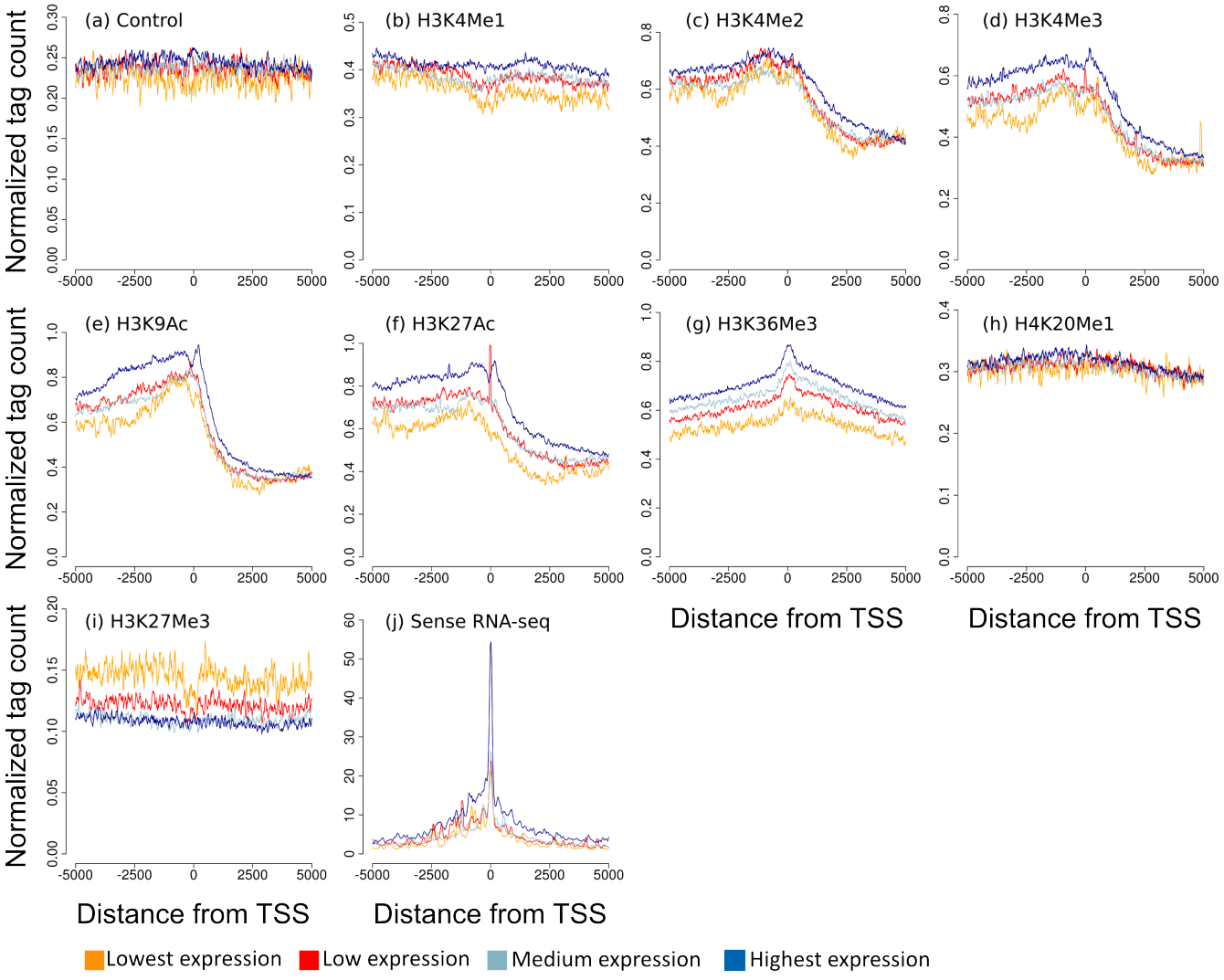
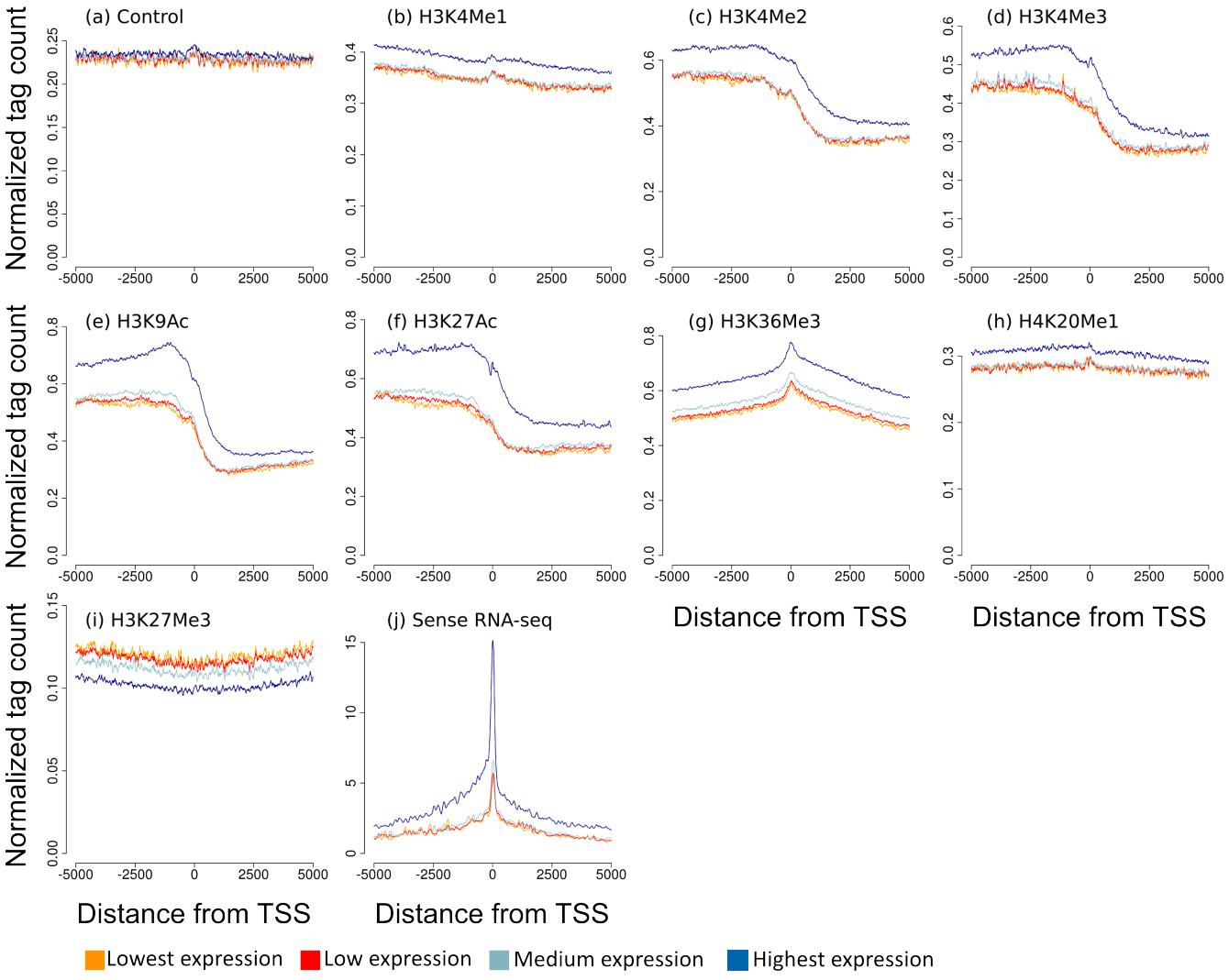
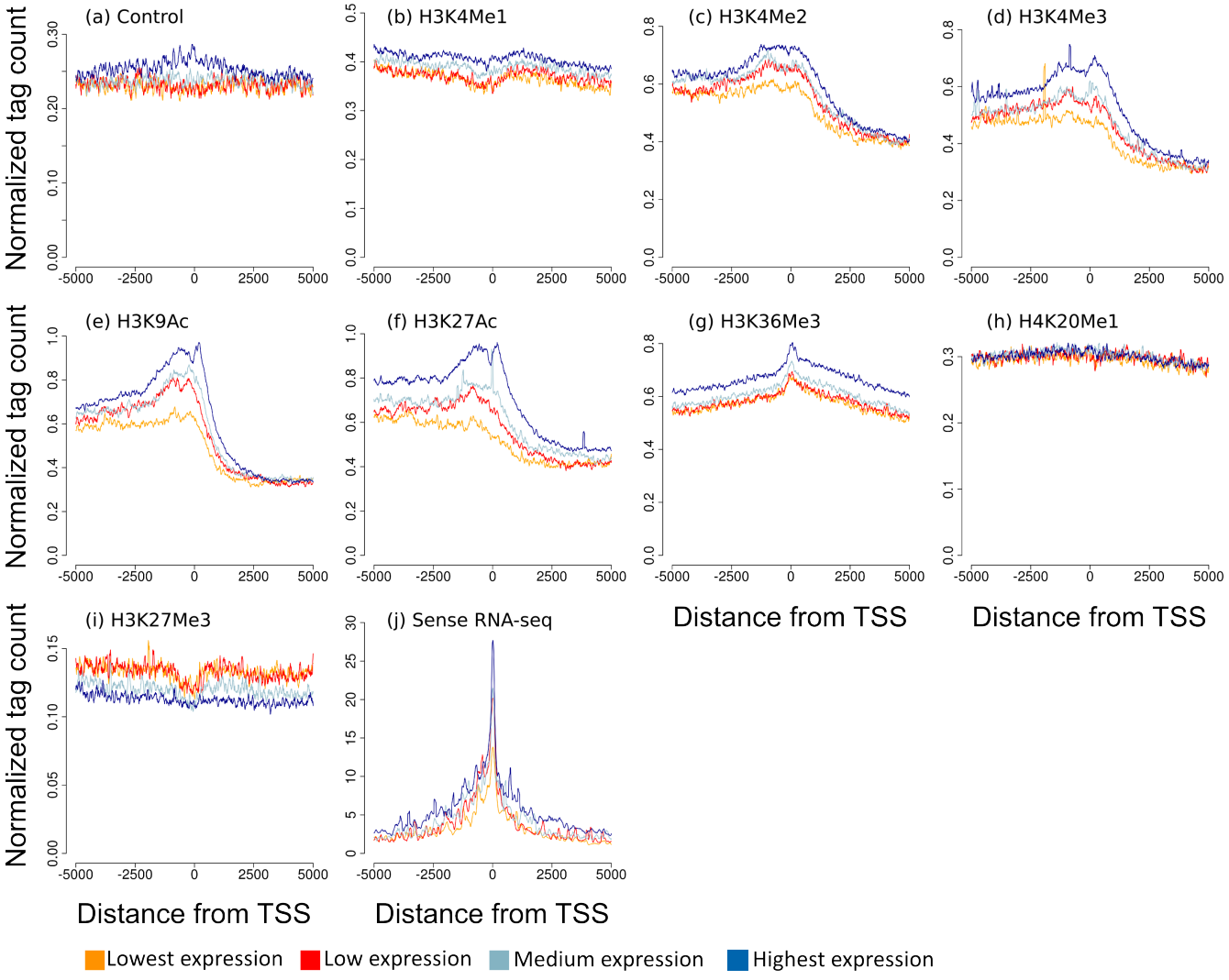


