

Figure S1. The UCSC Xena tool was used to explore the multi-omics data of the TCGA-COAD and READ datasets. Gene expression (RNAseq) was evaluated using the normalized $\log_2(\text{FPKM}+1)$, and somatic mutations (deleterious, splice, missense/inframe, intron/RNA, splice, silent and complex or unannotated mutations) were estimated using MuTect2 variant aggregation and masking. Mutations in the checkpoint molecules *CTLA-4*, *CD274* (*PD-L1*), *PDCD1* (*PD-1*), *PDCD1LG2* (*PD-L2*), *ADORA2A*, *HAVCR2*, *IDO1*, *IDO2*, *LAG3*, *TIGIT* and *VTCN1* do not affect their corresponding expression levels.

