



Research article

Identification of a novel snoRNA expression signature associated with overall survival in patients with lung adenocarcinoma: A comprehensive analysis based on RNA sequencing dataset

Linbo Zhang, Mei Xin and Peng Wang*

Department of Health Management and Division of Physical Examination, The First Affiliated Hospital of Guangxi Medical University, Shuang Yong Road 6, Nanning 530021, China

* **Correspondence:** Email: wangpeng@gxmu.edu.cn; Tel: +867715314316; Fax: +867715314316.

Supplementary

Table S1. Demographic data of 500 patients included in prognostic analysis in the TCGA LUAD cohort.

Variables	Events/total (n = 500)	MST (days)	Crude HR (95% CI)	Log-rank <i>P</i>
Age (years) ^a				0.386
≤ 65	74/215	1499	1	
> 65	99/264	1454	1.143 (0.845-1.546)	
Gender				0.754
Female	96/270	1454	1	
Male	86/230	1528	1.048 (0.783-1.403)	
Tumor Stage ^b				< 0.0001
Stage I	65/268	2620	1	
Stage II	54/119	1209	2.473 (1.719-3.559)	
Stage III	45/80	879	3.495 (2.383-5.126)	
Stage IV	16/25	826	3.819 (2.201-6.629)	
Tumor Stage ^b				< 0.0001
Stage I+II	119/387	1632	1	
Stage III+IV	61/105	826	2.585 (1.894-3.528)	

Notes: a Information of age was unavailable in 21 patients; b Information of tumor stage was unavailable in 8 patients.

Abbreviation: TCGA, The Cancer Genome Atlas; MST, median survival time; LUAD, lung adenocarcinoma; HR, hazard ratio; CI, confidence interval.

Table S2. Survival analysis results of snoRNA in TCGA LUAD cohort.

ID	Adjusted Pλ	HR	Low 95%CI	High 95%CI
snoU109 ENSG00000238832	0.009846284	1.482519	1.099398	1.999151
U8 ENSG00000239148	0.010418736	0.677437	0.502876	0.91259
SNORA70 ENSG00000206886	0.017173982	0.697903	0.51918	0.93815
U3 ENSG00000207119	0.030339121	0.720103	0.534974	0.969297
SNORA5A ENSG00000206838	0.036390775	1.369859	1.020138	1.83947
SNORD7 ENSG00000207297	0.037602647	0.73046	0.543267	0.982155
SNORD104 ENSG00000199753	0.044011334	0.736418	0.546781	0.991827
U3 ENSG00000221044	0.061070408	0.754489	0.561855	1.013168
SNORA5C ENSG00000201772	0.064416969	1.323813	0.983351	1.782152
SNORA9 ENSG00000252192	0.064465027	0.755091	0.560627	1.01701
SNORA54 ENSG00000207008	0.064595674	0.757066	0.56357	1.016997
SNORD88A ENSG00000221241	0.073531768	1.307652	0.974775	1.754204
SNORD15A ENSG00000206941	0.074320315	1.306531	0.974074	1.752457
SNORA15B-1 ENSG00000206785	0.076448663	1.304732	0.972126	1.751137
SNORD116-2 ENSG00000207001	0.080345273	0.769276	0.573324	1.0322
SNORA58 ENSG00000249020	0.081935056	0.76783	0.570156	1.034038
SNORA75 ENSG00000212440	0.084349736	1.296392	0.965422	1.740827
SNORA1B ENSG00000199405	0.090429978	0.775378	0.577583	1.040908
SNORA48 ENSG00000252774	0.094446457	0.776391	0.577112	1.044481
SNORA40 ENSG00000212579	0.09530474	1.285931	0.956945	1.728018
SNORD100 ENSG00000221500	0.100955346	1.279795	0.95305	1.718561
SNORA4 ENSG00000202434	0.111346735	1.269432	0.946381	1.702759
SNORA68B ENSG00000201388	0.11254249	1.267948	0.945713	1.699978
SNORA14B ENSG00000207181	0.133047892	1.25363	0.933435	1.68366
SNORA67 ENSG00000252473	0.134710487	0.797664	0.593161	1.072674
SNORA48 ENSG00000212445	0.138135285	0.800061	0.595757	1.074428
SNORA63 ENSG00000252448	0.138753662	0.799831	0.595083	1.075026
SNORA13 ENSG00000238363	0.140051313	1.253137	0.928607	1.691082
SNORD6 ENSG00000202314	0.143321549	0.802557	0.597792	1.077462
snoU13 ENSG00000239035	0.151273111	0.805883	0.600151	1.082141
SNORA55 ENSG00000201457	0.153307326	0.804736	0.59725	1.084304
SNORA19 ENSG00000222588	0.157703593	1.237208	0.920876	1.662203
U3 ENSG00000199370	0.1589506	0.80937	0.603033	1.086308
snoZ196 ENSG00000281780	0.159380062	0.809596	0.603253	1.086518
SNORA48 ENSG00000212391	0.162776254	0.810958	0.604247	1.088384
SNORA71B ENSG00000235408	0.164556606	0.809849	0.601508	1.090353
SNORA48 ENSG00000252824	0.167408043	1.232484	0.916014	1.658289
SNORA12 ENSG00000212342	0.169310076	1.231207	0.915201	1.656326
SNORA2B ENSG00000207313	0.171349492	1.228384	0.914812	1.64944
SNORA22C ENSG00000207344	0.171538134	1.228554	0.914639	1.65021
SNORA58 ENSG00000201003	0.172355995	1.23194	0.913027	1.662247

U8 ENSG00000239142	0.182608943	0.817994	0.608751	1.099157
SNORA19 ENSG00000207468	0.183535409	0.819415	0.610989	1.098941
SNORA12 ENSG00000212464	0.191792491	0.822773	0.61386	1.102786
SNORA11 ENSG00000221716	0.191966136	1.216808	0.906164	1.633945
SNORA23 ENSG00000201998	0.194120786	1.216918	0.904828	1.636652
SNORA33 ENSG00000200534	0.194376905	1.215797	0.905099	1.633149
SNORD91A ENSG00000212163	0.194412684	0.821893	0.611156	1.105298
SNORA22 ENSG00000199571	0.197931503	1.215233	0.903189	1.635085
U3 ENSG00000275154	0.216580302	0.830472	0.618533	1.115033
SNORD11 ENSG00000238317	0.216842057	0.829945	0.617414	1.115636
SNORA74D ENSG00000252213	0.221069435	1.201948	0.895229	1.613753
SNORA75 ENSG00000212533	0.221822435	1.200896	0.895272	1.610854
SNORD13P3 ENSG00000239128	0.228628884	0.835163	0.622892	1.11977
SNORA2A ENSG00000206612	0.229402818	0.835005	0.62228	1.12045
ACA64 ENSG00000239005	0.23456243	0.836468	0.623133	1.122841
SNORD94 ENSG00000208772	0.236344097	1.194711	0.889985	1.603773
SNORA76 ENSG00000252122	0.241472504	0.837873	0.623207	1.126482
SNORA22 ENSG00000206634	0.243124001	0.838842	0.62449	1.126769
SNORD67 ENSG00000212135	0.244847883	1.191579	0.88681	1.601088
SNORA70 ENSG00000200237	0.248461862	0.840795	0.626316	1.128721
SNORA59B ENSG00000266079	0.249798088	0.841494	0.627202	1.129002
SNORA65 ENSG00000201302	0.250737656	1.188037	0.885393	1.594131
SNORD53B ENSG00000265706	0.253048374	0.842552	0.628074	1.130271
U3 ENSG00000212479	0.255070891	1.187715	0.883181	1.597256
SNORD63B ENSG00000222937	0.255739573	0.84256	0.627042	1.132152
SNORD127 ENSG00000239043	0.255922496	0.841306	0.624431	1.133504
SNORA7 ENSG00000206913	0.264323867	0.845873	0.630467	1.134876
SNORD69 ENSG00000212452	0.269702837	0.846346	0.629349	1.138161
SNORA20 ENSG00000207392	0.276689809	1.177336	0.877309	1.579968
SNORD56 ENSG00000201151	0.285582822	1.173455	0.874917	1.57386
SNORA11F ENSG00000221164	0.287723276	1.175642	0.872404	1.584282
SNORD46 ENSG00000200913	0.289914008	0.852634	0.634654	1.145483
SNORD14E ENSG00000200879	0.290063412	1.171633	0.873679	1.5712
SNORA2 ENSG00000206647	0.301248252	1.167384	0.870521	1.565483
SNORA63C ENSG00000201448	0.306876167	0.857115	0.637673	1.152074
SNORD38 ENSG00000207199	0.31211422	1.16584	0.865812	1.569837
SNORA22B ENSG00000206603	0.316675223	1.161468	0.866488	1.556867
SNORA71C ENSG00000201512	0.317200796	1.162246	0.865656	1.560455
SNORD9 ENSG00000199436	0.323980052	0.860911	0.639306	1.15933
SNORA58B ENSG00000201129	0.324464729	1.159005	0.864191	1.554393
SNORA74C-1 ENSG00000265733	0.327188901	0.862466	0.641507	1.159532
SNORA75 ENSG00000212593	0.335050751	0.865256	0.644686	1.16129
SNORA31 ENSG00000251999	0.351467911	1.150841	0.856381	1.546549
SNORD45 ENSG00000252438	0.351792797	0.869831	0.648556	1.166601

SNORA27 ENSG00000200235	0.352884598	0.869382	0.647085	1.168047
SNORA80E ENSG00000207475	0.356973929	1.147451	0.856318	1.537566
SNORA51 ENSG00000206878	0.357427852	1.149371	0.854466	1.546056
SNORD116-6 ENSG00000207442	0.357652008	0.870604	0.648027	1.169628
SNORA4 ENSG00000251730	0.359009383	0.870812	0.647973	1.170286
ACA59 ENSG00000251775	0.359939049	0.870556	0.647004	1.171349
SNORA49 ENSG00000208892	0.361755206	1.14627	0.854826	1.53708
snoZ6 ENSG00000252200	0.374433086	0.875371	0.652574	1.174234
SNORA40B ENSG00000208308	0.377794469	0.874442	0.648995	1.178203
SNORD42B ENSG00000238423	0.384157714	1.141829	0.846983	1.539314
SNORD17 ENSG00000212232	0.389117093	1.138529	0.847454	1.52958
SNORA57 ENSG00000212567	0.390900466	1.138202	0.846824	1.529838
SNORA16 ENSG00000212293	0.394246648	0.879056	0.653464	1.182528
SNORA26 ENSG00000212517	0.39483389	1.136815	0.84608	1.527453
SNORA7 ENSG00000222604	0.414817031	0.884262	0.657939	1.188438
SNORD67 ENSG00000252427	0.414964922	1.130515	0.84175	1.518342
SNORD116-19 ENSG00000207460	0.423831912	0.886723	0.660447	1.190524
U8 ENSG00000238840	0.424308446	0.886933	0.660787	1.190476
SCARNA10 ENSG00000239002	0.429446613	1.126463	0.838362	1.513568
SNORA15B-2 ENSG00000207062	0.429878158	0.88835	0.662104	1.191907
snoU13 ENSG00000238326	0.431931446	1.12529	0.838328	1.510481
SNORA80A ENSG00000200792	0.434514505	1.126781	0.83527	1.520031
SNORA31 ENSG00000252050	0.436637969	0.889653	0.662639	1.194441
SNORD62B ENSG00000231587	0.439765283	0.88954	0.661006	1.197088
SNORA67 ENSG00000201619	0.443348798	1.122602	0.835229	1.508849
SNORD112 ENSG00000238966	0.444868361	0.891476	0.663929	1.197011
SNORD88 ENSG00000221611	0.449294572	1.120945	0.83394	1.506725
SNORA70F ENSG00000206869	0.451689401	0.892676	0.664183	1.199774
SNORA26 ENSG00000212187	0.453102238	1.119528	0.833559	1.503604
SNORD1B ENSG00000199961	0.455390697	0.894104	0.666421	1.199575
SNORD8 ENSG00000200785	0.455522874	1.119136	0.83271	1.504084
SNORA71D ENSG00000200354	0.463166914	1.11665	0.831579	1.499446
SNORD38C ENSG00000207109	0.463952384	0.895991	0.667815	1.202129
SNORA50A ENSG00000281910	0.464423498	0.895988	0.667599	1.202509
SNORA43 ENSG00000281863	0.468877879	1.116214	0.828979	1.502972
SNORD72 ENSG00000212296	0.474814703	1.115211	0.826953	1.50395
SNORA51 ENSG00000206898	0.475232153	0.897696	0.667522	1.207238
SNORD13E ENSG00000238311	0.482004582	0.899084	0.668361	1.209455
SNORA81 ENSG00000253092	0.482744996	0.899813	0.670081	1.208307
SNORA77 ENSG00000221083	0.485453348	0.900688	0.671337	1.208394
SNORD116-27 ENSG00000251896	0.487621728	0.901135	0.671627	1.209072
SNORD105B ENSG00000238531	0.488146473	0.90129	0.671828	1.209123
SNORD71 ENSG00000223224	0.48997498	1.109453	0.826114	1.489972
SNORD73B ENSG00000201264	0.491190554	0.901064	0.669794	1.212187

SNORD121A ENSG00000238886	0.491470126	1.108439	0.826671	1.486246
SNORA14 ENSG00000251922	0.494432539	0.901635	0.669943	1.213456
SNORA35B ENSG00000271907	0.495121103	1.108609	0.824379	1.490836
SCARNA18 ENSG00000238835	0.498442686	0.901986	0.669095	1.215937
SNORD59A ENSG00000207031	0.499918508	0.903249	0.672071	1.213947
ACA64 ENSG00000238934	0.50113928	1.10594	0.824738	1.483021
SNORD19 ENSG00000222345	0.501965815	0.90441	0.674508	1.212674
SNORA25 ENSG00000200075	0.502066468	0.903713	0.672425	1.214555
SNORD19B ENSG00000280904	0.502723211	0.904399	0.674124	1.213334
SNORD123 ENSG00000239112	0.503444553	1.106175	0.823093	1.486614
SNORD53 ENSG00000265145	0.50406566	1.105187	0.824161	1.48204
SNORA18 ENSG00000252719	0.504617801	1.106336	0.822191	1.488678
SNORD93 ENSG00000221740	0.50563792	1.104822	0.823797	1.481713
SNORA51 ENSG00000271798	0.510955455	1.10381	0.822243	1.481797
SNORA31 ENSG00000252349	0.515961842	0.906799	0.675009	1.218181
SNORD12B ENSG00000222365	0.516867607	1.101922	0.821667	1.477766
snoU13 ENSG00000239096	0.51993721	1.101199	0.820994	1.477038
SNORA38 ENSG00000200816	0.521829375	0.90813	0.676214	1.219584
SNORA53 ENSG00000212443	0.522003746	1.101659	0.819091	1.481709
SNORA62 ENSG00000202374	0.523120302	0.908863	0.677815	1.218667
SNORA73B ENSG00000200087	0.524959272	0.90906	0.677532	1.219705
U3 ENSG00000271817	0.525298723	0.909269	0.678005	1.219414
U3 ENSG00000200693	0.53636105	0.911413	0.679237	1.222952
SNORA51 ENSG00000207022	0.537689944	0.911726	0.679559	1.223212
SNORD56B ENSG00000207444	0.541082175	1.096756	0.815609	1.474817
SNORA16B ENSG00000201544	0.543222209	0.912789	0.680156	1.224989
SNORA70 ENSG00000201376	0.54810735	0.913432	0.67975	1.227448
SNORA26 ENSG00000212588	0.55222411	0.914309	0.68047	1.228506
snoU2_19 ENSG00000201592	0.557088564	1.092093	0.81386	1.465446
SNORA76 ENSG00000252904	0.562065751	1.091423	0.811998	1.467004
SNORA36 ENSG00000206731	0.564183127	1.08995	0.813324	1.460661
SNORA26 ENSG00000252236	0.566921216	1.089443	0.812559	1.460676
SNORA73 ENSG00000199977	0.573867122	1.087656	0.811541	1.457715
SNORD91B ENSG00000275084	0.574444074	0.919312	0.685379	1.23309
U3 ENSG00000199856	0.576744626	0.919396	0.684448	1.234994
snoU13 ENSG00000239129	0.581577569	1.086356	0.809159	1.458514
SNORA67 ENSG00000212338	0.58555004	0.921591	0.687191	1.235944
SNORD62A ENSG00000235284	0.590805559	1.08425	0.807369	1.456085
SNORA66 ENSG00000207523	0.59171479	0.921802	0.684567	1.241252
SNORD38 ENSG00000252408	0.595002663	0.923484	0.688605	1.238479
SNORA62 ENSG00000201157	0.597215378	1.082853	0.806018	1.454771
SNORD19 ENSG00000212493	0.598057599	1.082512	0.806161	1.453595
snoU109 ENSG00000238575	0.599981025	0.923191	0.684817	1.24454
SNORA80B ENSG00000206633	0.604088536	1.081486	0.804318	1.454166

SNORA30 ENSG00000200063	0.609231096	0.926402	0.691037	1.241933
SNORD116-26 ENSG00000251815	0.611342512	1.080047	0.802518	1.45355
SNORD111 ENSG00000252230	0.615199478	0.927158	0.690369	1.245162
SNORD11B ENSG00000271852	0.615316809	1.078419	0.803345	1.447681
SNORA81 ENSG00000238390	0.621465504	0.92856	0.69189	1.246187
SNORA71A ENSG00000225091	0.626606232	1.075729	0.801647	1.443519
SNORD121B ENSG00000238300	0.632354094	1.074025	0.801595	1.439043
SNORA2C ENSG00000221491	0.633696258	0.930477	0.691818	1.251467
U3 ENSG00000212182	0.634315672	0.931187	0.694152	1.249165
SNORA31 ENSG00000252096	0.635423264	1.073906	0.799744	1.442054
SNORA26 ENSG00000212624	0.636495925	0.931492	0.694002	1.250253
SNORD99 ENSG00000221539	0.638773124	0.930554	0.689011	1.256772
U8 ENSG00000238963	0.64011455	0.932246	0.694702	1.251013
SNORD56 ENSG00000200753	0.641379773	0.93257	0.695186	1.251013
SNORA80D ENSG00000207217	0.64785519	0.93363	0.69533	1.2536
SNORA38B ENSG00000200394	0.651335824	0.933989	0.694562	1.25595
SNORA70B ENSG00000206937	0.652905734	0.934886	0.697144	1.253704
SNORA69 ENSG00000212206	0.653500523	1.069811	0.796801	1.436361
SNORA70 ENSG00000251893	0.66182051	1.067751	0.795972	1.432328
SNORA70 ENSG00000202379	0.67143486	0.938576	0.700262	1.257992
SNORD60 ENSG00000206630	0.678404145	0.939712	0.700398	1.260796
SNORD116-24 ENSG00000207279	0.681432141	0.940258	0.700675	1.261763
SNORD124 ENSG00000238793	0.683713273	0.940336	0.69944	1.2642
SNORA70 ENSG00000252657	0.692501805	0.942346	0.702093	1.264814
SNORA25 ENSG00000201957	0.69889921	0.943592	0.703099	1.266346
snoU2-30 ENSG00000201882	0.70367585	1.059011	0.788118	1.423017
SNORD92 ENSG00000264994	0.707898495	1.058123	0.787384	1.421955
SNORA46 ENSG00000212371	0.708561009	0.945519	0.70485	1.268363
SNORD13P1 ENSG00000238498	0.7125295	1.056714	0.78799	1.417079
SNORA31 ENSG00000253059	0.732958072	0.949956	0.707333	1.275803
SCARNA12 ENSG00000238795	0.741476088	0.951804	0.709737	1.276432
SNORA31 ENSG00000253013	0.749220515	0.952978	0.70931	1.280354
SNORD48 ENSG00000201823	0.752553445	0.953097	0.70703	1.284801
SNORD14A ENSG00000272034	0.764564064	1.046202	0.778478	1.405998
SNORA79 ENSG00000221303	0.773729549	1.044154	0.777753	1.401804
SNORA28 ENSG00000272533	0.776152612	0.957786	0.71146	1.289397
SNORA12 ENSG00000212175	0.783600475	0.959802	0.716168	1.286317
SNORD3B-2 ENSG00000262074	0.784930041	0.959886	0.715357	1.288003
SNORD63 ENSG00000251987	0.786088446	1.041662	0.775724	1.39877
SNORD83A ENSG00000209482	0.790370478	0.960932	0.716282	1.289143
SNORA3 ENSG00000221639	0.794091009	0.961679	0.717128	1.289625
SNORA51 ENSG00000207171	0.794586587	0.961451	0.715161	1.292559
SNORD63 ENSG00000206989	0.794695926	1.039633	0.775783	1.393218
SNORD89 ENSG00000212283	0.795225312	0.961827	0.716877	1.290473

SNORD116-14 ENSG00000206621	0.808191497	0.964249	0.718683	1.293722
SNORD37 ENSG00000206775	0.808381634	1.037023	0.773017	1.391195
SNORD117 ENSG00000201785	0.811247003	0.964883	0.719546	1.29387
SNORD116-4 ENSG00000275529	0.81294139	0.965161	0.719522	1.29466
snoU13 ENSG00000239093	0.81482682	1.035727	0.772082	1.3894
SNORA63 ENSG00000201791	0.821167182	1.034727	0.769618	1.391159
SNORA2 ENSG00000202343	0.824259216	0.967309	0.721385	1.29707
SNORA77 ENSG00000221643	0.824678251	1.0337	0.770978	1.385949
U3 ENSG00000199851	0.824989788	0.967103	0.718974	1.300866
SNORD111 ENSG00000221066	0.827469243	1.033347	0.769366	1.387904
SNORA11B ENSG00000221102	0.829476099	1.033074	0.768299	1.389098
SNORA70 ENSG00000253042	0.835899136	0.969226	0.721073	1.302779
snoU13 ENSG00000239079	0.838298782	0.969804	0.722421	1.301899
SNORA46 ENSG00000207493	0.841210868	1.030582	0.76753	1.383789
SNORD51 ENSG00000207047	0.844413775	1.029803	0.768029	1.380799
SNORA74B ENSG00000212402	0.846723456	1.029528	0.766465	1.38288
SNORD101 ENSG00000206754	0.846775339	1.029263	0.7682	1.379044
SNORD3A ENSG00000263934	0.847765566	1.02912	0.767701	1.379557
SNORD36C ENSG00000252542	0.850964517	0.972219	0.724645	1.304377
SNORA24B ENSG00000206903	0.853807479	1.027952	0.766688	1.378248
SNORD58 ENSG00000212615	0.855732906	1.027917	0.763918	1.38315
SNORA48 ENSG00000212458	0.857439494	0.973445	0.725735	1.305703
SNORA31 ENSG00000199477	0.859525272	0.973763	0.7254	1.307161
SNORD15B ENSG00000207445	0.861132663	1.026452	0.766124	1.375238
SNORD116-1 ENSG00000207063	0.862101906	1.026561	0.763699	1.379899
SNORA63D ENSG00000201229	0.867504945	1.025379	0.763851	1.37645
SNORA60 ENSG00000199266	0.868261145	1.02518	0.764153	1.375371
SNORD18 ENSG00000200677	0.868820036	0.975468	0.726446	1.309855
SNORA47 ENSG00000238961	0.870863389	1.024939	0.761581	1.379367
SNORA73 ENSG00000222145	0.878315425	1.023281	0.762159	1.373865
SNORA75 ENSG00000206885	0.880584116	0.977661	0.728084	1.312791
SNORA70G ENSG00000206650	0.881888913	1.022465	0.76273	1.370646
SNORA18 ENSG00000206592	0.881894993	1.022698	0.760601	1.375111
SNORA3B ENSG00000212607	0.882039626	1.022475	0.762344	1.37137
SNORA43 ENSG00000252461	0.890601446	0.97963	0.730636	1.313479
SNORA14A ENSG00000201643	0.892898298	1.020332	0.761182	1.367712
SNORD115 ENSG00000212411	0.893769138	0.980164	0.730439	1.315265
snoU13 ENSG00000238295	0.898713029	0.981044	0.730644	1.317258
SNORA74 ENSG00000223111	0.899683118	0.981236	0.730925	1.31727
SNORA40 ENSG00000253047	0.900829325	0.981482	0.731482	1.316924
SNORD116-13 ENSG00000207137	0.902688362	0.981746	0.730702	1.319039
SNORD116 ENSG00000252985	0.902886276	0.981874	0.731891	1.31724
SNORD3B-1 ENSG00000265185	0.915899377	1.015976	0.757054	1.363453
SNORA57 ENSG00000223027	0.916829395	0.984463	0.733772	1.320802

SNORD65C ENSG00000212264	0.923074215	1.01464	0.755424	1.362804
SNORD111B ENSG00000221514	0.926533927	1.013963	0.755117	1.361539
SNORA30 ENSG00000206755	0.931020952	0.987108	0.735807	1.324236
U3 ENSG00000238297	0.933064119	0.987456	0.735504	1.325715
SNORA37 ENSG00000207233	0.933512302	1.012711	0.752677	1.362581
SNORD114-3 ENSG00000201839	0.934163969	1.012518	0.753731	1.360157
SNORA44 ENSG00000252840	0.935165502	1.012264	0.754651	1.357817
SNORA15 ENSG00000207168	0.936934698	1.011949	0.753999	1.358146
SNORA79B ENSG00000222489	0.937544863	1.012	0.750924	1.363846
SNORA74 ENSG00000252917	0.938048566	1.011815	0.752433	1.360611
SNORA42 ENSG00000200385	0.944958149	0.989625	0.736009	1.330632
SNORA72 ENSG00000200355	0.95116143	1.009247	0.751754	1.354938
SNORD12C ENSG00000209042	0.951350524	1.009164	0.752829	1.352779
snoU13 ENSG00000238372	0.95686062	1.008197	0.750052	1.355187
SNORA48 ENSG00000212181	0.960361891	0.992531	0.738476	1.333987
SNORA1 ENSG00000202059	0.972517969	0.994854	0.741779	1.33427
SNORA59A ENSG00000239149	0.972621504	0.994891	0.742566	1.332955
SNORA9B ENSG00000206897	0.975798954	0.995468	0.742281	1.335015
SNORA69 ENSG00000206622	0.976792312	0.995648	0.742166	1.335707
SNORA7B ENSG00000207088	0.976986855	0.995693	0.742622	1.335007
SNORA72 ENSG00000201944	0.982682449	1.003245	0.748762	1.34422
SNORA17 ENSG00000212461	0.983435348	0.99688	0.742197	1.338956
SNORA84 ENSG00000239183	0.985578173	1.002738	0.745498	1.34874
SNORA7 ENSG00000206976	0.986281721	1.002579	0.747495	1.344711
SNORA74A ENSG00000200959	0.99230388	1.00145	0.745998	1.344377
U3 ENSG00000212195	0.997049282	1.000554	0.745947	1.342065
SNORD70 ENSG00000212534	0.999101972	0.99983	0.743786	1.344016

Notes: λ adjusted for tumor stage.

Table S3. snoRNA co-expressed genes list

ID	ID	r	P value
SNORA5A	TARDBP	-0.32	0.002084
SNORA5A	ATF7	-0.308	0.002998
SNORA5A	SP2	-0.303	0.003477
SNORA5A	SF1	-0.295	0.004389
SNORA5A	PRKACA	-0.293	0.004649
SNORA5A	CTDNEP1	-0.29	0.005065
SNORA5A	HNRNPH3	-0.288	0.00536
SNORA5A	RAB5B	-0.285	0.005833
SNORA5A	ATN1	-0.284	0.005999
SNORA5A	SPPL3	-0.281	0.006522
SNORA5A	TBC1D17	-0.278	0.007085
SNORA5A	VAMP2	-0.278	0.007085
SNORA5A	CTDSP1	-0.274	0.007905
SNORA5A	RNF10	-0.274	0.007905
SNORA5A	SLC25A28	-0.27	0.008808
SNORA5A	NXF1	-0.268	0.009293
SNORA5A	PTPN23	-0.268	0.009293
SNORA5A	SETD1B	-0.263	0.010612
SNORA5A	HNRNPA3	-0.26	0.011481
SNORA5A	SRSF4	-0.256	0.012738
SNORA5A	DAZAP1	-0.254	0.013411
SNORA5A	IKZF4	-0.253	0.013759
SNORA5A	ULK1	-0.253	0.013759
SNORA5A	RNF44	-0.253	0.013759
SNORA5A	FBRS	-0.252	0.014115
SNORA5A	CIR1	-0.251	0.014479
SNORA5A	COPS7B	-0.251	0.014479
SNORA5A	C19orf54	-0.249	0.015233
SNORA5A	SETD1A	-0.245	0.016843
SNORA5A	ZNF444	-0.243	0.017703
SNORA5A	USB1	-0.241	0.018602
SNORA5A	SYVN1	-0.241	0.018602
SNORA5A	BET1L	-0.241	0.018602
SNORA5A	SLC35A4	-0.24	0.019065
SNORA5A	MNT	-0.24	0.019065
SNORA5A	CNOT3	-0.239	0.019539
SNORA5A	PLBD2	-0.238	0.020024
SNORA5A	CNKSR1	-0.237	0.020518
SNORA5A	TAF15	-0.237	0.020518
SNORA5A	SRRM1	-0.236	0.021024
SNORA5A	HNRNPA1	-0.236	0.021024
SNORA5A	CRTC2	-0.236	0.021024

SNORA5A	PRR14	-0.235	0.02154
SNORA5A	NPRL3	-0.235	0.02154
SNORA5A	DEXI	-0.234	0.022067
SNORA5A	TSPAN14	-0.233	0.022605
SNORA5A	MED25	-0.233	0.022605
SNORA5A	BRD4	-0.232	0.023155
SNORA5A	NAA60	-0.232	0.023155
SNORA5A	SUFU	-0.232	0.023155
SNORA5A	CAPZB	-0.231	0.023716
SNORA5A	ATXN2L	-0.23	0.024289
SNORA5A	PHF21A	-0.229	0.024874
SNORA5A	PPRC1	-0.229	0.024874
SNORA5A	HNRNPUL2	-0.227	0.026081
SNORA5A	ZRSR2	-0.226	0.026703
SNORA5A	GSK3A	-0.225	0.027338
SNORA5A	CCDC97	-0.225	0.027338
SNORA5A	R3HDM2	-0.225	0.027338
SNORA5A	BICRA	-0.225	0.027338
SNORA5A	RAB11B	-0.224	0.027986
SNORA5A	TP53I11	-0.223	0.028647
SNORA5A	PHACTR4	-0.223	0.028647
SNORA5A	UBALD1	-0.222	0.029321
SNORA5A	PNPLA2	-0.222	0.029321
SNORA5A	TMEM39B	-0.222	0.029321
SNORA5A	CAMTA2	-0.222	0.029321
SNORA5A	CPSF7	-0.221	0.030009
SNORA5A	TEX261	-0.221	0.030009
SNORA5A	YPEL3	-0.219	0.031427
SNORA5A	LZTS2	-0.219	0.031427
SNORA5A	ZNF213	-0.218	0.032157
SNORA5A	PRR13	-0.217	0.032902
SNORA5A	UBQLN2	-0.217	0.032902
SNORA5A	SYF2	-0.217	0.032902
SNORA5A	RNPEPL1	-0.217	0.032902
SNORA5A	RAB7A	-0.217	0.032902
SNORA5A	KIAA1522	-0.217	0.032902
SNORA5A	PABPN1	-0.217	0.032902
SNORA5A	FIZ1	-0.217	0.032902
SNORA5A	GATD1	-0.216	0.033661
SNORA5A	TMEM214	-0.216	0.033661
SNORA5A	INAFM1	-0.216	0.033661
SNORA5A	SIDT2	-0.216	0.033661
SNORA5A	MT-ND1	-0.215	0.034436
SNORA5A	FBRSL1	-0.215	0.034436

SNORA5A	JUND	-0.215	0.034436
SNORA5A	PHF1	-0.215	0.034436
SNORA5A	WDC1	-0.215	0.034436
SNORA5A	BLOC1S3	-0.214	0.035225
SNORA5A	DNAJB2	-0.214	0.035225
SNORA5A	SNRPA	-0.213	0.03603
SNORA5A	VEGFB	-0.213	0.03603
SNORA5A	KDM6B	-0.213	0.03603
SNORA5A	FAM222B	-0.213	0.03603
SNORA5A	FUS	-0.213	0.03603
SNORA5A	PCBP2	-0.212	0.036851
SNORA5A	MOB2	-0.212	0.036851
SNORA5A	ARHGAP17	-0.212	0.036851
SNORA5A	PTOV1	-0.212	0.036851
SNORA5A	SRCAP	-0.212	0.036851
SNORA5A	MBD6	-0.212	0.036851
SNORA5A	TATDN2	-0.212	0.036851
SNORA5A	CCDC92	-0.211	0.037687
SNORA5A	SMG9	-0.211	0.037687
SNORA5A	CIC	-0.211	0.037687
SNORA5A	SRRM2	-0.211	0.037687
SNORA5A	ARID1A	-0.21	0.038539
SNORA5A	PACS1	-0.21	0.038539
SNORA5A	ANP32B	-0.21	0.038539
SNORA5A	OAZ2	-0.21	0.038539
SNORA5A	ZNF580	-0.209	0.039408
SNORA5A	DYRK1B	-0.209	0.039408
SNORA5A	MMP24-AS1	-0.208	0.040294
SNORA5A	PITPNA	-0.208	0.040294
SNORA5A	TMEM175	-0.208	0.040294
SNORA5A	MEF2D	-0.208	0.040294
SNORA5A	MT-ND4	-0.207	0.041196
SNORA5A	HPS1	-0.206	0.042115
SNORA5A	FAM160A2	-0.206	0.042115
SNORA5A	NOL4L	-0.206	0.042115
SNORA5A	RAB4B	-0.206	0.042115
SNORA5A	DAZAP2	-0.205	0.043052
SNORA5A	CIZ1	-0.205	0.043052
SNORA5A	DVL3	-0.205	0.043052
SNORA5A	ATP6VOC	-0.205	0.043052
SNORA5A	ZMIZ1	-0.205	0.043052
SNORA5A	HECTD3	-0.205	0.043052
SNORA5A	WBP2	-0.204	0.044006
SNORA5A	SSBP3	-0.204	0.044006

SNORA5A	NCOA6	-0.203	0.044978
SNORA5A	RBPM5	-0.203	0.044978
SNORA5A	PRKD2	-0.203	0.044978
SNORA5A	HNRNPD	-0.202	0.045968
SNORA5A	TNK2	-0.201	0.046976
SNORA5A	CRTC3	-0.201	0.046976
SNORA5A	HNRNPUL1	-0.2	0.048003
SNORA5A	SORBS3	-0.2	0.048003
SNORA5A	ZER1	-0.2	0.048003
SNORA5A	INO80D	0.23	0.049197
SNORA5A	INVS	0.23	0.049197
SNORA5A	ZNF624	0.23	0.049197
SNORA5A	CYP51A1	0.23	0.049197
SNORA5A	KIF2A	0.23	0.049197
SNORA5A	ME2	0.23	0.049197
SNORA5A	MOB1A	0.23	0.049197
SNORA5A	SAMD11	0.23	0.049197
SNORA5A	CSNK1A1	0.23	0.049197
SNORA5A	ZDHHC4	0.23	0.049197
SNORA5A	ARAP2	0.231	0.048149
SNORA5A	PRR14L	0.231	0.048149
SNORA5A	MALSU1	0.231	0.048149
SNORA5A	PARP14	0.231	0.048149
SNORA5A	LHFPL2	0.231	0.048149
SNORA5A	TBL1XR1	0.231	0.048149
SNORA5A	CA5B	0.231	0.048149
SNORA5A	STYX	0.232	0.04712
SNORA5A	WAPL	0.232	0.04712
SNORA5A	INPP4B	0.232	0.04712
SNORA5A	FKBP14	0.232	0.04712
SNORA5A	ERCC8	0.232	0.04712
SNORA5A	ZNF658	0.232	0.04712
SNORA5A	GUCY1A3	0.232	0.04712
SNORA5A	ZNF443	0.232	0.04712
SNORA5A	EIF4E	0.232	0.04712
SNORA5A	AC135178.2	0.233	0.046109
SNORA5A	GFM2	0.233	0.046109
SNORA5A	AC010422.3	0.233	0.046109
SNORA5A	RTTN	0.233	0.046109
SNORA5A	FRK	0.233	0.046109
SNORA5A	DDX52	0.233	0.046109
SNORA5A	CC2D2B	0.233	0.046109
SNORA5A	C11orf65	0.233	0.046109
SNORA5A	FIGNL1	0.234	0.045116

SNORA5A	HSPA8	0.234	0.045116
SNORA5A	SYCP3	0.234	0.045116
SNORA5A	UTP15	0.234	0.045116
SNORA5A	ATP6V1A	0.234	0.045116
SNORA5A	CEP128	0.234	0.045116
SNORA5A	ITGAV	0.234	0.045116
SNORA5A	PLXNC1	0.235	0.044142
SNORA5A	PTPRC	0.235	0.044142
SNORA5A	GPATCH11	0.235	0.044142
SNORA5A	XKR9	0.235	0.044142
SNORA5A	ZNF14	0.235	0.044142
SNORA5A	ABCE1	0.235	0.044142
SNORA5A	PTPRG	0.235	0.044142
SNORA5A	MTR	0.235	0.044142
SNORA5A	ZZZ3	0.236	0.043185
SNORA5A	XRN2	0.236	0.043185
SNORA5A	CCZ1B	0.236	0.043185
SNORA5A	LACTB2	0.237	0.042246
SNORA5A	ZNF253	0.237	0.042246
SNORA5A	LIN9	0.237	0.042246
SNORA5A	SLC30A6	0.237	0.042246
SNORA5A	CEP97	0.237	0.042246
SNORA5A	VPS8	0.237	0.042246
SNORA5A	SCYL2	0.237	0.042246
SNORA5A	C1GALT1	0.237	0.042246
SNORA5A	KCNV2	0.238	0.041325
SNORA5A	CCDC88A	0.238	0.041325
SNORA5A	EEA1	0.238	0.041325
SNORA5A	FAM126B	0.238	0.041325
SNORA5A	ING3	0.238	0.041325
SNORA5A	HNRNPLL	0.238	0.041325
SNORA5A	ACTR8	0.239	0.04042
SNORA5A	CHM	0.239	0.04042
SNORA5A	IRAK4	0.239	0.04042
SNORA5A	SLC35B4	0.239	0.04042
SNORA5A	NUP205	0.239	0.04042
SNORA5A	KLRC3	0.239	0.04042
SNORA5A	TTC21B	0.239	0.04042
SNORA5A	TIFA	0.239	0.04042
SNORA5A	STK17B	0.24	0.039532
SNORA5A	ZNF611	0.24	0.039532
SNORA5A	UBE3A	0.24	0.039532
SNORA5A	PTPN22	0.24	0.039532
SNORA5A	GLIPR1L1	0.241	0.038661

SNORA5A	TBC1D12	0.241	0.038661
SNORA5A	ZNF714	0.241	0.038661
SNORA5A	PLEKHF2	0.241	0.038661
SNORA5A	ANKRD26	0.241	0.038661
SNORA5A	GPR65	0.241	0.038661
SNORA5A	DICER1	0.241	0.038661
SNORA5A	ZNF28	0.241	0.038661
SNORA5A	CD226	0.241	0.038661
SNORA5A	PAPOLG	0.241	0.038661
SNORA5A	DOCK11	0.242	0.037806
SNORA5A	STAM2	0.242	0.037806
SNORA5A	SCAF11	0.243	0.036968
SNORA5A	USP50	0.243	0.036968
SNORA5A	TMEM184C	0.243	0.036968
SNORA5A	PACRGL	0.243	0.036968
SNORA5A	TRAF6	0.243	0.036968
SNORA5A	NOC3L	0.243	0.036968
SNORA5A	TMTC3	0.243	0.036968
SNORA5A	SLC05A1	0.243	0.036968
SNORA5A	LRRC40	0.243	0.036968
SNORA5A	ASH1L	0.243	0.036968
SNORA5A	GTF2H2C	0.243	0.036968
SNORA5A	MTBP	0.243	0.036968
SNORA5A	TET2	0.244	0.036145
SNORA5A	MEF2C	0.244	0.036145
SNORA5A	ULK4	0.244	0.036145
SNORA5A	SLC39A9	0.244	0.036145
SNORA5A	UHMK1	0.244	0.036145
SNORA5A	SIKE1	0.244	0.036145
SNORA5A	DST	0.245	0.035338
SNORA5A	APOL6	0.245	0.035338
SNORA5A	ZNF551	0.245	0.035338
SNORA5A	AGO3	0.245	0.035338
SNORA5A	NSL1	0.245	0.035338
SNORA5A	KLRC4	0.245	0.035338
SNORA5A	NUP54	0.245	0.035338
SNORA5A	CREB1	0.245	0.035338
SNORA5A	C5orf42	0.245	0.035338
SNORA5A	ZSCAN20	0.245	0.035338
SNORA5A	CAMSAP2	0.246	0.034546
SNORA5A	SPATA5	0.246	0.034546
SNORA5A	PXT1	0.246	0.034546
SNORA5A	YTHDF3	0.246	0.034546
SNORA5A	ANKRD12	0.246	0.034546