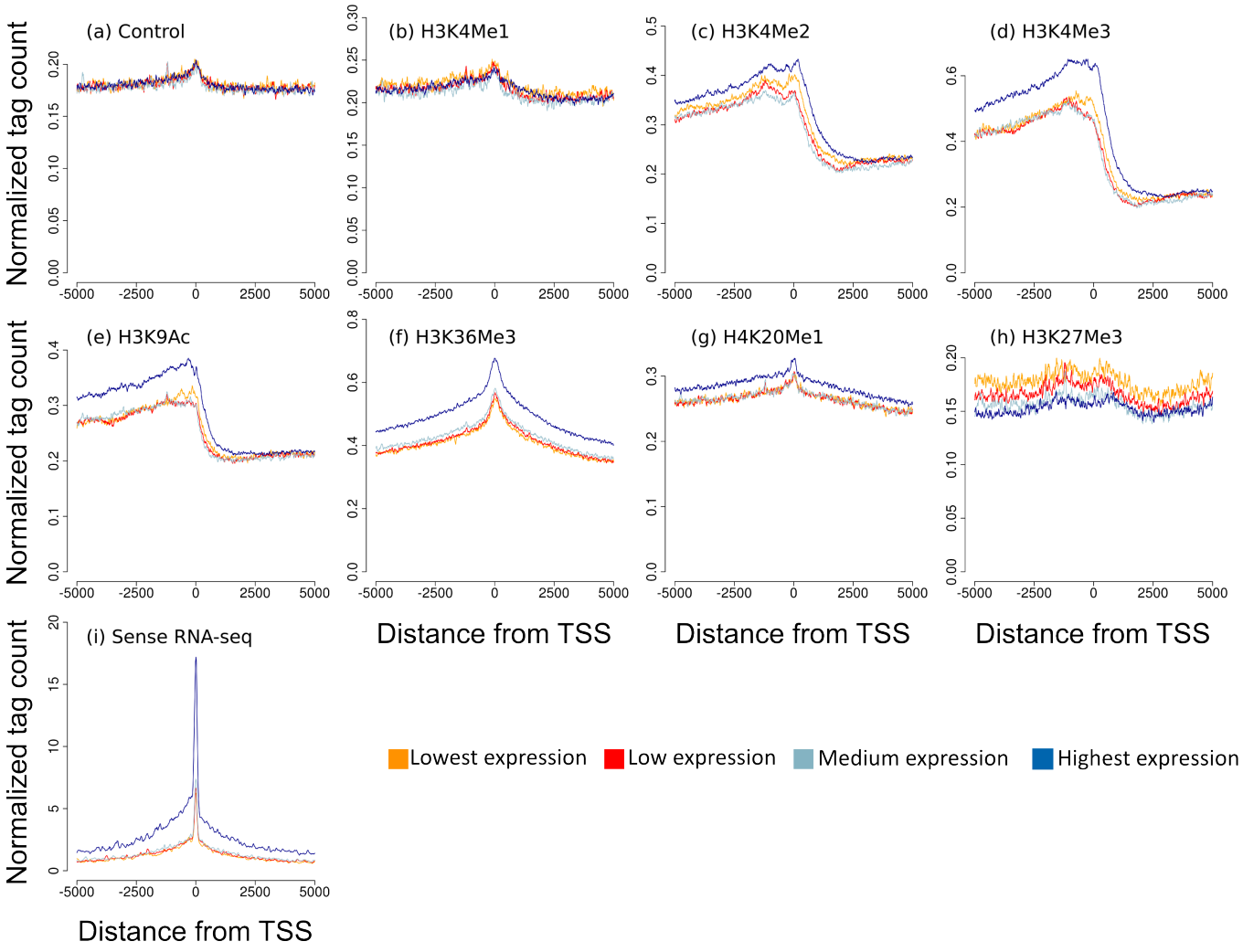
Supplementary Figure S63. Chromatin modification environment around exonic CAGE clusters in GM12878. Exonic CAGE clusters in the GM12878 cell type were identified using CAGE data from non-polyadenylated RNA from cytosol isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



