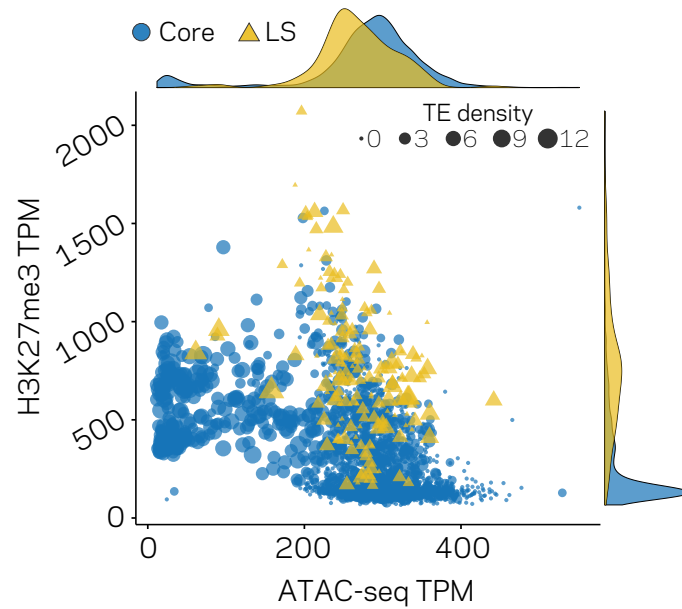


## Original Observations, shown in Fig. 4D



## Updated classifications based on consensus predictions

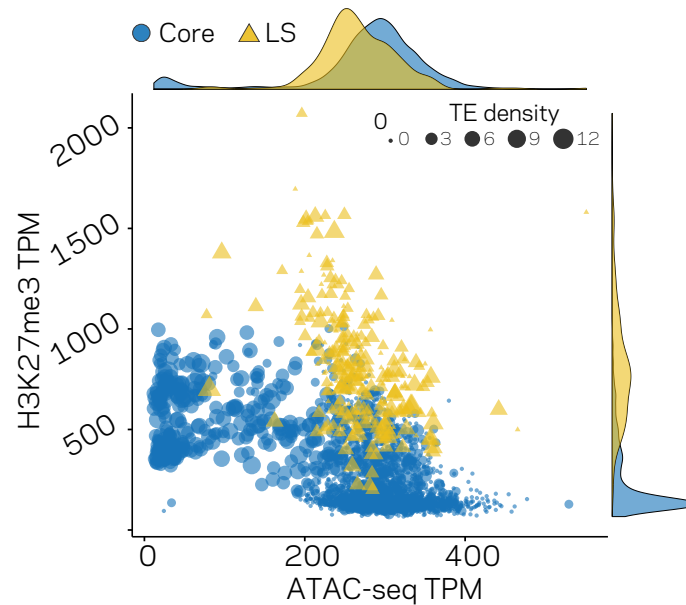


Figure 6- figure supplement 5. Genome model of core and LS regions defined by epigenetics and chromatin status. (Top) The genome of *V. dahliae* was split into 10 kb windows, and labeled as core or LS based on previous observations, shown in Fig. 4D, re-shown here for comparison. (Bottom) Same 10 kb genomic windows and data, but the regions are now defined as core and LS based on the consensus machine learning predictions. The core regions are shown in blue as circles. LS regions shown as yellow triangles. Points are plotted according to TPM ATAC-seq signal (x-axis) and H3K27me3 ChIP-seq TPM (y-axis). The size of each point is proportional to the number of TEs in the 10 kb window, shown as TE density. The marginal density plots are shown opposite of the respective axis.