

Fig.1: All genes are highly enriched in our list of DEGs and involved in Kegg pathway for kidney cancer except the marked star genes.

The most significant list of Go terms which highly enriched with our list of kidney DEGs:

950 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	apoptotic process	RT		453	3.8	5.9E-22	6.7E-18
<input type="checkbox"/>	GOTERM_BP_DIRECT	signal transduction	RT		838	7.0	3.7E-14	2.1E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	inflammatory response	RT		303	2.5	1.2E-13	4.0E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of catalytic activity	RT		280	2.3	1.4E-13	4.0E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of transcription from RNA polymerase II promoter	RT		792	6.6	5.4E-13	1.1E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of transcription, DNA-templated	RT		494	4.1	5.9E-13	1.1E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	intracellular protein transport	RT		245	2.1	3.0E-12	5.0E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of cell shape	RT		128	1.1	7.2E-12	1.0E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell migration	RT		204	1.7	1.2E-11	1.5E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	cytoplasmic translation	RT		81	0.7	1.3E-11	1.5E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell adhesion	RT		389	3.3	1.6E-11	1.7E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to drug	RT		220	1.8	1.8E-11	1.7E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	calcium-mediated signaling	RT		82	0.7	3.0E-11	2.6E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	intracellular signal transduction	RT		319	2.7	8.1E-11	6.6E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-tyrosine phosphorylation	RT		114	1.0	2.7E-10	2.0E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	small GTPase mediated signal transduction	RT		101	0.8	4.7E-10	3.3E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein phosphorylation	RT		345	2.9	3.2E-9	2.1E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	angiogenesis	RT		187	1.6	3.3E-9	2.1E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	kidney development	RT		98	0.8	3.7E-9	2.2E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell division	RT		270	2.3	4.0E-9	2.3E-6

Fig.3: Most significant list of BP in kidney cancer.

265 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosol	RT		3788	31.7	7.1E-129	1.2E-125
<input type="checkbox"/>	GOTERM_CC_DIRECT	membrane	RT		1876	15.7	8.2E-91	6.8E-88
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytoplasm	RT		3679	30.8	3.3E-79	1.8E-76
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleoplasm	RT		2682	22.4	1.9E-72	8.0E-70
<input type="checkbox"/>	GOTERM_CC_DIRECT	extracellular exosome	RT		1498	12.5	5.5E-35	1.8E-32
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleus	RT		3664	30.7	3.3E-32	9.3E-30
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrion	RT		1003	8.4	5.1E-31	1.2E-28
<input type="checkbox"/>	GOTERM_CC_DIRECT	focal adhesion	RT		344	2.9	5.1E-29	1.1E-26
<input type="checkbox"/>	GOTERM_CC_DIRECT	Golgi apparatus	RT		789	6.6	6.0E-26	1.1E-23
<input type="checkbox"/>	GOTERM_CC_DIRECT	intracellular membrane-bounded organelle	RT		700	5.9	1.2E-25	2.1E-23
<input type="checkbox"/>	GOTERM_CC_DIRECT	endoplasmic reticulum	RT		800	6.7	1.6E-25	2.5E-23
<input type="checkbox"/>	GOTERM_CC_DIRECT	endoplasmic reticulum membrane	RT		732	6.1	3.7E-22	5.1E-20
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell surface	RT		468	3.9	2.5E-21	3.2E-19
<input type="checkbox"/>	GOTERM_CC_DIRECT	perinuclear region of cytoplasm	RT		543	4.5	7.8E-20	9.3E-18
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytoplasmic vesicle	RT		250	2.1	1.0E-15	1.1E-13
<input type="checkbox"/>	GOTERM_CC_DIRECT	macromolecular complex	RT		489	4.1	8.5E-15	8.9E-13
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic ribosome	RT		74	0.6	1.0E-14	1.0E-12
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrial matrix	RT		290	2.4	1.2E-14	1.1E-12
<input type="checkbox"/>	GOTERM_CC_DIRECT	endosome	RT		240	2.0	9.5E-14	8.4E-12
<input type="checkbox"/>	GOTERM_CC_DIRECT	centrosome	RT		387	3.2	1.4E-13	1.2E-11
<input type="checkbox"/>	GOTERM_CC_DIRECT	Golgi membrane	RT		450	3.8	1.6E-13	1.3E-11
<input type="checkbox"/>	GOTERM_CC_DIRECT	neuronal cell body	RT		297	2.5	3.0E-13	2.3E-11
<input type="checkbox"/>	GOTERM_CC_DIRECT	receptor complex	RT		172	1.4	4.1E-13	3.0E-11
<input type="checkbox"/>	GOTERM_CC_DIRECT	basolateral plasma membrane	RT		186	1.6	4.8E-13	3.3E-11
<input type="checkbox"/>	GOTERM_CC_DIRECT	plasma membrane	RT		3027	25.3	8.1E-13	5.4E-11
<input type="checkbox"/>	GOTERM_CC_DIRECT	actin cytoskeleton	RT		197	1.6	4.7E-12	3.0E-10
<input type="checkbox"/>	GOTERM_CC_DIRECT	glutamatergic synapse	RT		270	2.3	1.7E-11	1.1E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	membrane raft	RT		190	1.6	4.4E-11	2.6E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	postsynaptic density	RT		200	1.7	6.6E-11	3.8E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	integral component of plasma membrane	RT		952	8.0	2.9E-10	1.6E-8
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrial inner membrane	RT		323	2.7	3.4E-10	1.8E-8

