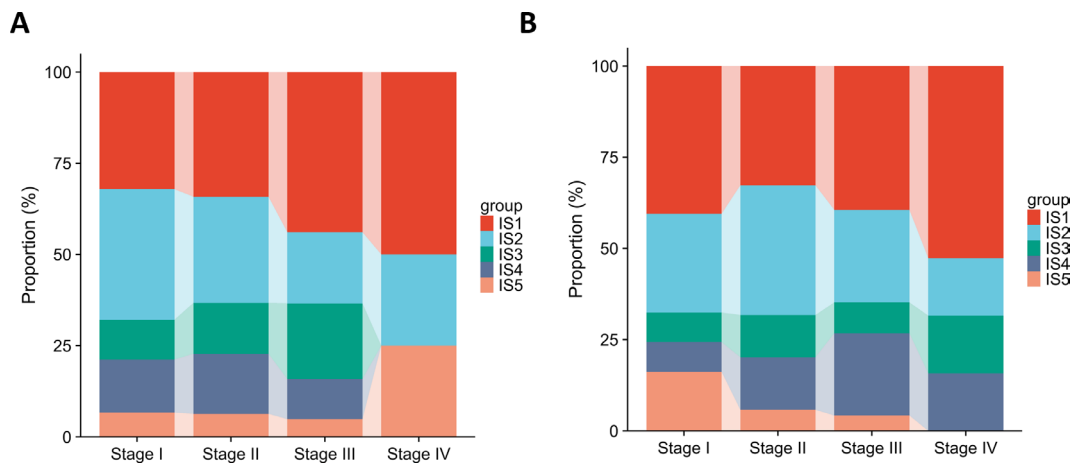
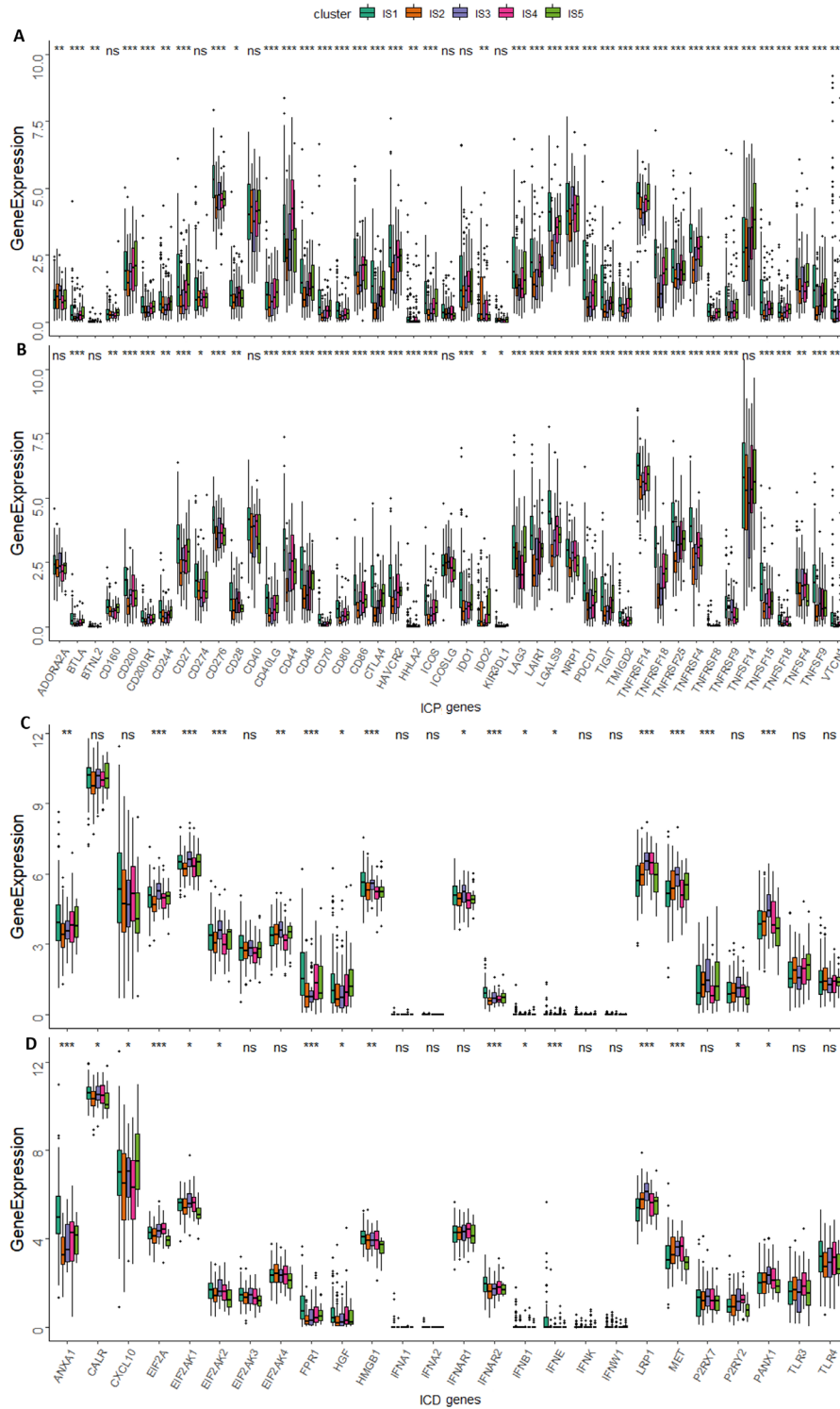


