Pathway	Gene ranks	NES	pval	padj
KEGG_ONE_CARBON_POOL_BY_FOLATE		1.58	3.2e-02	3.7e-01
KEGG_REGULATION_OF_AUTOPHAGY	Etino mercono de la companya de la c	1.50	5.8e-02	4.0e-01
KEGG_HOMOLOGOUS_RECOMBINATION	Time is a second control of the second contr	1.64	1.9e-02	2.9e-01
KEGG_SPLICEOSOME		1.80	8.1e-03	2.0e-01
KEGG_BASE_EXCISION_REPAIR	П ил по по том	1.42	6.6e-02	4.0e-01
KEGG_RIBOSOME		1.61	6.0e-03	2.0e-01
KEGG_LYSINE_DEGRADATION		1.37	5.9e-02	4.0e-01
KEGG_ARACHIDONIC_ACID_METABOLISM		1.34	9.0e-02	4.2e-01
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION		1.36	8.1e-02	4.0e-01
KEGG_PARKINSONS_DISEASE		1.33	6.3e-02	4.0e-01
KEGG_CHEMOKINE_SIGNALING_PATHWAY		-1.35	1.6e-02	2.8e-01
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	 	-1.42	7.6e-03	2.0e-01
KEGG_CELL_ADHESION_MOLECULES_CAMS		-1.45	9.3e-03	2.0e-01
KEGG_AXON_GUIDANCE		-1.48	2.2e-03	2.0e-01
KEGG_HEMATOPOIETIC_CELL_LINEAGE		-1.46	1.1e-02	2.1e-01
KEGG_ECM_RECEPTOR_INTERACTION		-1.54	4.8e-03	2.0e-01
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY		-1.52	6.3e-03	2.0e-01
KEGG_P53_SIGNALING_PATHWAY		-1.56	2.5e-03	2.0e-01
KEGG_SPHINGOLIPID_METABOLISM		-1.48	2.7e-02	3.6e-01
KEGG_RENIN_ANGIOTENSIN_SYSTEM		-1.52	2.5e-02	3.5e-01
	. 1000 2000 3000 4000			

Pathway	Gene ranks	NES	pval	padj
MOUSECYC_MM_PWY3DJ-0_ISOLEUCINE_DEGRADATION	[1.40	8.5e-02	3.7e-01
MOUSECYC_MM_PWY0-1334_NADH_TO_CYTOCHROME_I-BD-I_OXIDASE_ELECTRON_TRANSFER	I III I II I	1.66	1.1e-02	6.4e-02
MOUSECYC_MM_PWY0-1335_NADH_TO_CYTOCHROME_I-BO-I_OXIDASE_ELECTRON_TRANSFER	1 III I II	1.66	1.1e-02	6.4e-02
MOUSECYC_MM_PWY3DJ-86_VALINE_DEGRADATION	1 1111111 1 1 1 1 1 1 1 1 1 1 1 1 1	1.32	1.6e-01	4.3e-01
MOUSECYC_MM_PWY-4302_AEROBIC_RESPIRATIONELECTRON_DONOR_III		1.66	1.2e-02	6.4e-02
MOUSECYC_MM_PWY-3781_AEROBIC_RESPIRATIONELECTRON_DONOR_II		1.57	9.2e-03	6.4e-02
MOUSECYC_MM_TRNA-CHARGING-PWY_TRNA_CHARGING_PATHWAY		1.24	1.5e-01	4.3e-01
MOUSECYC_MM_PWY-5328_SUPERPATHWAY_OF_METHIONINE_DEGRADATION	I III i mar i i i i i i i i i i i i i i i i i i i	1.00	4.9e-01	7.3e-01
MOUSECYC_MM_PWY3DJ-1574_TCA_CYCLE_AND_MALATE_ASPARTATE_SHUTTLE_SUPERPATHWAY		1.00	4.7e-01	7.3e-01
MOUSECYC_MM_LIPASYN-PWY_PHOSPHOLIPASES	[] [] [] [] [] [] [] [] [] [] [] [] [] [0.94	5.3e-01	7.3e-01
MOUSECYC_MM_FAO-PWY_FATTY_ACID_BETA_OXIDATION_I	111 r r m r r	-0.70	8.5e-01	8.9e-01
MOUSECYC_MM_PWY-6352_3-PHOSPHOINOSITIDE_BIOSYNTHESIS		-0.79	7.5e-01	8.2e-01
MOUSECYC_MM_PWY3DJ-1_CYCLIC_AMP_BIOSYNTHESIS		-0.96	5.1e-01	7.3e-01
MOUSECYC_MM_PWY-6351_D-I-MYO-I-INOSITOL_1-4-5-TRISPHOSPHATE_BIOSYNTHESIS	to the company of the company of the second of the company of the	-0.88	6.5e-01	7.5e-01
MOUSECYC_MM_PWY-6353_PURINE_NUCLEOTIDES_DEGRADATION_II_AEROBIC	III i i i i i i i i i i i i i i i i i i	-0.87	6.5e-01	7.5e-01
