







Supplemental Figure 2 - Gene-level mutation frequencies in GENIE versus TCGA

Scatter plots comparing GENIE and TCGA mutation frequencies by gene, based on mappings between Oncotree and TCGA cancer types. Concordance was quantified by calculating root-mean-square deviation (RMSD) and weighted RMSD (wRMSD) from each gene to the diagonal line. Across the thirty three cancer types evaluated, the median wRMSD was 0.32 (interquartile range 0.13-0.55), with a few notable outliers at both the cancer and gene levels.