

Figure S8

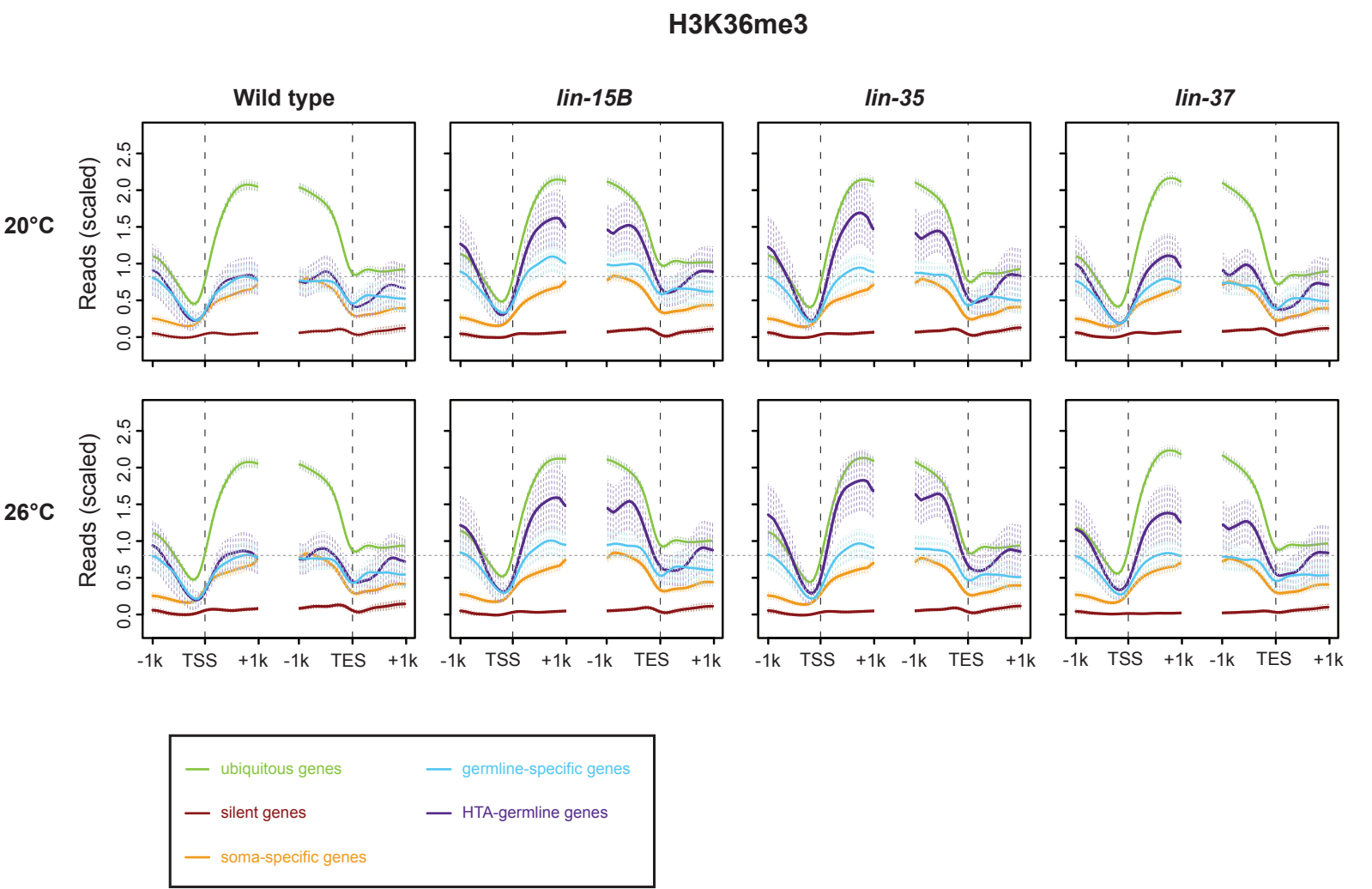


Figure S8: H3K36me3 increases on germline genes up-regulated in *synMuv B* mutants. Metagene profiles of mean H3K36me3 ChIP-seq signal 1kb upstream and downstream from the transcript start site (TSS) and transcript end site (TES) for genes that show ubiquitous, silent, soma-specific, germline-specific, or HTA-germline expression (see Materials and Methods for definitions of gene categories). Reads were scaled by dividing by the standard deviation and subtracting the 25th percentile. Horizontal dotted lines indicate the highest point for H3K36me3 reads over the gene body of germline-specific genes in wild type. Error bars indicate 95% confidence intervals for the mean. .