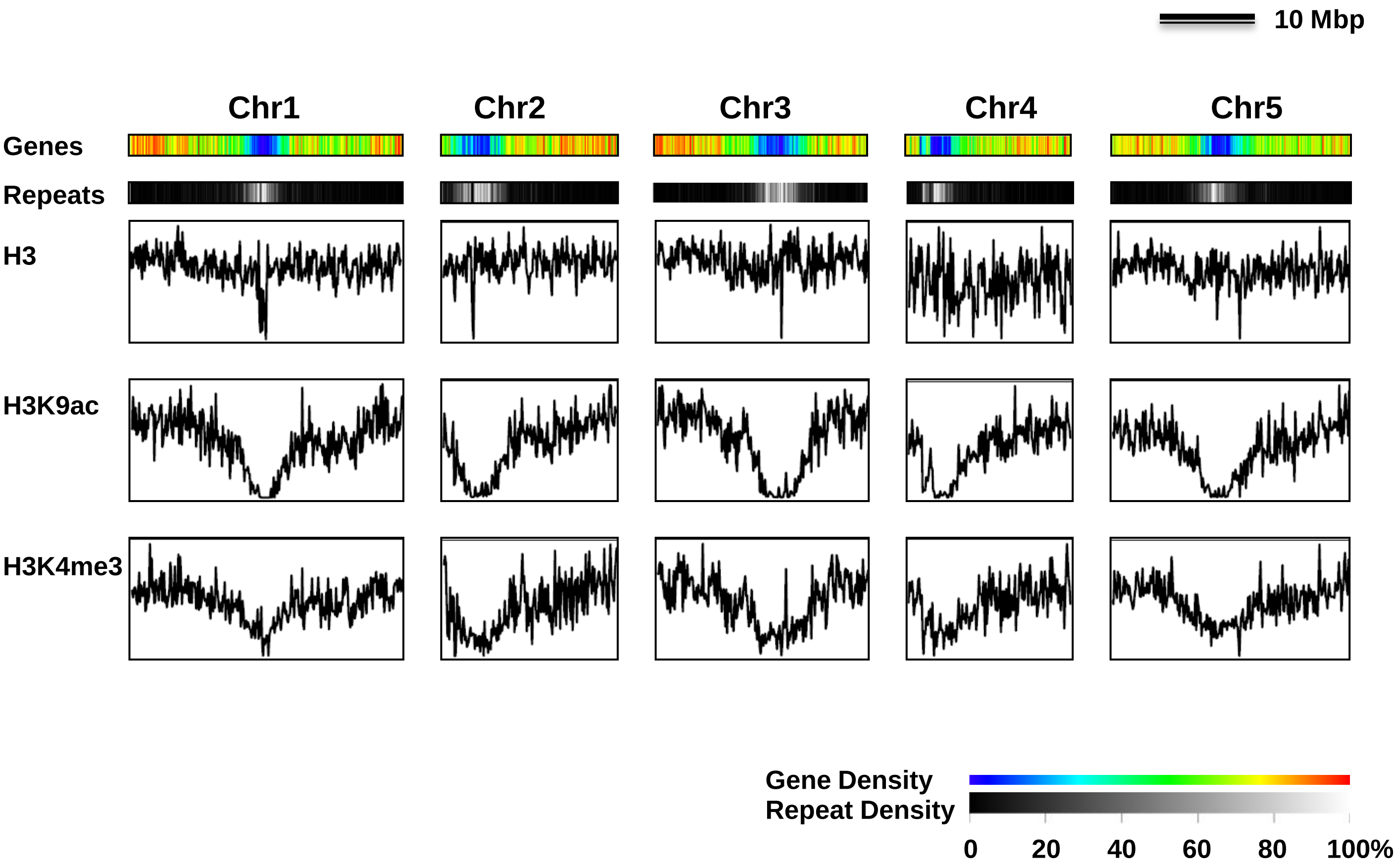
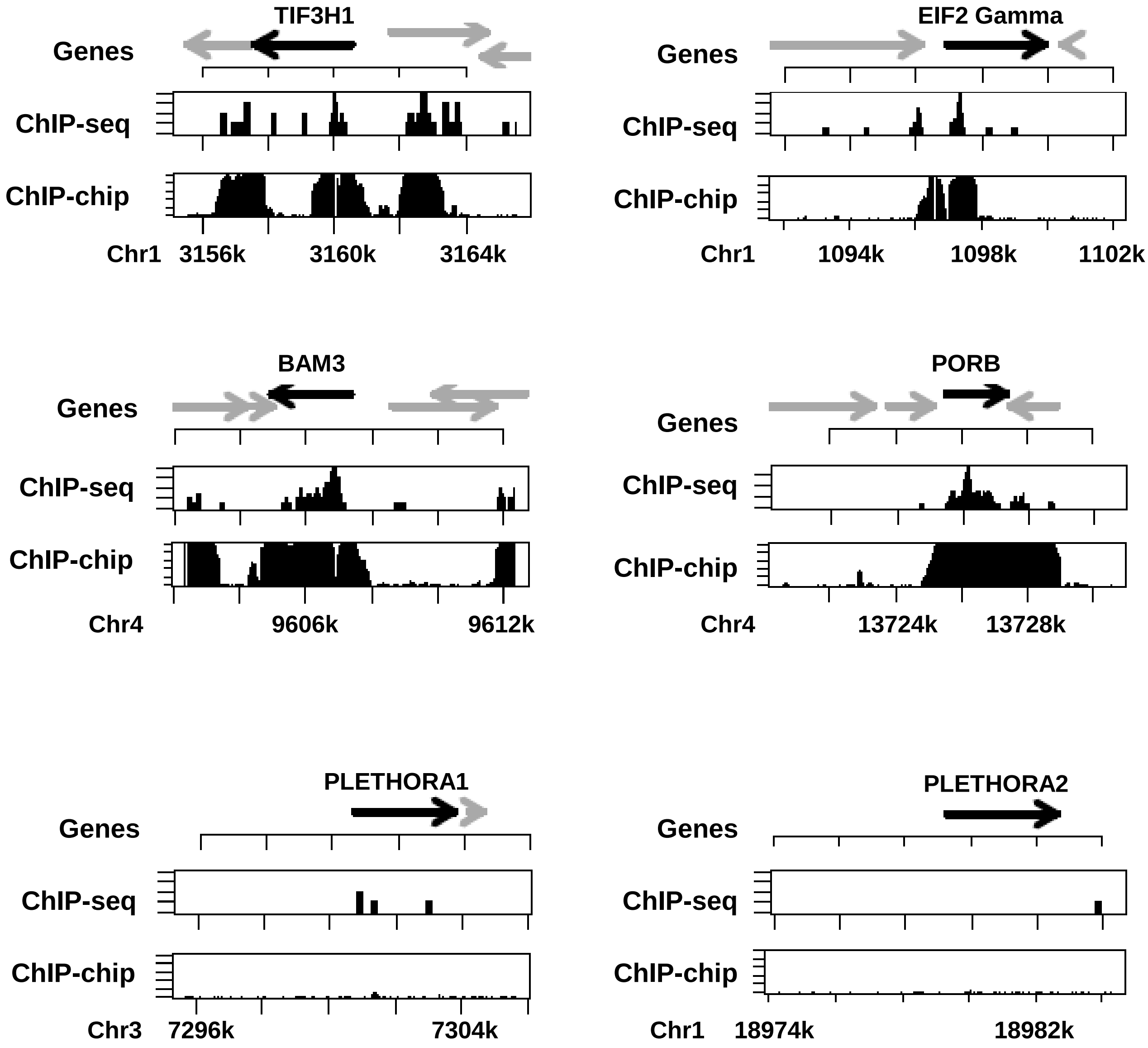
