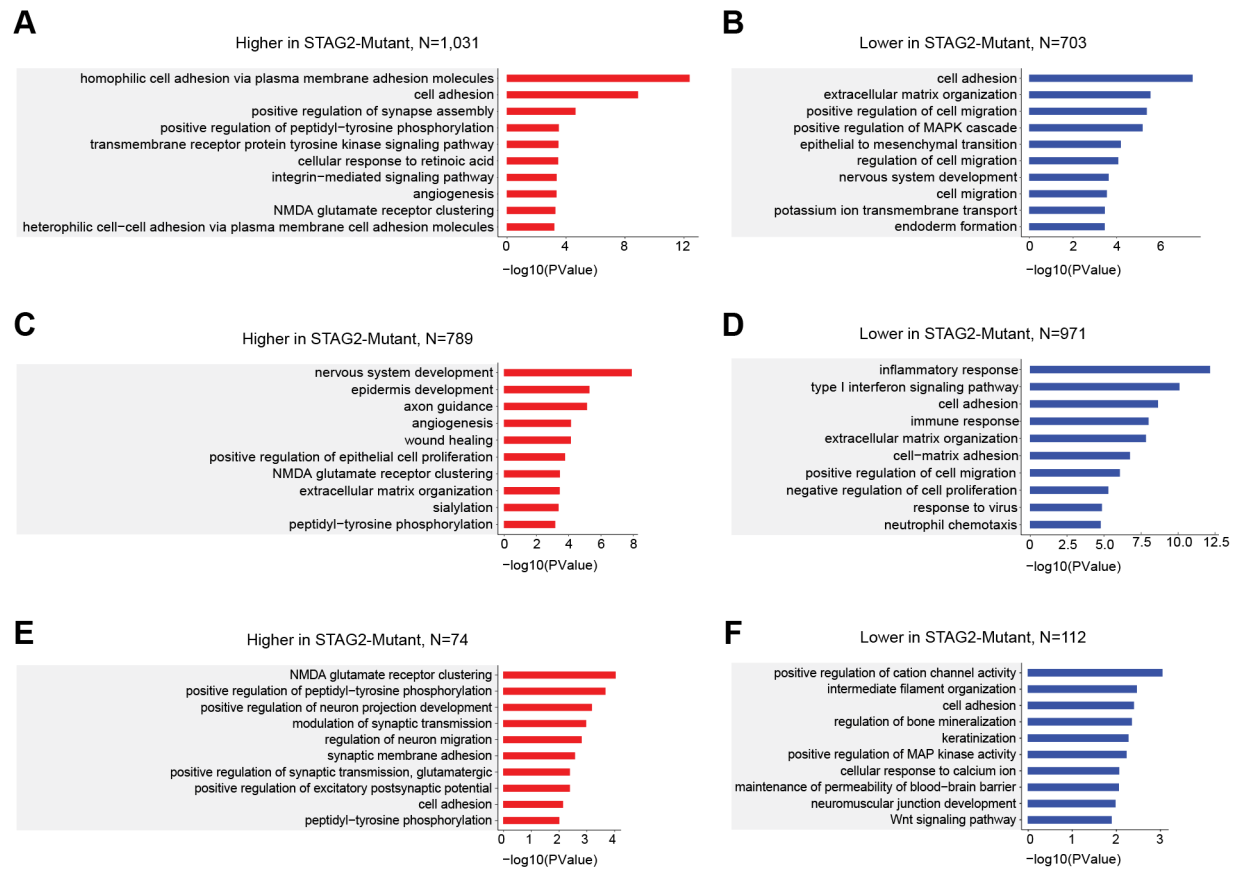
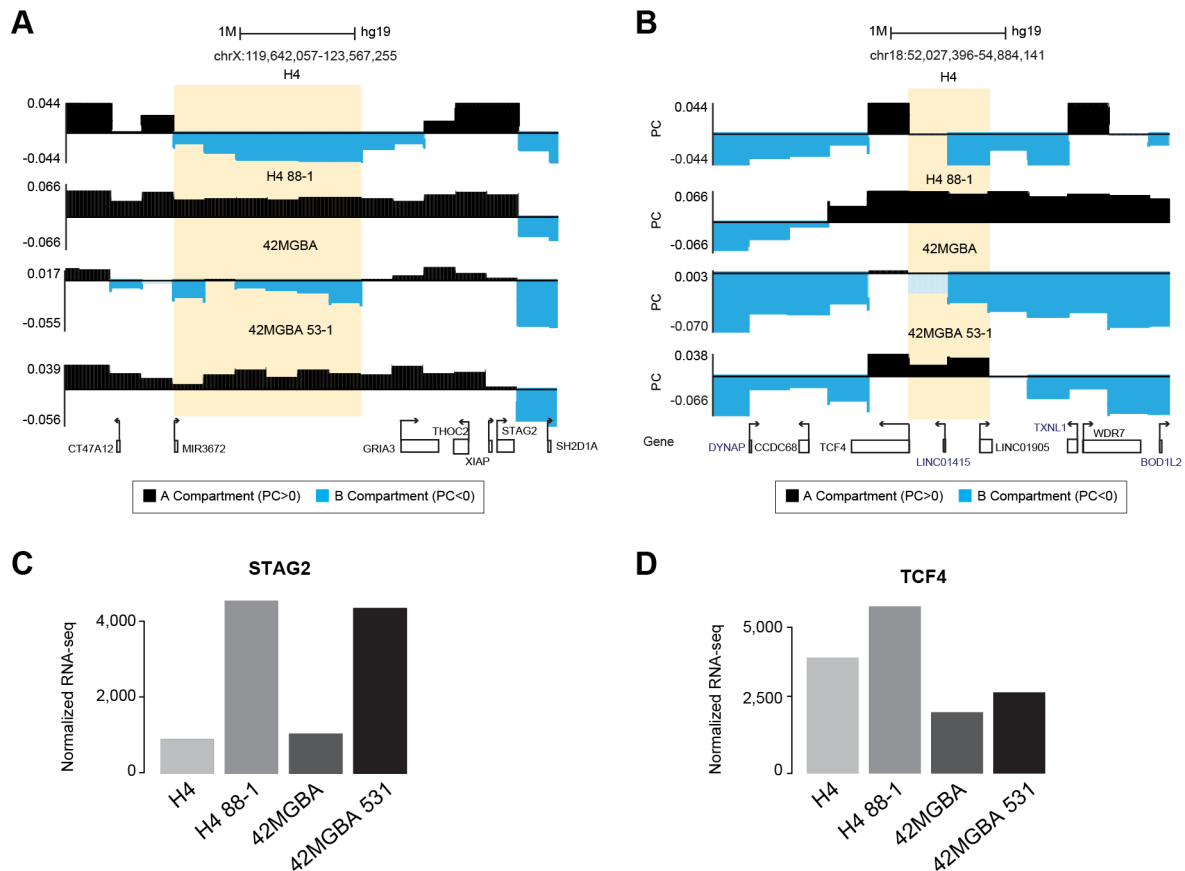
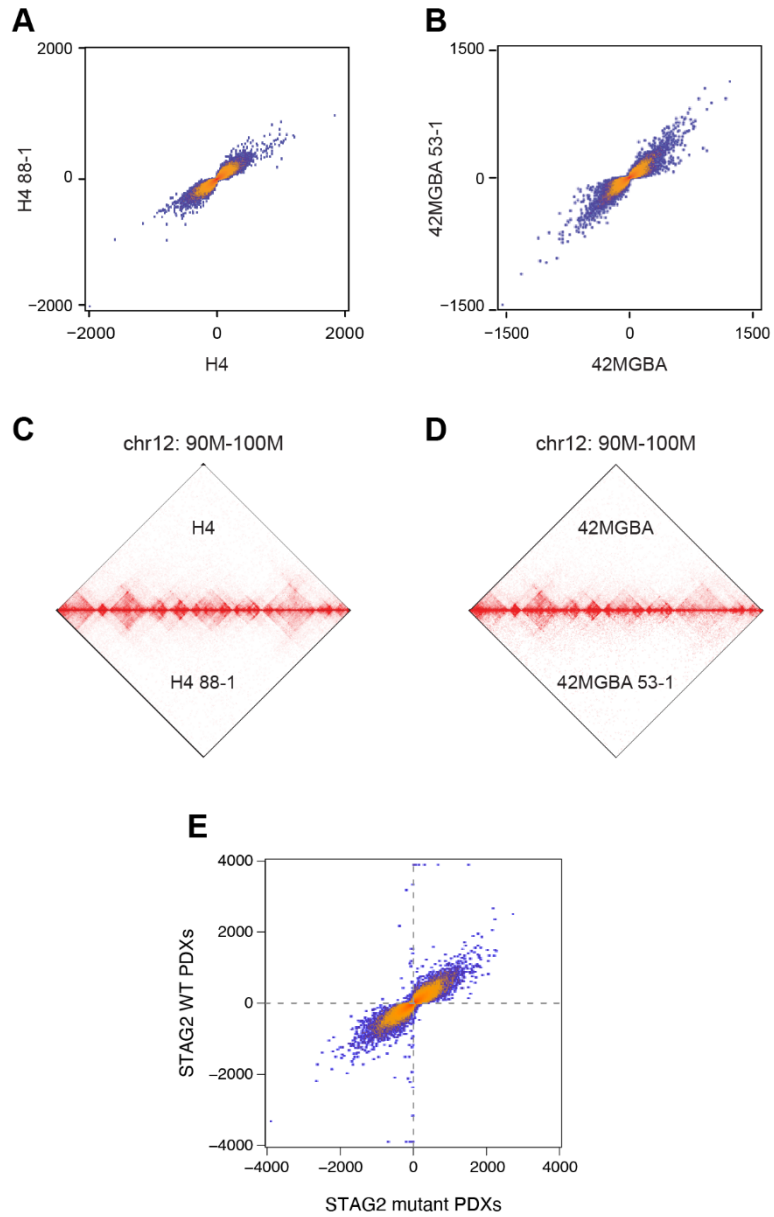




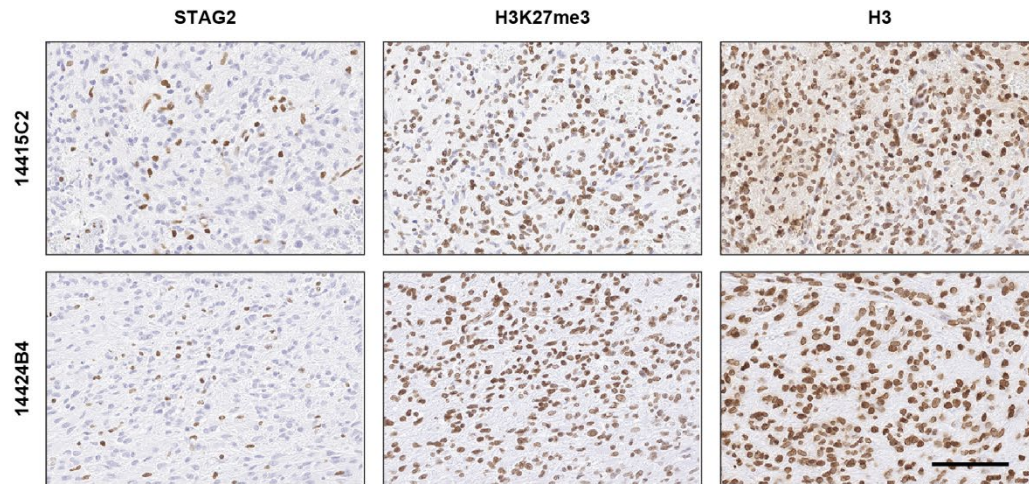
Supplementary Figure S1. Gene enrichment analysis of STAG2-regulated genes in (A,B) the H4 cell system, (C,D) the 42MGBA cell systems, and (E,F) the genes whose regulation by STAG2 was conserved between the H4 and 42MGBA cell systems.



Supplementary Figure S2. Conserved STAG2-regulated compartments switches. (A,B) Compartment diagrams depicting the effect of STAG2 correction on B to A compartment switching in the H4 and 42MGBA isogenic systems for the genomic regions containing (A) STAG2 and (B) TCF4. (C,D) Bar graphs showing RNA-seq data for the TCF4 and STAG2 genes in the H4 and 42MGBA isogenic systems, demonstrating that the conserved B to A compartment switches after STAG2 correction lead to the expected increase in gene expression.



Supplementary Figure S3. Effect of STAG2 correction on TADs in GBM. (A,B) Scatterplots indicating the effect of STAG2 mutation correction on directionality indices (DI; a measurement of TAD boundaries) in the (A) H4 and (B) 42MGBA isogenic systems. (C,D) Examples of TAD heatmap contact matrices at 40 kb resolution for (C) H4 isogenic system and (D) 42MGBA isogenic systems for a representative 10 Mb genomic region on chromosome 12. (E) Scatterplots comparing TADs in STAG2 mutant GBM PDXs (x axis) with TADs in STAG2 wild-type GBM PDXs (y axis).



Supplementary Figure S4. Immunohistochemistry with the antibodies indicated to two additional FFPE STAG2-mutant GBM primary tumors. Scale bar is 100 μ m.