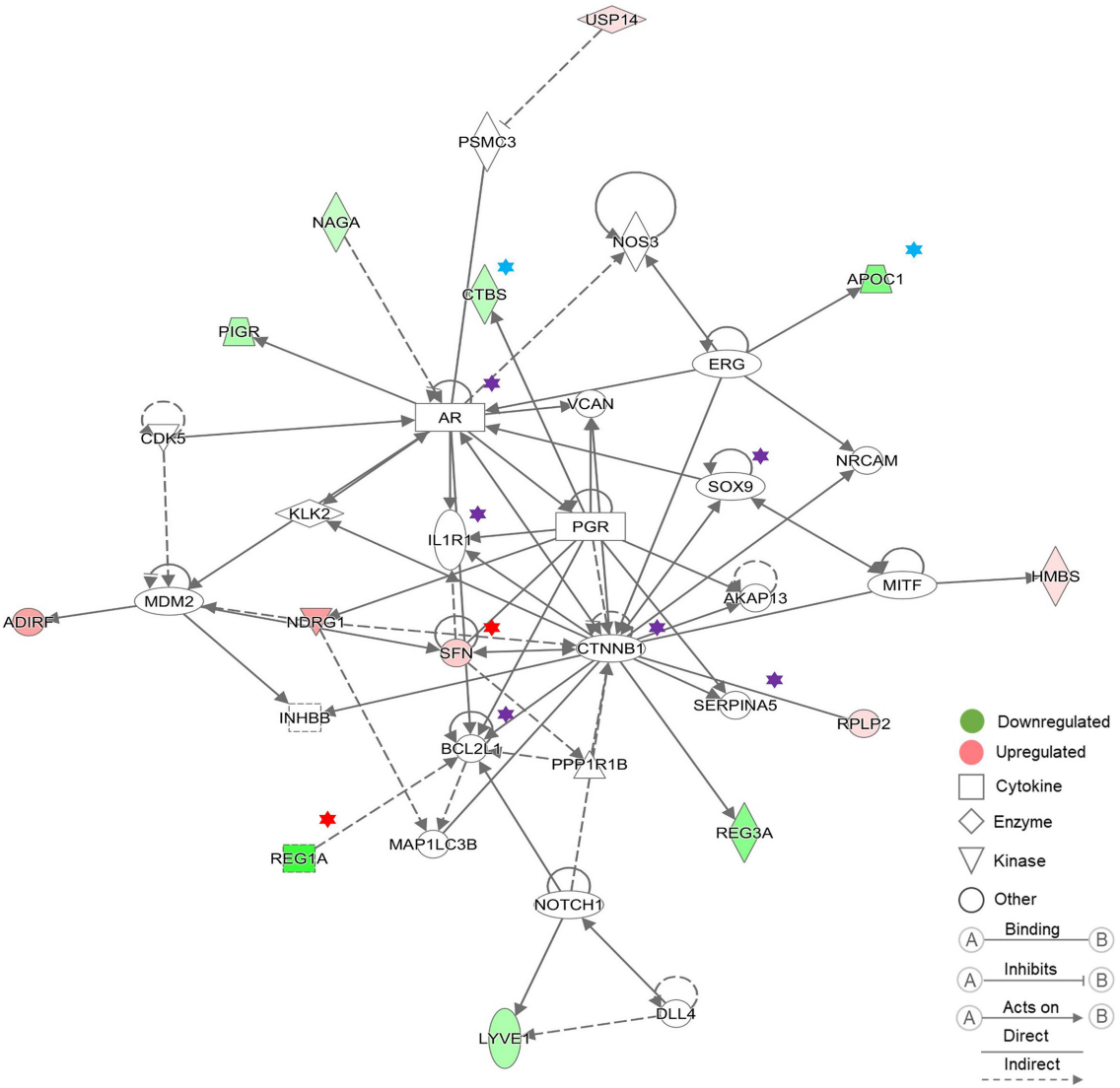

Figure S1 Network analysis identifying SFN and REG1A as important proteins in the process of cell death and survival, cellular movement, cellular growth and proliferation. It can be observed that SFN and REG1A could interact with CTNNB1, IL1R1, AR, and BCL2L1 proteins. In particular, binding with BCL2L1 may inhibit cell death, which could explain the high SFN expression in bladder cancer. Green indicates proteins that were significantly downregulated, whereas red indicates proteins that were significantly upregulated. Shapes indicate different functional categories of proteins (as defined in the inset). Lines indicate interactions among proteins within the network (as defined in the inset). Arrowheads indicate stimulatory interactions, whereas endcaps indicate inhibitory interactions. Solid lines indicate direct interactions, whereas dashed lines indicate indirect interactions. Red star-labeled proteins are the differential proteins identified in this experiment. Blue-star-labeled proteins are proteins mentioned in the literature, and purple-star-labeled proteins are closely related proteins.

