Table S6. Summary of Genomic Locations of hairy Transcription Repressor Binding Elements in the *cis*-Regulatory Regions of Genes Encoding TCA Cycle Enzymes

Gene ID	Fold Change	Size of *cis*-regulatory region*	hairy Binding Element	
			Location / Orientation	Sequence
l(1)G0030	-2.86	4154 bp	70-80 / -	catCACGCtcc
			1026-1036 / -	aagCACGCacc
			1088-1098 / +	gggCACGCttg
			1513-1523 / +	tggCACGCggg
Idh	-1.89	5496 bp	44-54 / +	cagCACGCtcc
			953-963 / +	gggCACGCact
			1152-1162 / +	cggCACGCgtt
			1807-1817 / +	acgCACGCtgc
			1983-1993 / +	ccaCACGCgcc
			3642-3652 / +	tgcCACGCgct
CG6439	-2.08	2500 bp	602-612 / -	agcCACGCtac
			865-875 / -	gtgCACGCcag
			1096-1106 / -	cgcCACGCgct
			2278-2288 / -	ggcCACGCgaa
l(1)G0156	-1.96	2500 bp	517-527 / -	aggCACGCcgg
			1022-1032 / -	ataCACGCgca
			1046-1056 / -	ataCACGCgtc
			2438-2448 / -	catCACGCgct
Nc73EF	-2.24	2500 bp	2161-2175 / -	aagCACGCgaa
			2259-2273 / -	gaaCACGCgg
CG33791	-1.76	4260 bp	2620-2634 / -	agcCACGCaac
CG7430	-3.03	2500 bp	920-930 / +	gatCACGCtcc
			931-941 / -	tagCACGCtgc
			2287-2297 / +	attCACGCtcc
Scsalpha	-2.38	2500 bp	ND***	
CG11963	-1.89	2500 bp	494-504 / -	cacCACGCccc
SdhB	-2.78	2500 bp	1259-1269 / -	cagCACGCcgc
			2176-2186 / -	tccCACGCggc
			2255-2265 / -	cacCACGCccc
			2354-2364 / +	aagCACGCgaa
CG10219	-1.59	2500 bp	550-560 / +	ttgCACGCtac
			1307-1317 / -	cggCACGCtga
			1439-1449 / -	cgtCACGCtcc
CG6666	-2.33	2500 bp	84-94 / +	tctCACGCgac
			996-1006 / +	gggCACGCtgt
			1565-1575 / +	tgcCACGCgct
l(1)G0255	-2.63	3652 bp	1048-1058 / -	cgcCACGCtac
			3167-3177 / +	gagCACGCctc
			3374-3384 / -	ctcCACGCgaa

CG6140	-1.75	2500 bp	816-826 / +	ataCACGCgat
CG4095	-2.70	2500 bp	85-95 / - 999-1009 / -	ctcCACGCgaa tggCACGCagc
CG5214	-2.63	2500 bp	1148-1158 / +	gaaCACGCgca
Sucb	NS**	2500 bp	ND	
CG10748	NS	2500 bp	ND	
CG10749	NS	2500 bp	ND	
CG14740	NS	2500 bp	ND	
CG4706	NS	2500 bp	ND	
CG5718	NS	2500 bp	514-528 / + 589-603 / - 1192-1206 / +	gatCACGCgcc tgaCACGCggc aaaCACGCgag
CG5599	NS	2500 bp	ND	
CG6629	1.76	2500 bp	ND	

Note: * *cis*-regulatory region includes 2000bp upstream of the first transcription start site and 500bp downstream of the last transcription start site. ** NS: Not Significant; ***ND: Not Detected