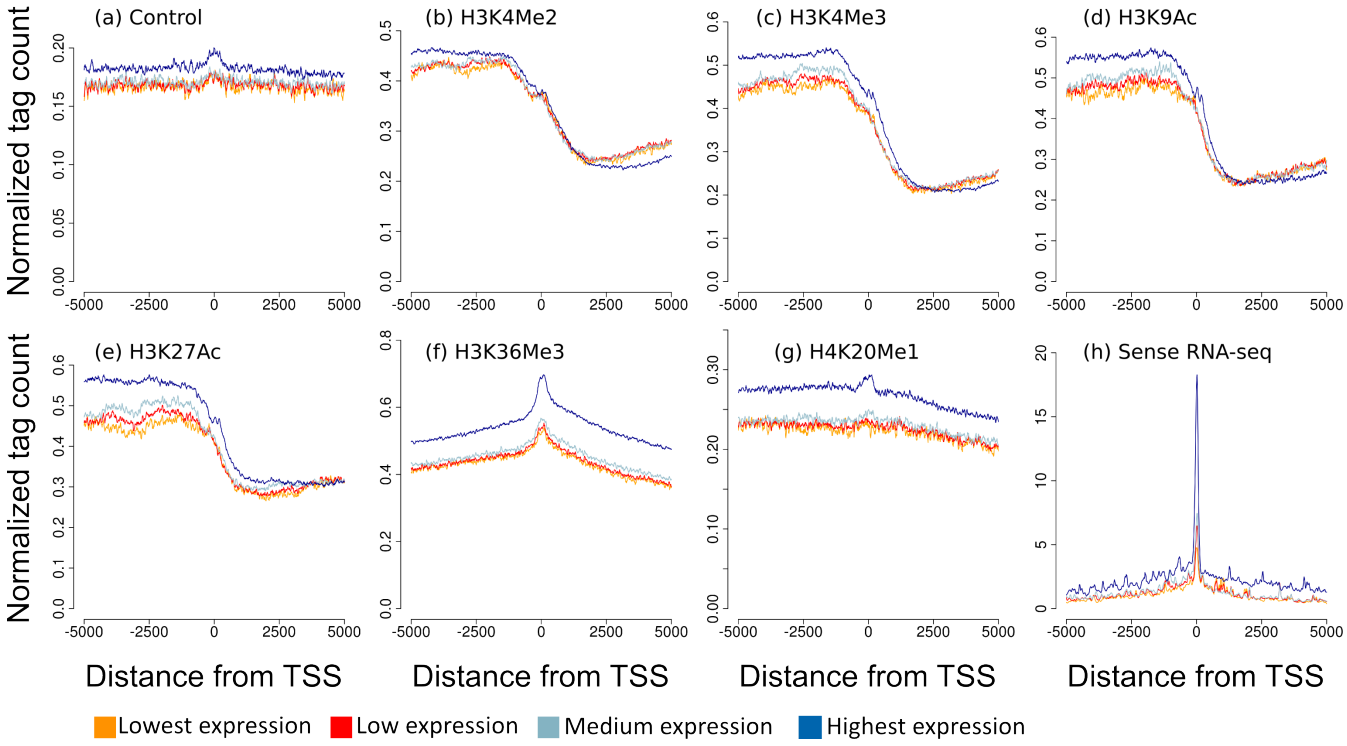
Supplementary Figure S64. Chromatin modification environment around exonic CAGE clusters in GM12878. Exonic CAGE clusters in the GM12878 cell type were identified using CAGE data from total RNA from nucleolus isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



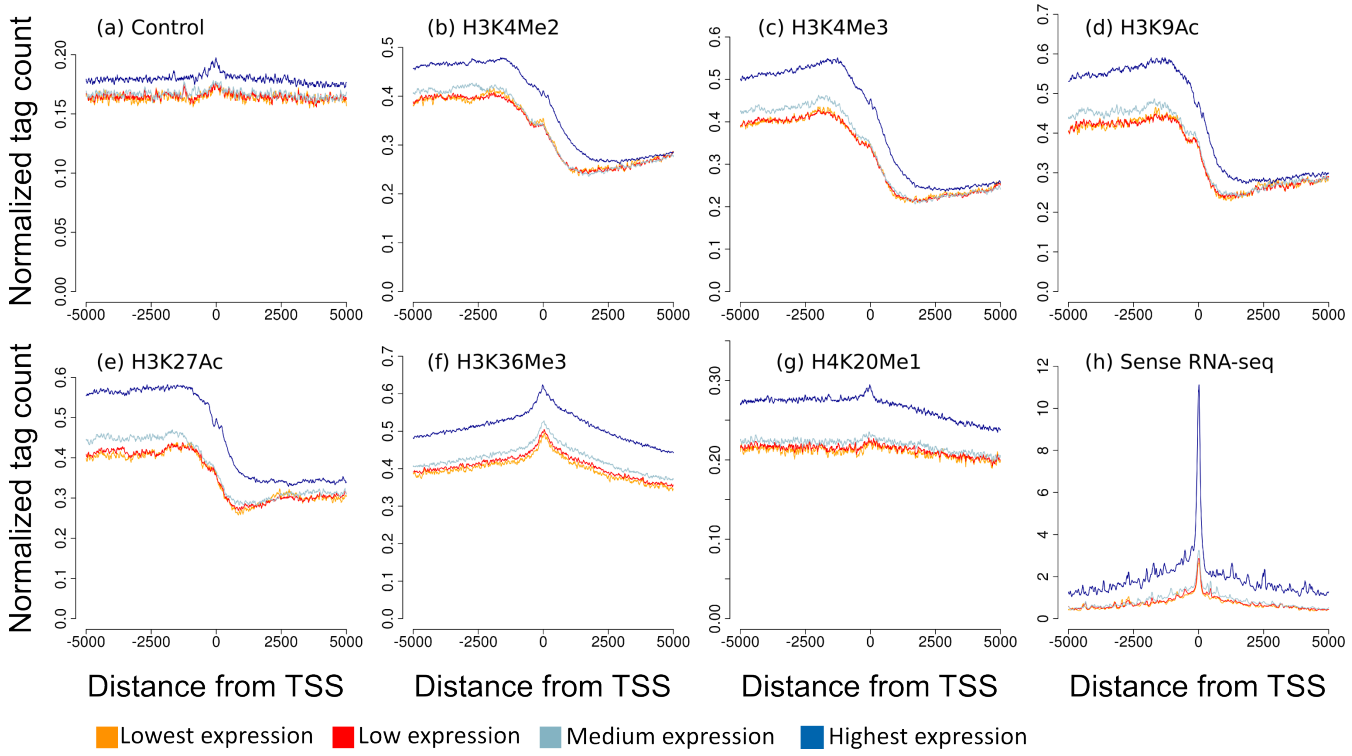
Supplementary Figure S65. Chromatin modification environment around exonic CAGE clusters in GM12878. Exonic CAGE clusters in the GM12878 cell type were identified using CAGE data from non-polyadenylated RNA from nucleus isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