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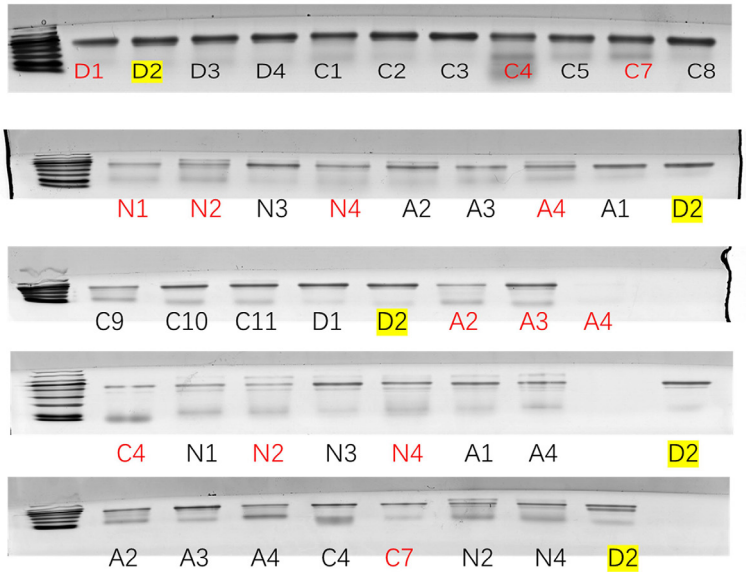

Figure S2 Coomassie blue staining is used for total protein quantification in urine samples. Because urine samples do not contain a suitable internal reference protein, we used the whole protein content of each sample as a loading control. In Coomassie Brilliant Blue quantification, when the sample runs through the separation gel, the electrophoresis was paused and the protein is concentrated in a small block to reduce the error in sample quantitation. In the gel pictures, the red-labeled sample represents an inaccurate sample in each quantification gel, and the D2 sample (yellow background) is an internal reference between quantification gels.

