

Name in the manuscript	Full Genotype
Control	<i>elav-GAL4/+</i>
Tau ^{R406W}	<i>elav-GAL4/+;UAS-Tau^{R406W}/+</i>
Tau ^{WT}	<i>elav-GAL4/+;UAS-Tau^{WT}/+</i>
Control+Gypsy-TRAP	<i>ovo-GAL80/+;GMR-GAL4/+;UAS-GFP/+</i>
Tau+Gypsy-TRAP	<i>ovo-GAL80/+;GMR-GAL4/+;UAS-GFP/GMR-Tau^{V337M}</i>
Control+piwi ^{RNAi-1}	<i>elav-GAL4/+;UAS-piwi^{v101658}/+</i>
Control+piwi ^{RNAi-2}	<i>elav-GAL4/+;UAS-piwi^{v22235}/+</i>
Control+piwi ^{OE}	<i>elav-GAL4/+;UAS-HA-piwi/+</i>
Control+flam ^{LOF1}	<i>elav-GAL4/flam^{OR}</i>
Control+flam ^{LOF2}	<i>elav-GAL4/flam^{KG00476}</i>
Tau+flam ^{LOF1}	<i>elav-GAL4/flam^{OR};UAS-Tau^{R406W}/+</i>
Tau+flam ^{LOF2}	<i>elav-GAL4/flam^{KG00476};UAS-Tau^{R406W}/+</i>
Tau+piwi ^{OE}	<i>elav-GAL4/+;UAS-HA-piwi/+;UAS-Tau^{R406W}</i>
Su(var)3-9 ^{LOF}	<i>elav-GAL4/+;Su(var)3-9²/+</i>
HP1 ^{LOF}	<i>elav-GAL4/+;Su(var)205⁵/+</i>

Supplementary Table 1 | Full *Drosophila* Genotypes.

(Included as an Excel spreadsheet)

Supplementary Table 2 | Differential expression analysis of transposable elements in *Drosophila* based on RNA-seq. The first column includes the FlyBase IDs of transposable elements, which are ordered based on *P*-values. The next six columns, computed using DESeq2, are: the mean of the normalized counts (basemean), the logarithm of the fold change (log2FoldChange), the standard error of the log2FoldChange (lfcSE), the two-sided Wald statistic defined as the log2FoldChange divided by lfcSE (stat), the *P*-value of the Wald test, and the Benjamini-Hochberg adjusted *P*-value (padj). The raw counts from RNA-seq are also included.

(Included as an Excel spreadsheet)

Supplementary Table 3 | Sequences of NanoString probes.

Generic Probe	Elements Recognized by Generic Probe
<i>297</i> {generic}	<i>297</i> {72 <i>297</i> {327 <i>297</i> {376 <i>297</i> {950
<i>blood</i> {generic}	<i>blood</i> {344 <i>blood</i> {488 <i>blood</i> {1094
<i>Burdock</i> {generic}	<i>Burdock</i> {1187 <i>Burdock</i> {1221
<i>copia</i> {generic}	<i>copia</i> {298 <i>copia</i> {342 <i>copia</i> {387 <i>copia</i> {539 <i>copia</i> {631 <i>copia</i> {837 <i>copia</i> {920 <i>copia</i> {988 <i>copia</i> {1016 <i>copia</i> {1349 <i>copia</i> {1391 <i>copia</i> {1467
<i>FB</i> {generic}	<i>FB</i> {CG17600 ^{FB-NOF} <i>a</i> <i>FB</i> {Pka-R1 ^{FB-NOF} <i>a</i>
<i>HMS-Beagle</i> {generic}	<i>HMS-Beagle</i> {347 <i>HMS-Beagle</i> {390
<i>jockey</i> {generic}	<i>jockey</i> {858 <i>jockey</i> {1447
<i>opus</i> {generic}	<i>opus</i> {292 <i>opus</i> {306 <i>opus</i> {1146
<i>pogo</i> {generic}	<i>pogo</i> {985 <i>pogo</i> {1061
<i>Quasimodo</i> {generic}	<i>Quasimodo</i> {360 <i>Quasimodo</i> {1100
<i>Tc1-2</i> {generic}	<i>Tc1-2</i> {3905 <i>Tc1-2</i> {4132

Supplementary Table 4 | Transposable elements recognized by “generic” NanoString probes.

(Included as an Excel spreadsheet)

Supplementary Table 5 | Differential expression analysis of piRNAs in *Drosophila*. The first column is the piRNA name sorted by *P*-value (two-sided Wald test), and the next six columns are similar to Supplementary Table 2, which is described above. In addition to raw counts, the sum of counts in each condition is included, as well as the ratio of the sum of the counts in tau transgenic samples over the sum of the counts in control samples. Because a piRNA can have multiple copies in the *Drosophila* genome, we included the number of copies (frequency) and their genomic locations, which are separated using a “*”. The last column is the sequence of the piRNA.

(Included as an Excel spreadsheet)

Supplementary Table 6 | Genomic locations of *Drosophila* piRNAs. The first column is the piRNA name sorted by *P*-value of two-sided tests. The chromosome, start, end, strand, sequence, number of copies (frequency), and the adjusted *P*-value from the small RNA-seq data are included. n=4 biologically independent replicates of each genotype, each consisting of RNA pooled from 6 heads. *P* values were calculated based on a two-sided Wald test, FDR.

(Included as an Excel spreadsheet)

Supplementary Table 7 | Differential expression of transposable elements in human tauopathy. In each of the first six sheets, the transposable elements are sorted based on the *P*-value corresponding to the tissue (cortex or cerebellum) and the condition specified in the sheet name. Columns are similar to Supplementary Table 2. The last two sheets are the clinical data including the diagnosis and the RIN of RNA samples. More detail on clinical information, including gender, age at death, apolipoprotein E (ApoE), sequencing flow cell batch, and post mortem interval is available at the Synapse.org website (cortex: <http://dx.doi.org/10.7303/syn5223705.3>, cerebellum: <http://dx.doi.org/10.7303/syn3817650.6>). *P* values were calculated based on a two-sided Wald test, FDR.

Antibody	Western Blotting	Immunostaining	Source
Actin	1:50,000		Abcam #ab8227
GFP	1:1,000		UCDavis/NIH NeuroMab #75-131
PCNA		1:200	Dako #M0879
piwi	1:500	1:50	Abcam #5207
cTau	1:2,000,000	1:10,000	Dako #A0024
Alexa555-conjugated secondary (rabbit)		1:200	Life Technologies #A21424
Biotin-conjugated secondary (rabbit)		1:200	Southern Biotech #4010-08
HRP-conjugated secondary (mouse)	1:10,000		Southern Biotech #1010-05
HRP-conjugated secondary (rabbit)	1:1,000		Southern Biotech #3010-05

Supplementary Table 8 | Antibody information.

(Included as an Excel spreadsheet)

Supplementary Table 9 | Statistical Analyses.

