



Figure 4- figure supplement 1. Principle component analysis for seven variables genome wide at 10 kb window. Each genomic window is shown as a point on the graph, with the windows in the core colored as blue circles and LS as yellow triangles. Colored ellipses show the confidence interval for the core and LS elements with a single large symbol to show the mean. The amount of variation for the first and second dimensions are shown in parentheses. mCG- Log2 weighted cytosine DNA methylation for CG; %GC - The percent GC sequence content; RNAseq-PDB- TPM for RNA-sequencing reads from Potato Dextrose Broth (PDB); H3K9me3 and H3K27me3 - TPM values of mapped reads from ChIP sequencing using anti-bodies against the respective histone modifications; ATAC-seq - TPM values of mapped reads from Assay for Transposase Accessible Chromatin.