

Supplementary Material

Table S1. P-values of the up- or down-regulated miRNAs in CFBE41o- and/or in IB3 with respect to 16HBE. We reported the p-values only for those miRNAs having a FC (log2) $\geq +2$ or FC (log2) ≤ -2 .

Up-regulated miRNA	p-value	
	CFBE41o-	IB3
miR-140-3p	.	0.013
miR-155-5p	0.011	0.024
miR-370-3p	0.039	0.04
miR-452-5p	>0.05	0.029
miR-486-5p	.	0.035
miR-493-3p	0.049	>0.05
miR-509-5p	>0.05	0.023
miR-886-5p	0.034	0.044
miR-10b-3p	0.045	0.008
miR-337-3p	0.035	0.104
miR-432-5p	0.015	0.059
miR-577-5p	0.028	0.048
miR-675-5p	.	0.017
miR-767-5p	.	0.025
miR-154-3p	0.046	.
miR-27b-5p	.	0.016
miR-505-5p	0.092	0.034
Down-regulated miRNA	p-value	
	CFBE41o-	IB3
miR-141-3p	.	0.022
miR-146a-5p	.	0.012
miR-183-5p	.	0.031
miR-193b-3p	0.038	.
miR-197-3p	0.013	.
miR-200b-3p	0.016	0.037
miR-200c-3p	.	0.017
miR-372-3p	>0.05	0.012
miR-483-5p	0.008	.
miR-501-5p	0.022	.
miR-511-5p	0.028	.
miR-574-3p	0.047	.
miR-616-3p	0.003	.
miR-124a-3p	>0.05	0.029
miR-183-3p	.	0.046
miR-193b-5p	.	0.017
miR-30c-1-3p	0.033	>0.05
miR-378a-3p	0.021	.
miR-616-5p	0.017	.
miR-942-5p	0.042	.
miR-1255B-5p	0.046	.
miR-1257	0.05	0.036
miR-335-3p	.	0.045
miR-9-3p	.	0.012

Table S2. Biological processes obtained from DIANA-miRPath V3.0 involving the 41 miRNAs deregulated in CF cell lines.

GO Category	Biological process	p-value	genes (n)	miRNAs (n)
GO:0034641	cellular nitrogen compound metabolic process	3.37E-253	2255	35
GO:0010467	gene expression	5.49E-156	427	33
GO:0009058	biosynthetic process	6.50E-155	1822	35
GO:0006464	cellular protein modification process	4.12E-109	1107	35
GO:0044281	small molecule metabolic process	2.74E-108	1109	35
GO:0044403	symbiosis. encompassing mutualism through parasitism	1.05E-104	352	33
GO:0016032	viral process	6.76E-103	320	33
GO:0009056	catabolic process	4.37E-94	944	34
GO:0044267	cellular protein metabolic process	2.56E-82	292	33
GO:0000278	mitotic cell cycle	5.13E-78	260	33
GO:0048011	neurotrophin TRK receptor signaling pathway	2.09E-67	173	35
GO:0022607	cellular component assembly	6.85E-65	636	34
GO:0006950	response to stress	1.44E-60	996	35
GO:0034655	nucleobase-containing compound catabolic process	1.47E-58	461	34
GO:0065003	macromolecular complex assembly	1.25E-57	455	33
GO:0008150	biological process	4.34E-55	6076	35
GO:0061024	membrane organization	1.16E-50	316	33
GO:0038095	Fc-epsilon receptor signaling pathway	2.30E-44	106	33
GO:0008219	cell death	1.36E-42	443	35
GO:0016071	mRNA metabolic process	1.78E-41	136	31
GO:0016070	RNA metabolic process	2.08E-40	153	32
GO:0006461	protein complex assembly	5.92E-38	372	33
GO:0007596	blood coagulation	1.84E-37	226	34
GO:0006259	DNA metabolic process	1.62E-36	377	33
GO:0043687	post-translational protein modification	4.56E-32	101	32
GO:0035666	TRIF-dependent toll-like receptor signaling pathway	1.32E-27	54	27
GO:0038123	toll-like receptor TLR1:TLR2 signaling pathway	2.62E-27	51	25
GO:0038124	toll-like receptor TLR6:TLR2 signaling pathway	2.62E-27	51	25
GO:0007173	epidermal growth factor receptor signaling pathway	4.17E-26	120	34
GO:0034166	toll-like receptor 10 signaling pathway	4.21E-26	48	25
GO:0002756	MyD88-independent toll-like receptor signaling pathway	9.45E-24	54	27
GO:0044255	cellular lipid metabolic process	3.84E-23	84	30
GO:0034162	toll-like receptor 9 signaling pathway	3.97E-22	51	27
GO:0034146	toll-like receptor 5 signaling pathway	6.73E-22	48	25
GO:0002376	immune system process	2.25E-21	621	35
GO:0018279	protein N-linked glycosylation via asparagine	2.45E-21	67	32
GO:0034142	toll-like receptor 4 signaling pathway	3.25E-20	63	27
GO:0034138	toll-like receptor 3 signaling pathway	7.32E-20	54	27
GO:0006921	cellular component disassembly involved in execution phase of apoptosis	8.38E-20	36	27
GO:0006325	chromatin organization	1.15E-18	80	33
GO:0002224	toll-like receptor signaling pathway	1.76E-18	68	30
GO:0034134	toll-like receptor 2 signaling pathway	2.34E-18	51	25
GO:0019058	viral life cycle	4.13E-18	64	27
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	4.94E-18	45	28

