**Table S1** Functional GO Biological Process enrichment analysis

| GO Biological Process Term | Count[†] | *p*-value[‡] | AC[§] | Protein name | Fold Enrichment[¶] | Benjamini[‖] |
|---|---|---|---|---|---|---|
| cellular metabolic process (GO:0044237) | 39 | 2,12E-07 | Q6NVY1 | 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial | 1.8 | 1,46E-04 |
| | | | P55809 | Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial | | |
| | | | P31939 | Bifunctional purine biosynthesis protein, PURH | | |
| | | | O95433 | Activator of 90 kDa heat shock protein ATPase homolog 1 | | |
| | | | P06576 | ATP synthase subunit beta, mitochondrial | | |
| | | | Q02790 | Peptidyl-prolyl cis-trans isomerase FKBP4 | | |
| | | | Q9NR45 | Sialic acid synthase | | |
| | | | Q9Y230 | RuvB-like 2 | | |
| | | | Q8NC51 | Plasminogen activator inhibitor 1 RNA-binding protein | | |
| | | | Q16851 | UTP--glucose-1-phosphate uridylyltransferase | | |
| | | | O96019 | Actin-like protein 6A | | |
| | | | P00352 | Retinal dehydrogenase 1 | | |
| | | | P09972 | Fructose-bisphosphate aldolase C | | |
| | | | P04083 | Annexin A1 | | |
| | | | O43684 | Mitotic checkpoint protein BUB3 | | |
| | | | P78371 | T-complex protein 1 subunit beta | | |
| | | | P09622 | Dihydrolipoyl dehydrogenase, mitochondrial | | |
| | | | P06733 | Alpha-enolase | | |
| | | | P13639 | Elongation factor 2 | | |
| | | | O75821 | Eukaryotic translation initiation factor 3 subunit G | | |
| | | | Q13347 | Eukaryotic translation initiation factor 3 subunit I | | |
| | | | Q15056 | Eukaryotic translation initiation factor 4H | | |
| | | | Q96IT0 | Fatty acid synthase | | |
| | | | P48637 | Glutathione synthetase | | |
| | | | P04406 | glyceraldehyde-3-phosphate dehydrogenase | | |
| | | | O95757 | Heat shock 70 kDa protein 4L | | |
| | | | P38646 | Stress-70 protein, mitochondrial | | |
| | | | P22626 | Heterogeneous nuclear ribonucleoproteins A2/B1 | | |
| | | | P07195 | Lactate dehydrogenase B | | |
| | | | Q9H3E1 | Methionine adenosyltransferase 2 subunit beta | | |
| | | | Q9H010 | S-methyl-5'-thioadenosine phosphorylase | | |
| | | | Q9UQ80 | Proliferation-associated protein 2G4 | | |
| | | | P62195 | 26S protease regulatory subunit 8 | | |
| | | | P25787 | Proteasome subunit alpha type-2 | | |
| | | | Q96J01 | THO complex subunit 3 | | |
| | | | P23246 | Splicing factor, proline- and glutamine-rich | | |
| | | | O60506 | Heterogeneous nuclear ribonucleoprotein Q | | |
| | | | P55072 | Transitional endoplasmic reticulum ATPase | | |
| | | | P17022 | Zinc finger protein 18 | | |
| | | | Q6NVY1 | 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial | | |
| | | | P31939 | Bifunctional purine biosynthesis protein, PURH | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | O95433 | Activator of 90 kDa heat shock protein ATPase homolog 1 | | |
| | | | P06576 | ATP synthase subunit beta, mitochondrial | | |
| | | | Q02790 | Peptidyl-prolyl cis-trans isomerase FKBP4 | | |
| | | | Q9NR45 | Sialic acid synthase | | |
| | | | Q9Y230 | RuvB-like 2 | | |
| | | | Q8NC51 | Plasminogen activator inhibitor 1 RNA-binding protein | | |
| | | | Q16851 | UTP--glucose-1-phosphate uridylyltransferase | | |
| | | | O96019 | Actin-like protein 6A | | |
| | | | P09972 | Fructose-bisphosphate aldolase C | | |
| | | | P04083 | Annexin A1 | | |
| | | | O43684 | Mitotic checkpoint protein BUB3 | | |
| | | | P78371 | T-complex protein 1 subunit beta | | |
| | | | P09622 | Dihydrolipoyl dehydrogenase, mitochondrial | | |
| | | | P06733 | Alpha-enolase | | |
| | | | P13639 | Elongation factor 2 | | |
| | | | O75821 | Eukaryotic translation initiation factor 3 subunit G | | |
| | | | Q13347 | Eukaryotic translation initiation factor 3 subunit I | | |
| | | | Q15056 | Eukaryotic translation initiation factor 4H | | |
| | | | Q96IT0 | Fatty acid synthase | | |
| | | | P48637 | Glutathione synthetase | | |
| | | | P04406 | glyceraldehyde-3-phosphate dehydrogenase | | |
