

Análisis de Enriquecimiento Funcional

Contraste: siRNA_02_vs_Control

Organismo: hsapiens

Archivos de entrada:

Resultados_Significativos_siRNA_02_vs_Control.txt
Resultados_Completos_siRNA_02_vs_Control.txt

Fuentes de datos: GO:MF, GO:BP, GO:CC, KEGG, REAC

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Resumen de Cobertura del Análisis

Total de genes significativos de entrada: 462

Genes mapeados en rutas enriquecidas: 423

Total de Genes Huérfanos: 39

Desglose de los Genes Huérfanos:

(Genes que NO están en las 616 rutas enriquecidas)

- Genes sin símbolo (NA o "): 14
- Genes con anotación no informativa (LOC..., si:..., zgc:...): 0
- Con símbolo real (pero en rutas no enriquecidas): 25

La tabla completa con los 39 genes huérfanos se ha guardado en 'genes_huerfanos_siRNA_02_vs_Control.txt'

Sección de Análisis: GO:MF – Funciones Moleculares

Total de términos enriquecidos en esta sección: 60

Términos 'Tope' (p-valor < 1e-16): 6

Términos que superan el 'tope' de significancia:

- *protein binding* (GO:0005515, p-val: 2.1e-21)
- *macromolecular conformation isomerase activity* (GO:0120543, p-val: 3.3e-18)
- *single-stranded DNA helicase activity* (GO:0017116, p-val: 7.8e-18)
- *ATP-dependent activity, acting on DNA* (GO:0008094, p-val: 1.2e-17)
- *catalytic activity, acting on DNA* (GO:0140097, p-val: 4.2e-17)
- *microtubule binding* (GO:0008017, p-val: 7.3e-17)

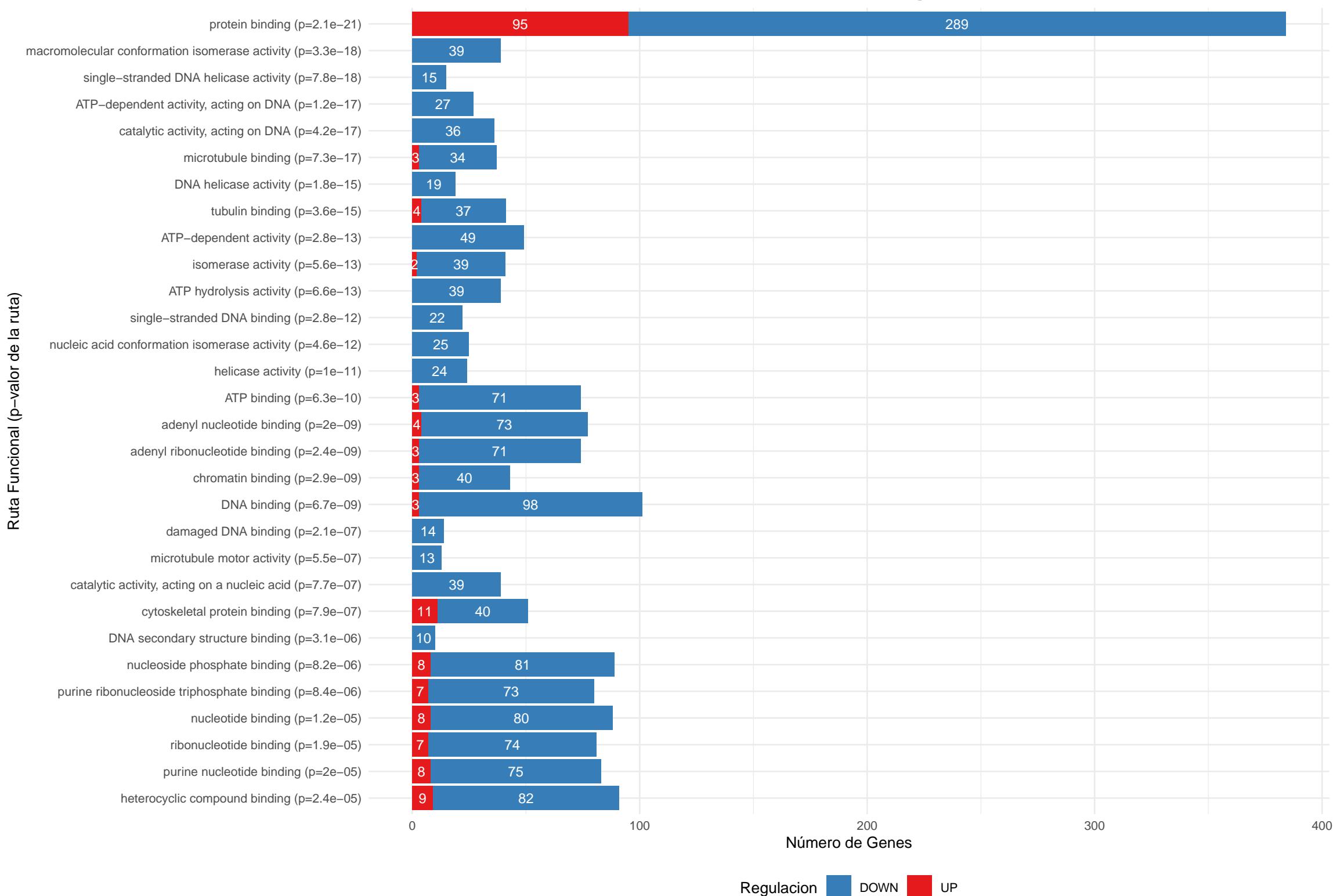
A continuación se muestran los gráficos de barras y tablas de genes para esta sección.

Volcano Plot – GO:MF – Funciones Moleculares

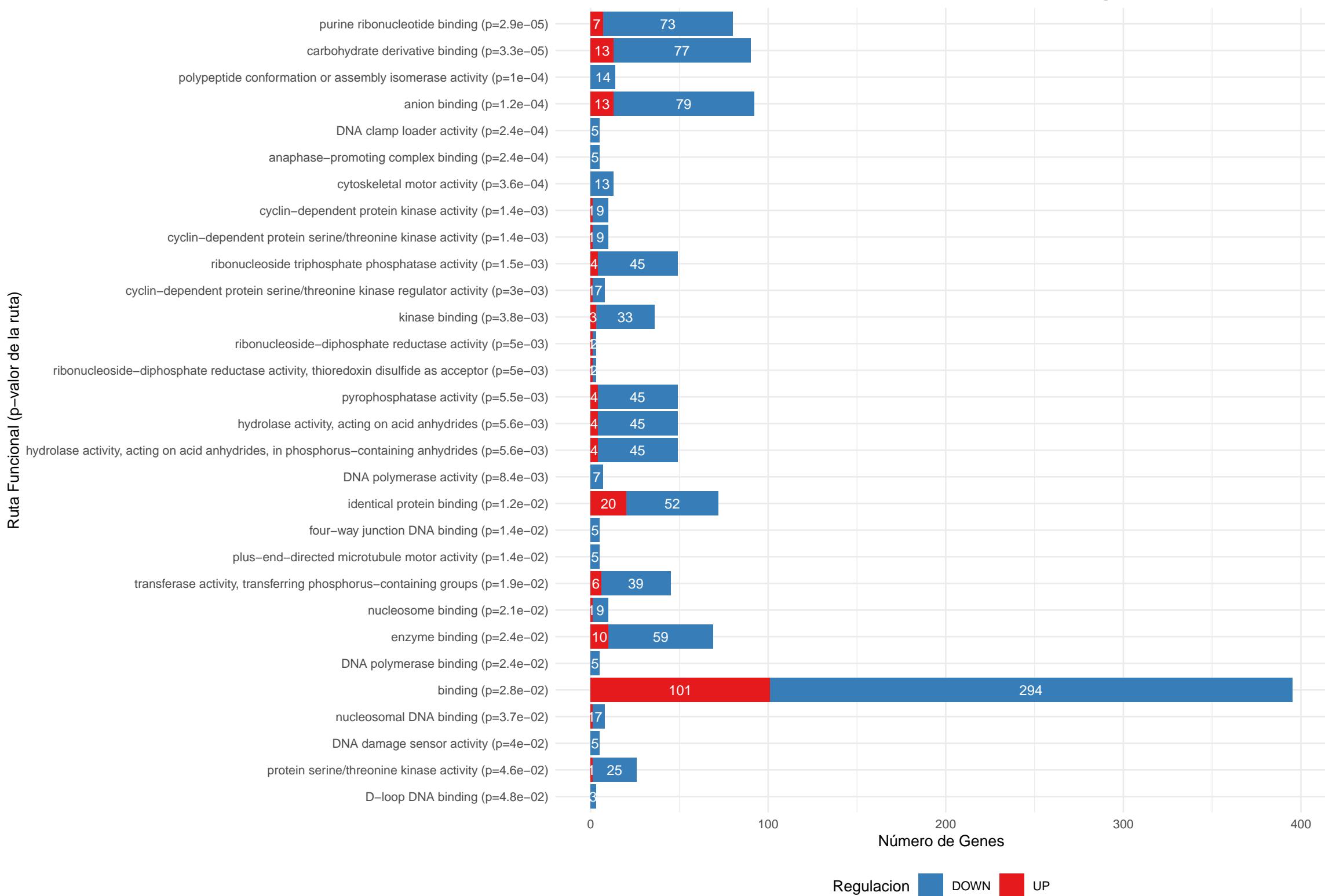
Mostrando 398 genes únicos mapeados en esta sección



GO:MF – Funciones Moleculares – Gráfico (Pág. 1 de 2)



GO:MF – Funciones Moleculares – Gráfico (Pág. 2 de 2)



Ruta: protein binding (Página 1 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8

Ruta: protein binding (Página 2 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000189057	FAM111B	DOWN	-2.315	2.29e-19	695.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3

Ruta: protein binding (Página 3 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000111665	CDCA3	DOWN	-1.647	8.37e-16	690.7
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG0000010438	PRSS3	UP	1.837	1.56e-15	633.6
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3

Ruta: protein binding (Página 4 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000137310	TCF19	DOWN	-1.639	1.12e-14	547.9
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000164466	SFXN1	DOWN	-1.129	2.57e-13	1052.2
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6

Ruta: protein binding (Página 5 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000133739	LRRCC1	DOWN	-1.272	1.80e-12	348.7
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000163584	RPL22L1	DOWN	-1.560	7.80e-11	4446.0
ENSG00000147394	ZNF185	UP	1.052	8.01e-11	1372.2
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4

Ruta: protein binding (Página 6 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG0000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG0000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG0000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG0000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG0000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG0000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG0000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG0000205208	C4orf46	DOWN	-1.302	2.82e-10	479.4
ENSG0000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG0000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG0000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG0000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG0000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG0000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG0000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG0000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG0000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG0000114346	ECT2	DOWN	-1.276	2.96e-09	617.4

Ruta: protein binding (Página 7 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5

Ruta: protein binding (Página 8 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000135451	TROAP	DOWN	-2.330	4.41e-08	64.0
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000213185	FAM24B	UP	1.490	3.18e-07	390.7
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000116667	C1orf21	UP	1.498	3.50e-07	528.0
ENSG00000129038	LOXL1	UP	1.441	3.55e-07	153.1
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2

Ruta: protein binding (Página 9 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000134802	SLC43A3	DOWN	-1.246	1.27e-06	585.6
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000163762	TM4SF18	DOWN	-1.139	5.20e-06	1676.0
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG0000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000146410	MTFR2	DOWN	-1.746	5.92e-06	145.6
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000139133	ALG10	DOWN	-1.541	8.66e-06	64.1

Ruta: protein binding (Página 10 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000132017	DCAF15	DOWN	-1.243	1.30e-05	122.0
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000139410	SDSL	UP	1.421	3.14e-05	75.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5

Ruta: protein binding (Página 11 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG0000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000144395	CCDC150	DOWN	-1.955	1.43e-04	53.6
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000160180	TFF3	UP	1.708	1.97e-04	44.6
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000074621	SLC24A1	UP	1.424	2.09e-04	124.7
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9

Ruta: protein binding (Página 12 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000166881	NEMP1	DOWN	-2.208	2.92e-04	75.0
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000189129	PLAC9	UP	1.249	4.04e-04	151.2
ENSG00000109452	INPP4B	UP	1.158	4.20e-04	146.5
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000138780	GSTCD	DOWN	-1.373	4.88e-04	110.9
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000162706	CADM3	UP	3.085	9.47e-04	20.3
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000128510	CPA4	UP	3.390	1.31e-03	31.5
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5

Ruta: protein binding (Página 13 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000228474	OST4	UP	1.044	5.07e-03	862.5
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG0000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5

Ruta: protein binding (Página 14 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000107719	PALD1	DOWN	-1.387	8.65e-03	67.9
ENSG00000100100	PIK3IP1	UP	1.413	8.65e-03	102.0
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000075303	SLC25A40	DOWN	-1.118	9.38e-03	169.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000101187	SLCO4A1	DOWN	-2.007	1.09e-02	29.9
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000166831	RBPM52	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7

Ruta: protein binding (Página 15 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000163596	ICA1L	DOWN	-1.027	1.99e-02	76.8
ENSG00000182667	NTM	UP	1.480	2.04e-02	41.9
ENSG00000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG00000151572	ANO4	UP	1.682	2.37e-02	39.8
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000250510	GPR162	UP	1.311	2.49e-02	51.7
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7
ENSG00000198885	ITPRIPL1	DOWN	-1.376	3.63e-02	64.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000121940	CLCC1	DOWN	-1.122	4.07e-02	81.5

Ruta: protein binding (Página 16 de 16)

Fuente: GO:MF | ID: GO:0005515 | Genes: 384 | p-valor ruta: 2.14e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000176244	ACBD7	DOWN	-1.260	4.14e-02	56.6
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000196247	ZNF107	DOWN	-1.028	4.60e-02	77.9
ENSG00000239779	WBP1	UP	1.901	4.62e-02	20.7
ENSG00000136925	TSTD2	DOWN	-2.222	4.79e-02	16.1
ENSG00000168060	NAALADL1	UP	1.226	4.82e-02	27.6
ENSG00000183048	SLC25A10	DOWN	-1.208	4.96e-02	35.4
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: macromolecular conformation isomerase activity (Página 1 de 2)

Fuente: GO:MF | ID: GO:0120543 | Genes: 39 | p–valor ruta: 3.31e–18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4

Ruta: macromolecular conformation isomerase activity (Página 2 de 2)

Fuente: GO:MF | ID: GO:0120543 | Genes: 39 | p-valor ruta: 3.31e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: single-stranded DNA helicase activity

Fuente: GO:MF | ID: GO:0017116 | Genes: 15 | p-valor ruta: 7.81e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: ATP-dependent activity, acting on DNA (Página 1 de 2)

Fuente: GO:MF | ID: GO:0008094 | Genes: 27 | p-valor ruta: 1.15e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: ATP-dependent activity, acting on DNA (Página 2 de 2)

Fuente: GO:MF | ID: GO:0008094 | Genes: 27 | p-valor ruta: 1.15e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: catalytic activity, acting on DNA (Página 1 de 2)

Fuente: GO:MF | ID: GO:0140097 | Genes: 36 | p–valor ruta: 4.25e–17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1

Ruta: catalytic activity, acting on DNA (Página 2 de 2)

Fuente: GO:MF | ID: GO:0140097 | Genes: 36 | p-valor ruta: 4.25e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: microtubule binding (Página 1 de 2)

Fuente: GO:MF | ID: GO:0008017 | Genes: 37 | p-valor ruta: 7.27e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3

Ruta: microtubule binding (Página 2 de 2)

Fuente: GO:MF | ID: GO:0008017 | Genes: 37 | p-valor ruta: 7.27e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8

Ruta: DNA helicase activity

Fuente: GO:MF | ID: GO:0003678 | Genes: 19 | p-valor ruta: 1.76e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: tubulin binding (Página 1 de 2)

Fuente: GO:MF | ID: GO:0015631 | Genes: 41 | p–valor ruta: 3.65e–15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	−1.581	1.18e−44	832.9
ENSG00000090889	KIF4A	DOWN	−1.513	7.98e−28	682.7
ENSG00000143228	NUF2	DOWN	−2.262	2.12e−27	1144.3
ENSG00000198901	PRC1	DOWN	−1.702	7.50e−27	475.6
ENSG00000075218	GTSE1	DOWN	−2.024	4.26e−25	327.8
ENSG00000089685	BIRC5	DOWN	−1.447	2.74e−24	999.2
ENSG00000138182	KIF20B	DOWN	−1.458	1.27e−20	1755.0
ENSG00000154839	SKA1	DOWN	−2.106	9.93e−20	265.9
ENSG00000137812	KNL1	DOWN	−1.964	1.50e−19	675.1
ENSG00000198624	CCDC69	UP	1.776	5.57e−17	255.3
ENSG00000237649	KIFC1	DOWN	−2.040	7.65e−17	505.4
ENSG00000165480	SKA3	DOWN	−1.586	1.14e−16	602.9
ENSG00000101447	FAM83D	DOWN	−1.989	5.57e−16	454.7
ENSG00000138160	KIF11	DOWN	−1.751	8.02e−14	450.4
ENSG0000012048	BRCA1	DOWN	−1.766	1.14e−12	390.2
ENSG00000076382	SPAG5	DOWN	−1.738	1.21e−12	384.3
ENSG00000131351	HAUS8	DOWN	−1.922	3.39e−12	203.9
ENSG00000117724	CENPF	DOWN	−1.603	6.29e−12	2801.9
ENSG00000142945	KIF2C	DOWN	−1.660	6.87e−11	313.0
ENSG00000168476	REEP4	DOWN	−1.127	2.04e−10	666.3
ENSG00000137807	KIF23	DOWN	−1.544	2.50e−10	400.6
ENSG00000151849	CPAP	DOWN	−1.564	4.65e−10	287.9
ENSG00000126787	DLGAP5	DOWN	−1.288	8.11e−10	969.9
ENSG00000186185	KIF18B	DOWN	−2.437	1.06e−09	148.7
ENSG00000139618	BRCA2	DOWN	−1.944	1.37e−09	326.9

Ruta: tubulin binding (Página 2 de 2)

Fuente: GO:MF | ID: GO:0015631 | Genes: 41 | p-valor ruta: 3.65e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2

Ruta: ATP-dependent activity (Página 1 de 2)

Fuente: GO:MF | ID: GO:0140657 | Genes: 49 | p-valor ruta: 2.83e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2

Ruta: ATP-dependent activity (Página 2 de 2)

Fuente: GO:MF | ID: GO:0140657 | Genes: 49 | p-valor ruta: 2.83e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: isomerase activity (Página 1 de 2)

Fuente: GO:MF | ID: GO:0016853 | Genes: 41 | p–valor ruta: 5.64e–13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4

Ruta: isomerase activity (Página 2 de 2)

Fuente: GO:MF | ID: GO:0016853 | Genes: 41 | p-valor ruta: 5.64e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG0000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000139410	SDSL	UP	1.421	3.14e-05	75.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000171451	DSEL	UP	1.321	2.18e-03	188.5
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: ATP hydrolysis activity (Página 1 de 2)

Fuente: GO:MF | ID: GO:0016887 | Genes: 39 | p–valor ruta: 6.61e–13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1

Ruta: ATP hydrolysis activity (Página 2 de 2)

Fuente: GO:MF | ID: GO:0016887 | Genes: 39 | p-valor ruta: 6.61e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG0000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG0000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: single-stranded DNA binding

Fuente: GO:MF | ID: GO:0003697 | Genes: 22 | p-valor ruta: 2.8e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: nucleic acid conformation isomerase activity

Fuente: GO:MF | ID: GO:0120545 | Genes: 25 | p–valor ruta: 4.59e–12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: helicase activity

Fuente: GO:MF | ID: GO:0004386 | Genes: 24 | p-valor ruta: 1.01e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: ATP binding (Página 1 de 3)

Fuente: GO:MF | ID: GO:0005524 | Genes: 74 | p–valor ruta: 6.31e–10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2

Ruta: ATP binding (Página 2 de 3)

Fuente: GO:MF | ID: GO:0005524 | Genes: 74 | p–valor ruta: 6.31e–10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1

Ruta: ATP binding (Página 3 de 3)

Fuente: GO:MF | ID: GO:0005524 | Genes: 74 | p-valor ruta: 6.31e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0

Ruta: adenyl nucleotide binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:0030554 | Genes: 77 | p–valor ruta: 1.96e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4

Ruta: adenyl nucleotide binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:0030554 | Genes: 77 | p–valor ruta: 1.96e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3

Ruta: adenyl nucleotide binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:0030554 | Genes: 77 | p–valor ruta: 1.96e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: adenyl nucleotide binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:0030554 | Genes: 77 | p–valor ruta: 1.96e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e–02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e–02	61.0

Ruta: adenyl ribonucleotide binding (Página 1 de 3)

Fuente: GO:MF | ID: GO:0032559 | Genes: 74 | p–valor ruta: 2.38e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2

Ruta: adenyl ribonucleotide binding (Página 2 de 3)

Fuente: GO:MF | ID: GO:0032559 | Genes: 74 | p–valor ruta: 2.38e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1

Ruta: adenyl ribonucleotide binding (Página 3 de 3)

Fuente: GO:MF | ID: GO:0032559 | Genes: 74 | p–valor ruta: 2.38e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100416	TRMU	DOWN	-1.100	2.40e–06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e–06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e–06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e–06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e–05	365.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e–05	265.1
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e–05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e–05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e–05	68.8
ENSG00000120539	MASTL	DOWN	-1.817	7.79e–05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e–05	105.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e–04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e–04	142.6
ENSG00000156136	DCK	DOWN	-1.080	9.96e–04	143.8
ENSG00000122966	CIT	DOWN	-1.673	2.35e–03	123.4
ENSG00000116830	TTF2	DOWN	-1.039	3.42e–03	336.7
ENSG00000186638	KIF24	DOWN	-2.074	4.52e–03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e–03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e–03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e–03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e–02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e–02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e–02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e–02	61.0

Ruta: chromatin binding (Página 1 de 2)

Fuente: GO:MF | ID: GO:0003682 | Genes: 43 | p–valor ruta: 2.86e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000119969	HELLS	DOWN	−1.592	1.29e−37	1124.3
ENSG00000131747	TOP2A	DOWN	−1.733	4.48e−31	5823.0
ENSG00000170312	CDK1	DOWN	−2.088	2.27e−25	1384.7
ENSG00000112312	GMNN	DOWN	−1.638	4.21e−24	861.3
ENSG00000132646	PCNA	DOWN	−1.372	6.33e−21	2475.7
ENSG00000156802	ATAD2	DOWN	−1.970	8.59e−20	682.4
ENSG00000136824	SMC2	DOWN	−1.424	3.27e−19	2147.1
ENSG00000113810	SMC4	DOWN	−1.484	8.40e−18	4283.1
ENSG00000106462	EZH2	DOWN	−1.170	1.57e−15	683.6
ENSG00000051180	RAD51	DOWN	−2.077	4.28e−15	291.4
ENSG00000146670	CDCA5	DOWN	−2.059	8.54e−13	175.9
ENSG00000167670	CHAF1A	DOWN	−1.749	1.16e−12	288.6
ENSG00000117724	CENPF	DOWN	−1.603	6.29e−12	2801.9
ENSG00000125885	MCM8	DOWN	−1.405	1.29e−11	278.7
ENSG00000077152	UBE2T	DOWN	−1.383	8.25e−11	1278.6
ENSG00000177084	POLE	DOWN	−2.215	8.53e−11	106.4
ENSG00000115163	CENPA	DOWN	−1.689	1.34e−10	297.0
ENSG00000100749	VRK1	DOWN	−1.501	2.14e−10	731.7
ENSG00000167513	CDT1	DOWN	−2.358	9.49e−10	138.1
ENSG00000166803	PCLAF	DOWN	−1.228	2.39e−09	4124.4
ENSG00000121152	NCAPH	DOWN	−2.359	4.90e−09	170.5
ENSG00000080839	RBL1	DOWN	−1.533	4.00e−08	151.5
ENSG00000101868	POLA1	DOWN	−1.208	4.18e−08	300.4
ENSG00000198554	WDHD1	DOWN	−1.420	1.64e−07	256.8
ENSG00000085840	ORC1	DOWN	−1.843	1.85e−06	100.1

Ruta: chromatin binding (Página 2 de 2)

Fuente: GO:MF | ID: GO:0003682 | Genes: 43 | p-valor ruta: 2.86e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2

Ruta: DNA binding (Página 1 de 5)

Fuente: GO:MF | ID: GO:0003677 | Genes: 101 | p-valor ruta: 6.68e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3

Ruta: DNA binding (Página 2 de 5)

Fuente: GO:MF | ID: GO:0003677 | Genes: 101 | p-valor ruta: 6.68e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1

Ruta: DNA binding (Página 3 de 5)

Fuente: GO:MF | ID: GO:0003677 | Genes: 101 | p-valor ruta: 6.68e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG0000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5

Ruta: DNA binding (Página 4 de 5)

Fuente: GO:MF | ID: GO:0003677 | Genes: 101 | p-valor ruta: 6.68e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: DNA binding (Página 5 de 5)

Fuente: GO:MF | ID: GO:0003677 | Genes: 101 | p-valor ruta: 6.68e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000196247	ZNF107	DOWN	-1.028	4.6e-02	77.9

Ruta: damaged DNA binding

Fuente: GO:MF | ID: GO:0003684 | Genes: 14 | p-valor ruta: 2.07e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8

Ruta: microtubule motor activity

Fuente: GO:MF | ID: GO:0003777 | Genes: 13 | p-valor ruta: 5.49e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8

Ruta: catalytic activity, acting on a nucleic acid (Página 1 de 2)

Fuente: GO:MF | ID: GO:0140640 | Genes: 39 | p-valor ruta: 7.7e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7

Ruta: catalytic activity, acting on a nucleic acid (Página 2 de 2)

Fuente: GO:MF | ID: GO:0140640 | Genes: 39 | p-valor ruta: 7.7e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: cytoskeletal protein binding (Página 1 de 3)

Fuente: GO:MF | ID: GO:0008092 | Genes: 51 | p–valor ruta: 7.87e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG0000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9

Ruta: cytoskeletal protein binding (Página 2 de 3)

Fuente: GO:MF | ID: GO:0008092 | Genes: 51 | p–valor ruta: 7.87e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8

Ruta: cytoskeletal protein binding (Página 3 de 3)

Fuente: GO:MF | ID: GO:0008092 | Genes: 51 | p-valor ruta: 7.87e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2

Ruta: DNA secondary structure binding

Fuente: GO:MF | ID: GO:0000217 | Genes: 10 | p-valor ruta: 3.09e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: nucleoside phosphate binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:1901265 | Genes: 89 | p–valor ruta: 8.22e–06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4

Ruta: nucleoside phosphate binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:1901265 | Genes: 89 | p–valor ruta: 8.22e–06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4

Ruta: nucleoside phosphate binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:1901265 | Genes: 89 | p–valor ruta: 8.22e–06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG0000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG0000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG0000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG0000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG0000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG0000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG0000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG0000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG0000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG0000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG0000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG0000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG0000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG0000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG0000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG0000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG0000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG0000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG0000154917	RAB6B	UP	1.410	4.24e-03	77.1

Ruta: nucleoside phosphate binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:1901265 | Genes: 89 | p–valor ruta: 8.22e–06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186638	KIF24	DOWN	-2.074	4.52e–03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e–03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e–03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e–03	109.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e–03	62.7
ENSG00000177106	EPS8L2	UP	2.621	8.00e–03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e–03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e–03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e–02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e–02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e–02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e–02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e–02	61.0
ENSG00000176244	ACBD7	DOWN	-1.260	4.14e–02	56.6

Ruta: purine ribonucleoside triphosphate binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:0035639 | Genes: 80 | p–valor ruta: 8.39e–06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2

Ruta: purine ribonucleoside triphosphate binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:0035639 | Genes: 80 | p–valor ruta: 8.39e–06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3

Ruta: purine ribonucleoside triphosphate binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:0035639 | Genes: 80 | p–valor ruta: 8.39e–06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: purine ribonucleoside triphosphate binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:0035639 | Genes: 80 | p-valor ruta: 8.39e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0

Ruta: nucleotide binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:0000166 | Genes: 88 | p–valor ruta: 1.22e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e–57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e–43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e–37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e–37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e–37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e–32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e–31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e–30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e–28	682.7
ENSG00000170312	CDK1	DOWN	-2.088	2.27e–25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e–24	659.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e–21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e–20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e–20	682.4
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e–19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e–19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e–19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e–18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e–18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e–18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e–18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e–18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e–17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e–17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e–17	505.4

Ruta: nucleotide binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:0000166 | Genes: 88 | p–valor ruta: 1.22e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4

Ruta: nucleotide binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:0000166 | Genes: 88 | p–valor ruta: 1.22e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG0000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG0000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG0000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG0000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG0000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG0000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG0000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG0000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG0000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG0000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG0000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG0000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG0000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG0000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG0000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG0000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG0000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG0000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG0000154917	RAB6B	UP	1.410	4.24e-03	77.1

Ruta: nucleotide binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:0000166 | Genes: 88 | p–valor ruta: 1.22e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186638	KIF24	DOWN	-2.074	4.52e–03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e–03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e–03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e–03	109.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e–03	62.7
ENSG00000177106	EPS8L2	UP	2.621	8.00e–03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e–03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e–03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e–02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e–02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e–02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e–02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e–02	61.0

Ruta: ribonucleotide binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:0032553 | Genes: 81 | p–valor ruta: 1.91e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e–57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e–43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e–37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e–37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e–37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e–32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e–31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e–30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e–28	682.7
ENSG00000170312	CDK1	DOWN	-2.088	2.27e–25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e–24	659.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e–21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e–20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e–20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e–19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e–19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e–18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e–18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e–18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e–18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e–18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e–17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e–17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e–17	505.4
ENSG00000167325	RRM1	DOWN	-1.219	2.43e–15	4069.2

Ruta: ribonucleotide binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:0032553 | Genes: 81 | p–valor ruta: 1.91e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3

Ruta: ribonucleotide binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:0032553 | Genes: 81 | p–valor ruta: 1.91e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0

Ruta: ribonucleotide binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:0032553 | Genes: 81 | p-valor ruta: 1.91e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0

Ruta: purine nucleotide binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:0017076 | Genes: 83 | p–valor ruta: 1.98e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e–57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e–43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e–37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e–37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e–37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e–32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e–31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e–30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e–28	682.7
ENSG00000170312	CDK1	DOWN	-2.088	2.27e–25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e–24	659.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e–21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e–20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e–20	682.4
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e–19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e–19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e–19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e–18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e–18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e–18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e–18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e–18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e–17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e–17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e–17	505.4

Ruta: purine nucleotide binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:0017076 | Genes: 83 | p–valor ruta: 1.98e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7

Ruta: purine nucleotide binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:0017076 | Genes: 83 | p–valor ruta: 1.98e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: purine nucleotide binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:0017076 | Genes: 83 | p-valor ruta: 1.98e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0

Ruta: heterocyclic compound binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:1901363 | Genes: 91 | p–valor ruta: 2.44e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e–57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e–43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e–37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e–37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e–37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e–32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e–31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e–30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e–28	682.7
ENSG00000170312	CDK1	DOWN	-2.088	2.27e–25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e–24	659.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e–21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e–20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e–20	682.4
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e–19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e–19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e–19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e–18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e–18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e–18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e–18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e–18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e–17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e–17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e–17	505.4

Ruta: heterocyclic compound binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:1901363 | Genes: 91 | p–valor ruta: 2.44e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4

Ruta: heterocyclic compound binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:1901363 | Genes: 91 | p–valor ruta: 2.44e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG0000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG0000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG0000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG0000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG0000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG0000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG0000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG0000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG0000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG0000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG0000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG0000139410	SDSL	UP	1.421	3.14e-05	75.7
ENSG0000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG0000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG0000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG0000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG0000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG0000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG0000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0

Ruta: heterocyclic compound binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:1901363 | Genes: 91 | p-valor ruta: 2.44e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0
ENSG00000176244	ACBD7	DOWN	-1.260	4.14e-02	56.6

Ruta: purine ribonucleotide binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:0032555 | Genes: 80 | p–valor ruta: 2.89e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2

Ruta: purine ribonucleotide binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:0032555 | Genes: 80 | p–valor ruta: 2.89e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3

Ruta: purine ribonucleotide binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:0032555 | Genes: 80 | p–valor ruta: 2.89e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: purine ribonucleotide binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:0032555 | Genes: 80 | p-valor ruta: 2.89e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0

Ruta: carbohydrate derivative binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:0097367 | Genes: 90 | p–valor ruta: 3.32e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000058085	LAMC2	UP	1.879	2.12e-17	204.8
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4

Ruta: carbohydrate derivative binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:0097367 | Genes: 90 | p–valor ruta: 3.32e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1

Ruta: carbohydrate derivative binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:0097367 | Genes: 90 | p–valor ruta: 3.32e–05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8

Ruta: carbohydrate derivative binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:0097367 | Genes: 90 | p-valor ruta: 3.32e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0

Ruta: polypeptide conformation or assembly isomerase activity

Fuente: GO:MF | ID: GO:0120544 | Genes: 14 | p-valor ruta: 9.98e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8

Ruta: anion binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:0043168 | Genes: 92 | p–valor ruta: 1.16e–04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4

Ruta: anion binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:0043168 | Genes: 92 | p–valor ruta: 1.16e–04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000147697	GSDMC	UP	2.564	1.66e-10	130.4
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1

Ruta: anion binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:0043168 | Genes: 92 | p–valor ruta: 1.16e–04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000139410	SDSL	UP	1.421	3.14e-05	75.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4

Ruta: anion binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:0043168 | Genes: 92 | p-valor ruta: 1.16e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0
ENSG00000176244	ACBD7	DOWN	-1.260	4.14e-02	56.6

Ruta: DNA clamp loader activity

Fuente: GO:MF | ID: GO:0003689 | Genes: 5 | p-valor ruta: 2.36e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: anaphase-promoting complex binding

Fuente: GO:MF | ID: GO:0010997 | Genes: 5 | p-valor ruta: 2.36e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: cytoskeletal motor activity

Fuente: GO:MF | ID: GO:0003774 | Genes: 13 | p-valor ruta: 3.62e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8

Ruta: cyclin-dependent protein kinase activity

Fuente: GO:MF | ID: GO:0097472 | Genes: 10 | p-valor ruta: 1.42e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: cyclin–dependent protein serine/threonine kinase activity

Fuente: GO:MF | ID: GO:0004693 | Genes: 10 | p–valor ruta: 1.42e–03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e–44	4228.1
ENSG00000134057	CCNB1	DOWN	–1.376	4.23e–30	1075.8
ENSG00000145386	CCNA2	DOWN	–1.856	3.17e–26	988.0
ENSG00000170312	CDK1	DOWN	–2.088	2.27e–25	1384.7
ENSG00000123374	CDK2	DOWN	–1.140	6.55e–11	1630.6
ENSG00000175305	CCNE2	DOWN	–2.245	2.83e–09	73.4
ENSG00000162063	CCNF	DOWN	–1.611	3.45e–07	160.0
ENSG00000157456	CCNB2	DOWN	–1.198	5.68e–07	582.1
ENSG00000123080	CDKN2C	DOWN	–1.693	2.28e–05	206.7
ENSG00000105173	CCNE1	DOWN	–1.268	2.65e–04	172.2

Ruta: ribonucleoside triphosphate phosphatase activity (Página 1 de 2)

Fuente: GO:MF | ID: GO:0017111 | Genes: 49 | p–valor ruta: 1.45e–03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4

Ruta: ribonucleoside triphosphate phosphatase activity (Página 2 de 2)

Fuente: GO:MF | ID: GO:0017111 | Genes: 49 | p–valor ruta: 1.45e–03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: cyclin-dependent protein serine/threonine kinase regulator activity

Fuente: GO:MF | ID: GO:0016538 | Genes: 8 | p-valor ruta: 2.96e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: kinase binding (Página 1 de 2)

Fuente: GO:MF | ID: GO:0019900 | Genes: 36 | p–valor ruta: 3.84e–03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e–44	4228.1
ENSG00000094804	CDC6	DOWN	–2.490	6.33e–43	452.0
ENSG00000178999	AURKB	DOWN	–2.095	1.44e–37	1004.1
ENSG00000131747	TOP2A	DOWN	–1.733	4.48e–31	5823.0
ENSG00000134057	CCNB1	DOWN	–1.376	4.23e–30	1075.8
ENSG00000198901	PRC1	DOWN	–1.702	7.50e–27	475.6
ENSG00000145386	CCNA2	DOWN	–1.856	3.17e–26	988.0
ENSG00000138376	BARD1	DOWN	–1.668	4.10e–24	474.1
ENSG00000132646	PCNA	DOWN	–1.372	6.33e–21	2475.7
ENSG00000120129	DUSP1	UP	1.436	1.44e–19	596.2
ENSG00000088325	TPX2	DOWN	–1.571	2.07e–16	1191.9
ENSG00000101447	FAM83D	DOWN	–1.989	5.57e–16	454.7
ENSG00000087586	AURKA	DOWN	–1.463	3.30e–14	1066.4
ENSG00000138160	KIF11	DOWN	–1.751	8.02e–14	450.4
ENSG00000112029	FBXO5	DOWN	–2.086	6.62e–13	325.6
ENSG00000129810	SGO1	DOWN	–2.322	5.66e–11	212.1
ENSG00000100749	VRK1	DOWN	–1.501	2.14e–10	731.7
ENSG00000151849	CPAP	DOWN	–1.564	4.65e–10	287.9
ENSG00000175305	CCNE2	DOWN	–2.245	2.83e–09	73.4
ENSG00000164045	CDC25A	DOWN	–1.398	3.62e–09	386.0
ENSG00000158402	CDC25C	DOWN	–2.102	8.88e–09	177.0
ENSG00000103995	CEP152	DOWN	–1.141	1.66e–08	311.4
ENSG00000101868	POLA1	DOWN	–1.208	4.18e–08	300.4
ENSG00000136861	CDK5RAP2	DOWN	–1.057	1.62e–07	406.3
ENSG00000118193	KIF14	DOWN	–1.556	2.88e–07	345.1

Ruta: kinase binding (Página 2 de 2)

Fuente: GO:MF | ID: GO:0019900 | Genes: 36 | p-valor ruta: 3.84e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: ribonucleoside-diphosphate reductase activity

Fuente: GO:MF | ID: GO:0061731 | Genes: 3 | p-valor ruta: 4.97e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1

Ruta: ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor

Fuente: GO:MF | ID: GO:0004748 | Genes: 3 | p-valor ruta: 4.97e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1

Ruta: pyrophosphatase activity (Página 1 de 2)

Fuente: GO:MF | ID: GO:0016462 | Genes: 49 | p–valor ruta: 5.49e–03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4

Ruta: pyrophosphatase activity (Página 2 de 2)

Fuente: GO:MF | ID: GO:0016462 | Genes: 49 | p–valor ruta: 5.49e–03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: hydrolase activity, acting on acid anhydrides (Página 1 de 2)

Fuente: GO:MF | ID: GO:0016817 | Genes: 49 | p–valor ruta: 5.61e–03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4

Ruta: hydrolase activity, acting on acid anhydrides (Página 2 de 2)

Fuente: GO:MF | ID: GO:0016817 | Genes: 49 | p–valor ruta: 5.61e–03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides (Página 1 de 2)

Fuente: GO:MF | ID: GO:0016818 | Genes: 49 | p-valor ruta: 5.61e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG0000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG0000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4

Ruta: hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides (Página 2 de 2)

Fuente: GO:MF | ID: GO:0016818 | Genes: 49 | p-valor ruta: 5.61e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: DNA polymerase activity

Fuente: GO:MF | ID: GO:0034061 | Genes: 7 | p-valor ruta: 8.37e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1

Ruta: identical protein binding (Página 1 de 3)

Fuente: GO:MF | ID: GO:0042802 | Genes: 72 | p-valor ruta: 1.23e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9

Ruta: identical protein binding (Página 2 de 3)

Fuente: GO:MF | ID: GO:0042802 | Genes: 72 | p–valor ruta: 1.23e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG0000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG0000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG0000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG0000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG0000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG0000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG0000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG0000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG0000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG0000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG0000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG0000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG0000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG0000139410	SDSL	UP	1.421	3.14e-05	75.7
ENSG0000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000167772	ANGPTL4	UP	1.032	4.49e-05	119.9

Ruta: identical protein binding (Página 3 de 3)

Fuente: GO:MF | ID: GO:0042802 | Genes: 72 | p-valor ruta: 1.23e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000160180	TFF3	UP	1.708	1.97e-04	44.6
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000162706	CADM3	UP	3.085	9.47e-04	20.3
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000166831	RBPM52	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000168060	NAALADL1	UP	1.226	4.82e-02	27.6
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: four-way junction DNA binding

Fuente: GO:MF | ID: GO:0000400 | Genes: 5 | p-valor ruta: 1.38e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: plus–end–directed microtubule motor activity

Fuente: GO:MF | ID: GO:0008574 | Genes: 5 | p–valor ruta: 1.38e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138182	KIF20B	DOWN	−1.458	1.27e−20	1755.0
ENSG00000138160	KIF11	DOWN	−1.751	8.02e−14	450.4
ENSG00000186185	KIF18B	DOWN	−2.437	1.06e−09	148.7
ENSG00000118193	KIF14	DOWN	−1.556	2.88e−07	345.1
ENSG00000163808	KIF15	DOWN	−1.624	1.04e−05	365.5

Ruta: transferase activity, transferring phosphorus-containing groups (Página 1 de 2)

Fuente: GO:MF | ID: GO:0016772 | Genes: 45 | p-valor ruta: 1.9e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7

Ruta: transferase activity, transferring phosphorus-containing groups (Página 2 de 2)

Fuente: GO:MF | ID: GO:0016772 | Genes: 45 | p-valor ruta: 1.9e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000100100	PIK3IP1	UP	1.413	8.65e-03	102.0
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0

Ruta: nucleosome binding

Fuente: GO:MF | ID: GO:0031491 | Genes: 10 | p-valor ruta: 2.14e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: enzyme binding (Página 1 de 3)

Fuente: GO:MF | ID: GO:0019899 | Genes: 69 | p–valor ruta: 2.41e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e–44	4228.1
ENSG00000094804	CDC6	DOWN	–2.490	6.33e–43	452.0
ENSG00000178999	AURKB	DOWN	–2.095	1.44e–37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e–34	4081.3
ENSG00000175063	UBE2C	DOWN	–1.912	1.62e–32	1424.6
ENSG00000131747	TOP2A	DOWN	–1.733	4.48e–31	5823.0
ENSG00000134057	CCNB1	DOWN	–1.376	4.23e–30	1075.8
ENSG00000198901	PRC1	DOWN	–1.702	7.50e–27	475.6
ENSG00000145386	CCNA2	DOWN	–1.856	3.17e–26	988.0
ENSG00000089685	BIRC5	DOWN	–1.447	2.74e–24	999.2
ENSG00000138376	BARD1	DOWN	–1.668	4.10e–24	474.1
ENSG00000112312	GMNN	DOWN	–1.638	4.21e–24	861.3
ENSG00000065328	MCM10	DOWN	–2.433	2.52e–23	492.5
ENSG00000132646	PCNA	DOWN	–1.372	6.33e–21	2475.7
ENSG00000055163	CYFIP2	UP	2.148	1.61e–20	318.2
ENSG00000120129	DUSP1	UP	1.436	1.44e–19	596.2
ENSG00000088325	TPX2	DOWN	–1.571	2.07e–16	1191.9
ENSG00000101447	FAM83D	DOWN	–1.989	5.57e–16	454.7
ENSG00000113368	LMNB1	DOWN	–1.225	1.98e–15	1268.3
ENSG00000051180	RAD51	DOWN	–2.077	4.28e–15	291.4
ENSG00000087586	AURKA	DOWN	–1.463	3.30e–14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e–14	663.5
ENSG00000138160	KIF11	DOWN	–1.751	8.02e–14	450.4
ENSG00000112029	FBXO5	DOWN	–2.086	6.62e–13	325.6
ENSG00000012048	BRCA1	DOWN	–1.766	1.14e–12	390.2

Ruta: enzyme binding (Página 2 de 3)

Fuente: GO:MF | ID: GO:0019899 | Genes: 69 | p-valor ruta: 2.41e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6

Ruta: enzyme binding (Página 3 de 3)

Fuente: GO:MF | ID: GO:0019899 | Genes: 69 | p-valor ruta: 2.41e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG0000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: DNA polymerase binding

Fuente: GO:MF | ID: GO:0070182 | Genes: 5 | p-valor ruta: 2.42e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3

Ruta: binding (Página 1 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8

Ruta: binding (Página 2 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG0000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG0000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG0000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG0000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG0000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG0000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG0000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG0000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG0000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG0000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG0000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG0000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG0000189057	FAM111B	DOWN	-2.315	2.29e-19	695.4
ENSG0000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG0000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4

Ruta: binding (Página 3 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000058085	LAMC2	UP	1.879	2.12e-17	204.8
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000111665	CDCA3	DOWN	-1.647	8.37e-16	690.7
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4

Ruta: binding (Página 4 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000010438	PRSS3	UP	1.837	1.56e-15	633.6
ENSG0000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG0000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG0000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG0000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG0000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG0000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG0000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG0000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG0000137310	TCF19	DOWN	-1.639	1.12e-14	547.9
ENSG0000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG0000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG0000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG0000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG0000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG0000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000163918	RFC4	DOWN	-1.722	2.38e-13	353.5

Ruta: binding (Página 5 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164466	SFXN1	DOWN	-1.129	2.57e-13	1052.2
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000133739	LRRCC1	DOWN	-1.272	1.80e-12	348.7
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0

Ruta: binding (Página 6 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163584	RPL22L1	DOWN	-1.560	7.80e-11	4446.0
ENSG00000147394	ZNF185	UP	1.052	8.01e-11	1372.2
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000147697	GSDMC	UP	2.564	1.66e-10	130.4
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000205208	C4orf46	DOWN	-1.302	2.82e-10	479.4
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1

Ruta: binding (Página 7 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4

Ruta: binding (Página 8 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000135451	TROAP	DOWN	-2.330	4.41e-08	64.0
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000213185	FAM24B	UP	1.490	3.18e-07	390.7
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0

Ruta: binding (Página 9 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000116667	C1orf21	UP	1.498	3.50e-07	528.0
ENSG00000129038	LOXL1	UP	1.441	3.55e-07	153.1
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000134802	SLC43A3	DOWN	-1.246	1.27e-06	585.6
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000163762	TM4SF18	DOWN	-1.139	5.20e-06	1676.0
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2

Ruta: binding (Página 10 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG0000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000146410	MTFR2	DOWN	-1.746	5.92e-06	145.6
ENSG00000210144	MT-TY	UP	1.058	6.14e-06	2317.5
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000139133	ALG10	DOWN	-1.541	8.66e-06	64.1
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000132017	DCAF15	DOWN	-1.243	1.30e-05	122.0
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0

Ruta: binding (Página 11 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000139410	SDSL	UP	1.421	3.14e-05	75.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG0000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000160352	ZNF714	DOWN	-1.576	1.17e-04	120.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000144395	CCDC150	DOWN	-1.955	1.43e-04	53.6
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2

Ruta: binding (Página 12 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000160180	TFF3	UP	1.708	1.97e-04	44.6
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000074621	SLC24A1	UP	1.424	2.09e-04	124.7
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000166881	NEMP1	DOWN	-2.208	2.92e-04	75.0
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000189129	PLAC9	UP	1.249	4.04e-04	151.2
ENSG00000109452	INPP4B	UP	1.158	4.20e-04	146.5
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000138780	GSTCD	DOWN	-1.373	4.88e-04	110.9
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000011638	LDAF1	UP	1.147	5.56e-04	173.9

Ruta: binding (Página 13 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000162706	CADM3	UP	3.085	9.47e-04	20.3
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000128510	CPA4	UP	3.390	1.31e-03	31.5
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3

Ruta: binding (Página 14 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000228474	OST4	UP	1.044	5.07e-03	862.5
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000107719	PALD1	DOWN	-1.387	8.65e-03	67.9
ENSG00000100100	PIK3IP1	UP	1.413	8.65e-03	102.0
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000075303	SLC25A40	DOWN	-1.118	9.38e-03	169.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4

Ruta: binding (Página 15 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000101187	SLCO4A1	DOWN	-2.007	1.09e-02	29.9
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000166831	RBPM2	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000163596	ICA1L	DOWN	-1.027	1.99e-02	76.8
ENSG00000182667	NTM	UP	1.480	2.04e-02	41.9
ENSG00000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG00000151572	ANO4	UP	1.682	2.37e-02	39.8
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000250510	GPR162	UP	1.311	2.49e-02	51.7
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1

Ruta: binding (Página 16 de 16)

Fuente: GO:MF | ID: GO:0005488 | Genes: 395 | p-valor ruta: 2.8e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7
ENSG00000198885	ITPRIPL1	DOWN	-1.376	3.63e-02	64.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000121940	CLCC1	DOWN	-1.122	4.07e-02	81.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000176244	ACBD7	DOWN	-1.260	4.14e-02	56.6
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000196247	ZNF107	DOWN	-1.028	4.60e-02	77.9
ENSG00000239779	WBP1	UP	1.901	4.62e-02	20.7
ENSG00000136925	TSTD2	DOWN	-2.222	4.79e-02	16.1
ENSG00000168060	NAALADL1	UP	1.226	4.82e-02	27.6
ENSG00000183048	SLC25A10	DOWN	-1.208	4.96e-02	35.4
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: nucleosomal DNA binding

Fuente: GO:MF | ID: GO:0031492 | Genes: 8 | p-valor ruta: 3.65e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: DNA damage sensor activity

Fuente: GO:MF | ID: GO:0140612 | Genes: 5 | p-valor ruta: 3.97e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: protein serine/threonine kinase activity (Página 1 de 2)

Fuente: GO:MF | ID: GO:0004674 | Genes: 26 | p–valor ruta: 4.57e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e–44	4228.1
ENSG00000178999	AURKB	DOWN	–2.095	1.44e–37	1004.1
ENSG00000134057	CCNB1	DOWN	–1.376	4.23e–30	1075.8
ENSG00000145386	CCNA2	DOWN	–1.856	3.17e–26	988.0
ENSG00000170312	CDK1	DOWN	–2.088	2.27e–25	1384.7
ENSG00000165304	MELK	DOWN	–1.524	2.74e–21	505.6
ENSG00000156970	BUB1B	DOWN	–1.960	1.47e–18	480.6
ENSG00000168078	PBK	DOWN	–1.893	4.67e–15	353.2
ENSG00000163781	TOPBP1	DOWN	–1.311	1.42e–14	788.6
ENSG00000087586	AURKA	DOWN	–1.463	3.30e–14	1066.4
ENSG00000123374	CDK2	DOWN	–1.140	6.55e–11	1630.6
ENSG00000169679	BUB1	DOWN	–1.427	8.07e–11	645.0
ENSG00000100749	VRK1	DOWN	–1.501	2.14e–10	731.7
ENSG00000175305	CCNE2	DOWN	–2.245	2.83e–09	73.4
ENSG00000112742	TTK	DOWN	–2.143	2.62e–08	332.0
ENSG00000142731	PLK4	DOWN	–1.552	2.41e–07	244.7
ENSG00000162063	CCNF	DOWN	–1.611	3.45e–07	160.0
ENSG00000157456	CCNB2	DOWN	–1.198	5.68e–07	582.1
ENSG00000117650	NEK2	DOWN	–1.675	2.88e–06	263.6
ENSG00000166851	PLK1	DOWN	–1.760	7.54e–06	86.4
ENSG0000006634	DBF4	DOWN	–1.342	9.85e–06	449.5
ENSG00000123080	CDKN2C	DOWN	–1.693	2.28e–05	206.7
ENSG00000120539	MASTL	DOWN	–1.817	7.79e–05	126.7
ENSG00000105173	CCNE1	DOWN	–1.268	2.65e–04	172.2
ENSG00000122966	CIT	DOWN	–1.673	2.35e–03	123.4

Ruta: protein serine/threonine kinase activity (Página 2 de 2)

Fuente: GO:MF | ID: GO:0004674 | Genes: 26 | p-valor ruta: 4.57e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000183765	CHEK2	DOWN	-1.03	5.41e-03	109.3

Ruta: D-loop DNA binding

Fuente: GO:MF | ID: GO:0062037 | Genes: 3 | p-valor ruta: 4.82e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8

Sección de Análisis: GO:BP – Procesos Biológicos

Total de términos enriquecidos en esta sección: 311

Términos 'Tope' (p–valor < 1e–16): 98

Términos que superan el 'tope' de significancia:

- *cell cycle process* (GO:0022402, p–val: 3.4e–105)
- *cell cycle* (GO:0007049, p–val: 5.2e–99)
- *mitotic cell cycle process* (GO:1903047, p–val: 1.4e–91)
- *mitotic cell cycle* (GO:0000278, p–val: 1.0e–87)
- *chromosome segregation* (GO:0007059, p–val: 3.8e–77)
- *regulation of cell cycle process* (GO:0010564, p–val: 4.2e–70)
- *chromosome organization* (GO:0051276, p–val: 3.3e–67)
- *nuclear chromosome segregation* (GO:0098813, p–val: 6.0e–64)
- *regulation of cell cycle* (GO:0051726, p–val: 1.4e–63)
- *nuclear division* (GO:0000280, p–val: 6.9e–61)

...y otros

A continuación se muestran los gráficos de barras y tablas de genes para esta sección.

