Figure S1. Downregulation of CTHRC1 expression decreases migration of bladder cancer cells. (A) The cells were transfected with control siRNA or CTHRC1 siRNA (siRNA-1 or siRNA-2) for 48 h, mRNA expression of CTHRC1 was tested by RT-qPCR. (B) Compared with negative control group, loss of CTHRC1 suppressed cell migration detected by Transwell assay in 5637 and TCCSUP cells. Data are presented as mean ± SD from three independent experiments. NC, negative control; si-1, CTHRC1 siRNA-1; si-2, CTHRC1 siRNA-2. ***P<0.001.

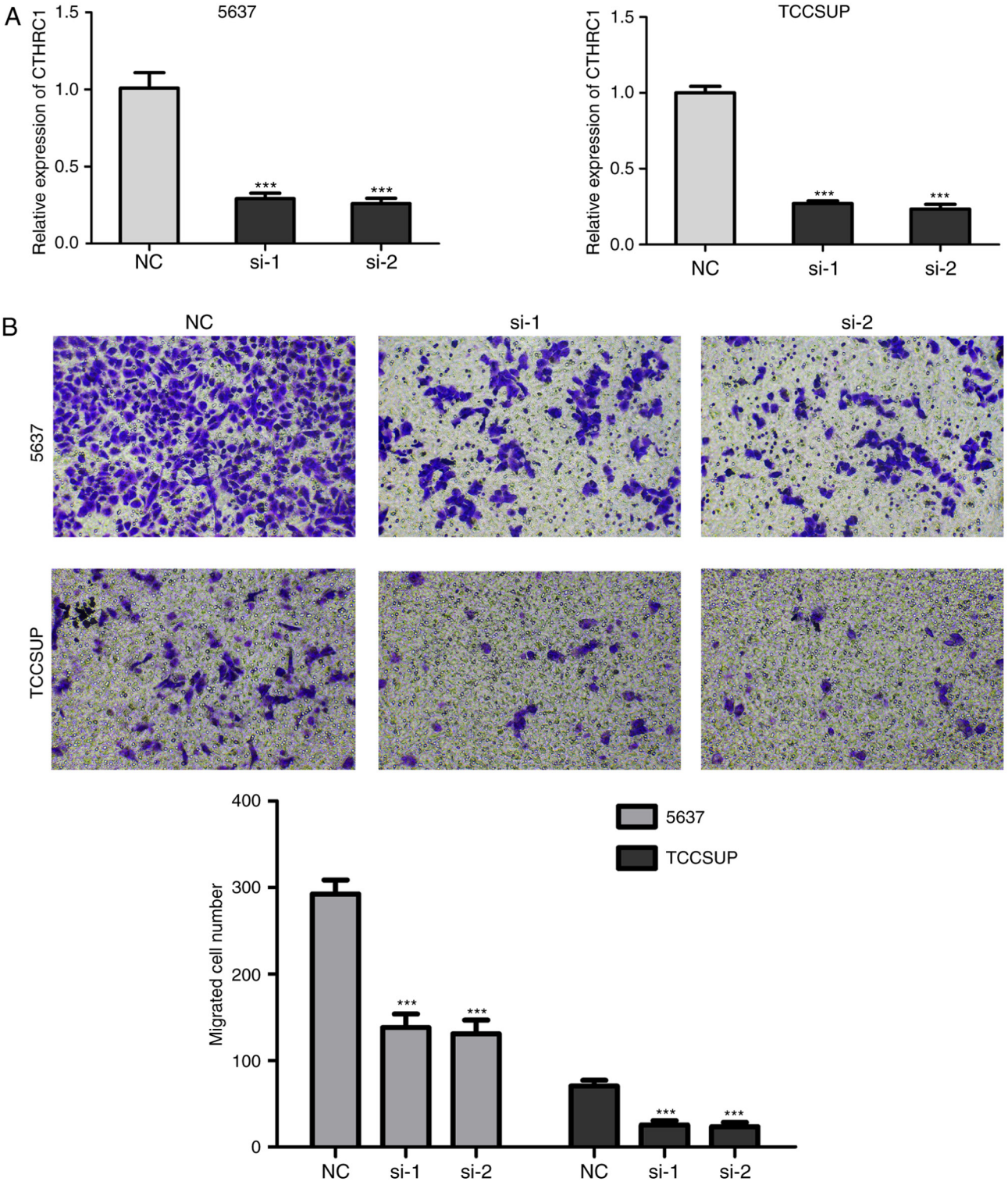

Table SI. Seventy-three differentially expressed genes between progressive and non-progressive groups.

