

Table S1 The clinical information of the samples in GSE68020 gene expression dataset

Sample ID	Type	Biological source	Gender	Age	Platform	Organism	Molecule
GSM1661273	High grade urothelial carcinoma	Urine specimen	Male	83	GPL10558	Homo sapiens	total RNA
GSM1661274	High grade urothelial carcinoma	Urine specimen	Male	72	GPL10558	Homo sapiens	total RNA
GSM1661275	High grade urothelial carcinoma	Urine specimen	Male	58	GPL10558	Homo sapiens	total RNA
GSM1661276	High grade urothelial carcinoma	Urine specimen	Male	66	GPL10558	Homo sapiens	total RNA
GSM1661277	High grade urothelial carcinoma	Urine specimen	NA	NA	GPL10558	Homo sapiens	total RNA
GSM1661278	High grade urothelial carcinoma	Urine specimen	Male	68	GPL10558	Homo sapiens	total RNA
GSM1661279	High grade urothelial carcinoma	Urine specimen	NA	NA	GPL10558	Homo sapiens	total RNA
GSM1661280	High grade urothelial carcinoma	Urine specimen	Male	59	GPL10558	Homo sapiens	total RNA
GSM1661281	High grade urothelial carcinoma	Urine specimen	Female	61	GPL10558	Homo sapiens	total RNA
GSM1661282	High grade urothelial carcinoma	Urine specimen	Female	73	GPL10558	Homo sapiens	total RNA
GSM1661283	High grade urothelial carcinoma	Urine specimen	NA	NA	GPL10558	Homo sapiens	total RNA
GSM1661284	High grade urothelial carcinoma	Urine specimen	Male	77	GPL10558	Homo sapiens	total RNA
GSM1661285	High grade urothelial carcinoma	Urine specimen	Male	82	GPL10558	Homo sapiens	total RNA
GSM1661286	High grade urothelial carcinoma	Urine specimen	Male	83	GPL10558	Homo sapiens	total RNA
GSM1661287	High grade urothelial carcinoma	Urine specimen	Male	79	GPL10558	Homo sapiens	total RNA
GSM1661288	High grade urothelial carcinoma	Urine specimen	NA	NA	GPL10558	Homo sapiens	total RNA
GSM1661289	High grade urothelial carcinoma	Urine specimen	Male	84	GPL10558	Homo sapiens	total RNA
GSM1661290	High grade urothelial carcinoma	Urine specimen	Male	74	GPL10558	Homo sapiens	total RNA
GSM1661291	High grade urothelial carcinoma	Urine specimen	NA	NA	GPL10558	Homo sapiens	total RNA
GSM1661292	High grade urothelial carcinoma	Urine specimen	Male	92	GPL10558	Homo sapiens	total RNA
GSM1661293	High grade urothelial carcinoma	Urine specimen	Male	52	GPL10558	Homo sapiens	total RNA
GSM1661294	High grade urothelial carcinoma	Urine specimen	NA	NA	GPL10558	Homo sapiens	total RNA
GSM1661295	High grade urothelial carcinoma	Urine specimen	NA	NA	GPL10558	Homo sapiens	total RNA
GSM1661296	High grade urothelial carcinoma	Urine specimen	Male	81	GPL10558	Homo sapiens	total RNA
GSM1661297	High grade urothelial carcinoma	Urine specimen	Female	70	GPL10558	Homo sapiens	total RNA
GSM1661298	High grade urothelial carcinoma	Urine specimen	Male	62	GPL10558	Homo sapiens	total RNA
GSM1661299	High grade urothelial carcinoma	Urine specimen	Male	83	GPL10558	Homo sapiens	total RNA
GSM1661300	High grade urothelial carcinoma	Urine specimen	Female	69	GPL10558	Homo sapiens	total RNA
GSM1661301	High grade urothelial carcinoma	Urine specimen	Male	56	GPL10558	Homo sapiens	total RNA
GSM1661302	High grade urothelial carcinoma	Urine specimen	Female	60	GPL10558	Homo sapiens	total RNA
GSM1661253	Benign	Urine specimen	NA	NA	GPL10558	Homo sapiens	total RNA
GSM1661254	Benign	Urine specimen	Female	88	GPL10558	Homo sapiens	total RNA
GSM1661255	Benign	Urine specimen	Male	40	GPL10558	Homo sapiens	total RNA
GSM1661256	Benign	Urine specimen	Female	48	GPL10558	Homo sapiens	total RNA
GSM1661257	Benign	Urine specimen	NA	NA	GPL10558	Homo sapiens	total RNA
GSM1661258	Benign	Urine specimen	Male	37	GPL10558	Homo sapiens	total RNA
GSM1661259	Benign	Urine specimen	Male	52	GPL10558	Homo sapiens	total RNA
GSM1661260	Benign	Urine specimen	Male	88	GPL10558	Homo sapiens	total RNA
GSM1661261	Benign	Urine specimen	Female	63	GPL10558	Homo sapiens	total RNA
GSM1661262	Benign	Urine specimen	Male	49	GPL10558	Homo sapiens	total RNA
GSM1661263	Benign	Urine specimen	Female	48	GPL10558	Homo sapiens	total RNA
GSM1661264	Benign	Urine specimen	Male	73	GPL10558	Homo sapiens	total RNA
GSM1661265	Benign	Urine specimen	Male	54	GPL10558	Homo sapiens	total RNA
GSM1661266	Benign	Urine specimen	NA	NA	GPL10558	Homo sapiens	total RNA
GSM1661267	Benign	Urine specimen	Male	33	GPL10558	Homo sapiens	total RNA
GSM1661268	Benign	Urine specimen	Female	44	GPL10558	Homo sapiens	total RNA
GSM1661269	Benign	Urine specimen	NA	NA	GPL10558	Homo sapiens	total RNA
GSM1661270	Benign	Urine specimen	NA	NA	GPL10558	Homo sapiens	total RNA
GSM1661271	Benign	Urine specimen	Male	74	GPL10558	Homo sapiens	total RNA
GSM1661272	Benign	Urine specimen	Female	46	GPL10558	Homo sapiens	total RNA

Table S2 Information for the DEGs shared across both GSE62080 profile and TCGA database ($|\log_2FC| \geq 0.5$ and P value < 0.05)