SNORA5A	ZFP1	0.246	0.034546
SNORA5A	RNF213	0.246	0.034546
SNORA5A	ZNF792	0.246	0.034546
SNORA5A	TRPS1	0.247	0.03377
SNORA5A	CPSF2	0.247	0.03377
SNORA5A	ADAT1	0.247	0.03377
SNORA5A	ZGRF1	0.248	0.033008
SNORA5A	AGTPBP1	0.248	0.033008
SNORA5A	AQR	0.248	0.033008
SNORA5A	C8orf37	0.248	0.033008
SNORA5A	PHC3	0.248	0.033008
SNORA5A	CCDC18	0.249	0.032261
SNORA5A	BTAF1	0.249	0.032261
SNORA5A	ZNF749	0.249	0.032261
SNORA5A	ERCC4	0.249	0.032261
SNORA5A	ATP11C	0.249	0.032261
SNORA5A	ZC3H12C	0.249	0.032261
SNORA5A	MAP4K3	0.249	0.032261
SNORA5A	MTHFD2L	0.249	0.032261
SNORA5A	CNOT6L	0.249	0.032261
SNORA5A	UBE2W	0.249	0.032261
SNORA5A	NAA35	0.25	0.031529
SNORA5A	CLDN12	0.25	0.031529
SNORA5A	STAG2	0.25	0.031529
SNORA5A	YAE1D1	0.25	0.031529
SNORA5A	UGGT2	0.25	0.031529
SNORA5A	CRLF3	0.25	0.031529
SNORA5A	ARL5A	0.25	0.031529
SNORA5A	GNA13	0.25	0.031529
SNORA5A	UBR3	0.25	0.031529
SNORA5A	JMJD1C	0.25	0.031529
SNORA5A	SLC25A32	0.251	0.030811
SNORA5A	PRKDC	0.251	0.030811
SNORA5A	ZNF780B	0.251	0.030811
SNORA5A	APC	0.251	0.030811
SNORA5A	GALK2	0.251	0.030811
SNORA5A	ANAPC1	0.252	0.030107
SNORA5A	USP15	0.252	0.030107
SNORA5A	DEPDC7	0.252	0.030107
SNORA5A	AASDH	0.252	0.030107
SNORA5A	CLLU1	0.253	0.029417
SNORA5A	ANKIB1	0.253	0.029417
SNORA5A	SLC30A1	0.253	0.029417
SNORA5A	NUDCD1	0.253	0.029417

SNORA5A	PDZD9	0.253	0.029417
SNORA5A	DDX6	0.253	0.029417
SNORA5A	SLF2	0.254	0.028741
SNORA5A	KMT2C	0.254	0.028741
SNORA5A	PTPRJ	0.254	0.028741
SNORA5A	IPP	0.254	0.028741
SNORA5A	SGTB	0.255	0.028078
SNORA5A	METTL2A	0.255	0.028078
SNORA5A	RANBP2	0.255	0.028078
SNORA5A	MPHOSPH9	0.255	0.028078
SNORA5A	ANKRD46	0.256	0.027428
SNORA5A	ZNF417	0.256	0.027428
SNORA5A	PLEKHA8	0.256	0.027428
SNORA5A	LARP4	0.256	0.027428
SNORA5A	THAP5	0.257	0.026792
SNORA5A	STXBP5	0.257	0.026792
SNORA5A	SMAD5	0.257	0.026792
SNORA5A	ABCA6	0.257	0.026792
SNORA5A	STXBP4	0.257	0.026792
SNORA5A	ZFP37	0.257	0.026792
SNORA5A	ZBTB1	0.257	0.026792
SNORA5A	MTERF1	0.258	0.026168
SNORA5A	CENPL	0.258	0.026168
SNORA5A	AC012309.1	0.258	0.026168
SNORA5A	AGL	0.259	0.025557
SNORA5A	FBXL13	0.259	0.025557
SNORA5A	C1orf74	0.259	0.025557
SNORA5A	DNAJC13	0.26	0.024958
SNORA5A	LYPLA1	0.26	0.024958
SNORA5A	AC093155.3	0.26	0.024958
SNORA5A	ITPR2	0.26	0.024958
SNORA5A	PPP2R3A	0.26	0.024958
SNORA5A	LCOR	0.261	0.024371
SNORA5A	DNAH11	0.261	0.024371
SNORA5A	CEPT1	0.261	0.024371
SNORA5A	ZNF35	0.262	0.023796
SNORA5A	COPB1	0.262	0.023796
SNORA5A	FBXL5	0.262	0.023796
SNORA5A	STX17	0.262	0.023796
SNORA5A	HUS1	0.262	0.023796
SNORA5A	PFKFB2	0.262	0.023796
SNORA5A	CTNNA2	0.262	0.023796
SNORA5A	ZNF484	0.263	0.023233
SNORA5A	MANEA	0.263	0.023233

SNORA5A	MLH3	0.263	0.023233
SNORA5A	TBC1D8B	0.263	0.023233
SNORA5A	ZNF136	0.263	0.023233
SNORA5A	ARHGAP5	0.263	0.023233
SNORA5A	DYNAP	0.263	0.023233
SNORA5A	ZNF701	0.263	0.023233
SNORA5A	DLEU1	0.264	0.022682
SNORA5A	UTP23	0.264	0.022682
SNORA5A	ZDHHC21	0.264	0.022682
SNORA5A	ABHD18	0.264	0.022682
SNORA5A	PHACTR2	0.265	0.022142
SNORA5A	IL21	0.265	0.022142
SNORA5A	KLHL28	0.265	0.022142
SNORA5A	ZNF138	0.265	0.022142
SNORA5A	STARD3NL	0.265	0.022142
SNORA5A	ZNF525	0.265	0.022142
SNORA5A	MPP6	0.265	0.022142
SNORA5A	APPBP2	0.265	0.022142
SNORA5A	PIKFYVE	0.266	0.021613
SNORA5A	ATXN1	0.266	0.021613
SNORA5A	SPTY2D1	0.266	0.021613
SNORA5A	ZNF708	0.266	0.021613
SNORA5A	HELZ	0.266	0.021613
SNORA5A	TMEM154	0.266	0.021613
SNORA5A	ANKRD50	0.266	0.021613
SNORA5A	RAB27B	0.267	0.021096
SNORA5A	BST1	0.267	0.021096
SNORA5A	TBC1D23	0.267	0.021096
SNORA5A	NCOA2	0.267	0.021096
SNORA5A	APO02495.2	0.267	0.021096
SNORA5A	N4BP2	0.267	0.021096
SNORA5A	XPO4	0.267	0.021096
SNORA5A	ANKRD31	0.268	0.020589
SNORA5A	PDS5B	0.268	0.020589
SNORA5A	KLRC4-KLRK1	0.268	0.020589
SNORA5A	ZNF564	0.268	0.020589
SNORA5A	ST7L	0.268	0.020589
SNORA5A	DOPEY1	0.268	0.020589
SNORA5A	KCNS2	0.268	0.020589
SNORA5A	ARHGAP12	0.269	0.020093
SNORA5A	ARHGAP18	0.269	0.020093
SNORA5A	ICE2	0.27	0.019607
SNORA5A	ZNF765	0.27	0.019607
SNORA5A	IP011	0.27	0.019607

SNORA5A	ATP7A	0.271	0.019132
SNORA5A	KRIT1	0.271	0.019132
SNORA5A	RAB19	0.271	0.019132
SNORA5A	AC006978.2	0.272	0.018666
SNORA5A	SLC25A2	0.272	0.018666
SNORA5A	BACH1	0.272	0.018666
SNORA5A	SPG11	0.272	0.018666
SNORA5A	ZNF791	0.272	0.018666
SNORA5A	ZNF736	0.272	0.018666
SNORA5A	CCNT1	0.272	0.018666
SNORA5A	DENND4A	0.272	0.018666
SNORA5A	TRAPPC8	0.273	0.018211
SNORA5A	FAN1	0.273	0.018211
SNORA5A	SFT2D2	0.273	0.018211
SNORA5A	KBTBD8	0.274	0.017765
SNORA5A	WDR7	0.274	0.017765
SNORA5A	TACR3	0.274	0.017765
SNORA5A	LPGAT1	0.275	0.017329
SNORA5A	MDN1	0.275	0.017329
SNORA5A	CD80	0.275	0.017329
SNORA5A	CASP8AP2	0.275	0.017329
SNORA5A	HIST1H1T	0.275	0.017329
SNORA5A	PPP1R15B	0.275	0.017329
SNORA5A	AC022335.1	0.276	0.016903
SNORA5A	RSBN1	0.276	0.016903
SNORA5A	MFSD4B	0.276	0.016903
SNORA5A	LPP	0.276	0.016903
SNORA5A	7-Mar	0.276	0.016903
SNORA5A	KLHL15	0.276	0.016903
SNORA5A	SOWAHB	0.276	0.016903
SNORA5A	TAF1B	0.277	0.016485
SNORA5A	GCC2	0.277	0.016485
SNORA5A	SUCO	0.277	0.016485
SNORA5A	POC1B-GALNT4	0.277	0.016485
SNORA5A	DOCK4	0.278	0.016077
SNORA5A	ZNF627	0.278	0.016077
SNORA5A	TAX1BP1	0.278	0.016077
SNORA5A	REL	0.278	0.016077
SNORA5A	MON2	0.279	0.015678
SNORA5A	IARS	0.279	0.015678
SNORA5A	THAP9	0.279	0.015678
SNORA5A	SPATA1	0.279	0.015678
SNORA5A	RNF133	0.279	0.015678
SNORA5A	TULP4	0.28	0.015287

SNORA5A	TTBK2	0.281	0.014905
SNORA5A	ATAD2B	0.281	0.014905
SNORA5A	CMTR2	0.281	0.014905
SNORA5A	CYP7B1	0.281	0.014905
SNORA5A	ZCCHC6	0.281	0.014905
SNORA5A	PDCL2	0.281	0.014905
SNORA5A	TRAPPC13	0.281	0.014905
SNORA5A	SMCHD1	0.281	0.014905
SNORA5A	TRAPPC11	0.281	0.014905
SNORA5A	SP3	0.282	0.014531
SNORA5A	MFSD8	0.282	0.014531
SNORA5A	ZMYM1	0.282	0.014531
SNORA5A	UEVLD	0.282	0.014531
SNORA5A	OXNAD1	0.282	0.014531
SNORA5A	PPP1R9A	0.283	0.014166
SNORA5A	ZFX	0.283	0.014166
SNORA5A	EXOC5	0.283	0.014166
SNORA5A	ABCA1	0.283	0.014166
SNORA5A	TTC37	0.283	0.014166
SNORA5A	CCDC134	0.284	0.013809
SNORA5A	TBC1D32	0.284	0.013809
SNORA5A	MPP5	0.284	0.013809
SNORA5A	KHDRBS2	0.284	0.013809
SNORA5A	7-Sep	0.285	0.01346
SNORA5A	BARD1	0.285	0.01346
SNORA5A	MIB1	0.285	0.01346
SNORA5A	KIAA1429	0.285	0.01346
SNORA5A	RP1	0.286	0.013118
SNORA5A	MSH3	0.286	0.013118
SNORA5A	KDM7A	0.286	0.013118
SNORA5A	ZNF823	0.287	0.012784
SNORA5A	REV3L	0.287	0.012784
SNORA5A	CASTOR2	0.287	0.012784
SNORA5A	CCDC36	0.287	0.012784
SNORA5A	TAOK1	0.287	0.012784
SNORA5A	TOR1AIP2	0.287	0.012784
SNORA5A	RB1CC1	0.287	0.012784
SNORA5A	RPA4	0.289	0.01214
SNORA5A	TLR4	0.289	0.01214
SNORA5A	GMFB	0.289	0.01214
SNORA5A	TMPPE	0.289	0.01214
SNORA5A	ZNRF2	0.289	0.01214
SNORA5A	INTS6	0.289	0.01214
SNORA5A	FAM151B	0.289	0.01214

SNORA5A	KIAA0895	0.29	0.011828
SNORA5A	G3BP2	0.29	0.011828
SNORA5A	ANKRD7	0.29	0.011828
SNORA5A	GPR34	0.29	0.011828
SNORA5A	DOCK10	0.291	0.011524
SNORA5A	SLC35F5	0.291	0.011524
SNORA5A	ZBTB37	0.291	0.011524
SNORA5A	MTMR8	0.292	0.011226
SNORA5A	RPAP2	0.292	0.011226
SNORA5A	SLC01B7	0.293	0.010936
SNORA5A	FAM208B	0.293	0.010936
SNORA5A	USP24	0.293	0.010936
SNORA5A	MED13	0.293	0.010936
SNORA5A	LIN54	0.293	0.010936
SNORA5A	SYDE2	0.293	0.010936
SNORA5A	ZNF625	0.294	0.010652
SNORA5A	CCDC117	0.294	0.010652
SNORA5A	B3GALNT2	0.295	0.010374
SNORA5A	FAM196B	0.295	0.010374
SNORA5A	QSER1	0.295	0.010374
SNORA5A	UBE4A	0.296	0.010103
SNORA5A	ZNF121	0.296	0.010103
SNORA5A	RNF169	0.296	0.010103
SNORA5A	KRBA2	0.296	0.010103
SNORA5A	ANKMY2	0.297	0.009839
SNORA5A	FAM126A	0.297	0.009839
SNORA5A	C16orf72	0.297	0.009839
SNORA5A	ITGA4	0.297	0.009839
SNORA5A	ZNF770	0.298	0.00958
SNORA5A	HELQ	0.298	0.00958
SNORA5A	NPAT	0.298	0.00958
SNORA5A	HIST1H2BD	0.298	0.00958
SNORA5A	FAM135A	0.299	0.009328
SNORA5A	RAB3GAP2	0.299	0.009328
SNORA5A	FBXO28	0.299	0.009328
SNORA5A	CUL5	0.3	0.009082
SNORA5A	UBR2	0.3	0.009082
SNORA5A	ZNF92	0.301	0.008841
SNORA5A	ZNF510	0.301	0.008841
SNORA5A	TTC39B	0.301	0.008841
SNORA5A	ERBIN	0.301	0.008841
SNORA5A	TANGO6	0.301	0.008841
SNORA5A	ZNF717	0.302	0.008606
SNORA5A	TFEC	0.302	0.008606

SNORA5A	TLR1	0.302	0.008606
SNORA5A	DDX60	0.303	0.008377
SNORA5A	GPR82	0.303	0.008377
SNORA5A	INTS2	0.304	0.008153
SNORA5A	PRMT3	0.304	0.008153
SNORA5A	ZNF555	0.304	0.008153
SNORA5A	CEP295NL	0.304	0.008153
SNORA5A	NUPL2	0.304	0.008153
SNORA5A	PARP8	0.304	0.008153
SNORA5A	MIER1	0.304	0.008153
SNORA5A	FAM19A2	0.305	0.007935
SNORA5A	ZNF727	0.305	0.007935
SNORA5A	AP003108.2	0.305	0.007935
SNORA5A	VPS41	0.306	0.007722
SNORA5A	ARFGEF2	0.307	0.007514
SNORA5A	RASA2	0.309	0.007113
SNORA5A	UBR5	0.31	0.00692
SNORA5A	ZNF518A	0.31	0.00692
SNORA5A	ATRX	0.31	0.00692
SNORA5A	KIAA1109	0.311	0.006731
SNORA5A	CEP295	0.311	0.006731
SNORA5A	SPRED1	0.311	0.006731
SNORA5A	NBAS	0.311	0.006731
SNORA5A	TRIP11	0.311	0.006731
SNORA5A	MAN1A2	0.312	0.006547
SNORA5A	FBXL4	0.312	0.006547
SNORA5A	USP38	0.312	0.006547
SNORA5A	EPS15	0.312	0.006547
SNORA5A	RAPGEF5	0.312	0.006547
SNORA5A	SMG8	0.313	0.006368
SNORA5A	ITCH	0.313	0.006368
SNORA5A	KPNA5	0.314	0.006193
SNORA5A	CTDSPL2	0.314	0.006193
SNORA5A	UBR1	0.314	0.006193
SNORA5A	USP33	0.314	0.006193
SNORA5A	EDEM3	0.315	0.006023
SNORA5A	RIC1	0.315	0.006023
SNORA5A	PMS2	0.315	0.006023
SNORA5A	GAPVD1	0.315	0.006023
SNORA5A	TNPO1	0.316	0.005856
SNORA5A	UBA6	0.316	0.005856
SNORA5A	PAPOLB	0.316	0.005856
SNORA5A	MACF1	0.317	0.005694
SNORA5A	SLC9C1	0.317	0.005694

SNORA5A	CFAP54	0.317	0.005694
SNORA5A	GPR88	0.318	0.005536
SNORA5A	FANCM	0.318	0.005536
SNORA5A	DGAT2L6	0.318	0.005536
SNORA5A	FBXW7	0.318	0.005536
SNORA5A	SLC25A46	0.319	0.005382
SNORA5A	CENPC	0.319	0.005382
SNORA5A	VCPIP1	0.319	0.005382
SNORA5A	WDR36	0.319	0.005382
SNORA5A	HIST1H3H	0.319	0.005382
SNORA5A	ZNF852	0.32	0.005232
SNORA5A	ZBTB38	0.32	0.005232
SNORA5A	CSNK1G3	0.32	0.005232
SNORA5A	DYNC2H1	0.32	0.005232
SNORA5A	CLDN20	0.321	0.005085
SNORA5A	ZNF669	0.321	0.005085
SNORA5A	ZNF680	0.322	0.004942
SNORA5A	ZNF644	0.322	0.004942
SNORA5A	JAK2	0.322	0.004942
SNORA5A	MTMR6	0.323	0.004803
SNORA5A	CHD1	0.323	0.004803
SNORA5A	BLID	0.323	0.004803
SNORA5A	MATR3	0.324	0.004668
SNORA5A	HSPA4L	0.324	0.004668
SNORA5A	CCDC83	0.324	0.004668
SNORA5A	PIK3CG	0.324	0.004668
SNORA5A	PRDM5	0.325	0.004536
SNORA5A	SWT1	0.325	0.004536
SNORA5A	ELF2	0.325	0.004536
SNORA5A	CPSF4L	0.325	0.004536
SNORA5A	TMEM106B	0.326	0.004407
SNORA5A	C3orf38	0.326	0.004407
SNORA5A	ZNF678	0.326	0.004407
SNORA5A	PARD6B	0.326	0.004407
SNORA5A	SULT1C3	0.327	0.004282
SNORA5A	HIST1H2BA	0.328	0.00416
SNORA5A	ZNF800	0.328	0.00416
SNORA5A	VPS13A	0.329	0.004041
SNORA5A	RIMS1	0.329	0.004041
SNORA5A	CA1	0.33	0.003925
SNORA5A	HDAC9	0.33	0.003925
SNORA5A	CDK13	0.33	0.003925
SNORA5A	ZNF106	0.33	0.003925
SNORA5A	TOGARAM1	0.33	0.003925

SNORA5A	PKD2L2	0.33	0.003925
SNORA5A	GPATCH2	0.33	0.003925
SNORA5A	MYO9A	0.331	0.003812
SNORA5A	RBM12B	0.331	0.003812
SNORA5A	MAN2A1	0.332	0.003702
SNORA5A	NBN	0.333	0.003595
SNORA5A	DGKE	0.334	0.003491
SNORA5A	USP45	0.334	0.003491
SNORA5A	CYP4A11	0.334	0.003491
SNORA5A	CFAP97	0.334	0.003491
SNORA5A	MLANA	0.335	0.00339
SNORA5A	HIST1H1C	0.335	0.00339
SNORA5A	PRKD3	0.335	0.00339
SNORA5A	AHR	0.335	0.00339
SNORA5A	VPS50	0.336	0.003291
SNORA5A	PTPN4	0.337	0.003195
SNORA5A	SLFN12L	0.337	0.003195
SNORA5A	BAZ2B	0.339	0.00301
SNORA5A	WASHC4	0.339	0.00301
SNORA5A	TMF1	0.339	0.00301
SNORA5A	FNIP1	0.34	0.002922
SNORA5A	STAG1	0.34	0.002922
SNORA5A	KBTBD2	0.34	0.002922
SNORA5A	NEK7	0.34	0.002922
SNORA5A	DCP2	0.341	0.002835
SNORA5A	ZNF283	0.341	0.002835
SNORA5A	ZNF407	0.341	0.002835
SNORA5A	RANBP6	0.341	0.002835
SNORA5A	CEP85L	0.342	0.002752
SNORA5A	RELL1	0.342	0.002752
SNORA5A	PIK3C2A	0.343	0.00267
SNORA5A	GSTCD	0.343	0.00267
SNORA5A	SYNE1	0.343	0.00267
SNORA5A	AVL9	0.343	0.00267
SNORA5A	SLC10A1	0.345	0.002513
SNORA5A	SHQ1	0.345	0.002513
SNORA5A	DPY19L4	0.345	0.002513
SNORA5A	ALG11	0.346	0.002438
SNORA5A	MAB21L1	0.347	0.002365
SNORA5A	TRPM7	0.347	0.002365
SNORA5A	ZNF543	0.347	0.002365
SNORA5A	ZNF562	0.347	0.002365
SNORA5A	EBLN2	0.348	0.002294
SNORA5A	ZNF426	0.349	0.002225

SNORA5A	ATP6V0A2	0.349	0.002225
SNORA5A	HCFC2	0.349	0.002225
SNORA5A	IKZF2	0.349	0.002225
SNORA5A	ATL3	0.349	0.002225
SNORA5A	KLHL7	0.35	0.002158
SNORA5A	ZFYVE16	0.35	0.002158
SNORA5A	USP37	0.35	0.002158
SNORA5A	DENND4C	0.351	0.002093
SNORA5A	EXPH5	0.351	0.002093
SNORA5A	MACC1	0.352	0.002029
SNORA5A	HEATR1	0.352	0.002029
SNORA5A	RLIM	0.352	0.002029
SNORA5A	TIGD4	0.353	0.001967
SNORA5A	ZNF148	0.353	0.001967
SNORA5A	MAP3K1	0.354	0.001907
SNORA5A	ZNF292	0.354	0.001907
SNORA5A	PUS7L	0.354	0.001907
SNORA5A	AC134669.2	0.354	0.001907
SNORA5A	PPP4R2	0.354	0.001907
SNORA5A	FER	0.355	0.001849
SNORA5A	BRCA2	0.356	0.001792
SNORA5A	PCNX1	0.356	0.001792
SNORA5A	ZBTB6	0.356	0.001792
SNORA5A	CCDC126	0.356	0.001792
SNORA5A	GTPBP10	0.356	0.001792
SNORA5A	GPATCH2L	0.357	0.001737
SNORA5A	SMIM18	0.358	0.001684
SNORA5A	ISPD	0.358	0.001684
SNORA5A	PATE4	0.358	0.001684
SNORA5A	FAT4	0.358	0.001684
SNORA5A	HOMER1	0.359	0.001632
SNORA5A	SLC5A3	0.36	0.001581
SNORA5A	CLASP2	0.36	0.001581
SNORA5A	ZNF441	0.361	0.001532
SNORA5A	NOTCH2NL	0.362	0.001485
SNORA5A	AL161911.1	0.362	0.001485
SNORA5A	TWISTNB	0.363	0.001438
SNORA5A	REST	0.363	0.001438
SNORA5A	LRBA	0.364	0.001393
SNORA5A	ZNF91	0.365	0.00135
SNORA5A	TNRC6B	0.365	0.00135
SNORA5A	SOCS4	0.366	0.001307
SNORA5A	SPINT4	0.366	0.001307
SNORA5A	FAM160A1	0.366	0.001307

SNORA5A	ZNF221	0.366	0.001307
SNORA5A	POLK	0.367	0.001266
SNORA5A	USP34	0.367	0.001266
SNORA5A	DMXL2	0.37	0.00115
SNORA5A	UHRF1BP1L	0.371	0.001113
SNORA5A	C6orf10	0.371	0.001113
SNORA5A	PURB	0.372	0.001078
SNORA5A	VMA21	0.372	0.001078
SNORA5A	RLF	0.372	0.001078
SNORA5A	FNDC9	0.372	0.001078
SNORA5A	ZNF12	0.373	0.001043
SNORA5A	OXR1	0.374	0.00101
SNORA5A	SLC30A7	0.374	0.00101
SNORA5A	ZNF141	0.375	0.000978
SNORA5A	DGKH	0.375	0.000978
SNORA5A	LIN7C	0.376	0.000946
SNORA5A	IMPG2	0.376	0.000946
SNORA5A	EVI5	0.378	0.000886
SNORA5A	HIST2H3C	0.378	0.000886
SNORA5A	SETX	0.378	0.000886
SNORA5A	HERC1	0.379	0.000857
SNORA5A	PPIP5K2	0.379	0.000857
SNORA5A	RC3H1	0.379	0.000857
SNORA5A	RIF1	0.379	0.000857
SNORA5A	ZNF808	0.38	0.000829
SNORA5A	PLEKHM3	0.38	0.000829
SNORA5A	SMARCA1	0.381	0.000802
SNORA5A	MYCBP2	0.381	0.000802
SNORA5A	ZC3H6	0.381	0.000802
SNORA5A	MFAP3	0.381	0.000802
SNORA5A	BBS9	0.381	0.000802
SNORA5A	ASCC3	0.382	0.000776
SNORA5A	C12orf40	0.382	0.000776
SNORA5A	SCLT1	0.382	0.000776
SNORA5A	SLC30A4	0.382	0.000776
SNORA5A	MGA	0.384	0.000726
SNORA5A	METTL25	0.385	0.000702
SNORA5A	ATR	0.386	0.000679
SNORA5A	SLC4A7	0.387	0.000657
SNORA5A	PTAR1	0.387	0.000657
SNORA5A	FOXN2	0.387	0.000657
SNORA5A	CEP192	0.388	0.000635
SNORA5A	MAP3K2	0.388	0.000635
SNORA5A	WDFY3	0.389	0.000614

SNORA5A	SCRG1	0.389	0.000614
SNORA5A	ZNF267	0.39	0.000594
SNORA5A	ZYG11B	0.39	0.000594
SNORA5A	ZNF845	0.391	0.000574
SNORA5A	KIF27	0.392	0.000555
SNORA5A	C3orf49	0.392	0.000555
SNORA5A	FAM208A	0.393	0.000536
SNORA5A	SRFBP1	0.394	0.000518
SNORA5A	AKAP9	0.396	0.000484
SNORA5A	GNL3L	0.397	0.000468
SNORA5A	ZNF81	0.397	0.000468
SNORA5A	SLC8A1	0.399	0.000436
SNORA5A	BDP1	0.399	0.000436
SNORA5A	CHD9	0.401	0.000407
SNORA5A	HIST2H3D	0.401	0.000407
SNORA5A	BMP2K	0.401	0.000407
SNORA5A	SLC2A13	0.401	0.000407
SNORA5A	HIST1H4K	0.401	0.000407
SNORA5A	AWAT1	0.403	0.00038
SNORA5A	LYST	0.403	0.00038
SNORA5A	HIST1H1A	0.405	0.000354
SNORA5A	GCNT7	0.406	0.000342
SNORA5A	LDHAL6B	0.407	0.00033
SNORA5A	SP4	0.407	0.00033
SNORA5A	DNAJB14	0.409	0.000308
SNORA5A	ATP8B4	0.409	0.000308
SNORA5A	BRWD1	0.41	0.000297
SNORA5A	SUMO4	0.412	0.000277
SNORA5A	FBXO40	0.412	0.000277
SNORA5A	MKLN1	0.414	0.000258
SNORA5A	OSBPL8	0.414	0.000258
SNORA5A	FGL2	0.415	0.000248
SNORA5A	HIST1H2AL	0.415	0.000248
SNORA5A	ZNF573	0.416	0.00024
SNORA5A	HIST1H3J	0.416	0.00024
SNORA5A	FRYL	0.416	0.00024
SNORA5A	KIAA0825	0.417	0.000231
SNORA5A	IL5	0.418	0.000223
SNORA5A	ZNF724	0.418	0.000223
SNORA5A	NAIP	0.419	0.000215
SNORA5A	AL449266.1	0.42	0.000208
SNORA5A	HIST1H2AH	0.422	0.000193
SNORA5A	MIOS	0.423	0.000186
SNORA5A	DENND1B	0.425	0.000173

SNORA5A	XRN1	0.426	0.000167
SNORA5A	ATP5L2	0.427	0.000161
SNORA5A	IFIT1B	0.431	0.000139
SNORA5A	ERVW-1	0.431	0.000139
SNORA5A	HIST1H3C	0.432	0.000134
SNORA5A	BTBD8	0.433	0.000129
SNORA5A	CDKL4	0.434	0.000124
SNORA5A	CRYBG3	0.435	0.000119
SNORA5A	HIPK3	0.436	0.000115
SNORA5A	MORC3	0.437	0.000111
SNORA5A	NRIP1	0.439	0.000103
SNORA5A	HIST1H2BL	0.439	0.000103
SNORA5A	HIST1H4L	0.439	0.000103
SNORA5A	LINC00238	0.44	9.90E-05
SNORA5A	ZNF410	0.441	9.53E-05
SNORA5A	CHRNA	0.441	9.53E-05
SNORA5A	VPS13B	0.442	9.17E-05
SNORA5A	ACSM6	0.447	7.58E-05
SNORA5A	HIST1H2AI	0.449	7.02E-05
SNORA5A	VPS13C	0.449	7.02E-05
SNORA5A	HIST1H3I	0.45	6.75E-05
SNORA5A	ZBTB41	0.45	6.75E-05
SNORA5A	HIST1H2AE	0.451	6.50E-05
SNORA5A	HIST1H2BN	0.453	6.01E-05
SNORA5A	TTN	0.454	5.78E-05
SNORA5A	HIST1H4F	0.454	5.78E-05
SNORA5A	UTP20	0.457	5.14E-05
SNORA5A	WDPCP	0.458	4.94E-05
SNORA5A	DNAH14	0.459	4.75E-05
SNORA5A	DMXL1	0.46	4.57E-05
SNORA5A	HIST1H2AG	0.464	3.90E-05
SNORA5A	TAS2R31	0.465	3.75E-05
SNORA5A	ANKAR	0.465	3.75E-05
SNORA5A	TAS2R43	0.466	3.60E-05
SNORA5A	LNPEP	0.469	3.19E-05
SNORA5A	HIST1H2BB	0.469	3.19E-05
SNORA5A	HIST2H2BF	0.469	3.19E-05
SNORA5A	HIST1H3G	0.473	2.72E-05
SNORA5A	HIST1H2BC	0.474	2.61E-05
SNORA5A	CEP350	0.477	2.31E-05
SNORA5A	HIST1H2B0	0.477	2.31E-05
SNORA5A	GDAP2	0.477	2.31E-05
SNORA5A	TCP11L2	0.478	2.22E-05
SNORA5A	HIST1H2BE	0.478	2.22E-05

SNORA5A	AL138752. 2	0. 48	2. 04E-05
SNORA5A	HIST1H3F	0. 48	2. 04E-05
SNORA5A	HIST1H2AJ	0. 481	1. 96E-05
SNORA5A	HIST1H2BJ	0. 483	1. 81E-05
SNORA5A	HIST1H2AB	0. 484	1. 73E-05
SNORA5A	C4orf45	0. 484	1. 73E-05
SNORA5A	HIST1H4J	0. 485	1. 66E-05
SNORA5A	HIST1H3A	0. 486	1. 60E-05
SNORA5A	HIST1H1B	0. 487	1. 53E-05
SNORA5A	RBM15	0. 488	1. 47E-05
SNORA5A	LTN1	0. 489	1. 41E-05
SNORA5A	HIST1H2AD	0. 491	1. 30E-05
SNORA5A	ZNF451	0. 494	1. 14E-05
SNORA5A	SHPRH	0. 494	1. 14E-05
SNORA5A	CRYBA1	0. 495	1. 09E-05
SNORA5A	HIST1H3D	0. 496	1. 05E-05
SNORA5A	AC092835. 1	0. 497	1. 01E-05
SNORA5A	ATM	0. 497	1. 01E-05
SNORA5A	HIST1H2AM	0. 499	9. 24E-06
SNORA5A	POMK	0. 502	8. 13E-06
SNORA5A	NBEAL1	0. 502	8. 13E-06
SNORA5A	GK3P	0. 503	7. 79E-06
SNORA5A	HIST1H2BH	0. 505	7. 14E-06
SNORA5A	ABRA	0. 506	6. 84E-06
SNORA5A	HIST1H4D	0. 507	6. 55E-06
SNORA5A	ANKRD36C	0. 508	6. 28E-06
SNORA5A	AC013394. 1	0. 51	5. 75E-06
SNORA5A	FAM217A	0. 512	5. 27E-06
SNORA5A	ZNF483	0. 512	5. 27E-06
SNORA5A	GNRHR	0. 513	5. 05E-06
SNORA5A	HIST4H4	0. 514	4. 83E-06
SNORA5A	APLF	0. 515	4. 63E-06
SNORA5A	HIST1H2BG	0. 516	4. 43E-06
SNORA5A	ZNF699	0. 516	4. 43E-06
SNORA5A	ANKRD36B	0. 517	4. 24E-06
SNORA5A	ZNF557	0. 517	4. 24E-06
SNORA5A	HIST1H3B	0. 519	3. 88E-06
SNORA5A	HIST1H2BF	0. 521	3. 55E-06
SNORA5A	AC087632. 1	0. 521	3. 55E-06
SNORA5A	HIST1H4A	0. 521	3. 55E-06
SNORA5A	ANKRD36	0. 529	2. 48E-06
SNORA5A	TAS2R19	0. 53	2. 37E-06
SNORA5A	C9orf131	0. 531	2. 27E-06
SNORA5A	CCSER1	0. 532	2. 17E-06

SNORA5A	LRRTM2	0.533	2.07E-06
SNORA5A	HIST1H2BI	0.536	1.81E-06
SNORA5A	ADAM20	0.536	1.81E-06
SNORA5A	IFNK	0.547	1.09E-06
SNORA5A	HIST2H2AB	0.55	9.48E-07
SNORA5A	HIST1H2BM	0.551	9.05E-07
SNORA5A	HIST1H4H	0.551	9.05E-07
SNORA5A	BIRC6	0.555	7.50E-07
SNORA5A	TAS2R3	0.569	3.85E-07
SNORA5A	ERCC6L2	0.572	3.33E-07
SNORA5A	TAS2R46	0.575	2.88E-07
SNORA5A	ZNF490	0.576	2.74E-07
SNORA5A	PBOV1	0.578	2.48E-07
SNORA5A	ZBED6	0.579	2.36E-07
SNORA5A	HIST1H1E	0.581	2.14E-07
SNORA5A	C10orf113	0.584	1.85E-07
SNORA5A	HIST1H1D	0.585	1.76E-07
SNORA5A	HIST1H4B	0.594	1.12E-07
SNORA5A	SNX13	0.596	1.01E-07
SNORA5A	CCDC7	0.598	9.17E-08
SNORA5A	HIST2H2AC	0.598	9.17E-08
SNORA5A	TROVE2	0.606	6.10E-08
SNORA5A	ZNF805	0.608	5.51E-08
SNORA5A	KCNJ13	0.611	4.72E-08
SNORA5A	BTBD18	0.614	4.04E-08
SNORA5A	KLHL11	0.633	1.48E-08
SNORA5A	MAB21L2	0.636	1.26E-08
SNORA5A	ZNF124	0.64	1.02E-08
SNORA5A	ZBTB20	0.64	1.02E-08
SNORA5A	PRSS48	0.641	9.65E-09
SNORA5A	TAS2R50	0.642	9.14E-09
SNORA5A	GPR52	0.653	5.01E-09
SNORA5A	TAS2R30	0.655	4.48E-09
SNORA5A	HIST1H4E	0.66	3.40E-09
SNORA5A	HIST1H4C	0.669	2.05E-09
SNORA5A	GPR22	0.67	1.94E-09
SNORA5A	TAS2R13	0.675	1.46E-09
SNORA5A	ZNF460	0.709	2.01E-10
SNORA5A	POU5F2	0.738	3.44E-11
SNORA5A	SNORA5A	1	1.72E-19
SNORA70	PDE6A	0.2	0.000303
SNORA70	CALR	0.201	0.000282
SNORA70	PATZ1	0.202	0.000262
SNORA70	XPOT	0.203	0.000244

SNORA70	CABP4	0.203	0.000244
SNORA70	ZNF689	0.203	0.000244
SNORA70	RRP36	0.204	0.000227
SNORA70	C6orf223	0.204	0.000227
SNORA70	OAZ2	0.204	0.000227
SNORA70	NME1-NME2	0.205	0.000211
SNORA70	FKBP10	0.206	0.000197
SNORA70	TMED2	0.206	0.000197
SNORA70	TM2D3	0.206	0.000197
SNORA70	ALX3	0.206	0.000197
SNORA70	EXT2	0.206	0.000197
SNORA70	CTBS	0.207	0.000183
SNORA70	SUV39H2	0.207	0.000183
SNORA70	PTPN20	0.207	0.000183
SNORA70	YIPF4	0.207	0.000183
SNORA70	ARFIP2	0.207	0.000183
SNORA70	PPIL1	0.207	0.000183
SNORA70	IFITM1	0.207	0.000183
SNORA70	ICE2	0.208	0.00017
SNORA70	HSP90B1	0.208	0.00017
SNORA70	C16orf58	0.208	0.00017
SNORA70	MCFD2	0.209	0.000158
SNORA70	MRS2	0.21	0.000146
SNORA70	AL161911.1	0.21	0.000146
SNORA70	ADPGK	0.211	0.000136
SNORA70	MESP1	0.211	0.000136
SNORA70	BPIFA2	0.211	0.000136
SNORA70	IDH3A	0.211	0.000136
SNORA70	CTSF	0.211	0.000136
SNORA70	TXNDC12	0.211	0.000136
SNORA70	PREB	0.212	0.000126
SNORA70	BSCL2	0.212	0.000126
SNORA70	NT5DC2	0.212	0.000126
SNORA70	MANF	0.214	0.000109
SNORA70	F7	0.214	0.000109
SNORA70	PARS2	0.214	0.000109
SNORA70	GRSF1	0.216	9.33E-05
SNORA70	ACRBP	0.217	8.64E-05
SNORA70	C2orf16	0.217	8.64E-05
SNORA70	SEC11A	0.218	8.01E-05
SNORA70	PRRT1	0.218	8.01E-05
SNORA70	KCNQ1	0.218	8.01E-05
SNORA70	TXNDC5	0.218	8.01E-05
SNORA70	SHMT2	0.218	8.01E-05

SNORA70	PEX6	0.221	6.35E-05
SNORA70	FBX08	0.223	5.43E-05
SNORA70	C12orf29	0.223	5.43E-05
SNORA70	RPN2	0.223	5.43E-05
SNORA70	ASCL2	0.224	5.02E-05
SNORA70	MAZ	0.226	4.29E-05
SNORA70	RCCD1	0.227	3.96E-05
SNORA70	TMEM263	0.228	3.66E-05
SNORA70	POLR2J2	0.229	3.37E-05
SNORA70	APH1B	0.229	3.37E-05
SNORA70	BHMGI	0.229	3.37E-05
SNORA70	TCTN3	0.23	3.11E-05
SNORA70	SLC2A14	0.231	2.87E-05
SNORA70	UBE2Q2	0.231	2.87E-05
SNORA70	LARGE2	0.231	2.87E-05
SNORA70	C4BPA	0.232	2.65E-05
SNORA70	PIGT	0.234	2.25E-05
SNORA70	TM7SF2	0.234	2.25E-05
SNORA70	ERGIC3	0.235	2.07E-05
SNORA70	MMP17	0.235	2.07E-05
SNORA70	TMEM176A	0.237	1.76E-05
SNORA70	ANAPC5	0.238	1.62E-05
SNORA70	PDIA3	0.238	1.62E-05
SNORA70	CMTM2	0.239	1.49E-05
SNORA70	PGM3	0.239	1.49E-05
SNORA70	ERP29	0.24	1.37E-05
SNORA70	PYG01	0.241	1.26E-05
SNORA70	TNFRSF18	0.241	1.26E-05
SNORA70	GJB7	0.242	1.16E-05
SNORA70	ZNF771	0.242	1.16E-05
SNORA70	UBE2J1	0.243	1.06E-05
SNORA70	FAM107B	0.244	9.75E-06
SNORA70	SNCAIP	0.244	9.75E-06
SNORA70	CRELD1	0.245	8.95E-06
SNORA70	FBX022	0.245	8.95E-06
SNORA70	FBN3	0.247	7.54E-06
SNORA70	TBX6	0.247	7.54E-06
SNORA70	FAM136A	0.247	7.54E-06
SNORA70	MOGS	0.247	7.54E-06
SNORA70	RWDD2A	0.248	6.91E-06
SNORA70	MT1H	0.25	5.81E-06
SNORA70	CXCR2	0.251	5.33E-06
SNORA70	P3H3	0.253	4.47E-06
SNORA70	POGLUT1	0.253	4.47E-06