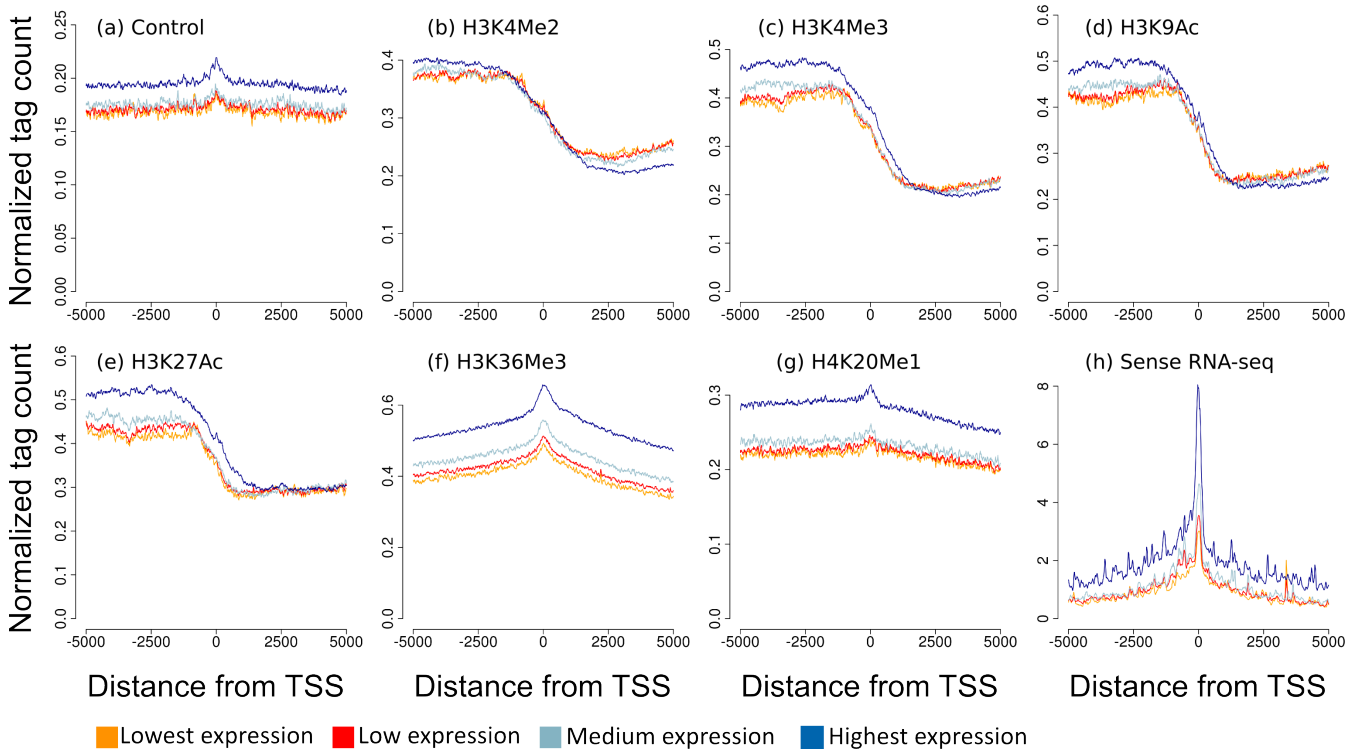
Supplementary Figure S66. Chromatin modification environment around exonic CAGE clusters in H1HESC. Exonic CAGE clusters in the H1HESC cell type were identified using CAGE data from non-polyadenylated RNA from whole-cell isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



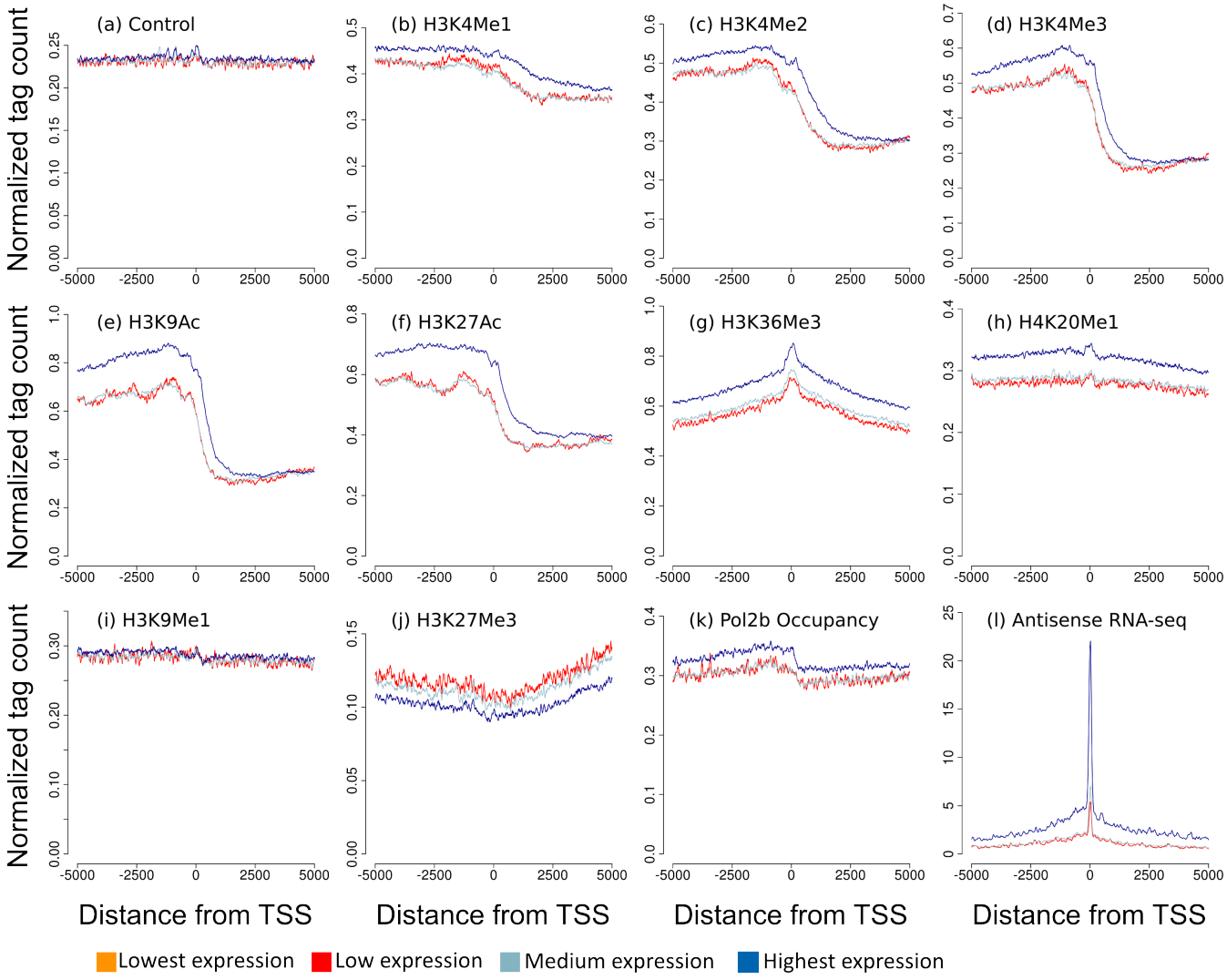
Supplementary Figure S67. Chromatin modification environment around exonic CAGE clusters in HepG2. Exonic CAGE clusters in the HepG2 cell type were identified using CAGE data from non-polyadenylated RNA from cytosol isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



