

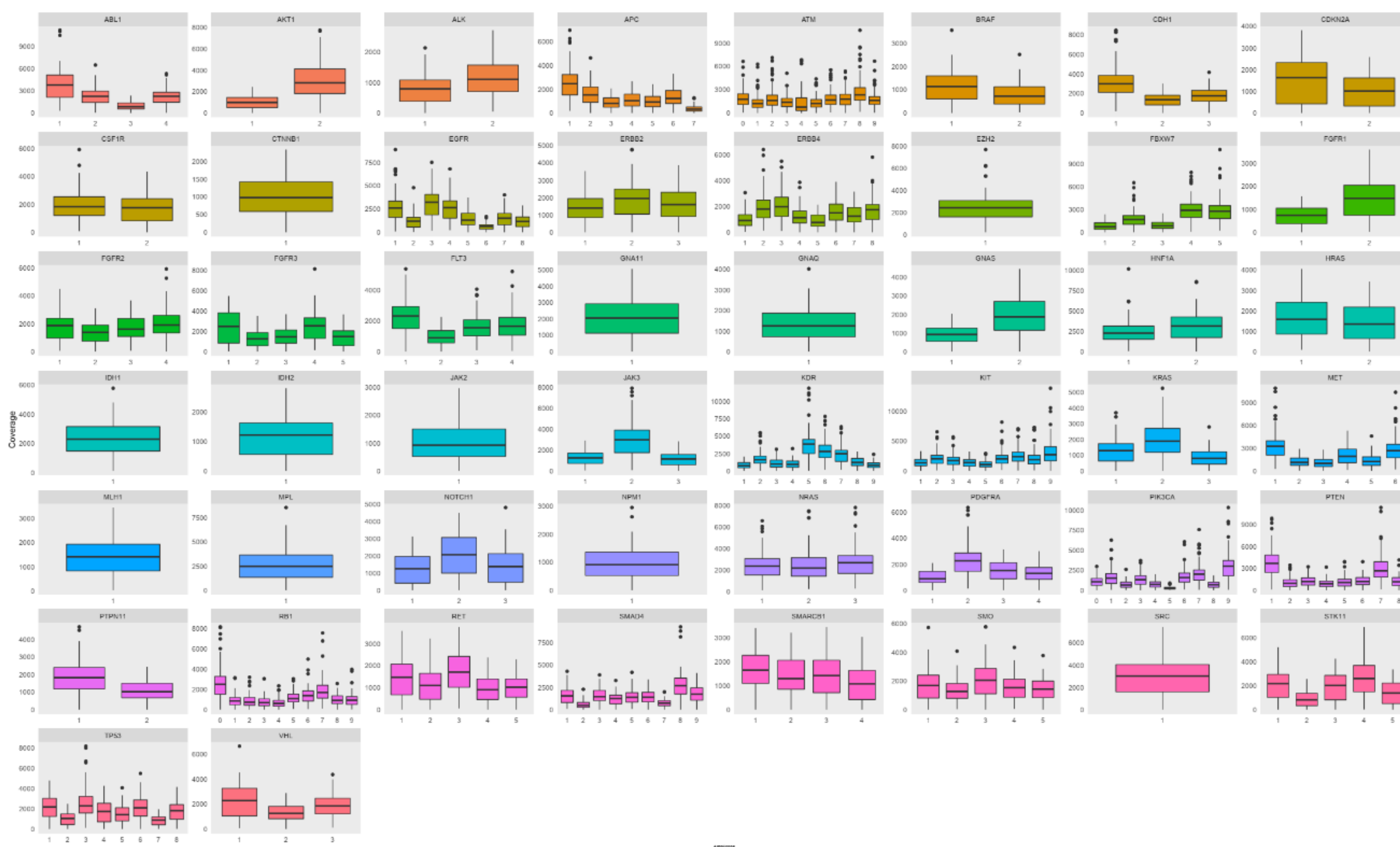


Figure S1. Boxplots reporting the median coverage of the 207 amplicons sequenced across the 50 genes for all precursor lesion samples. The average depth of all amplicons was 1631.5x per sample (ranging from 0x to 13823x).