



Research article

A methylomics-correlated nomogram predicts the recurrence free survival risk of kidney renal clear cell carcinoma

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Supplementary

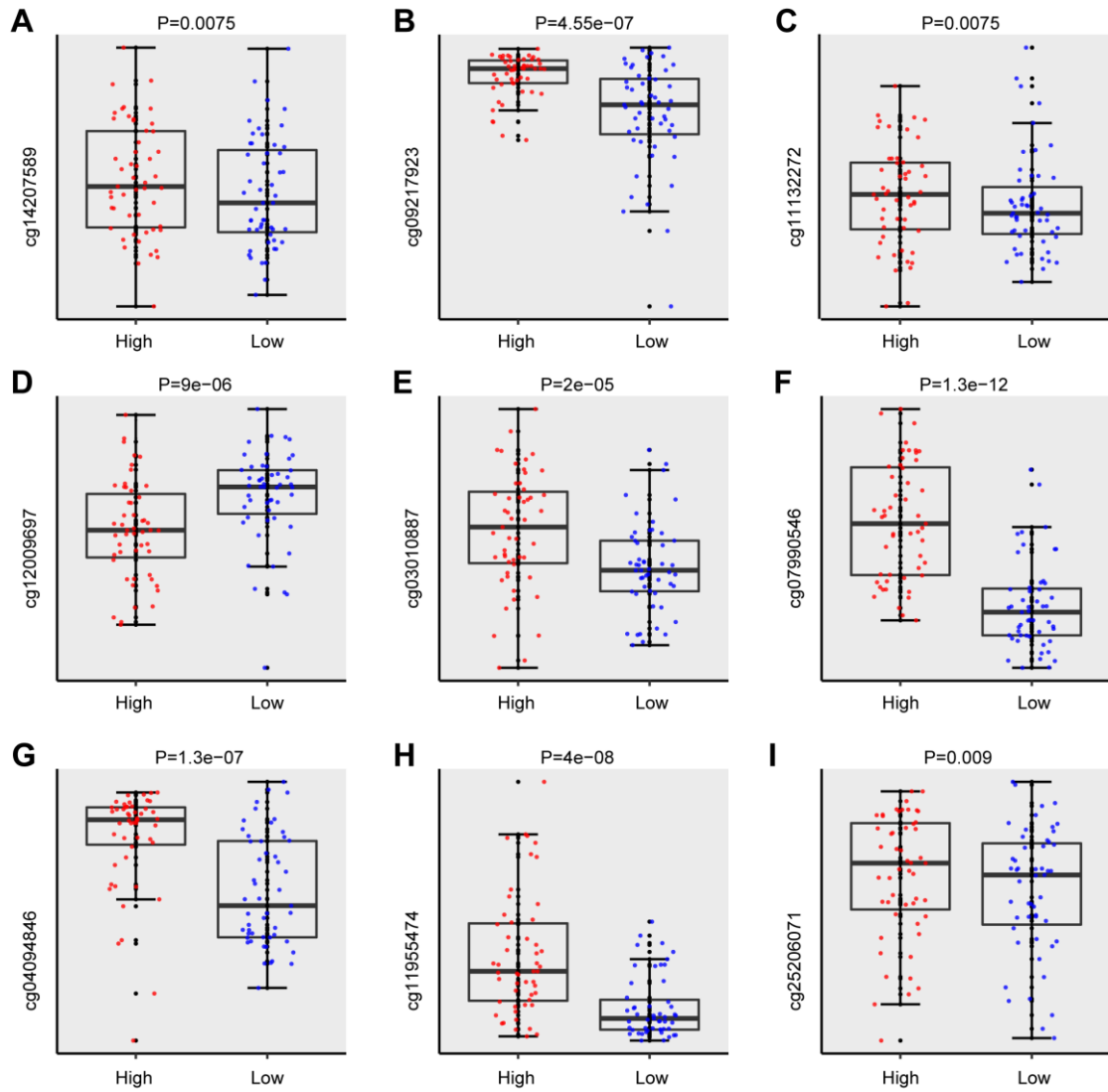


Figure S1. Boxplots of methylation β values against risk group in the entire E-MTAB-3274 dataset. Y-axis stood for the β -value of 9-DNA methylation sites respectively. The differences between the 2 groups were assessed by Mann-Whitney U test.

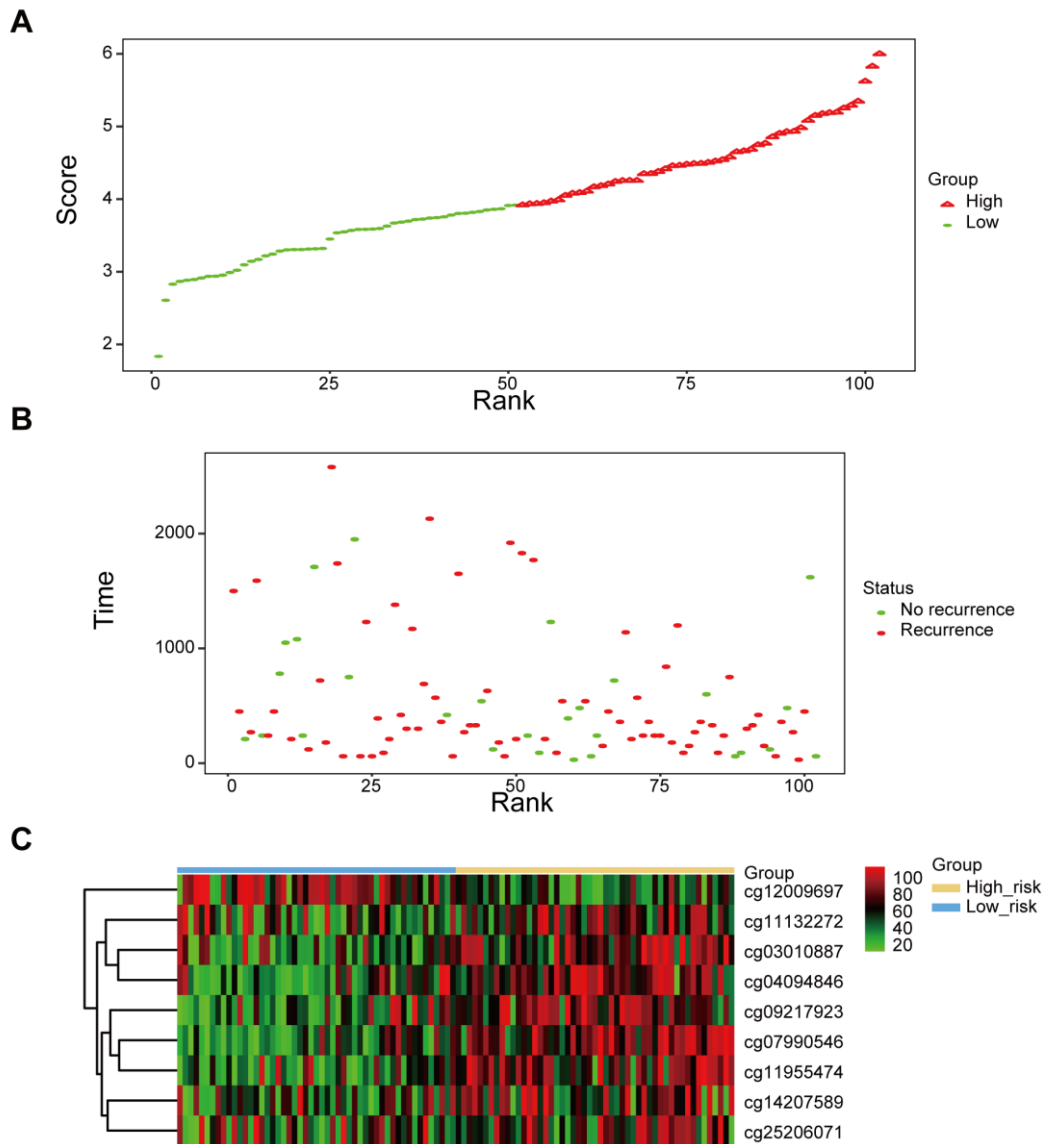


Figure S2. Methylation risk score analysis of the 102 KIRC patients from E-MTAB-3274. (A) Methylation risk score distribution against the rank of risk score. Median risk score was the cut-off point. (B) Recurrence status of KIRC patients. (C) Heatmap of 9 methylation sites expression profiles of KIRC patients.

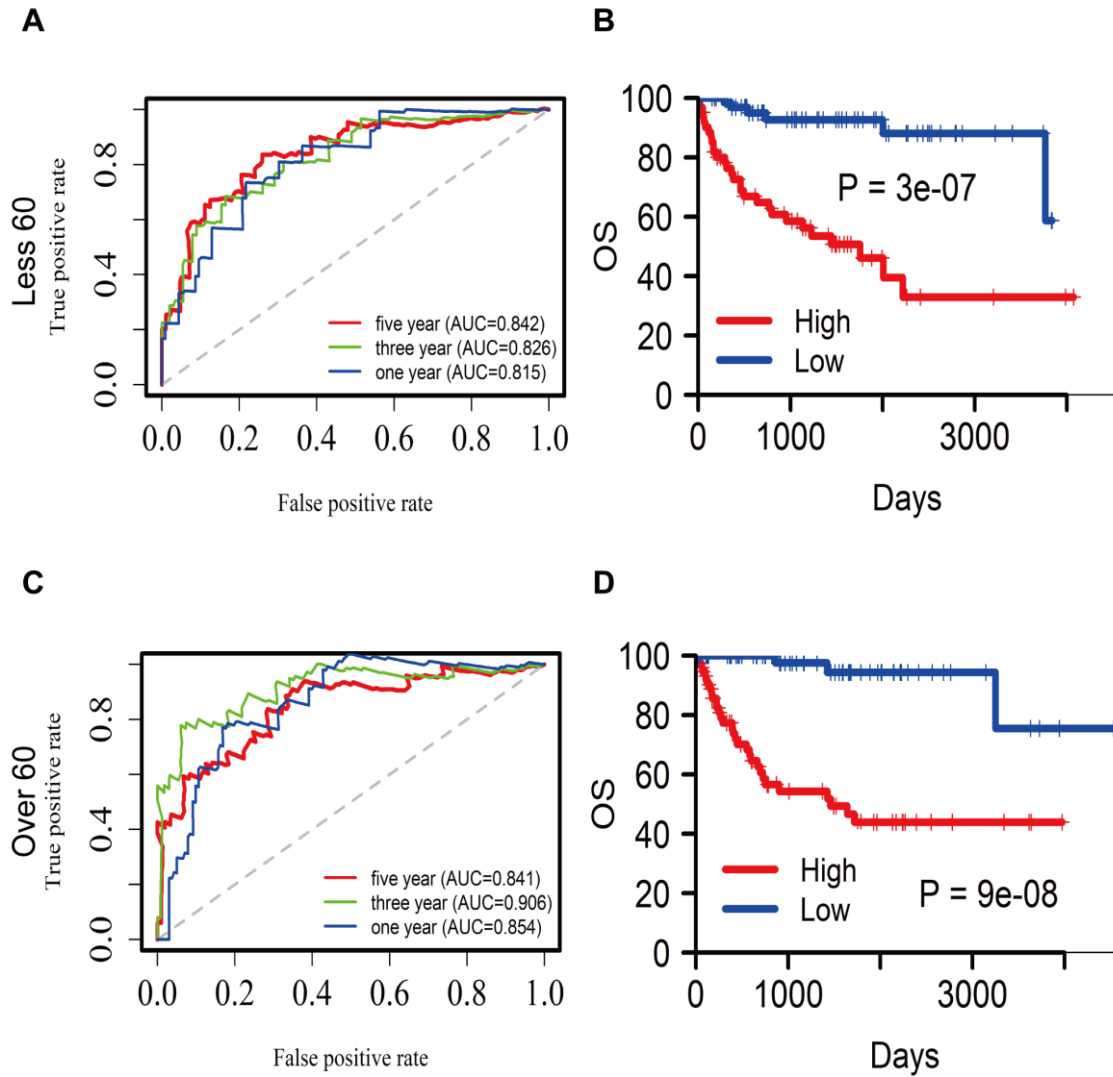


Figure S3. Kaplan-Meier and ROC analysis of patients with KIRC in sub-groups according to age, respectively. (A, B) Age less 60 years sub-group. (C, D) Age over 60 years sub-group. “High” and “Low” stood for the high risk score group and low risk score group, respectively. The median risk score was set as a cutoff.

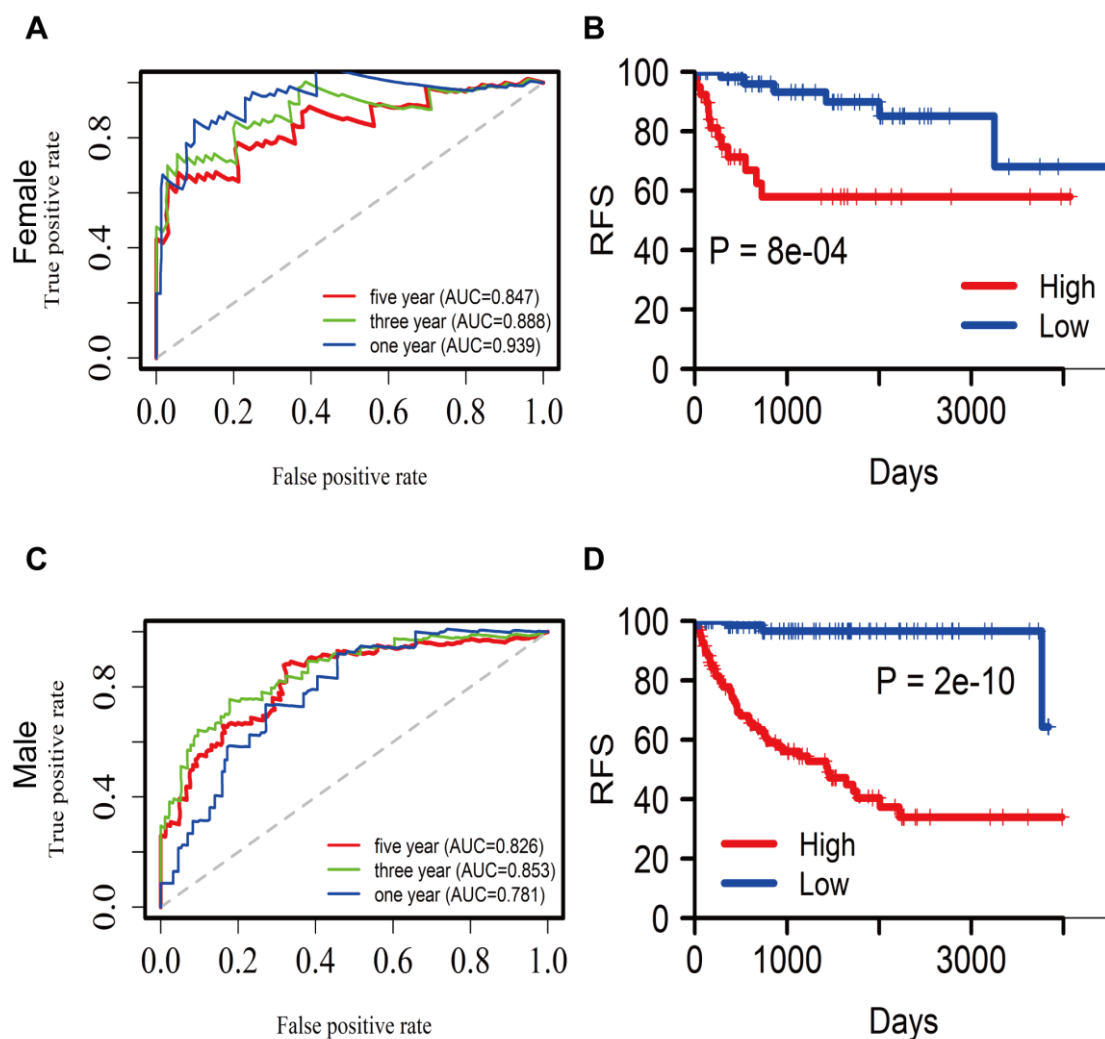


Figure S4. Kaplan-Meier and ROC analysis of patients with KIRC in sub-groups based on sex, respectively. (A, B) Female sub-group. (C, D) Male sub-group. “High” and “Low” represented the high risk score group and low risk score group, respectively. The median risk score was set as a cutoff.

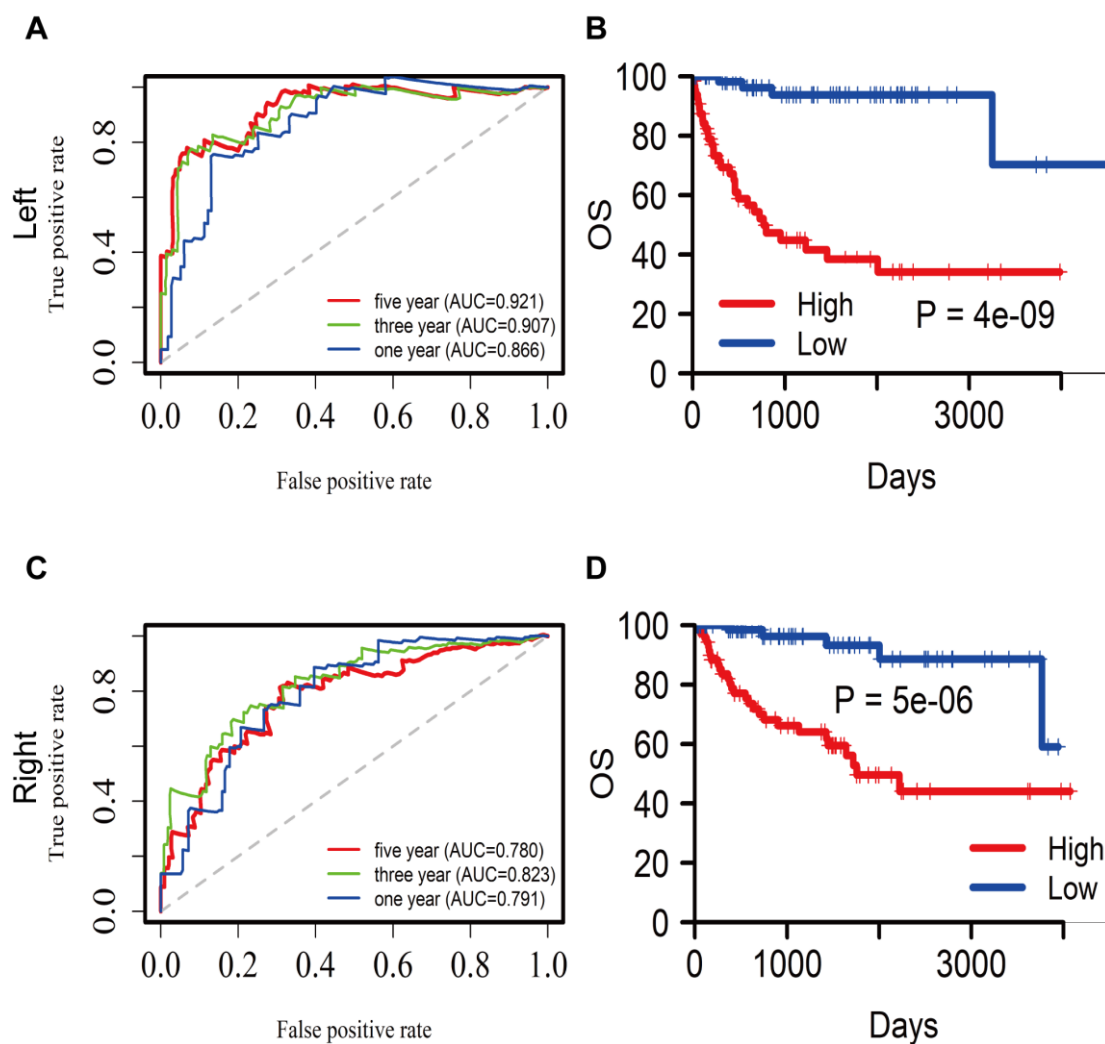


Figure S5. Kaplan-Meier and ROC analysis of patients with KIRC in sub-groups according to anatomic site, respectively. (A, B) Left side sub-group. (C, D) Right side sub-group. “High” and “Low” represented the high risk score group and low risk score group, respectively. The median risk score was set as a cutoff.

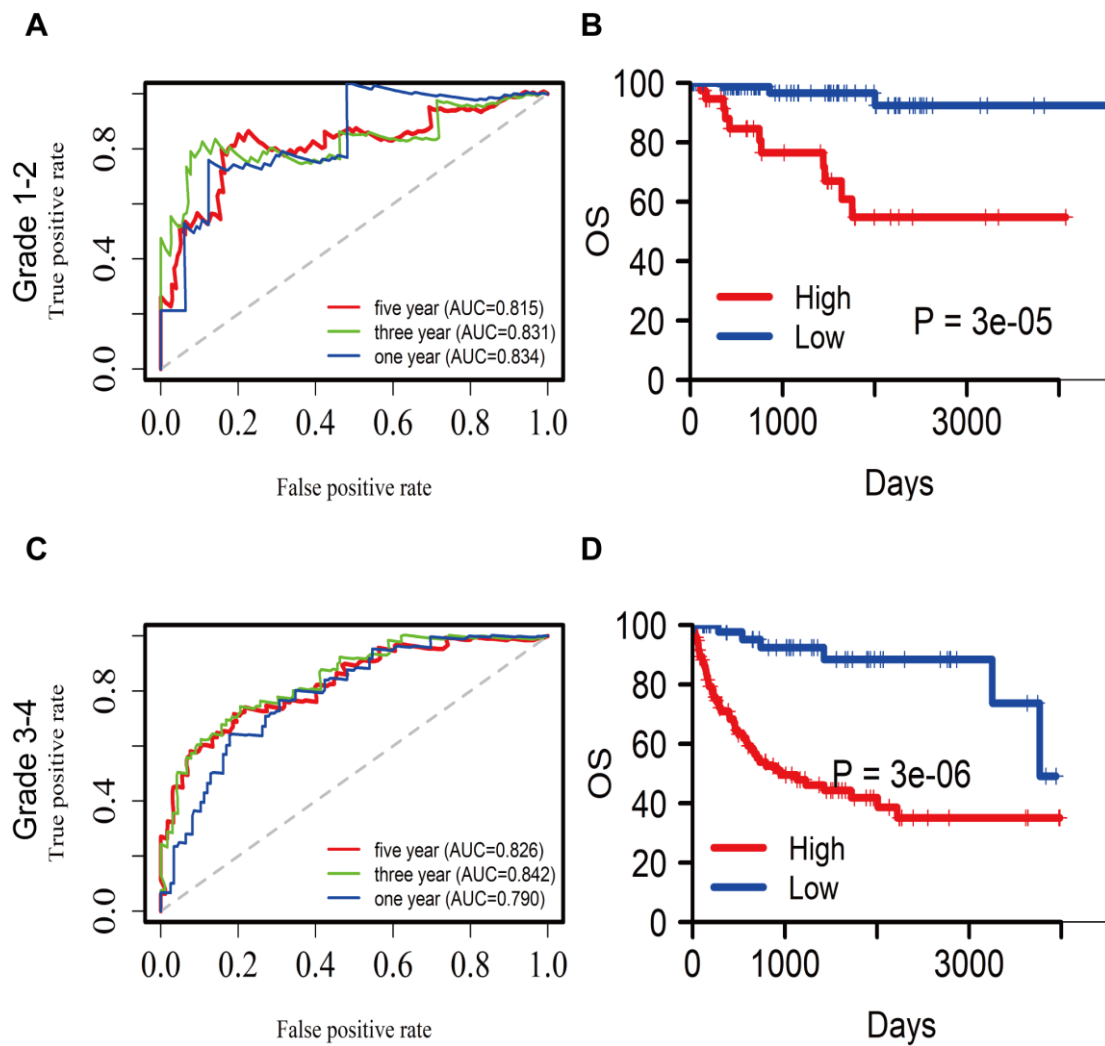


Figure S6. Kaplan-Meier and ROC analysis of patients with KIRC in sub-groups according to Grade, respectively. (A, B) Grade 1-2 sub-group. (C, D) Grade 3-4 sub-group. “High” and “Low” represented the high risk score group and low risk score group, respectively. The median risk score was set as a cutoff.

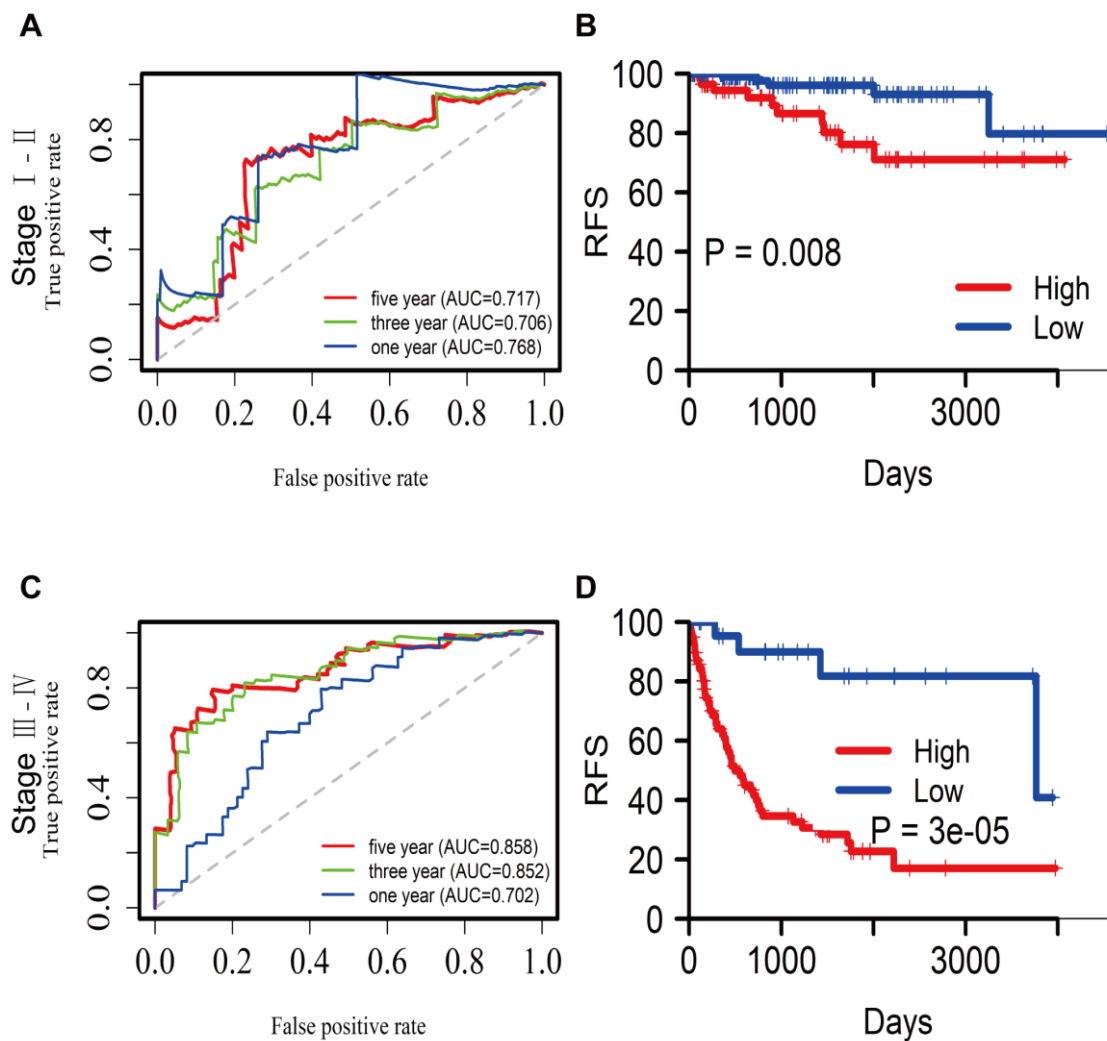
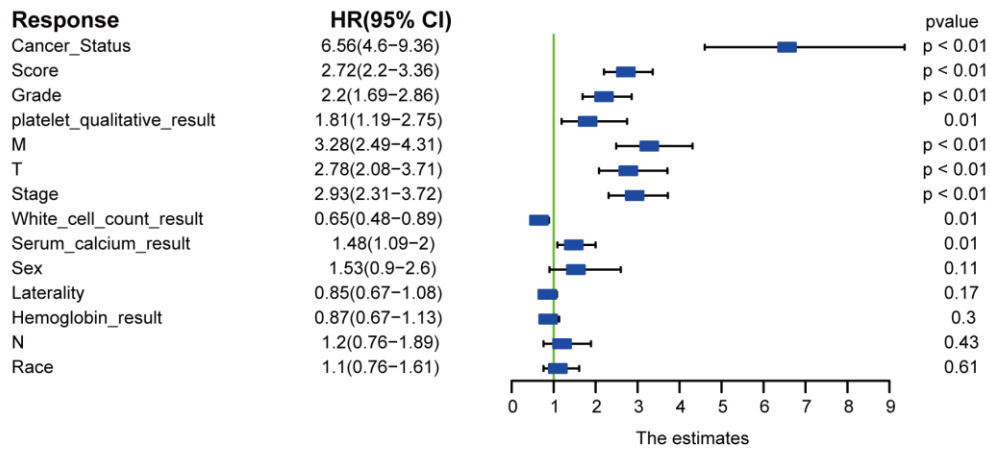


Figure S7. Kaplan-Meier and ROC analysis of patients with KIRC in sub-groups according to stage, respectively. (A, B) Stage I-II. (C, D) Stage III-IV. “High” and “Low” represented the high risk score group and low risk score group, respectively. The median risk score was set as a cutoff.

A



B

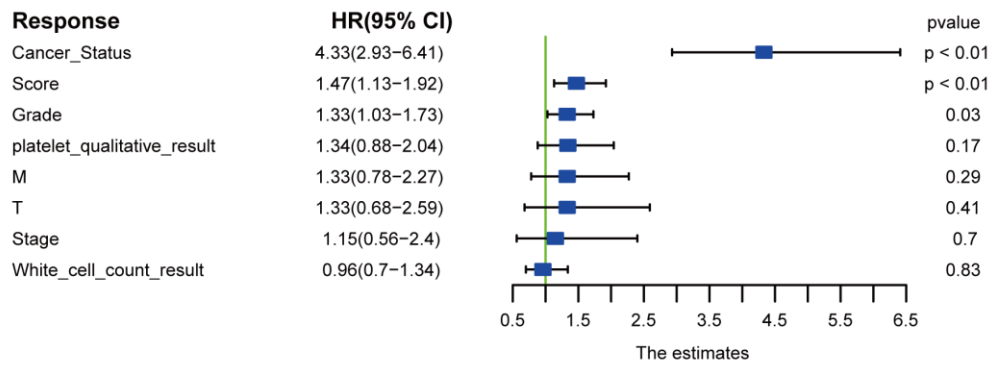


Figure S8. Forest plot summary of analysis of RFS. (A) Univariable Cox analysis of the risk score as well as other clinical variables. (B) Multivariable Cox analysis of the risk score and other clinical variables. The blue squares on the transverse lines stood for the hazard ratio (HR), and the black transverse lines stood for 95% CI. “Score” represents the risk scores computed based on the formula in Results section. “Response” means response variables, that is clinical variables with relatively complete clinical information.

Table S1. Hazard ratios and 95% CIs as well as P values of 942 methylation sites based on univariate Cox regression analysis.

Characteristics	Hazard.Ratio	CI 95%	P.value
cg00459623	22.00614	5.26691-91.94577	2.00E-05
cg07274590	54.85264	12.61063-238.59332	0
cg01054478	31.1449	7.39992-131.08313	0
cg04787024	18.45674	4.82437-70.61052	2.00E-05
cg04092800	17.80438	4.98177-63.63122	1.00E-05
cg04492228	54.66038	10.97058-272.34274	0
cg24603408	13.74559	4.45012-42.45754	1.00E-05
cg02416510	148.9806	20.71294-1071.56307	0
cg13677149	32.42541	8.00346-131.36904	0

cg12331331	0.03445	0.00801-0.14811	1.00E-05
cg26599006	19.24062	5.32724-69.49209	1.00E-05
cg05223720	16.4908	4.39561-61.86771	3.00E-05
cg14207589	36.10405	5.9434-219.3195	1.00E-04
cg09217923	371.5232	25.08762-5501.89574	2.00E-05
cg14427009	105.7427	14.85705-752.60704	0
cg02604524	13.496	5.12148-35.56439	0
cg02317400	36.58661	7.98462-167.64489	0
cg08637618	37.91938	9.19296-156.41085	0
cg09537620	14.34023	4.52945-45.4011	1.00E-05
cg11132272	23.23547	5.80606-92.98675	1.00E-05
cg12715421	54.17541	8.01551-366.16211	4.00E-05
cg16557178	40.89521	8.54046-195.82304	0
cg26199241	17.18001	4.37447-67.47174	5.00E-05
cg23376501	0.01813	0.00189-0.17362	5.00E-04
cg04681810	55.78887	10.70439-290.759	0
cg07539443	0.0554	0.01741-0.17625	0
cg03774463	46.21651	9.24385-231.06885	0
cg07014673	9.74527	3.51329-27.03171	1.00E-05
cg04727521	0.04807	0.01239-0.18644	1.00E-05
cg21697851	14.61757	4.07795-52.39727	4.00E-05
cg26189983	36.44784	6.97913-190.34522	2.00E-05
cg03002848	33.63685	7.5448-149.96268	0
cg03072621	16.48997	4.57833-59.39265	2.00E-05
cg22595460	25.77124	7.14037-93.01431	0
cg14202477	42.07641	7.18188-246.51271	3.00E-05
cg13459498	20.44679	4.60318-90.82234	7.00E-05
cg03565189	17.63435	3.9119-79.49335	0.00019
cg09287190	24.25193	4.39393-133.85641	0.00025
cg02388453	53.39232	6.64464-429.02879	0.00018
cg26546373	31.3572	5.30881-185.21544	0.00014
cg23153745	0.04806	0.01091-0.21161	6.00E-05
cg12436377	13.8874	4.42761-43.55842	1.00E-05
cg13389502	24.17538	4.34722-134.44206	0.00027
cg01715172	0.03992	0.0088-0.18103	3.00E-05
cg12338552	11.33691	3.23405-39.74138	0.00015
cg07135614	15.20589	4.47004-51.72645	1.00E-05
cg03690956	17.67119	4.73223-65.98812	2.00E-05
cg27508620	15.56793	4.05603-59.75318	6.00E-05
cg13349472	65.4312	6.4758-661.11411	4.00E-04
cg06555959	19.3815	4.55911-82.39381	6.00E-05
cg12764034	32.25088	7.56818-137.43325	0
cg27443071	9.30893	2.79851-30.96516	0.00027
cg00182273	0.00359	0.00016-0.0807	0.00039
cg05692123	10.38928	2.3826-45.30218	0.00184
cg16084872	20.25622	4.4424-92.36327	1.00E-04
cg12009697	0.0231	0.00383-0.13926	4.00E-05
cg00095431	35.72753	6.85978-186.07823	2.00E-05
cg16670307	27.75588	4.43617-173.66076	0.00038
cg14866167	48.40595	8.04549-291.23611	2.00E-05

cg18401406	50.32165	8.77255-288.65815	1.00E-05
cg19908556	8.12548	2.76327-23.89322	0.00014
cg24509810	23.30988	5.19493-104.59249	4.00E-05
cg05591728	0.05385	0.01229-0.23589	0.00011
cg05870739	8.57805	2.31576-31.77486	0.0013
cg03780851	18.3173	4.02525-83.35468	0.00017
cg26271045	9.66838	2.44805-38.18449	0.00121
cg03011535	22.32329	5.19348-95.95287	3.00E-05
cg24843474	11.18556	2.90814-43.02292	0.00044
cg18126442	25.11077	3.73842-168.6677	0.00091
cg17610800	17.25457	4.28062-69.55065	6.00E-05
cg03010887	49.57829	8.32037-295.42028	2.00E-05
cg07990546	18.1134	4.87865-67.25118	2.00E-05
cg10067304	0.05413	0.01016-0.28843	0.00063
cg04094846	20.87577	5.16955-84.30096	2.00E-05
cg04642923	32.36341	6.18064-169.46314	4.00E-05
cg01329434	35.52721	4.95366-254.79783	0.00038
cg23734418	9.53193	2.50571-36.26022	0.00094
cg16697438	32.95771	6.59011-164.82426	2.00E-05
cg24617171	29.68801	5.66545-155.57067	6.00E-05
cg06404175	7.07831	2.14815-23.32357	0.0013
cg03519907	10.04262	2.90829-34.67819	0.00026
cg05668996	22.1193	3.52516-138.79202	0.00095
cg11955474	15.1406	4.05056-56.59404	5.00E-05
cg05256504	29.20606	3.87689-220.02009	0.00106
cg08091192	15.32723	3.61692-64.9513	0.00021
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cg16348112	12.25341	2.88451-52.05249	0.00069
cg22546168	10.82908	2.65672-44.14049	0.00089
cg12650490	13.97967	2.97386-65.71633	0.00084
cg14038391	20.15205	4.0155-101.13436	0.00026
cg24570303	26.41615	5.20242-134.13232	8.00E-05
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cg02623400	14.45855	2.80356-74.56578	0.00141
cg11910782	0.0914	0.02188-0.38176	0.00104
cg26239391	14.63527	3.27242-65.45334	0.00045
cg24040115	0.03745	0.00566-0.24759	0.00065
cg08545493	9.89614	2.15771-45.38786	0.00318
cg00891278	31.39684	5.74085-171.71013	7.00E-05
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cg02251315	59.49296	5.3344-663.50723	9.00E-04
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cg06946708	21.26075	3.85112-117.37351	0.00045
cg03317505	0.03254	0.00432-0.24507	0.00088
cg18160691	21.53047	3.98881-116.21528	0.00036
cg08152546	21.58164	4.43448-105.03305	0.00014
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cg26266708	12.29716	2.32677-64.99147	0.00314