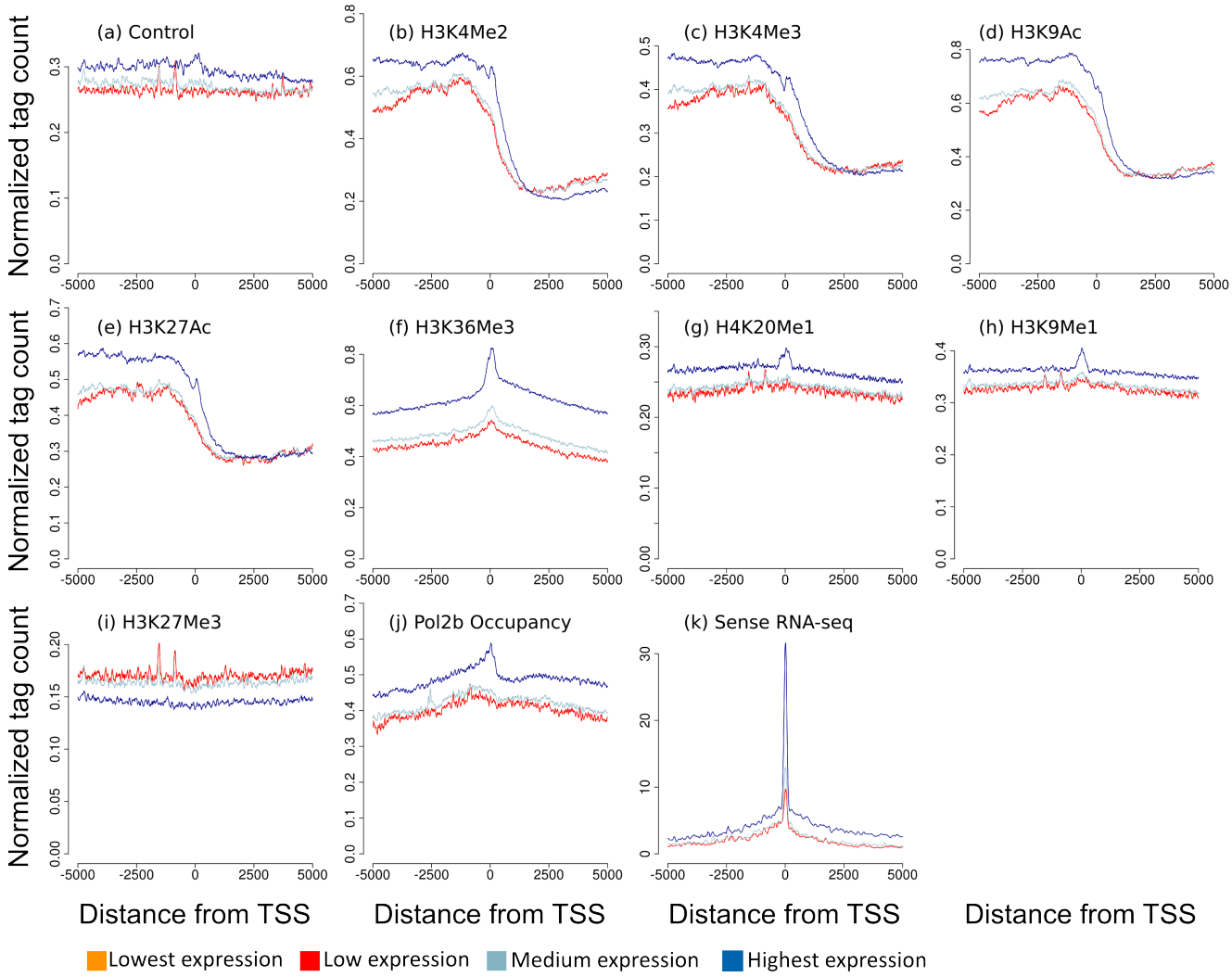
Supplementary Figure S68. Chromatin modification environment around exonic CAGE clusters in HepG2. Exonic CAGE clusters in the HepG2cell type were identified using CAGE data from total RNA from nucleolus isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



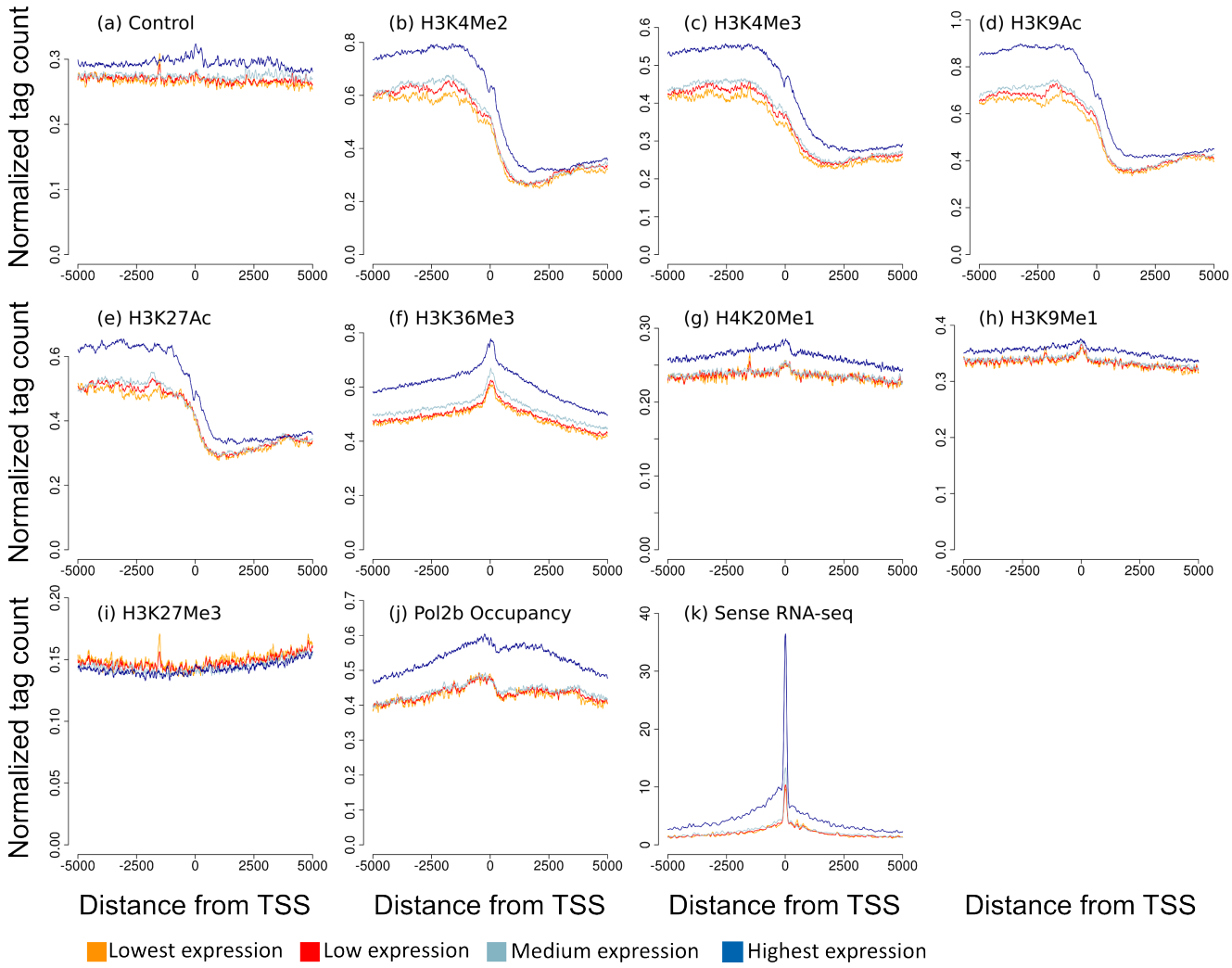
Supplementary Figure S69. Chromatin modification environment around exonic CAGE clusters in HepG2. Exonic CAGE clusters in the HepG2 cell type were identified using CAGE data from non-polyadenylated RNA from nucleus isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