Name	logFC (in GSE62080)	logFC (in TCGA)	Category
<i>GPT2</i>	1.37	1.09	Up-regulated gene
<i>SPINT2</i>	1.35	1.08	Up-regulated gene
<i>SUMO3</i>	1.35	0.52	Up-regulated gene
<i>SNRPG</i>	1.33	0.87	Up-regulated gene
<i>TUBB3</i>	1.28	2.51	Up-regulated gene
<i>CDR2L</i>	1.28	1.01	Up-regulated gene
<i>SPCS1</i>	1.24	0.60	Up-regulated gene
<i>STK36</i>	1.23	0.52	Up-regulated gene
<i>EBNA1BP2</i>	1.20	0.80	Up-regulated gene
<i>DDOST</i>	1.18	0.91	Up-regulated gene
<i>DKC1</i>	1.16	0.94	Up-regulated gene
<i>TXNDC12</i>	1.08	0.86	Up-regulated gene
<i>IGFBP3</i>	1.06	1.54	Up-regulated gene
<i>PAFAH1B3</i>	1.06	1.67	Up-regulated gene
<i>LSM2</i>	1.05	0.78	Up-regulated gene
<i>RPN1</i>	1.03	0.96	Up-regulated gene
<i>ATF5</i>	1.03	0.76	Up-regulated gene
<i>RCC2</i>	1.02	1.29	Up-regulated gene
<i>FASN</i>	0.93	1.50	Up-regulated gene
<i>KRTCAP2</i>	0.91	0.93	Up-regulated gene
<i>LMNB2</i>	0.91	1.21	Up-regulated gene
<i>SCAP</i>	0.91	0.60	Up-regulated gene
<i>POLR2H</i>	0.90	1.14	Up-regulated gene
<i>PTPRF</i>	0.90	0.52	Up-regulated gene
<i>RNASET2</i>	0.90	0.74	Up-regulated gene
<i>EFTUD2</i>	0.88	0.87	Up-regulated gene
<i>ENO1</i>	0.88	0.98	Up-regulated gene
<i>TMEM97</i>	0.87	1.27	Up-regulated gene
<i>AIMP2</i>	0.87	0.71	Up-regulated gene
<i>IFNGR2</i>	0.83	0.59	Up-regulated gene
<i>JTB</i>	0.83	0.82	Up-regulated gene
<i>GINS2</i>	0.83	1.65	Up-regulated gene
<i>EMG1</i>	0.82	1.00	Up-regulated gene
<i>ILF2</i>	0.81	0.80	Up-regulated gene
<i>BLCAP</i>	0.81	0.90	Up-regulated gene
<i>DNAJC9</i>	0.80	0.81	Up-regulated gene
<i>H2AFZ</i>	0.79	0.78	Up-regulated gene
<i>TFRC</i>	0.76	1.22	Up-regulated gene
<i>NOL7</i>	0.75	0.53	Up-regulated gene
<i>LASP1</i>	0.75	0.83	Up-regulated gene
<i>IGFL1</i>	0.75	4.09	Up-regulated gene
<i>BCAT2</i>	0.75	0.74	Up-regulated gene
<i>CCT2</i>	0.74	1.01	Up-regulated gene
<i>PSMB2</i>	0.72	0.86	Up-regulated gene
<i>PSMA5</i>	0.71	0.72	Up-regulated gene
<i>EIF2B5</i>	0.71	0.51	Up-regulated gene
<i>CNPY2</i>	0.71	1.03	Up-regulated gene
<i>PABPN1</i>	0.70	0.80	Up-regulated gene
<i>COIL</i>	0.70	0.70	Up-regulated gene
<i>SSR4</i>	0.69	0.56	Up-regulated gene
<i>INA</i>	0.68	2.12	Up-regulated gene
<i>TBCB</i>	0.67	0.51	Up-regulated gene
<i>LDHA</i>	0.67	0.59	Up-regulated gene
<i>RPS19</i>	0.67	0.50	Up-regulated gene
<i>MRPS26</i>	0.67	1.08	Up-regulated gene
<i>CACNB3</i>	0.66	1.27	Up-regulated gene
<i>TH</i>	0.66	2.49	Up-regulated gene
<i>NR2C2AP</i>	0.65	1.07	Up-regulated gene
<i>SLC5A6</i>	0.64	1.85	Up-regulated gene
<i>CHCHD4</i>	0.64	0.51	Up-regulated gene
<i>ERGIC3</i>	0.64	0.59	Up-regulated gene
<i>HOXB7</i>	0.64	1.17	Up-regulated gene
<i>RBM17</i>	0.64	0.64	Up-regulated gene

Table S2 (continued)

Table S2 (continued)

Name	logFC (in GSE62080)	logFC (in TCGA)	Category
TUBA1C	0.64	0.53	Up-regulated gene
POLR1C	0.63	0.58	Up-regulated gene
PNPO	0.63	0.67	Up-regulated gene
FCRLB	0.63	3.10	Up-regulated gene
BCAP31	0.62	0.66	Up-regulated gene
NAT10	0.62	0.60	Up-regulated gene
TOMM34	0.62	0.92	Up-regulated gene
KDEL2	0.62	0.71	Up-regulated gene
TFDP1	0.62	0.96	Up-regulated gene
CNIH4	0.62	0.63	Up-regulated gene
RPP21	0.62	0.80	Up-regulated gene
DHRS13	0.61	1.18	Up-regulated gene
NUP62	0.61	0.72	Up-regulated gene
IMP4	0.61	0.51	Up-regulated gene
B4GALT3	0.61	1.23	Up-regulated gene
H2AFY2	0.60	0.62	Up-regulated gene
TMEM99	0.60	0.69	Up-regulated gene
FAM58A	0.59	0.74	Up-regulated gene
TUFM	0.59	0.50	Up-regulated gene
POLR2G	0.58	0.92	Up-regulated gene
PSMB5	0.57	0.67	Up-regulated gene
CKS1B	0.57	1.57	Up-regulated gene
PSMB4	0.57	0.80	Up-regulated gene
RARRES1	0.57	2.40	Up-regulated gene
PTDSS1	0.56	0.87	Up-regulated gene
PTBP1	0.56	0.72	Up-regulated gene
ADCK2	0.56	0.58	Up-regulated gene
SNRNP70	0.56	0.64	Up-regulated gene
NSUN2	0.56	0.65	Up-regulated gene
CCT8	0.55	0.60	Up-regulated gene
MRPL11	0.55	0.55	Up-regulated gene
ERP29	0.54	0.51	Up-regulated gene
DNAJB11	0.53	1.03	Up-regulated gene
RRP1	0.53	0.86	Up-regulated gene
GAPDH	0.53	0.65	Up-regulated gene
NARF	0.53	0.76	Up-regulated gene
TMCO1	0.52	0.54	Up-regulated gene
GSTK1	0.52	0.53	Up-regulated gene
ATRIP	0.52	0.67	Up-regulated gene
ACLY	0.52	0.88	Up-regulated gene
MCM3	0.50	1.02	Up-regulated gene
CLPTM1L	0.50	0.82	Up-regulated gene
NIF3L1	0.50	0.59	Up-regulated gene
PPM1L	-0.51	-2.06	Down-regulated gene
XPNPEP2	-0.53	-3.69	Down-regulated gene
SLURP1	-0.56	-3.26	Down-regulated gene
TMPRSS11B	-0.57	-8.04	Down-regulated gene
SERPIN2	-0.57	-1.72	Down-regulated gene
RNF39	-0.58	-0.70	Down-regulated gene
FLG	-0.58	-1.41	Down-regulated gene
MSRA	-0.59	-0.58	Down-regulated gene
PNPLA7	-0.60	-1.51	Down-regulated gene
RBPM2	-0.63	-3.53	Down-regulated gene
PHLDA1	-0.64	-1.54	Down-regulated gene
RND3	-0.65	-1.52	Down-regulated gene
CSTA	-0.66	-2.22	Down-regulated gene
NKX6-2	-0.67	-2.91	Down-regulated gene
TCEAL2	-0.69	-3.12	Down-regulated gene
KLK11	-0.74	-2.64	Down-regulated gene
MUC21	-0.75	-6.30	Down-regulated gene
ZNF185	-0.78	-0.86	Down-regulated gene
VWF	-0.82	-1.02	Down-regulated gene
EMP1	-0.82	-2.81	Down-regulated gene

Table S2 (continued)

Table S2 (continued)