MOUSECYC_MM_PWY-4061_GLUTATHIONE-MEDIATED_DETOXIFICATION		-0.97	5.1e-01	7.3e-01
MOUSECYC_MM_PWY-5136_FATTY_ACID_BETA_OXIDATION_II_CORE_PATHWAY		-1.01	4.8e-01	7.3e-01
MOUSECYC_MM_PHOSLIPSYN-PWY_PHOSPHOLIPID_BIOSYNTHESIS_I		-0.99	5.0e-01	7.3e-01
MOUSECYC_MM_P1-PWY_SALVAGE_PATHWAYS_OF_PURINE_AND_PYRIMIDINE_NUCLEOTIDES	lui on on one of the second	-1.10	3.6e-01	7.3e-01
MOUSECYC_MM_GLYCOLYSIS_GLYCOLYSIS_I		-1.33	1.5e-01	4.3e-01
	0 250 500 750			

Pathway	Gene ranks	NES	pval	padj
INOH_MM_PROSTAGLANDIN_LEUKOTRIENE_METABOLISM	The first of the second of the	1.60	5.9e-02	6.8e-01
INOH_MM_LYSINE_DEGRADATION		1.49	6.3e-02	6.8e-01
INOH_MM_GLUTAMATE_GLUTAMINE_METABOLISM	Total management of the second	1.29	1.7e-01	9.6e-01
INOH_MM_FOLATE_METABOLISM	The first of the months of the control of the contr	1.26	1.7e-01	9.6e-01
INOH_MM_VALINE_LEUCINE_ISOLEUCINE_DEGRADATION	Etter en	1.19	2.4e-01	9.6e-01
INOH_MM_METHIONINE_CYSTEINE_METABOLISM	Total control of the second	1.03	4.1e-01	9.6e-01
INOH_MM_PYRUVATE_METABOLISM	Here we were the common to	1.07	3.7e-01	9.6e-01
INOH_MM_PROPANOATE_METABOLISM	The first of the second control of the secon	0.98	4.5e-01	9.6e-01
INOH_MM_GPCR_ADENOSINE_A2A_RECEPTOR	The material control of the second of the se	1.00	4.7e-01	9.6e-01
INOH_MM_NICOTINATE_NICOTINAMIDE_METABOLISM	THE COURT OF THE C	0.88	5.8e-01	9.6e-01
INOH_MM_GLYCINE_SERINE_METABOLISM	The first the first of the first term of the fir	0.93	5.8e-01	9.6e-01
INOH_MM_CITRATE_CYCLE	to material and control of the contr	0.89	6.2e-01	9.6e-01
INOH_MM_INSULIN		0.97	5.4e-01	9.6e-01
INOH_MM_GPCR_SIGNALING-G_ALPHA_S_PKA_AND_ERK		-0.95	6.0e-01	9.6e-01
INOH_MM_WNT_CANONICAL		-0.93	6.3e-01	9.6e-01
INOH_MM_GPCR_SIGNALING-CHOLERA_TOXIN		-0.97	5.7e-01	9.6e-01
INOH_MM_JAK_STAT_PATHWAY_AND_REGULATION		-1.00	5.1e-01	9.6e-01
INOH_MM_GPCR_SIGNALING-G_ALPHA_S_EPAC_AND_ERK		-0.98	5.3e-01	9.6e-01
INOH_MM_GPCR_SIGNALING-G_ALPHA_I		-1.00	4.9e-01	9.6e-01
INOH_MM_GPCR_SIGNALING-PERTUSSIS_TOXIN		-1.00	4.9e-01	9.6e-01
INOH_MM_PYRIMIDINE_NUCLEOTIDES_NUCLEOSIDES_METABOLISM		-0.92	5.9e-01	9.6e-01
INOH_MM_GPCR_SIGNALING-G_ALPHA_Q	11 HE 11 M 1 M M M 1 M 1 M 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H 1 H	-1.07	3.6e-01	9.6e-01
INOH_MM_TGF-BETA_SUPER_FAMILY_SIGNALING_PATHWAY_CANONICAL		-1.04	4.3e-01	9.6e-01
INOH_MM_HEDGEHOG		-0.99	5.0e-01	9.6e-01
INOH_MM_CD4_T_CELL_RECEPTOR_SIGNALING	# 11 T T # 11 TO TO TO TO THE TOTAL TO THE TOTAL TO THE TOTAL THE	-1.09	3.2e-01	9.6e-01
INOH_MM_CD4_T_CELL_RECEPTOR_SIGNALING-NFKB_CASCADE		-1.05	3.9e-01	9.6e-01
INOH_MM_NGF	tion to the control of the control o	-0.90	6.3e-01	9.6e-01
INOH_MM_GPCR_GROUPI_METABOTROPIC_GLUTAMATE_RECEPTOR	ti de la composition de la composition La composition de la	-0.95	5.6e-01	9.6e-01
