Secondary structure: β1 β2 αA β3 β4 β5 β6 β7

```
                                      β1            β2                    αA                          β3              β4            β5        β6    β7

Tudor.1      FBpp0071508  11    SKVDLYITHVDH-VGPYLKVYG---------HVNRDAASLISERIRNLLPTCFAIEPSWSVERQQALLIPGTFCIFKNINGPAPGDVEYRRIRVVSADLE------GQSMRAEIDFVDFGYKRTVD-SHDLMFPK
Tudor.2      FBpp0071508  410   LTYDVVISYVEN-GPYLFWVHL---------KSSDHDLSTMMGQIERTKLKALAQ---------APELGTACVARFSE-----DGHLYRAMVCAVYA----------QRYRVVYVDYGNSELLS-ASDLFQIP
Tudor.3      FBpp0071508  595   NDDAVEIRFIDS-PSNFYVQK---------VANIGKFEQLMDEMFSYYNANQRVPD--------QLILGAPCIVKC-------DQEWYRAEILRVDD--------SVIVRHVDFGYEQNVK-RHLIGHIA
Tudor.4      FBpp0071508  1016  SKEAASLSWWLS-PFQFYIVP----------KSVSAKYDNIMRDMREFYRQKQHQPL--------QLKVGSTVVVRQRK-----DNAILRATVTACNH-------MMRKYRVFCVDTGSLITVT-SEDIWQLE
Tudor.5      FBpp0071508  1214  -----------------------------------------------------------GQQIRGKFTSIRD-------MTSFKVQF-DYGNNVNFL----CTYDD
Tudor.6      FBpp0071508  1309  SSFQALVVYTAK-PYRVYVQP---------QAIVPSMQTLLDNMYEHYKAKGDSLK-----KFDVGQICAVRSS-----DGNWYRARISGKDS-----NAACFEVPYIDYGNTEEIK-RDDIKALD
Tudor.7      FBpp0071508  1617  DLDCVVLSHCDN-PAQFYVHP---------IDQLSKLNQLHENLQIVSPSLPQLM---------NVVNGADCVSMYSV-----DKCWYRAKIIDAE---------LMVLLFIDYGNTDCVS---DATDIK
Tudor.8      FBpp0071508  1795  SGCSCYISHVNG-ICDFFIQL---------ERDSKALELIELYLRKKDTLKPLE---------GFEKGLIVAALFED-----DELWYRAQLQKELP---------DSRYEVLFIDYGNTSTTS---KCLMLS
Tudor.9      FBpp0071508  1979  VTTKAIITHVEN-TSRIYLQF---------SEKDSLMDIICEKLNGSKLQPKTE---------KAAVDDMCVVQFAD-----DLEFYRSRILEVLE---------DDQYKVILIDYGNTTVVD---KLYELP
Tudor.10     FBpp0071508  2163  ENSECIISYGNS-PKSFYVQM---------KHNSADLDLIVKTLQSLKKEKLKKLI--------DPTTNSNGVCYSQE-----DACYYRCSIKSVLD---------PSQGFEVFLLDYGNTLVVP---EVWQLP
Tudor.11     FBpp0071508  2347  ELHNCVVVQFDG-PMSFYVQM---------ESDVPALEQMTDKLLDAEQDLPAFS--------DLKEGALCVAQFPE-----DEVFYRAQIRSKLD---------DGKCEVHFIDFGNNAVTQ---QFRQLP
CG9925.1     FBpp0082339  112   FKCRVTFMENDG-PIWVVHVA---------NVEAIERMTVNMQRCMQNKKMIRME------GVREDTLVAISV-------GDKVHRGHVLTVCQ-------KKQEANVRMIDHGQIVATP-FRDIYTIV
CG9925.2     FBpp0082339  271   LNPEVKVIRVFK-ANP-----------KHNEPQLALLQINVMGHVNADLNNRIAEKPRQPFTLPFPEQKSIFFAATRT-----KNGYRRAFLLDHIMK-------PRPTYLVYEMDEGRVSIAT---DLSRIP
CG9925.3     FBpp0082339  461   HDSIVFISHLVS-FKEVYIST----------PDAKQYAEIFKRLEYKCATITKSS-------DVSVGSIVLVVSK-----QMGHFRGEILSKDS-------GLFEVMNVDTGATQKVE-LAEIRSSC
CG9925.4     FBpp0082339  722   KVNLILMNADGL-PQTGYITAAYF------KDEKAAKEFEKILSLTSSQGACDHNVVPGY------VPNVGELCLAIYSE-----DKNWYRGVCQEVKD-------NMVKILFCDFGNTEYVA-VRHVKPIS
CG9684.1     FBpp0081342  136   SGAMVYITDFIS-SNRCYIRD----------ASESAERAFDEVCKKVNTIATLLPRIK------NPPPNRLCLVHF------NGMYVRAKMCKKLR--------EVSHLFLVDLGIKHSGP-FFDFKDIN
CG9684.2     FBpp0081342  477   EGIDLIVVDSTK-KNRGIFGAF----------DSTYASEFSALHSRLSEITDCEPY-----------KPVVREYVLARF-----EGSWYRGKVEQIIVV-----PRQQTKYRVMYLDYTNVEDIT-EMDIRRYP
CG4771.1     FBpp0083716  322   SGSKVRITAFEQ-TNVVYVRSA----------DIQIDIAYYTVLTEVMMLGKDASKLQS-------TPVCGQIVLYKF-------EGHMSRAMVLNVDN-------IKEIYVVFIDFGSVEVTQ-LERLYECS
CG4771.2     FBpp0083716  524   KNINVVVMDNTFIQCGFIYCTS----------IDLAYEVTKMQRDIQEYGEKIAKCATY------APPINELCIAKY-------EGKWRRGLSVELVG-------DGYPSILFIDYGNIVPTH-VTDIRPYP
CG14303.1    FBpp0083074  277   TDTLVRVRSVQS-PEDFYVQG-----------IHAAQRLREELDTFAHTLSDSSSVPP-----TIVVGQNYIIHHKD-----KDRYYRALVSQKLT-------NENLYNVFLTDIGVHLHVR-CSDFRVVP
CG14303.2    FBpp0083074  487   DVYMVQMLHVED-PQEFYVMRH----------DYEKKRLWLQFSLQEAMDRINISQLQ------NIFLGQLHLGCVLQS----GGQWKRASIEQILP-------DGYVLVHLVDEGPSQKVF-WDQLFVLP
CG14303.3    FBpp0083074  722   KRTTVNILYVRK-PDEFYVTLP----------HFQKAINNLQKSVQKAAAAMYQNMLPRT------DWQVGDMCYARVQANC-DSQALWYRGVVTGVIP---PGITCPIVRYQVHLRDLGELIDDVHSSSLANID
CG14303.4    FBpp0083074  1026  SVFTAIATNVTY-ECCIYLTLA----------SDKPFIEHMGNLLVREYKPLMDKQKERSTSY--TYKVGQAVVVTYHM-----DNMIYRGIVQRLEN-------NHNEYTVYYVDYGNMELVK-ADEMLPYA
CG14303.5    FBpp0083074  1404  KEFYCTVDNVLS-DTELQIAP-----------CLSEFTKHEISLIQETSTLIKDAEPLM-----EPKVGDLCLARYSR------DKQWYRANIKEISP-----ILSPTSEQVTYYIDFHDTEKVS-FNHLKVMP
Spindle-E.1  FBpp0082637  892   KTISGSITCIVN-CGKFFFQPQS---------FEECIRNMSEIFNAPQQLRNYVTNAS--AIAKGMMVLAKR------DSYFQRATVIRPEN-----QSNRQPMFYVRFIDYGNCTLLP-MQLMRLMP
Fs_1_Yb.1    FBpp0070462  825   GLIRFLVLVCYS-PAALAVRLSDQFP-----TAIRFLNFPMSDLGERVQRHYELEANRHMHP-----NPVPGEMAVVKN-------INRYERVHIVSVES-------NVMVLVQLLDTSTECFSYKTSQLYSCD
CG11133.1    FBpp0078210  520   GDVKVQLVKVYS-PTHFCVRLLEHLPP-----KGTWRMMEYSAVQEFRMQLTQIKEPRRYW------PPVAGAICMYHT-----TFTKERVRVLKVAAIKNTNIVQSDLTVKLQALDVDTRIFSTNCGKLFECP
CG31755.1    FBpp0079562  22    QEESILITHFVN-PHQFSYVR-------CIDVENSAMLVRQIEQDLKDYCSSERTKQ-------VYVEDERVIVRYQRWS-----PPKLVRGVVRRRQN-------EEYLVWILDYGFNLCCS-VWDLWPLP
CG31755.2    FBpp0079562  930   TLIRCKFLKAYD-PAHMAVMPMKY-KSKDSTIWIDVPYPSYPSTLVFKMSFGVPRKVHN------PCKINDVCFVQH-----KELLSRVRIVDNPA-----RPQVTVQLMDYGTELLQVKASQLLECP
Tejas.1      FBpp0086689  366   QRIRVQLVSLVN-PHNFNFWIY----------NDDFKDYEAQFANMQTFYESSESKNYTMPLF---LITTDHLCVVRC------TSGWERAKVLGYRS-----SNNKMTIEVELVGIDGIIRVS-QQNVKFLI
CG8920.1     FBpp0085592  558   HDWNMFISFCDS-TKIVWARM----------IDQIANFEELTKHIGRQMESPHFRQKVS-----KPYAQEVYLVEM-----PDGWNRVRAISVDE-------ETRSGRYHFIDFGDVAMFH-SEDLFHCP
CG8920.2     FBpp0085592  769   KTTPILVSHIND-DGDLMVLL----------RNDDLKFVERSIAQTVADLGEQDRVSYS---DLLHDRHIFVCDETVDGV---KQWFRGRLVTRPLN-----PDEESFDVYYVDDGRQRKAH-ISNIYRLE
CG8920.3     FBpp0085592  1034  AYFEVRVALSVN-PGHFAVQ----------PYKYYNQLQTLNKNLQEHCQKEAAKGVQPS----QLAIGEAYAAPDS-----EGVYHRVSIHKIYD-------EIIHVFRVFDVGDDGVIA-CDQLKTLN
Krimper.1    FBpp0086333  318   TIVTAVLASVDV-TDNCAYVAK----------WDESSDRIKKVLQRQLPLQELDQ-----------LPDYGDIFAVLDSI-----NNIIRTITINSSSA------GGGYDAYLIDFGEHIHFDGNETIFKLP
Krimper.2    FBpp0086333  570   SIVGILITFING-PTEVYGQFLD----------GSPPLVWDKKDVPENKRTFKS-------KPRLLDIVLALYS-----DGCFYRAQIIDEFP------SEYMIFYVDYGNTEFVP-LSCLAPCE
Papi.1       FBpp0077508  259   KPMEVYVSAVAS-PTKFWVQLI--------GPQSKKLDSMVQEMTSYYSSAENRAKHVLT----APYVGQIVAAVFKF-----DEKWYRAEIVDIMPNQYN----PKEQVIDLYFVDYGDSEYIS-PADICELR
Yu.1         FBpp0070761  417   INNDVVVSAVLS-GSHIFIQHPL--------HPSHPSLPLLQKQLYDSYSTMEAPLLP------SLELSAVCVIPI-------NDVWYRQVIVDTDP-------EDEERCVIKFLDFGGYMNVG-FNTLRQIR
Tudor-SN.1   FBpp0072419  701   NYENVIVTEITE-TLTFFAQSV----------ESGSKLESLMSKLHADFQSNPPIAGSY-----TPKRGDLVAAQFTL----DNQWYRAKVERVQG-------SNATVLYIDYGNKETLP-TNRLAALP
CG15042.1    FBpp0074390  74    IGTKLTGTVLLE-SLPVFYVTINGPGS-------KLLKCLAMGQVQLQELEQ--------LPDYGEIFAFYDKA------ENRISRIAINAPVH-------PMGYCAYMIDAAKYTNMSGMERIFALP
CG15042.2    FBpp0074390  266   SIVRVHVTRIVS-HAEFYARFADGPT----------VPTWSKSVMKRGTG----------DFRVWDIVLAPY-----QGRYRAKIVDIFR-------CRYRVYFLDFGITEYTS-KKNLTFCY
CG15930.1    FBpp0291095  285   SIFPIIMSCVFS-PCEFWFHIVPPQY-------AKNPVAEMTIDLNWFYRHTTISSYRAELP-SYFYKEGYICAAYS-----ECGWRRAMVLVTAP-----LDAQCVNIEYVDHALSVTLA-PNHLRFLP
CG13472.1    FBpp0075441  729   -----------------------------------------AWMMWQKGDLCMAKYWD-----DGRYYEAEITGVSE-------KTCVVFFMGYGNHEEVL-KVDILPIT
Smn.1        FBpp0075153  67    ---------------------------------------PVSFKVGDYARATYV------DGVDYEGAVVSINE-----EKGTCVLRYLGYENEQEVL-LVDLLPSW
CG17454.1    FBpp0289146  89    -----------------------------------------AKIWKKGDKCQAKWKE-----DRQYYDATIEDISS------TGEVNVIFDAYQNRSTTH-VNELRERT
CG3251.1     FBpp0077113  300   -----------------------------------------DYNFKVGAKCQVQLDTNR---RDLLSACYIQSIDK------KKSVCKVFIEEQGKLVDVP-SDNLHPLP
otu.1        FBpp0071181  334   -----------------------------------------DYNFKVGAKCKVELPN-----ETEMYTCHVQNISK------DKNYCHVFVERIGKEIVVP-YESLHPLP

                    1.......10........20........30........40........50........60........70........80........90........100.......110.......120.......130.....
```