Name	logFC (in GSE62080)	logFC (in TCGA)	Category
<i>FOSB</i>	-0.82	-3.78	Down-regulated gene
<i>ARHGAP10</i>	-0.83	-1.42	Down-regulated gene
<i>GADD45B</i>	-0.85	-2.57	Down-regulated gene
<i>IGFBP7</i>	-0.85	-0.77	Down-regulated gene
<i>ASPG</i>	-0.88	-0.98	Down-regulated gene
<i>ZFP36</i>	-0.88	-2.85	Down-regulated gene
<i>FAM46B</i>	-0.94	-2.98	Down-regulated gene
<i>ALOX12</i>	-0.95	-2.02	Down-regulated gene
<i>GPRC5A</i>	-0.95	-0.97	Down-regulated gene
<i>AVPI1</i>	-0.97	-1.03	Down-regulated gene
<i>NFKBIA</i>	-1.01	-0.73	Down-regulated gene
<i>LPIN1</i>	-1.03	-0.85	Down-regulated gene
<i>MYOM1</i>	-1.04	-4.44	Down-regulated gene
<i>SPRR1A</i>	-1.06	-1.98	Down-regulated gene
<i>SPINK7</i>	-1.11	-3.91	Down-regulated gene
<i>TP53INP2</i>	-1.12	-2.20	Down-regulated gene
<i>KLK12</i>	-1.16	-4.45	Down-regulated gene
<i>HSPB8</i>	-1.17	-3.09	Down-regulated gene
<i>A2ML1</i>	-1.17	-1.55	Down-regulated gene
<i>PPP1R15A</i>	-1.18	-1.34	Down-regulated gene
<i>DUSP5</i>	-1.18	-2.21	Down-regulated gene
<i>MXD1</i>	-1.18	-0.71	Down-regulated gene
<i>VASN</i>	-1.19	-0.90	Down-regulated gene
<i>IER3</i>	-1.20	-2.43	Down-regulated gene
<i>KLF15</i>	-1.23	-1.32	Down-regulated gene
<i>TMPRSS11D</i>	-1.24	-2.63	Down-regulated gene
<i>SLC25A23</i>	-1.28	-2.12	Down-regulated gene
<i>PPL</i>	-1.32	-1.33	Down-regulated gene
<i>ANXA1</i>	-1.34	-1.45	Down-regulated gene
<i>MALL</i>	-1.35	-1.51	Down-regulated gene
<i>ECM1</i>	-1.35	-1.49	Down-regulated gene
<i>AIF1L</i>	-1.35	-0.86	Down-regulated gene
<i>LOR</i>	-1.42	-1.59	Down-regulated gene
<i>KRT4</i>	-1.46	-4.70	Down-regulated gene
<i>SBSN</i>	-1.51	-1.54	Down-regulated gene
<i>SPINK5</i>	-1.57	-4.46	Down-regulated gene
<i>MAL</i>	-1.58	-1.80	Down-regulated gene
<i>KRT13</i>	-1.60	-2.31	Down-regulated gene
<i>GCNT3</i>	-1.61	-2.48	Down-regulated gene
<i>PRSS27</i>	-1.65	-2.21	Down-regulated gene
<i>CGNL1</i>	-1.67	-3.24	Down-regulated gene
<i>AQP2</i>	-1.72	-2.00	Down-regulated gene
<i>RHCG</i>	-1.85	-3.90	Down-regulated gene
<i>PITX1</i>	-1.93	-1.52	Down-regulated gene
<i>CRYAB</i>	-2.00	-3.56	Down-regulated gene
<i>CNFN</i>	-2.15	-3.09	Down-regulated gene
<i>SPRR3</i>	-2.16	-3.67	Down-regulated gene
<i>CRCT1</i>	-2.19	-2.71	Down-regulated gene
<i>KRT78</i>	-2.19	-3.67	Down-regulated gene
<i>CRNN</i>	-2.66	-8.48	Down-regulated gene

Table S3 KEGG pathway and GO terms enrichment analyses of hub genes

KEGG pathway analysis					
Terms	ID	Pathway	Count	P value	Gene ID
KEGG	hsa03020	RNA polymerase	2	7.77E-04	POLR2H POLR2G
KEGG	hsa03050	Proteasome	2	1.64E-03	PSMB2 PSMB4
KEGG	hsa03008	Ribosome biogenesis in eukaryotes	2	9.61E-03	DKC1 EMG1
GO terms analysis					
GO terms	GO ID	Description	Count	P value	Gene ID
BP	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	5	9.31E-06	SNRPG POLR2H EFTUD2 POLR2G PABPN1
BP	GO:0000398	mRNA splicing, via spliceosome	5	9.31E-06	SNRPG POLR2H EFTUD2 POLR2G PABPN1
BP	GO:0000375	RNA splicing, via transesterification reactions	5	9.85E-06	SNRPG POLR2H EFTUD2 POLR2G PABPN1
BP	GO:0006353	DNA-templated transcription, termination	3	2.96E-05	SNRPG POLR2H PABPN1
BP	GO:0008380	RNA splicing	5	3.05E-05	SNRPG POLR2H EFTUD2 POLR2G PABPN1
BP	GO:1903405	protein localization to nuclear body	2	3.35E-05	CCT2 DKC1
BP	GO:1904851	positive regulation of establishment of protein localization to telomere	2	3.35E-05	CCT2 DKC1
BP	GO:1904867	protein localization to Cajal body	2	3.35E-05	CCT2 DKC1
BP	GO:0070203	regulation of establishment of protein localization to telomere	2	4.09E-05	CCT2 DKC1
BP	GO:0070202	regulation of establishment of protein localization to chromosome	2	4.91E-05	CCT2 DKC1
BP	GO:1904816	positive regulation of protein localization to chromosome, telomeric region	2	4.91E-05	CCT2 DKC1
BP	GO:1990173	protein localization to nucleoplasm	2	4.91E-05	CCT2 DKC1
BP	GO:0006397	mRNA processing	5	5.57E-05	SNRPG POLR2H EFTUD2 POLR2G PABPN1
BP	GO:1904814	regulation of protein localization to chromosome, telomeric region	2	6.76E-05	CCT2 DKC1
BP	GO:1904874	positive regulation of telomerase RNA localization to Cajal body	2	7.80E-05	CCT2 DKC1
BP	GO:0070200	establishment of protein localization to telomere	2	8.91E-05	CCT2 DKC1
BP	GO:1904872	regulation of telomerase RNA localization to Cajal body	2	1.13E-04	CCT2 DKC1
BP	GO:0070268	cornification	3	1.26E-04	SPRR3 FLG LOR
BP	GO:0090670	RNA localization to Cajal body	2	1.27E-04	CCT2 DKC1
BP	GO:0090671	telomerase RNA localization to Cajal body	2	1.27E-04	CCT2 DKC1
BP	GO:0090672	telomerase RNA localization	2	1.27E-04	CCT2 DKC1
BP	GO:0090685	RNA localization to nucleus	2	1.27E-04	CCT2 DKC1
BP	GO:0070199	establishment of protein localization to chromosome	2	2.04E-04	CCT2 DKC1
BP	GO:0070198	protein localization to chromosome, telomeric region	2	2.79E-04	CCT2 DKC1
BP	GO:0006369	termination of RNA polymerase II transcription	2	3.43E-04	SNRPG PABPN1
BP	GO:0043487	regulation of RNA stability	3	3.80E-04	DKC1 PSMB2 PSMB4
BP	GO:0006370	7-methylguanosine mRNA capping	2	3.89E-04	POLR2H POLR2G
BP	GO:0009452	7-methylguanosine RNA capping	2	4.13E-04	POLR2H POLR2G
BP	GO:0018149	peptide cross-linking	2	4.13E-04	FLG LOR
BP	GO:0032212	positive regulation of telomere maintenance via telomerase	2	4.13E-04	CCT2 DKC1
BP	GO:0036260	RNA capping	2	4.13E-04	POLR2H POLR2G
BP	GO:0051973	positive regulation of telomerase activity	2	4.63E-04	CCT2 DKC1
BP	GO:1904358	positive regulation of telomere maintenance via telomere lengthening	2	4.89E-04	CCT2 DKC1
BP	GO:0050434	positive regulation of viral transcription	2	6.01E-04	POLR2H POLR2G
BP	GO:0034660	ncRNA metabolic process	4	6.63E-04	POLR2H DKC1 EMG1 POLR2G
BP	GO:0006403	RNA localization	3	7.73E-04	CCT2 DKC1 PABPN1
BP	GO:0051972	regulation of telomerase activity	2	8.24E-04	CCT2 DKC1
BP	GO:0032206	positive regulation of telomere maintenance	2	9.30E-04	CCT2 DKC1
BP	GO:0031424	keratinization	3	9.58E-04	SPRR3 FLG LOR
BP	GO:0032210	regulation of telomere maintenance via telomerase	2	1.00E-03	CCT2 DKC1
BP	GO:0006521	regulation of cellular amino acid metabolic process	2	1.33E-03	PSMB2 PSMB4
BP	GO:1904356	regulation of telomere maintenance via telomere lengthening	2	1.33E-03	CCT2 DKC1
BP	GO:0046782	regulation of viral transcription	2	1.46E-03	POLR2H POLR2G
BP	GO:2000573	positive regulation of DNA biosynthetic process	2	1.55E-03	CCT2 DKC1
BP	GO:0007004	telomere maintenance via telomerase	2	1.60E-03	CCT2 DKC1
BP	GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	2	1.69E-03	PSMB2 PSMB4
BP	GO:1903311	regulation of mRNA metabolic process	3	1.73E-03	PABPN1 PSMB2 PSMB4
BP	GO:0042795	snRNA transcription by RNA polymerase II	2	1.79E-03	POLR2H POLR2G
BP	GO:0009301	snRNA transcription	2	1.84E-03	POLR2H POLR2G
BP	GO:0035019	somatic stem cell population maintenance	2	1.84E-03	POLR2H POLR2G
BP	GO:1902036	regulation of hematopoietic stem cell differentiation	2	1.84E-03	PSMB2 PSMB4
BP	GO:0006283	transcription-coupled nucleotide-excision repair	2	1.89E-03	POLR2H POLR2G
BP	GO:0006278	RNA-dependent DNA biosynthetic process	2	1.95E-03	CCT2 DKC1
BP	GO:1900182	positive regulation of protein localization to nucleus	2	1.95E-03	CCT2 DKC1
BP	GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	2	2.00E-03	PSMB2 PSMB4
BP	GO:0016073	snRNA metabolic process	2	2.10E-03	POLR2H POLR2G

