

The top five enriched GO terms and KEGG and Reactome pathways for the involved DEGs from the meta-analysis of normal and cancer cell lines displayed by the ClueGO/CluePedia app in Cytoscape. Bp means biological process, Mf represents molecular function, FDR is equal to p-values < 0.05 adjusted by Benjamini- Hochberg false discovery rate, count introduces the number of DEGs included in a term or a pathway; % symbolizes count / all genes involved in a term or pathway.

Dataset	ID	Category	Term or pathway	P-value	FDR	Count	%
Normal	GO:0034470	Bp	ncRNA processing	0.00	0.00	47	10.15
Normal	GO:0006396	Bp	RNA processing	0.00	0.00	82	7.78
Normal	GO:0070972	Bp	protein localization to endoplasmic reticulum	0.00	0.00	22	14.38
Normal	GO:0034660	Bp	ncRNA metabolic process	0.00	0.00	50	8.98
Normal	GO:0045184	Bp	establishment of protein localization	0.00	0.00	125	6.50
Normal	GO:0140603	Mf	ATP hydrolysis activity	0.00	0.03	13	14.94
Normal	GO:0003676	Mf	nucleic acid binding	0.00	0.04	229	5.46
Normal	GO:0032553	Mf	ribonucleotide binding	0.00	0.04	127	5.65
Normal	GO:0008173	Mf	RNA methyltransferase activity	0.00	0.05	9	12.86
Normal	GO:0004860	Mf	protein kinase inhibitor activity	0.00	0.05	9	12.68
Normal	KEGG:03060	KEGG	Protein export	0.00	0.00	7	30.43
Normal	KEGG:05415	KEGG	Diabetic cardiomyopathy	0.00	0.01	20	9.85
Normal	KEGG:05012	KEGG	Parkinson disease	0.00	0.01	23	9.24
Normal	KEGG:05020	KEGG	Prion disease	0.00	0.01	25	9.16
Normal	KEGG:00190	KEGG	Oxidative phosphorylation	0.00	0.01	15	11.28
Normal	R-HSA:8953854	Reactome	Metabolism of RNA	0.00	0.00	58	8.62
Normal	R-HSA:75944	Reactome	Transcription from mitochondrial promoters	0.00	0.00	4	100.00
Normal	R-HSA:163282	Reactome	Mitochondrial transcription initiation	0.00	0.01	3	100.00
Normal	R-HSA:6799198	Reactome	Complex I biogenesis	0.00	0.02	10	17.54
Normal	R-HSA:1799339	Reactome	SRP-dependent cotranslational protein targeting to membrane	0.00	0.02	15	13.39
Cancer	GO:0045047	Bp	protein targeting to ER	0.00	0.00	11	9.02
Cancer	GO:0006412	Bp	translation	0.00	0.00	31	4.22
Cancer	GO:0043043	Bp	peptide biosynthetic process	0.00	0.00	32	4.18
Cancer	GO:0051668	Bp	localization within membrane	0.00	0.00	33	4.08
Cancer	GO:0072599	Bp	establishment of protein localization to endoplasmic reticulum	0.00	0.00	11	8.73
Cancer	GO:0140030	Mf	modification-dependent protein binding	0.00	0.00	13	7.69
Cancer	GO:0048027	Mf	mRNA 5'-UTR binding	0.00	0.00	6	20.69

Cancer	GO:0031593	Mf	polyubiquitin modification-dependent protein binding	0.00	0.01	6	11.32
Cancer	GO:0043539	Mf	protein serine/threonine kinase activator activity	0.00	0.01	5	11.63
Cancer	GO:0042393	Mf	histone binding	0.00	0.02	12	4.72
Cancer	KEGG:04141	KEGG	Protein processing in endoplasmic reticulum	0.00	0.00	10	5.85
Cancer	KEGG:03010	KEGG	Ribosome	0.00	0.00	10	6.33
Cancer	KEGG:03018	KEGG	RNA degradation	0.01	0.02	5	6.33
Cancer	KEGG:03060	KEGG	Protein export	0.01	0.02	3	13.04
Cancer	KEGG:05110	KEGG	Vibrio cholerae infection	0.01	0.02	4	8.00
Cancer	R-HSA:9711097	Reactome	Cellular response to starvation	0.00	0.00	14	8.97
Cancer	R-HSA:6791226	Reactome	Major pathway of rRNA processing in the nucleolus and cytosol	0.00	0.00	14	7.61
Cancer	R-HSA:156842	Reactome	Eukaryotic Translation Elongation	0.00	0.00	10	10.75
Cancer	R-HSA:8868773	Reactome	rRNA processing in the nucleus and cytosol	0.00	0.00	14	7.22
Cancer	R-HSA:72613	Reactome	Eukaryotic Translation Initiation	0.00	0.00	11	9.24