Four microRNAs Signature for Survival Prognosis in Colon Cancer using TCGA Data

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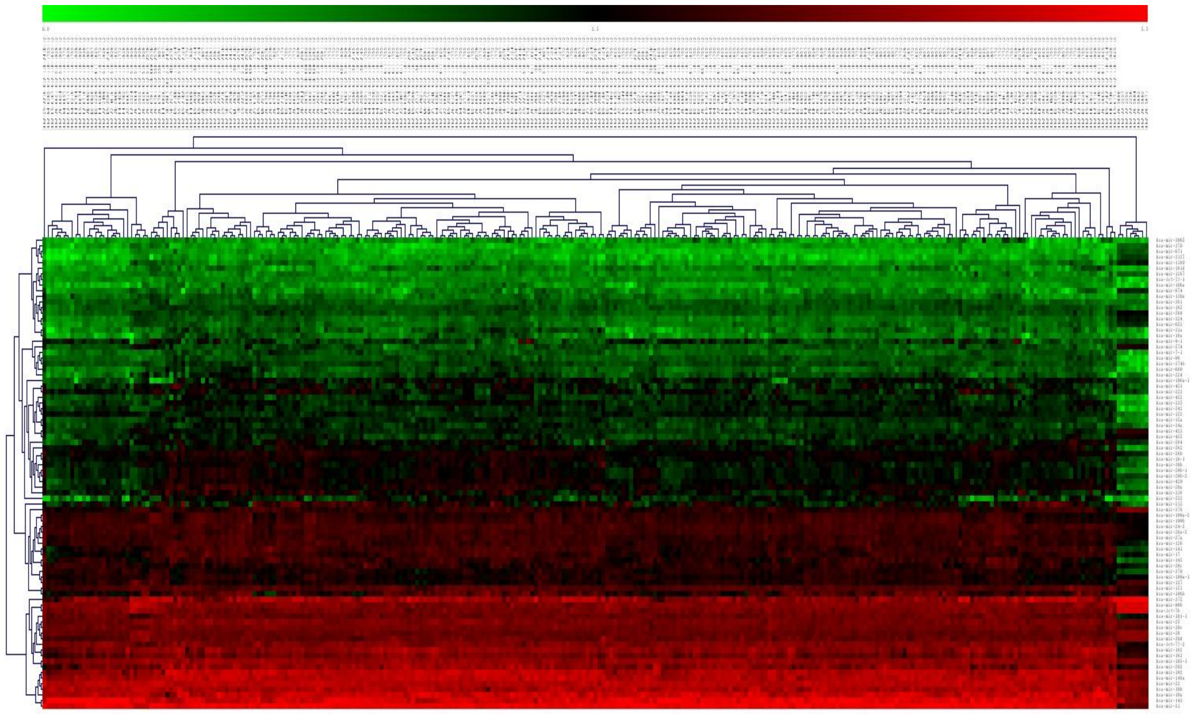
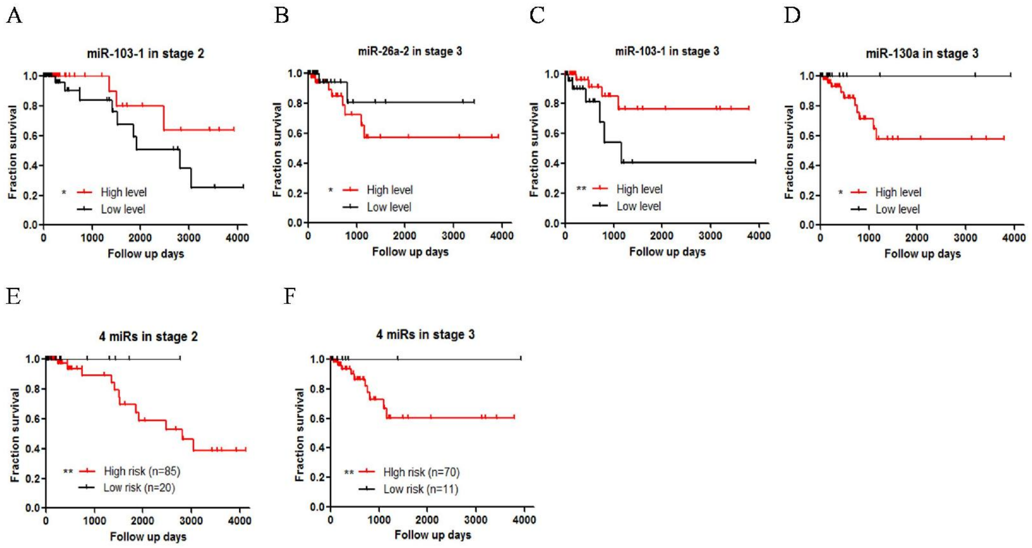
Supplemental figure s1



Supplemental figure s1. Hierarchical clustering of 84-miRNAs to classify cancer samples and non-cancer samples.

Supplemental figure s2



Supplemental figure s2. Four miRNAs signature in colon cancer stage 2 and stage 3. In the Kaplan-Meier survival analysis of four miRNAs one by one, results showed that only miR-103-1 was significant in stage 2 (A), while miR-26a-2, miR-103-1 and miR-130a were significant in stage 3 of patient survival (B, C and D). In the risk factor ranking aspect, score 2-4 was ranked as high risk, and score below 2 as low risk. Data showed the four miRNAs signature was significant both in stage 2 and stage 3 (E and F, **p<0.01).

