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Drome-CKII-α      -MTLPSAARVYTDVNAHKPDEYWDYENYVVDWGNQDDYQLVLRKLRGKGYSEVF EAINIT T
Tal-CKII-α       MMPFRSRARVYADVNTLRPQDYWDYESHLEWGGQDDYQLVLRKLRGKGYSEVF EAININN
Harsa-CKII-α     -MALPSRARVYADVNSHKPREYWDYESYVVDWGGQDDYQLVLRKLRGKGYSEVF EAINVTN
Oruab-CKII-α     -MALPSRGRVYADVNSHKPRDYWDYESYVVDWGGQDDYQLVLRKLRGKGYSEVF EAINVTN
                  *.: * .***:***: :* :*****.::::***:*****:*****:*****:..

Drome-CKII-α     TEKCVVKILKPVKKKKIKREIKILENLRGGTNIITLLAVVKDPVSRTPALIFEHVNN TDF
Tal-CKII-α       NEKCVVKILKPVKKKKIKREIKILENLRGGTNIITLQAVVKDPVSRTPALVFEHVNN TDF
Harsa-CKII-α     NEKCVVKILKPVKKKKIKREIKILENLRGGTNIITLQAVVKDPVSRTPALIFEHVNN TDF
Oruab-CKII-α     NEKCVVKILKPVKKKKIKREIKILENLRGGTNIITLQAVVKDPVSRTPALIFEHVNN TDF
                  .*****:*****:*****:*****:*****:*****:*****:*****

Drome-CKII-α     KQLYQTLTDYEIRYYLFELLKALDYCHSMGIMHRDVKPHNV MIDHENRKLRLIDWGLAEF
Tal-CKII-α       KQLYQTLNDYDIRYYLYELLKALDYCHSMGIMHRDVKPHNV MIDHENRKLRLIDWGLAEF
Harsa-CKII-α     KQLYQTLNDYDIRYYLYELLKALDYCHSMGIMHRDVKPHNV MIDHENRKLRLIDWGLAEF
Oruab-CKII-α     KQLYQTLTDYDIRYYLYELLKALDYCHSLGIMHRDVKPHNV MIDHENRKLRLIDWGLAEF
                  *****.:**.:***:***:*****:*****:*****:*****:*****:*****

Drome-CKII-α     YHPGQEYNVRVASRYFKGPELLVDYQMYDYSLDMWSLGCMLASMI FRKEPFFHGH DNYDQ
Tal-CKII-α       YHPGQEYNVRVASRYFKGPELLIDYQMYDYSLDMWSLGCMLASMI FRKEPFFHGH DNYDQ
Harsa-CKII-α     YHPGQEYNVRVASRYFKGPELLVDYQMYDYSLDMWSLGCMLASMI FRKEPFFHGH DNYDQ
Oruab-CKII-α     YHPGQEYNVRVASRYFKGPELLVDYQMYDYSLDMWSLGCMLASMI FRKEPFFHGH DNYDQ
                  *****.:*****:*****:*****:*****:*****:*****

Drome-CKII-α     LVRIAKVLGTEELYAYLDKYNIDLDPFRFDILQRHSRKRWERFVHSDNQHLV SPEALDFL
Tal-CKII-α       LVRIAKVLGTEELFEYVEKYHVELDPRFNDILGRHSRKRWERFVHSDNQHLV SPEALDFL
Harsa-CKII-α     LVRIAKVLGTEELFEYLDKYHIELDPRFNDILGRHSRKRWERFVHSDNQHLV SPEALDFL
Oruab-CKII-α     LVRIAKVLGTEELFEYLEKYHIELDPRFNDILGRHSRKRWERFVHSDNQHLV SPEALDFL
                  *****.:*.:**.:**.:*****:*** *****:*****:*****:*****

Drome-CKII-α     DKLLRYDHVDRLTAREAMAHPYFLPIVN--GQMNPNNQ-----
Tal-CKII-α       DKLLRYDHQERLTAHEAMEHPYFAPIVKDGIMIGSPPFPQPPPAVISGIQDE-----
Harsa-CKII-α     DKLLRYDHYERLTAREAMEHPYFYPIVKEQGRLTMVSSSPTPMTGSVPVGDHYRSSWRNN
Oruab-CKII-α     DKLLRYDHYERLTAREAMEHPYFYPIVKEQGRLTIVSSSPTPMPGSLPLDE-----
                  *****.:***:*** *****:***: * :

