

Supplementary Table 1. A total of 569 differentially expressed miRNAs in patients with colorectal cancer compared with normal controls, identified by microarray technique using orthogonal partial least squares analysis.

A, Up-regulated		
miRNA ID	Fold Change, CRC/normal	<i>p</i> value
MIMAT0014994	10.76	3.98813E-11
MIMAT0005872	4.53	3.70315E-06
MIMAT0002844	4.52	4.28565E-07
MIMAT0027666	4.33	6.79993E-10
MIMAT0027445	4.30	3.84578E-06
MIMAT0000268	4.24	1.46285E-10
MIMAT0004486	3.87	5.38685E-05
MIMAT0004672	3.41	0.00010228
MIMAT0001618	3.32	1.23074E-06
MIMAT0017982	3.31	5.95951E-08
MIMAT0001339	2.74	6.87294E-14
MIMAT0004589	2.66	1.9594E-12
MIMAT0003283	2.66	5.59066E-08
MIMAT0004986	2.64	1.20622E-08
MIMAT0027477	2.49	3.40426E-09
MIMAT0003230	2.49	0.000142673
MIMAT0018963	2.48	5.81046E-06
MIMAT0027499	2.30	1.0372E-05
MIMAT0001343	2.23	1.09494E-07
MIMAT0002819	2.22	7.34058E-07
MIMAT0005580	2.14	4.58138E-06
MIMAT0027525	2.13	9.87829E-07
MIMAT0004978	2.08	1.61145E-07
MIMAT0027691	2.08	0.000708814
MIMAT0006790	1.99	5.61841E-12
MIMAT0004947	1.94	2.91416E-05
MIMAT0027541	1.94	1.01452E-07
MIMAT0021124	1.81	0.000143943
MIMAT0027621	1.79	4.24682E-05
MIMAT0027505	1.78	4.05388E-09
MIMAT0000710, MIMAT0022834	1.77	7.91706E-05
MIMAT0005926	1.75	3.19561E-05
MIMAT0019214	1.73	2.01908E-05
MIMAT0019015	1.71	6.73398E-05
MIMAT0013518	1.69	0.000312523
MIMAT0004780	1.68	4.46266E-08
MIMAT0016921	1.67	2.04092E-12

MIMAT0027669	1.58	3.23467E-13
MIMAT0027459	1.57	0.000464184
MIMAT0019688	1.56	3.14801E-16
MIMAT0027614	1.56	1.36756E-25
MIMAT0018004	1.54	0.000434316
MIMAT0027671	1.54	1.05331E-06
MIMAT0023693	1.52	2.45372E-09
MIMAT0016864	1.51	4.21431E-08
MIMAT0028118	1.50	4.79735E-09
MIMAT0019809	1.49	8.71822E-06
MIMAT0019979	1.49	2.8825E-18
MIMAT0019747	1.48	1.18889E-07
MIMAT0019837	1.46	2.00497E-06
MIMAT0003881	1.45	4.98297E-07
MIMAT0003237	1.44	7.53405E-09
MIMAT0007889	1.43	1.87025E-05
MIMAT0027687	1.43	0.000379972
MIMAT0027495	1.42	2.9352E-05
MIMAT0007401	1.42	8.34203E-05
MIMAT0019226	1.41	0.000458605
MIMAT0005588	1.40	3.35436E-10
MIMAT0028120	1.40	3.09412E-07
MIMAT0027681	1.39	3.7476E-06
MIMAT0027675	1.37	2.52865E-06
MIMAT0027553	1.37	0.00067077
MIMAT0019213	1.36	6.50663E-05
MIMAT0005591	1.34	6.60625E-06
MIMAT0027624	1.33	3.62932E-06
MIMAT0027631	1.33	1.5094E-08
MIMAT0020956	1.33	4.78636E-23
MIMAT0021129	1.32	2.5634E-08
MIMAT0027419	1.32	0.000119942
MIMAT0019964	1.32	6.05132E-31
MIMAT0019011	1.32	2.64551E-07
MIMAT0027550	1.31	3.53839E-32
MIMAT0027384	1.31	3.93007E-07
MIMAT0027364	1.31	2.21393E-05
MIMAT0015057	1.31	1.37338E-05
MIMAT0027685	1.30	6.71272E-05
MIMAT0016909	1.30	1.45443E-12
MIMAT0000756	1.30	0.000159815
MIMAT0028116	1.30	2.01688E-07
MIMAT0019708	1.29	0.000857457

MIMAT0019738	1.29	2.52029E-05
MIMAT0018999	1.28	5.33901E-15
MIMAT0019710	1.28	7.55524E-11
MIMAT0027473	1.28	6.76955E-05
MIMAT0027413	1.27	2.29482E-08
MIMAT0019850	1.27	4.0856E-10
MIMAT0005584	1.26	2.44026E-10
MIMAT0018104	1.26	1.58689E-40
MIMAT0007884	1.25	4.94569E-10
MIMAT0002173	1.25	0.000420978
MIMAT0027527	1.25	1.23832E-06
MIMAT0019881	1.25	4.8881E-34
MIMAT0027659	1.25	3.9531E-09
MIMAT0019839	1.25	5.50499E-05
MIMAT0015069	1.24	1.42443E-12
MIMAT0019789	1.24	4.04688E-05
MIMAT0005589	1.24	2.59231E-07
MIMAT0005573	1.24	7.14602E-17
MIMAT0027362	1.24	3.89486E-05
MIMAT0028121	1.23	1.39866E-06
MIMAT0025479	1.23	0.000722147
MIMAT0022260	1.22	1.27147E-23
MIMAT0004945	1.22	4.66251E-35
MIMAT0028117	1.22	1.44289E-24
MIMAT0005592	1.22	9.96829E-16
MIMAT0015070	1.22	6.3329E-32
MIMAT0015065	1.22	2.51404E-27
MIMAT0005586	1.22	4.46712E-38
MIMAT0027399	1.21	3.83869E-06
MIMAT0006765	1.21	4.94846E-05
MIMAT0005593	1.21	9.90002E-09
MIMAT0022939	1.21	1.20557E-06
MIMAT0019700	1.20	5.19479E-07
MIMAT0000227	1.20	6.13552E-05
MIMAT0025848	1.20	0.000160669
MIMAT0022721	1.20	1.89851E-37
MIMAT0027617	1.20	0.000840204
MIMAT0027509	1.20	2.26473E-06
MIMAT0019772	1.20	4.99098E-05
MIMAT0022948	1.19	1.21209E-09
MIMAT0019740	1.19	6.38629E-32
MIMAT0011161	1.18	1.31464E-05
MIMAT0027485	1.18	1.46942E-06

MIMAT0005826	1.18	1.12767E-10
MIMAT0019940	1.18	3.98244E-08
MIMAT0027493	1.17	8.27527E-16
MIMAT0005951	1.17	0.000148317
MIMAT0027354	1.17	5.47924E-07
MIMAT0027673	1.16	0.000244901
MIMAT0007348	1.16	9.95621E-06
MIMAT0000752	1.16	2.2169E-07
MIMAT0027586	1.16	8.85884E-22
MIMAT0004951	1.16	8.68817E-17
MIMAT0027388	1.16	0.000441883
MIMAT0027626	1.16	3.53304E-05
MIMAT0003270	1.16	3.51036E-19
MIMAT0009451	1.16	5.48842E-10
MIMAT0027572	1.16	2.4416E-45
MIMAT0026477	1.15	1.95198E-20
MIMAT0015064	1.15	4.046E-22
MIMAT0027551	1.15	2.56932E-05
MIMAT0019854	1.15	4.27494E-07
MIMAT0019886	1.15	1.23503E-10
MIMAT0005583	1.15	1.55339E-27
MIMAT0027689	1.15	0.00025284
MIMAT0019826	1.15	4.07569E-06
MIMAT0027501	1.15	2.27946E-09
MIMAT0004982	1.15	2.09779E-18
MIMAT0019957	1.14	6.18721E-08
MIMAT0022286	1.14	0.000477977
MIMAT0018105	1.14	9.23171E-17
MIMAT0027507	1.14	3.49069E-05
MIMAT0027655	1.14	7.90947E-05
MIMAT0018968	1.14	7.76405E-23
MIMAT0015019	1.14	0.000218361
MIMAT0004983	1.13	9.36581E-17
MIMAT0018994	1.13	9.31044E-30
MIMAT0027661	1.13	1.3422E-07
MIMAT0005572	1.13	6.03698E-24
MIMAT0027356	1.13	0.000626914
MIMAT0027433	1.13	1.84865E-16
MIMAT0003888	1.13	0.000436354
MIMAT0030420	1.13	1.47007E-11
MIMAT0027591	1.13	7.43982E-05
MIMAT0016904	1.13	6.574E-05
MIMAT0027491	1.13	0.000724131

MIMAT0018099	1.12	1.01895E-06
MIMAT0019947	1.12	2.96118E-06
MIMAT0027360	1.12	1.48826E-07
MIMAT0027464	1.12	3.39031E-11
MIMAT0027511	1.12	4.73058E-14
MIMAT0028114	1.11	0.000686719
MIMAT0027455	1.11	6.86021E-06
MIMAT0025487	1.10	3.93615E-18
MIMAT0018949	1.10	1.0759E-18
MIMAT0016906	1.09	0.000682429
MIMAT0030414	1.09	1.94316E-22
MIMAT0017996	1.09	0.000909208
MIMAT0027650	1.09	1.18308E-23
MIMAT0028113	1.09	6.19313E-39
MIMAT0019807	1.09	3.39714E-20
MIMAT0004808	1.09	0.000257872
MIMAT0024616	1.08	5.8618E-18
MIMAT0004508	1.08	9.27256E-11
MIMAT0027427	1.08	0.000320801
MIMAT0027497	1.08	0.000384719
MIMAT0025844	1.08	3.20423E-09
MIMAT0012734	1.08	6.63364E-19
MIMAT0025852	1.08	4.63784E-15
MIMAT0027640	1.08	1.61811E-10
MIMAT0025476	1.08	6.78344E-05
MIMAT0018961	1.08	0.000351814
MIMAT0019788	1.07	1.50704E-16
MIMAT0027365	1.07	1.10119E-15
MIMAT0027482	1.07	1.54886E-30
MIMAT0027526	1.07	1.62324E-05
MIMAT0018352	1.07	5.942E-23
MIMAT0027658	1.07	3.89537E-13
MIMAT0019044	1.07	2.7948E-05
MIMAT0024599	1.07	1.19712E-18
MIMAT0022977	1.07	3.8826E-16
MIMAT0022967	1.06	7.88455E-12
MIMAT0019020	1.06	1.32706E-06
MIMAT0019743	1.06	8.32888E-06
MIMAT0018925	1.06	2.09168E-13
MIMAT0019808	1.06	7.66363E-05
MIMAT0004792	1.06	1.26271E-11
MIMAT0007881	1.06	6.66244E-31
MIMAT0004595	1.06	0.000236856

MIMAT0027590	1.06	1.51259E-17
MIMAT0025856	1.06	2.87366E-23
MIMAT0027496	1.05	1.03501E-10
MIMAT0027596	1.05	1.12804E-08
MIMAT0018929	1.05	1.77539E-17
MIMAT0023700	1.05	2.09249E-07
MIMAT0004952	1.05	0.000756233
MIMAT0027532	1.05	5.12199E-16
MIMAT0003326	1.05	6.33821E-17
MIMAT0012735	1.05	0.000127457
MIMAT0027602	1.05	0.000601778
MIMAT0019871	1.04	8.07992E-12
MIMAT0030999	1.04	4.25957E-29
MIMAT0024598	1.04	1.64057E-26
MIMAT0015082	1.04	2.35573E-07
MIMAT0027468	1.04	6.21763E-15
MIMAT0019885	1.04	3.52655E-07
MIMAT0019844	1.04	1.31547E-09
MIMAT0007347	1.04	2.66726E-14
MIMAT0019913	1.04	4.06948E-06
MIMAT0005922	1.04	6.02342E-08
MIMAT0007892	1.03	1.82104E-10
MIMAT0022941	1.03	1.03103E-14
MIMAT0027478	1.03	2.30412E-09
MIMAT0027462	1.03	6.63171E-14
MIMAT0030996	1.03	8.18196E-24
MIMAT0016889	1.03	1.36571E-08
MIMAT0019859	1.03	1.41786E-17
MIMAT0018076	1.02	1.29884E-09
MIMAT0025854	1.02	2.70013E-08
MIMAT0027600	1.02	4.94199E-10
MIMAT0018178	1.02	0.000146083
MIMAT0015058	1.02	0.000311673
MIMAT0027430	1.02	9.63375E-05
MIMAT0027359	1.02	1.92975E-19
MIMAT0015080	1.02	8.46838E-09
MIMAT0019027	1.02	3.10899E-05
MIMAT0019229	1.02	1.45871E-05
MIMAT0027506	1.02	6.17123E-06
MIMAT0023714	1.01	4.67037E-05
MIMAT0023715	1.01	2.81573E-05
MIMAT0019045	1.01	0.000618078
MIMAT0018087	1.01	0.000503668

B, Down-regulated

MIMAT0027355	0.99	1.8531E-08
MIMAT0019032	0.98	0.000248847
MIMAT0018002	0.98	1.43758E-09
MIMAT0013802	0.98	5.97728E-16
MIMAT0019053	0.97	3.96528E-12
MIMAT0004609	0.97	9.39274E-10
MIMAT0018085	0.97	8.19974E-12
MIMAT0019903	0.97	2.9412E-13
MIMAT0028111	0.97	1.60749E-06
MIMAT0019071	0.97	1.38421E-09
MIMAT0019791	0.96	1.19522E-07
MIMAT0027458	0.96	2.06857E-09
MIMAT0016907	0.96	3.17507E-16
MIMAT0016901	0.96	3.04798E-08
MIMAT0030986	0.96	1.32239E-05
MIMAT0015036	0.96	0.000161619
MIMAT0031095	0.96	3.10661E-08
MIMAT0027504	0.95	3.88192E-13
MIMAT0019711	0.95	3.14351E-08
MIMAT0019778	0.95	2.07123E-11
MIMAT0027654	0.95	3.66152E-09
MIMAT0027398	0.95	8.77009E-23
MIMAT0023713	0.94	1.63927E-14
MIMAT0022938	0.94	2.50738E-15
MIMAT0018976	0.94	1.54102E-12
MIMAT0019715	0.94	1.07153E-39
MIMAT0019777	0.94	1.70759E-09
MIMAT0027470	0.93	5.97849E-10
MIMAT0005867	0.93	3.34976E-13
MIMAT0004284	0.93	7.34197E-07
MIMAT0018960	0.93	8.60882E-18
MIMAT0027412	0.93	6.87098E-25
MIMAT0019739	0.93	2.96185E-18
MIMAT0023711	0.93	0.000230244
MIMAT0031178	0.93	2.72302E-12
MIMAT0016849	0.92	2.28415E-15
MIMAT0024615	0.92	5.48036E-12
MIMAT0015028	0.92	1.04431E-05
MIMAT0004687	0.92	5.28798E-12
MIMAT0027438	0.92	1.49477E-10
MIMAT0028115	0.92	8.2719E-22
MIMAT0019757	0.92	3.23531E-10

MIMAT0019838	0.92	3.73143E-15
MIMAT0027623	0.92	7.24504E-15
MIMAT0027377	0.92	4.5576E-12
MIMAT0027620	0.92	2.20744E-10
MIMAT0007890	0.92	1.14239E-19
MIMAT0027583	0.92	1.75255E-18
MIMAT0027540	0.92	4.05818E-10
MIMAT0019806	0.91	1.57576E-19
MIMAT0019849	0.91	6.47526E-19
MIMAT0019073	0.91	1.48744E-08
MIMAT0022693	0.91	2.42079E-20
MIMAT0019003	0.91	2.90256E-05
MIMAT0022694	0.91	0.000184285
MIMAT0018985	0.91	9.96065E-11
MIMAT0027431	0.91	1.11177E-09
MIMAT0019779	0.91	2.45927E-06
MIMAT0003307	0.90	0.000448136
MIMAT0005865	0.90	1.05726E-09
MIMAT0031119	0.90	6.42304E-07
MIMAT0004748	0.90	6.45485E-09
MIMAT0020924	0.90	1.00144E-14
MIMAT0022943	0.90	8.82585E-35
MIMAT0018444	0.90	1.86333E-17
MIMAT0019836	0.90	5.76413E-07
MIMAT0027432	0.88	3.43794E-09
MIMAT0004800	0.88	1.24901E-05
MIMAT0004561	0.88	5.75004E-22
MIMAT0021127	0.88	1.00783E-16
MIMAT0027490	0.87	1.15354E-12
MIMAT0003880	0.87	3.90936E-13
MIMAT0001631	0.87	1.30228E-05
MIMAT0023694	0.87	0.000763878
MIMAT0003282	0.87	1.00732E-08
MIMAT0030990	0.87	2.80497E-27
MIMAT0022709	0.87	1.40818E-09
MIMAT0022491	0.87	7.23071E-07
MIMAT0027474	0.87	2.3153E-50
MIMAT0023698	0.86	0.000218592
MIMAT0011163	0.86	2.73912E-09
MIMAT0027454	0.86	7.88962E-14
MIMAT0018072	0.86	2.97705E-09
MIMAT0027686	0.85	4.57835E-23
MIMAT0027383	0.85	2.23269E-33

MIMAT0016852	0.85	3.14244E-13
MIMAT0026612	0.85	0.000376814
MIMAT0028109	0.85	1.43605E-11
MIMAT0022838	0.85	0.00010789
MIMAT0004610	0.84	9.70083E-12
MIMAT0004679	0.84	6.81454E-11
MIMAT0027353	0.84	1.40039E-64
MIMAT0019050	0.83	1.3866E-13
MIMAT0027371	0.82	6.34556E-11
MIMAT0000078	0.82	4.33339E-06
MIMAT0000080	0.82	2.80592E-10
MIMAT0027514	0.82	1.22087E-14
MIMAT0019695	0.81	1.45843E-09
MIMAT0027392	0.81	3.0491E-34
MIMAT0027494	0.81	4.54649E-13
MIMAT0027414	0.81	3.30923E-37
MIMAT0000440	0.81	0.000803691
MIMAT0030979	0.80	1.86206E-13
MIMAT0000077	0.80	6.96253E-06
MIMAT0024782	0.80	2.42833E-18
MIMAT0019737	0.80	1.93105E-07
MIMAT0022698	0.79	1.20791E-14
MIMAT0004552	0.78	0.000502303
MIMAT0019006	0.78	2.18797E-07
MIMAT0004804	0.78	5.80044E-22
MIMAT0019072	0.78	2.79401E-06
MIMAT0025846	0.78	4.65066E-23
MIMAT0019946	0.77	4.18102E-06
MIMAT0018191	0.77	1.13987E-24
MIMAT0018945	0.77	1.3901E-08
MIMAT0025486	0.76	2.11714E-12
MIMAT0027674	0.76	2.24371E-29
MIMAT0027630	0.76	3.30855E-14
MIMAT0003240	0.76	3.6236E-10
MIMAT0019034	0.75	3.54005E-25
MIMAT0000418	0.75	5.67812E-10
MIMAT0019771	0.75	1.04136E-17
MIMAT0019867	0.75	1.38635E-11
MIMAT0027394	0.75	1.06916E-10
MIMAT0019082	0.74	1.19458E-07
MIMAT0007891	0.74	3.48935E-14
MIMAT0019211	0.74	5.03097E-12
MIMAT0022925	0.74	0.000305641

MIMAT0019033	0.74	2.42435E-06
MIMAT0015075	0.73	3.50163E-29
MIMAT0019835	0.72	5.32332E-12
MIMAT0018943	0.72	8.39144E-10
MIMAT0018110	0.72	0.000293487
MIMAT0027363	0.72	6.48151E-15
MIMAT0014996	0.72	1.27792E-44
MIMAT0027570	0.71	1.65722E-12
MIMAT0003337	0.71	5.58837E-05
MIMAT0027486	0.71	5.04146E-06
MIMAT0019776	0.70	3.29699E-48
MIMAT0000093	0.70	3.35174E-05
MIMAT0018967	0.70	6.38882E-07
MIMAT0019696	0.69	2.47179E-09
MIMAT0027530	0.69	3.44089E-07
MIMAT0019874	0.69	2.37336E-11
MIMAT0018944	0.69	1.59095E-24
MIMAT0019888	0.68	4.66613E-23
MIMAT0015023	0.68	8.01759E-06
MIMAT0004602	0.68	8.07369E-15
MIMAT0004496	0.67	1.7286E-05
MIMAT0027552	0.67	6.532E-32
MIMAT0000421	0.67	4.2841E-05
MIMAT0025847	0.66	4.05529E-27
MIMAT0018360	0.66	0.000500361
MIMAT0027492	0.66	0.00091614
MIMAT0000101	0.66	7.45952E-12
MIMAT0015030	0.66	1.49581E-11
MIMAT0000063	0.65	1.48918E-08
MIMAT0018971	0.65	1.24432E-15
MIMAT0027524	0.65	1.23875E-43
MIMAT0000722	0.65	8.12855E-24
MIMAT0018931	0.65	5.80942E-20
MIMAT0018003	0.65	8.45022E-33
MIMAT0015087	0.64	4.83095E-14
MIMAT0016878	0.64	1.79889E-63
MIMAT0027396	0.64	1.5459E-21
MIMAT0027684	0.63	4.42501E-22
MIMAT0000445	0.63	1.02607E-07
MIMAT0000075	0.63	0.000422021
MIMAT0019793	0.62	1.47918E-13
MIMAT0005458	0.61	6.9329E-15
MIMAT0002847	0.61	0.00017871

MIMAT0000417	0.61	6.18646E-06
MIMAT0028230	0.61	6.05391E-09
MIMAT0018084	0.61	2.0089E-05
MIMAT0029782	0.60	2.5155E-37
MIMAT0000076	0.60	0.000529846
MIMAT0003330	0.59	1.16295E-05
MIMAT0018349	0.59	8.03286E-19
MIMAT0000062	0.59	1.57287E-10
MIMAT0000104	0.59	2.31781E-14
MIMAT0027406	0.58	8.48602E-24
MIMAT0000070	0.58	1.11022E-08
MIMAT0019021	0.58	2.06219E-06
MIMAT0021033	0.58	6.51797E-13
MIMAT0019075	0.58	2.53771E-27
MIMAT0019953	0.57	1.24003E-06
MIMAT0016880	0.57	7.40496E-42
MIMAT0004592	0.55	3.25544E-08
MIMAT0004694	0.55	7.12984E-06
MIMAT0004970	0.55	9.8772E-39
MIMAT0019858	0.55	1.175E-07
MIMAT0017987	0.55	1.24434E-20
MIMAT0000084	0.53	1.39446E-05
MIMAT0026608	0.53	0.00011803
MIMAT0003228	0.53	3.101E-33
MIMAT0018986	0.53	2.31161E-40
MIMAT0000064	0.53	1.38044E-11
MIMAT0019899	0.52	8.92039E-19
MIMAT0027460	0.51	1.54447E-08
MIMAT0000449	0.51	0.000494802
MIMAT0019815	0.51	7.71338E-18
MIMAT0000065	0.51	1.45642E-13
MIMAT0000716	0.51	2.19557E-13
MIMAT0000415	0.51	0.000771894
MIMAT0014984	0.50	2.15853E-22
MIMAT0027408	0.50	1.99587E-11
MIMAT0015026	0.50	6.25248E-12
MIMAT0015053	0.50	8.03792E-13
MIMAT0027560	0.50	2.40213E-12
MIMAT0016867	0.49	0.000202368
MIMAT0004614	0.49	7.03437E-08
MIMAT0001413	0.49	7.89729E-07
MIMAT0015054	0.49	1.26147E-08
MIMAT0016851	0.49	1.22779E-09

MIMAT0004696	0.49	3.77712E-07
MIMAT0027400	0.48	9.49788E-15
MIMAT0027680	0.46	1.28791E-26
MIMAT0025855	0.46	1.35074E-12
MIMAT0000457	0.45	8.1553E-11
MIMAT0030987	0.45	1.15556E-44
MIMAT0000082	0.45	3.8243E-14
MIMAT0027520	0.45	1.90894E-27
MIMAT0018165	0.45	1.10972E-23
MIMAT0004949	0.44	1.47881E-21
MIMAT0000103	0.44	6.36762E-13
MIMAT0016854	0.44	4.84886E-05
MIMAT0031012	0.44	5.22544E-11
MIMAT0000068	0.44	5.32199E-09
MIMAT0000087	0.44	6.83078E-05
MIMAT0002877	0.43	7.20045E-22
MIMAT0005943	0.43	9.26245E-08
MIMAT0019827	0.43	0.000123096
MIMAT0005942	0.43	1.86948E-28
MIMAT0027420	0.43	1.13061E-32
MIMAT0026481	0.43	5.17452E-05
MIMAT0021120	0.43	7.61403E-24
MIMAT0019958	0.42	6.00789E-31
MIMAT0018958	0.42	2.75393E-09
MIMAT0019707	0.41	6.49506E-13
MIMAT0027642	0.41	3.34635E-18
MIMAT0018997	0.40	5.34534E-15
MIMAT0022833	0.40	3.76607E-15
MIMAT0026609	0.39	4.80916E-06
MIMAT0018185	0.38	2.42325E-18
MIMAT0003261	0.38	1.12873E-05
MIMAT0014986	0.38	2.193E-11
MIMAT0015017	0.37	0.000137984
MIMAT0019023	0.37	5.66371E-29
MIMAT0004498	0.37	3.49108E-10
MIMAT0019061	0.37	6.24493E-09
MIMAT0031005	0.35	2.12835E-10
MIMAT0005905	0.34	4.33122E-33
MIMAT0018351	0.33	4.98099E-06
MIMAT0002845, MIMAT0005455, MIMAT0005456	0.31	1.2431E-07
MIMAT0027662	0.31	3.94149E-22
MIMAT0027598	0.31	2.14508E-53

MIMAT0018005	0.31	4.29099E-40
MIMAT0030991	0.31	2.76753E-23
MIMAT0022839	0.31	4.28593E-10
MIMAT0027672	0.30	0.000336018
MIMAT0026917	0.30	4.85524E-06
MIMAT0002831, MIMAT0005449, MIMAT0005450, MIMAT0005451, MIMAT0005452, MIMAT0005454	0.30	4.51553E-06
MIMAT0021123	0.29	2.75653E-07
MIMAT0003340	0.29	1.74168E-29
MIMAT0016872	0.28	0.000872533
MIMAT0019848	0.28	4.30804E-33
MIMAT0019012	0.28	0.000120021
MIMAT0005576	0.28	4.16213E-05
MIMAT0019821	0.28	2.21437E-08
MIMAT0002816	0.28	4.5319E-08
MIMAT0019051	0.27	7.54677E-19
MIMAT0007349	0.27	8.58203E-26
MIMAT0027373	0.26	1.00763E-15
MIMAT0016853	0.26	4.62345E-05
MIMAT0030411	0.26	4.88066E-12
MIMAT0027361	0.24	3.69005E-10
MIMAT0000067	0.24	6.23033E-08
MIMAT0030429	0.23	9.47683E-11
MIMAT0025459	0.23	2.67648E-33
MIMAT0018962	0.22	0.00010486
MIMAT0004794	0.20	6.32038E-54
MIMAT0018200	0.20	3.26143E-22
MIMAT0027652	0.20	0.000655608
MIMAT0003320	0.19	2.00032E-48
MIMAT0000066	0.18	0.000160408
MIMAT0027556	0.18	5.19307E-09
MIMAT0019932	0.17	1.52221E-36
MIMAT0019031	0.16	5.32962E-43
MIMAT0022737	0.15	0.000230383
MIMAT0000454	0.15	8.17936E-11
MIMAT0016845	0.14	2.20351E-05
MIMAT0027357	0.14	6.69321E-06
MIMAT0026620	0.14	7.38251E-05
MIMAT0019796	0.14	1.05905E-09
MIMAT0019692	0.13	1.4665E-37
MIMAT0019081	0.13	6.06216E-36

MIMAT0004776	0.11	1.18477E-15
MIMAT0018103	0.10	0.000742349
MIMAT0027389	0.10	6.97628E-39
MIMAT0027618	0.07	4.6595E-23
MIMAT0015005	0.07	4.93078E-34
MIMAT0019941	0.07	1.84851E-16
MIMAT0015076	0.06	2.875E-16
MIMAT0027646	0.05	1.7854E-09
MIMAT0002835	0.05	2.00917E-05
MIMAT0026636	0.05	1.01685E-41
MIMAT0027502	0.04	0.000567824
MIMAT0000422	0.04	1.47809E-29
MIMAT0000414	0.01	2.49471E-22

CRC, colorectal cancer.

Supplementary Table 2. The details of statistics related to each of the binary classification models over the 100 iterations of leave-one-out cross validations.