Group labels (left margin): C, B, A

```
                                    αB          β8              αC               β9              β10            αD

Tudor.1      FBpp0071508  QPK--LLQNIPLHCFQYIVLGIC---------SEWDQTDLAEVRRLVVNQIV---KITVEPTQICDQ-----------------KFASLRWKD--------------FELNEFLVQQKQIG  204
Tudor.2      FBpp0071508  P----ELLEIKPFAFRFALAGTK----------EIEPIDDSMKRIFKKSAI-YRNFELTVQAPESV----------------GSMQTCHLNQN---------GTNMLELLRQLKNS  583
770          FBpp0071508  EK----HLEMPRQAIKCCLKGFE------NSELSEDKITDQFEMLAEESNIRRRTFSVRIFRIEPD------------GLNVVNLLAK-----------NLNVMKKLYKLSMP  770
Tudor.4      FBpp0071508  Q----RFADPPCMAHRCSFHSVV----------TNYDPLYIVDRMETFVPVNA--KVDCEFVSKEKSNQGSNT-----SSTCSYTVNIFVN-----------GASLRDMLVKAEFL  1200
Tudor.5      FBpp0071508  A---KFVKSNPNLARRFKEFYEG----------KSFALNVKNVCE----------NNIVHLRP--------------VMPLF----------------MEDRRSFICPYPV  1306
Tudor.6      FBpp0071508  A---KFYEHASGFAVEINLPI---------GRPSNDTKLKARISEILEEKV-------VTIKSIEVR----------RSHLIADVILEN----------NQSVIDLLKAEKLV  1482
Tudor.7      FBpp0071508  E---SMWSHIEPFCLPCALPI-----RPKGTADWVDAANGIFNESYSKVP--------RLEYLTQG----------DHYTTSYVNMYID----------GEDVAKKLIADGFA  1787
Tudor.8      FBpp0071508  ----EEIASLPSLSKKCSLQL---------PDAYISWSPEAEAKFAELTGEGE----LVFTTQLLKPG--------QDHVTIDLLLD-----------GENIIDRLLPLCQR  1966
Tudor.9      FBpp0071508  ----QEFTLIKPVAEICSM------EPSAIFEKNKALTLTTFDALLDSCK-----GVVAVEFVNKS----------ASPPVVRLTTKDKR--------SLKIYEHLQKLVQA  2153
Tudor.10     FBpp0071508  ----QEIEPIPSLALHCQL--------SKIPMDVSDEKLEEAFAALLEQHF--GELYEITTQPNEDE--------TKPLIAELRIN----------YKDFVQELVSTVTG  2339
Tudor.11     FBpp0071508  ----EELAKPARYSRHCEL---------DASTISKCDAALLQSFIDTRF--SETFQVEILATKGT-----------GTHVVRLFYQ-----------SKNISEKLQECQ--  2515
CG9925.1     FBpp0082339  ----PKMAESKAFAFRVQL-----------PTNTGVQDIKNLTLRML-------------------------------------------------------------  241
CG9925.2     FBpp0082339  ----SELLGLPSRVFAAQL-----------EDSVPEELETQGAELTVKFK-----------------------------------------------------------  411
CG9925.3     FBpp0082339  ----RFLENLPVCLMRVQLQN--VCNIPDAAVPVNNAAIQMLHKLCAQKE------LLKLNMVDAT-----------TSTVDLLFSSGD---------SRSLTTQMLPLIFT  636
CG9925.4     FBpp0082339  ------QDLLIAVNVTKCYI------------NGFDKSKNFAALEQFLVRKI--RFLCGVKKGPEPDT----------RLITIPDMETI------------LN----------  888
CG9684.1     FBpp0081342  ----DELKALPCSSQLVQL----------KNVLNCDYSNDVIAFNSKFVGKK--------YMATIKKCP-------GLHLVELVNTEM----------NFSVNEQLNAFFNS  306
CG9684.2     FBpp0081342  -----LDFTAPCATNLCVIDEFP--------HNPNAAQVSYLAEVLKVHQ----SVHIDSIK---------YINHIAVIK-----------SGSLIQKLLSL---  642
CG4771.1     FBpp0083716  ----SYLAGLTCYPVAVKL-------RGVPRRFVGPNIREVMYELDQSLV--FNIKYSSREYDTSK-----------GMQVVVMTEIDI----------NRSLNRLFKTILTP  500
CG4771.2     FBpp0083716  P----QFIFPIMTTQLDLIGV-----------PEKPTDEQIKWLDKNYP-----IGSVITCSEI-----------TFDEETNSYST----------RIEKLQEFLSLD--  691
CG14303.1    FBpp0083074  ----ERISHLPYSAVHCSLSEL---MPKNGESEWDSKASAFLKQIVQNN--PVRVIVKKALTYELH--------GVDLITSNYDT----------NISVRDSFLYCGLA  459
CG14303.2    FBpp0083074  -----QKFWDTGLAIKCCLADV--ETRAEHSYTWTPEGTTLFKQLTSNP-----RLYMDVISCTED---------LVYVSLHFERSNSE--------TTSVGVQLVAHGHC  670
CG14303.3    FBpp0083074  -----EADMRISSSAKRCHLHGIR-----PIGDEWSKDAIDFFMDQLKA-------YNEIHVTGRGRTEN-----SLSVILWGSLSILTGPF-[6]-YVNINKALLMAGMA  925
CG14303.4    FBpp0083074  -----PFPDLNAMCFLVELHGVR---------SKQGKYSLKEMDTVHLNLV--MKLSGVRIVDDETV-------GPNKIPKCQIKVG--------NVDIATMMIDSGMS  1210
CG14303.5    FBpp0083074  ----SQLFMFPLRSFCVKLHGIK-----RNKSFKEKSVRQALQACLCQH----PLVFARVHYPLNYYPNR-----PNCDADLIEVELYE---------NRHEKKLVYQSLC  1593
Spindle-E.1  FBpp0082637  RELTEQYGDLPPRVFECRLAMVQPSSVVSGNNRWSTAANDMLKTVAQCG------LIDIEVYSLFNN---------VAAVLIHMR----------DGIINDKLVELMLC  1079
Fs_1_Yb.1    FBpp0070462  K----IFKDSPREAMDLRILGLQ--PESLDRIWPDDARNLVRKDFFRRTHNKRNR-QFHAVVQSAI----------HRTIFVRNIY-----------DDEGNDLLSFVIN  1015
CG11133.1    FBpp0078210  -----EALQQEAPLACDLRLPGWV---PYFGERSWTEENIRNVNLILTQLP-KDHFLQAKILFVAAG--------TLFVQDLVAIMYADQFK-[4]-HLSLARRLVEATLV  729
CG31755.1    FBpp0079562  ----DHLSRSLCDFKEGGVALIA----PHSGSVWSRSAIESLDKQLEDAN--QLTFQVVHRGKSNR-------NFGLLKFRSSCQ---------TEDAANFLIKQDQG  207
CG31755.2    FBpp0079562  ----EQFRDLQQLAMDIRLSGLA----GSGQGGMWSTDSIQWVQDRFADIN--EEIMQITVDFGVLD-----------VAYVKEIALIEECPTML-[4]-KTFLRKELLRQGFA  1131
Tejas.1      FBpp0086689  ----KPFALLPRQCLAGRLAFIT----QCKSPNWTAEVVNFFHDMIL-----LRLLYAKVEAIKNN----------TAYLVLVDTESQGH--------TVNLNRSLIETGWV  553
CG8920.1     FBpp0085592  ----PQFLALPAQAVCLSMYALD--------KFEDHPHALQVLTKELD-------GQTVVAHVLTTEKQFL-[14]-RRACLVATLYDTSTAE---------DIHLNDLVAKRITK  754
CG8920.2     FBpp0085592  ANN-RALATFPPQAIPVRLHDVP---------EIGGHMLHRLRGLIPWRT----EALLKVVAMD---------GGKPLVNVFIREDPESMYM-----CVNIGLRLELEMAS  959