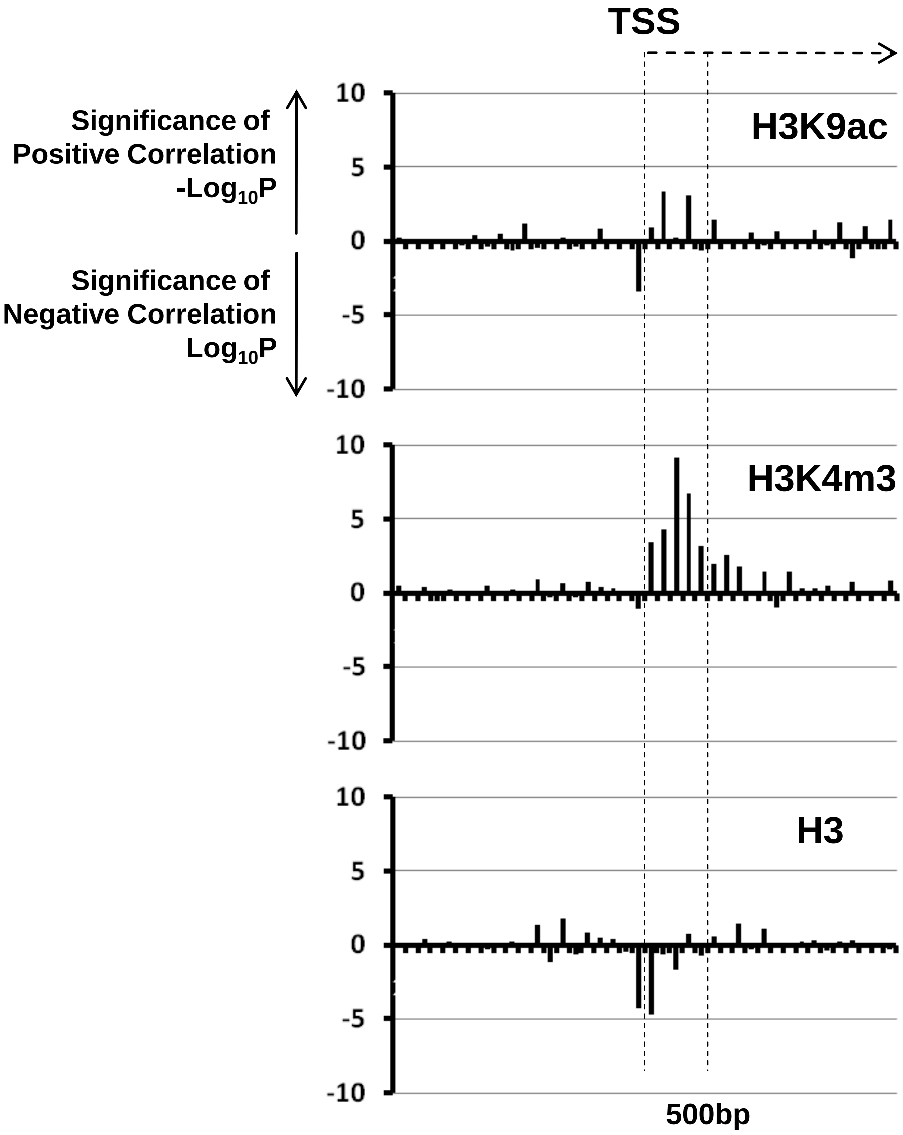


Supplementary Figure 1. Genome-wide view of H3, H3K9Ac and H3K4me3 densities in 100kb window. Y-axes are proportion of genomic region showing H3, H3K9Ac, H3K27me3 in 100kb window.