No. of LOO repeat	A, Using 569 DEMs			B, Using top three ranked features		
	Sn	Sp	ACC	Sn	Sp	ACC
1	1	1	1	0.94	0.99	0.98
2	1	0.98	0.99	0.96	0.99	0.98
3	1	1	1	0.91	0.98	0.96
4	1	1	1	0.90	0.99	0.98
5	1	0.97	0.98	0.96	0.99	0.98
6	1	0.99	1	0.95	0.99	0.98
7	1	1	1	0.94	1	0.99
8	1	0.99	0.99	0.97	0.99	0.98
9	1	1	1	0.98	0.98	0.98
10	1	0.99	1	0.97	1	0.99
11	1	0.99	1	1	0.99	0.99
12	1	0.97	0.98	1	1	1
13	1	0.99	0.99	1	0.95	0.97
14	1	0.99	0.99	0.98	0.99	0.99
15	1	1	1	0.93	1	0.99
16	1	1	1	1	0.99	1
17	1	0.96	0.97	0.95	0.98	0.98
18	1	1	1	0.98	1	1
19	1	0.99	0.99	0.95	0.98	0.97

20	1	0.98	0.98	1	0.99	1
21	1	1	1	0.86	0.99	0.96
22	1	0.97	0.98	1	0.98	0.99
23	1	0.99	1	0.95	1	0.99
24	1	0.99	1	0.88	0.99	0.97
25	1	0.99	0.99	0.94	0.99	0.98
26	1	1	1	0.91	0.99	0.97
27	1	0.99	1	0.98	0.97	0.97
28	1	0.99	0.99	0.95	0.99	0.98
29	1	0.99	0.99	1	1	1
30	1	0.99	0.99	0.98	0.98	0.98
31	1	1	1	0.98	0.99	0.99
32	1	0.99	1	0.93	1.00	0.98
33	1	1	1	1	0.99	1
34	1	1	1	0.95	0.97	0.97
35	1	0.99	1	1	0.99	0.99
36	1	1	1	0.98	0.98	0.98
37	1	0.99	1	0.92	0.99	0.98
38	1	1	1	0.93	0.99	0.98
39	1	0.99	1	0.92	0.99	0.97
40	1	0.99	1	0.94	0.99	0.98
41	1	1	1	0.97	0.99	0.98
42	1	1	1	0.96	0.97	0.97
43	1	1	1	0.96	0.98	0.98
44	1	0.99	1	1	1	1
45	1	1	1	0.95	0.97	0.97
46	1	0.99	1	0.94	1	0.99
47	1	0.99	1	0.98	1	1
48	1	0.99	1	1	0.97	0.98
49	1	0.99	0.99	0.92	0.98	0.97
50	1	0.99	1	1	0.99	1
51	1	1	1	1	1	1
52	1	1	1	0.91	1	0.98
53	1	0.99	1.00	0.95	0.99	0.98
54	1	1	1	0.96	0.99	0.98
55	1	0.97	0.98	0.90	0.99	0.97
56	1	0.99	1	1	0.99	0.99
57	1	0.99	1	0.90	0.96	0.94
58	1	0.97	0.98	0.95	0.99	0.98
59	1	1	1	1	0.99	1
60	1	0.99	1.00	0.92	0.99	0.98

61	1	0.99	1	0.98	1	1
62	1	1	1	0.98	0.99	0.99
63	1	1	1	1	0.97	0.98
64	1	1	1	0.97	0.99	0.99
65	1	1	1	1	0.97	0.98
66	1	1	1	0.96	0.99	0.99
67	1	0.99	1	0.91	1	0.98
68	1	1	1	0.98	0.99	0.99
69	1	1	1	1	0.99	1
70	1	0.99	0.99	0.94	0.99	0.98
71	1	0.99	1	0.93	0.99	0.97
72	1	0.99	1	0.96	1	0.99
73	1	0.99	1	0.95	0.99	0.98
74	1	1	1	1	0.99	0.99
75	1	0.99	1	0.92	0.98	0.97
76	1	1	1	0.93	0.99	0.98
77	1	1	1	0.94	1	0.99
78	1	0.98	0.99	0.98	0.99	0.99
79	1	1	1	0.96	0.99	0.98
80	1	0.98	0.99	0.98	0.99	0.99
81	1	0.99	0.99	0.96	0.99	0.98
82	1	0.98	0.99	0.97	0.99	0.98
83	1	0.99	1	0.98	0.99	0.99
84	1	0.99	0.99	0.97	0.99	0.99
85	1	0.99	1	0.98	0.99	0.99
86	1	0.99	0.99	0.98	1	1
87	1	1	1	0.91	0.97	0.96
88	1	0.99	1	0.92	0.97	0.96
89	1	0.99	0.99	1	0.98	0.99
90	1	0.99	0.99	0.96	0.99	0.99
91	1	1	1	0.87	0.98	0.95
92	1	0.99	1	0.93	0.99	0.98
93	1	0.99	1	0.93	0.98	0.96
94	1	1	1	0.98	0.99	0.99
95	1	0.99	1	1	1	1
96	1	1	1	1	0.99	0.99
97	1	0.99	1	1	0.98	0.99
98	1	1	1	0.95	0.99	0.98
99	1	1	1	0.98	0.99	0.99
100	1	1	1	0.97	0.99	0.99

DEM, differentially expressed miRNAs; LOO, leave-one-out; Sn, sensitivity; Sp, specificity; ACC, accuracy.

Supplementary Table 3. Signaling pathway enrichment analysis of the genes involved in the most important clusters in the protein-protein interaction network associated with colorectal cancer.

Cluster no.	Pathway ID (R-HAS-)	Pathway name	#Entities found	#Entities total	FDR
1	73857	RNA Polymerase II Transcription	281	1379	1.33E-15
	212436	Generic Transcription Pathway	281	1257	1.33E-15
	74160	Gene expression (Transcription)	281	1521	1.33E-15
2	156902	Peptide chain elongation	81	90	1.44E-15
	975956	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	79	96	1.44E-15
	72689	Formation of a pool of free 40S subunits	80	102	1.44E-15
	192823	Viral mRNA Translation	79	101	1.44E-15
	156827	L13a-mediated translational silencing of Ceruloplasmin expression	80	112	1.44E-15
	72706	GTP hydrolysis and joining of the 60S ribosomal subunit	80	113	1.44E-15
	1799339	SRP-dependent cotranslational protein targeting to membrane	79	113	1.44E-15
	72649	Translation initiation complex formation	34	59	1.44E-15
	72702	Ribosomal scanning and start codon recognition	34	59	1.44E-15
	156842	Eukaryotic Translation Elongation	81	95	1.44E-15
	6791226	Major pathway of rRNA processing in the nucleolus and cytosol	79	183	1.44E-15
	927802	Nonsense-Mediated Decay (NMD)	79	117	1.44E-15
	975957	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	79	117	1.44E-15
	72613	Eukaryotic Translation Initiation	80	120	1.44E-15
	72764	Eukaryotic Translation Termination	79	94	1.44E-15
	72737	Cap-dependent Translation Initiation	80	120	1.44E-15
	8868773	rRNA processing in the nucleus and cytosol	79	193	1.44E-15
72695	Formation of the ternary complex, and subsequently, the 43S complex	34	52	1.44E-15	
72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	34	60	1.44E-15	

72312	rRNA processing	79	203	1.44E-15
72766	Translation	82	294	1.44E-15
2408557	Selenocysteine synthesis	79	94	1.44E-15
9010553	Regulation of expression of SLITs and ROBOs	79	172	1.44E-15
9633012	Response of EIF2AK4 (GCN2) to amino acid deficiency	79	102	1.44E-15
392499	Metabolism of proteins	89	2012	1.44E-15
168273	Influenza Viral RNA Transcription and Replication	79	151	1.44E-15
2408522	Selenoamino acid metabolism	79	118	1.44E-15
376176	Signaling by ROBO receptors	79	218	1.44E-15
8953854	Metabolism of RNA	80	675	1.44E-15
5663205	Infectious disease	81	1040	1.44E-15
1643685	Disease	83	1735	1.44E-15
2262752	Cellular responses to stress	80	564	1.44E-15
8953897	Cellular responses to external stimuli	80	578	1.44E-15
168255	Influenza Infection	79	171	1.44E-15
422475	Axon guidance	79	558	1.44E-15
9675108	Nervous system development	79	584	1.44E-15
1266738	Developmental Biology	79	1100	1.44E-15
71291	Metabolism of amino acids and derivatives	79	376	1.44E-15
1430728	Metabolism	79	2142	1.44E-15
6790901	rRNA modification in the nucleus and cytosol	5	60	1.68E-03
936440	Negative regulators of DDX58/IFIH1 signaling	4	34	2.24E-03
5684264	MAP3K8 (TPL2)-dependent MAPK1/3 activation	3	16	3.07E-03
8876725	Protein methylation	3	17	3.66E-03
9613829	Chaperone Mediated Autophagy	3	22	6.93E-03
917937	Iron uptake and transport	4	58	1.14E-02
5357956	TNFR1-induced NFkappaB signaling pathway	3	30	1.68E-02
5656169	Termination of translesion DNA synthesis	3	32	1.95E-02
8948747	Regulation of PTEN localization	2	9	1.95E-02
3785653	Myoclonic epilepsy of Lafora	2	9	1.95E-02
8849469	PTK6 Regulates RTKs and Their Effectors AKT1 and DOK1	2	9	1.95E-02
937042	IRAK2 mediated activation of TAK1 complex	2	10	2.35E-02
8876493	InlA-mediated entry of Listeria monocytogenes into host cells	2	10	2.35E-02
168638	NOD1/2 Signaling Pathway	3	36	2.35E-02
5357905	Regulation of TNFR1 signaling	3	37	2.35E-02

168928	DDX58/IFIH1-mediated induction of interferon-alpha/beta	4	77	2.45E-02
9014325	TICAM1,TRAF6-dependent induction of TAK1 complex	2	11	2.52E-02
9645460	Alpha-protein kinase 1 signaling pathway	2	11	2.52E-02
1253288	Downregulation of ERBB4 signaling	2	11	2.52E-02
9637628	Modulation by Mtb of host immune system	2	11	2.52E-02
9664873	Pexophagy	2	11	2.52E-02
5689896	Ovarian tumor domain proteases	3	38	2.53E-02
110313	Translesion synthesis by Y family DNA polymerases bypasses lesions on DNA template	3	39	2.56E-02
5689877	Josephin domain DUBs	2	12	2.56E-02
9013973	TICAM1-dependent activation of IRF3/IRF7	2	12	2.56E-02
209560	NF-kB is activated and signals survival	2	13	2.87E-02
69231	Cyclin D associated events in G1	3	44	2.87E-02
69236	G1 Phase	3	44	2.87E-02
1358803	Downregulation of ERBB2:ERBB3 signaling	2	14	2.87E-02
937039	IRAK1 recruits IKK complex	2	14	2.87E-02
975144	IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation	2	14	2.87E-02
975110	TRAF6 mediated IRF7 activation in TLR7/8 or 9 signaling	2	14	2.87E-02
209543	p75NTR recruits signalling complexes	2	14	2.87E-02
75893	TNF signaling	3	47	2.96E-02
975163	IRAK2 mediated activation of TAK1 complex upon TLR7/8 or 9 stimulation	2	15	2.96E-02
174490	Membrane binding and targetting of GAG proteins	2	15	2.96E-02
174495	Synthesis And Processing Of GAG, GAGPOL Polyproteins	2	15	2.96E-02
3134975	Regulation of innate immune responses to cytosolic DNA	2	15	2.96E-02
2691230	Signaling by NOTCH1 HD Domain Mutants in Cancer	2	15	2.96E-02
2691232	Constitutive Signaling by NOTCH1 HD Domain Mutants	2	15	2.96E-02
73893	DNA Damage Bypass	3	48	2.96E-02
2122947	NOTCH1 Intracellular Domain Regulates Transcription	3	49	2.96E-02
937072	TRAF6-mediated induction of TAK1 complex within TLR4 complex	2	16	2.96E-02
110312	Translesion synthesis by REV1	2	16	2.96E-02
205043	NRIF signals cell death from the nucleus	2	16	2.96E-02

2173791	TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition)	2	16	2.96E-02
1295596	Spry regulation of FGF signaling	2	16	2.96E-02
3229121	Glycogen storage diseases	2	16	2.96E-02
3322077	Glycogen synthesis	2	16	2.96E-02
5656121	Translesion synthesis by POLI	2	17	2.96E-02
5655862	Translesion synthesis by POLK	2	17	2.96E-02
8875360	InlB-mediated entry of Listeria monocytogenes into host cell	2	17	2.96E-02
936964	Activation of IRF3/IRF7 mediated by TBK1/IKK epsilon	2	17	2.96E-02
193639	p75NTR signals via NF-kB	2	17	2.96E-02
9636383	Prevention of phagosomal-lysosomal fusion	2	18	2.96E-02
8854050	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	3	55	2.96E-02
174113	SCF-beta-TrCP mediated degradation of Emi1	3	55	2.96E-02
9604323	Negative regulation of NOTCH4 signaling	3	55	2.96E-02
110320	Translesion Synthesis by POLH	2	19	2.96E-02
168927	TICAM1, RIP1-mediated IKK complex recruitment	2	19	2.96E-02
6804760	Regulation of TP53 Activity through Methylation	2	19	2.96E-02
4641258	Degradation of DVL	3	57	2.96E-02
1236382	Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants	2	20	2.96E-02
5637815	Signaling by Ligand-Responsive EGFR Variants in Cancer	2	20	2.96E-02
5676590	NIK-->noncanonical NF-kB signaling	3	59	2.96E-02
2644603	Signaling by NOTCH1 in Cancer	3	59	2.96E-02
168643	Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways	3	59	2.96E-02
2894862	Constitutive Signaling by NOTCH1 HD+PEST Domain Mutants	3	59	2.96E-02
2894858	Signaling by NOTCH1 HD+PEST Domain Mutants in Cancer	3	59	2.96E-02
2644606	Constitutive Signaling by NOTCH1 PEST Domain Mutants	3	59	2.96E-02
2644602	Signaling by NOTCH1 PEST Domain Mutants in Cancer	3	59	2.96E-02
4641263	Regulation of FZD by ubiquitination	2	21	2.96E-02
6807004	Negative regulation of MET activity	2	21	2.96E-02
901032	ER Quality Control Compartment (ERQC)	2	21	2.96E-02
5675482	Regulation of necroptotic cell death	2	21	2.96E-02

187577	SCF(Skp2)-mediated degradation of p27/p21	3	60	2.96E-02
5607761	Dectin-1 mediated noncanonical NF- κ B signaling	3	60	2.96E-02
5610783	Degradation of GLI2 by the proteasome	3	60	2.96E-02
5610785	GLI3 is processed to GLI3R by the proteasome	3	60	2.96E-02
5610780	Degradation of GLI1 by the proteasome	3	60	2.96E-02
450321	JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1	2	22	2.96E-02
2979096	NOTCH2 Activation and Transmission of Signal to the Nucleus	2	22	2.96E-02
912631	Regulation of signaling by CBL	2	22	2.96E-02
5205685	Pink/Parkin Mediated Mitophagy	2	22	2.96E-02
450294	MAP kinase activation	3	63	2.96E-02
174048	APC/C:Cdc20 mediated degradation of Cyclin B	2	23	2.96E-02
2173795	Downregulation of SMAD2/3:SMAD4 transcriptional activity	2	23	2.96E-02
937041	IKK complex recruitment mediated by RIP1	2	23	2.96E-02
8876384	Listeria monocytogenes entry into host cells	2	23	2.96E-02
450302	activated TAK1 mediates p38 MAPK activation	2	23	2.96E-02
9637687	Suppression of phagosomal maturation	2	23	2.96E-02
5213460	RIPK1-mediated regulated necrosis	2	23	2.96E-02
5218859	Regulated Necrosis	2	23	2.96E-02
175474	Assembly Of The HIV Virion	2	24	3.21E-02
1169091	Activation of NF-kappaB in B cells	3	67	3.37E-02
5696397	Gap-filling DNA repair synthesis and ligation in GG-NER	2	25	3.46E-02
179409	APC-Cdc20 mediated degradation of Nek2A	2	25	3.46E-02
9013507	NOTCH3 Activation and Transmission of Signal to the Nucleus	2	25	3.46E-02
400253	Circadian Clock	3	68	3.50E-02
5658442	Regulation of RAS by GAPs	3	69	3.63E-02
2173788	Downregulation of TGF-beta receptor signaling	2	26	3.73E-02
901042	Calnexin/calreticulin cycle	2	26	3.73E-02
1643713	Signaling by EGFR in Cancer	2	26	3.73E-02
68949	Orc1 removal from chromatin	3	71	3.92E-02
448424	Interleukin-17 signaling	3	71	3.92E-02

8982491	Glycogen metabolism	2	27	4.00E-02
8939902	Regulation of RUNX2 expression and activity	3	74	4.20E-02
1980143	Signaling by NOTCH1	3	75	4.20E-02
5205647	Mitophagy	2	29	4.20E-02
8866652	Synthesis of active ubiquitin: roles of E1 and E2 enzymes	2	30	4.20E-02
110314	Recognition of DNA damage by PCNA-containing replication complex	2	30	4.20E-02
5654732	Negative regulation of FGFR3 signaling	2	30	4.20E-02
917729	Endosomal Sorting Complex Required For Transport (ESCRT)	2	31	4.20E-02
5689901	Metalloprotease DUBs	2	31	4.20E-02
182971	EGFR downregulation	2	31	4.20E-02
2122948	Activated NOTCH1 Transmits Signal to the Nucleus	2	31	4.20E-02
5654733	Negative regulation of FGFR4 signaling	2	31	4.20E-02
1169408	ISG15 antiviral mechanism	3	80	4.20E-02
176408	Regulation of APC/C activators between G1/S and early anaphase	3	80	4.20E-02
6806834	Signaling by MET	3	80	4.20E-02
8863795	Downregulation of ERBB2 signaling	2	32	4.20E-02
2173789	TGF-beta receptor signaling activates SMADs	2	32	4.20E-02
445989	TAK1 activates NFkB by phosphorylation and activation of IKKs complex	2	32	4.20E-02
2173796	SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	2	32	4.20E-02
1168372	Downstream signaling events of B Cell Receptor (BCR)	3	82	4.20E-02
1980145	Signaling by NOTCH2	2	33	4.20E-02
69202	Cyclin E associated events during G1/S transition	3	83	4.20E-02
195253	Degradation of beta-catenin by the destruction complex	3	83	4.20E-02
9013694	Signaling by NOTCH4	3	83	4.20E-02
9615710	Late endosomal microautophagy	2	34	4.20E-02
2559585	Oncogene Induced Senescence	2	34	4.20E-02
5663084	Diseases of carbohydrate metabolism	2	34	4.20E-02
69656	Cyclin A:Cdk2-associated events at S phase entry	3	85	4.20E-02
975871	MyD88 cascade initiated on plasma membrane	3	85	4.20E-02
168176	Toll Like Receptor 5 (TLR5) Cascade	3	85	4.20E-02
168142	Toll Like Receptor 10 (TLR10) Cascade	3	85	4.20E-02

5632684	Hedgehog 'on' state	3	85	4.20E-02
174143	APC/C-mediated degradation of cell cycle proteins	3	86	4.20E-02
453276	Regulation of mitotic cell cycle	3	86	4.20E-02
532668	N-glycan trimming in the ER and Calnexin/Calreticulin cycle	2	35	4.20E-02
5654726	Negative regulation of FGFR1 signaling	2	35	4.20E-02
5358351	Signaling by Hedgehog	4	150	4.20E-02
2565942	Regulation of PLK1 Activity at G2/M Transition	3	87	4.20E-02
162588	Budding and maturation of HIV virion	2	36	4.20E-02
6804757	Regulation of TP53 Degradation	2	36	4.20E-02
1169410	Antiviral mechanism by IFN-stimulated genes	3	89	4.20E-02
5654727	Negative regulation of FGFR2 signaling	2	37	4.20E-02
6806003	Regulation of TP53 Expression and Degradation	2	37	4.20E-02
69052	Switching of origins to a post-replicative state	3	90	4.20E-02
975138	TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	3	90	4.20E-02
975155	MyD88 dependent cascade initiated on endosome	3	91	4.20E-02
168181	Toll Like Receptor 7/8 (TLR7/8) Cascade	3	91	4.20E-02
5696394	DNA Damage Recognition in GG-NER	2	38	4.20E-02
6783310	Fanconi Anemia Pathway	2	38	4.20E-02
168164	Toll Like Receptor 3 (TLR3) Cascade	3	93	4.20E-02
8869496	TFAP2A acts as a transcriptional repressor during retinoic acid induced cell differentiation	1	5	4.20E-02
9637690	Response of Mtb to phagocytosis	2	39	4.20E-02
168138	Toll Like Receptor 9 (TLR9) Cascade	3	95	4.20E-02
8951664	Neddylaton	5	236	4.20E-02
166058	MyD88:MAL(TIRAP) cascade initiated on plasma membrane	3	96	4.20E-02
168188	Toll Like Receptor TLR6:TLR2 Cascade	3	96	4.20E-02
5696400	Dual Incision in GG-NER	2	41	4.29E-02
5675221	Negative regulation of MAPK pathway	2	41	4.29E-02
937061	TRIF(TICAM1)-mediated TLR4 signaling	3	97	4.31E-02
166166	MyD88-independent TLR4 cascade	3	97	4.31E-02
5607764	CLEC7A (Dectin-1) signaling	3	98	4.42E-02

3769402	Deactivation of the beta-catenin transactivating complex	2	42	4.48E-02
168179	Toll Like Receptor TLR1:TLR2 Cascade	3	99	4.53E-02
181438	Toll Like Receptor 2 (TLR2) Cascade	3	99	4.53E-02
5696395	Formation of Incision Complex in GG-NER	2	43	4.68E-02
5654743	Signaling by FGFR4	2	43	4.68E-02
5654741	Signaling by FGFR3	2	43	4.68E-02
1566977	Fibronectin matrix formation	1	6	4.68E-02
2644605	FBXW7 Mutants and NOTCH1 in Cancer	1	6	4.68E-02
2644607	Loss of Function of FBXW7 in Cancer and NOTCH1 Signaling	1	6	4.68E-02
9646399	Aggrephagy	2	44	4.87E-02
2173793	Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer	2	44	4.87E-02
9020702	Interleukin-1 signaling	3	102	4.88E-02
5668541	TNFR2 non-canonical NF-kB pathway	3	102	4.88E-02
72165	mRNA Splicing - Minor Pathway	43	52	8.88E-16
6803529	FGFR2 alternative splicing	21	26	8.88E-16
77595	Processing of Intronless Pre-mRNAs	14	19	8.88E-16
167242	Abortive elongation of HIV-1 transcript in the absence of Tat	16	23	8.88E-16
75067	Processing of Capped Intronless Pre-mRNA	19	28	8.88E-16
72187	mRNA 3'-end processing	33	57	8.88E-16
72163	mRNA Splicing - Major Pathway	104	180	8.88E-16
73856	RNA Polymerase II Transcription Termination	38	66	8.88E-16
72172	mRNA Splicing	104	188	8.88E-16
72086	mRNA Capping	16	29	8.88E-16
77075	RNA Pol II CTD phosphorylation and interaction with CE	14	27	8.88E-16
167160	RNA Pol II CTD phosphorylation and interaction with CE during HIV infection	14	27	8.88E-16
167158	Formation of the HIV-1 Early Elongation Complex	16	33	8.88E-16
113418	Formation of the Early Elongation Complex	16	33	8.88E-16
72203	Processing of Capped Intron-Containing Pre-mRNA	104	245	8.88E-16
167243	Tat-mediated HIV elongation arrest and recovery	14	35	8.88E-16
167238	Pausing and recovery of Tat-mediated HIV elongation	14	35	8.88E-16
167287	HIV elongation arrest and recovery	14	36	8.88E-16

167290	Pausing and recovery of HIV elongation	14	36	8.88E-16
167152	Formation of HIV elongation complex in the absence of HIV Tat	16	48	8.88E-16
72202	Transport of Mature Transcript to Cytoplasm	24	87	8.88E-16
159236	Transport of Mature mRNA derived from an Intron-Containing Transcript	21	78	8.88E-16
75955	RNA Polymerase II Transcription Elongation	16	61	8.88E-16
112382	Formation of RNA Pol II elongation complex	16	61	8.88E-16
167169	HIV Transcription Elongation	16	47	8.88E-16
6796648	TP53 Regulates Transcription of DNA Repair Genes	16	65	8.88E-16
167246	Tat-mediated elongation of the HIV-1 transcript	16	47	8.88E-16
6807505	RNA polymerase II transcribes snRNA genes	17	74	8.88E-16
167200	Formation of HIV-1 elongation complex containing HIV-1 Tat	16	47	8.88E-16
8851708	Signaling by FGFR2 IIIa TM	16	23	8.88E-16
8953854	Metabolism of RNA	113	675	8.88E-16
74160	Gene expression (Transcription)	57	1521	8.88E-16
73857	RNA Polymerase II Transcription	56	1379	8.88E-16
203927	MicroRNA (miRNA) biogenesis	12	24	8.88E-16
5654738	Signaling by FGFR2	21	78	8.88E-16
1839126	FGFR2 mutant receptor activation	16	38	8.88E-16
5655253	Signaling by FGFR2 in disease	16	49	8.88E-16
190236	Signaling by FGFR	21	95	8.88E-16
76042	RNA Polymerase II Transcription Initiation And Promoter Clearance	14	47	2.33E-15
167162	RNA Polymerase II HIV Promoter Escape	14	47	2.33E-15
73776	RNA Polymerase II Promoter Escape	14	47	2.33E-15
167161	HIV Transcription Initiation	14	47	2.33E-15
75953	RNA Polymerase II Transcription Initiation	14	47	2.33E-15
167172	Transcription of the HIV genome	16	74	2.33E-15
73779	RNA Polymerase II Transcription Pre-Initiation And Promoter Opening	14	47	2.33E-15
1226099	Signaling by FGFR in disease	16	73	2.33E-15
5601884	PIWI-interacting RNA (piRNA) biogenesis	12	29	6.66E-15
168325	Viral Messenger RNA Synthesis	14	52	8.66E-15
674695	RNA Polymerase II Pre-transcription Events	16	84	1.53E-14

6781823	Formation of TC-NER Pre-Incision Complex	13	53	3.00E-13
6781827	Transcription-Coupled Nucleotide Excision Repair (TC-NER)	13	78	3.62E-11
9018519	Estrogen-dependent gene expression	15	120	4.48E-11
168255	Influenza Infection	17	171	5.84E-11
6782210	Gap-filling DNA repair synthesis and ligation in TC-NER	12	64	6.34E-11
6782135	Dual incision in TC-NER	12	65	6.34E-11
168273	Influenza Viral RNA Transcription and Replication	16	151	8.15E-11
162599	Late Phase of HIV Life Cycle	16	152	8.98E-11
111367	SLBP independent Processing of Histone Pre-mRNAs	7	10	1.55E-10
162587	HIV Life Cycle	16	165	2.96E-10
77588	SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs	7	11	2.98E-10
5578749	Transcriptional regulation by small RNAs	12	80	6.67E-10
5696398	Nucleotide Excision Repair	13	110	1.96E-09
5617472	Activation of anterior HOX genes in hindbrain development during early embryogenesis	12	91	2.83E-09
5619507	Activation of HOX genes during differentiation	12	91	2.83E-09
211000	Gene Silencing by RNA	12	110	2.31E-08
8939211	ESR-mediated signaling	15	196	2.33E-08
162906	HIV Infection	16	248	7.51E-08
191859	snRNP Assembly	9	57	7.63E-08
194441	Metabolism of non-coding RNA	9	57	7.63E-08
927802	Nonsense-Mediated Decay (NMD)	11	117	3.68E-07
975957	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	11	117	3.68E-07
9006934	Signaling by Receptor Tyrosine Kinases	21	523	1.26E-06
9006931	Signaling by Nuclear Receptors	15	273	1.65E-06
73894	DNA Repair	16	313	1.71E-06
9010553	Regulation of expression of SLITs and ROBOs	12	172	2.22E-06
3700989	Transcriptional Regulation by TP53	17	367	2.81E-06
73780	RNA Polymerase III Chain Elongation	5	18	8.20E-06
376176	Signaling by ROBO receptors	12	218	2.49E-05
73980	RNA Polymerase III Transcription Termination	5	23	2.67E-05
5663202	Diseases of signal transduction by growth factor receptors and second messengers	16	393	3.12E-05

159231	Transport of Mature mRNA Derived from an Intronless Transcript	6	46	4.77E-05
76066	RNA Polymerase III Transcription Initiation From Type 2 Promoter	5	27	4.77E-05
159234	Transport of Mature mRNAs Derived from Intronless Transcripts	6	47	4.77E-05
76071	RNA Polymerase III Transcription Initiation From Type 3 Promoter	5	28	5.13E-05
76061	RNA Polymerase III Transcription Initiation From Type 1 Promoter	5	28	5.13E-05
73863	RNA Polymerase I Transcription Termination	5	31	8.31E-05
76046	RNA Polymerase III Transcription Initiation	5	36	1.68E-04
5250924	B-WICH complex positively regulates rRNA expression	6	60	1.84E-04
1834949	Cytosolic sensors of pathogen-associated DNA	6	63	2.40E-04
749476	RNA Polymerase III Abortive And Retractive Initiation	5	41	3.08E-04
74158	RNA Polymerase III Transcription	5	41	3.08E-04
975956	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	7	96	3.19E-04
73762	RNA Polymerase I Transcription Initiation	5	47	5.78E-04
5250913	Positive epigenetic regulation of rRNA expression	6	75	6.13E-04
1266738	Developmental Biology	25	1100	1.19E-03
73772	RNA Polymerase I Promoter Escape	5	60	1.75E-03
427413	NoRC negatively regulates rRNA expression	5	75	4.68E-03
5250941	Negative epigenetic regulation of rRNA expression	5	78	5.55E-03
73854	RNA Polymerase I Promoter Clearance	5	79	5.87E-03
212165	Epigenetic regulation of gene expression	6	117	6.07E-03
73864	RNA Polymerase I Transcription	5	80	6.19E-03
8950505	Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	3	37	2.48E-02
159227	Transport of the SLBP independent Mature mRNA	3	39	2.86E-02
159230	Transport of the SLBP Dependant Mature mRNA	3	40	3.07E-02
5663205	Infectious disease	20	1040	3.13E-02
6804116	TP53 Regulates Transcription of Genes Involved in G1 Cell Cycle Arrest	2	14	3.22E-02
9020591	Interleukin-12 signaling	3	46	4.38E-02
72764	Eukaryotic Translation Termination	4	94	4.38E-02
422475	Axon guidance	12	558	4.38E-02

	6804754	Regulation of TP53 Expression	1	2	4.38E-02
	450408	AUF1 (hnRNP D0) binds and destabilizes mRNA	3	56	4.94E-02
	447115	Interleukin-12 family signaling	3	56	4.94E-02
	211733	Regulation of activated PAK-2p34 by proteasome mediated degradation	31	50	4.44E-16
	8854050	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	34	55	4.44E-16
	174113	SCF-beta-TrCP mediated degradation of Emi1	34	55	4.44E-16
	75815	Ubiquitin-dependent degradation of Cyclin D	32	52	4.44E-16
	187577	SCF(Skp2)-mediated degradation of p27/p21	35	60	4.44E-16
	174084	Autodegradation of Cdh1 by Cdh1:APC/C	35	63	4.44E-16
	141424	Amplification of signal from the kinetochores	52	94	4.44E-16
	141444	Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal	52	94	4.44E-16
	174154	APC/C:Cdc20 mediated degradation of Securin	35	67	4.44E-16
	174178	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	37	72	4.44E-16
4	69618	Mitotic Spindle Checkpoint	55	110	4.44E-16
	174184	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	35	72	4.44E-16
	176409	APC/C:Cdc20 mediated degradation of mitotic proteins	36	75	4.44E-16
	179419	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint	35	73	4.44E-16
	176814	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	36	76	4.44E-16
	72702	Ribosomal scanning and start codon recognition	16	59	4.44E-16
	453276	Regulation of mitotic cell cycle	40	86	4.44E-16
	174143	APC/C-mediated degradation of cell cycle proteins	40	86	4.44E-16
	8951664	Neddylation	38	236	4.44E-16
	176408	Regulation of APC/C activators between G1/S and early anaphase	38	80	4.44E-16
	5689880	Ub-specific processing proteases	31	205	4.44E-16
	5688426	Deubiquitination	35	282	4.44E-16
	180534	Vpu mediated degradation of CD4	33	53	4.44E-16
	983168	Antigen processing: Ubiquitination & Proteasome degradation	39	309	4.44E-16