CG8920.3     FBpp0085592  ----PELRKLPKMALPAQLYGIQ-----LTDVVWSKENCVRFRELSLGQK--FIGIVRRMTKQKDG---------GRALCLELVDTSTPK--------DIKLHEILINEKHA  1218
Krimper.1    FBpp0086333  ---DDIKRLPAQAIRCDLINCD-------------IANMHCFVNTY-------IKIRVHENN--------NSTLVAEPVIDRLSRPT-[14]-DMAMLNEIDESTSD  500
Krimper.2    FBpp0086333  ----NVDSFKPHRVFSFHIEGIV-------RSKNLTHQKTIECIEYLKSKLL--NTEMNVHLVQRLPD---------GFLIRFLDD-----------WKYIPEQLLQRNYA  742
Papi.1       FBpp0077508  ----TDFLTLRFQAVECFLANVK-STIQTEPITWPKSSIAKFEELTEVAH--WRKLIARVVTYKERPRAT-[9]-GTPLPGVELFDPADNS---------ELNIADLMITQGFA  471
Yu.1         FBpp0070761  ----TDFMNVPFQSTECILSNIE-----PIGGTWSIEAAEILNKLTKGIV--LQAQVAGYNSHNLP----------EIFLFASLGPNN-----------VIFINKELVGRKLA  600
Tudor-SN.1   FBpp0072419  ----PAFSSEKPYATEYALALVA-------LPTDNEDKEEALRAFSEDVL--NHKVQLNVELKVTG---------SPNLATLRDPTT----------KVDFGKQLVAEGLV  880
CG15042.1    FBpp0074390  ----DDLKKLPALTIKCRLVNVA------------QMHIFITQN--------VRLRVLGSN----------GLELLVALIR-----------NRTNIRKIPSAQLP  233
CG15042.2    FBpp0074390  ----ELEKAQHNLAFRFEILGTR-----RQCPIPYINILEGIKHLEHTVL--RSDINVRIHNILKD---------GGYVIRLM-----------KHIHECHMIHLFDD  432
CG15930.1    FBpp0291095  ----LSFARTPPLVFRGKMSHVR-----PLANGWPKNGITAFQRMTFNR-----VLYAHVGELDTAQG----------IFSMRLSYDE----------TFVPTINDLIESRI  472
CG13472.1    FBpp0075441  D-----------------------------------------------------------------------------------------------------------  784
Smn.1        FBpp0075153  G-----------------------------------------------------------------------------------------------------------  123
CG17454.1    FBpp0289146  I-----------------------------------------------------------------------------------------------------------  145
CG3251.1     FBpp0077113  P-----------------------------------------------------------------------------------------------------------  359
otu.1        FBpp0071181  P-----------------------------------------------------------------------------------------------------------  391

                          ..140.......150.......160.......170.......180.......190.......200.......210.......220.......230.......240.........
```
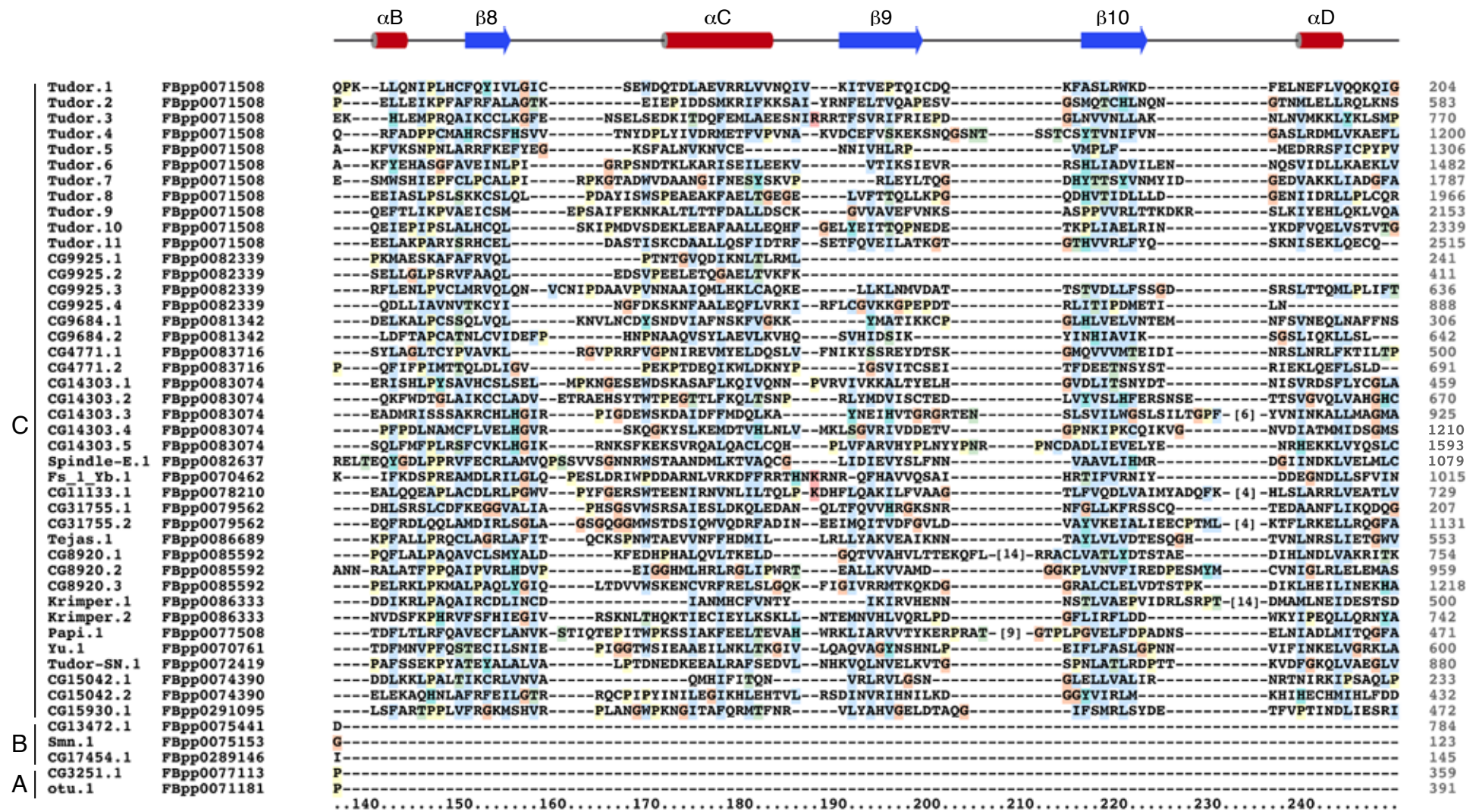
Figure S1. Alignment of all *Drosophila melanogaster* TUDOR and SMN domains including N- and C-terminal extensions
At the top, the secondary structure elements (blue: β-sheets; red: α-helices) as defined by Liu et al. (2011a) are depicted with β-strands in blue and α-helices in red. The alignment covers the entire extended TUDOR domain, including the N- and C-terminal extensions. Start and stop positions of each domain in the respective host protein are indicated at the beginning and at the end of the alignment as well as the corresponding FlyBase Protein ID. Residues were color coded using JalView (color option: ClustalX). To the left, the three groups (A: Otu group; B: Smn group; C: Tudor-extended group) are indicated.
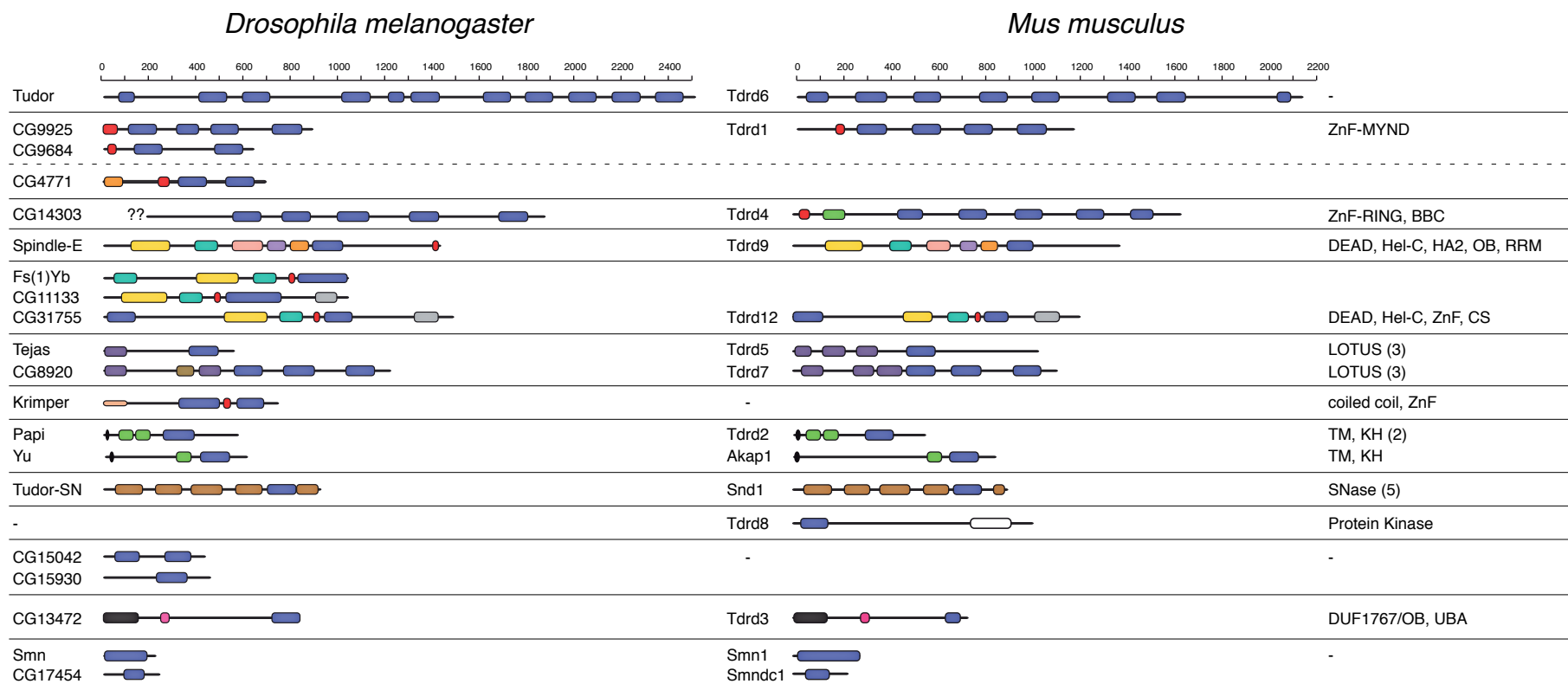
Figure S2. The Fly and Mouse TUDOR domain containing proteins
Cartoon depicting all *Drosophila melanogaster* proteins containing TUDOR/SMN domains (blue boxes) and their corresponding mouse counterparts. All other significant protein domains identified via HHPRED searches are indicated with colored boxes and their identity (mouse proteins only) is given to the right from N to C-terminus (ZnF: zinc finger; BBC: B-Box C-terminal domain; OB: Oligo-Nucleotide binding domain; RRM: RNA recognition motif; DEAD: DEAD Box RNA Helicase domain; Hel-C: Helicase C-term. domain; HA2: Helicase associated domain; Hydrol.: Hydrolase; CS: HSP20-like domain; TM: transmembrane domain; KH: K homology; SNase: Staphylococcus nuclease; DUF: domain of unknown function; UBA: ubiquitin associated domain). For CG14303, the '??' indicate the non-mapped N-terminus. The scale indicates amino acid positions. Based on the additional contained domains, the proteins were grouped into families, separated by horizontal lines.
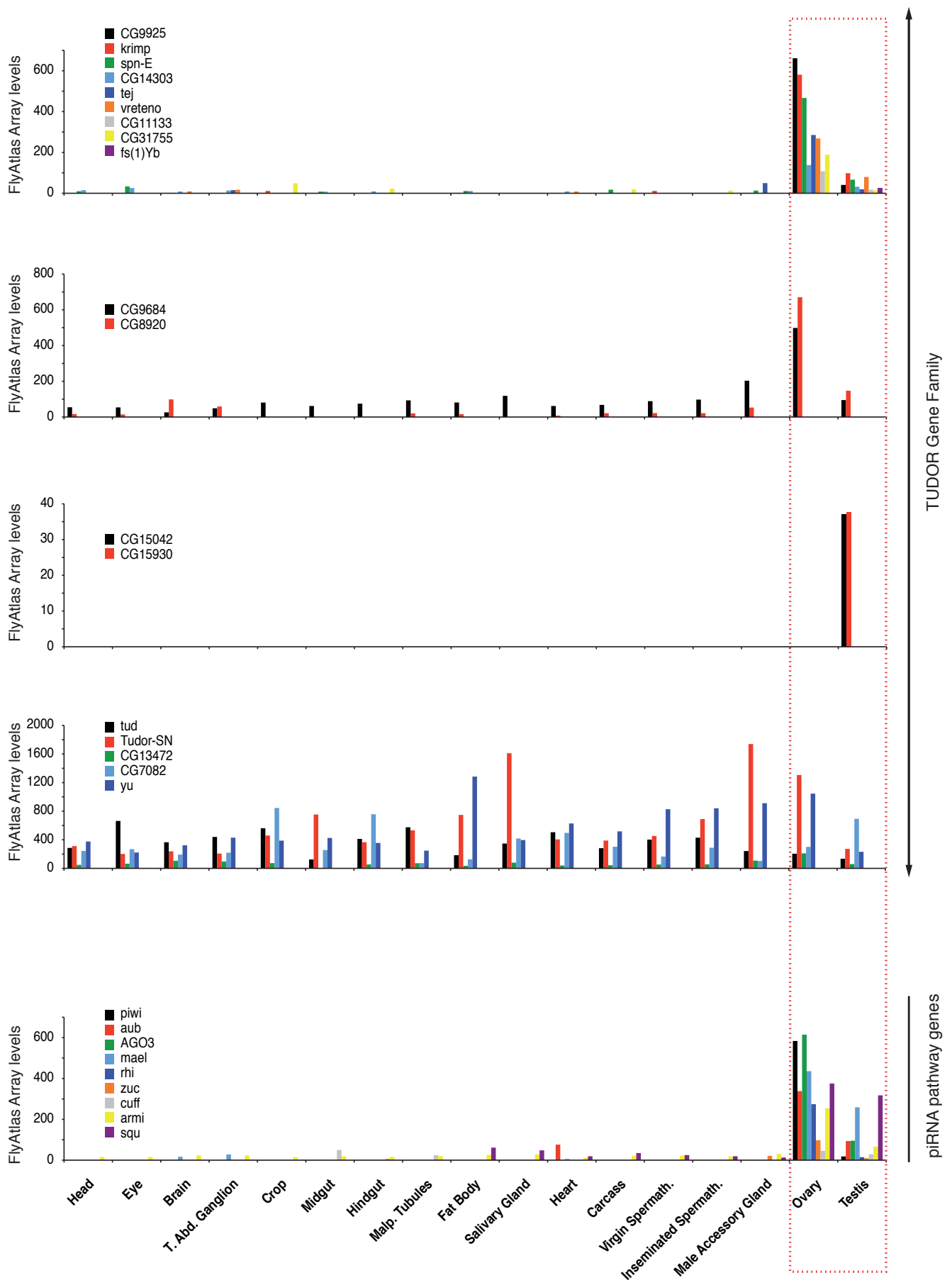
Figure S3. Adult Expression Patterns of TUDOR and piRNA pathway genes in _Drosophila_
Bar Diagrams depicting the detected expression levels of the indicated genes (color coded; legend given for each diagram) in the indicated tissues (bottom). All values are based on data from the adult FlyAtlas (www.flyatlas.org). TUDOR genes were split into gonad specific (first), gonad enriched (second), testes specific (third) and ubiquitous (fourth).
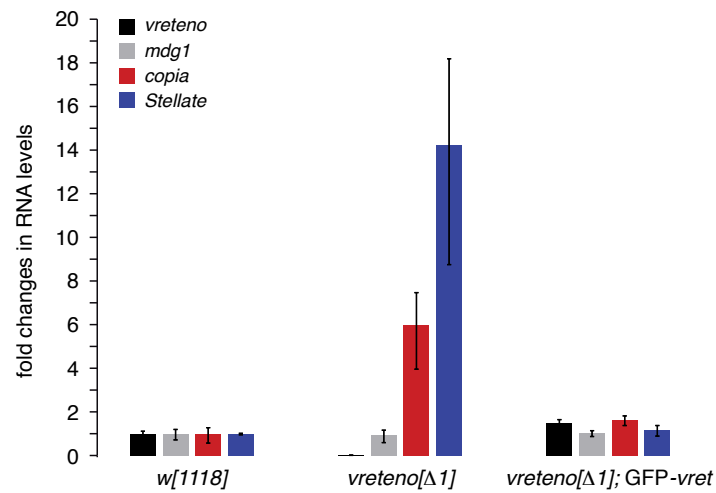
Figure S4. *vreteno* **is required for efficient transposon and** *Stellate* **silencing in testes**
Shown are changes in testes steady state RNA levels (normalized to *w[1118]* controls) of *vreteno*, the transposons *mdg1* and *copia* as well as of *Stellate* in *vreteno[Δ1]* flies compared to *vreteno[Δ1]* flies expressing a GFP-*vreteno* rescue construct (n=3; error bars indicate St. dev).

