Table SI. Clinical and pathological characteristics of patients with bladder cancer.

Sample no.	Sex	Age (years)	Tumor stage	Tumor grade	Metastasis	Smoking	Cigarettes per day	Professional risk factors	Family history	Recurrence	BCG therapy	MMC therapy
1	F	50	T2	G2	N0M0	+	20	-	-	R, 3rd	-	-
2	F	82	T2	G2	N0M0	-	-	+	-	Pr Tu	-	-
3	F	62	T1	G1	N0M0	+	10	-	-	R, 1st	-	+
4	F	61	T1	G2	N0M0	+	20	+	-	R, 3rd	-	-
5	F	65	T2	G3	N0M0	+	20	-	-	R, 2nd	-	-
6	F	61	T2	G3	N0M0	-	-	-	-	R, 3rd	-	-
7	M	82	T2	G2	N0M0	+	11	-	-	Pr Tu	-	-
8	M	82	T2	G3	N0M0	+	6	-	-	Pr Tu	-	-
9	M	76	T3	G3	N0M0	+	10	-	-	R, 1st	-	-
10	M	66	T1	G1	N0M0	-	-	-	-	R, 1st	+	-
11	M	78	T3b	G3	N0M0	-	-	+	-	R, 3d	-	-
12	M	78	T1	G1	N0M0	-	-	-	-	Pr Tu	-	-
13	M	73	T3	G3	N1M0	+	20	+	-	PrTu	-	-
14	M	67	T2	G3	N0M0	+	30	-	-	R, 2nd	-	+
15	M	63	T1	G2	N0M0	-	-	-	-	Pr Tu	-	-
16	M	63	Ta	G1	N0M0	+	10	-	-	Pr Tu	-	-
17	M	67	Ta	G1	N0M0	-	-	-	-	R, 2nd	-	-
18	M	63	T4	G3	N0M0	+	15	-	-	Pr Tu	-	-
19	M	64	Ta	G1	N0M0	+	20	-	-	Pr Tu	-	-
20	M	42	Ta	G1	N0M0	-	-	-	-	R, 2nd	-	-
21	M	77	T2a	G2	N0M0	-	-	-	-	PrTu	-	-
22	M	64	T2	G2	N0M0	-	-	-	-	R, 1st	-	-
23	M	61	T1	G2	N0M0	-	-	-	-	Pr Tu	-	-
24	M	62	T2a	G3	N0M0	-	-	-	-	R, 2nd	-	-
25	M	63	T1	G2	N0M0	-	-	-	-	R, 1st	-	+
26	M	63	T2b	G3	N0M0	-	-	-	-	R, 1st	-	+
27	M	77	T2b	G3	N0M0	-	-	-	-	R, 1st	-	-
28	M	79	T2b	G3	N1M0	-	-	-	-	R, 2nd	-	-
29	M	69	Ta	G1	N0M0	+	20	-	-	Pr Tu	-	-
30	M	66	T1	G1	N0M0	+	20	-	-	Pr Tu	-	-

F, female; M, male; '-'/'+', negative/positive for the tested category; BCG, bacillus Calmette-Guérin; MMC, mitomycin C; Tu, tumour; R, recurrent; Pr, primary.

Table SII. Number of detected CNVs distributed by chromosomal arm (p and q), tumour stage and grade.

