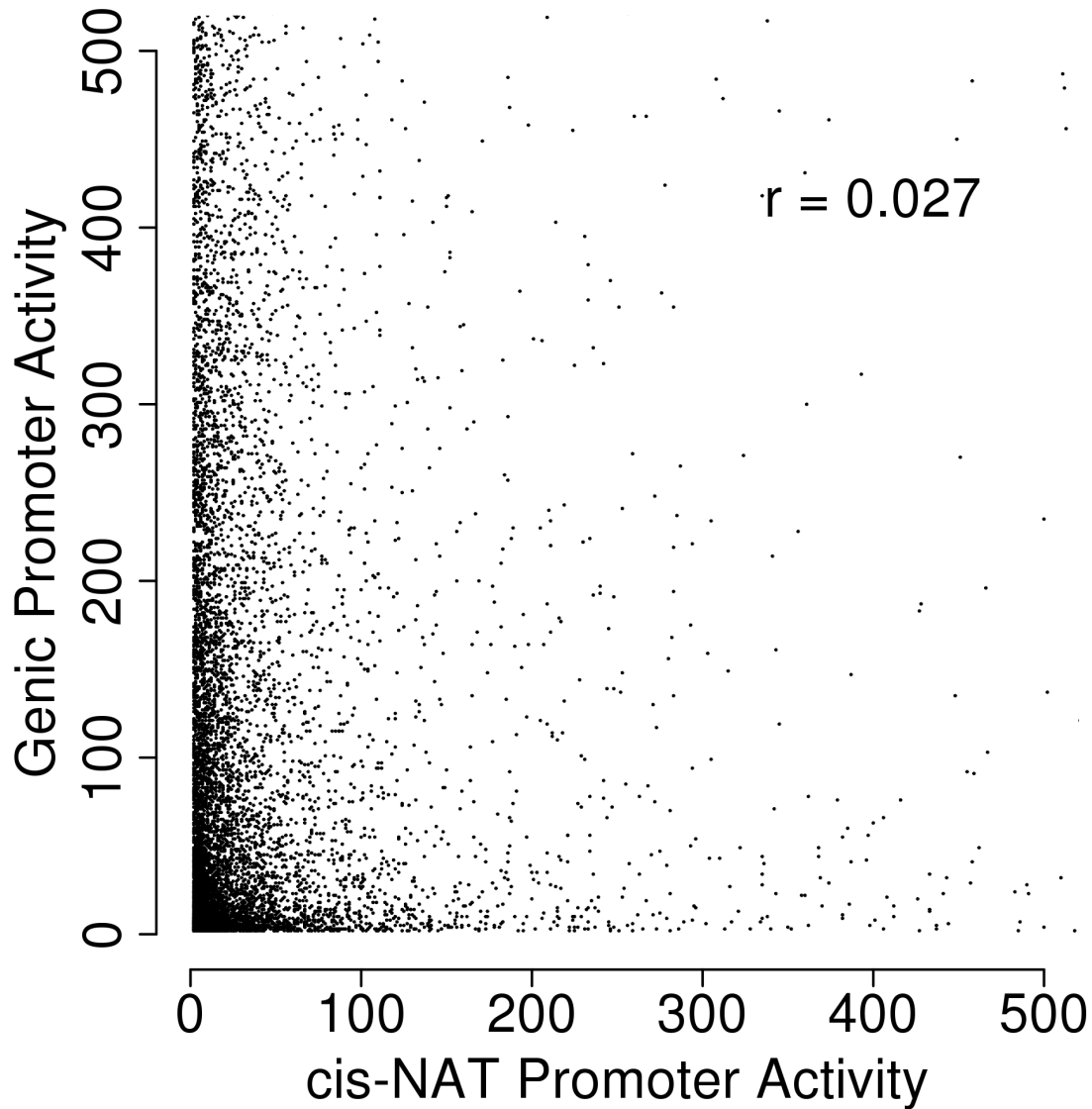
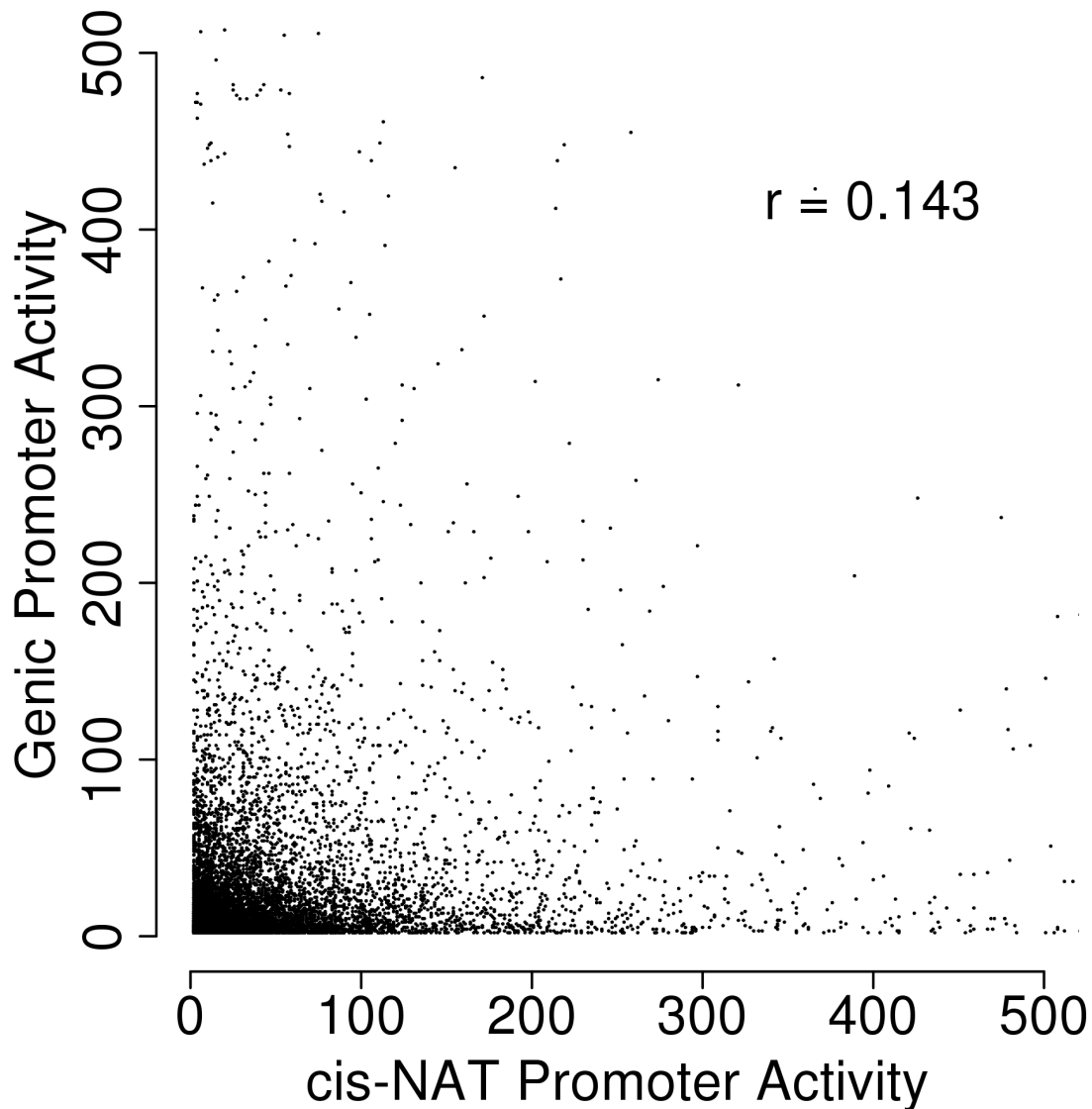


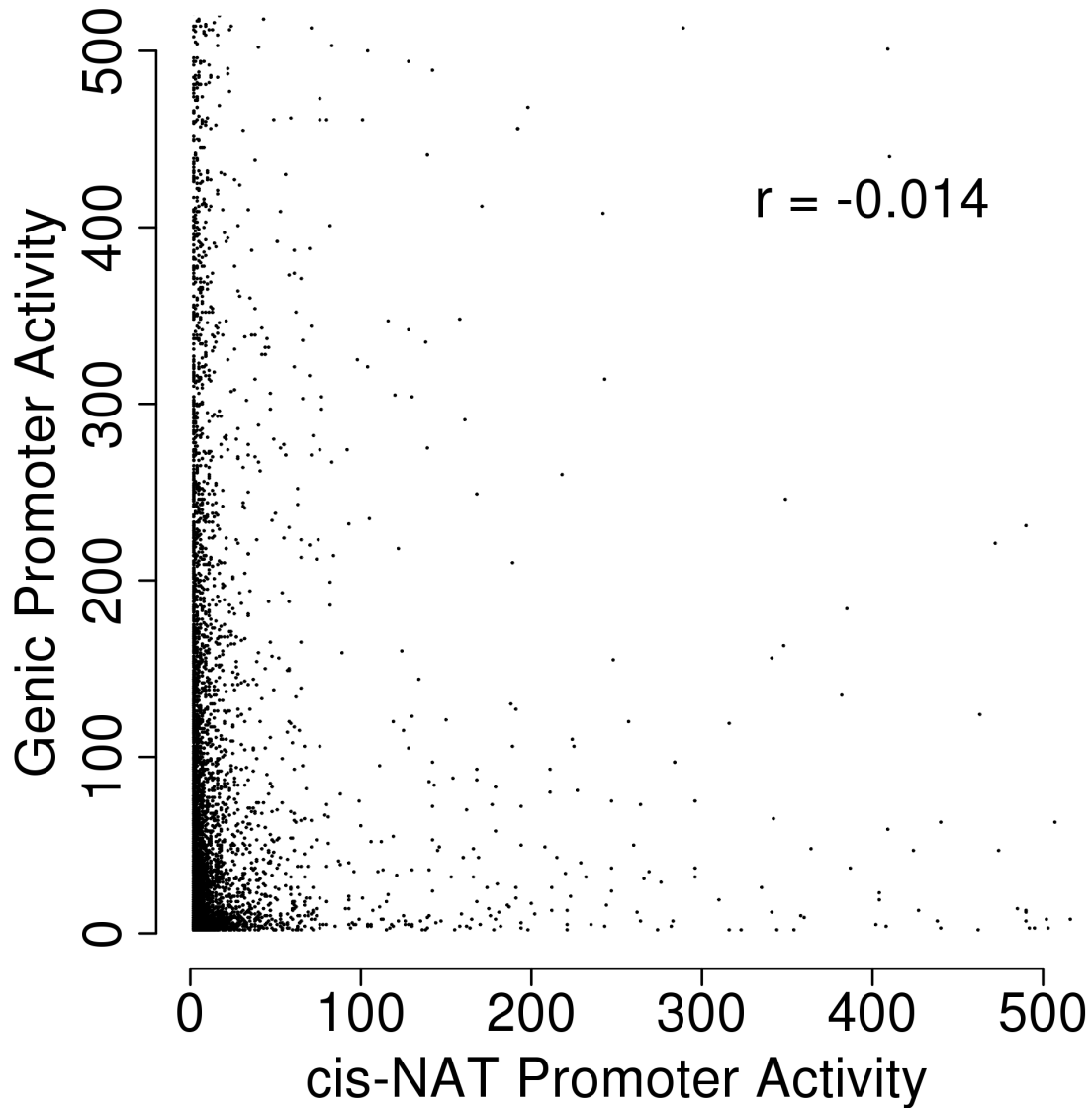
Supplementary Figure S79. Correlation between genic and cis-NAT promoter activity in GM12878. Cis-NAT promoters in the GM12878 cell type were identified using CAGE data from non-polyadenylated RNA from nucleus isolates. Activity of genic promoters and the sum of corresponding cis-NAT promoter activity was measured by CAGE tag counts. A Spearman rank correlation was used to determine the relationship between total cis-NAT promoter activity and genic promoter activity.



