

GSE64041.gsea.zip

WikiPathways

Type	Name	#Hits	Expected score	p-Value
enriched	mRNA Processing	120	0.000000	0.000000
enriched	Retinoblastoma Gene in Cancer	86	0.000000	0.000000
enriched	Cell Cycle	119	0.000000	0.000000
enriched	DNA IR-damage and cellular response via ATR	79	0.000000	0.000000
depleted	Complement and Coagulation Cascades	57	0.000000	0.000000
enriched	DNA Replication	42	0.000000	0.000000
depleted	Complement Activation	20	0.000000	0.000000
depleted	Metapathway biotransformation Phase I and II	166	0.000000	0.000000
enriched	DNA IR-Double Strand Breaks (DSBs) and cellular response via ATM	55	0.000000	0.000000
enriched	Parkin-Ubiquitin Proteasomal System pathway	67	0.000000	0.000000
depleted	Human Complement System	96	0.000000	0.000000
enriched	Proteasome Degradation	58	0.000000	0.000000
depleted	Nuclear Receptors Meta-Pathway	303	0.000000	0.000000
enriched	Pyrimidine metabolism	82	0.000000	0.000000
enriched	ATM Signaling Network in Development and Disease	45	0.000000	0.000000
enriched	Gastric Cancer Network 1	27	0.000000	0.000000
depleted	Biomarkers for urea cycle disorders	12	0.000000	0.000001
enriched	Ciliary landscape	211	0.000000	0.000001
depleted	Eicosanoid metabolism via Cyclo Oxygenases (COX)	30	0.000000	0.000001
enriched	FBXL10 enhancement of MAP/ERK signaling in diffuse large B-cell lymphoma	29	0.000000	0.000001
enriched	Cytoplasmic Ribosomal Proteins	76	0.000000	0.000002
depleted	Mitochondrial LC-Fatty Acid Beta-Oxidation	17	0.000000	0.000004
depleted	GPCRs, Class A Rhodopsin-like	249	0.000000	0.000004
depleted	PPAR Alpha Pathway	24	0.000000	0.000006
depleted	Tryptophan metabolism	40	0.000000	0.000008
enriched	G1 to S cell cycle control	63	0.000000	0.000010
enriched	The effect of progerin on the involved genes in Hutchinson-Gilford Progeria Syndrome	33	0.000000	0.000013
depleted	Arylamine metabolism	4	0.000000	0.000020
depleted	Fatty Acid Omega Oxidation	14	0.000000	0.000030
enriched	ATM Signaling Pathway	40	0.000000	0.000040
depleted	Amino Acid metabolism	89	0.000000	0.000041
depleted	Oxidation by Cytochrome P450	59	0.000000	0.000041
enriched	Translation Factors	47	0.000000	0.000055
depleted	Eicosanoid metabolism via Cytochrome P450 Mono-Oxygenases (CYP) pathway	9	0.000000	0.000073
enriched	Regulation of sister chromatid separation at the metaphase-anaphase transition	15	0.000000	0.000073
enriched	TGF-beta Signaling Pathway	130	0.000000	0.000073
depleted	Diclofenac Metabolic Pathway	4	0.000000	0.000098
depleted	Nuclear Receptors in Lipid Metabolism and Toxicity	34	0.000000	0.000132
depleted	Caffeine and Theobromine metabolism	3	0.000000	0.000141

enriched	Integrated Breast Cancer Pathway	150	0.000000	0.000160
enriched	Integrated Cancer Pathway	45	0.000000	0.000166
depleted	PPAR signaling pathway	64	0.000000	0.000185
depleted	Tamoxifen metabolism	16	0.000000	0.000240
depleted	Alanine and aspartate metabolism	12	0.000000	0.000241
depleted	Blood Clotting Cascade	22	0.000000	0.000241
enriched	Gastric Cancer Network 2	31	0.000000	0.000258
enriched	Eukaryotic Transcription Initiation	39	0.000000	0.000303
enriched	DNA Damage Response	68	0.000000	0.000312
enriched	Target Of Rapamycin (TOR) Signaling	35	0.000000	0.000322
enriched	miRNA Regulation of DNA Damage Response	80	0.000000	0.000362
depleted	Fatty Acid Beta Oxidation	31	0.000000	0.000748
enriched	Histone Modifications	62	0.000000	0.000748
enriched	Pathogenic Escherichia coli infection	54	0.000000	0.000820
depleted	Allograft Rejection	83	0.000000	0.000935
depleted	Amino Acid Metabolism Pathway Excerpt (Histidine catabolism extension)	5	0.000000	0.001191
enriched	Envelope proteins and their potential roles in EDMD physiopathology	46	0.000000	0.001318
depleted	Farnesoid X Receptor Pathway	19	0.000000	0.002304
depleted	Urea cycle and related diseases	9	0.000000	0.002467
depleted	Constitutive Androstane Receptor Pathway	27	0.000000	0.002669
depleted	Copper homeostasis	52	0.000000	0.003682
depleted	Phosphodiesterases in neuronal function	51	0.000000	0.003682
depleted	Statin Pathway	28	0.000000	0.004851
depleted	Urea cycle and associated pathways	20	0.000000	0.005093
depleted	NAD Biosynthesis II (from tryptophan)	8	0.000000	0.006363
depleted	Selenium Micronutrient Network	83	0.000000	0.006826
enriched	Hepatitis C and Hepatocellular Carcinoma	49	0.000000	0.008485
depleted	Eicosanoid Synthesis	24	0.000000	0.009329
depleted	Pregnane X Receptor pathway	27	0.000000	0.009758
depleted	Eicosanoid metabolism via Lipo Oxygenases (LOX)	27	0.000000	0.013333
depleted	Methionine metabolism leading to Sulphur Amino Acids and related disorders	10	0.000000	0.016252
enriched	DNA Mismatch Repair	9	0.000000	0.016402
enriched	p38 MAPK Signaling Pathway	34	0.000000	0.016402
enriched	TNF related weak inducer of apoptosis (TWEAK) Signaling Pathway	41	0.000000	0.016784
depleted	Ras Signaling	177	0.000000	0.017180
enriched	Wnt Signaling Pathway (Netpath)	51	0.000000	0.017180
depleted	Metabolic pathway of LDL, HDL and TG, including diseases	15	0.000000	0.019657
depleted	Estrogen Receptor Pathway	13	0.000000	0.020547
depleted	Valproic acid pathway	12	0.000000	0.023479
depleted	Vitamin B12 Metabolism	47	0.000000	0.023584
enriched	TNF alpha Signaling Pathway	89	0.000000	0.025145
depleted	Cancer immunotherapy by PD-1 blockade	22	0.000000	0.031314
enriched	Nucleotide Metabolism	19	0.000000	0.031314
depleted	Peptide GPCRs	74	0.000000	0.032785
depleted	Tyrosine Metabolism	4	0.000000	0.032785
depleted	Deregulation of Rab and Rab Effector Genes in Bladder Cancer	16	0.000000	0.036304
enriched	ATR Signaling	9	0.000000	0.037517
enriched	Androgen receptor signaling pathway	89	0.000000	0.037517
depleted	Estrogen metabolism	15	0.000000	0.037517
depleted	Biosynthesis and regeneration of tetrahydrobiopterin (BH4) and catabolism of phenylalanine, including diseases	2	0.000000	0.041556
enriched	Photodynamic therapy-induced unfolded protein response	27	0.000000	0.042900
depleted	Fatty Acid Biosynthesis	22	0.000000	0.043853

enriched	Homologous recombination	13	0.000000	0.044984
depleted	Vitamin A and Carotenoid Metabolism	42	0.000000	0.045705
depleted	Drug Induction of Bile Acid Pathway	17	0.000000	0.046130
enriched	Cholesterol Biosynthesis Pathway	15	0.000000	0.049943

GO - Molecular Function

Type	Name	#Hits	Expected score	p-Value
depleted	cofactor binding	481	0.000000	0.000000
depleted	oxidoreductase activity	679	0.000000	0.000000
depleted	coenzyme binding	279	0.000000	0.000000
depleted	olfactory receptor activity	361	0.000000	0.000000
enriched	ATPase activity	362	0.000000	0.000000
enriched	ribonucleoprotein complex binding	124	0.000000	0.000000
enriched	ATPase activity, coupled	233	0.000000	0.000000
enriched	single-stranded DNA binding	101	0.000000	0.000000
enriched	histone binding	192	0.000000	0.000000
depleted	heme binding	125	0.000000	0.000000
enriched	structural constituent of ribosome	149	0.000000	0.000000
depleted	antigen binding	54	0.000000	0.000000
enriched	chromatin binding	510	0.000000	0.000000
depleted	lipid binding	697	0.000000	0.000000
enriched	ubiquitin-like protein ligase binding	298	0.000000	0.000000
enriched	unfolded protein binding	117	0.000000	0.000000
enriched	DNA replication origin binding	23	0.000000	0.000000
enriched	ubiquitin protein ligase binding	282	0.000000	0.000000
depleted	lipid transporter activity	129	0.000000	0.000001
depleted	vitamin binding	131	0.000000	0.000001
enriched	cadherin binding	313	0.000000	0.000001
depleted	carbohydrate binding	253	0.000000	0.000002
enriched	DNA-dependent ATPase activity	77	0.000000	0.000002
enriched	helicase activity	134	0.000000	0.000002
depleted	serine-type endopeptidase activity	152	0.000000	0.000002
depleted	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavo-protein as one donor, and incorporation of one atom of oxygen	33	0.000000	0.000003
depleted	monooxygenase activity	94	0.000000	0.000003
depleted	organic acid binding	192	0.000000	0.000004
depleted	pyridoxal phosphate binding	51	0.000000	0.000008
depleted	aromatase activity	25	0.000000	0.000008
depleted	serine hydrolase activity	178	0.000000	0.000012
enriched	DNA polymerase binding	16	0.000000	0.000013
enriched	ubiquitin binding	74	0.000000	0.000016
depleted	carboxylic acid binding	183	0.000000	0.000017
depleted	serine-type peptidase activity	174	0.000000	0.000018
enriched	ubiquitin-like protein binding	94	0.000000	0.000018
enriched	mRNA binding	242	0.000000	0.000021
enriched	tubulin binding	335	0.000000	0.000021
depleted	cation channel activity	315	0.000000	0.000029
depleted	glutathione transferase activity	23	0.000000	0.000035
enriched	ubiquitin-like protein transferase activity	349	0.000000	0.000043
depleted	receptor regulator activity	477	0.000000	0.000044
depleted	steroid binding	91	0.000000	0.000044
enriched	transcription factor binding	649	0.000000	0.000048
enriched	heat shock protein binding	112	0.000000	0.000052
enriched	RNA methyltransferase activity	61	0.000000	0.000060

depleted	signaling receptor activator activity	448	0.000000	0.000064
enriched	damaged DNA binding	59	0.000000	0.000067
depleted	receptor ligand activity	442	0.000000	0.000074
depleted	acyl-CoA dehydrogenase activity	10	0.000000	0.000079
depleted	oxidoreductase activity, acting on the CH-CH group of donors	56	0.000000	0.000079
depleted	flavin adenine dinucleotide binding	76	0.000000	0.000080
depleted	cytokine receptor activity	94	0.000000	0.000085
depleted	arachidonic acid epoxigenase activity	14	0.000000	0.000098
enriched	transcription coregulator activity	544	0.000000	0.000119
depleted	potassium ion transmembrane transporter activity	151	0.000000	0.000137
enriched	protein kinase binding	630	0.000000	0.000151
enriched	modification-dependent protein binding	140	0.000000	0.000182
depleted	steroid hydroxylase activity	35	0.000000	0.000182
depleted	sterol binding	55	0.000000	0.000182
enriched	histone kinase activity	16	0.000000	0.000198
enriched	RNA helicase activity	71	0.000000	0.000215
depleted	heparin binding	168	0.000000	0.000245
depleted	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	114	0.000000	0.000245
depleted	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	149	0.000000	0.000262
depleted	iron ion binding	144	0.000000	0.000311
enriched	basal RNA polymerase II transcription machinery binding	53	0.000000	0.000314
enriched	snRNP binding	8	0.000000	0.000328
depleted	lyase activity	179	0.000000	0.000335
depleted	arachidonic acid monooxygenase activity	15	0.000000	0.000386
depleted	transaminase activity	21	0.000000	0.000416
depleted	ion channel activity	406	0.000000	0.000423
enriched	transcription coactivator activity	310	0.000000	0.000427
enriched	RNA polymerase II-specific DNA-binding transcription factor binding	278	0.000000	0.000487
depleted	metal ion transmembrane transporter activity	428	0.000000	0.000595
enriched	cell adhesion molecule binding	479	0.000000	0.000612
enriched	protein folding chaperone	25	0.000000	0.000681
depleted	lipopeptide binding	10	0.000000	0.000792
enriched	protein N-terminus binding	102	0.000000	0.000821
depleted	inorganic cation transmembrane transporter activity	557	0.000000	0.000880
enriched	ubiquitin-protein transferase activity	328	0.000000	0.001004
enriched	protein heterodimerization activity	430	0.000000	0.001085
enriched	DNA helicase activity	53	0.000000	0.001157
depleted	passive transmembrane transporter activity	445	0.000000	0.001333
depleted	potassium channel activity	117	0.000000	0.001372
depleted	Ras guanyl-nucleotide exchange factor activity	123	0.000000	0.001428
depleted	channel activity	444	0.000000	0.001428
enriched	chaperone binding	100	0.000000	0.001743
depleted	protein tyrosine kinase activity	133	0.000000	0.002108
enriched	exonuclease activity	74	0.000000	0.002275
depleted	monovalent inorganic cation transmembrane transporter activity	353	0.000000	0.002275
enriched	proton-transporting ATPase activity, rotational mechanism	22	0.000000	0.002372
depleted	voltage-gated ion channel activity	190	0.000000	0.002426
enriched	double-stranded DNA exodeoxyribonuclease activity	4	0.000000	0.003114
enriched	translation initiation factor activity	39	0.000000	0.003294
depleted	ligand-gated ion channel activity	126	0.000000	0.003358
enriched	proteasome binding	17	0.000000	0.003636
depleted	cargo receptor activity	75	0.000000	0.003689
depleted	molybdopterin cofactor binding	6	0.000000	0.003766