cg00786952	15.37755	3.55069-66.59804	0.00026
cg21100077	16.76785	3.46627-81.11345	0.00046
cg10486998	8.31939	1.77961-38.89173	0.00709
cg24902478	11.64344	2.53683-53.44069	0.00159
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cg22260952	7.07187	1.97423-25.33204	0.00266
cg27417609	17.6378	4.21795-73.7543	8.00E-05
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cg10245273	10.63862	2.4524-46.15073	0.00159
cg21458907	8.26758	1.91212-35.74722	0.00469
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cg00530805	0.03863	0.00551-0.27094	0.00106
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cg08554603	10.3055	2.76041-38.47376	0.00052
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cg04198912	0.12077	0.02924-0.4988	0.00349
cg22650617	6.85922	1.77383-26.52385	0.00526
cg23348789	27.38351	2.16441-346.44857	0.01058
cg20250426	11.52834	2.42369-54.83469	0.00212
cg23304923	17.52844	2.60125-118.11496	0.00326
cg19611002	0.09366	0.01724-0.50897	0.00611

cg13460850	6.30422	1.98009-20.07146	0.00183
cg22532314	32.26626	3.33957-311.75009	0.00268
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cg22859061	8.53655	1.7123-42.55828	0.00889
cg17603461	0.02348	0.00161-0.34144	0.00602
cg08261988	0.06505	0.00684-0.61835	0.01739
cg03723123	0.03364	0.00161-0.70151	0.02862
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cg18486235	7.35721	1.65168-32.77177	0.00884
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cg26909981	0.14255	0.04223-0.48115	0.0017
cg00475509	14.97339	2.92072-76.76282	0.00117
cg12599168	0.11884	0.02062-0.68487	0.01715
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cg11193681	0.05477	0.00638-0.46991	0.00808
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cg15902390	4.35574	1.55708-12.18465	0.00505
cg11128216	9.2442	2.61306-32.70307	0.00056
cg17187163	9.47279	2.01789-44.46907	0.00437
cg10105884	6.90132	1.33403-35.70246	0.02124
cg14658067	6.8379	1.65183-28.3062	0.00799
cg06086887	15.47563	2.72279-87.95932	0.002
cg15037541	8.16422	2.43075-27.4214	0.00068
cg15601050	31.19722	5.53847-175.72845	1.00E-04
cg04481096	4.46739	1.11137-17.95758	0.03497
cg05771369	11.02127	1.95246-62.21289	0.00657
cg20445727	0.08925	0.01619-0.49206	0.00554
cg05782651	0.07727	0.00985-0.60593	0.01482
cg19030994	0.17409	0.04788-0.63294	0.00794
cg00706913	0.04069	0.0056-0.29551	0.00155
cg26597242	4.00879	1.25426-12.81268	0.01918

cg02205073	0.17651	0.03294-0.94574	0.04286
cg13567299	0.08862	0.01484-0.52904	0.00785
cg25353450	6.19048	2.03858-18.79839	0.0013
cg05105069	6.17532	1.96686-19.38853	0.00182
cg14156405	6.33149	2.29798-17.44483	0.00036
cg08251815	5.69793	1.18282-27.4482	0.03006
cg15363435	0.07244	0.00869-0.60363	0.01524
cg16001495	11.03395	2.87368-42.36654	0.00047
cg21230493	9.05191	1.85203-44.24187	0.0065
cg18316256	7.70142	1.79688-33.00827	0.00597
cg02469604	11.74028	2.32505-59.28226	0.00287
cg26872100	25.65534	2.77526-237.16562	0.00424
cg02193580	0.10748	0.01692-0.6826	0.01804
cg27296089	0.11857	0.0215-0.65405	0.01439
cg08336425	0.11013	0.02034-0.59629	0.01047
cg25764105	12.22847	1.75088-85.40576	0.01158
cg21234506	0.14354	0.04422-0.46598	0.00123
cg12347346	7.97889	1.21893-52.22833	0.03027
cg27373604	9.63344	2.10074-44.17636	0.00355
cg16049598	0.08901	0.01051-0.75398	0.02649
cg12861797	9.63682	1.90782-48.67772	0.00611
cg18005337	410.2067	7.01192-23997.66057	0.00375
cg20429172	7.68367	1.5993-36.91534	0.01089
cg20574490	12.53081	2.07268-75.75779	0.00589
cg11457640	9.88914	1.88787-51.80178	0.00669
cg27207493	13.34234	2.16898-82.07462	0.00519
cg00155310	4.24038	1.35414-13.27839	0.01312
cg18708013	11.09786	2.4501-50.26826	0.00179
cg01210880	0.04076	0.00356-0.46701	0.01011
cg26144458	9.32798	2.22286-39.14379	0.00228
cg02644510	4.37254	1.26674-15.09313	0.01959
cg27011060	8.69577	2.31585-32.65167	0.00136
cg15374686	7.28768	1.6042-33.10708	0.01011
cg10795666	4.36336	1.19486-15.93395	0.02579
cg09810818	12.13872	2.33938-62.98623	0.00296
cg20405017	17.44531	3.67973-82.7069	0.00032
cg22186831	8.38389	2.36611-29.70679	0.00099
cg05112555	13.86156	2.5381-75.70344	0.0024
cg12590600	27.73971	4.71547-163.18463	0.00024
cg12283119	15.07589	2.54846-89.18413	0.00278
cg27492725	8.53473	1.55901-46.72303	0.01344
cg21742836	0.05757	0.00697-0.47535	0.00804
cg09285795	15.56857	2.20501-109.92232	0.00591
cg10361547	3.8673	1.32785-11.26335	0.01314
cg02673850	0.15659	0.02721-0.90132	0.03787
cg19409687	0.10507	0.01847-0.59756	0.01107
cg12510923	0.08058	0.0112-0.57993	0.01238
cg24408656	9.03215	1.86927-43.64257	0.00618
cg04635364	5.31628	1.43588-19.68326	0.01236
cg11229543	5.41128	1.22343-23.93421	0.02603

cg00378228	26.78008	2.80434-255.73625	0.0043
cg07713026	0.05741	0.00568-0.58053	0.01549
cg21915313	16.67399	2.16788-128.24618	0.00687
cg27553162	13.95801	2.36749-82.29242	0.00359
cg27172175	16.50245	2.9852-91.22692	0.00131
cg16799087	13.35295	1.87067-95.31435	0.00975
cg20082641	12.39739	2.8143-54.61228	0.00088
cg26987597	11.11487	2.5551-48.35059	0.00132
cg18479593	14.27145	3.51803-57.89443	2.00E-04
cg23944920	8.46304	1.66131-43.11238	0.01014
cg09570348	10.71343	1.86636-61.49794	0.00782
cg17566118	4.09867	1.27397-13.18645	0.01798
cg00666105	9.48576	1.80338-49.89497	0.0079
cg17568707	11.84945	2.48941-56.40265	0.0019
cg14197071	8.31651	2.25099-30.72624	0.00149
cg04211829	11.93985	2.45328-58.11002	0.00213
cg15657888	0.03667	0.00469-0.28674	0.00163
cg05104639	6.70198	1.59861-28.09719	0.00928
cg14526718	6.66362	1.33673-33.21824	0.02066
cg20035980	0.1543	0.04516-0.52722	0.00287
cg03464416	0.14689	0.02208-0.97719	0.04727
cg08042273	12.24562	2.15929-69.44639	0.00466
cg10779454	11.78213	1.87343-74.09842	0.00856
cg08296831	4.96697	1.176-20.97849	0.02922
cg14712531	11.20794	2.64484-47.49548	0.00104
cg23524524	0.16337	0.03321-0.80354	0.02581
cg12377327	0.23552	0.06195-0.89531	0.03382
cg26704293	0.14523	0.03192-0.66066	0.01255
cg10430690	16.5605	2.00075-137.07394	0.00924
cg17802464	0.11931	0.01405-1.01328	0.05143
cg08707617	7.24747	1.65155-31.80402	0.00867
cg20319604	0.14694	0.02984-0.72365	0.01839
cg14773365	13.02818	2.98335-56.89367	0.00064
cg10961604	11.65258	3.04375-44.61034	0.00034
cg21129864	12.80666	2.24571-73.0329	0.00409
cg02639634	18.03874	3.47091-93.74938	0.00058
cg04311403	7.76067	1.43252-42.04349	0.01746
cg10576817	0.11442	0.01791-0.73078	0.02194
cg01084827	0.077	0.00601-0.98601	0.04875
cg21429394	17.53655	2.85168-107.84212	0.002
cg00178359	11.15862	1.75942-70.77022	0.01048
cg13800209	17.31831	4.14726-72.31861	9.00E-05
cg04392209	0.03895	0.00191-0.795	0.03494
cg19426955	27.78122	3.62276-213.04114	0.00138
cg19767622	6.24597	1.48011-26.3576	0.01264
cg26651775	0.24785	0.06444-0.95334	0.04241
cg24055703	15.49207	2.12293-113.05341	0.00689
cg02581727	0.09399	0.01411-0.62595	0.01452
cg09687738	4.11827	1.21397-13.97076	0.02314
cg23637494	6.72901	1.2975-34.89766	0.0232

cg17489908	8.61484	2.00833-36.95378	0.00375
cg19585433	0.13351	0.03348-0.53236	0.00433
cg00006815	0.11667	0.01943-0.70056	0.01882
cg03099771	9.64808	1.65213-56.34279	0.01182
cg13270055	7.08526	1.35915-36.93548	0.02011
cg09166536	7.88839	1.38426-44.9532	0.02001
cg02407342	11.87935	3.27635-43.07204	0.00017
cg17345373	0.18027	0.03965-0.81965	0.0266
cg07172885	0.1076	0.01687-0.68647	0.01838
cg22097249	8.14636	2.16233-30.69053	0.00194
cg07429087	0.14308	0.03707-0.55229	0.00478
cg26806511	0.09229	0.01102-0.77264	0.02796
cg25950278	11.23202	2.35286-53.61915	0.00242
cg21109542	0.1527	0.02485-0.93827	0.04248
cg14471364	5.97982	1.63134-21.91949	0.00697
cg14097304	9.30097	2.56109-33.77785	7.00E-04
cg17236781	0.10971	0.01462-0.82352	0.03165
cg07963234	5.45936	1.70194-17.51215	0.00432
cg05554151	31.8047	2.89255-349.70509	0.00468
cg22813950	8.19661	1.32617-50.66039	0.02359
cg05559023	6.61671	1.36842-31.99372	0.01877
cg06104859	0.13332	0.03442-0.51647	0.00354
cg08097882	6.625	1.61755-27.13402	0.00858
cg01047586	6.61876	1.60894-27.22781	0.00882
cg06282524	5.71059	1.36175-23.94776	0.01721
cg04136185	11.30009	1.89968-67.21774	0.00769
cg10095226	8.83342	2.12356-36.74449	0.00274
cg14209781	12.33656	2.23218-68.18037	0.00397
cg08663552	22.10624	2.06349-236.82443	0.01051
cg21944224	23.94837	3.47837-164.88284	0.00125
cg08369368	10.80687	2.50513-46.61974	0.00142
cg00857536	0.0778	0.01417-0.42719	0.00329
cg16735881	10.80928	2.03538-57.40487	0.0052
cg17996619	4.97358	1.25675-19.6828	0.02228
cg06027835	0.19101	0.0372-0.98074	0.04734
cg26130581	0.0873	0.01433-0.53192	0.00818
cg10592454	12.66282	2.11039-75.97994	0.00549
cg15268456	10.42711	2.18672-49.72051	0.00326
cg20909686	8.19668	2.18674-30.72411	0.00181
cg00718539	20.30828	1.76063-234.24936	0.01581
cg27644869	12.71998	1.82305-88.7512	0.01029
cg07896193	0.11414	0.01563-0.83323	0.03237
cg15503722	4.01316	1.12521-14.31329	0.03221
cg14725109	0.05589	0.00418-0.74704	0.02923
cg10109146	0.09085	0.01112-0.74206	0.0252
cg20606555	18.31814	2.57059-130.53598	0.0037
cg27312652	11.81836	1.56724-89.12095	0.01658
cg18045515	2.70616	0.90601-8.08302	0.07456
cg00445126	12.31038	2.04811-73.99276	0.00608
cg03068068	0.09673	0.02684-0.34864	0.00036

cg04547675	6.07588	1.66177-22.21499	0.00638
cg17964359	0.10243	0.01283-0.81754	0.03155
cg13914094	5.99622	1.28286-28.02694	0.02281
cg01403532	7.21608	1.63246-31.89768	0.00915
cg24995836	6.14026	1.48856-25.32847	0.01207
cg26144594	6.00975	1.36747-26.41171	0.01758
cg23677243	4.09684	1.23042-13.64099	0.02157
cg23752828	0.17257	0.05097-0.58432	0.00475
cg26581449	0.11795	0.02126-0.6543	0.01448
cg15868105	6.79182	1.39309-33.11257	0.01778
cg22272888	0.22759	0.06798-0.76199	0.01636
cg12011522	12.39773	2.08833-73.60142	0.0056
cg16336989	0.16587	0.03093-0.88961	0.03604
cg25144893	4.06387	1.34231-12.30349	0.01311
cg15388196	6.34338	1.72268-23.35807	0.00547
cg21280392	0.08528	0.01025-0.70976	0.02278
cg24781737	0.13207	0.02216-0.78726	0.02624
cg24714905	9.35553	2.71302-32.2614	4.00E-04
cg02124059	0.10457	0.01258-0.86896	0.03662
cg14091713	0.15794	0.02871-0.86888	0.03388
cg06908232	0.18005	0.03516-0.92191	0.03963
cg03831206	0.0515	0.00396-0.67001	0.02346
cg11111740	4.04148	1.01221-16.13653	0.04802
cg14684434	8.4864	2.45575-29.3267	0.00072
cg09761040	5.50924	1.46911-20.66	0.0114
cg02763101	4.26026	1.07345-16.90799	0.03933
cg23074992	6.58539	1.43191-30.2865	0.01547
cg02904442	44.78666	3.92441-511.12025	0.00221
cg07499899	14.08307	2.14149-92.6142	0.00592
cg12157364	5.59988	1.42608-21.98931	0.01357
cg10983544	10.88554	2.0809-56.94412	0.00468
cg01615333	11.14765	1.53941-80.72586	0.01698
cg19580826	0.09252	0.01014-0.84404	0.03483
cg00605988	6.68541	1.16986-38.20535	0.03265
cg04159302	0.14213	0.03602-0.56077	0.00534
cg17044023	0.16653	0.02652-1.04558	0.05582
cg08499046	3.04904	0.89213-10.42068	0.07542
cg16199850	0.11049	0.02175-0.56121	0.00789
cg07210774	0.22711	0.05514-0.93541	0.04013
cg20743662	0.09313	0.01558-0.55682	0.00928
cg07398839	6.01121	1.08056-33.44069	0.04052
cg11756870	6.7902	1.36158-33.86282	0.01947
cg20340302	8.46266	2.16198-33.12552	0.00216
cg26105341	0.18149	0.032-1.02916	0.05392
cg00381755	15.15631	2.58812-88.757	0.00257
cg08425203	6.82734	1.46998-31.70959	0.01422
cg03679521	10.27603	1.64642-64.13731	0.01264
cg26795312	0.1884	0.04631-0.7664	0.01972
cg26429783	7.49901	1.10863-50.72497	0.03886
cg21872782	12.30742	2.20385-68.73093	0.00423

cg21019788	0.18412	0.035-0.96854	0.04575
cg23171231	11.5895	1.3634-98.51609	0.02484
cg24592892	11.84979	2.01694-69.61921	0.00621
cg20288000	8.86583	1.77925-44.1776	0.00774
cg15826897	7.21013	1.78014-29.20325	0.00564
cg27545611	3.93209	0.82001-18.85504	0.08692
cg18628255	0.12656	0.02915-0.54959	0.0058
cg01544903	9.5921	2.30697-39.88277	0.00187
cg14098847	10.25378	1.88429-55.79813	0.00708
cg22519102	0.17057	0.0362-0.80379	0.02534
cg24910675	0.18185	0.03004-1.10061	0.06351
cg17854454	3.56768	1.03047-12.35198	0.04471
cg14054928	10.45404	1.6076-67.98152	0.01401
cg17916960	10.37661	2.82246-38.14903	0.00043
cg13433278	6.78811	1.65021-27.92279	0.00795
cg18869840	19.90494	1.71158-231.48546	0.01688
cg22946648	0.14156	0.01679-1.19342	0.07227
cg08434396	0.12032	0.01858-0.77929	0.02631
cg03732411	0.22147	0.05095-0.96274	0.04437
cg24361079	0.13841	0.02388-0.80215	0.02739
cg18344930	6.36216	1.50513-26.89271	0.01187
cg12530021	0.08928	0.01353-0.58912	0.01209
cg24142775	0.17482	0.03115-0.98112	0.04752
cg01000615	6.88041	1.32179-35.81495	0.02194
cg21123686	12.1755	1.6319-90.84079	0.01479
cg10848980	0.18611	0.03525-0.98248	0.04761
cg02143487	6.62709	1.91665-22.91414	0.00281
cg09850561	0.16314	0.03214-0.82817	0.02871
cg04134528	8.48755	1.52664-47.18756	0.01455
cg06921685	0.10882	0.0112-1.05712	0.05587
cg08855449	10.40327	1.81919-59.49259	0.00847
cg18769303	0.29199	0.07515-1.1345	0.07545
cg03161309	0.15337	0.03629-0.64823	0.01079
cg14563954	7.21291	1.69376-30.71621	0.00752
cg21643178	0.10757	0.02448-0.47275	0.00316
cg26956007	0.22404	0.04464-1.12451	0.06916
cg02678482	0.08193	0.01163-0.57703	0.012
cg16316394	11.59519	1.64067-81.94704	0.01404
cg22824415	0.21748	0.04778-0.98997	0.0485
cg02410245	0.04024	0.00479-0.3378	0.00308
cg12999084	0.21067	0.05937-0.74749	0.01594
cg18135555	11.78585	1.38623-100.20433	0.02388
cg25027167	6.96268	1.07661-45.02914	0.0416
cg04929703	7.16579	1.37331-37.39042	0.01948
cg27274135	6.1882	1.69243-22.62655	0.00586
cg04345928	0.16436	0.03045-0.88714	0.0358
cg11521079	6.96562	1.82338-26.60992	0.00453
cg25205946	0.33372	0.11137-1.00002	0.05
cg04560225	3.89729	1.04879-14.48227	0.04225
cg16809762	0.10151	0.02683-0.38408	0.00075

cg26345105	9.17064	1.52034-55.31686	0.01565
cg23708288	0.21025	0.04026-1.0981	0.06446
cg07793148	6.04734	1.42758-25.61694	0.01455
cg18781988	3.8667	1.07761-13.87464	0.03802
cg18206027	4.14403	1.21746-14.10567	0.02292
cg11101117	20.05567	3.51624-114.39205	0.00074
cg20074774	0.2035	0.04056-1.02104	0.05303
cg02330362	0.18162	0.03323-0.99274	0.04902
cg23619357	4.96425	1.24303-19.82552	0.02334
cg01057599	0.08814	0.01045-0.74305	0.02555
cg22018083	11.82374	1.91632-72.95282	0.0078
cg25927227	0.09891	0.01368-0.71491	0.02188
cg23545906	0.0753	0.00824-0.6878	0.02193
cg21320573	0.10787	0.02514-0.46292	0.00273
cg20981089	0.16295	0.02243-1.18357	0.07291
cg07532353	3.8122	1.30125-11.1684	0.01468
cg02372786	5.20064	1.31313-20.59709	0.01888
cg26292521	5.92673	1.45934-24.0699	0.01283
cg04388383	0.2431	0.06479-0.91212	0.03606
cg21229153	0.09842	0.01326-0.7307	0.02341
cg17058724	0.26439	0.06891-1.01442	0.05249
cg05050657	5.45715	1.27605-23.33813	0.02209
cg19586382	0.15876	0.03346-0.75331	0.02053
cg08598654	8.70182	1.56557-48.36693	0.01343
cg27258050	0.24471	0.08498-0.70466	0.00909
cg05419227	0.10154	0.01219-0.84597	0.03446
cg04029630	0.23036	0.057-0.93107	0.03938
cg11950860	0.13246	0.02941-0.59659	0.00847
cg08623691	0.15259	0.02317-1.00482	0.05059
cg25436127	0.13998	0.02166-0.90453	0.03889
cg15317927	0.22529	0.04892-1.03757	0.0558
cg03335173	0.26528	0.07617-0.92395	0.03714
cg26331172	8.38243	1.93163-36.37608	0.00452
cg16645983	7.57806	1.38771-41.3826	0.01937
cg09923769	10.03543	2.042-49.31926	0.00453
cg25529889	0.16928	0.02709-1.05779	0.05745
cg05237970	0.10025	0.01019-0.98651	0.04865
cg16792302	6.11552	0.72381-51.67042	0.09629
cg06174815	0.12564	0.0145-1.08874	0.05973
cg13928116	0.20065	0.03713-1.08437	0.06206
cg10375890	2.39123	0.59668-9.58295	0.21836
cg02306630	14.00105	2.89204-67.78244	0.00104
cg26720125	9.27314	2.3204-37.05875	0.00163
cg05059648	0.25127	0.06003-1.05167	0.05863
cg24142603	0.12163	0.03416-0.43307	0.00115
cg25156485	0.19505	0.03859-0.986	0.04804
cg01984798	18.84335	1.94839-182.23898	0.01121
cg03933846	0.30922	0.08119-1.17776	0.0854
cg06512128	0.17292	0.03134-0.95416	0.04403
cg01056373	0.31179	0.08258-1.17719	0.08556

cg19622623	5.86503	1.43855-23.91196	0.01362
cg05368341	5.97135	1.17697-30.29544	0.03104
cg18064631	5.08879	1.22685-21.10746	0.02498
cg00253811	0.23721	0.04856-1.15866	0.07541
cg06030846	7.35072	1.25984-42.88871	0.02665
cg18925560	0.08289	0.00617-1.11401	0.06031
cg01166827	0.1406	0.03402-0.58108	0.00673
cg16132139	0.17477	0.02994-1.02011	0.05264
cg18597991	0.22678	0.05019-1.02471	0.05382
cg10511972	0.14309	0.02003-1.0223	0.05263
cg00525383	6.37745	1.15168-35.31537	0.03386
cg03870816	0.2163	0.05588-0.83724	0.02661
cg03219705	0.18788	0.03679-0.9596	0.04448
cg27483342	4.62403	0.9704-22.03391	0.05458
cg03718079	0.17427	0.02648-1.14676	0.06914
cg09906922	6.42093	0.84197-48.96669	0.07281
cg09994035	11.4086	2.00803-64.81791	0.00602
cg25367647	0.11895	0.01464-0.9662	0.04636
cg19814934	3.41492	1.15103-10.13151	0.02687
cg08410996	6.1297	1.72807-21.74291	0.005
cg03315557	9.12485	1.7846-46.6564	0.00792
cg02589074	0.18656	0.02803-1.24153	0.08252
cg16566391	0.18322	0.03418-0.98204	0.04758
cg10068408	16.87758	2.62918-108.34284	0.00289
cg05387565	0.10375	0.01258-0.85578	0.03532
cg14304817	6.38595	1.27155-32.07126	0.02434
cg17404000	0.09445	0.01018-0.87668	0.03792
cg08784129	10.30949	2.19791-48.35752	0.00309
cg26811372	3.68125	1.0177-13.31586	0.04695
cg08310088	0.09452	0.01625-0.5497	0.00864
cg00085732	7.58021	1.11169-51.68682	0.03863
cg07136610	0.11244	0.01377-0.91792	0.04136
cg08029969	10.53953	2.18596-50.81612	0.00334
cg01555661	0.20113	0.03378-1.19751	0.07808
cg19436320	8.03753	1.76512-36.59907	0.00705
cg09996779	0.23557	0.05513-1.00668	0.05106
cg03517379	0.16694	0.0257-1.08424	0.06076
cg00364758	0.34958	0.07875-1.55172	0.16692
cg20664065	0.1384	0.02106-0.90956	0.03953
cg12980127	4.89969	1.51103-15.88783	0.0081
cg17297238	7.52931	1.16719-48.57005	0.0338
cg04866639	0.33303	0.07725-1.43578	0.14026
cg11859478	0.15775	0.02064-1.2056	0.07511
cg12115302	10.20254	1.23377-84.3688	0.03117
cg26386673	10.38551	1.99682-54.01521	0.0054
cg06506080	0.13629	0.01504-1.23487	0.07634
cg00098732	4.47189	0.88536-22.58723	0.06989
cg22608646	0.12877	0.02453-0.67605	0.01541
cg06769752	0.21711	0.04029-1.16991	0.07551
cg17651959	6.87793	1.68878-28.01199	0.00712

cg07327405	0.12077	0.01744-0.83613	0.03225
cg27599792	8.45139	1.02186-69.89796	0.0477
cg00150874	16.50594	1.59421-170.8968	0.01872
cg08575537	5.02497	1.49947-16.83955	0.00888
cg09192059	0.22184	0.02469-1.9932	0.17887
cg00769799	0.26822	0.07053-1.01998	0.05349
cg09992746	8.04707	1.76025-36.78749	0.00716
cg06833823	0.2387	0.03678-1.54921	0.1333
cg05940452	10.71428	1.79294-64.02664	0.00932
cg02615468	0.28659	0.06163-1.33256	0.11098
cg07750402	0.34627	0.10867-1.10337	0.07288
cg16632346	0.14034	0.02959-0.66576	0.01343
cg12078211	0.17025	0.0352-0.82336	0.02769
cg25852925	0.26566	0.06075-1.16172	0.07827
cg03310203	0.17943	0.03497-0.92072	0.0395
cg04653083	0.23688	0.05598-1.00237	0.05038
cg16809293	8.04743	1.87107-34.61183	0.00508
cg05575921	12.32891	1.95516-77.74413	0.0075
cg08778681	0.29048	0.06364-1.32585	0.11052
cg03564727	0.43917	0.14669-1.31481	0.14135
cg13931285	13.15355	2.19809-78.71192	0.00476
cg21364077	4.38214	0.90191-21.29175	0.06696
cg01479413	0.33314	0.08547-1.29843	0.11326
cg18552380	5.65289	1.08528-29.44431	0.03967
cg03287877	0.12948	0.02287-0.73306	0.02083
cg21625817	5.92744	1.41857-24.76763	0.01472
cg16462075	0.11982	0.01505-0.95399	0.04502
cg10168149	4.24527	1.30697-13.7894	0.01616
cg03079395	6.03139	1.72265-21.11727	0.00494
cg23431897	0.32104	0.09078-1.1354	0.07791
cg10873964	0.17396	0.02637-1.14746	0.06921
cg13988667	0.20762	0.03091-1.39474	0.10575
cg13077262	21.71108	2.854-165.16178	0.00295
cg16679837	0.28687	0.05094-1.61542	0.15675
cg18725867	3.1082	0.81169-11.9022	0.09784
cg06443644	6.75325	1.192-38.26039	0.03089
cg17125742	0.21636	0.02888-1.62112	0.13628
cg23860088	0.12397	0.01321-1.16322	0.06761
cg21945665	0.16836	0.02328-1.21755	0.07757
cg05559795	0.25737	0.05115-1.29507	0.0997
cg03659340	0.19759	0.03237-1.20619	0.07894
cg15323528	6.45239	1.32561-31.40689	0.02094
cg22495388	6.80736	1.31778-35.16539	0.02206
cg19585278	3.98995	1.24106-12.82746	0.02021
cg22647546	7.23476	0.8375-62.49756	0.07205
cg01443426	8.16974	1.33553-49.97634	0.02302
cg15042310	4.29534	1.28572-14.34989	0.01787
cg01665555	4.6751	1.11017-19.68759	0.03552
cg15035911	4.24913	1.03761-17.40073	0.0443
cg22491141	7.52683	1.67988-33.72452	0.00834

cg08213689	6.55783	1.0774-39.91589	0.04126
cg23269489	0.11063	0.01235-0.99114	0.04908
cg25809290	5.55995	0.993-31.13105	0.05094
cg05656180	3.31625	0.6671-16.48551	0.14287
cg24195365	0.22186	0.04445-1.10737	0.06641
cg26133164	10.94386	2.1179-56.55048	0.0043
cg26328954	0.12171	0.02307-0.6422	0.01307
cg19047340	5.42225	1.14484-25.68127	0.03314
cg09072865	0.37661	0.12316-1.1517	0.08684
cg27438889	4.94378	0.85983-28.42543	0.07334
cg09195491	0.20952	0.03484-1.25993	0.08772
cg08115220	0.1602	0.01835-1.39874	0.09763
cg13993218	0.10791	0.01862-0.62522	0.01299
cg04143870	5.98838	1.09918-32.62492	0.03852
cg10055097	0.36808	0.12231-1.10765	0.07539
cg27248583	0.09934	0.00882-1.11868	0.0616
cg01062020	0.30383	0.08575-1.07655	0.06494
cg07145783	0.16648	0.03353-0.82667	0.02832
cg04402486	0.26001	0.06629-1.01981	0.05338
cg26672952	16.64082	2.22618-124.39084	0.00615
cg13848989	6.99121	1.52746-31.99886	0.01222
cg21839338	6.42969	0.91479-45.19176	0.06142
cg20883831	5.22662	1.32855-20.56187	0.01796
cg00450319	5.86674	1.15099-29.90339	0.03324
cg16641060	0.42319	0.15285-1.17163	0.09791
cg13613450	5.94543	1.16831-30.25589	0.03177
cg08215169	0.25505	0.05564-1.16907	0.0786
cg05537653	23.58497	2.29922-241.93009	0.00779
cg11675165	0.2787	0.05795-1.34026	0.11083
cg01581018	3.48113	0.79936-15.15993	0.09658
cg26584545	16.67413	2.69235-103.26547	0.00249
cg17658468	0.21178	0.04124-1.08741	0.06295
cg04487857	7.91914	1.66209-37.73129	0.00938
cg05288927	0.19784	0.0283-1.38321	0.10247
cg03102729	0.33697	0.0986-1.15164	0.08278
cg11016745	0.27801	0.06617-1.16801	0.08048
cg00652772	5.04166	1.2521-20.30067	0.02283
cg20477160	0.27895	0.07164-1.08619	0.06566
cg19013611	7.00697	1.39958-35.0803	0.01784
cg20442640	0.2326	0.05291-1.02253	0.05355
cg25825506	5.36951	1.36821-21.07256	0.01598
cg20501518	7.2713	1.35054-39.14853	0.0209
cg08108619	0.30122	0.08153-1.11295	0.07194
cg23906060	6.99594	0.93934-52.10376	0.05758
cg00936342	0.16993	0.03278-0.88079	0.03476
cg19800913	0.28428	0.0646-1.25111	0.09618
cg05219493	8.6903	1.74552-43.26595	0.00829
cg19741073	0.27195	0.06092-1.21402	0.08803
cg06241901	9.3877	1.78183-49.4599	0.00826
cg09786233	0.18388	0.02751-1.22887	0.08058

cg10543450	5.68696	1.39778-23.13785	0.0152
cg02538330	0.18342	0.02314-1.45414	0.10838
cg09988116	15.30419	2.30673-101.53695	0.00472
cg26359958	0.21381	0.03449-1.3256	0.09748
cg02264182	0.36779	0.10199-1.32632	0.12641
cg21113886	0.36637	0.07954-1.68752	0.19757
cg15189015	0.25424	0.07609-0.84944	0.02608
cg06714180	3.7026	0.94152-14.56078	0.06097
cg00301396	6.68127	1.20537-37.03361	0.02972
cg19506937	0.08989	0.01043-0.77499	0.02839
cg09054333	0.29619	0.06042-1.452	0.13357
cg06957447	4.84816	1.08951-21.57353	0.03822
cg05017302	9.8443	1.07715-89.96909	0.04279
cg19364021	0.16108	0.02987-0.86864	0.03369
cg23221544	0.08432	0.00904-0.78611	0.02991
cg26342575	0.29074	0.08105-1.04297	0.05804
cg08479532	0.43491	0.15699-1.20481	0.10925
cg25952964	7.6701	0.91075-64.5959	0.06093
cg13308964	6.55885	1.44297-29.8125	0.01491
cg18828303	0.37903	0.10412-1.37979	0.14112
cg11839979	0.20718	0.03743-1.14689	0.07139
cg20761810	0.37406	0.11279-1.24054	0.10793
cg15729404	7.51086	1.69475-33.28686	0.00794
cg02468250	5.75616	1.06699-31.05324	0.04181
cg10869271	0.16176	0.01883-1.38975	0.09691
cg08805386	0.09354	0.01127-0.77621	0.02819
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cg00258480	0.37114	0.10064-1.36868	0.13659
cg06899582	0.15982	0.0155-1.64771	0.12345
cg14974711	4.29415	0.92818-19.86653	0.06224
cg16949923	0.33231	0.0667-1.65568	0.17876
cg18275647	0.31616	0.08325-1.2007	0.09078
cg03559942	0.18492	0.04644-0.73638	0.01666
cg14430524	0.28405	0.07089-1.13828	0.07555
cg05973455	5.47644	0.90781-33.03712	0.06367
cg15347342	10.33016	1.94279-54.92737	0.00616
cg23623404	0.35871	0.09012-1.42776	0.14575
cg05114959	0.14754	0.01695-1.28429	0.08304
cg16594779	0.37118	0.09798-1.40623	0.14475
cg01860944	0.2386	0.0588-0.96832	0.04496
cg11700800	5.71927	1.10832-29.51309	0.03727
cg02248763	0.30367	0.06396-1.44188	0.13374
cg05117693	0.0845	0.0093-0.76788	0.0282
cg21988739	0.28928	0.07062-1.18499	0.0847
cg27254482	7.7102	1.39067-42.74711	0.01942
cg18466173	0.20128	0.0371-1.09204	0.06318
cg25549619	0.29555	0.0714-1.22338	0.09261

cg16403901	0.3645	0.1002-1.32599	0.12559
cg03065447	7.65904	1.82238-32.18919	0.00545
cg07213684	0.22707	0.03938-1.3094	0.09724
cg07581732	5.77749	1.17681-28.36423	0.03073
cg16059374	0.3649	0.1036-1.28522	0.11657
cg25016544	0.22118	0.03821-1.28041	0.09217
cg22417589	0.33883	0.09617-1.19373	0.09211
cg18452672	0.16516	0.0206-1.32441	0.08999
cg26936230	0.38356	0.11609-1.26727	0.11606
cg05969378	7.77458	1.40571-42.99896	0.01876
cg04258219	3.65571	0.96717-13.81787	0.05604
cg08867933	0.22336	0.04907-1.01674	0.05256
cg11107468	0.34187	0.08292-1.40954	0.13754
cg01162494	10.64381	0.92603-122.34013	0.05766
cg24772920	0.17795	0.02284-1.3863	0.09933
cg06783548	0.38139	0.12311-1.1815	0.09475
cg21912448	3.94291	0.77591-20.03641	0.09811
cg19929967	0.31648	0.07556-1.32561	0.11543
cg18112782	0.28549	0.07074-1.1522	0.07825
cg22039909	8.31407	1.62699-42.48575	0.01093
cg08590987	0.27978	0.07158-1.09354	0.06704
cg21304892	0.25759	0.05508-1.20472	0.08483
cg09695261	4.41258	1.01914-19.1051	0.04711
cg22050539	0.11167	0.01208-1.03194	0.05333
cg06793796	0.21984	0.05238-0.92268	0.03846
cg03806192	0.44592	0.15524-1.28092	0.13359
cg12280901	0.2046	0.03853-1.0865	0.06252
cg09070095	0.34852	0.08859-1.37113	0.13148
cg05134041	4.37587	1.02641-18.65554	0.04602
cg17531456	0.15084	0.0199-1.14342	0.06721
cg23218559	4.23917	1.0252-17.52885	0.04612
cg26647197	2.91563	0.81207-10.46814	0.10084
cg03266453	3.51495	0.64467-19.16459	0.14633
cg19194595	0.28483	0.0624-1.30016	0.10499
cg27147258	0.24262	0.04186-1.40633	0.11419
cg18557185	3.65559	0.60783-21.98534	0.15675
cg12813325	0.3349	0.07151-1.56846	0.16495
cg10950413	0.23989	0.05388-1.06816	0.06101
cg07184316	0.25928	0.06699-1.00352	0.0506
cg12910797	7.10215	0.64287-78.46133	0.10971
cg19474888	0.19649	0.04735-0.81541	0.02503
cg16306900	5.33875	0.65811-43.30956	0.11683
cg23690264	0.35597	0.1034-1.22547	0.1015
cg07061728	0.23844	0.03297-1.72447	0.15556
cg10697737	11.62609	1.87566-72.06317	0.0084
cg24620761	7.35803	1.30549-41.47158	0.02369
cg24789180	4.08139	0.68804-24.21032	0.12154
cg21327581	0.3599	0.10764-1.20334	0.09704
cg02698615	0.2836	0.05979-1.34526	0.11261
cg20018767	0.21741	0.03767-1.25484	0.08798

