Pathway	Gene ranks	NES	pval	padj
KEGG_DNA_REPLICATION		1.96	2.7e−03	5.2e−02
KEGG_MISMATCH_REPAIR		1.76	2.6e−03	5.2e−02
KEGG_BASE_EXCISION_REPAIR		1.85	2.7e−03	5.2e−02
KEGG_RIBOSOME		2.20	4.2e−03	5.7e−02
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM		1.62	1.9e−02	1.5e−01
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS		1.76	5.6e−03	6.1e−02
KEGG_SPLICEOSOME		2.05	5.1e−03	6.1e−02
KEGG_CITRATE_CYCLE_TCA_CYCLE		1.59	1.6e−02	1.5e−01
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION		1.72	3.3e−03	5.7e−02
KEGG_PYRIMIDINE_METABOLISM		1.59	4.2e−03	5.7e−02
KEGG_FOCAL_ADHESION		−1.50	2.3e−03	5.2e−02
KEGG_CHEMOKINE_SIGNALING_PATHWAY		−1.54	1.2e−03	5.0e−02
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY		−1.62	1.3e−03	5.0e−02
KEGG_P53_SIGNALING_PATHWAY		−1.56	6.8e−03	6.9e−02
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION		−1.57	5.4e−03	6.1e−02
KEGG_TIGHT_JUNCTION		−1.75	1.3e−03	5.0e−02
KEGG_AXON_GUIDANCE		−1.84	1.2e−03	5.0e−02
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS		−1.66	4.3e−03	5.7e−02
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION		−1.72	1.4e−03	5.0e−02
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE		−1.60	1.3e−02	1.2e−01

Pathway	Gene ranks	NES	pval	padj
MOUSECYC_MM_PWY3DJ−0_ISOLEUCINE_DEGRADATION		1.70	2.0e−03	4.3e−02
MOUSECYC_MM_PWY3DJ−86_VALINE_DEGRADATION		1.54	7.9e−03	4.3e−02
MOUSECYC_MM_TRNA−CHARGING−PWY_TRNA_CHARGING_PATHWAY		1.70	6.9e−03	4.3e−02
MOUSECYC_MM_PWY3DJ−1574_TCA_CYCLE_AND_MALATE_ASPARTATE_SHUTTLE_SUPERPATHWAY		1.44	5.1e−02	1.3e−01
MOUSECYC_MM_PWY−4302_AEROBIC_RESPIRATION__ELECTRON_DONOR_III		1.61	9.7e−03	4.3e−02
MOUSECYC_MM_PWY−3781_AEROBIC_RESPIRATION__ELECTRON_DONOR_II		1.67	7.4e−03	4.3e−02
MOUSECYC_MM_PWY0−1334_NADH_TO_CYTOCHROME_I−BD−I_OXIDASE_ELECTRON_TRANSFER		1.55	1.5e−02	4.6e−02
MOUSECYC_MM_PWY0−1335_NADH_TO_CYTOCHROME_I−BO−I_OXIDASE_ELECTRON_TRANSFER		1.55	1.5e−02	4.6e−02
MOUSECYC_MM_FAO−PWY_FATTY_ACID_BETA_OXIDATION_I		1.06	4.0e−01	6.4e−01
MOUSECYC_MM_PWY−5136_FATTY_ACID_BETA_OXIDATION_II_CORE_PATHWAY		1.00	4.8e−01	7.0e−01
MOUSECYC_MM_PWY−6353_PURINE_NUCLEOTIDES_DEGRADATION_II_AEROBIC		−0.79	7.5e−01	8.2e−01
MOUSECYC_MM_PWY−5044_PURINE_DEGRADATION_I_AEROBIC		−0.80	7.3e−01	8.2e−01
MOUSECYC_MM_PWY−4061_GLUTATHIONE−MEDIATED_DETOXIFICATION		−0.86	6.8e−01	8.2e−01
MOUSECYC_MM_P1−PWY_SALVAGE_PATHWAYS_OF_PURINE_AND_PYRIMIDINE_NUCLEOTIDES		−1.05	3.8e−01	6.4e−01
MOUSECYC_MM_PWY3DJ−1_CYCLIC_AMP_BIOSYNTHESIS		−1.45	2.4e−02	6.5e−02
MOUSECYC_MM_LIPASYN−PWY_PHOSPHOLIPASES		−1.33	1.3e−01	2.4e−01
MOUSECYC_MM_PWY−6352_3−PHOSPHOINOSITIDE_BIOSYNTHESIS		−1.35	1.3e−01	2.4e−01
MOUSECYC_MM_PWY−6351_D−I−MYO−I−INOSITOL_1−4−5−TRISPHOSPHATE_BIOSYNTHESIS		−1.44	6.4e−02	1.4e−01