| | | | O95757 | Heat shock 70 kDa protein 4L | | |
| | | | P38646 | Stress-70 protein, mitochondrial | | |
| | | | P22626 | Heterogeneous nuclear ribonucleoproteins A2/B1 | | |
| | | | P07195 | Lactate dehydrogenase B | | |
| | | | P28838 | Cytosol aminopeptidase | | |
| | | | Q9H3E1 | Methionine adenosyltransferase 2 subunit beta | | |
| | | | Q9H010 | S-methyl-5'-thioadenosine phosphorylase | | |
| | | | Q9UQ80 | Proliferation-associated protein 2G4 | | |
| | | | P62195 | 26S protease regulatory subunit 8 | | |
| | | | P25787 | Proteasome subunit alpha type-2 | | |
| | | | Q96J01 | THO complex subunit 3 | | |
| | | | P23246 | Splicing factor, proline- and glutamine-rich | | |
| | | | O60506 | Heterogeneous nuclear ribonucleoprotein Q | | |
| | | | P55072 | Transitional endoplasmic reticulum ATPase | | |
| | | | P17022 | 26S protease regulatory subunit 8 | | |
| | | | Q6NVY1 | 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial | | |
| | | | P55809 | Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial | | |
| | | | P31939 | Bifunctional purine biosynthesis protein, PURH | | |
| | | | O95433 | Activator of 90 kDa heat shock protein ATPase homolog 1 | | |
| | | | P06576 | ATP synthase subunit beta, mitochondrial | | |
| | | | Q02790 | Peptidyl-prolyl cis-trans isomerase FKBP4 | | |
| | | | Q9NR45 | Sialic acid synthase | | |
| | | | Q9Y230 | RuvB-like 2 | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | Q8NC51 | Plasminogen activator inhibitor 1 RNA-binding protein | | |
| | | | Q16851 | UTP--glucose-1-phosphate uridylyltransferase | | |
| | | | O96019 | Actin-like protein 6° | | |
| | | | P00352 | Retinal dehydrogenase 1 | | |
| | | | P09972 | Fructose-bisphosphate aldolase C | | |
| | | | P04083 | Annexin A1 | | |
| | | | O43684 | Mitotic checkpoint protein BUB3 | | |
| | | | P78371 | T-complex protein 1 subunit beta | | |
| | | | P09622 | Dihydrolipoyl dehydrogenase, mitochondrial | | |
| | | | P06733 | Alpha-enolase | | |
| | | | P13639 | Elongation factor 2 | | |
| | | | O75821 | Eukaryotic translation initiation factor 3 subunit G | | |
| | | | Q13347 | Eukaryotic translation initiation factor 3 subunit I | | |
| | | | Q15056 | Eukaryotic translation initiation factor 4H | | |
| | | | Q96IT0 | Fatty acid synthase | | |
| | | | P48637 | Glutathione synthetase | | |
| | | | P04406 | glyceraldehyde-3-phosphate dehydrogenase | | |
| | | | O95757 | Heat shock 70 kDa protein 4L | | |
| | | | P38646 | Stress-70 protein, mitochondrial | | |
| | | | P22626 | Heterogeneous nuclear ribonucleoproteins A2/B1 | | |
| | | | P07195 | Lactate dehydrogenase B | | |
| | | | P28838 | Cytosol aminopeptidase | | |
| | | | Q9H3E1 | Methionine adenosyltransferase 2 subunit beta | | |
| | | | Q9H010 | S-methyl-5'-thioadenosine phosphorylase | | |
| | | | Q9UQ80 | Proliferation-associated protein 2G4 | | |
| | | | P62195 | 26S protease regulatory subunit 8 | | |
| | | | P25787 | Proteasome subunit alpha type-2 | | |
| | | | Q96J01 | THO complex subunit 3 | | |
| | | | P23246 | Splicing factor, proline- and glutamine-rich | | |
| | | | O60506 | Heterogeneous nuclear ribonucleoprotein Q | | |
| | | | P55072 | Transitional endoplasmic reticulum ATPase | | |
| | | | P17022 | Zinc finger protein 18 | | |
| | | | Q6NVY1 | 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial | | |
| | | | P55809 | Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial | | |
| | | | P31939 | Bifunctional purine biosynthesis protein, PURH | | |
| | | | O95433 | Activator of 90 kDa heat shock protein ATPase homolog 1 | | |
| | | | P06576 | ATP synthase subunit beta, mitochondrial | | |
| | | | Q02790 | Peptidyl-prolyl cis-trans isomerase FKBP4 | | |
| | | | O14908 | PDZ domain-containing protein GIPC1 | | |
| | | | Q9NR45 | Sialic acid synthase | | |
| | | | Q9Y230 | RuvB-like 2 | | |
| | | | Q8NC51 | Plasminogen activator inhibitor 1 RNA-binding protein | | |