cg04029664	0.28701	0.06504-1.26647	0.09934
cg24536244	0.21714	0.03632-1.29804	0.09413
cg18216249	2.87886	0.64595-12.8305	0.16551
cg13300521	9.36708	1.31362-66.79441	0.02561
cg16152676	9.25134	1.02591-83.42596	0.04739
cg27109043	5.80629	1.34338-25.09561	0.01851
cg03222990	0.21056	0.04104-1.08031	0.06185
cg17851725	5.01323	0.91635-27.42673	0.063
cg14930065	7.53759	0.90823-62.55638	0.06137
cg06948492	2.90185	0.8454-9.96061	0.09044
cg07137581	0.2877	0.04912-1.68523	0.16718
cg06448603	7.18818	1.29856-39.79003	0.02387
cg23237972	3.11181	0.53716-18.02712	0.20531
cg12560320	6.23091	1.30266-29.80393	0.02196
cg21591452	6.81	1.19605-38.7744	0.03064
cg00297876	5.43439	1.30646-22.60505	0.01994
cg20801711	4.8699	0.8075-29.36972	0.08421
cg02856716	0.11205	0.01429-0.87873	0.03725
cg00624737	5.38479	0.86459-33.53738	0.07122
cg20081453	0.26706	0.068-1.04888	0.05855
cg00167275	0.14197	0.0174-1.15841	0.06835
cg01523763	4.34616	0.88321-21.38699	0.07073
cg21962901	4.51816	0.79849-25.5653	0.0881
cg18406472	0.40846	0.13414-1.24379	0.11503
cg02365303	0.17068	0.0325-0.89652	0.0367
cg14972002	0.15333	0.02363-0.99515	0.04941
cg06400167	0.29537	0.05328-1.63731	0.16281
cg20111321	7.35653	0.76438-70.80064	0.0841
cg08800033	0.29159	0.05913-1.43794	0.13007
cg01058070	5.65434	1.1745-27.22147	0.03073
cg00691830	3.8579	0.88301-16.85523	0.07272
cg27665489	0.29507	0.06664-1.30651	0.10788
cg23954206	0.34291	0.08809-1.33475	0.1227
cg25425140	4.25578	1.02814-17.61586	0.04569
cg26334166	17.62883	1.52058-204.3802	0.02172
cg19045344	4.36614	0.93663-20.35288	0.06057
cg05497345	5.74714	1.20228-27.47245	0.02847
cg09907936	2.60285	0.87376-7.75366	0.08586
cg08038219	0.10834	0.01708-0.68732	0.01839
cg13869648	0.49175	0.13054-1.85243	0.29422
cg26751631	0.16401	0.03138-0.85734	0.03216
cg02805922	0.23286	0.04666-1.16216	0.07561
cg03862854	5.47313	1.23298-24.29495	0.02539
cg27537972	5.87921	1.0983-31.47144	0.0385
cg12527112	0.3789	0.08796-1.63209	0.19274
cg10796749	0.21318	0.0488-0.93123	0.03991
cg10521480	6.99564	1.36265-35.9146	0.01977
cg04139223	2.66875	0.65715-10.83805	0.16981
cg21290313	6.68998	1.21968-36.69475	0.02862
cg09520414	0.16088	0.0171-1.51356	0.11014

cg14846442	6.0749	0.84268-43.79397	0.07343
cg07557423	2.82814	0.73806-10.8371	0.12931
cg07825508	0.35545	0.07892-1.60098	0.17796
cg01374431	0.27554	0.06296-1.206	0.08703
cg25892640	0.32322	0.0779-1.34104	0.11977
cg16676177	0.15314	0.02792-0.83988	0.0307
cg06431681	9.65316	1.21489-76.70094	0.03203
cg19658849	0.21352	0.04121-1.10622	0.06581
cg09418623	0.37189	0.07697-1.79681	0.2184
cg16161440	0.30219	0.04305-2.12112	0.22873
cg25746778	3.46427	0.87616-13.69746	0.07648
cg00346208	6.7818	1.90929-24.08905	0.00308
cg22913932	0.22025	0.03341-1.45212	0.11588
cg05532446	0.17903	0.02747-1.16699	0.0721
cg14318197	5.08411	1.4501-17.82516	0.01107
cg03432955	4.76919	0.96346-23.60766	0.05557
cg20407861	8.48639	1.81859-39.60154	0.00651
cg09496273	6.0359	0.79557-45.79355	0.08208
cg17010747	9.26885	1.60552-53.51023	0.0128
cg06965300	0.23788	0.04339-1.30419	0.09812
cg19043574	4.15133	0.9111-18.91504	0.06582
cg13504740	5.60307	0.92954-33.77425	0.06008
cg19062189	0.41854	0.14837-1.18066	0.09974
cg00361609	6.67	1.74649-25.47331	0.00551
cg22265142	0.27727	0.06985-1.10058	0.0682
cg26112661	0.13797	0.0191-0.99679	0.04963
cg22864689	0.13802	0.02694-0.70708	0.01751
cg09662907	0.21804	0.0329-1.44498	0.11446
cg03717424	6.14025	0.76686-49.16501	0.08729
cg00596763	7.87875	1.34323-46.2131	0.0222
cg13717446	3.03366	1.05571-8.71744	0.03934
cg13923018	0.37726	0.12588-1.13058	0.08172
cg05905814	0.25943	0.04544-1.48109	0.129
cg15692360	6.3653	1.13397-35.73012	0.03548
cg19867250	5.16169	1.02677-25.94848	0.04637
cg06158088	0.3494	0.09921-1.23055	0.10163
cg10446869	7.44242	1.34229-41.26514	0.02163
cg22575892	0.38184	0.12032-1.21175	0.10226
cg09742177	0.27783	0.06181-1.24889	0.09489
cg20047489	2.96417	0.82343-10.67039	0.09638
cg04101819	5.93437	0.84222-41.81399	0.07384
cg13840174	0.33809	0.07634-1.49724	0.15319
cg15673034	3.86708	1.13023-13.23119	0.03116
cg03332892	4.20788	0.86265-20.52535	0.07553
cg19965300	0.24179	0.055-1.063	0.06023
cg05062413	0.22224	0.0441-1.11988	0.06834
cg10105844	0.34948	0.08643-1.41308	0.14025
cg10800369	5.82992	0.99264-34.23997	0.05096
cg01794103	0.2561	0.08084-0.81127	0.02059
cg11717280	3.67744	0.86623-15.61201	0.07752

cg22455725	5.37652	0.99484-29.05696	0.05071
cg16456252	5.12116	1.25984-20.81714	0.02244
cg00877329	4.1614	0.74037-23.38997	0.10551
cg18771553	5.20239	0.63615-42.54514	0.12403
cg18891924	5.22507	1.47446-18.51615	0.01042
cg03575969	13.07471	1.5937-107.26525	0.01667
cg20686234	2.55056	0.65165-9.98286	0.17867
cg16088894	7.09469	1.18807-42.36657	0.03164
cg13375624	0.16963	0.0295-0.9754	0.04683
cg22975864	0.34409	0.07072-1.67428	0.18632
cg24533311	0.24779	0.03719-1.65106	0.14936
cg01074584	0.29186	0.07614-1.11874	0.07245
cg10632209	6.22681	1.03606-37.42369	0.04564
cg21056706	4.7673	1.24659-18.23149	0.02249
cg03392386	0.30128	0.10024-0.90551	0.03262
cg01353788	0.33084	0.07622-1.43604	0.13973
cg13486805	5.65474	0.99624-32.09663	0.0505
cg18755798	4.06967	0.56599-29.26215	0.16317
cg07516457	0.24319	0.04895-1.20832	0.08388
cg24260882	0.1459	0.0142-1.49929	0.10539
cg05637536	3.40787	0.64904-17.89351	0.14731
cg17678645	0.13133	0.01428-1.20816	0.07298
cg16857771	0.22631	0.02367-2.16381	0.19709
cg14804181	0.51125	0.20357-1.28394	0.15329
cg17418692	7.10591	1.4907-33.87269	0.01385
cg23687269	0.19934	0.03583-1.10908	0.06551
cg15037004	5.92049	0.38569-90.88235	0.20187
cg00426668	2.80448	0.87627-8.97573	0.08231
cg13535212	2.79744	0.67074-11.66725	0.158
cg22561883	0.40101	0.11997-1.34036	0.13776
cg09576209	6.53575	1.03853-41.13133	0.04547
cg04180086	2.44424	0.71042-8.40952	0.15629
cg26515460	4.3712	0.8193-23.3217	0.08423

Table S2. 9 DNA methylation signature-related biological pathways. ‘Cor’ represented the pearson correlations between the methylation risk score and GSVA score. ‘P value’ stood for significance of pearson correlations.

ID	corr	pvalue
RHODES_CANCER_META_SIGNATURE	0.4398	1.1E-14
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_CYTOCHROME_C_RELEASE	0.4385	1.3E-14
MORI_MATURE_B_LYMPHOCYTE_DN	0.4375	1.6E-14
BIOCARTA_RANMS_PATHWAY	0.4	5.5

	292	5E-
	62	14
	0.4	4.6
BURTON_ADIPOGENESIS_PEAK_AT_24HR	145	7E-
	92	13
	0.4	6.6
OHASHI_AURKA_TARGETS	121	2E-
	16	13
	0.4	6.9
NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP	117	3E-
	88	13
	0.4	7.1
BASSO_B_LYMPHOCYTE_NETWORK	116	1E-
	01	13
	0.4	9.1
SASAKI_ADULT_T_CELL_LEUKEMIA	097	9E-
	7	13
	0.4	9.7
BHATTACHARYA_EMBRYONIC_STEM_CELL	093	2E-
	68	13
	0.4	9.8
SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN	093	1E-
	02	13
	0.4	1.2
XU_CREBBP_TARGETS_UP	074	6E-
	97	12
	0.4	2.7
ZHAN_MULTIPLE_MYELOMA_CD1_UP	017	7E-
	38	12
	0.3	3.5
KAPOSI_LIVER_CANCER_MET_UP	999	4E-
	23	12
	0.3	6.0
LY_AGING_MIDDLE_DN	958	9E-
	66	12
	0.3	6.3
WANG_CISPLATIN_RESPONSE_AND_XPC_UP	955	1E-
	99	12
	0.3	6.9
PEART_HDAC_PROLIFERATION_CLUSTER_DN	948	9E-
	34	12
	0.3	7.3
NADERI_BREAST_CANCER_PROGNOSIS_UP	944	5E-
	48	12
	0.3	8.8
CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN	930	3E-
	59	12
	0.3	9.4
LI_LUNG_CANCER	925	5E-
	45	12

CAFFAREL_RESPONSE_TO_THC_24HR_3_DN	0.3	9.9
	921	0E-
	93	12
	0.3	1.0
LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_LARGE_VS_TINY_DN	915	7E-
	77	11
	0.3	1.0
DARWICHE_PAPILLOMA_RISK_HIGH_UP	914	9E-
	7	11
	0.3	1.0
WEBER_METHYLATED_ICP_IN_SPERM_DN	914	9E-
	24	11
	0.3	1.4
JOHANSSON_GLIOMAGENESIS_BY_PDGF_UP	894	1E-
	61	11
	0.3	1.4
LY_AGING_OLD_DN	891	7E-
	63	11
	0.3	1.5
LE_SKI_TARGETS_UP	887	5E-
	53	11
	0.3	1.6
SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP	882	5E-
	62	11
	0.3	1.6
SMID_BREAST_CANCER_LUMINAL_A_DN	880	9E-
	79	11
	0.3	1.7
LEI_HOXC8_TARGETS_UP	877	6E-
	85	11
	0.3	2.4
NOUSHMEHR_GBM_SILENCED_BY_METHYLATION	851	5E-
	93	11
	0.3	2.6
CHUANG_OXIDATIVE_STRESS_RESPONSE_DN	846	4E-
	34	11
	0.3	2.7
CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_UP	843	4E-
	3	11
	0.3	2.9
RHODES_UNDIFFERENTIATED_CANCER	838	1E-
	69	11
	0.3	4.0
REACTOME_TFAP2A_ACTS_AS_A_TRANSCRIPTIONAL_REPRESSOR_DURING_RETINOIC_ACID_INDUCED_CELL_DIFFERENTIATION	812	8E-
	02	11
	0.3	4.1
BAKER_HEMATOPOIESIS_STAT3_TARGETS	810	6E-
	41	11
	0.3	4.8
CAIRO_HEPATOBLASTOMA_POOR_SURVIVAL	798	2E-

	77	11
	0.3	5.4
HASEGAWA_TUMORIGENESIS_BY_RET_C634R	789	4E-
	14	11
	0.3	6.3
KEGG_P53_SIGNALING_PATHWAY	776	5E-
	86	11
	0.3	6.4
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	776	0E-
	23	11
	0.3	6.5
SWEET_KRAS_TARGETS_DN	774	5E-
	4	11
	0.3	7.3
BIOCARTA_RAN_PATHWAY	765	2E-
	42	11
	0.3	7.7
WEST_ADRENOCORTICAL_TUMOR_MARKERS_UP	760	9E-
	47	11
	0.3	8.8
CAFFAREL_RESPONSE_TO_THC_24HR_5_DN	749	9E-
	8	11
	0.3	9.6
MORI_PRE_BI_LYMPHOCYTE_UP	743	5E-
	18	11
	0.3	9.7
CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP	742	0E-
	74	11
	0.3	9.8
JECHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP	741	7E-
	39	11
	0.3	1.0
CUI_TCF21_TARGETS_2_UP	734	7E-
	46	10
	0.3	1.1
XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_UP	728	5E-
	89	10
	0.3	1.1
BASAKI_YBX1_TARGETS_UP	726	9E-
	3	10
	0.3	1.2
COLINA_TARGETS_OF_4EBP1_AND_4EBP2	722	4E-
	93	10
	0.3	1.5
MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN	703	7E-
	34	10
	0.3	1.6
AFFAR_YY1_TARGETS_DN	701	2E-
	18	10
LY_AGING_PREMATURE_DN	0.3	1.8

	688	9E-
	44	10
	0.3	2.0
REACTOME_PHOSPHORYLATION_OF_EMI1	681	4E-
	83	10
	0.3	2.0
WANG_ESOPHAGUS_CANCER_PROGRESSION_UP	680	8E-
	41	10
	0.3	2.1
LE_EGR2_TARGETS_UP	677	5E-
	69	10
	0.3	2.1
KRIEG_HYPOXIA_VIA_KDM3A	676	8E-
	61	10
	0.3	2.1
STANELLE_E2F1_TARGETS	676	9E-
	25	10
	0.3	2.3
LY_AGING_OLD_UP	671	3E-
	03	10
	0.3	2.6
REACTOME_INTERLEUKIN_20_FAMILY_SIGNALING	659	7E-
	68	10
	0.3	2.8
HU_GENOTOXIC_DAMAGE_4HR	655	0E-
	64	10
	0.3	2.9
BRUECKNER_TARGETS_OF_MIRLET7A3_DN	651	6E-
	05	10
	0.3	3.0
MEISSNER_BRAIN_HCP_WITH_H3K4ME2_AND_H3K27ME3	647	8E-
	76	10
	0.3	3.0
ZHAN_VARIABLE_EARLY_DIFFERENTIATION_GENES_DN	647	8E-
	64	10
	0.3	4.1
CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_UP	623	0E-
	61	10
	0.3	4.3
DARWICHE_PAPILLOMA_RISK_LOW_UP	619	3E-
	10	10
	0.3	4.6
BENPORATH_ES_CORE_NINE	613	1E-
	71	10
	0.3	4.8
THILLAINADESAN_ZNF217_TARGETS_UP	609	7E-
	07	10
	0.3	4.9
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP	607	7E-
	5	10

BOGNI_TREATMENT_RELATED_MYELOID_LEUKEMIA_UP	0.3	5.4
	599	9E-
	01	10
CHICAS_RB1_TARGETS_LOW_SERUM	0.3	5.6
	596	6E-
	34	10
GRADE_COLON_AND_RECTAL_CANCER_UP	0.3	5.6
	596	6E-
	33	10
KONG_E2F1_TARGETS	0.3	5.7
	594	7E-
	69	10
GROSS_HYPOXIA_VIA_HIF1A_UP	0.3	6.0
	590	7E-
	37	10
MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP	0.3	6.1
	588	8E-
	88	10
VETTER_TARGETS_OF_PRKCA_AND_ETS1_DN	0.3	6.4
	585	6E-
	07	10
HONMA_DOCETAXEL_RESISTANCE	0.3	6.7
	581	8E-
	02	10
LIAO_METASTASIS	0.3	6.9
	578	5E-
	88	10
SABATES_COLORECTAL_ADENOMA_UP	0.3	7.5
	572	3E-
	02	10
KANG_CISPLATIN_RESISTANCE_DN	0.3	7.5
	571	6E-
	59	10
FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_DN	0.3	7.5
	571	9E-
	26	10
FULCHER_INFLAMMATORY_RESPONSE_LLECTIN_VS_LPS_UP	0.3	7.8
	568	2E-
	68	10
VECCHI_GASTRIC_CANCER_EARLY_UP	0.3	7.9
	566	8E-
	99	10
PAL_PRMT5_TARGETS_UP	0.3	8.3
	563	2E-
	35	10
SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_UP	0.3	8.7
	558	6E-
	93	10
ROZANOV_MMP14_TARGETS_UP	0.3	8.9
	557	3E-

	25	10
	0.3	9.3
TARTE_PLASMA_CELL_VS_PLASMABLAST_DN	552	9E-
	91	10
	0.3	9.6
HU_GENOTOXIC_DAMAGE_24HR	551	0E-
		10
	0.3	1.1
APPIERTO_RESPONSE_TO_FENRETINIDE_DN	533	8E-
	46	09
	0.3	1.3
VANTVEER_BREAST_CANCER_ESR1_DN	520	6E-
	63	09
	0.3	1.3
YAGI_AML_RELAPSE_PROGNOSIS	520	6E-
	57	09
	0.3	1.4
PID_SYNDECAN_4_PATHWAY	514	6E-
	76	09
	0.3	1.5
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR	511	1E-
	51	09
	0.3	1.7
ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP	500	2E-
	23	09
	0.3	1.8
BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_UP	495	1E-
	61	09
	0.3	1.8
BIOCARTA_NPC_PATHWAY	494	4E-
	3	09
	0.3	2.1
CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN	480	5E-
	53	09
	0.3	2.1
PID_HIF1A_PATHWAY	479	8E-
	19	09
	0.3	2.2
REACTOME_UNFOLDED_PROTEIN_RESPONSE_UPR	477	1E-
	82	09
	0.3	2.2
MULLIGAN_NTF3_SIGNALING_VIA_INSR_AND_IGF1R_UP	476	6E-
	21	09
	0.3	2.2
NAGY_TFTC_COMPONENTS_HUMAN	474	9E-
	94	09
	0.3	2.3
RUIZ_TNC_TARGETS_DN	473	2E-
	51	09
	0.3	2.3
REACTOME_PLASMA_LIPOPROTEIN_ASSEMBLY		

	473	3E-
	4	09
	0.3	2.4
WHITEFORD_PEDIATRIC_CANCER_MARKERS	468	5E-
	97	09
	0.3	2.5
LOPEZ_MESOTELIOMA_SURVIVAL_TIME_UP	467	0E-
	11	09
	0.3	2.5
HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_1_DN	464	8E-
	36	09
	0.3	2.6
OLSSON_E2F3_TARGETS_DN	463	1E-
	08	09
	0.3	2.7
ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_DN	459	1E-
	81	09
	0.3	2.7
VANLOO_SP3_TARGETS_UP	458	4E-
	8	09
	0.3	2.7
WONG_EMBRYONIC_STEM_CELL_CORE	458	6E-
	07	09
	0.3	2.8
TOOKER_GEMCITABINE_RESISTANCE_DN	455	5E-
	33	09
	0.3	2.9
XU_HGF_SIGNALING_NOT_VIA_AKT1_48HR_UP	453	0E-
	82	09
	0.3	3.1
POMEROY_MEDULLOBLASTOMA_PROGNOSIS_DN	447	0E-
	83	09
	0.3	3.2
FOURNIER_ACINAR_DEVELOPMENT_LATE_2	443	5E-
	57	09
	0.3	3.2
MODY_HIPPOCAMPUS_PRENATAL	442	7E-
	93	09
	0.3	3.3
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14	440	6E-
	54	09
	0.3	4.1
TSENG_IRS1_TARGETS_UP	422	3E-
	01	09
	0.3	4.1
PID_FOXM1_PATHWAY	420	8E-
	8	09
	0.3	4.2
REACTOME_PCP_CE_PATHWAY	420	1E-
	22	09

CROONQUIST_NRAS_SIGNALING_DN	0.3	5.0
	403	8E-
	25	09
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CELL_DEATH_GENES	0.3	5.1
	401	5E-
	95	09
GOLDRATH_ANTIGEN_RESPONSE	0.3	5.3
	398	7E-
	21	09
FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN	0.3	5.5
	395	5E-
	19	09
CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP	0.3	5.7
	391	9E-
	27	09
AIYAR_COBRA1_TARGETS_UP	0.3	6.0
	386	8E-
	76	09
REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SIGNALING	0.3	6.1
	386	3E-
	07	09
SIMBULAN_PARP1_TARGETS_DN	0.3	6.2
	385	0E-
		09
DANG_MYC_TARGETS_UP	0.3	6.5
	380	0E-
	63	09
WEBER_METHYLATED_ICP_IN_FIBROBLAST	0.3	6.5
	380	0E-
	62	09
NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_UP	0.3	6.6
	378	8E-
	16	09
NADLER_OBESITY_UP	0.3	6.8
	376	2E-
	22	09
DELPUECH_FOXO3_TARGETS_DN	0.3	6.8
	375	7E-
	54	09
FOURNIER_ACINAR_DEVELOPMENT_LATE_DN	0.3	7.1
	371	6E-
	82	09
LINDGREN_BLADDER_CANCER_CLUSTER_1_DN	0.3	7.4
	368	1E-
	6	09
BERENJENO_TRANSFORMED_BY_RHOA_UP	0.3	7.5
	366	7E-
	59	09
SMID_BREAST_CANCER_BASAL_UP	0.3	8.0
	361	4E-

	11	09
	0.3	9.1
PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN	348	9E-
	64	09
	0.3	9.3
REACTOME_INTERLEUKIN_10_SIGNALING	347	0E-
	57	09
	0.3	9.3
REACTOME_CLEC7A_INFLAMMASOME_PATHWAY	347	5E-
	06	09
	0.3	1.0
LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_QTL	338	3E-
	13	08
	0.3	1.0
BURTON_ADIPOGENESIS_PEAK_AT_16HR	333	8E-
	23	08
	0.3	1.2
NAKAMURA_LUNG_CANCER	323	0E-
	63	08
	0.3	1.2
GREENBAUM_E2A_TARGETS_UP	322	1E-
	97	08
	0.3	1.2
LEI_HOXC8_TARGETS_DN	317	9E-
	26	08
	0.3	1.3
URS_ADIPOCYTE_DIFFERENTIATION_DN	316	0E-
	43	08
	0.3	1.3
HATADA_METHYLATED_IN_LUNG_CANCER_DN	313	4E-
	37	08
	0.3	1.3
REN_ALVEOLAR_RHABDOMYOSARCOMA_DN	313	4E-
	2	08
	0.3	1.3
LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN	311	6E-
	84	08
	0.3	1.3
NABA_SECRETED_FACTORS	311	7E-
	04	08
	0.3	1.4
SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP	306	4E-
	34	08
	0.3	1.5
PID_MYC_ACTIV_PATHWAY	300	3E-
	88	08
	0.3	1.6
REACTOME_RHO_GTPASE_EFFECTORS	294	4E-
	13	08
ENK_UV_RESPONSE_EPIDERMIS_UP	0.3	1.6

	293	6E-
	34	08
	0.3	1.7
REACTOME_SYNTHESIS_OF_5_EICOSATETRAENOIC_ACIDS	289	2E-
	57	08
	0.3	1.7
JAZAG_TGFB1_SIGNALING_VIA_SMAD4_UP	287	7E-
	34	08
	0.3	1.7
LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN	286	8E-
	63	08
	0.3	1.7
MATTHEWS_SKIN_CARCINOGENESIS_VIA_JUN	286	9E-
	11	08
	0.3	1.7
ZHAN_MULTIPLE_MYELOMA_PR_UP	285	9E-
	9	08
	0.3	1.8
DIRMEIER_LMP1_RESPONSE_LATE_UP	283	4E-
	28	08
	0.3	1.9
SHIN_B_CELL_LYMPHOMA_CLUSTER_8	280	1E-
	04	08
	0.3	1.9
WATANABE_COLON_CANCER_MSI_VS_MSS_UP	279	1E-
	64	08
	0.3	1.9
BRACHAT_RESPONSE_TO_CAMPTOTHECIN_DN	276	7E-
	89	08
	0.3	2.0
REACTOME_LINOLEIC_ACID_LA_METABOLISM	272	7E-
	22	08
	0.3	2.1
HENDRICKS_SMARCA4_TARGETS_UP	270	1E-
	61	08
	0.3	2.2
PRAMOONJAGO_SOX4_TARGETS_DN	266	0E-
	6	08
	0.3	2.2
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	264	3E-
	94	08
	0.3	2.2
CROMER_TUMORIGENESIS_UP	264	3E-
	89	08
	0.3	2.2
REACTOME_IRF3_MEDIATED_ACTIVATION_OF_TYPE_1_IFN	263	7E-
	57	08
	0.3	2.3
KAN_RESPONSE_TO_ARSENIC_TRIOXIDE	261	1E-
	62	08

KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	0.3	2.4
	256	3E-
	71	08
FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	0.3	2.4
	256	4E-
	5	08
REACTOME_TRANSPORT_OF_CONNEXONS_TO_THE_PLASMA_MEMBRAN E	0.3	2.5
	253	1E-
	88	08
HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP	0.3	2.5
	251	8E-
		08
PATIL_LIVER_CANCER	0.3	2.6
	249	2E-
	57	08
WANG_THOC1_TARGETS_UP	0.3	2.6
	249	2E-
	51	08
MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_UP	0.3	2.6
	248	4E-
	97	08
GRUETZMANN_PANCREATIC_CANCER_UP	0.3	2.9
	238	4E-
	66	08
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_UP	0.3	3.0
	235	3E-
	72	08
KUMAR_AUTOPHAGY_NETWORK	0.3	3.0
	234	7E-
	25	08
SHEPARD_BMYB_MORPHOLINO_DN	0.3	3.1
	232	3E-
	43	08
ROZANOV_MMP14_TARGETS_SUBSET	0.3	3.1
	231	5E-
	74	08
LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_UP	0.3	3.1
	231	7E-
	09	08
LY_AGING_MIDDLE_UP	0.3	3.3
	226	4E-
	27	08
LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_UP	0.3	3.3
	225	8E-
	03	08
VERRECCHIA_RESPONSE_TO_TGFB1_C5	0.3	3.4
	222	6E-
	83	08
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_I N_G1_CELL_CYCLE_ARREST	0.3	3.5
	220	4E-

	54	08
	0.3	3.6
ITO_PTTG1_TARGETS_DN	217	5E-
	5	08
	0.3	3.6
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_GRANU LOCYTE_DN	217	5E-
	5	08
	0.3	3.7
LEE_LIVER_CANCER_SURVIVAL_DN	214	6E-
	7	08
	0.3	3.8
BURTON_ADIPOGENESIS_8	213	0E-
	69	08
	0.3	3.8
NABA_ECM_REGULATORS	213	1E-
	34	08
	0.3	4.0
REACTOME_SYNTHESIS_OF_PROSTAGLANDINS_PG_AND_THROMBOXAN ES_TX	208	2E-
	13	08
	0.3	4.1
REACTOME_DEPOLYMERISATION_OF_THE_NUCLEAR_LAMINA	206	0E-
	27	08
	0.3	4.1
REACTOME_IRF3_MEDIATED_INDUCION_OF_TYPE_I_IFN	205	4E-
	19	08
	0.3	4.1
KIM_WT1_TARGETS_8HR_DN	204	6E-
	67	08
	0.3	4.3
REACTOME_WNT5A_DEPENDENT_INTERNALIZATION_OF_FZD4	201	0E-
	47	08
	0.3	4.3
INAMURA_LUNG_CANCER_SCC_UP	201	0E-
	44	08
	0.3	4.4
MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_DN	198	5E-
	2	08
	0.3	4.4
CROONQUIST_IL6_DEPRIVATION_DN	197	8E-
	49	08
	0.3	4.9
MOREIRA_RESPONSE_TO_TSA_UP	187	6E-
	47	08
	0.3	4.9
AMIT_SERUM_RESPONSE_480_MCF10A	187	8E-
	18	08
	0.3	5.0
ZAMORA_NOS2_TARGETS_UP	186	2E-
	29	08
WORSCHER_TUMOR_EVASION_AND_TOLEROGENICITY_DN	0.3	5.1

	184	2E-
	36	08
	0.3	5.3
BIOCARTA_IL4_PATHWAY	179	6E-
	76	08
	0.3	5.6
KATSANOUELAVL1_TARGETS_DN	174	3E-
	98	08
	0.3	6.0
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER	168	0E-
	77	08
	0.3	6.1
TOMIDA_METASTASIS_UP	166	2E-
	66	08
	0.3	6.2
IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_DN	164	6E-
	52	08
	0.3	6.5
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_DN	159	6E-
	77	08
	0.3	6.5
REACTOME_ACTIVATION_OF_IRF3_IRF7_MEDIATED_BY_TBK1_IKK_EPSILON	159	9E-
	44	08
	0.3	6.7
HAN_JNK_SIGNALING_DN	156	6E-
	88	08
	0.3	6.8
MORI_LARGE_PRE_BII_LYMPHOCYTE_UP	155	5E-
	57	08
	0.3	7.1
REACTOME_VLDL_ASSEMBLY	151	1E-
	78	08
	0.3	7.2
ISHIDA_E2F_TARGETS	149	5E-
	93	08
	0.3	7.2
SIMBULAN_UV_RESPONSE_NORMAL_UP	149	7E-
	64	08
	0.3	7.9
FRIDMAN_IMMORTALIZATION_DN	140	7E-
	45	08
	0.3	8.1
REACTOME_MITOTIC_G2_G2_M_PHASES	137	9E-
	68	08
	0.3	8.2
VANTVEER_BREAST_CANCER_BRCA1_UP	137	3E-
	14	08
	0.3	8.4
KONDO_COLON_CANCER_HCP_WITH_H3K27ME1	134	3E-
	76	08

PURBEY_TARGETS_OF_CTBP1_NOT_SATB1_UP	0.3	8.4
	134	4E-
	64	08
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_RED_UP	0.3	8.4
	134	6E-
	46	08
LI_WILMS_TUMOR	0.3	8.4
	134	9E-
	04	08
LIANG_SILENCED_BY_METHYLATION_2	0.3	8.6
	132	4E-
	35	08
NABA_MATRISOME_ASSOCIATED	0.3	8.7
	130	6E-
	91	08
MINGUEZ_LIVER_CANCER_VASCULAR_INVASION_UP	0.3	8.8
	130	3E-
	18	08
POOLA_INVASIVE_BREAST_CANCER_UP	0.3	9.0
	127	8E-
	26	08
WINTER_HYPOXIA_UP	0.3	9.2
	125	2E-
	81	08
LIU_VAV3_PROSTATE_CARCINOGENESIS_DN	0.3	9.2
	125	3E-
	63	08
WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN	0.3	9.8
	119	4E-
	17	08
REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM	0.3	9.9
	117	8E-
	83	08
KOBAYASHI_EGFR_SIGNALING_24HR_DN	0.3	1.0
	116	1E-
	83	07
BIOCARTA_SRCRPTP_PATHWAY	0.3	1.0
	116	1E-
	63	07
KORKOLA_YOLK_SAC_TUMOR_UP	0.3	1.0
	112	5E-
	28	07
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	0.3	1.1
	107	1E-
	33	07
YIH_RESPONSE_TO_ARSENITE_C5	0.3	1.1
	103	4E-
	91	07
CAIRO_HEPATOBLASTOMA_CLASSES_UP	0.3	1.1
	100	8E-

	89	07
	0.3	1.2
KANG_AR_TARGETS_UP	098	1E-
	09	07
	0.3	1.2
LENAOUR_DENDRITIC_CELL_MATURATION_DN	097	2E-
	56	07
	0.3	1.2
CUI_TCF21_TARGETS_UP	091	9E-
	49	07
	0.3	1.3
YOKOE_CANCER_TESTIS_ANTIGENS	090	1E-
	01	07
		1.3
KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP	0.3	1E-
	09	07
	0.3	1.3
KIM_TIAL1_TARGETS	087	5E-
	46	07
	0.3	1.3
WU_HBX_TARGETS_1_UP	085	7E-
	33	07
	0.3	1.3
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	084	9E-
	41	07
	0.3	1.4
SHEN_SMARCA2_TARGETS_DN	082	1E-
	34	07
	0.3	1.4
TANG_SENESCENCE_TP53_TARGETS_DN	081	3E-
	27	07
	0.3	1.5
HOFFMANN_PRE_BI_TO_LARGE_PRE_BII_LYMPHOCYTE_UP	074	3E-
	1	07
	0.3	1.5
REACTOME_TNFR1_MEDIATED_CERAMIDE_PRODUCTION	074	3E-
	06	07
	0.3	1.5
REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE	073	3E-
	98	07
	0.3	1.5
DARWICHE_SQUAMOUS_CELL_CARCINOMA_UP	073	4E-
	7	07
	0.3	1.5
REACTOME_G1_S_DNA_DAMAGE_CHECKPOINTS	073	4E-
	6	07
	0.3	1.5
REACTOME_RUNX1_AND_FOXP3_CONTROL_THE_DEVELOPMENT_OF_REGULATORY_T_LYMPHOCYTES_TREGS	070	8E-
	98	07
JOHANSSON_BRAIN_CANCER_EARLY_VS_LATE_UP	0.3	1.6

	069	0E-
	74	07
	0.3	1.6
FARMER_BREAST_CANCER_CLUSTER_2	069	0E-
	72	07
	0.3	1.6
REACTOME_ACTIVATION_OF_APC_C_AND_APC_C:CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	067	3E-
	99	07
	0.3	1.6
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_1	067	3E-
	95	07
	0.3	1.6
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TURQUOISE_DN	067	3E-
	68	07
	0.3	1.6
PUIFFE_INVASION_INHIBITED_BY_ASCITES_UP	067	4E-
	25	07
	0.3	1.6
GRAHAM_CML QUIESCENT_VS_NORMAL QUIESCENT_UP	064	8E-
	82	07
	0.3	1.6
REACTOME_REGULATION_OF_IFNA_SIGNALING	064	9E-
	05	07
	0.3	1.6
VERHAAK_GLIOMASTOMA_MESENCHYMAL	063	9E-
	78	07
	0.3	1.7
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_15	061	3E-
	56	07
	0.3	1.8
KYNG_DNA_DAMAGE_DN	052	9E-
	44	07
	0.3	1.9
WANG_METASTASIS_OF_BREAST_CANCER_ESR1_UP	050	3E-
	29	07
	0.3	1.9
REACTOME_RELEASE_OF_APOPTOTIC_FACTORS_FROM_THE_MITOCHONDRIA	048	7E-
	25	07
	0.3	1.9
OHASHI_AURKB_TARGETS	048	7E-
	02	07
	0.3	1.9
FERRANDO_HOX11_NEIGHBORS	047	9E-
	3	07
	0.3	2.0
NAKAMURA_METASTASIS	042	9E-
	13	07
	0.3	2.0
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM3	042	9E-
	07	07

KARLSSON_TGFB1_TARGETS_UP	0.3	2.0
	041	9E-
	98	07
	0.3	2.1
HOSHIDA_LIVER_CANCER_SUBCLASS_S1	039	3E-
	87	07
	0.3	2.1
REN_MIF_TARGETS_DN	038	7E-
	29	07
	0.3	2.1
REACTOME_THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AFTER_G2_CHECKPOINT	037	9E-
	11	07
	0.3	2.2
ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP	036	1E-
	43	07
	0.3	2.2
TERAMOTO_OPN_TARGETS_CLUSTER_6	035	3E-
	19	07
	0.3	2.3
MORI_IMMATURE_B_LYMPHOCYTE_DN	031	1E-
	62	07
	0.3	2.3
FUJIWARA_PARK2_IN_LIVER_CANCER_UP	031	2E-
	38	07
	0.3	2.3
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_25	028	8E-
	55	07
	0.3	2.3
ZHAN_V1_LATE_DIFFERENTIATION_GENES_DN	028	8E-
	33	07
	0.3	2.3
LINDSTEDT_DENDRITIC_CELL_MATURATION_A	028	9E-
	21	07
	0.3	2.4
NABA_PROTEOGLYCANS	027	0E-
	8	07
	0.3	2.4
CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_DN	026	3E-
	18	07
	0.3	2.5
REACTOME_MICRORNA_MIRNA_BIOGENESIS	023	1E-
	06	07
	0.3	2.5
AMIT_EGF_RESPONSE_480_MCF10A	022	1E-
	96	07
	0.3	2.5
WU_HBX_TARGETS_3_DN	019	8E-
	92	07
	0.3	2.6
SANSOM_APC_TARGETS_REQUIRE_MYC	017	4E-

