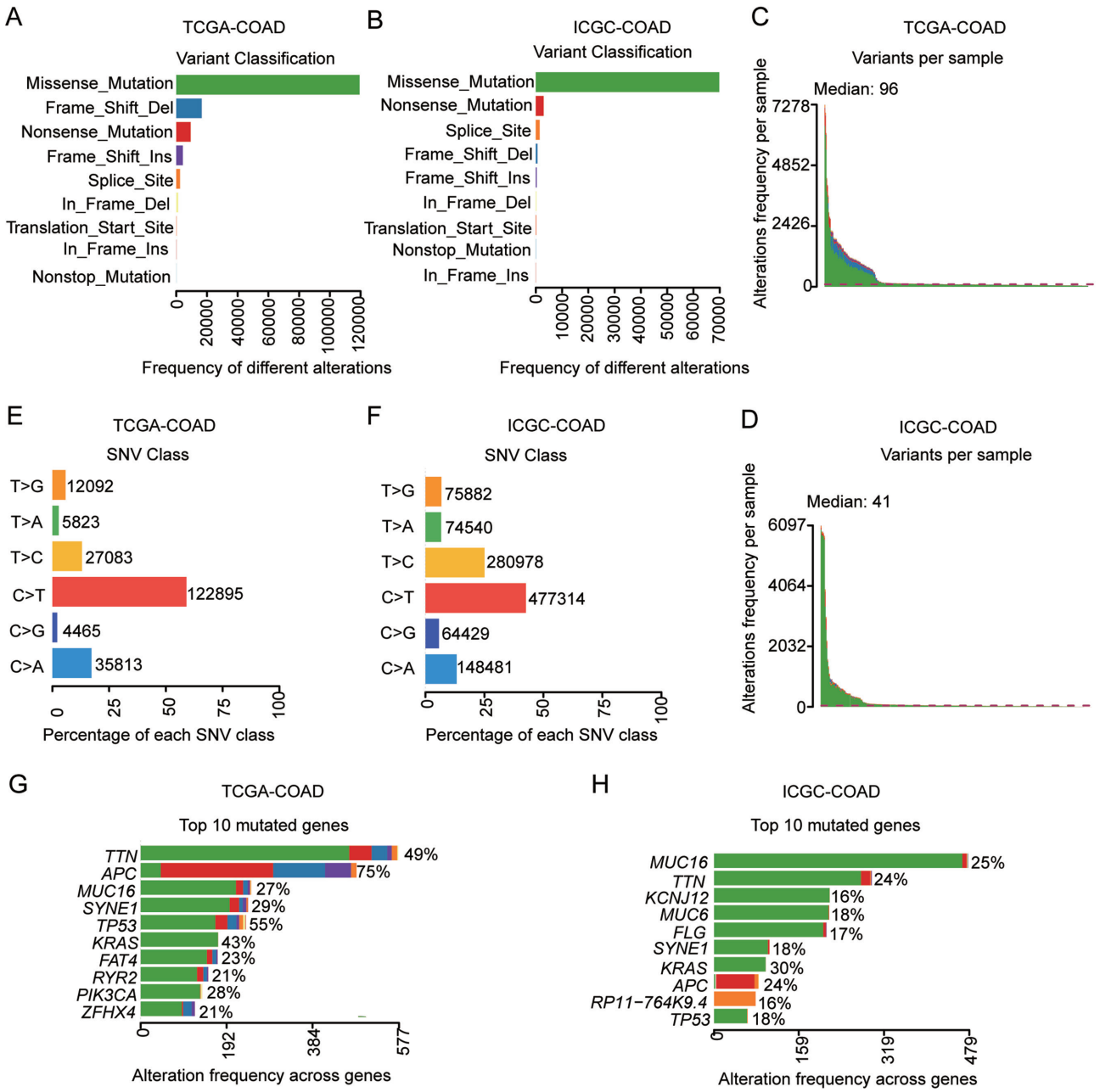

Figure S1 The landscape of genome somatic alteration in TCGA-COAD and ICGC-COAD cohorts. Variant classification of genome somatic alteration in the cohorts of TCGA-COAD (A) and ICGA-COAD (B). Variants per sample of genome somatic alteration in the cohorts of TCGA-COAD (C) and ICGA-COAD (D). SNV class analysis of genome somatic alteration in TCGA (E) and ICGA (F). Top 10 most commonly mutated genes in TCGA-COAD (G) and ICGC-COAD (H). TCGA, The Cancer Genome Atlas; COAD, colon adenocarcinoma; ICGC, International Cancer Genome Consortium; SNV, stable nuclear variant.