180585	Vif-mediated degradation of APOBEC3G	33	56	4.44E-16
1234176	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	32	66	4.44E-16
2467813	Separation of Sister Chromatids	87	190	4.44E-16
5689603	UCH proteinases	33	96	4.44E-16
4641258	Degradation of DVL	32	57	4.44E-16
68827	CDT1 association with the CDC6:ORC:origin complex	31	59	4.44E-16
69656	Cyclin A:Cdk2-associated events at S phase entry	36	85	4.44E-16
195253	Degradation of beta-catenin by the destruction complex	35	83	4.44E-16
6807070	PTEN Regulation	34	139	4.44E-16
69613	p53-Independent G1/S DNA damage checkpoint	31	52	4.44E-16
69610	p53-Independent DNA Damage Response	31	52	4.44E-16
69601	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	31	52	4.44E-16
5610780	Degradation of GLI1 by the proteasome	34	60	4.44E-16
4641257	Degradation of AXIN	31	55	4.44E-16
450408	AUF1 (hnRNP D0) binds and destabilizes mRNA	31	56	4.44E-16
69017	CDK-mediated phosphorylation and removal of Cdc6	35	72	4.44E-16
68949	Orc1 removal from chromatin	33	71	4.44E-16
69202	Cyclin E associated events during G1/S transition	35	83	4.44E-16
2500257	Resolution of Sister Chromatid Cohesion	52	126	4.44E-16
8948751	Regulation of PTEN stability and activity	31	69	4.44E-16
1234174	Cellular response to hypoxia	32	75	4.44E-16
69052	Switching of origins to a post-replicative state	37	90	4.44E-16
68882	Mitotic Anaphase	87	236	4.44E-16
5678895	Defective CFTR causes cystic fibrosis	31	61	4.44E-16
2555396	Mitotic Metaphase and Anaphase	87	237	4.44E-16
1257604	PIP3 activates AKT signaling	38	276	4.44E-16
5663220	RHO GTPases Activate Formins	54	141	4.44E-16
8939902	Regulation of RUNX2 expression and activity	34	74	4.44E-16
349425	Autodegradation of the E3 ubiquitin ligase COP1	31	52	4.44E-16
169911	Regulation of Apoptosis	31	53	4.44E-16
5610783	Degradation of GLI2 by the proteasome	34	60	4.44E-16

5610785	GLI3 is processed to GLI3R by the proteasome	34	60	4.44E-16
5658442	Regulation of RAS by GAPs	32	69	4.44E-16
68877	Mitotic Prometaphase	52	203	4.44E-16
69242	S Phase	40	161	4.44E-16
4615885	SUMOylation of DNA replication proteins	17	50	4.44E-16
69278	Cell Cycle, Mitotic	98	536	4.44E-16
9604323	Negative regulation of NOTCH4 signaling	33	55	4.44E-16
8941858	Regulation of RUNX3 expression and activity	31	55	4.44E-16
5676590	NIK-->noncanonical NF-kB signaling	33	59	4.44E-16
5362768	Hh mutants that don't undergo autocatalytic processing are degraded by ERAD	31	56	4.44E-16
5607761	Dectin-1 mediated noncanonical NF-kB signaling	33	60	4.44E-16
69275	G2/M Transition	39	198	4.44E-16
453274	Mitotic G2-G2/M phases	39	200	4.44E-16
9010553	Regulation of expression of SLITs and ROBOs	33	172	4.44E-16
9006925	Intracellular signaling by second messengers	38	316	4.44E-16
69615	G1/S DNA Damage Checkpoints	32	68	4.44E-16
597592	Post-translational protein modification	58	1417	4.44E-16
1640170	Cell Cycle	98	651	4.44E-16
1169091	Activation of NF-kappaB in B cells	33	67	4.44E-16
8852276	The role of GTSE1 in G2/M progression after G2 checkpoint	32	79	4.44E-16
5387390	Hh mutants abrogate ligand secretion	31	59	4.44E-16
4608870	Asymmetric localization of PCP proteins	31	64	4.44E-16
69620	Cell Cycle Checkpoints	87	274	4.44E-16
69563	p53-Dependent G1 DNA Damage Response	32	66	4.44E-16
69580	p53-Dependent G1/S DNA damage checkpoint	32	66	4.44E-16
69541	Stabilization of p53	31	57	4.44E-16
68886	M Phase	90	392	4.44E-16
162909	Host Interactions of HIV factors	50	144	4.44E-16
983169	Class I MHC mediated antigen processing & presentation	40	441	4.44E-16
201681	TCF dependent signaling in response to WNT	34	202	4.44E-16
350562	Regulation of ornithine decarboxylase (ODC)	27	51	4.44E-16
9020702	Interleukin-1 signaling	34	102	4.44E-16

195721	Signaling by WNT	37	299	4.44E-16
392499	Metabolism of proteins	74	2012	4.44E-16
5610787	Hedgehog 'off' state	34	114	4.44E-16
1168372	Downstream signaling events of B Cell Receptor (BCR)	33	82	4.44E-16
453279	Mitotic G1 phase and G1/S transition	35	149	4.44E-16
2871837	FCERI mediated NF-kB activation	33	167	4.44E-16
5673001	RAF/MAP kinase cascade	37	260	4.44E-16
1236978	Cross-presentation of soluble exogenous antigens (endosomes)	27	50	4.44E-16
9648025	EML4 and NUDC in mitotic spindle formation	52	117	4.44E-16
8878171	Transcriptional regulation by RUNX1	36	208	4.44E-16
1169408	ISG15 antiviral mechanism	20	80	4.44E-16
5668541	TNFR2 non-canonical NF-kB pathway	33	102	4.44E-16
157118	Signaling by NOTCH	36	206	4.44E-16
5358351	Signaling by Hedgehog	34	150	4.44E-16
195258	RHO GTPase Effectors	56	295	4.44E-16
5607764	CLEC7A (Dectin-1) signaling	33	98	4.44E-16
5684996	MAPK1/MAPK3 signaling	37	267	4.44E-16
194315	Signaling by Rho GTPases	56	426	4.44E-16
2262752	Cellular responses to stress	55	564	4.44E-16
68867	Assembly of the pre-replicative complex	31	68	4.44E-16
8878166	Transcriptional regulation by RUNX2	35	121	4.44E-16
202424	Downstream TCR signaling	33	116	4.44E-16
69206	G1/S Transition	35	131	4.44E-16
5632684	Hedgehog 'on' state	32	85	4.44E-16
8953854	Metabolism of RNA	48	675	4.44E-16
69239	Synthesis of DNA	37	119	4.44E-16
162582	Signal Transduction	106	2829	4.44E-16
8953897	Cellular responses to external stimuli	55	578	4.44E-16
8878159	Transcriptional regulation by RUNX3	32	96	4.44E-16
382556	ABC-family proteins mediated transport	32	103	4.44E-16
5683057	MAPK family signaling cascades	39	306	4.44E-16
446652	Interleukin-1 family signaling	34	141	4.44E-16
5619084	ABC transporter disorders	31	77	4.44E-16
5358346	Hedgehog ligand biogenesis	31	65	4.44E-16
8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	31	99	4.44E-16
9607240	FLT3 Signaling	37	278	4.44E-16

69306	DNA Replication	37	127	4.44E-16
162906	HIV Infection	50	248	4.44E-16
422475	Axon guidance	38	558	4.44E-16
5663202	Diseases of signal transduction by growth factor receptors and second messengers	42	393	4.44E-16
5621481	C-type lectin receptors (CLRs)	33	174	4.44E-16
9675108	Nervous system development	38	584	4.44E-16
376176	Signaling by ROBO receptors	33	218	4.44E-16
9013694	Signaling by NOTCH4	33	83	4.44E-16
5687128	MAPK6/MAPK4 signaling	33	89	4.44E-16
1236974	ER-Phagosome pathway	31	153	4.44E-16
1169410	Antiviral mechanism by IFN-stimulated genes	20	89	4.44E-16
69002	DNA Replication Pre-Initiation	31	85	4.44E-16
1236975	Antigen processing-Cross presentation	31	169	4.44E-16
5663205	Infectious disease	54	1040	4.44E-16
4086400	PCP/CE pathway	31	92	4.44E-16
3858494	Beta-catenin independent WNT signaling	33	144	4.44E-16
450531	Regulation of mRNA stability by proteins that bind AU-rich elements	31	88	4.44E-16
202403	TCR signaling	33	138	4.44E-16
983705	Signaling by the B Cell Receptor (BCR)	33	176	4.44E-16
351202	Metabolism of polyamines	27	59	4.44E-16
2454202	Fc epsilon receptor (FCERI) signaling	33	218	4.44E-16
1280215	Cytokine Signaling in Immune system	59	954	4.44E-16
5619115	Disorders of transmembrane transporters	44	180	4.44E-16
69481	G2/M Checkpoints	31	151	4.44E-16
449147	Signaling by Interleukins	38	456	4.44E-16
5357801	Programmed Cell Death	33	185	4.44E-16
109581	Apoptosis	33	180	4.44E-16
159227	Transport of the SLBP independent Mature mRNA	14	39	8.88E-16
74160	Gene expression (Transcription)	59	1521	8.88E-16
159230	Transport of the SLBP Dependant Mature mRNA	14	40	1.33E-15
165054	Rev-mediated nuclear export of HIV RNA	14	40	1.33E-15
177243	Interactions of Rev with host cellular proteins	14	42	2.22E-15
71291	Metabolism of amino acids and derivatives	30	376	3.11E-15

159231	Transport of Mature mRNA Derived from an Intronless Transcript	14	46	7.55E-15
5619107	Defective TPR may confer susceptibility towards thyroid papillary carcinoma (TPC)	13	36	8.88E-15
170822	Regulation of Glucokinase by Glucokinase Regulatory Protein	13	36	8.88E-15
72649	Translation initiation complex formation	15	59	9.33E-15
159234	Transport of Mature mRNAs Derived from Intronless Transcripts	14	47	9.77E-15
176033	Interactions of Vpr with host cellular proteins	14	47	9.77E-15
72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	15	60	1.20E-14
1643685	Disease	61	1735	2.22E-14
4085377	SUMOylation of SUMOylation proteins	13	39	2.44E-14
180746	Nuclear import of Rev protein	13	39	2.44E-14
4570464	SUMOylation of RNA binding proteins	14	51	2.98E-14
3301854	Nuclear Pore Complex (NPC) Disassembly	13	40	3.38E-14
168271	Transport of Ribonucleoproteins into the Host Nucleus	13	40	3.38E-14
168333	NEP/NS2 Interacts with the Cellular Export Machinery	13	42	6.22E-14
3232142	SUMOylation of ubiquitinylation proteins	13	43	8.39E-14
168274	Export of Viral Ribonucleoproteins from Nucleus	13	43	8.39E-14
180910	Vpr-mediated nuclear import of PICs	13	44	1.12E-13
168276	NS1 Mediated Effects on Host Pathways	13	46	1.46E-13
1280218	Adaptive Immune System	43	944	1.82E-13
4551638	SUMOylation of chromatin organization proteins	14	62	3.04E-13
72706	GTP hydrolysis and joining of the 60S ribosomal subunit	17	113	4.09E-13
9615933	Postmitotic nuclear pore complex (NPC) reformation	11	28	4.10E-13
5578749	Transcriptional regulation by small RNAs	15	80	5.43E-13
168325	Viral Messenger RNA Synthesis	13	52	6.75E-13
72737	Cap-dependent Translation Initiation	17	120	1.06E-12
72613	Eukaryotic Translation Initiation	17	120	1.06E-12
191859	snRNP Assembly	13	57	2.11E-12
194441	Metabolism of non-coding RNA	13	57	2.11E-12
2980766	Nuclear Envelope Breakdown	13	58	2.62E-12

3108232	SUMO E3 ligases SUMOylate target proteins	19	174	3.66E-12
162599	Late Phase of HIV Life Cycle	18	152	3.97E-12
156827	L13a-mediated translational silencing of Ceruloplasmin expression	16	112	4.78E-12
6784531	tRNA processing in the nucleus	13	62	5.97E-12
2990846	SUMOylation	19	180	6.55E-12
3108214	SUMOylation of DNA damage response and repair proteins	14	81	1.05E-11
162587	HIV Life Cycle	18	165	1.52E-11
168256	Immune System	67	2374	1.57E-11
382551	Transport of small molecules	35	731	1.83E-11
774815	Nucleosome assembly	12	54	2.24E-11
606279	Deposition of new CENPA-containing nucleosomes at the centromere	12	54	2.24E-11
72202	Transport of Mature Transcript to Cytoplasm	14	87	2.67E-11
211000	Gene Silencing by RNA	15	110	4.69E-11
3371453	Regulation of HSF1-mediated heat shock response	13	75	6.17E-11
159236	Transport of Mature mRNA derived from an Intron-Containing Transcript	13	78	9.95E-11
70171	Glycolysis	13	78	9.95E-11
212436	Generic Transcription Pathway	45	1257	1.59E-10
72695	Formation of the ternary complex, and subsequently, the 43S complex	11	52	2.88E-10
168273	Influenza Viral RNA Transcription and Replication	16	151	3.77E-10
913531	Interferon Signaling	21	289	4.10E-10
3371556	Cellular response to heat stress	13	95	1.08E-09
70326	Glucose metabolism	13	98	1.56E-09
168255	Influenza Infection	16	171	2.23E-09
5619102	SLC transporter disorders	13	103	2.83E-09
73857	RNA Polymerase II Transcription	45	1379	3.22E-09
179409	APC-Cdc20 mediated degradation of Nek2A	8	25	4.65E-09
72306	tRNA processing	13	113	8.47E-09
68875	Mitotic Prophase	13	119	1.56E-08
73886	Chromosome Maintenance	12	98	1.79E-08
2995410	Nuclear Envelope (NE) Reassembly	11	78	1.88E-08
1266738	Developmental Biology	38	1100	2.17E-08
174048	APC/C:Cdc20 mediated degradation of Cyclin B	7	23	7.07E-08
168249	Innate Immune System	38	1187	1.65E-07

5684264	MAP3K8 (TPL2)-dependent MAPK1/3 activation	6	16	2.17E-07
72689	Formation of a pool of free 40S subunits	11	102	2.79E-07
69231	Cyclin D associated events in G1	8	44	3.50E-07
69236	G1 Phase	8	44	3.50E-07
2565942	Regulation of PLK1 Activity at G2/M Transition	10	87	4.58E-07
72766	Translation	17	294	4.58E-07
71387	Metabolism of carbohydrates	17	300	6.05E-07
9610379	HCMV Late Events	13	173	7.54E-07
2559582	Senescence-Associated Secretory Phenotype (SASP)	9	80	2.01E-06
205043	NRIF signals cell death from the nucleus	5	16	4.47E-06
9609690	HCMV Early Events	13	208	5.68E-06
72203	Processing of Capped Intron- Containing Pre-mRNA	14	245	6.49E-06
2173789	TGF-beta receptor signaling activates SMADs	6	32	7.85E-06
8948747	Regulation of PTEN localization	4	9	1.22E-05
3785653	Myoclonic epilepsy of Lafora	4	9	1.22E-05
8849469	PTK6 Regulates RTKs and Their Effectors AKT1 and DOK1	4	9	1.22E-05
937042	IRAK2 mediated activation of TAK1 complex	4	10	1.85E-05
8876493	InlA-mediated entry of Listeria monocytogenes into host cells	4	10	1.85E-05
2559583	Cellular Senescence	11	165	1.88E-05
5696394	DNA Damage Recognition in GG- NER	6	38	2.07E-05
5689896	Ovarian tumor domain proteases	6	38	2.07E-05
8853884	Transcriptional Regulation by VENTX	6	38	2.07E-05
9014325	TICAM1, TRAF6-dependent induction of TAK1 complex	4	11	2.68E-05
9645460	Alpha-protein kinase 1 signaling pathway	4	11	2.68E-05
1253288	Downregulation of ERBB4 signaling	4	11	2.68E-05
9637628	Modulation by Mtb of host immune system	4	11	2.68E-05
9664873	Pexophagy	4	11	2.68E-05
3769402	Deactivation of the beta-catenin transactivating complex	6	42	3.62E-05
5689877	Josephin domain DUBs	4	12	3.76E-05
9013973	TICAM1-dependent activation of IRF3/IRF7	4	12	3.76E-05
2173788	Downregulation of TGF-beta receptor signaling	5	26	4.57E-05
209560	NF-kB is activated and signals survival	4	13	5.13E-05

400253	Circadian Clock	7	68	5.81E-05
9609646	HCMV Infection	13	262	6.40E-05
1358803	Downregulation of ERBB2:ERBB3 signaling	4	14	6.83E-05
937039	IRAK1 recruits IKK complex	4	14	6.83E-05
975144	IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation	4	14	6.83E-05
975110	TRAF6 mediated IRF7 activation in TLR7/8 or 9 signaling	4	14	6.83E-05
209543	p75NTR recruits signalling complexes	4	14	6.83E-05
2122947	NOTCH1 Intracellular Domain Regulates Transcription	6	49	8.49E-05
975163	IRAK2 mediated activation of TAK1 complex upon TLR7/8 or 9 stimulation	4	15	8.91E-05
174490	Membrane binding and targetting of GAG proteins	4	15	8.91E-05
174495	Synthesis And Processing Of GAG, GAGPOL Polyproteins	4	15	8.91E-05
3134975	Regulation of innate immune responses to cytosolic DNA	4	15	8.91E-05
2691230	Signaling by NOTCH1 HD Domain Mutants in Cancer	4	15	8.91E-05
2691232	Constitutive Signaling by NOTCH1 HD Domain Mutants	4	15	8.91E-05
110314	Recognition of DNA damage by PCNA-containing replication complex	5	30	8.98E-05
5689901	Metalloprotease DUBs	5	31	1.05E-04
937072	TRAF6-mediated induction of TAK1 complex within TLR4 complex	4	16	1.14E-04
110312	Translesion synthesis by REV1	4	16	1.14E-04
2173791	TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition)	4	16	1.14E-04
1295596	Spry regulation of FGF signaling	4	16	1.14E-04
3229121	Glycogen storage diseases	4	16	1.14E-04
3322077	Glycogen synthesis	4	16	1.14E-04
8863795	Downregulation of ERBB2 signaling	5	32	1.22E-04
5656121	Translesion synthesis by POLI	4	17	1.44E-04
5655862	Translesion synthesis by POLK	4	17	1.44E-04
8875360	InlB-mediated entry of Listeria monocytogenes into host cell	4	17	1.44E-04
936964	Activation of IRF3/IRF7 mediated by TBK1/IKK epsilon	4	17	1.44E-04
193639	p75NTR signals via NF-kB	4	17	1.44E-04
6806834	Signaling by MET	7	80	1.60E-04
2559585	Oncogene Induced Senescence	5	34	1.61E-04
446353	Cell-extracellular matrix interactions	4	18	1.79E-04

9636383	Prevention of phagosomal-lysosomal fusion	4	18	1.79E-04
532668	N-glycan trimming in the ER and Calnexin/Calreticulin cycle	5	35	1.85E-04
917937	Iron uptake and transport	6	58	1.92E-04
8848021	Signaling by PTK6	6	58	1.92E-04
9006927	Signaling by Non-Receptor Tyrosine Kinases	6	58	1.92E-04
176407	Conversion from APC/C:Cdc20 to APC/C:Cdh1 in late anaphase	4	19	1.92E-04
110320	Translesion Synthesis by POLH	4	19	1.92E-04
168927	TICAM1, RIP1-mediated IKK complex recruitment	4	19	1.92E-04
6804760	Regulation of TP53 Activity through Methylation	4	19	1.92E-04
1430728	Metabolism	46	2142	1.92E-04
2644603	Signaling by NOTCH1 in Cancer	6	59	1.92E-04
2894858	Signaling by NOTCH1 HD+PEST Domain Mutants in Cancer	6	59	1.92E-04
2644602	Signaling by NOTCH1 PEST Domain Mutants in Cancer	6	59	1.92E-04
2644606	Constitutive Signaling by NOTCH1 PEST Domain Mutants	6	59	1.92E-04
2894862	Constitutive Signaling by NOTCH1 HD+PEST Domain Mutants	6	59	1.92E-04
141405	Inhibition of the proteolytic activity of APC/C required for the onset of anaphase by mitotic spindle checkpoint components	4	20	1.92E-04
141430	Inactivation of APC/C via direct inhibition of the APC/C complex	4	20	1.92E-04
1236382	Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants	4	20	1.92E-04
5637815	Signaling by Ligand-Responsive EGFR Variants in Cancer	4	20	1.92E-04
4641263	Regulation of FZD by ubiquitination	4	21	1.92E-04
6807004	Negative regulation of MET activity	4	21	1.92E-04
901032	ER Quality Control Compartment (ERQC)	4	21	1.92E-04
5675482	Regulation of necroptotic cell death	4	21	1.92E-04
450294	MAP kinase activation	6	63	1.92E-04
5696400	Dual Incision in GG-NER	5	41	1.92E-04
9613829	Chaperone Mediated Autophagy	4	22	1.92E-04
450321	JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1	4	22	1.92E-04
2979096	NOTCH2 Activation and Transmission of Signal to the Nucleus	4	22	1.92E-04
912631	Regulation of signaling by CBL	4	22	1.92E-04
5205685	Pink/Parkin Mediated Mitophagy	4	22	1.92E-04

2173795	Downregulation of SMAD2/3:SMAD4 transcriptional activity	4	23	2.28E-04
937041	IKK complex recruitment mediated by RIP1	4	23	2.28E-04
8876384	Listeria monocytogenes entry into host cells	4	23	2.28E-04
450302	activated TAK1 mediates p38 MAPK activation	4	23	2.28E-04
9637687	Suppression of phagosomal maturation	4	23	2.28E-04
5213460	RIPK1-mediated regulated necrosis	4	23	2.28E-04
5218859	Regulated Necrosis	4	23	2.28E-04
5696395	Formation of Incision Complex in GG-NER	5	43	2.38E-04
175474	Assembly Of The HIV Virion	4	24	2.67E-04
1500931	Cell-Cell communication	8	130	2.74E-04
5696397	Gap-filling DNA repair synthesis and ligation in GG-NER	4	25	3.12E-04
9013507	NOTCH3 Activation and Transmission of Signal to the Nucleus	4	25	3.12E-04
448424	Interleukin-17 signaling	6	71	3.13E-04
901042	Calnexin/calreticulin cycle	4	26	3.61E-04
1643713	Signaling by EGFR in Cancer	4	26	3.61E-04
170834	Signaling by TGF-beta Receptor Complex	6	73	3.63E-04
73893	DNA Damage Bypass	5	48	3.93E-04
8982491	Glycogen metabolism	4	27	4.16E-04
1980143	Signaling by NOTCH1	6	75	4.18E-04
5205647	Mitophagy	4	29	5.43E-04
9009391	Extra-nuclear estrogen signaling	6	80	5.85E-04
6781823	Formation of TC-NER Pre-Incision Complex	5	53	6.13E-04
8866652	Synthesis of active ubiquitin: roles of E1 and E2 enzymes	4	30	6.16E-04
5654732	Negative regulation of FGFR3 signaling	4	30	6.16E-04
5357956	TNFR1-induced NFkappaB signaling pathway	4	30	6.16E-04
917729	Endosomal Sorting Complex Required For Transport (ESCRT)	4	31	6.95E-04
182971	EGFR downregulation	4	31	6.95E-04
2122948	Activated NOTCH1 Transmits Signal to the Nucleus	4	31	6.95E-04
5654733	Negative regulation of FGFR4 signaling	4	31	6.95E-04
5696399	Global Genome Nucleotide Excision Repair (GG-NER)	6	84	7.52E-04
5656169	Termination of translesion DNA synthesis	4	32	7.82E-04

445989	TAK1 activates NFkB by phosphorylation and activation of IKKs complex	4	32	7.82E-04
2173796	SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	4	32	7.82E-04
1227986	Signaling by ERBB2	5	56	7.84E-04
975871	MyD88 cascade initiated on plasma membrane	6	85	7.99E-04
168142	Toll Like Receptor 10 (TLR10) Cascade	6	85	7.99E-04
168176	Toll Like Receptor 5 (TLR5) Cascade	6	85	7.99E-04
1980145	Signaling by NOTCH2	4	33	8.76E-04
1170546	Prolactin receptor signaling	3	15	9.68E-04
9615710	Late endosomal microautophagy	4	34	9.77E-04
936440	Negative regulators of DDX58/IFIH1 signaling	4	34	9.77E-04
5663084	Diseases of carbohydrate metabolism	4	34	9.77E-04
975138	TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	6	90	1.07E-03
5654726	Negative regulation of FGFR1 signaling	4	35	1.09E-03
975155	MyD88 dependent cascade initiated on endosome	6	91	1.13E-03
168181	Toll Like Receptor 7/8 (TLR7/8) Cascade	6	91	1.13E-03
162588	Budding and maturation of HIV virion	4	36	1.20E-03
168638	NOD1/2 Signaling Pathway	4	36	1.20E-03
6804757	Regulation of TP53 Degradation	4	36	1.20E-03
1236394	Signaling by ERBB4	5	62	1.23E-03
168164	Toll Like Receptor 3 (TLR3) Cascade	6	93	1.26E-03
6802948	Signaling by high-kinase activity BRAF mutants	4	37	1.33E-03
5654727	Negative regulation of FGFR2 signaling	4	37	1.33E-03
6806003	Regulation of TP53 Expression and Degradation	4	37	1.33E-03
5357905	Regulation of TNFR1 signaling	4	37	1.33E-03
2559580	Oxidative Stress Induced Senescence	6	94	1.33E-03
8934593	Regulation of RUNX1 Expression and Activity	3	17	1.38E-03
168138	Toll Like Receptor 9 (TLR9) Cascade	6	95	1.41E-03
6782210	Gap-filling DNA repair synthesis and ligation in TC-NER	5	64	1.41E-03
6783310	Fanconi Anemia Pathway	4	38	1.47E-03
166058	MyD88:MAL(TIRAP) cascade initiated on plasma membrane	6	96	1.48E-03

168188	Toll Like Receptor TLR6:TLR2 Cascade	6	96	1.48E-03
6782135	Dual incision in TC-NER	5	65	1.51E-03
937061	TRIF(TICAM1)-mediated TLR4 signaling	6	97	1.56E-03
166166	MyD88-independent TLR4 cascade	6	97	1.56E-03
110313	Translesion synthesis by Y family DNA polymerases bypasses lesions on DNA template	4	39	1.61E-03
9637690	Response of Mtb to phagocytosis	4	39	1.61E-03
168179	Toll Like Receptor TLR1:TLR2 Cascade	6	99	1.73E-03
181438	Toll Like Receptor 2 (TLR2) Cascade	6	99	1.73E-03
176412	Phosphorylation of the APC/C	3	19	1.90E-03
5674135	MAP2K and MAPK activation	4	41	1.93E-03
5675221	Negative regulation of MAPK pathway	4	41	1.93E-03
9006936	Signaling by TGF-beta family members	6	102	2.01E-03
5654743	Signaling by FGFR4	4	43	2.29E-03
5654741	Signaling by FGFR3	4	43	2.29E-03
9646399	Aggrephagy	4	44	2.49E-03
2173793	Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer	4	44	2.49E-03
8856828	Clathrin-mediated endocytosis	7	145	2.61E-03
8849470	PTK6 Regulates Cell Cycle	2	6	2.72E-03
2644607	Loss of Function of FBXW7 in Cancer and NOTCH1 Signaling	2	6	2.72E-03
2644605	FBXW7 Mutants and NOTCH1 in Cancer	2	6	2.72E-03
5696398	Nucleotide Excision Repair	6	110	2.91E-03
204998	Cell death signalling via NRAGE, NRIF and NADE	5	76	2.95E-03
9649948	Signaling downstream of RAS mutants	4	47	3.15E-03
6802946	Signaling by moderate kinase activity BRAF mutants	4	47	3.15E-03
6802955	Paradoxical activation of RAF signaling by kinase inactive BRAF	4	47	3.15E-03
6802949	Signaling by RAS mutants	4	47	3.15E-03
75893	TNF signaling	4	47	3.15E-03
6798695	Neutrophil degranulation	14	480	3.21E-03
6781827	Transcription-Coupled Nucleotide Excision Repair (TC-NER)	5	78	3.30E-03
512988	Interleukin-3, Interleukin-5 and GM-CSF signaling	4	48	3.39E-03
9012852	Signaling by NOTCH3	4	49	3.65E-03

9634638	Estrogen-dependent nuclear events downstream of ESR-membrane signaling	3	24	3.65E-03
8939211	ESR-mediated signaling	8	196	3.66E-03
426496	Post-transcriptional silencing by small RNAs	2	7	3.67E-03
429947	Deadenylation of mRNA	3	25	4.09E-03
177929	Signaling by EGFR	4	52	4.49E-03
8948700	Competing endogenous RNAs (ceRNAs) regulate PTEN translation	2	8	4.75E-03
5654736	Signaling by FGFR1	4	54	5.12E-03
8943723	Regulation of PTEN mRNA translation	2	9	5.96E-03
426486	Small interfering RNA (siRNA) biogenesis	2	9	5.96E-03
166016	Toll Like Receptor 4 (TLR4) Cascade	6	129	6.24E-03
446728	Cell junction organization	5	92	6.55E-03
6804756	Regulation of TP53 Activity through Phosphorylation	5	92	6.55E-03
8874081	MET activates PTK2 signaling	3	30	6.75E-03
3000157	Laminin interactions	3	30	6.75E-03
168643	Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways	4	59	6.96E-03
5693565	Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	4	59	6.96E-03
8866654	E3 ubiquitin ligases ubiquitinate target proteins	4	60	7.37E-03
5693606	DNA Double Strand Break Response	4	60	7.37E-03
5626467	RHO GTPases activate IQGAPs	3	32	8.04E-03
1834949	Cytosolic sensors of pathogen-associated DNA	4	63	8.70E-03
196025	Formation of annular gap junctions	2	11	8.76E-03
193704	p75 NTR receptor-mediated signalling	5	99	8.81E-03
9033241	Peroxisomal protein import	4	64	9.18E-03
6802952	Signaling by BRAF and RAF fusions	4	66	1.02E-02
5685942	HDR through Homologous Recombination (HRR)	4	66	1.02E-02
190873	Gap junction degradation	2	12	1.03E-02
5663213	RHO GTPases Activate WASPs and WAVES	3	36	1.10E-02
8856825	Cargo recognition for clathrin-mediated endocytosis	5	105	1.11E-02
5467333	APC truncation mutants are not K63 polyubiquitinated	1	1	1.26E-02
8854518	AURKA Activation by TPX2	4	72	1.36E-02
445355	Smooth Muscle Contraction	3	39	1.37E-02

168898	Toll-like Receptor Cascades	6	156	1.48E-02	
6802957	Oncogenic MAPK signaling	4	74	1.49E-02	
8875878	MET promotes cell motility	3	41	1.56E-02	
372708	p130Cas linkage to MAPK signaling for integrins	2	15	1.58E-02	
354194	GRB2:SOS provides linkage to MAPK signaling for Integrins	2	15	1.58E-02	
3928662	EPHB-mediated forward signaling	3	42	1.66E-02	
168928	DDX58/IFIH1-mediated induction of interferon-alpha/beta	4	77	1.70E-02	
5654738	Signaling by FGFR2	4	78	1.77E-02	
391160	Signal regulatory protein family interactions	2	16	1.78E-02	
8852135	Protein ubiquitination	4	80	1.92E-02	
977225	Amyloid fiber formation	4	80	1.92E-02	
5693607	Processing of DNA double-strand break ends	4	81	2.00E-02	
9663891	Selective autophagy	4	82	2.08E-02	
9635486	Infection with Mycobacterium tuberculosis	4	82	2.08E-02	
9006931	Signaling by Nuclear Receptors	8	273	2.33E-02	
8854521	Interaction between PHLDA1 and AURKA	1	2	2.50E-02	
190236	Signaling by FGFR	4	95	3.32E-02	
9006934	Signaling by Receptor Tyrosine Kinases	12	523	3.40E-02	
429914	Deadenylation-dependent mRNA decay	3	56	3.47E-02	
5620912	Anchoring of the basal body to the plasma membrane	4	97	3.54E-02	
4420097	VEGFA-VEGFR2 Pathway	4	98	3.65E-02	
203927	MicroRNA (miRNA) biogenesis	2	24	3.75E-02	
73887	Death Receptor Signalling	5	147	3.97E-02	
9633012	Response of EIF2AK4 (GCN2) to amino acid deficiency	4	102	4.13E-02	
3700989	Transcriptional Regulation by TP53	9	367	4.42E-02	
1912408	Pre-NOTCH Transcription and Translation	3	62	4.46E-02	
2672351	Stimuli-sensing channels	4	107	4.77E-02	
194138	Signaling by VEGF	4	108	4.90E-02	
180897	Vpr-mediated induction of apoptosis by mitochondrial outer membrane permeabilization	1	4	4.93E-02	
354192	Integrin signaling	2	28	4.94E-02	
380284	Loss of proteins required for interphase microtubule organization from the centrosome	54	69	3.55E-15	
5	380259	Loss of Nlp from mitotic centrosomes	54	69	3.55E-15
8854518	AURKA Activation by TPX2	54	72	3.55E-15	

