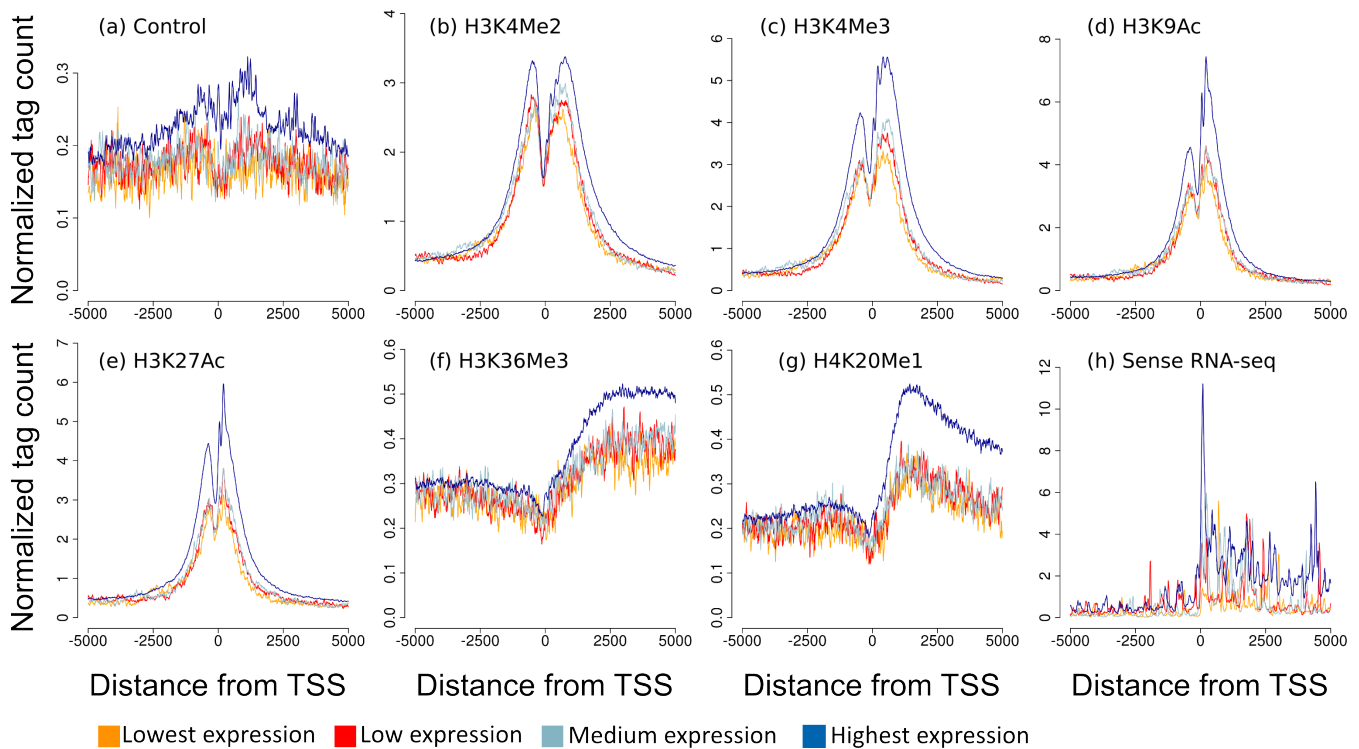
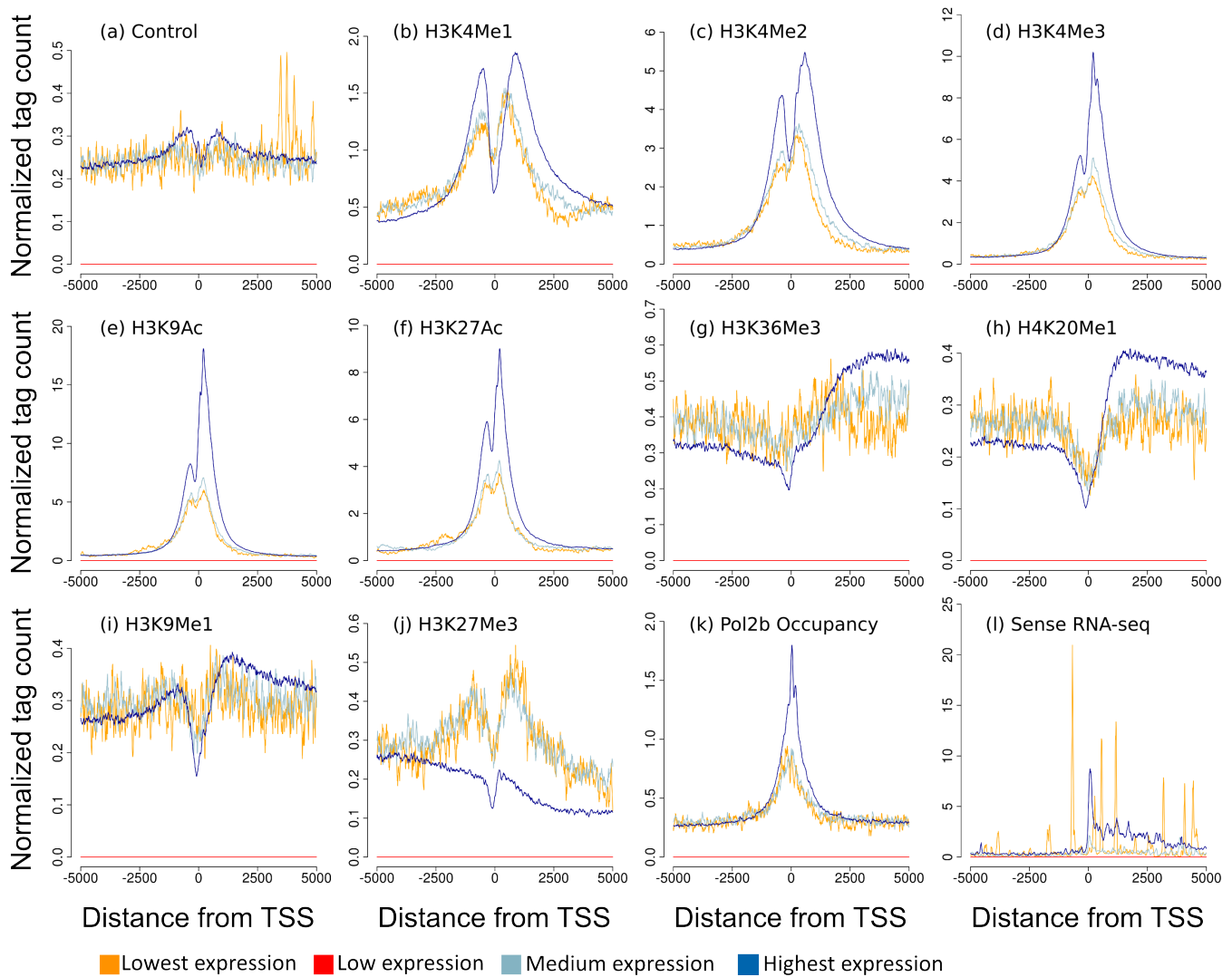


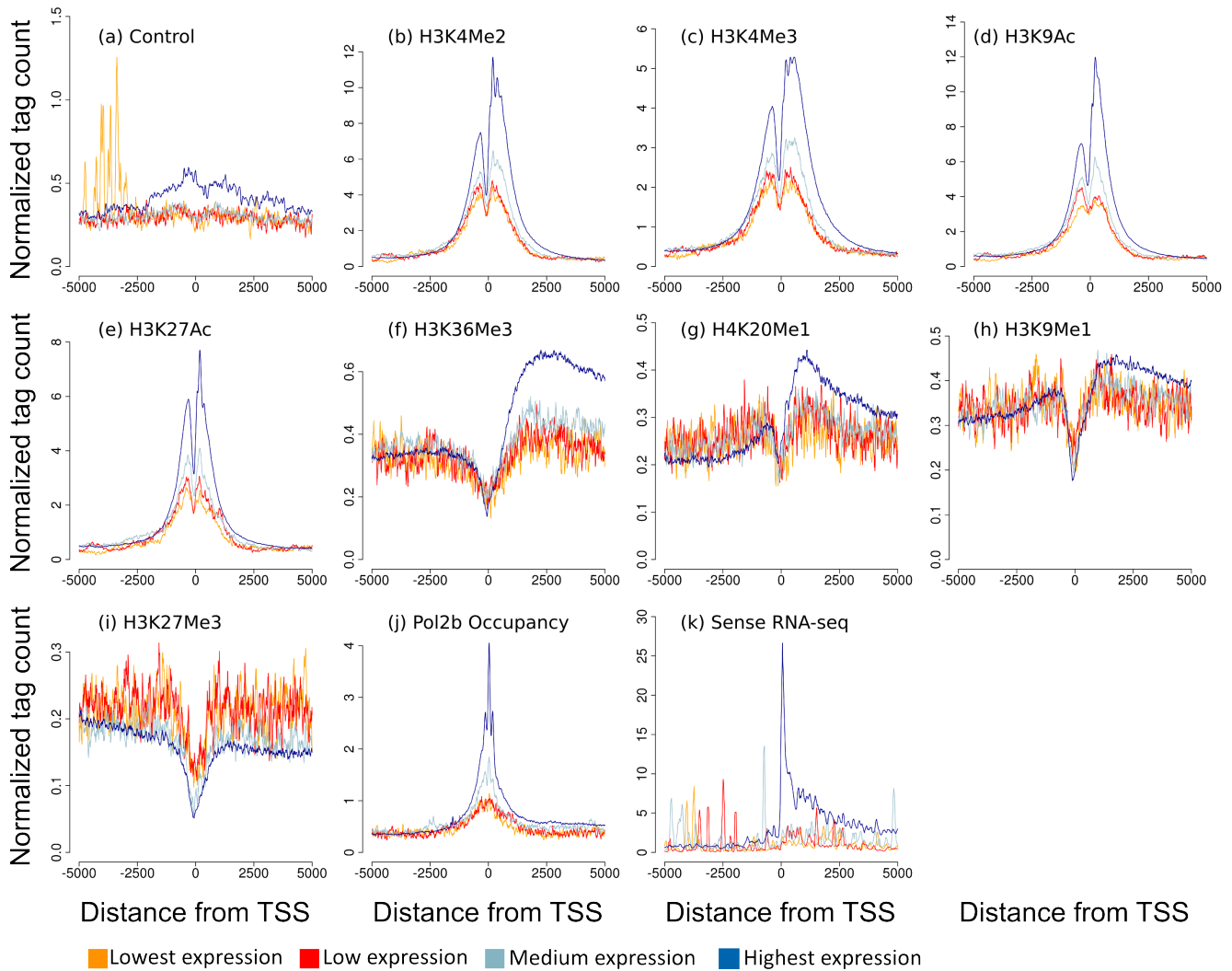
Supplementary Figure S51. Chromatin modification environment around genic promoters in HepG2. Genic promoters were taken from the UCSC genes set, and their activity measured using CAGE data from non-polyadenylated RNA from cytosol isolates from HepG2 cells. Genic promoters were divided into the same for bins as cis-NAT promoters for the same data set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the genic TSS (at position 0) were calculated for each bin.



