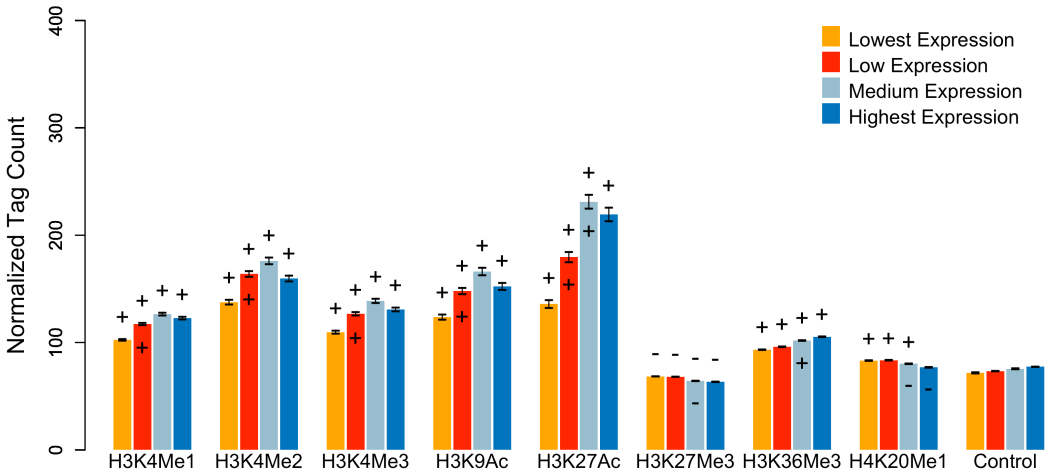
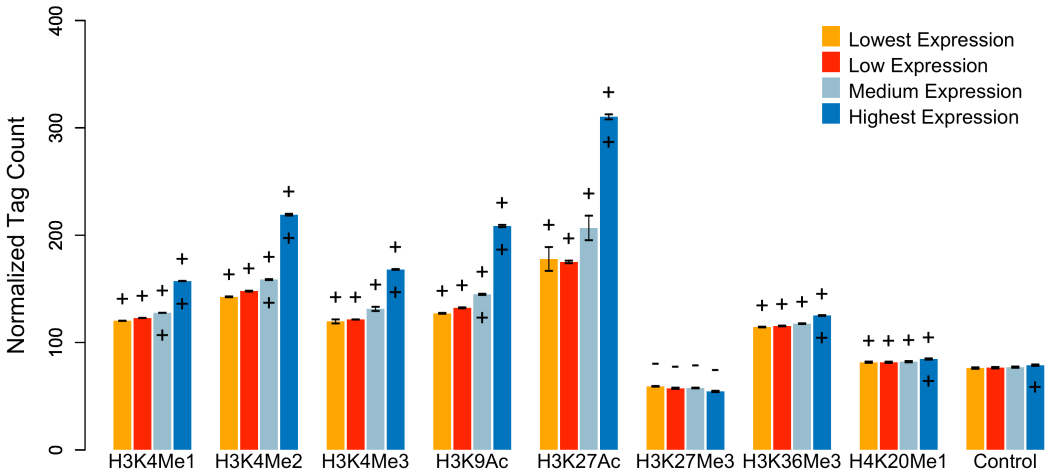
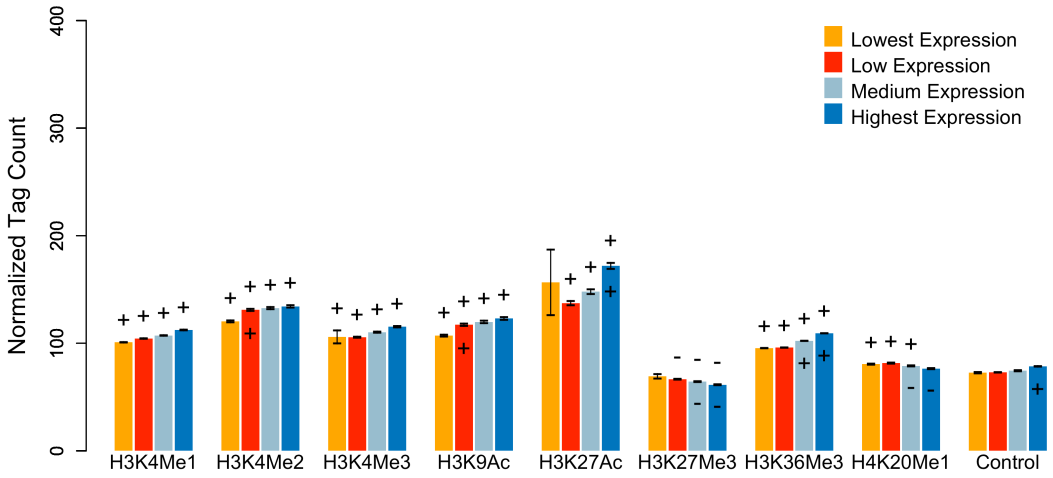


