Table S3: Predicted trans-membrane helices in the genes that are more than two fold up-regulated by the expression of dhh1 E182Q.

gene ID	dhh1 E182Q induced/uninduced	number of trans-membrane helices (predicted)	identity
	microarray		
Tb927.1.4630	8.8	-	conserved - TM
Tb10.6k15.2030	6.2	12	glucose transporter
Tb11.47.0021	5.4	-	conserved
Tb927.1.2160	4.8	-	calpain-like protein fragment
Tb927.3.3730	4.7	11	ABC transporter
Tb927.1.4550	4.3	3	conserved
Tb11.01.3915	4.2	-	RBP5
Tb11.02.1100	3.8	9	nucleoside transporter 8.1
Tb927.3.5080	3.7	-	conserved PSP1 domain
Tb10.6k15.3640	3.6	1	alternative oxidase
Tb927.8.4060	3.5	2	flagellum-adhesion glycoprotein
Tb10.389.0020	3.4	1	phosphatidic acid phosphatase
Tb927.5.360	3.4	1	ISG75
Tb10.61.2680	3.3	-	pyruvate kinase 1
Tb11.02.2360	3.3	-	unique - sig seq
Tb927.3.4270	3.1	-	conserved MORN repeat protein
Tb09.160.1520	3.1	1	conserved - TM
Tb10.6k15.2040	3.0	12	glucose transporter
Tb10.70.4080	2.9	-	conserved - sig seq
Tb927.7.6000	2.9	13	mitochondrial DNA ligase
Tb927.2.4670	2.8	4	conserved - TM
Tb927.4.1230	2.7	-	unique
Tb11.01.6420	2.6	-	conserved PIF1
Tb11.02.3760	2.6	2	conserved - TM
Tb10.389.0740	2.6	-	ZC3H38 zinc finger
Tb927.3.4100	2.5	14	conserved - TM
Tb927.1.2150	2.46	-	calpain-like protein fragment
Tb11.01.7600	2.38	11	amino acid transporter, putative
Tb927.8.5350	2.34	-	hypothetical protein, conserved
Tb10.61.0380	2.33	12	glycerol uptake protein, putative
Tb927.5.3850	2.33	-	conserved
Tb927.3.4070	2.32	12	conserved, MFS-1
Tb927.8.5050	2.30	-	conserved, OUT like cystein protease
Tb927.4.4000	2.29	11	amino acid transporter, putative
Tb927.4.4020	2.29	11	amino acid transporter, putative
Tb927.6.3480	2.27	-	RNA binding protein, putative
Tb927.7.5370	2.26	-	conserved, actin binding
Tb10.70.4590	2.25	-	conserved, sig seq
Tb927.7.5960	2.24	13	hypothetical protein, conserved
Tb10.61.1730	2.22	-	conserved
Tb927.3.1410	2.22	-	cytochrome c oxidase VII
Tb927.8.7980	2.21	14	TVPI
Tb11.02.2630	2.18	-	protein phosphotase
Tb09.244.2550	2.16	-	unique

Tb927.8.480	2.16	6	phosphatidic acid phosphatase protein
Tb09.160.5190	2.15	1	conserved sig seq
Tb927.1.700	2.15	-	phosphoglycerate kinase C
Tb927.5.890	2.15	10	oligosaccharyl transferase subunit, putative
Tb927.6.5090	2.14	9	conserved
Tb09.244.2750	2.13	-	conserved
Tb10.70.7100	2.12	-	serine carboxypeptidase III precursor
Tb927.2.2770	2.12	-	conserved
Tb927.8.4110	2.12	2	flagellum-adhesion glycoprotein, putative
Tb927.1.600	2.11	10	phosphate-repressible phosphate permease
Tb927.8.2930	2.11	-	mannosyl-oligosaccharide 1,2-alpha-mannosidase IB, putative
Tb927.5.4020	2.10	-	conserved, GPI anchor
Tb927.7.2160	2.10	-	conserved
Tb927.2.4610	2.09	-	branched-chain amino acid aminotransferase
Tb927.7.5550	2.09	-	conserved TLD
Tb11.02.4730	2.06	-	DNA repair/recombination helicase protein PIF1, putative
Tb927.8.7610	2.05	11	amino acid transporter 1
Tb927.5.610	2.04	2	acidic phosphatase
Tb10.389.1170	2.03	7	P-type H+-ATPase, putative
Tb927.7.5940	2.03	14	conserved, MFS-1
Tb09.211.3500	2.02	-	conserved sig seq
Tb927.3.3960	2.02	-	RNA binding protein, putative
Tb927.3.3930	2.00	-	RNA binding protein, putative