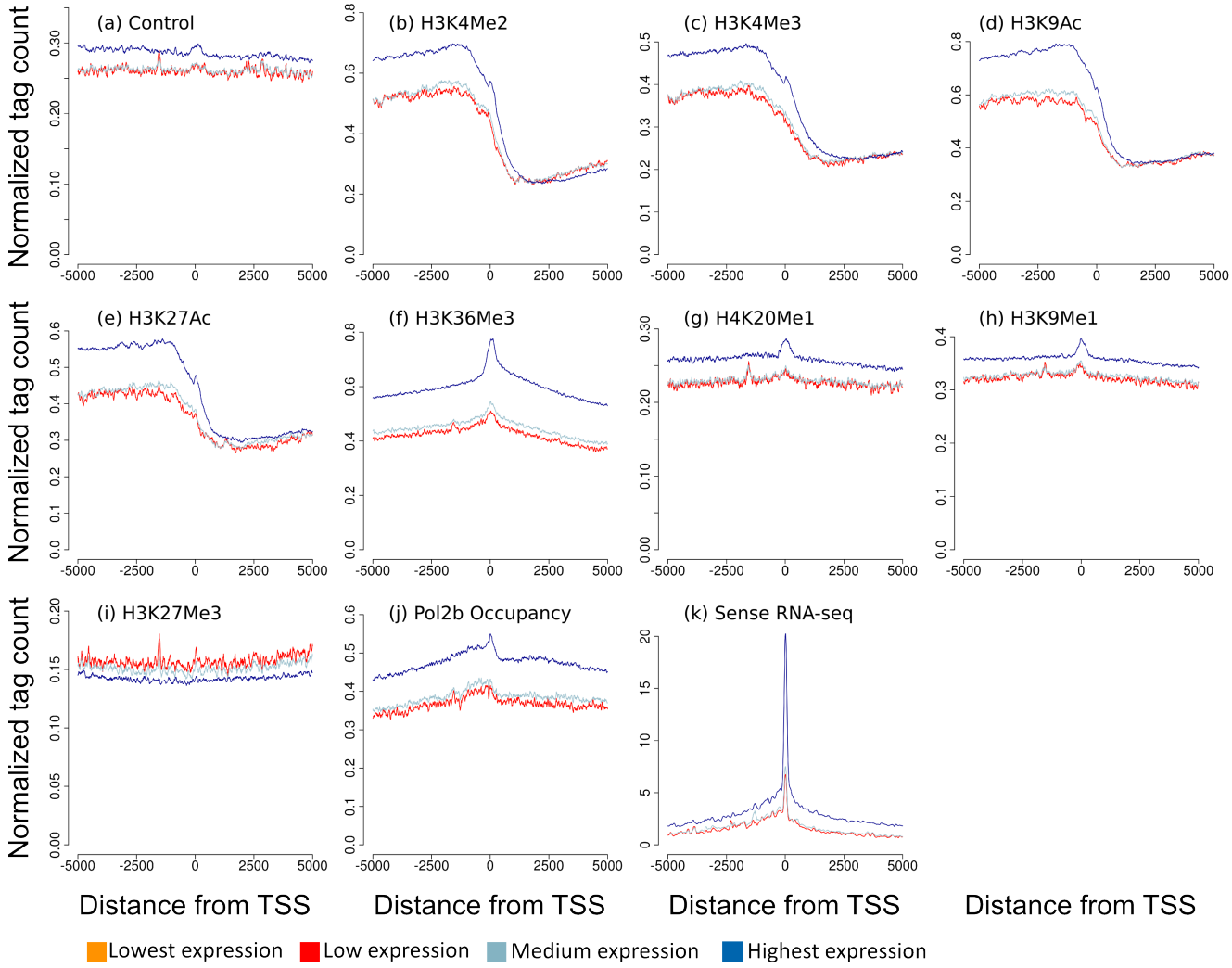
Supplementary Figure S70. Chromatin modification environment around exonic CAGE clusters in HUVEC. Exonic CAGE clusters in the HUVEC cell type were identified using CAGE data from non-polyadenylated RNA from cytosol isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



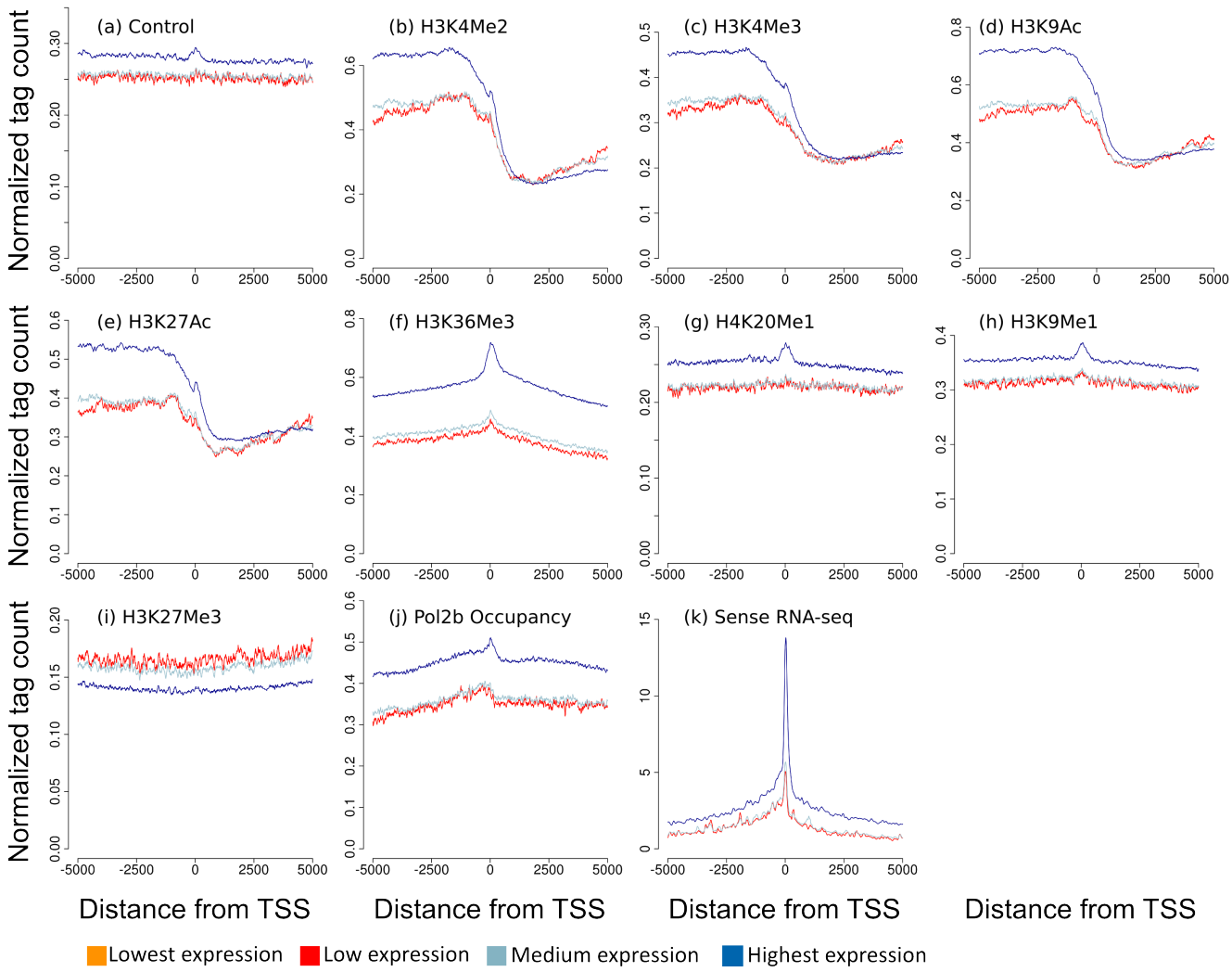
Supplementary Figure S71. Chromatin modification environment around exonic CAGE clusters in K562. Exonic CAGE clusters in the K562cell type were identified using CAGE data from non-polyadenylated RNA from cytosol isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