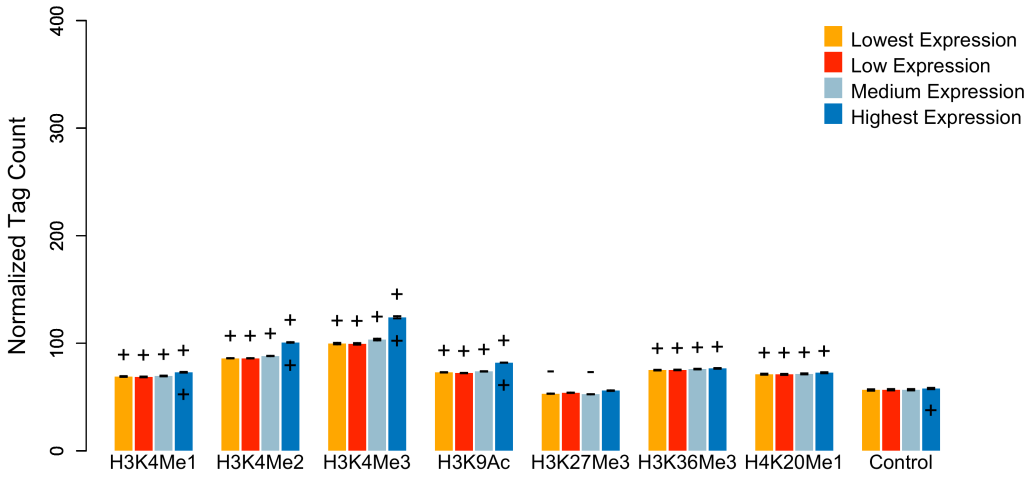
Supplementary Figure S1. Enrichment of chromatin modifications at cis-NAT promoters in GM12878. Cis-NAT promoters in the GM12878 cell type were identified using CAGE data from non-polyadenylated RNA from cytosol isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis-NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



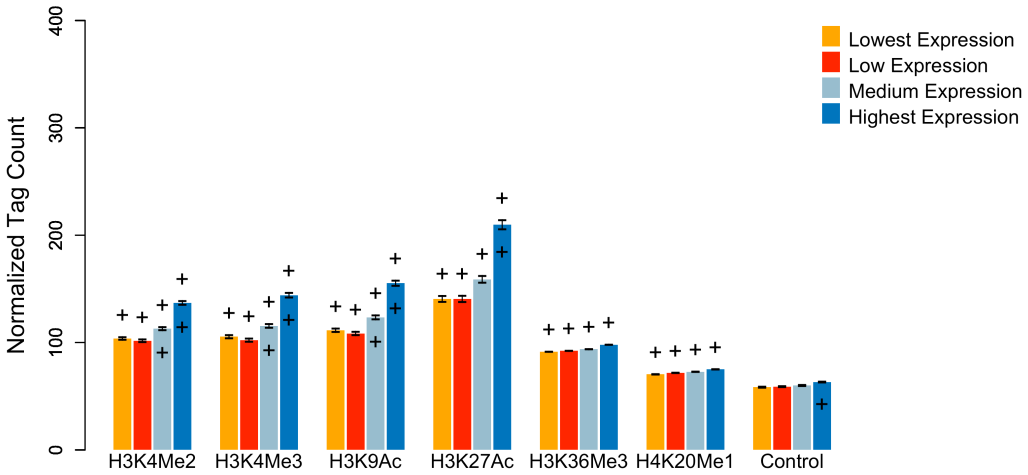
Supplementary Figure S2. Enrichment of chromatin modifications at cis-NAT promoters in GM12878. Cis-NAT promoters in the GM12878 cell type were identified using CAGE data from total RNA from nucleolus isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis-NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



