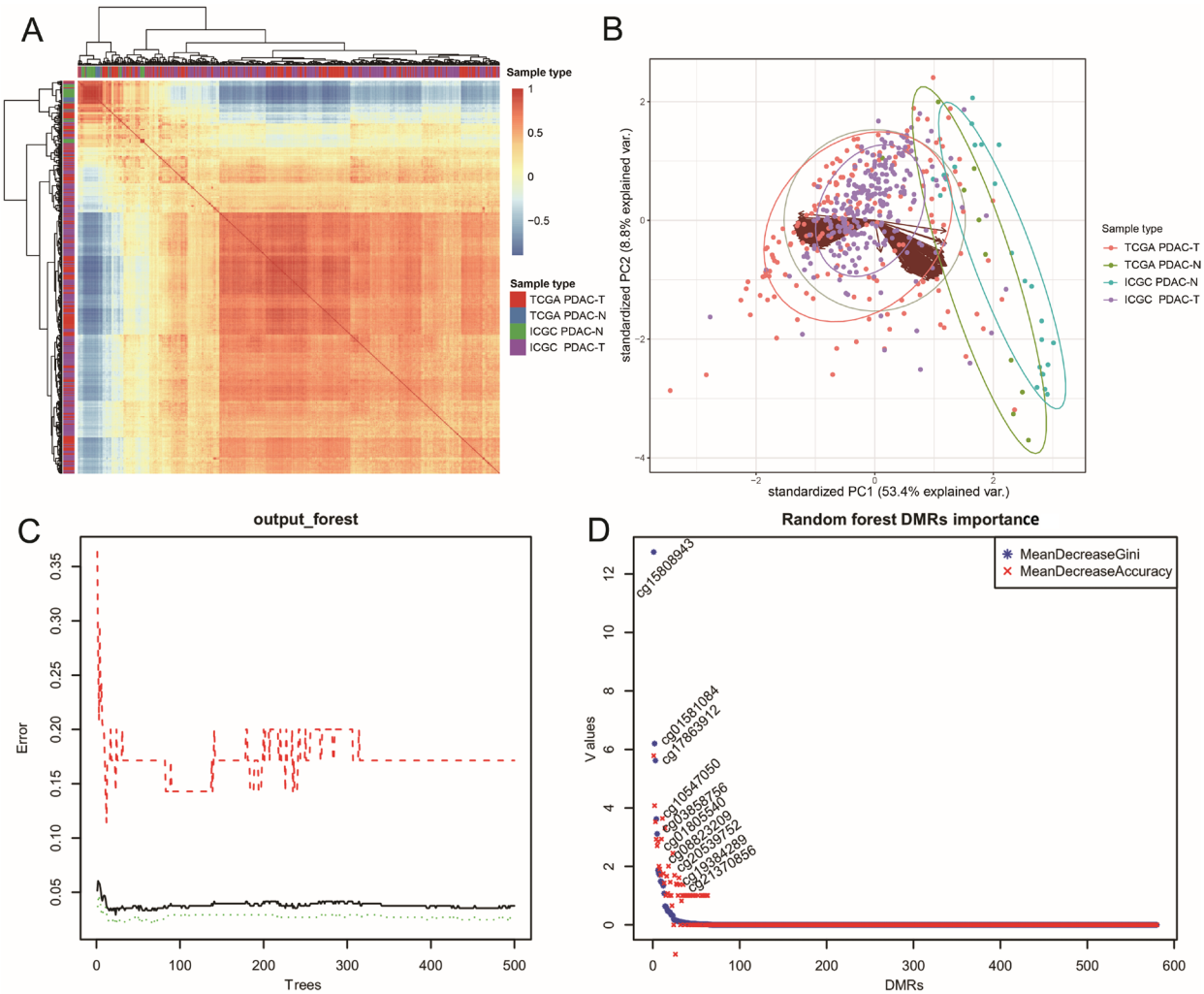

Figure S1 Data preprocessing in TCGA and ICGC datasets. (A) The similarity matrix of tumor and normal samples after merging TCGA and ICGC datasets. (B) PCA presenting correlations and differences among samples in TCGA and ICGC datasets. (C) Relationship between the number of trees and the classification error rate in the random forest model. (D) Importance of DMRs and the top 10 DMRs in the random forest model. TCGA, The Cancer Genome Atlas; PDAC, pancreatic ductal adenocarcinoma; ICGC, International Cancer Genome Consortium; DMRs, differentially methylated regions; PCA, principal component analysis.