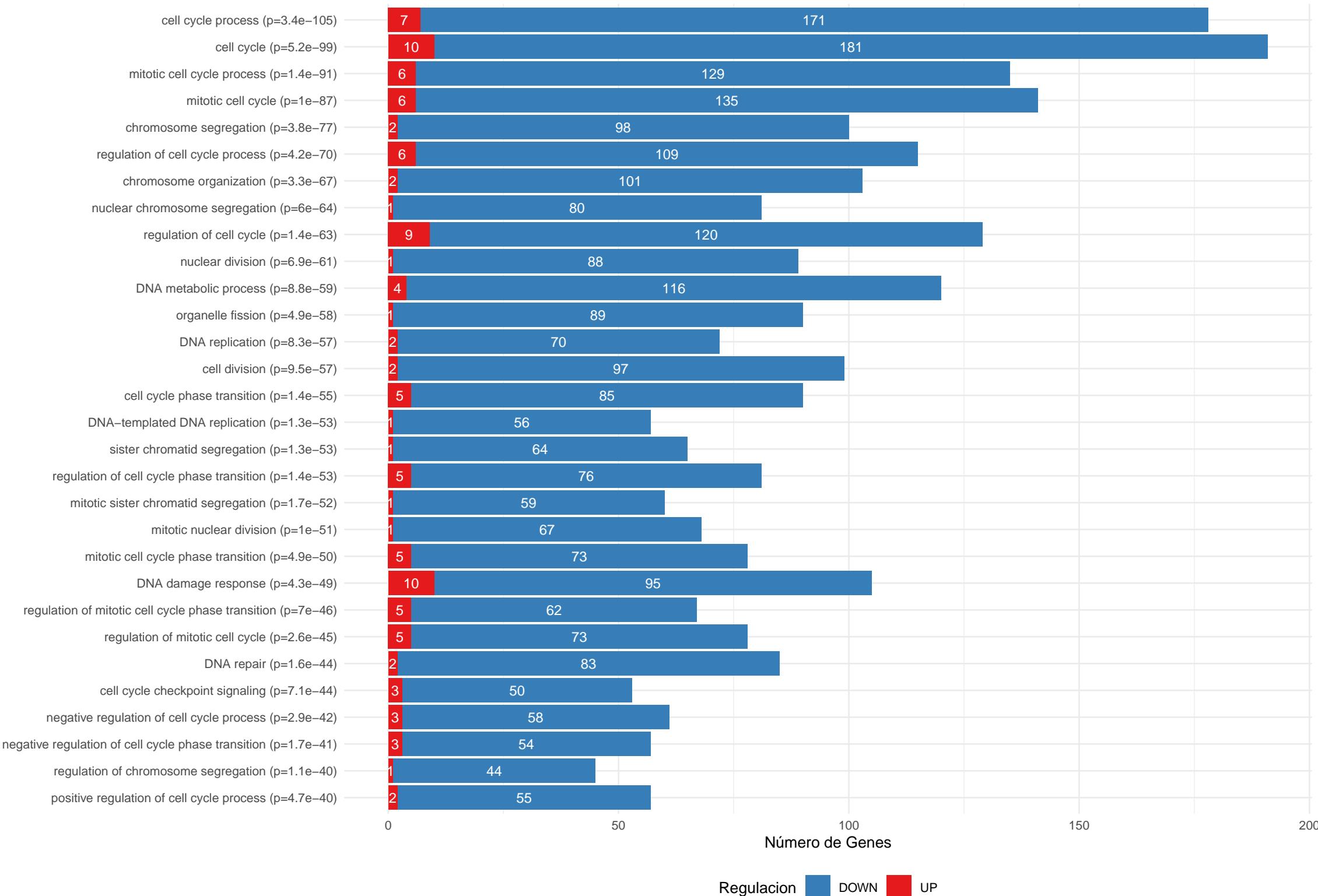
Volcano Plot – GO:BP – Procesos Biológicos

Mostrando 378 genes únicos mapeados en esta sección



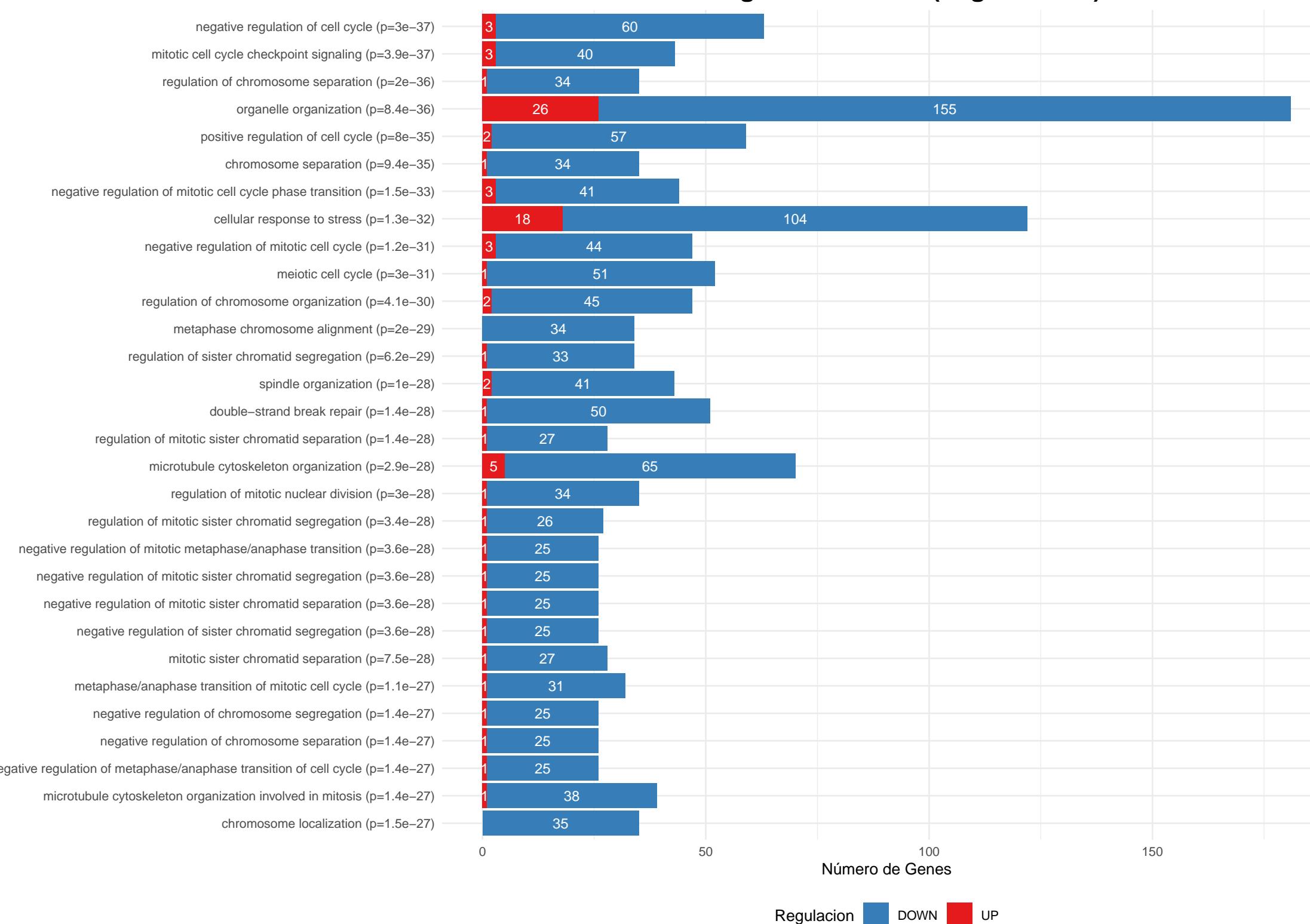
GO:BP – Procesos Biológicos – Gráfico (Pág. 1 de 11)

Ruta Funcional (p–valor de la ruta)



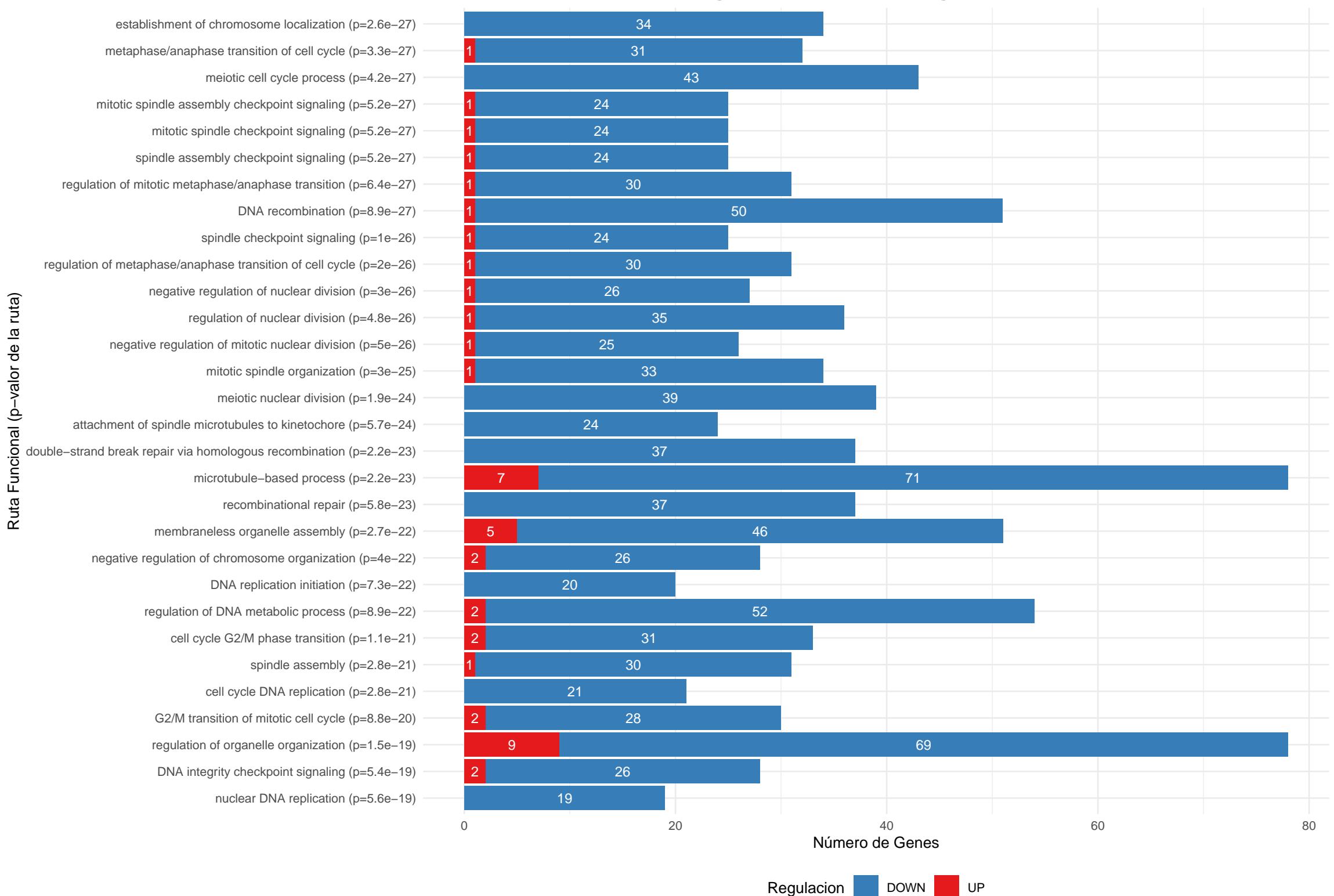
GO:BP – Procesos Biológicos – Gráfico (Pág. 2 de 11)

Ruta Funcional (p–valor de la ruta)

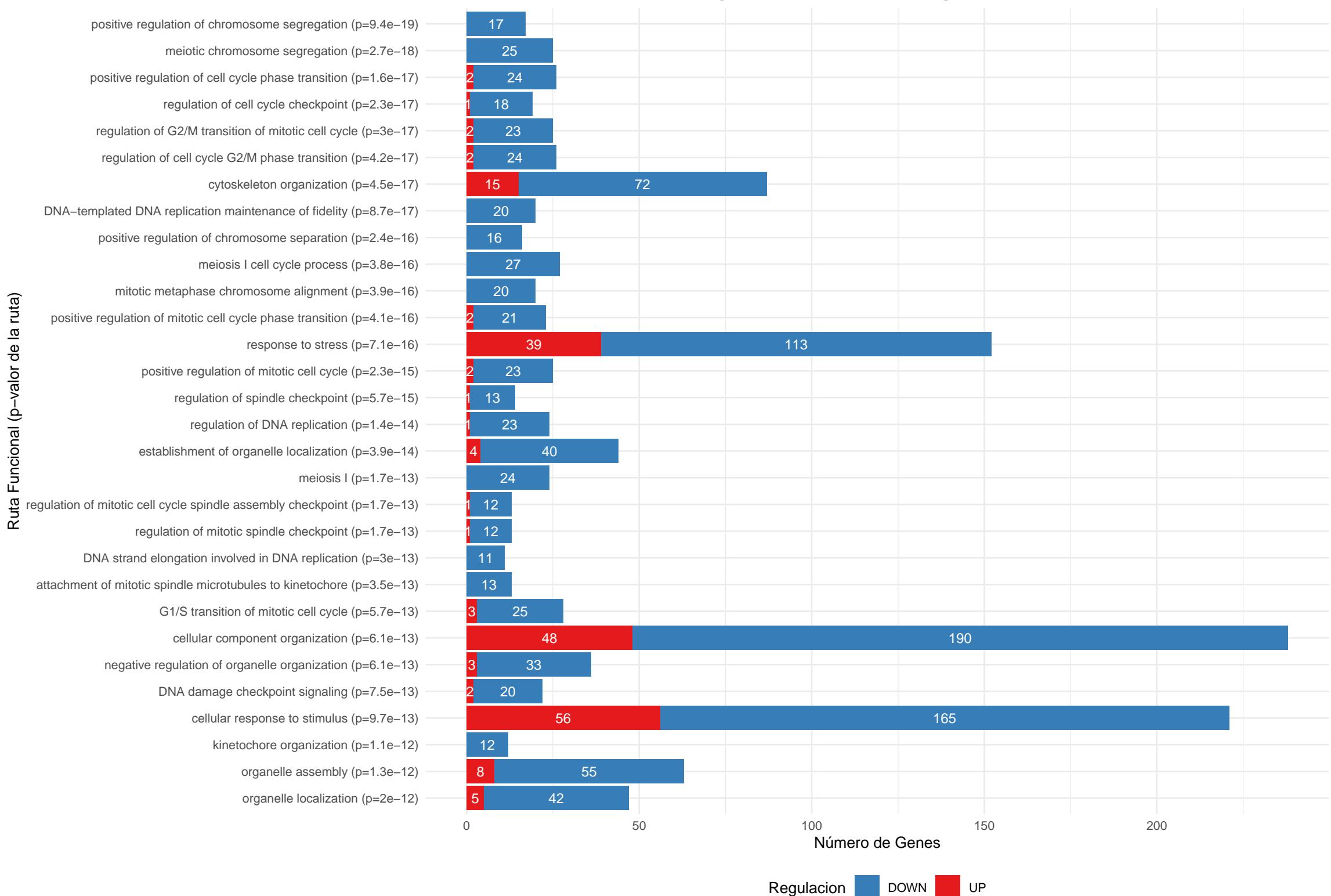


Regulacion █ DOWN █ UP

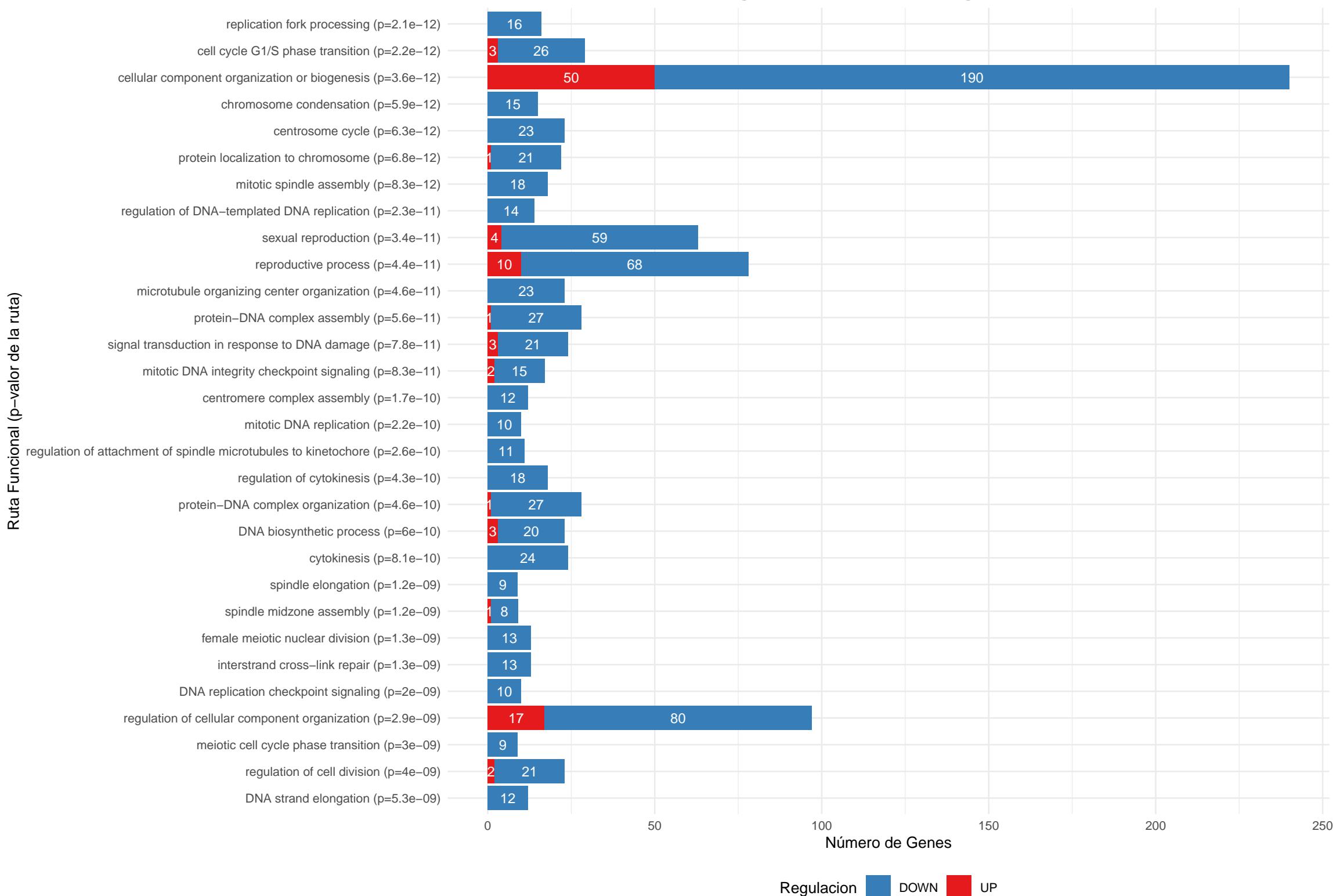
GO:BP – Procesos Biológicos – Gráfico (Pág. 3 de 11)



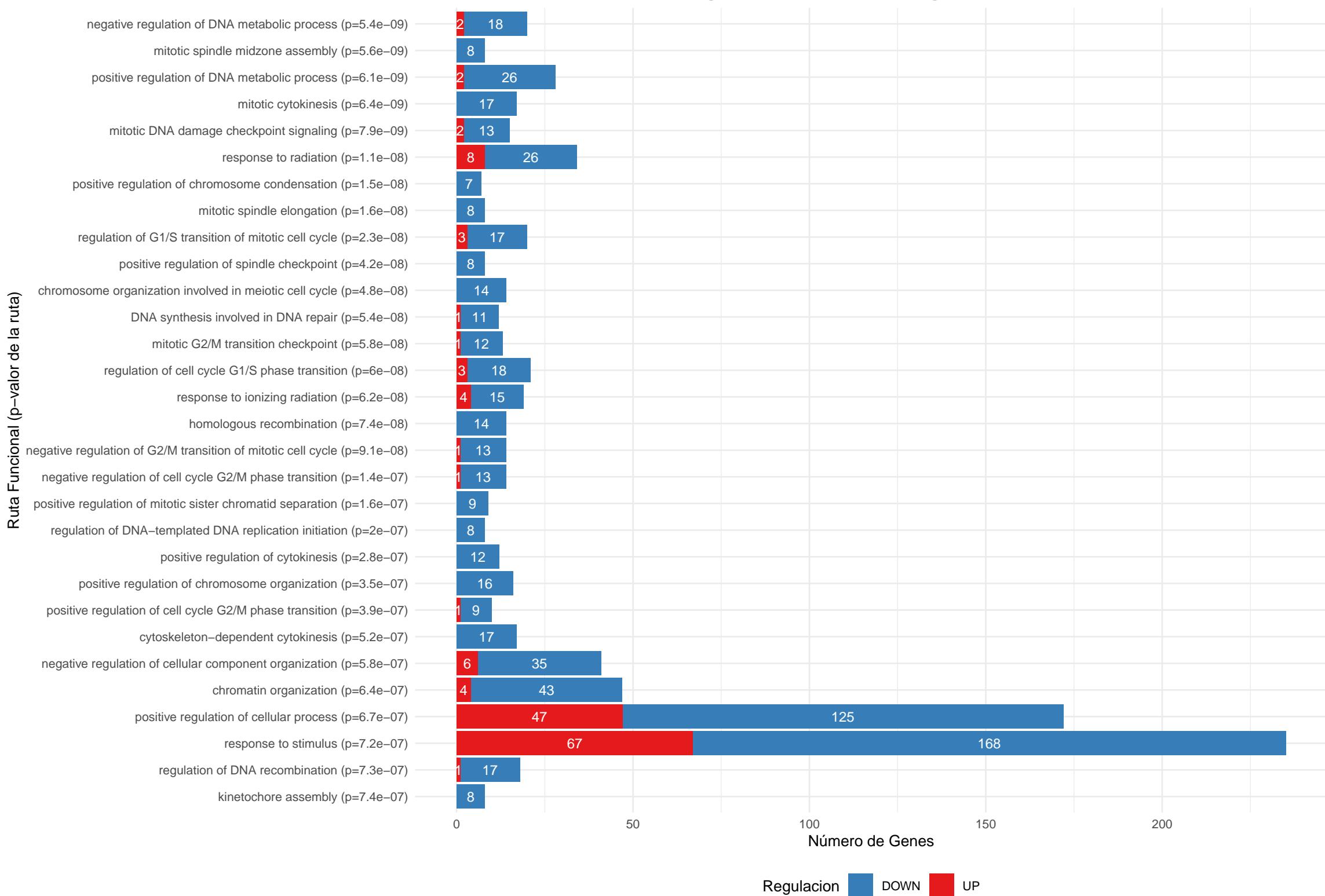
GO:BP – Procesos Biológicos – Gráfico (Pág. 4 de 11)



GO:BP – Procesos Biológicos – Gráfico (Pág. 5 de 11)

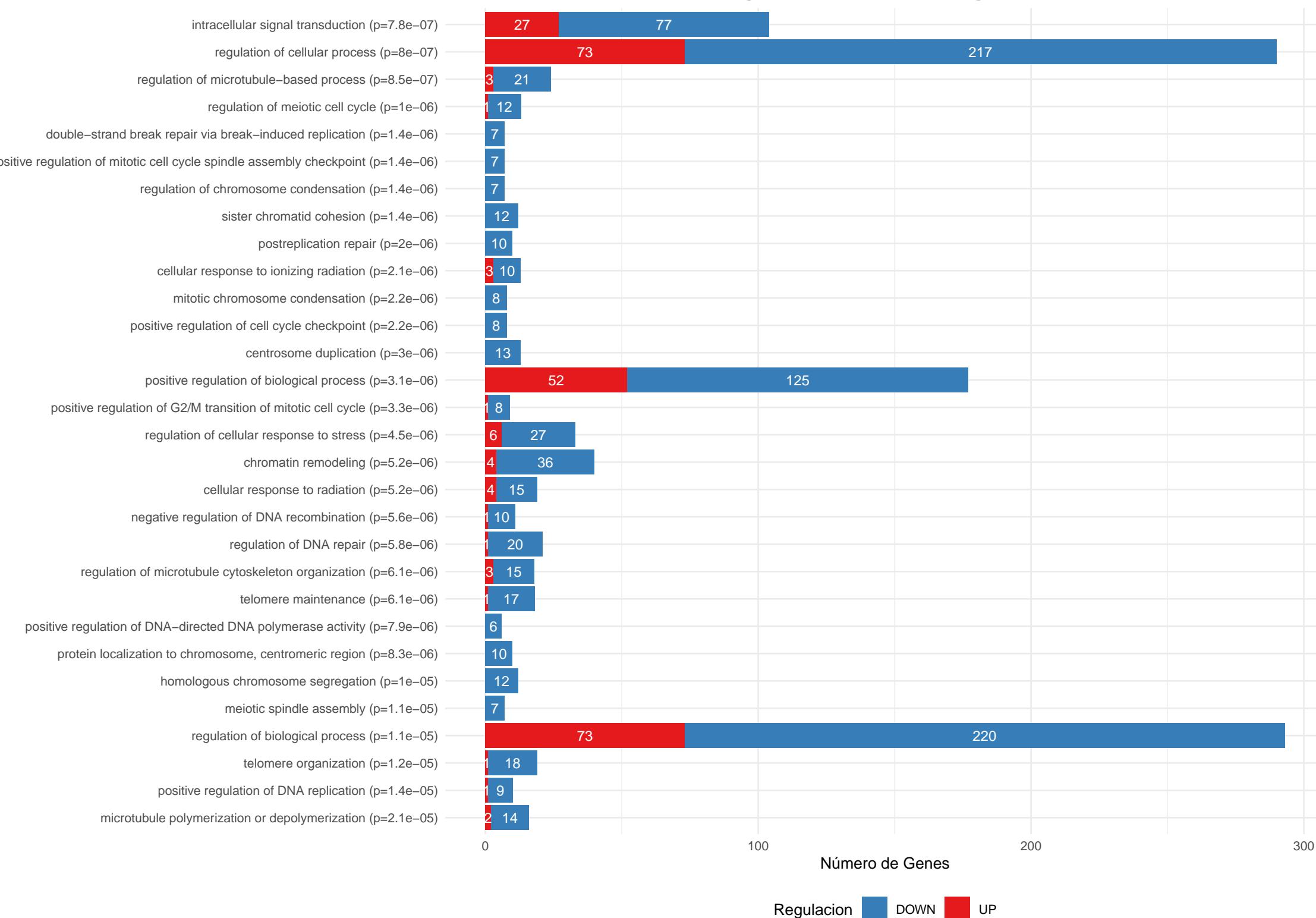


GO:BP – Procesos Biológicos – Gráfico (Pág. 6 de 11)

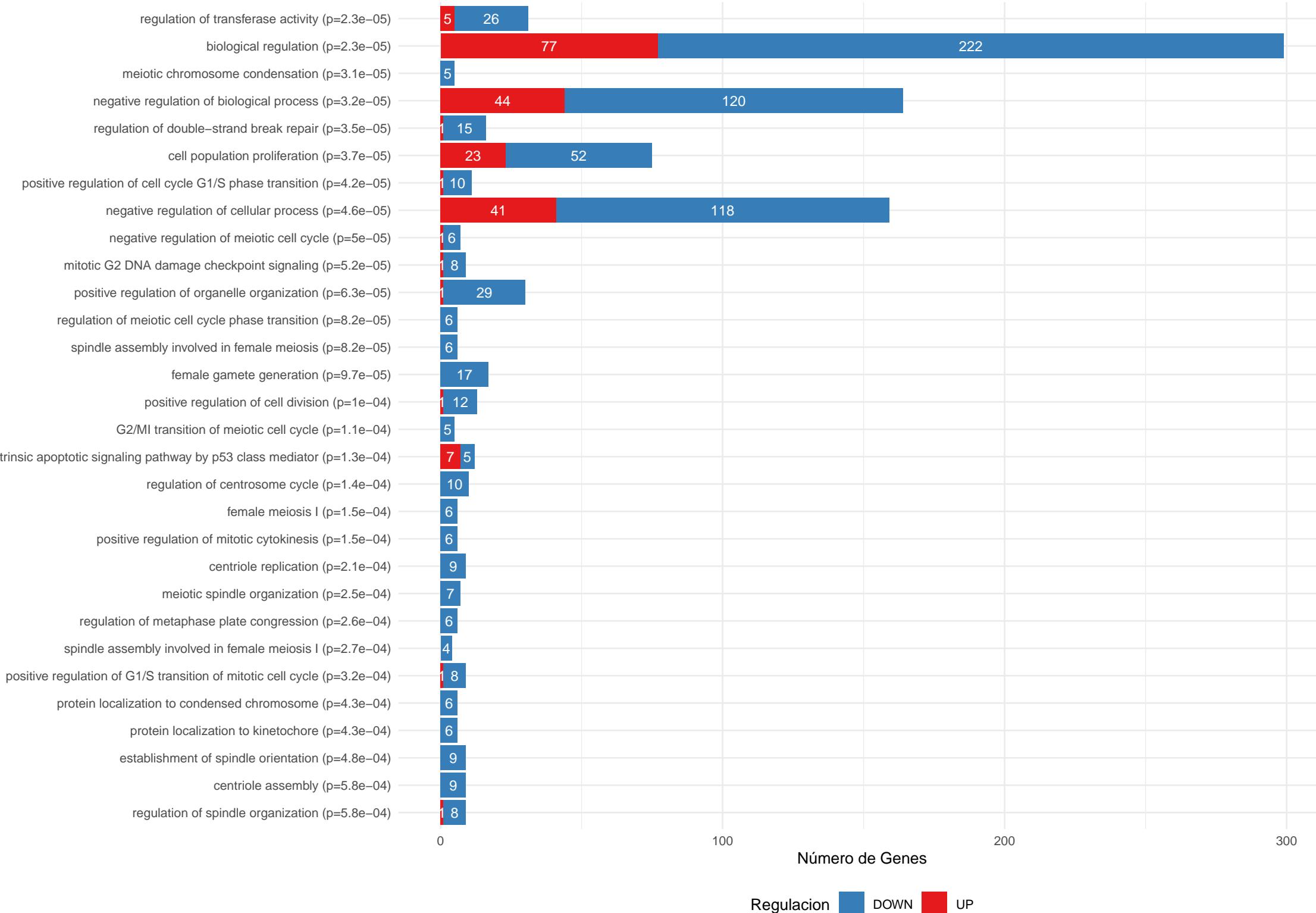


GO:BP – Procesos Biológicos – Gráfico (Pág. 7 de 11)

Ruta Funcional (p–valor de la ruta)

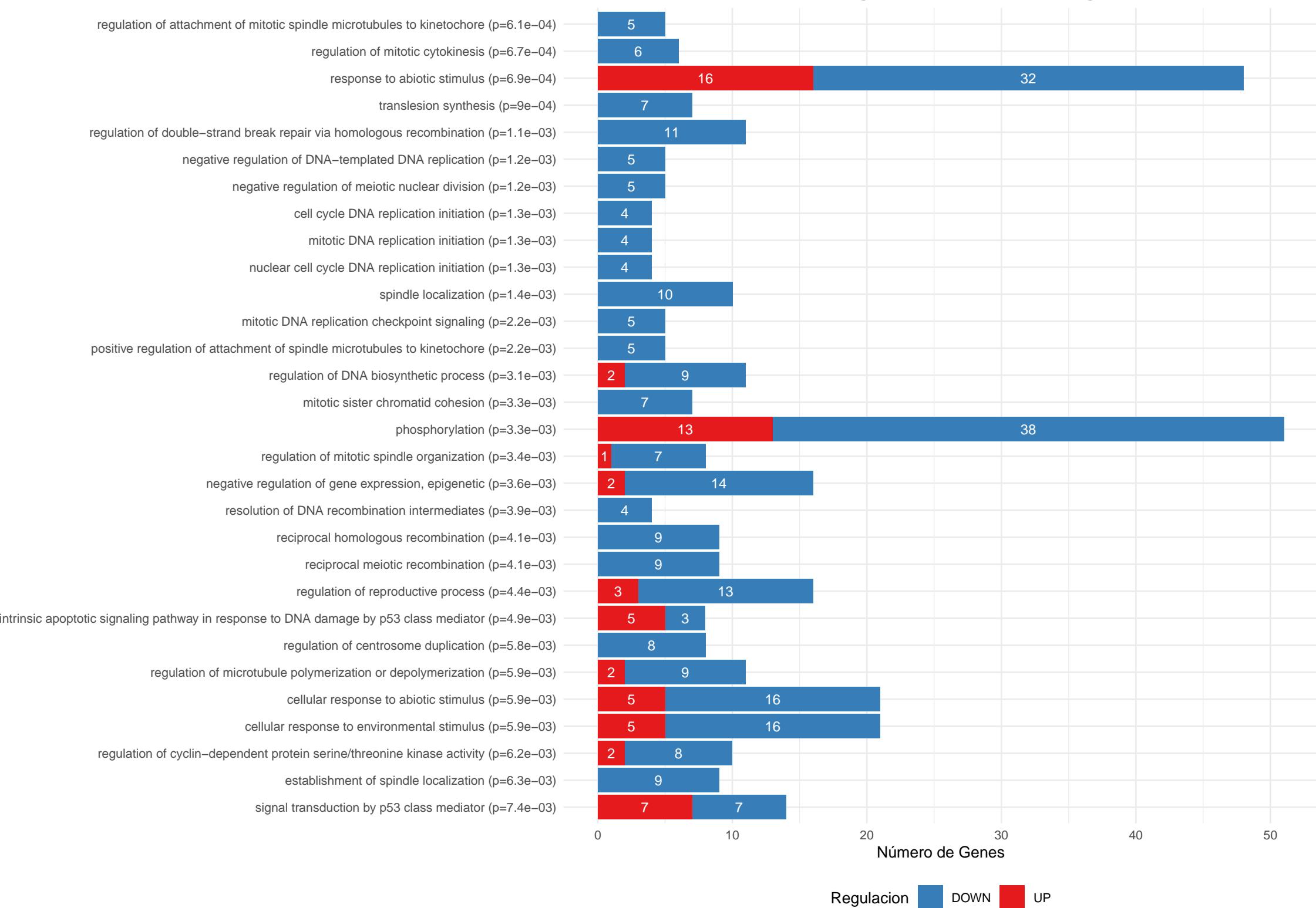


GO:BP – Procesos Biológicos – Gráfico (Pág. 8 de 11)



GO:BP – Procesos Biológicos – Gráfico (Pág. 9 de 11)

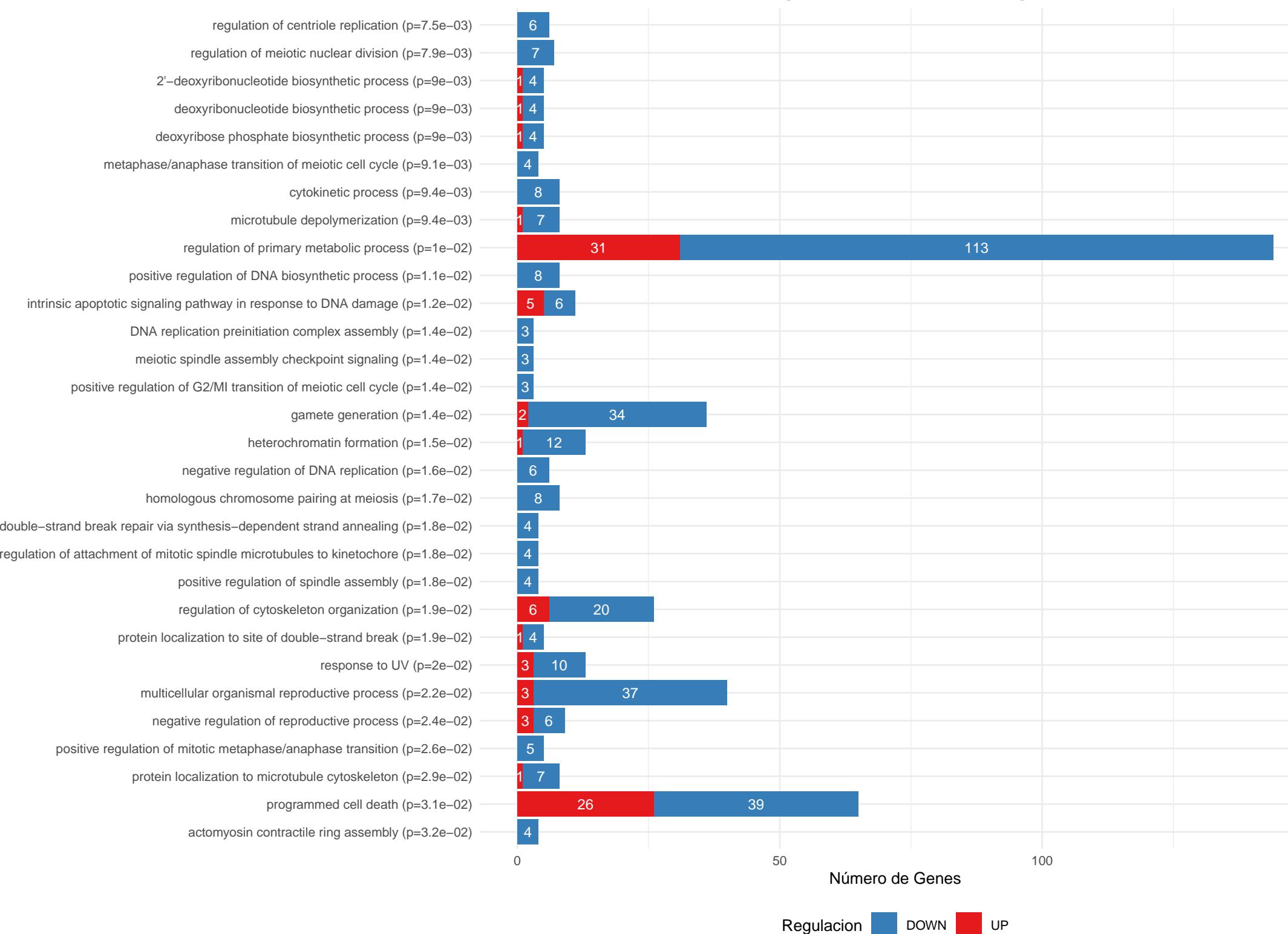
Ruta Funcional (p–valor de la ruta)



Regulación █ DOWN █ UP

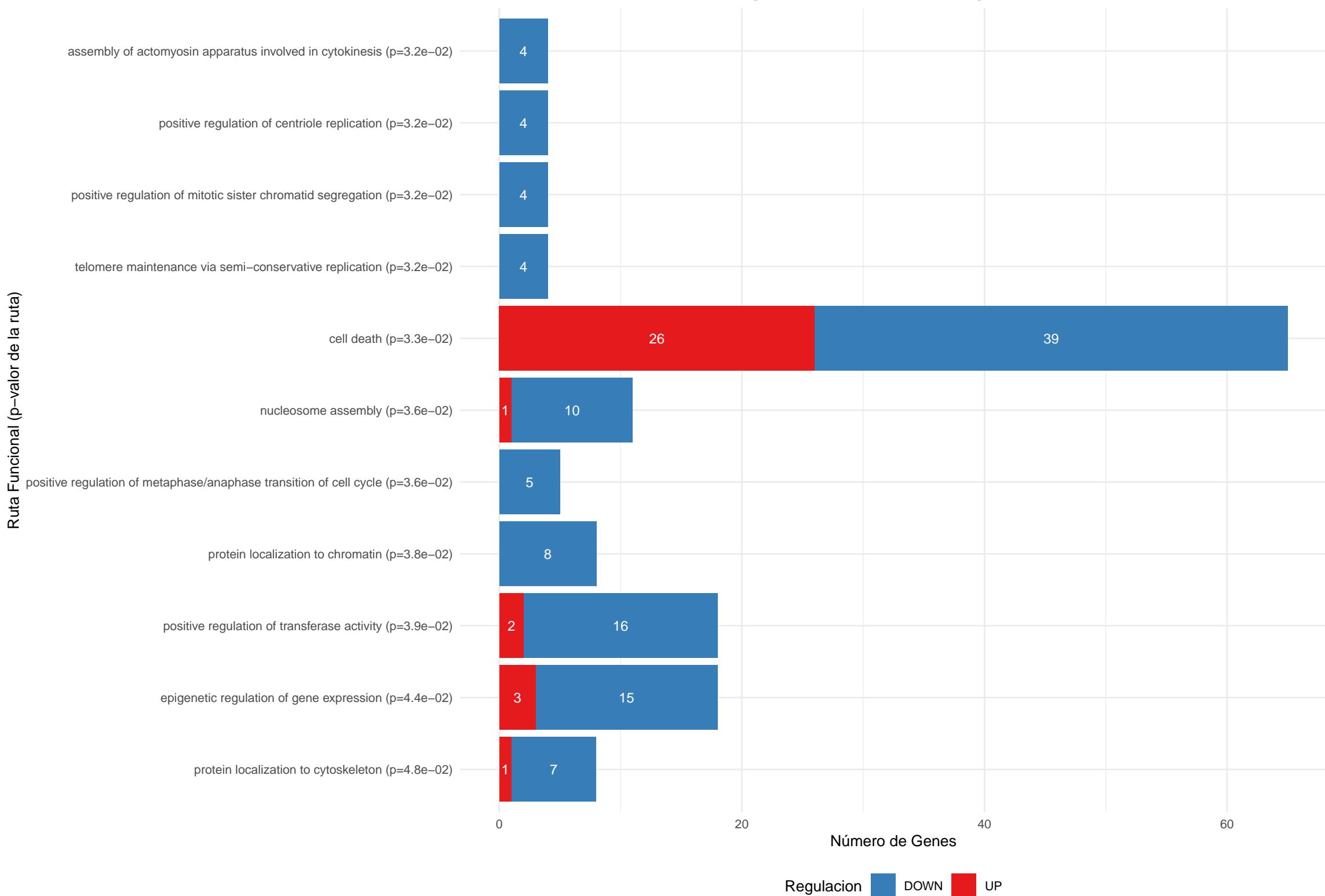
GO:BP – Procesos Biológicos – Gráfico (Pág. 10 de 11)

Ruta Funcional (p–valor de la ruta)



Regulacion DOWN UP

GO:BP – Procesos Biológicos – Gráfico (Pág. 11 de 11)



Ruta: cell cycle process (Página 1 de 8)

Fuente: GO:BP | ID: GO:0022402 | Genes: 178 | p-valor ruta: 3.35e-105

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6

Ruta: cell cycle process (Página 2 de 8)

Fuente: GO:BP | ID: GO:0022402 | Genes: 178 | p-valor ruta: 3.35e-105

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1

Ruta: cell cycle process (Página 3 de 8)

Fuente: GO:BP | ID: GO:0022402 | Genes: 178 | p-valor ruta: 3.35e-105

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3

Ruta: cell cycle process (Página 4 de 8)

Fuente: GO:BP | ID: GO:0022402 | Genes: 178 | p-valor ruta: 3.35e-105

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4

Ruta: cell cycle process (Página 5 de 8)

Fuente: GO:BP | ID: GO:0022402 | Genes: 178 | p-valor ruta: 3.35e-105

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7

Ruta: cell cycle process (Página 6 de 8)

Fuente: GO:BP | ID: GO:0022402 | Genes: 178 | p-valor ruta: 3.35e-105

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3

Ruta: cell cycle process (Página 7 de 8)

Fuente: GO:BP | ID: GO:0022402 | Genes: 178 | p-valor ruta: 3.35e-105

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6

Ruta: cell cycle process (Página 8 de 8)

Fuente: GO:BP | ID: GO:0022402 | Genes: 178 | p-valor ruta: 3.35e-105

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: cell cycle (Página 1 de 8)

Fuente: GO:BP | ID: GO:0007049 | Genes: 191 | p-valor ruta: 5.19e-99

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6

Ruta: cell cycle (Página 2 de 8)

Fuente: GO:BP | ID: GO:0007049 | Genes: 191 | p-valor ruta: 5.19e-99

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1

Ruta: cell cycle (Página 3 de 8)

Fuente: GO:BP | ID: GO:0007049 | Genes: 191 | p-valor ruta: 5.19e-99

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2

Ruta: cell cycle (Página 4 de 8)

Fuente: GO:BP | ID: GO:0007049 | Genes: 191 | p-valor ruta: 5.19e-99

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000068489	PRR11	DOWN	-1.033	9.90e-11	1510.0
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1

Ruta: cell cycle (Página 5 de 8)

Fuente: GO:BP | ID: GO:0007049 | Genes: 191 | p-valor ruta: 5.19e-99

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3

Ruta: cell cycle (Página 6 de 8)

Fuente: GO:BP | ID: GO:0007049 | Genes: 191 | p-valor ruta: 5.19e-99

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5

Ruta: cell cycle (Página 7 de 8)

Fuente: GO:BP | ID: GO:0007049 | Genes: 191 | p-valor ruta: 5.19e-99

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8

Ruta: cell cycle (Página 8 de 8)

Fuente: GO:BP | ID: GO:0007049 | Genes: 191 | p-valor ruta: 5.19e-99

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5

Ruta: mitotic cell cycle process (Página 1 de 6)

Fuente: GO:BP | ID: GO:1903047 | Genes: 135 | p-valor ruta: 1.39e-91

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8

Ruta: mitotic cell cycle process (Página 2 de 6)

Fuente: GO:BP | ID: GO:1903047 | Genes: 135 | p-valor ruta: 1.39e-91

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4

Ruta: mitotic cell cycle process (Página 3 de 6)

Fuente: GO:BP | ID: GO:1903047 | Genes: 135 | p-valor ruta: 1.39e-91

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDC45	DOWN	-2.059	8.54e-13	175.9
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1

Ruta: mitotic cell cycle process (Página 4 de 6)

Fuente: GO:BP | ID: GO:1903047 | Genes: 135 | p-valor ruta: 1.39e-91

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0

Ruta: mitotic cell cycle process (Página 5 de 6)

Fuente: GO:BP | ID: GO:1903047 | Genes: 135 | p-valor ruta: 1.39e-91

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5

Ruta: mitotic cell cycle process (Página 6 de 6)

Fuente: GO:BP | ID: GO:1903047 | Genes: 135 | p-valor ruta: 1.39e-91

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: mitotic cell cycle (Página 1 de 6)

Fuente: GO:BP | ID: GO:0000278 | Genes: 141 | p-valor ruta: 1.04e-87

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9

Ruta: mitotic cell cycle (Página 2 de 6)

Fuente: GO:BP | ID: GO:0000278 | Genes: 141 | p-valor ruta: 1.04e-87

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6

Ruta: mitotic cell cycle (Página 3 de 6)

Fuente: GO:BP | ID: GO:0000278 | Genes: 141 | p-valor ruta: 1.04e-87

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0

Ruta: mitotic cell cycle (Página 4 de 6)

Fuente: GO:BP | ID: GO:0000278 | Genes: 141 | p-valor ruta: 1.04e-87

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8

Ruta: mitotic cell cycle (Página 5 de 6)

Fuente: GO:BP | ID: GO:0000278 | Genes: 141 | p-valor ruta: 1.04e-87

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9

Ruta: mitotic cell cycle (Página 6 de 6)

Fuente: GO:BP | ID: GO:0000278 | Genes: 141 | p-valor ruta: 1.04e-87

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1

Ruta: chromosome segregation (Página 1 de 4)

Fuente: GO:BP | ID: GO:0007059 | Genes: 100 | p-valor ruta: 3.82e-77

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9

Ruta: chromosome segregation (Página 2 de 4)

Fuente: GO:BP | ID: GO:0007059 | Genes: 100 | p-valor ruta: 3.82e-77

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0

Ruta: chromosome segregation (Página 3 de 4)

Fuente: GO:BP | ID: GO:0007059 | Genes: 100 | p-valor ruta: 3.82e-77

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1

Ruta: chromosome segregation (Página 4 de 4)

Fuente: GO:BP | ID: GO:0007059 | Genes: 100 | p-valor ruta: 3.82e-77

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: regulation of cell cycle process (Página 1 de 5)

Fuente: GO:BP | ID: GO:0010564 | Genes: 115 | p-valor ruta: 4.24e-70

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1

Ruta: regulation of cell cycle process (Página 2 de 5)

Fuente: GO:BP | ID: GO:0010564 | Genes: 115 | p-valor ruta: 4.24e-70

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3

Ruta: regulation of cell cycle process (Página 3 de 5)

Fuente: GO:BP | ID: GO:0010564 | Genes: 115 | p-valor ruta: 4.24e-70

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000080839	RBL1	DOWN	-1.533	4.00e-08	151.5

Ruta: regulation of cell cycle process (Página 4 de 5)

Fuente: GO:BP | ID: GO:0010564 | Genes: 115 | p-valor ruta: 4.24e-70

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6

Ruta: regulation of cell cycle process (Página 5 de 5)

Fuente: GO:BP | ID: GO:0010564 | Genes: 115 | p-valor ruta: 4.24e-70

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: chromosome organization (Página 1 de 5)

Fuente: GO:BP | ID: GO:0051276 | Genes: 103 | p-valor ruta: 3.27e-67

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4

Ruta: chromosome organization (Página 2 de 5)

Fuente: GO:BP | ID: GO:0051276 | Genes: 103 | p-valor ruta: 3.27e-67

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0

Ruta: chromosome organization (Página 3 de 5)

Fuente: GO:BP | ID: GO:0051276 | Genes: 103 | p-valor ruta: 3.27e-67

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7

Ruta: chromosome organization (Página 4 de 5)

Fuente: GO:BP | ID: GO:0051276 | Genes: 103 | p-valor ruta: 3.27e-67

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: chromosome organization (Página 5 de 5)

Fuente: GO:BP | ID: GO:0051276 | Genes: 103 | p-valor ruta: 3.27e-67

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: nuclear chromosome segregation (Página 1 de 4)