380287	Centrosome maturation	60	81	3.55E-15
380270	Recruitment of mitotic centrosome proteins and complexes	60	81	3.55E-15
380320	Recruitment of NuMA to mitotic centrosomes	60	95	3.55E-15
179419	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint	18	73	3.55E-15
176409	APC/C:Cdc20 mediated degradation of mitotic proteins	18	75	3.55E-15
176814	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	18	76	3.55E-15
2500257	Resolution of Sister Chromatid Cohesion	22	126	3.55E-15
5620912	Anchoring of the basal body to the plasma membrane	54	97	3.55E-15
68877	Mitotic Prometaphase	72	203	3.55E-15
2467813	Separation of Sister Chromatids	36	190	3.55E-15
69275	G2/M Transition	75	198	3.55E-15
453274	Mitotic G2-G2/M phases	75	200	3.55E-15
5610787	Hedgehog 'off' state	21	114	3.55E-15
2565942	Regulation of PLK1 Activity at G2/M Transition	55	87	3.55E-15
8852276	The role of GTSE1 in G2/M progression after G2 checkpoint	18	79	3.55E-15
69278	Cell Cycle, Mitotic	91	536	3.55E-15
68886	M Phase	87	392	3.55E-15
1640170	Cell Cycle	91	651	3.55E-15
69620	Cell Cycle Checkpoints	36	274	3.55E-15
5617833	Cilium Assembly	54	202	3.55E-15
68882	Mitotic Anaphase	37	236	3.55E-15
2555396	Mitotic Metaphase and Anaphase	37	237	3.55E-15
5663220	RHO GTPases Activate Formins	22	141	3.55E-15
1852241	Organelle biogenesis and maintenance	55	298	3.55E-15
5358351	Signaling by Hedgehog	22	150	1.38E-14
174184	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	17	72	1.67E-14
174143	APC/C-mediated degradation of cell cycle proteins	18	86	1.80E-14
453276	Regulation of mitotic cell cycle	18	86	1.80E-14
9648025	EML4 and NUDC in mitotic spindle formation	20	117	1.80E-14
69618	Mitotic Spindle Checkpoint	19	110	7.51E-14
176408	Regulation of APC/C activators between G1/S and early anaphase	17	80	8.37E-14
174154	APC/C:Cdc20 mediated degradation of Securin	16	67	9.44E-14

174178	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	16	72	2.66E-13
5610783	Degradation of GLI2 by the proteasome	15	60	3.20E-13
5610785	GLI3 is processed to GLI3R by the proteasome	15	60	3.20E-13
195258	RHO GTPase Effectors	27	295	3.20E-13
174084	Autodegradation of Cdh1 by Cdh1:APC/C	15	63	6.40E-13
180585	Vif-mediated degradation of APOBEC3G	14	56	2.37E-12
69017	CDK-mediated phosphorylation and removal of Cdc6	15	72	3.88E-12
69242	S Phase	20	161	4.37E-12
211733	Regulation of activated PAK-2p34 by proteasome mediated degradation	13	50	1.02E-11
141444	Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal	16	94	1.10E-11
141424	Amplification of signal from the kinetochores	16	94	1.10E-11
69610	p53-Independent DNA Damage Response	13	52	1.49E-11
69613	p53-Independent G1/S DNA damage checkpoint	13	52	1.49E-11
69601	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	13	52	1.49E-11
75815	Ubiquitin-dependent degradation of Cyclin D	13	52	1.49E-11
1234176	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	14	66	1.70E-11
180534	Vpu mediated degradation of CD4	13	53	1.77E-11
169911	Regulation of Apoptosis	13	53	1.77E-11
8953897	Cellular responses to external stimuli	34	578	1.79E-11
195253	Degradation of beta-catenin by the destruction complex	15	83	2.15E-11
69615	G1/S DNA Damage Checkpoints	14	68	2.22E-11
174113	SCF-beta-TrCP mediated degradation of Emi1	13	55	2.63E-11
69656	Cyclin A:Cdk2-associated events at S phase entry	15	85	3.00E-11
450408	AUF1 (hnRNP D0) binds and destabilizes mRNA	13	56	3.06E-11
8878166	Transcriptional regulation by RUNX2	17	121	3.18E-11
2262752	Cellular responses to stress	33	564	4.14E-11
5687128	MAPK6/MAPK4 signaling	15	89	5.32E-11
69052	Switching of origins to a post-replicative state	15	90	5.78E-11

5610780	Degradation of GLI1 by the proteasome	13	60	6.45E-11
187577	SCF(Skp2)-mediated degradation of p27/p21	13	60	6.45E-11
1234174	Cellular response to hypoxia	14	75	6.45E-11
8878159	Transcriptional regulation by RUNX3	15	96	1.31E-10
69563	p53-Dependent G1 DNA Damage Response	13	66	1.97E-10
69580	p53-Dependent G1/S DNA damage checkpoint	13	66	1.97E-10
349425	Autodegradation of the E3 ubiquitin ligase COP1	12	52	2.02E-10
69202	Cyclin E associated events during G1/S transition	14	83	2.42E-10
5632684	Hedgehog 'on' state	14	85	3.03E-10
8854050	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	12	55	3.50E-10
4641257	Degradation of AXIN	12	55	3.50E-10
8941858	Regulation of RUNX3 expression and activity	12	55	3.50E-10
9604323	Negative regulation of NOTCH4 signaling	12	55	3.50E-10
5362768	Hh mutants that don't undergo autocatalytic processing are degraded by ERAD	12	56	4.30E-10
4641258	Degradation of DVL	12	57	4.78E-10
69541	Stabilization of p53	12	57	4.78E-10
376176	Signaling by ROBO receptors	20	218	4.78E-10
1280218	Adaptive Immune System	41	944	5.13E-10
422475	Axon guidance	31	558	5.46E-10
194315	Signaling by Rho GTPases	27	426	6.35E-10
8939902	Regulation of RUNX2 expression and activity	13	74	6.35E-10
68827	CDT1 association with the CDC6:ORC:origin complex	12	59	6.35E-10
5387390	Hh mutants abrogate ligand secretion	12	59	6.35E-10
5676590	NIK-->noncanonical NF-kB signaling	12	59	6.35E-10
69206	G1/S Transition	16	131	7.14E-10
5607761	Dectin-1 mediated noncanonical NF-kB signaling	12	60	7.67E-10
5678895	Defective CFTR causes cystic fibrosis	12	61	9.24E-10
9675108	Nervous system development	31	584	1.50E-09
4608870	Asymmetric localization of PCP proteins	12	64	1.59E-09
1236978	Cross-presentation of soluble exogenous antigens (endosomes)	11	50	1.68E-09
69239	Synthesis of DNA	15	119	1.68E-09

5358346	Hedgehog ligand biogenesis	12	65	1.68E-09
350562	Regulation of ornithine decarboxylase (ODC)	11	51	1.95E-09
9013694	Signaling by NOTCH4	13	83	2.11E-09
1169091	Activation of NF-kappaB in B cells	12	67	2.36E-09
162909	Host Interactions of HIV factors	16	144	2.47E-09
382556	ABC-family proteins mediated transport	14	103	2.61E-09
68867	Assembly of the pre-replicative complex	12	68	2.78E-09
6811436	COPI-independent Golgi-to-ER retrograde traffic	11	53	2.90E-09
8948751	Regulation of PTEN stability and activity	12	69	3.28E-09
5658442	Regulation of RAS by GAPs	12	69	3.28E-09
69306	DNA Replication	15	127	3.72E-09
453279	Mitotic G1 phase and G1/S transition	16	149	3.72E-09
450531	Regulation of mRNA stability by proteins that bind AU-rich elements	13	88	3.72E-09
68949	Orc1 removal from chromatin	12	71	3.94E-09
69481	G2/M Checkpoints	16	151	4.25E-09
3371497	HSP90 chaperone cycle for steroid hormone receptors (SHR)	11	57	5.38E-09
4086400	PCP/CE pathway	13	92	6.31E-09
9646399	Aggrephagy	10	44	6.94E-09
351202	Metabolism of polyamines	11	59	7.68E-09
8856688	Golgi-to-ER retrograde transport	15	137	9.67E-09
5619084	ABC transporter disorders	12	77	9.71E-09
1168372	Downstream signaling events of B Cell Receptor (BCR)	12	82	1.95E-08
69002	DNA Replication Pre-Initiation	12	85	2.89E-08
201681	TCF dependent signaling in response to WNT	17	202	3.67E-08
109581	Apoptosis	16	180	4.99E-08
5663202	Diseases of signal transduction by growth factor receptors and second messengers	23	393	6.06E-08
5357801	Programmed Cell Death	16	185	6.25E-08
202403	TCR signaling	14	138	7.73E-08
202424	Downstream TCR signaling	13	116	8.26E-08
5689603	UCH proteinases	12	96	9.35E-08
983168	Antigen processing: Ubiquitination & Proteasome degradation	20	309	1.04E-07
2132295	MHC class II antigen presentation	14	142	1.10E-07
5607764	CLEC7A (Dectin-1) signaling	12	98	1.17E-07
8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	12	99	1.30E-07

9010553	Regulation of expression of SLITs and ROBOs	15	172	1.65E-07
9020702	Interleukin-1 signaling	12	102	1.80E-07
5668541	TNFR2 non-canonical NF-kB pathway	12	102	1.80E-07
9663891	Selective autophagy	11	82	1.87E-07
5689880	Ub-specific processing proteases	16	205	2.54E-07
216083	Integrin cell surface interactions	11	85	2.68E-07
5683057	MAPK family signaling cascades	19	306	4.63E-07
5688426	Deubiquitination	18	282	6.97E-07
3858494	Beta-catenin independent WNT signaling	13	144	9.81E-07
5621481	C-type lectin receptors (CLRs)	14	174	1.29E-06
6807878	COPI-mediated anterograde transport	11	102	1.37E-06
195721	Signaling by WNT	18	299	1.37E-06
157118	Signaling by NOTCH	15	206	1.37E-06
6811442	Intra-Golgi and retrograde Golgi-to-ER traffic	15	206	1.37E-06
5684996	MAPK1/MAPK3 signaling	17	267	1.38E-06
162906	HIV Infection	16	248	2.66E-06
6807070	PTEN Regulation	12	139	3.95E-06
446652	Interleukin-1 family signaling	12	141	4.58E-06
1236975	Antigen processing-Cross presentation	13	169	4.85E-06
5673001	RAF/MAP kinase cascade	16	260	4.91E-06
174048	APC/C:Cdc20 mediated degradation of Cyclin B	6	23	5.50E-06
983169	Class I MHC mediated antigen processing & presentation	21	441	5.84E-06
8951664	Neddylation	15	236	7.36E-06
179409	APC-Cdc20 mediated degradation of Nek2A	6	25	8.86E-06
1236974	ER-Phagosome pathway	12	153	1.06E-05
9607240	FLT3 Signaling	16	278	1.15E-05
199977	ER to Golgi Anterograde Transport	12	155	1.21E-05
9006925	Intracellular signaling by second messengers	17	316	1.35E-05
1632852	Macroautophagy	11	137	2.28E-05
2871837	FCERI mediated NF-kB activation	12	167	2.55E-05
983705	Signaling by the B Cell Receptor (BCR)	12	176	4.30E-05
1266738	Developmental Biology	34	1100	4.54E-05
1257604	PIP3 activates AKT signaling	15	276	4.76E-05
5619115	Disorders of transmembrane transporters	12	180	5.37E-05
9612973	Autophagy	11	152	5.98E-05

2454202	Fc epsilon receptor (FCERI) signaling	13	218	7.38E-05
948021	Transport to the Golgi and subsequent modification	12	186	7.41E-05
72649	Translation initiation complex formation	7	59	1.15E-04
72702	Ribosomal scanning and start codon recognition	7	59	1.15E-04
72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	7	60	1.15E-04
438064	Post NMDA receptor activation events	8	84	1.15E-04
199991	Membrane Trafficking	23	635	1.22E-04
983189	Kinesins	7	64	1.56E-04
8878171	Transcriptional regulation by RUNX1	12	208	1.74E-04
3000170	Syndecan interactions	5	27	1.81E-04
373760	L1CAM interactions	9	121	2.45E-04
9619483	Activation of AMPK downstream of NMDARs	5	29	2.53E-04
162582	Signal Transduction	62	2829	2.79E-04
442755	Activation of NMDA receptors and postsynaptic events	8	97	3.13E-04
1445148	Translocation of SLC2A4 (GLUT4) to the plasma membrane	7	72	3.23E-04
449147	Signaling by Interleukins	18	456	3.30E-04
6811434	COPI-dependent Golgi-to-ER retrograde traffic	8	103	4.71E-04
597592	Post-translational protein modification	37	1417	5.25E-04
446353	Cell-extracellular matrix interactions	4	18	5.38E-04
176412	Phosphorylation of the APC/C	4	19	6.61E-04
176407	Conversion from APC/C:Cdc20 to APC/C:Cdh1 in late anaphase	4	19	6.61E-04
141405	Inhibition of the proteolytic activity of APC/C required for the onset of anaphase by mitotic spindle checkpoint components	4	20	8.03E-04
141430	Inactivation of APC/C via direct inhibition of the APC/C complex	4	20	8.03E-04
190840	Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	4	20	8.03E-04
8953854	Metabolism of RNA	22	675	8.35E-04
190872	Transport of connexons to the plasma membrane	4	21	9.65E-04
447041	CHL1 interactions	3	9	1.20E-03
389977	Post-chaperonin tubulin folding pathway	4	23	1.36E-03
1474244	Extracellular matrix organization	13	301	1.45E-03

446203	Asparagine N-linked glycosylation	13	305	1.64E-03
9609736	Assembly and cell surface presentation of NMDA receptors	5	44	1.72E-03
5653656	Vesicle-mediated transport	23	761	1.73E-03
69273	Cyclin A/B1/B2 associated events during G2/M transition	4	25	1.86E-03
1566948	Elastic fibre formation	5	45	1.90E-03
983231	Factors involved in megakaryocyte development and platelet production	9	160	1.91E-03
389960	Formation of tubulin folding intermediates by CCT/TriC	4	26	2.15E-03
389957	Prefoldin mediated transfer of substrate to CCT/TriC	4	28	2.83E-03
168256	Immune System	51	2374	2.87E-03
392499	Metabolism of proteins	45	2012	2.88E-03
3000178	ECM proteoglycans	6	76	3.11E-03
75035	Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	3	13	3.23E-03
1643685	Disease	40	1735	3.23E-03
2995410	Nuclear Envelope (NE) Reassembly	6	78	3.23E-03
72695	Formation of the ternary complex, and subsequently, the 43S complex	5	52	3.23E-03
5620924	Intraflagellar transport	5	54	3.23E-03
5467340	AXIN missense mutants destabilize the destruction complex	3	14	3.23E-03
5467348	Truncations of AMER1 destabilize the destruction complex	3	14	3.23E-03
5467337	APC truncation mutants have impaired AXIN binding	3	14	3.23E-03
4839735	AXIN mutants destabilize the destruction complex, activating WNT signaling	3	14	3.23E-03
4839748	AMER1 mutants destabilize the destruction complex	3	14	3.23E-03
4839744	truncated APC mutants destabilize the destruction complex	3	14	3.23E-03
156827	L13a-mediated translational silencing of Ceruloplasmin expression	7	112	3.36E-03
5626467	RHO GTPases activate IQGAPs	4	32	3.46E-03
9668328	Sealing of the nuclear envelope (NE) by ESCRT-III	4	32	3.46E-03
72706	GTP hydrolysis and joining of the 60S ribosomal subunit	7	113	3.53E-03
389958	Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding	4	33	3.88E-03
4839743	phosphorylation site mutants of CTNBN1 are not targeted to the proteasome by the destruction complex	3	15	3.93E-03

5339716	Misspliced GSK3beta mutants stabilize beta-catenin	3	15	3.93E-03
5358751	S45 mutants of beta-catenin aren't phosphorylated	3	15	3.93E-03
5358752	T41 mutants of beta-catenin aren't phosphorylated	3	15	3.93E-03
5358749	S37 mutants of beta-catenin aren't phosphorylated	3	15	3.93E-03
5358747	S33 mutants of beta-catenin aren't phosphorylated	3	15	3.93E-03
75892	Platelet Adhesion to exposed collagen	3	15	3.93E-03
446343	Localization of the PINCH-ILK-PARVIN complex to focal adhesions	2	4	4.53E-03
3000171	Non-integrin membrane-ECM interactions	5	59	4.72E-03
72737	Cap-dependent Translation Initiation	7	120	4.96E-03
72613	Eukaryotic Translation Initiation	7	120	4.96E-03
196299	Beta-catenin phosphorylation cascade	3	17	5.60E-03
2129379	Molecules associated with elastic fibres	4	38	6.46E-03
190861	Gap junction assembly	4	38	6.46E-03
212436	Generic Transcription Pathway	30	1257	7.92E-03
5663205	Infectious disease	26	1040	8.50E-03
109582	Hemostasis	20	726	9.27E-03
176417	Phosphorylation of Emi1	2	6	1.00E-02
1566977	Fibronectin matrix formation	2	6	1.00E-02
8955332	Carboxyterminal post-translational modifications of tubulin	4	43	1.00E-02
445144	Signal transduction by L1	3	21	1.01E-02
1280215	Cytokine Signaling in Immune system	24	954	1.15E-02
8862803	Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	3	22	1.15E-02
8863678	Neurodegenerative Diseases	3	22	1.15E-02
373753	Nephrin family interactions	3	23	1.31E-02
180024	DARPP-32 events	3	24	1.47E-02
9645723	Diseases of programmed cell death	3	24	1.47E-02
190828	Gap junction trafficking	4	49	1.59E-02
437239	Recycling pathway of L1	4	49	1.59E-02
2559582	Senescence-Associated Secretory Phenotype (SASP)	5	80	1.71E-02
72731	Recycling of eIF2:GDP	2	8	1.75E-02
446388	Regulation of cytoskeletal remodeling and cell spreading by IPP complex components	2	8	1.75E-02
428890	Role of ABL in ROBO-SLIT signaling	2	8	1.75E-02

157858	Gap junction trafficking and regulation	4	51	1.82E-02	
2465910	MASTL Facilitates Mitotic Progression	2	10	2.68E-02	
3000157	Laminin interactions	3	30	2.70E-02	
8874081	MET activates PTK2 signaling	3	30	2.70E-02	
114452	Activation of BH3-only proteins	3	30	2.70E-02	
9609690	HCMV Early Events	8	208	2.87E-02	
112314	Neurotransmitter receptors and postsynaptic signal transmission	8	208	2.87E-02	
4641262	Disassembly of the destruction complex and recruitment of AXIN to the membrane	3	31	2.95E-02	
73857	RNA Polymerase II Transcription	30	1379	2.95E-02	
1500931	Cell-Cell communication	6	130	3.17E-02	
4791275	Signaling by WNT in cancer	3	34	3.77E-02	
5689877	Josephin domain DUBs	2	12	3.79E-02	
442720	CREB1 phosphorylation through the activation of Adenylate Cyclase	2	12	3.79E-02	
9634600	Regulation of glycolysis by fructose 2,6-bisphosphate metabolism	2	12	3.79E-02	
6804757	Regulation of TP53 Degradation	3	36	4.39E-02	
6806003	Regulation of TP53 Expression and Degradation	3	37	4.72E-02	
5696394	DNA Damage Recognition in GG-NER	3	38	4.93E-02	
8853884	Transcriptional Regulation by VENTX	3	38	4.93E-02	
198323	AKT phosphorylates targets in the cytosol	2	14	4.93E-02	
71291	Metabolism of amino acids and derivatives	11	376	4.93E-02	
445355	Smooth Muscle Contraction	3	39	4.93E-02	
3134975	Regulation of innate immune responses to cytosolic DNA	2	15	4.93E-02	
111447	Activation of BAD and translocation to mitochondria	2	15	4.93E-02	
9648895	Response of EIF2AK1 (HRI) to heme deficiency	2	15	4.93E-02	
165159	mTOR signalling	3	40	4.93E-02	
8875878	MET promotes cell motility	3	41	4.93E-02	
1295596	Spry regulation of FGF signaling	2	16	4.93E-02	
1980143	Signaling by NOTCH1	4	75	4.93E-02	
5696395	Formation of Incision Complex in GG-NER	3	43	4.93E-02	
69231	Cyclin D associated events in G1	3	44	4.93E-02	
69236	G1 Phase	3	44	4.93E-02	
8948216	Collagen chain trimerization	3	44	4.93E-02	
7	5419276	Mitochondrial translation termination	29	88	3.19E-14

5368287	Mitochondrial translation	29	94	3.19E-14
5368286	Mitochondrial translation initiation	29	88	3.19E-14
5389840	Mitochondrial translation elongation	29	88	3.19E-14
72766	Translation	47	294	1.02E-13
5696399	Global Genome Nucleotide Excision Repair (GG-NER)	21	84	5.74E-09
418990	Adherens junctions interactions	14	33	1.32E-08
749476	RNA Polymerase III Abortive And Retractive Initiation	15	41	1.63E-08
74158	RNA Polymerase III Transcription	15	41	1.63E-08
6811558	PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	22	115	1.62E-07
2219530	Constitutive Signaling by Aberrant PI3K in Cancer	19	86	2.02E-07
5696398	Nucleotide Excision Repair	21	110	3.18E-07
199418	Negative regulation of the PI3K/AKT network	22	122	3.18E-07
5696394	DNA Damage Recognition in GG-NER	13	38	3.18E-07
69109	Leading Strand Synthesis	9	14	3.18E-07
69091	Polymerase switching	9	14	3.18E-07
1226099	Signaling by FGFR in disease	17	73	3.18E-07
112399	IRS-mediated signalling	15	55	3.18E-07
9006335	Signaling by Erythropoietin	11	26	4.13E-07
76066	RNA Polymerase III Transcription Initiation From Type 2 Promoter	11	27	5.79E-07
2428928	IRS-related events triggered by IGF1R	15	59	7.13E-07
76061	RNA Polymerase III Transcription Initiation From Type 1 Promoter	11	28	7.80E-07
74751	Insulin receptor signalling cascade	15	61	1.02E-06
2219528	PI3K/AKT Signaling in Cancer	20	113	1.10E-06
174411	Polymerase switching on the C-strand of the telomere	9	17	1.14E-06
2428924	IGF1R signaling cascade	15	62	1.14E-06
73980	RNA Polymerase III Transcription Termination	10	23	1.14E-06
176187	Activation of ATR in response to replication stress	12	37	1.14E-06
2404192	Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)	15	63	1.25E-06
69190	DNA strand elongation	11	32	2.18E-06
5663202	Diseases of signal transduction by growth factor receptors and second messengers	39	393	3.11E-06
109704	PI3K Cascade	13	50	3.18E-06
69186	Lagging Strand Synthesis	9	20	3.21E-06
69306	DNA Replication	20	127	4.65E-06
76046	RNA Polymerase III Transcription Initiation	11	36	5.83E-06

912631	Regulation of signaling by CBL	9	22	6.41E-06
1433557	Signaling by SCF-KIT	12	45	6.41E-06
421270	Cell-cell junction organization	14	65	8.46E-06
186763	Downstream signal transduction	10	31	1.13E-05
512988	Interleukin-3, Interleukin-5 and GM-CSF signaling	12	48	1.20E-05
9027276	Erythropoietin activates Phosphoinositide-3-kinase (PI3K)	7	12	1.23E-05
68962	Activation of the pre-replicative complex	10	33	1.88E-05
9006934	Signaling by Receptor Tyrosine Kinases	44	523	2.74E-05
74752	Signaling by Insulin receptor	15	85	3.32E-05
9607240	FLT3 Signaling	29	278	3.54E-05
174417	Telomere C-strand (Lagging Strand) Synthesis	9	28	3.75E-05
9027284	Erythropoietin activates RAS	7	15	4.57E-05
1059683	Interleukin-6 signaling	7	15	4.57E-05
5655253	Signaling by FGFR2 in disease	11	49	8.14E-05
5655332	Signaling by FGFR3 in disease	8	25	1.30E-04
8853338	Signaling by FGFR3 point mutants in cancer	8	25	1.30E-04
389960	Formation of tubulin folding intermediates by CCT/TriC	8	26	1.72E-04
5654696	Downstream signaling of activated FGFR2	9	35	1.90E-04
1799339	SRP-dependent cotranslational protein targeting to membrane	16	113	1.90E-04
6781827	Transcription-Coupled Nucleotide Excision Repair (TC-NER)	13	78	2.40E-04
389957	Prefoldin mediated transfer of substrate to CCT/TriC	8	28	2.75E-04
446728	Cell junction organization	14	92	3.07E-04
5684996	MAPK1/MAPK3 signaling	26	267	3.14E-04
69239	Synthesis of DNA	16	119	3.32E-04
5651801	PCNA-Dependent Long Patch Base Excision Repair	7	21	3.34E-04
190236	Signaling by FGFR	14	95	3.82E-04
110314	Recognition of DNA damage by PCNA-containing replication complex	8	30	3.95E-04
113510	E2F mediated regulation of DNA replication	7	22	4.19E-04
5683057	MAPK family signaling cascades	28	306	4.24E-04
1257604	PIP3 activates AKT signaling	26	276	4.85E-04
5673001	RAF/MAP kinase cascade	25	260	4.85E-04
5696400	Dual Incision in GG-NER	9	41	5.26E-04
5637810	Constitutive Signaling by EGFRvIII	6	16	5.99E-04
5637812	Signaling by EGFRvIII in Cancer	6	16	5.99E-04
1433559	Regulation of KIT signaling	6	16	5.99E-04

9006925	Intracellular signaling by second messengers	28	316	6.38E-04
390450	Folding of actin by CCT/TriC	5	10	6.41E-04
389958	Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding	8	33	6.64E-04
5654741	Signaling by FGFR3	9	43	7.02E-04
1500931	Cell-Cell communication	16	130	7.44E-04
5696397	Gap-filling DNA repair synthesis and ligation in GG-NER	7	25	7.44E-04
110373	Resolution of AP sites via the multiple-nucleotide patch replacement pathway	7	25	7.44E-04
180786	Extension of Telomeres	9	44	7.71E-04
451927	Interleukin-2 family signaling	9	45	9.12E-04
8853334	Signaling by FGFR3 fusions in cancer	5	11	9.24E-04
5654695	PI-3K cascade:FGFR2	7	26	9.48E-04
73780	RNA Polymerase III Chain Elongation	6	18	9.76E-04
449147	Signaling by Interleukins	35	456	1.22E-03
5655291	Signaling by FGFR4 in disease	5	12	1.27E-03
5654708	Downstream signaling of activated FGFR3	7	28	1.37E-03
5654699	SHC-mediated cascade:FGFR2	7	28	1.37E-03
76071	RNA Polymerase III Transcription Initiation From Type 3 Promoter	7	28	1.37E-03
6783589	Interleukin-6 family signaling	7	28	1.37E-03
186797	Signaling by PDGF	10	60	1.50E-03
69002	DNA Replication Pre-Initiation	12	85	1.54E-03
5637815	Signaling by Ligand-Responsive EGFR Variants in Cancer	6	20	1.54E-03
1236382	Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants	6	20	1.54E-03
5654700	FRS-mediated FGFR2 signaling	7	29	1.54E-03
9673770	Signaling by PDGFRA extracellular domain mutants	5	13	1.67E-03
9673767	Signaling by PDGFRA transmembrane, juxtamembrane and kinase domain mutants	5	13	1.67E-03
8856828	Clathrin-mediated endocytosis	16	145	2.00E-03
69242	S Phase	17	161	2.13E-03
177929	Signaling by EGFR	9	52	2.21E-03
187037	Signaling by NTRK1 (TRKA)	14	117	2.22E-03
69166	Removal of the Flap Intermediate	5	14	2.34E-03
6814122	Cooperation of PDCL (PhLP1) and TRiC/CCT in G-protein beta folding	8	42	2.40E-03
5654738	Signaling by FGFR2	11	78	2.40E-03
453279	Mitotic G1 phase and G1/S transition	16	149	2.43E-03
5656169	Termination of translesion DNA synthesis	7	32	2.50E-03

112412	SOS-mediated signalling	4	8	2.57E-03
5654743	Signaling by FGFR4	8	43	2.75E-03
69183	Processive synthesis on the lagging strand	5	15	2.88E-03
982772	Growth hormone receptor signaling	6	24	3.39E-03
166520	Signaling by NTRKs	15	139	3.55E-03
390466	Chaperonin-mediated protein folding	12	96	3.77E-03
198203	PI3K/AKT activation	4	9	4.00E-03
1266695	Interleukin-7 signaling	6	25	4.01E-03
4420097	VEGFA-VEGFR2 Pathway	12	98	4.01E-03
9665348	Signaling by ERBB2 ECD mutants	5	17	4.50E-03
1643713	Signaling by EGFR in Cancer	6	26	4.57E-03
383280	Nuclear Receptor transcription pathway	11	86	4.77E-03
1280215	Cytokine Signaling in Immune system	57	954	4.98E-03
73893	DNA Damage Bypass	8	48	5.00E-03
5654727	Negative regulation of FGFR2 signaling	7	37	5.22E-03
8875656	MET receptor recycling	4	10	5.26E-03
9020958	Interleukin-21 signaling	4	10	5.26E-03
69206	G1/S Transition	14	131	5.36E-03
912526	Interleukin receptor SHC signaling	6	27	5.56E-03
391251	Protein folding	12	102	5.66E-03
1839126	FGFR2 mutant receptor activation	7	38	6.09E-03
1834949	Cytosolic sensors of pathogen-associated DNA	9	63	6.19E-03
110313	Translesion synthesis by Y family DNA polymerases bypasses lesions on DNA template	7	39	6.19E-03
73933	Resolution of Abasic Sites (AP sites)	7	39	6.19E-03
69481	G2/M Checkpoints	15	151	6.35E-03
5654710	PI-3K cascade:FGFR3	5	19	6.46E-03
210993	Tie2 Signaling	5	19	6.46E-03
8875555	MET activates RAP1 and RAC1	4	11	6.54E-03
68689	CDC6 association with the ORC:origin complex	4	11	6.54E-03
5654716	Downstream signaling of activated FGFR4	6	29	7.01E-03
392499	Metabolism of proteins	103	2012	7.45E-03
6782135	Dual incision in TC-NER	9	65	7.50E-03
194138	Signaling by VEGF	12	108	8.03E-03
1660499	Synthesis of PIPs at the plasma membrane	8	53	8.20E-03
5655302	Signaling by FGFR1 in disease	7	41	8.24E-03
8853659	RET signaling	7	41	8.24E-03
2424491	DAP12 signaling	6	30	8.32E-03