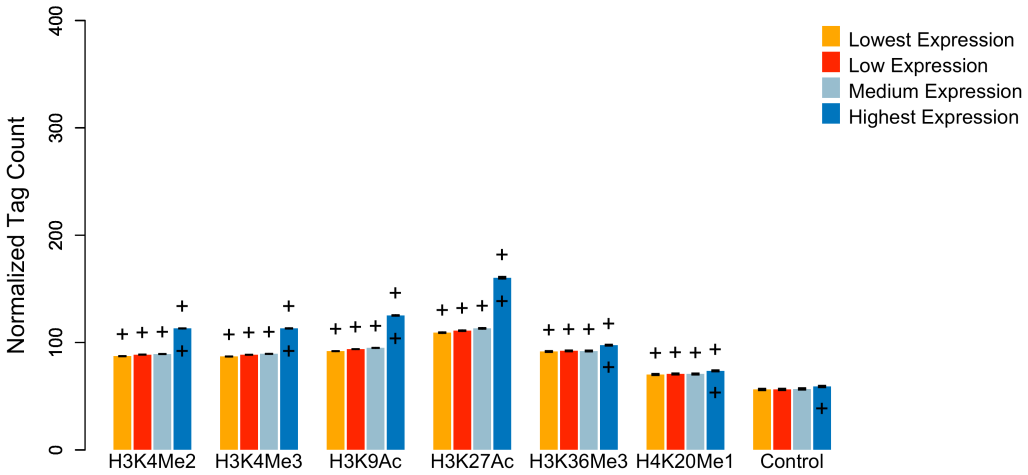
Supplementary Figure S3. Enrichment of chromatin modifications at cis-NAT promoters in GM12878. Cis-NAT promoters in the GM12878 cell type were identified using CAGE data from non-polyadenylated RNA from nucleus isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis-NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



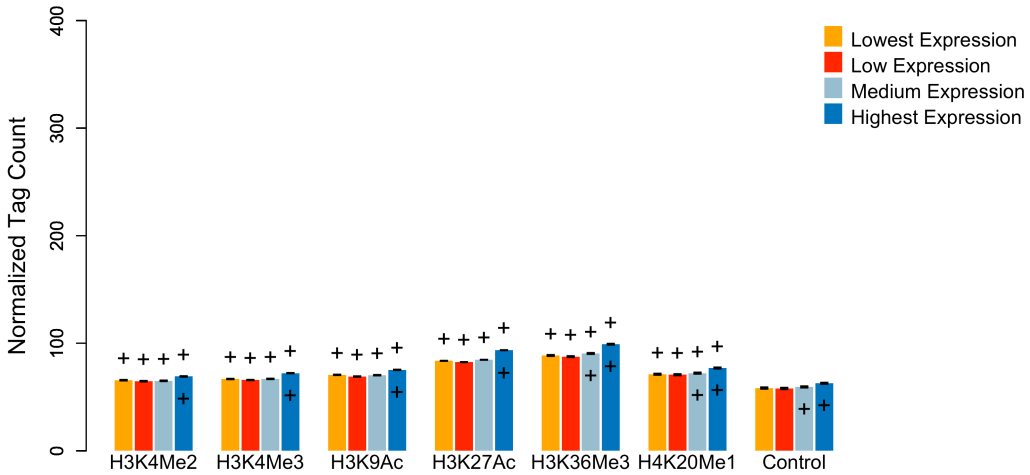
Supplementary Figure S4. Enrichment of chromatin modifications at cis-NAT promoters in H1HESC. Cis-NAT promoters in the H1HESC cell type were identified using CAGE data from total RNA from whole-cell isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis-NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



