**Table S5:** Genes down-regulated in bloodstream form cells (ratio bloodstream/procyclic <0.4) are shown in comparison with their ratio on dhh1 E182Q expression (induced/uninduced).

| gene ID | bloodstream/ procyclic | dhh1 E182Q induced/ uninduced | identity |
|---|---|---|---|
| | microarray | microarray | |
| Tb927.5.2260 | 0.09 | 0.38 | conserved META domain |
| Tb10.61.0980 | 0.10 | 0.23 | glycosomal malate dehydrogenase |
| Tb10.389.0770 | 0.10 | 1.30 | ZC3H37 |
| Tb11.02.4150 | 0.11 | 0.65 | pyruvate phosphate dikinase |
| Tb927.5.2170 | 0.12 | 0.36 | conserved META domain |
| Tb927.7.2640 | 0.13 | 0.78 | conserved |
| Tb927.5.4020 | 0.13 | 2.10 | unique - sig seq |
| Tb927.8.6170 | 0.13 | 0.62 | putative transketolase |
| Tb09.160.5480 | 0.14 | 0.51 | purine nucleoside transporter |
| Tb927.7.3020 | 0.15 | 0.75 | FMN nitroreductase? |
| Tb10.6k15.2020 | 0.15 | 0.98 | glucose transporter 2A |
| Tb10.6k15.3510 | 0.15 | 1.31 | CRAM |
| Tb927.5.1060 | 0.16 | 0.79 | mitochondrial processing peptidase, beta subunit |
| Tb927.4.3500 | 0.17 | 0.72 | conserved - TM |
| Tb927.5.2210 | 0.17 | 0.98 | conserved META domain |
| Tb11.02.0445 | 0.17 | 1.01 | conserved - sig seq |
| Tb927.5.2560 | 0.18 | 0.95 | conserved - TM |
| Tb11.02.3860 | 0.18 | 1.66 | major facilitator superfamily |
| Tb927.4.4940 | 0.19 | 0.86 | conserved |
| Tb927.7.2680 | 0.19 | 0.61 | ZC3H22 |
| Tb10.6k15.0280 | 0.20 | 1.04 | conserved esterase/lipase domain |
| Tb927.7.4970 | 0.20 | 1.45 | glutamine synthetase |
| Tb927.7.5950 | 0.20 | 1.14 | major facilitator superfamily |
| Tb11.02.1480 | 0.20 | 1.16 | mitochondrial processing peptidase alpha subunit |
| Tb927.8.2540 | 0.21 | 0.41 | 3-ketoacyl-CoA thiolase, putative |
| Tb10.70.2970 | 0.21 | 1.05 | Cytochrome bd ubiquinol oxidase, 14 kDa subunit |
| Tb09.160.4310 | 0.21 | 0.41 | glutamate dehydrogenase |
| Tb927.1.4100 | 0.22 | 0.96 | cytochrome oxidase subunit IV |
| Tb11.02.5400 | 0.22 | 0.60 | cystathionine beta-synthase, putative |
| Tb927.4.4620 | 0.22 | 1.55 | cytochrome oxidase subunit VIII |
| Tb927.8.4100 | 0.22 | 0.56 | conserved - TM |
| Tb11.01.4702 | 0.23 | 1.34 | cytochrome oxidase subunit X |
| Tb10.26.0790 | 0.23 | 1.12 | PSSA-2 surface glycoprotein |
| Tb927.3.700 | 0.23 | 0.84 | conserved - TM |