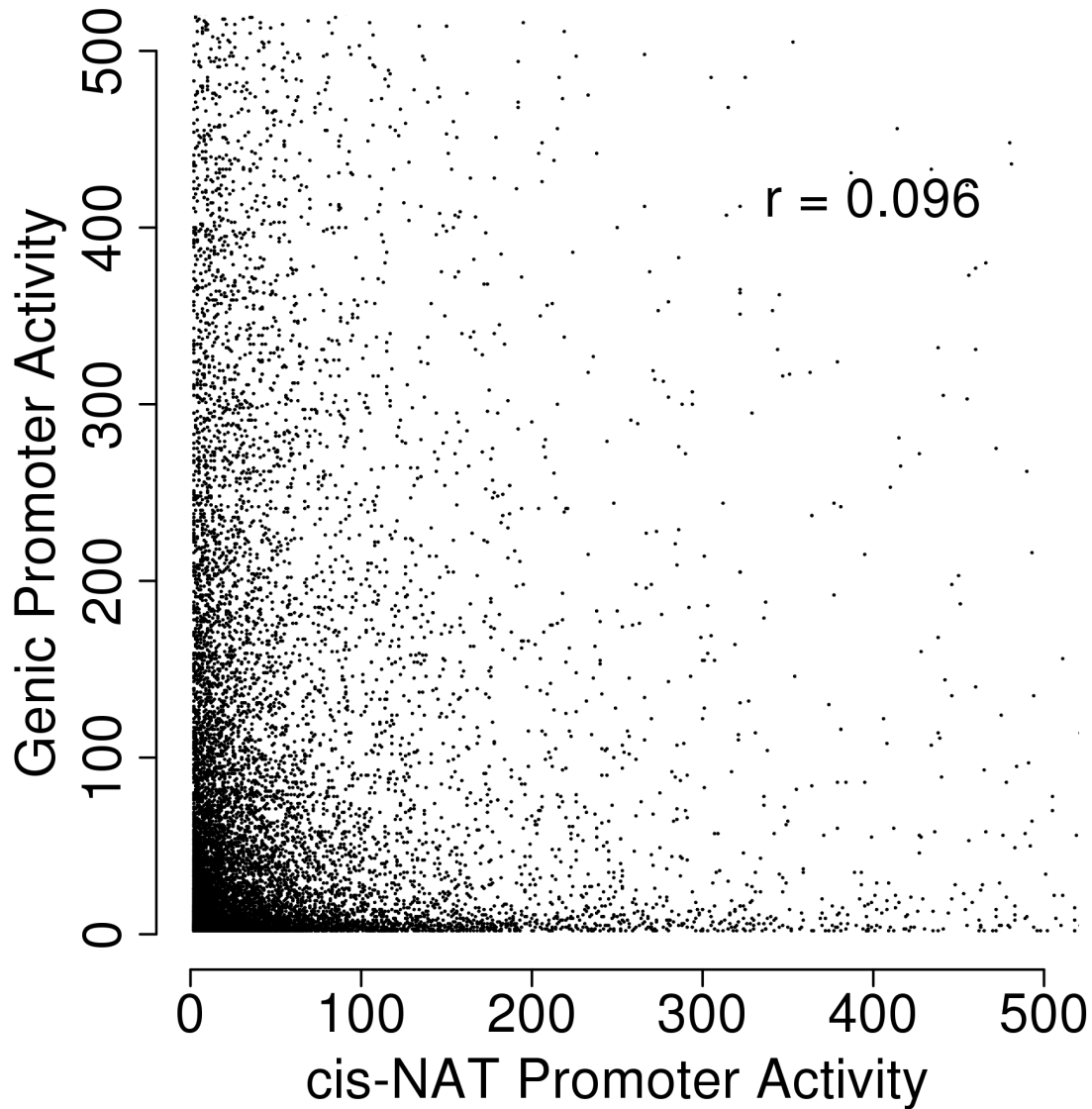
Supplementary Figure S80. Correlation between genic and cis-NAT promoter activity in H1HESC. Cis-NAT promoters in the H1HESC cell type were identified using CAGE data from non-polyadenylated RNA from whole-cell isolates. Activity of genic promoters and the sum of corresponding cis-NAT promoter activity was measured by CAGE tag counts. A Spearman rank correlation was used to determine the relationship between total cis-NAT promoter activity and genic promoter activity.



