

Supplementary Figures

Figure S1

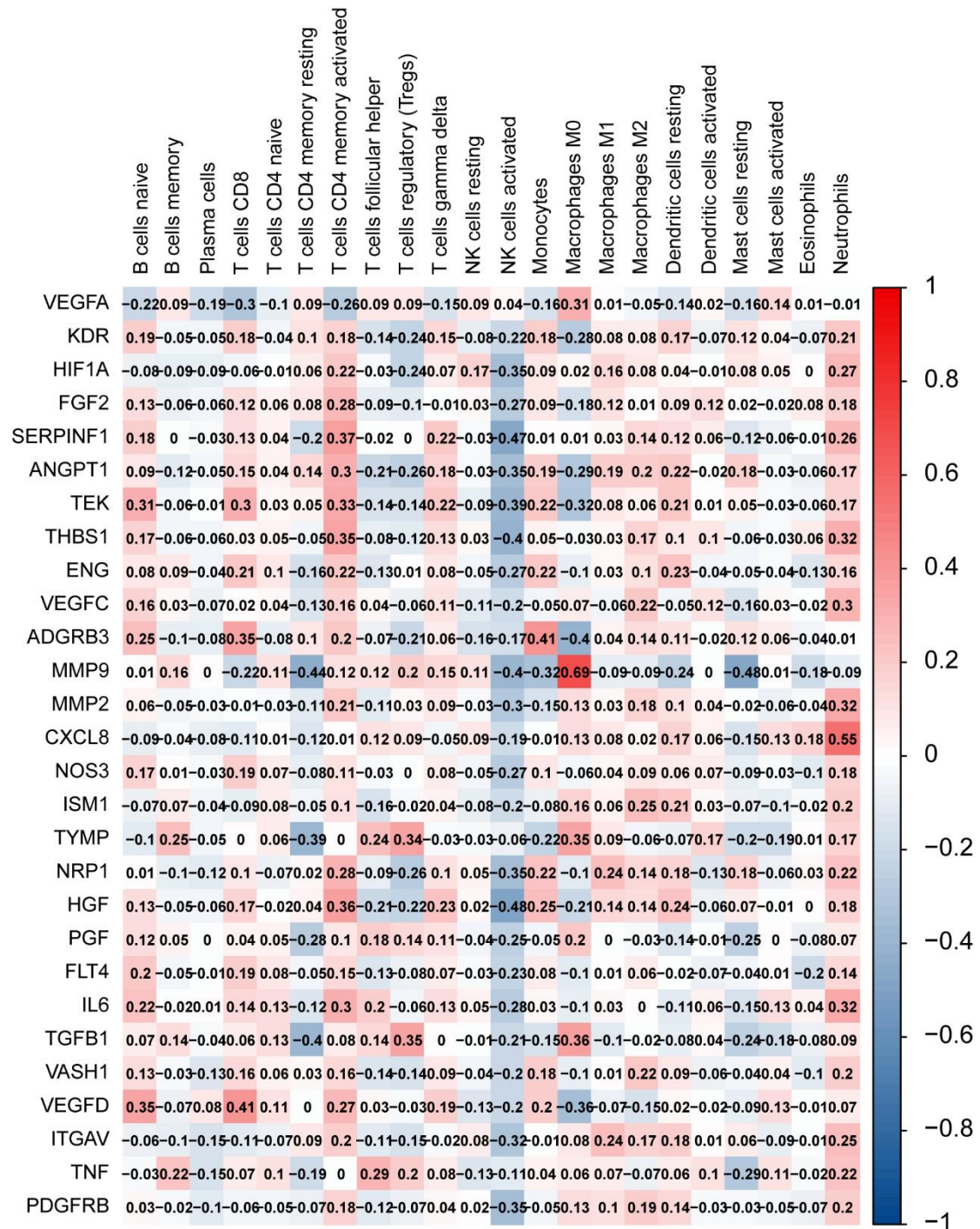


Figure S1. The correlation between 28 AIGs and the abundance of immune cells infiltration.