| | | | |
|---|---|---|---|
| Tb11.02.5490 | 0.24 | 1.39 | conserved - TM |
| Tb927.8.1890 | 0.24 | 0.98 | cytochrome c1, heme protein, mitochondrial |
| Tb927.3.4500 | 0.25 | 0.88 | fumarate hydratase, putative |
| Tb11.01.6650 | 0.25 | 1.04 | serine/threonine-protein kinase, putative NIMA-like |
| Tb11.02.4520 | 0.25 | 1.00 | amino acid permease/transporter, putative |
| Tb09.v1.0420 | 0.26 | 1.02 | conserved - TM |
| Tb09.160.2910 | 0.26 | 0.74 | tricarboxylate carrier, putative |
| Tb11.02.4080 | 0.26 | 0.79 | lanosterol 14-alpha-demethylase, cytochrome P450 |
| Tb10.6k15.2900 | 0.27 | 0.58 | ABC transporter, putative |
| Tb10.6k15.2180 | 0.27 | 1.79 | cytochrome oxidase subunit IX |
| Tb10.100.0160 | 0.27 | 1.79 | cytochrome oxidase subunit VI |
| Tb927.3.2880 | 0.28 | 1.04 | conserved - sig seq |
| Tb11.01.8200 | 0.29 | 1.04 | enoyl-CoA hydratase/isomerase family protein, putative |
| Tb927.7.7430 | 0.29 | 0.96 | ATP synthase F1 alpha chain, mitochondrial precursor |
| Tb09.211.1030 | 0.29 | 1.00 | phosphatidylcholine:ceramide cholinephosphotransferase 2 |
| Tb927.1.2260 | 0.29 | 0.33 | calpain-like protein fragment, putative |
| Tb09.244.2660 | 0.29 | 1.06 | conserved, tetratricopeptide repeat |
| Tb927.7.5550 | 0.29 | 2.09 | conserved TLD domain |
| Tb11.01.3860 | 0.30 | 1.34 | conserved - sig seq |
| Tb11.01.1740 | 0.30 | 0.84 | 2-oxoglutarate dehydrogenase E1 component |
| Tb10.389.0690 | 0.30 | 0.79 | mitochondrial 2-oxoglutarate/malate carrier protein |
| Tb927.3.1690 | 0.30 | 0.91 | conserved |
| Tb10.6k15.3610 | 0.31 | 1.33 | delta-6 fatty acid desaturase |
| Tb927.4.4730 | 0.31 | 0.87 | amino acid transporter |
| Tb10.26.0280 | 0.31 | 1.08 | conserved PSP1 domain |
| Tb11.02.4485 | 0.31 | 0.76 | cytochrome b5, putative |
| Tb927.3.3330 | 0.31 | 1.02 | heat shock protein 20, putative |
| Tb927.2.2140 | 0.31 | 1.15 | conserved - TM |
| Tb927.3.1410 | 0.32 | 2.22 | cytochrome oxidase subunit VII |
| Tb927.1.2100 | 0.32 | 0.60 | cysteine peptidase, Clan CA, family C2, putative |
| Tb09.211.4700 | 0.32 | 0.68 | reiske iron-sulfur protein , mitochondrial precursor |
| Tb10.70.2320 | 0.32 | 1.65 | sig seq conserved |
| Tb11.02.5500 | 0.33 | 1.25 | conserved - TM |
| Tb10.70.7760 | 0.33 | 0.81 | conserved - TM |
| Tb11.02.2310 | 0.33 | 0.46 | prostaglandin f synthase |
| Tb10.389.0070 | 0.33 | 0.66 | elongation factor TU, putative mitochondrial? |
| Tb927.2.4200 | 0.33 | 0.86 | protein kinase, plant homologues |
| Tb927.6.3880 | 0.33 | 0.95 | conserved |
| Tb927.1.1470 | 0.33 | 1.24 | conserved |
| Tb11.02.4120 | 0.34 | 0.98 | conserved - sig seq |
| Tb11.55.0023 | 0.34 | 0.65 | conserved |
| Tb927.7.5960 | 0.34 | 2.24 | major facilitator superfamily |

| | | | |
|---|---|---|---|
| Tb927.7.5980 | 0.35 | 1.99 | major facilitator superfamily |
| Tb927.7.4270 | 0.35 | 1.01 | conserved - TM |
| Tb11.01.3610 | 0.35 | 0.92 | membrane-bound acid phosphatase, putative |
| Tb927.3.680 | 0.35 | 1.21 | cytochrome P450, putative |
| Tb11.01.7170 | 0.35 | 1.02 | C-14 sterol reductase, putative |
| Tb927.7.1790 | 0.35 | 0.78 | adenine phosphoribosyltransferase, putative |
| Tb11.01.3915 | 0.35 | 4.21 | RBP5 |
| Tb09.160.4380 | 0.35 | 1.15 | succinate dehydrogenase, putative |
| Tb927.1.2230 | 0.36 | 0.49 | calpain-like protein fragment, putative |
| Tb927.7.210 | 0.36 | 1.67 | proline dehydrogenase |
| Tb927.7.4070 | 0.36 | 0.50 | cysteine peptidase, Clan CA, family C2, putative |
| Tb927.8.4010 | 0.36 | 0.64 | flagellum-adhesion glycoprotein |
| Tb09.160.1070 | 0.37 | 0.56 | sig seq conserved methyl transferase domain |
| Tb927.3.4650 | 0.37 | 0.65 | C-8 sterol isomerase, putative |
| Tb927.5.2160 | 0.37 | 1.05 | conserved META domain |
| Tb927.5.930 | 0.37 | 0.76 | NADH-dependent fumarate reductase |
| Tb09.160.4840 | 0.37 | 1.05 | conserved |
| Tb11.02.2450 | 0.37 | 1.38 | conserved - TM |
| Tb10.70.5380 | 0.37 | 0.79 | pyruvate dehydrogenase complex E3 binding protein |
| Tb10.406.0240 | 0.37 | 0.78 | dual-specificity phosphatase |
| Tb927.5.2430 | 0.37 | 1.79 | transporter MatE superfamily |
| Tb927.5.2570 | 0.38 | 0.93 | eIF3B |
| Tb11.39.0005 | 0.38 | 1.33 | conserved - TM |
| Tb927.6.2030 | 0.38 | 1.19 | protein kinase MEK/MAP/NPK |
| Tb927.8.1630 | 0.39 | 1.51 | GP63 |
| Tb10.6k15.2490 | 0.39 | 1.03 | TFIIF-stimulated CTD phosphatase |
| Tb927.6.4990 | 0.39 | 0.88 | ATP synthase, epsilon chain, putative |
| Tb927.7.7090 | 0.39 | 1.44 | conserved - TM |
| Tb927.3.2180 | 0.39 | 0.93 | conserved - TM |
| Tb11.02.0620 | 0.40 | 1.01 | nucleolar GTP-binding protein 1 |
| Tb927.2.4700 | 0.40 | 0.98 | conserved - TM |
| Tb09.211.3500 | 0.40 | 2.02 | conserved - sig seq |
| Tb09.244.2460 | 0.40 | 1.80 | BARP |
| Tb10.70.6340 | 0.40 | 0.71 | ATPase subunit 9, putative |
| Tb11.02.5660 | 0.40 | 0.80 | conserved - sig seq |