Table S3 (continued)

Table S3 (continued)

BP	GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	2	2.10E-03	PSMB2 PSMB4
BP	GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	2	2.16E-03	PSMB2 PSMB4
BP	GO:0030216	keratinocyte differentiation	3	2.17E-03	SPRR3 FLG LOR
BP	GO:0006368	transcription elongation from RNA polymerase II promoter	2	2.21E-03	POLR2H POLR2G
BP	GO:0010833	telomere maintenance via telomere lengthening	2	2.21E-03	CCT2 DKC1
BP	GO:0032204	regulation of telomere maintenance	2	2.21E-03	CCT2 DKC1
BP	GO:0033238	regulation of cellular amine metabolic process	2	2.27E-03	PSMB2 PSMB4
BP	GO:0031145	anaphase-promoting complex-dependent catabolic process	2	2.33E-03	PSMB2 PSMB4
BP	GO:0034502	protein localization to chromosome	2	2.38E-03	CCT2 DKC1
BP	GO:0060218	hematopoietic stem cell differentiation	2	2.44E-03	PSMB2 PSMB4
BP	GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	2	2.56E-03	PSMB2 PSMB4
BP	GO:1901532	regulation of hematopoietic progenitor cell differentiation	2	2.56E-03	PSMB2 PSMB4
BP	GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	2	3.18E-03	PSMB2 PSMB4
BP	GO:1902750	negative regulation of cell cycle G2/M phase transition	2	3.31E-03	PSMB2 PSMB4
BP	GO:0009913	epidermal cell differentiation	3	3.32E-03	SPRR3 FLG LOR
BP	GO:0070498	interleukin-1-mediated signaling pathway	2	3.59E-03	PSMB2 PSMB4
BP	GO:0006289	nucleotide-excision repair	2	3.66E-03	POLR2H POLR2G
BP	GO:0048524	positive regulation of viral process	2	3.73E-03	POLR2H POLR2G
BP	GO:0098781	ncRNA transcription	2	3.80E-03	POLR2H POLR2G
BP	GO:0006354	DNA-templated transcription, elongation	2	3.94E-03	POLR2H POLR2G
BP	GO:2000278	regulation of DNA biosynthetic process	2	3.94E-03	CCT2 DKC1
BP	GO:0006401	RNA catabolic process	3	3.95E-03	DKC1 PSMB2 PSMB4
BP	GO:0060071	Wnt signaling pathway, planar cell polarity pathway	2	4.02E-03	PSMB2 PSMB4
BP	GO:0008543	fibroblast growth factor receptor signaling pathway	2	4.16E-03	POLR2H POLR2G
BP	GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	2	4.16E-03	PSMB2 PSMB4
BP	GO:0090175	regulation of establishment of planar polarity	2	4.16E-03	PSMB2 PSMB4
BP	GO:0022613	ribonucleoprotein complex biogenesis	3	4.35E-03	SNRPG DKC1 EMG1
BP	GO:0002223	stimulatory C-type lectin receptor signaling pathway	2	4.47E-03	PSMB2 PSMB4
BP	GO:0060964	regulation of gene silencing by miRNA	2	4.47E-03	POLR2H POLR2G
BP	GO:0043620	regulation of DNA-templated transcription in response to stress	2	4.62E-03	PSMB2 PSMB4
BP	GO:0002220	innate immune response activating cell surface receptor signaling pathway	2	4.70E-03	PSMB2 PSMB4
BP	GO:2000736	regulation of stem cell differentiation	2	4.70E-03	PSMB2 PSMB4
BP	GO:0060147	regulation of posttranscriptional gene silencing	2	4.78E-03	POLR2H POLR2G
BP	GO:0060966	regulation of gene silencing by RNA	2	4.78E-03	POLR2H POLR2G
BP	GO:1900180	regulation of protein localization to nucleus	2	4.78E-03	CCT2 DKC1
BP	GO:0044106	cellular amine metabolic process	2	5.10E-03	PSMB2 PSMB4
BP	GO:0001736	establishment of planar polarity	2	5.27E-03	PSMB2 PSMB4
BP	GO:0007164	establishment of tissue polarity	2	5.27E-03	PSMB2 PSMB4
BP	GO:0043588	skin development	3	5.41E-03	SPRR3 FLG LOR
BP	GO:0009308	amine metabolic process	2	5.69E-03	PSMB2 PSMB4
BP	GO:0090263	positive regulation of canonical Wnt signaling pathway	2	6.31E-03	PSMB2 PSMB4
BP	GO:0044344	cellular response to fibroblast growth factor stimulus	2	6.59E-03	POLR2H POLR2G
BP	GO:0001738	morphogenesis of a polarized epithelium	2	6.68E-03	PSMB2 PSMB4
BP	GO:0060968	regulation of gene silencing	2	6.68E-03	POLR2H POLR2G
BP	GO:0008544	epidermis development	3	7.00E-03	SPRR3 FLG LOR
BP	GO:0035567	non-canonical Wnt signaling pathway	2	7.25E-03	PSMB2 PSMB4
BP	GO:0071774	response to fibroblast growth factor	2	7.25E-03	POLR2H POLR2G
BP	GO:0000723	telomere maintenance	2	8.14E-03	CCT2 DKC1
BP	GO:0006364	rRNA processing	2	8.14E-03	DKC1 EMG1
BP	GO:0071347	cellular response to interleukin-1	2	8.35E-03	PSMB2 PSMB4
BP	GO:0002244	hematopoietic progenitor cell differentiation	2	8.55E-03	PSMB2 PSMB4
BP	GO:0019827	stem cell population maintenance	2	8.55E-03	POLR2H POLR2G
BP	GO:0043488	regulation of mRNA stability	2	8.55E-03	PSMB2 PSMB4
BP	GO:0098727	maintenance of cell number	2	8.76E-03	POLR2H POLR2G
BP	GO:0032200	telomere organization	2	9.52E-03	CCT2 DKC1
BP	GO:0033209	tumor necrosis factor-mediated signaling pathway	2	9.52E-03	PSMB2 PSMB4
BP	GO:0038095	Fc-epsilon receptor signaling pathway	2	9.74E-03	PSMB2 PSMB4
BP	GO:0090090	negative regulation of canonical Wnt signaling pathway	2	9.74E-03	PSMB2 PSMB4
BP	GO:2001252	positive regulation of chromosome organization	2	9.74E-03	CCT2 DKC1
BP	GO:0030177	positive regulation of Wnt signaling pathway	2	9.85E-03	PSMB2 PSMB4
BP	GO:0002478	antigen processing and presentation of exogenous peptide antigen	2	1.03E-02	PSMB2 PSMB4
BP	GO:0019884	antigen processing and presentation of exogenous antigen	2	1.05E-02	PSMB2 PSMB4
BP	GO:0019083	viral transcription	2	1.06E-02	POLR2H POLR2G
BP	GO:0002862	negative regulation of inflammatory response to antigenic stimulus	1	1.07E-02	PSMB4

