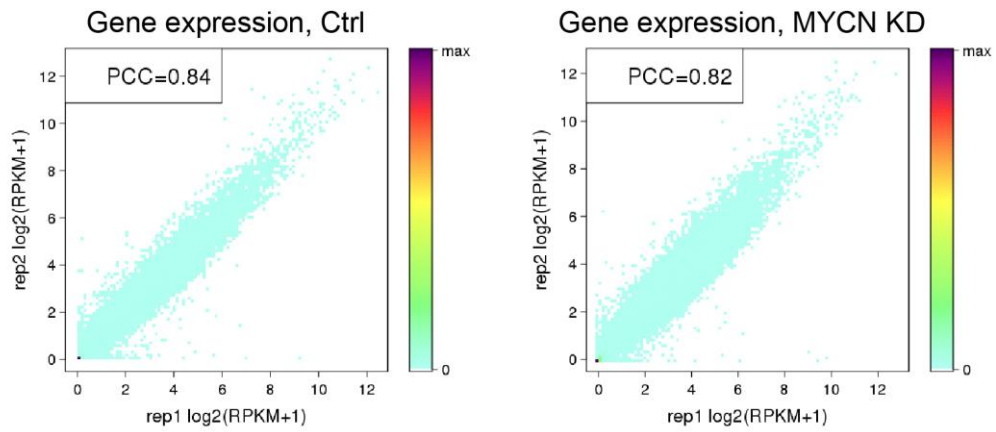
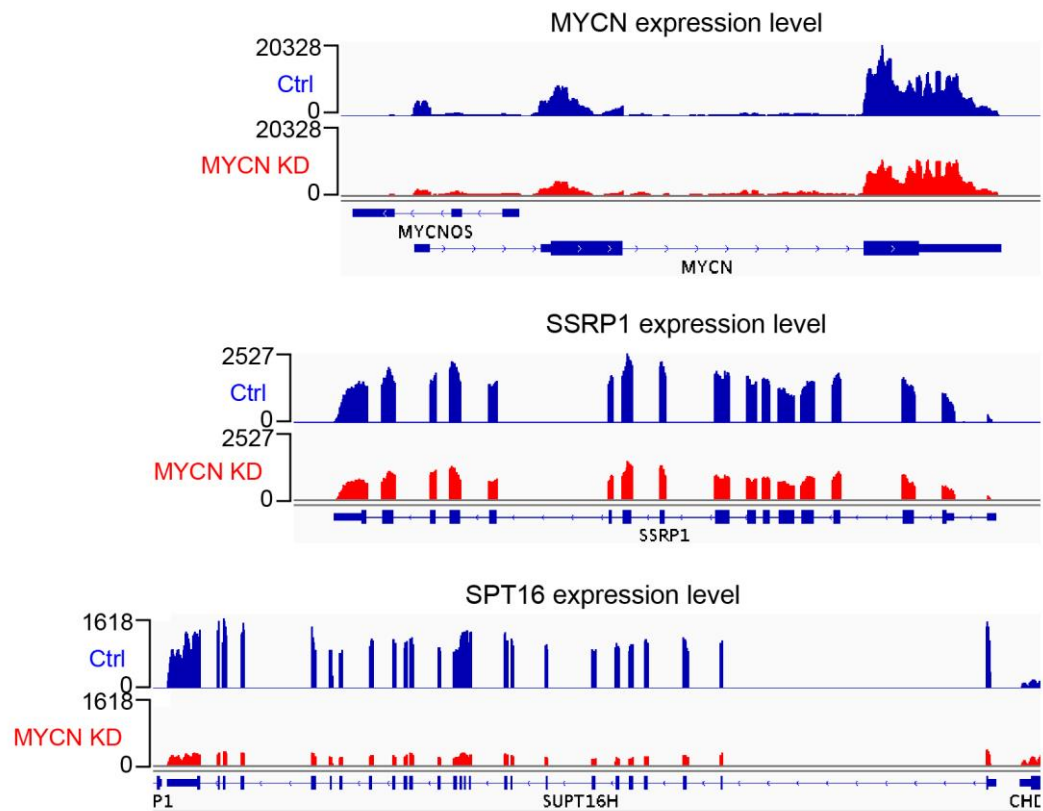


