

Drome-CYC	-----
Tal-BMAL1	EAAMAIIMSLLLEADAGLGGPAD-----
Pacle-BMAL1A	EAAMAVIMSLLLEADAGLGGPVDFSHLPWLP
Ep-BMAL1	EAAMAVIMSLLLEADAGLGEVDFSHLPWLP

Figure S5. Putative *Talitrus saltator* BMAL1 protein

Alignment of *Drosophila melanogaster* CYC (Drome-CYC; Accession No. AAF49107) with the *T. saltator* BMAL1 (Tal-BMAL1) deduced from the Trinity *de novo* transcriptome assembly, together with the top two tblastn species homologue sequences *Pacifastacus leniusculus* BMAL1A (Pacle-BMAL1A; Accession No. JQ670886) and *Eurydice pulchra* BMAL1 (Ep-BMAL1; Accession No. KC885968). '*' indicates identical amino acid residues in the two proteins, '.' and ':' indicate similar amino acid residues between the two proteins. In this figure SMART identified domains of bHLH domain, PAS domains and PAC domain are highlighted in yellow, green and blue respectively. Red text indicates sequence with high similarity to C-terminal transactivation domain of *Mus musculus* BMAL1.