

# Análisis de Enriquecimiento Funcional

*Contraste: SARS\_CoV\_2\_vs\_Mock*

Organismo: *hsapiens*

## **Archivos de entrada:**

*Resultados\_Significativos\_SARS\_CoV\_2\_vs\_Mock.txt*

*Resultados\_Completos\_SARS\_CoV\_2\_vs\_Mock.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: 530

Genes mapeados en rutas enriquecidas: 468

**Total de Genes Huérfanos: 62**

## Desglose de los Genes Huérfanos:

(Genes que NO están en las 616 rutas enriquecidas)

- Genes sin símbolo (NA o "): 62
- Genes con anotación no informativa (LOC..., si:..., zgc:...): 0
- Con símbolo real (pero en rutas no enriquecidas): 0

*La tabla completa con los 62 genes huérfanos se ha guardado en 'genes\_huerfanos\_SARS\_CoV\_2\_vs\_Mock.txt'*

# Sección de Análisis: GO:MF – Funciones Moleculares

Total de términos enriquecidos en esta sección: 27

Términos 'Tope' (p–valor < 1e–16): 1

## Términos que superan el 'tope' de significancia:

– cytokine activity (GO:0005125, p–val: 4.7e–17)

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

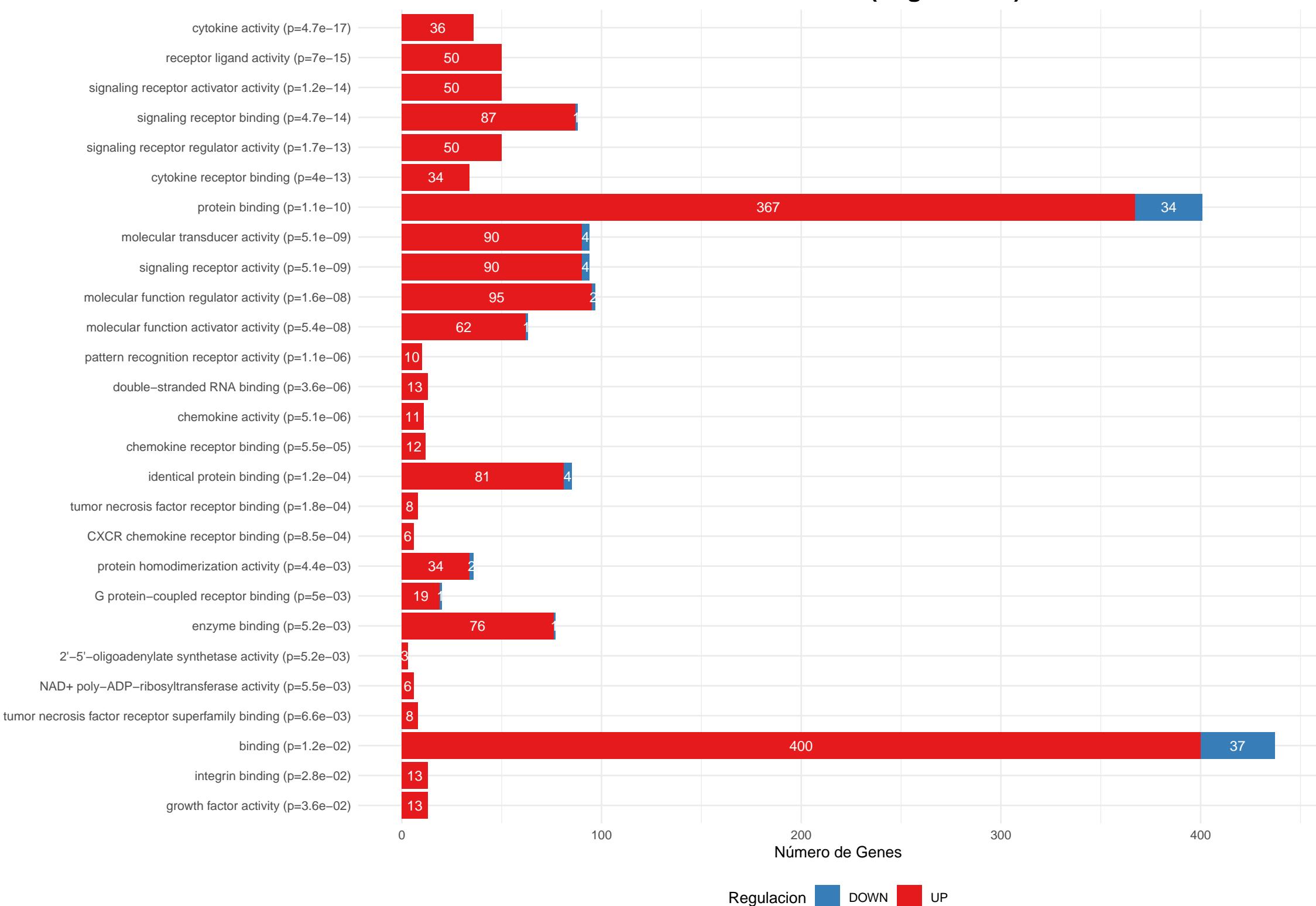
# Volcano Plot – GO:MF – Funciones Moleculares

Mostrando 442 genes únicos mapeados en esta sección



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

Ruta Funcional (p–valor de la ruta)



Regulacion ■ DOWN ■ UP

## Ruta: cytokine activity (Página 1 de 2)

Fuente: GO:MF | ID: GO:0005125 | Genes: 36 | p–valor ruta: 4.74e–17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e–242	2226.4
IL1B	NA	UP	4.202	1.58e–214	2230.2
CXCL10	NA	UP	6.079	8.12e–195	783.4
CXCL3	NA	UP	3.053	2.27e–187	4330.7
CXCL11	NA	UP	6.074	5.51e–176	710.1
CCL5	NA	UP	5.035	8.94e–165	656.3
CXCL2	NA	UP	3.371	1.67e–155	4155.4
INHBA	NA	UP	3.514	2.31e–143	1743.6
CX3CL1	NA	UP	3.114	2.67e–123	1760.3
TNFSF10	NA	UP	3.014	1.58e–112	3429.5
CSF2	NA	UP	7.043	2.08e–103	455.6
TNF	NA	UP	7.712	3.81e–103	573.0
IFNB1	NA	UP	10.001	4.69e–95	1340.6
IFNL1	NA	UP	8.179	1.68e–89	578.0
CCL2	NA	UP	2.562	2.63e–75	658.0
TNFRSF11B	NA	UP	2.247	4.76e–54	1332.4
CCL22	NA	UP	3.454	2.91e–50	168.7
CSF1	NA	UP	2.530	1.40e–49	467.4
LTB	NA	UP	3.555	2.50e–41	150.4
BMP2	NA	UP	2.237	3.69e–40	325.3
IFNL3	NA	UP	9.837	4.42e–30	365.0
IL12A	NA	UP	3.852	1.95e–28	83.7
IFNL2	NA	UP	11.372	1.86e–23	434.7

## Ruta: cytokine activity (Página 2 de 2)

Fuente: GO:MF | ID: GO:0005125 | Genes: 36 | p-valor ruta: 4.74e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF3	NA	UP	6.122	1.72e-19	56.0
IL15	NA	UP	2.012	2.28e-17	116.8
INHBE	NA	UP	5.109	1.59e-15	37.3
FLT3LG	NA	UP	2.346	6.32e-15	68.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFSF14	NA	UP	2.748	3.71e-07	23.0
CXCL9	NA	UP	4.099	4.37e-04	26.3
IL17C	NA	UP	4.636	3.13e-03	4.1
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: receptor ligand activity (Página 1 de 2)

Fuente: GO:MF | ID: GO:0048018 | Genes: 50 | p–valor ruta: 6.99e–15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e–242	2226.4
IL1B	NA	UP	4.202	1.58e–214	2230.2
CXCL10	NA	UP	6.079	8.12e–195	783.4
CXCL3	NA	UP	3.053	2.27e–187	4330.7
CXCL11	NA	UP	6.074	5.51e–176	710.1
CCL5	NA	UP	5.035	8.94e–165	656.3
CXCL2	NA	UP	3.371	1.67e–155	4155.4
INHBA	NA	UP	3.514	2.31e–143	1743.6
CX3CL1	NA	UP	3.114	2.67e–123	1760.3
STC2	NA	UP	2.729	3.17e–119	2626.1
TNFSF10	NA	UP	3.014	1.58e–112	3429.5
CSF2	NA	UP	7.043	2.08e–103	455.6
TNF	NA	UP	7.712	3.81e–103	573.0
CD274	NA	UP	5.204	1.23e–98	314.4
IFNB1	NA	UP	10.001	4.69e–95	1340.6
IFNL1	NA	UP	8.179	1.68e–89	578.0
CCL2	NA	UP	2.562	2.63e–75	658.0
SEMA7A	NA	UP	2.329	3.91e–69	7576.6
HBEGF	NA	UP	2.602	3.10e–57	415.2
TNFRSF11B	NA	UP	2.247	4.76e–54	1332.4
CCL22	NA	UP	3.454	2.91e–50	168.7
CSF1	NA	UP	2.530	1.40e–49	467.4
SEMA3A	NA	UP	2.276	5.71e–42	512.5

## Ruta: receptor ligand activity (Página 2 de 2)

Fuente: GO:MF | ID: GO:0048018 | Genes: 50 | p–valor ruta: 6.99e–15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LTB	NA	UP	3.555	2.50e–41	150.4
BMP2	NA	UP	2.237	3.69e–40	325.3
ULBP1	NA	UP	3.138	2.70e–38	151.4
EDN2	NA	UP	3.499	8.77e–31	90.3
IFNL3	NA	UP	9.837	4.42e–30	365.0
TYMP	NA	UP	2.001	2.11e–29	872.8
IL12A	NA	UP	3.852	1.95e–28	83.7
IFNL2	NA	UP	11.372	1.86e–23	434.7
FGF19	NA	UP	3.931	5.59e–21	52.8
CSF3	NA	UP	6.122	1.72e–19	56.0
IL15	NA	UP	2.012	2.28e–17	116.8
INHBE	NA	UP	5.109	1.59e–15	37.3
FLT3LG	NA	UP	2.346	6.32e–15	68.5
IL23A	NA	UP	2.189	2.05e–11	59.9
TNFSF13B	NA	UP	3.042	2.17e–11	34.7
TNFSF14	NA	UP	2.748	3.71e–07	23.0
COLEC10	NA	UP	2.878	4.02e–04	11.6
CXCL9	NA	UP	4.099	4.37e–04	26.3
LHB	NA	UP	3.522	1.50e–03	7.0
IL17C	NA	UP	4.636	3.13e–03	4.1
DLL1	NA	UP	2.171	4.40e–03	10.4
CD70	NA	UP	3.257	1.21e–02	4.7
IL34	NA	UP	2.794	2.41e–02	4.8
CCL17	NA	UP	3.441	3.89e–02	2.9
FGF18	NA	UP	2.038	4.86e–02	6.1

## Ruta: signaling receptor activator activity (Página 1 de 2)

Fuente: GO:MF | ID: GO:0030546 | Genes: 50 | p–valor ruta: 1.19e–14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e–242	2226.4
IL1B	NA	UP	4.202	1.58e–214	2230.2
CXCL10	NA	UP	6.079	8.12e–195	783.4
CXCL3	NA	UP	3.053	2.27e–187	4330.7
CXCL11	NA	UP	6.074	5.51e–176	710.1
CCL5	NA	UP	5.035	8.94e–165	656.3
CXCL2	NA	UP	3.371	1.67e–155	4155.4
INHBA	NA	UP	3.514	2.31e–143	1743.6
CX3CL1	NA	UP	3.114	2.67e–123	1760.3
STC2	NA	UP	2.729	3.17e–119	2626.1
TNFSF10	NA	UP	3.014	1.58e–112	3429.5
CSF2	NA	UP	7.043	2.08e–103	455.6
TNF	NA	UP	7.712	3.81e–103	573.0
CD274	NA	UP	5.204	1.23e–98	314.4
IFNB1	NA	UP	10.001	4.69e–95	1340.6
IFNL1	NA	UP	8.179	1.68e–89	578.0
CCL2	NA	UP	2.562	2.63e–75	658.0
SEMA7A	NA	UP	2.329	3.91e–69	7576.6
HBEGF	NA	UP	2.602	3.10e–57	415.2
TNFRSF11B	NA	UP	2.247	4.76e–54	1332.4
CCL22	NA	UP	3.454	2.91e–50	168.7
CSF1	NA	UP	2.530	1.40e–49	467.4
SEMA3A	NA	UP	2.276	5.71e–42	512.5

## Ruta: signaling receptor activator activity (Página 2 de 2)

Fuente: GO:MF | ID: GO:0030546 | Genes: 50 | p–valor ruta: 1.19e–14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LTB	NA	UP	3.555	2.50e–41	150.4
BMP2	NA	UP	2.237	3.69e–40	325.3
ULBP1	NA	UP	3.138	2.70e–38	151.4
EDN2	NA	UP	3.499	8.77e–31	90.3
IFNL3	NA	UP	9.837	4.42e–30	365.0
TYMP	NA	UP	2.001	2.11e–29	872.8
IL12A	NA	UP	3.852	1.95e–28	83.7
IFNL2	NA	UP	11.372	1.86e–23	434.7
FGF19	NA	UP	3.931	5.59e–21	52.8
CSF3	NA	UP	6.122	1.72e–19	56.0
IL15	NA	UP	2.012	2.28e–17	116.8
INHBE	NA	UP	5.109	1.59e–15	37.3
FLT3LG	NA	UP	2.346	6.32e–15	68.5
IL23A	NA	UP	2.189	2.05e–11	59.9
TNFSF13B	NA	UP	3.042	2.17e–11	34.7
TNFSF14	NA	UP	2.748	3.71e–07	23.0
COLEC10	NA	UP	2.878	4.02e–04	11.6
CXCL9	NA	UP	4.099	4.37e–04	26.3
LHB	NA	UP	3.522	1.50e–03	7.0
IL17C	NA	UP	4.636	3.13e–03	4.1
DLL1	NA	UP	2.171	4.40e–03	10.4
CD70	NA	UP	3.257	1.21e–02	4.7
IL34	NA	UP	2.794	2.41e–02	4.8
CCL17	NA	UP	3.441	3.89e–02	2.9
FGF18	NA	UP	2.038	4.86e–02	6.1

## Ruta: signaling receptor binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:0005102 | Genes: 88 | p-valor ruta: 4.68e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
STC2	NA	UP	2.729	3.17e-119	2626.1
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
TRAF1	NA	UP	4.730	5.65e-84	258.2

## Ruta: signaling receptor binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:0005102 | Genes: 88 | p–valor ruta: 4.68e–14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
THBS1	NA	UP	2.656	1.05e–77	3791.3
CCL2	NA	UP	2.562	2.63e–75	658.0
SEMA7A	NA	UP	2.329	3.91e–69	7576.6
STAT1	NA	UP	2.519	1.61e–68	9528.0
RND1	NA	UP	2.840	1.60e–62	337.7
NEDD4	NA	UP	2.433	4.99e–60	1678.5
HBEGF	NA	UP	2.602	3.10e–57	415.2
ISG15	NA	UP	2.482	5.90e–57	3807.9
TNFRSF11B	NA	UP	2.247	4.76e–54	1332.4
CCL22	NA	UP	3.454	2.91e–50	168.7
CSF1	NA	UP	2.530	1.40e–49	467.4
SEMA3A	NA	UP	2.276	5.71e–42	512.5
LTB	NA	UP	3.555	2.50e–41	150.4
BMP2	NA	UP	2.237	3.69e–40	325.3
ULBP1	NA	UP	3.138	2.70e–38	151.4
IRS2	NA	UP	2.254	1.06e–33	255.2
EDN2	NA	UP	3.499	8.77e–31	90.3
IFNL3	NA	UP	9.837	4.42e–30	365.0
TYMP	NA	UP	2.001	2.11e–29	872.8
IL12A	NA	UP	3.852	1.95e–28	83.7
VCAM1	NA	UP	4.737	4.28e–26	66.5
LIFR	NA	UP	2.213	9.30e–24	226.1
IFNL2	NA	UP	11.372	1.86e–23	434.7
CHAC1	NA	UP	3.022	3.43e–23	111.7
LAMA2	NA	UP	2.355	4.82e–21	125.5

## Ruta: signaling receptor binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:0005102 | Genes: 88 | p–valor ruta: 4.68e–14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FGF19	NA	UP	3.931	5.59e–21	52.8
ITGAM	NA	UP	2.447	1.39e–19	90.2
CSF3	NA	UP	6.122	1.72e–19	56.0
JAK2	NA	UP	2.081	1.26e–17	123.4
IL15	NA	UP	2.012	2.28e–17	116.8
INHBE	NA	UP	5.109	1.59e–15	37.3
BDKRB2	NA	UP	2.797	5.56e–15	55.1
FLT3LG	NA	UP	2.346	6.32e–15	68.5
MUC4	NA	UP	2.613	4.74e–12	55.4
IL23A	NA	UP	2.189	2.05e–11	59.9
TNFSF13B	NA	UP	3.042	2.17e–11	34.7
ACTN2	NA	UP	3.956	7.01e–09	20.3
SOCS1	NA	UP	2.012	6.54e–08	82.5
TLR6	NA	UP	2.680	9.77e–08	26.3
TNFSF14	NA	UP	2.748	3.71e–07	23.0
SYT1	NA	UP	2.659	1.62e–06	21.4
ICAM4	NA	UP	2.446	8.79e–06	22.0
FAP	NA	UP	3.233	1.87e–05	14.0
COLEC10	NA	UP	2.878	4.02e–04	11.6
CXCL9	NA	UP	4.099	4.37e–04	26.3
LHB	NA	UP	3.522	1.50e–03	7.0
LGR6	NA	UP	3.915	2.25e–03	6.0
IL17C	NA	UP	4.636	3.13e–03	4.1
HRG	NA	UP	2.971	4.00e–03	6.9
DLL1	NA	UP	2.171	4.40e–03	10.4

## Ruta: signaling receptor binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:0005102 | Genes: 88 | p-valor ruta: 4.68e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LY96	NA	UP	5.204	4.42e-03	3.4
EGFL6	NA	UP	3.034	6.01e-03	5.9
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
DLG2	NA	UP	3.028	3.83e-02	3.8
CCL17	NA	UP	3.441	3.89e-02	2.9
ASXL3	NA	UP	2.101	4.07e-02	6.6
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: signaling receptor regulator activity (Página 1 de 2)

Fuente: GO:MF | ID: GO:0030545 | Genes: 50 | p–valor ruta: 1.74e–13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e–242	2226.4
IL1B	NA	UP	4.202	1.58e–214	2230.2
CXCL10	NA	UP	6.079	8.12e–195	783.4
CXCL3	NA	UP	3.053	2.27e–187	4330.7
CXCL11	NA	UP	6.074	5.51e–176	710.1
CCL5	NA	UP	5.035	8.94e–165	656.3
CXCL2	NA	UP	3.371	1.67e–155	4155.4
INHBA	NA	UP	3.514	2.31e–143	1743.6
CX3CL1	NA	UP	3.114	2.67e–123	1760.3
STC2	NA	UP	2.729	3.17e–119	2626.1
TNFSF10	NA	UP	3.014	1.58e–112	3429.5
CSF2	NA	UP	7.043	2.08e–103	455.6
TNF	NA	UP	7.712	3.81e–103	573.0
CD274	NA	UP	5.204	1.23e–98	314.4
IFNB1	NA	UP	10.001	4.69e–95	1340.6
IFNL1	NA	UP	8.179	1.68e–89	578.0
CCL2	NA	UP	2.562	2.63e–75	658.0
SEMA7A	NA	UP	2.329	3.91e–69	7576.6
HBEGF	NA	UP	2.602	3.10e–57	415.2
TNFRSF11B	NA	UP	2.247	4.76e–54	1332.4
CCL22	NA	UP	3.454	2.91e–50	168.7
CSF1	NA	UP	2.530	1.40e–49	467.4
SEMA3A	NA	UP	2.276	5.71e–42	512.5

## Ruta: signaling receptor regulator activity (Página 2 de 2)

Fuente: GO:MF | ID: GO:0030545 | Genes: 50 | p–valor ruta: 1.74e–13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LTB	NA	UP	3.555	2.50e–41	150.4
BMP2	NA	UP	2.237	3.69e–40	325.3
ULBP1	NA	UP	3.138	2.70e–38	151.4
EDN2	NA	UP	3.499	8.77e–31	90.3
IFNL3	NA	UP	9.837	4.42e–30	365.0
TYMP	NA	UP	2.001	2.11e–29	872.8
IL12A	NA	UP	3.852	1.95e–28	83.7
IFNL2	NA	UP	11.372	1.86e–23	434.7
FGF19	NA	UP	3.931	5.59e–21	52.8
CSF3	NA	UP	6.122	1.72e–19	56.0
IL15	NA	UP	2.012	2.28e–17	116.8
INHBE	NA	UP	5.109	1.59e–15	37.3
FLT3LG	NA	UP	2.346	6.32e–15	68.5
IL23A	NA	UP	2.189	2.05e–11	59.9
TNFSF13B	NA	UP	3.042	2.17e–11	34.7
TNFSF14	NA	UP	2.748	3.71e–07	23.0
COLEC10	NA	UP	2.878	4.02e–04	11.6
CXCL9	NA	UP	4.099	4.37e–04	26.3
LHB	NA	UP	3.522	1.50e–03	7.0
IL17C	NA	UP	4.636	3.13e–03	4.1
DLL1	NA	UP	2.171	4.40e–03	10.4
CD70	NA	UP	3.257	1.21e–02	4.7
IL34	NA	UP	2.794	2.41e–02	4.8
CCL17	NA	UP	3.441	3.89e–02	2.9
FGF18	NA	UP	2.038	4.86e–02	6.1

## Ruta: cytokine receptor binding (Página 1 de 2)

Fuente: GO:MF | ID: GO:0005126 | Genes: 34 | p–valor ruta: 3.98e–13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e–242	2226.4
IL1B	NA	UP	4.202	1.58e–214	2230.2
CXCL10	NA	UP	6.079	8.12e–195	783.4
CXCL3	NA	UP	3.053	2.27e–187	4330.7
CXCL11	NA	UP	6.074	5.51e–176	710.1
CCL5	NA	UP	5.035	8.94e–165	656.3
CXCL2	NA	UP	3.371	1.67e–155	4155.4
CX3CL1	NA	UP	3.114	2.67e–123	1760.3
TNFSF10	NA	UP	3.014	1.58e–112	3429.5
CSF2	NA	UP	7.043	2.08e–103	455.6
TNF	NA	UP	7.712	3.81e–103	573.0
IFNB1	NA	UP	10.001	4.69e–95	1340.6
IFNL1	NA	UP	8.179	1.68e–89	578.0
TRAF1	NA	UP	4.730	5.65e–84	258.2
CCL2	NA	UP	2.562	2.63e–75	658.0
STAT1	NA	UP	2.519	1.61e–68	9528.0
CCL22	NA	UP	3.454	2.91e–50	168.7
CSF1	NA	UP	2.530	1.40e–49	467.4
LTB	NA	UP	3.555	2.50e–41	150.4
IL12A	NA	UP	3.852	1.95e–28	83.7
LIFR	NA	UP	2.213	9.30e–24	226.1
CSF3	NA	UP	6.122	1.72e–19	56.0
JAK2	NA	UP	2.081	1.26e–17	123.4

## Ruta: cytokine receptor binding (Página 2 de 2)

Fuente: GO:MF | ID: GO:0005126 | Genes: 34 | p-valor ruta: 3.98e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFSF14	NA	UP	2.748	3.71e-07	23.0
CXCL9	NA	UP	4.099	4.37e-04	26.3
CD70	NA	UP	3.257	1.21e-02	4.7
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: protein binding (Página 1 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0

## Ruta: protein binding (Página 2 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
EPSTI1	NA	UP	4.231	7.22e-130	564.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
SAMD9L	NA	UP	3.487	2.90e-126	1768.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
IKZF3	NA	UP	3.163	1.21e-120	1046.8
APOL6	NA	UP	3.196	9.56e-120	1648.2
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4

## Ruta: protein binding (Página 3 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ASNS	NA	UP	2.919	1.59e-113	1627.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
MB21D2	NA	UP	2.998	2.32e-111	911.2
XAF1	NA	UP	4.580	3.19e-111	427.9
IFI44	NA	UP	3.036	1.35e-108	3423.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
NUAK2	NA	UP	4.358	1.14e-107	489.1
RTP4	NA	UP	3.457	2.00e-107	589.0
TMEM140	NA	UP	3.747	6.77e-107	475.4
SP110	NA	UP	2.776	1.00e-106	1474.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
TRANK1	NA	UP	3.317	5.86e-102	541.3
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8

## Ruta: protein binding (Página 4 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TM4SF4	NA	DOWN	-2.482	1.83e-87	1021.7
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
RASGRP3	NA	UP	3.468	2.92e-82	392.1
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7

## Ruta: protein binding (Página 5 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
KRTAP2-3	NA	UP	2.722	7.97e-75	878.4
EGR1	NA	UP	2.472	2.61e-74	1149.5
HSH2D	NA	UP	2.613	6.29e-73	813.8
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
RND1	NA	UP	2.840	1.60e-62	337.7
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8

## Ruta: protein binding (Página 6 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TUFT1	NA	UP	2.001	1.00e-55	1905.9
FOSB	NA	UP	3.144	1.32e-55	267.7
ALDH1L2	NA	UP	3.029	4.52e-55	257.3
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
NAV2	NA	UP	2.370	3.20e-51	765.9
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
ANKRD33B	NA	UP	2.525	7.29e-50	317.4
CSF1	NA	UP	2.530	1.40e-49	467.4

## Ruta: protein binding (Página 7 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
APOL4	NA	UP	3.489	1.37e-42	132.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
PHF11	NA	UP	2.211	3.12e-37	302.1
ZC3H12C	NA	UP	2.109	3.86e-36	308.6
MT2A	NA	UP	2.437	2.24e-35	363.0
DUSP8	NA	UP	2.088	3.69e-35	551.5
SNRNP25	NA	DOWN	-2.131	4.01e-34	420.7
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
ANXA10	NA	DOWN	-2.270	2.83e-33	223.1
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7

## Ruta: protein binding (Página 8 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
EDN2	NA	UP	3.499	8.77e-31	90.3
BACH2	NA	UP	2.222	2.18e-30	209.0
LRRC45	NA	DOWN	-2.449	3.12e-30	356.2
PPM1K	NA	UP	2.192	3.89e-30	395.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
EPN3	NA	DOWN	-2.294	4.66e-30	335.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
HDX	NA	UP	2.521	1.83e-28	139.2
IL12A	NA	UP	3.852	1.95e-28	83.7
KIF21B	NA	UP	2.131	3.74e-27	240.5
RBM43	NA	UP	2.267	6.06e-27	246.6
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
BCL2L14	NA	UP	2.782	8.63e-26	122.3
MAST4	NA	UP	2.184	1.21e-25	197.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1
KRT6B	NA	UP	2.049	5.47e-24	321.4
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CHAC1	NA	UP	3.022	3.43e-23	111.7

## Ruta: protein binding (Página 9 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
DDO	NA	UP	2.846	3.84e-20	82.4
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
GIMAP2	NA	UP	2.542	5.46e-18	86.3
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8
FSD1L	NA	UP	2.523	4.34e-17	83.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DDC	NA	DOWN	-2.582	2.27e-16	72.0
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
INHBE	NA	UP	5.109	1.59e-15	37.3
RAET1L	NA	UP	2.665	2.71e-15	60.0
NAV3	NA	UP	2.285	2.77e-15	84.4

## Ruta: protein binding (Página 10 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HOGA1	NA	DOWN	-2.098	2.81e-15	96.4
GBX2	NA	UP	2.353	5.55e-15	78.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
DNAH17	NA	UP	3.324	3.42e-13	38.8
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PDZD2	NA	UP	4.182	1.86e-12	28.7
PLEKHG7	NA	UP	3.625	2.08e-12	31.8
MUC4	NA	UP	2.613	4.74e-12	55.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
KLHDC7B	NA	UP	3.660	1.88e-11	29.7
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
PPP4R4	NA	UP	3.423	6.94e-11	30.7
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3

## Ruta: protein binding (Página 11 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STX19	NA	UP	2.009	1.09e-08	99.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
C6orf58	NA	UP	2.512	2.12e-08	30.6
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
SULT1C2	NA	UP	2.136	2.10e-07	36.2
KCNV1	NA	UP	2.402	2.10e-07	37.9
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
AHRR	NA	UP	2.180	3.48e-07	33.9
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
BCAT1	NA	UP	2.723	7.42e-07	22.9
RBM11	NA	UP	2.506	8.83e-07	22.9
SAA4	NA	UP	2.563	9.46e-07	21.9
WFDC5	NA	UP	5.168	1.07e-06	13.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
COX6B2	NA	UP	2.208	1.76e-06	27.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4

## Ruta: protein binding (Página 12 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TAGAP	NA	UP	3.201	2.52e-06	16.1
HSD17B14	NA	UP	2.529	3.30e-06	21.4
RAB30	NA	UP	2.024	5.27e-06	28.7
COL4A1	NA	UP	6.589	5.89e-06	8.2
ACTBL2	NA	UP	2.242	5.97e-06	28.3
ADCY4	NA	UP	2.271	8.12e-06	23.6
BEST1	NA	UP	3.553	8.47e-06	13.3
ICAM4	NA	UP	2.446	8.79e-06	22.0
SERPINA10	NA	UP	6.459	9.50e-06	7.5
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
RAB36	NA	DOWN	-2.063	2.15e-05	24.7
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
BEST3	NA	UP	2.070	3.26e-05	23.9
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
SDS	NA	UP	4.527	5.38e-05	9.4
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
KIF6	NA	UP	4.867	1.75e-04	7.8
RHCG	NA	UP	2.107	1.84e-04	21.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
GFPT2	NA	UP	2.651	2.37e-04	12.7

## Ruta: protein binding (Página 13 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TMEM40	NA	UP	2.179	2.99e-04	16.5
UBQLNL	NA	UP	3.875	3.33e-04	7.9
TRPC4	NA	UP	5.730	3.71e-04	4.5
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
CCDC96	NA	DOWN	-2.033	4.86e-04	19.3
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
SLC38A4	NA	DOWN	-2.630	6.25e-04	12.4
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
HAND1	NA	UP	4.966	8.42e-04	5.1
ENKUR	NA	UP	3.518	8.61e-04	9.0
CNTN4	NA	UP	4.928	9.17e-04	5.0
SLC16A6	NA	UP	3.375	9.62e-04	7.8
TMEM160	NA	DOWN	-2.039	1.02e-03	686.6
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
RNF152	NA	UP	3.325	1.37e-03	7.5
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
LHB	NA	UP	3.522	1.50e-03	7.0
TBX15	NA	UP	2.824	1.94e-03	8.6

## Ruta: protein binding (Página 14 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KCNH3	NA	DOWN	-2.243	1.94e-03	12.5
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
RUFY4	NA	UP	4.136	2.15e-03	6.0
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0
KCNN1	NA	UP	3.883	2.55e-03	6.2
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
PATL2	NA	UP	2.215	2.72e-03	12.1
SUSD3	NA	UP	2.011	2.77e-03	13.3
SLCO5A1	NA	UP	2.814	2.87e-03	7.7
IL17C	NA	UP	4.636	3.13e-03	4.1
GBP6	NA	UP	2.233	3.24e-03	11.2
IPCEF1	NA	UP	4.035	3.69e-03	4.9
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
CCDC74A	NA	DOWN	-2.142	4.32e-03	11.1
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
KRT81	NA	UP	2.044	4.94e-03	15.2
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
SLC25A18	NA	DOWN	-2.816	5.67e-03	7.5
SDK2	NA	UP	2.715	5.83e-03	7.9
EGFL6	NA	UP	3.034	6.01e-03	5.9

## Ruta: protein binding (Página 15 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
RNF150	NA	UP	4.240	1.04e-02	3.1
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
TTLL6	NA	UP	2.577	1.74e-02	6.7
CAMK1G	NA	UP	4.059	1.79e-02	2.8
MSTO1	NA	DOWN	-2.110	1.81e-02	8.3
OLR1	NA	UP	2.655	1.81e-02	6.9
TBCEL	NA	UP	2.318	1.82e-02	7.1
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
FBXW10	NA	UP	2.019	1.90e-02	9.5
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8

## Ruta: protein binding (Página 16 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
CELF6	NA	UP	2.403	2.65e-02	5.6
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
SPRR2A	NA	UP	2.086	2.78e-02	7.8
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
INSC	NA	UP	3.872	3.01e-02	2.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7
HSD11B1	NA	UP	2.341	3.03e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8
TRIM69	NA	UP	3.519	3.21e-02	3.0
CR1L	NA	UP	3.479	3.30e-02	3.5
KCNE4	NA	UP	2.337	3.37e-02	5.7
DLG2	NA	UP	3.028	3.83e-02	3.8
ADAMTS4	NA	UP	3.293	3.88e-02	3.0
CCL17	NA	UP	3.441	3.89e-02	2.9
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
PPM1E	NA	UP	3.810	4.20e-02	2.4
NID2	NA	DOWN	-3.779	4.29e-02	2.9
PPEF1	NA	UP	3.725	4.31e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: protein binding (Página 17 de 17)

Fuente: GO:MF | ID: GO:0005515 | Genes: 401 | p-valor ruta: 1.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: molecular transducer activity (Página 1 de 4)

Fuente: GO:MF | ID: GO:0060089 | Genes: 94 | p-valor ruta: 5.1e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STC2	NA	UP	2.729	3.17e-119	2626.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
ADRB2	NA	UP	2.471	2.83e-79	954.4
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
NR1D1	NA	UP	2.475	2.08e-68	1229.5

## Ruta: molecular transducer activity (Página 2 de 4)

Fuente: GO:MF | ID: GO:0060089 | Genes: 94 | p-valor ruta: 5.1e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
HBEGF	NA	UP	2.602	3.10e-57	415.2
CD69	NA	UP	3.112	5.99e-57	257.2
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
IL15	NA	UP	2.012	2.28e-17	116.8

## Ruta: molecular transducer activity (Página 3 de 4)

Fuente: GO:MF | ID: GO:0060089 | Genes: 94 | p-valor ruta: 5.1e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
INHBE	NA	UP	5.109	1.59e-15	37.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PTGER2	NA	UP	3.006	1.95e-04	11.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9

## Ruta: molecular transducer activity (Página 4 de 4)

Fuente: GO:MF | ID: GO:0060089 | Genes: 94 | p-valor ruta: 5.1e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LHB	NA	UP	3.522	1.50e-03	7.0
LGR6	NA	UP	3.915	2.25e-03	6.0
IL17C	NA	UP	4.636	3.13e-03	4.1
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CCL17	NA	UP	3.441	3.89e-02	2.9
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: signaling receptor activity (Página 1 de 4)

Fuente: GO:MF | ID: GO:0038023 | Genes: 94 | p-valor ruta: 5.1e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STC2	NA	UP	2.729	3.17e-119	2626.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
ADRB2	NA	UP	2.471	2.83e-79	954.4
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
NR1D1	NA	UP	2.475	2.08e-68	1229.5

## Ruta: signaling receptor activity (Página 2 de 4)

Fuente: GO:MF | ID: GO:0038023 | Genes: 94 | p-valor ruta: 5.1e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
HBEGF	NA	UP	2.602	3.10e-57	415.2
CD69	NA	UP	3.112	5.99e-57	257.2
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
IL15	NA	UP	2.012	2.28e-17	116.8

## Ruta: signaling receptor activity (Página 3 de 4)

Fuente: GO:MF | ID: GO:0038023 | Genes: 94 | p-valor ruta: 5.1e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
INHBE	NA	UP	5.109	1.59e-15	37.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PTGER2	NA	UP	3.006	1.95e-04	11.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9

## Ruta: signaling receptor activity (Página 4 de 4)

Fuente: GO:MF | ID: GO:0038023 | Genes: 94 | p-valor ruta: 5.1e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LHB	NA	UP	3.522	1.50e-03	7.0
LGR6	NA	UP	3.915	2.25e-03	6.0
IL17C	NA	UP	4.636	3.13e-03	4.1
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CCL17	NA	UP	3.441	3.89e-02	2.9
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: molecular function regulator activity (Página 1 de 4)

Fuente: GO:MF | ID: GO:0098772 | Genes: 97 | p–valor ruta: 1.64e–08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e–242	2226.4
PPP1R15A	NA	UP	3.879	2.08e–241	8348.0
NFKBIA	NA	UP	4.079	6.66e–241	4955.3
TXNIP	NA	UP	3.401	2.30e–219	11419.4
IL1B	NA	UP	4.202	1.58e–214	2230.2
GBP1	NA	UP	4.090	2.07e–209	2026.7
CXCL10	NA	UP	6.079	8.12e–195	783.4
CXCL3	NA	UP	3.053	2.27e–187	4330.7
CXCL11	NA	UP	6.074	5.51e–176	710.1
CCL5	NA	UP	5.035	8.94e–165	656.3
CXCL2	NA	UP	3.371	1.67e–155	4155.4
INHBA	NA	UP	3.514	2.31e–143	1743.6
CX3CL1	NA	UP	3.114	2.67e–123	1760.3
STC2	NA	UP	2.729	3.17e–119	2626.1
TNFSF10	NA	UP	3.014	1.58e–112	3429.5
SERPINE1	NA	UP	4.807	1.12e–104	435.1
CSF2	NA	UP	7.043	2.08e–103	455.6
TNF	NA	UP	7.712	3.81e–103	573.0
CD274	NA	UP	5.204	1.23e–98	314.4
DTX3L	NA	UP	2.553	3.51e–96	2147.3
IFNB1	NA	UP	10.001	4.69e–95	1340.6
SERPINB9	NA	UP	2.439	1.35e–89	1138.5
IFNL1	NA	UP	8.179	1.68e–89	578.0

## Ruta: molecular function regulator activity (Página 2 de 4)

Fuente: GO:MF | ID: GO:0098772 | Genes: 97 | p–valor ruta: 1.64e–08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRC5	NA	UP	3.949	8.12e–88	414.4
RASGRP3	NA	UP	3.468	2.92e–82	392.1
ADRB2	NA	UP	2.471	2.83e–79	954.4
THBS1	NA	UP	2.656	1.05e–77	3791.3
PARP9	NA	UP	2.449	1.75e–75	2354.5
CCL2	NA	UP	2.562	2.63e–75	658.0
SEMA7A	NA	UP	2.329	3.91e–69	7576.6
JUN	NA	UP	2.450	1.10e–62	6693.5
NEDD4	NA	UP	2.433	4.99e–60	1678.5
HBEGF	NA	UP	2.602	3.10e–57	415.2
SERPINB2	NA	UP	2.344	2.67e–55	2507.0
TNFRSF11B	NA	UP	2.247	4.76e–54	1332.4
PDE4B	NA	UP	3.818	7.08e–52	171.4
CCL22	NA	UP	3.454	2.91e–50	168.7
CSF1	NA	UP	2.530	1.40e–49	467.4
EIF2AK2	NA	UP	2.142	3.22e–48	1460.0
SEMA3A	NA	UP	2.276	5.71e–42	512.5
BIRC3	NA	UP	2.146	8.30e–42	2602.9
LTB	NA	UP	3.555	2.50e–41	150.4
BMP2	NA	UP	2.237	3.69e–40	325.3
ULBP1	NA	UP	3.138	2.70e–38	151.4
RASGRP1	NA	UP	2.055	4.16e–34	336.9
IRS2	NA	UP	2.254	1.06e–33	255.2
EDN2	NA	UP	3.499	8.77e–31	90.3
IFNL3	NA	UP	9.837	4.42e–30	365.0

## Ruta: molecular function regulator activity (Página 3 de 4)

Fuente: GO:MF | ID: GO:0098772 | Genes: 97 | p–valor ruta: 1.64e–08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SPRY2	NA	UP	2.250	1.05e–29	211.9
TYMP	NA	UP	2.001	2.11e–29	872.8
SERPINB7	NA	UP	2.796	1.04e–28	127.7
IL12A	NA	UP	3.852	1.95e–28	83.7
RASGEF1B	NA	UP	2.113	4.74e–26	182.0
IFNL2	NA	UP	11.372	1.86e–23	434.7
NKX3–1	NA	UP	2.233	8.30e–23	132.4
FGF19	NA	UP	3.931	5.59e–21	52.8
NOD2	NA	UP	2.981	1.19e–19	80.5
CSF3	NA	UP	6.122	1.72e–19	56.0
BST2	NA	UP	4.284	3.82e–19	50.8
CASP1	NA	UP	2.494	1.49e–18	80.2
IL15	NA	UP	2.012	2.28e–17	116.8
GBP5	NA	UP	6.172	4.92e–17	48.7
INHBE	NA	UP	5.109	1.59e–15	37.3
FLT3LG	NA	UP	2.346	6.32e–15	68.5
NLRP3	NA	UP	4.366	3.67e–13	29.8
PLEKHG7	NA	UP	3.625	2.08e–12	31.8
ZEB2	NA	UP	3.419	5.95e–12	30.5
IL23A	NA	UP	2.189	2.05e–11	59.9
TNFSF13B	NA	UP	3.042	2.17e–11	34.7
PPP4R4	NA	UP	3.423	6.94e–11	30.7
CYTH4	NA	UP	2.691	3.08e–10	36.2
NLRP1	NA	UP	5.692	4.64e–09	21.6
SOCS1	NA	UP	2.012	6.54e–08	82.5

## Ruta: molecular function regulator activity (Página 4 de 4)

Fuente: GO:MF | ID: GO:0098772 | Genes: 97 | p–valor ruta: 1.64e–08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KCNV1	NA	UP	2.402	2.10e–07	37.9
TNFSF14	NA	UP	2.748	3.71e–07	23.0
WFDC5	NA	UP	5.168	1.07e–06	13.9
SYT1	NA	UP	2.659	1.62e–06	21.4
NUPR1	NA	UP	3.660	1.78e–06	14.5
TAGAP	NA	UP	3.201	2.52e–06	16.1
SERPINA10	NA	UP	6.459	9.50e–06	7.5
KCNK2	NA	DOWN	–3.579	2.55e–05	12.4
COLEC10	NA	UP	2.878	4.02e–04	11.6
CXCL9	NA	UP	4.099	4.37e–04	26.3
LRRC26	NA	DOWN	–2.795	1.47e–03	10.1
LHB	NA	UP	3.522	1.50e–03	7.0
IL17C	NA	UP	4.636	3.13e–03	4.1
HRG	NA	UP	2.971	4.00e–03	6.9
DLL1	NA	UP	2.171	4.40e–03	10.4
CD70	NA	UP	3.257	1.21e–02	4.7
RANBP3L	NA	UP	4.634	1.47e–02	2.2
VAV1	NA	UP	2.118	1.54e–02	7.9
IL34	NA	UP	2.794	2.41e–02	4.8
KCNE4	NA	UP	2.337	3.37e–02	5.7
CCL17	NA	UP	3.441	3.89e–02	2.9
FGF18	NA	UP	2.038	4.86e–02	6.1

## Ruta: molecular function activator activity (Página 1 de 3)

Fuente: GO:MF | ID: GO:0140677 | Genes: 63 | p–valor ruta: 5.37e–08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e–242	2226.4
PPP1R15A	NA	UP	3.879	2.08e–241	8348.0
IL1B	NA	UP	4.202	1.58e–214	2230.2
CXCL10	NA	UP	6.079	8.12e–195	783.4
CXCL3	NA	UP	3.053	2.27e–187	4330.7
CXCL11	NA	UP	6.074	5.51e–176	710.1
CCL5	NA	UP	5.035	8.94e–165	656.3
CXCL2	NA	UP	3.371	1.67e–155	4155.4
INHBA	NA	UP	3.514	2.31e–143	1743.6
CX3CL1	NA	UP	3.114	2.67e–123	1760.3
STC2	NA	UP	2.729	3.17e–119	2626.1
TNFSF10	NA	UP	3.014	1.58e–112	3429.5
CSF2	NA	UP	7.043	2.08e–103	455.6
TNF	NA	UP	7.712	3.81e–103	573.0
CD274	NA	UP	5.204	1.23e–98	314.4
IFNB1	NA	UP	10.001	4.69e–95	1340.6
IFNL1	NA	UP	8.179	1.68e–89	578.0
NLRC5	NA	UP	3.949	8.12e–88	414.4
RASGRP3	NA	UP	3.468	2.92e–82	392.1
CCL2	NA	UP	2.562	2.63e–75	658.0
SEMA7A	NA	UP	2.329	3.91e–69	7576.6
JUN	NA	UP	2.450	1.10e–62	6693.5
HBEGF	NA	UP	2.602	3.10e–57	415.2

## Ruta: molecular function activator activity (Página 2 de 3)

Fuente: GO:MF | ID: GO:0140677 | Genes: 63 | p–valor ruta: 5.37e–08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFRSF11B	NA	UP	2.247	4.76e–54	1332.4
CCL22	NA	UP	3.454	2.91e–50	168.7
CSF1	NA	UP	2.530	1.40e–49	467.4
SEMA3A	NA	UP	2.276	5.71e–42	512.5
LTB	NA	UP	3.555	2.50e–41	150.4
BMP2	NA	UP	2.237	3.69e–40	325.3
ULBP1	NA	UP	3.138	2.70e–38	151.4
EDN2	NA	UP	3.499	8.77e–31	90.3
IFNL3	NA	UP	9.837	4.42e–30	365.0
SPRY2	NA	UP	2.250	1.05e–29	211.9
TYMP	NA	UP	2.001	2.11e–29	872.8
IL12A	NA	UP	3.852	1.95e–28	83.7
IFNL2	NA	UP	11.372	1.86e–23	434.7
NKX3–1	NA	UP	2.233	8.30e–23	132.4
FGF19	NA	UP	3.931	5.59e–21	52.8
NOD2	NA	UP	2.981	1.19e–19	80.5
CSF3	NA	UP	6.122	1.72e–19	56.0
CASP1	NA	UP	2.494	1.49e–18	80.2
IL15	NA	UP	2.012	2.28e–17	116.8
INHBE	NA	UP	5.109	1.59e–15	37.3
FLT3LG	NA	UP	2.346	6.32e–15	68.5
IL23A	NA	UP	2.189	2.05e–11	59.9
TNFSF13B	NA	UP	3.042	2.17e–11	34.7
NLRP1	NA	UP	5.692	4.64e–09	21.6
TNFSF14	NA	UP	2.748	3.71e–07	23.0

## Ruta: molecular function activator activity (Página 3 de 3)

Fuente: GO:MF | ID: GO:0140677 | Genes: 63 | p–valor ruta: 5.37e–08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NUPR1	NA	UP	3.660	1.78e–06	14.5
TAGAP	NA	UP	3.201	2.52e–06	16.1
COLEC10	NA	UP	2.878	4.02e–04	11.6
CXCL9	NA	UP	4.099	4.37e–04	26.3
LRRC26	NA	DOWN	-2.795	1.47e–03	10.1
LHB	NA	UP	3.522	1.50e–03	7.0
IL17C	NA	UP	4.636	3.13e–03	4.1
DLL1	NA	UP	2.171	4.40e–03	10.4
CD70	NA	UP	3.257	1.21e–02	4.7
RANBP3L	NA	UP	4.634	1.47e–02	2.2
IL34	NA	UP	2.794	2.41e–02	4.8
CCL17	NA	UP	3.441	3.89e–02	2.9
FGF18	NA	UP	2.038	4.86e–02	6.1

## Ruta: pattern recognition receptor activity

Fuente: GO:MF | ID: GO:0038187 | Genes: 10 | p-valor ruta: 1.1e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIH1	NA	UP	4.035	2.22e-233	4525.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: double-stranded RNA binding

Fuente: GO:MF | ID: GO:0003725 | Genes: 13 | p-valor ruta: 3.63e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
DDX60L	NA	UP	3.765	2.46e-147	1804.9
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
OAS3	NA	UP	2.942	1.13e-87	8674.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
TLR3	NA	UP	2.508	1.99e-22	111.5
NLRP1	NA	UP	5.692	4.64e-09	21.6
SIDT1	NA	UP	2.642	2.81e-03	8.6

## Ruta: chemokine activity

Fuente: GO:MF | ID: GO:0008009 | Genes: 11 | p-valor ruta: 5.07e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CCL2	NA	UP	2.562	2.63e-75	658.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CXCL9	NA	UP	4.099	4.37e-04	26.3
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: chemokine receptor binding

Fuente: GO:MF | ID: GO:0042379 | Genes: 12 | p-valor ruta: 5.53e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CCL2	NA	UP	2.562	2.63e-75	658.0
STAT1	NA	UP	2.519	1.61e-68	9528.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CXCL9	NA	UP	4.099	4.37e-04	26.3
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: identical protein binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:0042802 | Genes: 85 | p–valor ruta: 1.18e–04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e–277	2472.4
ATF3	NA	UP	4.971	1.38e–261	2286.0
MX1	NA	UP	3.859	1.25e–245	5699.6
NFKBIA	NA	UP	4.079	6.66e–241	4955.3
IFIH1	NA	UP	4.035	2.22e–233	4525.3
TRIM22	NA	UP	5.650	1.01e–212	913.7
GBP1	NA	UP	4.090	2.07e–209	2026.7
GBP4	NA	UP	4.422	6.95e–185	1175.0
CCL5	NA	UP	5.035	8.94e–165	656.3
INHBA	NA	UP	3.514	2.31e–143	1743.6
TAP1	NA	UP	2.707	8.35e–123	5228.7
IKZF3	NA	UP	3.163	1.21e–120	1046.8
STC2	NA	UP	2.729	3.17e–119	2626.1
IFI16	NA	UP	3.151	2.12e–114	2583.4
TNFSF10	NA	UP	3.014	1.58e–112	3429.5
TNF	NA	UP	7.712	3.81e–103	573.0
ZBP1	NA	UP	6.242	1.22e–99	349.5
STAT2	NA	UP	2.337	1.85e–96	2004.6
IRAK2	NA	UP	2.666	3.46e–95	1164.5
SP100	NA	UP	2.428	1.62e–93	2653.7
CLDN2	NA	DOWN	-3.586	5.60e–89	498.3
TRAF1	NA	UP	4.730	5.65e–84	258.2
PTGS2	NA	UP	3.253	7.39e–80	3663.8

## Ruta: identical protein binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:0042802 | Genes: 85 | p–valor ruta: 1.18e–04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ADRB2	NA	UP	2.471	2.83e–79	954.4
IFI35	NA	UP	2.237	9.59e–79	2236.7
THBS1	NA	UP	2.656	1.05e–77	3791.3
PNPT1	NA	UP	2.411	6.12e–71	2101.8
PML	NA	UP	2.208	2.84e–70	2901.3
STAT1	NA	UP	2.519	1.61e–68	9528.0
PTX3	NA	UP	3.614	2.25e–68	237.4
OPTN	NA	UP	2.002	1.08e–67	1911.6
JUN	NA	UP	2.450	1.10e–62	6693.5
CREB5	NA	UP	2.714	3.43e–62	649.9
TRIM5	NA	UP	2.172	6.62e–61	1222.6
TRIM21	NA	UP	2.221	1.14e–60	888.8
GADD45A	NA	UP	2.255	1.32e–60	1140.5
CTH	NA	UP	2.488	2.75e–57	412.1
CD69	NA	UP	3.112	5.99e–57	257.2
SAMHD1	NA	UP	2.304	5.99e–57	1585.1
C1QTNF1	NA	UP	3.006	3.30e–52	250.8
CSF1	NA	UP	2.530	1.40e–49	467.4
EIF2AK2	NA	UP	2.142	3.22e–48	1460.0
APOBEC3G	NA	UP	2.120	1.48e–40	359.9
RASGRP1	NA	UP	2.055	4.16e–34	336.9
TYMP	NA	UP	2.001	2.11e–29	872.8
TLR3	NA	UP	2.508	1.99e–22	111.5
BST2	NA	UP	4.284	3.82e–19	50.8
CASP1	NA	UP	2.494	1.49e–18	80.2

## Ruta: identical protein binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:0042802 | Genes: 85 | p–valor ruta: 1.18e–04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GIMAP2	NA	UP	2.542	5.46e–18	86.3
JAK2	NA	UP	2.081	1.26e–17	123.4
GBP5	NA	UP	6.172	4.92e–17	48.7
HOGA1	NA	DOWN	-2.098	2.81e–15	96.4
LMO2	NA	UP	3.437	9.83e–12	31.2
ACTN2	NA	UP	3.956	7.01e–09	20.3
NR4A3	NA	UP	5.574	1.45e–08	20.2
TLR6	NA	UP	2.680	9.77e–08	26.3
TNFSF14	NA	UP	2.748	3.71e–07	23.0
RBM11	NA	UP	2.506	8.83e–07	22.9
SYT1	NA	UP	2.659	1.62e–06	21.4
HSD17B14	NA	UP	2.529	3.30e–06	21.4
BEST1	NA	UP	3.553	8.47e–06	13.3
FAP	NA	UP	3.233	1.87e–05	14.0
KCNK2	NA	DOWN	-3.579	2.55e–05	12.4
SDS	NA	UP	4.527	5.38e–05	9.4
RHCG	NA	UP	2.107	1.84e–04	21.0
SLC5A5	NA	UP	4.542	4.62e–04	6.8
KIT	NA	UP	3.650	6.24e–04	7.9
HAND1	NA	UP	4.966	8.42e–04	5.1
TBX15	NA	UP	2.824	1.94e–03	8.6
POU3F2	NA	UP	4.735	2.02e–03	4.5
VWF	NA	UP	3.390	1.16e–02	4.6
SCUBE1	NA	UP	2.508	1.26e–02	8.4
OLR1	NA	UP	2.655	1.81e–02	6.9

## Ruta: identical protein binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:0042802 | Genes: 85 | p-valor ruta: 1.18e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NPR3	NA	UP	2.789	1.87e-02	5.7
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
HSD11B1	NA	UP	2.341	3.03e-02	5.6
TRIM69	NA	UP	3.519	3.21e-02	3.0
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: tumor necrosis factor receptor binding

Fuente: GO:MF | ID: GO:0005164 | Genes: 8 | p-valor ruta: 1.84e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
TRAF1	NA	UP	4.730	5.65e-84	258.2
STAT1	NA	UP	2.519	1.61e-68	9528.0
LTB	NA	UP	3.555	2.50e-41	150.4
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFSF14	NA	UP	2.748	3.71e-07	23.0
CD70	NA	UP	3.257	1.21e-02	4.7

## Ruta: CXCR chemokine receptor binding

Fuente: GO:MF | ID: GO:0045236 | Genes: 6 | p-valor ruta: 8.49e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CXCL9	NA	UP	4.099	4.37e-04	26.3

## Ruta: protein homodimerization activity (Página 1 de 2)

Fuente: GO:MF | ID: GO:0042803 | Genes: 36 | p-valor ruta: 4.4e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ATF3	NA	UP	4.971	1.38e-261	2286.0
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
CCL5	NA	UP	5.035	8.94e-165	656.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
IKZF3	NA	UP	3.163	1.21e-120	1046.8
STC2	NA	UP	2.729	3.17e-119	2626.1
IRAK2	NA	UP	2.666	3.46e-95	1164.5
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CSF1	NA	UP	2.530	1.40e-49	467.4
TYMP	NA	UP	2.001	2.11e-29	872.8
BST2	NA	UP	4.284	3.82e-19	50.8
GBP5	NA	UP	6.172	4.92e-17	48.7
HOGA1	NA	DOWN	-2.098	2.81e-15	96.4
NR4A3	NA	UP	5.574	1.45e-08	20.2
RBM11	NA	UP	2.506	8.83e-07	22.9

## Ruta: protein homodimerization activity (Página 2 de 2)

Fuente: GO:MF | ID: GO:0042803 | Genes: 36 | p-valor ruta: 4.4e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FAP	NA	UP	3.233	1.87e-05	14.0
SDS	NA	UP	4.527	5.38e-05	9.4
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
NPR3	NA	UP	2.789	1.87e-02	5.7
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
HSD11B1	NA	UP	2.341	3.03e-02	5.6

## Ruta: G protein-coupled receptor binding

Fuente: GO:MF | ID: GO:0001664 | Genes: 20 | p-valor ruta: 5.02e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
RTP4	NA	UP	3.457	2.00e-107	589.0
CCL2	NA	UP	2.562	2.63e-75	658.0
STAT1	NA	UP	2.519	1.61e-68	9528.0
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CCL22	NA	UP	3.454	2.91e-50	168.7
EDN2	NA	UP	3.499	8.77e-31	90.3
JAK2	NA	UP	2.081	1.26e-17	123.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
CXCL9	NA	UP	4.099	4.37e-04	26.3
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CCL17	NA	UP	3.441	3.89e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: enzyme binding (Página 1 de 4)

Fuente: GO:MF | ID: GO:0019899 | Genes: 77 | p–valor ruta: 5.18e–03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e–277	2472.4
PPP1R15A	NA	UP	3.879	2.08e–241	8348.0
NFKBIA	NA	UP	4.079	6.66e–241	4955.3
TXNIP	NA	UP	3.401	2.30e–219	11419.4
TRIM22	NA	UP	5.650	1.01e–212	913.7
GBP1	NA	UP	4.090	2.07e–209	2026.7
CYP1A1	NA	UP	6.086	6.00e–198	811.0
DUSP1	NA	UP	3.521	2.54e–161	1829.2
IKZF3	NA	UP	3.163	1.21e–120	1046.8
PARP14	NA	UP	2.977	1.79e–119	2649.9
STC2	NA	UP	2.729	3.17e–119	2626.1
SERPINE1	NA	UP	4.807	1.12e–104	435.1
ZFP36	NA	UP	2.944	7.57e–104	1721.5
TNF	NA	UP	7.712	3.81e–103	573.0
STAT2	NA	UP	2.337	1.85e–96	2004.6
DTX3L	NA	UP	2.553	3.51e–96	2147.3
UBE2L6	NA	UP	2.518	5.99e–95	2683.8
SP100	NA	UP	2.428	1.62e–93	2653.7
SERPINB9	NA	UP	2.439	1.35e–89	1138.5
TRAF1	NA	UP	4.730	5.65e–84	258.2
RASGRP3	NA	UP	3.468	2.92e–82	392.1
PTGS2	NA	UP	3.253	7.39e–80	3663.8
KLF4	NA	UP	2.704	2.52e–79	645.9
ADRB2	NA	UP	2.471	2.83e–79	954.4
THBS1	NA	UP	2.656	1.05e–77	3791.3

## Ruta: enzyme binding (Página 2 de 4)

Fuente: GO:MF | ID: GO:0019899 | Genes: 77 | p–valor ruta: 5.18e–03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP9	NA	UP	2.449	1.75e–75	2354.5
EGR1	NA	UP	2.472	2.61e–74	1149.5
LGALS9	NA	UP	2.474	3.44e–71	1449.3
PML	NA	UP	2.208	2.84e–70	2901.3
ANKRD1	NA	UP	3.496	4.72e–69	335.9
STAT1	NA	UP	2.519	1.61e–68	9528.0
AKAP12	NA	UP	2.306	2.56e–67	3768.0
JUN	NA	UP	2.450	1.10e–62	6693.5
RND1	NA	UP	2.840	1.60e–62	337.7
PTAFR	NA	UP	3.014	4.62e–62	338.1
TRIM5	NA	UP	2.172	6.62e–61	1222.6
TRIM21	NA	UP	2.221	1.14e–60	888.8
GADD45A	NA	UP	2.255	1.32e–60	1140.5
NEDD4	NA	UP	2.433	4.99e–60	1678.5
BBC3	NA	UP	2.829	3.65e–57	503.1
ISG15	NA	UP	2.482	5.90e–57	3807.9
PER1	NA	UP	2.501	8.94e–44	469.6
IL15RA	NA	UP	2.045	1.16e–42	847.9
IRS2	NA	UP	2.254	1.06e–33	255.2
HDAC9	NA	UP	2.292	4.51e–32	2003.2
PRDM1	NA	UP	3.525	5.98e–31	99.0
SPRY2	NA	UP	2.250	1.05e–29	211.9
BCL3	NA	UP	2.067	4.65e–26	500.4
BCL2L14	NA	UP	2.782	8.63e–26	122.3
NKX3–1	NA	UP	2.233	8.30e–23	132.4

## Ruta: enzyme binding (Página 3 de 4)

Fuente: GO:MF | ID: GO:0019899 | Genes: 77 | p–valor ruta: 5.18e–03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOD2	NA	UP	2.981	1.19e–19	80.5
CSF3	NA	UP	6.122	1.72e–19	56.0
CASP1	NA	UP	2.494	1.49e–18	80.2
JAK2	NA	UP	2.081	1.26e–17	123.4
DDC	NA	DOWN	-2.582	2.27e–16	72.0
DUOXA2	NA	UP	4.650	3.36e–16	39.7
BDKRB2	NA	UP	2.797	5.56e–15	55.1
FLT3LG	NA	UP	2.346	6.32e–15	68.5
EGR2	NA	UP	3.090	6.72e–15	43.7
NLRP1	NA	UP	5.692	4.64e–09	21.6
NR4A3	NA	UP	5.574	1.45e–08	20.2
SOCS1	NA	UP	2.012	6.54e–08	82.5
NGFR	NA	UP	2.337	3.33e–07	30.0
ACTBL2	NA	UP	2.242	5.97e–06	28.3
ADCY4	NA	UP	2.271	8.12e–06	23.6
FAP	NA	UP	3.233	1.87e–05	14.0
SELE	NA	UP	5.745	2.05e–05	9.0
HIST1H1E	NA	UP	2.243	4.44e–05	25.9
KIT	NA	UP	3.650	6.24e–04	7.9
HAND1	NA	UP	4.966	8.42e–04	5.1
CEACAM20	NA	UP	5.412	1.17e–03	3.6
RNF152	NA	UP	3.325	1.37e–03	7.5
PEX5L	NA	UP	3.321	2.40e–03	7.0
VWF	NA	UP	3.390	1.16e–02	4.6
RFPL1	NA	UP	3.259	2.06e–02	4.1

## Ruta: enzyme binding (Página 4 de 4)

Fuente: GO:MF | ID: GO:0019899 | Genes: 77 | p-valor ruta: 5.18e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DLG2	NA	UP	3.028	3.83e-02	3.8
ADAMTS4	NA	UP	3.293	3.88e-02	3.0

## Ruta: 2'-5'-oligoadenylate synthetase activity

Fuente: GO:MF | ID: GO:0001730 | Genes: 3 | p-valor ruta: 5.24e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
OAS3	NA	UP	2.942	1.13e-87	8674.1

## Ruta: NAD+ poly-ADP-ribosyltransferase activity

Fuente: GO:MF | ID: GO:0003950 | Genes: 6 | p-valor ruta: 5.49e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TIPARP	NA	UP	3.093	1.11e-158	5401.6
PARP14	NA	UP	2.977	1.79e-119	2649.9
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
PARP12	NA	UP	2.297	5.64e-82	1665.8
PARP9	NA	UP	2.449	1.75e-75	2354.5
PARP10	NA	UP	2.093	5.71e-52	2376.2

## Ruta: tumor necrosis factor receptor superfamily binding

Fuente: GO:MF | ID: GO:0032813 | Genes: 8 | p-valor ruta: 6.6e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
TRAF1	NA	UP	4.730	5.65e-84	258.2
STAT1	NA	UP	2.519	1.61e-68	9528.0
LTB	NA	UP	3.555	2.50e-41	150.4
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFSF14	NA	UP	2.748	3.71e-07	23.0
CD70	NA	UP	3.257	1.21e-02	4.7

## Ruta: binding (Página 1 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0

## Ruta: binding (Página 2 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
CMPK2	NA	UP	4.677	1.14e-162	1687.4
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
CXCL2	NA	UP	3.371	1.67e-155	4155.4
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
EPSTI1	NA	UP	4.231	7.22e-130	564.5
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
SAMD9L	NA	UP	3.487	2.90e-126	1768.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
IKZF3	NA	UP	3.163	1.21e-120	1046.8
APOL6	NA	UP	3.196	9.56e-120	1648.2

## Ruta: binding (Página 3 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
MB21D2	NA	UP	2.998	2.32e-111	911.2
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
IFI44	NA	UP	3.036	1.35e-108	3423.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
NUAK2	NA	UP	4.358	1.14e-107	489.1
RTP4	NA	UP	3.457	2.00e-107	589.0
TMEM140	NA	UP	3.747	6.77e-107	475.4
SP110	NA	UP	2.776	1.00e-106	1474.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
TRANK1	NA	UP	3.317	5.86e-102	541.3
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6

## Ruta: binding (Página 4 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TM4SF4	NA	DOWN	-2.482	1.83e-87	1021.7
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
RASGRP3	NA	UP	3.468	2.92e-82	392.1
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PARP12	NA	UP	2.297	5.64e-82	1665.8
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9

## Ruta: binding (Página 5 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
SLFN5	NA	UP	2.917	1.64e-76	2317.0
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
KRTAP2-3	NA	UP	2.722	7.97e-75	878.4
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
HSH2D	NA	UP	2.613	6.29e-73	813.8
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4

## Ruta: binding (Página 6 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
NEURL3	NA	UP	2.464	1.53e-62	758.9
RND1	NA	UP	2.840	1.60e-62	337.7
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TUFT1	NA	UP	2.001	1.00e-55	1905.9
FOSB	NA	UP	3.144	1.32e-55	267.7
ALDH1L2	NA	UP	3.029	4.52e-55	257.3
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0

## Ruta: binding (Página 7 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
NAV2	NA	UP	2.370	3.20e-51	765.9
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
ANKRD33B	NA	UP	2.525	7.29e-50	317.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
APOL4	NA	UP	3.489	1.37e-42	132.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4

## Ruta: binding (Página 8 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PHF11	NA	UP	2.211	3.12e-37	302.1
ZC3H12C	NA	UP	2.109	3.86e-36	308.6
MT2A	NA	UP	2.437	2.24e-35	363.0
DUSP8	NA	UP	2.088	3.69e-35	551.5
ZNF267	NA	UP	2.059	1.30e-34	677.0
SNRNP25	NA	DOWN	-2.131	4.01e-34	420.7
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
ANXA10	NA	DOWN	-2.270	2.83e-33	223.1
C1R	NA	UP	2.188	3.06e-32	258.8
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
EDN2	NA	UP	3.499	8.77e-31	90.3
BACH2	NA	UP	2.222	2.18e-30	209.0
LRRC45	NA	DOWN	-2.449	3.12e-30	356.2
PPM1K	NA	UP	2.192	3.89e-30	395.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
EPN3	NA	DOWN	-2.294	4.66e-30	335.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
HDX	NA	UP	2.521	1.83e-28	139.2
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: binding (Página 9 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KIF21B	NA	UP	2.131	3.74e-27	240.5
RBM43	NA	UP	2.267	6.06e-27	246.6
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
BCL2L14	NA	UP	2.782	8.63e-26	122.3
MAST4	NA	UP	2.184	1.21e-25	197.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1
KRT6B	NA	UP	2.049	5.47e-24	321.4
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
DDO	NA	UP	2.846	3.84e-20	82.4
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2

## Ruta: binding (Página 10 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GIMAP2	NA	UP	2.542	5.46e-18	86.3
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8
FSD1L	NA	UP	2.523	4.34e-17	83.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DDC	NA	DOWN	-2.582	2.27e-16	72.0
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
INHBE	NA	UP	5.109	1.59e-15	37.3
RAET1L	NA	UP	2.665	2.71e-15	60.0
NAV3	NA	UP	2.285	2.77e-15	84.4
HOGA1	NA	DOWN	-2.098	2.81e-15	96.4
GBX2	NA	UP	2.353	5.55e-15	78.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
DNAH17	NA	UP	3.324	3.42e-13	38.8
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PDZD2	NA	UP	4.182	1.86e-12	28.7
PLEKHG7	NA	UP	3.625	2.08e-12	31.8
MUC4	NA	UP	2.613	4.74e-12	55.4

## Ruta: binding (Página 11 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
KLHDC7B	NA	UP	3.660	1.88e-11	29.7
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
PPP4R4	NA	UP	3.423	6.94e-11	30.7
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
STX19	NA	UP	2.009	1.09e-08	99.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
C6orf58	NA	UP	2.512	2.12e-08	30.6
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
BAHCC1	NA	UP	4.513	9.67e-08	16.6
TLR6	NA	UP	2.680	9.77e-08	26.3
SULT1C2	NA	UP	2.136	2.10e-07	36.2

## Ruta: binding (Página 12 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KCNV1	NA	UP	2.402	2.10e-07	37.9
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
AHRR	NA	UP	2.180	3.48e-07	33.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
BCAT1	NA	UP	2.723	7.42e-07	22.9
RBM11	NA	UP	2.506	8.83e-07	22.9
SAA4	NA	UP	2.563	9.46e-07	21.9
WFDC5	NA	UP	5.168	1.07e-06	13.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
COX6B2	NA	UP	2.208	1.76e-06	27.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
TAGAP	NA	UP	3.201	2.52e-06	16.1
HSD17B14	NA	UP	2.529	3.30e-06	21.4
RAB30	NA	UP	2.024	5.27e-06	28.7
COL4A1	NA	UP	6.589	5.89e-06	8.2
SP8	NA	UP	6.528	5.89e-06	8.0
ACTBL2	NA	UP	2.242	5.97e-06	28.3
ZNF442	NA	UP	2.573	6.55e-06	18.8

## Ruta: binding (Página 13 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ADCY4	NA	UP	2.271	8.12e-06	23.6
BEST1	NA	UP	3.553	8.47e-06	13.3
ICAM4	NA	UP	2.446	8.79e-06	22.0
ADAMTS6	NA	UP	2.602	8.90e-06	19.6
MMP13	NA	UP	5.406	9.23e-06	11.1
SERPINA10	NA	UP	6.459	9.50e-06	7.5
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
RAB36	NA	DOWN	-2.063	2.15e-05	24.7
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
BEST3	NA	UP	2.070	3.26e-05	23.9
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
SDS	NA	UP	4.527	5.38e-05	9.4
GLTPD2	NA	DOWN	-2.633	7.44e-05	17.8
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
KIF6	NA	UP	4.867	1.75e-04	7.8
RHCG	NA	UP	2.107	1.84e-04	21.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
GFPT2	NA	UP	2.651	2.37e-04	12.7
EGR3	NA	UP	2.096	2.87e-04	21.5

## Ruta: binding (Página 14 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TMEM40	NA	UP	2.179	2.99e-04	16.5
UBQLNL	NA	UP	3.875	3.33e-04	7.9
TRPC4	NA	UP	5.730	3.71e-04	4.5
ZNF382	NA	UP	2.028	3.78e-04	18.2
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
CCDC96	NA	DOWN	-2.033	4.86e-04	19.3
MKX	NA	UP	2.196	5.67e-04	15.1
CPXM1	NA	UP	2.128	5.77e-04	16.0
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
SLC38A4	NA	DOWN	-2.630	6.25e-04	12.4
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
GAL3ST4	NA	UP	2.371	7.40e-04	12.5
HAND1	NA	UP	4.966	8.42e-04	5.1
ENKUR	NA	UP	3.518	8.61e-04	9.0
CNTN4	NA	UP	4.928	9.17e-04	5.0
SLC16A6	NA	UP	3.375	9.62e-04	7.8
TMEM160	NA	DOWN	-2.039	1.02e-03	686.6
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6

## Ruta: binding (Página 15 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
PLA1A	NA	UP	3.622	1.35e-03	6.6
RNF152	NA	UP	3.325	1.37e-03	7.5
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
LHB	NA	UP	3.522	1.50e-03	7.0
TBX15	NA	UP	2.824	1.94e-03	8.6
KCNH3	NA	DOWN	-2.243	1.94e-03	12.5
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
RUFY4	NA	UP	4.136	2.15e-03	6.0
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0
KCNN1	NA	UP	3.883	2.55e-03	6.2
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
PATL2	NA	UP	2.215	2.72e-03	12.1
SUSD3	NA	UP	2.011	2.77e-03	13.3
SIDT1	NA	UP	2.642	2.81e-03	8.6
SLCO5A1	NA	UP	2.814	2.87e-03	7.7
IL17C	NA	UP	4.636	3.13e-03	4.1
GBP6	NA	UP	2.233	3.24e-03	11.2
IPCEF1	NA	UP	4.035	3.69e-03	4.9
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
CCDC74A	NA	DOWN	-2.142	4.32e-03	11.1

## Ruta: binding (Página 16 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
KRT81	NA	UP	2.044	4.94e-03	15.2
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
SLC25A18	NA	DOWN	-2.816	5.67e-03	7.5
SDK2	NA	UP	2.715	5.83e-03	7.9
EGFL6	NA	UP	3.034	6.01e-03	5.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
RNF150	NA	UP	4.240	1.04e-02	3.1
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
TTLL6	NA	UP	2.577	1.74e-02	6.7
CAMK1G	NA	UP	4.059	1.79e-02	2.8
MSTO1	NA	DOWN	-2.110	1.81e-02	8.3
OLR1	NA	UP	2.655	1.81e-02	6.9
TBCEL	NA	UP	2.318	1.82e-02	7.1
GLP2R	NA	UP	2.220	1.86e-02	8.9

## Ruta: binding (Página 17 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
FBXW10	NA	UP	2.019	1.90e-02	9.5
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
CELF6	NA	UP	2.403	2.65e-02	5.6
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
SPRR2A	NA	UP	2.086	2.78e-02	7.8
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
INSC	NA	UP	3.872	3.01e-02	2.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7
HSD11B1	NA	UP	2.341	3.03e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8
TRIM69	NA	UP	3.519	3.21e-02	3.0
CR1L	NA	UP	3.479	3.30e-02	3.5
KCNE4	NA	UP	2.337	3.37e-02	5.7
DLG2	NA	UP	3.028	3.83e-02	3.8
ADAMTS4	NA	UP	3.293	3.88e-02	3.0

## Ruta: binding (Página 18 de 18)

Fuente: GO:MF | ID: GO:0005488 | Genes: 437 | p-valor ruta: 1.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL17	NA	UP	3.441	3.89e-02	2.9
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
PPM1E	NA	UP	3.810	4.20e-02	2.4
NID2	NA	DOWN	-3.779	4.29e-02	2.9
PPEF1	NA	UP	3.725	4.31e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
PURG	NA	DOWN	-4.166	4.66e-02	1.7
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: integrin binding

Fuente: GO:MF | ID: GO:0005178 | Genes: 13 | p–valor ruta: 2.77e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e–214	2230.2
ICAM1	NA	UP	3.652	3.11e–204	19095.5
CX3CL1	NA	UP	3.114	2.67e–123	1760.3
THBS1	NA	UP	2.656	1.05e–77	3791.3
SEMA7A	NA	UP	2.329	3.91e–69	7576.6
ISG15	NA	UP	2.482	5.90e–57	3807.9
VCAM1	NA	UP	4.737	4.28e–26	66.5
ITGAM	NA	UP	2.447	1.39e–19	90.2
ACTN2	NA	UP	3.956	7.01e–09	20.3
ICAM4	NA	UP	2.446	8.79e–06	22.0
FAP	NA	UP	3.233	1.87e–05	14.0
EGFL6	NA	UP	3.034	6.01e–03	5.9
VWF	NA	UP	3.390	1.16e–02	4.6

## Ruta: growth factor activity

Fuente: GO:MF | ID: GO:0008083 | Genes: 13 | p-valor ruta: 3.58e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
INHBA	NA	UP	3.514	2.31e-143	1743.6
CSF2	NA	UP	7.043	2.08e-103	455.6
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7
FGF19	NA	UP	3.931	5.59e-21	52.8
CSF3	NA	UP	6.122	1.72e-19	56.0
INHBE	NA	UP	5.109	1.59e-15	37.3
IL34	NA	UP	2.794	2.41e-02	4.8
FGF18	NA	UP	2.038	4.86e-02	6.1

# Sección de Análisis: GO:BP – Procesos Biológicos

Total de términos enriquecidos en esta sección: 522

Términos 'Tope' (p–valor < 1e–16): 76

## Términos que superan el 'tope' de significancia:

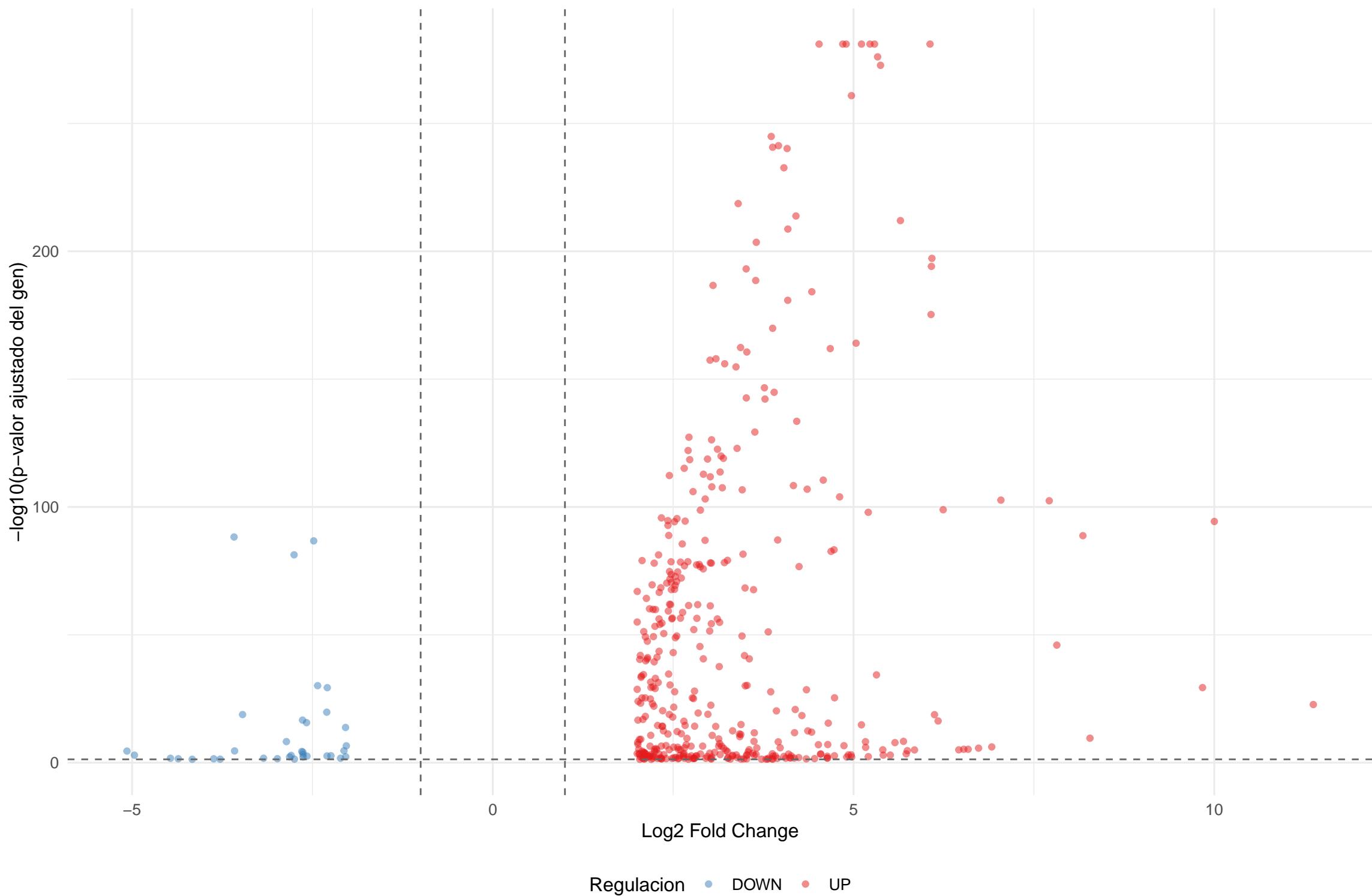
- *response to biotic stimulus* (GO:0009607, p–val: 8.0e–58)
- *response to other organism* (GO:0051707, p–val: 5.0e–56)
- *response to external biotic stimulus* (GO:0043207, p–val: 6.5e–56)
- *response to external stimulus* (GO:0009605, p–val: 3.7e–55)
- *defense response* (GO:0006952, p–val: 4.1e–55)
- *biological process involved in interspecies interaction between organisms* (GO:0044419, p–val: 1.2e–52)
- *response to peptide* (GO:1901652, p–val: 1.5e–46)
- *response to cytokine* (GO:0034097, p–val: 2.4e–46)
- *defense response to other organism* (GO:0098542, p–val: 3.6e–45)
- *defense response to symbiont* (GO:0140546, p–val: 3.9e–43)

...y otros

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

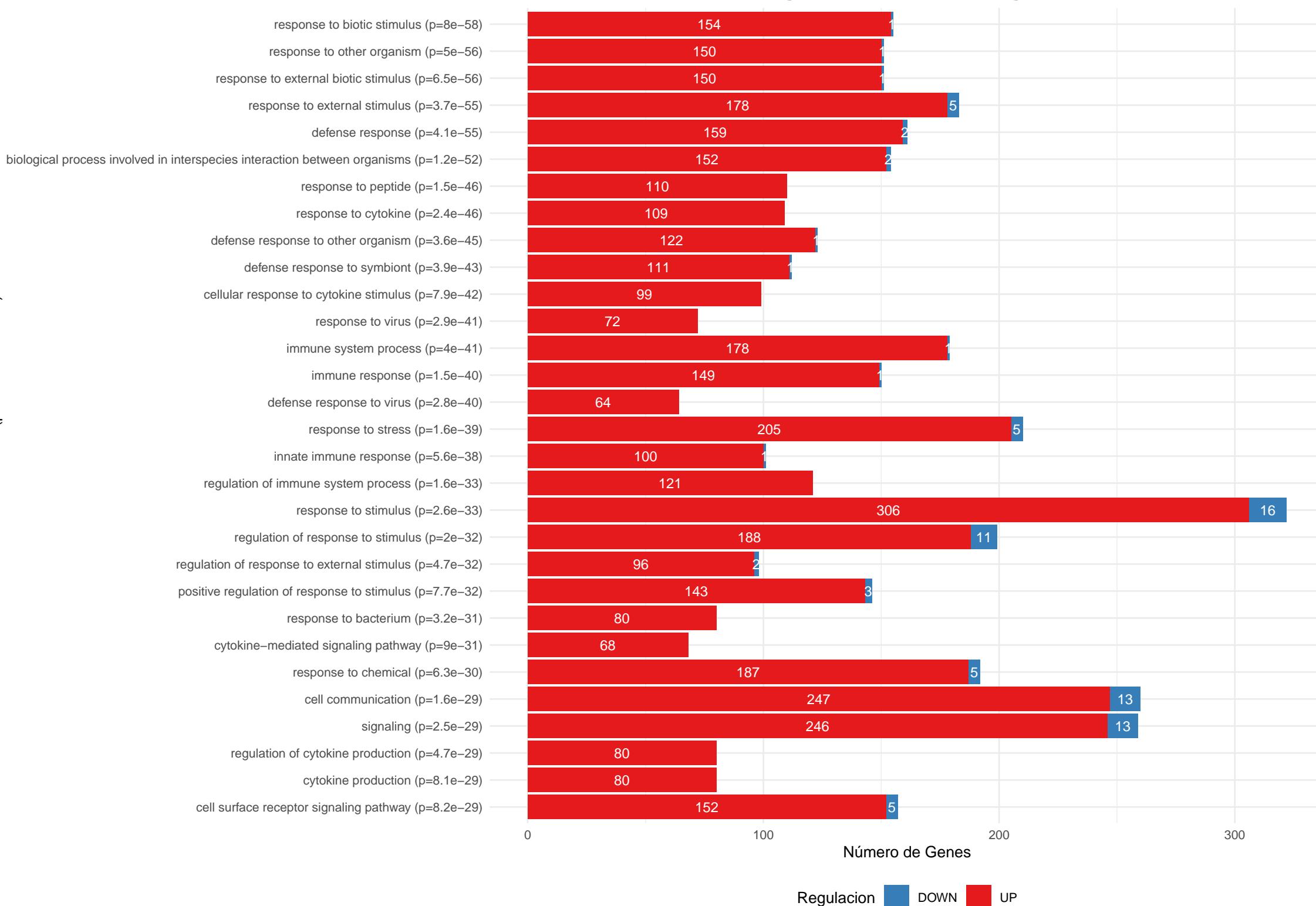
# Volcano Plot – GO:BP – Procesos Biológicos

Mostrando 434 genes únicos mapeados en esta sección



# GO:BP – Procesos Biológicos – Gráfico (Pág. 1 de 18)

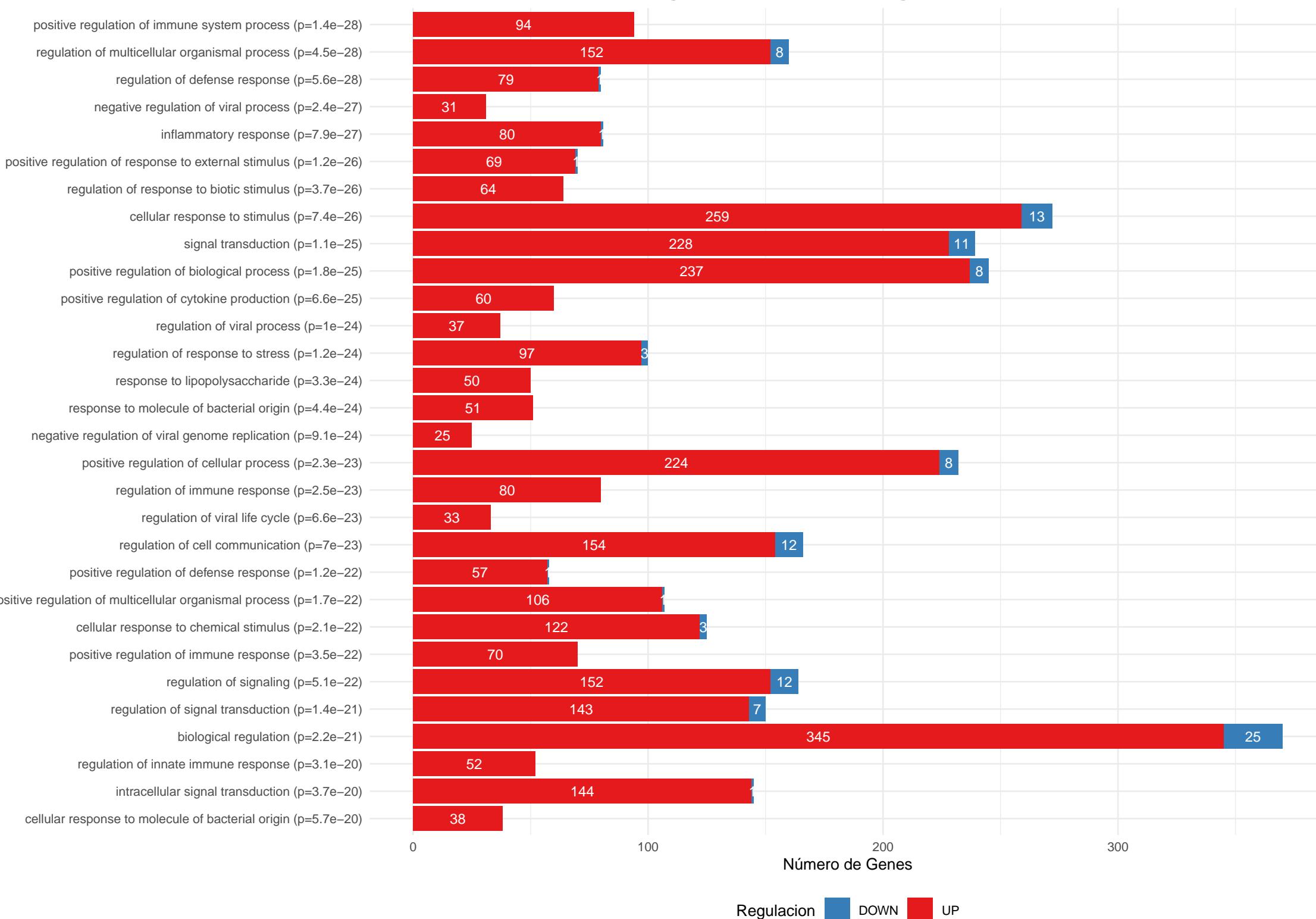
Ruta Funcional (p–valor de la ruta)



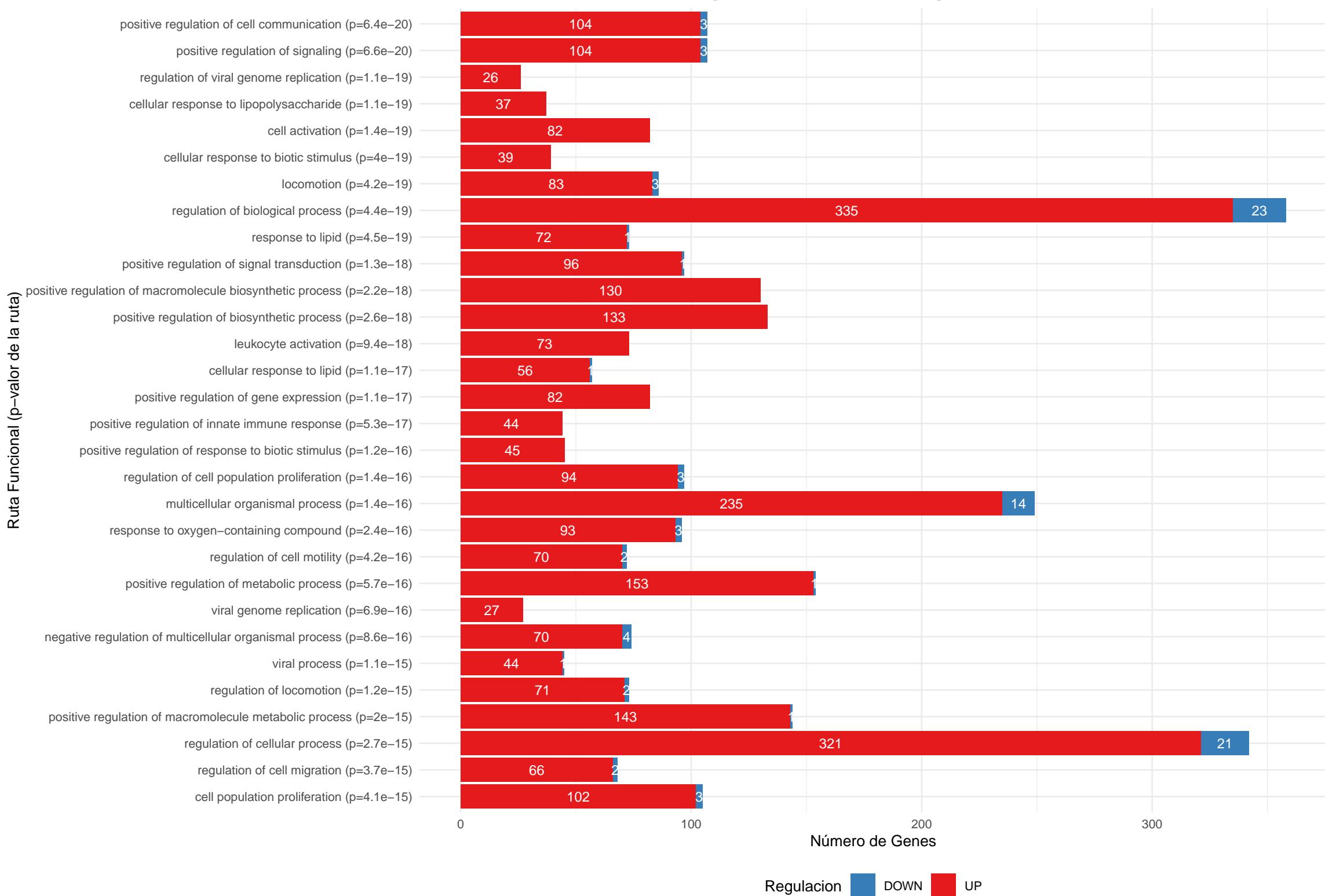
Regulacion  DOWN  UP

# GO:BP – Procesos Biológicos – Gráfico (Pág. 2 de 18 )

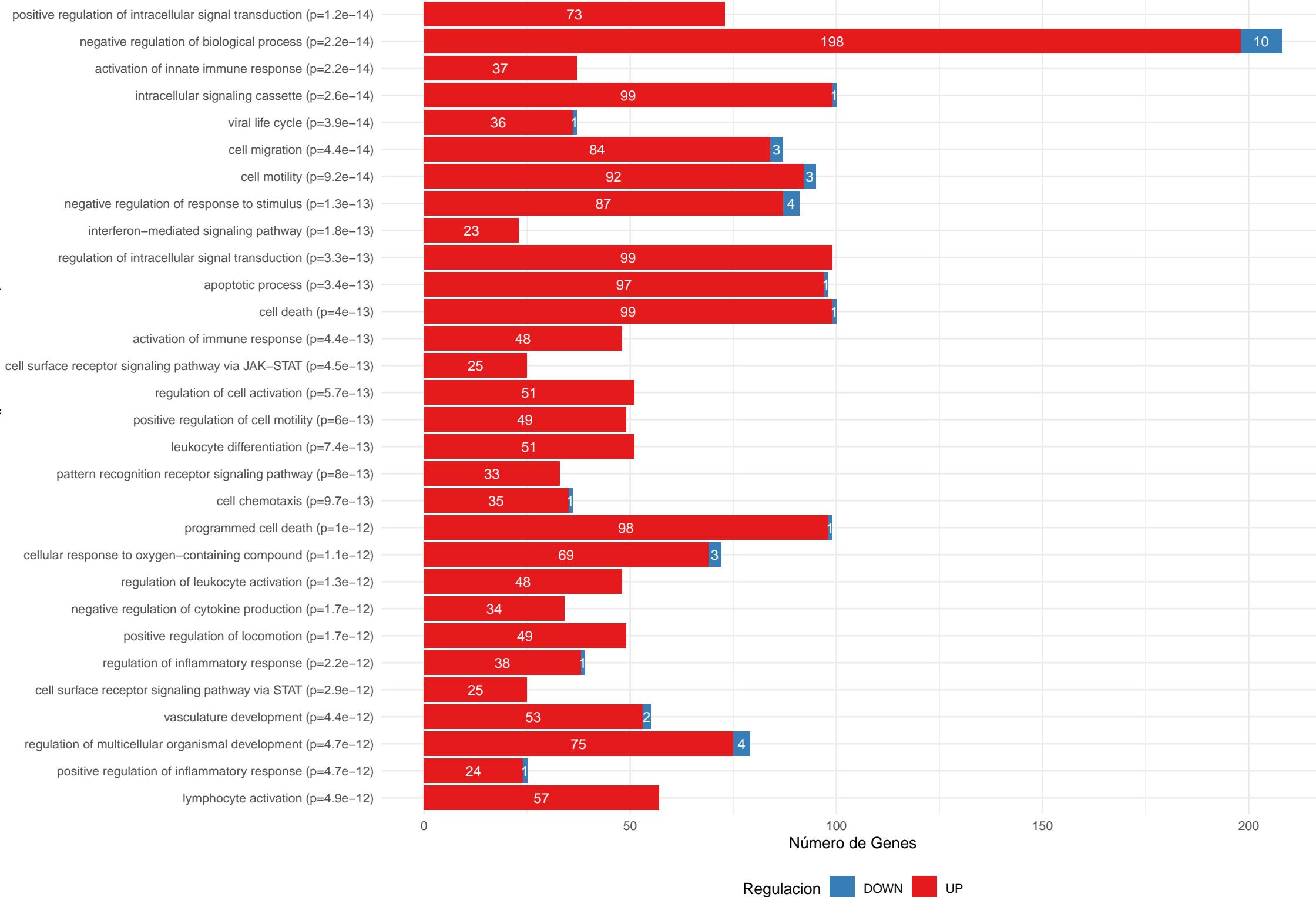
Ruta Funcional (p–valor de la ruta)