Table S3 (continued)

Table S3 (continued)

BP	GO:0006367	transcription initiation from RNA polymerase II promoter	2	1.08E-02	POLR2H POLR2G
BP	GO:0010565	regulation of cellular ketone metabolic process	2	1.08E-02	PSMB2 PSMB4
BP	GO:0061013	regulation of mRNA catabolic process	2	1.08E-02	PSMB2 PSMB4
BP	GO:0038061	NIK/NF-kappaB signaling	2	1.09E-02	PSMB2 PSMB4
BP	GO:0043902	positive regulation of multi-organism process	2	1.10E-02	POLR2H POLR2G
BP	GO:0050852	T cell receptor signaling pathway	2	1.10E-02	PSMB2 PSMB4
BP	GO:1905330	regulation of morphogenesis of an epithelium	2	1.11E-02	PSMB2 PSMB4
BP	GO:0070555	response to interleukin-1	2	1.13E-02	PSMB2 PSMB4
BP	GO:0010389	regulation of G2/M transition of mitotic cell cycle	2	1.16E-02	PSMB2 PSMB4
BP	GO:0048002	antigen processing and presentation of peptide antigen	2	1.19E-02	PSMB2 PSMB4
BP	GO:0016072	rRNA metabolic process	2	1.23E-02	DKC1 EMG1
BP	GO:0019080	viral gene expression	2	1.23E-02	POLR2H POLR2G
BP	GO:0071897	DNA biosynthetic process	2	1.24E-02	CCT2 DKC1
BP	GO:0001522	pseudouridine synthesis	1	1.24E-02	DKC1
BP	GO:0030178	negative regulation of Wnt signaling pathway	2	1.32E-02	PSMB2 PSMB4
BP	GO:0042254	ribosome biogenesis	2	1.37E-02	DKC1 EMG1
BP	GO:1902749	regulation of cell cycle G2/M phase transition	2	1.37E-02	PSMB2 PSMB4
BP	GO:0050792	regulation of viral process	2	1.39E-02	POLR2H POLR2G
BP	GO:0051131	chaperone-mediated protein complex assembly	1	1.42E-02	CCT2
BP	GO:0071456	cellular response to hypoxia	2	1.47E-02	PSMB2 PSMB4
BP	GO:0051084	'de novo' posttranslational protein folding	1	1.60E-02	CCT2
BP	GO:0019882	antigen processing and presentation	2	1.61E-02	PSMB2 PSMB4
BP	GO:0036294	cellular response to decreased oxygen levels	2	1.61E-02	PSMB2 PSMB4
BP	GO:0051054	positive regulation of DNA metabolic process	2	1.64E-02	CCT2 DKC1
BP	GO:0034504	protein localization to nucleus	2	1.65E-02	CCT2 DKC1
BP	GO:0050851	antigen receptor-mediated signaling pathway	2	1.66E-02	PSMB2 PSMB4
BP	GO:0006352	DNA-templated transcription, initiation	2	1.76E-02	POLR2H POLR2G
BP	GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	2	1.78E-02	POLR2H POLR2G
BP	GO:1901991	negative regulation of mitotic cell cycle phase transition	2	1.82E-02	PSMB2 PSMB4
BP	GO:0048863	stem cell differentiation	2	1.85E-02	PSMB2 PSMB4
BP	GO:0071453	cellular response to oxygen levels	2	1.85E-02	PSMB2 PSMB4
BP	GO:0000086	G2/M transition of mitotic cell cycle	2	1.87E-02	PSMB2 PSMB4
BP	GO:0038093	Fc receptor signaling pathway	2	1.91E-02	PSMB2 PSMB4
BP	GO:0042180	cellular ketone metabolic process	2	1.91E-02	PSMB2 PSMB4
BP	GO:0000154	rRNA modification	1	1.95E-02	DKC1
BP	GO:0006458	'de novo' protein folding	1	2.04E-02	CCT2
BP	GO:0061436	establishment of skin barrier	1	2.04E-02	FLG
BP	GO:2000027	regulation of animal organ morphogenesis	2	2.05E-02	PSMB2 PSMB4
BP	GO:1901988	negative regulation of cell cycle phase transition	2	2.11E-02	PSMB2 PSMB4
BP	GO:0002861	regulation of inflammatory response to antigenic stimulus	1	2.12E-02	PSMB4
BP	GO:0008334	histone mRNA metabolic process	1	2.12E-02	SNRPG
BP	GO:0042274	ribosomal small subunit biogenesis	1	2.12E-02	EMG1
BP	GO:0044839	cell cycle G2/M phase transition	2	2.16E-02	PSMB2 PSMB4
BP	GO:0016579	protein deubiquitination	2	2.20E-02	PSMB2 PSMB4
BP	GO:0060828	regulation of canonical Wnt signaling pathway	2	2.27E-02	PSMB2 PSMB4
BP	GO:0033561	regulation of water loss via skin	1	2.30E-02	FLG
BP	GO:0071356	cellular response to tumor necrosis factor	2	2.30E-02	PSMB2 PSMB4
BP	GO:0019054	modulation by virus of host process	1	2.39E-02	PABPN1
BP	GO:0070646	protein modification by small protein removal	2	2.41E-02	PSMB2 PSMB4
BP	GO:0045737	positive regulation of cyclin-dependent protein serine/threonine kinase activity	1	2.47E-02	CKS1B
BP	GO:0034612	response to tumor necrosis factor	2	2.60E-02	PSMB2 PSMB4
BP	GO:0006362	transcription elongation from RNA polymerase I promoter	1	2.65E-02	POLR2H
BP	GO:0000209	protein polyubiquitination	2	2.66E-02	PSMB2 PSMB4
BP	GO:0006363	termination of RNA polymerase I transcription	1	2.73E-02	POLR2H
BP	GO:0018279	protein N-linked glycosylation via asparagine	1	2.73E-02	RPN1
BP	GO:0044068	modulation by symbiont of host cellular process	1	2.73E-02	PABPN1
BP	GO:0034470	ncRNA processing	2	2.75E-02	DKC1 EMG1
BP	GO:0018196	peptidyl-asparagine modification	1	2.82E-02	RPN1
BP	GO:1904031	positive regulation of cyclin-dependent protein kinase activity	1	2.82E-02	CKS1B
BP	GO:0002758	innate immune response-activating signal transduction	2	2.84E-02	PSMB2 PSMB4
BP	GO:0006913	nucleocytoplasmic transport	2	2.91E-02	SNRPG PABPN1
BP	GO:0051169	nuclear transport	2	2.96E-02	SNRPG PABPN1
BP	GO:0045930	negative regulation of mitotic cell cycle	2	3.02E-02	PSMB2 PSMB4
BP	GO:0033044	regulation of chromosome organization	2	3.07E-02	CCT2 DKC1
BP	GO:0060070	canonical Wnt signaling pathway	2	3.07E-02	PSMB2 PSMB4
BP	GO:0006361	transcription initiation from RNA polymerase I promoter	1	3.08E-02	POLR2H
BP	GO:0007339	binding of sperm to zona pellucida	1	3.08E-02	CCT2

Table S3 (continued)

Table S3 (continued)