Fuente: GO:BP | ID: GO:0098813 | Genes: 81 | p-valor ruta: 6.05e-64

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7

Ruta: nuclear chromosome segregation (Página 2 de 4)

Fuente: GO:BP | ID: GO:0098813 | Genes: 81 | p-valor ruta: 6.05e-64

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4

Ruta: nuclear chromosome segregation (Página 3 de 4)

Fuente: GO:BP | ID: GO:0098813 | Genes: 81 | p-valor ruta: 6.05e-64

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: nuclear chromosome segregation (Página 4 de 4)

Fuente: GO:BP | ID: GO:0098813 | Genes: 81 | p-valor ruta: 6.05e-64

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: regulation of cell cycle (Página 1 de 6)

Fuente: GO:BP | ID: GO:0051726 | Genes: 129 | p-valor ruta: 1.41e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1

Ruta: regulation of cell cycle (Página 2 de 6)

Fuente: GO:BP | ID: GO:0051726 | Genes: 129 | p-valor ruta: 1.41e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9

Ruta: regulation of cell cycle (Página 3 de 6)

Fuente: GO:BP | ID: GO:0051726 | Genes: 129 | p-valor ruta: 1.41e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000068489	PRR11	DOWN	-1.033	9.90e-11	1510.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0

Ruta: regulation of cell cycle (Página 4 de 6)

Fuente: GO:BP | ID: GO:0051726 | Genes: 129 | p-valor ruta: 1.41e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG0000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5

Ruta: regulation of cell cycle (Página 5 de 6)

Fuente: GO:BP | ID: GO:0051726 | Genes: 129 | p-valor ruta: 1.41e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: regulation of cell cycle (Página 6 de 6)

Fuente: GO:BP | ID: GO:0051726 | Genes: 129 | p-valor ruta: 1.41e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5

Ruta: nuclear division (Página 1 de 4)

Fuente: GO:BP | ID: GO:0000280 | Genes: 89 | p-valor ruta: 6.92e-61

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9

Ruta: nuclear division (Página 2 de 4)

Fuente: GO:BP | ID: GO:0000280 | Genes: 89 | p-valor ruta: 6.92e-61

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1

Ruta: nuclear division (Página 3 de 4)

Fuente: GO:BP | ID: GO:0000280 | Genes: 89 | p-valor ruta: 6.92e-61

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2

Ruta: nuclear division (Página 4 de 4)

Fuente: GO:BP | ID: GO:0000280 | Genes: 89 | p-valor ruta: 6.92e-61

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: DNA metabolic process (Página 1 de 5)

Fuente: GO:BP | ID: GO:0006259 | Genes: 120 | p-valor ruta: 8.78e-59

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166801	FAM11A	DOWN	-1.546	4.63e-20	583.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000189057	FAM11B	DOWN	-2.315	2.29e-19	695.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6

Ruta: DNA metabolic process (Página 2 de 5)

Fuente: GO:BP | ID: GO:0006259 | Genes: 120 | p-valor ruta: 8.78e-59

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0

Ruta: DNA metabolic process (Página 3 de 5)

Fuente: GO:BP | ID: GO:0006259 | Genes: 120 | p-valor ruta: 8.78e-59

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG0000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG0000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG0000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG0000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG0000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG0000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG0000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG0000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG0000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG0000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG0000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG0000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG0000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG0000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG0000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG0000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG0000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG0000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG0000174371	EXO1	DOWN	-2.596	2.10e-06	101.7

Ruta: DNA metabolic process (Página 4 de 5)

Fuente: GO:BP | ID: GO:0006259 | Genes: 120 | p-valor ruta: 8.78e-59

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1

Ruta: DNA metabolic process (Página 5 de 5)

Fuente: GO:BP | ID: GO:0006259 | Genes: 120 | p-valor ruta: 8.78e-59

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: organelle fission (Página 1 de 4)

Fuente: GO:BP | ID: GO:0048285 | Genes: 90 | p-valor ruta: 4.88e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9

Ruta: organelle fission (Página 2 de 4)

Fuente: GO:BP | ID: GO:0048285 | Genes: 90 | p-valor ruta: 4.88e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1

Ruta: organelle fission (Página 3 de 4)

Fuente: GO:BP | ID: GO:0048285 | Genes: 90 | p-valor ruta: 4.88e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000146410	MTFR2	DOWN	-1.746	5.92e-06	145.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5

Ruta: organelle fission (Página 4 de 4)

Fuente: GO:BP | ID: GO:0048285 | Genes: 90 | p-valor ruta: 4.88e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG0000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: DNA replication (Página 1 de 4)

Fuente: GO:BP | ID: GO:0006260 | Genes: 90 | p-valor ruta: 8.3e-57

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000189057	FAM111B	DOWN	-2.315	2.29e-19	695.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9

Ruta: DNA replication (Página 2 de 4)

Fuente: GO:BP | ID: GO:0006260 | Genes: 90 | p-valor ruta: 8.3e-57

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9

Ruta: DNA replication (Página 3 de 4)

Fuente: GO:BP | ID: GO:0006260 | Genes: 90 | p-valor ruta: 8.3e-57

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8

Ruta: DNA replication (Página 4 de 4)

Fuente: GO:BP | ID: GO:0006260 | Genes: 90 | p-valor ruta: 8.3e-57

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: cell division (Página 1 de 4)

Fuente: GO:BP | ID: GO:0051301 | Genes: 99 | p-valor ruta: 9.46e-57

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1

Ruta: cell division (Página 2 de 4)

Fuente: GO:BP | ID: GO:0051301 | Genes: 99 | p-valor ruta: 9.46e-57

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000111665	CDCA3	DOWN	-1.647	8.37e-16	690.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000133739	LRRCC1	DOWN	-1.272	1.80e-12	348.7
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9

Ruta: cell division (Página 3 de 4)

Fuente: GO:BP | ID: GO:0051301 | Genes: 99 | p-valor ruta: 9.46e-57

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0

Ruta: cell division (Página 4 de 4)

Fuente: GO:BP | ID: GO:0051301 | Genes: 99 | p-valor ruta: 9.46e-57

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: cell cycle phase transition (Página 1 de 4)

Fuente: GO:BP | ID: GO:0044770 | Genes: 90 | p-valor ruta: 1.37e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3

Ruta: cell cycle phase transition (Página 2 de 4)

Fuente: GO:BP | ID: GO:0044770 | Genes: 90 | p-valor ruta: 1.37e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1

Ruta: cell cycle phase transition (Página 3 de 4)

Fuente: GO:BP | ID: GO:0044770 | Genes: 90 | p-valor ruta: 1.37e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1

Ruta: cell cycle phase transition (Página 4 de 4)

Fuente: GO:BP | ID: GO:0044770 | Genes: 90 | p-valor ruta: 1.37e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: DNA-templated DNA replication (Página 1 de 3)

Fuente: GO:BP | ID: GO:0006261 | Genes: 57 | p-valor ruta: 1.25e-53

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG0000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG0000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG0000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG0000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG0000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG0000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG0000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG0000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG0000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG0000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG0000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG0000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG0000125885	MCM8	DOWN	-1.405	1.29e-11	278.7

Ruta: DNA-templated DNA replication (Página 2 de 3)

Fuente: GO:BP | ID: GO:0006261 | Genes: 57 | p-valor ruta: 1.25e-53

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9

Ruta: DNA–templated DNA replication (Página 3 de 3)

Fuente: GO:BP | ID: GO:0006261 | Genes: 57 | p-valor ruta: 1.25e-53

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: sister chromatid segregation (Página 1 de 3)

Fuente: GO:BP | ID: GO:0000819 | Genes: 65 | p-valor ruta: 1.3e-53

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4

Ruta: sister chromatid segregation (Página 2 de 3)

Fuente: GO:BP | ID: GO:0000819 | Genes: 65 | p-valor ruta: 1.3e-53

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3

Ruta: sister chromatid segregation (Página 3 de 3)

Fuente: GO:BP | ID: GO:0000819 | Genes: 65 | p-valor ruta: 1.3e-53

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: regulation of cell cycle phase transition (Página 1 de 4)

Fuente: GO:BP | ID: GO:1901987 | Genes: 81 | p-valor ruta: 1.39e-53

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7

Ruta: regulation of cell cycle phase transition (Página 2 de 4)

Fuente: GO:BP | ID: GO:1901987 | Genes: 81 | p-valor ruta: 1.39e-53

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0

Ruta: regulation of cell cycle phase transition (Página 3 de 4)

Fuente: GO:BP | ID: GO:1901987 | Genes: 81 | p-valor ruta: 1.39e-53

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5

Ruta: regulation of cell cycle phase transition (Página 4 de 4)

Fuente: GO:BP | ID: GO:1901987 | Genes: 81 | p-valor ruta: 1.39e-53

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG0000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG0000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG0000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG0000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG0000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: mitotic sister chromatid segregation (Página 1 de 3)

Fuente: GO:BP | ID: GO:0000070 | Genes: 60 | p-valor ruta: 1.66e-52

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6

Ruta: mitotic sister chromatid segregation (Página 2 de 3)

Fuente: GO:BP | ID: GO:0000070 | Genes: 60 | p-valor ruta: 1.66e-52

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0

Ruta: mitotic sister chromatid segregation (Página 3 de 3)

Fuente: GO:BP | ID: GO:0000070 | Genes: 60 | p-valor ruta: 1.66e-52

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: mitotic nuclear division (Página 1 de 3)

Fuente: GO:BP | ID: GO:0140014 | Genes: 68 | p-valor ruta: 1.05e-51

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4

Ruta: mitotic nuclear division (Página 2 de 3)

Fuente: GO:BP | ID: GO:0140014 | Genes: 68 | p-valor ruta: 1.05e-51

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0

Ruta: mitotic nuclear division (Página 3 de 3)

Fuente: GO:BP | ID: GO:0140014 | Genes: 68 | p-valor ruta: 1.05e-51

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG0000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: mitotic cell cycle phase transition (Página 1 de 4)

Fuente: GO:BP | ID: GO:0044772 | Genes: 78 | p-valor ruta: 4.91e-50

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3

Ruta: mitotic cell cycle phase transition (Página 2 de 4)

Fuente: GO:BP | ID: GO:0044772 | Genes: 78 | p-valor ruta: 4.91e-50

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3

Ruta: mitotic cell cycle phase transition (Página 3 de 4)

Fuente: GO:BP | ID: GO:0044772 | Genes: 78 | p-valor ruta: 4.91e-50

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: mitotic cell cycle phase transition (Página 4 de 4)

Fuente: GO:BP | ID: GO:0044772 | Genes: 78 | p-valor ruta: 4.91e-50

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: DNA damage response (Página 1 de 5)

Fuente: GO:BP | ID: GO:0006974 | Genes: 105 | p-valor ruta: 4.31e-49

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4

Ruta: DNA damage response (Página 2 de 5)

Fuente: GO:BP | ID: GO:0006974 | Genes: 105 | p-valor ruta: 4.31e-49

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDC45	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMG2B	DOWN	-1.572	1.72e-11	2905.5
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4

Ruta: DNA damage response (Página 3 de 5)

Fuente: GO:BP | ID: GO:0006974 | Genes: 105 | p-valor ruta: 4.31e-49

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4

Ruta: DNA damage response (Página 4 de 5)

Fuente: GO:BP | ID: GO:0006974 | Genes: 105 | p-valor ruta: 4.31e-49

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: DNA damage response (Página 5 de 5)

Fuente: GO:BP | ID: GO:0006974 | Genes: 105 | p-valor ruta: 4.31e-49

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: regulation of mitotic cell cycle phase transition (Página 1 de 3)

Fuente: GO:BP | ID: GO:1901990 | Genes: 67 | p-valor ruta: 6.99e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6

Ruta: regulation of mitotic cell cycle phase transition (Página 2 de 3)

Fuente: GO:BP | ID: GO:1901990 | Genes: 67 | p-valor ruta: 6.99e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0

Ruta: regulation of mitotic cell cycle phase transition (Página 3 de 3)

Fuente: GO:BP | ID: GO:1901990 | Genes: 67 | p-valor ruta: 6.99e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: regulation of mitotic cell cycle (Página 1 de 4)

Fuente: GO:BP | ID: GO:0007346 | Genes: 78 | p-valor ruta: 2.63e-45

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3

Ruta: regulation of mitotic cell cycle (Página 2 de 4)

Fuente: GO:BP | ID: GO:0007346 | Genes: 78 | p-valor ruta: 2.63e-45

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4

Ruta: regulation of mitotic cell cycle (Página 3 de 4)

Fuente: GO:BP | ID: GO:0007346 | Genes: 78 | p-valor ruta: 2.63e-45

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8

Ruta: regulation of mitotic cell cycle (Página 4 de 4)

Fuente: GO:BP | ID: GO:0007346 | Genes: 78 | p-valor ruta: 2.63e-45

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: DNA repair (Página 1 de 4)

Fuente: GO:BP | ID: GO:0006281 | Genes: 85 | p-valor ruta: 1.61e-44

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0

Ruta: DNA repair (Página 2 de 4)

Fuente: GO:BP | ID: GO:0006281 | Genes: 85 | p-valor ruta: 1.61e-44

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG0000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG0000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG0000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG0000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG0000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG0000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG0000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG0000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG0000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG0000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG0000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG0000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG0000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG0000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG0000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG0000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG0000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG0000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8

Ruta: DNA repair (Página 3 de 4)

Fuente: GO:BP | ID: GO:0006281 | Genes: 85 | p-valor ruta: 1.61e-44

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0

Ruta: DNA repair (Página 4 de 4)

Fuente: GO:BP | ID: GO:0006281 | Genes: 85 | p-valor ruta: 1.61e-44

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: cell cycle checkpoint signaling (Página 1 de 3)

Fuente: GO:BP | ID: GO:0000075 | Genes: 53 | p-valor ruta: 7.14e-44

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1

Ruta: cell cycle checkpoint signaling (Página 2 de 3)

Fuente: GO:BP | ID: GO:0000075 | Genes: 53 | p-valor ruta: 7.14e-44

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: cell cycle checkpoint signaling (Página 3 de 3)

Fuente: GO:BP | ID: GO:0000075 | Genes: 53 | p-valor ruta: 7.14e-44

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: negative regulation of cell cycle process (Página 1 de 3)

Fuente: GO:BP | ID: GO:0010948 | Genes: 61 | p-valor ruta: 2.9e-42

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2

Ruta: negative regulation of cell cycle process (Página 2 de 3)

Fuente: GO:BP | ID: GO:0010948 | Genes: 61 | p-valor ruta: 2.9e-42

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0

Ruta: negative regulation of cell cycle process (Página 3 de 3)

Fuente: GO:BP | ID: GO:0010948 | Genes: 61 | p-valor ruta: 2.9e-42

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: negative regulation of cell cycle phase transition (Página 1 de 3)

Fuente: GO:BP | ID: GO:1901988 | Genes: 57 | p-valor ruta: 1.72e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2

Ruta: negative regulation of cell cycle phase transition (Página 2 de 3)

Fuente: GO:BP | ID: GO:1901988 | Genes: 57 | p-valor ruta: 1.72e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8

Ruta: negative regulation of cell cycle phase transition (Página 3 de 3)

Fuente: GO:BP | ID: GO:1901988 | Genes: 57 | p-valor ruta: 1.72e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: regulation of chromosome segregation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051983 | Genes: 45 | p-valor ruta: 1.09e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6

Ruta: regulation of chromosome segregation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051983 | Genes: 45 | p-valor ruta: 1.09e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: positive regulation of cell cycle process (Página 1 de 3)

Fuente: GO:BP | ID: GO:0090068 | Genes: 57 | p-valor ruta: 4.68e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1

Ruta: positive regulation of cell cycle process (Página 2 de 3)

Fuente: GO:BP | ID: GO:0090068 | Genes: 57 | p-valor ruta: 4.68e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0

Ruta: positive regulation of cell cycle process (Página 3 de 3)

Fuente: GO:BP | ID: GO:0090068 | Genes: 57 | p-valor ruta: 4.68e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: negative regulation of cell cycle (Página 1 de 3)

Fuente: GO:BP | ID: GO:0045786 | Genes: 63 | p-valor ruta: 2.95e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8

Ruta: negative regulation of cell cycle (Página 2 de 3)

Fuente: GO:BP | ID: GO:0045786 | Genes: 63 | p-valor ruta: 2.95e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9

Ruta: negative regulation of cell cycle (Página 3 de 3)

Fuente: GO:BP | ID: GO:0045786 | Genes: 63 | p-valor ruta: 2.95e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: mitotic cell cycle checkpoint signaling (Página 1 de 2)

Fuente: GO:BP | ID: GO:0007093 | Genes: 43 | p-valor ruta: 3.88e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9

Ruta: mitotic cell cycle checkpoint signaling (Página 2 de 2)

Fuente: GO:BP | ID: GO:0007093 | Genes: 43 | p-valor ruta: 3.88e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: regulation of chromosome separation (Página 1 de 2)

Fuente: GO:BP | ID: GO:1905818 | Genes: 35 | p-valor ruta: 2.02e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5

Ruta: regulation of chromosome separation (Página 2 de 2)

Fuente: GO:BP | ID: GO:1905818 | Genes: 35 | p-valor ruta: 2.02e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: organelle organization (Página 1 de 8)

Fuente: GO:BP | ID: GO:0006996 | Genes: 181 | p-valor ruta: 8.41e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3

Ruta: organelle organization (Página 2 de 8)

Fuente: GO:BP | ID: GO:0006996 | Genes: 181 | p-valor ruta: 8.41e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6

Ruta: organelle organization (Página 3 de 8)

Fuente: GO:BP | ID: GO:0006996 | Genes: 181 | p-valor ruta: 8.41e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9

Ruta: organelle organization (Página 4 de 8)

Fuente: GO:BP | ID: GO:0006996 | Genes: 181 | p-valor ruta: 8.41e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5

Ruta: organelle organization (Página 5 de 8)

Fuente: GO:BP | ID: GO:0006996 | Genes: 181 | p-valor ruta: 8.41e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000146410	MTFR2	DOWN	-1.746	5.92e-06	145.6

Ruta: organelle organization (Página 6 de 8)

Fuente: GO:BP | ID: GO:0006996 | Genes: 181 | p-valor ruta: 8.41e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000166881	NEMP1	DOWN	-2.208	2.92e-04	75.0
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5

Ruta: organelle organization (Página 7 de 8)

Fuente: GO:BP | ID: GO:0006996 | Genes: 181 | p-valor ruta: 8.41e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000181652	ATG9B	UP	1.052	9.34e-03	97.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1

Ruta: organelle organization (Página 8 de 8)

Fuente: GO:BP | ID: GO:0006996 | Genes: 181 | p-valor ruta: 8.41e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: positive regulation of cell cycle (Página 1 de 3)

Fuente: GO:BP | ID: GO:0045787 | Genes: 59 | p-valor ruta: 7.97e-35

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1

Ruta: positive regulation of cell cycle (Página 2 de 3)

Fuente: GO:BP | ID: GO:0045787 | Genes: 59 | p-valor ruta: 7.97e-35

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1

Ruta: positive regulation of cell cycle (Página 3 de 3)

Fuente: GO:BP | ID: GO:0045787 | Genes: 59 | p-valor ruta: 7.97e-35

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: chromosome separation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051304 | Genes: 35 | p-valor ruta: 9.43e-35

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5

Ruta: chromosome separation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051304 | Genes: 35 | p-valor ruta: 9.43e-35

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: negative regulation of mitotic cell cycle phase transition (Página 1 de 2)

Fuente: GO:BP | ID: GO:1901991 | Genes: 44 | p-valor ruta: 1.47e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1

Ruta: negative regulation of mitotic cell cycle phase transition (Página 2 de 2)

Fuente: GO:BP | ID: GO:1901991 | Genes: 44 | p-valor ruta: 1.47e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: cellular response to stress (Página 1 de 5)

Fuente: GO:BP | ID: GO:0033554 | Genes: 122 | p-valor ruta: 1.31e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6

Ruta: cellular response to stress (Página 2 de 5)

Fuente: GO:BP | ID: GO:0033554 | Genes: 122 | p-valor ruta: 1.31e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7

Ruta: cellular response to stress (Página 3 de 5)

Fuente: GO:BP | ID: GO:0033554 | Genes: 122 | p-valor ruta: 1.31e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG0000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG0000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG0000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG0000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG0000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG0000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG0000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG0000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG0000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG0000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG0000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG0000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG0000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG0000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG0000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG0000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG0000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG0000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3

Ruta: cellular response to stress (Página 4 de 5)

Fuente: GO:BP | ID: GO:0033554 | Genes: 122 | p-valor ruta: 1.31e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5

Ruta: cellular response to stress (Página 5 de 5)

Fuente: GO:BP | ID: GO:0033554 | Genes: 122 | p-valor ruta: 1.31e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG0000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: negative regulation of mitotic cell cycle (Página 1 de 2)

Fuente: GO:BP | ID: GO:0045930 | Genes: 47 | p-valor ruta: 1.21e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1

Ruta: negative regulation of mitotic cell cycle (Página 2 de 2)

Fuente: GO:BP | ID: GO:0045930 | Genes: 47 | p-valor ruta: 1.21e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: meiotic cell cycle (Página 1 de 3)

Fuente: GO:BP | ID: GO:0051321 | Genes: 52 | p-valor ruta: 3.02e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG0000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG0000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG0000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9

Ruta: meiotic cell cycle (Página 2 de 3)

Fuente: GO:BP | ID: GO:0051321 | Genes: 52 | p-valor ruta: 3.02e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6

Ruta: meiotic cell cycle (Página 3 de 3)

Fuente: GO:BP | ID: GO:0051321 | Genes: 52 | p-valor ruta: 3.02e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: regulation of chromosome organization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0033044 | Genes: 47 | p-valor ruta: 4.11e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6

Ruta: regulation of chromosome organization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0033044 | Genes: 47 | p-valor ruta: 4.11e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: metaphase chromosome alignment (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051310 | Genes: 34 | p-valor ruta: 2.04e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0

Ruta: metaphase chromosome alignment (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051310 | Genes: 34 | p-valor ruta: 2.04e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG0000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG0000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG0000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG0000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG0000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1

Ruta: regulation of sister chromatid segregation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0033045 | Genes: 34 | p-valor ruta: 6.19e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3

Ruta: regulation of sister chromatid segregation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0033045 | Genes: 34 | p-valor ruta: 6.19e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: spindle organization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0007051 | Genes: 43 | p-valor ruta: 1.04e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9

Ruta: spindle organization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0007051 | Genes: 43 | p-valor ruta: 1.04e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG0000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG0000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG0000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG0000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG0000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG0000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG0000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG0000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG0000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG0000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG0000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: double-strand break repair (Página 1 de 3)

Fuente: GO:BP | ID: GO:0006302 | Genes: 51 | p-valor ruta: 1.36e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4

Ruta: double-strand break repair (Página 2 de 3)

Fuente: GO:BP | ID: GO:0006302 | Genes: 51 | p-valor ruta: 1.36e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: double-strand break repair (Página 3 de 3)

Fuente: GO:BP | ID: GO:0006302 | Genes: 51 | p-valor ruta: 1.36e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: regulation of mitotic sister chromatid separation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0010965 | Genes: 28 | p-valor ruta: 1.42e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5

Ruta: regulation of mitotic sister chromatid separation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0010965 | Genes: 28 | p-valor ruta: 1.42e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: microtubule cytoskeleton organization (Página 1 de 3)

Fuente: GO:BP | ID: GO:0000226 | Genes: 70 | p-valor ruta: 2.87e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9

Ruta: microtubule cytoskeleton organization (Página 2 de 3)

Fuente: GO:BP | ID: GO:0000226 | Genes: 70 | p-valor ruta: 2.87e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3

Ruta: microtubule cytoskeleton organization (Página 3 de 3)

Fuente: GO:BP | ID: GO:0000226 | Genes: 70 | p-valor ruta: 2.87e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1

Ruta: regulation of mitotic nuclear division (Página 1 de 2)

Fuente: GO:BP | ID: GO:0007088 | Genes: 35 | p-valor ruta: 3.05e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5

Ruta: regulation of mitotic nuclear division (Página 2 de 2)

Fuente: GO:BP | ID: GO:0007088 | Genes: 35 | p-valor ruta: 3.05e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: regulation of mitotic sister chromatid segregation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0033047 | Genes: 27 | p-valor ruta: 3.38e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: regulation of mitotic sister chromatid segregation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0033047 | Genes: 27 | p-valor ruta: 3.38e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: negative regulation of mitotic metaphase/anaphase transition (Página 1 de 2)

Fuente: GO:BP | ID: GO:0045841 | Genes: 26 | p-valor ruta: 3.61e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: negative regulation of mitotic metaphase/anaphase transition (Página 2 de 2)

Fuente: GO:BP | ID: GO:0045841 | Genes: 26 | p-valor ruta: 3.61e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: negative regulation of mitotic sister chromatid segregation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0033048 | Genes: 26 | p-valor ruta: 3.61e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: negative regulation of mitotic sister chromatid segregation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0033048 | Genes: 26 | p-valor ruta: 3.61e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: negative regulation of mitotic sister chromatid separation (Página 1 de 2)

Fuente: GO:BP | ID: GO:2000816 | Genes: 26 | p-valor ruta: 3.61e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: negative regulation of mitotic sister chromatid separation (Página 2 de 2)

Fuente: GO:BP | ID: GO:2000816 | Genes: 26 | p-valor ruta: 3.61e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: negative regulation of sister chromatid segregation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0033046 | Genes: 26 | p-valor ruta: 3.61e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: negative regulation of sister chromatid segregation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0033046 | Genes: 26 | p-valor ruta: 3.61e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: mitotic sister chromatid separation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051306 | Genes: 28 | p-valor ruta: 7.55e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5

Ruta: mitotic sister chromatid separation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051306 | Genes: 28 | p-valor ruta: 7.55e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: metaphase/anaphase transition of mitotic cell cycle (Página 1 de 2)

Fuente: GO:BP | ID: GO:0007091 | Genes: 32 | p-valor ruta: 1.07e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0

Ruta: metaphase/anaphase transition of mitotic cell cycle (Página 2 de 2)

Fuente: GO:BP | ID: GO:0007091 | Genes: 32 | p-valor ruta: 1.07e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: negative regulation of chromosome segregation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051985 | Genes: 26 | p-valor ruta: 1.37e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: negative regulation of chromosome segregation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051985 | Genes: 26 | p-valor ruta: 1.37e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: negative regulation of chromosome separation (Página 1 de 2)

Fuente: GO:BP | ID: GO:1905819 | Genes: 26 | p-valor ruta: 1.37e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: negative regulation of chromosome separation (Página 2 de 2)

Fuente: GO:BP | ID: GO:1905819 | Genes: 26 | p-valor ruta: 1.37e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: negative regulation of metaphase/anaphase transition of cell cycle (Página 1 de 2)

Fuente: GO:BP | ID: GO:1902100 | Genes: 26 | p-valor ruta: 1.37e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: negative regulation of metaphase/anaphase transition of cell cycle (Página 2 de 2)

Fuente: GO:BP | ID: GO:1902100 | Genes: 26 | p-valor ruta: 1.37e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: microtubule cytoskeleton organization involved in mitosis (Página 1 de 2)

Fuente: GO:BP | ID: GO:1902850 | Genes: 39 | p-valor ruta: 1.37e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000276043	UHFR1	DOWN	-1.751	1.20e-08	161.5

Ruta: microtubule cytoskeleton organization involved in mitosis (Página 2 de 2)

Fuente: GO:BP | ID: GO:1902850 | Genes: 39 | p-valor ruta: 1.37e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: chromosome localization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0050000 | Genes: 35 | p-valor ruta: 1.47e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5

Ruta: chromosome localization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0050000 | Genes: 35 | p-valor ruta: 1.47e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1

Ruta: establishment of chromosome localization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051303 | Genes: 34 | p-valor ruta: 2.64e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0

Ruta: establishment of chromosome localization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051303 | Genes: 34 | p-valor ruta: 2.64e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1

Ruta: metaphase/anaphase transition of cell cycle (Página 1 de 2)

Fuente: GO:BP | ID: GO:0044784 | Genes: 32 | p-valor ruta: 3.29e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0

Ruta: metaphase/anaphase transition of cell cycle (Página 2 de 2)

Fuente: GO:BP | ID: GO:0044784 | Genes: 32 | p-valor ruta: 3.29e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: meiotic cell cycle process (Página 1 de 2)

Fuente: GO:BP | ID: GO:1903046 | Genes: 43 | p-valor ruta: 4.19e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0

Ruta: meiotic cell cycle process (Página 2 de 2)

Fuente: GO:BP | ID: GO:1903046 | Genes: 43 | p-valor ruta: 4.19e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: mitotic spindle assembly checkpoint signaling

Fuente: GO:BP | ID: GO:0007094 | Genes: 25 | p-valor ruta: 5.18e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG0000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: mitotic spindle checkpoint signaling

Fuente: GO:BP | ID: GO:0071174 | Genes: 25 | p-valor ruta: 5.18e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: spindle assembly checkpoint signaling

Fuente: GO:BP | ID: GO:0071173 | Genes: 25 | p-valor ruta: 5.18e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: regulation of mitotic metaphase/anaphase transition (Página 1 de 2)

Fuente: GO:BP | ID: GO:0030071 | Genes: 31 | p-valor ruta: 6.39e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3

Ruta: regulation of mitotic metaphase/anaphase transition (Página 2 de 2)

Fuente: GO:BP | ID: GO:0030071 | Genes: 31 | p-valor ruta: 6.39e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: DNA recombination (Página 1 de 3)

Fuente: GO:BP | ID: GO:0006310 | Genes: 51 | p-valor ruta: 8.86e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3

Ruta: DNA recombination (Página 2 de 3)

Fuente: GO:BP | ID: GO:0006310 | Genes: 51 | p-valor ruta: 8.86e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: DNA recombination (Página 3 de 3)

Fuente: GO:BP | ID: GO:0006310 | Genes: 51 | p-valor ruta: 8.86e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: spindle checkpoint signaling

Fuente: GO:BP | ID: GO:0031577 | Genes: 25 | p-valor ruta: 1.02e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG0000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: regulation of metaphase/anaphase transition of cell cycle (Página 1 de 2)

Fuente: GO:BP | ID: GO:1902099 | Genes: 31 | p-valor ruta: 1.99e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3

Ruta: regulation of metaphase/anaphase transition of cell cycle (Página 2 de 2)

Fuente: GO:BP | ID: GO:1902099 | Genes: 31 | p-valor ruta: 1.99e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: negative regulation of nuclear division (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051784 | Genes: 27 | p-valor ruta: 3.03e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: negative regulation of nuclear division (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051784 | Genes: 27 | p-valor ruta: 3.03e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: regulation of nuclear division (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051783 | Genes: 36 | p-valor ruta: 4.79e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9

Ruta: regulation of nuclear division (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051783 | Genes: 36 | p-valor ruta: 4.79e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: negative regulation of mitotic nuclear division (Página 1 de 2)

Fuente: GO:BP | ID: GO:0045839 | Genes: 26 | p-valor ruta: 5.01e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: negative regulation of mitotic nuclear division (Página 2 de 2)

Fuente: GO:BP | ID: GO:0045839 | Genes: 26 | p-valor ruta: 5.01e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: mitotic spindle organization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0007052 | Genes: 34 | p-valor ruta: 3.02e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG0000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG0000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG0000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG0000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG0000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG0000117650	NEK2	DOWN	-1.675	2.88e-06	263.6

Ruta: mitotic spindle organization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0007052 | Genes: 34 | p-valor ruta: 3.02e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG0000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: meiotic nuclear division (Página 1 de 2)

Fuente: GO:BP | ID: GO:0140013 | Genes: 39 | p-valor ruta: 1.88e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0

Ruta: meiotic nuclear division (Página 2 de 2)

Fuente: GO:BP | ID: GO:0140013 | Genes: 39 | p-valor ruta: 1.88e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: attachment of spindle microtubules to kinetochore

Fuente: GO:BP | ID: GO:0008608 | Genes: 24 | p-valor ruta: 5.7e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: double-strand break repair via homologous recombination (Página 1 de 2)

Fuente: GO:BP | ID: GO:0000724 | Genes: 37 | p-valor ruta: 2.17e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8

Ruta: double-strand break repair via homologous recombination (Página 2 de 2)

Fuente: GO:BP | ID: GO:0000724 | Genes: 37 | p-valor ruta: 2.17e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: microtubule-based process (Página 1 de 4)

Fuente: GO:BP | ID: GO:0007017 | Genes: 78 | p-valor ruta: 2.24e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6

Ruta: microtubule-based process (Página 2 de 4)

Fuente: GO:BP | ID: GO:0007017 | Genes: 78 | p-valor ruta: 2.24e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7

Ruta: microtubule-based process (Página 3 de 4)

Fuente: GO:BP | ID: GO:0007017 | Genes: 78 | p-valor ruta: 2.24e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7

Ruta: microtubule-based process (Página 4 de 4)

Fuente: GO:BP | ID: GO:0007017 | Genes: 78 | p-valor ruta: 2.24e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7

Ruta: recombinational repair (Página 1 de 2)

Fuente: GO:BP | ID: GO:0000725 | Genes: 37 | p-valor ruta: 5.83e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8

Ruta: recombinational repair (Página 2 de 2)

Fuente: GO:BP | ID: GO:0000725 | Genes: 37 | p-valor ruta: 5.83e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: membraneless organelle assembly (Página 1 de 3)

Fuente: GO:BP | ID: GO:0140694 | Genes: 51 | p-valor ruta: 2.66e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9

Ruta: membraneless organelle assembly (Página 2 de 3)

Fuente: GO:BP | ID: GO:0140694 | Genes: 51 | p-valor ruta: 2.66e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: membraneless organelle assembly (Página 3 de 3)

Fuente: GO:BP | ID: GO:0140694 | Genes: 51 | p-valor ruta: 2.66e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: negative regulation of chromosome organization (Página 1 de 2)

Fuente: GO:BP | ID: GO:2001251 | Genes: 28 | p-valor ruta: 4.04e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: negative regulation of chromosome organization (Página 2 de 2)

Fuente: GO:BP | ID: GO:2001251 | Genes: 28 | p-valor ruta: 4.04e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: DNA replication initiation

Fuente: GO:BP | ID: GO:0006270 | Genes: 25 | p-valor ruta: 7.3e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: regulation of DNA metabolic process (Página 1 de 3)

Fuente: GO:BP | ID: GO:0051052 | Genes: 54 | p-valor ruta: 8.91e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6

Ruta: regulation of DNA metabolic process (Página 2 de 3)

Fuente: GO:BP | ID: GO:0051052 | Genes: 54 | p-valor ruta: 8.91e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5

Ruta: regulation of DNA metabolic process (Página 3 de 3)

Fuente: GO:BP | ID: GO:0051052 | Genes: 54 | p-valor ruta: 8.91e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: cell cycle G2/M phase transition (Página 1 de 2)

Fuente: GO:BP | ID: GO:0044839 | Genes: 33 | p-valor ruta: 1.11e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3

Ruta: cell cycle G2/M phase transition (Página 2 de 2)

Fuente: GO:BP | ID: GO:0044839 | Genes: 33 | p-valor ruta: 1.11e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG0000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: spindle assembly (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051225 | Genes: 31 | p-valor ruta: 2.78e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG0000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG0000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG0000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG0000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG0000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG0000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG0000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG0000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9

Ruta: spindle assembly (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051225 | Genes: 31 | p-valor ruta: 2.78e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: cell cycle DNA replication

Fuente: GO:BP | ID: GO:0044786 | Genes: 21 | p-valor ruta: 2.81e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: G2/M transition of mitotic cell cycle (Página 1 de 2)

Fuente: GO:BP | ID: GO:0000086 | Genes: 30 | p-valor ruta: 8.83e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1

Ruta: G2/M transition of mitotic cell cycle (Página 2 de 2)

Fuente: GO:BP | ID: GO:0000086 | Genes: 30 | p-valor ruta: 8.83e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: regulation of organelle organization (Página 1 de 4)

Fuente: GO:BP | ID: GO:0033043 | Genes: 78 | p-valor ruta: 1.53e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7

Ruta: regulation of organelle organization (Página 2 de 4)

Fuente: GO:BP | ID: GO:0033043 | Genes: 78 | p-valor ruta: 1.53e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0

Ruta: regulation of organelle organization (Página 3 de 4)

Fuente: GO:BP | ID: GO:0033043 | Genes: 78 | p-valor ruta: 1.53e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7

Ruta: regulation of organelle organization (Página 4 de 4)

Fuente: GO:BP | ID: GO:0033043 | Genes: 78 | p-valor ruta: 1.53e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: DNA integrity checkpoint signaling (Página 1 de 2)

Fuente: GO:BP | ID: GO:0031570 | Genes: 28 | p-valor ruta: 5.36e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5

Ruta: DNA integrity checkpoint signaling (Página 2 de 2)

Fuente: GO:BP | ID: GO:0031570 | Genes: 28 | p-valor ruta: 5.36e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: nuclear DNA replication

Fuente: GO:BP | ID: GO:0033260 | Genes: 19 | p-valor ruta: 5.6e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: positive regulation of chromosome segregation

Fuente: GO:BP | ID: GO:0051984 | Genes: 17 | p-valor ruta: 9.44e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: meiotic chromosome segregation

Fuente: GO:BP | ID: GO:0045132 | Genes: 25 | p-valor ruta: 2.7e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: positive regulation of cell cycle phase transition (Página 1 de 2)

Fuente: GO:BP | ID: GO:1901989 | Genes: 26 | p-valor ruta: 1.64e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6

Ruta: positive regulation of cell cycle phase transition (Página 2 de 2)

Fuente: GO:BP | ID: GO:1901989 | Genes: 26 | p-valor ruta: 1.64e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: regulation of cell cycle checkpoint

Fuente: GO:BP | ID: GO:1901976 | Genes: 19 | p-valor ruta: 2.33e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: regulation of G2/M transition of mitotic cell cycle

Fuente: GO:BP | ID: GO:0010389 | Genes: 25 | p-valor ruta: 2.98e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8

Ruta: regulation of cell cycle G2/M phase transition (Página 1 de 2)

Fuente: GO:BP | ID: GO:1902749 | Genes: 26 | p-valor ruta: 4.2e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1

Ruta: regulation of cell cycle G2/M phase transition (Página 2 de 2)

Fuente: GO:BP | ID: GO:1902749 | Genes: 26 | p-valor ruta: 4.2e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8

Ruta: cytoskeleton organization (Página 1 de 4)

Fuente: GO:BP | ID: GO:0007010 | Genes: 87 | p-valor ruta: 4.53e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6

Ruta: cytoskeleton organization (Página 2 de 4)

Fuente: GO:BP | ID: GO:0007010 | Genes: 87 | p-valor ruta: 4.53e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5

Ruta: cytoskeleton organization (Página 3 de 4)

Fuente: GO:BP | ID: GO:0007010 | Genes: 87 | p-valor ruta: 4.53e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9

Ruta: cytoskeleton organization (Página 4 de 4)

Fuente: GO:BP | ID: GO:0007010 | Genes: 87 | p-valor ruta: 4.53e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: DNA-templated DNA replication maintenance of fidelity

Fuente: GO:BP | ID: GO:0045005 | Genes: 20 | p-valor ruta: 8.71e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: positive regulation of chromosome separation

Fuente: GO:BP | ID: GO:1905820 | Genes: 16 | p-valor ruta: 2.43e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: meiosis I cell cycle process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0061982 | Genes: 27 | p-valor ruta: 3.79e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6

Ruta: meiosis I cell cycle process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0061982 | Genes: 27 | p-valor ruta: 3.79e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: mitotic metaphase chromosome alignment

Fuente: GO:BP | ID: GO:0007080 | Genes: 20 | p-valor ruta: 3.92e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1

Ruta: positive regulation of mitotic cell cycle phase transition

Fuente: GO:BP | ID: GO:1901992 | Genes: 23 | p-valor ruta: 4.12e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDC45	DOWN	-2.059	8.54e-13	175.9
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: response to stress (Página 1 de 7)

Fuente: GO:BP | ID: GO:0006950 | Genes: 152 | p-valor ruta: 7.08e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1

Ruta: response to stress (Página 2 de 7)

Fuente: GO:BP | ID: GO:0006950 | Genes: 152 | p-valor ruta: 7.08e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG0000010438	PRSS3	UP	1.837	1.56e-15	633.6
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000120448	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6

Ruta: response to stress (Página 3 de 7)

Fuente: GO:BP | ID: GO:0006950 | Genes: 152 | p-valor ruta: 7.08e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000147697	GSDMC	UP	2.564	1.66e-10	130.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2

Ruta: response to stress (Página 4 de 7)

Fuente: GO:BP | ID: GO:0006950 | Genes: 152 | p-valor ruta: 7.08e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2

Ruta: response to stress (Página 5 de 7)

Fuente: GO:BP | ID: GO:0006950 | Genes: 152 | p-valor ruta: 7.08e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1

Ruta: response to stress (Página 6 de 7)

Fuente: GO:BP | ID: GO:0006950 | Genes: 152 | p-valor ruta: 7.08e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: response to stress (Página 7 de 7)

Fuente: GO:BP | ID: GO:0006950 | Genes: 152 | p-valor ruta: 7.08e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: positive regulation of mitotic cell cycle

Fuente: GO:BP | ID: GO:0045931 | Genes: 25 | p-valor ruta: 2.28e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: regulation of spindle checkpoint

Fuente: GO:BP | ID: GO:0090231 | Genes: 14 | p-valor ruta: 5.69e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: regulation of DNA replication

Fuente: GO:BP | ID: GO:0006275 | Genes: 24 | p-valor ruta: 1.38e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: establishment of organelle localization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051656 | Genes: 44 | p-valor ruta: 3.92e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDDA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000146670	CDDA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1

Ruta: establishment of organelle localization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051656 | Genes: 44 | p-valor ruta: 3.92e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7

Ruta: meiosis I

Fuente: GO:BP | ID: GO:0007127 | Genes: 24 | p-valor ruta: 1.68e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: regulation of mitotic cell cycle spindle assembly checkpoint

Fuente: GO:BP | ID: GO:0090266 | Genes: 13 | p-valor ruta: 1.71e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: regulation of mitotic spindle checkpoint

Fuente: GO:BP | ID: GO:1903504 | Genes: 13 | p-valor ruta: 1.71e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: DNA strand elongation involved in DNA replication

Fuente: GO:BP | ID: GO:0006271 | Genes: 11 | p-valor ruta: 3.02e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: attachment of mitotic spindle microtubules to kinetochore

Fuente: GO:BP | ID: GO:0051315 | Genes: 13 | p-valor ruta: 3.5e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: G1/S transition of mitotic cell cycle (Página 1 de 2)

Fuente: GO:BP | ID: GO:0000082 | Genes: 28 | p-valor ruta: 5.69e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7

Ruta: G1/S transition of mitotic cell cycle (Página 2 de 2)

Fuente: GO:BP | ID: GO:0000082 | Genes: 28 | p-valor ruta: 5.69e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8

Ruta: cellular component organization (Página 1 de 10)

Fuente: GO:BP | ID: GO:0016043 | Genes: 238 | p-valor ruta: 6.07e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0

Ruta: cellular component organization (Página 2 de 10)

Fuente: GO:BP | ID: GO:0016043 | Genes: 238 | p-valor ruta: 6.07e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG0000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG0000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG0000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG0000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG0000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG0000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG0000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG0000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG0000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG0000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG0000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3

Ruta: cellular component organization (Página 3 de 10)

Fuente: GO:BP | ID: GO:0016043 | Genes: 238 | p-valor ruta: 6.07e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3

Ruta: cellular component organization (Página 4 de 10)

Fuente: GO:BP | ID: GO:0016043 | Genes: 238 | p-valor ruta: 6.07e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1

Ruta: cellular component organization (Página 5 de 10)

Fuente: GO:BP | ID: GO:0016043 | Genes: 238 | p-valor ruta: 6.07e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3

Ruta: cellular component organization (Página 6 de 10)

Fuente: GO:BP | ID: GO:0016043 | Genes: 238 | p-valor ruta: 6.07e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000129038	LOXL1	UP	1.441	3.55e-07	153.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000146410	MTFR2	DOWN	-1.746	5.92e-06	145.6

Ruta: cellular component organization (Página 7 de 10)

Fuente: GO:BP | ID: GO:0016043 | Genes: 238 | p-valor ruta: 6.07e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2

Ruta: cellular component organization (Página 8 de 10)

Fuente: GO:BP | ID: GO:0016043 | Genes: 238 | p-valor ruta: 6.07e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000166881	NEMP1	DOWN	-2.208	2.92e-04	75.0
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3

Ruta: cellular component organization (Página 9 de 10)

Fuente: GO:BP | ID: GO:0016043 | Genes: 238 | p-valor ruta: 6.07e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG0000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000181652	ATG9B	UP	1.052	9.34e-03	97.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000172197	MBOAT1	DOWN	-1.396	1.61e-02	54.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8

Ruta: cellular component organization (Página 10 de 10)

Fuente: GO:BP | ID: GO:0016043 | Genes: 238 | p-valor ruta: 6.07e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000151572	ANO4	UP	1.682	2.37e-02	39.8
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000281344	HELLPAR	DOWN	-1.328	3.14e-02	46.9
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: negative regulation of organelle organization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0010639 | Genes: 36 | p-valor ruta: 6.13e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7

Ruta: negative regulation of organelle organization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0010639 | Genes: 36 | p-valor ruta: 6.13e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG0000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7

Ruta: DNA damage checkpoint signaling

Fuente: GO:BP | ID: GO:0000077 | Genes: 22 | p-valor ruta: 7.47e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: cellular response to stimulus (Página 1 de 9)

Fuente: GO:BP | ID: GO:0051716 | Genes: 221 | p-valor ruta: 9.67e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2

Ruta: cellular response to stimulus (Página 2 de 9)

Fuente: GO:BP | ID: GO:0051716 | Genes: 221 | p-valor ruta: 9.67e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2

Ruta: cellular response to stimulus (Página 3 de 9)

Fuente: GO:BP | ID: GO:0051716 | Genes: 221 | p-valor ruta: 9.67e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDDA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8

Ruta: cellular response to stimulus (Página 4 de 9)

Fuente: GO:BP | ID: GO:0051716 | Genes: 221 | p-valor ruta: 9.67e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164237	CMBL	UP	1.794	1.17e-09	471.4
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9

Ruta: cellular response to stimulus (Página 5 de 9)

Fuente: GO:BP | ID: GO:0051716 | Genes: 221 | p-valor ruta: 9.67e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8

Ruta: cellular response to stimulus (Página 6 de 9)

Fuente: GO:BP | ID: GO:0051716 | Genes: 221 | p-valor ruta: 9.67e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4

Ruta: cellular response to stimulus (Página 7 de 9)

Fuente: GO:BP | ID: GO:0051716 | Genes: 221 | p-valor ruta: 9.67e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000109452	INPP4B	UP	1.158	4.20e-04	146.5
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8

Ruta: cellular response to stimulus (Página 8 de 9)

Fuente: GO:BP | ID: GO:0051716 | Genes: 221 | p-valor ruta: 9.67e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG0000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: cellular response to stimulus (Página 9 de 9)

Fuente: GO:BP | ID: GO:0051716 | Genes: 221 | p-valor ruta: 9.67e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000100100	PIK3IP1	UP	1.413	8.65e-03	102.0
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000166831	RBPMS2	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000250510	GPR162	UP	1.311	2.49e-02	51.7
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: kinetochore organization

Fuente: GO:BP | ID: GO:0051383 | Genes: 12 | p-valor ruta: 1.12e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9

Ruta: organelle assembly (Página 1 de 3)

Fuente: GO:BP | ID: GO:0070925 | Genes: 63 | p-valor ruta: 1.3e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0

Ruta: organelle assembly (Página 2 de 3)

Fuente: GO:BP | ID: GO:0070925 | Genes: 63 | p-valor ruta: 1.3e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2

Ruta: organelle assembly (Página 3 de 3)

Fuente: GO:BP | ID: GO:0070925 | Genes: 63 | p-valor ruta: 1.3e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG0000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000181652	ATG9B	UP	1.052	9.34e-03	97.0
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5

Ruta: organelle localization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051640 | Genes: 47 | p-valor ruta: 2.05e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0

Ruta: organelle localization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051640 | Genes: 47 | p-valor ruta: 2.05e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7

Ruta: replication fork processing

Fuente: GO:BP | ID: GO:0031297 | Genes: 16 | p-valor ruta: 2.07e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: cell cycle G1/S phase transition (Página 1 de 2)

Fuente: GO:BP | ID: GO:0044843 | Genes: 29 | p-valor ruta: 2.16e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9

Ruta: cell cycle G1/S phase transition (Página 2 de 2)

Fuente: GO:BP | ID: GO:0044843 | Genes: 29 | p-valor ruta: 2.16e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8

Ruta: cellular component organization or biogenesis (Página 1 de 10)

Fuente: GO:BP | ID: GO:0071840 | Genes: 240 | p-valor ruta: 3.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0

Ruta: cellular component organization or biogenesis (Página 2 de 10)

Fuente: GO:BP | ID: GO:0071840 | Genes: 240 | p-valor ruta: 3.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG0000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG0000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG0000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG0000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG0000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG0000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG0000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG0000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG0000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG0000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG0000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3

Ruta: cellular component organization or biogenesis (Página 3 de 10)

Fuente: GO:BP | ID: GO:0071840 | Genes: 240 | p-valor ruta: 3.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3

Ruta: cellular component organization or biogenesis (Página 4 de 10)

Fuente: GO:BP | ID: GO:0071840 | Genes: 240 | p-valor ruta: 3.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1

Ruta: cellular component organization or biogenesis (Página 5 de 10)

Fuente: GO:BP | ID: GO:0071840 | Genes: 240 | p-valor ruta: 3.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3

Ruta: cellular component organization or biogenesis (Página 6 de 10)

Fuente: GO:BP | ID: GO:0071840 | Genes: 240 | p-valor ruta: 3.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000129038	LOXL1	UP	1.441	3.55e-07	153.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000146410	MTFR2	DOWN	-1.746	5.92e-06	145.6

Ruta: cellular component organization or biogenesis (Página 7 de 10)

Fuente: GO:BP | ID: GO:0071840 | Genes: 240 | p-valor ruta: 3.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2

Ruta: cellular component organization or biogenesis (Página 8 de 10)

Fuente: GO:BP | ID: GO:0071840 | Genes: 240 | p-valor ruta: 3.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000166881	NEMP1	DOWN	-2.208	2.92e-04	75.0
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1

Ruta: cellular component organization or biogenesis (Página 9 de 10)

Fuente: GO:BP | ID: GO:0071840 | Genes: 240 | p-valor ruta: 3.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000181652	ATG9B	UP	1.052	9.34e-03	97.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000172197	MBOAT1	DOWN	-1.396	1.61e-02	54.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6

Ruta: cellular component organization or biogenesis (Página 10 de 10)

Fuente: GO:BP | ID: GO:0071840 | Genes: 240 | p-valor ruta: 3.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000151572	ANO4	UP	1.682	2.37e-02	39.8
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000281344	HELLPAR	DOWN	-1.328	3.14e-02	46.9
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: chromosome condensation

Fuente: GO:BP | ID: GO:0030261 | Genes: 15 | p-valor ruta: 5.87e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: centrosome cycle

Fuente: GO:BP | ID: GO:0007098 | Genes: 23 | p-valor ruta: 6.33e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: protein localization to chromosome

Fuente: GO:BP | ID: GO:0034502 | Genes: 22 | p-valor ruta: 6.81e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3

Ruta: mitotic spindle assembly

Fuente: GO:BP | ID: GO:0090307 | Genes: 18 | p-valor ruta: 8.26e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: regulation of DNA-templated DNA replication

Fuente: GO:BP | ID: GO:0090329 | Genes: 14 | p-valor ruta: 2.28e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8

Ruta: sexual reproduction (Página 1 de 3)

