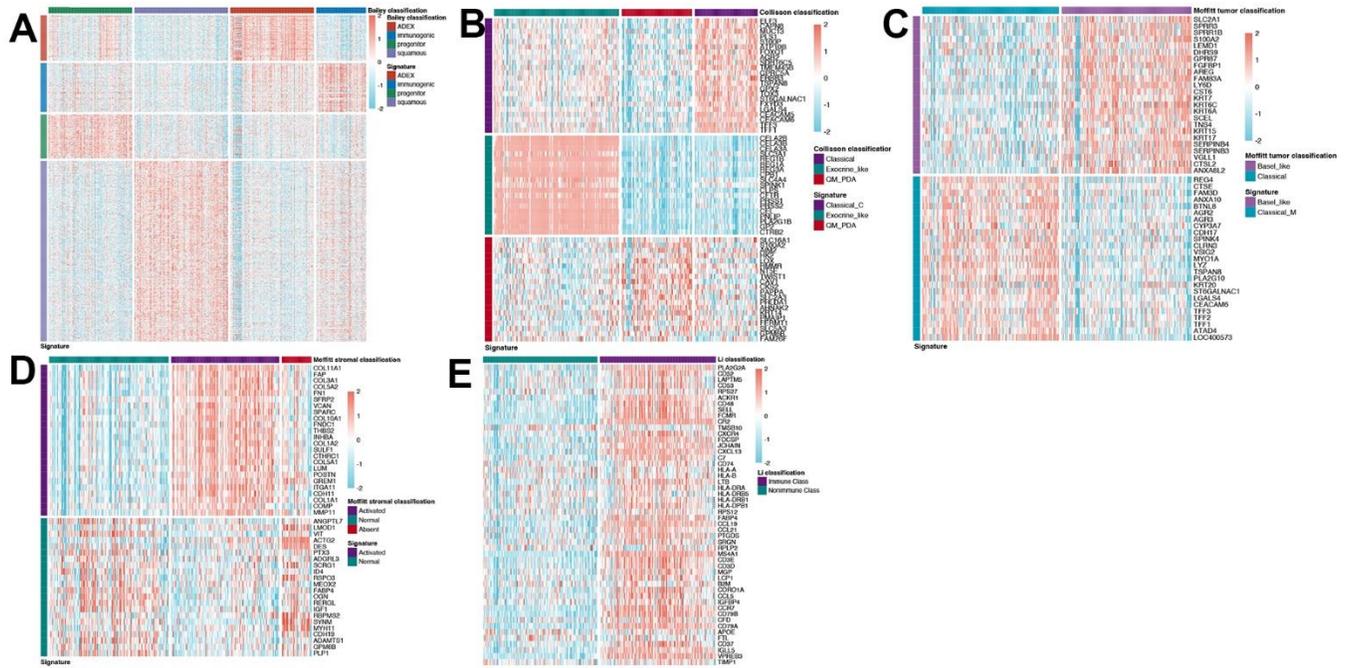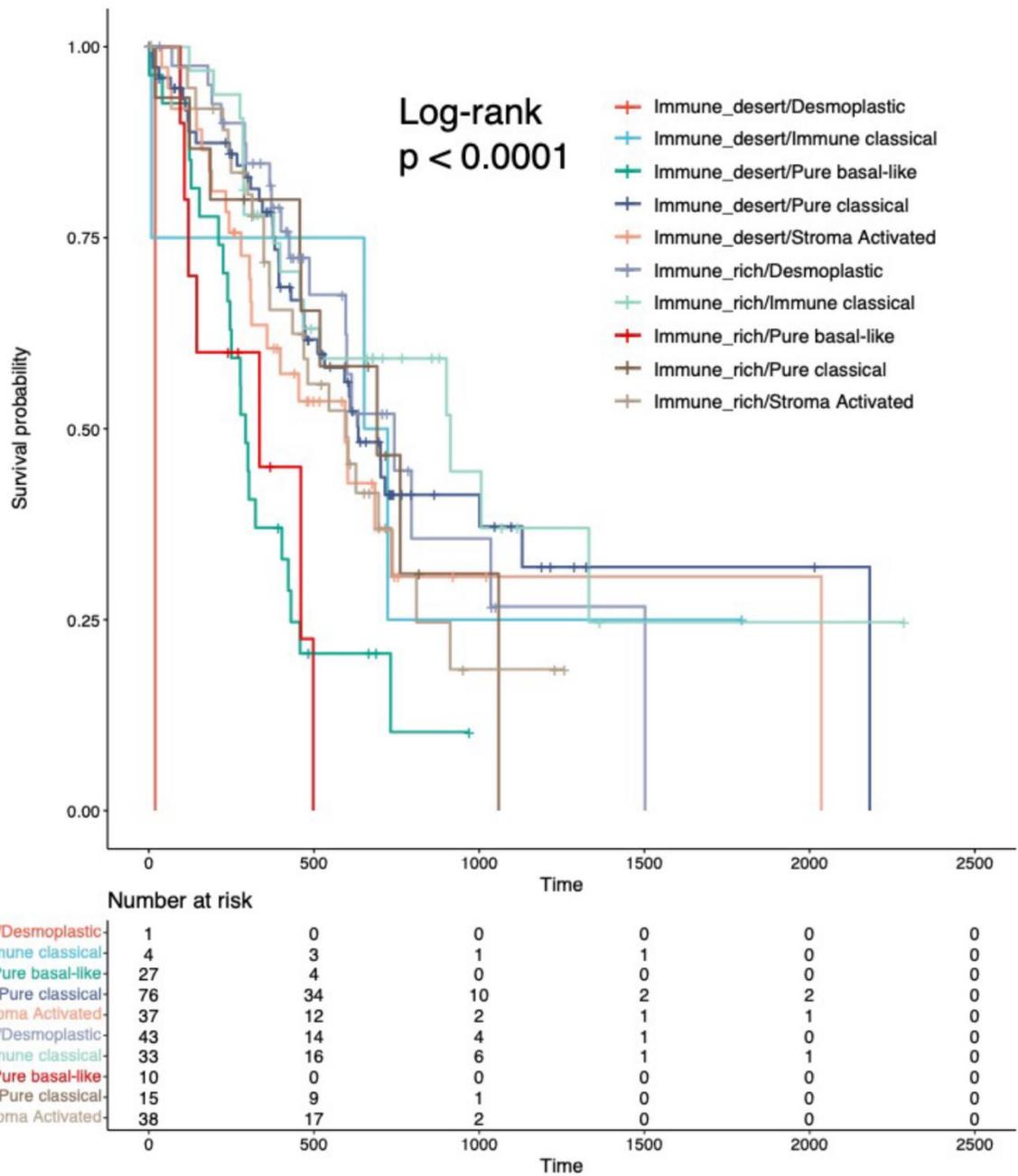**Supplementary Figure 1. Identification of TIME-related subtypes.** (**A**) The CDF plot of consensus clustering. (**B**) The PCA plot demonstrated the differences between the two clusters.

Supplementary Figure 2. Published PC subtypes prediction. Heatmap showed that we defined Bailey's classification (**A**), Collisson's