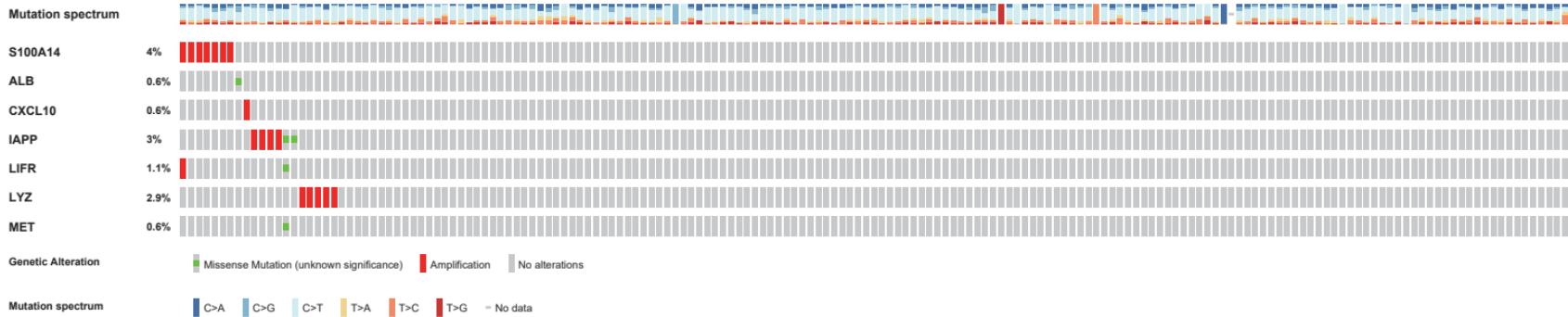


Figure S1. Flowchart of the whole study.

**A**

TCGA

**B**

ICGC

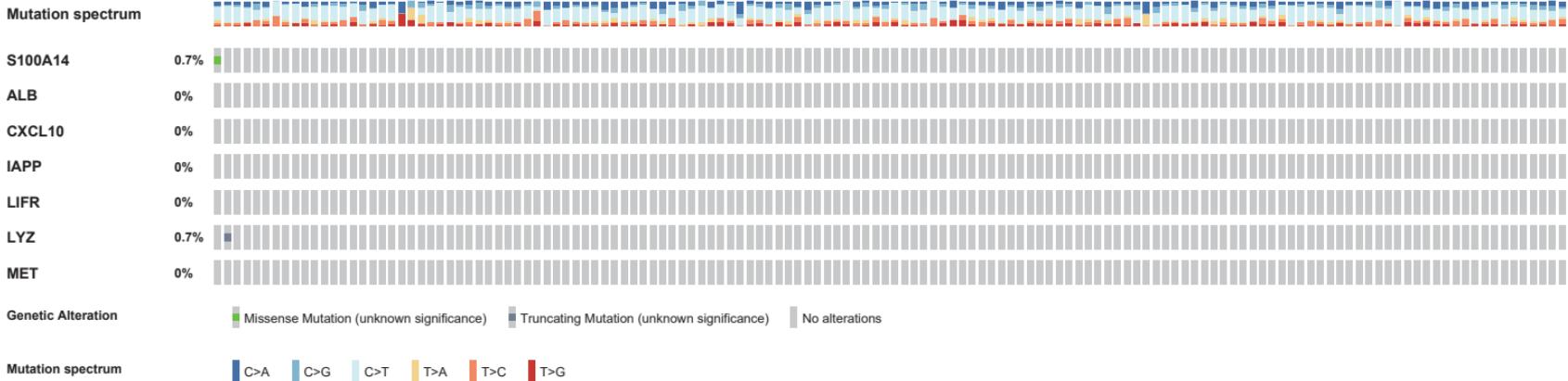
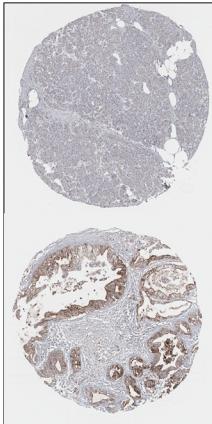


Figure S2. The mutation status of the seven hub IRGs in TCGA dataset (A) and ICGC dataset (B).

