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mel_9002      MAP-VDTWPKVDPVIVLVVLCQLIVLVDRIEWEMILTKROQLVCLNSIMVPEELRGHIPPETVHRARHYELHHTELQIWRVLDLITLDCBLLILGFPVFLWSAKTLCQKISQBIWITLDF
erecta_9002  MAP-VDTWPKVDPVIVLVVLCQLIVLVDRIEWEMILTKROQLVCLNSIMVPEELRGHIPPETVHRARHYELHHTELQIWRVLDLITLDCBLLILGFPVFLWSAKTLCQKISQBIWITLDF
yak_9002     MAP-VDTWPKVDPVIVLVVLCQLIVLVDRIEWEMILTKROQLVCLNSIMVPEELRGHIPPETVHRARHYELHHTELQIWRVLDLITLDCBLLILGFPVFLWSAKTLCQKISQBIWITLDF
anna_9002    MAPFEEWPKVDPVIVLVVLCQLIVLVDRIEWEMILTKROQLVCLNSIMVPEELRGHIPPETVHRARHYELHHTELQIWRVLDLITLDCBLLILGFPVFLWSAKTLCQKISQBIWITLDF
yak_30461    MFRTRHATPRCETAKLVVSS--IGSGSEFLYADATTRSFCAN-----PSWLNPFQNGMMETGPISEKPNPHDSQKSAASPLRRHFGQR-----
erect_30461  MTRTKHATPRCETAKLVVSS--IGSGSEFLYADATTRSFCAN-----PSWLNPFQNGMMETGPISEKPNPHDSQKSAASPLRRHFGQR-----
mel_30461_PD MTRTKHATPRCETAKLVVSS--IGSGSEFLYADATTRSFCAN-----PSWLNPFQNGMMETGPISEKPNPHDSQKSAASPLRRHFGQR-----
ana_30461    MIRTEHATPRCETAKLVVSS--ISSGQTKIYADSSRTFCAN-----PSWLTNSGRMVDSPVCEPAPMDYFKRABLFRRHFGTSSQTRVSEAA-----
consensus   Ma-yl-wfkcdpiikLVV-clivi-riwet---krq-s-can-impveelrgihpp-iyhrariyelh-telpikwdii-e-it-ce--rgfy-flw-l---tlq-t--e-witlif

mel_9002      VFYLTIIYICIRLPLVLIYDKCLELRYGMSGKFPWYLYCIGAMSNLSSQLVDFPDAAAIVPSVKFIGVYFLLWFWLFWAFVFLLVFVFLPCCIPCIGRQVVLPEGTALYMEVKKRVCDV
erecta_9002  VFYLTIIYICIRLPLVLIYDKCLELRYGMSGKFPWYLYCIGALSVLSSQLVDFPDAAAIVPSVQLIGVYFLLWFWLFWAFVFLLVFVFLPCCIPCIGRQVVLPEGTALYMEVKKRVCDV
yak_9002     VFYLTIIYICIRLPLVLIYDKCLELRYGMSGTRFPWYCYGCGALAILVSSQLVDFPDAAAIVPSVQLIGVYFLLWFWLFWAFVFLLVFVFLPCCIPCIGRQVVLPEGTALYMEVKKRVCDM
anna_9002    VFYLTIIYICIRLPLVLIYDKCLELRYGMRFRFPWYLYCIGVLIAMNLSQLVDFPDAAAIVPSVQLIGVYFLLWFWLFWAFVFLLVFVFLPCCIPCIGRQVVLPEGTALYMEVKKRVCDV
yak_30461    -----FDSEGMN-----ESGSAVDFQEKTIHWHT-----WLVKVRVFPBAOCVAIVKWKQDP-----FTEFLSSCCSWHLQSCMAWQLIISNR---MTDAKFCQSR
erect_30461  -----FDSEGMN-----ESWGAVGQDDKTIHWHT-----WLVKVRVFPBAOCVAIVKWKQDP-----FTEFLSSCCSWHLQSCMAWQLIISNR---MTDAKFCQSR
mel_30461_PD -----FDSEGMN-----AEFKNKTIHWHT-----WLVKVRVFPBAOCVAIVKWKQDP-----FTEFLSSCCSWHLQSCMAWQLIISNR---MTDAKFCQSR
ana_30461    -----KFRDELDDNVLSYNNDLVEKVPLEWHP-----ATVEEVDVPTQRAITVEYKRP-----VTDTRTFNINWHLQSCMAWQLIISNR---NPSAKCYQSR
consensus   vfylytiyicir-lpvli-dkcllelrygmrrkfpw-yc-ig-m-ily-qlvlpplq-Aivfsvkfigpyyffllwflfwaf-tllvfflpy--pcigr-qvvl---aly-e-k-vCdr