Figure S2

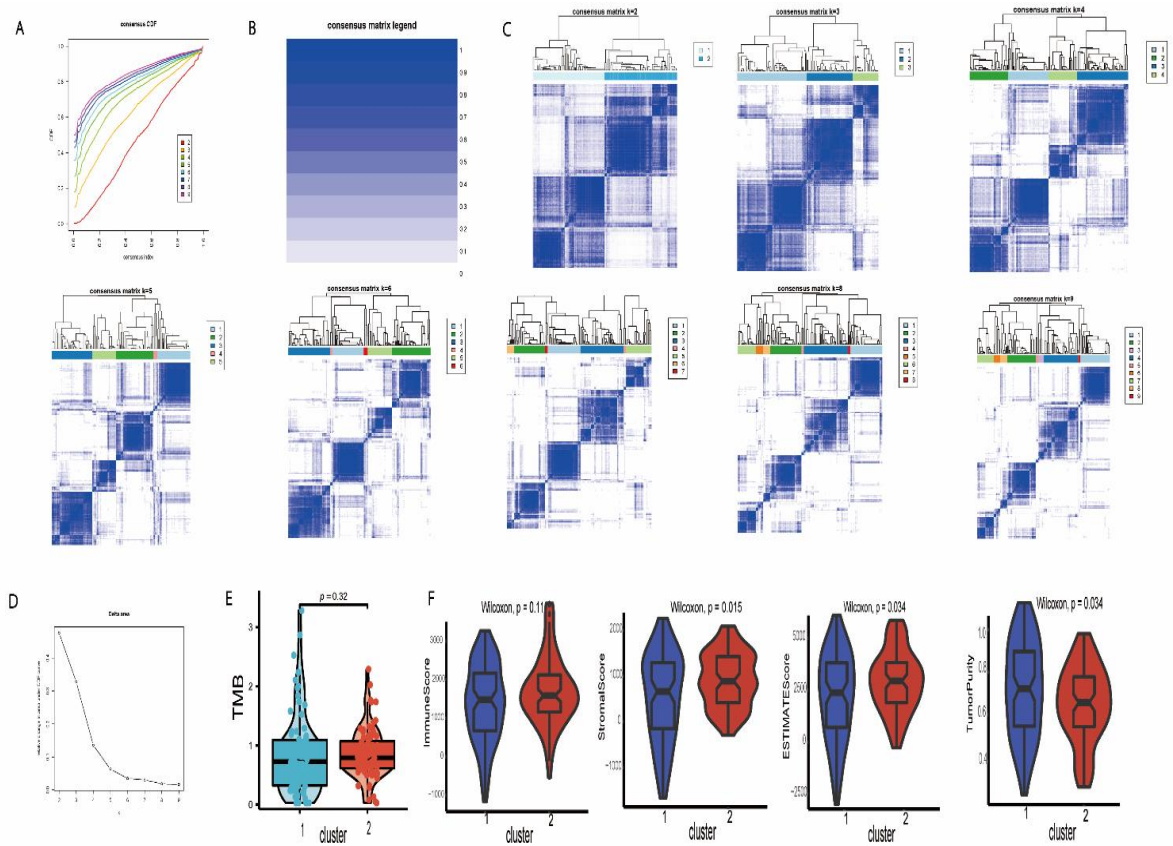


Figure S2. The characteristics of two distinct clusters.

(A-D) Consensus matrix heatmap defining clusters and their correlation area. (E) TMB between the two clusters. (F) Immune score, stromal score, ESTIMATE score and tumor purity between the two clusters ($P < 0.05$ *; $P < 0.01$ **; $P < 0.001$ ***).

