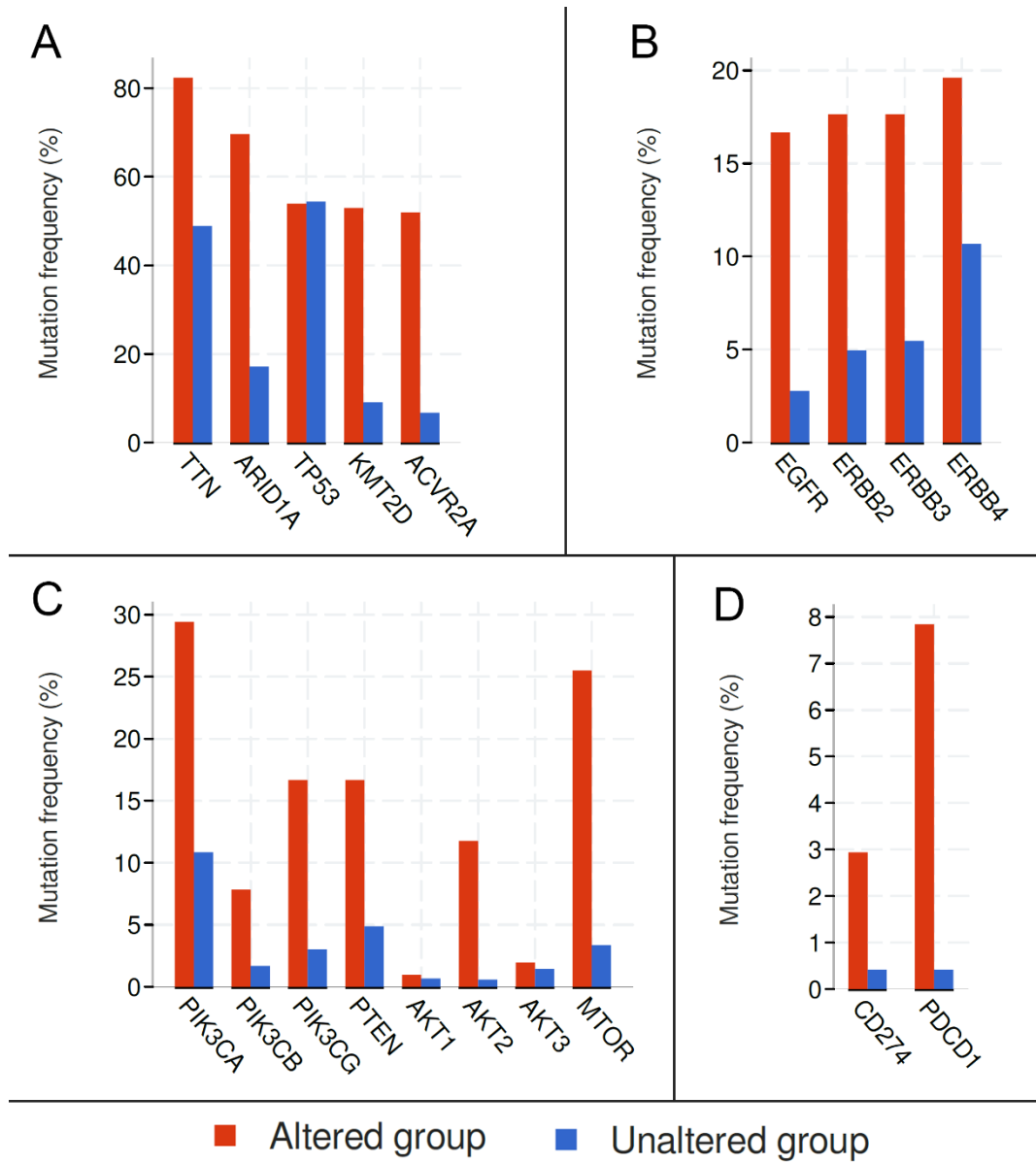


Supplementary Figure S1. Mutational count (mut/Mb) in MMR mutated versus MMR wild-type GEC in The Cancer Genome Atlas Network cohorts.



Supplementary Figure S2. Comparison between MMR-altered vs MMR-unaltered groups of genetic alteration frequency of the 5 most frequently altered genes in our analysis (A), EGFR family genes (B), PI3K/Akt family genes (C), and PD-1/PD-L1 genes (D).