

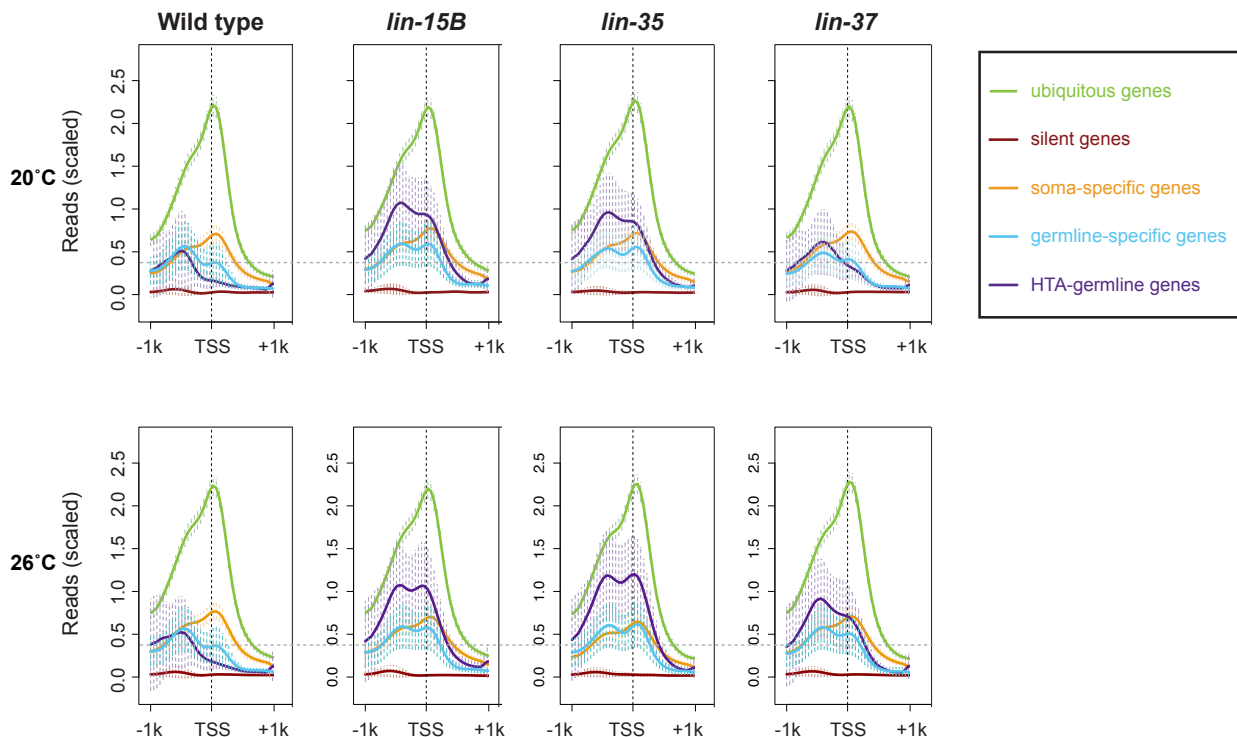
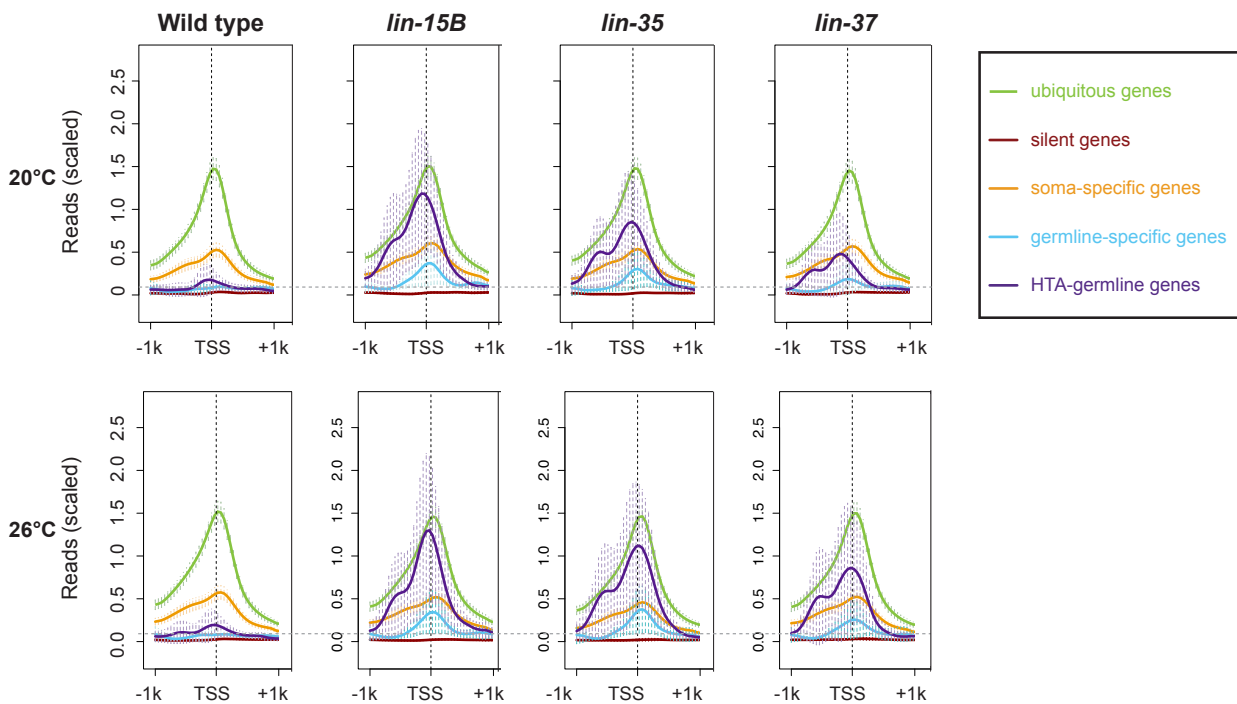
A H3K4me3 on all genes in each category**B** H3K4me3 on genes in category with a TSS > 2 kb from the closest TSS

Figure S9: Distribution and levels of H3K4me3 at the TSS of different categories of genes at 20°C and 26°C.

(A) Metagene profiles of mean H3K4me3 ChIP-seq signal 1kb upstream and downstream from the transcript start site (TSS) for genes that show ubiquitous, silent, soma-specific, germline-specific, or HTA-germline expression at 20°C and 26°C (see Materials and Methods for definitions of gene categories). (B) Metagene profiles of mean H3K4me3 ChIP-seq signal 1kb upstream and downstream from the transcript start site (TSS) for genes where the TSS is >2kb away from the TSS of neighboring genes at 20°C and 26°C in each category. For A and B, the horizontal dotted line is located at the highest level of reads over the TSS in wild type for genes in the germline-specific category. Reads were scaled by dividing by the standard deviation and subtracting the 25th percentile. Error bars indicate 95% confidence intervals for the mean.