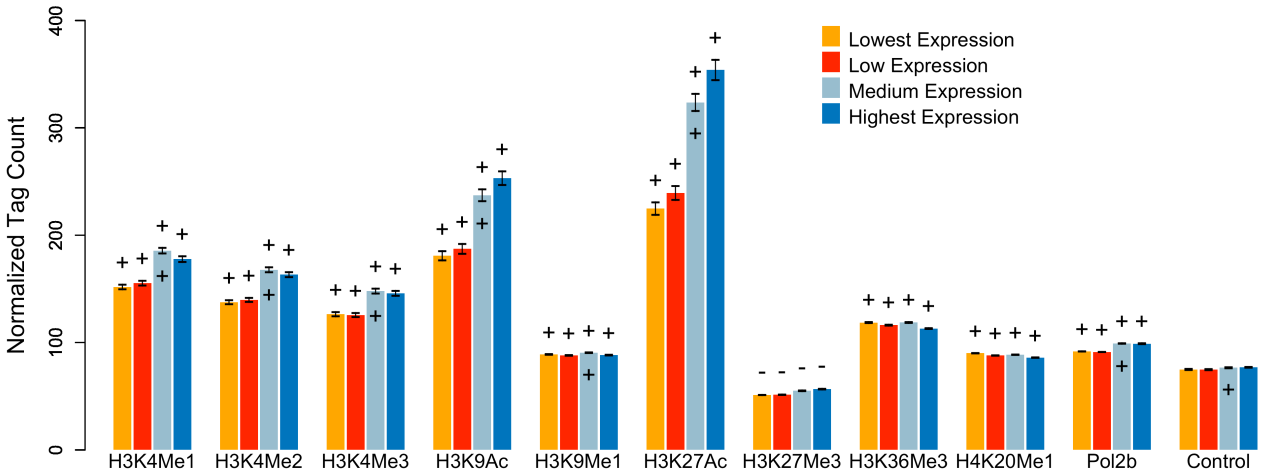
Supplementary Figure S5. Enrichment of chromatin modifications at cis-NAT promoters in HepG2. Cis-NAT promoters in the HepG2 cell type were identified using CAGE data from non-polyadenylated RNA from cytosol isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis- NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



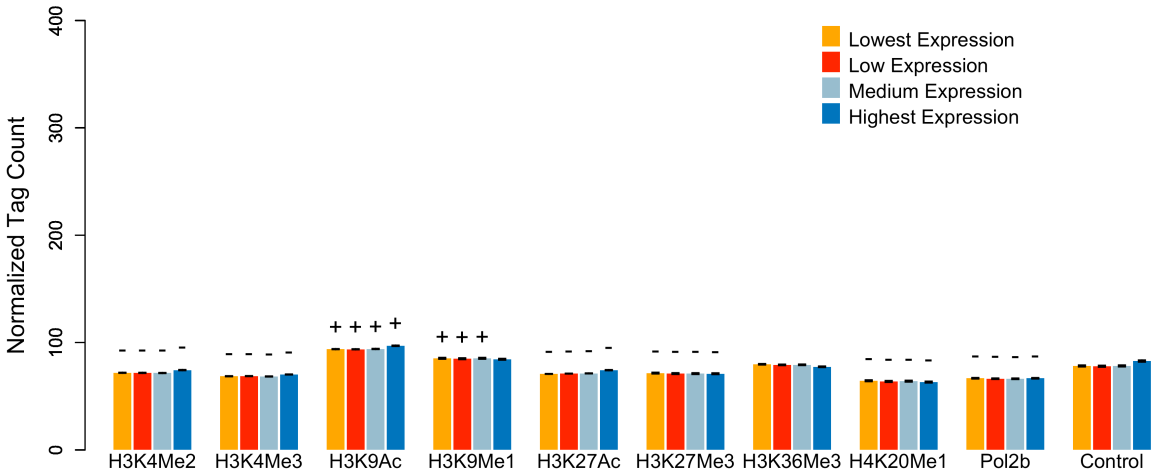
Supplementary Figure S6. Enrichment of chromatin modifications at cis-NAT promoters in HepG2. Cis-NAT promoters in the HepG2 cell type were identified using CAGE data from total RNA from nucleolus isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis-NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



