

Supplementary Figures

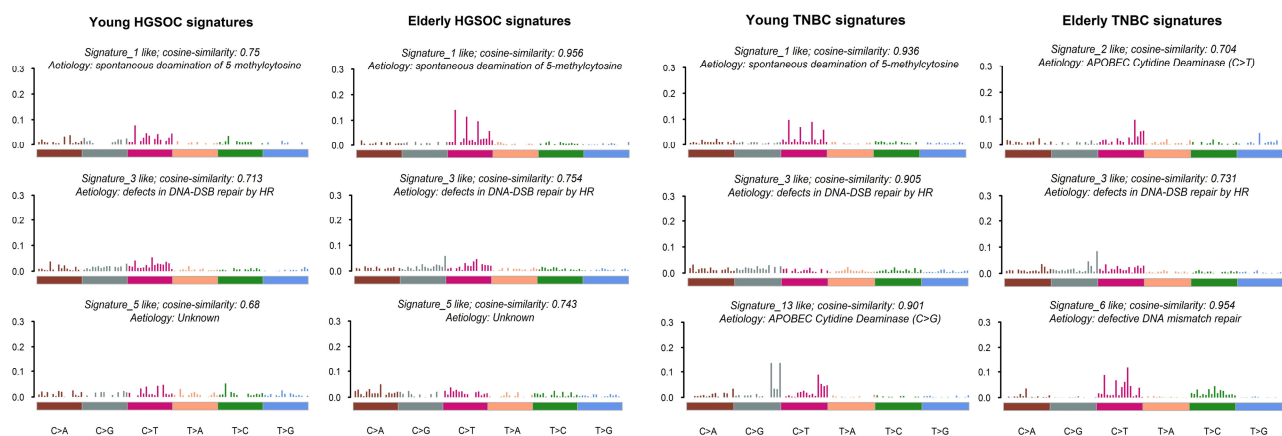


Figure S1. Mutational Signatures. For each signature, a barplot of the frequency distribution of single base substitutions in the trinucleotide context is shown.