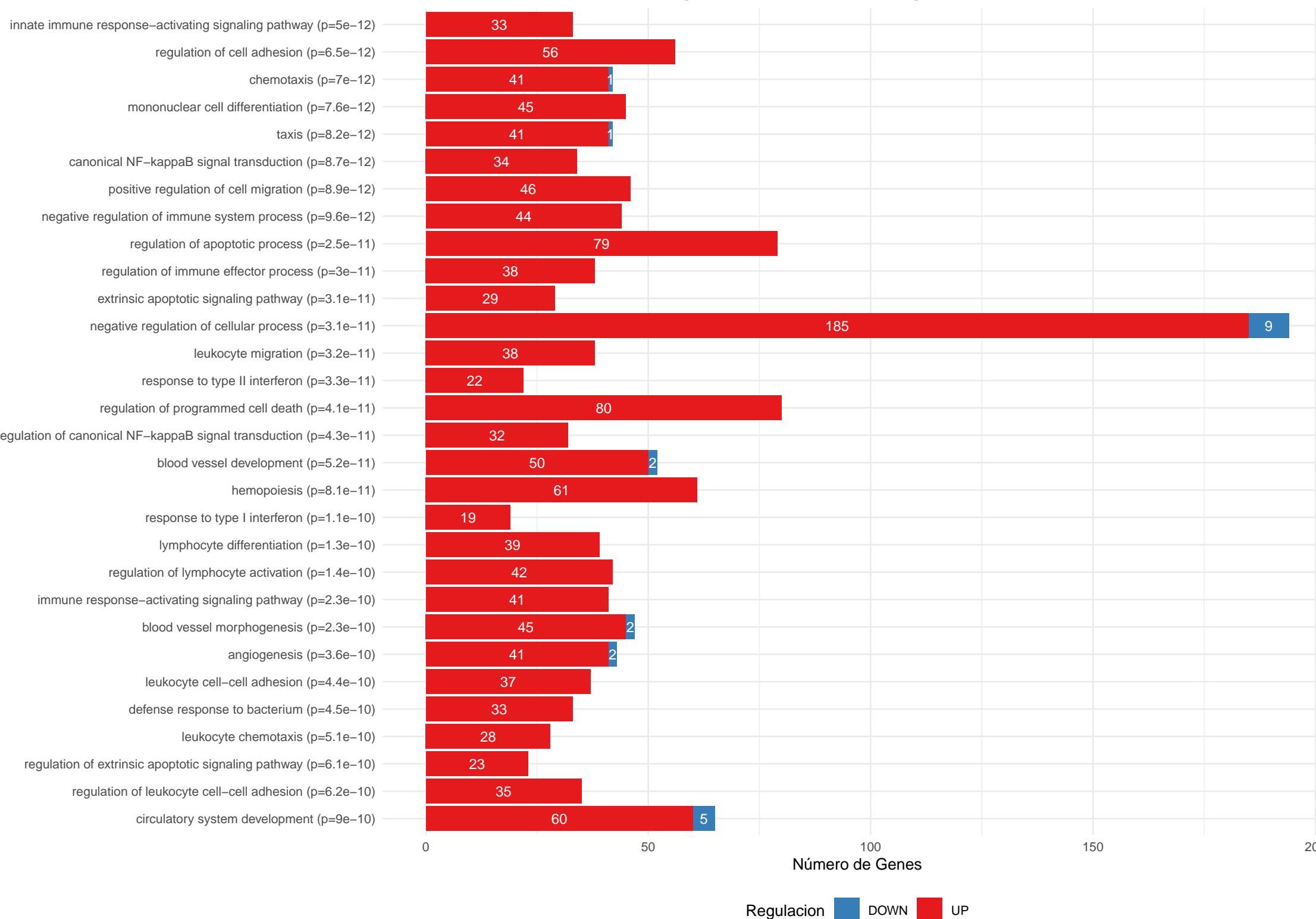
# GO:BP – Procesos Biológicos – Gráfico (Pág. 3 de 18 )



# GO:BP – Procesos Biológicos – Gráfico (Pág. 4 de 18 )

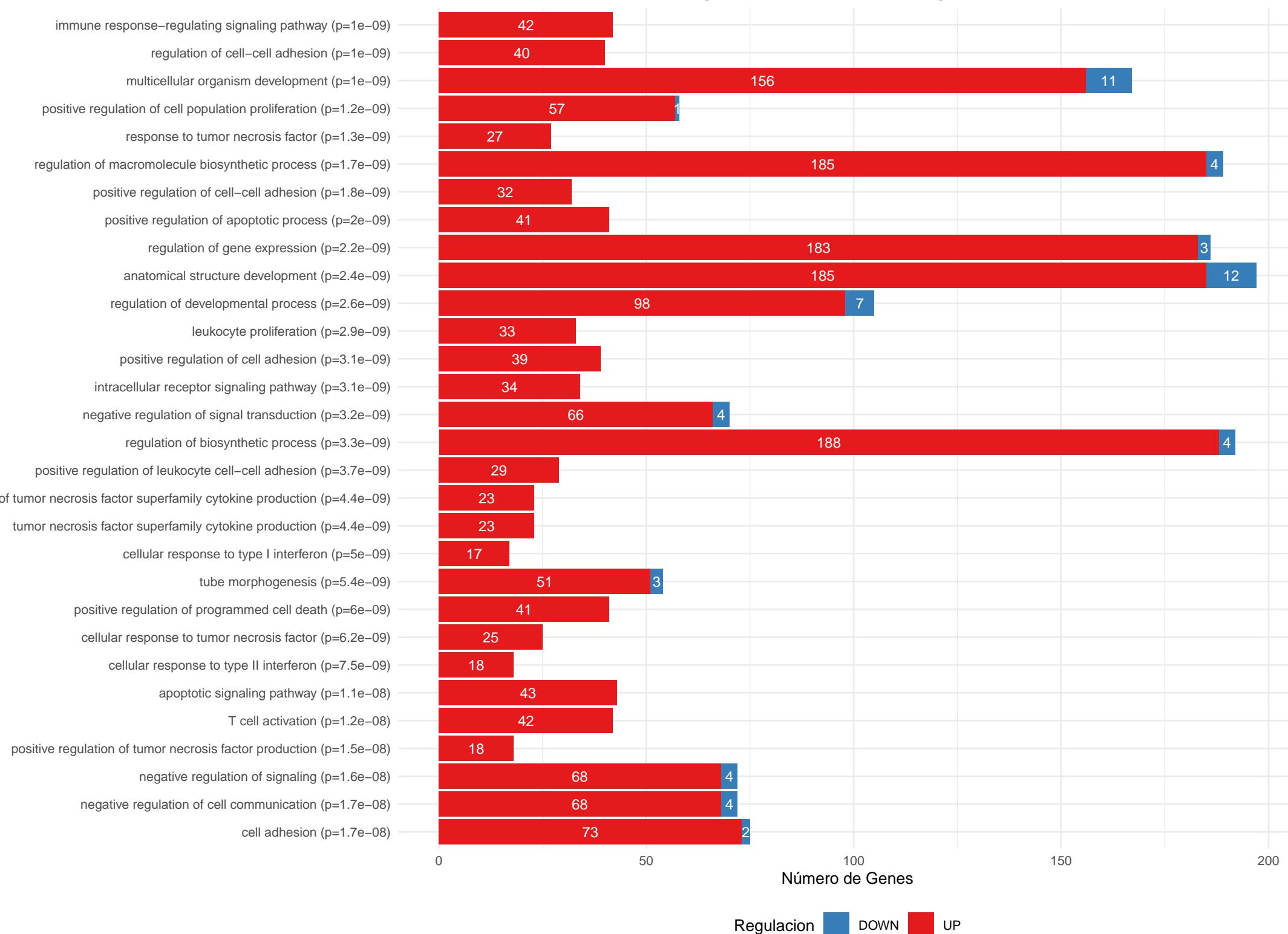


# GO:BP – Procesos Biológicos – Gráfico (Pág. 5 de 18 )



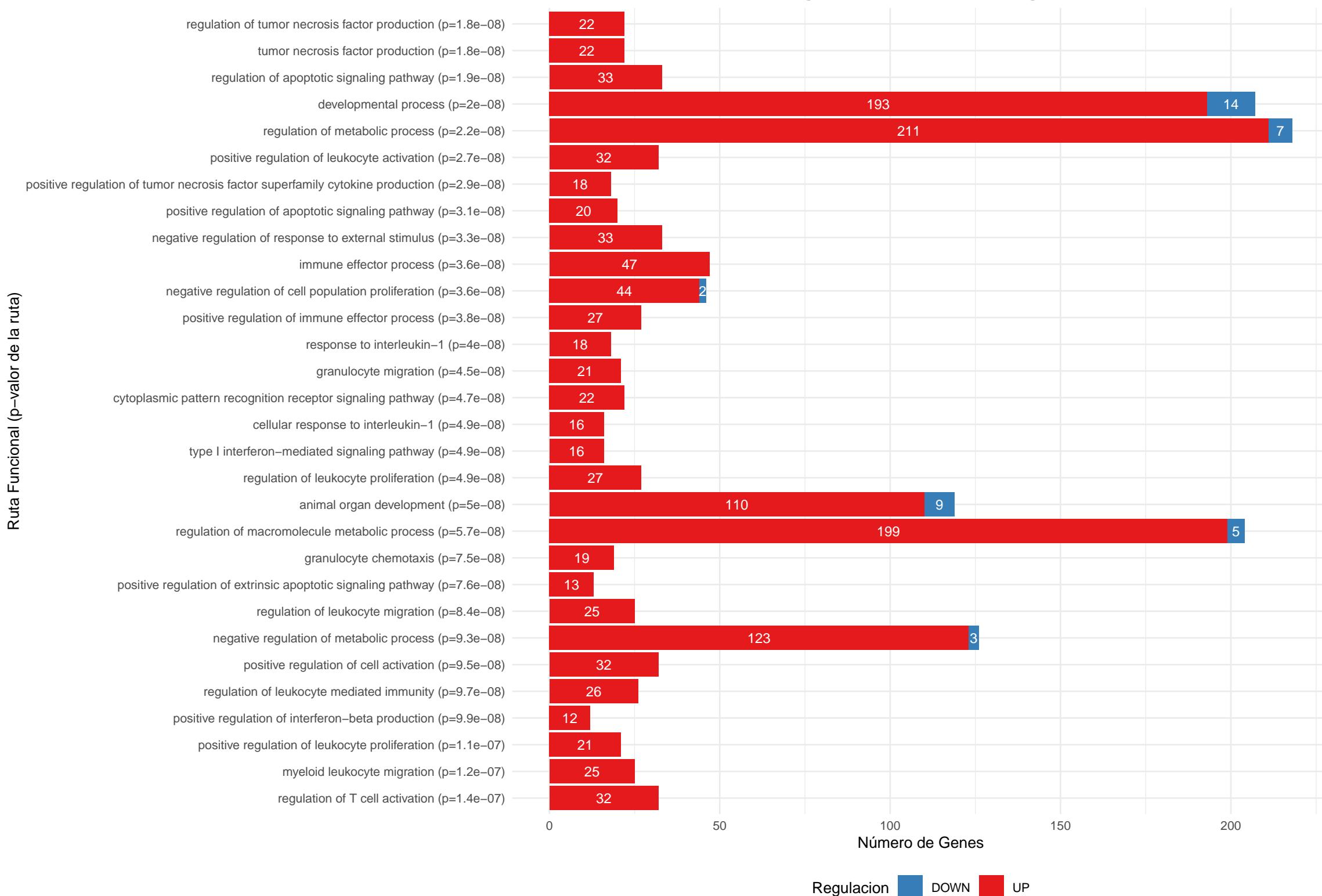
# GO:BP – Procesos Biológicos – Gráfico (Pág. 6 de 18 )

Ruta Funcional (p–valor de la ruta)

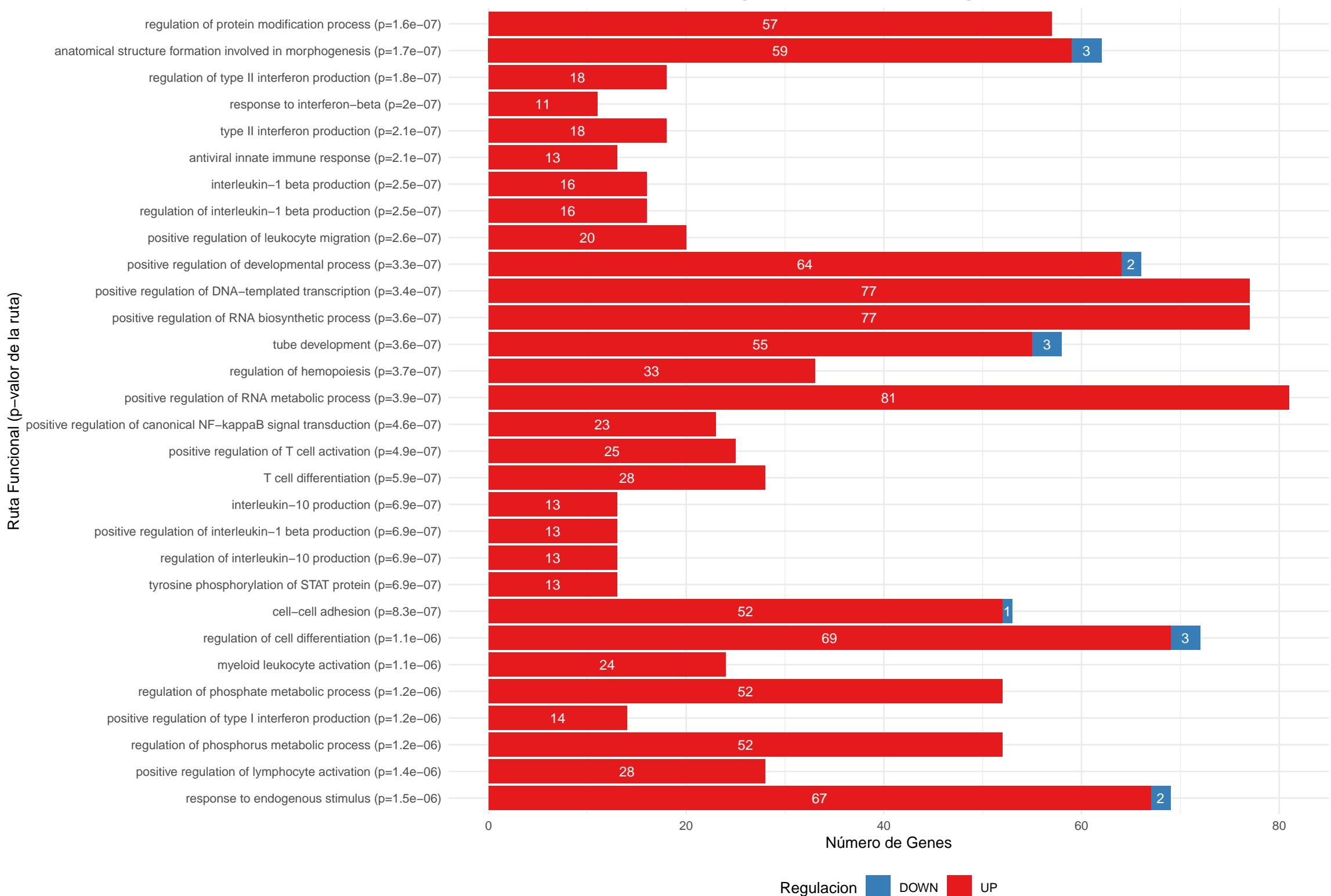


Regulacion    DOWN    UP

# GO:BP – Procesos Biológicos – Gráfico (Pág. 7 de 18 )

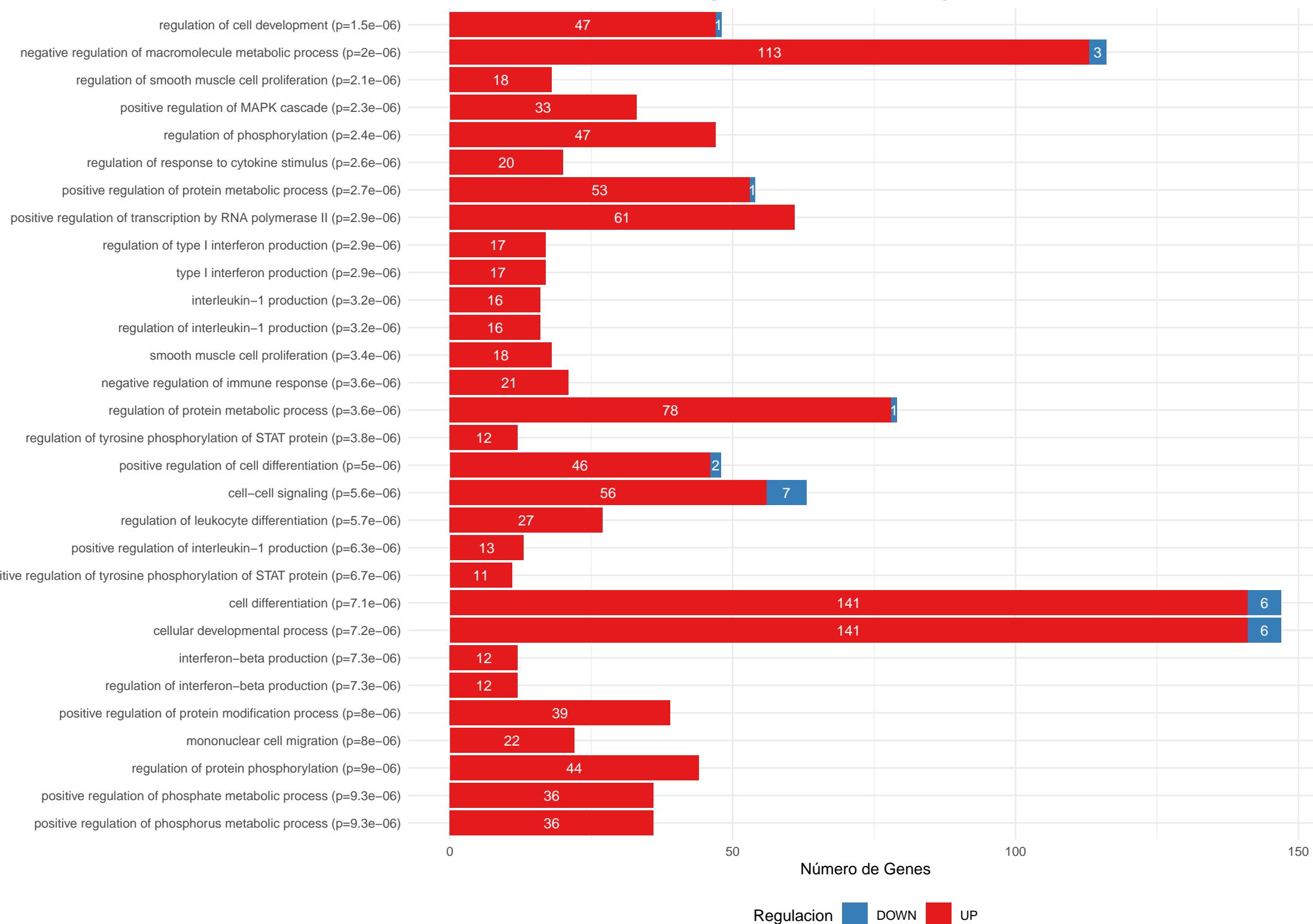


# GO:BP – Procesos Biológicos – Gráfico (Pág. 8 de 18 )



# GO:BP – Procesos Biológicos – Gráfico (Pág. 9 de 18)

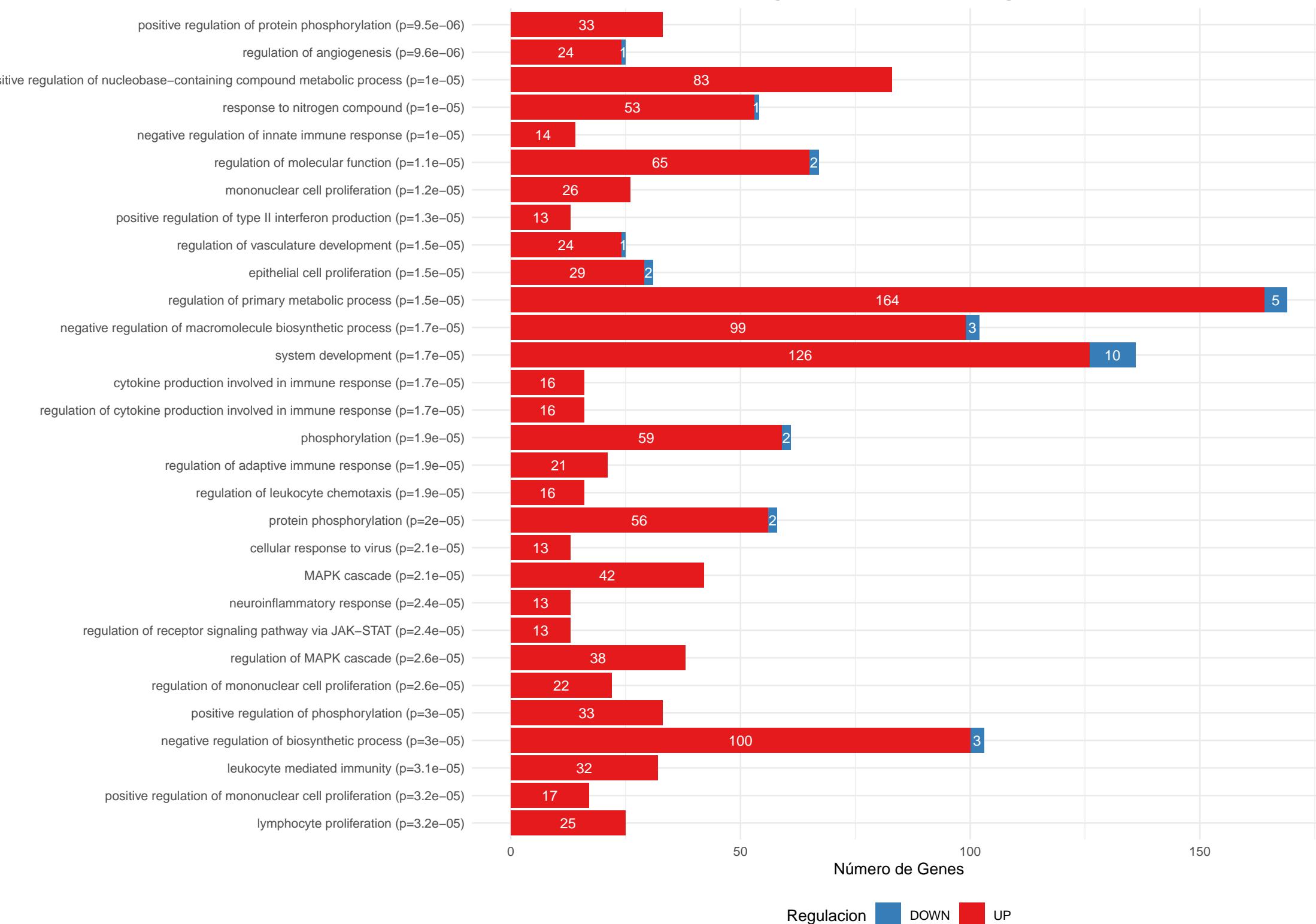
Ruta Funcional (p–valor de la ruta)



Regulacion    DOWN    UP

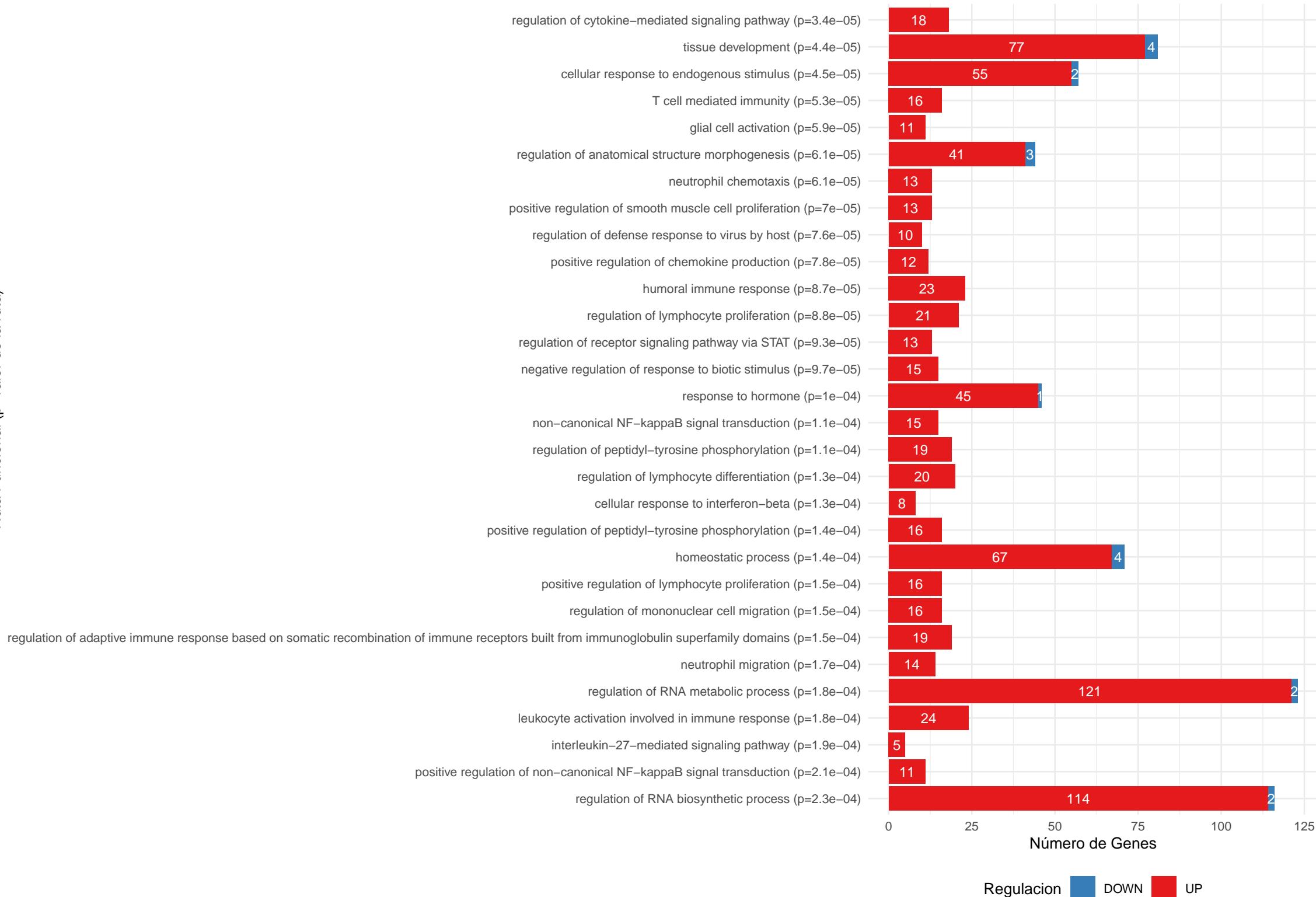
# GO:BP – Procesos Biológicos – Gráfico (Pág. 10 de 18 )

Ruta Funcional (p–valor de la ruta)



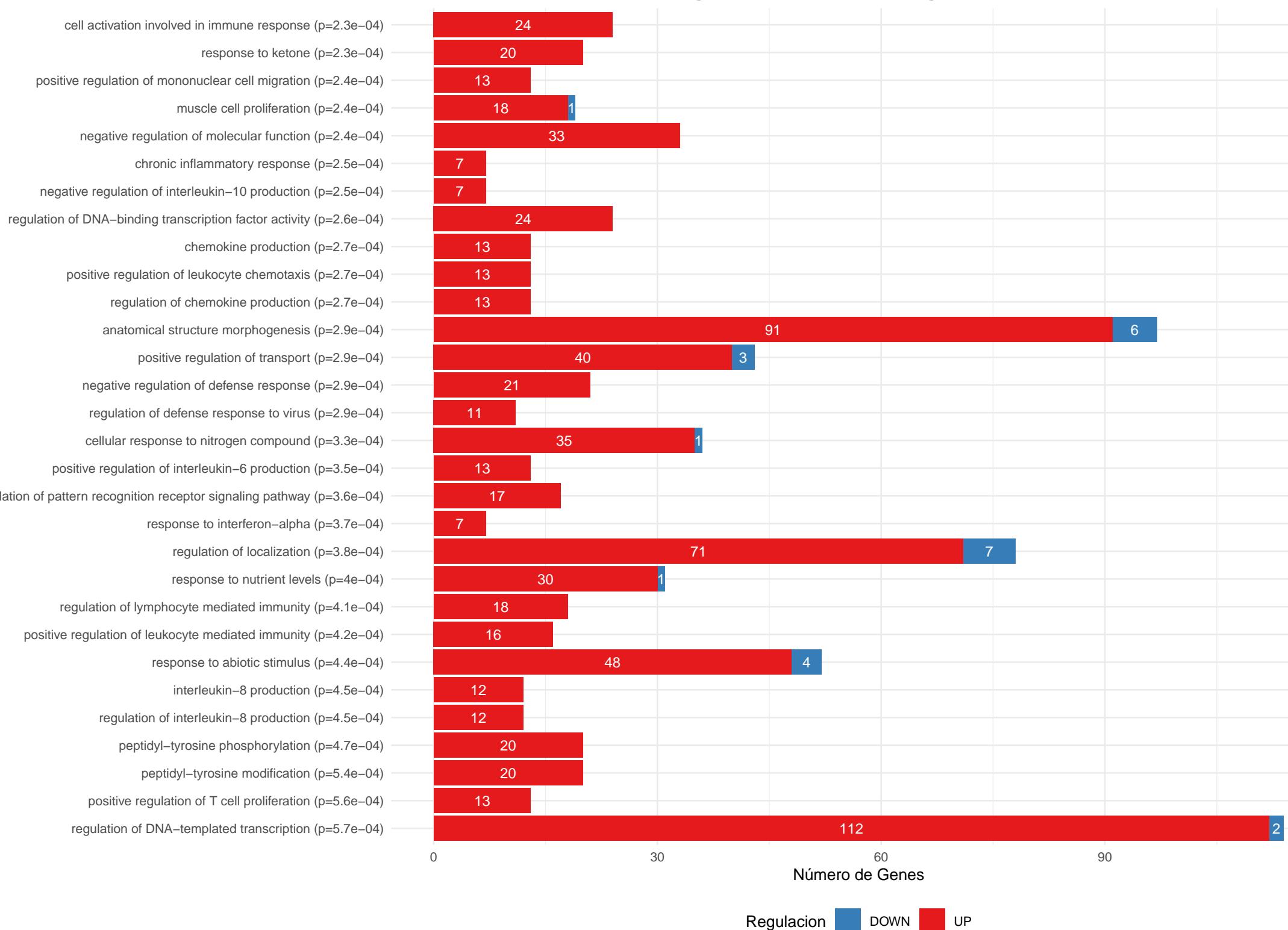
# GO:BP – Procesos Biológicos – Gráfico

Ruta Funcional (p–valor de la ruta)



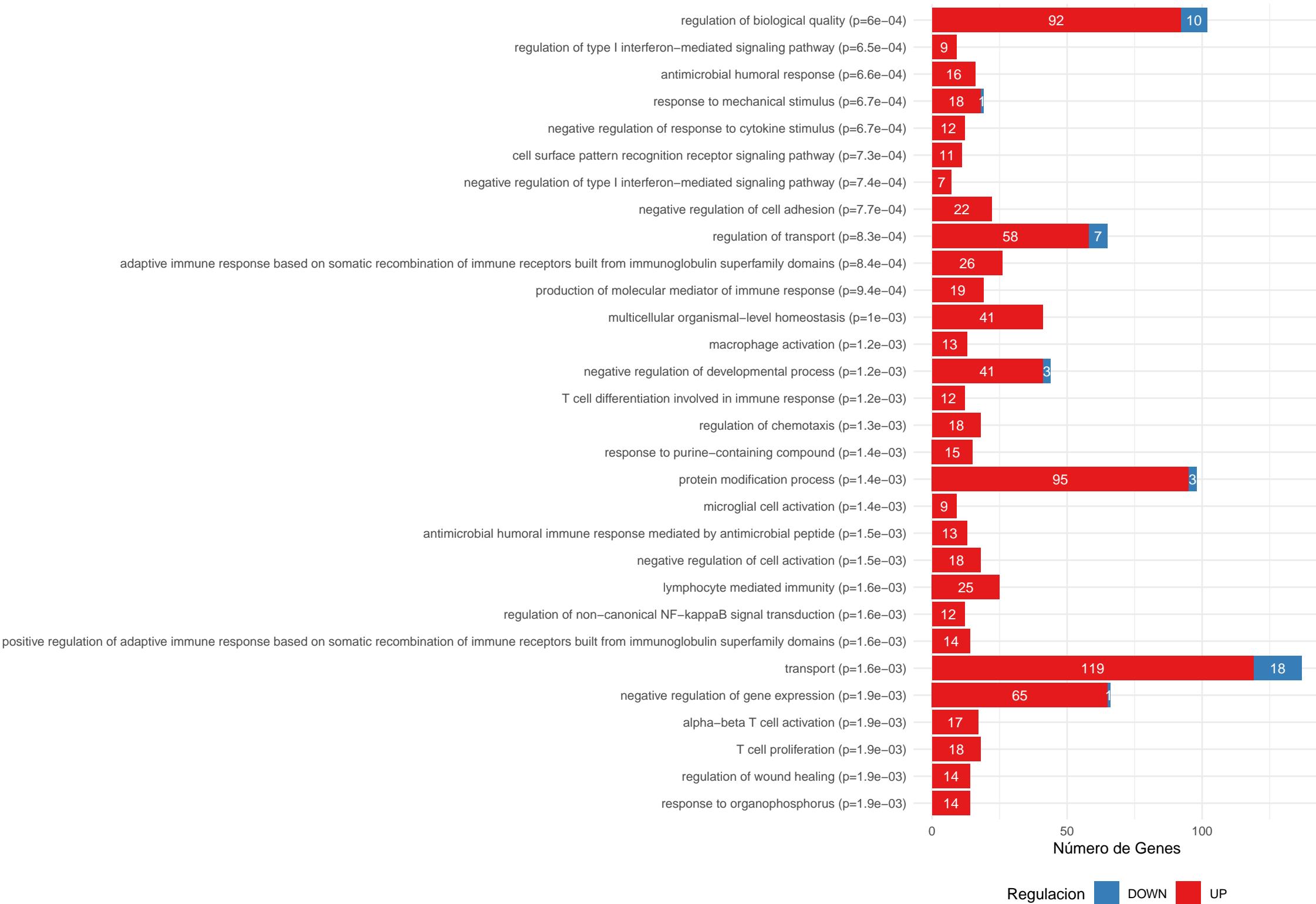
# GO:BP – Procesos Biológicos – Gráfico (Pág. 12 de 18)

Ruta Funcional (p–valor de la ruta)

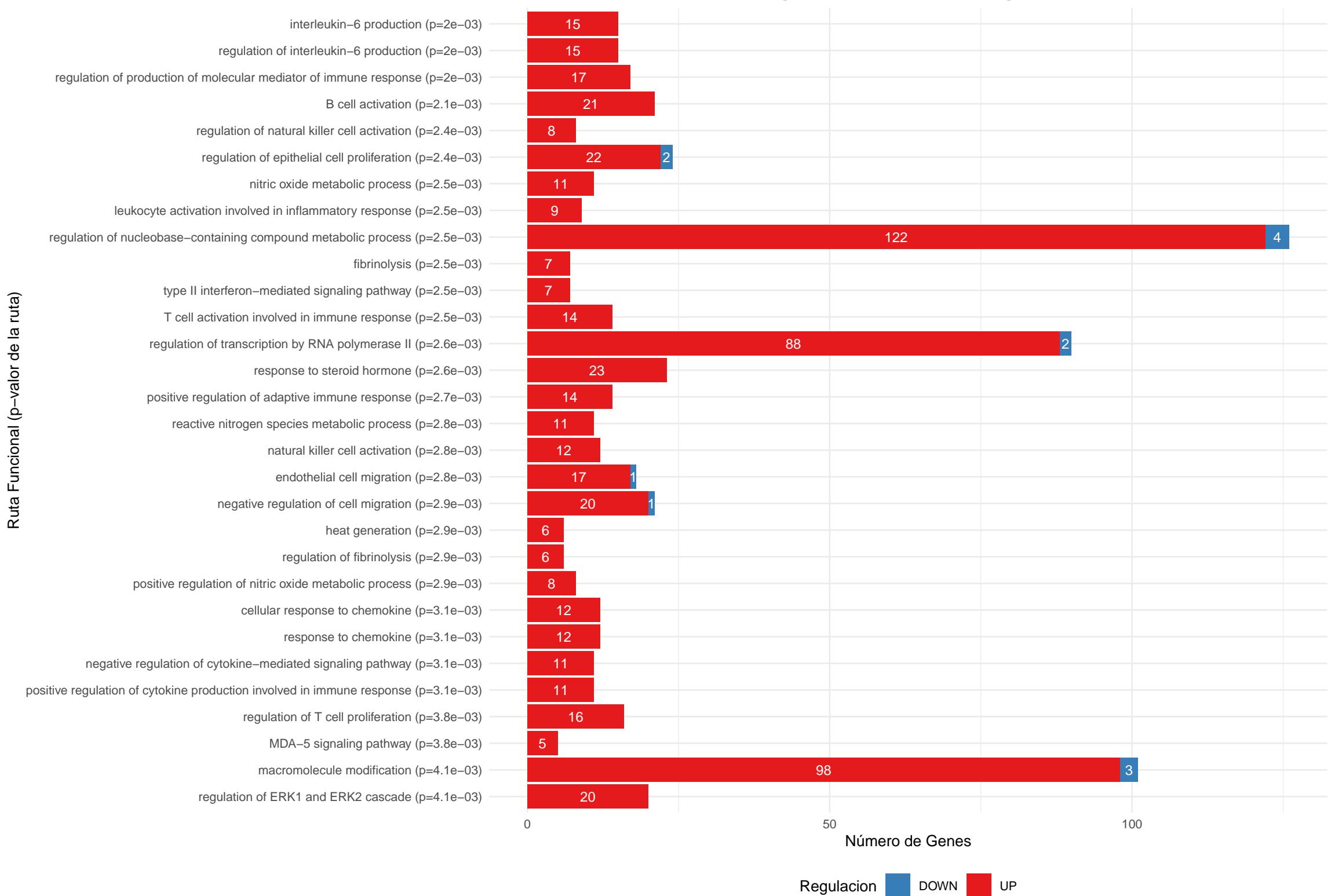


# GO:BP – Procesos Biológicos – Gr

Ruta Funcional (p–valor de la ruta)

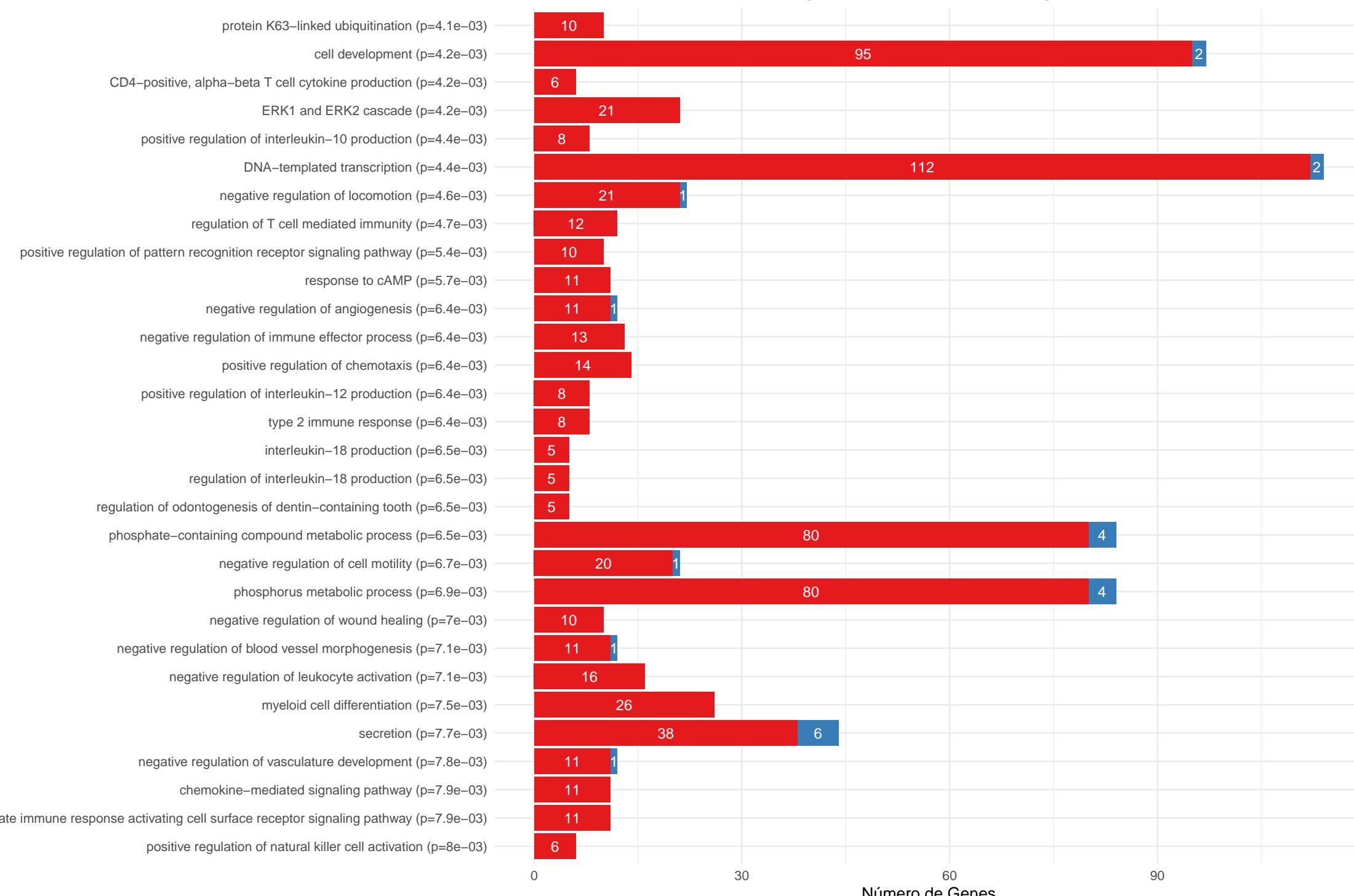


# GO:BP – Procesos Biológicos – Gráfico (Pág. 14 de 18)



# GO:BP – Procesos Biológicos – Gráfico (Pág. 15 de 18 )

Ruta Funcional (p–valor de la ruta)

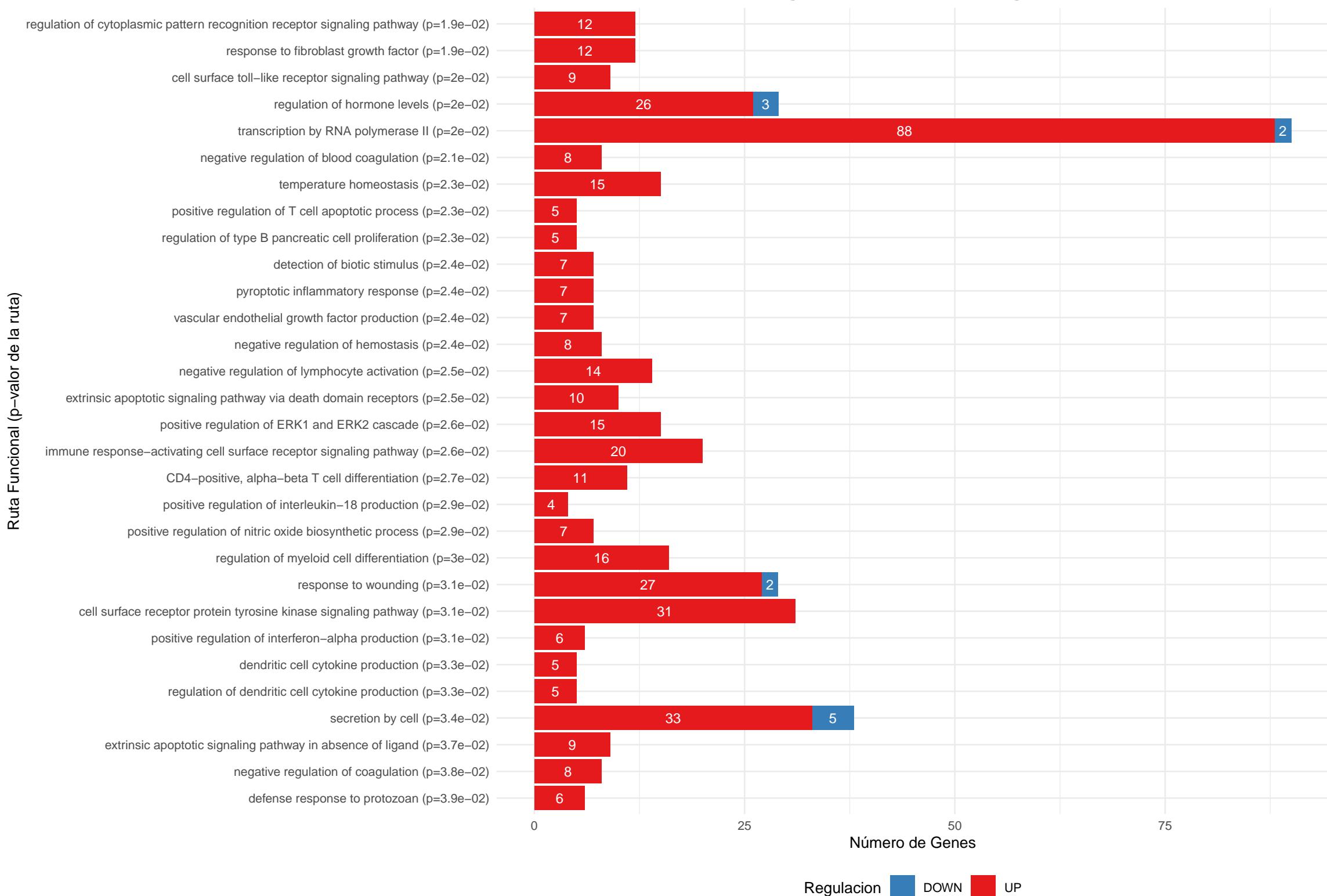


Regulacion DOWN UP

# GO:BP – Procesos Biológicos – Gráfico (Pág. 16 de 18)

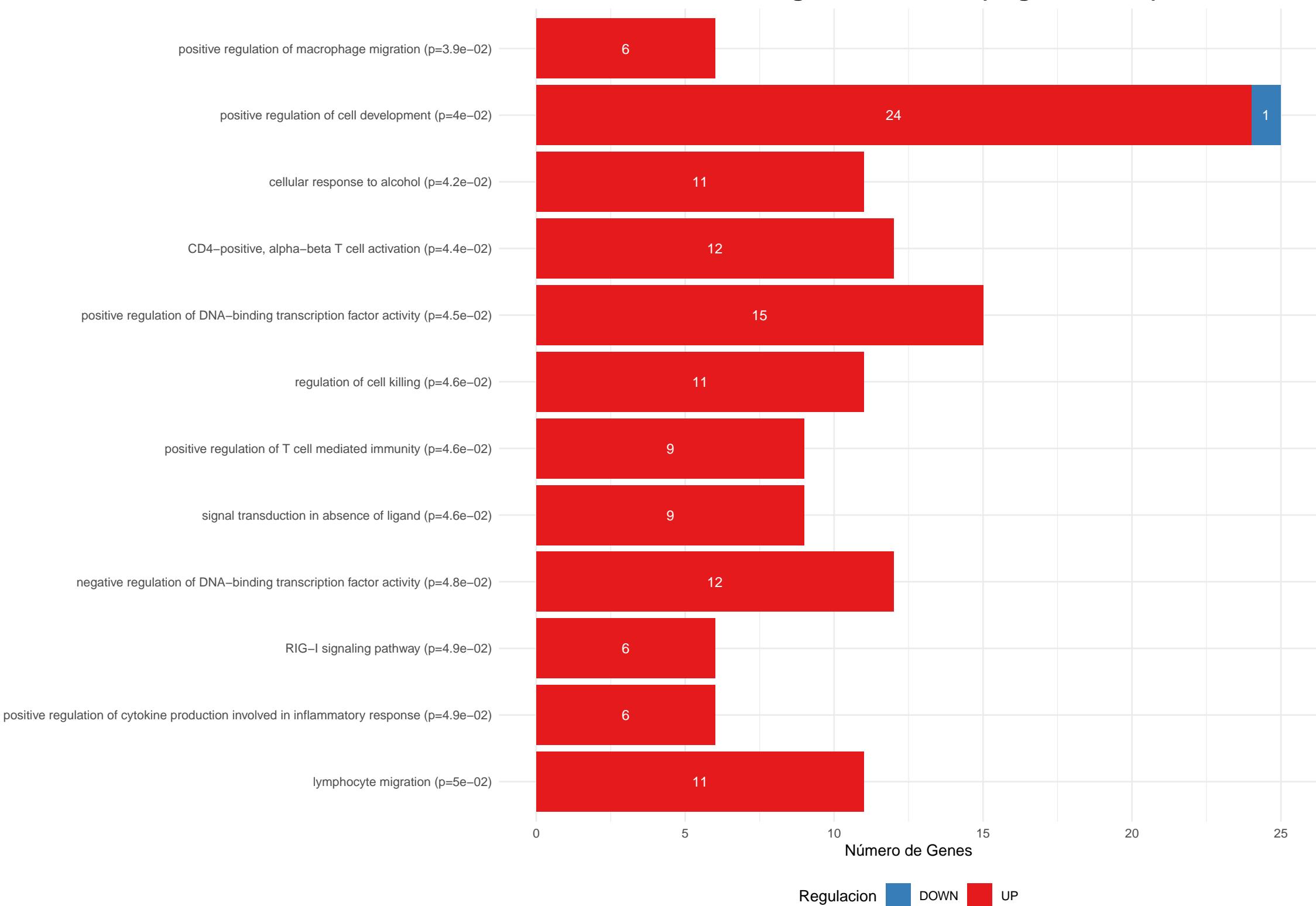


# GO:BP – Procesos Biológicos – Gráfico (Pág. 17 de 18 )



# GO:BP – Procesos Biológicos – Gráfico (Pág. 18 de 18 )

Ruta Funcional (p–valor de la ruta)



## Ruta: response to biotic stimulus (Página 1 de 7)

Fuente: GO:BP | ID: GO:0009607 | Genes: 155 | p-valor ruta: 8.04e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
IFI44L	NA	UP	4.088	1.50e-181	1679.8
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3

## Ruta: response to biotic stimulus (Página 2 de 7)

Fuente: GO:BP | ID: GO:0009607 | Genes: 155 | p-valor ruta: 8.04e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OASL	NA	UP	3.434	4.45e-163	4285.8
CMPK2	NA	UP	4.677	1.14e-162	1687.4
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
IFI44	NA	UP	3.036	1.35e-108	3423.4
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6

## Ruta: response to biotic stimulus (Página 3 de 7)

Fuente: GO:BP | ID: GO:0009607 | Genes: 155 | p-valor ruta: 8.04e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2

## Ruta: response to biotic stimulus (Página 4 de 7)

Fuente: GO:BP | ID: GO:0009607 | Genes: 155 | p-valor ruta: 8.04e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3

## Ruta: response to biotic stimulus (Página 5 de 7)

Fuente: GO:BP | ID: GO:0009607 | Genes: 155 | p-valor ruta: 8.04e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
PRDM1	NA	UP	3.525	5.98e-31	99.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6

## Ruta: response to biotic stimulus (Página 6 de 7)

Fuente: GO:BP | ID: GO:0009607 | Genes: 155 | p-valor ruta: 8.04e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CLEC4E	NA	UP	3.620	4.75e-09	26.0
KMO	NA	UP	5.165	6.24e-09	19.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
WFDC5	NA	UP	5.168	1.07e-06	13.9
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
PTGER2	NA	UP	3.006	1.95e-04	11.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
CEACAM20	NA	UP	5.412	1.17e-03	3.6
GBP6	NA	UP	2.233	3.24e-03	11.2
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
THBD	NA	UP	2.330	1.23e-02	7.3
PRG2	NA	UP	2.073	1.32e-02	9.7
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: response to biotic stimulus (Página 7 de 7)

Fuente: GO:BP | ID: GO:0009607 | Genes: 155 | p-valor ruta: 8.04e-58

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL34	NA	UP	2.794	2.41e-02	4.8
SPRR2A	NA	UP	2.086	2.78e-02	7.8
CCL17	NA	UP	3.441	3.89e-02	2.9
PPM1E	NA	UP	3.810	4.20e-02	2.4
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: response to other organism (Página 1 de 7)

Fuente: GO:BP | ID: GO:0051707 | Genes: 151 | p-valor ruta: 5.05e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
IFI44L	NA	UP	4.088	1.50e-181	1679.8
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8

## Ruta: response to other organism (Página 2 de 7)

Fuente: GO:BP | ID: GO:0051707 | Genes: 151 | p-valor ruta: 5.05e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CMPK2	NA	UP	4.677	1.14e-162	1687.4
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
IFI44	NA	UP	3.036	1.35e-108	3423.4
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3

## Ruta: response to other organism (Página 3 de 7)

Fuente: GO:BP | ID: GO:0051707 | Genes: 151 | p-valor ruta: 5.05e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3

## Ruta: response to other organism (Página 4 de 7)

Fuente: GO:BP | ID: GO:0051707 | Genes: 151 | p-valor ruta: 5.05e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9

## Ruta: response to other organism (Página 5 de 7)

Fuente: GO:BP | ID: GO:0051707 | Genes: 151 | p-valor ruta: 5.05e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C1R	NA	UP	2.188	3.06e-32	258.8
PRDM1	NA	UP	3.525	5.98e-31	99.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
KMO	NA	UP	5.165	6.24e-09	19.5

## Ruta: response to other organism (Página 6 de 7)

Fuente: GO:BP | ID: GO:0051707 | Genes: 151 | p-valor ruta: 5.05e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
WFDC5	NA	UP	5.168	1.07e-06	13.9
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
PTGER2	NA	UP	3.006	1.95e-04	11.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
CEACAM20	NA	UP	5.412	1.17e-03	3.6
GBP6	NA	UP	2.233	3.24e-03	11.2
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
THBD	NA	UP	2.330	1.23e-02	7.3
PRG2	NA	UP	2.073	1.32e-02	9.7
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SPRR2A	NA	UP	2.086	2.78e-02	7.8
CCL17	NA	UP	3.441	3.89e-02	2.9
PPM1E	NA	UP	3.810	4.20e-02	2.4

## Ruta: response to other organism (Página 7 de 7)

Fuente: GO:BP | ID: GO:0051707 | Genes: 151 | p-valor ruta: 5.05e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SRMS	NA	UP	3.88	4.55e-02	2.3

## Ruta: response to external biotic stimulus (Página 1 de 7)

Fuente: GO:BP | ID: GO:0043207 | Genes: 151 | p-valor ruta: 6.5e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
IFI44L	NA	UP	4.088	1.50e-181	1679.8
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8

## Ruta: response to external biotic stimulus (Página 2 de 7)

Fuente: GO:BP | ID: GO:0043207 | Genes: 151 | p-valor ruta: 6.5e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CMPK2	NA	UP	4.677	1.14e-162	1687.4
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
IFI44	NA	UP	3.036	1.35e-108	3423.4
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3

## Ruta: response to external biotic stimulus (Página 3 de 7)

Fuente: GO:BP | ID: GO:0043207 | Genes: 151 | p-valor ruta: 6.5e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRK5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3

## Ruta: response to external biotic stimulus (Página 4 de 7)

Fuente: GO:BP | ID: GO:0043207 | Genes: 151 | p-valor ruta: 6.5e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9

## Ruta: response to external biotic stimulus (Página 5 de 7)

Fuente: GO:BP | ID: GO:0043207 | Genes: 151 | p-valor ruta: 6.5e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C1R	NA	UP	2.188	3.06e-32	258.8
PRDM1	NA	UP	3.525	5.98e-31	99.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
KMO	NA	UP	5.165	6.24e-09	19.5

## Ruta: response to external biotic stimulus (Página 6 de 7)

Fuente: GO:BP | ID: GO:0043207 | Genes: 151 | p-valor ruta: 6.5e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
WFDC5	NA	UP	5.168	1.07e-06	13.9
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
PTGER2	NA	UP	3.006	1.95e-04	11.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
CEACAM20	NA	UP	5.412	1.17e-03	3.6
GBP6	NA	UP	2.233	3.24e-03	11.2
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
THBD	NA	UP	2.330	1.23e-02	7.3
PRG2	NA	UP	2.073	1.32e-02	9.7
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SPRR2A	NA	UP	2.086	2.78e-02	7.8
CCL17	NA	UP	3.441	3.89e-02	2.9
PPM1E	NA	UP	3.810	4.20e-02	2.4

## Ruta: response to external biotic stimulus (Página 7 de 7)

Fuente: GO:BP | ID: GO:0043207 | Genes: 151 | p-valor ruta: 6.5e-56

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SRMS	NA	UP	3.88	4.55e-02	2.3

## Ruta: response to external stimulus (Página 1 de 8)

Fuente: GO:BP | ID: GO:0009605 | Genes: 183 | p-valor ruta: 3.69e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
IFI44L	NA	UP	4.088	1.50e-181	1679.8
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3

## Ruta: response to external stimulus (Página 2 de 8)

Fuente: GO:BP | ID: GO:0009605 | Genes: 183 | p-valor ruta: 3.69e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OASL	NA	UP	3.434	4.45e-163	4285.8
CMPK2	NA	UP	4.677	1.14e-162	1687.4
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
IDO1	NA	UP	4.167	4.38e-109	394.2
IFI44	NA	UP	3.036	1.35e-108	3423.4
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6

## Ruta: response to external stimulus (Página 3 de 8)

Fuente: GO:BP | ID: GO:0009605 | Genes: 183 | p-valor ruta: 3.69e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7

## Ruta: response to external stimulus (Página 4 de 8)

Fuente: GO:BP | ID: GO:0009605 | Genes: 183 | p-valor ruta: 3.69e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
FOSB	NA	UP	3.144	1.32e-55	267.7
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5

## Ruta: response to external stimulus (Página 5 de 8)

Fuente: GO:BP | ID: GO:0009605 | Genes: 183 | p-valor ruta: 3.69e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
PER1	NA	UP	2.501	8.94e-44	469.6
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7

## Ruta: response to external stimulus (Página 6 de 8)

Fuente: GO:BP | ID: GO:0009605 | Genes: 183 | p-valor ruta: 3.69e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
DUOXA2	NA	UP	4.650	3.36e-16	39.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
KMO	NA	UP	5.165	6.24e-09	19.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
WFDC5	NA	UP	5.168	1.07e-06	13.9
NUPR1	NA	UP	3.660	1.78e-06	14.5

## Ruta: response to external stimulus (Página 7 de 8)

Fuente: GO:BP | ID: GO:0009605 | Genes: 183 | p-valor ruta: 3.69e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BEST1	NA	UP	3.553	8.47e-06	13.3
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
PTGER2	NA	UP	3.006	1.95e-04	11.0
EGR3	NA	UP	2.096	2.87e-04	21.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
CEACAM20	NA	UP	5.412	1.17e-03	3.6
LGR6	NA	UP	3.915	2.25e-03	6.0
GBP6	NA	UP	2.233	3.24e-03	11.2
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
THBD	NA	UP	2.330	1.23e-02	7.3
PRG2	NA	UP	2.073	1.32e-02	9.7
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1

## Ruta: response to external stimulus (Página 8 de 8)

Fuente: GO:BP | ID: GO:0009605 | Genes: 183 | p-valor ruta: 3.69e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
SPRR2A	NA	UP	2.086	2.78e-02	7.8
CCL17	NA	UP	3.441	3.89e-02	2.9
PPM1E	NA	UP	3.810	4.20e-02	2.4
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: defense response (Página 1 de 7)

Fuente: GO:BP | ID: GO:0006952 | Genes: 161 | p-valor ruta: 4.12e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
IFI44L	NA	UP	4.088	1.50e-181	1679.8
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8

## Ruta: defense response (Página 2 de 7)

Fuente: GO:BP | ID: GO:0006952 | Genes: 161 | p-valor ruta: 4.12e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5

## Ruta: defense response (Página 3 de 7)

Fuente: GO:BP | ID: GO:0006952 | Genes: 161 | p-valor ruta: 4.12e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3

## Ruta: defense response (Página 4 de 7)

Fuente: GO:BP | ID: GO:0006952 | Genes: 161 | p-valor ruta: 4.12e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
PER1	NA	UP	2.501	8.94e-44	469.6
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4

## Ruta: defense response (Página 5 de 7)

Fuente: GO:BP | ID: GO:0006952 | Genes: 161 | p-valor ruta: 4.12e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
DUOXA2	NA	UP	4.650	3.36e-16	39.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: defense response (Página 6 de 7)

Fuente: GO:BP | ID: GO:0006952 | Genes: 161 | p-valor ruta: 4.12e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DUOX1	NA	UP	3.131	5.18e-10	27.1
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
SAA4	NA	UP	2.563	9.46e-07	21.9
WFDC5	NA	UP	5.168	1.07e-06	13.9
NUPR1	NA	UP	3.660	1.78e-06	14.5
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PTGER2	NA	UP	3.006	1.95e-04	11.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
IL17C	NA	UP	4.636	3.13e-03	4.1
GBP6	NA	UP	2.233	3.24e-03	11.2
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
SCUBE1	NA	UP	2.508	1.26e-02	8.4
PRG2	NA	UP	2.073	1.32e-02	9.7
VAV1	NA	UP	2.118	1.54e-02	7.9

## Ruta: defense response (Página 7 de 7)

Fuente: GO:BP | ID: GO:0006952 | Genes: 161 | p-valor ruta: 4.12e-55

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
OLR1	NA	UP	2.655	1.81e-02	6.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SPRR2A	NA	UP	2.086	2.78e-02	7.8
CCL17	NA	UP	3.441	3.89e-02	2.9
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: biological process involved in interspecies interaction between organisms (Página 1 de 7)

Fuente: GO:BP | ID: GO:0044419 | Genes: 154 | p-valor ruta: 1.22e-52

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
IFI44L	NA	UP	4.088	1.50e-181	1679.8
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3

## Ruta: biological process involved in interspecies interaction between organisms (Página 2 de 7)

Fuente: GO:BP | ID: GO:0044419 | Genes: 154 | p-valor ruta: 1.22e-52

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OASL	NA	UP	3.434	4.45e-163	4285.8
CMPK2	NA	UP	4.677	1.14e-162	1687.4
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
IFI44	NA	UP	3.036	1.35e-108	3423.4
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6

## Ruta: biological process involved in interspecies interaction between organisms (Página 3 de 7)

Fuente: GO:BP | ID: GO:0044419 | Genes: 154 | p-valor ruta: 1.22e-52

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3

## Ruta: biological process involved in interspecies interaction between organisms (Página 4 de 7)

Fuente: GO:BP | ID: GO:0044419 | Genes: 154 | p-valor ruta: 1.22e-52

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3

## Ruta: biological process involved in interspecies interaction between organisms (Página 5 de 7)

Fuente: GO:BP | ID: GO:0044419 | Genes: 154 | p-valor ruta: 1.22e-52

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
PRDM1	NA	UP	3.525	5.98e-31	99.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6

## Ruta: biological process involved in interspecies interaction between organisms (Página 6 de 7)

Fuente: GO:BP | ID: GO:0044419 | Genes: 154 | p-valor ruta: 1.22e-52

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CLEC4E	NA	UP	3.620	4.75e-09	26.0
KMO	NA	UP	5.165	6.24e-09	19.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
WFDC5	NA	UP	5.168	1.07e-06	13.9
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
PTGER2	NA	UP	3.006	1.95e-04	11.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
CEACAM20	NA	UP	5.412	1.17e-03	3.6
GBP6	NA	UP	2.233	3.24e-03	11.2
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
THBD	NA	UP	2.330	1.23e-02	7.3
PRG2	NA	UP	2.073	1.32e-02	9.7
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: biological process involved in interspecies interaction between organisms (Página 7 de 7)

Fuente: GO:BP | ID: GO:0044419 | Genes: 154 | p-valor ruta: 1.22e-52

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SPRR2A	NA	UP	2.086	2.78e-02	7.8
CCL17	NA	UP	3.441	3.89e-02	2.9
PPM1E	NA	UP	3.810	4.20e-02	2.4
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: response to peptide (Página 1 de 5)

Fuente: GO:BP | ID: GO:1901652 | Genes: 110 | p-valor ruta: 1.51e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2

## Ruta: response to peptide (Página 2 de 5)

Fuente: GO:BP | ID: GO:1901652 | Genes: 110 | p-valor ruta: 1.51e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
XAF1	NA	UP	4.580	3.19e-111	427.9
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0

## Ruta: response to peptide (Página 3 de 5)

Fuente: GO:BP | ID: GO:1901652 | Genes: 110 | p-valor ruta: 1.51e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM21	NA	UP	2.221	1.14e-60	888.8
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
IL15RA	NA	UP	2.045	1.16e-42	847.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
MT2A	NA	UP	2.437	2.24e-35	363.0
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3

## Ruta: response to peptide (Página 4 de 5)

Fuente: GO:BP | ID: GO:1901652 | Genes: 110 | p-valor ruta: 1.51e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
PCK1	NA	UP	4.419	1.17e-12	29.6
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
DUOX1	NA	UP	3.131	5.18e-10	27.1
KMO	NA	UP	5.165	6.24e-09	19.5
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL10RA	NA	UP	3.172	3.66e-07	18.8
SELE	NA	UP	5.745	2.05e-05	9.0
IL18R1	NA	UP	2.088	8.75e-05	23.0
GFPT2	NA	UP	2.651	2.37e-04	12.7

## Ruta: response to peptide (Página 5 de 5)

Fuente: GO:BP | ID: GO:1901652 | Genes: 110 | p-valor ruta: 1.51e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
RUFY4	NA	UP	4.136	2.15e-03	6.0
GBP6	NA	UP	2.233	3.24e-03	11.2
CD70	NA	UP	3.257	1.21e-02	4.7
GBP7	NA	UP	4.177	1.61e-02	2.9
IL34	NA	UP	2.794	2.41e-02	4.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CCL17	NA	UP	3.441	3.89e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: response to cytokine (Página 1 de 5)

Fuente: GO:BP | ID: GO:0034097 | Genes: 109 | p-valor ruta: 2.38e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2

## Ruta: response to cytokine (Página 2 de 5)

Fuente: GO:BP | ID: GO:0034097 | Genes: 109 | p-valor ruta: 2.38e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
XAF1	NA	UP	4.580	3.19e-111	427.9
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0

## Ruta: response to cytokine (Página 3 de 5)

Fuente: GO:BP | ID: GO:0034097 | Genes: 109 | p-valor ruta: 2.38e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM21	NA	UP	2.221	1.14e-60	888.8
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
IL15RA	NA	UP	2.045	1.16e-42	847.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
MT2A	NA	UP	2.437	2.24e-35	363.0
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0

## Ruta: response to cytokine (Página 4 de 5)

Fuente: GO:BP | ID: GO:0034097 | Genes: 109 | p-valor ruta: 2.38e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
PCK1	NA	UP	4.419	1.17e-12	29.6
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
DUOX1	NA	UP	3.131	5.18e-10	27.1
KMO	NA	UP	5.165	6.24e-09	19.5
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL10RA	NA	UP	3.172	3.66e-07	18.8
SELE	NA	UP	5.745	2.05e-05	9.0
IL18R1	NA	UP	2.088	8.75e-05	23.0
GFPT2	NA	UP	2.651	2.37e-04	12.7
CXCL9	NA	UP	4.099	4.37e-04	26.3

## Ruta: response to cytokine (Página 5 de 5)

Fuente: GO:BP | ID: GO:0034097 | Genes: 109 | p-valor ruta: 2.38e-46

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KIT	NA	UP	3.650	6.24e-04	7.9
RUFY4	NA	UP	4.136	2.15e-03	6.0
GBP6	NA	UP	2.233	3.24e-03	11.2
CD70	NA	UP	3.257	1.21e-02	4.7
GBP7	NA	UP	4.177	1.61e-02	2.9
IL34	NA	UP	2.794	2.41e-02	4.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CCL17	NA	UP	3.441	3.89e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: defense response to other organism (Página 1 de 5)

Fuente: GO:BP | ID: GO:0098542 | Genes: 123 | p-valor ruta: 3.58e-45

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
IFI44L	NA	UP	4.088	1.50e-181	1679.8
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4

## Ruta: defense response to other organism (Página 2 de 5)

Fuente: GO:BP | ID: GO:0098542 | Genes: 123 | p-valor ruta: 3.58e-45

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3

## Ruta: defense response to other organism (Página 3 de 5)

Fuente: GO:BP | ID: GO:0098542 | Genes: 123 | p-valor ruta: 3.58e-45

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
NEURL3	NA	UP	2.464	1.53e-62	758.9
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1

## Ruta: defense response to other organism (Página 4 de 5)

Fuente: GO:BP | ID: GO:0098542 | Genes: 123 | p-valor ruta: 3.58e-45

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
PRDM1	NA	UP	3.525	5.98e-31	99.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
NLRP3	NA	UP	4.366	3.67e-13	29.8

## Ruta: defense response to other organism (Página 5 de 5)

Fuente: GO:BP | ID: GO:0098542 | Genes: 123 | p-valor ruta: 3.58e-45

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
WFDC5	NA	UP	5.168	1.07e-06	13.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
GBP6	NA	UP	2.233	3.24e-03	11.2
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
PRG2	NA	UP	2.073	1.32e-02	9.7
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SPRR2A	NA	UP	2.086	2.78e-02	7.8
CCL17	NA	UP	3.441	3.89e-02	2.9
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: defense response to symbiont (Página 1 de 5)

Fuente: GO:BP | ID: GO:0140546 | Genes: 112 | p-valor ruta: 3.9e-43

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5

## Ruta: defense response to symbiont (Página 2 de 5)

Fuente: GO:BP | ID: GO:0140546 | Genes: 112 | p-valor ruta: 3.9e-43

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8

## Ruta: defense response to symbiont (Página 3 de 5)

Fuente: GO:BP | ID: GO:0140546 | Genes: 112 | p-valor ruta: 3.9e-43

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
NEURL3	NA	UP	2.464	1.53e-62	758.9
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9

## Ruta: defense response to symbiont (Página 4 de 5)

Fuente: GO:BP | ID: GO:0140546 | Genes: 112 | p-valor ruta: 3.9e-43

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C1R	NA	UP	2.188	3.06e-32	258.8
PRDM1	NA	UP	3.525	5.98e-31	99.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
WFDC5	NA	UP	5.168	1.07e-06	13.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3

## Ruta: defense response to symbiont (Página 5 de 5)

Fuente: GO:BP | ID: GO:0140546 | Genes: 112 | p-valor ruta: 3.9e-43

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP6	NA	UP	2.233	3.24e-03	11.2
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SPRR2A	NA	UP	2.086	2.78e-02	7.8
CCL17	NA	UP	3.441	3.89e-02	2.9
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: cellular response to cytokine stimulus (Página 1 de 4)

Fuente: GO:BP | ID: GO:0071345 | Genes: 99 | p-valor ruta: 7.93e-42

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8

## Ruta: cellular response to cytokine stimulus (Página 2 de 4)

Fuente: GO:BP | ID: GO:0071345 | Genes: 99 | p-valor ruta: 7.93e-42

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9

## Ruta: cellular response to cytokine stimulus (Página 3 de 4)

Fuente: GO:BP | ID: GO:0071345 | Genes: 99 | p-valor ruta: 7.93e-42

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
MT2A	NA	UP	2.437	2.24e-35	363.0
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5

## Ruta: cellular response to cytokine stimulus (Página 4 de 4)

Fuente: GO:BP | ID: GO:0071345 | Genes: 99 | p-valor ruta: 7.93e-42

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
PCK1	NA	UP	4.419	1.17e-12	29.6
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
DUOX1	NA	UP	3.131	5.18e-10	27.1
KMO	NA	UP	5.165	6.24e-09	19.5
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL10RA	NA	UP	3.172	3.66e-07	18.8
IL18R1	NA	UP	2.088	8.75e-05	23.0
GFPT2	NA	UP	2.651	2.37e-04	12.7
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
RUFY4	NA	UP	4.136	2.15e-03	6.0
GBP6	NA	UP	2.233	3.24e-03	11.2
CD70	NA	UP	3.257	1.21e-02	4.7
GBP7	NA	UP	4.177	1.61e-02	2.9
IL34	NA	UP	2.794	2.41e-02	4.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CCL17	NA	UP	3.441	3.89e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: response to virus (Página 1 de 3)

Fuente: GO:BP | ID: GO:0009615 | Genes: 72 | p-valor ruta: 2.94e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
IFI44L	NA	UP	4.088	1.50e-181	1679.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
IFI16	NA	UP	3.151	2.12e-114	2583.4

## Ruta: response to virus (Página 2 de 3)

Fuente: GO:BP | ID: GO:0009615 | Genes: 72 | p-valor ruta: 2.94e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFI44	NA	UP	3.036	1.35e-108	3423.4
RTP4	NA	UP	3.457	2.00e-107	589.0
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFIT5	NA	UP	2.861	3.01e-78	749.8
PARP9	NA	UP	2.449	1.75e-75	2354.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1

## Ruta: response to virus (Página 3 de 3)

Fuente: GO:BP | ID: GO:0009615 | Genes: 72 | p-valor ruta: 2.94e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL22	NA	UP	3.454	2.91e-50	168.7
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: immune system process (Página 1 de 8)

Fuente: GO:BP | ID: GO:0002376 | Genes: 179 | p-valor ruta: 3.96e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
IFI44L	NA	UP	4.088	1.50e-181	1679.8
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3

## Ruta: immune system process (Página 2 de 8)

Fuente: GO:BP | ID: GO:0002376 | Genes: 179 | p-valor ruta: 3.96e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
IFI44	NA	UP	3.036	1.35e-108	3423.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6

## Ruta: immune system process (Página 3 de 8)

Fuente: GO:BP | ID: GO:0002376 | Genes: 179 | p-valor ruta: 3.96e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5

## Ruta: immune system process (Página 4 de 8)

Fuente: GO:BP | ID: GO:0002376 | Genes: 179 | p-valor ruta: 3.96e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0

## Ruta: immune system process (Página 5 de 8)

Fuente: GO:BP | ID: GO:0002376 | Genes: 179 | p-valor ruta: 3.96e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CH25H	NA	UP	7.817	1.04e-46	242.7
IL15RA	NA	UP	2.045	1.16e-42	847.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
C1R	NA	UP	2.188	3.06e-32	258.8
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
BACH2	NA	UP	2.222	2.18e-30	209.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2

## Ruta: immune system process (Página 6 de 8)

Fuente: GO:BP | ID: GO:0002376 | Genes: 179 | p-valor ruta: 3.96e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
ZBTB20	NA	UP	3.440	1.24e-15	47.6
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
WFDC5	NA	UP	5.168	1.07e-06	13.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
UBASH3A	NA	UP	5.845	1.05e-05	9.8
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7

## Ruta: immune system process (Página 7 de 8)

Fuente: GO:BP | ID: GO:0002376 | Genes: 179 | p-valor ruta: 3.96e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL18R1	NA	UP	2.088	8.75e-05	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
CEACAM20	NA	UP	5.412	1.17e-03	3.6
GBP6	NA	UP	2.233	3.24e-03	11.2
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
CD70	NA	UP	3.257	1.21e-02	4.7
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
OLR1	NA	UP	2.655	1.81e-02	6.9
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
SPRR2A	NA	UP	2.086	2.78e-02	7.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: immune system process (Página 8 de 8)

Fuente: GO:BP | ID: GO:0002376 | Genes: 179 | p-valor ruta: 3.96e-41

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CR1L	NA	UP	3.479	3.30e-02	3.5
CCL17	NA	UP	3.441	3.89e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: immune response (Página 1 de 6)

Fuente: GO:BP | ID: GO:0006955 | Genes: 150 | p-valor ruta: 1.49e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
IFI44L	NA	UP	4.088	1.50e-181	1679.8
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3

## Ruta: immune response (Página 2 de 6)

Fuente: GO:BP | ID: GO:0006955 | Genes: 150 | p-valor ruta: 1.49e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
IFI44	NA	UP	3.036	1.35e-108	3423.4
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8

## Ruta: immune response (Página 3 de 6)

Fuente: GO:BP | ID: GO:0006955 | Genes: 150 | p-valor ruta: 1.49e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
NEURL3	NA	UP	2.464	1.53e-62	758.9

## Ruta: immune response (Página 4 de 6)

Fuente: GO:BP | ID: GO:0006955 | Genes: 150 | p-valor ruta: 1.49e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
PRDM1	NA	UP	3.525	5.98e-31	99.0
BACH2	NA	UP	2.222	2.18e-30	209.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4

## Ruta: immune response (Página 5 de 6)

Fuente: GO:BP | ID: GO:0006955 | Genes: 150 | p-valor ruta: 1.49e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
WFDC5	NA	UP	5.168	1.07e-06	13.9

## Ruta: immune response (Página 6 de 6)

Fuente: GO:BP | ID: GO:0006955 | Genes: 150 | p-valor ruta: 1.49e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
GBP6	NA	UP	2.233	3.24e-03	11.2
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
CD70	NA	UP	3.257	1.21e-02	4.7
PRG2	NA	UP	2.073	1.32e-02	9.7
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SPRR2A	NA	UP	2.086	2.78e-02	7.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5
CCL17	NA	UP	3.441	3.89e-02	2.9
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: defense response to virus (Página 1 de 3)

Fuente: GO:BP | ID: GO:0051607 | Genes: 64 | p-valor ruta: 2.84e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
IFI44L	NA	UP	4.088	1.50e-181	1679.8
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
IFI16	NA	UP	3.151	2.12e-114	2583.4
RTP4	NA	UP	3.457	2.00e-107	589.0

## Ruta: defense response to virus (Página 2 de 3)

Fuente: GO:BP | ID: GO:0051607 | Genes: 64 | p-valor ruta: 2.84e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFIT5	NA	UP	2.861	3.01e-78	749.8
PARP9	NA	UP	2.449	1.75e-75	2354.5
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IFNL3	NA	UP	9.837	4.42e-30	365.0

## Ruta: defense response to virus (Página 3 de 3)

Fuente: GO:BP | ID: GO:0051607 | Genes: 64 | p-valor ruta: 2.84e-40

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: response to stress (Página 1 de 9)

Fuente: GO:BP | ID: GO:0006950 | Genes: 210 | p-valor ruta: 1.59e-39

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
IFI44L	NA	UP	4.088	1.50e-181	1679.8

## Ruta: response to stress (Página 2 de 9)

Fuente: GO:BP | ID: GO:0006950 | Genes: 210 | p-valor ruta: 1.59e-39

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
IDO1	NA	UP	4.167	4.38e-109	394.2
NUAK2	NA	UP	4.358	1.14e-107	489.1
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5

## Ruta: response to stress (Página 3 de 9)

Fuente: GO:BP | ID: GO:0006950 | Genes: 210 | p-valor ruta: 1.59e-39

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0

## Ruta: response to stress (Página 4 de 9)

Fuente: GO:BP | ID: GO:0006950 | Genes: 210 | p-valor ruta: 1.59e-39

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
JUN	NA	UP	2.450	1.10e-62	6693.5
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8

## Ruta: response to stress (Página 5 de 9)

Fuente: GO:BP | ID: GO:0006950 | Genes: 210 | p-valor ruta: 1.59e-39

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
PER1	NA	UP	2.501	8.94e-44	469.6
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4

## Ruta: response to stress (Página 6 de 9)

Fuente: GO:BP | ID: GO:0006950 | Genes: 210 | p-valor ruta: 1.59e-39

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
MT2A	NA	UP	2.437	2.24e-35	363.0
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
DUOXA2	NA	UP	4.650	3.36e-16	39.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1

## Ruta: response to stress (Página 7 de 9)

Fuente: GO:BP | ID: GO:0006950 | Genes: 210 | p-valor ruta: 1.59e-39

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
SCN3A	NA	UP	8.277	2.66e-10	27.0
DUOX1	NA	UP	3.131	5.18e-10	27.1
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
KMO	NA	UP	5.165	6.24e-09	19.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
RBM11	NA	UP	2.506	8.83e-07	22.9
SAA4	NA	UP	2.563	9.46e-07	21.9
WFDC5	NA	UP	5.168	1.07e-06	13.9
NUPR1	NA	UP	3.660	1.78e-06	14.5
SERPINA10	NA	UP	6.459	9.50e-06	7.5
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
FFAR2	NA	UP	3.253	4.81e-05	12.7

## Ruta: response to stress (Página 8 de 9)

Fuente: GO:BP | ID: GO:0006950 | Genes: 210 | p-valor ruta: 1.59e-39

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL18R1	NA	UP	2.088	8.75e-05	23.0
PTGER2	NA	UP	3.006	1.95e-04	11.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
RNF152	NA	UP	3.325	1.37e-03	7.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
IL17C	NA	UP	4.636	3.13e-03	4.1
GBP6	NA	UP	2.233	3.24e-03	11.2
IPCEF1	NA	UP	4.035	3.69e-03	4.9
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
VWF	NA	UP	3.390	1.16e-02	4.6
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
OLR1	NA	UP	2.655	1.81e-02	6.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1

## Ruta: response to stress (Página 9 de 9)

Fuente: GO:BP | ID: GO:0006950 | Genes: 210 | p-valor ruta: 1.59e-39

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
SPRR2A	NA	UP	2.086	2.78e-02	7.8
CCL17	NA	UP	3.441	3.89e-02	2.9
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: innate immune response (Página 1 de 5)

Fuente: GO:BP | ID: GO:0045087 | Genes: 101 | p-valor ruta: 5.61e-38

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
GBP4	NA	UP	4.422	6.95e-185	1175.0
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0

## Ruta: innate immune response (Página 2 de 5)

Fuente: GO:BP | ID: GO:0045087 | Genes: 101 | p-valor ruta: 5.61e-38

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRK5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3

## Ruta: innate immune response (Página 3 de 5)

Fuente: GO:BP | ID: GO:0045087 | Genes: 101 | p-valor ruta: 5.61e-38

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
NEURL3	NA	UP	2.464	1.53e-62	758.9
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
PRDM1	NA	UP	3.525	5.98e-31	99.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5

## Ruta: innate immune response (Página 4 de 5)

Fuente: GO:BP | ID: GO:0045087 | Genes: 101 | p-valor ruta: 5.61e-38

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
WFDC5	NA	UP	5.168	1.07e-06	13.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
GBP6	NA	UP	2.233	3.24e-03	11.2
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: innate immune response (Página 5 de 5)

Fuente: GO:BP | ID: GO:0045087 | Genes: 101 | p-valor ruta: 5.61e-38

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SRMS	NA	UP	3.88	4.55e-02	2.3

## Ruta: regulation of immune system process (Página 1 de 5)

Fuente: GO:BP | ID: GO:0002682 | Genes: 121 | p-valor ruta: 1.63e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1

## Ruta: regulation of immune system process (Página 2 de 5)

Fuente: GO:BP | ID: GO:0002682 | Genes: 121 | p-valor ruta: 1.63e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6

## Ruta: regulation of immune system process (Página 3 de 5)

Fuente: GO:BP | ID: GO:0002682 | Genes: 121 | p-valor ruta: 1.63e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
C1R	NA	UP	2.188	3.06e-32	258.8
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5

## Ruta: regulation of immune system process (Página 4 de 5)

Fuente: GO:BP | ID: GO:0002682 | Genes: 121 | p-valor ruta: 1.63e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5

## Ruta: regulation of immune system process (Página 5 de 5)

Fuente: GO:BP | ID: GO:0002682 | Genes: 121 | p-valor ruta: 1.63e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
UBASH3A	NA	UP	5.845	1.05e-05	9.8
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
CEACAM20	NA	UP	5.412	1.17e-03	3.6
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
CD70	NA	UP	3.257	1.21e-02	4.7
PRG2	NA	UP	2.073	1.32e-02	9.7
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: response to stimulus (Página 1 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL3	NA	UP	3.053	2.27e-187	4330.7

## Ruta: response to stimulus (Página 2 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP4	NA	UP	4.422	6.95e-185	1175.0
IFI44L	NA	UP	4.088	1.50e-181	1679.8
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
CMPK2	NA	UP	4.677	1.14e-162	1687.4
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1

## Ruta: response to stimulus (Página 3 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
IFI44	NA	UP	3.036	1.35e-108	3423.4
NUAK2	NA	UP	4.358	1.14e-107	489.1
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0

## Ruta: response to stimulus (Página 4 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
RASGRP3	NA	UP	3.468	2.92e-82	392.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
HSH2D	NA	UP	2.613	6.29e-73	813.8

## Ruta: response to stimulus (Página 5 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
NEURL3	NA	UP	2.464	1.53e-62	758.9
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9

## Ruta: response to stimulus (Página 6 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TUFT1	NA	UP	2.001	1.00e-55	1905.9
FOSB	NA	UP	3.144	1.32e-55	267.7
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2

## Ruta: response to stimulus (Página 7 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
MT2A	NA	UP	2.437	2.24e-35	363.0
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
C1R	NA	UP	2.188	3.06e-32	258.8
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
BACH2	NA	UP	2.222	2.18e-30	209.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
BCL2L14	NA	UP	2.782	8.63e-26	122.3
MAST4	NA	UP	2.184	1.21e-25	197.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7

## Ruta: response to stimulus (Página 8 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
DEPDC7	NA	UP	2.115	7.88e-19	114.2
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
DDC	NA	DOWN	-2.582	2.27e-16	72.0
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
INHBE	NA	UP	5.109	1.59e-15	37.3
RAET1L	NA	UP	2.665	2.71e-15	60.0
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7

## Ruta: response to stimulus (Página 9 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PLEKHG7	NA	UP	3.625	2.08e-12	31.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SCN3A	NA	UP	8.277	2.66e-10	27.0
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9

## Ruta: response to stimulus (Página 10 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RBM11	NA	UP	2.506	8.83e-07	22.9
SAA4	NA	UP	2.563	9.46e-07	21.9
WFDC5	NA	UP	5.168	1.07e-06	13.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
TAGAP	NA	UP	3.201	2.52e-06	16.1
RAB30	NA	UP	2.024	5.27e-06	28.7
COL4A1	NA	UP	6.589	5.89e-06	8.2
ADCY4	NA	UP	2.271	8.12e-06	23.6
BEST1	NA	UP	3.553	8.47e-06	13.3
MMP13	NA	UP	5.406	9.23e-06	11.1
SERPINA10	NA	UP	6.459	9.50e-06	7.5
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: response to stimulus (Página 11 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
PTGER2	NA	UP	3.006	1.95e-04	11.0
GFPT2	NA	UP	2.651	2.37e-04	12.7
EGR3	NA	UP	2.096	2.87e-04	21.5
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
RNF152	NA	UP	3.325	1.37e-03	7.5
LHB	NA	UP	3.522	1.50e-03	7.0
SLC1A2	NA	UP	2.752	2.07e-03	8.4
RUFY4	NA	UP	4.136	2.15e-03	6.0
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
IL17C	NA	UP	4.636	3.13e-03	4.1
GBP6	NA	UP	2.233	3.24e-03	11.2

## Ruta: response to stimulus (Página 12 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IPCEF1	NA	UP	4.035	3.69e-03	4.9
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
OLR1	NA	UP	2.655	1.81e-02	6.9
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: response to stimulus (Página 13 de 13)

Fuente: GO:BP | ID: GO:0050896 | Genes: 322 | p-valor ruta: 2.6e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
SPRR2A	NA	UP	2.086	2.78e-02	7.8
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
CR1L	NA	UP	3.479	3.30e-02	3.5
DLG2	NA	UP	3.028	3.83e-02	3.8
CCL17	NA	UP	3.441	3.89e-02	2.9
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
PPM1E	NA	UP	3.810	4.20e-02	2.4
PPEF1	NA	UP	3.725	4.31e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of response to stimulus (Página 1 de 8)

Fuente: GO:BP | ID: GO:0048583 | Genes: 199 | p-valor ruta: 2.03e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7

## Ruta: regulation of response to stimulus (Página 2 de 8)

Fuente: GO:BP | ID: GO:0048583 | Genes: 199 | p-valor ruta: 2.03e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2

## Ruta: regulation of response to stimulus (Página 3 de 8)

Fuente: GO:BP | ID: GO:0048583 | Genes: 199 | p-valor ruta: 2.03e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1

## Ruta: regulation of response to stimulus (Página 4 de 8)

Fuente: GO:BP | ID: GO:0048583 | Genes: 199 | p-valor ruta: 2.03e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2

## Ruta: regulation of response to stimulus (Página 5 de 8)

Fuente: GO:BP | ID: GO:0048583 | Genes: 199 | p-valor ruta: 2.03e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
C1R	NA	UP	2.188	3.06e-32	258.8
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
IFNL2	NA	UP	11.372	1.86e-23	434.7
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8

## Ruta: regulation of response to stimulus (Página 6 de 8)

Fuente: GO:BP | ID: GO:0048583 | Genes: 199 | p-valor ruta: 2.03e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7
RAET1L	NA	UP	2.665	2.71e-15	60.0
BDKRB2	NA	UP	2.797	5.56e-15	55.1
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0

## Ruta: regulation of response to stimulus (Página 7 de 8)

Fuente: GO:BP | ID: GO:0048583 | Genes: 199 | p-valor ruta: 2.03e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
TAGAP	NA	UP	3.201	2.52e-06	16.1
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
RBMS3	NA	UP	2.303	4.11e-04	18.6
KIT	NA	UP	3.650	6.24e-04	7.9
RNF152	NA	UP	3.325	1.37e-03	7.5
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: regulation of response to stimulus (Página 8 de 8)

Fuente: GO:BP | ID: GO:0048583 | Genes: 199 | p-valor ruta: 2.03e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
SALL1	NA	UP	4.345	3.20e-02	1.8
CR1L	NA	UP	3.479	3.30e-02	3.5
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of response to external stimulus (Página 1 de 4)

Fuente: GO:BP | ID: GO:0032101 | Genes: 98 | p-valor ruta: 4.72e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0

## Ruta: regulation of response to external stimulus (Página 2 de 4)

Fuente: GO:BP | ID: GO:0032101 | Genes: 98 | p-valor ruta: 4.72e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6

## Ruta: regulation of response to external stimulus (Página 3 de 4)

Fuente: GO:BP | ID: GO:0032101 | Genes: 98 | p-valor ruta: 4.72e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
RASGRP1	NA	UP	2.055	4.16e-34	336.9
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7

## Ruta: regulation of response to external stimulus (Página 4 de 4)

Fuente: GO:BP | ID: GO:0032101 | Genes: 98 | p-valor ruta: 4.72e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
THBD	NA	UP	2.330	1.23e-02	7.3
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: positive regulation of response to stimulus (Página 1 de 6)

Fuente: GO:BP | ID: GO:0048584 | Genes: 146 | p-valor ruta: 7.74e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5

## Ruta: positive regulation of response to stimulus (Página 2 de 6)

Fuente: GO:BP | ID: GO:0048584 | Genes: 146 | p-valor ruta: 7.74e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3

## Ruta: positive regulation of response to stimulus (Página 3 de 6)

Fuente: GO:BP | ID: GO:0048584 | Genes: 146 | p-valor ruta: 7.74e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2

## Ruta: positive regulation of response to stimulus (Página 4 de 6)

Fuente: GO:BP | ID: GO:0048584 | Genes: 146 | p-valor ruta: 7.74e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
C1R	NA	UP	2.188	3.06e-32	258.8
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL2L14	NA	UP	2.782	8.63e-26	122.3
IFNL2	NA	UP	11.372	1.86e-23	434.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
RAET1L	NA	UP	2.665	2.71e-15	60.0

## Ruta: positive regulation of response to stimulus (Página 5 de 6)

Fuente: GO:BP | ID: GO:0048584 | Genes: 146 | p-valor ruta: 7.74e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
DUOX1	NA	UP	3.131	5.18e-10	27.1
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
UBASH3A	NA	UP	5.845	1.05e-05	9.8
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4

## Ruta: positive regulation of response to stimulus (Página 6 de 6)

Fuente: GO:BP | ID: GO:0048584 | Genes: 146 | p-valor ruta: 7.74e-32

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
SALL1	NA	UP	4.345	3.20e-02	1.8
CR1L	NA	UP	3.479	3.30e-02	3.5
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: response to bacterium (Página 1 de 4)

Fuente: GO:BP | ID: GO:0009617 | Genes: 80 | p-valor ruta: 3.23e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
CXCL11	NA	UP	6.074	5.51e-176	710.1
CMPK2	NA	UP	4.677	1.14e-162	1687.4
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
IFI44	NA	UP	3.036	1.35e-108	3423.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6

## Ruta: response to bacterium (Página 2 de 4)

Fuente: GO:BP | ID: GO:0009617 | Genes: 80 | p-valor ruta: 3.23e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
IRAK2	NA	UP	2.666	3.46e-95	1164.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
ISG15	NA	UP	2.482	5.90e-57	3807.9
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4