Gene	logFC	AveExpr	t	P-value	adj.P-val	B
S100A8	2.616284	10.2681	5.784835	8.71E-08	0.000239	7.61287
CTHRC1	1.305433	8.872615	5.477642	3.34E-07	0.000521	6.377871
ST3GAL5	-1.44538	11.76679	-5.39169	4.84E-07	0.000521	6.038278
C15orf48	1.40029	8.503489	5.25318	8.74E-07	0.000654	5.496897
MPPED2	-1.00201	9.445783	-5.14421	1.38E-06	0.000886	5.076248
MTHFD2	1.109937	9.15472	5.004966	2.47E-06	0.001151	4.545863
CKAP2L	1.068286	8.755597	5.004287	2.47E-06	0.001151	4.543296
ADGRV1	-1.13175	10.08256	-4.96747	2.88E-06	0.001261	4.404425
PLA2G10	-1.37213	10.47551	-4.91865	3.52E-06	0.00138	4.221231
RBP1	1.317605	9.214859	4.912293	3.61E-06	0.001388	4.197442
S100A9	1.719036	9.521635	4.872143	4.25E-06	0.001514	4.047661
SNCAIP	1.143399	8.471094	4.803087	5.63E-06	0.001813	3.791737
UCHL1	1.161097	8.033512	4.802055	5.65E-06	0.001813	3.787926
C1orf132	-1.03207	10.61372	-4.73199	7.49E-06	0.002093	3.530547
CEP55	1.126034	8.9675	4.707079	8.28E-06	0.00218	3.439563
MT2A	1.350906	10.87136	4.684031	9.08E-06	0.002346	3.355663
SALL4	1.1294	9.090565	4.681937	9.15E-06	0.002346	3.348051
LDLR	1.01058	10.26729	4.628539	1.13E-05	0.002652	3.154692
ASPM	1.149184	9.047127	4.598048	1.28E-05	0.002921	3.044899
TESC	-1.66718	11.83294	-4.41372	2.62E-05	0.004839	2.390952
MMP11	1.004836	8.250277	4.393755	2.83E-05	0.004985	2.321154
IER3	1.011365	11.16186	4.381354	2.96E-05	0.005013	2.277904
IQGAP3	1.153042	10.26659	4.371333	3.08E-05	0.00504	2.243013
HMOX1	1.07022	8.889076	4.356832	3.26E-05	0.005211	2.192616
CDCA5	1.138662	9.670022	4.35526	3.28E-05	0.005211	2.18716
TK1	1.035956	9.306778	4.351765	3.32E-05	0.005211	2.175033
CXCL8	1.468332	8.438218	4.350853	3.33E-05	0.005211	2.171866
VSIG2	-1.22961	13.18074	-4.3452	3.40E-05	0.005235	2.152266
TRIP13	1.040746	9.219342	4.340153	3.47E-05	0.005253	2.134786
CDC42EP5	-1.07358	12.28925	-4.33285	3.57E-05	0.005359	2.1095
CALD1	1.235701	9.765445	4.269771	4.53E-05	0.006094	1.892368
TUBB2B	1.221333	8.077597	4.267562	4.57E-05	0.006102	1.884803
TPX2	1.06047	9.537993	4.243671	5.00E-05	0.006243	1.803143
FAM174B	-1.01738	12.04885	-4.21791	5.51E-05	0.006528	1.715432
COL1A1	1.010422	10.98172	4.169587	6.60E-05	0.006971	1.551895
CRTAC1	-2.1631	11.23426	-4.16139	6.80E-05	0.007108	1.524293
CCNB2	1.146609	9.608451	4.146929	7.18E-05	0.007302	1.475652
TUBB3	1.327576	9.174125	4.138748	7.40E-05	0.007371	1.448195
AEBP1	1.063788	9.441612	4.101946	8.48E-05	0.007761	1.325132
CDC20	1.247561	11.10241	4.048784	0.000103	0.008844	1.14871
GATA2	-1.02764	10.12721	-3.97812	0.000133	0.010137	0.916705
C10orf99	-1.4255	11.65366	-3.95457	0.000145	0.010329	0.840015
CAPNS2	-1.03975	10.09346	-3.93798	0.000154	0.01058	0.786187
KIF1A	1.005857	7.817419	3.928279	0.000159	0.010755	0.754784
PI3	1.512557	8.193847	3.918772	0.000165	0.011027	0.724064
S100A7	1.044081	7.651022	3.918392	0.000165	0.011027	0.722837
NUSAP1	1.006022	10.24964	3.916668	0.000166	0.011057	0.717273
MT1A	1.039829	10.89528	3.906927	0.000172	0.011332	0.685865
TOP2A	1.199474	10.34107	3.852008	0.000209	0.012936	0.509842
PHLDA1	1.028221	9.733357	3.785114	0.000265	0.014677	0.297872
FABP4	-1.79281	11.07259	-3.77993	0.00027	0.014776	0.281569
ALDH1L1	-1.30663	11.35777	-3.75689	0.000292	0.01514	0.209252
SLITRK6	-1.14176	9.937676	-3.75228	0.000297	0.015156	0.194813
MT1G	1.02263	8.479228	3.739219	0.000311	0.015527	0.154009
HOXB5	-1.23797	11.86574	-3.69604	0.000361	0.01687	0.019849
LINC01451	-1.25575	10.80815	-3.69297	0.000365	0.016958	0.010365
AQP3	-1.23958	10.43547	-3.64174	0.000435	0.018549	-0.14724
TRNP1	-1.06826	11.10609	-3.60995	0.000485	0.019544	-0.24419
LGALS1	1.028414	12.22033	3.608598	0.000487	0.019544	-0.2483

