Table S4: Genes up-regulated in bloodstream form cells (ratio bloodstream/procyclic >2.5) are shown in comparison with their ratio on dhh1 E182Q expression (induced/uninduced).

gene ID	bloodstream/ procyclic	dhh1 E182Q induced/ uninduced	identity
	microarray	microarray	
Tb927.3.4070	38.99	2.32	conserved - TM
Tb927.2.3270	19.69	1.03	ISG65
Tb927.2.3280	19.56	0.99	ISG65
Tb11.01.4950	18.3	1	RNA helicase
Tb10.70.5820	17.79	0.96	hexokinase
Tb927.4.4870	16.95	1.07	amino acid transporter
Tb927.3.600	14.36	1.02	unique
Tb927.5.1410	11.82	0.94	ISG64
Tb927.5.610	10.99	2.04	p'tase ISG-like
Tb927.5.1390	10.67	0.93	ISG64
Tb927.8.480	10.09	2.16	phosphatidic acid p'tase
Tb10.61.1750	9.82	1.73	C-terminal motor kinesin
Tb927.1.700	9.1	2.15	gPGK
Tb11.02.0010	8.94	1.14	N-term acylated conserved
Tb10.70.5290	8.8	1.76	MSP-C (gp63)
Tb10.389.0740	8.43	2.56	ZC3H38 zinc finger
Tb927.4.1230	7.79	2.72	unique
Tb927.8.6730	7.63	1.43	unknown - TM
Tb927.7.6490	7.15	1.78	unique - sig seq
Tb927.4.4580	6.84	1.56	conserved
Tb10.61.2680	6.57	3.31	pyruvate kinase 1
Tb10.6k15.3640	6.43	3.57	alternative oxidase
Tb927.2.3320	6.38	1	ISG65
Tb927.2.6000	6.34	1.17	GPI-PLC
Tb927.2.6210	6.29	0.99	iron/ascorbate oxidoreductase
Tb927.4.4020	6.28	2.29	AAT
Tb927.5.630	6.26	1.86	p'tase ISG-like
Tb927.7.7510	6.14	1.24	unique
Tb10.70.7750	6.03	1.49	conserved - TM
Tb09.211.3955	6.03	1.52	heat shock protein binding
Tb927.8.2780	6.02	1.3	RBP10
Tb11.02.5540	5.78	1.74	conserved - TM
Tb927.8.6710	5.75	1.5	conserved - TM
Tb927.7.6480	5.71	0.81	conserved
Tb927.5.310	5.7	1.93	clustered by GRESAG and iron asc oxidored

Tb927.5.1040	5.64	0.98	unique
Tb927.1.3830	5.58	1.48	glucose-6-phosphate isomerase
Tb09.160.3090	5.32	1.09	HSP70
Tb927.5.4570	5.27	1.38	conserved - TM
Tb10.70.5300	5.27	1.93	unique
Tb927.4.710	5.25	1.19	conserved
Tb10.389.0720	5.2	1.21	conserved
Tb927.5.350	5.14	1.09	ISG75
Tb10.6k15.2030	5.14	6.19	glucose transporter
Tb927.7.4260	5.12	1.61	conserved - TM
Tb10.70.5100	5.03	1.27	lysosomal alpha-mannosidase
Tb927.8.7780	5.01	1.49	conserved
Tb10.70.6350	5	0.70	conserved
Tb927.8.7970	4.81	1.31	unique
Tb927.3.4110	4.78	1.41	conserved - TM
Tb927.7.6570	4.77	1.04	conserved - sig seq
Tb927.7.2650	4.75	1.54	conserved
Tb10.6k15.3560	4.66	1.29	p'tase ISG-like
Tb11.01.0120	4.51	1.29	haloacid dehydrogenase-like
Tb10.61.3130	4.51	1.14	conserved
Tb927.2.6320	4.48	0.99	adenosine transporter
Tb927.5.360	4.46	3.4	ISG75
Tb11.01.3940	4.45	1.41	RBP9
Tb927.7.6600	4.4	1.54	conserved - sig seq
Tb09.160.5500	4.39	1.01	unique - TM
Tb11.01.3240	4.36	0.98	trans-sialidase
Tb10.61.0380	4.3	2.33	glycerol uptake
Tb10.6k15.2290	4.27	1.48	sig seq protein disulphide isomerase
Tb927.2.3340	4.26	1.01	conserved
Tb10.70.2420	4.21	1.08	GPI inositol deacylase
Tb09.211.3880	4.17	1.32	conserved - TM
Tb927.6.3120	4.15	1.22	DNA J
Tb927.5.4580	4.13	1.55	conserved - TM
Tb927.8.2280	4.12	0.82	conserved N-term acylated
Tb927.7.5060	3.99	1.32	Batten's disease cln3 like
Tb927.8.8030	3.96	1.16	conserved - TM
Tb927.1.4650	3.93	1.27	F-box protein
Tb927.8.6720	3.92	1.06	conserved - TM
Tb927.5.4010	3.89	1.3	unique - sig seq
Tb10.70.0040	3.88	1.36	yeast PNS1 unknown function
Tb927.6.560	3.85	1.28	TbCATB cys protease
Tb11.02.1565	3.83	1.02	leucine rich repeat near VSGs

