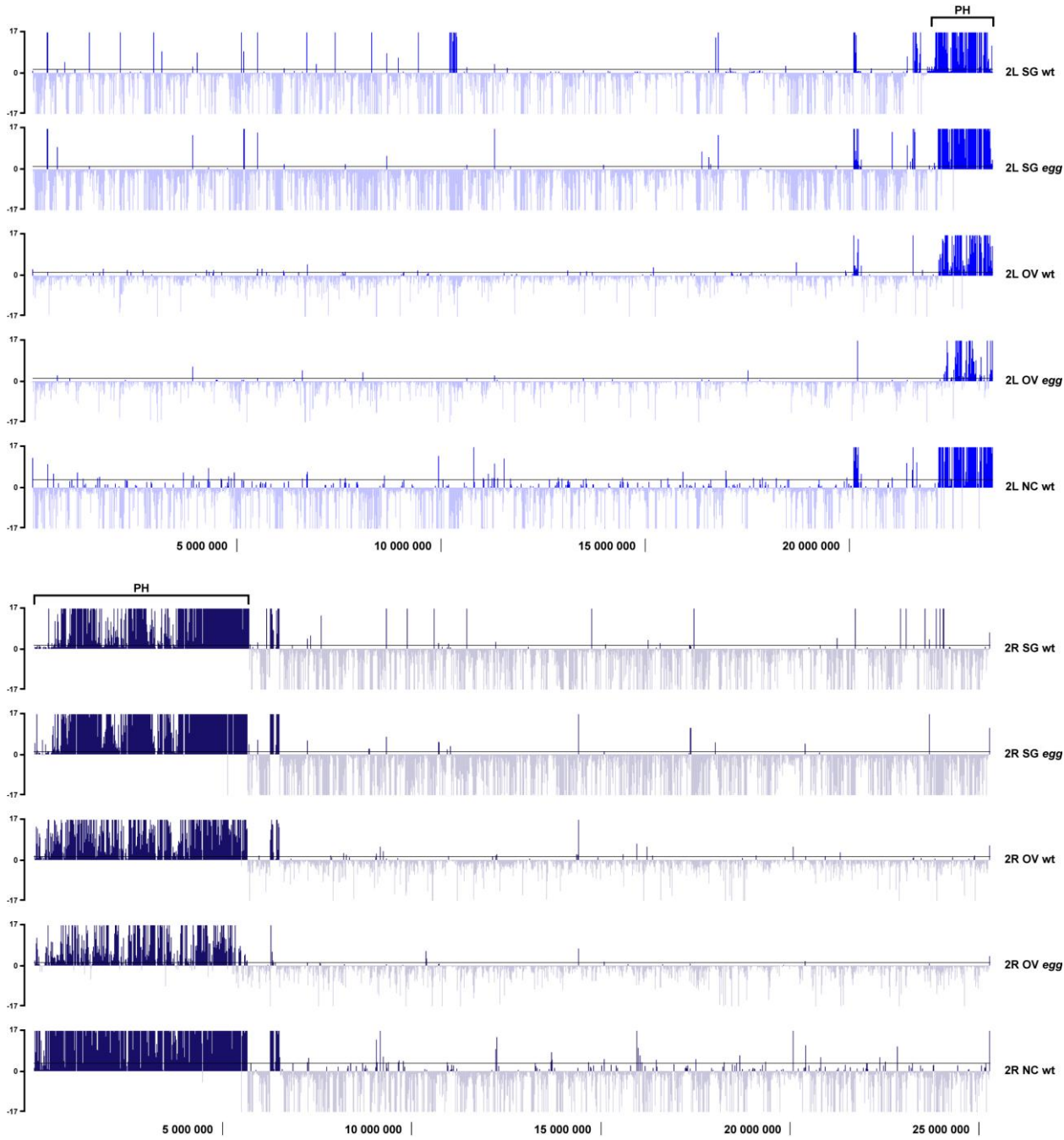
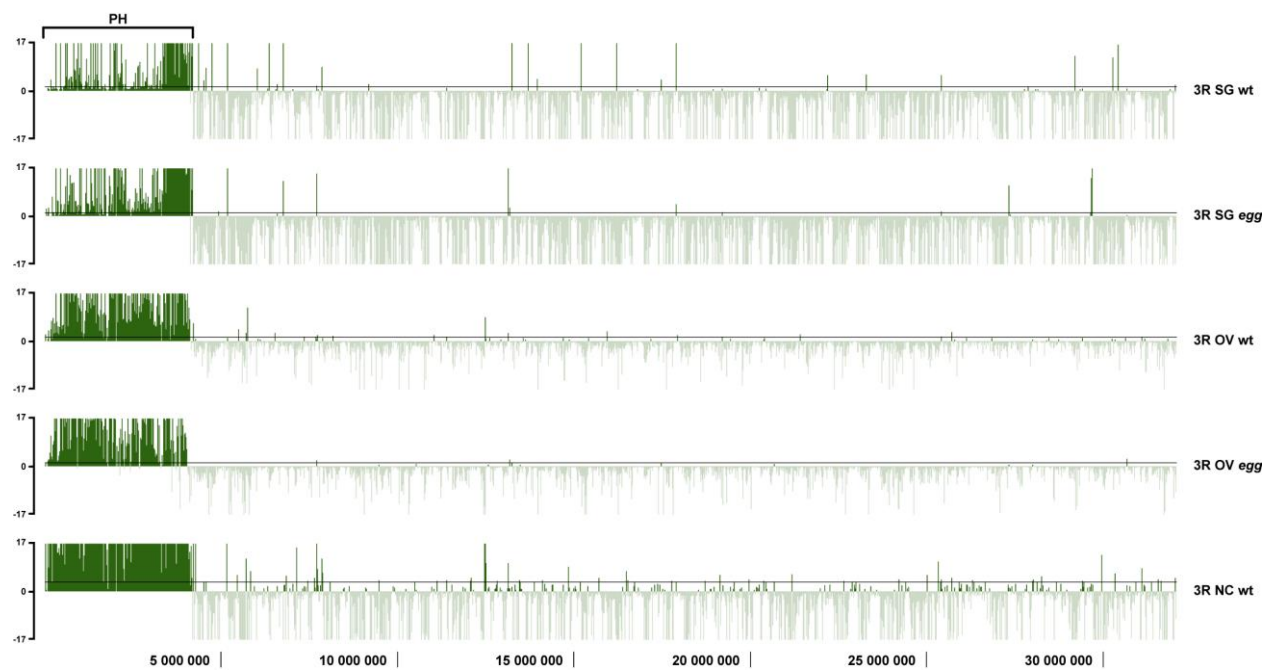
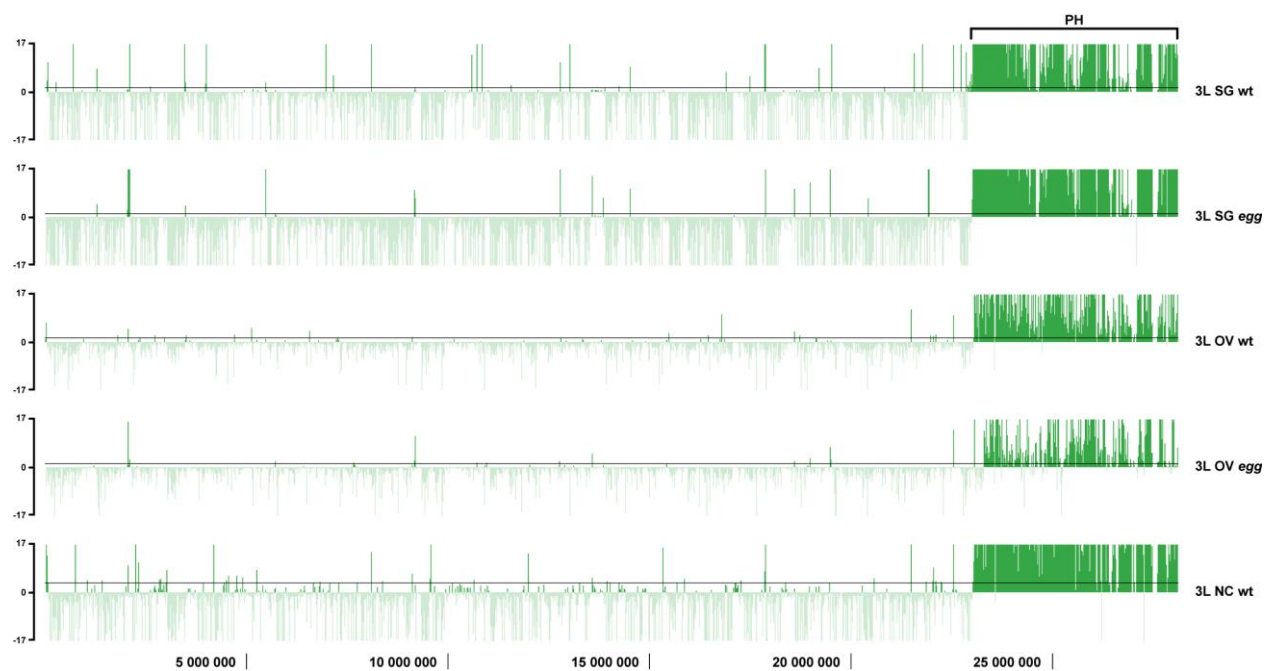
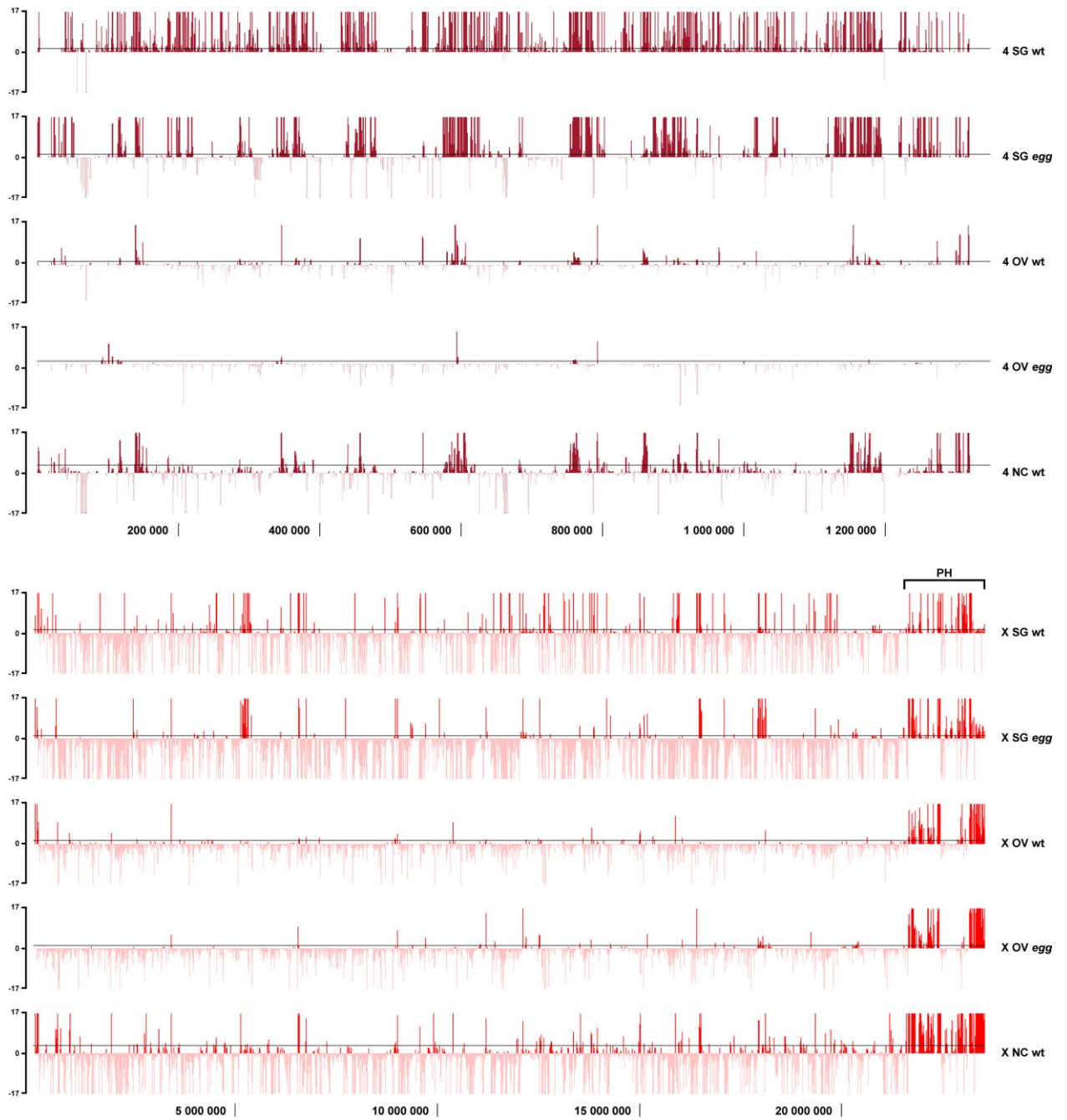


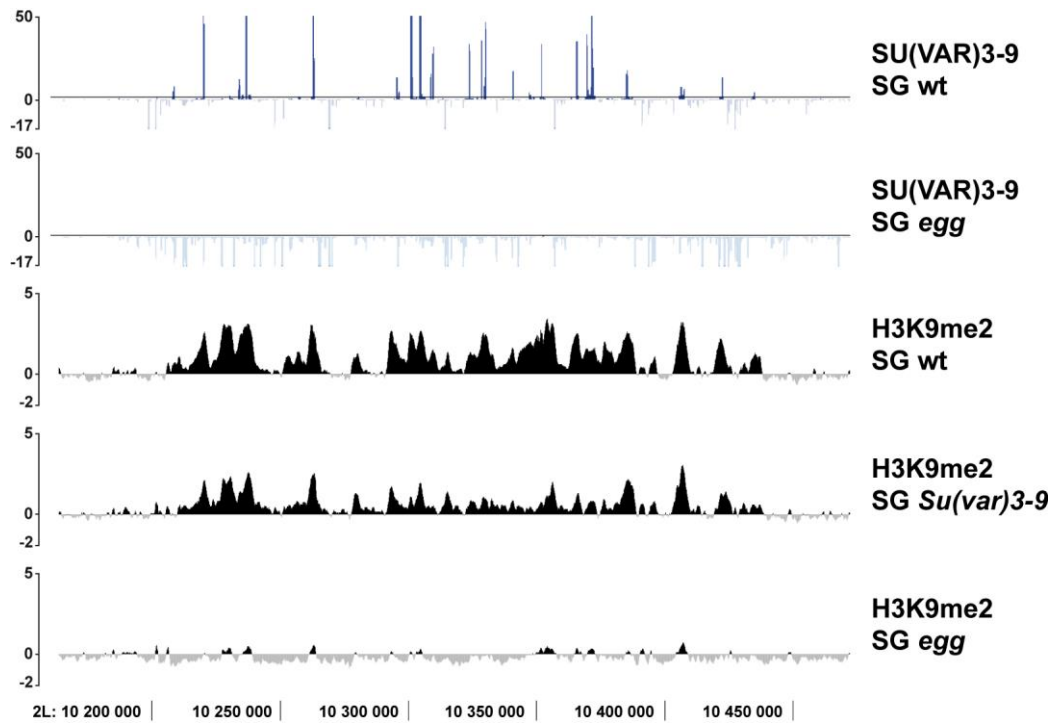
Supplementary materials



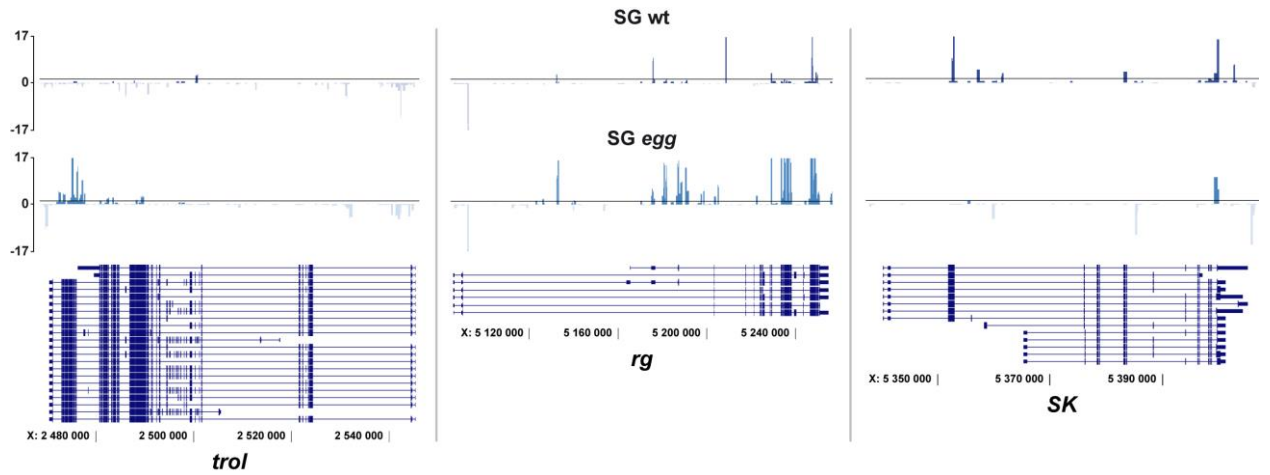




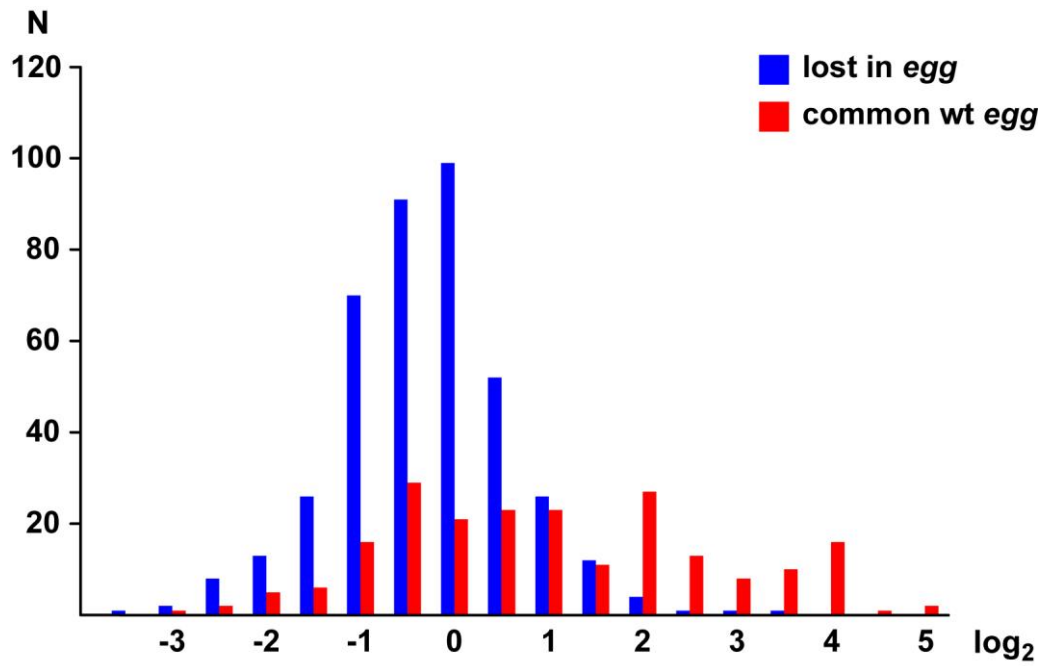
**Figure 1.