Captions for the supplementary figures

Supplementary Figure 1. Kaplan-Meier curves on validation sets using three risk level ArcTIL model comprising for predicting OS (A-E) and PFS (F), A. chemotherapy ovarian cohort (D1), B. chemotherapy cervical cohort (D2), C. radiotherapy cervical cohort (D3), D. chemotherapy endometrial cohort (D4), E. Radiotherapy endometrial cohort (D5), F. immunotherapy cohorts (D6-D8)

Supplementary Figure 2. Illustration of proximity graphs. Tissue slide images with a low-risk (top) and high-risk (bottom) patient. Each panel represents proximity graphs as well as corresponding convex hulls for a single cell family (green: epithelial TILs, orange: cancer-cells, cyan: S-TILs, blue: stromal non-lymphocyte cells). The background is color coded to differentiate the epithelium and surrounding stromal tissues on the tumor invasive front.

Supplementary Figure 3. Comparing prognostic ability of ArcTIL model with human readers of immune profile using average TIL count in WSI. Also ICC values shows the disagreement between pathologist derived TIL counts.

Supplementary Figure 4. Enrichment Analysis bar plots for TCGA patients. First row to 4th, demonstrate biological process, cellular components, molecular functions, and pathways.

Supplementary Figure 5. The association between the prognostic ArcTIL features and the enrichment scores of pathways

Supplementary Figure 6- **UMAP embedding of seven prognostic ArcTIL features** Each circle is associated with a patient, circles are color-coded according to **A.** the ArcTIL signature values, **B.** the ArcTIL risk group, **C.** cancer type and therapy regimen, **D.** race, **E.** tissue source sites

Captions for the supplementary tables

Supplementary Table 1. Evaluation of results in different supplemental experiments. The number in parentheses represents the number of cases for that specific validation set. In the column "Number of selected features and geographical region" (the abbreviation E, S, T represent epithelium, stroma, and tumor invasive front, respectively).

Supplementary Table 2. Pathologists' opinion on D_6, D_7, D_8 data set (average TIL count on three same field of view)

Supplementary Table 3. The list of genes that were shown to be significantly differentially regulated between high-ArcTIL risk and low-ArcTIL risk groups.

Supplementary Table 4. The list of central biological pathways and their involving genes, that were associated with the gene ontology analysis. Each pathway may include different number of genes.

Supplementary Table 5. Enrichment scores calculated using single sample gene set enrichment analysis (ssGSEA) for all 7 prognostic ArcTIL features, and all 22 biological pathways

Supplementary Table 6. P-values of pairwise comparison between all ATCTIL contributing features and all 22 biological pathways.

Supplementary Table 7. Performance of univariate Cox proportional hazards model analysis of OS across D_1-D_5 and PFS across D_6-D_8 using clinical and ArcTIL features, each cell contains HR, (95% CI) and p, respectively. Green-filled cells reflect the statistically significant results.

Supplementary Table 8. Performance of multivariable Cox proportional hazards model analysis of OS across D1-D5 and PFS across D6-D8 using individual ArcTIL features, each cell contains HR, (95% CI) and p. Green-filled cells reflect the statistically significant results.