classification (**B**), Moffitt's tumor classification (**C**), Moffitt's stromal classification (**D**) and Li's classification (**E**) based on the published classifier exemplar genes.

Supplementary Figure 3. Kaplan-Meier curves of overall survival were plotted according to the TIME subtype and Puleo's classification.
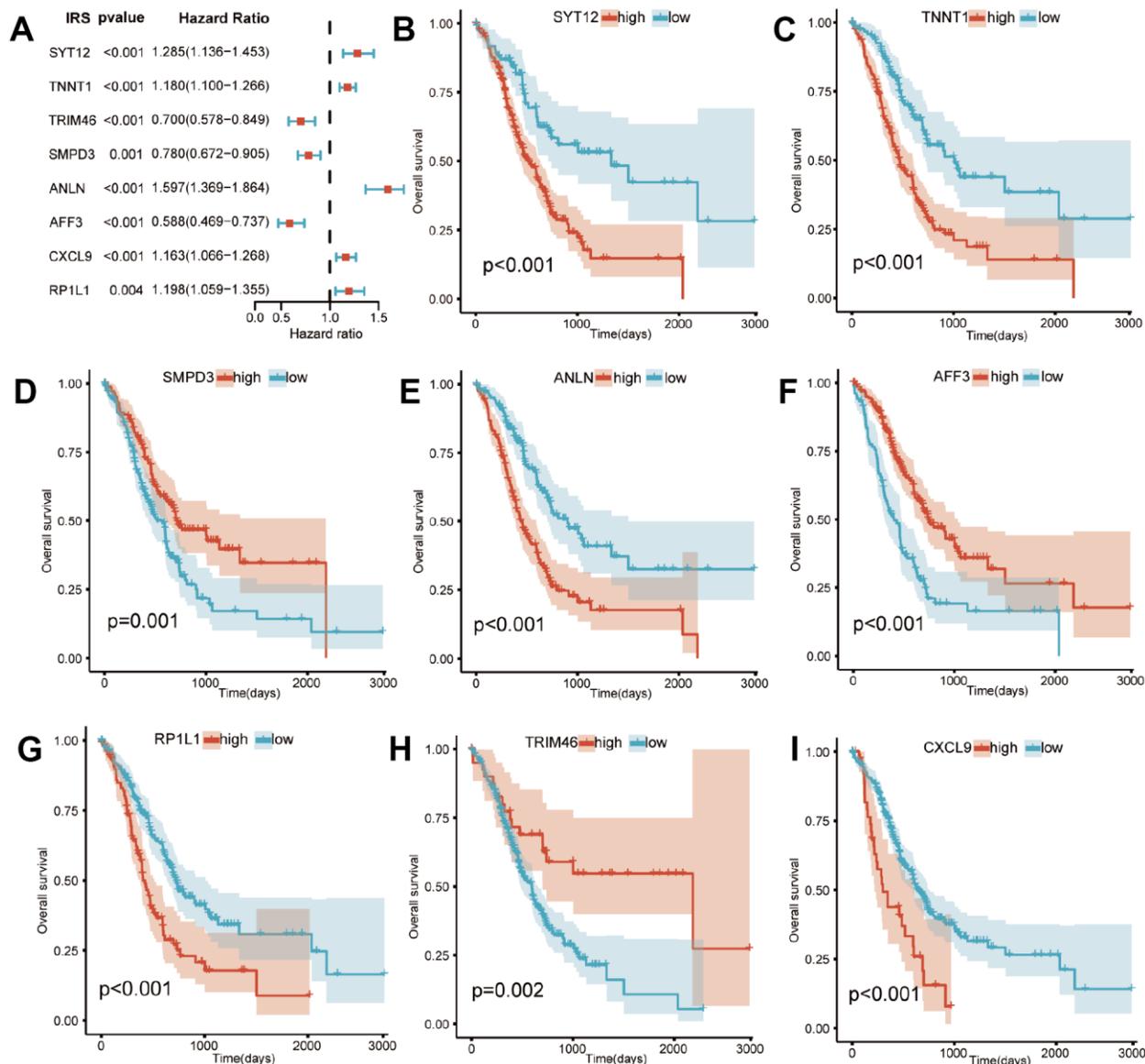
