

Figure S6 related to Figure 6. Mutation frequency and copy number loss analyses for TP53 target genes.

(A) Frequency of non-silent mutations and significantly mutated genes (SMGs) identified by MutSigCV in tumors with either wild type (wt) or mutant *TP53*, across all cancer types.

(B) Pie charts showing the mutation frequencies of the three TP53 core target genes found to be significantly mutated in the analysis in Figure 6B, dividing tumors by *TP53* status.

(C) Map of chromosome 6 indicating the position of the TP53 targets *ASCC3*, *PRDM1* and *SESN1*.

(D) Analysis of copy number loss frequencies for all genes (white) versus TP53 core target genes (blue). p-values were calculated with *t*-test. TP53 core target genes within a significantly lost region (Gistic2.0, $q < 0.01$) are marked in red and listed. The complete list of genomic loci with significant copy number variations can be found in Supplemental File S10.

(E) Analysis of copy number loss as in (D) for diverse tumor types.

(F) Analysis of copy number loss as in (D) for diverse tumor types, divided by *TP53* mutation status. Only those tumor types with sufficient numbers in each group were analyzed.

(G) Genomic positions of significant copy number losses (Gistic 2.0, $q < 0.01$) in TP53 wild type head and neck squamous cell carcinomas.

(H) Map of chromosome 11 highlighting the size of the significantly lost region in TP53 wild type head and neck squamous cell carcinomas and the position of the core TP53 targets in this region.

(I) Cumulative distribution plots for copy number loss frequencies identified with Gistic 2.0 in head and neck squamous cell carcinomas. The size of each point (gene) reflects the significance of the loss (*q*-value). TP53 wild type (green) and mutant (orange) tumors were analyzed and plotted separately. Genes highlighted in bold show a significant copy number loss (Gistic 2.0, $q < 0.01$).