

Figure S1 Supplementary information for the differential alternative splicing events. (A) Volcano plot showing differentially activated alternative splicing events between tumor and adjacent normal pancreas. (B) Heatmap showing top 100 differential alternative splicing events. (C) Bar plot showing the constitution of mutation types for the top 10 genes with the highest mutation percentage. (D) Bar plot showing the proportion of the specified type of variation of each gene in all samples of this type of variation. (E) Box plot showing differential expression of NMD mediators. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$. NMD, nonsense-mediated RNA decay.

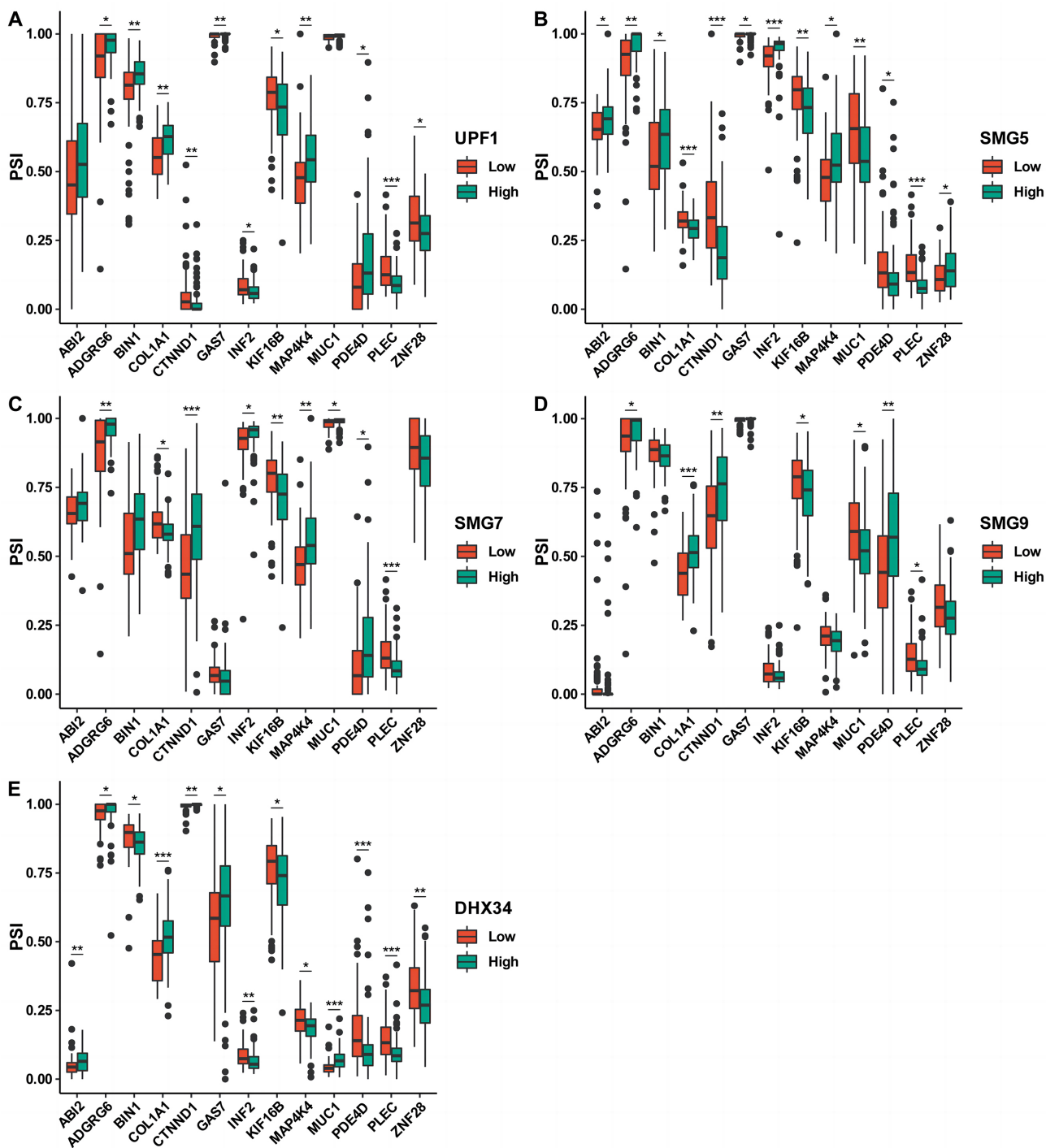


Figure S2 Box plot showing differential expression of genes encoding candidate tumor antigens between PAAD samples with higher or lower expression of each NMD regulator, including (A) *UPF1*; (B) *SMG5*; (C) *SMG7*; (D) *SMG9* and (E) *DHX34*. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$. PSI, percent spliced in; PAAD, pancreatic adenocarcinoma; NMD, nonsense-mediated RNA decay.

