



S3 Fig. Wide range of TMB (log10) with different size of targeted NGS panels (295- vs. 1021-gene panel). The mutation rate normalized by the size of the coding region covered. This correction results in similar median of TMB with wide range in the 295- and 1021-gene panel, respectively (median, 6; range, 2 to 227 and median: 7; range, 2 to 802; $p < 0.0001$). NGS, next generation sequencing; TMB, tumor mutational burden.