GO Category	Biological process	p-value	genes (n)	miRNAs (n)
GO:0008543	fibroblast growth factor receptor signaling pathway	1.19E-17	103	34
GO:0006987	activation of signaling protein activity involved in unfolded protein response	2.03E-17	44	28
GO:0006369	termination of RNA polymerase II transcription	7.91E-17	36	25
GO:0051403	stress-activated MAPK cascade	2.08E-16	40	25
GO:0031124	mRNA 3'-end processing	6.17E-16	33	25
GO:0030203	glycosaminoglycan metabolic process	9.24E-16	59	28
GO:0034330	cell junction organization	1.42E-15	84	32
GO:0007077	mitotic nuclear envelope disassembly	1.78E-15	28	23
GO:0000086	G2/M transition of mitotic cell cycle	5.33E-15	82	30
GO:0034329	cell junction assembly	8.39E-15	41	28
GO:0000082	G1/S transition of mitotic cell cycle	1.45E-14	100	29
GO:0006091	generation of precursor metabolites and energy	2.28E-14	148	33
GO:0022618	ribonucleoprotein complex assembly	4.89E-14	83	30
GO:0045087	innate immune response	6.67E-14	290	35
GO:0006605	protein targeting	9.63E-14	139	30
GO:0006367	transcription initiation from RNA polymerase II promoter	2.54E-13	108	33
GO:0030168	platelet activation	3.70E-13	91	34
GO:0008380	RNA splicing	4.59E-13	160	31
GO:0006790	sulfur compound metabolic process	8.57E-13	127	29
GO:0002755	MyD88-dependent toll-like receptor signaling pathway	2.12E-12	53	26
GO:0051439	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	6.23E-12	41	27
GO:0055086	nucleobase-containing small molecule metabolic process	9.64E-12	38	24
GO:0006767	water-soluble vitamin metabolic process	8.57E-11	37	23
GO:0048015	phosphatidylinositol-mediated signaling	1.24E-10	68	32
GO:0051186	cofactor metabolic process	1.42E-10	110	30
GO:0051437	positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	2.20E-10	38	27
GO:0035872	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	2.23E-10	26	21
GO:0019083	viral transcription	2.46E-10	41	20
GO:0006913	nucleocytoplasmic transport	3.14E-10	158	30
GO:0000288	nuclear-transcribed mRNA catabolic process. deadenylation-dependent decay	4.43E-10	37	27
GO:0007049	cell cycle	4.43E-10	376	33
GO:0030198	extracellular matrix organization	5.65E-10	156	34
GO:0008286	insulin receptor signaling pathway	1.10E-09	82	29
GO:0097193	intrinsic apoptotic signaling pathway	1.44E-09	41	29
GO:0006766	vitamin metabolic process	1.46E-09	38	23
GO:0006397	mRNA processing	2.44E-09	227	32
GO:0031145	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	2.93E-09	45	27
GO:0006112	energy reserve metabolic process	3.87E-09	48	30
GO:0000184	nuclear-transcribed mRNA catabolic process. nonsense-mediated decay	5.27E-09	66	26
GO:0050900	leukocyte migration	5.99E-09	56	29
GO:0042592	homeostatic process	6.34E-09	303	32
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	7.25E-09	59	26
GO:0050690	regulation of defense response to virus by virus	8.38E-09	19	22

