Table SII. Top 70 common hub genes that are expressed in lung, cervical and liver cancer.

SN	Gene symbol	Degree	Closeness
1	*CDK1*	75	0.56712
2	*CCNA2*	62	0.53488
3	*CDC20*	60	0.51493
4	*BUB1B*	59	0.49286
5	*CCNB1*	58	0.50735
6	*BUB1*	55	0.51238
7	*KIF11*	53	0.4726
8	*PLK1*	53	0.49522
9	*KIF20A*	50	0.46939
10	*DLGAP5*	47	0.48821
11	*TOP2A*	47	0.48821
12	*CENPF*	46	0.47586
13	*CCNB2*	45	0.4976
14	*CDCA8*	45	0.48821
15	*KIF2C*	44	0.46413
16	*CENPA*	42	0.45197
17	*ASPM*	41	0.44612
18	*BIRC5*	41	0.45395
19	*CDC45*	41	0.47586
20	*NUF2*	40	0.45495
21	*TPX2*	39	0.44421
22	*AURKB*	39	0.47696
23	*UBE2C*	38	0.46517
24	*CEP55*	37	0.44612
25	*CENPE*	36	0.45098
26	*NCAPG*	35	0.45695
27	*KIF4A*	34	0.43856
28	*NDC80*	33	0.43579
29	*MAD2L1*	33	0.45695
30	*CDC6*	33	0.45495
31	*AURKA*	32	0.44516
32	*TTK*	32	0.44516
33	*KIF23*	31	0.43215
34	*MCM4*	29	0.37843
35	*MCM5*	29	0.41818
36	*MCM7*	28	0.41903
37	*MCM6*	28	0.3723
38	*MCM2*	28	0.36898
39	*MCM3*	28	0.37163
40	*HJURP*	27	0.42418
41	*PBK*	27	0.43763

42	*ZWINT*	27	0.43035
43	*CHEK1*	27	0.45595
44	*MCM10*	27	0.41235
45	*PCNA*	25	0.44805
46	*NEK2*	24	0.42946
47	*RAD51*	24	0.43305
48	*EXO1*	23	0.45098
49	*KIF15*	22	0.39579
49	*PRC1*	22	0.41988
50	*MKI67*	22	0.42331
51	*RRM2*	22	0.43949
52	*CDT1*	22	0.43856
53	*WDHD1*	21	0.36316
55	*RACGAP1*	19	0.40588
56	*HMMR*	19	0.42331
57	*SPAG5*	18	0.41988
58	*CDCA3*	18	0.41153
59	*FOXM1*	18	0.4165
60	*POLE2*	18	0.35264
61	*CDC7*	18	0.36252
62	*KIF14*	17	0.36572
63	*BRCA2*	17	0.41483
64	*FEN1*	17	0.41235
65	*PTTG1*	16	0.41235
66	*RFC4*	16	0.38051
67	*KNL1*	15	0.38051
68	*CLSPN*	15	0.39961
69	*ORC1*	15	0.39808
70	*DBF4*	15	0.36063

Table SIII. Go function and pathway enrichment analysis of seven common genes in lung, cervical and liver cancer.

A, Biological process

Gene set	Description	Size	Expected value[a]	Ratio	P-value	FDR
GO:0000226	Microtubule cytoskeleton organization	540	2.2681	11.022	<2.2e-16	<2.2e-16
GO:0000278	Mitotic cell cycle	927	3.8936	15.924	<2.2e-16	<2.2e-16
GO:0006259	DNA metabolic process	970	4.0742	7.8544	<2.2e-16	<2.2e-16
GO:0007017	Microtubule-based process	729	3.0619	8.818	<2.2e-16	<2.2e-16
GO:0007049	Cell cycle	1739	7.3041	9.5837	<2.2e-16	<2.2e-16
GO:0007346	Regulation of mitotic cell cycle	578	2.4277	14.417	<2.2e-16	<2.2e-16
GO:0022402	Cell cycle process	1274	5.351	11.96	<2.2e-16	<2.2e-16
GO:0045786	Negative regulation of cell cycle	559	2.3479	11.5	<2.2e-16	<2.2e-16
GO:0045930	Negative regulation of mitotic cell cycle	256	1.0752	19.53	<2.2e-16	<2.2e-16
GO:0051726	Regulation of cell cycle	1106	4.6454	9.687	<2.2e-16	<2.2e-16