	52	07
	0.3	2.7
POS_HISTAMINE_RESPONSE_NETWORK	012	7E-
	79	07
	0.3	2.7
HINATA_NFKB_TARGETS_FIBROBLAST_UP	012	8E-
	37	07
	0.3	2.9
REACTOME_KERATAN_SULFATE_BIOSYNTHESIS	006	5E-
	07	07
	0.3	2.9
MUELLER_METHYLATED_IN_GLIOBLASTOMA	005	7E-
	21	07
	0.3	3.0
REACTOME_SYNTHESIS_OF_ACTIVE_UBIQUITIN:_ROLES_OF_E1_AND_E2_ENZYMES	003	3E-
	26	07
	0.3	3.0
FOSTER_TOLERANT_MACROPHAGE_UP	002	6E-
	34	07
	0.2	3.1
DASU_IL6_SIGNALING_UP	999	2E-
	96	07
	0.2	3.1
SASAI_TARGETS_OF_CXCR6_AND_PTCH1_UP	999	5E-
	07	07
	0.2	3.1
JAZAG_TGFB1_SIGNALING_UP	998	7E-
	4	07
	0.2	3.1
PID_IL27_PATHWAY	998	7E-
	4	07
	0.2	3.2
QI_PLASMACYTOMA_DN	997	0E-
	46	07
	0.2	3.2
CROSBY_E2F4_TARGETS	995	6E-
	61	07
	0.2	3.3
BENPORATH_PROLIFERATION	993	3E-
	36	07
	0.2	3.3
KARAKAS_TGFB1_SIGNALING	991	9E-
	36	07
	0.2	3.5
JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_UP	986	4E-
	68	07
	0.2	3.6
GENTLES_LEUKEMIC_STEM_CELL_DN	983	5E-
	47	07
MATTIOLI_MGUS_VS_PCL	0.2	3.8

	978	3E-
	52	07
	0.2	3.9
REACTOME_SYNTHESIS_OF_15_EICOSATETRAENOIC_ACID_DERIVATIVES	974	6E-
	72	07
	0.2	3.9
REICHERT_MITOSIS_LIN9_TARGETS	974	7E-
	53	07
	0.2	4.2
BENPORATH_ES_CORE_NINE_CORRELATED	967	5E-
	32	07
	0.2	4.2
REACTOME_APC_C:CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C:CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1	966	9E-
	26	07
	0.2	4.3
MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN	963	9E-
	96	07
	0.2	4.4
GAL_LEUKEMIC_STEM_CELL_DN	962	6E-
	12	07
	0.2	4.6
REACTOME_INTERLEUKIN_1_SIGNALING	956	9E-
	74	07
	0.2	4.7
CAIRO_PML_TARGETS_BOUND_BY_MYC_UP	955	5E-
	48	07
	0.2	4.7
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	955	5E-
	46	07
	0.2	4.8
BARIS_THYROID_CANCER_UP	954	1E-
	09	07
	0.2	4.9
PID_ARF6_DOWNSTREAM_PATHWAY	950	8E-
	41	07
	0.2	4.9
REACTOME_ADVANCED_GLYCOSYLATION_ENDPRODUCT_RECEPTOR_SIGNALING	950	9E-
	12	07
	0.2	5.0
BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_TRANS	949	1E-
	7	07
	0.2	5.0
CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_UP	949	2E-
	5	07
	0.2	5.0
HILLION_HMGA1B_TARGETS	949	2E-
	43	07
	0.2	5.0
REACTOME_SENESCENCE_ASSOCIATED_SECRETORY_PHENOTYPE_SASP	949	3E-
	23	07

HESS_TARGETS_OF_HOXA9_AND_MEIS1_UP	0.2	5.0
	948	6E-
	66	07
	0.2	5.2
BIOCARTA_EFP_PATHWAY	945	1E-
	53	07
	0.2	5.2
LANG_MYB_FAMILY_TARGETS	944	6E-
	49	07
	0.2	5.3
HAHTOLA_CTCL_CUTANEOUS	942	4E-
	84	07
	0.2	5.3
BRUINS_UVC_RESPONSE_LATE	941	9E-
	88	07
	0.2	5.4
REACTOME_G2_PHASE	940	7E-
	19	07
	0.2	5.5
CORRADETTI_MTOR_PATHWAY_REGULATORS_DN	939	0E-
	7	07
	0.2	5.5
PID_SYNDECAN_1_PATHWAY	939	2E-
	2	07
	0.2	5.6
PARK_TRETINOIN_RESPONSE_AND_RARA_PLZF_FUSION	936	8E-
	05	07
	0.2	5.8
REACTOME_INTERLEUKIN_12_FAMILY_SIGNALING	933	0E-
	95	07
	0.2	5.8
DOUGLAS_BMI1_TARGETS_UP	932	8E-
	38	07
	0.2	5.9
HASINA_NOL7_TARGETS_UP	931	2E-
	65	07
	0.2	5.9
ZEILSTRA_CD44_TARGETS_DN	931	4E-
	37	07
	0.2	5.9
LI_WILMS_TUMOR_ANAPLASTIC_UP	930	7E-
	76	07
	0.2	6.0
REACTOME_COLLAGEN_FORMATION	929	5E-
	35	07
	0.2	6.2
GERHOLD_ADIPOGENESIS_DN	926	0E-
	65	07
	0.2	6.5
RASHI_RESPONSE_TO_IONIZING_RADIATION_6	921	0E-

	53	07
	0.2	6.5
GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP	920	3E-
	97	07
	0.2	6.8
WANG_TARGETS_OF_MLL_CBP_FUSION_UP	916	1E-
	45	07
	0.2	6.9
MISSIAGLIA_REGULATED_BY_METHYLATION_DN	914	3E-
	49	07
	0.2	6.9
DANG_REGULATED_BY_MYC_UP	914	4E-
	41	07
	0.2	7.1
WHITFIELD_CELL_CYCLE_LITERATURE	911	5E-
	06	07
	0.2	7.2
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	909	8E-
	23	07
	0.2	7.3
REACTOME_LONG_TERM_POTENTIATION	908	4E-
	2	07
	0.2	7.4
REACTOME_REGULATION_OF_RUNX3_EXPRESSION_AND_ACTIVITY	906	6E-
	47	07
	0.2	7.5
KANG_DOXORUBICIN_RESISTANCE_UP	904	8E-
	7	07
	0.2	7.6
JAEGER_METASTASIS_UP	904	1E-
	29	07
	0.2	7.7
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR	901	9E-
	75	07
	0.2	7.8
HONRADO_BREAST_CANCER_BRCA1_VS_BRCA2	900	7E-
	61	07
	0.2	8.0
STEARMAN_TUMOR_FIELD_EFFECT_UP	898	1E-
	77	07
	0.2	8.2
WELCSH_BRCA1_TARGETS_DN	896	1E-
	07	07
	0.2	8.5
REACTOME_KERATAN_SULFATE_DEGRADATION	890	9E-
	98	07
	0.2	8.6
TSUTSUMI_FBXW8_TARGETS	889	7E-
	97	07
	0.2	8.9

	886	2E-
	84	07
	0.2	9.1
MCLACHLAN_DENTAL_CARIES_UP	884	2E-
	44	07
	0.2	9.5
SESTO_RESPONSE_TO_UV_C4	878	9E-
	9	07
	0.2	9.6
LIU_SMARCA4_TARGETS	877	8E-
	89	07
	0.2	9.7
WOO_LIVER_CANCER_RECURRENCE_UP	877	0E-
	68	07
	0.2	9.7
KOKKINAKIS_METHIONINE_DEPRIVATION_96HR_DN	877	2E-
	42	07
	0.2	9.8
REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM_EVENTS	876	4E-
	07	07
	0.2	1.0
KONG_E2F3_TARGETS	872	2E-
	23	06
	0.2	1.0
WANG_SMARCE1_TARGETS_DN	871	3E-
	46	06
	0.2	1.0
SHEPARD_BMYB_TARGETS	870	3E-
	93	06
	0.2	1.0
BLUM_RESPONSE_TO_SALIRASIB_DN	870	4E-
	37	06
	0.2	1.0
NABA_MATRISOME	868	5E-
	98	06
	0.2	1.0
LEI_MYB_TARGETS	866	7E-
	66	06
	0.2	1.0
SHIN_B_CELL_LYMPHOMA_CLUSTER_5	866	7E-
	56	06
	0.2	1.0
MEISSNER_NPC_ICP_WITH_H3_UNMETHYLATED	866	7E-
	36	06
	0.2	1.0
BIOCARTA_INFLAM_PATHWAY	866	8E-
	09	06
	0.2	1.0
REACTOME_INTERLEUKIN_27_SIGNALING	866	8E-
	08	06

EHRlich_ICF_SYNDROM_UP	0.2	1.0
	865	8E-
	78	06
	0.2	1.1
WILENSKY_RESPONSE_TO_DARAPLADIB	863	1E-
	12	06
	0.2	1.1
BRACHAT_RESPONSE_TO_METHOTREXATE_DN	862	1E-
	78	06
	0.2	1.1
KAAB_FAILED_HEART_VENTRICLE_DN	862	1E-
	41	06
	0.2	1.1
PARK_HSC_VS_MULTIPOTENT_PROGENITORS_DN	862	2E-
	12	06
	0.2	1.1
WHITFIELD_CELL_CYCLE_G2	861	2E-
	48	06
	0.2	1.1
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_16	859	5E-
		06
	0.2	1.1
COLLER_MYC_TARGETS_UP	858	5E-
	97	06
	0.2	1.1
LOPES_METHYLATED_IN_COLON_CANCER_UP	857	6E-
	68	06
	0.2	1.1
DER_IFN_GAMMA_RESPONSE_UP	856	7E-
	78	06
	0.2	1.1
REACTOME_RHO_GTPASES_ACTIVATE_FORMINS	856	8E-
	01	06
	0.2	1.2
PARK_APL_PATHOGENESIS_DN	854	0E-
	2	06
	0.2	1.2
FRIDMAN_SENESCENCE_UP	853	0E-
	8	06
	0.2	1.2
AZARE NEOPLASTIC_TRANSFORMATION_BY_STAT3_UP	851	3E-
	28	06
	0.2	1.2
NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP	850	4E-
	3	06
	0.2	1.2
WEIGEL_OXIDATIVE_STRESS_BY_TBH_AND_H2O2	849	5E-
	64	06
	0.2	1.2
BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN	846	9E-

	26	06
	0.2	1.3
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP	842	3E-
	9	06
REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT	0.2	1.3
_TRIC	842	3E-
	65	06
	0.2	1.3
DARWICHE_SKIN_TUMOR_PROMOTER_UP	841	5E-
	17	06
	0.2	1.3
SA_PROGRAMMED_CELL_DEATH	838	8E-
	01	06
	0.2	1.3
LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_LARGE_VS_TINY_UP	837	9E-
	44	06
	0.2	1.4
REACTOME_PENTOSE_PHOSPHATE_PATHWAY	836	1E-
	29	06
	0.2	1.4
REACTOME_ASYMMETRIC_LOCALIZATION_OF_PCP_PROTEINS	835	2E-
	07	06
	0.2	1.4
HILLION_HMGA1_TARGETS	834	3E-
	32	06
	0.2	1.4
MUNSHI_MULTIPLE_MYELOMA_DN	832	5E-
	41	06
	0.2	1.5
IRITANI_MAD1_TARGETS_DN	828	0E-
	73	06
	0.2	1.5
SERVITJA_ISLET_HNF1A_TARGETS_UP	827	1E-
	98	06
	0.2	1.5
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM1	827	1E-
	91	06
	0.2	1.5
KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN	826	4E-
	16	06
	0.2	1.5
REACTOME_CONDENSATION_OF_PROMETAPHASE_CHROMOSOMES	825	5E-
	49	06
	0.2	1.5
AMIT_EGF_RESPONSE_480_HELA	824	6E-
	33	06
	0.2	1.6
GRAHAM_CML QUIESCENT_VS_CML_DIVIDING_DN	821	1E-
	32	06
BIOCARTA_CHEMICAL_PATHWAY	0.2	1.6

	821	1E-
	21	06
	0.2	1.6
WEST_ADRENOCORTICAL_TUMOR_UP	820	2E-
	26	06
	0.2	1.6
NAGY_PCAF_COMPONENTS_HUMAN	819	4E-
	2	06
	0.2	1.6
SASAI_TARGETS_OF_CXCR6_AND_PTCH1_DN	817	6E-
	48	06
	0.2	1.6
CHEN_HOXA5_TARGETS_9HR_DN	815	9E-
	83	06
	0.2	1.7
REACTOME_PEPTIDE_HORMONE_BIOSYNTHESIS	812	4E-
	03	06
	0.2	1.7
HORIUCHI_WTAP_TARGETS_DN	809	9E-
	05	06
	0.2	1.8
FARMER_BREAST_CANCER_CLUSTER_4	806	3E-
	53	06
	0.2	1.8
REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE	806	3E-
	49	06
	0.2	1.8
REACTOME_TICAM1_DEPENDENT_ACTIVATION_OF_IRF3_IRF7	805	5E-
	44	06
	0.2	1.8
REACTOME_APC_C:CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	805	5E-
	27	06
	0.2	1.9
KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN	800	3E-
	67	06
	0.2	1.9
HASLINGER_B_CLL_WITH_CHROMOSOME_12_TRISOMY	799	4E-
	67	06
	0.2	1.9
MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP	798	6E-
	83	06
	0.2	1.9
MODY_HIPPOCAMPUS_NEONATAL	798	7E-
	09	06
	0.2	2.0
REACTOME_INFECTIOUS_DISEASE	795	1E-
	74	06
	0.2	2.0
REACTOME_ABC_TRANSPORTER_DISORDERS	795	2E-
	16	06

BURTON_ADIPOGENESIS_3	0.2	2.0
	794	3E-
	85	06
	0.2	2.0
MCMURRAY_TP53_HRAS_COOPERATION_RESPONSE_UP	791	8E-
	64	06
	0.2	2.1
REACTOME_STABILIZATION_OF_P53	790	1E-
	28	06
	0.2	2.1
TOMIDA_LUNG_CANCER_POOR_SURVIVAL	788	4E-
	78	06
	0.2	2.1
CHEN_METABOLIC_SYNDROM_NETWORK	787	6E-
	6	06
	0.2	2.1
SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY	786	9E-
	13	06
	0.2	2.2
HOLLMANN_APOPTOSIS_VIA_CD40_UP	785	0E-
	2	06
	0.2	2.2
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	784	2E-
	21	06
	0.2	2.2
MALONEY_RESPONSE_TO_17AAG_UP	783	4E-
	49	06
	0.2	2.2
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_MONOCYTE_DN	783	4E-
	34	06
	0.2	2.2
REACTOME_ASSEMBLY_OF_COLLAGEN_FIBRILS_AND_OTHER_MULTIMERIC_STRUCTURES	782	5E-
	97	06
	0.2	2.3
REACTOME_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES	779	1E-
	88	06
	0.2	2.3
NAGY_STAGA_COMPONENTS_HUMAN	778	4E-
	6	06
	0.2	2.3
BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN	777	5E-
	73	06
	0.2	2.3
KIM_ALL_DISORDERS_CALB1_CORR_DN	777	6E-
	36	06
	0.2	2.3
KYNG_RESPONSE_TO_H2O2_VIA_ERCC6	776	8E-
	62	06
	0.2	2.4
REACTOME_APOPTOTIC_FACTOR_MEDIATED_RESPONSE	775	0E-

	36	06
	0.2	2.4
REACTOME_NUCLEOTIDE_SALVAGE	774	2E-
	32	06
	0.2	2.4
XU_HGF_SIGNALING_NOT_VIA_AKT1_48HR_DN	773	4E-
	38	06
	0.2	2.4
MIKKELSEN_MEF_LCP_WITH_H3K4ME3	771	7E-
	98	06
	0.2	2.5
ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION	770	1E-
	35	06
	0.2	2.5
REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS	770	1E-
	14	06
	0.2	2.5
KIM_LIVER_CANCER_POOR_SURVIVAL_UP	769	3E-
	24	06
	0.2	2.5
REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	769	4E-
	07	06
	0.2	2.5
PID_P38_ALPHA_BETA_DOWNSTREAM_PATHWAY	767	6E-
	99	06
	0.2	2.5
RIZKI_TUMOR_INVASIVENESS_3D_DN	767	8E-
	05	06
	0.2	2.5
VANTVEER_BREAST_CANCER_METASTASIS_DN	766	9E-
	78	06
	0.2	2.6
CHEMELLO_SOLEUS_VS_EDL_MYOFIBERS_UP	762	7E-
	97	06
	0.2	2.7
REACTOME_BASIGIN_INTERACTIONS	760	3E-
	8	06
	0.2	2.7
BROWNE_HCMV_INFECTION_2HR_DN	759	6E-
	28	06
	0.2	2.7
ZHANG_BREAST_CANCER_PROGENITORS_DN	758	8E-
	33	06
	0.2	2.8
BIOCARTA_CYTOKINE_PATHWAY	757	2E-
		06
	0.2	2.8
BORCZUK_MALIGNANT_MESOTHELIOMA_UP	756	3E-
	61	06
	0.2	2.8
NAKAMURA_CANCER_MICROENVIRONMENT_DN		

	755	4E-
	88	06
	0.2	2.8
BLUM_RESPONSE_TO_SALIRASIB_UP	755	5E-
	71	06
	0.2	2.8
REACTOME_ACTIVATION_OF_MATRIX_METALLOPROTEINASES	754	7E-
	84	06
	0.2	2.8
LEE_EARLY_T_LYMPHOCYTE_UP	754	7E-
	73	06
	0.2	2.9
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_DN	753	0E-
	67	06
	0.2	2.9
SCHLINGEMANN_SKIN_CARCINOGENESIS_TPA_UP	753	0E-
	48	06
		2.9
REACTOME_COOPERATION_OF_PREFOLDIN_AND_TRIC_CCT_IN_ACTIN_AND_TUBULIN_FOLDING	0.2	1E-
	753	06
	0.2	2.9
DELYS_THYROID_CANCER_UP	752	3E-
	56	06
	0.2	2.9
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_CYCLE_ARREST	750	7E-
	92	06
	0.2	2.9
REACTOME_IRE1ALPHA_ACTIVATES_CHAPERONES	750	9E-
	01	06
	0.2	3.0
SANSOM_WNT_PATHWAY_REQUIRE_MYC	747	6E-
	22	06
	0.2	3.1
VISALA_RESPONSE_TO_HEAT_SHOCK_AND_AGING_DN	745	0E-
	71	06
	0.2	3.1
REACTOME_TNF_RECEPTOR_SUPERFAMILY_TNFSF_MEMBERS_MEDIATING_NON_CANONICAL_NF_KB_PATHWAY	745	1E-
	47	06
	0.2	3.1
SMID_BREAST_CANCER_RELAPSE_IN_LIVER_UP	745	2E-
	25	06
	0.2	3.1
LI_AMPLIFIED_IN_LUNG_CANCER	744	2E-
	92	06
	0.2	3.1
YU_MYC_TARGETS_UP	744	3E-
	72	06
	0.2	3.1
KIM_GLIS2_TARGETS_UP	743	7E-
	26	06

REACTOME_RECEPTOR_MEDIATED_MITOPHAGY	0.2	3.1
	743	7E-
	06	06
DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP	0.2	3.2
	742	0E-
	23	06
RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_SMAD4_UP	0.2	3.2
	741	1E-
	75	06
REACTOME_M_PHASE	0.2	3.2
	741	2E-
	57	06
RAMASWAMY_METASTASIS_UP	0.2	3.2
	740	3E-
	9	06
PID_INTEGRIN2_PATHWAY	0.2	3.2
	740	4E-
	78	06
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	0.2	3.2
	740	6E-
	01	06
GLINSKY_CANCER_DEATH_UP	0.2	3.2
	738	9E-
	85	06
REACTOME_CARBOXYTERMINAL_POST_TRANSLATIONAL_MODIFICATIO NS_OF_TUBULIN	0.2	3.3
	736	6E-
	6	06
REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY	0.2	3.3
	735	9E-
	55	06
HAMAI_APOPTOSIS_VIA_TRAIL_DN	0.2	3.3
	735	9E-
	55	06
MURAKAMI_UV_RESPONSE_1HR_UP	0.2	3.3
	735	9E-
	3	06
RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP	0.2	3.4
	734	2E-
	29	06
GOLUB_ALL_VS_AML_UP	0.2	3.4
	734	2E-
	28	06
PID_FRA_PATHWAY	0.2	3.5
	731	2E-
	02	06
REACTOME_INTERLEUKIN_1_FAMILY_SIGNALING	0.2	3.5
	730	4E-
	43	06
REACTOME_ACYL_CHAIN_REMODELLING_OF_PG	0.2	3.5
	729	5E-

	98	06
	0.2	3.6
REACTOME_SCAVENGING_BY_CLASS_B_RECEPTORS	727	2E-
	69	06
	0.2	3.6
STEGER_ADIPOGENESIS_DN	725	8E-
	94	06
	0.2	3.6
PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION	725	9E-
	57	06
	0.2	3.7
RODWELL_AGING_KIDNEY_UP	725	0E-
	21	06
	0.2	3.7
REACTOME_REGULATION_OF_CYTOSKELETAL_REMODELING_AND_CEL L_SPREADING_BY_IPP_COMPLEX_COMPONENTS	723	4E-
	81	06
	0.2	3.9
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP	718	3E-
	11	06
	0.2	3.9
MUELLER_PLURINET	716	7E-
	89	06
	0.2	4.0
GAVIN_FOXP3_TARGETS_CLUSTER_P6	715	3E-
	21	06
	0.2	4.0
HOLLEMAN_DAUNORUBICIN_ALL_UP	714	7E-
	01	06
	0.2	4.1
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_C DC6	710	8E-
	77	06
	0.2	4.2
ZHENG_IL22_SIGNALING_UP	709	2E-
	8	06
	0.2	4.2
RODWELL_AGING_KIDNEY_NO_BLOOD_UP	709	2E-
	56	06
	0.2	4.2
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_DN	708	5E-
	72	06
	0.2	4.2
ROVERSI_GLIOMA_COPY_NUMBER_UP	708	8E-
	02	06
	0.2	4.2
BOUDOUKHA_BOUND_BY_IGF2BP2	707	9E-
	66	06
	0.2	4.3
KESHELAVA_MULTIPLE_DRUG_RESISTANCE	706	3E-
	53	06
JIANG_VHL_TARGETS	0.2	4.3

	706	5E-
	09	06
	0.2	4.4
REACTOME_DNA_REPLICATION	703	3E-
	91	06
	0.2	4.4
AUJLA_IL22_AND_IL17A_SIGNALING	703	4E-
	8	06
	0.2	4.5
HOWLIN_CITED1_TARGETS_2_UP	701	1E-
	73	06
	0.2	4.6
DIRMEIER_LMP1_RESPONSE_LATE_DN	698	4E-
	57	06
	0.2	4.6
OISHI_CHOLANGIOMA_STEM_CELL_LIKE_DN	697	8E-
	5	06
	0.2	4.6
IIZUKA_LIVER_CANCER_PROGRESSION_L0_L1_DN	697	8E-
	36	06
	0.2	4.7
PID_DELTA_NP63_PATHWAY	696	1E-
	7	06
	0.2	4.7
RAGHAVACHARI_PLATELET_SPECIFIC_GENES	696	2E-
	42	06
	0.2	4.7
SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP	696	2E-
	38	06
	0.2	4.8
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	692	9E-
	11	06
	0.2	4.9
VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1	691	1E-
	73	06
	0.2	4.9
SOUCEK_MYC_TARGETS	690	7E-
	4	06
	0.2	4.9
REACTOME_ATTACHMENT_OF_GPI_ANCHOR_TO_UPAR	690	7E-
	2	06
	0.2	5.0
MARTENS_TRETINOIN_RESPONSE_DN	689	0E-
	6	06
	0.2	5.0
REICHERT_G1S_REGULATORS_AS_PI3K_TARGETS	688	5E-
	35	06
	0.2	5.0
AMIT_EGF_RESPONSE_120_MCF10A	688	6E-
	11	06

ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN	0.2	5.1
	687	0E-
	3	06
	0.2	5.2
REACTOME_APOBEC3G_MEDIATED_RESISTANCE_TO_HIV_1_INFECTION	684	0E-
	91	06
	0.2	5.2
WINNEPENNINGX_MELANOMA_METASTASIS_UP	684	0E-
	9	06
	0.2	5.2
SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP	684	3E-
	25	06
	0.2	5.2
PID_AURORA_A_PATHWAY	683	5E-
	87	06
	0.2	5.2
REACTOME_VLDL_CLEARANCE	683	5E-
	73	06
	0.2	5.3
EGUCHI_CELL_CYCLE_RB1_TARGETS	681	3E-
	94	06
	0.2	5.4
BALLIF_DEVELOPMENTAL_DISABILITY_P16_P12_DELETION	679	6E-
	18	06
	0.2	5.4
REACTOME_CELL_CYCLE_MITOTIC	679	6E-
	08	06
	0.2	5.4
REACTOME_ALTERNATIVE_COMPLEMENT_ACTIVATION	678	7E-
	97	06
	0.2	5.5
MARTINEZ_RB1_TARGETS_DN	676	9E-
	3	06
	0.2	5.6
HOLLEMAN_VINCRIStINE_RESISTANCE_B_ALL_DN	674	5E-
	99	06
	0.2	5.6
HUANG_FOXA2_TARGETS_DN	674	9E-
	17	06
	0.2	5.7
REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	673	1E-
	82	06
	0.2	5.8
SESTO_RESPONSE_TO_UV_C7	670	5E-
	74	06
	0.2	5.8
REACTOME_COPI_DEPENDENT_GOLGI_TO_ER_RETROGRADE_TRAFFIC	670	7E-
	47	06
	0.2	5.9
REACTOME_DEGRADATION_OF_DVL	669	3E-

	17	06
REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVE D_IN_DIFFERENTIATION_OF_MYELOID_CELLS	0.2 668	5.9 7E-
	38	06
VERRECCHIA_RESPONSE_TO_TGFB1_C4	0.2 667	6.0 0E-
	88	06
REACTOME_HDL_ASSEMBLY	0.2 667	6.0 2E-
	47	06
KIM_MYCL1_AMPLIFICATION_TARGETS_UP	0.2 667	6.0 3E-
	14	06
PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP	0.2 664	6.1 9E-
	03	06
CASTELLANO_NRAS_TARGETS_UP	0.2 658	6.5 1E-
	02	06
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	0.2 656	6.5 7E-
	86	06
YAGI_AML_WITH_T_8_21_TRANSLOCATION	0.2 655	6.6 5E-
	38	06
JOSEPH_RESPONSE_TO_SODIUM_BUTYRATE_UP	0.2 653	6.7 7E-
	29	06
HINATA_NFKB_TARGETS_KERATINOCYTE_UP	0.2 652	6.8 1E-
	48	06
BROWN_MYELOID_CELL_DEVELOPMENT_DN	0.2 651	6.8 5E-
	85	06
SCHLINGEMANN_SKIN_CARCINOGENESIS_TPA_DN	0.2 651	6.8 8E-
	3	06
TIAN_TNF_SIGNALING_VIA_NFKB	0.2 650	6.9 4E-
	22	06
REACTOME_CYTOSOLIC_SENSORS_OF_PATHOGEN_ASSOCIATED_DNA	0.2 648	7.0 2E-
	85	06
DAVIES_MULTIPLE_MYELOMA_VS_MGUS_DN	0.2 645	7.2 2E-
	46	06
KORKOLA_EMBRYONAL_CARCINOMA_UP	0.2 642	7.3 8E-
	79	06
REACTOME_INFLUENZA_INFECTION	0.2	7.4

	641	4E-
	78	06
	0.2	7.6
LIU_CD_X2_TARGETS_DN	637	9E-
	75	06
	0.2	7.7
KIM_WT1_TARGETS_12HR_DN	636	9E-
	26	06
	0.2	7.8
PUJANA_BRCA1_PCC_NETWORK	635	2E-
	72	06
	0.2	7.9
REACTOME_FORMYL_PEPTIDE_RECEPTORS_BIND_FORMYL_PEPTIDES_A ND_MANY_OTHER_LIGANDS	633	6E-
	6	06
	0.2	7.9
HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_UP	633	8E-
	32	06
	0.2	8.0
PID_IL4_2PATHWAY	632	7E-
	02	06
	0.2	8.1
HOUSTIS_ROS	631	0E-
	55	06
	0.2	8.1
ZHONG_SECRETOME_OF_LUNG_CANCER_AND_FIBROBLAST	630	8E-
	23	06
	0.2	8.1
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	630	9E-
	07	06
	0.2	8.2
ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_DN	629	2E-
	64	06
	0.2	8.4
PETROVA_ENDOTHELIUM_LYMPHATIC_VS_BLOOD_DN	625	9E-
	77	06
	0.2	8.5
OSADA_ASCL1_TARGETS_DN	624	6E-
	78	06
	0.2	8.5
SONG_TARGETS_OF_IE86_CMV_PROTEIN	624	7E-
	68	06
	0.2	8.5
NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_UP	624	7E-
	55	06
	0.2	8.5
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS ENDOSOMES	624	8E-
	47	06
	0.2	8.7
HAHTOLA_SEZARY_SYNDROM_UP	622	0E-
	78	06

LIANG_SILENCED_BY_METHYLATION_DN	0.2	8.9
	618	8E-
	84	06
	0.2	9.0
HUMMERICH_SKIN_CANCER_PROGRESSION_UP	617	5E-
	92	06
	0.2	9.0
FINETTI_BREAST_CANCER_KINOME_RED	617	7E-
	69	06
	0.2	9.1
REACTOME_STING_MEDIATED_INDUCION_OF_HOST_IMMUNE_RESPON	616	8E-
SES	13	06
	0.2	9.2
COATES_MACROPHAGE_M1_VS_M2_DN	615	5E-
	19	06
	0.2	9.3
HU_GENOTOXIN_ACTION_DIRECT_VS_INDIRECT_24HR	614	1E-
	5	06
	0.2	9.3
IIZUKA_LIVER_CANCER_PROGRESSION_G2_G3_DN	613	8E-
	5	06
	0.2	9.4
REACTOME_CELLULAR_RESPONSE_TO_HYPOXIA	612	5E-
	57	06
	0.2	9.5
REACTOME_SIGNALING_BY_ROBO_RECEPTORS	611	3E-
	59	06
	0.2	9.6
BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_UP	610	3E-
	26	06
	0.2	9.6
PETROVA_PROX1_TARGETS_UP	610	5E-
	02	06
	0.2	9.8
BOYALT_LIVER_CANCER_SUBCLASS_G5_DN	607	5E-
	53	06
	0.2	9.9
YANG_BREAST_CANCER_ESR1_BULK_DN	606	1E-
	77	06
	0.2	1.0
WANG_TUMOR_INVASIVENESS_UP	605	1E-
	06	05
	0.2	1.0
REACTOME_CELL_CYCLE_CHECKPOINTS	604	1E-
	35	05
	0.2	1.0
JACKSON_DNMT1_TARGETS_UP	602	2E-
	8	05
	0.2	1.0
HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN	601	3E-

	94	05
	0.2	1.0
BIOCARTA_ACETAMINOPHEN_PATHWAY	599	5E-
	99	05
	0.2	1.0
REACTOME_HIV_INFECTION	599	5E-
	65	05
	0.2	1.0
BIOCARTA_G2_PATHWAY	598	6E-
	41	05
	0.2	1.0
CASTELLANO_NRAS_TARGETS_DN	596	8E-
	74	05
	0.2	1.0
HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP	594	9E-
	64	05
	0.2	1.1
REACTOME_FBXL7_DOWN_REGULATES_AURKA_DURING_MITOTIC_ENTRY_AND_IN_EARLY_MITOSIS	593	0E-
	8	05
	0.2	1.1
REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	593	1E-
	11	05
	0.2	1.1
DAIRKEE_CANCER_PRONE_RESPONSE_BPA_E2	590	3E-
	84	05
	0.2	1.1
REACTOME_BH3_ONLY_PROTEINS_ASSOCIATE_WITH_AND_INACTIVATE_ANTI_APOPTOTIC_BCL_2_MEMBERS	587	6E-
	85	05
	0.2	1.1
LANDIS_ERBB2_BREAST_PRENEOPLASTIC_UP	587	6E-
	71	05
	0.2	1.1
KEGG_PYRIMIDINE_METABOLISM	587	6E-
	53	05
	0.2	1.1
RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POORLY_UP	587	6E-
	2	05
	0.2	1.1
MACLACHLAN_BRCA1_TARGETS_UP	587	6E-
	06	05
	0.2	1.1
GRAHAM_CML QUIESCENT_VS_CML_DIVIDING_UP	586	7E-
	79	05
	0.2	1.1
PID_MYC_PATHWAY	585	8E-
	47	05
	0.2	1.2
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	583	0E-
	33	05
	0.2	1.2
WATANABE_RECTAL_CANCER_RADIOOTHERAPY_RESPONSIVE_DN		

	583	0E-
	15	05
	0.2	1.2
WOOD_EBV_EBNA1_TARGETS_UP	581	1E-
	68	05
	0.2	1.2
CHICAS_RB1_TARGETS_CONFLUENT	579	4E-
	34	05
	0.2	1.2
KEGG_PROTEASOME	578	4E-
	66	05
	0.2	1.2
REACTOME_DEFECTIVE_ST3GAL3_CAUSES_MCT12_AND_EIEE15	576	6E-
	87	05
	0.2	1.3
OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_UP	573	0E-
	54	05
	0.2	1.3
CERIBELLI_GENES_INACTIVE_AND_BOUND_BY_NFY	573	0E-
	25	05
	0.2	1.3
GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN	570	3E-
	13	05
	0.2	1.3
REACTOME_RUNX2_REGULATES_CHONDROCYTE_MATURATION	570	3E-
	03	05
	0.2	1.3
BIOCARTA_CELLCYCLE_PATHWAY	569	4E-
	79	05
	0.2	1.3
REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	569	4E-
	67	05
	0.2	1.3
REACTOME_MRNA_DECAY_BY_5_TO_3_EXORIBONUCLEASE	569	4E-
	25	05
	0.2	1.3
MARTIN_VIRAL_GPCR_SIGNALING_DN	568	5E-
	86	05
	0.2	1.3
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	567	7E-
	01	05
	0.2	1.3
ANDERSEN_CHOLANGIOCARCINOMA_CLASS2	566	7E-
	99	05
	0.2	1.3
PID_RB_1PATHWAY	566	7E-
	83	05
	0.2	1.3
MATTHEWS_API1_TARGETS	566	7E-
	65	05

REACTOME_REGULATION_OF_RUNX2_EXPRESSION_AND_ACTIVITY	0.2	1.3
	566	8E-
	08	05
POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_UP	0.2	1.4
	564	0E-
	29	05
REACTOME_UCH_PROTEINASES	0.2	1.4
	564	0E-
	02	05
ONO_AML1_TARGETS_DN	0.2	1.4
	563	0E-
	62	05
ANASTASSIOU_MULTICANCER_INVASIVENESS_SIGNATURE	0.2	1.4
	563	1E-
	16	05
FERREIRA_EWINGS_SARCOMA_UNSTABLE_VS_STABLE_UP	0.2	1.4
	562	1E-
	81	05
LAMB_CCND1_TARGETS	0.2	1.4
	560	4E-
	16	05
ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP	0.2	1.4
	558	6E-
	78	05
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	0.2	1.4
	558	6E-
	65	05
BROWN_MYELOID_CELL_DEVELOPMENT_UP	0.2	1.4
	557	7E-
	63	05
LINDVALL_IMMORTALIZED_BY_TERT_DN	0.2	1.4
	556	8E-
	63	05
REACTOME_PIWI_INTERACTING_RNA_PIRNA_BIOGENESIS	0.2	1.5
	555	0E-
	51	05
PID_CASPASE_PATHWAY	0.2	1.5
	553	2E-
	7	05
BIOCARTA_SM_PATHWAY	0.2	1.5
	552	4E-
	3	05
KONDO_HYPOXIA	0.2	1.5
	552	4E-
	29	05
LOPEZ_MESOTHELIOMA_SURVIVAL_DN	0.2	1.5
	552	4E-
	07	05
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	0.2	1.5
	551	4E-

	97	05
	0.2	1.5
WONG_PROTEASOME_GENE_MODULE	550	6E-
	7	05
	0.2	1.5
BHAT_ESR1_TARGETS_NOT_VIA_AKT1_UP	548	9E-
	12	05
	0.2	1.6
HAHTOLA_CTCL_PATHOGENESIS	545	2E-
	8	05
	0.2	1.6
MARSHALL_VIRAL_INFECTION_RESPONSE_UP	545	2E-
	52	05
	0.2	1.6
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	545	2E-
	4	05
	0.2	1.6
REACTOME_DEFECTIVE_B4GALT1_CAUSES_B4GALT1_CDG_CDG_2D	544	4E-
	2	05
	0.2	1.6
HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP	542	6E-
	37	05
	0.2	1.6
BOYALT_LIVER_CANCER_SUBCLASS_G3_UP	542	6E-
	28	05
	0.2	1.6
REACTOME_PYRIMIDINE_SALVAGE	541	7E-
	88	05
	0.2	1.7
CROONQUIST_IL6_DEPRIVATION_UP	538	1E-
	54	05
	0.2	1.8
REACTOME_INTERLEUKIN_21_SIGNALING	532	0E-
	36	05
	0.2	1.8
BILD_MYC_ONCOGENIC_SIGNATURE	530	2E-
	67	05
	0.2	1.8
REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION	530	2E-
	55	05
	0.2	1.8
REACTOME_GENE_AND_PROTEIN_EXPRESSION_BY_JAK_STAT_SIGNALING_AFTER_INTERLEUKIN_12_STIMULATION	528	6E-
	09	05
	0.2	1.8
FERRANDO_TAL1_NEIGHBORS	527	7E-
	53	05
	0.2	1.8
REACTOME_PURINE_SALVAGE	526	8E-
	44	05
	0.2	1.8
CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN		

