










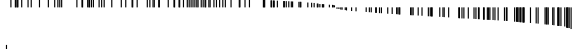
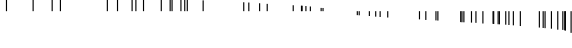



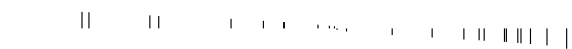





| Pathway | Gene ranks | NES | pval | padj |
|---|---|-------|---------|---------|
| endoplasmic reticulum unfolded protein response |  | 1.63 | 7.1e-03 | 1.0e+00 |
| cellular response to unfolded protein |  | 1.63 | 7.1e-03 | 1.0e+00 |
| regulation of response to external stimulus |  | 1.67 | 1.4e-02 | 1.0e+00 |
| cellular response to topologically incorrect protein |  | 1.57 | 2.1e-02 | 1.0e+00 |
| vasculature development |  | 1.58 | 2.0e-02 | 1.0e+00 |
| cardiovascular system development |  | 1.58 | 2.0e-02 | 1.0e+00 |
| myelin sheath |  | 1.59 | 1.7e-02 | 1.0e+00 |
| secretion by cell |  | 1.50 | 1.3e-02 | 1.0e+00 |
| secretion |  | 1.49 | 1.5e-02 | 1.0e+00 |
| RNA splicing |  | 1.40 | 1.7e-02 | 1.0e+00 |
| regulation of cellular protein metabolic process |  | -1.28 | 3.3e-02 | 1.0e+00 |
| chromatin |  | -1.43 | 3.2e-02 | 1.0e+00 |
| regulation of translation |  | -1.68 | 7.3e-03 | 1.0e+00 |
| regulation of cellular amide metabolic process |  | -1.76 | 8.1e-03 | 1.0e+00 |
| nucleolar part |  | -1.69 | 9.0e-03 | 1.0e+00 |
| positive regulation of cellular amide metabolic process |  | -1.53 | 3.2e-02 | 1.0e+00 |
| protein–DNA complex |  | -1.62 | 3.0e-02 | 1.0e+00 |
| enzyme activator activity |  | -1.66 | 2.9e-02 | 1.0e+00 |
| nuclease activity |  | -1.73 | 2.7e-02 | 1.0e+00 |
| small GTPase mediated signal transduction |  | -2.00 | 7.3e-03 | 1.0e+00 |

0 200 400 600 800