depleted	caffeine oxidase activity	4	0.000000	0.003793
enriched	snRNA binding	38	0.000000	0.004529
depleted	voltage-gated cation channel activity	136	0.000000	0.004532
depleted	cation transmembrane transporter activity	608	0.000000	0.004727
depleted	immunoglobulin binding	22	0.000000	0.004727
enriched	snoRNA binding	23	0.000000	0.004727
depleted	G protein-coupled peptide receptor activity	144	0.000000	0.004909
enriched	nucleoside binding	368	0.000000	0.006149
enriched	U1 snRNP binding	6	0.000000	0.006498
enriched	steroid hormone receptor binding	91	0.000000	0.006498
depleted	leukotriene-B4 20-monooxygenase activity	4	0.000000	0.006722
enriched	nuclear hormone receptor binding	152	0.000000	0.006722
enriched	nuclease activity	171	0.000000	0.006722
enriched	ribonucleoside binding	361	0.000000	0.006722
enriched	nucleosome binding	44	0.000000	0.006776
depleted	MHC class I protein complex binding	6	0.000000	0.007343
enriched	nuclear receptor binding	110	0.000000	0.007380
enriched	core promoter binding	54	0.000000	0.008013
depleted	hormone activity	111	0.000000	0.008314
enriched	TBP-class protein binding	22	0.000000	0.008549
enriched	translation regulator activity	122	0.000000	0.008846
depleted	enoyl-CoA hydratase activity	8	0.000000	0.009019
depleted	monocarboxylic acid transmembrane transporter activity	56	0.000000	0.009020
depleted	glycosaminoglycan binding	225	0.000000	0.009401
depleted	peptide receptor activity	149	0.000000	0.009401
enriched	purine nucleoside binding	361	0.000000	0.009811
enriched	translation factor activity, RNA binding	72	0.000000	0.010259
depleted	fatty-acyl-CoA binding	21	0.000000	0.010287
depleted	transmembrane receptor protein tyrosine kinase activity	62	0.000000	0.010287
enriched	methyltransferase activity	194	0.000000	0.010332
enriched	p53 binding	64	0.000000	0.010655
depleted	amide binding	327	0.000000	0.010657
depleted	neurotransmitter receptor activity	112	0.000000	0.010713
enriched	protein domain specific binding	672	0.000000	0.011136
depleted	Rho guanyl-nucleotide exchange factor activity	72	0.000000	0.011315
depleted	testosterone 6-beta-hydroxylase activity	4	0.000000	0.011315
depleted	peptidase inhibitor activity	176	0.000000	0.013309
depleted	scavenger receptor activity	51	0.000000	0.013322
depleted	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	117	0.000000	0.013540
enriched	RNA polymerase II complex binding	35	0.000000	0.014513
enriched	disordered domain specific binding	34	0.000000	0.014513
enriched	mRNA 3'-UTR binding	83	0.000000	0.015248
depleted	voltage-gated potassium channel activity	81	0.000000	0.015248
depleted	cholesterol binding	48	0.000000	0.016710
enriched	ribosome binding	51	0.000000	0.016710
enriched	telomeric DNA binding	36	0.000000	0.016740
enriched	rRNA methyltransferase activity	20	0.000000	0.016921
enriched	RNA polymerase core enzyme binding	43	0.000000	0.019581
enriched	ribosomal small subunit binding	14	0.000000	0.019581
enriched	GTP binding	353	0.000000	0.020164
enriched	RISC complex binding	3	0.000000	0.020532
depleted	endopeptidase inhibitor activity	169	0.000000	0.020803
enriched	microtubule binding	247	0.000000	0.021062
enriched	microtubule motor activity	75	0.000000	0.021238
depleted	alcohol dehydrogenase activity, zinc-dependent	7	0.000000	0.021358
enriched	RNA polymerase binding	57	0.000000	0.021537

depleted	calcium ion binding	660	0.000000	0.021537
enriched	S-adenosylmethionine-dependent methyltransferase activity	137	0.000000	0.021816
depleted	transforming growth factor beta receptor, inhibitory cytoplas-	2	0.000000	0.021933
	mic mediator activity			
enriched	protein kinase C inhibitor activity	3	0.000000	0.022388
enriched	histone deacetylase binding	108	0.000000	0.022869
depleted	cytokine activity	200	0.000000	0.023392
depleted	alcohol dehydrogenase (NAD+) activity	9	0.000000	0.023950
depleted	alcohol dehydrogenase [NAD(P)+] activity	9	0.000000	0.023950
depleted	glutathione hydrolase activity	6	0.000000	0.024320
depleted	T cell receptor binding	6	0.000000	0.024441
depleted	carbon-carbon lyase activity	49	0.000000	0.027203
depleted	channel regulator activity	130	0.000000	0.027203
enriched	core promoter sequence-specific DNA binding	44	0.000000	0.027927
depleted	guanyl-nucleotide exchange factor activity	193	0.000000	0.029852
depleted	organic anion transmembrane transporter activity	206	0.000000	0.029852
enriched	structural molecule activity	639	0.000000	0.029852
enriched	ubiquitin protein ligase activity	193	0.000000	0.029866
depleted	phosphatidylcholine-sterol O-acyltransferase activator activity	6	0.000000	0.030050
depleted	secondary active transmembrane transporter activity	235	0.000000	0.030050
enriched	RNA polymerase II general transcription initiation factor activ-	12	0.000000	0.031056
	ity			
depleted	primary amine oxidase activity	6	0.000000	0.031273
depleted	serine-type endopeptidase inhibitor activity	88	0.000000	0.032004
enriched	Hsp90 protein binding	37	0.000000	0.036766
enriched	odorant binding	81	0.000000	0.037024
depleted	FAD binding	31	0.000000	0.038213
depleted	estrogen 16-alpha-hydroxylase activity	8	0.000000	0.038213
enriched	mRNA CDS binding	3	0.000000	0.043223
depleted	sialic acid binding	12	0.000000	0.044748
depleted	palmitoyl-CoA oxidase activity	3	0.000000	0.045020
depleted	symporter activity	144	0.000000	0.046039
enriched	ubiquitin conjugating enzyme activity	37	0.000000	0.046039
enriched	5'-3' RNA polymerase activity	21	0.000000	0.046674
depleted	endopeptidase regulator activity	177	0.000000	0.049577

GO_- Biological Process

Type	Name	#Hits	Expected score	p-Value
enriched	DNA metabolic process	690	0.000000	0.000000
enriched	mRNA metabolic process	603	0.000000	0.000000
depleted	carboxylic acid catabolic process	244	0.000000	0.000000
enriched	DNA repair	461	0.000000	0.000000
enriched	mRNA processing	403	0.000000	0.000000
enriched	RNA splicing, via transesterification reactions	243	0.000000	0.000000
enriched	mRNA splicing, via spliceosome	238	0.000000	0.000000
enriched	cell division	383	0.000000	0.000000
enriched	RNA splicing	343	0.000000	0.000000
enriched	regulation of mitotic cell cycle	613	0.000000	0.000000
enriched	chromosome organization	379	0.000000	0.000000
enriched	rRNA processing	198	0.000000	0.000000
enriched	rRNA metabolic process	209	0.000000	0.000000
enriched	chromatin organization	646	0.000000	0.000000
enriched	regulation of cell cycle phase transition	437	0.000000	0.000000
enriched	cellular protein-containing complex assembly	690	0.000000	0.000000
enriched	regulation of mitotic cell cycle phase transition	405	0.000000	0.000000

depleted	cellular amino acid catabolic process	118	0.000000	0.000000
enriched	cell cycle	432	0.000000	0.000000
enriched	mitotic cell cycle phase transition	249	0.000000	0.000000
enriched	cell cycle phase transition	256	0.000000	0.000000
depleted	monocarboxylic acid metabolic process	485	0.000000	0.000000
enriched	negative regulation of cell cycle	548	0.000000	0.000000
enriched	DNA replication	154	0.000000	0.000000
enriched	regulation of cell cycle G2/M phase transition	208	0.000000	0.000000
enriched	viral process	584	0.000000	0.000000
enriched	ribonucleoprotein complex assembly	169	0.000000	0.000000
depleted	drug metabolic process	463	0.000000	0.000000
enriched	negative regulation of cell cycle process	313	0.000000	0.000000
enriched	regulation of G2/M transition of mitotic cell cycle	191	0.000000	0.000000
depleted	alpha-amino acid metabolic process	187	0.000000	0.000000
depleted	fatty acid metabolic process	293	0.000000	0.000000
enriched	posttranscriptional regulation of gene expression	476	0.000000	0.000000
enriched	protein-DNA complex assembly	178	0.000000	0.000000
enriched	regulation of chromosome organization	336	0.000000	0.000000
enriched	ribonucleoprotein complex biogenesis	67	0.000000	0.000000
enriched	double-strand break repair	175	0.000000	0.000000
enriched	G2/M transition of mitotic cell cycle	130	0.000000	0.000000
depleted	cellular amino acid metabolic process	271	0.000000	0.000000
enriched	mitotic cell cycle	139	0.000000	0.000000
depleted	complement activation	51	0.000000	0.000000
enriched	DNA recombination	186	0.000000	0.000000
enriched	cell cycle G2/M phase transition	132	0.000000	0.000000
enriched	negative regulation of mitotic cell cycle phase transition	209	0.000000	0.000000
enriched	negative regulation of mitotic cell cycle	299	0.000000	0.000000
depleted	fatty acid catabolic process	85	0.000000	0.000000
depleted	detection of chemical stimulus involved in sensory perception of smell	361	0.000000	0.000000
enriched	RNA biosynthetic process	603	0.000000	0.000000
enriched	covalent chromatin modification	355	0.000000	0.000000
depleted	detection of chemical stimulus involved in sensory perception	409	0.000000	0.000000
enriched	histone modification	348	0.000000	0.000000
enriched	protein ubiquitination	666	0.000000	0.000000
depleted	detection of chemical stimulus	441	0.000000	0.000000
depleted	detection of stimulus involved in sensory perception	464	0.000000	0.000000
enriched	nuclear transport	245	0.000000	0.000000
enriched	DNA conformation change	160	0.000000	0.000000
depleted	cofactor metabolic process	400	0.000000	0.000000
enriched	chromosome segregation	108	0.000000	0.000000
enriched	translational initiation	123	0.000000	0.000000
enriched	nucleocytoplasmic transport	242	0.000000	0.000000
enriched	protein catabolic process	425	0.000000	0.000000
enriched	regulation of signal transduction by p53 class mediator	176	0.000000	0.000000
enriched	regulation of chromosome segregation	99	0.000000	0.000000
enriched	microtubule-based process	603	0.000000	0.000000
enriched	proteasomal protein catabolic process	331	0.000000	0.000000
enriched	recombinational repair	94	0.000000	0.000000
depleted	xenobiotic metabolic process	109	0.000000	0.000000
enriched	mitotic cell cycle checkpoint	98	0.000000	0.000000
enriched	double-strand break repair via homologous recombination	93	0.000000	0.000000
enriched	organelle localization	463	0.000000	0.000000
enriched	regulation of mitotic nuclear division	159	0.000000	0.000000
enriched	tRNA metabolic process	180	0.000000	0.000000
enriched	anaphase-promoting complex-dependent catabolic process	81	0.000000	0.000000

enriched	positive regulation of DNA metabolic process	183	0.000000	0.000000
enriched	proteasome-mediated ubiquitin-dependent protein catabolic process	312	0.000000	0.000000
enriched	nuclear-transcribed mRNA catabolic process	177	0.000000	0.000000
depleted	complement activation, classical pathway	36	0.000000	0.000000
enriched	protein deubiquitination	251	0.000000	0.000000
enriched	spindle organization	124	0.000000	0.000000
enriched	transcription, DNA-templated	433	0.000000	0.000000
depleted	sensory perception	534	0.000000	0.000000
enriched	proteolysis involved in cellular protein catabolic process	550	0.000000	0.000000
enriched	protein modification by small protein removal	267	0.000000	0.000000
enriched	RNA catabolic process	228	0.000000	0.000000
enriched	mRNA catabolic process	195	0.000000	0.000000
enriched	positive regulation of organelle organization	593	0.000000	0.000000
depleted	detection of stimulus	604	0.000000	0.000000
enriched	negative regulation of cell cycle G2/M phase transition	99	0.000000	0.000000
enriched	ubiquitin-dependent protein catabolic process	480	0.000000	0.000000
enriched	RNA export from nucleus	118	0.000000	0.000000
depleted	regulation of complement activation	52	0.000000	0.000000
depleted	cellular lipid catabolic process	175	0.000000	0.000000
enriched	microtubule cytoskeleton organization	363	0.000000	0.000000
enriched	nuclear export	148	0.000000	0.000000
enriched	modification-dependent protein catabolic process	486	0.000000	0.000000
enriched	regulation of mRNA stability	171	0.000000	0.000000
enriched	cell cycle G1/S phase transition	99	0.000000	0.000000
enriched	nuclear chromosome segregation	47	0.000000	0.000000
enriched	DNA geometric change	105	0.000000	0.000000
enriched	chromatin assembly or disassembly	73	0.000000	0.000000
depleted	lipid catabolic process	273	0.000000	0.000000
enriched	nucleosome assembly	103	0.000000	0.000000
enriched	RNA 3'-end processing	115	0.000000	0.000000
enriched	telomere organization	93	0.000000	0.000000
enriched	RNA transport	175	0.000000	0.000000
enriched	regulation of sister chromatid segregation	79	0.000000	0.000000
enriched	positive regulation of cell cycle process	272	0.000000	0.000000
enriched	microtubule cytoskeleton organization involved in mitosis	98	0.000000	0.000000
enriched	viral transcription	100	0.000000	0.000000
enriched	G1/S transition of mitotic cell cycle	98	0.000000	0.000000
enriched	regulation of cellular response to stress	695	0.000000	0.000000
enriched	mitotic sister chromatid segregation	30	0.000000	0.000000
enriched	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	106	0.000000	0.000000
enriched	telomere maintenance	91	0.000000	0.000000
enriched	nucleobase-containing compound transport	221	0.000000	0.000000
enriched	protein localization to organelle	635	0.000000	0.000000
depleted	fatty acid oxidation	75	0.000000	0.000000
enriched	DNA duplex unwinding	97	0.000000	0.000000
depleted	alcohol metabolic process	303	0.000000	0.000000
enriched	regulation of translation	334	0.000000	0.000000
depleted	drug catabolic process	127	0.000000	0.000000
enriched	positive regulation of cell cycle	362	0.000000	0.000000
depleted	lipid oxidation	76	0.000000	0.000000
depleted	inflammatory response	418	0.000000	0.000000
depleted	regulation of humoral immune response	71	0.000000	0.000000
enriched	mitotic spindle organization	69	0.000000	0.000000
enriched	protein localization to endoplasmic reticulum	105	0.000000	0.000000
depleted	steroid metabolic process	240	0.000000	0.000000

enriched	sister chromatid segregation	33	0.000000	0.000000
enriched	nucleosome organization	141	0.000000	0.000000
enriched	negative regulation of G2/M transition of mitotic cell cycle	87	0.000000	0.000000
enriched	transcription-coupled nucleotide-excision repair	69	0.000000	0.000000
depleted	fatty acid beta-oxidation	53	0.000000	0.000000
enriched	positive regulation of chromosome organization	172	0.000000	0.000000
enriched	regulation of response to DNA damage stimulus	207	0.000000	0.000000
enriched	protein targeting to ER	90	0.000000	0.000000
enriched	regulation of DNA replication	106	0.000000	0.000000
enriched	spliceosomal snRNP assembly	36	0.000000	0.000000
enriched	establishment of protein localization to endoplasmic reticulum	94	0.000000	0.000000
enriched	negative regulation of chromosome organization	126	0.000000	0.000000
enriched	establishment of organelle localization	249	0.000000	0.000000
depleted	sulfur compound metabolic process	347	0.000000	0.000000
enriched	nucleic acid phosphodiester bond hydrolysis	273	0.000000	0.000000
enriched	regulation of cellular response to heat	76	0.000000	0.000000
enriched	CENP-A containing nucleosome assembly	29	0.000000	0.000000
enriched	regulation of mitotic sister chromatid separation	57	0.000000	0.000000
enriched	regulation of microtubule cytoskeleton organization	183	0.000000	0.000000
enriched	positive regulation of telomerase RNA localization to Cajal body	15	0.000000	0.000000
enriched	DNA damage checkpoint	66	0.000000	0.000000
enriched	protein polyubiquitination	287	0.000000	0.000000
enriched	positive regulation of DNA biosynthetic process	66	0.000000	0.000000
enriched	chromatin remodeling	147	0.000000	0.000000
enriched	DNA replication-independent nucleosome organization	38	0.000000	0.000000
enriched	translation	183	0.000000	0.000000
enriched	cotranslational protein targeting to membrane	82	0.000000	0.000000
enriched	DNA strand elongation	21	0.000000	0.000000
enriched	SRP-dependent cotranslational protein targeting to membrane	77	0.000000	0.000000
enriched	positive regulation of protein localization to Cajal body	9	0.000000	0.000000
enriched	nucleotide-excision repair	98	0.000000	0.000000
enriched	peptidyl-lysine modification	290	0.000000	0.000000
enriched	RNA modification	159	0.000000	0.000000
enriched	establishment of protein localization to organelle	384	0.000000	0.000000
enriched	double-strand break repair via nonhomologous end joining	57	0.000000	0.000000
enriched	DNA-templated transcription, termination	69	0.000000	0.000000
depleted	aromatic amino acid family metabolic process	39	0.000000	0.000000
enriched	response to ionizing radiation	140	0.000000	0.000000
enriched	regulation of microtubule-based process	214	0.000000	0.000000
enriched	tRNA processing	126	0.000000	0.000000
depleted	keratinization	161	0.000000	0.000000
enriched	DNA-templated transcription, elongation	84	0.000000	0.000000
enriched	DNA replication-independent nucleosome assembly	37	0.000000	0.000000
enriched	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	27	0.000000	0.000000
enriched	non-recombinational repair	59	0.000000	0.000000
enriched	RNA methylation	78	0.000000	0.000000
enriched	maturation of SSU-rRNA	38	0.000000	0.000000
enriched	protein folding	203	0.000000	0.000000
enriched	ATP-dependent chromatin remodeling	71	0.000000	0.000000
depleted	acute inflammatory response	61	0.000000	0.000000
enriched	regulation of DNA repair	116	0.000000	0.000001
depleted	high-density lipoprotein particle remodeling	15	0.000000	0.000001
enriched	mRNA export from nucleus	100	0.000000	0.000001
depleted	branched-chain amino acid catabolic process	21	0.000000	0.000001
depleted	innate immune response	425	0.000000	0.000001