Fuente: GO:BP | ID: GO:0019953 | Genes: 63 | p-valor ruta: 3.39e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6

Ruta: sexual reproduction (Página 2 de 3)

Fuente: GO:BP | ID: GO:0019953 | Genes: 63 | p-valor ruta: 3.39e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6

Ruta: sexual reproduction (Página 3 de 3)

Fuente: GO:BP | ID: GO:0019953 | Genes: 63 | p-valor ruta: 3.39e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: reproductive process (Página 1 de 4)

Fuente: GO:BP | ID: GO:0022414 | Genes: 78 | p-valor ruta: 4.45e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7

Ruta: reproductive process (Página 2 de 4)

Fuente: GO:BP | ID: GO:0022414 | Genes: 78 | p-valor ruta: 4.45e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164104	HMGFB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3

Ruta: reproductive process (Página 3 de 4)

Fuente: GO:BP | ID: GO:0022414 | Genes: 78 | p-valor ruta: 4.45e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: reproductive process (Página 4 de 4)

Fuente: GO:BP | ID: GO:0022414 | Genes: 78 | p-valor ruta: 4.45e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: microtubule organizing center organization

Fuente: GO:BP | ID: GO:0031023 | Genes: 23 | p-valor ruta: 4.61e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: protein–DNA complex assembly (Página 1 de 2)

Fuente: GO:BP | ID: GO:0065004 | Genes: 28 | p-valor ruta: 5.59e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2

Ruta: protein–DNA complex assembly (Página 2 de 2)

Fuente: GO:BP | ID: GO:0065004 | Genes: 28 | p-valor ruta: 5.59e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: signal transduction in response to DNA damage

Fuente: GO:BP | ID: GO:0042770 | Genes: 24 | p-valor ruta: 7.82e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: mitotic DNA integrity checkpoint signaling

Fuente: GO:BP | ID: GO:0044774 | Genes: 17 | p-valor ruta: 8.34e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: centromere complex assembly

Fuente: GO:BP | ID: GO:0034508 | Genes: 12 | p-valor ruta: 1.71e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9

Ruta: mitotic DNA replication

Fuente: GO:BP | ID: GO:1902969 | Genes: 10 | p-valor ruta: 2.17e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG0000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG0000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG0000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG0000093009	CDC45	DOWN	-1.677	3.83e-04	201.5

Ruta: regulation of attachment of spindle microtubules to kinetochore

Fuente: GO:BP | ID: GO:0051988 | Genes: 11 | p-valor ruta: 2.6e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: regulation of cytokinesis

Fuente: GO:BP | ID: GO:0032465 | Genes: 18 | p-valor ruta: 4.32e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4

Ruta: protein–DNA complex organization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0071824 | Genes: 28 | p-valor ruta: 4.59e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2

Ruta: protein–DNA complex organization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0071824 | Genes: 28 | p-valor ruta: 4.59e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: DNA biosynthetic process

Fuente: GO:BP | ID: GO:0071897 | Genes: 23 | p-valor ruta: 5.96e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5

Ruta: cytokinesis

Fuente: GO:BP | ID: GO:0000910 | Genes: 24 | p-valor ruta: 8.11e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4

Ruta: spindle elongation

Fuente: GO:BP | ID: GO:0051231 | Genes: 9 | p-valor ruta: 1.23e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: spindle midzone assembly

Fuente: GO:BP | ID: GO:0051255 | Genes: 9 | p-valor ruta: 1.23e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: female meiotic nuclear division

Fuente: GO:BP | ID: GO:0007143 | Genes: 13 | p-valor ruta: 1.28e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7

Ruta: interstrand cross-link repair

Fuente: GO:BP | ID: GO:0036297 | Genes: 13 | p-valor ruta: 1.28e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: DNA replication checkpoint signaling

Fuente: GO:BP | ID: GO:0000076 | Genes: 10 | p-valor ruta: 1.96e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: regulation of cellular component organization (Página 1 de 4)

Fuente: GO:BP | ID: GO:0051128 | Genes: 97 | p-valor ruta: 2.91e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0

Ruta: regulation of cellular component organization (Página 2 de 4)

Fuente: GO:BP | ID: GO:0051128 | Genes: 97 | p-valor ruta: 2.91e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9

Ruta: regulation of cellular component organization (Página 3 de 4)

Fuente: GO:BP | ID: GO:0051128 | Genes: 97 | p-valor ruta: 2.91e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: regulation of cellular component organization (Página 4 de 4)

Fuente: GO:BP | ID: GO:0051128 | Genes: 97 | p-valor ruta: 2.91e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG0000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000172197	MBOAT1	DOWN	-1.396	1.61e-02	54.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: meiotic cell cycle phase transition

Fuente: GO:BP | ID: GO:0044771 | Genes: 9 | p-valor ruta: 3.02e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1

Ruta: regulation of cell division

Fuente: GO:BP | ID: GO:0051302 | Genes: 23 | p-valor ruta: 3.98e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8

Ruta: DNA strand elongation (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-69190 | Genes: 33 | p-valor ruta: 5.32e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8

Ruta: DNA strand elongation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0022616 | Genes: 33 | p-valor ruta: 5.32e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: negative regulation of DNA metabolic process

Fuente: GO:BP | ID: GO:0051053 | Genes: 20 | p-valor ruta: 5.4e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: mitotic spindle midzone assembly

Fuente: GO:BP | ID: GO:0051256 | Genes: 8 | p-valor ruta: 5.55e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: positive regulation of DNA metabolic process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051054 | Genes: 28 | p-valor ruta: 6.09e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5

Ruta: positive regulation of DNA metabolic process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051054 | Genes: 28 | p-valor ruta: 6.09e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: mitotic cytokinesis

Fuente: GO:BP | ID: GO:0000281 | Genes: 17 | p-valor ruta: 6.44e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4

Ruta: mitotic DNA damage checkpoint signaling

Fuente: GO:BP | ID: GO:0044773 | Genes: 15 | p-valor ruta: 7.92e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: response to radiation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0009314 | Genes: 34 | p-valor ruta: 1.14e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3

Ruta: response to radiation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0009314 | Genes: 34 | p-valor ruta: 1.14e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000074621	SLC24A1	UP	1.424	2.09e-04	124.7
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: positive regulation of chromosome condensation

Fuente: GO:BP | ID: GO:1905821 | Genes: 7 | p-valor ruta: 1.47e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: mitotic spindle elongation

Fuente: GO:BP | ID: GO:0000022 | Genes: 8 | p-valor ruta: 1.64e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: regulation of G1/S transition of mitotic cell cycle

Fuente: GO:BP | ID: GO:2000045 | Genes: 20 | p-valor ruta: 2.28e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8

Ruta: positive regulation of spindle checkpoint

Fuente: GO:BP | ID: GO:0090232 | Genes: 8 | p-valor ruta: 4.19e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: chromosome organization involved in meiotic cell cycle

Fuente: GO:BP | ID: GO:0070192 | Genes: 14 | p-valor ruta: 4.83e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: DNA synthesis involved in DNA repair

Fuente: GO:BP | ID: GO:0000731 | Genes: 12 | p-valor ruta: 5.37e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1

Ruta: mitotic G2/M transition checkpoint

Fuente: GO:BP | ID: GO:0044818 | Genes: 13 | p-valor ruta: 5.79e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG0000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG0000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG0000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8

Ruta: regulation of cell cycle G1/S phase transition

Fuente: GO:BP | ID: GO:1902806 | Genes: 21 | p-valor ruta: 5.99e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8

Ruta: response to ionizing radiation

Fuente: GO:BP | ID: GO:0010212 | Genes: 19 | p-valor ruta: 6.21e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: homologous recombination

Fuente: GO:BP | ID: GO:0035825 | Genes: 14 | p-valor ruta: 7.42e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: negative regulation of G2/M transition of mitotic cell cycle

Fuente: GO:BP | ID: GO:0010972 | Genes: 14 | p-valor ruta: 9.14e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG0000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG0000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8

Ruta: negative regulation of cell cycle G2/M phase transition

Fuente: GO:BP | ID: GO:1902750 | Genes: 14 | p-valor ruta: 1.37e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8

Ruta: positive regulation of mitotic sister chromatid separation

Fuente: GO:BP | ID: GO:1901970 | Genes: 9 | p-valor ruta: 1.6e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: regulation of DNA-templated DNA replication initiation

Fuente: GO:BP | ID: GO:0030174 | Genes: 8 | p-valor ruta: 2.02e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1

Ruta: positive regulation of cytokinesis

Fuente: GO:BP | ID: GO:0032467 | Genes: 12 | p-valor ruta: 2.78e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4

Ruta: positive regulation of chromosome organization

Fuente: GO:BP | ID: GO:2001252 | Genes: 16 | p-valor ruta: 3.51e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: positive regulation of cell cycle G2/M phase transition

Fuente: GO:BP | ID: GO:1902751 | Genes: 10 | p-valor ruta: 3.89e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1

Ruta: cytoskeleton–dependent cytokinesis

Fuente: GO:BP | ID: GO:0061640 | Genes: 17 | p-valor ruta: 5.21e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4

Ruta: negative regulation of cellular component organization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051129 | Genes: 41 | p-valor ruta: 5.76e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5

Ruta: negative regulation of cellular component organization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051129 | Genes: 41 | p-valor ruta: 5.76e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: chromatin organization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0006325 | Genes: 47 | p-valor ruta: 6.38e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5

Ruta: chromatin organization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0006325 | Genes: 47 | p-valor ruta: 6.38e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: positive regulation of cellular process (Página 1 de 7)

Fuente: GO:BP | ID: GO:0048522 | Genes: 172 | p-valor ruta: 6.72e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4

Ruta: positive regulation of cellular process (Página 2 de 7)

Fuente: GO:BP | ID: GO:0048522 | Genes: 172 | p-valor ruta: 6.72e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000058085	LAMC2	UP	1.879	2.12e-17	204.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2

Ruta: positive regulation of cellular process (Página 3 de 7)

Fuente: GO:BP | ID: GO:0048522 | Genes: 172 | p-valor ruta: 6.72e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG0000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG0000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG0000164104	HMG2B	DOWN	-1.572	1.72e-11	2905.5
ENSG0000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG0000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG0000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG0000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG0000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG0000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG0000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG0000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4
ENSG0000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG0000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG0000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG0000122861	PLAU	UP	1.083	3.46e-09	730.9

Ruta: positive regulation of cellular process (Página 4 de 7)

Fuente: GO:BP | ID: GO:0048522 | Genes: 172 | p-valor ruta: 6.72e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9

Ruta: positive regulation of cellular process (Página 5 de 7)

Fuente: GO:BP | ID: GO:0048522 | Genes: 172 | p-valor ruta: 6.72e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG0000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2

Ruta: positive regulation of cellular process (Página 6 de 7)

Fuente: GO:BP | ID: GO:0048522 | Genes: 172 | p-valor ruta: 6.72e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG0000074621	SLC24A1	UP	1.424	2.09e-04	124.7
ENSG0000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG0000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG0000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG0000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG0000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG0000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG0000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG0000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG0000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG0000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG0000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG0000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG0000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG0000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG0000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG0000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG0000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG0000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG0000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: positive regulation of cellular process (Página 7 de 7)

Fuente: GO:BP | ID: GO:0048522 | Genes: 172 | p-valor ruta: 6.72e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000166831	RBPM32	DOWN	-1.538	1.19e-02	49.2
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000196247	ZNF107	DOWN	-1.028	4.60e-02	77.9

Ruta: response to stimulus (Página 1 de 10)

Fuente: GO:BP | ID: GO:0050896 | Genes: 235 | p-valor ruta: 7.22e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2

Ruta: response to stimulus (Página 2 de 10)

Fuente: GO:BP | ID: GO:0050896 | Genes: 235 | p-valor ruta: 7.22e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG0000010438	PRSS3	UP	1.837	1.56e-15	633.6
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6

Ruta: response to stimulus (Página 3 de 10)

Fuente: GO:BP | ID: GO:0050896 | Genes: 235 | p-valor ruta: 7.22e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDC45	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3

Ruta: response to stimulus (Página 4 de 10)

Fuente: GO:BP | ID: GO:0050896 | Genes: 235 | p-valor ruta: 7.22e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000147697	GSDMC	UP	2.564	1.66e-10	130.4
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164237	CMLB	UP	1.794	1.17e-09	471.4
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9

Ruta: response to stimulus (Página 5 de 10)

Fuente: GO:BP | ID: GO:0050896 | Genes: 235 | p-valor ruta: 7.22e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG0000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG0000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG0000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG0000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG0000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG0000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG0000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG0000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG0000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG0000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG0000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG0000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG0000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG0000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG0000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG0000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG0000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG0000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3

Ruta: response to stimulus (Página 6 de 10)

Fuente: GO:BP | ID: GO:0050896 | Genes: 235 | p-valor ruta: 7.22e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG0000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000129038	LOXL1	UP	1.441	3.55e-07	153.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: response to stimulus (Página 7 de 10)

Fuente: GO:BP | ID: GO:0050896 | Genes: 235 | p-valor ruta: 7.22e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000074621	SLC24A1	UP	1.424	2.09e-04	124.7
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0

Ruta: response to stimulus (Página 8 de 10)

Fuente: GO:BP | ID: GO:0050896 | Genes: 235 | p-valor ruta: 7.22e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000109452	INPP4B	UP	1.158	4.20e-04	146.5
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0

Ruta: response to stimulus (Página 9 de 10)

Fuente: GO:BP | ID: GO:0050896 | Genes: 235 | p-valor ruta: 7.22e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG0000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000100100	PIK3IP1	UP	1.413	8.65e-03	102.0
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000166831	RBPMS2	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6

Ruta: response to stimulus (Página 10 de 10)

Fuente: GO:BP | ID: GO:0050896 | Genes: 235 | p-valor ruta: 7.22e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000250510	GPR162	UP	1.311	2.49e-02	51.7
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: regulation of DNA recombination

Fuente: GO:BP | ID: GO:0000018 | Genes: 18 | p-valor ruta: 7.28e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: kinetochore assembly

Fuente: GO:BP | ID: GO:0051382 | Genes: 8 | p-valor ruta: 7.39e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9

Ruta: intracellular signal transduction (Página 1 de 5)

Fuente: GO:BP | ID: GO:0035556 | Genes: 104 | p-valor ruta: 7.77e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8

Ruta: intracellular signal transduction (Página 2 de 5)

Fuente: GO:BP | ID: GO:0035556 | Genes: 104 | p-valor ruta: 7.77e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG0000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG0000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG0000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG0000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG0000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG0000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG0000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG0000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG0000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG0000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4

Ruta: intracellular signal transduction (Página 3 de 5)

Fuente: GO:BP | ID: GO:0035556 | Genes: 104 | p-valor ruta: 7.77e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1

Ruta: intracellular signal transduction (Página 4 de 5)

Fuente: GO:BP | ID: GO:0035556 | Genes: 104 | p-valor ruta: 7.77e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000100100	PIK3IP1	UP	1.413	8.65e-03	102.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8

Ruta: intracellular signal transduction (Página 5 de 5)

Fuente: GO:BP | ID: GO:0035556 | Genes: 104 | p-valor ruta: 7.77e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5

Ruta: regulation of cellular process (Página 1 de 12)

Fuente: GO:BP | ID: GO:0050794 | Genes: 290 | p-valor ruta: 8e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1

Ruta: regulation of cellular process (Página 2 de 12)

Fuente: GO:BP | ID: GO:0050794 | Genes: 290 | p-valor ruta: 8e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6

Ruta: regulation of cellular process (Página 3 de 12)

Fuente: GO:BP | ID: GO:0050794 | Genes: 290 | p-valor ruta: 8e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG0000058085	LAMC2	UP	1.879	2.12e-17	204.8
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000137310	TCF19	DOWN	-1.639	1.12e-14	547.9
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8

Ruta: regulation of cellular process (Página 4 de 12)

Fuente: GO:BP | ID: GO:0050794 | Genes: 290 | p-valor ruta: 8e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0

Ruta: regulation of cellular process (Página 5 de 12)

Fuente: GO:BP | ID: GO:0050794 | Genes: 290 | p-valor ruta: 8e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000068489	PRR11	DOWN	-1.033	9.90e-11	1510.0
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4

Ruta: regulation of cellular process (Página 6 de 12)

Fuente: GO:BP | ID: GO:0050794 | Genes: 290 | p-valor ruta: 8e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1

Ruta: regulation of cellular process (Página 7 de 12)

Fuente: GO:BP | ID: GO:0050794 | Genes: 290 | p-valor ruta: 8e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0

Ruta: regulation of cellular process (Página 8 de 12)

Fuente: GO:BP | ID: GO:0050794 | Genes: 290 | p-valor ruta: 8e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG0000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG0000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG0000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG0000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG0000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG0000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG0000132017	DCAF15	DOWN	-1.243	1.30e-05	122.0
ENSG0000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG0000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG0000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG0000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG0000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG0000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG0000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG0000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG0000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG0000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG0000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG0000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG0000120539	MASTL	DOWN	-1.817	7.79e-05	126.7

Ruta: regulation of cellular process (Página 9 de 12)

Fuente: GO:BP | ID: GO:0050794 | Genes: 290 | p-valor ruta: 8e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000160352	ZNF714	DOWN	-1.576	1.17e-04	120.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000160180	TFF3	UP	1.708	1.97e-04	44.6
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000074621	SLC24A1	UP	1.424	2.09e-04	124.7
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000109452	INPP4B	UP	1.158	4.20e-04	146.5
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5

Ruta: regulation of cellular process (Página 10 de 12)

Fuente: GO:BP | ID: GO:0050794 | Genes: 290 | p-valor ruta: 8e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG0000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG0000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2

Ruta: regulation of cellular process (Página 11 de 12)

Fuente: GO:BP | ID: GO:0050794 | Genes: 290 | p-valor ruta: 8e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000100100	PIK3IP1	UP	1.413	8.65e-03	102.0
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000166831	RBPM2	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000172197	MBOAT1	DOWN	-1.396	1.61e-02	54.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: regulation of cellular process (Página 12 de 12)

Fuente: GO:BP | ID: GO:0050794 | Genes: 290 | p-valor ruta: 8e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000250510	GPR162	UP	1.311	2.49e-02	51.7
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000196247	ZNF107	DOWN	-1.028	4.60e-02	77.9
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: regulation of microtubule-based process

Fuente: GO:BP | ID: GO:0032886 | Genes: 24 | p-valor ruta: 8.47e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8

Ruta: regulation of meiotic cell cycle

Fuente: GO:BP | ID: GO:0051445 | Genes: 13 | p-valor ruta: 9.97e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2

Ruta: double-strand break repair via break-induced replication

Fuente: GO:BP | ID: GO:0000727 | Genes: 7 | p-valor ruta: 1.36e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5

Ruta: positive regulation of mitotic cell cycle spindle assembly checkpoint

Fuente: GO:BP | ID: GO:0090267 | Genes: 7 | p-valor ruta: 1.36e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: regulation of chromosome condensation

Fuente: GO:BP | ID: GO:0060623 | Genes: 7 | p-valor ruta: 1.36e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: sister chromatid cohesion

Fuente: GO:BP | ID: GO:0007062 | Genes: 12 | p-valor ruta: 1.44e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0

Ruta: postreplication repair

Fuente: GO:BP | ID: GO:0006301 | Genes: 10 | p-valor ruta: 2.05e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1

Ruta: cellular response to ionizing radiation

Fuente: GO:BP | ID: GO:0071479 | Genes: 13 | p-valor ruta: 2.1e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: mitotic chromosome condensation

Fuente: GO:BP | ID: GO:0007076 | Genes: 8 | p-valor ruta: 2.22e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: positive regulation of cell cycle checkpoint

Fuente: GO:BP | ID: GO:1901978 | Genes: 8 | p-valor ruta: 2.22e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: centrosome duplication

Fuente: GO:BP | ID: GO:0051298 | Genes: 13 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: positive regulation of biological process (Página 1 de 8)

Fuente: GO:BP | ID: GO:0048518 | Genes: 177 | p-valor ruta: 3.06e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4

Ruta: positive regulation of biological process (Página 2 de 8)

Fuente: GO:BP | ID: GO:0048518 | Genes: 177 | p-valor ruta: 3.06e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000058085	LAMC2	UP	1.879	2.12e-17	204.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDC45	DOWN	-2.059	8.54e-13	175.9

Ruta: positive regulation of biological process (Página 3 de 8)

Fuente: GO:BP | ID: GO:0048518 | Genes: 177 | p-valor ruta: 3.06e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG0000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG0000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG0000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG0000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG0000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG0000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG0000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG0000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG0000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG0000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG0000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG0000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG0000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4
ENSG0000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG0000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG0000114346	ECT2	DOWN	-1.276	2.96e-09	617.4

Ruta: positive regulation of biological process (Página 4 de 8)

Fuente: GO:BP | ID: GO:0048518 | Genes: 177 | p-valor ruta: 3.06e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG0000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3

Ruta: positive regulation of biological process (Página 5 de 8)

Fuente: GO:BP | ID: GO:0048518 | Genes: 177 | p-valor ruta: 3.06e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG0000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8

Ruta: positive regulation of biological process (Página 6 de 8)

Fuente: GO:BP | ID: GO:0048518 | Genes: 177 | p-valor ruta: 3.06e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000074621	SLC24A1	UP	1.424	2.09e-04	124.7
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7

Ruta: positive regulation of biological process (Página 7 de 8)

Fuente: GO:BP | ID: GO:0048518 | Genes: 177 | p-valor ruta: 3.06e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000166831	RBPM2	DOWN	-1.538	1.19e-02	49.2
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2

Ruta: positive regulation of biological process (Página 8 de 8)

Fuente: GO:BP | ID: GO:0048518 | Genes: 177 | p-valor ruta: 3.06e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166086	JAM3	DOWN	-1.293	4.5e-02	50.7
ENSG00000196247	ZNF107	DOWN	-1.028	4.6e-02	77.9

Ruta: positive regulation of G2/M transition of mitotic cell cycle

Fuente: GO:BP | ID: GO:0010971 | Genes: 9 | p-valor ruta: 3.34e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3

Ruta: regulation of cellular response to stress (Página 1 de 2)

Fuente: GO:BP | ID: GO:0080135 | Genes: 33 | p-valor ruta: 4.45e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1

Ruta: regulation of cellular response to stress (Página 2 de 2)

Fuente: GO:BP | ID: GO:0080135 | Genes: 33 | p-valor ruta: 4.45e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG0000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG0000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG0000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG0000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG0000133863	TEX15	DOWN	-1.716	1.77e-02	39.6

Ruta: chromatin remodeling (Página 1 de 2)

Fuente: GO:BP | ID: GO:0006338 | Genes: 40 | p-valor ruta: 5.19e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9

Ruta: chromatin remodeling (Página 2 de 2)

Fuente: GO:BP | ID: GO:0006338 | Genes: 40 | p-valor ruta: 5.19e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: cellular response to radiation

Fuente: GO:BP | ID: GO:0071478 | Genes: 19 | p-valor ruta: 5.19e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: negative regulation of DNA recombination

Fuente: GO:BP | ID: GO:0045910 | Genes: 11 | p-valor ruta: 5.64e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: regulation of DNA repair

Fuente: GO:BP | ID: GO:0006282 | Genes: 21 | p-valor ruta: 5.81e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6

Ruta: regulation of microtubule cytoskeleton organization

Fuente: GO:BP | ID: GO:0070507 | Genes: 18 | p-valor ruta: 6.12e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8

Ruta: telomere maintenance

Fuente: GO:BP | ID: GO:0000723 | Genes: 18 | p-valor ruta: 6.12e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: positive regulation of DNA-directed DNA polymerase activity

Fuente: GO:BP | ID: GO:1900264 | Genes: 6 | p-valor ruta: 7.88e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: protein localization to chromosome, centromeric region

Fuente: GO:BP | ID: GO:0071459 | Genes: 10 | p-valor ruta: 8.29e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3

Ruta: homologous chromosome segregation

Fuente: GO:BP | ID: GO:0045143 | Genes: 12 | p-valor ruta: 1.02e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: meiotic spindle assembly

Fuente: GO:BP | ID: GO:0090306 | Genes: 7 | p-valor ruta: 1.05e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1

Ruta: regulation of biological process (Página 1 de 12)

Fuente: GO:BP | ID: GO:0050789 | Genes: 293 | p-valor ruta: 1.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1

Ruta: regulation of biological process (Página 2 de 12)

Fuente: GO:BP | ID: GO:0050789 | Genes: 293 | p-valor ruta: 1.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8

Ruta: regulation of biological process (Página 3 de 12)

Fuente: GO:BP | ID: GO:0050789 | Genes: 293 | p-valor ruta: 1.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000058085	LAMC2	UP	1.879	2.12e-17	204.8
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000137310	TCF19	DOWN	-1.639	1.12e-14	547.9
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6

Ruta: regulation of biological process (Página 4 de 12)

Fuente: GO:BP | ID: GO:0050789 | Genes: 293 | p-valor ruta: 1.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDC45	DOWN	-2.059	8.54e-13	175.9
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6

Ruta: regulation of biological process (Página 5 de 12)

Fuente: GO:BP | ID: GO:0050789 | Genes: 293 | p-valor ruta: 1.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000068489	PRR11	DOWN	-1.033	9.90e-11	1510.0
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4

Ruta: regulation of biological process (Página 6 de 12)

Fuente: GO:BP | ID: GO:0050789 | Genes: 293 | p-valor ruta: 1.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3

Ruta: regulation of biological process (Página 7 de 12)

Fuente: GO:BP | ID: GO:0050789 | Genes: 293 | p-valor ruta: 1.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5

Ruta: regulation of biological process (Página 8 de 12)

Fuente: GO:BP | ID: GO:0050789 | Genes: 293 | p-valor ruta: 1.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG0000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000132017	DCAF15	DOWN	-1.243	1.30e-05	122.0
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7

Ruta: regulation of biological process (Página 9 de 12)

Fuente: GO:BP | ID: GO:0050789 | Genes: 293 | p-valor ruta: 1.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000160352	ZNF714	DOWN	-1.576	1.17e-04	120.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000160180	TFF3	UP	1.708	1.97e-04	44.6
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000074621	SLC24A1	UP	1.424	2.09e-04	124.7
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000109452	INPP4B	UP	1.158	4.20e-04	146.5

Ruta: regulation of biological process (Página 10 de 12)

Fuente: GO:BP | ID: GO:0050789 | Genes: 293 | p-valor ruta: 1.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG0000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG0000007908	SELE	DOWN	-4.746	5.26e-03	18.1

Ruta: regulation of biological process (Página 11 de 12)

Fuente: GO:BP | ID: GO:0050789 | Genes: 293 | p-valor ruta: 1.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000100100	PIK3IP1	UP	1.413	8.65e-03	102.0
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000166831	RBPM32	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000172197	MBOAT1	DOWN	-1.396	1.61e-02	54.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6

Ruta: regulation of biological process (Página 12 de 12)

Fuente: GO:BP | ID: GO:0050789 | Genes: 293 | p-valor ruta: 1.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000163596	ICA1L	DOWN	-1.027	1.99e-02	76.8
ENSG00000250510	GPR162	UP	1.311	2.49e-02	51.7
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000196247	ZNF107	DOWN	-1.028	4.60e-02	77.9
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: telomere organization

Fuente: GO:BP | ID: GO:0032200 | Genes: 19 | p-valor ruta: 1.16e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: positive regulation of DNA replication

Fuente: GO:BP | ID: GO:0045740 | Genes: 10 | p-valor ruta: 1.37e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: microtubule polymerization or depolymerization

Fuente: GO:BP | ID: GO:0031109 | Genes: 16 | p-valor ruta: 2.1e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8

Ruta: regulation of transferase activity (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051338 | Genes: 31 | p-valor ruta: 2.28e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: regulation of transferase activity (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051338 | Genes: 31 | p-valor ruta: 2.28e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1

Ruta: biological regulation (Página 1 de 12)

Fuente: GO:BP | ID: GO:0065007 | Genes: 299 | p-valor ruta: 2.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1

Ruta: biological regulation (Página 2 de 12)

Fuente: GO:BP | ID: GO:0065007 | Genes: 299 | p-valor ruta: 2.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8

Ruta: biological regulation (Página 3 de 12)

Fuente: GO:BP | ID: GO:0065007 | Genes: 299 | p-valor ruta: 2.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000058085	LAMC2	UP	1.879	2.12e-17	204.8
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000137310	TCF19	DOWN	-1.639	1.12e-14	547.9
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6

Ruta: biological regulation (Página 4 de 12)

Fuente: GO:BP | ID: GO:0065007 | Genes: 299 | p-valor ruta: 2.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3

Ruta: biological regulation (Página 5 de 12)

Fuente: GO:BP | ID: GO:0065007 | Genes: 299 | p-valor ruta: 2.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000068489	PRR11	DOWN	-1.033	9.90e-11	1510.0
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9

Ruta: biological regulation (Página 6 de 12)

Fuente: GO:BP | ID: GO:0065007 | Genes: 299 | p-valor ruta: 2.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4

Ruta: biological regulation (Página 7 de 12)

Fuente: GO:BP | ID: GO:0065007 | Genes: 299 | p-valor ruta: 2.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG0000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3

Ruta: biological regulation (Página 8 de 12)

Fuente: GO:BP | ID: GO:0065007 | Genes: 299 | p-valor ruta: 2.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000132017	DCAF15	DOWN	-1.243	1.30e-05	122.0
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000167772	ANGPTL4	UP	1.032	4.49e-05	119.9

Ruta: biological regulation (Página 9 de 12)

Fuente: GO:BP | ID: GO:0065007 | Genes: 299 | p-valor ruta: 2.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG0000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000160352	ZNF714	DOWN	-1.576	1.17e-04	120.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000160180	TFF3	UP	1.708	1.97e-04	44.6
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000074621	SLC24A1	UP	1.424	2.09e-04	124.7
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1

Ruta: biological regulation (Página 10 de 12)

Fuente: GO:BP | ID: GO:0065007 | Genes: 299 | p-valor ruta: 2.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000109452	INPP4B	UP	1.158	4.20e-04	146.5
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000128510	CPA4	UP	3.390	1.31e-03	31.5
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8

Ruta: biological regulation (Página 11 de 12)

Fuente: GO:BP | ID: GO:0065007 | Genes: 299 | p-valor ruta: 2.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000100100	PIK3IP1	UP	1.413	8.65e-03	102.0
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000181652	ATG9B	UP	1.052	9.34e-03	97.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000101187	SLCO4A1	DOWN	-2.007	1.09e-02	29.9
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000166831	RBPM52	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2

Ruta: biological regulation (Página 12 de 12)

Fuente: GO:BP | ID: GO:0065007 | Genes: 299 | p-valor ruta: 2.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000172197	MBOAT1	DOWN	-1.396	1.61e-02	54.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000163596	ICA1L	DOWN	-1.027	1.99e-02	76.8
ENSG00000151572	ANO4	UP	1.682	2.37e-02	39.8
ENSG00000250510	GPR162	UP	1.311	2.49e-02	51.7
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000196247	ZNF107	DOWN	-1.028	4.60e-02	77.9
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: meiotic chromosome condensation

Fuente: GO:BP | ID: GO:0010032 | Genes: 5 | p-valor ruta: 3.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0

Ruta: negative regulation of biological process (Página 1 de 7)

Fuente: GO:BP | ID: GO:0048519 | Genes: 164 | p-valor ruta: 3.21e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0

Ruta: negative regulation of biological process (Página 2 de 7)

Fuente: GO:BP | ID: GO:0048519 | Genes: 164 | p-valor ruta: 3.21e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6

Ruta: negative regulation of biological process (Página 3 de 7)

Fuente: GO:BP | ID: GO:0048519 | Genes: 164 | p-valor ruta: 3.21e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5

Ruta: negative regulation of biological process (Página 4 de 7)

Fuente: GO:BP | ID: GO:0048519 | Genes: 164 | p-valor ruta: 3.21e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7

Ruta: negative regulation of biological process (Página 5 de 7)

Fuente: GO:BP | ID: GO:0048519 | Genes: 164 | p-valor ruta: 3.21e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000074621	SLC24A1	UP	1.424	2.09e-04	124.7
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4

Ruta: negative regulation of biological process (Página 6 de 7)

Fuente: GO:BP | ID: GO:0048519 | Genes: 164 | p-valor ruta: 3.21e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000100100	PIK3IP1	UP	1.413	8.65e-03	102.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: negative regulation of biological process (Página 7 de 7)

Fuente: GO:BP | ID: GO:0048519 | Genes: 164 | p-valor ruta: 3.21e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166831	RBPM2	DOWN	-1.538	1.19e-02	49.2
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: regulation of double-strand break repair

Fuente: GO:BP | ID: GO:2000779 | Genes: 16 | p-valor ruta: 3.52e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6

Ruta: cell population proliferation (Página 1 de 3)

Fuente: GO:BP | ID: GO:0008283 | Genes: 75 | p-valor ruta: 3.7e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000058085	LAMC2	UP	1.879	2.12e-17	204.8
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2

Ruta: cell population proliferation (Página 2 de 3)

Fuente: GO:BP | ID: GO:0008283 | Genes: 75 | p-valor ruta: 3.7e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1

Ruta: cell population proliferation (Página 3 de 3)

Fuente: GO:BP | ID: GO:0008283 | Genes: 75 | p-valor ruta: 3.7e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000166831	RBPMS2	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: positive regulation of cell cycle G1/S phase transition

Fuente: GO:BP | ID: GO:1902808 | Genes: 11 | p-valor ruta: 4.17e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: negative regulation of cellular process (Página 1 de 7)

Fuente: GO:BP | ID: GO:0048523 | Genes: 159 | p-valor ruta: 4.58e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8

Ruta: negative regulation of cellular process (Página 2 de 7)

Fuente: GO:BP | ID: GO:0048523 | Genes: 159 | p-valor ruta: 4.58e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2

Ruta: negative regulation of cellular process (Página 3 de 7)

Fuente: GO:BP | ID: GO:0048523 | Genes: 159 | p-valor ruta: 4.58e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3

Ruta: negative regulation of cellular process (Página 4 de 7)

Fuente: GO:BP | ID: GO:0048523 | Genes: 159 | p-valor ruta: 4.58e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8

Ruta: negative regulation of cellular process (Página 5 de 7)

Fuente: GO:BP | ID: GO:0048523 | Genes: 159 | p-valor ruta: 4.58e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000074621	SLC24A1	UP	1.424	2.09e-04	124.7
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1

Ruta: negative regulation of cellular process (Página 6 de 7)

Fuente: GO:BP | ID: GO:0048523 | Genes: 159 | p-valor ruta: 4.58e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000154175	ABI3BP	UP	1.785	5.52e-03	87.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000100100	PIK3IP1	UP	1.413	8.65e-03	102.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000166831	RBPMS2	DOWN	-1.538	1.19e-02	49.2
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: negative regulation of cellular process (Página 7 de 7)

Fuente: GO:BP | ID: GO:0048523 | Genes: 159 | p-valor ruta: 4.58e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG0000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: negative regulation of meiotic cell cycle

Fuente: GO:BP | ID: GO:0051447 | Genes: 7 | p-valor ruta: 4.95e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2

Ruta: mitotic G2 DNA damage checkpoint signaling

Fuente: GO:BP | ID: GO:0007095 | Genes: 9 | p-valor ruta: 5.16e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8

Ruta: positive regulation of organelle organization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0010638 | Genes: 30 | p-valor ruta: 6.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0

Ruta: positive regulation of organelle organization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0010638 | Genes: 30 | p-valor ruta: 6.29e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: regulation of meiotic cell cycle phase transition

Fuente: GO:BP | ID: GO:1901993 | Genes: 6 | p-valor ruta: 8.25e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3

Ruta: spindle assembly involved in female meiosis

Fuente: GO:BP | ID: GO:0007056 | Genes: 6 | p-valor ruta: 8.25e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1

Ruta: female gamete generation

Fuente: GO:BP | ID: GO:0007292 | Genes: 17 | p-valor ruta: 9.66e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG0000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG0000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG0000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: positive regulation of cell division

Fuente: GO:BP | ID: GO:0051781 | Genes: 13 | p-valor ruta: 1.01e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4

Ruta: G2/MI transition of meiotic cell cycle

Fuente: GO:BP | ID: GO:0008315 | Genes: 5 | p-valor ruta: 1.05e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1

Ruta: intrinsic apoptotic signaling pathway by p53 class mediator

Fuente: GO:BP | ID: GO:0072332 | Genes: 12 | p-valor ruta: 1.25e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: regulation of centrosome cycle

Fuente: GO:BP | ID: GO:0046605 | Genes: 10 | p-valor ruta: 1.41e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: female meiosis I

Fuente: GO:BP | ID: GO:0007144 | Genes: 6 | p-valor ruta: 1.51e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1

Ruta: positive regulation of mitotic cytokinesis

Fuente: GO:BP | ID: GO:1903490 | Genes: 6 | p-valor ruta: 1.51e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: centriole replication

Fuente: GO:BP | ID: GO:0007099 | Genes: 9 | p-valor ruta: 2.11e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: meiotic spindle organization

Fuente: GO:BP | ID: GO:0000212 | Genes: 7 | p-valor ruta: 2.48e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1

Ruta: regulation of metaphase plate congression

Fuente: GO:BP | ID: GO:0090235 | Genes: 6 | p-valor ruta: 2.59e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: spindle assembly involved in female meiosis I

Fuente: GO:BP | ID: GO:0007057 | Genes: 4 | p-valor ruta: 2.71e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1

Ruta: positive regulation of G1/S transition of mitotic cell cycle

Fuente: GO:BP | ID: GO:1900087 | Genes: 9 | p-valor ruta: 3.21e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG0000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: protein localization to condensed chromosome

Fuente: GO:BP | ID: GO:1903083 | Genes: 6 | p-valor ruta: 4.25e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5

Ruta: protein localization to kinetochore

Fuente: GO:BP | ID: GO:0034501 | Genes: 6 | p-valor ruta: 4.25e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5

Ruta: establishment of spindle orientation

Fuente: GO:BP | ID: GO:0051294 | Genes: 9 | p-valor ruta: 4.76e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: centriole assembly

Fuente: GO:BP | ID: GO:0098534 | Genes: 9 | p-valor ruta: 5.77e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: regulation of spindle organization

Fuente: GO:BP | ID: GO:0090224 | Genes: 9 | p-valor ruta: 5.77e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1

Ruta: regulation of attachment of mitotic spindle microtubules to kinetochore

Fuente: GO:BP | ID: GO:1902423 | Genes: 5 | p-valor ruta: 6.12e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: regulation of mitotic cytokinesis

Fuente: GO:BP | ID: GO:1902412 | Genes: 6 | p-valor ruta: 6.7e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: response to abiotic stimulus (Página 1 de 2)

Fuente: GO:BP | ID: GO:0009628 | Genes: 48 | p-valor ruta: 6.87e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4

Ruta: response to abiotic stimulus (Página 2 de 2)

Fuente: GO:BP | ID: GO:0009628 | Genes: 48 | p-valor ruta: 6.87e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000074621	SLC24A1	UP	1.424	2.09e-04	124.7
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: translesion synthesis

Fuente: GO:BP | ID: GO:0019985 | Genes: 7 | p-valor ruta: 8.96e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1

Ruta: regulation of double-strand break repair via homologous recombination

Fuente: GO:BP | ID: GO:0010569 | Genes: 11 | p-valor ruta: 1.1e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6

Ruta: negative regulation of DNA-templated DNA replication

Fuente: GO:BP | ID: GO:2000104 | Genes: 5 | p-valor ruta: 1.2e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8

Ruta: negative regulation of meiotic nuclear division

Fuente: GO:BP | ID: GO:0045835 | Genes: 5 | p-valor ruta: 1.2e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2

Ruta: cell cycle DNA replication initiation

Fuente: GO:BP | ID: GO:1902292 | Genes: 4 | p-valor ruta: 1.34e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1

Ruta: mitotic DNA replication initiation

Fuente: GO:BP | ID: GO:1902975 | Genes: 4 | p-valor ruta: 1.34e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1

Ruta: nuclear cell cycle DNA replication initiation

Fuente: GO:BP | ID: GO:1902315 | Genes: 4 | p-valor ruta: 1.34e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1

Ruta: spindle localization

Fuente: GO:BP | ID: GO:0051653 | Genes: 10 | p-valor ruta: 1.35e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: mitotic DNA replication checkpoint signaling

Fuente: GO:BP | ID: GO:0033314 | Genes: 5 | p-valor ruta: 2.17e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1

Ruta: positive regulation of attachment of spindle microtubules to kinetochore

Fuente: GO:BP | ID: GO:0051987 | Genes: 5 | p-valor ruta: 2.17e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: regulation of DNA biosynthetic process

Fuente: GO:BP | ID: GO:2000278 | Genes: 11 | p-valor ruta: 3.14e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5

Ruta: mitotic sister chromatid cohesion

Fuente: GO:BP | ID: GO:0007064 | Genes: 7 | p-valor ruta: 3.3e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0

Ruta: phosphorylation (Página 1 de 3)

Fuente: GO:BP | ID: GO:0016310 | Genes: 51 | p-valor ruta: 3.35e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0

Ruta: phosphorylation (Página 2 de 3)

Fuente: GO:BP | ID: GO:0016310 | Genes: 51 | p-valor ruta: 3.35e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7

Ruta: phosphorylation (Página 3 de 3)

Fuente: GO:BP | ID: GO:0016310 | Genes: 51 | p-valor ruta: 3.35e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000093217	XYLB	DOWN	-1.226	3.2e-02	61

Ruta: regulation of mitotic spindle organization

Fuente: GO:BP | ID: GO:0060236 | Genes: 8 | p-valor ruta: 3.42e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1

Ruta: negative regulation of gene expression, epigenetic

Fuente: GO:BP | ID: GO:0045814 | Genes: 16 | p-valor ruta: 3.59e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5

Ruta: resolution of DNA recombination intermediates

Fuente: GO:BP | ID: GO:0071139 | Genes: 4 | p-valor ruta: 3.95e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: reciprocal homologous recombination

Fuente: GO:BP | ID: GO:0140527 | Genes: 9 | p-valor ruta: 4.14e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: reciprocal meiotic recombination

Fuente: GO:BP | ID: GO:0007131 | Genes: 9 | p-valor ruta: 4.14e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: regulation of reproductive process

Fuente: GO:BP | ID: GO:2000241 | Genes: 16 | p-valor ruta: 4.36e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2

Ruta: intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator

Fuente: GO:BP | ID: GO:0042771 | Genes: 8 | p-valor ruta: 4.86e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: regulation of centrosome duplication

Fuente: GO:BP | ID: GO:0010824 | Genes: 8 | p-valor ruta: 5.76e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7

Ruta: regulation of microtubule polymerization or depolymerization

Fuente: GO:BP | ID: GO:0031110 | Genes: 11 | p-valor ruta: 5.91e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8

Ruta: cellular response to abiotic stimulus

Fuente: GO:BP | ID: GO:0071214 | Genes: 21 | p-valor ruta: 5.95e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: cellular response to environmental stimulus

Fuente: GO:BP | ID: GO:0104004 | Genes: 21 | p-valor ruta: 5.95e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: regulation of cyclin-dependent protein serine/threonine kinase activity

Fuente: GO:BP | ID: GO:0000079 | Genes: 10 | p-valor ruta: 6.24e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG0000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1

Ruta: establishment of spindle localization

Fuente: GO:BP | ID: GO:0051293 | Genes: 9 | p-valor ruta: 6.31e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: signal transduction by p53 class mediator

Fuente: GO:BP | ID: GO:0072331 | Genes: 14 | p-valor ruta: 7.45e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: regulation of centriole replication

Fuente: GO:BP | ID: GO:0046599 | Genes: 6 | p-valor ruta: 7.53e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6

Ruta: regulation of meiotic nuclear division

Fuente: GO:BP | ID: GO:0040020 | Genes: 7 | p-valor ruta: 7.89e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2

Ruta: 2'-deoxyribonucleotide biosynthetic process

Fuente: GO:BP | ID: GO:0009265 | Genes: 5 | p-valor ruta: 8.98e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0

Ruta: deoxyribonucleotide biosynthetic process

Fuente: GO:BP | ID: GO:0009263 | Genes: 5 | p-valor ruta: 8.98e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0

Ruta: deoxyribose phosphate biosynthetic process

Fuente: GO:BP | ID: GO:0046385 | Genes: 5 | p-valor ruta: 8.98e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0

Ruta: metaphase/anaphase transition of meiotic cell cycle

Fuente: GO:BP | ID: GO:0044785 | Genes: 4 | p-valor ruta: 9.07e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0

Ruta: cytokinetic process

Fuente: GO:BP | ID: GO:0032506 | Genes: 8 | p-valor ruta: 9.36e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0

Ruta: microtubule depolymerization

Fuente: GO:BP | ID: GO:0007019 | Genes: 8 | p-valor ruta: 9.36e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8

Ruta: regulation of primary metabolic process (Página 1 de 6)

Fuente: GO:BP | ID: GO:0080090 | Genes: 144 | p-valor ruta: 1.02e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6

Ruta: regulation of primary metabolic process (Página 2 de 6)

Fuente: GO:BP | ID: GO:0080090 | Genes: 144 | p-valor ruta: 1.02e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6

Ruta: regulation of primary metabolic process (Página 3 de 6)

Fuente: GO:BP | ID: GO:0080090 | Genes: 144 | p-valor ruta: 1.02e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7

Ruta: regulation of primary metabolic process (Página 4 de 6)

Fuente: GO:BP | ID: GO:0080090 | Genes: 144 | p-valor ruta: 1.02e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0

Ruta: regulation of primary metabolic process (Página 5 de 6)

Fuente: GO:BP | ID: GO:0080090 | Genes: 144 | p-valor ruta: 1.02e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000160352	ZNF714	DOWN	-1.576	1.17e-04	120.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000160180	TFF3	UP	1.708	1.97e-04	44.6
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7

Ruta: regulation of primary metabolic process (Página 6 de 6)

Fuente: GO:BP | ID: GO:0080090 | Genes: 144 | p-valor ruta: 1.02e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000166831	RBPM32	DOWN	-1.538	1.19e-02	49.2
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000196247	ZNF107	DOWN	-1.028	4.60e-02	77.9

Ruta: positive regulation of DNA biosynthetic process

Fuente: GO:BP | ID: GO:2000573 | Genes: 8 | p-valor ruta: 1.09e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: intrinsic apoptotic signaling pathway in response to DNA damage

Fuente: GO:BP | ID: GO:0008630 | Genes: 11 | p-valor ruta: 1.16e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: DNA replication preinitiation complex assembly

Fuente: GO:BP | ID: GO:0071163 | Genes: 3 | p-valor ruta: 1.42e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5

Ruta: meiotic spindle assembly checkpoint signaling

Fuente: GO:BP | ID: GO:0033316 | Genes: 3 | p-valor ruta: 1.42e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0

Ruta: positive regulation of G2/M transition of meiotic cell cycle

Fuente: GO:BP | ID: GO:0110032 | Genes: 3 | p-valor ruta: 1.42e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3

Ruta: gamete generation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0007276 | Genes: 36 | p-valor ruta: 1.43e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG0000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG0000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG0000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG0000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG0000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG0000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG0000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1

Ruta: gamete generation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0007276 | Genes: 36 | p-valor ruta: 1.43e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: heterochromatin formation

Fuente: GO:BP | ID: GO:0031507 | Genes: 13 | p-valor ruta: 1.51e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6

Ruta: negative regulation of DNA replication

Fuente: GO:BP | ID: GO:0008156 | Genes: 6 | p-valor ruta: 1.63e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8

Ruta: homologous chromosome pairing at meiosis

Fuente: GO:BP | ID: GO:0007129 | Genes: 8 | p-valor ruta: 1.7e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: double-strand break repair via synthesis-dependent strand annealing

Fuente: GO:BP | ID: GO:0045003 | Genes: 4 | p-valor ruta: 1.79e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: positive regulation of attachment of mitotic spindle microtubules to kinetochore

Fuente: GO:BP | ID: GO:1902425 | Genes: 4 | p-valor ruta: 1.79e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: positive regulation of spindle assembly

Fuente: GO:BP | ID: GO:1905832 | Genes: 4 | p-valor ruta: 1.79e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6

Ruta: regulation of cytoskeleton organization (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051493 | Genes: 26 | p-valor ruta: 1.86e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2

Ruta: regulation of cytoskeleton organization (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051493 | Genes: 26 | p-valor ruta: 1.86e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166086	JAM3	DOWN	-1.293	4.5e-02	50.7

Ruta: protein localization to site of double-strand break

Fuente: GO:BP | ID: GO:1990166 | Genes: 5 | p-valor ruta: 1.9e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0

Ruta: response to UV

Fuente: GO:BP | ID: GO:0009411 | Genes: 13 | p-valor ruta: 2e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9

Ruta: multicellular organismal reproductive process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0048609 | Genes: 40 | p-valor ruta: 2.17e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG0000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG0000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG0000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG0000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG0000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG0000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG0000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG0000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG0000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3

Ruta: multicellular organismal reproductive process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0048609 | Genes: 40 | p-valor ruta: 2.17e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: negative regulation of reproductive process

Fuente: GO:BP | ID: GO:2000242 | Genes: 9 | p-valor ruta: 2.44e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2

Ruta: positive regulation of mitotic metaphase/anaphase transition

Fuente: GO:BP | ID: GO:0045842 | Genes: 5 | p-valor ruta: 2.64e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9

Ruta: protein localization to microtubule cytoskeleton

Fuente: GO:BP | ID: GO:0072698 | Genes: 8 | p-valor ruta: 2.92e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8

Ruta: programmed cell death (Página 1 de 3)

Fuente: GO:BP | ID: GO:0012501 | Genes: 65 | p-valor ruta: 3.11e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000147697	GSDMC	UP	2.564	1.66e-10	130.4

Ruta: programmed cell death (Página 2 de 3)

Fuente: GO:BP | ID: GO:0012501 | Genes: 65 | p-valor ruta: 3.11e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG0000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG0000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG0000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG0000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG0000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG0000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG0000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG0000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG0000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG0000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG0000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG0000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG0000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG0000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG0000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG0000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG0000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG0000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG0000242265	PEG10	DOWN	-1.056	2.33e-04	204.2

Ruta: programmed cell death (Página 3 de 3)

Fuente: GO:BP | ID: GO:0012501 | Genes: 65 | p-valor ruta: 3.11e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000181652	ATG9B	UP	1.052	9.34e-03	97.0
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7

Ruta: actomyosin contractile ring assembly

Fuente: GO:BP | ID: GO:0000915 | Genes: 4 | p-valor ruta: 3.17e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9

Ruta: assembly of actomyosin apparatus involved in cytokinesis

Fuente: GO:BP | ID: GO:0000912 | Genes: 4 | p-valor ruta: 3.17e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9

Ruta: positive regulation of centriole replication

Fuente: GO:BP | ID: GO:0046601 | Genes: 4 | p-valor ruta: 3.17e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6

Ruta: positive regulation of mitotic sister chromatid segregation

Fuente: GO:BP | ID: GO:0062033 | Genes: 4 | p-valor ruta: 3.17e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9

Ruta: telomere maintenance via semi-conservative replication

Fuente: GO:BP | ID: GO:0032201 | Genes: 4 | p-valor ruta: 3.17e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: cell death (Página 1 de 3)

Fuente: GO:BP | ID: GO:0008219 | Genes: 65 | p-valor ruta: 3.31e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000147697	GSDMC	UP	2.564	1.66e-10	130.4

Ruta: cell death (Página 2 de 3)

Fuente: GO:BP | ID: GO:0008219 | Genes: 65 | p-valor ruta: 3.31e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG0000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG0000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG0000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG0000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG0000151012	SLC7A11	DOWN	-1.015	1.38e-07	2765.3
ENSG0000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG0000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG0000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG0000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG0000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG0000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG0000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG0000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG0000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG0000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG0000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG0000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG0000167772	ANGPTL4	UP	1.032	4.49e-05	119.9
ENSG0000242265	PEG10	DOWN	-1.056	2.33e-04	204.2

