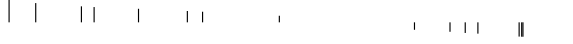
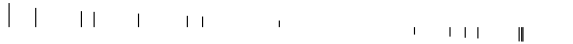

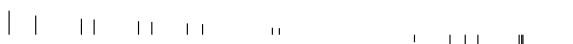
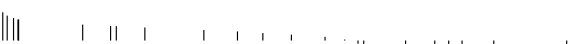








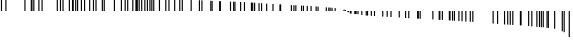
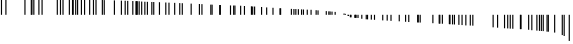







Pathway	Gene ranks	NES	pval	padj
endoplasmic reticulum unfolded protein response		1.66	1.3e-02	1.0e+00
cellular response to unfolded protein		1.66	1.3e-02	1.0e+00
regulation of response to external stimulus		1.68	8.2e-03	1.0e+00
cellular response to topologically incorrect protein		1.59	1.9e-02	1.0e+00
vasculature development		1.59	1.6e-02	1.0e+00
cardiovascular system development		1.59	1.6e-02	1.0e+00
myelin sheath		1.60	1.0e-02	1.0e+00
secretion by cell		1.49	1.1e-02	1.0e+00
secretion		1.49	1.2e-02	1.0e+00
RNA splicing		1.40	2.0e-02	1.0e+00
negative regulation of cellular metabolic process		-1.17	2.1e-02	1.0e+00
regulation of cellular protein metabolic process		-1.27	1.5e-02	1.0e+00
negative regulation of cellular biosynthetic process		-1.31	2.2e-02	1.0e+00
negative regulation of macromolecule biosynthetic process		-1.31	2.2e-02	1.0e+00
negative regulation of biosynthetic process		-1.35	1.1e-02	1.0e+00
regulation of translation		-1.61	7.3e-03	1.0e+00
regulation of cellular amide metabolic process		-1.71	7.5e-03	1.0e+00
nucleolar part		-1.70	1.7e-02	1.0e+00
protein-DNA complex		-1.63	2.4e-02	1.0e+00
small GTPase mediated signal transduction		-1.96	6.6e-03	1.0e+00

0 200 400 600 800