SNORA70	FCGR3B	0.261	2.18E-06
SNORA70	RCN2	0.262	1.99E-06
SNORA70	FMO1	0.263	1.82E-06
SNORA70	RNF215	0.264	1.66E-06
SNORA70	RBP3	0.265	1.52E-06
SNORA70	APC2	0.266	1.38E-06
SNORA70	RARS2	0.267	1.26E-06
SNORA70	TGIF2- C20orf24	0.268	1.15E-06
SNORA70	EPCAM	0.268	1.15E-06
SNORA70	TMED4	0.272	7.89E-07
SNORA70	TMEM106C	0.273	7.18E-07
SNORA70	PRR19	0.275	5.94E-07
SNORA70	SIAE	0.276	5.40E-07
SNORA70	PRDX4	0.283	2.74E-07
SNORA70	KLK11	0.288	1.67E-07
SNORA70	TMEM59L	0.29	1.37E-07
SNORA70	NLRP6	0.29	1.37E-07
SNORA70	CRLF1	0.293	1.01E-07
SNORA70	MT1G	0.293	1.01E-07
SNORA70	CERCAM	0.295	8.27E-08
SNORA70	TMEM132A	0.297	6.74E-08
SNORA70	RPL7L1	0.297	6.74E-08
SNORA70	AC007998.2	0.305	2.94E-08
SNORA70	PPP1R3F	0.307	2.38E-08
SNORA70	CXCR1	0.307	2.38E-08
SNORA70	CHID1	0.308	2.14E-08
SNORA70	SDF4	0.312	1.39E-08
SNORA70	DDOST	0.313	1.25E-08
SNORA70	CNPY3	0.319	6.52E-09
SNORA70	PITX2	0.319	6.52E-09
SNORA70	LRRC26	0.323	4.19E-09
SNORA70	COX18	0.328	2.39E-09
SNORA70	TCTN1	0.33	1.91E-09
SNORA70	TCN2	0.338	7.62E-10
SNORA70	NIPSNAP1	0.34	6.04E-10
SNORA70	TMED3	0.351	1.64E-10
SNORA70	PROK2	0.357	7.92E-11
SNORA70	VMO1	0.366	2.60E-11
SNORA70	FAM46A	0.369	1.78E-11
SNORA70	BSG	0.372	1.22E-11
SNORA70	CCDC36	0.378	5.63E-12
SNORA70	LHX8	0.397	4.54E-13
SNORA70	ATRAID	0.406	1.32E-13

SNORA70	LCN12	0.407	1.15E-13
SNORA70	SRMS	0.412	5.72E-14
SNORA70	AATK-AS1	0.444	5.35E-16
SNORA70	AC005020.2	0.444	5.35E-16
SNORA70	CD320	0.451	1.84E-16
SNORA70	TMEM225B	0.466	1.77E-17
SNORA70	KLK14	0.469	1.10E-17
SNORA70	CEP44	0.491	3.01E-19
SNORA70	PPIB	0.5	6.61E-20
SNORA70	KLK13	0.507	1.99E-20
SNORA70	C8B	0.509	1.41E-20
SNORA70	UBL4B	0.51	1.19E-20
SNORA70	KLK12	0.519	2.46E-21
SNORA70	RFK	0.527	5.93E-22
SNORA70	PDIA6	0.553	5.03E-24
SNORA70	MYDGF	0.557	2.37E-24
SNORA70	HBG2	0.603	2.76E-28
SNORA70	SIX2	0.663	7.02E-34
SNORA70	DPPA5	0.697	2.77E-37
SNORA70	ARID3C	0.718	1.80E-39
SNORA70	MST1	0.784	9.19E-47
SNORA70	IFITM5	0.88	1.65E-58
SNORA70	KIR3DX1	0.897	9.93E-61
SNORA70	SNORA70	1	4.33E-75
SNORD104	BMP2	-0.382	0.001734
SNORD104	PIK3CA	-0.371	0.002326
SNORD104	ACTR2	-0.365	0.002723
SNORD104	OTUD4	-0.364	0.002795
SNORD104	MORC3	-0.361	0.003021
SNORD104	CTTNBP2NL	-0.359	0.003181
SNORD104	LUZP1	-0.354	0.003615
SNORD104	SCAF8	-0.344	0.004648
SNORD104	SON	-0.339	0.005258
SNORD104	ELF1	-0.338	0.005389
SNORD104	NEK1	-0.335	0.005798
SNORD104	JAK1	-0.333	0.006086
SNORD104	REST	-0.332	0.006235
SNORD104	NPAT	-0.331	0.006387
SNORD104	MYCBP2	-0.328	0.006864
SNORD104	LRCH1	-0.328	0.006864
SNORD104	WDFY1	-0.328	0.006864
SNORD104	SERINC1	-0.328	0.006864
SNORD104	ANO6	-0.327	0.00703
SNORD104	CDC40	-0.326	0.0072

SNORD104	C16orf72	-0.322	0.007915
SNORD104	AKAP11	-0.321	0.008103
SNORD104	APC	-0.321	0.008103
SNORD104	MINDY2	-0.32	0.008296
SNORD104	BCLAF1	-0.319	0.008492
SNORD104	TRIP12	-0.317	0.008898
SNORD104	BACH1	-0.317	0.008898
SNORD104	BOD1L1	-0.314	0.009539
SNORD104	GAB1	-0.314	0.009539
SNORD104	DNAJC13	-0.313	0.009761
SNORD104	SETX	-0.31	0.010457
SNORD104	DDX6	-0.31	0.010457
SNORD104	ATP10D	-0.308	0.010945
SNORD104	MFAP3	-0.308	0.010945
SNORD104	SMARCA5	-0.307	0.011197
SNORD104	FRYL	-0.307	0.011197
SNORD104	TMEM184C	-0.306	0.011453
SNORD104	METTL14	-0.306	0.011453
SNORD104	OSBPL8	-0.306	0.011453
SNORD104	ZNF436	-0.305	0.011715
SNORD104	ATXN1	-0.302	0.012533
SNORD104	HIVEP2	-0.302	0.012533
SNORD104	HIPK1	-0.301	0.012817
SNORD104	UBE4A	-0.3	0.013106
SNORD104	SLC12A6	-0.299	0.013401
SNORD104	GTF2A1	-0.299	0.013401
SNORD104	ZC3H13	-0.299	0.013401
SNORD104	LATS1	-0.297	0.014009
SNORD104	LTN1	-0.296	0.014322
SNORD104	PTPN14	-0.296	0.014322
SNORD104	TRAPPC10	-0.294	0.014966
SNORD104	SLMAP	-0.294	0.014966
SNORD104	TBC1D5	-0.293	0.015298
SNORD104	NIN	-0.293	0.015298
SNORD104	USP34	-0.293	0.015298
SNORD104	AGPS	-0.293	0.015298
SNORD104	SH3D19	-0.293	0.015298
SNORD104	HECA	-0.292	0.015636
SNORD104	ZNF106	-0.292	0.015636
SNORD104	RIC1	-0.291	0.015981
SNORD104	ZNF845	-0.291	0.015981
SNORD104	STK4	-0.289	0.01669
SNORD104	CSGALNACT2	-0.289	0.01669
SNORD104	ZNF770	-0.288	0.017055

SNORD104	G3BP2	-0.288	0.017055
SNORD104	IFNAR1	-0.288	0.017055
SNORD104	FER	-0.288	0.017055
SNORD104	ARHGEF12	-0.288	0.017055
SNORD104	BBX	-0.288	0.017055
SNORD104	CLIC4	-0.288	0.017055
SNORD104	EEA1	-0.287	0.017427
SNORD104	ATP11B	-0.287	0.017427
SNORD104	EPS15	-0.287	0.017427
SNORD104	VCL	-0.286	0.017806
SNORD104	PIK3R1	-0.286	0.017806
SNORD104	USP9X	-0.286	0.017806
SNORD104	TMOD3	-0.285	0.018192
SNORD104	SP3	-0.283	0.018987
SNORD104	MYO1B	-0.283	0.018987
SNORD104	PLSCR4	-0.283	0.018987
SNORD104	CTR9	-0.283	0.018987
SNORD104	AFF1	-0.282	0.019395
SNORD104	ITPRIPL2	-0.282	0.019395
SNORD104	LIMS1	-0.281	0.019811
SNORD104	MTM1	-0.281	0.019811
SNORD104	ADAM10	-0.281	0.019811
SNORD104	AP4E1	-0.28	0.020235
SNORD104	OXSRI	-0.28	0.020235
SNORD104	TRAF6	-0.28	0.020235
SNORD104	TRAPPC11	-0.28	0.020235
SNORD104	USF3	-0.28	0.020235
SNORD104	DIS3	-0.279	0.020667
SNORD104	ZNF264	-0.279	0.020667
SNORD104	AFF4	-0.278	0.021107
SNORD104	LACC1	-0.278	0.021107
SNORD104	PBRM1	-0.277	0.021555
SNORD104	IQGAP1	-0.277	0.021555
SNORD104	LHFPL2	-0.277	0.021555
SNORD104	SLC25A24	-0.276	0.022012
SNORD104	TRIP11	-0.276	0.022012
SNORD104	DST	-0.275	0.022476
SNORD104	ERCC6L2	-0.275	0.022476
SNORD104	ZBTB38	-0.275	0.022476
SNORD104	AAK1	-0.275	0.022476
SNORD104	WDFY3	-0.275	0.022476
SNORD104	PJA2	-0.275	0.022476
SNORD104	GABPA	-0.275	0.022476
SNORD104	ZNF654	-0.274	0.022949

SNORD104	ARAP2	-0.274	0.022949
SNORD104	ZNF148	-0.274	0.022949
SNORD104	CREB1	-0.274	0.022949
SNORD104	CFAP97	-0.274	0.022949
SNORD104	CNOT6L	-0.274	0.022949
SNORD104	ETS1	-0.273	0.023431
SNORD104	ULBP3	-0.273	0.023431
SNORD104	AHNAK	-0.273	0.023431
SNORD104	RC3H2	-0.273	0.023431
SNORD104	MACF1	-0.272	0.023922
SNORD104	PCDHGC3	-0.272	0.023922
SNORD104	SNRK	-0.271	0.024421
SNORD104	RANBP2	-0.271	0.024421
SNORD104	RAPGEF2	-0.271	0.024421
SNORD104	ZBTB21	-0.271	0.024421
SNORD104	PIKFYVE	-0.27	0.02493
SNORD104	SPTY2D1	-0.27	0.02493
SNORD104	OSBPL11	-0.27	0.02493
SNORD104	PUM1	-0.27	0.02493
SNORD104	ELK3	-0.269	0.025447
SNORD104	ROCK1	-0.269	0.025447
SNORD104	REV3L	-0.269	0.025447
SNORD104	ASCC3	-0.269	0.025447
SNORD104	KMT2A	-0.269	0.025447
SNORD104	HSPG2	-0.269	0.025447
SNORD104	AIDA	-0.268	0.025974
SNORD104	CBL	-0.268	0.025974
SNORD104	ERCC4	-0.268	0.025974
SNORD104	SPTBN1	-0.268	0.025974
SNORD104	PRKG1	-0.267	0.02651
SNORD104	ARL13B	-0.267	0.02651
SNORD104	GOPC	-0.267	0.02651
SNORD104	LNPEP	-0.267	0.02651
SNORD104	ZYG11B	-0.267	0.02651
SNORD104	LRRFIP1	-0.267	0.02651
SNORD104	ZNF45	-0.267	0.02651
SNORD104	SLFN5	-0.266	0.027056
SNORD104	GNG12	-0.266	0.027056
SNORD104	TOP2B	-0.266	0.027056
SNORD104	XPO4	-0.266	0.027056
SNORD104	FRMD4B	-0.266	0.027056
SNORD104	LATS2	-0.266	0.027056
SNORD104	ATL3	-0.266	0.027056
SNORD104	PIK3R4	-0.265	0.027612

SNORD104	SSPN	-0.265	0.027612
SNORD104	UTP14C	-0.265	0.027612
SNORD104	NR1D2	-0.264	0.028177
SNORD104	LAMA2	-0.264	0.028177
SNORD104	MITF	-0.264	0.028177
SNORD104	BCL10	-0.264	0.028177
SNORD104	TAOK1	-0.264	0.028177
SNORD104	CLCN3	-0.264	0.028177
SNORD104	WAPL	-0.263	0.028752
SNORD104	TRAM2	-0.263	0.028752
SNORD104	DDX3X	-0.263	0.028752
SNORD104	HIVEP1	-0.263	0.028752
SNORD104	MAP3K2	-0.263	0.028752
SNORD104	PLXDC2	-0.263	0.028752
SNORD104	ZBTB44	-0.263	0.028752
SNORD104	MEF2A	-0.262	0.029337
SNORD104	PDS5B	-0.262	0.029337
SNORD104	CNOT1	-0.262	0.029337
SNORD104	PDCD6IP	-0.262	0.029337
SNORD104	RNF111	-0.262	0.029337
SNORD104	ATRX	-0.262	0.029337
SNORD104	CERS6	-0.261	0.029933
SNORD104	TRANK1	-0.261	0.029933
SNORD104	CDK17	-0.261	0.029933
SNORD104	ZFP91	-0.261	0.029933
SNORD104	FOXO3	-0.261	0.029933
SNORD104	ARSB	-0.26	0.030539
SNORD104	APAF1	-0.26	0.030539
SNORD104	PARP4	-0.26	0.030539
SNORD104	ITGAV	-0.26	0.030539
SNORD104	APBB2	-0.26	0.030539
SNORD104	ZNF611	-0.259	0.031155
SNORD104	PEAK1	-0.259	0.031155
SNORD104	QKI	-0.259	0.031155
SNORD104	AMOTL1	-0.259	0.031155
SNORD104	ANKRD17	-0.259	0.031155
SNORD104	RASA2	-0.259	0.031155
SNORD104	TMF1	-0.259	0.031155
SNORD104	MBNL2	-0.259	0.031155
SNORD104	EPB41L2	-0.258	0.031782
SNORD104	PANK3	-0.258	0.031782
SNORD104	AFAP1	-0.258	0.031782
SNORD104	ZEB1	-0.258	0.031782
SNORD104	APPL1	-0.258	0.031782

SNORD104	GOLIM4	-0.258	0.031782
SNORD104	ERBIN	-0.258	0.031782
SNORD104	CMTM6	-0.258	0.031782
SNORD104	KLF12	-0.257	0.03242
SNORD104	SMARCA1	-0.257	0.03242
SNORD104	CYLD	-0.257	0.03242
SNORD104	SPTAN1	-0.257	0.03242
SNORD104	FBXO28	-0.257	0.03242
SNORD104	RIF1	-0.257	0.03242
SNORD104	USP37	-0.257	0.03242
SNORD104	MYO5A	-0.256	0.033069
SNORD104	PALM2-AKAP2	-0.256	0.033069
SNORD104	RAB8B	-0.256	0.033069
SNORD104	MAN1A2	-0.255	0.033729
SNORD104	RSBN1	-0.255	0.033729
SNORD104	CAB39	-0.255	0.033729
SNORD104	USP25	-0.255	0.033729
SNORD104	FNDC3B	-0.255	0.033729
SNORD104	PTPN21	-0.254	0.0344
SNORD104	MAML2	-0.254	0.0344
SNORD104	ZNF197	-0.254	0.0344
SNORD104	CDK14	-0.254	0.0344
SNORD104	PIK3CB	-0.254	0.0344
SNORD104	EVI5	-0.253	0.035082
SNORD104	CDKL5	-0.253	0.035082
SNORD104	ARHGAP42	-0.253	0.035082
SNORD104	UTRN	-0.253	0.035082
SNORD104	TGFBR2	-0.253	0.035082
SNORD104	ZNF347	-0.253	0.035082
SNORD104	KIDINS220	-0.253	0.035082
SNORD104	PARVA	-0.253	0.035082
SNORD104	ZNF28	-0.253	0.035082
SNORD104	AP3B1	-0.253	0.035082
SNORD104	ALG11	-0.252	0.035776
SNORD104	KIF2A	-0.252	0.035776
SNORD104	RELL1	-0.252	0.035776
SNORD104	MFN2	-0.252	0.035776
SNORD104	SGMS2	-0.252	0.035776
SNORD104	EP300	-0.251	0.036482
SNORD104	MAP3K1	-0.251	0.036482
SNORD104	SSH1	-0.251	0.036482
SNORD104	EXOC6B	-0.251	0.036482
SNORD104	CSNK1G1	-0.251	0.036482
SNORD104	ITSN1	-0.251	0.036482

SNORD104	XRN1	-0.251	0.036482
SNORD104	TJP1	-0.25	0.037199
SNORD104	ZEB2	-0.25	0.037199
SNORD104	SCAF11	-0.249	0.037929
SNORD104	USP53	-0.249	0.037929
SNORD104	NRIP1	-0.249	0.037929
SNORD104	DOCK11	-0.249	0.037929
SNORD104	MYLK	-0.249	0.037929
SNORD104	SRFBP1	-0.249	0.037929
SNORD104	TOR1AIP1	-0.249	0.037929
SNORD104	ZMAT3	-0.249	0.037929
SNORD104	MPP5	-0.249	0.037929
SNORD104	ZNF221	-0.249	0.037929
SNORD104	SEC24B	-0.248	0.03867
SNORD104	SNX19	-0.248	0.03867
SNORD104	TRPS1	-0.248	0.03867
SNORD104	MYADM	-0.248	0.03867
SNORD104	SPOPL	-0.248	0.03867
SNORD104	FSTL1	-0.248	0.03867
SNORD104	EXOC2	-0.248	0.03867
SNORD104	ITCH	-0.248	0.03867
SNORD104	FBN1	-0.247	0.039424
SNORD104	WDR82	-0.247	0.039424
SNORD104	HIPK3	-0.247	0.039424
SNORD104	FEM1C	-0.247	0.039424
SNORD104	RAB3GAP1	-0.246	0.04019
SNORD104	CDK19	-0.246	0.04019
SNORD104	PAK2	-0.246	0.04019
SNORD104	STAG1	-0.246	0.04019
SNORD104	TBC1D14	-0.246	0.04019
SNORD104	RLIM	-0.246	0.04019
SNORD104	KLF11	-0.246	0.04019
SNORD104	FBXW11	-0.246	0.04019
SNORD104	CEP120	-0.245	0.040969
SNORD104	NOTCH2	-0.245	0.040969
SNORD104	VAMP3	-0.245	0.040969
SNORD104	DOCK7	-0.245	0.040969
SNORD104	MTOR	-0.245	0.040969
SNORD104	DENND4C	-0.245	0.040969
SNORD104	STX17	-0.245	0.040969
SNORD104	TAB2	-0.244	0.041761
SNORD104	CCNK	-0.244	0.041761
SNORD104	SUSD6	-0.244	0.041761
SNORD104	LPP	-0.244	0.041761

SNORD104	ZNFX1	-0.244	0.041761
SNORD104	GNAQ	-0.244	0.041761
SNORD104	GSK3B	-0.244	0.041761
SNORD104	LTBP1	-0.244	0.041761
SNORD104	ITGA4	-0.244	0.041761
SNORD104	VPS13D	-0.244	0.041761
SNORD104	YWHAB	-0.243	0.042565
SNORD104	FAM208A	-0.243	0.042565
SNORD104	GAS7	-0.243	0.042565
SNORD104	PDE5A	-0.243	0.042565
SNORD104	USP38	-0.243	0.042565
SNORD104	ZCCHC6	-0.243	0.042565
SNORD104	ARHGAP10	-0.243	0.042565
SNORD104	LRRC58	-0.243	0.042565
SNORD104	BTBD7	-0.243	0.042565
SNORD104	PIK3C2A	-0.242	0.043383
SNORD104	KPNA6	-0.242	0.043383
SNORD104	RNF38	-0.242	0.043383
SNORD104	ZNF543	-0.242	0.043383
SNORD104	KIF1B	-0.242	0.043383
SNORD104	TTBK2	-0.241	0.044214
SNORD104	PLXNC1	-0.241	0.044214
SNORD104	DNAJC16	-0.241	0.044214
SNORD104	RFX7	-0.241	0.044214
SNORD104	KIAA2026	-0.241	0.044214
SNORD104	PRKAR2A	-0.241	0.044214
SNORD104	ARID2	-0.241	0.044214
SNORD104	MCC	-0.241	0.044214
SNORD104	DYRK1A	-0.241	0.044214
SNORD104	PPP1R12A	-0.241	0.044214
SNORD104	MTPN	-0.241	0.044214
SNORD104	G3BP1	-0.241	0.044214
SNORD104	DMXL1	-0.241	0.044214
SNORD104	RASA1	-0.24	0.045058
SNORD104	TBCEL	-0.24	0.045058
SNORD104	DIP2B	-0.24	0.045058
SNORD104	MTF1	-0.24	0.045058
SNORD104	FBXL3	-0.24	0.045058
SNORD104	BMP2K	-0.24	0.045058
SNORD104	CHSY1	-0.24	0.045058
SNORD104	CDV3	-0.24	0.045058
SNORD104	DDR2	-0.239	0.045916
SNORD104	LRRC8C	-0.239	0.045916
SNORD104	ZFX	-0.239	0.045916

SNORD104	ARID1B	-0.239	0.045916
SNORD104	ITGB1	-0.239	0.045916
SNORD104	RB1	-0.239	0.045916
SNORD104	SAMD9	-0.239	0.045916
SNORD104	STARD13	-0.238	0.046788
SNORD104	PPP3CA	-0.238	0.046788
SNORD104	CAST	-0.238	0.046788
SNORD104	USP47	-0.238	0.046788
SNORD104	PICALM	-0.238	0.046788
SNORD104	PIK3CG	-0.238	0.046788
SNORD104	GNA13	-0.238	0.046788
SNORD104	RYBP	-0.238	0.046788
SNORD104	PHC3	-0.238	0.046788
SNORD104	CHIC1	-0.238	0.046788
SNORD104	TCF4	-0.237	0.047673
SNORD104	KIAA1551	-0.237	0.047673
SNORD104	ZNF134	-0.237	0.047673
SNORD104	PALLD	-0.237	0.047673
SNORD104	EPC2	-0.237	0.047673
SNORD104	DICER1	-0.237	0.047673
SNORD104	DAPP1	-0.237	0.047673
SNORD104	PTPRK	-0.237	0.047673
SNORD104	ABCA1	-0.237	0.047673
SNORD104	IGF2R	-0.236	0.048572
SNORD104	11-Sep	-0.236	0.048572
SNORD104	ZNF426	-0.236	0.048572
SNORD104	RSF1	-0.236	0.048572
SNORD104	NFAT5	-0.236	0.048572
SNORD104	DCP1A	-0.236	0.048572
SNORD104	KLHL28	-0.236	0.048572
SNORD104	SLC30A4	-0.236	0.048572
SNORD104	PIP4K2A	-0.236	0.048572
SNORD104	SETD7	-0.236	0.048572
SNORD104	STRN	-0.235	0.049486
SNORD104	ASXL2	-0.235	0.049486
SNORD104	ZNF624	-0.235	0.049486
SNORD104	AQR	-0.235	0.049486
SNORD104	TROVE2	-0.235	0.049486
SNORD104	TLN1	-0.235	0.049486
SNORD104	CALD1	-0.235	0.049486
SNORD104	ZNF268	-0.235	0.049486
SNORD104	RPS9	0.259	0.049882
SNORD104	FBRSL1	0.259	0.049882
SNORD104	STKLD1	0.259	0.049882

SNORD104	MFSD10	0.259	0.049882
SNORD104	FAM96B	0.259	0.049882
SNORD104	NEIL1	0.259	0.049882
SNORD104	TBCC	0.259	0.049882
SNORD104	BABAM1	0.259	0.049882
SNORD104	HES4	0.259	0.049882
SNORD104	SPG7	0.259	0.049882
SNORD104	LUC7L	0.26	0.048962
SNORD104	PET117	0.26	0.048962
SNORD104	C1orf122	0.26	0.048962
SNORD104	THOP1	0.26	0.048962
SNORD104	PICK1	0.26	0.048962
SNORD104	BATF	0.26	0.048962
SNORD104	TXNRD2	0.26	0.048962
SNORD104	TTC32	0.26	0.048962
SNORD104	ECSIT	0.26	0.048962
SNORD104	SRRM5	0.26	0.048962
SNORD104	SLC50A1	0.26	0.048962
SNORD104	PRPF31	0.26	0.048962
SNORD104	SWI5	0.26	0.048962
SNORD104	RNF167	0.26	0.048962
SNORD104	PYCR3	0.261	0.048057
SNORD104	MVK	0.261	0.048057
SNORD104	DDX51	0.261	0.048057
SNORD104	CYP2E1	0.261	0.048057
SNORD104	FAM186A	0.261	0.048057
SNORD104	LLGL2	0.261	0.048057
SNORD104	DMAP1	0.261	0.048057
SNORD104	R3HCC1	0.261	0.048057
SNORD104	SIRT4	0.261	0.048057
SNORD104	POLR2L	0.261	0.048057
SNORD104	CSAD	0.261	0.048057
SNORD104	IFI27L1	0.261	0.048057
SNORD104	SPIDR	0.261	0.048057
SNORD104	SF3B5	0.261	0.048057
SNORD104	NDUFB1	0.262	0.047166
SNORD104	SEN3	0.262	0.047166
SNORD104	RPUSD1	0.262	0.047166
SNORD104	MCRIP1	0.262	0.047166
SNORD104	NR1H2	0.262	0.047166
SNORD104	MYL6B	0.262	0.047166
SNORD104	CEP95	0.262	0.047166
SNORD104	RNF208	0.262	0.047166
SNORD104	UBL5	0.262	0.047166

SNORD104	PGP	0.262	0.047166
SNORD104	SGSH	0.262	0.047166
SNORD104	MUTYH	0.262	0.047166
SNORD104	SLC35B1	0.262	0.047166
SNORD104	CHMP6	0.263	0.046288
SNORD104	EPS8L2	0.263	0.046288
SNORD104	NRL	0.263	0.046288
SNORD104	C19orf53	0.263	0.046288
SNORD104	GALT	0.263	0.046288
SNORD104	MOSPD3	0.263	0.046288
SNORD104	FKBP11	0.264	0.045424
SNORD104	MRM3	0.264	0.045424
SNORD104	GIGYF1	0.264	0.045424
SNORD104	POLRMT	0.264	0.045424
SNORD104	C2CD4D	0.264	0.045424
SNORD104	SLC26A11	0.264	0.045424
SNORD104	RAMP1	0.264	0.045424
SNORD104	ANKRD23	0.264	0.045424
SNORD104	ALKBH2	0.264	0.045424
SNORD104	VPS9D1	0.264	0.045424
SNORD104	ZNF335	0.264	0.045424
SNORD104	ENGASE	0.265	0.044574
SNORD104	TMEM160	0.265	0.044574
SNORD104	LSM4	0.265	0.044574
SNORD104	MST1	0.265	0.044574
SNORD104	TECR	0.265	0.044574
SNORD104	C6orf226	0.265	0.044574
SNORD104	AC011498.1	0.265	0.044574
SNORD104	MYL5	0.265	0.044574
SNORD104	POLR2H	0.265	0.044574
SNORD104	LCN12	0.266	0.043738
SNORD104	LMNTD2	0.266	0.043738
SNORD104	CDK3	0.266	0.043738
SNORD104	TMEM91	0.266	0.043738
SNORD104	SHARPIN	0.266	0.043738
SNORD104	IMP3	0.266	0.043738
SNORD104	FAAP20	0.266	0.043738
SNORD104	DHRS4	0.266	0.043738
SNORD104	FPGS	0.266	0.043738
SNORD104	NME1	0.266	0.043738
SNORD104	SIVA1	0.266	0.043738
SNORD104	MSS51	0.266	0.043738
SNORD104	C12orf73	0.266	0.043738
SNORD104	FBXL6	0.266	0.043738

SNORD104	PRDX5	0.266	0.043738
SNORD104	MOGS	0.266	0.043738
SNORD104	WDR45	0.267	0.042915
SNORD104	SCNM1	0.267	0.042915
SNORD104	FAM229A	0.267	0.042915
SNORD104	ZNF446	0.267	0.042915
SNORD104	SELENOH	0.267	0.042915
SNORD104	MBD3	0.267	0.042915
SNORD104	SRRT	0.267	0.042915
SNORD104	ATP5J2-PTCD1	0.267	0.042915
SNORD104	RABGGTA	0.268	0.042104
SNORD104	BLOC1S1	0.268	0.042104
SNORD104	XAB2	0.268	0.042104
SNORD104	SAC3D1	0.268	0.042104
SNORD104	NCAPH2	0.268	0.042104
SNORD104	SMDT1	0.268	0.042104
SNORD104	EXOSC5	0.268	0.042104
SNORD104	PYCR1	0.268	0.042104
SNORD104	CLDN7	0.268	0.042104
SNORD104	CLPP	0.268	0.042104
SNORD104	SDCCAG3	0.268	0.042104
SNORD104	HYI	0.268	0.042104
SNORD104	FLYWCH2	0.268	0.042104
SNORD104	WDR13	0.268	0.042104
SNORD104	COX6A1	0.268	0.042104
SNORD104	CCDC137	0.268	0.042104
SNORD104	RPS24	0.269	0.041307
SNORD104	FLAD1	0.269	0.041307
SNORD104	C12orf10	0.269	0.041307
SNORD104	ATP5H	0.269	0.041307
SNORD104	PLEKHH3	0.269	0.041307
SNORD104	CXXC1	0.269	0.041307
SNORD104	TMEM60	0.269	0.041307
SNORD104	POMT1	0.269	0.041307
SNORD104	AP5Z1	0.269	0.041307
SNORD104	COX8A	0.269	0.041307
SNORD104	PARP10	0.269	0.041307
SNORD104	LAMTOR4	0.27	0.040523
SNORD104	GPRIN2	0.27	0.040523
SNORD104	NAA60	0.27	0.040523
SNORD104	UQCRB	0.27	0.040523
SNORD104	RPL18	0.27	0.040523
SNORD104	FBX044	0.27	0.040523
SNORD104	PSMG3	0.27	0.040523

SNORD104	PYM1	0.27	0.040523
SNORD104	COX6C	0.27	0.040523
SNORD104	YPEL3	0.271	0.039751
SNORD104	APBB3	0.271	0.039751
SNORD104	SAMD1	0.271	0.039751
SNORD104	MISP3	0.271	0.039751
SNORD104	VPS16	0.271	0.039751
SNORD104	ZNF771	0.271	0.039751
SNORD104	MIF	0.271	0.039751
SNORD104	FUK	0.271	0.039751
SNORD104	ZDHC12	0.271	0.039751
SNORD104	HSD17B10	0.272	0.038992
SNORD104	GSTP1	0.272	0.038992
SNORD104	SGF29	0.272	0.038992
SNORD104	MRPL58	0.272	0.038992
SNORD104	LRRC14	0.272	0.038992
SNORD104	RNF25	0.272	0.038992
SNORD104	BGLAP	0.272	0.038992
SNORD104	TMEM256	0.272	0.038992
SNORD104	SPSB2	0.272	0.038992
SNORD104	ABHD14A	0.272	0.038992
SNORD104	ZNF358	0.273	0.038245
SNORD104	RNASEK	0.273	0.038245
SNORD104	PWWP2B	0.273	0.038245
SNORD104	RPL13	0.273	0.038245
SNORD104	SLC38A10	0.273	0.038245
SNORD104	SUGP1	0.273	0.038245
SNORD104	MIGA2	0.273	0.038245
SNORD104	TECPR1	0.273	0.038245
SNORD104	RPL36A	0.273	0.038245
SNORD104	C20orf27	0.274	0.037511
SNORD104	ATP5G1	0.274	0.037511
SNORD104	SLC25A39	0.274	0.037511
SNORD104	SFXN4	0.274	0.037511
SNORD104	ZNF593	0.274	0.037511
SNORD104	BRMS1	0.274	0.037511
SNORD104	UNC119	0.274	0.037511
SNORD104	SMIM26	0.274	0.037511
SNORD104	ZNF76	0.274	0.037511
SNORD104	HID1	0.274	0.037511
SNORD104	TMEM175	0.274	0.037511
SNORD104	C1orf56	0.275	0.036788
SNORD104	ZBTB45	0.275	0.036788
SNORD104	PMF1-BGLAP	0.275	0.036788

SNORD104	SYCE1L	0.275	0.036788
SNORD104	RECQL5	0.275	0.036788
SNORD104	CES4A	0.275	0.036788
SNORD104	IMP4	0.275	0.036788
SNORD104	ANKRD39	0.275	0.036788
SNORD104	APBA3	0.276	0.036077
SNORD104	CAPN12	0.276	0.036077
SNORD104	AIFM2	0.276	0.036077
SNORD104	JTB	0.276	0.036077
SNORD104	SMIM22	0.276	0.036077
SNORD104	PREB	0.277	0.035378
SNORD104	SNRPB	0.277	0.035378
SNORD104	PPP6R2	0.277	0.035378
SNORD104	RALY	0.277	0.035378
SNORD104	ALKBH7	0.277	0.035378
SNORD104	ELMO3	0.277	0.035378
SNORD104	TPGS1	0.277	0.035378
SNORD104	RPS19BP1	0.277	0.035378
SNORD104	UCKL1	0.278	0.034691
SNORD104	RAB11B	0.278	0.034691
SNORD104	THOC6	0.278	0.034691
SNORD104	PGS1	0.278	0.034691
SNORD104	HS1BP3	0.278	0.034691
SNORD104	TRMT61A	0.278	0.034691
SNORD104	PSMG4	0.278	0.034691
SNORD104	GNPTG	0.278	0.034691
SNORD104	GCDH	0.278	0.034691
SNORD104	ASGR1	0.278	0.034691
SNORD104	C15orf61	0.278	0.034691
SNORD104	C19orf66	0.279	0.034015
SNORD104	SURF2	0.28	0.03335
SNORD104	EFCAB2	0.28	0.03335
SNORD104	ENDOG	0.28	0.03335
SNORD104	NOSIP	0.28	0.03335
SNORD104	GPAA1	0.28	0.03335
SNORD104	ILKAP	0.28	0.03335
SNORD104	ZNF837	0.28	0.03335
SNORD104	SPATA20	0.28	0.03335
SNORD104	GTPBP3	0.28	0.03335
SNORD104	OCEL1	0.281	0.032697
SNORD104	ZNF511	0.281	0.032697
SNORD104	AIP	0.281	0.032697
SNORD104	JOSD2	0.281	0.032697
SNORD104	COX17	0.281	0.032697

SNORD104	ERP29	0.281	0.032697
SNORD104	MAN2C1	0.281	0.032697
SNORD104	TAF1C	0.281	0.032697
SNORD104	JMJD6	0.282	0.032054
SNORD104	TIGD1	0.282	0.032054
SNORD104	TRADD	0.282	0.032054
SNORD104	SCRN2	0.282	0.032054
SNORD104	NUDT8	0.283	0.031423
SNORD104	GATD1	0.283	0.031423
SNORD104	KHK	0.283	0.031423
SNORD104	MPV17	0.283	0.031423
SNORD104	FKBP8	0.283	0.031423
SNORD104	NAA10	0.283	0.031423
SNORD104	EXOSC4	0.283	0.031423
SNORD104	KLHL17	0.284	0.030802
SNORD104	EXD3	0.284	0.030802
SNORD104	PSMD4	0.284	0.030802
SNORD104	BORCS8	0.284	0.030802
SNORD104	P4HTM	0.284	0.030802
SNORD104	ACTL10	0.284	0.030802
SNORD104	WDR830S	0.284	0.030802
SNORD104	NUP85	0.284	0.030802
SNORD104	SMUG1	0.284	0.030802
SNORD104	C9orf16	0.284	0.030802
SNORD104	MRPL57	0.285	0.030191
SNORD104	AAAS	0.285	0.030191
SNORD104	COQ4	0.285	0.030191
SNORD104	TMEM208	0.285	0.030191
SNORD104	MIIP	0.285	0.030191
SNORD104	MRPL43	0.286	0.029591
SNORD104	TRPT1	0.286	0.029591
SNORD104	CEP131	0.286	0.029591
SNORD104	MRI1	0.286	0.029591
SNORD104	TMEM59L	0.286	0.029591
SNORD104	UCN	0.286	0.029591
SNORD104	SSBP4	0.286	0.029591
SNORD104	NEURL4	0.286	0.029591
SNORD104	RBFA	0.286	0.029591
SNORD104	CDPF1	0.287	0.029002
SNORD104	ANKZF1	0.287	0.029002
SNORD104	ATG4D	0.287	0.029002
SNORD104	PMVK	0.287	0.029002
SNORD104	SLC16A11	0.287	0.029002
SNORD104	KIFC2	0.287	0.029002

SNORD104	PEX16	0.287	0.029002
SNORD104	D2HGDH	0.287	0.029002
SNORD104	CHCHD10	0.288	0.028422
SNORD104	UBALD1	0.288	0.028422
SNORD104	ESRRA	0.288	0.028422
SNORD104	RPS6KB2	0.288	0.028422
SNORD104	KMT5C	0.288	0.028422
SNORD104	USF1	0.288	0.028422
SNORD104	DPM2	0.289	0.027853
SNORD104	AGAP9	0.289	0.027853
SNORD104	CCDC24	0.289	0.027853
SNORD104	RPS20	0.289	0.027853
SNORD104	TMEM222	0.289	0.027853
SNORD104	ZNF444	0.289	0.027853
SNORD104	PPDPF	0.289	0.027853
SNORD104	GSDMD	0.289	0.027853
SNORD104	MGMT	0.289	0.027853
SNORD104	PIDD1	0.289	0.027853
SNORD104	C8G	0.289	0.027853
SNORD104	RPL37A	0.29	0.027293
SNORD104	MAGIX	0.29	0.027293
SNORD104	DAZAP1	0.29	0.027293
SNORD104	MUS81	0.29	0.027293
SNORD104	MCRS1	0.29	0.027293
SNORD104	NFKBIL1	0.29	0.027293
SNORD104	IFT43	0.29	0.027293
SNORD104	HRAS	0.29	0.027293
SNORD104	C19orf70	0.29	0.027293
SNORD104	FGFBP3	0.291	0.026743
SNORD104	EXOSC1	0.291	0.026743
SNORD104	NPRL2	0.291	0.026743
SNORD104	BOLA1	0.291	0.026743
SNORD104	SNRPA	0.292	0.026203
SNORD104	AP002990.1	0.292	0.026203
SNORD104	ETFB	0.292	0.026203
SNORD104	RNASEH2C	0.292	0.026203
SNORD104	LMBR1L	0.292	0.026203
SNORD104	TRAPPC12	0.292	0.026203
SNORD104	SIRT7	0.292	0.026203
SNORD104	FITM1	0.292	0.026203
SNORD104	TELO2	0.293	0.025672
SNORD104	SLC39A3	0.293	0.025672
SNORD104	PEX11G	0.293	0.025672
SNORD104	HOOK2	0.293	0.025672

SNORD104	ROMO1	0.293	0.025672
SNORD104	MAP2K2	0.293	0.025672
SNORD104	GPX4	0.294	0.02515
SNORD104	WNT4	0.294	0.02515
SNORD104	ROGDI	0.294	0.02515
SNORD104	CRACR2B	0.294	0.02515
SNORD104	NDUFB7	0.294	0.02515
SNORD104	MOB2	0.294	0.02515
SNORD104	JSRP1	0.294	0.02515
SNORD104	SPSB3	0.294	0.02515
SNORD104	DUS3L	0.294	0.02515
SNORD104	TIMM17B	0.294	0.02515
SNORD104	HAGH	0.294	0.02515
SNORD104	ATP5G2	0.295	0.024638
SNORD104	DHRS4L2	0.295	0.024638
SNORD104	NME2	0.295	0.024638
SNORD104	ZNF467	0.295	0.024638
SNORD104	SNRNP70	0.295	0.024638
SNORD104	BOLA2B	0.295	0.024638
SNORD104	ECI1	0.295	0.024638
SNORD104	STXBP2	0.295	0.024638
SNORD104	MTX1	0.295	0.024638
SNORD104	PRR22	0.295	0.024638
SNORD104	RBBP8NL	0.295	0.024638
SNORD104	BUD23	0.295	0.024638
SNORD104	NARF	0.296	0.024135
SNORD104	NPIP15	0.296	0.024135
SNORD104	FBXW5	0.296	0.024135
SNORD104	RAD9A	0.296	0.024135
SNORD104	ZNHIT1	0.296	0.024135
SNORD104	NAXE	0.296	0.024135
SNORD104	COA4	0.296	0.024135
SNORD104	NADSYN1	0.297	0.02364
SNORD104	DNAJC4	0.297	0.02364
SNORD104	MRPL24	0.297	0.02364
SNORD104	POLG2	0.297	0.02364
SNORD104	RHPN1	0.297	0.02364
SNORD104	NME4	0.297	0.02364
SNORD104	TRMT2A	0.297	0.02364
SNORD104	PPP1R16A	0.298	0.023155
SNORD104	GPR108	0.298	0.023155
SNORD104	GMPPA	0.298	0.023155
SNORD104	CLDND2	0.298	0.023155
SNORD104	SSR4	0.298	0.023155

