

Table SI. Cumulative analysis of the molecular pathways altered by the 20 selected miRNAs.

No.	KEGG pathway	P-value	No. of genes	No. of miRNAs		#	KEGG pathway	P-value	No. of genes	No. of miRNAs
1	Protein processing in endoplasmic reticulum (hsa04141)	2.35E-06	82	18		30	HIF-1 signaling pathway (hsa04066)	0.018482	44	15
2	Proteoglycans in cancer (hsa05205)	7.25E-09	90	17		31	Bladder cancer (hsa05219)	0.031409	20	15
3	Adherens junction (hsa04520)	1.84E-08	42	17		32	Regulation of actin cytoskeleton (hsa04810)	0.031409	77	15
4	FoxO signaling pathway (hsa04068)	4.91E-05	65	17		33	Non-small cell lung cancer (hsa05223)	0.035274	24	15
5	Endocytosis (hsa04144)	0.000134	90	17		34	Melanoma (hsa05218)	0.043902	29	15
6	Pathways in cancer (hsa05200)	0.000203	150	17		35	Renal cell carcinoma (hsa05211)	1.46E-06	35	14
7	Focal adhesion (hsa04510)	0.000354	89	17		36	p53 signaling pathway (hsa04115)	5.19E-05	38	14
8	HTLV-I infection (hsa05166)	0.000738	104	17		37	TNF signaling pathway (hsa04668)	0.000512	50	14
9	RNA transport (hsa03013)	0.00074	71	17		38	Central carbon metabolism in cancer (hsa05230)	0.003672	28	14
10	Insulin signaling pathway (hsa04910)	0.024143	57	17		39	mRNA surveillance pathway (hsa03015)	0.036725	40	14
11	PI3K-Akt signaling pathway (hsa04151)	0.040504	120	17		40	ECM-receptor interaction (hsa04512)	7.78E-15	34	13
12	Viral carcinogenesis (hsa05203)	8.36E-11	89	16		41	Small cell lung cancer (hsa05222)	7.16E-05	45	13
13	Ubiquitin mediated proteolysis (hsa04120)	5.71E-07	70	16		42	Bacterial invasion of epithelial cells (hsa05100)	8.05E-05	39	13
14	Hepatitis B (hsa05161)	3.93E-05	64	16		43	Pancreatic cancer (hsa05212)	0.000512	35	13
15	Chronic myeloid leukemia (hsa05220)	5.00E-05	39	16		44	Thyroid cancer (hsa05216)	0.009723	14	13
16	Glioma (hsa05214)	8.05E-05	32	16		45	Transcriptional misregulation in cancer (hsa05202)	0.031409	66	13
17	TGF-beta signaling pathway (hsa04350)	0.000203	39	16		46	Colorectal cancer (hsa05210)	3.93E-05	34	12
18	Prostate cancer (hsa05215)	0.000738	44	16		47	Progesterone-mediated oocyte maturation (hsa04914)	0.038369	37	12
19	Epstein-Barr virus infection (hsa05169)	0.003601	84	16		48	AMPK signaling pathway (hsa04152)	0.039664	52	12
20	Neurotrophin signaling pathway (hsa04722)	0.01193	50	16		49	Shigellosis (hsa05131)	0.005649	31	11
21	Huntington's disease (hsa05016)	0.015573	67	16		50	Lysine degradation (hsa00310)	5.33E-11	25	9
22	Thyroid hormone signaling pathway (hsa04919)	0.017277	48	16		51	Fatty acid metabolism (hsa01212)	0.034898	16	9
23	Pluripotency of stem cells (hsa04550)	0.043902	54	16		52	Sphingolipid metabolism (hsa00600)	0.041055	18	9
24	Hippo signaling pathway (hsa04390)	3.24E-10	70	15		53	Steroid biosynthesis (hsa00100)	0.006376	9	6
25	Cell cycle (hsa04110)	6.49E-10	68	15		54	Sulfur metabolism (hsa00920)	0.000804	6	5
26	Oocyte meiosis (hsa04114)	7.00E-09	56	15		55	Glycosaminoglycan biosynthesis - heparan sulfate / heparin (hsa00534)	0.019251	10	5
27	Sphingolipid signaling pathway (hsa04071)	0.001091	52	15		56	Fatty acid biosynthesis (hsa00061)	5.24E-08	6	4
28	Endometrial cancer (hsa05213)	0.003501	25	15		57	Sulfur relay system (hsa04122)	0.017056	6	3
29	Spliceosome (hsa03040)	0.017277	55	15						

The cancer-related molecular pathways are indicated in bold font.