ACCSCIENCE PUBLISHING

Eurasian Journal of Medicine and Oncology

ORIGINAL RESEARCH ARTICLE

Super-enhancer gene *C1QTNF6* as a prognostic biomarker and therapeutic target in bladder cancer: A machine learning-based multi-omics analysis

Supplementary File

Table S1. Differential gene expression in normal and tumor tissues of the bladder

Gene	ConMean	TreatMean	LogFC	*p*-value	False discovery rate
AR	3.065193	1.466546	−1.06356	5.69E-06	3.47E-05
NFIX	23.64465	6.321935	−1.90308	5.15E-09	1.27E-07
SIM2	0.456229	2.131414	2.223982	4.06E-07	3.66E-06
SRRM3	1.174595	2.464906	1.069369	0.015571	0.027351
NCEH1	3.785107	7.702418	1.024977	0.000228	0.000722
HILPDA	7.159024	27.42297	1.93755	1.44E-07	1.73E-06
ARHGEF37	6.436615	1.983332	−1.69838	2.44E-05	0.000116
MTHFD1L	2.593916	7.967584	1.61901	9.48E-10	3.71E-08
SLC45A3	2.071514	5.154112	1.315038	0.000487	0.001394
OR7E47P	2.047033	0.600059	−1.77036	7.47E-08	1.03E-06
KIAA0513	5.498994	2.050442	−1.42323	1.54E-09	4.81E-08
GRHL2	7.272963	15.07482	1.051525	8.25E-05	0.000315
P4HB	110.3674	234.3685	1.086465	1.19E-09	4.28E-08
RGS1	24.77323	12.35317	−1.0039	4.28E-05	0.000187
PRAC2	2.225657	0.868181	−1.35816	1.92E-05	9.79E-05
PRR15L	4.013679	11.26146	1.488397	0.009117	0.017311
PACSIN1	0.326366	0.910654	1.480411	0.002066	0.004749
CYP27A1	12.75799	5.717596	−1.15792	5.05E-07	4.27E-06
RHOB	376.9711	99.0636	−1.92803	3.00E-11	2.35E-09
DUSP1	795.2293	101.7625	−2.96616	1.86E-11	2.18E-09
ARID5B	24.46738	7.873129	−1.63585	1.59E-07	1.87E-06
LGALS3BP	122.1989	248.2506	1.022566	1.34E-05	7.45E-05
PDK4	62.70582	6.338913	−3.30629	9.09E-12	2.13E-09
TRIB1	86.8644	26.99226	−1.68622	0.000264	0.000821
SCARB1	3.657877	7.817009	1.09561	6.11E-05	0.000245
NFIC	19.70542	8.941002	−1.14008	2.67E-07	2.72E-06
DDIT4	50.92477	111.2761	1.127705	0.023691	0.039825
CHDH	0.232488	0.850955	1.871926	0.000185	0.000607
HCAR2	3.659574	9.221569	1.333336	0.005382	0.01107
ENO1	204.2592	433.3846	1.085247	1.91E-07	2.09E-06
CCDC134	1.39566	3.258969	1.223468	2.26E-08	4.07E-07
BTG2	418.8302	103.8899	−2.01131	9.35E-09	2.09E-07

(Cont'd...)