Fig.4: Most significant list of CC in kidney cancer.

221 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein binding	RT		8307	69.5	4.4E-175	1.7E-171
<input type="checkbox"/>	GOTERM_MF_DIRECT	identical protein binding	RT		1229	10.3	1.3E-30	2.5E-27
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP binding	RT		1053	8.8	1.2E-14	1.5E-11
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA binding	RT		992	8.3	4.3E-12	4.1E-9
<input type="checkbox"/>	GOTERM_MF_DIRECT	macromolecular complex binding	RT		306	2.6	2.5E-10	1.9E-7
<input type="checkbox"/>	GOTERM_MF_DIRECT	metal ion binding	RT		1700	14.2	1.7E-9	1.1E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein homodimerization activity	RT		496	4.2	3.6E-9	2.0E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	SH3 domain binding	RT		109	0.9	7.7E-9	3.6E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein tyrosine kinase activity	RT		95	0.8	3.0E-8	1.2E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin protein ligase binding	RT		226	1.9	4.6E-8	1.7E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	GTPase activator activity	RT		212	1.8	7.5E-8	2.6E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	actin filament binding	RT		171	1.4	1.3E-7	4.2E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein kinase binding	RT		357	3.0	2.4E-7	6.9E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	small GTPase binding	RT		210	1.8	2.9E-7	7.5E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	guanyl-nucleotide exchange factor activity	RT		176	1.5	3.0E-7	7.5E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	actin binding	RT		245	2.1	4.2E-7	9.9E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	oxidoreductase activity	RT		180	1.5	4.9E-7	1.1E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	signaling receptor activity	RT		173	1.4	6.2E-7	1.3E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	transmembrane receptor protein tyrosine kinase activity	RT		94	0.8	1.1E-6	2.1E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	cadherin binding	RT		227	1.9	2.4E-6	4.5E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	microtubule binding	RT		194	1.6	2.8E-6	5.0E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	receptor binding	RT		276	2.3	1.0E-5	1.8E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	integrin binding	RT		122	1.0	1.3E-5	2.1E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	protease binding	RT		86	0.7	2.3E-5	3.7E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	kinase binding	RT		81	0.7	2.8E-5	4.0E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	kinase activity	RT		164	1.4	2.8E-5	4.0E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein serine/threonine kinase activity	RT		271	2.3	3.2E-5	4.5E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	poly(U) RNA binding	RT		25	0.2	3.5E-5	4.7E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein binding, bridging	RT		82	0.7	3.9E-5	5.1E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein domain specific binding	RT		186	1.6	9.0E-5	1.1E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein C-terminal binding	RT		158	1.3	1.0E-4	1.3E-2

Fig.5: Most significant list of MF in kidney cancer.

The most significant list of Go terms which highly enriched with our list of lung DEGs:

Rerun Using Options Create Sublist

972 chart records [Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein phosphorylation	RT		376	3.1	3.7E-18	4.2E-14
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of transcription from RNA polymerase II promoter	RT		814	6.7	3.4E-16	2.0E-12
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell division	RT		289	2.4	9.4E-15	3.6E-11
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of transcription from RNA polymerase II promoter	RT		658	5.5	8.5E-14	2.4E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell cycle	RT		270	2.2	2.5E-13	5.8E-10
<input type="checkbox"/>	GOTERM_BP_DIRECT	apoptotic process	RT		429	3.6	5.5E-13	1.0E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	endocytosis	RT		167	1.4	1.2E-12	2.0E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein autophosphorylation	RT		147	1.2	5.9E-12	8.4E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	actin cytoskeleton organization	RT		147	1.2	1.3E-11	1.7E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	proteasome-mediated ubiquitin-dependent protein catabolic process	RT		166	1.4	1.6E-11	1.8E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	intracellular signal transduction	RT		323	2.7	2.6E-11	2.7E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of transcription, DNA-templated	RT		489	4.1	7.2E-11	6.8E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein transport	RT		314	2.6	9.7E-11	8.5E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	signal transduction	RT		825	6.8	1.5E-10	1.2E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell migration	RT		202	1.7	2.3E-10	1.7E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	inflammatory response	RT		293	2.4	7.6E-10	5.4E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to drug	RT		215	1.8	3.3E-9	2.2E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	regulation of catalytic activity	RT		268	2.2	4.4E-9	2.8E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of GTPase activity	RT		145	1.2	7.3E-9	4.4E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	small GTPase mediated signal transduction	RT		99	0.8	1.2E-8	6.4E-6