Tabor piRNA profile

position in transposon [bp]

normalized piRNA density per nt

heterozygote

spn-E-/-

Yb-/-

armi-/-

zuc-/-

vret-/-

ZAM piRNA profile

position in transposon [bp]

normalized piRNA density per nt

heterozygote

spn-E-/-

Yb-/-

armi-/-

zuc-/-

vret-/-
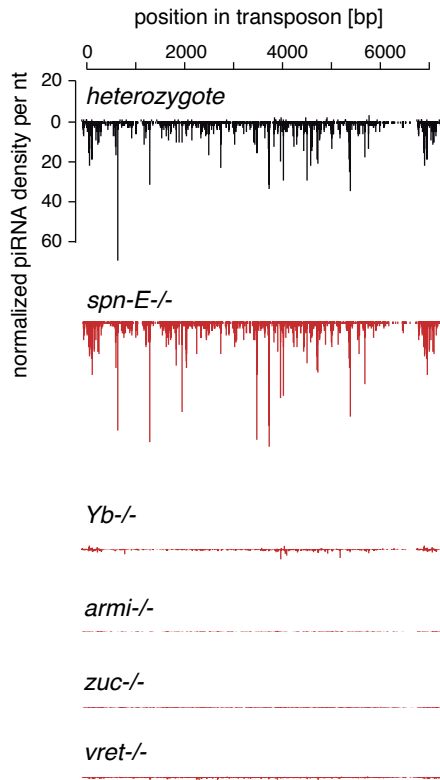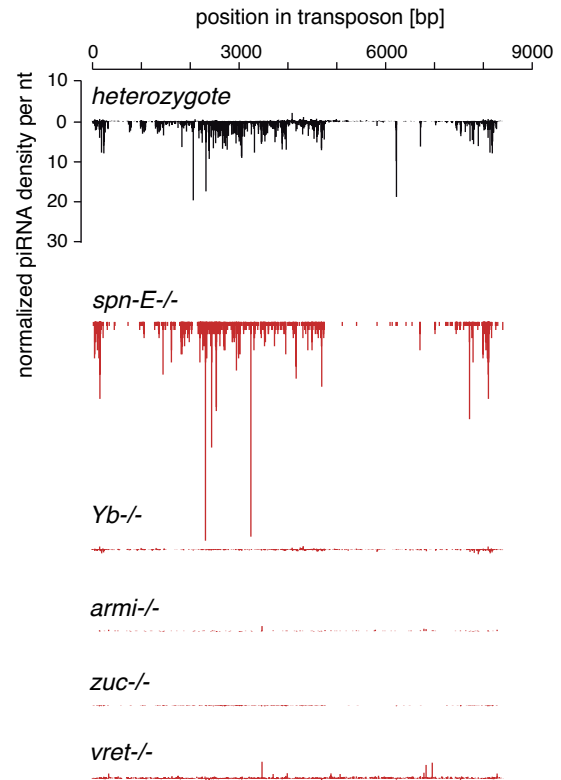
Figure S5. piRNA populations of somatic transposons collaps in *vreteno* mutants
Shown are normalized piRNA profiles obtained from heterozygote ovaries (black) in comparison to profiles obtained from indicated mutant ovaries (red) mapping to the soma dominant transposons *Tabor* and *ZAM* (sense and antisense piRNAs are indicated with peaks pointing up- and downwards).
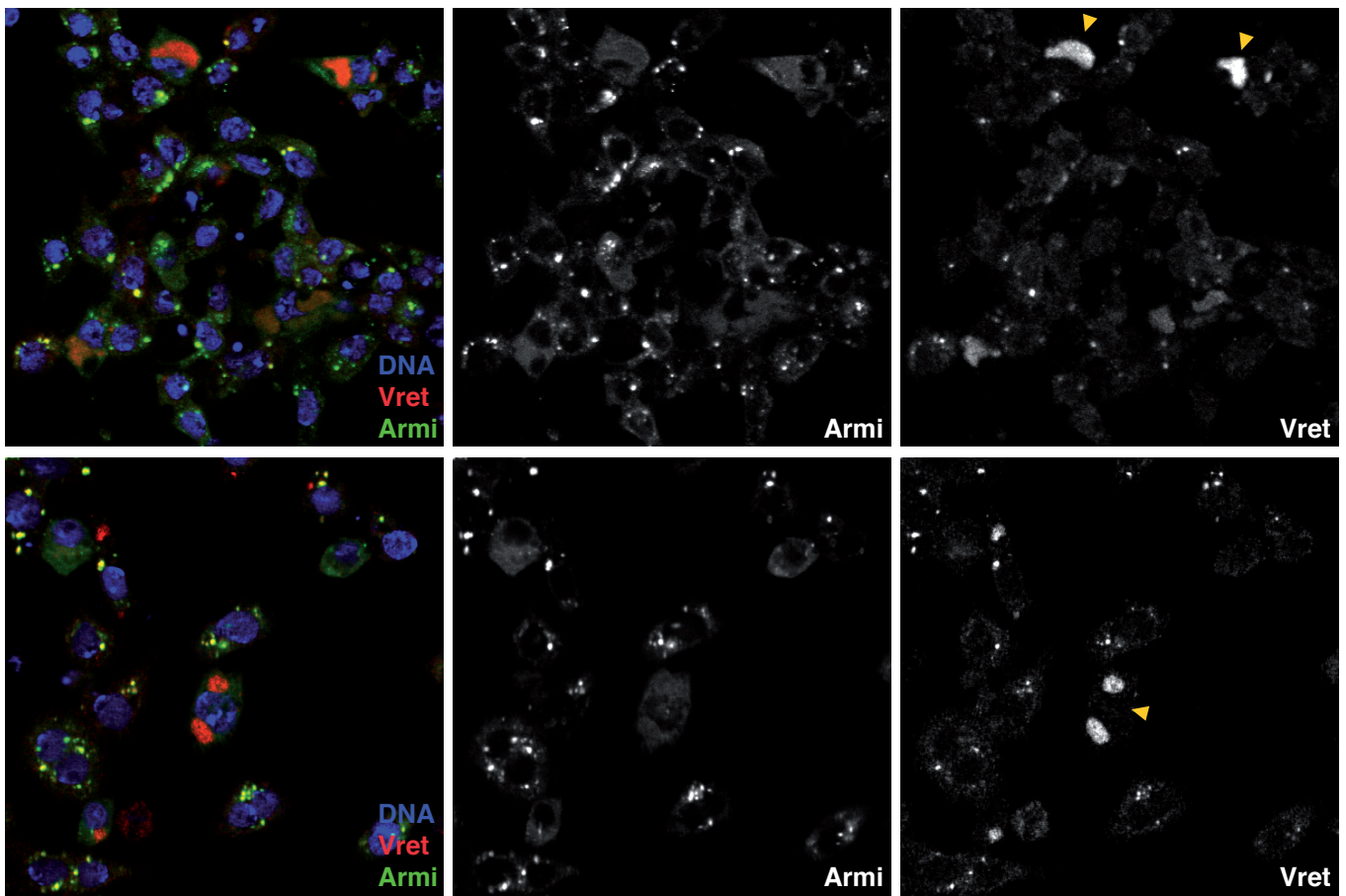
Figure S6. Vreteno localizes to Armi-foci in cultured somatic follicle stem cells
Shown are immunofluorescence images of fixed OSCs stained for Vreteno (red), Armitage (green) and DNA (blue). Two representative images are shown. Yellow arrowheads in the monochromatic Vreteno channel highlight the cells in which Yb-bodies have apparently dispersed, resulting in loss of Armitage foci and large cytoplasmic accumulations of Vreteno.