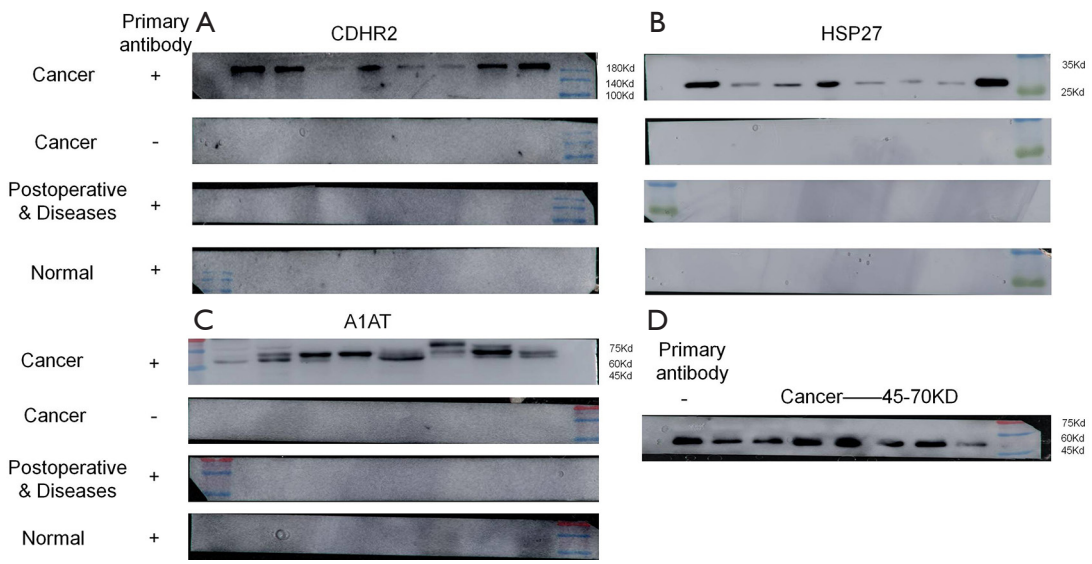

Figure S3 Elimination of impurity bands. Patients with bladder cancer often have hematuria, where blood is present in urine samples. Some of our candidate biomarker proteins have similar molecular weights and consequently run similarly on the gel; they are located in the blood-derived immunoglobulin (IgG) heavy and light chains. ABC) To exclude interference in the quantitation of biomarker candidate proteins from the presence of IgG in the sample, we used a secondary antibody that could distinguish between light and heavy chains. For proteins expected to run at a similar position to the IgG light chain, we use a secondary antibody that recognizes only the IgG heavy chain, and vice versa. D) A sample of gel without primary antibody, incubated with secondary antibody that detects both light and heavy IgG chains.

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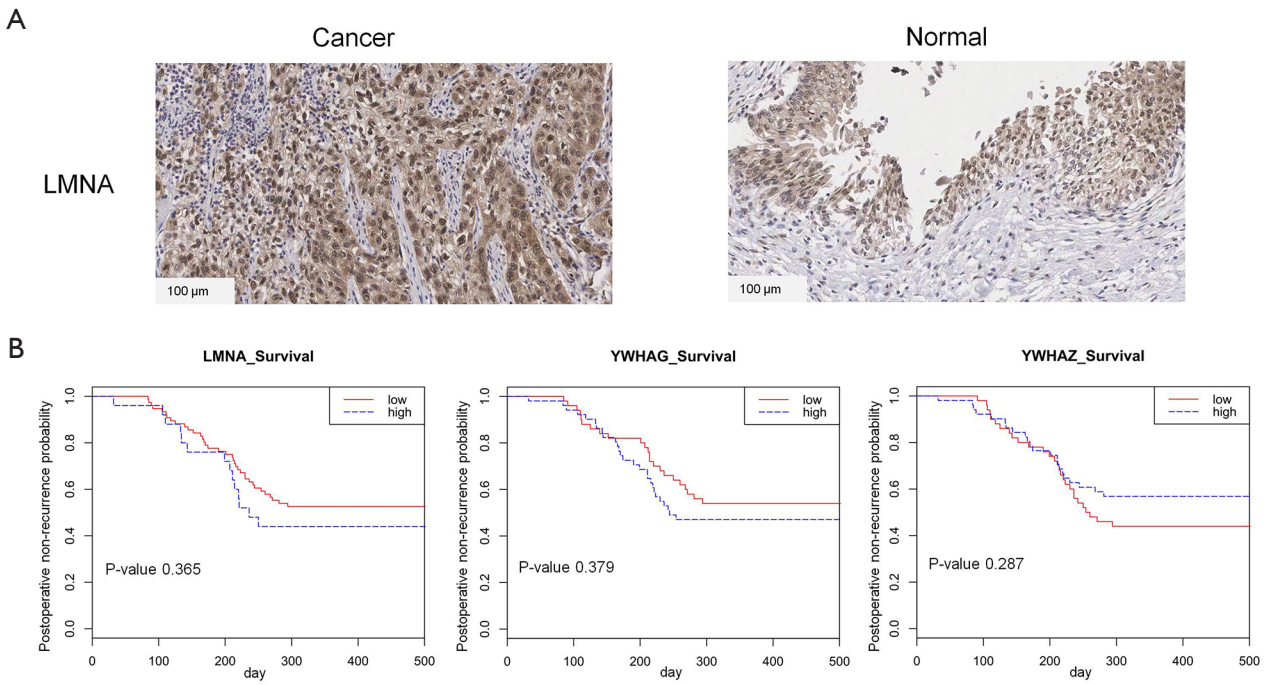

Figure S4 The probability of recurrence in patients with bladder cancer, stratified by gene expression data from TCGA. (A) Immunohistochemical analysis of LMNA protein expression levels in bladder cancer tissue chips. (B) The probability of recurrence of bladder cancer in patients, stratified by gene expression data, from TCGA. There are 101 bladder cancer gene expression data, set the recurrence time within 300 days as prone to recurrence population. Among them, 50 patients were relapse patients, and 51 patients were not easy to relapse. The results of TCGA data and MS, WB results revealed that the difference in expression of LMNA, YWHAG and YWHAZ are closely related to bladder cancer. These proteins may predict the prognosis of patients beyond 200 days postoperatively.

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