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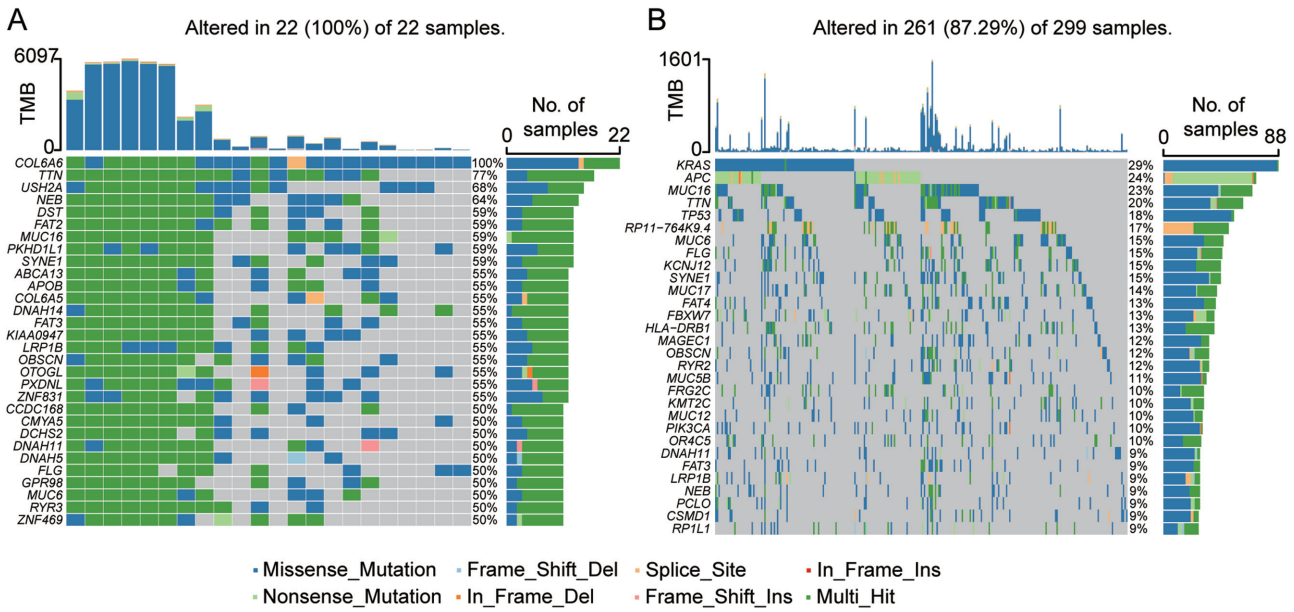

Figure S2 SNPs of the top 30 mutated genes in the *COL6A6*-MUT (A) and *COL6A6*-WT (B) groups in the ICGC-COAD cohort. TMB, tumor mutational burden; SNPs, single nucleotide polymorphisms; *COL6A6*, collagen type VI alpha 6 chain; MUT, mutation; WT, wild-type; ICGC, International Cancer Genome Consortium; COAD, colon adenocarcinoma.

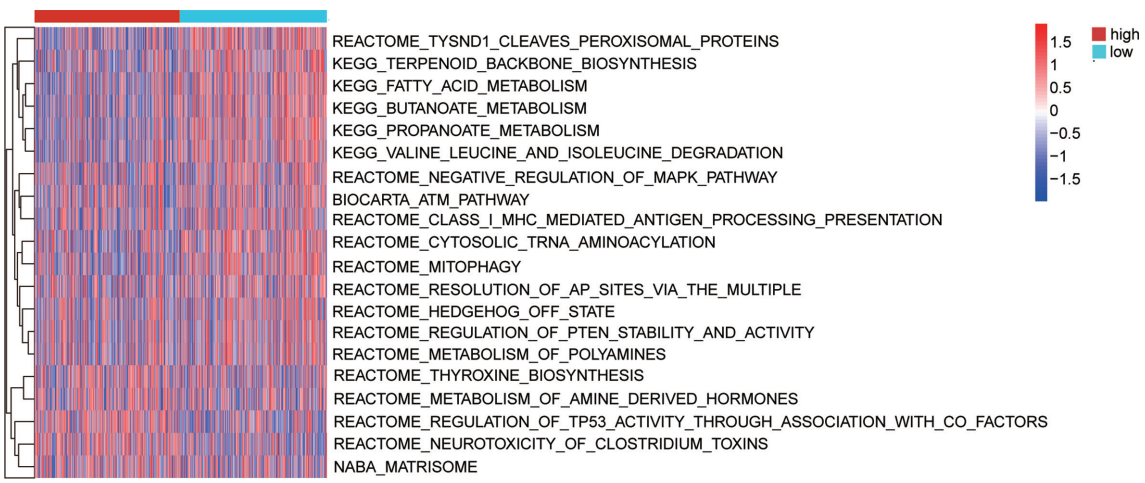

Figure S3 GSVA analyses of the differential pathways enriched in the two risk groups. KEGG, Kyoto Encyclopedia of Genes and Genomes; GSVA, gene set variation analysis.