https://dx.doi.org/10.21037/jgo-23-985

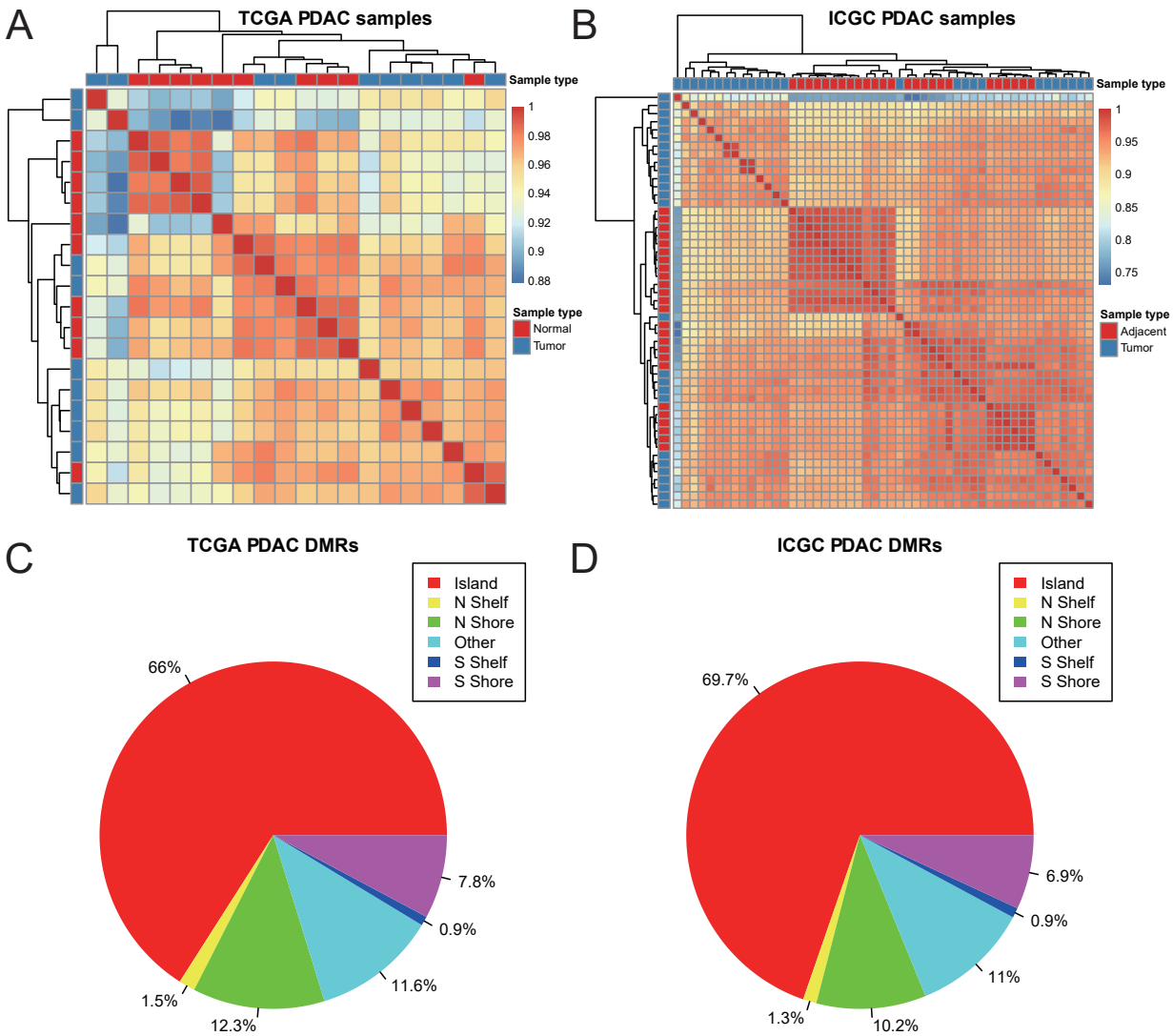

Figure S2 Analysis of internal consistency between tumor and normal groups, and the distribution of DMRs in TCGA and ICGC datasets. (A,B) Internal consistency between tumor and normal samples from TCGA and ICGC datasets. (C,D) Distribution of types of DMRs in the genome between TCGA and ICGC datasets. Islands were the most common affected sites in both datasets. TCGA, The Cancer Genome Atlas; PDAC, pancreatic ductal adenocarcinoma; ICGC, International Cancer Genome Consortium; DMRs, differentially methylated regions.