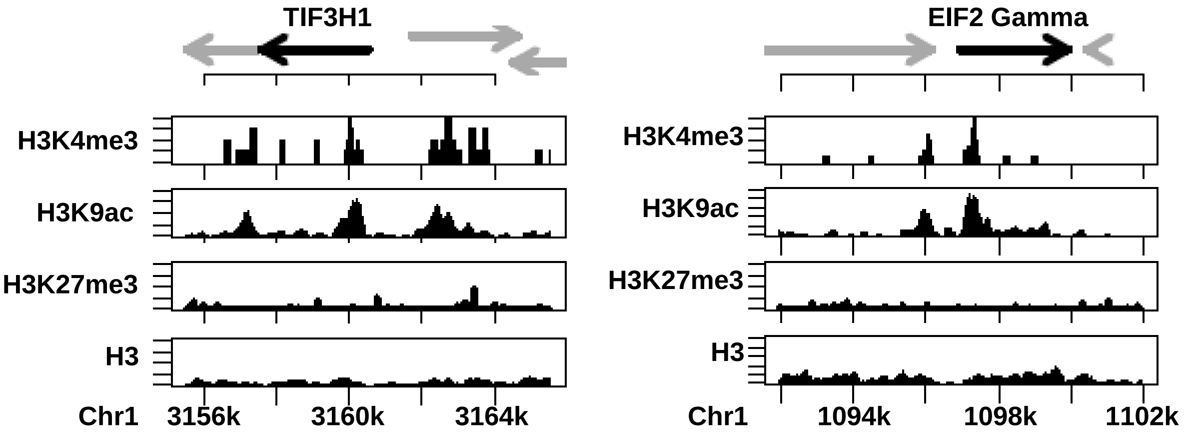


Supplementary Figure 2. Comparison of H3K4me3 distributions from our ChIP-seq and ChIP-chip. Using ChIP-seq, we could identify occupations of histone modification in high resolution. The results from ChIP-chip data may be different from that of ChIP-seq due to limitation of probe composition and cross-hybridization among homologous sequences in ChIP-chip. ChIP-chip data of H3K4me3 were obtained from Zhang et al.

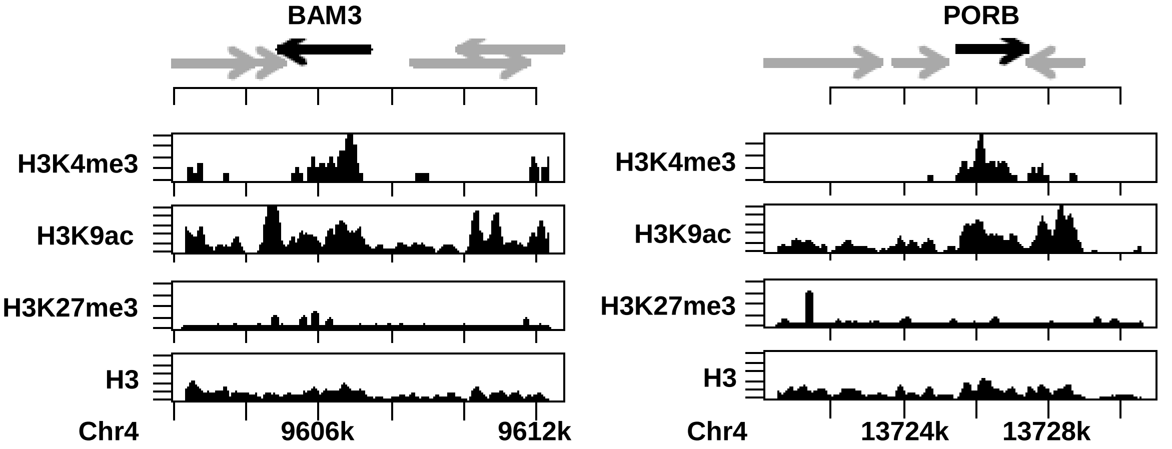


Supplementary Figure 3. Multiple linear regression with transcription level and chromatin modifications at each position around TSS.