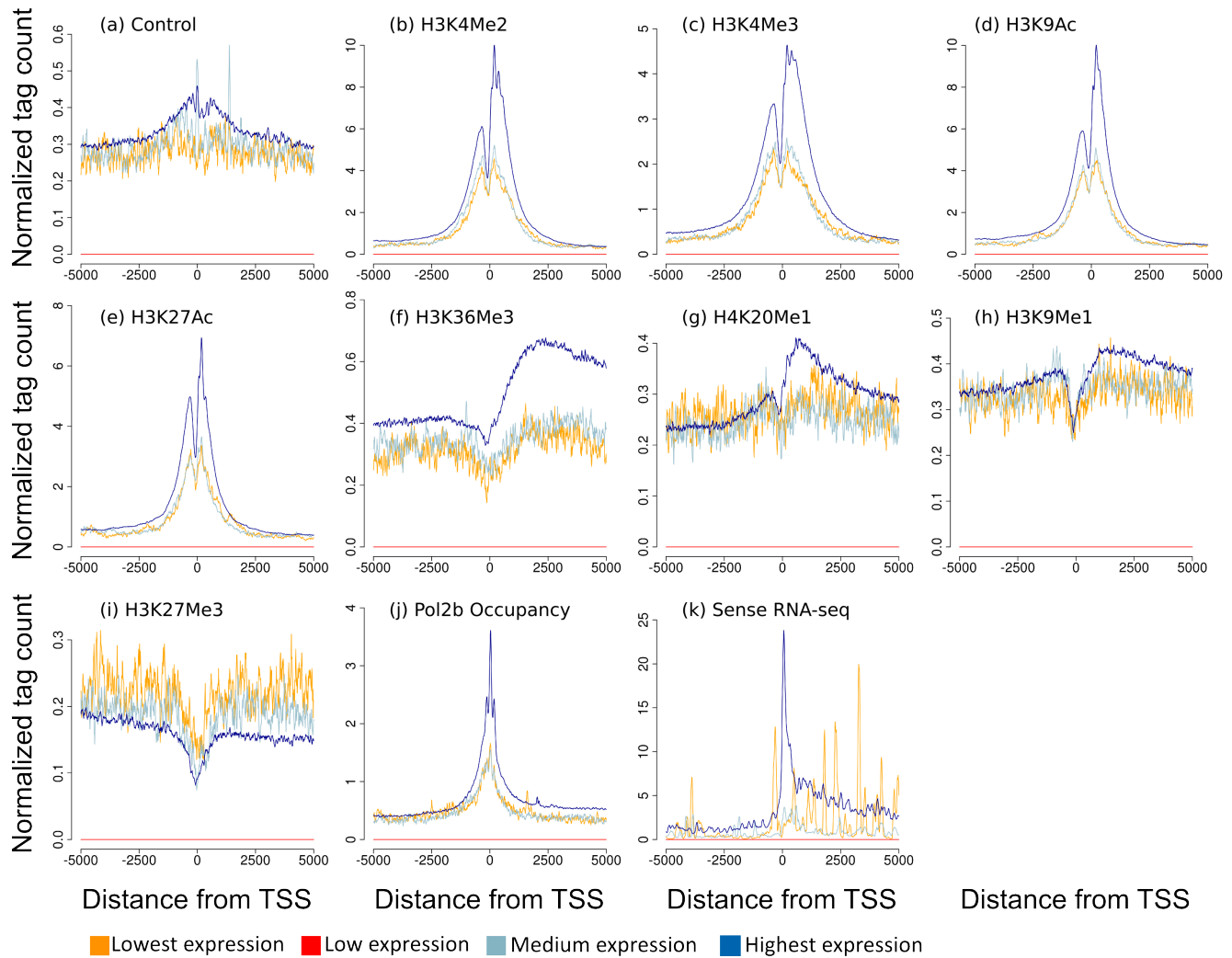
Supplementary Figure S53. Chromatin modification environment around genic promoters in HepG2. Genic promoters were taken from the UCSC genes set, and their activity measured using CAGE data from non-polyadenylated RNA from nucleus isolates from HepG2 cells. Genic promoters were divided into the same for bins as cis-NAT promoters for the same data set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows \pm 5kb of the genic TSS (at position 0) were calculated for each bin.



