

Figure S4

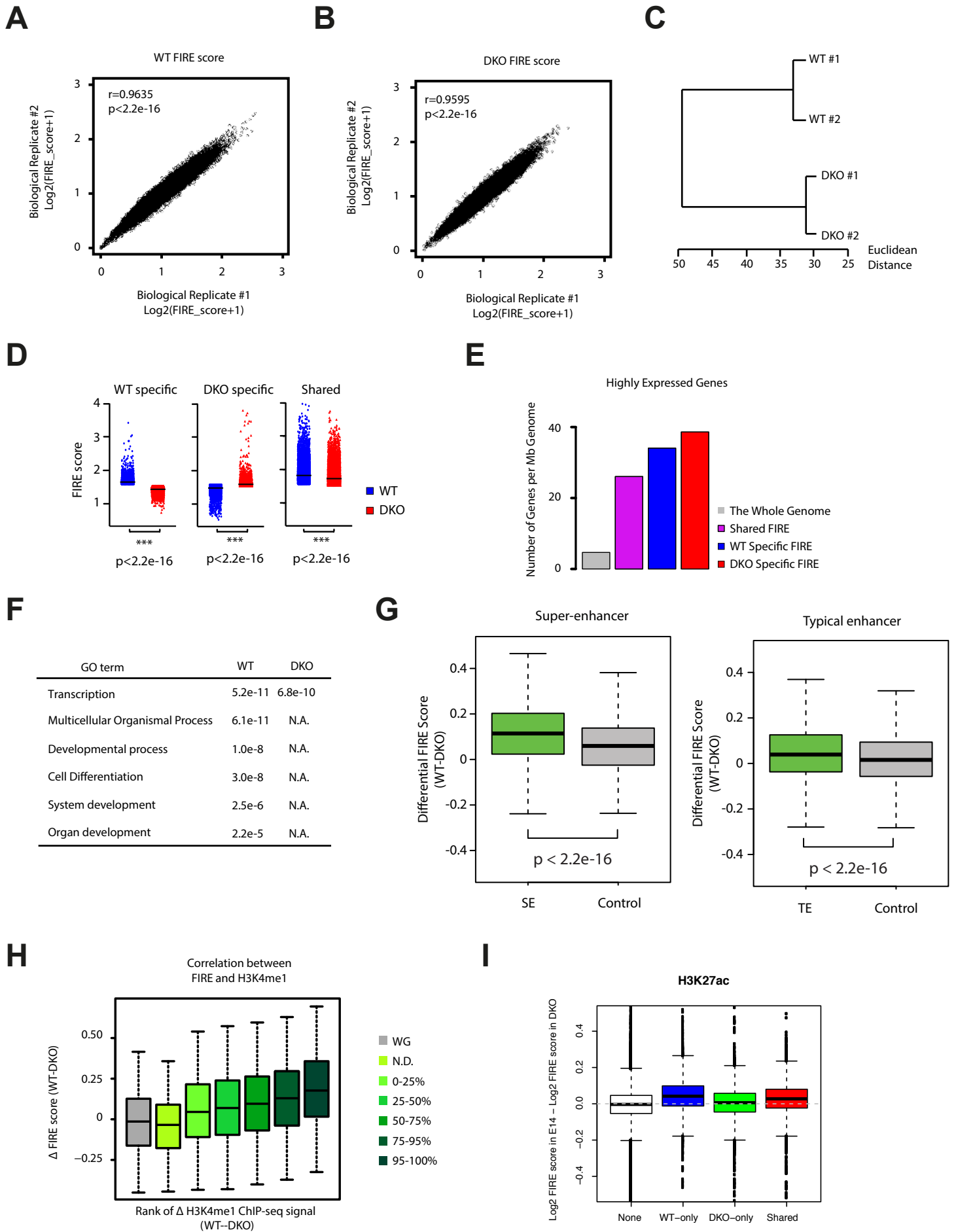


Figure S4. H3K4me1 is Required for FIREs, Related to Figure 2

(A, B) Scatter plots showing comparison of FIRE score between two biological replicates of WT cells (B) and DKO cells (C), respectively. Insets show the Pearson correlation coefficient r and p value.

(C) Cluster analysis using Pearson correlation coefficient r between samples. The x-axis represents the maximum possible Euclidean distance between samples belonging to two different clusters. From the dendrogram, we observed that two biological replicates of the same condition first clustered together, indicating that the variation between two biological replicates of the same condition is less than the variation between wild type cells and mutant cells.

(D) Jittered scatter plot showing FIRE score of different categories of FIREs. Note that in the shared FIREs, WT cells show higher FIRE score than DKO cells. The p value is computed with Mann-Whitney U test.

(E) The gene density of expressed genes (FPKM \geq 1) per Mb DNA sequences in FIREs are significantly higher than the average genome.

(F) Gene ontology analysis of genes located in WT and DKO specific FIREs respectively. The genes in WT-specific FIREs are more functionally related to cell differentiation and development. The Benjamini-adjusted p values are shown in each category.

(G) Box plot showing change of FIRE score at super-enhancers (left) and typical enhancers (right) is significantly higher than at other genomic regions with similar FIRE score.

(H) Boxplot showing the correlation between the change of H3K4me1 and change of FIRE score throughout the genome. The change of H3K4me1 is classified in different quantiles according to the change of the input normalized RPKM value. Note that only 19% of bins that showed detectable change of H3K4me1 were included in the analysis. The other 81% of bins were indicated as 'N.D.' in the figure. The data of all the bins were included (WG) for comparison. Y-axis shows the change of FIRE score for the indicated bins.

(I) Boxplot showing that change of H3K27ac signal is correlated with change of FIRE scores. Similar to Figure 4D, the 10-kb bins were categorized to 4 groups: I, no H3K27ac peaks in either cell type; II, with WT specific H3K27ac peaks only; III, with DKO specific H3K27ac peaks only; IV, with shared H3K27ac peaks. y-axis shows Log₂ transformed fold change of FIRE score between WT and DKO cells.