**A S100A14**

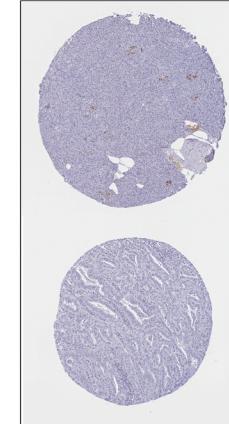
Normal tissue  
Patient id: 1647  
Staining: Not detected  
Intensity: Weak  
Quantity: <25%

Adenocarcinoma  
Patient id: 956  
Staining: High  
Intensity: Strong  
Quantity: 75%-25%

**B ALB**

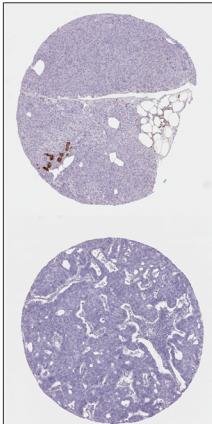
Normal tissue  
Patient id: 2329  
Staining: Not detected  
Intensity: Negative  
Quantity: None

Adenocarcinoma  
Patient id: 4595  
Staining: Medium  
Intensity: Moderate  
Quantity: >75%

**C IAPP**

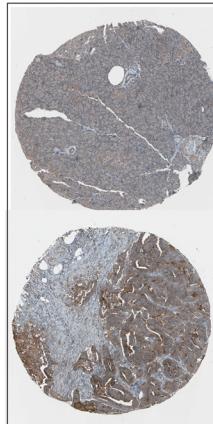
Normal tissue  
Patient id: 2162  
Staining: Not detected  
Intensity: Negative  
Quantity: None

Adenocarcinoma  
Patient id: 3851  
Staining: Not detected  
Intensity: Negative  
Quantity: None

**D LYZ**

Normal tissue  
Patient id: 2162  
Staining: Medium  
Intensity: Strong  
Quantity: <25%

Adenocarcinoma  
Patient id: 3614  
Staining: Not detected  
Intensity: Negative  
Quantity: None

**E MET**

Normal tissue  
Patient id: 2220  
Staining: Low  
Intensity: Weak  
Quantity: >75%

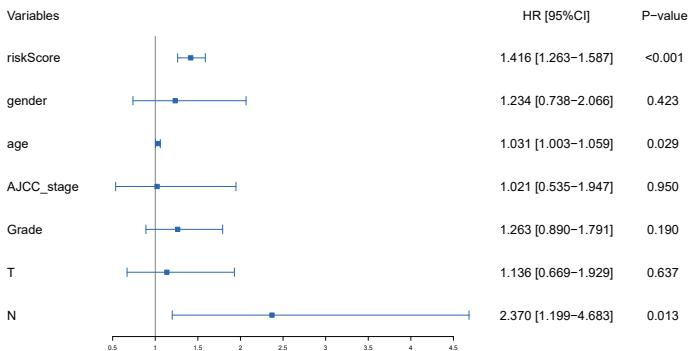
Adenocarcinoma  
Patient id: 1647  
Staining: Medium  
Intensity: Moderate  
Quantity: >75%

Figure S3. Representative images of hub IRGs expression status except CXCL10 and LIFR in normal pancreas and PC tissues. (The expression information of CXCL10 and LIFR was unavailable in HPA database)