enriched	regulation of chromosome separation	61	0.000000	0.000001
enriched	regulation of proteasomal ubiquitin-dependent protein catabolic process	120	0.000000	0.000001
enriched	regulation of mitotic metaphase/anaphase transition	51	0.000000	0.000001
enriched	mRNA transport	139	0.000000	0.000001
enriched	transcription by RNA polymerase II	306	0.000000	0.000001
enriched	regulation of telomerase RNA localization to Cajal body	18	0.000000	0.000001
depleted	defense response to other organism	648	0.000000	0.000001
enriched	ciliary basal body-plasma membrane docking	94	0.000000	0.000001
enriched	regulation of establishment of protein localization to chromosome	12	0.000000	0.000001
enriched	peptide biosynthetic process	205	0.000000	0.000001
enriched	ncRNA transcription	93	0.000000	0.000001
depleted	lipid transport	278	0.000000	0.000001
enriched	regulation of DNA-dependent DNA replication	48	0.000000	0.000001
enriched	protein localization to chromosome	61	0.000000	0.000001
depleted	complement activation, alternative pathway	13	0.000000	0.000001
enriched	positive regulation of protein localization to chromosome, telomeric region	12	0.000000	0.000001
enriched	regulation of protein catabolic process	371	0.000000	0.000002
depleted	reverse cholesterol transport	14	0.000000	0.000002
enriched	regulation of ubiquitin-dependent protein catabolic process	145	0.000000	0.000002
enriched	regulation of DNA biosynthetic process	105	0.000000	0.000003
depleted	acute-phase response	37	0.000000	0.000003
enriched	regulation of cellular protein localization	524	0.000000	0.000004
enriched	regulation of telomere maintenance	77	0.000000	0.000004
enriched	regulation of gene silencing	122	0.000000	0.000004
enriched	DNA replication initiation	30	0.000000	0.000004
enriched	membrane docking	176	0.000000	0.000004
enriched	ribosomal large subunit biogenesis	28	0.000000	0.000005
depleted	sensory perception of chemical stimulus	162	0.000000	0.000005
enriched	interstrand cross-link repair	48	0.000000	0.000005
enriched	positive regulation of cellular protein localization	317	0.000000	0.000005
depleted	icosanoid metabolic process	100	0.000000	0.000005
depleted	plasma lipoprotein particle remodeling	26	0.000000	0.000006
depleted	ribonucleotide metabolic process	308	0.000000	0.000006
enriched	regulation of translational initiation	72	0.000000	0.000006
enriched	negative regulation of mitotic nuclear division	40	0.000000	0.000006
enriched	double-strand break repair via break-induced replication	11	0.000000	0.000006
depleted	nucleoside phosphate metabolic process	426	0.000000	0.000006
depleted	organic anion transport	433	0.000000	0.000006
depleted	regulation of cell activation	533	0.000000	0.000006
enriched	DNA strand elongation involved in DNA replication	16	0.000000	0.000006
enriched	positive regulation of translation	120	0.000000	0.000006
enriched	mRNA 3'-end processing	74	0.000000	0.000006
depleted	neurotransmitter metabolic process	86	0.000000	0.000008
depleted	adaptive immune response	223	0.000000	0.000008
depleted	nucleotide metabolic process	419	0.000000	0.000008
depleted	B cell receptor signaling pathway	39	0.000000	0.000009
depleted	lipid homeostasis	129	0.000000	0.000009
enriched	regulation of cellular protein catabolic process	239	0.000000	0.000009
depleted	glutathione derivative biosynthetic process	21	0.000000	0.000010
enriched	tRNA export from nucleus	32	0.000000	0.000011
enriched	regulation of DNA-templated transcription in response to stress	117	0.000000	0.000011
depleted	ribose phosphate metabolic process	317	0.000000	0.000012
enriched	protein monoubiquitination	63	0.000000	0.000012

enriched	regulation of transcription from RNA polymerase II promoter	111	0.000000	0.000012
	in response to stress			
enriched	methylation	292	0.000000	0.000012
enriched	histone exchange	45	0.000000	0.000013
depleted	purine nucleotide metabolic process	312	0.000000	0.000014
enriched	protein localization to kinetochore	12	0.000000	0.000014
enriched	rRNA modification	34	0.000000	0.000014
enriched	negative regulation of mitotic sister chromatid separation	27	0.000000	0.000015
enriched	regulation of gene expression, epigenetic	182	0.000000	0.000016
enriched	interleukin-1-mediated signaling pathway	94	0.000000	0.000017
enriched	histone ubiquitination	39	0.000000	0.000017
enriched	positive regulation of establishment of protein localization to telomere	10	0.000000	0.000018
enriched	establishment of protein localization to membrane	230	0.000000	0.000020
enriched	DNA biosynthetic process	97	0.000000	0.000021
depleted	long-chain fatty acid metabolic process	102	0.000000	0.000024
enriched	signal transduction involved in DNA damage checkpoint	70	0.000000	0.000025
enriched	ribosome biogenesis	25	0.000000	0.000025
enriched	DNA-templated transcription, initiation	190	0.000000	0.000026
depleted	regulation of ion transport	663	0.000000	0.000026
depleted	short-chain fatty acid catabolic process	9	0.000000	0.000027
enriched	regulation of protein ubiquitination	194	0.000000	0.000028
enriched	positive regulation of telomere maintenance	48	0.000000	0.000028
enriched	positive regulation of viral transcription	41	0.000000	0.000029
enriched	cleavage involved in rRNA processing	21	0.000000	0.000029
enriched	spindle assembly	68	0.000000	0.000029
enriched	snRNA transcription by RNA polymerase II	69	0.000000	0.000033
enriched	protein-containing complex disassembly	220	0.000000	0.000034
enriched	negative regulation of mitotic metaphase/anaphase transition	24	0.000000	0.000037
enriched	regulation of cellular amino acid metabolic process	60	0.000000	0.000038
depleted	sensory perception of smell	128	0.000000	0.000038
enriched	DNA-dependent DNA replication	34	0.000000	0.000040
enriched	regulation of gene silencing by miRNA	81	0.000000	0.000044
enriched	mitotic DNA integrity checkpoint	49	0.000000	0.000044
enriched	signal transduction involved in cell cycle checkpoint	71	0.000000	0.000046
depleted	cell-cell adhesion	470	0.000000	0.000049
enriched	NIK/NF-kappaB signaling	63	0.000000	0.000051
depleted	histidine catabolic process to glutamate and formamide	4	0.000000	0.000052
depleted	histidine catabolic process to glutamate and formate	4	0.000000	0.000052
depleted	epoxygenase P450 pathway	18	0.000000	0.000052
enriched	regulation of proteasomal protein catabolic process	175	0.000000	0.000057
depleted	neurotransmitter catabolic process	20	0.000000	0.000058
enriched	Golgi organization	112	0.000000	0.000060
enriched	antigen processing and presentation of peptide antigen	178	0.000000	0.000060
enriched	kinetochore organization	16	0.000000	0.000064
enriched	regulation of mRNA processing	135	0.000000	0.000068
enriched	snRNA transcription	70	0.000000	0.000068
enriched	antigen processing and presentation	203	0.000000	0.000068
depleted	unsaturated fatty acid metabolic process	96	0.000000	0.000069
enriched	RNA localization	22	0.000000	0.000070
depleted	arachidonic acid metabolic process	51	0.000000	0.000071
depleted	second-messenger-mediated signaling	325	0.000000	0.000071
depleted	dicarboxylic acid metabolic process	89	0.000000	0.000072
depleted	negative regulation of locomotion	306	0.000000	0.000072
enriched	nucleotide-excision repair, DNA incision, 5'-to lesion	35	0.000000	0.000076
enriched	signal transduction in response to DNA damage	101	0.000000	0.000076
enriched	positive regulation of cell cycle phase transition	91	0.000000	0.000077

depleted	regulated exocytosis	651	0.000000	0.000077
depleted	antibiotic metabolic process	98	0.000000	0.000082
depleted	negative regulation of cellular component movement	296	0.000000	0.000083
enriched	regulation of centrosome cycle	55	0.000000	0.000097
enriched	transcription elongation from RNA polymerase II promoter	69	0.000000	0.000097
enriched	protein localization to chromosome, centromeric region	16	0.000000	0.000101
depleted	cellular modified amino acid metabolic process	184	0.000000	0.000108
enriched	regulation of viral transcription	62	0.000000	0.000112
depleted	anion transport	553	0.000000	0.000112
enriched	RNA phosphodiester bond hydrolysis	143	0.000000	0.000113
enriched	regulation of cytoskeleton organization	507	0.000000	0.000118
enriched	DNA replication checkpoint	16	0.000000	0.000126
depleted	acylglycerol homeostasis	31	0.000000	0.000126
enriched	organelle transport along microtubule	72	0.000000	0.000126
depleted	triglyceride homeostasis	31	0.000000	0.000126
depleted	diterpenoid metabolic process	99	0.000000	0.000128
enriched	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	81	0.000000	0.000128
depleted	regulation of lipid metabolic process	385	0.000000	0.000128
enriched	cytoplasmic translation	35	0.000000	0.000131
enriched	regulation of hematopoietic progenitor cell differentiation	85	0.000000	0.000138
enriched	protein sumoylation	60	0.000000	0.000140
enriched	cytoskeleton-dependent intracellular transport	165	0.000000	0.000143
depleted	hormone metabolic process	192	0.000000	0.000145
enriched	postreplication repair	53	0.000000	0.000157
enriched	positive regulation of proteasomal protein catabolic process	102	0.000000	0.000157
enriched	regulation of cell cycle G1/S phase transition	163	0.000000	0.000166
enriched	regulation of macroautophagy	166	0.000000	0.000171
enriched	positive regulation of cellular protein catabolic process	138	0.000000	0.000171
depleted	sterol metabolic process	131	0.000000	0.000178
depleted	positive regulation of lipid metabolic process	139	0.000000	0.000182
enriched	mitotic cytokinesis	49	0.000000	0.000185
enriched	nucleotide-excision repair, DNA incision	39	0.000000	0.000187
enriched	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	13	0.000000	0.000187
depleted	lipid modification	196	0.000000	0.000189
depleted	negative regulation of cell motility	263	0.000000	0.000191
enriched	tRNA modification	86	0.000000	0.000194
enriched	ribosomal small subunit biogenesis	17	0.000000	0.000198
depleted	carbohydrate metabolic process	442	0.000000	0.000212
depleted	detoxification of copper ion	15	0.000000	0.000213
enriched	regulation of mitotic spindle organization	35	0.000000	0.000219
enriched	positive regulation of proteolysis involved in cellular protein catabolic process	117	0.000000	0.000219
enriched	histone monoubiquitination	29	0.000000	0.000221
enriched	peptide metabolic process	321	0.000000	0.000233
enriched	mitotic G2/M transition checkpoint	26	0.000000	0.000237
depleted	serine family amino acid catabolic process	11	0.000000	0.000237
depleted	metal ion homeostasis	605	0.000000	0.000238
enriched	positive regulation of viral process	102	0.000000	0.000249
depleted	signaling	647	0.000000	0.000255
enriched	regulation of autophagy	316	0.000000	0.000257
enriched	positive regulation of protein catabolic process	210	0.000000	0.000262
enriched	regulation of hematopoietic stem cell differentiation	72	0.000000	0.000262
depleted	serine family amino acid metabolic process	36	0.000000	0.000262
enriched	DNA replication-dependent nucleosome assembly	10	0.000000	0.000264
enriched	maturation of LSU-rRNA	20	0.000000	0.000264

enriched	positive regulation of ubiquitin-dependent protein catabolic process	94	0.000000	0.000264
enriched	regulation of protein localization to nucleus	117	0.000000	0.000264
enriched	response to endoplasmic reticulum stress	242	0.000000	0.000273
depleted	regulation of lipoprotein lipase activity	22	0.000000	0.000274
depleted	cation homeostasis	683	0.000000	0.000277
depleted	monoterpenoid metabolic process	6	0.000000	0.000277
enriched	sister chromatid cohesion	39	0.000000	0.000277
depleted	short-chain fatty acid metabolic process	17	0.000000	0.000281
enriched	organelle assembly	487	0.000000	0.000293
depleted	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	234	0.000000	0.000301
enriched	mitotic spindle assembly checkpoint	22	0.000000	0.000301
depleted	positive regulation of immune response	679	0.000000	0.000316
enriched	protein acetylation	134	0.000000	0.000316
enriched	telomere maintenance via semi-conservative replication	24	0.000000	0.000316
depleted	humoral immune response	202	0.000000	0.000337
enriched	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	67	0.000000	0.000346
enriched	regulation of protein stability	271	0.000000	0.000355
depleted	cellular detoxification	95	0.000000	0.000369
enriched	chaperone-mediated protein folding	55	0.000000	0.000374
depleted	acyl-CoA metabolic process	93	0.000000	0.000383
depleted	cornification	114	0.000000	0.000383
enriched	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	93	0.000000	0.000403
depleted	nicotinamide nucleotide metabolic process	33	0.000000	0.000406
enriched	establishment of chromosome localization	60	0.000000	0.000438
enriched	regulation of telomere maintenance via telomere lengthening	57	0.000000	0.000459
depleted	cholesterol metabolic process	116	0.000000	0.000480
enriched	regulation of transcription from RNA polymerase II promoter in response to hypoxia	76	0.000000	0.000489
depleted	negative regulation of cell migration	249	0.000000	0.000501
depleted	retinoid metabolic process	93	0.000000	0.000513
depleted	regulation of chemotaxis	202	0.000000	0.000520
enriched	metaphase plate congression	44	0.000000	0.000524
enriched	positive regulation of mitotic cell cycle	147	0.000000	0.000527
enriched	tRNA aminoacylation	48	0.000000	0.000541
enriched	protein targeting to membrane	137	0.000000	0.000574
depleted	visual perception	201	0.000000	0.000576
depleted	coenzyme biosynthetic process	132	0.000000	0.000592
enriched	antigen processing and presentation of exogenous peptide antigen via MHC class I	71	0.000000	0.000638
enriched	retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum	81	0.000000	0.000643
depleted	platelet degranulation	120	0.000000	0.000653
enriched	regulation of rRNA processing	12	0.000000	0.000658
enriched	regulation of telomere maintenance via telomerase	52	0.000000	0.000663
depleted	regulation of ion transmembrane transport	457	0.000000	0.000668
depleted	calcium-mediated signaling	140	0.000000	0.000674
depleted	regulation of lipid catabolic process	50	0.000000	0.000687
depleted	complement activation, lectin pathway	9	0.000000	0.000688
depleted	cellular response to copper ion	27	0.000000	0.000700
depleted	lipid biosynthetic process	534	0.000000	0.000700
enriched	positive regulation of rRNA processing	9	0.000000	0.000710
enriched	tRNA aminoacylation for protein translation	45	0.000000	0.000713
enriched	negative regulation of RNA splicing	24	0.000000	0.000720
depleted	choline catabolic process	6	0.000000	0.000746