Figure S3

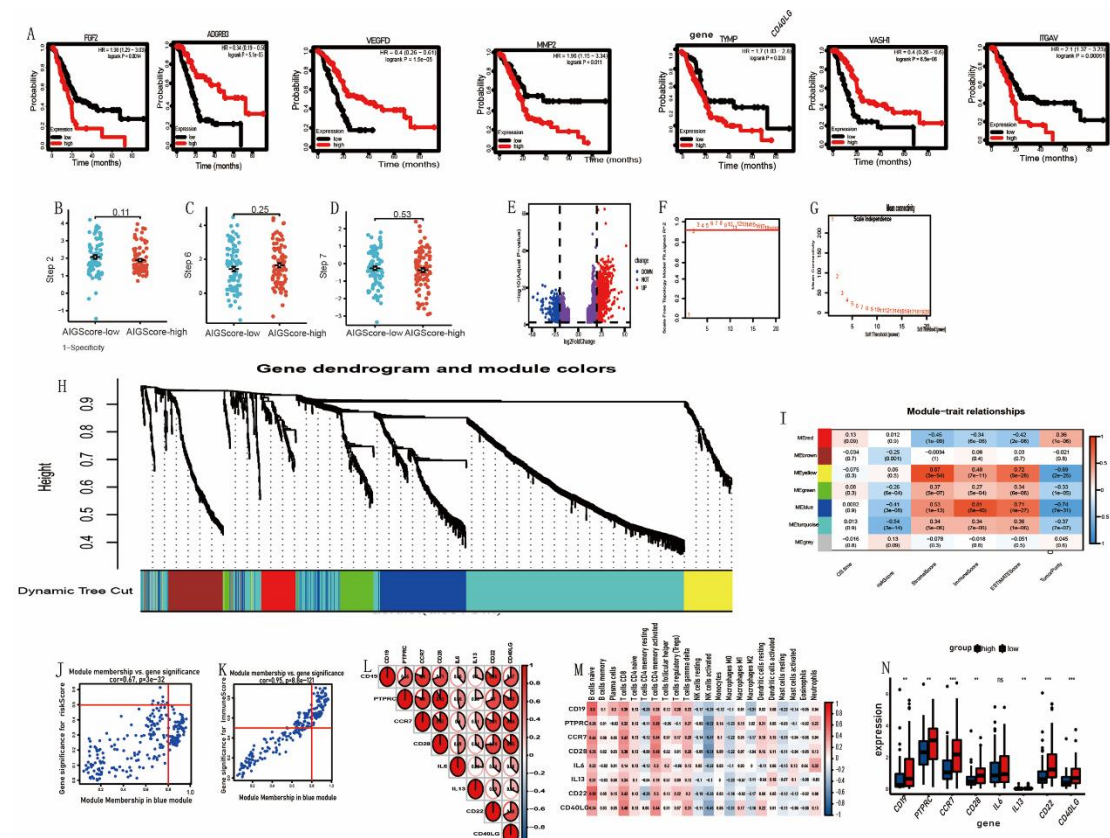


Figure S3. TME of the AIGScore and WGCNA based on the seven AIGs.

(A) Kaplan-Meier curves of the seven AIGs. (B-D) The cancer-immunity cycle in AIGScore-high and AIGScore-low groups. (E) The volcano plot of DEGs between AIGScore-high and AIGScore-low group. (F-G) Analysis of network topology for soft powers. (H) Gene dendrogram and module colors. (I) Heatmap between module eigengenes and traits. (J-K) Scatter plot of module eigengenes in the blue module. (L) The correlation analysis between the hub genes. (M) The correlation analysis between the hub genes and immune cells. (N) The expression of the hub genes in AIGScore-high and AIGScore-low groups.

A VEGF **B** FGF2 **C** ADGRB3

D PAAD_GSE111672

E FGF2

F ITGAV **G** MMP2 **H** TYMP **I** VASH1

J ADGRB3 is NOT detected in the dataset **K** VEGFD is NOT detected in the dataset

L

M

N

O

MMP2 P(v)=5.8E-02
FGF2 P(v)=1.76E-01
ADGRB3 P(v)=6.76E-10
VEGFD P(v)=9.74E-05

ITGAV P(v)=3.82E-01
TYMP P(v)=1.69E-04
VASH1 P(v)=2.35E-04

n=C1:57;C2:32;C3=40;C4=1;C6=21
C1 (wound healing);
C2 (IFN-gamma dominant)
C3 (inflammatory)
C4 (lymphocyte depleted)
C5 (immunologically quiet)
C6 (TGF-b dominant)

(A-C) UMAP displayed the distribution of FGF2, ADGRB3 and VEGFD expression at a single-cell level in CRA001160 set. (D-K) UMAP displayed the distribution of the seven AIGs expression at a single-cell level in GSE111672 set. (L-N) The relationship between CNAs of FGF2, ADGRB3 and VEGFD and tumor-infiltrating immune cells. (O) The seven AIGs mRNA expression in different immune-molecular subtypes in TISIDB database ($P < 0.05$ *; $P < 0.01$ **; $P < 0.001$ ***).