Supplemental table s1. Summary of 84 microRNAs expression level

microRNA	Mean of Tumor (log, n=268)	Mean of Nontumor (log, n=8)	Expression level in colon cancer
hsa-mir-21	5.31±0.02	3.57±0.03	Up
hsa-mir-101-1	3.75±0.03	2.31±0.02	Up
hsa-mir-379	2.89±0.03	1.7±0.01	Up
hsa-mir-98	1.71±0.03	0.5±0.03	Up
hsa-mir-542	2.18±0.03	0.6±0.04	Up
hsa-mir-335	2.26±0.04	0.96±0.03	Up
hsa-mir-452	2.06±0.04	0.68±0.04	Up
hsa-mir-141	3.15±0.04	1.87±0.01	Up
hsa-mir-182	4.16±0.04	2.87±0.02	Up
hsa-mir-142	3.07±0.05	1.49±0.03	Up
hsa-let-7f-2	4.01±0.03	2.84±0.03	Up
hsa-mir-29b-1	2.48±0.04	1.12±0.03	Up
hsa-mir-582	2.43±0.04	1.05±0.04	Up
hsa-mir-20a	2.69±0.05	1.29±0.03	Up
hsa-mir-203	4.09±0.05	3.06±0.03	Up
hsa-mir-126	3.16±0.03	2.27±0.03	Up
hsa-mir-552	2.12±0.08	0.81±0.04	Up
hsa-mir-429	2.53±0.05	1.6±0.03	Up
hsa-mir-152	2.26±0.03	1.3±0.02	Up
hsa-mir-374b	1.87±0.03	0.7±0.04	Up
hsa-mir-15a	2.09±0.03	1.11±0.04	Up
hsa-mir-660	1.67±0.04	0.61±0.04	Up
hsa-mir-183	3.85±0.04	3.18±0.02	Up
hsa-mir-10a	4.82±0.04	4.02±0.03	Up
hsa-mir-16-1	2.61±0.03	1.64±0.03	Up
hsa-mir-17	3.08±0.04	2.28±0.03	Up
hsa-mir-29b-2	2.49±0.04	1.91±0.01	Up
hsa-mir-148a	4.63±0.04	3.79±0.03	Up
hsa-mir-29c	2.99±0.04	2.3±0.03	Up
hsa-mir-199b	3.17±0.03	2.62±0.02	Up
hsa-mir-30b	2.44±0.04	1.64±0.04	Up
hsa-mir-7-1	1.65±0.04	0.88±0.05	Up
hsa-mir-181d	1.28±0.05	0.75±0.02	Up
hsa-mir-196a-1	2.24±0.07	1.78±0.02	Up
hsa-mir-199a-1	2.84±0.03	2.52±0.01	Up
hsa-mir-192	4.6±0.05	4.06±0.02	Up
hsa-mir-223	2.41±0.06	1.8±0.03	Up
hsa-mir-215	2.64±0.08	1.51±0.06	Up
hsa-mir-151	3.45±0.03	2.96±0.02	Up
hsa-mir-451	2.28±0.06	1.7±0.03	Up
hsa-mir-199a-2	3.07±0.03	2.69±0.01	Up
hsa-mir-143	5.14±0.05	4.24±0.05	Up
hsa-mir-26b	2.74±0.03	2.22±0.02	Up
hsa-mir-33a	1.49±0.06	0.95±0.05	Up
hsa-mir-10b	4.52±0.03	4.01±0.03	Up
hsa-mir-338	2.51±0.06	1.99±0.03	Up
hsa-mir-224	1.8±0.05	1.35±0.04	Up
hsa-mir-27a	3.16±0.03	2.63±0.02	Up
hsa-mir-25	3.94±0.03	3.68±0.01	Up
hsa-mir-24-2	3.29±0.02	2.7±0.02	Up
hsa-mir-196b	3.16±0.07	2.87±0.04	Up
hsa-mir-106a	1.06±0.04	0.58±0.04	Up
hsa-mir-22	4.67±0.02	4.22±0.02	Up
hsa-mir-30e	3.86±0.02	3.47±0.02	Up
hsa-mir-3065	1.01±0.05	0.76±0.02	Up
hsa-mir-34a	2.02±0.04	1.51±0.04	Up
hsa-mir-26a-2	3.23±0.02	2.78±0.03	Up
hsa-mir-381	1.63±0.03	1.43±0.01	Up
hsa-mir-130a	1.41±0.04	1.2±0.03	Up
hsa-mir-18a	1.35±0.06	0.87±0.05	Up
hsa-let-7f-1	1.23±0.02	0.59±0.04	Up
hsa-mir-9-1	2.01±0.06	1.85±0.01	Up
hsa-mir-103-1	4.22±0.03	3.96±0.02	Up
hsa-mir-185	1.77±0.03	1.38±0.03	Up
hsa-mir-584	2.38±0.06	2±0.02	Down
hsa-let-7b	3.91±0.03	5.03±0.01	Down

hsa-mir-28	3.71±0.02	4.12±0.01	Down
hsa-mir-30d	3.7±0.03	4.09±0.01	Down
hsa-mir-423	2.14±0.03	3.06±0.01	Down
hsa-mir-375	4.29±0.06	5.4±0.01	Down
hsa-mir-378	3.02±0.04	3.94±0.01	Down
hsa-mir-589	1.72±0.03	2.49±0.01	Down
hsa-mir-455	2.1±0.04	2.73±0.01	Down
hsa-mir-127	2.87±0.04	3.37±0.01	Down
hsa-mir-574	1.73±0.04	2.87±0.01	Down
hsa-mir-324	1.45±0.03	2.29±0.01	Down
hsa-mir-1180	1.1±0.04	2.21±0.01	Down
hsa-mir-874	1.24±0.05	2.11±0.01	Down
hsa-mir-3127	0.82±0.04	1.88±0.02	Down
hsa-mir-671	0.81±0.03	1.67±0.01	Down
hsa-mir-370	0.88±0.04	1.56±0.01	Down
hsa-mir-1287	1.18±0.03	1.62±0.01	Down
hsa-mir-652	1.46±0.04	2.1±0.01	Down
hsa-mir-99b	4.05±0.03	5.08±0.01	Down

Supplemental table s2. Four miRNAs signature for survival analysis

Patients	Status(dead =1, alive=0)	Follow up days	miR-148a	miR-26a-2	miR-130a	miR-103-1	miRNA Index
TCGA-G4-6626	1	1422	1	1	1	1	4
TCGA-G4-6294	1	858	1	1	1	1	4
TCGA-AZ-6608	1	59	1	1	1	1	4
TCGA-AZ-6606	1	357	1	1	1	1	4
TCGA-AZ-6603	1	899	1	1	1	1	4
TCGA-AZ-6600	1	368	1	1	1	1	4
TCGA-AZ-6599	1	206	1	1	1	1	4
TCGA-DM-A1D4	1	2821	1	1	1	1	4
TCGA-DM-A28G	1	1849	1	1	1	1	4
TCGA-DM-A1D6	1	1518	1	1	1	1	4
TCGA-DM-A0XF	1	1162	1	1	1	1	4
TCGA-DM-A288	1	427	1	1	1	1	4
TCGA-DM-A1D8	1	383	1	1	1	1	4
TCGA-DM-A1D7	1	0	1	1	1	1	4
TCGA-DM-A282	0	4122	1	1	1	1	4
TCGA-G4-6625	0	2673	1	1	1	1	4
TCGA-G4-6306	0	1359	1	1	1	1	4
TCGA-A6-2672	0	503	1	1	1	1	4
TCGA-G4-6295	0	254	1	1	1	1	4
TCGA-A6-6138	0	182	1	1	1	1	4
TCGA-A6-6649	0	147	1	1	1	1	4
TCGA-CM-6680	0	91	1	1	1	1	4
TCGA-NH-A6GC	0	40	1	1	1	1	4
TCGA-AA-3496	0	31	1	1	1	1	4
TCGA-F4-6806	0	20	1	1	1	1	4
TCGA-F4-6808	0	14	1	1	1	1	4
TCGA-4N-A93T	0	8	1	1	1	1	4
TCGA-CM-5862	1	153	1	1	1	0	3
TCGA-AZ-6598	1	1503	1	1	1	0	3
TCGA-A6-A565	1	494	1	1	1	0	3
TCGA-5M-AAT6	1	290	1	1	1	0	3
TCGA-DM-A28C	1	2475	1	1	1	0	3
TCGA-DM-A1DB	1	1348	1	1	1	0	3
TCGA-DM-A28F	1	1094	1	1	1	0	3
TCGA-DM-A1D9	0	3920	1	1	1	0	3
TCGA-DM-A1D0	0	3625	1	1	1	0	3
TCGA-5M-AATE	0	1200	1	1	1	0	3
TCGA-G4-6317	0	894	1	1	1	0	3
TCGA-G4-6320	0	678	1	1	1	0	3
TCGA-CK-4947	0	534	1	1	1	0	3
TCGA-D5-5537	0	456	1	1	1	0	3
TCGA-AU-3779	0	441	1	1	1	0	3
TCGA-QL-A97D	0	295	1	1	1	0	3
TCGA-D5-6529	0	260	1	1	1	0	3
TCGA-CM-6172	0	212	1	1	1	0	3
TCGA-AY-A8YK	0	209	1	1	1	0	3
TCGA-G4-6323	0	201	1	1	1	0	3
TCGA-A6-6137	0	195	1	1	1	0	3
TCGA-A6-6650	0	173	1	1	1	0	3
TCGA-NH-A6GB	0	170	1	1	1	0	3
TCGA-NH-A8F7	0	158	1	1	1	0	3
TCGA-A6-6141	0	130	1	1	1	0	3
TCGA-AD-6888	0	128	1	1	1	0	3