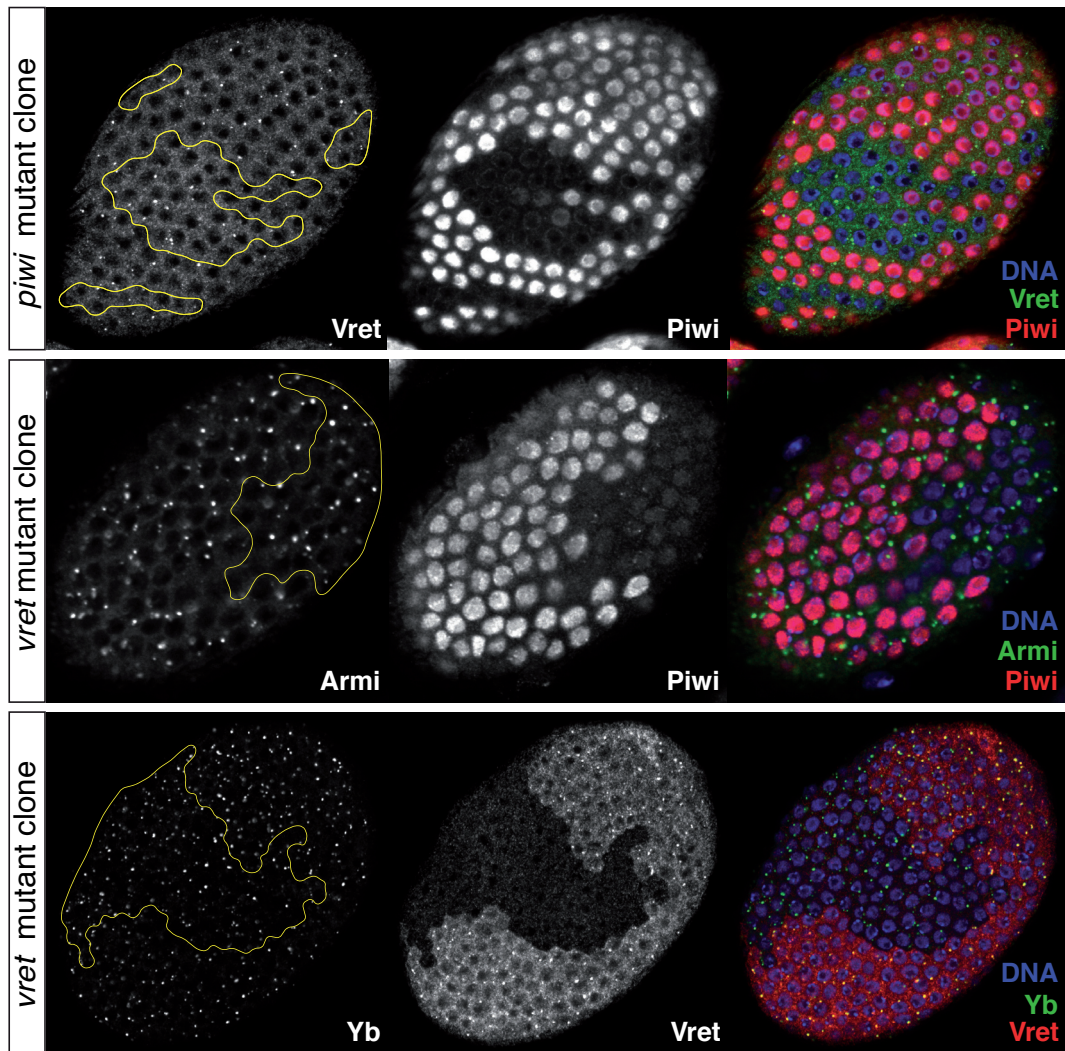
Figure S7. Vreteno localization is independent of Piwi and its levels do not affect Yb-body formation.
Immunostainings of Vret, Armi, Yb, Piwi and DNA (blue) in egg chambers, where clones of cells mutant for the indicated genes (left) have been induced in the follicular epithelium (clone borders indicated by a yellow line). The right panels show the merge of all three channels, the monochrome panels the individual channels as indicated.
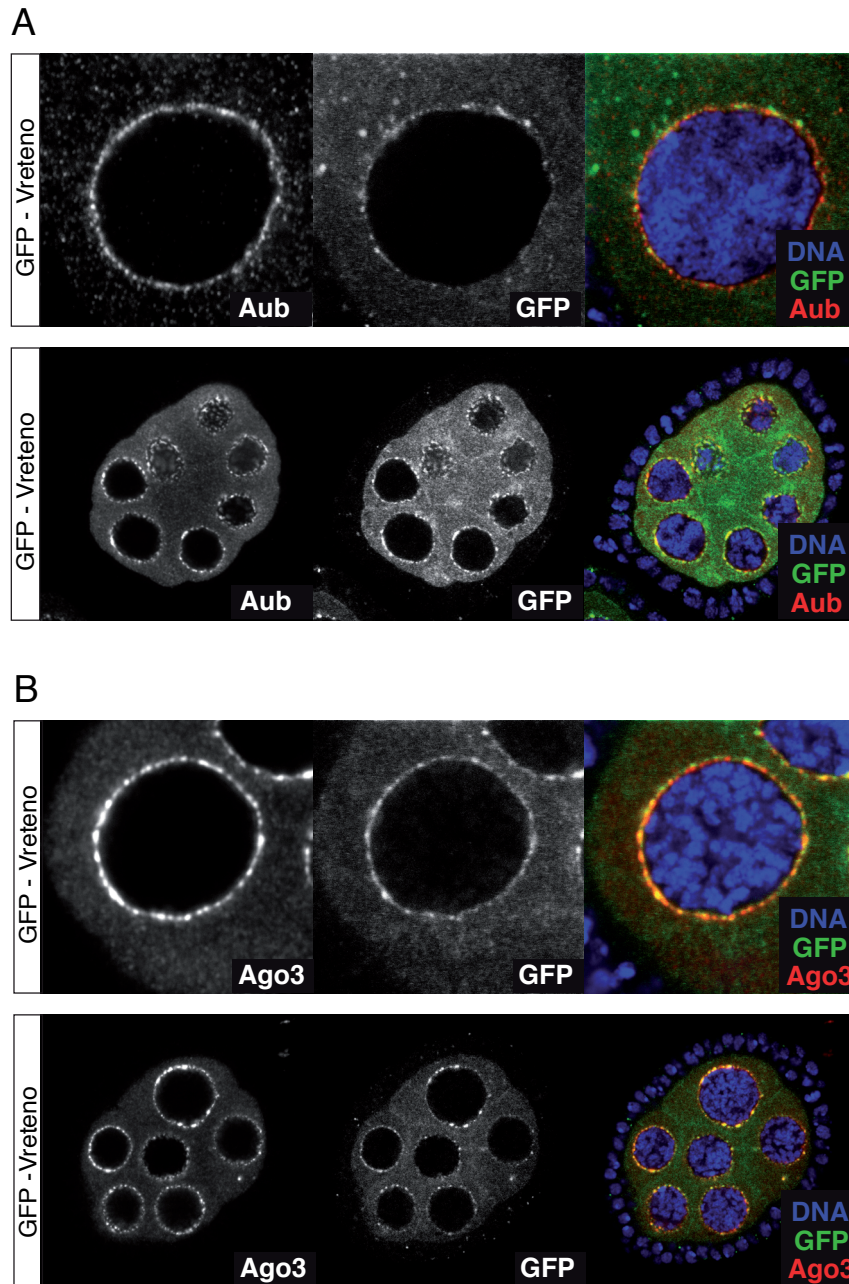
Figure S8. Vreteno localizes to nuage in nurse cells in close proximity to Aubergine and Ago3.
(A) Immunostainings of GFP-Vret (green), Aubergine (red) and DNA (blue) in an entire egg chamber (lower panel) or focused on an individual nurse cell nucleus (upper panels). The right panels show the merge of all three channels where co-localization results in yellow. **(B)** Immunostainings of GFP-Vret (green), Ago3(red) and DNA (blue) in an entire egg chamber (lower panel) or focused on an individual nurse cell nucleus (upper panels). The right panels show the merge of all three channels where co-localization results in yellow.