SNORD104	CHTOP	0.298	0.023155
SNORD104	NDUFS8	0.299	0.022678
SNORD104	RBM10	0.299	0.022678
SNORD104	ZNF653	0.299	0.022678
SNORD104	TSSC4	0.299	0.022678
SNORD104	C10orf35	0.299	0.022678
SNORD104	ARSA	0.299	0.022678
SNORD104	RAB17	0.299	0.022678
SNORD104	SLC25A11	0.3	0.02221
SNORD104	CC2D1A	0.3	0.02221
SNORD104	C14orf93	0.3	0.02221
SNORD104	CHTF18	0.3	0.02221
SNORD104	RHBDL1	0.3	0.02221
SNORD104	TRAPPC1	0.3	0.02221
SNORD104	SLC25A10	0.3	0.02221
SNORD104	AL162231.1	0.301	0.02175
SNORD104	RAB40C	0.301	0.02175
SNORD104	METTL17	0.301	0.02175
SNORD104	HSPB9	0.301	0.02175
SNORD104	INO80E	0.301	0.02175
SNORD104	HAUS7	0.301	0.02175
SNORD104	TAF10	0.301	0.02175
SNORD104	DPM3	0.301	0.02175
SNORD104	RPS19	0.301	0.02175
SNORD104	ZGPAT	0.301	0.02175
SNORD104	CLK2	0.302	0.021298
SNORD104	KIAA0895L	0.302	0.021298
SNORD104	CCDC124	0.302	0.021298
SNORD104	KIFC3	0.302	0.021298
SNORD104	TACO1	0.302	0.021298
SNORD104	SWSAP1	0.302	0.021298
SNORD104	CTU1	0.303	0.020855
SNORD104	STK25	0.303	0.020855
SNORD104	SH2B1	0.304	0.02042
SNORD104	RFXANK	0.304	0.02042
SNORD104	PSMC5	0.304	0.02042
SNORD104	TMUB1	0.304	0.02042
SNORD104	DDRGK1	0.304	0.02042
SNORD104	TMEM205	0.304	0.02042
SNORD104	KAZALD1	0.305	0.019992
SNORD104	GPS1	0.305	0.019992
SNORD104	HINT2	0.305	0.019992
SNORD104	RAB4B	0.305	0.019992
SNORD104	C8orf82	0.305	0.019992

SNORD104	SPRYD4	0.305	0.019992
SNORD104	UNK	0.305	0.019992
SNORD104	MYDGF	0.306	0.019573
SNORD104	RPL38	0.306	0.019573
SNORD104	SEC61B	0.306	0.019573
SNORD104	SH3GLB2	0.306	0.019573
SNORD104	CCDC107	0.307	0.019161
SNORD104	FAM173A	0.307	0.019161
SNORD104	ZFAND2B	0.307	0.019161
SNORD104	ARIH2OS	0.307	0.019161
SNORD104	FRS3	0.308	0.018757
SNORD104	NDUFA11	0.308	0.018757
SNORD104	PCGF1	0.308	0.018757
SNORD104	MRPS34	0.308	0.018757
SNORD104	SPPL2B	0.308	0.018757
SNORD104	ANKS3	0.309	0.01836
SNORD104	YDJC	0.309	0.01836
SNORD104	ULK3	0.309	0.01836
SNORD104	RABEP2	0.309	0.01836
SNORD104	MAMDC4	0.309	0.01836
SNORD104	TARBP2	0.31	0.017971
SNORD104	ANAPC11	0.31	0.017971
SNORD104	MED11	0.31	0.017971
SNORD104	TMUB2	0.31	0.017971
SNORD104	TMEM238	0.31	0.017971
SNORD104	NDUFA1	0.31	0.017971
SNORD104	RPLP2	0.311	0.017589
SNORD104	AGAP6	0.311	0.017589
SNORD104	FAM50A	0.311	0.017589
SNORD104	ZGLP1	0.311	0.017589
SNORD104	LINC00116	0.311	0.017589
SNORD104	RHBDD3	0.311	0.017589
SNORD104	AARSD1	0.311	0.017589
SNORD104	PPOX	0.311	0.017589
SNORD104	BORCS6	0.312	0.017214
SNORD104	LZTS2	0.312	0.017214
SNORD104	RNF113A	0.312	0.017214
SNORD104	PNKP	0.312	0.017214
SNORD104	PTOV1	0.312	0.017214
SNORD104	SCO2	0.312	0.017214
SNORD104	GADD45GIP1	0.312	0.017214
SNORD104	EPOR	0.312	0.017214
SNORD104	MMAB	0.312	0.017214
SNORD104	MZT2A	0.313	0.016846

SNORD104	WBP1	0.313	0.016846
SNORD104	ZNHIT2	0.313	0.016846
SNORD104	ZFYVE27	0.313	0.016846
SNORD104	FAAP100	0.314	0.016485
SNORD104	GPS2	0.314	0.016485
SNORD104	LAMTOR2	0.314	0.016485
SNORD104	MACROD1	0.314	0.016485
SNORD104	TRMU	0.314	0.016485
SNORD104	NANOS3	0.314	0.016485
SNORD104	TRAF2	0.314	0.016485
SNORD104	NUBP2	0.314	0.016485
SNORD104	PCP2	0.315	0.01613
SNORD104	MFSD3	0.315	0.01613
SNORD104	PHKG2	0.315	0.01613
SNORD104	CD320	0.315	0.01613
SNORD104	COPE	0.315	0.01613
SNORD104	MRPL27	0.316	0.015783
SNORD104	PRR14	0.316	0.015783
SNORD104	MRPL28	0.316	0.015783
SNORD104	LENG1	0.316	0.015783
SNORD104	EMC6	0.316	0.015783
SNORD104	NPEPL1	0.316	0.015783
SNORD104	NDUFS7	0.316	0.015783
SNORD104	EMC9	0.317	0.015442
SNORD104	CCDC12	0.317	0.015442
SNORD104	DDX39A	0.317	0.015442
SNORD104	NDUFB8	0.317	0.015442
SNORD104	AUP1	0.317	0.015442
SNORD104	RPL37	0.317	0.015442
SNORD104	SNTA1	0.317	0.015442
SNORD104	FMC1	0.317	0.015442
SNORD104	IRF3	0.318	0.015108
SNORD104	PQBP1	0.318	0.015108
SNORD104	WASHC1	0.318	0.015108
SNORD104	COASY	0.318	0.015108
SNORD104	GALK1	0.319	0.01478
SNORD104	RABGEF1	0.32	0.014458
SNORD104	SGSM2	0.32	0.014458
SNORD104	RPS15	0.32	0.014458
SNORD104	B3GAT3	0.32	0.014458
SNORD104	TMC06	0.321	0.014142
SNORD104	NDUFA3	0.321	0.014142
SNORD104	SLC27A5	0.321	0.014142
SNORD104	DNPH1	0.321	0.014142

SNORD104	MRM1	0.322	0.013833
SNORD104	RING1	0.322	0.013833
SNORD104	NTHL1	0.322	0.013833
SNORD104	SPRN	0.322	0.013833
SNORD104	ANO9	0.322	0.013833
SNORD104	ZNF688	0.322	0.013833
SNORD104	TCIRG1	0.323	0.013529
SNORD104	NR2C2AP	0.323	0.013529
SNORD104	DPP7	0.323	0.013529
SNORD104	NIT1	0.323	0.013529
SNORD104	C17orf49	0.324	0.013232
SNORD104	MRPL23	0.324	0.013232
SNORD104	PHPT1	0.324	0.013232
SNORD104	INO80B	0.324	0.013232
SNORD104	SERF2	0.325	0.01294
SNORD104	NOL3	0.326	0.012654
SNORD104	RNF215	0.326	0.012654
SNORD104	B3GNTL1	0.326	0.012654
SNORD104	CNPY2	0.326	0.012654
SNORD104	ANKRD16	0.326	0.012654
SNORD104	RAB24	0.327	0.012374
SNORD104	POLR2J	0.327	0.012374
SNORD104	RANGRF	0.327	0.012374
SNORD104	CLASRP	0.328	0.012099
SNORD104	TUT1	0.328	0.012099
SNORD104	VPS28	0.328	0.012099
SNORD104	STX10	0.328	0.012099
SNORD104	GADD45G	0.328	0.012099
SNORD104	TMEM161A	0.329	0.011829
SNORD104	ATG4B	0.329	0.011829
SNORD104	CDK10	0.329	0.011829
SNORD104	DHPS	0.329	0.011829
SNORD104	GFER	0.33	0.011565
SNORD104	BCS1L	0.33	0.011565
SNORD104	NDUFB11	0.33	0.011565
SNORD104	FAM110A	0.33	0.011565
SNORD104	PTDSS2	0.33	0.011565
SNORD104	PUS1	0.331	0.011306
SNORD104	PMF1	0.331	0.011306
SNORD104	SDF2L1	0.331	0.011306
SNORD104	NARFL	0.331	0.011306
SNORD104	PPAN	0.331	0.011306
SNORD104	CENPX	0.332	0.011052
SNORD104	HSBP1L1	0.332	0.011052

SNORD104	MBLAC1	0.332	0.011052
SNORD104	ARL16	0.332	0.011052
SNORD104	NUDT14	0.333	0.010804
SNORD104	ZNF205	0.333	0.010804
SNORD104	NECAB3	0.333	0.010804
SNORD104	MRPL41	0.333	0.010804
SNORD104	PRKRIP1	0.333	0.010804
SNORD104	TMEM134	0.334	0.01056
SNORD104	INAFM1	0.334	0.01056
SNORD104	USE1	0.335	0.010321
SNORD104	SIGIRR	0.335	0.010321
SNORD104	TIMM44	0.335	0.010321
SNORD104	IL12B	0.336	0.010087
SNORD104	CAPN10	0.336	0.010087
SNORD104	LSM7	0.336	0.010087
SNORD104	CYHR1	0.336	0.010087
SNORD104	CCDC57	0.337	0.009858
SNORD104	ZNF775	0.337	0.009858
SNORD104	NAA38	0.338	0.009634
SNORD104	EGFL7	0.338	0.009634
SNORD104	C19orf43	0.338	0.009634
SNORD104	SIRT6	0.338	0.009634
SNORD104	SSNA1	0.338	0.009634
SNORD104	CENPT	0.338	0.009634
SNORD104	PIM3	0.338	0.009634
SNORD104	SDR39U1	0.339	0.009414
SNORD104	CUEDC2	0.339	0.009414
SNORD104	C19orf24	0.339	0.009414
SNORD104	TEN1-CDK3	0.339	0.009414
SNORD104	DUSP28	0.339	0.009414
SNORD104	DPH7	0.34	0.009198
SNORD104	NDUFV1	0.341	0.008987
SNORD104	PFDN6	0.341	0.008987
SNORD104	FBXL8	0.341	0.008987
SNORD104	DXO	0.342	0.00878
SNORD104	DOHH	0.342	0.00878
SNORD104	FASTK	0.342	0.00878
SNORD104	RGL3	0.343	0.008578
SNORD104	FAM98C	0.343	0.008578
SNORD104	SAPCD1	0.345	0.008185
SNORD104	RABAC1	0.346	0.007995
SNORD104	PPCDC	0.346	0.007995
SNORD104	RASSF7	0.347	0.007809
SNORD104	PAM16	0.347	0.007809

SNORD104	TIMM13	0.347	0.007809
SNORD104	LIN7B	0.348	0.007627
SNORD104	FAM3A	0.348	0.007627
SNORD104	ZNF524	0.348	0.007627
SNORD104	RPP25L	0.349	0.007448
SNORD104	CHKB	0.349	0.007448
SNORD104	UFSP1	0.349	0.007448
SNORD104	SAT2	0.349	0.007448
SNORD104	MRPL55	0.349	0.007448
SNORD104	NDUFA7	0.35	0.007273
SNORD104	CEBPD	0.35	0.007273
SNORD104	CCDC130	0.35	0.007273
SNORD104	MXD3	0.351	0.007102
SNORD104	TRMT1	0.351	0.007102
SNORD104	CHCHD1	0.352	0.006935
SNORD104	ATP5D	0.352	0.006935
SNORD104	BPIFB4	0.352	0.006935
SNORD104	ANKRD13D	0.352	0.006935
SNORD104	STK32C	0.352	0.006935
SNORD104	PTGES2	0.352	0.006935
SNORD104	UQCC3	0.353	0.006771
SNORD104	RSAD1	0.353	0.006771
SNORD104	TYSND1	0.353	0.006771
SNORD104	EIF2B4	0.354	0.006611
SNORD104	PCED1A	0.354	0.006611
SNORD104	RHOT2	0.355	0.006454
SNORD104	SNRNP35	0.356	0.0063
SNORD104	METTL23	0.356	0.0063
SNORD104	SLC25A28	0.357	0.00615
SNORD104	POP5	0.357	0.00615
SNORD104	HSF4	0.357	0.00615
SNORD104	ARL6IP4	0.358	0.006003
SNORD104	ACBD4	0.358	0.006003
SNORD104	HEXDC	0.36	0.005718
SNORD104	PET100	0.36	0.005718
SNORD104	FKBP2	0.361	0.00558
SNORD104	PIN1	0.361	0.00558
SNORD104	CBX8	0.361	0.00558
SNORD104	EDF1	0.362	0.005446
SNORD104	ZNF580	0.362	0.005446
SNORD104	ATPIF1	0.362	0.005446
SNORD104	ODF3B	0.362	0.005446
SNORD104	ITPA	0.363	0.005314
SNORD104	H1FX	0.363	0.005314

SNORD104	TEPSIN	0.363	0.005314
SNORD104	DECR2	0.364	0.005185
SNORD104	ADCK5	0.364	0.005185
SNORD104	RPP21	0.364	0.005185
SNORD104	DCXR	0.365	0.005059
SNORD104	NOXA1	0.365	0.005059
SNORD104	ZNF513	0.365	0.005059
SNORD104	E4F1	0.366	0.004936
SNORD104	MRPL12	0.366	0.004936
SNORD104	MRPS21	0.366	0.004936
SNORD104	ABHD17A	0.366	0.004936
SNORD104	CCDC159	0.367	0.004815
SNORD104	C1orf35	0.367	0.004815
SNORD104	KAT2A	0.369	0.004582
SNORD104	FDX2	0.37	0.004469
SNORD104	C17orf62	0.37	0.004469
SNORD104	NME3	0.37	0.004469
SNORD104	COMMD4	0.371	0.004359
SNORD104	RRNAD1	0.372	0.004251
SNORD104	C9orf172	0.372	0.004251
SNORD104	LRRC45	0.373	0.004146
SNORD104	TAZ	0.373	0.004146
SNORD104	CDK5RAP3	0.373	0.004146
SNORD104	ZNF692	0.374	0.004043
SNORD104	GLI4	0.374	0.004043
SNORD104	CCDC183	0.374	0.004043
SNORD104	HDAC10	0.377	0.003748
SNORD104	TRABD	0.377	0.003748
SNORD104	CDK5RAP1	0.379	0.003563
SNORD104	TMEM259	0.379	0.003563
SNORD104	MSH5-SAPCD1	0.379	0.003563
SNORD104	TP53I13	0.381	0.003385
SNORD104	MZT2B	0.382	0.0033
SNORD104	METTL26	0.384	0.003135
SNORD104	NDUFAF8	0.384	0.003135
SNORD104	MCRIP2	0.388	0.002826
SNORD104	SCAND1	0.393	0.00248
SNORD104	DUS1L	0.395	0.002353
SNORD104	RPS28	0.398	0.002173
SNORD104	KRTCAP2	0.4	0.002061
SNORD104	ZNF414	0.406	0.001754
SNORD104	PPP1R35	0.407	0.001707
SNORD104	SELENOO	0.408	0.001661
SNORD104	ACADVL	0.408	0.001661

SNORD104	RFNG	0.411	0.001531
SNORD104	MRPL38	0.413	0.001449
SNORD104	POLL	0.413	0.001449
SNORD104	TSEN54	0.414	0.00141
SNORD104	COMTD1	0.417	0.001298
SNORD104	FBXL15	0.418	0.001262
SNORD104	MRPS26	0.432	0.000851
SNORD104	CCS	0.436	0.000759
SNORD104	WDR83	0.44	0.000676
SNORD104	NAT9	0.442	0.000638
SNORD104	QTRT1	0.452	0.000475
SNORD104	ASPSCR1	0.453	0.000461
SNORD104	C9orf142	0.457	0.000409
SNORD104	NT5C	0.462	0.000352
SNORD104	C19orf60	0.492	0.000138
SNORD104	OXLD1	0.495	0.000125
SNORD104	SNORD104	1	4.19E-15
snoU109	RBM5	-0.364	0.000316
snoU109	NKTR	-0.352	0.000497
snoU109	MDM4	-0.345	0.000643
snoU109	AHSA2	-0.342	0.000717
snoU109	MSS51	-0.34	0.000771
snoU109	GOLGA8B	-0.337	0.000859
snoU109	SRSF5	-0.337	0.000859
snoU109	RBM6	-0.336	0.00089
snoU109	N4BP2L2	-0.335	0.000923
snoU109	LUC7L3	-0.334	0.000956
snoU109	GNRH1	-0.331	0.001063
snoU109	ANKRD23	-0.322	0.001454
snoU109	MZF1	-0.322	0.001454
snoU109	KIAA0907	-0.321	0.001505
snoU109	UBAP1L	-0.32	0.001557
snoU109	CRYGS	-0.32	0.001557
snoU109	C8orf44	-0.317	0.001725
snoU109	POLI	-0.316	0.001784
snoU109	ARGLU1	-0.315	0.001846
snoU109	AGAP6	-0.314	0.001909
snoU109	DDX39B	-0.314	0.001909
snoU109	TIA1	-0.313	0.001974
snoU109	CSAD	-0.311	0.002111
snoU109	ZNF169	-0.31	0.002182
snoU109	ELMOD3	-0.31	0.002182
snoU109	GPS2	-0.309	0.002256
snoU109	CLK1	-0.309	0.002256

snoU109	AC022400.6	-0.309	0.002256
snoU109	PCF11	-0.307	0.00241
snoU109	C3orf35	-0.305	0.002574
snoU109	JMJD7-PLA2G4B	-0.305	0.002574
snoU109	ZNF276	-0.304	0.00266
snoU109	PAN2	-0.304	0.00266
snoU109	FNBP4	-0.304	0.00266
snoU109	CBWD3	-0.304	0.00266
snoU109	CHKB	-0.304	0.00266
snoU109	FAM193B	-0.304	0.00266
snoU109	CCDC66	-0.303	0.002749
snoU109	HNRNPDL	-0.303	0.002749
snoU109	TRIM52	-0.302	0.00284
snoU109	TRIM66	-0.301	0.002933
snoU109	CCNL2	-0.3	0.00303
snoU109	PIGL	-0.299	0.003129
snoU109	DDX5	-0.299	0.003129
snoU109	PDE6C	-0.299	0.003129
snoU109	TTLL3	-0.298	0.003232
snoU109	APBB3	-0.296	0.003446
snoU109	PNISR	-0.294	0.003673
snoU109	VAMP1	-0.294	0.003673
snoU109	TUBGCP6	-0.294	0.003673
snoU109	CDK3	-0.293	0.003792
snoU109	DFNB59	-0.293	0.003792
snoU109	ERICH6B	-0.292	0.003914
snoU109	L3MBTL1	-0.292	0.003914
snoU109	HMBOX1	-0.291	0.004039
snoU109	HYPK	-0.291	0.004039
snoU109	NISCH	-0.291	0.004039
snoU109	CATSPER2	-0.291	0.004039
snoU109	MAN2C1	-0.291	0.004039
snoU109	TTC14	-0.291	0.004039
snoU109	HNRNPH1	-0.29	0.004169
snoU109	DDX17	-0.289	0.004302
snoU109	ZNF692	-0.289	0.004302
snoU109	NEIL1	-0.289	0.004302
snoU109	RSRP1	-0.288	0.004438
snoU109	CLHC1	-0.288	0.004438
snoU109	GOLGA8N	-0.288	0.004438
snoU109	SEC31B	-0.288	0.004438
snoU109	ZNF589	-0.287	0.004579
snoU109	LY6G5B	-0.286	0.004724
snoU109	C6orf163	-0.285	0.004873

snoU109	LENG8	-0.285	0.004873
snoU109	TARBP1	-0.284	0.005026
snoU109	LINC01125	-0.283	0.005183
snoU109	AC023509.3	-0.283	0.005183
snoU109	ENOSF1	-0.282	0.005345
snoU109	SNRNP70	-0.282	0.005345
snoU109	KCNIP2	-0.282	0.005345
snoU109	EPM2AIP1	-0.282	0.005345
snoU109	TEPSIN	-0.281	0.005512
snoU109	KIAA0895L	-0.281	0.005512
snoU109	CDK5RAP3	-0.281	0.005512
snoU109	HEMK1	-0.281	0.005512
snoU109	SUGP2	-0.28	0.005683
snoU109	TSSK3	-0.28	0.005683
snoU109	WDR27	-0.28	0.005683
snoU109	CDRT4	-0.278	0.006039
snoU109	ATG16L2	-0.278	0.006039
snoU109	ENGASE	-0.277	0.006225
snoU109	FAM229A	-0.277	0.006225
snoU109	ZNF852	-0.277	0.006225
snoU109	PCED1A	-0.277	0.006225
snoU109	PLXNB1	-0.277	0.006225
snoU109	IP6K2	-0.276	0.006416
snoU109	CBWD6	-0.276	0.006416
snoU109	NPHP3	-0.276	0.006416
snoU109	ZNF354B	-0.275	0.006612
snoU109	TAF1C	-0.275	0.006612
snoU109	TEN1-CDK3	-0.274	0.006814
snoU109	ADAT2	-0.274	0.006814
snoU109	APO01931.1	-0.273	0.007021
snoU109	CPT1B	-0.272	0.007233
snoU109	RGL4	-0.272	0.007233
snoU109	PRPF39	-0.272	0.007233
snoU109	ZNF514	-0.271	0.007452
snoU109	RBM25	-0.27	0.007676
snoU109	STK36	-0.27	0.007676
snoU109	ZNF10	-0.27	0.007676
snoU109	MTG1	-0.269	0.007907
snoU109	MASP2	-0.269	0.007907
snoU109	SPRN	-0.269	0.007907
snoU109	CFAP44	-0.269	0.007907
snoU109	NXF1	-0.268	0.008143
snoU109	CARF	-0.268	0.008143
snoU109	ASB14	-0.268	0.008143

snoU109	ACCS	-0.267	0.008386
snoU109	DCAF8	-0.267	0.008386
snoU109	D2HGDH	-0.267	0.008386
snoU109	C5orf63	-0.266	0.008635
snoU109	BBS1	-0.266	0.008635
snoU109	ZNF224	-0.266	0.008635
snoU109	CDK10	-0.266	0.008635
snoU109	GOLGA6L9	-0.265	0.008891
snoU109	PP2D1	-0.265	0.008891
snoU109	EIF4A1	-0.265	0.008891
snoU109	FAM217A	-0.265	0.008891
snoU109	ZNF248	-0.265	0.008891
snoU109	ZNF587	-0.264	0.009154
snoU109	NADSYN1	-0.264	0.009154
snoU109	DUSP28	-0.264	0.009154
snoU109	PHYKPL	-0.264	0.009154
snoU109	RBM39	-0.264	0.009154
snoU109	PAXBP1	-0.262	0.0097
snoU109	MTERF2	-0.262	0.0097
snoU109	AKAP17A	-0.262	0.0097
snoU109	CLK2	-0.262	0.0097
snoU109	AC090004.1	-0.262	0.0097
snoU109	CCNL1	-0.262	0.0097
snoU109	PPP6R2	-0.261	0.009984
snoU109	C3orf62	-0.261	0.009984
snoU109	SENP7	-0.261	0.009984
snoU109	ZRANB2	-0.261	0.009984
snoU109	ZNF662	-0.261	0.009984
snoU109	TRMT10B	-0.261	0.009984
snoU109	AC011511.1	-0.26	0.010275
snoU109	TAS2R10	-0.26	0.010275
snoU109	DMTF1	-0.26	0.010275
snoU109	CYP2R1	-0.26	0.010275
snoU109	NR2C2	-0.26	0.010275
snoU109	LHX4	-0.259	0.010574
snoU109	RGL3	-0.259	0.010574
snoU109	LINCO0854	-0.259	0.010574
snoU109	ECHDC2	-0.258	0.010881
snoU109	AC020915.1	-0.258	0.010881
snoU109	CCDC84	-0.258	0.010881
snoU109	SLC25A27	-0.258	0.010881
snoU109	EBLN2	-0.258	0.010881
snoU109	MAT2A	-0.258	0.010881
snoU109	CIRBP	-0.257	0.011195

snoU109	ING5	-0.257	0.011195
snoU109	LRRC39	-0.257	0.011195
snoU109	INTS6L	-0.257	0.011195
snoU109	AARSD1	-0.257	0.011195
snoU109	PLA2G6	-0.256	0.011517
snoU109	ZNF814	-0.256	0.011517
snoU109	CEP95	-0.256	0.011517
snoU109	AGAP5	-0.256	0.011517
snoU109	PABPC1L	-0.256	0.011517
snoU109	WASHC1	-0.255	0.011848
snoU109	AGAP9	-0.255	0.011848
snoU109	REV1	-0.253	0.012534
snoU109	ANKZF1	-0.253	0.012534
snoU109	EDRF1	-0.253	0.012534
snoU109	MATR3	-0.252	0.012891
snoU109	CCDC14	-0.252	0.012891
snoU109	ASB16	-0.252	0.012891
snoU109	ZNF33A	-0.252	0.012891
snoU109	SAPCD1	-0.251	0.013256
snoU109	GCNT7	-0.251	0.013256
snoU109	CHKB-CPT1B	-0.251	0.013256
snoU109	ZGLP1	-0.251	0.013256
snoU109	PIDD1	-0.251	0.013256
snoU109	MSH5	-0.25	0.01363
snoU109	LIME1	-0.25	0.01363
snoU109	ABCA5	-0.25	0.01363
snoU109	ZNF546	-0.25	0.01363
snoU109	CLASRP	-0.25	0.01363
snoU109	LBHD1	-0.25	0.01363
snoU109	LUC7L	-0.249	0.014014
snoU109	OGT	-0.249	0.014014
snoU109	KLHDC4	-0.249	0.014014
snoU109	DNAH1	-0.249	0.014014
snoU109	UCP3	-0.248	0.014407
snoU109	ZBTB40	-0.248	0.014407
snoU109	RBM14-RBM4	-0.248	0.014407
snoU109	GDF9	-0.248	0.014407
snoU109	CAPN10	-0.248	0.014407
snoU109	LMNTD2	-0.247	0.01481
snoU109	SRSF11	-0.247	0.01481
snoU109	AMT	-0.247	0.01481
snoU109	SETD4	-0.247	0.01481
snoU109	SFI1	-0.247	0.01481
snoU109	CLK4	-0.247	0.01481

snoU109	AP003108.2	-0.247	0.01481
snoU109	NPEPL1	-0.247	0.01481
snoU109	ZNF23	-0.246	0.015223
snoU109	BRICD5	-0.246	0.015223
snoU109	ZNF444	-0.246	0.015223
snoU109	MYL5	-0.246	0.015223
snoU109	NEURL4	-0.246	0.015223
snoU109	EP400NL	-0.245	0.015646
snoU109	EME2	-0.245	0.015646
snoU109	BGLAP	-0.245	0.015646
snoU109	ZBTB37	-0.245	0.015646
snoU109	ACSF3	-0.245	0.015646
snoU109	ZBTB25	-0.244	0.016079
snoU109	MAMDC4	-0.244	0.016079
snoU109	ACO09690.1	-0.244	0.016079
snoU109	SPATA1	-0.244	0.016079
snoU109	NICN1	-0.244	0.016079
snoU109	GLI4	-0.244	0.016079
snoU109	WDR73	-0.244	0.016079
snoU109	MYSM1	-0.243	0.016522
snoU109	AL353588.1	-0.243	0.016522
snoU109	LMBR1L	-0.243	0.016522
snoU109	TSSK4	-0.243	0.016522
snoU109	HDAC10	-0.243	0.016522
snoU109	TMEM110-	-0.243	0.016522
	MUSTN1		
snoU109	EZH1	-0.242	0.016977
snoU109	METTL17	-0.242	0.016977
snoU109	EXD3	-0.242	0.016977
snoU109	SRSF6	-0.242	0.016977
snoU109	ZNF700	-0.241	0.017442
snoU109	FAM186A	-0.241	0.017442
snoU109	NBEAL2	-0.241	0.017442
snoU109	SPDYA	-0.241	0.017442
snoU109	JMJD7	-0.24	0.017919
snoU109	ZNF345	-0.24	0.017919
snoU109	RNF207	-0.24	0.017919
snoU109	KLC1	-0.24	0.017919
snoU109	ACBD4	-0.239	0.018406
snoU109	SGSM2	-0.239	0.018406
snoU109	ZFC3H1	-0.239	0.018406
snoU109	SPATA6L	-0.239	0.018406
snoU109	ARIH2OS	-0.239	0.018406
snoU109	GABPB2	-0.239	0.018406

snoU109	ZNF333	-0.239	0.018406
snoU109	PAN3	-0.238	0.018906
snoU109	HEXDC	-0.238	0.018906
snoU109	VCPKMT	-0.238	0.018906
snoU109	ANKAR	-0.238	0.018906
snoU109	PPOX	-0.238	0.018906
snoU109	SLC25A34	-0.237	0.019417
snoU109	C1orf100	-0.237	0.019417
snoU109	STX16-NPEPL1	-0.237	0.019417
snoU109	TCTE3	-0.237	0.019417
snoU109	MRPS25	-0.237	0.019417
snoU109	POLG2	-0.237	0.019417
snoU109	ZNF337	-0.237	0.019417
snoU109	ZNF621	-0.237	0.019417
snoU109	ACO06254.1	-0.237	0.019417
snoU109	ATAT1	-0.236	0.01994
snoU109	GOLGA6L10	-0.236	0.01994
snoU109	RSAD1	-0.236	0.01994
snoU109	PLA2G4B	-0.236	0.01994
snoU109	SETDB2	-0.236	0.01994
snoU109	TMEM262	-0.235	0.020476
snoU109	CCDC130	-0.235	0.020476
snoU109	CCNT2	-0.235	0.020476
snoU109	AL136295.4	-0.235	0.020476
snoU109	NOXA1	-0.235	0.020476
snoU109	ARPC4-TTLL3	-0.235	0.020476
snoU109	AL133352.1	-0.234	0.021024
snoU109	MRNIP	-0.234	0.021024
snoU109	ANO9	-0.234	0.021024
snoU109	PTCH2	-0.233	0.021584
snoU109	FBXW12	-0.233	0.021584
snoU109	NPIPA1	-0.232	0.022158
snoU109	KRTAP5-1	-0.232	0.022158
snoU109	TIGD1	-0.232	0.022158
snoU109	AC096887.1	-0.232	0.022158
snoU109	ZNF782	-0.232	0.022158
snoU109	C6orf201	-0.232	0.022158
snoU109	RPAIN	-0.232	0.022158
snoU109	UVSSA	-0.231	0.022745
snoU109	DDX47	-0.231	0.022745
snoU109	BTAF1	-0.23	0.023345
snoU109	ANKMY1	-0.23	0.023345
snoU109	SAP25	-0.23	0.023345
snoU109	ZNF7	-0.23	0.023345

snoU109	TRMU	-0.23	0.023345
snoU109	BRD8	-0.229	0.02396
snoU109	CORT	-0.229	0.02396
snoU109	ZNF513	-0.229	0.02396
snoU109	FAM47E	-0.228	0.024588
snoU109	COL27A1	-0.228	0.024588
snoU109	KAT2A	-0.228	0.024588
snoU109	MUSTN1	-0.228	0.024588
snoU109	WSB1	-0.227	0.02523
snoU109	AGAP4	-0.227	0.02523
snoU109	TADA2A	-0.227	0.02523
snoU109	CHMP4A	-0.227	0.02523
snoU109	U2AF1L4	-0.226	0.025887
snoU109	SGK494	-0.226	0.025887
snoU109	ANKHD1	-0.226	0.025887
snoU109	SPTY2D1-AS1	-0.226	0.025887
snoU109	CDK11A	-0.226	0.025887
snoU109	PRR25	-0.225	0.026558
snoU109	ALKBH6	-0.225	0.026558
snoU109	MSH5-SAPCD1	-0.225	0.026558
snoU109	NUDT13	-0.225	0.026558
snoU109	LRP5L	-0.225	0.026558
snoU109	RTEL1- TNFRSF6B	-0.225	0.026558
snoU109	ZNF517	-0.224	0.027245
snoU109	PKD2L2	-0.224	0.027245
snoU109	GTF2IRD2	-0.224	0.027245
snoU109	CC2D2B	-0.224	0.027245
snoU109	ANKS3	-0.223	0.027946
snoU109	P4HTM	-0.223	0.027946
snoU109	AL121594.3	-0.223	0.027946
snoU109	PGBD4	-0.223	0.027946
snoU109	SLC9C1	-0.223	0.027946
snoU109	INO80B	-0.223	0.027946
snoU109	NAA16	-0.223	0.027946
snoU109	CRTC1	-0.223	0.027946
snoU109	ZNF83	-0.223	0.027946
snoU109	OFD1	-0.222	0.028664
snoU109	ZNF133	-0.222	0.028664
snoU109	TRPV1	-0.222	0.028664
snoU109	GGA1	-0.222	0.028664
snoU109	C20orf96	-0.222	0.028664
snoU109	MRPL38	-0.222	0.028664
snoU109	GABRR2	-0.222	0.028664

snoU109	SLC25A45	-0.222	0.028664
snoU109	TIAF1	-0.222	0.028664
snoU109	ZNF580	-0.222	0.028664
snoU109	CTC1	-0.221	0.029397
snoU109	GATD1	-0.221	0.029397
snoU109	TVP23C	-0.221	0.029397
snoU109	AC009119.2	-0.221	0.029397
snoU109	ABCA10	-0.221	0.029397
snoU109	C5orf56	-0.221	0.029397
snoU109	ANKRD61	-0.221	0.029397
snoU109	CALCOCO1	-0.221	0.029397
snoU109	ANKHD1- EIF4EBP3	-0.22	0.030146
snoU109	TAS2R20	-0.22	0.030146
snoU109	NFKBID	-0.22	0.030146
snoU109	ZBTB3	-0.22	0.030146
snoU109	CES4A	-0.22	0.030146
snoU109	MBTD1	-0.22	0.030146
snoU109	OR10AD1	-0.22	0.030146
snoU109	KLHL17	-0.219	0.030911
snoU109	ZNF785	-0.219	0.030911
snoU109	FGFR10P	-0.219	0.030911
snoU109	GNG3	-0.219	0.030911
snoU109	FBXL8	-0.219	0.030911
snoU109	SPG7	-0.219	0.030911
snoU109	HSF4	-0.219	0.030911
snoU109	ZBTB48	-0.219	0.030911
snoU109	DNAJC27	-0.218	0.031693
snoU109	PGS1	-0.218	0.031693
snoU109	CEP83	-0.218	0.031693
snoU109	STRADA	-0.218	0.031693
snoU109	EPOR	-0.218	0.031693
snoU109	RBM33	-0.218	0.031693
snoU109	SCRN2	-0.218	0.031693
snoU109	MYH7B	-0.217	0.032492
snoU109	CXorf65	-0.217	0.032492
snoU109	MICAL1	-0.217	0.032492
snoU109	CARD8	-0.217	0.032492
snoU109	NIPSNAP3B	-0.217	0.032492
snoU109	NOL12	-0.217	0.032492
snoU109	NEK8	-0.216	0.033309
snoU109	AC244197.3	-0.216	0.033309
snoU109	ARHGAP8	-0.216	0.033309
snoU109	ZNF594	-0.216	0.033309

snoU109	LAT	-0.216	0.033309
snoU109	SPATA25	-0.216	0.033309
snoU109	U2AF1L5	-0.216	0.033309
snoU109	IRF9	-0.215	0.034142
snoU109	SDR39U1	-0.215	0.034142
snoU109	HEXIM2	-0.215	0.034142
snoU109	BORCS8	-0.215	0.034142
snoU109	KLHDC1	-0.215	0.034142
snoU109	ANKDD1A	-0.215	0.034142
snoU109	CENPT	-0.215	0.034142
snoU109	ATG4B	-0.215	0.034142
snoU109	WDR92	-0.215	0.034142
snoU109	FAM186B	-0.215	0.034142
snoU109	KMT5C	-0.215	0.034142
snoU109	ANAPC4	-0.215	0.034142
snoU109	ZBED5	-0.214	0.034994
snoU109	ULK3	-0.214	0.034994
snoU109	WDR6	-0.214	0.034994
snoU109	AL365205.1	-0.214	0.034994
snoU109	CUL9	-0.214	0.034994
snoU109	PTBP2	-0.214	0.034994
snoU109	INCA1	-0.214	0.034994
snoU109	OSBPL7	-0.213	0.035863
snoU109	AC040162.1	-0.213	0.035863
snoU109	SCART1	-0.213	0.035863
snoU109	NDST2	-0.213	0.035863
snoU109	ZNF789	-0.213	0.035863
snoU109	PCBD2	-0.213	0.035863
snoU109	SPDYE1	-0.213	0.035863
snoU109	ARL17A	-0.212	0.036751
snoU109	UBXN11	-0.212	0.036751
snoU109	CXXC1	-0.212	0.036751
snoU109	AD000671.2	-0.212	0.036751
snoU109	FITM1	-0.212	0.036751
snoU109	METTL3	-0.211	0.037658
snoU109	FAM209A	-0.211	0.037658
snoU109	CRIPAK	-0.211	0.037658
snoU109	WBP1	-0.211	0.037658
snoU109	RAPSN	-0.211	0.037658
snoU109	CLEC2D	-0.211	0.037658
snoU109	CENPC	-0.211	0.037658
snoU109	GPR61	-0.211	0.037658
snoU109	OTUD3	-0.211	0.037658
snoU109	ACADVL	-0.211	0.037658

snoU109	ADAMTS13	-0.211	0.037658
snoU109	KCNAB3	-0.21	0.038583
snoU109	INTU	-0.21	0.038583
snoU109	RECQL5	-0.21	0.038583
snoU109	CCDC57	-0.21	0.038583
snoU109	ZC3H12D	-0.21	0.038583
snoU109	ZFYVE27	-0.21	0.038583
snoU109	ZNF195	-0.21	0.038583
snoU109	HEATR9	-0.21	0.038583
snoU109	RC3H1	-0.21	0.038583
snoU109	DENND4B	-0.21	0.038583
snoU109	RNPC3	-0.209	0.039528
snoU109	GOLGA8A	-0.209	0.039528
snoU109	ZNF182	-0.209	0.039528
snoU109	LRRC14	-0.209	0.039528
snoU109	TRAF5	-0.209	0.039528
snoU109	TSPOAP1	-0.209	0.039528
snoU109	SLC2A11	-0.209	0.039528
snoU109	SPIN3	-0.209	0.039528
snoU109	ZNF236	-0.209	0.039528
snoU109	AC072022.1	-0.208	0.040492
snoU109	ZNF8	-0.208	0.040492
snoU109	ZNF226	-0.208	0.040492
snoU109	NDUFAF7	-0.208	0.040492
snoU109	PICK1	-0.208	0.040492
snoU109	MRPL53	-0.208	0.040492
snoU109	CYHR1	-0.208	0.040492
snoU109	AC068896.1	-0.208	0.040492
snoU109	SPPL2B	-0.208	0.040492
snoU109	IL11RA	-0.208	0.040492
snoU109	NSMCE4A	-0.207	0.041476
snoU109	ITGB1BP2	-0.207	0.041476
snoU109	MRI1	-0.207	0.041476
snoU109	KRTAP5-9	-0.207	0.041476
snoU109	CCDC188	-0.207	0.041476
snoU109	SLC35E2	-0.207	0.041476
snoU109	PLGLB1	-0.206	0.042481
snoU109	ACAP3	-0.206	0.042481
snoU109	AKAP8L	-0.206	0.042481
snoU109	ZNF251	-0.206	0.042481
snoU109	LRRC27	-0.206	0.042481
snoU109	ZNF540	-0.206	0.042481
snoU109	CLK3	-0.206	0.042481
snoU109	SPACA6	-0.206	0.042481

snoU109	DIP2A	-0.206	0.042481
snoU109	AP1G2	-0.206	0.042481
snoU109	KIFC2	-0.206	0.042481
snoU109	ZNF91	-0.206	0.042481
snoU109	PRCD	-0.205	0.043505
snoU109	USPL1	-0.205	0.043505
snoU109	PRPF4B	-0.205	0.043505
snoU109	ODF3B	-0.205	0.043505
snoU109	VPS13A	-0.204	0.044551
snoU109	CCER2	-0.204	0.044551
snoU109	ZNF446	-0.204	0.044551
snoU109	VMAC	-0.204	0.044551
snoU109	SPACA4	-0.204	0.044551
snoU109	PGGHG	-0.204	0.044551
snoU109	ZNF44	-0.204	0.044551
snoU109	LRIT3	-0.204	0.044551
snoU109	WDR90	-0.203	0.045618
snoU109	ADCK5	-0.203	0.045618
snoU109	AC005726.2	-0.203	0.045618
snoU109	SRSF2	-0.203	0.045618
snoU109	AC012651.1	-0.203	0.045618
snoU109	C19orf18	-0.203	0.045618
snoU109	FAM160B2	-0.203	0.045618
snoU109	CLDN20	-0.202	0.046706
snoU109	ACAD11	-0.202	0.046706
snoU109	NBPF12	-0.202	0.046706
snoU109	CHRNA10	-0.202	0.046706
snoU109	DOPEY1	-0.202	0.046706
snoU109	NPIP4	-0.202	0.046706
snoU109	ESR2	-0.202	0.046706
snoU109	TRABD	-0.202	0.046706
snoU109	ZMAT1	-0.202	0.046706
snoU109	SPDYE5	-0.202	0.046706
snoU109	CTRL	-0.201	0.047816
snoU109	CELF6	-0.201	0.047816
snoU109	MAPK15	-0.201	0.047816
snoU109	NOXRED1	-0.201	0.047816
snoU109	POLL	-0.201	0.047816
snoU109	STX16	-0.201	0.047816
snoU109	OR5K2	-0.201	0.047816
snoU109	NR2C1	-0.2	0.048948
snoU109	SLC25A16	-0.2	0.048948
snoU109	CREBZF	-0.2	0.048948
snoU109	AC055811.2	-0.2	0.048948

