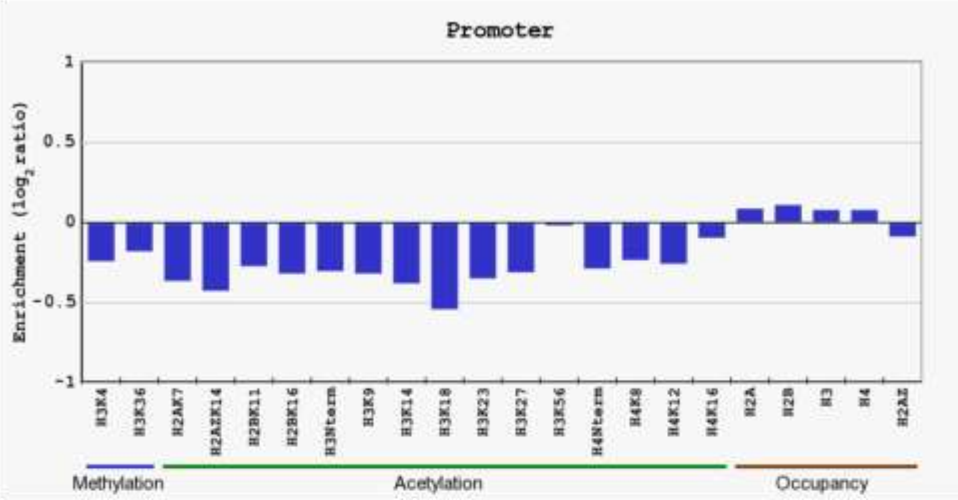
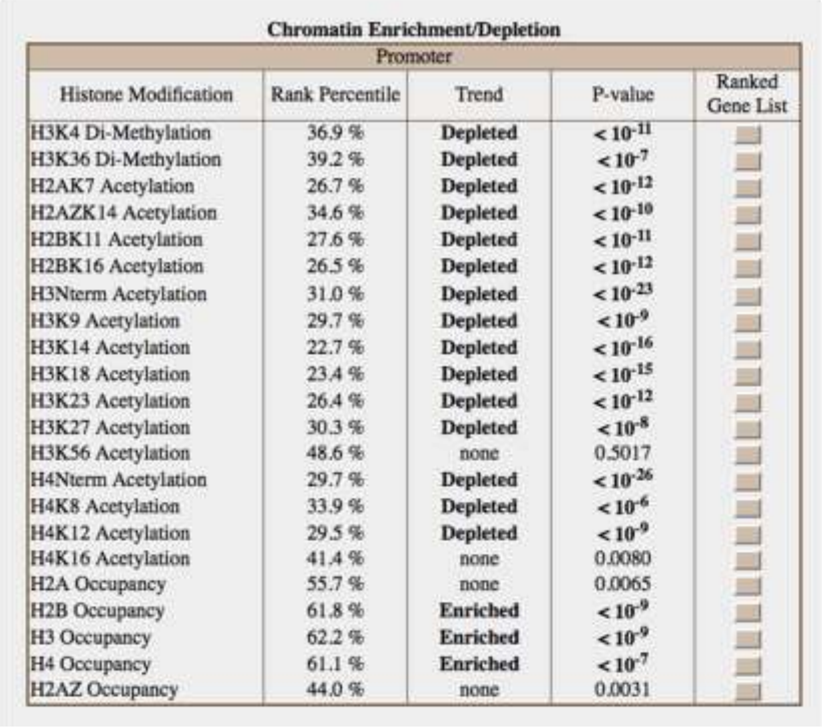
A



B



**Chromatin Enrichment/Depletion**

| Promoter | | | | |
|---|---|---|---|---|
| Histone Modification | Rank Percentile | Trend | P-value | Ranked Gene List |
| H3K4 Di-Methylation | 36.9 % | **Depleted** | $< 10^{-11}$ | |
| H3K36 Di-Methylation | 39.2 % | **Depleted** | $< 10^{-7}$ | |
| H2AK7 Acetylation | 26.7 % | **Depleted** | $< 10^{-12}$ | |
| H2AZK14 Acetylation | 34.6 % | **Depleted** | $< 10^{-10}$ | |
| H2BK11 Acetylation | 27.6 % | **Depleted** | $< 10^{-11}$ | |
| H2BK16 Acetylation | 26.5 % | **Depleted** | $< 10^{-12}$ | |
| H3Nterm Acetylation | 31.0 % | **Depleted** | $< 10^{-23}$ | |
| H3K9 Acetylation | 29.7 % | **Depleted** | $< 10^{-9}$ | |
| H3K14 Acetylation | 22.7 % | **Depleted** | $< 10^{-16}$ | |
| H3K18 Acetylation | 23.4 % | **Depleted** | $< 10^{-15}$ | |
| H3K23 Acetylation | 26.4 % | **Depleted** | $< 10^{-12}$ | |
| H3K27 Acetylation | 30.3 % | **Depleted** | $< 10^{-8}$ | |
| H3K56 Acetylation | 48.6 % | none | 0.5017 | |
| H4Nterm Acetylation | 29.7 % | **Depleted** | $< 10^{-26}$ | |
| H4K8 Acetylation | 33.9 % | **Depleted** | $< 10^{-6}$ | |
| H4K12 Acetylation | 29.5 % | **Depleted** | $< 10^{-9}$ | |
| H4K16 Acetylation | 41.4 % | none | 0.0080 | |
| H2A Occupancy | 55.7 % | none | 0.0065 | |
| H2B Occupancy | 61.8 % | **Enriched** | $< 10^{-9}$ | |
| H3 Occupancy | 62.2 % | **Enriched** | $< 10^{-9}$ | |
| H4 Occupancy | 61.1 % | **Enriched** | $< 10^{-7}$ | |
| H2AZ Occupancy | 44.0 % | none | 0.0031 | |

Figure S4. Genes repressed by the H2A R78 sprocket arginine residue have high levels of promoter histone occupancy and low levels of active histone post-translational modifications. (A) Histone occupancy and histone modification levels in the promoter regions of 290 genes repressed by H2A R78 (i.e., genes with induced expression in the H2A R78A mutant). Analysis was performed on published ChIP-chip data sets using the web-based database ChromatinDB (O'CONNOR AND WYRICK 2007). Note, histone modification data were normalized by nucleosome occupancy levels. (B) Statistical analysis of the data shown in part A showing enrichment or depletion of histone occupancy or post-translational modifications.

.