

S3. Text

D virilis CCAP-R genomic DNA:

<https://www.ncbi.nlm.nih.gov/nuccore/1805215796?report=graph&v=3415416:3456792>

In *D melanogaster*, PC and PD isoforms are predicted; the latter by stop suppression, and it contains an additional BBS, **SFSADE**

Blastp searches of *D virilis* reveal only a predicted PC isoform. Here looking for a STOP Suppression-generated PD isoform orthologue

The following sequence (starting at 3416271 bp of ([NW_022587377.1](#)), and including termination of the predicted PC orthologue, shows that *D virilis* also contains the potential for expression of a similar stop-suppressed PD isoform which features an additional BBS: **SFSDAE**

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Q R Y D S W R I Q P A S V Q R L R S T G   F1
  R G M I A G A F N P Q A F N V C G P R A   F2
  E V * * L A H S T R K R S T F A V H G P   F3
1 CAGAGGTATGATAGCTGGCGCATTCAACCCGCAAGCGTTCAACGTTTGCAGTCCACGGGC   60
  ----:----|----:----|----:----|----:----|----:----|----:----|
R R P S A M R S F Y K * I A S A H C R L   F1
  D V L Q R C G V S I S K L P A P T V G Y   F2
  T S F S D A E F L * V N C Q R P L * A I   F3
61 CGACGTCCTTCAGCGATGCGGAGTTTCTATAAGTAAATTGCCAGCGCCCACTGTAGGCTA   120
  ----:----|----:----|----:----|----:----|----:----|----:----|
* E A * T I S A I V V C A * R M P K S N   F1
  R R L R Q * V R * L C V H S E C P N R I   F2
  G G L D N K C D S C V C I A N A Q I E Y   F3
121 TAGGAGGCTTAGACAATAAGTGCGATAGTTGTGTGTGCATAGCGAATGCCCAAATCGAAT   180
  ----:----|----:----|----:----|----:----|----:----|----:----|
I Y T Y T Y M H N V R V L R C A T N F N   F1
  Y I H T H I C I M C V Y L G V L R I S M   F2
  I Y I H I Y A * C A C T * V C Y E F Q C   F3
181 ATATATACATACACATATATGCATAATGTGCGTGTACTTAGGTGTGCTACGAATTTCAAT   240
  ----:----|----:----|----:----|----:----|----:----|----:----|
A C I S H C N L F * V F M Q L A C N Y Y   F1
  H V F P I A I Y S K Y L C N * L V T T I   F2
  M Y F P L Q F I L S I Y A I S L * L L *   F3
241 GCATGTATTTCCCATTGCAATTTATTCTAAGTATTTATGCAATTAGCTTGTAACACTACTAT   300
  ----:----|----:----|----:----|----:----|----:----|----:----|
K T K L I Q L N E N L T C I G H R F X   F1
  K Q N L F N * M R T * H A L G I D L   F2
  N K T Y S T K * E L N M H W A S I X   F3
301 AAAACAAAACCTTATTCAACTAAATGAGAAGTAAACATGCATTGGGCATCGATTTA   355
  ----:----|----:----|----:----|----:----|----:----|----:----|
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