## Ruta: response to bacterium (Página 3 de 4)

Fuente: GO:BP | ID: GO:0009617 | Genes: 80 | p-valor ruta: 3.23e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
KMO	NA	UP	5.165	6.24e-09	19.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
WFDC5	NA	UP	5.168	1.07e-06	13.9
SELE	NA	UP	5.745	2.05e-05	9.0
PTGER2	NA	UP	3.006	1.95e-04	11.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
CEACAM20	NA	UP	5.412	1.17e-03	3.6
GBP6	NA	UP	2.233	3.24e-03	11.2
LY96	NA	UP	5.204	4.42e-03	3.4
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: response to bacterium (Página 4 de 4)

Fuente: GO:BP | ID: GO:0009617 | Genes: 80 | p-valor ruta: 3.23e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PRG2	NA	UP	2.073	1.32e-02	9.7
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
SPRR2A	NA	UP	2.086	2.78e-02	7.8
PPM1E	NA	UP	3.810	4.20e-02	2.4

## Ruta: cytokine-mediated signaling pathway (Página 1 de 3)

Fuente: GO:BP | ID: GO:0019221 | Genes: 68 | p-valor ruta: 9.04e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5

## Ruta: cytokine-mediated signaling pathway (Página 2 de 3)

Fuente: GO:BP | ID: GO:0019221 | Genes: 68 | p-valor ruta: 9.04e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
STAT1	NA	UP	2.519	1.61e-68	9528.0
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: cytokine-mediated signaling pathway (Página 3 de 3)

Fuente: GO:BP | ID: GO:0019221 | Genes: 68 | p-valor ruta: 9.04e-31

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IFITM2	NA	UP	2.649	6.22e-17	64.2
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
DUOX1	NA	UP	3.131	5.18e-10	27.1
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL10RA	NA	UP	3.172	3.66e-07	18.8
IL18R1	NA	UP	2.088	8.75e-05	23.0
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
CD70	NA	UP	3.257	1.21e-02	4.7
IL34	NA	UP	2.794	2.41e-02	4.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: response to chemical (Página 1 de 8)

Fuente: GO:BP | ID: GO:0042221 | Genes: 192 | p-valor ruta: 6.28e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
CMPK2	NA	UP	4.677	1.14e-162	1687.4
DUSP1	NA	UP	3.521	2.54e-161	1829.2

## Ruta: response to chemical (Página 2 de 8)

Fuente: GO:BP | ID: GO:0042221 | Genes: 192 | p-valor ruta: 6.28e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7

## Ruta: response to chemical (Página 3 de 8)

Fuente: GO:BP | ID: GO:0042221 | Genes: 192 | p-valor ruta: 6.28e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1

## Ruta: response to chemical (Página 4 de 8)

Fuente: GO:BP | ID: GO:0042221 | Genes: 192 | p-valor ruta: 6.28e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
FOSB	NA	UP	3.144	1.32e-55	267.7
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
MT2A	NA	UP	2.437	2.24e-35	363.0

## Ruta: response to chemical (Página 5 de 8)

Fuente: GO:BP | ID: GO:0042221 | Genes: 192 | p-valor ruta: 6.28e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
DDC	NA	DOWN	-2.582	2.27e-16	72.0
ZBTB20	NA	UP	3.440	1.24e-15	47.6
BDKRB2	NA	UP	2.797	5.56e-15	55.1

## Ruta: response to chemical (Página 6 de 8)

Fuente: GO:BP | ID: GO:0042221 | Genes: 192 | p-valor ruta: 6.28e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
COL4A1	NA	UP	6.589	5.89e-06	8.2

## Ruta: response to chemical (Página 7 de 8)

Fuente: GO:BP | ID: GO:0042221 | Genes: 192 | p-valor ruta: 6.28e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
MMP13	NA	UP	5.406	9.23e-06	11.1
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
NPTX1	NA	UP	2.102	1.13e-04	22.3
PTGER2	NA	UP	3.006	1.95e-04	11.0
GFPT2	NA	UP	2.651	2.37e-04	12.7
EGR3	NA	UP	2.096	2.87e-04	21.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
LHB	NA	UP	3.522	1.50e-03	7.0
SLC1A2	NA	UP	2.752	2.07e-03	8.4
RUFY4	NA	UP	4.136	2.15e-03	6.0
LGR6	NA	UP	3.915	2.25e-03	6.0
GBP6	NA	UP	2.233	3.24e-03	11.2
IPCEF1	NA	UP	4.035	3.69e-03	4.9
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
CD70	NA	UP	3.257	1.21e-02	4.7

## Ruta: response to chemical (Página 8 de 8)

Fuente: GO:BP | ID: GO:0042221 | Genes: 192 | p-valor ruta: 6.28e-30

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
THBD	NA	UP	2.330	1.23e-02	7.3
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
IL13RA2	NA	UP	2.568	3.02e-02	4.7
DLG2	NA	UP	3.028	3.83e-02	3.8
CCL17	NA	UP	3.441	3.89e-02	2.9
TP63	NA	UP	3.788	4.09e-02	2.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: cell communication (Página 1 de 11)

Fuente: GO:BP | ID: GO:0007154 | Genes: 260 | p-valor ruta: 1.59e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6

## Ruta: cell communication (Página 2 de 11)

Fuente: GO:BP | ID: GO:0007154 | Genes: 260 | p-valor ruta: 1.59e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8

## Ruta: cell communication (Página 3 de 11)

Fuente: GO:BP | ID: GO:0007154 | Genes: 260 | p-valor ruta: 1.59e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
RASGRP3	NA	UP	3.468	2.92e-82	392.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1

## Ruta: cell communication (Página 4 de 11)

Fuente: GO:BP | ID: GO:0007154 | Genes: 260 | p-valor ruta: 1.59e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HSH2D	NA	UP	2.613	6.29e-73	813.8
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TUFT1	NA	UP	2.001	1.00e-55	1905.9

## Ruta: cell communication (Página 5 de 11)

Fuente: GO:BP | ID: GO:0007154 | Genes: 260 | p-valor ruta: 1.59e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8

## Ruta: cell communication (Página 6 de 11)

Fuente: GO:BP | ID: GO:0007154 | Genes: 260 | p-valor ruta: 1.59e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
BCL2L14	NA	UP	2.782	8.63e-26	122.3
MAST4	NA	UP	2.184	1.21e-25	197.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
DDO	NA	UP	2.846	3.84e-20	82.4
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
DEPDC7	NA	UP	2.115	7.88e-19	114.2
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: cell communication (Página 7 de 11)

Fuente: GO:BP | ID: GO:0007154 | Genes: 260 | p-valor ruta: 1.59e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
INHBE	NA	UP	5.109	1.59e-15	37.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PLEKHG7	NA	UP	3.625	2.08e-12	31.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
STX19	NA	UP	2.009	1.09e-08	99.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0

## Ruta: cell communication (Página 8 de 11)

Fuente: GO:BP | ID: GO:0007154 | Genes: 260 | p-valor ruta: 1.59e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
TAGAP	NA	UP	3.201	2.52e-06	16.1
RAB30	NA	UP	2.024	5.27e-06	28.7
COL4A1	NA	UP	6.589	5.89e-06	8.2
ADCY4	NA	UP	2.271	8.12e-06	23.6
BEST1	NA	UP	3.553	8.47e-06	13.3
UBASH3A	NA	UP	5.845	1.05e-05	9.8
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
PTGER2	NA	UP	3.006	1.95e-04	11.0
EGR3	NA	UP	2.096	2.87e-04	21.5

## Ruta: cell communication (Página 9 de 11)

Fuente: GO:BP | ID: GO:0007154 | Genes: 260 | p-valor ruta: 1.59e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
MPZ	NA	UP	2.002	2.88e-04	19.4
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
GAL3ST4	NA	UP	2.371	7.40e-04	12.5
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6
RNF152	NA	UP	3.325	1.37e-03	7.5
LHB	NA	UP	3.522	1.50e-03	7.0
SLC1A2	NA	UP	2.752	2.07e-03	8.4
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0
KCNN1	NA	UP	3.883	2.55e-03	6.2
IL17C	NA	UP	4.636	3.13e-03	4.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8

## Ruta: cell communication (Página 10 de 11)

Fuente: GO:BP | ID: GO:0007154 | Genes: 260 | p-valor ruta: 1.59e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RP1L1	NA	UP	2.162	5.43e-03	10.3
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0

## Ruta: cell communication (Página 11 de 11)

Fuente: GO:BP | ID: GO:0007154 | Genes: 260 | p-valor ruta: 1.59e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
DLG2	NA	UP	3.028	3.83e-02	3.8
CCL17	NA	UP	3.441	3.89e-02	2.9
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: signaling (Página 1 de 11)

Fuente: GO:BP | ID: GO:0023052 | Genes: 259 | p-valor ruta: 2.53e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6

## Ruta: signaling (Página 2 de 11)

Fuente: GO:BP | ID: GO:0023052 | Genes: 259 | p-valor ruta: 2.53e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8

## Ruta: signaling (Página 3 de 11)

Fuente: GO:BP | ID: GO:0023052 | Genes: 259 | p-valor ruta: 2.53e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
RASGRP3	NA	UP	3.468	2.92e-82	392.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1

## Ruta: signaling (Página 4 de 11)

Fuente: GO:BP | ID: GO:0023052 | Genes: 259 | p-valor ruta: 2.53e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HSH2D	NA	UP	2.613	6.29e-73	813.8
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TUFT1	NA	UP	2.001	1.00e-55	1905.9

## Ruta: signaling (Página 5 de 11)

Fuente: GO:BP | ID: GO:0023052 | Genes: 259 | p-valor ruta: 2.53e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8

## Ruta: signaling (Página 6 de 11)

Fuente: GO:BP | ID: GO:0023052 | Genes: 259 | p-valor ruta: 2.53e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
BCL2L14	NA	UP	2.782	8.63e-26	122.3
MAST4	NA	UP	2.184	1.21e-25	197.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
DEPDC7	NA	UP	2.115	7.88e-19	114.2
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3

## Ruta: signaling (Página 7 de 11)

Fuente: GO:BP | ID: GO:0023052 | Genes: 259 | p-valor ruta: 2.53e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
INHBE	NA	UP	5.109	1.59e-15	37.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PLEKHG7	NA	UP	3.625	2.08e-12	31.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
STX19	NA	UP	2.009	1.09e-08	99.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5

## Ruta: signaling (Página 8 de 11)

Fuente: GO:BP | ID: GO:0023052 | Genes: 259 | p-valor ruta: 2.53e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
TAGAP	NA	UP	3.201	2.52e-06	16.1
RAB30	NA	UP	2.024	5.27e-06	28.7
COL4A1	NA	UP	6.589	5.89e-06	8.2
ADCY4	NA	UP	2.271	8.12e-06	23.6
BEST1	NA	UP	3.553	8.47e-06	13.3
UBASH3A	NA	UP	5.845	1.05e-05	9.8
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
PTGER2	NA	UP	3.006	1.95e-04	11.0
EGR3	NA	UP	2.096	2.87e-04	21.5
MPZ	NA	UP	2.002	2.88e-04	19.4

## Ruta: signaling (Página 9 de 11)

Fuente: GO:BP | ID: GO:0023052 | Genes: 259 | p-valor ruta: 2.53e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
GAL3ST4	NA	UP	2.371	7.40e-04	12.5
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6
RNF152	NA	UP	3.325	1.37e-03	7.5
LHB	NA	UP	3.522	1.50e-03	7.0
SLC1A2	NA	UP	2.752	2.07e-03	8.4
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0
KCNN1	NA	UP	3.883	2.55e-03	6.2
IL17C	NA	UP	4.636	3.13e-03	4.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3

## Ruta: signaling (Página 10 de 11)

Fuente: GO:BP | ID: GO:0023052 | Genes: 259 | p-valor ruta: 2.53e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: signaling (Página 11 de 11)

Fuente: GO:BP | ID: GO:0023052 | Genes: 259 | p-valor ruta: 2.53e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SALL1	NA	UP	4.345	3.20e-02	1.8
DLG2	NA	UP	3.028	3.83e-02	3.8
CCL17	NA	UP	3.441	3.89e-02	2.9
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of cytokine production (Página 1 de 4)

Fuente: GO:BP | ID: GO:0001817 | Genes: 80 | p-valor ruta: 4.73e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1

## Ruta: regulation of cytokine production (Página 2 de 4)

Fuente: GO:BP | ID: GO:0001817 | Genes: 80 | p-valor ruta: 4.73e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
LTB	NA	UP	3.555	2.50e-41	150.4
HDAC9	NA	UP	2.292	4.51e-32	2003.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5

## Ruta: regulation of cytokine production (Página 3 de 4)

Fuente: GO:BP | ID: GO:0001817 | Genes: 80 | p-valor ruta: 4.73e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
CEACAM20	NA	UP	5.412	1.17e-03	3.6
SRGN	NA	UP	2.093	3.80e-03	11.0
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4

## Ruta: regulation of cytokine production (Página 4 de 4)

Fuente: GO:BP | ID: GO:0001817 | Genes: 80 | p-valor ruta: 4.73e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PRG2	NA	UP	2.073	1.32e-02	9.7
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: cytokine production (Página 1 de 4)

Fuente: GO:BP | ID: GO:0001816 | Genes: 80 | p-valor ruta: 8.09e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1

## Ruta: cytokine production (Página 2 de 4)

Fuente: GO:BP | ID: GO:0001816 | Genes: 80 | p-valor ruta: 8.09e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
LTB	NA	UP	3.555	2.50e-41	150.4
HDAC9	NA	UP	2.292	4.51e-32	2003.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5

## Ruta: cytokine production (Página 3 de 4)

Fuente: GO:BP | ID: GO:0001816 | Genes: 80 | p-valor ruta: 8.09e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
CEACAM20	NA	UP	5.412	1.17e-03	3.6
SRGN	NA	UP	2.093	3.80e-03	11.0
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4

## Ruta: cytokine production (Página 4 de 4)

Fuente: GO:BP | ID: GO:0001816 | Genes: 80 | p-valor ruta: 8.09e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PRG2	NA	UP	2.073	1.32e-02	9.7
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: cell surface receptor signaling pathway (Página 1 de 7)

Fuente: GO:BP | ID: GO:0007166 | Genes: 157 | p-valor ruta: 8.23e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4

## Ruta: cell surface receptor signaling pathway (Página 2 de 7)

Fuente: GO:BP | ID: GO:0007166 | Genes: 157 | p-valor ruta: 8.23e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
IFI35	NA	UP	2.237	9.59e-79	2236.7

## Ruta: cell surface receptor signaling pathway (Página 3 de 7)

Fuente: GO:BP | ID: GO:0007166 | Genes: 157 | p-valor ruta: 8.23e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9

## Ruta: cell surface receptor signaling pathway (Página 4 de 7)

Fuente: GO:BP | ID: GO:0007166 | Genes: 157 | p-valor ruta: 8.23e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
HIVEP1	NA	UP	2.014	1.06e-24	282.1
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2

## Ruta: cell surface receptor signaling pathway (Página 5 de 7)

Fuente: GO:BP | ID: GO:0007166 | Genes: 157 | p-valor ruta: 8.23e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IFITM2	NA	UP	2.649	6.22e-17	64.2
BDKRB2	NA	UP	2.797	5.56e-15	55.1
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
DUOX1	NA	UP	3.131	5.18e-10	27.1
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
RUNX2	NA	UP	3.983	1.50e-06	15.2
COL4A1	NA	UP	6.589	5.89e-06	8.2
UBASH3A	NA	UP	5.845	1.05e-05	9.8
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
COLEC10	NA	UP	2.878	4.02e-04	11.6

## Ruta: cell surface receptor signaling pathway (Página 6 de 7)

Fuente: GO:BP | ID: GO:0007166 | Genes: 157 | p-valor ruta: 8.23e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
FLRT1	NA	UP	5.509	1.11e-03	3.8
LGR6	NA	UP	3.915	2.25e-03	6.0
IL17C	NA	UP	4.636	3.13e-03	4.1
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
CD70	NA	UP	3.257	1.21e-02	4.7
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
GLP2R	NA	UP	2.220	1.86e-02	8.9
ALPK2	NA	UP	3.025	2.06e-02	4.7
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: cell surface receptor signaling pathway (Página 7 de 7)

Fuente: GO:BP | ID: GO:0007166 | Genes: 157 | p-valor ruta: 8.23e-29

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SALL1	NA	UP	4.345	3.20e-02	1.8
CCL17	NA	UP	3.441	3.89e-02	2.9
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: positive regulation of immune system process (Página 1 de 4)

Fuente: GO:BP | ID: GO:0002684 | Genes: 94 | p-valor ruta: 1.45e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8

## Ruta: positive regulation of immune system process (Página 2 de 4)

Fuente: GO:BP | ID: GO:0002684 | Genes: 94 | p-valor ruta: 1.45e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9

## Ruta: positive regulation of immune system process (Página 3 de 4)

Fuente: GO:BP | ID: GO:0002684 | Genes: 94 | p-valor ruta: 1.45e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
C1R	NA	UP	2.188	3.06e-32	258.8
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2

## Ruta: positive regulation of immune system process (Página 4 de 4)

Fuente: GO:BP | ID: GO:0002684 | Genes: 94 | p-valor ruta: 1.45e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
TNFSF14	NA	UP	2.748	3.71e-07	23.0
UBASH3A	NA	UP	5.845	1.05e-05	9.8
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: regulation of multicellular organismal process (Página 1 de 7)

Fuente: GO:BP | ID: GO:0051239 | Genes: 160 | p-valor ruta: 4.53e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5

## Ruta: regulation of multicellular organismal process (Página 2 de 7)

Fuente: GO:BP | ID: GO:0051239 | Genes: 160 | p-valor ruta: 4.53e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5

## Ruta: regulation of multicellular organismal process (Página 3 de 7)

Fuente: GO:BP | ID: GO:0051239 | Genes: 160 | p-valor ruta: 4.53e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2

## Ruta: regulation of multicellular organismal process (Página 4 de 7)

Fuente: GO:BP | ID: GO:0051239 | Genes: 160 | p-valor ruta: 4.53e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1

## Ruta: regulation of multicellular organismal process (Página 5 de 7)

Fuente: GO:BP | ID: GO:0051239 | Genes: 160 | p-valor ruta: 4.53e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: regulation of multicellular organismal process (Página 6 de 7)

Fuente: GO:BP | ID: GO:0051239 | Genes: 160 | p-valor ruta: 4.53e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
CEACAM20	NA	UP	5.412	1.17e-03	3.6
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
POU3F2	NA	UP	4.735	2.02e-03	4.5
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
BMPER	NA	UP	4.906	6.28e-03	2.6
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7

## Ruta: regulation of multicellular organismal process (Página 7 de 7)

Fuente: GO:BP | ID: GO:0051239 | Genes: 160 | p-valor ruta: 4.53e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
KCNE4	NA	UP	2.337	3.37e-02	5.7
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of defense response (Página 1 de 4)

Fuente: GO:BP | ID: GO:0031347 | Genes: 80 | p-valor ruta: 5.55e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4

## Ruta: regulation of defense response (Página 2 de 4)

Fuente: GO:BP | ID: GO:0031347 | Genes: 80 | p-valor ruta: 5.55e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
MAP3K8	NA	UP	2.825	4.57e-78	640.1
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8

## Ruta: regulation of defense response (Página 3 de 4)

Fuente: GO:BP | ID: GO:0031347 | Genes: 80 | p-valor ruta: 5.55e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
NUPR1	NA	UP	3.660	1.78e-06	14.5
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7

## Ruta: regulation of defense response (Página 4 de 4)

Fuente: GO:BP | ID: GO:0031347 | Genes: 80 | p-valor ruta: 5.55e-28

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
COLEC10	NA	UP	2.878	4.02e-04	11.6
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: negative regulation of viral process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0048525 | Genes: 31 | p-valor ruta: 2.37e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
MX1	NA	UP	3.859	1.25e-245	5699.6
IFIH1	NA	UP	4.035	2.22e-233	4525.3
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
OAS3	NA	UP	2.942	1.13e-87	8674.1
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFIT5	NA	UP	2.861	3.01e-78	749.8
STAT1	NA	UP	2.519	1.61e-68	9528.0
PTX3	NA	UP	3.614	2.25e-68	237.4
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7

## Ruta: negative regulation of viral process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0048525 | Genes: 31 | p-valor ruta: 2.37e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
BST2	NA	UP	4.284	3.82e-19	50.8
IFITM2	NA	UP	2.649	6.22e-17	64.2
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: inflammatory response (Página 1 de 4)

Fuente: GO:BP | ID: GO:0006954 | Genes: 81 | p-valor ruta: 7.87e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
IRAK2	NA	UP	2.666	3.46e-95	1164.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IFI35	NA	UP	2.237	9.59e-79	2236.7

## Ruta: inflammatory response (Página 2 de 4)

Fuente: GO:BP | ID: GO:0006954 | Genes: 81 | p-valor ruta: 7.87e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM21	NA	UP	2.221	1.14e-60	888.8
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
VCAM1	NA	UP	4.737	4.28e-26	66.5
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2

## Ruta: inflammatory response (Página 3 de 4)

Fuente: GO:BP | ID: GO:0006954 | Genes: 81 | p-valor ruta: 7.87e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
SAA4	NA	UP	2.563	9.46e-07	21.9
NUPR1	NA	UP	3.660	1.78e-06	14.5
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PTGER2	NA	UP	3.006	1.95e-04	11.0
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
IL17C	NA	UP	4.636	3.13e-03	4.1
LY96	NA	UP	5.204	4.42e-03	3.4
SCUBE1	NA	UP	2.508	1.26e-02	8.4

## Ruta: inflammatory response (Página 4 de 4)

Fuente: GO:BP | ID: GO:0006954 | Genes: 81 | p-valor ruta: 7.87e-27

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C3AR1	NA	UP	4.639	1.59e-02	2.2
OLR1	NA	UP	2.655	1.81e-02	6.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: positive regulation of response to external stimulus (Página 1 de 3)

Fuente: GO:BP | ID: GO:0032103 | Genes: 70 | p-valor ruta: 1.23e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6

## Ruta: positive regulation of response to external stimulus (Página 2 de 3)

Fuente: GO:BP | ID: GO:0032103 | Genes: 70 | p-valor ruta: 1.23e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
TRIM5	NA	UP	2.172	6.62e-61	1222.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2

## Ruta: positive regulation of response to external stimulus (Página 3 de 3)

Fuente: GO:BP | ID: GO:0032103 | Genes: 70 | p-valor ruta: 1.23e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
TNFSF14	NA	UP	2.748	3.71e-07	23.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
THBD	NA	UP	2.330	1.23e-02	7.3
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: regulation of response to biotic stimulus (Página 1 de 3)

Fuente: GO:BP | ID: GO:0002831 | Genes: 64 | p-valor ruta: 3.74e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6

## Ruta: regulation of response to biotic stimulus (Página 2 de 3)

Fuente: GO:BP | ID: GO:0002831 | Genes: 64 | p-valor ruta: 3.74e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: regulation of response to biotic stimulus (Página 3 de 3)

Fuente: GO:BP | ID: GO:0002831 | Genes: 64 | p-valor ruta: 3.74e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CASP1	NA	UP	2.494	1.49e-18	80.2
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: cellular response to stimulus (Página 1 de 11)

Fuente: GO:BP | ID: GO:0051716 | Genes: 272 | p-valor ruta: 7.39e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8

## Ruta: cellular response to stimulus (Página 2 de 11)

Fuente: GO:BP | ID: GO:0051716 | Genes: 272 | p-valor ruta: 7.39e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CMPK2	NA	UP	4.677	1.14e-162	1687.4
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5

## Ruta: cellular response to stimulus (Página 3 de 11)

Fuente: GO:BP | ID: GO:0051716 | Genes: 272 | p-valor ruta: 7.39e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
RASGRP3	NA	UP	3.468	2.92e-82	392.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1

## Ruta: cellular response to stimulus (Página 4 de 11)

Fuente: GO:BP | ID: GO:0051716 | Genes: 272 | p-valor ruta: 7.39e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
HSH2D	NA	UP	2.613	6.29e-73	813.8
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5

## Ruta: cellular response to stimulus (Página 5 de 11)

Fuente: GO:BP | ID: GO:0051716 | Genes: 272 | p-valor ruta: 7.39e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TUFT1	NA	UP	2.001	1.00e-55	1905.9
FOSB	NA	UP	3.144	1.32e-55	267.7
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9

## Ruta: cellular response to stimulus (Página 6 de 11)

Fuente: GO:BP | ID: GO:0051716 | Genes: 272 | p-valor ruta: 7.39e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
MT2A	NA	UP	2.437	2.24e-35	363.0
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
BCL2L14	NA	UP	2.782	8.63e-26	122.3
MAST4	NA	UP	2.184	1.21e-25	197.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CHAC1	NA	UP	3.022	3.43e-23	111.7

## Ruta: cellular response to stimulus (Página 7 de 11)

Fuente: GO:BP | ID: GO:0051716 | Genes: 272 | p-valor ruta: 7.39e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
DEPDC7	NA	UP	2.115	7.88e-19	114.2
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
ZBTB20	NA	UP	3.440	1.24e-15	47.6
INHBE	NA	UP	5.109	1.59e-15	37.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PLEKHG7	NA	UP	3.625	2.08e-12	31.8

## Ruta: cellular response to stimulus (Página 8 de 11)

Fuente: GO:BP | ID: GO:0051716 | Genes: 272 | p-valor ruta: 7.39e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
TAGAP	NA	UP	3.201	2.52e-06	16.1

## Ruta: cellular response to stimulus (Página 9 de 11)

Fuente: GO:BP | ID: GO:0051716 | Genes: 272 | p-valor ruta: 7.39e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RAB30	NA	UP	2.024	5.27e-06	28.7
COL4A1	NA	UP	6.589	5.89e-06	8.2
ADCY4	NA	UP	2.271	8.12e-06	23.6
UBASH3A	NA	UP	5.845	1.05e-05	9.8
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
PTGER2	NA	UP	3.006	1.95e-04	11.0
EGR3	NA	UP	2.096	2.87e-04	21.5
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6
RNF152	NA	UP	3.325	1.37e-03	7.5
LHB	NA	UP	3.522	1.50e-03	7.0

## Ruta: cellular response to stimulus (Página 10 de 11)

Fuente: GO:BP | ID: GO:0051716 | Genes: 272 | p-valor ruta: 7.39e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SLC1A2	NA	UP	2.752	2.07e-03	8.4
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
IL17C	NA	UP	4.636	3.13e-03	4.1
IPCEF1	NA	UP	4.035	3.69e-03	4.9
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7

## Ruta: cellular response to stimulus (Página 11 de 11)

Fuente: GO:BP | ID: GO:0051716 | Genes: 272 | p-valor ruta: 7.39e-26

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
DLG2	NA	UP	3.028	3.83e-02	3.8
CCL17	NA	UP	3.441	3.89e-02	2.9
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: signal transduction (Página 1 de 10)

Fuente: GO:BP | ID: GO:0007165 | Genes: 239 | p-valor ruta: 1.15e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6

## Ruta: signal transduction (Página 2 de 10)

Fuente: GO:BP | ID: GO:0007165 | Genes: 239 | p-valor ruta: 1.15e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8

## Ruta: signal transduction (Página 3 de 10)

Fuente: GO:BP | ID: GO:0007165 | Genes: 239 | p-valor ruta: 1.15e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
RASGRP3	NA	UP	3.468	2.92e-82	392.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
HSH2D	NA	UP	2.613	6.29e-73	813.8

## Ruta: signal transduction (Página 4 de 10)

Fuente: GO:BP | ID: GO:0007165 | Genes: 239 | p-valor ruta: 1.15e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TUFT1	NA	UP	2.001	1.00e-55	1905.9
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4

## Ruta: signal transduction (Página 5 de 10)

Fuente: GO:BP | ID: GO:0007165 | Genes: 239 | p-valor ruta: 1.15e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: signal transduction (Página 6 de 10)

Fuente: GO:BP | ID: GO:0007165 | Genes: 239 | p-valor ruta: 1.15e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
BCL2L14	NA	UP	2.782	8.63e-26	122.3
MAST4	NA	UP	2.184	1.21e-25	197.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
DEPDC7	NA	UP	2.115	7.88e-19	114.2
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
INHBE	NA	UP	5.109	1.59e-15	37.3

## Ruta: signal transduction (Página 7 de 10)

Fuente: GO:BP | ID: GO:0007165 | Genes: 239 | p-valor ruta: 1.15e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PLEKHG7	NA	UP	3.625	2.08e-12	31.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5

## Ruta: signal transduction (Página 8 de 10)

Fuente: GO:BP | ID: GO:0007165 | Genes: 239 | p-valor ruta: 1.15e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TAGAP	NA	UP	3.201	2.52e-06	16.1
RAB30	NA	UP	2.024	5.27e-06	28.7
COL4A1	NA	UP	6.589	5.89e-06	8.2
ADCY4	NA	UP	2.271	8.12e-06	23.6
UBASH3A	NA	UP	5.845	1.05e-05	9.8
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
PTGER2	NA	UP	3.006	1.95e-04	11.0
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6
RNF152	NA	UP	3.325	1.37e-03	7.5
LHB	NA	UP	3.522	1.50e-03	7.0
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0

## Ruta: signal transduction (Página 9 de 10)

Fuente: GO:BP | ID: GO:0007165 | Genes: 239 | p-valor ruta: 1.15e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL17C	NA	UP	4.636	3.13e-03	4.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: signal transduction (Página 10 de 10)

Fuente: GO:BP | ID: GO:0007165 | Genes: 239 | p-valor ruta: 1.15e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
CCL17	NA	UP	3.441	3.89e-02	2.9
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of biological process (Página 1 de 10)

Fuente: GO:BP | ID: GO:0048518 | Genes: 245 | p-valor ruta: 1.79e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8

## Ruta: positive regulation of biological process (Página 2 de 10)

Fuente: GO:BP | ID: GO:0048518 | Genes: 245 | p-valor ruta: 1.79e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6

## Ruta: positive regulation of biological process (Página 3 de 10)

Fuente: GO:BP | ID: GO:0048518 | Genes: 245 | p-valor ruta: 1.79e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2

## Ruta: positive regulation of biological process (Página 4 de 10)

Fuente: GO:BP | ID: GO:0048518 | Genes: 245 | p-valor ruta: 1.79e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0

## Ruta: positive regulation of biological process (Página 5 de 10)

Fuente: GO:BP | ID: GO:0048518 | Genes: 245 | p-valor ruta: 1.79e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
ZNF267	NA	UP	2.059	1.30e-34	677.0
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
C1R	NA	UP	2.188	3.06e-32	258.8
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3

## Ruta: positive regulation of biological process (Página 6 de 10)

Fuente: GO:BP | ID: GO:0048518 | Genes: 245 | p-valor ruta: 1.79e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
HIVEP1	NA	UP	2.014	1.06e-24	282.1
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8

## Ruta: positive regulation of biological process (Página 7 de 10)

Fuente: GO:BP | ID: GO:0048518 | Genes: 245 | p-valor ruta: 1.79e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
RAET1L	NA	UP	2.665	2.71e-15	60.0
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
DUOX1	NA	UP	3.131	5.18e-10	27.1
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3

## Ruta: positive regulation of biological process (Página 8 de 10)

Fuente: GO:BP | ID: GO:0048518 | Genes: 245 | p-valor ruta: 1.79e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
SYNPO2	NA	UP	3.603	1.95e-04	9.0
EGR3	NA	UP	2.096	2.87e-04	21.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CEACAM20	NA	UP	5.412	1.17e-03	3.6

## Ruta: positive regulation of biological process (Página 9 de 10)

Fuente: GO:BP | ID: GO:0048518 | Genes: 245 | p-valor ruta: 1.79e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RNF152	NA	UP	3.325	1.37e-03	7.5
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
RUFY4	NA	UP	4.136	2.15e-03	6.0
LGR6	NA	UP	3.915	2.25e-03	6.0
PATL2	NA	UP	2.215	2.72e-03	12.1
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
EGFL6	NA	UP	3.034	6.01e-03	5.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
TTLL6	NA	UP	2.577	1.74e-02	6.7

## Ruta: positive regulation of biological process (Página 10 de 10)

Fuente: GO:BP | ID: GO:0048518 | Genes: 245 | p-valor ruta: 1.79e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
SALL1	NA	UP	4.345	3.20e-02	1.8
CR1L	NA	UP	3.479	3.30e-02	3.5
CCL17	NA	UP	3.441	3.89e-02	2.9
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of cytokine production (Página 1 de 3)

Fuente: GO:BP | ID: GO:0001819 | Genes: 60 | p-valor ruta: 6.62e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3

## Ruta: positive regulation of cytokine production (Página 2 de 3)

Fuente: GO:BP | ID: GO:0001819 | Genes: 60 | p-valor ruta: 6.62e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
LTB	NA	UP	3.555	2.50e-41	150.4
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2

## Ruta: positive regulation of cytokine production (Página 3 de 3)

Fuente: GO:BP | ID: GO:0001819 | Genes: 60 | p-valor ruta: 6.62e-25

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
CEACAM20	NA	UP	5.412	1.17e-03	3.6
LY96	NA	UP	5.204	4.42e-03	3.4
PRG2	NA	UP	2.073	1.32e-02	9.7
C3AR1	NA	UP	4.639	1.59e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: regulation of viral process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0050792 | Genes: 37 | p-valor ruta: 1.03e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
MX1	NA	UP	3.859	1.25e-245	5699.6
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TRIM22	NA	UP	5.650	1.01e-212	913.7
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
OAS3	NA	UP	2.942	1.13e-87	8674.1
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFIT5	NA	UP	2.861	3.01e-78	749.8
LGALS9	NA	UP	2.474	3.44e-71	1449.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
PTX3	NA	UP	3.614	2.25e-68	237.4
TRIM5	NA	UP	2.172	6.62e-61	1222.6

## Ruta: regulation of viral process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0050792 | Genes: 37 | p-valor ruta: 1.03e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
BST2	NA	UP	4.284	3.82e-19	50.8
IFITM2	NA	UP	2.649	6.22e-17	64.2
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
GBP7	NA	UP	4.177	1.61e-02	2.9
RFPL1	NA	UP	3.259	2.06e-02	4.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of response to stress (Página 1 de 4)

Fuente: GO:BP | ID: GO:0080134 | Genes: 100 | p-valor ruta: 1.25e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5

## Ruta: regulation of response to stress (Página 2 de 4)

Fuente: GO:BP | ID: GO:0080134 | Genes: 100 | p-valor ruta: 1.25e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3

## Ruta: regulation of response to stress (Página 3 de 4)

Fuente: GO:BP | ID: GO:0080134 | Genes: 100 | p-valor ruta: 1.25e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
RASGRP1	NA	UP	2.055	4.16e-34	336.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: regulation of response to stress (Página 4 de 4)

Fuente: GO:BP | ID: GO:0080134 | Genes: 100 | p-valor ruta: 1.25e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
DUOX1	NA	UP	3.131	5.18e-10	27.1
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
THBD	NA	UP	2.330	1.23e-02	7.3
VAV1	NA	UP	2.118	1.54e-02	7.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: response to lipopolysaccharide (Página 1 de 2)

Fuente: GO:BP | ID: GO:0032496 | Genes: 50 | p-valor ruta: 3.27e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CMPK2	NA	UP	4.677	1.14e-162	1687.4
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IRAK2	NA	UP	2.666	3.46e-95	1164.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5

## Ruta: response to lipopolysaccharide (Página 2 de 2)

Fuente: GO:BP | ID: GO:0032496 | Genes: 50 | p-valor ruta: 3.27e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
KMO	NA	UP	5.165	6.24e-09	19.5
IL10RA	NA	UP	3.172	3.66e-07	18.8
SELE	NA	UP	5.745	2.05e-05	9.0
PTGER2	NA	UP	3.006	1.95e-04	11.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
LY96	NA	UP	5.204	4.42e-03	3.4
THBD	NA	UP	2.330	1.23e-02	7.3
TLR9	NA	UP	2.952	1.98e-02	4.6
PPM1E	NA	UP	3.810	4.20e-02	2.4

## Ruta: response to molecule of bacterial origin (Página 1 de 3)

Fuente: GO:BP | ID: GO:0002237 | Genes: 51 | p-valor ruta: 4.44e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CMPK2	NA	UP	4.677	1.14e-162	1687.4
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IRAK2	NA	UP	2.666	3.46e-95	1164.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5

## Ruta: response to molecule of bacterial origin (Página 2 de 3)

Fuente: GO:BP | ID: GO:0002237 | Genes: 51 | p-valor ruta: 4.44e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
KMO	NA	UP	5.165	6.24e-09	19.5
TLR6	NA	UP	2.680	9.77e-08	26.3
IL10RA	NA	UP	3.172	3.66e-07	18.8
SELE	NA	UP	5.745	2.05e-05	9.0
PTGER2	NA	UP	3.006	1.95e-04	11.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
LY96	NA	UP	5.204	4.42e-03	3.4
THBD	NA	UP	2.330	1.23e-02	7.3
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: response to molecule of bacterial origin (Página 3 de 3)

Fuente: GO:BP | ID: GO:0002237 | Genes: 51 | p-valor ruta: 4.44e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PPM1E	NA	UP	3.81	4.2e-02	2.4

## Ruta: negative regulation of viral genome replication

Fuente: GO:BP | ID: GO:0045071 | Genes: 25 | p-valor ruta: 9.14e-24

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
MX1	NA	UP	3.859	1.25e-245	5699.6
IFIH1	NA	UP	4.035	2.22e-233	4525.3
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
OAS3	NA	UP	2.942	1.13e-87	8674.1
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFIT5	NA	UP	2.861	3.01e-78	749.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
BST2	NA	UP	4.284	3.82e-19	50.8
IFITM2	NA	UP	2.649	6.22e-17	64.2
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of cellular process (Página 1 de 10)

Fuente: GO:BP | ID: GO:0048522 | Genes: 232 | p-valor ruta: 2.3e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1

## Ruta: positive regulation of cellular process (Página 2 de 10)

Fuente: GO:BP | ID: GO:0048522 | Genes: 232 | p-valor ruta: 2.3e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
IFITM1	NA	UP	3.632	5.16e-130	784.8
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7

## Ruta: positive regulation of cellular process (Página 3 de 10)

Fuente: GO:BP | ID: GO:0048522 | Genes: 232 | p-valor ruta: 2.3e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6

## Ruta: positive regulation of cellular process (Página 4 de 10)

Fuente: GO:BP | ID: GO:0048522 | Genes: 232 | p-valor ruta: 2.3e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4

## Ruta: positive regulation of cellular process (Página 5 de 10)

Fuente: GO:BP | ID: GO:0048522 | Genes: 232 | p-valor ruta: 2.3e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
ZNF267	NA	UP	2.059	1.30e-34	677.0
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4

## Ruta: positive regulation of cellular process (Página 6 de 10)

Fuente: GO:BP | ID: GO:0048522 | Genes: 232 | p-valor ruta: 2.3e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BCL2L14	NA	UP	2.782	8.63e-26	122.3
HIVEP1	NA	UP	2.014	1.06e-24	282.1
LIFR	NA	UP	2.213	9.30e-24	226.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
RAET1L	NA	UP	2.665	2.71e-15	60.0
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8

## Ruta: positive regulation of cellular process (Página 7 de 10)

Fuente: GO:BP | ID: GO:0048522 | Genes: 232 | p-valor ruta: 2.3e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
DUOX1	NA	UP	3.131	5.18e-10	27.1
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
FAP	NA	UP	3.233	1.87e-05	14.0

## Ruta: positive regulation of cellular process (Página 8 de 10)

Fuente: GO:BP | ID: GO:0048522 | Genes: 232 | p-valor ruta: 2.3e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
SYNPO2	NA	UP	3.603	1.95e-04	9.0
EGR3	NA	UP	2.096	2.87e-04	21.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CEACAM20	NA	UP	5.412	1.17e-03	3.6
RNF152	NA	UP	3.325	1.37e-03	7.5
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
RUFY4	NA	UP	4.136	2.15e-03	6.0
LGR6	NA	UP	3.915	2.25e-03	6.0
PATL2	NA	UP	2.215	2.72e-03	12.1
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4

## Ruta: positive regulation of cellular process (Página 9 de 10)

Fuente: GO:BP | ID: GO:0048522 | Genes: 232 | p-valor ruta: 2.3e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LY96	NA	UP	5.204	4.42e-03	3.4
EGFL6	NA	UP	3.034	6.01e-03	5.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
SCUBE1	NA	UP	2.508	1.26e-02	8.4
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
TTLL6	NA	UP	2.577	1.74e-02	6.7
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
SALL1	NA	UP	4.345	3.20e-02	1.8
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: positive regulation of cellular process (Página 10 de 10)

Fuente: GO:BP | ID: GO:0048522 | Genes: 232 | p-valor ruta: 2.3e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of immune response (Página 1 de 4)

Fuente: GO:BP | ID: GO:0050776 | Genes: 80 | p-valor ruta: 2.49e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5

## Ruta: regulation of immune response (Página 2 de 4)

Fuente: GO:BP | ID: GO:0050776 | Genes: 80 | p-valor ruta: 2.49e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
IFNL3	NA	UP	9.837	4.42e-30	365.0

## Ruta: regulation of immune response (Página 3 de 4)

Fuente: GO:BP | ID: GO:0050776 | Genes: 80 | p-valor ruta: 2.49e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL12A	NA	UP	3.852	1.95e-28	83.7
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9

## Ruta: regulation of immune response (Página 4 de 4)

Fuente: GO:BP | ID: GO:0050776 | Genes: 80 | p-valor ruta: 2.49e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: regulation of viral life cycle (Página 1 de 2)

Fuente: GO:BP | ID: GO:1903900 | Genes: 33 | p-valor ruta: 6.65e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
MX1	NA	UP	3.859	1.25e-245	5699.6
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TRIM22	NA	UP	5.650	1.01e-212	913.7
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
OAS3	NA	UP	2.942	1.13e-87	8674.1
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFIT5	NA	UP	2.861	3.01e-78	749.8
LGALS9	NA	UP	2.474	3.44e-71	1449.3
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7

## Ruta: regulation of viral life cycle (Página 2 de 2)

Fuente: GO:BP | ID: GO:1903900 | Genes: 33 | p-valor ruta: 6.65e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
BST2	NA	UP	4.284	3.82e-19	50.8
IFITM2	NA	UP	2.649	6.22e-17	64.2
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
GBP7	NA	UP	4.177	1.61e-02	2.9
RFPL1	NA	UP	3.259	2.06e-02	4.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of cell communication (Página 1 de 7)

Fuente: GO:BP | ID: GO:0010646 | Genes: 166 | p-valor ruta: 7.04e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IRF1	NA	UP	3.512	7.87e-194	2808.9
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
NUAK2	NA	UP	4.358	1.14e-107	489.1

## Ruta: regulation of cell communication (Página 2 de 7)

Fuente: GO:BP | ID: GO:0010646 | Genes: 166 | p-valor ruta: 7.04e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5

## Ruta: regulation of cell communication (Página 3 de 7)

Fuente: GO:BP | ID: GO:0010646 | Genes: 166 | p-valor ruta: 7.04e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9

## Ruta: regulation of cell communication (Página 4 de 7)

Fuente: GO:BP | ID: GO:0010646 | Genes: 166 | p-valor ruta: 7.04e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
DDO	NA	UP	2.846	3.84e-20	82.4
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: regulation of cell communication (Página 5 de 7)

Fuente: GO:BP | ID: GO:0010646 | Genes: 166 | p-valor ruta: 7.04e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
GBP5	NA	UP	6.172	4.92e-17	48.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
EGR2	NA	UP	3.090	6.72e-15	43.7
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
CYTH4	NA	UP	2.691	3.08e-10	36.2
KMO	NA	UP	5.165	6.24e-09	19.5
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
TAGAP	NA	UP	3.201	2.52e-06	16.1
BEST1	NA	UP	3.553	8.47e-06	13.3

## Ruta: regulation of cell communication (Página 6 de 7)

Fuente: GO:BP | ID: GO:0010646 | Genes: 166 | p-valor ruta: 7.04e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
UBASH3A	NA	UP	5.845	1.05e-05	9.8
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
RBMS3	NA	UP	2.303	4.11e-04	18.6
KIT	NA	UP	3.650	6.24e-04	7.9
CNTN4	NA	UP	4.928	9.17e-04	5.0
RNF152	NA	UP	3.325	1.37e-03	7.5
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of cell communication (Página 7 de 7)

Fuente: GO:BP | ID: GO:0010646 | Genes: 166 | p-valor ruta: 7.04e-23

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of defense response (Página 1 de 3)

Fuente: GO:BP | ID: GO:0031349 | Genes: 58 | p-valor ruta: 1.17e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1

## Ruta: positive regulation of defense response (Página 2 de 3)

Fuente: GO:BP | ID: GO:0031349 | Genes: 58 | p-valor ruta: 1.17e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTGS2	NA	UP	3.253	7.39e-80	3663.8
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
MAP3K8	NA	UP	2.825	4.57e-78	640.1
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
TRIM5	NA	UP	2.172	6.62e-61	1222.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0

## Ruta: positive regulation of defense response (Página 3 de 3)

Fuente: GO:BP | ID: GO:0031349 | Genes: 58 | p-valor ruta: 1.17e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
NUPR1	NA	UP	3.660	1.78e-06	14.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: positive regulation of multicellular organismal process (Página 1 de 5)

Fuente: GO:BP | ID: GO:0051240 | Genes: 107 | p-valor ruta: 1.7e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8

## Ruta: positive regulation of multicellular organismal process (Página 2 de 5)

Fuente: GO:BP | ID: GO:0051240 | Genes: 107 | p-valor ruta: 1.7e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
IL15RA	NA	UP	2.045	1.16e-42	847.9
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9

## Ruta: positive regulation of multicellular organismal process (Página 3 de 5)

Fuente: GO:BP | ID: GO:0051240 | Genes: 107 | p-valor ruta: 1.7e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5

## Ruta: positive regulation of multicellular organismal process (Página 4 de 5)

Fuente: GO:BP | ID: GO:0051240 | Genes: 107 | p-valor ruta: 1.7e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
LRRN3	NA	UP	6.733	2.08e-06	9.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
CEACAM20	NA	UP	5.412	1.17e-03	3.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
BMPER	NA	UP	4.906	6.28e-03	2.6
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2

## Ruta: positive regulation of multicellular organismal process (Página 5 de 5)

Fuente: GO:BP | ID: GO:0051240 | Genes: 107 | p-valor ruta: 1.7e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
TP63	NA	UP	3.788	4.09e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: cellular response to chemical stimulus (Página 1 de 5)

Fuente: GO:BP | ID: GO:0070887 | Genes: 125 | p-valor ruta: 2.11e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CMPK2	NA	UP	4.677	1.14e-162	1687.4
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CXCL2	NA	UP	3.371	1.67e-155	4155.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STC2	NA	UP	2.729	3.17e-119	2626.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0

## Ruta: cellular response to chemical stimulus (Página 2 de 5)

Fuente: GO:BP | ID: GO:0070887 | Genes: 125 | p-valor ruta: 2.11e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CD274	NA	UP	5.204	1.23e-98	314.4
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2

## Ruta: cellular response to chemical stimulus (Página 3 de 5)

Fuente: GO:BP | ID: GO:0070887 | Genes: 125 | p-valor ruta: 2.11e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BBC3	NA	UP	2.829	3.65e-57	503.1
CD69	NA	UP	3.112	5.99e-57	257.2
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
CH25H	NA	UP	7.817	1.04e-46	242.7
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
MT2A	NA	UP	2.437	2.24e-35	363.0
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: cellular response to chemical stimulus (Página 4 de 5)

Fuente: GO:BP | ID: GO:0070887 | Genes: 125 | p-valor ruta: 2.11e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
BDKRB2	NA	UP	2.797	5.56e-15	55.1
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RBM11	NA	UP	2.506	8.83e-07	22.9
SYT1	NA	UP	2.659	1.62e-06	21.4
COL4A1	NA	UP	6.589	5.89e-06	8.2
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
NPTX1	NA	UP	2.102	1.13e-04	22.3
PTGER2	NA	UP	3.006	1.95e-04	11.0

## Ruta: cellular response to chemical stimulus (Página 5 de 5)

Fuente: GO:BP | ID: GO:0070887 | Genes: 125 | p-valor ruta: 2.11e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
LHB	NA	UP	3.522	1.50e-03	7.0
SLC1A2	NA	UP	2.752	2.07e-03	8.4
IPCEF1	NA	UP	4.035	3.69e-03	4.9
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
DLG2	NA	UP	3.028	3.83e-02	3.8
CCL17	NA	UP	3.441	3.89e-02	2.9
TP63	NA	UP	3.788	4.09e-02	2.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: positive regulation of immune response (Página 1 de 3)

Fuente: GO:BP | ID: GO:0050778 | Genes: 70 | p-valor ruta: 3.53e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1

## Ruta: positive regulation of immune response (Página 2 de 3)

Fuente: GO:BP | ID: GO:0050778 | Genes: 70 | p-valor ruta: 3.53e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8

## Ruta: positive regulation of immune response (Página 3 de 3)

Fuente: GO:BP | ID: GO:0050778 | Genes: 70 | p-valor ruta: 3.53e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP5	NA	UP	6.172	4.92e-17	48.7
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: regulation of signaling (Página 1 de 7)

Fuente: GO:BP | ID: GO:0023051 | Genes: 164 | p-valor ruta: 5.09e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IRF1	NA	UP	3.512	7.87e-194	2808.9
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
NUAK2	NA	UP	4.358	1.14e-107	489.1

## Ruta: regulation of signaling (Página 2 de 7)

Fuente: GO:BP | ID: GO:0023051 | Genes: 164 | p-valor ruta: 5.09e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5

## Ruta: regulation of signaling (Página 3 de 7)

Fuente: GO:BP | ID: GO:0023051 | Genes: 164 | p-valor ruta: 5.09e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9

## Ruta: regulation of signaling (Página 4 de 7)

Fuente: GO:BP | ID: GO:0023051 | Genes: 164 | p-valor ruta: 5.09e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0

## Ruta: regulation of signaling (Página 5 de 7)

Fuente: GO:BP | ID: GO:0023051 | Genes: 164 | p-valor ruta: 5.09e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
GBP5	NA	UP	6.172	4.92e-17	48.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
EGR2	NA	UP	3.090	6.72e-15	43.7
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
CYTH4	NA	UP	2.691	3.08e-10	36.2
KMO	NA	UP	5.165	6.24e-09	19.5
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
TAGAP	NA	UP	3.201	2.52e-06	16.1
BEST1	NA	UP	3.553	8.47e-06	13.3
UBASH3A	NA	UP	5.845	1.05e-05	9.8
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4

## Ruta: regulation of signaling (Página 6 de 7)

Fuente: GO:BP | ID: GO:0023051 | Genes: 164 | p-valor ruta: 5.09e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
RBMS3	NA	UP	2.303	4.11e-04	18.6
KIT	NA	UP	3.650	6.24e-04	7.9
CNTN4	NA	UP	4.928	9.17e-04	5.0
RNF152	NA	UP	3.325	1.37e-03	7.5
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7

## Ruta: regulation of signaling (Página 7 de 7)

Fuente: GO:BP | ID: GO:0023051 | Genes: 164 | p-valor ruta: 5.09e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of signal transduction (Página 1 de 6)

Fuente: GO:BP | ID: GO:0009966 | Genes: 150 | p-valor ruta: 1.38e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IRF1	NA	UP	3.512	7.87e-194	2808.9
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1

## Ruta: regulation of signal transduction (Página 2 de 6)

Fuente: GO:BP | ID: GO:0009966 | Genes: 150 | p-valor ruta: 1.38e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0

## Ruta: regulation of signal transduction (Página 3 de 6)

Fuente: GO:BP | ID: GO:0009966 | Genes: 150 | p-valor ruta: 1.38e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0

## Ruta: regulation of signal transduction (Página 4 de 6)

Fuente: GO:BP | ID: GO:0009966 | Genes: 150 | p-valor ruta: 1.38e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PER1	NA	UP	2.501	8.94e-44	469.6
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: regulation of signal transduction (Página 5 de 6)

Fuente: GO:BP | ID: GO:0009966 | Genes: 150 | p-valor ruta: 1.38e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP5	NA	UP	6.172	4.92e-17	48.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
CYTH4	NA	UP	2.691	3.08e-10	36.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
TAGAP	NA	UP	3.201	2.52e-06	16.1
UBASH3A	NA	UP	5.845	1.05e-05	9.8
IL18R1	NA	UP	2.088	8.75e-05	23.0
RBMS3	NA	UP	2.303	4.11e-04	18.6
KIT	NA	UP	3.650	6.24e-04	7.9
RNF152	NA	UP	3.325	1.37e-03	7.5
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4

## Ruta: regulation of signal transduction (Página 6 de 6)

Fuente: GO:BP | ID: GO:0009966 | Genes: 150 | p-valor ruta: 1.38e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: biological regulation (Página 1 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL3	NA	UP	3.053	2.27e-187	4330.7

## Ruta: biological regulation (Página 2 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5

## Ruta: biological regulation (Página 3 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
NUAK2	NA	UP	4.358	1.14e-107	489.1
SP110	NA	UP	2.776	1.00e-106	1474.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2

## Ruta: biological regulation (Página 4 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ETV7	NA	UP	4.688	2.39e-83	278.8
RASGRP3	NA	UP	3.468	2.92e-82	392.1
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
HSH2D	NA	UP	2.613	6.29e-73	813.8
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8

## Ruta: biological regulation (Página 5 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
RND1	NA	UP	2.840	1.60e-62	337.7
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1

## Ruta: biological regulation (Página 6 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TUFT1	NA	UP	2.001	1.00e-55	1905.9
FOSB	NA	UP	3.144	1.32e-55	267.7
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
NAV2	NA	UP	2.370	3.20e-51	765.9
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
FUT3	NA	UP	2.139	2.84e-41	355.7

## Ruta: biological regulation (Página 7 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
MT2A	NA	UP	2.437	2.24e-35	363.0
DUSP8	NA	UP	2.088	3.69e-35	551.5
MIR155HG	NA	UP	5.318	4.66e-35	99.1
ZNF267	NA	UP	2.059	1.30e-34	677.0
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
C1R	NA	UP	2.188	3.06e-32	258.8
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
EDN2	NA	UP	3.499	8.77e-31	90.3
BACH2	NA	UP	2.222	2.18e-30	209.0
PPM1K	NA	UP	2.192	3.89e-30	395.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
HDX	NA	UP	2.521	1.83e-28	139.2
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: biological regulation (Página 8 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
BCL2L14	NA	UP	2.782	8.63e-26	122.3
MAST4	NA	UP	2.184	1.21e-25	197.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
DDO	NA	UP	2.846	3.84e-20	82.4
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
DEPDC7	NA	UP	2.115	7.88e-19	114.2
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: biological regulation (Página 9 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
INHBE	NA	UP	5.109	1.59e-15	37.3
RAET1L	NA	UP	2.665	2.71e-15	60.0
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PLEKHG7	NA	UP	3.625	2.08e-12	31.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SCN3A	NA	UP	8.277	2.66e-10	27.0
CYTH4	NA	UP	2.691	3.08e-10	36.2

## Ruta: biological regulation (Página 10 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DUOX1	NA	UP	3.131	5.18e-10	27.1
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
STX19	NA	UP	2.009	1.09e-08	99.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
KCNV1	NA	UP	2.402	2.10e-07	37.9
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
AHRR	NA	UP	2.180	3.48e-07	33.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RBM11	NA	UP	2.506	8.83e-07	22.9

## Ruta: biological regulation (Página 11 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
TAGAP	NA	UP	3.201	2.52e-06	16.1
RAB30	NA	UP	2.024	5.27e-06	28.7
COL4A1	NA	UP	6.589	5.89e-06	8.2
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
ADCY4	NA	UP	2.271	8.12e-06	23.6
BEST1	NA	UP	3.553	8.47e-06	13.3
SERPINA10	NA	UP	6.459	9.50e-06	7.5
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
BEST3	NA	UP	2.070	3.26e-05	23.9
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
XKR9	NA	UP	3.541	5.84e-05	11.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3

## Ruta: biological regulation (Página 12 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RHCG	NA	UP	2.107	1.84e-04	21.0
PTGER2	NA	UP	3.006	1.95e-04	11.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
EGR3	NA	UP	2.096	2.87e-04	21.5
MPZ	NA	UP	2.002	2.88e-04	19.4
ZNF382	NA	UP	2.028	3.78e-04	18.2
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
GAL3ST4	NA	UP	2.371	7.40e-04	12.5
HAND1	NA	UP	4.966	8.42e-04	5.1
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
RNF152	NA	UP	3.325	1.37e-03	7.5
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
LHB	NA	UP	3.522	1.50e-03	7.0

## Ruta: biological regulation (Página 13 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
KCNH3	NA	DOWN	-2.243	1.94e-03	12.5
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
RUFY4	NA	UP	4.136	2.15e-03	6.0
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
SLC17A4	NA	DOWN	-2.298	2.32e-03	11.5
PEX5L	NA	UP	3.321	2.40e-03	7.0
KCNN1	NA	UP	3.883	2.55e-03	6.2
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
PATL2	NA	UP	2.215	2.72e-03	12.1
IL17C	NA	UP	4.636	3.13e-03	4.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
EGFL6	NA	UP	3.034	6.01e-03	5.9
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6

## Ruta: biological regulation (Página 14 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
SLC9B1	NA	UP	4.128	1.36e-02	3.1
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
TTLL6	NA	UP	2.577	1.74e-02	6.7
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
SLC9C2	NA	UP	3.943	2.11e-02	2.8
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9

## Ruta: biological regulation (Página 15 de 15)

Fuente: GO:BP | ID: GO:0065007 | Genes: 370 | p-valor ruta: 2.18e-21

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CELF6	NA	UP	2.403	2.65e-02	5.6
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
INSC	NA	UP	3.872	3.01e-02	2.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
CR1L	NA	UP	3.479	3.30e-02	3.5
KCNE4	NA	UP	2.337	3.37e-02	5.7
DLG2	NA	UP	3.028	3.83e-02	3.8
CCL17	NA	UP	3.441	3.89e-02	2.9
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
PURG	NA	DOWN	-4.166	4.66e-02	1.7
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of innate immune response (Página 1 de 3)

Fuente: GO:BP | ID: GO:0045088 | Genes: 52 | p-valor ruta: 3.1e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9

## Ruta: regulation of innate immune response (Página 2 de 3)

Fuente: GO:BP | ID: GO:0045088 | Genes: 52 | p-valor ruta: 3.1e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
LY96	NA	UP	5.204	4.42e-03	3.4

## Ruta: regulation of innate immune response (Página 3 de 3)

Fuente: GO:BP | ID: GO:0045088 | Genes: 52 | p-valor ruta: 3.1e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: intracellular signal transduction (Página 1 de 6)

Fuente: GO:BP | ID: GO:0035556 | Genes: 145 | p-valor ruta: 3.7e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNFSF10	NA	UP	3.014	1.58e-112	3429.5

## Ruta: intracellular signal transduction (Página 2 de 6)

Fuente: GO:BP | ID: GO:0035556 | Genes: 145 | p-valor ruta: 3.7e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NUAK2	NA	UP	4.358	1.14e-107	489.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
SP100	NA	UP	2.428	1.62e-93	2653.7
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
RASGRP3	NA	UP	3.468	2.92e-82	392.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5

## Ruta: intracellular signal transduction (Página 3 de 6)

Fuente: GO:BP | ID: GO:0035556 | Genes: 145 | p-valor ruta: 3.7e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
RND1	NA	UP	2.840	1.60e-62	337.7
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
TUFT1	NA	UP	2.001	1.00e-55	1905.9
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6

## Ruta: intracellular signal transduction (Página 4 de 6)

Fuente: GO:BP | ID: GO:0035556 | Genes: 145 | p-valor ruta: 3.7e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
MAST4	NA	UP	2.184	1.21e-25	197.5
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
DEPDC7	NA	UP	2.115	7.88e-19	114.2
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7

## Ruta: intracellular signal transduction (Página 5 de 6)

Fuente: GO:BP | ID: GO:0035556 | Genes: 145 | p-valor ruta: 3.7e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BDKRB2	NA	UP	2.797	5.56e-15	55.1
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PLEKHG7	NA	UP	3.625	2.08e-12	31.8
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
CYTH4	NA	UP	2.691	3.08e-10	36.2
NLRP1	NA	UP	5.692	4.64e-09	21.6
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
TAGAP	NA	UP	3.201	2.52e-06	16.1
RAB30	NA	UP	2.024	5.27e-06	28.7
ADCY4	NA	UP	2.271	8.12e-06	23.6
SELE	NA	UP	5.745	2.05e-05	9.0
IL18R1	NA	UP	2.088	8.75e-05	23.0
NCALD	NA	UP	2.037	3.82e-04	17.1
KIT	NA	UP	3.650	6.24e-04	7.9
RNF152	NA	UP	3.325	1.37e-03	7.5

## Ruta: intracellular signal transduction (Página 6 de 6)

Fuente: GO:BP | ID: GO:0035556 | Genes: 145 | p-valor ruta: 3.7e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PEX5L	NA	UP	3.321	2.40e-03	7.0
RP1L1	NA	UP	2.162	5.43e-03	10.3
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: cellular response to molecule of bacterial origin (Página 1 de 2)

Fuente: GO:BP | ID: GO:0071219 | Genes: 38 | p-valor ruta: 5.74e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CMPK2	NA	UP	4.677	1.14e-162	1687.4
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IRAK2	NA	UP	2.666	3.46e-95	1164.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
CCL2	NA	UP	2.562	2.63e-75	658.0
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
PDE4B	NA	UP	3.818	7.08e-52	171.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2

## Ruta: cellular response to molecule of bacterial origin (Página 2 de 2)

Fuente: GO:BP | ID: GO:0071219 | Genes: 38 | p-valor ruta: 5.74e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KMO	NA	UP	5.165	6.24e-09	19.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6
PPM1E	NA	UP	3.810	4.20e-02	2.4

## Ruta: positive regulation of cell communication (Página 1 de 5)

Fuente: GO:BP | ID: GO:0010647 | Genes: 107 | p-valor ruta: 6.36e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4

## Ruta: positive regulation of cell communication (Página 2 de 5)

Fuente: GO:BP | ID: GO:0010647 | Genes: 107 | p-valor ruta: 6.36e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4

## Ruta: positive regulation of cell communication (Página 3 de 5)

Fuente: GO:BP | ID: GO:0010647 | Genes: 107 | p-valor ruta: 6.36e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
BCL2L14	NA	UP	2.782	8.63e-26	122.3
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
GBP5	NA	UP	6.172	4.92e-17	48.7
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: positive regulation of cell communication (Página 4 de 5)

Fuente: GO:BP | ID: GO:0010647 | Genes: 107 | p-valor ruta: 6.36e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KMO	NA	UP	5.165	6.24e-09	19.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9

## Ruta: positive regulation of cell communication (Página 5 de 5)

Fuente: GO:BP | ID: GO:0010647 | Genes: 107 | p-valor ruta: 6.36e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of signaling (Página 1 de 5)

Fuente: GO:BP | ID: GO:0023056 | Genes: 107 | p-valor ruta: 6.64e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4

## Ruta: positive regulation of signaling (Página 2 de 5)

Fuente: GO:BP | ID: GO:0023056 | Genes: 107 | p-valor ruta: 6.64e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4

## Ruta: positive regulation of signaling (Página 3 de 5)

Fuente: GO:BP | ID: GO:0023056 | Genes: 107 | p-valor ruta: 6.64e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
BCL2L14	NA	UP	2.782	8.63e-26	122.3
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
GBP5	NA	UP	6.172	4.92e-17	48.7
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: positive regulation of signaling (Página 4 de 5)

Fuente: GO:BP | ID: GO:0023056 | Genes: 107 | p-valor ruta: 6.64e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KMO	NA	UP	5.165	6.24e-09	19.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9

## Ruta: positive regulation of signaling (Página 5 de 5)

Fuente: GO:BP | ID: GO:0023056 | Genes: 107 | p-valor ruta: 6.64e-20

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of viral genome replication (Página 1 de 2)

Fuente: GO:BP | ID: GO:0045069 | Genes: 26 | p-valor ruta: 1.08e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
MX1	NA	UP	3.859	1.25e-245	5699.6
IFIH1	NA	UP	4.035	2.22e-233	4525.3
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
OAS3	NA	UP	2.942	1.13e-87	8674.1
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFIT5	NA	UP	2.861	3.01e-78	749.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
BST2	NA	UP	4.284	3.82e-19	50.8
IFITM2	NA	UP	2.649	6.22e-17	64.2
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
GBP7	NA	UP	4.177	1.61e-02	2.9

## Ruta: regulation of viral genome replication (Página 2 de 2)

Fuente: GO:BP | ID: GO:0045069 | Genes: 26 | p-valor ruta: 1.08e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: cellular response to lipopolysaccharide (Página 1 de 2)

Fuente: GO:BP | ID: GO:0071222 | Genes: 37 | p-valor ruta: 1.12e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CMPK2	NA	UP	4.677	1.14e-162	1687.4
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IRAK2	NA	UP	2.666	3.46e-95	1164.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
CCL2	NA	UP	2.562	2.63e-75	658.0
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
PDE4B	NA	UP	3.818	7.08e-52	171.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2

## Ruta: cellular response to lipopolysaccharide (Página 2 de 2)

Fuente: GO:BP | ID: GO:0071222 | Genes: 37 | p-valor ruta: 1.12e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KMO	NA	UP	5.165	6.24e-09	19.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6
PPM1E	NA	UP	3.810	4.20e-02	2.4

## Ruta: cell activation (Página 1 de 4)

Fuente: GO:BP | ID: GO:0001775 | Genes: 82 | p-valor ruta: 1.39e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
PLAT	NA	UP	2.447	4.98e-113	6662.1
IDO1	NA	UP	4.167	4.38e-109	394.2
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0

## Ruta: cell activation (Página 2 de 4)

Fuente: GO:BP | ID: GO:0001775 | Genes: 82 | p-valor ruta: 1.39e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
CD69	NA	UP	3.112	5.99e-57	257.2
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8

## Ruta: cell activation (Página 3 de 4)

Fuente: GO:BP | ID: GO:0001775 | Genes: 82 | p-valor ruta: 1.39e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
IL18R1	NA	UP	2.088	8.75e-05	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7

## Ruta: cell activation (Página 4 de 4)

Fuente: GO:BP | ID: GO:0001775 | Genes: 82 | p-valor ruta: 1.39e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
THBD	NA	UP	2.330	1.23e-02	7.3
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: cellular response to biotic stimulus (Página 1 de 2)

Fuente: GO:BP | ID: GO:0071216 | Genes: 39 | p-valor ruta: 4.04e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CMPK2	NA	UP	4.677	1.14e-162	1687.4
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IRAK2	NA	UP	2.666	3.46e-95	1164.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
CCL2	NA	UP	2.562	2.63e-75	658.0
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
PDE4B	NA	UP	3.818	7.08e-52	171.4

## Ruta: cellular response to biotic stimulus (Página 2 de 2)

Fuente: GO:BP | ID: GO:0071216 | Genes: 39 | p-valor ruta: 4.04e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KMO	NA	UP	5.165	6.24e-09	19.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6
PPM1E	NA	UP	3.810	4.20e-02	2.4

## Ruta: locomotion (Página 1 de 4)

Fuente: GO:BP | ID: GO:0040011 | Genes: 86 | p-valor ruta: 4.19e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CXCL2	NA	UP	3.371	1.67e-155	4155.4
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2

## Ruta: locomotion (Página 2 de 4)

Fuente: GO:BP | ID: GO:0040011 | Genes: 86 | p-valor ruta: 4.19e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
CH25H	NA	UP	7.817	1.04e-46	242.7
SEMA3A	NA	UP	2.276	5.71e-42	512.5
FUT3	NA	UP	2.139	2.84e-41	355.7
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9

## Ruta: locomotion (Página 3 de 4)

Fuente: GO:BP | ID: GO:0040011 | Genes: 86 | p-valor ruta: 4.19e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
DUOXA2	NA	UP	4.650	3.36e-16	39.7
NAV3	NA	UP	2.285	2.77e-15	84.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
DUOX1	NA	UP	3.131	5.18e-10	27.1
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
SYNPO2	NA	UP	3.603	1.95e-04	9.0
EGR3	NA	UP	2.096	2.87e-04	21.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0

## Ruta: locomotion (Página 4 de 4)

Fuente: GO:BP | ID: GO:0040011 | Genes: 86 | p-valor ruta: 4.19e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
TTLL6	NA	UP	2.577	1.74e-02	6.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of biological process (Página 1 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL3	NA	UP	3.053	2.27e-187	4330.7

## Ruta: regulation of biological process (Página 2 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5

## Ruta: regulation of biological process (Página 3 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
NUAK2	NA	UP	4.358	1.14e-107	489.1
SP110	NA	UP	2.776	1.00e-106	1474.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2

## Ruta: regulation of biological process (Página 4 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ETV7	NA	UP	4.688	2.39e-83	278.8
RASGRP3	NA	UP	3.468	2.92e-82	392.1
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
HSH2D	NA	UP	2.613	6.29e-73	813.8
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8

## Ruta: regulation of biological process (Página 5 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
RND1	NA	UP	2.840	1.60e-62	337.7
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1

## Ruta: regulation of biological process (Página 6 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TUFT1	NA	UP	2.001	1.00e-55	1905.9
FOSB	NA	UP	3.144	1.32e-55	267.7
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2

## Ruta: regulation of biological process (Página 7 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
MT2A	NA	UP	2.437	2.24e-35	363.0
DUSP8	NA	UP	2.088	3.69e-35	551.5
MIR155HG	NA	UP	5.318	4.66e-35	99.1
ZNF267	NA	UP	2.059	1.30e-34	677.0
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
C1R	NA	UP	2.188	3.06e-32	258.8
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
EDN2	NA	UP	3.499	8.77e-31	90.3
BACH2	NA	UP	2.222	2.18e-30	209.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
HDX	NA	UP	2.521	1.83e-28	139.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9

## Ruta: regulation of biological process (Página 8 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
BCL2L14	NA	UP	2.782	8.63e-26	122.3
MAST4	NA	UP	2.184	1.21e-25	197.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
DDO	NA	UP	2.846	3.84e-20	82.4
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
DEPDC7	NA	UP	2.115	7.88e-19	114.2
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8

## Ruta: regulation of biological process (Página 9 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
INHBE	NA	UP	5.109	1.59e-15	37.3
RAET1L	NA	UP	2.665	2.71e-15	60.0
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PLEKHG7	NA	UP	3.625	2.08e-12	31.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
SSTR2	NA	UP	2.031	8.80e-10	53.9

## Ruta: regulation of biological process (Página 10 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
STX19	NA	UP	2.009	1.09e-08	99.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
AHRR	NA	UP	2.180	3.48e-07	33.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4

## Ruta: regulation of biological process (Página 11 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TAGAP	NA	UP	3.201	2.52e-06	16.1
RAB30	NA	UP	2.024	5.27e-06	28.7
COL4A1	NA	UP	6.589	5.89e-06	8.2
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
ADCY4	NA	UP	2.271	8.12e-06	23.6
BEST1	NA	UP	3.553	8.47e-06	13.3
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
BEST3	NA	UP	2.070	3.26e-05	23.9
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
PTGER2	NA	UP	3.006	1.95e-04	11.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
EGR3	NA	UP	2.096	2.87e-04	21.5
MPZ	NA	UP	2.002	2.88e-04	19.4
ZNF382	NA	UP	2.028	3.78e-04	18.2
NCALD	NA	UP	2.037	3.82e-04	17.1

## Ruta: regulation of biological process (Página 12 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
GAL3ST4	NA	UP	2.371	7.40e-04	12.5
HAND1	NA	UP	4.966	8.42e-04	5.1
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
RNF152	NA	UP	3.325	1.37e-03	7.5
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
LHB	NA	UP	3.522	1.50e-03	7.0
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
RUFY4	NA	UP	4.136	2.15e-03	6.0
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0

## Ruta: regulation of biological process (Página 13 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KCNN1	NA	UP	3.883	2.55e-03	6.2
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
PATL2	NA	UP	2.215	2.72e-03	12.1
IL17C	NA	UP	4.636	3.13e-03	4.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
EGFL6	NA	UP	3.034	6.01e-03	5.9
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9

## Ruta: regulation of biological process (Página 14 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TTLL6	NA	UP	2.577	1.74e-02	6.7
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
CELF6	NA	UP	2.403	2.65e-02	5.6
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
INSC	NA	UP	3.872	3.01e-02	2.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
CR1L	NA	UP	3.479	3.30e-02	3.5
KCNE4	NA	UP	2.337	3.37e-02	5.7
DLG2	NA	UP	3.028	3.83e-02	3.8
CCL17	NA	UP	3.441	3.89e-02	2.9
ASXL3	NA	UP	2.101	4.07e-02	6.6

## Ruta: regulation of biological process (Página 15 de 15)

Fuente: GO:BP | ID: GO:0050789 | Genes: 358 | p-valor ruta: 4.38e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
PURG	NA	DOWN	-4.166	4.66e-02	1.7
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: response to lipid (Página 1 de 3)

Fuente: GO:BP | ID: GO:0033993 | Genes: 73 | p-valor ruta: 4.46e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CMPK2	NA	UP	4.677	1.14e-162	1687.4
CXCL2	NA	UP	3.371	1.67e-155	4155.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STC2	NA	UP	2.729	3.17e-119	2626.1
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IRAK2	NA	UP	2.666	3.46e-95	1164.5
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9

## Ruta: response to lipid (Página 2 de 3)

Fuente: GO:BP | ID: GO:0033993 | Genes: 73 | p-valor ruta: 4.46e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
NEDD4	NA	UP	2.433	4.99e-60	1678.5
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NKX3-1	NA	UP	2.233	8.30e-23	132.4
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: response to lipid (Página 3 de 3)

Fuente: GO:BP | ID: GO:0033993 | Genes: 73 | p-valor ruta: 4.46e-19

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
SSTR2	NA	UP	2.031	8.80e-10	53.9
KMO	NA	UP	5.165	6.24e-09	19.5
NR4A3	NA	UP	5.574	1.45e-08	20.2
IL10RA	NA	UP	3.172	3.66e-07	18.8
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
PTGER2	NA	UP	3.006	1.95e-04	11.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
LY96	NA	UP	5.204	4.42e-03	3.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
THBD	NA	UP	2.330	1.23e-02	7.3
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
TP63	NA	UP	3.788	4.09e-02	2.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: positive regulation of signal transduction (Página 1 de 4)

Fuente: GO:BP | ID: GO:0009967 | Genes: 97 | p-valor ruta: 1.34e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6

## Ruta: positive regulation of signal transduction (Página 2 de 4)

Fuente: GO:BP | ID: GO:0009967 | Genes: 97 | p-valor ruta: 1.34e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9

## Ruta: positive regulation of signal transduction (Página 3 de 4)

Fuente: GO:BP | ID: GO:0009967 | Genes: 97 | p-valor ruta: 1.34e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
BCL2L14	NA	UP	2.782	8.63e-26	122.3
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0

## Ruta: positive regulation of signal transduction (Página 4 de 4)

Fuente: GO:BP | ID: GO:0009967 | Genes: 97 | p-valor ruta: 1.34e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NUPR1	NA	UP	3.660	1.78e-06	14.5
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of macromolecule biosynthetic process (Página 1 de 6)

Fuente: GO:BP | ID: GO:0010557 | Genes: 130 | p-valor ruta: 2.19e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5

## Ruta: positive regulation of macromolecule biosynthetic process (Página 2 de 6)

Fuente: GO:BP | ID: GO:0010557 | Genes: 130 | p-valor ruta: 2.19e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6

## Ruta: positive regulation of macromolecule biosynthetic process (Página 3 de 6)

Fuente: GO:BP | ID: GO:0010557 | Genes: 130 | p-valor ruta: 2.19e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
IRS2	NA	UP	2.254	1.06e-33	255.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
SPRY2	NA	UP	2.250	1.05e-29	211.9

## Ruta: positive regulation of macromolecule biosynthetic process (Página 4 de 6)

Fuente: GO:BP | ID: GO:0010557 | Genes: 130 | p-valor ruta: 2.19e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3

## Ruta: positive regulation of macromolecule biosynthetic process (Página 5 de 6)

Fuente: GO:BP | ID: GO:0010557 | Genes: 130 | p-valor ruta: 2.19e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
RBMS3	NA	UP	2.303	4.11e-04	18.6
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CEACAM20	NA	UP	5.412	1.17e-03	3.6
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SALL1	NA	UP	4.345	3.20e-02	1.8

## Ruta: positive regulation of macromolecule biosynthetic process (Página 6 de 6)

Fuente: GO:BP | ID: GO:0010557 | Genes: 130 | p-valor ruta: 2.19e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of biosynthetic process (Página 1 de 6)

Fuente: GO:BP | ID: GO:0009891 | Genes: 133 | p-valor ruta: 2.62e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5

## Ruta: positive regulation of biosynthetic process (Página 2 de 6)

Fuente: GO:BP | ID: GO:0009891 | Genes: 133 | p-valor ruta: 2.62e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6

## Ruta: positive regulation of biosynthetic process (Página 3 de 6)

Fuente: GO:BP | ID: GO:0009891 | Genes: 133 | p-valor ruta: 2.62e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
IRS2	NA	UP	2.254	1.06e-33	255.2
PRDM1	NA	UP	3.525	5.98e-31	99.0

## Ruta: positive regulation of biosynthetic process (Página 4 de 6)

Fuente: GO:BP | ID: GO:0009891 | Genes: 133 | p-valor ruta: 2.62e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SPRY2	NA	UP	2.250	1.05e-29	211.9
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6

## Ruta: positive regulation of biosynthetic process (Página 5 de 6)

Fuente: GO:BP | ID: GO:0009891 | Genes: 133 | p-valor ruta: 2.62e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
RBMS3	NA	UP	2.303	4.11e-04	18.6
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CEACAM20	NA	UP	5.412	1.17e-03	3.6
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: positive regulation of biosynthetic process (Página 6 de 6)

Fuente: GO:BP | ID: GO:0009891 | Genes: 133 | p-valor ruta: 2.62e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: leukocyte activation (Página 1 de 3)

Fuente: GO:BP | ID: GO:0045321 | Genes: 73 | p-valor ruta: 9.43e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IDO1	NA	UP	4.167	4.38e-109	394.2
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2

## Ruta: leukocyte activation (Página 2 de 3)

Fuente: GO:BP | ID: GO:0045321 | Genes: 73 | p-valor ruta: 9.43e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
CD69	NA	UP	3.112	5.99e-57	257.2
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6

## Ruta: leukocyte activation (Página 3 de 3)

Fuente: GO:BP | ID: GO:0045321 | Genes: 73 | p-valor ruta: 9.43e-18

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
IL18R1	NA	UP	2.088	8.75e-05	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: cellular response to lipid (Página 1 de 3)

Fuente: GO:BP | ID: GO:0071396 | Genes: 57 | p-valor ruta: 1.06e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CMPK2	NA	UP	4.677	1.14e-162	1687.4
CXCL2	NA	UP	3.371	1.67e-155	4155.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IRAK2	NA	UP	2.666	3.46e-95	1164.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1

## Ruta: cellular response to lipid (Página 2 de 3)

Fuente: GO:BP | ID: GO:0071396 | Genes: 57 | p-valor ruta: 1.06e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM5	NA	UP	2.172	6.62e-61	1222.6
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
NKX3-1	NA	UP	2.233	8.30e-23	132.4
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
SSTR2	NA	UP	2.031	8.80e-10	53.9
KMO	NA	UP	5.165	6.24e-09	19.5
NR4A3	NA	UP	5.574	1.45e-08	20.2
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
PTGER2	NA	UP	3.006	1.95e-04	11.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8

## Ruta: cellular response to lipid (Página 3 de 3)

Fuente: GO:BP | ID: GO:0071396 | Genes: 57 | p-valor ruta: 1.06e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LY96	NA	UP	5.204	4.42e-03	3.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
TP63	NA	UP	3.788	4.09e-02	2.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: positive regulation of gene expression (Página 1 de 4)

Fuente: GO:BP | ID: GO:0010628 | Genes: 82 | p-valor ruta: 1.07e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1

## Ruta: positive regulation of gene expression (Página 2 de 4)

Fuente: GO:BP | ID: GO:0010628 | Genes: 82 | p-valor ruta: 1.07e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
PRDM1	NA	UP	3.525	5.98e-31	99.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4

## Ruta: positive regulation of gene expression (Página 3 de 4)

Fuente: GO:BP | ID: GO:0010628 | Genes: 82 | p-valor ruta: 1.07e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NLRP3	NA	UP	4.366	3.67e-13	29.8
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
RUNX2	NA	UP	3.983	1.50e-06	15.2
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
RBMS3	NA	UP	2.303	4.11e-04	18.6
KIT	NA	UP	3.650	6.24e-04	7.9
CEACAM20	NA	UP	5.412	1.17e-03	3.6
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4

## Ruta: positive regulation of gene expression (Página 4 de 4)

Fuente: GO:BP | ID: GO:0010628 | Genes: 82 | p-valor ruta: 1.07e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: positive regulation of innate immune response (Página 1 de 2)

Fuente: GO:BP | ID: GO:0045089 | Genes: 44 | p-valor ruta: 5.28e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
NR1D1	NA	UP	2.475	2.08e-68	1229.5

## Ruta: positive regulation of innate immune response (Página 2 de 2)

Fuente: GO:BP | ID: GO:0045089 | Genes: 44 | p-valor ruta: 5.28e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM5	NA	UP	2.172	6.62e-61	1222.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: positive regulation of response to biotic stimulus (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002833 | Genes: 45 | p-valor ruta: 1.16e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
NR1D1	NA	UP	2.475	2.08e-68	1229.5

## Ruta: positive regulation of response to biotic stimulus (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002833 | Genes: 45 | p-valor ruta: 1.16e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM5	NA	UP	2.172	6.62e-61	1222.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
HRG	NA	UP	2.971	4.00e-03	6.9
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of cell population proliferation (Página 1 de 4)

Fuente: GO:BP | ID: GO:0042127 | Genes: 97 | p-valor ruta: 1.39e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1

## Ruta: regulation of cell population proliferation (Página 2 de 4)

Fuente: GO:BP | ID: GO:0042127 | Genes: 97 | p-valor ruta: 1.39e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
FUT3	NA	UP	2.139	2.84e-41	355.7
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: regulation of cell population proliferation (Página 3 de 4)

Fuente: GO:BP | ID: GO:0042127 | Genes: 97 | p-valor ruta: 1.39e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
LIFR	NA	UP	2.213	9.30e-24	226.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
FLT3LG	NA	UP	2.346	6.32e-15	68.5
KLF9	NA	UP	2.555	7.01e-13	66.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SSTR2	NA	UP	2.031	8.80e-10	53.9
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4

## Ruta: regulation of cell population proliferation (Página 4 de 4)

Fuente: GO:BP | ID: GO:0042127 | Genes: 97 | p-valor ruta: 1.39e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTGER2	NA	UP	3.006	1.95e-04	11.0
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
POU3F2	NA	UP	4.735	2.02e-03	4.5
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
CD70	NA	UP	3.257	1.21e-02	4.7
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
IL34	NA	UP	2.794	2.41e-02	4.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: multicellular organismal process (Página 1 de 10)

Fuente: GO:BP | ID: GO:0032501 | Genes: 249 | p-valor ruta: 1.44e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8

## Ruta: multicellular organismal process (Página 2 de 10)

Fuente: GO:BP | ID: GO:0032501 | Genes: 249 | p-valor ruta: 1.44e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9

## Ruta: multicellular organismal process (Página 3 de 10)

Fuente: GO:BP | ID: GO:0032501 | Genes: 249 | p-valor ruta: 1.44e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
IFI35	NA	UP	2.237	9.59e-79	2236.7
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5

## Ruta: multicellular organismal process (Página 4 de 10)

Fuente: GO:BP | ID: GO:0032501 | Genes: 249 | p-valor ruta: 1.44e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TUFT1	NA	UP	2.001	1.00e-55	1905.9
FOSB	NA	UP	3.144	1.32e-55	267.7
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
NAV2	NA	UP	2.370	3.20e-51	765.9
THEMIS2	NA	UP	2.550	2.88e-50	403.0
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
LTB	NA	UP	3.555	2.50e-41	150.4

## Ruta: multicellular organismal process (Página 5 de 10)

Fuente: GO:BP | ID: GO:0032501 | Genes: 249 | p-valor ruta: 1.44e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
KRT6B	NA	UP	2.049	5.47e-24	321.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
DDO	NA	UP	2.846	3.84e-20	82.4
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: multicellular organismal process (Página 6 de 10)

Fuente: GO:BP | ID: GO:0032501 | Genes: 249 | p-valor ruta: 1.44e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DDC	NA	DOWN	-2.582	2.27e-16	72.0
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
DNAAF3	NA	DOWN	-2.041	1.75e-14	101.4
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
MUC4	NA	UP	2.613	4.74e-12	55.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
PPP4R4	NA	UP	3.423	6.94e-11	30.7
SCN3A	NA	UP	8.277	2.66e-10	27.0
DUOX1	NA	UP	3.131	5.18e-10	27.1

## Ruta: multicellular organismal process (Página 7 de 10)

Fuente: GO:BP | ID: GO:0032501 | Genes: 249 | p-valor ruta: 1.44e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
BAHCC1	NA	UP	4.513	9.67e-08	16.6
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
COL4A1	NA	UP	6.589	5.89e-06	8.2
SP8	NA	UP	6.528	5.89e-06	8.0
ACTBL2	NA	UP	2.242	5.97e-06	28.3
BEST1	NA	UP	3.553	8.47e-06	13.3

## Ruta: multicellular organismal process (Página 8 de 10)

Fuente: GO:BP | ID: GO:0032501 | Genes: 249 | p-valor ruta: 1.44e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ADAMTS6	NA	UP	2.602	8.90e-06	19.6
MMP13	NA	UP	5.406	9.23e-06	11.1
SERPINA10	NA	UP	6.459	9.50e-06	7.5
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
EGR3	NA	UP	2.096	2.87e-04	21.5
MPZ	NA	UP	2.002	2.88e-04	19.4
TRPC4	NA	UP	5.730	3.71e-04	4.5
NCALD	NA	UP	2.037	3.82e-04	17.1
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
ENKUR	NA	UP	3.518	8.61e-04	9.0
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
LHB	NA	UP	3.522	1.50e-03	7.0
TBX15	NA	UP	2.824	1.94e-03	8.6

## Ruta: multicellular organismal process (Página 9 de 10)

Fuente: GO:BP | ID: GO:0032501 | Genes: 249 | p-valor ruta: 1.44e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
KRT81	NA	UP	2.044	4.94e-03	15.2
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
SDK2	NA	UP	2.715	5.83e-03	7.9
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9

## Ruta: multicellular organismal process (Página 10 de 10)

Fuente: GO:BP | ID: GO:0032501 | Genes: 249 | p-valor ruta: 1.44e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OLR1	NA	UP	2.655	1.81e-02	6.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
SPRR2A	NA	UP	2.086	2.78e-02	7.8
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
INSC	NA	UP	3.872	3.01e-02	2.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7
HSD11B1	NA	UP	2.341	3.03e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8
KCNE4	NA	UP	2.337	3.37e-02	5.7
ADAMTS4	NA	UP	3.293	3.88e-02	3.0
TP63	NA	UP	3.788	4.09e-02	2.3
PPEF1	NA	UP	3.725	4.31e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: response to oxygen-containing compound (Página 1 de 4)

Fuente: GO:BP | ID: GO:1901700 | Genes: 96 | p-valor ruta: 2.4e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CMPK2	NA	UP	4.677	1.14e-162	1687.4
CXCL2	NA	UP	3.371	1.67e-155	4155.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STC2	NA	UP	2.729	3.17e-119	2626.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5

## Ruta: response to oxygen-containing compound (Página 2 de 4)

Fuente: GO:BP | ID: GO:1901700 | Genes: 96 | p-valor ruta: 2.4e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
IRS2	NA	UP	2.254	1.06e-33	255.2

## Ruta: response to oxygen-containing compound (Página 3 de 4)

Fuente: GO:BP | ID: GO:1901700 | Genes: 96 | p-valor ruta: 2.4e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HDAC9	NA	UP	2.292	4.51e-32	2003.2
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NKX3-1	NA	UP	2.233	8.30e-23	132.4
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0

## Ruta: response to oxygen-containing compound (Página 4 de 4)

Fuente: GO:BP | ID: GO:1901700 | Genes: 96 | p-valor ruta: 2.4e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL10RA	NA	UP	3.172	3.66e-07	18.8
MMP13	NA	UP	5.406	9.23e-06	11.1
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
NPTX1	NA	UP	2.102	1.13e-04	22.3
PTGER2	NA	UP	3.006	1.95e-04	11.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
SLC1A2	NA	UP	2.752	2.07e-03	8.4
LY96	NA	UP	5.204	4.42e-03	3.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
THBD	NA	UP	2.330	1.23e-02	7.3
RET	NA	UP	2.793	1.44e-02	5.5
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of cell motility (Página 1 de 3)

Fuente: GO:BP | ID: GO:2000145 | Genes: 72 | p-valor ruta: 4.21e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1

## Ruta: regulation of cell motility (Página 2 de 3)

Fuente: GO:BP | ID: GO:2000145 | Genes: 72 | p-valor ruta: 4.21e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
SEMA3A	NA	UP	2.276	5.71e-42	512.5
FUT3	NA	UP	2.139	2.84e-41	355.7
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
DUOXA2	NA	UP	4.650	3.36e-16	39.7
NAV3	NA	UP	2.285	2.77e-15	84.4
ZEB2	NA	UP	3.419	5.95e-12	30.5

## Ruta: regulation of cell motility (Página 3 de 3)

Fuente: GO:BP | ID: GO:2000145 | Genes: 72 | p-valor ruta: 4.21e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL23A	NA	UP	2.189	2.05e-11	59.9
DUOX1	NA	UP	3.131	5.18e-10	27.1
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
TTLL6	NA	UP	2.577	1.74e-02	6.7
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of metabolic process (Página 1 de 7)

Fuente: GO:BP | ID: GO:0009893 | Genes: 154 | p-valor ruta: 5.66e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
KLF6	NA	UP	2.653	7.59e-116	4943.3

## Ruta: positive regulation of metabolic process (Página 2 de 7)

Fuente: GO:BP | ID: GO:0009893 | Genes: 154 | p-valor ruta: 5.66e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5

## Ruta: positive regulation of metabolic process (Página 3 de 7)

Fuente: GO:BP | ID: GO:0009893 | Genes: 154 | p-valor ruta: 5.66e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8

## Ruta: positive regulation of metabolic process (Página 4 de 7)

Fuente: GO:BP | ID: GO:0009893 | Genes: 154 | p-valor ruta: 5.66e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PDE4B	NA	UP	3.818	7.08e-52	171.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2

## Ruta: positive regulation of metabolic process (Página 5 de 7)

Fuente: GO:BP | ID: GO:0009893 | Genes: 154 | p-valor ruta: 5.66e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8

## Ruta: positive regulation of metabolic process (Página 6 de 7)

Fuente: GO:BP | ID: GO:0009893 | Genes: 154 | p-valor ruta: 5.66e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR3	NA	UP	2.096	2.87e-04	21.5
RBMS3	NA	UP	2.303	4.11e-04	18.6
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CEACAM20	NA	UP	5.412	1.17e-03	3.6
RNF152	NA	UP	3.325	1.37e-03	7.5
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
RUFY4	NA	UP	4.136	2.15e-03	6.0
PATL2	NA	UP	2.215	2.72e-03	12.1
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6

## Ruta: positive regulation of metabolic process (Página 7 de 7)

Fuente: GO:BP | ID: GO:0009893 | Genes: 154 | p-valor ruta: 5.66e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: viral genome replication (Página 1 de 2)

Fuente: GO:BP | ID: GO:0019079 | Genes: 27 | p-valor ruta: 6.89e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
MX1	NA	UP	3.859	1.25e-245	5699.6
IFIH1	NA	UP	4.035	2.22e-233	4525.3
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
OAS3	NA	UP	2.942	1.13e-87	8674.1
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFIT5	NA	UP	2.861	3.01e-78	749.8
CCL2	NA	UP	2.562	2.63e-75	658.0
ISG15	NA	UP	2.482	5.90e-57	3807.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
BST2	NA	UP	4.284	3.82e-19	50.8
IFITM2	NA	UP	2.649	6.22e-17	64.2
APOBEC3D	NA	UP	2.051	7.01e-10	51.0

## Ruta: viral genome replication (Página 2 de 2)

Fuente: GO:BP | ID: GO:0019079 | Genes: 27 | p-valor ruta: 6.89e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP7	NA	UP	4.177	1.61e-02	2.9
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of multicellular organismal process (Página 1 de 3)

Fuente: GO:BP | ID: GO:0051241 | Genes: 74 | p-valor ruta: 8.6e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STC2	NA	UP	2.729	3.17e-119	2626.1
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4

## Ruta: negative regulation of multicellular organismal process (Página 2 de 3)

Fuente: GO:BP | ID: GO:0051241 | Genes: 74 | p-valor ruta: 8.6e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
THBS1	NA	UP	2.656	1.05e-77	3791.3
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CD69	NA	UP	3.112	5.99e-57	257.2
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BMP2	NA	UP	2.237	3.69e-40	325.3
HDAC9	NA	UP	2.292	4.51e-32	2003.2
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
IL15	NA	UP	2.012	2.28e-17	116.8
NAV3	NA	UP	2.285	2.77e-15	84.4

## Ruta: negative regulation of multicellular organismal process (Página 3 de 3)

Fuente: GO:BP | ID: GO:0051241 | Genes: 74 | p-valor ruta: 8.6e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
LST1	NA	UP	6.916	7.00e-07	10.5
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
IL18R1	NA	UP	2.088	8.75e-05	23.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
THBD	NA	UP	2.330	1.23e-02	7.3
PRG2	NA	UP	2.073	1.32e-02	9.7
GBP7	NA	UP	4.177	1.61e-02	2.9
NPR3	NA	UP	2.789	1.87e-02	5.7
ALPK2	NA	UP	3.025	2.06e-02	4.7
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: viral process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0016032 | Genes: 45 | p-valor ruta: 1.07e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
MX1	NA	UP	3.859	1.25e-245	5699.6
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TRIM22	NA	UP	5.650	1.01e-212	913.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFIT5	NA	UP	2.861	3.01e-78	749.8
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0

## Ruta: viral process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0016032 | Genes: 45 | p-valor ruta: 1.07e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LGALS9	NA	UP	2.474	3.44e-71	1449.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
PTX3	NA	UP	3.614	2.25e-68	237.4
JUN	NA	UP	2.450	1.10e-62	6693.5
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
PARP10	NA	UP	2.093	5.71e-52	2376.2
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
BST2	NA	UP	4.284	3.82e-19	50.8
IFITM2	NA	UP	2.649	6.22e-17	64.2
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
GBP7	NA	UP	4.177	1.61e-02	2.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
RFPL1	NA	UP	3.259	2.06e-02	4.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of locomotion (Página 1 de 3)

