

Table S2 The validation of top 11 hub DEGs using 12 topological analysis methods of Cytoscape plugin cytoHubba in the PPI networks of small cell lung cancer

MCODE		MCC		Betweenness		BottleNeck		Closeness		ClusteringCoefficient		Degree		DMNC		EcCentricity		EPC		MNC		Radiality		Stress	
Rank	Gene	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score
1	MSH2	MSH2	86,430	CDKN2A	1,348.78	CDKN2A	53	PLK1	30.97	KIF1A	1.00	PLK1	17	ESCO2	0.72	CDH2	0.19	BRCA1	16.28	BRCA1	15	CDKN2A	8.06	CDKN2A	3,120
2	PCNA	PCNA	86,426	CDH2	1,276.61	CDH2	49	BRCA1	30.14	DONSON	1.00	BRCA1	16	FANCA	0.71	NRCAM	0.16	PLK1	16.27	PLK1	15	PLK1	8.03	CDH2	2,706
3	RFC3	RFC3	86,412	C3	900.00	BRCA1	26	MSH2	28.89	MAOA	1.00	PCNA	15	USP1	0.71	SCG3	0.16	MSH2	16.25	RFC3	14	BRCA1	7.98	C3	1,800
4	RFC5	RFC5	86,406	GNG4	766.00	PLK1	13	PCNA	28.00	TPH1	1.00	RFC3	14	GMNN	0.70	C3	0.16	PCNA	16.10	MSH2	14	MSH2	7.91	PLK1	1,718
5	PLK1	PLK1	85,780	PLK1	612.11	C3	11	RFC3	27.84	CEP78	1.00	MSH2	14	PCNA	0.68	CDKN2A	0.16	RFC3	16.07	RRM1	13	GMNN	7.84	GNG4	1,486
6	RRM1	RRM1	85,758	GRP	604.00	MSH2	10	RRM1	27.67	CCL21	1.00	RRM1	13	RFC5	0.66	ISL1	0.16	RFC5	15.98	RFC5	13	CDH2	7.74	BRCA1	1,236
7	BRCA1	BRCA1	81,423	BRCA1	430.66	GNG4	9	GMNN	27.55	FANCA	1.00	RFC5	13	RRM1	0.64	PCSK1	0.13	RRM1	15.73	PCNA	13	STMN1	7.67	GRP	1,144
8	GMNN	GMNN	80,689	DDC	316.00	GRP	7	CDKN2A	27.32	USP1	1.00	GMNN	12	MCM6	0.63	SCN8A	0.13	MCM6	15.54	MCM6	12	RRM1	7.64	MSH2	1,028
9	MCM6	MCM6	45,438	MSH2	308.22	STMN1	6	RFC5	27.17	CENPI	0.83	MCM6	12	ASF1B	0.62	PMAIP1	0.13	GMNN	15.28	GMNN	11	RFC3	7.60	KIFC1	780
10	ESCO2	ESCO2	40,327	GMNN	248.54	DDC	4	MCM6	26.67	ESCO2	0.67	ESCO2	10	MSH2	0.62	CDKN2C	0.13	ESCO2	14.56	ESCO2	9	PCNA	7.59	STMN1	780
11	ASF1B	ASF1B	5,071	PCNA	244.83	PCNA	4	ESCO2	25.50	RFC5	0.67	ASF1B	10	RFC3	0.61	CCL21	0.13	ASF1B	14.49	ASF1B	9	RFC5	7.57	PCNA	766
	Reference (11 genes)	11/11		5/11		4/11		10/11		2/11		11/11		9/11		0/11		11/11		11/11		8/11		4/11	

PPI, protein-protein interaction; MCODE, Molecular Complex Detection; EPC, Percolated Component; MNC, Maximum Neighborhood Component; DMNC, Density of Maximum Neighborhood Component; MCC, Maximal Clique Centrality.

Table S3 The validation of top 8 hub DEGs using 12 topological analysis methods of Cytoscape plugin cytoHubba in the PPI networks of non-small cell lung cancer

MCODE		MCC		Betweenness		BottleNeck		Closeness		ClusteringCoefficient		Degree		DMNC		EcCentricity		EPC		MNC		Radiality		Stress	
Rank	Gene	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score
1	S100A2	S100A2	4	SLC7A11	6	SLC7A11	2	SLC7A11	3.50	SERPINB5	1.00	S100A2	3	S100A2	0.31	S100A2	0.31	NQO1	3.18	S100A2	3	SLC7A11	1.44	SLC7A11	8
2	KRT6A	KRT6A	4	NQO1	2	GCLC	2	NQO1	3.50	SPRR1A	1.00	KRT6A	3	KRT6A	0.31	KRT6A	0.31	GCLC	3.16	KRT6A	3	NQO1	1.44	NQO1	4
3	NQO1	NQO1	4	GCLC	2	PSAT1	1	GCLC	3.50	AKR1B10	1.00	SLC7A11	3	NQO1	0.31	SLC7A11	0.19	SLC7A11	3.12	NQO1	3	GCLC	1.44	GCLC	4
4	GCLC	GCLC	4	S100A2	1	SERPINB5	1	S100A2	3.00	S100A2	0.67	NQO1	3	GCLC	0.31	NQO1	0.19	AKR1B10	2.86	GCLC	3	AKR1B10	1.25	S100A2	2
5	SLC7A11	SLC7A11	3	KRT6A	1	SPRR1A	1	KRT6A	3.00	KRT6A	0.67	GCLC	3	SERPINB5	0.31	GCLC	0.19	KRT6A	2.86	SERPINB5	2	PSAT1	1.15	KRT6A	2
6	SERPINB5	SERPINB5	2	PSAT1	0	S100A2	1	AKR1B10	2.83	NQO1	0.67	SERPINB5	2	SPRR1A	0.31	SERPINB5	0.15	S100A2	2.85	SPRR1A	2	S100A2	0.92	PSAT1	0
7	SPRR1A	SPRR1A	2	SERPINB5	0	KRT6A	1	SERPINB5	2.50	GCLC	0.67	SPRR1A	2	SLC7A11	0.31	SPRR1A	0.15	SERPINB5	2.63	SLC7A11	2	KRT6A	0.92	SERPINB5	0
8	AKR1B10	AKR1B10	2	SPRR1A	0	STEAP1	1	SPRR1A	2.50	SLC7A11	0.33	AKR1B10	2	AKR1B10	0.31	STEAP1	0.15	SPRR1A	2.62	AKR1B10	2	SERPINB5	0.82	SPRR1A	0
	Reference (8 genes)	8/8		7/8		6/8		8/8		8/8		8/8		8/8		7/8		8/8		8/8		7/8		7/8	

PPI, protein-protein interaction; MCODE, Molecular Complex Detection; EPC, Percolated Component; MNC, Maximum Neighborhood Component; DMNC, Density of Maximum Neighborhood Component; MCC, Maximal Clique Centrality.