TCGA-A6-6140	0	125	1	1	1	0	3
TCGA-D5-6532	0	107	1	1	1	0	3
TCGA-D5-6535	0	10	1	1	1	0	3
TCGA-T9-A92H	0	0	1	1	1	0	3
TCGA-F4-6461	0	0	1	1	1	0	3
TCGA-AA-3511	0	0	1	1	1	0	3
TCGA-G4-6298	1	715	0	1	1	1	3
TCGA-AZ-6605	1	159	0	1	1	1	3
TCGA-AZ-6601	1	3042	0	1	1	1	3
TCGA-AZ-5403	1	1910	0	1	1	1	3
TCGA-AZ-4616	1	156	0	1	1	1	3
TCGA-AZ-4323	1	43	0	1	1	1	3
TCGA-A6-4105	1	442	1	0	1	1	3
TCGA-DM-A28A	1	805	1	0	1	1	3
TCGA-DM-A0XD	1	743	0	1	1	1	3
TCGA-DM-A280	1	236	0	1	1	1	3
TCGA-DM-A28E	0	3530	0	1	1	1	3
TCGA-G4-6303	0	1882	0	1	1	1	3
TCGA-G4-6628	0	1606	0	1	1	1	3
TCGA-G4-6310	0	1205	0	1	1	1	3
TCGA-G4-6586	0	741	0	1	1	1	3
TCGA-CM-4751	0	607	0	1	1	1	3
TCGA-G4-6321	0	572	0	1	1	1	3
TCGA-A6-2675	0	515	0	1	1	1	3
TCGA-CM-6164	0	487	0	1	1	1	3
TCGA-CM-5861	0	335	0	1	1	1	3
TCGA-A6-5661	0	306	0	1	1	1	3
TCGA-CM-5863	0	304	0	1	1	1	3
TCGA-CM-5860	0	304	0	1	1	1	3
TCGA-A6-5665	0	286	0	1	1	1	3
TCGA-D5-6530	0	271	1	1	0	1	3
TCGA-A6-6648	0	253	1	1	0	1	3
TCGA-NH-A6GA	0	182	1	0	1	1	3
TCGA-A6-6654	0	178	0	1	1	1	3
TCGA-A6-6782	0	164	0	1	1	1	3
TCGA-NH-A8F7	0	158	1	0	1	1	3
TCGA-3L-AA1B	0	154	1	0	1	1	3
TCGA-CM-6677	0	153	0	1	1	1	3
TCGA-CM-6676	0	153	0	1	1	1	3
TCGA-CM-6674	0	150	0	1	1	1	3
TCGA-D5-6929	0	146	1	0	1	1	3
TCGA-CM-6679	0	122	0	1	1	1	3
TCGA-CM-6678	0	122	0	1	1	1	3
TCGA-D5-6920	0	112	1	0	1	1	3
TCGA-D5-6924	0	89	1	0	1	1	3
TCGA-CK-6747	0	89	1	0	1	1	3
TCGA-F4-6703	0	56	0	1	1	1	3
TCGA-F4-6704	0	47	0	1	1	1	3
TCGA-F4-6855	0	42	0	1	1	1	3
TCGA-F4-6809	0	39	0	1	1	1	3
TCGA-AD-6901	0	31	0	1	1	1	3
TCGA-AA-3489	0	31	0	1	1	1	3
TCGA-D5-5539	0	30	0	1	1	1	3
TCGA-D5-6932	0	19	0	1	1	1	3
TCGA-F4-6854	0	16	1	0	1	1	3
TCGA-AD-6963	0	3	0	1	1	1	3
TCGA-AD-6548	0	3	0	1	1	1	3
TCGA-AD-5900	0	2	0	1	1	1	3
TCGA-F4-6570	0	0	0	1	1	1	3
TCGA-F4-6569	0	0	0	1	1	1	3
TCGA-F4-6460	0	0	1	0	1	1	3
TCGA-F4-6459	0	0	0	1	1	1	3
TCGA-A6-A566	1	758	0	1	1	0	2
TCGA-DM-A1DA	1	228	1	0	1	0	2
TCGA-DM-A1HB	0	3786	0	1	1	0	2
TCGA-DM-A0X9	0	3429	1	0	1	0	2
TCGA-DM-A28H	0	3423	1	0	1	0	2
TCGA-CK-4948	0	3116	0	1	1	0	2
TCGA-DM-A28K	0	2835	1	0	1	0	2
TCGA-G4-6299	0	2077	0	1	1	0	2
TCGA-WS-AB45	0	2038	1	0	1	0	2
TCGA-A6-A56B	0	1595	1	0	1	0	2
TCGA-G4-6307	0	1485	0	1	1	0	2
TCGA-CK-5912	0	1466	1	1	0	0	2
TCGA-CK-4950	0	1227	1	1	0	0	2
TCGA-G4-6311	0	1112	0	1	1	0	2
TCGA-G4-6315	0	937	0	1	1	0	2
TCGA-RU-A8FL	0	921	1	0	1	0	2
TCGA-G4-6317	0	894	0	1	1	0	2
TCGA-QG-A5YV	0	821	1	0	1	0	2
TCGA-G4-6588	0	644	0	1	1	0	2