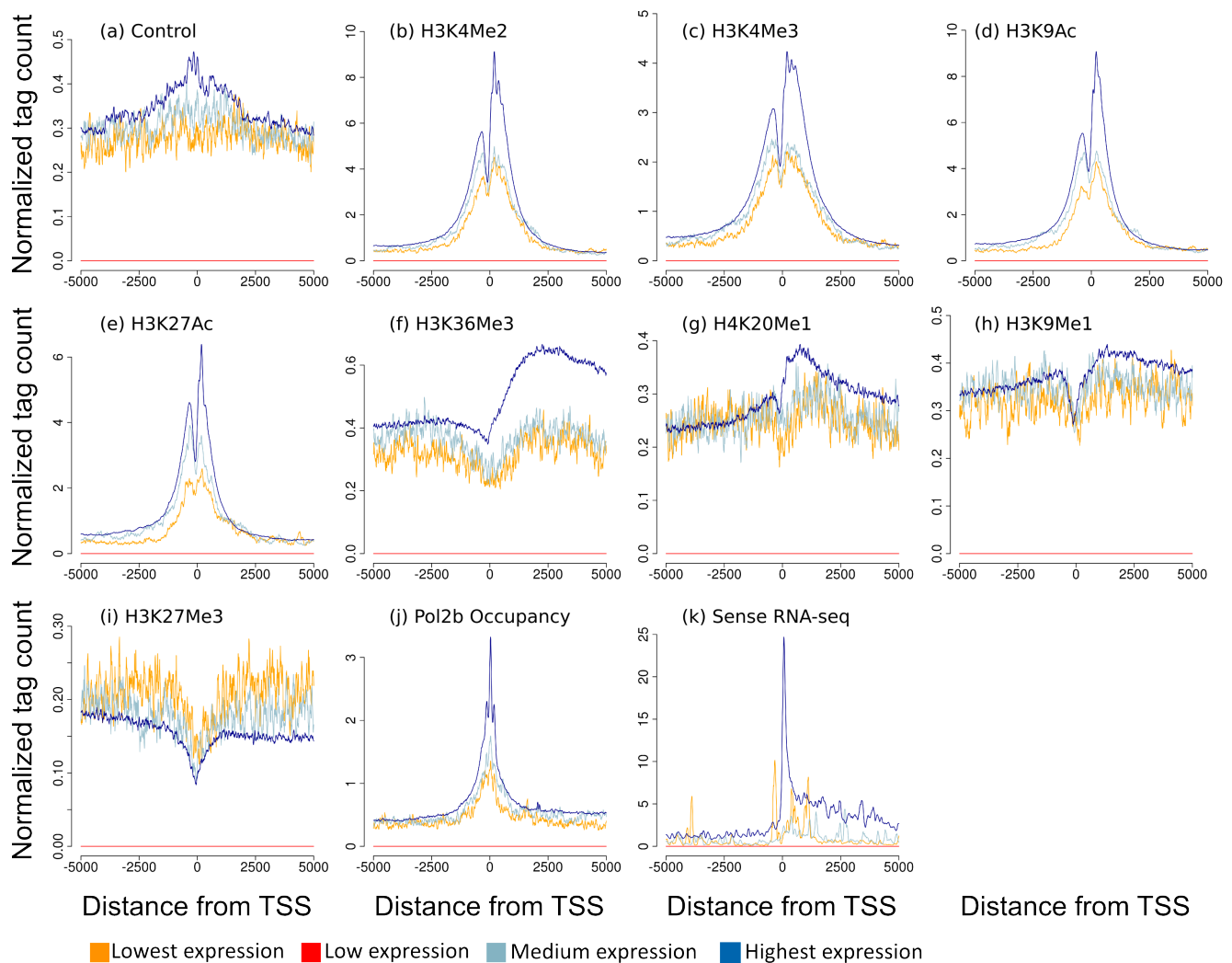
Supplementary Figure S54. Chromatin modification environment around genic promoters in HUVEC. Genic promoters were taken from the UCSC genes set, and their activity measured using CAGE data from non-polyadenylated RNA from cytosol isolates from HUVEC cells. Genic promoters were divided into the same for bins as cis-NAT promoters for the same data set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the genic TSS (at position 0) were calculated for each bin.