Tb927.8.2080	3.81	1.12	hypothetical conserved near snoRNAs
Tb927.6.440	3.77	1.05	HpHb receptor
Tb09.244.2160	3.76	1.65	unique between RHS and ESAG
Tb927.4.4860	3.75	1.19	amino acid transporter
Tb927.7.300	3.74	1.12	UDP-Ga/lUDP-GlcNAc glycosyltransferase
Tb10.70.1850	3.74	1.21	ZC3H32
Tb927.8.2070	3.73	0.95	conserved
Tb927.1.1500	3.7	0.98	conserved
Tb927.8.3720	3.69	1.36	conserved - TM
Tb927.4.3980	3.66	1.22	DNA J
Tb927.4.5310	3.64	1.22	S/T PKA
Tb927.8.3170	3.63	1.05	conserved
Tb927.5.370	3.63	1.02	ISG75
Tb927.8.4430	3.61	1.01	nucleoside (uridine) phosphorylase
Tb927.7.4650	3.6	1.38	SNF2 DNA repair protein
Tb10.70.1370	3.59	1.47	fructose-bisphosphate aldolase, glycosomal
Tb927.8.7100	3.58	0.87	S/T protein kinase PKA?
Tb10.70.5230	3.56	1.25	TM with DNA J domain
Tb927.5.1440	3.53	0.97	downstream of ISG64 related to ESAG8
Tb927.3.2610	3.53	1.21	GPI inositol deacylase 2
Tb11.02.0730	3.48	1.21	metacaspase 1
Tb927.2.6150	3.47	1	AT2 adenosine transporter 2
Tb10.70.3070	3.39	1.16	TFIIF-stimulated CTD phosphatase
Tb10.70.5060	3.36	1.5	conserved (calpain like cys protease?)
Tb927.8.4060	3.33	3.54	flagellum adhesion glycoprotein
Tb927.7.1300	3.25	1.6	protein disulphide isomerase
Tb927.4.3480	3.22	1.15	unique - TM
Tb927.5.3660	3.2	1.21	conserved
Tb927.2.2490	3.18	1.71	unique - TM
Tb11.47.0001	3.16	1.42	TM ISG65-related
Tb11.01.0220	3.16	1.84	conserved
Tb09.211.4740	3.11	1.02	conserved methyltransferase?
Tb10.61.2670	3.08	1.45	conserved
Tb10.61.2650	3.08	1.3	aquaglyceroporin
Tb11.02.3050	3.07	1.25	conserved - TM
Tb10.389.0390	3.07	1.22	conserved - TM
Tb10.6k15.0880	3.04	1.08	unique
Tb11.02.5680	3.02	1.6	conserved - TM
Tb927.2.1700	3.01	1.19	conserved - TM
Tb927.8.4340	2.97	1.15	conserved - TM
Tb927.4.2380	2.97	1.08	sarcalumenin
Tb927.6.410	2.96	0.96	conserved