TCGA-A6-5656	0	462	0	1	1	0	2
TCGA-A6-5656	0	462	0	1	1	0	2
TCGA-QG-A5Z2	0	449	1	0	1	0	2
TCGA-QG-A5YW	0	399	1	0	1	0	2
TCGA-A6-5660	0	342	0	1	1	0	2
TCGA-CM-5349	0	335	0	1	1	0	2
TCGA-CM-5868	0	304	0	1	1	0	2
TCGA-D5-6536	0	287	1	1	0	0	2
TCGA-CM-6169	0	243	0	1	1	0	2
TCGA-CM-6170	0	242	0	1	1	0	2
TCGA-D5-6534	0	241	0	1	1	0	2
TCGA-AY-A71X	0	235	1	0	1	0	2
TCGA-AY-5543	0	230	1	1	0	0	2
TCGA-CM-6165	0	212	0	1	1	0	2
TCGA-CM-6162	0	212	0	1	1	0	2
TCGA-CM-6171	0	182	1	1	0	0	2
TCGA-A6-6650	0	173	1	0	1	0	2
TCGA-A6-6650	0	173	1	0	1	0	2
TCGA-AY-A69D	0	168	1	0	1	0	2
TCGA-NH-A8F8	0	167	0	1	1	0	2
TCGA-4T-AA8H	0	160	1	0	1	0	2
TCGA-AY-A54L	0	158	1	0	1	0	2
TCGA-A6-6781	0	158	1	0	1	0	2
TCGA-A6-6781	0	158	0	1	1	0	2
TCGA-A6-6781	0	158	0	1	1	0	2
TCGA-NH-A50V	0	154	1	0	1	0	2
TCGA-D5-6539	0	145	1	1	0	0	2
TCGA-A6-6652	0	135	1	0	1	0	2
TCGA-A6-6142	0	134	0	1	1	0	2
TCGA-CM-6167	0	122	0	1	1	0	2
TCGA-A6-A5ZU	0	117	1	0	1	0	2
TCGA-D5-6541	0	108	0	1	1	0	2
TCGA-CM-6163	0	90	0	1	1	0	2
TCGA-A6-6780	0	87	0	1	1	0	2
TCGA-NH-A5IV	0	85	0	1	1	0	2
TCGA-AD-6899	0	48	1	0	1	0	2
TCGA-AA-3660	0	31	1	1	0	0	2
TCGA-AA-3697	0	30	1	1	0	0	2
TCGA-AD-6964	0	23	0	1	1	0	2
TCGA-D5-6928	0	20	0	1	1	0	2
TCGA-AD-A5EK	0	13	1	0	1	0	2
TCGA-CA-5797	0	8	0	1	1	0	2
TCGA-AY-6196	0	6	0	1	1	0	2
TCGA-CA-5255	0	2	0	1	1	0	2
TCGA-F4-6463	0	0	0	1	1	0	2
TCGA-AA-3712	0	0	0	1	1	0	2
TCGA-AA-3662	0	0	1	1	0	0	2
TCGA-CK-6746	0	-2	1	1	0	0	2
TCGA-AZ-6607	1	97	0	1	0	1	2
TCGA-DM-A285	1	186	0	0	1	1	2
TCGA-DM-A1HA	0	3924	0	1	0	1	2
TCGA-CK-6751	0	3136	0	0	1	1	2
TCGA-DM-A28M	0	2775	0	0	1	1	2
TCGA-G4-6627	0	1434	0	1	0	1	2
TCGA-G4-6309	0	1386	0	0	1	1	2
TCGA-G4-6302	0	1310	0	0	1	1	2
TCGA-G4-6314	0	1031	0	0	1	1	2
TCGA-CM-6166	0	424	0	0	1	1	2
TCGA-A6-5657	0	367	0	0	1	1	2
TCGA-A6-5664	0	362	0	0	1	1	2
TCGA-CM-5344	0	304	0	0	1	1	2
TCGA-A6-6651	0	249	0	0	1	1	2
TCGA-D5-6922	0	134	0	0	1	1	2
TCGA-D5-6927	0	67	0	0	1	1	2
TCGA-CK-6748	0	61	0	0	1	1	2
TCGA-D5-6930	0	46	0	0	1	1	2
TCGA-D5-6898	0	45	0	0	1	1	2
TCGA-D5-6931	0	43	1	0	0	1	2
TCGA-D5-6923	0	43	0	0	1	1	2
TCGA-D5-7000	0	41	0	0	1	1	2
TCGA-D5-6533	0	40	0	1	0	1	2
TCGA-AD-6890	0	24	0	0	1	1	2
TCGA-AD-6895	0	22	0	0	1	1	2
TCGA-F4-6807	0	16	0	0	1	1	2
TCGA-F4-6805	0	16	0	0	1	1	2
TCGA-AD-6965	0	6	0	0	1	1	2
TCGA-CA-5254	0	5	0	0	1	1	2
TCGA-CA-6718	0	3	0	0	1	1	2
TCGA-NH-A50U	1	334	0	0	1	0	1
TCGA-CK-5916	1	643	0	1	0	0	1
TCGA-A6-A567	1	1881	0	0	1	0	1

TCGA-5M-AAT4	1	49	0	0	1	0	1
TCGA-G4-6293	0	3203	1	0	0	0	1
TCGA-G4-6297	0	2289	0	1	0	0	1
TCGA-G4-6304	0	1631	0	0	1	0	1
TCGA-AZ-5407	0	1395	1	0	0	0	1
TCGA-CK-5914	0	669	0	0	1	0	1
TCGA-G4-6322	0	547	1	0	0	0	1
TCGA-QG-A5YX	0	526	0	0	1	0	1
TCGA-CK-4952	0	475	1	0	0	0	1
TCGA-A6-5656	0	462	0	0	1	0	1
TCGA-CM-5348	0	393	0	1	0	0	1
TCGA-A6-5667	0	320	0	0	1	0	1
TCGA-A6-5662	0	297	0	1	0	0	1
TCGA-A6-5659	0	286	0	0	1	0	1
TCGA-D5-6538	0	246	1	0	0	0	1
TCGA-A6-5666	0	244	1	0	0	0	1
TCGA-D5-5538	0	204	0	1	0	0	1
TCGA-QG-A5Z1	0	202	0	0	1	0	1
TCGA-D5-5541	0	202	0	1	0	0	1
TCGA-CM-4743	0	184	0	1	0	0	1
TCGA-CM-6168	0	181	0	0	1	0	1
TCGA-AY-6386	0	169	1	0	0	0	1
TCGA-NH-A50T	0	125	0	0	1	0	1
TCGA-D5-6926	0	95	0	0	1	0	1
TCGA-A6-6653	0	91	0	0	1	0	1
TCGA-A6-6780	0	87	1	0	0	0	1
TCGA-CM-5864	0	61	1	0	0	0	1
TCGA-AA-3663	0	31	1	0	0	0	1
TCGA-AA-3713	0	30	0	1	0	0	1
TCGA-F4-6856	0	20	0	0	1	0	1
TCGA-CA-5796	0	12	1	0	0	0	1
TCGA-CA-6715	0	2	1	0	0	0	1
TCGA-CK-5915	0	0	1	0	0	0	1
TCGA-AD-A5EJ	0	0	0	0	1	0	1
TCGA-AA-3655	0	0	1	0	0	0	1
TCGA-A6-5665	0	286	0	0	0	1	1
TCGA-CM-6675	0	153	0	0	0	1	1
TCGA-CA-6719	0	41	0	0	0	1	1
TCGA-CA-6717	0	10	0	0	0	1	1
TCGA-CA-6716	0	8	0	0	0	1	1
TCGA-AD-6889	0	1720	0	0	0	0	0
TCGA-CK-5913	0	853	0	0	0	0	0
TCGA-A6-5661	0	306	0	0	0	0	0
TCGA-CM-6161	0	212	0	0	0	0	0
TCGA-AU-6004	0	203	0	0	0	0	0
TCGA-D5-5540	0	198	0	0	0	0	0
TCGA-D5-6540	0	186	0	0	0	0	0
TCGA-D5-6537	0	137	0	0	0	0	0
TCGA-AY-6197	0	113	0	0	0	0	0
TCGA-A6-6780	0	87	0	0	0	0	0
TCGA-AM-5821	0	28	0	0	0	0	0
TCGA-D5-6531	0	17	0	0	0	0	0
TCGA-AM-5820	0	14	0	0	0	0	0

Supplemental table s3. Gene targets of four miRNAs

miR-148a	miR-26a-2	miR-130a	miR-103-1
ATP6AP2	POLR3G	SLAIN1	FGFRL1
MEOX2	CHORDC1	MDM4	RNF38
GLRX5	THAP2	KDM2A	PPP6R2
C5orf30	STRADB	KLF7	TRIAP1
SNN	ARPP19	PAN3	MED26
GADD45A	MTX2	ENPP5	GJE1
ARL8B	ZDHHC6	FBXO28	NPAS3
NPTN	ART3	MYBL1	ANO3
NPEPL1	MAB21L1	ACVR1	PRKAG3
MITF	BID	CPEB1	ARIH2
CLCN6	SRP19	CHST1	NEK10
CDK5R1	PALM3	RTCA	ARMC1
TMEM54	FAM98A	SYBU	FAM103A1
C18orf25	SERP1	IRF1	AGFG1
SOS2	CREBZF	RPS6KA5	TFRC
HLA-DQB2	GMDS	MAF	NEIL1
S1PR1	HMGA1	DYNLL2	CACNA2D1
QKI	EZH2	SBF2	GPRIN3
INO80	PMAIP1	RNF38	SPATS2L
RTN4	HMGA2	TSHZ1	RPSAP58
CCT6A	UBE2W	EREG	C5orf60
B4GALT5	MTFMT	RAI2	TPD52
TMED7	TAF13	NFIA	C7orf55