	526	9E-
	13	05
	0.2	1.9
NOJIMA_SFRP2_TARGETS_UP	525	0E-
	03	05
	0.2	1.9
WANG_TNF_TARGETS	522	5E-
	36	05
	0.2	1.9
KEGG_SULFUR_METABOLISM	521	6E-
	57	05
	0.2	1.9
KAMIKUBO_MYELOID_CEBPA_NETWORK	521	6E-
	53	05
	0.2	2.0
SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN	517	2E-
	7	05
	0.2	2.0
REACTOME_CELL_CYCLE	516	4E-
	56	05
	0.2	2.0
SMIRNOV_RESPONSE_TO_IR_6HR_DN	514	7E-
	32	05
	0.2	2.0
FUJIWARA_PARK2_HEPATOCYTE_PROLIFERATION_DN	512	9E-
	99	05
	0.2	2.0
MANALO_HYPOXIA_DN	512	9E-
	92	05
	0.2	2.1
KYNG_RESPONSE_TO_H2O2	512	0E-
	39	05
	0.2	2.1
REACTOME_RNA_POLYMERASE_III_CHAIN_ELONGATION	509	5E-
	38	05
	0.2	2.1
BOQUEST_STEM_CELL_UP	509	6E-
	26	05
	0.2	2.2
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN	504	4E-
	5	05
	0.2	2.2
LEE_LIVER_CANCER_HEPATOBLAST	503	6E-
	11	05
	0.2	2.3
REACTOME_ASSEMBLY_AND_CELL_SURFACE_PRESENTATION_OF_NMD A_RECEPTORS	499	2E-
	96	05
	0.2	2.3
BURTON_ADIPOGENESIS_4	496	8E-
	31	05

MARKEY_RB1_ACUTE_LOF_DN	495	0.2	2.3
	98	9E-	05
REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21	492	0.2	2.4
	88	5E-	05
REACTOME_REGULATION_OF_EXPRESSION_OF_SLITS_AND_ROBOS	492	0.2	2.4
	02	6E-	05
PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP	491	0.2	2.4
	84	7E-	05
CESLER_BRAIN_QTL_CIS	491	0.2	2.4
	17	8E-	05
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_R EQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHEC KPOINT_COMPONENTS	488	0.2	2.5
	6	3E-	05
LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER	487	0.2	2.5
	15	6E-	05
REACTOME_GOLGI_CISTERNAE_PERICENTRIOLAR_STACK_REORGANIZA TION	486	0.2	2.5
	86	8E-	05
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_ RECEPTORS_BY_RECRUITING_THEM_TO_CLATHRIN_ADAPTERS	482	0.2	2.6
	38	6E-	05
ZHAN_EARLY_DIFFERENTIATION_GENES_DN	482	0.2	2.6
	32	6E-	05
CHICAS_RB1_TARGETS_GROWING	481	0.2	2.6
	62	7E-	05
REACTOME_DEFECTIVE_CHST6_CAUSES_MCDC1	480	0.2	2.6
	63	9E-	05
RICKMAN_HEAD_AND_NECK_CANCER_B	480	0.2	2.7
	37	0E-	05
VANDESLUIS_COMMD1_TARGETS_GROUP_3_DN	479	0.2	2.7
	37	2E-	05
FONTAINE_FOLLICULAR_THYROID_ADENOMA_DN	478	0.2	2.7
	79	3E-	05
BENPORATH_MYC_TARGETS_WITH_EBOX	478	0.2	2.7
	64	3E-	05
REACTOME_CELLULAR_RESPONSES_TO_EXTERNAL_STIMULI	474	0.2	2.8
	474	1E-	

	95	05
	0.2	2.8
FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP	471	9E-
	56	05
	0.2	2.9
REACTOME_LEADING_STRAND_SYNTHESIS	470	0E-
	87	05
	0.2	2.9
MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_DN	469	2E-
	98	05
	0.2	2.9
BIOCARTA_IL10_PATHWAY	469	3E-
	6	05
	0.2	2.9
REACTOME_DEFECTIVE_CFTR_CAUSES_CYSTIC_FIBROSIS	468	5E-
	77	05
	0.2	2.9
BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP	468	5E-
	66	05
	0.2	2.9
BIOCARTA_STEM_PATHWAY	468	6E-
	11	05
	0.2	2.9
LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN	467	7E-
	74	05
	0.2	2.9
LIN_TUMOR_ESCAPE_FROM_IMMUNE_ATTACK	467	9E-
	11	05
	0.2	3.0
CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP	465	2E-
	55	05
	0.2	3.0
MELLMAN_TUT1_TARGETS_UP	464	5E-
	52	05
	0.2	3.0
GALINDO_IMMUNE_RESPONSE_TO_ENTEROTOXIN	463	8E-
	07	05
	0.2	3.0
REACTOME_CLEC7A_DECTIN_1_SIGNALING	462	9E-
	69	05
	0.2	3.1
REACTOME_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR _TC_NER	461	1E-
	77	05
	0.2	3.1
REACTOME_NEF_MEDIATED_CD4_DOWN_REGULATION	458	8E-
	96	05
	0.2	3.2
WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_UP	457	2E-
	28	05
RIZKI_TUMOR_INVASIVENESS_2D_DN	0.2	3.2

	455	5E-
	99	05
	0.2	3.2
REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION	455	7E-
	34	05
	0.2	3.3
LIAO_HAVE_SOX4_BINDING_SITES	452	4E-
	3	05
	0.2	3.3
REACTOME_DEGRADATION_OF_AXIN	451	8E-
		05
	0.2	3.3
REACTOME_MITOTIC_G1_G1_S_PHASES	450	8E-
	72	05
	0.2	3.4
HOLLERN_EMT_BREAST_TUMOR_UP	449	1E-
	58	05
	0.2	3.4
REACTOME_NUCLEAR_ENVELOPE_REASSEMBLY	448	6E-
	02	05
	0.2	3.4
BAKER_HEMATOPOESIS_STAT1_TARGETS	447	6E-
	9	05
	0.2	3.4
GHANDHI_BYSTANDER_IRRADIATION_UP	447	7E-
	61	05
	0.2	3.5
DELASERNA_MYOD_TARGETS_DN	445	1E-
	93	05
	0.2	3.5
REACTOME_ATF4_ACTIVATES_GENES_IN_RESPONSE_TO_ENDOPLASMIC _RETICULUM_STRESS	445	1E-
	86	05
	0.2	3.5
SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP	445	3E-
	3	05
	0.2	3.5
REACTOME_DISEASES_OF_GLYCOSYLATION	443	7E-
	78	05
	0.2	3.5
HOLLERN_ADENOMYOEPITHELIAL_BREAST_TUMOR	443	9E-
	15	05
	0.2	3.6
TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL_UP	442	0E-
	73	05
	0.2	3.6
REACTOME_DNA_REPLICATION_PRE_INITIATION	442	1E-
	13	05
	0.2	3.6
ONDER_CDH1_SIGNALING_VIA_CTNNB1	441	3E-
	7	05

REACTOME_REGULATION_OF_APOPTOSIS	441	0.2	3.6
	26	4E-	05
REACTOME_DISPLACEMENT_OF_DNA_GLYCOSYLASE_BY_APEX1	441	0.2	3.6
	03	4E-	05
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_B IND_AU_RICH_ELEMENTS	441	0.2	3.6
	01	4E-	05
MARTORIATI_MDM4_TARGETS_FETAL_LIVER_UP	440	0.2	3.6
	84	5E-	05
REACTOME_CELLULAR_RESPONSES_TO_STRESS	440	0.2	3.6
	05	7E-	05
NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON	439	0.2	3.6
	63	8E-	05
TSUNODA_CISPLATIN_RESISTANCE_UP	439	0.2	3.7
	03	0E-	05
REACTOME_MITOPHAGY	438	0.2	3.7
	89	0E-	05
REACTOME_WNT5A_DEPENDENT_INTERNALIZATION_OF_FZD2_FZD5_AN D_ROR2	437	0.2	3.7
	88	3E-	05
KRASNOSELSKAYA_ILF3_TARGETS_DN	437	0.2	3.7
	26	5E-	05
MIKKELSEN_ES_LCP_WITH_H3K4ME3_AND_H3K27ME3	436	0.2	3.7
	45	7E-	05
QI_HYPOXIA_TARGETS_OF_HIF1A_AND_FOXA2	436	0.2	3.7
	13	8E-	05
REACTOME_NEGATIVE_REGULATION_OF_NOTCH4_SIGNALING	435	0.2	3.8
	29	1E-	05
HELLER_SILENCED_BY_METHYLATION_UP	434	0.2	3.8
	98	1E-	05
JL_CARCINOGENESIS_BY_KRAS_AND_STK11_DN	433	0.2	3.8
	58	6E-	05
RAY_ALZHEIMERS_DISEASE	433	0.2	3.8
	38	6E-	05
REACTOME_G2_M_CHECKPOINTS	432	0.2	3.8
	432	8E-	

	57	05
	0.2	3.9
RUTELLA_RESPONSE_TO_HGF_UP	432	0E-
	21	05
	0.2	3.9
REACTOME_MTORC1_MEDIATED_SIGNALLING	430	3E-
	99	05
	0.2	3.9
REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVE D_IN_WNT_SIGNALING	430	5E-
	37	05
	0.2	3.9
BIOCARTA_FREE_PATHWAY	429	8E-
	36	05
	0.2	4.0
REN_BOUND_BY_E2F	428	1E-
	26	05
	0.2	4.0
REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_C CT_TRIC	427	3E-
	61	05
	0.2	4.0
JACKSON_DNMT1_TARGETS_DN	426	5E-
	92	05
	0.2	4.0
REACTOME_HEDGEHOG_LIGAND_BIOGENESIS	426	5E-
	9	05
	0.2	4.0
ROPERO_HDAC2_TARGETS	426	6E-
	6	05
	0.2	4.1
PID_PLK1_PATHWAY	425	1E-
	14	05
	0.2	4.1
JOHANSSON_GLIOMAGENESIS_BY_PDGF_DN	422	8E-
	99	05
	0.2	4.1
REACTOME_GOLGI_TO_ER_RETROGRADE_TRANSPORT	422	9E-
	55	05
	0.2	4.2
POS_RESPONSE_TO_HISTAMINE_DN	422	0E-
	14	05
	0.2	4.2
MARTINEZ_TP53_TARGETS_DN	421	3E-
	13	05
	0.2	4.2
REACTOME_HIGHLY_CALCIIUM_PERMEABLE_POSTSYNAPTIC_NICOTINIC _ACETYLCHOLINE_RECEPTORS	420	4E-
	96	05
	0.2	4.3
WU_HBX_TARGETS_3_UP	417	6E-
	21	05
REACTOME_CROSSLINKING_OF_COLLAGEN_FIBRILS	0.2	4.4

	416	0E-
	07	05
	0.2	4.4
PACHER_TARGETS_OF_IGF1_AND_IGF2_UP	414	6E-
	22	05
	0.2	4.4
VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP	413	9E-
	3	05
	0.2	4.5
OZANNE_API_TARGETS_UP	413	0E-
	16	05
	0.2	4.5
REACTOME_PERK_REGULATES_GENE_EXPRESSION	411	5E-
	61	05
	0.2	4.5
HOLLEMAN_VINCRIStINE_RESISTANCE_ALL_DN	410	8E-
	68	05
	0.2	4.5
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_UP	410	9E-
	42	05
	0.2	4.5
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_TP53	410	9E-
	32	05
	0.2	4.6
GROSS_HYPOXIA_VIA_ELK3_AND_HIF1A_DN	409	1E-
	81	05
	0.2	4.6
GHANDHI_DIRECT_IRRADIATION_UP	409	4E-
	09	05
	0.2	4.6
YU_BAP1_TARGETS	408	6E-
	3	05
	0.2	4.6
BURTON_ADIPOGENESIS_PEAK_AT_8HR	408	7E-
	11	05
	0.2	4.6
WANG_CISPLATIN_RESPONSE_AND_XPC_DN	408	7E-
	04	05
	0.2	4.6
SCHWAB_TARGETS_OF_BMYB_POLYMORPHIC_VARIANTS_UP	407	8E-
	67	05
	0.2	4.7
REACTOME_AUF1_HNRNP_D0_BINDS_AND_DESTABILIZES_MRNA	407	0E-
	28	05
	0.2	4.7
REACTOME_CHYLOMICRON_ASSEMBLY	407	0E-
	16	05
	0.2	4.7
MUNSHI_MULTIPLE_MYELOMA_UP	406	3E-
	24	05

REACTOME_NUCLEOTIDE_EXCISION_REPAIR	0.2	4.7
	405	6E-
	46	05
HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_UP	0.2	4.8
	403	2E-
	75	05
REACTOME_INTERACTION_WITH_CUMULUS_CELLS_AND_THE_ZONA_PELLUCIDA	0.2	4.8
	403	4E-
	23	05
MURAKAMI_UV_RESPONSE_1HR_DN	0.2	4.8
	402	8E-
	16	05
BIOCARTA_PTC1_PATHWAY	0.2	4.9
	399	6E-
	9	05
AMIT_EGF_RESPONSE_240_MCF10A	0.2	4.9
	399	7E-
	85	05
REACTOME_C_TYPE_LECTIN_RECEPTORS_CLRS	0.2	5.0
	399	0E-
	06	05
REACTOME_DEGRADATION_OF_GLI1_BY_THE_PROTEASOME	0.2	5.0
	398	2E-
	38	05
REACTOME_ACTIVATION_OF_NIMA_KINASES_NEK9_NEK6_NEK7	0.2	5.0
	397	4E-
	89	05
DELASERNA_MYOD_TARGETS_UP	0.2	5.0
	396	8E-
	91	05
LE_NEURONAL_DIFFERENTIATION_DN	0.2	5.0
	396	9E-
	53	05
PID_UPA_UPAR_PATHWAY	0.2	5.1
	394	6E-
	81	05
MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_UP	0.2	5.1
	394	6E-
	65	05
REACTOME_RESOLUTION_OF_ABASIC_SITES_AP_SITES	0.2	5.2
	393	2E-
	26	05
REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_DIFFERENTIATION_OF_HSCS	0.2	5.2
	393	2E-
	09	05
BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_24HR_DN	0.2	5.2
	392	4E-
	69	05
MATZUK_SPERMATOCYTE	0.2	5.2
	392	6E-

	21	05
	0.2	5.2
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SULFATE	391	9E-
	35	05
	0.2	5.3
PID_P73PATHWAY	391	0E-
	23	05
	0.2	5.3
FUNG_IL2_TARGETS_WITH_STAT5_BINDING_SITES	390	1E-
	87	05
	0.2	5.3
REACTOME_MAPK6_MAPK4_SIGNALING	390	3E-
	35	05
	0.2	5.3
LI_INDUCED_T_TO_NATURAL_KILLER_UP	390	4E-
	15	05
	0.2	5.3
REACTOME_SIGNAL_REGULATORY_PROTEIN_FAMILY_INTERACTIONS	390	4E-
	06	05
	0.2	5.3
CAFFAREL_RESPONSE_TO_THC_DN	389	6E-
	66	05
	0.2	5.3
RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP	388	9E-
	74	05
	0.2	5.4
SA_REG_CASCADE_OF_CYCLIN_EXPR	387	4E-
	52	05
	0.2	5.4
ZHAN_MULTIPLE_MYELOMA_CD2_DN	386	7E-
	91	05
	0.2	5.7
REACTOME_DISEASES_ASSOCIATED_WITH_GLYCOSAMINOGLYCAN_ME TABOLISM	379	6E-
	92	05
	0.2	5.7
VERRECCHIA_RESPONSE_TO_TGFB1_C3	379	6E-
	91	05
	0.2	5.7
DUTERTRE ESTRADIOL_RESPONSE_24HR_UP	379	8E-
	35	05
	0.2	5.9
PUJANA_CHEK2_PCC_NETWORK	375	4E-
	75	05
	0.2	5.9
QI_PLASMACYTOMA_UP	375	7E-
	1	05
	0.2	5.9
PID_ATR_PATHWAY	374	9E-
	63	05
REACTOME_INTERLEUKIN_9_SIGNALING	0.2	6.1

	371	1E-
	94	05
	0.2	6.1
ZHENG_GLIOMASTOMA_PLASTICITY_UP	371	2E-
	74	05
	0.2	6.1
CUI_GLUCOSE_DEPRIVATION	371	4E-
	25	05
	0.2	6.1
MAHAJAN_RESPONSE_TO_IL1A_UP	370	9E-
	14	05
	0.2	6.2
BURTON_ADIPOGENESIS_PEAK_AT_0HR	368	7E-
	33	05
	0.2	6.4
PID_SYNDECAN_2_PATHWAY	364	6E-
	29	05
	0.2	6.5
FLECHNER_PBL_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP	362	5E-
	33	05
	0.2	6.7
BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL_TRANS	359	0E-
	35	05
	0.2	6.7
HWANG_PROSTATE_CANCER_MARKERS	358	4E-
	48	05
	0.2	6.7
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING	358	5E-
	36	05
	0.2	6.8
JI_RESPONSE_TO_FSH_UP	357	0E-
	31	05
	0.2	6.8
LEE_INTRATHYMIC_T_PROGENITOR	357	1E-
	1	05
	0.2	6.8
KASLER_HDAC7_TARGETS_1_UP	356	6E-
	05	05
	0.2	6.9
RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN	353	7E-
	98	05
	0.2	7.0
REACTOME_BASE_EXCISION_REPAIR	352	7E-
	02	05
	0.2	7.1
REACTOME_COMPLEMENT_CASCADE	349	8E-
	91	05
	0.2	7.1
KEGG_BASE_EXCISION_REPAIR	349	9E-
	74	05

BIOCARTA_DNAFRAGMENT_PATHWAY	0.2	7.2
	348	6E-
	29	05
KRIGE_AMINO_ACID_DEPRIVATION	0.2	7.2
	348	7E-
	17	05
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	0.2	7.3
	347	1E-
	44	05
AMUNDSON_RESPONSE_TO_ARSENITE	0.2	7.4
	345	0E-
	74	05
REACTOME_DECTIN_1_MEDIATED_NONCANONICAL_NF_KB_SIGNALING	0.2	7.4
	344	6E-
	57	05
JIANG_HYPOXIA_CANCER	0.2	7.4
	344	9E-
	06	05
MULLIGHAN_NPM1_MUTATED_SIGNATURE_2_DN	0.2	7.5
	343	3E-
	26	05
CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP	0.2	7.5
	342	9E-
	3	05
CHOW_RASSF1_TARGETS_UP	0.2	7.6
	341	1E-
	82	05
REACTOME_COLLAGEN_DEGRADATION	0.2	7.6
	340	7E-
	79	05
KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_DN	0.2	7.7
	338	9E-
	74	05
REACTOME_COLLAGEN_BIOSYNTHESIS_AND_MODIFYING_ENZYMES	0.2	7.9
	336	3E-
	26	05
KEGG_CELL_CYCLE	0.2	8.0
	334	3E-
	41	05
BIOCARTA_CASPASE_PATHWAY	0.2	8.3
	329	1E-
	82	05
PID_AURORA_B_PATHWAY	0.2	8.3
	328	7E-
	79	05
DAZARD_UV_RESPONSE_CLUSTER_G1	0.2	8.4
	328	1E-
	1	05
REACTOME_EARLY_PHASE_OF_HIV_LIFE_CYCLE	0.2	8.4
	327	3E-

	77	05
	0.2	8.4
DACOSTA_UV_RESPONSE_VIA_ERCC3_UP	327	3E-
	7	05
	0.2	8.4
DORMOY_ELAVL1_TARGETS	327	6E-
	37	05
	0.2	8.5
MARKS_HDAC_TARGETS_UP	326	0E-
	57	05
	0.2	8.5
XU_RESPONSE_TO_TRETINOIN_UP	325	8E-
	28	05
	0.2	8.6
DAVICIONI_MOLECULAR_ARMS_VS_ERMS_DN	324	2E-
	75	05
	0.2	8.6
RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN	324	5E-
	17	05
	0.2	8.6
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_UP	323	9E-
	64	05
	0.2	8.7
BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN	322	5E-
	67	05
	0.2	8.7
BIOCARTA_P35ALZHEIMERS_PATHWAY	322	7E-
	29	05
	0.2	8.8
MIKKELSEN_NPC_LCP_WITH_H3K4ME3	320	6E-
	94	05
	0.2	8.8
TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP	320	7E-
	73	05
	0.2	8.9
BIOCARTA_IL22BP_PATHWAY	319	6E-
	4	05
	0.2	9.1
BIOCARTA_TH1TH2_PATHWAY	316	2E-
	87	05
	0.2	9.1
CHIARADONNA NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_DN	316	3E-
	74	05
	0.2	9.1
HELLEBREKERS_SILENCED_DURING_TUMOR_ANGIOGENESIS	316	4E-
	6	05
	0.2	9.1
ODONNELL_TFRC_TARGETS_DN	316	4E-
	55	05
REACTOME_CD22_MEDIATED_BCR_REGULATION	0.2	9.3

	313	4E-
	6	05
	0.2	9.3
WANG_TARGETS_OF_MLL_CBP_FUSION_DN	313	6E-
	3	05
	0.2	9.5
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_12	310	2E-
	86	05
	0.2	9.5
WHITFIELD_CELL_CYCLE_G2_M	310	6E-
	26	05
	0.2	9.6
ZERBINI_RESPONSE_TO_SULINDAC_DN	309	3E-
	28	05
	0.2	9.6
MANN_RESPONSE_TO_AMIFOSTINE_UP	309	3E-
	26	05
	0.2	9.6
LIAN_LIPA_TARGETS_3M	308	8E-
	59	05
	0.2	9.6
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	308	8E-
	58	05
	0.2	9.8
BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_DN	306	2E-
	59	05
	0.2	9.9
ZHANG_PROLIFERATING_VS QUIESCENT	304	4E-
	82	05
	0.2	9.9
REACTOME_MITOTIC_SPINDLE_CHECKPOINT	304	6E-
	59	05
	0.2	9.9
PID_LIS1_PATHWAY	304	8E-
	28	05
	0.2	9.9
PID_ILK_PATHWAY	304	8E-
	25	05
	0.2	0.0
REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM	303	001
	76	
	0.2	0.0
GROSS_HYPOXIA_VIA_ELK3_ONLY_DN	302	001
	7	01
	0.2	0.0
IGLESIAS_E2F_TARGETS_DN	302	001
	47	01
	0.2	0.0
YANG_BCL3_TARGETS_DN	301	001
	67	02

BIOCARTA_ERAD_PATHWAY	0.2	0.0
	301	001
	66	02
	0.2	0.0
MULLIGHAN_MLL_SIGNATURE_1_UP	301	001
	45	02
	0.2	0.0
REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_C_STRAND_OF_THE_TEL OMERE	300	001
	05	03
	0.2	0.0
KEGG_DNA_REPLICATION	298	001
	32	04
	0.2	0.0
FAELT_B_CLL_WITH_VH3_21_UP	298	001
	298	04
	0.2	0.0
REACTOME_DUAL_INCISION_IN_TC_NER	297	001
	58	05
	0.2	0.0
YAMASHITA_METHYLATED_IN_PROSTATE_CANCER	297	001
	05	05
	0.2	0.0
HUANG_GATA2_TARGETS_UP	296	001
	18	06
	0.2	0.0
HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN	296	001
	296	06
	0.2	0.0
WHITESIDE_CISPLATIN_RESISTANCE_DN	295	001
	79	06
	0.2	0.0
SCIEN_INVERSED_TARGETS_OF_TP53_AND_TP73_UP	295	001
	65	06
	0.2	0.0
MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INHIBITORS_D N	292	001
	84	08
	0.2	0.0
REACTOME_CONVERSION_FROM_APC_C: CDC20_TO_APC_C: CDH1_IN_LAT E_ANAPHASE	291	001
	97	09
	0.2	0.0
TSENG_ADIPOGENIC_POTENTIAL_UP	289	001
	24	11
	0.2	0.0
PURBEY_TARGETS_OF_CTBP1_AND_SATB1_UP	288	001
	84	11
	0.2	0.0
GENTILE_UV_RESPONSE_CLUSTER_D1	288	001
	59	12
	0.2	0.0
GARY_CD5_TARGETS_UP	288	001

	15	12
	0.2	0.0
KEGG_BASAL_CELL_CARCINOMA	287	001
	32	13
	0.2	0.0
REACTOME_RECYCLING_OF EIF2:GDP	285	001
	68	14
	0.2	0.0
SEMBA_FHIT_TARGETS_DN	284	001
	7	15
	0.2	0.0
BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_48HR_DN	284	001
	16	15
	0.2	0.0
WORSCHER_TUMOR_EVASION_AND_TOLEROGENICITY_UP	283	001
	87	15
	0.2	0.0
MARKEY_RB1_CHRONIC_LOF_UP	282	001
	56	17
	0.2	0.0
BIOCARTA_CELL2CELL_PATHWAY	280	001
	42	18
	0.2	0.0
GAVIN_FOXP3_TARGETS_CLUSTER_T7	280	001
	32	18
	0.2	0.0
MARKEY_RB1_ACUTE_LOF_UP	276	001
	43	22
	0.2	0.0
WU_APOPTOSIS_BY_CDKN1A_VIA_TP53	275	001
	69	22
	0.2	0.0
LI_DCP2_BOUND_MRNA	275	001
	69	22
	0.2	0.0
BROWNE_HCMV_INFECTION_14HR_DN	275	001
	12	23
	0.2	0.0
SERVITJA_LIVER_HNF1A_TARGETS_UP	274	001
	75	23
	0.2	0.0
VANTVEER_BREAST_CANCER_POOR_PROGNOSIS	274	001
	47	23
	0.2	0.0
REACTOME_REGULATION_OF_INNATE_IMMUNE_RESPONSES_TO_CYTOSOLIC_DNA	270	001
	98	26
	0.2	0.0
REACTOME_SYNTHESIS_OF_UDP_N_ACETYL_GLUCOSAMINE	269	001
	9	27
	0.2	0.0
LEE_TARGETS_OF_PTCH1_AND_SUFU_UP		

	267	001
	35	3
	0.2	0.0
NOJIMA_SFRP2_TARGETS_DN	267	001
	22	3
	0.2	0.0
NABA_CORE_MATRISOME	266	001
	16	31
	0.2	0.0
YANG_BREAST_CANCER_ESR1_DN	262	001
	73	34
	0.2	0.0
KUMAR_TARGETS_OF_MLL_AF9_FUSION	262	001
	56	34
	0.2	0.0
FURUKAWA_DUSP6_TARGETS_PCI35_DN	262	001
	35	
	0.2	0.0
OZEN_MIR125B1_TARGETS	260	001
	53	36
	0.2	0.0
KAMMINGA_EZH2_TARGETS	260	001
	39	36
	0.2	0.0
REACTOME_INTERLEUKIN_12_SIGNALING	258	001
	2	38
	0.2	0.0
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	258	001
	06	38
	0.2	0.0
KORKOLA_CORRELATED_WITH_POU5F1	256	001
	78	4
	0.2	0.0
REACTOME_TRAF3_DEPENDENT_IRF_ACTIVATION_PATHWAY	254	001
	32	42
	0.2	0.0
BHAT_ESR1_TARGETS_VIA_AKT1_UP	253	001
	42	43
	0.2	0.0
RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_MAPK1_DN	250	001
	4	46
	0.2	0.0
SMID_BREAST_CANCER_LUMINAL_B_DN	248	001
	65	48
	0.2	0.0
WILLIAMS_ESR1_TARGETS_UP	248	001
	34	48
	0.2	0.0
BIOCARTA GRANULOCYTES_PATHWAY	247	001
	2	49

REACTOME_HSF1_DEPENDENT_TRANSACTIVATION	0.2	0.0
	245	001
	07	52
HUMMERICH_MALIGNANT_SKIN_TUMOR_UP	0.2	0.0
	243	001
	31	53
BOYERINAS_ONCOFETAL_TARGETS_OF_LET7A1	0.2	0.0
	243	001
	04	54
REACTOME_METABOLISM_OF_POLYAMINES	0.2	0.0
	242	001
	97	54
GHO_ATF5_TARGETS_DN	0.2	0.0
	242	001
	6	54
REACTOME_INNATE_IMMUNE_SYSTEM	0.2	0.0
	241	001
	86	55
DODD_NASOPHARYNGEAL_CARCINOMA_DN	0.2	0.0
	241	001
	64	55
LINDGREN_BLADDER_CANCER_CLUSTER_3_UP	0.2	0.0
	240	001
	4	57
DACOSTA_ERCC3_ALLELE_XPCS_VS_TTD_UP	0.2	0.0
	240	001
	13	57
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.2	0.0
	239	001
	22	58
KANNAN_TP53_TARGETS_UP	0.2	0.0
	238	001
	34	59
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	0.2	0.0
	235	001
	44	62
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX3	0.2	0.0
	232	001
	86	65
ZHAN_V2_LATE_DIFFERENTIATION_GENES	0.2	0.0
	232	001
	78	65
MULLIGHAN_NPM1_MUTATED_SIGNATURE_1_DN	0.2	0.0
	231	001
	96	66
HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_DN	0.2	0.0
	231	001
	53	67
HELLER_HDAC_TARGETS_DN	0.2	0.0
	230	001

	1	68
REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVE	0.2	0.0
D_IN_DIFFERENTIATION_OF_KERATINOCYTES	229	001
	2	69
	0.2	0.0
HOLLEMAN_ASPARAGINASE_RESISTANCE_ALL_DN	227	001
	28	72
	0.2	0.0
HUMMERICH_SKIN_CANCER_PROGRESSION_DN	227	001
	26	72
	0.2	0.0
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	226	001
	76	72
	0.2	0.0
SANSOM_APC_MYC_TARGETS	224	001
	61	75
	0.2	0.0
REACTOME_DEX_H_BOX_HELICASES_ACTIVATE_TYPE_I_IFN_AND_INFL	224	001
AMMATORY_CYTOKINES_PRODUCTION	09	75
	0.2	0.0
REACTOME_RRNA_PROCESSING_IN_THE_NUCLEUS_AND_CYTOSOL	224	001
	06	75
	0.2	0.0
MURAKAMI_UV_RESPONSE_6HR_DN	221	001
	97	78
	0.2	0.0
REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_TR	221	001
ANSPORT_AND_UPTAKE_BY_INSULIN_LIKE_GROWTH_FACTOR_BINDING	9	78
_PROTEINS_IGFBPS		
	0.2	0.0
REACTOME_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR_GG_NE	221	001
R	84	78
	0.2	0.0
GNATENKO_PLATELET_SIGNATURE	220	001
	58	8
	0.2	0.0
BIOCARTA_DC_PATHWAY	220	001
	04	8
	0.2	0.0
KEGG_RNA_POLYMERASE	219	001
	33	81
	0.2	0.0
VILIMAS_NOTCH1_TARGETS_UP	218	001
	1	83
	0.2	0.0
JEPSEN_SMRT_TARGETS	216	001
	28	85
	0.2	0.0
LAU_APOPTOSIS_CDKN2A_UP	215	001
	98	85
	0.2	0.0
REACTOME_HEDGEHOG_ON_STATE		

	215	001
	53	86
	0.2	0.0
PUJANA_BRCA2_PCC_NETWORK	213	001
	37	89
	0.2	0.0
FISCHER_G2_M_CELL_CYCLE	211	001
	3	92
	0.2	0.0
WU_APOPTOSIS_BY_CDKN1A_NOT_VIA_TP53	210	001
	72	92
	0.2	0.0
REACTOME_THE_NLRP3_INFLAMMASOME	209	001
	94	93
	0.2	0.0
REACTOME_G2_M_DNA_REPLICATION_CHECKPOINT	207	001
	73	96
	0.2	0.0
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_16	206	001
	4	98
	0.2	0.0
CHEOK_RESPONSE_TO_HD_MTX_UP	205	001
	91	99
	0.2	0.0
SCHUHMACHER_MYC_TARGETS_UP	205	001
	55	99
	0.2	0.0
REACTOME_EXTRINSIC_PATHWAY_OF_FIBRIN_CLOT_FORMATION	203	002
	19	02
	0.2	0.0
BIOCARTA_IL5_PATHWAY	202	002
	29	04
	0.2	0.0
REACTOME_ALPHA_LINOLENIC_OMEGA3_AND_LINOLEIC_OMEGA6_ACID_METABOLISM	198	002
	63	09
	0.2	0.0
GAURNIER_PSMD4_TARGETS	198	002
	21	09
	0.2	0.0
LOPEZ_MBD_TARGETS	196	002
	26	12
	0.2	0.0
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_SMALL_RNAS	196	002
	04	13
	0.2	0.0
REACTOME_FCERI_MEDIATED_NF_KB_ACTIVATION	195	002
	05	14
	0.2	0.0
REACTOME_REGULATION_OF_PTEN_STABILITY_AND_ACTIVITY	190	002
	58	21

	0.2	0.0
REACTOME_NEUTROPHIL_DEGRANULATION	189	002
	88	22
	0.2	0.0
LU_TUMOR_VASCULATURE_UP	189	002
	79	22
	0.2	0.0
GOLUB_ALL_VS_AML_DN	188	002
	98	23
	0.2	0.0
COLDREN_GEFITINIB_RESISTANCE_UP	188	002
	57	24
	0.2	0.0
VANDESLUIS_COMMD1_TARGETS_GROUP_4_DN	187	002
	33	26
	0.2	0.0
BIOCARTA_REELIN_PATHWAY	186	002
	05	28
	0.2	0.0
SHIN_B_CELL_LYMPHOMA_CLUSTER_9	185	002
	66	28
	0.2	0.0
KYNG_DNA_DAMAGE_BY_4NQO_OR_UV	184	002
	87	29
	0.2	0.0
SESTO_RESPONSE_TO_UV_C6	184	002
	5	3
	0.2	0.0
TERAMOTO_OPN_TARGETS_CLUSTER_7	183	002
	74	31
	0.2	0.0
REACTOME_ATTENUATION_PHASE	182	002
	59	33
	0.2	0.0
REACTOME_HIV_ELONGATION_ARREST_AND_RECOVERY	182	002
	16	34
	0.2	0.0
BIOCARTA_SLRP_PATHWAY	181	002
	36	35
	0.2	0.0
NATSUME_RESPONSE_TO_INTERFERON_BETA_DN	181	002
	25	35
	0.2	0.0
REACTOME_EXTENSION_OF_TELOMERES	180	002
	58	36
	0.2	0.0
SCHRAETS_MLL_TARGETS_DN	180	002
	52	36
	0.2	0.0
HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_DN	179	002

	28	38
	0.2	0.0
BURTON_ADIPOGENESIS_7	178	002
	95	39
	0.2	0.0
NIKOLSKY_BREAST_CANCER_17Q11_Q21_AMPLICON	178	002
	62	39
	0.2	0.0
DAUER_STAT3_TARGETS_UP	178	002
	47	4
	0.2	0.0
RAMPON_ENRICHED_LEARNING_ENVIRONMENT_LATE_UP	177	002
	95	4
	0.2	0.0
NADERI_BREAST_CANCER_PROGNOSIS_DN	177	002
	55	41
	0.2	0.0
REACTOME_BINDING_AND_UPTAKE_OF_LIGANDS_BY_SCAVENGER_RECEPTORS	176	002
	55	43
	0.2	0.0
PLASARI_TGFB1_TARGETS_10HR_UP	174	002
	42	46
	0.2	0.0
REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM	171	002
	75	51
	0.2	0.0
REACTOME_FORMATION_OF_HIV_ELONGATION_COMPLEX_IN_THE_ABSENCE_OF_HIV_TAT	170	002
	84	52
	0.2	0.0
REACTOME_VITAMINS	170	002
	24	53
	0.2	0.0
BASSO_CD40_SIGNALING_UP	169	002
	41	55
	0.2	0.0
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	168	002
	69	56
	0.2	0.0
REACTOME_RRNA_PROCESSING	167	002
	59	58
	0.2	0.0
REACTOME_CHROMOSOME_MAINTENANCE	166	002
	65	59
	0.2	0.0
SIG_REGULATION_OF_THE_ACTIN_CYTOSKELETON_BY_RHO_GTPASES	165	002
	18	62
	0.2	0.0
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	164	002
	81	63
	0.2	0.0
MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTROPHY_UP	164	002