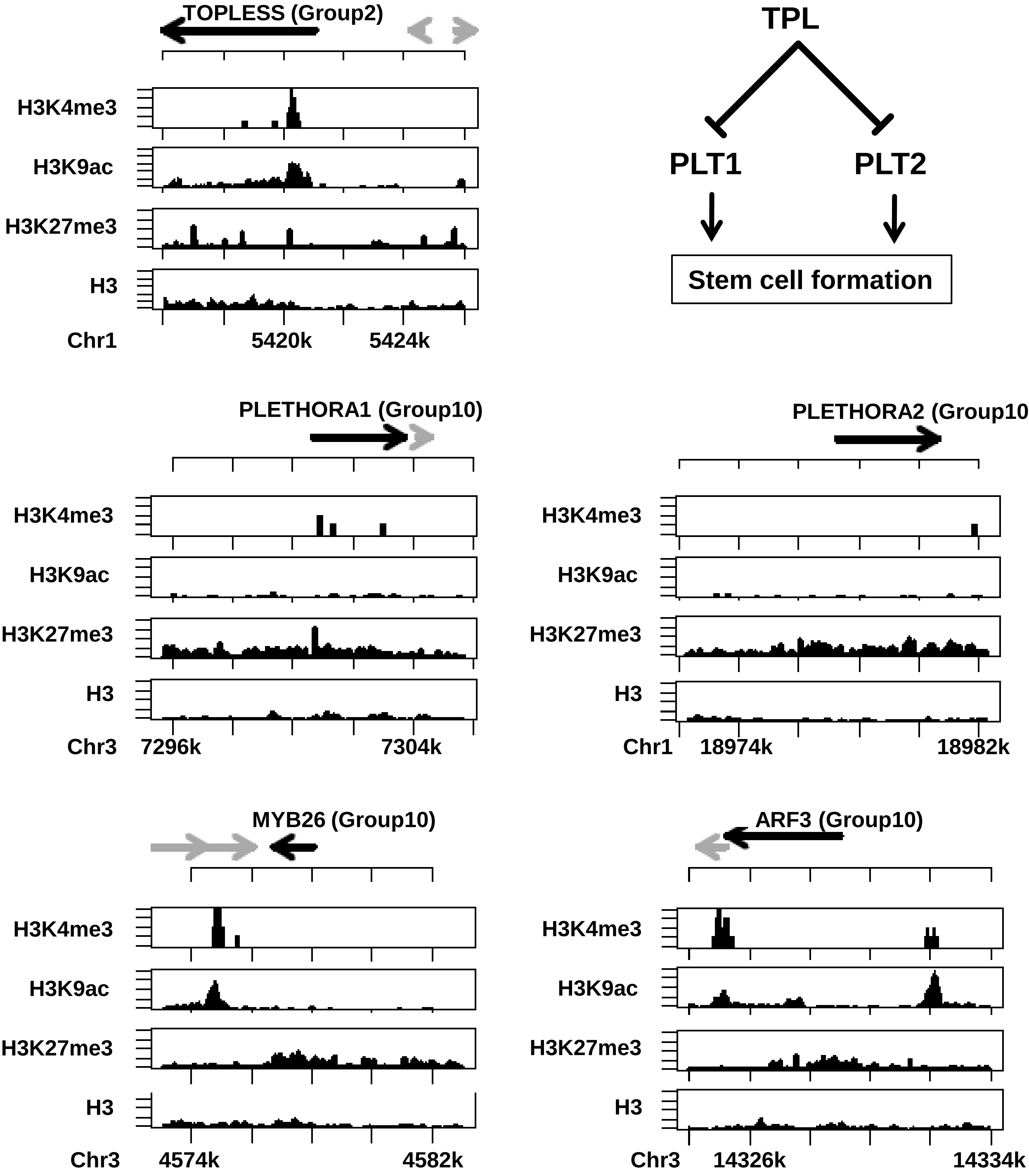
Translation Initiation Factors (Group1)



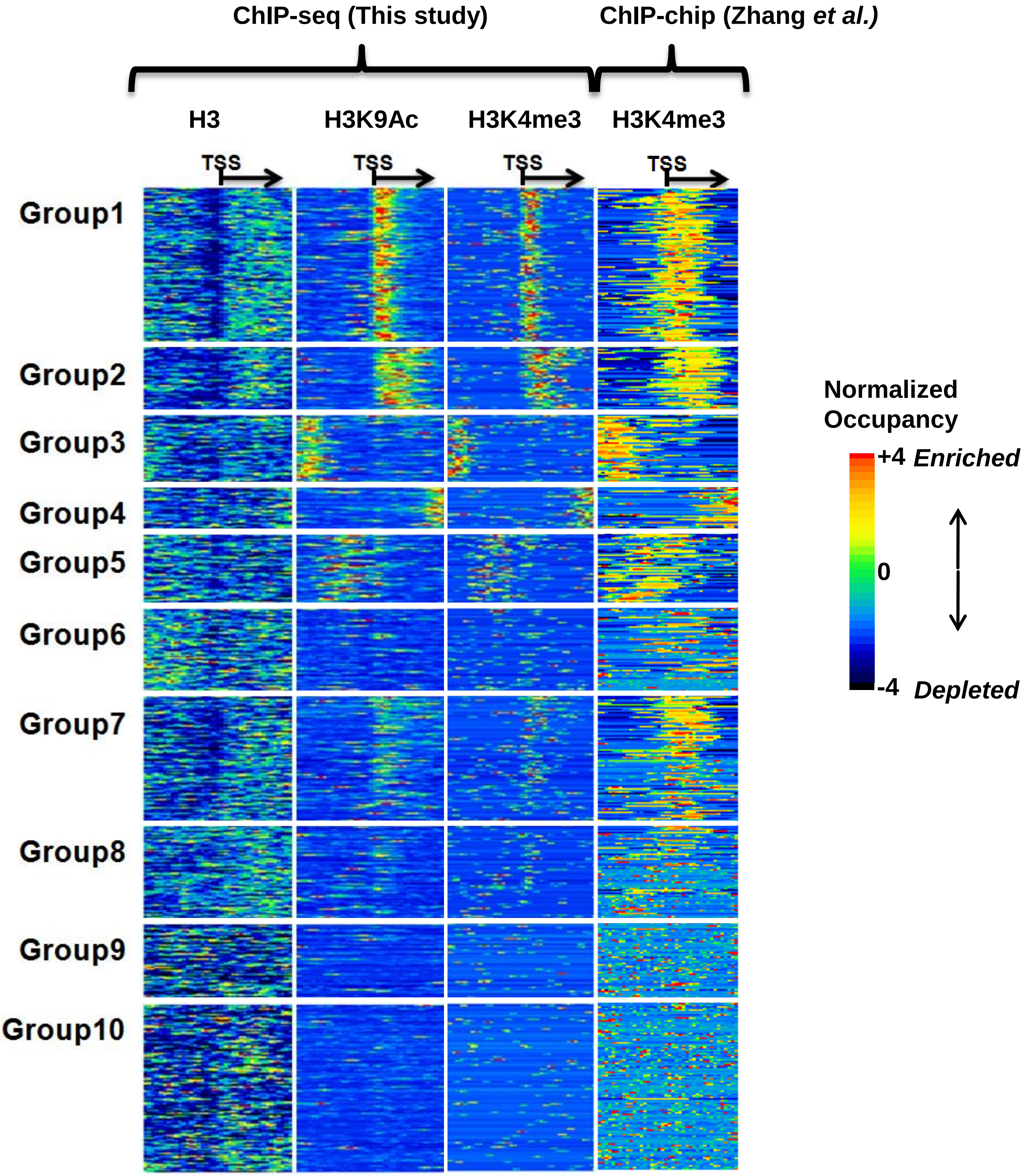
Photosynthesis genes (Group 2)



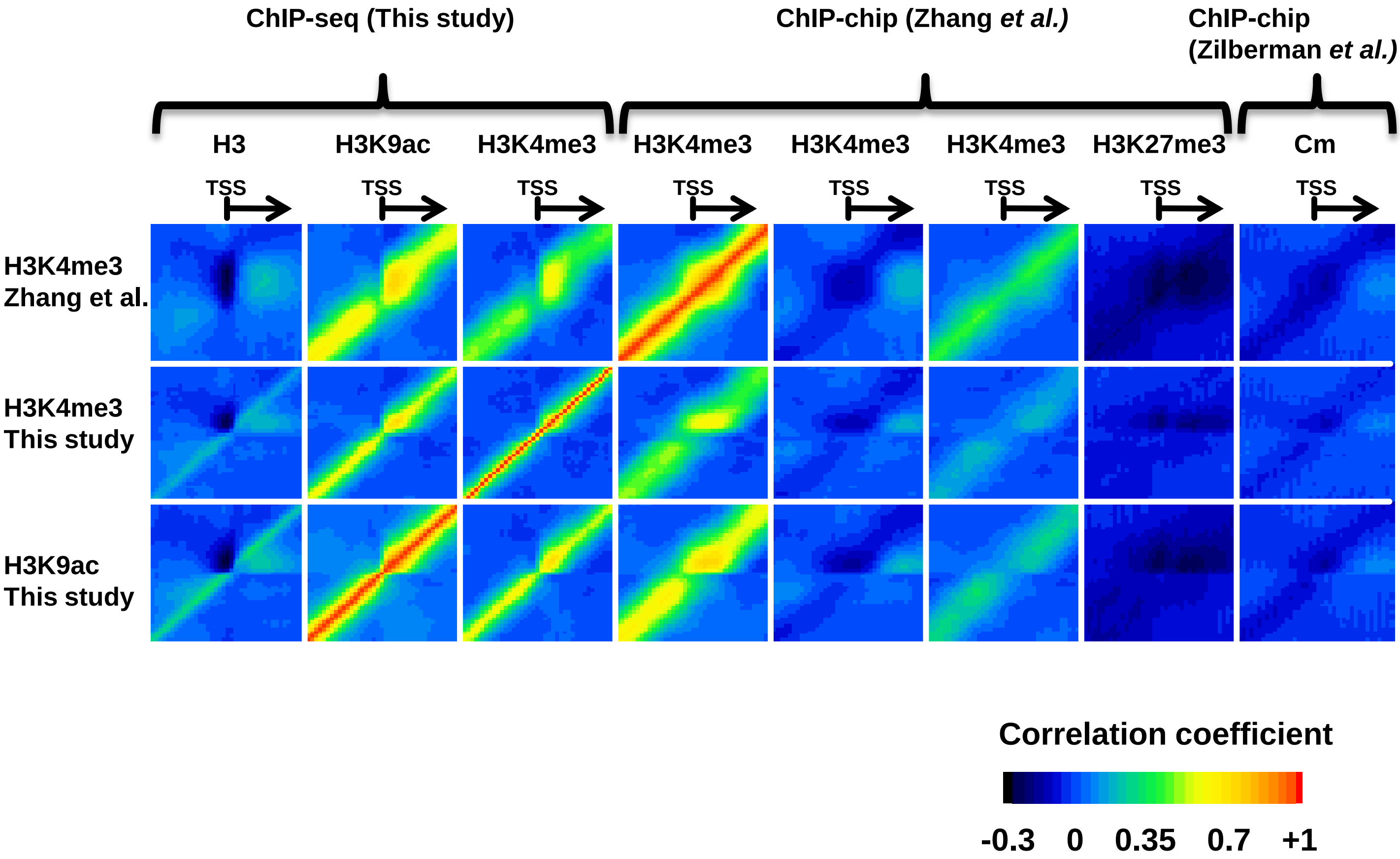
Supplementary Figure 4. Detailed view of the genes in Group1 and Group2. Normalized occupancy of H3K4me3, H3K9ac and H3 around TIF3H1 (AT1G10840, Translation Initiation Factor H1) and EIF2 gamma (AT1G04170, Eukayotic Initiation Factor 2 gamma subunit). H3K27me3 is from ChIP-chip. BAM3(AT4G17090) encodes chloroplast beta-amylase. Inhibition of BAM3 by RNAi leads to failure of maltose accumulation during cold shock. PORB(AT4G27440, protochlorophyllide oxidoreductase B) encodes light-dependent NADPH and involved in chlorophyll biosynthesis and photosynthesis pathway.