GO Category	Biological process	p-value	genes (n)	miRNAs (n)
GO:0016192	vesicle-mediated transport	1.24E-08	384	33
GO:0008645	hexose transport	1.31E-08	23	24
GO:0006892	post-Golgi vesicle-mediated transport	1.47E-08	30	26
GO:0006271	DNA strand elongation involved in DNA replication	1.69E-08	21	13
GO:1900740	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	3.64E-08	20	23
GO:0002576	platelet degranulation	4.97E-08	35	27
GO:0010827	regulation of glucose transport	7.01E-08	20	22
GO:0051436	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	7.42E-08	33	27
GO:0022617	extracellular matrix disassembly	8.02E-08	48	26
GO:0051604	protein maturation	8.20E-08	89	30
GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway	1.56E-07	16	15
GO:0000096	sulfur amino acid metabolic process	1.60E-07	18	14
GO:0097190	apoptotic signaling pathway	2.69E-07	62	30
GO:0006415	translational termination	3.82E-07	44	24
GO:0051084	'de novo' posttranslational protein folding	5.64E-07	24	21
GO:0006644	phospholipid metabolic process	5.64E-07	71	28
GO:0030204	chondroitin sulfate metabolic process	6.11E-07	25	19
GO:0007411	axon guidance	1.16E-06	179	34
GO:0032201	telomere maintenance via semi-conservative replication	1.47E-06	14	11
GO:0046474	glycerophospholipid biosynthetic process	1.50E-06	38	22
GO:0032481	positive regulation of type I interferon production	2.50E-06	32	26
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	2.52E-06	53	28
GO:0006928	cellular component movement	2.52E-06	50	31
GO:0007010	cytoskeleton organization	2.80E-06	246	34
GO:0019221	cytokine-mediated signaling pathway	3.22E-06	125	31
GO:0000398	mRNA splicing, via spliceosome	4.27E-06	108	31
GO:0006406	mRNA export from nucleus	4.29E-06	46	28
GO:0006366	transcription from RNA polymerase II promoter	4.38E-06	244	34
GO:0006629	lipid metabolic process	5.29E-06	436	35
GO:0007179	transforming growth factor beta receptor signaling pathway	5.42E-06	84	33
GO:0046209	nitric oxide metabolic process	5.59E-06	15	17
GO:0042339	keratan sulfate metabolic process	1.14E-05	17	18
GO:0001701	in utero embryonic development	1.34E-05	148	33
GO:0006661	phosphatidylinositol biosynthetic process	1.36E-05	31	25
GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	1.72E-05	17	21
GO:0032480	negative regulation of type I interferon production	1.72E-05	21	21
GO:0034660	ncRNA metabolic process	2.27E-05	14	15
GO:0060337	type I interferon signaling pathway	2.27E-05	34	23
GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle	2.31E-05	19	23
GO:0048870	cell motility	3.08E-05	199	33
GO:0060397	JAK-STAT cascade involved in growth hormone signaling pathway	3.14E-05	15	13
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	3.29E-05	33	25
GO:0008283	cell proliferation	3.70E-05	241	33

