

**Table S1** Seventy coexpression genes from cBioPortal significantly associated with exportins mutations

Gene	Correlated gene	Cytoband	Spearman correlation	P value	q value
<i>XPO1</i>	<i>MSH2</i>	2p21-p16.3	0.641877	2.24E-61	3.26E-57
	<i>CIP2A</i>	3q13.13	0.641211	3.26E-61	3.26E-57
	<i>POLQ</i>	3q13.33	0.634575	1.30E-59	8.67E-56
	<i>SGO1</i>	3p24.3	0.626094	1.27E-57	6.35E-54
	<i>BUB1</i>	2q13	0.625131	2.12E-57	8.47E-54
	<i>KIF15</i>	3p21.31	0.624534	2.91E-57	9.28E-54
	<i>CKAP2L</i>	2q14.1	0.624323	3.25E-57	9.28E-54
	<i>SASS6</i>	1p21.2	0.615186	3.76E-55	9.38E-52
	<i>TOP2A</i>	17q21.2	0.6122	1.72E-54	3.81E-51
	<i>FANCD2</i>	3p25.3	0.611041	3.08E-54	6.15E-51
<i>CSE1L</i>	<i>AURKA</i>	20q13.2	0.700738	1.48E-77	2.97E-73
	<i>EXO1</i>	1q43	0.69397	1.70E-75	1.70E-71
	<i>MCM10</i>	10p13	0.688483	7.23E-74	4.81E-70
	<i>TPX2</i>	20q11.21	0.687557	1.35E-73	6.74E-70
	<i>DEPDC1</i>	1p31.3	0.685141	6.81E-73	2.72E-69
	<i>TTK</i>	6q14.1	0.684709	9.07E-73	3.02E-69
	<i>NEK2</i>	1q32.3	0.684272	1.21E-72	3.46E-69
	<i>AUNIP</i>	1p36.11	0.683399	2.16E-72	5.40E-69
	<i>KIF2C</i>	1p34.1	0.68287	3.07E-72	6.81E-69
	<i>NCAPG</i>	4p15.31	0.681813	6.16E-72	1.23E-68
<i>XPOT</i>	<i>MARS1</i>	12q13.3	0.744383	2.24E-92	4.48E-88
	<i>MTHFD2</i>	2p13.1	0.721019	4.34E-84	4.33E-80
	<i>SHMT2</i>	12q13.3	0.706987	1.65E-79	1.10E-75
	<i>RACGAP1</i>	12q13.12	0.68551	5.32E-73	2.66E-69
	<i>NUP107</i>	12q15	0.657224	3.04E-65	1.04E-61
	<i>PARPBP</i>	12q23.2	0.657157	3.16E-65	1.04E-61
	<i>TIMELESS</i>	12q13.3	0.656922	3.64E-65	1.04E-61
	<i>CCT2</i>	12q15	0.64397	6.86E-62	1.71E-58
	<i>DEPDC1</i>	1p31.3	0.636069	5.72E-60	1.27E-56
	<i>DENR</i>	12q24.31	0.634317	1.50E-59	2.92E-56
<i>XPO4</i>	<i>MPHOSPH8</i>	13q12.11	0.689765	3.03E-74	6.06E-70
	<i>AKAP11</i>	13q14.11	0.645737	2.50E-62	2.50E-58
	<i>ZC3H13</i>	13q14.13	0.618045	8.64E-56	5.76E-52
	<i>PDS5B</i>	13q13.1	0.615207	3.72E-55	1.86E-51
	<i>ZMYM2</i>	13q12.11	0.611824	2.08E-54	8.29E-51