snoU109	IBA57	-0.2	0.048948
snoU109	ZFP3	-0.2	0.048948
snoU109	TIMP3	0.2	0.044061
snoU109	PAQR7	0.2	0.044061
snoU109	CDC42	0.2	0.044061
snoU109	TUBB6	0.2	0.044061
snoU109	EMP3	0.2	0.044061
snoU109	KIRREL	0.2	0.044061
snoU109	RAB10	0.2	0.044061
snoU109	UBE2Z	0.2	0.044061
snoU109	DDB1	0.2	0.044061
snoU109	COL5A1	0.201	0.043025
snoU109	GNG12	0.201	0.043025
snoU109	CARHSP1	0.201	0.043025
snoU109	BAG5	0.201	0.043025
snoU109	SPDYE3	0.201	0.043025
snoU109	PRPS1	0.202	0.04201
snoU109	GPAT3	0.202	0.04201
snoU109	UBC	0.202	0.04201
snoU109	NEK6	0.202	0.04201
snoU109	EIF2S2	0.202	0.04201
snoU109	SEMA3A	0.202	0.04201
snoU109	SPTLC1	0.202	0.04201
snoU109	CAST	0.202	0.04201
snoU109	LRRC8E	0.202	0.04201
snoU109	CDH11	0.203	0.041015
snoU109	PRR11	0.203	0.041015
snoU109	DCTN5	0.203	0.041015
snoU109	FAM83D	0.203	0.041015
snoU109	CTSB	0.203	0.041015
snoU109	DRAP1	0.203	0.041015
snoU109	PINK1	0.203	0.041015
snoU109	FGF1	0.203	0.041015
snoU109	THY1	0.203	0.041015
snoU109	IRS1	0.203	0.041015
snoU109	PHF13	0.203	0.041015
snoU109	PBX3	0.203	0.041015
snoU109	PYGL	0.204	0.04004
snoU109	ZFAND3	0.204	0.04004
snoU109	KDELC2	0.204	0.04004
snoU109	CTHRC1	0.204	0.04004
snoU109	ASAP1	0.204	0.04004
snoU109	MAP7D3	0.204	0.04004
snoU109	RTCA	0.204	0.04004

snoU109	AGPAT1	0.205	0.039085
snoU109	MMP3	0.205	0.039085
snoU109	RNF4	0.205	0.039085
snoU109	OSTM1	0.205	0.039085
snoU109	PATL1	0.205	0.039085
snoU109	SFRP2	0.205	0.039085
snoU109	ZFP91	0.205	0.039085
snoU109	ACTN4	0.205	0.039085
snoU109	CD70	0.205	0.039085
snoU109	RWDD1	0.205	0.039085
snoU109	LYAR	0.205	0.039085
snoU109	ENO1	0.205	0.039085
snoU109	YWHAH	0.205	0.039085
snoU109	ORC3	0.205	0.039085
snoU109	RBMS1	0.206	0.038149
snoU109	STK17A	0.206	0.038149
snoU109	TMEM159	0.206	0.038149
snoU109	ATG5	0.206	0.038149
snoU109	LAMC2	0.206	0.038149
snoU109	TNFAIP1	0.206	0.038149
snoU109	LUZP1	0.206	0.038149
snoU109	ULBP2	0.206	0.038149
snoU109	MICB	0.207	0.037233
snoU109	EI24	0.207	0.037233
snoU109	TMEM196	0.207	0.037233
snoU109	ACTN1	0.207	0.037233
snoU109	CHMP2B	0.207	0.037233
snoU109	GPR1	0.207	0.037233
snoU109	ANTXR1	0.208	0.036335
snoU109	FAP	0.208	0.036335
snoU109	VGLL4	0.208	0.036335
snoU109	AZIN1	0.208	0.036335
snoU109	ZDHHC5	0.208	0.036335
snoU109	SMARCAL1	0.208	0.036335
snoU109	ADAM17	0.208	0.036335
snoU109	CLIC1	0.209	0.035456
snoU109	TMEM50A	0.209	0.035456
snoU109	ARCN1	0.209	0.035456
snoU109	PRRG4	0.209	0.035456
snoU109	TRIM4	0.209	0.035456
snoU109	AIG1	0.209	0.035456
snoU109	GNA12	0.209	0.035456
snoU109	RAB32	0.209	0.035456
snoU109	SLC2A1	0.21	0.034594

snoU109	COL5A2	0.21	0.034594
snoU109	TCF19	0.21	0.034594
snoU109	EDIL3	0.21	0.034594
snoU109	SND1	0.21	0.034594
snoU109	TACSTD2	0.21	0.034594
snoU109	COL11A1	0.21	0.034594
snoU109	TMEM184C	0.211	0.033751
snoU109	C7orf49	0.211	0.033751
snoU109	DIAPH1	0.211	0.033751
snoU109	CHRM2	0.211	0.033751
snoU109	TMEM185A	0.211	0.033751
snoU109	LINC00998	0.211	0.033751
snoU109	TTC4	0.211	0.033751
snoU109	ZNF185	0.211	0.033751
snoU109	UBE2C	0.212	0.032926
snoU109	FN1	0.212	0.032926
snoU109	MID2	0.212	0.032926
snoU109	LYPD3	0.212	0.032926
snoU109	SETD7	0.212	0.032926
snoU109	CEP41	0.213	0.032118
snoU109	TMEM158	0.213	0.032118
snoU109	CASP2	0.213	0.032118
snoU109	SLC44A1	0.213	0.032118
snoU109	NRBF2	0.213	0.032118
snoU109	CD44	0.213	0.032118
snoU109	KPNA3	0.213	0.032118
snoU109	COL8A2	0.214	0.031327
snoU109	ARSI	0.214	0.031327
snoU109	CYP51A1	0.214	0.031327
snoU109	RAB14	0.214	0.031327
snoU109	TAF5L	0.214	0.031327
snoU109	CUL4B	0.215	0.030552
snoU109	FAM26E	0.215	0.030552
snoU109	SNX3	0.216	0.029794
snoU109	STYXL1	0.216	0.029794
snoU109	GJA5	0.216	0.029794
snoU109	ABCE1	0.216	0.029794
snoU109	CTNNAL1	0.216	0.029794
snoU109	NCS1	0.216	0.029794
snoU109	PSMD2	0.216	0.029794
snoU109	IGF2BP2	0.216	0.029794
snoU109	TMBIM1	0.216	0.029794
snoU109	VTA1	0.216	0.029794
snoU109	SOAT1	0.217	0.029053

snoU109	SH3GL1	0.217	0.029053
snoU109	SLC35E1	0.217	0.029053
snoU109	FIS1	0.217	0.029053
snoU109	PTBP3	0.217	0.029053
snoU109	SLC35F6	0.217	0.029053
snoU109	HYAL4	0.217	0.029053
snoU109	CAMK2N1	0.217	0.029053
snoU109	CDC27	0.217	0.029053
snoU109	XPO6	0.217	0.029053
snoU109	SUMO3	0.217	0.029053
snoU109	GPR107	0.217	0.029053
snoU109	CARM1	0.217	0.029053
snoU109	TMEM140	0.218	0.028327
snoU109	CD40	0.218	0.028327
snoU109	AL355102.2	0.218	0.028327
snoU109	MET	0.218	0.028327
snoU109	LOX	0.218	0.028327
snoU109	RAB9A	0.219	0.027617
snoU109	CPA2	0.219	0.027617
snoU109	LRP12	0.219	0.027617
snoU109	SURF4	0.219	0.027617
snoU109	KLHL5	0.22	0.026923
snoU109	RASAL2	0.22	0.026923
snoU109	CFL1	0.22	0.026923
snoU109	SNX7	0.22	0.026923
snoU109	GJC1	0.22	0.026923
snoU109	FNDC3B	0.22	0.026923
snoU109	TPST1	0.22	0.026923
snoU109	HTATSF1	0.22	0.026923
snoU109	COL3A1	0.22	0.026923
snoU109	HBP1	0.221	0.026243
snoU109	CNNM4	0.221	0.026243
snoU109	COL1A2	0.221	0.026243
snoU109	CERCAM	0.221	0.026243
snoU109	NCEH1	0.221	0.026243
snoU109	RBM18	0.221	0.026243
snoU109	BCAR3	0.221	0.026243
snoU109	PIM1	0.222	0.025579
snoU109	JPT2	0.222	0.025579
snoU109	THBS2	0.222	0.025579
snoU109	CNN3	0.222	0.025579
snoU109	ERLIN1	0.222	0.025579
snoU109	ADAMTS12	0.222	0.025579
snoU109	CCNK	0.222	0.025579

snoU109	UBE2L5P	0.222	0.025579
snoU109	ARHGAP10	0.222	0.025579
snoU109	WDFY1	0.222	0.025579
snoU109	TMEM250	0.223	0.024929
snoU109	RHOC	0.223	0.024929
snoU109	COL10A1	0.223	0.024929
snoU109	TUBA1B	0.224	0.024293
snoU109	EIF5A2	0.224	0.024293
snoU109	FAS	0.224	0.024293
snoU109	PTTG1IP	0.224	0.024293
snoU109	PEA15	0.224	0.024293
snoU109	SRRD	0.224	0.024293
snoU109	VKORC1L1	0.225	0.023672
snoU109	TMEM41A	0.226	0.023064
snoU109	SMS	0.226	0.023064
snoU109	APH1A	0.226	0.023064
snoU109	IGDCC4	0.226	0.023064
snoU109	SLC9A6	0.226	0.023064
snoU109	LRRC15	0.227	0.02247
snoU109	RELA	0.227	0.02247
snoU109	POSTN	0.228	0.021889
snoU109	ADCK2	0.228	0.021889
snoU109	ANGPTL2	0.228	0.021889
snoU109	RAB23	0.228	0.021889
snoU109	NAMPT	0.228	0.021889
snoU109	TOR1B	0.228	0.021889
snoU109	VANGL1	0.229	0.021321
snoU109	IDO1	0.229	0.021321
snoU109	RPF2	0.23	0.020767
snoU109	CDSN	0.23	0.020767
snoU109	RAB31	0.23	0.020767
snoU109	HK1	0.23	0.020767
snoU109	SHCBP1	0.231	0.020224
snoU109	PUDP	0.231	0.020224
snoU109	TPBG	0.231	0.020224
snoU109	LAYN	0.231	0.020224
snoU109	POM121C	0.232	0.019695
snoU109	KCTD5	0.232	0.019695
snoU109	PGM1	0.232	0.019695
snoU109	PITPNB	0.232	0.019695
snoU109	HCCS	0.232	0.019695
snoU109	RAD23B	0.232	0.019695
snoU109	GJB2	0.232	0.019695
snoU109	NCK1	0.232	0.019695

snoU109	PDAP1	0.233	0.019177
snoU109	NRAS	0.233	0.019177
snoU109	CLSTN1	0.233	0.019177
snoU109	SSTR2	0.233	0.019177
snoU109	SPARC	0.234	0.018671
snoU109	EMP1	0.234	0.018671
snoU109	MRGPRX3	0.234	0.018671
snoU109	ARNTL2	0.234	0.018671
snoU109	PGM2	0.234	0.018671
snoU109	NDUFA5	0.234	0.018671
snoU109	PUS7	0.234	0.018671
snoU109	ACTG1	0.235	0.018177
snoU109	TOR1A	0.235	0.018177
snoU109	SYS1	0.235	0.018177
snoU109	CAVIN1	0.235	0.018177
snoU109	ACVR1	0.236	0.017695
snoU109	MAPKAP1	0.236	0.017695
snoU109	VAMP7	0.236	0.017695
snoU109	COL6A1	0.237	0.017224
snoU109	TGM4	0.237	0.017224
snoU109	METTL9	0.237	0.017224
snoU109	ARHGAP29	0.237	0.017224
snoU109	IL13RA1	0.237	0.017224
snoU109	NRP2	0.237	0.017224
snoU109	POFUT1	0.237	0.017224
snoU109	TTPAL	0.237	0.017224
snoU109	UBE2R2	0.237	0.017224
snoU109	F8A1	0.238	0.016764
snoU109	PPP1R18	0.238	0.016764
snoU109	CHST11	0.238	0.016764
snoU109	DEGS1	0.238	0.016764
snoU109	VTI1B	0.238	0.016764
snoU109	HPRT1	0.239	0.016314
snoU109	BACH1	0.239	0.016314
snoU109	DCLRE1B	0.239	0.016314
snoU109	MFSD14B	0.239	0.016314
snoU109	PDGFC	0.24	0.015876
snoU109	T	0.24	0.015876
snoU109	TMEM200B	0.24	0.015876
snoU109	RAB7A	0.24	0.015876
snoU109	RAD23A	0.24	0.015876
snoU109	INHBA	0.24	0.015876
snoU109	BMT2	0.241	0.015447
snoU109	VAMP3	0.241	0.015447

snoU109	FLNC	0.241	0.015447
snoU109	ANTXR2	0.241	0.015447
snoU109	NTAN1	0.242	0.015029
snoU109	RAB11FIP5	0.242	0.015029
snoU109	CLIP2	0.242	0.015029
snoU109	PRPF4	0.242	0.015029
snoU109	LRRC8A	0.242	0.015029
snoU109	TNFAIP6	0.243	0.014621
snoU109	ZCRB1	0.243	0.014621
snoU109	AXL	0.244	0.014223
snoU109	GPR87	0.244	0.014223
snoU109	ILK	0.244	0.014223
snoU109	MUL1	0.244	0.014223
snoU109	MAP4	0.244	0.014223
snoU109	KPNA4	0.244	0.014223
snoU109	ITGB5	0.244	0.014223
snoU109	B4GALT5	0.244	0.014223
snoU109	APP	0.245	0.013834
snoU109	HNRNPCL1	0.245	0.013834
snoU109	EFNB2	0.245	0.013834
snoU109	PCDH7	0.245	0.013834
snoU109	SLC35F2	0.245	0.013834
snoU109	SLAIN2	0.246	0.013455
snoU109	EPHB4	0.246	0.013455
snoU109	DCBLD2	0.246	0.013455
snoU109	MAP7D1	0.246	0.013455
snoU109	CMTM3	0.246	0.013455
snoU109	CRYGD	0.246	0.013455
snoU109	VGLL2	0.246	0.013455
snoU109	TMEM127	0.246	0.013455
snoU109	ACTR2	0.246	0.013455
snoU109	LDOC1	0.246	0.013455
snoU109	MCFD2	0.247	0.013085
snoU109	MSANTD3	0.247	0.013085
snoU109	GREM1	0.248	0.012724
snoU109	CLDN4	0.248	0.012724
snoU109	M6PR	0.249	0.012371
snoU109	NRBP1	0.249	0.012371
snoU109	SSPN	0.249	0.012371
snoU109	STIM1	0.249	0.012371
snoU109	BRCC3	0.249	0.012371
snoU109	IL27RA	0.249	0.012371
snoU109	FOSL1	0.249	0.012371
snoU109	FSTL1	0.249	0.012371

snoU109	CLIC4	0.249	0.012371
snoU109	GTPBP10	0.249	0.012371
snoU109	HS3ST3A1	0.249	0.012371
snoU109	WBP11	0.25	0.012028
snoU109	ALKBH4	0.25	0.012028
snoU109	FAM220A	0.25	0.012028
snoU109	DNAJC2	0.251	0.011693
snoU109	SNAI1	0.251	0.011693
snoU109	YWHAG	0.251	0.011693
snoU109	HMGA1	0.251	0.011693
snoU109	TUBA1C	0.251	0.011693
snoU109	PDLIM5	0.251	0.011693
snoU109	TMEM248	0.252	0.011366
snoU109	PICALM	0.252	0.011366
snoU109	BRI3	0.253	0.011047
snoU109	ZYX	0.254	0.010737
snoU109	RALA	0.254	0.010737
snoU109	ERO1A	0.254	0.010737
snoU109	AIDA	0.255	0.010434
snoU109	AFAP1	0.255	0.010434
snoU109	DDX18	0.256	0.010139
snoU109	SLC25A40	0.256	0.010139
snoU109	SDCBP	0.256	0.010139
snoU109	RIN2	0.256	0.010139
snoU109	TAB2	0.257	0.009851
snoU109	NF2	0.257	0.009851
snoU109	B4GALT1	0.257	0.009851
snoU109	VCL	0.258	0.00957
snoU109	FHL2	0.258	0.00957
snoU109	IL1RAPL1	0.258	0.00957
snoU109	CD109	0.258	0.00957
snoU109	NAA15	0.258	0.00957
snoU109	STAU1	0.259	0.009297
snoU109	NETO1	0.259	0.009297
snoU109	SZRD1	0.259	0.009297
snoU109	ACTR3	0.259	0.009297
snoU109	SH3GLB1	0.259	0.009297
snoU109	OSTN	0.26	0.009031
snoU109	DNAJB6	0.26	0.009031
snoU109	ITGB1	0.26	0.009031
snoU109	RINT1	0.26	0.009031
snoU109	ADAMTSL1	0.26	0.009031
snoU109	SERPINE2	0.261	0.008771
snoU109	RNF11	0.261	0.008771

snoU109	PALLD	0.261	0.008771
snoU109	ABCF2	0.261	0.008771
snoU109	ORC5	0.261	0.008771
snoU109	POT1	0.262	0.008518
snoU109	CAPZB	0.262	0.008518
snoU109	IDS	0.262	0.008518
snoU109	SLC10A3	0.262	0.008518
snoU109	MMP14	0.263	0.008272
snoU109	STEAP2	0.263	0.008272
snoU109	LIMS1	0.265	0.007798
snoU109	CHCHD3	0.265	0.007798
snoU109	TAF6	0.265	0.007798
snoU109	RRAGC	0.265	0.007798
snoU109	GNAI3	0.267	0.007349
snoU109	CAB39	0.267	0.007349
snoU109	THAP5	0.268	0.007134
snoU109	ARL2BP	0.268	0.007134
snoU109	UBE2D1	0.268	0.007134
snoU109	MSN	0.268	0.007134
snoU109	IRAK1	0.269	0.006924
snoU109	PI4K2A	0.269	0.006924
snoU109	SPATS2L	0.269	0.006924
snoU109	GNB1	0.27	0.006719
snoU109	MAPRE1	0.27	0.006719
snoU109	AP1S1	0.271	0.00652
snoU109	WDR1	0.271	0.00652
snoU109	BCL7B	0.271	0.00652
snoU109	NME7	0.272	0.006326
snoU109	MBTPS2	0.272	0.006326
snoU109	IFT22	0.272	0.006326
snoU109	COLGALT1	0.272	0.006326
snoU109	PLIN3	0.273	0.006138
snoU109	TOMM34	0.273	0.006138
snoU109	LYPD5	0.274	0.005954
snoU109	CNOT4	0.275	0.005776
snoU109	PRR16	0.276	0.005602
snoU109	PRPF19	0.276	0.005602
snoU109	TPM4	0.277	0.005433
snoU109	EXOC4	0.277	0.005433
snoU109	PLBD2	0.278	0.005269
snoU109	ARHGEF5	0.279	0.005109
snoU109	ZNF277	0.279	0.005109
snoU109	CDCP1	0.281	0.004803
snoU109	RAP2C	0.281	0.004803

snoU109	SDC4	0.281	0.004803
snoU109	PAK2	0.282	0.004656
snoU109	GLIPR1	0.282	0.004656
snoU109	CAP1	0.282	0.004656
snoU109	OLFML2A	0.282	0.004656
snoU109	SMURF1	0.283	0.004513
snoU109	IL23A	0.283	0.004513
snoU109	CUX1	0.283	0.004513
snoU109	PTP4A2	0.283	0.004513
snoU109	ENOX2	0.284	0.004374
snoU109	UBE2H	0.285	0.004239
snoU109	ANKIB1	0.285	0.004239
snoU109	ACTB	0.285	0.004239
snoU109	GNB2	0.285	0.004239
snoU109	ADGRE1	0.286	0.004108
snoU109	PANX1	0.288	0.003856
snoU109	VEGFC	0.288	0.003856
snoU109	TWF1	0.291	0.003505
snoU109	LMBR1	0.291	0.003505
snoU109	STEAP1	0.292	0.003395
snoU109	CSTB	0.293	0.003288
snoU109	ICMT	0.293	0.003288
snoU109	DCBLD1	0.293	0.003288
snoU109	UBE3C	0.293	0.003288
snoU109	TIMP2	0.293	0.003288
snoU109	SEMA3C	0.294	0.003184
snoU109	CAV2	0.294	0.003184
snoU109	CLDN12	0.296	0.002985
snoU109	TMEM185B	0.297	0.002889
snoU109	SERINC3	0.298	0.002797
snoU109	LIMK1	0.298	0.002797
snoU109	ORAI2	0.299	0.002707
snoU109	COPS6	0.302	0.002453
snoU109	TNPO3	0.302	0.002453
snoU109	TNFRSF12A	0.302	0.002453
snoU109	FGF5	0.304	0.002296
snoU109	MMGT1	0.305	0.002221
snoU109	HMGA2	0.308	0.00201
snoU109	ZNF114	0.308	0.00201
snoU109	ANO6	0.31	0.001879
snoU109	EXT1	0.31	0.001879
snoU109	ELF4	0.311	0.001817
snoU109	CCDC86	0.312	0.001756
snoU109	PLAU	0.32	0.001335

snoU109	DSE	0.32	0.001335
snoU109	PTPN12	0.328	0.001009
snoU109	ARPC1B	0.33	0.00094
snoU109	ARPC1A	0.332	0.000875
snoU109	TMCC3	0.333	0.000845
snoU109	DLD	0.337	0.000731
snoU109	ELK3	0.338	0.000705
snoU109	YWHAB	0.338	0.000705
snoU109	OR4C6	0.34	0.000656
snoU109	EIF4H	0.34	0.000656
snoU109	SRPK2	0.343	0.000588
snoU109	ARMC10	0.344	0.000566
snoU109	DUS4L	0.344	0.000566
snoU109	CALU	0.347	0.000507
snoU109	SNX12	0.348	0.000488
snoU109	CORO1C	0.353	0.000405
snoU109	SBDS	0.354	0.00039
snoU109	CDA	0.356	0.000361
snoU109	PNPLA8	0.357	0.000348
snoU109	SH3KBP1	0.358	0.000335
snoU109	PLOD3	0.358	0.000335
snoU109	TES	0.359	0.000322
snoU109	GCC1	0.367	0.000237
snoU109	CDH3	0.37	0.00021
snoU109	FOXB1	0.378	0.000153
snoU109	PSMC2	0.379	0.000147
snoU109	CCDC71L	0.38	0.000141
snoU109	ACP7	0.381	0.000136
snoU109	RALB	0.382	0.00013
snoU109	TMEM109	0.383	0.000125
snoU109	MDFIC	0.385	0.000116
snoU109	CBLL1	0.394	7.98E-05
snoU109	FAM3C	0.394	7.98E-05
snoU109	WASL	0.394	7.98E-05
snoU109	MTPN	0.397	7.04E-05
snoU109	SFRP1	0.404	5.24E-05
snoU109	COG5	0.417	2.99E-05
snoU109	SYPL1	0.459	4.39E-06
snoU109	BCAP29	0.526	1.45E-07
snoU109	snoU109	1	1.89E-23
U3	COLGALT1	-0.279	0.00053
U3	PLAUR	-0.264	0.001023
U3	MMP14	-0.256	0.001435
U3	ACTB	-0.255	0.001496

U3	ADAMTS4	-0.247	0.002078
U3	PARVB	-0.244	0.002345
U3	GPR4	-0.242	0.00254
U3	NCS1	-0.241	0.002643
U3	ABL2	-0.237	0.003095
U3	YWHAG	-0.234	0.003478
U3	SH3GL1	-0.233	0.003615
U3	SPHK1	-0.233	0.003615
U3	HIF1A	-0.229	0.004215
U3	RIPK2	-0.228	0.004378
U3	TPM4	-0.226	0.004722
U3	COL6A2	-0.226	0.004722
U3	KLF16	-0.226	0.004722
U3	FSCN1	-0.224	0.00509
U3	COL6A1	-0.223	0.005284
U3	HDGF	-0.222	0.005484
U3	MAP4K4	-0.221	0.005691
U3	RASAL2	-0.22	0.005905
U3	NRBP1	-0.22	0.005905
U3	ZBTB2	-0.218	0.006356
U3	COL1A1	-0.218	0.006356
U3	S100A16	-0.217	0.006592
U3	RND3	-0.217	0.006592
U3	TNFRSF1A	-0.217	0.006592
U3	SLC27A4	-0.216	0.006836
U3	LAMB1	-0.216	0.006836
U3	CD3EAP	-0.213	0.007619
U3	ARPC1B	-0.213	0.007619
U3	TBXA2R	-0.212	0.007897
U3	NUMBL	-0.211	0.008185
U3	PLIN3	-0.211	0.008185
U3	RELB	-0.211	0.008185
U3	THY1	-0.211	0.008185
U3	TUBB6	-0.21	0.008481
U3	RPS6KA4	-0.21	0.008481
U3	CCDC71L	-0.209	0.008787
U3	CFL1	-0.208	0.009103
U3	TNPO3	-0.208	0.009103
U3	ITPRIP	-0.208	0.009103
U3	GARS	-0.207	0.00943
U3	FOSL2	-0.207	0.00943
U3	GAS2L1	-0.207	0.00943
U3	SEMA6B	-0.207	0.00943
U3	MAPK1IP1L	-0.207	0.00943

U3	RBMS1	-0.206	0.009766
U3	ZYX	-0.206	0.009766
U3	RALA	-0.206	0.009766
U3	COL5A2	-0.205	0.010113
U3	COL1A2	-0.205	0.010113
U3	PTBP3	-0.205	0.010113
U3	SAPCD2	-0.205	0.010113
U3	EIF3B	-0.205	0.010113
U3	TIMP2	-0.205	0.010113
U3	JPT1	-0.204	0.010471
U3	RFX8	-0.204	0.010471
U3	ADAM12	-0.204	0.010471
U3	TATDN2	-0.204	0.010471
U3	COL5A1	-0.201	0.011614
U3	EMP1	-0.201	0.011614
U3	PVR	-0.201	0.011614
U3	LMNB2	-0.201	0.011614
U3	LMNA	-0.201	0.011614
U3	VASP	-0.201	0.011614
U3	PUS7	-0.201	0.011614
U3	COL5A3	-0.201	0.011614
U3	COL3A1	-0.201	0.011614
U3	RRP1B	-0.2	0.012019
U3	KRBOX4	0.2	0.020526
U3	ALG13	0.2	0.020526
U3	C17orf75	0.2	0.020526
U3	F11	0.2	0.020526
U3	TMEM125	0.2	0.020526
U3	ELMOD3	0.2	0.020526
U3	TMX4	0.2	0.020526
U3	AK9	0.201	0.019877
U3	ACBD4	0.201	0.019877
U3	ZNF641	0.201	0.019877
U3	TSSK4	0.201	0.019877
U3	ZSCAN26	0.201	0.019877
U3	TTLL2	0.201	0.019877
U3	LGALS8	0.201	0.019877
U3	MRPL21	0.201	0.019877
U3	ARMCX1	0.202	0.019246
U3	FAM46D	0.202	0.019246
U3	MALL	0.202	0.019246
U3	FMO4	0.202	0.019246
U3	DFFB	0.202	0.019246
U3	ANKDD1B	0.202	0.019246

U3	GOLGA6L9	0.203	0.018633
U3	SLC35E2B	0.203	0.018633
U3	CENPS	0.203	0.018633
U3	CLEC18C	0.203	0.018633
U3	JMJD7-PLA2G4B	0.203	0.018633
U3	GPRASP2	0.203	0.018633
U3	SCIN	0.203	0.018633
U3	POLR2M	0.203	0.018633
U3	KIAA1191	0.204	0.018036
U3	SLC25A4	0.204	0.018036
U3	CRY2	0.204	0.018036
U3	SRSF8	0.204	0.018036
U3	FBX038	0.204	0.018036
U3	MDP1	0.205	0.017457
U3	REV1	0.205	0.017457
U3	PHKB	0.205	0.017457
U3	BBS1	0.205	0.017457
U3	ANAPC15	0.205	0.017457
U3	PCBD2	0.205	0.017457
U3	MCCC1	0.205	0.017457
U3	CBX7	0.206	0.016894
U3	CCDC189	0.206	0.016894
U3	IFT46	0.206	0.016894
U3	ZC2HC1C	0.206	0.016894
U3	RTL5	0.206	0.016894
U3	NGT1	0.206	0.016894
U3	ARSD	0.206	0.016894
U3	DDO	0.207	0.016347
U3	PHYKPL	0.207	0.016347
U3	NICN1	0.207	0.016347
U3	LCA5L	0.208	0.015815
U3	FBX048	0.208	0.015815
U3	SLC24A1	0.208	0.015815
U3	GGTLC1	0.208	0.015815
U3	NCMAP	0.209	0.015299
U3	GOLGA6L10	0.209	0.015299
U3	MBOAT1	0.209	0.015299
U3	SLC25A14	0.21	0.014798
U3	CYP39A1	0.21	0.014798
U3	BSCL2	0.21	0.014798
U3	CD99L2	0.21	0.014798
U3	C1orf210	0.21	0.014798
U3	FAM200B	0.21	0.014798
U3	TMEM62	0.21	0.014798

U3	CTSF	0.21	0.014798
U3	KCTD18	0.21	0.014798
U3	ZNF75D	0.212	0.013838
U3	SLC15A2	0.212	0.013838
U3	CGNL1	0.212	0.013838
U3	ZNF821	0.212	0.013838
U3	CYP4B1	0.213	0.013379
U3	GGA2	0.213	0.013379
U3	KIAA0141	0.213	0.013379
U3	IKZF5	0.214	0.012934
U3	ANKRA2	0.214	0.012934
U3	UBL7	0.214	0.012934
U3	ZMAT1	0.214	0.012934
U3	C18orf32	0.215	0.012502
U3	MLYCD	0.215	0.012502
U3	NOL12	0.215	0.012502
U3	PIGBOS1	0.216	0.012083
U3	ENPP5	0.216	0.012083
U3	C15orf40	0.216	0.012083
U3	SH2B1	0.217	0.011676
U3	RUFY3	0.217	0.011676
U3	ATP6V1G2	0.217	0.011676
U3	EDC3	0.218	0.011281
U3	ICE2	0.218	0.011281
U3	DCTN4	0.218	0.011281
U3	RSL24D1	0.218	0.011281
U3	IL11RA	0.218	0.011281
U3	DIS3L	0.219	0.010899
U3	GRAMD2	0.219	0.010899
U3	PREPL	0.22	0.010528
U3	ZNF785	0.22	0.010528
U3	FUCA1	0.22	0.010528
U3	ZNF346	0.22	0.010528
U3	RMND5B	0.22	0.010528
U3	FAM13B	0.22	0.010528
U3	APH1B	0.22	0.010528
U3	GTF2IRD2	0.22	0.010528
U3	TRIM68	0.22	0.010528
U3	KBTD4	0.221	0.010168
U3	AP002360.1	0.221	0.010168
U3	SORL1	0.221	0.010168
U3	MPL	0.221	0.010168
U3	KLHDC2	0.221	0.010168
U3	AKR7A2	0.222	0.009819

U3	ANGPTL5	0.222	0.009819
U3	AMELX	0.222	0.009819
U3	RWDD2A	0.224	0.009153
U3	PIPOX	0.224	0.009153
U3	ZNF354B	0.225	0.008836
U3	CCDC30	0.225	0.008836
U3	ZNF540	0.225	0.008836
U3	ZFP3	0.225	0.008836
U3	MAPK10	0.225	0.008836
U3	USP3	0.225	0.008836
U3	GLS2	0.225	0.008836
U3	ABCC6	0.226	0.008528
U3	GGA1	0.226	0.008528
U3	ZNF19	0.226	0.008528
U3	BEND5	0.227	0.00823
U3	GEMIN8	0.227	0.00823
U3	ADCY9	0.227	0.00823
U3	TRIM52	0.227	0.00823
U3	CTSH	0.228	0.007941
U3	FAM76A	0.228	0.007941
U3	THAP6	0.228	0.007941
U3	C15orf61	0.228	0.007941
U3	BBS10	0.229	0.007662
U3	SELENOP	0.229	0.007662
U3	RPLP1	0.229	0.007662
U3	HRC	0.23	0.007391
U3	FRZB	0.23	0.007391
U3	HADH	0.23	0.007391
U3	FGF21	0.23	0.007391
U3	AL139353.1	0.231	0.007129
U3	ANKRD54	0.231	0.007129
U3	CYP2R1	0.231	0.007129
U3	ZBED8	0.231	0.007129
U3	FUNDC2	0.232	0.006875
U3	TSGA10IP	0.232	0.006875
U3	PAN2	0.232	0.006875
U3	TOX3	0.232	0.006875
U3	TMEM50B	0.233	0.006629
U3	FAM221B	0.234	0.006392
U3	TXNDC16	0.234	0.006392
U3	C16orf58	0.234	0.006392
U3	GDF10	0.234	0.006392
U3	ZSCAN12	0.235	0.006162
U3	BEX2	0.235	0.006162

U3	PARP16	0.236	0.005939
U3	SDR42E1	0.237	0.005724
U3	MEAF6	0.237	0.005724
U3	GAL	0.237	0.005724
U3	MAP10	0.237	0.005724
U3	ZBTB3	0.238	0.005516
U3	CLK4	0.238	0.005516
U3	RABL2A	0.239	0.005314
U3	NRAP	0.239	0.005314
U3	CD302	0.239	0.005314
U3	BBS4	0.239	0.005314
U3	TRIM63	0.24	0.00512
U3	TSPOAP1	0.24	0.00512
U3	CERS4	0.241	0.004931
U3	HSBP1	0.242	0.00475
U3	SLC25A42	0.242	0.00475
U3	SPATA6	0.242	0.00475
U3	RNF113B	0.243	0.004574
U3	NKX6-3	0.244	0.004404
U3	BEX4	0.244	0.004404
U3	SNX1	0.244	0.004404
U3	SST	0.245	0.00424
U3	RCHY1	0.245	0.00424
U3	CCDC121	0.246	0.004081
U3	ARMCX6	0.246	0.004081
U3	PTGDR2	0.246	0.004081
U3	ADCY5	0.246	0.004081
U3	BRD8	0.246	0.004081
U3	INCA1	0.246	0.004081
U3	ING4	0.247	0.003928
U3	ZNF157	0.248	0.00378
U3	TMEM63C	0.248	0.00378
U3	ZNF774	0.248	0.00378
U3	PKIG	0.249	0.003637
U3	WBP1	0.25	0.003499
U3	APITD1-CORT	0.255	0.002878
U3	PCP4	0.255	0.002878
U3	MAGT1	0.257	0.002659
U3	WDR73	0.257	0.002659
U3	THAP10	0.258	0.002556
U3	TMEM8B	0.258	0.002556
U3	FBXO9	0.259	0.002456
U3	ZBED5	0.261	0.002267
U3	MASP2	0.261	0.002267

U3	KIAA0319L	0.261	0.002267
U3	CPT1A	0.264	0.002008
U3	TCEAL8	0.264	0.002008
U3	LRRC49	0.265	0.001928
U3	TCEANC	0.267	0.001776
U3	RSPH6A	0.268	0.001705
U3	RSG1	0.269	0.001636
U3	CLK3	0.27	0.001569
U3	TSSK3	0.272	0.001444
U3	ABAT	0.273	0.001385
U3	SLC35E2	0.273	0.001385
U3	HACD3	0.274	0.001328
U3	TIMM10B	0.274	0.001328
U3	CARF	0.274	0.001328
U3	TSPYL2	0.277	0.00117
U3	SARM1	0.278	0.001122
U3	UGT3A1	0.278	0.001122
U3	NOTO	0.278	0.001122
U3	KSR2	0.279	0.001075
U3	BSDC1	0.279	0.001075
U3	MYOZ1	0.281	0.000987
U3	MTFR1L	0.281	0.000987
U3	UNC13C	0.283	0.000905
U3	DNALI1	0.283	0.000905
U3	RBL2	0.284	0.000867
U3	DNAJC27	0.287	0.000761
U3	SPIN3	0.288	0.000728
U3	FAM219B	0.292	0.00061
U3	SEC11C	0.295	0.000534
U3	MAGEB17	0.297	0.000488
U3	SENP8	0.304	0.000354
U3	ZNF280D	0.316	0.000202
U3	GGT7	0.329	0.000107
U3	SPOCK3	0.338	6.82E-05
U3	MAGEH1	0.35	3.67E-05
U3	U3	1	4.93E-33

Table S4. Functional enrichment results of snoRNA co-expressed genes.