Fuente: GO:BP | ID: GO:0040012 | Genes: 73 | p-valor ruta: 1.18e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0

## Ruta: regulation of locomotion (Página 2 de 3)

Fuente: GO:BP | ID: GO:0040012 | Genes: 73 | p-valor ruta: 1.18e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTAFR	NA	UP	3.014	4.62e-62	338.1
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
SEMA3A	NA	UP	2.276	5.71e-42	512.5
FUT3	NA	UP	2.139	2.84e-41	355.7
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
DUOXA2	NA	UP	4.650	3.36e-16	39.7
NAV3	NA	UP	2.285	2.77e-15	84.4

## Ruta: regulation of locomotion (Página 3 de 3)

Fuente: GO:BP | ID: GO:0040012 | Genes: 73 | p-valor ruta: 1.18e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
DUOX1	NA	UP	3.131	5.18e-10	27.1
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
TTLL6	NA	UP	2.577	1.74e-02	6.7
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of macromolecule metabolic process (Página 1 de 6)

Fuente: GO:BP | ID: GO:0010604 | Genes: 144 | p-valor ruta: 2.01e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4

## Ruta: positive regulation of macromolecule metabolic process (Página 2 de 6)

Fuente: GO:BP | ID: GO:0010604 | Genes: 144 | p-valor ruta: 2.01e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2

## Ruta: positive regulation of macromolecule metabolic process (Página 3 de 6)

Fuente: GO:BP | ID: GO:0010604 | Genes: 144 | p-valor ruta: 2.01e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6

## Ruta: positive regulation of macromolecule metabolic process (Página 4 de 6)

Fuente: GO:BP | ID: GO:0010604 | Genes: 144 | p-valor ruta: 2.01e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7

## Ruta: positive regulation of macromolecule metabolic process (Página 5 de 6)

Fuente: GO:BP | ID: GO:0010604 | Genes: 144 | p-valor ruta: 2.01e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
RBMS3	NA	UP	2.303	4.11e-04	18.6
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CEACAM20	NA	UP	5.412	1.17e-03	3.6
TBX15	NA	UP	2.824	1.94e-03	8.6

## Ruta: positive regulation of macromolecule metabolic process (Página 6 de 6)

Fuente: GO:BP | ID: GO:0010604 | Genes: 144 | p-valor ruta: 2.01e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of cellular process (Página 1 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1

## Ruta: regulation of cellular process (Página 2 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
XAF1	NA	UP	4.580	3.19e-111	427.9

## Ruta: regulation of cellular process (Página 3 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
NUAK2	NA	UP	4.358	1.14e-107	489.1
SP110	NA	UP	2.776	1.00e-106	1474.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
RASGRP3	NA	UP	3.468	2.92e-82	392.1

## Ruta: regulation of cellular process (Página 4 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
HSH2D	NA	UP	2.613	6.29e-73	813.8
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6

## Ruta: regulation of cellular process (Página 5 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
RND1	NA	UP	2.840	1.60e-62	337.7
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TUFT1	NA	UP	2.001	1.00e-55	1905.9
FOSB	NA	UP	3.144	1.32e-55	267.7
SERPINB2	NA	UP	2.344	2.67e-55	2507.0

## Ruta: regulation of cellular process (Página 6 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4

## Ruta: regulation of cellular process (Página 7 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DUSP8	NA	UP	2.088	3.69e-35	551.5
MIR155HG	NA	UP	5.318	4.66e-35	99.1
ZNF267	NA	UP	2.059	1.30e-34	677.0
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
EDN2	NA	UP	3.499	8.77e-31	90.3
BACH2	NA	UP	2.222	2.18e-30	209.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
HDX	NA	UP	2.521	1.83e-28	139.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
BCL2L14	NA	UP	2.782	8.63e-26	122.3
MAST4	NA	UP	2.184	1.21e-25	197.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1

## Ruta: regulation of cellular process (Página 8 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
DDO	NA	UP	2.846	3.84e-20	82.4
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
DEPDC7	NA	UP	2.115	7.88e-19	114.2
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
INHBE	NA	UP	5.109	1.59e-15	37.3

## Ruta: regulation of cellular process (Página 9 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RAET1L	NA	UP	2.665	2.71e-15	60.0
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PLEKHG7	NA	UP	3.625	2.08e-12	31.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3

## Ruta: regulation of cellular process (Página 10 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
TAGAP	NA	UP	3.201	2.52e-06	16.1
RAB30	NA	UP	2.024	5.27e-06	28.7
COL4A1	NA	UP	6.589	5.89e-06	8.2
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
ADCY4	NA	UP	2.271	8.12e-06	23.6
BEST1	NA	UP	3.553	8.47e-06	13.3

## Ruta: regulation of cellular process (Página 11 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
PTGER2	NA	UP	3.006	1.95e-04	11.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
EGR3	NA	UP	2.096	2.87e-04	21.5
ZNF382	NA	UP	2.028	3.78e-04	18.2
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8

## Ruta: regulation of cellular process (Página 12 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CEACAM20	NA	UP	5.412	1.17e-03	3.6
RNF152	NA	UP	3.325	1.37e-03	7.5
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
LHB	NA	UP	3.522	1.50e-03	7.0
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
RUFY4	NA	UP	4.136	2.15e-03	6.0
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
PATL2	NA	UP	2.215	2.72e-03	12.1
IL17C	NA	UP	4.636	3.13e-03	4.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
EGFL6	NA	UP	3.034	6.01e-03	5.9
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0

## Ruta: regulation of cellular process (Página 13 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
TTLL6	NA	UP	2.577	1.74e-02	6.7
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
CELF6	NA	UP	2.403	2.65e-02	5.6

## Ruta: regulation of cellular process (Página 14 de 14)

Fuente: GO:BP | ID: GO:0050794 | Genes: 342 | p-valor ruta: 2.73e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
INSC	NA	UP	3.872	3.01e-02	2.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
CR1L	NA	UP	3.479	3.30e-02	3.5
CCL17	NA	UP	3.441	3.89e-02	2.9
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
PURG	NA	DOWN	-4.166	4.66e-02	1.7
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of cell migration (Página 1 de 3)

Fuente: GO:BP | ID: GO:0030334 | Genes: 68 | p-valor ruta: 3.68e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1

## Ruta: regulation of cell migration (Página 2 de 3)

Fuente: GO:BP | ID: GO:0030334 | Genes: 68 | p-valor ruta: 3.68e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
SEMA3A	NA	UP	2.276	5.71e-42	512.5
FUT3	NA	UP	2.139	2.84e-41	355.7
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
NAV3	NA	UP	2.285	2.77e-15	84.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
NR4A3	NA	UP	5.574	1.45e-08	20.2

## Ruta: regulation of cell migration (Página 3 de 3)

Fuente: GO:BP | ID: GO:0030334 | Genes: 68 | p-valor ruta: 3.68e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: cell population proliferation (Página 1 de 5)

Fuente: GO:BP | ID: GO:0008283 | Genes: 105 | p-valor ruta: 4.13e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0

## Ruta: cell population proliferation (Página 2 de 5)

Fuente: GO:BP | ID: GO:0008283 | Genes: 105 | p-valor ruta: 4.13e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3

## Ruta: cell population proliferation (Página 3 de 5)

Fuente: GO:BP | ID: GO:0008283 | Genes: 105 | p-valor ruta: 4.13e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SPRY2	NA	UP	2.250	1.05e-29	211.9
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
LIFR	NA	UP	2.213	9.30e-24	226.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBX2	NA	UP	2.353	5.55e-15	78.3
FLT3LG	NA	UP	2.346	6.32e-15	68.5
KLF9	NA	UP	2.555	7.01e-13	66.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SSTR2	NA	UP	2.031	8.80e-10	53.9
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1

## Ruta: cell population proliferation (Página 4 de 5)

Fuente: GO:BP | ID: GO:0008283 | Genes: 105 | p-valor ruta: 4.13e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
PTGER2	NA	UP	3.006	1.95e-04	11.0
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
POU3F2	NA	UP	4.735	2.02e-03	4.5
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
CD70	NA	UP	3.257	1.21e-02	4.7
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1

## Ruta: cell population proliferation (Página 5 de 5)

Fuente: GO:BP | ID: GO:0008283 | Genes: 105 | p-valor ruta: 4.13e-15

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL34	NA	UP	2.794	2.41e-02	4.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of intracellular signal transduction (Página 1 de 3)

Fuente: GO:BP | ID: GO:1902533 | Genes: 73 | p-valor ruta: 1.21e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6

## Ruta: positive regulation of intracellular signal transduction (Página 2 de 3)

Fuente: GO:BP | ID: GO:1902533 | Genes: 73 | p-valor ruta: 1.21e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ANKRD1	NA	UP	3.496	4.72e-69	335.9
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: positive regulation of intracellular signal transduction (Página 3 de 3)

Fuente: GO:BP | ID: GO:1902533 | Genes: 73 | p-valor ruta: 1.21e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR6	NA	UP	2.680	9.77e-08	26.3
NPR1	NA	UP	3.131	3.66e-07	19.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of biological process (Página 1 de 9)

Fuente: GO:BP | ID: GO:0048519 | Genes: 208 | p-valor ruta: 2.18e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2

## Ruta: negative regulation of biological process (Página 2 de 9)

Fuente: GO:BP | ID: GO:0048519 | Genes: 208 | p-valor ruta: 2.18e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3

## Ruta: negative regulation of biological process (Página 3 de 9)

Fuente: GO:BP | ID: GO:0048519 | Genes: 208 | p-valor ruta: 2.18e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
ETV7	NA	UP	4.688	2.39e-83	278.8
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8

## Ruta: negative regulation of biological process (Página 4 de 9)

Fuente: GO:BP | ID: GO:0048519 | Genes: 208 | p-valor ruta: 2.18e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
RND1	NA	UP	2.840	1.60e-62	337.7
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
FOSB	NA	UP	3.144	1.32e-55	267.7
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4

## Ruta: negative regulation of biological process (Página 5 de 9)

Fuente: GO:BP | ID: GO:0048519 | Genes: 208 | p-valor ruta: 2.18e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
XRN1	NA	UP	2.115	6.38e-50	984.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
MT2A	NA	UP	2.437	2.24e-35	363.0
DUSP8	NA	UP	2.088	3.69e-35	551.5
MIR155HG	NA	UP	5.318	4.66e-35	99.1
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4

## Ruta: negative regulation of biological process (Página 6 de 9)

Fuente: GO:BP | ID: GO:0048519 | Genes: 208 | p-valor ruta: 2.18e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IFITM2	NA	UP	2.649	6.22e-17	64.2
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
KLF9	NA	UP	2.555	7.01e-13	66.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
SSTR2	NA	UP	2.031	8.80e-10	53.9
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1

## Ruta: negative regulation of biological process (Página 7 de 9)

Fuente: GO:BP | ID: GO:0048519 | Genes: 208 | p-valor ruta: 2.18e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
BEST3	NA	UP	2.070	3.26e-05	23.9
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CNTN4	NA	UP	4.928	9.17e-04	5.0
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2

## Ruta: negative regulation of biological process (Página 8 de 9)

Fuente: GO:BP | ID: GO:0048519 | Genes: 208 | p-valor ruta: 2.18e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RNF152	NA	UP	3.325	1.37e-03	7.5
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
THBD	NA	UP	2.330	1.23e-02	7.3
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
RANBP3L	NA	UP	4.634	1.47e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
NPR3	NA	UP	2.789	1.87e-02	5.7
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
IKZF1	NA	UP	2.283	2.21e-02	6.8
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8

## Ruta: negative regulation of biological process (Página 9 de 9)

Fuente: GO:BP | ID: GO:0048519 | Genes: 208 | p-valor ruta: 2.18e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CR1L	NA	UP	3.479	3.30e-02	3.5
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: activation of innate immune response (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002218 | Genes: 37 | p-valor ruta: 2.25e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
NR1D1	NA	UP	2.475	2.08e-68	1229.5
TRIM5	NA	UP	2.172	6.62e-61	1222.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2

## Ruta: activation of innate immune response (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002218 | Genes: 37 | p-valor ruta: 2.25e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: intracellular signaling cassette (Página 1 de 4)

Fuente: GO:BP | ID: GO:0141124 | Genes: 100 | p-valor ruta: 2.64e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
CCL20	NA	UP	3.959	5.09e-242	2226.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
TRAF1	NA	UP	4.730	5.65e-84	258.2
RASGRP3	NA	UP	3.468	2.92e-82	392.1
KLF4	NA	UP	2.704	2.52e-79	645.9

## Ruta: intracellular signaling cassette (Página 2 de 4)

Fuente: GO:BP | ID: GO:0141124 | Genes: 100 | p-valor ruta: 2.64e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ADRB2	NA	UP	2.471	2.83e-79	954.4
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
RND1	NA	UP	2.840	1.60e-62	337.7
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0

## Ruta: intracellular signaling cassette (Página 3 de 4)

Fuente: GO:BP | ID: GO:0141124 | Genes: 100 | p-valor ruta: 2.64e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PER1	NA	UP	2.501	8.94e-44	469.6
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
PLEKHG7	NA	UP	3.625	2.08e-12	31.8
IL23A	NA	UP	2.189	2.05e-11	59.9
CYTH4	NA	UP	2.691	3.08e-10	36.2
LRP2	NA	UP	3.144	3.22e-08	22.0

## Ruta: intracellular signaling cassette (Página 4 de 4)

Fuente: GO:BP | ID: GO:0141124 | Genes: 100 | p-valor ruta: 2.64e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
TAGAP	NA	UP	3.201	2.52e-06	16.1
RAB30	NA	UP	2.024	5.27e-06	28.7
SELE	NA	UP	5.745	2.05e-05	9.0
IL18R1	NA	UP	2.088	8.75e-05	23.0
NCALD	NA	UP	2.037	3.82e-04	17.1
KIT	NA	UP	3.650	6.24e-04	7.9
PEX5L	NA	UP	3.321	2.40e-03	7.0
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: viral life cycle (Página 1 de 2)

Fuente: GO:BP | ID: GO:0019058 | Genes: 37 | p-valor ruta: 3.87e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
MX1	NA	UP	3.859	1.25e-245	5699.6
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TRIM22	NA	UP	5.650	1.01e-212	913.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
OAS3	NA	UP	2.942	1.13e-87	8674.1
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFIT5	NA	UP	2.861	3.01e-78	749.8
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5

## Ruta: viral life cycle (Página 2 de 2)

Fuente: GO:BP | ID: GO:0019058 | Genes: 37 | p-valor ruta: 3.87e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ISG15	NA	UP	2.482	5.90e-57	3807.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
BST2	NA	UP	4.284	3.82e-19	50.8
IFITM2	NA	UP	2.649	6.22e-17	64.2
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
GBP7	NA	UP	4.177	1.61e-02	2.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
RFPL1	NA	UP	3.259	2.06e-02	4.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: cell migration (Página 1 de 4)

Fuente: GO:BP | ID: GO:0016477 | Genes: 87 | p-valor ruta: 4.4e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CXCL2	NA	UP	3.371	1.67e-155	4155.4
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5

## Ruta: cell migration (Página 2 de 4)

Fuente: GO:BP | ID: GO:0016477 | Genes: 87 | p-valor ruta: 4.4e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
CH25H	NA	UP	7.817	1.04e-46	242.7
SEMA3A	NA	UP	2.276	5.71e-42	512.5
FUT3	NA	UP	2.139	2.84e-41	355.7
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: cell migration (Página 3 de 4)

Fuente: GO:BP | ID: GO:0016477 | Genes: 87 | p-valor ruta: 4.4e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
SYNPO2	NA	UP	3.603	1.95e-04	9.0
EGR3	NA	UP	2.096	2.87e-04	21.5
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
POU3F2	NA	UP	4.735	2.02e-03	4.5
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9

## Ruta: cell migration (Página 4 de 4)

Fuente: GO:BP | ID: GO:0016477 | Genes: 87 | p-valor ruta: 4.4e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: cell motility (Página 1 de 4)

Fuente: GO:BP | ID: GO:0048870 | Genes: 95 | p-valor ruta: 9.23e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CXCL2	NA	UP	3.371	1.67e-155	4155.4
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5

## Ruta: cell motility (Página 2 de 4)

Fuente: GO:BP | ID: GO:0048870 | Genes: 95 | p-valor ruta: 9.23e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
CH25H	NA	UP	7.817	1.04e-46	242.7
SEMA3A	NA	UP	2.276	5.71e-42	512.5
FUT3	NA	UP	2.139	2.84e-41	355.7
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2

## Ruta: cell motility (Página 3 de 4)

Fuente: GO:BP | ID: GO:0048870 | Genes: 95 | p-valor ruta: 9.23e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
DUOXA2	NA	UP	4.650	3.36e-16	39.7
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
DNAH17	NA	UP	3.324	3.42e-13	38.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
DUOX1	NA	UP	3.131	5.18e-10	27.1
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0
ACTBL2	NA	UP	2.242	5.97e-06	28.3
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
SYNPO2	NA	UP	3.603	1.95e-04	9.0
EGR3	NA	UP	2.096	2.87e-04	21.5
CXCL9	NA	UP	4.099	4.37e-04	26.3

## Ruta: cell motility (Página 4 de 4)

Fuente: GO:BP | ID: GO:0048870 | Genes: 95 | p-valor ruta: 9.23e-14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KIT	NA	UP	3.650	6.24e-04	7.9
ENKUR	NA	UP	3.518	8.61e-04	9.0
POU3F2	NA	UP	4.735	2.02e-03	4.5
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
SLC9B1	NA	UP	4.128	1.36e-02	3.1
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
TTLL6	NA	UP	2.577	1.74e-02	6.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of response to stimulus (Página 1 de 4)

Fuente: GO:BP | ID: GO:0048585 | Genes: 91 | p-valor ruta: 1.26e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4

## Ruta: negative regulation of response to stimulus (Página 2 de 4)

Fuente: GO:BP | ID: GO:0048585 | Genes: 91 | p-valor ruta: 1.26e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IFI35	NA	UP	2.237	9.59e-79	2236.7
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1

## Ruta: negative regulation of response to stimulus (Página 3 de 4)

Fuente: GO:BP | ID: GO:0048585 | Genes: 91 | p-valor ruta: 1.26e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
PER1	NA	UP	2.501	8.94e-44	469.6
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BDKRB2	NA	UP	2.797	5.56e-15	55.1
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
IL10RA	NA	UP	3.172	3.66e-07	18.8
RUNX2	NA	UP	3.983	1.50e-06	15.2
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0

## Ruta: negative regulation of response to stimulus (Página 4 de 4)

Fuente: GO:BP | ID: GO:0048585 | Genes: 91 | p-valor ruta: 1.26e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RBMS3	NA	UP	2.303	4.11e-04	18.6
RNF152	NA	UP	3.325	1.37e-03	7.5
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
THBD	NA	UP	2.330	1.23e-02	7.3
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
CR1L	NA	UP	3.479	3.30e-02	3.5
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: interferon-mediated signaling pathway

Fuente: GO:BP | ID: GO:0140888 | Genes: 23 | p-valor ruta: 1.81e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
ZBP1	NA	UP	6.242	1.22e-99	349.5
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
STAT1	NA	UP	2.519	1.61e-68	9528.0
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
IFNL3	NA	UP	9.837	4.42e-30	365.0
IFNL2	NA	UP	11.372	1.86e-23	434.7
JAK2	NA	UP	2.081	1.26e-17	123.4
IFITM2	NA	UP	2.649	6.22e-17	64.2

## Ruta: regulation of intracellular signal transduction (Página 1 de 4)

Fuente: GO:BP | ID: GO:1902531 | Genes: 99 | p-valor ruta: 3.25e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
NUAK2	NA	UP	4.358	1.14e-107	489.1
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9

## Ruta: regulation of intracellular signal transduction (Página 2 de 4)

Fuente: GO:BP | ID: GO:1902531 | Genes: 99 | p-valor ruta: 3.25e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0

## Ruta: regulation of intracellular signal transduction (Página 3 de 4)

Fuente: GO:BP | ID: GO:1902531 | Genes: 99 | p-valor ruta: 3.25e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PER1	NA	UP	2.501	8.94e-44	469.6
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
BCL3	NA	UP	2.067	4.65e-26	500.4
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
IL23A	NA	UP	2.189	2.05e-11	59.9
CYTH4	NA	UP	2.691	3.08e-10	36.2
TLR6	NA	UP	2.680	9.77e-08	26.3

## Ruta: regulation of intracellular signal transduction (Página 4 de 4)

Fuente: GO:BP | ID: GO:1902531 | Genes: 99 | p-valor ruta: 3.25e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NPR1	NA	UP	3.131	3.66e-07	19.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
TAGAP	NA	UP	3.201	2.52e-06	16.1
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
RNF152	NA	UP	3.325	1.37e-03	7.5
PEX5L	NA	UP	3.321	2.40e-03	7.0
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: apoptotic process (Página 1 de 4)

Fuente: GO:BP | ID: GO:0006915 | Genes: 98 | p-valor ruta: 3.41e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1

## Ruta: apoptotic process (Página 2 de 4)

Fuente: GO:BP | ID: GO:0006915 | Genes: 98 | p-valor ruta: 3.41e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CTH	NA	UP	2.488	2.75e-57	412.1

## Ruta: apoptotic process (Página 3 de 4)

Fuente: GO:BP | ID: GO:0006915 | Genes: 98 | p-valor ruta: 3.41e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BBC3	NA	UP	2.829	3.65e-57	503.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
PPM1K	NA	UP	2.192	3.89e-30	395.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
ZEB2	NA	UP	3.419	5.95e-12	30.5
NLRP1	NA	UP	5.692	4.64e-09	21.6

## Ruta: apoptotic process (Página 4 de 4)

Fuente: GO:BP | ID: GO:0006915 | Genes: 98 | p-valor ruta: 3.41e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ACTN2	NA	UP	3.956	7.01e-09	20.3
LRP2	NA	UP	3.144	3.22e-08	22.0
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
XKR9	NA	UP	3.541	5.84e-05	11.9
NPTX1	NA	UP	2.102	1.13e-04	22.3
EGR3	NA	UP	2.096	2.87e-04	21.5
RNF152	NA	UP	3.325	1.37e-03	7.5
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
CD70	NA	UP	3.257	1.21e-02	4.7
RET	NA	UP	2.793	1.44e-02	5.5
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TRIM69	NA	UP	3.519	3.21e-02	3.0
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: cell death (Página 1 de 4)

Fuente: GO:BP | ID: GO:0008219 | Genes: 100 | p-valor ruta: 4.05e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1

## Ruta: cell death (Página 2 de 4)

Fuente: GO:BP | ID: GO:0008219 | Genes: 100 | p-valor ruta: 4.05e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5

## Ruta: cell death (Página 3 de 4)

Fuente: GO:BP | ID: GO:0008219 | Genes: 100 | p-valor ruta: 4.05e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CTH	NA	UP	2.488	2.75e-57	412.1
BBC3	NA	UP	2.829	3.65e-57	503.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
PPM1K	NA	UP	2.192	3.89e-30	395.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
ZEB2	NA	UP	3.419	5.95e-12	30.5

## Ruta: cell death (Página 4 de 4)

Fuente: GO:BP | ID: GO:0008219 | Genes: 100 | p-valor ruta: 4.05e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRP1	NA	UP	5.692	4.64e-09	21.6
ACTN2	NA	UP	3.956	7.01e-09	20.3
LRP2	NA	UP	3.144	3.22e-08	22.0
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
XKR9	NA	UP	3.541	5.84e-05	11.9
NPTX1	NA	UP	2.102	1.13e-04	22.3
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
RNF152	NA	UP	3.325	1.37e-03	7.5
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
CD70	NA	UP	3.257	1.21e-02	4.7
RET	NA	UP	2.793	1.44e-02	5.5
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TRIM69	NA	UP	3.519	3.21e-02	3.0
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: activation of immune response (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002253 | Genes: 48 | p-valor ruta: 4.38e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
NR1D1	NA	UP	2.475	2.08e-68	1229.5
TRIM5	NA	UP	2.172	6.62e-61	1222.6
PDE4B	NA	UP	3.818	7.08e-52	171.4

## Ruta: activation of immune response (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002253 | Genes: 48 | p-valor ruta: 4.38e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
THEMIS2	NA	UP	2.550	2.88e-50	403.0
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
C1R	NA	UP	2.188	3.06e-32	258.8
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: cell surface receptor signaling pathway via JAK–STAT

Fuente: GO:BP | ID: GO:0007259 | Genes: 25 | p-valor ruta: 4.52e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL10RA	NA	UP	3.172	3.66e-07	18.8
KIT	NA	UP	3.650	6.24e-04	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9

## Ruta: regulation of cell activation (Página 1 de 3)

Fuente: GO:BP | ID: GO:0050865 | Genes: 51 | p-valor ruta: 5.7e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
CD69	NA	UP	3.112	5.99e-57	257.2
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
THEMIS2	NA	UP	2.550	2.88e-50	403.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9

## Ruta: regulation of cell activation (Página 2 de 3)

Fuente: GO:BP | ID: GO:0050865 | Genes: 51 | p-valor ruta: 5.7e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRS2	NA	UP	2.254	1.06e-33	255.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
HRG	NA	UP	2.971	4.00e-03	6.9
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of cell activation (Página 3 de 3)

Fuente: GO:BP | ID: GO:0050865 | Genes: 51 | p-valor ruta: 5.7e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: positive regulation of cell motility (Página 1 de 2)

Fuente: GO:BP | ID: GO:2000147 | Genes: 49 | p-valor ruta: 6e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BMP2	NA	UP	2.237	3.69e-40	325.3

## Ruta: positive regulation of cell motility (Página 2 de 2)

Fuente: GO:BP | ID: GO:2000147 | Genes: 49 | p-valor ruta: 6e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
JAK2	NA	UP	2.081	1.26e-17	123.4
DUOXA2	NA	UP	4.650	3.36e-16	39.7
IL23A	NA	UP	2.189	2.05e-11	59.9
DUOX1	NA	UP	3.131	5.18e-10	27.1
NR4A3	NA	UP	5.574	1.45e-08	20.2
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: leukocyte differentiation (Página 1 de 3)

Fuente: GO:BP | ID: GO:0002521 | Genes: 51 | p-valor ruta: 7.38e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3

## Ruta: leukocyte differentiation (Página 2 de 3)

Fuente: GO:BP | ID: GO:0002521 | Genes: 51 | p-valor ruta: 7.38e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
CSF3	NA	UP	6.122	1.72e-19	56.0
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CLEC4E	NA	UP	3.620	4.75e-09	26.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RUNX2	NA	UP	3.983	1.50e-06	15.2
IL18R1	NA	UP	2.088	8.75e-05	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: leukocyte differentiation (Página 3 de 3)

Fuente: GO:BP | ID: GO:0002521 | Genes: 51 | p-valor ruta: 7.38e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: pattern recognition receptor signaling pathway (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002221 | Genes: 33 | p-valor ruta: 7.97e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
NR1D1	NA	UP	2.475	2.08e-68	1229.5
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7

## Ruta: pattern recognition receptor signaling pathway (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002221 | Genes: 33 | p-valor ruta: 7.97e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: cell chemotaxis (Página 1 de 2)

Fuente: GO:BP | ID: GO:0060326 | Genes: 36 | p-valor ruta: 9.68e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
HBEGF	NA	UP	2.602	3.10e-57	415.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
CH25H	NA	UP	7.817	1.04e-46	242.7
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0

## Ruta: cell chemotaxis (Página 2 de 2)

Fuente: GO:BP | ID: GO:0060326 | Genes: 36 | p-valor ruta: 9.68e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FFAR2	NA	UP	3.253	4.81e-05	12.7
EGR3	NA	UP	2.096	2.87e-04	21.5
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: programmed cell death (Página 1 de 4)

Fuente: GO:BP | ID: GO:0012501 | Genes: 99 | p-valor ruta: 1.01e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
MX1	NA	UP	3.859	1.25e-245	5699.6
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1

## Ruta: programmed cell death (Página 2 de 4)

Fuente: GO:BP | ID: GO:0012501 | Genes: 99 | p-valor ruta: 1.01e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CTH	NA	UP	2.488	2.75e-57	412.1

## Ruta: programmed cell death (Página 3 de 4)

Fuente: GO:BP | ID: GO:0012501 | Genes: 99 | p-valor ruta: 1.01e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BBC3	NA	UP	2.829	3.65e-57	503.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
PPM1K	NA	UP	2.192	3.89e-30	395.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
ZEB2	NA	UP	3.419	5.95e-12	30.5
NLRP1	NA	UP	5.692	4.64e-09	21.6

## Ruta: programmed cell death (Página 4 de 4)

Fuente: GO:BP | ID: GO:0012501 | Genes: 99 | p-valor ruta: 1.01e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ACTN2	NA	UP	3.956	7.01e-09	20.3
LRP2	NA	UP	3.144	3.22e-08	22.0
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
XKR9	NA	UP	3.541	5.84e-05	11.9
NPTX1	NA	UP	2.102	1.13e-04	22.3
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
RNF152	NA	UP	3.325	1.37e-03	7.5
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
CD70	NA	UP	3.257	1.21e-02	4.7
RET	NA	UP	2.793	1.44e-02	5.5
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TRIM69	NA	UP	3.519	3.21e-02	3.0
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: cellular response to oxygen-containing compound (Página 1 de 3)

Fuente: GO:BP | ID: GO:1901701 | Genes: 72 | p-valor ruta: 1.08e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CMPK2	NA	UP	4.677	1.14e-162	1687.4
CXCL2	NA	UP	3.371	1.67e-155	4155.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IRAK2	NA	UP	2.666	3.46e-95	1164.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2

## Ruta: cellular response to oxygen-containing compound (Página 2 de 3)

Fuente: GO:BP | ID: GO:1901701 | Genes: 72 | p-valor ruta: 1.08e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
SSTR2	NA	UP	2.031	8.80e-10	53.9
KMO	NA	UP	5.165	6.24e-09	19.5

## Ruta: cellular response to oxygen-containing compound (Página 3 de 3)

Fuente: GO:BP | ID: GO:1901701 | Genes: 72 | p-valor ruta: 1.08e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
NPTX1	NA	UP	2.102	1.13e-04	22.3
PTGER2	NA	UP	3.006	1.95e-04	11.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
SLC1A2	NA	UP	2.752	2.07e-03	8.4
LY96	NA	UP	5.204	4.42e-03	3.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of leukocyte activation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002694 | Genes: 48 | p-valor ruta: 1.32e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
CD69	NA	UP	3.112	5.99e-57	257.2
THEMIS2	NA	UP	2.550	2.88e-50	403.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2

## Ruta: regulation of leukocyte activation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002694 | Genes: 48 | p-valor ruta: 1.32e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: negative regulation of cytokine production (Página 1 de 2)

Fuente: GO:BP | ID: GO:0001818 | Genes: 34 | p-valor ruta: 1.74e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
GBP1	NA	UP	4.090	2.07e-209	2026.7
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
HDAC9	NA	UP	2.292	4.51e-32	2003.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8

## Ruta: negative regulation of cytokine production (Página 2 de 2)

Fuente: GO:BP | ID: GO:0001818 | Genes: 34 | p-valor ruta: 1.74e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NAV3	NA	UP	2.285	2.77e-15	84.4
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
SRGN	NA	UP	2.093	3.80e-03	11.0
DLL1	NA	UP	2.171	4.40e-03	10.4
PRG2	NA	UP	2.073	1.32e-02	9.7
GBP7	NA	UP	4.177	1.61e-02	2.9

## Ruta: positive regulation of locomotion (Página 1 de 2)

Fuente: GO:BP | ID: GO:0040017 | Genes: 49 | p-valor ruta: 1.75e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BMP2	NA	UP	2.237	3.69e-40	325.3

## Ruta: positive regulation of locomotion (Página 2 de 2)

Fuente: GO:BP | ID: GO:0040017 | Genes: 49 | p-valor ruta: 1.75e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
JAK2	NA	UP	2.081	1.26e-17	123.4
DUOXA2	NA	UP	4.650	3.36e-16	39.7
IL23A	NA	UP	2.189	2.05e-11	59.9
DUOX1	NA	UP	3.131	5.18e-10	27.1
NR4A3	NA	UP	5.574	1.45e-08	20.2
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of inflammatory response (Página 1 de 2)

Fuente: GO:BP | ID: GO:0050727 | Genes: 39 | p-valor ruta: 2.19e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
CCL5	NA	UP	5.035	8.94e-165	656.3
USP18	NA	UP	3.900	1.42e-145	1151.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
MAP3K8	NA	UP	2.825	4.57e-78	640.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
NR1D1	NA	UP	2.475	2.08e-68	1229.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2

## Ruta: regulation of inflammatory response (Página 2 de 2)

Fuente: GO:BP | ID: GO:0050727 | Genes: 39 | p-valor ruta: 2.19e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
NUPR1	NA	UP	3.660	1.78e-06	14.5
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: cell surface receptor signaling pathway via STAT

Fuente: GO:BP | ID: GO:0097696 | Genes: 25 | p-valor ruta: 2.93e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
IFNL2	NA	UP	11.372	1.86e-23	434.7
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL10RA	NA	UP	3.172	3.66e-07	18.8
KIT	NA	UP	3.650	6.24e-04	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9

## Ruta: vasculature development (Página 1 de 3)

Fuente: GO:BP | ID: GO:0001944 | Genes: 55 | p-valor ruta: 4.4e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CTH	NA	UP	2.488	2.75e-57	412.1
CYP1B1	NA	UP	2.786	9.33e-53	766.0
BMP2	NA	UP	2.237	3.69e-40	325.3
HDAC9	NA	UP	2.292	4.51e-32	2003.2

## Ruta: vasculature development (Página 2 de 3)

Fuente: GO:BP | ID: GO:0001944 | Genes: 55 | p-valor ruta: 4.4e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
LRP2	NA	UP	3.144	3.22e-08	22.0
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
COL4A1	NA	UP	6.589	5.89e-06	8.2
ADAMTS6	NA	UP	2.602	8.90e-06	19.6
FAP	NA	UP	3.233	1.87e-05	14.0
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
C3AR1	NA	UP	4.639	1.59e-02	2.2

## Ruta: vasculature development (Página 3 de 3)

Fuente: GO:BP | ID: GO:0001944 | Genes: 55 | p-valor ruta: 4.4e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of multicellular organismal development (Página 1 de 4)

Fuente: GO:BP | ID: GO:2000026 | Genes: 79 | p-valor ruta: 4.71e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6

## Ruta: regulation of multicellular organismal development (Página 2 de 4)

Fuente: GO:BP | ID: GO:2000026 | Genes: 79 | p-valor ruta: 4.71e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
PRDM1	NA	UP	3.525	5.98e-31	99.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
FUT1	NA	UP	2.765	4.55e-26	104.9
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
CSF3	NA	UP	6.122	1.72e-19	56.0
IL15	NA	UP	2.012	2.28e-17	116.8
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8

## Ruta: regulation of multicellular organismal development (Página 3 de 4)

Fuente: GO:BP | ID: GO:2000026 | Genes: 79 | p-valor ruta: 4.71e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
C3AR1	NA	UP	4.639	1.59e-02	2.2
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0

## Ruta: regulation of multicellular organismal development (Página 4 de 4)

Fuente: GO:BP | ID: GO:2000026 | Genes: 79 | p-valor ruta: 4.71e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of inflammatory response

Fuente: GO:BP | ID: GO:0050729 | Genes: 25 | p-valor ruta: 4.73e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
IFI35	NA	UP	2.237	9.59e-79	2236.7
MAP3K8	NA	UP	2.825	4.57e-78	640.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
TLR3	NA	UP	2.508	1.99e-22	111.5
CASP1	NA	UP	2.494	1.49e-18	80.2
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
NUPR1	NA	UP	3.660	1.78e-06	14.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: lymphocyte activation (Página 1 de 3)

Fuente: GO:BP | ID: GO:0046649 | Genes: 57 | p-valor ruta: 4.86e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
THEMIS2	NA	UP	2.550	2.88e-50	403.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4

## Ruta: lymphocyte activation (Página 2 de 3)

Fuente: GO:BP | ID: GO:0046649 | Genes: 57 | p-valor ruta: 4.86e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CLEC4E	NA	UP	3.620	4.75e-09	26.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
IL18R1	NA	UP	2.088	8.75e-05	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2

## Ruta: lymphocyte activation (Página 3 de 3)

Fuente: GO:BP | ID: GO:0046649 | Genes: 57 | p-valor ruta: 4.86e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: innate immune response–activating signaling pathway (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002758 | Genes: 33 | p-valor ruta: 4.99e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
NR1D1	NA	UP	2.475	2.08e-68	1229.5
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7

## Ruta: innate immune response–activating signaling pathway (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002758 | Genes: 33 | p-valor ruta: 4.99e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of cell adhesion (Página 1 de 3)

Fuente: GO:BP | ID: GO:0030155 | Genes: 56 | p-valor ruta: 6.45e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF4	NA	UP	2.704	2.52e-79	645.9
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0

## Ruta: regulation of cell adhesion (Página 2 de 3)

Fuente: GO:BP | ID: GO:0030155 | Genes: 56 | p-valor ruta: 6.45e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
CSF1	NA	UP	2.530	1.40e-49	467.4
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
LAMA2	NA	UP	2.355	4.82e-21	125.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
HRG	NA	UP	2.971	4.00e-03	6.9

## Ruta: regulation of cell adhesion (Página 3 de 3)

Fuente: GO:BP | ID: GO:0030155 | Genes: 56 | p-valor ruta: 6.45e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DLL1	NA	UP	2.171	4.40e-03	10.4
EGFL6	NA	UP	3.034	6.01e-03	5.9
CD70	NA	UP	3.257	1.21e-02	4.7
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: chemotaxis (Página 1 de 2)

Fuente: GO:BP | ID: GO:0006935 | Genes: 42 | p-valor ruta: 7.04e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
CH25H	NA	UP	7.817	1.04e-46	242.7
SEMA3A	NA	UP	2.276	5.71e-42	512.5
EDN2	NA	UP	3.499	8.77e-31	90.3
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: chemotaxis (Página 2 de 2)

Fuente: GO:BP | ID: GO:0006935 | Genes: 42 | p-valor ruta: 7.04e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
EGR3	NA	UP	2.096	2.87e-04	21.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
HRG	NA	UP	2.971	4.00e-03	6.9
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: mononuclear cell differentiation (Página 1 de 2)

Fuente: GO:BP | ID: GO:1903131 | Genes: 45 | p-valor ruta: 7.6e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
CSF2	NA	UP	7.043	2.08e-103	455.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
IRF7	NA	UP	3.210	5.72e-79	2126.1
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
VCAM1	NA	UP	4.737	4.28e-26	66.5

## Ruta: mononuclear cell differentiation (Página 2 de 2)

Fuente: GO:BP | ID: GO:1903131 | Genes: 45 | p-valor ruta: 7.6e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BCL3	NA	UP	2.067	4.65e-26	500.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CLEC4E	NA	UP	3.620	4.75e-09	26.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RUNX2	NA	UP	3.983	1.50e-06	15.2
IL18R1	NA	UP	2.088	8.75e-05	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: taxis (Página 1 de 2)

Fuente: GO:BP | ID: GO:0042330 | Genes: 42 | p-valor ruta: 8.17e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
CH25H	NA	UP	7.817	1.04e-46	242.7
SEMA3A	NA	UP	2.276	5.71e-42	512.5
EDN2	NA	UP	3.499	8.77e-31	90.3
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: taxis (Página 2 de 2)

Fuente: GO:BP | ID: GO:0042330 | Genes: 42 | p-valor ruta: 8.17e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
EGR3	NA	UP	2.096	2.87e-04	21.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
HRG	NA	UP	2.971	4.00e-03	6.9
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: canonical NF-kappaB signal transduction (Página 1 de 2)

Fuente: GO:BP | ID: GO:0007249 | Genes: 34 | p-valor ruta: 8.71e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
TRAF1	NA	UP	4.730	5.65e-84	258.2
KLF4	NA	UP	2.704	2.52e-79	645.9
IFIT5	NA	UP	2.861	3.01e-78	749.8
LGALS9	NA	UP	2.474	3.44e-71	1449.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
CTH	NA	UP	2.488	2.75e-57	412.1
PER1	NA	UP	2.501	8.94e-44	469.6
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
BCL3	NA	UP	2.067	4.65e-26	500.4

## Ruta: canonical NF–kappaB signal transduction (Página 2 de 2)

Fuente: GO:BP | ID: GO:0007249 | Genes: 34 | p–valor ruta: 8.71e–12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR3	NA	UP	2.508	1.99e–22	111.5
NOD2	NA	UP	2.981	1.19e–19	80.5
BST2	NA	UP	4.284	3.82e–19	50.8
CASP1	NA	UP	2.494	1.49e–18	80.2
TLR6	NA	UP	2.680	9.77e–08	26.3
GBP7	NA	UP	4.177	1.61e–02	2.9
TLR9	NA	UP	2.952	1.98e–02	4.6
RFPL1	NA	UP	3.259	2.06e–02	4.1
TMEM106A	NA	UP	2.485	2.20e–02	7.2

## Ruta: positive regulation of cell migration (Página 1 de 2)

Fuente: GO:BP | ID: GO:0030335 | Genes: 46 | p-valor ruta: 8.92e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BMP2	NA	UP	2.237	3.69e-40	325.3

## Ruta: positive regulation of cell migration (Página 2 de 2)

Fuente: GO:BP | ID: GO:0030335 | Genes: 46 | p-valor ruta: 8.92e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
JAK2	NA	UP	2.081	1.26e-17	123.4
IL23A	NA	UP	2.189	2.05e-11	59.9
NR4A3	NA	UP	5.574	1.45e-08	20.2
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
LGR6	NA	UP	3.915	2.25e-03	6.0
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of immune system process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002683 | Genes: 44 | p-valor ruta: 9.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
IDO1	NA	UP	4.167	4.38e-109	394.2
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5

## Ruta: negative regulation of immune system process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002683 | Genes: 44 | p-valor ruta: 9.57e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
LST1	NA	UP	6.916	7.00e-07	10.5
UBASH3A	NA	UP	5.845	1.05e-05	9.8
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
DLL1	NA	UP	2.171	4.40e-03	10.4
PRG2	NA	UP	2.073	1.32e-02	9.7
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of apoptotic process (Página 1 de 4)

Fuente: GO:BP | ID: GO:0042981 | Genes: 79 | p-valor ruta: 2.49e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
ASNS	NA	UP	2.919	1.59e-113	1627.6
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
CD274	NA	UP	5.204	1.23e-98	314.4

## Ruta: regulation of apoptotic process (Página 2 de 4)

Fuente: GO:BP | ID: GO:0042981 | Genes: 79 | p-valor ruta: 2.49e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CTH	NA	UP	2.488	2.75e-57	412.1
BBC3	NA	UP	2.829	3.65e-57	503.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
CYP1B1	NA	UP	2.786	9.33e-53	766.0
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4

## Ruta: regulation of apoptotic process (Página 3 de 4)

Fuente: GO:BP | ID: GO:0042981 | Genes: 79 | p-valor ruta: 2.49e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
ZEB2	NA	UP	3.419	5.95e-12	30.5
NLRP1	NA	UP	5.692	4.64e-09	21.6
ACTN2	NA	UP	3.956	7.01e-09	20.3
LRP2	NA	UP	3.144	3.22e-08	22.0
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
EGR3	NA	UP	2.096	2.87e-04	21.5
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5

## Ruta: regulation of apoptotic process (Página 4 de 4)

Fuente: GO:BP | ID: GO:0042981 | Genes: 79 | p-valor ruta: 2.49e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of immune effector process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002697 | Genes: 38 | p-valor ruta: 2.95e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
DDX60	NA	UP	3.015	7.43e-79	1999.9
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
PTAFR	NA	UP	3.014	4.62e-62	338.1
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8

## Ruta: regulation of immune effector process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002697 | Genes: 38 | p-valor ruta: 2.95e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
NR4A3	NA	UP	5.574	1.45e-08	20.2
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
KIT	NA	UP	3.650	6.24e-04	7.9
PRG2	NA	UP	2.073	1.32e-02	9.7
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: extrinsic apoptotic signaling pathway (Página 1 de 2)

Fuente: GO:BP | ID: GO:0097191 | Genes: 29 | p-valor ruta: 3.05e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
TRAF1	NA	UP	4.730	5.65e-84	258.2
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL2L14	NA	UP	2.782	8.63e-26	122.3
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: extrinsic apoptotic signaling pathway (Página 2 de 2)

Fuente: GO:BP | ID: GO:0097191 | Genes: 29 | p-valor ruta: 3.05e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
CD70	NA	UP	3.257	1.21e-02	4.7
RET	NA	UP	2.793	1.44e-02	5.5
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: negative regulation of cellular process (Página 1 de 8)

Fuente: GO:BP | ID: GO:0048523 | Genes: 194 | p-valor ruta: 3.11e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT3	NA	UP	4.898	0.00e+00	4866.8
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8

## Ruta: negative regulation of cellular process (Página 2 de 8)

Fuente: GO:BP | ID: GO:0048523 | Genes: 194 | p-valor ruta: 3.11e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0

## Ruta: negative regulation of cellular process (Página 3 de 8)

Fuente: GO:BP | ID: GO:0048523 | Genes: 194 | p-valor ruta: 3.11e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
ETV7	NA	UP	4.688	2.39e-83	278.8
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
IFI35	NA	UP	2.237	9.59e-79	2236.7
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
TDRD7	NA	UP	2.129	5.72e-65	1011.2

## Ruta: negative regulation of cellular process (Página 4 de 8)

Fuente: GO:BP | ID: GO:0048523 | Genes: 194 | p-valor ruta: 3.11e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JUN	NA	UP	2.450	1.10e-62	6693.5
RND1	NA	UP	2.840	1.60e-62	337.7
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
FOSB	NA	UP	3.144	1.32e-55	267.7
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
XRN1	NA	UP	2.115	6.38e-50	984.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOBEC3G	NA	UP	2.120	1.48e-40	359.9

## Ruta: negative regulation of cellular process (Página 5 de 8)

Fuente: GO:BP | ID: GO:0048523 | Genes: 194 | p-valor ruta: 3.11e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
MIR155HG	NA	UP	5.318	4.66e-35	99.1
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
ZBTB20	NA	UP	3.440	1.24e-15	47.6

## Ruta: negative regulation of cellular process (Página 6 de 8)

Fuente: GO:BP | ID: GO:0048523 | Genes: 194 | p-valor ruta: 3.11e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NAV3	NA	UP	2.285	2.77e-15	84.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
KLF9	NA	UP	2.555	7.01e-13	66.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
SSTR2	NA	UP	2.031	8.80e-10	53.9
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4

## Ruta: negative regulation of cellular process (Página 7 de 8)

Fuente: GO:BP | ID: GO:0048523 | Genes: 194 | p-valor ruta: 3.11e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CNTN4	NA	UP	4.928	9.17e-04	5.0
RNF152	NA	UP	3.325	1.37e-03	7.5
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: negative regulation of cellular process (Página 8 de 8)

Fuente: GO:BP | ID: GO:0048523 | Genes: 194 | p-valor ruta: 3.11e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
RANBP3L	NA	UP	4.634	1.47e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
NPR3	NA	UP	2.789	1.87e-02	5.7
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
IKZF1	NA	UP	2.283	2.21e-02	6.8
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: leukocyte migration (Página 1 de 2)

Fuente: GO:BP | ID: GO:0050900 | Genes: 38 | p-valor ruta: 3.2e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
CD69	NA	UP	3.112	5.99e-57	257.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
CH25H	NA	UP	7.817	1.04e-46	242.7
EDN2	NA	UP	3.499	8.77e-31	90.3

## Ruta: leukocyte migration (Página 2 de 2)

Fuente: GO:BP | ID: GO:0050900 | Genes: 38 | p-valor ruta: 3.2e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: response to type II interferon

Fuente: GO:BP | ID: GO:0034341 | Genes: 22 | p-valor ruta: 3.33e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
GBP4	NA	UP	4.422	6.95e-185	1175.0
CCL5	NA	UP	5.035	8.94e-165	656.3
IFITM1	NA	UP	3.632	5.16e-130	784.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
NLRC5	NA	UP	3.949	8.12e-88	414.4
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
TRIM21	NA	UP	2.221	1.14e-60	888.8
TLR3	NA	UP	2.508	1.99e-22	111.5
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
GBP6	NA	UP	2.233	3.24e-03	11.2
GBP7	NA	UP	4.177	1.61e-02	2.9

## Ruta: regulation of programmed cell death (Página 1 de 4)

Fuente: GO:BP | ID: GO:0043067 | Genes: 80 | p-valor ruta: 4.13e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
ASNS	NA	UP	2.919	1.59e-113	1627.6
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
CD274	NA	UP	5.204	1.23e-98	314.4

## Ruta: regulation of programmed cell death (Página 2 de 4)

Fuente: GO:BP | ID: GO:0043067 | Genes: 80 | p-valor ruta: 4.13e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CTH	NA	UP	2.488	2.75e-57	412.1
BBC3	NA	UP	2.829	3.65e-57	503.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
CYP1B1	NA	UP	2.786	9.33e-53	766.0
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4

## Ruta: regulation of programmed cell death (Página 3 de 4)

Fuente: GO:BP | ID: GO:0043067 | Genes: 80 | p-valor ruta: 4.13e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
ZEB2	NA	UP	3.419	5.95e-12	30.5
NLRP1	NA	UP	5.692	4.64e-09	21.6
ACTN2	NA	UP	3.956	7.01e-09	20.3
LRP2	NA	UP	3.144	3.22e-08	22.0
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4

## Ruta: regulation of programmed cell death (Página 4 de 4)

Fuente: GO:BP | ID: GO:0043067 | Genes: 80 | p-valor ruta: 4.13e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RET	NA	UP	2.793	1.44e-02	5.5
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of canonical NF-kappaB signal transduction (Página 1 de 2)

Fuente: GO:BP | ID: GO:0043122 | Genes: 32 | p-valor ruta: 4.34e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
TRAF1	NA	UP	4.730	5.65e-84	258.2
KLF4	NA	UP	2.704	2.52e-79	645.9
IFIT5	NA	UP	2.861	3.01e-78	749.8
LGALS9	NA	UP	2.474	3.44e-71	1449.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
CTH	NA	UP	2.488	2.75e-57	412.1
PER1	NA	UP	2.501	8.94e-44	469.6
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: regulation of canonical NF-kappaB signal transduction (Página 2 de 2)

Fuente: GO:BP | ID: GO:0043122 | Genes: 32 | p-valor ruta: 4.34e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
TLR6	NA	UP	2.680	9.77e-08	26.3
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: blood vessel development (Página 1 de 3)

Fuente: GO:BP | ID: GO:0001568 | Genes: 52 | p-valor ruta: 5.21e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3

## Ruta: blood vessel development (Página 2 de 3)

Fuente: GO:BP | ID: GO:0001568 | Genes: 52 | p-valor ruta: 5.21e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
LRP2	NA	UP	3.144	3.22e-08	22.0
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
COL4A1	NA	UP	6.589	5.89e-06	8.2
ADAMTS6	NA	UP	2.602	8.90e-06	19.6
FAP	NA	UP	3.233	1.87e-05	14.0
EGR3	NA	UP	2.096	2.87e-04	21.5
HAND1	NA	UP	4.966	8.42e-04	5.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
C3AR1	NA	UP	4.639	1.59e-02	2.2
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: blood vessel development (Página 3 de 3)

Fuente: GO:BP | ID: GO:0001568 | Genes: 52 | p-valor ruta: 5.21e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: hemopoiesis (Página 1 de 3)

Fuente: GO:BP | ID: GO:0030097 | Genes: 61 | p-valor ruta: 8.05e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
TIPARP	NA	UP	3.093	1.11e-158	5401.6
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0

## Ruta: hemopoiesis (Página 2 de 3)

Fuente: GO:BP | ID: GO:0030097 | Genes: 61 | p-valor ruta: 8.05e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
FLT3LG	NA	UP	2.346	6.32e-15	68.5
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CLEC4E	NA	UP	3.620	4.75e-09	26.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1

## Ruta: hemopoiesis (Página 3 de 3)

Fuente: GO:BP | ID: GO:0030097 | Genes: 61 | p-valor ruta: 8.05e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RUNX2	NA	UP	3.983	1.50e-06	15.2
IL18R1	NA	UP	2.088	8.75e-05	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: response to type I interferon

Fuente: GO:BP | ID: GO:0034340 | Genes: 19 | p-valor ruta: 1.11e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
MX1	NA	UP	3.859	1.25e-245	5699.6
IFIH1	NA	UP	4.035	2.22e-233	4525.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZBP1	NA	UP	6.242	1.22e-99	349.5
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
CH25H	NA	UP	7.817	1.04e-46	242.7
IFITM2	NA	UP	2.649	6.22e-17	64.2

## Ruta: lymphocyte differentiation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0030098 | Genes: 39 | p-valor ruta: 1.34e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: lymphocyte differentiation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0030098 | Genes: 39 | p-valor ruta: 1.34e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CLEC4E	NA	UP	3.620	4.75e-09	26.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RUNX2	NA	UP	3.983	1.50e-06	15.2
IL18R1	NA	UP	2.088	8.75e-05	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of lymphocyte activation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051249 | Genes: 42 | p-valor ruta: 1.37e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
THEMIS2	NA	UP	2.550	2.88e-50	403.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: regulation of lymphocyte activation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051249 | Genes: 42 | p-valor ruta: 1.37e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: immune response–activating signaling pathway (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002757 | Genes: 41 | p–valor ruta: 2.28e–10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e–277	2472.4
NFKBIA	NA	UP	4.079	6.66e–241	4955.3
IFIH1	NA	UP	4.035	2.22e–233	4525.3
GBP1	NA	UP	4.090	2.07e–209	2026.7
IRF1	NA	UP	3.512	7.87e–194	2808.9
OASL	NA	UP	3.434	4.45e–163	4285.8
OAS1	NA	UP	3.011	3.81e–158	5273.1
TNF	NA	UP	7.712	3.81e–103	573.0
DHX58	NA	UP	2.877	1.75e–99	953.6
CD274	NA	UP	5.204	1.23e–98	314.4
ZC3HAV1	NA	UP	2.427	2.20e–95	2512.8
IRAK2	NA	UP	2.666	3.46e–95	1164.5
OAS3	NA	UP	2.942	1.13e–87	8674.1
IRF7	NA	UP	3.210	5.72e–79	2126.1
DDX60	NA	UP	3.015	7.43e–79	1999.9
IFI35	NA	UP	2.237	9.59e–79	2236.7
SLC15A3	NA	UP	4.245	2.06e–77	254.6
NR1D1	NA	UP	2.475	2.08e–68	1229.5
PDE4B	NA	UP	3.818	7.08e–52	171.4
THEMIS2	NA	UP	2.550	2.88e–50	403.0
EIF2AK2	NA	UP	2.142	3.22e–48	1460.0
BIRC3	NA	UP	2.146	8.30e–42	2602.9
NFKBIZ	NA	UP	2.037	4.06e–41	2486.2
TLR3	NA	UP	2.508	1.99e–22	111.5

## Ruta: immune response–activating signaling pathway (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002757 | Genes: 41 | p-valor ruta: 2.28e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: blood vessel morphogenesis (Página 1 de 2)

Fuente: GO:BP | ID: GO:0048514 | Genes: 47 | p-valor ruta: 2.29e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9

## Ruta: blood vessel morphogenesis (Página 2 de 2)

Fuente: GO:BP | ID: GO:0048514 | Genes: 47 | p-valor ruta: 2.29e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
TLR3	NA	UP	2.508	1.99e-22	111.5
GBX2	NA	UP	2.353	5.55e-15	78.3
LRP2	NA	UP	3.144	3.22e-08	22.0
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
COL4A1	NA	UP	6.589	5.89e-06	8.2
FAP	NA	UP	3.233	1.87e-05	14.0
EGR3	NA	UP	2.096	2.87e-04	21.5
HAND1	NA	UP	4.966	8.42e-04	5.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
C3AR1	NA	UP	4.639	1.59e-02	2.2
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: angiogenesis (Página 1 de 2)

Fuente: GO:BP | ID: GO:0001525 | Genes: 43 | p-valor ruta: 3.59e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: angiogenesis (Página 2 de 2)

Fuente: GO:BP | ID: GO:0001525 | Genes: 43 | p-valor ruta: 3.59e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FUT1	NA	UP	2.765	4.55e-26	104.9
TLR3	NA	UP	2.508	1.99e-22	111.5
GBX2	NA	UP	2.353	5.55e-15	78.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
COL4A1	NA	UP	6.589	5.89e-06	8.2
FAP	NA	UP	3.233	1.87e-05	14.0
EGR3	NA	UP	2.096	2.87e-04	21.5
HAND1	NA	UP	4.966	8.42e-04	5.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
C3AR1	NA	UP	4.639	1.59e-02	2.2
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: leukocyte cell–cell adhesion (Página 1 de 2)

Fuente: GO:BP | ID: GO:0007159 | Genes: 37 | p–valor ruta: 4.41e–10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e–214	2230.2
ICAM1	NA	UP	3.652	3.11e–204	19095.5
IRF1	NA	UP	3.512	7.87e–194	2808.9
CCL5	NA	UP	5.035	8.94e–165	656.3
IDO1	NA	UP	4.167	4.38e–109	394.2
TNF	NA	UP	7.712	3.81e–103	573.0
CD274	NA	UP	5.204	1.23e–98	314.4
IFNB1	NA	UP	10.001	4.69e–95	1340.6
IFNL1	NA	UP	8.179	1.68e–89	578.0
KLF4	NA	UP	2.704	2.52e–79	645.9
MAP3K8	NA	UP	2.825	4.57e–78	640.1
CCL2	NA	UP	2.562	2.63e–75	658.0
LGALS9	NA	UP	2.474	3.44e–71	1449.3
PTAFR	NA	UP	3.014	4.62e–62	338.1
CD69	NA	UP	3.112	5.99e–57	257.2
NFKBIZ	NA	UP	2.037	4.06e–41	2486.2
RASGRP1	NA	UP	2.055	4.16e–34	336.9
IL12A	NA	UP	3.852	1.95e–28	83.7
VCAM1	NA	UP	4.737	4.28e–26	66.5
NOD2	NA	UP	2.981	1.19e–19	80.5
JAK2	NA	UP	2.081	1.26e–17	123.4
IL15	NA	UP	2.012	2.28e–17	116.8
NLRP3	NA	UP	4.366	3.67e–13	29.8

## Ruta: leukocyte cell–cell adhesion (Página 2 de 2)

Fuente: GO:BP | ID: GO:0007159 | Genes: 37 | p–valor ruta: 4.41e–10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PCK1	NA	UP	4.419	1.17e–12	29.6
IL23A	NA	UP	2.189	2.05e–11	59.9
TNFSF13B	NA	UP	3.042	2.17e–11	34.7
NR4A3	NA	UP	5.574	1.45e–08	20.2
SOCS1	NA	UP	2.012	6.54e–08	82.5
TNFSF14	NA	UP	2.748	3.71e–07	23.0
SELE	NA	UP	5.745	2.05e–05	9.0
EGR3	NA	UP	2.096	2.87e–04	21.5
PDCD1LG2	NA	UP	4.546	4.10e–04	7.2
CD70	NA	UP	3.257	1.21e–02	4.7
VAV1	NA	UP	2.118	1.54e–02	7.9
OLR1	NA	UP	2.655	1.81e–02	6.9

## Ruta: defense response to bacterium (Página 1 de 2)

Fuente: GO:BP | ID: GO:0042742 | Genes: 33 | p-valor ruta: 4.53e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
OAS1	NA	UP	3.011	3.81e-158	5273.1
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
RNF213	NA	UP	2.528	1.50e-73	6034.1
OPTN	NA	UP	2.002	1.08e-67	1911.6
ISG15	NA	UP	2.482	5.90e-57	3807.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0

## Ruta: defense response to bacterium (Página 2 de 2)

Fuente: GO:BP | ID: GO:0042742 | Genes: 33 | p-valor ruta: 4.53e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
WFDC5	NA	UP	5.168	1.07e-06	13.9
GBP6	NA	UP	2.233	3.24e-03	11.2
PRG2	NA	UP	2.073	1.32e-02	9.7
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
SPRR2A	NA	UP	2.086	2.78e-02	7.8

## Ruta: leukocyte chemotaxis (Página 1 de 2)

Fuente: GO:BP | ID: GO:0030595 | Genes: 28 | p-valor ruta: 5.08e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
CH25H	NA	UP	7.817	1.04e-46	242.7
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9

## Ruta: leukocyte chemotaxis (Página 2 de 2)

Fuente: GO:BP | ID: GO:0030595 | Genes: 28 | p-valor ruta: 5.08e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: regulation of extrinsic apoptotic signaling pathway

Fuente: GO:BP | ID: GO:2001236 | Genes: 23 | p-valor ruta: 6.1e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
TRAF1	NA	UP	4.730	5.65e-84	258.2
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
LTB	NA	UP	3.555	2.50e-41	150.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
TLR6	NA	UP	2.680	9.77e-08	26.3
RET	NA	UP	2.793	1.44e-02	5.5
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of leukocyte cell–cell adhesion (Página 1 de 2)

Fuente: GO:BP | ID: GO:1903037 | Genes: 35 | p–valor ruta: 6.23e–10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e–214	2230.2
IRF1	NA	UP	3.512	7.87e–194	2808.9
CCL5	NA	UP	5.035	8.94e–165	656.3
IDO1	NA	UP	4.167	4.38e–109	394.2
TNF	NA	UP	7.712	3.81e–103	573.0
CD274	NA	UP	5.204	1.23e–98	314.4
IFNB1	NA	UP	10.001	4.69e–95	1340.6
IFNL1	NA	UP	8.179	1.68e–89	578.0
KLF4	NA	UP	2.704	2.52e–79	645.9
MAP3K8	NA	UP	2.825	4.57e–78	640.1
CCL2	NA	UP	2.562	2.63e–75	658.0
LGALS9	NA	UP	2.474	3.44e–71	1449.3
PTAFR	NA	UP	3.014	4.62e–62	338.1
CD69	NA	UP	3.112	5.99e–57	257.2
NFKBIZ	NA	UP	2.037	4.06e–41	2486.2
RASGRP1	NA	UP	2.055	4.16e–34	336.9
IL12A	NA	UP	3.852	1.95e–28	83.7
VCAM1	NA	UP	4.737	4.28e–26	66.5
NOD2	NA	UP	2.981	1.19e–19	80.5
JAK2	NA	UP	2.081	1.26e–17	123.4
IL15	NA	UP	2.012	2.28e–17	116.8
NLRP3	NA	UP	4.366	3.67e–13	29.8
PCK1	NA	UP	4.419	1.17e–12	29.6

## Ruta: regulation of leukocyte cell–cell adhesion (Página 2 de 2)

Fuente: GO:BP | ID: GO:1903037 | Genes: 35 | p–valor ruta: 6.23e–10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL23A	NA	UP	2.189	2.05e–11	59.9
TNFSF13B	NA	UP	3.042	2.17e–11	34.7
NR4A3	NA	UP	5.574	1.45e–08	20.2
SOCS1	NA	UP	2.012	6.54e–08	82.5
TNFSF14	NA	UP	2.748	3.71e–07	23.0
SELE	NA	UP	5.745	2.05e–05	9.0
EGR3	NA	UP	2.096	2.87e–04	21.5
PDCD1LG2	NA	UP	4.546	4.10e–04	7.2
CD70	NA	UP	3.257	1.21e–02	4.7
VAV1	NA	UP	2.118	1.54e–02	7.9

## Ruta: circulatory system development (Página 1 de 3)

Fuente: GO:BP | ID: GO:0072359 | Genes: 65 | p-valor ruta: 9e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CTH	NA	UP	2.488	2.75e-57	412.1

## Ruta: circulatory system development (Página 2 de 3)

Fuente: GO:BP | ID: GO:0072359 | Genes: 65 | p-valor ruta: 9e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CYP1B1	NA	UP	2.786	9.33e-53	766.0
BMP2	NA	UP	2.237	3.69e-40	325.3
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
DNAAF3	NA	DOWN	-2.041	1.75e-14	101.4
ACTN2	NA	UP	3.956	7.01e-09	20.3
LRP2	NA	UP	3.144	3.22e-08	22.0
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
COL4A1	NA	UP	6.589	5.89e-06	8.2
ADAMTS6	NA	UP	2.602	8.90e-06	19.6
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
EGR3	NA	UP	2.096	2.87e-04	21.5

## Ruta: circulatory system development (Página 3 de 3)

Fuente: GO:BP | ID: GO:0072359 | Genes: 65 | p-valor ruta: 9e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4
C3AR1	NA	UP	4.639	1.59e-02	2.2
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: immune response-regulating signaling pathway (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002764 | Genes: 42 | p-valor ruta: 9.97e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
TLR3	NA	UP	2.508	1.99e-22	111.5

## Ruta: immune response-regulating signaling pathway (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002764 | Genes: 42 | p-valor ruta: 9.97e-10

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
KIT	NA	UP	3.650	6.24e-04	7.9
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of cell-cell adhesion (Página 1 de 2)

Fuente: GO:BP | ID: GO:0022407 | Genes: 40 | p-valor ruta: 1.03e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IDO1	NA	UP	4.167	4.38e-109	394.2
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF4	NA	UP	2.704	2.52e-79	645.9
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
CD69	NA	UP	3.112	5.99e-57	257.2
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: regulation of cell-cell adhesion (Página 2 de 2)

Fuente: GO:BP | ID: GO:0022407 | Genes: 40 | p-valor ruta: 1.03e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9

## Ruta: multicellular organism development (Página 1 de 7)

Fuente: GO:BP | ID: GO:0007275 | Genes: 167 | p-valor ruta: 1.05e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
STC2	NA	UP	2.729	3.17e-119	2626.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0

## Ruta: multicellular organism development (Página 2 de 7)

Fuente: GO:BP | ID: GO:0007275 | Genes: 167 | p-valor ruta: 1.05e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KLF10	NA	UP	2.626	2.92e-86	1224.1
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
TDRD7	NA	UP	2.129	5.72e-65	1011.2
RND1	NA	UP	2.840	1.60e-62	337.7
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5

## Ruta: multicellular organism development (Página 3 de 7)

Fuente: GO:BP | ID: GO:0007275 | Genes: 167 | p-valor ruta: 1.05e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
NAV2	NA	UP	2.370	3.20e-51	765.9
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7

## Ruta: multicellular organism development (Página 4 de 7)

Fuente: GO:BP | ID: GO:0007275 | Genes: 167 | p-valor ruta: 1.05e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
DDC	NA	DOWN	-2.582	2.27e-16	72.0
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
DNAAF3	NA	DOWN	-2.041	1.75e-14	101.4
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
PPP4R4	NA	UP	3.423	6.94e-11	30.7

## Ruta: multicellular organism development (Página 5 de 7)

Fuente: GO:BP | ID: GO:0007275 | Genes: 167 | p-valor ruta: 1.05e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
BAHCC1	NA	UP	4.513	9.67e-08	16.6
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
COL4A1	NA	UP	6.589	5.89e-06	8.2
SP8	NA	UP	6.528	5.89e-06	8.0
ACTBL2	NA	UP	2.242	5.97e-06	28.3
ADAMTS6	NA	UP	2.602	8.90e-06	19.6
MMP13	NA	UP	5.406	9.23e-06	11.1
SERPINA10	NA	UP	6.459	9.50e-06	7.5
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
PKP1	NA	UP	3.076	9.16e-05	12.8

## Ruta: multicellular organism development (Página 6 de 7)

Fuente: GO:BP | ID: GO:0007275 | Genes: 167 | p-valor ruta: 1.05e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NPTX1	NA	UP	2.102	1.13e-04	22.3
EGR3	NA	UP	2.096	2.87e-04	21.5
MPZ	NA	UP	2.002	2.88e-04	19.4
TRPC4	NA	UP	5.730	3.71e-04	4.5
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
ENKUR	NA	UP	3.518	8.61e-04	9.0
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
LHB	NA	UP	3.522	1.50e-03	7.0
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
SDK2	NA	UP	2.715	5.83e-03	7.9
BMPER	NA	UP	4.906	6.28e-03	2.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2

## Ruta: multicellular organism development (Página 7 de 7)

Fuente: GO:BP | ID: GO:0007275 | Genes: 167 | p-valor ruta: 1.05e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C3AR1	NA	UP	4.639	1.59e-02	2.2
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
INSC	NA	UP	3.872	3.01e-02	2.4
HSD11B1	NA	UP	2.341	3.03e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8
ADAMTS4	NA	UP	3.293	3.88e-02	3.0
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of cell population proliferation (Página 1 de 3)

Fuente: GO:BP | ID: GO:0008284 | Genes: 58 | p-valor ruta: 1.17e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SERPINB7	NA	UP	2.796	1.04e-28	127.7

## Ruta: positive regulation of cell population proliferation (Página 2 de 3)

Fuente: GO:BP | ID: GO:0008284 | Genes: 58 | p-valor ruta: 1.17e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
LIFR	NA	UP	2.213	9.30e-24	226.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
FLT3LG	NA	UP	2.346	6.32e-15	68.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
CD70	NA	UP	3.257	1.21e-02	4.7

## Ruta: positive regulation of cell population proliferation (Página 3 de 3)

Fuente: GO:BP | ID: GO:0008284 | Genes: 58 | p-valor ruta: 1.17e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: response to tumor necrosis factor (Página 1 de 2)

Fuente: GO:BP | ID: GO:0034612 | Genes: 27 | p-valor ruta: 1.3e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
GBP1	NA	UP	4.090	2.07e-209	2026.7
CCL5	NA	UP	5.035	8.94e-165	656.3
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9
VCAM1	NA	UP	4.737	4.28e-26	66.5
NKX3-1	NA	UP	2.233	8.30e-23	132.4
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
PCK1	NA	UP	4.419	1.17e-12	29.6
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SELE	NA	UP	5.745	2.05e-05	9.0

## Ruta: response to tumor necrosis factor (Página 2 de 2)

Fuente: GO:BP | ID: GO:0034612 | Genes: 27 | p-valor ruta: 1.3e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CD70	NA	UP	3.257	1.21e-02	4.7
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of macromolecule biosynthetic process (Página 1 de 8)

Fuente: GO:BP | ID: GO:0010556 | Genes: 189 | p-valor ruta: 1.67e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CCL5	NA	UP	5.035	8.94e-165	656.3
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8

## Ruta: regulation of macromolecule biosynthetic process (Página 2 de 8)

Fuente: GO:BP | ID: GO:0010556 | Genes: 189 | p-valor ruta: 1.67e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1

## Ruta: regulation of macromolecule biosynthetic process (Página 3 de 8)

Fuente: GO:BP | ID: GO:0010556 | Genes: 189 | p-valor ruta: 1.67e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNPI1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6

## Ruta: regulation of macromolecule biosynthetic process (Página 4 de 8)

Fuente: GO:BP | ID: GO:0010556 | Genes: 189 | p-valor ruta: 1.67e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
MIR155HG	NA	UP	5.318	4.66e-35	99.1
ZNF267	NA	UP	2.059	1.30e-34	677.0
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0

## Ruta: regulation of macromolecule biosynthetic process (Página 5 de 8)

Fuente: GO:BP | ID: GO:0010556 | Genes: 189 | p-valor ruta: 1.67e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
SERPINB7	NA	UP	2.796	1.04e-28	127.7
HDX	NA	UP	2.521	1.83e-28	139.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8

## Ruta: regulation of macromolecule biosynthetic process (Página 6 de 8)

Fuente: GO:BP | ID: GO:0010556 | Genes: 189 | p-valor ruta: 1.67e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
UBASH3A	NA	UP	5.845	1.05e-05	9.8
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
FFAR2	NA	UP	3.253	4.81e-05	12.7

## Ruta: regulation of macromolecule biosynthetic process (Página 7 de 8)

Fuente: GO:BP | ID: GO:0010556 | Genes: 189 | p-valor ruta: 1.67e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
ZNF382	NA	UP	2.028	3.78e-04	18.2
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CEACAM20	NA	UP	5.412	1.17e-03	3.6
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of macromolecule biosynthetic process (Página 8 de 8)

Fuente: GO:BP | ID: GO:0010556 | Genes: 189 | p-valor ruta: 1.67e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
CELF6	NA	UP	2.403	2.65e-02	5.6
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PURG	NA	DOWN	-4.166	4.66e-02	1.7
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of cell–cell adhesion (Página 1 de 2)

Fuente: GO:BP | ID: GO:0022409 | Genes: 32 | p–valor ruta: 1.77e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e–214	2230.2
CCL5	NA	UP	5.035	8.94e–165	656.3
CX3CL1	NA	UP	3.114	2.67e–123	1760.3
TNF	NA	UP	7.712	3.81e–103	573.0
CD274	NA	UP	5.204	1.23e–98	314.4
MAP3K8	NA	UP	2.825	4.57e–78	640.1
CCL2	NA	UP	2.562	2.63e–75	658.0
LGALS9	NA	UP	2.474	3.44e–71	1449.3
PTAFR	NA	UP	3.014	4.62e–62	338.1
FUT3	NA	UP	2.139	2.84e–41	355.7
NFKBIZ	NA	UP	2.037	4.06e–41	2486.2
RASGRP1	NA	UP	2.055	4.16e–34	336.9
IL12A	NA	UP	3.852	1.95e–28	83.7
VCAM1	NA	UP	4.737	4.28e–26	66.5
NOD2	NA	UP	2.981	1.19e–19	80.5
JAK2	NA	UP	2.081	1.26e–17	123.4
IL15	NA	UP	2.012	2.28e–17	116.8
NLRP3	NA	UP	4.366	3.67e–13	29.8
PCK1	NA	UP	4.419	1.17e–12	29.6
IL23A	NA	UP	2.189	2.05e–11	59.9
TNFSF13B	NA	UP	3.042	2.17e–11	34.7
NR4A3	NA	UP	5.574	1.45e–08	20.2
SOCS1	NA	UP	2.012	6.54e–08	82.5

## Ruta: positive regulation of cell–cell adhesion (Página 2 de 2)

Fuente: GO:BP | ID: GO:0022409 | Genes: 32 | p–valor ruta: 1.77e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFSF14	NA	UP	2.748	3.71e–07	23.0
SELE	NA	UP	5.745	2.05e–05	9.0
PKP1	NA	UP	3.076	9.16e–05	12.8
EGR3	NA	UP	2.096	2.87e–04	21.5
PDCD1LG2	NA	UP	4.546	4.10e–04	7.2
CD70	NA	UP	3.257	1.21e–02	4.7
VAV1	NA	UP	2.118	1.54e–02	7.9

## Ruta: positive regulation of apoptotic process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0043065 | Genes: 41 | p-valor ruta: 2.03e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
PTGS2	NA	UP	3.253	7.39e-80	3663.8
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
BBC3	NA	UP	2.829	3.65e-57	503.1
CYP1B1	NA	UP	2.786	9.33e-53	766.0

## Ruta: positive regulation of apoptotic process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0043065 | Genes: 41 | p-valor ruta: 2.03e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL2L14	NA	UP	2.782	8.63e-26	122.3
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
HRG	NA	UP	2.971	4.00e-03	6.9
RET	NA	UP	2.793	1.44e-02	5.5
RFPL1	NA	UP	3.259	2.06e-02	4.1
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of gene expression (Página 1 de 8)

Fuente: GO:BP | ID: GO:0010468 | Genes: 186 | p-valor ruta: 2.2e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CCL5	NA	UP	5.035	8.94e-165	656.3
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8

## Ruta: regulation of gene expression (Página 2 de 8)

Fuente: GO:BP | ID: GO:0010468 | Genes: 186 | p-valor ruta: 2.2e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1

## Ruta: regulation of gene expression (Página 3 de 8)

Fuente: GO:BP | ID: GO:0010468 | Genes: 186 | p-valor ruta: 2.2e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNPI1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6

## Ruta: regulation of gene expression (Página 4 de 8)

Fuente: GO:BP | ID: GO:0010468 | Genes: 186 | p-valor ruta: 2.2e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
MIR155HG	NA	UP	5.318	4.66e-35	99.1
ZNF267	NA	UP	2.059	1.30e-34	677.0
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7

## Ruta: regulation of gene expression (Página 5 de 8)

Fuente: GO:BP | ID: GO:0010468 | Genes: 186 | p-valor ruta: 2.2e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BACH2	NA	UP	2.222	2.18e-30	209.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
SERPINB7	NA	UP	2.796	1.04e-28	127.7
HDX	NA	UP	2.521	1.83e-28	139.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6

## Ruta: regulation of gene expression (Página 6 de 8)

Fuente: GO:BP | ID: GO:0010468 | Genes: 186 | p-valor ruta: 2.2e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
UBASH3A	NA	UP	5.845	1.05e-05	9.8
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5

## Ruta: regulation of gene expression (Página 7 de 8)

Fuente: GO:BP | ID: GO:0010468 | Genes: 186 | p-valor ruta: 2.2e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZNF382	NA	UP	2.028	3.78e-04	18.2
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CEACAM20	NA	UP	5.412	1.17e-03	3.6
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8

## Ruta: regulation of gene expression (Página 8 de 8)

Fuente: GO:BP | ID: GO:0010468 | Genes: 186 | p-valor ruta: 2.2e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
CELF6	NA	UP	2.403	2.65e-02	5.6
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PURG	NA	DOWN	-4.166	4.66e-02	1.7
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: anatomical structure development (Página 1 de 8)

Fuente: GO:BP | ID: GO:0048856 | Genes: 197 | p-valor ruta: 2.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNFSF10	NA	UP	3.014	1.58e-112	3429.5

## Ruta: anatomical structure development (Página 2 de 8)

Fuente: GO:BP | ID: GO:0048856 | Genes: 197 | p-valor ruta: 2.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
TM4SF4	NA	DOWN	-2.482	1.83e-87	1021.7
KLF10	NA	UP	2.626	2.92e-86	1224.1
ETV7	NA	UP	4.688	2.39e-83	278.8
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8

## Ruta: anatomical structure development (Página 3 de 8)

Fuente: GO:BP | ID: GO:0048856 | Genes: 197 | p-valor ruta: 2.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
TDRD7	NA	UP	2.129	5.72e-65	1011.2
RND1	NA	UP	2.840	1.60e-62	337.7
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TUFT1	NA	UP	2.001	1.00e-55	1905.9
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
NAV2	NA	UP	2.370	3.20e-51	765.9
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6

## Ruta: anatomical structure development (Página 4 de 8)

Fuente: GO:BP | ID: GO:0048856 | Genes: 197 | p-valor ruta: 2.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
KRT6B	NA	UP	2.049	5.47e-24	321.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8

## Ruta: anatomical structure development (Página 5 de 8)

Fuente: GO:BP | ID: GO:0048856 | Genes: 197 | p-valor ruta: 2.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
DDC	NA	DOWN	-2.582	2.27e-16	72.0
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
DNAAF3	NA	DOWN	-2.041	1.75e-14	101.4
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
PPP4R4	NA	UP	3.423	6.94e-11	30.7
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
BAHCC1	NA	UP	4.513	9.67e-08	16.6

## Ruta: anatomical structure development (Página 6 de 8)

Fuente: GO:BP | ID: GO:0048856 | Genes: 197 | p-valor ruta: 2.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
COL4A1	NA	UP	6.589	5.89e-06	8.2
SP8	NA	UP	6.528	5.89e-06	8.0
ACTBL2	NA	UP	2.242	5.97e-06	28.3
ADAMTS6	NA	UP	2.602	8.90e-06	19.6
MMP13	NA	UP	5.406	9.23e-06	11.1
SERPINA10	NA	UP	6.459	9.50e-06	7.5
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
XKR9	NA	UP	3.541	5.84e-05	11.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
RHCG	NA	UP	2.107	1.84e-04	21.0
EGR3	NA	UP	2.096	2.87e-04	21.5
MPZ	NA	UP	2.002	2.88e-04	19.4

## Ruta: anatomical structure development (Página 7 de 8)

Fuente: GO:BP | ID: GO:0048856 | Genes: 197 | p-valor ruta: 2.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRPC4	NA	UP	5.730	3.71e-04	4.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
MKX	NA	UP	2.196	5.67e-04	15.1
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
ENKUR	NA	UP	3.518	8.61e-04	9.0
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
LHB	NA	UP	3.522	1.50e-03	7.0
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
KRT81	NA	UP	2.044	4.94e-03	15.2
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
SDK2	NA	UP	2.715	5.83e-03	7.9
KRT9	NA	UP	4.973	6.24e-03	2.7
BMPER	NA	UP	4.906	6.28e-03	2.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4

## Ruta: anatomical structure development (Página 8 de 8)

Fuente: GO:BP | ID: GO:0048856 | Genes: 197 | p-valor ruta: 2.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
INSC	NA	UP	3.872	3.01e-02	2.4
HSD11B1	NA	UP	2.341	3.03e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8
ADAMTS4	NA	UP	3.293	3.88e-02	3.0
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of developmental process (Página 1 de 5)

Fuente: GO:BP | ID: GO:0050793 | Genes: 105 | p-valor ruta: 2.57e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
STC2	NA	UP	2.729	3.17e-119	2626.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4

## Ruta: regulation of developmental process (Página 2 de 5)

Fuente: GO:BP | ID: GO:0050793 | Genes: 105 | p-valor ruta: 2.57e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0

## Ruta: regulation of developmental process (Página 3 de 5)

Fuente: GO:BP | ID: GO:0050793 | Genes: 105 | p-valor ruta: 2.57e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
FUT1	NA	UP	2.765	4.55e-26	104.9
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2

## Ruta: regulation of developmental process (Página 4 de 5)

Fuente: GO:BP | ID: GO:0050793 | Genes: 105 | p-valor ruta: 2.57e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
CNTN4	NA	UP	4.928	9.17e-04	5.0
POU3F2	NA	UP	4.735	2.02e-03	4.5
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
BMPER	NA	UP	4.906	6.28e-03	2.6
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9

## Ruta: regulation of developmental process (Página 5 de 5)

Fuente: GO:BP | ID: GO:0050793 | Genes: 105 | p-valor ruta: 2.57e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: leukocyte proliferation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0070661 | Genes: 33 | p-valor ruta: 2.95e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
CSF2	NA	UP	7.043	2.08e-103	455.6
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CSF1	NA	UP	2.530	1.40e-49	467.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFRSF9	NA	UP	4.642	8.23e-08	94.1

## Ruta: leukocyte proliferation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0070661 | Genes: 33 | p-valor ruta: 2.95e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
CD70	NA	UP	3.257	1.21e-02	4.7
NPR3	NA	UP	2.789	1.87e-02	5.7
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: positive regulation of cell adhesion (Página 1 de 2)

Fuente: GO:BP | ID: GO:0045785 | Genes: 39 | p-valor ruta: 3.07e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
CSF1	NA	UP	2.530	1.40e-49	467.4
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
LAMA2	NA	UP	2.355	4.82e-21	125.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: positive regulation of cell adhesion (Página 2 de 2)

Fuente: GO:BP | ID: GO:0045785 | Genes: 39 | p-valor ruta: 3.07e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
HRG	NA	UP	2.971	4.00e-03	6.9
EGFL6	NA	UP	3.034	6.01e-03	5.9
CD70	NA	UP	3.257	1.21e-02	4.7
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: intracellular receptor signaling pathway (Página 1 de 2)

Fuente: GO:BP | ID: GO:0030522 | Genes: 34 | p-valor ruta: 3.14e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
SP100	NA	UP	2.428	1.62e-93	2653.7
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PML	NA	UP	2.208	2.84e-70	2901.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
BIRC3	NA	UP	2.146	8.30e-42	2602.9
BMP2	NA	UP	2.237	3.69e-40	325.3
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: intracellular receptor signaling pathway (Página 2 de 2)

Fuente: GO:BP | ID: GO:0030522 | Genes: 34 | p-valor ruta: 3.14e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NR1I2	NA	UP	2.428	6.42e-12	59.1
NLRP1	NA	UP	5.692	4.64e-09	21.6
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: negative regulation of signal transduction (Página 1 de 3)

Fuente: GO:BP | ID: GO:0009968 | Genes: 70 | p-valor ruta: 3.16e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9

## Ruta: negative regulation of signal transduction (Página 2 de 3)

Fuente: GO:BP | ID: GO:0009968 | Genes: 70 | p-valor ruta: 3.16e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ADRB2	NA	UP	2.471	2.83e-79	954.4
IFI35	NA	UP	2.237	9.59e-79	2236.7
THBS1	NA	UP	2.656	1.05e-77	3791.3
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
PDE4B	NA	UP	3.818	7.08e-52	171.4
PER1	NA	UP	2.501	8.94e-44	469.6
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BDKRB2	NA	UP	2.797	5.56e-15	55.1

## Ruta: negative regulation of signal transduction (Página 3 de 3)

Fuente: GO:BP | ID: GO:0009968 | Genes: 70 | p-valor ruta: 3.16e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
UBASH3A	NA	UP	5.845	1.05e-05	9.8
RBMS3	NA	UP	2.303	4.11e-04	18.6
RNF152	NA	UP	3.325	1.37e-03	7.5
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: regulation of biosynthetic process (Página 1 de 8)

Fuente: GO:BP | ID: GO:0009889 | Genes: 192 | p-valor ruta: 3.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CCL5	NA	UP	5.035	8.94e-165	656.3
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8

## Ruta: regulation of biosynthetic process (Página 2 de 8)

Fuente: GO:BP | ID: GO:0009889 | Genes: 192 | p-valor ruta: 3.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1

## Ruta: regulation of biosynthetic process (Página 3 de 8)

Fuente: GO:BP | ID: GO:0009889 | Genes: 192 | p-valor ruta: 3.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNPI1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1

## Ruta: regulation of biosynthetic process (Página 4 de 8)

Fuente: GO:BP | ID: GO:0009889 | Genes: 192 | p-valor ruta: 3.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
MIR155HG	NA	UP	5.318	4.66e-35	99.1
ZNF267	NA	UP	2.059	1.30e-34	677.0
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7

## Ruta: regulation of biosynthetic process (Página 5 de 8)

Fuente: GO:BP | ID: GO:0009889 | Genes: 192 | p-valor ruta: 3.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
SERPINB7	NA	UP	2.796	1.04e-28	127.7
HDX	NA	UP	2.521	1.83e-28	139.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7

## Ruta: regulation of biosynthetic process (Página 6 de 8)

Fuente: GO:BP | ID: GO:0009889 | Genes: 192 | p-valor ruta: 3.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
UBASH3A	NA	UP	5.845	1.05e-05	9.8
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6

## Ruta: regulation of biosynthetic process (Página 7 de 8)

Fuente: GO:BP | ID: GO:0009889 | Genes: 192 | p-valor ruta: 3.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
ZNF382	NA	UP	2.028	3.78e-04	18.2
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CEACAM20	NA	UP	5.412	1.17e-03	3.6
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5

## Ruta: regulation of biosynthetic process (Página 8 de 8)

Fuente: GO:BP | ID: GO:0009889 | Genes: 192 | p-valor ruta: 3.35e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
CELF6	NA	UP	2.403	2.65e-02	5.6
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PURG	NA	DOWN	-4.166	4.66e-02	1.7
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of leukocyte cell–cell adhesion (Página 1 de 2)

Fuente: GO:BP | ID: GO:1903039 | Genes: 29 | p–valor ruta: 3.7e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e–214	2230.2
CCL5	NA	UP	5.035	8.94e–165	656.3
TNF	NA	UP	7.712	3.81e–103	573.0
CD274	NA	UP	5.204	1.23e–98	314.4
MAP3K8	NA	UP	2.825	4.57e–78	640.1
CCL2	NA	UP	2.562	2.63e–75	658.0
LGALS9	NA	UP	2.474	3.44e–71	1449.3
PTAFR	NA	UP	3.014	4.62e–62	338.1
NFKBIZ	NA	UP	2.037	4.06e–41	2486.2
RASGRP1	NA	UP	2.055	4.16e–34	336.9
IL12A	NA	UP	3.852	1.95e–28	83.7
VCAM1	NA	UP	4.737	4.28e–26	66.5
NOD2	NA	UP	2.981	1.19e–19	80.5
JAK2	NA	UP	2.081	1.26e–17	123.4
IL15	NA	UP	2.012	2.28e–17	116.8
NLRP3	NA	UP	4.366	3.67e–13	29.8
PCK1	NA	UP	4.419	1.17e–12	29.6
IL23A	NA	UP	2.189	2.05e–11	59.9
TNFSF13B	NA	UP	3.042	2.17e–11	34.7
NR4A3	NA	UP	5.574	1.45e–08	20.2
SOCS1	NA	UP	2.012	6.54e–08	82.5
TNFSF14	NA	UP	2.748	3.71e–07	23.0
SELE	NA	UP	5.745	2.05e–05	9.0

## Ruta: positive regulation of leukocyte cell–cell adhesion (Página 2 de 2)

Fuente: GO:BP | ID: GO:1903039 | Genes: 29 | p-valor ruta: 3.7e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9

## Ruta: regulation of tumor necrosis factor superfamily cytokine production

Fuente: GO:BP | ID: GO:1903555 | Genes: 23 | p-valor ruta: 4.4e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IFIH1	NA	UP	4.035	2.22e-233	4525.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CD274	NA	UP	5.204	1.23e-98	314.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
IL23A	NA	UP	2.189	2.05e-11	59.9
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: tumor necrosis factor superfamily cytokine production

Fuente: GO:BP | ID: GO:0071706 | Genes: 23 | p-valor ruta: 4.4e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IFIH1	NA	UP	4.035	2.22e-233	4525.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CD274	NA	UP	5.204	1.23e-98	314.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
IL23A	NA	UP	2.189	2.05e-11	59.9
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: cellular response to type I interferon

Fuente: GO:BP | ID: GO:0071357 | Genes: 17 | p-valor ruta: 5.04e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZBP1	NA	UP	6.242	1.22e-99	349.5
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
IFITM2	NA	UP	2.649	6.22e-17	64.2

## Ruta: tube morphogenesis (Página 1 de 3)

Fuente: GO:BP | ID: GO:0035239 | Genes: 54 | p-valor ruta: 5.39e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0

## Ruta: tube morphogenesis (Página 2 de 3)

Fuente: GO:BP | ID: GO:0035239 | Genes: 54 | p-valor ruta: 5.39e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
GBX2	NA	UP	2.353	5.55e-15	78.3
LRP2	NA	UP	3.144	3.22e-08	22.0
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
COL4A1	NA	UP	6.589	5.89e-06	8.2
FAP	NA	UP	3.233	1.87e-05	14.0
EGR3	NA	UP	2.096	2.87e-04	21.5
HAND1	NA	UP	4.966	8.42e-04	5.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
SALL1	NA	UP	4.345	3.20e-02	1.8

## Ruta: tube morphogenesis (Página 3 de 3)

Fuente: GO:BP | ID: GO:0035239 | Genes: 54 | p-valor ruta: 5.39e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of programmed cell death (Página 1 de 2)

Fuente: GO:BP | ID: GO:0043068 | Genes: 41 | p-valor ruta: 5.96e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
PTGS2	NA	UP	3.253	7.39e-80	3663.8
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
AKAP12	NA	UP	2.306	2.56e-67	3768.0
JUN	NA	UP	2.450	1.10e-62	6693.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
BBC3	NA	UP	2.829	3.65e-57	503.1
CYP1B1	NA	UP	2.786	9.33e-53	766.0

## Ruta: positive regulation of programmed cell death (Página 2 de 2)

Fuente: GO:BP | ID: GO:0043068 | Genes: 41 | p-valor ruta: 5.96e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL2L14	NA	UP	2.782	8.63e-26	122.3
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
HRG	NA	UP	2.971	4.00e-03	6.9
RET	NA	UP	2.793	1.44e-02	5.5
RFPL1	NA	UP	3.259	2.06e-02	4.1
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: cellular response to tumor necrosis factor

Fuente: GO:BP | ID: GO:0071356 | Genes: 25 | p-valor ruta: 6.18e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
GBP1	NA	UP	4.090	2.07e-209	2026.7
CCL5	NA	UP	5.035	8.94e-165	656.3
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
TRAF1	NA	UP	4.730	5.65e-84	258.2
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9
VCAM1	NA	UP	4.737	4.28e-26	66.5
NKX3-1	NA	UP	2.233	8.30e-23	132.4
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
PCK1	NA	UP	4.419	1.17e-12	29.6
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CD70	NA	UP	3.257	1.21e-02	4.7
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: cellular response to type II interferon

Fuente: GO:BP | ID: GO:0071346 | Genes: 18 | p-valor ruta: 7.53e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
GBP4	NA	UP	4.422	6.95e-185	1175.0
CCL5	NA	UP	5.035	8.94e-165	656.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
NLRC5	NA	UP	3.949	8.12e-88	414.4
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
TLR3	NA	UP	2.508	1.99e-22	111.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
GBP6	NA	UP	2.233	3.24e-03	11.2
GBP7	NA	UP	4.177	1.61e-02	2.9

## Ruta: apoptotic signaling pathway (Página 1 de 2)

Fuente: GO:BP | ID: GO:0097190 | Genes: 43 | p-valor ruta: 1.11e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
CTH	NA	UP	2.488	2.75e-57	412.1
BBC3	NA	UP	2.829	3.65e-57	503.1
CYP1B1	NA	UP	2.786	9.33e-53	766.0

## Ruta: apoptotic signaling pathway (Página 2 de 2)

Fuente: GO:BP | ID: GO:0097190 | Genes: 43 | p-valor ruta: 1.11e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
JAK2	NA	UP	2.081	1.26e-17	123.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
CD70	NA	UP	3.257	1.21e-02	4.7
RET	NA	UP	2.793	1.44e-02	5.5
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: T cell activation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0042110 | Genes: 42 | p-valor ruta: 1.16e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: T cell activation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0042110 | Genes: 42 | p-valor ruta: 1.16e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CLEC4E	NA	UP	3.620	4.75e-09	26.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
IL18R1	NA	UP	2.088	8.75e-05	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9

## Ruta: positive regulation of tumor necrosis factor production

Fuente: GO:BP | ID: GO:0032760 | Genes: 18 | p-valor ruta: 1.51e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IFIH1	NA	UP	4.035	2.22e-233	4525.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
OAS3	NA	UP	2.942	1.13e-87	8674.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
IL23A	NA	UP	2.189	2.05e-11	59.9
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: negative regulation of signaling (Página 1 de 3)

Fuente: GO:BP | ID: GO:0023057 | Genes: 72 | p-valor ruta: 1.6e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8

## Ruta: negative regulation of signaling (Página 2 de 3)

Fuente: GO:BP | ID: GO:0023057 | Genes: 72 | p-valor ruta: 1.6e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IFI35	NA	UP	2.237	9.59e-79	2236.7
THBS1	NA	UP	2.656	1.05e-77	3791.3
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
PDE4B	NA	UP	3.818	7.08e-52	171.4
PER1	NA	UP	2.501	8.94e-44	469.6
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: negative regulation of signaling (Página 3 de 3)

