



S4 Fig. Tumor mutation burden correlated with the number of non-*BRCA* homologous recombination DNA damage repair (HR-DDR) genes. Spearman's correlation analysis showed a linear correlation (coefficient=0.221) with marginal p-value ($p=0.068$) between tumor mutation burden (TMB) value and number of non-*BRCA1/2* HR-related gene aberrations.