6806834	Signaling by MET	10	80	8.58E-03
9020558	Interleukin-2 signaling	4	12	8.58E-03
3928662	EPHB-mediated forward signaling	7	42	8.58E-03
4641262	Disassembly of the destruction complex and recruitment of AXIN to the membrane	6	31	8.58E-03
389513	CTLA4 inhibitory signaling	5	21	8.58E-03
5654704	SHC-mediated cascade:FGFR3	5	21	8.58E-03
5654221	Phospholipase C-mediated cascade; FGFR2	5	21	8.58E-03
9671555	Signaling by PDGFR in disease	5	21	8.58E-03
6785807	Interleukin-4 and Interleukin-13 signaling	12	111	8.64E-03
8851907	MET activates PI3K/AKT signaling	3	6	1.02E-02
68616	Assembly of the ORC complex at the origin of replication	3	6	1.02E-02
113501	Inhibition of replication initiation of damaged DNA by RB1/E2F1	4	13	1.03E-02
164843	2-LTR circle formation	4	13	1.03E-02
5654706	FRS-mediated FGFR3 signaling	5	22	1.05E-02
3371497	HSP90 chaperone cycle for steroid hormone receptors (SHR)	8	57	1.10E-02
157579	Telomere Maintenance	9	71	1.17E-02
9006927	Signaling by Non-Receptor Tyrosine Kinases	8	58	1.23E-02
8848021	Signaling by PTK6	8	58	1.23E-02
8851708	Signaling by FGFR2 IIIa TM	5	23	1.27E-02
190241	FGFR2 ligand binding and activation	5	23	1.27E-02
4791275	Signaling by WNT in cancer	6	34	1.33E-02
2033514	FGFR3 mutant receptor activation	4	14	1.34E-02
1839130	Signaling by activated point mutants of FGFR3	4	14	1.34E-02
877312	Regulation of IFNG signaling	4	14	1.34E-02
114604	GPVI-mediated activation cascade	6	35	1.53E-02
9027283	Erythropoietin activates STAT5	3	7	1.58E-02
9027277	Erythropoietin activates Phospholipase C gamma (PLCG)	3	7	1.58E-02
73894	DNA Repair	23	313	1.60E-02
2023837	Signaling by FGFR2 amplification mutants	2	2	1.67E-02
162592	Integration of provirus	4	15	1.72E-02
5099900	WNT5A-dependent internalization of FZD4	4	15	1.72E-02
8849471	PTK6 Regulates RHO GTPases, RAS GTPase and MAP kinases	4	15	1.72E-02
69278	Cell Cycle, Mitotic	34	536	1.80E-02
2682334	EPH-Ephrin signaling	10	92	1.80E-02
110312	Translesion synthesis by REV1	4	16	1.80E-02

6782210	Gap-filling DNA repair synthesis and ligation in TC-NER	8	64	1.85E-02
8873719	RAB geranylgeranylation	8	65	2.03E-02
9009391	Extra-nuclear estrogen signaling	9	80	2.12E-02
390471	Association of TriC/CCT with target proteins during biosynthesis	6	39	2.16E-02
5656121	Translesion synthesis by POLI	4	17	2.23E-02
5655862	Translesion synthesis by POLK	4	17	2.23E-02
177539	Autointegration results in viral DNA circles	3	9	2.64E-02
113507	E2F-enabled inhibition of pre-replication complex formation	3	9	2.64E-02
8985947	Interleukin-9 signaling	3	9	2.64E-02
175567	Integration of viral DNA into host genomic DNA	3	9	2.64E-02
5654736	Signaling by FGFR1	7	54	2.66E-02
9664565	Signaling by ERBB2 KD Mutants	5	29	2.81E-02
9649913	RAS GTPase cycle mutants	2	3	3.06E-02
432722	Golgi Associated Vesicle Biogenesis	7	56	3.22E-02
5654732	Negative regulation of FGFR3 signaling	5	30	3.22E-02
1227990	Signaling by ERBB2 in Cancer	5	30	3.22E-02
2033519	Activated point mutants of FGFR2	4	19	3.27E-02
110320	Translesion Synthesis by POLH	4	19	3.27E-02
881907	Gastrin-CREB signalling pathway via PKC and MAPK	4	19	3.27E-02
9034015	Signaling by NTRK3 (TRKC)	4	19	3.27E-02
195721	Signaling by WNT	21	299	3.28E-02
2179392	EGFR Transactivation by Gastrin	3	10	3.52E-02
1445148	Translocation of SLC2A4 (GLUT4) to the plasma membrane	8	72	3.66E-02
5673000	RAF activation	5	31	3.68E-02
5654720	PI-3K cascade:FGFR4	4	20	3.90E-02
5218921	VEGFR2 mediated cell proliferation	4	20	3.90E-02
8854214	TBC/RABGAPs	6	45	4.21E-02
199992	trans-Golgi Network Vesicle Budding	8	74	4.27E-02
174437	Removal of the Flap Intermediate from the C-strand	3	11	4.55E-02
2586552	Signaling by Leptin	3	11	4.55E-02
6807004	Negative regulation of MET activity	4	21	4.60E-02
2172127	DAP12 interactions	6	47	4.60E-02
69620	Cell Cycle Checkpoints	19	274	4.60E-02
5654719	SHC-mediated cascade:FGFR4	4	22	4.60E-02
5621575	CD209 (DC-SIGN) signaling	4	22	4.60E-02
162594	Early Phase of HIV Life Cycle	4	22	4.60E-02
8851805	MET activates RAS signaling	3	12	4.60E-02
8984722	Interleukin-35 Signalling	3	12	4.60E-02

	9634285	Constitutive Signaling by Overexpressed ERBB2	3	12	4.60E-02
	180689	APOBEC3G mediated resistance to HIV-1 infection	3	12	4.60E-02
	5654687	Downstream signaling of activated FGFR1	5	35	4.78E-02
	418597	G alpha (z) signalling events	6	49	4.96E-02
	437239	Recycling pathway of L1	6	49	4.96E-02
	5654712	FRS-mediated FGFR4 signaling	4	23	5.00E-02
	5620922	BBSome-mediated cargo-targeting to cilium	4	23	5.00E-02
	5362768	Hh mutants that don't undergo autocatalytic processing are degraded by ERAD	3	56	9.30E-04
	5387390	Hh mutants abrogate ligand secretion	3	59	9.30E-04
	5678895	Defective CFTR causes cystic fibrosis	3	61	9.30E-04
	5358346	Hedgehog ligand biogenesis	3	65	9.30E-04
	5619084	ABC transporter disorders	3	77	1.22E-03
	382556	ABC-family proteins mediated transport	3	103	2.37E-03
	5358351	Signaling by Hedgehog	3	150	3.76E-03
	5619115	Disorders of transmembrane transporters	3	180	3.76E-03
	211733	Regulation of activated PAK-2p34 by proteasome mediated degradation	2	50	3.76E-03
	1236978	Cross-presentation of soluble exogenous antigens (endosomes)	2	50	3.76E-03
	350562	Regulation of ornithine decarboxylase (ODC)	2	51	3.76E-03
14	69610	p53-Independent DNA Damage Response	2	52	3.76E-03
	69601	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	2	52	3.76E-03
	69613	p53-Independent G1/S DNA damage checkpoint	2	52	3.76E-03
	75815	Ubiquitin-dependent degradation of Cyclin D	2	52	3.76E-03
	349425	Autodegradation of the E3 ubiquitin ligase COP1	2	52	3.76E-03
	180534	Vpu mediated degradation of CD4	2	53	3.76E-03
	169911	Regulation of Apoptosis	2	53	3.76E-03
	8854050	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	2	55	3.76E-03
	174113	SCF-beta-TrCP mediated degradation of Emi1	2	55	3.76E-03
	4641257	Degradation of AXIN	2	55	3.76E-03
	9604323	Negative regulation of NOTCH4 signaling	2	55	3.76E-03
	8941858	Regulation of RUNX3 expression and activity	2	55	3.76E-03

450408	AUF1 (hnRNP D0) binds and destabilizes mRNA	2	56	3.76E-03
180585	Vif-mediated degradation of APOBEC3G	2	56	3.76E-03
4641258	Degradation of DVL	2	57	3.76E-03
69541	Stabilization of p53	2	57	3.76E-03
68827	CDT1 association with the CDC6:ORC:origin complex	2	59	3.76E-03
5676590	NIK-->noncanonical NF-kB signaling	2	59	3.76E-03
351202	Metabolism of polyamines	2	59	3.76E-03
5610780	Degradation of GLI1 by the proteasome	2	60	3.76E-03
5610783	Degradation of GLI2 by the proteasome	2	60	3.76E-03
5610785	GLI3 is processed to GLI3R by the proteasome	2	60	3.76E-03
187577	SCF(Skp2)-mediated degradation of p27/p21	2	60	3.76E-03
5607761	Dectin-1 mediated noncanonical NF-kB signaling	2	60	3.76E-03
174084	Autodegradation of Cdh1 by Cdh1:APC/C	2	63	3.76E-03
4608870	Asymmetric localization of PCP proteins	2	64	3.76E-03
1234176	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	2	66	3.76E-03
69580	p53-Dependent G1/S DNA damage checkpoint	2	66	3.76E-03
69563	p53-Dependent G1 DNA Damage Response	2	66	3.76E-03
174154	APC/C:Cdc20 mediated degradation of Securin	2	67	3.76E-03
1169091	Activation of NF-kappaB in B cells	2	67	3.76E-03
68867	Assembly of the pre-replicative complex	2	68	3.76E-03
69615	G1/S DNA Damage Checkpoints	2	68	3.76E-03
5688426	Deubiquitination	3	282	3.76E-03
5658442	Regulation of RAS by GAPs	2	69	3.76E-03
8948751	Regulation of PTEN stability and activity	2	69	3.76E-03
68949	Orc1 removal from chromatin	2	71	3.76E-03
174178	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	2	72	3.76E-03
174184	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	2	72	3.76E-03
69017	CDK-mediated phosphorylation and removal of Cdc6	2	72	3.76E-03

179419	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint	2	73	3.76E-03
8939902	Regulation of RUNX2 expression and activity	2	74	3.76E-03
176409	APC/C:Cdc20 mediated degradation of mitotic proteins	2	75	3.76E-03
1234174	Cellular response to hypoxia	2	75	3.76E-03
176814	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	2	76	3.86E-03
8852276	The role of GTSE1 in G2/M progression after G2 checkpoint	2	79	4.17E-03
176408	Regulation of APC/C activators between G1/S and early anaphase	2	80	4.27E-03
1168372	Downstream signaling events of B Cell Receptor (BCR)	2	82	4.49E-03
69202	Cyclin E associated events during G1/S transition	2	83	4.59E-03
9013694	Signaling by NOTCH4	2	83	4.59E-03
195253	Degradation of beta-catenin by the destruction complex	2	83	4.59E-03
5632684	Hedgehog 'on' state	2	85	4.64E-03
69656	Cyclin A:Cdk2-associated events at S phase entry	2	85	4.64E-03
69002	DNA Replication Pre-Initiation	2	85	4.64E-03
453276	Regulation of mitotic cell cycle	2	86	4.64E-03
174143	APC/C-mediated degradation of cell cycle proteins	2	86	4.64E-03
450531	Regulation of mRNA stability by proteins that bind AU-rich elements	2	88	4.64E-03
5687128	MAPK6/MAPK4 signaling	2	89	4.64E-03
69052	Switching of origins to a post-replicative state	2	90	4.64E-03
4086400	PCP/CE pathway	2	92	4.64E-03
5689603	UCH proteinases	2	96	4.64E-03
8878159	Transcriptional regulation by RUNX3	2	96	4.64E-03
5607764	CLEC7A (Dectin-1) signaling	2	98	4.64E-03
8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	2	99	4.64E-03
5668541	TNFR2 non-canonical NF-kB pathway	2	102	4.64E-03
9020702	Interleukin-1 signaling	2	102	4.64E-03
5663202	Diseases of signal transduction by growth factor receptors and second messengers	3	393	4.64E-03
5610787	Hedgehog 'off' state	2	114	4.64E-03
202424	Downstream TCR signaling	2	116	4.64E-03

69239	Synthesis of DNA	2	119	4.64E-03
8878166	Transcriptional regulation by RUNX2	2	121	4.80E-03
69306	DNA Replication	2	127	5.27E-03
69206	G1/S Transition	2	131	5.59E-03
202403	TCR signaling	2	138	6.19E-03
6807070	PTEN Regulation	2	139	6.28E-03
446652	Interleukin-1 family signaling	2	141	6.45E-03
162909	Host Interactions of HIV factors	2	144	6.72E-03
3858494	Beta-catenin independent WNT signaling	2	144	6.72E-03
453279	Mitotic G1 phase and G1/S transition	2	149	7.18E-03
69481	G2/M Checkpoints	2	151	7.36E-03
1236974	ER-Phagosome pathway	2	153	7.55E-03
69242	S Phase	2	161	8.33E-03
2871837	FCERI mediated NF-kB activation	2	167	8.94E-03
1236975	Antigen processing-Cross presentation	2	169	9.15E-03
9010553	Regulation of expression of SLITs and ROBOs	2	172	9.46E-03
5621481	C-type lectin receptors (CLRs)	2	174	9.67E-03
983705	Signaling by the B Cell Receptor (BCR)	2	176	9.89E-03
109581	Apoptosis	2	180	1.03E-02
5689877	Josephin domain DUBs	1	12	1.05E-02
3371511	HSF1 activation	1	12	1.05E-02
5357801	Programmed Cell Death	2	185	1.09E-02
2262752	Cellular responses to stress	3	564	1.12E-02
2467813	Separation of Sister Chromatids	2	190	1.14E-02
8953897	Cellular responses to external stimuli	3	578	1.20E-02
69275	G2/M Transition	2	198	1.24E-02
453274	Mitotic G2-G2/M phases	2	200	1.26E-02
201681	TCF dependent signaling in response to WNT	2	202	1.29E-02
5689880	Ub-specific processing proteases	2	205	1.32E-02
157118	Signaling by NOTCH	2	206	1.34E-02
8878171	Transcriptional regulation by RUNX1	2	208	1.36E-02
8876725	Protein methylation	1	17	1.48E-02
376176	Signaling by ROBO receptors	2	218	1.49E-02
2454202	Fc epsilon receptor (FCERI) signaling	2	218	1.49E-02
110320	Translesion Synthesis by POLH	1	19	1.66E-02
8951664	Neddylaton	2	236	1.73E-02
68882	Mitotic Anaphase	2	236	1.73E-02

	2555396	Mitotic Metaphase and Anaphase	2	237	1.74E-02
	162906	HIV Infection	2	248	1.90E-02
	5673001	RAF/MAP kinase cascade	2	260	2.07E-02
	5684996	MAPK1/MAPK3 signaling	2	267	2.18E-02
	382551	Transport of small molecules	3	731	2.25E-02
	69620	Cell Cycle Checkpoints	2	274	2.29E-02
	1257604	PIP3 activates AKT signaling	2	276	2.32E-02
	9607240	FLT3 Signaling	2	278	2.35E-02
	195721	Signaling by WNT	2	299	2.69E-02
	5683057	MAPK family signaling cascades	2	306	2.81E-02
	983168	Antigen processing: Ubiquitination & Proteasome degradation	2	309	2.86E-02
	9006925	Intracellular signaling by second messengers	2	316	2.98E-02
	532668	N-glycan trimming in the ER and Calnexin/Calreticulin cycle	1	35	3.03E-02
	5689896	Ovarian tumor domain proteases	1	38	3.29E-02
	110313	Translesion synthesis by Y family DNA polymerases bypasses lesions on DNA template	1	39	3.37E-02
	9646399	Aggrephagy	1	44	3.80E-02
	71291	Metabolism of amino acids and derivatives	2	376	4.11E-02
	73893	DNA Damage Bypass	1	48	4.13E-02
	68886	M Phase	2	392	4.43E-02
	202430	Translocation of ZAP-70 to Immunological synapse	15	38	1.33E-12
	202427	Phosphorylation of CD3 and TCR zeta chains	15	41	1.78E-12
	389948	PD-1 signaling	15	42	1.78E-12
	2132295	MHC class II antigen presentation	23	142	1.78E-12
	202433	Generation of second messenger molecules	15	53	3.05E-11
	388841	Costimulation by the CD28 family	15	88	2.83E-08
	202424	Downstream TCR signaling	15	116	9.49E-07
	202403	TCR signaling	15	138	7.83E-06
25	877300	Interferon gamma signaling	16	172	2.04E-05
	194840	Rho GTPase cycle	13	141	2.68E-04
	194315	Signaling by Rho GTPases	23	426	5.27E-04
	75158	TRAIL signaling	4	8	1.00E-03
	6811436	COPI-independent Golgi-to-ER retrograde traffic	7	53	4.00E-03
	75035	Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	4	13	5.46E-03
	913531	Interferon Signaling	16	289	6.49E-03
	6807878	COPI-mediated anterograde transport	9	102	6.49E-03

	199977	ER to Golgi Anterograde Transport	11	155	7.46E-03
	5628897	TP53 Regulates Metabolic Genes	8	88	1.03E-02
	8856688	Golgi-to-ER retrograde transport	10	137	1.03E-02
	1445148	Translocation of SLC2A4 (GLUT4) to the plasma membrane	7	72	1.48E-02
	109606	Intrinsic Pathway for Apoptosis	6	53	1.62E-02
	190840	Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	4	20	1.64E-02
	6811442	Intra-Golgi and retrograde Golgi-to-ER traffic	12	206	1.73E-02
	5675482	Regulation of necroptotic cell death	4	21	1.73E-02
	190872	Transport of connexons to the plasma membrane	4	21	1.73E-02
	3371497	HSP90 chaperone cycle for steroid hormone receptors (SHR)	6	57	1.90E-02
	948021	Transport to the Golgi and subsequent modification	11	186	2.08E-02
	5213460	RIPK1-mediated regulated necrosis	4	23	2.08E-02
	5218859	Regulated Necrosis	4	23	2.08E-02
	3371378	Regulation by c-FLIP	3	11	2.39E-02
	69416	Dimerization of procaspase-8	3	11	2.39E-02
	9646399	Aggrephagy	5	44	2.96E-02
	9609736	Assembly and cell surface presentation of NMDA receptors	5	44	2.96E-02
	73887	Death Receptor Signalling	9	147	3.82E-02
	9619483	Activation of AMPK downstream of NMDARs	4	29	3.94E-02
	5218900	CASP8 activity is inhibited	3	14	3.94E-02
	75108	Activation, myristoylation of BID and translocation to mitochondria	2	4	4.20E-02
	111447	Activation of BAD and translocation to mitochondria	3	15	4.67E-02
	8863795	Downregulation of ERBB2 signaling	4	32	4.67E-02
	5626467	RHO GTPases activate IQGAPs	4	32	4.67E-02
	9668328	Sealing of the nuclear envelope (NE) by ESCRT-III	4	32	4.67E-02
	156711	Polo-like kinase mediated events	3	16	4.96E-02
	1362300	Transcription of E2F targets under negative control by p107 (RBL1) and p130 (RBL2) in complex with HDAC1	3	16	4.96E-02
	380972	Energy dependent regulation of mTOR by LKB1-AMPK	9	29	1.30E-07
	165159	mTOR signalling	9	40	1.04E-06
29	166208	mTORC1-mediated signalling	6	23	1.35E-04
	449147	Signaling by Interleukins	18	456	3.63E-03
	380994	ATF4 activates genes in response to endoplasmic reticulum stress	5	27	3.67E-03

	429958	mRNA decay by 3' to 5' exoribonuclease	4	16	5.84E-03
	381042	PERK regulates gene expression	5	32	5.84E-03
	9639288	Amino acids regulate mTORC1	6	55	6.72E-03
	6785807	Interleukin-4 and Interleukin-13 signaling	8	111	7.13E-03
	8943724	Regulation of PTEN gene transcription	6	60	8.63E-03
	5628897	TP53 Regulates Metabolic Genes	7	88	8.82E-03
	9006925	Intracellular signaling by second messengers	13	316	1.19E-02
	379716	Cytosolic tRNA aminoacylation	4	24	1.37E-02
	1632852	Macroautophagy	8	137	1.71E-02
	5260271	Diseases of Immune System	4	27	1.71E-02
	5602358	Diseases associated with the TLR signaling cascade	4	27	1.71E-02
	9612973	Autophagy	8	152	2.91E-02
	429914	Deadenylation-dependent mRNA decay	5	56	2.91E-02
	1257604	PIP3 activates AKT signaling	11	276	2.97E-02
	168898	Toll-like Receptor Cascades	8	156	3.00E-02
	9648895	Response of EIF2AK1 (HRI) to heme deficiency	3	15	3.06E-02
	9614657	FOXO-mediated transcription of cell death genes	3	16	3.38E-02
	450513	Tristetraprolin (TTP, ZFP36) binds and destabilizes mRNA	3	17	3.38E-02
	450604	KSRP (KHSRP) binds and destabilizes mRNA	3	17	3.38E-02
	450385	Butyrate Response Factor 1 (BRF1) binds and destabilizes mRNA	3	17	3.38E-02
	168188	Toll Like Receptor TLR6:TLR2 Cascade	6	96	3.38E-02
	166058	MyD88:MAL(TIRAP) cascade initiated on plasma membrane	6	96	3.38E-02
	181438	Toll Like Receptor 2 (TLR2) Cascade	6	99	3.76E-02
	168179	Toll Like Receptor TLR1:TLR2 Cascade	6	99	3.76E-02
	379724	tRNA Aminoacylation	4	42	4.32E-02
	446652	Interleukin-1 family signaling	7	141	4.42E-02
	5419276	Mitochondrial translation termination	1	88	3.26E-02
35	5389840	Mitochondrial translation elongation	1	88	3.26E-02
	5368286	Mitochondrial translation initiation	1	88	3.26E-02
	5368287	Mitochondrial translation	1	94	3.26E-02
	162710	Synthesis of glycosylphosphatidylinositol (GPI)	6	18	9.20E-10
38	163125	Post-translational modification: synthesis of GPI-anchored proteins	6	94	8.05E-06
	9640463	Wax biosynthesis	2	4	1.81E-03

	8848584	Wax and plasmalogen biosynthesis	2	7	4.06E-03
	5628897	TP53 Regulates Metabolic Genes	8	88	4.07E-03
	5218920	VEGFR2 mediated vascular permeability	5	27	4.07E-03
	442742	CREB1 phosphorylation through NMDA receptor-mediated activation of RAS signaling	5	29	4.07E-03
	111932	CaMK IV-mediated phosphorylation of CREB	3	10	2.41E-02
	1538133	G0 and Early G1	4	27	2.51E-02
39	1362300	Transcription of E2F targets under negative control by p107 (RBL1) and p130 (RBL2) in complex with HDAC1	3	16	4.12E-02
	4420097	VEGFA-VEGFR2 Pathway	6	98	4.12E-02
	3700989	Transcriptional Regulation by TP53	12	367	4.12E-02
	1632852	Macroautophagy	7	137	4.12E-02
	165158	Activation of AKT2	2	4	4.12E-02
	611105	Respiratory electron transport	6	101	4.12E-02
	909733	Interferon alpha/beta signaling	4	184	3.87E-07
	877300	Interferon gamma signaling	4	250	6.16E-07
	913531	Interferon Signaling	4	392	2.15E-06
	1236977	Endosomal/Vacuolar pathway	3	82	2.15E-06
	983170	Antigen Presentation: Folding, assembly and peptide loading of class I MHC	3	102	4.14E-06
	1236974	ER-Phagosome pathway	3	165	1.17E-05
	1236975	Antigen processing-Cross presentation	3	187	1.69E-05
45	198933	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	3	316	4.06E-05
	1280215	Cytokine Signaling in Immune system	4	1261	5.70E-05
	983169	Class I MHC mediated antigen processing & presentation	3	465	1.28E-04
	1280218	Adaptive Immune System	3	999	1.24E-03
	168256	Immune System	4	2823	1.43E-03
	2424491	DAP12 signaling	1	36	9.88E-03
	2172127	DAP12 interactions	1	53	1.45E-02
	2142789	Ubiquinol biosynthesis	1	8	1.26E-02
	8978934	Metabolism of cofactors	1	19	1.50E-02
48	1268020	Mitochondrial protein import	1	65	3.40E-02
	9609507	Protein localization	1	166	4.31E-02
	196854	Metabolism of vitamins and cofactors	1	192	4.97E-02
	977606	Regulation of Complement cascade	2	135	4.88E-03
50	166658	Complement cascade	2	146	4.88E-03

	198933	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	2	297	1.20E-02
	168256	Immune System	3	2374	3.18E-02
	1280218	Adaptive Immune System	2	944	3.18E-02
	2219530	Constitutive Signaling by Aberrant PI3K in Cancer	1	86	3.18E-02
	983695	Antigen activates B Cell Receptor (BCR) leading to generation of second messengers	1	95	3.18E-02
	2219528	PI3K/AKT Signaling in Cancer	1	113	3.18E-02
	6811558	PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	1	115	3.18E-02
	168249	Innate Immune System	2	1187	3.18E-02
	199418	Negative regulation of the PI3K/AKT network	1	122	3.18E-02
	909733	Interferon alpha/beta signaling	1	137	3.56E-02
	983705	Signaling by the B Cell Receptor (BCR)	1	176	4.56E-02
54	8931987	RUNX1 regulates estrogen receptor mediated transcription	1	6	2.53E-02
55	189483	Heme degradation	1	15	7.35E-03
	189445	Metabolism of porphyrins	1	28	7.35E-03
69	4724325	Defective ALG8 causes ALG8-CDG (CDG-1h)	1	1	1.68E-02
70	5632681	Ligand-receptor interactions	3	8	6.33E-03
	5658034	HHAT G278V abrogates palmitoylation of Hh-Np	2	4	3.92E-02
	3928663	EPHA-mediated growth cone collapse	3	29	3.95E-07
	3928665	EPH-ephrin mediated repulsion of cells	3	51	1.07E-06
77	2682334	EPH-Ephrin signaling	3	92	4.19E-06
	422475	Axon guidance	3	558	4.53E-04
	9675108	Nervous system development	3	584	5.18E-04
	1266738	Developmental Biology	3	1100	3.34E-03
	1369062	ABC transporters in lipid homeostasis	2	18	7.71E-03
	9603798	Class I peroxisomal membrane protein import	2	20	7.71E-03
86	382556	ABC-family proteins mediated transport	3	103	7.71E-03
	5619088	Defective SLC39A4 causes acrodermatitis enteropathica, zinc-deficiency type (AEZ)	1	1	1.50E-02
	375276	Peptide ligand-binding receptors	3	198	2.89E-02
	1369007	Mitochondrial ABC transporters	1	4	3.99E-02
90	174490	Membrane binding and targeting of GAG proteins	3	15	1.19E-03
	174495	Synthesis And Processing Of GAG, GAGPOL Polyproteins	3	15	1.19E-03

5693567	HDR through Homologous Recombination (HRR) or Single Strand Annealing (SSA)	5	114	1.19E-03
5693538	Homology Directed Repair	5	120	1.19E-03
175474	Assembly Of The HIV Virion	3	24	2.04E-03
5693532	DNA Double-Strand Break Repair	5	148	2.17E-03
69473	G2/M DNA damage checkpoint	4	78	2.24E-03
5693607	Processing of DNA double-strand break ends	4	81	2.27E-03
917729	Endosomal Sorting Complex Required For Transport (ESCRT)	3	31	2.45E-03
9610379	HCMV Late Events	5	173	2.59E-03
9615710	Late endosomal microautophagy	3	34	2.59E-03
162588	Budding and maturation of HIV virion	3	36	2.78E-03
73894	DNA Repair	6	313	3.79E-03
5693571	Nonhomologous End-Joining (NHEJ)	3	52	6.83E-03
912446	Meiotic recombination	3	56	7.41E-03
5693565	Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	3	59	8.00E-03
5693606	DNA Double Strand Break Response	3	60	8.40E-03
9609646	HCMV Infection	5	262	9.07E-03
69481	G2/M Checkpoints	4	151	9.07E-03
1500620	Meiosis	3	88	1.93E-02
5693554	Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA)	2	26	2.24E-02
5602358	Diseases associated with the TLR signaling cascade	2	27	2.24E-02
5260271	Diseases of Immune System	2	27	2.24E-02
5602410	TLR3 deficiency - HSE	1	1	2.24E-02
5579006	Defective GSS causes Glutathione synthetase deficiency (GSS deficiency)	1	1	2.24E-02
5689901	Metalloprotease DUBs	2	31	2.50E-02
5693568	Resolution of D-loop Structures through Holliday Junction Intermediates	2	32	2.50E-02
73728	RNA Polymerase I Promoter Opening	2	32	2.50E-02
171306	Packaging Of Telomere Ends	2	33	2.50E-02
5693537	Resolution of D-Loop Structures	2	33	2.50E-02
1474165	Reproduction	3	114	2.50E-02
5334118	DNA methylation	2	34	2.50E-02

5625886	Activated PKN1 stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3	2	36	2.79E-02
427359	SIRT1 negatively regulates rRNA expression	2	37	2.80E-02
110331	Cleavage of the damaged purine	2	38	2.80E-02
73927	Depurination	2	39	2.80E-02
110330	Recognition and association of DNA glycosylase with site containing an affected purine	2	39	2.80E-02
5602566	TICAM1 deficiency - HSE	1	2	2.80E-02
5602415	UNC93B1 deficiency - HSE	1	2	2.80E-02
212300	PRC2 methylates histones and DNA	2	42	2.81E-02
5693579	Homologous DNA Pairing and Strand Exchange	2	42	2.81E-02
110329	Cleavage of the damaged pyrimidine	2	42	2.81E-02
73928	Depyrimidination	2	42	2.81E-02
110328	Recognition and association of DNA glycosylase with site containing an affected pyrimidine	2	42	2.81E-02
69620	Cell Cycle Checkpoints	4	274	2.81E-02
2299718	Condensation of Prophase Chromosomes	2	45	2.86E-02
427389	ERCC6 (CSB) and EHMT2 (G9a) positively regulate rRNA expression	2	45	2.86E-02
73929	Base-Excision Repair, AP Site Formation	2	46	2.98E-02
5602571	TRAF3 deficiency - HSE	1	3	3.36E-02
162599	Late Phase of HIV Life Cycle	3	152	3.53E-02
9612973	Autophagy	3	152	3.53E-02
195258	RHO GTPase Effectors	4	295	3.60E-02
774815	Nucleosome assembly	2	54	3.60E-02
606279	Deposition of new CENPA-containing nucleosomes at the centromere	2	54	3.60E-02
71406	Pyruvate metabolism and Citric Acid (TCA) cycle	2	55	3.60E-02
162587	HIV Life Cycle	3	165	3.60E-02
9616222	Transcriptional regulation of granulopoiesis	2	59	3.60E-02
3214815	HDACs deacetylate histones	2	60	3.72E-02
1221632	Meiotic synapsis	2	60	3.72E-02
73772	RNA Polymerase I Promoter Escape	2	60	3.72E-02
5250924	B-WICH complex positively regulates rRNA expression	2	60	3.72E-02
201722	Formation of the beta-catenin:TCF transactivating complex	2	60	3.72E-02
2559586	DNA Damage/Telomere Stress Induced Senescence	2	61	3.83E-02

1428517	The citric acid (TCA) cycle and respiratory electron transport	3	176	3.93E-02
1912408	Pre-NOTCH Transcription and Translation	2	62	3.95E-02
5625740	RHO GTPases activate PKNs	2	63	4.08E-02
5685942	HDR through Homologous Recombination (HRR)	2	66	4.15E-02
8936459	RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	2	66	4.15E-02
9013957	TLR3-mediated TICAM1-dependent programmed cell death	1	6	4.15E-02
157579	Telomere Maintenance	2	71	4.15E-02
73884	Base Excision Repair	2	74	4.15E-02
427413	NoRC negatively regulates rRNA expression	2	75	4.15E-02
5250913	Positive epigenetic regulation of rRNA expression	2	75	4.15E-02
5250941	Negative epigenetic regulation of rRNA expression	2	78	4.15E-02
1912422	Pre-NOTCH Expression and Processing	2	78	4.15E-02
73854	RNA Polymerase I Promoter Clearance	2	79	4.15E-02
5578749	Transcriptional regulation by small RNAs	2	80	4.25E-02
73864	RNA Polymerase I Transcription	2	80	4.25E-02
2559582	Senescence-Associated Secretory Phenotype (SASP)	2	80	4.25E-02
977225	Amyloid fiber formation	2	80	4.25E-02
2562578	TRIF-mediated programmed cell death	1	9	4.99E-02

FDR, false discovery rate.