Supplementary Table 1

gene	label	name	tudor_clan_domains
FBgn0003044	Pcl	Polycomblike	53-BP1_Tudor
FBgn0250818	CG34360		53-BP1_Tudor
FBgn0038780	CG5060		53-BP1_Tudor
FBgn0051151	wge	winged eye	53-BP1_Tudor
FBgn0023509	mip130	Myb-interacting protein 130	53-BP1_Tudor
FBgn0050390	CG30390		53-BP1_Tudor,DUF1325
FBgn0032169	CG4709		53-BP1_Tudor,SMN
FBgn0028734	Fmr1	Fmr1	Agenet,53-BP1_Tudor
FBgn0034255	CG18186		Chromo
FBgn0030854	CG8289		Chromo
FBgn0044324	Chro	Chromator	Chromo
FBgn0023395	Chd3	Chd3	Chromo
FBgn0013591	Mi-2	Mi-2	Chromo
FBgn0086902	kis	kismet	Chromo
FBgn0250786	Chd1	Chromodomain-helicase-DNA-binding protein 1	Chromo
FBgn0003042	Pc	Polycomb	Chromo
FBgn0003600	Su(var)3-9	Suppressor of variegation 3-9	Chromo
FBgn0028965	A16	A16	Chromo
FBgn0027914	Gen	XPG-like endonuclease	Chromo
FBgn0031613	HP6	Heterochromatin protein 6	Chromo_shadow
FBgn0259922	CG42448		Chromo_shadow
FBgn0030994	CG14193		Chromo_shadow
FBgn0003607	Su(var)205	Suppressor of variegation 205	Chromo_shadow,Chromo
FBgn0030082	HP1b	HP1b	Chromo_shadow,Chromo
FBgn0037675	HP1e	HP1e	Chromo_shadow,Chromo
FBgn0039019	HP1c	HP1c	Chromo_shadow,Chromo
FBgn0004400	rhi	rhino	Chromo_shadow,Chromo
FBgn0032475	Sfmbt	Scm-related gene containing four mbt domains	MBT
FBgn0003334	Scm	Sex comb on midleg	MBT
FBgn0038016	MBD-R2	MBD-R2	MBT,53-BP1_Tudor
FBgn0086908	egg	eggless	MBT,53-BP1_Tudor
FBgn0002441	l(3)mbt	lethal (3) malignant brain tumor	MBT,Tudor-knot
FBgn0039743	CG7946		PWWP
FBgn0033155	CG1845		PWWP
FBgn0043456	CG4747		PWWP
FBgn0031023	CG14200		PWWP
FBgn0038190	CG9926		PWWP
FBgn0039559	Mes-4	Mes-4	PWWP
FBgn0016754	sba	six-banded	PWWP
FBgn0033752	CG8569		PWWP
FBgn0039863	CG1815		PWWP
FBgn0036882	CG9279		PWWP
FBgn0020503	CLIP-190	Cytoplasmic linker protein 190	PWWP
FBgn0085451	CG34422		PWWP,53-BP1_Tudor,Tudor-knot,Chromo
FBgn0011785	BRWD3	BRWD3	SMN
FBgn0036467	CG12310		SMN
FBgn0051268	CG31268		SMN
FBgn0259241	CG42339		SMN
FBgn0038191	CG9925		TUDOR
FBgn0037583	CG9684		TUDOR
FBgn0039018	CG4771		TUDOR
FBgn0033921	CG8589		TUDOR
FBgn0031401	CG7082		TUDOR
FBgn0029764	yu	yu	TUDOR
FBgn0035121	Tudor-SN	Tudor-SN	TUDOR
FBgn0003483	spn-E	spindle E	TUDOR
FBgn0029754	CG15930		TUDOR
FBgn0034098	krimp	krimper	TUDOR
FBgn0030937	CG15042		TUDOR
FBgn0037205	CG11133		TUDOR
FBgn0051755	CG31755		TUDOR
FBgn0000928	fs(1)Yb	female sterile (1) Yb	TUDOR
FBgn0003891	tud	tudor	TUDOR
FBgn0038633	CG14303		TUDOR
FBgn0027529	CG8920		TUDOR

FBgn0003023	otu	ovarian tumor	TUDOR
FBgn0031622	CG3251		TUDOR
FBgn0036450	CG13472		TUDOR,SMN
FBgn0039977	CG17454		TUDOR,SMN
FBgn0036641	Smn	survival motor neuron	TUDOR,SMN
FBgn0034975	enok	enoki mushroom	Tudor-knot
FBgn0026080	Tip60	Tip60	Tudor-knot
FBgn0014340	mof	males absent on the first	Tudor-knot
FBgn0027378	MRG15	MRG15	Tudor-knot
FBgn0002775	msl-3	male-specific lethal 3	Tudor-knot
FBgn0039585	CG1894		Tudor-knot

Supplementary Table 2A
this table lists the raw counts of 23-30mer small RNAs that map with up to 3 mismatches
to the indicated transposons (from Repbase) in antisense orientation.

#TP	ZucMut	ZucHet	ArmiMut	ArmiHet	Fs1YbMut	Fs1YbHet	VretMut	VretHet
GYPSY6A_LTR	97	2521	42	1855	947	2143	802	4476
DM412B_LTR	1378	32722	1527	48441	6182	19121	2035	58834
STALKER3_LTR	34	1880	12	1727	518	1024	139	4206
GYPSY12A_LTR	17	438	6	449	346	515	27	510
DMTOM1_LTR	3	56	1	63	31	41	14	77
BATUMI	43581	108401	21970	108450	105682	161040	59856	128518
DMSAT6	1	12	3	11	13	11	1	10
ACCORD	799	28448	840	40484	27183	34841	3159	62863
TLD3	19	230	14	122	74	95	34	209
GTWIN	1587	75721	136	92222	4748	19474	4657	168692
PEN2	0	0	0	0	1	0	0	0
INVADER3	3574	35224	8770	23828	43761	51587	1303	13088
HETRP	4144	29908	3852	16439	15304	73977	4033	11782
TART	2566	116067	2608	91599	112408	142211	8669	95882
LTRMDG3	445	5033	711	2440	3436	7542	333	2154
PROTOP_A	23501	22911	10835	22749	11919	20057	30847	28848
QUASIMODO2-I	571	44515	164	11247	9821	9220	1013	14357
GYPSY11	13	176	2	136	77	154	29	264
MARINER2	2	49	0	22	31	32	10	33
DOC2	2010	28340	1331	16483	22688	18080	2431	23040
COPIA2LTR	335	609	142	711	558	1219	1954	1814
S	2943	9717	1068	5354	3091	4870	848	8944
STALKER4	60984	309121	34776	363296	143910	417014	87495	322716
PEN1	0	0	0	0	1	0	0	0
DIVER2	319	8386	198	7468	6320	5635	1207	12167
SAR	204	96	73	225	79	316	187	141
TC1-2	118	4768	42	4418	3036	3642	151	2597
ACCORD2	487	29104	192	20781	18556	23209	1153	33485
FROGGER	5	204	2	116	106	137	18	198
INVADER6	2659	65074	884	45323	24189	49730	2238	52300
MDG3	10989	41569	8276	19762	41292	60944	1387	20294
DNAREP1	55	3756	19	2361	1413	2200	169	2211
ROO	77745	412727	43983	405566	312266	480554	96228	317238
Transib5	97	2795	43	2269	3349	3780	380	3942
DMRPR	0	0	0	0	0	0	0	0
INVADER4	576	9983	1112	9543	10593	9650	778	9301
DMRT1C	22	1524	7	709	777	913	49	1888
MDG1	7031	155867	4158	162877	29219	118023	18868	286447
Transib1	46	3039	17	1579	783	1547	67	2085
HELENA_RT	26	740	9	1052	672	954	178	1140
RSP	2874	695	76	96	265	274	552	650
LOOPER1	69	4492	23	2781	1472	2574	189	2943
S2	7	92	2	86	64	94	19	161
DIVER	541	34067	734	23497	17485	11185	1039	24270
LINEJ1	1413	61586	606	37437	36915	42340	2625	47357
ALA	0	0	0	0	0	0	0	0
FW3	26	389	22	375	341	390	81	586
DOC3	4336	40993	2663	30692	35865	36331	5447	34662
DM412	8321	270760	3328	337464	39605	187076	18113	469794
INVADER1	4015	21972	4586	36423	31300	50284	7957	22514
INVADER5	4	48	2	33	63	52	5	40
TLD1	0	11	0	27	19	19	0	25
G7	3	51	1	43	43	38	4	33
PEN4	0	0	0	0	0	0	0	0
Transib4	5	65	2	40	25	43	7	78
GYPSY2	478	30560	189	20703	18139	24554	1639	37980
JOCKEY2	592	2568	821	3243	1251	2585	556	4014
DM1731	1342	24641	4106	31713	30464	37698	1123	24255
XDMR	27	218	6	143	51	86	46	75
ZAM	453	10528	124	9261	747	5798	821	16933
TC1	8	388	3	393	162	251	17	447