## Univariable Cox Regression Analysis

A

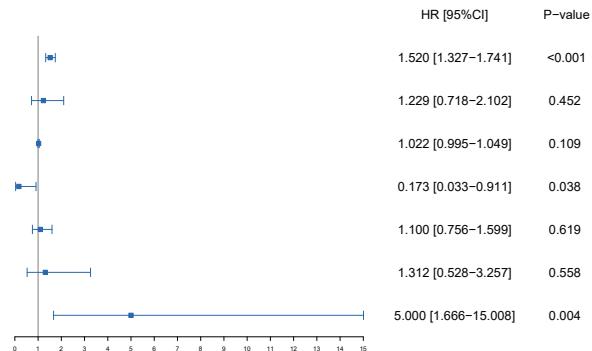
Training set



## Multivariable Cox Regression Analysis

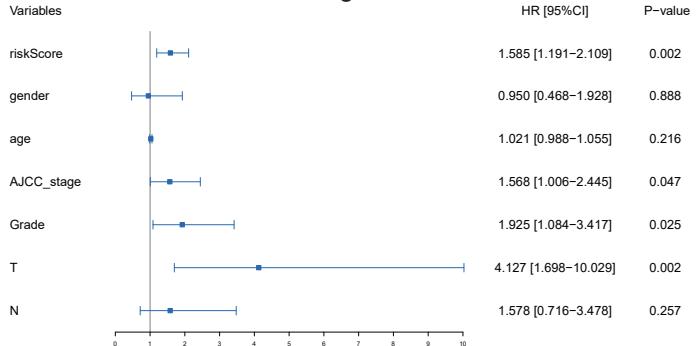
B

Training set



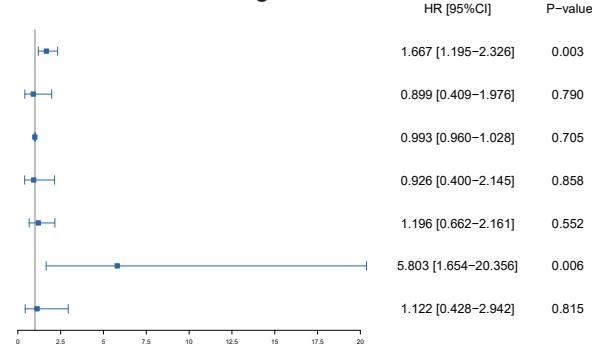
C

Testing set



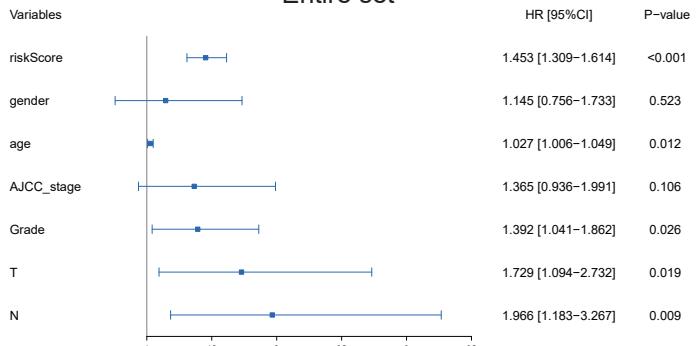
D

Testing set



E

Entire set



F

Entire set

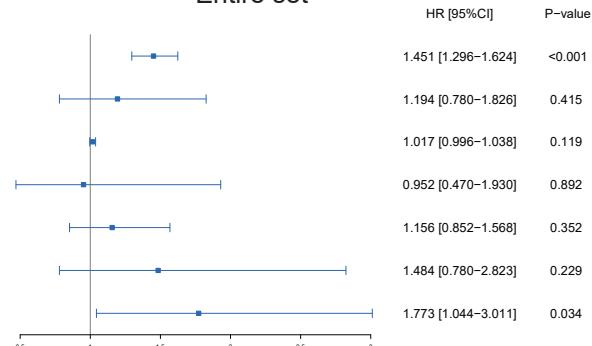


Figure S4. Independence of the risk signature and the other clinical variables, including, age, tumor grade, AJCC\_stage and gender. (A, C, E) Univariate Cox regression analyses in the training set, testing set and entire set. (B, D, F) Multivariate Cox regression analyses in the training set testing set and entire set.

