

Motif	Logo		Occurrences		Other algorithms that identified the regulatory element		
	Consensus	Reverse consensus	Three treated strains	All four treated strains	MEME-DREME	BioProspector	SCOPE
DAF-16 Associated Element (DAE) CTTATCA			19%	24%	✓	✓	✓
			25%	25%	✓	✓	✓
			15%	-	✗	✓	✗
TATA box GTATA(T/A)(T/A)AG			22%	12%	✓	✗	✓
			12%	-	✗	✗	✗
?			-	15%	✗	✗	✗

Figure S6. Ethosuximide-responsive genes are enriched for a DAF-16 Associated Element (DAE) motif. To identify candidate regulatory sequence motifs for ethosuximide-responsive genes, 200 bp upstream regions for each of promoter sequences of common DEGs were mined for overrepresented motifs using the ‘oligo-analysis’ and ‘peak-motifs analysis’ option of RSAT web server. Repeat analyses were also performed using multiple motif analysing packages. Table shows overrepresented consensus motifs found by RSAT peak-motifs analysis containing a graphic representation of the motifs identified and their reverse complements, along with the extent of agreement with BioProspector, MEME and SCOPE packages.