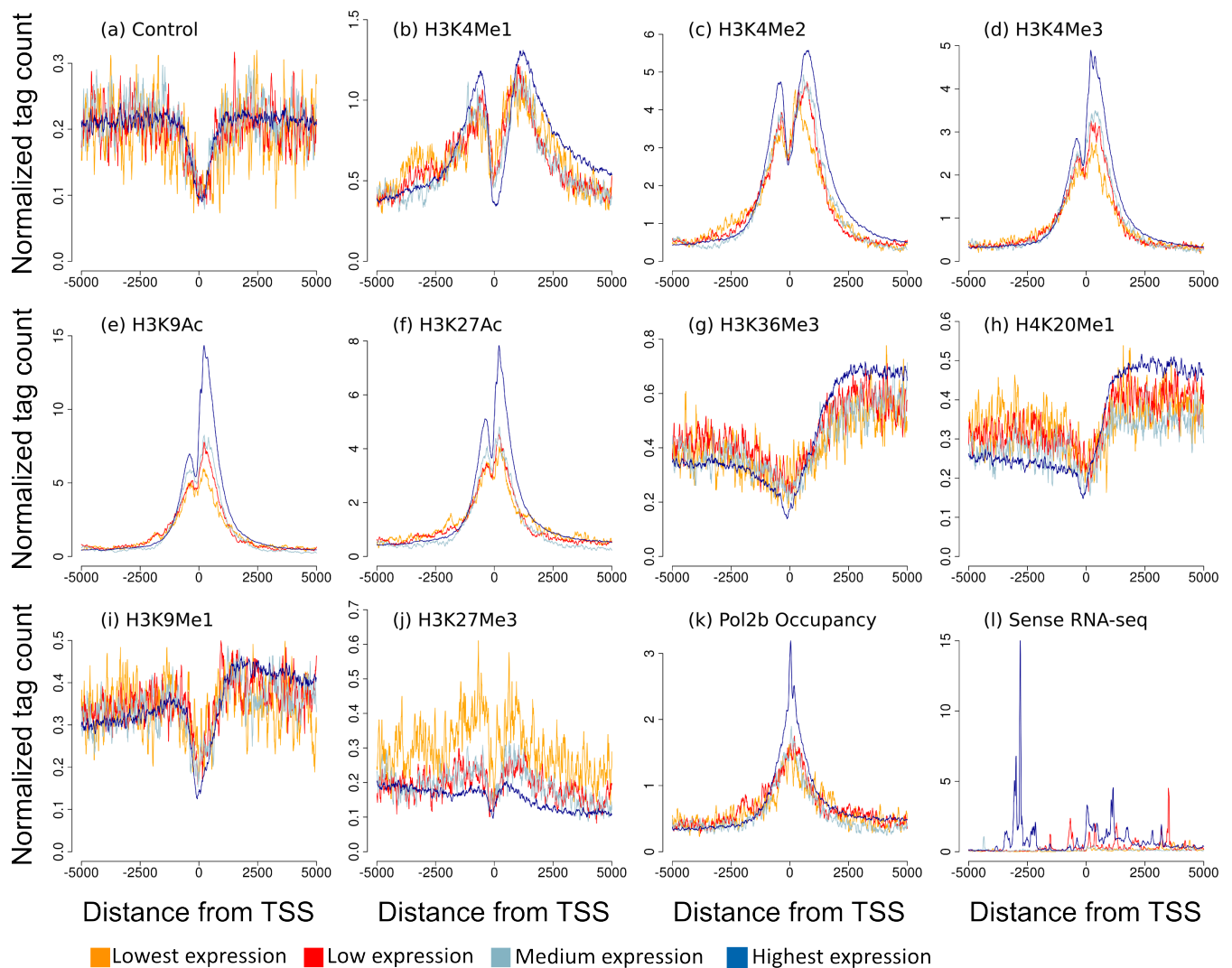
Supplementary Figure S56. Chromatin modification environment around genic promoters in K562. Genic promoters were taken from the UCSC genes set, and their activity measured using CAGE data from polyadenylated RNA from cytosol isolates from K562 cells. Genic promoters were divided into the same for bins as cis-NAT promoters for the same data set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the genic TSS (at position 0) were calculated for each bin.



Supplementary Figure S57. Chromatin modification environment around genic promoters in K562. Genic promoters were taken from the UCSC genes set, and their activity measured using CAGE data from total RNA from nucleolus isolates from K562 cells. Genic promoters were divided into the same for bins as cis-NAT promoters for the same data set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the genic TSS (at position 0) were calculated for each bin.



Supplementary Figure S58. Chromatin modification environment around genic promoters in K562. Genic promoters were taken from the UCSC genes set, and their activity measured using CAGE data from total RNA from nucleoplasm isolates from K562 cells. Genic promoters were divided into the same for bins as cis-NAT promoters for the same data set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the genic TSS (at position 0) were calculated for each bin.



Supplementary Figure S61. Chromatin modification environment around genic promoters in NHEK. Genic promoters were taken from the UCSC genes set, and their activity measured using CAGE data from non-polyadenylated RNA from cytosol isolates from NHEK cells. Genic promoters were divided into the same for bins as cis-NAT promoters for the same data set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the genic TSS (at position 0) were calculated for each bin.

