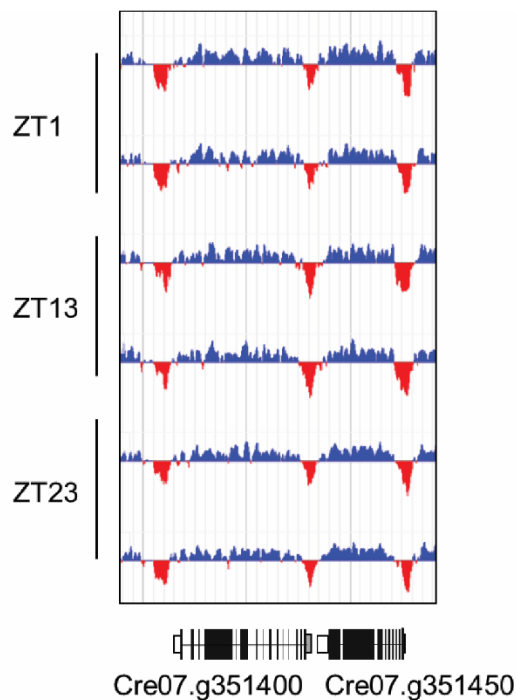
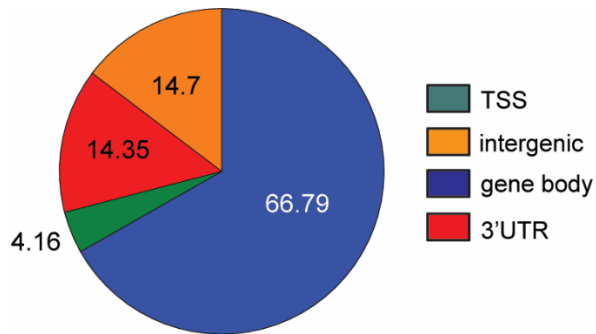


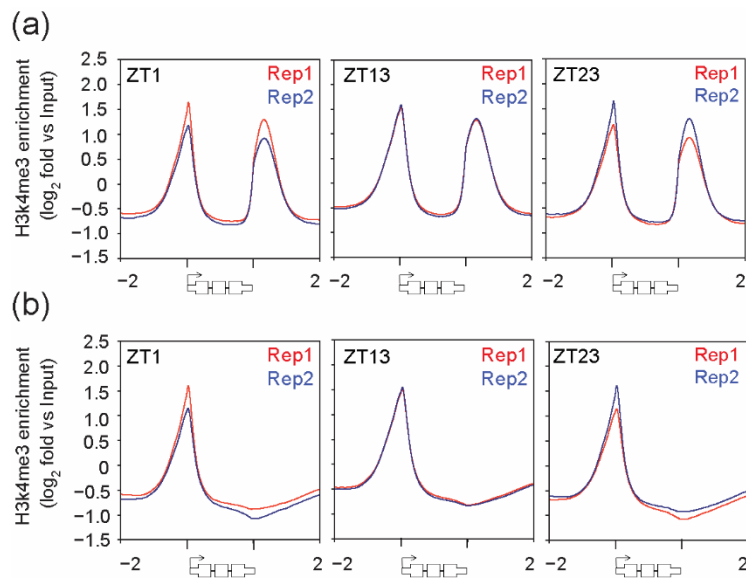
Supporting Figure 1. Cross-reactivity of H3K4me1 and H3K4me3 antibodies against *Chlamydomonas* cell lysate. Whole-cell protein lysates corresponding to 2×10^5 cells from *Chlamydomonas* were separated on an SDS-containing polyacrylamide (15% monomer) gel and analyzed by immuno-detection using antibodies against histone H3K4me1 or histone H3K4me3 as indicated.