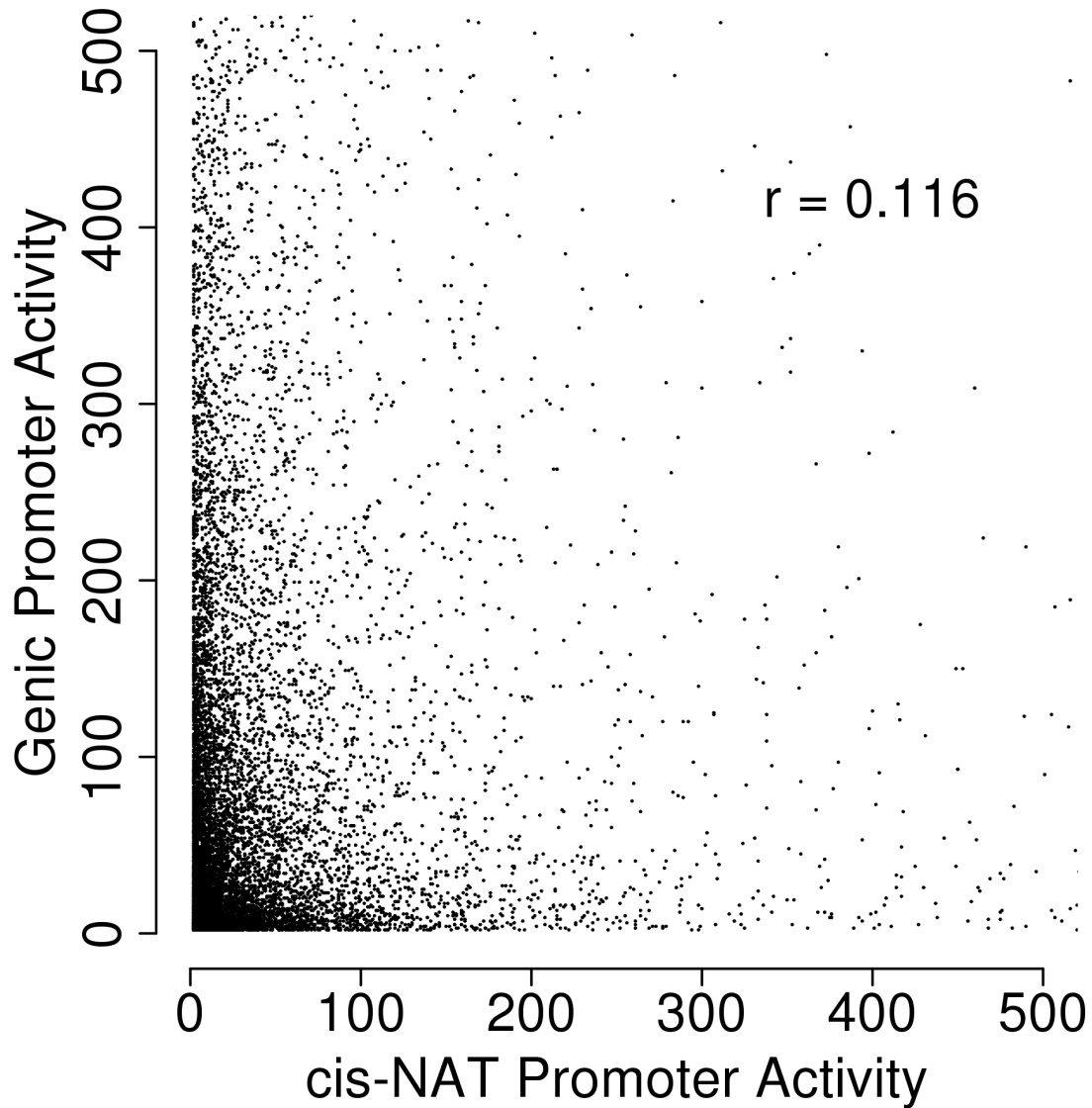
Supplementary Figure S81. Correlation between genic and cis-NAT promoter activity in HepG2. Cis-NAT promoters in the HepG2 cell type were identified using CAGE data from non-polyadenylated RNA from nucleus isolates. Activity of genic promoters and the sum of corresponding cis-NAT promoter activity was measured by CAGE tag counts. A Spearman rank correlation was used to determine the relationship between total cis-NAT promoter activity and genic promoter activity.