enriched	signal transduction by p53 class mediator	117	0.000000	0.000746
enriched	regulation of sister chromatid cohesion	21	0.000000	0.000751
enriched	positive regulation of Wnt signaling pathway	174	0.000000	0.000755
enriched	7-methylguanosine RNA capping	33	0.000000	0.000760
enriched	regulation of spindle assembly	26	0.000000	0.000768
depleted	myeloid leukocyte activation	561	0.000000	0.000774
enriched	transcription elongation from RNA polymerase I promoter	27	0.000000	0.000820
depleted	negative regulation of wound healing	71	0.000000	0.000837
enriched	negative regulation of DNA-dependent DNA replication	19	0.000000	0.000840
enriched	regulation of G1/S transition of mitotic cell cycle	149	0.000000	0.000864
depleted	fatty acid beta-oxidation using acyl-CoA dehydrogenase	9	0.000000	0.000873
enriched	spliceosomal complex assembly	25	0.000000	0.000888
depleted	response to zinc ion	51	0.000000	0.000899
depleted	neuron remodeling	12	0.000000	0.000981
depleted	regulation of inflammatory response	327	0.000000	0.000981
depleted	activation of immune response	467	0.000000	0.000992
depleted	generation of precursor metabolites and energy	359	0.000000	0.000992
depleted	sensory perception of light stimulus	205	0.000000	0.001038
enriched	RNA-dependent DNA biosynthetic process	25	0.000000	0.001046
depleted	exogenous drug catabolic process	22	0.000000	0.001065
enriched	intracellular transport of virus	52	0.000000	0.001065
enriched	negative regulation of mRNA splicing, via spliceosome	20	0.000000	0.001130
enriched	regulation of cytokinesis	84	0.000000	0.001130
depleted	vitamin metabolic process	121	0.000000	0.001141
depleted	glyoxylate metabolic process	10	0.000000	0.001185
enriched	regulation of chromatin organization	187	0.000000	0.001185
enriched	protein stabilization	175	0.000000	0.001246
enriched	proteasome assembly	14	0.000000	0.001256
depleted	tryptophan metabolic process	12	0.000000	0.001256
enriched	mitotic DNA replication initiation	4	0.000000	0.001293
depleted	regulation of interferon-gamma production	94	0.000000	0.001306
enriched	mitotic metaphase plate congression	34	0.000000	0.001332
depleted	potassium ion transmembrane transport	153	0.000000	0.001332
depleted	regulation of ERK1 and ERK2 cascade	272	0.000000	0.001342
depleted	positive regulation of MAPK cascade	516	0.000000	0.001350
depleted	positive regulation of ERK1 and ERK2 cascade	195	0.000000	0.001374
depleted	response to copper ion	39	0.000000	0.001397
depleted	tryptophan catabolic process	10	0.000000	0.001397
enriched	negative regulation of response to DNA damage stimulus	75	0.000000	0.001413
depleted	response to molecule of bacterial origin	295	0.000000	0.001433
enriched	response to unfolded protein	64	0.000000	0.001433
enriched	regulation of mitotic spindle assembly	19	0.000000	0.001499
enriched	positive regulation of canonical Wnt signaling pathway	143	0.000000	0.001508
depleted	glycine metabolic process	15	0.000000	0.001518
depleted	regulation of cytokine production	670	0.000000	0.001578
enriched	regulation of double-strand break repair	73	0.000000	0.001578
enriched	7-methylguanosine mRNA capping	32	0.000000	0.001656
enriched	mitotic DNA damage checkpoint	40	0.000000	0.001682
depleted	isoprenoid metabolic process	124	0.000000	0.001726
enriched	microtubule-based movement	253	0.000000	0.001740
depleted	amine metabolic process	62	0.000000	0.001805
enriched	positive regulation of telomere maintenance via telomerase	34	0.000000	0.001834
depleted	aldehyde catabolic process	11	0.000000	0.001894
depleted	response to lipopolysaccharide	281	0.000000	0.001900
enriched	RNA (guanine-N7)-methylation	6	0.000000	0.002004
enriched	DNA unwinding involved in DNA replication	15	0.000000	0.002046

enriched	post-translational protein modification	351	0.000000	0.002046
depleted	cell activation involved in immune response	590	0.000000	0.002059
enriched	positive regulation of telomerase activity	36	0.000000	0.002062
enriched	positive regulation of telomere maintenance via telomere lengthening	36	0.000000	0.002062
depleted	negative regulation of lipid catabolic process	19	0.000000	0.002102
enriched	positive regulation of chromosome segregation	27	0.000000	0.002178
enriched	regulation of DNA-templated transcription, elongation	48	0.000000	0.002178
enriched	telomere maintenance via telomerase	22	0.000000	0.002178
depleted	ethanol catabolic process	11	0.000000	0.002194
depleted	kynurenine metabolic process	11	0.000000	0.002239
enriched	attachment of spindle microtubules to kinetochore	21	0.000000	0.002356
depleted	cellular metal ion homeostasis	540	0.000000	0.002356
depleted	neuropeptide signaling pathway	101	0.000000	0.002390
depleted	cytokine secretion	47	0.000000	0.002399
depleted	regulation of body fluid levels	371	0.000000	0.002416
enriched	transcription initiation from RNA polymerase II promoter	158	0.000000	0.002416
enriched	rRNA methylation	24	0.000000	0.002623
enriched	termination of RNA polymerase I transcription	29	0.000000	0.002652
enriched	regulation of nucleocytoplasmic transport	103	0.000000	0.002730
enriched	termination of RNA polymerase II transcription	33	0.000000	0.002734
depleted	lymphocyte activation	329	0.000000	0.002734
enriched	positive regulation of mitotic cell cycle phase transition	77	0.000000	0.002734
enriched	ribosomal small subunit assembly	14	0.000000	0.002734
enriched	positive regulation of DNA repair	62	0.000000	0.002786
depleted	cellular aldehyde metabolic process	55	0.000000	0.002807
enriched	vesicle cytoskeletal trafficking	46	0.000000	0.002859
enriched	regulation of RNA splicing	129	0.000000	0.002887
depleted	regulation of hormone levels	506	0.000000	0.002906
depleted	potassium ion transport	162	0.000000	0.002915
depleted	cholesterol efflux	22	0.000000	0.002969
enriched	mitotic spindle assembly	28	0.000000	0.002992
depleted	positive regulation of cell activation	316	0.000000	0.003047
depleted	negative regulation of immune system process	428	0.000000	0.003059
enriched	Wnt signaling pathway, planar cell polarity pathway	95	0.000000	0.003065
enriched	internal protein amino acid acetylation	116	0.000000	0.003065
enriched	meiotic sister chromatid cohesion, centromeric	4	0.000000	0.003070
enriched	regulation of centrosome duplication	40	0.000000	0.003090
depleted	amino-acid betaine metabolic process	16	0.000000	0.003108
enriched	establishment of localization in cell	279	0.000000	0.003233
depleted	regulation of heart contraction	226	0.000000	0.003257
enriched	amide biosynthetic process	322	0.000000	0.003329
depleted	NAD biosynthetic process	28	0.000000	0.003333
depleted	cell-cell signaling	571	0.000000	0.003375
depleted	cellular ion homeostasis	627	0.000000	0.003375
enriched	negative regulation of DNA replication	34	0.000000	0.003392
enriched	histone H4 acetylation	53	0.000000	0.003415
depleted	regulation of lymphocyte activation	414	0.000000	0.003429
depleted	zinc ion homeostasis	32	0.000000	0.003472
enriched	negative regulation of gene expression, epigenetic	65	0.000000	0.003708
depleted	regulation of phagocytosis	88	0.000000	0.003753
enriched	regulation of DNA recombination	100	0.000000	0.003797
depleted	leukocyte activation involved in immune response	586	0.000000	0.003816
enriched	mitochondrion organization	295	0.000000	0.003822
enriched	antigen processing and presentation of peptide antigen via MHC class I	91	0.000000	0.003858
depleted	histidine metabolic process	10	0.000000	0.003859

enriched	regulation of transcription elongation from RNA polymerase II promoter	30	0.000000	0.003872
enriched	histone acetylation	106	0.000000	0.004105
depleted	cellular cation homeostasis	614	0.000000	0.004197
enriched	double-strand break repair via alternative nonhomologous end joining	3	0.000000	0.004197
enriched	protein targeting	297	0.000000	0.004197
depleted	positive regulation of phosphatidylinositol 3-kinase signaling	84	0.000000	0.004206
depleted	positive regulation of lipid biosynthetic process	77	0.000000	0.004214
depleted	monocarboxylic acid transport	134	0.000000	0.004453
enriched	aromatic compound catabolic process	404	0.000000	0.004527
depleted	cholesterol homeostasis	78	0.000000	0.004527
enriched	Golgi vesicle transport	317	0.000000	0.004606
enriched	positive regulation of DNA-templated transcription, elongation	28	0.000000	0.004606
depleted	regulation of cell adhesion	657	0.000000	0.004646
depleted	cellular amino acid biosynthetic process	75	0.000000	0.004785
enriched	anterograde synaptic vesicle transport	13	0.000000	0.004830
depleted	response to metal ion	349	0.000000	0.004990
depleted	blood coagulation, intrinsic pathway	16	0.000000	0.005008
enriched	transferrin transport	35	0.000000	0.005044
enriched	peptidyl-lysine acetylation	113	0.000000	0.005251
enriched	ER overload response	12	0.000000	0.005255
depleted	negative regulation of dendritic cell apoptotic process	7	0.000000	0.005346
depleted	ketone body biosynthetic process	9	0.000000	0.005413
depleted	peroxisome organization	71	0.000000	0.005437
enriched	internal peptidyl-lysine acetylation	111	0.000000	0.005464
enriched	negative regulation of ubiquitin-dependent protein catabolic process	45	0.000000	0.005530
depleted	cholesterol transport	50	0.000000	0.005530
enriched	transcription initiation from RNA polymerase I promoter	31	0.000000	0.005556
enriched	histone phosphorylation	28	0.000000	0.005604
enriched	regulation of establishment of planar polarity	109	0.000000	0.005648
depleted	leukotriene B4 catabolic process	4	0.000000	0.005670
depleted	regulation of leukocyte proliferation	216	0.000000	0.005675
depleted	phagocytosis, recognition	20	0.000000	0.005804
enriched	positive regulation by host of viral transcription	17	0.000000	0.005875
enriched	spindle localization	50	0.000000	0.005987
depleted	sterol homeostasis	79	0.000000	0.006061
enriched	RNA phosphodiester bond hydrolysis, endonucleolytic	68	0.000000	0.006079
depleted	regulation of fatty acid metabolic process	79	0.000000	0.006355
enriched	IRES-dependent viral translational initiation	10	0.000000	0.006624
enriched	regulation of mRNA splicing, via spliceosome	97	0.000000	0.006917
depleted	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	200	0.000000	0.006979
depleted	sterol transport	53	0.000000	0.007061
depleted	regulation of blood coagulation	79	0.000000	0.007140
depleted	negative regulation of coagulation	52	0.000000	0.007261
depleted	regulation of leukocyte mediated cytotoxicity	69	0.000000	0.007261
enriched	nuclear envelope organization	46	0.000000	0.007281
enriched	mitotic DNA replication checkpoint	10	0.000000	0.007306
enriched	positive regulation of response to DNA damage stimulus	94	0.000000	0.007320
enriched	positive regulation of intracellular transport	202	0.000000	0.007358
enriched	cellular response to ionizing radiation	66	0.000000	0.007457
enriched	protein K63-linked ubiquitination	36	0.000000	0.007572
enriched	vesicle transport along microtubule	41	0.000000	0.007590
depleted	cellular zinc ion homeostasis	29	0.000000	0.007607

enriched	signal transduction involved in mitotic G1 DNA damage check-point	57	0.000000	0.007843
enriched	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	4	0.000000	0.009005
depleted	4-hydroxyproline catabolic process	3	0.000000	0.009217
depleted	glutathione metabolic process	50	0.000000	0.009332
enriched	regulation of translational fidelity	20	0.000000	0.009335
enriched	positive regulation of DNA replication	37	0.000000	0.009373
enriched	histone H2A ubiquitination	22	0.000000	0.009392
enriched	negative regulation of G0 to G1 transition	37	0.000000	0.009392
enriched	mismatch repair	29	0.000000	0.009401
enriched	positive regulation of protein localization to nucleus	74	0.000000	0.009401
enriched	pre-replicative complex assembly involved in nuclear cell cycle DNA replication	7	0.000000	0.009401
depleted	regulation of Ras protein signal transduction	230	0.000000	0.009848
depleted	leucine catabolic process	6	0.000000	0.009932
depleted	phospholipid transport	85	0.000000	0.009966
depleted	regulation of small GTPase mediated signal transduction	327	0.000000	0.010110
depleted	ethanol oxidation	12	0.000000	0.010115
depleted	regulation of fatty acid oxidation	27	0.000000	0.010151
depleted	establishment of protein localization to peroxisome	64	0.000000	0.010339
depleted	protein targeting to peroxisome	64	0.000000	0.010339
depleted	response to nutrient	205	0.000000	0.010353
enriched	positive regulation of cell cycle G2/M phase transition	30	0.000000	0.010437
depleted	negative regulation of blood coagulation	50	0.000000	0.010608
enriched	error-free translesion synthesis	20	0.000000	0.010660
depleted	glyoxylate catabolic process	3	0.000000	0.010660
enriched	histone deubiquitination	22	0.000000	0.010767
depleted	carboxylic acid transport	273	0.000000	0.010806
depleted	interleukin-1 secretion	11	0.000000	0.010869
enriched	negative regulation of canonical Wnt signaling pathway	174	0.000000	0.011035
depleted	2-oxoglutarate metabolic process	16	0.000000	0.011268
depleted	positive regulation of neuron projection regeneration	8	0.000000	0.011367
enriched	transcription by RNA polymerase III	39	0.000000	0.011402
depleted	leukocyte migration	296	0.000000	0.011428
enriched	DNA damage response, detection of DNA damage	37	0.000000	0.011470
enriched	DNA damage response, signal transduction by p53 class mediator	78	0.000000	0.011956
enriched	Fc-epsilon receptor signaling pathway	112	0.000000	0.011956
enriched	histone H2A monoubiquitination	17	0.000000	0.011956
enriched	negative regulation of G1/S transition of mitotic cell cycle	102	0.000000	0.011956
depleted	negative regulation of lipid metabolic process	74	0.000000	0.011956
depleted	peptidyl-tyrosine phosphorylation	143	0.000000	0.011956
enriched	meiotic chromosome segregation	16	0.000000	0.012358
depleted	acetyl-CoA metabolic process	30	0.000000	0.012491
depleted	sulfation	16	0.000000	0.012567
enriched	rRNA 3'-end processing	9	0.000000	0.012640
depleted	positive regulation of cholesterol esterification	9	0.000000	0.013107
enriched	protein localization to chromatin	24	0.000000	0.013398
depleted	regulation of cholesterol esterification	12	0.000000	0.013398
enriched	nuclear envelope reassembly	18	0.000000	0.013597
enriched	cytoskeleton-dependent cytokinesis	73	0.000000	0.013621
depleted	glutamate metabolic process	26	0.000000	0.013628
enriched	telomere maintenance via telomere lengthening	28	0.000000	0.013852
enriched	stimulatory C-type lectin receptor signaling pathway	107	0.000000	0.013880
enriched	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	56	0.000000	0.013882

