**Table S2. A list of proteins identified to be significantly up- or down- regulated in Fe-limited cells by *QSpec* from analyses of 4 biological splits from each culture.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  | **Global ID number** | **Protein Function** | ***QSpec*** | **Cellular Processes** |
|  | **Protein abundance**  **Log2 fold change** |
|  | **Down-regulated proteins in Fe-limited cells** | 224015655 | nickel ABC transporter periplasmic protein | -2.87 | **TRANSPORTER,AAmet** |
|  | 118411185 | 30S ribosomal protein S4 | -1.63 | **TRANSLATION** |
|  | 223994385 | chloroplast 50S ribosomal protein L15 | -1.61 | **TRANSLATION** |
|  | 223993577 | Predicted Protein | -1.38 |  |
|  | 209583663 | Predicted protein B0432.4 | -1.26 |  |
|  | 223998678 | Phosphoenolpyruvate carboxylase (PEPC2) | -1.24 | **PHOTO, ENERGY** |
|  | 118411124 | 50S ribosomal protein L1 | -1.21 | **TRANSLATION** |
|  | 224007537 | ATP binding | -1.13 | **DNA, REG, ENERGY** |
|  | 224002675 | ribosomal protein L22 | -1.12 | **TRANSLATION** |
|  | 224010633 | COG1233: Phytoene dehydrogenase and related proteins | -1.09 | **OXI-RED** |
|  | 224009938 | RsuA 16S rRNA U516 pseudouridine synthase | -1.08 | **TRANSLATION** |
|  | 118411203 | 50S ribosomal protein L5 | -1.08 | **TRANSLATION** |
|  | 223994299 | Predicted proteins -PFAM: HEC/Ndc80p family | -0.98 | **DNA** |
|  | 118411141 | cell division protein FtsH-like protein | -0.96 | **CD, DNA PROT\_deg** |
|  | 223993621 | proteophosphoglycan ppg4 | -0.95 | **CMI, CARBmet** |
|  | 223995685 | Predicted cell division protein FtsH2 | -0.88 | **CD, DNA PROT\_deg** |
|  | 118411191 | 50S ribosomal protein L4 | -0.85 | **TRANSLATION** |
|  | 118411193 | 50S ribosomal protein L2 | -0.84 | **TRANSLATION** |
|  | 209583588 | SHM1 glycine hydroxymethyltransferase | -0.82 | **AAmet** |
|  | 224007497 | Predicted: nicotinamide nucleotide transhydrogenase | -0.82 | **OXI-RED** |
|  | 118411222 | 30S ribosomal protein S6 | -0.82 | **TRANSLATION** |
|  | 209586173 | Ribosomal protein L3 | -0.81 | **TRANSLATION** |
|  | 223993421 | Muc19: mucin 19 | -0.81 | **CMI** |
|  | 223996073 | phosphoribosylpyrophosphate synthetase | -0.8 | **PPP** |
|  | 118411201 | 50S ribosomal protein L14 | -0.8 | **TRANSLATION** |
|  | 223998400 | heat shock protein 83 | -0.79 | **REG** |
|  | 118411123 | 50S ribosomal protein L11 | -0.78 | **TRANSLATION** |
|  | 224008965 | 60S ribosomal protein L6 CgRPL6 | -0.78 | **TRANSLATION** |
|  | 224006742 | 30S ribosomal protein S1 | -0.77 | **TRANSLATION** |
|  | 118411126 | 30S ribosomal protein S2 | -0.77 | **TRANSLATION** |
|  | 224014104 | Predicted protein | -0.76 |  |
|  | 224015517 | Predicted protein- DNA binding domain | -0.73 | **DNA** |
|  | 224013552 | pyruvate dehydrogenase (lipoamide) beta | -0.72 | **Glyc, AAmet** |
|  | 223999739 | chloroplast light harvesting protein isoform 12 | -0.7 | **PHOTO** |
|  | 224009568 | Predicted protein | -0.67 |  |
|  | 224009197 | Predicted protein similar to CG9888-PA | -0.67 | **TRANSLATION** |
|  | 118411109 | ATP synthase CF0 B' chain subunit II | -0.64 | **ENERGY** |
|  | 224015308 | Photosystem I light harvesting proteins | -0.64 | **PHOTO** |
|  | 223995405 | Predicted protein | -0.64 |  |
