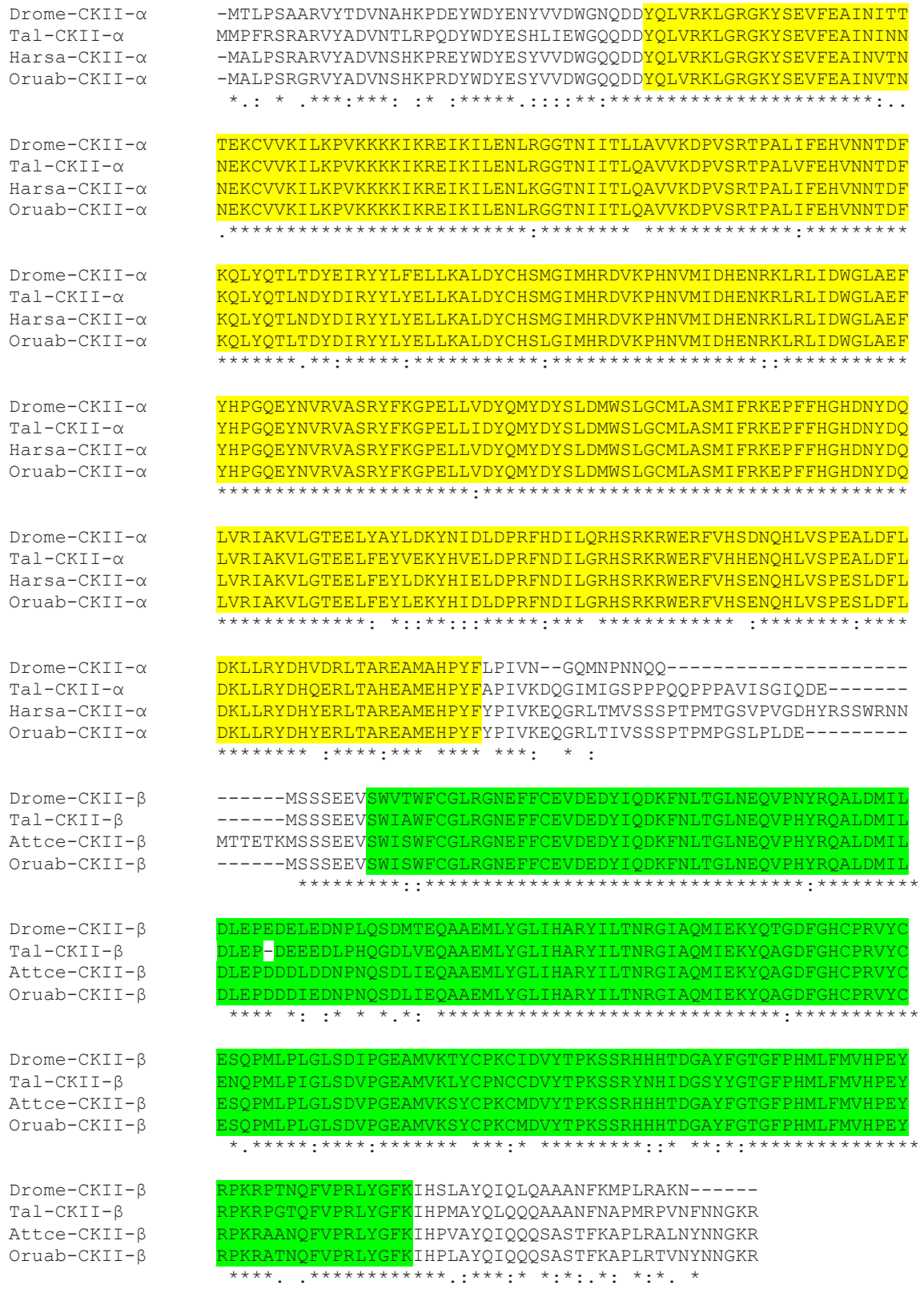

Figure S6. Putative *Talitrus saltator* CASEIN KINASE II α and β (CKII-α and CKII-β) proteins

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.