



S4 Fig. The correlation of TMB normalized by the percentage of patients evaluated by TMB in the different size of targeted NGS panels (295- vs. 1021-gene panel). The mutation rate normalized by the size of the coding region covered. This correlation of TMB value among all enrolled patients were closely similar in the 295- and 1021-gene panel ($R^2=0.9655$). NGS, next generation sequencing; TMB, tumor mutational burden.