GO Category	Biological process	p-value	genes (n)	miRNAs (n)
GO:0006368	transcription elongation from RNA polymerase II promoter	4.61E-05	36	26
GO:0050999	regulation of nitric-oxide synthase activity	5.17E-05	15	17
GO:0048205	COPI coating of Golgi vesicle	5.28E-05	10	16
GO:0006521	regulation of cellular amino acid metabolic process	5.28E-05	24	20
GO:0006351	transcription. DNA-templated	5.28E-05	859	35
GO:0030968	endoplasmic reticulum unfolded protein response	8.18E-05	57	29
GO:0000375	RNA splicing. via transesterification reactions	0.000102049	19	20
GO:0050434	positive regulation of viral transcription	0.000103833	23	22
GO:0006488	dolichol-linked oligosaccharide biosynthetic process	0.000106306	22	21
GO:0043647	inositol phosphate metabolic process	0.000106306	22	22
GO:0042339	keratan sulfate biosynthetic process	0.000180241	14	17
GO:0050427	3'-phosphoadenosine 5'-phosphosulfate metabolic process	0.000224807	11	12
GO:0030148	sphingolipid biosynthetic process	0.000239673	23	18
GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	0.000345327	20	20
GO:0035338	long-chain fatty-acyl-CoA biosynthetic process	0.00049414	10	14
GO:0000722	telomere maintenance via recombination	0.000669146	15	12
GO:0007265	Ras protein signal transduction	0.001021521	47	26
GO:0006520	cellular amino acid metabolic process	0.001140156	147	30
GO:0008334	histone mRNA metabolic process	0.00118673	8	8
GO:0000209	protein polyubiquitination	0.001279147	67	29
GO:0044237	cellular metabolic process	0.001596324	61	26
GO:0043066	negative regulation of apoptotic process	0.001660219	272	34
GO:0034332	adherens junction organization	0.001846359	21	20
GO:0030521	androgen receptor signaling pathway	0.002037271	28	26
GO:0006399	tRNA metabolic process	0.002181761	64	24
GO:0060334	regulation of interferon-gamma-mediated signaling pathway	0.002263687	13	18
GO:0005975	carbohydrate metabolic process	0.002506841	334	33
GO:0007219	Notch signaling pathway	0.002510244	80	31
GO:0009615	response to virus	0.003090984	74	29
GO:0015949	nucleobase-containing small molecule interconversion	0.003324755	9	16
GO:0007050	cell cycle arrest	0.003324755	74	31
GO:0046134	pyrimidine nucleoside biosynthetic process	0.003556838	5	6
GO:0007009	plasma membrane organization	0.003556838	51	25
GO:0070830	tight junction assembly	0.003556838	25	28
GO:0006665	sphingolipid metabolic process	0.003902361	43	22
GO:0006006	glucose metabolic process	0.003961835	61	29
GO:0006283	transcription-coupled nucleotide-excision repair	0.004232824	23	17
GO:0006687	glycosphingolipid metabolic process	0.004232824	22	18
GO:0071377	cellular response to glucagon stimulus	0.004232824	17	23
GO:0009653	anatomical structure morphogenesis	0.004237345	40	26
GO:0051056	regulation of small GTPase mediated signal transduction	0.004238983	77	30
GO:0045216	cell-cell junction organization	0.004857154	32	27
GO:0000186	activation of MAPKK activity	0.004857154	38	28
GO:0043065	positive regulation of apoptotic process	0.005513545	173	33
GO:0075733	intracellular transport of virus	0.005865826	10	17
GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I. TAP-dependent	0.007387847	34	25
GO:0071456	cellular response to hypoxia	0.007756361	62	32

GO Category	Biological process	p-value	genes (n)	miRNAs (n)
GO:0006413	translational initiation	0.008707043	86	28
GO:0015758	glucose transport	0.008990645	31	25
GO:0033572	transferrin transport	0.009935887	16	17
GO:0006695	cholesterol biosynthetic process	0.011510426	24	22
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	0.012594171	35	25
GO:0071897	DNA biosynthetic process	0.012668295	21	15
GO:0006206	pyrimidine nucleobase metabolic process	0.013991932	12	11
GO:0007202	activation of phospholipase C activity	0.0156007	24	25
GO:0031293	membrane protein intracellular domain proteolysis	0.016987961	10	12
GO:0042059	negative regulation of epidermal growth factor receptor signaling pathway	0.017008235	22	23
GO:0030705	cytoskeleton-dependent intracellular transport	0.017307944	39	27
GO:0019432	triglyceride biosynthetic process	0.0174461	21	19
GO:0006986	response to unfolded protein	0.0174461	32	29
GO:0006501	C-terminal protein lipidation	0.018021323	12	13
GO:0043928	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	0.018465887	16	16
GO:0051028	mRNA transport	0.019343771	41	26
GO:0000098	sulfur amino acid catabolic process	0.022138392	5	6
GO:0019068	virion assembly	0.026967385	11	13
GO:0048208	COPII vesicle coating	0.026967385	11	16
GO:0006024	glycosaminoglycan biosynthetic process	0.029232789	20	17
GO:0051092	positive regulation of NF-kappaB transcription factor activity	0.030334674	74	27
GO:0019054	modulation by virus of host process	0.030511746	3	7
GO:0007249	I-kappaB kinase/NF-kappaB signaling	0.030511746	24	17
GO:0008285	negative regulation of cell proliferation	0.030511746	210	32
GO:0090382	phagosome maturation	0.032535694	16	16
GO:0006915	apoptotic process	0.033979822	315	35
GO:0046718	viral entry into host cell	0.037227481	12	16
GO:0006810	transport	0.038273379	1314	34
GO:2000145	regulation of cell motility	0.039498848	10	21
GO:0050796	regulation of insulin secretion	0.03958616	39	27
GO:0060333	interferon-gamma-mediated signaling pathway	0.040836329	32	24
GO:0070301	cellular response to hydrogen peroxide	0.041340222	33	23
GO:0034080	CENP-A containing nucleosome assembly	0.043284074	17	19
GO:0030574	collagen catabolic process	0.04607994	28	19
GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	0.046446249	42	29
GO:0051149	positive regulation of muscle cell differentiation	0.046795909	13	20
GO:0071479	cellular response to ionizing radiation	0.047111848	23	22