Table SI. Continued.

Gene	logFC	AveExpr	t	P-value	adj.P-val	B
DHCR24	1.029073	9.656127	3.585732	0.000527	0.020572	-0.31762
CELSR3	1.021632	9.82799	3.546345	0.000601	0.022143	-0.43625
KRT14	1.14603	8.035243	3.448087	0.000834	0.027237	-0.72784
S100A10	1.014374	12.31694	3.434618	0.000872	0.027791	-0.76732
ANXA10	-1.61755	10.93114	-3.39571	0.00099	0.030074	-0.88069
KRT6C	1.035091	7.526387	3.394376	0.000995	0.03011	-0.88455
RARRES1	1.481894	9.94185	3.382856	0.001033	0.030826	-0.91792
SNAR-A1	1.293101	11.82894	3.367125	0.001087	0.031511	-0.96333
HSD17B2	-1.12619	11.72026	-3.36587	0.001091	0.031511	-0.96695
SERPINA3	1.262736	8.637332	3.346628	0.001162	0.033078	-1.02226
TNNT1	1.187132	8.814036	3.295625	0.001369	0.036188	-1.16767
TM4SF1	1.00501	11.43228	3.24192	0.001624	0.040886	-1.31887
FGFR3	-1.07311	12.94174	-3.2352	0.001659	0.041412	-1.33766
CAPN9	-1.01183	8.602061	-3.18893	0.001918	0.044762	-1.46612

Table SII. Primer sequences of the mRNAs used for RT-qPCR.

Gene	Primer sequence (Forward)	Primer sequence (Reverse)
AEBP1	AGACCACGCCATCTTCCG	CCTTGTTGTTCTCCCACTCG
COL1A1	CGATGGATTCCAGTTCGAGT	TTTTGAGGGGGTTCAGTTTG
CTHRC1	GTGGCTCACTTCGGCTAAAAT	CACTAATCCAGCACCAATTCCTT
MMP11	CCGCAACCGACAGAAGAGG	ATCGCTCCATACCTTTAGGGC
*S100*A8	GGAATTTCCATGCCGTCTACAG	GCTGCCACGCCCATCTTTAT
*SNCA*IP	GTTTATGCAAGAACAGGGCATCT	ATCCAAGGTAGCCATGCTGTG
β-*actin*	CATGTACGTTGCTATCCAGGC	CTCCTTAATGTCACGCACGAT

Table SIII. Forty-seven prognosis-related genes.