Fuente: GO:BP | ID: GO:0023057 | Genes: 72 | p-valor ruta: 1.6e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BDKRB2	NA	UP	2.797	5.56e-15	55.1
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FFAR2	NA	UP	3.253	4.81e-05	12.7
RBMS3	NA	UP	2.303	4.11e-04	18.6
RNF152	NA	UP	3.325	1.37e-03	7.5
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3

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

Fuente: GO:BP | ID: GO:0010648 | Genes: 72 | p-valor ruta: 1.65e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8

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

Fuente: GO:BP | ID: GO:0010648 | Genes: 72 | p-valor ruta: 1.65e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IFI35	NA	UP	2.237	9.59e-79	2236.7
THBS1	NA	UP	2.656	1.05e-77	3791.3
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
OPTN	NA	UP	2.002	1.08e-67	1911.6
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
PDE4B	NA	UP	3.818	7.08e-52	171.4
PER1	NA	UP	2.501	8.94e-44	469.6
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: negative regulation of cell communication (Página 3 de 3)

Fuente: GO:BP | ID: GO:0010648 | Genes: 72 | p-valor ruta: 1.65e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BDKRB2	NA	UP	2.797	5.56e-15	55.1
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FFAR2	NA	UP	3.253	4.81e-05	12.7
RBMS3	NA	UP	2.303	4.11e-04	18.6
RNF152	NA	UP	3.325	1.37e-03	7.5
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
TP63	NA	UP	3.788	4.09e-02	2.3
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: cell adhesion (Página 1 de 3)

Fuente: GO:BP | ID: GO:0007155 | Genes: 75 | p-valor ruta: 1.66e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
KLF4	NA	UP	2.704	2.52e-79	645.9
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
CD69	NA	UP	3.112	5.99e-57	257.2

## Ruta: cell adhesion (Página 2 de 3)

Fuente: GO:BP | ID: GO:0007155 | Genes: 75 | p-valor ruta: 1.66e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
THEMIS2	NA	UP	2.550	2.88e-50	403.0
CSF1	NA	UP	2.530	1.40e-49	467.4
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
LAMA2	NA	UP	2.355	4.82e-21	125.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PDZD2	NA	UP	4.182	1.86e-12	28.7
MUC4	NA	UP	2.613	4.74e-12	55.4
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2

## Ruta: cell adhesion (Página 3 de 3)

Fuente: GO:BP | ID: GO:0007155 | Genes: 75 | p-valor ruta: 1.66e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFSF14	NA	UP	2.748	3.71e-07	23.0
ICAM4	NA	UP	2.446	8.79e-06	22.0
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
MPZ	NA	UP	2.002	2.88e-04	19.4
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
SDK2	NA	UP	2.715	5.83e-03	7.9
EGFL6	NA	UP	3.034	6.01e-03	5.9
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
OLR1	NA	UP	2.655	1.81e-02	6.9
CLSTN2	NA	UP	2.773	2.49e-02	4.9
DLG2	NA	UP	3.028	3.83e-02	3.8
NID2	NA	DOWN	-3.779	4.29e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of tumor necrosis factor production

Fuente: GO:BP | ID: GO:0032680 | Genes: 22 | p-valor ruta: 1.81e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IFIH1	NA	UP	4.035	2.22e-233	4525.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
ZFP36	NA	UP	2.944	7.57e-104	1721.5
OAS3	NA	UP	2.942	1.13e-87	8674.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
IL23A	NA	UP	2.189	2.05e-11	59.9
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: tumor necrosis factor production

Fuente: GO:BP | ID: GO:0032640 | Genes: 22 | p-valor ruta: 1.81e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IFIH1	NA	UP	4.035	2.22e-233	4525.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
ZFP36	NA	UP	2.944	7.57e-104	1721.5
OAS3	NA	UP	2.942	1.13e-87	8674.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
IL23A	NA	UP	2.189	2.05e-11	59.9
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: regulation of apoptotic signaling pathway (Página 1 de 2)

Fuente: GO:BP | ID: GO:2001233 | Genes: 33 | p-valor ruta: 1.9e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
CTH	NA	UP	2.488	2.75e-57	412.1
BBC3	NA	UP	2.829	3.65e-57	503.1
LTB	NA	UP	3.555	2.50e-41	150.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
NKX3-1	NA	UP	2.233	8.30e-23	132.4

## Ruta: regulation of apoptotic signaling pathway (Página 2 de 2)

Fuente: GO:BP | ID: GO:2001233 | Genes: 33 | p-valor ruta: 1.9e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
RET	NA	UP	2.793	1.44e-02	5.5
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: developmental process (Página 1 de 9)

Fuente: GO:BP | ID: GO:0032502 | Genes: 207 | p-valor ruta: 2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4

## Ruta: developmental process (Página 2 de 9)

Fuente: GO:BP | ID: GO:0032502 | Genes: 207 | p-valor ruta: 2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
TM4SF4	NA	DOWN	-2.482	1.83e-87	1021.7
KLF10	NA	UP	2.626	2.92e-86	1224.1
ETV7	NA	UP	4.688	2.39e-83	278.8
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLFN5	NA	UP	2.917	1.64e-76	2317.0
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2

## Ruta: developmental process (Página 3 de 9)

Fuente: GO:BP | ID: GO:0032502 | Genes: 207 | p-valor ruta: 2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
TDRD7	NA	UP	2.129	5.72e-65	1011.2
RND1	NA	UP	2.840	1.60e-62	337.7
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TUFT1	NA	UP	2.001	1.00e-55	1905.9
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
NAV2	NA	UP	2.370	3.20e-51	765.9
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4

## Ruta: developmental process (Página 4 de 9)

Fuente: GO:BP | ID: GO:0032502 | Genes: 207 | p-valor ruta: 2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
KRT6B	NA	UP	2.049	5.47e-24	321.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5

## Ruta: developmental process (Página 5 de 9)

Fuente: GO:BP | ID: GO:0032502 | Genes: 207 | p-valor ruta: 2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
DDC	NA	DOWN	-2.582	2.27e-16	72.0
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
DNAAF3	NA	DOWN	-2.041	1.75e-14	101.4
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
PPP4R4	NA	UP	3.423	6.94e-11	30.7
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
ACTN2	NA	UP	3.956	7.01e-09	20.3

## Ruta: developmental process (Página 6 de 9)

Fuente: GO:BP | ID: GO:0032502 | Genes: 207 | p-valor ruta: 2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
BAHCC1	NA	UP	4.513	9.67e-08	16.6
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
COL4A1	NA	UP	6.589	5.89e-06	8.2
SP8	NA	UP	6.528	5.89e-06	8.0
ACTBL2	NA	UP	2.242	5.97e-06	28.3
ADAMTS6	NA	UP	2.602	8.90e-06	19.6
MMP13	NA	UP	5.406	9.23e-06	11.1
SERPINA10	NA	UP	6.459	9.50e-06	7.5
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6

## Ruta: developmental process (Página 7 de 9)

Fuente: GO:BP | ID: GO:0032502 | Genes: 207 | p-valor ruta: 2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FFAR2	NA	UP	3.253	4.81e-05	12.7
XKR9	NA	UP	3.541	5.84e-05	11.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
RHCG	NA	UP	2.107	1.84e-04	21.0
EGR3	NA	UP	2.096	2.87e-04	21.5
MPZ	NA	UP	2.002	2.88e-04	19.4
TRPC4	NA	UP	5.730	3.71e-04	4.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
MKX	NA	UP	2.196	5.67e-04	15.1
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
ENKUR	NA	UP	3.518	8.61e-04	9.0
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
LHB	NA	UP	3.522	1.50e-03	7.0
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9

## Ruta: developmental process (Página 8 de 9)

Fuente: GO:BP | ID: GO:0032502 | Genes: 207 | p-valor ruta: 2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DLL1	NA	UP	2.171	4.40e-03	10.4
KRT81	NA	UP	2.044	4.94e-03	15.2
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
SDK2	NA	UP	2.715	5.83e-03	7.9
EGFL6	NA	UP	3.034	6.01e-03	5.9
KRT9	NA	UP	4.973	6.24e-03	2.7
BMPER	NA	UP	4.906	6.28e-03	2.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
INSC	NA	UP	3.872	3.01e-02	2.4
HSD11B1	NA	UP	2.341	3.03e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8

## Ruta: developmental process (Página 9 de 9)

Fuente: GO:BP | ID: GO:0032502 | Genes: 207 | p-valor ruta: 2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ADAMTS4	NA	UP	3.293	3.88e-02	3.0
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of metabolic process (Página 1 de 9)

Fuente: GO:BP | ID: GO:0019222 | Genes: 218 | p-valor ruta: 2.2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
BATF2	NA	UP	4.213	3.12e-134	731.0
ZNFX1	NA	UP	2.719	5.31e-128	6490.5

## Ruta: regulation of metabolic process (Página 2 de 9)

Fuente: GO:BP | ID: GO:0019222 | Genes: 218 | p-valor ruta: 2.2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7

## Ruta: regulation of metabolic process (Página 3 de 9)

Fuente: GO:BP | ID: GO:0019222 | Genes: 218 | p-valor ruta: 2.2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0

## Ruta: regulation of metabolic process (Página 4 de 9)

Fuente: GO:BP | ID: GO:0019222 | Genes: 218 | p-valor ruta: 2.2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
ARRDC4	NA	UP	2.305	2.76e-44	631.5

## Ruta: regulation of metabolic process (Página 5 de 9)

Fuente: GO:BP | ID: GO:0019222 | Genes: 218 | p-valor ruta: 2.2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PER1	NA	UP	2.501	8.94e-44	469.6
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
MIR155HG	NA	UP	5.318	4.66e-35	99.1
ZNF267	NA	UP	2.059	1.30e-34	677.0
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
SERPINB7	NA	UP	2.796	1.04e-28	127.7
HDX	NA	UP	2.521	1.83e-28	139.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8

## Ruta: regulation of metabolic process (Página 6 de 9)

Fuente: GO:BP | ID: GO:0019222 | Genes: 218 | p-valor ruta: 2.2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3

## Ruta: regulation of metabolic process (Página 7 de 9)

Fuente: GO:BP | ID: GO:0019222 | Genes: 218 | p-valor ruta: 2.2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
IL10RA	NA	UP	3.172	3.66e-07	18.8
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
SYNPO2	NA	UP	3.603	1.95e-04	9.0
EGR3	NA	UP	2.096	2.87e-04	21.5

## Ruta: regulation of metabolic process (Página 8 de 9)

Fuente: GO:BP | ID: GO:0019222 | Genes: 218 | p-valor ruta: 2.2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZNF382	NA	UP	2.028	3.78e-04	18.2
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CEACAM20	NA	UP	5.412	1.17e-03	3.6
RNF152	NA	UP	3.325	1.37e-03	7.5
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
RUFY4	NA	UP	4.136	2.15e-03	6.0
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
NPR3	NA	UP	2.789	1.87e-02	5.7

## Ruta: regulation of metabolic process (Página 9 de 9)

Fuente: GO:BP | ID: GO:0019222 | Genes: 218 | p-valor ruta: 2.2e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
CELF6	NA	UP	2.403	2.65e-02	5.6
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
PURG	NA	DOWN	-4.166	4.66e-02	1.7
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of leukocyte activation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002696 | Genes: 32 | p-valor ruta: 2.67e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5

## Ruta: positive regulation of leukocyte activation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002696 | Genes: 32 | p-valor ruta: 2.67e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
TNFSF14	NA	UP	2.748	3.71e-07	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: positive regulation of tumor necrosis factor superfamily cytokine production

Fuente: GO:BP | ID: GO:1903557 | Genes: 18 | p-valor ruta: 2.93e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IFIH1	NA	UP	4.035	2.22e-233	4525.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
OAS3	NA	UP	2.942	1.13e-87	8674.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
IL23A	NA	UP	2.189	2.05e-11	59.9
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: positive regulation of apoptotic signaling pathway

Fuente: GO:BP | ID: GO:2001235 | Genes: 20 | p-valor ruta: 3.06e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ATF3	NA	UP	4.971	1.38e-261	2286.0
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
BBC3	NA	UP	2.829	3.65e-57	503.1
LTB	NA	UP	3.555	2.50e-41	150.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
NKX3-1	NA	UP	2.233	8.30e-23	132.4
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
NUPR1	NA	UP	3.660	1.78e-06	14.5
RET	NA	UP	2.793	1.44e-02	5.5
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: negative regulation of response to external stimulus (Página 1 de 2)

Fuente: GO:BP | ID: GO:0032102 | Genes: 33 | p-valor ruta: 3.33e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1

## Ruta: negative regulation of response to external stimulus (Página 2 de 2)

Fuente: GO:BP | ID: GO:0032102 | Genes: 33 | p-valor ruta: 3.33e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
NOD2	NA	UP	2.981	1.19e-19	80.5
IL10RA	NA	UP	3.172	3.66e-07	18.8
FAP	NA	UP	3.233	1.87e-05	14.0
HRG	NA	UP	2.971	4.00e-03	6.9
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: immune effector process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002252 | Genes: 47 | p-valor ruta: 3.56e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
PTX3	NA	UP	3.614	2.25e-68	237.4
PTAFR	NA	UP	3.014	4.62e-62	338.1
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4

## Ruta: immune effector process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002252 | Genes: 47 | p-valor ruta: 3.56e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
CD70	NA	UP	3.257	1.21e-02	4.7
PRG2	NA	UP	2.073	1.32e-02	9.7
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: negative regulation of cell population proliferation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0008285 | Genes: 46 | p-valor ruta: 3.63e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8
IDO1	NA	UP	4.167	4.38e-109	394.2
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0

## Ruta: negative regulation of cell population proliferation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0008285 | Genes: 46 | p-valor ruta: 3.63e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMP2	NA	UP	2.237	3.69e-40	325.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
JAK2	NA	UP	2.081	1.26e-17	123.4
KLF9	NA	UP	2.555	7.01e-13	66.8
SSTR2	NA	UP	2.031	8.80e-10	53.9
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
LST1	NA	UP	6.916	7.00e-07	10.5
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
RFPL1	NA	UP	3.259	2.06e-02	4.1
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of immune effector process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002699 | Genes: 27 | p-valor ruta: 3.8e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
DDX60	NA	UP	3.015	7.43e-79	1999.9
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
PTAFR	NA	UP	3.014	4.62e-62	338.1
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
NR4A3	NA	UP	5.574	1.45e-08	20.2
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
KIT	NA	UP	3.650	6.24e-04	7.9

## Ruta: positive regulation of immune effector process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002699 | Genes: 27 | p-valor ruta: 3.8e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: response to interleukin-1

Fuente: GO:BP | ID: GO:0070555 | Genes: 18 | p-valor ruta: 4.03e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
CCL5	NA	UP	5.035	8.94e-165	656.3
ZBP1	NA	UP	6.242	1.22e-99	349.5
IRAK2	NA	UP	2.666	3.46e-95	1164.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
NKX3-1	NA	UP	2.233	8.30e-23	132.4
PCK1	NA	UP	4.419	1.17e-12	29.6
KMO	NA	UP	5.165	6.24e-09	19.5
SELE	NA	UP	5.745	2.05e-05	9.0
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: granulocyte migration

Fuente: GO:BP | ID: GO:0097530 | Genes: 21 | p-valor ruta: 4.53e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
EDN2	NA	UP	3.499	8.77e-31	90.3
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
CXCL9	NA	UP	4.099	4.37e-04	26.3
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: cytoplasmic pattern recognition receptor signaling pathway

Fuente: GO:BP | ID: GO:0002753 | Genes: 22 | p-valor ruta: 4.66e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
SLC15A3	NA	UP	4.245	2.06e-77	254.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: cellular response to interleukin-1

Fuente: GO:BP | ID: GO:0071347 | Genes: 16 | p-valor ruta: 4.93e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
CCL5	NA	UP	5.035	8.94e-165	656.3
ZBP1	NA	UP	6.242	1.22e-99	349.5
IRAK2	NA	UP	2.666	3.46e-95	1164.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
NKX3-1	NA	UP	2.233	8.30e-23	132.4
PCK1	NA	UP	4.419	1.17e-12	29.6
KMO	NA	UP	5.165	6.24e-09	19.5
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: type I interferon-mediated signaling pathway

Fuente: GO:BP | ID: GO:0060337 | Genes: 16 | p-valor ruta: 4.93e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZBP1	NA	UP	6.242	1.22e-99	349.5
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
IFITM2	NA	UP	2.649	6.22e-17	64.2

## Ruta: regulation of leukocyte proliferation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0070663 | Genes: 27 | p-valor ruta: 4.95e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
CSF2	NA	UP	7.043	2.08e-103	455.6
CD274	NA	UP	5.204	1.23e-98	314.4
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CSF1	NA	UP	2.530	1.40e-49	467.4
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
LST1	NA	UP	6.916	7.00e-07	10.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
CD70	NA	UP	3.257	1.21e-02	4.7

## Ruta: regulation of leukocyte proliferation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0070663 | Genes: 27 | p-valor ruta: 4.95e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: animal organ development (Página 1 de 5)

Fuente: GO:BP | ID: GO:0048513 | Genes: 119 | p-valor ruta: 5e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
TIPARP	NA	UP	3.093	1.11e-158	5401.6
INHBA	NA	UP	3.514	2.31e-143	1743.6
STC2	NA	UP	2.729	3.17e-119	2626.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
ETV7	NA	UP	4.688	2.39e-83	278.8
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
CCL2	NA	UP	2.562	2.63e-75	658.0

## Ruta: animal organ development (Página 2 de 5)

Fuente: GO:BP | ID: GO:0048513 | Genes: 119 | p-valor ruta: 5e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
PTX3	NA	UP	3.614	2.25e-68	237.4
TDRD7	NA	UP	2.129	5.72e-65	1011.2
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
TUFT1	NA	UP	2.001	1.00e-55	1905.9
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
PER1	NA	UP	2.501	8.94e-44	469.6
SEMA3A	NA	UP	2.276	5.71e-42	512.5
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2

## Ruta: animal organ development (Página 3 de 5)

Fuente: GO:BP | ID: GO:0048513 | Genes: 119 | p-valor ruta: 5e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
KRT6B	NA	UP	2.049	5.47e-24	321.4
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
DDC	NA	DOWN	-2.582	2.27e-16	72.0
GBX2	NA	UP	2.353	5.55e-15	78.3
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
DNAAF3	NA	DOWN	-2.041	1.75e-14	101.4
PCK1	NA	UP	4.419	1.17e-12	29.6
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SSTR2	NA	UP	2.031	8.80e-10	53.9

## Ruta: animal organ development (Página 4 de 5)

Fuente: GO:BP | ID: GO:0048513 | Genes: 119 | p-valor ruta: 5e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
COL4A1	NA	UP	6.589	5.89e-06	8.2
ADAMTS6	NA	UP	2.602	8.90e-06	19.6
MMP13	NA	UP	5.406	9.23e-06	11.1
SERPINA10	NA	UP	6.459	9.50e-06	7.5
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
MKX	NA	UP	2.196	5.67e-04	15.1
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CNTN4	NA	UP	4.928	9.17e-04	5.0
LHB	NA	UP	3.522	1.50e-03	7.0
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
SRGN	NA	UP	2.093	3.80e-03	11.0
DLL1	NA	UP	2.171	4.40e-03	10.4
KRT81	NA	UP	2.044	4.94e-03	15.2

## Ruta: animal organ development (Página 5 de 5)

Fuente: GO:BP | ID: GO:0048513 | Genes: 119 | p-valor ruta: 5e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
SDK2	NA	UP	2.715	5.83e-03	7.9
KRT9	NA	UP	4.973	6.24e-03	2.7
BMPER	NA	UP	4.906	6.28e-03	2.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
HSD11B1	NA	UP	2.341	3.03e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of macromolecule metabolic process (Página 1 de 9)

Fuente: GO:BP | ID: GO:0060255 | Genes: 204 | p-valor ruta: 5.68e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1

## Ruta: regulation of macromolecule metabolic process (Página 2 de 9)

Fuente: GO:BP | ID: GO:0060255 | Genes: 204 | p-valor ruta: 5.68e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5

## Ruta: regulation of macromolecule metabolic process (Página 3 de 9)

Fuente: GO:BP | ID: GO:0060255 | Genes: 204 | p-valor ruta: 5.68e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6

## Ruta: regulation of macromolecule metabolic process (Página 4 de 9)

Fuente: GO:BP | ID: GO:0060255 | Genes: 204 | p-valor ruta: 5.68e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2

## Ruta: regulation of macromolecule metabolic process (Página 5 de 9)

Fuente: GO:BP | ID: GO:0060255 | Genes: 204 | p-valor ruta: 5.68e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
MIR155HG	NA	UP	5.318	4.66e-35	99.1
ZNF267	NA	UP	2.059	1.30e-34	677.0
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
SERPINB7	NA	UP	2.796	1.04e-28	127.7
HDX	NA	UP	2.521	1.83e-28	139.2
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2

## Ruta: regulation of macromolecule metabolic process (Página 6 de 9)

Fuente: GO:BP | ID: GO:0060255 | Genes: 204 | p-valor ruta: 5.68e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0

## Ruta: regulation of macromolecule metabolic process (Página 7 de 9)

Fuente: GO:BP | ID: GO:0060255 | Genes: 204 | p-valor ruta: 5.68e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
AHRR	NA	UP	2.180	3.48e-07	33.9
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
UBASH3A	NA	UP	5.845	1.05e-05	9.8
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
SYNPO2	NA	UP	3.603	1.95e-04	9.0
EGR3	NA	UP	2.096	2.87e-04	21.5
ZNF382	NA	UP	2.028	3.78e-04	18.2
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CEACAM20	NA	UP	5.412	1.17e-03	3.6
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6

## Ruta: regulation of macromolecule metabolic process (Página 8 de 9)

Fuente: GO:BP | ID: GO:0060255 | Genes: 204 | p-valor ruta: 5.68e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
CELF6	NA	UP	2.403	2.65e-02	5.6
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
PPM1E	NA	UP	3.810	4.20e-02	2.4

## Ruta: regulation of macromolecule metabolic process (Página 9 de 9)

Fuente: GO:BP | ID: GO:0060255 | Genes: 204 | p-valor ruta: 5.68e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SFRP1	NA	UP	2.711	4.51e-02	3.8
PURG	NA	DOWN	-4.166	4.66e-02	1.7
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: granulocyte chemotaxis

Fuente: GO:BP | ID: GO:0071621 | Genes: 19 | p-valor ruta: 7.47e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
EDN2	NA	UP	3.499	8.77e-31	90.3
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
CXCL9	NA	UP	4.099	4.37e-04	26.3
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: positive regulation of extrinsic apoptotic signaling pathway

Fuente: GO:BP | ID: GO:2001238 | Genes: 13 | p-valor ruta: 7.57e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ATF3	NA	UP	4.971	1.38e-261	2286.0
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
LTB	NA	UP	3.555	2.50e-41	150.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
TLR6	NA	UP	2.680	9.77e-08	26.3
RET	NA	UP	2.793	1.44e-02	5.5
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of leukocyte migration

Fuente: GO:BP | ID: GO:0002685 | Genes: 25 | p-valor ruta: 8.4e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
CD69	NA	UP	3.112	5.99e-57	257.2
CSF1	NA	UP	2.530	1.40e-49	467.4
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: negative regulation of metabolic process (Página 1 de 6)

Fuente: GO:BP | ID: GO:0009892 | Genes: 126 | p-valor ruta: 9.26e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1

## Ruta: negative regulation of metabolic process (Página 2 de 6)

Fuente: GO:BP | ID: GO:0009892 | Genes: 126 | p-valor ruta: 9.26e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
ETV7	NA	UP	4.688	2.39e-83	278.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9

## Ruta: negative regulation of metabolic process (Página 3 de 6)

Fuente: GO:BP | ID: GO:0009892 | Genes: 126 | p-valor ruta: 9.26e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
PARP10	NA	UP	2.093	5.71e-52	2376.2
XRN1	NA	UP	2.115	6.38e-50	984.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
PER1	NA	UP	2.501	8.94e-44	469.6
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
MIR155HG	NA	UP	5.318	4.66e-35	99.1
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0

## Ruta: negative regulation of metabolic process (Página 4 de 6)

Fuente: GO:BP | ID: GO:0009892 | Genes: 126 | p-valor ruta: 9.26e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
IL15	NA	UP	2.012	2.28e-17	116.8
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5

## Ruta: negative regulation of metabolic process (Página 5 de 6)

Fuente: GO:BP | ID: GO:0009892 | Genes: 126 | p-valor ruta: 9.26e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
HAND1	NA	UP	4.966	8.42e-04	5.1
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
DLL1	NA	UP	2.171	4.40e-03	10.4
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
GBP7	NA	UP	4.177	1.61e-02	2.9
NPR3	NA	UP	2.789	1.87e-02	5.7
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: negative regulation of metabolic process (Página 6 de 6)

Fuente: GO:BP | ID: GO:0009892 | Genes: 126 | p-valor ruta: 9.26e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of cell activation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0050867 | Genes: 32 | p-valor ruta: 9.48e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5

## Ruta: positive regulation of cell activation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0050867 | Genes: 32 | p-valor ruta: 9.48e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
TNFSF14	NA	UP	2.748	3.71e-07	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of leukocyte mediated immunity (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002703 | Genes: 26 | p-valor ruta: 9.72e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: regulation of leukocyte mediated immunity (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002703 | Genes: 26 | p-valor ruta: 9.72e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CR1L	NA	UP	3.479	3.3e-02	3.5

## Ruta: positive regulation of interferon–beta production

Fuente: GO:BP | ID: GO:0032728 | Genes: 12 | p-valor ruta: 9.93e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
ARRDC4	NA	UP	2.305	2.76e-44	631.5
TLR3	NA	UP	2.508	1.99e-22	111.5
ZBTB20	NA	UP	3.440	1.24e-15	47.6
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: positive regulation of leukocyte proliferation

Fuente: GO:BP | ID: GO:0070665 | Genes: 21 | p-valor ruta: 1.05e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CSF2	NA	UP	7.043	2.08e-103	455.6
CD274	NA	UP	5.204	1.23e-98	314.4
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CSF1	NA	UP	2.530	1.40e-49	467.4
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
CD70	NA	UP	3.257	1.21e-02	4.7
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: myeloid leukocyte migration

Fuente: GO:BP | ID: GO:0097529 | Genes: 25 | p-valor ruta: 1.21e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
EDN2	NA	UP	3.499	8.77e-31	90.3
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: regulation of T cell activation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0050863 | Genes: 32 | p-valor ruta: 1.42e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7

## Ruta: regulation of T cell activation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0050863 | Genes: 32 | p-valor ruta: 1.42e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9

## Ruta: regulation of protein modification process (Página 1 de 3)

Fuente: GO:BP | ID: GO:0031399 | Genes: 57 | p-valor ruta: 1.64e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PML	NA	UP	2.208	2.84e-70	2901.3
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5

## Ruta: regulation of protein modification process (Página 2 de 3)

Fuente: GO:BP | ID: GO:0031399 | Genes: 57 | p-valor ruta: 1.64e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
PARP10	NA	UP	2.093	5.71e-52	2376.2
CSF1	NA	UP	2.530	1.40e-49	467.4
ARRDC4	NA	UP	2.305	2.76e-44	631.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
BDKRB2	NA	UP	2.797	5.56e-15	55.1
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NUPR1	NA	UP	3.660	1.78e-06	14.5
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9

## Ruta: regulation of protein modification process (Página 3 de 3)

Fuente: GO:BP | ID: GO:0031399 | Genes: 57 | p-valor ruta: 1.64e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: anatomical structure formation involved in morphogenesis (Página 1 de 3)

Fuente: GO:BP | ID: GO:0048646 | Genes: 62 | p-valor ruta: 1.68e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0

## Ruta: anatomical structure formation involved in morphogenesis (Página 2 de 3)

Fuente: GO:BP | ID: GO:0048646 | Genes: 62 | p-valor ruta: 1.68e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMP2	NA	UP	2.237	3.69e-40	325.3
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
ACTN2	NA	UP	3.956	7.01e-09	20.3
LRP2	NA	UP	3.144	3.22e-08	22.0
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
COL4A1	NA	UP	6.589	5.89e-06	8.2
FAP	NA	UP	3.233	1.87e-05	14.0
EGR3	NA	UP	2.096	2.87e-04	21.5
CXCL9	NA	UP	4.099	4.37e-04	26.3
HAND1	NA	UP	4.966	8.42e-04	5.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9

## Ruta: anatomical structure formation involved in morphogenesis (Página 3 de 3)

Fuente: GO:BP | ID: GO:0048646 | Genes: 62 | p-valor ruta: 1.68e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DLL1	NA	UP	2.171	4.40e-03	10.4
SDK2	NA	UP	2.715	5.83e-03	7.9
BMPER	NA	UP	4.906	6.28e-03	2.6
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of type II interferon production

Fuente: GO:BP | ID: GO:0032649 | Genes: 18 | p-valor ruta: 1.81e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNL1	NA	UP	8.179	1.68e-89	578.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ISG15	NA	UP	2.482	5.90e-57	3807.9
PDE4B	NA	UP	3.818	7.08e-52	171.4
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL23A	NA	UP	2.189	2.05e-11	59.9
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL18R1	NA	UP	2.088	8.75e-05	23.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: response to interferon–beta

Fuente: GO:BP | ID: GO:0035456 | Genes: 11 | p-valor ruta: 2.03e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFITM1	NA	UP	3.632	5.16e-130	784.8
IFI16	NA	UP	3.151	2.12e-114	2583.4
XAF1	NA	UP	4.580	3.19e-111	427.9
IFNB1	NA	UP	10.001	4.69e-95	1340.6
PNPT1	NA	UP	2.411	6.12e-71	2101.8
STAT1	NA	UP	2.519	1.61e-68	9528.0
TLR3	NA	UP	2.508	1.99e-22	111.5
BST2	NA	UP	4.284	3.82e-19	50.8
IFITM2	NA	UP	2.649	6.22e-17	64.2

## Ruta: type II interferon production

Fuente: GO:BP | ID: GO:0032609 | Genes: 18 | p-valor ruta: 2.08e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNL1	NA	UP	8.179	1.68e-89	578.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ISG15	NA	UP	2.482	5.90e-57	3807.9
PDE4B	NA	UP	3.818	7.08e-52	171.4
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL23A	NA	UP	2.189	2.05e-11	59.9
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL18R1	NA	UP	2.088	8.75e-05	23.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: antiviral innate immune response

Fuente: GO:BP | ID: GO:0140374 | Genes: 13 | p-valor ruta: 2.14e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
MX1	NA	UP	3.859	1.25e-245	5699.6
IFIH1	NA	UP	4.035	2.22e-233	4525.3
CXCL10	NA	UP	6.079	8.12e-195	783.4
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
NLRP1	NA	UP	5.692	4.64e-09	21.6

## Ruta: interleukin-1 beta production

Fuente: GO:BP | ID: GO:0032611 | Genes: 16 | p-valor ruta: 2.47e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
TLR6	NA	UP	2.680	9.77e-08	26.3
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: regulation of interleukin-1 beta production

Fuente: GO:BP | ID: GO:0032651 | Genes: 16 | p-valor ruta: 2.47e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
TLR6	NA	UP	2.680	9.77e-08	26.3
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: positive regulation of leukocyte migration

Fuente: GO:BP | ID: GO:0002687 | Genes: 20 | p-valor ruta: 2.65e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
CSF1	NA	UP	2.530	1.40e-49	467.4
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SELE	NA	UP	5.745	2.05e-05	9.0
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: positive regulation of developmental process (Página 1 de 3)

Fuente: GO:BP | ID: GO:0051094 | Genes: 66 | p-valor ruta: 3.31e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9

## Ruta: positive regulation of developmental process (Página 2 de 3)

Fuente: GO:BP | ID: GO:0051094 | Genes: 66 | p-valor ruta: 3.31e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
FUT1	NA	UP	2.765	4.55e-26	104.9
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
LRRN3	NA	UP	6.733	2.08e-06	9.4
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
CXCL9	NA	UP	4.099	4.37e-04	26.3

## Ruta: positive regulation of developmental process (Página 3 de 3)

Fuente: GO:BP | ID: GO:0051094 | Genes: 66 | p-valor ruta: 3.31e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KIT	NA	UP	3.650	6.24e-04	7.9
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of DNA-templated transcription (Página 1 de 4)

Fuente: GO:BP | ID: GO:0045893 | Genes: 77 | p-valor ruta: 3.4e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
KLF10	NA	UP	2.626	2.92e-86	1224.1
KLF4	NA	UP	2.704	2.52e-79	645.9

## Ruta: positive regulation of DNA-templated transcription (Página 2 de 4)

Fuente: GO:BP | ID: GO:0045893 | Genes: 77 | p-valor ruta: 3.4e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
FOSB	NA	UP	3.144	1.32e-55	267.7
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: positive regulation of DNA-templated transcription (Página 3 de 4)

Fuente: GO:BP | ID: GO:0045893 | Genes: 77 | p-valor ruta: 3.4e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
EGR4	NA	UP	2.643	5.77e-04	12.2
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3

## Ruta: positive regulation of DNA-templated transcription (Página 4 de 4)

Fuente: GO:BP | ID: GO:0045893 | Genes: 77 | p-valor ruta: 3.4e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of RNA biosynthetic process (Página 1 de 4)

Fuente: GO:BP | ID: GO:1902680 | Genes: 77 | p-valor ruta: 3.59e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
KLF10	NA	UP	2.626	2.92e-86	1224.1
KLF4	NA	UP	2.704	2.52e-79	645.9

## Ruta: positive regulation of RNA biosynthetic process (Página 2 de 4)

Fuente: GO:BP | ID: GO:1902680 | Genes: 77 | p-valor ruta: 3.59e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
FOSB	NA	UP	3.144	1.32e-55	267.7
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: positive regulation of RNA biosynthetic process (Página 3 de 4)

Fuente: GO:BP | ID: GO:1902680 | Genes: 77 | p-valor ruta: 3.59e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
EGR4	NA	UP	2.643	5.77e-04	12.2
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3

## Ruta: positive regulation of RNA biosynthetic process (Página 4 de 4)

Fuente: GO:BP | ID: GO:1902680 | Genes: 77 | p-valor ruta: 3.59e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: tube development (Página 1 de 3)

Fuente: GO:BP | ID: GO:0035295 | Genes: 58 | p-valor ruta: 3.65e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
HDAC9	NA	UP	2.292	4.51e-32	2003.2

## Ruta: tube development (Página 2 de 3)

Fuente: GO:BP | ID: GO:0035295 | Genes: 58 | p-valor ruta: 3.65e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
GBX2	NA	UP	2.353	5.55e-15	78.3
LRP2	NA	UP	3.144	3.22e-08	22.0
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
COL4A1	NA	UP	6.589	5.89e-06	8.2
FAP	NA	UP	3.233	1.87e-05	14.0
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
NPR3	NA	UP	2.789	1.87e-02	5.7

## Ruta: tube development (Página 3 de 3)

Fuente: GO:BP | ID: GO:0035295 | Genes: 58 | p-valor ruta: 3.65e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
HSD11B1	NA	UP	2.341	3.03e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of hemopoiesis (Página 1 de 2)

Fuente: GO:BP | ID: GO:1903706 | Genes: 33 | p-valor ruta: 3.7e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
IKZF3	NA	UP	3.163	1.21e-120	1046.8
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
PRDM1	NA	UP	3.525	5.98e-31	99.0
TLR3	NA	UP	2.508	1.99e-22	111.5
CSF3	NA	UP	6.122	1.72e-19	56.0
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6

## Ruta: regulation of hemopoiesis (Página 2 de 2)

Fuente: GO:BP | ID: GO:1903706 | Genes: 33 | p-valor ruta: 3.7e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
EGR3	NA	UP	2.096	2.87e-04	21.5
DLL1	NA	UP	2.171	4.40e-03	10.4
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: positive regulation of RNA metabolic process (Página 1 de 4)

Fuente: GO:BP | ID: GO:0051254 | Genes: 81 | p-valor ruta: 3.92e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4

## Ruta: positive regulation of RNA metabolic process (Página 2 de 4)

Fuente: GO:BP | ID: GO:0051254 | Genes: 81 | p-valor ruta: 3.92e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KLF10	NA	UP	2.626	2.92e-86	1224.1
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
FOSB	NA	UP	3.144	1.32e-55	267.7
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5

## Ruta: positive regulation of RNA metabolic process (Página 3 de 4)

Fuente: GO:BP | ID: GO:0051254 | Genes: 81 | p-valor ruta: 3.92e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
EGR4	NA	UP	2.643	5.77e-04	12.2
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5

## Ruta: positive regulation of RNA metabolic process (Página 4 de 4)

Fuente: GO:BP | ID: GO:0051254 | Genes: 81 | p-valor ruta: 3.92e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR9	NA	UP	2.952	1.98e-02	4.6
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of canonical NF-kappaB signal transduction

Fuente: GO:BP | ID: GO:0043123 | Genes: 23 | p-valor ruta: 4.56e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFIT5	NA	UP	2.861	3.01e-78	749.8
LGALS9	NA	UP	2.474	3.44e-71	1449.3
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
CTH	NA	UP	2.488	2.75e-57	412.1
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: positive regulation of T cell activation

Fuente: GO:BP | ID: GO:0050870 | Genes: 25 | p-valor ruta: 4.92e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CD274	NA	UP	5.204	1.23e-98	314.4
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFSF14	NA	UP	2.748	3.71e-07	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9

## Ruta: T cell differentiation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0030217 | Genes: 28 | p-valor ruta: 5.86e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
PRDM1	NA	UP	3.525	5.98e-31	99.0
BCL3	NA	UP	2.067	4.65e-26	500.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
RUNX2	NA	UP	3.983	1.50e-06	15.2
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: T cell differentiation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0030217 | Genes: 28 | p-valor ruta: 5.86e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
VAV1	NA	UP	2.118	1.54e-02	7.9

## Ruta: interleukin–10 production

Fuente: GO:BP | ID: GO:0032613 | Genes: 13 | p-valor ruta: 6.9e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ISG15	NA	UP	2.482	5.90e-57	3807.9
BCL3	NA	UP	2.067	4.65e-26	500.4
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
DLL1	NA	UP	2.171	4.40e-03	10.4
PRG2	NA	UP	2.073	1.32e-02	9.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: positive regulation of interleukin–1 beta production

Fuente: GO:BP | ID: GO:0032731 | Genes: 13 | p-valor ruta: 6.9e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
TLR6	NA	UP	2.680	9.77e-08	26.3
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: regulation of interleukin-10 production

Fuente: GO:BP | ID: GO:0032653 | Genes: 13 | p-valor ruta: 6.9e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ISG15	NA	UP	2.482	5.90e-57	3807.9
BCL3	NA	UP	2.067	4.65e-26	500.4
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
DLL1	NA	UP	2.171	4.40e-03	10.4
PRG2	NA	UP	2.073	1.32e-02	9.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: tyrosine phosphorylation of STAT protein

Fuente: GO:BP | ID: GO:0007260 | Genes: 13 | p-valor ruta: 6.9e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNL1	NA	UP	8.179	1.68e-89	578.0
PARP9	NA	UP	2.449	1.75e-75	2354.5
IL12A	NA	UP	3.852	1.95e-28	83.7
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
KIT	NA	UP	3.650	6.24e-04	7.9

## Ruta: cell-cell adhesion (Página 1 de 3)

Fuente: GO:BP | ID: GO:0098609 | Genes: 53 | p-valor ruta: 8.33e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IDO1	NA	UP	4.167	4.38e-109	394.2
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
KLF4	NA	UP	2.704	2.52e-79	645.9
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
CD69	NA	UP	3.112	5.99e-57	257.2
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9

## Ruta: cell-cell adhesion (Página 2 de 3)

Fuente: GO:BP | ID: GO:0098609 | Genes: 53 | p-valor ruta: 8.33e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFSF14	NA	UP	2.748	3.71e-07	23.0
ICAM4	NA	UP	2.446	8.79e-06	22.0
SELE	NA	UP	5.745	2.05e-05	9.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
MPZ	NA	UP	2.002	2.88e-04	19.4
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
KIT	NA	UP	3.650	6.24e-04	7.9
CNTN4	NA	UP	4.928	9.17e-04	5.0
SDK2	NA	UP	2.715	5.83e-03	7.9
CD70	NA	UP	3.257	1.21e-02	4.7
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9

## Ruta: cell-cell adhesion (Página 3 de 3)

Fuente: GO:BP | ID: GO:0098609 | Genes: 53 | p-valor ruta: 8.33e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OLR1	NA	UP	2.655	1.81e-02	6.9
CLSTN2	NA	UP	2.773	2.49e-02	4.9
DLG2	NA	UP	3.028	3.83e-02	3.8

## Ruta: regulation of cell differentiation (Página 1 de 3)

Fuente: GO:BP | ID: GO:0045595 | Genes: 72 | p-valor ruta: 1.11e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
CTH	NA	UP	2.488	2.75e-57	412.1

## Ruta: regulation of cell differentiation (Página 2 de 3)

Fuente: GO:BP | ID: GO:0045595 | Genes: 72 | p-valor ruta: 1.11e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: regulation of cell differentiation (Página 3 de 3)

Fuente: GO:BP | ID: GO:0045595 | Genes: 72 | p-valor ruta: 1.11e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
CNTN4	NA	UP	4.928	9.17e-04	5.0
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: myeloid leukocyte activation

Fuente: GO:BP | ID: GO:0002274 | Genes: 24 | p-valor ruta: 1.15e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
BATF2	NA	UP	4.213	3.12e-134	731.0
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
CSF1	NA	UP	2.530	1.40e-49	467.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
EDN2	NA	UP	3.499	8.77e-31	90.3
TLR3	NA	UP	2.508	1.99e-22	111.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: regulation of phosphate metabolic process (Página 1 de 3)

Fuente: GO:BP | ID: GO:0019220 | Genes: 52 | p-valor ruta: 1.17e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9

## Ruta: regulation of phosphate metabolic process (Página 2 de 3)

Fuente: GO:BP | ID: GO:0019220 | Genes: 52 | p-valor ruta: 1.17e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRS2	NA	UP	2.254	1.06e-33	255.2
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
ZBTB20	NA	UP	3.440	1.24e-15	47.6
BDKRB2	NA	UP	2.797	5.56e-15	55.1
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NUPR1	NA	UP	3.660	1.78e-06	14.5
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
P2RY6	NA	UP	2.536	8.76e-03	7.0
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of phosphate metabolic process (Página 3 de 3)

Fuente: GO:BP | ID: GO:0019220 | Genes: 52 | p-valor ruta: 1.17e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of type I interferon production

Fuente: GO:BP | ID: GO:0032481 | Genes: 14 | p-valor ruta: 1.18e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
ISG15	NA	UP	2.482	5.90e-57	3807.9
ARRDC4	NA	UP	2.305	2.76e-44	631.5
TLR3	NA	UP	2.508	1.99e-22	111.5
ZBTB20	NA	UP	3.440	1.24e-15	47.6
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of phosphorus metabolic process (Página 1 de 3)

Fuente: GO:BP | ID: GO:0051174 | Genes: 52 | p-valor ruta: 1.21e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9

## Ruta: regulation of phosphorus metabolic process (Página 2 de 3)

Fuente: GO:BP | ID: GO:0051174 | Genes: 52 | p-valor ruta: 1.21e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRS2	NA	UP	2.254	1.06e-33	255.2
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
ZBTB20	NA	UP	3.440	1.24e-15	47.6
BDKRB2	NA	UP	2.797	5.56e-15	55.1
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NUPR1	NA	UP	3.660	1.78e-06	14.5
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
P2RY6	NA	UP	2.536	8.76e-03	7.0
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of phosphorus metabolic process (Página 3 de 3)

Fuente: GO:BP | ID: GO:0051174 | Genes: 52 | p-valor ruta: 1.21e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of lymphocyte activation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051251 | Genes: 28 | p-valor ruta: 1.36e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CD274	NA	UP	5.204	1.23e-98	314.4
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFSF14	NA	UP	2.748	3.71e-07	23.0
EGR3	NA	UP	2.096	2.87e-04	21.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2

## Ruta: positive regulation of lymphocyte activation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051251 | Genes: 28 | p-valor ruta: 1.36e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: response to endogenous stimulus (Página 1 de 3)

Fuente: GO:BP | ID: GO:0009719 | Genes: 69 | p-valor ruta: 1.49e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
STC2	NA	UP	2.729	3.17e-119	2626.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1

## Ruta: response to endogenous stimulus (Página 2 de 3)

Fuente: GO:BP | ID: GO:0009719 | Genes: 69 | p-valor ruta: 1.49e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NEDD4	NA	UP	2.433	4.99e-60	1678.5
FOSB	NA	UP	3.144	1.32e-55	267.7
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
JAK2	NA	UP	2.081	1.26e-17	123.4
EGR2	NA	UP	3.090	6.72e-15	43.7
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
SSTR2	NA	UP	2.031	8.80e-10	53.9
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2

## Ruta: response to endogenous stimulus (Página 3 de 3)

Fuente: GO:BP | ID: GO:0009719 | Genes: 69 | p-valor ruta: 1.49e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
PTGER2	NA	UP	3.006	1.95e-04	11.0
EGR3	NA	UP	2.096	2.87e-04	21.5
SLC5A5	NA	UP	4.542	4.62e-04	6.8
FLRT1	NA	UP	5.509	1.11e-03	3.8
LHB	NA	UP	3.522	1.50e-03	7.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: regulation of cell development (Página 1 de 2)

Fuente: GO:BP | ID: GO:0060284 | Genes: 48 | p-valor ruta: 1.5e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2

## Ruta: regulation of cell development (Página 2 de 2)

Fuente: GO:BP | ID: GO:0060284 | Genes: 48 | p-valor ruta: 1.5e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
TLR3	NA	UP	2.508	1.99e-22	111.5
CSF3	NA	UP	6.122	1.72e-19	56.0
IL15	NA	UP	2.012	2.28e-17	116.8
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of macromolecule metabolic process (Página 1 de 5)

Fuente: GO:BP | ID: GO:0010605 | Genes: 116 | p-valor ruta: 2.02e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5

## Ruta: negative regulation of macromolecule metabolic process (Página 2 de 5)

Fuente: GO:BP | ID: GO:0010605 | Genes: 116 | p-valor ruta: 2.02e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
ETV7	NA	UP	4.688	2.39e-83	278.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0

## Ruta: negative regulation of macromolecule metabolic process (Página 3 de 5)

Fuente: GO:BP | ID: GO:0010605 | Genes: 116 | p-valor ruta: 2.02e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
PARP10	NA	UP	2.093	5.71e-52	2376.2
XRN1	NA	UP	2.115	6.38e-50	984.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
MIR155HG	NA	UP	5.318	4.66e-35	99.1
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4

## Ruta: negative regulation of macromolecule metabolic process (Página 4 de 5)

Fuente: GO:BP | ID: GO:0010605 | Genes: 116 | p-valor ruta: 2.02e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HIVEP1	NA	UP	2.014	1.06e-24	282.1
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RUNX2	NA	UP	3.983	1.50e-06	15.2
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
PKP1	NA	UP	3.076	9.16e-05	12.8
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
HAND1	NA	UP	4.966	8.42e-04	5.1

## Ruta: negative regulation of macromolecule metabolic process (Página 5 de 5)

Fuente: GO:BP | ID: GO:0010605 | Genes: 116 | p-valor ruta: 2.02e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
DLL1	NA	UP	2.171	4.40e-03	10.4
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
GBP7	NA	UP	4.177	1.61e-02	2.9
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of smooth muscle cell proliferation

Fuente: GO:BP | ID: GO:0048660 | Genes: 18 | p-valor ruta: 2.13e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BMP2	NA	UP	2.237	3.69e-40	325.3
IL12A	NA	UP	3.852	1.95e-28	83.7
JAK2	NA	UP	2.081	1.26e-17	123.4
NR4A3	NA	UP	5.574	1.45e-08	20.2
NPR1	NA	UP	3.131	3.66e-07	19.1
P2RY6	NA	UP	2.536	8.76e-03	7.0

## Ruta: positive regulation of MAPK cascade (Página 1 de 2)

Fuente: GO:BP | ID: GO:0043410 | Genes: 33 | p-valor ruta: 2.26e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
GADD45A	NA	UP	2.255	1.32e-60	1140.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3

## Ruta: positive regulation of MAPK cascade (Página 2 de 2)

Fuente: GO:BP | ID: GO:0043410 | Genes: 33 | p-valor ruta: 2.26e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KIT	NA	UP	3.650	6.24e-04	7.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: regulation of phosphorylation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0042325 | Genes: 47 | p-valor ruta: 2.35e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
SPRY2	NA	UP	2.250	1.05e-29	211.9

## Ruta: regulation of phosphorylation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0042325 | Genes: 47 | p-valor ruta: 2.35e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
BDKRB2	NA	UP	2.797	5.56e-15	55.1
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of response to cytokine stimulus

Fuente: GO:BP | ID: GO:0060759 | Genes: 20 | p-valor ruta: 2.62e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IFIH1	NA	UP	4.035	2.22e-233	4525.3
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
PARP14	NA	UP	2.977	1.79e-119	2649.9
ZBP1	NA	UP	6.242	1.22e-99	349.5
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
CASP1	NA	UP	2.494	1.49e-18	80.2

## Ruta: positive regulation of protein metabolic process (Página 1 de 3)

Fuente: GO:BP | ID: GO:0051247 | Genes: 54 | p-valor ruta: 2.7e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
TIPARP	NA	UP	3.093	1.11e-158	5401.6
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PML	NA	UP	2.208	2.84e-70	2901.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2

## Ruta: positive regulation of protein metabolic process (Página 2 de 3)

Fuente: GO:BP | ID: GO:0051247 | Genes: 54 | p-valor ruta: 2.7e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CSF1	NA	UP	2.530	1.40e-49	467.4
ARRDC4	NA	UP	2.305	2.76e-44	631.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
LRP2	NA	UP	3.144	3.22e-08	22.0
TLR6	NA	UP	2.680	9.77e-08	26.3
NUPR1	NA	UP	3.660	1.78e-06	14.5
PKP1	NA	UP	3.076	9.16e-05	12.8
KIT	NA	UP	3.650	6.24e-04	7.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1

## Ruta: positive regulation of protein metabolic process (Página 3 de 3)

Fuente: GO:BP | ID: GO:0051247 | Genes: 54 | p-valor ruta: 2.7e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of transcription by RNA polymerase II (Página 1 de 3)

Fuente: GO:BP | ID: GO:0045944 | Genes: 61 | p-valor ruta: 2.86e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
NLRC5	NA	UP	3.949	8.12e-88	414.4
KLF10	NA	UP	2.626	2.92e-86	1224.1
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
EGR1	NA	UP	2.472	2.61e-74	1149.5
CSRNP1	NA	UP	2.529	4.65e-70	673.2

## Ruta: positive regulation of transcription by RNA polymerase II (Página 2 de 3)

Fuente: GO:BP | ID: GO:0045944 | Genes: 61 | p-valor ruta: 2.86e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
FOSB	NA	UP	3.144	1.32e-55	267.7
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
NR4A3	NA	UP	5.574	1.45e-08	20.2
RUNX2	NA	UP	3.983	1.50e-06	15.2

## Ruta: positive regulation of transcription by RNA polymerase II (Página 3 de 3)

Fuente: GO:BP | ID: GO:0045944 | Genes: 61 | p-valor ruta: 2.86e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
EGR4	NA	UP	2.643	5.77e-04	12.2
HAND1	NA	UP	4.966	8.42e-04	5.1
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
TLR9	NA	UP	2.952	1.98e-02	4.6
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of type I interferon production

Fuente: GO:BP | ID: GO:0032479 | Genes: 17 | p-valor ruta: 2.9e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
XAF1	NA	UP	4.580	3.19e-111	427.9
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
ARRDC4	NA	UP	2.305	2.76e-44	631.5
TLR3	NA	UP	2.508	1.99e-22	111.5
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: type I interferon production

Fuente: GO:BP | ID: GO:0032606 | Genes: 17 | p-valor ruta: 2.9e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
XAF1	NA	UP	4.580	3.19e-111	427.9
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
ARRDC4	NA	UP	2.305	2.76e-44	631.5
TLR3	NA	UP	2.508	1.99e-22	111.5
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBP7	NA	UP	4.177	1.61e-02	2.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: interleukin-1 production

Fuente: GO:BP | ID: GO:0032612 | Genes: 16 | p-valor ruta: 3.25e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
TLR6	NA	UP	2.680	9.77e-08	26.3
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: regulation of interleukin-1 production

Fuente: GO:BP | ID: GO:0032652 | Genes: 16 | p-valor ruta: 3.25e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
TLR6	NA	UP	2.680	9.77e-08	26.3
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: smooth muscle cell proliferation

Fuente: GO:BP | ID: GO:0048659 | Genes: 18 | p-valor ruta: 3.4e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BMP2	NA	UP	2.237	3.69e-40	325.3
IL12A	NA	UP	3.852	1.95e-28	83.7
JAK2	NA	UP	2.081	1.26e-17	123.4
NR4A3	NA	UP	5.574	1.45e-08	20.2
NPR1	NA	UP	3.131	3.66e-07	19.1
P2RY6	NA	UP	2.536	8.76e-03	7.0

## Ruta: negative regulation of immune response

Fuente: GO:BP | ID: GO:0050777 | Genes: 21 | p-valor ruta: 3.58e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
NOD2	NA	UP	2.981	1.19e-19	80.5
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: regulation of protein metabolic process (Página 1 de 4)

Fuente: GO:BP | ID: GO:0051246 | Genes: 79 | p-valor ruta: 3.63e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
LAMP3	NA	UP	3.644	2.72e-189	1627.7
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
INHBA	NA	UP	3.514	2.31e-143	1743.6
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0

## Ruta: regulation of protein metabolic process (Página 2 de 4)

Fuente: GO:BP | ID: GO:0051246 | Genes: 79 | p-valor ruta: 3.63e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PML	NA	UP	2.208	2.84e-70	2901.3
PTX3	NA	UP	3.614	2.25e-68	237.4
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: regulation of protein metabolic process (Página 3 de 4)

Fuente: GO:BP | ID: GO:0051246 | Genes: 79 | p-valor ruta: 3.63e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BCL3	NA	UP	2.067	4.65e-26	500.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
BDKRB2	NA	UP	2.797	5.56e-15	55.1
IL23A	NA	UP	2.189	2.05e-11	59.9
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NUPR1	NA	UP	3.660	1.78e-06	14.5
PKP1	NA	UP	3.076	9.16e-05	12.8
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
PATL2	NA	UP	2.215	2.72e-03	12.1
HRG	NA	UP	2.971	4.00e-03	6.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9

## Ruta: regulation of protein metabolic process (Página 4 de 4)

Fuente: GO:BP | ID: GO:0051246 | Genes: 79 | p-valor ruta: 3.63e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of tyrosine phosphorylation of STAT protein

Fuente: GO:BP | ID: GO:0042509 | Genes: 12 | p-valor ruta: 3.83e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNL1	NA	UP	8.179	1.68e-89	578.0
PARP9	NA	UP	2.449	1.75e-75	2354.5
IL12A	NA	UP	3.852	1.95e-28	83.7
JAK2	NA	UP	2.081	1.26e-17	123.4
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
KIT	NA	UP	3.650	6.24e-04	7.9

## Ruta: positive regulation of cell differentiation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0045597 | Genes: 48 | p-valor ruta: 5.05e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
LAMA2	NA	UP	2.355	4.82e-21	125.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8

## Ruta: positive regulation of cell differentiation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0045597 | Genes: 48 | p-valor ruta: 5.05e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: cell-cell signaling (Página 1 de 3)

Fuente: GO:BP | ID: GO:0007267 | Genes: 63 | p-valor ruta: 5.59e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
CCL2	NA	UP	2.562	2.63e-75	658.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
CCL22	NA	UP	3.454	2.91e-50	168.7
PCK2	NA	UP	2.226	5.13e-50	969.9
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
NKX3-1	NA	UP	2.233	8.30e-23	132.4

## Ruta: cell-cell signaling (Página 2 de 3)

Fuente: GO:BP | ID: GO:0007267 | Genes: 63 | p-valor ruta: 5.59e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LAMA2	NA	UP	2.355	4.82e-21	125.5
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8
EGR2	NA	UP	3.090	6.72e-15	43.7
KMO	NA	UP	5.165	6.24e-09	19.5
STX19	NA	UP	2.009	1.09e-08	99.7
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
SYT1	NA	UP	2.659	1.62e-06	21.4
BEST1	NA	UP	3.553	8.47e-06	13.3
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
NPTX1	NA	UP	2.102	1.13e-04	22.3
EGR3	NA	UP	2.096	2.87e-04	21.5
MPZ	NA	UP	2.002	2.88e-04	19.4
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
GAL3ST4	NA	UP	2.371	7.40e-04	12.5
CNTN4	NA	UP	4.928	9.17e-04	5.0
LHB	NA	UP	3.522	1.50e-03	7.0
SLC1A2	NA	UP	2.752	2.07e-03	8.4

## Ruta: cell-cell signaling (Página 3 de 3)

Fuente: GO:BP | ID: GO:0007267 | Genes: 63 | p-valor ruta: 5.59e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KCNN1	NA	UP	3.883	2.55e-03	6.2
IL17C	NA	UP	4.636	3.13e-03	4.1
DLL1	NA	UP	2.171	4.40e-03	10.4
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
DLG2	NA	UP	3.028	3.83e-02	3.8
CCL17	NA	UP	3.441	3.89e-02	2.9
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: regulation of leukocyte differentiation (Página 1 de 2)

Fuente: GO:BP | ID: GO:1902105 | Genes: 27 | p-valor ruta: 5.74e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
IKZF3	NA	UP	3.163	1.21e-120	1046.8
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
PRDM1	NA	UP	3.525	5.98e-31	99.0
TLR3	NA	UP	2.508	1.99e-22	111.5
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
EGR3	NA	UP	2.096	2.87e-04	21.5
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of leukocyte differentiation (Página 2 de 2)

Fuente: GO:BP | ID: GO:1902105 | Genes: 27 | p-valor ruta: 5.74e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL34	NA	UP	2.794	2.41e-02	4.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: positive regulation of interleukin-1 production

Fuente: GO:BP | ID: GO:0032732 | Genes: 13 | p-valor ruta: 6.28e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
TLR6	NA	UP	2.680	9.77e-08	26.3
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: positive regulation of tyrosine phosphorylation of STAT protein

Fuente: GO:BP | ID: GO:0042531 | Genes: 11 | p-valor ruta: 6.74e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNL1	NA	UP	8.179	1.68e-89	578.0
PARP9	NA	UP	2.449	1.75e-75	2354.5
IL12A	NA	UP	3.852	1.95e-28	83.7
JAK2	NA	UP	2.081	1.26e-17	123.4
IL23A	NA	UP	2.189	2.05e-11	59.9
KIT	NA	UP	3.650	6.24e-04	7.9

## Ruta: cell differentiation (Página 1 de 6)

Fuente: GO:BP | ID: GO:0030154 | Genes: 147 | p-valor ruta: 7.05e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6

## Ruta: cell differentiation (Página 2 de 6)

Fuente: GO:BP | ID: GO:0030154 | Genes: 147 | p-valor ruta: 7.05e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
SLFN5	NA	UP	2.917	1.64e-76	2317.0
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
TDRD7	NA	UP	2.129	5.72e-65	1011.2
RND1	NA	UP	2.840	1.60e-62	337.7
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2

## Ruta: cell differentiation (Página 3 de 6)

Fuente: GO:BP | ID: GO:0030154 | Genes: 147 | p-valor ruta: 7.05e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
NAV2	NA	UP	2.370	3.20e-51	765.9
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
KRT6B	NA	UP	2.049	5.47e-24	321.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8

## Ruta: cell differentiation (Página 4 de 6)

Fuente: GO:BP | ID: GO:0030154 | Genes: 147 | p-valor ruta: 7.05e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
BAHCC1	NA	UP	4.513	9.67e-08	16.6
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0

## Ruta: cell differentiation (Página 5 de 6)

Fuente: GO:BP | ID: GO:0030154 | Genes: 147 | p-valor ruta: 7.05e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LST1	NA	UP	6.916	7.00e-07	10.5
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
COL4A1	NA	UP	6.589	5.89e-06	8.2
ACTBL2	NA	UP	2.242	5.97e-06	28.3
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
RHCG	NA	UP	2.107	1.84e-04	21.0
EGR3	NA	UP	2.096	2.87e-04	21.5
TRPC4	NA	UP	5.730	3.71e-04	4.5
CXCL9	NA	UP	4.099	4.37e-04	26.3
MKX	NA	UP	2.196	5.67e-04	15.1
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
LGR6	NA	UP	3.915	2.25e-03	6.0
DLL1	NA	UP	2.171	4.40e-03	10.4

## Ruta: cell differentiation (Página 6 de 6)

Fuente: GO:BP | ID: GO:0030154 | Genes: 147 | p-valor ruta: 7.05e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KRT81	NA	UP	2.044	4.94e-03	15.2
RP1L1	NA	UP	2.162	5.43e-03	10.3
SDK2	NA	UP	2.715	5.83e-03	7.9
EGFL6	NA	UP	3.034	6.01e-03	5.9
KRT9	NA	UP	4.973	6.24e-03	2.7
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
INSC	NA	UP	3.872	3.01e-02	2.4
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: cellular developmental process (Página 1 de 6)

Fuente: GO:BP | ID: GO:0048869 | Genes: 147 | p-valor ruta: 7.17e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6

## Ruta: cellular developmental process (Página 2 de 6)

Fuente: GO:BP | ID: GO:0048869 | Genes: 147 | p-valor ruta: 7.17e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
SLFN5	NA	UP	2.917	1.64e-76	2317.0
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
TDRD7	NA	UP	2.129	5.72e-65	1011.2
RND1	NA	UP	2.840	1.60e-62	337.7
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2

## Ruta: cellular developmental process (Página 3 de 6)

Fuente: GO:BP | ID: GO:0048869 | Genes: 147 | p-valor ruta: 7.17e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
NAV2	NA	UP	2.370	3.20e-51	765.9
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
KRT6B	NA	UP	2.049	5.47e-24	321.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8

## Ruta: cellular developmental process (Página 4 de 6)

Fuente: GO:BP | ID: GO:0048869 | Genes: 147 | p-valor ruta: 7.17e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
BAHCC1	NA	UP	4.513	9.67e-08	16.6
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0

## Ruta: cellular developmental process (Página 5 de 6)

Fuente: GO:BP | ID: GO:0048869 | Genes: 147 | p-valor ruta: 7.17e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LST1	NA	UP	6.916	7.00e-07	10.5
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
COL4A1	NA	UP	6.589	5.89e-06	8.2
ACTBL2	NA	UP	2.242	5.97e-06	28.3
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
RHCG	NA	UP	2.107	1.84e-04	21.0
EGR3	NA	UP	2.096	2.87e-04	21.5
TRPC4	NA	UP	5.730	3.71e-04	4.5
CXCL9	NA	UP	4.099	4.37e-04	26.3
MKX	NA	UP	2.196	5.67e-04	15.1
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
LGR6	NA	UP	3.915	2.25e-03	6.0
DLL1	NA	UP	2.171	4.40e-03	10.4

## Ruta: cellular developmental process (Página 6 de 6)

Fuente: GO:BP | ID: GO:0048869 | Genes: 147 | p-valor ruta: 7.17e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KRT81	NA	UP	2.044	4.94e-03	15.2
RP1L1	NA	UP	2.162	5.43e-03	10.3
SDK2	NA	UP	2.715	5.83e-03	7.9
EGFL6	NA	UP	3.034	6.01e-03	5.9
KRT9	NA	UP	4.973	6.24e-03	2.7
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
INSC	NA	UP	3.872	3.01e-02	2.4
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: interferon–beta production

Fuente: GO:BP | ID: GO:0032608 | Genes: 12 | p-valor ruta: 7.25e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
ARRDC4	NA	UP	2.305	2.76e-44	631.5
TLR3	NA	UP	2.508	1.99e-22	111.5
ZBTB20	NA	UP	3.440	1.24e-15	47.6
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of interferon-beta production

Fuente: GO:BP | ID: GO:0032648 | Genes: 12 | p-valor ruta: 7.25e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
ARRDC4	NA	UP	2.305	2.76e-44	631.5
TLR3	NA	UP	2.508	1.99e-22	111.5
ZBTB20	NA	UP	3.440	1.24e-15	47.6
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: positive regulation of protein modification process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0031401 | Genes: 39 | p-valor ruta: 8.02e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PML	NA	UP	2.208	2.84e-70	2901.3
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
ARRDC4	NA	UP	2.305	2.76e-44	631.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4

## Ruta: positive regulation of protein modification process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0031401 | Genes: 39 | p-valor ruta: 8.02e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR6	NA	UP	2.680	9.77e-08	26.3
NUPR1	NA	UP	3.660	1.78e-06	14.5
KIT	NA	UP	3.650	6.24e-04	7.9
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: mononuclear cell migration

Fuente: GO:BP | ID: GO:0071674 | Genes: 22 | p-valor ruta: 8.03e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
CSF1	NA	UP	2.530	1.40e-49	467.4
CH25H	NA	UP	7.817	1.04e-46	242.7
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: regulation of protein phosphorylation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0001932 | Genes: 44 | p-valor ruta: 8.99e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5

## Ruta: regulation of protein phosphorylation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0001932 | Genes: 44 | p-valor ruta: 8.99e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
BDKRB2	NA	UP	2.797	5.56e-15	55.1
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of phosphate metabolic process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0045937 | Genes: 36 | p-valor ruta: 9.27e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0

## Ruta: positive regulation of phosphate metabolic process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0045937 | Genes: 36 | p-valor ruta: 9.27e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
ZBTB20	NA	UP	3.440	1.24e-15	47.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR6	NA	UP	2.680	9.77e-08	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
P2RY6	NA	UP	2.536	8.76e-03	7.0
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of phosphorus metabolic process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0010562 | Genes: 36 | p-valor ruta: 9.27e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0

## Ruta: positive regulation of phosphorus metabolic process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0010562 | Genes: 36 | p-valor ruta: 9.27e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
ZBTB20	NA	UP	3.440	1.24e-15	47.6
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR6	NA	UP	2.680	9.77e-08	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
P2RY6	NA	UP	2.536	8.76e-03	7.0
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of protein phosphorylation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0001934 | Genes: 33 | p-valor ruta: 9.51e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: positive regulation of protein phosphorylation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0001934 | Genes: 33 | p-valor ruta: 9.51e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR6	NA	UP	2.680	9.77e-08	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of angiogenesis

Fuente: GO:BP | ID: GO:0045765 | Genes: 25 | p-valor ruta: 9.64e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
FUT1	NA	UP	2.765	4.55e-26	104.9
TLR3	NA	UP	2.508	1.99e-22	111.5
NPR1	NA	UP	3.131	3.66e-07	19.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
C3AR1	NA	UP	4.639	1.59e-02	2.2
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: positive regulation of nucleobase-containing compound metabolic process (Página 1 de 4)

Fuente: GO:BP | ID: GO:0045935 | Genes: 83 | p-valor ruta: 1e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4

## Ruta: positive regulation of nucleobase-containing compound metabolic process (Página 2 de 4)

Fuente: GO:BP | ID: GO:0045935 | Genes: 83 | p-valor ruta: 1e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KLF10	NA	UP	2.626	2.92e-86	1224.1
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4

## Ruta: positive regulation of nucleobase-containing compound metabolic process (Página 3 de 4)

Fuente: GO:BP | ID: GO:0045935 | Genes: 83 | p-valor ruta: 1e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
EGR4	NA	UP	2.643	5.77e-04	12.2
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1

## Ruta: positive regulation of nucleobase-containing compound metabolic process (Página 4 de 4)

Fuente: GO:BP | ID: GO:0045935 | Genes: 83 | p-valor ruta: 1e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: response to nitrogen compound (Página 1 de 3)

Fuente: GO:BP | ID: GO:1901698 | Genes: 54 | p-valor ruta: 1.04e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
INHBA	NA	UP	3.514	2.31e-143	1743.6
STC2	NA	UP	2.729	3.17e-119	2626.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
EGR1	NA	UP	2.472	2.61e-74	1149.5
PNPT1	NA	UP	2.411	6.12e-71	2101.8
STAT1	NA	UP	2.519	1.61e-68	9528.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9

## Ruta: response to nitrogen compound (Página 2 de 3)

Fuente: GO:BP | ID: GO:1901698 | Genes: 54 | p-valor ruta: 1.04e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
XRN1	NA	UP	2.115	6.38e-50	984.6
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
DUOX2	NA	UP	4.348	3.03e-29	71.2
VCAM1	NA	UP	4.737	4.28e-26	66.5
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
DUOX1	NA	UP	3.131	5.18e-10	27.1
NLRP1	NA	UP	5.692	4.64e-09	21.6
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
MMP13	NA	UP	5.406	9.23e-06	11.1
SLC5A5	NA	UP	4.542	4.62e-04	6.8
SLC1A2	NA	UP	2.752	2.07e-03	8.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: response to nitrogen compound (Página 3 de 3)

Fuente: GO:BP | ID: GO:1901698 | Genes: 54 | p-valor ruta: 1.04e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: negative regulation of innate immune response

Fuente: GO:BP | ID: GO:0045824 | Genes: 14 | p-valor ruta: 1.05e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
DHX58	NA	UP	2.877	1.75e-99	953.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1

## Ruta: regulation of molecular function (Página 1 de 3)

Fuente: GO:BP | ID: GO:0065009 | Genes: 67 | p-valor ruta: 1.09e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT1	NA	UP	4.523	0.00e+00	6073.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
IFI16	NA	UP	3.151	2.12e-114	2583.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3

## Ruta: regulation of molecular function (Página 2 de 3)

Fuente: GO:BP | ID: GO:0065009 | Genes: 67 | p-valor ruta: 1.09e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTX3	NA	UP	3.614	2.25e-68	237.4
JUN	NA	UP	2.450	1.10e-62	6693.5
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
ACTN2	NA	UP	3.956	7.01e-09	20.3
TLR6	NA	UP	2.680	9.77e-08	26.3

## Ruta: regulation of molecular function (Página 3 de 3)

Fuente: GO:BP | ID: GO:0065009 | Genes: 67 | p-valor ruta: 1.09e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NUPR1	NA	UP	3.660	1.78e-06	14.5
IL18R1	NA	UP	2.088	8.75e-05	23.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
P2RY6	NA	UP	2.536	8.76e-03	7.0
VAV1	NA	UP	2.118	1.54e-02	7.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: mononuclear cell proliferation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0032943 | Genes: 26 | p-valor ruta: 1.23e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CSF1	NA	UP	2.530	1.40e-49	467.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7

## Ruta: mononuclear cell proliferation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0032943 | Genes: 26 | p-valor ruta: 1.23e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: positive regulation of type II interferon production

Fuente: GO:BP | ID: GO:0032729 | Genes: 13 | p-valor ruta: 1.27e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
IFNL1	NA	UP	8.179	1.68e-89	578.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ISG15	NA	UP	2.482	5.90e-57	3807.9
PDE4B	NA	UP	3.818	7.08e-52	171.4
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL23A	NA	UP	2.189	2.05e-11	59.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of vasculature development

Fuente: GO:BP | ID: GO:1901342 | Genes: 25 | p-valor ruta: 1.45e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
FUT1	NA	UP	2.765	4.55e-26	104.9
TLR3	NA	UP	2.508	1.99e-22	111.5
NPR1	NA	UP	3.131	3.66e-07	19.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
C3AR1	NA	UP	4.639	1.59e-02	2.2
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: epithelial cell proliferation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0050673 | Genes: 31 | p-valor ruta: 1.46e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL5	NA	UP	5.035	8.94e-165	656.3
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
IRS2	NA	UP	2.254	1.06e-33	255.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
NKX3-1	NA	UP	2.233	8.30e-23	132.4
NOD2	NA	UP	2.981	1.19e-19	80.5
KLF9	NA	UP	2.555	7.01e-13	66.8
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
FAP	NA	UP	3.233	1.87e-05	14.0
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9

## Ruta: epithelial cell proliferation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0050673 | Genes: 31 | p-valor ruta: 1.46e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
BMPER	NA	UP	4.906	6.28e-03	2.6
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of primary metabolic process (Página 1 de 7)

Fuente: GO:BP | ID: GO:0080090 | Genes: 169 | p-valor ruta: 1.51e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
KLF6	NA	UP	2.653	7.59e-116	4943.3

## Ruta: regulation of primary metabolic process (Página 2 de 7)

Fuente: GO:BP | ID: GO:0080090 | Genes: 169 | p-valor ruta: 1.51e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9

## Ruta: regulation of primary metabolic process (Página 3 de 7)

Fuente: GO:BP | ID: GO:0080090 | Genes: 169 | p-valor ruta: 1.51e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9

## Ruta: regulation of primary metabolic process (Página 4 de 7)

Fuente: GO:BP | ID: GO:0080090 | Genes: 169 | p-valor ruta: 1.51e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PARP10	NA	UP	2.093	5.71e-52	2376.2
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
HDX	NA	UP	2.521	1.83e-28	139.2
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: regulation of primary metabolic process (Página 5 de 7)

Fuente: GO:BP | ID: GO:0080090 | Genes: 169 | p-valor ruta: 1.51e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2

## Ruta: regulation of primary metabolic process (Página 6 de 7)

Fuente: GO:BP | ID: GO:0080090 | Genes: 169 | p-valor ruta: 1.51e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
SYNPO2	NA	UP	3.603	1.95e-04	9.0
EGR3	NA	UP	2.096	2.87e-04	21.5
ZNF382	NA	UP	2.028	3.78e-04	18.2
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1

## Ruta: regulation of primary metabolic process (Página 7 de 7)

Fuente: GO:BP | ID: GO:0080090 | Genes: 169 | p-valor ruta: 1.51e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
CELF6	NA	UP	2.403	2.65e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
PURG	NA	DOWN	-4.166	4.66e-02	1.7
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of macromolecule biosynthetic process (Página 1 de 5)

Fuente: GO:BP | ID: GO:0010558 | Genes: 102 | p-valor ruta: 1.67e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4

## Ruta: negative regulation of macromolecule biosynthetic process (Página 2 de 5)

Fuente: GO:BP | ID: GO:0010558 | Genes: 102 | p-valor ruta: 1.67e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
ETV7	NA	UP	4.688	2.39e-83	278.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
FOSB	NA	UP	3.144	1.32e-55	267.7

## Ruta: negative regulation of macromolecule biosynthetic process (Página 3 de 5)

Fuente: GO:BP | ID: GO:0010558 | Genes: 102 | p-valor ruta: 1.67e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP10	NA	UP	2.093	5.71e-52	2376.2
XRN1	NA	UP	2.115	6.38e-50	984.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
MIR155HG	NA	UP	5.318	4.66e-35	99.1
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: negative regulation of macromolecule biosynthetic process (Página 4 de 5)

Fuente: GO:BP | ID: GO:0010558 | Genes: 102 | p-valor ruta: 1.67e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RUNX2	NA	UP	3.983	1.50e-06	15.2
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
PKP1	NA	UP	3.076	9.16e-05	12.8
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
HAND1	NA	UP	4.966	8.42e-04	5.1
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
DLL1	NA	UP	2.171	4.40e-03	10.4
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
GBP7	NA	UP	4.177	1.61e-02	2.9
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3

## Ruta: negative regulation of macromolecule biosynthetic process (Página 5 de 5)

Fuente: GO:BP | ID: GO:0010558 | Genes: 102 | p-valor ruta: 1.67e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: system development (Página 1 de 6)

Fuente: GO:BP | ID: GO:0048731 | Genes: 136 | p-valor ruta: 1.7e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3

## Ruta: system development (Página 2 de 6)

Fuente: GO:BP | ID: GO:0048731 | Genes: 136 | p-valor ruta: 1.7e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
TDRD7	NA	UP	2.129	5.72e-65	1011.2
RND1	NA	UP	2.840	1.60e-62	337.7
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
NAV2	NA	UP	2.370	3.20e-51	765.9
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
LTB	NA	UP	3.555	2.50e-41	150.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3

## Ruta: system development (Página 3 de 6)

Fuente: GO:BP | ID: GO:0048731 | Genes: 136 | p-valor ruta: 1.7e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
DDC	NA	DOWN	-2.582	2.27e-16	72.0
NAV3	NA	UP	2.285	2.77e-15	84.4
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
DNAAF3	NA	DOWN	-2.041	1.75e-14	101.4

## Ruta: system development (Página 4 de 6)

Fuente: GO:BP | ID: GO:0048731 | Genes: 136 | p-valor ruta: 1.7e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
SSTR2	NA	UP	2.031	8.80e-10	53.9
ACTN2	NA	UP	3.956	7.01e-09	20.3
LRP2	NA	UP	3.144	3.22e-08	22.0
BAHCC1	NA	UP	4.513	9.67e-08	16.6
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
COL4A1	NA	UP	6.589	5.89e-06	8.2
ACTBL2	NA	UP	2.242	5.97e-06	28.3
ADAMTS6	NA	UP	2.602	8.90e-06	19.6
MMP13	NA	UP	5.406	9.23e-06	11.1
SERPINA10	NA	UP	6.459	9.50e-06	7.5
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPTX1	NA	UP	2.102	1.13e-04	22.3
EGR3	NA	UP	2.096	2.87e-04	21.5
MPZ	NA	UP	2.002	2.88e-04	19.4
TRPC4	NA	UP	5.730	3.71e-04	4.5

## Ruta: system development (Página 5 de 6)

Fuente: GO:BP | ID: GO:0048731 | Genes: 136 | p-valor ruta: 1.7e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
LHB	NA	UP	3.522	1.50e-03	7.0
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
SDK2	NA	UP	2.715	5.83e-03	7.9
BMPER	NA	UP	4.906	6.28e-03	2.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
C3AR1	NA	UP	4.639	1.59e-02	2.2
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7

## Ruta: system development (Página 6 de 6)

Fuente: GO:BP | ID: GO:0048731 | Genes: 136 | p-valor ruta: 1.7e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL34	NA	UP	2.794	2.41e-02	4.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
INSC	NA	UP	3.872	3.01e-02	2.4
HSD11B1	NA	UP	2.341	3.03e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8
ADAMTS4	NA	UP	3.293	3.88e-02	3.0
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: cytokine production involved in immune response

Fuente: GO:BP | ID: GO:0002367 | Genes: 16 | p-valor ruta: 1.71e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
NR4A3	NA	UP	5.574	1.45e-08	20.2
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
PRG2	NA	UP	2.073	1.32e-02	9.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of cytokine production involved in immune response

Fuente: GO:BP | ID: GO:0002718 | Genes: 16 | p-valor ruta: 1.71e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
NR4A3	NA	UP	5.574	1.45e-08	20.2
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
PRG2	NA	UP	2.073	1.32e-02	9.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: phosphorylation (Página 1 de 3)

Fuente: GO:BP | ID: GO:0016310 | Genes: 61 | p-valor ruta: 1.86e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
NUAK2	NA	UP	4.358	1.14e-107	489.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4

## Ruta: phosphorylation (Página 2 de 3)

Fuente: GO:BP | ID: GO:0016310 | Genes: 61 | p-valor ruta: 1.86e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
MAST4	NA	UP	2.184	1.21e-25	197.5
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
BDKRB2	NA	UP	2.797	5.56e-15	55.1
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NPR1	NA	UP	3.131	3.66e-07	19.1
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
RET	NA	UP	2.793	1.44e-02	5.5
CAMK1G	NA	UP	4.059	1.79e-02	2.8

## Ruta: phosphorylation (Página 3 de 3)

Fuente: GO:BP | ID: GO:0016310 | Genes: 61 | p-valor ruta: 1.86e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of adaptive immune response

Fuente: GO:BP | ID: GO:0002819 | Genes: 21 | p-valor ruta: 1.87e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: regulation of leukocyte chemotaxis

Fuente: GO:BP | ID: GO:0002688 | Genes: 16 | p-valor ruta: 1.93e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CSF1	NA	UP	2.530	1.40e-49	467.4
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: protein phosphorylation (Página 1 de 3)

Fuente: GO:BP | ID: GO:0006468 | Genes: 58 | p-valor ruta: 2.03e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
NUAK2	NA	UP	4.358	1.14e-107	489.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BMP2	NA	UP	2.237	3.69e-40	325.3

## Ruta: protein phosphorylation (Página 2 de 3)

Fuente: GO:BP | ID: GO:0006468 | Genes: 58 | p-valor ruta: 2.03e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
MAST4	NA	UP	2.184	1.21e-25	197.5
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
BDKRB2	NA	UP	2.797	5.56e-15	55.1
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NPR1	NA	UP	3.131	3.66e-07	19.1
SYNPO2	NA	UP	3.603	1.95e-04	9.0
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
RET	NA	UP	2.793	1.44e-02	5.5
CAMK1G	NA	UP	4.059	1.79e-02	2.8
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7

## Ruta: protein phosphorylation (Página 3 de 3)

Fuente: GO:BP | ID: GO:0006468 | Genes: 58 | p-valor ruta: 2.03e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: cellular response to virus

Fuente: GO:BP | ID: GO:0098586 | Genes: 13 | p-valor ruta: 2.08e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IFIH1	NA	UP	4.035	2.22e-233	4525.3
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: MAPK cascade (Página 1 de 2)

Fuente: GO:BP | ID: GO:0000165 | Genes: 42 | p-valor ruta: 2.11e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
RASGRP3	NA	UP	3.468	2.92e-82	392.1
ADRB2	NA	UP	2.471	2.83e-79	954.4
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
GADD45A	NA	UP	2.255	1.32e-60	1140.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
SEMA3A	NA	UP	2.276	5.71e-42	512.5

## Ruta: MAPK cascade (Página 2 de 2)

Fuente: GO:BP | ID: GO:0000165 | Genes: 42 | p-valor ruta: 2.11e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: neuroinflammatory response

Fuente: GO:BP | ID: GO:0150076 | Genes: 13 | p-valor ruta: 2.44e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
NR1D1	NA	UP	2.475	2.08e-68	1229.5
TLR3	NA	UP	2.508	1.99e-22	111.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NUPR1	NA	UP	3.660	1.78e-06	14.5
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of receptor signaling pathway via JAK–STAT

Fuente: GO:BP | ID: GO:0046425 | Genes: 13 | p-valor ruta: 2.44e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
PARP14	NA	UP	2.977	1.79e-119	2649.9
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
BCL3	NA	UP	2.067	4.65e-26	500.4
JAK2	NA	UP	2.081	1.26e-17	123.4
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL10RA	NA	UP	3.172	3.66e-07	18.8
KIT	NA	UP	3.650	6.24e-04	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9

## Ruta: regulation of MAPK cascade (Página 1 de 2)

Fuente: GO:BP | ID: GO:0043408 | Genes: 38 | p-valor ruta: 2.58e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TRIM5	NA	UP	2.172	6.62e-61	1222.6
GADD45A	NA	UP	2.255	1.32e-60	1140.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9

## Ruta: regulation of MAPK cascade (Página 2 de 2)

Fuente: GO:BP | ID: GO:0043408 | Genes: 38 | p-valor ruta: 2.58e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2
IL34	NA	UP	2.794	2.41e-02	4.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: regulation of mononuclear cell proliferation

Fuente: GO:BP | ID: GO:0032944 | Genes: 22 | p-valor ruta: 2.62e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CSF1	NA	UP	2.530	1.40e-49	467.4
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
LST1	NA	UP	6.916	7.00e-07	10.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: positive regulation of phosphorylation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0042327 | Genes: 33 | p-valor ruta: 2.97e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: positive regulation of phosphorylation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0042327 | Genes: 33 | p-valor ruta: 2.97e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR6	NA	UP	2.680	9.77e-08	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of biosynthetic process (Página 1 de 5)

Fuente: GO:BP | ID: GO:0009890 | Genes: 103 | p-valor ruta: 2.98e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4

## Ruta: negative regulation of biosynthetic process (Página 2 de 5)

Fuente: GO:BP | ID: GO:0009890 | Genes: 103 | p-valor ruta: 2.98e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
ETV7	NA	UP	4.688	2.39e-83	278.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
TDRD7	NA	UP	2.129	5.72e-65	1011.2
JUN	NA	UP	2.450	1.10e-62	6693.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
FOSB	NA	UP	3.144	1.32e-55	267.7

## Ruta: negative regulation of biosynthetic process (Página 3 de 5)

Fuente: GO:BP | ID: GO:0009890 | Genes: 103 | p-valor ruta: 2.98e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP10	NA	UP	2.093	5.71e-52	2376.2
XRN1	NA	UP	2.115	6.38e-50	984.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
MIR155HG	NA	UP	5.318	4.66e-35	99.1
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: negative regulation of biosynthetic process (Página 4 de 5)

Fuente: GO:BP | ID: GO:0009890 | Genes: 103 | p-valor ruta: 2.98e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RUNX2	NA	UP	3.983	1.50e-06	15.2
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
PKP1	NA	UP	3.076	9.16e-05	12.8
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
HAND1	NA	UP	4.966	8.42e-04	5.1
MIR146A	NA	UP	2.592	1.50e-03	10.3
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
DLL1	NA	UP	2.171	4.40e-03	10.4
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
GBP7	NA	UP	4.177	1.61e-02	2.9
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6

## Ruta: negative regulation of biosynthetic process (Página 5 de 5)

Fuente: GO:BP | ID: GO:0009890 | Genes: 103 | p-valor ruta: 2.98e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: leukocyte mediated immunity (Página 1 de 2)

Fuente: GO:BP | ID: GO:0002443 | Genes: 32 | p-valor ruta: 3.1e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IRF7	NA	UP	3.210	5.72e-79	2126.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
NR4A3	NA	UP	5.574	1.45e-08	20.2

## Ruta: leukocyte mediated immunity (Página 2 de 2)

Fuente: GO:BP | ID: GO:0002443 | Genes: 32 | p-valor ruta: 3.1e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: positive regulation of mononuclear cell proliferation

Fuente: GO:BP | ID: GO:0032946 | Genes: 17 | p-valor ruta: 3.2e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CD274	NA	UP	5.204	1.23e-98	314.4
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CSF1	NA	UP	2.530	1.40e-49	467.4
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: lymphocyte proliferation

Fuente: GO:BP | ID: GO:0046651 | Genes: 25 | p-valor ruta: 3.2e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of cytokine-mediated signaling pathway

Fuente: GO:BP | ID: GO:0001959 | Genes: 18 | p-valor ruta: 3.39e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
PARP14	NA	UP	2.977	1.79e-119	2649.9
ZBP1	NA	UP	6.242	1.22e-99	349.5
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
CASP1	NA	UP	2.494	1.49e-18	80.2

## Ruta: tissue development (Página 1 de 4)

Fuente: GO:BP | ID: GO:0009888 | Genes: 81 | p-valor ruta: 4.36e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
INHBA	NA	UP	3.514	2.31e-143	1743.6
IKZF3	NA	UP	3.163	1.21e-120	1046.8
STC2	NA	UP	2.729	3.17e-119	2626.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
EGR1	NA	UP	2.472	2.61e-74	1149.5
PML	NA	UP	2.208	2.84e-70	2901.3

## Ruta: tissue development (Página 2 de 4)

Fuente: GO:BP | ID: GO:0009888 | Genes: 81 | p-valor ruta: 4.36e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
TUFT1	NA	UP	2.001	1.00e-55	1905.9
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
SEMA3A	NA	UP	2.276	5.71e-42	512.5
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
KRT6B	NA	UP	2.049	5.47e-24	321.4
NKX3-1	NA	UP	2.233	8.30e-23	132.4
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
GBX2	NA	UP	2.353	5.55e-15	78.3

## Ruta: tissue development (Página 3 de 4)

Fuente: GO:BP | ID: GO:0009888 | Genes: 81 | p-valor ruta: 4.36e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR2	NA	UP	3.090	6.72e-15	43.7
PCK1	NA	UP	4.419	1.17e-12	29.6
ACTN2	NA	UP	3.956	7.01e-09	20.3
LRP2	NA	UP	3.144	3.22e-08	22.0
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
COL4A1	NA	UP	6.589	5.89e-06	8.2
MMP13	NA	UP	5.406	9.23e-06	11.1
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
PKP1	NA	UP	3.076	9.16e-05	12.8
RHCG	NA	UP	2.107	1.84e-04	21.0
HAND1	NA	UP	4.966	8.42e-04	5.1
POU3F2	NA	UP	4.735	2.02e-03	4.5
SRGN	NA	UP	2.093	3.80e-03	11.0
DLL1	NA	UP	2.171	4.40e-03	10.4
KRT81	NA	UP	2.044	4.94e-03	15.2
KRT9	NA	UP	4.973	6.24e-03	2.7
BMPER	NA	UP	4.906	6.28e-03	2.6
SCUBE1	NA	UP	2.508	1.26e-02	8.4
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
IKZF1	NA	UP	2.283	2.21e-02	6.8

## Ruta: tissue development (Página 4 de 4)

Fuente: GO:BP | ID: GO:0009888 | Genes: 81 | p-valor ruta: 4.36e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: cellular response to endogenous stimulus (Página 1 de 3)

Fuente: GO:BP | ID: GO:0071495 | Genes: 57 | p-valor ruta: 4.54e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
ZFP36	NA	UP	2.944	7.57e-104	1721.5
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2

## Ruta: cellular response to endogenous stimulus (Página 2 de 3)

Fuente: GO:BP | ID: GO:0071495 | Genes: 57 | p-valor ruta: 4.54e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
JAK2	NA	UP	2.081	1.26e-17	123.4
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
SSTR2	NA	UP	2.031	8.80e-10	53.9
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
PTGER2	NA	UP	3.006	1.95e-04	11.0
EGR3	NA	UP	2.096	2.87e-04	21.5
SLC5A5	NA	UP	4.542	4.62e-04	6.8
FLRT1	NA	UP	5.509	1.11e-03	3.8
LHB	NA	UP	3.522	1.50e-03	7.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4

## Ruta: cellular response to endogenous stimulus (Página 3 de 3)

Fuente: GO:BP | ID: GO:0071495 | Genes: 57 | p-valor ruta: 4.54e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: T cell mediated immunity

Fuente: GO:BP | ID: GO:0002456 | Genes: 16 | p-valor ruta: 5.33e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
CD70	NA	UP	3.257	1.21e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: glial cell activation

Fuente: GO:BP | ID: GO:0061900 | Genes: 11 | p-valor ruta: 5.9e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
TLR3	NA	UP	2.508	1.99e-22	111.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of anatomical structure morphogenesis (Página 1 de 2)

Fuente: GO:BP | ID: GO:0022603 | Genes: 44 | p-valor ruta: 6.08e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
SP100	NA	UP	2.428	1.62e-93	2653.7
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CSF1	NA	UP	2.530	1.40e-49	467.4
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BMP2	NA	UP	2.237	3.69e-40	325.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
FUT1	NA	UP	2.765	4.55e-26	104.9

## Ruta: regulation of anatomical structure morphogenesis (Página 2 de 2)

Fuente: GO:BP | ID: GO:0022603 | Genes: 44 | p-valor ruta: 6.08e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR3	NA	UP	2.508	1.99e-22	111.5
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
KIT	NA	UP	3.650	6.24e-04	7.9
POU3F2	NA	UP	4.735	2.02e-03	4.5
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
BMPER	NA	UP	4.906	6.28e-03	2.6
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: neutrophil chemotaxis

Fuente: GO:BP | ID: GO:0030593 | Genes: 13 | p-valor ruta: 6.09e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PDE4B	NA	UP	3.818	7.08e-52	171.4
EDN2	NA	UP	3.499	8.77e-31	90.3
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
CXCL9	NA	UP	4.099	4.37e-04	26.3
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2

## Ruta: positive regulation of smooth muscle cell proliferation

Fuente: GO:BP | ID: GO:0048661 | Genes: 13 | p-valor ruta: 7.04e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
JAK2	NA	UP	2.081	1.26e-17	123.4
NR4A3	NA	UP	5.574	1.45e-08	20.2
P2RY6	NA	UP	2.536	8.76e-03	7.0

## Ruta: regulation of defense response to virus by host

Fuente: GO:BP | ID: GO:0050691 | Genes: 10 | p-valor ruta: 7.62e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
DTX3L	NA	UP	2.553	3.51e-96	2147.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: positive regulation of chemokine production

Fuente: GO:BP | ID: GO:0032722 | Genes: 12 | p-valor ruta: 7.75e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNF	NA	UP	7.712	3.81e-103	573.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: humoral immune response

Fuente: GO:BP | ID: GO:0006959 | Genes: 23 | p-valor ruta: 8.74e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
CCL2	NA	UP	2.562	2.63e-75	658.0
CCL22	NA	UP	3.454	2.91e-50	168.7
C1R	NA	UP	2.188	3.06e-32	258.8
BCL3	NA	UP	2.067	4.65e-26	500.4
NOD2	NA	UP	2.981	1.19e-19	80.5
WFDC5	NA	UP	5.168	1.07e-06	13.9
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
HRG	NA	UP	2.971	4.00e-03	6.9
SPRR2A	NA	UP	2.086	2.78e-02	7.8
CR1L	NA	UP	3.479	3.30e-02	3.5
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: regulation of lymphocyte proliferation

Fuente: GO:BP | ID: GO:0050670 | Genes: 21 | p-valor ruta: 8.8e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
LGALS9	NA	UP	2.474	3.44e-71	1449.3
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
LST1	NA	UP	6.916	7.00e-07	10.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of receptor signaling pathway via STAT

Fuente: GO:BP | ID: GO:1904892 | Genes: 13 | p-valor ruta: 9.35e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
PARP14	NA	UP	2.977	1.79e-119	2649.9
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
BCL3	NA	UP	2.067	4.65e-26	500.4
JAK2	NA	UP	2.081	1.26e-17	123.4
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL10RA	NA	UP	3.172	3.66e-07	18.8
KIT	NA	UP	3.650	6.24e-04	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9

## Ruta: negative regulation of response to biotic stimulus

Fuente: GO:BP | ID: GO:0002832 | Genes: 15 | p-valor ruta: 9.72e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1

## Ruta: response to hormone (Página 1 de 2)

Fuente: GO:BP | ID: GO:0009725 | Genes: 46 | p-valor ruta: 1.04e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
STC2	NA	UP	2.729	3.17e-119	2626.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
PTGS2	NA	UP	3.253	7.39e-80	3663.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
NEDD4	NA	UP	2.433	4.99e-60	1678.5
FOSB	NA	UP	3.144	1.32e-55	267.7
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9