Chromosome	Arm	pTa	pT1	pT2	pT3	pT4	G1	G2	G3	CNVs per chromosomal arm
1	p	1	1	7	2	1	1	4	7	12
1	q	1	1	10	4	0	1	5	10	16
2	p	1	0	6	1	0	1	4	3	8
2	q	1	0	13	1	0	1	7	7	15
3	p	1	0	6	0	0	1	0	6	7
3	q	1	0	6	0	0	1	1	5	7
4	p	1	2	7	1	0	1	6	4	11
4	q	2	0	14	0	0	2	8	6	16
5	p	1	1	8	0	0	2	4	4	10
5	q	2	0	15	0	0	2	9	7	18
6	p	2	3	16	2	0	4	9	10	23
6	q	1	0	12	0	0	1	5	7	13
7	p	1	0	4	2	0	1	2	4	7
7	q	2	0	8	0	0	2	6	2	10
8	p	1	0	5	2	0	1	1	6	8
8	q	1	0	11	0	0	1	4	7	12
9	p	3	6	16	0	0	7	13	5	25
9	q	1	15	3	0	0	7	12	4	23
10	p	1	0	12	0	0	1	8	4	13
10	q	1	1	8	0	0	1	7	2	10
11	p	1	1	2	1	0	2	1	2	5
11	q	1	1	5	2	4	2	3	8	13
12	p	1	0	1	0	0	1	0	1	2
12	q	1	2	1	0	0	3	0	1	4
13	p	0	0	0	0	0	0	0	0	0
13	q	1	1	8	0	0	2	5	3	10
14	p	0	0	0	0	0	0	0	0	0
14	q	1	1	5	2	0	2	3	4	9
15	p	0	0	0	0	0	0	0	0	0
15	q	1	0	4	1	0	1	0	5	6
16	p	1	0	3	0	0	1	2	1	4
16	q	1	0	3	0	0	1	1	2	4
17	p	1	0	5	1	0	1	3	3	7
17	q	2	0	11	0	1	2	7	5	14
18	p	2	0	3	0	0	2	2	1	5
18	q	1	1	6	0	0	2	5	1	8
19	p	1	0	5	0	0	1	2	3	6
19	q	1	0	8	0	0	1	4	4	9
20	p	1	1	7	0	0	2	3	4	9
20	q	1	1	5	1	0	2	1	5	8
21	p	0	0	0	0	0	0	0	0	0
21	q	1	0	0	0	0	1	0	0	1
22	p	0	0	0	0	0	0	0	0	0
22	q	1	0	7	0	0	1	6	1	8
X	p	3	4	6	5	1	6	2	11	19
X	q	4	3	12	9	2	6	7	17	30
Y	p	4	10	18	6	2	10	12	18	40
Y	q	6	10	15	6	2	12	10	17	39

T, tumor stage; G, grade; p, short arm of the chromosome; q, long arm of the chromosome; CNV, copy number variation.

Table SIII. Genes located in the detected LOH regions.

Cytoband	Genes
p12.1-p11.1	*BMP5; COL21A1; DST; BEND6; KIAA1586; ZNF451; BAG2; RAB23; PRIM2; GUSBL2*
q21.3	*PPP1R9A; PON1; PON3; PON2; ASB4; PDK4; DYNC1I1; SLC25A13; MIR591; SHFM1; DLX6AS; DLX6; DLX5; ACN9; TAC1; ASNS; MGC72080; OCM2*
q22.1q22.2	*GATS; PVRIG; SPDYE3; PMS2L13; PILRB; PILRA; ZCWPW1; MEPCE; C7orf47; C7orf61; TSC22D4; C7orf51; AGFG2; SAP25; LRCH4; FBXO24; PCOLCE; MOSPD3; MOSPD3; TFR2; ACTL6B; GNB2; GIGYF1; POP7; EPO; ZAN; EPHB4; SLC12A9; TRIP6; SRRT; UFSP1; ACHE; MUC12; MUC17; TRIM56; SERPINE1; AP1S1; VGF; C7orf52; MOGAT3; PLOD3; ZNHIT1; CLDN15; FIS1; RABL5; EMID2; MYL10; CUX1; SH2B2; SPDYE6; PRKRIP1; ORAI2; ALKBH4; LRWD1; POLR2J; POLR2J3; SPDYE2L; RASA4; POLR2J2; SPDYE2L; FAM185A; FBXL13; LRRC17; ARMC10; NAPEPLD; RPL19P12; DPY19L2P2; PMPCB; DNAJC2; PSMC2; SLC26A5; SLC26A5; RELN; ORC5L; LHFPL3*
q14.1q14.2	*FAM181B; PRCP; C11orf82; RAB30; PCF11; ANKRD42; CCDC90B; DLG2; TMEM126B; TMEM126A; CREBZF; CCDC89; SYTL2; CCDC83; PICALM; EED; C11orf73*
q25.1-q25.3	*ACOX1; C17orf106; CDK3; EVPL; SRP68; GALR2; ZACN; EXOC7; FOXJ1; RNF157; FAM100B; QRICH2; PRPSAP1; SPHK1; UBE2O; AANAT; RHBDF2; CYGB; PRCD; SNORD1C; SNORD1B; SNORD1A; ST6GALNAC2; ST6GALNAC1; MXRA7; JMJD6; C17* or *f95; SFRS2; MIR636; MFSD11; MGAT5B; C17orf86; SCARNA16; SEC14L1; SEPT9; FLJ45079; TNRC6C; TMC6; TMC8; C17orf99; SYNGR2; TK1; AFMID; AFMID; BIRC5; EPR-1; LOC283999; SOCS3; PGS1; DNAH17; CYTH1; USP36; TIMP2; LGALS3BP; CANT1; C1QTNF1; ENGASE; HRNBP3*

LOH, loss of heterozygosity regions.