Tb927.6.400	2.95	0.86	peptidase M20/M25/M40
Tb11.02.3950	2.91	1.64	ABC transporter
Tb927.8.4890	2.89	1.23	sig seq ERO1
Tb927.5.2000	2.89	0.99	unique
Tb927.3.4100	2.89	2.5	conserved - TM
Tb11.01.7530	2.88	1.51	conserved - TM
Tb927.3.4230	2.85	1.78	serine peptidase, clan SB, family S8-like protein
Tb927.5.2330	2.84	0.81	conserved P13K domain
Tb927.8.6590	2.81	1.04	conserved glut-S-transferase - sig seq
Tb927.6.940	2.81	0.98	cysteine peptidase, Clan CD, family C13, putative
Tb11.02.2730	2.81	0.90	conserved - TM
Tb10.70.7090	2.81	1.37	serine peptidase, Clan SC, Family S10
Tb11.01.2580	2.8	1.77	conserved pumilio RNA bp
Tb927.2.2770	2.79	2.12	conserved
Tb11.12.0008	2.79	1.13	conserved - TM
Tb927.3.5080	2.78	3.69	conserved
Tb10.389.0920	2.77	1.18	conserved
Tb11.01.6140	2.76	1.85	conserved
Tb927.5.1990	2.75	1.4	unique - sig seq
Tb927.6.1330	2.72	1.03	unique - sig seq
Tb09.160.3740	2.7	1.16	conserved
Tb927.8.6450	2.68	1.98	inhibitor of cysteine peptidase chagasin family
Tb927.8.4110	2.68	2.12	flagellum-adhesion glycoprotein
Tb927.2.5320	2.67	0.75	conserved - TM
Tb10.70.5020	2.67	0.64	IFT81
Tb927.6.2830	2.65	1.38	RabGAP GYP1
Tb10.70.3660	2.65	0.90	proteasome activator protein PA26
Tb11.47.0026	2.63	1.55	conserved
Tb10.70.4700	2.63	0.90	splicing factor PTSR1 interacting protein
Tb11.02.2210	2.61	0.87	protein kinase A regulatory subunit
Tb10.6k15.1690	2.61	1.22	conserved - TM
Tb10.389.1780	2.61	1.21	sig seq conserved
Tb11.01.3580	2.59	1.05	conserved
Tb927.7.4500	2.58	0.68	conserved
Tb927.4.2520	2.58	0.94	SIR2 deacetylase
Tb10.389.1250	2.58	1.36	conserved - TM
Tb927.8.7270	2.57	0.99	conserved ERGIC Golgi
Tb927.7.3000	2.56	0.85	kinesin, putative
Tb927.5.2300	2.56	1.00	formin, putative
Tb09.v1.0650	2.56	1.14	conserved - TM
Tb11.02.2780	2.54	1.07	conserved TPR domain
Tb10.70.2020	2.54	1.03	ZC3H31 zinc finger

Tb09.211.4240	2.53	1.22	phosphoinositide-binding protein, nexin 2
Tb927.7.5790	2.52	1.28	protein disulphide isomerase
Tb09.211.2410	2.52	1.11	protein kinase A catalytic subunit
Tb927.6.1460	2.51	1.12	cyclin 3
Tb927.3.3270	2.51	0.52	phosphofructokinase-6-phospho-1-fructokinase
Tb11.12.0016	2.51	1.18	glutathionylspermidine synthetase
Tb11.02.5280	2.51	1.00	glycerol-3-phosphate dehydrogenase
Tb927.8.3730	2.5	1.03	conserved - TM
Tb927.3.5410	2.5	1.04	conserved - TM
Tb11.02.2470	2.5	1.37	conserved possible E3 Ub lig