```
Drome-SGG          MSGRPRTSSFAEGNK-QSPSLVLGGVKTCSRDGSKITTVVATPGQGTDRVQEVSYTDTKV
Tal-SGG            MSGRPRTTSFAEGNKGPLAAVNFPGMKISSKDGNKVTTVVATAGLGSDRPQEVSYMDTKV
Athro-GSK-III      MSGRPRTTSFAEGNK-PPTNPPLGGMKISSKDGSKVTTVVASAGAGPDRPQEVGYTDTKV
Linhu-GSK-III      MSGRPRTTSFAEGNK-PPANPPLGGMKISSKDGSKVTTVVATPGAGPDRPQEVAYTDTKV
                   *******:*******   .   : *:* .*:**.*:*****:.* *.** ***.* ****

Drome-SGG          IGNGSFGVVFQAKLCDTGELVAIKKVLQDRRFKNRELQIMRKLEHCNIVKLLYFFYSSGE
Tal-SGG            IGNGSFGVVFQAKLVESGELVAIKKVLQDKRFKNRELQIMRRLEHCNIVELKYFFYSCGD
Athro-GSK-III      IGNGSFGVVYQAKLCDTGEMVAIKKVLQDKRFKNRELQIMRRLEHCNIVKLKYFFYSSGD
Linhu-GSK-III      IGNGSFGVVYQAKLCDSGEMVAIKKVLQDKRFKNRELQIMRRLEHCNIVKLKYFFYSSGD
                   *********:**** ::**:*********:***********:*******:* *****.*:

Drome-SGG          KRDEVFLNLVLEYIPETVYKVARQYAKTKQTIPINFIRLYMYQLFRSLAYIHSLGICHRD
Tal-SGG            KKDEVFLNLVLEYVPETIYKVARHHGKQKQTIPMSYIKLYMYQLFRSLAYMHALGVCHRD
Athro-GSK-III      KKDEVYLNLVLEYIPETVYKVARHYSKSKQTIPISFIKLYMYQLFRSLAYIHSLGICHRD
Linhu-GSK-III      KKDEVYLNLVLEYIPETVYKVARHYSKSKQTIPISFIKLYMYQLFRSLAYIHSLGICHRD
                   *:***:*******:***:*****::.* *****:.:*:************:*:**:****

Drome-SGG          IKPQNLLLDPETAVLKLCDFGSAKQLLHGEPNVSYICSRYYRAPELIFGAINYTTKIDVW
Tal-SGG            IKPQNLLVDPETGVLKLCDFGSAKHLVRGEPNVSYICSRYYRAPELIFGATDYTTNIDVW
Athro-GSK-III      IKPQNLLLDPETGVLKLCDFGSAKHLVKGEPNVSYICSRYYRAPELIFGAIDYTTKIDVW
Linhu-GSK-III      IKPQNLLLDPDTGVLKLCDFGSAKHLVKGEPNVSYICSRYYRAPELIFGAIDYTTKIDVW
                   *******:**:*.***********:*::********************** :***:****

Drome-SGG          SAGCVLAELLLGQPIFPGDSGVDQLVEVIKVLGTPTREQIREMNPNYTEFKFPQIKSHPW
Tal-SGG            SAGCVLSELLLAQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKSHPW
Athro-GSK-III      SAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKSHPW
Linhu-GSK-III      SAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTRDQIREMNPNYTEFKFPQIKSHPW
                   ******:****.***************:*********:**********************

Drome-SGG          QKVFRIRTPTEAINLVSLLLEYTPSARITPLKACAHPFFDELRMEGNHTLPNGRDMPPLF
Tal-SGG            QKVFRQRTPEDAINLVSRLLEYTPSARISPLQACTHRFFDELREPN-TRLPNNRPLPPLF
Athro-GSK-III      QKVFRARTPPEAMELVARLLEYTPSLRWTPLQACAHSFFNELREQG-TRLPNGRELPPLF
Linhu-GSK-III      QKVFRARTPPEAMDLVARLLEYTPSLRMTPLQACAHSFFNELREQG-TRLPSGRELPPLF
                   ***** *** :*::**: ******* * :**:**:* **:***  .   **..* :****

Drome-SGG          NFTEHELSIQPSLVPQLLPKHLQNASGPGGNRPSAGGAASIAASGSTSVSSTGSGASVEG
Tal-SGG            NFTELELKIQPELASKLIPSHYQS------------------------------------
Athro-GSK-III      NFTEQELQIQPTLNSILIPKYMQ-------------------------------------
Linhu-GSK-III      NFTEHELRIQPVLNSMLIPKYMQSTA----------------------------------
                   **** ** *** * . *:*.: *

Drome-SGG          SAQPQSQGTAAAAGSGSGGATAGTGGASAGGPGSGNNSSSGGASGAPSAVAAGGANAAVA
Tal-SGG            ---------------------------ESGGSG------GGAVGSEAPTGAAGGS-----
Athro-GSK-III      ---------------------------TADNPG------AQSEASNVTAGASGNSSDNSA
Linhu-GSK-III      ---------------------AATTTGTEGNPGSGGGGGGQSDTTGATASASGNSNDNSV
                                                ...*      . .     .: *:*.:

Drome-SGG          GGAGGGGGAGAATAAATATGAIGATNAGGANVTGSQSNSALNSSGSGGSGNGEAAGSGSG
Tal-SGG            -----------------------VTSANTATAAGAE------------------------
Athro-GSK-III      N---------------------ISTPTTTQNTDPSQSNMA--------------------
Linhu-GSK-III      TNP---------------NTTANTSTTNTQNIDPNSSNMA--------------------
                                           : :   .    .

Drome-SGG          SGSGSGGGNGGDNDAGDSGAIASGGGAAETEAAASG
Tal-SGG            ------------------------------------
Athro-GSK-III      ------------------------------------
Linhu-GSK-III      ------------------------------------
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Figure S14. Putative *Talitrus saltator* SHAGGY (SGG) protein

Alignment of *Drosophila melanogaster* SGG (Drome-SGG; Accession no. AAN09084) with the *T. saltator* SGG (Tal-SGG) deduced from the Trinity *de novo* transcriptome assembly, together with the top two tblastn species homologue sequences *Athalia rosae* GSK-III

(Athro-GSK-III; Accession No. XM_012400594) and *Linepithema humile* GSK-III (Linhu-GSK-III; Accession No. XM_012372547). '*' 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.