Table S3. Molecular functions obtained from DIANA-miRPath V3.0 involving the 41 miRNAs deregulated in CF cell lines.

GO Category	Molecular function	p-value	genes (n)	miRNAs (n)
GO:0043167	ion binding	2.61E-147	2469	35
GO:0019899	enzyme binding	4.12E-88	693	35
GO:0003674	molecular function	2.36E-76	6242	35
GO:0003723	RNA binding	7.63E-68	906	35
GO:0000988	protein binding transcription factor activity	1.35E-48	273	33
GO:0001071	nucleic acid binding transcription factor activity	2.76E-28	417	33
GO:0008092	cytoskeletal protein binding	2.44E-23	335	35
GO:0044822	poly(A) RNA binding	4.48E-23	731	35
GO:0030234	enzyme regulator activity	5.21E-17	336	34
GO:0032182	small conjugating protein binding	6.74E-08	50	26
GO:0008135	translation factor activity. nucleic acid binding	6.74E-08	61	28
GO:0008134	transcription factor binding	3.40E-05	245	33
GO:0003713	transcription coactivator activity	0.000609893	139	32
GO:0003714	transcription corepressor activity	0.000749689	110	32
GO:0016874	ligase activity	0.01191857	225	33
GO:0008289	lipid binding	0.015077687	215	32
GO:0030674	protein binding. bridging	0.040668335	58	29

Table S4. Cellular components obtained from DIANA-miRPath V3.0 involving the 41 miRNAs deregulated in CF cell lines.

GO Category	Cellular component	p-value	genes (n)	miRNAs (n)
GO:0043226	organelle	0	4471	35
GO:0005829	cytosol	3.53E-113	1361	35
GO:0005654	nucleoplasm	1.87E-108	700	34
GO:0043234	protein complex	2.13E-98	1700	35
GO:0005575	cellular component	6.02E-70	6289	35
GO:0005815	microtubule organizing center	1.21E-16	214	32
GO:0005925	focal adhesion	1.11E-06	246	34
GO:0005768	endosome	0.00022551	247	33
GO:0005788	endoplasmic reticulum lumen	0.002166475	70	29
GO:0005773	vacuole	0.002166475	112	32
GO:0043202	lysosomal lumen	0.003304427	25	19
GO:0000139	Golgi membrane	0.005445425	163	34
GO:0031093	platelet alpha granule lumen	0.034354719	16	23

Table S5. KEGG pathway analysis of the genes deriving from the protein-protein interaction analysis reported in Figure 5.