	163	002
	31	65
	0.2	0.0
REACTOME_MITOTIC_PROMETAPHASE	162	002
	5	67
	0.2	0.0
RUNNE_GENDER_EFFECT_UP	162	002
	15	67
	0.2	0.0
REACTOME_TELOMERE_MAINTENANCE	161	002
	98	68
	0.2	0.0
REACTOME_SIGNALING_BY_INTERLEUKINS	161	002
	86	68
	0.2	0.0
REACTOME_SLBP_DEPENDENT_PROCESSING_OF_REPLICATION_DEPENDENT_HISTONE_PRE_MRNAS	159	002
	03	73
	0.2	0.0
WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP	157	002
	6	76
	0.2	0.0
REACTOME_ELASTIC_FIBRE_FORMATION	156	002
	21	78
	0.2	0.0
SCHIEDEREIT_IKK_INTERACTING_PROTEINS	153	002
	17	84
	0.2	0.0
KOHOUTEK_CCNT1_TARGETS	150	002
	74	89
	0.2	0.0
REACTOME_RUNX3_REGULATES_YAP1_MEDIATED_TRANSCRIPTION	150	002
	28	9
	0.2	0.0
REACTOME_SUMOYLATION_OF_DNA_REPLICATION_PROTEINS	149	002
	12	92
	0.2	0.0
GRADE_COLON_VS_RECTAL_CANCER_DN	147	002
	28	95
	0.2	0.0
REACTOME_MRNA_CAPPING	146	002
	75	96
	0.2	0.0
LIAN_LIPA_TARGETS_6M	146	002
	27	97
	0.2	0.0
BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_B	144	003
	88	
	0.2	0.0
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_UP	143	003
	74	02

	0.2	0.0
REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_TERMINATION	143	003
	54	03
	0.2	0.0
BROWNE_HCMV_INFECTION_8HR_DN	142	003
	07	06
	0.2	0.0
REACTOME_TCR_SIGNALING	141	003
	57	07
	0.2	0.0
REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS	138	003
	82	12
	0.2	0.0
REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES	137	003
	97	14
	0.2	0.0
MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_DN	136	003
	69	17
	0.2	0.0
BIOCARTA_NEUTROPHIL_PATHWAY	135	003
	94	19
	0.2	0.0
REACTOME_FORMATION_OF_TC_NER_PRE_INCISION_COMPLEX	133	003
	55	24
	0.2	0.0
CHANG_POU5F1_TARGETS_DN	131	003
	81	27
	0.2	0.0
REACTOME_ALPHA_DEFENSINS	131	003
	73	28
	0.2	0.0
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	131	003
	38	28
	0.2	0.0
SAGIV_CD24_TARGETS_DN	130	003
	54	3
	0.2	0.0
CROONQUIST_STROMAL_STIMULATION_UP	127	003
	61	37
	0.2	0.0
NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_DN	127	003
	46	37
	0.2	0.0
KEGG_PURINE_METABOLISM	126	003
	25	4
	0.2	0.0
RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_MAPK1_UP	126	003
	06	4
	0.2	0.0
REACTOME_PHASE_1_INACTIVATION_OF_FAST_NAPLUS_CHANNELS	125	003

	48	41
	0.2	0.0
TAKAO_RESPONSE_TO_UVB_RADIATION_UP	125	003
	37	42
	0.2	0.0
BIOCARTA_PEP1_PATHWAY	125	003
	25	42
	0.2	0.0
BIOCARTA_P27_PATHWAY	124	003
	47	44
	0.2	0.0
KANG_FLUOROURACIL_RESISTANCE_UP	124	003
	36	44
	0.2	0.0
CARDOSO_RESPONSE_TO_GAMMA_RADIATION_AND_3AB	122	003
	6	48
	0.2	0.0
REACTOME_TRANSCRIPTIONAL_REGULATION_OF_GRANULOPOIESIS	122	003
	59	48
	0.2	0.0
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GLOBO_SERIES	119	003
	39	55
	0.2	0.0
HAHTOLA_MYCOSIS_FUNGOIDES_UP	117	003
	96	59
	0.2	0.0
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	114	003
	06	68
	0.2	0.0
BURTON_ADIPOGENESIS_2	113	003
	97	68
	0.2	0.0
MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTROPHY_DN	112	003
	85	71
	0.2	0.0
REACTOME_FGFR2_MUTANT_RECEPTOR_ACTIVATION	112	003
	2	73
	0.2	0.0
MCBRYAN_PUBERTAL_BREAST_6_7WK_DN	111	003
	65	74
	0.2	0.0
NABA_ECM_GLYCOPROTEINS	109	003
	98	78
	0.2	0.0
REACTOME_CONDENSATION_OF_PROPHASE_CHROMOSOMES	108	003
	37	82
	0.2	0.0
REACTOME_INTERLEUKIN_35_SIGNALLING	107	003
	92	83
	0.2	0.0
REACTOME_PROTON_COUPLED_MONOCARBOXYLATE_TRANSPORT		

	105	003
	74	89
	0.2	0.0
PID_IL23_PATHWAY	105	003
	01	91
	0.2	0.0
LEIN_MIDBRAIN_MARKERS	103	003
	84	94
	0.2	0.0
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	103	003
	59	94
	0.2	0.0
SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A12	102	003
	48	97
	0.2	0.0
ELVIDGE_HIF1A_AND_HIF2A_TARGETS_UP	100	004
	32	03
	0.2	0.0
REACTOME_TRANSCRIPTION_OF_THE_HIV_GENOME	100	004
	04	03
	0.2	0.0
PHONG_TNF_RESPONSE_VIA_P38_PARTIAL	099	004
	63	04
	0.2	0.0
CHIARETTI_ACUTE_LYMPHOBLASTIC_LEUKEMIA_ZAP70	098	004
	4	08
	0.2	0.0
SASAKI_TARGETS_OF_TP73_AND_TP63	097	004
	54	1
	0.2	0.0
DELACROIX_RARG_BOUND_MEF	095	004
	97	14
	0.2	0.0
REACTOME_INTERLEUKIN_2_SIGNALING	095	004
	67	15
	0.2	0.0
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_1	095	004
	59	15
	0.2	0.0
BIOCARTA_NKT_PATHWAY	093	004
	85	2
	0.2	0.0
PARENT_MTOR_SIGNALING_DN	093	004
	62	21
	0.2	0.0
PID_INTEGRIN5_PATHWAY	093	004
	32	21
	0.2	0.0
OSAWA_TNF_TARGETS	092	004
	8	23

PID_E2F_PATHWAY	0.2	0.0
	092	004
	43	24
KORKOLA_SEMINOMA_UP	0.2	0.0
	090	004
	06	3
BIOCARTA_IL6_PATHWAY	0.2	0.0
	087	004
		39
LU_TUMOR_ENDOTHELIAL_MARKERS_UP	0.2	0.0
	086	004
	66	4
PID_P38_MK2_PATHWAY	0.2	0.0
	084	004
	23	47
REACTOME_ANTIMICROBIAL_PEPTIDES	0.2	0.0
	084	004
	12	47
REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTI DE_PATCH_REPLACEMENT_PATHWAY	0.2	0.0
	083	004
	16	5
DOANE_BREAST_CANCER_ESR1_DN	0.2	0.0
	083	004
	12	5
REACTOME_TELOMERE_EXTENSION_BY_TELOMERASE	0.2	0.0
	082	004
	5	52
REACTOME_S_PHASE	0.2	0.0
	079	004
	79	6
REACTOME_REGULATION_OF_IFNG_SIGNALING	0.2	0.0
	079	004
	53	61
CHICAS_RB1_TARGETS_SENESCENT	0.2	0.0
	077	004
	93	66
SMITH_TERT_TARGETS_UP	0.2	0.0
	076	004
	17	71
UDAYAKUMAR_MED1_TARGETS_UP	0.2	0.0
	075	004
	6	73
SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC	0.2	0.0
	075	004
	44	73
MULLIGHAN_MLL_SIGNATURE_2_UP	0.2	0.0
	075	004
	17	74
REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION	0.2	0.0
	074	004

	95	75
	0.2	0.0
WANG_METHYLATED_IN_BREAST_CANCER	074	004
	63	76
	0.2	0.0
ZHAN_MULTIPLE_MYELOMA_HP_DN	072	004
	71	82
	0.2	0.0
PID_AMB2_NEUTROPHILS_PATHWAY	068	004
	64	94
	0.2	0.0
REACTOME_DNA_STRAND_ELONGATION	067	004
	05	99
	0.2	0.0
ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_UP	065	005
	79	04
	0.2	0.0
REACTOME_INTERLEUKIN_18_SIGNALING	064	005
	65	07
	0.2	0.0
PID_INTEGRIN_A4B1_PATHWAY	064	005
	57	08
	0.2	0.0
SAMOLS_TARGETS_OF_KHSV_MIRNAS_DN	062	005
	71	14
	0.2	0.0
BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_48HR_UP	062	005
	14	15
	0.2	0.0
BIOCARTA_HBX_PATHWAY	062	005
	07	16
	0.2	0.0
YIH_RESPONSE_TO_ARSENITE_C3	061	005
	93	16
	0.2	0.0
SA_MMP_CYTOKINE_CONNECTION	061	005
	31	18
	0.2	0.0
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM2	060	005
	59	21
	0.2	0.0
REACTOME_BINDING_OF_TCF_LEF:CTNNB1_TO_TARGET_GENE_PROMOTERS	060	005
	56	21
	0.2	0.0
MACLACHLAN_BRCA1_TARGETS_DN	060	005
	33	21
	0.2	0.0
FUJII_YBX1_TARGETS_DN	059	005
	75	23
	0.2	0.0
REACTOME_NEURODEGENERATIVE_DISEASES	060	005

	059	005
	59	24
	0.2	0.0
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	058	005
	49	28
	0.2	0.0
WANG_RESPONSE_TO_BEXAROTENE_UP	058	005
	43	28
	0.2	0.0
REACTOME_HIV_LIFE_CYCLE	056	005
	84	33
	0.2	0.0
LIANG_SILENCED_BY_METHYLATION_UP	056	005
	06	36
	0.2	0.0
BIOCARTA_SUMO_PATHWAY	055	005
	21	39
	0.2	0.0
DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_UP	054	005
	51	41
	0.2	0.0
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13	054	005
	46	41
	0.2	0.0
LI_WILMS_TUMOR_VS_FETAL_KIDNEY_2_UP	054	005
	13	43
	0.2	0.0
KEGG_HEMATOPOIETIC_CELL_LINEAGE	054	005
	01	43
	0.2	0.0
REACTOME_RHO_GTPASES_ACTIVATE_IQGAPS	053	005
	54	45
	0.2	0.0
REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_F OR_GAG_SYNTHESIS	053	005
	27	46
	0.2	0.0
BROWNE_HCMV_INFECTION_16HR_DN	053	005
	23	46
	0.2	0.0
PUJANA_BREAST_CANCER_LIT_INT_NETWORK	053	005
	2	46
	0.2	0.0
MURAKAMI_UV_RESPONSE_24HR	052	005
	62	48
	0.2	0.0
BIOCARTA_PCAF_PATHWAY	049	005
	71	58
	0.2	0.0
MIKKELSEN_ES_ICP_WITH_H3K27ME3	048	005
	79	61

REACTOME_NEGATIVE_REGULATION_OF_NMDA_RECEPTOR_MEDIATED _NEURONAL_TRANSMISSION	0.2 048	0.0 005
	35	63
BIOCARTA_IFNA_PATHWAY	0.2 048	0.0 005
	32	63
REACTOME_METABOLISM_OF_RNA	0.2 047	0.0 005
	59	66
SANSOM_APC_TARGETS_UP	0.2 046	0.0 005
	25	71
REACTOME_PCNA_DEPENDENT_LONG_PATCH_BASE_EXCISION_REPAIR	0.2 045	0.0 005
	92	72
REACTOME_DDX58_IFIH1_MEDIATED_INDUCION_OF_INTERFERON_ALP HA_BETA	0.2 045	0.0 005
	84	72
ENGELMANN_CANCER_PROGENITORS_DN	0.2 045	0.0 005
	27	74
REACTOME_GAP_FILLING_DNA_REPAIR_SYNTHESIS_AND_LIGATION_IN_ GG_NER	0.2 045	0.0 005
	03	75
MARCHINI TRABECTEDIN_RESISTANCE_DN	0.2 044	0.0 005
	47	77
BAKKER_FOXO3_TARGETS_DN	0.2 043	0.0 005
	51	81
BOYALT_LIVER_CANCER_SUBCLASS_G56_DN	0.2 041	0.0 005
	88	87
KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_DN	0.2 041	0.0 005
		9
DEMAGALHAES_AGING_UP	0.2 040	0.0 005
	75	91
CASTELLANO_HRAS_TARGETS_DN	0.2 040	0.0 005
	43	92
WORSCHICH_TUMOR_REJECTION_UP	0.2 038	0.0 005
	76	98
ONO_FOXP3_TARGETS_UP	0.2 037	0.0 006
	7	02
KEGG_PRIMARY_IMMUNODEFICIENCY	0.2 036	0.0 006

	86	06
	0.2	0.0
MARZEC_IL2_SIGNALING_UP	036	006
	74	06
	0.2	0.0
ONKEN_UVEAL_MELANOMA_UP	035	006
	93	09
	0.2	0.0
REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS	035	006
	48	11
	0.2	0.0
APPEL_IMATINIB_RESPONSE	035	006
	13	
	0.2	0.0
REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS	034	006
	74	14
	0.2	0.0
REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_INITIATION	033	006
	97	17
	0.2	0.0
VALK_AML_CLUSTER_15	032	006
	29	23
	0.2	0.0
ZHAN_LATE_DIFFERENTIATION_GENES_DN	031	006
	88	25
	0.2	0.0
REACTOME_HS_GAG_DEGRADATION	031	006
	42	27
	0.2	0.0
PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_DN	029	006
	36	
	0.2	0.0
MCGARVEY_SILENCED_BY_METHYLATION_IN_COLON_CANCER	027	006
	25	44
	0.2	0.0
NGUYEN_NOTCH1_TARGETS_UP	025	006
	81	49
	0.2	0.0
AGARWAL_AKT_PATHWAY_TARGETS	023	006
	87	57
	0.2	0.0
REACTOME_EUKARYOTIC_TRANSLATION_INITIATION	023	006
	24	6
	0.2	0.0
STEARMAN_LUNG_CANCER_EARLY_VS_LATE_DN	022	006
	64	63
	0.2	0.0
REACTOME_POST_TRANSLATIONAL_MODIFICATION:_SYNTHESIS_OF_GP I_ANCHORED_PROTEINS	022	006
	12	65
	0.2	0.0
MORI_SMALL_PRE_BII_LYMPHOCYTE_UP		

	021	006
	66	67
	0.2	0.0
SWEET_KRAS_ONCOGENIC_SIGNATURE	021	006
	38	68
	0.2	0.0
WEI_MYCN_TARGETS_WITH_E_BOX	019	006
	32	77
	0.2	0.0
BAE_BRCA1_TARGETS_UP	019	006
	17	77
	0.2	0.0
REACTOME_DEGRADATION_OF_BETA_CATENIN_BY_THE_DESTRUCTION_COMPLEX	018	006
	67	79
	0.2	0.0
REACTOME_DOWNSTREAM_TCR_SIGNALING	018	006
	32	81
	0.2	0.0
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	016	006
	9	87
	0.2	0.0
VERNOCHET_ADIPOGENESIS	016	006
	83	87
	0.2	0.0
DURCHDEWALD_SKIN_CARCINOGENESIS_UP	016	006
	66	88
	0.2	0.0
PID_ARF_3PATHWAY	015	006
	83	91
	0.2	0.0
REACTOME_CHK1_CHK2_CDS1_MEDIATED_INACTIVATION_OF_CYCLIN_B:CDK1_COMPLEX	015	006
	44	93
	0.2	0.0
SUH_COEXPRESSED_WITH_ID1_AND_ID2_UP	014	006
	7	96
	0.2	0.0
SCHLOSSER_SERUM_RESPONSE_UP	013	007
	75	01
	0.2	0.0
ONDER_CDH1_TARGETS_3_DN	012	007
	78	05
	0.2	0.0
BIOCARTA_IL2_PATHWAY	009	007
	16	21
	0.2	0.0
CHO_NR4A1_TARGETS	009	007
	07	21
	0.2	0.0
MARTINEZ_RB1_AND_TP53_TARGETS_DN	007	007
	89	27

REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CELL_CYCLE_GENES	0.2	0.0
	007	007
	45	29
	0.2	0.0
SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_UP	005	007
	63	37
	0.2	0.0
KEGG_HOMOLOGOUS_RECOMBINATION	005	007
	39	38
	0.2	0.0
NIKOLSKY_BREAST_CANCER_20Q11_AMPLICON	004	007
	32	43
	0.2	0.0
RHEIN_ALL_GLUCOCORTICOID_THERAPY_UP	004	007
	07	44
	0.2	0.0
BIOCARTA_PLK3_PATHWAY	003	007
	26	48
	0.2	0.0
SENESE_HDAC1_AND_HDAC2_TARGETS_UP	002	007
	98	49
	0.2	0.0
NIKOLSKY_BREAST_CANCER_11Q12_Q14_AMPLICON	002	007
	24	53
	0.2	0.0
REACTOME_DNA_METHYLATION	000	007
	74	6
	0.2	0.0
REACTOME_POSITIVE_EPIGENETIC_REGULATION_OF_RRNA_EXPRESSION	000	007
	39	62
	0.1	0.0
WEBER_METHYLATED_IN_COLON_CANCER	999	007
	85	64
	0.1	0.0
REACTOME_LAGGING_STRAND_SYNTHESIS	999	007
	24	67
	0.1	0.0
KEGG_PRION_DISEASES	998	007
	85	69
	0.1	0.0
BENPORATH_CYCLING_GENES	998	007
	61	7
	0.1	0.0
CHIARETTI_T_ALL_REFRACTORY_TO_THERAPY	997	007
	68	74
	0.1	0.0
REACTOME_SIGNALING_BY_FGFR2_IIIa_TM	996	007
	2	82
	0.1	0.0
MCCABE_HOXC6_TARGETS_CANCER_UP	995	007

	48	85
	0.1	0.0
VIETOR_IFRD1_TARGETS	994	007
	43	9
	0.1	0.0
PARK_TRETINOIN_RESPONSE	994	007
	17	92
	0.1	0.0
REACTOME_CHYLOMICRON_CLEARANCE	989	008
	96	12
	0.1	0.0
ROESSLER_LIVER_CANCER_METASTASIS_UP	989	008
	95	13
	0.1	0.0
DORN_ADENOVIRUS_INFECTION_12HR_DN	989	008
	91	13
	0.1	0.0
REACTOME_RRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL	988	008
	59	19
	0.1	0.0
TSAI_DNAJB4_TARGETS_DN	985	008
	57	35
	0.1	0.0
VILIMAS_NOTCH1_TARGETS_DN	985	008
	32	36
	0.1	0.0
TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN	984	008
	67	4
	0.1	0.0
KENNY_CTNNB1_TARGETS_UP	983	008
	38	46
	0.1	0.0
HOLLMANN_APOPTOSIS_VIA_CD40_DN	982	008
	71	5
	0.1	0.0
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN	982	008
	56	51
	0.1	0.0
REACTOME_SUMO_IS_TRANSFERRED_FROM_E1_TO_E2_UBE2I_UBC9	980	008
	51	61
	0.1	0.0
PETRETTO_BLOOD_PRESSURE_UP	980	008
	42	62
	0.1	0.0
REACTOME_REGULATION_OF_TLR_BY_ENDOGENOUS_LIGAND	979	008
	61	66
	0.1	0.0
GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_DN	979	008
	28	68
	0.1	0.0
SHEPARD_CRUSH_AND_BURN_MUTANT_UP		

	978	008
	85	7
	0.1	0.0
CLASPER_LYMPHATIC_VESSELS_DURING_METASTASIS_DN	978	008
	63	71
	0.1	0.0
PID_INTEGRIN3_PATHWAY	978	008
	63	71
	0.1	0.0
MILI_PSEUDOPODIA_HAPTOTAXIS_DN	976	008
	98	8
	0.1	0.0
MARTINELLI_IMMATURE_NEUTROPHIL_DN	975	008
	74	87
	0.1	0.0
MARKEY_RB1_CHRONIC_LOF_DN	975	008
	68	87
	0.1	0.0
JI_CARCIANOGENESIS_BY_KRAS_AND_STK11_UP	974	008
	38	95
	0.1	0.0
SCIAN_INVERSED_TARGETS_OF_TP53_AND_TP73_DN	974	008
	15	96
	0.1	0.0
RIGGI_EWING_SARCOMA_PROGENITOR_DN	973	008
	74	98
	0.1	0.0
NIKOLSKY_BREAST_CANCER_8Q23_Q24_AMPLICON	973	008
	69	98
	0.1	0.0
REACTOME DISSOLUTION_OF_FIBRIN_CLOT	972	009
	38	06
	0.1	0.0
MISSIAGLIA_REGULATED_BY_METHYLATION_UP	971	009
	26	12
	0.1	0.0
REACTOME_DUAL_INCISION_IN_GG_NER	970	009
	64	15
	0.1	0.0
KAUFFMANN_DNA_REPLICATION_GENES	969	009
	94	19
	0.1	0.0
BIOCARTA_ALTERNATIVE_PATHWAY	968	009
	33	28
	0.1	0.0
REACTOME_HIGHLY_CALCIIUM_PERMEABLE_NICOTINIC_ACETYLCHOLINE_RECEPTORS	968	009
	04	3
	0.1	0.0
REACTOME_HSF1_ACTIVATION	967	009
	62	32

REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S	0.1	0.0
	966	009
	76	37
	0.1	0.0
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	965	009
	32	46
	0.1	0.0
REACTOME_DISINHIBITION_OF_SNARE_FORMATION	963	009
	55	56
	0.1	0.0
TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL_UP	962	009
	3	63
	0.1	0.0
WIERENGA_STAT5A_TARGETS_UP	962	009
	1	65
	0.1	0.0
SCHAEFFER_PROSTATE_DEVELOPMENT_12HR_DN	960	009
	52	74
	0.1	0.0
WAKABAYASHI_ADIPOGENESIS_PPARG_BOUND_8D	960	009
	33	75
	0.1	0.0
MATZUK_MATERNAL_EFFECT	959	009
	87	78
	0.1	0.0
ELLWOOD_MYC_TARGETS_UP	959	009
	41	81
	0.1	0.0
KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS	957	009
	86	9
	0.1	0.0
RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP	957	009
	63	91
	0.1	0.0
REACTOME_P130CAS_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRINS	954	010
	52	1
	0.1	0.0
LEIN_NEURON_MARKERS	954	010
	09	13
	0.1	0.0
SENESE_HDAC2_TARGETS_DN	953	010
	28	18
	0.1	0.0
VILLANUEVA_LIVER_CANCER_KRT19_UP	952	010
	61	22
	0.1	0.0
REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHESIS	952	010
	54	22
	0.1	0.0
REACTOME_THE_ROLE_OF_NEF_IN_HIV_1_REPLICATION_AND_DISEASE_PATHOGENESIS	951	010

	62	28
	0.1	0.0
GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3	950	010
	57	35
	0.1	0.0
BILANGES_RAPAMYCIN_SENSITIVE_VIA_TSC1_AND_TSC2	950	010
	55	35
	0.1	0.0
REACTOME_NUCLEOBASE_BIOSYNTHESIS	950	010
	42	36
	0.1	0.0
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_9	950	010
	26	37
	0.1	0.0
REACTOME_RNA_POLYMERASE_I_PROMOTER_ESCAPE	950	010
	21	37
	0.1	0.0
PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN	949	010
	99	38
	0.1	0.0
RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POORLY_DN	949	010
	19	43
	0.1	0.0
LEE_CALORIE_RESTRICTION_MUSCLE_UP	949	010
	18	44
	0.1	0.0
GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_DN	949	010
	05	44
	0.1	0.0
NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON	946	010
	84	59
	0.1	0.0
BIOCARTA_MITOCHONDRIA_PATHWAY	945	010
	52	67
	0.1	0.0
KOYAMA_SEMA3B_TARGETS_UP	945	010
	29	69
	0.1	0.0
REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_COMPLEX	944	010
	34	75
	0.1	0.0
HOLLERN_MICROACINAR_BREAST_TUMOR_DN	943	010
	47	8
	0.1	0.0
AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP	943	010
	32	81
	0.1	0.0
SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_1	943	010
	26	82
	0.1	0.0
BIOCARTA_CLASSIC_PATHWAY	943	010

	941	010
	95	9
	0.1	0.0
FU_INTERACT_WITH_ALKBH8	941	010
	38	94
	0.1	0.0
LINDVALL_IMMORTALIZED_BY_TERT_UP	940	011
	11	03
	0.1	0.0
HOFFMAN_CLOCK_TARGETS_DN	938	011
	93	1
	0.1	0.0
REACTOME_VITAMIN_B2_RIBOFLAVIN_METABOLISM	938	011
	63	12
	0.1	0.0
DANG_BOUND_BY_MYC	938	011
	26	15
	0.1	0.0
REACTOME_G0_AND_EARLY_G1	938	011
	01	17
	0.1	0.0
REACTOME_REGULATION_OF_RAS_BY_GAPS	937	011
	95	17
	0.1	0.0
PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP	936	011
	11	3
	0.1	0.0
CAFFAREL_RESPONSE_TO_THC_8HR_5_DN	936	011
	07	3
	0.1	0.0
LU_EZH2_TARGETS_UP	935	011
	43	34
	0.1	0.0
REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND	933	011
	58	47
	0.1	0.0
FERNANDEZ_BOUND_BY_MYC	933	011
	07	5
	0.1	0.0
REACTOME_NUCLEOSOME_ASSEMBLY	930	011
	82	66
	0.1	0.0
REACTOME_CYCLIN_A:CDK2_ASSOCIATED_EVENTS_AT_S_PHASE_ENTR Y	929	011
	03	79
	0.1	0.0
THUM_MIR21_TARGETS_HEART_DISEASE_DN	928	011
	75	81
	0.1	0.0
CHIARADONNA NEOPLASTIC_TRANSFORMATION_CDC25_DN	928	011
	05	86

KIM_GASTRIC_CANCER_CHEMOSENSITIVITY	0.1	0.0
	927	011
	19	92
REACTOME_RECOGNITION_OF_DNA_DAMAGE_BY_PCNA_CONTAINING_REPLICATION_COMPLEX	0.1	0.0
	927	011
		93
	0.1	0.0
REACTOME_ECM_PROTEOGLYCANS	926	011
	99	93
	0.1	0.0
REACTOME_METABOLISM_OF_NUCLEOTIDES	925	012
	95	01
	0.1	0.0
BIOCARTA_IL2RB_PATHWAY	925	012
	61	03
	0.1	0.0
REACTOME_RAB_GERANYLGERANYLATION	925	012
	19	06
	0.1	0.0
PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP	921	012
	03	37
	0.1	0.0
KEGG_ALZHEIMERS_DISEASE	920	012
	82	38
	0.1	0.0
SESTO_RESPONSE_TO_UV_C8	918	012
	41	56
	0.1	0.0
REACTOME_BIOSYNTHESIS_OF_EPA_DERIVED_SPMS	918	012
	11	59
	0.1	0.0
BIOCARTA_RB_PATHWAY	917	012
	41	64
	0.1	0.0
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	916	012
	11	74
	0.1	0.0
MCBRYAN_TERMINAL_END_BUD_UP	916	012
	02	74
	0.1	0.0
WIELAND_UP_BY_HBV_INFECTION	913	012
	28	96
	0.1	0.0
ZHONG_SECRETOME_OF_LUNG_CANCER_AND_MACROPHAGE	910	013
	45	18
	0.1	0.0
FERRARI_RESPONSE_TO_FENRETINIDE_UP	909	013
	91	22
	0.1	0.0
GAJATE_RESPONSE_TO TRABECTEDIN_UP	909	013

	32	26
	0.1	0.0
WIERENGA_PML_INTERACTOME	907	013
	87	38
	0.1	0.0
REACTOME_PROTEIN_FOLDING	907	013
	46	41
	0.1	0.0
SENESE_HDAC1_AND_HDAC2_TARGETS_DN	907	013
	24	43
	0.1	0.0
BIOCARTA_P38MAPK_PATHWAY	907	013
	11	44
	0.1	0.0
REACTOME_UNWINDING_OF_DNA	905	013
	84	54
	0.1	0.0
KRIEG_HYPOXIA_NOT_VIA_KDM3A	905	013
	62	56
	0.1	0.0
REACTOME_KSRP_KHSRP_BINDS_AND_DESTABILIZES_MRNA	904	013
	35	66
	0.1	0.0
PYEON_HPV_POSITIVE_TUMORS_DN	903	013
	52	73
	0.1	0.0
BECKER_TAMOXIFEN_RESISTANCE_UP	902	013
	5	81
	0.1	0.0
KALMA_E2F1_TARGETS	900	013
	72	96
	0.1	0.0
YAN_ESCAPE_FROM_ANOIKIS	899	014
	04	1
	0.1	0.0
PETRETTO_CARDIAC_HYPERTROPHY	898	014
	95	11
	0.1	0.0
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	898	014
	63	13
	0.1	0.0
SARTIPY_NORMAL_AT_INSULIN_RESISTANCE_UP	898	014
	38	16
	0.1	0.0
PID_TCR_RAS_PATHWAY	897	014
	35	24
	0.1	0.0
REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	896	014
	896	36
	0.1	0.0
REACTOME_GDP_FUCOSE_BIOSYNTHESIS	896	014

	894	014
	97	44
	0.1	0.0
HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_2_UP	893	014
	6	56
	0.1	0.0
GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_UP	893	014
	52	57
	0.1	0.0
BIOCARTA_AKAP95_PATHWAY	893	014
	26	59
	0.1	0.0
HSIAO_HOUSEKEEPING_GENES	891	014
	57	74
	0.1	0.0
PUJANA_BRCA_CENTERED_NETWORK	891	014
	51	74
	0.1	0.0
NUTT_GBM_VS_AO_GLIOMA_UP	891	014
	13	78
	0.1	0.0
KLEIN_TARGETS_OF_BCR_ABL1_FUSION	888	015
	01	05
	0.1	0.0
BROWNE_HCMV_INFECTION_18HR_DN	883	015
	51	45
	0.1	0.0
BREDEMEYER_RAG_SIGNALING_VIA_ATM_NOT_VIA_NFKB_UP	881	015
	4	65
	0.1	0.0
SHIRAISHI_PLZF_TARGETS_UP	881	015
	29	66
	0.1	0.0
REACTOME_SYNDECAN_INTERACTIONS	879	015
	3	84
	0.1	0.0
NGO_MALIGNANT_GLIOMA_1P_LOH	878	015
	2	94
	0.1	0.0
LIEN_BREAST_CARCINOMA_METAPLASTIC	878	015
	18	95
	0.1	0.0
UROSEVIC_RESPONSE_TO_IMIQUIMOD	876	016
	83	07
	0.1	0.0
PIONTEK_PKD1_TARGETS_DN	874	016
	88	26
	0.1	0.0
GU_PDEF_TARGETS_UP	874	016
	25	32

	0.1	0.0
LIN_MELANOMA_COPY_NUMBER_UP	873	016
	93	35
	0.1	0.0
GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP	872	016
	82	46
	0.1	0.0
PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP	871	016
	42	59
	0.1	0.0
REACTOME_NEF_MEDIATED_CD8_DOWN_REGULATION	871	016
	11	62
	0.1	0.0
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX1	869	016
	16	81
	0.1	0.0
SUNG_METASTASIS_STROMA_UP	867	016
	59	97
	0.1	0.0
BIOCARTA_COMP_PATHWAY	866	017
	3	09
	0.1	0.0
KEGG_RIBOSOME	865	017
	22	2
	0.1	0.0
REACTOME_ABORTIVE_ELONGATION_OF_HIV_1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT	865	017
	1	21
	0.1	0.0
BOSCO_TH1_CYTOTOXIC_MODULE	863	017
	9	34
	0.1	0.0
BIOCARTA_UCALPAIN_PATHWAY	862	017
	97	43
	0.1	0.0
JIANG_AGING_HYPOTHALAMUS_UP	862	017
	67	46
	0.1	0.0
BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_UP	862	017
	13	51
	0.1	0.0
JOHNSTONE_PARVB_TARGETS_2_UP	860	017
	36	7
	0.1	0.0
MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH	860	017
	12	72
	0.1	0.0
BIOCARTA_BLYMPHOCYTE_PATHWAY	860	017
	06	73
	0.1	0.0
MIKKELSEN_DEDIFFERENTIATED_STATE_DN	859	017

	53	78
	0.1	0.0
REACTOME_KINESINS	859	017
	42	79
	0.1	0.0
HUANG_FOXA2_TARGETS_UP	859	017
	37	8
	0.1	0.0
ALCALAY_AML_BY_NPM1_LOCALIZATION_DN	859	017
	33	8
	0.1	0.0
PASINI_SUZ12_TARGETS_DN	858	017
	42	9
	0.1	0.0
REACTOME_OPSINS	855	018
	71	18
	0.1	0.0
KANG_IMMORTALIZED_BY_TERT_DN	855	018
	33	22
	0.1	0.0
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_29	854	018
	87	27
	0.1	0.0
REACTOME_METABOLISM_OF_CARBOHYDRATES	851	018
	22	66
	0.1	0.0
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	850	018
	29	76
	0.1	0.0
REACTOME_HIGHLY_SODIUM_PERMEABLE_ACETYLCHOLINE_NICOTINIC_RECEPTORS	849	018
	07	89
	0.1	0.0
REACTOME_BASE_EXCISION_REPAIR_AP_SITE_FORMATION	848	018
	95	91
	0.1	0.0
BIOCARTA_STATHMIN_PATHWAY	844	019
	4	41
	0.1	0.0
VERRECCHIA_EARLY_RESPONSE_TO_TGFB1	842	019
	92	58
	0.1	0.0
MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_DN	842	019
	33	64
	0.1	0.0
REACTOME_PRC2_METHYLATES_HISTONES_AND_DNA	841	019
	7	72
	0.1	0.0
TESAR_ALK_TARGETS_HUMAN_ES_4D_DN	841	019
	49	74
	0.1	0.0
POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_DN	841	019

	841	019
	22	77
	0.1	0.0
SASAI_RESISTANCE_TO_NEOPLASTIC_TRANSFORMATION	837	020
	82	16
	0.1	0.0
CHUNG_BLISTER_CYTOTOXICITY_UP	837	020
	25	23
	0.1	0.0
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX2	835	020
	26	46
	0.1	0.0
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	835	020
	18	47
	0.1	0.0
KIM_MYCL1_AMPLIFICATION_TARGETS_DN	833	020
	59	66
	0.1	0.0
NADELLA_PRKAR1A_TARGETS_DN	832	020
	85	75
	0.1	0.0
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CASPASE_ACTIVATORS_AND_CASPASES	831	020
	81	87
	0.1	0.0
WESTON_VEGFA_TARGETS_12HR	831	020
	01	97
	0.1	0.0
STREICHER_LSM1_TARGETS_DN	829	021
	86	1
	0.1	0.0
REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS	828	021
	85	23
	0.1	0.0
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	828	021
	13	31
	0.1	0.0
REACTOME_FERTILIZATION	827	021
	7	37
	0.1	0.0
WILSON_PROTEASES_AT_TUMOR_BONE_INTERFACE_DN	826	021
	87	47
	0.1	0.0
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_15	826	021
	3	54
	0.1	0.0
BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS	825	021
	68	61
	0.1	0.0
REACTOME_NEF_MEDIATED_DOWNREGULATION_OF_MHC_CLASS_I_COMPLEX_CELL_SURFACE_EXPRESSION	821	022
	39	15

SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX4_UP	0.1	0.0
	820	022
	66	24
	0.1	0.0
RICKMAN_HEAD_AND_NECK_CANCER_F	819	022
	43	4
	0.1	0.0
REACTOME_GRB2:SOS_PROVIDES_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRINS	818	022
	5	52
	0.1	0.0
HOLLERN_PAPILLARY_BREAST_TUMOR	818	022
	21	56
	0.1	0.0
REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_1_PROMOTER	818	022
	04	58
	0.1	0.0
SU_THYMUS	817	022
	2	69
	0.1	0.0
REACTOME_WNT_MEDIATED_ACTIVATION_OF_DVL	816	022
	85	73
	0.1	0.0
REACTOME_COPI_INDEPENDENT_GOLGI_TO_ER_RETROGRADE_TRAFFIC	814	022
	96	98
	0.1	0.0
LUI_THYROID_CANCER_PAX8_PPARG_DN	812	023
	09	35
	0.1	0.0
LUDWICZEK_TREATING_IRON_OVERLOAD	812	023
	06	36
	0.1	0.0
PID_IL2_STAT5_PATHWAY	810	023
	88	52
	0.1	0.0
KRASNOSELSKAYA_ILF3_TARGETS_UP	809	023
	48	7
	0.1	0.0
WALLACE_PROSTATE_CANCER_RACE_UP	808	023
	77	8
	0.1	0.0
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_MONOCYTE_UP	808	023
	24	87
	0.1	0.0
KEGG_BLADDER_CANCER	807	023
	99	9
	0.1	0.0
DORN_ADENOVIRUS_INFECTION_32HR_UP	807	024
	32	
	0.1	0.0
JAIN_NFKB_SIGNALING	805	024