Supplementary Figures and Figure legend

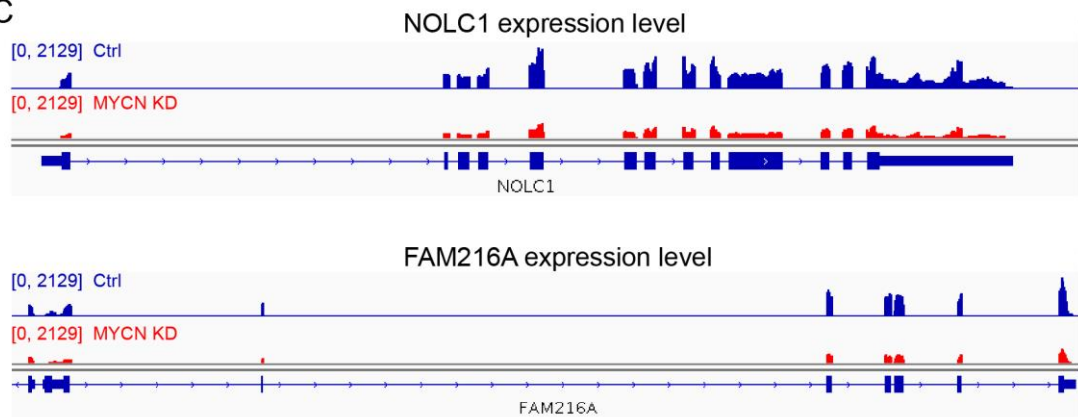
A



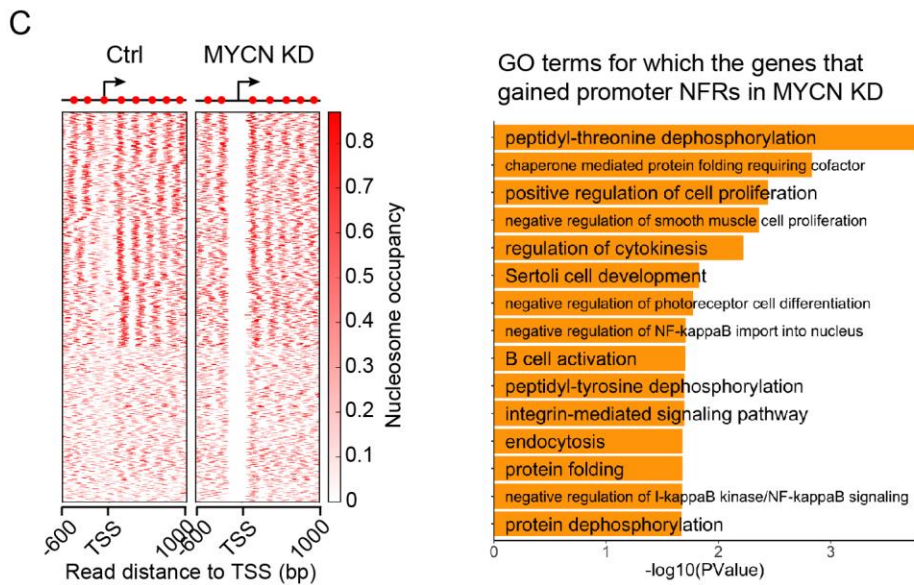