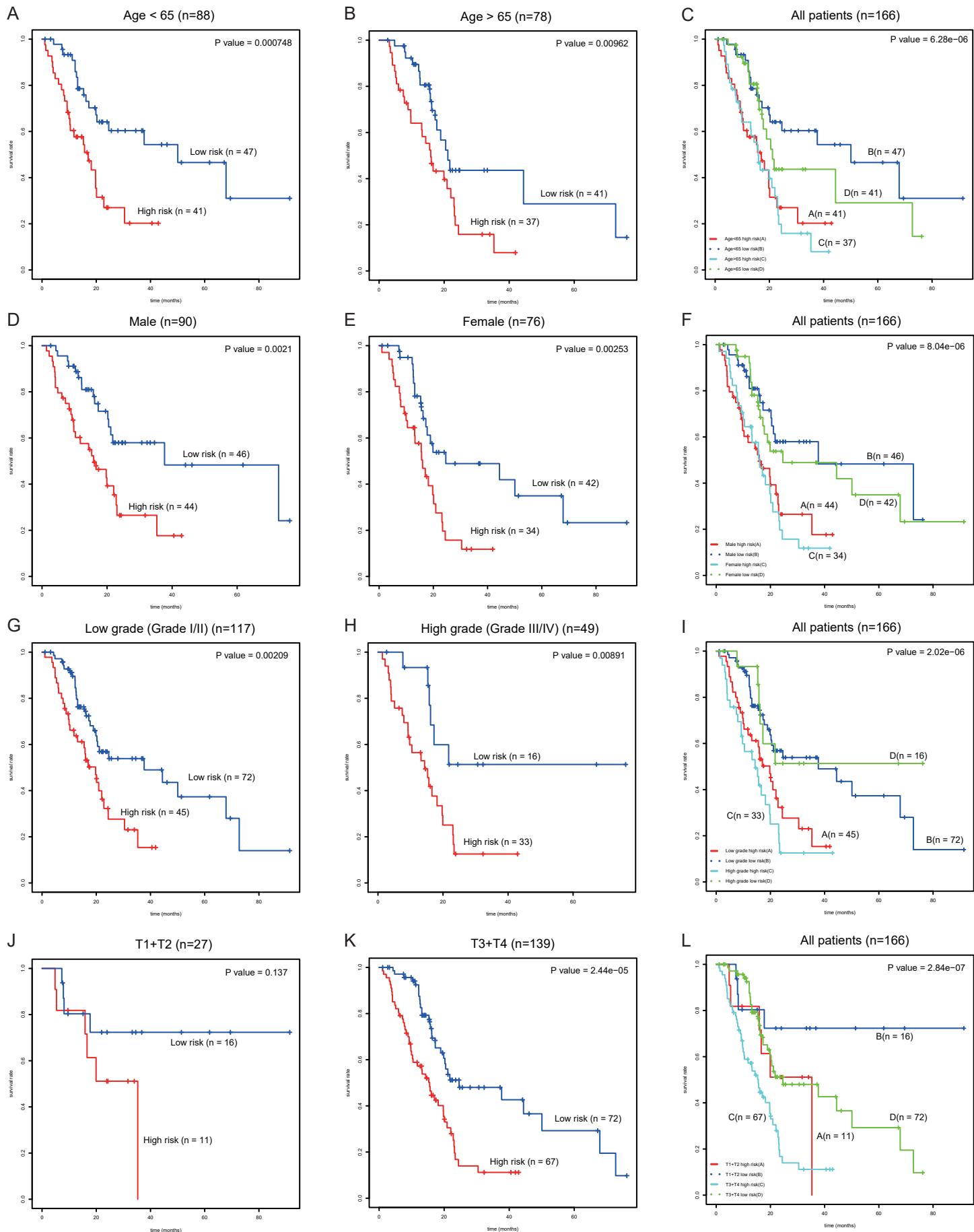


Figure S5. Stratification analyses of all patients using the risk signature. (A-C) The Kaplan-Meier analysis of the younger stratum (age  $\leq 65$ , n=88), older stratum (age  $> 65$ , n=78) and all patients with PC (n=166). (D-F) The Kaplan-Meier analysis of the male stratum (n=90), female stratum n=76) and all patients with PC (n=166). (G-I) The Kaplan-Meier analysis of the Grade I/II stratum (n=117), Grade III/IV stratum (n=49) and all patients with PC (n=166). (J-L) The Kaplan-Meier analysis of the T1+T2 stratum (n=27), T3+T4 stratum (n=139) and all patients with PC (n=166).