depleted	cellular oxidant detoxification	84	0.000000	0.013940
enriched	mitotic spindle midzone assembly	7	0.000000	0.014395
depleted	tyrosine metabolic process	10	0.000000	0.014454
enriched	import into nucleus	105	0.000000	0.014611
depleted	positive regulation of cell adhesion	386	0.000000	0.014945
depleted	negative regulation of hemostasis	51	0.000000	0.015115
depleted	monosaccharide metabolic process	183	0.000000	0.015342
enriched	response to radiation	410	0.000000	0.015390
enriched	negative regulation of cell cycle G1/S phase transition	105	0.000000	0.015419
depleted	pressure natriuresis	3	0.000000	0.015435
enriched	histone lysine methylation	72	0.000000	0.015720
depleted	leukocyte degranulation	485	0.000000	0.016016
depleted	positive regulation of T cell proliferation	91	0.000000	0.016274
enriched	regulation of telomerase activity	47	0.000000	0.016371
enriched	positive regulation of gene expression, epigenetic	62	0.000000	0.016570
enriched	regulation of canonical Wnt signaling pathway	278	0.000000	0.016570
enriched	negative regulation of proteasomal ubiquitin-dependent protein catabolic process	33	0.000000	0.016573
depleted	regulation of fibrinolysis	14	0.000000	0.016573
enriched	regulation of centriole replication	21	0.000000	0.016789
enriched	somatic diversification of immunoglobulins	32	0.000000	0.016789
depleted	cellular response to metal ion	180	0.000000	0.017024
depleted	tyrosine catabolic process	5	0.000000	0.017865
depleted	amino-acid betaine catabolic process	3	0.000000	0.018294
enriched	histone mRNA metabolic process	24	0.000000	0.018294
depleted	choline metabolic process	9	0.000000	0.018357
depleted	blood coagulation	158	0.000000	0.018483
depleted	sulfur amino acid metabolic process	36	0.000000	0.018550
depleted	positive regulation of fibrinolysis	4	0.000000	0.018593
depleted	phospholipid homeostasis	12	0.000000	0.019873
depleted	response to bacterium	305	0.000000	0.019873
enriched	establishment of spindle localization	45	0.000000	0.020103
depleted	retinol metabolic process	40	0.000000	0.020316
depleted	negative regulation of cell population proliferation	658	0.000000	0.020509
depleted	hemostasis	164	0.000000	0.020771
enriched	nucleotide-excision repair, DNA gap filling	23	0.000000	0.020993
enriched	regulation of ATP metabolic process	112	0.000000	0.021032
depleted	cellular ketone body metabolic process	10	0.000000	0.021088
enriched	regulation of attachment of spindle microtubules to kinetochore	12	0.000000	0.021290
depleted	fatty acid biosynthetic process	103	0.000000	0.021688
depleted	response to estradiol	132	0.000000	0.021688
enriched	beta-catenin-TCF complex assembly	29	0.000000	0.021715
depleted	regulation of T cell proliferation	152	0.000000	0.021763
enriched	RNA 5'-end processing	19	0.000000	0.021764
depleted	regulation of phosphatidylinositol 3-kinase signaling	118	0.000000	0.022049
enriched	alternative mRNA splicing, via spliceosome	16	0.000000	0.022172
depleted	L-alanine catabolic process	4	0.000000	0.022323
depleted	L-alanine metabolic process	4	0.000000	0.022323
enriched	kinetochore assembly	11	0.000000	0.022555
enriched	cellular response to heat	69	0.000000	0.022703
depleted	cyclic-nucleotide-mediated signaling	166	0.000000	0.022862
depleted	negative regulation of hydrolase activity	421	0.000000	0.022862
enriched	regulation of cell division	159	0.000000	0.022967
enriched	regulation of double-strand break repair via homologous recombination	44	0.000000	0.022967
depleted	positive regulation of lymphocyte activation	263	0.000000	0.023082
enriched	endoplasmic reticulum unfolded protein response	100	0.000000	0.023335

depleted	cellular biogenic amine metabolic process	53	0.000000	0.023577
depleted	interferon-gamma production	9	0.000000	0.023743
depleted	omega-hydroxylase P450 pathway	9	0.000000	0.023795
enriched	positive regulation of DNA-dependent DNA replication	12	0.000000	0.023795
depleted	regulation of cytosolic calcium ion concentration	328	0.000000	0.023795
depleted	positive regulation of lipase activity	70	0.000000	0.023955
depleted	cAMP-mediated signaling	143	0.000000	0.023991
depleted	histidine catabolic process	8	0.000000	0.023991
depleted	negative regulation of ruffle assembly	5	0.000000	0.024378
enriched	negative regulation of centrosome duplication	12	0.000000	0.024402
enriched	regulation of CD40 signaling pathway	6	0.000000	0.025942
enriched	metaphase/anaphase transition of mitotic cell cycle	4	0.000000	0.026316
enriched	regulation of transcription involved in G1/S transition of mitotic cell cycle	28	0.000000	0.026419
enriched	attachment of mitotic spindle microtubules to kinetochore	11	0.000000	0.026464
depleted	neutrophil activation	480	0.000000	0.026523
depleted	positive regulation of cytosolic calcium ion concentration	284	0.000000	0.026563
depleted	negative regulation of cytokine production	265	0.000000	0.027229
enriched	regulation of cyclin-dependent protein serine/threonine kinase activity	96	0.000000	0.027772
depleted	coagulation	160	0.000000	0.028062
enriched	histone methylation	90	0.000000	0.028439
depleted	negative regulation of chemotaxis	54	0.000000	0.028439
depleted	defense response to bacterium	215	0.000000	0.028685
enriched	maturation of 5.8S rRNA	11	0.000000	0.028685
enriched	mitotic chromosome movement towards spindle pole	4	0.000000	0.028738
depleted	positive regulation of cell-cell adhesion	247	0.000000	0.028817
enriched	DNA packaging	48	0.000000	0.029694
depleted	regulation of triglyceride metabolic process	33	0.000000	0.029725
depleted	neutrophil activation involved in immune response	471	0.000000	0.029774
enriched	microtubule organizing center organization	63	0.000000	0.030507
enriched	positive regulation of cell cycle arrest	78	0.000000	0.030664
enriched	membrane organization	643	0.000000	0.031079
depleted	cell-cell adhesion via plasma-membrane adhesion molecules	231	0.000000	0.031211
enriched	protein K11-linked ubiquitination	27	0.000000	0.031480
depleted	L-kynurenine metabolic process	7	0.000000	0.031669
enriched	negative regulation of proteolysis involved in cellular protein catabolic process	66	0.000000	0.031752
depleted	aspartate catabolic process	4	0.000000	0.031831
enriched	positive regulation of nucleocytoplasmic transport	63	0.000000	0.031831
depleted	response to inorganic substance	497	0.000000	0.032486
enriched	formation of cytoplasmic translation initiation complex	15	0.000000	0.032863
enriched	mitotic cytokinetic process	19	0.000000	0.032997
enriched	positive regulation of proteolysis	343	0.000000	0.033118
depleted	regulation of cholesterol transport	45	0.000000	0.033181
enriched	mitochondrial translational termination	88	0.000000	0.033883
depleted	T cell selection	26	0.000000	0.034297
depleted	regulation of response to wounding	165	0.000000	0.034450
enriched	mitotic spindle elongation	2	0.000000	0.034670
depleted	response to fatty acid	84	0.000000	0.034806
depleted	calcium ion homeostasis	440	0.000000	0.035057
enriched	positive regulation of centrosome duplication	8	0.000000	0.035589
depleted	positive regulation of bicellular tight junction assembly	6	0.000000	0.036156
enriched	establishment of protein localization to mitochondrion	61	0.000000	0.036231
depleted	fibrinolysis	22	0.000000	0.036231
enriched	positive regulation of protein ubiquitination	111	0.000000	0.036616
depleted	pyrimidine nucleobase catabolic process	3	0.000000	0.036616

depleted	thymine catabolic process	3	0.000000	0.036616
depleted	thymine metabolic process	3	0.000000	0.036616
enriched	mitotic chromosome condensation	17	0.000000	0.036744
depleted	icosanoid biosynthetic process	36	0.000000	0.036914
enriched	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	7	0.000000	0.037022
enriched	mitochondrial RNA metabolic process	42	0.000000	0.037022
depleted	cytolysis	24	0.000000	0.037091
depleted	cellular calcium ion homeostasis	427	0.000000	0.037425
depleted	regulation of vasculature development	310	0.000000	0.037641
enriched	cellular response to unfolded protein	25	0.000000	0.037721
depleted	cellular carbohydrate metabolic process	158	0.000000	0.037741
depleted	response to growth factor	302	0.000000	0.037813
depleted	phospholipid efflux	11	0.000000	0.037842
depleted	triglyceride-rich lipoprotein particle remodeling	11	0.000000	0.037842
depleted	regulation of cell-cell adhesion	389	0.000000	0.038169
enriched	histone H2A acetylation	17	0.000000	0.038201
enriched	tRNA methylation	39	0.000000	0.038201
depleted	neutrophil degranulation	467	0.000000	0.038323
depleted	'de novo' NAD biosynthetic process from tryptophan	6	0.000000	0.039158
enriched	tumor necrosis factor-mediated signaling pathway	113	0.000000	0.039331
enriched	negative regulation of double-strand break repair	29	0.000000	0.039355
depleted	lymphocyte differentiation	196	0.000000	0.039826
depleted	negative regulation of peptidase activity	238	0.000000	0.039826
depleted	steroid biosynthetic process	124	0.000000	0.039826
enriched	telomere capping	14	0.000000	0.039889
enriched	protein refolding	28	0.000000	0.039962
enriched	positive regulation of intracellular protein transport	149	0.000000	0.040254
enriched	exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	8	0.000000	0.041551
enriched	translational termination	96	0.000000	0.041867
enriched	regulation of cell cycle arrest	103	0.000000	0.042019
enriched	Golgi reassembly	4	0.000000	0.042266
depleted	glucuronate catabolic process to xylulose 5-phosphate	5	0.000000	0.042388
enriched	translesion synthesis	41	0.000000	0.042926
enriched	negative regulation of cellular protein catabolic process	81	0.000000	0.043333
depleted	arginine metabolic process	16	0.000000	0.043339
enriched	regulation of protein import	56	0.000000	0.043506
enriched	Fc receptor signaling pathway	170	0.000000	0.044190
enriched	mitotic sister chromatid cohesion	12	0.000000	0.044190
depleted	ADP biosynthetic process	5	0.000000	0.045009
depleted	regulation of adaptive immune response	155	0.000000	0.045009
depleted	low-density lipoprotein particle remodeling	13	0.000000	0.045522
enriched	ER-nucleus signaling pathway	35	0.000000	0.045571
depleted	positive regulation of axon regeneration	7	0.000000	0.045621
depleted	hexose metabolic process	150	0.000000	0.045938
enriched	regulation of stem cell differentiation	114	0.000000	0.045994
enriched	plus-end-directed organelle transport along microtubule	8	0.000000	0.046296
depleted	chemical synaptic transmission	306	0.000000	0.046433
enriched	CRD-mediated mRNA stabilization	5	0.000000	0.046642
enriched	mitochondrial translational elongation	87	0.000000	0.046642
enriched	mitophagy	6	0.000000	0.046886
depleted	regulation of T cell activation	305	0.000000	0.047015
depleted	cellular response to zinc ion	22	0.000000	0.047092
enriched	regulation of transcription by RNA polymerase I	32	0.000000	0.047919

depleted	sarcosine metabolic process	2	0.000000	0.047919
depleted	regulation of natural killer cell mediated immunity	38	0.000000	0.048523
depleted	response to erythropoietin	5	0.000000	0.048563
enriched	nucleotide-excision repair, preincision complex stabilization	19	0.000000	0.048761
enriched	positive regulation of protein complex assembly	224	0.000000	0.048761
enriched	innate immune response activating cell surface receptor signaling pathway	110	0.000000	0.048914
depleted	L-phenylalanine catabolic process	11	0.000000	0.049048
depleted	lipid hydroxylation	6	0.000000	0.049423
enriched	negative regulation of DNA repair	31	0.000000	0.049423
enriched	DNA replication, removal of RNA primer	4	0.000000	0.049993

Reactome_Pathways

Type	Name	#Hits	Expected score	p-Value
enriched	Separation of Sister Chromatids	186	0.000000	0.000000
enriched	mRNA Splicing - Major Pathway	176	0.000000	0.000000
enriched	Major pathway of rRNA processing in the nucleolus and cytosol	166	0.000000	0.000000
enriched	Resolution of Sister Chromatid Cohesion	122	0.000000	0.000000
enriched	Processing of DNA double-strand break ends	95	0.000000	0.000000
enriched	Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal	92	0.000000	0.000000
enriched	G2/M DNA damage checkpoint	82	0.000000	0.000000
enriched	Mitotic Prometaphase	109	0.000000	0.000000
enriched	Meiotic recombination	77	0.000000	0.000000
enriched	RHO GTPases Activate Formins	136	0.000000	0.000000
enriched	RNA Polymerase I Promoter Escape	82	0.000000	0.000000
enriched	Transcriptional regulation by small RNAs	96	0.000000	0.000000
enriched	ERCC6 (CSB) and EHMT2 (G9a) positively regulate rRNA expression	67	0.000000	0.000000
enriched	Deposition of new CENPA-containing nucleosomes at the centromere	68	0.000000	0.000000
enriched	NoRC negatively regulates rRNA expression	98	0.000000	0.000000
enriched	B-WICH complex positively regulates rRNA expression	82	0.000000	0.000000
enriched	HDACs deacetylate histones	88	0.000000	0.000000
enriched	RUNX1 regulates transcription of genes involved in differentiation of HSCs	122	0.000000	0.000000
enriched	PRC2 methylates histones and DNA	65	0.000000	0.000000
enriched	Condensation of Prophase Chromosomes	66	0.000000	0.000000
enriched	DNA methylation	57	0.000000	0.000000
enriched	HATs acetylate histones	134	0.000000	0.000000
enriched	Formation of the beta-catenin:TCF transactivating complex	80	0.000000	0.000000
enriched	UCH proteinases	98	0.000000	0.000000
enriched	Regulation of TP53 Activity through Phosphorylation	90	0.000000	0.000000
enriched	RNA Polymerase I Promoter Opening	55	0.000000	0.000000
enriched	Senescence-Associated Secretory Phenotype (SASP)	102	0.000000	0.000000
enriched	Estrogen-dependent gene expression	142	0.000000	0.000000
enriched	SIRT1 negatively regulates rRNA expression	60	0.000000	0.000000
depleted	Olfactory Signaling Pathway	363	0.000000	0.000000
enriched	Activated PKN1 stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3	59	0.000000	0.000000
enriched	RMTs methylate histone arginines	72	0.000000	0.000000
enriched	Oxidative Stress Induced Senescence	116	0.000000	0.000000
enriched	rRNA modification in the nucleus and cytosol	58	0.000000	0.000000
enriched	Ub-specific processing proteases	194	0.000000	0.000000
enriched	Nonhomologous End-Joining (NHEJ)	67	0.000000	0.000000
enriched	DNA Damage/Telomere Stress Induced Senescence	62	0.000000	0.000000