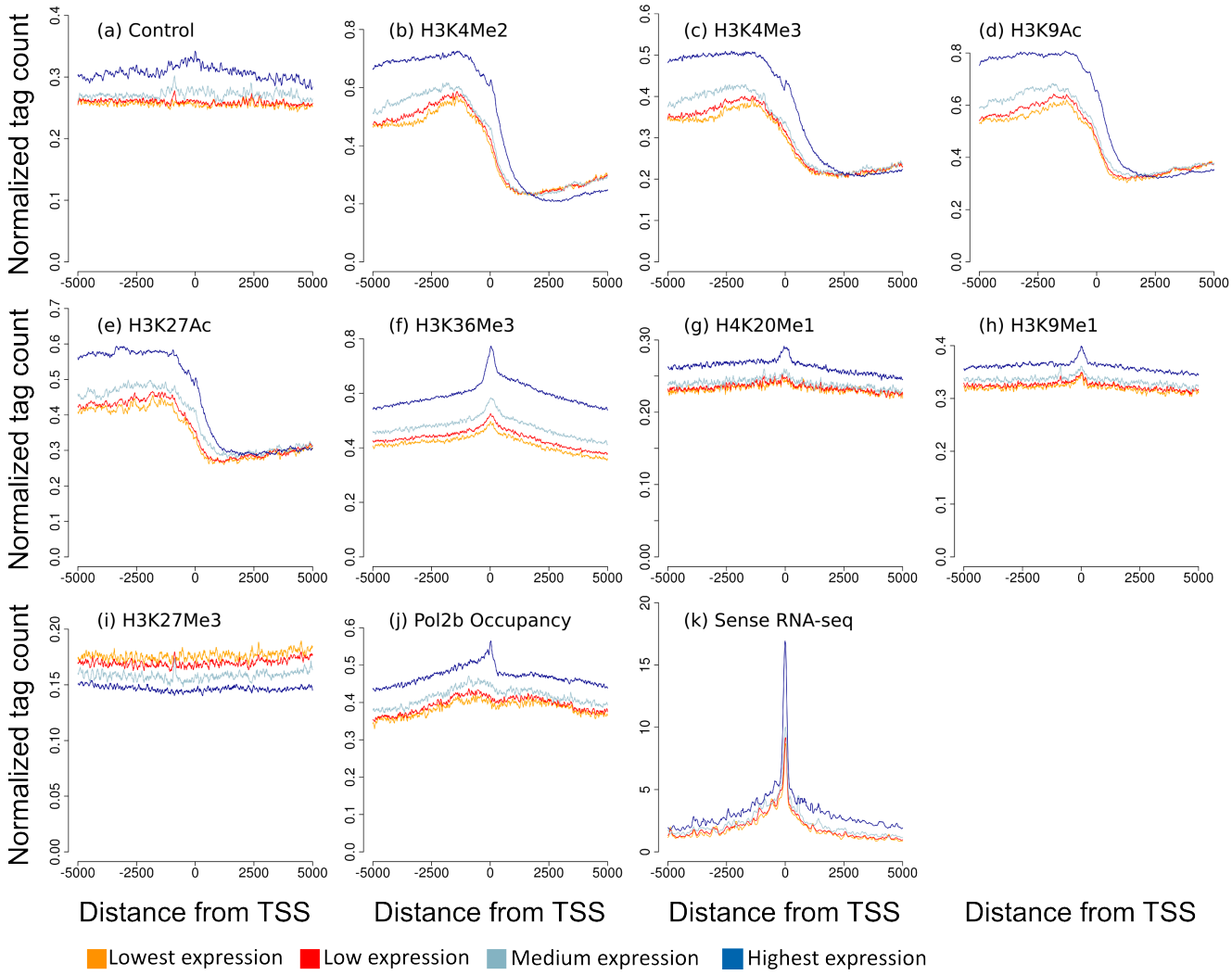
Supplementary Figure S72. Chromatin modification environment around exonic CAGE clusters in K562. Exonic CAGE clusters in the K562cell type were identified using CAGE data from polyadenylated RNA from cytosol isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



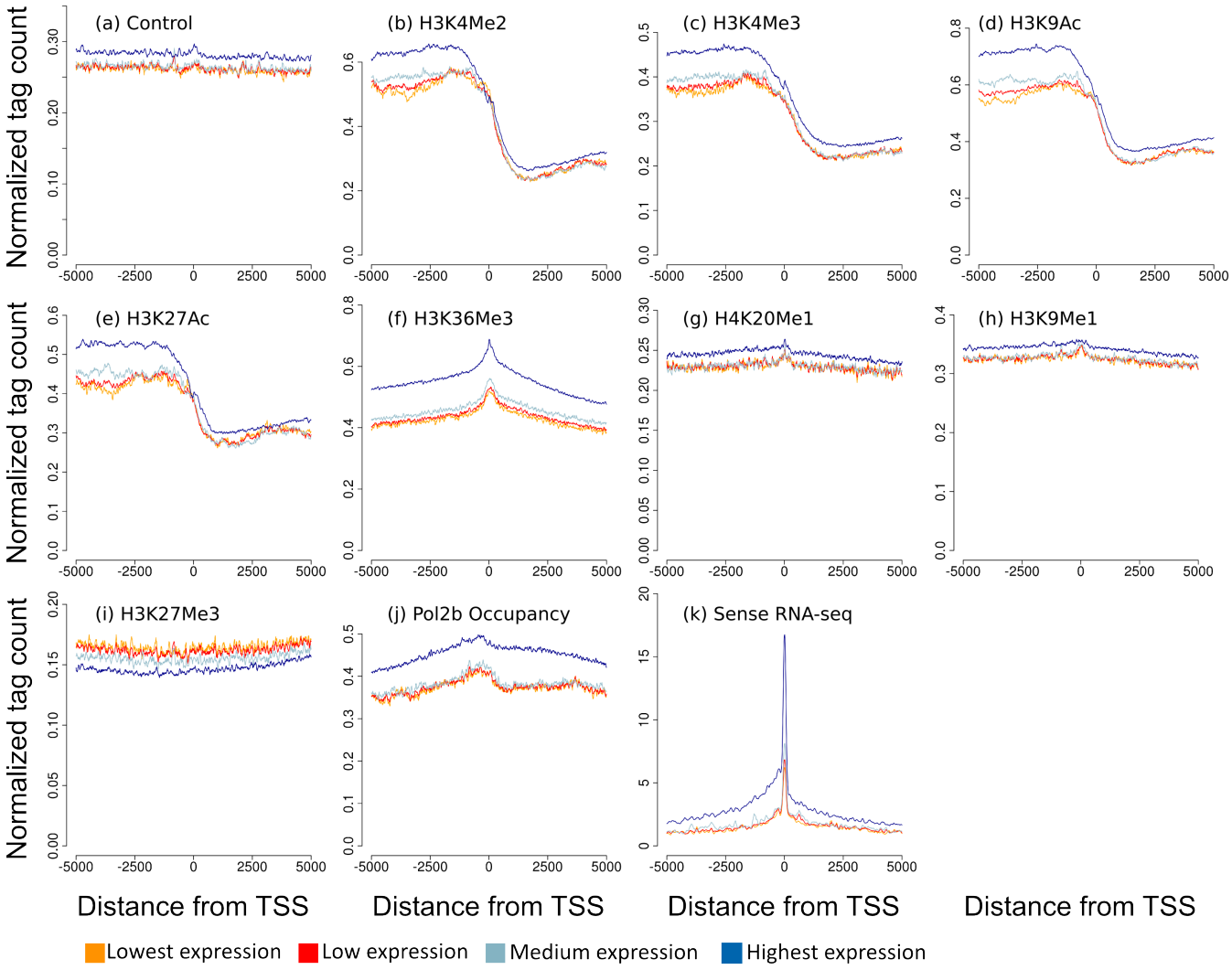
Supplementary Figure S73. Chromatin modification environment around exonic CAGE clusters in K562. Exonic CAGE clusters in the K562 cell type were identified using CAGE data from total RNA from nucleolus isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