## Ruta: response to hormone (Página 2 de 2)

Fuente: GO:BP | ID: GO:0009725 | Genes: 46 | p-valor ruta: 1.04e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PER1	NA	UP	2.501	8.94e-44	469.6
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
NKX3-1	NA	UP	2.233	8.30e-23	132.4
JAK2	NA	UP	2.081	1.26e-17	123.4
EGR2	NA	UP	3.090	6.72e-15	43.7
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
SSTR2	NA	UP	2.031	8.80e-10	53.9
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
PTGER2	NA	UP	3.006	1.95e-04	11.0
SLC5A5	NA	UP	4.542	4.62e-04	6.8
LHB	NA	UP	3.522	1.50e-03	7.0
P2RY6	NA	UP	2.536	8.76e-03	7.0
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: non-canonical NF-kappaB signal transduction

Fuente: GO:BP | ID: GO:0038061 | Genes: 15 | p-valor ruta: 1.09e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
LGALS9	NA	UP	2.474	3.44e-71	1449.3
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR6	NA	UP	2.680	9.77e-08	26.3
TNFSF14	NA	UP	2.748	3.71e-07	23.0
IL18R1	NA	UP	2.088	8.75e-05	23.0
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of peptidyl-tyrosine phosphorylation

Fuente: GO:BP | ID: GO:0050730 | Genes: 19 | p-valor ruta: 1.1e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNL1	NA	UP	8.179	1.68e-89	578.0
PARP9	NA	UP	2.449	1.75e-75	2354.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
IL34	NA	UP	2.794	2.41e-02	4.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of lymphocyte differentiation

Fuente: GO:BP | ID: GO:0045619 | Genes: 20 | p-valor ruta: 1.31e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
IKZF3	NA	UP	3.163	1.21e-120	1046.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
EGR3	NA	UP	2.096	2.87e-04	21.5
TLR9	NA	UP	2.952	1.98e-02	4.6
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: cellular response to interferon-beta

Fuente: GO:BP | ID: GO:0035458 | Genes: 8 | p-valor ruta: 1.33e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
PNPT1	NA	UP	2.411	6.12e-71	2101.8
STAT1	NA	UP	2.519	1.61e-68	9528.0
TLR3	NA	UP	2.508	1.99e-22	111.5
IFITM2	NA	UP	2.649	6.22e-17	64.2

## Ruta: positive regulation of peptidyl-tyrosine phosphorylation

Fuente: GO:BP | ID: GO:0050731 | Genes: 16 | p-valor ruta: 1.36e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNL1	NA	UP	8.179	1.68e-89	578.0
PARP9	NA	UP	2.449	1.75e-75	2354.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
KIT	NA	UP	3.650	6.24e-04	7.9
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: homeostatic process (Página 1 de 3)

Fuente: GO:BP | ID: GO:0042592 | Genes: 71 | p-valor ruta: 1.43e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STC2	NA	UP	2.729	3.17e-119	2626.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0

## Ruta: homeostatic process (Página 2 de 3)

Fuente: GO:BP | ID: GO:0042592 | Genes: 71 | p-valor ruta: 1.43e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NR1D1	NA	UP	2.475	2.08e-68	1229.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
CSF1	NA	UP	2.530	1.40e-49	467.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
MT2A	NA	UP	2.437	2.24e-35	363.0
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
LAMA2	NA	UP	2.355	4.82e-21	125.5
NOD2	NA	UP	2.981	1.19e-19	80.5
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
ZBTB20	NA	UP	3.440	1.24e-15	47.6
PCK1	NA	UP	4.419	1.17e-12	29.6
MUC4	NA	UP	2.613	4.74e-12	55.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8

## Ruta: homeostatic process (Página 3 de 3)

Fuente: GO:BP | ID: GO:0042592 | Genes: 71 | p-valor ruta: 1.43e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFSF14	NA	UP	2.748	3.71e-07	23.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
NPTX1	NA	UP	2.102	1.13e-04	22.3
RHCG	NA	UP	2.107	1.84e-04	21.0
TRPC4	NA	UP	5.730	3.71e-04	4.5
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
DLL1	NA	UP	2.171	4.40e-03	10.4
RP1L1	NA	UP	2.162	5.43e-03	10.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
SLC9B1	NA	UP	4.128	1.36e-02	3.1
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
SLC9C2	NA	UP	3.943	2.11e-02	2.8
IKZF1	NA	UP	2.283	2.21e-02	6.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
SPRR2A	NA	UP	2.086	2.78e-02	7.8
GPR27	NA	DOWN	-4.359	2.89e-02	1.9

## Ruta: positive regulation of lymphocyte proliferation

Fuente: GO:BP | ID: GO:0050671 | Genes: 16 | p-valor ruta: 1.5e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CD274	NA	UP	5.204	1.23e-98	314.4
LGALS9	NA	UP	2.474	3.44e-71	1449.3
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of mononuclear cell migration

Fuente: GO:BP | ID: GO:0071675 | Genes: 16 | p-valor ruta: 1.5e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
CSF1	NA	UP	2.530	1.40e-49	467.4
IL12A	NA	UP	3.852	1.95e-28	83.7
TNFSF14	NA	UP	2.748	3.71e-07	23.0
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

# on of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily

Fuente: GO:BP | ID: GO:0002822 | Genes: 19 | p-valor ruta: 1.52e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: neutrophil migration

Fuente: GO:BP | ID: GO:1990266 | Genes: 14 | p-valor ruta: 1.74e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PDE4B	NA	UP	3.818	7.08e-52	171.4
EDN2	NA	UP	3.499	8.77e-31	90.3
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
CXCL9	NA	UP	4.099	4.37e-04	26.3
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2

## Ruta: regulation of RNA metabolic process (Página 1 de 5)

Fuente: GO:BP | ID: GO:0051252 | Genes: 123 | p-valor ruta: 1.76e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4

## Ruta: regulation of RNA metabolic process (Página 2 de 5)

Fuente: GO:BP | ID: GO:0051252 | Genes: 123 | p-valor ruta: 1.76e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5

## Ruta: regulation of RNA metabolic process (Página 3 de 5)

Fuente: GO:BP | ID: GO:0051252 | Genes: 123 | p-valor ruta: 1.76e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
HDX	NA	UP	2.521	1.83e-28	139.2
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1

## Ruta: regulation of RNA metabolic process (Página 4 de 5)

Fuente: GO:BP | ID: GO:0051252 | Genes: 123 | p-valor ruta: 1.76e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8

## Ruta: regulation of RNA metabolic process (Página 5 de 5)

Fuente: GO:BP | ID: GO:0051252 | Genes: 123 | p-valor ruta: 1.76e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
ZNF382	NA	UP	2.028	3.78e-04	18.2
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
CELF6	NA	UP	2.403	2.65e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PURG	NA	DOWN	-4.166	4.66e-02	1.7
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: leukocyte activation involved in immune response

Fuente: GO:BP | ID: GO:0002366 | Genes: 24 | p-valor ruta: 1.83e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
ICAM1	NA	UP	3.652	3.11e-204	19095.5
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
BCL3	NA	UP	2.067	4.65e-26	500.4
ITGAM	NA	UP	2.447	1.39e-19	90.2
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: interleukin–27–mediated signaling pathway

Fuente: GO:BP | ID: GO:0070106 | Genes: 5 | p-valor ruta: 1.87e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
MX1	NA	UP	3.859	1.25e-245	5699.6
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
STAT1	NA	UP	2.519	1.61e-68	9528.0

## Ruta: positive regulation of non-canonical NF-kappaB signal transduction

Fuente: GO:BP | ID: GO:1901224 | Genes: 11 | p-valor ruta: 2.08e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
LGALS9	NA	UP	2.474	3.44e-71	1449.3
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
IL18R1	NA	UP	2.088	8.75e-05	23.0
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of RNA biosynthetic process (Página 1 de 5)

Fuente: GO:BP | ID: GO:2001141 | Genes: 116 | p-valor ruta: 2.26e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6

## Ruta: regulation of RNA biosynthetic process (Página 2 de 5)

Fuente: GO:BP | ID: GO:2001141 | Genes: 116 | p-valor ruta: 2.26e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNPI1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6

## Ruta: regulation of RNA biosynthetic process (Página 3 de 5)

Fuente: GO:BP | ID: GO:2001141 | Genes: 116 | p-valor ruta: 2.26e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
HDX	NA	UP	2.521	1.83e-28	139.2
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0

## Ruta: regulation of RNA biosynthetic process (Página 4 de 5)

Fuente: GO:BP | ID: GO:2001141 | Genes: 116 | p-valor ruta: 2.26e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
ZNF382	NA	UP	2.028	3.78e-04	18.2

## Ruta: regulation of RNA biosynthetic process (Página 5 de 5)

Fuente: GO:BP | ID: GO:2001141 | Genes: 116 | p-valor ruta: 2.26e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PURG	NA	DOWN	-4.166	4.66e-02	1.7
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: cell activation involved in immune response

Fuente: GO:BP | ID: GO:0002263 | Genes: 24 | p-valor ruta: 2.32e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
ICAM1	NA	UP	3.652	3.11e-204	19095.5
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
BCL3	NA	UP	2.067	4.65e-26	500.4
ITGAM	NA	UP	2.447	1.39e-19	90.2
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: response to ketone

Fuente: GO:BP | ID: GO:1901654 | Genes: 20 | p-valor ruta: 2.35e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TXNIP	NA	UP	3.401	2.30e-219	11419.4
CYP1A1	NA	UP	6.086	6.00e-198	811.0
INHBA	NA	UP	3.514	2.31e-143	1743.6
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
PTGER4	NA	UP	2.548	1.70e-71	568.2
PTAFR	NA	UP	3.014	4.62e-62	338.1
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
NKX3-1	NA	UP	2.233	8.30e-23	132.4
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PTGER2	NA	UP	3.006	1.95e-04	11.0
SLC5A5	NA	UP	4.542	4.62e-04	6.8
P2RY6	NA	UP	2.536	8.76e-03	7.0
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: positive regulation of mononuclear cell migration

Fuente: GO:BP | ID: GO:0071677 | Genes: 13 | p-valor ruta: 2.37e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CSF1	NA	UP	2.530	1.40e-49	467.4
IL12A	NA	UP	3.852	1.95e-28	83.7
TNFSF14	NA	UP	2.748	3.71e-07	23.0
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: muscle cell proliferation

Fuente: GO:BP | ID: GO:0033002 | Genes: 19 | p-valor ruta: 2.42e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BMP2	NA	UP	2.237	3.69e-40	325.3
IL12A	NA	UP	3.852	1.95e-28	83.7
JAK2	NA	UP	2.081	1.26e-17	123.4
NR4A3	NA	UP	5.574	1.45e-08	20.2
NPR1	NA	UP	3.131	3.66e-07	19.1
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
P2RY6	NA	UP	2.536	8.76e-03	7.0

## Ruta: negative regulation of molecular function (Página 1 de 2)

Fuente: GO:BP | ID: GO:0044092 | Genes: 33 | p-valor ruta: 2.43e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT1	NA	UP	4.523	0.00e+00	6073.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
DUSP1	NA	UP	3.521	2.54e-161	1829.2
IFI16	NA	UP	3.151	2.12e-114	2583.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
PARP9	NA	UP	2.449	1.75e-75	2354.5
PTX3	NA	UP	3.614	2.25e-68	237.4
JUN	NA	UP	2.450	1.10e-62	6693.5
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2

## Ruta: negative regulation of molecular function (Página 2 de 2)

Fuente: GO:BP | ID: GO:0044092 | Genes: 33 | p-valor ruta: 2.43e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BCL3	NA	UP	2.067	4.65e-26	500.4
JAK2	NA	UP	2.081	1.26e-17	123.4
ACTN2	NA	UP	3.956	7.01e-09	20.3
NUPR1	NA	UP	3.660	1.78e-06	14.5
HAND1	NA	UP	4.966	8.42e-04	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
PPM1E	NA	UP	3.810	4.20e-02	2.4
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: chronic inflammatory response

Fuente: GO:BP | ID: GO:0002544 | Genes: 7 | p-valor ruta: 2.48e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL5	NA	UP	5.035	8.94e-165	656.3
IDO1	NA	UP	4.167	4.38e-109	394.2
TNF	NA	UP	7.712	3.81e-103	573.0
THBS1	NA	UP	2.656	1.05e-77	3791.3
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
VCAM1	NA	UP	4.737	4.28e-26	66.5

## Ruta: negative regulation of interleukin–10 production

Fuente: GO:BP | ID: GO:0032693 | Genes: 7 | p-valor ruta: 2.48e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
IL23A	NA	UP	2.189	2.05e-11	59.9
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
DLL1	NA	UP	2.171	4.40e-03	10.4
PRG2	NA	UP	2.073	1.32e-02	9.7

## Ruta: regulation of DNA–binding transcription factor activity

Fuente: GO:BP | ID: GO:0051090 | Genes: 24 | p–valor ruta: 2.6e–04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e–277	2472.4
NFKBIA	NA	UP	4.079	6.66e–241	4955.3
IL1B	NA	UP	4.202	1.58e–214	2230.2
TRIM22	NA	UP	5.650	1.01e–212	913.7
TNF	NA	UP	7.712	3.81e–103	573.0
IRAK2	NA	UP	2.666	3.46e–95	1164.5
SP100	NA	UP	2.428	1.62e–93	2653.7
NLRC5	NA	UP	3.949	8.12e–88	414.4
TRAF1	NA	UP	4.730	5.65e–84	258.2
LGALS9	NA	UP	2.474	3.44e–71	1449.3
TRIM5	NA	UP	2.172	6.62e–61	1222.6
TRIM21	NA	UP	2.221	1.14e–60	888.8
CYP1B1	NA	UP	2.786	9.33e–53	766.0
PARP10	NA	UP	2.093	5.71e–52	2376.2
EIF2AK2	NA	UP	2.142	3.22e–48	1460.0
BMP2	NA	UP	2.237	3.69e–40	325.3
BCL3	NA	UP	2.067	4.65e–26	500.4
NOD2	NA	UP	2.981	1.19e–19	80.5
NUPR1	NA	UP	3.660	1.78e–06	14.5
IL18R1	NA	UP	2.088	8.75e–05	23.0
KIT	NA	UP	3.650	6.24e–04	7.9
HAND1	NA	UP	4.966	8.42e–04	5.1
PROX1	NA	UP	2.195	4.92e–02	5.7

## Ruta: chemokine production

Fuente: GO:BP | ID: GO:0032602 | Genes: 13 | p-valor ruta: 2.69e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNF	NA	UP	7.712	3.81e-103	573.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF4	NA	UP	2.704	2.52e-79	645.9
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: positive regulation of leukocyte chemotaxis

Fuente: GO:BP | ID: GO:0002690 | Genes: 13 | p-valor ruta: 2.69e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CSF1	NA	UP	2.530	1.40e-49	467.4
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: regulation of chemokine production

Fuente: GO:BP | ID: GO:0032642 | Genes: 13 | p-valor ruta: 2.69e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNF	NA	UP	7.712	3.81e-103	573.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF4	NA	UP	2.704	2.52e-79	645.9
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: anatomical structure morphogenesis (Página 1 de 4)

Fuente: GO:BP | ID: GO:0009653 | Genes: 97 | p-valor ruta: 2.86e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
SP100	NA	UP	2.428	1.62e-93	2653.7
ETV7	NA	UP	4.688	2.39e-83	278.8
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
RNF213	NA	UP	2.528	1.50e-73	6034.1
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6

## Ruta: anatomical structure morphogenesis (Página 2 de 4)

Fuente: GO:BP | ID: GO:0009653 | Genes: 97 | p-valor ruta: 2.86e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
TUFT1	NA	UP	2.001	1.00e-55	1905.9
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
CSF1	NA	UP	2.530	1.40e-49	467.4
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BMP2	NA	UP	2.237	3.69e-40	325.3
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5

## Ruta: anatomical structure morphogenesis (Página 3 de 4)

Fuente: GO:BP | ID: GO:0009653 | Genes: 97 | p-valor ruta: 2.86e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
COL4A1	NA	UP	6.589	5.89e-06	8.2
SP8	NA	UP	6.528	5.89e-06	8.0
ACTBL2	NA	UP	2.242	5.97e-06	28.3
MMP13	NA	UP	5.406	9.23e-06	11.1
FAP	NA	UP	3.233	1.87e-05	14.0
NPTX1	NA	UP	2.102	1.13e-04	22.3
EGR3	NA	UP	2.096	2.87e-04	21.5
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
CNTN4	NA	UP	4.928	9.17e-04	5.0

## Ruta: anatomical structure morphogenesis (Página 4 de 4)

Fuente: GO:BP | ID: GO:0009653 | Genes: 97 | p-valor ruta: 2.86e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FLRT1	NA	UP	5.509	1.11e-03	3.8
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
LGR6	NA	UP	3.915	2.25e-03	6.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
SDK2	NA	UP	2.715	5.83e-03	7.9
BMPER	NA	UP	4.906	6.28e-03	2.6
RET	NA	UP	2.793	1.44e-02	5.5
C3AR1	NA	UP	4.639	1.59e-02	2.2
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
ALPK2	NA	UP	3.025	2.06e-02	4.7
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of transport (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051050 | Genes: 43 | p-valor ruta: 2.86e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
CCL2	NA	UP	2.562	2.63e-75	658.0
ANKRD1	NA	UP	3.496	4.72e-69	335.9
PTX3	NA	UP	3.614	2.25e-68	237.4
PTAFR	NA	UP	3.014	4.62e-62	338.1
NEDD4	NA	UP	2.433	4.99e-60	1678.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PCK2	NA	UP	2.226	5.13e-50	969.9
IL15RA	NA	UP	2.045	1.16e-42	847.9
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: positive regulation of transport (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051050 | Genes: 43 | p-valor ruta: 2.86e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
NPR1	NA	UP	3.131	3.66e-07	19.1
SYT1	NA	UP	2.659	1.62e-06	21.4
SELE	NA	UP	5.745	2.05e-05	9.0
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
SLC1A2	NA	UP	2.752	2.07e-03	8.4
DLL1	NA	UP	2.171	4.40e-03	10.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
GPR27	NA	DOWN	-4.359	2.89e-02	1.9

## Ruta: negative regulation of defense response

Fuente: GO:BP | ID: GO:0031348 | Genes: 21 | p-valor ruta: 2.88e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
DHX58	NA	UP	2.877	1.75e-99	953.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF4	NA	UP	2.704	2.52e-79	645.9
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
TRIM21	NA	UP	2.221	1.14e-60	888.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
NOD2	NA	UP	2.981	1.19e-19	80.5
IL10RA	NA	UP	3.172	3.66e-07	18.8

## Ruta: regulation of defense response to virus

Fuente: GO:BP | ID: GO:0050688 | Genes: 11 | p-valor ruta: 2.89e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
HERC5	NA	UP	3.386	1.24e-123	1735.7
DTX3L	NA	UP	2.553	3.51e-96	2147.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: cellular response to nitrogen compound (Página 1 de 2)

Fuente: GO:BP | ID: GO:1901699 | Genes: 36 | p-valor ruta: 3.33e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
INHBA	NA	UP	3.514	2.31e-143	1743.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
EGR1	NA	UP	2.472	2.61e-74	1149.5
STAT1	NA	UP	2.519	1.61e-68	9528.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
VCAM1	NA	UP	4.737	4.28e-26	66.5
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ACTN2	NA	UP	3.956	7.01e-09	20.3

## Ruta: cellular response to nitrogen compound (Página 2 de 2)

Fuente: GO:BP | ID: GO:1901699 | Genes: 36 | p-valor ruta: 3.33e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NGFR	NA	UP	2.337	3.33e-07	30.0
SLC5A5	NA	UP	4.542	4.62e-04	6.8
SLC1A2	NA	UP	2.752	2.07e-03	8.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: positive regulation of interleukin-6 production

Fuente: GO:BP | ID: GO:0032755 | Genes: 13 | p-valor ruta: 3.45e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ZBTB20	NA	UP	3.440	1.24e-15	47.6
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: regulation of pattern recognition receptor signaling pathway

Fuente: GO:BP | ID: GO:0062207 | Genes: 17 | p-valor ruta: 3.64e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
OASL	NA	UP	3.434	4.45e-163	4285.8
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
NR1D1	NA	UP	2.475	2.08e-68	1229.5
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NOD2	NA	UP	2.981	1.19e-19	80.5
GBP5	NA	UP	6.172	4.92e-17	48.7
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: response to interferon-alpha

Fuente: GO:BP | ID: GO:0035455 | Genes: 7 | p-valor ruta: 3.66e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
MX2	NA	UP	5.374	1.90e-273	1682.8
LAMP3	NA	UP	3.644	2.72e-189	1627.7
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFITM1	NA	UP	3.632	5.16e-130	784.8
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BST2	NA	UP	4.284	3.82e-19	50.8
IFITM2	NA	UP	2.649	6.22e-17	64.2

## Ruta: regulation of localization (Página 1 de 4)

Fuente: GO:BP | ID: GO:0032879 | Genes: 78 | p-valor ruta: 3.81e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
MX2	NA	UP	5.374	1.90e-273	1682.8
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STC2	NA	UP	2.729	3.17e-119	2626.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
DTX3L	NA	UP	2.553	3.51e-96	2147.3
SP100	NA	UP	2.428	1.62e-93	2653.7
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3

## Ruta: regulation of localization (Página 2 de 4)

Fuente: GO:BP | ID: GO:0032879 | Genes: 78 | p-valor ruta: 3.81e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
BBC3	NA	UP	2.829	3.65e-57	503.1
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: regulation of localization (Página 3 de 4)

Fuente: GO:BP | ID: GO:0032879 | Genes: 78 | p-valor ruta: 3.81e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15	NA	UP	2.012	2.28e-17	116.8
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
SYT1	NA	UP	2.659	1.62e-06	21.4
BEST1	NA	UP	3.553	8.47e-06	13.3
SELE	NA	UP	5.745	2.05e-05	9.0
BEST3	NA	UP	2.070	3.26e-05	23.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
PKP1	NA	UP	3.076	9.16e-05	12.8
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
SLC1A2	NA	UP	2.752	2.07e-03	8.4
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1

## Ruta: regulation of localization (Página 4 de 4)

Fuente: GO:BP | ID: GO:0032879 | Genes: 78 | p-valor ruta: 3.81e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: response to nutrient levels (Página 1 de 2)

Fuente: GO:BP | ID: GO:0031667 | Genes: 31 | p-valor ruta: 3.98e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
NUAK2	NA	UP	4.358	1.14e-107	489.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
VCAM1	NA	UP	4.737	4.28e-26	66.5
NOD2	NA	UP	2.981	1.19e-19	80.5
PCK1	NA	UP	4.419	1.17e-12	29.6

## Ruta: response to nutrient levels (Página 2 de 2)

Fuente: GO:BP | ID: GO:0031667 | Genes: 31 | p-valor ruta: 3.98e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZEB2	NA	UP	3.419	5.95e-12	30.5
SSTR2	NA	UP	2.031	8.80e-10	53.9
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
RNF152	NA	UP	3.325	1.37e-03	7.5
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of lymphocyte mediated immunity

Fuente: GO:BP | ID: GO:0002706 | Genes: 18 | p-valor ruta: 4.13e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
VAV1	NA	UP	2.118	1.54e-02	7.9
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: positive regulation of leukocyte mediated immunity

Fuente: GO:BP | ID: GO:0002705 | Genes: 16 | p-valor ruta: 4.23e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
VAV1	NA	UP	2.118	1.54e-02	7.9

## Ruta: response to abiotic stimulus (Página 1 de 3)

Fuente: GO:BP | ID: GO:0009628 | Genes: 52 | p-valor ruta: 4.42e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5

## Ruta: response to abiotic stimulus (Página 2 de 3)

Fuente: GO:BP | ID: GO:0009628 | Genes: 52 | p-valor ruta: 4.42e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BBC3	NA	UP	2.829	3.65e-57	503.1
FOSB	NA	UP	3.144	1.32e-55	267.7
PER1	NA	UP	2.501	8.94e-44	469.6
BMP2	NA	UP	2.237	3.69e-40	325.3
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CASP1	NA	UP	2.494	1.49e-18	80.2
BDKRB2	NA	UP	2.797	5.56e-15	55.1
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NLRP1	NA	UP	5.692	4.64e-09	21.6
KMO	NA	UP	5.165	6.24e-09	19.5
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0
BEST1	NA	UP	3.553	8.47e-06	13.3
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
KIT	NA	UP	3.650	6.24e-04	7.9
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
SLC1A2	NA	UP	2.752	2.07e-03	8.4
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: response to abiotic stimulus (Página 3 de 3)

Fuente: GO:BP | ID: GO:0009628 | Genes: 52 | p-valor ruta: 4.42e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: interleukin-8 production

Fuente: GO:BP | ID: GO:0032637 | Genes: 12 | p-valor ruta: 4.53e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
KLF4	NA	UP	2.704	2.52e-79	645.9
LGALS9	NA	UP	2.474	3.44e-71	1449.3
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
TLR6	NA	UP	2.680	9.77e-08	26.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of interleukin–8 production

Fuente: GO:BP | ID: GO:0032677 | Genes: 12 | p-valor ruta: 4.53e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
KLF4	NA	UP	2.704	2.52e-79	645.9
LGALS9	NA	UP	2.474	3.44e-71	1449.3
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
TLR6	NA	UP	2.680	9.77e-08	26.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: peptidyl-tyrosine phosphorylation

Fuente: GO:BP | ID: GO:0018108 | Genes: 20 | p-valor ruta: 4.72e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNL1	NA	UP	8.179	1.68e-89	578.0
PARP9	NA	UP	2.449	1.75e-75	2354.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
IL34	NA	UP	2.794	2.41e-02	4.8
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: peptidyl-tyrosine modification

Fuente: GO:BP | ID: GO:0018212 | Genes: 20 | p-valor ruta: 5.4e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNL1	NA	UP	8.179	1.68e-89	578.0
PARP9	NA	UP	2.449	1.75e-75	2354.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
KIT	NA	UP	3.650	6.24e-04	7.9
HRG	NA	UP	2.971	4.00e-03	6.9
IL34	NA	UP	2.794	2.41e-02	4.8
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: positive regulation of T cell proliferation

Fuente: GO:BP | ID: GO:0042102 | Genes: 13 | p-valor ruta: 5.56e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CD274	NA	UP	5.204	1.23e-98	314.4
LGALS9	NA	UP	2.474	3.44e-71	1449.3
VCAM1	NA	UP	4.737	4.28e-26	66.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7

## Ruta: regulation of DNA-templated transcription (Página 1 de 5)

Fuente: GO:BP | ID: GO:0006355 | Genes: 114 | p-valor ruta: 5.7e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6

## Ruta: regulation of DNA-templated transcription (Página 2 de 5)

Fuente: GO:BP | ID: GO:0006355 | Genes: 114 | p-valor ruta: 5.7e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNPI1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6

## Ruta: regulation of DNA-templated transcription (Página 3 de 5)

Fuente: GO:BP | ID: GO:0006355 | Genes: 114 | p-valor ruta: 5.7e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
HDX	NA	UP	2.521	1.83e-28	139.2
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: regulation of DNA-templated transcription (Página 4 de 5)

Fuente: GO:BP | ID: GO:0006355 | Genes: 114 | p-valor ruta: 5.7e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
ZNF382	NA	UP	2.028	3.78e-04	18.2
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2

## Ruta: regulation of DNA-templated transcription (Página 5 de 5)

Fuente: GO:BP | ID: GO:0006355 | Genes: 114 | p-valor ruta: 5.7e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PURG	NA	DOWN	-4.166	4.66e-02	1.7
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of biological quality (Página 1 de 5)

Fuente: GO:BP | ID: GO:0065008 | Genes: 102 | p-valor ruta: 6.04e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL6	NA	UP	6.060	0.00e+00	1698.5
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CCL5	NA	UP	5.035	8.94e-165	656.3
TIPARP	NA	UP	3.093	1.11e-158	5401.6
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STC2	NA	UP	2.729	3.17e-119	2626.1
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3

## Ruta: regulation of biological quality (Página 2 de 5)

Fuente: GO:BP | ID: GO:0065008 | Genes: 102 | p-valor ruta: 6.04e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
AKAP12	NA	UP	2.306	2.56e-67	3768.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
NAV2	NA	UP	2.370	3.20e-51	765.9
PCK2	NA	UP	2.226	5.13e-50	969.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
EDN2	NA	UP	3.499	8.77e-31	90.3
PPM1K	NA	UP	2.192	3.89e-30	395.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
NKX3-1	NA	UP	2.233	8.30e-23	132.4
DDO	NA	UP	2.846	3.84e-20	82.4
NOD2	NA	UP	2.981	1.19e-19	80.5
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3

## Ruta: regulation of biological quality (Página 3 de 5)

Fuente: GO:BP | ID: GO:0065008 | Genes: 102 | p-valor ruta: 6.04e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DUOXA2	NA	UP	4.650	3.36e-16	39.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
EGR2	NA	UP	3.090	6.72e-15	43.7
ZEB2	NA	UP	3.419	5.95e-12	30.5
SCN3A	NA	UP	8.277	2.66e-10	27.0
DUOX1	NA	UP	3.131	5.18e-10	27.1
ACTN2	NA	UP	3.956	7.01e-09	20.3
KCNV1	NA	UP	2.402	2.10e-07	37.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
LST1	NA	UP	6.916	7.00e-07	10.5
LRRN3	NA	UP	6.733	2.08e-06	9.4
BEST1	NA	UP	3.553	8.47e-06	13.3
SERPINA10	NA	UP	6.459	9.50e-06	7.5
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
XKR9	NA	UP	3.541	5.84e-05	11.9
NPTX1	NA	UP	2.102	1.13e-04	22.3
PTGER2	NA	UP	3.006	1.95e-04	11.0
NCALD	NA	UP	2.037	3.82e-04	17.1
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
CNTN4	NA	UP	4.928	9.17e-04	5.0

## Ruta: regulation of biological quality (Página 4 de 5)

Fuente: GO:BP | ID: GO:0065008 | Genes: 102 | p-valor ruta: 6.04e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LHB	NA	UP	3.522	1.50e-03	7.0
KCNH3	NA	DOWN	-2.243	1.94e-03	12.5
CACNA1I	NA	UP	2.173	2.19e-03	14.9
SLC17A4	NA	DOWN	-2.298	2.32e-03	11.5
PATL2	NA	UP	2.215	2.72e-03	12.1
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
VWF	NA	UP	3.390	1.16e-02	4.6
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
SLC9B1	NA	UP	4.128	1.36e-02	3.1
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
TTLL6	NA	UP	2.577	1.74e-02	6.7
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
SLC9C2	NA	UP	3.943	2.11e-02	2.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
INSC	NA	UP	3.872	3.01e-02	2.4
KCNE4	NA	UP	2.337	3.37e-02	5.7

## Ruta: regulation of biological quality (Página 5 de 5)

Fuente: GO:BP | ID: GO:0065008 | Genes: 102 | p-valor ruta: 6.04e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DLG2	NA	UP	3.028	3.83e-02	3.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of type I interferon-mediated signaling pathway

Fuente: GO:BP | ID: GO:0060338 | Genes: 9 | p-valor ruta: 6.52e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
ZBP1	NA	UP	6.242	1.22e-99	349.5
STAT2	NA	UP	2.337	1.85e-96	2004.6
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1

## Ruta: antimicrobial humoral response

Fuente: GO:BP | ID: GO:0019730 | Genes: 16 | p-valor ruta: 6.57e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CCL2	NA	UP	2.562	2.63e-75	658.0
CCL22	NA	UP	3.454	2.91e-50	168.7
BCL3	NA	UP	2.067	4.65e-26	500.4
NOD2	NA	UP	2.981	1.19e-19	80.5
WFDC5	NA	UP	5.168	1.07e-06	13.9
CXCL9	NA	UP	4.099	4.37e-04	26.3
HRG	NA	UP	2.971	4.00e-03	6.9
SPRR2A	NA	UP	2.086	2.78e-02	7.8
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: response to mechanical stimulus

Fuente: GO:BP | ID: GO:0009612 | Genes: 19 | p-valor ruta: 6.7e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
PTGER4	NA	UP	2.548	1.70e-71	568.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
FOSB	NA	UP	3.144	1.32e-55	267.7
TLR3	NA	UP	2.508	1.99e-22	111.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CASP1	NA	UP	2.494	1.49e-18	80.2
TNFSF14	NA	UP	2.748	3.71e-07	23.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
KIT	NA	UP	3.650	6.24e-04	7.9

## Ruta: negative regulation of response to cytokine stimulus

Fuente: GO:BP | ID: GO:0060761 | Genes: 12 | p-valor ruta: 6.71e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
PARP14	NA	UP	2.977	1.79e-119	2649.9
STAT2	NA	UP	2.337	1.85e-96	2004.6
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF4	NA	UP	2.704	2.52e-79	645.9
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4

## Ruta: cell surface pattern recognition receptor signaling pathway

Fuente: GO:BP | ID: GO:0002752 | Genes: 11 | p-valor ruta: 7.26e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFI35	NA	UP	2.237	9.59e-79	2236.7
NR1D1	NA	UP	2.475	2.08e-68	1229.5
NOD2	NA	UP	2.981	1.19e-19	80.5
TLR6	NA	UP	2.680	9.77e-08	26.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
LY96	NA	UP	5.204	4.42e-03	3.4

## Ruta: negative regulation of type I interferon-mediated signaling pathway

Fuente: GO:BP | ID: GO:0060339 | Genes: 7 | p-valor ruta: 7.43e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
STAT2	NA	UP	2.337	1.85e-96	2004.6
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1

## Ruta: negative regulation of cell adhesion

Fuente: GO:BP | ID: GO:0007162 | Genes: 22 | p-valor ruta: 7.74e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IDO1	NA	UP	4.167	4.38e-109	394.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
RND1	NA	UP	2.840	1.60e-62	337.7
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
BMP2	NA	UP	2.237	3.69e-40	325.3
JAK2	NA	UP	2.081	1.26e-17	123.4
SOCS1	NA	UP	2.012	6.54e-08	82.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
HRG	NA	UP	2.971	4.00e-03	6.9

## Ruta: regulation of transport (Página 1 de 3)

Fuente: GO:BP | ID: GO:0051049 | Genes: 65 | p-valor ruta: 8.34e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
MX2	NA	UP	5.374	1.90e-273	1682.8
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STC2	NA	UP	2.729	3.17e-119	2626.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5

## Ruta: regulation of transport (Página 2 de 3)

Fuente: GO:BP | ID: GO:0051049 | Genes: 65 | p-valor ruta: 8.34e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTX3	NA	UP	3.614	2.25e-68	237.4
PTAFR	NA	UP	3.014	4.62e-62	338.1
NEDD4	NA	UP	2.433	4.99e-60	1678.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NPR1	NA	UP	3.131	3.66e-07	19.1
SYT1	NA	UP	2.659	1.62e-06	21.4
BEST1	NA	UP	3.553	8.47e-06	13.3

## Ruta: regulation of transport (Página 3 de 3)

Fuente: GO:BP | ID: GO:0051049 | Genes: 65 | p-valor ruta: 8.34e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SELE	NA	UP	5.745	2.05e-05	9.0
BEST3	NA	UP	2.070	3.26e-05	23.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
SLC1A2	NA	UP	2.752	2.07e-03	8.4
DLL1	NA	UP	2.171	4.40e-03	10.4
P2RY6	NA	UP	2.536	8.76e-03	7.0
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SFRP1	NA	UP	2.711	4.51e-02	3.8

# immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains

Fuente: GO:BP | ID: GO:0002460 | Genes: 26 | p-valor ruta: 8.44e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
C1R	NA	UP	2.188	3.06e-32	258.8
BACH2	NA	UP	2.222	2.18e-30	209.0
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
CD70	NA	UP	3.257	1.21e-02	4.7
IL13RA2	NA	UP	2.568	3.02e-02	4.7

# immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains

Fuente: GO:BP | ID: GO:0002460 | Genes: 26 | p-valor ruta: 8.44e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CR1L	NA	UP	3.479	3.3e-02	3.5

## Ruta: production of molecular mediator of immune response

Fuente: GO:BP | ID: GO:0002440 | Genes: 19 | p-valor ruta: 9.45e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
NR4A3	NA	UP	5.574	1.45e-08	20.2
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
PRG2	NA	UP	2.073	1.32e-02	9.7
TLR9	NA	UP	2.952	1.98e-02	4.6
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: multicellular organismal-level homeostasis (Página 1 de 2)

Fuente: GO:BP | ID: GO:0048871 | Genes: 41 | p-valor ruta: 9.95e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
PDE4B	NA	UP	3.818	7.08e-52	171.4
CSF1	NA	UP	2.530	1.40e-49	467.4
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
EDN2	NA	UP	3.499	8.77e-31	90.3
LAMA2	NA	UP	2.355	4.82e-21	125.5
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: multicellular organismal-level homeostasis (Página 2 de 2)

Fuente: GO:BP | ID: GO:0048871 | Genes: 41 | p-valor ruta: 9.95e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
MUC4	NA	UP	2.613	4.74e-12	55.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
RP1L1	NA	UP	2.162	5.43e-03	10.3
NPR3	NA	UP	2.789	1.87e-02	5.7
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
SPRR2A	NA	UP	2.086	2.78e-02	7.8

## Ruta: macrophage activation

Fuente: GO:BP | ID: GO:0042116 | Genes: 13 | p-valor ruta: 1.21e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
THBS1	NA	UP	2.656	1.05e-77	3791.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
EDN2	NA	UP	3.499	8.77e-31	90.3
TLR3	NA	UP	2.508	1.99e-22	111.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: negative regulation of developmental process (Página 1 de 2)

Fuente: GO:BP | ID: GO:0051093 | Genes: 44 | p-valor ruta: 1.23e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
STC2	NA	UP	2.729	3.17e-119	2626.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CD69	NA	UP	3.112	5.99e-57	257.2
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
SEMA3A	NA	UP	2.276	5.71e-42	512.5
BMP2	NA	UP	2.237	3.69e-40	325.3
SPRY2	NA	UP	2.250	1.05e-29	211.9

## Ruta: negative regulation of developmental process (Página 2 de 2)

Fuente: GO:BP | ID: GO:0051093 | Genes: 44 | p-valor ruta: 1.23e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
SOCS1	NA	UP	2.012	6.54e-08	82.5
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
KIT	NA	UP	3.650	6.24e-04	7.9
CNTN4	NA	UP	4.928	9.17e-04	5.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
RANBP3L	NA	UP	4.634	1.47e-02	2.2
ALPK2	NA	UP	3.025	2.06e-02	4.7
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: T cell differentiation involved in immune response

Fuente: GO:BP | ID: GO:0002292 | Genes: 12 | p-valor ruta: 1.25e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BCL3	NA	UP	2.067	4.65e-26	500.4
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: regulation of chemotaxis

Fuente: GO:BP | ID: GO:0050920 | Genes: 18 | p-valor ruta: 1.25e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CSF1	NA	UP	2.530	1.40e-49	467.4
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
HRG	NA	UP	2.971	4.00e-03	6.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: response to purine-containing compound

Fuente: GO:BP | ID: GO:0014074 | Genes: 15 | p-valor ruta: 1.4e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
PNPT1	NA	UP	2.411	6.12e-71	2101.8
STAT1	NA	UP	2.519	1.61e-68	9528.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
XRN1	NA	UP	2.115	6.38e-50	984.6
PER1	NA	UP	2.501	8.94e-44	469.6
DUOX2	NA	UP	4.348	3.03e-29	71.2
PCK1	NA	UP	4.419	1.17e-12	29.6
DUOX1	NA	UP	3.131	5.18e-10	27.1
SLC5A5	NA	UP	4.542	4.62e-04	6.8
P2RY6	NA	UP	2.536	8.76e-03	7.0
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: protein modification process (Página 1 de 4)

Fuente: GO:BP | ID: GO:0036211 | Genes: 98 | p-valor ruta: 1.42e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
USP18	NA	UP	3.900	1.42e-145	1151.2
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
PLAT	NA	UP	2.447	4.98e-113	6662.1
NUAK2	NA	UP	4.358	1.14e-107	489.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
IFNL1	NA	UP	8.179	1.68e-89	578.0
TRAF1	NA	UP	4.730	5.65e-84	258.2

## Ruta: protein modification process (Página 2 de 4)

Fuente: GO:BP | ID: GO:0036211 | Genes: 98 | p-valor ruta: 1.42e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP12	NA	UP	2.297	5.64e-82	1665.8
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
DAPP1	NA	UP	2.456	1.42e-72	922.6
PML	NA	UP	2.208	2.84e-70	2901.3
NEURL3	NA	UP	2.464	1.53e-62	758.9
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
PARP10	NA	UP	2.093	5.71e-52	2376.2
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
OTUD1	NA	UP	2.871	3.76e-46	418.8
ARRDC4	NA	UP	2.305	2.76e-44	631.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9

## Ruta: protein modification process (Página 3 de 4)

Fuente: GO:BP | ID: GO:0036211 | Genes: 98 | p-valor ruta: 1.42e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FUT3	NA	UP	2.139	2.84e-41	355.7
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PPM1K	NA	UP	2.192	3.89e-30	395.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
MAST4	NA	UP	2.184	1.21e-25	197.5
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
BDKRB2	NA	UP	2.797	5.56e-15	55.1
EGR2	NA	UP	3.090	6.72e-15	43.7
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NPR1	NA	UP	3.131	3.66e-07	19.1
NUPR1	NA	UP	3.660	1.78e-06	14.5

## Ruta: protein modification process (Página 4 de 4)

Fuente: GO:BP | ID: GO:0036211 | Genes: 98 | p-valor ruta: 1.42e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SYNPO2	NA	UP	3.603	1.95e-04	9.0
GFPT2	NA	UP	2.651	2.37e-04	12.7
KIT	NA	UP	3.650	6.24e-04	7.9
RNF152	NA	UP	3.325	1.37e-03	7.5
HRG	NA	UP	2.971	4.00e-03	6.9
RET	NA	UP	2.793	1.44e-02	5.5
TTLL6	NA	UP	2.577	1.74e-02	6.7
CAMK1G	NA	UP	4.059	1.79e-02	2.8
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
TRIM69	NA	UP	3.519	3.21e-02	3.0
PPM1E	NA	UP	3.810	4.20e-02	2.4
PPEF1	NA	UP	3.725	4.31e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: microglial cell activation

Fuente: GO:BP | ID: GO:0001774 | Genes: 9 | p-valor ruta: 1.43e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
TLR3	NA	UP	2.508	1.99e-22	111.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: antimicrobial humoral immune response mediated by antimicrobial peptide

Fuente: GO:BP | ID: GO:0061844 | Genes: 13 | p-valor ruta: 1.5e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CCL2	NA	UP	2.562	2.63e-75	658.0
CCL22	NA	UP	3.454	2.91e-50	168.7
NOD2	NA	UP	2.981	1.19e-19	80.5
CXCL9	NA	UP	4.099	4.37e-04	26.3
HRG	NA	UP	2.971	4.00e-03	6.9
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: negative regulation of cell activation

Fuente: GO:BP | ID: GO:0050866 | Genes: 18 | p-valor ruta: 1.54e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
CD69	NA	UP	3.112	5.99e-57	257.2
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
SOCS1	NA	UP	2.012	6.54e-08	82.5
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
LST1	NA	UP	6.916	7.00e-07	10.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
THBD	NA	UP	2.330	1.23e-02	7.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: lymphocyte mediated immunity

Fuente: GO:BP | ID: GO:0002449 | Genes: 25 | p-valor ruta: 1.57e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IRF7	NA	UP	3.210	5.72e-79	2126.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
NOD2	NA	UP	2.981	1.19e-19	80.5
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: regulation of non-canonical NF-kappaB signal transduction

Fuente: GO:BP | ID: GO:1901222 | Genes: 12 | p-valor ruta: 1.58e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
LGALS9	NA	UP	2.474	3.44e-71	1449.3
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
IL18R1	NA	UP	2.088	8.75e-05	23.0
TLR9	NA	UP	2.952	1.98e-02	4.6

# Regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin su

Fuente: GO:BP | ID: GO:0002824 | Genes: 14 | p-valor ruta: 1.58e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: transport (Página 1 de 6)

Fuente: GO:BP | ID: GO:0006810 | Genes: 137 | p-valor ruta: 1.62e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
MX2	NA	UP	5.374	1.90e-273	1682.8
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
APOL6	NA	UP	3.196	9.56e-120	1648.2
STC2	NA	UP	2.729	3.17e-119	2626.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DTX3L	NA	UP	2.553	3.51e-96	2147.3
SP100	NA	UP	2.428	1.62e-93	2653.7

## Ruta: transport (Página 2 de 6)

Fuente: GO:BP | ID: GO:0006810 | Genes: 137 | p-valor ruta: 1.62e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
NEDD4	NA	UP	2.433	4.99e-60	1678.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
APOL4	NA	UP	3.489	1.37e-42	132.9

## Ruta: transport (Página 3 de 6)

Fuente: GO:BP | ID: GO:0006810 | Genes: 137 | p-valor ruta: 1.62e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
APOL3	NA	UP	2.918	2.49e-41	209.0
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
BACH2	NA	UP	2.222	2.18e-30	209.0
PPM1K	NA	UP	2.192	3.89e-30	395.9
EPN3	NA	DOWN	-2.294	4.66e-30	335.3
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
NKX3-1	NA	UP	2.233	8.30e-23	132.4
BCL2A1	NA	UP	4.192	1.64e-21	55.1
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8
DUOXA2	NA	UP	4.650	3.36e-16	39.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
EGR2	NA	UP	3.090	6.72e-15	43.7
NR1I2	NA	UP	2.428	6.42e-12	59.1
SCN3A	NA	UP	8.277	2.66e-10	27.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3

## Ruta: transport (Página 4 de 6)

Fuente: GO:BP | ID: GO:0006810 | Genes: 137 | p-valor ruta: 1.62e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STX19	NA	UP	2.009	1.09e-08	99.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
KCNV1	NA	UP	2.402	2.10e-07	37.9
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
SYT1	NA	UP	2.659	1.62e-06	21.4
KCNT2	NA	UP	2.262	3.16e-06	26.9
RAB30	NA	UP	2.024	5.27e-06	28.7
BEST1	NA	UP	3.553	8.47e-06	13.3
SELE	NA	UP	5.745	2.05e-05	9.0
RAB36	NA	DOWN	-2.063	2.15e-05	24.7
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
BEST3	NA	UP	2.070	3.26e-05	23.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
XKR9	NA	UP	3.541	5.84e-05	11.9
GLTPD2	NA	DOWN	-2.633	7.44e-05	17.8
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
RHCG	NA	UP	2.107	1.84e-04	21.0
TRPC4	NA	UP	5.730	3.71e-04	4.5
NCALD	NA	UP	2.037	3.82e-04	17.1

## Ruta: transport (Página 5 de 6)

Fuente: GO:BP | ID: GO:0006810 | Genes: 137 | p-valor ruta: 1.62e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
SLC38A4	NA	DOWN	-2.630	6.25e-04	12.4
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
SLC16A6	NA	UP	3.375	9.62e-04	7.8
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
KCNH3	NA	DOWN	-2.243	1.94e-03	12.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
CACNA1I	NA	UP	2.173	2.19e-03	14.9
SLC17A4	NA	DOWN	-2.298	2.32e-03	11.5
PEX5L	NA	UP	3.321	2.40e-03	7.0
KCNN1	NA	UP	3.883	2.55e-03	6.2
SIDT1	NA	UP	2.642	2.81e-03	8.6
SLCO5A1	NA	UP	2.814	2.87e-03	7.7
IPCEF1	NA	UP	4.035	3.69e-03	4.9
DLL1	NA	UP	2.171	4.40e-03	10.4
SLC25A18	NA	DOWN	-2.816	5.67e-03	7.5
P2RY6	NA	UP	2.536	8.76e-03	7.0
SLC9B1	NA	UP	4.128	1.36e-02	3.1
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
SLC6A7	NA	UP	3.822	1.73e-02	3.5

## Ruta: transport (Página 6 de 6)

Fuente: GO:BP | ID: GO:0006810 | Genes: 137 | p-valor ruta: 1.62e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OLR1	NA	UP	2.655	1.81e-02	6.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
SLC9C2	NA	UP	3.943	2.11e-02	2.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
IL13RA2	NA	UP	2.568	3.02e-02	4.7
KCNE4	NA	UP	2.337	3.37e-02	5.7
DLG2	NA	UP	3.028	3.83e-02	3.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: negative regulation of gene expression (Página 1 de 3)

Fuente: GO:BP | ID: GO:0010629 | Genes: 66 | p-valor ruta: 1.88e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
GBP1	NA	UP	4.090	2.07e-209	2026.7
TIPARP	NA	UP	3.093	1.11e-158	5401.6
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
IFI16	NA	UP	3.151	2.12e-114	2583.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF4	NA	UP	2.704	2.52e-79	645.9

## Ruta: negative regulation of gene expression (Página 2 de 3)

Fuente: GO:BP | ID: GO:0010629 | Genes: 66 | p-valor ruta: 1.88e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
TDRD7	NA	UP	2.129	5.72e-65	1011.2
PARP10	NA	UP	2.093	5.71e-52	2376.2
XRN1	NA	UP	2.115	6.38e-50	984.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
MIR155HG	NA	UP	5.318	4.66e-35	99.1
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
ZBTB20	NA	UP	3.440	1.24e-15	47.6
NAV3	NA	UP	2.285	2.77e-15	84.4
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: negative regulation of gene expression (Página 3 de 3)

Fuente: GO:BP | ID: GO:0010629 | Genes: 66 | p-valor ruta: 1.88e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
PKP1	NA	UP	3.076	9.16e-05	12.8
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
RBMS3	NA	UP	2.303	4.11e-04	18.6
MIR146A	NA	UP	2.592	1.50e-03	10.3
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
DLL1	NA	UP	2.171	4.40e-03	10.4
MEG9	NA	UP	4.115	1.26e-02	3.2
PRG2	NA	UP	2.073	1.32e-02	9.7
GBP7	NA	UP	4.177	1.61e-02	2.9
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: alpha–beta T cell activation

Fuente: GO:BP | ID: GO:0046631 | Genes: 17 | p-valor ruta: 1.88e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IRF1	NA	UP	3.512	7.87e-194	2808.9
CD274	NA	UP	5.204	1.23e-98	314.4
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: T cell proliferation

Fuente: GO:BP | ID: GO:0042098 | Genes: 18 | p-valor ruta: 1.89e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
LGALS9	NA	UP	2.474	3.44e-71	1449.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
VCAM1	NA	UP	4.737	4.28e-26	66.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TNFSF14	NA	UP	2.748	3.71e-07	23.0
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7

## Ruta: regulation of wound healing

Fuente: GO:BP | ID: GO:0061041 | Genes: 14 | p-valor ruta: 1.91e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
THBS1	NA	UP	2.656	1.05e-77	3791.3
HBEGF	NA	UP	2.602	3.10e-57	415.2
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
FAP	NA	UP	3.233	1.87e-05	14.0
HRG	NA	UP	2.971	4.00e-03	6.9
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: response to organophosphorus

Fuente: GO:BP | ID: GO:0046683 | Genes: 14 | p-valor ruta: 1.91e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
PNPT1	NA	UP	2.411	6.12e-71	2101.8
STAT1	NA	UP	2.519	1.61e-68	9528.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PER1	NA	UP	2.501	8.94e-44	469.6
DUOX2	NA	UP	4.348	3.03e-29	71.2
PCK1	NA	UP	4.419	1.17e-12	29.6
DUOX1	NA	UP	3.131	5.18e-10	27.1
SLC5A5	NA	UP	4.542	4.62e-04	6.8
P2RY6	NA	UP	2.536	8.76e-03	7.0
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: interleukin–6 production

Fuente: GO:BP | ID: GO:0032635 | Genes: 15 | p-valor ruta: 1.98e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ZBTB20	NA	UP	3.440	1.24e-15	47.6
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: regulation of interleukin–6 production

Fuente: GO:BP | ID: GO:0032675 | Genes: 15 | p-valor ruta: 1.98e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ZBTB20	NA	UP	3.440	1.24e-15	47.6
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: regulation of production of molecular mediator of immune response

Fuente: GO:BP | ID: GO:0002700 | Genes: 17 | p-valor ruta: 2.02e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
NR4A3	NA	UP	5.574	1.45e-08	20.2
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
PRG2	NA	UP	2.073	1.32e-02	9.7
TLR9	NA	UP	2.952	1.98e-02	4.6
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: B cell activation

Fuente: GO:BP | ID: GO:0042113 | Genes: 21 | p-valor ruta: 2.05e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFNB1	NA	UP	10.001	4.69e-95	1340.6
THEMIS2	NA	UP	2.550	2.88e-50	403.0
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
CD70	NA	UP	3.257	1.21e-02	4.7
TLR9	NA	UP	2.952	1.98e-02	4.6
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of natural killer cell activation

Fuente: GO:BP | ID: GO:0032814 | Genes: 8 | p-valor ruta: 2.38e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15RA	NA	UP	2.045	1.16e-42	847.9
RASGRP1	NA	UP	2.055	4.16e-34	336.9
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL12A	NA	UP	3.852	1.95e-28	83.7
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
PGLYRP2	NA	UP	4.867	2.30e-07	15.6

## Ruta: regulation of epithelial cell proliferation

Fuente: GO:BP | ID: GO:0050678 | Genes: 24 | p-valor ruta: 2.41e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL5	NA	UP	5.035	8.94e-165	656.3
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
NKX3-1	NA	UP	2.233	8.30e-23	132.4
NOD2	NA	UP	2.981	1.19e-19	80.5
KLF9	NA	UP	2.555	7.01e-13	66.8
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
EGR3	NA	UP	2.096	2.87e-04	21.5
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: nitric oxide metabolic process

Fuente: GO:BP | ID: GO:0046209 | Genes: 11 | p-valor ruta: 2.45e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
CYP1A1	NA	UP	6.086	6.00e-198	811.0
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PTX3	NA	UP	3.614	2.25e-68	237.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3
AHRR	NA	UP	2.180	3.48e-07	33.9
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: leukocyte activation involved in inflammatory response

Fuente: GO:BP | ID: GO:0002269 | Genes: 9 | p-valor ruta: 2.45e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
TLR3	NA	UP	2.508	1.99e-22	111.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of nucleobase–containing compound metabolic process (Página 1 de 6)

Fuente: GO:BP | ID: GO:0019219 | Genes: 126 | p-valor ruta: 2.48e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
OAS1	NA	UP	3.011	3.81e-158	5273.1
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4

## Ruta: regulation of nucleobase–containing compound metabolic process (Página 2 de 6)

Fuente: GO:BP | ID: GO:0019219 | Genes: 126 | p-valor ruta: 2.48e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5

## Ruta: regulation of nucleobase–containing compound metabolic process (Página 3 de 6)

Fuente: GO:BP | ID: GO:0019219 | Genes: 126 | p-valor ruta: 2.48e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
XRN1	NA	UP	2.115	6.38e-50	984.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
HDX	NA	UP	2.521	1.83e-28	139.2
BCL3	NA	UP	2.067	4.65e-26	500.4

## Ruta: regulation of nucleobase–containing compound metabolic process (Página 4 de 6)

Fuente: GO:BP | ID: GO:0019219 | Genes: 126 | p-valor ruta: 2.48e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
RBM11	NA	UP	2.506	8.83e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
SP8	NA	UP	6.528	5.89e-06	8.0

## Ruta: regulation of nucleobase–containing compound metabolic process (Página 5 de 6)

Fuente: GO:BP | ID: GO:0019219 | Genes: 126 | p-valor ruta: 2.48e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZNF442	NA	UP	2.573	6.55e-06	18.8
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
ZNF382	NA	UP	2.028	3.78e-04	18.2
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
PATL2	NA	UP	2.215	2.72e-03	12.1
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
CELF6	NA	UP	2.403	2.65e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PURG	NA	DOWN	-4.166	4.66e-02	1.7

## Ruta: regulation of nucleobase–containing compound metabolic process (Página 6 de 6)

Fuente: GO:BP | ID: GO:0019219 | Genes: 126 | p-valor ruta: 2.48e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: fibrinolysis

Fuente: GO:BP | ID: GO:0042730 | Genes: 7 | p-valor ruta: 2.5e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
FAP	NA	UP	3.233	1.87e-05	14.0
HRG	NA	UP	2.971	4.00e-03	6.9
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: type II interferon-mediated signaling pathway

Fuente: GO:BP | ID: GO:0060333 | Genes: 7 | p-valor ruta: 2.5e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRF1	NA	UP	3.512	7.87e-194	2808.9
PARP14	NA	UP	2.977	1.79e-119	2649.9
SP100	NA	UP	2.428	1.62e-93	2653.7
NLRC5	NA	UP	3.949	8.12e-88	414.4
PARP9	NA	UP	2.449	1.75e-75	2354.5
STAT1	NA	UP	2.519	1.61e-68	9528.0
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: T cell activation involved in immune response

Fuente: GO:BP | ID: GO:0002286 | Genes: 14 | p-valor ruta: 2.51e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BCL3	NA	UP	2.067	4.65e-26	500.4
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: regulation of transcription by RNA polymerase II (Página 1 de 4)

Fuente: GO:BP | ID: GO:0006357 | Genes: 90 | p-valor ruta: 2.59e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
NLRC5	NA	UP	3.949	8.12e-88	414.4
KLF10	NA	UP	2.626	2.92e-86	1224.1
ETV7	NA	UP	4.688	2.39e-83	278.8

## Ruta: regulation of transcription by RNA polymerase II (Página 2 de 4)

Fuente: GO:BP | ID: GO:0006357 | Genes: 90 | p-valor ruta: 2.59e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
FOSB	NA	UP	3.144	1.32e-55	267.7
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7

## Ruta: regulation of transcription by RNA polymerase II (Página 3 de 4)

Fuente: GO:BP | ID: GO:0006357 | Genes: 90 | p-valor ruta: 2.59e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BACH2	NA	UP	2.222	2.18e-30	209.0
HDX	NA	UP	2.521	1.83e-28	139.2
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
NR4A3	NA	UP	5.574	1.45e-08	20.2
RUNX2	NA	UP	3.983	1.50e-06	15.2
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
PKP1	NA	UP	3.076	9.16e-05	12.8

## Ruta: regulation of transcription by RNA polymerase II (Página 4 de 4)

Fuente: GO:BP | ID: GO:0006357 | Genes: 90 | p-valor ruta: 2.59e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR3	NA	UP	2.096	2.87e-04	21.5
ZNF382	NA	UP	2.028	3.78e-04	18.2
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
PURG	NA	DOWN	-4.166	4.66e-02	1.7
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: response to steroid hormone

Fuente: GO:BP | ID: GO:0048545 | Genes: 23 | p-valor ruta: 2.6e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TXNIP	NA	UP	3.401	2.30e-219	11419.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
NEDD4	NA	UP	2.433	4.99e-60	1678.5
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9
PER1	NA	UP	2.501	8.94e-44	469.6
NKX3-1	NA	UP	2.233	8.30e-23	132.4
JAK2	NA	UP	2.081	1.26e-17	123.4
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
SSTR2	NA	UP	2.031	8.80e-10	53.9
NR4A3	NA	UP	5.574	1.45e-08	20.2
PTGER2	NA	UP	3.006	1.95e-04	11.0
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: positive regulation of adaptive immune response

Fuente: GO:BP | ID: GO:0002821 | Genes: 14 | p-valor ruta: 2.74e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: reactive nitrogen species metabolic process

Fuente: GO:BP | ID: GO:2001057 | Genes: 11 | p-valor ruta: 2.78e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
CYP1A1	NA	UP	6.086	6.00e-198	811.0
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PTX3	NA	UP	3.614	2.25e-68	237.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3
AHRR	NA	UP	2.180	3.48e-07	33.9
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: natural killer cell activation

Fuente: GO:BP | ID: GO:0030101 | Genes: 12 | p-valor ruta: 2.78e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL12A	NA	UP	3.852	1.95e-28	83.7
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL18R1	NA	UP	2.088	8.75e-05	23.0
VAV1	NA	UP	2.118	1.54e-02	7.9

## Ruta: endothelial cell migration

Fuente: GO:BP | ID: GO:0043542 | Genes: 18 | p-valor ruta: 2.82e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
HDAC9	NA	UP	2.292	4.51e-32	2003.2
EDN2	NA	UP	3.499	8.77e-31	90.3
FUT1	NA	UP	2.765	4.55e-26	104.9
ZEB2	NA	UP	3.419	5.95e-12	30.5
FAP	NA	UP	3.233	1.87e-05	14.0
EGR3	NA	UP	2.096	2.87e-04	21.5
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
BMPER	NA	UP	4.906	6.28e-03	2.6
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of cell migration

Fuente: GO:BP | ID: GO:0030336 | Genes: 21 | p-valor ruta: 2.87e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DUSP1	NA	UP	3.521	2.54e-161	1829.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
BST2	NA	UP	4.284	3.82e-19	50.8
NAV3	NA	UP	2.285	2.77e-15	84.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
NGFR	NA	UP	2.337	3.33e-07	30.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: heat generation

Fuente: GO:BP | ID: GO:0031649 | Genes: 6 | p-valor ruta: 2.9e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4

## Ruta: regulation of fibrinolysis

Fuente: GO:BP | ID: GO:0051917 | Genes: 6 | p-valor ruta: 2.9e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
FAP	NA	UP	3.233	1.87e-05	14.0
HRG	NA	UP	2.971	4.00e-03	6.9
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: positive regulation of nitric oxide metabolic process

Fuente: GO:BP | ID: GO:1904407 | Genes: 8 | p-valor ruta: 2.94e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PTX3	NA	UP	3.614	2.25e-68	237.4
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3
TMEM106A	NA	UP	2.485	2.20e-02	7.2

## Ruta: cellular response to chemokine

Fuente: GO:BP | ID: GO:1990869 | Genes: 12 | p-valor ruta: 3.1e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CCL2	NA	UP	2.562	2.63e-75	658.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CXCL9	NA	UP	4.099	4.37e-04	26.3
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: response to chemokine

Fuente: GO:BP | ID: GO:1990868 | Genes: 12 | p-valor ruta: 3.1e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CCL2	NA	UP	2.562	2.63e-75	658.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CXCL9	NA	UP	4.099	4.37e-04	26.3
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: negative regulation of cytokine-mediated signaling pathway

Fuente: GO:BP | ID: GO:0001960 | Genes: 11 | p-valor ruta: 3.14e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
PARP14	NA	UP	2.977	1.79e-119	2649.9
STAT2	NA	UP	2.337	1.85e-96	2004.6
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4

## Ruta: positive regulation of cytokine production involved in immune response

Fuente: GO:BP | ID: GO:0002720 | Genes: 11 | p-valor ruta: 3.14e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
NLRP3	NA	UP	4.366	3.67e-13	29.8
NR4A3	NA	UP	5.574	1.45e-08	20.2
FFAR2	NA	UP	3.253	4.81e-05	12.7
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9

## Ruta: regulation of T cell proliferation

Fuente: GO:BP | ID: GO:0042129 | Genes: 16 | p-valor ruta: 3.76e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
CCL5	NA	UP	5.035	8.94e-165	656.3
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
LGALS9	NA	UP	2.474	3.44e-71	1449.3
VCAM1	NA	UP	4.737	4.28e-26	66.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CD70	NA	UP	3.257	1.21e-02	4.7

## Ruta: MDA–5 signaling pathway

Fuente: GO:BP | ID: GO:0039530 | Genes: 5 | p-valor ruta: 3.84e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIH1	NA	UP	4.035	2.22e-233	4525.3
DHX58	NA	UP	2.877	1.75e-99	953.6
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9

## Ruta: macromolecule modification (Página 1 de 5)

Fuente: GO:BP | ID: GO:0043412 | Genes: 101 | p-valor ruta: 4.07e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
USP18	NA	UP	3.900	1.42e-145	1151.2
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
PLAT	NA	UP	2.447	4.98e-113	6662.1
NUAK2	NA	UP	4.358	1.14e-107	489.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
IFNL1	NA	UP	8.179	1.68e-89	578.0
TRAF1	NA	UP	4.730	5.65e-84	258.2

## Ruta: macromolecule modification (Página 2 de 5)

Fuente: GO:BP | ID: GO:0043412 | Genes: 101 | p-valor ruta: 4.07e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP12	NA	UP	2.297	5.64e-82	1665.8
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
DAPP1	NA	UP	2.456	1.42e-72	922.6
PML	NA	UP	2.208	2.84e-70	2901.3
NEURL3	NA	UP	2.464	1.53e-62	758.9
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
OTUD1	NA	UP	2.871	3.76e-46	418.8
ARRDC4	NA	UP	2.305	2.76e-44	631.5

## Ruta: macromolecule modification (Página 3 de 5)

Fuente: GO:BP | ID: GO:0043412 | Genes: 101 | p-valor ruta: 4.07e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BIRC3	NA	UP	2.146	8.30e-42	2602.9
FUT3	NA	UP	2.139	2.84e-41	355.7
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PPM1K	NA	UP	2.192	3.89e-30	395.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
MAST4	NA	UP	2.184	1.21e-25	197.5
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
BDKRB2	NA	UP	2.797	5.56e-15	55.1
EGR2	NA	UP	3.090	6.72e-15	43.7
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
SOCS1	NA	UP	2.012	6.54e-08	82.5

## Ruta: macromolecule modification (Página 4 de 5)

Fuente: GO:BP | ID: GO:0043412 | Genes: 101 | p-valor ruta: 4.07e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR6	NA	UP	2.680	9.77e-08	26.3
NPR1	NA	UP	3.131	3.66e-07	19.1
NUPR1	NA	UP	3.660	1.78e-06	14.5
SYNPO2	NA	UP	3.603	1.95e-04	9.0
GFPT2	NA	UP	2.651	2.37e-04	12.7
KIT	NA	UP	3.650	6.24e-04	7.9
RNF152	NA	UP	3.325	1.37e-03	7.5
HRG	NA	UP	2.971	4.00e-03	6.9
RET	NA	UP	2.793	1.44e-02	5.5
TTLL6	NA	UP	2.577	1.74e-02	6.7
CAMK1G	NA	UP	4.059	1.79e-02	2.8
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
TRIM69	NA	UP	3.519	3.21e-02	3.0
PPM1E	NA	UP	3.810	4.20e-02	2.4
PPEF1	NA	UP	3.725	4.31e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: macromolecule modification (Página 5 de 5)

Fuente: GO:BP | ID: GO:0043412 | Genes: 101 | p-valor ruta: 4.07e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: regulation of ERK1 and ERK2 cascade

Fuente: GO:BP | ID: GO:0070372 | Genes: 20 | p-valor ruta: 4.08e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
TLR9	NA	UP	2.952	1.98e-02	4.6
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: protein K63-linked ubiquitination

Fuente: GO:BP | ID: GO:0070534 | Genes: 10 | p-valor ruta: 4.11e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM22	NA	UP	5.650	1.01e-212	913.7
TRAF1	NA	UP	4.730	5.65e-84	258.2
RNF213	NA	UP	2.528	1.50e-73	6034.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
PARP10	NA	UP	2.093	5.71e-52	2376.2
ARRDC4	NA	UP	2.305	2.76e-44	631.5
NOD2	NA	UP	2.981	1.19e-19	80.5
RNF152	NA	UP	3.325	1.37e-03	7.5

## Ruta: cell development (Página 1 de 4)

Fuente: GO:BP | ID: GO:0048468 | Genes: 97 | p-valor ruta: 4.16e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IRF1	NA	UP	3.512	7.87e-194	2808.9
TIPARP	NA	UP	3.093	1.11e-158	5401.6
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
NEB	NA	DOWN	-2.754	5.16e-82	703.7
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
EGR1	NA	UP	2.472	2.61e-74	1149.5

## Ruta: cell development (Página 2 de 4)

Fuente: GO:BP | ID: GO:0048468 | Genes: 97 | p-valor ruta: 4.16e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
TDRD7	NA	UP	2.129	5.72e-65	1011.2
RND1	NA	UP	2.840	1.60e-62	337.7
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
CD69	NA	UP	3.112	5.99e-57	257.2
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
EDN2	NA	UP	3.499	8.77e-31	90.3
VCAM1	NA	UP	4.737	4.28e-26	66.5

## Ruta: cell development (Página 3 de 4)

Fuente: GO:BP | ID: GO:0048468 | Genes: 97 | p-valor ruta: 4.16e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BCL3	NA	UP	2.067	4.65e-26	500.4
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBX2	NA	UP	2.353	5.55e-15	78.3
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ACTN2	NA	UP	3.956	7.01e-09	20.3
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
LST1	NA	UP	6.916	7.00e-07	10.5
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4
ACTBL2	NA	UP	2.242	5.97e-06	28.3

## Ruta: cell development (Página 4 de 4)

Fuente: GO:BP | ID: GO:0048468 | Genes: 97 | p-valor ruta: 4.16e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL18R1	NA	UP	2.088	8.75e-05	23.0
NPTX1	NA	UP	2.102	1.13e-04	22.3
EGR3	NA	UP	2.096	2.87e-04	21.5
MKX	NA	UP	2.196	5.67e-04	15.1
KIT	NA	UP	3.650	6.24e-04	7.9
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
POU3F2	NA	UP	4.735	2.02e-03	4.5
LGR6	NA	UP	3.915	2.25e-03	6.0
DLL1	NA	UP	2.171	4.40e-03	10.4
RP1L1	NA	UP	2.162	5.43e-03	10.3
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: CD4-positive, alpha-beta T cell cytokine production

Fuente: GO:BP | ID: GO:0035743 | Genes: 6 | p-valor ruta: 4.16e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IFNB1	NA	UP	10.001	4.69e-95	1340.6
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: ERK1 and ERK2 cascade

Fuente: GO:BP | ID: GO:0070371 | Genes: 21 | p-valor ruta: 4.19e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
TLR9	NA	UP	2.952	1.98e-02	4.6
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: positive regulation of interleukin–10 production

Fuente: GO:BP | ID: GO:0032733 | Genes: 8 | p-valor ruta: 4.4e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CD274	NA	UP	5.204	1.23e-98	314.4
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ISG15	NA	UP	2.482	5.90e-57	3807.9
BCL3	NA	UP	2.067	4.65e-26	500.4
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: DNA-templated transcription (Página 1 de 5)

Fuente: GO:BP | ID: GO:0006351 | Genes: 114 | p-valor ruta: 4.4e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6

## Ruta: DNA–templated transcription (Página 2 de 5)

Fuente: GO:BP | ID: GO:0006351 | Genes: 114 | p-valor ruta: 4.4e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
KLF10	NA	UP	2.626	2.92e-86	1224.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6

## Ruta: DNA-templated transcription (Página 3 de 5)

Fuente: GO:BP | ID: GO:0006351 | Genes: 114 | p-valor ruta: 4.4e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
HDX	NA	UP	2.521	1.83e-28	139.2
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: DNA-templated transcription (Página 4 de 5)

Fuente: GO:BP | ID: GO:0006351 | Genes: 114 | p-valor ruta: 4.4e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
EGR3	NA	UP	2.096	2.87e-04	21.5
ZNF382	NA	UP	2.028	3.78e-04	18.2
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2

## Ruta: DNA–templated transcription (Página 5 de 5)

Fuente: GO:BP | ID: GO:0006351 | Genes: 114 | p-valor ruta: 4.4e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KIT	NA	UP	3.650	6.24e-04	7.9
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8
PURG	NA	DOWN	-4.166	4.66e-02	1.7
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of locomotion

Fuente: GO:BP | ID: GO:0040013 | Genes: 22 | p-valor ruta: 4.62e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
DUSP1	NA	UP	3.521	2.54e-161	1829.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
BST2	NA	UP	4.284	3.82e-19	50.8
NAV3	NA	UP	2.285	2.77e-15	84.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
NGFR	NA	UP	2.337	3.33e-07	30.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of T cell mediated immunity

Fuente: GO:BP | ID: GO:0002709 | Genes: 12 | p-valor ruta: 4.72e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
ULBP1	NA	UP	3.138	2.70e-38	151.4
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: positive regulation of pattern recognition receptor signaling pathway

Fuente: GO:BP | ID: GO:0062208 | Genes: 10 | p-valor ruta: 5.38e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
OASL	NA	UP	3.434	4.45e-163	4285.8
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
SLC15A3	NA	UP	4.245	2.06e-77	254.6
GBP5	NA	UP	6.172	4.92e-17	48.7
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: response to cAMP

Fuente: GO:BP | ID: GO:0051591 | Genes: 11 | p-valor ruta: 5.67e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PNPT1	NA	UP	2.411	6.12e-71	2101.8
STAT1	NA	UP	2.519	1.61e-68	9528.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PER1	NA	UP	2.501	8.94e-44	469.6
DUOX2	NA	UP	4.348	3.03e-29	71.2
PCK1	NA	UP	4.419	1.17e-12	29.6
DUOX1	NA	UP	3.131	5.18e-10	27.1
SLC5A5	NA	UP	4.542	4.62e-04	6.8
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: negative regulation of angiogenesis

Fuente: GO:BP | ID: GO:0016525 | Genes: 12 | p-valor ruta: 6.4e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CXCL10	NA	UP	6.079	8.12e-195	783.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
SPRY2	NA	UP	2.250	1.05e-29	211.9
NPR1	NA	UP	3.131	3.66e-07	19.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9

## Ruta: negative regulation of immune effector process

Fuente: GO:BP | ID: GO:0002698 | Genes: 13 | p-valor ruta: 6.4e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
PRG2	NA	UP	2.073	1.32e-02	9.7
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: positive regulation of chemotaxis

Fuente: GO:BP | ID: GO:0050921 | Genes: 14 | p-valor ruta: 6.41e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CSF1	NA	UP	2.530	1.40e-49	467.4
EDN2	NA	UP	3.499	8.77e-31	90.3
IL12A	NA	UP	3.852	1.95e-28	83.7
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF14	NA	UP	2.748	3.71e-07	23.0
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: positive regulation of interleukin-12 production

Fuente: GO:BP | ID: GO:0032735 | Genes: 8 | p-valor ruta: 6.43e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRF1	NA	UP	3.512	7.87e-194	2808.9
IDO1	NA	UP	4.167	4.38e-109	394.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
LTB	NA	UP	3.555	2.50e-41	150.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: type 2 immune response

Fuente: GO:BP | ID: GO:0042092 | Genes: 8 | p-valor ruta: 6.43e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IDO1	NA	UP	4.167	4.38e-109	394.2
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
BCL3	NA	UP	2.067	4.65e-26	500.4
NOD2	NA	UP	2.981	1.19e-19	80.5
NLRP3	NA	UP	4.366	3.67e-13	29.8

## Ruta: interleukin–18 production

Fuente: GO:BP | ID: GO:0032621 | Genes: 5 | p-valor ruta: 6.46e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNF	NA	UP	7.712	3.81e-103	573.0
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of interleukin-18 production

Fuente: GO:BP | ID: GO:0032661 | Genes: 5 | p-valor ruta: 6.46e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNF	NA	UP	7.712	3.81e-103	573.0
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of odontogenesis of dentin-containing tooth

Fuente: GO:BP | ID: GO:0042487 | Genes: 5 | p-valor ruta: 6.46e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2

## Ruta: phosphate-containing compound metabolic process (Página 1 de 4)

Fuente: GO:BP | ID: GO:0006796 | Genes: 84 | p-valor ruta: 6.54e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CMPK2	NA	UP	4.677	1.14e-162	1687.4
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IDO1	NA	UP	4.167	4.38e-109	394.2
NUAK2	NA	UP	4.358	1.14e-107	489.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0

## Ruta: phosphate-containing compound metabolic process (Página 2 de 4)

Fuente: GO:BP | ID: GO:0006796 | Genes: 84 | p-valor ruta: 6.54e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTAFR	NA	UP	3.014	4.62e-62	338.1
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
ALDH1L2	NA	UP	3.029	4.52e-55	257.3
PDE4B	NA	UP	3.818	7.08e-52	171.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
PPM1K	NA	UP	2.192	3.89e-30	395.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7
MAST4	NA	UP	2.184	1.21e-25	197.5
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8

## Ruta: phosphate-containing compound metabolic process (Página 3 de 4)

Fuente: GO:BP | ID: GO:0006796 | Genes: 84 | p-valor ruta: 6.54e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZBTB20	NA	UP	3.440	1.24e-15	47.6
BDKRB2	NA	UP	2.797	5.56e-15	55.1
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
KMO	NA	UP	5.165	6.24e-09	19.5
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NPR1	NA	UP	3.131	3.66e-07	19.1
NUPR1	NA	UP	3.660	1.78e-06	14.5
ADCY4	NA	UP	2.271	8.12e-06	23.6
SYNPO2	NA	UP	3.603	1.95e-04	9.0
GFPT2	NA	UP	2.651	2.37e-04	12.7
KIT	NA	UP	3.650	6.24e-04	7.9
PLA1A	NA	UP	3.622	1.35e-03	6.6
SLC17A4	NA	DOWN	-2.298	2.32e-03	11.5
HRG	NA	UP	2.971	4.00e-03	6.9
SLC25A18	NA	DOWN	-2.816	5.67e-03	7.5
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
CAMK1G	NA	UP	4.059	1.79e-02	2.8
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: phosphate-containing compound metabolic process (Página 4 de 4)

Fuente: GO:BP | ID: GO:0006796 | Genes: 84 | p-valor ruta: 6.54e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
DLG2	NA	UP	3.028	3.83e-02	3.8
PPM1E	NA	UP	3.810	4.20e-02	2.4
PPEF1	NA	UP	3.725	4.31e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of cell motility

Fuente: GO:BP | ID: GO:2000146 | Genes: 21 | p-valor ruta: 6.7e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DUSP1	NA	UP	3.521	2.54e-161	1829.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
GADD45A	NA	UP	2.255	1.32e-60	1140.5
CD69	NA	UP	3.112	5.99e-57	257.2
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
BST2	NA	UP	4.284	3.82e-19	50.8
NAV3	NA	UP	2.285	2.77e-15	84.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
NGFR	NA	UP	2.337	3.33e-07	30.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: phosphorus metabolic process (Página 1 de 4)

Fuente: GO:BP | ID: GO:0006793 | Genes: 84 | p-valor ruta: 6.87e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
CMPK2	NA	UP	4.677	1.14e-162	1687.4
DUSP1	NA	UP	3.521	2.54e-161	1829.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
IDO1	NA	UP	4.167	4.38e-109	394.2
NUAK2	NA	UP	4.358	1.14e-107	489.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0

## Ruta: phosphorus metabolic process (Página 2 de 4)

Fuente: GO:BP | ID: GO:0006793 | Genes: 84 | p-valor ruta: 6.87e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTAFR	NA	UP	3.014	4.62e-62	338.1
GADD45A	NA	UP	2.255	1.32e-60	1140.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
ALDH1L2	NA	UP	3.029	4.52e-55	257.3
PDE4B	NA	UP	3.818	7.08e-52	171.4
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
PPM1K	NA	UP	2.192	3.89e-30	395.9
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
IL12A	NA	UP	3.852	1.95e-28	83.7
MAST4	NA	UP	2.184	1.21e-25	197.5
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8

## Ruta: phosphorus metabolic process (Página 3 de 4)

Fuente: GO:BP | ID: GO:0006793 | Genes: 84 | p-valor ruta: 6.87e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZBTB20	NA	UP	3.440	1.24e-15	47.6
BDKRB2	NA	UP	2.797	5.56e-15	55.1
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
KMO	NA	UP	5.165	6.24e-09	19.5
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NPR1	NA	UP	3.131	3.66e-07	19.1
NUPR1	NA	UP	3.660	1.78e-06	14.5
ADCY4	NA	UP	2.271	8.12e-06	23.6
SYNPO2	NA	UP	3.603	1.95e-04	9.0
GFPT2	NA	UP	2.651	2.37e-04	12.7
KIT	NA	UP	3.650	6.24e-04	7.9
PLA1A	NA	UP	3.622	1.35e-03	6.6
SLC17A4	NA	DOWN	-2.298	2.32e-03	11.5
HRG	NA	UP	2.971	4.00e-03	6.9
SLC25A18	NA	DOWN	-2.816	5.67e-03	7.5
P2RY6	NA	UP	2.536	8.76e-03	7.0
RET	NA	UP	2.793	1.44e-02	5.5
CAMK1G	NA	UP	4.059	1.79e-02	2.8
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: phosphorus metabolic process (Página 4 de 4)

Fuente: GO:BP | ID: GO:0006793 | Genes: 84 | p-valor ruta: 6.87e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
DLG2	NA	UP	3.028	3.83e-02	3.8
PPM1E	NA	UP	3.810	4.20e-02	2.4
PPEF1	NA	UP	3.725	4.31e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of wound healing

Fuente: GO:BP | ID: GO:0061045 | Genes: 10 | p-valor ruta: 6.96e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
THBS1	NA	UP	2.656	1.05e-77	3791.3
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
FAP	NA	UP	3.233	1.87e-05	14.0
HRG	NA	UP	2.971	4.00e-03	6.9
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: negative regulation of blood vessel morphogenesis

Fuente: GO:BP | ID: GO:2000181 | Genes: 12 | p-valor ruta: 7.06e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CXCL10	NA	UP	6.079	8.12e-195	783.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
SPRY2	NA	UP	2.250	1.05e-29	211.9
NPR1	NA	UP	3.131	3.66e-07	19.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9

## Ruta: negative regulation of leukocyte activation

Fuente: GO:BP | ID: GO:0002695 | Genes: 16 | p-valor ruta: 7.09e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
CD69	NA	UP	3.112	5.99e-57	257.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
LST1	NA	UP	6.916	7.00e-07	10.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: myeloid cell differentiation (Página 1 de 2)

Fuente: GO:BP | ID: GO:0030099 | Genes: 26 | p-valor ruta: 7.5e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
IFI16	NA	UP	3.151	2.12e-114	2583.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
ISG15	NA	UP	2.482	5.90e-57	3807.9
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
TLR3	NA	UP	2.508	1.99e-22	111.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
IKZF1	NA	UP	2.283	2.21e-02	6.8
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: myeloid cell differentiation (Página 2 de 2)

Fuente: GO:BP | ID: GO:0030099 | Genes: 26 | p-valor ruta: 7.5e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: secretion (Página 1 de 2)

Fuente: GO:BP | ID: GO:0046903 | Genes: 44 | p-valor ruta: 7.73e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
PTGS2	NA	UP	3.253	7.39e-80	3663.8
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PCK2	NA	UP	2.226	5.13e-50	969.9
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: secretion (Página 2 de 2)

Fuente: GO:BP | ID: GO:0046903 | Genes: 44 | p-valor ruta: 7.73e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
KMO	NA	UP	5.165	6.24e-09	19.5
STX19	NA	UP	2.009	1.09e-08	99.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
STX11	NA	UP	2.909	3.34e-07	21.9
NPR1	NA	UP	3.131	3.66e-07	19.1
SYT1	NA	UP	2.659	1.62e-06	21.4
BEST1	NA	UP	3.553	8.47e-06	13.3
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
TRPC4	NA	UP	5.730	3.71e-04	4.5
KIT	NA	UP	3.650	6.24e-04	7.9
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: negative regulation of vasculature development

Fuente: GO:BP | ID: GO:1901343 | Genes: 12 | p-valor ruta: 7.78e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CXCL10	NA	UP	6.079	8.12e-195	783.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
GADD45A	NA	UP	2.255	1.32e-60	1140.5
SPRY2	NA	UP	2.250	1.05e-29	211.9
NPR1	NA	UP	3.131	3.66e-07	19.1
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9

## Ruta: chemokine-mediated signaling pathway

Fuente: GO:BP | ID: GO:0070098 | Genes: 11 | p-valor ruta: 7.91e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CCL2	NA	UP	2.562	2.63e-75	658.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CXCL9	NA	UP	4.099	4.37e-04	26.3
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: innate immune response activating cell surface receptor signaling pathway

Fuente: GO:BP | ID: GO:0002220 | Genes: 11 | p-valor ruta: 7.91e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFI35	NA	UP	2.237	9.59e-79	2236.7
NR1D1	NA	UP	2.475	2.08e-68	1229.5
NOD2	NA	UP	2.981	1.19e-19	80.5
TLR6	NA	UP	2.680	9.77e-08	26.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
LY96	NA	UP	5.204	4.42e-03	3.4

## Ruta: positive regulation of natural killer cell activation

Fuente: GO:BP | ID: GO:0032816 | Genes: 6 | p-valor ruta: 8.03e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15RA	NA	UP	2.045	1.16e-42	847.9
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: regulation of response to wounding

Fuente: GO:BP | ID: GO:1903034 | Genes: 15 | p-valor ruta: 8.08e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
HBEGF	NA	UP	2.602	3.10e-57	415.2
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
FAP	NA	UP	3.233	1.87e-05	14.0
HRG	NA	UP	2.971	4.00e-03	6.9
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: myeloid leukocyte differentiation

Fuente: GO:BP | ID: GO:0002573 | Genes: 18 | p-valor ruta: 9.12e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
IFI16	NA	UP	3.151	2.12e-114	2583.4
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
TLR3	NA	UP	2.508	1.99e-22	111.5
CSF3	NA	UP	6.122	1.72e-19	56.0
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
KIT	NA	UP	3.650	6.24e-04	7.9
IL34	NA	UP	2.794	2.41e-02	4.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: cellular response to fibroblast growth factor stimulus

Fuente: GO:BP | ID: GO:0044344 | Genes: 12 | p-valor ruta: 9.43e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL5	NA	UP	5.035	8.94e-165	656.3
ZFP36	NA	UP	2.944	7.57e-104	1721.5
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
FGF19	NA	UP	3.931	5.59e-21	52.8
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
EGR3	NA	UP	2.096	2.87e-04	21.5
FLRT1	NA	UP	5.509	1.11e-03	3.8
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: immune response-regulating cell surface receptor signaling pathway

Fuente: GO:BP | ID: GO:0002768 | Genes: 22 | p-valor ruta: 9.58e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
GBP1	NA	UP	4.090	2.07e-209	2026.7
OAS1	NA	UP	3.011	3.81e-158	5273.1
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFI35	NA	UP	2.237	9.59e-79	2236.7
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CLEC4E	NA	UP	3.620	4.75e-09	26.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
KIT	NA	UP	3.650	6.24e-04	7.9
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2

## Ruta: establishment of localization (Página 1 de 6)

Fuente: GO:BP | ID: GO:0051234 | Genes: 146 | p-valor ruta: 9.91e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
APOL6	NA	UP	3.196	9.56e-120	1648.2
STC2	NA	UP	2.729	3.17e-119	2626.1
PLAT	NA	UP	2.447	4.98e-113	6662.1
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5

## Ruta: establishment of localization (Página 2 de 6)

Fuente: GO:BP | ID: GO:0051234 | Genes: 146 | p-valor ruta: 9.91e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DTX3L	NA	UP	2.553	3.51e-96	2147.3
SP100	NA	UP	2.428	1.62e-93	2653.7
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
NEDD4	NA	UP	2.433	4.99e-60	1678.5
BBC3	NA	UP	2.829	3.65e-57	503.1
PHLDB2	NA	UP	2.315	8.68e-55	764.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8

## Ruta: establishment of localization (Página 3 de 6)

Fuente: GO:BP | ID: GO:0051234 | Genes: 146 | p-valor ruta: 9.91e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
APOL4	NA	UP	3.489	1.37e-42	132.9
APOL3	NA	UP	2.918	2.49e-41	209.0
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
BACH2	NA	UP	2.222	2.18e-30	209.0
PPM1K	NA	UP	2.192	3.89e-30	395.9
EPN3	NA	DOWN	-2.294	4.66e-30	335.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
NKX3-1	NA	UP	2.233	8.30e-23	132.4
BCL2A1	NA	UP	4.192	1.64e-21	55.1
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7

## Ruta: establishment of localization (Página 4 de 6)

Fuente: GO:BP | ID: GO:0051234 | Genes: 146 | p-valor ruta: 9.91e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DUOXA2	NA	UP	4.650	3.36e-16	39.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
EGR2	NA	UP	3.090	6.72e-15	43.7
NR1I2	NA	UP	2.428	6.42e-12	59.1
SCN3A	NA	UP	8.277	2.66e-10	27.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
STX19	NA	UP	2.009	1.09e-08	99.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
KCNV1	NA	UP	2.402	2.10e-07	37.9
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
SYT1	NA	UP	2.659	1.62e-06	21.4
KCNT2	NA	UP	2.262	3.16e-06	26.9
RAB30	NA	UP	2.024	5.27e-06	28.7
BEST1	NA	UP	3.553	8.47e-06	13.3
SELE	NA	UP	5.745	2.05e-05	9.0
RAB36	NA	DOWN	-2.063	2.15e-05	24.7
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
BEST3	NA	UP	2.070	3.26e-05	23.9

## Ruta: establishment of localization (Página 5 de 6)

Fuente: GO:BP | ID: GO:0051234 | Genes: 146 | p-valor ruta: 9.91e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FFAR2	NA	UP	3.253	4.81e-05	12.7
XKR9	NA	UP	3.541	5.84e-05	11.9
GLTPD2	NA	DOWN	-2.633	7.44e-05	17.8
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
RHCG	NA	UP	2.107	1.84e-04	21.0
TRPC4	NA	UP	5.730	3.71e-04	4.5
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
SLC38A4	NA	DOWN	-2.630	6.25e-04	12.4
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
SLC16A6	NA	UP	3.375	9.62e-04	7.8
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
KCNH3	NA	DOWN	-2.243	1.94e-03	12.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
CACNA1I	NA	UP	2.173	2.19e-03	14.9
SLC17A4	NA	DOWN	-2.298	2.32e-03	11.5
PEX5L	NA	UP	3.321	2.40e-03	7.0
KCNN1	NA	UP	3.883	2.55e-03	6.2
SIDT1	NA	UP	2.642	2.81e-03	8.6
SLCO5A1	NA	UP	2.814	2.87e-03	7.7

## Ruta: establishment of localization (Página 6 de 6)

Fuente: GO:BP | ID: GO:0051234 | Genes: 146 | p-valor ruta: 9.91e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IPCEF1	NA	UP	4.035	3.69e-03	4.9
DLL1	NA	UP	2.171	4.40e-03	10.4
SLC25A18	NA	DOWN	-2.816	5.67e-03	7.5
P2RY6	NA	UP	2.536	8.76e-03	7.0
SLC9B1	NA	UP	4.128	1.36e-02	3.1
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
SLC6A7	NA	UP	3.822	1.73e-02	3.5
OLR1	NA	UP	2.655	1.81e-02	6.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
SLC9C2	NA	UP	3.943	2.11e-02	2.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
INSC	NA	UP	3.872	3.01e-02	2.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7
KCNE4	NA	UP	2.337	3.37e-02	5.7
DLG2	NA	UP	3.028	3.83e-02	3.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: enzyme-linked receptor protein signaling pathway (Página 1 de 2)

Fuente: GO:BP | ID: GO:0007167 | Genes: 43 | p-valor ruta: 1.02e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
INHBA	NA	UP	3.514	2.31e-143	1743.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
EGR1	NA	UP	2.472	2.61e-74	1149.5
PML	NA	UP	2.208	2.84e-70	2901.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
JUN	NA	UP	2.450	1.10e-62	6693.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
HIVEP1	NA	UP	2.014	1.06e-24	282.1
LIFR	NA	UP	2.213	9.30e-24	226.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
JAK2	NA	UP	2.081	1.26e-17	123.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1

## Ruta: enzyme-linked receptor protein signaling pathway (Página 2 de 2)

Fuente: GO:BP | ID: GO:0007167 | Genes: 43 | p-valor ruta: 1.02e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
NGFR	NA	UP	2.337	3.33e-07	30.0
NPR1	NA	UP	3.131	3.66e-07	19.1
RUNX2	NA	UP	3.983	1.50e-06	15.2
COL4A1	NA	UP	6.589	5.89e-06	8.2
KIT	NA	UP	3.650	6.24e-04	7.9
FLRT1	NA	UP	5.509	1.11e-03	3.8
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
BMPER	NA	UP	4.906	6.28e-03	2.6
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: negative regulation of fibrinolysis

Fuente: GO:BP | ID: GO:0051918 | Genes: 5 | p-valor ruta: 1.03e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
HRG	NA	UP	2.971	4.00e-03	6.9
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: regulation of natural killer cell differentiation

Fuente: GO:BP | ID: GO:0032823 | Genes: 5 | p-valor ruta: 1.03e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15RA	NA	UP	2.045	1.16e-42	847.9
RASGRP1	NA	UP	2.055	4.16e-34	336.9
PRDM1	NA	UP	3.525	5.98e-31	99.0
IL15	NA	UP	2.012	2.28e-17	116.8
PGLYRP2	NA	UP	4.867	2.30e-07	15.6

## Ruta: cellular response to ketone

Fuente: GO:BP | ID: GO:1901655 | Genes: 12 | p-valor ruta: 1.04e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KLF4	NA	UP	2.704	2.52e-79	645.9
PTGER4	NA	UP	2.548	1.70e-71	568.2
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
JAK2	NA	UP	2.081	1.26e-17	123.4
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PTGER2	NA	UP	3.006	1.95e-04	11.0
SLC5A5	NA	UP	4.542	4.62e-04	6.8
P2RY6	NA	UP	2.536	8.76e-03	7.0
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: peptidyl–amino acid modification (Página 1 de 2)

Fuente: GO:BP | ID: GO:0018193 | Genes: 34 | p–valor ruta: 1.05e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IFIH1	NA	UP	4.035	2.22e–233	4525.3
CCL5	NA	UP	5.035	8.94e–165	656.3
NCOA7	NA	UP	3.032	5.52e–127	2619.1
PARP14	NA	UP	2.977	1.79e–119	2649.9
CSF2	NA	UP	7.043	2.08e–103	455.6
TNF	NA	UP	7.712	3.81e–103	573.0
IFNB1	NA	UP	10.001	4.69e–95	1340.6
IFNL1	NA	UP	8.179	1.68e–89	578.0
PTGS2	NA	UP	3.253	7.39e–80	3663.8
PARP9	NA	UP	2.449	1.75e–75	2354.5
EGR1	NA	UP	2.472	2.61e–74	1149.5
PML	NA	UP	2.208	2.84e–70	2901.3
GADD45A	NA	UP	2.255	1.32e–60	1140.5
CTH	NA	UP	2.488	2.75e–57	412.1
HBEGF	NA	UP	2.602	3.10e–57	415.2
HDAC9	NA	UP	2.292	4.51e–32	2003.2
SPRY2	NA	UP	2.250	1.05e–29	211.9
IL12A	NA	UP	3.852	1.95e–28	83.7
NOD2	NA	UP	2.981	1.19e–19	80.5
CSF3	NA	UP	6.122	1.72e–19	56.0
JAK2	NA	UP	2.081	1.26e–17	123.4
IL15	NA	UP	2.012	2.28e–17	116.8
BDKRB2	NA	UP	2.797	5.56e–15	55.1
EGR2	NA	UP	3.090	6.72e–15	43.7