Supplementary Table 4. Biological process analysis of the genes involved in the most important clusters in the protein-protein interaction network associated with colorectal cancer.

Cluster no.	GO ID	GO Term	#Entities found	FDR
	GO:0000981	DNA-binding transcription factor activity, RNA polymerase II-specific	356	0/00E+00
	GO:0003700	DNA-binding transcription factor activity	359	1/42E-283
	GO:0006355	regulation of transcription, DNA-templated	383	1/41E-249
	GO:1903506	regulation of nucleic acid-templated transcription	383	2/16E-246
	GO:2001141	regulation of RNA biosynthetic process	383	4/94E-246
	GO:0006351	transcription, DNA-templated	383	3/42E-241
	GO:0097659	nucleic acid-templated transcription	383	6/56E-239
	GO:0032774	RNA biosynthetic process	383	2/97E-238
	GO:0006357	regulation of transcription by RNA polymerase II	358	2/97E-238
	GO:0051252	regulation of RNA metabolic process	383	5/52E-235
	GO:0006366	transcription by RNA polymerase II	359	1/16E-231
	GO:2000112	regulation of cellular macromolecule biosynthetic process	383	1/54E-228
	GO:0010556	regulation of macromolecule biosynthetic process	383	2/76E-223
	GO:0019219	regulation of nucleobase-containing compound metabolic process	383	1/07E-221
	GO:0034654	nucleobase-containing compound biosynthetic process	383	1/59E-215
	GO:0031326	regulation of cellular biosynthetic process	383	1/94E-215
	GO:0018130	heterocycle biosynthetic process	383	4/07E-213
	GO:0009889	regulation of biosynthetic process	383	1/70E-212
	GO:0019438	aromatic compound biosynthetic process	383	2/41E-212
1	GO:0010468	regulation of gene expression	383	1/47E-208
	GO:1901362	organic cyclic compound biosynthetic process	383	2/27E-207
	GO:0016070	RNA metabolic process	383	1/48E-202
	GO:0034645	cellular macromolecule biosynthetic process	383	2/01E-194
	GO:0044271	cellular nitrogen compound biosynthetic process	383	9/85E-192
	GO:0009059	macromolecule biosynthetic process	383	4/15E-190
	GO:0090304	nucleic acid metabolic process	383	9/62E-186
	GO:0010467	gene expression	383	8/85E-180
	GO:0051171	regulation of nitrogen compound metabolic process	383	9/11E-166
	GO:0006139	nucleobase-containing compound metabolic process	383	1/08E-165
	GO:0046483	heterocycle metabolic process	383	1/65E-161
	GO:0080090	regulation of primary metabolic process	383	6/34E-161
	GO:0006725	cellular aromatic compound metabolic process	383	1/92E-160
	GO:0044249	cellular biosynthetic process	383	1/34E-159
	GO:0060255	regulation of macromolecule metabolic process	383	1/92E-159
	GO:0031323	regulation of cellular metabolic process	383	1/86E-157
	GO:1901576	organic substance biosynthetic process	383	2/75E-157
	GO:1901360	organic cyclic compound metabolic process	383	3/39E-155
	GO:0034641	cellular nitrogen compound metabolic process	383	2/38E-148
	GO:0019222	regulation of metabolic process	383	1/12E-146

	GO:0044260	cellular macromolecule metabolic process	383	3/67E-114
	GO:0006614	SRP-dependent cotranslational protein targeting to membrane	74	3/65E-158
	GO:0006613	cotranslational protein targeting to membrane	74	1/39E-156
	GO:0045047	protein targeting to ER	74	1/31E-151
	GO:0072599	establishment of protein localization to endoplasmic reticulum	74	2/48E-150
	GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	74	3/20E-146
	GO:0070972	protein localization to endoplasmic reticulum	74	7/71E-143
	GO:0006413	translational initiation	76	4/17E-135
	GO:0019083	viral transcription	74	3/18E-131
	GO:0000956	nuclear-transcribed mRNA catabolic process	75	5/90E-128
	GO:0019080	viral gene expression	74	1/54E-127
	GO:0006612	protein targeting to membrane	74	4/30E-127
	GO:0006402	mRNA catabolic process	76	3/35E-110
	GO:0090150	establishment of protein localization to membrane	75	9/21E-110
	GO:0006401	RNA catabolic process	76	1/82E-107
	GO:0006412	translation	80	4/66E-101
	GO:0006605	protein targeting	74	2/42E-100
	GO:0043043	peptide biosynthetic process	80	1/16E-99
	GO:0006518	peptide metabolic process	81	7/92E-93
	GO:0043604	amide biosynthetic process	80	1/69E-92
	GO:0034655	nucleobase-containing compound catabolic process	76	2/04E-90
2	GO:0072594	establishment of protein localization to organelle	74	2/12E-90
	GO:0072657	protein localization to membrane	75	7/56E-90
	GO:0046700	heterocycle catabolic process	76	1/43E-87
	GO:0044270	cellular nitrogen compound catabolic process	76	1/53E-87
	GO:0019439	aromatic compound catabolic process	76	1/04E-86
	GO:0043603	cellular amide metabolic process	82	1/49E-85
	GO:1901361	organic cyclic compound catabolic process	76	3/78E-85
	GO:0016032	viral process	76	2/83E-81
	GO:0016071	mRNA metabolic process	76	4/30E-81
	GO:0044403	symbiont process	76	1/32E-78
	GO:0044265	cellular macromolecule catabolic process	79	5/25E-78
	GO:0033365	protein localization to organelle	75	4/20E-76
	GO:0009057	macromolecule catabolic process	80	1/97E-73
	GO:0006886	intracellular protein transport	75	2/45E-69
	GO:0042254	ribosome biogenesis	40	1/06E-44
	GO:0022613	ribonucleoprotein complex biogenesis	43	2/57E-40
	GO:0002181	cytoplasmic translation	29	2/89E-40
	GO:0006364	rRNA processing	28	6/71E-30
	GO:0042273	ribosomal large subunit biogenesis	20	3/48E-28
	GO:0042255	ribosome assembly	20	4/48E-28
	GO:0016072	rRNA metabolic process	28	9/50E-28
	GO:0042274	ribosomal small subunit biogenesis	18	4/74E-24

	GO:0034470	ncRNA processing	28	1/11E-22
	GO:0022618	ribonucleoprotein complex assembly	23	9/68E-20
	GO:0071826	ribonucleoprotein complex subunit organization	23	2/51E-19
	GO:0034660	ncRNA metabolic process	28	3/23E-18
	GO:0000027	ribosomal large subunit assembly	11	2/36E-16
	GO:0000028	ribosomal small subunit assembly	9	6/84E-14
	GO:0030490	maturation of SSU-rRNA	8	7/16E-09
	GO:1990948	ubiquitin ligase inhibitor activity	5	1/44E-08
	GO:0055105	ubiquitin-protein transferase inhibitor activity	5	2/54E-08
	GO:1904667	negative regulation of ubiquitin protein ligase activity	5	1/56E-07
	GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	6	4/79E-07
	GO:0000470	maturation of LSU-rRNA	5	1/56E-06
	GO:0051438	regulation of ubiquitin-protein transferase activity	7	2/79E-06
	GO:0051444	negative regulation of ubiquitin-protein transferase activity	5	2/89E-06
	GO:0055106	ubiquitin-protein transferase regulator activity	5	6/66E-06
	GO:1902255	positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator	3	1/96E-05
	GO:1904666	regulation of ubiquitin protein ligase activity	5	2/24E-05
	GO:1901798	positive regulation of signal transduction by p53 class mediator	5	3/06E-05
	GO:0031397	negative regulation of protein ubiquitination	6	1/53E-04
	GO:2000059	negative regulation of ubiquitin-dependent protein catabolic process	5	1/98E-04
	GO:1903321	negative regulation of protein modification by small protein conjugation or removal	6	2/28E-04
	GO:0045727	positive regulation of translation	6	8/92E-04
	GO:1903051	negative regulation of proteolysis involved in cellular protein catabolic process	5	8/98E-04
	GO:0071428	rRNA-containing ribonucleoprotein complex export from nucleus	3	1/43E-03
	GO:1903363	negative regulation of cellular protein catabolic process	5	2/03E-03
	GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	3	5/27E-03
	GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	4	5/92E-03
	GO:0035872	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	3	7/16E-03
	GO:1902253	regulation of intrinsic apoptotic signaling pathway by p53 class mediator	3	7/22E-03
	GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway	3	7/81E-03
	GO:0006301	postreplication repair	3	7/98E-03
	GO:0019985	translesion synthesis	3	8/64E-03
	GO:0042769	DNA damage response, detection of DNA damage	3	8/65E-03
	GO:0000731	DNA synthesis involved in DNA repair	3	1/15E-02
	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	86	1/53E-126
3	GO:0000398	mRNA splicing, via spliceosome	86	1/53E-126
	GO:0000375	RNA splicing, via transesterification reactions	86	3/03E-126
	GO:0008380	RNA splicing	86	1/55E-116
	GO:0006397	mRNA processing	87	1/47E-110

GO:0006396	RNA processing	92	1/15E-98
GO:0016071	mRNA metabolic process	90	9/51E-97
GO:0031124	mRNA 3'-end processing	37	5/53E-51
GO:0031123	RNA 3'-end processing	37	7/12E-45
GO:0050684	regulation of mRNA processing	28	4/52E-31
GO:0006405	RNA export from nucleus	28	7/28E-31
GO:0051028	mRNA transport	29	6/30E-30
GO:0006406	mRNA export from nucleus	26	7/85E-30
GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	26	7/85E-30
GO:0071426	ribonucleoprotein complex export from nucleus	27	8/59E-30
GO:0071166	ribonucleoprotein complex localization	27	9/99E-30
GO:0050657	nucleic acid transport	30	1/41E-28
GO:0050658	RNA transport	30	1/41E-28
GO:1903311	regulation of mRNA metabolic process	34	2/40E-28
GO:0051236	establishment of RNA localization	30	3/66E-28
GO:0051168	nuclear export	29	7/09E-28
GO:0006403	RNA localization	31	1/82E-27
GO:0015931	nucleobase-containing compound transport	31	1/97E-27
GO:0006611	protein export from nucleus	28	2/72E-27
GO:0006913	nucleocytoplasmic transport	32	8/06E-25
GO:0051169	nuclear transport	32	1/05E-24
GO:0043484	regulation of RNA splicing	23	3/36E-24
GO:0006353	DNA-templated transcription, termination	20	9/15E-24
GO:0048024	regulation of mRNA splicing, via spliceosome	20	1/63E-22
GO:0006369	termination of RNA polymerase II transcription	16	1/95E-22
GO:0022618	ribonucleoprotein complex assembly	26	1/75E-21
GO:0071826	ribonucleoprotein complex subunit organization	26	5/27E-21
GO:0000245	spliceosomal complex assembly	17	9/69E-21
GO:0031503	protein-containing complex localization	27	1/29E-20
GO:0000380	alternative mRNA splicing, via spliceosome	17	2/59E-19
GO:0045292	mRNA cis splicing, via spliceosome	13	8/29E-18
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	15	2/11E-17
GO:0022613	ribonucleoprotein complex biogenesis	28	2/14E-17
GO:0006379	mRNA cleavage	11	8/75E-17
GO:1903312	negative regulation of mRNA metabolic process	15	8/28E-16
GO:0048025	negative regulation of mRNA splicing, via spliceosome	10	8/55E-16
GO:0033119	negative regulation of RNA splicing	10	2/53E-14
GO:0050686	negative regulation of mRNA processing	10	3/07E-13
GO:0006378	mRNA polyadenylation	12	3/93E-13
GO:0043631	RNA polyadenylation	12	5/48E-13
GO:0006370	7-methylguanosine mRNA capping	10	7/26E-13
GO:0008543	fibroblast growth factor receptor signaling pathway	14	1/00E-12
GO:0009452	7-methylguanosine RNA capping	10	2/09E-12

GO:0036260	RNA capping	10	2/09E-12
GO:0044344	cellular response to fibroblast growth factor stimulus	15	2/28E-12
GO:0071774	response to fibroblast growth factor	15	5/66E-12
GO:0042795	snRNA transcription by RNA polymerase II	11	6/16E-11
GO:0009301	snRNA transcription	11	6/96E-11
GO:0006376	mRNA splice site selection	9	1/39E-10
GO:0006402	mRNA catabolic process	19	5/76E-10
GO:0050434	positive regulation of viral transcription	9	6/74E-10
GO:0016073	snRNA metabolic process	11	1/86E-09
GO:0098789	pre-mRNA cleavage required for polyadenylation	6	4/45E-09
GO:0098781	ncRNA transcription	11	7/11E-09
GO:0098787	mRNA cleavage involved in mRNA processing	6	7/14E-09
GO:0006368	transcription elongation from RNA polymerase II promoter	10	1/95E-08
GO:0006354	DNA-templated transcription, elongation	11	2/62E-08
GO:0046782	regulation of viral transcription	9	4/63E-08
GO:0090501	RNA phosphodiester bond hydrolysis	12	5/71E-08
GO:0031440	regulation of mRNA 3'-end processing	7	1/95E-07
GO:0031047	gene silencing by RNA	12	2/59E-07
GO:0048524	positive regulation of viral process	10	2/94E-07
GO:1903313	positive regulation of mRNA metabolic process	9	3/19E-07
GO:0033120	positive regulation of RNA splicing	7	4/01E-07
GO:0008334	histone mRNA metabolic process	6	6/53E-07
GO:0019080	viral gene expression	12	6/89E-07
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	10	7/99E-07
GO:0000956	nuclear-transcribed mRNA catabolic process	12	1/31E-06
GO:0050685	positive regulation of mRNA processing	6	3/15E-06
GO:0035194	posttranscriptional gene silencing by RNA	10	6/38E-06
GO:0016441	posttranscriptional gene silencing	10	6/53E-06
GO:1903241	U2-type prespliceosome assembly	3	6/76E-06
GO:0003899	DNA-directed 5'-3' RNA polymerase activity	6	9/07E-06
GO:0001055	RNA polymerase II activity	4	1/11E-05
GO:0019083	viral transcription	10	2/08E-05
GO:0048255	mRNA stabilization	6	2/71E-05
GO:0035195	gene silencing by miRNA	9	3/09E-05
GO:0060968	regulation of gene silencing	9	3/14E-05
GO:0043902	positive regulation of multi-organism process	10	3/18E-05
GO:0060964	regulation of gene silencing by miRNA	8	3/26E-05
GO:0060147	regulation of posttranscriptional gene silencing	8	3/41E-05
GO:0060966	regulation of gene silencing by RNA	8	3/41E-05
GO:0043489	RNA stabilization	6	4/95E-05
GO:1902373	negative regulation of mRNA catabolic process	6	5/73E-05
GO:1902369	negative regulation of RNA catabolic process	6	1/26E-04
GO:0000389	mRNA 3'-splice site recognition	3	2/50E-04

	GO:0035019	somatic stem cell population maintenance	6	2/54E-04
	GO:0006289	nucleotide-excision repair	7	3/05E-04
	GO:0048026	positive regulation of mRNA splicing, via spliceosome	4	3/49E-04
	GO:0006283	transcription-coupled nucleotide-excision repair	6	3/70E-04
	GO:0001054	RNA polymerase I activity	3	1/02E-03
	GO:0031442	positive regulation of mRNA 3'-end processing	3	1/02E-03
	GO:0001056	RNA polymerase III activity	3	2/28E-03
	GO:0006388	tRNA splicing, via endonucleolytic cleavage and ligation	3	2/59E-03
	GO:0000394	RNA splicing, via endonucleolytic cleavage and ligation	3	2/91E-03
	GO:0000387	spliceosomal snRNP assembly	4	3/12E-03
	GO:1900363	regulation of mRNA polyadenylation	3	4/09E-03
	GO:0019081	viral translation	3	4/41E-03
	GO:0070935	3'-UTR-mediated mRNA stabilization	3	6/00E-03
	GO:0016538	cyclin-dependent protein serine/threonine kinase regulator activity	3	7/05E-03
	GO:0006383	transcription by RNA polymerase III	4	7/50E-03
	GO:0006361	transcription initiation from RNA polymerase I promoter	3	1/21E-02
	GO:0045815	positive regulation of gene expression, epigenetic	4	1/24E-02
	GO:0045616	regulation of keratinocyte differentiation	3	1/25E-02
	GO:0046824	positive regulation of nucleocytoplasmic transport	4	1/32E-02
	GO:0006362	transcription elongation from RNA polymerase I promoter	3	1/32E-02
	GO:0032786	positive regulation of DNA-templated transcription, elongation	3	1/37E-02
	GO:0032481	positive regulation of type I interferon production	4	1/38E-02
	GO:0006363	termination of RNA polymerase I transcription	3	1/39E-02
	GO:0006446	regulation of translational initiation	4	1/49E-02
	GO:0043616	keratinocyte proliferation	3	1/80E-02
	GO:0061014	positive regulation of mRNA catabolic process	3	1/80E-02
	GO:0010837	regulation of keratinocyte proliferation	3	1/89E-02
	GO:0032784	regulation of DNA-templated transcription, elongation	3	2/20E-02
	GO:0000278	mitotic cell cycle	59	3/39E-34
	GO:1903047	mitotic cell cycle process	55	3/69E-33
	GO:0010608	posttranscriptional regulation of gene expression	49	6/96E-33
	GO:0031145	anaphase-promoting complex-dependent catabolic process	26	4/70E-32
	GO:1901990	regulation of mitotic cell cycle phase transition	38	4/82E-26
	GO:0007346	regulation of mitotic cell cycle	44	1/23E-25
	GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	22	1/93E-25
4	GO:1901987	regulation of cell cycle phase transition	38	6/40E-25
	GO:0070498	interleukin-1-mediated signaling pathway	22	8/90E-24
	GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	21	3/51E-23
	GO:0044772	mitotic cell cycle phase transition	39	4/36E-23
	GO:0045930	negative regulation of mitotic cell cycle	32	1/48E-22
	GO:1902750	negative regulation of cell cycle G2/M phase transition	22	3/67E-22
	GO:1901988	negative regulation of cell cycle phase transition	29	5/00E-22
	GO:0044770	cell cycle phase transition	39	5/44E-22

GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	21	6/21E-22
GO:1901991	negative regulation of mitotic cell cycle phase transition	28	1/25E-21
GO:1902749	regulation of cell cycle G2/M phase transition	27	1/43E-21
GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	22	2/69E-21
GO:0006521	regulation of cellular amino acid metabolic process	18	3/49E-21
GO:0010389	regulation of G2/M transition of mitotic cell cycle	26	4/07E-21
GO:0043620	regulation of DNA-templated transcription in response to stress	22	9/61E-21
GO:0010948	negative regulation of cell cycle process	31	7/53E-20
GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	18	1/09E-19
GO:1902036	regulation of hematopoietic stem cell differentiation	18	1/09E-19
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	19	1/48E-19
GO:0034655	nucleobase-containing compound catabolic process	37	1/68E-19
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	18	2/43E-19
GO:0002223	stimulatory C-type lectin receptor signaling pathway	20	4/40E-19
GO:0044839	cell cycle G2/M phase transition	27	5/35E-19
GO:0071347	cellular response to interleukin-1	23	5/62E-19
GO:0002220	innate immune response activating cell surface receptor signaling pathway	20	6/69E-19
GO:0043488	regulation of mRNA stability	23	9/23E-19
GO:0033238	regulation of cellular amine metabolic process	18	1/09E-18
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	30	1/10E-18
GO:0061013	regulation of mRNA catabolic process	24	1/11E-18
GO:0071456	cellular response to hypoxia	24	1/11E-18
GO:0000086	G2/M transition of mitotic cell cycle	26	1/69E-18
GO:0043487	regulation of RNA stability	23	1/80E-18
GO:0060218	hematopoietic stem cell differentiation	18	2/17E-18
GO:1901532	regulation of hematopoietic progenitor cell differentiation	18	2/17E-18
GO:0046700	heterocycle catabolic process	37	2/73E-18
GO:0044270	cellular nitrogen compound catabolic process	37	2/83E-18
GO:0016579	protein deubiquitination	26	3/44E-18
GO:0036294	cellular response to decreased oxygen levels	24	6/05E-18
GO:0019439	aromatic compound catabolic process	37	6/39E-18
GO:0038061	NIK/NF-kappaB signaling	22	9/34E-18
GO:0003743	translation initiation factor activity	15	1/47E-17
GO:0070646	protein modification by small protein removal	26	1/56E-17
GO:0070555	response to interleukin-1	23	1/69E-17
GO:0006511	ubiquitin-dependent protein catabolic process	33	5/43E-17
GO:0071453	cellular response to oxygen levels	24	5/72E-17
GO:0045786	negative regulation of cell cycle	35	6/11E-17
GO:0019941	modification-dependent protein catabolic process	33	7/46E-17
GO:0002478	antigen processing and presentation of exogenous peptide antigen	21	7/79E-17
GO:0010498	proteasomal protein catabolic process	30	8/17E-17
GO:0001736	establishment of planar polarity	19	9/27E-17

GO:0007164	establishment of tissue polarity	19	9/27E-17
GO:0035567	non-canonical Wnt signaling pathway	20	9/46E-17
GO:0043632	modification-dependent macromolecule catabolic process	33	1/19E-16
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	18	1/28E-16
GO:0019884	antigen processing and presentation of exogenous antigen	21	1/48E-16
GO:0090175	regulation of establishment of planar polarity	18	1/66E-16
GO:0090263	positive regulation of canonical Wnt signaling pathway	19	2/08E-16
GO:0048002	antigen processing and presentation of peptide antigen	21	3/35E-16
GO:2000736	regulation of stem cell differentiation	18	4/62E-16
GO:0001738	morphogenesis of a polarized epithelium	19	5/64E-16
GO:0062012	regulation of small molecule metabolic process	29	1/06E-15
GO:0001666	response to hypoxia	26	2/73E-15
GO:0090090	negative regulation of canonical Wnt signaling pathway	20	2/76E-15
GO:0006402	mRNA catabolic process	26	2/99E-15
GO:0033209	tumor necrosis factor-mediated signaling pathway	20	3/01E-15
GO:1903311	regulation of mRNA metabolic process	25	4/84E-15
GO:0044106	cellular amine metabolic process	18	5/18E-15
GO:0036293	response to decreased oxygen levels	26	6/11E-15
GO:0038095	Fc-epsilon receptor signaling pathway	19	1/31E-14
GO:0034508	centromere complex assembly	13	1/32E-14
GO:0010565	regulation of cellular ketone metabolic process	20	1/34E-14
GO:0002183	cytoplasmic translational initiation	12	1/36E-14
GO:0009308	amine metabolic process	18	1/76E-14
GO:0030177	positive regulation of Wnt signaling pathway	19	1/84E-14
GO:0006401	RNA catabolic process	26	1/86E-14
GO:0140014	mitotic nuclear division	23	3/31E-14
GO:1905330	regulation of morphogenesis of an epithelium	19	3/63E-14
GO:0070482	response to oxygen levels	26	3/73E-14
GO:0030178	negative regulation of Wnt signaling pathway	20	4/20E-14
GO:0002758	innate immune response-activating signal transduction	23	9/59E-14
GO:0038093	Fc receptor signaling pathway	21	1/02E-13
GO:0008135	translation factor activity, RNA binding	15	1/08E-13
GO:0090079	translation regulator activity, nucleic acid binding	16	1/74E-13
GO:0016055	Wnt signaling pathway	27	3/02E-13
GO:0198738	cell-cell signaling by wnt	27	3/38E-13
GO:0050852	T cell receptor signaling pathway	20	3/46E-13
GO:0002244	hematopoietic progenitor cell differentiation	18	4/30E-13
GO:0002218	activation of innate immune response	23	6/17E-13
GO:0000280	nuclear division	25	1/22E-12
GO:0034080	CENP-A containing nucleosome assembly	11	1/65E-12
GO:0061641	CENP-A containing chromatin organization	11	1/65E-12
GO:2000027	regulation of animal organ morphogenesis	20	2/01E-12
GO:0031055	chromatin remodeling at centromere	11	2/67E-12

GO:0043687	post-translational protein modification	23	3/09E-12
GO:0042180	cellular ketone metabolic process	20	3/19E-12
GO:0060828	regulation of canonical Wnt signaling pathway	20	6/71E-12
GO:0098813	nuclear chromosome segregation	20	7/06E-12
GO:0071356	cellular response to tumor necrosis factor	21	8/02E-12
GO:0045182	translation regulator activity	16	8/22E-12
GO:0048285	organelle fission	25	8/90E-12
GO:0001732	formation of cytoplasmic translation initiation complex	8	9/43E-12
GO:0045089	positive regulation of innate immune response	23	1/64E-11
GO:0006336	DNA replication-independent nucleosome assembly	11	2/67E-11
GO:0000070	mitotic sister chromatid segregation	16	2/75E-11
GO:0034724	DNA replication-independent nucleosome organization	11	3/19E-11
GO:0006413	translational initiation	17	3/41E-11
GO:0060964	regulation of gene silencing by miRNA	14	3/46E-11
GO:0034612	response to tumor necrosis factor	21	3/78E-11
GO:0048863	stem cell differentiation	19	3/99E-11
GO:0060147	regulation of posttranscriptional gene silencing	14	4/62E-11
GO:0060966	regulation of gene silencing by RNA	14	4/62E-11
GO:0030111	regulation of Wnt signaling pathway	21	8/05E-11
GO:0075733	intracellular transport of virus	11	8/96E-11
GO:0043486	histone exchange	11	1/05E-10
GO:0060070	canonical Wnt signaling pathway	20	1/09E-10
GO:0035195	gene silencing by miRNA	15	1/48E-10
GO:0046794	transport of virus	11	1/69E-10
GO:0043044	ATP-dependent chromatin remodeling	12	2/60E-10
GO:0035194	posttranscriptional gene silencing by RNA	15	3/64E-10
GO:0016441	posttranscriptional gene silencing	15	3/90E-10
GO:0050851	antigen receptor-mediated signaling pathway	20	5/30E-10
GO:0000819	sister chromatid segregation	16	6/63E-10
GO:0065004	protein-DNA complex assembly	17	8/43E-10
GO:0006409	tRNA export from nucleus	9	9/99E-10
GO:0071431	tRNA-containing ribonucleoprotein complex export from nucleus	9	9/99E-10
GO:0051383	kinetochore organization	8	1/00E-09
GO:0051031	tRNA transport	9	1/54E-09
GO:0044766	multi-organism transport	11	1/99E-09
GO:0050000	chromosome localization	11	1/99E-09
GO:0060968	regulation of gene silencing	14	2/28E-09
GO:0031047	gene silencing by RNA	15	2/64E-09
GO:0097064	ncRNA export from nucleus	9	4/14E-09
GO:0002181	cytoplasmic translation	12	5/27E-09
GO:0071824	protein-DNA complex subunit organization	17	8/81E-09
GO:0071426	ribonucleoprotein complex export from nucleus	13	1/56E-08
GO:0071166	ribonucleoprotein complex localization	13	1/66E-08

GO:0004298	threonine-type endopeptidase activity	7	2/42E-08
GO:0070003	threonine-type peptidase activity	7	2/42E-08
GO:0006405	RNA export from nucleus	13	2/66E-08
GO:0008608	attachment of spindle microtubules to kinetochore	8	3/24E-08
GO:0051303	establishment of chromosome localization	10	3/43E-08
GO:0006406	mRNA export from nucleus	12	4/06E-08
GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	12	4/06E-08
GO:0050657	nucleic acid transport	15	4/49E-08
GO:0050658	RNA transport	15	4/49E-08
GO:0051310	metaphase plate congression	9	5/22E-08
GO:0010499	proteasomal ubiquitin-independent protein catabolic process	7	5/58E-08
GO:0051236	establishment of RNA localization	15	6/83E-08
GO:0015931	nucleobase-containing compound transport	16	7/26E-08
GO:0006611	protein export from nucleus	14	7/96E-08
GO:0019080	viral gene expression	14	1/03E-07
GO:0006338	chromatin remodeling	13	1/19E-07
GO:0006110	regulation of glycolytic process	10	1/27E-07
GO:0030811	regulation of nucleotide catabolic process	10	1/39E-07
GO:0051168	nuclear export	14	1/93E-07
GO:0022618	ribonucleoprotein complex assembly	15	2/31E-07
GO:0051028	mRNA transport	13	2/68E-07
GO:0043470	regulation of carbohydrate catabolic process	10	2/85E-07
GO:1900034	regulation of cellular response to heat	10	3/09E-07
GO:0006096	glycolytic process	11	3/67E-07
GO:0051382	kinetochore assembly	6	3/89E-07
GO:0006757	ATP generation from ADP	11	3/92E-07
GO:0071826	ribonucleoprotein complex subunit organization	15	3/95E-07
GO:0006403	RNA localization	15	5/42E-07
GO:2001169	regulation of ATP biosynthetic process	10	5/78E-07
GO:0016458	gene silencing	15	5/82E-07
GO:0042866	pyruvate biosynthetic process	11	6/06E-07
GO:0051196	regulation of coenzyme metabolic process	10	6/17E-07
GO:0046031	ADP metabolic process	11	7/78E-07
GO:0006334	nucleosome assembly	11	8/79E-07
GO:1902416	positive regulation of mRNA binding	5	1/45E-06
GO:0006165	nucleoside diphosphate phosphorylation	11	1/62E-06
GO:0009135	purine nucleoside diphosphate metabolic process	11	1/81E-06
GO:0009179	purine ribonucleoside diphosphate metabolic process	11	1/81E-06
GO:0046939	nucleotide phosphorylation	11	1/81E-06
GO:0051983	regulation of chromosome segregation	10	1/84E-06
GO:0009185	ribonucleoside diphosphate metabolic process	11	2/00E-06
GO:0016925	protein sumoylation	9	2/10E-06
GO:1905216	positive regulation of RNA binding	5	2/13E-06

