Pathway	Gene ranks	NES	pval	padj
KEGG_PYRUVATE_METABOLISM		1.83	2.6e-03	1.0e-01
KEGG_PENTOSE_PHOSPHATE_PATHWAY		1.64	1.7e-02	1.4e-01
KEGG_BUTANOATE_METABOLISM		1.74	7.4e-03	1.2e-01
KEGG_PROPANOATE_METABOLISM	Homeon is a more and a contract of the contrac	1.73	1.2e-02	1.3e-01
KEGG_HISTIDINE_METABOLISM		1.65	1.5e-02	1.4e-01
KEGG_FATTY_ACID_METABOLISM		1.71	1.0e-02	1.2e-01
KEGG_TRYPTOPHAN_METABOLISM		1.64	1.0e-02	1.2e-01
KEGG_LYSINE_DEGRADATION		1.64	1.5e-02	1.4e-01
KEGG_PROTEASOME		1.60	2.0e-02	1.6e-01
KEGG_OXIDATIVE_PHOSPHORYLATION		1.63	8.8e-03	1.2e-01
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON		-1.42	1.1e-02	1.3e-01
KEGG_FOCAL_ADHESION		-1.47	4.2e-03	1.2e-01
KEGG_PATHWAYS_IN_CANCER		-1.53	1.4e-03	8.3e-02
KEGG_CELL_ADHESION_MOLECULES_CAMS		-1.55	6.0e-03	1.2e-01
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION		-1.67	1.5e-03	8.3e-02
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY		-1.58	9.1e-03	1.2e-01
KEGG_ECM_RECEPTOR_INTERACTION		-1.61	3.1e-03	1.0e-01
KEGG_VIRAL_MYOCARDITIS		-1.58	9.5e-03	1.2e-01
KEGG_SMALL_CELL_LUNG_CANCER		-1.69	1.5e-03	8.3e-02
KEGG_DNA_REPLICATION		-1.68	6.8e-03	1.2e-01
	i 1000 2000 3000 4000			

Pathway	Gene ranks	NES	pval	padj
MOUSECYC_MM_PWY-4061_GLUTATHIONE-MEDIATED_DETOXIFICATION		1.62	1.7e-02	2.0e-01
MOUSECYC_MM_TRNA-CHARGING-PWY_TRNA_CHARGING_PATHWAY		1.41	6.9e-02	2.1e-01
MOUSECYC_MM_PWY0-1334_NADH_TO_CYTOCHROME_I-BD-I_OXIDASE_ELECTRON_TRANSFER		1.42	5.6e-02	2.0e-01
MOUSECYC_MM_PWY0-1335_NADH_TO_CYTOCHROME_I-BO-I_OXIDASE_ELECTRON_TRANSFER		1.42	5.6e-02	2.0e-01
MOUSECYC_MM_PWY-4302_AEROBIC_RESPIRATIONELECTRON_DONOR_III		1.42	5.4e-02	2.0e-01
MOUSECYC_MM_PWY-3781_AEROBIC_RESPIRATIONELECTRON_DONOR_II		1.41	5.1e-02	2.0e-01
MOUSECYC_MM_PWY-5044_PURINE_DEGRADATION_I_AEROBIC		1.05	4.1e-01	7.9e-01
MOUSECYC_MM_PHOSLIPSYN-PWY_PHOSPHOLIPID_BIOSYNTHESIS_I		0.96	5.3e-01	8.6e-01
MOUSECYC_MM_PWY-6353_PURINE_NUCLEOTIDES_DEGRADATION_II_AEROBIC		0.91	5.9e-01	8.6e-01
MOUSECYC_MM_PWY-5136_FATTY_ACID_BETA_OXIDATION_II_CORE_PATHWAY		0.90	6.2e-01	8.6e-01
MOUSECYC_MM_FAO-PWY_FATTY_ACID_BETA_OXIDATION_I		0.90	6.1e-01	8.6e-01
MOUSECYC_MM_PWY3DJ-0_ISOLEUCINE_DEGRADATION		-1.15	3.2e-01	6.7e-01
MOUSECYC_MM_P1-PWY_SALVAGE_PATHWAYS_OF_PURINE_AND_PYRIMIDINE_NUCLEOTIDES		-1.40	8.5e-02	2.2e-01
MOUSECYC_MM_PWY3DJ-86_VALINE_DEGRADATION	1	-1.35	1.4e-01	3.3e-01
MOUSECYC_MM_PWY-6352_3-PHOSPHOINOSITIDE_BIOSYNTHESIS		-1.48	5.3e-02	2.0e-01
	0 200 400 600 800			