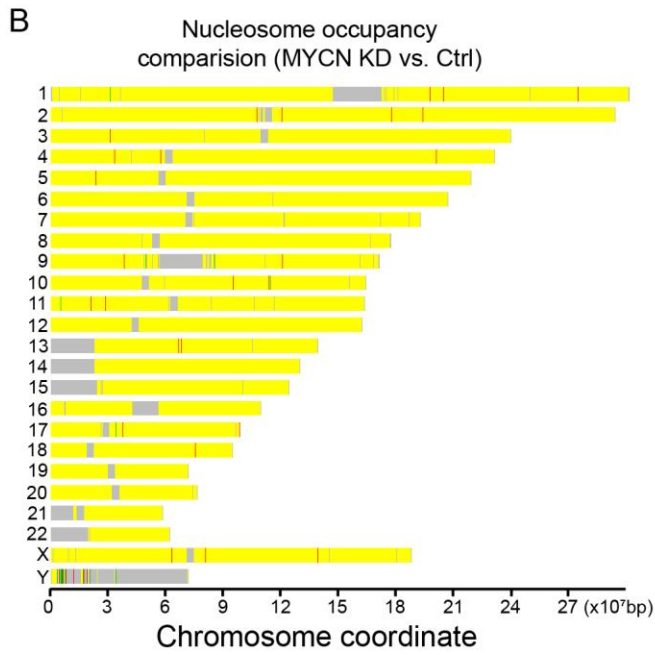
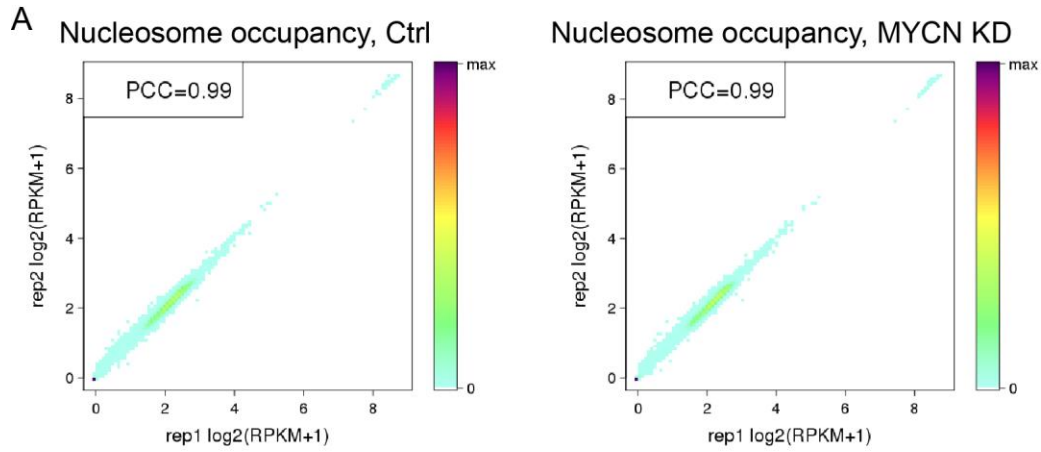
B



