Pathway	Gene ranks	NES	pval	padj
KEGG_SPLICEOSOME		2.82	2.9e-03	1.7e-02
KEGG_MISMATCH_REPAIR		1.98	2.2e-03	1.7e-02
KEGG_DNA_REPLICATION	1	2.08	2.3e-03	1.7e-02
KEGG_HOMOLOGOUS_RECOMBINATION	IIII i i i i i i i i i i i i i i i i i	2.00	2.3e-03	1.7e-02
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	I HOUR RECORD FOR A SECOND SEC	2.10	2.4e-03	1.7e-02
KEGG_RNA_DEGRADATION	IMINITURE REPORT OF A CONTROL O	2.22	2.5e-03	1.7e-02
KEGG_BASAL_TRANSCRIPTION_FACTORS	111####################################	1.96	2.3e-03	1.7e-02
KEGG_NUCLEOTIDE_EXCISION_REPAIR	The termination of the second	2.07	2.5e-03	1.7e-02
KEGG_PROTEASOME	Ⅲ III III	2.03	2.4e-03	1.7e-02
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	If the constraints of the second sec	1.90	2.3e-03	1.7e-02
KEGG_RIBOSOME		2.09	2.7e-03	1.7e-02
KEGG_PYRIMIDINE_METABOLISM		2.03	2.8e-03	1.7e-02
KEGG_CELL_CYCLE	100111000000000000000000000000000000000	1.96	2.9e-03	1.7e-02
KEGG_PURINE_METABOLISM		1.66	2.9e-03	1.7e-02
KEGG_CHEMOKINE_SIGNALING_PATHWAY		-1.68	1.5e-03	1.7e-02
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS		-1.60	3.0e-03	1.7e-02
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY		-1.63	1.5e-03	1.7e-02
KEGG_JAK_STAT_SIGNALING_PATHWAY		-1.63	1.5e-03	1.7e-02
KEGG_FOCAL_ADHESION		-1.77	1.5e-03	1.7e-02
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION		-1.93	1.5e-03	1.7e-02
KEGG_PEROXISOME		-1.78	1.6e-03	1.7e-02
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION		-1.69	3.3e-03	1.7e-02
KEGG_CELL_ADHESION_MOLECULES_CAMS		-1.91	1.5e-03	1.7e-02
KEGG_INOSITOL_PHOSPHATE_METABOLISM	Total to the second control of the second co	-1.68	3.4e-03	1.7e-02
KEGG_HEMATOPOIETIC_CELL_LINEAGE	T 1 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-1.82	1.6e-03	1.7e-02
KEGG_PPAR_SIGNALING_PATHWAY		-1.75	3.2e-03	1.7e-02
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION		-1.70	3.4e-03	1.7e-02
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY		-1.87	1.6e-03	1.7e-02
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM		-1.84	1.6e-03	1.7e-02
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	The first of the second of the	-1.79	3.4e-03	1.7e-02
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION		-1.73	1.7e-03	1.7e-02
