Table S2: Genes more than 1.33 fold down-regulated in response to DHH1 overexpression. For all genes, the ratio on the dhh1 E182Q microarray is shown.

gene ID	DHH1 overexpression induced/uninduced	dhh1 E182Q induced/uninduced	identity
	microarray	microarray	
Tb927.6.3490	0.488	0.353	ZFP1
Tb09.160.5480	0.595	0.510	purine nucleoside transporter TbNT10
Tb11.02.2310	0.645	0.461	prostaglandin f synthase
Tb927.6.700	0.645	0.394	alanyl-tRNA synthetase, putative
Tb927.8.2540	0.654	0.412	3-ketoacyl-CoA thiolase, putative
Tb11.02.0290	0.658	0.313	succinyl-coA:3-ketoacid-CoA transferase, mitochondrial
Tb10.70.0820	0.667	0.433	universal minicircle sequence binding protein
Tb927.3.930	0.671	0.508	dynein heavy chain, putative
Tb11.01.0725	0.680	0.820	cation transporter, putative
Tb10.6k15.3850	0.690	0.595	glyceraldehyde 3-phosphate dehydrogenase cytosolic
Tb10.61.0980	0.699	0.228	glycosomal malate dehydrogenase
Tb11.02.0760	0.699	0.518	dynein heavy chain, putative
Tb927.4.1330	0.699	0.694	DNA topoisomerase IB large subunit
Tb11.01.0720	0.730	0.365	cation transporter, putative
Tb927.5.3330	0.730	0.787	hypothetical protein
Tb927.7.920	0.730	0.654	dynein heavy chain, putative
Tb11.03.0390	0.735	0.478	protein phosphatase 2C, putative
Tb927.1.2260	0.735	0.331	calpain-like protein fragment, putative
Tb927.7.5210	0.735	0.633	conserved, DUF89
Tb927.7.960	0.735	0.680	protein kinase, putative
Tb11.02.0030	0.741	0.758	dynein heavy chain, putative
Tb11.02.4440	0.741	0.658	aminopeptidase, putative
Tb11.46.0009	0.741	0.685	zink finger protein, putative
Tb09.160.3590	0.746	0.503	cAMP-specific phosphodiesterase
Tb927.2.4710	0.746	0.559	RNA-binding protein, putative