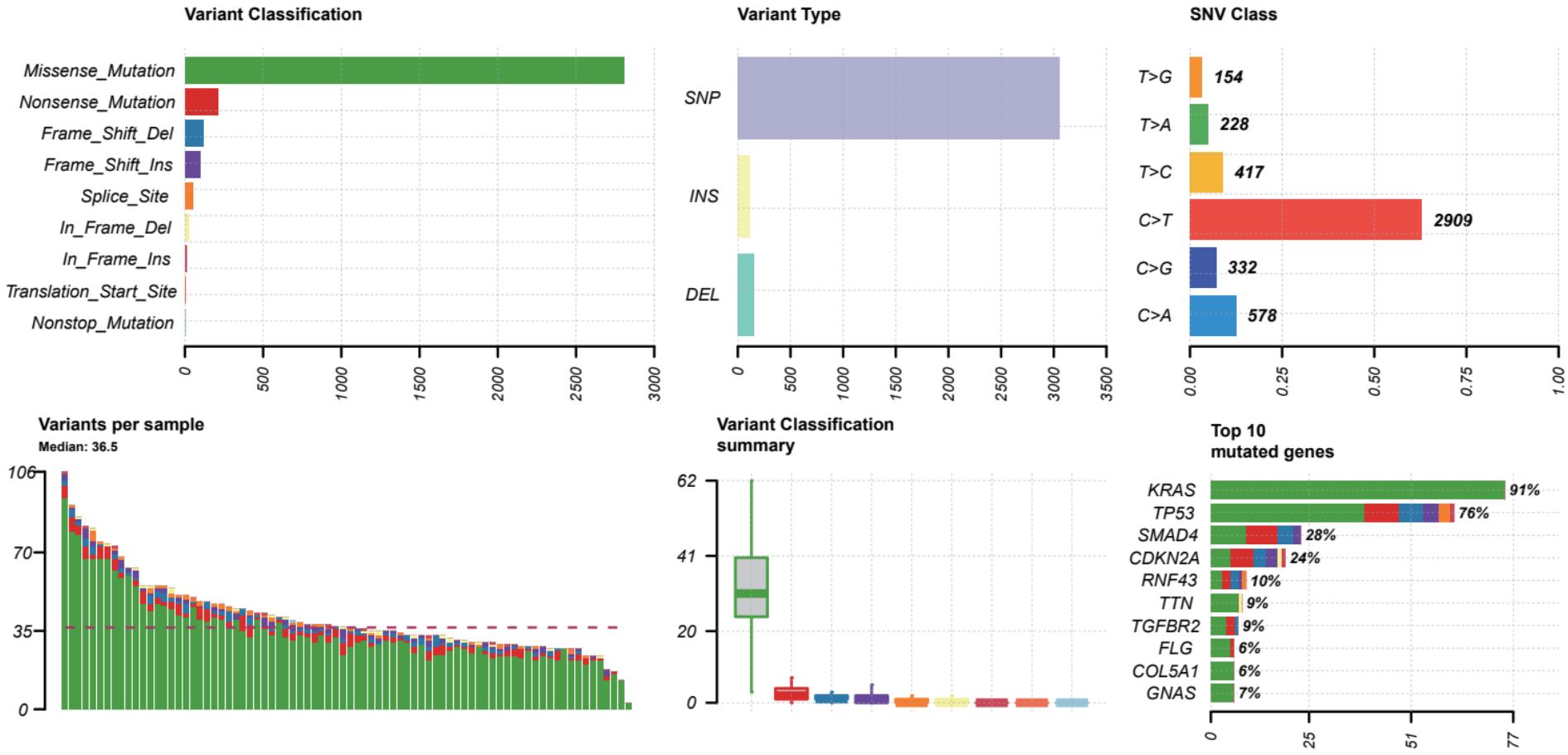


Figure S6: The mutation profiles of patients in S100A14 high expression group.