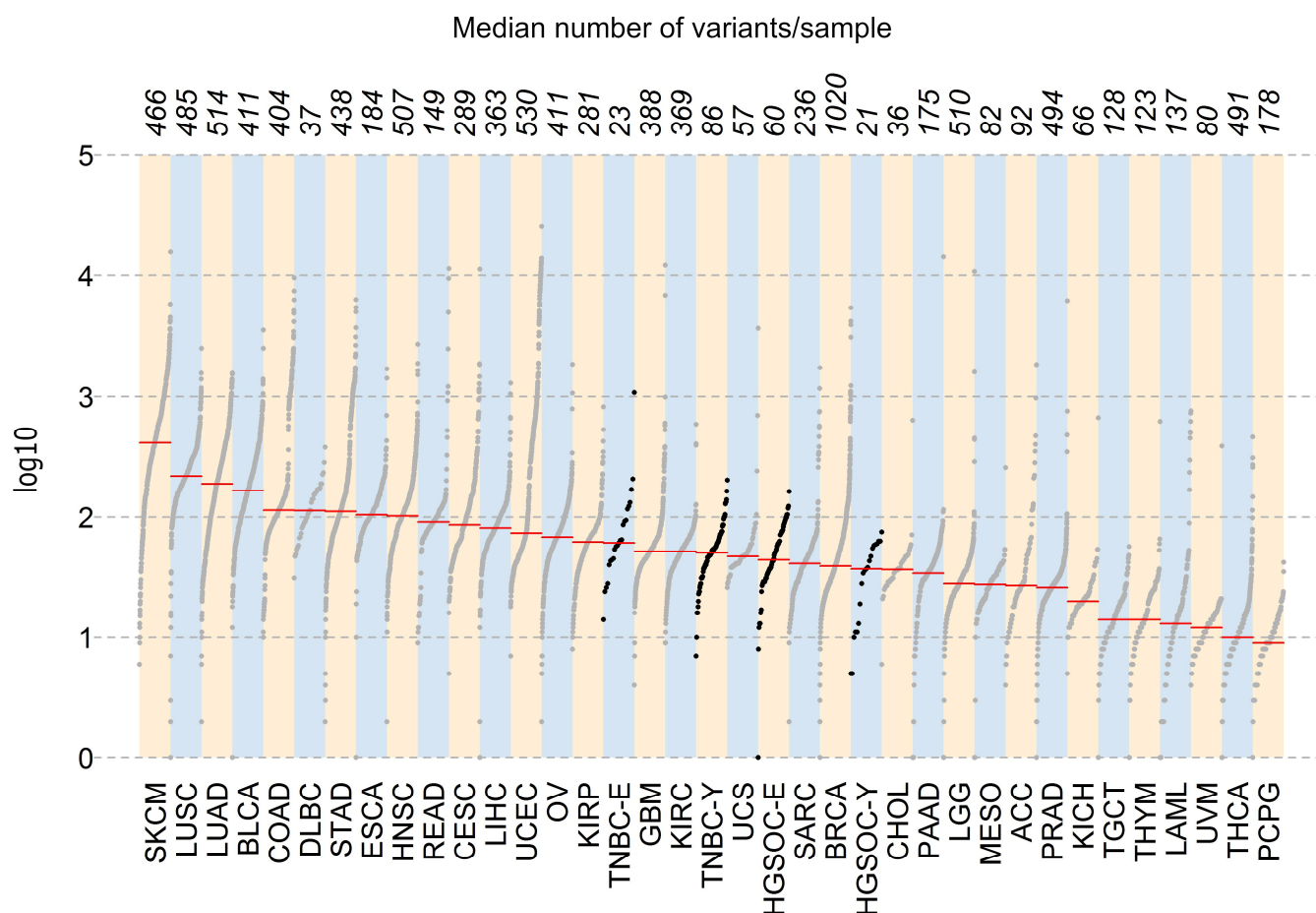


Figure S2. Number of non-synonymous coding variants per sample. The dot plot shows the distribution and median number (red line) of non-synonymous coding variants per sample in TCGA cohorts and those displayed in this work. Each point represents a patient (patients from our selected series are highlighted in bold). Y-axis: Number of non-synonymous coding variants (\log_{10}); X-axis: bottom: cohorts names; top: number of patients. HGSOE-Y: Young HGSOE patients; HGSOE-E: Elderly HGSOE patients; TNBC-Y: Young TNBC patients; TNBC-E: HGSOE-Y vs TCGA OV: $p=4.3 \times 10^{-6}$; HGSOE-E vs TCGA OV: $p=1.8 \times 10^{-5}$; TNBC-Y vs TCGA BRCA: $p=0.019$; TNBC-E vs TCGA BRCA: $p=0.0091$.