B, Cellular component

Gene set	Description	Size	Expect	Ratio	P-value	FDR
GO:0044430	Cytoskeletal part	1621	6.0801	6.5788	<2.2e-16	<2.2e-16
GO:0015630	Microtubule cytoskeleton	1165	4.3697	9.3827	<2.2e-16	<2.2e-16
GO:0005694	Chromosome	1014	3.8034	11.569	<2.2e-16	<2.2e-16
GO:0044427	Chromosomal part	886	3.3233	12.337	<2.2e-16	<2.2e-16
GO:0005815	Microtubule organizing center	722	2.7081	9.97	<2.2e-16	<2.2e-16
GO:0000228	Nuclear chromosome	573	2.1492	13.493	<2.2e-16	<2.2e-16
GO:0044454	Nuclear chromosome part	535	2.0067	12.458	<2.2e-16	<2.2e-16
GO:0098687	Chromosomal region	331	1.2415	28.996	<2.2e-16	<2.2e-16
GO:0000793	Condensed chromosome	223	0.83644	31.084	<2.2e-16	<2.2e-16
GO:0000794	Condensed nuclear chromosome	100	0.37509	34.659	<2.2e-16	<2.2e-16

C, Molecular function

Gene set	Description	Size	Expect	Ratio	P-value	FDR
GO:0005524	ATP binding	1453	5.5781	5.916	<2.2e-16	<2.2e-16
GO:0008017	Microtubule binding	239	0.91752	14.169	5.36E-12	1.10E-09
GO:0008144	Drug binding	1707	6.5532	5.0357	1.11E-16	5.20E-14
GO:0015631	Tubulin binding	321	1.2323	11.361	1.46E-11	2.70E-09
GO:0017076	Purine nucleotide binding	1865	7.1597	4.6091	1.67E-15	3.90E-13
GO:0030554	Adenyl nucleotide binding	1522	5.843	5.6478	<2.2e-16	<2.2e-16
GO:0032553	Ribonucleotide binding	1865	7.1597	4.6091	1.67E-15	3.90E-13
GO:0032555	Purine ribonucleotide binding	1850	7.1022	4.6465	1.33E-15	3.90E-13
GO:0032559	adenyl ribonucleotide binding	1509	5.7931	5.6965	<2.2e-16	<2.2e-16
GO:0035639	Purine ribonucleoside triphosphate binding	1786	6.8565	4.813	4.44E-16	1.70E-13

[a]Expected value defines the enrichment of genes in comparison to the reference gene set [Zhang B, Kirov S and Snoddy J: WebGestalt: an integrated system for exploring gene sets in various biological contexts. Nucleic Acids Res 33 (Web Server issue): W741-W748, 2005].

Table SIV. KEGG pathways analysis of seven common genes in lung, cervical, and liver cancer.

Gene set	Description	Size	Leading edge number	ES	NES	P-value	FDR
hsa03030	DNA replication	10	10	-0.7167	-2.6242	<2.2e-16	0.00271
hsa04914	Progesterone-mediated oocyte maturation	8	8	-0.5323	-1.7956	0.01587	0.02713
hsa04110	Cell cycle	24	21	-0.3426	-1.8231	<2.2e-16	0.03527
hsa04114	Oocyte meiosis	9	8	-0.3887	-1.3888	0.09836	0.137
hsa04218	Cellular senescence	6	6	0.29688	0.78304	0.73023	0.73861
hsa05166	Human T-cell leukemia virus 1 infection	8	6	-0.1656	-0.56411	0.96939	0.9669
hsa04115	p53 signaling pathway	5	5	0.32308	0.79843	0.69693	1

Table SV. Binding affinity of inhibitors with the common genes present in at least two types of cancer.