	17	29
	0.1	0.0
SINGH_NFE2L2_TARGETS	801	024
	42	81
	0.1	0.0
ZHU_CMV_ALL_UP	800	024
	87	89
	0.1	0.0
REACTOME_INTERLEUKIN_15_SIGNALING	800	024
	64	92
	0.1	0.0
YAMANAKA_GLIOMASTOMA_SURVIVAL_UP	799	025
	81	04
	0.1	0.0
CHEN_HOXA5_TARGETS_6HR_DN	799	025
	64	06
	0.1	0.0
SANSOM_APC_TARGETS	799	025
	34	1
	0.1	0.0
REACTOME_UNBLOCKING_OF_NMDA_RECEPTORS_Glutamate_Binding_AND_Activation	796	025
	18	55
	0.1	0.0
BIDUS_METASTASIS_DN	796	025
	06	57
	0.1	0.0
MIKKELSEN_IPS_ICP_WITH_H3K27ME3	794	025
	54	79
	0.1	0.0
IGLESIAS_E2F_TARGETS_UP	793	026
	1	
	0.1	0.0
REACTOME_RNA_POLYMERASE_II_PRE_TRANSCRIPTION_EVENTS	791	026
	94	17
	0.1	0.0
PUJANA_XPRSS_INT_NETWORK	791	026
	92	17
	0.1	0.0
REACTOME_MOLECULES_ASSOCIATED_WITH_ELASTIC_FIBRES	791	026
	28	27
	0.1	0.0
REACTOME_NONSENSE_MEDIATED_DECAY_NMD_INDEPENDENT_OF_THE_EXON_JUNCTION_COMPLEX_EJC	790	026
	7	35
	0.1	0.0
BROCKE_APOPTOSIS_REVERSED_BY_IL6	790	026
	44	39
	0.1	0.0
REACTOME_GAMMA_CARBOXYLATION_TRANSPORT_AND_AMINO_TERMINAL_CLEAVAGE_OF_PROTEINS	789	026
	76	49
	0.1	0.0
REACTOME_OTHER_INTERLEUKIN_SIGNALING		

	789	026
	35	55
	0.1	0.0
REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT	788	026
	58	67
	0.1	0.0
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	788	026
	42	69
	0.1	0.0
PID_PRL_SIGNALING_EVENTS_PATHWAY	786	026
	82	93
	0.1	0.0
BIOCARTA_MSP_PATHWAY	783	027
	65	41
	0.1	0.0
GROSS_HYPOXIA_VIA_ELK3_UP	782	027
	78	55
	0.1	0.0
NAISHIRO_CTNNB1_TARGETS_WITH_LEF1_MOTIF	782	027
	7	56
	0.1	0.0
REACTOME_SMAC_XIAP_REGULATED_APOPTOTIC_RESPONSE	782	027
	59	58
	0.1	0.0
STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN	779	028
	24	1
	0.1	0.0
WEINMANN_ADAPTATION_TO_HYPOXIA_DN	779	028
	08	13
	0.1	0.0
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_DN	778	028
	96	14
	0.1	0.0
REACTOME_DNA_REPAIR	778	028
	62	2
	0.1	0.0
CHIARADONNA_NEOPLASTIC_TRANSFORMATION_CDC25_UP	777	028
	28	41
	0.1	0.0
WANG_NEOPLASTIC_TRANSFORMATION_BY_CCND1_MYC	775	028
	77	65
	0.1	0.0
WEIGEL_OXIDATIVE_STRESS_RESPONSE	775	028
	72	66
	0.1	0.0
FINETTI_BREAST_CANCER_KINOME_GREEN	775	028
	34	72
	0.1	0.0
REACTOME_EPH_EPHRIN_MEDIATED_REPULSION_OF_CELLS	774	028
	51	85

	0.1	0.0
DITTMER_PTHLH_TARGETS_UP	774	028
	49	85
	0.1	0.0
REACTOME_RECRUITMENT_OF_NUMA_TO_MITOTIC_CENTROSOMES	771	029
	46	35
	0.1	0.0
HUMMERICH_BENIGN_SKIN_TUMOR_UP	771	029
	17	39
	0.1	0.0
REACTOME_TRANSLATION	771	029
	04	41
	0.1	0.0
VISALA_AGING_LYMPHOCYTE_UP	770	029
	59	49
	0.1	0.0
ZHU_CMV_ALL_DN	770	029
	46	51
	0.1	0.0
XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN	768	029
	7	8
	0.1	0.0
HUMMEL_BURKITTTS_LYMPHOMA_DN	768	029
	64	81
	0.1	0.0
FISCHER_DREAM_TARGETS	766	030
	67	14
	0.1	0.0
REACTOME_RUNX3_REGULATES_P14_ARF	765	030
	95	26
	0.1	0.0
REACTOME_GP1B_IX_V_ACTIVATION_SIGNALLING	765	030
	73	29
	0.1	0.0
PUJANA_ATM_PCC_NETWORK	764	030
	764	58
	0.1	0.0
RAMPON_ENRICHED_LEARNING_ENVIRONMENT_EARLY_DN	763	030
	82	62
	0.1	0.0
REACTOME_DNA_DAMAGE_RECOGNITION_IN_GG_NER	762	030
	96	76
	0.1	0.0
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	762	030
	47	85
	0.1	0.0
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_ELONGATION	762	030
	34	87
	0.1	0.0
TSUNODA_CISPLATIN_RESISTANCE_DN	761	030

	71	98
	0.1	0.0
GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_UP	761	031
	27	05
	0.1	0.0
RUAN_RESPONSE_TO_TNF_UP	761	031
	26	05
	0.1	0.0
HALMOS_CEBPA_TARGETS_UP	759	031
	56	35
	0.1	0.0
SWEET_KRAS_TARGETS_UP	758	031
	2	58
	0.1	0.0
GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN	757	031
	79	66
	0.1	0.0
PID_IL12_2PATHWAY	757	031
	78	66
	0.1	0.0
PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP	756	031
	66	85
	0.1	0.0
REACTOME_AMYLOID_FIBER_FORMATION	756	031
	64	86
	0.1	0.0
VALK_AML_CLUSTER_5	756	031
	29	92
	0.1	0.0
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP	756	031
	21	93
	0.1	0.0
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17	755	032
	58	04
	0.1	0.0
PHONG_TNF_RESPONSE_NOT_VIA_P38	755	032
	18	11
	0.1	0.0
MARSON_FOXP3_TARGETS_UP	754	032
	6	22
	0.1	0.0
TONG_INTERACT_WITH_PTTG1	754	032
	29	27
	0.1	0.0
LUI_THYROID_CANCER_CLUSTER_4	753	032
	96	33
	0.1	0.0
REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION	753	032
	35	44
	0.1	0.0
BIOCARTA_THELPER_PATHWAY	753	032

	752	032
	17	65
	0.1	0.0
KAYO_AGING_MUSCLE_UP	752	032
	13	66
	0.1	0.0
DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXO1_FUSION_DN	751	032
	46	78
	0.1	0.0
ZHU_SKIL_TARGETS_UP	748	033
	59	3
	0.1	0.0
BIOCARTA_LAIR_PATHWAY	747	033
	97	41
	0.1	0.0
CHESLER_BRAIN_HIGHEST_GENETIC_VARIANCE	746	033
	49	69
	0.1	0.0
BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_C	746	033
	36	71
	0.1	0.0
MARTENS_BOUND_BY_PML_RARA_FUSION	745	033
	05	95
	0.1	0.0
REACTOME_NONSENSE_MEDIATED_DECAY_NMD	743	034
	97	16
	0.1	0.0
REACTOME_METALLOTHIONEINS_BIND_METALS	743	034
	44	26
	0.1	0.0
VERHAAK_AML_WITH_NPM1_MUTATED_UP	741	034
	63	6
	0.1	0.0
HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_UP	741	034
	47	63
	0.1	0.0
ELVIDGE_HYPOXIA_DN	738	035
	08	27
	0.1	0.0
PID_CMYB_PATHWAY	735	035
	84	71
	0.1	0.0
ONDER_CDH1_TARGETS_1_UP	735	035
	61	75
	0.1	0.0
THUM_MIR21_TARGETS_HEART_DISEASE_UP	735	035
	54	77
	0.1	0.0
LINDGREN_BLADDER_CANCER_CLUSTER_2B	734	036
	07	06

	0.1	0.0
CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_DN	733	036
	19	23
	0.1	0.0
SANCHEZ_MDM2_TARGETS	732	036
	29	41
	0.1	0.0
ZAMORA_NOS2_TARGETS_DN	731	036
	68	53
	0.1	0.0
JU_AGING_TERC_TARGETS_UP	728	037
	06	26
	0.1	0.0
ZHANG_INTERFERON_RESPONSE	727	037
	58	35
	0.1	0.0
GROSS_HYPOXIA_VIA_ELK3_ONLY_UP	726	037
	04	67
	0.1	0.0
NEMETH_INFLAMMATORY_RESPONSE_LPS_UP	725	037
	95	69
	0.1	0.0
REACTOME_SUMOYLATION_OF_IMMUNE_RESPONSE_PROTEINS	723	038
	29	23
	0.1	0.0
RAMALHO_STEMNESS_DN	722	038
	5	4
	0.1	0.0
LEE_AGING_CEREBELLUM_UP	721	038
	22	66
	0.1	0.0
MULLIGHAN_NPM1_SIGNATURE_3_DN	720	038
	06	91
	0.1	0.0
REACTOME_NUCLEAR_ENVELOPE_BREAKDOWN	719	038
	75	97
	0.1	0.0
GARCIA_TARGETS_OF_FL11_AND_DAX1_DN	719	039
	52	02
	0.1	0.0
ABBUD_LIF_SIGNALING_1_UP	719	039
	03	13
	0.1	0.0
ALFANO_MYC_TARGETS	719	039
	01	13
	0.1	0.0
REACTOME_SIGNALING_BY_NOTCH4	718	039
	89	16
	0.1	0.0
SASSON_RESPONSE_TO_GONADOTROPHINS_UP	718	039

	15	31
	0.1	0.0
REACTOME_HDL_REMODELING	716	039
	05	76
	0.1	0.0
BIOCARTA_SODD_PATHWAY	713	040
	5	31
	0.1	0.0
BIOCARTA_NDKDYNAMIN_PATHWAY	710	040
	48	97
	0.1	0.0
PLASARI_NFIC_TARGETS_BASAL_DN	707	041
	68	6
	0.1	0.0
PECE_MAMMARY_STEM_CELL_UP	707	041
	65	6
	0.1	0.0
SENESE_HDAC2_TARGETS_UP	706	041
	9	77
	0.1	0.0
REACTOME_DEPURINATION	706	041
	22	92
	0.1	0.0
RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN	705	042
	53	08
	0.1	0.0
DARWICHE_SKIN_TUMOR_PROMOTER_DN	705	042
	11	17
	0.1	0.0
VERRECCHIA_RESPONSE_TO_TGFB1_C1	704	042
	84	24
	0.1	0.0
GEISS_RESPONSE_TO_DSRNA_DN	704	042
	83	24
	0.1	0.0
LEIN_MEDULLA_MARKERS	701	042
	71	95
	0.1	0.0
BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_48HR_DN	701	043
	44	02
	0.1	0.0
REACTOME_GENE_SILENCING_BY_RNA	700	043
	99	12
	0.1	0.0
ZHU_CMV_24_HR_UP	700	043
	73	18
	0.1	0.0
REACTOME_PTEN_REGULATION	700	043
	28	28
	0.1	0.0
MURAKAMI_UV_RESPONSE_6HR_UP		

	698	043
	79	63
	0.1	0.0
NAKAMURA_METASTASIS_MODEL_DN	697	043
	64	9
	0.1	0.0
KORKOLA_TERATOMA	696	044
	32	21
	0.1	0.0
REACTOME_SERINE_BIOSYNTHESIS	695	044
	79	34
	0.1	0.0
ZHU_CMV_24_HR_DN	695	044
	5	4
	0.1	0.0
PEDERSEN_TARGETS_OF_611CTF_ISOFORM_OF_ERBB2	695	044
	47	41
	0.1	0.0
PID_WNT_SIGNALING_PATHWAY	694	044
	89	55
	0.1	0.0
REACTOME_EPIGENETIC_REGULATION_OF_GENE_EXPRESSION	692	045
	96	01
	0.1	0.0
REACTOME_SCAVENGING_BY_CLASS_F_RECEPTORS	691	045
	99	24
	0.1	0.0
CHEN_ETV5_TARGETS_TESTIS	691	045
	11	46
	0.1	0.0
REACTOME_GALACTOSE_CATABOLISM	688	046
	1	19
	0.1	0.0
REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS	686	046
	65	55
	0.1	0.0
REACTOME_SELENOAMINO_ACID_METABOLISM	686	046
	64	55
	0.1	0.0
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_ERYT HROCYTE_UP	686	046
	43	6
	0.1	0.0
MARSON_FOXP3_TARGETS_DN	685	046
	88	74
	0.1	0.0
CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN	683	047
	91	23
	0.1	0.0
CHOW_RASSF1_TARGETS_DN	683	047
	22	41

SCIBETTA_KDM5B_TARGETS_DN	0.1	0.0
	682	047
	58	57
	0.1	0.0
NAKAMURA_BRONCHIAL_AND_BRONCHIOLAR_EPITHELIA	680	048
	38	13
	0.1	0.0
KAUFFMANN_MELANOMA_RELAPSE_UP	680	048
	19	18
	0.1	0.0
FIGUEROA_AML_METHYLATION_CLUSTER_2_DN	680	048
	15	19
	0.1	0.0
PID_INTEGRIN_A9B1_PATHWAY	679	048
	78	28
	0.1	0.0
KUMAMOTO_RESPONSE_TO_NUTLIN_3A_UP	679	048
	08	46
	0.1	0.0
REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER	678	048
	82	53
	0.1	0.0
VANASSE_BCL2_TARGETS_DN	676	049
	81	05
	0.1	0.0
SA_G1_AND_S_PHASES	676	049
	72	07
	0.1	0.0
SYED ESTRADIOL_RESPONSE	675	049
	83	3
	0.1	0.0
REACTOME_LYSOSOME_VESICLE_BIOGENESIS	675	049
	83	3
	0.1	0.0
REACTOME_INFLAMMASOMES	675	049
	48	39
	0.1	0.0
ABE_INNER_EAR	674	049
	27	71
	0.1	0.0
DORN_ADENOVIRUS_INFECTION_24HR_DN	673	049
	77	84
	0.1	0.0
REACTOME_AXON_GUIDANCE	673	049
	18	05
	0.1	0.0
KOINUMA_COLON_CANCER_MSI_DN	671	050
	12	54
	0.1	0.0
SAKAI_CHRONIC_HEPATITIS_VS_LIVER_CANCER_DN	671	050

	09	55
	0.1	0.0
BORLAK_LIVER_CANCER_EGF_UP	670	050
	25	78
	0.1	0.0
DORN_ADENOVIRUS_INFECTION_48HR_DN	669	050
	71	92
	0.1	0.0
SCHLESINGER_METHYLATED_IN_COLON_CANCER	669	051
	05	1
	0.1	0.0
CHIN_BREAST_CANCER_COPY_NUMBER_UP	667	051
	92	4
	0.1	0.0
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	666	051
	78	71
	0.1	0.0
REACTOME_CD28_DEPENDENT_VAV1_PATHWAY	665	052
	23	14
	0.1	0.0
REACTOME_SIGNALING_BY_WNT	664	052
	73	27
	0.1	0.0
DAZARD_UV_RESPONSE_CLUSTER_G28	664	052
	44	35
	0.1	0.0
MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED	664	052
	25	41
	0.1	0.0
REACTOME_REMOVAL_OF_AMINOTERMINAL_PROPEPTIDES_FROM_GAMMA_CARBOXYLATED_PROTEINS	662	052
	4	92
	0.1	0.0
MARSON_FOXP3_CORE_DIRECT_TARGETS	661	053
	8	08
	0.1	0.0
REACTOME_RESPONSE_TO_METAL_IONS	661	053
	7	11
	0.1	0.0
ENK_UV_RESPONSE_KERATINOCYTE_UP	661	053
	49	17
	0.1	0.0
KYNG_DNA_DAMAGE_BY_UV	657	054
	58	27
	0.1	0.0
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_DN	656	054
	3	64
	0.1	0.0
BOYLAN_MULTIPLE_MYELOMA_PCA1_UP	655	054
	28	93
	0.1	0.0
FUNG_IL2_SIGNALING_1		

	655	054
	16	96
	0.1	0.0
HAHTOLA_MYCOSIS_FUNGOIDES_CD4_UP	655	054
	14	97
	0.1	0.0
MORI_EMU_MYC_LYMPHOMA_BY_ONSET_TIME_DN	654	055
	98	02
	0.1	0.0
YIH_RESPONSE_TO_ARSENITE_C4	654	055
	91	04
	0.1	0.0
KORKOLA_SEMINOMA_DN	654	055
	09	27
	0.1	0.0
SANA_TNF_SIGNALING_UP	654	055
	07	28
	0.1	0.0
ZHAN_MULTIPLE_MYELOMA_DN	650	056
	96	19
	0.1	0.0
SASSON_FSH_RESPONSE	650	056
	23	4
	0.1	0.0
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	649	056
	61	58
	0.1	0.0
KEGG_CARDIAC_MUSCLE_CONTRACTION	649	056
	32	67
	0.1	0.0
PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_DN	649	056
	28	68
	0.1	0.0
MARTIN_NFKB_TARGETS_DN	648	056
	8	82
	0.1	0.0
JEON_SMAD6_TARGETS_UP	647	057
	21	29
	0.1	0.0
HEIDENBLAD_AMPLIFIED_IN_PANCREATIC_CANCER	645	057
	92	68
	0.1	0.0
TAVOR_CEBPA_TARGETS_UP	645	057
	35	85
	0.1	0.0
SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_DN	644	058
	08	24
	0.1	0.0
REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N_GLYCAN_BIOSYTHESIS	644	058
	04	25

	0.1	0.0
REACTOME_MAP2K_AND_MAPK_ACTIVATION	643	058
	88	3
	0.1	0.0
WAESCH_ANAPHASE_PROMOTING_COMPLEX	642	058
	64	67
	0.1	0.0
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	641	058
	79	93
	0.1	0.0
REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACTIVATION_OF_IKKS_COMPLEX	641	059
	28	09
	0.1	0.0
SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP	641	059
	09	15
	0.1	0.0
REACTOME_PROCESSING_AND_ACTIVATION_OF_SUMO	639	059
	53	63
	0.1	0.0
REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT	639	059
	17	74
	0.1	0.0
SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_DN	637	060
	84	15
	0.1	0.0
REACTOME_SIGNALING_BY_ACTIVIN	637	060
	3	32
	0.1	0.0
REACTOME_TNF_SIGNALING	637	060
	28	33
	0.1	0.0
WIERENGA_STAT5A_TARGETS_GROUP2	635	060
	61	85
	0.1	0.0
CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN	635	060
	22	98
	0.1	0.0
BIOCARTA_TERT_PATHWAY	634	061
	57	18
	0.1	0.0
REACTOME_HEDGEHOG_OFF_STATE	634	061
	13	32
	0.1	0.0
KLEIN_PRIMARY EFFUSION_LYMPHOMA_DN	633	061
	37	56
	0.1	0.0
GRAESSMANN_APOPTOSIS_BY_SERUM_DEPRIVATION_DN	632	061
	99	68
	0.1	0.0
LEE_LIVER_CANCER_E2F1_UP	631	062

	65	11
	0.1	0.0
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	631	062
	06	3
	0.1	0.0
ZHOU_TNF_SIGNALING_4HR	629	062
	32	86
	0.1	0.0
REACTOME_SEMA3A_PAK_DEPENDENT_AXON_REPULSION	628	062
	96	98
	0.1	0.0
JISON_SICKLE_CELL_DISEASE_UP	627	063
	96	31
	0.1	0.0
ALCALA_APOPTOSIS	626	063
	84	67
	0.1	0.0
POMEROY_MEDULLOBLASTOMA_PROGNOSIS_UP	626	063
	78	69
	0.1	0.0
PID_INTEGRIN1_PATHWAY	625	064
	85	064
	0.1	0.0
QI_HYPOXIA	625	064
	38	15
	0.1	0.0
WONG_ENDMETRIUM_CANCER_UP	625	064
	25	2
	0.1	0.0
BIOCARTA_D4GDI_PATHWAY	623	064
	36	83
	0.1	0.0
HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_4NM_DN	623	064
	07	92
	0.1	0.0
MIKKELSEN_MCV6_LCP_WITH_H3K4ME3	621	065
	82	34
	0.1	0.0
BIOCARTA_MONOCYTE_PATHWAY	621	065
	62	41
	0.1	0.0
REACTOME_ELEVATION_OF_CYTOSOLIC_CA2PLUS_LEVELS	620	065
	38	82
	0.1	0.0
REACTOME_REGULATION_OF_TNFR1_SIGNALING	618	066
	69	4
	0.1	0.0
VALK_AML_WITH_11Q23_REARRANGED	617	066
	57	78
	0.1	0.0
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	617	066

	616	067
	55	13
	0.1	0.0
KAAB_FAILED_HEART_ATRIUM_UP	616	067
	31	21
	0.1	0.0
WALLACE_PROSTATE_CANCER_UP	615	067
	68	43
	0.1	0.0
REACTOME_O_GLYCOSYLATION_OF_TSR_DOMAIN_CONTAINING_PROTEINS	614	067
	54	82
	0.1	0.0
HAN_JNK_SINGALING_UP	613	068
	69	12
	0.1	0.0
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	613	068
	31	25
	0.1	0.0
KANNAN_TP53_TARGETS_DN	612	068
	88	4
	0.1	0.0
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_21	612	068
	27	62
	0.1	0.0
GALE_APL_WITH_FLT3_MUTATED_DN	612	068
	11	67
	0.1	0.0
KEGG_NUCLEOTIDE_EXCISION_REPAIR	611	068
	56	87
	0.1	0.0
KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS_AND_CYCLIC_RGD	610	069
	43	27
	0.1	0.0
WHITESIDE_CISPLATIN_RESISTANCE_UP	610	069
	21	34
	0.1	0.0
COURTOIS_SENESCENCE_TRIGGERS	610	069
	15	36
	0.1	0.0
NIKOLSKY_BREAST_CANCER_19P13_AMPLICON	609	069
	85	47
	0.1	0.0
REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS	609	069
	7	52
	0.1	0.0
MOHANKUMAR_HOXA1_TARGETS_UP	607	070
	81	2
	0.1	0.0
BIOCARTA_SKP2E2F_PATHWAY	606	070
	56	65

	0.1	0.0
BIOCARTA_TCYTOTOXIC_PATHWAY	606	070
	11	81
	0.1	0.0
GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_DN	605	070
	96	86
	0.1	0.0
REACTOME_TCF_DEPENDENT_SIGNALING_IN_RESPONSE_TO_WNT	605	070
	83	91
	0.1	0.0
OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP_UP	604	071
	22	49
	0.1	0.0
KIM_ALL_DISORDERS_DURATION_CORR_DN	604	071
	604	57
	0.1	0.0
KERLEY_RESPONSE_TO_CISPLATIN_UP	603	071
	54	74
	0.1	0.0
DASU_IL6_SIGNALING_SCAR_UP	603	071
	04	93
	0.1	0.0
BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN	602	072
	07	28
	0.1	0.0
REACTOME_FORMATION_OF_THE_BETA_CATENIN:TCF_TRANSACTIVATING_COMPLEX	600	072
	46	87
	0.1	0.0
REACTOME_RHO_GTPASES_ACTIVATE_NADPH_OXIDASES	598	073
	3	68
	0.1	0.0
REACTOME_SIGNALING_BY_NOTCH	597	073
	63	93
	0.1	0.0
SHAFFER_IRF4_TARGETS_IN_ACTIVATED_DENDRITIC_CELL	597	073
	45	99
	0.1	0.0
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_THE_AP_2_TFAP2_FAMILY_OF_TRANSCRIPTION_FACTORS	597	074
	36	03
	0.1	0.0
MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP	597	074
	24	08
	0.1	0.0
REACTOME_INTEGRATION_OF_PROVIRUS	595	074
	65	67
	0.1	0.0
REACTOME_METABOLISM_OF_INGESTED_SEMET_SEC_MESEC_INTO_H2SE	595	074
	34	79
	0.1	0.0
REACTOME_SUMO_IS_CONJUGATED_TO_E1_UBA2:SAE1	595	074

	23	83
	0.1	0.0
VALK_AML_WITH_CEBPA	593	075
	97	31
	0.1	0.0
CHIARETTI_T_ALL_RELAPSE_PROGNOSIS	592	075
	94	7
	0.1	0.0
REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	592	075
	85	74
	0.1	0.0
REACTOME_TERMINATION_OF_TRANSLESION_DNA_SYNTHESIS	592	075
	79	76
	0.1	0.0
ISHIDA_TARGETS_OF_SYT_SSX_FUSIONS	592	075
	43	9
	0.1	0.0
NAKAJIMA_MAST_CELL	592	075
	43	9
	0.1	0.0
RIZ_ERYTHROID_DIFFERENTIATION	592	076
	07	
	0.1	0.0
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP	591	076
	43	28
	0.1	0.0
NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON	591	076
	27	35
	0.1	0.0
REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION_IN_TLR7_8_OR_9_SIGNALING	590	076
	91	48
	0.1	0.0
KIM_WT1_TARGETS_DN	590	076
	53	63
	0.1	0.0
REACTOME_HYALURONAN_METABOLISM	589	076
	7	95
	0.1	0.0
YANAGISAWA_LUNG_CANCER_RECURRENCE	589	077
	38	08
	0.1	0.0
REACTOME_RUNX3_REGULATES_WNT_SIGNALING	588	077
	17	55
	0.1	0.0
CEBALLOS_TARGETS_OF_TP53_AND_MYC_DN	586	078
	01	4
	0.1	0.0
KEGG_SPLICEOSOME	585	078
	66	54
	0.1	0.0
DER_IFN_ALPHA_RESPONSE_UP		

	585	078
	49	61
	0.1	0.0
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	584	079
	22	11
	0.1	0.0
MARTINEZ_RESPONSE_TO_TRABECTEDIN_UP	584	079
	14	14
	0.1	0.0
OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP_DN	583	079
	15	54
	0.1	0.0
SHEPARD_CRUSH_AND_BURN_MUTANT_DN	582	079
	76	69
	0.1	0.0
GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP	582	079
	4	84
	0.1	0.0
SASSON_RESPONSE_TO_FORSKOLIN_DN	581	080
	43	23
	0.1	0.0
DUTERTRE ESTRADIOL_RESPONSE_6HR_UP	579	081
	34	08
	0.1	0.0
TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN	578	081
	49	42
	0.1	0.0
BIOCARTA_FIBRINOLYSIS_PATHWAY	577	082
		03
	0.1	0.0
NABA_COLLAGENS	576	082
	39	29
	0.1	0.0
REACTOME_COLLAGEN_CHAIN_TRIMERIZATION	576	082
	39	29
	0.1	0.0
GENTILE_UV_HIGH_DOSE_UP	573	083
	08	66
	0.1	0.0
SHIN_B_CELL_LYMPHOMA_CLUSTER_3	572	083
	76	79
	0.1	0.0
REACTOME_RNA_POLYMERASE_II_TRANSCRIBES_SNRNA_GENES	571	084
	67	25
	0.1	0.0
BERENJENO_ROCK_SIGNALING_NOT_VIA_RHOA_UP	568	085
	71	51
	0.1	0.0
MARKS_HDAC_TARGETS_DN	568	085
	63	54

	0.1	0.0
BIOCARTA_FBW7_PATHWAY	568	085
	09	77
	0.1	0.0
WEBER_METHYLATED_LCP_IN_FIBROBLAST_UP	567	086
	25	13
	0.1	0.0
RODRIGUES_DCC_TARGETS_UP	567	086
	08	2
	0.1	0.0
FOURNIER_ACINAR_DEVELOPMENT_EARLY_DN	566	086
	39	5
	0.1	0.0
REACTOME_PINK_PARKIN_MEDIATED_MITOPHAGY	566	086
	34	52
	0.1	0.0
LEE_BMP2_TARGETS_DN	565	086
	92	71
	0.1	0.0
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_10	565	087
	22	01
	0.1	0.0
KIM_LRRC3B_TARGETS	565	087
	07	07
	0.1	0.0
BIOCARTA_IL17_PATHWAY	564	087
	57	29
	0.1	0.0
PID_ANTHRAX_PATHWAY	564	087
	44	35
	0.1	0.0
REACTOME_SCAVENGING_BY_CLASS_A_RECEPTORS	563	087
	79	63
	0.1	0.0
BENPORATH_ES_2	562	088
	9	02
	0.1	0.0
REACTOME_EPH_EPHRIN_SIGNALING	560	089
	63	02
	0.1	0.0
FINAK_BREAST_CANCER_SDPP_SIGNATURE	560	089
	36	14
	0.1	0.0
VISALA_AGING_LYMPHOCYTE_DN	560	089
	07	27
	0.1	0.0
HAN_SATB1_TARGETS_UP	559	089
	74	41
	0.1	0.0
GAVIN_FOXP3_TARGETS_CLUSTER_P3	559	089

	66	45
	0.1	0.0
HELLER_HDAC_TARGETS_UP	558	089
	61	91
	0.1	0.0
KEGG_VIRAL_MYOCARDITIS	557	090
	43	44
	0.1	0.0
PID_P53_DOWNSTREAM_PATHWAY	557	090
	17	56
	0.1	0.0
BASSO_HAIRY_CELL_LEUKEMIA_DN	557	090
	64	
	0.1	0.0
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	556	090
	32	94
	0.1	0.0
SESTO_RESPONSE_TO_UV_C3	554	091
	91	58
	0.1	0.0
KANG_IMMORTALIZED_BY_TERT_UP	553	092
	91	04
	0.1	0.0
KYNG_RESPONSE_TO_H2O2_VIA_ERCC6_DN	553	092
	36	29
	0.1	0.0
REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_TERMINATION	552	092
	27	79
	0.1	0.0
WIEDERSCHAIN_TARGETS_OF_BMI1_AND_PCGF2	551	093
	18	29
REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHO L_LIPID_LINKED_OLIGOSACCHARIDE_LLO_AND_TRANSFER_TO_A_NASC ENT_PROTEIN	548	094
	17	69
	0.1	0.0
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_DNA_REPAIR_GENES	548	094
	1	72
	0.1	0.0
MILI_PSEUDOPODIA_CHEMOTAXIS_DN	547	095
	25	11
	0.1	0.0
KUWANO_RNA_STABILIZED_BY_NO	547	095
	24	12
	0.1	0.0
HELLER_SILENCED_BY_METHYLATION_DN	547	095
	06	21
	0.1	0.0
BIOCARTA_TRKA_PATHWAY	546	095
	85	3
BIOCARTA_NOS1_PATHWAY	0.1	0.0

	546	095
	5	47
	0.1	0.0
BIOCARTA_EXTRINSIC_PATHWAY	544	096
	84	25
	0.1	0.0
MATTIOLI_MGUS_VS_MULTIPLE_MYELOMA	544	096
	51	41
	0.1	0.0
REACTOME_INTERLEUKIN_1_PROCESSING	543	096
	72	78
	0.1	0.0
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	542	097
	76	24
	0.1	0.0
REACTOME_ACTIVATION_OF_CASPASES_THROUGH_APOPTOSOME_MEDIATED_CLEAVAGE	540	098
	61	28
	0.1	0.0
SANA_RESPONSE_TO_IFNG_DN	538	099
	81	15
	0.1	0.0
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	538	099
	71	2
	0.1	0.0
RICKMAN_METASTASIS_DN	536	100
	96	05
	0.1	0.0
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN	536	100
	77	15
	0.1	0.0
NIKOLSKY_BREAST_CANCER_17Q21_Q25_AMPLICON	536	100
	76	15
	0.1	0.0
REACTOME_HYALURONAN_BIOSYNTHESIS_AND_EXPORT	533	101
	85	59
	0.1	0.0
REACTOME_HOST_INTERACTIONS_WITH_INFLUENZA_FACTORS	533	101
	11	96
	0.1	0.0
KIM_WT1_TARGETS_UP	531	102
	84	59
	0.1	0.0
REACTOME_CYP2E1_REACTIONS	530	103
	57	24
	0.1	0.0
KEGG_N_GLYCAN_BIOSYNTHESIS	530	103
	18	43
	0.1	0.0
REACTOME_GLYCEROPHOSPHOLIPID_CATABOLISM	528	104
	99	03

LEE_LIVER_CANCER_MYC_DN	0.1	0.0
	528	104
	05	51
	0.1	0.0
REACTOME_COMMON_PATHWAY_OF_FIBRIN_CLOT_FORMATION	527	104
	58	75
	0.1	0.0
TAVOR_CEBPA_TARGETS_DN	527	104
	39	85
	0.1	0.0
HEIDENBLAD_AMPLIFIED_IN_SOFT_TISSUE_CANCER	523	106
	28	97
	0.1	0.0
KUNINGER_IGF1_VS_PDGF_B_TARGETS_DN	523	107
	05	09
	0.1	0.0
LUI_THYROID_CANCER_CLUSTER_3	522	107
	98	12
	0.1	0.0
HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_DN	522	107
	52	36
	0.1	0.0
ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN	521	107
	37	97
	0.1	0.0
OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_DN	520	108
	1	64
	0.1	0.0
REACTOME_TRAFFICKING_AND_PROCESSING_OF_ENDOSOMAL_TLR	519	108
	63	88
	0.1	0.0
MATZUK_POSTIMPLANTATION_AND_POSTPARTUM	518	109
	53	47
	0.1	0.0
KEGG_HUNTINGTONS_DISEASE	518	109
	07	72
	0.1	0.0
KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQO_IN_WS	517	110
	18	19
	0.1	0.0
ONO_FOXP3_TARGETS_DN	515	110
	92	86
	0.1	0.0
ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN	515	110
	77	94
	0.1	0.0
HUANG_DASATINIB_RESISTANCE_UP	515	111
	03	34
	0.1	0.0
BIOCARTA_LYMPHOCYTE_PATHWAY	512	112

	62	65
	0.1	0.0
BRUINS_UVC_RESPONSE_MIDDLE	512	112
	42	76
	0.1	0.0
ANDERSEN_LIVER_CANCER_KRT19_UP	511	113
	83	08
	0.1	0.0
DAIRKEE_CANCER_PRONE_RESPONSE_BPA	510	114
	09	03
	0.1	0.0
MATSUDA_NATURAL_KILLER_DIFFERENTIATION	508	114
	4	97
	0.1	0.0
KEGG_ETHER_LIPID_METABOLISM	507	115
	9	25
	0.1	0.0
MA_MYELOID_DIFFERENTIATION_UP	507	115
	75	33
	0.1	0.0
REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA	507	115
	11	69
	0.1	0.0
GAVIN_IL2_RESPONSIVE_FOXP3_TARGETS_UP	506	116
	52	02
	0.1	0.0
LIAN_NEUTROPHIL_GRANULE_CONSTITUENTS	506	116
	46	05
	0.1	0.0
REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_PHOSPHORYL ATION	506	116
	36	11
	0.1	0.0
PROVENZANI_METASTASIS_DN	505	116
	89	37
	0.1	0.0
CAFFAREL_RESPONSE_TO_THC_8HR_3_DN	504	117
	1	37
	0.1	0.0
GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_UP	503	117
	61	65
	0.1	0.0
CHENG_RESPONSE_TO_NICKEL_ACETATE	502	118
	47	3
	0.1	0.0
WEBER_METHYLATED_LCP_IN_SPERM_UP	501	118
	63	78
	0.1	0.0
LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_UP	501	118
	53	84
LIM_MAMMARY_LUMINAL_PROGENITOR_UP	0.1	0.0

	500	119
	69	32
	0.1	0.0
KUUSELO_PANCREATIC_CANCER_19Q13_AMPLIFICATION	499	119
	78	84
	0.1	0.0
REACTOME_HOMOLOGY_DIRECTED_REPAIR	498	120
	87	37
	0.1	0.0
ROETH_TERT_TARGETS_DN	498	120
	52	57
	0.1	0.0
MAEKAWA_ATF2_TARGETS	497	121
	01	45
	0.1	0.0
REACTOME_INTERACTIONS_OF_REV_WITH_HOST_CELLULAR_PROTEINS	494	123
	21	
	0.1	0.0
MCBRYAN_PUBERTAL_BREAST_3_4WK_DN	493	123
	76	35
	0.1	0.0
LEE_CALORIE_RESTRICTION_NEOCORTEX_UP	493	123
	75	36
	0.1	0.0
HOLLEMAN_VINCRIStINE_RESISTANCE_ALL_UP	493	123
	47	52
	0.1	0.0
LEE_LIVER_CANCER_DENA_UP	493	123
	25	65
	0.1	0.0
ZIRN_TRETINOIN_RESPONSE_WT1_UP	492	124
	34	19
	0.1	0.0
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_11	491	124
	94	43
	0.1	0.0
REACTOME_CRMP5_IN_SEMA3A_SIGNALING	491	124
	65	6
	0.1	0.0
ABBUD_LIF_SIGNALING_2_UP	490	125
	76	13
	0.1	0.0
SCHAEFFER_SOX9_TARGETS_IN_PROSTATE_DEVELOPMENT_DN	490	125
	69	17
	0.1	0.0
REACTOME_NONCANONICAL_ACTIVATION_OF_NOTCH3	489	125
	84	69
	0.1	0.0
BROWNE_HCMV_INFECTION_1HR_DN	489	126
	25	04