BP	GO:0061077	chaperone-mediated protein folding	1	3.08E-02	CCT2
BP	GO:1901998	toxin transport	1	3.08E-02	CCT2
CC	GO:0001533	cornified envelope	3	8.10E-06	SPRR3 FLG LOR
CC	GO:0019774	proteasome core complex, beta-subunit complex	2	4.27E-05	PSMB2 PSMB4
CC	GO:0005665	RNA polymerase II, core complex	2	6.05E-05	POLR2H POLR2G
CC	GO:0005839	proteasome core complex	2	1.47E-04	PSMB2 PSMB4
CC	GO:0071007	U2-type catalytic step 2 spliceosome	2	3.34E-04	SNRPG EFTUD2
CC	GO:0046540	U4/U6 x U5 tri-snRNP complex	2	5.10E-04	SNRPG EFTUD2
CC	GO:0097526	spliceosomal tri-snRNP complex	2	5.10E-04	SNRPG EFTUD2
CC	GO:0071005	U2-type precatalytic spliceosome	2	8.58E-04	SNRPG EFTUD2
CC	GO:0071011	precatalytic spliceosome	2	8.58E-04	SNRPG EFTUD2
CC	GO:0000502	proteasome complex	2	1.38E-03	PSMB2 PSMB4
CC	GO:1905369	endopeptidase complex	2	1.43E-03	PSMB2 PSMB4
CC	GO:0016591	RNA polymerase II, holoenzyme	2	1.87E-03	POLR2H POLR2G
CC	GO:1905368	peptidase complex	2	1.92E-03	PSMB2 PSMB4
CC	GO:0015030	Cajal body	2	2.08E-03	DKC1 EFTUD2
CC	GO:0005684	U2-type spliceosomal complex	2	2.14E-03	SNRPG EFTUD2
CC	GO:0097525	spliceosomal snRNP complex	2	2.25E-03	SNRPG EFTUD2
CC	GO:0071013	catalytic step 2 spliceosome	2	2.48E-03	SNRPG EFTUD2
CC	GO:0000428	DNA-directed RNA polymerase complex	2	2.60E-03	POLR2H POLR2G
CC	GO:0055029	nuclear DNA-directed RNA polymerase complex	2	2.60E-03	POLR2H POLR2G
CC	GO:0030532	small nuclear ribonucleoprotein complex	2	2.72E-03	SNRPG EFTUD2
CC	GO:0030880	RNA polymerase complex	2	2.79E-03	POLR2H POLR2G
CC	GO:0120114	Sm-like protein family complex	2	3.38E-03	SNRPG EFTUD2
CC	GO:0072588	box H/ACA RNP complex	1	9.07E-03	DKC1
CC	GO:0005681	spliceosomal complex	2	9.11E-03	SNRPG EFTUD2
CC	GO:0005687	U4 snRNP	1	9.97E-03	SNRPG
CC	GO:0034709	methylosome	1	1.09E-02	SNRPG
CC	GO:0042405	nuclear inclusion body	1	1.09E-02	PABPN1
CC	GO:0061695	transferase complex, transferring phosphorus-containing groups	2	1.15E-02	POLR2H POLR2G
CC	GO:0008250	oligosaccharyltransferase complex	1	1.18E-02	RPN1
CC	GO:0034719	SMN-Sm protein complex	1	1.54E-02	SNRPG
CC	GO:0005697	telomerase holoenzyme complex	1	1.72E-02	DKC1
CC	GO:0101031	chaperone complex	1	1.72E-02	CCT2
CC	GO:0005689	U12-type spliceosomal complex	1	2.16E-02	SNRPG
CC	GO:0005732	small nucleolar ribonucleoprotein complex	1	2.34E-02	DKC1
CC	GO:0005685	U1 snRNP	1	2.52E-02	SNRPG
MF	GO:0030280	structural constituent of epidermis	2	7.54E-05	FLG LOR
MF	GO:0004298	threonine-type endopeptidase activity	2	1.73E-04	PSMB2 PSMB4
MF	GO:0070003	threonine-type peptidase activity	2	1.73E-04	PSMB2 PSMB4

Note: BP, biological process; CC, cellular component; MF, molecular function

Table S4 (continued)

SNRPG	CCT2	POLR2H	RPN1	DKC1	EFTUD2	EMG1	POLR2G	SPRR3	PSMB2	PABPN1	CKS1B	PSMB4	FLG	LOR	EBNA1BP2	ILF2	H2AFZ
					hsa-miR-301b-5p				hsa-miR-4670-3p								
					hsa-miR-1275				hsa-miR-4778-5p								
					hsa-miR-301a-5p				hsa-let-7a-2-3p								
									hsa-miR-651-5p								
									hsa-miR-6807-5p								
									hsa-let-7g-3p								
									hsa-miR-6758-5p								
									hsa-miR-4668-5p								
									hsa-miR-221-5p								
									hsa-miR-9500								
									hsa-miR-3153								
									hsa-miR-378j								
									hsa-miR-6839-5p								
									hsa-miR-629-3p								
									hsa-miR-4531								
									hsa-miR-7856-5p								
									hsa-miR-5739								
									hsa-miR-7151-3p								
									hsa-miR-641								
									hsa-miR-1248								
									hsa-miR-3688-3p								
									hsa-miR-4672								
									hsa-miR-3617-5p								
									hsa-miR-891b								
									hsa-miR-629-5p								
									hsa-miR-5006-5p								
									hsa-miR-4695-5p								
									hsa-miR-668-5p								
									hsa-miR-3143								
									hsa-miR-5699-3p								
									hsa-miR-6832-5p								
									hsa-miR-4659b-3p								
									hsa-miR-4659a-3p								
									hsa-miR-6884-5p								
									hsa-miR-8084								
									hsa-miR-3675-3p								
									hsa-miR-6839-3p								
									hsa-miR-6805-5p								
									hsa-miR-485-5p								
									hsa-miR-4421								
									hsa-miR-339-5p								
									hsa-miR-4524a-3p								
									hsa-miR-4478								
									hsa-miR-451b								
									hsa-miR-6856-5p								
									hsa-miR-548c-3p								
									hsa-miR-4477a								
									hsa-miR-4738-3p								
									hsa-miR-4490								
									hsa-miR-4680-3p								
									hsa-miR-5571-5p								
									hsa-miR-4676-3p								
									hsa-miR-6165								
									hsa-miR-892c-3p								
									hsa-miR-6078								
									hsa-miR-302e								
									hsa-miR-3978								
									hsa-miR-891a-3p								
									hsa-miR-452-5p								
									hsa-miR-3529-3p								
									hsa-miR-7977								
									hsa-miR-4713-5p								
									hsa-miR-6077								
									hsa-miR-561-3p								
									hsa-miR-135a-3p								

Table S5 The most significantly enriched signal transduction pathways enriched in phenotype of high and low expression of SNRPG and DKC1 in BC cell lines