## Ruta: peptidyl–amino acid modification (Página 2 de 2)

Fuente: GO:BP | ID: GO:0018193 | Genes: 34 | p–valor ruta: 1.05e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PCK1	NA	UP	4.419	1.17e–12	29.6
IL23A	NA	UP	2.189	2.05e–11	59.9
SOCS1	NA	UP	2.012	6.54e–08	82.5
KIT	NA	UP	3.650	6.24e–04	7.9
HRG	NA	UP	2.971	4.00e–03	6.9
TTLL6	NA	UP	2.577	1.74e–02	6.7
IL34	NA	UP	2.794	2.41e–02	4.8
SFRP1	NA	UP	2.711	4.51e–02	3.8
SRMS	NA	UP	3.880	4.55e–02	2.3

## Ruta: regulation of extrinsic apoptotic signaling pathway via death domain receptors

Fuente: GO:BP | ID: GO:1902041 | Genes: 8 | p-valor ruta: 1.09e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
ICAM1	NA	UP	3.652	3.11e-204	19095.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
SP100	NA	UP	2.428	1.62e-93	2653.7
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: positive regulation of lymphocyte mediated immunity

Fuente: GO:BP | ID: GO:0002708 | Genes: 13 | p-valor ruta: 1.17e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
VAV1	NA	UP	2.118	1.54e-02	7.9

## Ruta: alpha–beta T cell differentiation

Fuente: GO:BP | ID: GO:0046632 | Genes: 13 | p–valor ruta: 1.27e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IRF1	NA	UP	3.512	7.87e–194	2808.9
PTGER4	NA	UP	2.548	1.70e–71	568.2
LGALS9	NA	UP	2.474	3.44e–71	1449.3
CD69	NA	UP	3.112	5.99e–57	257.2
NFKBIZ	NA	UP	2.037	4.06e–41	2486.2
PRDM1	NA	UP	3.525	5.98e–31	99.0
BCL3	NA	UP	2.067	4.65e–26	500.4
NLRP3	NA	UP	4.366	3.67e–13	29.8
IL23A	NA	UP	2.189	2.05e–11	59.9
SOCS1	NA	UP	2.012	6.54e–08	82.5
IL18R1	NA	UP	2.088	8.75e–05	23.0

## Ruta: regulation of extrinsic apoptotic signaling pathway in absence of ligand

Fuente: GO:BP | ID: GO:2001239 | Genes: 8 | p-valor ruta: 1.29e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
KLF4	NA	UP	2.704	2.52e-79	645.9
RET	NA	UP	2.793	1.44e-02	5.5

## Ruta: interleukin-12 production

Fuente: GO:BP | ID: GO:0032615 | Genes: 9 | p-valor ruta: 1.33e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRF1	NA	UP	3.512	7.87e-194	2808.9
IDO1	NA	UP	4.167	4.38e-109	394.2
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
LTB	NA	UP	3.555	2.50e-41	150.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of interleukin-12 production

Fuente: GO:BP | ID: GO:0032655 | Genes: 9 | p-valor ruta: 1.33e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRF1	NA	UP	3.512	7.87e-194	2808.9
IDO1	NA	UP	4.167	4.38e-109	394.2
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
LTB	NA	UP	3.555	2.50e-41	150.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: positive regulation of defense response to virus by host

Fuente: GO:BP | ID: GO:0002230 | Genes: 7 | p-valor ruta: 1.33e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM22	NA	UP	5.650	1.01e-212	913.7
DTX3L	NA	UP	2.553	3.51e-96	2147.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
IL23A	NA	UP	2.189	2.05e-11	59.9

## Ruta: regulation of type 2 immune response

Fuente: GO:BP | ID: GO:0002828 | Genes: 7 | p-valor ruta: 1.33e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IDO1	NA	UP	4.167	4.38e-109	394.2
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
NOD2	NA	UP	2.981	1.19e-19	80.5
NLRP3	NA	UP	4.366	3.67e-13	29.8

## Ruta: positive regulation of molecular function (Página 1 de 2)

Fuente: GO:BP | ID: GO:0044093 | Genes: 40 | p-valor ruta: 1.37e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
TNF	NA	UP	7.712	3.81e-103	573.0
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
SP100	NA	UP	2.428	1.62e-93	2653.7
TRAF1	NA	UP	4.730	5.65e-84	258.2
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
ARRDC4	NA	UP	2.305	2.76e-44	631.5
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
EDN2	NA	UP	3.499	8.77e-31	90.3
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: positive regulation of molecular function (Página 2 de 2)

Fuente: GO:BP | ID: GO:0044093 | Genes: 40 | p-valor ruta: 1.37e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
ACTN2	NA	UP	3.956	7.01e-09	20.3
TLR6	NA	UP	2.680	9.77e-08	26.3
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
P2RY6	NA	UP	2.536	8.76e-03	7.0
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: localization (Página 1 de 7)

Fuente: GO:BP | ID: GO:0051179 | Genes: 160 | p-valor ruta: 1.42e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL10	NA	UP	6.079	8.12e-195	783.4
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
APOL6	NA	UP	3.196	9.56e-120	1648.2
STC2	NA	UP	2.729	3.17e-119	2626.1
PLAT	NA	UP	2.447	4.98e-113	6662.1

## Ruta: localization (Página 2 de 7)

Fuente: GO:BP | ID: GO:0051179 | Genes: 160 | p-valor ruta: 1.42e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NUAK2	NA	UP	4.358	1.14e-107	489.1
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
DTX3L	NA	UP	2.553	3.51e-96	2147.3
SP100	NA	UP	2.428	1.62e-93	2653.7
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6

## Ruta: localization (Página 3 de 7)

Fuente: GO:BP | ID: GO:0051179 | Genes: 160 | p-valor ruta: 1.42e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
PHLDB2	NA	UP	2.315	8.68e-55	764.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
PCK2	NA	UP	2.226	5.13e-50	969.9
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
APOL4	NA	UP	3.489	1.37e-42	132.9
APOL3	NA	UP	2.918	2.49e-41	209.0
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
BACH2	NA	UP	2.222	2.18e-30	209.0
PPM1K	NA	UP	2.192	3.89e-30	395.9
EPN3	NA	DOWN	-2.294	4.66e-30	335.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4

## Ruta: localization (Página 4 de 7)

Fuente: GO:BP | ID: GO:0051179 | Genes: 160 | p-valor ruta: 1.42e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NKX3-1	NA	UP	2.233	8.30e-23	132.4
BCL2A1	NA	UP	4.192	1.64e-21	55.1
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
DUOXA2	NA	UP	4.650	3.36e-16	39.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
EGR2	NA	UP	3.090	6.72e-15	43.7
NR1I2	NA	UP	2.428	6.42e-12	59.1
SCN3A	NA	UP	8.277	2.66e-10	27.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
STX19	NA	UP	2.009	1.09e-08	99.7
NR4A3	NA	UP	5.574	1.45e-08	20.2
LRP2	NA	UP	3.144	3.22e-08	22.0
KCNV1	NA	UP	2.402	2.10e-07	37.9
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
NPR1	NA	UP	3.131	3.66e-07	19.1

## Ruta: localization (Página 5 de 7)

Fuente: GO:BP | ID: GO:0051179 | Genes: 160 | p-valor ruta: 1.42e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL10RA	NA	UP	3.172	3.66e-07	18.8
SYT1	NA	UP	2.659	1.62e-06	21.4
KCNT2	NA	UP	2.262	3.16e-06	26.9
RAB30	NA	UP	2.024	5.27e-06	28.7
BEST1	NA	UP	3.553	8.47e-06	13.3
SELE	NA	UP	5.745	2.05e-05	9.0
RAB36	NA	DOWN	-2.063	2.15e-05	24.7
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
BEST3	NA	UP	2.070	3.26e-05	23.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
XKR9	NA	UP	3.541	5.84e-05	11.9
GLTPD2	NA	DOWN	-2.633	7.44e-05	17.8
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
RHCG	NA	UP	2.107	1.84e-04	21.0
TRPC4	NA	UP	5.730	3.71e-04	4.5
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
SLC38A4	NA	DOWN	-2.630	6.25e-04	12.4
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
SLC16A6	NA	UP	3.375	9.62e-04	7.8
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2

## Ruta: localization (Página 6 de 7)

Fuente: GO:BP | ID: GO:0051179 | Genes: 160 | p-valor ruta: 1.42e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
KCNH3	NA	DOWN	-2.243	1.94e-03	12.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
CACNA1I	NA	UP	2.173	2.19e-03	14.9
SLC17A4	NA	DOWN	-2.298	2.32e-03	11.5
PEX5L	NA	UP	3.321	2.40e-03	7.0
KCNN1	NA	UP	3.883	2.55e-03	6.2
SIDT1	NA	UP	2.642	2.81e-03	8.6
SLCO5A1	NA	UP	2.814	2.87e-03	7.7
IPCEF1	NA	UP	4.035	3.69e-03	4.9
SRGN	NA	UP	2.093	3.80e-03	11.0
DLL1	NA	UP	2.171	4.40e-03	10.4
SLC25A18	NA	DOWN	-2.816	5.67e-03	7.5
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
SLC9B1	NA	UP	4.128	1.36e-02	3.1
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
SLC6A7	NA	UP	3.822	1.73e-02	3.5
MSTO1	NA	DOWN	-2.110	1.81e-02	8.3
OLR1	NA	UP	2.655	1.81e-02	6.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1

## Ruta: localization (Página 7 de 7)

Fuente: GO:BP | ID: GO:0051179 | Genes: 160 | p-valor ruta: 1.42e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SLC9C2	NA	UP	3.943	2.11e-02	2.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
INSC	NA	UP	3.872	3.01e-02	2.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7
TRIM69	NA	UP	3.519	3.21e-02	3.0
KCNE4	NA	UP	2.337	3.37e-02	5.7
DLG2	NA	UP	3.028	3.83e-02	3.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: response to nematode

Fuente: GO:BP | ID: GO:0009624 | Genes: 4 | p-valor ruta: 1.46e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CYP1A1	NA	UP	6.086	6.00e-198	811.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
PTGER4	NA	UP	2.548	1.70e-71	568.2
PTGER2	NA	UP	3.006	1.95e-04	11.0

## Ruta: cellular response to hormone stimulus (Página 1 de 2)

Fuente: GO:BP | ID: GO:0032870 | Genes: 32 | p-valor ruta: 1.58e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
ZFP36	NA	UP	2.944	7.57e-104	1721.5
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
FOSB	NA	UP	3.144	1.32e-55	267.7
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PCK2	NA	UP	2.226	5.13e-50	969.9
PER1	NA	UP	2.501	8.94e-44	469.6
IRS2	NA	UP	2.254	1.06e-33	255.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
NKX3-1	NA	UP	2.233	8.30e-23	132.4
JAK2	NA	UP	2.081	1.26e-17	123.4
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
SSTR2	NA	UP	2.031	8.80e-10	53.9
ACTN2	NA	UP	3.956	7.01e-09	20.3
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
PTGER2	NA	UP	3.006	1.95e-04	11.0

## Ruta: cellular response to hormone stimulus (Página 2 de 2)

Fuente: GO:BP | ID: GO:0032870 | Genes: 32 | p-valor ruta: 1.58e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SLC5A5	NA	UP	4.542	4.62e-04	6.8
LHB	NA	UP	3.522	1.50e-03	7.0
P2RY6	NA	UP	2.536	8.76e-03	7.0
GLP2R	NA	UP	2.220	1.86e-02	8.9
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TP63	NA	UP	3.788	4.09e-02	2.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: positive regulation of monocyte chemotactic protein–1 production

Fuente: GO:BP | ID: GO:0071639 | Genes: 5 | p-valor ruta: 1.58e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
OAS3	NA	UP	2.942	1.13e-87	8674.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
NOD2	NA	UP	2.981	1.19e-19	80.5

## Ruta: toll-like receptor signaling pathway

Fuente: GO:BP | ID: GO:0002224 | Genes: 10 | p-valor ruta: 1.62e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRF1	NA	UP	3.512	7.87e-194	2808.9
CD274	NA	UP	5.204	1.23e-98	314.4
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IRF7	NA	UP	3.210	5.72e-79	2126.1
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
TLR3	NA	UP	2.508	1.99e-22	111.5
TLR6	NA	UP	2.680	9.77e-08	26.3
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: B cell differentiation

Fuente: GO:BP | ID: GO:0030183 | Genes: 14 | p-valor ruta: 1.62e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
INHBA	NA	UP	3.514	2.31e-143	1743.6
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFNB1	NA	UP	10.001	4.69e-95	1340.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
HDAC9	NA	UP	2.292	4.51e-32	2003.2
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
TLR9	NA	UP	2.952	1.98e-02	4.6
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of neuroinflammatory response

Fuente: GO:BP | ID: GO:0150077 | Genes: 7 | p-valor ruta: 1.64e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
NR1D1	NA	UP	2.475	2.08e-68	1229.5
NUPR1	NA	UP	3.660	1.78e-06	14.5

## Ruta: protein metabolic process (Página 1 de 6)

Fuente: GO:BP | ID: GO:0019538 | Genes: 140 | p-valor ruta: 1.67e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
LAMP3	NA	UP	3.644	2.72e-189	1627.7
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
DUSP1	NA	UP	3.521	2.54e-161	1829.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
NCOA7	NA	UP	3.032	5.52e-127	2619.1
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
APOL6	NA	UP	3.196	9.56e-120	1648.2
PARP14	NA	UP	2.977	1.79e-119	2649.9
PLAT	NA	UP	2.447	4.98e-113	6662.1
NUAK2	NA	UP	4.358	1.14e-107	489.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0

## Ruta: protein metabolic process (Página 2 de 6)

Fuente: GO:BP | ID: GO:0019538 | Genes: 140 | p-valor ruta: 1.67e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
TRAF1	NA	UP	4.730	5.65e-84	258.2
PARP12	NA	UP	2.297	5.64e-82	1665.8
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
PARP9	NA	UP	2.449	1.75e-75	2354.5
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
DAPP1	NA	UP	2.456	1.42e-72	922.6
PML	NA	UP	2.208	2.84e-70	2901.3
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1

## Ruta: protein metabolic process (Página 3 de 6)

Fuente: GO:BP | ID: GO:0019538 | Genes: 140 | p-valor ruta: 1.67e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
OTUD1	NA	UP	2.871	3.76e-46	418.8
ARRDC4	NA	UP	2.305	2.76e-44	631.5
APOL4	NA	UP	3.489	1.37e-42	132.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
FUT3	NA	UP	2.139	2.84e-41	355.7
BMP2	NA	UP	2.237	3.69e-40	325.3
DUSP8	NA	UP	2.088	3.69e-35	551.5
RASGRP1	NA	UP	2.055	4.16e-34	336.9
C1R	NA	UP	2.188	3.06e-32	258.8
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PPM1K	NA	UP	2.192	3.89e-30	395.9
SPRY2	NA	UP	2.250	1.05e-29	211.9

## Ruta: protein metabolic process (Página 4 de 6)

Fuente: GO:BP | ID: GO:0019538 | Genes: 140 | p-valor ruta: 1.67e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL12A	NA	UP	3.852	1.95e-28	83.7
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
MAST4	NA	UP	2.184	1.21e-25	197.5
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
DUOXA2	NA	UP	4.650	3.36e-16	39.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
EGR2	NA	UP	3.090	6.72e-15	43.7
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
NPR1	NA	UP	3.131	3.66e-07	19.1
NUPR1	NA	UP	3.660	1.78e-06	14.5
ADAMTS6	NA	UP	2.602	8.90e-06	19.6

## Ruta: protein metabolic process (Página 5 de 6)

Fuente: GO:BP | ID: GO:0019538 | Genes: 140 | p-valor ruta: 1.67e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
MMP13	NA	UP	5.406	9.23e-06	11.1
FAP	NA	UP	3.233	1.87e-05	14.0
PKP1	NA	UP	3.076	9.16e-05	12.8
SYNPO2	NA	UP	3.603	1.95e-04	9.0
GFPT2	NA	UP	2.651	2.37e-04	12.7
UBQLNL	NA	UP	3.875	3.33e-04	7.9
COLEC10	NA	UP	2.878	4.02e-04	11.6
CPXM1	NA	UP	2.128	5.77e-04	16.0
KIT	NA	UP	3.650	6.24e-04	7.9
GAL3ST4	NA	UP	2.371	7.40e-04	12.5
RNF152	NA	UP	3.325	1.37e-03	7.5
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
PATL2	NA	UP	2.215	2.72e-03	12.1
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
RNF150	NA	UP	4.240	1.04e-02	3.1
THBD	NA	UP	2.330	1.23e-02	7.3
RET	NA	UP	2.793	1.44e-02	5.5
SLC6A7	NA	UP	3.822	1.73e-02	3.5
TTLL6	NA	UP	2.577	1.74e-02	6.7
CAMK1G	NA	UP	4.059	1.79e-02	2.8
OLR1	NA	UP	2.655	1.81e-02	6.9
TBCEL	NA	UP	2.318	1.82e-02	7.1
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2

## Ruta: protein metabolic process (Página 6 de 6)

Fuente: GO:BP | ID: GO:0019538 | Genes: 140 | p-valor ruta: 1.67e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
ALPK2	NA	UP	3.025	2.06e-02	4.7
IL34	NA	UP	2.794	2.41e-02	4.8
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
TRIM69	NA	UP	3.519	3.21e-02	3.0
ADAMTS4	NA	UP	3.293	3.88e-02	3.0
PPM1E	NA	UP	3.810	4.20e-02	2.4
PPEF1	NA	UP	3.725	4.31e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of RNA biosynthetic process (Página 1 de 3)

Fuente: GO:BP | ID: GO:1902679 | Genes: 52 | p-valor ruta: 1.74e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ATF3	NA	UP	4.971	1.38e-261	2286.0
TXNIP	NA	UP	3.401	2.30e-219	11419.4
TRIM22	NA	UP	5.650	1.01e-212	913.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
ETV7	NA	UP	4.688	2.39e-83	278.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5

## Ruta: negative regulation of RNA biosynthetic process (Página 2 de 3)

Fuente: GO:BP | ID: GO:1902679 | Genes: 52 | p-valor ruta: 1.74e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FOSB	NA	UP	3.144	1.32e-55	267.7
PARP10	NA	UP	2.093	5.71e-52	2376.2
PER1	NA	UP	2.501	8.94e-44	469.6
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
BMP2	NA	UP	2.237	3.69e-40	325.3
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7
BACH2	NA	UP	2.222	2.18e-30	209.0
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
NR4A3	NA	UP	5.574	1.45e-08	20.2
RUNX2	NA	UP	3.983	1.50e-06	15.2
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
SALL1	NA	UP	4.345	3.20e-02	1.8
TP63	NA	UP	3.788	4.09e-02	2.3

## Ruta: negative regulation of RNA biosynthetic process (Página 3 de 3)

Fuente: GO:BP | ID: GO:1902679 | Genes: 52 | p-valor ruta: 1.74e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SFRP1	NA	UP	2.711	4.51e-02	3.8
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: positive regulation of interleukin-8 production

Fuente: GO:BP | ID: GO:0032757 | Genes: 9 | p-valor ruta: 1.74e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
FFAR2	NA	UP	3.253	4.81e-05	12.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: export from cell (Página 1 de 2)

Fuente: GO:BP | ID: GO:0140352 | Genes: 41 | p-valor ruta: 1.86e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PCK2	NA	UP	2.226	5.13e-50	969.9
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
KMO	NA	UP	5.165	6.24e-09	19.5
STX19	NA	UP	2.009	1.09e-08	99.7

## Ruta: export from cell (Página 2 de 2)

Fuente: GO:BP | ID: GO:0140352 | Genes: 41 | p-valor ruta: 1.86e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NR4A3	NA	UP	5.574	1.45e-08	20.2
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
STX11	NA	UP	2.909	3.34e-07	21.9
SYT1	NA	UP	2.659	1.62e-06	21.4
KCNT2	NA	UP	2.262	3.16e-06	26.9
BEST1	NA	UP	3.553	8.47e-06	13.3
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
KIT	NA	UP	3.650	6.24e-04	7.9
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
IL13RA2	NA	UP	2.568	3.02e-02	4.7
KCNE4	NA	UP	2.337	3.37e-02	5.7
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: regulation of cytoplasmic pattern recognition receptor signaling pathway

Fuente: GO:BP | ID: GO:0039531 | Genes: 12 | p-valor ruta: 1.95e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
OASL	NA	UP	3.434	4.45e-163	4285.8
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
DDX60	NA	UP	3.015	7.43e-79	1999.9
SLC15A3	NA	UP	4.245	2.06e-77	254.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
GBP5	NA	UP	6.172	4.92e-17	48.7
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: response to fibroblast growth factor

Fuente: GO:BP | ID: GO:0071774 | Genes: 12 | p-valor ruta: 1.95e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL5	NA	UP	5.035	8.94e-165	656.3
ZFP36	NA	UP	2.944	7.57e-104	1721.5
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
SPRY2	NA	UP	2.250	1.05e-29	211.9
FGF19	NA	UP	3.931	5.59e-21	52.8
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
EGR3	NA	UP	2.096	2.87e-04	21.5
FLRT1	NA	UP	5.509	1.11e-03	3.8
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: cell surface toll-like receptor signaling pathway

Fuente: GO:BP | ID: GO:0140895 | Genes: 9 | p-valor ruta: 1.98e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFI35	NA	UP	2.237	9.59e-79	2236.7
NR1D1	NA	UP	2.475	2.08e-68	1229.5
NOD2	NA	UP	2.981	1.19e-19	80.5
TLR6	NA	UP	2.680	9.77e-08	26.3
LY96	NA	UP	5.204	4.42e-03	3.4

## Ruta: regulation of hormone levels (Página 1 de 2)

Fuente: GO:BP | ID: GO:0010817 | Genes: 29 | p-valor ruta: 2.05e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CCL5	NA	UP	5.035	8.94e-165	656.3
TIPARP	NA	UP	3.093	1.11e-158	5401.6
INHBA	NA	UP	3.514	2.31e-143	1743.6
STC2	NA	UP	2.729	3.17e-119	2626.1
TNF	NA	UP	7.712	3.81e-103	573.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
NR1D1	NA	UP	2.475	2.08e-68	1229.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PCK2	NA	UP	2.226	5.13e-50	969.9
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
DUOX2	NA	UP	4.348	3.03e-29	71.2
NKX3-1	NA	UP	2.233	8.30e-23	132.4
DDO	NA	UP	2.846	3.84e-20	82.4
JAK2	NA	UP	2.081	1.26e-17	123.4
DUOXA2	NA	UP	4.650	3.36e-16	39.7
DUOX1	NA	UP	3.131	5.18e-10	27.1
FFAR2	NA	UP	3.253	4.81e-05	12.7
SLC5A5	NA	UP	4.542	4.62e-04	6.8
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
LHB	NA	UP	3.522	1.50e-03	7.0

## Ruta: regulation of hormone levels (Página 2 de 2)

Fuente: GO:BP | ID: GO:0010817 | Genes: 29 | p-valor ruta: 2.05e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SLC17A4	NA	DOWN	-2.298	2.32e-03	11.5
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: transcription by RNA polymerase II (Página 1 de 4)

Fuente: GO:BP | ID: GO:0006366 | Genes: 90 | p-valor ruta: 2.05e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
ATF3	NA	UP	4.971	1.38e-261	2286.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
BATF2	NA	UP	4.213	3.12e-134	731.0
NCOA7	NA	UP	3.032	5.52e-127	2619.1
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
IKZF3	NA	UP	3.163	1.21e-120	1046.8
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
HELZ2	NA	UP	3.181	3.07e-108	5185.4
SP110	NA	UP	2.776	1.00e-106	1474.2
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SP100	NA	UP	2.428	1.62e-93	2653.7
NLRC5	NA	UP	3.949	8.12e-88	414.4
KLF10	NA	UP	2.626	2.92e-86	1224.1
ETV7	NA	UP	4.688	2.39e-83	278.8

## Ruta: transcription by RNA polymerase II (Página 2 de 4)

Fuente: GO:BP | ID: GO:0006366 | Genes: 90 | p-valor ruta: 2.05e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
PARP9	NA	UP	2.449	1.75e-75	2354.5
EGR1	NA	UP	2.472	2.61e-74	1149.5
CSRNP1	NA	UP	2.529	4.65e-70	673.2
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HIVEP2	NA	UP	2.631	1.74e-59	905.3
FOSB	NA	UP	3.144	1.32e-55	267.7
PER1	NA	UP	2.501	8.94e-44	469.6
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
ZNF267	NA	UP	2.059	1.30e-34	677.0
HDAC9	NA	UP	2.292	4.51e-32	2003.2
ZBTB10	NA	UP	2.456	4.07e-31	257.7
PRDM1	NA	UP	3.525	5.98e-31	99.0
MXD3	NA	DOWN	-2.428	7.76e-31	352.7

## Ruta: transcription by RNA polymerase II (Página 3 de 4)

Fuente: GO:BP | ID: GO:0006366 | Genes: 90 | p-valor ruta: 2.05e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BACH2	NA	UP	2.222	2.18e-30	209.0
HDX	NA	UP	2.521	1.83e-28	139.2
BCL3	NA	UP	2.067	4.65e-26	500.4
HIVEP1	NA	UP	2.014	1.06e-24	282.1
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
ZBTB20	NA	UP	3.440	1.24e-15	47.6
GBX2	NA	UP	2.353	5.55e-15	78.3
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
ZEB2	NA	UP	3.419	5.95e-12	30.5
NR1I2	NA	UP	2.428	6.42e-12	59.1
LMO2	NA	UP	3.437	9.83e-12	31.2
IL23A	NA	UP	2.189	2.05e-11	59.9
NR4A3	NA	UP	5.574	1.45e-08	20.2
RUNX2	NA	UP	3.983	1.50e-06	15.2
SP8	NA	UP	6.528	5.89e-06	8.0
ZNF442	NA	UP	2.573	6.55e-06	18.8
HIST1H1E	NA	UP	2.243	4.44e-05	25.9
PKP1	NA	UP	3.076	9.16e-05	12.8

## Ruta: transcription by RNA polymerase II (Página 4 de 4)

Fuente: GO:BP | ID: GO:0006366 | Genes: 90 | p-valor ruta: 2.05e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
EGR3	NA	UP	2.096	2.87e-04	21.5
ZNF382	NA	UP	2.028	3.78e-04	18.2
MKX	NA	UP	2.196	5.67e-04	15.1
EGR4	NA	UP	2.643	5.77e-04	12.2
HAND1	NA	UP	4.966	8.42e-04	5.1
TBX15	NA	UP	2.824	1.94e-03	8.6
POU3F2	NA	UP	4.735	2.02e-03	4.5
DLL1	NA	UP	2.171	4.40e-03	10.4
TLR9	NA	UP	2.952	1.98e-02	4.6
IKZF1	NA	UP	2.283	2.21e-02	6.8
SALL1	NA	UP	4.345	3.20e-02	1.8
ASXL3	NA	UP	2.101	4.07e-02	6.6
TP63	NA	UP	3.788	4.09e-02	2.3
PURG	NA	DOWN	-4.166	4.66e-02	1.7
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: negative regulation of blood coagulation

Fuente: GO:BP | ID: GO:0030195 | Genes: 8 | p-valor ruta: 2.09e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
FAP	NA	UP	3.233	1.87e-05	14.0
HRG	NA	UP	2.971	4.00e-03	6.9
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: temperature homeostasis

Fuente: GO:BP | ID: GO:0001659 | Genes: 15 | p-valor ruta: 2.27e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
G0S2	NA	UP	3.773	6.27e-143	896.4
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
ADRB2	NA	UP	2.471	2.83e-79	954.4
EGR1	NA	UP	2.472	2.61e-74	1149.5
NR1D1	NA	UP	2.475	2.08e-68	1229.5
EDN2	NA	UP	3.499	8.77e-31	90.3
NOD2	NA	UP	2.981	1.19e-19	80.5
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL18R1	NA	UP	2.088	8.75e-05	23.0
NPR3	NA	UP	2.789	1.87e-02	5.7

## Ruta: positive regulation of T cell apoptotic process

Fuente: GO:BP | ID: GO:0070234 | Genes: 5 | p-valor ruta: 2.32e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL5	NA	UP	5.035	8.94e-165	656.3
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
LGALS9	NA	UP	2.474	3.44e-71	1449.3
BBC3	NA	UP	2.829	3.65e-57	503.1

## Ruta: regulation of type B pancreatic cell proliferation

Fuente: GO:BP | ID: GO:0061469 | Genes: 5 | p-valor ruta: 2.32e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NR1D1	NA	UP	2.475	2.08e-68	1229.5
IRS2	NA	UP	2.254	1.06e-33	255.2
NR4A3	NA	UP	5.574	1.45e-08	20.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: detection of biotic stimulus

Fuente: GO:BP | ID: GO:0009595 | Genes: 7 | p-valor ruta: 2.41e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOD2	NA	UP	2.981	1.19e-19	80.5
NLRP3	NA	UP	4.366	3.67e-13	29.8
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
FAP	NA	UP	3.233	1.87e-05	14.0
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: pyroptotic inflammatory response

Fuente: GO:BP | ID: GO:0070269 | Genes: 7 | p-valor ruta: 2.41e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP1	NA	UP	4.090	2.07e-209	2026.7
ZBP1	NA	UP	6.242	1.22e-99	349.5
TRIM21	NA	UP	2.221	1.14e-60	888.8
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7
ZEB2	NA	UP	3.419	5.95e-12	30.5
NLRP1	NA	UP	5.692	4.64e-09	21.6

## Ruta: vascular endothelial growth factor production

Fuente: GO:BP | ID: GO:0010573 | Genes: 7 | p-valor ruta: 2.41e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C3AR1	NA	UP	4.639	1.59e-02	2.2

## Ruta: negative regulation of hemostasis

Fuente: GO:BP | ID: GO:1900047 | Genes: 8 | p-valor ruta: 2.43e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
FAP	NA	UP	3.233	1.87e-05	14.0
HRG	NA	UP	2.971	4.00e-03	6.9
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: negative regulation of lymphocyte activation

Fuente: GO:BP | ID: GO:0051250 | Genes: 14 | p-valor ruta: 2.48e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
INHBA	NA	UP	3.514	2.31e-143	1743.6
IDO1	NA	UP	4.167	4.38e-109	394.2
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
LST1	NA	UP	6.916	7.00e-07	10.5
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: extrinsic apoptotic signaling pathway via death domain receptors

Fuente: GO:BP | ID: GO:0008625 | Genes: 10 | p-valor ruta: 2.51e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
ATF3	NA	UP	4.971	1.38e-261	2286.0
ICAM1	NA	UP	3.652	3.11e-204	19095.5
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
SP100	NA	UP	2.428	1.62e-93	2653.7
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
THBS1	NA	UP	2.656	1.05e-77	3791.3
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: positive regulation of ERK1 and ERK2 cascade

Fuente: GO:BP | ID: GO:0070374 | Genes: 15 | p-valor ruta: 2.58e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
ICAM1	NA	UP	3.652	3.11e-204	19095.5
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
BMP2	NA	UP	2.237	3.69e-40	325.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
FGF19	NA	UP	3.931	5.59e-21	52.8
NOD2	NA	UP	2.981	1.19e-19	80.5
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: immune response–activating cell surface receptor signaling pathway

Fuente: GO:BP | ID: GO:0002429 | Genes: 20 | p-valor ruta: 2.6e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
GBP1	NA	UP	4.090	2.07e-209	2026.7
OAS1	NA	UP	3.011	3.81e-158	5273.1
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFI35	NA	UP	2.237	9.59e-79	2236.7
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
NR4A3	NA	UP	5.574	1.45e-08	20.2
TLR6	NA	UP	2.680	9.77e-08	26.3
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FFAR2	NA	UP	3.253	4.81e-05	12.7
COLEC10	NA	UP	2.878	4.02e-04	11.6
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2

## Ruta: CD4-positive, alpha-beta T cell differentiation

Fuente: GO:BP | ID: GO:0043367 | Genes: 11 | p-valor ruta: 2.65e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BCL3	NA	UP	2.067	4.65e-26	500.4
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: positive regulation of interleukin-18 production

Fuente: GO:BP | ID: GO:0032741 | Genes: 4 | p-valor ruta: 2.87e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNF	NA	UP	7.712	3.81e-103	573.0
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: positive regulation of nitric oxide biosynthetic process

Fuente: GO:BP | ID: GO:0045429 | Genes: 7 | p-valor ruta: 2.91e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
KLF4	NA	UP	2.704	2.52e-79	645.9
PTX3	NA	UP	3.614	2.25e-68	237.4
JAK2	NA	UP	2.081	1.26e-17	123.4
TLR6	NA	UP	2.680	9.77e-08	26.3

## Ruta: regulation of myeloid cell differentiation

Fuente: GO:BP | ID: GO:0045637 | Genes: 16 | p-valor ruta: 3.04e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
INHBA	NA	UP	3.514	2.31e-143	1743.6
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
ISG15	NA	UP	2.482	5.90e-57	3807.9
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CSF1	NA	UP	2.530	1.40e-49	467.4
TLR3	NA	UP	2.508	1.99e-22	111.5
CSF3	NA	UP	6.122	1.72e-19	56.0
IL23A	NA	UP	2.189	2.05e-11	59.9
DLL1	NA	UP	2.171	4.40e-03	10.4
IL34	NA	UP	2.794	2.41e-02	4.8
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: response to wounding (Página 1 de 2)

Fuente: GO:BP | ID: GO:0009611 | Genes: 29 | p-valor ruta: 3.06e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
KLF4	NA	UP	2.704	2.52e-79	645.9
THBS1	NA	UP	2.656	1.05e-77	3791.3
HBEGF	NA	UP	2.602	3.10e-57	415.2
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
DUOX2	NA	UP	4.348	3.03e-29	71.2
TLR3	NA	UP	2.508	1.99e-22	111.5
JAK2	NA	UP	2.081	1.26e-17	123.4
DUOX1	NA	UP	3.131	5.18e-10	27.1
SERPINA10	NA	UP	6.459	9.50e-06	7.5
FAP	NA	UP	3.233	1.87e-05	14.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
SLC1A2	NA	UP	2.752	2.07e-03	8.4
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
HRG	NA	UP	2.971	4.00e-03	6.9

## Ruta: response to wounding (Página 2 de 2)

Fuente: GO:BP | ID: GO:0009611 | Genes: 29 | p-valor ruta: 3.06e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VWF	NA	UP	3.390	1.16e-02	4.6
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
VAV1	NA	UP	2.118	1.54e-02	7.9

## Ruta: cell surface receptor protein tyrosine kinase signaling pathway (Página 1 de 2)

Fuente: GO:BP | ID: GO:0007169 | Genes: 31 | p-valor ruta: 3.09e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TIPARP	NA	UP	3.093	1.11e-158	5401.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
ADRB2	NA	UP	2.471	2.83e-79	954.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
CSRNP1	NA	UP	2.529	4.65e-70	673.2
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CSF1	NA	UP	2.530	1.40e-49	467.4
BMP2	NA	UP	2.237	3.69e-40	325.3
IRS2	NA	UP	2.254	1.06e-33	255.2
SPRY2	NA	UP	2.250	1.05e-29	211.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
FGF19	NA	UP	3.931	5.59e-21	52.8
JAK2	NA	UP	2.081	1.26e-17	123.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
NR4A3	NA	UP	5.574	1.45e-08	20.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
COL4A1	NA	UP	6.589	5.89e-06	8.2
KIT	NA	UP	3.650	6.24e-04	7.9
FLRT1	NA	UP	5.509	1.11e-03	3.8

## Ruta: cell surface receptor protein tyrosine kinase signaling pathway (Página 2 de 2)

Fuente: GO:BP | ID: GO:0007169 | Genes: 31 | p-valor ruta: 3.09e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: positive regulation of interferon–alpha production

Fuente: GO:BP | ID: GO:0032727 | Genes: 6 | p-valor ruta: 3.11e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIH1	NA	UP	4.035	2.22e-233	4525.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
TLR3	NA	UP	2.508	1.99e-22	111.5
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: dendritic cell cytokine production

Fuente: GO:BP | ID: GO:0002371 | Genes: 5 | p-valor ruta: 3.32e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
KIT	NA	UP	3.650	6.24e-04	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: regulation of dendritic cell cytokine production

Fuente: GO:BP | ID: GO:0002730 | Genes: 5 | p-valor ruta: 3.32e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
BST2	NA	UP	4.284	3.82e-19	50.8
KIT	NA	UP	3.650	6.24e-04	7.9
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: secretion by cell (Página 1 de 2)

Fuente: GO:BP | ID: GO:0032940 | Genes: 38 | p-valor ruta: 3.43e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
INHBA	NA	UP	3.514	2.31e-143	1743.6
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PCK2	NA	UP	2.226	5.13e-50	969.9
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
KMO	NA	UP	5.165	6.24e-09	19.5
STX19	NA	UP	2.009	1.09e-08	99.7

## Ruta: secretion by cell (Página 2 de 2)

Fuente: GO:BP | ID: GO:0032940 | Genes: 38 | p-valor ruta: 3.43e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NR4A3	NA	UP	5.574	1.45e-08	20.2
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
STX11	NA	UP	2.909	3.34e-07	21.9
SYT1	NA	UP	2.659	1.62e-06	21.4
BEST1	NA	UP	3.553	8.47e-06	13.3
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
FFAR2	NA	UP	3.253	4.81e-05	12.7
KIT	NA	UP	3.650	6.24e-04	7.9
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: extrinsic apoptotic signaling pathway in absence of ligand

Fuente: GO:BP | ID: GO:0097192 | Genes: 9 | p-valor ruta: 3.67e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
KLF4	NA	UP	2.704	2.52e-79	645.9
BCL2A1	NA	UP	4.192	1.64e-21	55.1
RET	NA	UP	2.793	1.44e-02	5.5

## Ruta: negative regulation of coagulation

Fuente: GO:BP | ID: GO:0050819 | Genes: 8 | p-valor ruta: 3.76e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
FAP	NA	UP	3.233	1.87e-05	14.0
HRG	NA	UP	2.971	4.00e-03	6.9
THBD	NA	UP	2.330	1.23e-02	7.3

## Ruta: defense response to protozoan

Fuente: GO:BP | ID: GO:0042832 | Genes: 6 | p-valor ruta: 3.93e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
GBP1	NA	UP	4.090	2.07e-209	2026.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
BATF2	NA	UP	4.213	3.12e-134	731.0
BCL3	NA	UP	2.067	4.65e-26	500.4
GBP6	NA	UP	2.233	3.24e-03	11.2
GBP7	NA	UP	4.177	1.61e-02	2.9

## Ruta: positive regulation of macrophage migration

Fuente: GO:BP | ID: GO:1905523 | Genes: 6 | p-valor ruta: 3.93e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
THBS1	NA	UP	2.656	1.05e-77	3791.3
CSF1	NA	UP	2.530	1.40e-49	467.4
C3AR1	NA	UP	4.639	1.59e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: positive regulation of cell development

Fuente: GO:BP | ID: GO:0010720 | Genes: 25 | p-valor ruta: 3.99e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNF	NA	UP	7.712	3.81e-103	573.0
KLF10	NA	UP	2.626	2.92e-86	1224.1
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL15	NA	UP	2.012	2.28e-17	116.8
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
IL23A	NA	UP	2.189	2.05e-11	59.9
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
EGR3	NA	UP	2.096	2.87e-04	21.5
KIT	NA	UP	3.650	6.24e-04	7.9
RET	NA	UP	2.793	1.44e-02	5.5
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: cellular response to alcohol

Fuente: GO:BP | ID: GO:0097306 | Genes: 11 | p-valor ruta: 4.17e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
INHBA	NA	UP	3.514	2.31e-143	1743.6
KLF4	NA	UP	2.704	2.52e-79	645.9
PTGER4	NA	UP	2.548	1.70e-71	568.2
CYP1B1	NA	UP	2.786	9.33e-53	766.0
XRN1	NA	UP	2.115	6.38e-50	984.6
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PTGER2	NA	UP	3.006	1.95e-04	11.0
SLC5A5	NA	UP	4.542	4.62e-04	6.8
P2RY6	NA	UP	2.536	8.76e-03	7.0
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: CD4-positive, alpha-beta T cell activation

Fuente: GO:BP | ID: GO:0035710 | Genes: 12 | p-valor ruta: 4.43e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
CD274	NA	UP	5.204	1.23e-98	314.4
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
CD69	NA	UP	3.112	5.99e-57	257.2
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BCL3	NA	UP	2.067	4.65e-26	500.4
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: positive regulation of DNA-binding transcription factor activity

Fuente: GO:BP | ID: GO:0051091 | Genes: 15 | p-valor ruta: 4.51e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
TNF	NA	UP	7.712	3.81e-103	573.0
IRAK2	NA	UP	2.666	3.46e-95	1164.5
SP100	NA	UP	2.428	1.62e-93	2653.7
TRAF1	NA	UP	4.730	5.65e-84	258.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BMP2	NA	UP	2.237	3.69e-40	325.3
NOD2	NA	UP	2.981	1.19e-19	80.5
IL18R1	NA	UP	2.088	8.75e-05	23.0
KIT	NA	UP	3.650	6.24e-04	7.9

## Ruta: regulation of cell killing

Fuente: GO:BP | ID: GO:0031341 | Genes: 11 | p-valor ruta: 4.56e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ICAM1	NA	UP	3.652	3.11e-204	19095.5
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
ITGAM	NA	UP	2.447	1.39e-19	90.2
RAET1L	NA	UP	2.665	2.71e-15	60.0
IL23A	NA	UP	2.189	2.05e-11	59.9
VAV1	NA	UP	2.118	1.54e-02	7.9
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: positive regulation of T cell mediated immunity

Fuente: GO:BP | ID: GO:0002711 | Genes: 9 | p-valor ruta: 4.63e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ULBP1	NA	UP	3.138	2.70e-38	151.4
IL12A	NA	UP	3.852	1.95e-28	83.7
RAET1L	NA	UP	2.665	2.71e-15	60.0
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: signal transduction in absence of ligand

Fuente: GO:BP | ID: GO:0038034 | Genes: 9 | p-valor ruta: 4.63e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
KLF4	NA	UP	2.704	2.52e-79	645.9
BCL2A1	NA	UP	4.192	1.64e-21	55.1
RET	NA	UP	2.793	1.44e-02	5.5

## Ruta: negative regulation of DNA-binding transcription factor activity

Fuente: GO:BP | ID: GO:0043433 | Genes: 12 | p-valor ruta: 4.79e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
SP100	NA	UP	2.428	1.62e-93	2653.7
NLRC5	NA	UP	3.949	8.12e-88	414.4
TRIM21	NA	UP	2.221	1.14e-60	888.8
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
BCL3	NA	UP	2.067	4.65e-26	500.4
NUPR1	NA	UP	3.660	1.78e-06	14.5
HAND1	NA	UP	4.966	8.42e-04	5.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: RIG-I signaling pathway

Fuente: GO:BP | ID: GO:0039529 | Genes: 6 | p-valor ruta: 4.92e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OASL	NA	UP	3.434	4.45e-163	4285.8
DHX58	NA	UP	2.877	1.75e-99	953.6
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
OAS3	NA	UP	2.942	1.13e-87	8674.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9

## Ruta: positive regulation of cytokine production involved in inflammatory response

Fuente: GO:BP | ID: GO:1900017 | Genes: 6 | p-valor ruta: 4.92e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNF	NA	UP	7.712	3.81e-103	573.0
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
GBP5	NA	UP	6.172	4.92e-17	48.7
TLR6	NA	UP	2.680	9.77e-08	26.3

## Ruta: lymphocyte migration

Fuente: GO:BP | ID: GO:0072676 | Genes: 11 | p-valor ruta: 4.97e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CCL2	NA	UP	2.562	2.63e-75	658.0
CD69	NA	UP	3.112	5.99e-57	257.2
CH25H	NA	UP	7.817	1.04e-46	242.7
TNFSF14	NA	UP	2.748	3.71e-07	23.0
RET	NA	UP	2.793	1.44e-02	5.5

## Sección de Análisis: GO:CC – Componentes Celulares

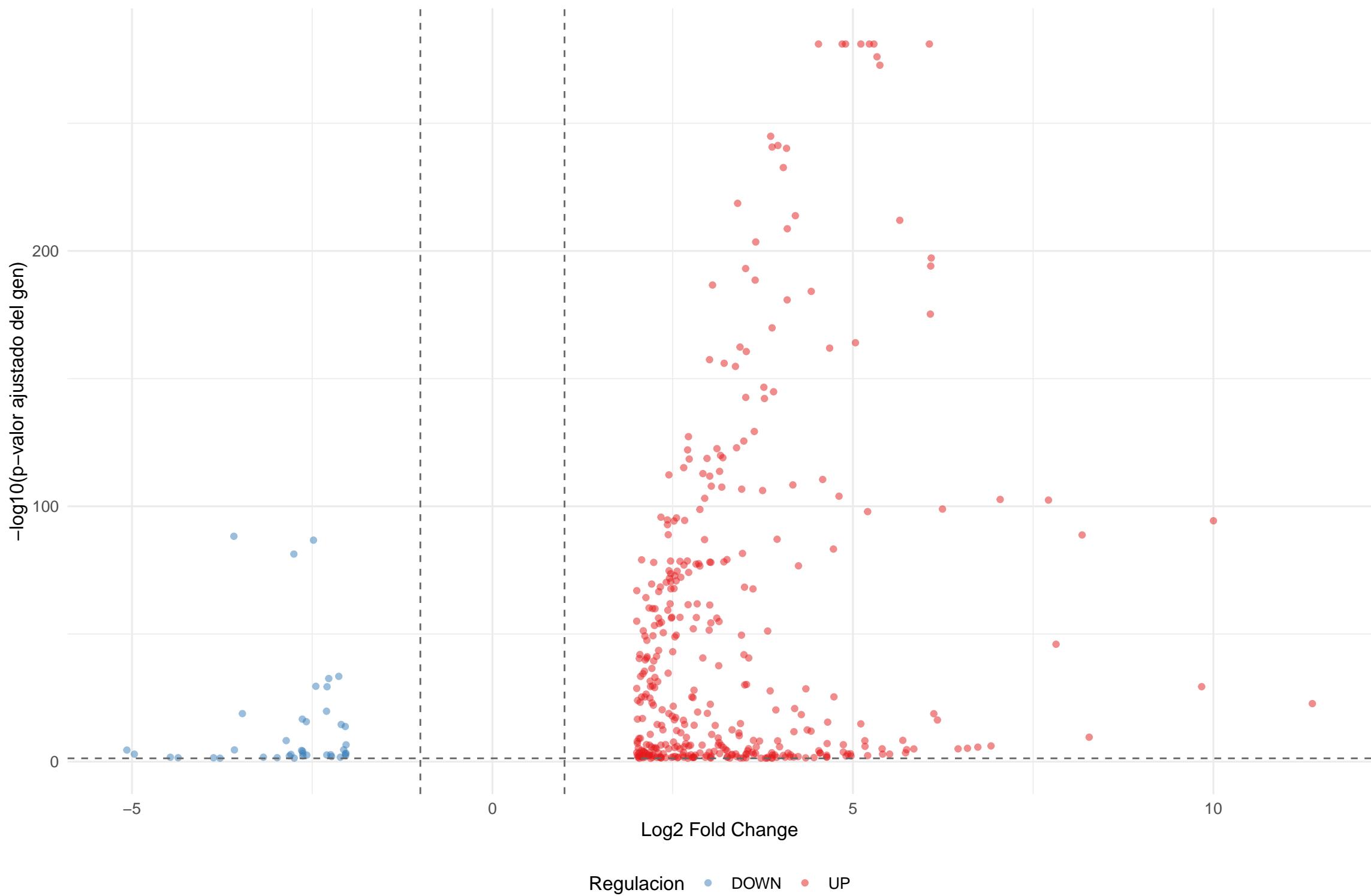
Total de términos enriquecidos en esta sección: 13

Términos 'Tope' (p–valor < 1e–16): 0

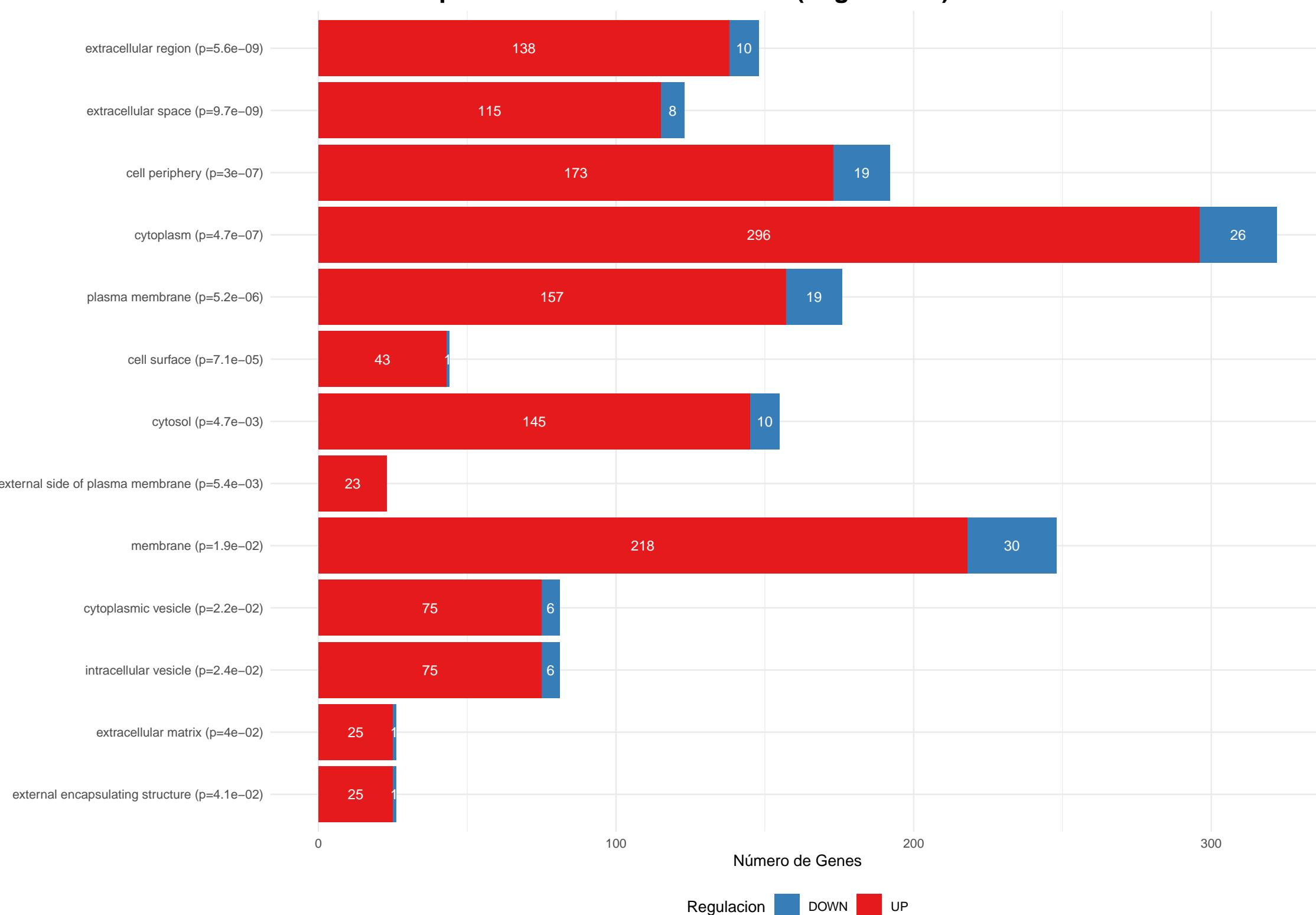
A continuación se muestran los gráficos de barras y tablas de genes para esta sección.

# Volcano Plot – GO:CC – Componentes Celulares

Mostrando 421 genes únicos mapeados en esta sección



# GO:CC – Componentes Celulares – Gráfico (Pág. 1 de 1 )



## Ruta: extracellular region (Página 1 de 6)

Fuente: GO:CC | ID: GO:0005576 | Genes: 148 | p-valor ruta: 5.58e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
CXCL2	NA	UP	3.371	1.67e-155	4155.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
APOL6	NA	UP	3.196	9.56e-120	1648.2
STC2	NA	UP	2.729	3.17e-119	2626.1
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6

## Ruta: extracellular region (Página 2 de 6)

Fuente: GO:CC | ID: GO:0005576 | Genes: 148 | p-valor ruta: 5.58e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1
NEB	NA	DOWN	-2.754	5.16e-82	703.7
IFI35	NA	UP	2.237	9.59e-79	2236.7
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTX3	NA	UP	3.614	2.25e-68	237.4
CREB5	NA	UP	2.714	3.43e-62	649.9
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
ISG15	NA	UP	2.482	5.90e-57	3807.9
TUFT1	NA	UP	2.001	1.00e-55	1905.9
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
ALDH1L2	NA	UP	3.029	4.52e-55	257.3
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
ARRDC4	NA	UP	2.305	2.76e-44	631.5
IL15RA	NA	UP	2.045	1.16e-42	847.9
APOL4	NA	UP	3.489	1.37e-42	132.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5

## Ruta: extracellular region (Página 3 de 6)

Fuente: GO:CC | ID: GO:0005576 | Genes: 148 | p-valor ruta: 5.58e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
FUT3	NA	UP	2.139	2.84e-41	355.7
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
C1R	NA	UP	2.188	3.06e-32	258.8
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
EPN3	NA	DOWN	-2.294	4.66e-30	335.3
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
KRT6B	NA	UP	2.049	5.47e-24	321.4
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
ITGAM	NA	UP	2.447	1.39e-19	90.2
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
IL15	NA	UP	2.012	2.28e-17	116.8

## Ruta: extracellular region (Página 4 de 6)

Fuente: GO:CC | ID: GO:0005576 | Genes: 148 | p-valor ruta: 5.58e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DDC	NA	DOWN	-2.582	2.27e-16	72.0
INHBE	NA	UP	5.109	1.59e-15	37.3
RAET1L	NA	UP	2.665	2.71e-15	60.0
FLT3LG	NA	UP	2.346	6.32e-15	68.5
NLRP3	NA	UP	4.366	3.67e-13	29.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PDZD2	NA	UP	4.182	1.86e-12	28.7
MUC4	NA	UP	2.613	4.74e-12	55.4
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
C6orf58	NA	UP	2.512	2.12e-08	30.6
LRP2	NA	UP	3.144	3.22e-08	22.0
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
NGFR	NA	UP	2.337	3.33e-07	30.0
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SAA4	NA	UP	2.563	9.46e-07	21.9
WFDC5	NA	UP	5.168	1.07e-06	13.9
LRRN3	NA	UP	6.733	2.08e-06	9.4
COL4A1	NA	UP	6.589	5.89e-06	8.2
ACTBL2	NA	UP	2.242	5.97e-06	28.3
ICAM4	NA	UP	2.446	8.79e-06	22.0
ADAMTS6	NA	UP	2.602	8.90e-06	19.6

## Ruta: extracellular region (Página 5 de 6)

Fuente: GO:CC | ID: GO:0005576 | Genes: 148 | p-valor ruta: 5.58e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
MMP13	NA	UP	5.406	9.23e-06	11.1
SERPINA10	NA	UP	6.459	9.50e-06	7.5
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
NPTX1	NA	UP	2.102	1.13e-04	22.3
RHCG	NA	UP	2.107	1.84e-04	21.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
CPXM1	NA	UP	2.128	5.77e-04	16.0
KIT	NA	UP	3.650	6.24e-04	7.9
GAL3ST4	NA	UP	2.371	7.40e-04	12.5
CNTN4	NA	UP	4.928	9.17e-04	5.0
FLRT1	NA	UP	5.509	1.11e-03	3.8
PLA1A	NA	UP	3.622	1.35e-03	6.6
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
LHB	NA	UP	3.522	1.50e-03	7.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
IL17C	NA	UP	4.636	3.13e-03	4.1
GBP6	NA	UP	2.233	3.24e-03	11.2
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4

## Ruta: extracellular region (Página 6 de 6)

Fuente: GO:CC | ID: GO:0005576 | Genes: 148 | p-valor ruta: 5.58e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LY96	NA	UP	5.204	4.42e-03	3.4
KRT81	NA	UP	2.044	4.94e-03	15.2
EGFL6	NA	UP	3.034	6.01e-03	5.9
KRT9	NA	UP	4.973	6.24e-03	2.7
BMPER	NA	UP	4.906	6.28e-03	2.6
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
PRG2	NA	UP	2.073	1.32e-02	9.7
OLR1	NA	UP	2.655	1.81e-02	6.9
NPR3	NA	UP	2.789	1.87e-02	5.7
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8
SPRR2A	NA	UP	2.086	2.78e-02	7.8
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5
ADAMTS4	NA	UP	3.293	3.88e-02	3.0
CCL17	NA	UP	3.441	3.89e-02	2.9
NID2	NA	DOWN	-3.779	4.29e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: extracellular space (Página 1 de 5)

Fuente: GO:CC | ID: GO:0005615 | Genes: 123 | p-valor ruta: 9.71e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
CXCL2	NA	UP	3.371	1.67e-155	4155.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STC2	NA	UP	2.729	3.17e-119	2626.1
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
IFNB1	NA	UP	10.001	4.69e-95	1340.6
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
OAS3	NA	UP	2.942	1.13e-87	8674.1

## Ruta: extracellular space (Página 2 de 5)

Fuente: GO:CC | ID: GO:0005615 | Genes: 123 | p-valor ruta: 9.71e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NEB	NA	DOWN	-2.754	5.16e-82	703.7
IFI35	NA	UP	2.237	9.59e-79	2236.7
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PTX3	NA	UP	3.614	2.25e-68	237.4
CREB5	NA	UP	2.714	3.43e-62	649.9
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
ALDH1L2	NA	UP	3.029	4.52e-55	257.3
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
APOL4	NA	UP	3.489	1.37e-42	132.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
LTB	NA	UP	3.555	2.50e-41	150.4
FUT3	NA	UP	2.139	2.84e-41	355.7
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
EDN2	NA	UP	3.499	8.77e-31	90.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
EPN3	NA	DOWN	-2.294	4.66e-30	335.3

## Ruta: extracellular space (Página 3 de 5)

Fuente: GO:CC | ID: GO:0005615 | Genes: 123 | p-valor ruta: 9.71e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DUOX2	NA	UP	4.348	3.03e-29	71.2
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
KRT6B	NA	UP	2.049	5.47e-24	321.4
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
FGF19	NA	UP	3.931	5.59e-21	52.8
SOSTDC1	NA	DOWN	-2.301	1.81e-20	114.8
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
IL15	NA	UP	2.012	2.28e-17	116.8
DDC	NA	DOWN	-2.582	2.27e-16	72.0
INHBE	NA	UP	5.109	1.59e-15	37.3
RAET1L	NA	UP	2.665	2.71e-15	60.0
FLT3LG	NA	UP	2.346	6.32e-15	68.5
PCK1	NA	UP	4.419	1.17e-12	29.6
MUC4	NA	UP	2.613	4.74e-12	55.4
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3

## Ruta: extracellular space (Página 4 de 5)

Fuente: GO:CC | ID: GO:0005615 | Genes: 123 | p-valor ruta: 9.71e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C6orf58	NA	UP	2.512	2.12e-08	30.6
LRP2	NA	UP	3.144	3.22e-08	22.0
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
TNFSF14	NA	UP	2.748	3.71e-07	23.0
SAA4	NA	UP	2.563	9.46e-07	21.9
WFDC5	NA	UP	5.168	1.07e-06	13.9
LRRN3	NA	UP	6.733	2.08e-06	9.4
COL4A1	NA	UP	6.589	5.89e-06	8.2
ACTBL2	NA	UP	2.242	5.97e-06	28.3
MMP13	NA	UP	5.406	9.23e-06	11.1
SERPINA10	NA	UP	6.459	9.50e-06	7.5
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
RHCG	NA	UP	2.107	1.84e-04	21.0
COLEC10	NA	UP	2.878	4.02e-04	11.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
CPXM1	NA	UP	2.128	5.77e-04	16.0
KIT	NA	UP	3.650	6.24e-04	7.9
GAL3ST4	NA	UP	2.371	7.40e-04	12.5
FLRT1	NA	UP	5.509	1.11e-03	3.8
PLA1A	NA	UP	3.622	1.35e-03	6.6
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
LHB	NA	UP	3.522	1.50e-03	7.0

## Ruta: extracellular space (Página 5 de 5)

Fuente: GO:CC | ID: GO:0005615 | Genes: 123 | p-valor ruta: 9.71e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
IL17C	NA	UP	4.636	3.13e-03	4.1
GBP6	NA	UP	2.233	3.24e-03	11.2
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
KRT81	NA	UP	2.044	4.94e-03	15.2
EGFL6	NA	UP	3.034	6.01e-03	5.9
KRT9	NA	UP	4.973	6.24e-03	2.7
BMPER	NA	UP	4.906	6.28e-03	2.6
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
PRG2	NA	UP	2.073	1.32e-02	9.7
NPR3	NA	UP	2.789	1.87e-02	5.7
IL34	NA	UP	2.794	2.41e-02	4.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5
ADAMTS4	NA	UP	3.293	3.88e-02	3.0
CCL17	NA	UP	3.441	3.89e-02	2.9
NID2	NA	DOWN	-3.779	4.29e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: cell periphery (Página 1 de 8)

Fuente: GO:CC | ID: GO:0071944 | Genes: 192 | p-valor ruta: 2.96e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
LAMP3	NA	UP	3.644	2.72e-189	1627.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
RASGRP3	NA	UP	3.468	2.92e-82	392.1

## Ruta: cell periphery (Página 2 de 8)

Fuente: GO:CC | ID: GO:0071944 | Genes: 192 | p-valor ruta: 2.96e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
ADRB2	NA	UP	2.471	2.83e-79	954.4
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
PTX3	NA	UP	3.614	2.25e-68	237.4
AKAP12	NA	UP	2.306	2.56e-67	3768.0
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
NAV2	NA	UP	2.370	3.20e-51	765.9
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4

## Ruta: cell periphery (Página 3 de 8)

Fuente: GO:CC | ID: GO:0071944 | Genes: 192 | p-valor ruta: 2.96e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ARRDC4	NA	UP	2.305	2.76e-44	631.5
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
ANXA10	NA	DOWN	-2.270	2.83e-33	223.1
LRRC45	NA	DOWN	-2.449	3.12e-30	356.2
EPN3	NA	DOWN	-2.294	4.66e-30	335.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
LIFR	NA	UP	2.213	9.30e-24	226.1
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: cell periphery (Página 4 de 8)

Fuente: GO:CC | ID: GO:0071944 | Genes: 192 | p-valor ruta: 2.96e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IFITM2	NA	UP	2.649	6.22e-17	64.2
DUOXA2	NA	UP	4.650	3.36e-16	39.7
INHBE	NA	UP	5.109	1.59e-15	37.3
RAET1L	NA	UP	2.665	2.71e-15	60.0
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PDZD2	NA	UP	4.182	1.86e-12	28.7
MUC4	NA	UP	2.613	4.74e-12	55.4
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SCN3A	NA	UP	8.277	2.66e-10	27.0
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
ACTN2	NA	UP	3.956	7.01e-09	20.3
STX19	NA	UP	2.009	1.09e-08	99.7
LRP2	NA	UP	3.144	3.22e-08	22.0
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
KCNV1	NA	UP	2.402	2.10e-07	37.9
RAB26	NA	DOWN	-2.030	2.53e-07	50.4

## Ruta: cell periphery (Página 5 de 8)

Fuente: GO:CC | ID: GO:0071944 | Genes: 192 | p-valor ruta: 2.96e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
SYT1	NA	UP	2.659	1.62e-06	21.4
LRRN3	NA	UP	6.733	2.08e-06	9.4
KCNT2	NA	UP	2.262	3.16e-06	26.9
COL4A1	NA	UP	6.589	5.89e-06	8.2
ADCY4	NA	UP	2.271	8.12e-06	23.6
BEST1	NA	UP	3.553	8.47e-06	13.3
ICAM4	NA	UP	2.446	8.79e-06	22.0
ADAMTS6	NA	UP	2.602	8.90e-06	19.6
MMP13	NA	UP	5.406	9.23e-06	11.1
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
BEST3	NA	UP	2.070	3.26e-05	23.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
XKR9	NA	UP	3.541	5.84e-05	11.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
RHCG	NA	UP	2.107	1.84e-04	21.0

## Ruta: cell periphery (Página 6 de 8)

Fuente: GO:CC | ID: GO:0071944 | Genes: 192 | p-valor ruta: 2.96e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PTGER2	NA	UP	3.006	1.95e-04	11.0
MPZ	NA	UP	2.002	2.88e-04	19.4
TRPC4	NA	UP	5.730	3.71e-04	4.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
SLC38A4	NA	DOWN	-2.630	6.25e-04	12.4
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
CNTN4	NA	UP	4.928	9.17e-04	5.0
SLC16A6	NA	UP	3.375	9.62e-04	7.8
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
KCNH3	NA	DOWN	-2.243	1.94e-03	12.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
SLC17A4	NA	DOWN	-2.298	2.32e-03	11.5
KCNN1	NA	UP	3.883	2.55e-03	6.2
SUSD3	NA	UP	2.011	2.77e-03	13.3
SIDT1	NA	UP	2.642	2.81e-03	8.6
SLCO5A1	NA	UP	2.814	2.87e-03	7.7

## Ruta: cell periphery (Página 7 de 8)

Fuente: GO:CC | ID: GO:0071944 | Genes: 192 | p-valor ruta: 2.96e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IPCEF1	NA	UP	4.035	3.69e-03	4.9
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
SDK2	NA	UP	2.715	5.83e-03	7.9
EGFL6	NA	UP	3.034	6.01e-03	5.9
BMPER	NA	UP	4.906	6.28e-03	2.6
P2RY6	NA	UP	2.536	8.76e-03	7.0
VWF	NA	UP	3.390	1.16e-02	4.6
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
PRG2	NA	UP	2.073	1.32e-02	9.7
SLC9B1	NA	UP	4.128	1.36e-02	3.1
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
SLC6A7	NA	UP	3.822	1.73e-02	3.5
CAMK1G	NA	UP	4.059	1.79e-02	2.8
OLR1	NA	UP	2.655	1.81e-02	6.9
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7

## Ruta: cell periphery (Página 8 de 8)

Fuente: GO:CC | ID: GO:0071944 | Genes: 192 | p-valor ruta: 2.96e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SLC9C2	NA	UP	3.943	2.11e-02	2.8
TMEM106A	NA	UP	2.485	2.20e-02	7.2
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
SPRR2A	NA	UP	2.086	2.78e-02	7.8
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
INSC	NA	UP	3.872	3.01e-02	2.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5
KCNE4	NA	UP	2.337	3.37e-02	5.7
DLG2	NA	UP	3.028	3.83e-02	3.8
ADAMTS4	NA	UP	3.293	3.88e-02	3.0
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
NID2	NA	DOWN	-3.779	4.29e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: cytoplasm (Página 1 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
CYP1A1	NA	UP	6.086	6.00e-198	811.0
IRF1	NA	UP	3.512	7.87e-194	2808.9
LAMP3	NA	UP	3.644	2.72e-189	1627.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
IFI44L	NA	UP	4.088	1.50e-181	1679.8
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8

## Ruta: cytoplasm (Página 2 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CMPK2	NA	UP	4.677	1.14e-162	1687.4
DUSP1	NA	UP	3.521	2.54e-161	1829.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNFAIP2	NA	UP	3.214	1.01e-156	3768.7
DDX60L	NA	UP	3.765	2.46e-147	1804.9
USP18	NA	UP	3.900	1.42e-145	1151.2
INHBA	NA	UP	3.514	2.31e-143	1743.6
G0S2	NA	UP	3.773	6.27e-143	896.4
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
SAMD9L	NA	UP	3.487	2.90e-126	1768.5
HERC5	NA	UP	3.386	1.24e-123	1735.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
IKZF3	NA	UP	3.163	1.21e-120	1046.8
APOL6	NA	UP	3.196	9.56e-120	1648.2
PARP14	NA	UP	2.977	1.79e-119	2649.9
STC2	NA	UP	2.729	3.17e-119	2626.1
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
ASNS	NA	UP	2.919	1.59e-113	1627.6
PLAT	NA	UP	2.447	4.98e-113	6662.1
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
IFI44	NA	UP	3.036	1.35e-108	3423.4

## Ruta: cytoplasm (Página 3 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HELZ2	NA	UP	3.181	3.07e-108	5185.4
RTP4	NA	UP	3.457	2.00e-107	589.0
SERPINE1	NA	UP	4.807	1.12e-104	435.1
ZFP36	NA	UP	2.944	7.57e-104	1721.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
RASGRP3	NA	UP	3.468	2.92e-82	392.1
NEB	NA	DOWN	-2.754	5.16e-82	703.7
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6

## Ruta: cytoplasm (Página 4 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
SAMD9	NA	UP	2.877	2.46e-77	6330.7
PARP9	NA	UP	2.449	1.75e-75	2354.5
KRTAP2-3	NA	UP	2.722	7.97e-75	878.4
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
HSH2D	NA	UP	2.613	6.29e-73	813.8
DAPP1	NA	UP	2.456	1.42e-72	922.6
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
NR1D1	NA	UP	2.475	2.08e-68	1229.5
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
TDRD7	NA	UP	2.129	5.72e-65	1011.2

## Ruta: cytoplasm (Página 5 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NEURL3	NA	UP	2.464	1.53e-62	758.9
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
TUFT1	NA	UP	2.001	1.00e-55	1905.9
FOSB	NA	UP	3.144	1.32e-55	267.7
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
ALDH1L2	NA	UP	3.029	4.52e-55	257.3
PHLDB2	NA	UP	2.315	8.68e-55	764.5
CYP1B1	NA	UP	2.786	9.33e-53	766.0
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
THEMIS2	NA	UP	2.550	2.88e-50	403.0
PCK2	NA	UP	2.226	5.13e-50	969.9
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7

## Ruta: cytoplasm (Página 6 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ARRDC4	NA	UP	2.305	2.76e-44	631.5
PER1	NA	UP	2.501	8.94e-44	469.6
IL15RA	NA	UP	2.045	1.16e-42	847.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOL3	NA	UP	2.918	2.49e-41	209.0
FUT3	NA	UP	2.139	2.84e-41	355.7
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
ULBP1	NA	UP	3.138	2.70e-38	151.4
ZC3H12C	NA	UP	2.109	3.86e-36	308.6
MT2A	NA	UP	2.437	2.24e-35	363.0
DUSP8	NA	UP	2.088	3.69e-35	551.5
SNRNP25	NA	DOWN	-2.131	4.01e-34	420.7
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
ANXA10	NA	DOWN	-2.270	2.83e-33	223.1
HDAC9	NA	UP	2.292	4.51e-32	2003.2
PRDM1	NA	UP	3.525	5.98e-31	99.0
BACH2	NA	UP	2.222	2.18e-30	209.0
LRRC45	NA	DOWN	-2.449	3.12e-30	356.2
PPM1K	NA	UP	2.192	3.89e-30	395.9
EPN3	NA	DOWN	-2.294	4.66e-30	335.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2

## Ruta: cytoplasm (Página 7 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SERPINB7	NA	UP	2.796	1.04e-28	127.7
IL12A	NA	UP	3.852	1.95e-28	83.7
KIF21B	NA	UP	2.131	3.74e-27	240.5
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
BCL2L14	NA	UP	2.782	8.63e-26	122.3
MAST4	NA	UP	2.184	1.21e-25	197.5
HIVEP1	NA	UP	2.014	1.06e-24	282.1
KRT6B	NA	UP	2.049	5.47e-24	321.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
FGF19	NA	UP	3.931	5.59e-21	52.8
DDO	NA	UP	2.846	3.84e-20	82.4
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
GIMAP2	NA	UP	2.542	5.46e-18	86.3
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: cytoplasm (Página 8 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
DDC	NA	DOWN	-2.582	2.27e-16	72.0
DUOXA2	NA	UP	4.650	3.36e-16	39.7
ZBTB20	NA	UP	3.440	1.24e-15	47.6
RAET1L	NA	UP	2.665	2.71e-15	60.0
HOGA1	NA	DOWN	-2.098	2.81e-15	96.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
EGR2	NA	UP	3.090	6.72e-15	43.7
DNAAF3	NA	DOWN	-2.041	1.75e-14	101.4
DNAH17	NA	UP	3.324	3.42e-13	38.8
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PDZD2	NA	UP	4.182	1.86e-12	28.7
MUC4	NA	UP	2.613	4.74e-12	55.4
ZEB2	NA	UP	3.419	5.95e-12	30.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
PPP4R4	NA	UP	3.423	6.94e-11	30.7
SCN3A	NA	UP	8.277	2.66e-10	27.0

## Ruta: cytoplasm (Página 9 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
APOBEC3D	NA	UP	2.051	7.01e-10	51.0
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
NDUFA4L2	NA	UP	3.705	8.81e-09	20.2
STX19	NA	UP	2.009	1.09e-08	99.7
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
SULT1C2	NA	UP	2.136	2.10e-07	36.2
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
AHRR	NA	UP	2.180	3.48e-07	33.9
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
BCAT1	NA	UP	2.723	7.42e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4

## Ruta: cytoplasm (Página 10 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
COX6B2	NA	UP	2.208	1.76e-06	27.2
NUPR1	NA	UP	3.660	1.78e-06	14.5
TAGAP	NA	UP	3.201	2.52e-06	16.1
HSD17B14	NA	UP	2.529	3.30e-06	21.4
RAB30	NA	UP	2.024	5.27e-06	28.7
COL4A1	NA	UP	6.589	5.89e-06	8.2
ACTBL2	NA	UP	2.242	5.97e-06	28.3
ADCY4	NA	UP	2.271	8.12e-06	23.6
BEST1	NA	UP	3.553	8.47e-06	13.3
SERPINA10	NA	UP	6.459	9.50e-06	7.5
UBASH3A	NA	UP	5.845	1.05e-05	9.8
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
RAB36	NA	DOWN	-2.063	2.15e-05	24.7
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TEX15	NA	DOWN	-2.648	4.18e-05	16.6
SDS	NA	UP	4.527	5.38e-05	9.4
GLTPD2	NA	DOWN	-2.633	7.44e-05	17.8
PKP1	NA	UP	3.076	9.16e-05	12.8
NPTX1	NA	UP	2.102	1.13e-04	22.3
KIF6	NA	UP	4.867	1.75e-04	7.8
RHCG	NA	UP	2.107	1.84e-04	21.0
SYNPO2	NA	UP	3.603	1.95e-04	9.0
GFPT2	NA	UP	2.651	2.37e-04	12.7
UBQLNL	NA	UP	3.875	3.33e-04	7.9

## Ruta: cytoplasm (Página 11 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRPC4	NA	UP	5.730	3.71e-04	4.5
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
RBMS3	NA	UP	2.303	4.11e-04	18.6
SLC5A5	NA	UP	4.542	4.62e-04	6.8
CCDC96	NA	DOWN	-2.033	4.86e-04	19.3
KIT	NA	UP	3.650	6.24e-04	7.9
EXOC3L1	NA	UP	3.152	6.83e-04	8.6
GAL3ST4	NA	UP	2.371	7.40e-04	12.5
HAND1	NA	UP	4.966	8.42e-04	5.1
ENKUR	NA	UP	3.518	8.61e-04	9.0
TMEM160	NA	DOWN	-2.039	1.02e-03	686.6
FLRT1	NA	UP	5.509	1.11e-03	3.8
PLA1A	NA	UP	3.622	1.35e-03	6.6
RNF152	NA	UP	3.325	1.37e-03	7.5
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
LHB	NA	UP	3.522	1.50e-03	7.0
RUFY4	NA	UP	4.136	2.15e-03	6.0
LGR6	NA	UP	3.915	2.25e-03	6.0
PEX5L	NA	UP	3.321	2.40e-03	7.0
VASH1	NA	DOWN	-2.576	2.72e-03	9.0
PATL2	NA	UP	2.215	2.72e-03	12.1
SIDT1	NA	UP	2.642	2.81e-03	8.6
GBP6	NA	UP	2.233	3.24e-03	11.2
IPCEF1	NA	UP	4.035	3.69e-03	4.9

## Ruta: cytoplasm (Página 12 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SRGN	NA	UP	2.093	3.80e-03	11.0
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
KRT81	NA	UP	2.044	4.94e-03	15.2
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
RP1L1	NA	UP	2.162	5.43e-03	10.3
SLC25A18	NA	DOWN	-2.816	5.67e-03	7.5
KRT9	NA	UP	4.973	6.24e-03	2.7
RNF150	NA	UP	4.240	1.04e-02	3.1
CPED1	NA	UP	2.030	1.13e-02	9.6
VWF	NA	UP	3.390	1.16e-02	4.6
THBD	NA	UP	2.330	1.23e-02	7.3
PRG2	NA	UP	2.073	1.32e-02	9.7
RET	NA	UP	2.793	1.44e-02	5.5
RANBP3L	NA	UP	4.634	1.47e-02	2.2
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
TTLL6	NA	UP	2.577	1.74e-02	6.7
CAMK1G	NA	UP	4.059	1.79e-02	2.8
MSTO1	NA	DOWN	-2.110	1.81e-02	8.3
OLR1	NA	UP	2.655	1.81e-02	6.9
TBCEL	NA	UP	2.318	1.82e-02	7.1
FBXW10	NA	UP	2.019	1.90e-02	9.5

## Ruta: cytoplasm (Página 13 de 13)

Fuente: GO:CC | ID: GO:0005737 | Genes: 322 | p-valor ruta: 4.71e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
RFPL1	NA	UP	3.259	2.06e-02	4.1
IKZF1	NA	UP	2.283	2.21e-02	6.8
CLSTN2	NA	UP	2.773	2.49e-02	4.9
CELF6	NA	UP	2.403	2.65e-02	5.6
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
SPRR2A	NA	UP	2.086	2.78e-02	7.8
NOTUM	NA	DOWN	-3.868	2.99e-02	3.0
INSC	NA	UP	3.872	3.01e-02	2.4
HSD11B1	NA	UP	2.341	3.03e-02	5.6
SALL1	NA	UP	4.345	3.20e-02	1.8
TRIM69	NA	UP	3.519	3.21e-02	3.0
CR1L	NA	UP	3.479	3.30e-02	3.5
DLG2	NA	UP	3.028	3.83e-02	3.8
TP63	NA	UP	3.788	4.09e-02	2.3
PPM1E	NA	UP	3.810	4.20e-02	2.4
PPEF1	NA	UP	3.725	4.31e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
FGF18	NA	UP	2.038	4.86e-02	6.1
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: plasma membrane (Página 1 de 8)

Fuente: GO:CC | ID: GO:0005886 | Genes: 176 | p-valor ruta: 5.22e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
LAMP3	NA	UP	3.644	2.72e-189	1627.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
IFITM1	NA	UP	3.632	5.16e-130	784.8
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PARP14	NA	UP	2.977	1.79e-119	2649.9
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
RASGRP3	NA	UP	3.468	2.92e-82	392.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0

## Ruta: plasma membrane (Página 2 de 8)

Fuente: GO:CC | ID: GO:0005886 | Genes: 176 | p-valor ruta: 5.22e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ADRB2	NA	UP	2.471	2.83e-79	954.4
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
ARRDC4	NA	UP	2.305	2.76e-44	631.5
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3

## Ruta: plasma membrane (Página 3 de 8)

Fuente: GO:CC | ID: GO:0005886 | Genes: 176 | p-valor ruta: 5.22e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ULBP1	NA	UP	3.138	2.70e-38	151.4
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
ANXA10	NA	DOWN	-2.270	2.83e-33	223.1
LRRC45	NA	DOWN	-2.449	3.12e-30	356.2
EPN3	NA	DOWN	-2.294	4.66e-30	335.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
LIFR	NA	UP	2.213	9.30e-24	226.1
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
IFITM2	NA	UP	2.649	6.22e-17	64.2
DUOXA2	NA	UP	4.650	3.36e-16	39.7
RAET1L	NA	UP	2.665	2.71e-15	60.0
BDKRB2	NA	UP	2.797	5.56e-15	55.1

## Ruta: plasma membrane (Página 4 de 8)

Fuente: GO:CC | ID: GO:0005886 | Genes: 176 | p-valor ruta: 5.22e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
FLT3LG	NA	UP	2.346	6.32e-15	68.5
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PDZD2	NA	UP	4.182	1.86e-12	28.7
MUC4	NA	UP	2.613	4.74e-12	55.4
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SCN3A	NA	UP	8.277	2.66e-10	27.0
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
ACTN2	NA	UP	3.956	7.01e-09	20.3
STX19	NA	UP	2.009	1.09e-08	99.7
LRP2	NA	UP	3.144	3.22e-08	22.0
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
KCNV1	NA	UP	2.402	2.10e-07	37.9
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5

## Ruta: plasma membrane (Página 5 de 8)

Fuente: GO:CC | ID: GO:0005886 | Genes: 176 | p-valor ruta: 5.22e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SYT1	NA	UP	2.659	1.62e-06	21.4
KCNT2	NA	UP	2.262	3.16e-06	26.9
ADCY4	NA	UP	2.271	8.12e-06	23.6
BEST1	NA	UP	3.553	8.47e-06	13.3
ICAM4	NA	UP	2.446	8.79e-06	22.0
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
BEST3	NA	UP	2.070	3.26e-05	23.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
XKR9	NA	UP	3.541	5.84e-05	11.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
RHCG	NA	UP	2.107	1.84e-04	21.0
PTGER2	NA	UP	3.006	1.95e-04	11.0
MPZ	NA	UP	2.002	2.88e-04	19.4
TRPC4	NA	UP	5.730	3.71e-04	4.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
SLC38A4	NA	DOWN	-2.630	6.25e-04	12.4
CNTN4	NA	UP	4.928	9.17e-04	5.0

## Ruta: plasma membrane (Página 6 de 8)

Fuente: GO:CC | ID: GO:0005886 | Genes: 176 | p-valor ruta: 5.22e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SLC16A6	NA	UP	3.375	9.62e-04	7.8
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
KCNH3	NA	DOWN	-2.243	1.94e-03	12.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
SLC17A4	NA	DOWN	-2.298	2.32e-03	11.5
KCNN1	NA	UP	3.883	2.55e-03	6.2
SUSD3	NA	UP	2.011	2.77e-03	13.3
SIDT1	NA	UP	2.642	2.81e-03	8.6
SLCO5A1	NA	UP	2.814	2.87e-03	7.7
IPCEF1	NA	UP	4.035	3.69e-03	4.9
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
SDK2	NA	UP	2.715	5.83e-03	7.9
P2RY6	NA	UP	2.536	8.76e-03	7.0
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
SLC9B1	NA	UP	4.128	1.36e-02	3.1
RET	NA	UP	2.793	1.44e-02	5.5

## Ruta: plasma membrane (Página 7 de 8)

Fuente: GO:CC | ID: GO:0005886 | Genes: 176 | p-valor ruta: 5.22e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
SLC6A7	NA	UP	3.822	1.73e-02	3.5
CAMK1G	NA	UP	4.059	1.79e-02	2.8
OLR1	NA	UP	2.655	1.81e-02	6.9
GLP2R	NA	UP	2.220	1.86e-02	8.9
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
SLC9C2	NA	UP	3.943	2.11e-02	2.8
TMEM106A	NA	UP	2.485	2.20e-02	7.2
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
SPRR2A	NA	UP	2.086	2.78e-02	7.8
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
INSC	NA	UP	3.872	3.01e-02	2.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CR1L	NA	UP	3.479	3.30e-02	3.5
KCNE4	NA	UP	2.337	3.37e-02	5.7
DLG2	NA	UP	3.028	3.83e-02	3.8
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
NID2	NA	DOWN	-3.779	4.29e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: plasma membrane (Página 8 de 8)

Fuente: GO:CC | ID: GO:0005886 | Genes: 176 | p-valor ruta: 5.22e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SRMS	NA	UP	3.88	4.55e-02	2.3

## Ruta: cell surface (Página 1 de 2)

Fuente: GO:CC | ID: GO:0009986 | Genes: 44 | p-valor ruta: 7.1e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
LAMP3	NA	UP	3.644	2.72e-189	1627.7
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
PLAT	NA	UP	2.447	4.98e-113	6662.1
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
THBS1	NA	UP	2.656	1.05e-77	3791.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
HBEGF	NA	UP	2.602	3.10e-57	415.2
CD69	NA	UP	3.112	5.99e-57	257.2
IL15RA	NA	UP	2.045	1.16e-42	847.9
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
DUOX2	NA	UP	4.348	3.03e-29	71.2
VCAM1	NA	UP	4.737	4.28e-26	66.5
LIFR	NA	UP	2.213	9.30e-24	226.1
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
BST2	NA	UP	4.284	3.82e-19	50.8
RAET1L	NA	UP	2.665	2.71e-15	60.0
FLT3LG	NA	UP	2.346	6.32e-15	68.5
DUOX1	NA	UP	3.131	5.18e-10	27.1
CLEC4E	NA	UP	3.620	4.75e-09	26.0

## Ruta: cell surface (Página 2 de 2)

Fuente: GO:CC | ID: GO:0009986 | Genes: 44 | p-valor ruta: 7.1e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LRP2	NA	UP	3.144	3.22e-08	22.0
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
NGFR	NA	UP	2.337	3.33e-07	30.0
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
TRPC4	NA	UP	5.730	3.71e-04	4.5
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
CXCL9	NA	UP	4.099	4.37e-04	26.3
KIT	NA	UP	3.650	6.24e-04	7.9
CEACAM20	NA	UP	5.412	1.17e-03	3.6
SLC1A2	NA	UP	2.752	2.07e-03	8.4
HRG	NA	UP	2.971	4.00e-03	6.9
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
CLSTN2	NA	UP	2.773	2.49e-02	4.9
IL13RA2	NA	UP	2.568	3.02e-02	4.7
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: cytosol (Página 1 de 7)

Fuente: GO:CC | ID: GO:0005829 | Genes: 155 | p-valor ruta: 4.72e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
IRF1	NA	UP	3.512	7.87e-194	2808.9
GBP4	NA	UP	4.422	6.95e-185	1175.0
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
HERC5	NA	UP	3.386	1.24e-123	1735.7
IKZF3	NA	UP	3.163	1.21e-120	1046.8
PARP14	NA	UP	2.977	1.79e-119	2649.9
KLF6	NA	UP	2.653	7.59e-116	4943.3
IFI16	NA	UP	3.151	2.12e-114	2583.4

## Ruta: cytosol (Página 2 de 7)

Fuente: GO:CC | ID: GO:0005829 | Genes: 155 | p-valor ruta: 4.72e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ASNS	NA	UP	2.919	1.59e-113	1627.6
XAF1	NA	UP	4.580	3.19e-111	427.9
IDO1	NA	UP	4.167	4.38e-109	394.2
HELZ2	NA	UP	3.181	3.07e-108	5185.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
ZBP1	NA	UP	6.242	1.22e-99	349.5
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
ZC3HAV1	NA	UP	2.427	2.20e-95	2512.8
IRAK2	NA	UP	2.666	3.46e-95	1164.5
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
TRAF1	NA	UP	4.730	5.65e-84	258.2
NEB	NA	DOWN	-2.754	5.16e-82	703.7
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
KLF4	NA	UP	2.704	2.52e-79	645.9
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
DDX60	NA	UP	3.015	7.43e-79	1999.9
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
SAMD9	NA	UP	2.877	2.46e-77	6330.7

## Ruta: cytosol (Página 3 de 7)

Fuente: GO:CC | ID: GO:0005829 | Genes: 155 | p-valor ruta: 4.72e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP9	NA	UP	2.449	1.75e-75	2354.5
KRTAP2-3	NA	UP	2.722	7.97e-75	878.4
RNF213	NA	UP	2.528	1.50e-73	6034.1
DAPP1	NA	UP	2.456	1.42e-72	922.6
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
ANKRD1	NA	UP	3.496	4.72e-69	335.9
STAT1	NA	UP	2.519	1.61e-68	9528.0
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
RND1	NA	UP	2.840	1.60e-62	337.7
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
CTH	NA	UP	2.488	2.75e-57	412.1
BBC3	NA	UP	2.829	3.65e-57	503.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
FOSB	NA	UP	3.144	1.32e-55	267.7
PHLDB2	NA	UP	2.315	8.68e-55	764.5
PARP10	NA	UP	2.093	5.71e-52	2376.2
PDE4B	NA	UP	3.818	7.08e-52	171.4
XRN1	NA	UP	2.115	6.38e-50	984.6
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
CH25H	NA	UP	7.817	1.04e-46	242.7

## Ruta: cytosol (Página 4 de 7)

Fuente: GO:CC | ID: GO:0005829 | Genes: 155 | p-valor ruta: 4.72e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PER1	NA	UP	2.501	8.94e-44	469.6
BIRC3	NA	UP	2.146	8.30e-42	2602.9
APOBEC3G	NA	UP	2.120	1.48e-40	359.9
ULBP1	NA	UP	3.138	2.70e-38	151.4
MT2A	NA	UP	2.437	2.24e-35	363.0
SNRNP25	NA	DOWN	-2.131	4.01e-34	420.7
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
BACH2	NA	UP	2.222	2.18e-30	209.0
LRRC45	NA	DOWN	-2.449	3.12e-30	356.2
SPRY2	NA	UP	2.250	1.05e-29	211.9
TYMP	NA	UP	2.001	2.11e-29	872.8
DUOX2	NA	UP	4.348	3.03e-29	71.2
BCL3	NA	UP	2.067	4.65e-26	500.4
BCL2L14	NA	UP	2.782	8.63e-26	122.3
HIVEP1	NA	UP	2.014	1.06e-24	282.1
KRT6B	NA	UP	2.049	5.47e-24	321.4
CHAC1	NA	UP	3.022	3.43e-23	111.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
BCL2A1	NA	UP	4.192	1.64e-21	55.1
DDO	NA	UP	2.846	3.84e-20	82.4
NOD2	NA	UP	2.981	1.19e-19	80.5
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: cytosol (Página 5 de 7)

Fuente: GO:CC | ID: GO:0005829 | Genes: 155 | p-valor ruta: 4.72e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15	NA	UP	2.012	2.28e-17	116.8
DDC	NA	DOWN	-2.582	2.27e-16	72.0
DUOXA2	NA	UP	4.650	3.36e-16	39.7
FLT3LG	NA	UP	2.346	6.32e-15	68.5
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PCK1	NA	UP	4.419	1.17e-12	29.6
PDZD2	NA	UP	4.182	1.86e-12	28.7
ZEB2	NA	UP	3.419	5.95e-12	30.5
PPP4R4	NA	UP	3.423	6.94e-11	30.7
CYTH4	NA	UP	2.691	3.08e-10	36.2
SSTR2	NA	UP	2.031	8.80e-10	53.9
NLRP1	NA	UP	5.692	4.64e-09	21.6
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
SOCS1	NA	UP	2.012	6.54e-08	82.5
SULT1C2	NA	UP	2.136	2.10e-07	36.2
NGFR	NA	UP	2.337	3.33e-07	30.0
AHRR	NA	UP	2.180	3.48e-07	33.9
IL10RA	NA	UP	3.172	3.66e-07	18.8
LST1	NA	UP	6.916	7.00e-07	10.5
BCAT1	NA	UP	2.723	7.42e-07	22.9
RUNX2	NA	UP	3.983	1.50e-06	15.2
SYT1	NA	UP	2.659	1.62e-06	21.4

## Ruta: cytosol (Página 6 de 7)

Fuente: GO:CC | ID: GO:0005829 | Genes: 155 | p-valor ruta: 4.72e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TAGAP	NA	UP	3.201	2.52e-06	16.1
HSD17B14	NA	UP	2.529	3.30e-06	21.4
BEST1	NA	UP	3.553	8.47e-06	13.3
UBASH3A	NA	UP	5.845	1.05e-05	9.8
SDS	NA	UP	4.527	5.38e-05	9.4
GLTPD2	NA	DOWN	-2.633	7.44e-05	17.8
SYNPO2	NA	UP	3.603	1.95e-04	9.0
GFPT2	NA	UP	2.651	2.37e-04	12.7
UBQLNL	NA	UP	3.875	3.33e-04	7.9
NCALD	NA	UP	2.037	3.82e-04	17.1
RBMS3	NA	UP	2.303	4.11e-04	18.6
PEX5L	NA	UP	3.321	2.40e-03	7.0
KRT81	NA	UP	2.044	4.94e-03	15.2
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
KRT9	NA	UP	4.973	6.24e-03	2.7
VAV1	NA	UP	2.118	1.54e-02	7.9
TTLL6	NA	UP	2.577	1.74e-02	6.7
MSTO1	NA	DOWN	-2.110	1.81e-02	8.3
FBXW10	NA	UP	2.019	1.90e-02	9.5
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
RFPL1	NA	UP	3.259	2.06e-02	4.1
IKZF1	NA	UP	2.283	2.21e-02	6.8
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
SPRR2A	NA	UP	2.086	2.78e-02	7.8
TRIM69	NA	UP	3.519	3.21e-02	3.0

## Ruta: cytosol (Página 7 de 7)

Fuente: GO:CC | ID: GO:0005829 | Genes: 155 | p-valor ruta: 4.72e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
DLG2	NA	UP	3.028	3.83e-02	3.8
PPEF1	NA	UP	3.725	4.31e-02	2.4
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3
PROX1	NA	UP	2.195	4.92e-02	5.7

## Ruta: external side of plasma membrane

Fuente: GO:CC | ID: GO:0009897 | Genes: 23 | p–valor ruta: 5.38e–03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ICAM1	NA	UP	3.652	3.11e–204	19095.5
CXCL10	NA	UP	6.079	8.12e–195	783.4
TNF	NA	UP	7.712	3.81e–103	573.0
CD274	NA	UP	5.204	1.23e–98	314.4
THBS1	NA	UP	2.656	1.05e–77	3791.3
SEMA7A	NA	UP	2.329	3.91e–69	7576.6
CD69	NA	UP	3.112	5.99e–57	257.2
ULBP1	NA	UP	3.138	2.70e–38	151.4
VCAM1	NA	UP	4.737	4.28e–26	66.5
LIFR	NA	UP	2.213	9.30e–24	226.1
ITGAM	NA	UP	2.447	1.39e–19	90.2
RAET1L	NA	UP	2.665	2.71e–15	60.0
CLEC4E	NA	UP	3.620	4.75e–09	26.0
LRP2	NA	UP	3.144	3.22e–08	22.0
TNFRSF9	NA	UP	4.642	8.23e–08	94.1
SELE	NA	UP	5.745	2.05e–05	9.0
COLEC10	NA	UP	2.878	4.02e–04	11.6
PDCD1LG2	NA	UP	4.546	4.10e–04	7.2
CXCL9	NA	UP	4.099	4.37e–04	26.3
KIT	NA	UP	3.650	6.24e–04	7.9
THBD	NA	UP	2.330	1.23e–02	7.3
SCUBE1	NA	UP	2.508	1.26e–02	8.4
IL13RA2	NA	UP	2.568	3.02e–02	4.7

