













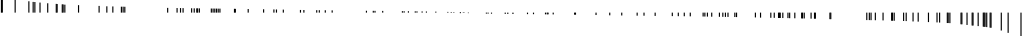

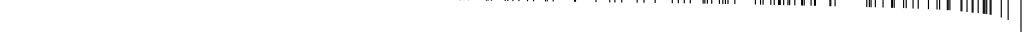










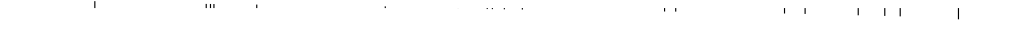
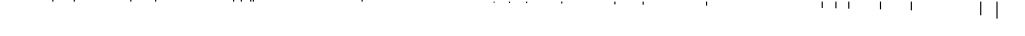








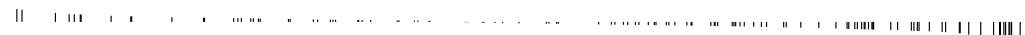







0 1000 2000 3000 4000



Pathway	Gene ranks	NES	pval	padj
INOH_MM_PROSTAGLANDIN_LEUKOTRIENE_METABOLISM		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		1.29	1.7e-01	9.6e-01
INOH_MM_FOLATE_METABOLISM		1.26	1.7e-01	9.6e-01
INOH_MM_VALINE_LEUCINE_ISOLEUCINE_DEGRADATION		1.19	2.4e-01	9.6e-01
INOH_MM_METHIONINE_CYSTEINE_METABOLISM		1.03	4.1e-01	9.6e-01
INOH_MM_PYRUVATE_METABOLISM		1.07	3.7e-01	9.6e-01
INOH_MM_PROPANOATE_METABOLISM		0.98	4.5e-01	9.6e-01
INOH_MM_GPCR_ADENOSINE_A2A_RECEPTOR		1.00	4.7e-01	9.6e-01
INOH_MM_NICOTINATE_NICOTINAMIDE_METABOLISM		0.88	5.8e-01	9.6e-01
INOH_MM_GLYCINE_SERINE_METABOLISM		0.93	5.8e-01	9.6e-01
INOH_MM_CITRATE_CYCLE		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		-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		-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		-0.90	6.3e-01	9.6e-01
INOH_MM_GPCR_GROUPI_METABOTROPIC_GLUTAMATE_RECEPTOR		-0.95	5.6e-01	9.6e-01
INOH_MM_EGF		-0.97	5.3e-01	9.6e-01
INOH_MM_PENTOSE_PHOSPHATE_CYCLE		-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_GLUONEOGENESIS		-1.12	3.4e-01	9.6e-01
INOH_MM_JAK_STAT_MOLECULARVARIATION_1		-1.23	1.7e-01	9.6e-01
INOH_MM_PDGF		-1.22	1.9e-01	9.6e-01
INOH_MM_BMP2_SIGNALING_TAK1		-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		-1.35	6.9e-02	6.8e-01
INOH_MM_INTEGRIN		-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		-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