https://dx.doi.org/10.21037/jgo-23-985

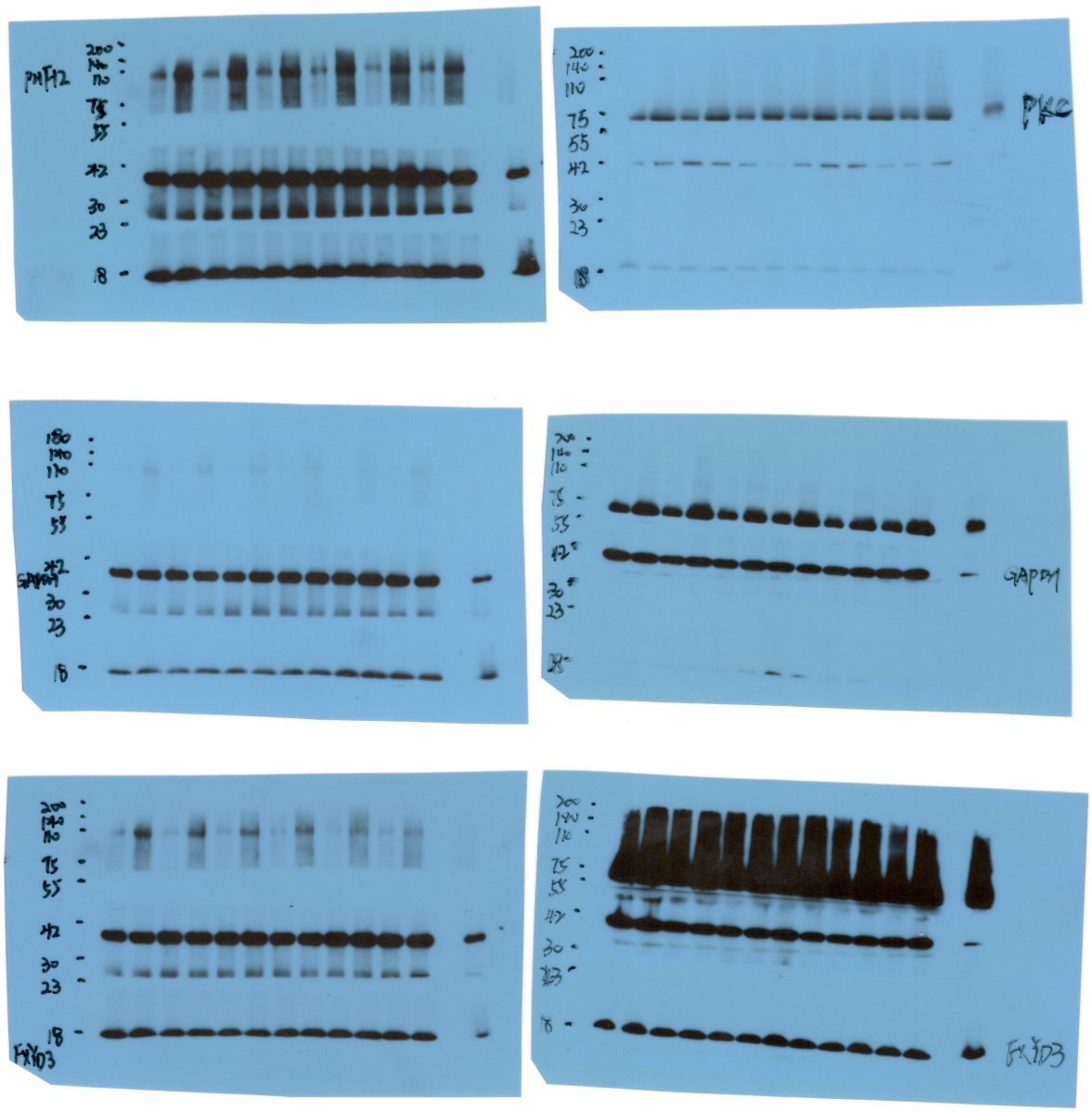

Figure S3 Raw western blotting images.

https://dx.doi.org/10.21037/jgo-23-985