INOH_MM_EGF	ti di kanan di manan kanan kanan Manan kanan ka	-0.97	5.3e-01	9.6e-01
INOH_MM_PENTOSE_PHOSPHATE_CYCLE	territoria de la companya de la comp	-0.93	5.9e-01	9.6e-01
INOH_MM_CD4_T_CELL_RECEPTOR_SIGNALING-ERK_CASCADE		-1.03	4.6e-01	9.6e-01
INOH_MM_CD4_T_CELL_RECEPTOR_SIGNALING-JNK_CASCADE		-1.08	4.0e-01	9.6e-01
INOH_MM_IGF_SIGNALING		– 1.10	3.7e-01	9.6e-01
INOH_MM_GLYCOLYSIS_GLUCONEOGENESIS		– 1.12	3.4e-01	9.6e-01
INOH_MM_JAK_STAT_MOLECULARVARIATION_1	The second of th	-1.23	1.7e-01	9.6e-01
INOH_MM_PDGF	. — тет сторож от том от т	-1.22	1.9e-01	9.6e-01
INOH_MM_BMP2_SIGNALING_TAK1	en de la companya de La companya de la co	–1.06	4.3e-01	9.6e-01
INOH_MM_JAK_STAT_MOLECULARVARIATION_2		-1.27	1.4e-01	9.6e-01
INOH_MM_AMINOSUGARS_METABOLISM		-1.13	3.4e-01	9.6e-01
INOH_MM_TNF	11	-1.35	6.9e-02	6.8e-01
INOH_MM_INTEGRIN	H 1 111 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-1.49	3.5e-03	2.4e-01
INOH_MM_INOSITOL_PHOSPHATE_METABOLISM		-1.37	6.5e-02	6.8e-01
INOH_MM_TGF-BETA_SIGNALING_TAK1	The state of the s	-1.25	2.0e-01	9.6e-01
INOH_MM_BMP2_SIGNALING_TGF-BETA_MV		-1.41	4.5e-02	6.8e-01
INOH_MM_FAS		-1.47	4.7e-02	6.8e-01
	0 300 600 900			

Pathway	Gene ranks	NES	pval	padj
WIKIPATHWAYS_MM_EICOSANOID_SYNTHESIS-WP167		1.74	6.1e-03	1.8e-01
WIKIPATHWAYS_MM_ONE_CARBON_METABOLISM-WP241		1.60	3.6e-02	2.5e-01
WIKIPATHWAYS_MM_GLYCOGEN_METABOLISM-WP500		1.64	2.8e-02	2.1e-01
WIKIPATHWAYS_MM_OXIDATIVE_PHOSPHORYLATION-WP623	I III пп пп т т телен не н	1.59	2.4e-02	2.1e-01
WIKIPATHWAYS_MM_DIURNALLY_REGULATED_GENES_WITH_CIRCADIAN_ORTHOLOGS-WP410		1.56	2.6e-02	2.1e-01
WIKIPATHWAYS_MM_HYPOTHETICAL_NETWORK_FOR_DRUG_ADDICTION-WP666	11 100	1.33	1.6e-01	5.1e-01
WIKIPATHWAYS_MM_ELECTRON_TRANSPORT_CHAIN-WP111		1.60	5.4e-03	1.8e-01
WIKIPATHWAYS_MM_TOR_SIGNALING-WP1471		1.38	9.1e-02	3.7e-01
WIKIPATHWAYS_MM_HEART_DEVELOPMENT-WP1591		1.33	1.2e-01	4.5e-01
WIKIPATHWAYS_MM_MRNA_PROCESSING-WP411		1.60	8.0e-03	1.9e-01
WIKIPATHWAYS_MM_FOCAL_ADHESION-WP306		-1.40	1.2e-02	2.0e-01
WIKIPATHWAYS_MM_MAPK_SIGNALING_PATHWAY-WP382		-1.48	5.6e-03	1.8e-01
WIKIPATHWAYS_MM_APOPTOSIS-WP254		-1.42	2.2e-02	2.1e-01
WIKIPATHWAYS_MM_APOPTOSIS_MODULATION_AND_SIGNALING-WP1772		-1.46	2.0e-02	2.1e-01
WIKIPATHWAYS_MM_IL-4_SIGNALING_PATHWAY-WP395		-1.45	2.6e-02	2.1e-01
WIKIPATHWAYS_MM_TWEAK_SIGNALING_PATHWAY-WP2036	T	-1.51	2.2e-02	2.1e-01
WIKIPATHWAYS_MM_NOD_PATHWAY-WP1433		-1.55	1.8e-02	2.1e-01
WIKIPATHWAYS_MM_FAS_PATHWAY_AND_STRESS_INDUCTION_OF_HSP_REGULATION-WP314		-1.60	5.3e-03	1.8e-01
WIKIPATHWAYS_MM_SIGNAL_TRANSDUCTION_OF_S1P_RECEPTOR-WP26		-1.57	1.0e-02	2.0e-01
WIKIPATHWAYS_MM_APOPTOSIS_MODULATION_BY_HSP70-WP384		-1.53	2.7e-02	2.1e-01
	0 1000 2000			