```
Drome-DCO         -MELRVGNKYRLGRKIGSGSFGDIYLGTTINTGEEVAIKLECIRTKHPQLHIESKFYKTM
Tal-DBT           -MELRVGNKYRLGRKIGSGSFGDIYLGTNISTAEEVAIKLECIKTKHPQLHIESKFYKMM
Ep-CKI-ε          MMELRVGNKYRLGRKIGSGSFGDIYLGTNISTGEEVAIKLECIKTKHPQLHIESKFYKMM
Cioin-CKI         -MELRVGNKYRLGRKIGSGSFGDIYLGTNISTGEEVAIKLECVKTKHPQLHIESKFYKMM
                   ***************************.*.*.*********::************** *

Drome-DCO         QGGIGIPRIIWCGSEGDYNVMVMELLGPSLEDLFNFCSRRFSLKTVLLLADQMISRIDYI
Tal-DBT           AGGVGIPAIKWCGSEGDYNVMVMELLGPSLEDLFNFCTRKFSLKTVLLLADQLITRIEYI
Ep-CKI-ε          AGGVGIPSIKWCGSEGDYNVMVMELLGPSLEDLFNFCSRKFFLKTVLLLADQLITRIEYI
Cioin-CKI         QGGVGIPTVKWCGAEGDYNVLVMELLGPSLEDLFNFCSRKFSLKTVLLLADQLISRIEFI
                   **:*** : ***:******:****************:*:* **********:*:**::*

Drome-DCO         HSRDFIHRDIKPDNFLMGLGKKGNLVYIIDFGLAKKFRDARSLKHIPYRENKNLTGTARY
Tal-DBT           HSKNFIHRDIKPDNFLMGLGKKGNLVYIIDFGLAKKYRDPRTHQHIPYRENKNLTGTARY
Ep-CKI-ε          HSKNFIHRDIKPDNFLMGLGKKGNLVYIIDFGLAKKYRDSRTHLHIPYRENKNLTGTARY
Cioin-CKI         HSKNFIHRDIKPDNFLMGLGKKGNLVYIIDFGLAKKYRDGRTHQHIPYRENKNLTGTARY
                  **::********************************:** *:  ****************

Drome-DCO         ASINTHLGIEQSRRDDLESLGYVLMYFNLGALPWQGLKAANKRQKYERISEKKLSTSIVV
Tal-DBT           ASVNTHLGIEQSRRDDLESLGYILMYFNRGSLPWQGLKAATKRQKYERISEKKMQTRIED
Ep-CKI-ε          ASVNTHLGIEQSRRDDLESLGYVLMYFNRGSLPWQGLKAATKRQKYERISEKKMQTPIEE
Cioin-CKI         ASINTHLGIEQSRRDDLESLGYILMYFNLGTLPWQGLKAATKRQKYERISEKKMSTPIEL
                  **:*******************:***** *:*********.************:.* *

Drome-DCO         LCKGFPSEFVNYLNFCRQMHFDQRPDYCHLRKLFRNLFHRLGFTYDYVFDWNLLKFGGPR
Tal-DBT           LCKGFPAEFATYLNVCRTLRFEEKPDYSHLRQLFRQLFHRQGFTYDYVFDWNLLKFVSEH
Ep-CKI-ε          LCKSFPNEFATYLNFCRSLRFEEKPDYSYLRQLFRQLFHRQGFTYDYVFDWNMLKFGGPR
Cioin-CKI         LCKGHPSEFATYLNYCRSLRFDDKPDYSYLRQLFRNLFHRQGFTYDYVFDWNMLKFGNRS
                  ***..* **..*** ** ::*:::***.:**:***:**** ***********:***  .

Drome-DCO         NPQAIQQAQDGADG----------------------------------------------
Tal-DBT           PSSKQHQQQQQ-------------------------------------------------
Ep-CKI-ε          NQEEG-DRRDRGSNRPQGT-----------------------------------------
Cioin-CKI         STDDGKDHRTSASRGLVGSSATRQASTQKKLVVRQSSTMSKAKSKVSSWLTSSVVLHPKK
                    .   : :
```

Figure S8. Putative *Talitrus saltator* DOUBLTETIME (DBT) protein

Alignment of *Drosophila melanogaster* DCO (Drome-DCO; Accession No. AAF57110) with the *T. saltator* DBT (Tal-DBT) deduced from the Trinity *de novo* transcriptome assembly, together with the top two tblastn species homologue sequences *Eurydice pulchra* CKI-ε (Ep-CKI-ε; Accession No. KC885972) and *Ciona intestinalis* CKI (Cioin-CKI; Accession No. XM_002125796). 5' and 3' sequence removed from all sequences except Tal-DBT. '*' indicates identical amino acid residues in the two proteins, '.' and ':' indicate similar amino acid residues between the two proteins. In this figure a SMART identified serine/threonine protein kinase catalytic domain is highlighted in yellow.