SNRPG				
Gene set name	ES	NES	adj. p-val	FDR
The most significantly gene sets enriched in phenotype of high expression of SNRPG in BC cell lines				
Cell cycle	0.67	1.92	0.00E+00	3.00E-03
RNA polymerase	0.81	1.91	0.00E+00	2.00E-03
Pyrimidine metabolism	0.63	1.87	0.00E+00	4.00E-03
DNA replication	0.81	1.78	0.00E+00	1.20E-02
Oocyte meiosis	0.55	1.7	0.00E+00	3.00E-02
Purine metabolism	0.51	1.69	2.00E-03	2.60E-02
Spliceosome	0.72	1.79	4.00E-03	1.40E-02
Mismatch repair	0.75	1.72	8.00E-03	2.60E-02
Basal transcription factors	0.58	1.63	8.00E-03	5.30E-02
Proteasome	0.71	1.7	1.40E-02	2.70E-02
NOD like receptor signaling pathway	0.44	1.42	1.90E-02	2.22E-01
RNA degradation	0.62	1.67	2.20E-02	3.70E-02
Progesterone mediated oocyte maturation	0.49	1.53	3.60E-02	1.45E-01
Homologous recombination	0.68	1.58	3.80E-02	9.50E-02
Epithelial cell signaling in helicobacter pylori infection	0.43	1.42	4.30E-02	2.18E-01
The most significantly gene sets enriched in phenotype of low expression of SNRPG in BC cell lines				
Olfactory transduction	-0.4	-1.51	0.00E+00	4.52E-01
Other glycan degradation	-0.77	-1.77	2.00E-03	6.80E-02
Glycosaminoglycan degradation	-0.66	-1.66	8.00E-03	1.96E-01
Lysosome	-0.47	-1.58	8.00E-03	3.17E-01
Linoleic acid metabolism	-0.63	-1.46	3.40E-02	5.91E-01
Arachidonic acid metabolism	-0.53	-1.45	4.00E-02	5.00E-01
PPAR signaling pathway	-0.43	-1.35	4.20E-02	6.29E-01
ABC transporters	-0.46	-1.38	5.00E-02	6.69E-01
DKC1				
Gene set name	ES	NES	adj. p-val	FDR
The most significantly gene sets enriched in phenotype of high expression of DKC1 in BC cell lines				
Glyoxylate and dicarboxylate metabolism	0.77	1.85	0.00E+00	2.11E-02
Pyrimidine metabolism	0.62	1.84	0.00E+00	1.20E-02
Citrate cycle tca cycle	0.75	1.76	2.04E-03	1.78E-02
DNA replication	0.77	1.74	4.03E-03	2.20E-02
Cell cycle	0.61	1.75	4.10E-03	2.08E-02
Huntingtons disease	0.55	1.78	4.12E-03	2.05E-02
Purine metabolism	0.49	1.59	6.11E-03	6.12E-02
RNA polymerase	0.77	1.82	6.21E-03	1.11E-02
Cysteine and methionine metabolism	0.56	1.60	7.95E-03	6.21E-02
Ribosome	0.82	1.66	8.18E-03	5.16E-02
Pyruvate metabolism	0.61	1.64	8.32E-03	5.78E-02
Parkinsons disease	0.58	1.76	1.02E-02	2.02E-02
Aminoacyl trna biosynthesis	0.69	1.62	1.19E-02	5.66E-02
Proteasome	0.73	1.73	1.23E-02	2.23E-02
Mismatch repair	0.70	1.62	2.05E-02	5.30E-02
Spliceosome	0.66	1.62	2.48E-02	6.07E-02
Beta alanine metabolism	0.66	1.63	2.84E-02	5.65E-02
Alzheimers disease	0.45	1.51	2.88E-02	1.07E-01
Glycolysis gluconeogenesis	0.54	1.52	3.29E-02	1.07E-01
Fructose and mannose metabolism	0.53	1.50	3.87E-02	1.19E-01
GAP junction	0.39	1.36	3.87E-02	2.54E-01
Base excision repair	0.60	1.58	3.99E-02	6.83E-02
NOD like receptor signaling pathway	0.42	1.34	4.34E-02	2.53E-01
Nucleotide excision repair	0.56	1.50	4.70E-02	1.14E-01
The most significantly gene sets enriched in phenotype of low expression of DKC1 in BC cell lines				
Glycosylphosphatidylinositol gpi anchor biosynthesis	-0.62	-1.61	1.54E-02	5.52E-01
Alpha linolenic acid metabolism	-0.73	-1.60	2.40E-02	3.18E-01
Other glycan degradation	-0.67	-1.55	4.98E-02	3.85E-01

ES: enrichment score; NES: normalized enrichment score; NOM: nominal; FDR: false discovery rate.

Gene sets with adj. p-val are considered as significant.

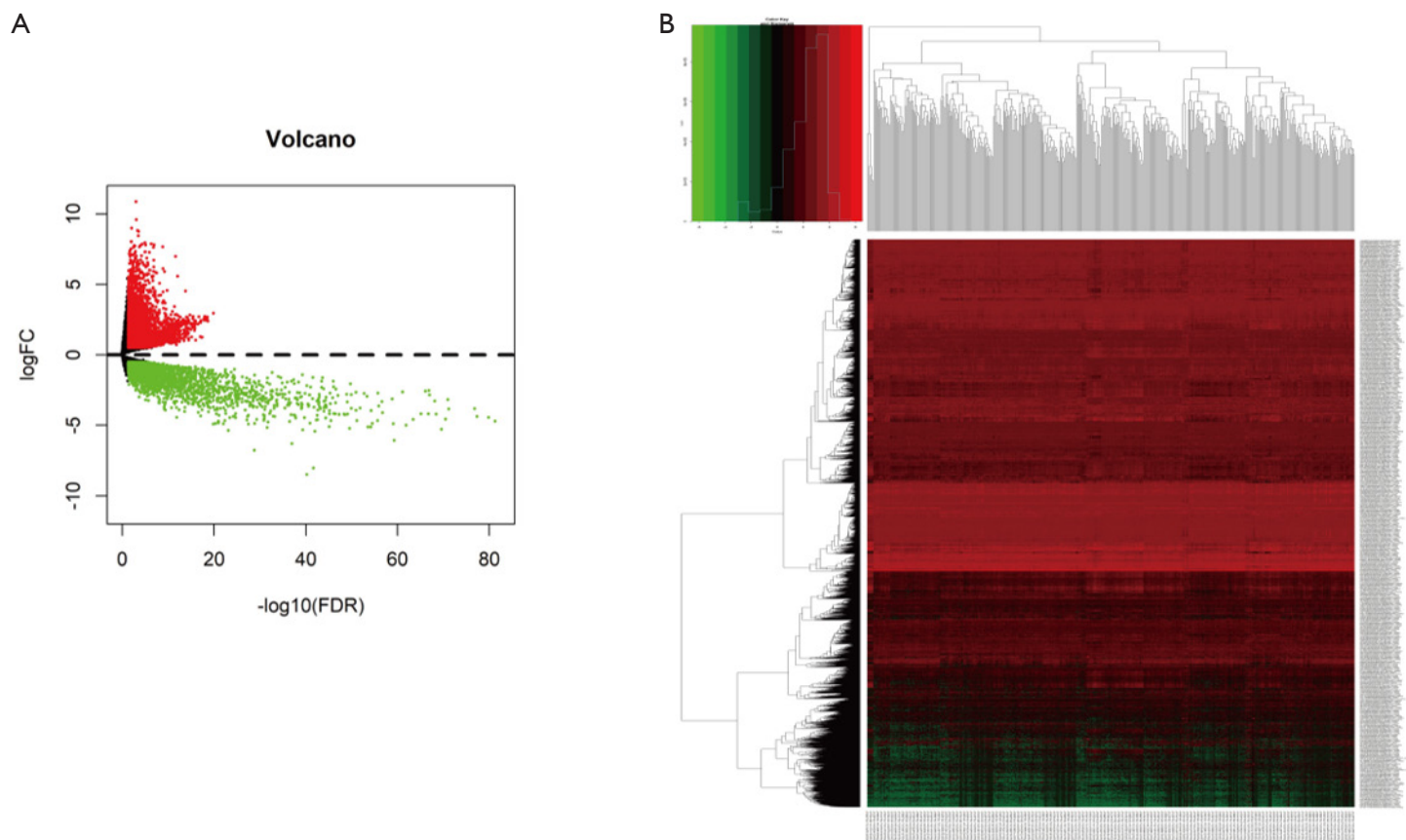


Figure S1 Identification of DEGs in HGBC. (A) Volcano plot and (B) heatmap of mRNAs in HGBC and adjacent non-carcinoma bladder tissues. Significant DE mRNAs in 387 HGBC and 19 adjacent noncancer bladder tissues from TCGA database were identified, and 4906 upregulated and 2952 downregulated DEGs were obtained with the thresholds of $|\text{Log}_2 \text{FC}| > 0.5$ and adj. P value < 0.05 . Green indicates down-regulated genes, red indicates up-regulated genes and black indicates genes with unchanged expression.