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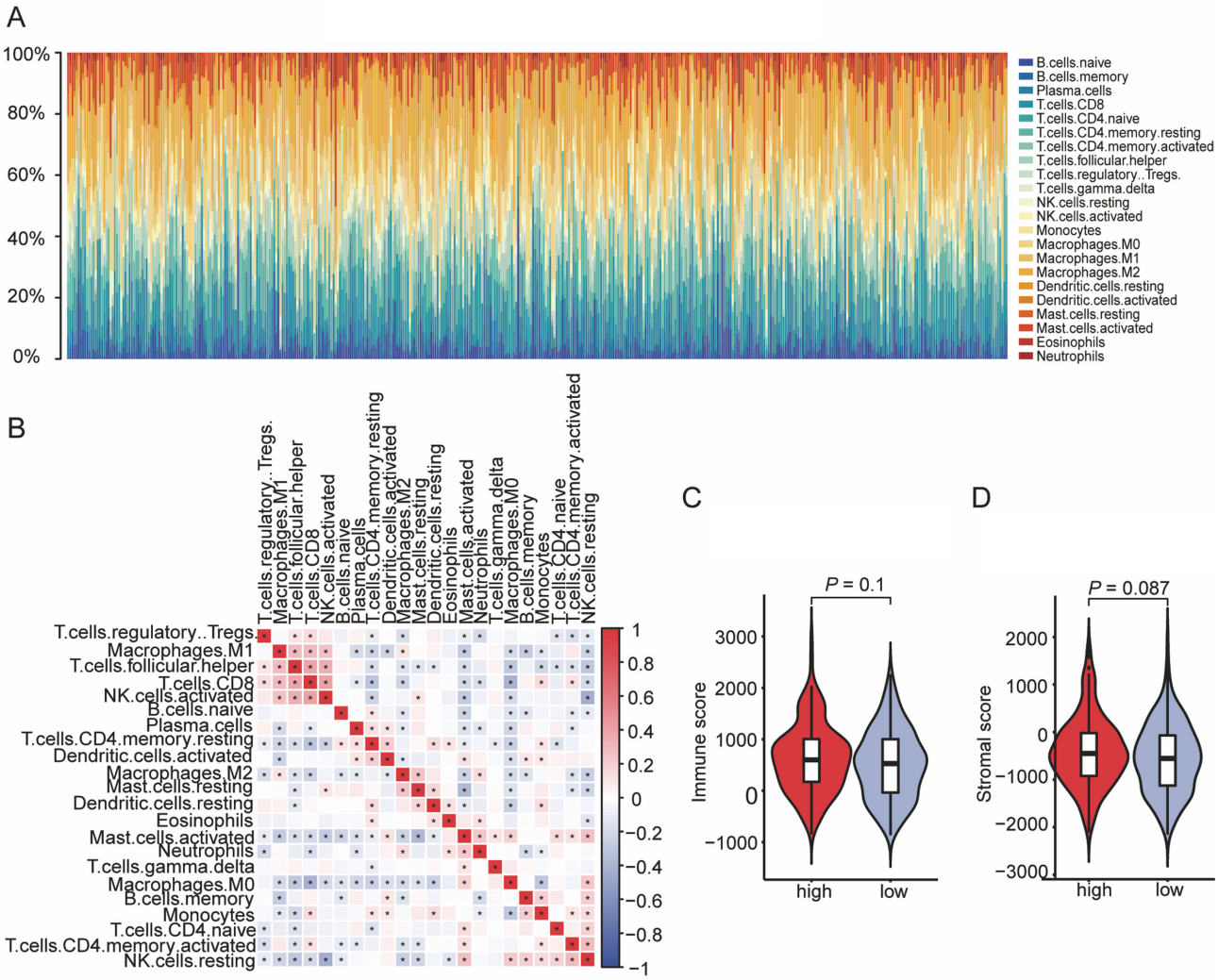

Figure S4 Immune cell infiltration analysis of TCGA-COAD cohort. (A) The immune landscape of the COAD microenvironment. (B) The correlationship among the immune cells in the TME of COAD. (C) The immune score was not significantly different between the two risk groups. (D) The stromal score was not significantly different between the two risk groups. NK, natural killer; TCGA, The Cancer Genome Atlas; COAD, colon adenocarcinoma; TME, tumor microenvironment.

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