Term	Count	%	P value
GO:0000786~nucleosome	56	1.888702	1.87E-22
GO:0005634~nucleus	1002	33.79427	8.31E-19
GO:0005515~protein binding	1549	52.24283	3.86E-18
GO:0005654~nucleoplasm	565	19.05565	2.08E-17
GO:0003676~nucleic acid binding	238	8.026981	1.29E-13
GO:0003677~DNA binding	365	12.31029	1.74E-13
GO:0006334~nucleosome assembly	52	1.753794	4.08E-13
GO:0045815~positive regulation of gene expression, epigenetic	34	1.146712	3.81E-12
GO:0032200~telomere organization	20	0.674536	1.80E-10
GO:0006355~regulation of transcription, DNA-templated	317	10.6914	2.09E-10
GO:0044822~poly(A) RNA binding	251	8.46543	2.84E-10
GO:0046872~metal ion binding	416	14.03035	5.57E-10
GO:0000183~chromatin silencing at rDNA	23	0.775717	8.79E-10
GO:0016607~nuclear speck	65	2.192243	9.53E-10
GO:0000788~nuclear nucleosome	24	0.809444	7.37E-09
GO:0006335~DNA replication-dependent nucleosome assembly	20	0.674536	1.30E-08
GO:0005925~focal adhesion	101	3.406408	1.94E-08
GO:0000228~nuclear chromosome	26	0.876897	2.46E-08
GO:0006351~transcription, DNA-templated	377	12.71501	2.13E-07
GO:0045814~negative regulation of gene expression, epigenetic	24	0.809444	2.36E-07
GO:0051290~protein heterotetramerization	21	0.708263	7.22E-07
GO:0016020~membrane	405	13.65936	1.22E-06
GO:0031047~gene silencing by RNA	38	1.281619	1.52E-06
GO:0000166~nucleotide binding	88	2.96796	1.64E-06
GO:0005737~cytoplasm	880	29.6796	2.59E-06
GO:0008380~RNA splicing	48	1.618887	1.11E-05
GO:0045653~negative regulation of megakaryocyte differentiation	12	0.404722	1.13E-05
GO:0004674~protein serine/threonine kinase activity	90	3.035413	1.32E-05
GO:0000398~mRNA splicing, via spliceosome	59	1.989882	1.68E-05
GO:0000784~nuclear chromosome, telomeric region	39	1.315346	2.14E-05
GO:0004842~ubiquitin-protein transferase activity	80	2.698145	2.32E-05
GO:0034080~CENP-A containing nucleosome assembly	19	0.640809	2.41E-05
GO:0006352~DNA-templated transcription, initiation	17	0.573356	2.77E-05
GO:0060968~regulation of gene silencing	9	0.303541	3.07E-05
GO:0016233~telomere capping	13	0.438449	3.96E-05
GO:0006303~double-strand break repair via nonhomologous end joining	23	0.775717	8.87E-05
GO:0006396~RNA processing	30	1.011804	1.83E-04

GO:0042393~histone binding	35	1.180438	2.85E-04
GO:0005524~ATP binding	278	9.376054	2.93E-04
GO:0005788~endoplasmic reticulum lumen	48	1.618887	3.16E-04
GO:0010494~cytoplasmic stress granule	15	0.505902	3.83E-04
GO:0006468~protein phosphorylation	97	3.271501	4.70E-04
GO:0098641~cadherin binding involved in cell-cell adhesion	67	2.259696	5.27E-04
GO:0005913~cell-cell adherens junction	71	2.394604	6.60E-04
GO:0080182~histone H3-K4 trimethylation	9	0.303541	6.74E-04
GO:0003723~RNA binding	113	3.81113	6.97E-04
GO:0006336~DNA replication-independent nucleosome assembly	12	0.404722	8.39E-04
GO:0043234~protein complex	86	2.900506	9.59E-04
GO:0000712~resolution of meiotic recombination intermediates	9	0.303541	0.001169
GO:0046982~protein heterodimerization activity	97	3.271501	0.001232
GO:0019013~viral nucleocapsid	12	0.404722	0.001453
GO:0098609~cell-cell adhesion	61	2.057336	0.001501
GO:0005622~intracellular	238	8.026981	0.001507
GO:0005815~microtubule organizing center	38	1.281619	0.001638
GO:0015031~protein transport	83	2.799325	0.001782
GO:0006281~DNA repair	54	1.821248	0.001793
GO:0004672~protein kinase activity	77	2.596965	0.00189
GO:0071821~FANCM-MHF complex	5	0.168634	0.002172
GO:0005829~cytosol	549	18.51602	0.002188
GO:0016567~protein ubiquitination	76	2.563238	0.002301
GO:0006397~mRNA processing	43	1.450253	0.002356
GO:0043484~regulation of RNA splicing	12	0.404722	0.00242
GO:0016442~RISC complex	7	0.236088	0.002564
GO:0044267~cellular protein metabolic process	31	1.045531	0.002664
GO:0006974~cellular response to DNA damage stimulus	48	1.618887	0.003022
GO:0006623~protein targeting to vacuole	6	0.202361	0.003055
GO:0042470~melanosome	27	0.910624	0.003076
GO:0005739~mitochondrion	234	7.892074	0.003748
GO:0060271~cilium morphogenesis	34	1.146712	0.003763
GO:0035987~endodermal cell differentiation	11	0.370995	0.00462
GO:0005681~spliceosomal complex	25	0.84317	0.004859
GO:0019003~GDP binding	17	0.573356	0.005797
GO:0051726~regulation of cell cycle	31	1.045531	0.005805
GO:0006369~termination of RNA polymerase II transcription	19	0.640809	0.005915
GO:0032886~regulation of microtubule-based process	6	0.202361	0.006013
GO:0031124~mRNA 3'-end processing	16	0.539629	0.006042
GO:1903506~regulation of nucleic acid-templated transcription	8	0.269815	0.006072

GO:0016032~viral process	63	2.124789	0.00618
GO:0090503~RNA phosphodiester bond hydrolysis, exonucleolytic	11	0.370995	0.006221
GO:0004386~helicase activity	23	0.775717	0.008193
GO:0043928~exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	11	0.370995	0.008222
GO:0015629~actin cytoskeleton	47	1.58516	0.008386
GO:0001568~blood vessel development	13	0.438449	0.008668
GO:0000932~cytoplasmic mRNA processing body	21	0.708263	0.009144
GO:0045335~phagocytic vesicle	13	0.438449	0.009151
GO:0033038~bitter taste receptor activity	10	0.337268	0.009288
GO:0003700~transcription factor activity, sequence-specific DNA binding	175	5.902192	0.009651
GO:0005730~nucleolus	153	5.160202	0.010704
GO:0030199~collagen fibril organization	13	0.438449	0.010822
GO:0051020~GTPase binding	10	0.337268	0.012305
GO:0015986~ATP synthesis coupled proton transport	9	0.303541	0.012418
GO:0003735~structural constituent of ribosome	48	1.618887	0.012474
GO:0005743~mitochondrial inner membrane	84	2.833052	0.013476
GO:0043161~proteasome-mediated ubiquitin-dependent protein catabolic process	44	1.48398	0.014028
GO:0035097~histone methyltransferase complex	9	0.303541	0.01462
GO:0005178~integrin binding	26	0.876897	0.015066
GO:0043001~Golgi to plasma membrane protein transport	10	0.337268	0.015149
GO:0031297~replication fork processing	10	0.337268	0.015149
GO:0006405~RNA export from nucleus	16	0.539629	0.015239
GO:0007249~I-kappaB kinase/NF-kappaB signaling	17	0.573356	0.015465
GO:0045732~positive regulation of protein catabolic process	17	0.573356	0.015465
GO:0043240~Fanconi anaemia nuclear complex	7	0.236088	0.016293
GO:0003713~transcription coactivator activity	52	1.753794	0.016479
GO:0006607~NLS-bearing protein import into nucleus	9	0.303541	0.01655
GO:0051010~microtubule plus-end binding	6	0.202361	0.017529
GO:0005759~mitochondrial matrix	64	2.158516	0.017971
GO:0031492~nucleosomal DNA binding	14	0.472175	0.018343
GO:0055037~recycling endosome	26	0.876897	0.01867
GO:0032007~negative regulation of TOR signaling	10	0.337268	0.019379
GO:0003712~transcription cofactor activity	19	0.640809	0.019451
GO:0005694~chromosome	25	0.84317	0.019549
GO:0005911~cell-cell junction	37	1.247892	0.020288
GO:0016584~nucleosome positioning	5	0.168634	0.022495
GO:0010008~endosome membrane	39	1.315346	0.02314
GO:0003680~AT DNA binding	5	0.168634	0.023181
GO:0005776~autophagosome	17	0.573356	0.023323
GO:1904837~beta-catenin-TCF complex assembly	13	0.438449	0.023755

GO:0010467~gene expression	14	0.472175	0.024283
GO:0032981~mitochondrial respiratory chain complex I assembly	17	0.573356	0.024311
GO:0006241~CTP biosynthetic process	6	0.202361	0.025408
GO:0006228~UTP biosynthetic process	6	0.202361	0.025408
GO:0017156~calcium ion regulated exocytosis	6	0.202361	0.025408
GO:0034329~cell junction assembly	6	0.202361	0.025408
GO:0005765~lysosomal membrane	54	1.821248	0.026138
GO:0003684~damaged DNA binding	17	0.573356	0.026176
GO:0043422~protein kinase B binding	6	0.202361	0.02631
GO:0045859~regulation of protein kinase activity	11	0.370995	0.026322
GO:0051015~actin filament binding	30	1.011804	0.027215
GO:0007264~small GTPase mediated signal transduction	50	1.686341	0.0274
GO:0007569~cell aging	9	0.303541	0.027616
GO:0045053~protein retention in Golgi apparatus	4	0.134907	0.027744
GO:0036498~IRE1-mediated unfolded protein response	16	0.539629	0.028369
GO:0035004~phosphatidylinositol 3-kinase activity	4	0.134907	0.028414
GO:0017112~Rab guanyl-nucleotide exchange factor activity	10	0.337268	0.031848
GO:0035861~site of double-strand break	10	0.337268	0.032785
GO:0016301~kinase activity	49	1.652614	0.032997
GO:0006342~chromatin silencing	13	0.438449	0.033375
GO:0051865~protein autoubiquitination	14	0.472175	0.033411
GO:2000785~regulation of autophagosome assembly	7	0.236088	0.034051
GO:0006376~mRNA splice site selection	7	0.236088	0.034051
GO:0042826~histone deacetylase binding	24	0.809444	0.034737
GO:0032947~protein complex scaffold	12	0.404722	0.034862
GO:0030695~GTPase regulator activity	7	0.236088	0.035382
GO:2000786~positive regulation of autophagosome assembly	5	0.168634	0.035681
GO:0042921~glucocorticoid receptor signaling pathway	5	0.168634	0.035681
GO:0006474~N-terminal protein amino acid acetylation	5	0.168634	0.035681
GO:0006220~pyrimidine nucleotide metabolic process	5	0.168634	0.035681
GO:0035988~chondrocyte proliferation	5	0.168634	0.035681
GO:0042787~protein ubiquitination involved in ubiquitin-dependent protein catabolic process	33	1.112985	0.036
GO:0032006~regulation of TOR signaling	6	0.202361	0.036219
GO:0006183~GTP biosynthetic process	6	0.202361	0.036219
GO:0036002~pre-mRNA binding	5	0.168634	0.036727
GO:0010629~negative regulation of gene expression	30	1.011804	0.038456
GO:0006289~nucleotide-excision repair	12	0.404722	0.039027
GO:0005794~Golgi apparatus	148	4.991568	0.042698
GO:0070979~protein K11-linked ubiquitination	9	0.303541	0.042954
GO:0035329~hippo signaling	9	0.303541	0.042954
GO:0002224~toll-like receptor signaling pathway	9	0.303541	0.042954

GO:0031293~membrane protein intracellular domain proteolysis	7	0.236088	0.044678
GO:0006493~protein O-linked glycosylation	10	0.337268	0.044845
GO:0005942~phosphatidylinositol 3-kinase complex	6	0.202361	0.045614
GO:0030140~trans-Golgi network transport vesicle	6	0.202361	0.045614
GO:0042800~histone methyltransferase activity (H3-K4 specific)	7	0.236088	0.04637
GO:0090544~BAF-type complex	4	0.134907	0.046558
GO:0030670~phagocytic vesicle membrane	15	0.505902	0.048677
GO:0005840~ribosome	34	1.146712	0.048791
GO:0090382~phagosome maturation	4	0.134907	0.049265
GO:0010659~cardiac muscle cell apoptotic process	4	0.134907	0.049265
GO:0010606~positive regulation of cytoplasmic mRNA processing body assembly	4	0.134907	0.049265
GO:0061157~mRNA destabilization	4	0.134907	0.049265
GO:0071044~histone mRNA catabolic process	6	0.202361	0.049459
GO:0070208~protein heterotrimerization	6	0.202361	0.049459
GO:0043508~negative regulation of JUN kinase activity	6	0.202361	0.049459
GO:0046835~carbohydrate phosphorylation	8	0.269815	0.049658
GO:0051439~regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	8	0.269815	0.049658
hsa05322:Systemic lupus erythematosus	57	1.922428	6.53E-16
hsa05034:Alcoholism	60	2.023609	1.34E-11
hsa05203:Viral carcinogenesis	62	2.091062	1.14E-09
hsa04510:Focal adhesion	51	1.720067	2.67E-05
hsa04611:Platelet activation	34	1.146712	2.55E-04
hsa04120:Ubiquitin mediated proteolysis	35	1.180438	3.27E-04
hsa03018:RNA degradation	23	0.775717	4.76E-04
hsa05146:Amoebiasis	28	0.944351	8.52E-04
hsa04810:Regulation of actin cytoskeleton	46	1.551433	0.001278
hsa03460:Fanconi anemia pathway	17	0.573356	0.001447
hsa05131:Shigellosis	19	0.640809	0.001845
hsa05100:Bacterial invasion of epithelial cells	21	0.708263	0.003532
hsa04512:ECM-receptor interaction	22	0.74199	0.006074
hsa03040:Spliceosome	30	1.011804	0.006817
hsa00310:Lysine degradation	15	0.505902	0.008672
hsa05205:Proteoglycans in cancer	40	1.349073	0.013439
hsa04932:Non-alcoholic fatty liver disease (NAFLD)	31	1.045531	0.021899
hsa00514:Other types of O-glycan biosynthesis	8	0.269815	0.023671
hsa04144:Endocytosis	45	1.517707	0.027059
hsa05202:Transcriptional misregulation in cancer	33	1.112985	0.029623
hsa05010:Alzheimer's disease	33	1.112985	0.031962
hsa04014:Ras signaling pathway	42	1.416526	0.035097
hsa04130:SNARE interactions in vesicular transport	10	0.337268	0.035834

hsa05130:Pathogenic Escherichia coli infection	13	0.438449	0.040132
hsa05110:Vibrio cholerae infection	13	0.438449	0.045911
hsa05213:Endometrial cancer	13	0.438449	0.045911
hsa05012:Parkinson's disease	28	0.944351	0.046896

Table S5. Survival analysis results of snoRNA co-expressed genes.

ID	Adjusted P λ	HR	Low 95%CI	High 95%CI
TMEM125	0.000356165	0.578513	0.428393	0.781238
PGS1	0.000363967	0.577403	0.426916	0.780937
MYOZ1	0.000369327	0.582389	0.432504	0.784216
ERO1A	0.000392872	1.728346	1.277152	2.338937
ZC3H12D	0.000474359	0.579888	0.427192	0.787163
PTGDR2	0.000488276	0.585503	0.433377	0.791028
CD302	0.000559	0.590579	0.437894	0.796503
BEX4	0.000584648	0.584529	0.430417	0.793821
STEAP1	0.00060434	1.692439	1.252921	2.286138
GJB2	0.000608617	1.697384	1.254276	2.297031
PSMD2	0.000719324	1.682359	1.244505	2.274263
TMEM50B	0.000741909	0.598854	0.444581	0.806661
SLC25A42	0.000923857	0.600442	0.444022	0.811965
ACTB	0.000947335	1.660237	1.229224	2.242379
IKZF4	0.000988955	0.607456	0.451534	0.817221
ZNF451	0.001026182	0.604762	0.447919	0.816525
BBS1	0.001080507	0.605854	0.448613	0.818209
SLC2A1	0.001180792	1.649636	1.21906	2.232293
SETDB2	0.001281433	0.603951	0.444329	0.820915
EXT1	0.001300465	1.635424	1.211798	2.207144
B4GALT1	0.001380547	1.636787	1.210237	2.213674
CFL1	0.001634697	1.624343	1.201094	2.19674
PLAUR	0.001745915	1.614752	1.196211	2.179736
FOSL2	0.001837039	1.615881	1.194797	2.185369
PVR	0.001859836	1.604062	1.191134	2.16014
GSK3A	0.002003782	1.601928	1.188025	2.160032
YWHAG	0.002057354	1.613491	1.190234	2.187263
VTA1	0.002072811	1.597837	1.185761	2.153118
SPATA6	0.002152778	0.626061	0.464194	0.844371
RPS19	0.002174709	1.59292	1.182795	2.145254
CERS4	0.002288464	0.627695	0.46535	0.846677
FOSL1	0.002399161	1.597458	1.180568	2.161563
RIPK2	0.002685982	1.581776	1.172484	2.133944
RAD23A	0.002790653	1.579981	1.170658	2.132424
GLS2	0.002812808	0.635139	0.471563	0.855457
PRCD	0.002852792	0.633909	0.469848	0.855257
C1GALT1	0.002995662	1.566168	1.164613	2.106176
PSMC5	0.003227038	1.568809	1.162584	2.116976
ADAMTS4	0.003371228	1.568819	1.160977	2.119932
BEND5	0.003396582	0.639883	0.474643	0.862649
HIST1H2BF	0.003457934	1.55813	1.157422	2.097565
EPOR	0.003543001	0.640348	0.474581	0.864016

FBXO9	0.003733125	0.64054	0.474018	0.865561
KLHL11	0.003771029	0.642703	0.476548	0.86679
ZFP3	0.003828606	0.637212	0.469506	0.864822
CENPC	0.003922078	0.646607	0.480804	0.869587
IL12B	0.003988977	0.647025	0.481063	0.870243
IKZF5	0.004037896	0.646736	0.48051	0.870464
ZNF141	0.0043509	0.649289	0.482525	0.873688
AL162231.1	0.004531816	0.650465	0.483347	0.875365
RTL5	0.004602106	0.645569	0.476963	0.873778
SNX7	0.004735857	1.533064	1.139714	2.062171
NBN	0.004873062	1.533023	1.138605	2.064068
VANGL1	0.004925498	1.536887	1.139059	2.07366
RALA	0.005004094	1.530533	1.137018	2.060242
VEGFC	0.00502607	1.529843	1.136693	2.058971
CYP4B1	0.005081996	0.649521	0.48028	0.878399
KPNA4	0.005342986	1.529342	1.13419	2.062164
CDCP1	0.005354586	1.528783	1.133982	2.061038
FNDC3B	0.005405132	1.533268	1.134592	2.072033
CARHSP1	0.005891964	1.519839	1.128245	2.047349
PPOX	0.00594846	0.652602	0.481476	0.884549
EZH1	0.005959744	0.653796	0.482953	0.885075
ITGB1	0.006014246	1.520792	1.127625	2.051045
SLC44A1	0.006072468	1.525526	1.128237	2.062712
COLGALT1	0.006085468	1.513559	1.125617	2.035206
PCDH7	0.006252861	1.511825	1.124164	2.033169
EMC6	0.006402356	1.513705	1.123606	2.03924
ACTN4	0.006410888	1.526366	1.126185	2.068748
GCDH	0.006503164	0.660902	0.490448	0.890597
THAP10	0.006648162	1.517633	1.122878	2.051167
MAPK1IP1L	0.006718793	1.516318	1.122172	2.048904
ZSCAN26	0.006812388	0.661814	0.490782	0.892449
MTHFD2L	0.007305973	0.667292	0.496542	0.89676
MALSU1	0.00743635	1.507549	1.116176	2.036152
MTERF1	0.007632113	1.49811	1.113223	2.016067
WDTC1	0.007694112	0.666874	0.495048	0.898339
WDR1	0.007694306	1.498935	1.113047	2.018609
HEMK1	0.007799758	0.66722	0.49524	0.898923
ACP7	0.007808562	1.497101	1.112071	2.01544
FRZB	0.007810186	0.666346	0.494089	0.898658
UBR3	0.007814011	0.667848	0.496015	0.899208
DNAJC27	0.008140542	0.668078	0.495542	0.900686
PAPOLG	0.008142427	0.66895	0.496665	0.900999
SMS	0.008177867	1.497818	1.11026	2.02066
S100A16	0.008192359	1.49589	1.109815	2.016271

MMP14	0.008430378	1.490948	1.107656	2.006874
AC068896.1	0.008510832	0.668665	0.495453	0.902432
POSTN	0.008520947	1.493479	1.107681	2.013649
PIK3R1	0.008527204	0.670693	0.498041	0.903196
ABAT	0.008698006	0.67049	0.497397	0.903818
FAM83D	0.008771624	1.501333	1.107899	2.034481
RND3	0.00882861	1.48599	1.104757	1.99878
DNALI1	0.008850109	0.671201	0.497984	0.904669
ZNF708	0.008858611	0.667843	0.493617	0.903564
SENP8	0.008980742	0.674979	0.502613	0.906457
LRRC27	0.009135509	0.669724	0.495451	0.905299
MCRS1	0.009170558	1.489017	1.103682	2.008887
ZNF546	0.00955368	0.673461	0.499422	0.908148
STK17B	0.009652936	0.676261	0.50287	0.909437
PTPRC	0.010150746	0.67156	0.495732	0.90975
CD3EAP	0.0103048	1.474922	1.096052	1.984757
PGM2	0.010392633	1.478267	1.096262	1.993387
KLK13	0.010441426	0.679794	0.505926	0.913415
EIF4E	0.010473006	1.475722	1.095477	1.987953
AC006978.2	0.01085613	0.676026	0.500187	0.913681
ATL3	0.010899882	1.475219	1.093608	1.989991
ZNF785	0.010929105	0.677329	0.501756	0.914339
RNF4	0.010950619	1.477692	1.09382	1.996283
HIST1H4A	0.011287463	1.466971	1.090645	1.973147
ATP8B4	0.011290218	0.67523	0.49833	0.914928
ZNF483	0.011501686	0.673811	0.496084	0.915212
SLC15A2	0.011905717	0.683812	0.508507	0.919551
ITGA4	0.01193875	0.680311	0.503826	0.918617
SLCO1B7	0.012048653	1.461645	1.086826	1.965731
MMP3	0.012138792	1.463095	1.086723	1.969817
TSPOAP1	0.012146813	0.679343	0.502183	0.919003
RBP3	0.012340492	1.464125	1.086136	1.973659
CCDC137	0.012407466	1.461385	1.085448	1.967525
KIAA1109	0.012473078	0.681635	0.504637	0.920714
MRPL12	0.012663275	1.465087	1.085098	1.978142
C3orf62	0.012769476	0.682876	0.505771	0.921998
ATP11B	0.012967229	1.457061	1.082736	1.960797
CLEC2D	0.013042097	0.686498	0.510117	0.923865
STKLD1	0.013070185	0.686114	0.50956	0.923841
C6orf201	0.013342244	0.686991	0.510277	0.924903
MBOAT1	0.013673283	0.688531	0.51179	0.926307
TBCC	0.013678211	0.689492	0.513065	0.926586
ZNF727	0.013944683	0.688739	0.511633	0.927152
ACTR2	0.014187998	1.459622	1.078904	1.974687

FKBP11	0.014407108	0.691447	0.514527	0.9292
SLC25A16	0.014443904	0.690428	0.513105	0.929031
LAMC2	0.014596235	1.44983	1.076108	1.953341
AIG1	0.015019006	1.445825	1.074171	1.946068
TMEM63C	0.015049795	0.693964	0.516923	0.931639
ZNF791	0.015140557	0.682546	0.501525	0.928905
HCCS	0.015141556	1.455778	1.075207	1.971053
DCBLD2	0.015195895	1.443953	1.073345	1.942525
CC2D2B	0.015276225	0.689241	0.510245	0.93103
TWF1	0.01531419	1.447012	1.073411	1.950645
CCDC86	0.01544688	1.443025	1.072432	1.941683
BMT2	0.015448918	0.692237	0.514005	0.932273
EIF3B	0.016138433	1.449679	1.071235	1.961819
COL6A1	0.016263318	1.435498	1.068916	1.927798
RNF38	0.016618604	0.695941	0.5173	0.936272
ASH1L	0.017241618	0.696697	0.517453	0.938031
DOCK4	0.017262017	0.696874	0.517664	0.938124
BCAR3	0.017263446	1.438084	1.06636	1.939387
SIDT2	0.017401925	0.69785	0.518795	0.938704
RNPEPL1	0.017987948	1.434694	1.063885	1.934746
ZNF573	0.018053639	0.695948	0.515332	0.939866
FBXO44	0.018163048	0.697958	0.517911	0.940596
MSANTD3	0.018173829	1.436967	1.063659	1.941296
MYL5	0.018192936	0.69915	0.519491	0.940941
GPR1	0.018482643	1.430895	1.062054	1.927832
FUCA1	0.018557825	0.701452	0.522144	0.942335
AMT	0.018682296	0.698516	0.517983	0.941971
SH2B1	0.018931312	0.697352	0.516076	0.942304
GNAI3	0.018982353	1.432882	1.060957	1.935187
ZNF555	0.019018564	0.695359	0.513259	0.942068
G3BP1	0.019254285	1.431289	1.060043	1.932554
UEVLD	0.019314814	1.422635	1.058841	1.911422
FAM76A	0.019388672	0.701643	0.52133	0.944321
RCCD1	0.019395596	1.42616	1.059056	1.920514
SEMA3A	0.019455054	1.42294	1.058516	1.912828
PAK2	0.019732702	1.422766	1.057783	1.913685
SHCBP1	0.01985076	1.43448	1.058858	1.943353
GADD45G	0.020038541	0.702255	0.521346	0.945941
ZDHHC5	0.020069947	1.426659	1.05738	1.924905
PKD2L2	0.02018572	0.703384	0.522708	0.946512
USF3	0.020359836	0.703276	0.522344	0.946881
PIK3CG	0.020872442	0.699353	0.516347	0.947219
KCNQ1	0.021117204	0.704286	0.522802	0.948768
HMGA1	0.021617515	1.43105	1.053999	1.942984

LOX	0.021633183	1.420348	1.052801	1.916209
AL139353.1	0.021633986	0.708184	0.527552	0.950664
GAL	0.021899339	1.415588	1.051652	1.905467
AGPS	0.022103124	1.427389	1.052425	1.935947
CAMK2N1	0.02236196	1.411609	1.050146	1.897491
DOPEY1	0.022365018	0.705574	0.523094	0.951713
MBTPS2	0.022516107	1.414646	1.050107	1.905731
ZNF780B	0.022532589	0.707965	0.526198	0.952522
NUP54	0.022638929	1.413963	1.049752	1.904538
ZNF136	0.02266763	0.704824	0.521708	0.952212
UBR2	0.022904201	0.707346	0.524914	0.953182
CCDC30	0.022975532	0.707524	0.525078	0.953363
KMT2C	0.022985572	0.709173	0.527348	0.953691
HECTD3	0.02306086	0.708958	0.526964	0.953806
GARS	0.023092995	1.418131	1.049133	1.916911
ADAM10	0.023126123	1.416747	1.048916	1.913568
HIST1H2BD	0.023215724	1.40976	1.048003	1.89639
HS3ST3A1	0.023252947	1.408227	1.047764	1.8927
IL23A	0.023284568	1.410638	1.047937	1.898874
CCNT2	0.023305414	0.707848	0.52515	0.954106
ABCC6	0.024221058	0.709701	0.52669	0.956303
RBPM5	0.024514119	0.710141	0.526978	0.956966
MRM3	0.024586471	1.409103	1.0449	1.900249
PRRT1	0.024612318	1.40455	1.044411	1.888872
PIK3CB	0.024774427	1.403354	1.043949	1.886491
LMNB2	0.024815033	1.403592	1.043885	1.887249
ZNF490	0.024975294	0.712058	0.529141	0.958207
PRKAR2A	0.025105901	0.712744	0.529955	0.958578
NUDCD1	0.025185392	1.424505	1.045017	1.941802
SYS1	0.025306423	0.714983	0.532866	0.959341
SLC30A7	0.026029903	1.399735	1.040976	1.882136
SGF29	0.026094023	0.713092	0.529386	0.960546
VAMP2	0.026475231	0.715022	0.531686	0.961577
DNAH1	0.027008952	0.711272	0.525889	0.962005
PDCD6IP	0.027157398	1.394483	1.038234	1.872973
KCTD5	0.02716929	1.400458	1.038711	1.888189
SLC8A1	0.027659934	0.716181	0.53209	0.963963
NCS1	0.027668954	1.395081	1.037268	1.876326
DXO	0.028379507	0.717447	0.533144	0.96546
AC007998.2	0.028643001	1.39521	1.035371	1.88011
ZNF248	0.029224948	0.71869	0.534059	0.967151
MBTD1	0.029353927	0.716773	0.531231	0.967121
WBP2	0.029391001	0.720247	0.536095	0.967656
CCDC189	0.02941848	0.717561	0.532277	0.967342

PRPF4B	0.029485865	0.716299	0.530434	0.967293
ZNF852	0.02956018	0.7158	0.529658	0.967359
METTL9	0.029622033	1.395829	1.033536	1.885119
SETD1B	0.029667731	0.718829	0.533822	0.967954
VPS13D	0.02967594	0.719787	0.535167	0.968096
ACTG1	0.029853389	1.389051	1.032605	1.868538
ZC3H6	0.029892311	0.721661	0.537611	0.968721
LARGE2	0.029950798	0.720184	0.535462	0.96863
LIME1	0.030137232	1.390177	1.032156	1.872384
EIF4H	0.030402524	1.393542	1.031899	1.881928
ING4	0.030429277	0.719637	0.534228	0.969394
RHOC	0.03091993	1.387569	1.03053	1.868309
FBN3	0.030992827	0.722332	0.537511	0.970703
HIST1H4H	0.031149775	1.386461	1.030036	1.86622
TGFBR2	0.031209527	0.722784	0.537949	0.971127
DMAP1	0.031414215	0.721699	0.536215	0.971344
HIST4H4	0.031432029	0.722537	0.537389	0.971475
VAMP1	0.031544318	0.721977	0.536488	0.971598
CCDC18	0.032036293	1.381272	1.028108	1.85575
KLK12	0.032393947	0.72575	0.541074	0.973458
SYNE1	0.03247085	0.72302	0.53711	0.973278
SDR42E1	0.032557328	0.724487	0.539122	0.973586
CAMTA2	0.032569332	0.720746	0.533787	0.973188
HMBOX1	0.032576304	0.720283	0.533124	0.973148
RASAL2	0.032584254	1.383886	1.027305	1.864238
IRS1	0.032778965	1.380474	1.026755	1.85605
JOSD2	0.032784416	1.378529	1.026627	1.851054
LHFPL2	0.033410336	1.384782	1.025912	1.869186
ARPC1A	0.033438713	1.381302	1.02566	1.860261
RTCA	0.033886629	1.378702	1.024742	1.854925
SMARCAL1	0.034015852	1.392716	1.025304	1.891787
SLC2A11	0.034112028	0.726168	0.540118	0.976306
SCLT1	0.034168031	1.374132	1.02401	1.843965
ZNF641	0.034296696	0.725214	0.538587	0.976509
ZNF10	0.034618937	0.72642	0.540028	0.977146
GK3P	0.034694769	1.38032	1.02346	1.861611
DNAJC2	0.034864303	1.3802	1.023167	1.861818
TNPO3	0.034879148	1.376585	1.022952	1.852469
CRY2	0.035184048	0.725751	0.538572	0.977985
SH3GL1	0.035253128	1.3752	1.022258	1.849999
FAM13B	0.035409692	0.727231	0.540496	0.978481
ENPP5	0.03602582	0.726805	0.539348	0.979414
DDX52	0.036177763	1.382301	1.021076	1.871317
NAIP	0.036300179	0.723014	0.53368	0.979518

SNAI1	0.036580549	1.371187	1.019895	1.843477
CAPN12	0.036694986	0.727814	0.540223	0.980547
CHMP2B	0.037124074	1.369401	1.018944	1.840393
HERC1	0.037357032	0.728432	0.540548	0.981621
ARIH2OS	0.03848863	0.733084	0.546326	0.983684
MIF	0.038607668	1.372889	1.016745	1.853782
SEN3	0.038637679	1.367621	1.016494	1.840039
CD99L2	0.03864515	0.732585	0.545472	0.983883
LHX8	0.038700916	1.366526	1.016353	1.837347
AK9	0.038859661	0.732215	0.544759	0.984177
COL1A1	0.039168366	1.365957	1.015612	1.837156
UBA6	0.039218253	1.368441	1.015627	1.843817
LTBP1	0.039514453	1.363256	1.014986	1.831028
PRR11	0.04019588	1.369012	1.014147	1.84805
KIAA0895L	0.040610868	0.731646	0.542503	0.986733
EMP3	0.040773029	1.363438	1.013097	1.834933
SWT1	0.041199111	0.73454	0.546239	0.987751
CARM1	0.041233319	1.358917	1.012277	1.824259
HRAS	0.041864242	1.363308	1.011473	1.837526
TCP11L2	0.042440385	0.732835	0.542771	0.989454
SARM1	0.043076314	0.735009	0.545443	0.990457
TXNDC5	0.043140802	0.736143	0.547051	0.990596
NEK8	0.043216517	0.735065	0.545416	0.990658
PLEKHM3	0.043934284	0.736085	0.546351	0.991707
POLR2H	0.04403208	1.355573	1.008164	1.822697
FAM219B	0.044184061	0.738257	0.549346	0.992133
MZT2A	0.044199827	1.354661	1.00791	1.820704
PDLIM5	0.044287196	1.354086	1.007776	1.819401
MTBP	0.044418098	1.357399	1.007654	1.828537
RLIM	0.044788618	1.354622	1.007084	1.822094
LATS2	0.044811035	1.352018	1.007008	1.815232
PHKB	0.044851421	0.740031	0.551446	0.993108
FMC1	0.044899212	0.739327	0.550373	0.993152
GRAMD2	0.045235539	0.738691	0.549182	0.993593
TMEM158	0.045590749	1.357334	1.006009	1.831352
SAPCD2	0.045658799	1.353014	1.005852	1.819996
FAN1	0.046046774	0.738846	0.5488	0.994704
ZNF678	0.046586176	0.739172	0.548877	0.995442
FAM186B	0.046589028	0.740449	0.550758	0.995472
KSR2	0.046839276	0.738777	0.548106	0.995777
ZNF441	0.046852039	0.738956	0.54836	0.995797
PARS2	0.04697279	0.739895	0.549655	0.995977
CLASP2	0.047478346	0.741762	0.552042	0.996683
ANKDD1B	0.047735123	0.740033	0.549296	0.997

BTBD18	0.047846146	0.738532	0.546999	0.997129
WDR6	0.047945217	0.740702	0.550131	0.997289
NICN1	0.048112861	0.739949	0.548895	0.997503
GOLGA6L9	0.048308786	0.740895	0.55015	0.997773
LACTB2	0.048444927	1.347866	1.002041	1.813043
AP002495.2	0.048595772	0.74302	0.55309	0.998171
SNTA1	0.048627577	0.740815	0.5498	0.998194
DFFB	0.04878525	0.740184	0.548752	0.998398
ZNF589	0.04881131	0.740487	0.54918	0.998435
ADAM12	0.048907221	1.350173	1.001439	1.820348
LYPD3	0.049262401	1.356622	1.000985	1.838613
FAM136A	0.049925352	1.347108	1.000097	1.814524
NDST2	0.04992818	0.740146	0.547868	0.999906
FITM1	0.050806178	0.742579	0.550848	1.001044
DMXL1	0.050944603	0.745494	0.555092	1.001207
TAF15	0.051046407	1.341594	0.998664	1.802283
REV3L	0.051190747	0.743697	0.552239	1.001533
FSCN1	0.051231321	1.346506	0.99841	1.815965
APPL1	0.051277786	0.745064	0.554214	1.001634
ABCA5	0.051286096	0.742869	0.550939	1.001661
FPGS	0.051443441	0.746318	0.55597	1.001835
CTSH	0.051955226	0.745593	0.554529	1.002489
CRELD1	0.052105902	0.746251	0.555406	1.002672
UTP15	0.052304708	1.341458	0.997076	1.804787
C12orf29	0.052520819	1.346512	0.996764	1.81898
CHCHD3	0.053029836	1.348181	0.996103	1.824702
REV1	0.0530703	0.745423	0.553499	1.003898
SDCBP	0.053117995	1.340124	0.996071	1.803015
EPC2	0.053354367	0.74636	0.554703	1.004237
KBTBD2	0.053638129	1.342687	0.995397	1.811146
RBL2	0.054300271	0.746921	0.554894	1.005402
C5orf56	0.054377049	0.742783	0.548653	1.005602
ENDOG	0.0544446119	0.748656	0.5574	1.005538
RPF2	0.054685944	1.34098	0.994123	1.808859
KLK11	0.055083022	0.747853	0.555759	1.006343
SIRT4	0.055376299	0.748604	0.55669	1.00668
CD109	0.055377339	1.338907	0.993311	1.804746
GGA2	0.055433149	0.74528	0.551662	1.006853
HPRT1	0.055457017	1.338217	0.993226	1.80304
GMFB	0.055872458	1.340048	0.992689	1.808954
COL11A1	0.05594504	1.338766	0.992625	1.805613
NRBP1	0.056234493	1.33713	0.992307	1.801778
GOLGA8N	0.056834666	0.749294	0.556749	1.008428
ITGAV	0.057246624	1.33574	0.991127	1.800174

UQCC3	0.057468954	1.334042	0.990903	1.796006
DDO	0.057859826	0.751397	0.559246	1.00957
HMGA2	0.057879666	1.331765	0.990475	1.790655
ULK3	0.05843188	0.751424	0.558911	1.010249
RFX8	0.058719882	1.331596	0.989499	1.791964
FAT4	0.058988262	0.750685	0.557426	1.010946
FRS3	0.059030301	0.751052	0.557954	1.010977
OGT	0.059145794	0.743835	0.547006	1.011491
ZMAT1	0.059867251	0.749931	0.555711	1.01203
LYAR	0.060924662	1.337043	0.986771	1.81165
PABPC1L	0.061325192	0.75264	0.558877	1.01358
SIKE1	0.061620141	1.324657	0.986412	1.778887
POLK	0.06215806	0.754353	0.560954	1.01443
MASP2	0.062277794	0.753471	0.559534	1.014629
PLIN3	0.062389016	1.325895	0.985507	1.783849
COL1A2	0.062389427	1.323759	0.985589	1.777959
ANP32B	0.062408759	1.325734	0.985491	1.783447
HIST2H2AB	0.062576019	1.323728	0.985383	1.778248
FAM107B	0.062720608	1.325015	0.985172	1.782089
ZEB2	0.062915056	0.751363	0.55592	1.015517
RUFY3	0.063359734	0.75288	0.557946	1.015919
SGSH	0.063645596	0.755945	0.562445	1.016014
MTPN	0.063934497	1.331397	0.983555	1.802255
TECPR1	0.06398993	0.755294	0.561234	1.016454
BSDC1	0.064147057	0.757182	0.564028	1.016484
SLC27A4	0.064242817	1.322692	0.983591	1.778701
MFN2	0.064427741	0.757349	0.564109	1.016786
SSBP3	0.064453338	0.755661	0.561505	1.01695
ZNF76	0.064481808	0.756483	0.562747	1.016916
ZC3H12C	0.064611743	1.322051	0.983217	1.777654
GDF10	0.064622575	0.755783	0.561587	1.017132
SPOCK3	0.065053892	1.322749	0.982704	1.78046
MVK	0.06506643	0.75718	0.563453	1.017516
TTLL2	0.065396188	0.753015	0.556873	1.018243
CUL9	0.065726755	0.751852	0.554892	1.018722
TPBG	0.0657479	1.319172	0.982124	1.77189
LYPD5	0.065961702	1.323037	0.981705	1.783048
LRCH1	0.066003441	1.320043	0.981807	1.774802
RNF11	0.066461759	0.75806	0.563943	1.018994
HIST1H3J	0.066698609	1.319259	0.981102	1.773968
PDZD9	0.066902982	0.759513	0.565911	1.019347
TSSK4	0.067072218	0.755692	0.559931	1.019894
EXOSC5	0.067184794	1.31951	0.980571	1.775605
ACTN1	0.067340865	1.316782	0.98055	1.76831

KIAA0895	0.067400396	1.315306	0.980566	1.764317
ZBTB38	0.067427632	1.318105	0.980388	1.772156
SELENOP	0.067463454	0.757149	0.561929	1.02019
ATG5	0.067929131	1.319391	0.979787	1.776703
ASB14	0.068175873	0.758095	0.562951	1.020885
SLC16A11	0.068589398	0.75983	0.565377	1.021162
KPNA5	0.068777957	0.760254	0.565918	1.021324
CDH3	0.068855982	1.315359	0.97904	1.767211
KIF27	0.068885508	0.759373	0.564493	1.021532
FBXO48	0.068928085	0.76083	0.566719	1.021427
PHF1	0.068944505	0.754234	0.55655	1.022135
SCNM1	0.068997564	1.316988	0.978798	1.772027
CTDNEP1	0.069026519	1.318139	0.978701	1.775302
PICALM	0.069182278	1.320798	0.978383	1.783052
SLC35F2	0.069325938	1.320364	0.978257	1.78211
CORO1C	0.069446663	1.317701	0.978287	1.774874
HNRNPD	0.069678076	1.316363	0.978125	1.771564
PRPF31	0.069883261	1.313684	0.978073	1.764454
UGGT2	0.069909377	1.317127	0.977838	1.774141
HOMER1	0.070246917	1.314792	0.97763	1.768233
PATE4	0.070316467	1.31404	0.977605	1.766257
SLC25A32	0.070456404	1.317096	0.977271	1.775088
TUBA1B	0.070468737	1.321255	0.977001	1.78681
ATAT1	0.070532013	0.759987	0.564454	1.023256
IL11RA	0.07082363	0.755914	0.557992	1.024038
FHL2	0.070892553	1.312579	0.977105	1.763233
COL6A2	0.070935245	1.31085	0.977171	1.758472
POLL	0.071043198	0.760851	0.565487	1.023709
CAST	0.071174655	1.312889	0.976797	1.764623
CRTC1	0.071463345	0.757772	0.560474	1.024523
RELA	0.071560115	1.312685	0.976417	1.764762
ZNF333	0.071591523	0.758206	0.561068	1.024611
STXBP5	0.071986784	1.313219	0.975947	1.767047
ZNF185	0.072624437	1.313309	0.975293	1.768476
PGP	0.073004896	1.313272	0.97491	1.76907
ARNTL2	0.073204192	1.320798	0.974185	1.790736
SLC30A1	0.073238692	1.31284	0.974703	1.768281
SLC26A11	0.073634753	0.763435	0.567979	1.026152
FKBP10	0.073791329	1.310689	0.974299	1.763222
GABPA	0.074056072	1.309392	0.974128	1.760043
AFAP1	0.074355254	1.308139	0.973922	1.757047
RPS6KB2	0.074892724	0.765165	0.569952	1.027241
ETFB	0.07507067	1.306555	0.973333	1.753857
ATXN1	0.075496662	0.764419	0.568437	1.027971

TMEM59L	0.07562022	0.765414	0.569923	1.027962
DGKE	0.075692923	0.764931	0.569124	1.028104
FBXL8	0.076227428	0.764328	0.567874	1.028745
GTF2A1	0.076441858	1.306764	0.971972	1.756874
ZNF510	0.076848908	0.765889	0.569964	1.029164
SPDYE1	0.076916153	1.305464	0.971613	1.754027
COL5A3	0.077670371	1.303001	0.971085	1.748366
ZNF564	0.078000576	0.766292	0.569941	1.030288
TTC39B	0.07812231	0.763824	0.566001	1.030787
ZNF662	0.078213372	0.766664	0.570405	1.03045
NAMPT	0.078799121	1.30346	0.969963	1.751623
OTUD3	0.079485575	0.766945	0.570129	1.031704
ZNF436	0.079658387	0.768138	0.571913	1.03169
GPRIN2	0.079816796	0.762968	0.5637	1.032679
ZYX	0.079923068	1.299692	0.969224	1.742838
CD80	0.079973877	0.765926	0.568251	1.032365
PIKFYVE	0.079982459	0.767799	0.571197	1.032072
TCEANC	0.080122694	0.763876	0.564948	1.032849
BAZ2B	0.080339225	0.767164	0.569995	1.032536
SEN7	0.080953359	0.767192	0.569696	1.033154
ZNF14	0.081107976	0.768496	0.571667	1.033094
YDJC	0.081306876	1.304168	0.967509	1.757972
CNPY3	0.081339525	0.768848	0.572094	1.033268
METTL25	0.081393586	0.769167	0.57257	1.033268
XPOT	0.08155167	1.300764	0.967593	1.748656
RPL18	0.081584706	1.298305	0.967792	1.741693
GAS2L1	0.081643091	1.30012	0.967568	1.74697
TOR1AIP1	0.081762211	0.769721	0.573242	1.033543
MAP4K4	0.081832361	1.301218	0.967287	1.750428
CYP4A11	0.081857088	0.766704	0.568423	1.034151
AIP	0.082173796	0.770011	0.573474	1.033904
LRRC58	0.082213478	1.300058	0.96704	1.747756
BACH1	0.082530113	1.299433	0.966804	1.746502
SEC11C	0.082545517	0.767821	0.569803	1.034654
MEAF6	0.082610573	0.770413	0.573871	1.034269
PRPF19	0.082866803	1.303715	0.966077	1.759356
WSB1	0.083168034	0.768787	0.570986	1.035109
MGMT	0.083632359	0.771605	0.575203	1.035069
C18orf32	0.083945388	0.771349	0.574625	1.035422
RAPGEF5	0.083945912	0.768377	0.569909	1.035959
MMP24-AS1	0.084027766	0.771109	0.574199	1.035547
CD226	0.084620539	0.767118	0.567547	1.036865
SPIN3	0.084659488	0.769377	0.571103	1.036487
SYDE2	0.084964377	0.770792	0.573184	1.036527