Ruta: cell death (Página 3 de 3)

Fuente: GO:BP | ID: GO:0008219 | Genes: 65 | p-valor ruta: 3.31e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000181652	ATG9B	UP	1.052	9.34e-03	97.0
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7

Ruta: nucleosome assembly

Fuente: GO:BP | ID: GO:0006334 | Genes: 11 | p-valor ruta: 3.58e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: positive regulation of metaphase/anaphase transition of cell cycle

Fuente: GO:BP | ID: GO:1902101 | Genes: 5 | p-valor ruta: 3.6e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9

Ruta: protein localization to chromatin

Fuente: GO:BP | ID: GO:0071168 | Genes: 8 | p-valor ruta: 3.77e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3

Ruta: positive regulation of transferase activity

Fuente: GO:BP | ID: GO:0051347 | Genes: 18 | p-valor ruta: 3.88e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG0000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000181634	TNFSF15	UP	1.161	3.19e-06	323.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1

Ruta: epigenetic regulation of gene expression

Fuente: GO:BP | ID: GO:0040029 | Genes: 18 | p-valor ruta: 4.44e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000162595	DIRAS3	UP	2.006	2.02e-10	93.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5

Ruta: protein localization to cytoskeleton

Fuente: GO:BP | ID: GO:0044380 | Genes: 8 | p-valor ruta: 4.82e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8

Sección de Análisis: GO:CC – Componentes Celulares

Total de términos enriquecidos en esta sección: 95

Términos 'Tope' (p–valor < 1e–16): 22

Términos que superan el 'tope' de significancia:

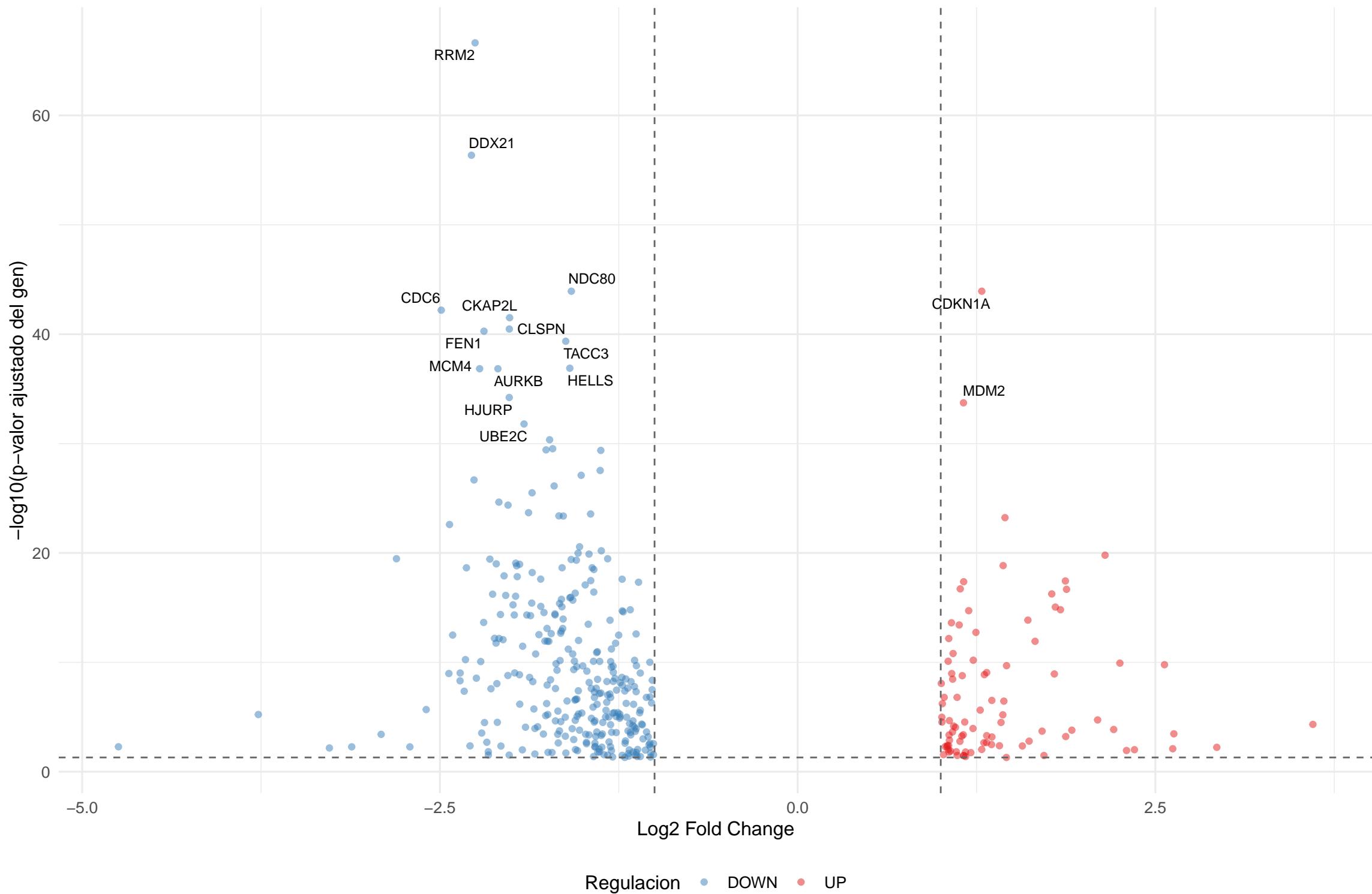
- *chromosome* (GO:0005694, p–val: 6.4e–63)
- *chromosomal region* (GO:0098687, p–val: 1.5e–55)
- *condensed chromosome* (GO:0000793, p–val: 3.4e–46)
- *intracellular membraneless organelle* (GO:0043232, p–val: 2.6e–41)
- *membraneless organelle* (GO:0043228, p–val: 2.6e–41)
- *chromosome, centromeric region* (GO:0000775, p–val: 4.9e–41)
- *nucleoplasm* (GO:0005654, p–val: 3.0e–37)
- *microtubule cytoskeleton* (GO:0015630, p–val: 3.5e–36)
- *condensed chromosome, centromeric region* (GO:0000779, p–val: 2.4e–34)
- *spindle* (GO:0005819, p–val: 2.3e–31)

...y otros

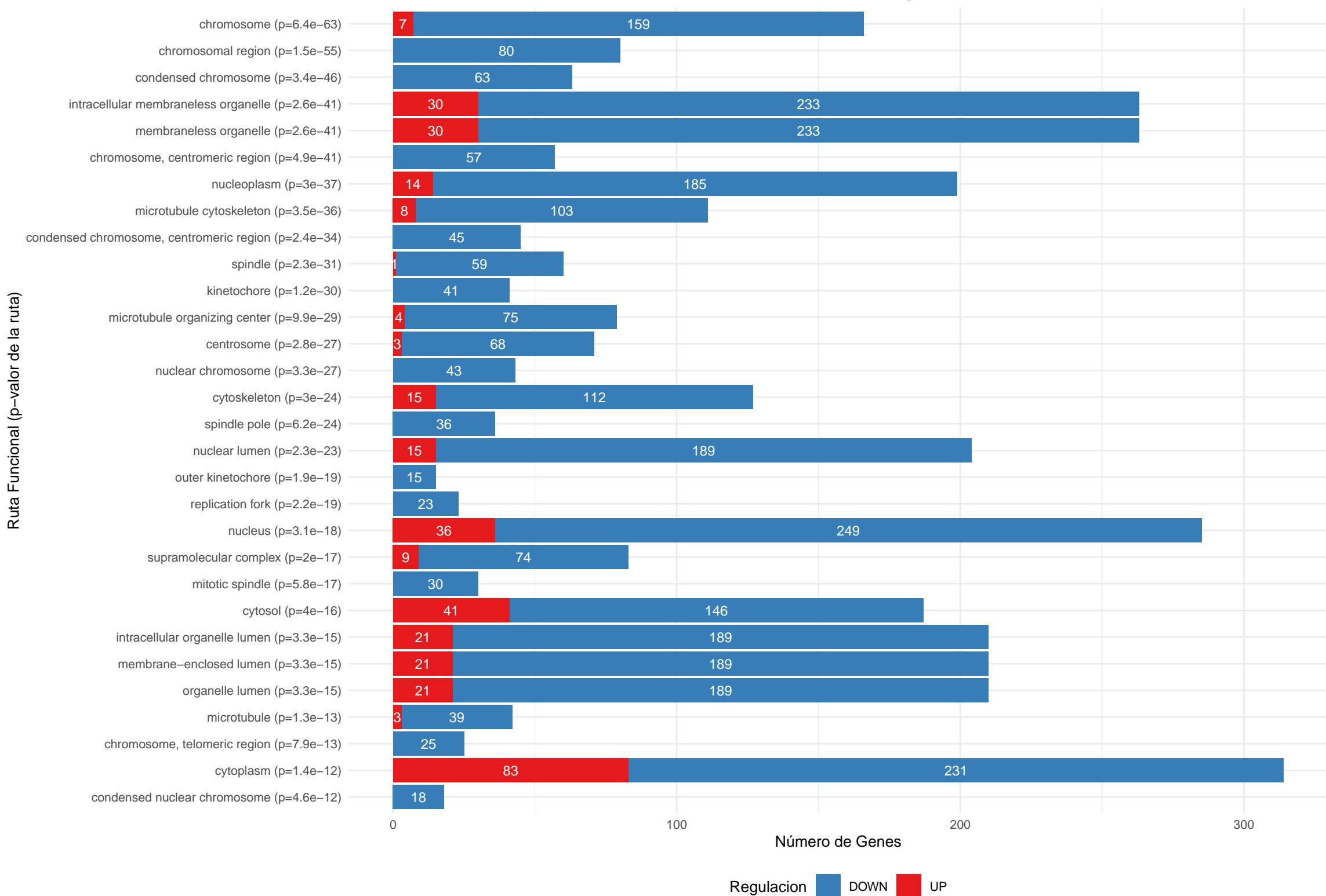
A continuación se muestran los gráficos de barras y tablas de genes para esta sección.

Volcano Plot – GO:CC – Componentes Celulares

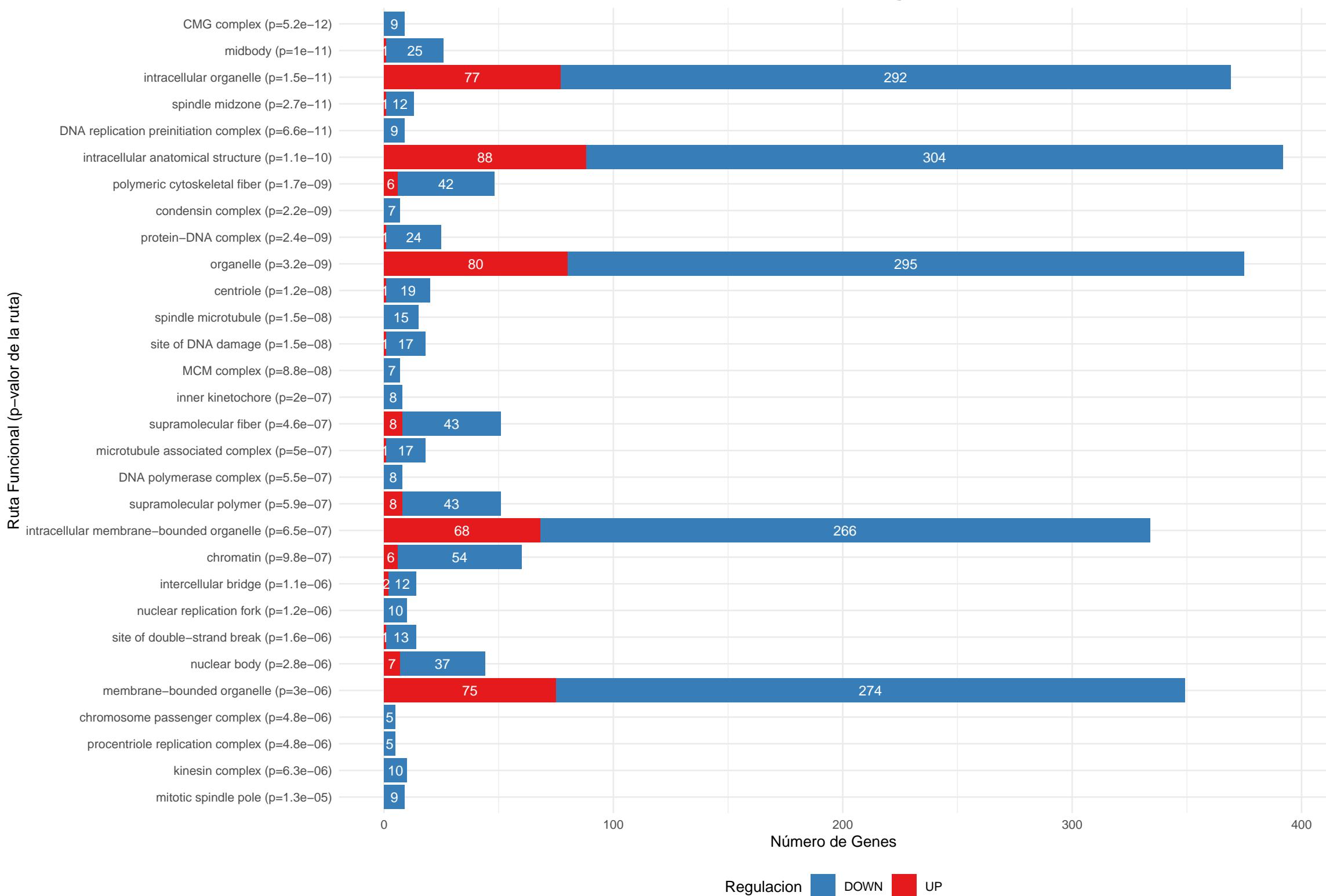
Mostrando 395 genes únicos mapeados en esta sección



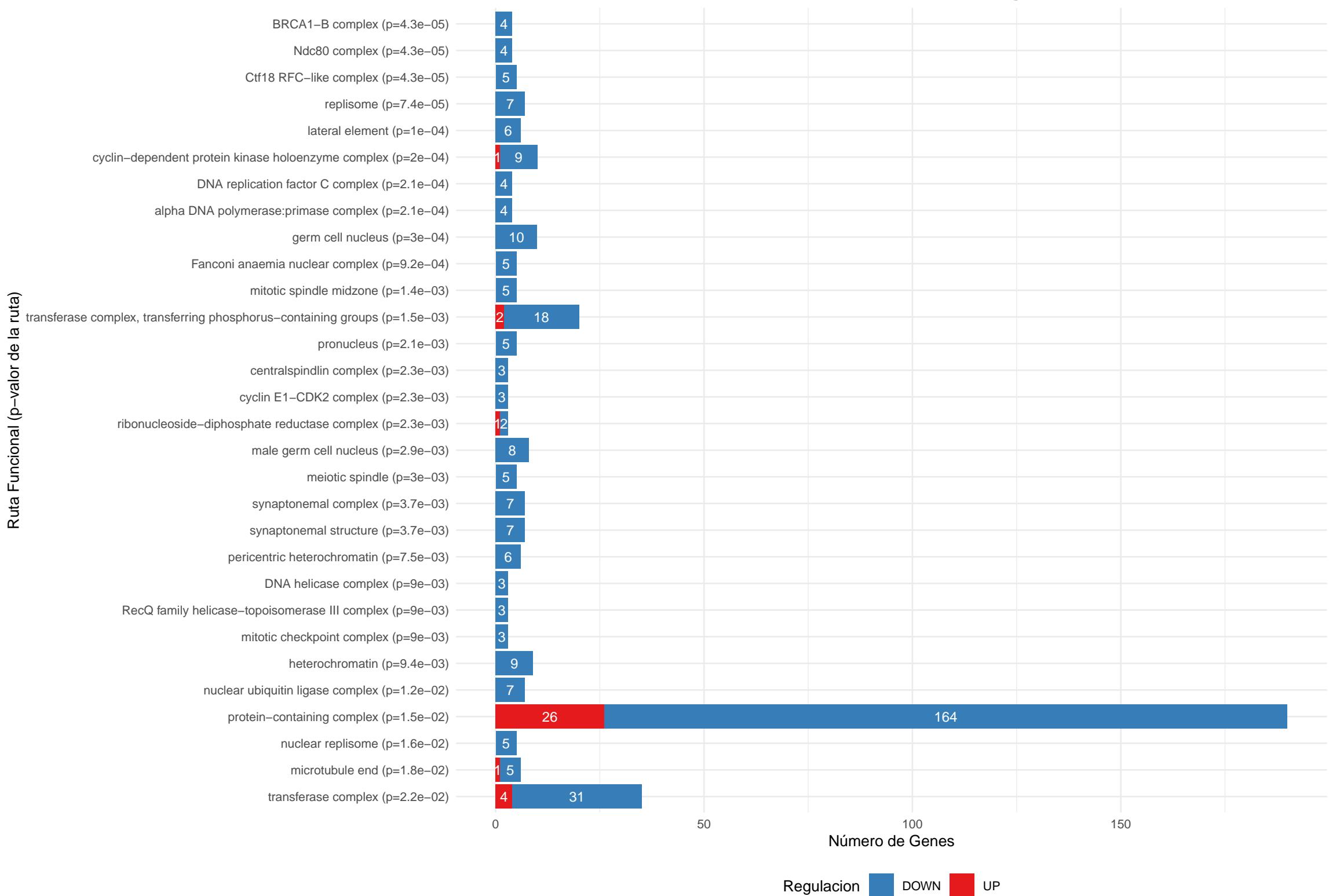
GO:CC – Componentes Celulares – Gráfico (Pág. 1 de 4)



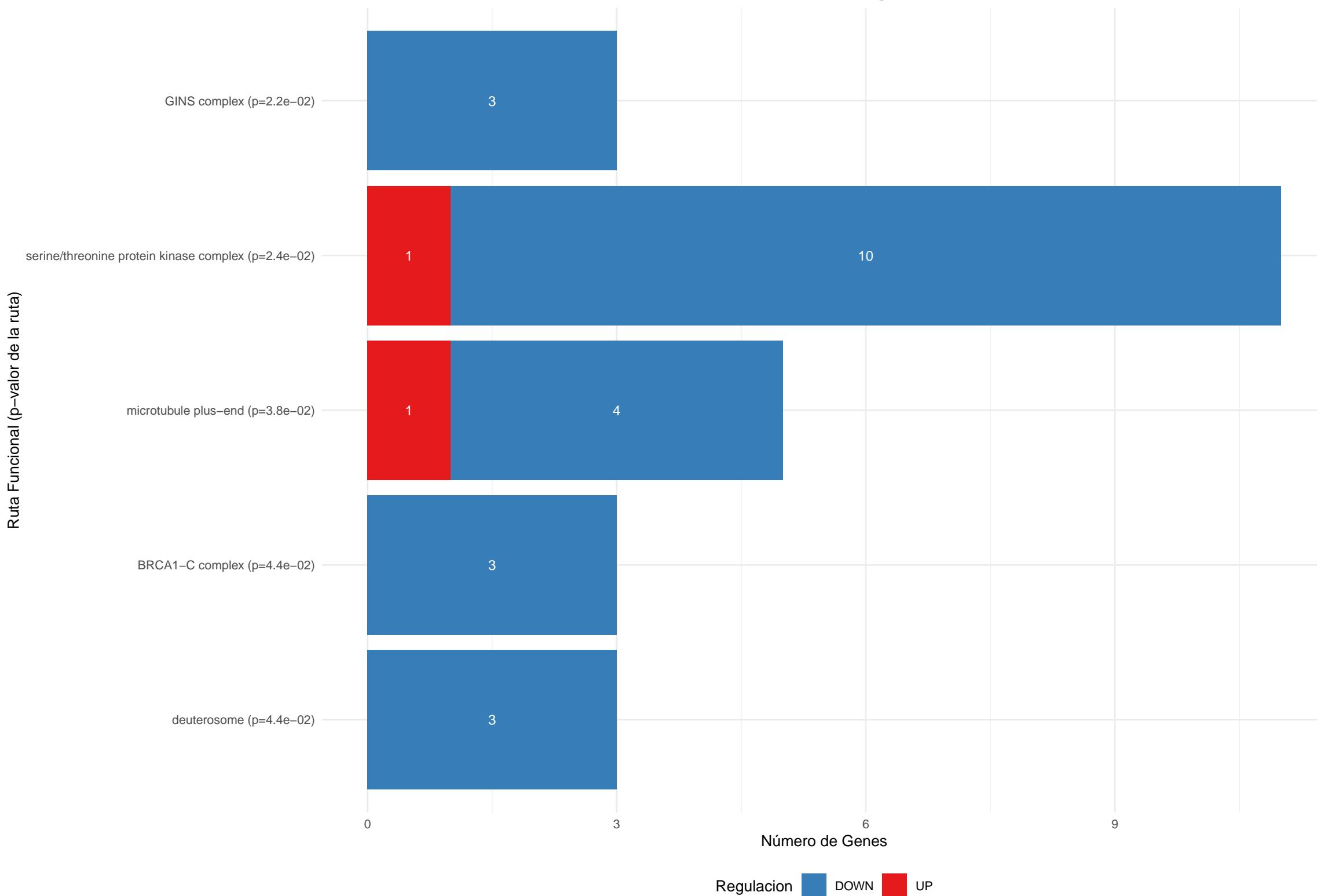
GO:CC – Componentes Celulares – Gráfico (Pág. 2 de 4)



GO:CC – Componentes Celulares – Gráfico (Pág. 3 de 4)



GO:CC – Componentes Celulares – Gráfico (Pág. 4 de 4)



Ruta: chromosome (Página 1 de 7)

Fuente: GO:CC | ID: GO:0005694 | Genes: 166 | p-valor ruta: 6.44e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1

Ruta: chromosome (Página 2 de 7)

Fuente: GO:CC | ID: GO:0005694 | Genes: 166 | p-valor ruta: 6.44e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000189057	FAM111B	DOWN	-2.315	2.29e-19	695.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8

Ruta: chromosome (Página 3 de 7)

Fuente: GO:CC | ID: GO:0005694 | Genes: 166 | p-valor ruta: 6.44e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000146670	CDC45	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMG2B	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4

Ruta: chromosome (Página 4 de 7)

Fuente: GO:CC | ID: GO:0005694 | Genes: 166 | p-valor ruta: 6.44e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1

Ruta: chromosome (Página 5 de 7)

Fuente: GO:CC | ID: GO:0005694 | Genes: 166 | p-valor ruta: 6.44e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8

Ruta: chromosome (Página 6 de 7)

Fuente: GO:CC | ID: GO:0005694 | Genes: 166 | p-valor ruta: 6.44e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3

Ruta: chromosome (Página 7 de 7)

Fuente: GO:CC | ID: GO:0005694 | Genes: 166 | p-valor ruta: 6.44e-63

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2

Ruta: chromosomal region (Página 1 de 4)

Fuente: GO:CC | ID: GO:0098687 | Genes: 80 | p-valor ruta: 1.46e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9

Ruta: chromosomal region (Página 2 de 4)

Fuente: GO:CC | ID: GO:0098687 | Genes: 80 | p-valor ruta: 1.46e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4

Ruta: chromosomal region (Página 3 de 4)

Fuente: GO:CC | ID: GO:0098687 | Genes: 80 | p–valor ruta: 1.46e–55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3

Ruta: chromosomal region (Página 4 de 4)

Fuente: GO:CC | ID: GO:0098687 | Genes: 80 | p-valor ruta: 1.46e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: condensed chromosome (Página 1 de 3)

Fuente: GO:CC | ID: GO:0000793 | Genes: 63 | p–valor ruta: 3.39e–46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	−1.581	1.18e−44	832.9
ENSG00000178999	AURKB	DOWN	−2.095	1.44e−37	1004.1
ENSG00000123485	HJURP	DOWN	−2.015	6.13e−35	695.4
ENSG00000131747	TOP2A	DOWN	−1.733	4.48e−31	5823.0
ENSG00000134057	CCNB1	DOWN	−1.376	4.23e−30	1075.8
ENSG00000143228	NUF2	DOWN	−2.262	2.12e−27	1144.3
ENSG00000089685	BIRC5	DOWN	−1.447	2.74e−24	999.2
ENSG00000154839	SKA1	DOWN	−2.106	9.93e−20	265.9
ENSG00000152253	SPC25	DOWN	−1.943	1.08e−19	456.4
ENSG00000137812	KNL1	DOWN	−1.964	1.50e−19	675.1
ENSG00000136824	SMC2	DOWN	−1.424	3.27e−19	2147.1
ENSG00000156970	BUB1B	DOWN	−1.960	1.47e−18	480.6
ENSG00000113810	SMC4	DOWN	−1.484	8.40e−18	4283.1
ENSG00000102384	CENPI	DOWN	−1.554	4.76e−17	603.3
ENSG00000165480	SKA3	DOWN	−1.586	1.14e−16	602.9
ENSG00000163535	SGO2	DOWN	−1.592	1.26e−16	1142.8
ENSG00000100162	CENPM	DOWN	−1.651	1.75e−16	256.1
ENSG00000151725	CENPU	DOWN	−1.858	3.84e−16	603.3
ENSG00000051180	RAD51	DOWN	−2.077	4.28e−15	291.4
ENSG00000163781	TOPBP1	DOWN	−1.311	1.42e−14	788.6
ENSG00000087586	AURKA	DOWN	−1.463	3.30e−14	1066.4
ENSG00000149636	DSN1	DOWN	−1.642	8.03e−14	568.7
ENSG00000122952	ZWINT	DOWN	−1.652	1.40e−13	998.2
ENSG00000164109	MAD2L1	DOWN	−1.656	2.19e−13	684.6
ENSG00000148773	MKI67	DOWN	−1.808	2.94e−13	1720.7

Ruta: condensed chromosome (Página 2 de 3)

Fuente: GO:CC | ID: GO:0000793 | Genes: 63 | p–valor ruta: 3.39e–46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000012048	BRCA1	DOWN	−1.766	1.14e−12	390.2
ENSG0000076382	SPAG5	DOWN	−1.738	1.21e−12	384.3
ENSG00000146918	NCAPG2	DOWN	−1.301	6.06e−12	556.6
ENSG00000117724	CENPF	DOWN	−1.603	6.29e−12	2801.9
ENSG00000164104	HMGB2	DOWN	−1.572	1.72e−11	2905.5
ENSG00000129810	SGO1	DOWN	−2.322	5.66e−11	212.1
ENSG00000123374	CDK2	DOWN	−1.140	6.55e−11	1630.6
ENSG00000142945	KIF2C	DOWN	−1.660	6.87e−11	313.0
ENSG00000169679	BUB1	DOWN	−1.427	8.07e−11	645.0
ENSG00000117399	CDC20	DOWN	−1.306	8.53e−11	1077.9
ENSG00000115163	CENPA	DOWN	−1.689	1.34e−10	297.0
ENSG00000144554	FANCD2	DOWN	−1.681	5.26e−10	378.0
ENSG00000167513	CDT1	DOWN	−2.358	9.49e−10	138.1
ENSG0000010292	NCAPD2	DOWN	−1.100	9.61e−10	894.2
ENSG00000139618	BRCA2	DOWN	−1.944	1.37e−09	326.9
ENSG00000121152	NCAPH	DOWN	−2.359	4.90e−09	170.5
ENSG00000138778	CENPE	DOWN	−1.289	5.56e−09	2554.3
ENSG00000161888	SPC24	DOWN	−1.240	7.21e−09	360.5
ENSG00000112742	TTK	DOWN	−2.143	2.62e−08	332.0
ENSG0000031691	CENPQ	DOWN	−1.420	5.20e−08	308.3
ENSG00000123219	CENPK	DOWN	−1.375	6.42e−08	355.1
ENSG00000117650	NEK2	DOWN	−1.675	2.88e−06	263.6
ENSG00000151503	NCAPD3	DOWN	−1.281	4.01e−06	180.0
ENSG00000184445	KNTC1	DOWN	−1.292	4.45e−06	133.5
ENSG00000166851	PLK1	DOWN	−1.760	7.54e−06	86.4

Ruta: condensed chromosome (Página 3 de 3)

Fuente: GO:CC | ID: GO:0000793 | Genes: 63 | p-valor ruta: 3.39e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: intracellular membraneless organelle (Página 1 de 11)

Fuente: GO:CC | ID: GO:0043232 | Genes: 263 | p-valor ruta: 2.56e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2

Ruta: intracellular membraneless organelle (Página 2 de 11)

Fuente: GO:CC | ID: GO:0043232 | Genes: 263 | p-valor ruta: 2.56e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG0000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG0000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG0000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG0000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG0000166801	FAM11A	DOWN	-1.546	4.63e-20	583.1
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG0000189057	FAM11B	DOWN	-2.315	2.29e-19	695.4
ENSG0000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG0000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG0000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG0000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG0000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG0000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG0000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG0000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1

Ruta: intracellular membraneless organelle (Página 3 de 11)

Fuente: GO:CC | ID: GO:0043232 | Genes: 263 | p-valor ruta: 2.56e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2

Ruta: intracellular membraneless organelle (Página 4 de 11)

Fuente: GO:CC | ID: GO:0043232 | Genes: 263 | p-valor ruta: 2.56e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000133739	LRRCC1	DOWN	-1.272	1.80e-12	348.7
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6

Ruta: intracellular membraneless organelle (Página 5 de 11)

Fuente: GO:CC | ID: GO:0043232 | Genes: 263 | p-valor ruta: 2.56e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000163584	RPL22L1	DOWN	-1.560	7.80e-11	4446.0
ENSG00000147394	ZNF185	UP	1.052	8.01e-11	1372.2
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000149548	CCDC15	DOWN	-1.977	9.27e-10	145.8
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4

Ruta: intracellular membraneless organelle (Página 6 de 11)

Fuente: GO:CC | ID: GO:0043232 | Genes: 263 | p-valor ruta: 2.56e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3

Ruta: intracellular membraneless organelle (Página 7 de 11)

Fuente: GO:CC | ID: GO:0043232 | Genes: 263 | p-valor ruta: 2.56e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000120647	CCDC77	DOWN	-1.339	2.44e-06	215.8
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0

Ruta: intracellular membraneless organelle (Página 8 de 11)

Fuente: GO:CC | ID: GO:0043232 | Genes: 263 | p-valor ruta: 2.56e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000293495		DOWN	-1.307	5.02e-05	261.4
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8

Ruta: intracellular membraneless organelle (Página 9 de 11)

Fuente: GO:CC | ID: GO:0043232 | Genes: 263 | p-valor ruta: 2.56e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9

Ruta: intracellular membraneless organelle (Página 10 de 11)

Fuente: GO:CC | ID: GO:0043232 | Genes: 263 | p-valor ruta: 2.56e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG0000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000166831	RBPM52	DOWN	-1.538	1.19e-02	49.2
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8

Ruta: intracellular membraneless organelle (Página 11 de 11)

Fuente: GO:CC | ID: GO:0043232 | Genes: 263 | p-valor ruta: 2.56e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000174669	SLC29A2	DOWN	-1.426	4.13e-02	38.9
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: membraneless organelle (Página 1 de 11)

Fuente: GO:CC | ID: GO:0043228 | Genes: 263 | p-valor ruta: 2.64e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2

Ruta: membraneless organelle (Página 2 de 11)

Fuente: GO:CC | ID: GO:0043228 | Genes: 263 | p-valor ruta: 2.64e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG0000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG0000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG0000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG0000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG0000166801	FAM11A	DOWN	-1.546	4.63e-20	583.1
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG0000189057	FAM11B	DOWN	-2.315	2.29e-19	695.4
ENSG0000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG0000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG0000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG0000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG0000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG0000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG0000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG0000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1

Ruta: membraneless organelle (Página 3 de 11)

Fuente: GO:CC | ID: GO:0043228 | Genes: 263 | p-valor ruta: 2.64e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2

Ruta: membraneless organelle (Página 4 de 11)

Fuente: GO:CC | ID: GO:0043228 | Genes: 263 | p-valor ruta: 2.64e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000133739	LRRCC1	DOWN	-1.272	1.80e-12	348.7
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6

Ruta: membraneless organelle (Página 5 de 11)

Fuente: GO:CC | ID: GO:0043228 | Genes: 263 | p-valor ruta: 2.64e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000163584	RPL22L1	DOWN	-1.560	7.80e-11	4446.0
ENSG00000147394	ZNF185	UP	1.052	8.01e-11	1372.2
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000149548	CCDC15	DOWN	-1.977	9.27e-10	145.8
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4

Ruta: membraneless organelle (Página 6 de 11)

Fuente: GO:CC | ID: GO:0043228 | Genes: 263 | p-valor ruta: 2.64e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3

Ruta: membraneless organelle (Página 7 de 11)

Fuente: GO:CC | ID: GO:0043228 | Genes: 263 | p-valor ruta: 2.64e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000120647	CCDC77	DOWN	-1.339	2.44e-06	215.8
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0

Ruta: membraneless organelle (Página 8 de 11)

Fuente: GO:CC | ID: GO:0043228 | Genes: 263 | p-valor ruta: 2.64e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000293495		DOWN	-1.307	5.02e-05	261.4
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8

Ruta: membraneless organelle (Página 9 de 11)

Fuente: GO:CC | ID: GO:0043228 | Genes: 263 | p-valor ruta: 2.64e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9

Ruta: membraneless organelle (Página 10 de 11)

Fuente: GO:CC | ID: GO:0043228 | Genes: 263 | p-valor ruta: 2.64e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG0000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000166831	RBPM2	DOWN	-1.538	1.19e-02	49.2
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8

Ruta: membraneless organelle (Página 11 de 11)

Fuente: GO:CC | ID: GO:0043228 | Genes: 263 | p-valor ruta: 2.64e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000174669	SLC29A2	DOWN	-1.426	4.13e-02	38.9
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: chromosome, centromeric region (Página 1 de 3)

Fuente: GO:CC | ID: GO:0000775 | Genes: 57 | p-valor ruta: 4.9e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6

Ruta: chromosome, centromeric region (Página 2 de 3)

Fuente: GO:CC | ID: GO:0000775 | Genes: 57 | p-valor ruta: 4.9e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3

Ruta: chromosome, centromeric region (Página 3 de 3)

Fuente: GO:CC | ID: GO:0000775 | Genes: 57 | p-valor ruta: 4.9e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: nucleoplasm (Página 1 de 8)

Fuente: GO:CC | ID: GO:0005654 | Genes: 199 | p-valor ruta: 3.02e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3

Ruta: nucleoplasm (Página 2 de 8)

Fuente: GO:CC | ID: GO:0005654 | Genes: 199 | p-valor ruta: 3.02e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG0000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG0000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG0000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG0000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG0000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG0000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG0000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG0000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG0000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG0000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG0000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG0000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG0000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG0000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG0000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG0000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG0000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7

Ruta: nucleoplasm (Página 3 de 8)

Fuente: GO:CC | ID: GO:0005654 | Genes: 199 | p-valor ruta: 3.02e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6

Ruta: nucleoplasm (Página 4 de 8)

Fuente: GO:CC | ID: GO:0005654 | Genes: 199 | p-valor ruta: 3.02e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGCB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4

Ruta: nucleoplasm (Página 5 de 8)

Fuente: GO:CC | ID: GO:0005654 | Genes: 199 | p-valor ruta: 3.02e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3

Ruta: nucleoplasm (Página 6 de 8)

Fuente: GO:CC | ID: GO:0005654 | Genes: 199 | p-valor ruta: 3.02e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3

Ruta: nucleoplasm (Página 7 de 8)

Fuente: GO:CC | ID: GO:0005654 | Genes: 199 | p-valor ruta: 3.02e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0

Ruta: nucleoplasm (Página 8 de 8)

Fuente: GO:CC | ID: GO:0005654 | Genes: 199 | p-valor ruta: 3.02e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000183048	SLC25A10	DOWN	-1.208	4.96e-02	35.4

Ruta: microtubule cytoskeleton (Página 1 de 5)

Fuente: GO:CC | ID: GO:0015630 | Genes: 111 | p-valor ruta: 3.53e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9

Ruta: microtubule cytoskeleton (Página 2 de 5)

Fuente: GO:CC | ID: GO:0015630 | Genes: 111 | p-valor ruta: 3.53e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000133739	LRRCC1	DOWN	-1.272	1.80e-12	348.7
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9

Ruta: microtubule cytoskeleton (Página 3 de 5)

Fuente: GO:CC | ID: GO:0015630 | Genes: 111 | p-valor ruta: 3.53e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000149548	CCDC15	DOWN	-1.977	9.27e-10	145.8
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6

Ruta: microtubule cytoskeleton (Página 4 de 5)

Fuente: GO:CC | ID: GO:0015630 | Genes: 111 | p-valor ruta: 3.53e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000120647	CCDC77	DOWN	-1.339	2.44e-06	215.8
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6

Ruta: microtubule cytoskeleton (Página 5 de 5)

Fuente: GO:CC | ID: GO:0015630 | Genes: 111 | p-valor ruta: 3.53e-36

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2

Ruta: condensed chromosome, centromeric region (Página 1 de 2)

Fuente: GO:CC | ID: GO:0000779 | Genes: 45 | p-valor ruta: 2.4e-34

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9

Ruta: condensed chromosome, centromeric region (Página 2 de 2)

Fuente: GO:CC | ID: GO:0000779 | Genes: 45 | p-valor ruta: 2.4e-34

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG0000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG0000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: spindle (Página 1 de 3)

Fuente: GO:CC | ID: GO:0005819 | Genes: 60 | p-valor ruta: 2.34e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6

Ruta: spindle (Página 2 de 3)

Fuente: GO:CC | ID: GO:0005819 | Genes: 60 | p-valor ruta: 2.34e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5

Ruta: spindle (Página 3 de 3)

Fuente: GO:CC | ID: GO:0005819 | Genes: 60 | p-valor ruta: 2.34e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: kinetochore (Página 1 de 2)

Fuente: GO:CC | ID: GO:0000776 | Genes: 41 | p–valor ruta: 1.22e–30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	−1.581	1.18e−44	832.9
ENSG00000178999	AURKB	DOWN	−2.095	1.44e−37	1004.1
ENSG00000123485	HJURP	DOWN	−2.015	6.13e−35	695.4
ENSG00000134057	CCNB1	DOWN	−1.376	4.23e−30	1075.8
ENSG00000143228	NUF2	DOWN	−2.262	2.12e−27	1144.3
ENSG00000089685	BIRC5	DOWN	−1.447	2.74e−24	999.2
ENSG00000154839	SKA1	DOWN	−2.106	9.93e−20	265.9
ENSG00000152253	SPC25	DOWN	−1.943	1.08e−19	456.4
ENSG00000137812	KNL1	DOWN	−1.964	1.50e−19	675.1
ENSG00000156970	BUB1B	DOWN	−1.960	1.47e−18	480.6
ENSG00000102384	CENPI	DOWN	−1.554	4.76e−17	603.3
ENSG00000165480	SKA3	DOWN	−1.586	1.14e−16	602.9
ENSG00000163535	SGO2	DOWN	−1.592	1.26e−16	1142.8
ENSG00000100162	CENPM	DOWN	−1.651	1.75e−16	256.1
ENSG00000151725	CENPU	DOWN	−1.858	3.84e−16	603.3
ENSG00000087586	AURKA	DOWN	−1.463	3.30e−14	1066.4
ENSG00000149636	DSN1	DOWN	−1.642	8.03e−14	568.7
ENSG00000122952	ZWINT	DOWN	−1.652	1.40e−13	998.2
ENSG00000164109	MAD2L1	DOWN	−1.656	2.19e−13	684.6
ENSG00000076382	SPAG5	DOWN	−1.738	1.21e−12	384.3
ENSG00000117724	CENPF	DOWN	−1.603	6.29e−12	2801.9
ENSG00000129810	SGO1	DOWN	−2.322	5.66e−11	212.1
ENSG00000142945	KIF2C	DOWN	−1.660	6.87e−11	313.0
ENSG00000169679	BUB1	DOWN	−1.427	8.07e−11	645.0
ENSG00000117399	CDC20	DOWN	−1.306	8.53e−11	1077.9

Ruta: kinetochore (Página 2 de 2)

Fuente: GO:CC | ID: GO:0000776 | Genes: 41 | p-valor ruta: 1.22e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: microtubule organizing center (Página 1 de 4)

Fuente: GO:CC | ID: GO:0005815 | Genes: 79 | p-valor ruta: 9.86e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG0000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG0000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG0000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG0000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG0000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG0000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG0000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG0000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG0000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG0000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG0000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2

Ruta: microtubule organizing center (Página 2 de 4)

Fuente: GO:CC | ID: GO:0005815 | Genes: 79 | p–valor ruta: 9.86e–29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000133739	LRRCC1	DOWN	-1.272	1.80e-12	348.7
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000149548	CCDC15	DOWN	-1.977	9.27e-10	145.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7

Ruta: microtubule organizing center (Página 3 de 4)

Fuente: GO:CC | ID: GO:0005815 | Genes: 79 | p-valor ruta: 9.86e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000120647	CCDC77	DOWN	-1.339	2.44e-06	215.8
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: microtubule organizing center (Página 4 de 4)

Fuente: GO:CC | ID: GO:0005815 | Genes: 79 | p-valor ruta: 9.86e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG0000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG0000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG0000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5

Ruta: centrosome (Página 1 de 3)

Fuente: GO:CC | ID: GO:0005813 | Genes: 71 | p–valor ruta: 2.82e–27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e–44	832.9
ENSG0000169607	CKAP2L	DOWN	-2.013	3.11e–42	1388.2
ENSG0000013810	TACC3	DOWN	-1.621	4.44e–40	2085.0
ENSG0000178999	AURKB	DOWN	-2.095	1.44e–37	1004.1
ENSG0000134057	CCNB1	DOWN	-1.376	4.23e–30	1075.8
ENSG0000145386	CCNA2	DOWN	-1.856	3.17e–26	988.0
ENSG0000170312	CDK1	DOWN	-2.088	2.27e–25	1384.7
ENSG0000132646	PCNA	DOWN	-1.372	6.33e–21	2475.7
ENSG0000138182	KIF20B	DOWN	-1.458	1.27e–20	1755.0
ENSG0000138180	CEP55	DOWN	-1.583	3.98e–20	905.8
ENSG0000154839	SKA1	DOWN	-2.106	9.93e–20	265.9
ENSG0000118655	DCLRE1B	DOWN	-2.051	1.24e–18	122.3
ENSG0000156970	BUB1B	DOWN	-1.960	1.47e–18	480.6
ENSG0000112118	MCM3	DOWN	-1.112	4.76e–18	989.6
ENSG0000237649	KIFC1	DOWN	-2.040	7.65e–17	505.4
ENSG0000101412	E2F1	DOWN	-1.971	9.08e–17	232.3
ENSG0000165480	SKA3	DOWN	-1.586	1.14e–16	602.9
ENSG0000151725	CENPU	DOWN	-1.858	3.84e–16	603.3
ENSG0000123473	STIL	DOWN	-1.696	3.74e–15	372.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e–15	291.4
ENSG0000163781	TOPBP1	DOWN	-1.311	1.42e–14	788.6
ENSG0000087586	AURKA	DOWN	-1.463	3.30e–14	1066.4
ENSG0000143476	DTL	DOWN	-2.411	3.23e–13	299.1
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e–12	384.3
ENSG0000133739	LRRCC1	DOWN	-1.272	1.80e–12	348.7

Ruta: centrosome (Página 2 de 3)

Fuente: GO:CC | ID: GO:0005813 | Genes: 71 | p-valor ruta: 2.82e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000149548	CCDC15	DOWN	-1.977	9.27e-10	145.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1

Ruta: centrosome (Página 3 de 3)

Fuente: GO:CC | ID: GO:0005813 | Genes: 71 | p–valor ruta: 2.82e–27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000120647	CCDC77	DOWN	-1.339	2.44e-06	215.8
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: nuclear chromosome (Página 1 de 2)

Fuente: GO:CC | ID: GO:0000228 | Genes: 43 | p-valor ruta: 3.3e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4

Ruta: nuclear chromosome (Página 2 de 2)

Fuente: GO:CC | ID: GO:0000228 | Genes: 43 | p-valor ruta: 3.3e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: cytoskeleton (Página 1 de 6)

Fuente: GO:CC | ID: GO:0005856 | Genes: 127 | p-valor ruta: 2.98e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3

Ruta: cytoskeleton (Página 2 de 6)

Fuente: GO:CC | ID: GO:0005856 | Genes: 127 | p-valor ruta: 2.98e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000133739	LRRCC1	DOWN	-1.272	1.80e-12	348.7
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6

Ruta: cytoskeleton (Página 3 de 6)

Fuente: GO:CC | ID: GO:0005856 | Genes: 127 | p-valor ruta: 2.98e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000147394	ZNF185	UP	1.052	8.01e-11	1372.2
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000149548	CCDC15	DOWN	-1.977	9.27e-10	145.8
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3

Ruta: cytoskeleton (Página 4 de 6)

Fuente: GO:CC | ID: GO:0005856 | Genes: 127 | p-valor ruta: 2.98e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000120647	CCDC77	DOWN	-1.339	2.44e-06	215.8
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7

Ruta: cytoskeleton (Página 5 de 6)

Fuente: GO:CC | ID: GO:0005856 | Genes: 127 | p-valor ruta: 2.98e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5

Ruta: cytoskeleton (Página 6 de 6)

Fuente: GO:CC | ID: GO:0005856 | Genes: 127 | p-valor ruta: 2.98e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: spindle pole (Página 1 de 2)

Fuente: GO:CC | ID: GO:0000922 | Genes: 36 | p-valor ruta: 6.23e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3

Ruta: spindle pole (Página 2 de 2)

Fuente: GO:CC | ID: GO:0000922 | Genes: 36 | p-valor ruta: 6.23e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: nuclear lumen (Página 1 de 9)

Fuente: GO:CC | ID: GO:0031981 | Genes: 204 | p-valor ruta: 2.31e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3

Ruta: nuclear lumen (Página 2 de 9)

Fuente: GO:CC | ID: GO:0031981 | Genes: 204 | p-valor ruta: 2.31e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG0000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG0000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG0000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG0000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG0000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG0000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG0000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG0000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG0000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG0000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG0000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG0000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG0000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG0000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG0000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG0000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG0000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7

Ruta: nuclear lumen (Página 3 de 9)

Fuente: GO:CC | ID: GO:0031981 | Genes: 204 | p-valor ruta: 2.31e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6

Ruta: nuclear lumen (Página 4 de 9)

Fuente: GO:CC | ID: GO:0031981 | Genes: 204 | p-valor ruta: 2.31e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGCB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4

Ruta: nuclear lumen (Página 5 de 9)

Fuente: GO:CC | ID: GO:0031981 | Genes: 204 | p-valor ruta: 2.31e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7

Ruta: nuclear lumen (Página 6 de 9)

Fuente: GO:CC | ID: GO:0031981 | Genes: 204 | p-valor ruta: 2.31e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG0000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8

Ruta: nuclear lumen (Página 7 de 9)

Fuente: GO:CC | ID: GO:0031981 | Genes: 204 | p-valor ruta: 2.31e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000293495		DOWN	-1.307	5.02e-05	261.4
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: nuclear lumen (Página 8 de 9)

Fuente: GO:CC | ID: GO:0031981 | Genes: 204 | p-valor ruta: 2.31e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1

Ruta: nuclear lumen (Página 9 de 9)

Fuente: GO:CC | ID: GO:0031981 | Genes: 204 | p-valor ruta: 2.31e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000174669	SLC29A2	DOWN	-1.426	4.13e-02	38.9
ENSG00000183048	SLC25A10	DOWN	-1.208	4.96e-02	35.4

Ruta: outer kinetochore

Fuente: GO:CC | ID: GO:0000940 | Genes: 15 | p-valor ruta: 1.9e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2

Ruta: replication fork

Fuente: GO:CC | ID: GO:0005657 | Genes: 23 | p-valor ruta: 2.2e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: nucleus (Página 1 de 12)

Fuente: GO:CC | ID: GO:0005634 | Genes: 285 | p-valor ruta: 3.13e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3

Ruta: nucleus (Página 2 de 12)

Fuente: GO:CC | ID: GO:0005634 | Genes: 285 | p-valor ruta: 3.13e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000189057	FAM111B	DOWN	-2.315	2.29e-19	695.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6

Ruta: nucleus (Página 3 de 12)

Fuente: GO:CC | ID: GO:0005634 | Genes: 285 | p-valor ruta: 3.13e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000137310	TCF19	DOWN	-1.639	1.12e-14	547.9

Ruta: nucleus (Página 4 de 12)

Fuente: GO:CC | ID: GO:0005634 | Genes: 285 | p-valor ruta: 3.13e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6

Ruta: nucleus (Página 5 de 12)

Fuente: GO:CC | ID: GO:0005634 | Genes: 285 | p-valor ruta: 3.13e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000068489	PRR11	DOWN	-1.033	9.90e-11	1510.0
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7

Ruta: nucleus (Página 6 de 12)

Fuente: GO:CC | ID: GO:0005634 | Genes: 285 | p-valor ruta: 3.13e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG0000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG0000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG0000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG0000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG0000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG0000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG0000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG0000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG0000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG0000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG0000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG0000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG0000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG0000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG0000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG0000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG0000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG0000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG0000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG0000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG0000100479	POLE2	DOWN	-1.692	2.50e-08	173.1

Ruta: nucleus (Página 7 de 12)

Fuente: GO:CC | ID: GO:0005634 | Genes: 285 | p-valor ruta: 3.13e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9

Ruta: nucleus (Página 8 de 12)

Fuente: GO:CC | ID: GO:0005634 | Genes: 285 | p-valor ruta: 3.13e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3

Ruta: nucleus (Página 9 de 12)

Fuente: GO:CC | ID: GO:0005634 | Genes: 285 | p-valor ruta: 3.13e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000293495		DOWN	-1.307	5.02e-05	261.4
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000160352	ZNF714	DOWN	-1.576	1.17e-04	120.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000166881	NEMP1	DOWN	-2.208	2.92e-04	75.0
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4

Ruta: nucleus (Página 10 de 12)

Fuente: GO:CC | ID: GO:0005634 | Genes: 285 | p-valor ruta: 3.13e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6

Ruta: nucleus (Página 11 de 12)

Fuente: GO:CC | ID: GO:0005634 | Genes: 285 | p-valor ruta: 3.13e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000166831	RBPMS2	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: nucleus (Página 12 de 12)

Fuente: GO:CC | ID: GO:0005634 | Genes: 285 | p-valor ruta: 3.13e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000121940	CLCC1	DOWN	-1.122	4.07e-02	81.5
ENSG00000146842	TMEM209	DOWN	-1.100	4.09e-02	64.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000174669	SLC29A2	DOWN	-1.426	4.13e-02	38.9
ENSG00000196247	ZNF107	DOWN	-1.028	4.60e-02	77.9
ENSG00000183048	SLC25A10	DOWN	-1.208	4.96e-02	35.4

Ruta: supramolecular complex (Página 1 de 4)

