



Figure S5 (legend on next page).

Figure S5 related to Figure 4. TP53 activates a core transcriptional program across diverse cell types.

(A) Pie charts showing the fraction of early direct genes with TP53 peak within 2.5 kb from TSS.

(B) Box and whisker plot depicts differences in fold changes (RPKM) of TP53 core and cell type-specific direct genes in non-tumor cell lines (foreskin fibroblasts BJ, retinal epithelial cells RPE1, primary lung fibroblasts IMR90) exposed to Nutlin and induced pluripotent stem cells treated with doxorubicin. Statistics: Mann-Whitney U test, $p < 0.01$. See also Supplemental File S7.

(C) Manhattan plot showing ChIP-seq analysis of TP53 occupancy. Numbers in parentheses indicate number of TP53 peaks identified as cell type-specific for each cell line.

(D) ChIP-seq data from the ENCODE project data was analyzed to determine the binding patterns of diverse transcription factors in HCT116 and MCF7 cell lines. Numbers of peaks occupying the same genomic sites in both cell lines (± 100 bp) are represented in diagram overlaps. Sequences of the *de novo* identified sequence motifs are shown in the bottom panels.

(E) Motif enrichment analysis for various transcription factors in HCT116 versus MCF7 cells. Frequency of the top identified motif was compared with its background occurrence across the genome.