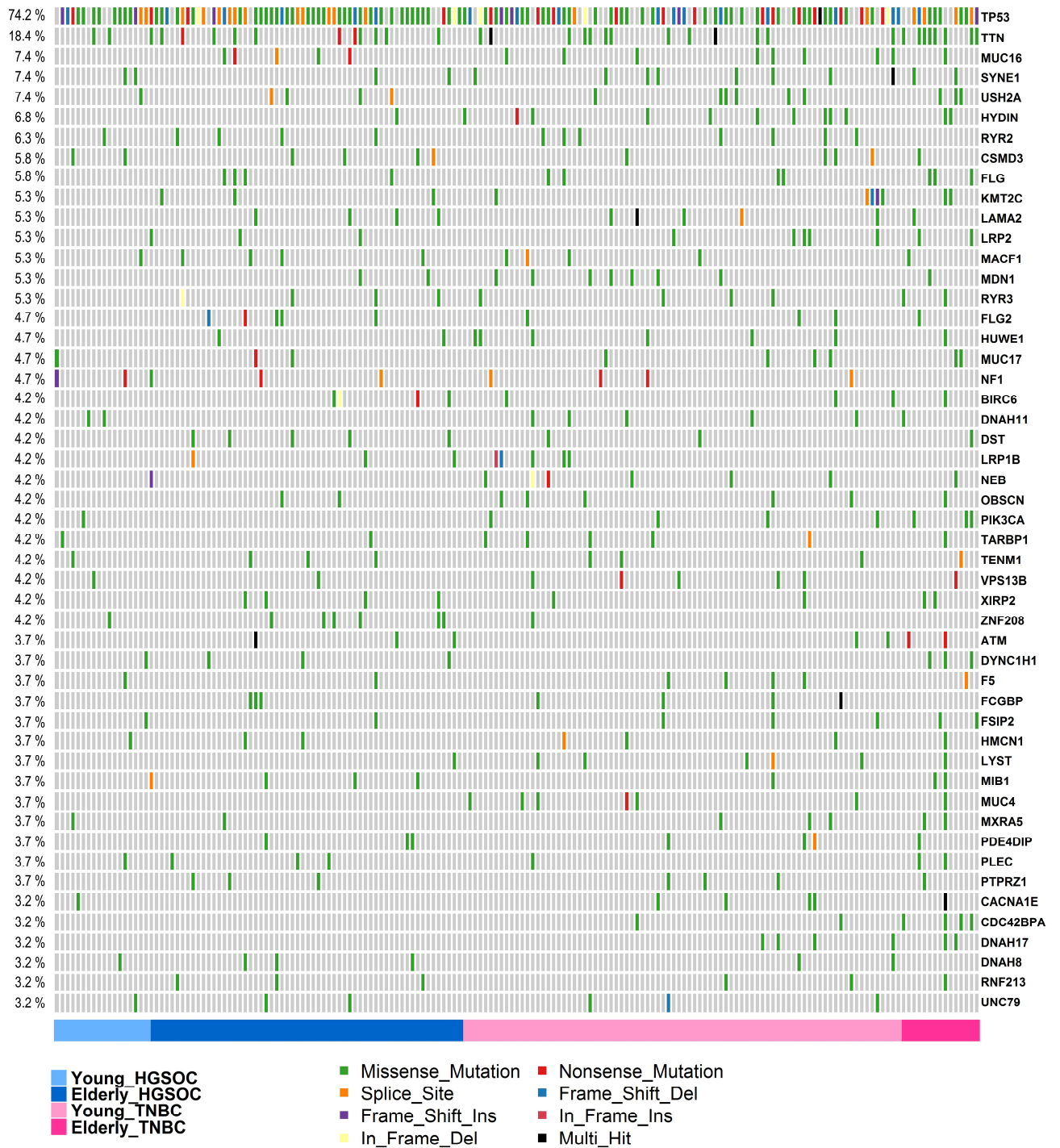


Figure S3. Overlapped frequently affected genes classified according to its variant type. Each column represents a patient and each line a gene (177 samples shown).

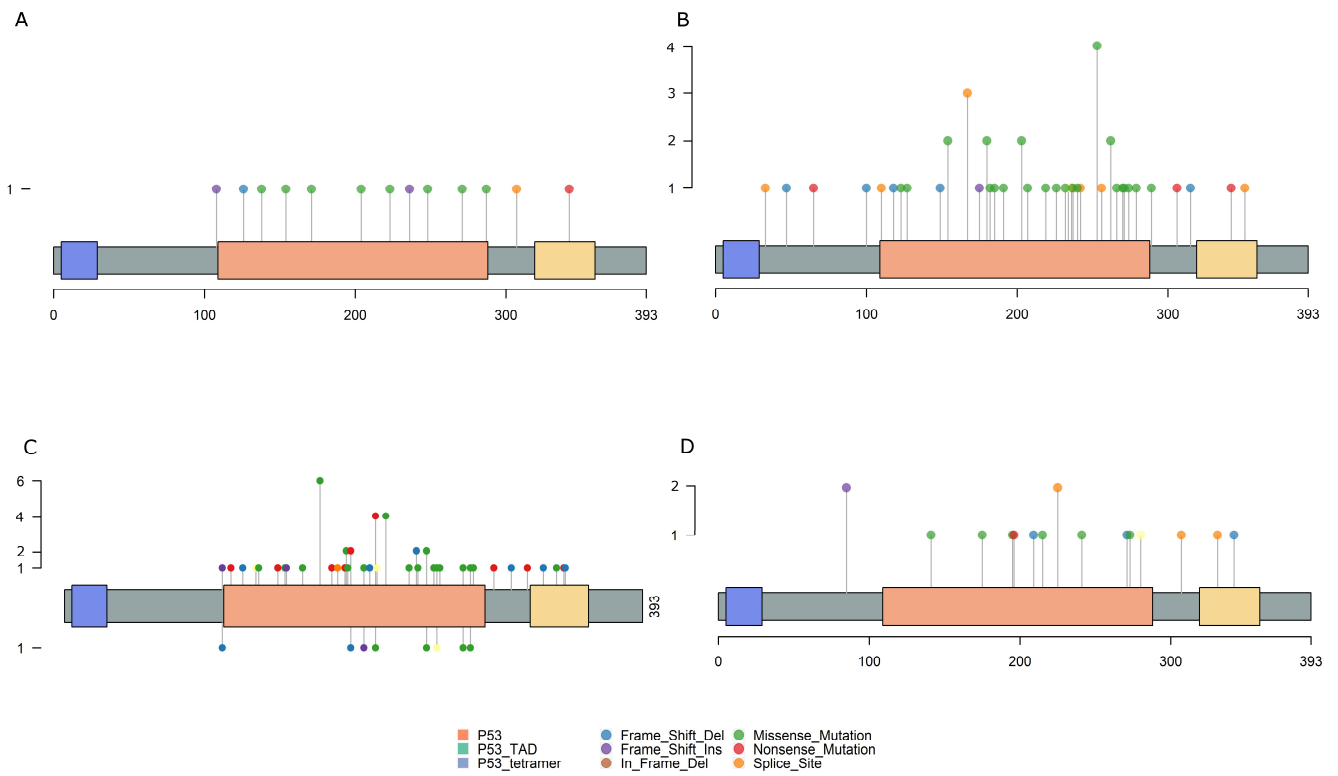


Figure S4. *TP53* variants. (A) Young HGSOc patients; (B) Elderly HGSOc patients; (C) Young TNBC patients; (D) Elderly TNBC patients. Y-axis: number of variants; X-axis: amino acid position and domains; P53: P53 DNA-binding domains; P53 Tetramer: P53 tetramerization motif; P53 TAD: P53 transactivation motif.