|  | 118411155 | cytochrome b6-f complex subunit IV | -0.63 | **OXI-RED, PHOTO** |
|  | 223998931 | adenosinetriphosphatase | -0.63 | **ENERGY** |
|  | 118411180 | photosystem II reaction center protein D1 | -0.61 | **PHOTO** |
|  | 224001616 | ATPase, E1-E2 type | -0.58 | **ENERGY** |
|  | 118411153 | photosystem I ferredoxin-binding protein | -0.58 | **PHOTO** |
|  | 118411220 | ATP-dependent clp protease ATP-binding subunit | -0.58 | **ENERGY** |
|  | 223996813 | ribosomal protein S4, Y-linked | -0.57 | **TRANSLATION** |
|  | 223992923 | Predicted Porin protein | -0.57 | **TRANSPORTER** |
|  | 118411137 | cytochrome f | -0.56 | **PHOTO** |
|  | 118411190 | 50S ribosomal protein L3 | -0.56 | **TRANSLATION** |
|  | 224003409 | Predicted Protein No BLAST result | -0.54 |  |
|  | 118411135 | ATP synthase CF1 epsilon chain | -0.54 | **ENERGY** |
|  | 224010635 | geranyl-geranyl reductase | -0.53 | **OXI-RED** |
|  | 224003107 | oxygen-evolving enhancer protein 1 precursor | -0.51 | **PHOTO** |
|  | 118411112 | ATP synthase CF1 alpha chain | -0.5 | **ENERGY** |
|  | **Up-regulated proteins in Fe-limited cells** | 224005154 | phosphoglycerate kinase precursor | 0.5 | **Glyc** |
|  | 224011888 | predicted translation elongation factor G | 0.5 | **TRANSLATION, CD** |
|  | 223994191 | Predicted protein | 0.59 |  |
|  | 224002408 | aconitate hydratase 2 (citrate hydro-lyase 2) (aconitase 2) | 0.59 | **CARBmet, ENERGY** |
|  | 223993043 | glyceraldehyde-3-phosphate dehydrogenase precursor | 0.6 | **Glyc** |
|  | 224009658 | phosphoadenosine-phosphosulphate reductase | 0.6 | **OXI-RED, ENERGY** |
|  | 223993867 | putative CDC48/ATPase | 0.63 | **ENERGY** |
|  | 224000661 | fructose-1,6-bisphosphate aldolase precursor | 0.65 | **Glyc** |
|  | 223996511 | Spermine synthase | 0.66 | **CMI** |
|  | 209583455 | copper-induced girdle band-associated cell surface protein | 0.67 | **CMI** |
|  | 223998614 | Predicted protein | 0.68 |  |
|  | 223999927 | Phosphoglucomutase, cytoplasmic (PGM) | 0.69 | **Glyc** |
|  | 223997268 | manganese superoxide dismutase | 0.69 | **OXI-RED** |
|  | 223999217 | phosphoribulokinase | 0.71 | **ENERGY** |
|  | 224012331 | ascorbate peroxidase | 0.73 | **CARBmet, AAmet** |
|  | 223993279 | 2-isopropylmalate synthase A | 0.73 | **AAmet** |
|  | 118411218 | translation elongation factor Tu | 0.76 | **TRANSLATION, CD** |
|  | 223999031 | CbbX protein homolog | 0.76 | **ENERGY** |
|  | 224007002 | Adenosine kinase | 0.77 | **TRANSLATION** |
|  | 224007705 | elongation factor alpha-like protein | 0.77 | **TRANSLATION, CD** |
|  | 223993031 | Fe transporter Ftr1 | 0.78 | **TRANSPORTER, IT** |
|  | 224010100 | histone H2A.1 | 0.79 | **REG** |
|  | 224001660 | GDP-mannose dehydratase | 0.82 | **CARBmet** |
|  | 224013212 | fucoxanthin chlorophyll a/c binding protein | 0.87 | **PHOTO** |
|  | 224012529 | HSP70-like protein | 0.87 | **CMI** |
|  | 224000862 | putative signal-transduction protein with CBS domains | 0.87 | **REG** |
|  | 223992617 | putative aminotransferase AGD2 | 0.87 | **AAmet** |
|  | 223995719 | membrane-associated 30 kD protein-like | 0.89 | **CMI, REG** |
|  | 223999607 | clathrin binding | 0.91 | **IT** |
|  | 224013082 | N-acetylornithine aminotransferase | 0.91 | **AAmet** |