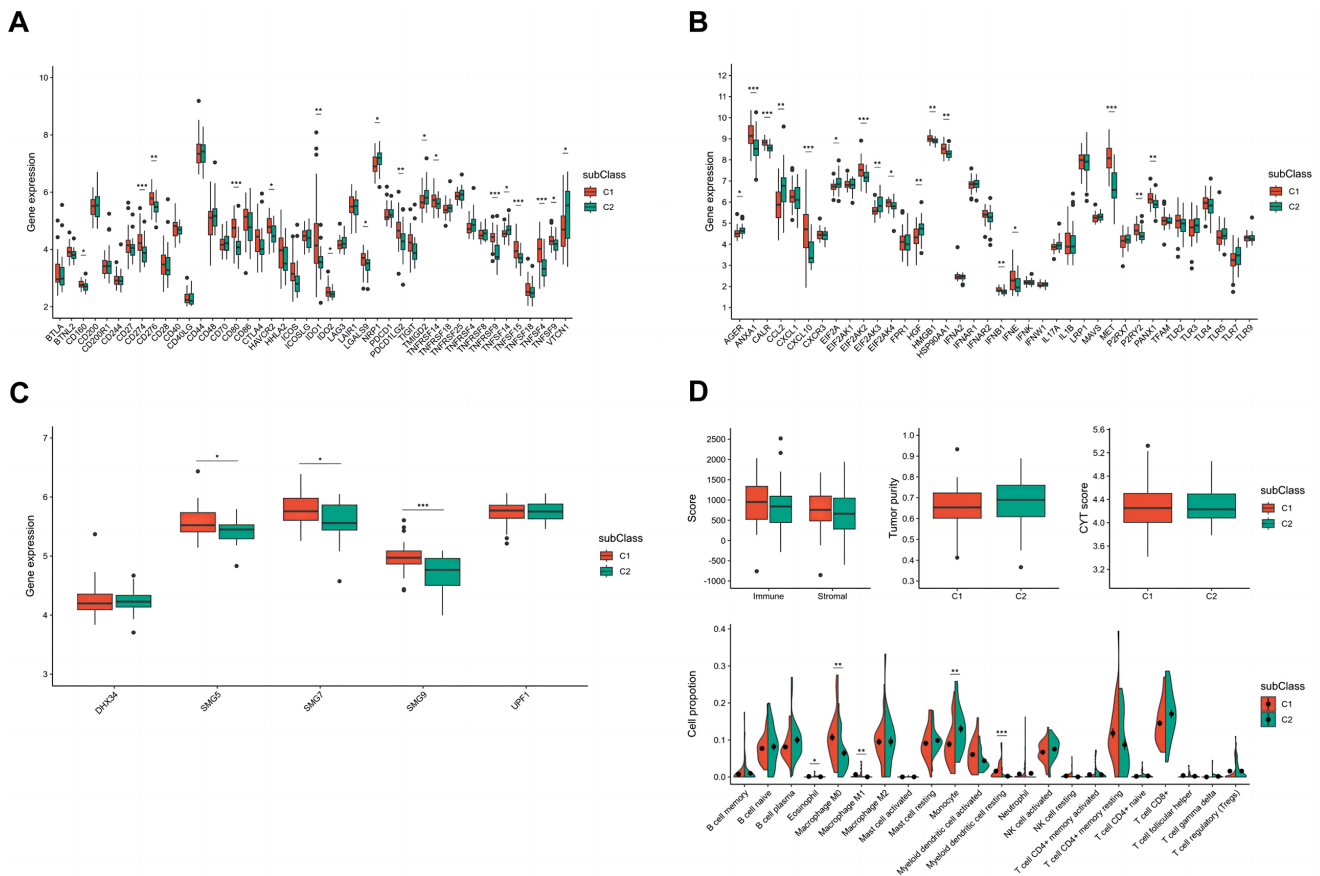


Figure S3 Supplementary information for the expression pattern of immune regulators in GSE62452 dataset. (A) Expression differences of immune checkpoints between subtypes based on GSE62452 data. (B) Expression differences of immune regulatory factors in GSE62452. (C) Expression differences of NMD factors between subtypes based on GSE62452 data. (D) Differences in immune score, stromal score, tumor purity, CYT score and proportion of immune cells between the two subtypes in GSE62452 data. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$. CYT, cytolytic activity; NMD, nonsense-mediated RNA decay.