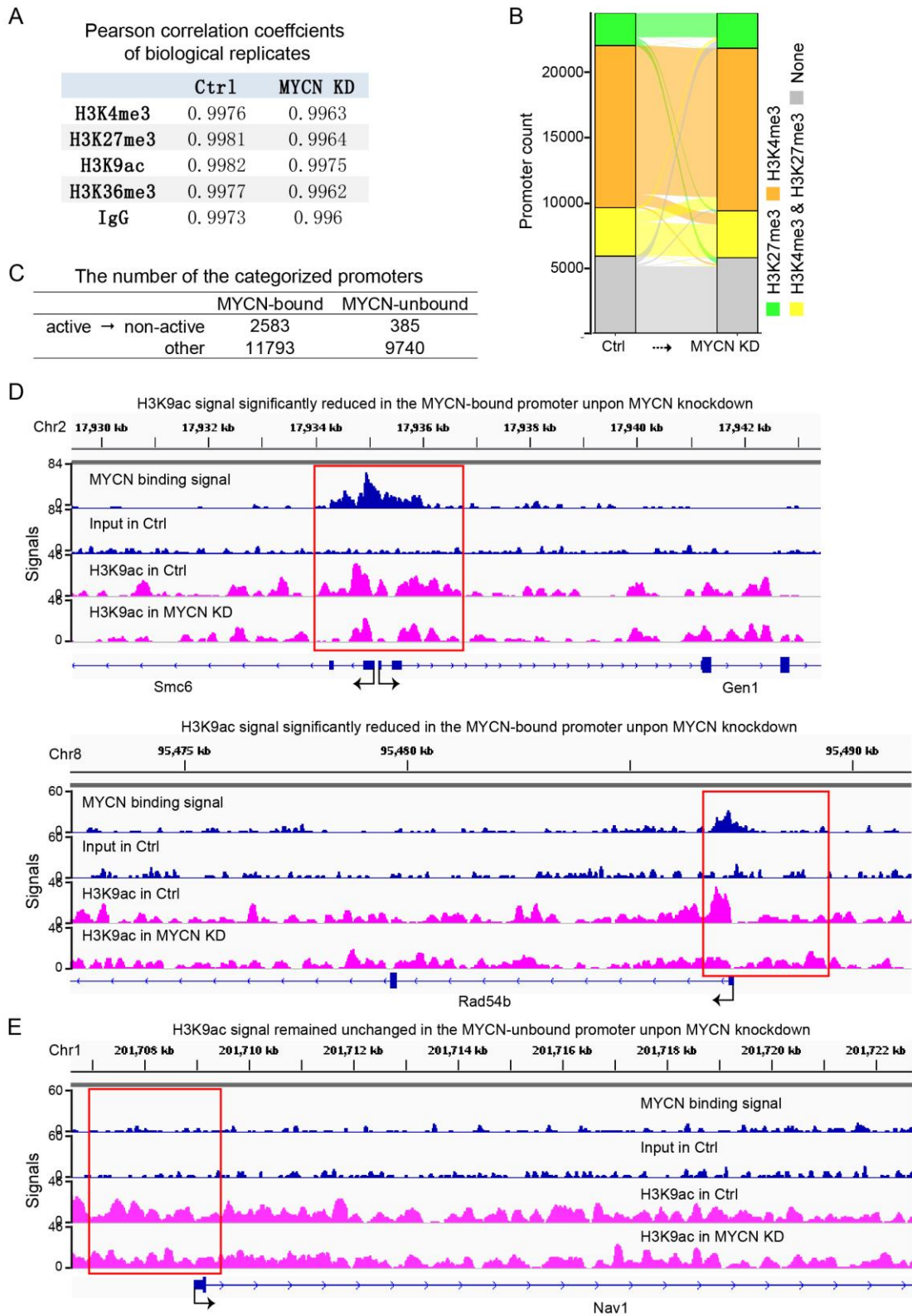
C



Supplementary Figure S1 | Knockdown of MYCN down-regulates the expression of FACT in neuroblastoma. **(A)** RNA-seq data are highly reproducible. **(B)** Track view of RNA-seq density shows greatly decreased expression levels of MYCN, SPT16, and SSRP1 after MYCN knockdown. **(C)** Track view of RNA-seq density shows greatly decreased expression levels of MYCN target genes *Nolc1* and *Fam216a* after MYCN knockdown.