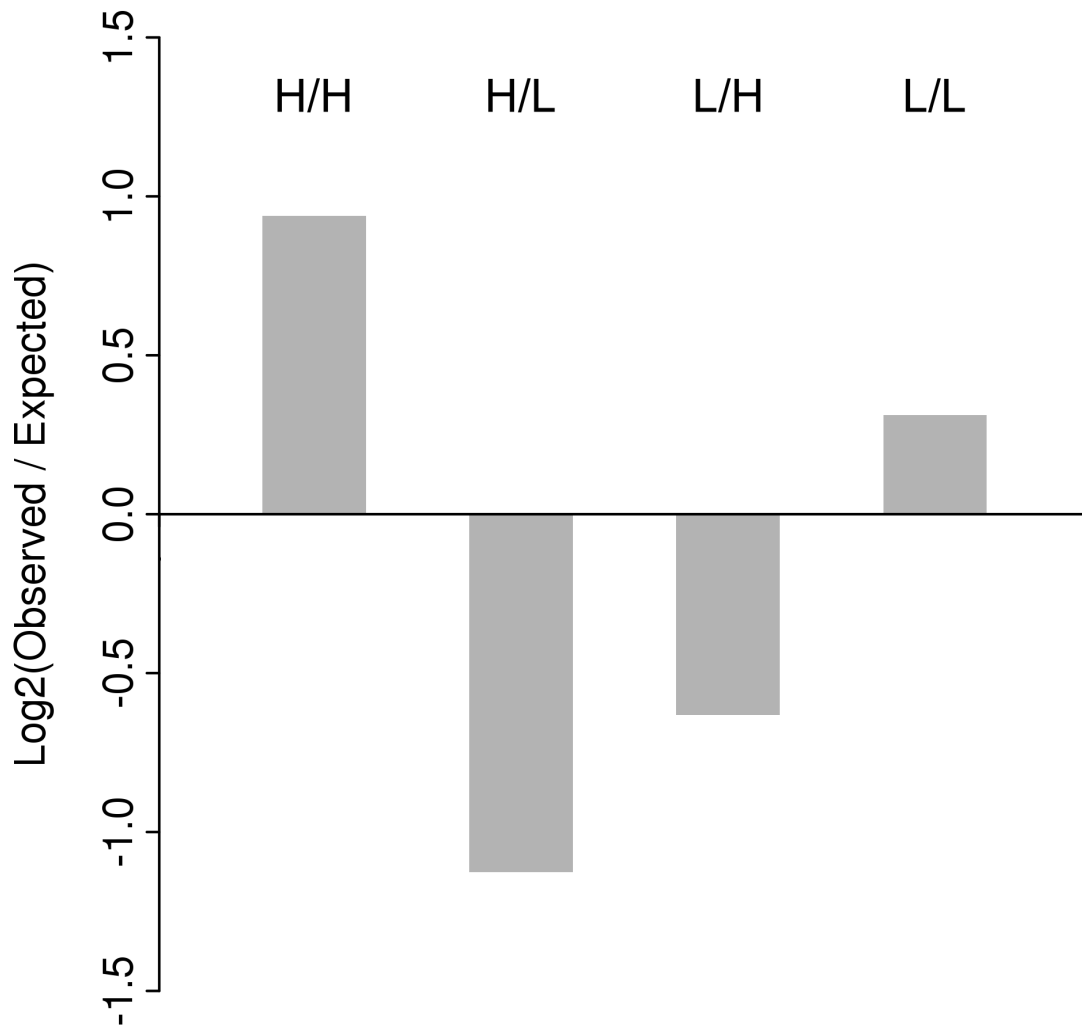
Supplementary Figure S82. Correlation between genic and cis-NAT promoter activity in HUVEC. Cis-NAT promoters in the HUVEC cell type were identified using CAGE data from non-polyadenylated RNA from cytosol isolates. Activity of genic promoters and the sum of corresponding cis-NAT promoter activity was measured by CAGE tag counts. A Spearman rank correlation was used to determine the relationship between total cis-NAT promoter activity and genic promoter activity.



