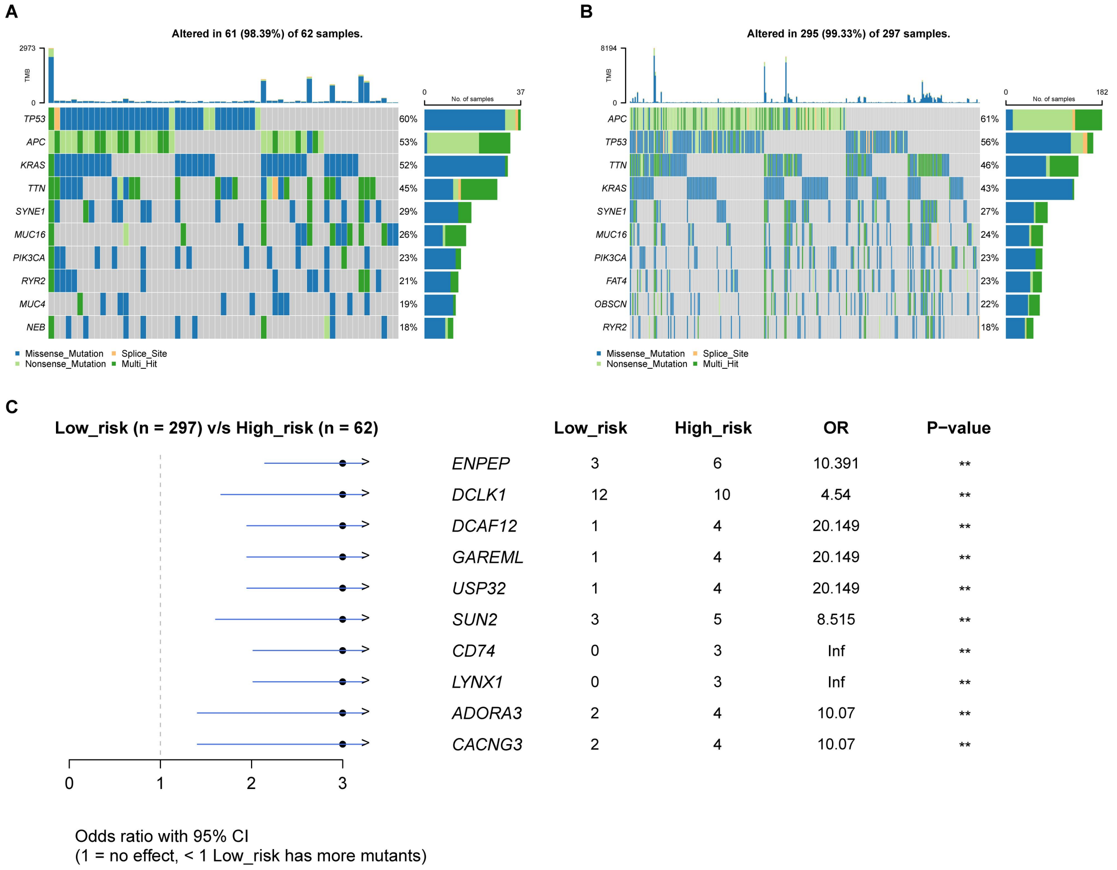

Figure S1. Somatic mutation analysis in two NRGS risk groups. (A) The top 10 mutated genes in the high NRGS risk group. (B) The top 10 mutated genes in the low NRGS risk group. (C) Differences in mutated genes between the two groups. ** $p<0.01$.

Figure S2. Based on the TISCH database to locate the expression situations of ASB9, CCDC8, COPS7A, COPS8, DCAF7, FBXL16, FBXO15, PALB2, PSMA5 and RNF7 in immune and nonimmune cells in CRC single-cell datasets.