

SUPPLEMENTARY TABLES

Supplementary Table 4. Module analysis of co-DEGs using MCODE of Cytoscope.

MCODE_Cluster	MCODE_Node_Status	MCODE_Score	name	TopologicalCoefficient
Cluster 1	Clustered	21.32307692	CDK1	0.24610988
Cluster 1	Clustered	21.32307692	CCNB1	0.28399209
Cluster 1	Clustered	21.32307692	CDC20	0.29765066
Cluster 1	Clustered	21.32307692	KIF11	0.32624113
Cluster 1	Clustered	21.32307692	TOP2A	0.33646245
Cluster 1	Clustered	21.32307692	CDCA8	0.34704034
Cluster 1	Clustered	21.32307692	BUB1B	0.36419753
Cluster 1	Seed	21.32307692	ASPM	0.36976744
Cluster 1	Clustered	21.32307692	DLGAP5	0.38181271
Cluster 1	Clustered	21.32307692	NDC80	0.35257453
Cluster 1	Clustered	21.32307692	KIF2C	0.40125
Cluster 1	Clustered	21.32307692	CENPF	0.40493421
Cluster 1	Clustered	21.32307692	TTK	0.40350877
Cluster 1	Clustered	21.32307692	KIF20A	0.40773229
Cluster 1	Clustered	18.8034188	RRM2	0.34723854
Cluster 1	Clustered	21.32307692	NUSAP1	0.41392318
Cluster 1	Clustered	20.51	NCAPG	0.40590278
Cluster 1	Clustered	20.37	TPX2	0.40785714
Cluster 1	Clustered	20.37	CEP55	0.41801471
Cluster 1	Clustered	20.69565217	UBE2C	0.42312009
Cluster 1	Clustered	19.98290598	PBK	0.44112903
Cluster 1	Clustered	18	ESPL1	0.39016897
Cluster 1	Clustered	20.44	KIF4A	0.45512821
Cluster 1	Clustered	19.60474308	KIF15	0.44137931
Cluster 1	Clustered	19.49275362	SPAG5	0.45767196
Cluster 1	Clustered	20.69565217	MELK	0.46383929
Cluster 1	Clustered	18.90952381	NUF2	0.45238095
Cluster 1	Clustered	19.76284585	KIF23	0.43717728
Cluster 1	Clustered	17.81052632	PRC1	0.41557223
Cluster 1	Clustered	18.81904762	PTTG1	0.46615385
Cluster 1	Clustered	18.90952381	MKI67	0.48839662
Cluster 1	Clustered	17.90526316	CDCA3	0.50185185
Cluster 2	Clustered	14	KNTC1	0.48070175
Cluster 2	Clustered	14	CENPU	0.47387387
Cluster 2	Clustered	14	ZWINT	0.45855856
Cluster 2	Clustered	14	RCC2	0.48841699
Cluster 2	Clustered	14	CDCA5	0.48841699
Cluster 3	Clustered	5.727272727	PCNA	0.23539618
Cluster 3	Clustered	5.785714286	MCM10	0.22094361
Cluster 3	Clustered	5.5	FEN1	0.31566265
Cluster 3	Clustered	5	DTL	0.34993614
Cluster 3	Clustered	5	DNA2	0.40613027
Cluster 3	Clustered	5	TIMELESS	0.41666667
Cluster 3	Clustered	5.785714286	ORC6	0.35030864
Cluster 3	Clustered	5	RMI2	0.44387755

Cluster 3	Seed	6	CHTF18	0.53571429
Cluster 3	Clustered	5.785714286	CDC7	0.30892857
Cluster 3	Clustered	5	RAD51AP1	0.52857143
Cluster 4	Clustered	7.418181818	MCM3	0.26919476
Cluster 4	Clustered	8	MCM7	0.26763285
Cluster 4	Seed	8	MCM2	0.25791624
Cluster 5	Clustered	3.771428571	RFC4	0.19430761
Cluster 5	Seed	4.581818182	POLE2	0.2029321
Cluster 5	Clustered	4	ISG15	0.50641026
Cluster 6	Clustered	2	LAMC1	0.66666667
Cluster 6	Seed	2	SPARCL1	0.83333333
Cluster 6	Clustered	2	STC2	0.83333333
Cluster 7	Seed	2	VIM	1
Cluster 7	Clustered	2	TNNI3	1
Cluster 7	Clustered	2	TNNT1	1
Cluster 8	Seed	2	KAT2B	0.43333333
Cluster 8	Clustered	2	E2F3	0.53333333
Cluster 8	Clustered	2	MEF2C	0.75
Cluster 9	Clustered	2	GAPDH	1
Cluster 9	Clustered	2	TPI1	1
Cluster 9	seed	2	GPI	1

Supplementary Table 5. Hub genes evaluated by PPI network analysis Degree>40 or the seed genes in MOCODE analysis of Cytoscape.