Fig.6: Most significant list of BP in lung cancer.

278 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosol	RT		3794	31.5	3.5E-121	5.8E-118
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytoplasm	RT		3711	30.8	8.1E-80	6.8E-77
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleoplasm	RT		2721	22.6	8.6E-78	4.8E-75
<input type="checkbox"/>	GOTERM_CC_DIRECT	membrane	RT		1843	15.3	1.3E-73	5.4E-71
<input type="checkbox"/>	GOTERM_CC_DIRECT	nucleus	RT		3799	31.5	7.9E-51	2.7E-48
<input type="checkbox"/>	GOTERM_CC_DIRECT	extracellular exosome	RT		1465	12.1	7.2E-25	2.0E-22
<input type="checkbox"/>	GOTERM_CC_DIRECT	endoplasmic reticulum membrane	RT		746	6.2	1.3E-24	3.3E-22
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrion	RT		976	8.1	5.0E-22	1.1E-19
<input type="checkbox"/>	GOTERM_CC_DIRECT	Golgi apparatus	RT		776	6.4	9.0E-21	1.7E-18
<input type="checkbox"/>	GOTERM_CC_DIRECT	endoplasmic reticulum	RT		784	6.5	1.2E-19	2.0E-17
<input type="checkbox"/>	GOTERM_CC_DIRECT	focal adhesion	RT		324	2.7	1.2E-18	1.9E-16
<input type="checkbox"/>	GOTERM_CC_DIRECT	intracellular membrane-bounded organelle	RT		680	5.6	1.6E-18	2.3E-16
<input type="checkbox"/>	GOTERM_CC_DIRECT	perinuclear region of cytoplasm	RT		532	4.4	2.9E-15	3.8E-13
<input type="checkbox"/>	GOTERM_CC_DIRECT	centrosome	RT		393	3.3	1.5E-14	1.8E-12
<input type="checkbox"/>	GOTERM_CC_DIRECT	microtubule	RT		249	2.1	2.4E-14	2.7E-12
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell surface	RT		445	3.7	5.9E-13	6.2E-11
<input type="checkbox"/>	GOTERM_CC_DIRECT	macromolecular complex	RT		485	4.0	8.6E-13	8.5E-11
<input type="checkbox"/>	GOTERM_CC_DIRECT	ficolin-1-rich granule lumen	RT		107	0.9	1.8E-12	1.7E-10
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytoplasmic vesicle	RT		243	2.0	2.8E-12	2.5E-10
<input type="checkbox"/>	GOTERM_CC_DIRECT	Golgi membrane	RT		447	3.7	7.4E-12	6.2E-10
<input type="checkbox"/>	GOTERM_CC_DIRECT	nuclear membrane	RT		185	1.5	3.1E-11	2.5E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell-cell junction	RT		152	1.3	3.5E-11	2.7E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	nuclear envelope	RT		153	1.3	5.1E-11	3.7E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	actin cytoskeleton	RT		195	1.6	9.5E-11	6.7E-9
<input type="checkbox"/>	GOTERM_CC_DIRECT	lysosome	RT		226	1.9	5.9E-10	4.0E-8
<input type="checkbox"/>	GOTERM_CC_DIRECT	neuronal cell body	RT		288	2.4	8.7E-10	5.6E-8
<input type="checkbox"/>	GOTERM_CC_DIRECT	postsynaptic density	RT		198	1.6	1.1E-9	6.9E-8
<input type="checkbox"/>	GOTERM_CC_DIRECT	microtubule organizing center	RT		127	1.1	1.2E-9	7.5E-8
<input type="checkbox"/>	GOTERM_CC_DIRECT	glutamatergic synapse	RT		265	2.2	2.3E-9	1.3E-7
<input type="checkbox"/>	GOTERM_CC_DIRECT	endosome membrane	RT		188	1.6	2.3E-9	1.3E-7
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrial matrix	RT		275	2.3	3.7E-9	2.0E-7

Fig.7: Most significant list of CC in lung cancer.

