

Table S2. Relating mRNA stability to gene function using a Gene Ontology (GO) analysis in the WT line (the 200 most stable genes)

| GO term | | | Continued | | |
|---|----------|----------|--|----------|----------|
| Biological process | P value | FDR | intracellular part | 1.03E-04 | 6.84E-03 |
| cytoplasmic translation | 3.71E-14 | 2.75E-10 | intracellular | 1.06E-04 | 6.70E-03 |
| translation | 2.57E-11 | 9.55E-08 | cell part | 3.23E-04 | 1.86E-02 |
| cellular protein metabolic process | 1.44E-06 | 9.72E-04 | cell | 3.23E-04 | 1.94E-02 |
| protein metabolic process | 9.18E-05 | 3.58E-02 | ferritin complex | 1.00E-03 | 4.86E-02 |
| cellular macromolecule metabolic process | 4.99E-06 | 2.64E-03 | protein complex | 8.68E-04 | 4.58E-02 |
| cellular process | 3.60E-05 | 1.57E-02 | macromolecular complex | 7.83E-07 | 9.01E-05 |
| cellular macromolecule biosynthetic process | 5.42E-07 | 4.46E-04 | cytosolic large ribosomal subunit | 7.55E-12 | 3.18E-09 |
| macromolecule biosynthetic process | 9.42E-07 | 6.99E-04 | cytosolic part | 5.72E-12 | 3.62E-09 |
| organic substance biosynthetic process | 1.18E-05 | 5.49E-03 | cytosol | 3.24E-08 | 5.12E-06 |
| biosynthetic process | 8.67E-06 | 4.29E-03 | cytoplasmic part | 5.08E-09 | 1.07E-06 |
| cellular biosynthetic process | 4.37E-06 | 2.49E-03 | cytoplasm | 3.55E-05 | 2.99E-03 |
| peptide biosynthetic process | 3.53E-11 | 8.73E-08 | large ribosomal subunit | 6.64E-09 | 1.20E-06 |
| peptide metabolic process | 1.24E-10 | 1.85E-07 | ribosomal subunit | 9.63E-11 | 2.44E-08 |
| cellular amide metabolic process | 8.80E-10 | 1.09E-06 | intracellular organelle part | 2.96E-05 | 2.67E-03 |
| cellular nitrogen compound metabolic process | 2.53E-06 | 1.56E-03 | intracellular organelle | 4.92E-05 | 3.89E-03 |
| organonitrogen compound biosynthetic process | 5.27E-08 | 5.59E-05 | organelle | 5.21E-05 | 3.87E-03 |
| amide biosynthetic process | 8.29E-11 | 1.54E-07 | organelle part | 7.24E-05 | 5.09E-03 |
| cellular nitrogen compound biosynthetic process | 5.75E-08 | 5.33E-05 | intracellular ribonucleoprotein complex | 1.46E-06 | 1.42E-04 |
| gene expression | 3.87E-05 | 1.60E-02 | ribonucleoprotein complex | 1.46E-06 | 1.54E-04 |
| ribosome assembly | 1.27E-04 | 4.72E-02 | ribosome | 2.83E-11 | 8.96E-09 |
| Molecular function complete | | | intracellular non-membrane-bounded organelle | 4.53E-07 | 6.37E-05 |
| structural constituent of ribosome | 4.83E-11 | 1.27E-07 | non-membrane-bounded organelle | 4.53E-07 | 5.74E-05 |
| structural molecule activity | 7.85E-06 | 6.89E-03 | cytosolic ribosome | 2.40E-14 | 3.03E-11 |
| RNA binding | 7.35E-07 | 9.68E-04 | cytosolic small ribosomal subunit | 3.90E-04 | 2.15E-02 |
| Cellular component complete | | | | | |
| intracellular ferritin complex | 1.00E-03 | 5.06E-02 | | | |

Significant GO terms and relevant P values and FDR (False Discovery rate) are shown. FDR cutoff = 0.05.