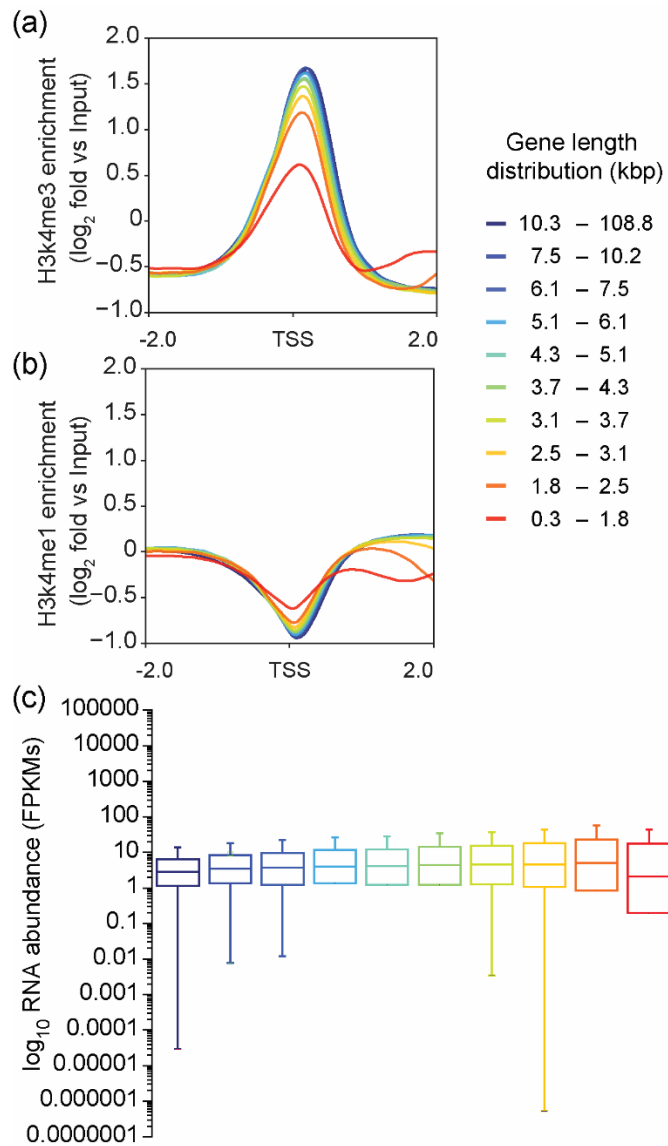
Supporting Figure 2. Genome browser view of H3K4me1 depleted regions at a representative genomic region. Shown are replicate ChIP-seq tracks from samples taken at Zeitgeber Time (ZT): ZT1, ZT13 and ZT23 as indicated. Introns are drawn as black line, exons as black bars, 5'UTRs are shown as white bars, while 3'UTRs are shown as grey bars.



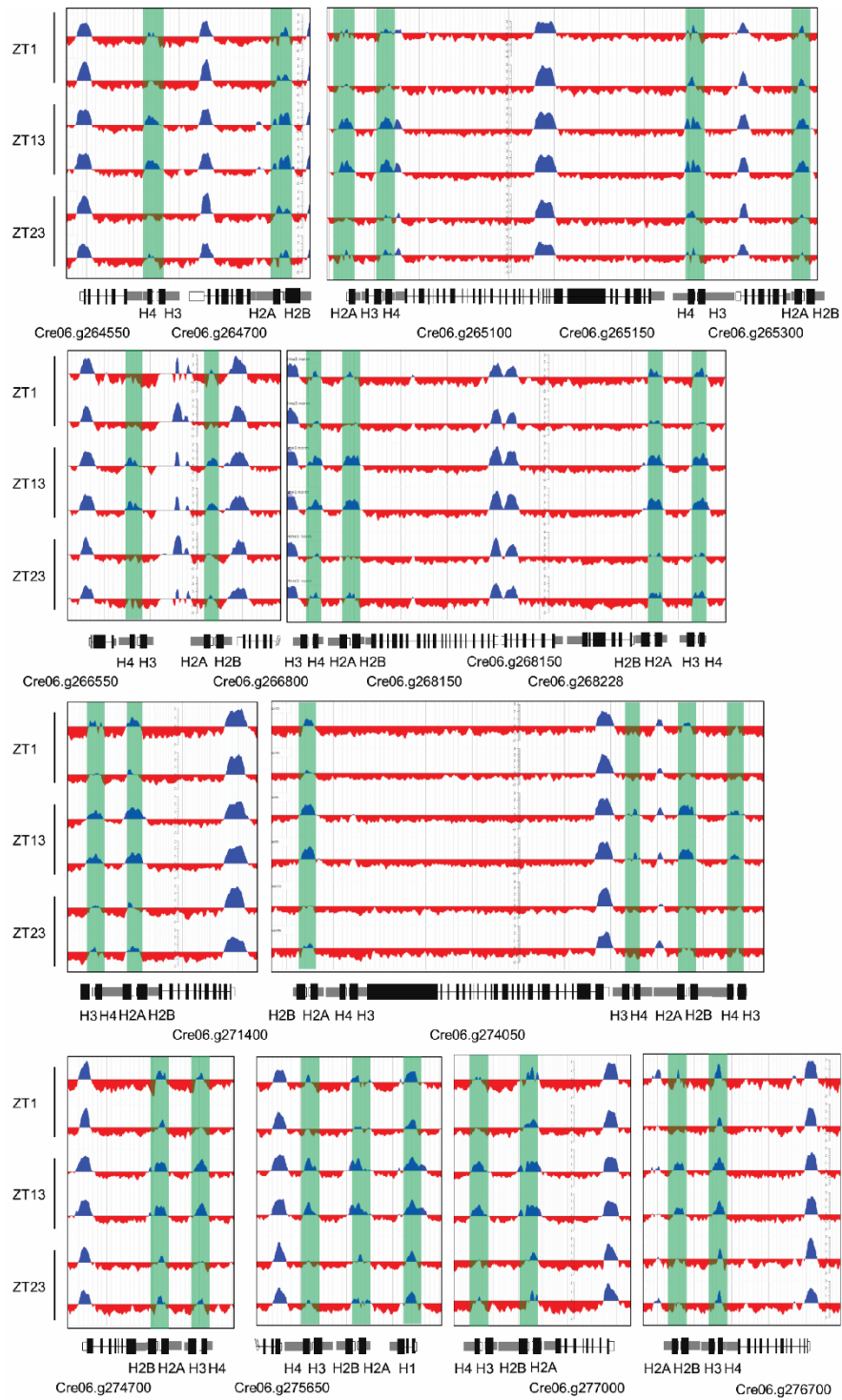
Supporting Figure 3. Relative distribution of genomic features such as transcription start sites (TSSs, cyan), intergenic regions (orange), gene bodies – introns and exons (blue) and 3'UTRs (red) in the *Chlamydomonas* genome.