enriched	Regulation of expression of SLITs and ROBOs	159	0.000000	0.000000
enriched	Meiotic synapsis	74	0.000000	0.000000
depleted	Regulation of Complement cascade	45	0.000000	0.000000
enriched	Packaging Of Telomere Ends	48	0.000000	0.000000
enriched	Cleavage of the damaged purine	52	0.000000	0.000000
enriched	Recognition and association of DNA glycosylase with site containing an affected purine	52	0.000000	0.000000
enriched	Presynaptic phase of homologous DNA pairing and strand exchange	38	0.000000	0.000000
enriched	SRP-dependent cotranslational protein targeting to membrane	100	0.000000	0.000000
enriched	Cleavage of the damaged pyrimidine	57	0.000000	0.000000
enriched	Recognition and association of DNA glycosylase with site containing an affected pyrimidine	57	0.000000	0.000000
enriched	Activation of anterior HOX genes in hindbrain development during early embryogenesis	113	0.000000	0.000000
enriched	Orc1 removal from chromatin	71	0.000000	0.000000
enriched	snRNP Assembly	50	0.000000	0.000000
enriched	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	72	0.000000	0.000000
enriched	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	72	0.000000	0.000000
enriched	Unwinding of DNA	12	0.000000	0.000000
enriched	mRNA Splicing - Minor Pathway	52	0.000000	0.000000
enriched	Pre-NOTCH Transcription and Translation	85	0.000000	0.000000
enriched	The role of GTSE1 in G2/M progression after G2 checkpoint	77	0.000000	0.000000
enriched	HDR through Homologous Recombination (HRR)	47	0.000000	0.000000
enriched	E3 ubiquitin ligases ubiquitinate target proteins	58	0.000000	0.000000
enriched	Activation of ATR in response to replication stress	37	0.000000	0.000000
enriched	L13a-mediated translational silencing of Ceruloplasmin expression	97	0.000000	0.000000
enriched	CDK-mediated phosphorylation and removal of Cdc6	72	0.000000	0.000000
enriched	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	103	0.000000	0.000000
enriched	Regulation of HSF1-mediated heat shock response	65	0.000000	0.000000
depleted	Initial triggering of complement	15	0.000000	0.000000
enriched	Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	74	0.000000	0.000000
enriched	SUMOylation of chromatin organization proteins	65	0.000000	0.000000
enriched	GTP hydrolysis and joining of the 60S ribosomal subunit	98	0.000000	0.000000
enriched	Recruitment of NuMA to mitotic centrosomes	92	0.000000	0.000000
enriched	Transcriptional regulation of granulopoiesis	82	0.000000	0.000000
enriched	APC/C:Cdc20 mediated degradation of Securin	67	0.000000	0.000000
enriched	SCF(Skp2)-mediated degradation of p27/p21	60	0.000000	0.000000
enriched	Gap-filling DNA repair synthesis and ligation in TC-NER	62	0.000000	0.000000
enriched	Regulation of PLK1 Activity at G2/M Transition	87	0.000000	0.000000
enriched	Autodegradation of Cdh1 by Cdh1:APC/C	63	0.000000	0.000000
enriched	Formation of a pool of free 40S subunits	88	0.000000	0.000000
enriched	NIK- γ noncanonical NF-kB signaling	59	0.000000	0.000000
enriched	AURKA Activation by TPX2	72	0.000000	0.000000
enriched	Recruitment of mitotic centrosome proteins and complexes	80	0.000000	0.000000
enriched	tRNA processing in the nucleus	54	0.000000	0.000000
enriched	Dectin-1 mediated noncanonical NF-kB signaling	60	0.000000	0.000000
enriched	Antigen processing: Ubiquitination & Proteasome degradation	302	0.000000	0.000000
enriched	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	52	0.000000	0.000000
enriched	SUMOylation of DNA damage response and repair proteins	73	0.000000	0.000000
enriched	Amyloid fiber formation	100	0.000000	0.000000
enriched	CDT1 association with the CDC6:ORC:origin complex	59	0.000000	0.000000
depleted	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	117	0.000000	0.000000

enriched	Metalloprotease DUBs	35	0.000000	0.000000
enriched	AUF1 (hnRNP D0) binds and destabilizes mRNA	55	0.000000	0.000000
enriched	Loss of Nlp from mitotic centrosomes	69	0.000000	0.000000
enriched	Loss of proteins required for interphase microtubule organization from the centrosome	69	0.000000	0.000000
enriched	RNA Polymerase II Transcription Termination	63	0.000000	0.000000
enriched	Regulation of ornithine decarboxylase (ODC)	51	0.000000	0.000000
enriched	Activation of the pre-replicative complex	33	0.000000	0.000000
enriched	HDR through Single Strand Annealing (SSA)	37	0.000000	0.000000
enriched	Resolution of D-loop Structures through Holliday Junction Intermediates	30	0.000000	0.000000
enriched	RNA Polymerase II Pre-transcription Events	80	0.000000	0.000000
enriched	Dual incision in TC-NER	62	0.000000	0.000000
enriched	Negative regulation of NOTCH4 signaling	54	0.000000	0.000000
enriched	Degradation of beta-catenin by the destruction complex	68	0.000000	0.000000
enriched	Ubiquitin-dependent degradation of Cyclin D	52	0.000000	0.000000
enriched	Regulation of activated PAK-2p34 by proteasome mediated degradation	50	0.000000	0.000000
depleted	Keratinization	131	0.000000	0.000000
enriched	Prefoldin mediated transfer of substrate to CCT/TriC	28	0.000000	0.000000
depleted	Terminal pathway of complement	8	0.000000	0.000000
enriched	Degradation of AXIN	55	0.000000	0.000000
enriched	Homologous DNA Pairing and Strand Exchange	24	0.000000	0.000000
enriched	RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	89	0.000000	0.000000
enriched	Regulation of RUNX3 expression and activity	55	0.000000	0.000000
enriched	Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA)	24	0.000000	0.000000
enriched	SCF-beta-TrCP mediated degradation of Emi1	55	0.000000	0.000000
enriched	Transport of Mature mRNA derived from an Intron-Containing Transcript	68	0.000000	0.000000
enriched	SUMOylation of DNA replication proteins	42	0.000000	0.000000
enriched	Anchoring of the basal body to the plasma membrane	97	0.000000	0.000000
enriched	G2/M Checkpoints	51	0.000000	0.000001
enriched	PKMTs methylate histone lysines	67	0.000000	0.000001
enriched	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	83	0.000000	0.000001
enriched	Condensation of Prometaphase Chromosomes	10	0.000000	0.000001
enriched	Neddylation	228	0.000000	0.000001
depleted	Glutathione conjugation	22	0.000000	0.000001
enriched	Processing of Capped Intron-Containing Pre-mRNA	34	0.000000	0.000001
enriched	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	54	0.000000	0.000001
depleted	Formation of the cornified envelope	127	0.000000	0.000001
enriched	Nuclear import of Rev protein	31	0.000000	0.000001
enriched	COPI-dependent Golgi-to-ER retrograde traffic	97	0.000000	0.000001
enriched	Regulation of PTEN gene transcription	60	0.000000	0.000001
enriched	Autodegradation of the E3 ubiquitin ligase COP1	52	0.000000	0.000001
enriched	G1/S-Specific Transcription	28	0.000000	0.000001
enriched	Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	13	0.000000	0.000001
enriched	SUMOylation of RNA binding proteins	42	0.000000	0.000001
enriched	Degradation of DVL	57	0.000000	0.000001
enriched	Cyclin A/B1/B2 associated events during G2/M transition	25	0.000000	0.000002
enriched	TP53 Regulates Transcription of DNA Repair Genes	61	0.000000	0.000002
enriched	Viral mRNA Translation	77	0.000000	0.000002
depleted	Branched-chain amino acid catabolism	19	0.000000	0.000002
enriched	Eukaryotic Translation Termination	81	0.000000	0.000002

enriched	Regulation of PTEN stability and activity	68	0.000000	0.000003
enriched	Formation of TC-NER Pre-Incision Complex	51	0.000000	0.000004
enriched	Formation of the ternary complex, and subsequently, the 43S complex	45	0.000000	0.000004
enriched	Cytosolic tRNA aminoacylation	23	0.000000	0.000004
enriched	Vif-mediated degradation of APOBEC3G	54	0.000000	0.000004
enriched	Folding of actin by CCT/TriC	10	0.000000	0.000004
enriched	HIV Transcription Initiation	45	0.000000	0.000005
enriched	RNA Polymerase II HIV Promoter Escape	45	0.000000	0.000005
enriched	RNA Polymerase II Promoter Escape	45	0.000000	0.000005
enriched	RNA Polymerase II Transcription Initiation	45	0.000000	0.000005
enriched	RNA Polymerase II Transcription Initiation And Promoter Clearance	45	0.000000	0.000005
enriched	RNA Polymerase II Transcription Pre-Initiation And Promoter Opening	45	0.000000	0.000005
enriched	Transcription of the HIV genome	45	0.000000	0.000005
depleted	Scavenging of heme from plasma	12	0.000000	0.000005
enriched	RNA Polymerase I Transcription Initiation	45	0.000000	0.000005
enriched	Vpu mediated degradation of CD4	52	0.000000	0.000005
depleted	Lectin pathway of complement activation	8	0.000000	0.000006
enriched	Nuclear Pore Complex (NPC) Disassembly	33	0.000000	0.000006
enriched	Activation of NF-kappaB in B cells	67	0.000000	0.000006
enriched	Translation initiation complex formation	51	0.000000	0.000006
enriched	Peptide chain elongation	77	0.000000	0.000007
enriched	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	65	0.000000	0.000007
enriched	Cross-presentation of soluble exogenous antigens (endosomes)	48	0.000000	0.000008
enriched	Rev-mediated nuclear export of HIV RNA	32	0.000000	0.000009
depleted	Gamma-carboxylation of protein precursors	9	0.000000	0.000010
enriched	RNA polymerase II transcribes snRNA genes	73	0.000000	0.000010
depleted	Removal of aminoterminal propeptides from gamma-carboxylated proteins	9	0.000000	0.000010
enriched	Interleukin-1 signaling	87	0.000000	0.000012
enriched	Hh mutants that don't undergo autocatalytic processing are degraded by ERAD	56	0.000000	0.000014
enriched	Viral Messenger RNA Synthesis	41	0.000000	0.000015
enriched	Hedgehog ligand biogenesis	60	0.000000	0.000016
enriched	Asymmetric localization of PCP proteins	64	0.000000	0.000020
enriched	COPI-mediated anterograde transport	98	0.000000	0.000022
enriched	mRNA 3'-end processing	54	0.000000	0.000023
enriched	Polo-like kinase mediated events	16	0.000000	0.000023
enriched	Transcription-Coupled Nucleotide Excision Repair (TC-NER)	42	0.000000	0.000025
enriched	NS1 Mediated Effects on Host Pathways	35	0.000000	0.000026
enriched	Selenocysteine synthesis	81	0.000000	0.000027
enriched	Ribosomal scanning and start codon recognition	51	0.000000	0.000028
enriched	CLEC7A (Dectin-1) signaling	78	0.000000	0.000028
enriched	NEP/NS2 Interacts with the Cellular Export Machinery	29	0.000000	0.000030
enriched	Defective CFTR causes cystic fibrosis	60	0.000000	0.000034
enriched	Degradation of GLI2 by the proteasome	60	0.000000	0.000034
enriched	GLI3 is processed to GLI3R by the proteasome	60	0.000000	0.000034
enriched	MAPK6/MAPK4 signaling	89	0.000000	0.000039
enriched	Transport of the SLBP Dependant Mature mRNA	33	0.000000	0.000039
enriched	FCERI mediated NF-kB activation	81	0.000000	0.000039
enriched	TNFR2 non-canonical NF-kB pathway	68	0.000000	0.000041
enriched	Dual Incision in GG-NER	39	0.000000	0.000045
depleted	Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus	8	0.000000	0.000052
enriched	HDMS demethylate histones	46	0.000000	0.000056

enriched	Polymerase switching	14	0.000000	0.000063
enriched	Polymerase switching on the C-strand of the telomere	14	0.000000	0.000063
enriched	Transport of Mature mRNA Derived from an Intronless Transcript	39	0.000000	0.000063
depleted	Metallothioneins bind metals	11	0.000000	0.000065
enriched	Regulation of RUNX2 expression and activity	73	0.000000	0.000068
depleted	Aflatoxin activation and detoxification	18	0.000000	0.000068
depleted	Biosynthesis of maresin-like SPMs	6	0.000000	0.000068
enriched	ER-Phagosome pathway	78	0.000000	0.000068
depleted	Intrinsic Pathway of Fibrin Clot Formation	21	0.000000	0.000068
enriched	Translocation of SLC2A4 (GLUT4) to the plasma membrane	71	0.000000	0.000068
enriched	Switching of origins to a post-replicative state	6	0.000000	0.000069
enriched	Formation of the Early Elongation Complex	32	0.000000	0.000075
enriched	Formation of the HIV-1 Early Elongation Complex	32	0.000000	0.000075
enriched	ABC-family proteins mediated transport	80	0.000000	0.000077
enriched	Vpr-mediated nuclear import of PICs	31	0.000000	0.000078
enriched	Formation of RNA Pol II elongation complex	58	0.000000	0.000080
enriched	Transport of Ribonucleoproteins into the Host Nucleus	29	0.000000	0.000081
enriched	RNA Polymerase II Transcription Elongation	56	0.000000	0.000085
enriched	Fanconi Anemia Pathway	37	0.000000	0.000086
enriched	Kinesins	59	0.000000	0.000094
enriched	DNA Damage Recognition in GG-NER	37	0.000000	0.000099
depleted	Eicosanoids	12	0.000000	0.000101
enriched	Selenoamino acid metabolism	10	0.000000	0.000110
depleted	Glyoxylate metabolism and glycine degradation	28	0.000000	0.000112
enriched	Transport of the SLBP independent Mature mRNA	32	0.000000	0.000112
depleted	Fatty acids	14	0.000000	0.000116
enriched	Degradation of GLI1 by the proteasome	60	0.000000	0.000117
enriched	HSP90 chaperone cycle for steroid hormone receptors (SHR)	54	0.000000	0.000150
enriched	Recognition of DNA damage by PCNA-containing replication complex	30	0.000000	0.000158
depleted	Translocation of ZAP-70 to Immunological synapse	17	0.000000	0.000163
enriched	Assembly of the pre-replicative complex	15	0.000000	0.000175
enriched	Regulation of RAS by GAPs	66	0.000000	0.000175
enriched	HDR through MMEJ (alt-NHEJ)	10	0.000000	0.000179
depleted	Choline catabolism	6	0.000000	0.000184
enriched	Formation of HIV elongation complex in the absence of HIV Tat	45	0.000000	0.000217
enriched	Formation of HIV-1 elongation complex containing HIV-1 Tat	43	0.000000	0.000220
enriched	Tat-mediated elongation of the HIV-1 transcript	41	0.000000	0.000221
enriched	RNA Polymerase III Transcription Initiation From Type 2 Promoter	27	0.000000	0.000237
enriched	Mitotic Telophase/Cytokinesis	3	0.000000	0.000242
enriched	SUMOylation of ubiquitylation proteins	36	0.000000	0.000250
depleted	Xenobiotics	21	0.000000	0.000252
enriched	Transcriptional Regulation by E2F6	34	0.000000	0.000275
depleted	HDL remodeling	8	0.000000	0.000276
enriched	Formation of tubulin folding intermediates by CCT/TriC	25	0.000000	0.000277
enriched	SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs	11	0.000000	0.000286
enriched	RNA Pol II CTD phosphorylation and interaction with CE	26	0.000000	0.000288
enriched	RNA Pol II CTD phosphorylation and interaction with CE during HIV infection	26	0.000000	0.000288
enriched	SUMOylation of SUMOylation proteins	31	0.000000	0.000331
enriched	mRNA Capping	28	0.000000	0.000342
enriched	Hedgehog 'on' state	73	0.000000	0.000363
enriched	Initiation of Nuclear Envelope Reformation	13	0.000000	0.000503