216 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein binding	RT		8340	69.1	2.7E-166	1.0E-162
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP binding	RT		1103	9.1	1.8E-24	3.3E-21
<input type="checkbox"/>	GOTERM_MF_DIRECT	identical protein binding	RT		1183	9.8	3.3E-18	4.1E-15
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA binding	RT		1013	8.4	9.5E-15	8.9E-12
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein kinase binding	RT		376	3.1	1.5E-11	1.1E-8
<input type="checkbox"/>	GOTERM_MF_DIRECT	small GTPase binding	RT		223	1.8	3.0E-11	1.9E-8
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin protein ligase binding	RT		236	2.0	5.7E-11	3.1E-8
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein homodimerization activity	RT		507	4.2	6.5E-11	3.1E-8
<input type="checkbox"/>	GOTERM_MF_DIRECT	actin binding	RT		253	2.1	5.9E-9	2.5E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	metal ion binding	RT		1706	14.1	7.1E-9	2.7E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein serine/threonine kinase activity	RT		285	2.4	4.8E-8	1.6E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein kinase activity	RT		275	2.3	1.1E-7	3.6E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	macromolecular complex binding	RT		297	2.5	2.0E-7	5.8E-5
<input type="checkbox"/>	GOTERM_MF_DIRECT	guanylyl-nucleotide exchange factor activity	RT		176	1.5	6.1E-7	1.6E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATPase activity	RT		253	2.1	9.2E-7	2.3E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	SH3 domain binding	RT		105	0.9	1.0E-6	2.4E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	actin filament binding	RT		168	1.4	2.5E-6	5.4E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein domain specific binding	RT		193	1.6	3.0E-6	6.3E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein C-terminus binding	RT		156	1.3	3.8E-6	7.3E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	kinase activity	RT		168	1.4	3.9E-6	7.3E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	double-stranded RNA binding	RT		64	0.5	4.3E-6	7.6E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA polymerase II sequence-specific DNA binding transcription factor binding	RT		142	1.2	5.6E-6	9.6E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcription factor binding	RT		156	1.3	6.0E-6	9.9E-4
<input type="checkbox"/>	GOTERM_MF_DIRECT	magnesium ion binding	RT		171	1.4	1.2E-5	1.8E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	microtubule binding	RT		192	1.6	1.8E-5	2.7E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	calcium ion binding	RT		503	4.2	1.9E-5	2.7E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	cadherin binding	RT		224	1.9	2.6E-5	3.6E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein tyrosine kinase activity	RT		89	0.7	2.8E-5	3.8E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	transcription regulatory region sequence-specific DNA binding	RT		172	1.4	4.6E-5	6.0E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	enzyme binding	RT		270	2.2	6.1E-5	7.6E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	chromatin binding	RT		319	2.6	6.7E-5	8.1E-3

Fig.8: Most significant list of MF in lung cancer.

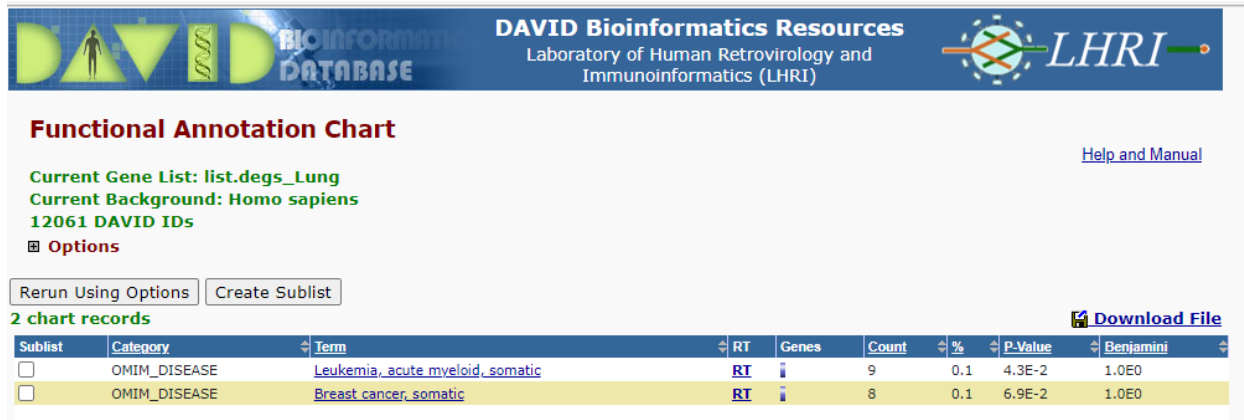


Fig.9: The related OMIM diseases of our lung DEGs.