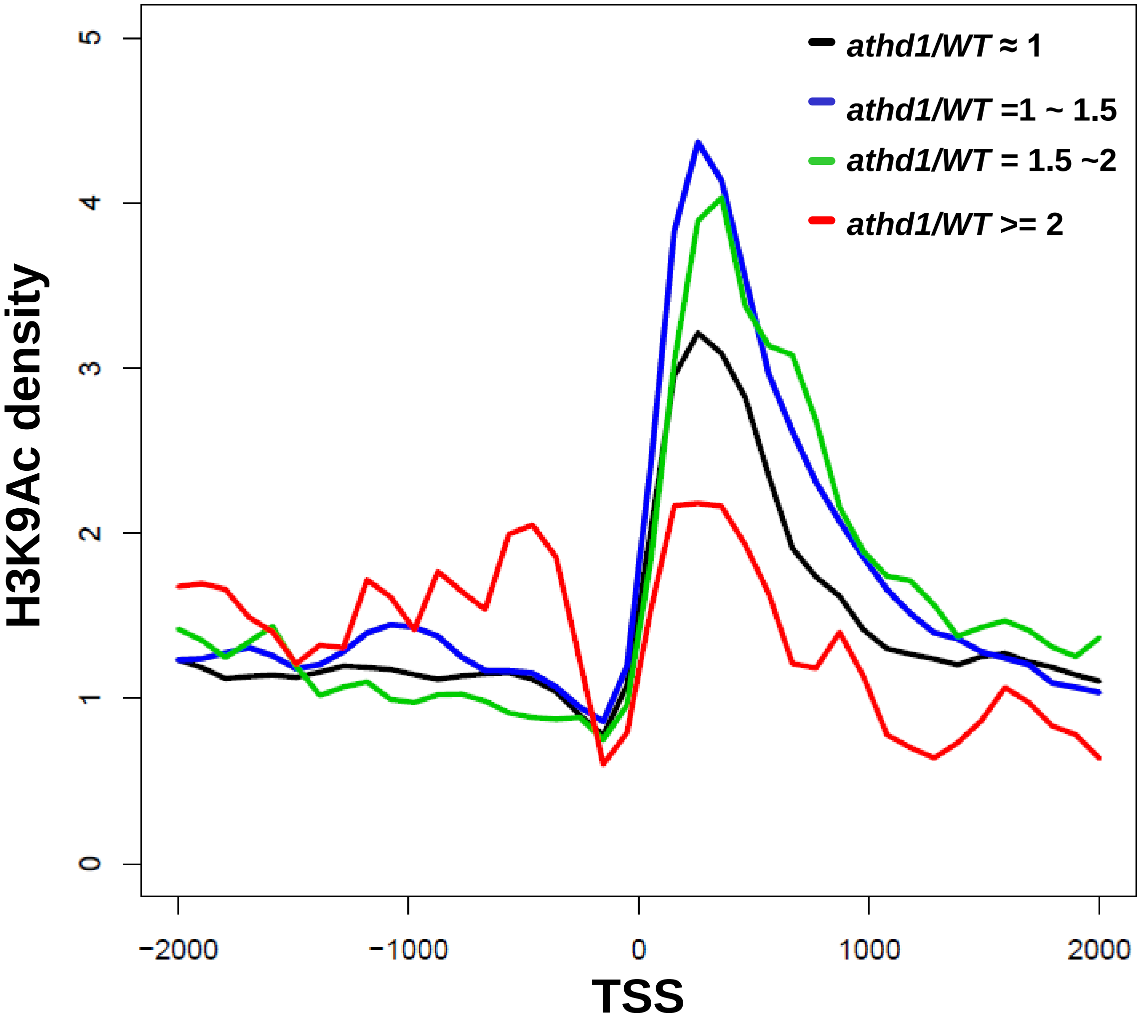
Supplementary Figure 5. **Detailed view of histone modifications around transcription factors involved in pattern specification.** PLT1 (AT3G20840, PLETHORA1) and PLT2 (AT1G51190, PLETHORA2) are essential genes for formation of stem cells. These genes show extensive H3K27m3 around and within genes. PLT1 and PLT2 are co-repressed by TPL (AT1G15750, TOPLESS). TPL show high level of H3K4m3 and H3K9Ac at the 5' end of gene.



Supplementary Figure 6. Comparison of H3K4me3 distribution using two H3K4me3 genome-wide ChIP data sources. Individual rows stand for occupancy of histone modification. The signals from ChIP-chip data show wider distribution. That may be because ChIP-chip values are affected by probe composition and probe length.



Supplementary Figure 7. **Consistent relationships among histone modifications**



Supplementary Figure 8. H3K9Ac enrichment around gene sets up-regulated in AtHD1 mutants with fold changes ≈1, 1~1.5, 1.5~2 and greater than 2.