**Supplemental Figure Legends:**

**Supplemental Figure 1:** Clinical and pathological information for the cohort employed in the present study.

**Supplemental Figure 2:** (A) Specific genes that define the immunological signatures as indicated. (B) Application of immunological signatures to TCGA data (n=183 cases) definetwo principle subtypes as shown by unsuperverised clustering analysis. (C) Interrogation of specific genes by unsupervised clustering analysis in TCGA data (n=183 cases).

**Supplemental Figure 3:** (A) Quantitation of the median survival associated with each of the indicated markers (B) Representative staining of PDL1 expression at the edge of the tumor. The association with overall survival was determined by Kaplan-Meier analysis, and association with stromal type was determined by t-test. \*\*p<0.01.

**Supplemental Figure 4:** (A) Correlation analysis of the indicated immune-regulatory marker gene expression with overall survival. Heatmap depicts Spearman correlation. (B) Correlation values of the indicated gene expression vs. overall survival. \*p<0.05, \*\*p<0.01, \*\*\*p<0.001.

**Supplemental Figure 5:** (A) Summary of cutpoints utilized in the random-forest clustering of biomarkers. (B) Median survival for each of the random-forest clusters. (C) Summary of the KRAS mutations observed in each cluster.