DCP2
MXD1
RAB34
ITGA9
PRNP
SZRD1
HOMER1
DDX6
MMD
MRAS
BARHL2
OTX2
ZDHHC7
PNRC2
CCDC144A
PIGA
MAFB
ST8SIA3
WDR47
STX3
RNF219
WDR20
SNX3
PTPRA
TNRC6A
AGO4
C15orf27
UBAP2L
LYSMD2
EOGT
MMP15
ARRDC3
CTSA
USP48
CDC14A
ARFIP1
MTMR9
KAT7
ZNF274
PPP1R10
BAI3
ABCB7
MDM4
SPRYD7
PPP6R1
C1GALT1
CCDC6
CABP7
PHAX
SNX27
SOS1
SMIM12
C7orf60
NRAS
FBXO28
NR2C2AP
SESTD1
FEZ2
NPTX1
NCKIPSD
DDAH1
CDK19
ELAVL4
KLF6
ERRFI1
VMP1
FXR1
SMS
BICC1
EIF4E3
MARCH3
MTF1
KLF5
PNPLA6
C3orf58
TGFA
UCP3
ARPC3
GPR52
TEX26
SLC38A2
REEP3
BLOC1S2
BOD1L2
FRAT2
NAP1L5
TOB1
FAM98B
NUS1
LOXL2
RDH14
ZBTB37
KLHL42
SLC25A16
UBE2G1
COMMD8
PRKCD
MSMO1
CHAC1
ARPP21
RHOQ
ACBD5
ZDHHC20
OSBPL11
RHOU
ADM
IPPK
WBSCR16
GPALPP1
SMAD1
TMEM106B
RGS4
MARCH11
STRBP
TTC13
SKP2
LRRC2
CCDC28A
ANKS1B
SNN
CDC6
TM4SF18
ZNF410
GNPNAT1
DDX52
BOD1
ZFC3H1
PTEN
NABP1
FAM214B
ARMCX2
STK39
CDK8
MNX1
RNF141
ACSL3
EPC1
ADAM9
RCN2
ASPN
DYRK1A
MINPP1
ATF2
SYT10
ACTR3
DCDC2
GBP3
RCN1
SHC4
EIF4G2
HOXA5
CKS2
MTM1
PFDN4
SKIDA1
SRSF2
ZBTB18
IGF1
WDR20
FICD
C7orf60
HABP4
FRZB
MMGT1
SH3D19
GJA1
VPS37A
HPRT1
TMEM55A
PPARG
CALM2
CCDC126
DDX6
ZMAT3
CD69
ESR1
RAP2C
PMEPA1
TSC1
BTG1
KCNJ10
PIGA
TES
C4orf36
PURG
TROVE2
LDLR
ULK2
RRAGD
CBFB
TGFBR2
HS3ST5
CHMP3
HBP1
ZNF217
RNF103-CHMP3
NPNT
HOXB1
ZNF3
KALRN
MIER1
FOSL1
MID1IP1
CPEB3
ACBD5
ARHGAP12
C9orf69
ST18
CDK19
SPG20
UBC
MEOX2
TRERF1
COX8C
SLC2A4RG
FAM175B
FNDC4
PTEN
KCNA4
MTMR6
DSEL
SLC6A6
C5orf30
LONRF1
SNAP25
CPEB2
KLF3
HIVEP2
ATP2B2
QKI
EPC2
KIF2B
TMEM47
CKMT1A
AGO4
GPC6
DLEU7
SNCG
WDR61
ZHX1
GREM2
CPA6
PTCHD3
OR52E8
AP006621.5
SH2D4B
CST3
RP11-664D7.4
LCN15
OR4M1
DUS1L
PPP2R3C
PNPLA2
CDC14A
MIF4GD
TWF1
KRTAP20-2
ZNRF2
UNC80
GFOD1
PTEN
PRKCE
AGO1
PATE4
AC068987.1
HTR2A
ERLIN1
B3GALT4
HELLS
NUDCD2
RPL34
NRIP1
CDKN1C
BST1
PDCD10
ARHGAP17
LDOC1
SNURF
ATP13A4
EIF5
AXIN2
LAPTM4A
PTPLB
PPP6C
TK2
RDH11
RRAGC
KIAA0247
VAPB
AC007461.1
CD80
TMEM221
NAA60
RP11-826N14.2
JAKMIP2
AMMECR1
EPHA3
SNX12
RET
KRTAP20-1
PHF19
CDK5R1
SNX3
RPUSD1
SH3BP4
C14orf105
RP11-1026M7.2
SMPD1