Fuente: GO:CC | ID: GO:0099080 | Genes: 83 | p–valor ruta: 2.03e–17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	−1.581	1.18e−44	832.9
ENSG00000178999	AURKB	DOWN	−2.095	1.44e−37	1004.1
ENSG00000123485	HJURP	DOWN	−2.015	6.13e−35	695.4
ENSG00000134057	CCNB1	DOWN	−1.376	4.23e−30	1075.8
ENSG00000090889	KIF4A	DOWN	−1.513	7.98e−28	682.7
ENSG00000143228	NUF2	DOWN	−2.262	2.12e−27	1144.3
ENSG00000198901	PRC1	DOWN	−1.702	7.50e−27	475.6
ENSG00000170312	CDK1	DOWN	−2.088	2.27e−25	1384.7
ENSG00000075218	GTSE1	DOWN	−2.024	4.26e−25	327.8
ENSG00000089685	BIRC5	DOWN	−1.447	2.74e−24	999.2
ENSG00000138376	BARD1	DOWN	−1.668	4.10e−24	474.1
ENSG00000138182	KIF20B	DOWN	−1.458	1.27e−20	1755.0
ENSG00000154839	SKA1	DOWN	−2.106	9.93e−20	265.9
ENSG00000152253	SPC25	DOWN	−1.943	1.08e−19	456.4
ENSG00000137812	KNL1	DOWN	−1.964	1.50e−19	675.1
ENSG00000156970	BUB1B	DOWN	−1.960	1.47e−18	480.6
ENSG00000102384	CENPI	DOWN	−1.554	4.76e−17	603.3
ENSG00000237649	KIFC1	DOWN	−2.040	7.65e−17	505.4
ENSG00000165480	SKA3	DOWN	−1.586	1.14e−16	602.9
ENSG00000163535	SGO2	DOWN	−1.592	1.26e−16	1142.8
ENSG00000100162	CENPM	DOWN	−1.651	1.75e−16	256.1
ENSG00000088325	TPX2	DOWN	−1.571	2.07e−16	1191.9
ENSG00000151725	CENPU	DOWN	−1.858	3.84e−16	603.3
ENSG00000113368	LMNB1	DOWN	−1.225	1.98e−15	1268.3
ENSG00000087586	AURKA	DOWN	−1.463	3.30e−14	1066.4

Ruta: supramolecular complex (Página 2 de 4)

Fuente: GO:CC | ID: GO:0099080 | Genes: 83 | p–valor ruta: 2.03e–17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3

Ruta: supramolecular complex (Página 3 de 4)

Fuente: GO:CC | ID: GO:0099080 | Genes: 83 | p–valor ruta: 2.03e–17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8

Ruta: supramolecular complex (Página 4 de 4)

Fuente: GO:CC | ID: GO:0099080 | Genes: 83 | p-valor ruta: 2.03e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000166831	RBPM2	DOWN	-1.538	1.19e-02	49.2
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: mitotic spindle (Página 1 de 2)

Fuente: GO:CC | ID: GO:0072686 | Genes: 30 | p–valor ruta: 5.81e–17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3

Ruta: mitotic spindle (Página 2 de 2)

Fuente: GO:CC | ID: GO:0072686 | Genes: 30 | p-valor ruta: 5.81e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4

Ruta: cytosol (Página 1 de 8)

Fuente: GO:CC | ID: GO:0005829 | Genes: 187 | p-valor ruta: 4.01e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7

Ruta: cytosol (Página 2 de 8)

Fuente: GO:CC | ID: GO:0005829 | Genes: 187 | p-valor ruta: 4.01e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000111665	CDCA3	DOWN	-1.647	8.37e-16	690.7
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4

Ruta: cytosol (Página 3 de 8)

Fuente: GO:CC | ID: GO:0005829 | Genes: 187 | p-valor ruta: 4.01e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000147697	GSDMC	UP	2.564	1.66e-10	130.4

Ruta: cytosol (Página 4 de 8)

Fuente: GO:CC | ID: GO:0005829 | Genes: 187 | p-valor ruta: 4.01e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000205208	C4orf46	DOWN	-1.302	2.82e-10	479.4
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164237	CMBL	UP	1.794	1.17e-09	471.4
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6

Ruta: cytosol (Página 5 de 8)

Fuente: GO:CC | ID: GO:0005829 | Genes: 187 | p-valor ruta: 4.01e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9

Ruta: cytosol (Página 6 de 8)

Fuente: GO:CC | ID: GO:0005829 | Genes: 187 | p-valor ruta: 4.01e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000139410	SDSL	UP	1.421	3.14e-05	75.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG0000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2

Ruta: cytosol (Página 7 de 8)

Fuente: GO:CC | ID: GO:0005829 | Genes: 187 | p-valor ruta: 4.01e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000109452	INPP4B	UP	1.158	4.20e-04	146.5
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6

Ruta: cytosol (Página 8 de 8)

Fuente: GO:CC | ID: GO:0005829 | Genes: 187 | p-valor ruta: 4.01e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000107719	PALD1	DOWN	-1.387	8.65e-03	67.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000166831	RBPM2	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7

Ruta: intracellular organelle lumen (Página 1 de 9)

Fuente: GO:CC | ID: GO:0070013 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3

Ruta: intracellular organelle lumen (Página 2 de 9)

Fuente: GO:CC | ID: GO:0070013 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG0000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG0000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG0000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG0000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG0000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG0000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG0000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG0000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG0000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG0000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG0000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG0000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG0000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG0000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG0000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG0000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG0000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7

Ruta: intracellular organelle lumen (Página 3 de 9)

Fuente: GO:CC | ID: GO:0070013 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000010438	PRSS3	UP	1.837	1.56e-15	633.6
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDC45	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3

Ruta: intracellular organelle lumen (Página 4 de 9)

Fuente: GO:CC | ID: GO:0070013 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000161513	FDXR	UP	1.086	1.56e-11	595.0
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9

Ruta: intracellular organelle lumen (Página 5 de 9)

Fuente: GO:CC | ID: GO:0070013 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8

Ruta: intracellular organelle lumen (Página 6 de 9)

Fuente: GO:CC | ID: GO:0070013 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4

Ruta: intracellular organelle lumen (Página 7 de 9)

Fuente: GO:CC | ID: GO:0070013 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000293495		DOWN	-1.307	5.02e-05	261.4
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6

Ruta: intracellular organelle lumen (Página 8 de 9)

Fuente: GO:CC | ID: GO:0070013 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7

Ruta: intracellular organelle lumen (Página 9 de 9)

Fuente: GO:CC | ID: GO:0070013 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000174669	SLC29A2	DOWN	-1.426	4.13e-02	38.9
ENSG00000183048	SLC25A10	DOWN	-1.208	4.96e-02	35.4

Ruta: membrane–enclosed lumen (Página 1 de 9)

Fuente: GO:CC | ID: GO:0031974 | Genes: 210 | p–valor ruta: 3.34e–15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	–2.280	4.37e–57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e–44	4228.1
ENSG00000080986	NDC80	DOWN	–1.581	1.18e–44	832.9
ENSG00000094804	CDC6	DOWN	–2.490	6.33e–43	452.0
ENSG00000092853	CLSPN	DOWN	–2.015	3.37e–41	1306.1
ENSG00000168496	FEN1	DOWN	–2.192	5.29e–41	1595.8
ENSG00000104738	MCM4	DOWN	–2.222	1.44e–37	1173.0
ENSG00000178999	AURKB	DOWN	–2.095	1.44e–37	1004.1
ENSG00000123485	HJURP	DOWN	–2.015	6.13e–35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e–34	4081.3
ENSG00000175063	UBE2C	DOWN	–1.912	1.62e–32	1424.6
ENSG00000131747	TOP2A	DOWN	–1.733	4.48e–31	5823.0
ENSG00000100297	MCM5	DOWN	–1.712	2.96e–30	468.0
ENSG00000111247	RAD51AP1	DOWN	–1.758	3.76e–30	411.5
ENSG00000134057	CCNB1	DOWN	–1.376	4.23e–30	1075.8
ENSG00000090889	KIF4A	DOWN	–1.513	7.98e–28	682.7
ENSG00000143228	NUF2	DOWN	–2.262	2.12e–27	1144.3
ENSG00000198901	PRC1	DOWN	–1.702	7.50e–27	475.6
ENSG00000145386	CCNA2	DOWN	–1.856	3.17e–26	988.0
ENSG00000170312	CDK1	DOWN	–2.088	2.27e–25	1384.7
ENSG00000075218	GTSE1	DOWN	–2.024	4.26e–25	327.8
ENSG00000076003	MCM6	DOWN	–1.881	2.08e–24	659.3
ENSG00000089685	BIRC5	DOWN	–1.447	2.74e–24	999.2
ENSG00000138376	BARD1	DOWN	–1.668	4.10e–24	474.1
ENSG00000112312	GMNN	DOWN	–1.638	4.21e–24	861.3

Ruta: membrane–enclosed lumen (Página 2 de 9)

Fuente: GO:CC | ID: GO:0031974 | Genes: 210 | p–valor ruta: 3.34e–15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000065328	MCM10	DOWN	−2.433	2.52e−23	492.5
ENSG0000132646	PCNA	DOWN	−1.372	6.33e−21	2475.7
ENSG0000011426	ANLN	DOWN	−1.534	1.05e−20	1912.3
ENSG0000138182	KIF20B	DOWN	−1.458	1.27e−20	1755.0
ENSG0000165244	ZNF367	DOWN	−2.804	3.39e−20	156.1
ENSG0000168411	RFWD3	DOWN	−1.328	3.39e−20	1082.9
ENSG0000166801	FAM11A	DOWN	−1.546	4.63e−20	583.1
ENSG0000156802	ATAD2	DOWN	−1.970	8.59e−20	682.4
ENSG0000137812	KNL1	DOWN	−1.964	1.50e−19	675.1
ENSG0000166508	MCM7	DOWN	−1.646	2.26e−19	1030.4
ENSG0000136824	SMC2	DOWN	−1.424	3.27e−19	2147.1
ENSG0000118655	DCLRE1B	DOWN	−2.051	1.24e−18	122.3
ENSG0000091651	ORC6	DOWN	−1.796	2.46e−18	386.3
ENSG0000172716	SLFN11	DOWN	−1.226	2.51e−18	752.8
ENSG0000112118	MCM3	DOWN	−1.112	4.76e−18	989.6
ENSG0000113810	SMC4	DOWN	−1.484	8.40e−18	4283.1
ENSG0000132436	FIGNL1	DOWN	−1.425	3.78e−17	624.9
ENSG0000102384	CENPI	DOWN	−1.554	4.76e−17	603.3
ENSG0000184661	CDCA2	DOWN	−2.132	5.90e−17	528.1
ENSG0000101412	E2F1	DOWN	−1.971	9.08e−17	232.3
ENSG0000163535	SGO2	DOWN	−1.592	1.26e−16	1142.8
ENSG0000100162	CENPM	DOWN	−1.651	1.75e−16	256.1
ENSG0000088325	TPX2	DOWN	−1.571	2.07e−16	1191.9
ENSG0000151725	CENPU	DOWN	−1.858	3.84e−16	603.3
ENSG0000134690	CDCA8	DOWN	−1.664	4.17e−16	833.7

Ruta: membrane–enclosed lumen (Página 3 de 9)

Fuente: GO:CC | ID: GO:0031974 | Genes: 210 | p–valor ruta: 3.34e–15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000010438	PRSS3	UP	1.837	1.56e–15	633.6
ENSG0000106462	EZH2	DOWN	–1.170	1.57e–15	683.6
ENSG0000172667	ZMAT3	UP	1.195	1.91e–15	2971.2
ENSG0000113368	LMNB1	DOWN	–1.225	1.98e–15	1268.3
ENSG0000101003	GINS1	DOWN	–1.773	2.82e–15	374.2
ENSG0000123473	STIL	DOWN	–1.696	3.74e–15	372.6
ENSG0000051180	RAD51	DOWN	–2.077	4.28e–15	291.4
ENSG0000187741	FANCA	DOWN	–1.866	5.41e–15	107.5
ENSG0000163781	TOPBP1	DOWN	–1.311	1.42e–14	788.6
ENSG0000171320	ESCO2	DOWN	–2.194	2.27e–14	284.8
ENSG0000087586	AURKA	DOWN	–1.463	3.30e–14	1066.4
ENSG0000131981	LGALS3	UP	1.129	3.85e–14	663.5
ENSG0000149636	DSN1	DOWN	–1.642	8.03e–14	568.7
ENSG0000122952	ZWINT	DOWN	–1.652	1.40e–13	998.2
ENSG0000164109	MAD2L1	DOWN	–1.656	2.19e–13	684.6
ENSG0000163918	RFC4	DOWN	–1.722	2.38e–13	353.5
ENSG0000148773	MKI67	DOWN	–1.808	2.94e–13	1720.7
ENSG0000143476	DTL	DOWN	–2.411	3.23e–13	299.1
ENSG0000140451	PIF1	DOWN	–2.118	6.42e–13	126.2
ENSG0000112029	FBXO5	DOWN	–2.086	6.62e–13	325.6
ENSG0000146670	CDC45	DOWN	–2.059	8.54e–13	175.9
ENSG0000131153	GINS2	DOWN	–1.531	1.00e–12	334.0
ENSG0000012048	BRCA1	DOWN	–1.766	1.14e–12	390.2
ENSG0000076382	SPAG5	DOWN	–1.738	1.21e–12	384.3
ENSG0000175643	RMI2	DOWN	–2.108	1.76e–12	174.3

Ruta: membrane–enclosed lumen (Página 4 de 9)

Fuente: GO:CC | ID: GO:0031974 | Genes: 210 | p–valor ruta: 3.34e–15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000146918	NCAPG2	DOWN	−1.301	6.06e−12	556.6
ENSG00000117724	CENPF	DOWN	−1.603	6.29e−12	2801.9
ENSG00000162607	USP1	DOWN	−1.400	1.07e−11	1193.8
ENSG00000125885	MCM8	DOWN	−1.405	1.29e−11	278.7
ENSG00000161513	FDXR	UP	1.086	1.56e−11	595.0
ENSG00000129195	PIMREG	DOWN	−1.831	1.72e−11	267.5
ENSG00000164104	HMGGB2	DOWN	−1.572	1.72e−11	2905.5
ENSG00000129810	SGO1	DOWN	−2.322	5.66e−11	212.1
ENSG00000123374	CDK2	DOWN	−1.140	6.55e−11	1630.6
ENSG00000169679	BUB1	DOWN	−1.427	8.07e−11	645.0
ENSG00000077152	UBE2T	DOWN	−1.383	8.25e−11	1278.6
ENSG00000117399	CDC20	DOWN	−1.306	8.53e−11	1077.9
ENSG00000177084	POLE	DOWN	−2.215	8.53e−11	106.4
ENSG00000087494	PTHLH	UP	2.252	1.19e−10	97.1
ENSG00000115163	CENPA	DOWN	−1.689	1.34e−10	297.0
ENSG00000100749	VRK1	DOWN	−1.501	2.14e−10	731.7
ENSG00000101057	MYBL2	DOWN	−1.290	2.23e−10	706.9
ENSG00000137807	KIF23	DOWN	−1.544	2.50e−10	400.6
ENSG00000144554	FANCD2	DOWN	−1.681	5.26e−10	378.0
ENSG00000049541	RFC2	DOWN	−1.473	6.43e−10	250.2
ENSG00000167513	CDT1	DOWN	−2.358	9.49e−10	138.1
ENSG0000010292	NCAPD2	DOWN	−1.100	9.61e−10	894.2
ENSG00000186185	KIF18B	DOWN	−2.437	1.06e−09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e−09	1061.1
ENSG00000139618	BRCA2	DOWN	−1.944	1.37e−09	326.9

Ruta: membrane–enclosed lumen (Página 5 de 9)

Fuente: GO:CC | ID: GO:0031974 | Genes: 210 | p–valor ruta: 3.34e–15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164938	TP53INP1	UP	1.151	1.66e–09	893.9
ENSG00000166803	PCLAF	DOWN	–1.228	2.39e–09	4124.4
ENSG00000175305	CCNE2	DOWN	–2.245	2.83e–09	73.4
ENSG00000114346	ECT2	DOWN	–1.276	2.96e–09	617.4
ENSG00000159055	MIS18A	DOWN	–1.201	3.32e–09	460.4
ENSG00000164045	CDC25A	DOWN	–1.398	3.62e–09	386.0
ENSG00000221829	FANCG	DOWN	–1.727	3.98e–09	141.4
ENSG00000121152	NCAPH	DOWN	–2.359	4.90e–09	170.5
ENSG00000145604	SKP2	DOWN	–1.333	5.70e–09	594.2
ENSG00000136982	DSCC1	DOWN	–1.851	5.81e–09	116.7
ENSG00000161888	SPC24	DOWN	–1.240	7.21e–09	360.5
ENSG00000158402	CDC25C	DOWN	–2.102	8.88e–09	177.0
ENSG00000276043	UHRF1	DOWN	–1.751	1.20e–08	161.5
ENSG00000103995	CEP152	DOWN	–1.141	1.66e–08	311.4
ENSG00000129534	MIS18BP1	DOWN	–1.187	2.29e–08	990.4
ENSG00000185480	PARPBP	DOWN	–1.442	2.48e–08	364.2
ENSG00000100479	POLE2	DOWN	–1.692	2.50e–08	173.1
ENSG00000140525	FANCI	DOWN	–1.266	3.48e–08	536.3
ENSG00000080839	RBL1	DOWN	–1.533	4.00e–08	151.5
ENSG00000101868	POLA1	DOWN	–1.208	4.18e–08	300.4
ENSG00000031691	CENPQ	DOWN	–1.420	5.20e–08	308.3
ENSG00000123219	CENPK	DOWN	–1.375	6.42e–08	355.1
ENSG00000111445	RFC5	DOWN	–1.386	7.25e–08	347.4
ENSG00000144354	CDCA7	DOWN	–1.327	9.78e–08	445.1
ENSG00000198554	WDHD1	DOWN	–1.420	1.64e–07	256.8

Ruta: membrane–enclosed lumen (Página 6 de 9)

Fuente: GO:CC | ID: GO:0031974 | Genes: 210 | p–valor ruta: 3.34e–15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4

Ruta: membrane–enclosed lumen (Página 7 de 9)

Fuente: GO:CC | ID: GO:0031974 | Genes: 210 | p–valor ruta: 3.34e–15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138092	CENPO	DOWN	-1.362	3.13e–05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e–05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e–05	824.3
ENSG00000137337	MDC1	DOWN	-1.090	4.40e–05	151.5
ENSG00000293495		DOWN	-1.307	5.02e–05	261.4
ENSG00000189060	H1–0	DOWN	-1.085	5.21e–05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e–05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e–05	126.7
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e–04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e–04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e–04	128.5
ENSG00000085872	CHERP	DOWN	-1.134	2.05e–04	192.1
ENSG00000242265	PEG10	DOWN	-1.056	2.33e–04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e–04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e–04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e–04	172.2
ENSG00000038427	VCAN	UP	2.629	3.44e–04	39.3
ENSG00000133119	RFC3	DOWN	-1.777	3.63e–04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e–04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e–04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e–04	57.9
ENSG00000176697	BDNF	UP	1.321	5.08e–04	151.5
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e–04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e–04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e–04	142.6

Ruta: membrane–enclosed lumen (Página 8 de 9)

Fuente: GO:CC | ID: GO:0031974 | Genes: 210 | p–valor ruta: 3.34e–15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7

Ruta: membrane–enclosed lumen (Página 9 de 9)

Fuente: GO:CC | ID: GO:0031974 | Genes: 210 | p–valor ruta: 3.34e–15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000184500	PROS1	UP	1.173	1.59e–02	71.6
ENSG00000184162	NR2C2AP	DOWN	–1.128	1.72e–02	241.3
ENSG00000138346	DNA2	DOWN	–1.620	1.96e–02	111.6
ENSG00000100206	DMC1	DOWN	–1.836	2.41e–02	15.3
ENSG00000184635	ZNF93	DOWN	–1.354	2.76e–02	86.5
ENSG00000108423	TUBD1	DOWN	–1.008	2.79e–02	124.1
ENSG00000136492	BRIP1	DOWN	–2.016	3.04e–02	163.3
ENSG00000203780	FANK1	UP	1.721	3.31e–02	30.7
ENSG00000174669	SLC29A2	DOWN	–1.426	4.13e–02	38.9
ENSG00000183048	SLC25A10	DOWN	–1.208	4.96e–02	35.4

Ruta: organelle lumen (Página 1 de 9)

Fuente: GO:CC | ID: GO:0043233 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3

Ruta: organelle lumen (Página 2 de 9)

Fuente: GO:CC | ID: GO:0043233 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG0000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG0000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG0000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG0000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG0000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG0000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG0000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG0000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG0000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG0000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG0000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG0000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG0000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG0000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG0000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG0000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG0000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG0000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG0000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG0000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7

Ruta: organelle lumen (Página 3 de 9)

Fuente: GO:CC | ID: GO:0043233 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000010438	PRSS3	UP	1.837	1.56e-15	633.6
ENSG0000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG0000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG0000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG0000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG0000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG0000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG0000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG0000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG0000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000146670	CDC45	DOWN	-2.059	8.54e-13	175.9
ENSG0000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG0000175643	RMI2	DOWN	-2.108	1.76e-12	174.3

Ruta: organelle lumen (Página 4 de 9)

Fuente: GO:CC | ID: GO:0043233 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000161513	FDXR	UP	1.086	1.56e-11	595.0
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9

Ruta: organelle lumen (Página 5 de 9)

Fuente: GO:CC | ID: GO:0043233 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8

Ruta: organelle lumen (Página 6 de 9)

Fuente: GO:CC | ID: GO:0043233 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4

Ruta: organelle lumen (Página 7 de 9)

Fuente: GO:CC | ID: GO:0043233 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000293495		DOWN	-1.307	5.02e-05	261.4
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6

Ruta: organelle lumen (Página 8 de 9)

Fuente: GO:CC | ID: GO:0043233 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7

Ruta: organelle lumen (Página 9 de 9)

Fuente: GO:CC | ID: GO:0043233 | Genes: 210 | p-valor ruta: 3.34e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000174669	SLC29A2	DOWN	-1.426	4.13e-02	38.9
ENSG00000183048	SLC25A10	DOWN	-1.208	4.96e-02	35.4

Ruta: microtubule (Página 1 de 2)

Fuente: GO:CC | ID: GO:0005874 | Genes: 42 | p-valor ruta: 1.29e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1

Ruta: microtubule (Página 2 de 2)

Fuente: GO:CC | ID: GO:0005874 | Genes: 42 | p-valor ruta: 1.29e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2

Ruta: chromosome, telomeric region

Fuente: GO:CC | ID: GO:0000781 | Genes: 25 | p–valor ruta: 7.93e–13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: cytoplasm (Página 1 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3

Ruta: cytoplasm (Página 2 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG0000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6

Ruta: cytoplasm (Página 3 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG0000058085	LAMC2	UP	1.879	2.12e-17	204.8
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000111665	CDCA3	DOWN	-1.647	8.37e-16	690.7
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG0000010438	PRSS3	UP	1.837	1.56e-15	633.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5

Ruta: cytoplasm (Página 4 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000164466	SFXN1	DOWN	-1.129	2.57e-13	1052.2
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000133739	LRRK2	DOWN	-1.272	1.80e-12	348.7
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000161513	FDXR	UP	1.086	1.56e-11	595.0

Ruta: cytoplasm (Página 5 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000147394	ZNF185	UP	1.052	8.01e-11	1372.2
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000068489	PRR11	DOWN	-1.033	9.90e-11	1510.0
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000147697	GSDMC	UP	2.564	1.66e-10	130.4
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000205208	C4orf46	DOWN	-1.302	2.82e-10	479.4
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1

Ruta: cytoplasm (Página 6 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164237	CMBL	UP	1.794	1.17e-09	471.4
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0

Ruta: cytoplasm (Página 7 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000135451	TROAP	DOWN	-2.330	4.41e-08	64.0
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG0000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG0000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000129038	LOXL1	UP	1.441	3.55e-07	153.1
ENSG0000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2

Ruta: cytoplasm (Página 8 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000146410	MTFR2	DOWN	-1.746	5.92e-06	145.6
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000139133	ALG10	DOWN	-1.541	8.66e-06	64.1
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7

Ruta: cytoplasm (Página 9 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000139410	SDSL	UP	1.421	3.14e-05	75.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000175600	SUGCT	UP	2.209	1.39e-04	54.4
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000160180	TFF3	UP	1.708	1.97e-04	44.6

Ruta: cytoplasm (Página 10 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG0000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG0000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG0000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG0000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG0000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG0000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG0000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG0000109452	INPP4B	UP	1.158	4.20e-04	146.5
ENSG0000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG0000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG0000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG0000138780	GSTCD	DOWN	-1.373	4.88e-04	110.9
ENSG0000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG0000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG0000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG0000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG0000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG0000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG0000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG0000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG0000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG0000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: cytoplasm (Página 11 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000087299	L2HGDH	DOWN	-1.318	1.89e-03	70.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000171451	DSEL	UP	1.321	2.18e-03	188.5
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000228474	OST4	UP	1.044	5.07e-03	862.5
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: cytoplasm (Página 12 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000107719	PALD1	DOWN	-1.387	8.65e-03	67.9
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000181652	ATG9B	UP	1.052	9.34e-03	97.0
ENSG00000075303	SLC25A40	DOWN	-1.118	9.38e-03	169.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000185352	HS6ST3	UP	2.354	9.79e-03	25.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000166831	RBPM2	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000172197	MBOAT1	DOWN	-1.396	1.61e-02	54.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000163596	ICA1L	DOWN	-1.027	1.99e-02	76.8
ENSG00000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1

Ruta: cytoplasm (Página 13 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 314 | p-valor ruta: 1.37e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000281344	HELLPAR	DOWN	-1.328	3.14e-02	46.9
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000121940	CLCC1	DOWN	-1.122	4.07e-02	81.5
ENSG00000146842	TMEM209	DOWN	-1.100	4.09e-02	64.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000183048	SLC25A10	DOWN	-1.208	4.96e-02	35.4
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: condensed nuclear chromosome

Fuente: GO:CC | ID: GO:0000794 | Genes: 18 | p-valor ruta: 4.55e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: CMG complex

Fuente: GO:CC | ID: GO:0071162 | Genes: 9 | p-valor ruta: 5.23e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5

Ruta: midbody (Página 1 de 2)

Fuente: GO:CC | ID: GO:0030496 | Genes: 26 | p-valor ruta: 1.01e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8

Ruta: midbody (Página 2 de 2)

Fuente: GO:CC | ID: GO:0030496 | Genes: 26 | p-valor ruta: 1.01e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1

Ruta: intracellular organelle (Página 1 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7

Ruta: intracellular organelle (Página 2 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000189057	FAM111B	DOWN	-2.315	2.29e-19	695.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4

Ruta: intracellular organelle (Página 3 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG0000010438	PRSS3	UP	1.837	1.56e-15	633.6
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6

Ruta: intracellular organelle (Página 4 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000137310	TCF19	DOWN	-1.639	1.12e-14	547.9
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000164466	SFXN1	DOWN	-1.129	2.57e-13	1052.2
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1

Ruta: intracellular organelle (Página 5 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000133739	LRRCC1	DOWN	-1.272	1.80e-12	348.7
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000161513	FDXR	UP	1.086	1.56e-11	595.0
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000163584	RPL22L1	DOWN	-1.560	7.80e-11	4446.0

Ruta: intracellular organelle (Página 6 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000147394	ZNF185	UP	1.052	8.01e-11	1372.2
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG0000068489	PRR11	DOWN	-1.033	9.90e-11	1510.0
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000149548	CCDC15	DOWN	-1.977	9.27e-10	145.8
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9

Ruta: intracellular organelle (Página 7 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2

Ruta: intracellular organelle (Página 8 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000129038	LOXL1	UP	1.441	3.55e-07	153.1
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7

Ruta: intracellular organelle (Página 9 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000120647	CCDC77	DOWN	-1.339	2.44e-06	215.8
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000146410	MTFR2	DOWN	-1.746	5.92e-06	145.6
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: intracellular organelle (Página 10 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000139133	ALG10	DOWN	-1.541	8.66e-06	64.1
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000293495		DOWN	-1.307	5.02e-05	261.4
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9

Ruta: intracellular organelle (Página 11 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000160352	ZNF714	DOWN	-1.576	1.17e-04	120.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000175600	SUGCT	UP	2.209	1.39e-04	54.4
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000160180	TFF3	UP	1.708	1.97e-04	44.6
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000166881	NEMP1	DOWN	-2.208	2.92e-04	75.0
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: intracellular organelle (Página 12 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG0000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000087299	L2HGDH	DOWN	-1.318	1.89e-03	70.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000171451	DSEL	UP	1.321	2.18e-03	188.5
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8

Ruta: intracellular organelle (Página 13 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000228474	OST4	UP	1.044	5.07e-03	862.5
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG0000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000181652	ATG9B	UP	1.052	9.34e-03	97.0

Ruta: intracellular organelle (Página 14 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000075303	SLC25A40	DOWN	-1.118	9.38e-03	169.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000185352	HS6ST3	UP	2.354	9.79e-03	25.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000166831	RBPM2	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000172197	MBOAT1	DOWN	-1.396	1.61e-02	54.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000163596	ICA1L	DOWN	-1.027	1.99e-02	76.8
ENSG00000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: intracellular organelle (Página 15 de 15)

Fuente: GO:CC | ID: GO:0043229 | Genes: 369 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000121940	CLCC1	DOWN	-1.122	4.07e-02	81.5
ENSG00000146842	TMEM209	DOWN	-1.100	4.09e-02	64.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000174669	SLC29A2	DOWN	-1.426	4.13e-02	38.9
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000196247	ZNF107	DOWN	-1.028	4.60e-02	77.9
ENSG00000183048	SLC25A10	DOWN	-1.208	4.96e-02	35.4
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: spindle midzone

Fuente: GO:CC | ID: GO:0051233 | Genes: 13 | p-valor ruta: 2.72e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: DNA replication preinitiation complex

Fuente: GO:CC | ID: GO:0031261 | Genes: 9 | p-valor ruta: 6.58e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5

Ruta: intracellular anatomical structure (Página 1 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7

Ruta: intracellular anatomical structure (Página 2 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000165304	MELK	DOWN	-1.524	2.74e-21	505.6
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000189057	FAM111B	DOWN	-2.315	2.29e-19	695.4

Ruta: intracellular anatomical structure (Página 3 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000174307	PHLDA3	UP	1.160	4.29e-18	611.8
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000065357	DGKA	UP	1.136	1.94e-17	694.1
ENSG00000058085	LAMC2	UP	1.879	2.12e-17	204.8
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7

Ruta: intracellular anatomical structure (Página 4 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000111665	CDCA3	DOWN	-1.647	8.37e-16	690.7
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG0000010438	PRSS3	UP	1.837	1.56e-15	633.6
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000113368	LMBN1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000137310	TCF19	DOWN	-1.639	1.12e-14	547.9
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2

Ruta: intracellular anatomical structure (Página 5 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000164466	SFXN1	DOWN	-1.129	2.57e-13	1052.2
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000133739	LRRCC1	DOWN	-1.272	1.80e-12	348.7
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000161513	FDXR	UP	1.086	1.56e-11	595.0
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5

Ruta: intracellular anatomical structure (Página 6 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000163584	RPL22L1	DOWN	-1.560	7.80e-11	4446.0
ENSG00000147394	ZNF185	UP	1.052	8.01e-11	1372.2
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000068489	PRR11	DOWN	-1.033	9.90e-11	1510.0
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000147697	GSDMC	UP	2.564	1.66e-10	130.4
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000205208	C4orf46	DOWN	-1.302	2.82e-10	479.4
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9

Ruta: intracellular anatomical structure (Página 7 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000149548	CCDC15	DOWN	-1.977	9.27e-10	145.8
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164237	CMBL	UP	1.794	1.17e-09	471.4
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0

Ruta: intracellular anatomical structure (Página 8 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000135451	TROAP	DOWN	-2.330	4.41e-08	64.0
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000078596	ITM2A	UP	1.114	1.60e-07	523.0

Ruta: intracellular anatomical structure (Página 9 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000129038	LOXL1	UP	1.441	3.55e-07	153.1
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000120647	CCDC77	DOWN	-1.339	2.44e-06	215.8
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6

Ruta: intracellular anatomical structure (Página 10 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG0000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000146410	MTFR2	DOWN	-1.746	5.92e-06	145.6
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000139133	ALG10	DOWN	-1.541	8.66e-06	64.1
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7

Ruta: intracellular anatomical structure (Página 11 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000139410	SDSL	UP	1.421	3.14e-05	75.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG00000293495		DOWN	-1.307	5.02e-05	261.4
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG0000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000160352	ZNF714	DOWN	-1.576	1.17e-04	120.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000175600	SUGCT	UP	2.209	1.39e-04	54.4
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2

Ruta: intracellular anatomical structure (Página 12 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000160180	TFF3	UP	1.708	1.97e-04	44.6
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000166881	NEMP1	DOWN	-2.208	2.92e-04	75.0
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000109452	INPP4B	UP	1.158	4.20e-04	146.5
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000138780	GSTCD	DOWN	-1.373	4.88e-04	110.9
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000011638	LDAF1	UP	1.147	5.56e-04	173.9

Ruta: intracellular anatomical structure (Página 13 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000087299	L2HGDH	DOWN	-1.318	1.89e-03	70.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000171451	DSEL	UP	1.321	2.18e-03	188.5
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5

Ruta: intracellular anatomical structure (Página 14 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000228474	OST4	UP	1.044	5.07e-03	862.5
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000107719	PALD1	DOWN	-1.387	8.65e-03	67.9
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000181652	ATG9B	UP	1.052	9.34e-03	97.0
ENSG00000075303	SLC25A40	DOWN	-1.118	9.38e-03	169.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000185352	HS6ST3	UP	2.354	9.79e-03	25.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: intracellular anatomical structure (Página 15 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000166831	RBPM2	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000172197	MBOAT1	DOWN	-1.396	1.61e-02	54.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000163596	ICA1L	DOWN	-1.027	1.99e-02	76.8
ENSG00000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5

Ruta: intracellular anatomical structure (Página 16 de 16)

Fuente: GO:CC | ID: GO:0005622 | Genes: 392 | p-valor ruta: 1.07e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168298	H1–4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000281344	HELLPAR	DOWN	-1.328	3.14e-02	46.9
ENSG00000093217	XYLB	DOWN	-1.226	3.20e-02	61.0
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000121940	CLCC1	DOWN	-1.122	4.07e-02	81.5
ENSG00000146842	TMEM209	DOWN	-1.100	4.09e-02	64.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000174669	SLC29A2	DOWN	-1.426	4.13e-02	38.9
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000196247	ZNF107	DOWN	-1.028	4.60e-02	77.9
ENSG00000183048	SLC25A10	DOWN	-1.208	4.96e-02	35.4
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: polymeric cytoskeletal fiber (Página 1 de 2)

Fuente: GO:CC | ID: GO:0099513 | Genes: 48 | p–valor ruta: 1.66e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e–37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e–28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e–27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e–25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e–25	327.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e–24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e–20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e–20	265.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e–17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e–16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e–16	1191.9
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e–15	1268.3
ENSG00000087586	AURKA	DOWN	-1.463	3.30e–14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e–14	450.4
ENSG00000135480	KRT7	UP	1.056	6.68e–13	1505.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e–12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e–12	203.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e–11	313.0
ENSG00000152229	PSTPIP2	UP	1.460	2.03e–10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e–10	666.3
ENSG00000137807	KIF23	DOWN	-1.544	2.50e–10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e–10	287.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e–09	148.7
ENSG00000171345	KRT19	UP	1.305	1.34e–09	596.8
ENSG00000066279	ASPM	DOWN	-1.873	2.39e–09	1354.9

Ruta: polymeric cytoskeletal fiber (Página 2 de 2)

Fuente: GO:CC | ID: GO:0099513 | Genes: 48 | p–valor ruta: 1.66e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: condensin complex

Fuente: GO:CC | ID: GO:0000796 | Genes: 7 | p-valor ruta: 2.23e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: protein–DNA complex

Fuente: GO:CC | ID: GO:0032993 | Genes: 25 | p–valor ruta: 2.39e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000189060	H1–0	DOWN	-1.085	5.21e-05	1363.7
ENSG0000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000187837	H1–2	DOWN	-1.365	3.54e-04	328.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000124575	H1–3	DOWN	-2.710	5.40e-03	36.2
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000168298	H1–4	DOWN	-2.161	3.04e-02	24.3

Ruta: organelle (Página 1 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000169607	CKAP2L	DOWN	-2.013	3.11e-42	1388.2
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7

Ruta: organelle (Página 2 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000189057	FAM111B	DOWN	-2.315	2.29e-19	695.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1

Ruta: organelle (Página 3 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171241	SHCBP1	DOWN	-1.855	6.20e-19	594.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG00000178882	RFLNA	UP	1.801	8.90e-16	246.4
ENSG0000010438	PRSS3	UP	1.837	1.56e-15	633.6

Ruta: organelle (Página 4 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000137310	TCF19	DOWN	-1.639	1.12e-14	547.9
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000164466	SFXN1	DOWN	-1.129	2.57e-13	1052.2
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7

Ruta: organelle (Página 5 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000133739	LRRCC1	DOWN	-1.272	1.80e-12	348.7
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000161513	FDXR	UP	1.086	1.56e-11	595.0
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0

Ruta: organelle (Página 6 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163584	RPL22L1	DOWN	-1.560	7.80e-11	4446.0
ENSG00000147394	ZNF185	UP	1.052	8.01e-11	1372.2
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000068489	PRR11	DOWN	-1.033	9.90e-11	1510.0
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000149548	CCDC15	DOWN	-1.977	9.27e-10	145.8
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164237	CMBL	UP	1.794	1.17e-09	471.4

Ruta: organelle (Página 7 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000163507	CIP2A	DOWN	-1.457	7.01e-09	711.6
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4

Ruta: organelle (Página 8 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000175455	CCDC14	DOWN	-1.128	4.84e-08	463.9
ENSG0000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0

Ruta: organelle (Página 9 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000129038	LOXL1	UP	1.441	3.55e-07	153.1
ENSG0000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000120647	CCDC77	DOWN	-1.339	2.44e-06	215.8
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000146410	MTFR2	DOWN	-1.746	5.92e-06	145.6

Ruta: organelle (Página 10 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000139133	ALG10	DOWN	-1.541	8.66e-06	64.1
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7

Ruta: organelle (Página 11 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000293495		DOWN	-1.307	5.02e-05	261.4
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000160352	ZNF714	DOWN	-1.576	1.17e-04	120.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000175600	SUGCT	UP	2.209	1.39e-04	54.4
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000160180	TFF3	UP	1.708	1.97e-04	44.6
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000166881	NEMP1	DOWN	-2.208	2.92e-04	75.0

Ruta: organelle (Página 12 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG0000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG0000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG0000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG0000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG0000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG0000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG0000138780	GSTCD	DOWN	-1.373	4.88e-04	110.9
ENSG0000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG0000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG0000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG0000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG0000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG0000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG0000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG0000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG0000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG0000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG0000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG0000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG0000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG0000087299	L2HGDH	DOWN	-1.318	1.89e-03	70.4
ENSG0000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0

Ruta: organelle (Página 13 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000171451	DSEL	UP	1.321	2.18e-03	188.5
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000228474	OST4	UP	1.044	5.07e-03	862.5
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000007908	SELE	DOWN	-4.746	5.26e-03	18.1
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1

Ruta: organelle (Página 14 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000181652	ATG9B	UP	1.052	9.34e-03	97.0
ENSG00000075303	SLC25A40	DOWN	-1.118	9.38e-03	169.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000185352	HS6ST3	UP	2.354	9.79e-03	25.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000158164	TMSB15A	DOWN	-1.177	1.01e-02	120.4
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000166831	RBPMS2	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000172197	MBOAT1	DOWN	-1.396	1.61e-02	54.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3

Ruta: organelle (Página 15 de 15)

Fuente: GO:CC | ID: GO:0043226 | Genes: 375 | p-valor ruta: 3.22e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000163596	ICA1L	DOWN	-1.027	1.99e-02	76.8
ENSG00000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000121940	CLCC1	DOWN	-1.122	4.07e-02	81.5
ENSG00000146842	TMEM209	DOWN	-1.100	4.09e-02	64.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000174669	SLC29A2	DOWN	-1.426	4.13e-02	38.9
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000196247	ZNF107	DOWN	-1.028	4.60e-02	77.9
ENSG00000183048	SLC25A10	DOWN	-1.208	4.96e-02	35.4
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: centriole

Fuente: GO:CC | ID: GO:0005814 | Genes: 20 | p-valor ruta: 1.24e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000133739	LRRCC1	DOWN	-1.272	1.80e-12	348.7
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000161996	WDR90	DOWN	-1.301	1.18e-02	97.1
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5

Ruta: spindle microtubule

Fuente: GO:CC | ID: GO:0005876 | Genes: 15 | p-valor ruta: 1.46e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1

Ruta: site of DNA damage

Fuente: GO:CC | ID: GO:0090734 | Genes: 18 | p-valor ruta: 1.52e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: MCM complex

Fuente: GO:CC | ID: GO:0042555 | Genes: 7 | p-valor ruta: 8.76e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5

Ruta: inner kinetochore

Fuente: GO:CC | ID: GO:0000939 | Genes: 8 | p-valor ruta: 1.96e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: supramolecular fiber (Página 1 de 3)

Fuente: GO:CC | ID: GO:0099512 | Genes: 51 | p–valor ruta: 4.56e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9

Ruta: supramolecular fiber (Página 2 de 3)

Fuente: GO:CC | ID: GO:0099512 | Genes: 51 | p–valor ruta: 4.56e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2

Ruta: supramolecular fiber (Página 3 de 3)

Fuente: GO:CC | ID: GO:0099512 | Genes: 51 | p-valor ruta: 4.56e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166086	JAM3	DOWN	-1.293	4.5e-02	50.7

Ruta: microtubule associated complex

Fuente: GO:CC | ID: GO:0005875 | Genes: 18 | p-valor ruta: 4.96e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG0000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8

Ruta: DNA polymerase complex

Fuente: GO:CC | ID: GO:0042575 | Genes: 8 | p-valor ruta: 5.45e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: supramolecular polymer (Página 1 de 3)

Fuente: GO:CC | ID: GO:0099081 | Genes: 51 | p–valor ruta: 5.88e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000152229	PSTPIP2	UP	1.460	2.03e-10	656.1
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9

Ruta: supramolecular polymer (Página 2 de 3)

Fuente: GO:CC | ID: GO:0099081 | Genes: 51 | p–valor ruta: 5.88e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000136108	CKAP2	DOWN	-1.032	1.47e-07	822.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2

Ruta: supramolecular polymer (Página 3 de 3)

Fuente: GO:CC | ID: GO:0099081 | Genes: 51 | p–valor ruta: 5.88e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166086	JAM3	DOWN	-1.293	4.5e–02	50.7

Ruta: intracellular membrane–bounded organelle (Página 1 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8

Ruta: intracellular membrane–bounded organelle (Página 2 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000189057	FAM111B	DOWN	-2.315	2.29e-19	695.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8

Ruta: intracellular membrane–bounded organelle (Página 3 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG0000010438	PRSS3	UP	1.837	1.56e-15	633.6
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1

Ruta: intracellular membrane–bounded organelle (Página 4 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000213347	MXD3	DOWN	−1.980	4.67e−15	153.5
ENSG00000168078	PBK	DOWN	−1.893	4.67e−15	353.2
ENSG00000187741	FANCA	DOWN	−1.866	5.41e−15	107.5
ENSG00000137310	TCF19	DOWN	−1.639	1.12e−14	547.9
ENSG00000163781	TOPBP1	DOWN	−1.311	1.42e−14	788.6
ENSG00000171320	ESCO2	DOWN	−2.194	2.27e−14	284.8
ENSG00000185088	RPS27L	UP	1.075	2.43e−14	18190.8
ENSG00000087586	AURKA	DOWN	−1.463	3.30e−14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e−14	663.5
ENSG00000138160	KIF11	DOWN	−1.751	8.02e−14	450.4
ENSG00000149636	DSN1	DOWN	−1.642	8.03e−14	568.7
ENSG00000122952	ZWINT	DOWN	−1.652	1.40e−13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e−13	2447.2
ENSG00000164109	MAD2L1	DOWN	−1.656	2.19e−13	684.6
ENSG00000163918	RFC4	DOWN	−1.722	2.38e−13	353.5
ENSG00000164466	SFXN1	DOWN	−1.129	2.57e−13	1052.2
ENSG00000148773	MKI67	DOWN	−1.808	2.94e−13	1720.7
ENSG00000143476	DTL	DOWN	−2.411	3.23e−13	299.1
ENSG00000058804	NDC1	DOWN	−1.251	3.27e−13	1000.3
ENSG00000140451	PIF1	DOWN	−2.118	6.42e−13	126.2
ENSG00000112029	FBXO5	DOWN	−2.086	6.62e−13	325.6
ENSG00000135480	KRT7	UP	1.056	6.68e−13	1505.2
ENSG00000146670	CDDA5	DOWN	−2.059	8.54e−13	175.9
ENSG00000131153	GINS2	DOWN	−1.531	1.00e−12	334.0
ENSG0000012048	BRCA1	DOWN	−1.766	1.14e−12	390.2

Ruta: intracellular membrane–bounded organelle (Página 5 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG0000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000161513	FDXR	UP	1.086	1.56e-11	595.0
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000068489	PRR11	DOWN	-1.033	9.90e-11	1510.0
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7

Ruta: intracellular membrane–bounded organelle (Página 6 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2

Ruta: intracellular membrane–bounded organelle (Página 7 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1
ENSG00000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1

Ruta: intracellular membrane–bounded organelle (Página 8 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000129038	LOXL1	UP	1.441	3.55e-07	153.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2

Ruta: intracellular membrane–bounded organelle (Página 9 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG0000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000146410	MTFR2	DOWN	-1.746	5.92e-06	145.6
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000139133	ALG10	DOWN	-1.541	8.66e-06	64.1
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000293495		DOWN	-1.307	5.02e-05	261.4

Ruta: intracellular membrane–bounded organelle (Página 10 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000189060	H1–0	DOWN	−1.085	5.21e−05	1363.7
ENSG00000153044	CENPH	DOWN	−1.151	6.14e−05	228.9
ENSG00000185567	AHNAK2	UP	1.090	6.76e−05	1004.7
ENSG00000120539	MASTL	DOWN	−1.817	7.79e−05	126.7
ENSG00000174059	CD34	DOWN	−1.139	8.34e−05	273.4
ENSG00000127423	AUNIP	DOWN	−1.836	1.12e−04	67.0
ENSG00000160352	ZNF714	DOWN	−1.576	1.17e−04	120.0
ENSG00000111602	TIMELESS	DOWN	−1.128	1.19e−04	370.8
ENSG00000175600	SUGCT	UP	2.209	1.39e−04	54.4
ENSG00000163071	SPATA18	UP	1.916	1.60e−04	96.2
ENSG00000181544	FANCB	DOWN	−1.664	1.85e−04	111.2
ENSG00000146263	MMS22L	DOWN	−1.185	1.85e−04	128.5
ENSG00000160180	TFF3	UP	1.708	1.97e−04	44.6
ENSG00000085872	CHERP	DOWN	−1.134	2.05e−04	192.1
ENSG00000162407	PLPP3	UP	1.082	2.32e−04	395.0
ENSG00000242265	PEG10	DOWN	−1.056	2.33e−04	204.2
ENSG00000149503	INCENP	DOWN	−1.404	2.34e−04	103.9
ENSG00000077514	POLD3	DOWN	−1.169	2.56e−04	290.9
ENSG00000105173	CCNE1	DOWN	−1.268	2.65e−04	172.2
ENSG00000166881	NEMP1	DOWN	−2.208	2.92e−04	75.0
ENSG00000038427	VCAN	UP	2.629	3.44e−04	39.3
ENSG00000187837	H1–2	DOWN	−1.365	3.54e−04	328.9
ENSG00000133119	RFC3	DOWN	−1.777	3.63e−04	302.9
ENSG00000178343	SHISA3	DOWN	−1.481	3.80e−04	120.0
ENSG00000093009	CDC45	DOWN	−1.677	3.83e−04	201.5

Ruta: intracellular membrane–bounded organelle (Página 11 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG0000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG0000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG0000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG0000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG0000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG0000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000087299	L2HGDH	DOWN	-1.318	1.89e-03	70.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000171451	DSEL	UP	1.321	2.18e-03	188.5
ENSG0000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5

Ruta: intracellular membrane–bounded organelle (Página 12 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000026103	FAS	UP	1.355	3.32e–03	176.7
ENSG00000116830	TTF2	DOWN	–1.039	3.42e–03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e–03	4115.5
ENSG00000099937	SERPIND1	UP	1.055	4.11e–03	226.3
ENSG00000154917	RAB6B	UP	1.410	4.24e–03	77.1
ENSG00000197061	H4C3	DOWN	–2.289	4.36e–03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e–03	66.3
ENSG00000165490	DDIAS	DOWN	–1.415	4.97e–03	91.3
ENSG00000228474	OST4	UP	1.044	5.07e–03	862.5
ENSG00000157404	KIT	UP	1.031	5.08e–03	131.8
ENSG00000178966	RMI1	DOWN	–1.308	5.27e–03	243.9
ENSG00000128408	RIBC2	DOWN	–3.116	5.36e–03	19.6
ENSG00000124575	H1–3	DOWN	–2.710	5.40e–03	36.2
ENSG00000183765	CHEK2	DOWN	–1.030	5.41e–03	109.3
ENSG00000134222	PSRC1	DOWN	–1.418	5.55e–03	157.1
ENSG00000198056	PRIM1	DOWN	–1.368	5.76e–03	62.7
ENSG00000178573	MAF	UP	2.929	5.95e–03	18.9
ENSG00000156509	FBXO43	DOWN	–3.272	6.77e–03	15.2
ENSG00000181652	ATG9B	UP	1.052	9.34e–03	97.0
ENSG00000075303	SLC25A40	DOWN	–1.118	9.38e–03	169.0
ENSG00000126215	XRCC3	DOWN	–1.553	9.49e–03	57.7
ENSG00000185352	HS6ST3	UP	2.354	9.79e–03	25.7
ENSG00000109805	NCAPG	DOWN	–1.924	1.00e–02	293.9
ENSG00000129484	PARP2	DOWN	–1.064	1.06e–02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e–02	38.4

Ruta: intracellular membrane–bounded organelle (Página 13 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166831	RBPM2	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000172197	MBOAT1	DOWN	-1.396	1.61e-02	54.9
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000163596	ICA1L	DOWN	-1.027	1.99e-02	76.8
ENSG00000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5
ENSG00000168298	H1–4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7

Ruta: intracellular membrane–bounded organelle (Página 14 de 14)

Fuente: GO:CC | ID: GO:0043231 | Genes: 334 | p–valor ruta: 6.48e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000118242	MREG	UP	1.163	3.42e–02	59.7
ENSG00000121940	CLCC1	DOWN	–1.122	4.07e–02	81.5
ENSG00000146842	TMEM209	DOWN	–1.100	4.09e–02	64.5
ENSG00000141376	BCAS3	UP	1.174	4.09e–02	37.2
ENSG00000174669	SLC29A2	DOWN	–1.426	4.13e–02	38.9
ENSG00000166086	JAM3	DOWN	–1.293	4.50e–02	50.7
ENSG00000196247	ZNF107	DOWN	–1.028	4.60e–02	77.9
ENSG00000183048	SLC25A10	DOWN	–1.208	4.96e–02	35.4
ENSG00000197070	ARRDC1	UP	1.459	4.99e–02	23.9

Ruta: chromatin (Página 1 de 3)

Fuente: GO:CC | ID: GO:0000785 | Genes: 60 | p–valor ruta: 9.84e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000189057	FAM111B	DOWN	-2.315	2.29e-19	695.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4

Ruta: chromatin (Página 2 de 3)

Fuente: GO:CC | ID: GO:0000785 | Genes: 60 | p–valor ruta: 9.84e–07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG0000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9

Ruta: chromatin (Página 3 de 3)

Fuente: GO:CC | ID: GO:0000785 | Genes: 60 | p-valor ruta: 9.84e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2

Ruta: intercellular bridge

Fuente: GO:CC | ID: GO:0045171 | Genes: 14 | p-valor ruta: 1.07e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000138180	CEP55	DOWN	-1.583	3.98e-20	905.8
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000128591	FLNC	UP	1.008	2.93e-05	441.4
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG0000041880	PARP3	UP	1.061	1.32e-03	127.5