enriched	Defective TPR may confer susceptibility towards thyroid papillary carcinoma (TPC)	29	0.000000	0.000512
enriched	Regulation of Glucokinase by Glucokinase Regulatory Protein	29	0.000000	0.000512
enriched	ISG15 antiviral mechanism	69	0.000000	0.000525
depleted	Common Pathway of Fibrin Clot Formation	22	0.000000	0.000572
depleted	PD-1 signaling	21	0.000000	0.000596
enriched	Amino acids regulate mTORC1	54	0.000000	0.000642
depleted	Platelet degranulation	126	0.000000	0.000677
enriched	RNA Polymerase III Transcription Initiation From Type 1 Promoter	28	0.000000	0.000702
enriched	G2/M DNA replication checkpoint	5	0.000000	0.000708
depleted	G alpha (i) signalling events	250	0.000000	0.000744
depleted	G alpha (q) signalling events	170	0.000000	0.000840
enriched	MHC class II antigen presentation	121	0.000000	0.000840
depleted	Generation of second messenger molecules	31	0.000000	0.000864
enriched	Translesion Synthesis by POLH	19	0.000000	0.000896
depleted	Phosphorylation of CD3 and TCR zeta chains	20	0.000000	0.001006
enriched	Post-chaperonin tubulin folding pathway	21	0.000000	0.001026
enriched	SLBP independent Processing of Histone Pre-mRNAs	10	0.000000	0.001079
enriched	mTORC1-mediated signalling	23	0.000000	0.001166
depleted	Activation of C3 and C5	6	0.000000	0.001313
enriched	PCNA-Dependent Long Patch Base Excision Repair	21	0.000000	0.001332
enriched	mTOR signalling	17	0.000000	0.001400
enriched	COPI-independent Golgi-to-ER retrograde traffic	51	0.000000	0.001411
enriched	Removal of the Flap Intermediate	14	0.000000	0.001511
depleted	Ficolins bind to repetitive carbohydrate structures on the target cell surface	5	0.000000	0.001592
enriched	Gap-filling DNA repair synthesis and ligation in GG-NER	25	0.000000	0.001592
enriched	Transcription of E2F targets under negative control by DREAM complex	19	0.000000	0.001762
enriched	Formation of Incision Complex in GG-NER	40	0.000000	0.001928
depleted	Peroxisomal protein import	60	0.000000	0.001928
enriched	APC-Cdc20 mediated degradation of Nek2A	25	0.000000	0.001964
depleted	Classical antibody-mediated complement activation	6	0.000000	0.001965
enriched	Abortive elongation of HIV-1 transcript in the absence of Tat	23	0.000000	0.002082
enriched	Processive synthesis on the lagging strand	10	0.000000	0.002353
enriched	Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	36	0.000000	0.002378
enriched	Downstream TCR signaling	96	0.000000	0.002631
depleted	Ethanol oxidation	12	0.000000	0.002927
depleted	CYP2E1 reactions	9	0.000000	0.003052
enriched	Synthesis of active ubiquitin: roles of E1 and E2 enzymes	29	0.000000	0.003052
enriched	RNA Polymerase III Abortive And Retractive Initiation	41	0.000000	0.003340
enriched	Transcription of E2F targets under negative control by p107 (RBL1) and p130 (RBL2) in complex with HDAC1	16	0.000000	0.003459
enriched	Transferrin endocytosis and recycling	30	0.000000	0.003555
depleted	Metabolism of ingested SeMet, Sec, MeSec into H2Se	7	0.000000	0.003555
enriched	Signal attenuation	9	0.000000	0.003585
depleted	G alpha (s) signalling events	139	0.000000	0.003653
enriched	Regulation of APC/C activators between G1/S and early anaphase	24	0.000000	0.003751
enriched	Nuclear Envelope Breakdown	9	0.000000	0.003864
enriched	RNA Polymerase I Transcription Termination	31	0.000000	0.004031
enriched	HIV elongation arrest and recovery	34	0.000000	0.004489
enriched	Pausing and recovery of HIV elongation	34	0.000000	0.004489
enriched	RNA Polymerase III Transcription Initiation From Type 3 Promoter	28	0.000000	0.004574
enriched	Pausing and recovery of Tat-mediated HIV elongation	32	0.000000	0.004773

enriched	TFAP2A acts as a transcriptional repressor during retinoic acid induced cell differentiation	5	0.000000	0.004773
enriched	Tat-mediated HIV elongation arrest and recovery	32	0.000000	0.004773
depleted	Propionyl-CoA catabolism	5	0.000000	0.004845
depleted	Recycling of bile acids and salts	16	0.000000	0.004845
enriched	ATF4 activates genes in response to endoplasmic reticulum stress	27	0.000000	0.005134
depleted	Tyrosine catabolism	5	0.000000	0.005283
depleted	Post-translational modification: synthesis of GPI-anchored proteins	65	0.000000	0.005358
enriched	Golgi Associated Vesicle Biogenesis	54	0.000000	0.005763
enriched	Chromatin modifying enzymes	17	0.000000	0.005948
enriched	Regulation of the apoptosome activity	11	0.000000	0.006117
depleted	Synthesis of epoxy (EET) and dihydroxyeicosatrienoic acids (DHET)	8	0.000000	0.006122
enriched	Cytosolic sensors of pathogen-associated DNA	22	0.000000	0.006654
depleted	DDX58/IFIH1-mediated induction of interferon-alpha/beta	17	0.000000	0.006660
depleted	MET Receptor Activation	6	0.000000	0.006688
enriched	APC/C:Cdc20 mediated degradation of Cyclin B	23	0.000000	0.007000
enriched	APC/C:Cdc20 mediated degradation of mitotic proteins	20	0.000000	0.007103
depleted	Cell surface interactions at the vascular wall	84	0.000000	0.007103
enriched	Inactivation of APC/C via direct inhibition of the APC/C complex	20	0.000000	0.007103
depleted	Nicotinamide salvaging	19	0.000000	0.007103
depleted	Synthesis of (16-20)-hydroxyeicosatetraenoic acids (HETE)	9	0.000000	0.007110
depleted	Histidine catabolism	8	0.000000	0.007186
depleted	Reuptake of GABA	4	0.000000	0.007621
enriched	Mismatch repair (MMR) directed by MSH2:MSH6 (MutSalpha)	14	0.000000	0.007984
enriched	Ion channel transport	23	0.000000	0.008626
depleted	Synthesis of Ketone Bodies	8	0.000000	0.008830
enriched	Mitochondrial translation initiation	86	0.000000	0.009685
enriched	Mitochondrial translation termination	86	0.000000	0.009685
depleted	Signaling by MST1	5	0.000000	0.009685
enriched	Cholesterol biosynthesis	20	0.000000	0.010720
enriched	RHO GTPases activate IQGAPs	32	0.000000	0.011075
enriched	TP53 Regulates Transcription of Genes Involved in G2 Cell Cycle Arrest	18	0.000000	0.011493
depleted	Miscellaneous substrates	12	0.000000	0.012182
enriched	Inhibition of the proteolytic activity of APC/C required for the onset of anaphase by mitotic spindle checkpoint components	2	0.000000	0.012205
depleted	Formation of xylulose-5-phosphate	5	0.000000	0.013593
depleted	ABC transporters in lipid homeostasis	18	0.000000	0.015922
enriched	Phosphorylation of the APC/C	19	0.000000	0.016167
depleted	Neutrophil degranulation	463	0.000000	0.016297
enriched	Recycling of eIF2:GDP	8	0.000000	0.016406
enriched	NOTCH3 Activation and Transmission of Signal to the Nucleus	23	0.000000	0.016535
enriched	Association of TriC/CCT with target proteins during biosynthesis	37	0.000000	0.017598
enriched	tRNA modification in the nucleus and cytosol	37	0.000000	0.017814
depleted	G alpha (12/13) signalling events	76	0.000000	0.018031
depleted	Acetylation	2	0.000000	0.018848
enriched	KSRP (KHSRP) binds and destabilizes mRNA	17	0.000000	0.018848
enriched	Macroautophagy	66	0.000000	0.018848
enriched	Phosphorylation of Emi1	6	0.000000	0.018848
depleted	Extrinsic Pathway of Fibrin Clot Formation	5	0.000000	0.018895
enriched	Insulin receptor recycling	24	0.000000	0.018895
enriched	Attenuation phase	13	0.000000	0.020487
depleted	Peroxisomal lipid metabolism	4	0.000000	0.020555

depleted	Tryptophan catabolism	14	0.000000	0.021457
enriched	Mitochondrial translation elongation	86	0.000000	0.021490
depleted	AKT-mediated inactivation of FOXO1A	4	0.000000	0.022629
enriched	Telomere Extension By Telomerase	6	0.000000	0.022750
enriched	Intraflagellar transport	54	0.000000	0.024269
enriched	Formation of annular gap junctions	11	0.000000	0.024355
depleted	Peptide ligand-binding receptors	103	0.000000	0.024567
enriched	TP53 regulates transcription of several additional cell death genes whose specific roles in p53-dependent apoptosis remain uncertain	14	0.000000	0.025397
enriched	Noncanonical activation of NOTCH3	8	0.000000	0.026099
enriched	Evasion of Oncogene Induced Senescence Due to Defective p16INK4A binding to CDK4	2	0.000000	0.028487
enriched	Evasion of Oxidative Stress Induced Senescence Due to Defective p16INK4A binding to CDK4	2	0.000000	0.028487
enriched	G0 and Early G1	18	0.000000	0.028487
depleted	Interferon gamma signaling	76	0.000000	0.028487
enriched	XBP1(S) activates chaperone genes	46	0.000000	0.028986
depleted	Conjugation of salicylate with glycine	6	0.000000	0.030071
depleted	Nicotinate metabolism	12	0.000000	0.030635
enriched	MASTL Facilitates Mitotic Progression	10	0.000000	0.031109
enriched	Establishment of Sister Chromatid Cohesion	11	0.000000	0.031114
enriched	RNA Polymerase III Chain Elongation	18	0.000000	0.031605
depleted	NR1H3 & NR1H2 regulate gene expression linked to cholesterol transport and efflux	35	0.000000	0.032038
depleted	Defective MMAA causes methylmalonic aciduria type cblA	2	0.000000	0.034028
depleted	Defective MUT causes methylmalonic aciduria mut type	2	0.000000	0.034028
depleted	Interleukin-33 signaling	3	0.000000	0.034110
enriched	Energy dependent regulation of mTOR by LKB1-AMPK	29	0.000000	0.035166
depleted	Alternative complement activation	5	0.000000	0.035631
enriched	Downregulation of TGF-beta receptor signaling	26	0.000000	0.036691
enriched	RHO GTPases Activate WASPs and WAVES	35	0.000000	0.042898
enriched	Cytosolic iron-sulfur cluster assembly	12	0.000000	0.043497
depleted	Defective ABCA1 causes Tangier disease	2	0.000000	0.043497
enriched	Insulin effects increased synthesis of Xylulose-5-Phosphate	2	0.000000	0.044385
depleted	Synthesis of bile acids and bile salts via 7alpha-hydroxycholesterol	23	0.000000	0.045287
enriched	TP53 Regulates Metabolic Genes	82	0.000000	0.045301
depleted	Neurexins and neuroligins	56	0.000000	0.045732
enriched	Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	22	0.000000	0.046692
enriched	Regulation of actin dynamics for phagocytic cup formation	59	0.000000	0.046725
enriched	SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	32	0.000000	0.047422
enriched	SOS-mediated signalling	7	0.000000	0.048794
enriched	mRNA decay by 3' to 5' exoribonuclease	16	0.000000	0.048794
depleted	mitochondrial fatty acid beta-oxidation of unsaturated fatty acids	6	0.000000	0.048794

GO_-_Cellular_Component

Type	Name	#Hits	Expected score	p-Value
enriched	ribonucleoprotein complex	615	0.000000	0.000000
enriched	transferase complex	687	0.000000	0.000000
enriched	spliceosomal complex	175	0.000000	0.000000
enriched	chromosome	201	0.000000	0.000000
enriched	kinetochore	117	0.000000	0.000000
enriched	catalytic step 2 spliceosome	81	0.000000	0.000000

enriched	centrosome	474	0.000000	0.000000
enriched	preribosome	71	0.000000	0.000000
depleted	blood microparticle	109	0.000000	0.000000
enriched	cell-substrate adherens junction	389	0.000000	0.000000
enriched	cell-substrate junction	393	0.000000	0.000000
enriched	spindle	195	0.000000	0.000000
enriched	focal adhesion	386	0.000000	0.000000
enriched	condensed chromosome kinetochore	87	0.000000	0.000000
enriched	microtubule organizing center	619	0.000000	0.000000
enriched	proteasome complex	57	0.000000	0.000000
enriched	microtubule	362	0.000000	0.000000
enriched	methyltransferase complex	93	0.000000	0.000000
enriched	U2-type spliceosomal complex	88	0.000000	0.000000
depleted	mitochondrial matrix	349	0.000000	0.000000
enriched	adherens junction	520	0.000000	0.000000
enriched	spindle pole	133	0.000000	0.000000
enriched	small nuclear ribonucleoprotein complex	59	0.000000	0.000000
depleted	collagen-containing extracellular matrix	370	0.000000	0.000000
enriched	chromosome, telomeric region	113	0.000000	0.000000
enriched	U2-type precatalytic spliceosome	50	0.000000	0.000000
depleted	high-density lipoprotein particle	23	0.000000	0.000000
enriched	precatalytic spliceosome	51	0.000000	0.000000
depleted	extracellular matrix	495	0.000000	0.000000
enriched	Cajal body	50	0.000000	0.000000
enriched	spliceosomal snRNP complex	53	0.000000	0.000000
enriched	nuclear chromosome, telomeric region	84	0.000000	0.000000
enriched	nuclear speck	384	0.000000	0.000000
depleted	receptor complex	375	0.000000	0.000000
enriched	midbody	153	0.000000	0.000000
enriched	chromosome, centromeric region	65	0.000000	0.000000
depleted	external side of plasma membrane	280	0.000000	0.000000
enriched	condensed nuclear chromosome outer kinetochore	4	0.000000	0.000000
depleted	protein-lipid complex	35	0.000000	0.000000
depleted	lipoprotein particle	33	0.000000	0.000000
depleted	plasma lipoprotein particle	33	0.000000	0.000000
enriched	ubiquitin ligase complex	271	0.000000	0.000001
enriched	U4/U6 x U5 tri-snRNP complex	29	0.000000	0.000001
enriched	small-subunit processome	35	0.000000	0.000002
enriched	nuclear chromosome	53	0.000000	0.000002
enriched	U12-type spliceosomal complex	25	0.000000	0.000003
depleted	peroxisomal matrix	47	0.000000	0.000003
enriched	large ribosomal subunit	108	0.000000	0.000006
depleted	cell surface	599	0.000000	0.000007
depleted	membrane attack complex	7	0.000000	0.000007
enriched	proteasome accessory complex	17	0.000000	0.000010
depleted	T cell receptor complex	14	0.000000	0.000014
enriched	telomerase holoenzyme complex	19	0.000000	0.000015
enriched	protein-DNA complex	131	0.000000	0.000016
enriched	nuclear envelope	171	0.000000	0.000019
enriched	RNA polymerase II transcription factor complex	155	0.000000	0.000025
enriched	mitotic spindle	84	0.000000	0.000025
enriched	mitotic spindle pole	22	0.000000	0.000026
enriched	spindle microtubule	47	0.000000	0.000029
enriched	chaperone complex	21	0.000000	0.000031
enriched	nuclear transcription factor complex	194	0.000000	0.000031
enriched	condensed chromosome	51	0.000000	0.000033