Figure S5

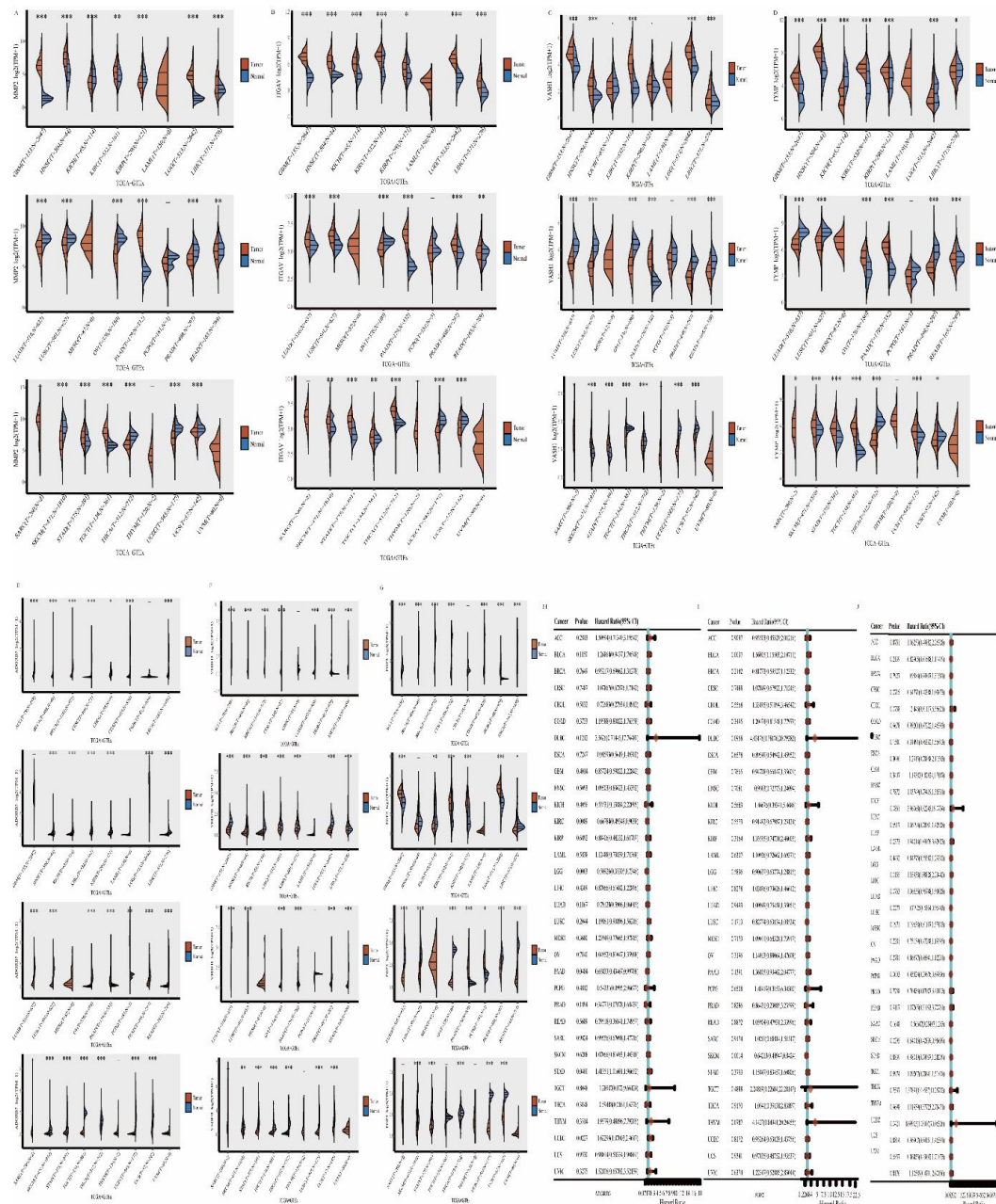


Figure S5. The expression of the seven AIGs across cancers and their prognostic value.

(A-G) The expression distribution of the seven AIGs in tumor tissues and normal tissues. (H-J) Forest plots showed the results of univariate cox regression analysis of the three AIGs in pan-cancer. ($P < 0.05$ *; $P < 0.01$ **; $P < 0.001$ ***).