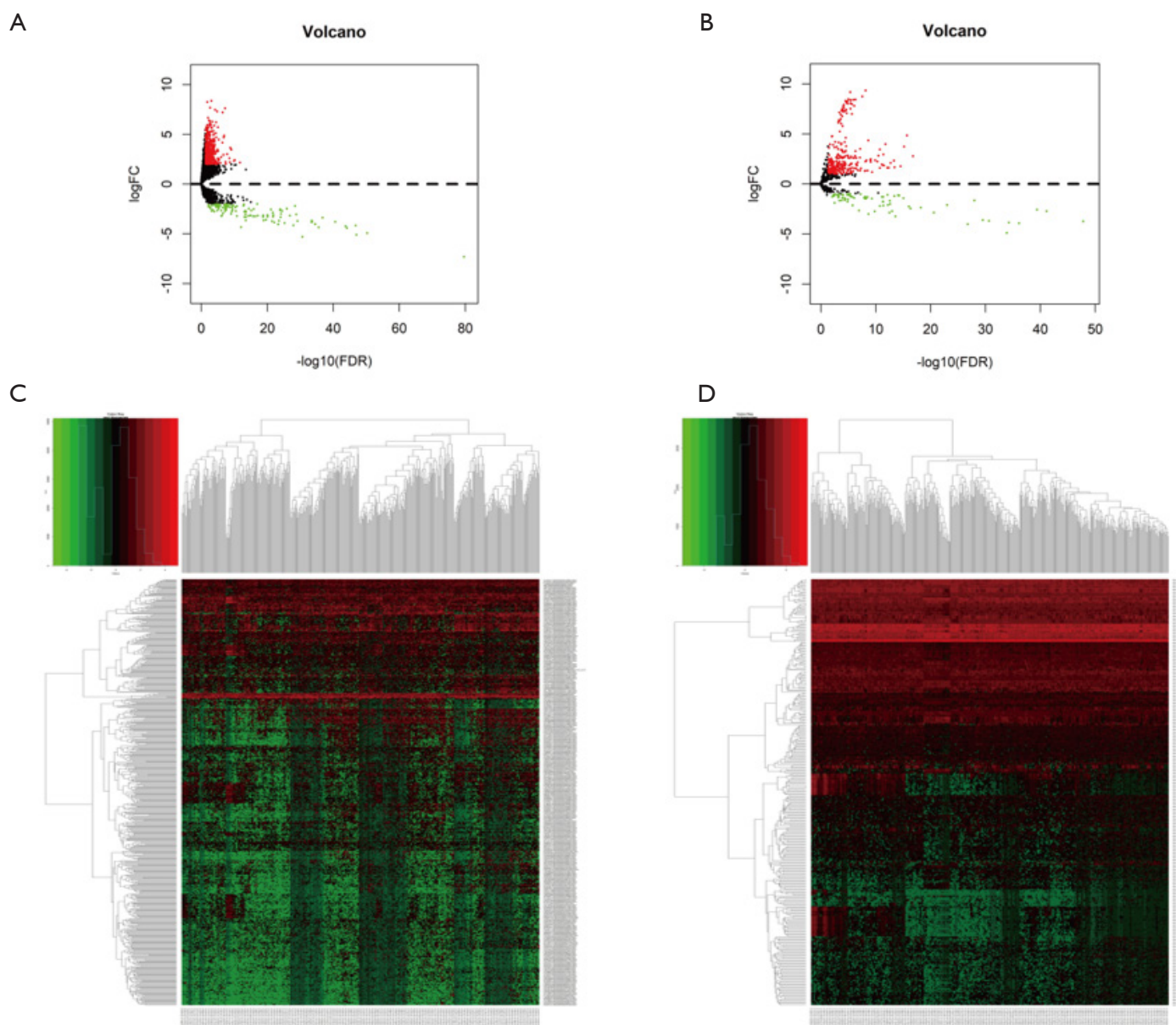


Figure S2 DElncRNAs and DE miRNAs in patients with HGBC. (A) Volcano plot and (B) heatmap of DElncRNAs in HGBC and adjacent non-carcinoma bladder tissues. The DElncRNAs were identified with the thresholds of $|\text{Log}_2 \text{FC}| > 2.0$ and adj. P value < 0.05 . (C) Volcano plot and (D) heatmap of DE miRNAs in HGBC and adjacent non-carcinoma bladder tissues. The DE miRNAs were identified with the thresholds of $|\text{Log}_2 \text{FC}| > 1.0$ and adj. P value < 0.05 . Green indicates down-regulated genes, red indicates up-regulated genes and black indicates genes with unchanged expression.

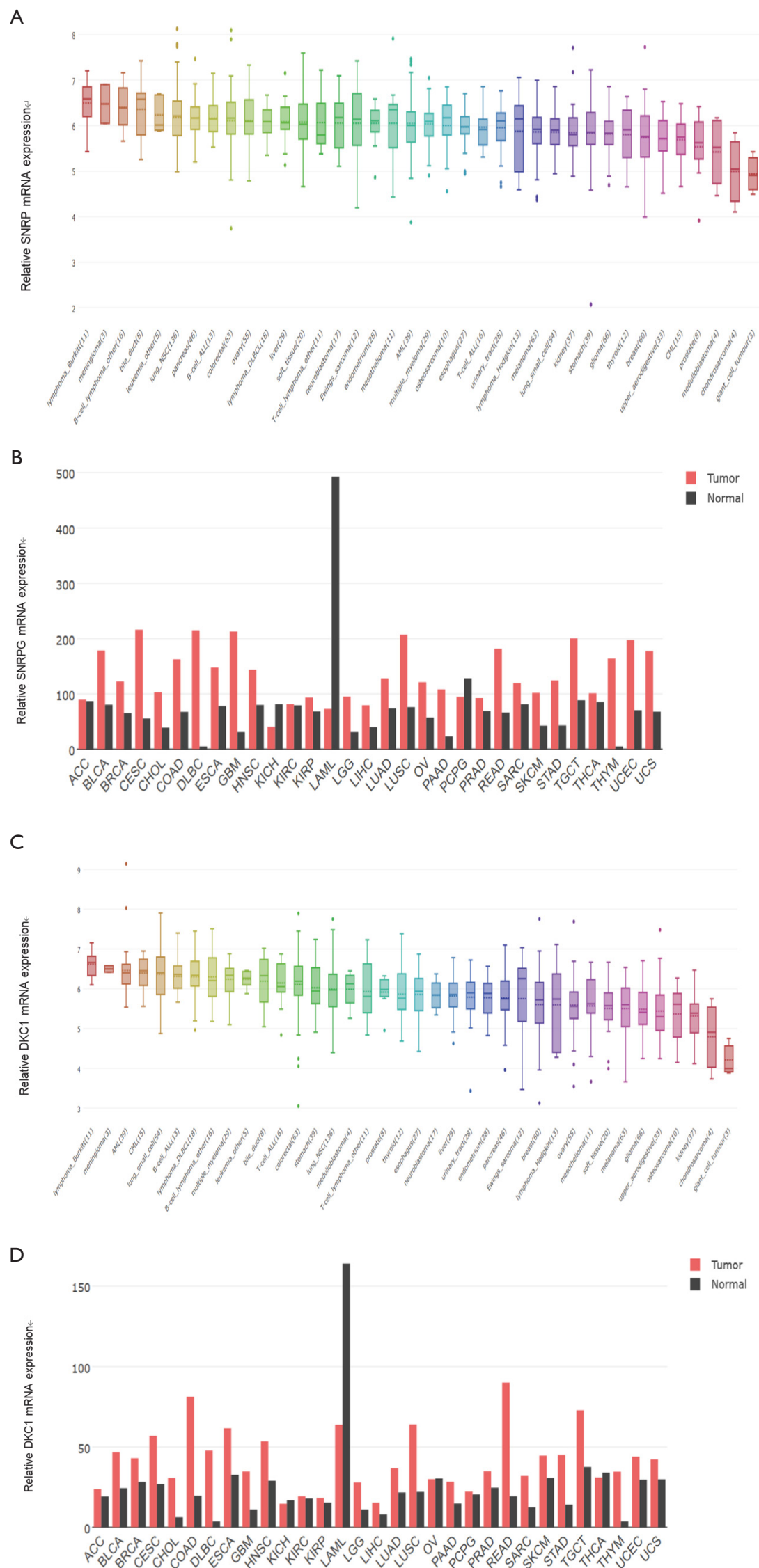


Figure S3 *SNRPG* and *DKC1* expression in various cancer cell lines and cancer tissues. (A) *SNRPG* mRNA-expression in various cancer cell lines obtained from Cancer Cell Line Encyclopedia database. The abscissa is the tumor type and sample size, and the ordinate is the expression of *SNRPG*. (B) *SNRPG* mRNA-expression in various cancer tissues obtained from GEPIA database. The red bar represents tumor tissue sample, and the gray bar represents non-cancerous tissue samples. Expression data were sorted depending on tumor type. (C) *DKC1* mRNA-expression in various cancer cell lines. (D) *DKC1* mRNA-expression in various cancer tissues.