Supplemental table s4. GO Term of Biological Process

Term	Count	p value	Genes
GO:0045449~regulation of transcription	66	0.007	SLC2A4RG, EZH2, PPARG, MITF, RHOQ, CBFB, ZBTB37, EPC1, RNF141, S1PR1, MIER1, MED26, FOSL1, ZHX1, OTX2, BARHL2, ESR1, CDK8, HMGA2, MXD1, TRERF1, HMGA1, ZNF3, NRIP1, TAF13, MTF1, KDM2A, EREG, CD80, BTG1, UBC, MNX1, ST18, MDM4, ACVR1, ZNF274, TSHZ1, MYBL1, ATF2, NPAS3, BLOC1S2, HOXA5, HBP1, HELLS, KLF5, POLR3G, MAF, KLF6, KLF7, CREBZF, MAFB, IGF1, SMAD1, RPS6KA5, CDKN1C, HOXB1, ZNF217, PHF19, MEOX2, PNRC2, IRF1, HIVEP2, HABP4, NFIA, KLF3, ZNF410
GO:0006350~transcription	55	0.008	SLC2A4RG, EZH2, PPARG, MITF, CBFB, ZBTB37, EPC1, MIER1, MED26, FOSL1, ZHX1, BARHL2, CDK8, ESR1, HMGA2, MXD1, TRERF1, HMGA1, ZNF3, NRIP1, TAF13, MTF1, EREG, KDM2A, MNX1, ST18, ZNF274, TSHZ1, MYBL1, RRAGC, ATF2, TROVE2, NPAS3, HOXA5, HBP1, HELLS, POLR3G, MAF, KLF5, KLF6, KLF7, CREBZF, MAFB, PPP1R10, SMAD1, HOXB1, ZNF217, PHF19, PNRC2, IRF1, HIVEP2, HABP4, NFIA, ZNF410, KLF3
GO:0006355~regulation of transcription, DNA-dependent	47	0.013	ZNF274, SLC2A4RG, TSHZ1, MITF, PPARG, EZH2, RHOQ, MYBL1, CBFB, ATF2, EPC1, RNF141, NPAS3, S1PR1, HOXA5, MED26, FOSL1, HELLS, POLR3G, MAF, KLF5, KLF6, KLF7, CREBZF, MAFB, ZHX1, BARHL2, OTX2, ESR1, IGF1, SMAD1, HMGA2, HMGA1, TRERF1, ZNF3, NRIP1, RPS6KA5, CDKN1C, HOXB1, MTF1, MEOX2, MNX1, IRF1, HIVEP2, MDM4, ST18, NFIA
GO:0051252~regulation of RNA metabolic process	47	0.018	ZNF274, SLC2A4RG, TSHZ1, MITF, PPARG, EZH2, RHOQ, MYBL1, CBFB, ATF2, EPC1, RNF141, NPAS3, S1PR1, HOXA5, MED26, FOSL1, HELLS, POLR3G, MAF, KLF5, KLF6, KLF7, CREBZF, MAFB, ZHX1, BARHL2, OTX2, ESR1, IGF1, SMAD1, HMGA2, HMGA1, TRERF1, ZNF3, NRIP1, RPS6KA5, CDKN1C, HOXB1, MTF1, MEOX2, MNX1, IRF1, HIVEP2, MDM4, ST18, NFIA
GO:0007242~intracellular signaling cascade	36	0.011	PRKAG3, MRAS, RHOQ, RHOU, RRAGC, TMED7, TRIAP1, S1PR1, SOS1, SOS2, TGFA, DDAH1, SHC4, ADAM9, RET, RAP2C, ESR1, DCDC2, IGF1, SMAD1, STRADB, PRKCE, HOMER1, PRKCD, NRIP1, RPS6KA5, NRAS, CD80, ADM, RGS4, RAB34, CKS2, ARL8B, PMEPA1, KALRN, HTR2A
GO:0010604~positive regulation of macromolecule metabolic process	30	0.001	MITF, PPARG, RHOQ, GJA1, CBFB, EPC1, S1PR1, BLOC1S2, FOSL1, ADAM9, MAF, KLF5, KLF6, KLF7, MAFB, BARHL2, ESR1, IGF1, SMAD1, HMGA1, TRERF1, NRIP1, HOXB1, MTF1, EREG, CD80, UBC, IRF1, SH3D19, ACVR1
GO:0006793~phosphorus metabolic process	30	0.009	CDK19, PPP6C, CDK5R1, CDC14A, PTEN, MTM1, TGFA, STK39, MTMR9, MTMR6, ADAM9, MINPP1, RET, TWF1, PAN3, TGFBR2, PTPRA, CDK8, NEK10, STRADB, PRKCE, PRKCD, EPHA3, RPS6KA5, SBF2, ULK2, DYRK1A, IPPK, KALRN, ACVR1
GO:0006796~phosphate metabolic process	30	0.009	CDK19, PPP6C, CDK5R1, CDC14A, PTEN, MTM1, TGFA, STK39, MTMR9, MTMR6, ADAM9, MINPP1, RET, TWF1, PAN3, TGFBR2, PTPRA, CDK8, NEK10, STRADB, PRKCE, PRKCD, EPHA3, RPS6KA5, SBF2, ULK2, DYRK1A, IPPK, KALRN, ACVR1
GO:0031328~positive regulation of cellular biosynthetic process	28	0.000	PPARG, MITF, RHOQ, CBFB, EPC1, S1PR1, BLOC1S2, DDAH1, FOSL1, MAF, KLF5, KLF6, KLF7, MAFB, BARHL2, ARPP19, IGF1, SMAD1, HMGA1, TRERF1, NRIP1, HOXB1, EREG, CD80, MTF1, UBC, IRF1, ACVR1
GO:0009891~positive regulation of biosynthetic process	28	0.000	PPARG, MITF, RHOQ, CBFB, EPC1, S1PR1, BLOC1S2, DDAH1, FOSL1, MAF, KLF5, KLF6, KLF7, MAFB, BARHL2, ARPP19, IGF1, SMAD1, HMGA1, TRERF1, NRIP1, HOXB1, EREG, CD80, MTF1, UBC, IRF1, ACVR1
GO:0051173~positive regulation of nitrogen compound metabolic process	27	0.000	PPARG, MITF, RHOQ, HPRT1, CBFB, EPC1, S1PR1, BLOC1S2, DDAH1, FOSL1, MAF, KLF5, KLF6, KLF7, MAFB, IGF1, SMAD1, HMGA1, TRERF1, NRIP1, HOXB1, EREG, CD80, MTF1, UBC, IRF1, ACVR1
GO:0042127~regulation of cell proliferation	27	0.003	PPARG, MITF, FGFRL1, GJA1, PTEN, S1PR1, BLOC1S2, TGFA, AXIN2, FOSL1, KLF5, CDC6, TGFBR2, IGF1, SMAD1, CDKN1C, NRAS, EREG, TSC1, CD80, ADM, BTG1, MDM4, MAB21L1, LDOC1, TOB1, HTR2A
GO:0010557~positive regulation of macromolecule biosynthetic process	26	0.001	PPARG, MITF, RHOQ, CBFB, EPC1, S1PR1, BLOC1S2, FOSL1, MAF, KLF5, KLF6, KLF7, MAFB, BARHL2, IGF1, SMAD1, HMGA1, TRERF1, NRIP1, HOXB1, EREG, CD80, MTF1, UBC, IRF1, ACVR1
GO:0010628~positive regulation of gene expression	25	0.000	KLF5, MAF, KLF6, KLF7, MAFB, MITF, PPARG, ESR1, IGF1, RHOQ, SMAD1, HMGA1, TRERF1, CBFB, NRIP1, EPC1, HOXB1, S1PR1, MTF1, BLOC1S2, CD80, UBC, IRF1, FOSL1, ACVR1
GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	25	0.001	KLF5, MAF, KLF6, KLF7, MAFB, MITF, PPARG, IGF1, RHOQ, SMAD1, HMGA1, TRERF1, CBFB, NRIP1, EPC1, HOXB1, S1PR1, MTF1, BLOC1S2, CD80, EREG, UBC, IRF1, FOSL1, ACVR1
GO:0008219~cell death	25	0.004	BID, RTN4, PDCD10, VAPB, ZMAT3, MMD, GJA1, PMAIP1, HPRT1, PTEN, PNPLA6, RRAGC, FXR1, TRIAP1, EIF4G2, NRAS, SOS1, SOS2, SPG20, UBC, MDM4, AXIN2, GADD45A, HTR2A, KALRN
GO:0016265~death	25	0.005	BID, RTN4, PDCD10, VAPB, ZMAT3, MMD, GJA1, PMAIP1, HPRT1, PTEN, PNPLA6, RRAGC, FXR1, TRIAP1, EIF4G2, NRAS, SOS1, SOS2, SPG20, UBC, MDM4, AXIN2, GADD45A, HTR2A, KALRN
GO:0042981~regulation of apoptosis	25	0.016	BID, RTN4, CDK5R1, ZMAT3, MITF, SKP2, ESR1, IGF1, PMAIP1, STRADB, PRKCE, PTEN, NRAS, TRIAP1, BLOC1S2, BTG1, SOS1, SOS2, UBC, PRNP, FOSL1, HELLS, KALRN, ACVR1, ADAM9
GO:0043067~regulation of programmed cell death	25	0.018	BID, RTN4, CDK5R1, ZMAT3, MITF, SKP2, ESR1, IGF1, PMAIP1, STRADB, PRKCE, PTEN, NRAS, TRIAP1, BLOC1S2, BTG1, SOS1, SOS2, UBC, PRNP, FOSL1, HELLS, KALRN, ACVR1, ADAM9
GO:0010941~regulation of cell death	25	0.018	BID, RTN4, CDK5R1, ZMAT3, MITF, SKP2, ESR1, IGF1, PMAIP1, STRADB, PRKCE, PTEN, NRAS, TRIAP1, BLOC1S2, BTG1, SOS1, SOS2, UBC, PRNP, FOSL1, HELLS, KALRN, ACVR1, ADAM9
GO:0045941~positive regulation of transcription	24	0.000	KLF5, MAF, KLF6, KLF7, MAFB, PPARG, MITF, IGF1, RHOQ, SMAD1, TRERF1, HMGA1, CBFB, NRIP1, EPC1, HOXB1, S1PR1, CD80, BLOC1S2, MTF1, UBC, IRF1, FOSL1, ACVR1
GO:0006357~regulation of transcription from RNA polymerase II promoter	23	0.018	MAF, KLF6, KLF7, MAFB, PPARG, MITF, BARHL2, IGF1, RHOQ, SMAD1, CBFB, NRIP1, CDKN1C, EPC1, HOXB1, S1PR1, MTF1, MED26, IRF1, MNX1, MDM4, ST18, FOSL1
GO:0006468~protein amino acid phosphorylation	21	0.025	CDK19, RET, TWF1, CDK5R1, PAN3, TGFBR2, PTPRA, CDK8, NEK10, STRADB, PRKCE, PRKCD, EPHA3, RPS6KA5, ULK2, DYRK1A, TGFA, STK39, KALRN, ADAM9, ACVR1
GO:0030182~neuron differentiation	20	0.001	KLF7, RET, CDK5R1, STX3, OTX2, BARHL2, GJA1, HPRT1, PTEN, CDKN1C, ATP2B2, S1PR1, ADM, DYNLL2, ULK2, UBC, MNX1, SNAP25, FEZ2, KALRN
GO:0045893~positive regulation of transcription, DNA-dependent	19	0.004	MAF, KLF6, KLF7, MAFB, PPARG, MITF, IGF1, RHOQ, SMAD1, TRERF1, HMGA1, CBFB, NRIP1, EPC1, HOXB1, S1PR1, MTF1, IRF1, FOSL1
GO:0051254~positive regulation of RNA metabolic process	19	0.004	MAF, KLF6, KLF7, MAFB, PPARG, MITF, IGF1, RHOQ, SMAD1, TRERF1, HMGA1, CBFB, NRIP1, EPC1, HOXB1, S1PR1, MTF1, IRF1, FOSL1
GO:0042325~regulation of phosphorylation	18	0.007	CDC6, CDK5R1, TGFBR2, IGF1, STRADB, PRKCE, PRKCD, PTEN, CDKN1C, CD80, TSC1, EREG, RGS4, CKS2, TGFA, GADD45A, HTR2A, ADAM9
GO:0051174~regulation of phosphorus metabolic process	18	0.010	CDC6, CDK5R1, TGFBR2, IGF1, STRADB, PRKCE, PRKCD, PTEN, CDKN1C, CD80, TSC1, EREG, RGS4, CKS2, TGFA, GADD45A, HTR2A, ADAM9
GO:0019220~regulation of phosphate metabolic process	18	0.010	CDC6, CDK5R1, TGFBR2, IGF1, STRADB, PRKCE, PRKCD, PTEN, CDKN1C, CD80, TSC1, EREG, RGS4, CKS2, TGFA, GADD45A, HTR2A, ADAM9
GO:0048666~neuron development	17	0.001	KLF7, RET, CDK5R1, STX3, OTX2, GJA1, HPRT1, PTEN, CDKN1C, ATP2B2, ADM, DYNLL2, ULK2, UBC, SNAP25, FEZ2, KALRN
GO:0008285~negative regulation of cell proliferation	17	0.001	CDC6, FGFRL1, PPARG, TGFBR2, GJA1, SMAD1, PTEN, CDKN1C, ADM, TSC1, EREG, BTG1, MDM4, AXIN2, LDOC1, FOSL1, TOB1
GO:0032268~regulation of cellular protein metabolic	17	0.017	EIF4E3, CPEB2, EIF5, BARHL2, IGF1, CPEB1, PRKCE, PRKCD, EIF4G2, CD80, TSC1, UBC, QKI, SH3D19, MIF4GD, TNRC6A, ADAM9