mel_9002      VGFPMKRVFPIKTRFMQNSNAYFYGSCLLKRVIPTDILLNKGKBPNEIHPYEVGRGLNMQVAGVVCHELGHWKHGHFYKATIIMKIHFPIITMGLFGLFFHSPOLYMAVGFASGVMPPII
erecta_9002  VGFPMKRVFPIKTRFMQNSNAYFYGSCLLKRVIPTDILLNKGKBPNEIHPYEVGRGLNMQVAGVVCHELGHWKHGHFYKATIIMKIHFPIITMGLFGLFFHSPOLYMAVGFASGVMPPII
yak_9002     VGFPMKRVFPIKTRFMQNSNAYFYGSCLLKRVIPTDILLNKGKBPNEIHPYEVGRGLNMQVAGVVCHELGHWKHGHFYKATIIMKIHFPIITMGLFGLFFHSPOLYMAVGFASGVMPPII
anna_9002    VGFPMKRVFPIKTRFMQNSNAYFYGSCLLKRVIPTDILLNKGKBPNEIHPYEVGRGLNMQVAGVVCHELGHWKHGHFYKATIIMKIHFPIITMGLFGLFFHSPOLYMAVGFASGVMPPII
yak_30461    IKKTMDFVNCVLDPELEQDNSVSKDCSPPLAALTEKVFVGGATGMLKLNLDLELQEKLRNRYKRLVE-----
erect_30461  IKKTMDFVNCVLDPELEQDNSVSKDCSPPLAALTEKVFVGGATGMLKLNLDLELQEKLRNRYKRLVE-----
mel_30461_PD IKKTMDFVNCVLDSEVEEKTFTKDCSPPLAALTEKVFVGGATGMLKLNLDLELQEKLRNRYKRLVE-----
ana_30461    IRKTMDFVNTVPEPELFDSSSEDDGALVPLSMKVQSASHMLKLNLDLELQEKLRNRYKQDS-----
consensus   vg-pmDrv-iiVtr-mqgsnayf-gScllkrivi-tl-lnk-klnei-p-vgr-lt-igv-gvvcchelghwkghfykatiimkihftmglfglffh-p-lymavgf-gv-pii

mel_9002      VGFIIIVLRFAMTPYLLANVLMWLNLRFFEYAADFAHRMGYSIQLRMALVKIYADHMSFPVYDQCYARWHHTHTPTILORLAYQOKLDVKAMNAGTY
erecta_9002  VGFIIIVLRFAMTPYLLANVLMWLNLRFFEYAADFAHRMGYSIQLRMALVKIYADHMSFPVYDQCYARWHHTHTPTILORLAYQOKLDGRAMNAGS
yak_9002     VGFIIIVLRFAMTPYLLANVLMWLNLRFFEYAADFAHRMGYSIQLRMALVKIYADHMSFPVYDQCYARWHHTHTPTILORLAYQOKLDKAMNNT--
anna_9002    VGFIIIVLRFAMTPYLLANVLMWLNLRFFEYAADFAHRMGYSIQLRMALVKIYADHMSFPVYDQCYARWHHTHTPTILORLAYQOKLDNKETSKK--
yak_30461    -----
erect_30461  -----
mel_30461_PD -----
ana_30461    -----
consensus   vgfiiivlkfaltpyl-lanvlmwlwlnrrfeyaadkfah-mgysi-lrmalvkiyadhmsfpvyd-cyarwhhthtptil-fl-yqqkld-k-----

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Figure S5 Clustal W alignment of *CG9002* and *CG30461* from the *Drosophila* subgroup (*D.melanogaster*, *D. erecta*, *D. yakuba*, *D. annasae*), indicating sequence homology. Significant similarity reveals itself when *CG30461* is aligned solely with *CG9002* sequences from the most recently evolved members of the *Drosophila* genus. The HEXXH zinc ion binding site is indicated with asterisks (*).

Thompson, J. D., D. G. Higgins, and T. J. Gibson, 1994 Clustal W: improving the sensitivity of progressive multiple sequence alignments through sequence weighting, position specific gap penalties and weight matrix choice. *Nucl. Acids Res.* **22**: 4673-4680.