Ruta: nuclear replication fork

Fuente: GO:CC | ID: GO:0043596 | Genes: 10 | p-valor ruta: 1.21e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: site of double-strand break

Fuente: GO:CC | ID: GO:0035861 | Genes: 14 | p-valor ruta: 1.62e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: nuclear body (Página 1 de 2)

Fuente: GO:CC | ID: GO:0016604 | Genes: 44 | p-valor ruta: 2.8e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9

Ruta: nuclear body (Página 2 de 2)

Fuente: GO:CC | ID: GO:0016604 | Genes: 44 | p-valor ruta: 2.8e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: membrane–bounded organelle (Página 1 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG0000013810	TACC3	DOWN	-1.621	4.44e-40	2085.0
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8

Ruta: membrane–bounded organelle (Página 2 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000103034	NDRG4	UP	1.449	5.95e-24	944.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000165244	ZNF367	DOWN	-2.804	3.39e-20	156.1
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000120129	DUSP1	UP	1.436	1.44e-19	596.2
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000092621	PHGDH	DOWN	-1.436	2.26e-19	340.9
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000189057	FAM111B	DOWN	-2.315	2.29e-19	695.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3

Ruta: membrane–bounded organelle (Página 3 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000137463	MGARP	UP	1.871	3.65e-18	353.0
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000198624	CCDC69	UP	1.776	5.57e-17	255.3
ENSG00000184661	CDCA2	DOWN	-2.132	5.90e-17	528.1
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000109084	TMEM97	DOWN	-1.795	7.74e-16	1175.3
ENSG0000010438	PRSS3	UP	1.837	1.56e-15	633.6
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4

Ruta: membrane–bounded organelle (Página 4 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG0000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG0000168078	PBK	DOWN	-1.893	4.67e-15	353.2
ENSG0000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG0000137310	TCF19	DOWN	-1.639	1.12e-14	547.9
ENSG0000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG0000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG0000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG0000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG0000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG0000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG0000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG0000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG0000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000164466	SFXN1	DOWN	-1.129	2.57e-13	1052.2
ENSG0000148773	MKI67	DOWN	-1.808	2.94e-13	1720.7
ENSG0000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG0000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG0000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000135480	KRT7	UP	1.056	6.68e-13	1505.2
ENSG0000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG0000131153	GINS2	DOWN	-1.531	1.00e-12	334.0

Ruta: membrane–bounded organelle (Página 5 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000253368	TRNP1	UP	1.659	1.20e-12	706.9
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000161513	FDXR	UP	1.086	1.56e-11	595.0
ENSG00000129195	PIMREG	DOWN	-1.831	1.72e-11	267.5
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000244509	APOBEC3C	UP	1.228	6.46e-11	685.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000068489	PRR11	DOWN	-1.033	9.90e-11	1510.0
ENSG00000087494	PTHLH	UP	2.252	1.19e-10	97.1
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000168476	REEP4	DOWN	-1.127	2.04e-10	666.3

Ruta: membrane–bounded organelle (Página 6 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000126787	DLGAP5	DOWN	-1.288	8.11e-10	969.9
ENSG00000154678	PDE1C	UP	1.321	8.66e-10	661.0
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164237	CMBL	UP	1.794	1.17e-09	471.4
ENSG00000171345	KRT19	UP	1.305	1.34e-09	596.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4

Ruta: membrane–bounded organelle (Página 7 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000126453	BCL2L12	DOWN	-1.016	4.35e-09	808.5
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000197956	S100A6	UP	1.004	8.52e-09	42660.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000213186	TRIM59	DOWN	-1.226	1.24e-08	289.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000185480	PARPBP	DOWN	-1.442	2.48e-08	364.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000144354	CDCA7	DOWN	-1.327	9.78e-08	445.1

Ruta: membrane–bounded organelle (Página 8 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000078596	ITM2A	UP	1.114	1.60e-07	523.0
ENSG00000119632	IFI27L2	UP	1.024	1.60e-07	879.6
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000186193	SAPCD2	DOWN	-1.543	2.30e-07	304.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000109743	BST1	UP	1.357	3.05e-07	142.3
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000129038	LOXL1	UP	1.441	3.55e-07	153.1
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG0000072163	LIMS2	UP	1.276	2.35e-06	210.9
ENSG00000100416	TRMU	DOWN	-1.100	2.40e-06	131.4
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0

Ruta: membrane–bounded organelle (Página 9 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164087	POC1A	DOWN	-1.256	4.03e-06	220.8
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000186767	SPIN4	DOWN	-1.531	5.23e-06	201.2
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000146410	MTFR2	DOWN	-1.746	5.92e-06	145.6
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000139133	ALG10	DOWN	-1.541	8.66e-06	64.1
ENSG00000213853	EMP2	DOWN	-1.268	9.16e-06	258.3
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000138587	MNS1	DOWN	-1.441	1.31e-05	251.7
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000142669	SH3BGRL3	UP	1.168	2.89e-05	423.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2

Ruta: membrane–bounded organelle (Página 10 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000170779	CDCA4	DOWN	-1.174	3.99e-05	824.3
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000138356	AOX1	UP	3.601	4.75e-05	33.7
ENSG00000293495		DOWN	-1.307	5.02e-05	261.4
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000185567	AHNAK2	UP	1.090	6.76e-05	1004.7
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000127423	AUNIP	DOWN	-1.836	1.12e-04	67.0
ENSG00000160352	ZNF714	DOWN	-1.576	1.17e-04	120.0
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000175600	SUGCT	UP	2.209	1.39e-04	54.4
ENSG00000163071	SPATA18	UP	1.916	1.60e-04	96.2
ENSG00000185347	TEDC1	DOWN	-1.524	1.61e-04	68.1
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000160180	TFF3	UP	1.708	1.97e-04	44.6
ENSG00000085872	CHERP	DOWN	-1.134	2.05e-04	192.1
ENSG00000162407	PLPP3	UP	1.082	2.32e-04	395.0
ENSG00000242265	PEG10	DOWN	-1.056	2.33e-04	204.2

Ruta: membrane–bounded organelle (Página 11 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000166881	NEMP1	DOWN	-2.208	2.92e-04	75.0
ENSG00000038427	VCAN	UP	2.629	3.44e-04	39.3
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000178343	SHISA3	DOWN	-1.481	3.80e-04	120.0
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000150593	PDCD4	UP	1.058	4.42e-04	284.2
ENSG00000138780	GSTCD	DOWN	-1.373	4.88e-04	110.9
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG00000011638	LDAF1	UP	1.147	5.56e-04	173.9
ENSG00000182010	RTKN2	DOWN	-1.623	5.70e-04	82.4
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000156136	DCK	DOWN	-1.080	9.96e-04	143.8
ENSG00000179750	APOBEC3B	DOWN	-1.565	1.15e-03	54.2
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: membrane–bounded organelle (Página 12 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000159167	STC1	UP	1.618	1.62e-03	112.1
ENSG00000110031	LPXN	UP	1.134	1.68e-03	561.4
ENSG00000087299	L2HGDH	DOWN	-1.318	1.89e-03	70.4
ENSG00000106511	MEOX2	DOWN	-2.172	2.03e-03	49.0
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000171451	DSEL	UP	1.321	2.18e-03	188.5
ENSG00000129295	DNAAF11	UP	1.302	2.26e-03	91.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000176974	SHMT1	DOWN	-1.206	2.50e-03	116.0
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000135842	NIBAN1	DOWN	-1.475	2.76e-03	52.0
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000099937	SERPIND1	UP	1.055	4.11e-03	226.3
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000165490	DDIAS	DOWN	-1.415	4.97e-03	91.3
ENSG00000228474	OST4	UP	1.044	5.07e-03	862.5
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000128408	RIBC2	DOWN	-3.116	5.36e-03	19.6
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2

Ruta: membrane–bounded organelle (Página 13 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000134222	PSRC1	DOWN	-1.418	5.55e-03	157.1
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000181652	ATG9B	UP	1.052	9.34e-03	97.0
ENSG00000075303	SLC25A40	DOWN	-1.118	9.38e-03	169.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000185352	HS6ST3	UP	2.354	9.79e-03	25.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000125848	FLRT3	UP	2.298	1.15e-02	38.4
ENSG00000166831	RBPM32	DOWN	-1.538	1.19e-02	49.2
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000075702	WDR62	DOWN	-2.162	1.49e-02	19.4
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7
ENSG00000149929	HIRIP3	DOWN	-1.385	1.55e-02	79.7
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000184500	PROS1	UP	1.173	1.59e-02	71.6
ENSG00000172197	MBOAT1	DOWN	-1.396	1.61e-02	54.9
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6

Ruta: membrane–bounded organelle (Página 14 de 14)

Fuente: GO:CC | ID: GO:0043227 | Genes: 349 | p-valor ruta: 3e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000186462	NAP1L2	UP	1.210	1.81e-02	44.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000163596	ICA1L	DOWN	-1.027	1.99e-02	76.8
ENSG00000084444	FAM234B	DOWN	-1.183	2.23e-02	86.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000126950	TMEM35A	UP	1.019	2.76e-02	364.1
ENSG00000184635	ZNF93	DOWN	-1.354	2.76e-02	86.5
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1
ENSG00000129028	THAP10	DOWN	-1.132	2.96e-02	48.5
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000067445	TRO	UP	1.115	3.27e-02	57.6
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5
ENSG00000203780	FANK1	UP	1.721	3.31e-02	30.7
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7
ENSG00000158163	DZIP1L	DOWN	-1.180	3.76e-02	30.5
ENSG00000121940	CLCC1	DOWN	-1.122	4.07e-02	81.5
ENSG00000146842	TMEM209	DOWN	-1.100	4.09e-02	64.5
ENSG00000141376	BCAS3	UP	1.174	4.09e-02	37.2
ENSG00000174669	SLC29A2	DOWN	-1.426	4.13e-02	38.9
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7
ENSG00000196247	ZNF107	DOWN	-1.028	4.60e-02	77.9
ENSG00000183048	SLC25A10	DOWN	-1.208	4.96e-02	35.4
ENSG00000197070	ARRDC1	UP	1.459	4.99e-02	23.9

Ruta: chromosome passenger complex

Fuente: GO:CC | ID: GO:0032133 | Genes: 5 | p-valor ruta: 4.78e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: procentriole replication complex

Fuente: GO:CC | ID: GO:0120099 | Genes: 5 | p-valor ruta: 4.78e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6

Ruta: kinesin complex

Fuente: GO:CC | ID: GO:0005871 | Genes: 10 | p-valor ruta: 6.28e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2

Ruta: mitotic spindle pole

Fuente: GO:CC | ID: GO:0097431 | Genes: 9 | p-valor ruta: 1.26e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000101447	FAM83D	DOWN	-1.989	5.57e-16	454.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000170264	FAM161A	DOWN	-1.241	9.45e-06	269.8

Ruta: BRCA1–B complex

Fuente: GO:CC | ID: GO:0070532 | Genes: 4 | p-valor ruta: 4.31e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Ndc80 complex

Fuente: GO:CC | ID: GO:0031262 | Genes: 4 | p-valor ruta: 4.31e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5

Ruta: Ctf18 RFC-like complex

Fuente: GO:CC | ID: GO:0031390 | Genes: 5 | p-valor ruta: 4.32e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: replisome

Fuente: GO:CC | ID: GO:0030894 | Genes: 7 | p-valor ruta: 7.42e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: lateral element

Fuente: GO:CC | ID: GO:0000800 | Genes: 6 | p-valor ruta: 1.03e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG0000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: cyclin-dependent protein kinase holoenzyme complex

Fuente: GO:CC | ID: GO:0000307 | Genes: 10 | p-valor ruta: 1.99e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: DNA replication factor C complex

Fuente: GO:CC | ID: GO:0005663 | Genes: 4 | p-valor ruta: 2.12e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: alpha DNA polymerase:primase complex

Fuente: GO:CC | ID: GO:0005658 | Genes: 4 | p-valor ruta: 2.12e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: germ cell nucleus

Fuente: GO:CC | ID: GO:0043073 | Genes: 10 | p-valor ruta: 3e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8

Ruta: Fanconi anaemia nuclear complex

Fuente: GO:CC | ID: GO:0043240 | Genes: 5 | p-valor ruta: 9.18e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6

Ruta: mitotic spindle midzone

Fuente: GO:CC | ID: GO:1990023 | Genes: 5 | p-valor ruta: 1.41e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3

Ruta: transferase complex, transferring phosphorus-containing groups

Fuente: GO:CC | ID: GO:0061695 | Genes: 20 | p-valor ruta: 1.53e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: pronucleus

Fuente: GO:CC | ID: GO:0045120 | Genes: 5 | p-valor ruta: 2.08e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8

Ruta: centalspindlin complex

Fuente: GO:CC | ID: GO:0097149 | Genes: 3 | p-valor ruta: 2.29e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9

Ruta: cyclin E1–CDK2 complex

Fuente: GO:CC | ID: GO:0097134 | Genes: 3 | p-valor ruta: 2.29e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: ribonucleoside-diphosphate reductase complex

Fuente: GO:CC | ID: GO:0005971 | Genes: 3 | p-valor ruta: 2.29e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1

Ruta: male germ cell nucleus

Fuente: GO:CC | ID: GO:0001673 | Genes: 8 | p-valor ruta: 2.95e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG0000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6

Ruta: meiotic spindle

Fuente: GO:CC | ID: GO:0072687 | Genes: 5 | p-valor ruta: 2.97e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG0000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: synaptonemal complex

Fuente: GO:CC | ID: GO:0000795 | Genes: 7 | p-valor ruta: 3.65e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: synaptonemal structure

Fuente: GO:CC | ID: GO:0099086 | Genes: 7 | p-valor ruta: 3.65e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG0000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: pericentric heterochromatin

Fuente: GO:CC | ID: GO:0005721 | Genes: 6 | p-valor ruta: 7.47e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: DNA helicase complex

Fuente: GO:CC | ID: GO:0033202 | Genes: 3 | p-valor ruta: 9.02e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9

Ruta: RecQ family helicase–topoisomerase III complex

Fuente: GO:CC | ID: GO:0031422 | Genes: 3 | p-valor ruta: 9.02e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9

Ruta: mitotic checkpoint complex

Fuente: GO:CC | ID: GO:0033597 | Genes: 3 | p-valor ruta: 9.02e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9

Ruta: heterochromatin

Fuente: GO:CC | ID: GO:0000792 | Genes: 9 | p-valor ruta: 9.36e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000119969	HELLS	DOWN	-1.592	1.29e-37	1124.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: nuclear ubiquitin ligase complex

Fuente: GO:CC | ID: GO:0000152 | Genes: 7 | p-valor ruta: 1.22e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9

Ruta: protein-containing complex (Página 1 de 8)

Fuente: GO:CC | ID: GO:0032991 | Genes: 190 | p-valor ruta: 1.55e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9

Ruta: protein-containing complex (Página 2 de 8)

Fuente: GO:CC | ID: GO:0032991 | Genes: 190 | p-valor ruta: 1.55e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000058085	LAMC2	UP	1.879	2.12e-17	204.8
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000165480	SKA3	DOWN	-1.586	1.14e-16	602.9
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000123473	STIL	DOWN	-1.696	3.74e-15	372.6
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000024526	DEPDC1	DOWN	-1.695	4.67e-15	597.1
ENSG00000213347	MXD3	DOWN	-1.980	4.67e-15	153.5
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5

Ruta: protein-containing complex (Página 3 de 8)

Fuente: GO:CC | ID: GO:0032991 | Genes: 190 | p-valor ruta: 1.55e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167779	IGFBP6	UP	1.609	1.39e-14	353.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000185088	RPS27L	UP	1.075	2.43e-14	18190.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000164104	HMGGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000163584	RPL22L1	DOWN	-1.560	7.80e-11	4446.0

Ruta: protein-containing complex (Página 4 de 8)

Fuente: GO:CC | ID: GO:0032991 | Genes: 190 | p-valor ruta: 1.55e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100629	CEP128	DOWN	-2.025	1.61e-09	110.3
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4

Ruta: protein-containing complex (Página 5 de 8)

Fuente: GO:CC | ID: GO:0032991 | Genes: 190 | p-valor ruta: 1.55e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000178726	THBD	UP	1.434	6.31e-06	145.8

Ruta: protein-containing complex (Página 6 de 8)

Fuente: GO:CC | ID: GO:0032991 | Genes: 190 | p-valor ruta: 1.55e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000132017	DCAF15	DOWN	-1.243	1.30e-05	122.0
ENSG00000156113	KCNMA1	UP	2.096	1.85e-05	78.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000174059	CD34	DOWN	-1.139	8.34e-05	273.4
ENSG00000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9

Ruta: protein-containing complex (Página 7 de 8)

Fuente: GO:CC | ID: GO:0032991 | Genes: 190 | p-valor ruta: 1.55e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000213626	LBH	UP	1.358	6.71e-04	90.3
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000011332	DPF1	DOWN	-1.417	2.44e-03	50.8
ENSG00000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000116830	TTF2	DOWN	-1.039	3.42e-03	336.7
ENSG00000118181	RPS25	UP	1.046	3.91e-03	4115.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000228474	OST4	UP	1.044	5.07e-03	862.5
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2

Ruta: protein-containing complex (Página 8 de 8)

Fuente: GO:CC | ID: GO:0032991 | Genes: 190 | p-valor ruta: 1.55e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000177106	EPS8L2	UP	2.621	8.00e-03	16.6
ENSG00000156049	GNA14	UP	1.287	9.28e-03	50.0
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000166963	MAP1A	UP	1.057	1.65e-02	148.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3
ENSG00000281344	HELLPAR	DOWN	-1.328	3.14e-02	46.9
ENSG00000118242	MREG	UP	1.163	3.42e-02	59.7
ENSG00000121940	CLCC1	DOWN	-1.122	4.07e-02	81.5
ENSG00000166086	JAM3	DOWN	-1.293	4.50e-02	50.7

Ruta: nuclear replisome

Fuente: GO:CC | ID: GO:0043601 | Genes: 5 | p-valor ruta: 1.63e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: microtubule end

Fuente: GO:CC | ID: GO:1990752 | Genes: 6 | p-valor ruta: 1.82e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000066279	ASPM	DOWN	-1.873	2.39e-09	1354.9
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7

Ruta: transferase complex (Página 1 de 2)

Fuente: GO:CC | ID: GO:1990234 | Genes: 35 | p–valor ruta: 2.18e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e–44	4228.1
ENSG00000175063	UBE2C	DOWN	−1.912	1.62e–32	1424.6
ENSG00000134057	CCNB1	DOWN	−1.376	4.23e–30	1075.8
ENSG00000145386	CCNA2	DOWN	−1.856	3.17e–26	988.0
ENSG00000170312	CDK1	DOWN	−2.088	2.27e–25	1384.7
ENSG00000138376	BARD1	DOWN	−1.668	4.10e–24	474.1
ENSG00000132646	PCNA	DOWN	−1.372	6.33e–21	2475.7
ENSG00000156970	BUB1B	DOWN	−1.960	1.47e–18	480.6
ENSG00000112118	MCM3	DOWN	−1.112	4.76e–18	989.6
ENSG00000106462	EZH2	DOWN	−1.170	1.57e–15	683.6
ENSG00000051180	RAD51	DOWN	−2.077	4.28e–15	291.4
ENSG00000143476	DTL	DOWN	−2.411	3.23e–13	299.1
ENSG00000012048	BRCA1	DOWN	−1.766	1.14e–12	390.2
ENSG00000123374	CDK2	DOWN	−1.140	6.55e–11	1630.6
ENSG00000117399	CDC20	DOWN	−1.306	8.53e–11	1077.9
ENSG00000177084	POLE	DOWN	−2.215	8.53e–11	106.4
ENSG00000139618	BRCA2	DOWN	−1.944	1.37e–09	326.9
ENSG00000175305	CCNE2	DOWN	−2.245	2.83e–09	73.4
ENSG00000145604	SKP2	DOWN	−1.333	5.70e–09	594.2
ENSG00000100479	POLE2	DOWN	−1.692	2.50e–08	173.1
ENSG00000101868	POLA1	DOWN	−1.208	4.18e–08	300.4
ENSG00000162063	CCNF	DOWN	−1.611	3.45e–07	160.0
ENSG00000157456	CCNB2	DOWN	−1.198	5.68e–07	582.1
ENSG00000070950	RAD18	DOWN	−1.104	4.13e–06	250.3
ENSG00000014138	POLA2	DOWN	−1.508	4.34e–06	201.8

Ruta: transferase complex (Página 2 de 2)

Fuente: GO:CC | ID: GO:1990234 | Genes: 35 | p-valor ruta: 2.18e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG0000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG0000132017	DCAF15	DOWN	-1.243	1.30e-05	122.0
ENSG0000161040	FBXL13	UP	1.103	8.80e-05	278.1
ENSG0000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG0000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG0000133302	SLF1	DOWN	-1.032	2.51e-03	270.0
ENSG0000228474	OST4	UP	1.044	5.07e-03	862.5
ENSG0000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG0000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: GINS complex

Fuente: GO:CC | ID: GO:0000811 | Genes: 3 | p-valor ruta: 2.22e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1

Ruta: serine/threonine protein kinase complex

Fuente: GO:CC | ID: GO:1902554 | Genes: 11 | p-valor ruta: 2.4e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000162063	CCNF	DOWN	-1.611	3.45e-07	160.0
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: microtubule plus-end

Fuente: GO:CC | ID: GO:0035371 | Genes: 5 | p-valor ruta: 3.83e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000076382	SPAG5	DOWN	-1.738	1.21e-12	384.3
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000105270	CLIP3	UP	1.109	1.51e-02	143.7

Ruta: BRCA1–C complex

Fuente: GO:CC | ID: GO:0070533 | Genes: 3 | p-valor ruta: 4.38e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9

Ruta: deuterosome

Fuente: GO:CC | ID: GO:0098536 | Genes: 3 | p-valor ruta: 4.38e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000156876	SASS6	DOWN	-1.300	2.51e-04	236.6

Sección de Análisis: REAC – Rutas Reactome

Total de términos enriquecidos en esta sección: 134

Términos 'Tope' (p–valor < 1e–16): 33

Términos que superan el 'tope' de significancia:

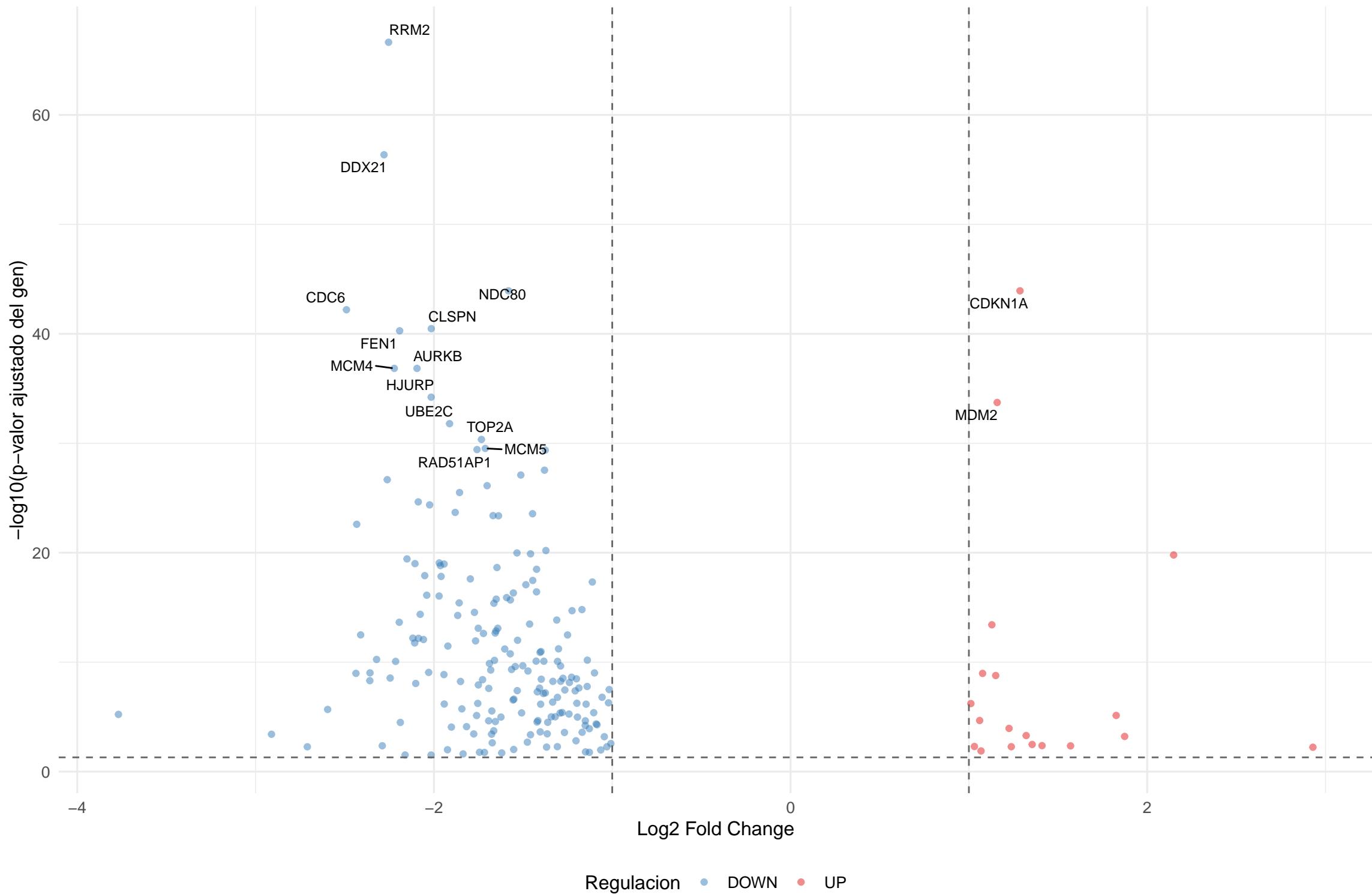
- Cell Cycle (REAC:R-HSA-1640170, p–val: 8.3e–95)
- Cell Cycle, Mitotic (REAC:R-HSA-69278, p–val: 2.0e–78)
- Cell Cycle Checkpoints (REAC:R-HSA-69620, p–val: 2.3e–58)
- Mitotic Prometaphase (REAC:R-HSA-68877, p–val: 3.7e–32)
- M Phase (REAC:R-HSA-68886, p–val: 1.3e–30)
- Resolution of Sister Chromatid Cohesion (REAC:R-HSA-2500257, p–val: 2.1e–28)
- Amplification of signal from the kinetochores (REAC:R-HSA-141424, p–val: 2.3e–28)
- Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal (REAC:R-HSA-141444, p–val: 2.3e–28)
- Mitotic G1 phase and G1/S transition (REAC:R-HSA-453279, p–val: 1.3e–27)
- S Phase (REAC:R-HSA-69242, p–val: 4.2e–27)

...y otros

A continuación se muestran los gráficos de barras y tablas de genes para esta sección.

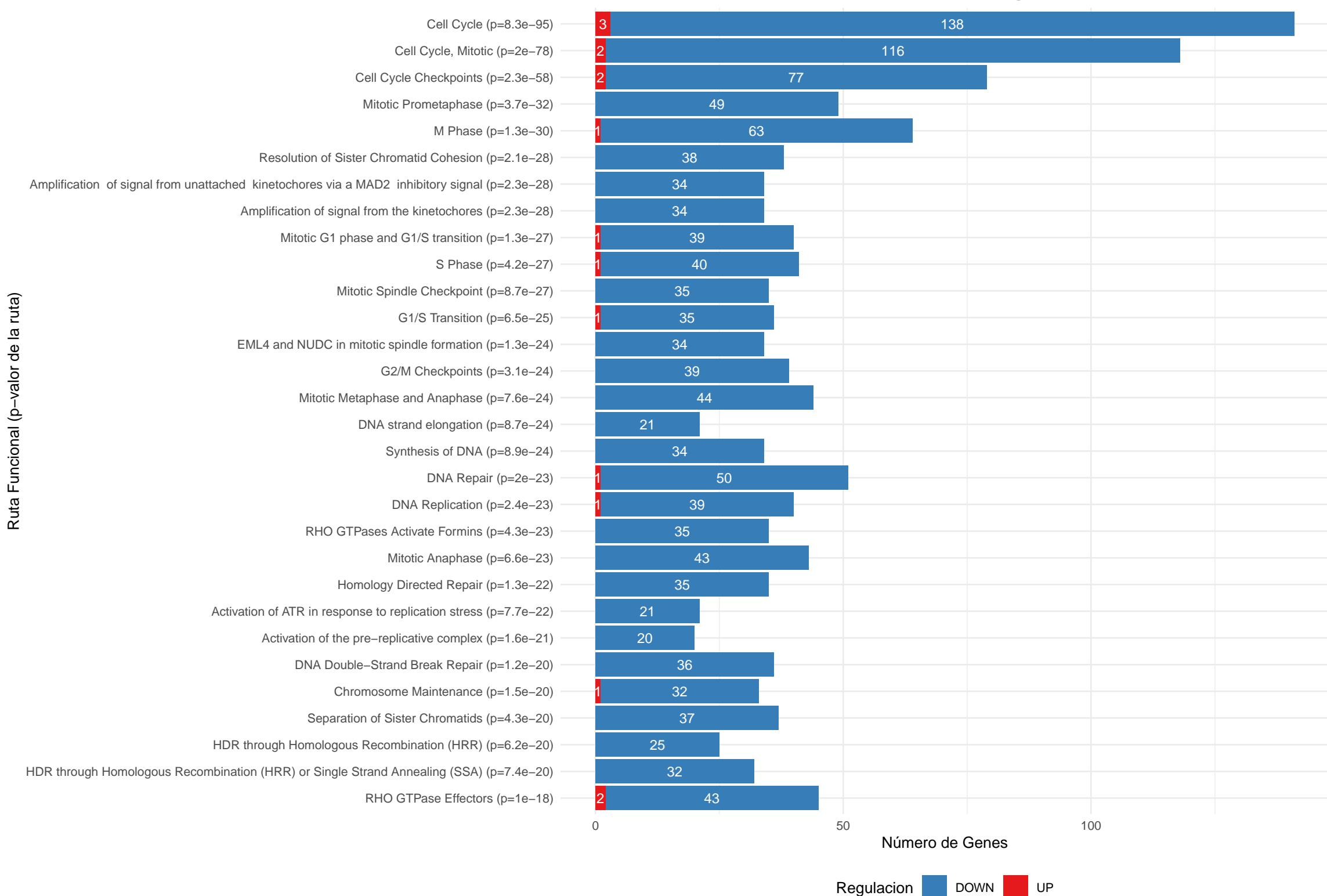
Volcano Plot – REAC – Rutas Reactome

Mostrando 208 genes únicos mapeados en esta sección



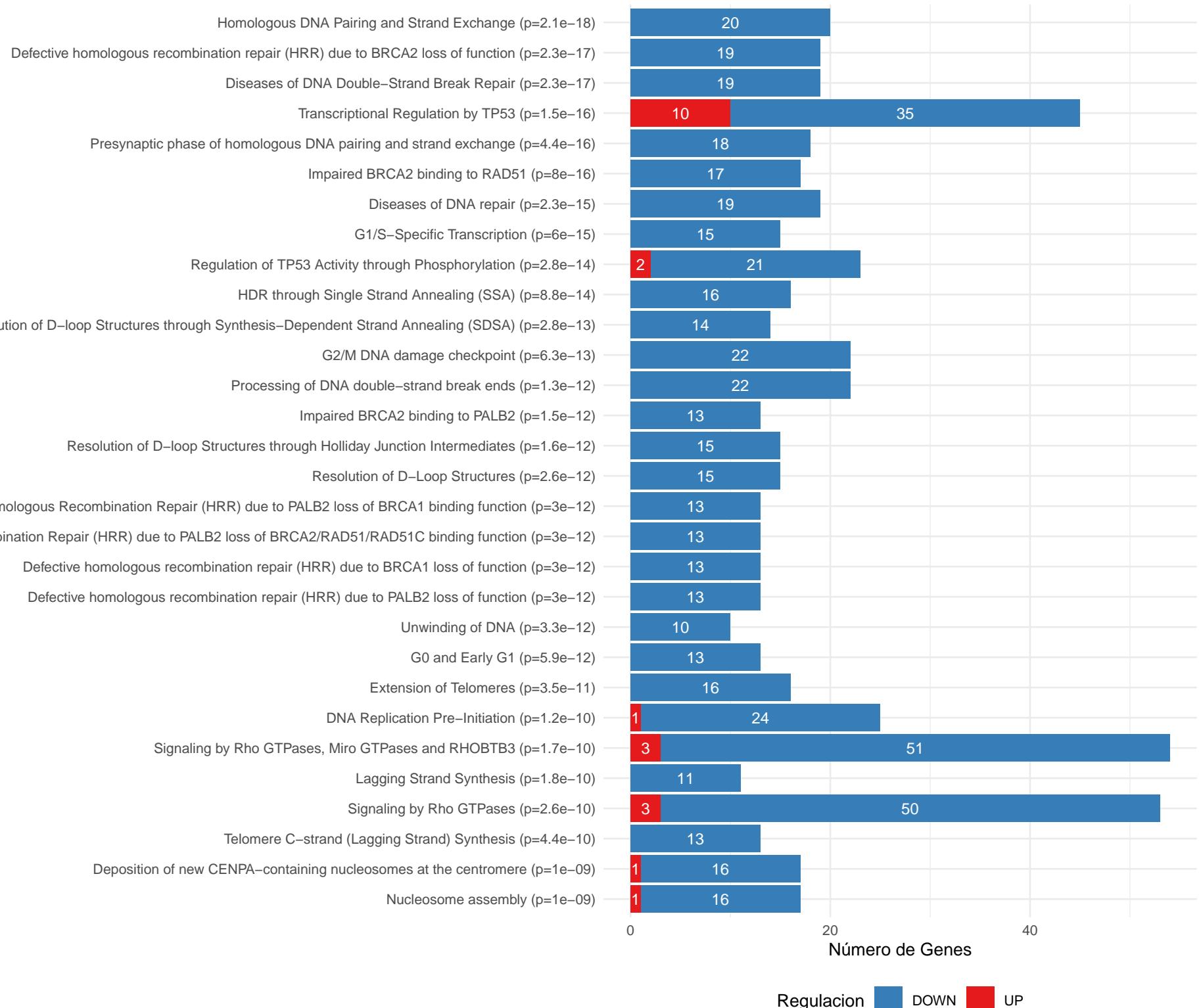
Regulacion ● DOWN ● UP

REAC – Rutas Reactome – Gráfico (Pág. 1 de 5)



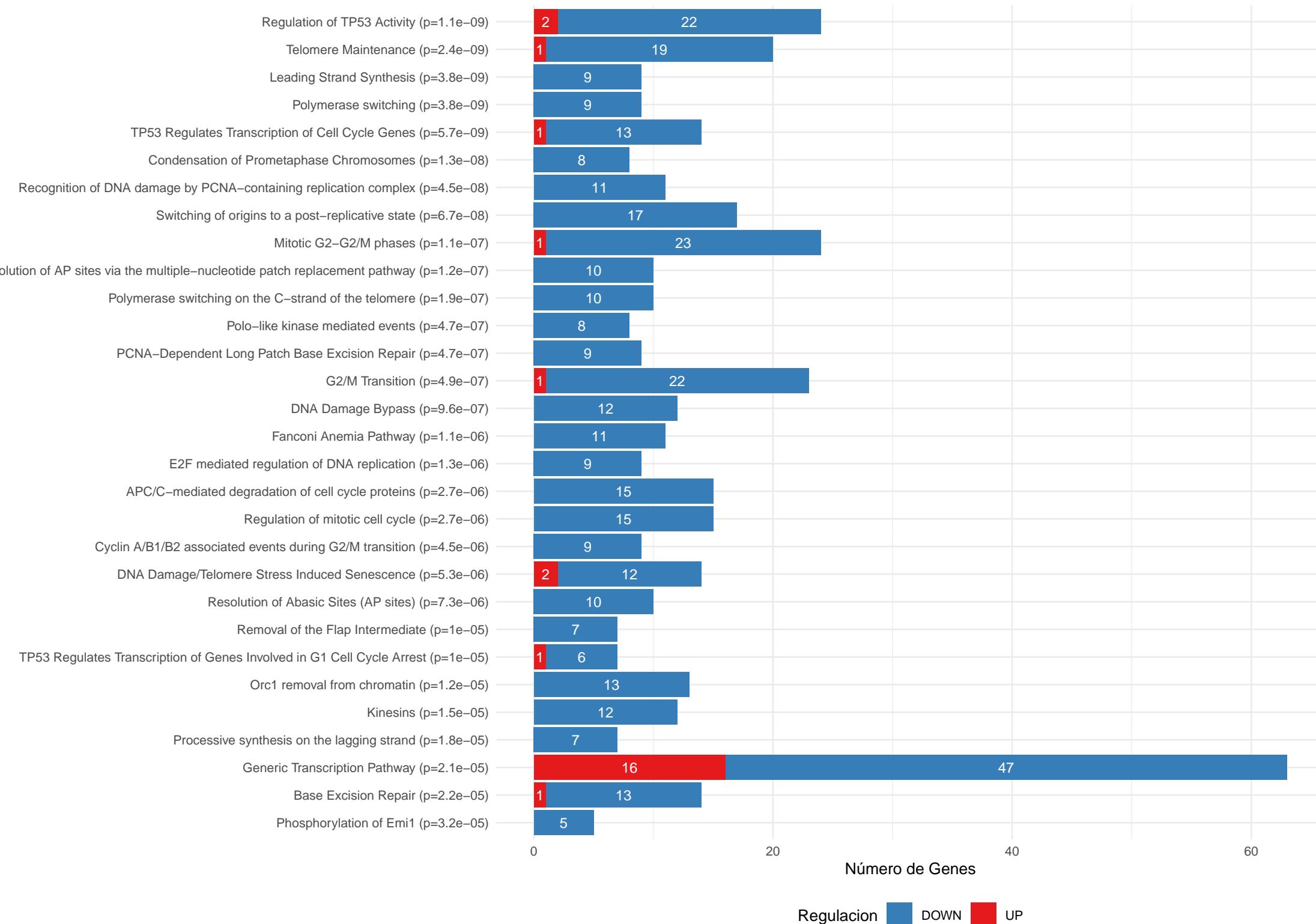
REAC – Rutas Reactome – Gráfico (Pág. 2 de

Ruta Funcional (p–valor de la ruta)



Regulación █ DOWN █ UP

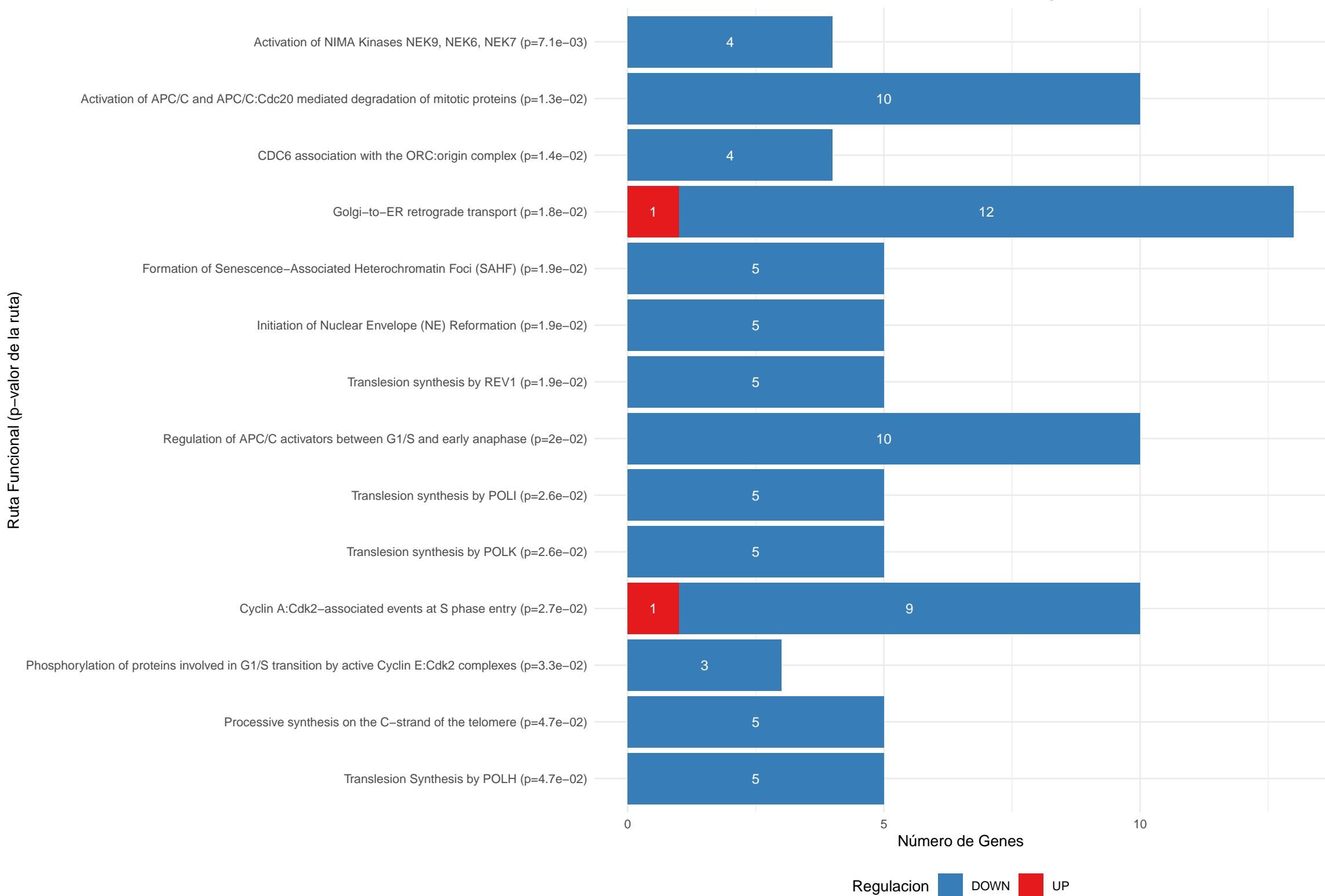
REAC – Rutas Reactome – Gráfico (Pág. 3 de 5)



REAC – Rutas Reactome – Gráfico (Pág. 4 de 5)



REAC – Rutas Reactome – Gráfico (Pág. 5 de 5)



Ruta: Cell Cycle (Página 1 de 6)

Fuente: REAC | ID: REAC:R-HSA-1640170 | Genes: 141 | p-valor ruta: 8.29e-95

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9

Ruta: Cell Cycle (Página 2 de 6)

Fuente: REAC | ID: REAC:R-HSA-1640170 | Genes: 141 | p-valor ruta: 8.29e-95

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6

Ruta: Cell Cycle (Página 3 de 6)

Fuente: REAC | ID: REAC:R-HSA-1640170 | Genes: 141 | p-valor ruta: 8.29e-95

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1

Ruta: Cell Cycle (Página 4 de 6)

Fuente: REAC | ID: REAC:R-HSA-1640170 | Genes: 141 | p-valor ruta: 8.29e-95

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3

Ruta: Cell Cycle (Página 5 de 6)

Fuente: REAC | ID: REAC:R-HSA-1640170 | Genes: 141 | p-valor ruta: 8.29e-95

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG0000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9

Ruta: Cell Cycle (Página 6 de 6)

Fuente: REAC | ID: REAC:R-HSA-1640170 | Genes: 141 | p-valor ruta: 8.29e-95

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Cell Cycle, Mitotic (Página 1 de 5)

Fuente: REAC | ID: REAC:R-HSA-69278 | Genes: 118 | p-valor ruta: 1.99e-78

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1

Ruta: Cell Cycle, Mitotic (Página 2 de 5)

Fuente: REAC | ID: REAC:R-HSA-69278 | Genes: 118 | p-valor ruta: 1.99e-78

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG0000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9

Ruta: Cell Cycle, Mitotic (Página 3 de 5)

Fuente: REAC | ID: REAC:R-HSA-69278 | Genes: 118 | p-valor ruta: 1.99e-78

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4

Ruta: Cell Cycle, Mitotic (Página 4 de 5)

Fuente: REAC | ID: REAC:R-HSA-69278 | Genes: 118 | p-valor ruta: 1.99e-78

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4

Ruta: Cell Cycle, Mitotic (Página 5 de 5)

Fuente: REAC | ID: REAC:R-HSA-69278 | Genes: 118 | p-valor ruta: 1.99e-78

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: Cell Cycle Checkpoints (Página 1 de 4)

Fuente: REAC | ID: REAC:R-HSA-69620 | Genes: 79 | p-valor ruta: 2.32e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6

Ruta: Cell Cycle Checkpoints (Página 2 de 4)

Fuente: REAC | ID: REAC:R-HSA-69620 | Genes: 79 | p-valor ruta: 2.32e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5

Ruta: Cell Cycle Checkpoints (Página 3 de 4)

Fuente: REAC | ID: REAC:R-HSA-69620 | Genes: 79 | p-valor ruta: 2.32e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG0000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG0000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3

Ruta: Cell Cycle Checkpoints (Página 4 de 4)

Fuente: REAC | ID: REAC:R-HSA-69620 | Genes: 79 | p-valor ruta: 2.32e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Mitotic Prometaphase (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-68877 | Genes: 49 | p-valor ruta: 3.72e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0

Ruta: Mitotic Prometaphase (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-68877 | Genes: 49 | p-valor ruta: 3.72e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: M Phase (Página 1 de 3)

Fuente: REAC | ID: REAC:R-HSA-68886 | Genes: 64 | p-valor ruta: 1.33e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9

Ruta: M Phase (Página 2 de 3)

Fuente: REAC | ID: REAC:R-HSA-68886 | Genes: 64 | p-valor ruta: 1.33e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5

Ruta: M Phase (Página 3 de 3)

Fuente: REAC | ID: REAC:R-HSA-68886 | Genes: 64 | p-valor ruta: 1.33e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: Resolution of Sister Chromatid Cohesion (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-2500257 | Genes: 38 | p-valor ruta: 2.14e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0

Ruta: Resolution of Sister Chromatid Cohesion (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-2500257 | Genes: 38 | p-valor ruta: 2.14e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-141444 | Genes: 34 | p-valor ruta: 2.34e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3

Ruta: Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-141444 | Genes: 34 | p-valor ruta: 2.34e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: Amplification of signal from the kinetochores (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-141424 | Genes: 34 | p-valor ruta: 2.34e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3

Ruta: Amplification of signal from the kinetochores (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-141424 | Genes: 34 | p-valor ruta: 2.34e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: Mitotic G1 phase and G1/S transition (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-453279 | Genes: 40 | p-valor ruta: 1.31e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4

Ruta: Mitotic G1 phase and G1/S transition (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-453279 | Genes: 40 | p-valor ruta: 1.31e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: S Phase (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-69242 | Genes: 41 | p-valor ruta: 4.18e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4

Ruta: S Phase (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-69242 | Genes: 41 | p-valor ruta: 4.18e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: Mitotic Spindle Checkpoint (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-69618 | Genes: 35 | p-valor ruta: 8.75e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5

Ruta: Mitotic Spindle Checkpoint (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-69618 | Genes: 35 | p-valor ruta: 8.75e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG0000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG0000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG0000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG0000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG0000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG0000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG0000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG0000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG0000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: G1/S Transition (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-69206 | Genes: 36 | p-valor ruta: 6.47e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2

Ruta: G1/S Transition (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-69206 | Genes: 36 | p-valor ruta: 6.47e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG0000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG0000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG0000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: EML4 and NUDC in mitotic spindle formation (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-9648025 | Genes: 34 | p-valor ruta: 1.34e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3

Ruta: EML4 and NUDC in mitotic spindle formation (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-9648025 | Genes: 34 | p-valor ruta: 1.34e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: G2/M Checkpoints (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-69481 | Genes: 39 | p-valor ruta: 3.06e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1

Ruta: G2/M Checkpoints (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-69481 | Genes: 39 | p-valor ruta: 3.06e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Mitotic Metaphase and Anaphase (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-2555396 | Genes: 44 | p-valor ruta: 7.57e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDC45	DOWN	-2.059	8.54e-13	175.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1

Ruta: Mitotic Metaphase and Anaphase (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-2555396 | Genes: 44 | p-valor ruta: 7.57e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG0000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: DNA strand elongation (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-69190 | Genes: 33 | p-valor ruta: 5.32e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8

Ruta: DNA strand elongation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0022616 | Genes: 33 | p-valor ruta: 5.32e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: Synthesis of DNA (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-69239 | Genes: 34 | p-valor ruta: 8.91e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4

Ruta: Synthesis of DNA (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-69239 | Genes: 34 | p-valor ruta: 8.91e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG0000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG0000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: DNA Repair (Página 1 de 3)

Fuente: REAC | ID: REAC:R-HSA-73894 | Genes: 51 | p-valor ruta: 1.97e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1

Ruta: DNA Repair (Página 2 de 3)

Fuente: REAC | ID: REAC:R-HSA-73894 | Genes: 51 | p-valor ruta: 1.97e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: DNA Repair (Página 3 de 3)

Fuente: REAC | ID: REAC:R-HSA-73894 | Genes: 51 | p-valor ruta: 1.97e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: DNA Replication (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-69306 | Genes: 40 | p-valor ruta: 2.39e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4

Ruta: DNA Replication (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-69306 | Genes: 40 | p-valor ruta: 2.39e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: RHO GTPases Activate Formins (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-5663220 | Genes: 35 | p-valor ruta: 4.27e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3

Ruta: RHO GTPases Activate Formins (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-5663220 | Genes: 35 | p-valor ruta: 4.27e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: Mitotic Anaphase (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-68882 | Genes: 43 | p-valor ruta: 6.61e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0

Ruta: Mitotic Anaphase (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-68882 | Genes: 43 | p-valor ruta: 6.61e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG0000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: Homology Directed Repair (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-5693538 | Genes: 35 | p-valor ruta: 1.25e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8

Ruta: Homology Directed Repair (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-5693538 | Genes: 35 | p-valor ruta: 1.25e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Activation of ATR in response to replication stress

Fuente: REAC | ID: REAC:R-HSA-176187 | Genes: 21 | p-valor ruta: 7.74e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5

Ruta: Activation of the pre-replicative complex

Fuente: REAC | ID: REAC:R-HSA-68962 | Genes: 20 | p-valor ruta: 1.55e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: DNA Double–Strand Break Repair (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-5693532 | Genes: 36 | p–valor ruta: 1.21e–20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8

Ruta: DNA Double–Strand Break Repair (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-5693532 | Genes: 36 | p–valor ruta: 1.21e–20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Chromosome Maintenance (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-73886 | Genes: 33 | p-valor ruta: 1.49e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9

Ruta: Chromosome Maintenance (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-73886 | Genes: 33 | p-valor ruta: 1.49e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG0000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG0000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG0000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG0000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG0000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG0000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: Separation of Sister Chromatids (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-2467813 | Genes: 37 | p-valor ruta: 4.35e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3

Ruta: Separation of Sister Chromatids (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-2467813 | Genes: 37 | p-valor ruta: 4.35e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG0000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: HDR through Homologous Recombination (HRR)

Fuente: REAC | ID: REAC:R-HSA-5685942 | Genes: 25 | p-valor ruta: 6.19e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: HDR through Homologous Recombination (HRR) or Single Strand Annealing (SSA) (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-5693567 | Genes: 32 | p-valor ruta: 7.43e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9

Ruta: HDR through Homologous Recombination (HRR) or Single Strand Annealing (SSA) (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-5693567 | Genes: 32 | p-valor ruta: 7.43e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: RHO GTPase Effectors (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-195258 | Genes: 45 | p-valor ruta: 1.04e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3