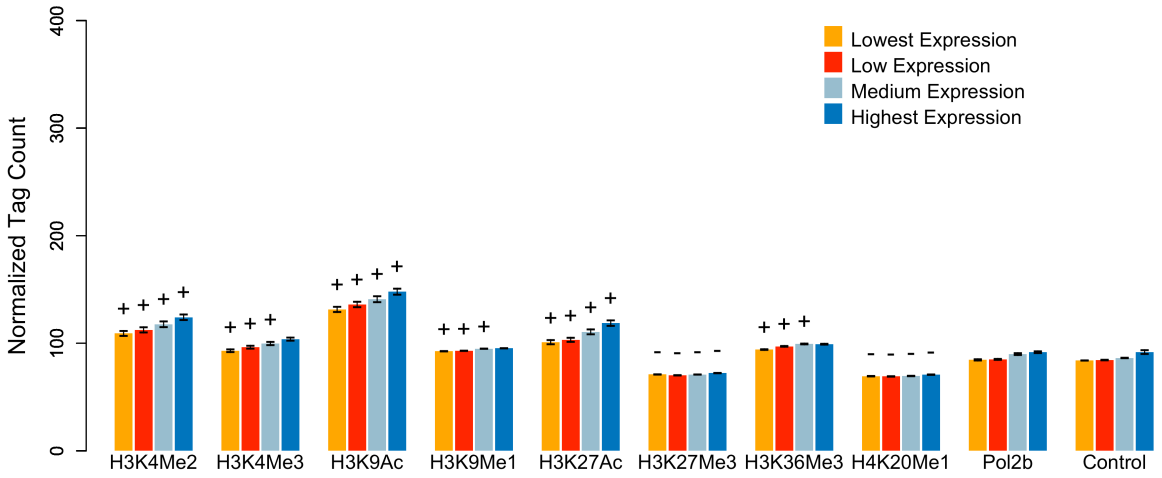
Supplementary Figure S7. Enrichment of chromatin modifications at cis-NAT promoters in HepG2. Cis-NAT promoters in the HepG2 cell type were identified using CAGE data from non-polyadenylated RNA from nucleus isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis- NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



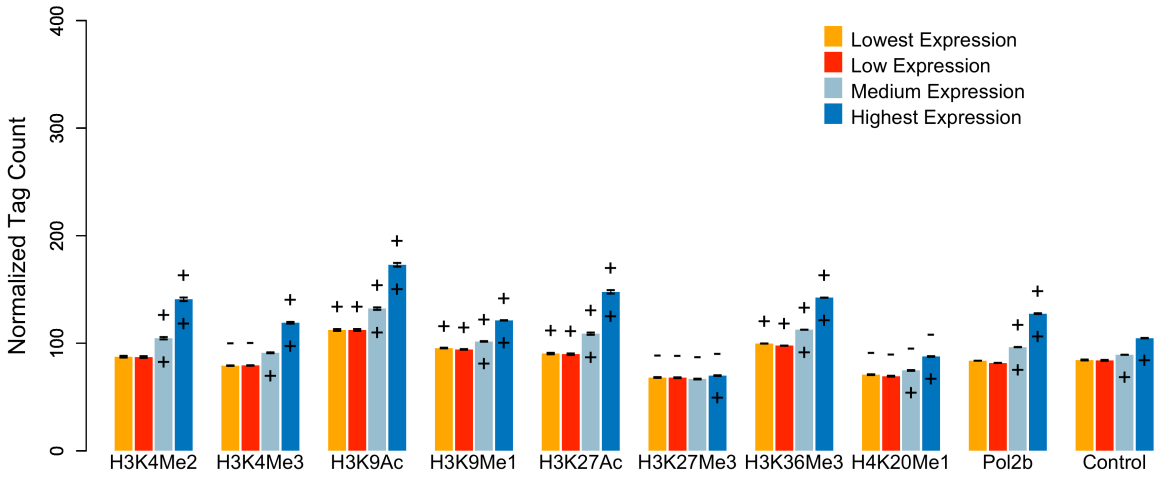
Supplementary Figure S8. Enrichment of chromatin modifications at cis-NAT promoters in HUVEC. Cis-NAT promoters in the HUVEC cell type were identified using CAGE data from non-polyadenylated RNA from cytosol isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis- NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



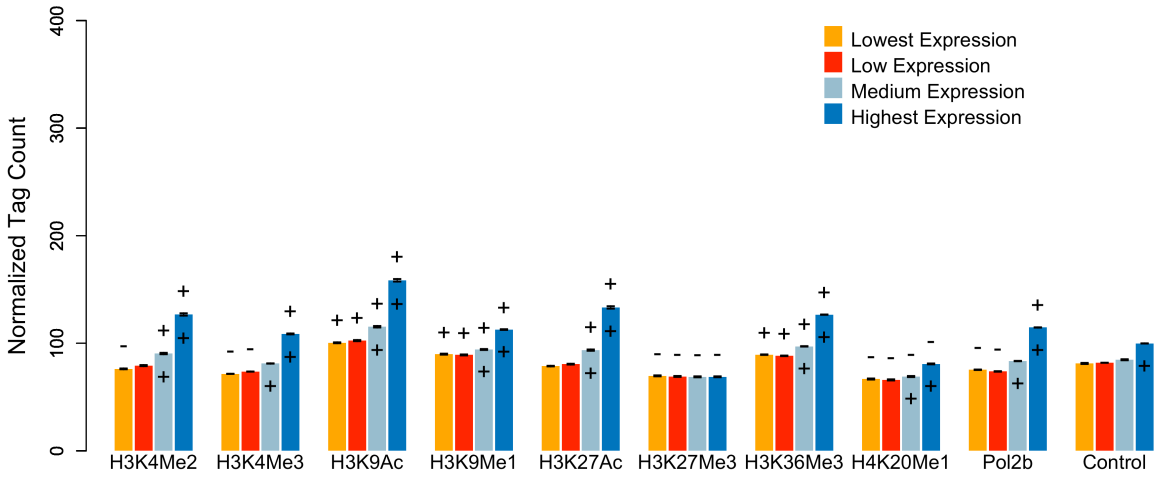
Supplementary Figure S9. Enrichment of chromatin modifications at cis-NAT promoters in K562. Cis-NAT promoters in the K562 cell type were identified using CAGE data from non-polyadenylated RNA from cytosol isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis- NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