Pathway	Gene ranks	NES	pval	padj
INOH_MM_BUTANOATE_METABOLISM		1.65	1.5e−02	3.5e−01
INOH_MM_CITRATE_CYCLE		1.72	7.6e−03	3.5e−01
INOH_MM_TYROSINE_METABOLISM		1.35	8.4e−02	3.5e−01
INOH_MM_GLYCINE_SERINE_METABOLISM		1.38	8.0e−02	3.5e−01
INOH_MM_VALINE_LEUCINE_ISOLEUCINE_DEGRADATION		1.36	8.7e−02	3.5e−01
INOH_MM_HEDGEHOG		1.27	5.7e−02	3.5e−01
INOH_MM_PYRUVATE_METABOLISM		1.09	3.1e−01	5.7e−01
INOH_MM_PYRIMIDINE_NUCLEOTIDES_NUCLEOSIDES_METABOLISM		1.12	2.2e−01	5.4e−01
INOH_MM_IL−1_JNK		1.14	2.0e−01	5.4e−01
INOH_MM_IL−1_P38		1.12	2.4e−01	5.4e−01
INOH_MM_GPCR_SIGNALING−G_ALPHA_Q		−1.24	8.6e−02	3.5e−01
INOH_MM_GPCR_SIGNALING−G_ALPHA_S_EPAC_AND_ERK		−1.24	9.2e−02	3.5e−01
INOH_MM_GPCR_SIGNALING−G_ALPHA_I		−1.25	9.0e−02	3.5e−01
INOH_MM_GPCR_SIGNALING−PERTUSSIS_TOXIN		−1.25	9.0e−02	3.5e−01
INOH_MM_GPCR_SIGNALING−CHOLERA_TOXIN		−1.28	5.5e−02	3.5e−01
INOH_MM_VEGF		−1.29	4.0e−02	3.5e−01
INOH_MM_GPCR_SIGNALING−G_ALPHA_S_PKA_AND_ERK		−1.31	2.9e−02	3.5e−01
INOH_MM_CD4_T_CELL_RECEPTOR_SIGNALING−NFKB_CASCADE		−1.39	4.6e−02	3.5e−01
INOH_MM_B_CELL_RECEPTOR_SIGNALING		−1.45	2.2e−02	3.5e−01
INOH_MM_PDGF		−1.36	7.7e−02	3.5e−01
INOH_MM_HGF		−1.38	7.7e−02	3.5e−01
INOH_MM_GPCR_ADENOSINE_A2A_RECEPTOR		−1.41	6.4e−02	3.5e−01

Pathway	Gene ranks	NES	pval	padj
WIKIPATHWAYS_MM_CHOLESTEROL_BIOSYNTHESIS−WP197		1.68	9.0e−03	8.3e−02
WIKIPATHWAYS_MM_DNA_REPLICATION−WP466		1.74	7.7e−03	8.3e−02
WIKIPATHWAYS_MM_CYTOPLASMIC_RIBOSOMAL_PROTEINS−WP477		1.67	7.7e−03	8.3e−02
WIKIPATHWAYS_MM_GLYCOLYSIS_AND_GLUCONEOGENESIS−WP534		1.58	1.5e−02	1.0e−01
WIKIPATHWAYS_MM_ELECTRON_TRANSPORT_CHAIN−WP111		1.77	3.1e−03	8.3e−02
WIKIPATHWAYS_MM_FAS_PATHWAY_AND_STRESS_INDUCTION_OF_HSP_REGULATION−WP314		1.50	2.8e−02	1.3e−01
WIKIPATHWAYS_MM_MRNA_PROCESSING−WP411		1.84	3.8e−03	8.3e−02
WIKIPATHWAYS_MM_TCA_CYCLE−WP78		1.39	5.9e−02	2.2e−01
WIKIPATHWAYS_MM_FOLATE_METABOLISM−WP176		1.50	2.1e−02	1.1e−01
WIKIPATHWAYS_MM_OXIDATIVE_PHOSPHORYLATION−WP623		1.37	6.1e−02	2.2e−01
WIKIPATHWAYS_MM_FOCAL_ADHESION−WP306		−1.51	5.0e−03	8.3e−02
WIKIPATHWAYS_MM_CALCIUM_REGULATION_IN_THE_CARDIAC_CELL−WP536		−1.58	2.7e−03	8.3e−02
WIKIPATHWAYS_MM_MYOMETRIAL_RELAXATION_AND_CONTRACTION_PATHWAYS−WP289		−1.61	2.6e−03	8.3e−02
WIKIPATHWAYS_MM_SENESCENCE_AND_AUTOPHAGY−WP615		−1.61	5.7e−03	8.3e−02
WIKIPATHWAYS_MM_MICRORNAS_IN_CARDIOMYOCYTE_HYPERTROPHY−WP1544		−1.62	4.4e−03	8.3e−02
WIKIPATHWAYS_MM_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY		−1.59	8.9e−03	8.3e−02
WIKIPATHWAYS_MM_NOTCH_SIGNALING_PATHWAY−WP61		−1.58	1.1e−02	9.3e−02
WIKIPATHWAYS_MM_LEPTIN_SIGNALING_PATHWAY−WP2034		−1.67	4.7e−03	8.3e−02
WIKIPATHWAYS_MM_SIGNALING_OF_HEPATOCYTE_GROWTH_FACTOR_RECEPTOR−WP313		−1.68	6.6e−03	8.3e−02
WIKIPATHWAYS_MM_EPO_RECEPTOR_SIGNALING−WP581		−1.66	1.2e−02	9.7e−02