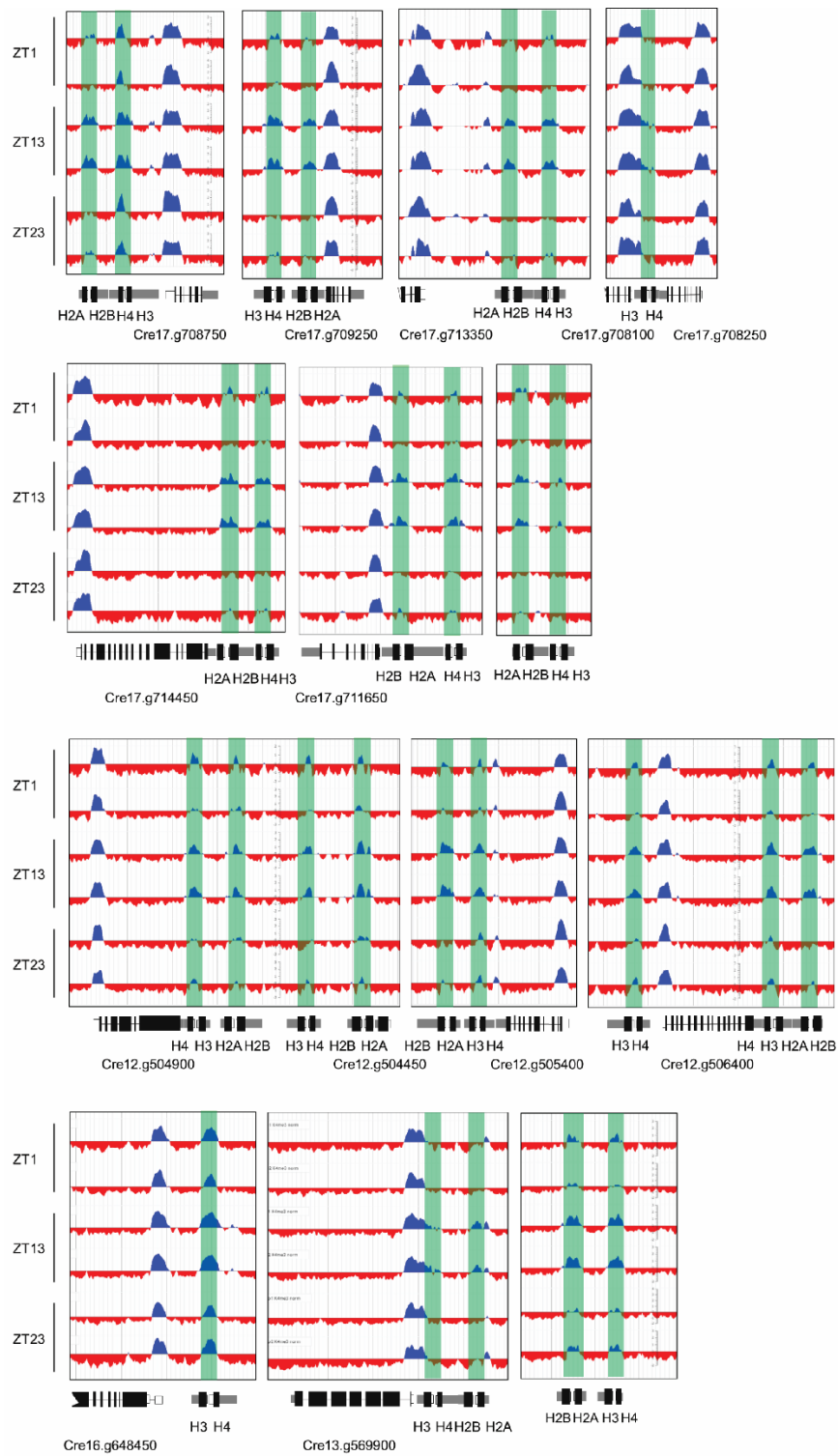
Supporting Figure 4. Gene wide distribution of H3K4me3 along two different subsets of *Chlamydomonas* genes. Graphs showing density plots of H3K4me3 enrichment from two independent replications in red or blue, respectively, at each of three time points. The first subset (a) constitutes 5643 genes where the TTS of the reference gene is adjacent to the TSS of its neighboring gene, while the subset of 7438 genes in (b) show genes in a tail-to-tail configuration where the TTS of the reference gene is adjacent to the TTS of its neighboring gene (tail to tail orientation). For these profiles, each gene was scaled to the same length and signal enrichments were displayed for the scaled gene lengths and 2kb upstream/downstream of its transcription start site (TSS)/termination site (TTS).



