SUPPLEMENTARY FIGURE LEGENDS

Supplementary Figure 1. Fraction of genome altered (FGA%). FGA according to **(A)** grade and **(B)** stage (Median FGA values are shown). FGA and *TP53* mutation status according to **(C)** grade and **(D)** stage.

Supplementary Figure 2. 8q22.2-q22.3 amplification in UC. (A) 1Mb resolution aCGH detection of 8q22.2-q22.3 amplification in four T1G3 tumors. Results are represented as individual chromosome 8 plots of log2 ratio versus distance along chromosome (Mb). **(B)** Schematic representation illustrating the minimal region of amplification at 8q22.2-q22.3 and candidate genes. BAC array clones covering amplified (black boxes) and nonamplified (grey boxes) regions are shown. Dashed lines define the minimal region according to 1Mb aCGH data from the current study (left-hand boundary) and mapping data taken from the study of Heidenblad *et al*. (2008) (right-hand boundary). **(C)** Real-time PCR analysis of candidate genes from the 8q22.2-q22.3 minimal region. The relative expression of candidate genes (*YWHAZ*, *ANKRD46*, *SNX31*, *ZNF706* and *GRHL2*) was determined by real-time RT-PCR. Levels of expression were normalised to *SDHA* (Hs00417200_m1) and measured relative to a pool of uncultured normal human urothelial cells (P0). Tumors with copy number gain (blue bars) or amplification (red bars) of 8q22.2-q22.3 are highlighted. Pearson correlations were performed between DNA copy number and gene expression for 8q22.2-q22.3 candidate genes. Correlation coefficients (r) and p-values values are shown.

Supplementary Figure 3. Relationship between *PTEN* loss, *RB1* loss and *TP53* mutation status and time to metastasis. Kaplan-Meier plots of metastasis-free survival in patients with ≥T2 tumors stratified according to the copy number status (loss [-] or no loss [+]) of the *PTEN* and *RB1* regions, and *TP53* mutation status (mutant [mut] or wildtype [wt]). (A) *PTEN* copy number loss (B) *RB1* copy number loss (C) *PTEN* and *RB1* copy number loss, (D) *TP53* mutation status and (E) *TP53* mutation status and *PTEN* copy number loss. Log-rank tests were used to evaluate statistical differences between groups with p-values being shown on individual plots. Please note that 9 patients had metastasis at diagnosis.

Supplementary Figure 4. Copy number (CN), mutation status (MS), loss of heterozygosity analysis (LOH) and immunohistochemistry (IHC) data for all tumors (n=160).

Supplementary Figure 5. Unsupervised hierarchical cluster analysis of aCGH data from all tumor samples and genome-wide frequency plots of copy number alterations in individual ≥T2 clusters. Each tumor was scored for copy number gains and losses and these were assigned a copy number class (2 high-level gain, 1 gain, 0 no change, -1 loss; -2 high-level loss). Copy number class data was used in one-way hierarchical cluster analysis of **(A)** all 160 tumors and **(B)** 42 stage ≥T2 tumors. Each column of the heat map represents one sample and each row represents the genomic positions of individual BAC clones on the array. Green=copy number gain; Red=copy number loss. Chromosome number is shown on the left-hand side of the heat map. A colour code for stages and grades is shown at the bottom of panel **(A)**. Three main clusters of ≥T2 tumors were identified and these are indicated by the colour bars at the top of the figure: Cluster 1 = blue, Cluster 2 = yellow, Cluster 3 = grey. The *TP53* and *FGFR3* mutation status of each tumor is also shown at the top of panel **(B)** (Black box = mutant; white box = wildtype) along with FGA group (A-D). Frequency plots of copy number events for individual ≥T2 clusters are presented in panel **(C)** with copy number gains shown in green and losses in red.

Supplementary Figure 6. Loss and gain in tumors from individual Ta, T1 and ≥T2 clusters. The x-axis corresponds to individual tumors arranged according to cluster assignment in Ta, T1 and ≥T2 tumor subgroups. The y-axis corresponds to either **(A)** the number of clones reporting gain (above the zero line) or loss (below the zero line) or **(B)** the number of gain events (above the zero line) and loss events (below the zero line) in each tumor. Whole chromosome arm gains or losses were counted as single events whereas independent copy number alterations on the same chromosome arm were each scored as single events.