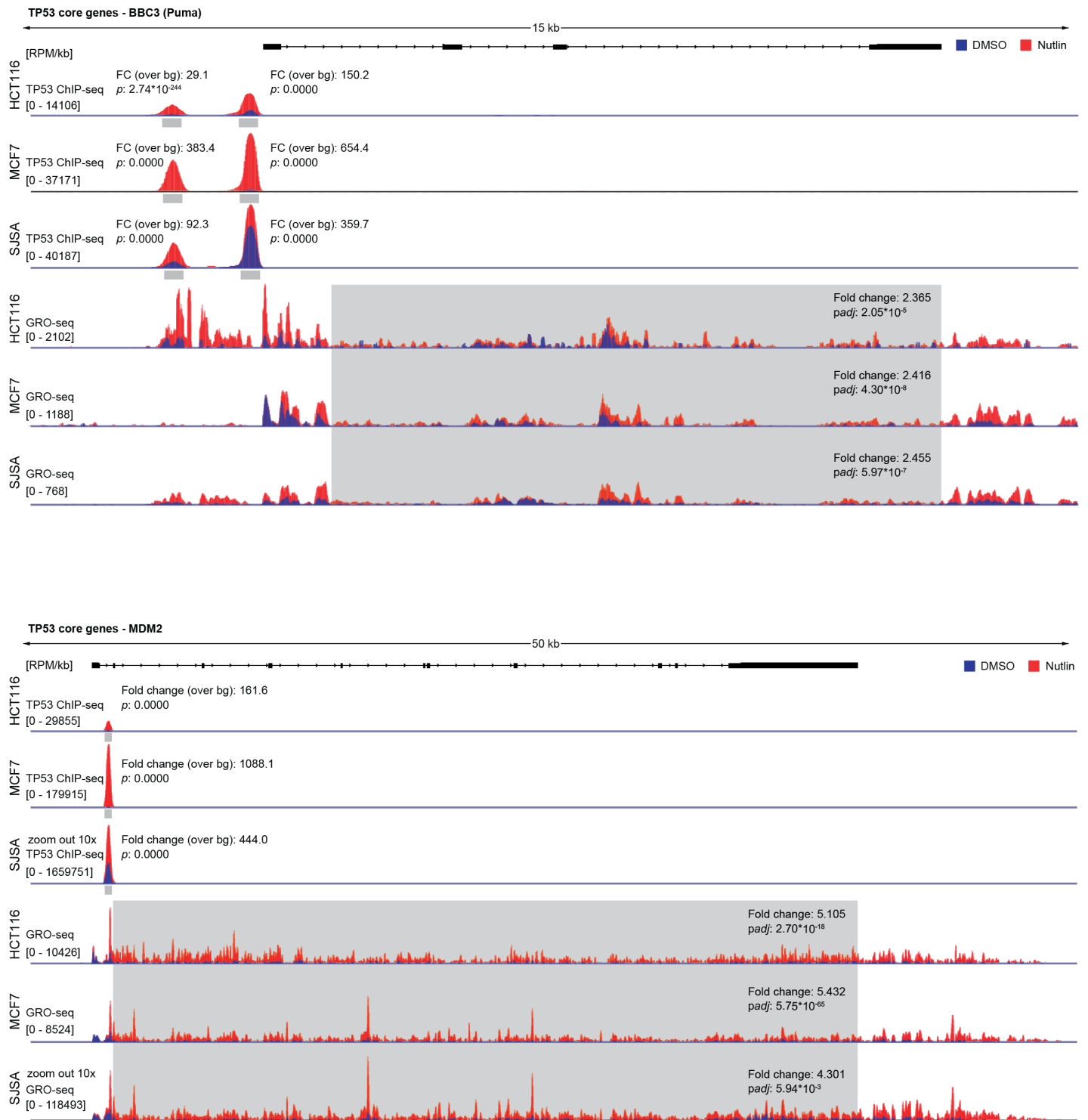
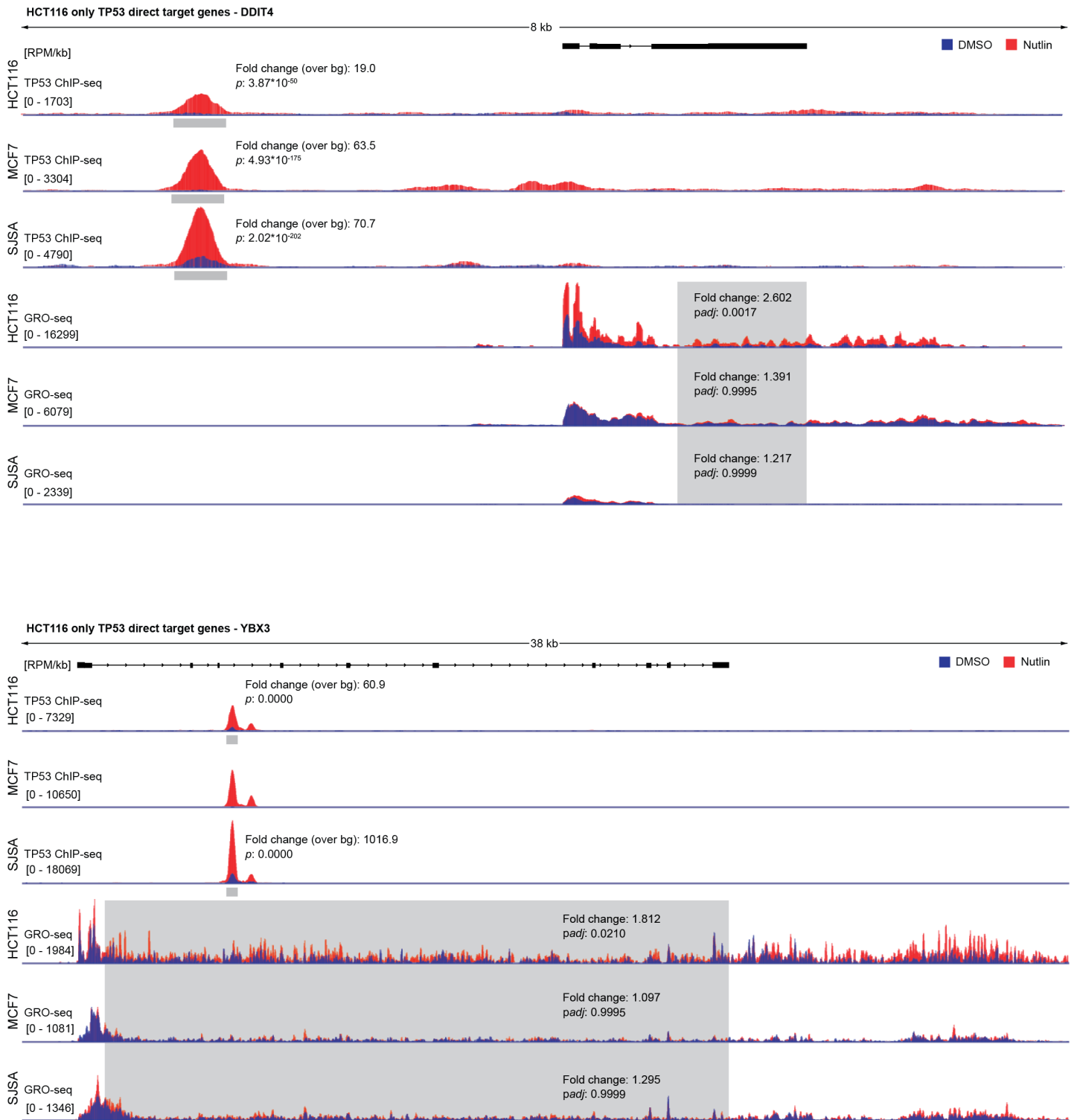
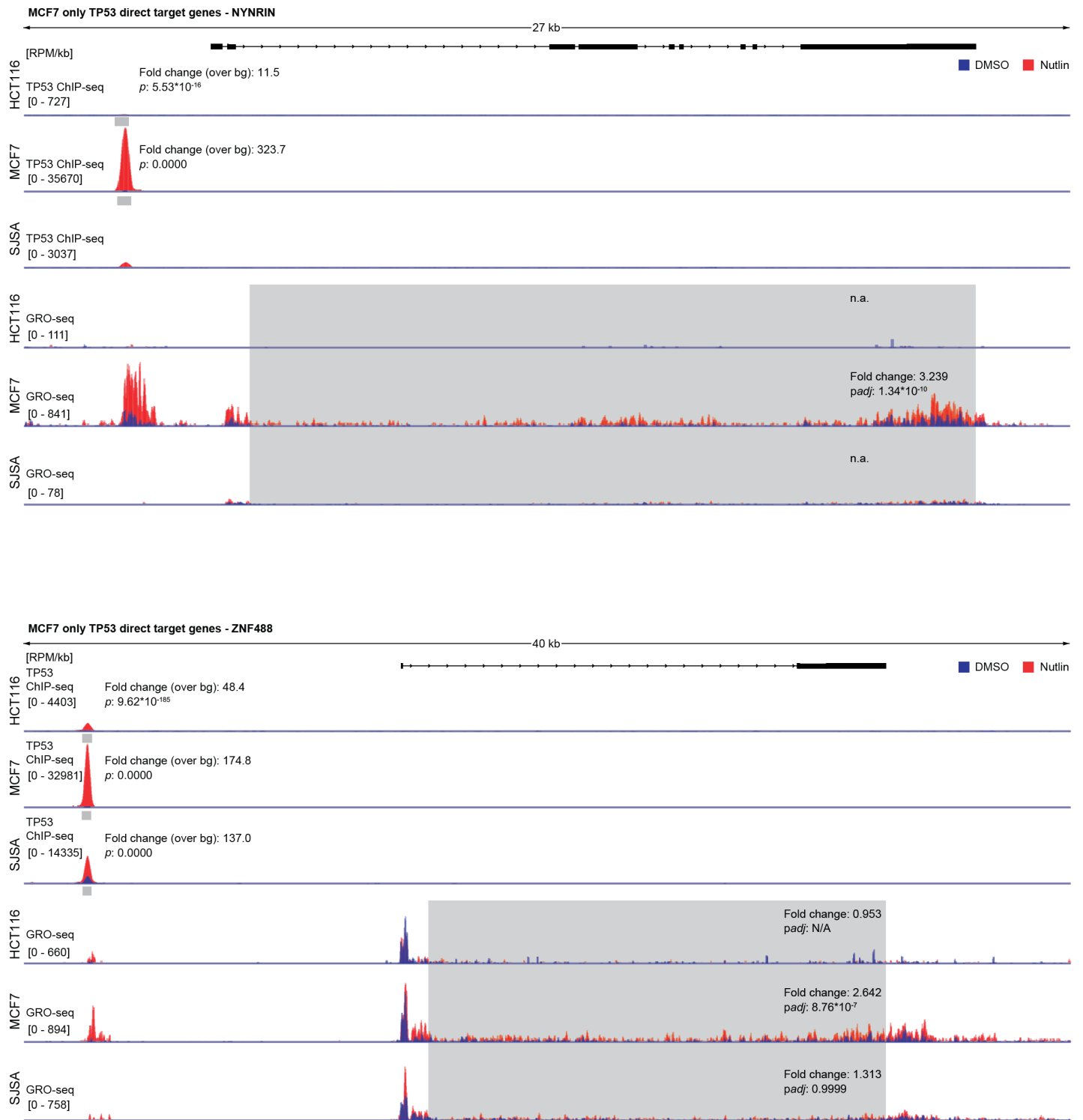
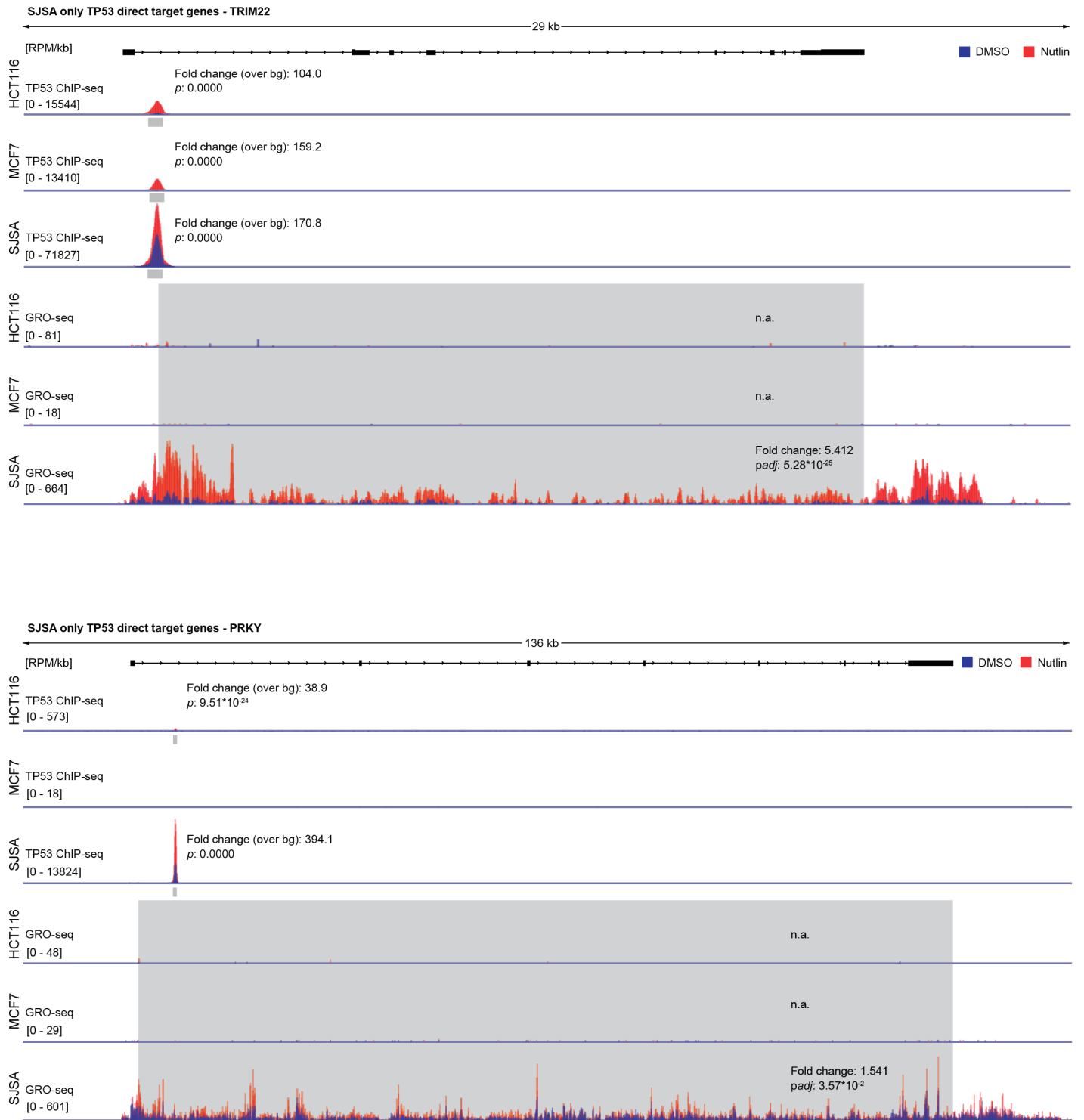


**A****Figure S3** (continued on next page, legend follows).

**B**

**Figure S3** (continued on next page, legend follows).

**C****Figure S3** (continued on next page, legend follows).

**D****Figure S3** (legend on next page).

**Figure S3 related to Figure 2.**

Genome browser tracks show TP53 ChIP-seq and GRO-seq reads in HCT116, MCF7, and SJSA cell lines. Panels depict examples of genes activated by Nutlin either in all cell lines (A) or in a cell type-specific fashion (B-D). Grey boxes below the TP53 ChIP-seq tracks mark positions of TP53 peaks identified by Homer. Associated fold changes and p values were calculated by Homer findPeaks. Large grey boxes over the GRO-seq tracks show the gene body area (from TSS +1kb to TTS) used to compare read densities from DMSO- and Nutlin-treated samples by DESeq2. n.a. denotes transcriptionally inactive genes as determined by FStitch.