

**Supplementary figure 1.** Scan view of bladder urothelial carcinoma liquid-based cytology (Papanicolau, Aperio ImageScope) and representative cytomorphologic features of (A) urothelial carcinoma cells and (B) benign urothelial cells (Papanicolau, x 40, Aperio ImageScope).

**Supplementary figure 2.** Workflow of protein markers selection for immunostaining validation.

**Supplementary figure 3.** Correlation among technical and biological replicates.

**Supplementary figure 4.** Correlation between cell counts and MS intensities.

**Supplementary figure 5.** Normalization of cytology samples.

**Supplementary Figure 6.** Heat map demonstrating unsupervised hierarchical clustering of 112 differentially expressed proteins (DEPs) in 10 benign urothelial lesion and bladder urothelial carcinoma samples.

**Supplementary figure 7.** Dynamic range of urothelial carcinoma FFPE samples. Highlighted data points indicate the six proteins selected using cross-platform based analysis.

**Supplementary Figure 8.** Correlation among biological replicates in Urothelial Carcinoma FFPE samples.

**Supplementary Figure 9.** Representative images of histology (left, H&E, original magnification x100) and immunohistochemistry staining of AHNAK in urinary urothelial carcinoma tissue sample (right, original magnification x100 and x400 (inlet), respectively).

**Supplementary Figure 10.** Prognostic significance of 11 protein candidates from individual datasets, SurvExpress.

**Supplementary Figure 11.** Prognostic significance of 11 protein candidates from individual datasets, the Human Protein Atlas.