Description	observed gene count	background gene count	FDR	Genes
MicroRNAs in cancer	23	149	2.05e-08	CDK6.CDKN1A.CREBBP.DNMT3B.E2F3.EP300.FOXP1.GRB2.HMGA2.MCL1.MDM4.NOTCH1.NRAS.PIM1.PRKCE.RHOA.SHC1.SOS1.STAT3.STMN1.VEGFA.ZEB1.ZEB2
Endocrine resistance	16	95	2.62e-06	CDKN1A.E2F3.ESR1.GRB2.IGF1R.JAG1.JAG2.MAPK3.MAPK8.NOTCH1.NRAS.PIK3R1.RPS6KB1.SHC1.SOS1.SP1
EGFR tyrosine kinase inhibitor resistance	14	78	6.62e-06	GRB2.IGF1R.IL6R.KDR.MAPK3.NF1.NRAS.NRG1.PIK3R1.RPS6KB1.SHC1.SOS1.STAT3.VEGFA
FoxO signalling pathway	17	130	8.77e-06	BCL6.CCNB1.CDKN1A.CREBBP.EP300.GABARAPL1.GRB2.IGF1R.MAPK3.MAPK8.NRAS.PIK3R1.PRKAA2.SETD7.SMAD2.SOS1.STAT3
Hepatitis B	18	142	8.77e-06	ATP6AP1.CDK6.CDKN1A.CREB3L2.CREBBP.DDX3X.E2F3.EP300.GRB2.MAP3K1.MAPK3.MAPK8.MAVS.NFATC1.NRAS.PIK3R1.STAT2.STAT3
Pathways in cancer	36	515	8.77e-06	CBL.CDK6.CDKN1A.CREBBP.E2F3.EP300.ESR1.ETS1.GLI3.GNA13.GRB2.IGF1R.IL6R.ITGA3.ITGB1.JAG1.JAG2.KIT.LAMC1.LRP6.MAPK3.MAPK8.NOTCH1.NRAS.PIK3R1.PIM1.RALGDS.RHOA.ROCK2.RPS6KB1.SMAD2.SOS1.SP1.STAT2.STAT3.VEGFA
Proteoglycans in cancer	21	195	8.77e-06	CBL.CDKN1A.ESR1.GRB2.IGF1R.ITGB1.KDR.MAPK3.MSN.NRAS.PIK3R1.PTPN11.RHOA.ROCK2.RPS6KB1.RRAS.SMAD2.SOS1.STAT3.TFAP4.VEGFA
Breast cancer	18	147	8.77e-06	CDK6.CDKN1A.E2F3.ESR1.GRB2.IGF1R.JAG1.JAG2.KIT.LRP6.MAPK3.NOTCH1.NRAS.PIK3R1.RPS6KB1.SHC1.SOS1.SP1
Human papillomavirus infection	25	317	6.93e-05	CDK6.CDKN1A.CREB3L2.CREBBP.EP300.GRB2.HLA-A.HLA-C.INADL.ITGA3.ITGB1.JAG1.LAMC1.MAML1.MAPK3.NOTCH1.NRAS.PIK3R1.PPP2CB.RPS6KB1.SOS1.STAT2.TSC1.TYK2.VEGFA
Ras signalling pathway	20	228	0.0001	ETS1.GRB2.IGF1R.KDR.KIT.MAPK3.MAPK8.NF1.NRAS.NTRK2.PIK3R1.PTPN11.RAB5B.RALGDS.REL.RHOA.RRAS.SHC1.SOS1.VEGFA. PTPN11=Shp2; IGF1R=RTK; kit=rtk; REL=NFKB; KDR=RTk; NTRK2=RTK
Choline metabolism in cancer	13	98	0.0001	GRB2.MAPK3.MAPK8.NRAS.PIK3R1.RALGDS.RPS6KB1.SLC22A5.SLC44A2.SOS1.SP1.TSC1.WASF3
Renal cell carcinoma	11	68	0.0001	CDKN1A.CREBBP.EP300.ETS1.GRB2.MAPK3.NRAS.PIK3R1.PTPN11.SOS1.VEGFA
Adherens junction	11	71	0.0001	CREBBP.CTNND1.EP300.IGF1R.MAP3K7.MAPK3.PTPRB.RHOA.SMAD2.SNAI2.WASF3