A, Microtubule inhibitors

SN	Name	Target	Score	Binding affinity	
				NDC80	DLGAP5
1	Cytochalasin B	ACTB	-98.19	-7.8	-7.3
2	Vindesine	TUBB, TUBB1	-93.24	-7.8	-7
3	Vinorelbine	TUBB	-91.59	-7.2	-6.4
4	Epothilone	TUBA1A, TUBA1B, TUBA1C, TUBA3C, TUBA4A, TUBA8, TUBB, TUBB1, TUBB3, TUBB4A, TUBB4B	-67.97	-6.2	-6.1
5	Paclitaxel	TUBB, NR1I2, ABCB1, BCL2, CYP2C8, MAP2, MAP4, MAPT, TLR4, TUBB1	-99.86	-6.2	-5.9
6	Docetaxel	TUBB, BCL2, MAP2, MAP4, MAPT, NR1I2, TUBB1	-91.42	-6.2	-5.5
7	Podophyllotoxin	IGF1R, CASP3, TOP2A, TUBA4A, TUBB	-99.87	-5.6	-5.4
8	Flubendazole	TUBB	-99.84	-5.6	-6.1
9	Noscapine	BDKRB2, SIGMAR1	-74.28	-5.4	-5.5
10	ABT-751	TUBB	-99.79	-5.2	-5.8
11	Vincristine	TUBB, TUBA4A	-99.8	-5.2	-6
12	Mebendazole	TUBA1A, TUBB, TUBB4B	-99.81	-5.2	-6.2
13	Griseofulvin	KRT12	-54.25	-4.9	-5.2
14	Triclabendazole	DNMT1	-61.31	-4.7	-5.5
15	Albendazole	CYP1A2, CYP2J2, TUBA1A, TUBB, TUBB4B	-99.77	-4.2	-5.1

B, TOP2A

SN	Name	Target	Score	Binding affinity
1	Etoposide	TOP2A, CYP2E1, CYP3A5, TOP2B	-80.77	-9.1
2	Pidorubicine	TOP2A	-76.25	-8.8
3	Idarubicin	TOP2A	-49.8	-8.7
4	Teniposide	TOP2A, CYP3A5	-96.26	-8.6
5	Daunorubicin	TOP2A, TOP2B	-64.86	-8.6
6	Doxorubicin	TOP2A	-91.76	-8.5
7	Pirarubicin	TOP2A	-78.13	-8.4
8	Ellipticine	TOP2A, TOP2B	-70.39	-7.8
9	Levofloxacin	TOP2A	-30.64	-7.7
10	Genistein	CFTR, ESR2, EGFR, ESR1, ESRRA, ESRRB, ESRRG, NCOA1, NCOA2, PPARG, PTK2B, TOP2A, TRPC5	33.22	-7.4
11	Mitoxantrone	TOP2A, PIM1	-33.8	-7.1
12	Mazoxane	TOP2A, TOP2B	-69.9	-6.8
13	Moxifloxacin	TOP2A	53.95	-6.7
14	Podophyllotoxin	IGF1R, CASP3, TOP2A, TUBA4A, TUBB	-99.87	-6.5
15	Pefloxacin	TOP2A	-30.23	-6.4
16	Elesclomol	TOP2A	68.91	-6.3
17	Ofloxacin	TOP2A	-33.57	-6.1
18	Temozolomide	TOP2A	99.92	-5.8

C, CDC

SN	Name	Target	Score	Binding affinity
1	Menadione	AOX1, BGLAP, F10, F2, F7, F9, GGCX, NQO1, NQO2, PKM, PROC, PROS1, PROZ, VKORC1, VKORC1L1	-99.4	-6.5
2	NSC-663284	CDC25A, CDC25B, CDC25C	-96.48	-6

Table SVI. Effects of the high expression of unique DEGs on the survival of patients with lung, cervical and liver cancer.

A, Lung cancer

SN	Gene symbol	Survival
1	*ALDOC*	HIGH
2	*FN1*	LOW
3	*SNRPG*	HIGH

B, Cervical cancer

SN	Gene symbol	Survival
1	*CSF2*	LOW
2	*SCD*	LOW
3	*DNAJC9*	HIGH
4	*FANCM*	HIGH
5	*USP18*	HIGH
6	*FASN*	LOW
7	*RUNX1*	LOW
8	*NASP*	HIGH

C, Liver cancer

SN	Gene symbol	Survival
1	*NDUSF3*	LOW
2	*RPS21*	LOW
3	*RPL38*	LOW
4	*RPL8*	LOW
5	*SHARPIN*	LOW
6	*RPSA*	LOW
7	*RBCK1*	LOW
8	*RIPK2*	LOW
9	*RPS5*	LOW
10	*TRAF5*	LOW
11	*APOC3*	HIGH
12	*ECHS1*	HIGH
13	*SARDH*	HIGH
14	*HSD17B8*	HIGH
15	*CYP2C9*	HIGH
16	*CYP2C8*	HIGH
17	*MT-CO1*	HIGH
18	*MT-CYB*	HIGH
19	*ABAT*	HIGH
20	*ACADS*	HIGH
21	*AKRIDI*	HIGH
22	*AGXT2*	HIGH
23	*ACAA1*	HIGH