|  | 224013261 | Predicted 3-oxoacyl-[acyl-carrier-protein] synthase | 0.92 | **FA** |
|  | 118411104 | ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | 0.94 | **PHOTO** |
|  | 224001930 | COG0473: Isocitrate/isopropylmalate dehydrogenase | 1.02 | **AAmet** |
|  | 224002995 | elongation factor 2 | 1.03 | **TRANSLATION** |
|  | 224001430 | ATPREP1/ATZNMP; metalloendopeptidase | 1.07 | **PROT\_deg** |
|  | 224006554 | Tubulin alpha-2 chain | 1.1 | **CMI, IT** |
|  | 209583661 | GTPAse: T06D8.1b | 1.1 | **REG, CD, IT** |
|  | 224010070 | serine hydroxymethyltransferase | 1.14 | **AAmet** |
|  | 223993519 | ADP-ribosylation factor | 1.14 | **IT, REG** |
|  | 224013196 | stress-inducible protein STI1 homolog | 1.17 | **REG** |
|  | 223999013 | protein kinase, putative | 1.18 | **CARBmet, AAmet** |
|  | 224001286 | 2nd Hit Predicted protein CBG01077 | 1.19 | **DNA** |
|  | 118411164 | Rubisco expression protein | 1.19 | **PHOTO** |
|  | 223992817 | predicted protein | 1.21 |  |
|  | 224003531 | Pyruvate dehydrogenase | 1.21 | **AAmet, Glyc, OXI-RED** |
|  | 223999929 | UDP-glucose pyrophosphorylase | 1.23 | **CARBmet, PPP** |
|  | 209583468 | copper-induced girdle band-associated cell surface protein | 1.24 | **CMI, CD** |
|  | 223998024 | 14-3-3 regulatory protein | 1.25 | **REG** |
|  | 223994125 | cysD: ATP-sulfurylase | 1.3 | **ENERGY** |
|  | 223993693 | Predicted: Bromodomain; RING3 | 1.35 | **CD, TRANSLATION** |
|  | 223997516 | Aspartate-semialdehyde dehydrogenase, USG-1 related | 1.36 | **AAmet** |
|  | 224001278 | enolase | 1.37 | **Glyc** |
|  | 223994119 | Predicted HSP70 heat shock 70kD protein 4 | 1.39 | **REG** |
|  | 224001636 | predicted protein cgd4\_200 | 1.39 |  |
|  | 223996962 | proliferating cell nuclear antigen | 1.49 | **DNA** |
|  | 223999219 | Phosphofructokinase | 1.5 | **Glyc** |
|  | 224008957 | Predicted protein: ProSite- Protamine P1 signature | 1.53 | **CD, AAmet** |
|  | 224008733 | similar to coatomer protein complex, subunit gamma 2 | 1.54 | **TRANS** |
|  | 223993357 | Tubulin beta chain (Beta tubulin) | 1.56 | **CMI** |
|  | 223995669 | Predicted RNA Helicase | 1.58 | **TRANSLATION** |
|  | 224013856 | Hmg protein 1.2, isoform c | 1.6 | **DNA** |
|  | 223999447 | asparagine synthetase | 1.63 | **AAmet** |
|  | 224009908 | aspartate-ammonia ligase | 1.63 | **AAmet** |
|  | 223997294 | fructose-bisphosphate aldolase | 1.65 | **Glyc** |
|  | 209586218 | Predicted protein related to NonF protein | 1.68 | **REG, PROT\_deg** |
|  | 224012695 | ClpB protein | 1.7 | **PROT\_deg** |
|  | 224014576 | COG0166: Glucose-6-phosphate isomerase | 1.75 | **Glyc** |
|  | 223997294 | fructose-1,6-biphosphate aldolase precursor | 1.78 | **Glyc** |
|  | 224015421 | phosphoesterase | 1.79 | **AAmet** |
|  | 224009534 | UDP-glucose 6-dehydrogenase | 1.8 | **OXI-RED, PPP** |
|  | 224010838 | metalloendopeptidase | 1.81 | **PROT\_deg** |
|  | 223996381 | chloroplast cysteine synthase 1 precursor | 1.87 | **AAmet** |
|  | 224013436 | Predicted protein MG01320.4 | 1.89 | **CARBmet** |
|  | 223993045 | transketolase | 1.91 | **PPP** |
|  | 224013544 | Predicted protein | 1.94 |  |
|  | 224012106 | Predicted protein UM04584.1 | 2.14 | **AAmet** |
|  | 223997748 | Predicted protein | 2.3 | **OXI-RED** |