GO:0034605	cellular response to heat	11	2/60E-06
GO:0031497	chromatin assembly	11	3/06E-06
GO:1902415	regulation of mRNA binding	5	3/09E-06
GO:0051783	regulation of nuclear division	13	3/76E-06
GO:1900371	regulation of purine nucleotide biosynthetic process	10	3/86E-06
GO:0030808	regulation of nucleotide biosynthetic process	10	4/08E-06
GO:0006999	nuclear pore organization	5	4/31E-06
GO:0010965	regulation of mitotic sister chromatid separation	8	4/60E-06
GO:0051193	regulation of cofactor metabolic process	10	4/80E-06
GO:0009408	response to heat	12	4/91E-06
GO:0006754	ATP biosynthetic process	11	5/33E-06
GO:0019359	nicotinamide nucleotide biosynthetic process	11	5/33E-06
GO:0019363	pyridine nucleotide biosynthetic process	11	5/33E-06
GO:0043467	regulation of generation of precursor metabolites and energy	11	5/33E-06
GO:1903578	regulation of ATP metabolic process	10	5/33E-06
GO:1905214	regulation of RNA binding	5	5/73E-06
GO:0009132	nucleoside diphosphate metabolic process	11	5/79E-06
GO:0051306	mitotic sister chromatid separation	8	6/93E-06
GO:0007088	regulation of mitotic nuclear division	12	7/22E-06
GO:1905818	regulation of chromosome separation	8	7/45E-06
GO:0072525	pyridine-containing compound biosynthetic process	11	7/53E-06
GO:0006446	regulation of translational initiation	8	8/64E-06
GO:0034728	nucleosome organization	11	8/65E-06
GO:0071459	protein localization to chromosome, centromeric region	6	9/25E-06
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	11	9/58E-06
GO:0035278	miRNA mediated inhibition of translation	5	9/68E-06
GO:0040033	negative regulation of translation, ncRNA-mediated	5	9/68E-06
GO:0045974	regulation of translation, ncRNA-mediated	5	9/68E-06
GO:0009145	purine nucleoside triphosphate biosynthetic process	11	9/94E-06
GO:0006333	chromatin assembly or disassembly	11	1/03E-05
GO:0006090	pyruvate metabolic process	11	1/12E-05
GO:0009201	ribonucleoside triphosphate biosynthetic process	11	1/40E-05
GO:0033047	regulation of mitotic sister chromatid segregation	8	1/56E-05
GO:0007093	mitotic cell cycle checkpoint	11	1/87E-05
GO:0019083	viral transcription	11	1/94E-05
GO:1900542	regulation of purine nucleotide metabolic process	10	1/97E-05
GO:0009166	nucleotide catabolic process	11	2/15E-05
GO:0006140	regulation of nucleotide metabolic process	10	3/02E-05
GO:0009142	nucleoside triphosphate biosynthetic process	11	3/08E-05
GO:1901292	nucleoside phosphate catabolic process	11	3/08E-05
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	7	3/61E-05
GO:0006323	DNA packaging	11	4/16E-05
GO:0016052	carbohydrate catabolic process	11	4/16E-05

GO:0044784	metaphase/anaphase transition of cell cycle	7	4/56E-05
GO:0033045	regulation of sister chromatid segregation	8	4/59E-05
GO:0007080	mitotic metaphase plate congression	6	6/34E-05
GO:0019362	pyridine nucleotide metabolic process	11	6/45E-05
GO:0046496	nicotinamide nucleotide metabolic process	11	6/45E-05
GO:1902850	microtubule cytoskeleton organization involved in mitosis	9	6/47E-05
GO:0051304	chromosome separation	8	7/05E-05
GO:1905616	regulation of miRNA mediated inhibition of translation	3	7/06E-05
GO:1905618	positive regulation of miRNA mediated inhibition of translation	3	7/06E-05
GO:0006109	regulation of carbohydrate metabolic process	11	7/12E-05
GO:0034501	protein localization to kinetochore	5	9/76E-05
GO:0072524	pyridine-containing compound metabolic process	11	9/82E-05
GO:0017056	structural constituent of nuclear pore	5	1/13E-04
GO:2000816	negative regulation of mitotic sister chromatid separation	6	1/20E-04
GO:1905819	negative regulation of chromosome separation	6	1/45E-04
GO:0002191	cap-dependent translational initiation	3	1/58E-04
GO:0097010	eukaryotic translation initiation factor 4F complex assembly	3	1/58E-04
GO:0051315	attachment of mitotic spindle microtubules to kinetochore	4	2/18E-04
GO:0033048	negative regulation of mitotic sister chromatid segregation	6	2/43E-04
GO:0030071	regulation of mitotic metaphase/anaphase transition	6	3/67E-04
GO:0033046	negative regulation of sister chromatid segregation	6	3/67E-04
GO:0051985	negative regulation of chromosome segregation	6	4/25E-04
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	6	4/52E-04
GO:0045931	positive regulation of mitotic cell cycle	9	5/48E-04
GO:0045839	negative regulation of mitotic nuclear division	6	5/49E-04
GO:0007094	mitotic spindle assembly checkpoint	5	8/02E-04
GO:0031577	spindle checkpoint	5	8/02E-04
GO:0071173	spindle assembly checkpoint	5	8/02E-04
GO:0071174	mitotic spindle checkpoint	5	8/02E-04
GO:0034502	protein localization to chromosome	7	8/14E-04
GO:0017148	negative regulation of translation	8	9/26E-04
GO:0051651	maintenance of location in cell	7	9/94E-04
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	5	1/02E-03
GO:1902100	negative regulation of metaphase/anaphase transition of cell cycle	5	1/20E-03
GO:0051292	nuclear pore complex assembly	3	1/43E-03
GO:0000132	establishment of mitotic spindle orientation	4	1/55E-03
GO:0051784	negative regulation of nuclear division	6	1/57E-03
GO:0032507	maintenance of protein location in cell	6	1/79E-03
GO:0031109	microtubule polymerization or depolymerization	7	1/99E-03
GO:0040001	establishment of mitotic spindle localization	4	3/87E-03
GO:0006997	nucleus organization	7	3/94E-03
GO:0051294	establishment of spindle orientation	4	4/11E-03
GO:0046931	pore complex assembly	3	5/41E-03

GO:0007052	mitotic spindle organization	6	7/13E-03
GO:0043248	proteasome assembly	3	8/78E-03
GO:0075522	IRES-dependent viral translational initiation	3	8/78E-03
GO:0007044	cell-substrate junction assembly	6	9/13E-03
GO:0007229	integrin-mediated signaling pathway	6	9/13E-03
GO:1900087	positive regulation of G1/S transition of mitotic cell cycle	4	9/30E-03
GO:0051293	establishment of spindle localization	4	9/53E-03
GO:0045185	maintenance of protein location	6	1/09E-02
GO:0099518	vesicle cytoskeletal trafficking	3	1/15E-02
GO:0099170	postsynaptic modulation of chemical synaptic transmission	3	1/19E-02
GO:0045727	positive regulation of translation	6	1/23E-02
GO:0007019	microtubule depolymerization	4	1/23E-02
GO:0072595	maintenance of protein localization in organelle	4	1/23E-02
GO:0019081	viral translation	3	1/24E-02
GO:0051653	spindle localization	4	1/37E-02
GO:0000717	nucleotide-excision repair, DNA duplex unwinding	3	1/44E-02
GO:0045947	negative regulation of translational initiation	3	1/50E-02
GO:1902808	positive regulation of cell cycle G1/S phase transition	4	1/54E-02
GO:0090630	activation of GTPase activity	5	1/57E-02
GO:1901992	positive regulation of mitotic cell cycle phase transition	5	1/57E-02
GO:0000715	nucleotide-excision repair, DNA damage recognition	3	1/72E-02
GO:0034629	cellular protein-containing complex localization	3	1/83E-02
GO:0070911	global genome nucleotide-excision repair	3	1/83E-02
GO:0031529	ruffle organization	3	2/14E-02
GO:2000637	positive regulation of gene silencing by miRNA	3	2/56E-02
GO:0060148	positive regulation of posttranscriptional gene silencing	3	2/66E-02
GO:0031050	dsRNA processing	3	2/74E-02
GO:0070918	production of small RNA involved in gene silencing by RNA	3	2/74E-02
GO:0035196	production of miRNAs involved in gene silencing by miRNA	3	2/95E-02
GO:1900027	regulation of ruffle assembly	3	2/99E-02
GO:0006294	nucleotide-excision repair, preincision complex assembly	3	3/07E-02
GO:0045737	positive regulation of cyclin-dependent protein serine/threonine kinase activity	3	3/13E-02
GO:0051642	centrosome localization	3	3/13E-02
GO:0071549	cellular response to dexamethasone stimulus	3	3/18E-02
GO:0006296	nucleotide-excision repair, DNA incision, 5'-to lesion	3	3/30E-02
GO:0097178	ruffle assembly	3	3/34E-02
GO:1900024	regulation of substrate adhesion-dependent cell spreading	3	3/37E-02
GO:1904031	positive regulation of cyclin-dependent protein kinase activity	3	3/37E-02
GO:0044783	G1 DNA damage checkpoint	4	3/63E-02
GO:0042769	DNA damage response, detection of DNA damage	3	3/64E-02
GO:0097421	liver regeneration	3	3/69E-02
GO:0071548	response to dexamethasone	3	3/70E-02
GO:0031571	mitotic G1 DNA damage checkpoint	4	3/76E-02

	GO:0044819	mitotic G1/S transition checkpoint	4	3/76E-02
	GO:0016504	peptidase activator activity	3	3/81E-02
	GO:0021955	central nervous system neuron axonogenesis	3	3/81E-02
	GO:0033683	nucleotide-excision repair, DNA incision	3	3/82E-02
	GO:0010389	regulation of G2/M transition of mitotic cell cycle	52	1/00E-59
	GO:0097711	ciliary basal body-plasma membrane docking	43	1/77E-59
	GO:1902749	regulation of cell cycle G2/M phase transition	52	6/82E-58
	GO:0000086	G2/M transition of mitotic cell cycle	52	5/38E-54
	GO:1901990	regulation of mitotic cell cycle phase transition	60	2/30E-53
	GO:0044839	cell cycle G2/M phase transition	52	1/63E-52
	GO:1901987	regulation of cell cycle phase transition	60	1/71E-51
	GO:0044772	mitotic cell cycle phase transition	62	2/39E-49
	GO:0140056	organelle localization by membrane tethering	43	3/71E-49
	GO:0000278	mitotic cell cycle	73	1/51E-47
	GO:0044770	cell cycle phase transition	62	1/68E-47
	GO:1903047	mitotic cell cycle process	68	9/10E-46
	GO:0007346	regulation of mitotic cell cycle	61	1/90E-43
	GO:0022402	cell cycle process	75	4/40E-41
	GO:0010564	regulation of cell cycle process	62	4/40E-40
	GO:0060271	cilium assembly	45	1/20E-37
	GO:0044782	cilium organization	45	5/86E-37
	GO:0120031	plasma membrane bounded cell projection assembly	50	2/75E-35
	GO:0030031	cell projection assembly	50	7/27E-35
5	GO:0051726	regulation of cell cycle	66	5/74E-34
	GO:0070925	organelle assembly	55	2/26E-32
	GO:0051640	organelle localization	51	1/38E-31
	GO:0000226	microtubule cytoskeleton organization	46	7/02E-31
	GO:0031023	microtubule organizing center organization	23	1/34E-19
	GO:0007098	centrosome cycle	20	2/80E-16
	GO:0007051	spindle organization	20	5/37E-15
	GO:0007020	microtubule nucleation	11	6/41E-13
	GO:0031109	microtubule polymerization or depolymerization	16	1/14E-12
	GO:0007099	centriole replication	11	3/36E-11
	GO:0046785	microtubule polymerization	13	4/20E-11
	GO:0070507	regulation of microtubule cytoskeleton organization	18	4/45E-11
	GO:0098534	centriole assembly	11	6/03E-11
	GO:1902850	microtubule cytoskeleton organization involved in mitosis	15	7/43E-11
	GO:0051298	centrosome duplication	13	1/00E-10
	GO:0032886	regulation of microtubule-based process	18	4/56E-10
	GO:0002478	antigen processing and presentation of exogenous peptide antigen	15	5/29E-09
	GO:0031589	cell-substrate adhesion	20	6/05E-09
	GO:0019884	antigen processing and presentation of exogenous antigen	15	8/24E-09
	GO:0048002	antigen processing and presentation of peptide antigen	15	1/44E-08

GO:0007052	mitotic spindle organization	12	1/89E-08
GO:0140014	mitotic nuclear division	18	2/15E-08
GO:0051225	spindle assembly	12	2/45E-08
GO:0007160	cell-matrix adhesion	16	4/62E-08
GO:0000070	mitotic sister chromatid segregation	13	2/33E-07
GO:0000819	sister chromatid segregation	14	3/22E-07
GO:0031122	cytoplasmic microtubule organization	9	3/33E-07
GO:0031145	anaphase-promoting complex-dependent catabolic process	10	6/46E-07
GO:1905508	protein localization to microtubule organizing center	7	9/61E-07
GO:0007369	gastrulation	13	1/01E-06
GO:0051418	microtubule nucleation by microtubule organizing center	5	1/82E-06
GO:0098813	nuclear chromosome segregation	15	2/28E-06
GO:0044380	protein localization to cytoskeleton	8	4/74E-06
GO:0051258	protein polymerization	15	5/61E-06
GO:0051983	regulation of chromosome segregation	10	5/84E-06
GO:0001618	virus receptor activity	9	7/36E-06
GO:0051321	meiotic cell cycle	14	8/45E-06
GO:0034453	microtubule anchoring	6	9/87E-06
GO:0051306	mitotic sister chromatid separation	8	2/12E-05
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	9	2/48E-05
GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	9	3/26E-05
GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	9	3/97E-05
GO:0003743	translation initiation factor activity	7	4/48E-05
GO:0072698	protein localization to microtubule cytoskeleton	7	4/48E-05
GO:0051415	microtubule nucleation by interphase microtubule organizing center	4	6/46E-05
GO:0007229	integrin-mediated signaling pathway	9	7/39E-05
GO:0032388	positive regulation of intracellular transport	12	8/41E-05
GO:0002183	cytoplasmic translational initiation	6	9/42E-05
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	7	1/18E-04
GO:0044784	metaphase/anaphase transition of cell cycle	7	1/54E-04
GO:0051293	establishment of spindle localization	6	1/54E-04
GO:0010965	regulation of mitotic sister chromatid separation	7	1/96E-04
GO:0051017	actin filament bundle assembly	10	2/08E-04
GO:0061572	actin filament bundle organization	10	2/36E-04
GO:0090316	positive regulation of intracellular protein transport	10	2/45E-04
GO:0046718	viral entry into host cell	9	2/51E-04
GO:0051304	chromosome separation	8	2/64E-04
GO:1905818	regulation of chromosome separation	7	3/05E-04
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	8	3/32E-04
GO:0051653	spindle localization	6	3/55E-04
GO:0097742	de novo centriole assembly	3	4/01E-04
GO:0098535	de novo centriole assembly involved in multi-ciliated epithelial cell differentiation	3	4/01E-04

GO:0098639	collagen binding involved in cell-matrix adhesion	3	4/01E-04
GO:0046605	regulation of centrosome cycle	7	4/99E-04
GO:0030260	entry into host cell	9	5/42E-04
GO:0044409	entry into host	9	5/42E-04
GO:0051806	entry into cell of other organism involved in symbiotic interaction	9	5/42E-04
GO:0051828	entry into other organism involved in symbiotic interaction	9	5/42E-04
GO:0051494	negative regulation of cytoskeleton organization	9	5/62E-04
GO:0033047	regulation of mitotic sister chromatid segregation	7	6/02E-04
GO:0007044	cell-substrate junction assembly	8	6/58E-04
GO:0040001	establishment of mitotic spindle localization	5	6/62E-04
GO:0051294	establishment of spindle orientation	5	7/51E-04
GO:0001704	formation of primary germ layer	8	7/51E-04
GO:0031110	regulation of microtubule polymerization or depolymerization	7	7/54E-04
GO:0051310	metaphase plate congression	6	7/66E-04
GO:1902750	negative regulation of cell cycle G2/M phase transition	8	8/11E-04
GO:0046599	regulation of centriole replication	5	8/17E-04
GO:0010457	centriole-centriole cohesion	4	8/79E-04
GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	7	8/83E-04
GO:0031032	actomyosin structure organization	10	1/10E-03
GO:0030071	regulation of mitotic metaphase/anaphase transition	6	1/11E-03
GO:0098634	cell-matrix adhesion mediator activity	3	1/19E-03
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	6	1/38E-03
GO:0033045	regulation of sister chromatid segregation	7	1/44E-03
GO:0008135	translation factor activity, RNA binding	7	1/51E-03
GO:0010824	regulation of centrosome duplication	6	1/56E-03
GO:0030010	establishment of cell polarity	8	1/74E-03
GO:0007045	cell-substrate adherens junction assembly	7	1/84E-03
GO:0048041	focal adhesion assembly	7	1/84E-03
GO:1903251	multi-ciliated epithelial cell differentiation	3	2/62E-03
GO:0007080	mitotic metaphase plate congression	5	2/73E-03
GO:0033627	cell adhesion mediated by integrin	6	2/81E-03
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	5	2/94E-03
GO:0034333	adherens junction assembly	7	2/96E-03
GO:0051303	establishment of chromosome localization	6	3/31E-03
GO:0030038	contractile actin filament bundle assembly	7	3/37E-03
GO:0032231	regulation of actin filament bundle assembly	7	3/37E-03
GO:0043149	stress fiber assembly	7	3/37E-03
GO:0007019	microtubule depolymerization	5	3/38E-03
GO:1902100	negative regulation of metaphase/anaphase transition of cell cycle	5	3/38E-03
GO:0051261	protein depolymerization	7	3/45E-03
GO:0050000	chromosome localization	6	3/59E-03
GO:0000132	establishment of mitotic spindle orientation	4	4/11E-03

GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	6	4/22E-03
GO:2000816	negative regulation of mitotic sister chromatid separation	5	4/51E-03
GO:0031113	regulation of microtubule polymerization	5	5/18E-03
GO:1905819	negative regulation of chromosome separation	5	5/18E-03
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	6	5/21E-03
GO:0090079	translation regulator activity, nucleic acid binding	7	5/53E-03
GO:0034454	microtubule anchoring at centrosome	3	5/59E-03
GO:0033048	negative regulation of mitotic sister chromatid segregation	5	7/88E-03
GO:0031116	positive regulation of microtubule polymerization	4	7/92E-03
GO:0051497	negative regulation of stress fiber assembly	4	7/92E-03
GO:0072393	microtubule anchoring at microtubule organizing center	3	8/57E-03
GO:0048333	mesodermal cell differentiation	4	8/63E-03
GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	7	8/71E-03
GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	6	8/84E-03
GO:0090307	mitotic spindle assembly	5	8/98E-03
GO:0001736	establishment of planar polarity	7	9/51E-03
GO:0007164	establishment of tissue polarity	7	9/51E-03
GO:1902904	negative regulation of supramolecular fiber organization	7	9/51E-03
GO:0033046	negative regulation of sister chromatid segregation	5	9/84E-03
GO:0032232	negative regulation of actin filament bundle assembly	4	9/96E-03
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	6	1/05E-02
GO:0051492	regulation of stress fiber assembly	6	1/05E-02
GO:0051985	negative regulation of chromosome segregation	5	1/07E-02
GO:0043620	regulation of DNA-templated transcription in response to stress	7	1/09E-02
GO:0031112	positive regulation of microtubule polymerization or depolymerization	4	1/13E-02
GO:0070498	interleukin-1-mediated signaling pathway	6	1/30E-02
GO:0001732	formation of cytoplasmic translation initiation complex	3	1/31E-02
GO:0051315	attachment of mitotic spindle microtubules to kinetochore	3	1/31E-02
GO:0008608	attachment of spindle microtubules to kinetochore	4	1/33E-02
GO:0006521	regulation of cellular amino acid metabolic process	5	1/33E-02
GO:0045839	negative regulation of mitotic nuclear division	5	1/34E-02
GO:0001738	morphogenesis of a polarized epithelium	7	1/42E-02
GO:0110020	regulation of actomyosin structure organization	6	1/54E-02
GO:0044319	wound healing, spreading of cells	4	1/57E-02
GO:0090505	epiboly involved in wound healing	4	1/57E-02
GO:0090504	epiboly	4	1/61E-02
GO:1903078	positive regulation of protein localization to plasma membrane	3	1/61E-02
GO:0002181	cytoplasmic translation	6	1/62E-02
GO:0035313	wound healing, spreading of epidermal cells	3	1/64E-02
GO:0031111	negative regulation of microtubule polymerization or depolymerization	4	1/72E-02
GO:0007094	mitotic spindle assembly checkpoint	4	1/98E-02
GO:0031577	spindle checkpoint	4	1/98E-02

GO:0071173	spindle assembly checkpoint	4	1/98E-02
GO:0071174	mitotic spindle checkpoint	4	1/98E-02
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	6	2/03E-02
GO:0090175	regulation of establishment of planar polarity	6	2/15E-02
GO:0035987	endodermal cell differentiation	4	2/17E-02
GO:0040019	positive regulation of embryonic development	4	2/17E-02
GO:1902036	regulation of hematopoietic stem cell differentiation	5	2/38E-02
GO:0071711	basement membrane organization	3	2/43E-02
GO:0002223	stimulatory C-type lectin receptor signaling pathway	6	2/43E-02
GO:0051784	negative regulation of nuclear division	5	2/46E-02
GO:0002220	innate immune response activating cell surface receptor signaling pathway	6	2/53E-02
GO:0030397	membrane disassembly	3	2/58E-02
GO:0031269	pseudopodium assembly	3	2/58E-02
GO:0051081	nuclear envelope disassembly	3	2/58E-02
GO:0000717	nucleotide-excision repair, DNA duplex unwinding	3	2/77E-02
GO:0031268	pseudopodium organization	3	2/77E-02
GO:0001706	endoderm formation	4	2/83E-02
GO:0051898	negative regulation of protein kinase B signaling	3	3/00E-02
GO:1901879	regulation of protein depolymerization	5	3/14E-02
GO:0033238	regulation of cellular amine metabolic process	5	3/33E-02
GO:1901992	positive regulation of mitotic cell cycle phase transition	5	3/58E-02
GO:0042073	intraciliary transport	3	3/58E-02
GO:0000715	nucleotide-excision repair, DNA damage recognition	3	3/59E-02
GO:0060218	hematopoietic stem cell differentiation	5	3/62E-02
GO:1901532	regulation of hematopoietic progenitor cell differentiation	5	3/62E-02
GO:0070911	global genome nucleotide-excision repair	3	3/65E-02
GO:0051445	regulation of meiotic cell cycle	4	3/71E-02
GO:0006998	nuclear envelope organization	4	4/03E-02
GO:0007026	negative regulation of microtubule depolymerization	3	4/04E-02
GO:1902117	positive regulation of organelle assembly	5	4/23E-02
GO:0002011	morphogenesis of an epithelial sheet	4	4/28E-02
GO:0010677	negative regulation of cellular carbohydrate metabolic process	4	4/28E-02
GO:0010712	regulation of collagen metabolic process	3	4/41E-02
GO:0015459	potassium channel regulator activity	3	4/41E-02
GO:0010470	regulation of gastrulation	3	4/47E-02
GO:1901016	regulation of potassium ion transmembrane transporter activity	3	4/58E-02
GO:0048332	mesoderm morphogenesis	4	4/59E-02
GO:1901381	positive regulation of potassium ion transmembrane transport	3	4/63E-02
GO:0007212	dopamine receptor signaling pathway	3	4/79E-02
GO:0045724	positive regulation of cilium assembly	3	4/79E-02
GO:0033137	negative regulation of peptidyl-serine phosphorylation	3	4/82E-02
GO:1902751	positive regulation of cell cycle G2/M phase transition	3	4/82E-02
GO:0043268	positive regulation of potassium ion transport	3	4/86E-02

	GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	93	3/41E-108
	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	93	1/70E-81
	GO:0098609	cell-cell adhesion	121	3/42E-59
	GO:0016339	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	34	1/13E-42
	GO:0044331	cell-cell adhesion mediated by cadherin	21	6/45E-21
	GO:0007043	cell-cell junction assembly	25	1/94E-13
	GO:0070125	mitochondrial translational elongation	19	1/18E-11
	GO:0070126	mitochondrial translational termination	19	1/44E-11
	GO:0045216	cell-cell junction organization	25	1/51E-10
	GO:0006415	translational termination	19	3/62E-10
	GO:0034332	adherens junction organization	23	1/32E-09
	GO:0006414	translational elongation	20	2/03E-08
	GO:0035004	phosphatidylinositol 3-kinase activity	15	2/15E-08
	GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	49	2/24E-08
	GO:0032543	mitochondrial translation	19	3/51E-08
	GO:0034329	cell junction assembly	27	5/34E-08
	GO:0043624	cellular protein complex disassembly	23	4/00E-07
	GO:0140053	mitochondrial gene expression	19	7/72E-07
	GO:0034330	cell junction organization	28	1/27E-06
	GO:0007167	enzyme linked receptor protein signaling pathway	58	1/66E-06
7	GO:2000573	positive regulation of DNA biosynthetic process	14	2/43E-06
	GO:0032984	protein-containing complex disassembly	27	3/05E-06
	GO:0046854	phosphatidylinositol phosphorylation	15	3/22E-06
	GO:0046834	lipid phosphorylation	16	4/99E-06
	GO:0032989	cellular component morphogenesis	59	8/61E-06
	GO:0006260	DNA replication	26	1/02E-05
	GO:0000902	cell morphogenesis	55	1/16E-05
	GO:0014065	phosphatidylinositol 3-kinase signaling	19	1/19E-05
	GO:0016303	1-phosphatidylinositol-3-kinase activity	8	2/54E-05
	GO:0051897	positive regulation of protein kinase B signaling	19	3/35E-05
	GO:0006259	DNA metabolic process	54	3/62E-05
	GO:0006261	DNA-dependent DNA replication	18	5/06E-05
	GO:0035005	1-phosphatidylinositol-4-phosphate 3-kinase activity	5	6/55E-05
	GO:0001727	lipid kinase activity	12	7/36E-05
	GO:0036092	phosphatidylinositol-3-phosphate biosynthetic process	8	9/76E-05
	GO:0033260	nuclear DNA replication	11	1/03E-04
	GO:0006270	DNA replication initiation	9	1/12E-04
	GO:0052742	phosphatidylinositol kinase activity	8	1/56E-04
	GO:0048015	phosphatidylinositol-mediated signaling	19	1/85E-04
	GO:0000723	telomere maintenance	18	1/87E-04
	GO:1900182	positive regulation of protein localization to nucleus	12	1/87E-04
	GO:0032201	telomere maintenance via semi-conservative replication	8	1/94E-04
	GO:0071375	cellular response to peptide hormone stimulus	25	2/13E-04

GO:0048017	inositol lipid-mediated signaling	19	2/33E-04
GO:0043550	regulation of lipid kinase activity	11	2/53E-04
GO:0051896	regulation of protein kinase B signaling	21	2/59E-04
GO:2000278	regulation of DNA biosynthetic process	15	2/72E-04
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	13	3/11E-04
GO:0043491	protein kinase B signaling	22	3/74E-04
GO:0032200	telomere organization	18	4/16E-04
GO:1904869	regulation of protein localization to Cajal body	5	4/95E-04
GO:1904871	positive regulation of protein localization to Cajal body	5	4/95E-04
GO:0044786	cell cycle DNA replication	11	5/08E-04
GO:0043551	regulation of phosphatidylinositol 3-kinase activity	10	5/27E-04
GO:1903405	protein localization to nuclear body	5	8/30E-04
GO:1904851	positive regulation of establishment of protein localization to telomere	5	8/30E-04
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	15	8/83E-04
GO:0042791	5S class rRNA transcription by RNA polymerase III	4	8/88E-04
GO:0042797	tRNA transcription by RNA polymerase III	4	8/88E-04
GO:0007416	synapse assembly	17	8/89E-04
GO:0050808	synapse organization	28	9/08E-04
GO:0006296	nucleotide-excision repair, DNA incision, 5'-to lesion	8	9/14E-04
GO:0051054	positive regulation of DNA metabolic process	20	1/62E-03
GO:0033683	nucleotide-excision repair, DNA incision	8	1/78E-03
GO:1990173	protein localization to nucleoplasm	5	2/00E-03
GO:0004471	malate dehydrogenase (decarboxylating) (NAD ⁺) activity	4	2/01E-03
GO:0004473	malate dehydrogenase (decarboxylating) (NADP ⁺) activity	4	2/01E-03
GO:0006383	transcription by RNA polymerase III	9	2/35E-03
GO:0060249	anatomical structure homeostasis	29	2/66E-03
GO:0007260	tyrosine phosphorylation of STAT protein	11	2/80E-03
GO:0070203	regulation of establishment of protein localization to telomere	5	2/91E-03
GO:0032869	cellular response to insulin stimulus	18	3/59E-03
GO:0004470	malic enzyme activity	4	3/91E-03
GO:0009304	tRNA transcription	4	3/91E-03
GO:0035771	interleukin-4-mediated signaling pathway	4	3/91E-03
GO:0070202	regulation of establishment of protein localization to chromosome	5	4/14E-03
GO:1904816	positive regulation of protein localization to chromosome, telomeric region	5	4/14E-03
GO:0071897	DNA biosynthetic process	18	4/33E-03
GO:0071897	DNA biosynthetic process	18	4/33E-03
GO:0022411	cellular component disassembly	30	5/61E-03
GO:1901653	cellular response to peptide	25	5/80E-03
GO:0016055	Wnt signaling pathway	29	6/40E-03
GO:0198738	cell-cell signaling by wnt	29	6/67E-03
GO:0198738	cell-cell signaling by wnt	29	6/67E-03
GO:0000995	RNA polymerase III general transcription initiation factor activity	4	6/82E-03
GO:0075713	establishment of integrated proviral latency	4	6/82E-03