M4DM	1007	1344	557	2107	1899	2887	1223	2729
QUASIMODO2-LTR	189	3476	139	2191	2000	2519	228	2899
DM297	38812	213721	7138	288019	162021	380655	34943	333093
BURDOCK	728	46273	296	26774	26904	30477	2974	40870
BS	1345	53920	359	41004	34089	50471	2041	44540
COPIA	9499	15762	20532	44219	28185	60125	7054	36067
PROTOP_B	15078	16023	6992	14876	8962	13893	22175	18416
TAHRE	1879	61358	746	36881	30077	47691	6976	62452
DOC6	1670	31487	1016	22146	8515	14824	1250	19501
G5	109	5041	74	5214	10160	7148	286	7928
FW	180343	332458	127402	308490	204087	235846	149840	302042
DMRT1A	3465	165599	1379	131193	135617	157803	13404	143919
TLD2	11	704	1	470	134	326	39	737
DOC4	16	732	2	377	451	448	81	967
DOC5	86	4029	39	3881	3513	3159	272	5446
ROVER	1143	38223	1270	57502	11307	28729	4184	97115
DMCR1A	33215	74290	20850	78918	59635	80445	41028	83073
TABOR	3126	142029	915	66046	5252	125609	7686	94074
MICROPIA	6724	24440	6376	29067	40087	63692	3268	22360
ROOA	1305	75828	493	53944	38370	65337	2568	46756
DMHMR2	623	12227	152	5104	4653	6486	1860	8670
R1-2	7	215	4	155	187	160	16	179
GYPSY8	221	19327	49	5606	6444	6342	282	10472
ARS406	1785	670	1139	441	343	1736	893	755
IVK	1101	38364	761	24938	27568	30862	1761	25968
MAX	72102	286753	16063	212047	195127	233856	49357	206279
BS2	2389	101346	807	82456	79428	100581	6285	87017
PROTOP	43793	61404	20580	52411	44750	82868	39255	58297
BLOOD	2604	111437	3298	97950	241547	162272	5883	119228
FB4	546	490	169	420	383	1891	1463	1724
G4	181	9798	81	8670	5024	7596	621	8628
I	635	40335	596	25739	23111	20342	1933	34365
BARI	25306	18046	8467	16634	16929	10421	7619	26591
DMHMR1	14	222	10	193	242	160	145	567
COPIA2I	6254	15085	2494	11491	12077	10348	5660	12619
FUSHI	0	0	0	0	0	0	0	0
ALUII	3	4	3	5	4	5	5	6
BAGGINS1	5790	55230	5015	33337	36033	38331	8808	39345
QUASIMODO	1654	29995	5531	55306	52596	95512	6745	49666
G5A	21	925	5	676	704	772	51	1084
POGON1	75	309	50	373	199	312	65	460
Transib-N1	0	2	0	5	3	4	0	3
G2	2930	42007	3063	50130	31785	33079	5972	50000
DMRP1	0	0	0	1	0	0	0	2
IDEFIX	645	22790	1098	20493	23656	28790	2355	29259
R2	350	29321	129	9711	9577	8746	628	15087
TRANSPAC	281	22259	109	10662	7192	8320	882	12035
BLASTOPIA	3307	46589	5737	48428	74833	104142	1454	29453
DM176	22632	71658	18910	95940	66147	61209	13913	113089
GYPSY3	323	23268	153	13268	11213	22802	1372	18623
TRANSIB2	3545	18219	1314	12845	16653	20695	1178	13107
NTS	6222	22425	2599	3855	2763	5786	3266	7179
GYPSY9	3	308	3	245	216	212	16	234
GYPSY12	1742	41350	2161	39436	27541	52156	4632	49803
DOC	219113	390869	75007	190911	208756	260108	129523	193104
G6	1144	35443	714	20462	74708	85817	1174	22809
GYPSY7	58	3849	18	1806	1615	1858	98	1611
TART_B1	1196	70136	2064	45495	184495	231569	5617	84953
GYPSY	826	46772	368	22393	18658	19784	2323	34844
NOMAD	41353	309011	2538	89759	155151	156313	16040	89768
R1	51022	286739	40397	116622	166842	180826	48810	189292
BS4	0	19	1	9	17	21	0	10
HETA	4778	94328	1307	70882	26633	53380	15765	79338
G	975	64037	2488	45424	47731	39336	12943	79748
FW2	14	448	12	385	485	517	70	467
POGO	7125	13818	3630	16938	8288	12200	1367	12117
STALKER2	14139	66003	7194	75972	35137	88825	20186	92249

BEL	983	49215	3024	35552	53716	42046	2220	34789
PLACW	1	4	0	5	5	7	3	12
GYPSY6	1290	40096	543	26140	20379	20652	3901	41936
HOBO	121	1748	77	2245	4393	5535	366	2070
INVADER2	8534	42497	11419	31943	22462	21460	2741	34058
CIRCE	2844	24163	4740	36527	29734	63183	11952	38875
DMRT1B	5150	271702	2493	188024	168162	193999	20495	199542
GYPSY5	974	63388	97	37495	1316	55096	3512	62182
G3	4	457	4	298	348	450	50	421
TRANSIB3	3	160	1	242	60	92	12	440
GYPSY10	190	11350	25	8966	1676	8190	592	14464
DMLTR5	192	1693	202	3700	3978	8193	129	2039
FTZ	0	0	0	0	0	0	0	0
HMSBEAGLE_I	6455	36692	14892	57164	96395	125998	2642	33230
GYPSY4	2501	59095	2335	57480	33732	36478	4628	68495
HELITRON1	0	4	0	5	7	12	1	10
BS3	51	3221	32	1992	3190	3304	99	2846
TIRANT	8	1125	1	106	65	79	441	133

Supplementary Table 2B
all heterozygote libraries were scaled to 1 million repeat derived 23-30mer small RNAs
each mutant library was normalized too its respective het lobrary via non-TE derived endogenous siRNAs (see Malone et al. 2009)
the spn-E data was taken from Malone et al. 2009
elements colored in red are germline dominant, in yellow are intermediate and in green are soma dominant (according to Malone et al. 2009)

