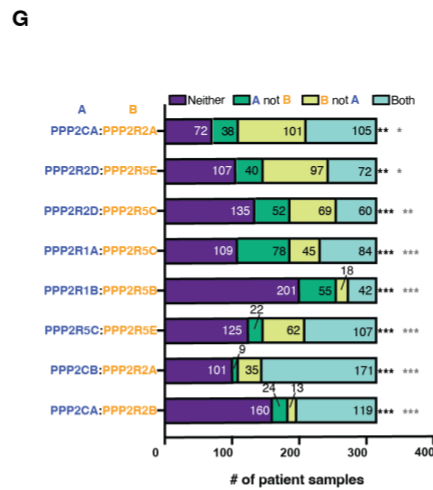
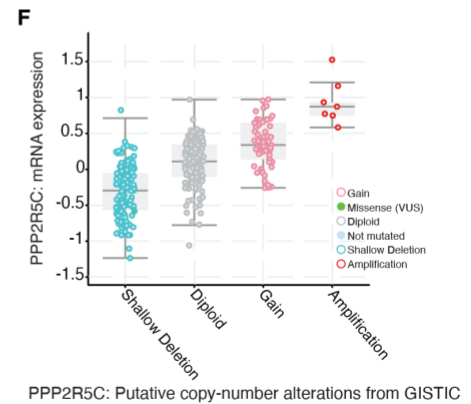
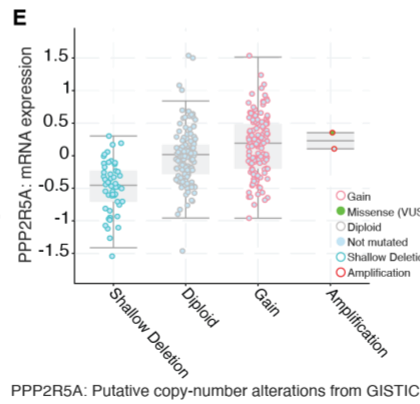
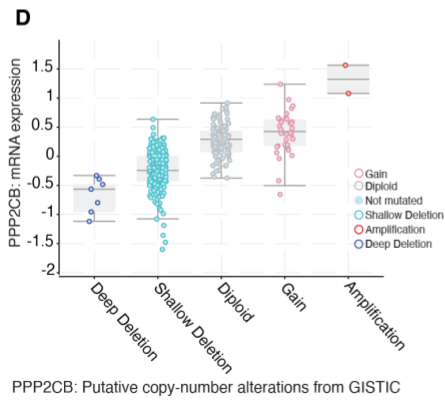
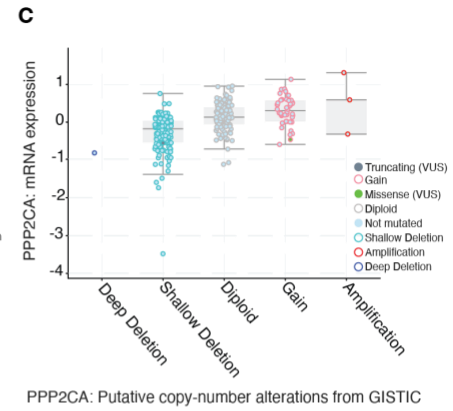
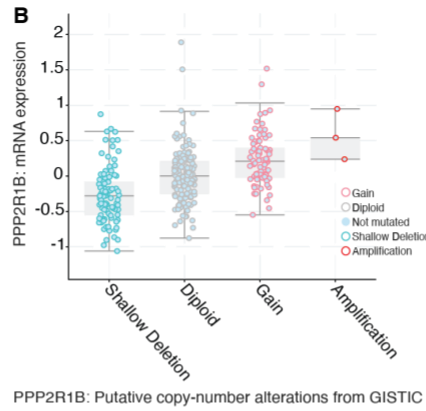
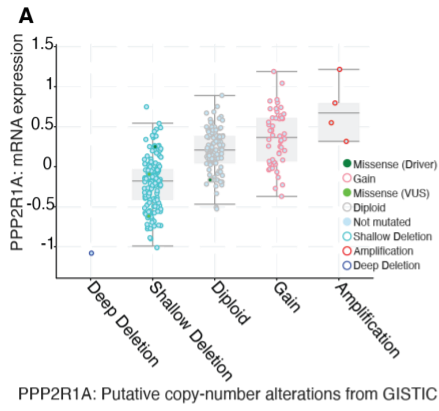


Supplementary Figure 1



Supplementary Figure 1 – PP2A family genes mRNA profiles show putative copy-number alterations proportionally correlate with their respective mRNA expression levels. Shallow and deep deletion, diploid, gain and amplification copy-number alterations for A) PPP2R1A, B) PPP2R1B, C) PPP2CA, D) PPP2CB, E) PPP2R5A, F) PPP2R5C, relative its own mRNA expression levels. G) Analysis of statistically significant co-occurrences in PP2A genes using panel C's data. *** $p < 0.001$, ** $p < 0.01$; *** $q < 0.001$, ** $q < 0.01$, * $q < 0.05$. Tendency – co-occurrence. Statistical analysis provided by cBioPortal. H) Individual patient tumor data analysis showing frequency of PP2A genes heterozygous loss as well as co-occurrence profiles. Each bar represents an individual tumor, for which grey signifies negative and blue positive for Hetloss.