** General view of SU(VAR)3-9 binding profiles in the chromosomes from all the samples. SG – salivary glands, OV – juvenile ovaries (mainly consisting of germarium cells), NC – mature nurse cells, wt – wild type, *egg* – *eggless* mutation. Data for SG *egg*, OV wt, and OV *egg* are obtained in the present study, data for SG wt and NC wt are taken from [28]. PH – pericentric heterochromatin. Axis labels are the same as in **Figure 2**.



**Figure S2.** SU(VAR)3-9 binding (colored profiles) and H3K9me2 distribution (black profiles) in the region 31B-E of the chromosome arm 2L in salivary glands (SG) of wild type (wt), *egg*, and *Su(var)3-9* mutant larvae. SU(VAR)3-9 SG wt profile is taken from [28]. H3K9me2 profiles have been retrieved from the raw data reported by [35]. Axis labels are the same as in **Figure 7**.



**Figure S3.** SU(VAR)3-9 binding profiles across the genes *trol*, *rg*, and *SK* in the salivary glands (SG) of wild type (wt) and *egg* mutant larvae. SU(VAR)3-9 SG wt profile is taken from [28]. Axis labels are the same as in **Figure 2**.



**Figure S4.** Distribution of gene numbers in “lost in *egg*” and “common wt *egg*” gene sets, based on the relative contribution of *Su(var)3-9* vs *egg* to H3K9me2 levels. For each gene, the difference between *egg* and wild type values, as well as between *Su(var)3-9* and wild type values are calculated as log ratio. The latter is subtracted from the former. X axis shows the resulting values (in increments of 0.5), Y axis shows the number of genes in each group (N).