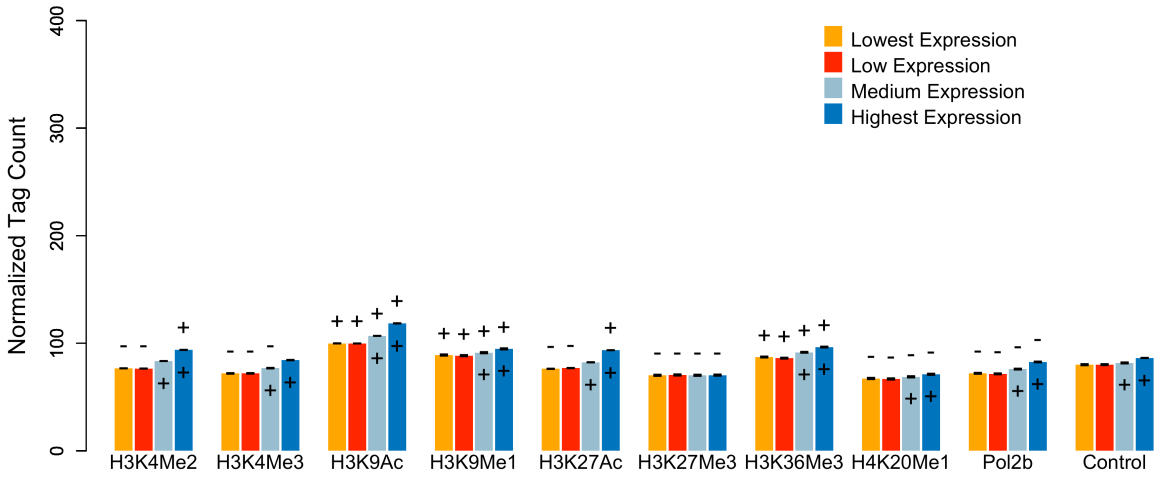
Supplementary Figure S10. Enrichment of chromatin modifications at cis-NAT promoters in K562. Cis-NAT promoters in the K562 cell type were identified using CAGE data from polyadenylated RNA from cytosol isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis-NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



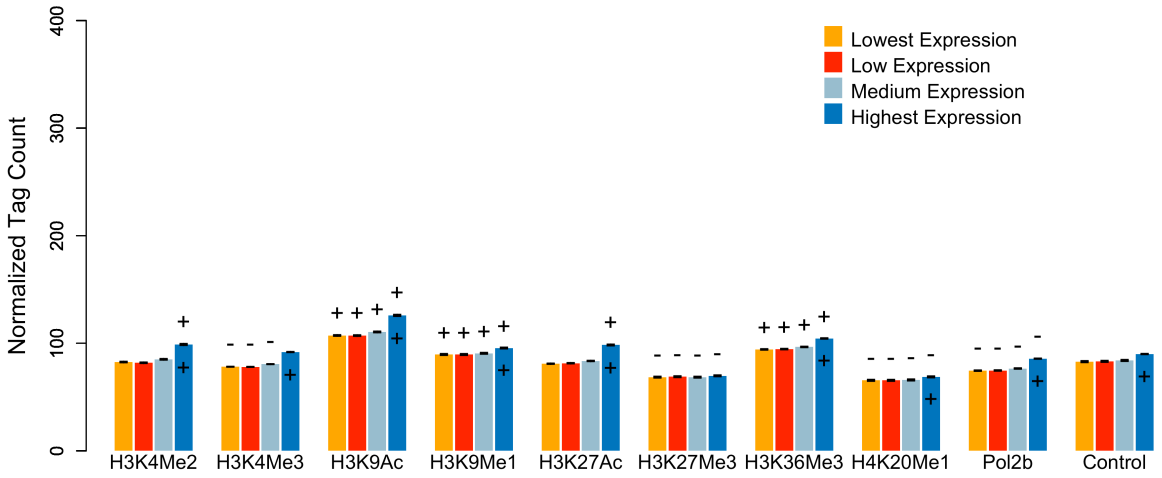
Supplementary Figure S11. Enrichment of chromatin modifications at cis-NAT promoters in K562. Cis-NAT promoters in the K562 cell type were identified using CAGE data from total RNA from nucleolus isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis-NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