Ruta: RHO GTPase Effectors (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-195258 | Genes: 45 | p-valor ruta: 1.04e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: Homologous DNA Pairing and Strand Exchange

Fuente: REAC | ID: REAC:R-HSA-5693579 | Genes: 20 | p-valor ruta: 2.07e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Defective homologous recombination repair (HRR) due to BRCA2 loss of function

Fuente: REAC | ID: REAC:R-HSA-9701190 | Genes: 19 | p-valor ruta: 2.26e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Diseases of DNA Double–Strand Break Repair

Fuente: REAC | ID: REAC:R-HSA-9675136 | Genes: 19 | p–valor ruta: 2.26e–17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Transcriptional Regulation by TP53 (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-3700989 | Genes: 45 | p-valor ruta: 1.47e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3

Ruta: Transcriptional Regulation by TP53 (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-3700989 | Genes: 45 | p-valor ruta: 1.47e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Presynaptic phase of homologous DNA pairing and strand exchange

Fuente: REAC | ID: REAC:R-HSA-5693616 | Genes: 18 | p-valor ruta: 4.37e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Impaired BRCA2 binding to RAD51

Fuente: REAC | ID: REAC:R-HSA-9709570 | Genes: 17 | p-valor ruta: 7.98e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Diseases of DNA repair

Fuente: REAC | ID: REAC:R-HSA-9675135 | Genes: 19 | p-valor ruta: 2.29e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: G1/S-Specific Transcription

Fuente: REAC | ID: REAC:R-HSA-69205 | Genes: 15 | p-valor ruta: 6.01e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000228716	DHFR	DOWN	-1.307	1.64e-07	193.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5

Ruta: Regulation of TP53 Activity through Phosphorylation

Fuente: REAC | ID: REAC:R-HSA-6804756 | Genes: 23 | p-valor ruta: 2.82e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: HDR through Single Strand Annealing (SSA)

Fuente: REAC | ID: REAC:R-HSA-5685938 | Genes: 16 | p-valor ruta: 8.77e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Resolution of D-loop Structures through Synthesis–Dependent Strand Annealing (SDSA)

Fuente: REAC | ID: REAC:R-HSA-5693554 | Genes: 14 | p-valor ruta: 2.79e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: G2/M DNA damage checkpoint

Fuente: REAC | ID: REAC:R-HSA-69473 | Genes: 22 | p-valor ruta: 6.26e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Processing of DNA double-strand break ends

Fuente: REAC | ID: REAC:R-HSA-5693607 | Genes: 22 | p-valor ruta: 1.28e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000092853	CLSPN	DOWN	-2.015	3.37e-41	1306.1
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Impaired BRCA2 binding to PALB2

Fuente: REAC | ID: REAC:R-HSA-9709603 | Genes: 13 | p-valor ruta: 1.49e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Resolution of D-loop Structures through Holliday Junction Intermediates

Fuente: REAC | ID: REAC:R-HSA-5693568 | Genes: 15 | p-valor ruta: 1.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Resolution of D–Loop Structures

Fuente: REAC | ID: REAC:R-HSA-5693537 | Genes: 15 | p–valor ruta: 2.57e–12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132436	FIGNL1	DOWN	-1.425	3.78e-17	624.9
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Defective HDR through Homologous Recombination Repair (HRR) due to PALB2 loss of BRCA1 binding function

Fuente: REAC | ID: REAC:R-HSA-9704331 | Genes: 13 | p-valor ruta: 3.04e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Defective HDR through Homologous Recombination Repair (HRR) due to PALB2 loss of BRCA2/RAD51/RAD51C binding fu

Fuente: REAC | ID: REAC:R-HSA-9704646 | Genes: 13 | p-valor ruta: 3.04e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Defective homologous recombination repair (HRR) due to BRCA1 loss of function

Fuente: REAC | ID: REAC:R-HSA-9701192 | Genes: 13 | p-valor ruta: 3.04e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Defective homologous recombination repair (HRR) due to PALB2 loss of function

Fuente: REAC | ID: REAC:R-HSA-9701193 | Genes: 13 | p-valor ruta: 3.04e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000111247	RAD51AP1	DOWN	-1.758	3.76e-30	411.5
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Unwinding of DNA

Fuente: REAC | ID: REAC:R-HSA-176974 | Genes: 10 | p-valor ruta: 3.27e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5

Ruta: G0 and Early G1

Fuente: REAC | ID: REAC:R-HSA-1538133 | Genes: 13 | p-valor ruta: 5.94e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: Extension of Telomeres

Fuente: REAC | ID: REAC:R-HSA-180786 | Genes: 16 | p-valor ruta: 3.54e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: DNA Replication Pre-Initiation

Fuente: REAC | ID: REAC:R-HSA-69002 | Genes: 25 | p-valor ruta: 1.2e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: Signaling by Rho GTPases, Miro GTPases and RHOBTB3 (Página 1 de 3)

Fuente: REAC | ID: REAC:R-HSA-9716542 | Genes: 54 | p-valor ruta: 1.67e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0

Ruta: Signaling by Rho GTPases, Miro GTPases and RHOBTB3 (Página 2 de 3)

Fuente: REAC | ID: REAC:R-HSA-9716542 | Genes: 54 | p-valor ruta: 1.67e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4

Ruta: Signaling by Rho GTPases, Miro GTPases and RHOBTB3 (Página 3 de 3)

Fuente: REAC | ID: REAC:R-HSA-9716542 | Genes: 54 | p-valor ruta: 1.67e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: Lagging Strand Synthesis

Fuente: REAC | ID: REAC:R-HSA-69186 | Genes: 11 | p-valor ruta: 1.75e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: Signaling by Rho GTPases (Página 1 de 3)

Fuente: REAC | ID: REAC:R-HSA-194315 | Genes: 53 | p-valor ruta: 2.61e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000120802	TMPO	DOWN	-1.380	2.88e-28	1824.8
ENSG00000143228	NUF2	DOWN	-2.262	2.12e-27	1144.3
ENSG00000198901	PRC1	DOWN	-1.702	7.50e-27	475.6
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000011426	ANLN	DOWN	-1.534	1.05e-20	1912.3
ENSG00000055163	CYFIP2	UP	2.148	1.61e-20	318.2
ENSG00000198826	ARHGAP11A	DOWN	-2.151	3.69e-20	649.7
ENSG00000154839	SKA1	DOWN	-2.106	9.93e-20	265.9
ENSG00000152253	SPC25	DOWN	-1.943	1.08e-19	456.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000163535	SGO2	DOWN	-1.592	1.26e-16	1142.8
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000149636	DSN1	DOWN	-1.642	8.03e-14	568.7
ENSG00000122952	ZWINT	DOWN	-1.652	1.40e-13	998.2
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0

Ruta: Signaling by Rho GTPases (Página 2 de 3)

Fuente: REAC | ID: REAC:R-HSA-194315 | Genes: 53 | p-valor ruta: 2.61e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000035499	DEPDC1B	DOWN	-2.029	8.66e-10	209.4
ENSG00000114346	ECT2	DOWN	-1.276	2.96e-09	617.4
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161888	SPC24	DOWN	-1.240	7.21e-09	360.5
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000183856	IQGAP3	DOWN	-1.408	2.35e-08	134.5
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000139734	DIAPH3	DOWN	-1.147	6.88e-07	672.6
ENSG00000184445	KNTC1	DOWN	-1.292	4.45e-06	133.5
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000167842	MIS12	DOWN	-1.151	2.27e-05	287.2
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000186871	ERCC6L	DOWN	-1.902	8.55e-05	105.9
ENSG00000008517	IL32	UP	1.225	1.13e-04	212.8
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7

Ruta: Signaling by Rho GTPases (Página 3 de 3)

Fuente: REAC | ID: REAC:R-HSA-194315 | Genes: 53 | p-valor ruta: 2.61e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000122966	CIT	DOWN	-1.673	2.35e-03	123.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: Telomere C–strand (Lagging Strand) Synthesis

Fuente: REAC | ID: REAC:R-HSA-174417 | Genes: 13 | p–valor ruta: 4.41e–10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	−2.192	5.29e−41	1595.8
ENSG00000132646	PCNA	DOWN	−1.372	6.33e−21	2475.7
ENSG00000163918	RFC4	DOWN	−1.722	2.38e−13	353.5
ENSG00000049541	RFC2	DOWN	−1.473	6.43e−10	250.2
ENSG00000136982	DSCC1	DOWN	−1.851	5.81e−09	116.7
ENSG00000101868	POLA1	DOWN	−1.208	4.18e−08	300.4
ENSG00000111445	RFC5	DOWN	−1.386	7.25e−08	347.4
ENSG0000014138	POLA2	DOWN	−1.508	4.34e−06	201.8
ENSG00000197299	BLM	DOWN	−2.188	3.23e−05	68.8
ENSG00000077514	POLD3	DOWN	−1.169	2.56e−04	290.9
ENSG00000133119	RFC3	DOWN	−1.777	3.63e−04	302.9
ENSG00000198056	PRIM1	DOWN	−1.368	5.76e−03	62.7
ENSG00000138346	DNA2	DOWN	−1.620	1.96e−02	111.6

Ruta: Deposition of new CENPA-containing nucleosomes at the centromere

Fuente: REAC | ID: REAC:R-HSA-606279 | Genes: 17 | p-valor ruta: 1.02e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: Nucleosome assembly

Fuente: REAC | ID: REAC:R-HSA-774815 | Genes: 17 | p-valor ruta: 1.02e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123485	HJURP	DOWN	-2.015	6.13e-35	695.4
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000102384	CENPI	DOWN	-1.554	4.76e-17	603.3
ENSG00000100162	CENPM	DOWN	-1.651	1.75e-16	256.1
ENSG00000151725	CENPU	DOWN	-1.858	3.84e-16	603.3
ENSG00000115163	CENPA	DOWN	-1.689	1.34e-10	297.0
ENSG00000159055	MIS18A	DOWN	-1.201	3.32e-09	460.4
ENSG00000129534	MIS18BP1	DOWN	-1.187	2.29e-08	990.4
ENSG00000031691	CENPQ	DOWN	-1.420	5.20e-08	308.3
ENSG00000123219	CENPK	DOWN	-1.375	6.42e-08	355.1
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000138092	CENPO	DOWN	-1.362	3.13e-05	159.3
ENSG00000153044	CENPH	DOWN	-1.151	6.14e-05	228.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000120334	CENPL	DOWN	-1.203	1.53e-03	114.7
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: Regulation of TP53 Activity

Fuente: REAC | ID: REAC:R-HSA-5633007 | Genes: 24 | p-valor ruta: 1.06e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Telomere Maintenance

Fuente: REAC | ID: REAC:R-HSA-157579 | Genes: 20 | p-valor ruta: 2.43e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: Leading Strand Synthesis

Fuente: REAC | ID: REAC:R-HSA-69109 | Genes: 9 | p-valor ruta: 3.75e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: Polymerase switching

Fuente: REAC | ID: REAC:R-HSA-69091 | Genes: 9 | p-valor ruta: 3.75e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: TP53 Regulates Transcription of Cell Cycle Genes

Fuente: REAC | ID: REAC:R-HSA-6791312 | Genes: 14 | p-valor ruta: 5.68e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: Condensation of Prometaphase Chromosomes

Fuente: REAC | ID: REAC:R-HSA-2514853 | Genes: 8 | p-valor ruta: 1.3e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG0000010292	NCAPD2	DOWN	-1.100	9.61e-10	894.2
ENSG00000121152	NCAPH	DOWN	-2.359	4.90e-09	170.5
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000109805	NCAPG	DOWN	-1.924	1.00e-02	293.9

Ruta: Recognition of DNA damage by PCNA-containing replication complex

Fuente: REAC | ID: REAC:R-HSA-110314 | Genes: 11 | p-valor ruta: 4.54e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: Switching of origins to a post-replicative state

Fuente: REAC | ID: REAC:R-HSA-69052 | Genes: 17 | p-valor ruta: 6.7e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG0000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG0000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG0000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG0000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG0000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG0000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG0000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG0000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG0000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG0000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG0000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG0000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG0000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG0000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG0000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: Mitotic G2–G2/M phases

Fuente: REAC | ID: REAC:R-HSA-453274 | Genes: 24 | p-valor ruta: 1.07e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG0000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG0000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4

Ruta: Resolution of AP sites via the multiple–nucleotide patch replacement pathway

Fuente: REAC | ID: REAC:R-HSA-110373 | Genes: 10 | p-valor ruta: 1.21e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8

Ruta: Polymerase switching on the C-strand of the telomere

Fuente: REAC | ID: REAC:R-HSA-174411 | Genes: 10 | p-valor ruta: 1.92e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: Polo-like kinase mediated events

Fuente: REAC | ID: REAC:R-HSA-156711 | Genes: 8 | p-valor ruta: 4.65e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4

Ruta: PCNA–Dependent Long Patch Base Excision Repair

Fuente: REAC | ID: REAC:R-HSA-5651801 | Genes: 9 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: G2/M Transition

Fuente: REAC | ID: REAC:R-HSA-69275 | Genes: 23 | p-valor ruta: 4.94e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG0000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG0000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000117724	CENPF	DOWN	-1.603	6.29e-12	2801.9
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4

Ruta: DNA Damage Bypass

Fuente: REAC | ID: REAC:R-HSA-73893 | Genes: 12 | p-valor ruta: 9.63e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000070950	RAD18	DOWN	-1.104	4.13e-06	250.3
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: Fanconi Anemia Pathway

Fuente: REAC | ID: REAC:R-HSA-6783310 | Genes: 11 | p-valor ruta: 1.13e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000118655	DCLRE1B	DOWN	-2.051	1.24e-18	122.3
ENSG00000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG00000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG00000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG00000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5

Ruta: E2F mediated regulation of DNA replication

Fuente: REAC | ID: REAC:R-HSA-113510 | Genes: 9 | p-valor ruta: 1.25e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: APC/C-mediated degradation of cell cycle proteins

Fuente: REAC | ID: REAC:R-HSA-174143 | Genes: 15 | p-valor ruta: 2.71e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: Regulation of mitotic cell cycle

Fuente: REAC | ID: REAC:R-HSA-453276 | Genes: 15 | p-valor ruta: 2.71e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: Cyclin A/B1/B2 associated events during G2/M transition

Fuente: REAC | ID: REAC:R-HSA-69273 | Genes: 9 | p-valor ruta: 4.47e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: DNA Damage/Telomere Stress Induced Senescence

Fuente: REAC | ID: REAC:R-HSA-2559586 | Genes: 14 | p-valor ruta: 5.26e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: Resolution of Abasic Sites (AP sites)

Fuente: REAC | ID: REAC:R-HSA-73933 | Genes: 10 | p-valor ruta: 7.32e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8

Ruta: Removal of the Flap Intermediate

Fuente: REAC | ID: REAC:R-HSA-69166 | Genes: 7 | p-valor ruta: 9.98e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: TP53 Regulates Transcription of Genes Involved in G1 Cell Cycle Arrest

Fuente: REAC | ID: REAC:R-HSA-6804116 | Genes: 7 | p-valor ruta: 9.98e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: Orc1 removal from chromatin

Fuente: REAC | ID: REAC:R-HSA-68949 | Genes: 13 | p-valor ruta: 1.19e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1

Ruta: Kinesins

Fuente: REAC | ID: REAC:R-HSA-983189 | Genes: 12 | p-valor ruta: 1.47e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2

Ruta: Processive synthesis on the lagging strand

Fuente: REAC | ID: REAC:R-HSA-69183 | Genes: 7 | p-valor ruta: 1.83e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: Generic Transcription Pathway (Página 1 de 3)

Fuente: REAC | ID: REAC:R-HSA-212436 | Genes: 63 | p-valor ruta: 2.11e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9

Ruta: Generic Transcription Pathway (Página 2 de 3)

Fuente: REAC | ID: REAC:R-HSA-212436 | Genes: 63 | p-valor ruta: 2.11e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG0000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG0000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG0000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG0000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG0000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG0000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG0000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG0000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG0000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG0000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG0000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG0000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG0000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG0000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG0000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG0000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG0000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7

Ruta: Generic Transcription Pathway (Página 3 de 3)

Fuente: REAC | ID: REAC:R-HSA-212436 | Genes: 63 | p-valor ruta: 2.11e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Base Excision Repair

Fuente: REAC | ID: REAC:R-HSA-73884 | Genes: 14 | p-valor ruta: 2.21e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: Phosphorylation of Emi1

Fuente: REAC | ID: REAC:R-HSA-176417 | Genes: 5 | p-valor ruta: 3.18e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: Termination of translesion DNA synthesis

Fuente: REAC | ID: REAC:R-HSA-5656169 | Genes: 9 | p-valor ruta: 3.51e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: Cellular Senescence

Fuente: REAC | ID: REAC:R-HSA-2559583 | Genes: 20 | p-valor ruta: 5.73e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: Gap-filling DNA repair synthesis and ligation in GG-NER

Fuente: REAC | ID: REAC:R-HSA-5696397 | Genes: 8 | p-valor ruta: 6.26e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: Transcription of E2F targets under negative control by DREAM complex

Fuente: REAC | ID: REAC:R-HSA-1362277 | Genes: 7 | p-valor ruta: 8.47e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4

Ruta: Mitotic Prophase

Fuente: REAC | ID: REAC:R-HSA-68875 | Genes: 16 | p-valor ruta: 1.49e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000120539	MASTL	DOWN	-1.817	7.79e-05	126.7
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: Translesion synthesis by Y family DNA polymerases bypasses lesions on DNA template

Fuente: REAC | ID: REAC:R-HSA-110313 | Genes: 9 | p-valor ruta: 2.27e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: DNA replication initiation

Fuente: GO:BP | ID: GO:0006270 | Genes: 25 | p-valor ruta: 7.3e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7

Ruta: Assembly of the pre-replicative complex

Fuente: REAC | ID: REAC:R-HSA-68867 | Genes: 16 | p-valor ruta: 3.32e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: Dual Incision in GG-NER

Fuente: REAC | ID: REAC:R-HSA-5696400 | Genes: 9 | p-valor ruta: 3.58e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8

Ruta: Transcription of E2F targets under negative control by p107 (RBL1) and p130 (RBL2) in complex with HDAC1

Fuente: REAC | ID: REAC:R-HSA-1362300 | Genes: 6 | p-valor ruta: 5.59e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4

Ruta: RNA Polymerase II Transcription (Página 1 de 3)

Fuente: REAC | ID: REAC:R-HSA-73857 | Genes: 63 | p-valor ruta: 6.17e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9

Ruta: RNA Polymerase II Transcription (Página 2 de 3)

Fuente: REAC | ID: REAC:R-HSA-73857 | Genes: 63 | p-valor ruta: 6.17e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG0000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG0000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG0000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG0000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG0000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG0000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG0000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG0000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG0000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG0000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG0000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG0000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG0000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG0000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG0000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG0000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG0000176697	BDNF	UP	1.321	5.08e-04	151.5
ENSG0000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG0000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG0000026103	FAS	UP	1.355	3.32e-03	176.7

Ruta: RNA Polymerase II Transcription (Página 3 de 3)

Fuente: REAC | ID: REAC:R-HSA-73857 | Genes: 63 | p-valor ruta: 6.17e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: E2F-enabled inhibition of pre-replication complex formation

Fuente: REAC | ID: REAC:R-HSA-113507 | Genes: 5 | p-valor ruta: 6.26e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1

Ruta: AURKA Activation by TPX2

Fuente: REAC | ID: REAC:R-HSA-8854518 | Genes: 11 | p-valor ruta: 8.39e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000072571	HMMR	DOWN	-1.334	4.49e-07	600.7
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: Meiotic recombination

Fuente: REAC | ID: REAC:R-HSA-912446 | Genes: 12 | p-valor ruta: 8.89e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG0000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG0000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG0000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG0000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG0000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG0000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG0000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: Condensation of Prophase Chromosomes

Fuente: REAC | ID: REAC:R-HSA-2299718 | Genes: 11 | p-valor ruta: 9.68e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000136824	SMC2	DOWN	-1.424	3.27e-19	2147.1
ENSG00000113810	SMC4	DOWN	-1.484	8.40e-18	4283.1
ENSG00000146918	NCAPG2	DOWN	-1.301	6.06e-12	556.6
ENSG00000151503	NCAPD3	DOWN	-1.281	4.01e-06	180.0
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: Diseases of programmed cell death

Fuente: REAC | ID: REAC:R-HSA-9645723 | Genes: 13 | p-valor ruta: 1.05e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG0000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7

Ruta: Cyclin D associated events in G1

Fuente: REAC | ID: REAC:R-HSA-69231 | Genes: 9 | p-valor ruta: 1.22e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: G1 Phase

Fuente: REAC | ID: REAC:R-HSA-69236 | Genes: 9 | p-valor ruta: 1.22e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: Aberrant regulation of mitotic G1/S transition in cancer due to RB1 defects

Fuente: REAC | ID: REAC:R-HSA-9659787 | Genes: 6 | p-valor ruta: 1.32e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: Defective binding of RB1 mutants to E2F1,(E2F2, E2F3)

Fuente: REAC | ID: REAC:R-HSA-9661069 | Genes: 6 | p-valor ruta: 1.32e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: Aberrant regulation of mitotic cell cycle due to RB1 defects

Fuente: REAC | ID: REAC:R-HSA-9687139 | Genes: 8 | p-valor ruta: 1.37e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: Gene expression (Transcription) (Página 1 de 3)

Fuente: REAC | ID: REAC:R-HSA-74160 | Genes: 67 | p-valor ruta: 1.64e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000165732	DDX21	DOWN	-2.280	4.37e-57	5364.7
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000156802	ATAD2	DOWN	-1.970	8.59e-20	682.4
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000088325	TPX2	DOWN	-1.571	2.07e-16	1191.9
ENSG00000106462	EZH2	DOWN	-1.170	1.57e-15	683.6
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131981	LGALS3	UP	1.129	3.85e-14	663.5
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6

Ruta: Gene expression (Transcription) (Página 2 de 3)

Fuente: REAC | ID: REAC:R-HSA-74160 | Genes: 67 | p-valor ruta: 1.64e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000164938	TP53INP1	UP	1.151	1.66e-09	893.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000276043	UHRF1	DOWN	-1.751	1.20e-08	161.5
ENSG00000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000146374	RSPO3	UP	1.826	7.38e-06	66.8
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000168209	DDIT4	UP	1.060	2.15e-05	278.6
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000137337	MDC1	DOWN	-1.090	4.40e-05	151.5
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000176697	BDNF	UP	1.321	5.08e-04	151.5

Ruta: Gene expression (Transcription) (Página 3 de 3)

Fuente: REAC | ID: REAC:R-HSA-74160 | Genes: 67 | p-valor ruta: 1.64e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000101945	SUV39H1	DOWN	-1.476	2.05e-03	64.9
ENSG00000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000157404	KIT	UP	1.031	5.08e-03	131.8
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000173535	TNFRSF10C	UP	1.238	5.32e-03	54.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000178573	MAF	UP	2.929	5.95e-03	18.9
ENSG00000117450	PRDX1	UP	1.068	1.29e-02	543.8
ENSG00000197020	ZNF100	DOWN	-1.150	1.58e-02	103.2
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000184162	NR2C2AP	DOWN	-1.128	1.72e-02	241.3
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: TP53 Regulates Transcription of Genes Involved in G2 Cell Cycle Arrest

Fuente: REAC | ID: REAC:R-HSA-6804114 | Genes: 6 | p-valor ruta: 1.94e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5

Ruta: Diseases of mitotic cell cycle

Fuente: REAC | ID: REAC:R-HSA-9675126 | Genes: 8 | p-valor ruta: 2.12e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: HDR through MMEJ (alt-NHEJ)

Fuente: REAC | ID: REAC:R-HSA-5685939 | Genes: 5 | p-valor ruta: 3.69e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8

Ruta: COPI-dependent Golgi-to-ER retrograde traffic

Fuente: REAC | ID: REAC:R-HSA-6811434 | Genes: 12 | p-valor ruta: 4e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2

Ruta: Meiosis

Fuente: REAC | ID: REAC:R-HSA-1500620 | Genes: 13 | p-valor ruta: 4.02e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG00000188486	H2AX	DOWN	-1.320	9.84e-06	1365.6
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000180573	H2AC6	UP	1.874	6.10e-04	49.4
ENSG00000197061	H4C3	DOWN	-2.289	4.36e-03	3115.3
ENSG00000276368	H2AC14	DOWN	-1.744	1.71e-02	46.7
ENSG00000133863	TEX15	DOWN	-1.716	1.77e-02	39.6
ENSG00000100206	DMC1	DOWN	-1.836	2.41e-02	15.3

Ruta: Regulation of PLK1 Activity at G2/M Transition

Fuente: REAC | ID: REAC:R-HSA-2565942 | Genes: 11 | p-valor ruta: 5.09e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000131351	HAUS8	DOWN	-1.922	3.39e-12	203.9
ENSG00000151849	CPAP	DOWN	-1.564	4.65e-10	287.9
ENSG00000103995	CEP152	DOWN	-1.141	1.66e-08	311.4
ENSG00000136861	CDK5RAP2	DOWN	-1.057	1.62e-07	406.3
ENSG00000142731	PLK4	DOWN	-1.552	2.41e-07	244.7
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: SUMOylation of DNA replication proteins

Fuente: REAC | ID: REAC:R-HSA-4615885 | Genes: 8 | p-valor ruta: 5.63e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG0000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000134690	CDCA8	DOWN	-1.664	4.17e-16	833.7
ENSG0000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG0000058804	NDC1	DOWN	-1.251	3.27e-13	1000.3
ENSG00000149503	INCENP	DOWN	-1.404	2.34e-04	103.9

Ruta: Apoptosis induced DNA fragmentation

Fuente: REAC | ID: REAC:R-HSA-140342 | Genes: 5 | p-valor ruta: 5.88e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000164104	HMGB2	DOWN	-1.572	1.72e-11	2905.5
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: Activation of NIMA Kinases NEK9, NEK6, NEK7

Fuente: REAC | ID: REAC:R-HSA-2980767 | Genes: 4 | p-valor ruta: 7.07e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins

Fuente: REAC | ID: REAC:R-HSA-176814 | Genes: 10 | p-valor ruta: 1.26e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000117650	NEK2	DOWN	-1.675	2.88e-06	263.6
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: CDC6 association with the ORC:origin complex

Fuente: REAC | ID: REAC:R-HSA-68689 | Genes: 4 | p-valor ruta: 1.39e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1

Ruta: Golgi-to-ER retrograde transport

Fuente: REAC | ID: REAC:R-HSA-8856688 | Genes: 13 | p-valor ruta: 1.77e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000161800	RACGAP1	DOWN	-1.754	5.89e-07	175.9
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000154917	RAB6B	UP	1.410	4.24e-03	77.1

Ruta: Formation of Senescence–Associated Heterochromatin Foci (SAHF)

Fuente: REAC | ID: REAC:R-HSA-2559584 | Genes: 5 | p-valor ruta: 1.87e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000189060	H1-0	DOWN	-1.085	5.21e-05	1363.7
ENSG00000187837	H1-2	DOWN	-1.365	3.54e-04	328.9
ENSG00000124575	H1-3	DOWN	-2.710	5.40e-03	36.2
ENSG00000168298	H1-4	DOWN	-2.161	3.04e-02	24.3

Ruta: Initiation of Nuclear Envelope (NE) Reformation

Fuente: REAC | ID: REAC:R-HSA-2995383 | Genes: 5 | p-valor ruta: 1.87e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000113368	LMNB1	DOWN	-1.225	1.98e-15	1268.3
ENSG00000100749	VRK1	DOWN	-1.501	2.14e-10	731.7
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1

Ruta: Translesion synthesis by REV1

Fuente: REAC | ID: REAC:R-HSA-110312 | Genes: 5 | p-valor ruta: 1.87e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: Regulation of APC/C activators between G1/S and early anaphase

Fuente: REAC | ID: REAC:R-HSA-176408 | Genes: 10 | p-valor ruta: 1.96e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000175063	UBE2C	DOWN	-1.912	1.62e-32	1424.6
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4

Ruta: Translesion synthesis by POLI

Fuente: REAC | ID: REAC:R-HSA-5656121 | Genes: 5 | p-valor ruta: 2.6e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: Translesion synthesis by POLK

Fuente: REAC | ID: REAC:R-HSA-5655862 | Genes: 5 | p-valor ruta: 2.6e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: Cyclin A:Cdk2–associated events at S phase entry

Fuente: REAC | ID: REAC:R-HSA-69656 | Genes: 10 | p-valor ruta: 2.7e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: Phosphorylation of proteins involved in G1/S transition by active Cyclin E:Cdk2 complexes

Fuente: REAC | ID: REAC:R-HSA-69200 | Genes: 3 | p-valor ruta: 3.33e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: Processive synthesis on the C-strand of the telomere

Fuente: REAC | ID: REAC:R-HSA-174414 | Genes: 5 | p-valor ruta: 4.68e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: Translesion Synthesis by POLH

Fuente: REAC | ID: REAC:R-HSA-110320 | Genes: 5 | p-valor ruta: 4.68e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Sección de Análisis: KEGG – Rutas Metabólicas

Total de términos enriquecidos en esta sección: 16

Términos 'Tope' (p-valor < 1e-16): 2

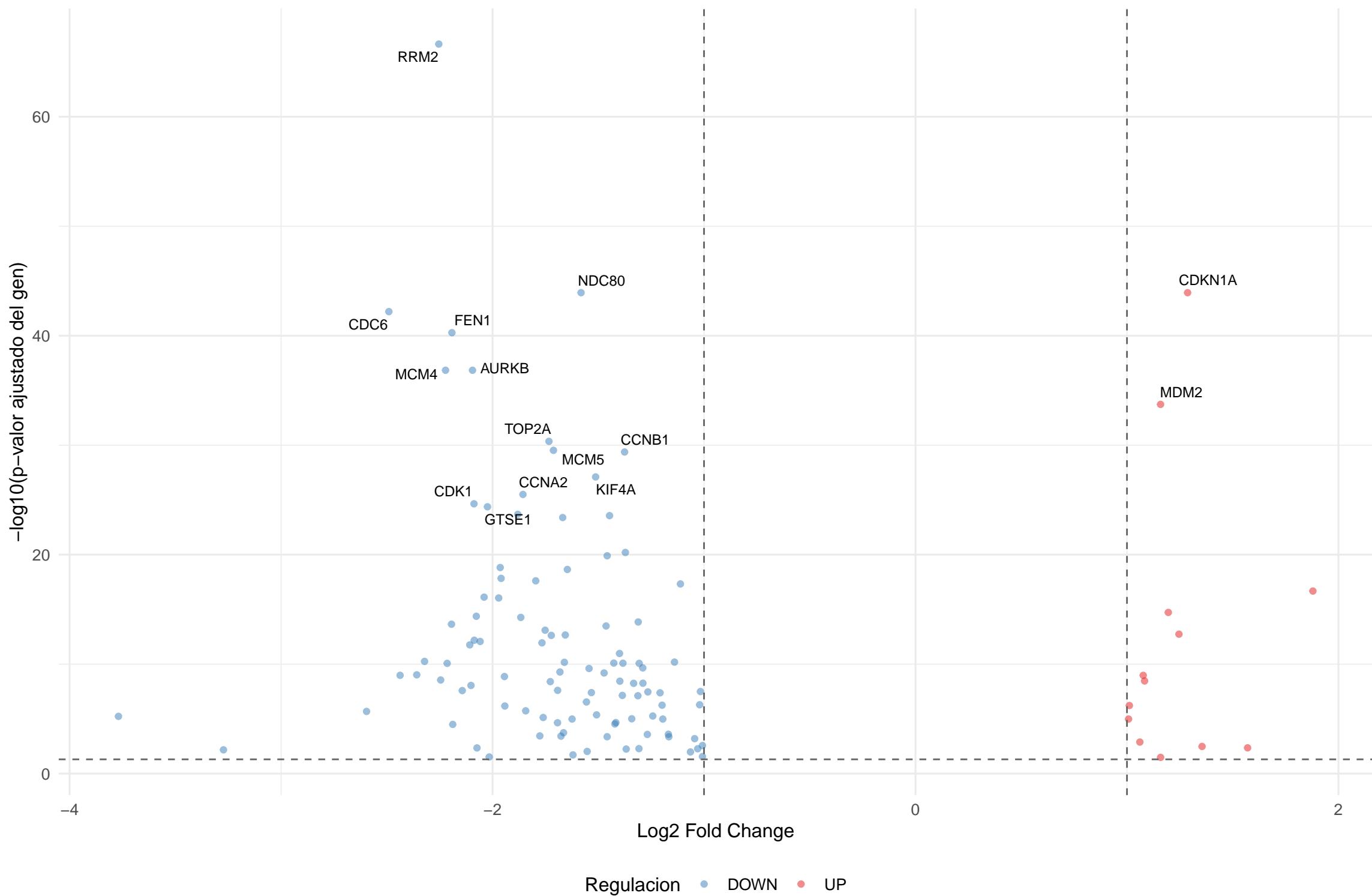
Términos que superan el 'tope' de significancia:

- *Cell cycle* (KEGG:04110, p-val: 4.3e-37)
- *DNA replication* (KEGG:03030, p-val: 1.1e-18)

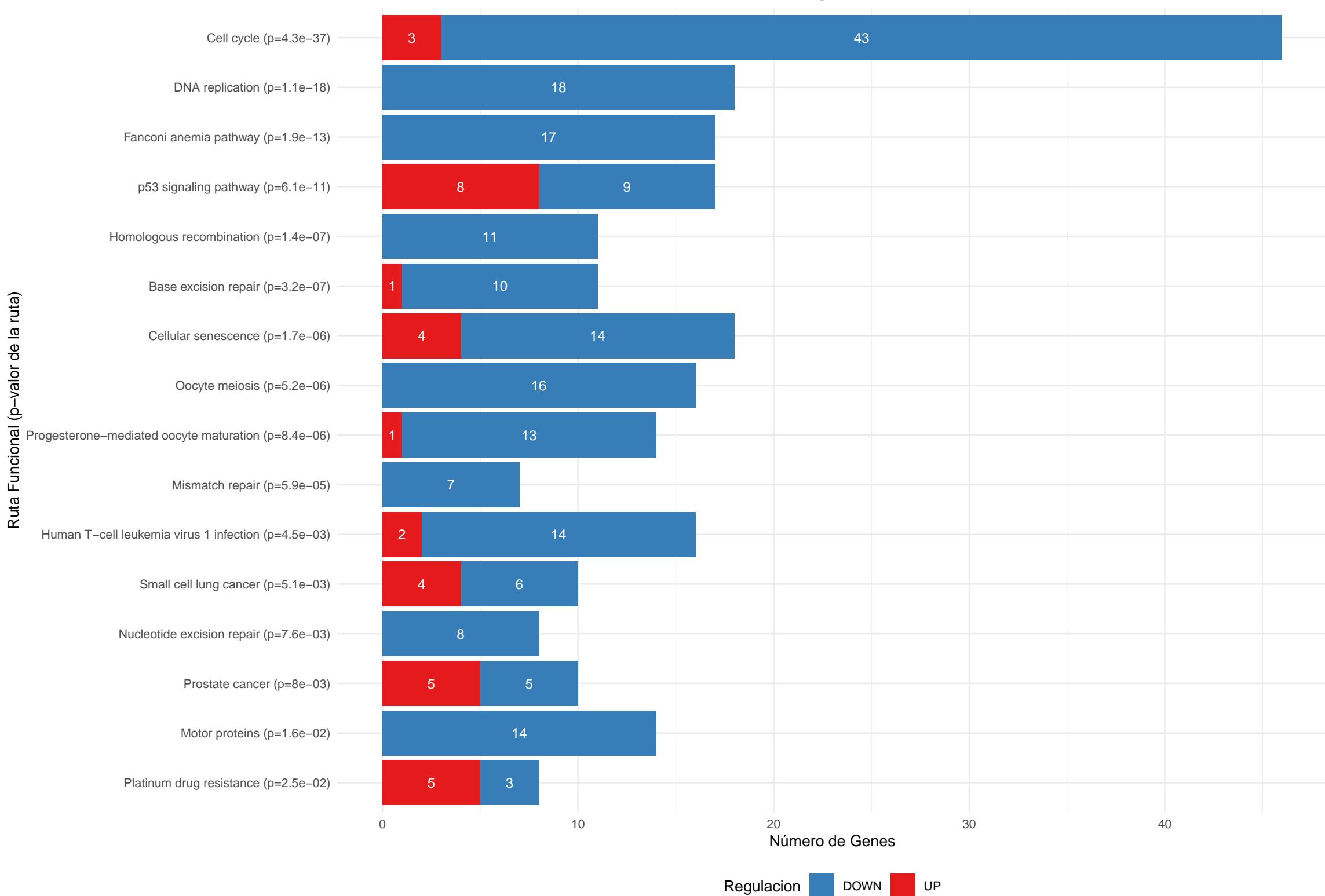
A continuación se muestran los gráficos de barras y tablas de genes para esta sección.

Volcano Plot – KEGG – Rutas Metabólicas

Mostrando 115 genes únicos mapeados en esta sección



KEGG – Rutas Metabólicas – Gráfico (Pág. 1 de 1)



Ruta: Cell cycle (Página 1 de 2)

Fuente: KEGG | ID: KEGG:04110 | Genes: 46 | p-valor ruta: 4.31e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000080986	NDC80	DOWN	-1.581	1.18e-44	832.9
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000178999	AURKB	DOWN	-2.095	1.44e-37	1004.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000137812	KNL1	DOWN	-1.964	1.50e-19	675.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000146670	CDCA5	DOWN	-2.059	8.54e-13	175.9
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0

Ruta: Cell cycle (Página 2 de 2)

Fuente: KEGG | ID: KEGG:04110 | Genes: 46 | p-valor ruta: 4.31e-37

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000112742	TTK	DOWN	-2.143	2.62e-08	332.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000071539	TRIP13	DOWN	-1.313	7.76e-08	472.3
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5

Ruta: DNA replication (Página 1 de 4)

Fuente: GO:BP | ID: GO:0006260 | Genes: 90 | p-valor ruta: 8.3e-57

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000094804	CDC6	DOWN	-2.490	6.33e-43	452.0
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000104738	MCM4	DOWN	-2.222	1.44e-37	1173.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000100297	MCM5	DOWN	-1.712	2.96e-30	468.0
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000076003	MCM6	DOWN	-1.881	2.08e-24	659.3
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG00000112312	GMNN	DOWN	-1.638	4.21e-24	861.3
ENSG00000065328	MCM10	DOWN	-2.433	2.52e-23	492.5
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000168411	RFWD3	DOWN	-1.328	3.39e-20	1082.9
ENSG00000166801	FAM111A	DOWN	-1.546	4.63e-20	583.1
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000166508	MCM7	DOWN	-1.646	2.26e-19	1030.4
ENSG00000189057	FAM111B	DOWN	-2.315	2.29e-19	695.4
ENSG00000091651	ORC6	DOWN	-1.796	2.46e-18	386.3
ENSG00000172716	SLFN11	DOWN	-1.226	2.51e-18	752.8
ENSG00000167900	TK1	DOWN	-1.446	3.41e-18	448.9

Ruta: DNA replication (Página 2 de 4)

Fuente: GO:BP | ID: GO:0006260 | Genes: 90 | p-valor ruta: 8.3e-57

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000112118	MCM3	DOWN	-1.112	4.76e-18	989.6
ENSG00000167325	RRM1	DOWN	-1.219	2.43e-15	4069.2
ENSG00000101003	GINS1	DOWN	-1.773	2.82e-15	374.2
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG00000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG00000171320	ESCO2	DOWN	-2.194	2.27e-14	284.8
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000143476	DTL	DOWN	-2.411	3.23e-13	299.1
ENSG00000140451	PIF1	DOWN	-2.118	6.42e-13	126.2
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000131153	GINS2	DOWN	-1.531	1.00e-12	334.0
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000167670	CHAF1A	DOWN	-1.749	1.16e-12	288.6
ENSG00000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG00000125885	MCM8	DOWN	-1.405	1.29e-11	278.7
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000167513	CDT1	DOWN	-2.358	9.49e-10	138.1
ENSG0000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9

Ruta: DNA replication (Página 3 de 4)

Fuente: GO:BP | ID: GO:0006260 | Genes: 90 | p-valor ruta: 8.3e-57

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000166803	PCLAF	DOWN	-1.228	2.39e-09	4124.4
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000136982	DSCC1	DOWN	-1.851	5.81e-09	116.7
ENSG00000159147	DONSON	DOWN	-1.164	5.81e-09	483.0
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000101868	POLA1	DOWN	-1.208	4.18e-08	300.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000198554	WDHD1	DOWN	-1.420	1.64e-07	256.8
ENSG00000181938	GINS3	DOWN	-1.401	6.93e-07	303.1
ENSG00000160957	RECQL4	DOWN	-1.430	1.26e-06	132.1
ENSG00000085840	ORC1	DOWN	-1.843	1.85e-06	100.1
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000014138	POLA2	DOWN	-1.508	4.34e-06	201.8
ENSG00000006634	DBF4	DOWN	-1.342	9.85e-06	449.5
ENSG00000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG00000176208	ATAD5	DOWN	-1.554	2.03e-05	261.1
ENSG00000129173	E2F8	DOWN	-1.655	2.67e-05	135.0
ENSG00000183763	TRAIP	DOWN	-2.099	3.08e-05	53.4
ENSG00000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG00000111602	TIMELESS	DOWN	-1.128	1.19e-04	370.8

Ruta: DNA replication (Página 4 de 4)

Fuente: GO:BP | ID: GO:0006260 | Genes: 90 | p-valor ruta: 8.3e-57

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000146263	MMS22L	DOWN	-1.185	1.85e-04	128.5
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000093009	CDC45	DOWN	-1.677	3.83e-04	201.5
ENSG00000051341	POLQ	DOWN	-2.911	3.87e-04	70.1
ENSG00000159259	CHAF1B	DOWN	-1.411	5.99e-04	124.5
ENSG00000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG00000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000198056	PRIM1	DOWN	-1.368	5.76e-03	62.7
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6
ENSG00000138346	DNA2	DOWN	-1.620	1.96e-02	111.6

Ruta: Fanconi anemia pathway

Fuente: KEGG | ID: KEGG:03460 | Genes: 17 | p-valor ruta: 1.87e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000187741	FANCA	DOWN	-1.866	5.41e-15	107.5
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG0000175643	RMI2	DOWN	-2.108	1.76e-12	174.3
ENSG0000162607	USP1	DOWN	-1.400	1.07e-11	1193.8
ENSG0000077152	UBE2T	DOWN	-1.383	8.25e-11	1278.6
ENSG0000144554	FANCD2	DOWN	-1.681	5.26e-10	378.0
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000221829	FANCG	DOWN	-1.727	3.98e-09	141.4
ENSG0000140525	FANCI	DOWN	-1.266	3.48e-08	536.3
ENSG0000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000181544	FANCB	DOWN	-1.664	1.85e-04	111.2
ENSG0000131944	FAAP24	DOWN	-1.458	4.29e-04	57.9
ENSG0000187790	FANCM	DOWN	-1.044	6.47e-04	142.6
ENSG0000164053	ATRIP	DOWN	-1.008	2.74e-03	97.5
ENSG0000178966	RMI1	DOWN	-1.308	5.27e-03	243.9
ENSG0000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: p53 signaling pathway

Fuente: KEGG | ID: KEGG:04115 | Genes: 17 | p-valor ruta: 6.07e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000171848	RRM2	DOWN	-2.254	2.30e-67	1984.3
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000075218	GTSE1	DOWN	-2.024	4.26e-25	327.8
ENSG00000172667	ZMAT3	UP	1.195	1.91e-15	2971.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000048392	RRM2B	UP	1.077	1.07e-09	1061.1
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7
ENSG00000149212	SESN3	UP	1.570	4.45e-03	66.3
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5

Ruta: Homologous recombination

Fuente: KEGG | ID: KEGG:03440 | Genes: 11 | p-valor ruta: 1.4e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000138376	BARD1	DOWN	-1.668	4.10e-24	474.1
ENSG0000051180	RAD51	DOWN	-2.077	4.28e-15	291.4
ENSG0000163781	TOPBP1	DOWN	-1.311	1.42e-14	788.6
ENSG0000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG0000139618	BRCA2	DOWN	-1.944	1.37e-09	326.9
ENSG0000196584	XRCC2	DOWN	-1.942	6.71e-07	129.3
ENSG0000101773	RBBP8	DOWN	-1.195	1.05e-05	442.9
ENSG0000197299	BLM	DOWN	-2.188	3.23e-05	68.8
ENSG0000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG0000126215	XRCC3	DOWN	-1.553	9.49e-03	57.7
ENSG0000136492	BRIP1	DOWN	-2.016	3.04e-02	163.3

Ruta: Base excision repair

Fuente: KEGG | ID: KEGG:03410 | Genes: 11 | p-valor ruta: 3.2e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000168496	FEN1	DOWN	-2.192	5.29e-41	1595.8
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9
ENSG00000041880	PARP3	UP	1.061	1.32e-03	127.5
ENSG00000129484	PARP2	DOWN	-1.064	1.06e-02	254.8

Ruta: Cellular senescence

Fuente: KEGG | ID: KEGG:04218 | Genes: 18 | p-valor ruta: 1.65e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000101057	MYBL2	DOWN	-1.290	2.23e-10	706.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000080839	RBL1	DOWN	-1.533	4.00e-08	151.5
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000183814	LIN9	DOWN	-1.417	2.19e-05	123.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5

Ruta: Oocyte meiosis

Fuente: KEGG | ID: KEGG:04114 | Genes: 16 | p-valor ruta: 5.24e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000112029	FBXO5	DOWN	-2.086	6.62e-13	325.6
ENSG00000129810	SGO1	DOWN	-2.322	5.66e-11	212.1
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000156509	FBXO43	DOWN	-3.272	6.77e-03	15.2

Ruta: Progesterone-mediated oocyte maturation

Fuente: KEGG | ID: KEGG:04914 | Genes: 14 | p-valor ruta: 8.39e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000134057	CCNB1	DOWN	-1.376	4.23e-30	1075.8
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000170312	CDK1	DOWN	-2.088	2.27e-25	1384.7
ENSG00000087586	AURKA	DOWN	-1.463	3.30e-14	1066.4
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000169679	BUB1	DOWN	-1.427	8.07e-11	645.0
ENSG00000164045	CDC25A	DOWN	-1.398	3.62e-09	386.0
ENSG00000158402	CDC25C	DOWN	-2.102	8.88e-09	177.0
ENSG00000101224	CDC25B	DOWN	-1.021	5.18e-07	347.3
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000166851	PLK1	DOWN	-1.760	7.54e-06	86.4
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2

Ruta: Mismatch repair

Fuente: KEGG | ID: KEGG:03430 | Genes: 7 | p-valor ruta: 5.95e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG0000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000174371	EXO1	DOWN	-2.596	2.10e-06	101.7
ENSG0000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: Human T-cell leukemia virus 1 infection

Fuente: KEGG | ID: KEGG:05166 | Genes: 16 | p-valor ruta: 4.54e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000145386	CCNA2	DOWN	-1.856	3.17e-26	988.0
ENSG00000156970	BUB1B	DOWN	-1.960	1.47e-18	480.6
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000164109	MAD2L1	DOWN	-1.656	2.19e-13	684.6
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000117399	CDC20	DOWN	-1.306	8.53e-11	1077.9
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000164611	PTTG1	DOWN	-1.017	3.21e-08	3814.8
ENSG00000157456	CCNB2	DOWN	-1.198	5.68e-07	582.1
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000123080	CDKN2C	DOWN	-1.693	2.28e-05	206.7
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000117394	SLC2A1	DOWN	-1.166	4.34e-04	200.8
ENSG00000183765	CHEK2	DOWN	-1.030	5.41e-03	109.3

Ruta: Small cell lung cancer

Fuente: KEGG | ID: KEGG:05222 | Genes: 10 | p-valor ruta: 5.08e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000058085	LAMC2	UP	1.879	2.12e-17	204.8
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000145604	SKP2	DOWN	-1.333	5.70e-09	594.2
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2
ENSG00000130222	GADD45G	UP	1.159	3.31e-02	58.5

Ruta: Nucleotide excision repair

Fuente: KEGG | ID: KEGG:03420 | Genes: 8 | p-valor ruta: 7.64e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000132646	PCNA	DOWN	-1.372	6.33e-21	2475.7
ENSG00000163918	RFC4	DOWN	-1.722	2.38e-13	353.5
ENSG00000177084	POLE	DOWN	-2.215	8.53e-11	106.4
ENSG00000049541	RFC2	DOWN	-1.473	6.43e-10	250.2
ENSG00000100479	POLE2	DOWN	-1.692	2.50e-08	173.1
ENSG00000111445	RFC5	DOWN	-1.386	7.25e-08	347.4
ENSG00000077514	POLD3	DOWN	-1.169	2.56e-04	290.9
ENSG00000133119	RFC3	DOWN	-1.777	3.63e-04	302.9

Ruta: Prostate cancer

Fuente: KEGG | ID: KEGG:05215 | Genes: 10 | p-valor ruta: 8.01e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000101412	E2F1	DOWN	-1.971	9.08e-17	232.3
ENSG00000104368	PLAT	UP	1.246	1.84e-13	2447.2
ENSG00000123374	CDK2	DOWN	-1.140	6.55e-11	1630.6
ENSG00000175305	CCNE2	DOWN	-2.245	2.83e-09	73.4
ENSG00000122861	PLAU	UP	1.083	3.46e-09	730.9
ENSG00000007968	E2F2	DOWN	-3.769	5.92e-06	21.4
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000105173	CCNE1	DOWN	-1.268	2.65e-04	172.2

Ruta: Motor proteins

Fuente: KEGG | ID: KEGG:04814 | Genes: 14 | p-valor ruta: 1.56e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000090889	KIF4A	DOWN	-1.513	7.98e-28	682.7
ENSG00000138182	KIF20B	DOWN	-1.458	1.27e-20	1755.0
ENSG00000237649	KIFC1	DOWN	-2.040	7.65e-17	505.4
ENSG00000138160	KIF11	DOWN	-1.751	8.02e-14	450.4
ENSG00000142945	KIF2C	DOWN	-1.660	6.87e-11	313.0
ENSG00000137807	KIF23	DOWN	-1.544	2.50e-10	400.6
ENSG00000186185	KIF18B	DOWN	-2.437	1.06e-09	148.7
ENSG00000138778	CENPE	DOWN	-1.289	5.56e-09	2554.3
ENSG00000118193	KIF14	DOWN	-1.556	2.88e-07	345.1
ENSG00000112984	KIF20A	DOWN	-1.242	5.50e-06	464.0
ENSG00000163808	KIF15	DOWN	-1.624	1.04e-05	365.5
ENSG00000079616	KIF22	DOWN	-1.422	2.93e-05	211.2
ENSG00000186638	KIF24	DOWN	-2.074	4.52e-03	18.8
ENSG00000108423	TUBD1	DOWN	-1.008	2.79e-02	124.1

Ruta: Platinum drug resistance

Fuente: KEGG | ID: KEGG:01524 | Genes: 8 | p-valor ruta: 2.5e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ENSG00000124762	CDKN1A	UP	1.287	1.18e-44	4228.1
ENSG00000135679	MDM2	UP	1.159	1.88e-34	4081.3
ENSG00000131747	TOP2A	DOWN	-1.733	4.48e-31	5823.0
ENSG00000089685	BIRC5	DOWN	-1.447	2.74e-24	999.2
ENSG00000012048	BRCA1	DOWN	-1.766	1.14e-12	390.2
ENSG00000105327	BBC3	UP	1.011	6.06e-07	2011.2
ENSG00000171608	PIK3CD	UP	1.008	1.05e-05	265.1
ENSG00000026103	FAS	UP	1.355	3.32e-03	176.7