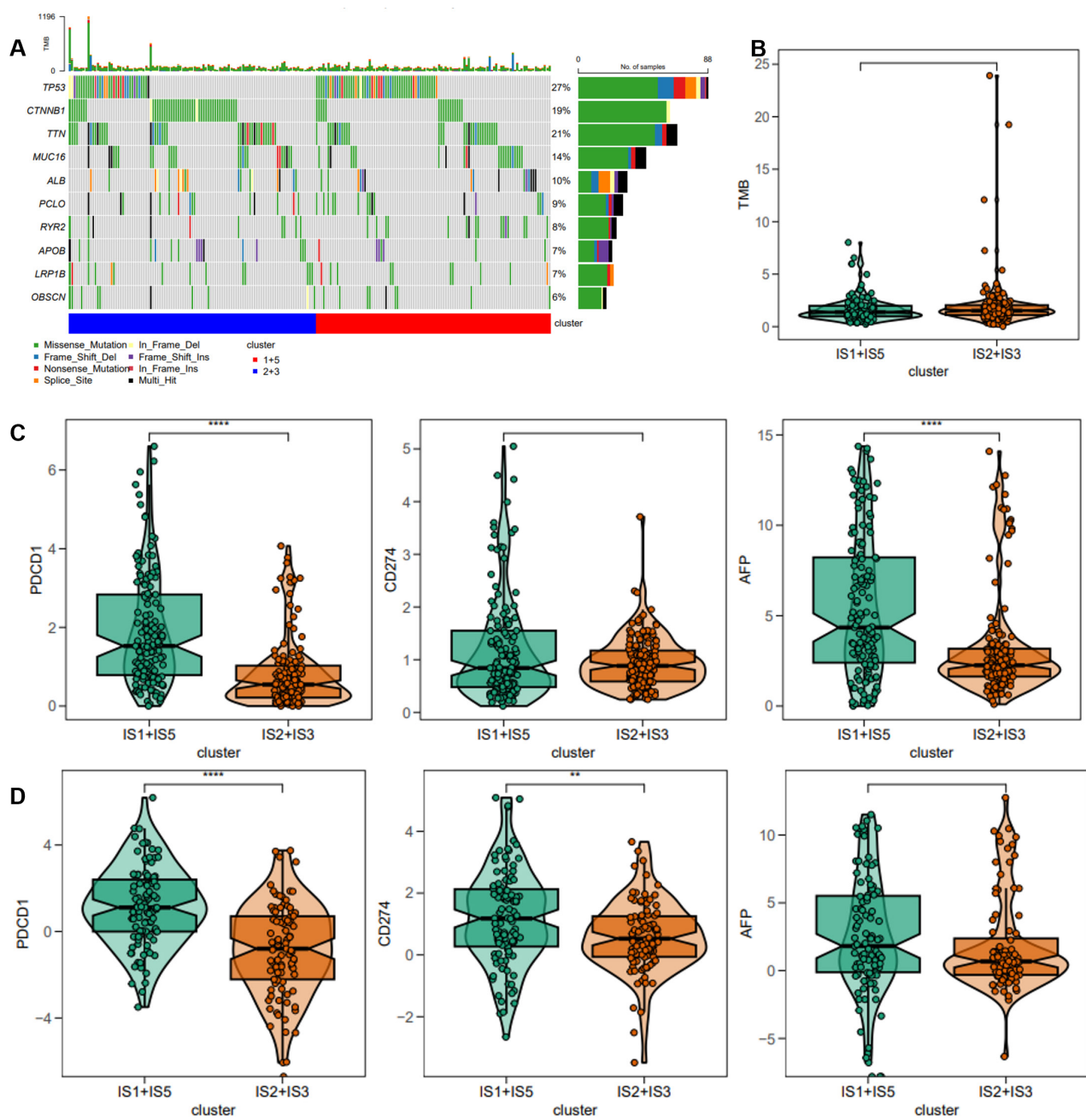
**Figure S1** Validation in the GEO database. (A) Expression of the 6 target genes in GSE84402. (B) Expression of the 6 target genes in GSE101685. \*\*\*,  $P < 0.001$ . GEO, Gene Expression Omnibus.



**Figure S2** Stacked histogram of immunophenotypes and staging of HCC. (A) TCGA; (B) ICGC. HCC, hepatocellular carcinoma; TCGA, The Cancer Genome Atlas; ICGC, International Cancer Genome Consortium.



**Figure S3** The relationship between immunophenotyping and immunotherapeutic targets. (A,B) Differential expression of ICP genes among the HCC immunophenotypes in (A) TCGA and (B) ICGC cohorts. (C,D) Differential expression of ICD modulator genes among the LIHC immune subtypes in (C) TCGA and (D) ICGC cohorts. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ . ns, no statistical differences; ICP, immune checkpoint; HCC, hepatocellular carcinoma; TCGA, The Cancer Genome Atlas; ICGC, International Cancer Genome Consortium; ICD, immunogenic cell death modulator.



**Figure S4** Association between immunophenotypes and molecular characteristics. (A) Ten highly mutated genes in HCC immunophenotypes in TCGA cohorts; (B) association between immunophenotypes and TMB; (C,D) association between immunophenotypes and Tumor marker genes expression in immunophenotypes in TCGA cohorts (C) and ICGC cohorts (D). \*\*,  $P < 0.01$ ; \*\*\*\*,  $P < 0.0001$ . TMB, tumor mutation burden; HCC, hepatocellular carcinoma; TCGA, The Cancer Genome Atlas; ICGC, International Cancer Genome Consortium.