#TP	ZucMut	ZucHet	zuc_log 2 ratio	ArmiMut	ArmiHet	armi_log 2 ratio	Fs1YbMut	Fs1YbHet	yb_log2_ratio	VretMut	VretHet	vret-log2_ratio	spnE-log2_ratio
PROTOP_A	680	1413	1.054244095	927	1593	0.781545759	715	1232	0.78488102	1254	1712	0.449316679	4.10
HETA	138	5816	5.394133133	112	4962	5.472530049	1598	3279	1.037122746	641	4707	2.877262425	6.75
NOMAD	1197	19052	3.992520108	217	6284	4.855734413	9309	9603	0.044803158	652	5326	3.030502676	5.01
DOC	6342	24099	1.925935899	6414	13365	1.059244869	12525	15979	0.351331495	5263	11457	1.122145307	4.23
DMRT1B	149	16752	6.812234755	213	13163	5.948331915	10090	11918	0.240235869	833	11839	3.82932411	6.33
TAHRE	54	3783	6.120140299	64	2582	5.339000117	1805	2930	0.699094746	283	3705	3.708251394	6.38
G6_DM	33	2185	6.044267578	61	1433	4.552321063	4482	5272	0.234039114	48	1353	4.826074449	4.16
R1_DM	1477	17679	3.581472597	3454	8165	1.24096169	10010	11108	0.150158005	1983	11231	2.501340348	4.86
FW_DM	5220	20498	1.97335448	10894	21597	0.987277582	12245	14488	0.242699231	6089	17920	1.557301936	4.00
TART	74	7156	6.590218677	223	6413	4.845757857	6744	8736	0.373326733	352	5689	4.013298079	4.97
I_DM	18	2487	7.080057666	51	1802	5.143941647	1387	1250	-0.150079769	79	2039	4.698001982	0.93
BATUMI	1261	6684	2.405532672	1879	7592	2.014865062	6341	9893	0.641727789	2432	7625	1.648378224	6.16
MAX	2087	17680	3.082623209	1374	14845	3.434012588	11707	14366	0.295245411	2006	12238	2.609245909	6.24
BEL	28	3034	6.73668868	259	2489	3.266842461	3223	2583	-0.319344933	90	2064	4.515975193	6.07
DM1731	39	1519	5.289530042	351	2220	2.660710612	1828	2316	0.341420989	46	1439	4.978827912	5.53
BS2	69	6249	6.497664297	69	5773	6.386353777	4766	6179	0.374676607	255	5163	4.337288195	6.58
DM297	1123	13177	3.552079802	610	20164	5.045942059	9721	23384	1.266341598	1420	19762	3.798825221	3.14
INVADER4	17	616	5.206258522	95	668	2.812727868	636	593	-0.100471993	32	552	4.125519341	4.39
ROO	2250	25447	3.499291833	3761	28393	2.916360579	18736	29521	0.655961448	3910	18821	2.267012509	4.07
DM176	655	4418	2.753689509	1617	6717	2.05442486	3969	3760	-0.077893542	565	6709	3.568928732	2.18
QUASIMODO	48	1849	5.271616704	473	3872	3.03326554	3156	5867	0.894767305	274	2947	3.426343777	1.05
GYPSY3	9	1435	7.261595047	13	929	6.149717238	673	1401	1.05802644	56	1105	4.308708676	1.02
GYPSY4	72	3644	5.65338492	200	4024	4.333007391	2024	2241	0.146947159	188	4064	4.433513474	1.43
BLOOD	75	6871	6.510280878	282	6857	4.603823972	14493	9969	-0.539851464	239	7074	4.887002803	0.54
STALKER4	1765	19059	3.432594793	2974	25434	3.096423359	8634	25618	1.56896736	3555	19146	2.428968192	1.29
IDEFIX	19	1405	6.233883766	94	1435	3.933623022	1419	1769	0.317400027	96	1736	4.181057063	0.04
ROVER_DM	33	2357	6.154469519	109	4026	5.212153518	678	1765	1.379329962	170	5762	5.082714954	0.36
GYPSY	24	2884	6.914285341	31	1568	5.638640027	1119	1215	0.118578183	94	2067	4.452824757	0.19
STALKER2	409	4069	3.313777325	615	5319	3.112043521	2108	5457	1.372013151	820	5473	2.738153779	0.92
DM412	241	16694	6.115039705	285	23625	6.375376147	2376	11492	2.273908391	736	27872	5.242906433	0.31
GYPSY2	14	1884	7.089415927	16	1449	6.486751578	1088	1508	0.470901532	67	2253	5.080327711	0.58
MDG1	204	9610	5.561367622	356	11403	5.003191109	1753	7250	2.048127713	767	16995	4.470230382	0.31
GTWIN	46	4669	6.667245243	12	6456	9.116802276	285	1196	2.070195793	189	10008	5.72482243	-0.06
GYPSY10	5	700	6.991474881	2	628	8.197834378	101	503	2.322879689	24	858	5.156701162	-0.01
TABOR	90	8757	6.596649758	78	4624	5.884997419	315	7716	4.613967498	312	5581	4.159466732	-0.03
ZAM	13	649	5.629502346	11	648	5.934197742	45	356	2.990413572	33	1005	4.912287129	-0.33
GYPSY5	28	3908	7.115069979	8	2625	8.305939545	79	3385	5.421754574	143	3689	4.692107835	-0.64

Supplementary Table 3

Identified Proteins that were more than 10fold enriched (quantitative mass-spec analysis) in Vreteno-GFP immuno-precipitates compared to a control sample (wildtype ovaries). Ribosomal proteins were excluded.

protein ID	gene name	peptide coverage [%]	# unique peptides	# of peptides	iTRAQ enrichment
FBpp0076182	Hsp27	26.3	2	5	16x
FBpp0083716	CG4771	54.9	30	37	13x
FBpp0073872	CG9281	5.4	3	3	12x
FBpp0079562	CG31755	33.0	35	42	10x
FBpp0078210	CG11133	35.0	26	34	10x

Supplementary Table 4

VDRC lines used in this study

Tudor-SN	19011GD
yu	48006GD
CG13472	32193GD
tej	24181GD
CG8920	28998GD
CG4771	34897GD
CG9925	29329GD
CG9684	24090GD
CG7082	2553GD
spn-E	21374GD
CG11133	18149GD
tud	24031GD
CG31755	100190KK
CG14303	17474GD
fs(1)Yb	25437GD
armi	16205GD
zuc	48764GD

Supplementary Table 5

Primers for shRNA construct cloning

CG9925_top	ctagcagtAAAGTGTATGTTCAAACATTAtagttatattcaagcataTAATGTTTGAACATACACTTTgcg
CG9925_bottom	aattcgcAAAGTGTATGTTCAAACATTAtatgcttgaatataactaTAATGTTTGAACATACACTTTactg
CG31755_top	ctagcagtAAGGTTCAAAGTATCAGCGAAtagttatattcaagcataTTCGCTGATACTTTGAACCTTgcg
CG31755_bottom	aattcgcAAGGTTCAAAGTATCAGCGAAtatgcttgaatataactaTTCGCTGATACTTTGAACCTTactg
CG9684_top	ctagcagtAAGGATATCAATGATGAGTTAtagttatattcaagcataTAACTCATCATTGATATCCTTgcg
CG9684_bottom	aattcgcAAGGATATCAATGATGAGTTAtatgcttgaatataactaTAACTCATCATTGATATCCTTactg
yu_top	ctagcagtCAGCAAGTCGATGAACATCAAtagttatattcaagcataTTGATGTTCATCGACTTGCTGgcg
yu_bottom	aattcgcCAGCAAGTCGATGAACATCAAtatgcttgaatataactaTTGATGTTCATCGACTTGCTGactg
CG13472_top	ctagcagtCTGCAGCGAAATCGACAAATAtagttatattcaagcataTATTTGTCGATTTCGCTGCAGgcg
CG13472_bottom	aattcgcCTGCAGCGAAATCGACAAATAtatgcttgaatataactaTATTTGTCGATTTCGCTGCAGactg
Tudor-SN_top	ctagcagtTAGAAGAAGTGCCTAAAGAAAtagttatattcaagcataTTTCTTTAGGCACTTCTTCTAgcg
Tudor-SN_bottom	aattcgcTAGAAGAAGTGCCTAAAGAAAtatgcttgaatataactaTTTCTTTAGGCACTTCTTCTAactg
CG8920_top	ctagcagtCAGCATGTATGCGTTGGATAAtagttatattcaagcataTTATCCAACGCATACATGCTGgcg
CG8920_bottom	aattcgcCAGCATGTATGCGTTGGATAAtatgcttgaatataactaTTATCCAACGCATACATGCTGactg
CG7082_top	ctagcagtCACCCACAACAAGTTAATCAAtagttatattcaagcataTTGATTAACTTGTTGTGGGTGgcg
CG7082_bottom	aattcgcCACCCACAACAAGTTAATCAAtatgcttgaatataactaTTGATTAACTTGTTGTGGGTGactg
tud_top	ctagcagtCAGATTGACTACTAAAGATAAtagttatattcaagcataTTATCTTTAGTAGTCAATCTGgcg
tud_bottom	aattcgcCAGATTGACTACTAAAGATAAtatgcttgaatataactaTTATCTTTAGTAGTCAATCTGactg
CG4771_top	ctagcagtCAGCTGGAAAGACTGTATGAAtagttatattcaagcataTTCATACAGTCTTTCCAGCTGgcg
CG4771_bottom	aattcgcCAGCTGGAAAGACTGTATGAAtatgcttgaatataactaTTCATACAGTCTTTCCAGCTGactg
CG11133_bottom	aattcgcCAGCTGGAAGATGAAAGTAAAtatgcttgaatataactaTTTACTTTCATCTTCCAGCTGactg
CG11133_top	ctagcagtCAGCTGGAAGATGAAAGTAAAtagttatattcaagcataTTTACTTTCATCTTCCAGCTGgcg
CG8589_top	ctagcagtCTCCAAGTCATTGAAAGTTAAtagttatattcaagcataTTAACTTTCAATGACTTGGAGgcg

CG8589_bottom	aattcgcCTCCAAGTCATTGAAAGTTAAtatgcttgaatataactaTTAACTTTCAATGACTTGGAGactg
CG14303_top	ctagcagtCCGGAGGATTTCTATGTTCAAtagttatattcaagcataTTGAACATAGAAATCCTCCGGgcg
CG14303_bottom	aattcgcCCGGAGGATTTCTATGTTCAAtatgcttgaatataactaTTGAACATAGAAATCCTCCGGactg
spn-E_top	ctagcagtCTCGAAGAAGCTATTATTATAtagttatattcaagcataTATAATAATAGCTTCTTCGAGgcg
spn-E_bottom	aattcgcCTCGAAGAAGCTATTATTATAtatgcttgaatataactaTATAATAATAGCTTCTTCGAGactg
krimp_top	ctagcagtCAGATTGGGAGACTACGAATAtagttatattcaagcataTATTCGTAGTCTCCCAATCTGgcg
krimp_bottom	aattcgcCAGATTGGGAGACTACGAATAtatgcttgaatataactaTATTCGTAGTCTCCCAATCTGactg
fs(1)yb_top	ctagcagtCAGCTGCGATAAGATCTTCAAtagttatattcaagcataTTGAAGATCTTATCGCAGCTGgcg
fs(1)yb_bottom	aattcgcCAGCTGCGATAAGATCTTCAAtatgcttgaatataactaTTGAAGATCTTATCGCAGCTGactg

Supplementary Table 6

QPCR primers used in this study:

rp49_for	CCGCTTCAAGGGACAGTATCTG
rp49_rev	ATCTCGCCGCAGTAAACGC
HeT-A_for	CGCGCGGAACCCATCTTCAGA
HeT-A_rev	CGCCGCAGTCGTTTGGTGAGT
blood_for	AACAATAGAAAGAAGCCACCGAAC
blood_rev	AGTCATGGACTATTGAGGGTGTTG
ZAM_for	ACTTGACCTGGATACACTCACAAC
ZAM_rev	GAGTATTACGGCGACTAGGGATAC
HP1c_for	GTGCGAAGAGATCCAGAAGC
HP1c_rev	AGTCGAACTCGTCGCAGAAC
CG6985_for	ACCGCATTTGGAAATTAGCC
CG6985_rev	ATTCCGATTGGGTGAACTCC
vret_for	TGGCCAACAATGAACCTCTT
vret_rev	GACTTCCACTGAGCCAATGC
CG31755_for	TTCAAACAAACACTTGGCTTCC
CG31755_rev	AAAAACCCATCCGAAAGAAGTG
CG11133_for	CAGATTTTCCCAACTGTATGAGTGT
CG11133_rev	AATGCAGTCTTCTCCTGAGTATGG