## Ruta: membrane (Página 1 de 10)

Fuente: GO:CC | ID: GO:0016020 | Genes: 248 | p-valor ruta: 1.88e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL6	NA	UP	6.060	0.00e+00	1698.5
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
PPP1R15A	NA	UP	3.879	2.08e-241	8348.0
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL10	NA	UP	6.079	8.12e-195	783.4
LAMP3	NA	UP	3.644	2.72e-189	1627.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
IFITM1	NA	UP	3.632	5.16e-130	784.8
ZNFX1	NA	UP	2.719	5.31e-128	6490.5
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TAP1	NA	UP	2.707	8.35e-123	5228.7
APOL6	NA	UP	3.196	9.56e-120	1648.2
PARP14	NA	UP	2.977	1.79e-119	2649.9
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
HELZ2	NA	UP	3.181	3.07e-108	5185.4

## Ruta: membrane (Página 2 de 10)

Fuente: GO:CC | ID: GO:0016020 | Genes: 248 | p-valor ruta: 1.88e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
RTP4	NA	UP	3.457	2.00e-107	589.0
TMEM140	NA	UP	3.747	6.77e-107	475.4
SERPINE1	NA	UP	4.807	1.12e-104	435.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
OAS3	NA	UP	2.942	1.13e-87	8674.1
TM4SF4	NA	DOWN	-2.482	1.83e-87	1021.7
TRAF1	NA	UP	4.730	5.65e-84	258.2
RASGRP3	NA	UP	3.468	2.92e-82	392.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
ADRB2	NA	UP	2.471	2.83e-79	954.4
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6

## Ruta: membrane (Página 3 de 10)

Fuente: GO:CC | ID: GO:0016020 | Genes: 248 | p-valor ruta: 1.88e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PARP9	NA	UP	2.449	1.75e-75	2354.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
DAPP1	NA	UP	2.456	1.42e-72	922.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
PNPT1	NA	UP	2.411	6.12e-71	2101.8
PML	NA	UP	2.208	2.84e-70	2901.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
OPTN	NA	UP	2.002	1.08e-67	1911.6
AKAP12	NA	UP	2.306	2.56e-67	3768.0
RND1	NA	UP	2.840	1.60e-62	337.7
PTAFR	NA	UP	3.014	4.62e-62	338.1
NEDD4	NA	UP	2.433	4.99e-60	1678.5
HBEGF	NA	UP	2.602	3.10e-57	415.2
BBC3	NA	UP	2.829	3.65e-57	503.1
CD69	NA	UP	3.112	5.99e-57	257.2
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
PHLDB2	NA	UP	2.315	8.68e-55	764.5
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CYP1B1	NA	UP	2.786	9.33e-53	766.0
C1QTNF1	NA	UP	3.006	3.30e-52	250.8
PDE4B	NA	UP	3.818	7.08e-52	171.4
XRN1	NA	UP	2.115	6.38e-50	984.6
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0

## Ruta: membrane (Página 4 de 10)

Fuente: GO:CC | ID: GO:0016020 | Genes: 248 | p-valor ruta: 1.88e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CH25H	NA	UP	7.817	1.04e-46	242.7
ARRDC4	NA	UP	2.305	2.76e-44	631.5
IL15RA	NA	UP	2.045	1.16e-42	847.9
SEMA3A	NA	UP	2.276	5.71e-42	512.5
APOL3	NA	UP	2.918	2.49e-41	209.0
LTB	NA	UP	3.555	2.50e-41	150.4
FUT3	NA	UP	2.139	2.84e-41	355.7
BMP2	NA	UP	2.237	3.69e-40	325.3
ULBP1	NA	UP	3.138	2.70e-38	151.4
PHF11	NA	UP	2.211	3.12e-37	302.1
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
ANXA10	NA	DOWN	-2.270	2.83e-33	223.1
LRRC45	NA	DOWN	-2.449	3.12e-30	356.2
EPN3	NA	DOWN	-2.294	4.66e-30	335.3
SPRY2	NA	UP	2.250	1.05e-29	211.9
DUOX2	NA	UP	4.348	3.03e-29	71.2
VCAM1	NA	UP	4.737	4.28e-26	66.5
FUT1	NA	UP	2.765	4.55e-26	104.9
BCL3	NA	UP	2.067	4.65e-26	500.4
RASGEF1B	NA	UP	2.113	4.74e-26	182.0
BCL2L14	NA	UP	2.782	8.63e-26	122.3
LIFR	NA	UP	2.213	9.30e-24	226.1
TLR3	NA	UP	2.508	1.99e-22	111.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1

## Ruta: membrane (Página 5 de 10)

Fuente: GO:CC | ID: GO:0016020 | Genes: 248 | p-valor ruta: 1.88e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LAMA2	NA	UP	2.355	4.82e-21	125.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SCGN	NA	DOWN	-3.468	1.52e-19	60.9
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
GIMAP2	NA	UP	2.542	5.46e-18	86.3
JAK2	NA	UP	2.081	1.26e-17	123.4
SYT12	NA	DOWN	-2.637	2.26e-17	74.3
FSD1L	NA	UP	2.523	4.34e-17	83.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
DUOXA2	NA	UP	4.650	3.36e-16	39.7
RAET1L	NA	UP	2.665	2.71e-15	60.0
NAV3	NA	UP	2.285	2.77e-15	84.4
HOGA1	NA	DOWN	-2.098	2.81e-15	96.4
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
KLF9	NA	UP	2.555	7.01e-13	66.8
PDZD2	NA	UP	4.182	1.86e-12	28.7
MUC4	NA	UP	2.613	4.74e-12	55.4
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SCN3A	NA	UP	8.277	2.66e-10	27.0

## Ruta: membrane (Página 6 de 10)

Fuente: GO:CC | ID: GO:0016020 | Genes: 248 | p-valor ruta: 1.88e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CYTH4	NA	UP	2.691	3.08e-10	36.2
DUOX1	NA	UP	3.131	5.18e-10	27.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
ANXA13	NA	DOWN	-2.861	5.73e-09	29.3
KMO	NA	UP	5.165	6.24e-09	19.5
ACTN2	NA	UP	3.956	7.01e-09	20.3
NDUFA4L2	NA	UP	3.705	8.81e-09	20.2
STX19	NA	UP	2.009	1.09e-08	99.7
LRP2	NA	UP	3.144	3.22e-08	22.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
KCNV1	NA	UP	2.402	2.10e-07	37.9
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
RAB26	NA	DOWN	-2.030	2.53e-07	50.4
NGFR	NA	UP	2.337	3.33e-07	30.0
STX11	NA	UP	2.909	3.34e-07	21.9
NPR1	NA	UP	3.131	3.66e-07	19.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LST1	NA	UP	6.916	7.00e-07	10.5
SYT1	NA	UP	2.659	1.62e-06	21.4
COX6B2	NA	UP	2.208	1.76e-06	27.2
LRRN3	NA	UP	6.733	2.08e-06	9.4

## Ruta: membrane (Página 7 de 10)

Fuente: GO:CC | ID: GO:0016020 | Genes: 248 | p-valor ruta: 1.88e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
KCNT2	NA	UP	2.262	3.16e-06	26.9
RAB30	NA	UP	2.024	5.27e-06	28.7
COL4A1	NA	UP	6.589	5.89e-06	8.2
ACTBL2	NA	UP	2.242	5.97e-06	28.3
ADCY4	NA	UP	2.271	8.12e-06	23.6
BEST1	NA	UP	3.553	8.47e-06	13.3
ICAM4	NA	UP	2.446	8.79e-06	22.0
FAP	NA	UP	3.233	1.87e-05	14.0
SELE	NA	UP	5.745	2.05e-05	9.0
RAB36	NA	DOWN	-2.063	2.15e-05	24.7
KCNK2	NA	DOWN	-3.579	2.55e-05	12.4
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
BEST3	NA	UP	2.070	3.26e-05	23.9
FFAR2	NA	UP	3.253	4.81e-05	12.7
XKR9	NA	UP	3.541	5.84e-05	11.9
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
RHCG	NA	UP	2.107	1.84e-04	21.0
PTGER2	NA	UP	3.006	1.95e-04	11.0
MPZ	NA	UP	2.002	2.88e-04	19.4
TMEM40	NA	UP	2.179	2.99e-04	16.5
TRPC4	NA	UP	5.730	3.71e-04	4.5
NCALD	NA	UP	2.037	3.82e-04	17.1
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2

## Ruta: membrane (Página 8 de 10)

Fuente: GO:CC | ID: GO:0016020 | Genes: 248 | p-valor ruta: 1.88e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CXCL9	NA	UP	4.099	4.37e-04	26.3
SLC5A5	NA	UP	4.542	4.62e-04	6.8
KIT	NA	UP	3.650	6.24e-04	7.9
SLC38A4	NA	DOWN	-2.630	6.25e-04	12.4
GAL3ST4	NA	UP	2.371	7.40e-04	12.5
CNTN4	NA	UP	4.928	9.17e-04	5.0
SLC16A6	NA	UP	3.375	9.62e-04	7.8
TMEM160	NA	DOWN	-2.039	1.02e-03	686.6
FLRT1	NA	UP	5.509	1.11e-03	3.8
CEACAM20	NA	UP	5.412	1.17e-03	3.6
ABCG5	NA	DOWN	-4.967	1.17e-03	6.2
PLA1A	NA	UP	3.622	1.35e-03	6.6
RNF152	NA	UP	3.325	1.37e-03	7.5
LRRC26	NA	DOWN	-2.795	1.47e-03	10.1
KCNH3	NA	DOWN	-2.243	1.94e-03	12.5
SLC1A2	NA	UP	2.752	2.07e-03	8.4
CACNA1I	NA	UP	2.173	2.19e-03	14.9
LGR6	NA	UP	3.915	2.25e-03	6.0
SLC17A4	NA	DOWN	-2.298	2.32e-03	11.5
PEX5L	NA	UP	3.321	2.40e-03	7.0
KCNN1	NA	UP	3.883	2.55e-03	6.2
SUSD3	NA	UP	2.011	2.77e-03	13.3
SIDT1	NA	UP	2.642	2.81e-03	8.6
SLCO5A1	NA	UP	2.814	2.87e-03	7.7
IPCEF1	NA	UP	4.035	3.69e-03	4.9

## Ruta: membrane (Página 9 de 10)

Fuente: GO:CC | ID: GO:0016020 | Genes: 248 | p-valor ruta: 1.88e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
HRG	NA	UP	2.971	4.00e-03	6.9
DLL1	NA	UP	2.171	4.40e-03	10.4
LY96	NA	UP	5.204	4.42e-03	3.4
GAS2	NA	DOWN	-2.038	5.05e-03	13.8
SLC25A18	NA	DOWN	-2.816	5.67e-03	7.5
SDK2	NA	UP	2.715	5.83e-03	7.9
EGFL6	NA	UP	3.034	6.01e-03	5.9
KRT9	NA	UP	4.973	6.24e-03	2.7
RGS9BP	NA	DOWN	-2.629	6.39e-03	8.3
P2RY6	NA	UP	2.536	8.76e-03	7.0
TMEM52	NA	DOWN	-2.231	9.92e-03	9.2
RNF150	NA	UP	4.240	1.04e-02	3.1
CD70	NA	UP	3.257	1.21e-02	4.7
THBD	NA	UP	2.330	1.23e-02	7.3
SCUBE1	NA	UP	2.508	1.26e-02	8.4
SLC9B1	NA	UP	4.128	1.36e-02	3.1
RET	NA	UP	2.793	1.44e-02	5.5
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
SLC6A7	NA	UP	3.822	1.73e-02	3.5
CAMK1G	NA	UP	4.059	1.79e-02	2.8
MSTO1	NA	DOWN	-2.110	1.81e-02	8.3
OLR1	NA	UP	2.655	1.81e-02	6.9
GLP2R	NA	UP	2.220	1.86e-02	8.9

## Ruta: membrane (Página 10 de 10)

Fuente: GO:CC | ID: GO:0016020 | Genes: 248 | p-valor ruta: 1.88e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NPR3	NA	UP	2.789	1.87e-02	5.7
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
ALPK2	NA	UP	3.025	2.06e-02	4.7
SLC9C2	NA	UP	3.943	2.11e-02	2.8
TMEM106A	NA	UP	2.485	2.20e-02	7.2
CLSTN2	NA	UP	2.773	2.49e-02	4.9
SLC8A2	NA	UP	4.460	2.55e-02	1.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
SPRR2A	NA	UP	2.086	2.78e-02	7.8
GPR27	NA	DOWN	-4.359	2.89e-02	1.9
INSC	NA	UP	3.872	3.01e-02	2.4
IL13RA2	NA	UP	2.568	3.02e-02	4.7
HSD11B1	NA	UP	2.341	3.03e-02	5.6
CR1L	NA	UP	3.479	3.30e-02	3.5
KCNE4	NA	UP	2.337	3.37e-02	5.7
DLG2	NA	UP	3.028	3.83e-02	3.8
ADAMTS4	NA	UP	3.293	3.88e-02	3.0
TPBGL	NA	DOWN	-2.750	4.11e-02	4.4
NID2	NA	DOWN	-3.779	4.29e-02	2.9
SFRP1	NA	UP	2.711	4.51e-02	3.8
SRMS	NA	UP	3.880	4.55e-02	2.3

## Ruta: cytoplasmic vesicle (Página 1 de 4)

Fuente: GO:CC | ID: GO:0031410 | Genes: 81 | p–valor ruta: 2.17e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e–214	2230.2
GBP1	NA	UP	4.090	2.07e–209	2026.7
LAMP3	NA	UP	3.644	2.72e–189	1627.7
GBP4	NA	UP	4.422	6.95e–185	1175.0
ARRDC3	NA	UP	3.879	1.32e–170	3146.8
SAMD9L	NA	UP	3.487	2.90e–126	1768.5
TAP1	NA	UP	2.707	8.35e–123	5228.7
PLAT	NA	UP	2.447	4.98e–113	6662.1
SERPINE1	NA	UP	4.807	1.12e–104	435.1
TNF	NA	UP	7.712	3.81e–103	573.0
CD274	NA	UP	5.204	1.23e–98	314.4
DTX3L	NA	UP	2.553	3.51e–96	2147.3
IRAK2	NA	UP	2.666	3.46e–95	1164.5
AMOTL2	NA	UP	2.069	9.30e–80	4829.0
ADRB2	NA	UP	2.471	2.83e–79	954.4
IRF7	NA	UP	3.210	5.72e–79	2126.1
THBS1	NA	UP	2.656	1.05e–77	3791.3
SLC15A3	NA	UP	4.245	2.06e–77	254.6
PML	NA	UP	2.208	2.84e–70	2901.3
PTX3	NA	UP	3.614	2.25e–68	237.4
OPTN	NA	UP	2.002	1.08e–67	1911.6
NEURL3	NA	UP	2.464	1.53e–62	758.9
PTAFR	NA	UP	3.014	4.62e–62	338.1
TRIM21	NA	UP	2.221	1.14e–60	888.8
HBEGF	NA	UP	2.602	3.10e–57	415.2

## Ruta: cytoplasmic vesicle (Página 2 de 4)

Fuente: GO:CC | ID: GO:0031410 | Genes: 81 | p–valor ruta: 2.17e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PDE4B	NA	UP	3.818	7.08e–52	171.4
ARRDC4	NA	UP	2.305	2.76e–44	631.5
IL15RA	NA	UP	2.045	1.16e–42	847.9
EPN3	NA	DOWN	-2.294	4.66e–30	335.3
IL12A	NA	UP	3.852	1.95e–28	83.7
KIF21B	NA	UP	2.131	3.74e–27	240.5
VCAM1	NA	UP	4.737	4.28e–26	66.5
RASGEF1B	NA	UP	2.113	4.74e–26	182.0
TLR3	NA	UP	2.508	1.99e–22	111.5
NOD2	NA	UP	2.981	1.19e–19	80.5
ITGAM	NA	UP	2.447	1.39e–19	90.2
SCGN	NA	DOWN	-3.468	1.52e–19	60.9
CSF3	NA	UP	6.122	1.72e–19	56.0
BST2	NA	UP	4.284	3.82e–19	50.8
JAK2	NA	UP	2.081	1.26e–17	123.4
SYT12	NA	DOWN	-2.637	2.26e–17	74.3
IL15	NA	UP	2.012	2.28e–17	116.8
GBP5	NA	UP	6.172	4.92e–17	48.7
IFITM2	NA	UP	2.649	6.22e–17	64.2
BDKRB2	NA	UP	2.797	5.56e–15	55.1
CLEC4E	NA	UP	3.620	4.75e–09	26.0
ANXA13	NA	DOWN	-2.861	5.73e–09	29.3
ACTN2	NA	UP	3.956	7.01e–09	20.3
STX19	NA	UP	2.009	1.09e–08	99.7
LRP2	NA	UP	3.144	3.22e–08	22.0

## Ruta: cytoplasmic vesicle (Página 3 de 4)

Fuente: GO:CC | ID: GO:0031410 | Genes: 81 | p–valor ruta: 2.17e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SOCS1	NA	UP	2.012	6.54e–08	82.5
TLR6	NA	UP	2.680	9.77e–08	26.3
RAB26	NA	DOWN	-2.030	2.53e–07	50.4
NGFR	NA	UP	2.337	3.33e–07	30.0
STX11	NA	UP	2.909	3.34e–07	21.9
SYT1	NA	UP	2.659	1.62e–06	21.4
PKP1	NA	UP	3.076	9.16e–05	12.8
NPTX1	NA	UP	2.102	1.13e–04	22.3
RHCG	NA	UP	2.107	1.84e–04	21.0
NCALD	NA	UP	2.037	3.82e–04	17.1
COLEC10	NA	UP	2.878	4.02e–04	11.6
KIT	NA	UP	3.650	6.24e–04	7.9
EXOC3L1	NA	UP	3.152	6.83e–04	8.6
ENKUR	NA	UP	3.518	8.61e–04	9.0
FLRT1	NA	UP	5.509	1.11e–03	3.8
PLA1A	NA	UP	3.622	1.35e–03	6.6
RUFY4	NA	UP	4.136	2.15e–03	6.0
GBP6	NA	UP	2.233	3.24e–03	11.2
SRGN	NA	UP	2.093	3.80e–03	11.0
HRG	NA	UP	2.971	4.00e–03	6.9
DLL1	NA	UP	2.171	4.40e–03	10.4
LY96	NA	UP	5.204	4.42e–03	3.4
VWF	NA	UP	3.390	1.16e–02	4.6
PRG2	NA	UP	2.073	1.32e–02	9.7
RET	NA	UP	2.793	1.44e–02	5.5

## Ruta: cytoplasmic vesicle (Página 4 de 4)

Fuente: GO:CC | ID: GO:0031410 | Genes: 81 | p-valor ruta: 2.17e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
OLR1	NA	UP	2.655	1.81e-02	6.9
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
SPRR2A	NA	UP	2.086	2.78e-02	7.8

## Ruta: intracellular vesicle (Página 1 de 4)

Fuente: GO:CC | ID: GO:0097708 | Genes: 81 | p-valor ruta: 2.35e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
LAMP3	NA	UP	3.644	2.72e-189	1627.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
ARRDC3	NA	UP	3.879	1.32e-170	3146.8
SAMD9L	NA	UP	3.487	2.90e-126	1768.5
TAP1	NA	UP	2.707	8.35e-123	5228.7
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
CD274	NA	UP	5.204	1.23e-98	314.4
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
AMOTL2	NA	UP	2.069	9.30e-80	4829.0
ADRB2	NA	UP	2.471	2.83e-79	954.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
THBS1	NA	UP	2.656	1.05e-77	3791.3
SLC15A3	NA	UP	4.245	2.06e-77	254.6
PML	NA	UP	2.208	2.84e-70	2901.3
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
NEURL3	NA	UP	2.464	1.53e-62	758.9
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM21	NA	UP	2.221	1.14e-60	888.8
HBEGF	NA	UP	2.602	3.10e-57	415.2

## Ruta: intracellular vesicle (Página 2 de 4)

Fuente: GO:CC | ID: GO:0097708 | Genes: 81 | p–valor ruta: 2.35e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PDE4B	NA	UP	3.818	7.08e–52	171.4
ARRDC4	NA	UP	2.305	2.76e–44	631.5
IL15RA	NA	UP	2.045	1.16e–42	847.9
EPN3	NA	DOWN	-2.294	4.66e–30	335.3
IL12A	NA	UP	3.852	1.95e–28	83.7
KIF21B	NA	UP	2.131	3.74e–27	240.5
VCAM1	NA	UP	4.737	4.28e–26	66.5
RASGEF1B	NA	UP	2.113	4.74e–26	182.0
TLR3	NA	UP	2.508	1.99e–22	111.5
NOD2	NA	UP	2.981	1.19e–19	80.5
ITGAM	NA	UP	2.447	1.39e–19	90.2
SCGN	NA	DOWN	-3.468	1.52e–19	60.9
CSF3	NA	UP	6.122	1.72e–19	56.0
BST2	NA	UP	4.284	3.82e–19	50.8
JAK2	NA	UP	2.081	1.26e–17	123.4
SYT12	NA	DOWN	-2.637	2.26e–17	74.3
IL15	NA	UP	2.012	2.28e–17	116.8
GBP5	NA	UP	6.172	4.92e–17	48.7
IFITM2	NA	UP	2.649	6.22e–17	64.2
BDKRB2	NA	UP	2.797	5.56e–15	55.1
CLEC4E	NA	UP	3.620	4.75e–09	26.0
ANXA13	NA	DOWN	-2.861	5.73e–09	29.3
ACTN2	NA	UP	3.956	7.01e–09	20.3
STX19	NA	UP	2.009	1.09e–08	99.7
LRP2	NA	UP	3.144	3.22e–08	22.0

## Ruta: intracellular vesicle (Página 3 de 4)

Fuente: GO:CC | ID: GO:0097708 | Genes: 81 | p–valor ruta: 2.35e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SOCS1	NA	UP	2.012	6.54e–08	82.5
TLR6	NA	UP	2.680	9.77e–08	26.3
RAB26	NA	DOWN	-2.030	2.53e–07	50.4
NGFR	NA	UP	2.337	3.33e–07	30.0
STX11	NA	UP	2.909	3.34e–07	21.9
SYT1	NA	UP	2.659	1.62e–06	21.4
PKP1	NA	UP	3.076	9.16e–05	12.8
NPTX1	NA	UP	2.102	1.13e–04	22.3
RHCG	NA	UP	2.107	1.84e–04	21.0
NCALD	NA	UP	2.037	3.82e–04	17.1
COLEC10	NA	UP	2.878	4.02e–04	11.6
KIT	NA	UP	3.650	6.24e–04	7.9
EXOC3L1	NA	UP	3.152	6.83e–04	8.6
ENKUR	NA	UP	3.518	8.61e–04	9.0
FLRT1	NA	UP	5.509	1.11e–03	3.8
PLA1A	NA	UP	3.622	1.35e–03	6.6
RUFY4	NA	UP	4.136	2.15e–03	6.0
GBP6	NA	UP	2.233	3.24e–03	11.2
SRGN	NA	UP	2.093	3.80e–03	11.0
HRG	NA	UP	2.971	4.00e–03	6.9
DLL1	NA	UP	2.171	4.40e–03	10.4
LY96	NA	UP	5.204	4.42e–03	3.4
VWF	NA	UP	3.390	1.16e–02	4.6
PRG2	NA	UP	2.073	1.32e–02	9.7
RET	NA	UP	2.793	1.44e–02	5.5

## Ruta: intracellular vesicle (Página 4 de 4)

Fuente: GO:CC | ID: GO:0097708 | Genes: 81 | p-valor ruta: 2.35e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
OLR1	NA	UP	2.655	1.81e-02	6.9
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
SPRR2A	NA	UP	2.086	2.78e-02	7.8

## Ruta: extracellular matrix (Página 1 de 2)

Fuente: GO:CC | ID: GO:0031012 | Genes: 26 | p–valor ruta: 3.97e–02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ICAM1	NA	UP	3.652	3.11e–204	19095.5
SERPINE1	NA	UP	4.807	1.12e–104	435.1
SERPINB9	NA	UP	2.439	1.35e–89	1138.5
THBS1	NA	UP	2.656	1.05e–77	3791.3
LGALS9	NA	UP	2.474	3.44e–71	1449.3
SEMA7A	NA	UP	2.329	3.91e–69	7576.6
PTX3	NA	UP	3.614	2.25e–68	237.4
TNFRSF11B	NA	UP	2.247	4.76e–54	1332.4
NAV2	NA	UP	2.370	3.20e–51	765.9
TLR3	NA	UP	2.508	1.99e–22	111.5
LAMA2	NA	UP	2.355	4.82e–21	125.5
INHBE	NA	UP	5.109	1.59e–15	37.3
MUC4	NA	UP	2.613	4.74e–12	55.4
LRRN3	NA	UP	6.733	2.08e–06	9.4
COL4A1	NA	UP	6.589	5.89e–06	8.2
ADAMTS6	NA	UP	2.602	8.90e–06	19.6
MMP13	NA	UP	5.406	9.23e–06	11.1
FLRT1	NA	UP	5.509	1.11e–03	3.8
HRG	NA	UP	2.971	4.00e–03	6.9
EGFL6	NA	UP	3.034	6.01e–03	5.9
BMPER	NA	UP	4.906	6.28e–03	2.6
VWF	NA	UP	3.390	1.16e–02	4.6
PRG2	NA	UP	2.073	1.32e–02	9.7
ADAMTS4	NA	UP	3.293	3.88e–02	3.0
NID2	NA	DOWN	–3.779	4.29e–02	2.9

## Ruta: extracellular matrix (Página 2 de 2)

Fuente: GO:CC | ID: GO:0031012 | Genes: 26 | p-valor ruta: 3.97e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SFRP1	NA	UP	2.711	4.51e-02	3.8

## Ruta: external encapsulating structure (Página 1 de 2)

Fuente: GO:CC | ID: GO:0030312 | Genes: 26 | p-valor ruta: 4.08e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
ICAM1	NA	UP	3.652	3.11e-204	19095.5
SERPINE1	NA	UP	4.807	1.12e-104	435.1
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
THBS1	NA	UP	2.656	1.05e-77	3791.3
LGALS9	NA	UP	2.474	3.44e-71	1449.3
SEMA7A	NA	UP	2.329	3.91e-69	7576.6
PTX3	NA	UP	3.614	2.25e-68	237.4
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
NAV2	NA	UP	2.370	3.20e-51	765.9
TLR3	NA	UP	2.508	1.99e-22	111.5
LAMA2	NA	UP	2.355	4.82e-21	125.5
INHBE	NA	UP	5.109	1.59e-15	37.3
MUC4	NA	UP	2.613	4.74e-12	55.4
LRRN3	NA	UP	6.733	2.08e-06	9.4
COL4A1	NA	UP	6.589	5.89e-06	8.2
ADAMTS6	NA	UP	2.602	8.90e-06	19.6
MMP13	NA	UP	5.406	9.23e-06	11.1
FLRT1	NA	UP	5.509	1.11e-03	3.8
HRG	NA	UP	2.971	4.00e-03	6.9
EGFL6	NA	UP	3.034	6.01e-03	5.9
BMPER	NA	UP	4.906	6.28e-03	2.6
VWF	NA	UP	3.390	1.16e-02	4.6
PRG2	NA	UP	2.073	1.32e-02	9.7
ADAMTS4	NA	UP	3.293	3.88e-02	3.0
NID2	NA	DOWN	-3.779	4.29e-02	2.9

## Ruta: external encapsulating structure (Página 2 de 2)

Fuente: GO:CC | ID: GO:0030312 | Genes: 26 | p-valor ruta: 4.08e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
SFRP1	NA	UP	2.711	4.51e-02	3.8

# Sección de Análisis: REAC – Rutas Reactome

Total de términos enriquecidos en esta sección: 18

Términos 'Tope' (p-valor < 1e-16): 4

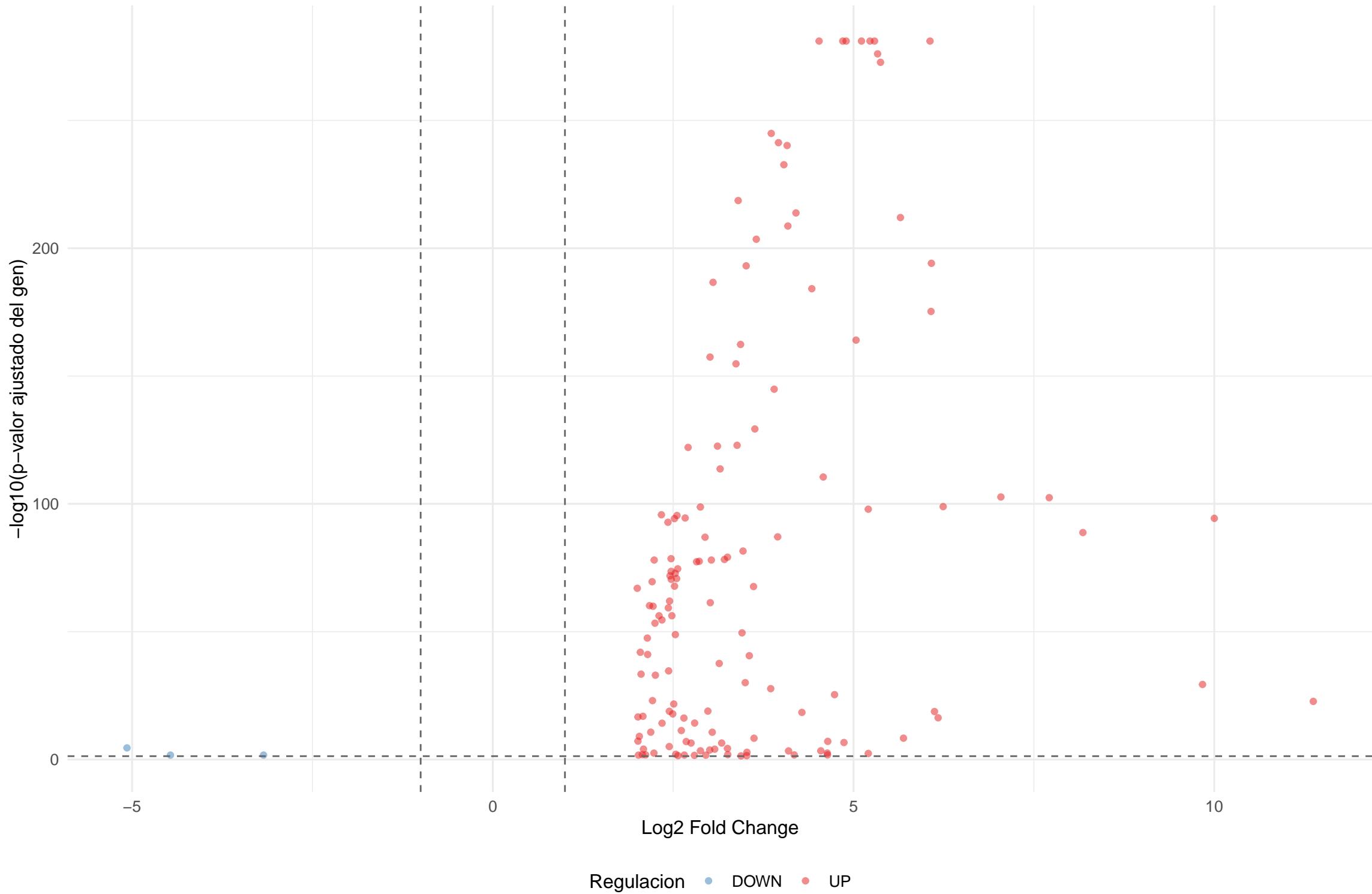
## Términos que superan el 'tope' de significancia:

- *Cytokine Signaling in Immune system* (REAC:R-HSA-1280215, p-val: 2.6e-33)
- *Interferon Signaling* (REAC:R-HSA-913531, p-val: 2.7e-22)
- *Interferon alpha/beta signaling* (REAC:R-HSA-909733, p-val: 8.6e-22)
- *Immune System* (REAC:R-HSA-168256, p-val: 3.0e-17)

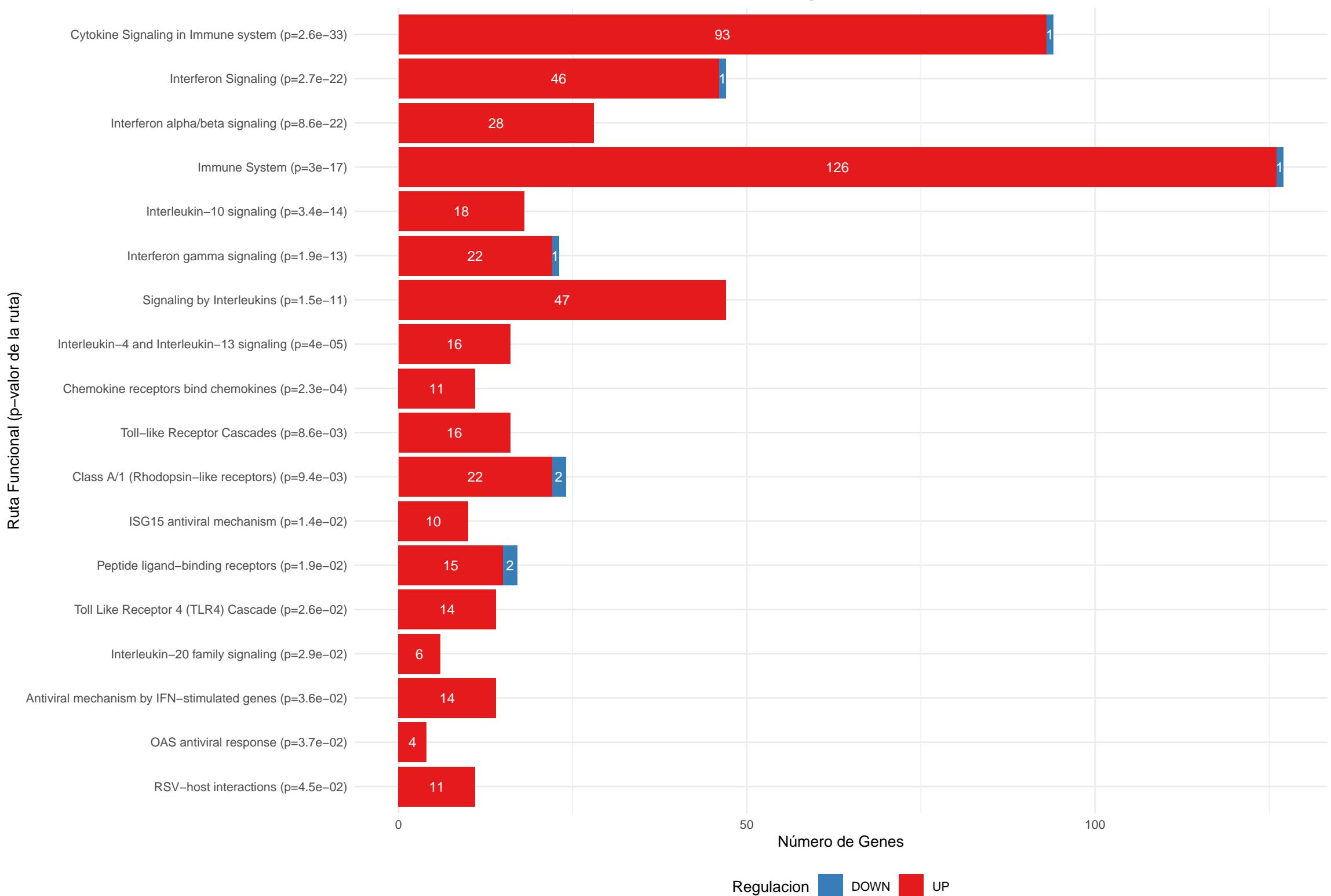
A continuación se muestran los gráficos de barras y tablas de genes para esta sección.

# Volcano Plot – REAC – Rutas Reactome

Mostrando 143 genes únicos mapeados en esta sección



# REAC – Rutas Reactome – Gráfico (Pág. 1 de 1 )



## Ruta: Cytokine Signaling in Immune system (Página 1 de 4)

Fuente: REAC | ID: REAC:R-HSA-1280215 | Genes: 94 | p-valor ruta: 2.57e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
GBP4	NA	UP	4.422	6.95e-185	1175.0
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
HERC5	NA	UP	3.386	1.24e-123	1735.7

## Ruta: Cytokine Signaling in Immune system (Página 2 de 4)

Fuente: REAC | ID: REAC:R-HSA-1280215 | Genes: 94 | p-valor ruta: 2.57e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
XAF1	NA	UP	4.580	3.19e-111	427.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
IRF7	NA	UP	3.210	5.72e-79	2126.1
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6

## Ruta: Cytokine Signaling in Immune system (Página 3 de 4)

Fuente: REAC | ID: REAC:R-HSA-1280215 | Genes: 94 | p-valor ruta: 2.57e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
MT2A	NA	UP	2.437	2.24e-35	363.0
IRS2	NA	UP	2.254	1.06e-33	255.2
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: Cytokine Signaling in Immune system (Página 4 de 4)

Fuente: REAC | ID: REAC:R-HSA-1280215 | Genes: 94 | p-valor ruta: 2.57e-33

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
FLT3LG	NA	UP	2.346	6.32e-15	68.5
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
IL18R1	NA	UP	2.088	8.75e-05	23.0
IL17C	NA	UP	4.636	3.13e-03	4.1
GBP6	NA	UP	2.233	3.24e-03	11.2
CD70	NA	UP	3.257	1.21e-02	4.7
VAV1	NA	UP	2.118	1.54e-02	7.9
GBP7	NA	UP	4.177	1.61e-02	2.9
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
IL34	NA	UP	2.794	2.41e-02	4.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: Interferon Signaling (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-913531 | Genes: 47 | p-valor ruta: 2.72e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IRF1	NA	UP	3.512	7.87e-194	2808.9
GBP4	NA	UP	4.422	6.95e-185	1175.0
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
HERC5	NA	UP	3.386	1.24e-123	1735.7
XAF1	NA	UP	4.580	3.19e-111	427.9
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
ISG20	NA	UP	3.029	9.45e-79	1021.0

## Ruta: Interferon Signaling (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-913531 | Genes: 47 | p-valor ruta: 2.72e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
EGR1	NA	UP	2.472	2.61e-74	1149.5
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
MT2A	NA	UP	2.437	2.24e-35	363.0
VCAM1	NA	UP	4.737	4.28e-26	66.5
BST2	NA	UP	4.284	3.82e-19	50.8
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
GBP6	NA	UP	2.233	3.24e-03	11.2
GBP7	NA	UP	4.177	1.61e-02	2.9
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2

## Ruta: Interferon alpha/beta signaling (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-909733 | Genes: 28 | p-valor ruta: 8.56e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
IRF1	NA	UP	3.512	7.87e-194	2808.9
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
XAF1	NA	UP	4.580	3.19e-111	427.9
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7
IFIT5	NA	UP	2.861	3.01e-78	749.8
EGR1	NA	UP	2.472	2.61e-74	1149.5
STAT1	NA	UP	2.519	1.61e-68	9528.0
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0

## Ruta: Interferon alpha/beta signaling (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-909733 | Genes: 28 | p-valor ruta: 8.56e-22

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
BST2	NA	UP	4.284	3.82e-19	50.8
IFITM2	NA	UP	2.649	6.22e-17	64.2
SOCS1	NA	UP	2.012	6.54e-08	82.5

## Ruta: Immune System (Página 1 de 6)

Fuente: REAC | ID: REAC:R-HSA-168256 | Genes: 127 | p-valor ruta: 3e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT2	NA	UP	5.291	0.00e+00	12201.7
IFIT3	NA	UP	4.898	0.00e+00	4866.8
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
GBP4	NA	UP	4.422	6.95e-185	1175.0
CCL5	NA	UP	5.035	8.94e-165	656.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4

## Ruta: Immune System (Página 2 de 6)

Fuente: REAC | ID: REAC:R-HSA-168256 | Genes: 127 | p-valor ruta: 3e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
USP18	NA	UP	3.900	1.42e-145	1151.2
IFITM1	NA	UP	3.632	5.16e-130	784.8
HERC5	NA	UP	3.386	1.24e-123	1735.7
TAP1	NA	UP	2.707	8.35e-123	5228.7
IFI16	NA	UP	3.151	2.12e-114	2583.4
XAF1	NA	UP	4.580	3.19e-111	427.9
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
DHX58	NA	UP	2.877	1.75e-99	953.6
CD274	NA	UP	5.204	1.23e-98	314.4
STAT2	NA	UP	2.337	1.85e-96	2004.6
DTX3L	NA	UP	2.553	3.51e-96	2147.3
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
SP100	NA	UP	2.428	1.62e-93	2653.7
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
OAS3	NA	UP	2.942	1.13e-87	8674.1
RASGRP3	NA	UP	3.468	2.92e-82	392.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
IRF7	NA	UP	3.210	5.72e-79	2126.1
ISG20	NA	UP	3.029	9.45e-79	1021.0
IFI35	NA	UP	2.237	9.59e-79	2236.7

## Ruta: Immune System (Página 3 de 6)

Fuente: REAC | ID: REAC:R-HSA-168256 | Genes: 127 | p-valor ruta: 3e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT5	NA	UP	2.861	3.01e-78	749.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
EGR1	NA	UP	2.472	2.61e-74	1149.5
RNF213	NA	UP	2.528	1.50e-73	6034.1
DAPP1	NA	UP	2.456	1.42e-72	922.6
LGALS9	NA	UP	2.474	3.44e-71	1449.3
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
PTX3	NA	UP	3.614	2.25e-68	237.4
OPTN	NA	UP	2.002	1.08e-67	1911.6
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9

## Ruta: Immune System (Página 4 de 6)

Fuente: REAC | ID: REAC:R-HSA-168256 | Genes: 127 | p-valor ruta: 3e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LTB	NA	UP	3.555	2.50e-41	150.4
ULBP1	NA	UP	3.138	2.70e-38	151.4
MT2A	NA	UP	2.437	2.24e-35	363.0
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IRS2	NA	UP	2.254	1.06e-33	255.2
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
BST2	NA	UP	4.284	3.82e-19	50.8
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
GBP5	NA	UP	6.172	4.92e-17	48.7
IFITM2	NA	UP	2.649	6.22e-17	64.2
FLT3LG	NA	UP	2.346	6.32e-15	68.5
MUC4	NA	UP	2.613	4.74e-12	55.4
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
NLRP1	NA	UP	5.692	4.64e-09	21.6

## Ruta: Immune System (Página 5 de 6)

Fuente: REAC | ID: REAC:R-HSA-168256 | Genes: 127 | p-valor ruta: 3e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CLEC4E	NA	UP	3.620	4.75e-09	26.0
SOCS1	NA	UP	2.012	6.54e-08	82.5
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
TLR6	NA	UP	2.680	9.77e-08	26.3
PGLYRP2	NA	UP	4.867	2.30e-07	15.6
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
ICAM4	NA	UP	2.446	8.79e-06	22.0
IL18R1	NA	UP	2.088	8.75e-05	23.0
PKP1	NA	UP	3.076	9.16e-05	12.8
COLEC10	NA	UP	2.878	4.02e-04	11.6
PDCD1LG2	NA	UP	4.546	4.10e-04	7.2
IL17C	NA	UP	4.636	3.13e-03	4.1
GBP6	NA	UP	2.233	3.24e-03	11.2
LY96	NA	UP	5.204	4.42e-03	3.4
CD70	NA	UP	3.257	1.21e-02	4.7
PRG2	NA	UP	2.073	1.32e-02	9.7
VAV1	NA	UP	2.118	1.54e-02	7.9
C3AR1	NA	UP	4.639	1.59e-02	2.2
GBP7	NA	UP	4.177	1.61e-02	2.9
OLR1	NA	UP	2.655	1.81e-02	6.9
FBXW10	NA	UP	2.019	1.90e-02	9.5
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
IL34	NA	UP	2.794	2.41e-02	4.8

## Ruta: Immune System (Página 6 de 6)

Fuente: REAC | ID: REAC:R-HSA-168256 | Genes: 127 | p-valor ruta: 3e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL13RA2	NA	UP	2.568	3.02e-02	4.7
TRIM69	NA	UP	3.519	3.21e-02	3.0

## Ruta: Interleukin–10 signaling

Fuente: REAC | ID: REAC:R-HSA-6783783 | Genes: 18 | p–valor ruta: 3.39e–14

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e–242	2226.4
IL1B	NA	UP	4.202	1.58e–214	2230.2
ICAM1	NA	UP	3.652	3.11e–204	19095.5
CXCL10	NA	UP	6.079	8.12e–195	783.4
CCL5	NA	UP	5.035	8.94e–165	656.3
CXCL2	NA	UP	3.371	1.67e–155	4155.4
CSF2	NA	UP	7.043	2.08e–103	455.6
TNF	NA	UP	7.712	3.81e–103	573.0
PTGS2	NA	UP	3.253	7.39e–80	3663.8
CCL2	NA	UP	2.562	2.63e–75	658.0
PTAFR	NA	UP	3.014	4.62e–62	338.1
CCL22	NA	UP	3.454	2.91e–50	168.7
CSF1	NA	UP	2.530	1.40e–49	467.4
IL12A	NA	UP	3.852	1.95e–28	83.7
CSF3	NA	UP	6.122	1.72e–19	56.0
IL10RA	NA	UP	3.172	3.66e–07	18.8

## Ruta: Interferon gamma signaling

Fuente: REAC | ID: REAC:R-HSA-877300 | Genes: 23 | p-valor ruta: 1.86e-13

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
TRIM22	NA	UP	5.650	1.01e-212	913.7
GBP1	NA	UP	4.090	2.07e-209	2026.7
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IRF1	NA	UP	3.512	7.87e-194	2808.9
GBP4	NA	UP	4.422	6.95e-185	1175.0
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
SP100	NA	UP	2.428	1.62e-93	2653.7
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
PML	NA	UP	2.208	2.84e-70	2901.3
PTAFR	NA	UP	3.014	4.62e-62	338.1
TRIM5	NA	UP	2.172	6.62e-61	1222.6
TRIM21	NA	UP	2.221	1.14e-60	888.8
MT2A	NA	UP	2.437	2.24e-35	363.0
VCAM1	NA	UP	4.737	4.28e-26	66.5
JAK2	NA	UP	2.081	1.26e-17	123.4
GBP5	NA	UP	6.172	4.92e-17	48.7
SOCS1	NA	UP	2.012	6.54e-08	82.5
GBP6	NA	UP	2.233	3.24e-03	11.2
GBP7	NA	UP	4.177	1.61e-02	2.9
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2

## Ruta: Signaling by Interleukins (Página 1 de 2)

Fuente: REAC | ID: REAC:R-HSA-449147 | Genes: 47 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
USP18	NA	UP	3.900	1.42e-145	1151.2
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNL1	NA	UP	8.179	1.68e-89	578.0
NLRC5	NA	UP	3.949	8.12e-88	414.4
PTGS2	NA	UP	3.253	7.39e-80	3663.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
LGALS9	NA	UP	2.474	3.44e-71	1449.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
PTAFR	NA	UP	3.014	4.62e-62	338.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
CCL22	NA	UP	3.454	2.91e-50	168.7

## Ruta: Signaling by Interleukins (Página 2 de 2)

Fuente: REAC | ID: REAC:R-HSA-449147 | Genes: 47 | p-valor ruta: 1.5e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
IRS2	NA	UP	2.254	1.06e-33	255.2
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL10RA	NA	UP	3.172	3.66e-07	18.8
IL18R1	NA	UP	2.088	8.75e-05	23.0
IL17C	NA	UP	4.636	3.13e-03	4.1
VAV1	NA	UP	2.118	1.54e-02	7.9
IL34	NA	UP	2.794	2.41e-02	4.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: Interleukin–4 and Interleukin–13 signaling

Fuente: REAC | ID: REAC:R-HSA-6785807 | Genes: 16 | p-valor ruta: 4.04e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
CCL2	NA	UP	2.562	2.63e-75	658.0
STAT1	NA	UP	2.519	1.61e-68	9528.0
CCL22	NA	UP	3.454	2.91e-50	168.7
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: Chemokine receptors bind chemokines

Fuente: REAC | ID: REAC:R-HSA-380108 | Genes: 11 | p-valor ruta: 2.27e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CCL2	NA	UP	2.562	2.63e-75	658.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CXCL9	NA	UP	4.099	4.37e-04	26.3
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: Toll-like Receptor Cascades

Fuente: REAC | ID: REAC:R-HSA-168898 | Genes: 16 | p-valor ruta: 8.58e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
USP18	NA	UP	3.900	1.42e-145	1151.2
IRAK2	NA	UP	2.666	3.46e-95	1164.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
MAP3K8	NA	UP	2.825	4.57e-78	640.1
OPTN	NA	UP	2.002	1.08e-67	1911.6
JUN	NA	UP	2.450	1.10e-62	6693.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
TLR3	NA	UP	2.508	1.99e-22	111.5
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: Class A/1 (Rhodopsin-like receptors)

Fuente: REAC | ID: REAC:R-HSA-373076 | Genes: 24 | p-valor ruta: 9.41e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
ADRB2	NA	UP	2.471	2.83e-79	954.4
CCL2	NA	UP	2.562	2.63e-75	658.0
PTGER4	NA	UP	2.548	1.70e-71	568.2
PTAFR	NA	UP	3.014	4.62e-62	338.1
CCL22	NA	UP	3.454	2.91e-50	168.7
EDN2	NA	UP	3.499	8.77e-31	90.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
FFAR2	NA	UP	3.253	4.81e-05	12.7
PTGER2	NA	UP	3.006	1.95e-04	11.0
CXCL9	NA	UP	4.099	4.37e-04	26.3
LHB	NA	UP	3.522	1.50e-03	7.0
P2RY6	NA	UP	2.536	8.76e-03	7.0
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: ISG15 antiviral mechanism

Fuente: REAC | ID: REAC:R-HSA-1169408 | Genes: 10 | p-valor ruta: 1.45e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
USP18	NA	UP	3.900	1.42e-145	1151.2
HERC5	NA	UP	3.386	1.24e-123	1735.7
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
STAT1	NA	UP	2.519	1.61e-68	9528.0
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0

## Ruta: Peptide ligand–binding receptors

Fuente: REAC | ID: REAC:R-HSA-375276 | Genes: 17 | p-valor ruta: 1.87e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CCL2	NA	UP	2.562	2.63e-75	658.0
CCL22	NA	UP	3.454	2.91e-50	168.7
EDN2	NA	UP	3.499	8.77e-31	90.3
BDKRB2	NA	UP	2.797	5.56e-15	55.1
SSTR2	NA	UP	2.031	8.80e-10	53.9
NPBWR1	NA	DOWN	-5.071	2.93e-05	12.3
CXCL9	NA	UP	4.099	4.37e-04	26.3
C3AR1	NA	UP	4.639	1.59e-02	2.2
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: Toll Like Receptor 4 (TLR4) Cascade

Fuente: REAC | ID: REAC:R-HSA-166016 | Genes: 14 | p-valor ruta: 2.62e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
USP18	NA	UP	3.900	1.42e-145	1151.2
IRAK2	NA	UP	2.666	3.46e-95	1164.5
NLRC5	NA	UP	3.949	8.12e-88	414.4
IRF7	NA	UP	3.210	5.72e-79	2126.1
MAP3K8	NA	UP	2.825	4.57e-78	640.1
OPTN	NA	UP	2.002	1.08e-67	1911.6
JUN	NA	UP	2.450	1.10e-62	6693.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
SOCS1	NA	UP	2.012	6.54e-08	82.5
TLR6	NA	UP	2.680	9.77e-08	26.3
LY96	NA	UP	5.204	4.42e-03	3.4

## Ruta: Interleukin–20 family signaling

Fuente: REAC | ID: REAC:R-HSA-8854691 | Genes: 6 | p-valor ruta: 2.86e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
STAT1	NA	UP	2.519	1.61e-68	9528.0
IFNL3	NA	UP	9.837	4.42e-30	365.0
IFNL2	NA	UP	11.372	1.86e-23	434.7
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: Antiviral mechanism by IFN-stimulated genes

Fuente: REAC | ID: REAC:R-HSA-1169410 | Genes: 14 | p-valor ruta: 3.55e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
USP18	NA	UP	3.900	1.42e-145	1151.2
HERC5	NA	UP	3.386	1.24e-123	1735.7
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
OAS3	NA	UP	2.942	1.13e-87	8674.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0

## Ruta: OAS antiviral response

Fuente: REAC | ID: REAC:R-HSA-8983711 | Genes: 4 | p-valor ruta: 3.74e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
OASL	NA	UP	3.434	4.45e-163	4285.8
OAS1	NA	UP	3.011	3.81e-158	5273.1
OAS3	NA	UP	2.942	1.13e-87	8674.1

## Ruta: RSV–host interactions

Fuente: REAC | ID: REAC:R-HSA-9833110 | Genes: 11 | p-valor ruta: 4.51e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
HERC5	NA	UP	3.386	1.24e-123	1735.7
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
UBE2L6	NA	UP	2.518	5.99e-95	2683.8
ISG15	NA	UP	2.482	5.90e-57	3807.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
TLR3	NA	UP	2.508	1.99e-22	111.5
TLR6	NA	UP	2.680	9.77e-08	26.3
LY96	NA	UP	5.204	4.42e-03	3.4

# Sección de Análisis: KEGG – Rutas Metabólicas

Total de términos enriquecidos en esta sección: 36

Términos 'Tope' (p-valor < 1e-16): 1

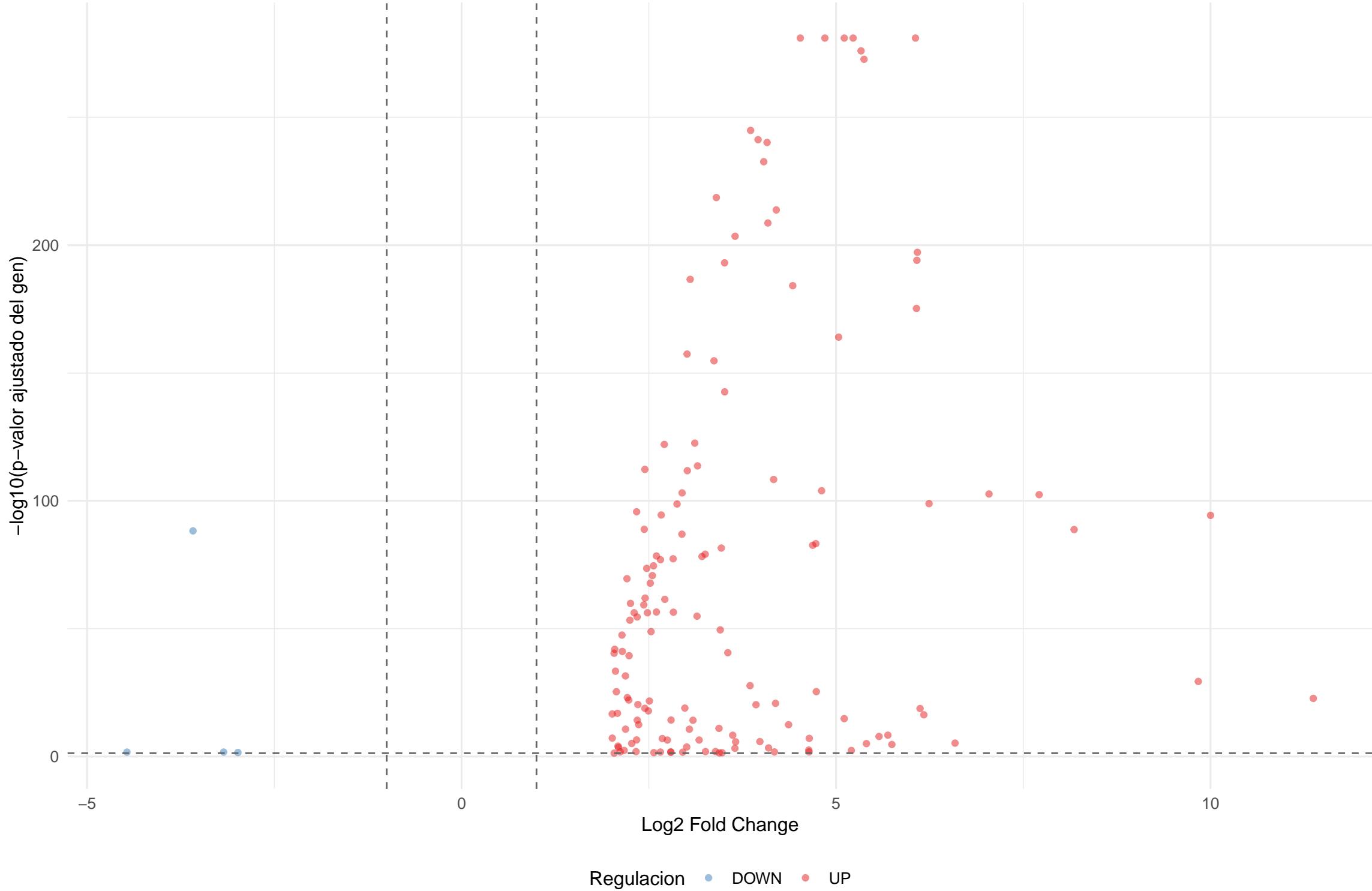
## Términos que superan el 'tope' de significancia:

- *TNF signaling pathway* (KEGG:04668, p-val: 1.8e-17)

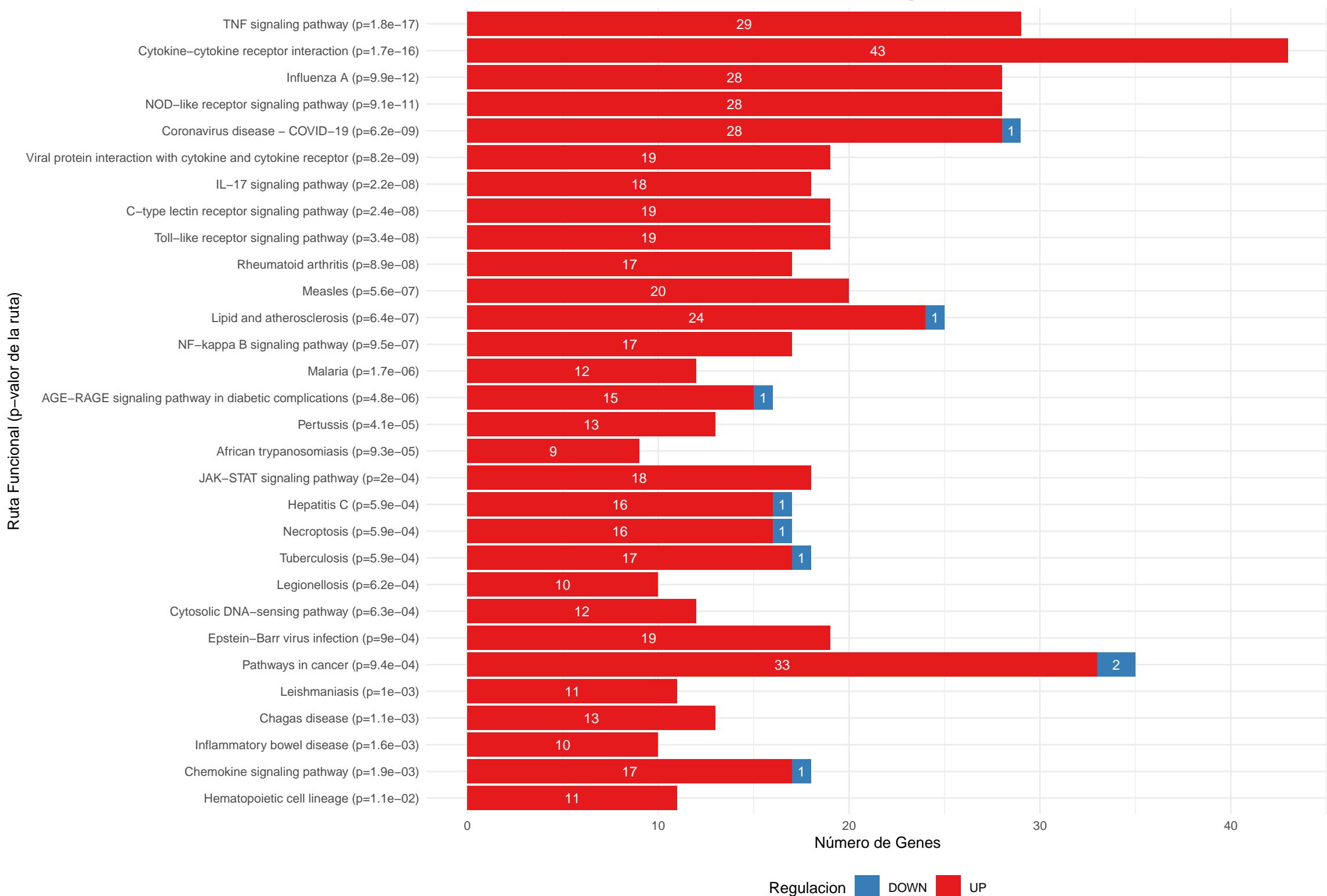
A continuación se muestran los gráficos de barras y tablas de genes para esta sección.

# Volcano Plot – KEGG – Rutas Metabólicas

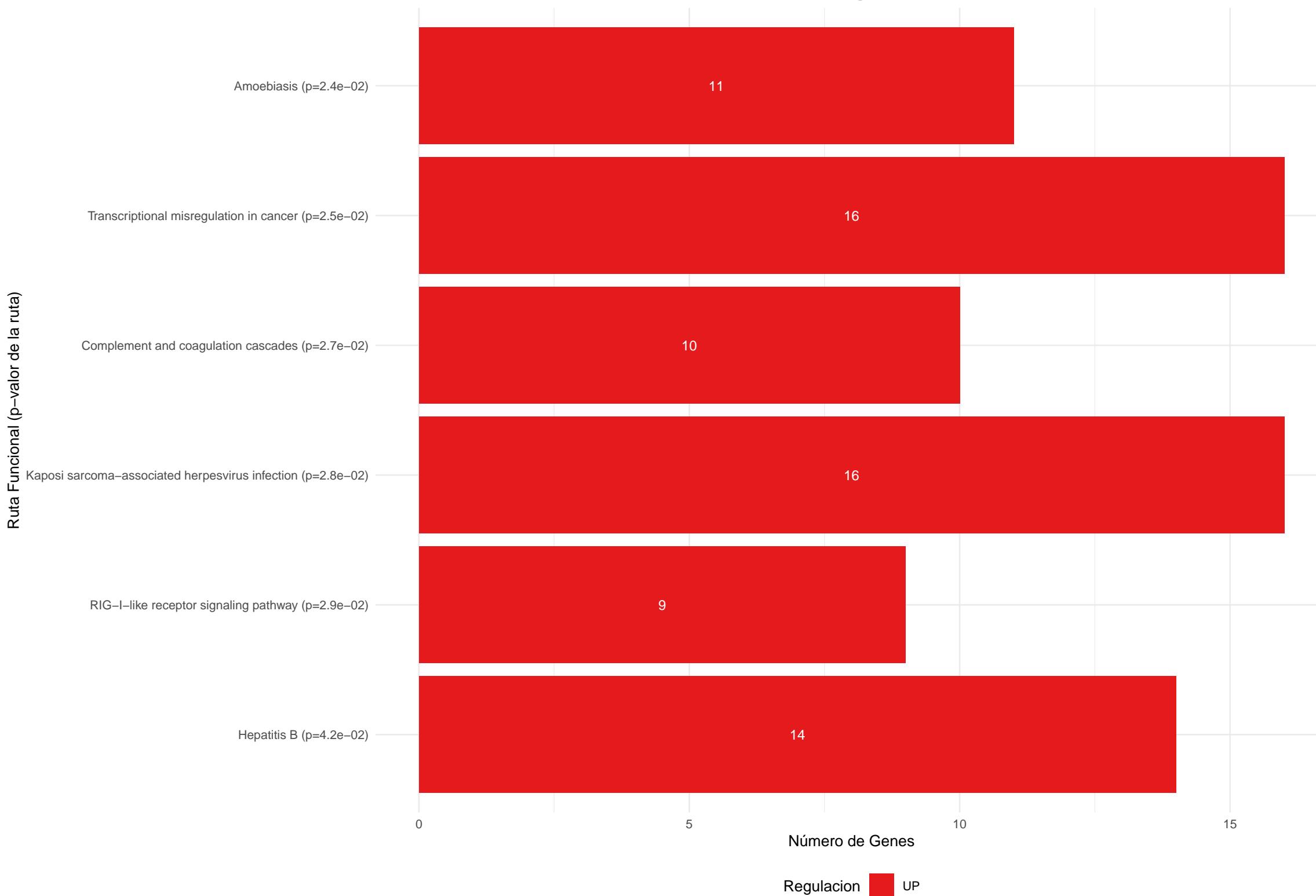
Mostrando 145 genes únicos mapeados en esta sección



# KEGG – Rutas Metabólicas – Gráfico (Pág. 1 de 2)



## KEGG – Rutas Metabólicas – Gráfico (Pág. 2 de 2 )



## Ruta: TNF signaling pathway (Página 1 de 2)

Fuente: KEGG | ID: KEGG:04668 | Genes: 29 | p-valor ruta: 1.77e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
IRF1	NA	UP	3.512	7.87e-194	2808.9
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
MAP3K8	NA	UP	2.825	4.57e-78	640.1
CCL2	NA	UP	2.562	2.63e-75	658.0
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
CSF1	NA	UP	2.530	1.40e-49	467.4
BIRC3	NA	UP	2.146	8.30e-42	2602.9
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL3	NA	UP	2.067	4.65e-26	500.4

## Ruta: TNF signaling pathway (Página 2 de 2)

Fuente: KEGG | ID: KEGG:04668 | Genes: 29 | p-valor ruta: 1.77e-17

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NOD2	NA	UP	2.981	1.19e-19	80.5
IL15	NA	UP	2.012	2.28e-17	116.8
SELE	NA	UP	5.745	2.05e-05	9.0
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: Cytokine–cytokine receptor interaction (Página 1 de 2)

Fuente: KEGG | ID: KEGG:04060 | Genes: 43 | p-valor ruta: 1.67e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
INHBA	NA	UP	3.514	2.31e-143	1743.6
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
CCL2	NA	UP	2.562	2.63e-75	658.0
TNFRSF11B	NA	UP	2.247	4.76e-54	1332.4
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
IL15RA	NA	UP	2.045	1.16e-42	847.9
LTB	NA	UP	3.555	2.50e-41	150.4
BMP2	NA	UP	2.237	3.69e-40	325.3
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: Cytokine–cytokine receptor interaction (Página 2 de 2)

Fuente: KEGG | ID: KEGG:04060 | Genes: 43 | p-valor ruta: 1.67e-16

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CSF3	NA	UP	6.122	1.72e-19	56.0
IL15	NA	UP	2.012	2.28e-17	116.8
INHBE	NA	UP	5.109	1.59e-15	37.3
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFRSF9	NA	UP	4.642	8.23e-08	94.1
NGFR	NA	UP	2.337	3.33e-07	30.0
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
IL18R1	NA	UP	2.088	8.75e-05	23.0
CXCL9	NA	UP	4.099	4.37e-04	26.3
IL17C	NA	UP	4.636	3.13e-03	4.1
CD70	NA	UP	3.257	1.21e-02	4.7
IL34	NA	UP	2.794	2.41e-02	4.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: Influenza A (Página 1 de 2)

Fuente: KEGG | ID: KEGG:05164 | Genes: 28 | p-valor ruta: 9.93e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
CCL2	NA	UP	2.562	2.63e-75	658.0
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5

## Ruta: Influenza A (Página 2 de 2)

Fuente: KEGG | ID: KEGG:05164 | Genes: 28 | p-valor ruta: 9.93e-12

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
NLRP3	NA	UP	4.366	3.67e-13	29.8

## Ruta: NOD-like receptor signaling pathway (Página 1 de 2)

Fuente: KEGG | ID: KEGG:04621 | Genes: 28 | p-valor ruta: 9.08e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
TXNIP	NA	UP	3.401	2.30e-219	11419.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
GBP1	NA	UP	4.090	2.07e-209	2026.7
CXCL3	NA	UP	3.053	2.27e-187	4330.7
GBP4	NA	UP	4.422	6.95e-185	1175.0
CCL5	NA	UP	5.035	8.94e-165	656.3
OAS1	NA	UP	3.011	3.81e-158	5273.1
CXCL2	NA	UP	3.371	1.67e-155	4155.4
IFI16	NA	UP	3.151	2.12e-114	2583.4
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
CCL2	NA	UP	2.562	2.63e-75	658.0
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NOD2	NA	UP	2.981	1.19e-19	80.5
CASP1	NA	UP	2.494	1.49e-18	80.2
GBP5	NA	UP	6.172	4.92e-17	48.7

## Ruta: NOD-like receptor signaling pathway (Página 2 de 2)

Fuente: KEGG | ID: KEGG:04621 | Genes: 28 | p-valor ruta: 9.08e-11

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRP3	NA	UP	4.366	3.67e-13	29.8
NLRP1	NA	UP	5.692	4.64e-09	21.6
GBP7	NA	UP	4.177	1.61e-02	2.9

## Ruta: Coronavirus disease – COVID–19 (Página 1 de 2)

Fuente: KEGG | ID: KEGG:05171 | Genes: 29 | p–valor ruta: 6.19e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL6	NA	UP	6.060	0.00e+00	1698.5
MX2	NA	UP	5.374	1.90e–273	1682.8
MX1	NA	UP	3.859	1.25e–245	5699.6
NFKBIA	NA	UP	4.079	6.66e–241	4955.3
IFIH1	NA	UP	4.035	2.22e–233	4525.3
IL1B	NA	UP	4.202	1.58e–214	2230.2
CXCL10	NA	UP	6.079	8.12e–195	783.4
OAS1	NA	UP	3.011	3.81e–158	5273.1
CSF2	NA	UP	7.043	2.08e–103	455.6
TNF	NA	UP	7.712	3.81e–103	573.0
STAT2	NA	UP	2.337	1.85e–96	2004.6
IFNB1	NA	UP	10.001	4.69e–95	1340.6
OAS3	NA	UP	2.942	1.13e–87	8674.1
CCL2	NA	UP	2.562	2.63e–75	658.0
STAT1	NA	UP	2.519	1.61e–68	9528.0
JUN	NA	UP	2.450	1.10e–62	6693.5
HBEGF	NA	UP	2.602	3.10e–57	415.2
ISG15	NA	UP	2.482	5.90e–57	3807.9
EIF2AK2	NA	UP	2.142	3.22e–48	1460.0
C1R	NA	UP	2.188	3.06e–32	258.8
IL12A	NA	UP	3.852	1.95e–28	83.7
TLR3	NA	UP	2.508	1.99e–22	111.5
CSF3	NA	UP	6.122	1.72e–19	56.0
CASP1	NA	UP	2.494	1.49e–18	80.2

## Ruta: Coronavirus disease – COVID–19 (Página 2 de 2)

Fuente: KEGG | ID: KEGG:05171 | Genes: 29 | p–valor ruta: 6.19e–09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NLRP3	NA	UP	4.366	3.67e–13	29.8
VWF	NA	UP	3.390	1.16e–02	4.6
C3AR1	NA	UP	4.639	1.59e–02	2.2
AGTR1	NA	DOWN	–3.177	1.87e–02	5.1

## Ruta: Viral protein interaction with cytokine and cytokine receptor

Fuente: KEGG | ID: KEGG:04061 | Genes: 19 | p-valor ruta: 8.19e-09

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
CCL2	NA	UP	2.562	2.63e-75	658.0
CCL22	NA	UP	3.454	2.91e-50	168.7
CSF1	NA	UP	2.530	1.40e-49	467.4
IL10RA	NA	UP	3.172	3.66e-07	18.8
TNFSF14	NA	UP	2.748	3.71e-07	23.0
IL18R1	NA	UP	2.088	8.75e-05	23.0
CXCL9	NA	UP	4.099	4.37e-04	26.3
IL34	NA	UP	2.794	2.41e-02	4.8
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: IL-17 signaling pathway

Fuente: KEGG | ID: KEGG:04657 | Genes: 18 | p-valor ruta: 2.24e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
CCL2	NA	UP	2.562	2.63e-75	658.0
JUN	NA	UP	2.450	1.10e-62	6693.5
FOSB	NA	UP	3.144	1.32e-55	267.7
CSF3	NA	UP	6.122	1.72e-19	56.0
MMP13	NA	UP	5.406	9.23e-06	11.1
IL17C	NA	UP	4.636	3.13e-03	4.1
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: C-type lectin receptor signaling pathway

Fuente: KEGG | ID: KEGG:04625 | Genes: 19 | p-valor ruta: 2.41e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
PTGS2	NA	UP	3.253	7.39e-80	3663.8
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
CCL22	NA	UP	3.454	2.91e-50	168.7
IL12A	NA	UP	3.852	1.95e-28	83.7
BCL3	NA	UP	2.067	4.65e-26	500.4
CASP1	NA	UP	2.494	1.49e-18	80.2
EGR2	NA	UP	3.090	6.72e-15	43.7
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
EGR3	NA	UP	2.096	2.87e-04	21.5
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: Toll-like receptor signaling pathway

Fuente: KEGG | ID: KEGG:04620 | Genes: 19 | p-valor ruta: 3.4e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
MAP3K8	NA	UP	2.825	4.57e-78	640.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR3	NA	UP	2.508	1.99e-22	111.5
TLR6	NA	UP	2.680	9.77e-08	26.3
CXCL9	NA	UP	4.099	4.37e-04	26.3
LY96	NA	UP	5.204	4.42e-03	3.4
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: Rheumatoid arthritis

Fuente: KEGG | ID: KEGG:05323 | Genes: 17 | p-valor ruta: 8.91e-08

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
CCL20	NA	UP	3.959	5.09e-242	2226.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CCL2	NA	UP	2.562	2.63e-75	658.0
JUN	NA	UP	2.450	1.10e-62	6693.5
CSF1	NA	UP	2.530	1.40e-49	467.4
LTB	NA	UP	3.555	2.50e-41	150.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
TNFSF13B	NA	UP	3.042	2.17e-11	34.7

## Ruta: Measles

Fuente: KEGG | ID: KEGG:05162 | Genes: 20 | p-valor ruta: 5.61e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
OAS1	NA	UP	3.011	3.81e-158	5273.1
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
BBC3	NA	UP	2.829	3.65e-57	503.1
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
IL12A	NA	UP	3.852	1.95e-28	83.7
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: Lipid and atherosclerosis

Fuente: KEGG | ID: KEGG:05417 | Genes: 25 | p-valor ruta: 6.4e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CYP1A1	NA	UP	6.086	6.00e-198	811.0
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
CCL2	NA	UP	2.562	2.63e-75	658.0
JUN	NA	UP	2.450	1.10e-62	6693.5
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
NLRP3	NA	UP	4.366	3.67e-13	29.8
TLR6	NA	UP	2.680	9.77e-08	26.3
SELE	NA	UP	5.745	2.05e-05	9.0
LY96	NA	UP	5.204	4.42e-03	3.4
VAV1	NA	UP	2.118	1.54e-02	7.9
OLR1	NA	UP	2.655	1.81e-02	6.9
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2

## Ruta: NF-kappa B signaling pathway

Fuente: KEGG | ID: KEGG:04064 | Genes: 17 | p-valor ruta: 9.51e-07

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL2	NA	UP	3.371	1.67e-155	4155.4
TNF	NA	UP	7.712	3.81e-103	573.0
TRAF1	NA	UP	4.730	5.65e-84	258.2
PTGS2	NA	UP	3.253	7.39e-80	3663.8
GADD45A	NA	UP	2.255	1.32e-60	1140.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
LTB	NA	UP	3.555	2.50e-41	150.4
VCAM1	NA	UP	4.737	4.28e-26	66.5
BCL2A1	NA	UP	4.192	1.64e-21	55.1
TNFSF13B	NA	UP	3.042	2.17e-11	34.7
TNFSF14	NA	UP	2.748	3.71e-07	23.0
LY96	NA	UP	5.204	4.42e-03	3.4

## Ruta: Malaria

Fuente: KEGG | ID: KEGG:05144 | Genes: 12 | p-valor ruta: 1.72e-06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
TNF	NA	UP	7.712	3.81e-103	573.0
THBS1	NA	UP	2.656	1.05e-77	3791.3
CCL2	NA	UP	2.562	2.63e-75	658.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
CSF3	NA	UP	6.122	1.72e-19	56.0
SELE	NA	UP	5.745	2.05e-05	9.0
TLR9	NA	UP	2.952	1.98e-02	4.6
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: AGE–RAGE signaling pathway in diabetic complications

Fuente: KEGG | ID: KEGG:04933 | Genes: 16 | p–valor ruta: 4.8e–06

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e–214	2230.2
ICAM1	NA	UP	3.652	3.11e–204	19095.5
SERPINE1	NA	UP	4.807	1.12e–104	435.1
TNF	NA	UP	7.712	3.81e–103	573.0
CCL2	NA	UP	2.562	2.63e–75	658.0
EGR1	NA	UP	2.472	2.61e–74	1149.5
STAT1	NA	UP	2.519	1.61e–68	9528.0
JUN	NA	UP	2.450	1.10e–62	6693.5
VCAM1	NA	UP	4.737	4.28e–26	66.5
JAK2	NA	UP	2.081	1.26e–17	123.4
COL4A1	NA	UP	6.589	5.89e–06	8.2
SELE	NA	UP	5.745	2.05e–05	9.0
THBD	NA	UP	2.330	1.23e–02	7.3
AGTR1	NA	DOWN	-3.177	1.87e–02	5.1

## Ruta: Pertussis

Fuente: KEGG | ID: KEGG:05133 | Genes: 13 | p-valor ruta: 4.06e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
IRF1	NA	UP	3.512	7.87e-194	2808.9
TNF	NA	UP	7.712	3.81e-103	573.0
JUN	NA	UP	2.450	1.10e-62	6693.5
C1R	NA	UP	2.188	3.06e-32	258.8
IL12A	NA	UP	3.852	1.95e-28	83.7
ITGAM	NA	UP	2.447	1.39e-19	90.2
CASP1	NA	UP	2.494	1.49e-18	80.2
NLRP3	NA	UP	4.366	3.67e-13	29.8
IL23A	NA	UP	2.189	2.05e-11	59.9
LY96	NA	UP	5.204	4.42e-03	3.4

## Ruta: African trypanosomiasis

Fuente: KEGG | ID: KEGG:05143 | Genes: 9 | p-valor ruta: 9.26e-05

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
ICAM1	NA	UP	3.652	3.11e-204	19095.5
IDO1	NA	UP	4.167	4.38e-109	394.2
TNF	NA	UP	7.712	3.81e-103	573.0
IL12A	NA	UP	3.852	1.95e-28	83.7
VCAM1	NA	UP	4.737	4.28e-26	66.5
SELE	NA	UP	5.745	2.05e-05	9.0
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: JAK–STAT signaling pathway

Fuente: KEGG | ID: KEGG:04630 | Genes: 18 | p-valor ruta: 1.95e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
CSF2	NA	UP	7.043	2.08e-103	455.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IFNL1	NA	UP	8.179	1.68e-89	578.0
STAT1	NA	UP	2.519	1.61e-68	9528.0
IL15RA	NA	UP	2.045	1.16e-42	847.9
IFNL3	NA	UP	9.837	4.42e-30	365.0
IL12A	NA	UP	3.852	1.95e-28	83.7
LIFR	NA	UP	2.213	9.30e-24	226.1
IFNL2	NA	UP	11.372	1.86e-23	434.7
CSF3	NA	UP	6.122	1.72e-19	56.0
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
IL23A	NA	UP	2.189	2.05e-11	59.9
SOCS1	NA	UP	2.012	6.54e-08	82.5
IL10RA	NA	UP	3.172	3.66e-07	18.8
IL13RA2	NA	UP	2.568	3.02e-02	4.7

## Ruta: Hepatitis C

Fuente: KEGG | ID: KEGG:05160 | Genes: 17 | p-valor ruta: 5.91e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IFIT1	NA	UP	4.523	0.00e+00	6073.5
OAS2	NA	UP	4.850	0.00e+00	6634.3
RSAD2	NA	UP	5.110	0.00e+00	2686.5
MX2	NA	UP	5.374	1.90e-273	1682.8
MX1	NA	UP	3.859	1.25e-245	5699.6
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
CXCL10	NA	UP	6.079	8.12e-195	783.4
OAS1	NA	UP	3.011	3.81e-158	5273.1
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
CLDN2	NA	DOWN	-3.586	5.60e-89	498.3
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
TLR3	NA	UP	2.508	1.99e-22	111.5

## Ruta: Necroptosis

Fuente: KEGG | ID: KEGG:04217 | Genes: 17 | p-valor ruta: 5.91e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNFSF10	NA	UP	3.014	1.58e-112	3429.5
TNF	NA	UP	7.712	3.81e-103	573.0
ZBP1	NA	UP	6.242	1.22e-99	349.5
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
BIRC3	NA	UP	2.146	8.30e-42	2602.9
TLR3	NA	UP	2.508	1.99e-22	111.5
CASP1	NA	UP	2.494	1.49e-18	80.2
JAK2	NA	UP	2.081	1.26e-17	123.4
PLA2G4C	NA	UP	2.364	3.45e-13	59.8
NLRP3	NA	UP	4.366	3.67e-13	29.8
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2

## Ruta: Tuberculosis

Fuente: KEGG | ID: KEGG:05152 | Genes: 18 | p-valor ruta: 5.93e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
IRAK2	NA	UP	2.666	3.46e-95	1164.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
STAT1	NA	UP	2.519	1.61e-68	9528.0
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
IL23A	NA	UP	2.189	2.05e-11	59.9
CLEC4E	NA	UP	3.620	4.75e-09	26.0
TLR6	NA	UP	2.680	9.77e-08	26.3
IL10RA	NA	UP	3.172	3.66e-07	18.8
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
TLR9	NA	UP	2.952	1.98e-02	4.6
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: Legionellosis

Fuente: KEGG | ID: KEGG:05134 | Genes: 10 | p-valor ruta: 6.15e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL2	NA	UP	3.371	1.67e-155	4155.4
TNF	NA	UP	7.712	3.81e-103	573.0
IL12A	NA	UP	3.852	1.95e-28	83.7
ITGAM	NA	UP	2.447	1.39e-19	90.2
CASP1	NA	UP	2.494	1.49e-18	80.2
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: Cytosolic DNA-sensing pathway

Fuente: KEGG | ID: KEGG:04623 | Genes: 12 | p-valor ruta: 6.31e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL10	NA	UP	6.079	8.12e-195	783.4
CCL5	NA	UP	5.035	8.94e-165	656.3
IFI16	NA	UP	3.151	2.12e-114	2583.4
ZBP1	NA	UP	6.242	1.22e-99	349.5
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
SAMHD1	NA	UP	2.304	5.99e-57	1585.1
CASP1	NA	UP	2.494	1.49e-18	80.2
NLRP3	NA	UP	4.366	3.67e-13	29.8

## Ruta: Epstein–Barr virus infection

Fuente: KEGG | ID: KEGG:05169 | Genes: 19 | p-valor ruta: 9.01e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
OAS2	NA	UP	4.850	0.00e+00	6634.3
IL6	NA	UP	6.060	0.00e+00	1698.5
TNFAIP3	NA	UP	5.334	9.38e-277	2472.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL10	NA	UP	6.079	8.12e-195	783.4
OAS1	NA	UP	3.011	3.81e-158	5273.1
TAP1	NA	UP	2.707	8.35e-123	5228.7
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
OAS3	NA	UP	2.942	1.13e-87	8674.1
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
NEDD4	NA	UP	2.433	4.99e-60	1678.5
ISG15	NA	UP	2.482	5.90e-57	3807.9
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0

## Ruta: Pathways in cancer (Página 1 de 2)

Fuente: KEGG | ID: KEGG:05200 | Genes: 35 | p-valor ruta: 9.43e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
STAT2	NA	UP	2.337	1.85e-96	2004.6
TRAF1	NA	UP	4.730	5.65e-84	258.2
RASGRP3	NA	UP	3.468	2.92e-82	392.1
PTGS2	NA	UP	3.253	7.39e-80	3663.8
PMAIP1	NA	UP	2.602	3.62e-79	1786.6
PTGER4	NA	UP	2.548	1.70e-71	568.2
PML	NA	UP	2.208	2.84e-70	2901.3
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
GADD45A	NA	UP	2.255	1.32e-60	1140.5
BBC3	NA	UP	2.829	3.65e-57	503.1
IL15RA	NA	UP	2.045	1.16e-42	847.9
BIRC3	NA	UP	2.146	8.30e-42	2602.9
BMP2	NA	UP	2.237	3.69e-40	325.3
RASGRP1	NA	UP	2.055	4.16e-34	336.9
IL12A	NA	UP	3.852	1.95e-28	83.7
NKX3-1	NA	UP	2.233	8.30e-23	132.4
LAMA2	NA	UP	2.355	4.82e-21	125.5
FGF19	NA	UP	3.931	5.59e-21	52.8
JAK2	NA	UP	2.081	1.26e-17	123.4
IL15	NA	UP	2.012	2.28e-17	116.8
BDKRB2	NA	UP	2.797	5.56e-15	55.1
FLT3LG	NA	UP	2.346	6.32e-15	68.5

## Ruta: Pathways in cancer (Página 2 de 2)

Fuente: KEGG | ID: KEGG:05200 | Genes: 35 | p-valor ruta: 9.43e-04

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL23A	NA	UP	2.189	2.05e-11	59.9
COL4A1	NA	UP	6.589	5.89e-06	8.2
ADCY4	NA	UP	2.271	8.12e-06	23.6
PTGER2	NA	UP	3.006	1.95e-04	11.0
KIT	NA	UP	3.650	6.24e-04	7.9
DLL1	NA	UP	2.171	4.40e-03	10.4
RET	NA	UP	2.793	1.44e-02	5.5
AGTR1	NA	DOWN	-3.177	1.87e-02	5.1
CAMK2B	NA	DOWN	-4.468	1.91e-02	2.2
FGF18	NA	UP	2.038	4.86e-02	6.1

## Ruta: Leishmaniasis

Fuente: KEGG | ID: KEGG:05140 | Genes: 11 | p-valor ruta: 1.01e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
PTGS2	NA	UP	3.253	7.39e-80	3663.8
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
IL12A	NA	UP	3.852	1.95e-28	83.7
ITGAM	NA	UP	2.447	1.39e-19	90.2
JAK2	NA	UP	2.081	1.26e-17	123.4
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: Chagas disease

Fuente: KEGG | ID: KEGG:05142 | Genes: 13 | p-valor ruta: 1.1e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IL1B	NA	UP	4.202	1.58e-214	2230.2
CCL5	NA	UP	5.035	8.94e-165	656.3
SERPINE1	NA	UP	4.807	1.12e-104	435.1
TNF	NA	UP	7.712	3.81e-103	573.0
IFNB1	NA	UP	10.001	4.69e-95	1340.6
CCL2	NA	UP	2.562	2.63e-75	658.0
JUN	NA	UP	2.450	1.10e-62	6693.5
IL12A	NA	UP	3.852	1.95e-28	83.7
BDKRB2	NA	UP	2.797	5.56e-15	55.1
TLR6	NA	UP	2.680	9.77e-08	26.3
TLR9	NA	UP	2.952	1.98e-02	4.6

## Ruta: Inflammatory bowel disease

Fuente: KEGG | ID: KEGG:05321 | Genes: 10 | p-valor ruta: 1.58e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
TNF	NA	UP	7.712	3.81e-103	573.0
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
IL12A	NA	UP	3.852	1.95e-28	83.7
NOD2	NA	UP	2.981	1.19e-19	80.5
IL23A	NA	UP	2.189	2.05e-11	59.9
IL18R1	NA	UP	2.088	8.75e-05	23.0

## Ruta: Chemokine signaling pathway

Fuente: KEGG | ID: KEGG:04062 | Genes: 18 | p-valor ruta: 1.86e-03

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
CCL20	NA	UP	3.959	5.09e-242	2226.4
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
CXCL10	NA	UP	6.079	8.12e-195	783.4
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL11	NA	UP	6.074	5.51e-176	710.1
CCL5	NA	UP	5.035	8.94e-165	656.3
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CX3CL1	NA	UP	3.114	2.67e-123	1760.3
STAT2	NA	UP	2.337	1.85e-96	2004.6
CCL2	NA	UP	2.562	2.63e-75	658.0
STAT1	NA	UP	2.519	1.61e-68	9528.0
CCL22	NA	UP	3.454	2.91e-50	168.7
JAK2	NA	UP	2.081	1.26e-17	123.4
ADCY4	NA	UP	2.271	8.12e-06	23.6
CXCL9	NA	UP	4.099	4.37e-04	26.3
VAV1	NA	UP	2.118	1.54e-02	7.9
GRK4	NA	DOWN	-2.986	2.78e-02	4.3
CCL17	NA	UP	3.441	3.89e-02	2.9

## Ruta: Hematopoietic cell lineage

Fuente: KEGG | ID: KEGG:04640 | Genes: 11 | p-valor ruta: 1.05e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL1A	NA	UP	5.228	0.00e+00	4828.4
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
CSF1	NA	UP	2.530	1.40e-49	467.4
ITGAM	NA	UP	2.447	1.39e-19	90.2
CSF3	NA	UP	6.122	1.72e-19	56.0
FLT3LG	NA	UP	2.346	6.32e-15	68.5
KIT	NA	UP	3.650	6.24e-04	7.9
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: Amoebiasis

Fuente: KEGG | ID: KEGG:05146 | Genes: 11 | p-valor ruta: 2.45e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
IL1B	NA	UP	4.202	1.58e-214	2230.2
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL2	NA	UP	3.371	1.67e-155	4155.4
CSF2	NA	UP	7.043	2.08e-103	455.6
TNF	NA	UP	7.712	3.81e-103	573.0
SERPINB9	NA	UP	2.439	1.35e-89	1138.5
IL12A	NA	UP	3.852	1.95e-28	83.7
LAMA2	NA	UP	2.355	4.82e-21	125.5
ITGAM	NA	UP	2.447	1.39e-19	90.2
COL4A1	NA	UP	6.589	5.89e-06	8.2

## Ruta: Transcriptional misregulation in cancer

Fuente: KEGG | ID: KEGG:05202 | Genes: 16 | p-valor ruta: 2.5e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
PLAT	NA	UP	2.447	4.98e-113	6662.1
CSF2	NA	UP	7.043	2.08e-103	455.6
TRAF1	NA	UP	4.730	5.65e-84	258.2
ETV7	NA	UP	4.688	2.39e-83	278.8
PML	NA	UP	2.208	2.84e-70	2901.3
GADD45A	NA	UP	2.255	1.32e-60	1140.5
BIRC3	NA	UP	2.146	8.30e-42	2602.9
NFKBIZ	NA	UP	2.037	4.06e-41	2486.2
BCL2A1	NA	UP	4.192	1.64e-21	55.1
ITGAM	NA	UP	2.447	1.39e-19	90.2
LMO2	NA	UP	3.437	9.83e-12	31.2
NR4A3	NA	UP	5.574	1.45e-08	20.2
NGFR	NA	UP	2.337	3.33e-07	30.0
RUNX2	NA	UP	3.983	1.50e-06	15.2
NUPR1	NA	UP	3.660	1.78e-06	14.5

## Ruta: Complement and coagulation cascades

Fuente: KEGG | ID: KEGG:04610 | Genes: 10 | p-valor ruta: 2.74e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
PLAT	NA	UP	2.447	4.98e-113	6662.1
SERPINE1	NA	UP	4.807	1.12e-104	435.1
SERPINB2	NA	UP	2.344	2.67e-55	2507.0
C1R	NA	UP	2.188	3.06e-32	258.8
ITGAM	NA	UP	2.447	1.39e-19	90.2
BDKRB2	NA	UP	2.797	5.56e-15	55.1
VWF	NA	UP	3.390	1.16e-02	4.6
THBD	NA	UP	2.330	1.23e-02	7.3
C3AR1	NA	UP	4.639	1.59e-02	2.2
CR1L	NA	UP	3.479	3.30e-02	3.5

## Ruta: Kaposi sarcoma–associated herpesvirus infection

Fuente: KEGG | ID: KEGG:05167 | Genes: 16 | p-valor ruta: 2.81e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
ICAM1	NA	UP	3.652	3.11e-204	19095.5
CXCL3	NA	UP	3.053	2.27e-187	4330.7
CXCL2	NA	UP	3.371	1.67e-155	4155.4
ZFP36	NA	UP	2.944	7.57e-104	1721.5
CSF2	NA	UP	7.043	2.08e-103	455.6
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
PTGS2	NA	UP	3.253	7.39e-80	3663.8
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
EIF2AK2	NA	UP	2.142	3.22e-48	1460.0
TLR3	NA	UP	2.508	1.99e-22	111.5
JAK2	NA	UP	2.081	1.26e-17	123.4

## Ruta: RIG-I-like receptor signaling pathway

Fuente: KEGG | ID: KEGG:04622 | Genes: 9 | p-valor ruta: 2.89e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
CXCL10	NA	UP	6.079	8.12e-195	783.4
TNF	NA	UP	7.712	3.81e-103	573.0
DHX58	NA	UP	2.877	1.75e-99	953.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
ISG15	NA	UP	2.482	5.90e-57	3807.9
IL12A	NA	UP	3.852	1.95e-28	83.7

## Ruta: Hepatitis B

Fuente: KEGG | ID: KEGG:05161 | Genes: 14 | p-valor ruta: 4.21e-02

gene_id	symbol	Regulacion	log2FoldChange	padj	baseMean
IL6	NA	UP	6.060	0.00e+00	1698.5
NFKBIA	NA	UP	4.079	6.66e-241	4955.3
IFIH1	NA	UP	4.035	2.22e-233	4525.3
TNF	NA	UP	7.712	3.81e-103	573.0
STAT2	NA	UP	2.337	1.85e-96	2004.6
IFNB1	NA	UP	10.001	4.69e-95	1340.6
IRF7	NA	UP	3.210	5.72e-79	2126.1
STAT1	NA	UP	2.519	1.61e-68	9528.0
JUN	NA	UP	2.450	1.10e-62	6693.5
CREB5	NA	UP	2.714	3.43e-62	649.9
TLR3	NA	UP	2.508	1.99e-22	111.5
JAK2	NA	UP	2.081	1.26e-17	123.4
EGR2	NA	UP	3.090	6.72e-15	43.7
EGR3	NA	UP	2.096	2.87e-04	21.5