KEGG_FATTY_ACID_METABOLISM		-1.80	1.7e-03	1.7e-02
KEGG_LEISHMANIA_INFECTION		-2.00	1.6e-03	1.7e-02
KEGG_ECM_RECEPTOR_INTERACTION	1 11 111 1 11 11 11 11	-2.02	1.6e-03	1.7e-02
KEGG_LYSOSOME		-2.27	1.5e-03	1.7e-02
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Pathway	Gene ranks	NES	pval	padj
MOUSECYC_MM_PWY3DJ-213_TARGETED_PROTEIN_DEGRADATION		2.20	1.9e-03	7.0e-03
MOUSECYC_MM_TRNA-CHARGING-PWY_TRNA_CHARGING_PATHWAY		2.13	1.8e-03	7.0e-03
MOUSECYC_MM_PWY3DJ-1574_TCA_CYCLE_AND_MALATE_ASPARTATE_SHUTTLE_SUPERPATHWAY	l I III III	1.59	1.6e-02	2.7e-02
MOUSECYC_MM_PWY-3781_AEROBIC_RESPIRATIONELECTRON_DONOR_II		1.76	1.7e-03	7.0e-03
MOUSECYC_MM_PWY-4302_AEROBIC_RESPIRATIONELECTRON_DONOR_III		1.65	1.8e-03	7.0e-03
MOUSECYC_MM_PWY0-1334_NADH_TO_CYTOCHROME_I-BD-I_OXIDASE_ELECTRON_TRANSFER		1.62	5.3e-03	1.2e-02
MOUSECYC_MM_PWY0-1335_NADH_TO_CYTOCHROME_I-BO-I_OXIDASE_ELECTRON_TRANSFER		1.62	5.3e-03	1.2e-02
MOUSECYC_MM_P1-PWY_SALVAGE_PATHWAYS_OF_PURINE_AND_PYRIMIDINE_NUCLEOTIDES		1.22	2.0e-01	2.6e-01
MOUSECYC_MM_GLYCOLYSIS_GLYCOLYSIS_I	11 1 1 11 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1.02	4.3e-01	5.2e-01
MOUSECYC_MM_PWY-5328_SUPERPATHWAY_OF_METHIONINE_DEGRADATION		0.87	6.3e-01	7.0e-01
MOUSECYC_MM_PWY-6353_PURINE_NUCLEOTIDES_DEGRADATION_II_AEROBIC		-0.97	4.8e-01	5.5e-01
MOUSECYC_MM_PWY-4061_GLUTATHIONE-MEDIATED_DETOXIFICATION		-1.34	9.0e-02	1.2e-01
MOUSECYC_MM_FAO-PWY_FATTY_ACID_BETA_OXIDATION_I		-1.37	6.7e-02	9.8e-02
MOUSECYC_MM_PWY3DJ-1_CYCLIC_AMP_BIOSYNTHESIS		-1.63	4.6e-03	1.2e-02
MOUSECYC_MM_PWY-6351_D-I-MYO-I-INOSITOL_1-4-5-TRISPHOSPHATE_BIOSYNTHESIS		-1.68	6.7e-03	1.3e-02
MOUSECYC_MM_PWY3DJ-86_VALINE_DEGRADATION		-1.55	1.7e-02	2.7e-02
MOUSECYC_MM_LIPASYN-PWY_PHOSPHOLIPASES		-1.87	2.2e-03	7.0e-03
MOUSECYC_MM_PWY3DJ-0_ISOLEUCINE_DEGRADATION		-1.62	8.6e-03	1.6e-02
MOUSECYC_MM_PWY-5136_FATTY_ACID_BETA_OXIDATION_II_CORE_PATHWAY		-1.75	2.2e-03	7.0e-03
MOUSECYC_MM_PWY-6352_3-PHOSPHOINOSITIDE_BIOSYNTHESIS		-1.88	2.2e-03	7.0e-03
	0 250 500 750			

Pathway	Gene ranks	NES	pval	padj
INOH_MM_IL-1_JNK		2.23	3.7e-03	2.1e-02
INOH_MM_FOLATE_METABOLISM		1.88	3.0e-03	2.1e-02
INOH_MM_IL-1_P38		2.21	3.7e-03	2.1e-02
INOH_MM_TLR_JNK		2.18	3.7e-03	2.1e-02
INOH_MM_TLR_P38		2.14	3.7e-03	2.1e-02
INOH_MM_TNF		2.13	3.6e-03	2.1e-02