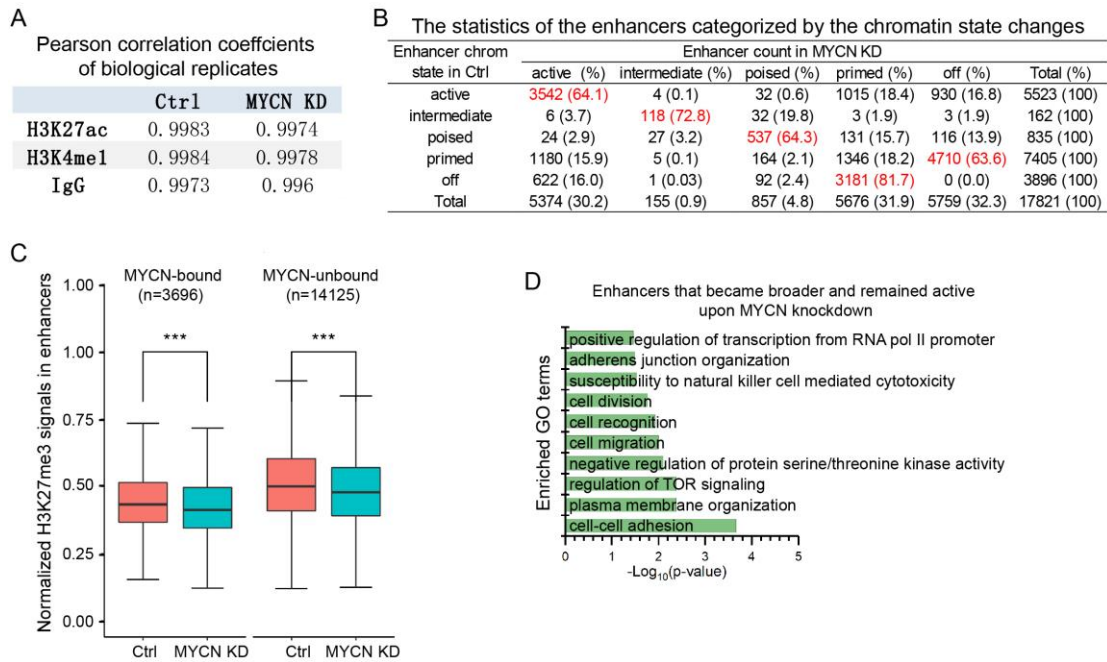


Supplementary Figure S2 | Global nucleosome occupancy profiles. **(A)** The genome is scanned with a 10-kb window and nucleosome occupancy is calculated and normalized as RPM (Reads Per Million mapped reads) for each window. The high correlation of the global nucleosome occupancy between the biological replicates indicates the high reproducibility (PCC: Pearson Correlation Coefficient). **(B)** Limited variations in nucleosome occupancy across the genome after MYCN knockdown compared with the control. The ratio of normalized nucleosome occupancy within each window is presented by a color. Red indicates read count in MYCN knockdown is at least 2 fold of that in the control. Green indicates read count in MYCN knockdown is less than half of that in the control. Yellow indicates the ratio is less than two folds. Grey indicates regions of Ns in the genome. **(C)** NFR formation in the promoter regions of a set of genes after MYCN knockdown through nucleosome eviction (left heatmap). Significantly enriched GO terms for this set of genes (right bar plot).



Supplementary Figure S3 | Histone modification changes in the promoters upon MYCN knockdown. **(A)** The ChIP-seq data of histone modifications are highly

reproducible. **(B)** The alluvial plot shows the dynamics of histone modifications (HMs) in the promoters upon MYCN knockdown. **(C)** There are significantly higher portion of MYCN-bound promoters than MYCN-unbound promoters whose chromatin state changes from active to non-active upon MYCN knockdown ($p < 0.001$, Chi square test). **(D)** Track view of MYCN binding and H3K9ac signals in the MYCN-bound promoter (marked in the red box) of the representative DNA repair-related genes *Smc6*, *Cen1*, *Rad54b*. **(E)** Track view of MYCN binding and H3K9ac signals in the MYCN-unbound promoter (marked in the red box) of the representative gene *Nav1*.



Supplementary Figure S4 | Histone modification changes in the enhancers upon MYCN knockdown. **(A)** The ChIP-seq data of histone modifications are highly reproducible. **(B)** The statistics of the enhancers categorized by the chromatin state changes upon MYCN knockdown. **(C)** H3K27me3 signals are significantly reduced in both MYCN-bound and MYCN-unbound enhancers upon MYCN knockdown (***: $p < 0.001$, Wilcoxon rank sum test). **(D)** GO terms for which the enhancers are enriched whose width becomes larger and remains an active chromatin state upon MYCN knockdown.