enriched	condensed chromosome outer kinetochore	13	0.000000	0.000043
enriched	SMN-Sm protein complex	15	0.000000	0.000047
enriched	small nucleolar ribonucleoprotein complex	21	0.000000	0.000056
depleted	peroxisome	101	0.000000	0.000063
enriched	ribonucleoprotein granule	219	0.000000	0.000068
depleted	plasma membrane protein complex	517	0.000000	0.000072
depleted	ion channel complex	275	0.000000	0.000084
enriched	replication fork	31	0.000000	0.000084
enriched	nuclear ubiquitin ligase complex	40	0.000000	0.000089
enriched	alpha DNA polymerase:primase complex	5	0.000000	0.000100
depleted	cation channel complex	202	0.000000	0.000103
enriched	histone methyltransferase complex	66	0.000000	0.000105
enriched	microtubule cytoskeleton	139	0.000000	0.000105
enriched	preribosome, large subunit precursor	22	0.000000	0.000107
enriched	melanosome	98	0.000000	0.000114
depleted	transmembrane transporter complex	297	0.000000	0.000122
enriched	proteasome regulatory particle, lid subcomplex	8	0.000000	0.000123
enriched	site of double-strand break	55	0.000000	0.000125
enriched	methylosome	12	0.000000	0.000125
depleted	chylomicron	13	0.000000	0.000126
enriched	MCM complex	9	0.000000	0.000127
enriched	microtubule associated complex	145	0.000000	0.000128
enriched	cytoplasmic ribonucleoprotein granule	208	0.000000	0.000134
enriched	Ndc80 complex	4	0.000000	0.000138
enriched	nucleosome	65	0.000000	0.000202
enriched	supramolecular fiber	658	0.000000	0.000214
depleted	platelet dense granule lumen	14	0.000000	0.000215
enriched	cytosolic large ribosomal subunit	51	0.000000	0.000234
enriched	site of DNA damage	73	0.000000	0.000234
enriched	spindle midzone	32	0.000000	0.000241
depleted	platelet alpha granule lumen	64	0.000000	0.000260
enriched	90S preribosome	11	0.000000	0.000281
depleted	immunoglobulin complex	11	0.000000	0.000281
enriched	lamin filament	5	0.000000	0.000347
depleted	very-low-density lipoprotein particle	19	0.000000	0.000449
enriched	replication fork protection complex	8	0.000000	0.000459
enriched	transcription factor TFIIIC complex	13	0.000000	0.000459
enriched	centralspindlin complex	3	0.000000	0.000471
enriched	U4 snRNP	8	0.000000	0.000524
enriched	chaperonin-containing T-complex	10	0.000000	0.000593
enriched	U5 snRNP	15	0.000000	0.000609
enriched	transcription factor TFIID complex	34	0.000000	0.000615
enriched	U2-type catalytic step 2 spliceosome	30	0.000000	0.000682
depleted	vesicle lumen	316	0.000000	0.000684
depleted	keratin filament	74	0.000000	0.000692
enriched	nuclear matrix	106	0.000000	0.000692
enriched	proteasome regulatory particle	8	0.000000	0.000692
enriched	U2 snRNP	17	0.000000	0.000720
enriched	fibrillar center	125	0.000000	0.000730
enriched	small ribosomal subunit	63	0.000000	0.000794
enriched	host cell	53	0.000000	0.000852
enriched	ribosome	91	0.000000	0.001208
enriched	ficolin-1-rich granule lumen	120	0.000000	0.001247
enriched	ATPase complex	77	0.000000	0.001258
depleted	cytoplasmic vesicle lumen	314	0.000000	0.001411
depleted	spherical high-density lipoprotein particle	8	0.000000	0.001411

enriched	transcription factor complex	352	0.000000	0.001559
depleted	intermediate filament	170	0.000000	0.001567
enriched	nuclear membrane	279	0.000000	0.001841
enriched	aminoacyl-tRNA synthetase multienzyme complex	11	0.000000	0.002018
enriched	cytosolic small ribosomal subunit	35	0.000000	0.002083
enriched	U7 snRNP	7	0.000000	0.002420
depleted	anchored component of membrane	160	0.000000	0.002576
enriched	mitotic spindle midzone	11	0.000000	0.002774
enriched	MLL1 complex	27	0.000000	0.002874
depleted	cell-cell junction	431	0.000000	0.003540
enriched	senescence-associated heterochromatin focus	3	0.000000	0.003659
depleted	secretory granule lumen	310	0.000000	0.003707
enriched	cullin-RING ubiquitin ligase complex	148	0.000000	0.003856
enriched	cyclin B1-CDK1 complex	2	0.000000	0.003928
enriched	polysomal ribosome	26	0.000000	0.004293
enriched	preribosome, small subunit precursor	12	0.000000	0.004415
enriched	eukaryotic 48S preinitiation complex	14	0.000000	0.004724
enriched	eukaryotic translation initiation factor 3 complex	14	0.000000	0.004724
enriched	eukaryotic 43S preinitiation complex	16	0.000000	0.005201
enriched	NuA4 histone acetyltransferase complex	20	0.000000	0.005282
enriched	histone pre-mRNA 3'end processing complex	6	0.000000	0.006361
enriched	proteasome regulatory particle, base subcomplex	11	0.000000	0.006485
depleted	basolateral plasma membrane	193	0.000000	0.006666
enriched	HAUS complex	8	0.000000	0.007707
enriched	condensin complex	8	0.000000	0.007707
enriched	centriole	135	0.000000	0.008191
enriched	kinesin complex	52	0.000000	0.008413
enriched	condensed nuclear chromosome	29	0.000000	0.008629
enriched	cytoplasmic stress granule	60	0.000000	0.009172
enriched	transcriptionally active chromatin	22	0.000000	0.012974
enriched	euchromatin	35	0.000000	0.013026
enriched	heterochromatin	68	0.000000	0.013128
enriched	histone acetyltransferase complex	81	0.000000	0.013341
depleted	tight junction	124	0.000000	0.014019
depleted	immunoglobulin complex, circulating	7	0.000000	0.017965
depleted	perikaryon	135	0.000000	0.017965
depleted	intermediate-density lipoprotein particle	5	0.000000	0.018266
enriched	nuclear pore outer ring	9	0.000000	0.018367
enriched	cytosolic proteasome complex	7	0.000000	0.019467
enriched	exon-exon junction complex	11	0.000000	0.020655
enriched	Sin3-type complex	13	0.000000	0.021169
enriched	BRCA1-A complex	7	0.000000	0.022885
enriched	Ino80 complex	13	0.000000	0.025246
enriched	perinuclear region of cytoplasm	671	0.000000	0.025246
depleted	microvillus	62	0.000000	0.027293
enriched	pronucleus	16	0.000000	0.027293
enriched	transcription export complex	9	0.000000	0.028113
depleted	potassium channel complex	84	0.000000	0.028668
depleted	pentameric IgM immunoglobulin complex	2	0.000000	0.031657
enriched	ubiquitin conjugating enzyme complex	9	0.000000	0.031941
depleted	membrane microdomain	296	0.000000	0.033010
enriched	replisome	2	0.000000	0.033010
enriched	histone deacetylase complex	66	0.000000	0.033719
enriched	box H/ACA snoRNP complex	5	0.000000	0.035208
depleted	bicellular tight junction	117	0.000000	0.035602
enriched	nuclear inner membrane	48	0.000000	0.036802

depleted	alpha-beta T cell receptor complex	5	0.000000	0.037882
enriched	cohesin complex	12	0.000000	0.038701
enriched	GIN5 complex	3	0.000000	0.039385
depleted	dimeric IgA immunoglobulin complex	2	0.000000	0.040079
enriched	mitotic spindle microtubule	3	0.000000	0.040079
depleted	monomeric IgA immunoglobulin complex	2	0.000000	0.040079
depleted	secretory IgA immunoglobulin complex	2	0.000000	0.040079
depleted	secretory dimeric IgA immunoglobulin complex	2	0.000000	0.040079
depleted	fibrinogen complex	8	0.000000	0.042153
depleted	membrane raft	295	0.000000	0.042718
enriched	box C/D snoRNP complex	6	0.000000	0.043368
enriched	TIM23 mitochondrial import inner membrane translocase complex	9	0.000000	0.048718
enriched	anaphase-promoting complex	18	0.000000	0.048861

KEGG - Pathways

Type	Name	#Hits	Expected score	p-Value
enriched	Spliceosome	127	0.000000	0.000000
depleted	Complement and coagulation cascades	78	0.000000	0.000000
enriched	Cell cycle	123	0.000000	0.000000
depleted	Olfactory transduction	395	0.000000	0.000000
enriched	RNA transport	145	0.000000	0.000000
depleted	Drug metabolism - cytochrome P450	56	0.000000	0.000000
depleted	Valine, leucine and isoleucine degradation	47	0.000000	0.000000
depleted	Chemical carcinogenesis	65	0.000000	0.000000
enriched	Ribosome biogenesis in eukaryotes	72	0.000000	0.000000
depleted	Fatty acid degradation	43	0.000000	0.000000
depleted	Neuroactive ligand-receptor interaction	329	0.000000	0.000000
enriched	Viral carcinogenesis	192	0.000000	0.000000
depleted	Glycine, serine and threonine metabolism	37	0.000000	0.000000
enriched	Ribosome	121	0.000000	0.000000
depleted	Metabolism of xenobiotics by cytochrome P450	60	0.000000	0.000000
enriched	DNA replication	36	0.000000	0.000000
enriched	Homologous recombination	40	0.000000	0.000000
enriched	Ubiquitin mediated proteolysis	132	0.000000	0.000000
depleted	Propanoate metabolism	34	0.000000	0.000000
depleted	Retinol metabolism	51	0.000000	0.000000
depleted	Tryptophan metabolism	40	0.000000	0.000000
enriched	Fanconi anemia pathway	51	0.000000	0.000001
enriched	Proteasome	45	0.000000	0.000001
depleted	Carbon metabolism	114	0.000000	0.000001
enriched	Alcoholism	171	0.000000	0.000002
enriched	Systemic lupus erythematosus	119	0.000000	0.000005
depleted	Histidine metabolism	22	0.000000	0.000009
depleted	Cytokine-cytokine receptor interaction	278	0.000000	0.000010
enriched	Basal transcription factors	41	0.000000	0.000012
enriched	Protein processing in endoplasmic reticulum	160	0.000000	0.000012
depleted	Caffeine metabolism	4	0.000000	0.000016
depleted	Glyoxylate and dicarboxylate metabolism	29	0.000000	0.000018
enriched	Mismatch repair	23	0.000000	0.000019
depleted	Cell adhesion molecules (CAMs)	137	0.000000	0.000020
depleted	beta-Alanine metabolism	30	0.000000	0.000021
depleted	Butanoate metabolism	26	0.000000	0.000026
depleted	Tyrosine metabolism	35	0.000000	0.000041
enriched	Endocytosis	233	0.000000	0.000069

enriched	Nucleotide excision repair	43	0.000000	0.000081
depleted	PPAR signaling pathway	70	0.000000	0.000116
depleted	Staphylococcus aureus infection	86	0.000000	0.000116
enriched	RNA polymerase	30	0.000000	0.000133
depleted	Drug metabolism - other enzymes	65	0.000000	0.000150
enriched	mRNA surveillance pathway	82	0.000000	0.000152
enriched	Lysosome	121	0.000000	0.000176
depleted	Arginine and proline metabolism	47	0.000000	0.000287
depleted	Hematopoietic cell lineage	91	0.000000	0.000292
depleted	Peroxisome	78	0.000000	0.000541
depleted	Arginine biosynthesis	19	0.000000	0.000571
depleted	Bile secretion	71	0.000000	0.000581
enriched	MicroRNAs in cancer	158	0.000000	0.000581
enriched	Bacterial invasion of epithelial cells	72	0.000000	0.000662
enriched	Cellular senescence	151	0.000000	0.001516
depleted	Alanine, aspartate and glutamate metabolism	34	0.000000	0.001550
enriched	Aminoacyl-tRNA biosynthesis	44	0.000000	0.001637
depleted	B cell receptor signaling pathway	78	0.000000	0.002452
depleted	Prion diseases	35	0.000000	0.003044
depleted	Natural killer cell mediated cytotoxicity	111	0.000000	0.003421
depleted	Biosynthesis of amino acids	72	0.000000	0.003552
enriched	Oocyte meiosis	118	0.000000	0.003552
depleted	Steroid hormone biosynthesis	47	0.000000	0.003709
depleted	Th1 and Th2 cell differentiation	90	0.000000	0.003929
enriched	Shigellosis	65	0.000000	0.004884
depleted	Arachidonic acid metabolism	58	0.000000	0.005080
enriched	Epithelial cell signaling in Helicobacter pylori infection	68	0.000000	0.005080
depleted	Fatty acid metabolism	54	0.000000	0.006010
enriched	Necroptosis	149	0.000000	0.007044
depleted	Porphyrin and chlorophyll metabolism	32	0.000000	0.007074
enriched	Vibrio cholerae infection	49	0.000000	0.008686
depleted	Glutamatergic synapse	111	0.000000	0.011615
enriched	Human T-cell leukemia virus 1 infection	212	0.000000	0.014352
depleted	Nicotinate and nicotinamide metabolism	36	0.000000	0.014927
depleted	Ascorbate and aldarate metabolism	17	0.000000	0.015391
depleted	Calcium signaling pathway	190	0.000000	0.015862
depleted	cAMP signaling pathway	213	0.000000	0.018800
depleted	Th17 cell differentiation	105	0.000000	0.021444
depleted	Synthesis and degradation of ketone bodies	9	0.000000	0.023289
depleted	Asthma	28	0.000000	0.024846
depleted	Mineral absorption	57	0.000000	0.025156
depleted	Renin secretion	69	0.000000	0.025156
depleted	Pyruvate metabolism	39	0.000000	0.026868
depleted	Inflammatory bowel disease (IBD)	63	0.000000	0.028306
depleted	Pathways in cancer	517	0.000000	0.028306
enriched	Base excision repair	32	0.000000	0.028314
enriched	Chronic myeloid leukemia	75	0.000000	0.028637
depleted	Glycerolipid metabolism	59	0.000000	0.028637
depleted	Glycolysis / Gluconeogenesis	66	0.000000	0.028637
depleted	Phenylalanine metabolism	16	0.000000	0.028637
enriched	Small cell lung cancer	92	0.000000	0.029498
enriched	Protein export	23	0.000000	0.034196
depleted	Glutathione metabolism	53	0.000000	0.034371
enriched	Colorectal cancer	85	0.000000	0.039543
depleted	Cholesterol metabolism	46	0.000000	0.039894
depleted	ABC transporters	45	0.000000	0.042963

enriched	Choline metabolism in cancer	96	0.000000	0.042963
depleted	Fluid shear stress and atherosclerosis	134	0.000000	0.047031