process			
GO:0030030~cell projection organization	16	0.004	KLF5, KLF7, CDK5R1, STX3, OTX2, GJA1, HPRT1, PTEN, ATP2B2, ADM, TSC1, ULK2, UBC, SNAP25, FEZ2, KALRN
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	16	0.004	MAF, KLF6, MAFB, PPARG, MITF, IGF1, RHOQ, SMAD1, CBFB, NRIP1, EPC1, HOXB1, S1PR1, MTF1, IRF1, FOSL1
GO:0051338~regulation of transferase activity	15	0.010	CDC6, CDK5R1, TGFBR2, PPARG, STRADB, PTEN, CDKN1C, TSC1, EREG, RGS4, CKS2, TGFA, GADD45A, HTR2A, ADAM9
GO:0010608~posttranscriptional regulation of gene expression	14	0.000	EIF4E3, CPEB2, EIF5, BARHL2, CPEB1, SMAD1, PTEN, PRKCD, EIF4G2, TSC1, QKI, MDM4, TNRC6A, MIF4GD
GO:0007167~enzyme linked receptor protein signaling pathway	14	0.012	RET, TGFBR2, PTPRA, RHOQ, SMAD1, GREM2, PTEN, EPHA3, RPS6KA5, EREG, SOS1, ADAM9, TOB1, ACVR1
GO:0045859~regulation of protein kinase activity	14	0.013	CDC6, CDK5R1, TGFBR2, STRADB, PTEN, CDKN1C, TSC1, EREG, RGS4, CKS2, TGFA, GADD45A, HTR2A, ADAM9
GO:0043549~regulation of kinase activity	14	0.017	CDC6, CDK5R1, TGFBR2, STRADB, PTEN, CDKN1C, TSC1, EREG, RGS4, CKS2, TGFA, GADD45A, HTR2A, ADAM9
GO:0032989~cellular component morphogenesis	14	0.036	CDK5R1, KLF7, AGFG1, OTX2, GJA1, STRADB, HPRT1, ATP2B2, ADM, ULK2, UBC, SNAP25, FEZ2, KALRN
GO:0008284~positive regulation of cell proliferation	14	0.047	KLF5, NRAS, S1PR1, EREG, BLOC1S2, CD80, ADM, TGFBR2, TGFA, IGF1, MDM4, MAB21L1, FOSL1, HTR2A
GO:0048514~blood vessel morphogenesis	13	0.001	RTN4, KLF5, TGFBR2, PTEN, PNPLA6, S1PR1, MEOX2, NUS1, EREG, QKI, TGFA, C1GALT1, ACVR1
GO:0001568~blood vessel development	13	0.002	RTN4, KLF5, TGFBR2, PTEN, PNPLA6, S1PR1, MEOX2, NUS1, EREG, QKI, TGFA, C1GALT1, ACVR1
GO:0001944~vasculature development	13	0.003	RTN4, KLF5, TGFBR2, PTEN, PNPLA6, S1PR1, MEOX2, NUS1, EREG, QKI, TGFA, C1GALT1, ACVR1
GO:0031175~neuron projection development	13	0.003	KLF7, CDK5R1, STX3, ADM, ULK2, OTX2, UBC, GJA1, HPRT1, SNAP25, PTEN, FEZ2, KALRN
GO:0000902~cell morphogenesis	13	0.036	ATP2B2, KLF7, CDK5R1, ADM, ULK2, OTX2, UBC, GJA1, STRADB, HPRT1, SNAP25, FEZ2, KALRN
GO:0001525~angiogenesis	12	0.000	KLF5, RTN4, S1PR1, NUS1, MEOX2, EREG, TGFBR2, TGFA, PTEN, C1GALT1, PNPLA6, ACVR1
GO:0010647~positive regulation of cell communication	12	0.045	CDKN1C, TMED7, NRAS, CD80, EREG, MIER1, SOS1, UBC, ESR1, TGFA, GJA1, IGF1
GO:0051726~regulation of cell cycle	12	0.048	CDKN1C, TRIAP1, CDC6, CDK5R1, EREG, SKP2, CKS2, TGFA, IGF1, FOSL1, GADD45A, PTEN
GO:0051960~regulation of nervous system development	11	0.003	RTN4, ACTR3, CDK5R1, BARHL2, PPARG, UBC, NPTN, IGF1, SMAD1, SNAP25, KALRN
GO:0048812~neuron projection morphogenesis	11	0.007	KLF7, CDK5R1, ADM, ULK2, OTX2, UBC, GJA1, HPRT1, SNAP25, FEZ2, KALRN
GO:0045321~leukocyte activation	11	0.016	KLF6, CD80, TGFBR2, IRF1, HPRT1, TPD52, PRKCD, HELLS, CBFB, ZNF3, ADAM9
GO:0048858~cell projection morphogenesis	11	0.017	KLF7, CDK5R1, ADM, ULK2, OTX2, UBC, GJA1, HPRT1, SNAP25, FEZ2, KALRN
GO:0032990~cell part morphogenesis	11	0.022	KLF7, CDK5R1, ADM, ULK2, OTX2, UBC, GJA1, HPRT1, SNAP25, FEZ2, KALRN
GO:0001775~cell activation	11	0.044	KLF6, CD80, TGFBR2, IRF1, HPRT1, TPD52, PRKCD, HELLS, CBFB, ZNF3, ADAM9
GO:0006351~transcription, DNA-dependent	11	0.048	KLF5, MAF, TROVE2, TAF13, ZNF217, EREG, MED26, ESR1, IRF1, FOSL1, CBFB
GO:0006417~regulation of translation	10	0.001	EIF4G2, EIF4E3, CPEB2, TSC1, BARHL2, EIF5, QKI, CPEB1, MIF4GD, TNRC6A
GO:0060284~regulation of cell development	10	0.015	RTN4, ACTR3, CDK5R1, BTG1, BARHL2, PPARG, UBC, NPTN, SMAD1, KALRN
GO:0048667~cell morphogenesis involved in neuron differentiation	10	0.017	ATP2B2, KLF7, CDK5R1, ULK2, OTX2, UBC, HPRT1, SNAP25, FEZ2, KALRN
GO:0000904~cell morphogenesis involved in differentiation	10	0.040	ATP2B2, KLF7, CDK5R1, ULK2, OTX2, UBC, HPRT1, SNAP25, FEZ2, KALRN
GO:0010648~negative regulation of cell communication	10	0.044	TSC1, RGS4, EZH2, AXIN2, FRZB, PRKCD, PTEN, TOB1, HTR2A, ACVR1
GO:0046578~regulation of Ras protein signal transduction	9	0.044	NRAS, FICD, S1PR1, AGFG1, TSC1, SOS1, SOS2, IGF1, KALRN
GO:0007517~muscle organ development	9	0.045	MTM1, TSC1, MEOX2, MRAS, IGF1, HOMER1, PTEN, FXR1, SERP1
GO:0044087~regulation of cellular component biogenesis	8	0.017	ACTR3, S1PR1, TSC1, ARPC3, UBC, RHOQ, SNAP25, PTEN
GO:0016311~dephosphorylation	8	0.026	MTM1, PPP6C, CDC14A, SBF2, PTPRA, MTMR9, MTMR6, PTEN
GO:0050767~regulation of neurogenesis	8	0.037	RTN4, ACTR3, CDK5R1, BARHL2, PPARG, NPTN, SMAD1, KALRN
GO:0009894~regulation of catabolic process	7	0.009	CST3, GJA1, IGF1, PNPLA2, SH3D19, MDM4, ADAM9
GO:0051329~interphase of mitotic cell cycle	7	0.013	CDKN1C, PPP6C, CDC6, SKP2, RHOU, GADD45A, ACVR1
GO:0051325~interphase	7	0.015	CDKN1C, PPP6C, CDC6, SKP2, RHOU, GADD45A, ACVR1
GO:0007568~aging	7	0.017	NRAS, TFRC, ADM, LOXL2, PRKCD, PTEN, HTR2A
GO:0050804~regulation of synaptic transmission	7	0.043	ATP2B2, NRAS, SNCG, UBC, NPTN, PATE4, HTR2A
GO:0000079~regulation of cyclin-dependent protein kinase activity	6	0.003	CDKN1C, CDC6, CDK5R1, CKS2, GADD45A, PTEN
GO:0040029~regulation of gene expression, epigenetic	6	0.015	EPC1, CREBZF, SMAD1, HMGA1, TNRC6A, HELLS