Drome-CKII-β     -----MSSSEEVSWVTWFCGLRGNEFFCEVDEDIQDKFNLTGLNEQVPHYRQALDMIL
Tal-CKII-β       -----MSSSEEVSWIAWFCGLRGNEFFCEVDEDIQDKFNLTGLNEQVPHYRQALDMIL
Attce-CKII-β     MTTETKMSSSEEVSWISWFCGLRGNEFFCEVDEDIQDKFNLTGLNEQVPHYRQALDMIL
Oruab-CKII-β     -----MSSSEEVSWISWFCGLRGNEFFCEVDEDIQDKFNLTGLNEQVPHYRQALDMIL
                  *****.:*****:*****:*****:*****:*****:*****

Drome-CKII-β     DLEPEDELEDNPLQSDMTEQAAMLYGLIHARYILTNRGIAQMI EKYQAGDFGH CPRVYC
Tal-CKII-β       DLEF-DEEEDLPHQD LVEQAAMLYGLIHARYILTNRGIAQMI EKYQAGDFGH CPRVYC
Attce-CKII-β     DLEPDDDLDDNPNQSDLIEQAAMLYGLIHARYILTNRGIAQMI EKYQAGDFGH CPRVYC
Oruab-CKII-β     DLEPDDDIEDNPNQSDLIEQAAMLYGLIHARYILTNRGIAQMI EKYQAGDFGH CPRVYC
                  **** *.: :* * *.: *****:*****:*****:*****:*****

Drome-CKII-β     ESQPMLPLGLSDIPGEAMVKTYCPKCIDVYTPKSSRHHHTDGAYFGTGFPHMLFMVHPEY
Tal-CKII-β       ENQPMLPIGLSDVPGEAMVKLYCPNCCDVYTPKSSRYNHIDGSY YGTGFPHMLFMVHPEY
Attce-CKII-β     ESQPMLPLGLSDVPGEAMVKSYPKCMDVYTPKSSRHHHTDGAYFGTGFPHMLFMVHPEY
Oruab-CKII-β     ESQPMLPLGLSDVPGEAMVKSYPKCMDVYTPKSSRHHHTDGAYFGTGFPHMLFMVHPEY
                  *.*****:*****:***** *****:*****:*****:*****:*****

Drome-CKII-β     RPKRPTNQFVPRLYGFIHSLAYQIQQAANFKMPLRAKN-----
Tal-CKII-β       RPKRPGTQFVPRLYGFIHPMAYQIQQAANFNAPMRPVNFNNGKR
Attce-CKII-β     RPKRAANQFVPRLYGFIHPVAYQIQQSASTFKAPLRALN YNNGKR
Oruab-CKII-β     RPKRATNQFVPRLYGFIHPLAYQIQQSASTFKAPLR TVNYNNGKR
                  ****. .*****:*****:***:* *:*:*.: *:*.*

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Figure S6. Putative *Talitrus saltator* CASEIN KINASE II α and β (CKII- α and CKII- β) proteins

Alignment of *Drosophila melanogaster* CKII- α and CKII- β (Drome-CKII- α and Drome-CKII- β ; Accession No.s AAN11415 and AAF48093 respectively) with the *T. saltator* CKII- α and CKII- β (Tal-CKII- α and Tal-CKII- β) deduced from the Trinity *de novo* transcriptome assembly, together with the top two Tal-

CKII- α tblastn species homologue sequences *Harpegnathos saltator* CKII- α (Harsa-CKII- α ; Accession No. XM_011140473) and *Orussus abietinus* CKII- α (Oruab-CKII- α ; Accession No. XM_01242321) and the top two Tal-CKII- β tblastn species homologue sequences *Atta cephalotes* CKII- β (Attce-CKII- β ; Accession No. XM_012208415) and *Orussus abietinus* CKII- β (Oruab-CKII- β ; Accession No. XM_012432316). 3' sequence removed from Harsa-CKII- α . '*' 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 serine/threonine protein kinase catalytic domain and casein kinase regulatory subunit domain are highlighted in yellow and green respectively.