Description	observed gene count	background gene count	FDR	Genes
Pancreatic cancer	11	74	0.0002	CDK6.CDKN1A.E2F3.MAPK3.MAPK8.PIK3R1.RALGDS.RPS6KB1.SMAD2.STAT3.VEGFA
PI3K-Akt signalling pathway	25	348	0.0002	CDK6.CDKN1A.CREB3L2.GRB2.IGF1R.IL6R.ITGA3.ITGB1.KDR.KIT.LAMC1.MAPK3.MCL1.MYB.NRAS.NTRK2.PHLPP2.PIK3R1.PPP2CB.PRKAA2.RPS6KB1.SOS1.TSC1.VEGFA.YWHAG
Autophagy - animal	14	125	0.0002	AKT1S1.GABARAPL1.IGF1R.MAP3K7.MAPK3.MAPK8.NRAS.PIK3R1.PPP2CB.PRKAA2.RAB7A.RPS6KB1.RRAS.TSC1
Chronic myeloid leukemia	11	76	0.0002	CBL.CDK6.CDKN1A.E2F3.GRB2.MAPK3.NRAS.PIK3R1.PTPN11.SHC1.SOS1
Kaposi's sarcoma-associated herpesvirus infection	17	183	0.0002	CDK6.CDKN1A.CREBBP.E2F3.EP300.GABARAPL1.HLA-A.HLA-C.MAPK3.MAPK8.NFATC1.NRAS.PIK3R1.STAT2.STAT3.TYK2.VEGFA
Tight junction	16	167	0.0002	ACTR2.F11R.INADL.ITGB1.MAP3K1.MAPK8.MSN.MYH9.PPP2CB.PRKAA2.PRKE.RAB8B.RHOA.ROCK2.TJAP1.TJP2
Prostate cancer	12	97	0.0003	CDKN1A.CREB3L2.CREBBP.E2F3.EP300.GRB2.IGF1R.MAPK3.NRAS.PIK3R1.SOS1.ZEB1
Neurotrophin signalling pathway	13	116	0.0003	GRB2.IRAK1.IRAK4.MAP3K1.MAPK3.MAPK8.NRAS.NTRK2.PIK3R1.PTPN11.RHOA.SHC1.SOS1
ErbB signalling pathway	11	83	0.0003	CBL.CDKN1A.GRB2.MAPK3.MAPK8.NRAS.NRG1.PIK3R1.RPS6KB1.SHC1.SOS1
Glioma	10	68	0.0003	CDK6.CDKN1A.E2F3.GRB2.IGF1R.MAPK3.NRAS.PIK3R1.SHC1.SOS1
Prolactin signalling pathway	10	69	0.0003	ESR1.GRB2.MAPK3.MAPK8.NRAS.PIK3R1.SHC1.SOCS6.SOS1.STAT3
Cellular senescence	15	156	0.0003	CCNB1.CDK6.CDKN1A.E2F3.ETS1.HLA-A.HLA-C.MAPK3.NFATC1.NRAS.PIK3R1.RRAS.SMAD2.TRAF3IP2.TSC1
Colorectal cancer	11	85	0.0003	CDKN1A.GRB2.MAPK3.MAPK8.NRAS.PIK3R1.RALGDS.RHOA.RPS6KB1.SMAD2.SOS1
Jak-STAT signalling pathway	15	160	0.0004	CDKN1A.CREBBP.EP300.GRB2.IL11.IL6R.MCL1.PIK3R1.PIM1.PTPN11.SOCS6.SOS1.STAT2.STAT3.TYK2
Viral carcinogenesis	16	183	0.0005	CDK6.CDKN1A.CREB3L2.CREBBP.DDX3X.EP300.GRB2.HLA-A.HLA-C.MAPK3.NRAS.PIK3R1.REL.RHOA.STAT3.YWHAG
Hepatitis C	13	131	0.0007	CDKN1A.GRB2.MAPK3.MAPK8.MAVS.NRAS.PIK3R1.PPARA.PPP2CB.SOS1.STAT2.STAT3.TYK2
HIF-1 signalling pathway	11	98	0.0009	CDKN1A.CREBBP.EP300.IGF1R.IL6R.LDHA.MAPK3.PIK3R1.RPS6KB1.STAT3.VEGFA
Focal adhesion	16	197	0.0009	ARHGAP5.GRB2.IGF1R.ITGA3.ITGB1.KDR.LAMC1.MAPK3.MAPK8.PARVB.PIK3R1.RHOA.ROCK2.SHC1.SOS1.VEGFA
TGF-beta signalling pathway	10	83	0.0009	CREBBP.EP300.MAPK3.PPP2CB.RHOA.RPS6KB1.SMAD2.SMAD5.SMURF2.SP1
Acute myeloid leukemia	9	66	0.0009	GRB2.KIT.MAPK3.NRAS.PIK3R1.PIM1.RPS6KB1.SOS1.STAT3