GO:1904874	positive regulation of telomerase RNA localization to Cajal body	5	7/74E-03
GO:0006297	nucleotide-excision repair, DNA gap filling	6	8/47E-03
GO:0051347	positive regulation of transferase activity	36	8/97E-03
GO:0072657	protein localization to membrane	33	9/70E-03
GO:0000082	G1/S transition of mitotic cell cycle	19	9/84E-03
GO:0016307	phosphatidylinositol phosphate kinase activity	5	1/02E-02
GO:0035591	signaling adaptor activity	11	1/03E-02
GO:1900180	regulation of protein localization to nucleus	12	1/05E-02
GO:0019043	establishment of viral latency	4	1/10E-02
GO:0038127	ERBB signaling pathway	14	1/19E-02
GO:0034061	DNA polymerase activity	11	1/19E-02
GO:0042509	regulation of tyrosine phosphorylation of STAT protein	10	1/26E-02
GO:0006384	transcription initiation from RNA polymerase III promoter	5	1/32E-02
GO:0070102	interleukin-6-mediated signaling pathway	5	1/32E-02
GO:1904814	regulation of protein localization to chromosome, telomeric region	5	1/32E-02
GO:0030258	lipid modification	20	1/51E-02
GO:1901699	cellular response to nitrogen compound	34	1/51E-02
GO:0048010	vascular endothelial growth factor receptor signaling pathway	11	1/70E-02
GO:0007268	chemical synaptic transmission	35	1/75E-02
GO:0098916	anterograde trans-synaptic signaling	35	1/75E-02
GO:0042769	DNA damage response, detection of DNA damage	7	1/88E-02
GO:0046488	phosphatidylinositol metabolic process	16	1/89E-02
GO:0032868	response to insulin	19	2/20E-02
GO:0071417	cellular response to organonitrogen compound	31	2/22E-02
GO:0007259	receptor signaling pathway via JAK-STAT	14	2/22E-02
GO:0043434	response to peptide hormone	26	2/37E-02
GO:0016615	malate dehydrogenase activity	4	2/42E-02
GO:0019042	viral latency	4	2/42E-02
GO:0038089	positive regulation of cell migration by vascular endothelial growth factor signaling pathway	4	2/42E-02
GO:0038110	interleukin-2-mediated signaling pathway	4	2/42E-02
GO:0044843	cell cycle G1/S phase transition	19	2/44E-02
GO:1904872	regulation of telomerase RNA localization to Cajal body	5	2/65E-02
GO:0097696	receptor signaling pathway via STAT	14	2/98E-02
GO:0007265	Ras protein signal transduction	26	3/04E-02
GO:0007173	epidermal growth factor receptor signaling pathway	12	3/15E-02
GO:0090670	RNA localization to Cajal body	5	3/26E-02
GO:0090671	telomerase RNA localization to Cajal body	5	3/26E-02
GO:0090672	telomerase RNA localization	5	3/26E-02
GO:0090685	RNA localization to nucleus	5	3/26E-02
GO:1903725	regulation of phospholipid metabolic process	10	3/33E-02
GO:0071352	cellular response to interleukin-2	4	3/37E-02
GO:0032481	positive regulation of type I interferon production	9	3/62E-02
GO:0002768	immune response-regulating cell surface receptor signaling pathway	28	4/29E-02

	GO:0051052	regulation of DNA metabolic process	25	4/42E-02
	GO:0006108	malate metabolic process	4	4/60E-02
	GO:0006616	SRP-dependent cotranslational protein targeting to membrane, translocation	4	4/60E-02
	GO:0070669	response to interleukin-2	4	4/60E-02
	GO:0022407	regulation of cell-cell adhesion	24	4/61E-02
	GO:0070972	protein localization to endoplasmic reticulum	12	4/62E-02
	GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	6	4/90E-02
	GO:1900739	regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	6	1/37E-04
	GO:1900740	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	6	1/37E-04
	GO:0001844	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	6	2/50E-04
	GO:1905477	positive regulation of protein localization to membrane	10	2/61E-04
	GO:1901030	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	6	4/84E-04
	GO:1903749	positive regulation of establishment of protein localization to mitochondrion	7	9/81E-04
	GO:0010822	positive regulation of mitochondrion organization	9	1/57E-03
	GO:1901028	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	6	1/63E-03
	GO:0051204	protein insertion into mitochondrial membrane	6	2/17E-03
	GO:0008379	thioredoxin peroxidase activity	3	2/74E-03
	GO:1903747	regulation of establishment of protein localization to mitochondrion	7	3/10E-03
	GO:0031532	actin cytoskeleton reorganization	8	3/54E-03
	GO:0097345	mitochondrial outer membrane permeabilization	6	5/39E-03
	GO:1902110	positive regulation of mitochondrial membrane permeability involved in apoptotic process	6	7/25E-03
25	GO:2000249	regulation of actin cytoskeleton reorganization	5	7/61E-03
	GO:0002763	positive regulation of myeloid leukocyte differentiation	6	7/65E-03
	GO:0010821	regulation of mitochondrion organization	10	7/68E-03
	GO:0051920	peroxiredoxin activity	3	8/49E-03
	GO:0045651	positive regulation of macrophage differentiation	4	8/49E-03
	GO:1905475	regulation of protein localization to membrane	10	9/58E-03
	GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	7	1/16E-02
	GO:1902108	regulation of mitochondrial membrane permeability involved in apoptotic process	6	1/17E-02
	GO:1902686	mitochondrial outer membrane permeabilization involved in programmed cell death	6	1/17E-02
	GO:0035794	positive regulation of mitochondrial membrane permeability	6	1/32E-02
	GO:0051205	protein insertion into membrane	6	1/32E-02
	GO:0004521	endoribonuclease activity	6	1/37E-02
	GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	7	1/38E-02
	GO:1905710	positive regulation of membrane permeability	6	1/44E-02
	GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	7	1/53E-02
	GO:0008637	apoptotic mitochondrial changes	8	1/54E-02

	GO:0016893	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	5	1/95E-02
	GO:0045649	regulation of macrophage differentiation	4	2/20E-02
	GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	6	2/89E-02
	GO:0046902	regulation of mitochondrial membrane permeability	6	3/17E-02
	GO:1903078	positive regulation of protein localization to plasma membrane	3	3/22E-02
	GO:2000756	regulation of peptidyl-lysine acetylation	3	3/22E-02
	GO:0070585	protein localization to mitochondrion	8	3/28E-02
	GO:0045445	myoblast differentiation	6	3/61E-02
	GO:0072384	organelle transport along microtubule	6	3/61E-02
	GO:0010825	positive regulation of centrosome duplication	3	4/50E-02
	GO:0002755	MyD88-dependent toll-like receptor signaling pathway	7	2/54E-07
	GO:0032008	positive regulation of TOR signaling	6	6/05E-06
	GO:0071230	cellular response to amino acid stimulus	7	1/24E-05
	GO:0016241	regulation of macroautophagy	10	1/32E-05
	GO:0031929	TOR signaling	8	7/99E-05
	GO:0032006	regulation of TOR signaling	7	2/21E-04
	GO:0034614	cellular response to reactive oxygen species	9	3/63E-04
	GO:0043200	response to amino acid	7	7/33E-04
	GO:0009267	cellular response to starvation	8	8/00E-04
	GO:0034198	cellular response to amino acid starvation	5	8/80E-04
	GO:1990928	response to amino acid starvation	5	1/09E-03
	GO:1901222	regulation of NIK/NF-kappaB signaling	7	1/15E-03
	GO:1901224	positive regulation of NIK/NF-kappaB signaling	6	1/37E-03
	GO:0004896	cytokine receptor activity	6	2/08E-03
	GO:0070301	cellular response to hydrogen peroxide	6	6/12E-03
	GO:0010508	positive regulation of autophagy	6	7/63E-03
29	GO:0099518	vesicle cytoskeletal trafficking	3	1/05E-02
	GO:0008089	anterograde axonal transport	3	2/02E-02
	GO:1903432	regulation of TORC1 signaling	3	2/11E-02
	GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	3	2/70E-02
	GO:0072665	protein localization to vacuole	3	2/70E-02
	GO:0032729	positive regulation of interferon-gamma production	4	3/07E-02
	GO:0047496	vesicle transport along microtubule	3	3/32E-02
	GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	3	3/32E-02
	GO:0016180	snRNA processing	3	3/33E-02
	GO:0016239	positive regulation of macroautophagy	4	3/37E-02
	GO:0038202	TORC1 signaling	3	3/48E-02
	GO:0043928	exonucleolytic catabolism of deadenylated mRNA	3	3/48E-02
	GO:0150076	neuroinflammatory response	4	3/49E-02
	GO:0038034	signal transduction in absence of ligand	4	3/63E-02
	GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	4	3/63E-02
	GO:0000291	nuclear-transcribed mRNA catabolic process, exonucleolytic	3	3/78E-02
	GO:0043038	amino acid activation	3	3/98E-02

	GO:0061900	glial cell activation	3	4/58E-02
	GO:2000351	regulation of endothelial cell apoptotic process	3	4/58E-02
	GO:0071260	cellular response to mechanical stimulus	4	4/65E-02
	GO:0016254	preassembly of GPI anchor in ER membrane	6	2/28E-12
	GO:0006506	GPI anchor biosynthetic process	6	1/25E-10
	GO:0006505	GPI anchor metabolic process	6	1/38E-10
	GO:0009247	glycolipid biosynthetic process	6	1/16E-08
	GO:0006497	protein lipidation	6	1/18E-07
	GO:0042158	lipoprotein biosynthetic process	6	1/38E-07
	GO:1903509	liposaccharide metabolic process	6	2/46E-07
38	GO:0006664	glycolipid metabolic process	6	2/69E-07
	GO:0006661	phosphatidylinositol biosynthetic process	6	4/52E-07
	GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	4	3/08E-06
	GO:0016903	oxidoreductase activity, acting on the aldehyde or oxo group of donors	4	5/89E-06
	GO:0004032	alditol:NADP+ 1-oxidoreductase activity	3	5/97E-06
	GO:0008106	alcohol dehydrogenase (NADP+) activity	3	1/69E-05
	GO:0004033	aldo-keto reductase (NADP) activity	3	1/72E-05
	GO:0033522	histone H2A ubiquitination	5	4/05E-05
	GO:0007006	mitochondrial membrane organization	8	2/49E-04
	GO:0044502	positive regulation of signal transduction in other organism	3	3/48E-04
	GO:0052470	modulation by host of symbiont signal transduction pathway	3	3/48E-04
	GO:0052525	positive regulation by host of symbiont signal transduction pathway	3	3/48E-04
	GO:0052526	positive regulation by organism of signal transduction in other organism involved in symbiotic interaction	3	3/48E-04
	GO:0075205	modulation by host of symbiont cAMP-mediated signal transduction	3	3/48E-04
	GO:0075206	positive regulation by host of symbiont cAMP-mediated signal transduction	3	3/48E-04
	GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	4	4/16E-04
	GO:0019646	aerobic electron transport chain	4	4/16E-04
	GO:0032411	positive regulation of transporter activity	7	4/70E-04
	GO:0051343	positive regulation of cyclic-nucleotide phosphodiesterase activity	3	7/95E-04
39	GO:1904427	positive regulation of calcium ion transmembrane transport	6	9/20E-04
	GO:0016574	histone ubiquitination	5	9/63E-04
	GO:0051823	regulation of synapse structural plasticity	3	1/08E-03
	GO:0044501	modulation of signal transduction in other organism	3	1/46E-03
	GO:0052250	modulation of signal transduction in other organism involved in symbiotic interaction	3	1/46E-03
	GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	5	1/72E-03
	GO:0010856	adenylate cyclase activator activity	3	1/88E-03
	GO:0010857	calcium-dependent protein kinase activity	3	1/88E-03
	GO:1903044	protein localization to membrane raft	3	1/88E-03
	GO:0004129	cytochrome-c oxidase activity	4	2/05E-03
	GO:0015002	heme-copper terminal oxidase activity	4	2/05E-03
	GO:0016676	oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor	4	2/05E-03

GO:0060316	positive regulation of ryanodine-sensitive calcium-release channel activity	3	2/36E-03
GO:0016675	oxidoreductase activity, acting on a heme group of donors	4	2/48E-03
GO:0032414	positive regulation of ion transmembrane transporter activity	6	2/61E-03
GO:0010882	regulation of cardiac muscle contraction by calcium ion signaling	4	2/66E-03
GO:0043539	protein serine/threonine kinase activator activity	4	2/66E-03
GO:0051342	regulation of cyclic-nucleotide phosphodiesterase activity	3	2/79E-03
GO:0060074	synapse maturation	4	3/16E-03
GO:0086064	cell communication by electrical coupling involved in cardiac conduction	4	3/16E-03
GO:0097327	response to antineoplastic agent	6	3/33E-03
GO:0043388	positive regulation of DNA binding	5	3/85E-03
GO:0060315	negative regulation of ryanodine-sensitive calcium-release channel activity	3	4/70E-03
GO:0010644	cell communication by electrical coupling	4	4/78E-03
GO:0010524	positive regulation of calcium ion transport into cytosol	5	5/09E-03
GO:0005513	detection of calcium ion	3	5/41E-03
GO:0072542	protein phosphatase activator activity	3	5/41E-03
GO:1901844	regulation of cell communication by electrical coupling involved in cardiac conduction	3	5/41E-03
GO:0014733	regulation of skeletal muscle adaptation	3	6/14E-03
GO:0051280	negative regulation of release of sequestered calcium ion into cytosol	3	6/14E-03
GO:1901021	positive regulation of calcium ion transmembrane transporter activity	4	6/18E-03
GO:0031952	regulation of protein autophosphorylation	3	6/95E-03
GO:0032206	positive regulation of telomere maintenance	3	6/95E-03
GO:0019855	calcium channel inhibitor activity	3	7/05E-03
GO:0090129	positive regulation of synapse maturation	3	7/05E-03
GO:0019211	phosphatase activator activity	3	8/01E-03
GO:0051284	positive regulation of sequestering of calcium ion	3	8/01E-03
GO:0010649	regulation of cell communication by electrical coupling	3	1/04E-02
GO:0035518	histone H2A monoubiquitination	3	1/04E-02
GO:0042775	mitochondrial ATP synthesis coupled electron transport	5	1/10E-02
GO:0042773	ATP synthesis coupled electron transport	5	1/12E-02
GO:0015278	calcium-release channel activity	3	1/14E-02
GO:0090128	regulation of synapse maturation	3	1/40E-02
GO:0010523	negative regulation of calcium ion transport into cytosol	3	1/54E-02
GO:0048168	regulation of neuronal synaptic plasticity	3	1/65E-02
GO:0035307	positive regulation of protein dephosphorylation	4	1/70E-02
GO:0043949	regulation of cAMP-mediated signaling	4	1/70E-02
GO:0010801	negative regulation of peptidyl-threonine phosphorylation	3	1/95E-02
GO:0051279	regulation of release of sequestered calcium ion into cytosol	5	2/00E-02
GO:0021762	substantia nigra development	3	2/11E-02
GO:0032873	negative regulation of stress-activated MAPK cascade	3	2/11E-02
GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	3	2/11E-02
GO:0010881	regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	3	2/31E-02
GO:0043501	skeletal muscle adaptation	3	2/31E-02

GO:0032516	positive regulation of phosphoprotein phosphatase activity	3	2/46E-02
GO:0014075	response to amine	3	2/53E-02
GO:0050850	positive regulation of calcium-mediated signaling	3	2/53E-02
GO:0061003	positive regulation of dendritic spine morphogenesis	3	2/85E-02
GO:0060999	positive regulation of dendritic spine development	3	2/91E-02
GO:2000351	regulation of endothelial cell apoptotic process	3	2/91E-02
GO:0022400	regulation of rhodopsin mediated signaling pathway	3	2/92E-02
GO:2000352	negative regulation of endothelial cell apoptotic process	3	2/92E-02
GO:0086065	cell communication involved in cardiac conduction	4	2/96E-02
GO:0035306	positive regulation of dephosphorylation	4	3/03E-02
GO:0010390	histone monoubiquitination	3	3/06E-02
GO:2001259	positive regulation of cation channel activity	4	3/10E-02
GO:0043950	positive regulation of cAMP-mediated signaling	3	3/11E-02
GO:0031954	positive regulation of protein autophosphorylation	3	3/13E-02
GO:0048169	regulation of long-term neuronal synaptic plasticity	3	3/13E-02
GO:0010799	regulation of peptidyl-threonine phosphorylation	3	3/25E-02
GO:0010880	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	3	3/25E-02
GO:0010800	positive regulation of peptidyl-threonine phosphorylation	3	3/37E-02
GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	3	3/55E-02
GO:0061001	regulation of dendritic spine morphogenesis	3	3/55E-02
GO:0016056	rhodopsin mediated signaling pathway	3	3/57E-02
GO:1901020	negative regulation of calcium ion transmembrane transporter activity	3	3/57E-02
GO:0031060	regulation of histone methylation	4	3/65E-02
GO:0005246	calcium channel regulator activity	3	3/65E-02
GO:0061647	histone H3-K9 modification	3	3/65E-02
GO:0060314	regulation of ryanodine-sensitive calcium-release channel activity	3	3/66E-02
GO:1903779	regulation of cardiac conduction	4	3/71E-02
GO:0051569	regulation of histone H3-K4 methylation	3	3/73E-02
GO:0005219	ryanodine-sensitive calcium-release channel activity	3	3/85E-02
GO:0014808	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	3	3/85E-02
GO:0044091	membrane biogenesis	3	3/86E-02
GO:0014888	striated muscle adaptation	3	3/87E-02
GO:1903170	negative regulation of calcium ion transmembrane transport	3	3/89E-02
GO:1903514	release of sequestered calcium ion into cytosol by endoplasmic reticulum	3	3/89E-02
GO:0050849	negative regulation of calcium-mediated signaling	3	3/91E-02
GO:2001222	regulation of neuron migration	3	4/01E-02
GO:2001258	negative regulation of cation channel activity	3	4/01E-02
GO:0016248	channel inhibitor activity	3	4/12E-02
GO:0071709	membrane assembly	3	4/12E-02
GO:0050775	positive regulation of dendrite morphogenesis	3	4/13E-02
GO:0007603	phototransduction, visible light	3	4/14E-02
GO:0008200	ion channel inhibitor activity	3	4/14E-02
GO:0010922	positive regulation of phosphatase activity	3	4/14E-02

	GO:0018023	peptidyl-lysine trimethylation	3	4/23E-02
	GO:1904036	negative regulation of epithelial cell apoptotic process	3	4/23E-02
	GO:0046329	negative regulation of JNK cascade	3	4/30E-02
	GO:0002729	positive regulation of natural killer cell cytokine production	3	7/45E-10
	GO:0002370	natural killer cell cytokine production	3	1/14E-09
	GO:0002484	antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway	3	1/14E-09
	GO:0002486	antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway, TAP-independent	3	1/14E-09
	GO:0002727	regulation of natural killer cell cytokine production	3	1/14E-09
	GO:0002480	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent	3	2/31E-09
	GO:0002476	antigen processing and presentation of endogenous peptide antigen via MHC class Ib	3	4/01E-09
	GO:0002428	antigen processing and presentation of peptide antigen via MHC class Ib	3	4/93E-09
	GO:0045953	negative regulation of natural killer cell mediated cytotoxicity	3	1/10E-08
	GO:0002716	negative regulation of natural killer cell mediated immunity	3	1/24E-08
	GO:0002475	antigen processing and presentation via MHC class Ib	3	1/62E-08
	GO:0002483	antigen processing and presentation of endogenous peptide antigen	3	1/62E-08
45	GO:0019885	antigen processing and presentation of endogenous peptide antigen via MHC class I	3	1/62E-08
	GO:0001911	negative regulation of leukocyte mediated cytotoxicity	3	2/67E-08
	GO:0031342	negative regulation of cell killing	3	3/56E-08
	GO:0001916	positive regulation of T cell mediated cytotoxicity	3	3/65E-08
	GO:0019883	antigen processing and presentation of endogenous antigen	3	5/53E-08
	GO:0002717	positive regulation of natural killer cell mediated immunity	3	6/51E-08
	GO:0042267	natural killer cell mediated cytotoxicity	3	6/57E-08
	GO:0001914	regulation of T cell mediated cytotoxicity	3	8/64E-08
	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	3	8/86E-08
	GO:0045824	negative regulation of innate immune response	3	8/86E-08
	GO:0002711	positive regulation of T cell mediated immunity	3	1/26E-07
	GO:0002704	negative regulation of leukocyte mediated immunity	3	1/27E-07
	GO:0001913	T cell mediated cytotoxicity	3	1/32E-07
	GO:0002707	negative regulation of lymphocyte mediated immunity	3	1/42E-07
	GO:0002715	regulation of natural killer cell mediated immunity	3	1/42E-07
	GO:0042269	regulation of natural killer cell mediated cytotoxicity	3	1/48E-07
	GO:0098960	postsynaptic neurotransmitter receptor activity	7	2/05E-07
	GO:0070681	glutaminyI-tRNA ^{Gln} biosynthesis via transamidation	3	9/23E-07
	GO:0007214	gamma-aminobutyric acid signaling pathway	4	5/59E-05
	GO:0099565	chemical synaptic transmission, postsynaptic	7	5/79E-05
70	GO:0071420	cellular response to histamine	3	1/26E-04
	GO:0034776	response to histamine	3	2/58E-04
	GO:0098962	regulation of postsynaptic neurotransmitter receptor activity	3	4/45E-04
	GO:1904315	transmitter-gated ion channel activity involved in regulation of postsynaptic membrane potential	4	5/29E-04

	GO:0099529	neurotransmitter receptor activity involved in regulation of postsynaptic membrane potential	4	6/55E-04
	GO:0005253	anion channel activity	5	1/10E-03
	GO:0043517	positive regulation of DNA damage response, signal transduction by p53 class mediator	3	1/19E-03
	GO:0008333	endosome to lysosome transport	4	1/46E-03
	GO:0085029	extracellular matrix assembly	3	1/62E-03
	GO:0043038	amino acid activation	3	1/88E-03
	GO:1901798	positive regulation of signal transduction by p53 class mediator	3	3/23E-03
	GO:0043039	tRNA aminoacylation	3	3/44E-03
	GO:0060384	innervation	3	3/52E-03
	GO:0043516	regulation of DNA damage response, signal transduction by p53 class mediator	3	3/73E-03
	GO:0030857	negative regulation of epithelial cell differentiation	3	4/94E-03
	GO:0060119	inner ear receptor cell development	3	5/44E-03
	GO:0006829	zinc ion transport	4	8/02E-06
	GO:0005385	zinc ion transmembrane transporter activity	3	1/54E-04
71	GO:0072509	divalent inorganic cation transmembrane transporter activity	3	1/59E-04
	GO:0071577	zinc ion transmembrane transport	3	1/79E-04
	GO:0046915	transition metal ion transmembrane transporter activity	3	3/12E-04
	GO:0005003	ephrin receptor activity	3	1/33E-08
77	GO:0005005	transmembrane-ephrin receptor activity	3	1/64E-08
	GO:0004966	galanin receptor activity	3	9/54E-08
86	GO:0008188	neuropeptide receptor activity	3	8/74E-06
	GO:0043162	ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	3	4/17E-05
	GO:0002227	innate immune response in mucosa	3	1/29E-04
	GO:0046794	transport of virus	3	1/31E-04
	GO:0075733	intracellular transport of virus	3	2/20E-04
90	GO:0002385	mucosal immune response	3	2/71E-04
	GO:0002251	organ or tissue specific immune response	3	2/79E-04
	GO:0032608	interferon-beta production	3	3/16E-04
	GO:0032648	regulation of interferon-beta production	3	3/68E-04
	GO:0019731	antibacterial humoral response	3	3/79E-04

GO, gene ontology; FDR, false discovery rate.

Supplementary Table 5. A list of 110 important (hub) genes for colorectal cancer with high centralities in the protein-protein interaction network.

HGNC symbol	Protein ID	Degree	Betweenness	Closeness	Eccentricity	DEM target
GNAT1	P11488	127	0.00023800	0.3299	6	Yes
OTX1	P32242	146	0.00250829	0.3379	6	Yes
ZNF526	Q8TF50	83	0.00076300	0.3387	6	Yes
GLP1R	P43220	87	0.00114699	0.3412	6	Yes
TAZ	Q16635	117	0.00045800	0.3416	6	Yes
VKORC1	Q9BQB6	98	0.00122438	0.3454	6	Yes
AGTRAP	Q6RW13	92	0.00029600	0.3480	6	Yes
RETREG3	Q86VR2	156	0.00135059	0.3485	6	Yes
CTDSPL	O15194	91	0.00031700	0.3493	6	Yes
LYPD3	O95274	119	0.00045600	0.3494	6	Yes
ARL6IP1	Q15041	98	0.00093700	0.3500	6	Yes
FAM189B	P81408	93	0.00034200	0.3512	6	Yes
CDK15	Q96Q40	101	0.00058400	0.3517	6	Yes
GNG5	P63218	189	0.00048000	0.3519	6	Yes
GMCL1	Q96IK5	106	0.00069700	0.3531	6	Yes
USHBP1	Q8N6Y0	131	0.00025000	0.3538	6	Yes
CHRM1	P11229	103	0.00043300	0.3539	6	Yes
CCHCR1	Q8TD31	115	0.00022600	0.3540	6	Yes
ATP6V1B1	P15313	100	0.00037200	0.3540	6	Yes
GNA14	O95837	138	0.00049700	0.3541	6	Yes
STX4	Q12846	88	0.00027700	0.3545	6	Yes
PARP2	Q9UGN5	104	0.00037100	0.3547	6	Yes
TSC22D4	Q9Y3Q8	84	0.00027600	0.3555	6	Yes
CHRM3	P20309	116	0.00055000	0.3557	6	Yes
CTNNA3	Q9UI47	190	0.00123594	0.3557	6	Yes
PEX5	P50542	92	0.00069900	0.3559	6	Yes
PLGRKT	Q9HBL7	144	0.00033300	0.3563	6	Yes
RAB8A	P61006	133	0.00037100	0.3581	6	Yes
CREB3	O43889	130	0.00121667	0.3589	6	Yes
CETN2	P41208	92	0.00024000	0.3599	6	Yes
SNX6	Q9UNH7	86	0.00102078	0.3611	6	Yes
SAV1	Q9H4B6	106	0.00034300	0.3615	6	Yes
APOB	P04114	93	0.00060300	0.3618	6	Yes
PNMA1	Q8ND90	140	0.00049600	0.3623	6	Yes
GNAQ	P50148	173	0.00086900	0.3625	6	Yes
PIP4K2A	P48426	119	0.00032300	0.3631	6	Yes
LNX2	Q8N448	93	0.00046800	0.3631	6	Yes
CBX6	O95503	116	0.00027000	0.3633	6	Yes
TLR4	O00206	111	0.00058400	0.3635	6	Yes

ITSN1	Q15811	139	0.00025800	0.3636	6	Yes
DDX46	Q7L014	89	0.00077400	0.3638	6	Yes
SKIL	P12757	110	0.00037700	0.3641	6	Yes
SPRTN	Q9H040	94	0.00028100	0.3642	6	Yes
MRM3	Q9HC36	85	0.00028600	0.3647	6	Yes
MMP9	P14780	112	0.00033800	0.3652	6	Yes
MMP2	P08253	85	0.00028800	0.3659	6	Yes
GRK2	P25098	88	0.00022900	0.3662	6	Yes
CDIPT	O14735	104	0.00067300	0.3666	6	Yes
PDE4DIP	Q5VU43	131	0.00054000	0.3668	6	Yes
TFAP4	Q01664	110	0.00024400	0.3671	6	Yes
BAG4	O95429	121	0.00050200	0.3674	6	Yes
TTC1	Q99614	104	0.00024100	0.3684	6	Yes
NUDCD3	Q8IVD9	132	0.00051100	0.3688	6	Yes
TJP2	Q9UDY2	103	0.00065800	0.3691	6	Yes
SYVN1	Q86TM6	95	0.00036700	0.3692	6	Yes
ECSIT	Q9BQ95	117	0.00041100	0.3703	6	Yes
RAB10	P61026	86	0.00030900	0.3707	6	Yes
MED21	Q13503	131	0.00026000	0.3712	6	Yes
GNB5	O14775	218	0.00106626	0.3716	6	Yes
PDK1	Q15118	319	0.00200559	0.3720	6	Yes
ERRFI1	Q9UJM3	97	0.00074700	0.3731	6	Yes
CNTRL	Q7Z7A1	191	0.00028000	0.3732	6	Yes
MYB	P10242	126	0.00043400	0.3736	6	Yes
ELOC	Q15369	180	0.00037700	0.3754	6	Yes
SLX4	Q8IY92	139	0.00029300	0.3755	6	Yes
PRNP	P04156	105	0.00026600	0.3756	6	Yes
FKBP4	Q02790	92	0.00035700	0.3758	6	Yes
FZR1	Q9UM11	205	0.00041400	0.3776	6	Yes
CDK8	P49336	143	0.00030400	0.3777	6	Yes
SUV39H1	O43463	189	0.00073400	0.3779	6	Yes
RNF11	Q9Y3C5	109	0.00022900	0.3785	6	Yes
PSMB2	P49721	193	0.00057800	0.3792	6	Yes
RAD23A	P54725	166	0.00025800	0.3798	6	Yes
ODF2	Q5BJF6	124	0.00023300	0.3806	6	Yes
ERBIN	Q96RT1	110	0.00050200	0.3815	6	Yes
SP3	Q02447	123	0.00036900	0.3818	6	Yes
WT1	P19544	114	0.00032000	0.3823	6	Yes
FLOT1	O75955	114	0.00026600	0.3827	6	Yes
MAP1LC3B	Q9GZQ8	171	0.00041500	0.3828	6	Yes
PSMB5	P28074	175	0.00056100	0.3836	6	Yes
UBE2L3	P68036	148	0.00055200	0.3855	6	Yes
NOS3	P29474	92	0.00026300	0.3866	6	Yes

EPS15	P42566	114	0.00023900	0.3873	6	Yes
ANXA1	P04083	119	0.00023700	0.3874	6	Yes
PLEC	Q15149	133	0.00024500	0.3927	6	Yes
UBB	P62988	205	0.00032600	0.3934	6	Yes
ATP5F1B	P06576	161	0.00077800	0.3934	6	Yes
ITCH	Q96J02	188	0.00052400	0.3945	6	Yes
SRSF3	P84103	198	0.00027100	0.3960	6	Yes
GNGT1	P63211	86	0.00025600	0.3496	6	No
SLAMF1	Q13291	121	0.00046700	0.3532	6	No
PLAUR	Q03405	85	0.00031500	0.3555	6	No
CACNA1A	O00555	109	0.00061200	0.3568	6	No
HLA-C	P10321	97	0.00050900	0.3584	6	No
SGTA	O43765	106	0.00050700	0.3666	6	No
MTNR1B	P49286	118	0.00050300	0.3674	6	No
CHMP4B	Q9H444	112	0.00041300	0.3683	6	No
CTSB	P07858	68	0.00043100	0.3690	6	No
KRT31	Q15323	126	0.00049800	0.3701	6	No
ELOB	Q15370	170	0.00029200	0.3711	6	No
JMJD6	Q6NYC1	130	0.00030800	0.3714	6	No
MAPK8IP2	Q13387	103	0.00061300	0.3741	6	No
MED23	Q9ULK4	147	0.00028700	0.3752	6	No
UBQLN4	Q9NRR5	201	0.00102799	0.3764	6	No
MTNR1A	P48039	128	0.00099400	0.3797	6	No
USP2	O75604	113	0.00031600	0.3810	6	No
SNRPE	P62304	309	0.00045300	0.3828	6	No
A2M	P01023	143	0.00101806	0.3831	6	No
HSPA2	P54652	163	0.00078600	0.3901	6	No
PSMC2	P35998	174	0.00031400	0.3933	6	No

HGNC, HUGO Gene Nomenclature Committee; DEM, differentially expressed miRNA.