HELZ	0.08498287	0.771446	0.574213	1.036425
MSH3	0.085106695	1.296506	0.964718	1.742405
MACF1	0.085149568	0.770131	0.572033	1.036833
SLC35A4	0.085499729	1.298599	0.964142	1.749078
NPRL2	0.08557609	0.771291	0.573644	1.037036
UBE2R2	0.085902209	1.296245	0.964019	1.742965
DNAJB6	0.086514776	1.296679	0.963416	1.745224
MTFR1L	0.087204585	0.773132	0.575702	1.038269
PIGL	0.087255723	0.772092	0.574014	1.038523
HIST1H2BC	0.087268329	1.294369	0.962983	1.739793
ANO9	0.087292642	0.770971	0.572207	1.03878
EIF2S2	0.087544608	1.294449	0.962726	1.740472
SSR4	0.087576639	0.77381	0.576586	1.038495
NRAS	0.088743519	1.295863	0.96149	1.74652
FAAP20	0.089059693	1.291559	0.961694	1.734569
C6orf223	0.089128271	1.291943	0.96159	1.735788
MALL	0.089182119	0.774373	0.576632	1.039925
RGL4	0.089420504	0.771447	0.571823	1.04076
STX16-NPEPL1	0.089567158	0.769874	0.569235	1.041231
HIST1H2AL	0.089707988	1.292674	0.960991	1.738837
ZNF138	0.08976758	1.291727	0.961047	1.736189
GPRASP2	0.090129206	0.775118	0.577324	1.040676
BMP2K	0.090358122	0.772954	0.573733	1.041352
HIST1H3D	0.090459875	1.291231	0.960493	1.735856
KDELC2	0.090856917	1.294562	0.95975	1.746176
TTC21B	0.090882744	0.773433	0.574222	1.041755
DPY19L4	0.091386954	1.291456	0.95965	1.737987
ZNF653	0.091646198	1.291155	0.959459	1.737522
SLC25A40	0.091660962	1.291031	0.95946	1.737187
SLC35F6	0.091775215	1.292493	0.959184	1.741624
DCLRE1B	0.09193417	1.291135	0.959208	1.737921
ZNF106	0.093058248	0.774546	0.574863	1.04359
PGM1	0.093064301	1.291474	0.958177	1.740706
NIPSNAP3B	0.093270387	0.775647	0.576525	1.043543
ZFYVE27	0.093437359	0.775332	0.575929	1.043772
SAMD9	0.093550421	1.287194	0.958289	1.728986
DDX60	0.093693171	1.289441	0.957883	1.735764
IRAK1	0.093722312	1.285779	0.958319	1.725133
MSS51	0.093996892	0.775812	0.576411	1.044191
SPATA6L	0.094368957	0.777203	0.578464	1.044221
HIST1H2BO	0.094829614	1.288097	0.957072	1.733615
PSMG3	0.095194653	1.286844	0.95692	1.730516
ZNF714	0.095890729	0.77686	0.577121	1.045726
AC012651.1	0.095940407	0.77514	0.574318	1.046183

ASAP1	0.095990489	1.286315	0.956309	1.730201
SUSD6	0.096052409	0.776983	0.577238	1.045848
ZNF276	0.096711009	0.776862	0.576702	1.046492
CIRBP	0.096946966	0.77772	0.57797	1.046504
STEAP2	0.097058305	1.283976	0.955715	1.724986
MCCC1	0.09723178	0.77934	0.580454	1.046373
SDR39U1	0.097388635	0.7779	0.578035	1.046871
UFSP1	0.098774206	0.778613	0.578485	1.047976
C7orf49	0.098918717	1.283345	0.954237	1.72596
ZNF182	0.099733694	0.772055	0.567385	1.050554
PCF11	0.100092859	0.778683	0.577928	1.049175
FKBP2	0.100161813	1.283158	0.953224	1.727292
TUBB6	0.100378788	1.280415	0.953436	1.71953
LGALS8	0.101046508	0.780917	0.581087	1.049466
PRR19	0.101061123	1.280815	0.952814	1.721729
PYGL	0.101367264	1.284938	0.951961	1.734385
ZNF280D	0.101670838	0.780255	0.579692	1.050209
ZNF23	0.101766128	0.780288	0.579698	1.050287
SLC25A14	0.101832292	0.775727	0.572243	1.051568
ZNF75D	0.101888958	0.773564	0.568713	1.052203
RAB27B	0.102030433	1.278108	0.952415	1.715177
DCP1A	0.102145279	0.780103	0.579204	1.050683
ZMAT3	0.102329193	0.782869	0.58364	1.050108
LIMK1	0.102351039	1.280656	0.951774	1.723183
SNCAIP	0.102404659	0.781735	0.581743	1.05048
STXBP2	0.102771696	0.782157	0.58225	1.050698
AC134669.2	0.102887655	0.780041	0.578732	1.051377
RAB11FIP5	0.102937862	1.280112	0.951373	1.722443
TMEM41A	0.104085109	1.277008	0.950909	1.714939
FAS	0.104620299	0.783288	0.583187	1.052047
GGT7	0.104685212	0.783684	0.583805	1.051995
ZNF414	0.104763629	0.783009	0.582657	1.052253
KLF16	0.10498325	1.275403	0.950432	1.711488
FGL2	0.105102286	0.780277	0.578009	1.053327
TMEM127	0.105780169	1.276072	0.949686	1.71463
ZNF540	0.105894223	0.776605	0.571618	1.055102
SOCS4	0.106837994	1.274134	0.949147	1.710395
GSK3B	0.106963267	1.276172	0.94872	1.716644
PUS7L	0.107202234	1.273385	0.948978	1.70869
DEXI	0.107216031	0.785209	0.585072	1.053806
METTL3	0.10726957	0.783481	0.582195	1.054357
KIFC2	0.108077802	0.784066	0.582764	1.054904
ZNF253	0.108142968	0.784729	0.583826	1.054766
ZNF44	0.108597082	0.782182	0.579404	1.055928

AP3B1	0.108782694	1.272558	0.947861	1.708481
FBXO22	0.108852082	1.275894	0.947255	1.718551
KRBOX4	0.108858686	0.784494	0.583088	1.055469
MRI1	0.10886616	0.785277	0.584379	1.055242
ANGPTL5	0.108946593	0.786284	0.586006	1.055011
KIF1B	0.109020648	0.786037	0.585561	1.05515
AL365205.1	0.10916089	0.785446	0.584514	1.055451
ATP6V1G2	0.109409858	0.785014	0.583678	1.0558
RPA4	0.110453528	1.272452	0.946563	1.710541
SPATA5	0.110547469	1.277582	0.94562	1.726081
FAM3C	0.110926645	1.272238	0.946228	1.710571
CTHRC1	0.111230052	1.272353	0.94597	1.711346
ZNF821	0.111431242	0.785609	0.58368	1.057397
IGF2BP2	0.111889706	1.271343	0.945628	1.70925
HIST1H4D	0.112154758	1.270978	0.945484	1.708526
SHMT2	0.112207096	1.271874	0.945288	1.711293
CALCOCO1	0.113243335	0.787358	0.58571	1.058428
UBC	0.113456565	1.270493	0.944557	1.708897
MRPL21	0.113944221	1.269477	0.94436	1.706522
MEF2C	0.114467788	0.788491	0.587013	1.059123
ASB16	0.114514496	0.788613	0.587193	1.059124
ITSN1	0.114751853	1.266935	0.944196	1.699991
HES4	0.114986755	1.267543	0.943906	1.702146
SSPN	0.115229306	1.268356	0.943572	1.704931
VPS8	0.115356447	1.26934	0.943296	1.70808
RPS6KA4	0.115369051	1.266797	0.943749	1.700425
TMTC3	0.115482368	1.274032	0.942346	1.722466
HIST1H4E	0.11593413	1.266169	0.943433	1.699308
SMIM18	0.116495394	1.26782	0.942701	1.705068
C6orf163	0.116559332	1.266468	0.942902	1.701069
ZNF417	0.116688399	0.785106	0.580311	1.062176
INCA1	0.11683517	0.78856	0.585998	1.06114
HACD3	0.117133668	1.267037	0.942359	1.703579
OSTN	0.117623477	1.2649	0.942388	1.697784
SLMAP	0.117856347	1.265708	0.942059	1.700547
SUGP1	0.117924097	0.788432	0.585267	1.062121
NISCH	0.118005995	0.788195	0.584832	1.062273
UVSSA	0.118323936	0.790328	0.588256	1.061815
MAN2C1	0.118817917	0.790062	0.587576	1.062328
TRABD	0.118928003	0.791242	0.589506	1.062015
MPL	0.118956452	0.789644	0.586808	1.062591
ZNF83	0.119826237	0.790299	0.587499	1.063105
ARL13B	0.12039376	0.792291	0.590585	1.062887
RABL2A	0.120970036	0.791429	0.588862	1.063678

DIP2B	0.121003458	1.267792	0.939275	1.711208
CARF	0.121109985	0.791402	0.588751	1.063806
NEIL1	0.121808901	0.791457	0.588517	1.064377
TSPYL2	0.121817077	0.78914	0.584615	1.065217
AL353588.1	0.122143005	0.791745	0.588846	1.064556
TET2	0.122148125	0.791538	0.588495	1.064635
CES4A	0.12233639	0.791636	0.588572	1.064759
ARHGAP10	0.122438401	1.262878	0.93917	1.698159
COL5A1	0.122611999	1.26258	0.9391	1.697484
NRL	0.122652103	0.791285	0.587833	1.065153
VCL	0.122857848	1.262947	0.938844	1.698935
MYCBP2	0.123040924	0.792806	0.59022	1.064927
TLR4	0.123088996	0.791766	0.588442	1.065346
PINK1	0.123278623	0.793604	0.59146	1.064836
AVL9	0.123974649	1.2616	0.938289	1.696316
ACTR8	0.124098363	0.793991	0.591736	1.065377
SCRN2	0.124232539	0.793284	0.590476	1.06575
ANTXR2	0.124737312	1.260314	0.93799	1.693398
ACAD11	0.125243491	0.791663	0.587264	1.067203
KRBA2	0.125366045	0.79334	0.590046	1.066677
MRPL27	0.125903796	1.258268	0.937561	1.688677
PET100	0.126093274	0.794918	0.59239	1.066688
APH1B	0.12658575	0.79529	0.592795	1.066955
PCP2	0.126714316	0.793133	0.589073	1.067882
CLHC1	0.127273356	0.794171	0.590576	1.067952
PICK1	0.127649748	0.794618	0.591163	1.068092
ANKRD13D	0.127849052	0.795229	0.592113	1.068022
CC2D1A	0.12797372	0.791101	0.585048	1.069725
ZNF557	0.128150306	0.79093	0.584677	1.069941
SUMO3	0.128388968	1.259227	0.935548	1.694891
TTC32	0.128664781	0.79557	0.59232	1.068563
FAM196B	0.128968692	1.257057	0.935596	1.688969
JPT1	0.129018133	1.257339	0.935499	1.689901
ABCF2	0.129450916	1.258637	0.934904	1.694469
PNISR	0.130021089	0.793038	0.587389	1.070686
MRS2	0.130083616	0.796307	0.592931	1.069441
PCGF1	0.130108921	0.797416	0.594816	1.069024
ZNF345	0.130195583	0.796139	0.592593	1.0696
BRCA2	0.130316073	1.257964	0.934424	1.693529
C19orf18	0.130349623	0.795542	0.591503	1.069964
ACTR3	0.130562202	1.255431	0.934805	1.686026
OR5K2	0.130823601	1.255383	0.934628	1.686219
NPIPA1	0.130846064	0.79566	0.591478	1.070326
KCNS2	0.131807993	0.795365	0.590536	1.071239

LSM4	0.131891538	1.255001	0.933949	1.686417
TBC1D17	0.132032814	0.795294	0.590314	1.071453
TCF19	0.132043057	1.258064	0.933156	1.696099
STRADA	0.132258553	0.796317	0.59196	1.071223
PANX1	0.132507992	1.261125	0.932134	1.706231
MBLAC1	0.133129273	1.255581	0.932935	1.689812
PALLD	0.133187196	1.255789	0.932846	1.690533
NR2C2	0.133477748	0.796999	0.592576	1.071944
PRKD3	0.133609263	0.79822	0.594611	1.071548
NCK1	0.133808539	1.253868	0.932841	1.685374
MZT2B	0.13393999	1.25424	0.932663	1.686695
MTMR8	0.134056491	0.793038	0.58554	1.074065
PPP3CA	0.134083108	1.253421	0.932749	1.684338
HAGH	0.13440641	0.798017	0.593904	1.07228
LLGL2	0.13454652	0.798604	0.59485	1.07215
AKAP8L	0.134584094	0.797091	0.592233	1.07281
PLAU	0.134736435	1.252033	0.932607	1.680864
ZNF292	0.135036073	0.798458	0.594378	1.072608
CCDC121	0.135152573	0.798393	0.594215	1.072729
ALKBH4	0.135174898	0.796186	0.590414	1.073674
ALX3	0.13547616	0.799645	0.596225	1.072466
GPR34	0.135599008	0.794504	0.587343	1.074734
PTPN22	0.136184706	0.797405	0.59205	1.073986
PTBP2	0.136370793	0.799241	0.595129	1.073358
ZDHHC21	0.136440957	0.798776	0.594295	1.073612
LAMTOR4	0.136708102	0.79978	0.595908	1.073401
SPHK1	0.136858377	1.252247	0.931064	1.684226
VTI1B	0.137251307	1.25064	0.931169	1.679717
UBE2Z	0.137490607	1.251249	0.930857	1.681917
ZNF625	0.137940193	0.79843	0.593027	1.074976
RNF44	0.137995855	1.249632	0.93089	1.677514
JMJD7-PLA2G4B	0.138327734	0.798573	0.5931	1.075228
CXCR2	0.138992734	0.798288	0.592312	1.075892
PEX16	0.139569581	0.800482	0.595846	1.075397
MICAL1	0.140152273	0.799833	0.594464	1.076151
RAB11B	0.140421478	0.800632	0.595728	1.076014
STXBP4	0.140484451	0.801427	0.597079	1.075712
PSMC2	0.14066943	1.251301	0.928623	1.686104
UBXN11	0.141258721	0.800043	0.594336	1.076948
ABHD14A	0.141298669	0.800013	0.594266	1.076994
CARD8	0.141361999	0.798444	0.591523	1.077748
SAC3D1	0.141602867	1.247267	0.928972	1.674619
STAM2	0.141626657	0.802308	0.598105	1.076229
TUBA1C	0.142652175	1.250584	0.927421	1.686354

CYLD	0.142785095	0.799222	0.592236	1.07855
BRI3	0.143047942	1.250101	0.927267	1.685332
MAP2K2	0.143635354	1.245131	0.928118	1.670426
NUBP2	0.143858138	0.803127	0.59855	1.077626
C16orf58	0.144203518	0.802908	0.598015	1.078
TTBK2	0.144823582	0.802873	0.597682	1.078507
CDA	0.144881464	1.251233	0.92571	1.691226
MAGEH1	0.144979901	0.795409	0.584669	1.08211
MGA	0.145010761	0.803246	0.598252	1.078483
CCNL2	0.145845277	0.802157	0.595985	1.079651
GNGT1	0.145964004	1.244289	0.926752	1.670625
UBE2D1	0.146041882	1.246316	0.926174	1.677117
C20orf96	0.147373614	0.802825	0.596481	1.080551
METTL17	0.148005301	0.804256	0.598709	1.080369
RELB	0.149077758	1.241232	0.925462	1.664743
BSG	0.15005794	1.243683	0.924148	1.673702
TRPM7	0.150128408	0.803696	0.596802	1.082313
NME3	0.150437907	0.806185	0.601044	1.081343
ZGPAT	0.150795679	0.80418	0.597361	1.082603
GPR87	0.150981687	1.243532	0.923567	1.674346
CHRM2	0.151169644	0.806723	0.601676	1.081649
MRNIP	0.151236302	0.80377	0.59645	1.083152
MTR	0.151948986	0.806557	0.601047	1.082335
RING1	0.152320517	0.80649	0.600768	1.082658
CALU	0.152533679	1.243665	0.922488	1.676664
KIDINS220	0.153305907	0.80716	0.601527	1.083089
BRMS1	0.153539311	1.240215	0.922769	1.666868
C8orf37	0.153775865	1.240908	0.922419	1.669365
ZNF680	0.15378802	0.806718	0.600539	1.083684
CENPL	0.154497598	1.24149	0.921777	1.672093
TBX6	0.15503703	1.238661	0.922213	1.663696
CRTC2	0.155273037	0.806491	0.599497	1.084955
VASP	0.155338629	1.237148	0.922442	1.65922
PARP8	0.155786219	0.807871	0.601721	1.084648
CLLU1	0.15604696	0.807074	0.600197	1.085259
CRLF1	0.156192858	0.807772	0.601371	1.085014
MRPL53	0.156399772	1.237178	0.921738	1.660569
SEMA3C	0.156683048	1.239745	0.92082	1.66913
ZNF133	0.156928963	0.805759	0.59749	1.086625
WASHC4	0.156957891	1.238811	0.920905	1.66646
DYNC2H1	0.156970196	0.807687	0.600888	1.085659
RSPH6A	0.157032348	0.805459	0.596915	1.086862
TMEM176A	0.157107638	0.809062	0.603271	1.085054
CEP95	0.157175998	0.806273	0.598292	1.086552

CBX7	0.157326101	0.80182	0.590376	1.088994
SMG9	0.157396308	1.236367	0.921319	1.659147
SNX3	0.157401711	1.237141	0.921093	1.661633
NT5DC2	0.157468863	0.809215	0.603389	1.085252
NUDT14	0.157922878	0.808896	0.602628	1.085766
PHF21A	0.158423071	0.808222	0.601216	1.086504
DNAJC13	0.158637176	1.236216	0.920553	1.660122
ANKRD12	0.158796291	0.809027	0.602489	1.086369
C19orf24	0.159250244	1.235761	0.920287	1.659379
GJA5	0.15954226	0.809956	0.603827	1.086452
FAM160A1	0.159566017	0.809251	0.60256	1.086843
EDIL3	0.1608356	0.810494	0.604239	1.087154
PTTG1IP	0.161064667	1.240648	0.917663	1.677312
ZNF814	0.161934743	0.808566	0.600329	1.089034
SPSB3	0.161937625	0.810121	0.603104	1.088197
SHARPIN	0.162018523	1.23516	0.918667	1.660689
CCNK	0.162119303	1.237237	0.917982	1.667521
ZCRB1	0.162463996	1.236513	0.917974	1.665587
ZNF517	0.162756307	0.810445	0.603338	1.088647
MTF1	0.16298677	0.810549	0.603426	1.088766
WBP11	0.163951132	1.237715	0.916642	1.671251
MRPS34	0.164050038	1.23589	0.917131	1.665437
LIN7B	0.164169364	0.81126	0.604199	1.08928
ZBTB44	0.164224586	0.811156	0.603989	1.089379
ADAT1	0.164471293	0.812307	0.605953	1.088934
CA1	0.16572413	0.812555	0.605873	1.089744
C1orf210	0.165916588	0.811038	0.603064	1.090735
ADCY9	0.166071833	0.811208	0.603303	1.090758
NBAS	0.166147834	0.810752	0.602453	1.091071
RBMS1	0.16621431	1.235	0.916001	1.665089
MYO9A	0.166356873	0.812495	0.605499	1.090256
BUD23	0.166545916	1.234974	0.915795	1.665394
RNF167	0.166830497	1.231357	0.916734	1.65396
CGNL1	0.167002468	0.810462	0.601571	1.091888
SH3GLB1	0.167048027	1.233633	0.915887	1.661613
PLOD3	0.167378156	1.229827	0.916863	1.649618
SP2	0.167653896	0.811476	0.603119	1.091814
DENND4A	0.16766586	0.810898	0.602075	1.09215
CLDN7	0.167707568	1.230712	0.916377	1.652871
TBCEL	0.168098546	0.812307	0.604428	1.091681
LRRC26	0.168505567	0.813227	0.605917	1.091467
TSSK3	0.168625706	0.810329	0.600648	1.09321
NUMBL	0.168909764	1.242333	0.911965	1.692379
SLC12A6	0.169259604	0.812596	0.604461	1.092397

ARMC10	0.169326668	1.231557	0.91508	1.657485
ZFX	0.169527317	1.231508	0.914968	1.657558
GNG12	0.17063566	1.227823	0.915442	1.6468
TSPAN14	0.171078855	1.228159	0.915055	1.648398
PARVB	0.17205199	1.228615	0.914295	1.650994
TMEM8B	0.172130387	0.811934	0.602062	1.094965
RNF213	0.172791742	1.228261	0.913944	1.650674
AP002360.1	0.173315392	0.814748	0.606663	1.094205
KDM7A	0.17352043	0.815052	0.607131	1.094179
KLHDC4	0.173826202	0.814945	0.606808	1.094472
FGF1	0.17399619	0.815593	0.607918	1.094215
MED25	0.174286143	0.815071	0.606846	1.094742
HBP1	0.175315633	0.816064	0.608228	1.09492
C15orf40	0.175365574	1.225289	0.913313	1.643832
SND1	0.175713934	0.814605	0.605406	1.096094
FAM126B	0.175930615	0.816526	0.608815	1.095101
SPATS2L	0.17647389	1.224938	0.912742	1.643919
CYP7B1	0.176717655	1.22721	0.911829	1.651675
ZNF654	0.176731408	0.816459	0.608362	1.095737
PKIG	0.176786874	0.813385	0.602742	1.097644
LIN54	0.177134806	1.225884	0.912013	1.647774
BEX2	0.177881825	0.81527	0.605716	1.097321
ZNF226	0.177933789	1.222963	0.912505	1.639047
TMEM185B	0.178113691	1.22646	0.911209	1.650779
ARPC1B	0.178370056	1.224465	0.911726	1.644478
EDEM3	0.178459339	1.223432	0.912022	1.641171
ZNF484	0.178736588	0.815367	0.605539	1.097904
SLC2A13	0.178744298	1.224847	0.911364	1.646159
C19orf54	0.178933276	1.224752	0.911279	1.646056
PTPN4	0.179037844	0.815924	0.606432	1.097787
CPA2	0.179144227	0.817264	0.608838	1.09704
TAS2R19	0.17937109	1.223472	0.911446	1.642319
LAMB1	0.180346257	1.22287	0.911052	1.641411
LARP4	0.180394319	1.223137	0.91093	1.642347
SMIM22	0.180423483	1.224504	0.910441	1.646906
GSTCD	0.180641618	1.224287	0.910381	1.646432
RPAIN	0.180686795	0.817763	0.609118	1.097876
VPS13C	0.181299569	0.815347	0.60444	1.099846
BOLA1	0.181327905	1.221873	0.910794	1.639199
GPR61	0.181423888	0.817709	0.608716	1.098457
NR2C2AP	0.182427626	0.81915	0.610954	1.098293
ZFP91	0.18292392	1.221007	0.91012	1.638089
MFSD8	0.18296733	0.818777	0.610045	1.098927
NR1H2	0.18297487	0.818821	0.610125	1.098904

TRIM52	0.183035937	0.81519	0.603433	1.101258
MFSD14B	0.183749502	1.223014	0.908907	1.645672
ARID1B	0.183825538	0.81796	0.608189	1.100083
C15orf61	0.183864464	0.81902	0.610126	1.099435
GOPC	0.183919753	1.22149	0.909341	1.640791
ASPSR1	0.183985599	0.818325	0.608796	1.099968
ARAP2	0.183989648	1.220825	0.909533	1.638656
REL	0.184107214	0.817479	0.607189	1.1006
TRPS1	0.18445802	1.220312	0.90943	1.637468
STYX	0.184489394	1.222524	0.908625	1.644863
E4F1	0.184554632	0.818004	0.607971	1.100597
MESP1	0.184774157	0.819384	0.610425	1.099873
CNOT1	0.184829634	0.819747	0.611073	1.099682
LRRC8A	0.185021616	1.220016	0.909192	1.637101
C14orf93	0.185368339	1.220617	0.908766	1.639482
EEA1	0.185562324	0.818525	0.608517	1.10101
SRMS	0.185837834	0.81979	0.610741	1.100396
HIST1H1E	0.186762309	1.218509	0.908677	1.633985
ATP5D	0.186776107	1.219593	0.908277	1.637615
ODF3B	0.186817258	0.819609	0.610006	1.101235
VKORC1L1	0.18708216	0.820494	0.611536	1.100853
DNPH1	0.187417895	1.219142	0.908051	1.636811
TFEC	0.188399774	0.816207	0.60308	1.104654
NTAN1	0.188637228	1.218804	0.907435	1.637012
CLDN4	0.189970963	1.216851	0.907347	1.631929
EMC9	0.190252562	1.219024	0.906375	1.63952
GOLIM4	0.190339798	1.217962	0.906715	1.63605
TPM4	0.190348948	1.21706	0.907043	1.633038
SPTLC1	0.190637594	1.221101	0.905375	1.64693
THAP5	0.190795704	0.822136	0.613075	1.102487
ZNF19	0.190819371	0.821148	0.611226	1.103165
RBM5	0.191550699	0.819112	0.607147	1.105075
CPT1B	0.191568828	1.217764	0.906047	1.636726
SBDS	0.191678996	1.217904	0.905928	1.637316
DLD	0.191733166	1.223264	0.903903	1.655461
INHBA	0.191904872	1.217923	0.905785	1.637626
ZFAND2B	0.191938099	0.822281	0.612883	1.103223
RNF10	0.192842818	1.215165	0.906256	1.62937
NSMCE4A	0.192948992	0.822807	0.613456	1.103604
DIAPH1	0.19296281	1.216007	0.905867	1.632328
ELK3	0.193178033	1.215539	0.905914	1.630988
NETO1	0.193783297	1.2167	0.905113	1.635551
UBE2C	0.194192172	1.21855	0.904167	1.642246
UBE2Q2	0.194250897	1.215938	0.905121	1.633488

GREM1	0.194440351	1.21757	0.904388	1.639204
HNRNPA1	0.194557827	1.217104	0.904494	1.637757
ZNF467	0.194831054	1.214285	0.905404	1.628543
ADAM20	0.194875657	0.822438	0.611984	1.105263
NCOA2	0.195015259	1.214758	0.905113	1.630333
ALKBH6	0.195316059	1.214773	0.904928	1.630706
AC006254.1	0.195370728	0.818904	0.605199	1.108073
ZFP1	0.195856493	0.823984	0.614483	1.104911
SLC24A1	0.19646681	0.823735	0.61377	1.105527
ITPR2	0.19744215	0.822316	0.610717	1.107229
RNF169	0.197609761	0.82339	0.612662	1.106599
TRMT10B	0.197681743	0.823148	0.612179	1.106822
ANTXR1	0.197799661	1.213166	0.904071	1.627937
RALB	0.19806124	1.216717	0.902536	1.640268
C6orf226	0.19828705	0.825197	0.615784	1.105824
MPP6	0.198689504	1.213752	0.903314	1.630876
CTDSP1	0.19876785	1.213039	0.903547	1.628541
BLOC1S3	0.19944828	1.212127	0.903502	1.626174
LMNA	0.200109372	1.213699	0.902491	1.632222
CEP41	0.200574941	1.212671	0.902621	1.629222
ELF2	0.201174375	0.825744	0.615657	1.10752
CCDC188	0.201528451	0.824221	0.612643	1.108869
LCA5L	0.201654513	0.826059	0.61606	1.107641
CLIC4	0.202806425	1.212226	0.901478	1.630091
UBE2J1	0.202930465	0.825657	0.614789	1.108852
PIK3R4	0.203189399	1.211966	0.901356	1.629612
JAK2	0.20332154	0.82377	0.61107	1.110508
HTATSF1	0.203790963	1.20958	0.901964	1.622111
CCDC36	0.203807582	0.825577	0.614286	1.109545
TRIP12	0.204661531	1.214002	0.899663	1.63817
DST	0.20515646	1.209295	0.901281	1.622574
PTAR1	0.205738493	0.825819	0.613967	1.11077
PIM3	0.205802471	1.210555	0.900388	1.62757
DNAJB2	0.206500543	0.827476	0.616809	1.110095
LPGAT1	0.206811461	1.21185	0.899263	1.633094
NRIP1	0.207128849	1.208643	0.900396	1.622418
HIST1H4C	0.207592842	0.82802	0.617409	1.110476
LRRRC15	0.20781353	1.209686	0.899565	1.626721
RAPSN	0.207858915	0.823305	0.608357	1.1142
CHRNA	0.207921091	0.825373	0.612246	1.112691
HPS1	0.207984281	0.82826	0.61771	1.110577
RSF1	0.208125316	1.207815	0.900158	1.620623
ARID1A	0.20869847	0.827484	0.615946	1.111672
LRRTM2	0.208751402	0.827936	0.616787	1.11137

SORBS3	0.208862081	0.82722	0.615377	1.111988
CD320	0.208969833	0.828205	0.617212	1.111325
TMEM250	0.20936078	1.209116	0.898895	1.626398
DCXR	0.20947678	0.828568	0.617704	1.111415
ANKRD46	0.209654308	0.827942	0.616437	1.112015
EP300	0.2097237	0.827407	0.615389	1.11247
SLC35B1	0.210000398	0.828826	0.617987	1.111596
POLR2L	0.210274108	1.206491	0.899463	1.618322
ERCC4	0.210483673	0.828926	0.617986	1.111866
GOLGA6L10	0.210528296	0.82845	0.617059	1.112259
FLYWCH2	0.21067347	0.826424	0.613136	1.113906
SNX1	0.211128164	0.828949	0.617775	1.11231
SLC39A9	0.211363379	1.209445	0.897585	1.62966
ACAP3	0.211375706	0.828442	0.616706	1.112874
AP1G2	0.211486045	0.826094	0.612183	1.114751
SLC35E2B	0.211883927	0.829174	0.617905	1.11268
ATP11C	0.212327372	1.206956	0.898076	1.622071
CLPP	0.212685463	1.20568	0.898412	1.618036
RAD23B	0.212774423	1.20832	0.897235	1.627263
PURB	0.213102073	1.205475	0.898259	1.617762
POC1B-GALNT4	0.213744753	0.829468	0.617728	1.113787
ZBTB21	0.213893268	0.829809	0.618323	1.113629
RPS24	0.214039327	1.205278	0.897803	1.618058
AC040162.1	0.215236559	1.205792	0.896889	1.621086
ATAD2B	0.21529646	0.829681	0.617521	1.114734
CLCN3	0.215798239	1.206057	0.896449	1.622595
PLXNC1	0.215958131	0.827338	0.612762	1.117053
PPP2R3A	0.216019783	0.830485	0.618779	1.114623
SPRYD4	0.216289936	0.830659	0.619008	1.114678
PEA15	0.216314085	1.204209	0.896955	1.616715
GNL3L	0.216388087	1.203143	0.897378	1.613091
ZBTB40	0.216582897	0.829158	0.616004	1.11607
ZNF689	0.216754695	0.831449	0.620346	1.114389
KIAA1191	0.216893246	1.20409	0.896674	1.616899
PDIA3	0.217318903	1.204688	0.896167	1.619422
UBAP1L	0.217463666	0.828945	0.615243	1.116876
ZNF775	0.217723741	0.830401	0.617941	1.115908
TRAF6	0.217784631	0.83021	0.617549	1.116103
VCPIP1	0.217824041	1.205179	0.89566	1.62166
SLC2A14	0.21787133	1.20287	0.896648	1.613674
RAB9A	0.218056084	1.205745	0.895278	1.623876
TAB2	0.218136211	1.203977	0.896008	1.617799
MRGPRX3	0.218280846	1.202796	0.896446	1.613836
SAMD11	0.21852503	1.203284	0.896091	1.615786

SPDYE5	0.218542163	0.83112	0.619005	1.115922
LRRC8C	0.218833036	0.831155	0.618956	1.116102
WDFY1	0.21929065	1.202817	0.895859	1.614951
XRN2	0.219564269	1.201746	0.896178	1.611504
C19orf53	0.219680402	1.203189	0.89547	1.616654
ESRRA	0.219933111	1.202181	0.895774	1.613397
ARSA	0.220563904	0.832202	0.620297	1.116497
TMX4	0.22146471	0.831822	0.619205	1.117445
GGA1	0.221472952	0.830293	0.616243	1.118692
TMEM106B	0.221618081	1.206063	0.893071	1.628749
FANCM	0.2216726	1.206169	0.892992	1.629178
KHDRBS2	0.221765167	0.828411	0.612498	1.120437
SDF4	0.222016412	1.204009	0.893761	1.621953
SLCO5A1	0.222453703	1.201206	0.894773	1.612585
SZRD1	0.223173813	0.831562	0.618024	1.11888
SRSF8	0.223435058	0.832941	0.6206	1.117937
AQR	0.224767523	1.205243	0.891614	1.629193
PUDP	0.225009203	1.201593	0.893139	1.616576
COPS6	0.225172063	1.202369	0.892691	1.619475
CTSF	0.225483826	0.831819	0.617608	1.120327
ZNF624	0.225609095	0.834151	0.6221	1.118482
SLC25A45	0.225816622	0.832677	0.619144	1.119853
AUP1	0.225835285	1.200354	0.893236	1.613068
RAP2C	0.226139093	1.199069	0.893656	1.60886
JSRP1	0.226294113	0.833402	0.620369	1.11959
GPR108	0.226424595	0.834094	0.621668	1.119107
ACADVL	0.226520198	1.199182	0.893388	1.609645
RC3H1	0.22657491	0.833985	0.621396	1.119304
PPIL1	0.226633725	1.2008	0.892576	1.615459
HIST1H2AI	0.226684407	1.198552	0.893587	1.607597
ANKHD1	0.226878516	0.831703	0.616829	1.121428
MSH5	0.226893416	0.833272	0.61988	1.120125
AGL	0.226998526	1.198586	0.893394	1.608034
ANKDD1A	0.227134978	0.830663	0.614707	1.122488
AC093155.3	0.227290439	0.834712	0.622536	1.119203
SLC25A27	0.227662618	0.832259	0.617599	1.121527
CDPF1	0.22771643	0.834925	0.622784	1.119326
ZNF621	0.227970776	0.834219	0.621303	1.120099
PPP6R2	0.228367854	0.833149	0.619057	1.121282
SDCCAG3	0.228811806	1.197675	0.892795	1.606667
CTU1	0.229067232	1.198179	0.892415	1.608705
HCFC2	0.229196055	0.833177	0.618785	1.121851
MST1	0.229469775	0.834132	0.620544	1.121237
DPM2	0.230172952	0.834847	0.621667	1.12113

CCDC134	0.230859434	1.198248	0.89137	1.610778
VCPKMT	0.231047396	0.835001	0.621625	1.121619
G3BP2	0.231120845	1.197392	0.891627	1.608014
AGTPBP1	0.231411822	0.835265	0.622	1.121652
IP6K2	0.231440557	0.83393	0.619371	1.122816
LCN12	0.231732076	0.835316	0.621974	1.121835
EXOC5	0.231937196	1.1982	0.890783	1.61171
RASA1	0.232034436	1.19585	0.891848	1.603476
C10orf113	0.232316673	1.196273	0.891487	1.605262
MTERF2	0.232475487	0.835583	0.622207	1.122132
PIGT	0.232644304	1.196406	0.89124	1.606063
ZNF91	0.233240063	0.83489	0.620544	1.123274
SNRPA	0.233437453	1.200691	0.888742	1.622134
RAB3GAP1	0.233820761	1.197914	0.889854	1.612621
LDOC1	0.233863915	1.196178	0.890664	1.60649
CA5B	0.234003048	0.832935	0.616407	1.125524
COA4	0.234475404	1.197349	0.889756	1.611278
SRSF4	0.23467401	0.836023	0.62221	1.123309
RSG1	0.235022138	0.837209	0.624416	1.122519
PHYKPL	0.23507661	0.834601	0.619252	1.124839
NAA35	0.235099308	0.83481	0.619655	1.124672
CNKSR1	0.235318532	0.836333	0.62257	1.123494
GJB7	0.235375361	1.194705	0.890529	1.602778
CSGALNACT2	0.235445802	1.196494	0.889622	1.609221
LAMA2	0.235519995	0.836391	0.622606	1.123586
WDR83	0.23583323	0.835292	0.620315	1.124773
LRP12	0.235871118	1.194762	0.890224	1.60348
POGLUT1	0.236103848	0.836043	0.621688	1.124306
ZNF347	0.236329613	0.835812	0.621144	1.12467
MID2	0.237522126	0.837214	0.623446	1.124278
TOX3	0.23755614	1.195618	0.888862	1.608239
INTS6L	0.237664053	0.8313	0.611747	1.129649
GPR22	0.23767823	0.837762	0.624471	1.123903
SOAT1	0.237989544	1.195749	0.888554	1.609147
CLIC1	0.238192841	1.193994	0.889304	1.603077
ANKRD17	0.238302943	0.836358	0.621446	1.125592
HIST2H2BF	0.238496572	1.193372	0.889441	1.601158
PATZ1	0.238784265	0.837399	0.623319	1.125005
ST7L	0.23896213	1.19385	0.888945	1.603337
TEX261	0.239029845	0.838063	0.62454	1.124587
ARSD	0.239104132	0.838362	0.625105	1.124372
AC022335.1	0.239381627	1.192751	0.889256	1.599826
EXOC6B	0.239423987	1.192787	0.889215	1.599997
SPIDR	0.239713075	0.838137	0.624421	1.125001

FBR5	0.240109634	0.838232	0.624453	1.125196
RBM6	0.240582014	0.835532	0.618914	1.127965
COL5A2	0.240597169	1.194794	0.887562	1.608377
SHPRH	0.240648939	0.835314	0.618458	1.12821
CHSY1	0.240964376	1.192332	0.888586	1.599909
DNAJC4	0.240972572	0.839066	0.625777	1.125053
TVP23C	0.24123617	0.837999	0.623549	1.126201
FOXB1	0.241378042	0.839219	0.625924	1.125199
DMTF1	0.241715901	0.838102	0.623568	1.126447
PTBP3	0.242030023	1.197766	0.885272	1.620568
RBM15	0.242561626	1.191035	0.888353	1.596847
ARHGAP18	0.242562839	0.837969	0.62297	1.127168
GOLGA8B	0.242761501	0.83821	0.623371	1.12709
ADGRE1	0.242791509	0.838862	0.62466	1.126516
PREPL	0.243354935	0.839859	0.626431	1.126004
HIST1H1D	0.243449447	1.191954	0.887396	1.601038
RMND5B	0.243971268	0.839731	0.625935	1.126553
WNT4	0.245080042	0.84006	0.62616	1.127029
KIAA0319L	0.245139055	0.84006	0.626137	1.127071
SIX2	0.245231866	0.840151	0.626282	1.127053
TMEM256	0.245531215	1.192111	0.886158	1.603697
USE1	0.245678815	0.839516	0.624838	1.127953
TMEM132A	0.246303484	1.190156	0.886733	1.597405
TIMM10B	0.246318905	0.838414	0.622384	1.129429
WBP1	0.246335406	0.840311	0.626174	1.127679
HIST1H2BI	0.246405334	0.840156	0.625836	1.127871
HIST1H2BM	0.246576618	1.189153	0.887099	1.594054
RAPGEF2	0.246745544	0.840076	0.625543	1.128185
WDPCP	0.246821191	0.840106	0.625572	1.128211
ECHDC2	0.246918966	0.838909	0.623137	1.129395
CTC1	0.247120421	0.839493	0.624227	1.128993
POLR2M	0.247156013	1.194779	0.883882	1.61503
MOB1A	0.247183167	1.193192	0.884682	1.609288
C5orf42	0.247226197	0.840465	0.626134	1.128162
CDK11A	0.247751292	1.189322	0.886365	1.59583
C9orf142	0.247806047	0.840122	0.625221	1.12889
USP50	0.247912776	0.84065	0.626239	1.128471
CHID1	0.247944136	0.841025	0.62698	1.128143
THY1	0.247993496	1.188919	0.886441	1.59461
SLC10A3	0.248143345	1.189415	0.886101	1.596554
MLYCD	0.248864039	0.840438	0.625441	1.12934
ABCA6	0.249212588	0.835619	0.615668	1.134148
SFRP2	0.249908425	1.188694	0.885504	1.595696
ZNF644	0.250357621	1.188648	0.885281	1.595972