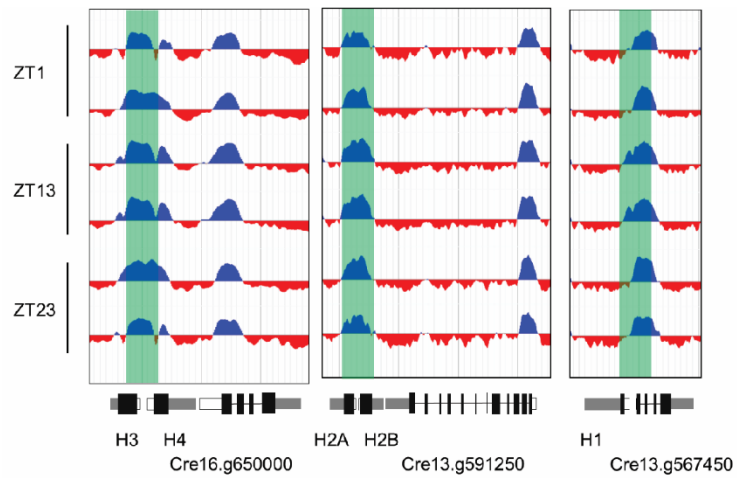
Supporting Figure 5. Correlation between gene length, histone lysine 4 methylation and gene expression. Density blots showing (a) H3K4me3 enrichment and (b) H3K4me1 enrichment against input in all time points. Genes were separated in groups by gene length from 1 to 10. (c) Boxplots showing expression values in FPKMs of all gene groups (1 to 10).



Supporting Figure 6. Genome browser view of dynamic histone H3K4me3 peaks at replication dependent expressed histone gene loci. Shown are replicate ChIP-seq tracks from samples taken at ZT1, ZT13 and ZT23 as indicated. displaying H3K4me3 enrichment at histone gene promoters are highlighted in green. Introns are drawn as black line, exons as black bars, 5'UTRs are shown as white bars, while 3'UTRs are shown as grey bars.



Supporting Figure 7. Genome browser view of dynamic histone H3K4me3 peaks at replication dependent expressed histone gene loci. Shown are replicate ChIP-seq tracks from samples taken at ZT1, ZT13 and ZT23 as indicated. displaying H3K4me3 enrichment at histone gene promoters are highlighted in green. Introns are drawn as black line, exons as black bars, 5'UTRs are shown as white bars, while 3'UTRs are shown as grey bars.



Supporting Figure 8. Genome browser view of stable histone H3K4me3 peaks at replication independent expressed histone gene loci. Shown are replicate ChIP-seq tracks from samples taken at ZT1, ZT13 and ZT23 as indicated. Introns are drawn as black line, exons as black bars, 5'UTRs are shown as white bars, while 3'UTRs are shown as grey bars.