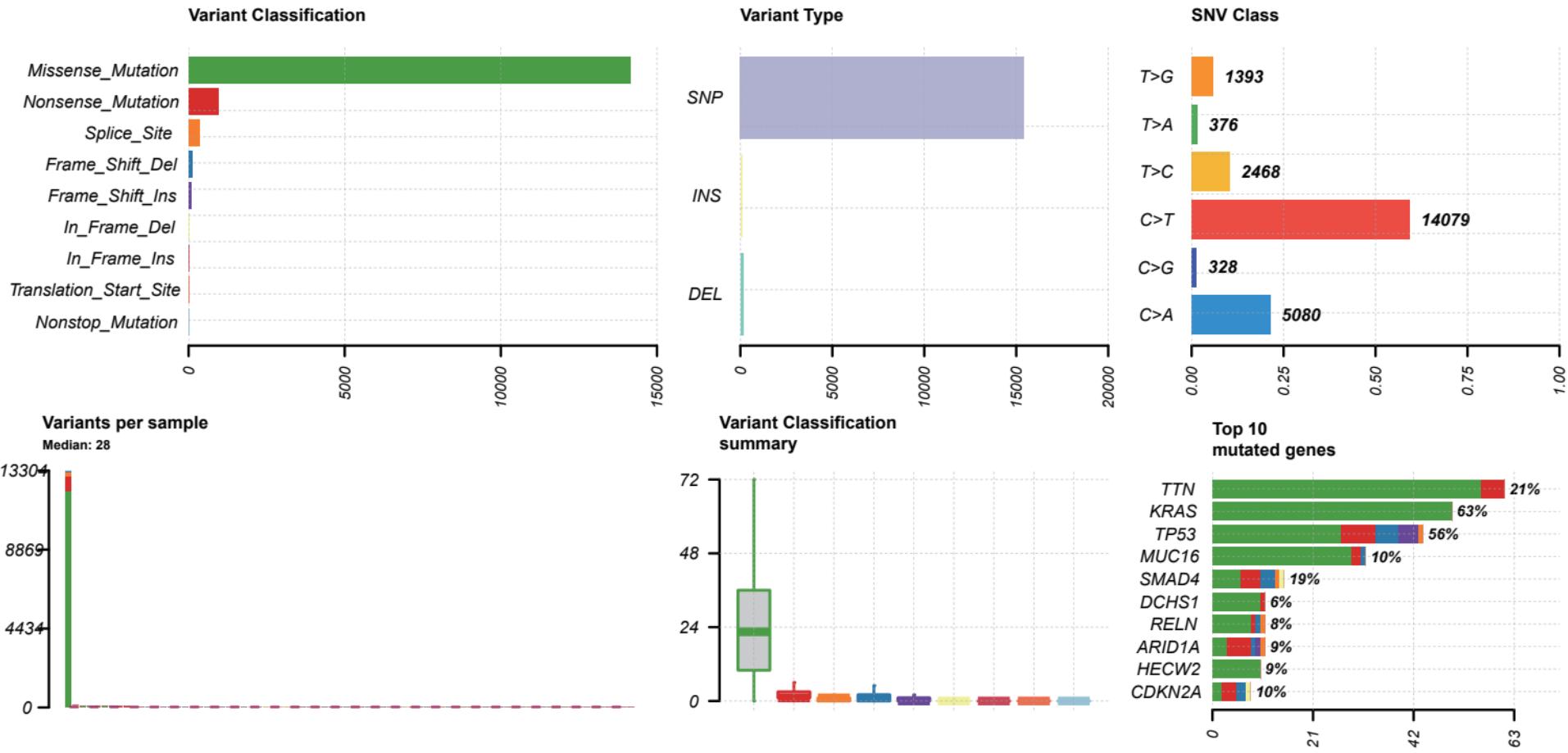


Figure S7: The mutation profiles of patients in S100A14 low expression group.