| | | | Q16851 | UTP--glucose-1-phosphate uridylyltransferase | | |
| | | | Q96HG5 | Actin, cytoplasmic 1 | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | P63261 | Actin, cytoplasmic 2 | | |
| | | | O96019 | Actin-like protein 6° | | |
| | | | P00352 | Retinal dehydrogenase 1 | | |
| | | | P09972 | Fructose-bisphosphate aldolase C | | |
| | | | P04083 | Annexin A1 | | |
| | | | O43684 | Mitotic checkpoint protein BUB3 | | |
| | | | P78371 | T-complex protein 1 subunit beta | | |
| | | | P09622 | Dihydrolipoyl dehydrogenase, mitochondrial | | |
| | | | P06733 | Alpha-enolase | | |
| | | | P13639 | Elongation factor 2 | | |
| | | | O75821 | Eukaryotic translation initiation factor 3 subunit G | | |
| | | | Q13347 | Eukaryotic translation initiation factor 3 subunit I | | |
| | | | Q15056 | Eukaryotic translation initiation factor 4H | | |
| | | | Q96IT0 | Fatty acid synthase | | |
| | | | P06396 | Gelsolin | | |
| | | | P48637 | Glutathione synthetase | | |
| | | | P04406 | glyceraldehyde-3-phosphate dehydrogenase | | |
| | | | O95757 | Heat shock 70 kDa protein 4L | | |
| | | | P38646 | Stress-70 protein, mitochondrial | | |
| | | | P22626 | Heterogeneous nuclear ribonucleoproteins A2/B1 | | |
| | | | P07195 | Lactate dehydrogenase B | | |
| | | | Q9H3E1 | Methionine adenosyltransferase 2 subunit beta | | |
| | | | Q9H010 | S-methyl-5'-thioadenosine phosphorylase | | |
| | | | Q9UQ80 | Proliferation-associated protein 2G4 | | |
| | | | P62195 | 26S protease regulatory subunit 8 | | |
| | | | P25787 | Proteasome subunit alpha type-2 | | |
| | | | P30101 | Protein disulfide-isomerase A3 | | |
| | | | Q96J01 | THO complex subunit 3 | | |
| | | | P23246 | Splicing factor, proline- and glutamine-rich | | |
| | | | O60506 | Heterogeneous nuclear ribonucleoprotein Q | | |
| | | | P55072 | Transitional endoplasmic reticulum ATPase | | |
| | | | P17022 | Zinc finger protein 18 | | |
| protein folding (GO:0006457) | 6 | 2,38E-04 | O95433 | Activator of 90 kDa heat shock protein ATPase homolog 1; | 10.4 | 4,00E-02 |
| | | | Q02790 | Peptidyl-prolyl cis-trans isomerase FKBP4; | | |
| | | | Q9Y230 | RuvB-like 2; | | |
| | | | P78371 | T-complex protein 1 subunit beta; | | |
| | | | O95757 | Heat shock 70 kDa protein 4L; | | |
| | | | P38646 | Stress-70 protein, mitochondrial | | |
| glycolysis (GO:0006096) | 4 | 4,45E-04 | P09972 | Fructose-bisphosphate aldolase C | 26.1 | 4,90E-02 |
| glucose catabolic process (GO:0006007) | | 8,26E-04 | P06733 | Alpha-enolase | 21.2 | 7,80E-02 |
| monosaccharide catabolic process (GO:0046365) | | 1,49E-03 | P04406 | glyceraldehyde-3-phosphate dehydrogenase | 17.3 | 8,80E-02 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| hexose catabolic process (GO:0019320) |  | 1,37E-03 | P07195 | Lactate dehydrogenase B | 17.8 | 9,90E-02 |
| glucose metabolic process (GO:0006006) | 5 | 1,40E-03 | P09972<br>P06733<br>P04406<br>P07195<br>Q16851 | Fructose-bisphosphate aldolase C<br>Alpha-enolase<br>glyceraldehyde-3-phosphate dehydrogenase<br>Lactate dehydrogenase B<br>UTP--glucose-1-phosphate uridylyltransferase | 10.1 | 9,10E-02 |
| cellular carbohydrate catabolic process (GO:0044275) | 7 | 1,35E-03 | Q9NR45<br>P09972<br>P06733<br>P04406<br>P07195<br>Q16851<br>Q9H3E1 | Sialic acid synthase<br>Fructose-bisphosphate aldolase C<br>Alpha-enolase<br>glyceraldehyde-3-phosphate dehydrogenase<br>Lactate dehydrogenase B<br>UTP--glucose-1-phosphate uridylyltransferase<br>Methionine adenosyltransferase 2 subunit beta | 5.5 | 1,00E-01 |

[†] Count indicates the number of the proteins /genes of our list involved in an enriched GO term.

[‡] *p*-value with a modified Fisher exact test was used to select the top enriched categories

[§] Accesion number in Swiss-Prot/UniprotKB (www.uniprot.org/).

[¶] Fold enrichment indicates the magnitude of enrichment

[‖] Benjamini multiple testing was performed to globally correct the *p*-value controlling family-wide false discovery rate ($p$-value $\leq 0.1$).