	0.1	0.0
GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_UP	489	126
	19	07
	0.1	0.0
WANG_RECURRENT_LIVER_CANCER_UP	488	126
	73	35
	0.1	0.0
LUCAS_HNF4A_TARGETS_DN	487	127
	23	26
	0.1	0.0
REACTOME_ATF6_ATF6_ALPHA_ACTIVATES_CHAPERONE_GENES	485	128
	73	17
	0.1	0.0
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN	483	129
	6	48
	0.1	0.0
REACTOME_NCAM1_INTERACTIONS	483	129
	33	64
	0.1	0.0
GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN	483	129
	85	
	0.1	0.0
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN	482	129
	87	93
	0.1	0.0
MORI_IMMATURE_B_LYMPHOCYTE_UP	482	130
	15	38
	0.1	0.0
BOYLAN_MULTIPLE_MYELOMA_D_CLUSTER_DN	481	131
	13	01
	0.1	0.0
REACTOME_DEFENSINS	480	131
	18	6
	0.1	0.0
BIOCARTA_CSK_PATHWAY	479	131
	69	91
	0.1	0.0
JAATINEN_HEMATOPOIETIC_STEM_CELL_DN	479	131
	63	94
	0.1	0.0
REACTOME_PLATELET_SENSITIZATION_BY_LDL	479	131
	58	98
	0.1	0.0
BIOCARTA_CTLA4_PATHWAY	478	132
	7	53
	0.1	0.0
TAKAO_RESPONSE_TO_UVB_RADIATION_DN	477	133
	81	09
	0.1	0.0
REACTOME_INTERLEUKIN_7_SIGNALING	477	133

	51	28
	0.1	0.0
GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN	477	133
	29	42
	0.1	0.0
BAUS_TFF2_TARGETS_UP	476	133
	72	78
	0.1	0.0
SMIRNOV_RESPONSE_TO_IR_6HR_UP	475	134
	65	46
	0.1	0.0
LIN_APC_TARGETS	475	134
	07	83
	0.1	0.0
MAGRANGEAS_MULTIPLE_MYELOMA_IPLL_VS_IPLK_UP	475	134
	06	84
	0.1	0.0
NADLER_HYPERGLYCEMIA_AT_OBESITY	474	135
	35	29
	0.1	0.0
BIOCARTA_BIOPEPTIDES_PATHWAY	474	135
	3	32
	0.1	0.0
BIOCARTA_P53HYPOXIA_PATHWAY	474	135
	18	4
	0.1	0.0
SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_DN	473	135
	7	71
	0.1	0.0
SAKAI_TUMOR_INFILTRATING_MONOCYTES_DN	473	136
	18	04
	0.1	0.0
XU_HGF_SIGNALING_NOT_VIA_AKT1_6HR	472	136
	93	2
	0.1	0.0
LIU_LIVER_CANCER	471	136
	81	92
	0.1	0.0
AMIT_SERUM_RESPONSE_20_MCF10A	470	137
	83	56
	0.1	0.0
THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP	469	138
	52	41
	0.1	0.0
MARIADASON_RESPONSE_TO_CURCUMIN_SULINDAC_7	469	138
	46	45
	0.1	0.0
BERENJENO_TRANSFORMED_BY_RHOA_DN	467	139
	55	71
	0.1	0.0
KORKOLA_TERATOMA_UP		

	466	140
	42	45
	0.1	0.0
REACTOME_SUMOYLATION_OF_DNA_METHYLATION_PROTEINS	466	140
	32	52
	0.1	0.0
XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR	466	140
	27	55
	0.1	0.0
APPIERTO_RESPONSE_TO_FENRETINIDE_UP	465	141
	42	11
	0.1	0.0
PID_NFAT_TFPATHWAY	465	141
	06	36
	0.1	0.0
RIZKI_TUMOR_INVASIVENESS_3D_UP	464	141
	23	9
	0.1	0.0
HAHTOLA_SEZARY_SYNDROM_DN	463	142
	49	4
	0.1	0.0
PID_GLYPICAN_1PATHWAY	463	142
	39	47
	0.1	0.0
BIOCARTA_SHH_PATHWAY	463	142
	39	47
	0.1	0.0
REACTOME_TRNA_PROCESSING_IN_THE_NUCLEUS	463	142
	12	65
	0.1	0.0
REACTOME_MITOTIC_PROPHASE	462	142
	97	76
	0.1	0.0
WINTER_HYPOXIA_METAGENE	461	143
	36	84
	0.1	0.0
INGRAM_SHH_TARGETS_DN	458	145
	94	48
	0.1	0.0
WU_ALZHEIMER_DISEASE_DN	458	145
	24	96
	0.1	0.0
DIRMEIER_LMP1_RESPONSE_EARLY	457	146
	77	28
	0.1	0.0
REACTOME_DEFECTIVE_B4GALT7_CAUSES_EDS_PROGEROID_TYPE	457	146
	17	69
	0.1	0.0
MIKKELSEN_PLURIPOTENT_STATE_DN	454	148
	47	56

	0.1	0.0
SHI_SPARC_TARGETS_UP	454	148
	17	77
	0.1	0.0
IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_UP	453	149
	43	28
	0.1	0.0
MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_DN	452	149
	72	78
	0.1	0.0
HUTTMANN_B_CLL_POOR_SURVIVAL_UP	452	150
	28	09
	0.1	0.0
REACTOME_INTERLEUKIN_RECEPTOR_SHC_SIGNALING	449	151
	69	91
	0.1	0.0
MORI_LARGE_PRE_BII_LYMPHOCYTE_DN	449	151
	6	98
	0.1	0.0
GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN	449	152
	53	03
	0.1	0.0
MCDOWELL_ACUTE_LUNG_INJURY_UP	449	152
	21	25
	0.1	0.0
GALIE_TUMOR_ANGIOGENESIS	448	152
	25	94
	0.1	0.0
REACTOME_G1_PHASE	447	153
	92	17
	0.1	0.0
YEMELYANOV_GR_TARGETS_DN	446	153
	93	88
	0.1	0.0
REACTOME_PHOSPHATE_BOND_HYDROLYSIS_BY_NUDT_PROTEINS	445	154
	97	58
	0.1	0.0
REACTOME_FGFR2_ALTERNATIVE_SPLICING	445	154
	78	71
	0.1	0.0
REACTOME_TOLL_LIKE_RECEPTOR_CASCADES	444	155
	98	29
	0.1	0.0
REACTOME_FCGR_ACTIVATION	444	155
	95	31
	0.1	0.0
ZHOU_INFLAMMATORY_RESPONSE_FIMA_UP	444	155
	87	36
	0.1	0.0
SHIN_B_CELL_LYMPHOMA_CLUSTER_1	444	155

	23	83
	0.1	0.0
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_YELLOW_DN	443	156
	76	17
	0.1	0.0
RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN	443	156
	07	67
	0.1	0.0
BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_DN	442	157
	52	07
	0.1	0.0
REACTOME_RUNX2_REGULATES_GENES_INVOLVED_IN_CELL_MIGRATION	442	157
	12	36
	0.1	0.0
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	441	158
	13	09
	0.1	0.0
BIOCARTA_EOSINOPHILS_PATHWAY	441	158
	04	16
	0.1	0.0
REACTOME_MINERALOCORTICOID_BIOSYNTHESIS	440	158
	98	2
	0.1	0.0
REACTOME_GPCR_LIGAND_BINDING	440	158
	28	71
	0.1	0.0
PID_IL6_7_PATHWAY	439	159
	88	01
	0.1	0.0
REACTOME_SIGNALING_BY_NTRK3_TRKC	439	159
	76	1
	0.1	0.0
LIU_PROSTATE_CANCER_UP	438	159
	62	94
	0.1	0.0
WU_CELL_MIGRATION	438	160
	52	02
	0.1	0.0
GAVIN_PDE3B_TARGETS	438	160
	45	07
	0.1	0.0
NAKAJIMA_EOSINOPHIL	438	160
	02	39
	0.1	0.0
KEGG_OTHER_GLYCAN_DEGRADATION	436	161
	31	66
	0.1	0.0
ZHENG_RESPONSE_TO_ARSENITE_UP	436	161
	22	73
	0.1	0.0
WIERENGA_STAT5A_TARGETS_GROUP1		

	435	162
	04	62
	0.1	0.0
ONO_AML1_TARGETS_UP	434	163
	29	18
	0.1	0.0
SWEET_LUNG_CANCER_KRAS_UP	431	165
	86	02
	0.1	0.0
REACTOME_CYTOCHROME_C_MEDIATED_APOPTOTIC_RESPONSE	431	165
	56	25
	0.1	0.0
PARK_APL_PATHOGENESIS_UP	431	165
	5	3
	0.1	0.0
BIOCARTA_CDC25_PATHWAY	430	166
	04	42
	0.1	0.0
BIOCARTA_CTL_PATHWAY	429	166
	74	64
	0.1	0.0
REACTOME_SOS_MEDIATED_SIGNALLING	429	167
	2	07
	0.1	0.0
YAGUE_PRETUMOR_DRUG_RESISTANCE_DN	428	167
	57	55
	0.1	0.0
WANG_TUMOR_INVASIVENESS_DN	426	169
	1	47
	0.1	0.0
FARMER_BREAST_CANCER_CLUSTER_1	425	169
	61	85
	0.1	0.0
REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION	425	169
	52	92
	0.1	0.0
MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA_VHL_UP	423	171
	98	12
	0.1	0.0
PODAR_RESPONSE_TO_ADAPHOSTIN_UP	423	171
	91	18
	0.1	0.0
REACTOME_NEGATIVE_REGULATION_OF_TCF_DEPENDENT_SIGNALING_BY_WNT_LIGAND_ANTAGONISTS	423	171
	43	56
	0.1	0.0
CHEN_ETV5_TARGETS_SERTOLI	422	172
	71	13
	0.1	0.0
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	422	172
	37	4

	0.1	0.0
BIOCARTA_TCRA_PATHWAY	422	172
	15	57
	0.1	0.0
NAKAMURA_METASTASIS_MODEL_UP	421	172
	76	88
	0.1	0.0
REACTOME_ACYL_CHAIN_REMODELLING_OF_PI	419	174
	56	64
	0.1	0.0
REACTOME_POLB_DEPENDENT_LONG_PATCH_BASE_EXCISION_REPAIR	419	174
	14	98
	0.1	0.0
KEGG_LEISHMANIA_INFECTIION	418	175
	44	54
	0.1	0.0
GILMORE_CORE_NFKB_PATHWAY	415	178
	38	01
	0.1	0.0
EHLERS_ANEUPLOIDY_DN	414	178
	88	42
	0.1	0.0
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	412	180
	25	58
	0.1	0.0
REACTOME_DISEASES_ASSOCIATED_WITH_N_GLYCOSYLATION_OF_PROTEINS	412	180
	09	71
	0.1	0.0
GRATIAS_RETINOBLASTOMA_16Q24	412	180
	01	78
	0.1	0.0
REACTOME_TRIGLYCERIDE_CATABOLISM	411	180
	97	8
	0.1	0.0
JIANG_TIP30_TARGETS_DN	411	181
	18	46
	0.1	0.0
HUPER_BREAST_BASAL_VS_LUMINAL_DN	409	182
	9	52
	0.1	0.0
KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAMMA_IN_OLD	409	182
	81	59
	0.1	0.0
LINDGREN_BLADDER_CANCER_HIGH_RECURRENCE	408	183
	3	85
	0.1	0.0
NUYTEN_EZH2_TARGETS_DN	407	184
	39	62
	0.1	0.0
REACTOME_INTERLEUKIN_2_FAMILY_SIGNALING	406	185

	63	26
	0.1	0.0
DASU_IL6_SIGNALING_SCAR_DN	406	185
	31	53
	0.1	0.0
BIOCARTA_TCAPOPTOSIS_PATHWAY	406	185
	19	63
	0.1	0.0
DORN_ADENOVIRUS_INFECTION_32HR_DN	404	186
	69	91
	0.1	0.0
VALK_AML_CLUSTER_13	404	187
	18	34
	0.1	0.0
GENTILE_UV_RESPONSE_CLUSTER_D7	404	187
	02	48
	0.1	0.0
REACTOME_DERMATAN_SULFATE_BIOSYNTHESIS	403	188
	17	2
	0.1	0.0
NIKOLSKY_BREAST_CANCER_7P15_AMPLICON	402	188
	93	4
	0.1	0.0
WAGSCHAL_EHMT2_TARGETS_UP	401	189
	7	45
	0.1	0.0
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_4	401	189
	22	87
	0.1	0.0
REACTOME_MEIOTIC_RECOMBINATION	400	190
	73	29
	0.1	0.0
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	400	190
	31	66
	0.1	0.0
CHOI_ATL_STAGE_PREDICTOR	399	191
	68	2
	0.1	0.0
REACTOME_REGULATION_OF_RUNX1_EXPRESSION_AND_ACTIVITY	397	192
	64	98
	0.1	0.0
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	393	196
	32	78
	0.1	0.0
REACTOME_HEME_DEGRADATION	393	196
	2	89
	0.1	0.0
REACTOME_2_LTR_CIRCLE_FORMATION	392	197
	86	19
WOOD_EBV_EBNA1_TARGETS_DN	0.1	0.0

	390	198
	97	88
	0.1	0.0
REACTOME_COPI_MEDIATED_ANTEROGRADE_TRANSPORT	390	199
	76	07
	0.1	0.0
BIOCARTA_FXR_PATHWAY	390	199
	31	47
	0.1	0.0
REACTOME_SEMAPHORIN_INTERACTIONS	389	200
	23	44
	0.1	0.0
PURBEY_TARGETS_OF_CTBP1_NOT_SATB1_DN	389	200
	16	51
	0.1	0.0
BENPORATH_ES_1	389	200
	01	65
	0.1	0.0
GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_UP	388	201
	02	54
	0.1	0.0
AMIT_EGF_RESPONSE_240_HELA	387	201
	99	57
	0.1	0.0
REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES	387	201
	61	91
	0.1	0.0
PETROVA_PROX1_TARGETS_DN	387	202
	18	31
	0.1	0.0
REACTOME_TRANSLESION_SYNTHESIS_BY_Y_FAMILY_DNA_POLYMERASES_BYPASSES_LESIONS_ON_DNA_TEMPLATE	386	202
	94	52
	0.1	0.0
PID_TCR_PATHWAY	383	205
	64	55
	0.1	0.0
LINDSTEDT_DENDRITIC_CELL_MATURATION_C	383	205
	63	56
	0.1	0.0
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	380	208
	85	13
	0.1	0.0
REACTOME_GAP_JUNCTION_ASSEMBLY	379	209
	61	3
	0.1	0.0
LEE_AGING_NEOCORTEX_UP	379	209
	42	47
	0.1	0.0
JIANG_HYPOXIA_VIA_VHL	377	210
	99	82

	0.1	0.0
GRASEMANN_RETINOBLASTOMA_WITH_6P_AMPLIFICATION	377	211
	07	68
	0.1	0.0
RUTELLA_RESPONSE_TO_HGF_DN	376	211
	9	85
	0.1	0.0
MIKKELSEN_IPS_LCP_WITH_H3K4ME3	376	212
	23	49
	0.1	0.0
KEGG_MISMATCH_REPAIR	376	212
	13	58
	0.1	0.0
MIKKELSEN_NPC_ICP_WITH_H3K27ME3	374	214
	44	18
	0.1	0.0
BILANGES_SERUM_SENSITIVE_VIA_TSC1	374	214
	42	2
	0.1	0.0
REACTOME_BIOSYNTHESIS_OF_E_SERIES_18_S_RESOLVINS	374	214
	28	34
	0.1	0.0
ROY_WOUND_BLOOD_VESSEL_UP	373	215
	4	18
	0.1	0.0
TENEDINI_MEGAKARYOCYTE_MARKERS	371	216
	96	57
	0.1	0.0
XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN	371	216
	82	7
	0.1	0.0
FUNG_IL2_TARGETS_WITH_STAT5_BINDING_SITES_T1	371	217
	16	35
	0.1	0.0
CAMPS_COLON_CANCER_COPY_NUMBER_UP	370	217
	52	96
	0.1	0.0
ONGUSAHA_BRCA1_TARGETS_UP	370	218
	29	19
	0.1	0.0
PIEPOLI_LGI1_TARGETS_DN	368	219
	85	59
	0.1	0.0
AZARE_NEOPLASTIC_TRANSFORMATION_BY_STAT3_DN	367	220
	75	67
	0.1	0.0
TSAI_RESPONSE_TO_IONIZING_RADIATION	367	221
	11	29
	0.1	0.0
VALK_AML_CLUSTER_6	366	221

	53	87
	0.1	0.0
MANN_RESPONSE_TO_AMIFOSTINE_DN	362	225
	92	46
	0.1	0.0
PURBEY_TARGETS_OF_CTBP1_AND_SATB1_DN	360	227
	65	73
	0.1	0.0
LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_UP	360	227
	42	96
	0.1	0.0
REACTOME_NEGATIVE_EPIGENETIC_REGULATION_OF_RRNA_EXPRESSION	358	230
	22	2
	0.1	0.0
BOYALT_LIVER_CANCER_SUBCLASS_G23_UP	356	231
	82	62
	0.1	0.0
BENPORATH_MYC_MAX_TARGETS	356	231
	59	86
	0.1	0.0
GHO_ATF5_TARGETS_UP	356	232
	41	04
	0.1	0.0
KRIEG_KDM3A_TARGETS_NOT_HYPOXIA	356	232
	04	43
	0.1	0.0
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_7	355	232
	87	6
	0.1	0.0
KOHOUTEK_CCNT2_TARGETS	354	234
	28	24
	0.1	0.0
REACTOME_ESTROGEN_BIOSYNTHESIS	354	234
	22	3
	0.1	0.0
SASSON_RESPONSE_TO_FORSKOLIN_UP	353	235
	06	5
	0.1	0.0
HUPER_BREAST_BASAL_VS_LUMINAL_UP	352	235
	96	6
	0.1	0.0
HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN	352	235
	84	72
	0.1	0.0
BORCZUK_MALIGNANT_MESOTHELIOMA_DN	352	235
	72	85
	0.1	0.0
LEIN_PONS_MARKERS	351	237
	59	02
	0.1	0.0
KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV_IN_WS		

	351	237
	28	35
	0.1	0.0
RAMPON_ENRICHED_LEARNING_ENVIRONMENT_EARLY_UP	351	237
	05	59
	0.1	0.0
REACTOME_DNA_DAMAGE_TELOMERE_STRESS_INDUCED_SENESCENCE	350	237
	78	87
	0.1	0.0
REACTOME_MET_ACTIVATES_PTK2_SIGNALING	350	237
	67	99
	0.1	0.0
BIOCARTA_RECK_PATHWAY	350	238
	31	36
	0.1	0.0
MEISSNER_NPC_HCP_WITH_H3K4ME2	349	239
	35	38
	0.1	0.0
REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS	348	239
	79	97
	0.1	0.0
BIOCARTA_PML_PATHWAY	348	240
	24	54
	0.1	0.0
PID_IL8_CXCR2_PATHWAY	346	242
	79	08
	0.1	0.0
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	346	242
	33	58
	0.1	0.0
WILCOX_RESPONSE_TO_PROGESTERONE_DN	345	243
	17	81
	0.1	0.0
REACTOME_SIGNALING_BY_LEPTIN	343	245
	51	59
	0.1	0.0
REACTOME_TYROSINE_CATABOLISM	342	246
	77	39
	0.1	0.0
MIKKELSEN_ES_LCP_WITH_H3K4ME3	342	247
	17	04
	0.1	0.0
MCBRYAN_TERMINAL_END_BUD_DN	341	247
	84	39
	0.1	0.0
SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP	340	248
	56	78
	0.1	0.0
REACTOME_TYPE_I_HEMIDESMOSOME_ASSEMBLY	338	250
	76	75

	0.1	0.0
REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	338	251
	49	05
	0.1	0.0
BAFNA_MUC4_TARGETS_UP	338	251
	23	34
	0.1	0.0
NAKAMURA_ADIPOGENESIS_LATE_DN	336	253
	51	22
	0.1	0.0
ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP	336	253
	34	41
	0.1	0.0
RADAEVA_RESPONSE_TO_IFNA1_UP	335	254
	72	1
	0.1	0.0
WUNDER_INFLAMMATORY_RESPONSE_AND_CHOLESTEROL_UP	335	254
		9
	0.1	0.0
TOMLINS_METASTASIS_UP	334	255
	43	53
	0.1	0.0
REACTOME_DEFECTIVE_CHST14_CAUSES_EDS_MUSCULOCONTRACTURAL_TYPE	334	255
	15	84
	0.1	0.0
ZHAN_MULTIPLE_MYELOMA_SUBGROUPS	332	257
	94	2
	0.1	0.0
REACTOME_BIOSYNTHESIS_OF_SPECIALIZED_PRORESOLVING_MEDIATORS_SPMS	331	258
	57	74
	0.1	0.0
REACTOME_MRNA_SPLICING	331	258
	51	8
	0.1	0.0
ROSS_AML_WITH_MLL_FUSIONS	330	259
	73	68
	0.1	0.0
GOUYER_TUMOR_INVASIVENESS	330	260
	45	26
	0.1	0.0
PID_INTEGRIN4_PATHWAY	330	260
	43	02
	0.1	0.0
REACTOME_ERYTHROPOIETIN_ACTIVATES_RAS	327	263
	23	66
	0.1	0.0
LE_NEURONAL_DIFFERENTIATION_UP	326	264
	75	2
	0.1	0.0
REACTOME_ACYL_CHAIN_REMODELLING_OF_PS	325	266

	09	11
REACTOME_N_GLYCAN_TRIMMING_IN_THE_ER_AND_CALNEXIN_CALRETICULIN_CYCLE	0.1	0.0
	324	266
	54	75
	0.1	0.0
VERNELL_RETINOBLASTOMA_PATHWAY_UP	323	267
	77	65
	0.1	0.0
REACTOME_PECAM1_INTERACTIONS	323	268
	39	08
	0.1	0.0
SASSON_RESPONSE_TO_GONADOTROPHINS_DN	322	269
	35	29
	0.1	0.0
ZHANG_RESPONSE_TO_CANTHARIDIN_DN	320	271
	89	
	0.1	0.0
CAFFAREL_RESPONSE_TO_THC_24HR_5_UP	319	272
	6	51
	0.1	0.0
RAY_TUMORIGENESIS_BY_ERBB2_CDC25A_UP	319	272
	52	6
	0.1	0.0
PID_P38_ALPHA_BETA_PATHWAY	319	272
	5	63
	0.1	0.0
ONGUSAHA_TP53_TARGETS	319	273
	08	12
	0.1	0.0
REACTOME_SYNTHESIS_OF_LIPOXINS_LX	318	273
	46	86
	0.1	0.0
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	316	276
	55	12
	0.1	0.0
MEISSNER_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3	316	276
	32	4
	0.1	0.0
XU_CREBBP_TARGETS_DN	315	277
	35	56
	0.1	0.0
REACTOME_TRIGLYCERIDE_METABOLISM	315	277
	3	62
	0.1	0.0
AMIT_EGF_RESPONSE_120_HELA	314	278
	23	89
	0.1	0.0
JEON_SMAD6_TARGETS_DN	312	280
	97	41
	0.1	0.0
GROSS_ELK3_TARGETS_DN		

	312	280
	89	51
REACTOME_DISEASES_ASSOCIATED_WITH_GLYCOSYLATION_PRECURSOR_BIOSYNTHESIS	0.1	0.0
	311	282
		8
	0.1	0.0
KEGG_ECM_RECEPTOR_INTERACTION	309	285
	08	14
	0.1	0.0
KIM_WT1_TARGETS_8HR_UP	307	286
	57	99
	0.1	0.0
SU_TESTIS	307	287
	35	26
	0.1	0.0
PODAR_RESPONSE_TO_ADAPHOSTIN_DN	305	289
	46	6
	0.1	0.0
BROWNE_HCMV_INFECTION_24HR_UP	302	293
	51	27
	0.1	0.0
REACTOME_RHO_GTPASES_ACTIVATE_RHOTEKIN_AND_RHOPHILINS	302	293
	16	71
	0.1	0.0
PETRETTO_LEFT_VENTRICLE_MASS_QTL_CIS_UP	301	294
	64	37
	0.1	0.0
REACTOME_PLASMA_LIPOPROTEIN_ASSEMBLY_REMODELING_AND_CLEARENCE	301	294
	29	81
	0.1	0.0
SABATES_COLORECTAL_ADENOMA_SIZE_UP	300	295
	37	97
	0.1	0.0
REACTOME_TRNA_PROCESSING_IN_THE_MITOCHONDRION	300	295
	35	99
	0.1	0.0
KANG_FLUOROURACIL_RESISTANCE_DN	300	296
	06	36
	0.1	0.0
KAAB_HEART_ATRIUM_VS_VENTRICLE_UP	299	297
	55	
	0.1	0.0
DANG_REGULATED_BY_MYC_DN	298	297
	85	89
	0.1	0.0
YAGI_AML_FAB_MARKERS	293	304
	64	57
	0.1	0.0
SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN	292	306
		7

REACTOME_TRANSLOCATION_OF_ZAP_70_TO_IMMUNOLOGICAL_SYNAPSE	0.1	0.0
	290	308
	72	37
	0.1	0.0
PASTURAL_RIZ1_TARGETS_UP	290	308
	28	95
	0.1	0.0
RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN	290	309
	2	06
	0.1	0.0
DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_DN	289	309
	94	4
	0.1	0.0
VALK_AML_CLUSTER_9	289	309
	85	51
	0.1	0.0
BIOCARTA_NO2IL12_PATHWAY	289	309
	69	72
	0.1	0.0
GRAHAM_CML QUIESCENT_VS_NORMAL_DIVIDING_DN	287	312
	5	61
	0.1	0.0
BIOCARTA_PARKIN_PATHWAY	287	312
	44	68
	0.1	0.0
JIANG_HYPOXIA_NORMAL	286	314
	45	
	0.1	0.0
WEIGEL_OXIDATIVE_STRESS_BY_HNE_AND_TBH	283	317
	84	49
	0.1	0.0
ABRAMSON_INTERACT_WITH_AIRE	28	322
	28	67
	0.1	0.0
REACTOME_RAS_ACTIVATION_UPON_CA2PLUS_INFLUX_THROUGH_NMDA_RECEPTOR	279	323
	43	45
	0.1	0.0
ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_UP	276	327
	8	06
	0.1	0.0
GILDEA_METASTASIS	276	327
	67	23
	0.1	0.0
ZERBINI_RESPONSE_TO_SULINDAC_UP	276	327
	25	8
	0.1	0.0
LI_WILMS_TUMOR_ANAPLASTIC_DN	276	327
	14	95
	0.1	0.0
REACTOME_PROCESSING_OF_DNA_DOUBLE_STRAND_BREAK_ENDS	275	329

	31	1
	0.1	0.0
HUANG_GATA2_TARGETS_DN	274	330
	3	51
	0.1	0.0
PID_IL12_STAT4_PATHWAY	273	331
	73	29
	0.1	0.0
STARK_HYPPOCAMPUS_22Q11_DELETION_DN	271	334
	67	17
	0.1	0.0
REACTOME_TRNA_PROCESSING	271	334
	23	79
	0.1	0.0
SEKI_INFLAMMATORY_RESPONSE_LPS_UP	270	335
	73	5
	0.1	0.0
REACTOME_PD_1_SIGNALING	269	337
	59	09
	0.1	0.0
YANG_BCL3_TARGETS_UP	268	338
	77	25
	0.1	0.0
REACTOME_MITOCHONDRIAL_TRANSLATION	267	339
	93	44
	0.1	0.0
REACTOME_SIGNALING_BY_MODERATE_KINASE_ACTIVITY_BRAF_MUTANTS	266	341
	36	68
	0.1	0.0
GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_DN	265	342
	88	36
	0.1	0.0
REACTOME_SIRT1_NEGATIVELY_REGULATES_RRNA_EXPRESSION	264	344
	36	55
	0.1	0.0
LIU_TARGETS_OF_VMYB_VS_CMYB_DN	264	344
	26	7
	0.1	0.0
BOYALT_LIVER_CANCER_SUBCLASS_G12_UP	263	345
	84	29
	0.1	0.0
PEART_HDAC_PROLIFERATION_CLUSTER_UP	260	349
	92	52
	0.1	0.0
CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_DN	260	350
	24	51
	0.1	0.0
GERHOLD_RESPONSE_TO_TZD_DN	257	354
	74	18
	0.1	0.0
TARTE_PLASMA_CELL_VS_PLASMABLAST_UP		

	257	354
	61	38
	0.1	0.0
PID_CD8_TCR_DOWNSTREAM_PATHWAY	257	354
	28	85
	0.1	0.0
REACTOME_ACTIVATION_OF_C3_AND_C5	257	354
	26	89
	0.1	0.0
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_UP	257	354
	23	93
	0.1	0.0
REACTOME_NEGATIVE_REGULATION_OF_ACTIVITY_OF_TFAP2_AP_2_FAMILY_TRANSCRIPTION_FACTORS	256	355
	55	93
	0.1	0.0
BIOCARTA_CPSF_PATHWAY	256	356
	47	05
	0.1	0.0
BIOCARTA_ASBCELL_PATHWAY	254	358
	95	31
	0.1	0.0
LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN	254	358
	86	44
	0.1	0.0
REACTOME_HEMOSTASIS	253	360
	64	26
	0.1	0.0
EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_UP	251	363
	71	15
	0.1	0.0
DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP	251	363
	62	29
	0.1	0.0
NAKAMURA_ADIPOGENESIS_LATE_UP	249	365
	96	79
	0.1	0.0
REACTOME_ZBP1_DAI_MEDIATED_INDUCATION_OF_TYPE_I_IFNS	249	366
	34	74
	0.1	0.0
GOUYER_TATI_TARGETS_DN	244	374
	56	03
	0.1	0.0
BLALOCK_ALZHEIMERS_DISEASE_UP	244	374
	47	18
	0.1	0.0
KORKOLA_EMBRYONAL_CARCINOMA_DN	244	374
	1	75
	0.1	0.0
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	242	376
	91	58

	0.1	0.0
STEIN_ESRRA_TARGETS_RESPONSIVE_TO_ESTROGEN_DN	242	376
	77	8
	0.1	0.0
BOWIE_RESPONSE_TO_TAMOXIFEN	242	377
	12	82
	0.1	0.0
DAZARD_UV_RESPONSE_CLUSTER_G5	242	377
	02	97
	0.1	0.0
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	241	378
	79	33
	0.1	0.0
MAYBURD_RESPONSE_TO_L663536_UP	240	380
	41	48
	0.1	0.0
REACTOME_TANDEM_PORE_DOMAIN_POTASSIUM_CHANNELS	240	380
	12	93
	0.1	0.0
TSENG_ADIPOGENIC_POTENTIAL_DN	239	382
	01	68
	0.1	0.0
REACTOME_EPHB_MEDIATED_FORWARD_SIGNALING	238	383
	56	38
	0.1	0.0
ZHONG_SECRETOME_OF_LUNG_CANCER_AND_ENDOTHELIUM	237	384
	57	94
	0.1	0.0
BIOCARTA_ION_PATHWAY	236	387
	15	19
	0.1	0.0
NAKAMURA_ADIPOGENESIS_EARLY_DN	235	388
	41	36
	0.1	0.0
REACTOME_YAP1_AND_WWTR1_TAZ_STIMULATED_GENE_EXPRESSION	235	388
	35	47
	0.1	0.0
REACTOME_CD28_CO_STIMULATION	233	391
	28	77
	0.1	0.0
GALI_TP53_TARGETS_APOPTOTIC_UP	229	397
	65	63
	0.1	0.0
TURJANSKI_MAPK8_AND_MAPK9_TARGETS	228	399
	46	57
	0.1	0.0
BIOCARTA_IL3_PATHWAY	227	400
	81	63
	0.1	0.0
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_C ONTAINING_RECEPTOR_NLR_SIGNALING_PATHWAYS	226	403

	29	12
REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_BCR_LEADING_T O_GENERATION_OF_SECOND_MESSENGERS	0.1	0.0
	224	405
	77	62
	0.1	0.0
WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN	224	405
	75	65
	0.1	0.0
SMITH_TERT_TARGETS_DN	223	407
	87	11
	0.1	0.0
BIOCARTA_CBL_PATHWAY	221	411
	11	71
	0.1	0.0
REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR	220	412
	51	71
	0.1	0.0
DAZARD_UV_RESPONSE_CLUSTER_G3	220	413
	11	37
	0.1	0.0
KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP	218	415
	6	92
	0.1	0.0
RICKMAN_HEAD_AND_NECK_CANCER_C	218	416
	38	28
	0.1	0.0
REACTOME_DNA_DAMAGE_BYPASS	218	416
	07	81
	0.1	0.0
LEE_METASTASIS_AND_RNA_PROCESSING_UP	216	419
	68	16
	0.1	0.0
BASSO_CD40_SIGNALING_DN	215	421
	45	25
	0.1	0.0
COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOMASTOMA_UP	215	421
	09	87
	0.1	0.0
REACTOME_CROSS_PRESENTATION_OF_PARTICULATE_EXOGENOUS_AN TIGENS_PHAGOSOMES	214	422
	84	3
	0.1	0.0
DARWICHE_SQUAMOUS_CELL_CARCINOMA_DN	213	424
	69	26
	0.1	0.0
WESTON_VEGFA_TARGETS_6HR	212	425
	83	73
	0.1	0.0
TURJANSKI_MAPK14_TARGETS	212	427
	02	13
	0.1	0.0
SMID_BREAST_CANCER_NORMAL_LIKE_UP		

	208	432
	91	53
	0.1	0.0
PRAMOONJAGO_SOX4_TARGETS_UP	208	432
	74	82
	0.1	0.0
LIU_VAV3_PROSTATE_CARCINOGENESIS_UP	208	433
	59	09
	0.1	0.0
HOLLEMAN_PREDNISOLONE_RESISTANCE_B_ALL_UP	206	436
	69	4
	0.1	0.0
REACTOME_SYNTHESIS_OF_GDP_MANNOSE	204	440
	59	11
	0.1	0.0
YAMAZAKI_TCEB3_TARGETS_DN	202	443
	6	64
	0.1	0.0
BIOCARTA_BBCELL_PATHWAY	201	445
	43	72
	0.1	0.0
PID_HIV_NEF_PATHWAY	200	446
	77	92
	0.1	0.0
PLASARI_NFIC_TARGETS_BASAL_UP	200	446
	76	93
	0.1	0.0
REACTOME_SEROTONIN_RECEPTORS	200	446
	73	98
	0.1	0.0
REACTOME_NECTIN_NECL_TRANS_HETERODIMERIZATION	199	449
	28	59
	0.1	0.0
REACTOME_DEFECTIVE_EXT2_CAUSES_EXOSTOSES_2	197	453
	25	25
	0.1	0.0
REACTOME_REPRODUCTION	196	455
	13	28
	0.1	0.0
REACTOME_SIGNALING_BY_FGFR2_IN_DISEASE	195	456
	73	02
	0.1	0.0
SANSOM_APC_TARGETS_DN	195	457
	12	12
	0.1	0.0
TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_DN	194	458
	39	47
	0.1	0.0
KEGG_RNA_DEGRADATION	194	458
	25	71

	0.1	0.0
REACTOME_ERYTHROPOIETIN_ACTIVATES_STAT5	194	459
	03	11
	0.1	0.0
LEE_NAIVE_T_LYMPHOCYTE	193	460
	01	98
	0.1	0.0
COLLIS_PRKDC_REGULATORS	192	462
	05	77
	0.1	0.0
LEE_CALORIE_RESTRICTION_MUSCLE_DN	191	463
	9	04
	0.1	0.0
TESAR_ALK_TARGETS_HUMAN_ES_5D_DN	190	465
	77	12
	0.1	0.0
REACTOME_MUCOPOLYSACCHARIDOSES	190	465
	73	19
	0.1	0.0
CHESLER_BRAIN_D6MIT150_QTL_TRANS	190	466
	23	13
	0.1	0.0
CHANG_POU5F1_TARGETS_UP	187	471
	56	11
	0.1	0.0
NAKAYAMA_FRA2_TARGETS	185	474
	98	07
	0.1	0.0
REACTOME_SYNTHESIS_OF_12_EICOSATETRAENOIC_ACID_DERIVATIVES	185	474
	49	99
	0.1	0.0
PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_UP	182	480
	82	04
	0.1	0.0
REACTOME_RMTS METHYLATE HISTONE ARGININES	181	482
	76	06
	0.1	0.0
REACTOME_CREB1_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII_CAMKK_CAMKIV_CASCASDE	181	482
	61	35
	0.1	0.0
MOOHA_VOXPPOS	180	484
	34	79
	0.1	0.0
GERY_CEBP_TARGETS	180	485
	22	01
	0.1	0.0
LEIN_LOCALIZED_TO_PROXIMAL_DENDRITES	178	488
	4	5
	0.1	0.0
REACTOME_FANCONI_ANEMIA_PATHWAY	176	491

	81	58
	0.1	0.0
TAKADA_GASTRIC_CANCER_COPY_NUMBER_UP	176	491
	66	88
	0.1	0.0
ENGELMANN_CANCER_PROGENITORS_UP	176	492
	09	99
	0.1	0.0
REACTOME_METABOLISM_OF_NON_CODING_RNA	172	499
	6	82