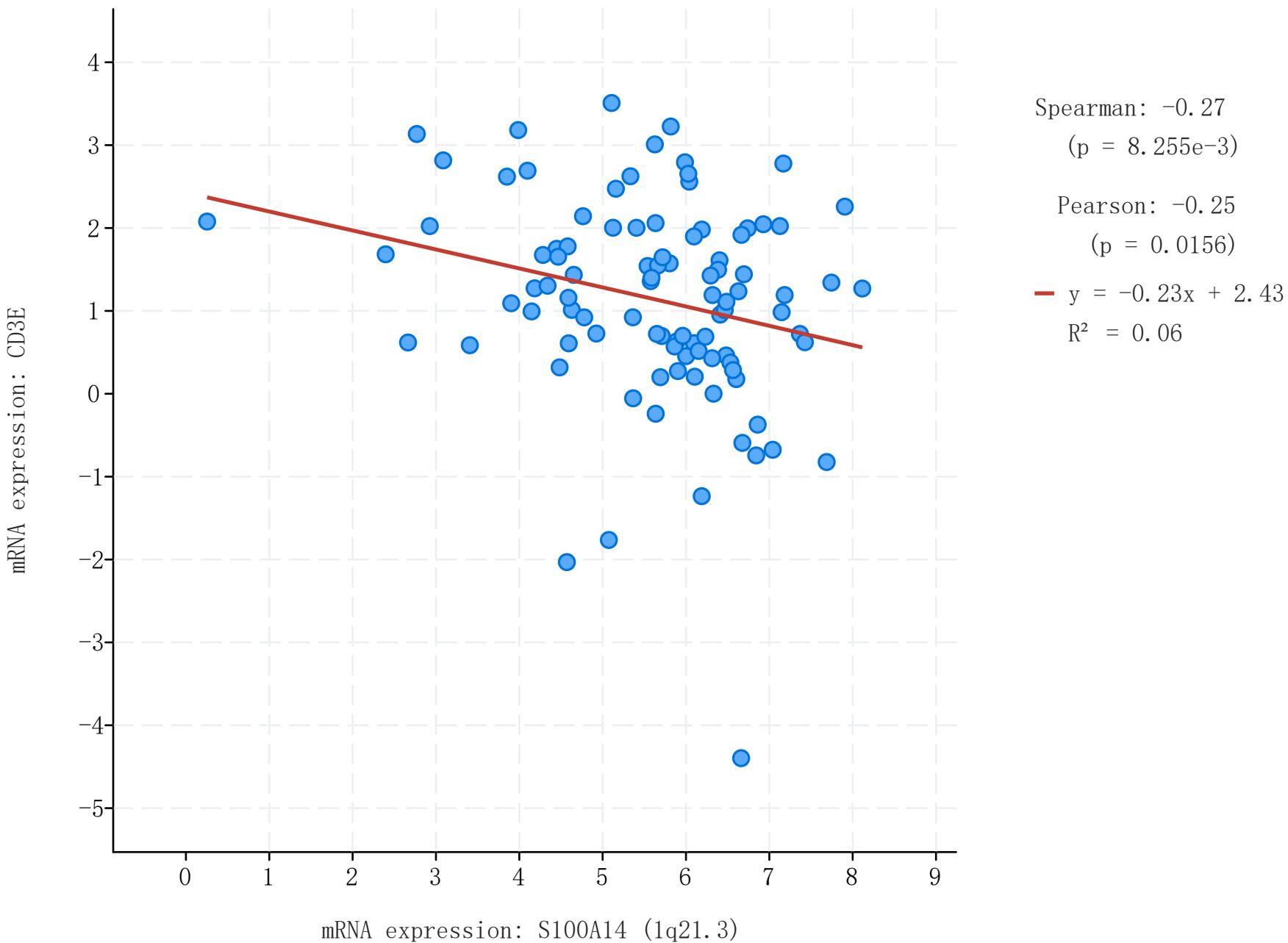


Figure S8: Correlation analysis of S100A14 and CD3E in the Bailey P. et al. cohort.