Supplemental Figure S1: Representative SDS-PAGE retrieved from the separation of urinary proteins of some animals enrolled in the present study.

Supplemental Figure S2: Venn diagram highlighting the interindividual variability of identified proteins within each group.

Supplemental Figure S3: Urine zymography of some urine samples from animals enrolled in the present study.

Supplemental Figure S4: ClueGo + CluePedia analysis of protein-protein interaction considering unique proteins identified in the urine of CONT, BBN1 and BBN2 subjects. Blue nodes refer to biological processes prevalent in BBN2 animals, pink nodes represent the ones prevalent in BBN1 animals whereas yellow nodes represent the ones widespread in healthy animals.

Supplemental Figure S5: Slot-blot analysis of urinary C-reactive protein (A), osteopontin (B) and IL-6 (C). Values are presented as mean ± standard deviation of optical density (OD), expressed in arbitrary units (a.u.), retrieved from the analysis of individual samples *per* group (duplicates of n=7). Representative immunoblots are presented above the respective histograms.

(*$p < 0.05$ vs CONT or BBN1).

Supplemental Figure S6: ClueGo+CluePedia analysis of protein-protein interaction considering common proteins present in significant distinct levels (based on emPAI values) in the urine of CONT, BBN1 and BBN2 animals. Green nodes refer to biological processes positively regulated whereas red nodes refer to the ones negatively regulated in animals with urothelial carcinoma.

Supplemental Figure S7: Summary of the biological processes more prevalent in BBN1 (A) and in BBN2 (B) based on protein clustering analysis (Figure 6).

Supplemental Figure S8: ClueGo+CluePedia analysis of protein-protein interaction considering the unique proteins identified in the urine of 3 bladder cancer patients (high-grade disease; blue nodes) and the ones identified in 10 healthy subjects (pink nodes).