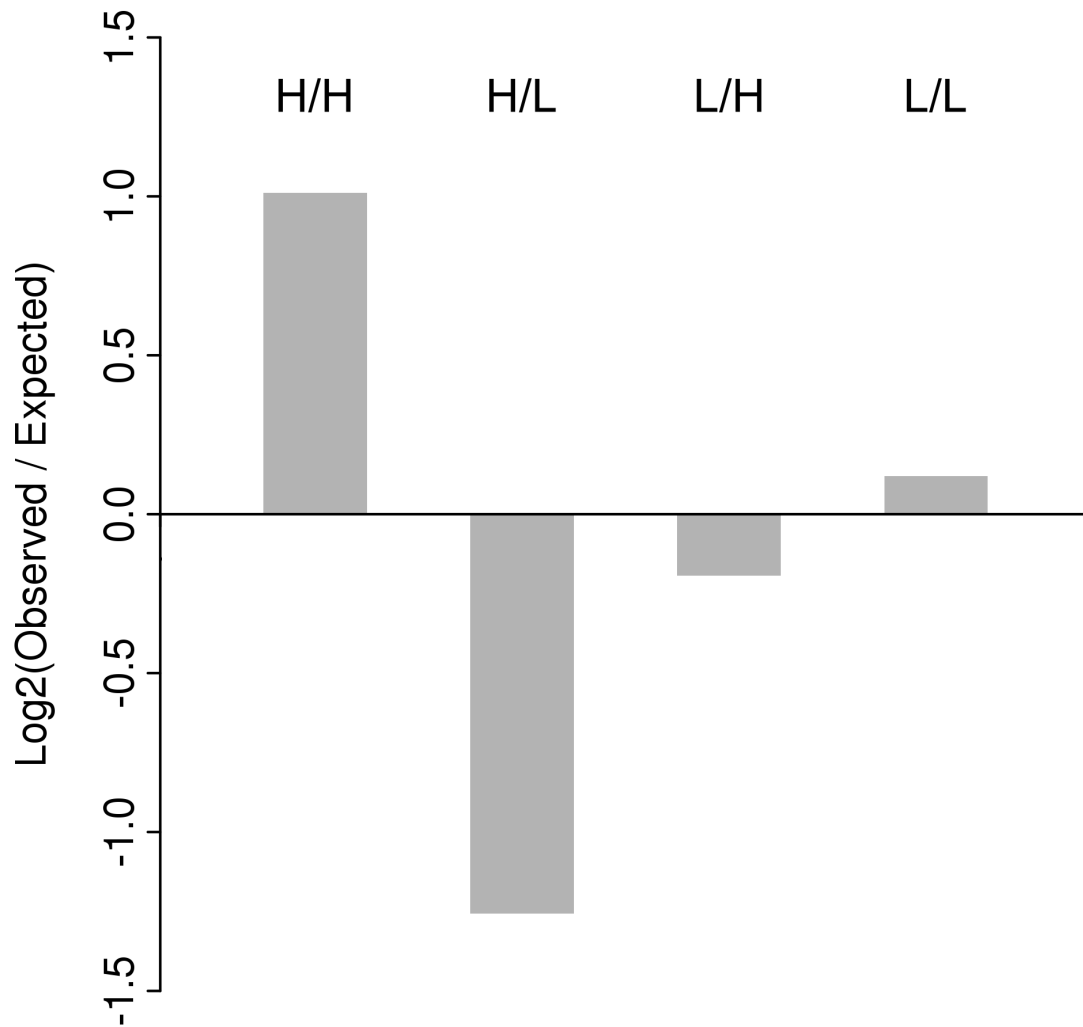
Supplementary Figure S83. Correlation between genic and cis-NAT promoter activity in K562. Cis-NAT promoters in the K562 cell type were identified using CAGE data from non-polyadenylated RNA from nucleus isolates. Activity of genic promoters and the sum of corresponding cis-NAT promoter activity was measured by CAGE tag counts. A Spearman rank correlation was used to determine the relationship between total cis-NAT promoter activity and genic promoter activity.



Supplementary Figure S84. Correlation between genic and cis-NAT promoter activity in NHEK. Cis-NAT promoters in the NHEK cell type were identified using CAGE data from non-polyadenylated RNA from nucleus isolates. Activity of genic promoters and the sum of corresponding cis-NAT promoter activity was measured by CAGE tag counts. A Spearman rank correlation was used to determine the relationship between total cis-NAT promoter activity and genic promoter activity.



Supplementary Figure S85. Association of cis-NAT promoter activity and genic promoter activity for cis-NAT promoters distal to genic promoters. Cis-NAT and genic promoters were classified into high (H) and low (L) categories based on their activity levels across all cell types analyzed here. The observed versus expected levels of association between the resulting four possible category combinations – 1) high cis-NAT & high gene (HH), 2) high cis-NAT & low gene (HL), 3) low cis-NAT & high gene (L/H), 4) low cis-NAT & low gene (L/L) – were then computed using association mining.



Supplementary Figure S86. Association of cis-NAT promoter activity and genic promoter activity for cis-NAT promoters proximal to genic promoters. Cis-NAT and genic promoters were classified into high (H) and low (L) categories based on their activity levels across all cell types analyzed here. The observed versus expected levels of association between the resulting four possible category combinations – 1) high cis-NAT & high gene (HH), 2) high cis-NAT & low gene (HL), 3) low cis-NAT & high gene (L/H), 4) low cis-NAT & low gene (L/L) – were then computed using association mining.