**Table S1** (continued)

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Gene	Correlated gene	Cytoband	Spearman correlation	P value	q value	
XPO5	<i>RNF6</i>	13q12.13	0.598986	1.18E-51	3.92E-48	
	<i>PAN3</i>	13q12.2	0.588217	1.93E-49	5.42E-46	
	<i>UTP14C</i>	13q14.3	0.587966	2.17E-49	5.42E-46	
	<i>NUBP2</i>	16p13.3	-0.57778	2.26E-47	5.02E-44	
	<i>RBM26</i>	13q31.1	0.573814	1.33E-46	2.65E-43	
	<i>RPL7L1</i>	6p21.1	0.714013	9.10E-82	1.82E-77	
	<i>ABCF1</i>	6p21.33	0.696581	2.78E-76	2.77E-72	
	<i>HSP90AB1</i>	6p21.1	0.693764	1.96E-75	1.31E-71	
	<i>PPP2R5D</i>	6p21.1	0.692099	6.17E-75	3.08E-71	
	<i>CDC5L</i>	6p21.1	0.67489	5.49E-70	2.20E-66	
	<i>NUP153</i>	6p22.3	0.673024	1.81E-69	6.01E-66	
	<i>E2F3</i>	6p22.3	0.663314	7.66E-67	2.19E-63	
	<i>UHRF1BP1</i>	6p21.31	0.661677	2.08E-66	5.19E-63	
	<i>SRPK1</i>	6p21.31	0.65548	8.59E-65	1.91E-61	
	<i>BYSL</i>	6p21.1	0.639986	6.49E-61	1.30E-57	
XPO6	<i>GTF3C1</i>	16p12.1	0.633405	2.47E-59	4.83E-55	
	<i>ATXN2L</i>	16p11.2	0.632172	4.84E-59	4.83E-55	
	<i>TBC1D10B</i>	16p11.2	0.582673	2.48E-48	1.65E-44	
	<i>USP31</i>	16p12.2	0.542899	5.74E-41	2.87E-37	
	<i>SETD1A</i>	16p11.2	0.530376	7.59E-39	3.03E-35	
	<i>DNMT1</i>	19p13.2	0.52713	2.61E-38	8.68E-35	
	<i>RNF40</i>	16p11.2	0.52402	8.39E-38	2.39E-34	
	<i>ZNF646</i>	16p11.2	0.497943	9.55E-34	2.39E-30	
	<i>KCTD5</i>	16p13.3	0.497237	1.22E-33	2.70E-30	
	<i>ZNF598</i>	16p13.3	0.492875	5.35E-33	1.07E-29	
	XPO7	<i>WRN</i>	8p12	0.766202	5.63E-101	1.12E-96
		<i>CCAR2</i>	8p21.3	0.751744	3.54E-95	3.54E-91
<i>TNKS</i>		8p23.1	0.744803	1.56E-92	1.04E-88	
<i>ENTPD4</i>		8p21.3	0.715342	3.34E-82	1.67E-78	
<i>CNOT7</i>		8p22	0.67032	9.96E-69	3.98E-65	
<i>CCDC25</i>		8p21.1	0.658894	1.12E-65	3.72E-62	
<i>MCPH1</i>		8p23.1	0.656895	3.70E-65	1.06E-61	
<i>PCM1</i>		8p22	0.644464	5.18E-62	1.29E-58	
<i>INTS9</i>		8p21.1	0.643534	8.78E-62	1.95E-58	
<i>MTMR9</i>		8p23.1	0.641088	3.50E-61	6.98E-58	

**Table S2** The enrichment analysis of differently expressed exportins and the 69 most frequently altered neighbor genes in LUAD and LUSC from the cBioPortal and DAVID databases

Category	Term	Count	P value	Fold enrichment
GOTERM_BP_DIRECT	GO: 0007067; mitotic nuclear division	9	3.03E-06	9.828824142
GOTERM_BP_DIRECT	GO: 0051301; cell division	10	4.47E-06	7.738248848
GOTERM_BP_DIRECT	GO: 0006281; DNA repair	8	2.21E-05	9.220041181
GOTERM_BP_DIRECT	GO: 0007062; sister chromatid cohesion	5	5.33E-04	13.14751018
GOTERM_BP_DIRECT	GO: 0006974; cellular response to DNA damage stimulus	6	9.42E-04	7.812655087
GOTERM_BP_DIRECT	GO: 0008283; cell proliferation	7	0.0020821	5.179975322
GOTERM_BP_DIRECT	GO: 0051321; meiotic cell cycle	3	0.0067577	23.89753321
GOTERM_BP_DIRECT	GO: 1901796; regulation of signal transduction by p53 class mediator	4	0.0103605	8.73673257
GOTERM_BP_DIRECT	GO: 0000086; G2/M transition of mitotic cell cycle	4	0.0135485	7.907699553
GOTERM_BP_DIRECT	GO: 0006260; DNA replication	4	0.0187911	6.989386056
GOTERM_CC_DIRECT	GO: 0005654; nucleoplasm	34	7.47E-12	3.477550287
GOTERM_CC_DIRECT	GO: 0005813; centrosome	11	1.85E-06	7.352699531
GOTERM_CC_DIRECT	GO: 0000776; kinetochore	6	8.79E-06	21.09259259
GOTERM_CC_DIRECT	GO: 0005730; nucleolus	13	3.15E-05	4.319428238
GOTERM_CC_DIRECT	GO: 0000922; spindle pole	6	3.72E-05	15.67431193
GOTERM_MF_DIRECT	GO: 0005515; protein binding	59	1.53E-10	1.717767889
GOTERM_MF_DIRECT	GO: 0005524; ATP binding	18	3.54E-05	3.079537853
GOTERM_MF_DIRECT	GO: 0044822; poly(A) RNA binding	13	0.0011181	2.945124406
GOTERM_MF_DIRECT	GO: 0003677; DNA binding	16	0.0014439	2.44466167
GOTERM_MF_DIRECT	GO: 0016887; ATPase activity	5	0.0054088	6.988325882
KEGG_PATHWAY	hsa04114; oocyte meiosis	4	0.0044007	11.26781327
KEGG_PATHWAY	hsa04110; cell cycle	3	0.0541553	7.564882698
KEGG_PATHWAY	hsa00670; one carbon pool by folate	2	0.0593964	31.26818182
KEGG_PATHWAY	hsa03430; mismatch repair	2	0.0680107	27.18972332

LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.