```
Drome-VRI    MSIVCTLEQKVNFFKAAATTKNLLILKNNTDTNYINNYKQDNPSNNKFPRIQAQSNNSHL
Tal-VRI      ----------------------------MTAVMQN----------------------V
Cluma-VRI    ------------------------------------------------------------
Acypi-VRI    --------------------------MVADTANSYHHQQKTQQQQP-----------


Drome-VRI    QHQQQLQQKLAQLHHYSQQKLSGSDFPYGPRPPTGGKEEKLLLLAPPGKLYPEASVSTAM
Tal-VRI      LQREIMVAETVKSYPYP--------------------------------ALLPLA
Cluma-VRI    -------VMVTELHHQE----SG-------APINGG------------------TIQRNI
Acypi-VRI    QQLNQHQHQQQQQHHHQ-----------------------------------QQQQKL
                         : :

Drome-VRI    PEVLSGTPTNSHNKANIAMMNNVRLSNISPTLSMNGSSNEASNLHPLSMYGGSISPQSND
Tal-VRI      QQGLNYSCTTSSCGPSLLPQALGQPYPAQASPIMERNHVGRARNAPSLGANVSSTPSG--
Cluma-VRI    DSGLS-KSCHYSNDSSVLML---RSDSMSPTMMS-----EMGDEH----YSKDSSPNS--
Acypi-VRI    HQQQQQQLHQIHLQRQQQQQ---QEQNSGGAMPQYCSDMEQSGGPGSMRYDDSVSPGP--
                 .  .        .     :     :       .      . . :*

Drome-VRI    SGMSDSLGKYVPGSGYGDGMMAQSPSQGGNGPQ---SALTAAQKELFSQRKQREFTPDNK
Tal-VRI      ---------------------LGASGMIGAN-----SALLKDSIFAQRKQREFIPDSK
Cluma-VRI    --------------------PTPYDG-----------SVKRKDIFSQRKQREFIPDAK
Acypi-VRI    --------------------ESPGPGEPYPPGFDLTAHLQHKEFFAQRKQREFIPDNK
                             *              :..:*:******* ** *

Drome-VRI    KDESYWDRRRRNNEAAKRSREKRRYNDMVLEQRVIELTKENHVLKAQLDAIRDKFNISGE
Tal-VRI      KDESYWDRRRRNNEAAKRSREKRRFNDMILEQRVIELSKENHILRAQLTALENKFHVKGE
Cluma-VRI    KDDSYWDRRRRNNEAAKRSREKRRFNDMVLEQRVIELTKENHVLKAQLDAIKDKYNISGE
Acypi-VRI    KDESYWDRRRRNNEAAKRSREKRRFNDMILEQRVVELSKENHVLKAQLSAIKDKFGISGE
             **:.********************:***.*****:**.****:*:*** *:..:* :..**

Drome-VRI    NLVSVEKILASLPTSEQVLSNTKRAKMSGSGGSSSGSSPSGSGSGEGSPQGGHNGYPVGP
Tal-VRI      GLVNEEQVLSSMPQADQILSLTRRSNLSLLSMTSP----------------------TS
Cluma-VRI    NLVSVDQIMATLPTSEQVLSLTKR----------------------------------
Acypi-VRI    AVVSVEQVMASLPTNEQVLSITKRPKLSTSSSSSS--------------------VG-
              :*. .::::::* :*:** *:*

Drome-VRI    PLSPLIYGPNGNARPEATVKSVHHIHHAGVAPPPTHLQQLVVPQSQTQHLYQPQPQQHQP
Tal-VRI      LLSPTSMPSTSPAP---------------------------------------------P
Cluma-VRI    ------------------------------------------------------------
Acypi-VRI    ------YSQNGSG---------------------------------------------P

Drome-VRI    HQQQQISQPPQQQQQQQEPSPSAGSSSPVISDPHNRPPSTTIANLQVQLQQALNRNVRPE
Tal-VRI      QQSSHSEDDHHFAVPQYSQHQHMEQSLPSPPQSNARSQSPDYYQRDVPLQAQSSQ-----
Cluma-VRI    ------------------------------------------------------------
Acypi-VRI    IPTSVIHQPVQSTTPKMNGSRTMAVHSPTAT-----------------------------

Drome-VRI    DLDSLRKVVAAGALYNAAAVVGAPPPPPSAGLYVPAPSAYKDHLEAAAAWSHNVEAAVSS
Tal-VRI      ----------------------------------------------AHSTYSSESHHLYES
Cluma-VRI    ------------------------------------------------------------
Acypi-VRI    ------------------------------------------------------------

Drome-VRI    SAVDAVSSSSVSGSAASVLNLSRRACSPSYEHMLSSTTSSTLSSASSSGAVSGDDEQEHE
Tal-VRI      TALNLSSRSSRSPNNMDCCYEQNRSLDYGGSSLPHKLRHKNQQHNTHSMSNNFNNPSCPM
Cluma-VRI    ------------------------------------------------------------
Acypi-VRI    ------------------------------------------------------------

Drome-VRI    PAHMAPLQLQRSSPQQGSDANNCLPLKLRHKSHLGDKDAAATALLSLQHIKQEPNCSRAS
Tal-VRI      GRPLSTSPLQDQMPPTSPHHYQQISSPMMVNGQHSGTRSSTSPSSPTSSHMLYPIKSEPI
Cluma-VRI    ------------------------------------------------------------
Acypi-VRI    ------------------------------------------------------------
```

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Drome-VRI      PPAWNDGGDNSSDERDSGISIASAEWTAQLQRKLLAPKEANVVTSAERDQMLKSQLERLE
Tal-VRI        SREAGEESPGSSDDRDSGISLASSPPLSGAQSYPSSNRDSTEDMDCDSEQQLRVELQRLA
Cluma-VRI      ------------------------------------------------------------
Acypi-VRI      ------------------------------------------------------------


Drome-VRI      SEVASIKMILAE--------------
Tal-VRI        TEVRSLKSIISRNVDSNRQRDSPPRR
Cluma-VRI      --------------------------
Acypi-VRI      --------------------------
```

Figure S16. Putative *Talitrus saltator* VRILLE (VRI) protein

Alignment of *Drosophila melanogaster* VRI (Drome-VRI; Accession No. AAF52237) with the *T. saltator* VRI (Tal-VRI) deduced from the Trinity *de novo* transcriptome assembly, together with the top two tblastn species homologue sequences *Clunio marinus* VRI (Cluma-VRI; Accession No. JQ011276) and *Acyrthosiphon pisum* VRI (Acypi-VRI; Accession No. FM998650). '*' 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 basic region leucin zipper domain is highlighted in yellow.