Entrez ID	Gene symbol	Description	Alternate names	Chromosome	Map location
63922	CHTF18	chromosome transmission fidelity factor 18	C16orf41 C321D2.2 C321D2.3 C321D2.4 CHL12 Ctf18 RUVBL	16	16p13.3
4171	MCM2	minichromosome maintenance complex component 2	BM28 CCNL1 CDCL1 D3S3194 MITOTIN cdc19	3	3q21
5427	POLE2	polymerase (DNA directed), epsilon 2, accessory subunit	DPE2	14	14q21-q22
8404	SPARCL1	SPARC-like 1 (hevin)	MAST 9 MAST9 PIG33 SC1	4	4q22.1
7431	VIM	vimentin	CTRCT30 HEL113	10	10p13
8850	KAT2B	K(lysine) acetyltransferase 2B	CAF P/CAF PCAF	3	3p24
983	CDK1	cyclin-dependent kinase 1	CDC2 CDC28A P34CDC2	10	10q21.1
891	CCNB1	cyclin B1	CCNB	5	5q12
991	CDC20	cell division cycle 20	CDC20A bA276H19.3 p55CDC	1	1p34.1
3832	KIF11	kinesin family member 11	EG5 HKSP KNSL1 MCLMR TRIP5	10	10q24.1
7153	TOP2A	topoisomerase (DNA) II alpha 170kDa	TOP2 TP2A	17	17q21-q22
55143	CDCA8	cell division cycle associated 8	BOR BOREALIN DasraB MESRGP	1	1p34.3
701	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	BUB1beta BUBR1 Bub1A MAD3L MVA1 SSK1 hBUBR1	15	15q15
259266	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	ASP Calmbp1 MCPH5	1	1q31
9787	DLGAP5	discs, large (Drosophila) homolog-associated protein 5	DLG7 HURP	14	14q22.3
10403	NDC80	NDC80 kinetochore complex component	HEC HEC1 HsHec1 KNTC2 TID3 hsNDC80	18	18p11.32

Supplementary Table 6. KEGG enrichment of core genes and EMT regulators.

Pathway ID	Description	Count in gene set	False Discovery Rate
hsa04520	Adherens junction	4 of 71	1.77E-05
hsa04390	Hippo signaling pathway	3 of 152	0.0059
hsa05216	Thyroid cancer	2 of 37	0.0067
hsa05205	Proteoglycans in cancer	3 of 195	0.0067
hsa05213	Endometrial cancer	2 of 58	0.008
hsa05130	Pathogenic Escherichia coli infection	2 of 53	0.008
hsa05412	Arrhythmogenic right ventricular cardiomyopathy	2 of 72	0.0103
hsa05100	bacterial invasion of Epithelial cells	2 of 72	0.0103
hsa05215	Prostate cancer	2 of 97	0.0142
hsa04514	cell adhesion molecules(CAMs)	2 of 139	0.0254
hsa05226	Gastric cancer	2 of 147	0.0257
hsa05206	MicroRNAs in cancer	2 of 149	0.0257
hsa05202	Transcriptional misregulation in cancer	2 of 169	0.0284
hsa04015	Rap1 signaling pathway	2 of 203	0.0373

Supplementary Table 7. Primers used for the real-time PCR.

Gene	Primers	Sequences (5'-3')
β -actin	Forward	CCACGAAACTACCTTCAACTCC
	Reverse	GTGATCTCCTTCTGCATCCTGT
ELF3	Forward	GCAAACACCCTGGACTTGAC
	Reverse	CTGTCCTTCATCACGGTGC
TFAP2A	Forward	ATATCCGTTACGCCGATCC
	Reverse	CCTCGCAGTCCTCGTACTTG
BUB1B	Forward	GGGATGGGTCCCTTCTGGAAA
	Reverse	GGCATTTCAGAATCCGCACAA
NDC80	Forward	CCTGGTGTTTTTGATGACCGC
	Reverse	TCCAGTTTCCTGACACGACC