Gene	HR	z	P-value
S100A8	7.830655	4.029455	5.59E-05
CALD1	22.38987	4.026384	5.66E-05
MMP11	33.56195	3.923761	8.72E-05
S100A7	10.53794	3.547227	0.000389
RBP1	15.78129	3.385329	0.000711
S100A9	8.993549	3.353873	0.000797
CXCL8	6.382744	3.350264	0.000807
TM4SF1	16.23584	3.123533	0.001787
MT2A	14.19763	3.111916	0.001859
COL1A1	32.39193	3.109558	0.001874
TUBB3	8.387168	3.107418	0.001887
CTHRC1	11.01053	3.070486	0.002137
UCHL1	9.277582	3.059547	0.002217
PI3	4.111562	2.973928	0.00294
TRNP1	0.100338	-2.96769	0.003
ALDH1L1	0.160398	-2.96055	0.003071
LDLR	22.76789	2.933066	0.003356
AEBP1	15.409	2.916913	0.003535
SNCAIP	10.37518	2.887205	0.003887
RARRES1	4.840064	2.865804	0.00416
TESC	0.168587	-2.84032	0.004507
CEP55	13.89391	2.836372	0.004563
DHCR24	10.69487	2.798617	0.005132
TRIP13	10.61833	2.54447	0.010944
C15orf48	6.518766	2.538233	0.011141
KRT6C	4.18997	2.536931	0.011183
KRT14	4.137938	2.536381	0.0112
CKAP2L	10.69759	2.5345	0.011261
MTHFD2	11.99478	2.517412	0.011822
MPPED2	0.072696	-2.49905	0.012453
SERPINA3	3.630553	2.495782	0.012568
TK1	10.56297	2.475758	0.013295
ASPM	8.475569	2.448461	0.014347
IER3	14.97865	2.416685	0.015663
CCNB2	7.757663	2.387543	0.016961
LGALS1	11.66876	2.3519	0.018678
SALL4	8.563573	2.307186	0.021044
C1orf132	0.086426	-2.30252	0.021306
CDCA5	8.185368	2.297489	0.021591
KIF1A	5.53531	2.288953	0.022082
TOP2A	6.578768	2.23633	0.02533
ST3GAL5	0.193739	-2.22471	0.0261
MT1A	8.790546	2.200867	0.027745
C10orf99	0.228046	-2.15108	0.03147
SNAR-A1	4.651799	2.12428	0.033647
IQGAP3	7.814429	2.112671	0.034629
TNNT1	3.298667	2.054723	0.039906
HMOX1	4.673005	1.891316	0.058582
HOXB5	0.226702	-1.87649	0.060588
SLITRK6	0.262731	-1.8652	0.062153
NUSAP1	5.718373	1.805471	0.071001
TPX2	5.132744	1.786075	0.074087
FABP4	0.410608	-1.77787	0.075425
TUBB2B	3.070328	1.774257	0.076021
CDC20	4.487852	1.723968	0.084714
MT1G	3.947411	1.720222	0.085392
CAPNS2	0.247824	-1.69422	0.090223
PLA2G10	0.293977	-1.59957	0.109695
AQP3	0.358377	-1.55966	0.11884

Table SIII. Continued.

Gene	HR	z	P-value
CELSR3	3.488559	1.541265	0.123252
GATA2	0.260258	-1.52481	0.127306
S100A10	3.949086	1.418281	0.156109
PHLDA1	3.374863	1.408453	0.158997
CRTAC1	0.53282	-1.34862	0.177459
FAM174B	0.405796	-1.20311	0.228936
ANXA10	0.598318	-1.06534	0.286724
LINC01451	0.509408	-1.00209	0.3163
CDC42EP5	0.418563	-0.99832	0.318125
VSIG2	0.510378	-0.82321	0.410386
FGFR3	0.568543	-0.80987	0.418013
HSD17B2	0.57293	-0.78247	0.433936
ADGRV1	0.525696	-0.73184	0.464267
CAPN9	0.658496	-0.59767	0.550063