Table S1. ***(Continued)***

Gene	ConMean	TreatMean	LogFC	*p*-value	False discovery rate
JUNB	607.7429	204.8598	−1.56882	9.59E-07	7.14E-06
TACC1	23.36781	9.523459	−1.29497	1.59E-06	1.10E-05
NT5DC3	7.242825	1.380087	−2.39179	0.018168	0.031212
ATOH8	4.668418	2.33261	−1.00099	9.35E-06	5.48E-05
HCAR1	1.165645	4.382701	1.910692	0.000172	0.000567
SLC6A6	4.017567	9.102266	1.179904	1.80E-05	9.28E-05
SLC50A1	14.42668	37.11667	1.363328	1.66E-08	3.25E-07
MNX1-AS1	0.34894	1.969848	2.497035	3.23E-06	2.10E-05
SLC16A3	7.940506	19.74695	1.314327	0.000114	0.000413
PVT1	1.181159	3.186099	1.431588	1.14E-06	8.22E-06
LGI4	3.953273	0.931775	−2.08499	1.57E-11	2.18E-09
PKMYT1	1.417395	5.406131	1.931355	2.65E-09	7.78E-08
QRICH2	0.343757	0.831513	1.274349	0.000546	0.001523
PDE4D	5.354969	1.342398	−1.99607	7.84E-10	3.68E-08
NFIB	9.050587	3.77701	−1.26077	1.76E-07	2.02E-06
CPEB4	6.354266	2.45897	−1.36967	2.57E-08	4.35E-07
KRT8	163.6022	384.1081	1.23132	0.000228	0.000722
IL6R	4.085716	1.914863	−1.09335	2.12E-05	0.000104
IER5L	2.456936	11.19705	2.188186	1.16E-10	6.80E-09
AHNAK	99.44439	42.02612	−1.2426	5.51E-07	4.54E-06
TMEM184A	4.942806	10.23834	1.05058	0.002139	0.004869
SEC14L2	0.982761	2.971456	1.596257	2.12E-05	0.000104
GADD45B	119.8627	23.96978	−2.32209	5.68E-08	8.07E-07
C1QTNF6	1.449172	8.857617	2.61169	6.56E-10	3.42E-08
SLC25A10	5.324908	12.3816	1.217369	6.56E-05	0.000261
SOX4	12.52633	43.10065	1.782746	5.68E-08	8.07E-07
PLEKHG4B	0.057757	0.936432	4.019108	0.004116	0.008734
LINC01605	0.358196	1.618785	2.176088	0.001327	0.003242
PFKFB4	0.65906	3.786866	2.522523	4.57E-12	2.13E-09
CPEB3	1.191083	0.582289	−1.03247	5.00E-07	4.27E-06
HIC1	2.902878	1.225029	−1.24467	2.60E-08	4.35E-07
ESRP1	15.93994	32.70942	1.03706	5.03E-05	0.000213
ATP11A	1.336866	2.729187	1.029616	0.000782	0.002072
CSGALNACT1	6.686824	1.797497	−1.89533	6.35E-11	4.26E-09
ADRB2	2.858482	1.346884	−1.08562	1.26E-05	7.10E-05
SLC16A7	1.778477	0.883329	−1.00962	3.39E-07	3.18E-06
FAM234B	1.790248	3.641899	1.024531	0.003107	0.006809
CBX8	1.029934	3.37051	1.710415	2.38E-11	2.23E-09
PPFIA3	1.572173	3.447387	1.132744	0.000137	0.000478
RASSF3	38.63807	9.564166	−2.01431	9.58E-05	0.000354
ATAD2	2.886711	8.945223	1.631691	7.91E-09	1.85E-07
STARD8	2.405518	1.033024	−1.21947	1.18E-07	1.46E-06

(Cont'd...)

Table S1. ***(Continued)***

Gene	ConMean	TreatMean	LogFC	*p*-value	False discovery rate
CDC42EP3	12.56339	4.689142	−1.42183	0.000152	0.000513
S100A11	942.8115	2015.144	1.095842	1.37E-05	7.56E-05
SIX1	0.551618	2.261646	2.03563	7.46E-07	5.70E-06
CIRBP-AS1	0.682207	1.372768	1.008806	9.00E-05	0.000335
NDUFA4L2	13.21293	34.55348	1.38688	0.011399	0.021131
KIF22	9.370072	23.00101	1.295565	1.14E-08	2.44E-07
PRIM1	1.856004	4.914974	1.404984	1.17E-07	1.46E-06
UCA1	13.45594	58.86523	2.129172	0.019702	0.033602
SREBF1	10.56884	26.32116	1.316406	1.17E-06	8.33E-06
NANOS3	0.349376	0.739263	1.081305	0.003617	0.007746

Notes: “ConMean” refers to the control mean; “TreatMean” refers to the treatment mean; “LogFC” refers to the log fold change; “*p*-value” refers to the *p*-value; and “FDR” refers to the false discovery rate