Figure S6

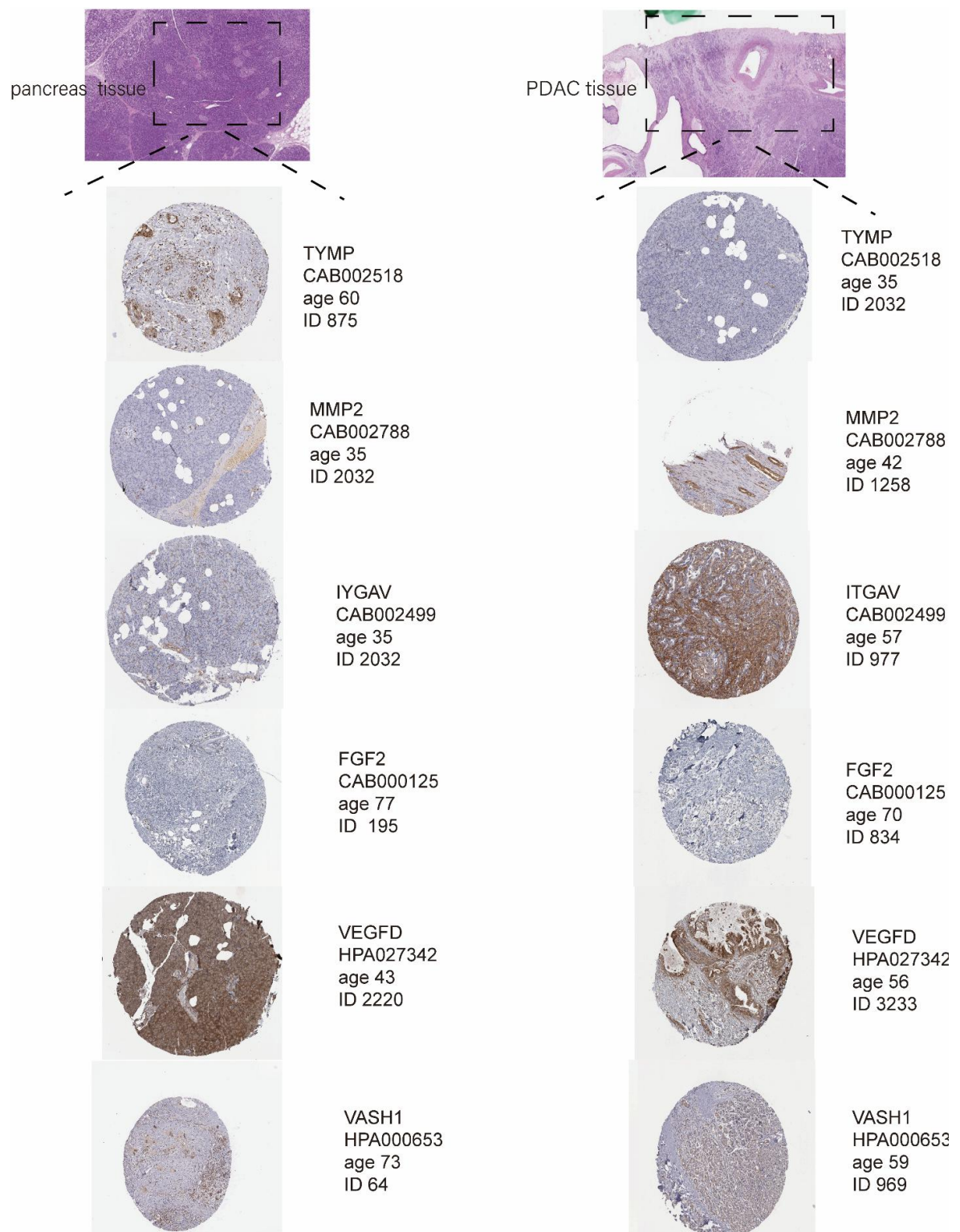


Figure S6. Immunohistochemistry of the AIGs in PDAC tissues and paired paraneoplastic tissues.

Supplementary Tables

Table S1. Online databases information.

Table S2. The primer sequences of seven AIGs and GAPDH used for RT-qPCR.

Table S3. The gene symbol used in this work from GeneCards database.

Table S4. The differentially expressed genes between the two clusters.

Table S5. The differences in anti-cancer immune response between risk subtypes of angiogenesis.

Table S6. The potential therapeutic agents for TYMP and MMP2.