



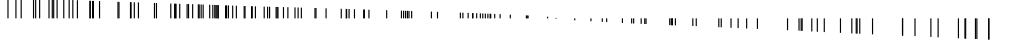
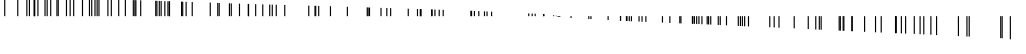





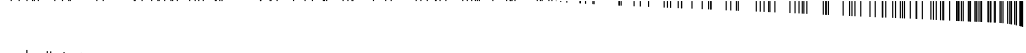










Pathway	Gene ranks	NES	pval	padj
NADH REPAIR		2.17	2.9e-04	5.3e-04
THIAMIN SALVAGE III		2.01	2.9e-04	5.3e-04
TRNA SPLICING		2.82	2.9e-04	5.3e-04
ALL-TRANS-DECAPRENYL DIPHOSPHATE BIOSYNTHESIS		2.38	2.9e-04	5.3e-04
4-AMINOBUTYRATE DEGRADATION I		1.41	6.3e-03	8.7e-03
SPERMINE AND SPERMDINE DEGRADATION I		1.27	4.0e-02	5.0e-02
TYROSINE BIOSYNTHESIS IV		1.11	1.8e-01	2.0e-01
METHYLMALONYL PATHWAY		1.06	2.8e-01	3.2e-01
PYRIMIDINE RIBONUCLEOTIDES INTERCONVERSION		1.05	3.2e-01	3.6e-01
PREGNENOLONE BIOSYNTHESIS		1.03	3.7e-01	4.0e-01
MYO-INOSITOL BIOSYNTHESIS		-2.23	1.6e-04	3.0e-04
VALINE DEGRADATION I		-1.99	1.6e-04	3.0e-04
S-ADENOSYL-L-METHIONINE BIOSYNTHESIS		-1.77	1.6e-04	3.0e-04
CITRULLINE-NITRIC OXIDE CYCLE		-1.68	1.6e-04	3.0e-04
GLYCINE CLEAVAGE		-1.84	1.5e-04	3.0e-04
GALACTOSE DEGRADATION I (LELOIR PATHWAY)		-2.06	1.5e-04	3.0e-04
CITRULLINE DEGRADATION		-1.89	1.5e-04	3.0e-04
5-AMINOIMIDAZOLE RIBONUCLEOTIDE BIOSYNTHESIS I		-1.79	1.5e-04	3.0e-04
UDP-N-Acetyl-D-glucosamine BIOSYNTHESIS II		-2.02	1.5e-04	3.0e-04
CYSTEINE BIOSYNTHESIS/HOMOCYSTEINE DEGRADATION		-1.92	1.5e-04	3.0e-04