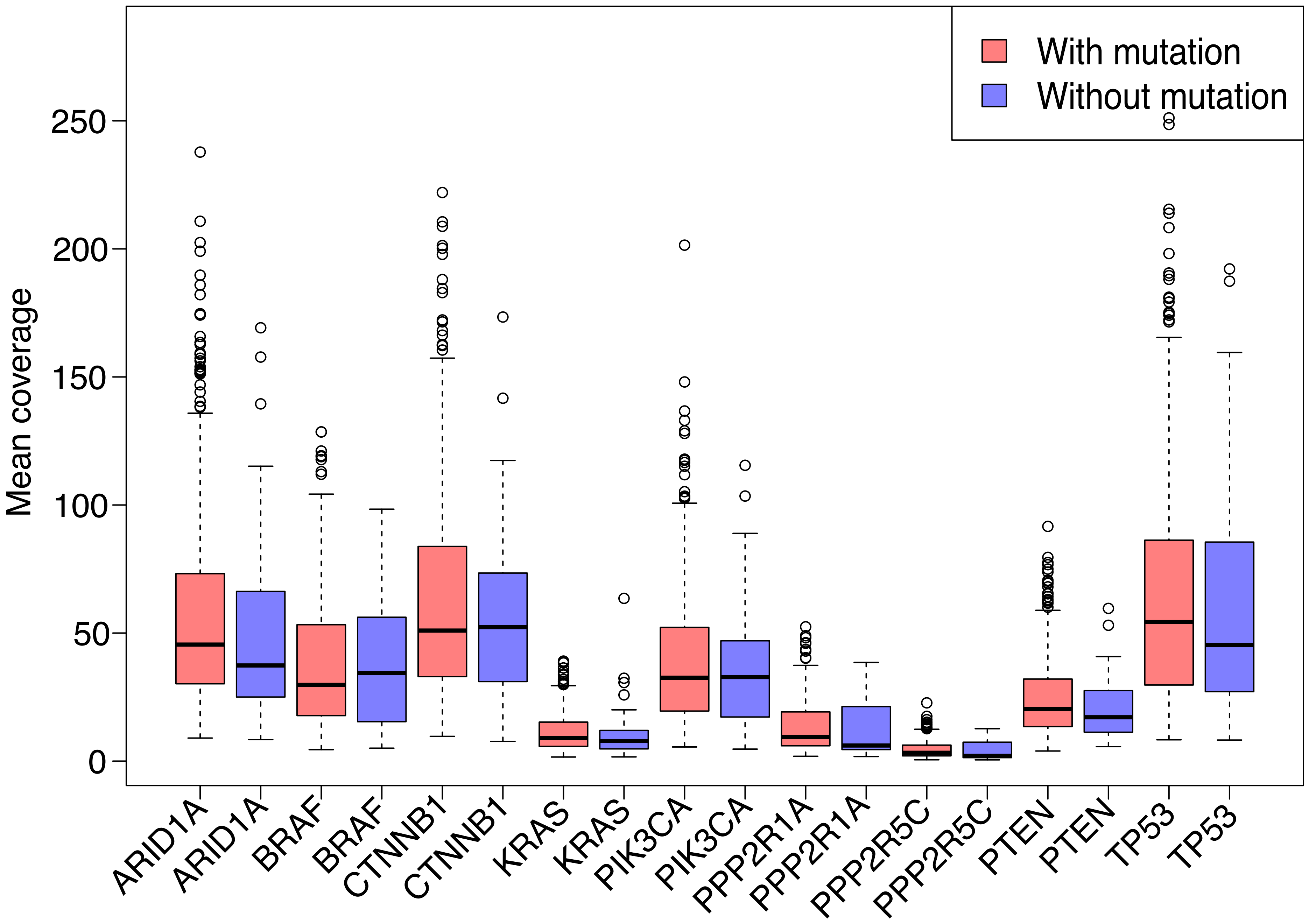

Figure S2: Boxplots of the mean-coverage of each gene in the cases with and without mutations. Cases with mutations (red) and without mutations (blue), with mean-coverage defined as the number of reads covering each coding position of a gene. The cases with and without mutations have similar coverage, therefore it is unlikely these cases are not false negatives in the genes analyzed. It can be noted that KRAS, PPP2R1A and PPP2R5C have relatively lower coverage; however both PPP2R1A and PPP2R5C have lower coverage due to not being sequenced in 64 cases. Previously validated somatic PPP2R1A mutations were added in subsequent analysis.