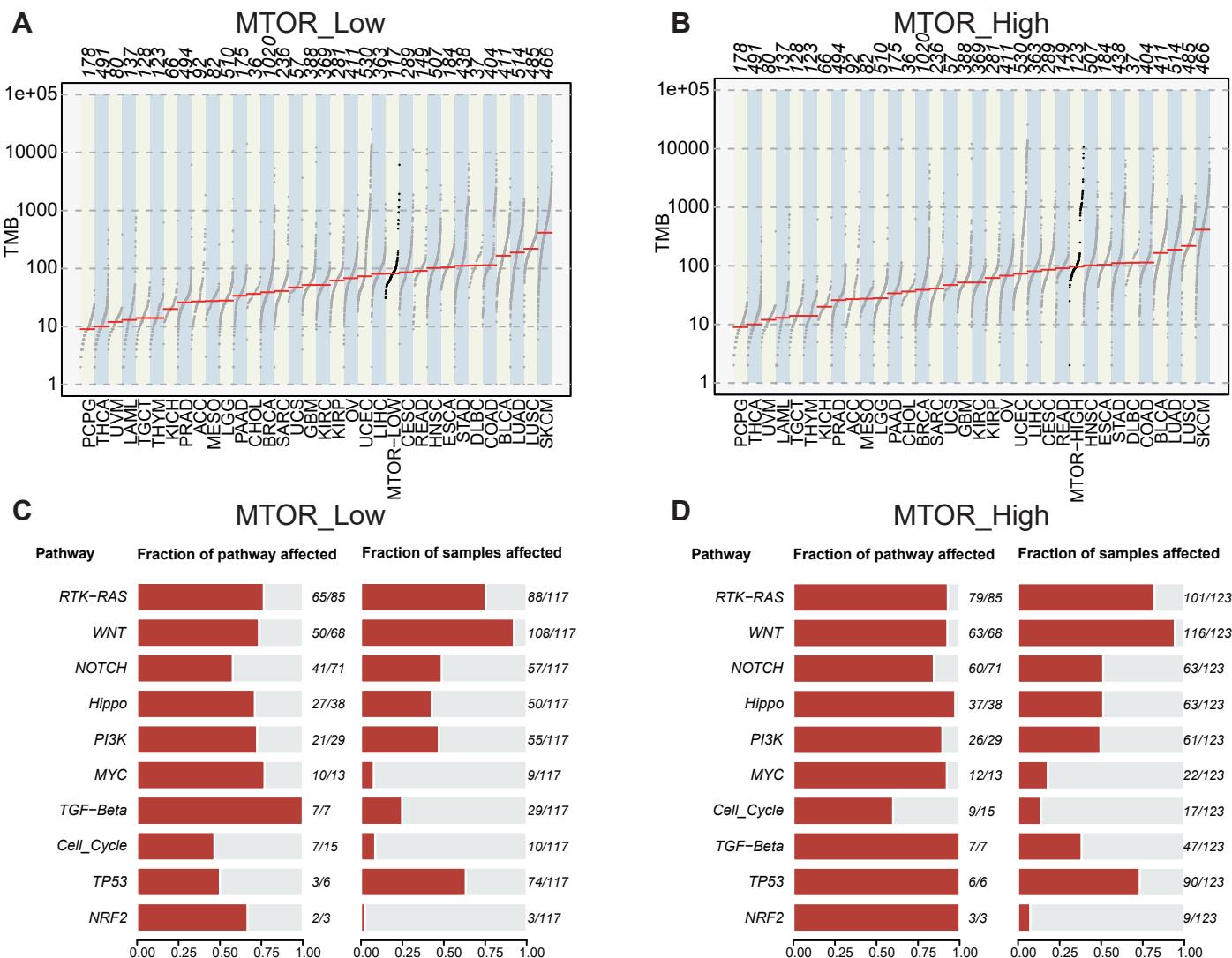


Supplementary Fig.1



A-B TMB of the low and high *MTOR* expression groups was compared with different cancer cohorts in TCGA. Every dot represents a sample, and the red horizontal lines represent the median numbers of mutations in the respective cancer types. **C-D** Differences in the proportions of affected pathways between the low and high *MTOR* expression groups. TMB, tumor mutational burden; TCGA, The Cancer Genome Atlas.