INOH_MM_IL-1_NFKB		2.09	3.7e-03	2.1e-02
INOH_MM_TLR_NFKB		2.05	3.7e-03	2.1e-02
INOH_MM_HEDGEHOG		1.97	3.7e-03	2.1e-02
INOH_MM_PYRIMIDINE_NUCLEOTIDES_NUCLEOSIDES_METABOLISM		1.72	6.4e-03	3.4e-02
INOH_MM_CD4_T_CELL_RECEPTOR_SIGNALING-JNK_CASCADE		-1.38	7.5e-02	1.7e-01
INOH_MM_BMP2_SIGNALING_TGF-BETA_MV		-1.46	2.9e-02	7.1e-02
INOH_MM_TGF-BETA_SIGNALING_TAK1		-1.31	1.2e-01	2.6e-01
INOH_MM_INOSITOL_PHOSPHATE_METABOLISM		-1.59	1.2e-02	4.0e-02
INOH_MM_HISTIDINE_DEGRADATION		-1.38	8.0e-02	1.8e-01
INOH_MM_VALINE_LEUCINE_ISOLEUCINE_DEGRADATION		-1.57	1.9e-02	5.2e-02
INOH_MM_INTEGRIN		-1.93	1.3e-03	2.1e-02
INOH_MM_JAK_STAT_MOLECULARVARIATION_1		-1.79	1.4e-03	2.1e-02
INOH_MM_JAK_STAT_MOLECULARVARIATION_2		-1.72	1.5e-03	2.1e-02
INOH_MM_PROPANOATE_METABOLISM		-1.55	1.6e-02	4.5e-02
	0 300 600 900 1200			

Pathway	Gene ranks	NES	pval	padj
WIKIPATHWAYS_MM_MRNA_PROCESSING-WP411		2.66	2.0e-03	1.8e-02
WIKIPATHWAYS_MM_DNA_REPLICATION-WP466		2.14	2.0e-03	1.8e-02
WIKIPATHWAYS_MM_EUKARYOTIC_TRANSCRIPTION_INITIATION-WP405		2.08	2.0e-03	1.8e-02
WIKIPATHWAYS_MM_TRANSLATION_FACTORS-WP107		2.03	2.0e-03	1.8e-02
WIKIPATHWAYS_MM_G1_TO_S_CELL_CYCLE_CONTROL-WP45	 	1.99	2.1e-03	1.8e-02
WIKIPATHWAYS_MM_INTEGRATED_CANCER_PATHWAY-WP1971		1.68	5.8e-03	3.7e-02
WIKIPATHWAYS_MM_CELL_CYCLE-WP179		2.02	2.0e-03	1.8e-02
WIKIPATHWAYS_MM_PROTEASOME_DEGRADATION-WP183		1.76	2.0e-03	1.8e-02
WIKIPATHWAYS_MM_DNA_DAMAGE_RESPONSE-WP707		1.75	2.0e-03	1.8e-02
WIKIPATHWAYS_MM_CYTOPLASMIC_RIBOSOMAL_PROTEINS-WP477		1.61	7.9e-03	4.5e-02
WIKIPATHWAYS_MM_FOCAL_ADHESION-WP306		-1.93	1.9e-03	1.8e-02
WIKIPATHWAYS_MM_IL-4_SIGNALING_PATHWAY-WP395		-1.61	5.9e-03	3.7e-02
WIKIPATHWAYS_MM_TOLL-LIKE_RECEPTOR_SIGNALING_PATHWAY-WP75		-1.90	2.0e-03	1.8e-02
WIKIPATHWAYS_MM_SENESCENCE_AND_AUTOPHAGY-WP615		-1.94	2.0e-03	1.8e-02
WIKIPATHWAYS_MM_TGF_BETA_SIGNALING_PATHWAY-WP560		-1.89	3.9e-03	2.9e-02
WIKIPATHWAYS_MM_COMPLEMENT_AND_COAGULATION_CASCADES-WP558		-1.75	2.0e-03	1.8e-02
WIKIPATHWAYS_MM_INFLAMMATORY_RESPONSE_PATHWAY-WP453		-1.74	4.1e-03	2.9e-02
WIKIPATHWAYS_MM_TYPE_II_INTERFERON_SIGNALING_IFNG-WP619		-1.76	2.0e-03	1.8e-02
WIKIPATHWAYS_MM_MATRIX_METALLOPROTEINASES-WP129		-1.74	4.0e-03	2.9e-02
WIKIPATHWAYS_MM_MONOAMINE_TRANSPORT-WP727		-1.82	2.0e-03	1.8e-02
	0 1000 2000			