GO:0010959~regulation of metal ion transport	6	0.018	ATP2B2, CACNA2D1, GJA1, HOMER1, CALM2, HTR2A
GO:0031344~regulation of cell projection organization	6	0.026	RTN4, ACTR3, BARHL2, RHOQ, SMAD1, KALRN
GO:0043269~regulation of ion transport	6	0.038	ATP2B2, CACNA2D1, GJA1, HOMER1, CALM2, HTR2A
GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway	6	0.044	TGFBR2, SMAD1, GREM2, ADAM9, TOB1, ACVR1
GO:0009896~positive regulation of catabolic process	5	0.013	GJA1, IGF1, PNPLA2, SH3D19, ADAM9
GO:0031329~regulation of cellular catabolic process	5	0.027	CST3, IGF1, PNPLA2, SH3D19, ADAM9
GO:0051924~regulation of calcium ion transport	5	0.040	ATP2B2, CACNA2D1, GJA1, HOMER1, CALM2
GO:0010975~regulation of neuron projection development	5	0.042	RTN4, ACTR3, BARHL2, SMAD1, KALRN
GO:0048661~positive regulation of smooth muscle cell proliferation	4	0.020	S1PR1, EREG, TGFBR2, IGF1
GO:0031331~positive regulation of cellular catabolic process	4	0.029	IGF1, PNPLA2, SH3D19, ADAM9
GO:0051147~regulation of muscle cell differentiation	4	0.036	EREG, BTG1, EZH2, UBC
GO:0045667~regulation of osteoblast differentiation	4	0.046	SMAD1, AXIN2, TOB1, ACVR1
GO:0045742~positive regulation of epidermal growth factor receptor signaling pathway	3	0.017	EREG, SOS1, TGFA
GO:0050773~regulation of dendrite development	3	0.031	ACTR3, SMAD1, KALRN
GO:0010469~regulation of receptor activity	3	0.044	EREG, TGFA, PRKCD

Supplemental table s5. GO Term of Cellular Component

Term	Count	p Value	Genes
GO:0000932~cytoplasmic	5	0.001	DCP2, PNRC2, CPEB1, TNRC6A, DDX6
GO:0005768~endosome	15	0.001	MMGT1, LDLR, SNX27, GNPNAT1, MMD, VPS37A, GJA1, MARCH3,
GO:0030426~growth cone	5	0.014	CDK5R1, STX3, TSC1, OTX2, SNAP25
GO:0030427~site of polarized	5	0.015	CDK5R1, STX3, TSC1, OTX2, SNAP25
GO:0043025~cell soma	8	0.027	RTN4, ATP2B2, SNCG, CDK5R1, AGFG1, SOS1, ESR1, KALRN
GO:0009897~external side of	8	0.029	S1PR1, CD80, ATP6AP2, CD69, GPC6, TGFBR2, MMP15, ADAM9
GO:0043005~neuron projection	12	0.037	ATP2B2, ANKS1B, SNCG, CDK5R1, STX3, TSC1, OTX2, ESR1, CPEB1,
GO:0031225~anchored to	9	0.038	NRAS, ART3, BST1, GPC6, PALM3, RHOQ, PRNP, RHOU, SNAP25
GO:0045202~synapse	12	0.046	ACTR3, ANKS1B, CDK5R1, SYT10, SOS1, NPTN, CPEB1, HOMER1,