



Supplemental Figure S11: Strand distribution of the piRNAs mapping to MutsuDr.

The shown coverage is the result of the sum of mapped small-RNAseq reads from all zebrafish samples (oocyte, 12 time course embryos, adult male whole-body and adult female tail) after being normalized over the total reads between 28 and 32 of each experiment. The sense read counts, marked in black, are separated from the antisense reads, marked in red. On the X axis the length of the MutsuDr element is indicated.