Supplementary Figure 4. Validation of IRS. (**A**) Forest plot of univariate cox analysis based on the training set. (**B**–**I**) The survival analysis is based on the expression of IRS genes.
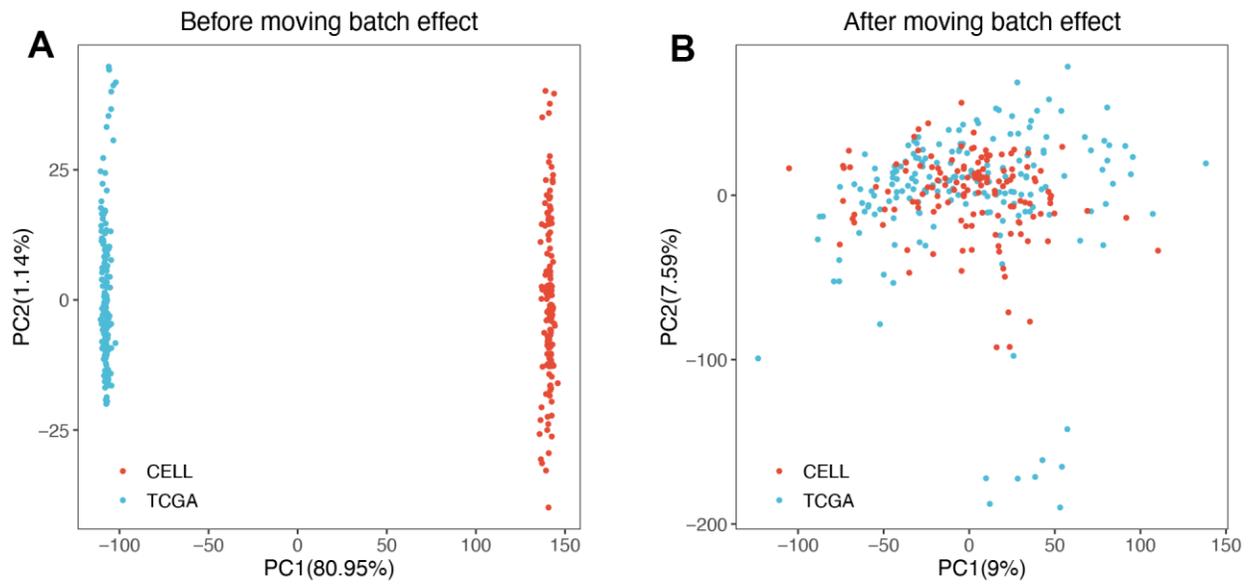
Supplementary Figure 5. Evaluation of the results of batch effect correction. The principal component analysis (PCA) before (**A**) and after (**B**) batch effect correction on Meta-cohort.