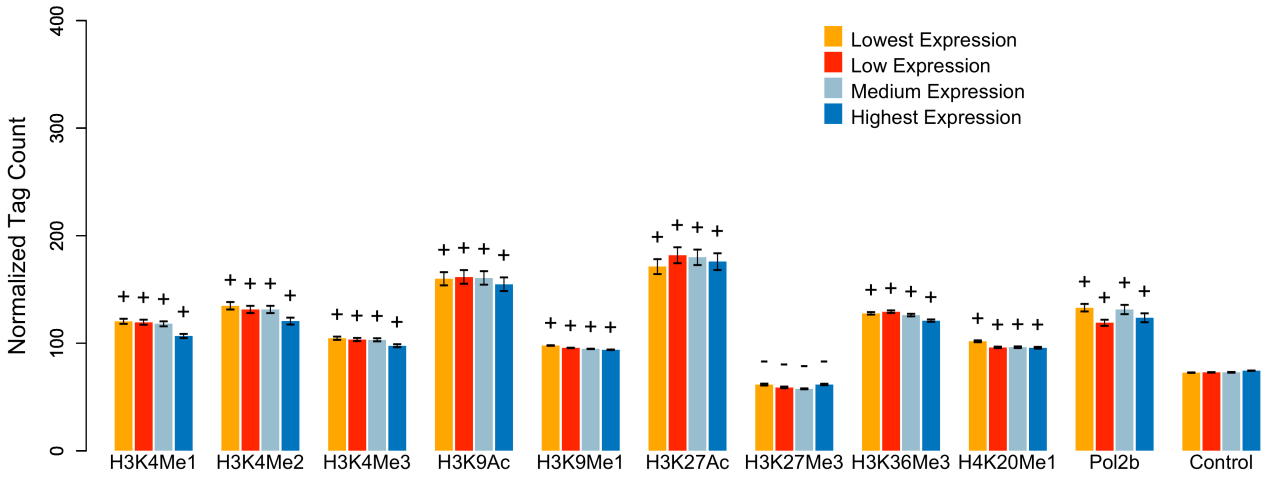
Supplementary Figure S12. Enrichment of chromatin modifications at cis-NAT promoters in K562. Cis-NAT promoters in the K562 cell type were identified using CAGE data from total RNA from nucleoplasm isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis-NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



Supplementary Figure S13. Enrichment of chromatin modifications at cis-NAT promoters in K562. Cis-NAT promoters in the K562 cell type were identified using CAGE data from non-polyadenylated RNA from nucleus isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis- NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



Supplementary Figure S14. Enrichment of chromatin modifications at cis-NAT promoters in K562. Cis-NAT promoters in the K562 cell type were identified using CAGE data from polyadenylated RNA from nucleus isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis- NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.



Supplementary Figure S15. Enrichment of chromatin modifications at cis-NAT promoters in NHEK. Cis-NAT promoters in the NHEK cell type were identified using CAGE data from non-polyadenylated RNA from cytosol isolates. Cis-NAT promoters were divided into 4 bins based on their activity (lowest to highest), and the normalized average numbers of ChIP-seq reads from each histone modification +/- 5 kb of the cis- NAT TSS were calculated for each bin. A '+' or '-' above a bar indicates that the number of ChIP-seq reads for that bin and modification is significantly higher or lower, respectively, than the control for that bin ($P < 0.001$). A '+' or '-' within a bar indicates that a bin is significantly enriched or depleted, respectively, for the histone modification compared to the next lowest activity bin ($P < 0.001$). Error bars shown are the standard error of the mean.