Description	observed gene count	background gene count	FDR	Genes
Non-small cell lung cancer	9	66	0.0009	CDK6.CDKN1A.E2F3.GRB2.MAPK3.NRAS.PIK3R1.SOS1.STAT3
MAPK signalling pathway	20	293	0.0011	ELK4.GRB2.IGF1R.IRAK1.IRAK4.KDR.KIT.MAP3K1.MAP3K7.MAPK3.MAPK8.NF1.NFATC1.NRAS.NTRK2.RRAS.SOS1.STMN1.TAOK1.VEGFA
HTLV-I infection	18	250	0.0012	CANX.CDC23.CDKN1A.CREBBP.E2F3.ELK4.EP300.ETS1.HLA-A.HLA.MAP3K1.MAPK8.MYB.NFATC1.NRAS.PIK3R1.RRAS.SMAD2
Hepatocellular carcinoma	14	163	0.0012	CDK6.CDKN1A.DPF3.E2F3.GRB2.IGF1R.LRP6.MAPK3.NRAS.PIK3R1.RPS6KB1.SHC1.SMAD2.SOS1
Phospholipase D signalling pathway	13	145	0.0013	GNA13.GRB2.KIT.MAPK3.NRAS.PIK3R1.PTPN11.RALGDS.RHOA.RRAS.SHC1.SOS1.TSC1
Endocytosis	17	242	0.0023	ARFGEF2.CBL.GIT2.HLA-A.HLA-C.IGF1R.LDLRAP1.PSD3.RAB22A.RAB5B.RAB7A.RHOA.SMAD2.SMURF2.VPS35.VPS4B.WIPF1
AGE-RAGE signalling pathway in diabetic complications	10	98	0.0026	MAPK3.MAPK8.NFATC1.NRAS.PIK3R1.PIM1.PRKCE.SMAD2.STAT3.VEGFA
Notch signalling pathway	7	48	0.0028	CREBBP.EP300.JAG1.JAG2.MAML1.NOTCH1.PSENEN
Influenza A	13	168	0.0044	ADAR.CREBBP.EP300.IL18.IRAK4.IVNS1ABP.KPNA2.MAPK3.MAPK8.MAVS.PIK3R1.STAT2.TYK2
mTOR signalling pathway	12	148	0.0047	AKT1S1.GRB2.IGF1R.LRP6.MAPK3.NRAS.PIK3R1.PRKAA2.RHOA.RPS6KB1.SOS1.TSC1
Toxoplasmosis	10	109	0.0051	IRAK1.IRAK4.ITGB1.LAMC1.MAP3K7.MAPK3.MAPK8.PPIF.STAT3.TYK2
cAMP signalling pathway	14	195	0.0052	CREB3L2.CREBBP.EP300.GLI3.GRIA2.MAPK3.MAPK8.MC2R.NFATC1.PIK3R1.PPARA.RHOA.ROCK2.RRAS
Apelin signalling pathway	11	133	0.0061	GABARAPL1.GNA13.JAG1.MAPK3.NRAS.PRKAA2.PRKCE.RPS6KB1.RRAS.RYR3.SMAD2
Measles	11	133	0.0061	ADAR.CDK6.IRAK1.IRAK4.MAP3K7.MAVS.MSN.PIK3R1.STAT2.STAT3.TYK2
Insulin signalling pathway	11	134	0.0062	CBL.GRB2.MAPK3.MAPK8.NRAS.PIK3R1.PRKAA2.RPS6KB1.SHC1.SOS1.TSC1
Sphingolipid signalling pathway	10	116	0.0071	CERS2.GNA13.MAPK3.MAPK8.NRAS.PIK3R1.PPP2CB.PRKCE.RHOA.ROCK2
Signalling pathways regulating pluripotency of stem cells	11	138	0.0074	GRB2.IGF1R.MAPK3.MEIS1.NRAS.PCGF2.PIK3R1.REST.SMAD2.SMAD5.STAT3