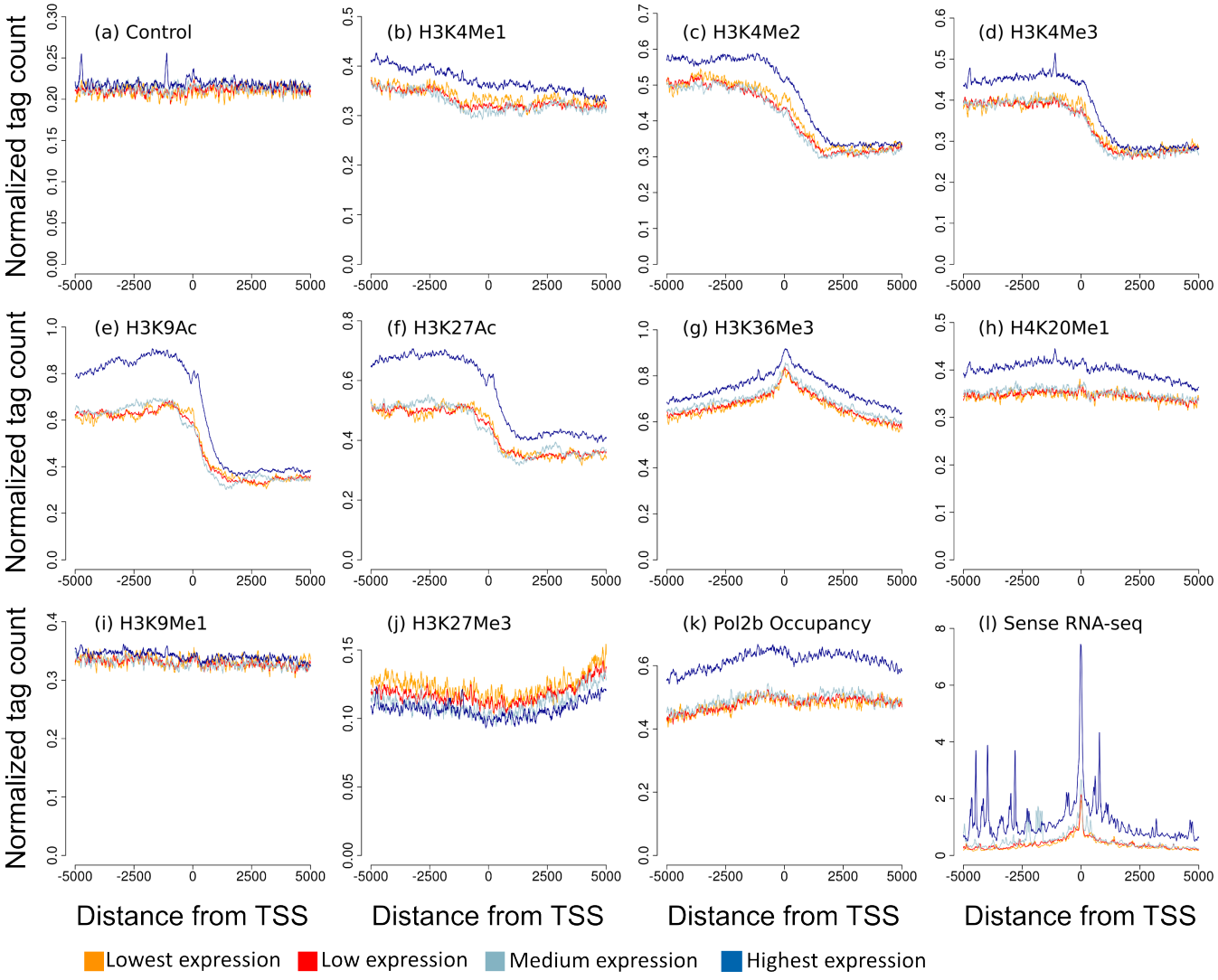
Supplementary Figure S74. Chromatin modification environment around exonic CAGE clusters in K562. Exonic CAGE clusters in the K562 cell type were identified using CAGE data from total RNA from nucleoplasm isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



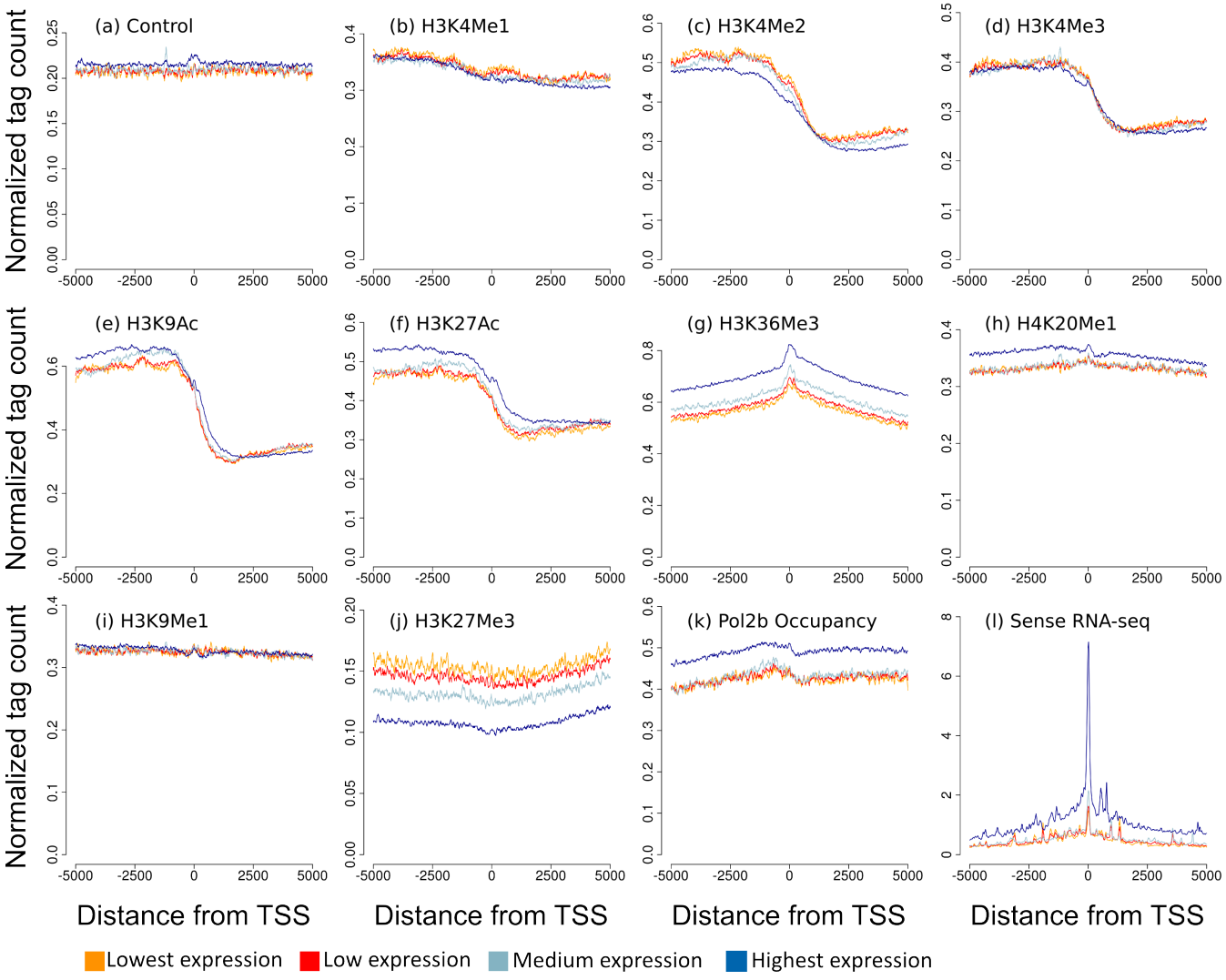
Supplementary Figure S75. Chromatin modification environment around exonic CAGE clusters in K562. Exonic CAGE clusters in the K562 cell type were identified using CAGE data from non-polyadenylated RNA from nucleus isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



Supplementary Figure S76. Chromatin modification environment around exonic CAGE clusters in K562. Exonic CAGE clusters in the K562 cell type were identified using CAGE data from polyadenylated RNA from nucleus isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



Supplementary Figure S77. Chromatin modification environment around exonic CAGE clusters in NHEK. Exonic CAGE clusters in the NHEK cell type were identified using CAGE data from non-polyadenylated RNA from cytosol isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.



Supplementary Figure S78. Chromatin modification environment around exonic CAGE clusters in NHEK. Exonic CAGE clusters in the NHEK cell type were identified using CAGE data from non-polyadenylated RNA from nucleus isolates. Exonic CAGE clusters were divided into the same four bins as cis-NAT promoters from the CAGE same set, and the normalized average numbers of ChIP-seq reads in 10 base-pair windows +/- 5kb of the exonic CAGE cluster peak (at position 0) were calculated for each bin.