Pathway	Gene ranks	NES	pval	padj
INOH_MM_PROPANOATE_METABOLISM		1.74	5.3e-03	8.6e-02
INOH_MM_PYRUVATE_METABOLISM		1.84	2.7e-03	8.6e-02
INOH_MM_LYSINE_DEGRADATION		1.69	5.3e-03	8.6e-02
INOH_MM_BUTANOATE_METABOLISM		1.57	5.2e-02	2.9e-01
INOH_MM_HISTIDINE_DEGRADATION		1.60	4.2e-02	2.6e-01
INOH_MM_VALINE_LEUCINE_ISOLEUCINE_DEGRADATION		1.59	2.4e-02	1.9e-01
INOH_MM_GLYCOLYSIS_GLUCONEOGENESIS	HIII 11 11 11 1 1 1 1 1 1 1 1 1 1 1 1 1	1.55	2.6e-02	1.9e-01
INOH_MM_TRYPTOPHAN_DEGRADATION		1.57	2.6e-02	1.9e-01
INOH_MM_FRUCTOSE_MANNOSE_METABOLISM		1.40	9.6e-02	4.9e-01
INOH_MM_ARGININE_PROLINE_METABOLISM		1.27	1.2e-01	5.2e-01
INOH_MM_JAK_STAT_PATHWAY_AND_REGULATION		-1.05	3.4e-01	5.9e-01
INOH_MM_VEGF		-1.06	3.1e-01	5.9e-01
INOH_MM_EPO_SIGNALING		-1.07	3.1e-01	5.9e-01
INOH_MM_IL-7_SIGNALING		-1.08	2.9e-01	5.9e-01
INOH_MM_TLR_ECSIT_MEKK1_JNK		-1.13	3.0e-01	5.9e-01
INOH_MM_TLR_ECSIT_MEKK1_P38		-1.19	2.2e-01	5.9e-01
INOH_MM_IGF_SIGNALING		-1.33	1.1e-01	5.1e-01
INOH_MM_HGF		-1.35	1.0e-01	4.9e-01
INOH_MM_BMP2_SIGNALING_TAK1		-1.18	2.6e-01	5.9e-01
INOH_MM_INTEGRIN		-1.65	1.6e-03	8.6e-02
INOH_MM_JAK_STAT_MOLECULARVARIATION_1		-1.52	6.3e-03	8.6e-02
INOH_MM_PDGF		-1.48	2.8e-02	1.9e-01
INOH_MM_JAK_STAT_MOLECULARVARIATION_2		-1.50	2.0e-02	1.9e-01
	0 300 600 900			

Pathway	Gene ranks	NES	pval	padj
WIKIPATHWAYS_MM_MITOCHONDRIAL_LC-FATTY_ACID_BETA-OXIDATION-WP368	Internal control of the second	1.61	3.0e-02	3.4e-01
WIKIPATHWAYS_MM_FATTY_ACID_BIOSYNTHESIS-WP357	I marina di sociali di seriesa di	1.57	4.5e-02	3.9e-01
WIKIPATHWAYS_MM_FATTY_ACID_BETA_OXIDATION-WP143	I и шинти то	1.64	1.2e-02	1.9e-01
WIKIPATHWAYS_MM_PROTEASOME_DEGRADATION-WP183	111111 1 10 11000 1 0000 1 10000 10 11 11	1.79	6.7e-03	1.9e-01
WIKIPATHWAYS_MM_TCA_CYCLE-WP78	Hit in a contract of a contract of the contrac	1.50	4.2e-02	3.9e-01
WIKIPATHWAYS_MM_ELECTRON_TRANSPORT_CHAIN-WP111		1.72	7.8e-03	1.9e-01
WIKIPATHWAYS_MM_OXIDATIVE_PHOSPHORYLATION-WP623	H I I I H 100 I I I I I I I I I I I I I I I I I I	1.50	5.1e-02	3.9e-01
WIKIPATHWAYS_MM_CYTOPLASMIC_RIBOSOMAL_PROTEINS-WP477	III (1.30	1.1e-01	5.0e-01
WIKIPATHWAYS_MM_ALZHEIMERS_DISEASE-WP2059		1.23	1.1e-01	5.0e-01
WIKIPATHWAYS_MM_G_PROTEIN_SIGNALING_PATHWAYS-WP35		1.28	8.8e-02	5.0e-01
WIKIPATHWAYS_MM_CELL_CYCLE-WP179		-1.28	1.1e-01	5.0e-01
WIKIPATHWAYS_MM_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY-WP138		-1.32	9.9e-02	5.0e-01
WIKIPATHWAYS_MM_FOCAL_ADHESION-WP306	1111 1 m	-1.47	9.3e-03	1.9e-01
WIKIPATHWAYS_MM_SENESCENCE_AND_AUTOPHAGY-WP615		-1.40	4.8e-02	3.9e-01
WIKIPATHWAYS_MM_TOLL-LIKE_RECEPTOR_SIGNALING_PATHWAY-WP75		-1.44	2.7e-02	3.4e-01
WIKIPATHWAYS_MM_ENDOCHONDRAL_OSSIFICATION-WP474		-1.36	8.8e-02	5.0e-01
WIKIPATHWAYS_MM_TGF_BETA_SIGNALING_PATHWAY-WP560	ш т п п п	-1.37	9.2e-02	5.0e-01
WIKIPATHWAYS_MM_LEPTIN_SIGNALING_PATHWAY-WP2034	III 1 1	-1.39	6.7e-02	4.8e-01
WIKIPATHWAYS_MM_STRIATED_MUSCLE_CONTRACTION-WP383		-1.35	1.1e-01	5.0e-01
WIKIPATHWAYS_MM_EBV_LMP1_SIGNALING-WP262		-1.39	9.9e-02	5.0e-01
WIKIPATHWAYS_MM_MITOCHONDRIAL_GENE_EXPRESSION-WP391		-1.39	1.0e-01	5.0e-01
WIKIPATHWAYS_MM_INTEGRATED_CANCER_PATHWAY-WP1971	t e e e e e e e e e e e e e e e e e e e	-1.54	9.0e-03	1.9e-01
WIKIPATHWAYS_MM_DNA_REPLICATION-WP466	· · · · · · · · · · · · · · · · · · ·	-1.61	2.9e-03	1.9e-01
WIKIPATHWAYS_MM_INFLAMMATORY_RESPONSE_PATHWAY-WP453		-1.50	3.7e-02	3.9e-01
WIKIPATHWAYS_MM_TYPE_II_INTERFERON_SIGNALING_IFNG-WP619	to the second of	-1.55	1.0e-02	1.9e-01
WIKIPATHWAYS_MM_MONOAMINE_TRANSPORT-WP727		-1.54	1.4e-02	1.9e-01
	0 500 1000 1500 2000 2500			