UBE2W	0.250394766	0.840168	0.6243	1.130677
CUL4B	0.250861725	1.189375	0.884621	1.599119
PTPN23	0.251086079	0.84123	0.626169	1.130156
XPO4	0.251892559	1.188213	0.884665	1.595914
MIIP	0.252585053	0.842018	0.627174	1.130458
ZNF580	0.253572371	0.841866	0.626482	1.131298
VPS9D1	0.253619826	0.842229	0.627199	1.130982
RBM39	0.2538899	0.841885	0.626396	1.131504
LYST	0.254412088	0.840491	0.623377	1.133223
NRAP	0.254590699	0.841275	0.62489	1.132589
NKTR	0.255541616	0.841507	0.624988	1.133037
NOL3	0.256087703	1.185435	0.883852	1.589922
TRPT1	0.256389943	0.843658	0.629018	1.131538
HIST1H2BG	0.256430825	1.186012	0.883353	1.59237
COASY	0.256887751	1.189678	0.881119	1.606292
THAP9	0.257453302	0.843987	0.629276	1.131959
AKAP9	0.257465255	0.843599	0.628482	1.132347
PARVA	0.25775142	0.84421	0.629614	1.131948
PSMD4	0.257787066	1.185767	0.882744	1.59281
PPP1R15B	0.257801788	1.186518	0.882326	1.595583
SAPCD1	0.258087715	0.843235	0.627498	1.133143
PIN1	0.259460196	0.84415	0.628827	1.133203
ZNF157	0.259542606	0.843643	0.627762	1.133763
AD000671.2	0.259573508	0.842413	0.625248	1.135006
CLIP2	0.260240742	1.183518	0.88264	1.586962
SUMO4	0.260548612	1.183296	0.882595	1.586445
ANGPTL2	0.261211014	1.184918	0.881336	1.593072
TAS2R13	0.2620064	0.845401	0.630397	1.133735
CCDC124	0.262370604	1.18338	0.881559	1.588535
DUSP28	0.262611377	0.845598	0.630565	1.133959
RFX7	0.263253847	1.182442	0.881603	1.58594
TAS2R46	0.26327449	1.185094	0.880108	1.595768
PRDX4	0.26350417	1.184251	0.880454	1.592871
AP1S1	0.263877751	1.182874	0.881022	1.588146
SLC27A5	0.263980304	1.182356	0.881258	1.586329
ARCN1	0.264033648	1.184008	0.880301	1.592496
ING3	0.264093726	0.845524	0.62984	1.135069
DRAP1	0.264657371	1.181974	0.881106	1.585578
SEC31B	0.264767937	0.843833	0.626111	1.137265
PCBP2	0.264918041	1.184373	0.879612	1.594725
TMEM50A	0.26593452	0.846087	0.630282	1.135784
STARD3NL	0.266318886	1.183096	0.879568	1.591369
CHD9	0.266918731	0.844229	0.626081	1.138387
SUCO	0.267339479	1.180999	0.880208	1.584578

SRFBP1	0.267447355	1.181358	0.879944	1.586017
PAM16	0.267826329	1.180898	0.880003	1.584676
IFITM5	0.267881718	0.846934	0.631272	1.136274
SSBP4	0.268386288	0.844438	0.625936	1.139215
DPH7	0.268770284	0.846904	0.630865	1.136926
HADH	0.26898278	0.84749	0.631993	1.136467
HSF4	0.269108324	0.84601	0.628887	1.138093
CREBZF	0.269456899	0.845974	0.628679	1.138375
DENND1B	0.269515353	0.846243	0.62921	1.138137
C3orf38	0.269754249	0.846752	0.630168	1.137774
UGT3A1	0.270078159	0.847466	0.631519	1.137256
ZNF524	0.270648921	1.179309	0.879396	1.581506
NANOS3	0.271062518	0.847737	0.631699	1.13766
FSTL1	0.271131761	1.179591	0.878972	1.583025
MISP3	0.271615924	0.847362	0.630706	1.138441
ZNF124	0.271929119	0.848011	0.63193	1.137978
KIAA1429	0.272569009	1.179656	0.878157	1.584668
FAM126A	0.272613764	1.179675	0.878122	1.584781
LIN9	0.272823971	1.180611	0.87746	1.588497
HIST1H2AD	0.273034285	1.178893	0.878354	1.582266
ZNF717	0.273289758	0.848457	0.632329	1.138457
GATD1	0.273778916	0.847751	0.630672	1.139548
CASP2	0.273949956	1.182723	0.875609	1.597553
PLA2G4B	0.274168744	0.848005	0.631048	1.139552
ZNF213	0.274378341	0.848312	0.631606	1.139371
LATS1	0.274528643	1.177624	0.878298	1.578959
NXF1	0.27522324	0.847312	0.629199	1.141035
MCFD2	0.276244509	1.180217	0.875834	1.590386
THBS2	0.276720005	1.178511	0.876591	1.584421
UTP14C	0.27691056	0.849741	0.633602	1.13961
DDR2	0.277341946	0.848677	0.631215	1.141059
RSBN1	0.277383317	0.849423	0.632755	1.140282
MTMR6	0.277697904	0.848969	0.631686	1.140993
MAPRE1	0.277765991	1.178559	0.875997	1.585624
RNF133	0.278165045	0.850096	0.63386	1.140099
NUP85	0.278264639	1.177435	0.876403	1.581866
KIAA2026	0.27873366	0.849976	0.633388	1.140627
RASSF7	0.278747567	0.849788	0.632989	1.14084
RCHY1	0.27882218	0.849959	0.633319	1.140706
NOC3L	0.279049955	1.178315	0.875449	1.585958
KRIT1	0.279451657	0.850225	0.633632	1.140856
GLIPR1L1	0.280715635	0.85032	0.63334	1.141636
LIMS1	0.28084162	1.175267	0.876332	1.576174
ROGDI	0.280961156	0.849279	0.631062	1.142952

ING5	0.280998847	0.85076	0.634155	1.14135
AC005726.2	0.281060369	1.1752	0.876256	1.576132
BORCS8	0.281066578	0.849946	0.63242	1.142292
ATP6V0C	0.281220324	1.176593	0.875321	1.581556
PNKP	0.281659316	0.849668	0.631606	1.143015
MYDGF	0.281748205	1.175958	0.875425	1.579665
ERCC6L2	0.28178779	0.849623	0.631463	1.143155
UTRN	0.281806126	0.850696	0.633708	1.141984
ZNF33A	0.282085683	0.849967	0.632067	1.142985
OR10AD1	0.282736966	0.850815	0.633596	1.142504
FER	0.283117237	1.174596	0.875527	1.575822
TMCO6	0.28334812	1.176022	0.874525	1.581462
HIST1H2AE	0.283872689	1.175189	0.874757	1.578803
PUS7	0.284237621	1.174935	0.874718	1.578193
AIFM2	0.284585179	1.174894	0.874557	1.578373
SMUG1	0.284691412	1.176009	0.87381	1.582721
AMELX	0.286372426	1.17332	0.874581	1.574101
RCN2	0.288879485	1.173857	0.872903	1.578572
ULBP2	0.289343655	1.172012	0.873821	1.571962
SAT2	0.289380681	0.848776	0.626709	1.149531
TRMU	0.289811259	1.171734	0.873749	1.571344
EPM2AIP1	0.289857749	0.853075	0.635612	1.144939
TARBP1	0.289908297	0.85287	0.635156	1.145209
ERBIN	0.290207607	1.17134	0.873789	1.570217
CHTF18	0.290264678	1.171428	0.873702	1.570607
CCDC92	0.290540076	0.85332	0.635869	1.145135
MON2	0.290766221	0.852567	0.63418	1.146158
DIS3L	0.290934483	0.852842	0.634698	1.14596
TRIM63	0.292213387	1.173221	0.871518	1.57937
MUSTN1	0.292241234	0.852692	0.633871	1.147052
RFXANK	0.292385094	0.853712	0.635987	1.145973
ALG13	0.292867082	1.171263	0.872424	1.572464
HSP90B1	0.292997247	1.171468	0.872223	1.573377
EXPH5	0.29319915	0.852662	0.633434	1.147763
TPGS1	0.293425	1.170517	0.872608	1.570134
BBS9	0.293864696	0.853745	0.635483	1.146971
MATR3	0.294984757	0.853892	0.635363	1.147584
TOR1B	0.295395843	1.169794	0.872031	1.569232
RECQL5	0.296285492	0.854612	0.636397	1.147652
MLH3	0.296522484	0.85465	0.636385	1.147773
SETD1A	0.296591951	0.854634	0.636325	1.147841
TIMM13	0.296642393	1.16951	0.871554	1.569328
EI24	0.296687438	1.172924	0.869303	1.582591
NAA15	0.297445572	1.172791	0.86898	1.582819

PLBD2	0.297525274	1.170155	0.870663	1.572668
APC2	0.297599846	1.169275	0.871201	1.569333
GGTLC1	0.298182919	0.854975	0.636438	1.148553
C17orf75	0.298264933	0.854705	0.635827	1.148931
C12orf73	0.298315835	1.168902	0.871066	1.568573
VMO1	0.298432226	0.855997	0.638537	1.147515
HNRNPUL1	0.29868628	1.171785	0.868971	1.580123
CATSPER2	0.298973091	0.854832	0.635822	1.149279
SLC25A24	0.299167825	1.169113	0.870475	1.570206
ABRA	0.300131799	0.856216	0.638351	1.148437
POT1	0.300157241	1.169472	0.869711	1.572551
CEP83	0.301028832	0.855821	0.637151	1.149539
DCTN4	0.301081417	0.856757	0.639151	1.148451
HIST2H2AC	0.301422084	1.168047	0.869986	1.568225
USP24	0.301923847	0.856665	0.638624	1.14915
MRPL28	0.302549936	1.167518	0.869743	1.567244
MANEA	0.30294307	0.85676	0.638435	1.149747
ZNF551	0.303668776	0.856761	0.638154	1.150254
MRPL41	0.304089116	1.166983	0.869288	1.566625
RAB19	0.305124238	1.166726	0.868914	1.56661
TCIRG1	0.305385603	0.855917	0.635658	1.152496
BOD1L1	0.305546712	1.166758	0.868669	1.567137
METTL23	0.305682153	1.167292	0.868234	1.569357
FKBP8	0.306327962	0.857592	0.638923	1.151101
DGKH	0.306401824	1.166703	0.868253	1.567742
PTPN12	0.306649015	1.165248	0.869116	1.562279
SLC25A39	0.306837595	1.166143	0.868404	1.565965
ADAMTS12	0.306846834	1.167461	0.8675	1.571141
SULT1C3	0.306905036	1.166495	0.868128	1.567406
PIK3CA	0.307139579	1.166434	0.868045	1.567393
EXOC2	0.307157699	0.858033	0.639559	1.151138
CAV2	0.307180192	1.16554	0.868636	1.563928
ERCC8	0.307551862	1.165646	0.868367	1.564695
UNC13C	0.308735257	0.858065	0.639015	1.152204
HIVEP1	0.309515544	0.857034	0.636465	1.154041
TBC1D5	0.309520401	0.85805	0.638676	1.152775
CSNK1G3	0.310042115	1.164678	0.867719	1.563266
EIF5A2	0.31079755	1.164746	0.867273	1.564251
PLXDC2	0.31162779	0.857832	0.637379	1.154536
IFT22	0.311790334	0.858184	0.638082	1.154208
HNRNPA3	0.311933943	1.163748	0.86737	1.561397
ZNF426	0.311999989	0.859173	0.640163	1.153109
YWHAB	0.312243261	1.164664	0.866565	1.56531
PTPRG	0.312682142	0.859096	0.63973	1.153684

CBX8	0.312711012	0.858789	0.639047	1.154093
ZNF283	0.312754292	1.16277	0.867623	1.55832
GPATCH11	0.312844632	0.859243	0.639988	1.153613
PUM1	0.313425867	0.859133	0.63952	1.154161
HSPB9	0.313688637	0.859956	0.641223	1.153302
NBEAL1	0.314110833	0.859105	0.639192	1.154679
PITPNB	0.314116709	1.16716	0.863819	1.577024
FAM209A	0.314161234	1.165352	0.865064	1.56988
GPR82	0.314203013	0.856363	0.633162	1.158247
HNRNPLL	0.31436783	0.858776	0.63837	1.15528
SIRT7	0.314591411	0.860124	0.641241	1.15372
SIGIRR	0.314628003	0.857135	0.634678	1.157564
LINC00116	0.314769551	1.163468	0.86607	1.56299
SRRT	0.314875645	1.163563	0.865946	1.563468
DUS3L	0.315072808	0.860283	0.641403	1.153855
OXNAD1	0.315692731	1.162465	0.866294	1.559891
TMEM185A	0.316606564	1.161723	0.866342	1.557813
ZNF525	0.316654709	1.161618	0.866391	1.557445
TRAPPC13	0.317072373	0.860696	0.641535	1.154726
ZNF774	0.317592516	0.86002	0.639842	1.155964
ADCK5	0.317694944	0.860941	0.641832	1.154848
ARSI	0.317733874	1.161457	0.86594	1.557825
COX8A	0.318391831	1.163037	0.86446	1.564738
TBC1D8B	0.319350218	0.86082	0.640921	1.156167
SRSF11	0.319635814	0.860581	0.640281	1.156679
PDAP1	0.319879194	1.165165	0.86214	1.574696
TIMP2	0.320325623	1.162007	0.864178	1.56248
BARD1	0.3204349	1.16489	0.86204	1.574136
PCED1A	0.32101233	0.860712	0.640032	1.157482
KPNA6	0.32156373	0.861017	0.640491	1.157472
GPR52	0.321776518	0.861838	0.642227	1.156545
FAM220A	0.321892194	1.161447	0.863756	1.561736
JMJD1C	0.322309473	0.861243	0.6407	1.157703
RHBDD3	0.3223452	1.159912	0.864637	1.556023
LMBR1	0.322406759	1.162395	0.862793	1.566034
GRSF1	0.322449552	1.16101	0.86378	1.560517
LDHAL6B	0.322925349	1.160136	0.864168	1.557471
MYADM	0.323310545	1.159159	0.864682	1.553923
CRLF3	0.32391025	0.862178	0.642148	1.157599
TIMM17B	0.324330036	1.160703	0.863012	1.561082
TOMM34	0.324783662	1.162	0.861818	1.566741
DDX6	0.325739147	0.862477	0.642099	1.158492
TEPSIN	0.326007848	0.862392	0.641804	1.158796
IBA57	0.326369422	0.863002	0.643024	1.158234

SSH1	0.327270366	0.861862	0.640128	1.160403
NAT9	0.327552558	0.863314	0.643258	1.158649
NUDT8	0.327615993	0.863148	0.642863	1.158917
RYBP	0.328405876	0.863865	0.644158	1.158508
ZNF148	0.328437306	0.862927	0.642046	1.159797
NUPL2	0.328489491	1.157889	0.86291	1.553702
MAPK15	0.328545301	0.863103	0.642397	1.159636
C3orf49	0.330755324	0.864475	0.644609	1.159334
WDR27	0.331542564	0.863326	0.64172	1.16146
SELENOH	0.332098018	0.864182	0.643424	1.160682
MRM1	0.332340648	0.864209	0.64339	1.160816
OAZ2	0.332812598	0.865129	0.645277	1.159887
RHOT2	0.333021078	0.864062	0.642792	1.161501
ACCS	0.333310204	0.863618	0.641678	1.16232
FBXL6	0.333409459	0.86514	0.645067	1.160293
HYI	0.333415036	0.864298	0.643168	1.161456
ATP5G1	0.333510396	1.159337	0.859162	1.564387
ZNF792	0.333906436	0.864861	0.644243	1.161028
ITPRIP	0.333931942	1.155458	0.861904	1.548993
TAS2R50	0.334173615	1.155451	0.861782	1.549194
TAF1C	0.334461713	0.86487	0.644046	1.161408
REST	0.334466335	1.155907	0.86128	1.55132
SMAD5	0.334686146	0.865144	0.644576	1.161188
ITGB5	0.334831215	1.155475	0.86142	1.54991
FNDC9	0.335036257	1.155965	0.860936	1.552095
CCDC107	0.335299728	1.156538	0.860357	1.554681
DYRK1A	0.336026098	0.865996	0.645977	1.160951
IGF2R	0.337326575	0.866068	0.645633	1.161767
ARID3C	0.337861248	1.154861	0.860309	1.550261
PNPLA8	0.337943526	0.865637	0.644412	1.162808
PRPF4	0.338591317	1.154389	0.860294	1.549022
RAB10	0.338741104	1.158722	0.856842	1.566959
BLOC1S1	0.339181392	1.155607	0.859033	1.55457
SLC35E2	0.341430597	0.866813	0.645712	1.163622
AC096887.1	0.341630407	0.866319	0.644507	1.164469
SERPINE2	0.341716051	1.153601	0.859275	1.548742
ABCE1	0.341867821	1.154632	0.858381	1.553129
AC009690.1	0.341964868	1.153588	0.859155	1.548924
NDUFA11	0.342678939	0.86681	0.645212	1.164515
FAM98C	0.342682365	0.867546	0.646892	1.163464
CDV3	0.34272205	1.153117	0.859131	1.547703
COMMD4	0.342866144	1.152911	0.85922	1.54699
RTTN	0.343563634	1.152258	0.859375	1.544957
ADAM17	0.343577923	0.864329	0.63921	1.168732

CD40	0.343605476	0.866781	0.64478	1.165217
OSBPL7	0.343769334	0.867534	0.646438	1.164251
BCL7B	0.344088433	1.154765	0.857102	1.555805
ZBTB3	0.34434193	0.867942	0.647145	1.164071
TECR	0.34457317	1.152115	0.858962	1.545318
KLHL17	0.344774535	0.867366	0.645655	1.165209
POLI	0.345088703	0.867672	0.646232	1.164991
HIST1H2BN	0.345137936	1.152749	0.858158	1.548469
TRAPPC10	0.345486507	0.866916	0.644344	1.166369
HINT2	0.346001205	0.867848	0.646276	1.165385
UBR1	0.346426467	0.868512	0.647632	1.164724
ZFC3H1	0.346615726	1.152582	0.857516	1.549179
NPAT	0.346929192	0.8685	0.647407	1.165098
MAMDC4	0.347067721	1.15172	0.857974	1.546036
FGF5	0.347137655	1.154527	0.855675	1.557754
CCDC117	0.347461266	0.867749	0.645471	1.166572
USP33	0.348920215	0.86863	0.64692	1.166325
SPPL3	0.349414974	1.15152	0.856905	1.547429
LMBR1L	0.35010855	0.868133	0.645304	1.167908
GOLGA8A	0.350426064	0.868277	0.645509	1.167923
TIGD4	0.350844527	0.869866	0.649012	1.165875
FAM46D	0.350926744	0.869745	0.6487	1.166112
UCKL1	0.351220775	0.868168	0.644943	1.168656
HIPK3	0.351604911	0.869757	0.64846	1.166576
WDR83OS	0.351736608	0.869029	0.646723	1.16775
RANGRF	0.351967012	0.869575	0.647895	1.167103
CCDC66	0.352169726	0.868296	0.644859	1.169151
DVL3	0.35224781	1.149503	0.857074	1.541709
BOLA2B	0.35227828	1.149647	0.85694	1.542335
FLNC	0.352609739	1.149876	0.856577	1.543605
AC010422.3	0.353637534	1.150261	0.855719	1.546188
N4BP2L2	0.353975379	0.869364	0.64661	1.168856
SLC10A1	0.354980124	0.870334	0.648462	1.168121
TAF10	0.35539136	1.1489	0.85593	1.54215
CNOT3	0.355840214	1.148235	0.856252	1.539785
IPP	0.356128376	0.870183	0.647654	1.169171
ZNF7	0.356321192	0.8696	0.646222	1.170192
CDC27	0.356839075	1.149195	0.854924	1.544757
JMJD6	0.356942459	1.148449	0.855496	1.541721
RELL1	0.357109692	1.149358	0.854645	1.545699
ZNF513	0.357535751	0.871253	0.649587	1.16856
TNFRSF12A	0.357877276	1.148092	0.855307	1.541102
ZNF627	0.358122491	0.871555	0.65006	1.16852
FUK	0.359671471	0.871471	0.64925	1.169754

FGFR1OP	0.359724191	1.147003	0.855262	1.538261
FRYL	0.359979842	1.146709	0.855378	1.537265
HIST1H2BJ	0.360137724	1.147222	0.85486	1.539572
PACS1	0.360346394	1.147997	0.854091	1.54304
CERS6	0.360601382	1.147325	0.854529	1.540443
TMEM248	0.360834245	1.147294	0.854433	1.540533
TMEM109	0.360891512	0.871892	0.649748	1.169984
TBC1D32	0.361047308	0.871075	0.647775	1.171352
DPM3	0.361297832	0.872062	0.649985	1.170014
DDX39B	0.361713685	0.870447	0.646039	1.172806
C6orf10	0.361956249	0.871284	0.647901	1.171686
BCL10	0.363264428	1.14576	0.854476	1.536342
CHCHD1	0.363295369	1.146954	0.853432	1.541428
PRKACA	0.363609537	0.872056	0.649051	1.171684
CUL5	0.364981533	0.873016	0.650763	1.171175
TRIM68	0.36547605	0.873293	0.65122	1.171097
APC	0.365563699	0.873241	0.651061	1.171241
ME2	0.365816961	0.87276	0.649826	1.172177
ASGR1	0.366055413	0.873399	0.651237	1.171347
FOXN2	0.366250632	1.145137	0.853455	1.536507
IMPG2	0.366386736	1.146833	0.851908	1.543859
COX18	0.366741161	0.8735	0.651203	1.171681
DCBLD1	0.367821532	1.144706	0.853009	1.53615
LINC00854	0.367960183	0.870323	0.643228	1.177597
KLHDC1	0.368113681	0.872802	0.649004	1.173773
TRAM2	0.369538122	1.143525	0.853151	1.532728
MCRIP2	0.369702721	0.874195	0.651667	1.172711
SPPL2B	0.369739724	0.873189	0.649265	1.17434
IL1RAPL1	0.37072904	1.145233	0.851016	1.541167
PIP4K2A	0.370859912	1.14339	0.85258	1.533392
AC092835.1	0.371122666	0.873773	0.650096	1.17441
RP1	0.371167677	1.143196	0.852591	1.532853
FIZ1	0.371502251	1.14391	0.851781	1.536229
NOTO	0.371730814	0.875061	0.652915	1.172788
RHPN1	0.372981665	0.874587	0.651286	1.174451
PCP4	0.373004368	0.874923	0.652077	1.173926
THOP1	0.373473955	1.143153	0.851421	1.534846
LRBA	0.374295308	0.875134	0.652062	1.174519
PALM2-AKAP2	0.374514906	0.874609	0.65072	1.17553
UBE3C	0.376254614	1.145205	0.848107	1.546378
MAB21L2	0.376349705	0.875431	0.651947	1.175525
BET1L	0.376843502	0.876119	0.653397	1.174759
ZGRF1	0.376909212	1.14118	0.851401	1.529587
RC3H2	0.376935061	1.141607	0.851	1.531451

RPP25L	0.377164059	1.142037	0.85049	1.533526
PIPOX	0.377225297	0.875154	0.65093	1.176615
FAM173A	0.378242464	1.142373	0.849616	1.536005
DDX3X	0.378353356	1.141026	0.850787	1.530277
SCIN	0.378360132	0.876711	0.654211	1.174885
SCAF11	0.378930386	1.143004	0.848678	1.539403
HIST1H2BB	0.378934225	0.876394	0.653218	1.17582
NTHL1	0.379010885	0.876791	0.654143	1.175222
NCEH1	0.379046387	1.141389	0.850091	1.532504
MTM1	0.379159829	0.874668	0.648982	1.178837
VEGFB	0.379172959	1.141174	0.850222	1.531691
PREB	0.379614791	1.141663	0.849541	1.534232
GPAT3	0.380359342	1.143492	0.847473	1.542908
RRP1B	0.380509905	1.140415	0.850217	1.529664
HIST2H3D	0.380807951	1.140124	0.850329	1.528682
HIST1H2BA	0.380961997	0.87695	0.653739	1.176373
CEP128	0.381412095	1.139894	0.850224	1.528255
TMEM196	0.381596804	1.140182	0.849862	1.529677
UBL4B	0.381698722	1.14051	0.849505	1.531201
SCART1	0.381848529	0.875709	0.650391	1.179086
GCNT7	0.381930805	0.875329	0.649443	1.179783
ZNF789	0.382275025	0.87717	0.65374	1.176961
PLEKHH3	0.382594113	0.877389	0.654143	1.176826
TLR1	0.384035264	0.877722	0.654366	1.177316
DDX17	0.384766764	0.876087	0.650112	1.180609
CREB1	0.385163509	0.877758	0.653997	1.178077
CAB39	0.38545922	1.139434	0.848528	1.530073
C17orf62	0.385852421	1.139911	0.847874	1.532536
CIC	0.388212889	1.138557	0.847904	1.528843
BABAM1	0.388753916	0.878962	0.655474	1.178651
AC009119.2	0.38882939	0.878944	0.655398	1.178738
ZBTB2	0.388843347	1.137617	0.848464	1.525312
MAGEB17	0.389378974	1.137416	0.848375	1.524932
AATK-AS1	0.38962588	1.137639	0.848033	1.526146
RNPC3	0.389933128	0.877335	0.651027	1.182312
C4BPA	0.39014969	0.876144	0.648044	1.184532
MSH5-SAPCD1	0.390229263	0.878508	0.653765	1.180511
KLHL15	0.390403744	1.137774	0.847494	1.52748
YWHAH	0.390449207	1.137935	0.847317	1.52823
TRAPPC12	0.390777488	0.87861	0.65379	1.180739
CAP1	0.390918445	0.878712	0.653983	1.180666
ADPGK	0.391446145	0.879069	0.65464	1.180438
TUBGCP6	0.391926629	0.878727	0.653607	1.181384
RAB32	0.391979176	1.137256	0.847161	1.526687

AARSD1	0.392476012	0.879187	0.65451	1.180991
CALD1	0.392722065	1.136276	0.847714	1.523065
HIST1H3F	0.393483615	1.137532	0.8461	1.529346
PATL1	0.393489699	1.136911	0.846697	1.526598
ANAPC1	0.39376752	0.87861	0.652567	1.182952
TMOD3	0.395023916	1.140484	0.842432	1.543986
CCDC183	0.395355108	0.87988	0.655034	1.181905
MYSM1	0.395731086	0.879338	0.653548	1.183135
FAM47E	0.395975203	0.879681	0.654291	1.182713
PGBD4	0.396506177	0.880685	0.65655	1.181337
ABCA10	0.396615623	0.879776	0.654262	1.183021
ZBTB6	0.396864437	0.880793	0.656668	1.181411
DHPS	0.396917929	1.136367	0.845413	1.527456
RLF	0.397045304	0.880498	0.655867	1.182064
BRCC3	0.397824175	1.135423	0.845859	1.524114
COL3A1	0.398277842	1.13555	0.845494	1.525113
ETS1	0.398564018	0.880705	0.655756	1.18282
GCC1	0.398630247	1.134831	0.846016	1.522242
CCS	0.399173837	0.880568	0.655167	1.183514
ZNF169	0.399292268	0.879791	0.653197	1.184989
SNX12	0.399657769	1.134645	0.845658	1.522387
RSRP1	0.400469807	0.879688	0.652456	1.186057
PLEKHF2	0.400917554	0.881884	0.657716	1.182455
TMED3	0.401574983	1.135449	0.843846	1.527822
CABP4	0.401714097	0.881785	0.657143	1.18322
GAS7	0.401772425	0.87938	0.651155	1.187595
DOHH	0.402305669	1.1337	0.845202	1.520672
NEK1	0.402426525	0.881922	0.657191	1.183502
NME1	0.402429431	1.134112	0.844725	1.522637
SRRM5	0.402553679	1.133531	0.845239	1.520153
GPS1	0.403544501	0.881015	0.654474	1.185971
SMARCA5	0.40379001	1.13383	0.844287	1.52267
PPP1R3F	0.404241329	1.133375	0.844504	1.521058
SEC61B	0.404383778	1.13354	0.844263	1.521934
CTBS	0.404799644	1.135179	0.842395	1.529725
ARMCX1	0.404826698	0.882384	0.657355	1.184445
MINDY2	0.405428755	0.882044	0.656258	1.185512
CAPN10	0.405596477	0.882409	0.657101	1.184971
CPSF4L	0.405967541	0.882294	0.656661	1.185457
INTU	0.406265755	0.882456	0.656943	1.185384
ZNF724	0.406871352	0.881905	0.655315	1.186845
CAPZB	0.407348745	1.134061	0.84216	1.527139
SF1	0.407607344	0.883358	0.658649	1.18473
LUZP1	0.407637201	1.13196	0.844143	1.517912

C8G	0.408106318	0.883076	0.657736	1.185619
KLHL28	0.408825586	1.131375	0.844114	1.516393
LUC7L3	0.409006669	0.883144	0.657534	1.186165
P4HTM	0.409349601	0.882621	0.656079	1.187389
ROCK1	0.409798053	0.883717	0.658647	1.185697
LYPLA1	0.410277243	1.13332	0.84135	1.526611
USPL1	0.410322439	0.883375	0.657568	1.186723
HIST1H2AM	0.410517454	1.131427	0.843166	1.518238
NRBF2	0.41137866	1.131827	0.842296	1.520881
MYO1B	0.411564844	0.884206	0.659148	1.186106
ARPC4-TTLL3	0.411719343	1.131675	0.842272	1.520516
BMPR2	0.411928237	0.884111	0.658758	1.186554
CD70	0.412189602	1.130312	0.843434	1.514765
TNK2	0.412591572	0.883556	0.657082	1.188088
YPEL3	0.413372411	0.884116	0.658172	1.187625
SLC25A4	0.413754825	0.884777	0.659685	1.186673
APAF1	0.414907088	0.883177	0.655158	1.190555
LRRC14	0.415681086	0.884393	0.657909	1.188842
FBXW5	0.416566114	1.131338	0.840033	1.523663
KIR3DX1	0.417073358	1.129714	0.84147	1.516694
FBXO28	0.417078901	1.131223	0.839878	1.523634
DCP2	0.417254808	1.12885	0.842285	1.51291
VPS13B	0.417773384	0.885147	0.658952	1.188986
MPP5	0.417868384	1.128979	0.841824	1.514086
NDUFAF7	0.417992299	0.885727	0.660339	1.188045
INVS	0.418106001	1.129412	0.841239	1.516299
AGO3	0.418259509	0.885511	0.659676	1.188658
RPS19BP1	0.418388956	1.129274	0.841234	1.51594
C9orf131	0.418546233	0.884589	0.657209	1.190637
RIF1	0.418666179	1.130238	0.840065	1.520642
MEF2D	0.419526718	0.885999	0.660392	1.188678
FAP	0.419636703	1.129898	0.839906	1.520014
LSM7	0.419691255	0.885027	0.657844	1.190667
HIST1H3H	0.420354733	1.128209	0.841322	1.512923
CPT1A	0.421630775	1.127581	0.841317	1.511247
SYF2	0.422019077	0.886271	0.660047	1.190031
DPP7	0.422317029	0.88684	0.661381	1.189156
PRR13	0.422520571	1.129542	0.838737	1.521175
SRSF2	0.423637105	1.126874	0.841014	1.509899
NPEPL1	0.423973348	0.885888	0.658243	1.192261
BPIFA2	0.424861709	0.886651	0.659828	1.191447
FNBP4	0.424958074	0.88612	0.658423	1.192559
MNT	0.425481149	1.128054	0.838751	1.517145
KLK14	0.425617741	0.887609	0.661977	1.190145

RBM10	0.426045472	0.886671	0.65938	1.192309
PITPNA	0.426178135	0.887576	0.661658	1.190632
VGLL2	0.427258357	1.126383	0.839621	1.511086
ZNF808	0.427302979	0.887867	0.661938	1.19091
HIST1H2AJ	0.427504938	1.126193	0.839697	1.510439
PRKDC	0.427599837	1.127005	0.838757	1.514312
FAM221B	0.428164038	0.887077	0.659531	1.193128
ATP5L2	0.429032078	0.888442	0.662699	1.191083
PRR14	0.429080228	0.887857	0.661162	1.192279
CASP8AP2	0.429517954	1.126155	0.838663	1.512199
RNASEK	0.430616676	1.126208	0.838015	1.513512
HSD17B10	0.430962491	1.125814	0.838266	1.511997
DEGS1	0.43185912	1.126777	0.836715	1.517395
PGGHG	0.43231039	0.888578	0.661669	1.193303
CPSF2	0.432468167	1.127055	0.836076	1.519303
KBTBD8	0.432519567	0.885957	0.654779	1.198755
CLDN12	0.43257323	1.127161	0.835902	1.519906
DDX5	0.432846403	0.887667	0.659071	1.195551
ZNF121	0.43387415	1.124182	0.838527	1.507149
DDX51	0.434431124	0.889411	0.662943	1.193244
ALKBH2	0.434592543	1.124383	0.837915	1.508789
BICRA	0.434622904	0.88852	0.660534	1.195197
TXNDC12	0.435031814	1.124897	0.837102	1.511636
PDE5A	0.435131332	0.889139	0.661934	1.194332
ADCY5	0.435650352	0.88958	0.662867	1.193833
ZNF221	0.435974481	0.887496	0.657286	1.198335
APP	0.43600973	1.124135	0.837434	1.508991
CEP120	0.436319475	0.889018	0.661112	1.195492
ZRANB2	0.436691891	0.889732	0.662821	1.194322
ZNF837	0.436796347	0.889546	0.66229	1.194782
BRICD5	0.436978249	1.123769	0.837329	1.508196
TATDN2	0.437527695	1.124135	0.836618	1.510462
EXOSC4	0.437942654	1.124407	0.836085	1.512156
NEK6	0.438088421	0.890196	0.663446	1.194444
ANKRA2	0.438476369	0.890026	0.662835	1.19509
RRP36	0.438514415	1.123875	0.83638	1.510192
AP003108.2	0.438705769	0.890246	0.663313	1.194816
LUC7L	0.438967957	0.889925	0.662358	1.195677
ATF7	0.439496954	1.123711	0.836037	1.510369
UBE4A	0.441340969	1.123733	0.835013	1.512282
C9orf16	0.441518058	0.891357	0.665048	1.194678
NFKBID	0.442586306	0.890933	0.663468	1.196383
ANKMY2	0.442704486	1.122026	0.836244	1.505472
STX17	0.443145428	0.890403	0.661828	1.197923

C8B	0.443318348	0.89013	0.661031	1.19863
KCNAB3	0.443698871	1.123775	0.833681	1.514811
MAB21L1	0.443847795	0.891675	0.664893	1.195807
POMT1	0.444278314	0.889907	0.660026	1.199853
LENG8	0.444288081	0.890851	0.66252	1.197875
PPP1R9A	0.444410998	0.891977	0.665454	1.195608
GJC1	0.444415782	1.121871	0.8355	1.506399
ZNHIT2	0.444669338	1.12366	0.833283	1.515226
BPIFB4	0.444790035	0.891835	0.664915	1.196198
NPIPB15	0.44533977	0.891599	0.664052	1.197118
MED11	0.445381761	1.121511	0.835397	1.505615
WDR36	0.445497627	1.121402	0.835462	1.505206
ANAPC5	0.445987355	0.888348	0.655169	1.204517
HDGF	0.446026395	1.124707	0.831322	1.52163
DOCK11	0.446298891	0.891608	0.663662	1.197845
FBXL15	0.446453228	0.892332	0.665524	1.196435
RB1CC1	0.44697713	1.121816	0.834175	1.508642
AC090004.1	0.447169993	0.891516	0.663042	1.198718
ANKRD26	0.447492957	0.892331	0.665074	1.197242
TUT1	0.448002941	1.121923	0.833491	1.510168
ITGB1BP2	0.44812889	1.12191	0.833437	1.51023
TMEM154	0.448333492	1.121984	0.833239	1.510788
VGLL4	0.449090316	1.12103	0.833951	1.506933
PAPOLB	0.449399617	0.892919	0.665826	1.197467
TGIF2-C20orf24	0.449940568	0.893024	0.665873	1.197663
7-Sep	0.449978976	1.120126	0.834541	1.50344
SH3GLB2	0.450706771	0.89304	0.665586	1.198224
CEBPD	0.450707801	0.893114	0.665784	1.198066
KMT2A	0.450794652	0.892674	0.664567	1.199078
MYH7B	0.450838541	0.892716	0.66466	1.199022
EVI5	0.45092068	0.893279	0.666134	1.197878
UBE2H	0.451298271	1.121656	0.832003	1.512148
SGSM2	0.451524722	0.893227	0.665735	1.198458
KAZALD1	0.45191793	1.119412	0.83434	1.501886
SORL1	0.452463815	0.893064	0.66489	1.199543
SURF2	0.452898473	0.8929	0.664259	1.20024
CLDN20	0.453129419	1.119943	0.833046	1.505645
MXD3	0.45464463	1.118138	0.834396	1.498367
SPACA4	0.454715259	1.118535	0.833877	1.500366
GPS2	0.454755956	0.892908	0.663472	1.201686
PHC3	0.454771238	1.119097	0.833168	1.503152
TMEM62	0.454899229	0.89414	0.666731	1.199114
TAS2R30	0.454980781	0.894438	0.667502	1.198528
NME4	0.455132255	1.119019	0.833065	1.503129

CRIPAK	0.456085005	0.893318	0.663995	1.201842
USP3	0.456630099	0.893279	0.663652	1.202358
HELQ	0.456721053	0.894712	0.667489	1.199286
SPATA1	0.456983639	0.894026	0.665516	1.200997
IMP4	0.456996875	1.118503	0.832675	1.502445
OXSR1	0.457041587	1.118826	0.832256	1.50407
PEX6	0.457427107	1.118785	0.832096	1.504249
MEF2A	0.457944839	0.89486	0.667358	1.199918
ZER1	0.45833844	0.894301	0.665668	1.20146
TNPO1	0.459013657	1.118959	0.831012	1.50668
DENND4B	0.45925777	1.116953	0.833338	1.497092
ATP7A	0.459281313	1.117793	0.832294	1.501225
APH1A	0.459473011	0.893843	0.66393	1.203373
EPB41L2	0.460295766	0.893318	0.662143	1.205202
ADCK2	0.460543541	1.116995	0.832586	1.498558
VAMP3	0.46117459	0.89511	0.666627	1.201905
FAM208B	0.461473066	1.116879	0.832222	1.498902
PTPRJ	0.461477334	1.117151	0.831883	1.500243
OXR1	0.461523292	0.895706	0.6681	1.200852
PIGBOS1	0.461712689	0.895575	0.667659	1.201294
CDRT4	0.463080149	0.894985	0.665449	1.203697
BIRC6	0.463158698	0.895845	0.667763	1.20183
PITX2	0.463176161	1.116303	0.832007	1.497743
NIPSNAP1	0.463542337	0.89578	0.667418	1.202278
EMP1	0.463799915	1.1162	0.831794	1.49785
HBG2	0.464188996	0.895296	0.665807	1.203883
ZNF658	0.464409155	0.895716	0.66686	1.203111
ELMOD3	0.464541264	1.117044	0.830334	1.502753
CCNT1	0.464630778	1.116518	0.830941	1.500241
NFAT5	0.464763075	0.896325	0.668375	1.202018
SSNA1	0.466226846	0.896398	0.667932	1.203011
ABHD18	0.46635637	0.896716	0.668749	1.202394
KLRC3	0.466552886	1.115374	0.831323	1.496481
MT-ND1	0.467522074	0.896568	0.667827	1.203655
OCEL1	0.468113592	0.89558	0.664846	1.206388
EXOSC1	0.468138004	0.897078	0.668962	1.202982
CXCR1	0.468417891	0.896547	0.667374	1.204417
GEMIN8	0.468649895	0.894583	0.661872	1.209114
FBXL4	0.468934121	0.896437	0.66684	1.205084
NR1D2	0.469187325	0.897351	0.669254	1.20319
HIST1H3B	0.469210639	1.114894	0.830471	1.496728
ANKHD1- EIF4EBP3	0.469234379	0.896703	0.667442	1.204714
RAB40C	0.469836055	0.896967	0.667905	1.204587

HAUS7	0.470104397	1.114345	0.830678	1.494882
PSMG4	0.470650999	1.113961	0.83087	1.493505
ARFIP2	0.471371271	0.896769	0.666675	1.206278
SRSF6	0.471723588	0.896928	0.666958	1.206193
CHD1	0.471819183	1.113782	0.830457	1.493768
AKR7A2	0.472025551	0.897368	0.668042	1.205417
TCTN1	0.472051067	0.897998	0.66978	1.203978
ZNF770	0.472199043	1.115471	0.828079	1.502604
GPATCH2L	0.472519236	1.114124	0.829632	1.496174
WDFY3	0.47323494	1.113202	0.830427	1.492267
HIST1H1A	0.473634226	0.898229	0.66972	1.204706
ANAPC4	0.474523892	0.898552	0.670225	1.204664
ZNF700	0.475564657	0.896886	0.665118	1.209415
CHKB-CPT1B	0.475828585	1.114072	0.827863	1.499231
HNRNPH3	0.475835104	1.113887	0.828101	1.4983
ZSCAN12	0.475842447	0.898726	0.670122	1.205315
CDK3	0.476153326	1.11288	0.829234	1.49355
ZNF823	0.476854931	0.899021	0.670495	1.205434
COPB1	0.478297426	0.898342	0.667949	1.208203
PNPLA2	0.478917824	0.899108	0.669819	1.206887
RANBP6	0.479838295	0.89948	0.670449	1.206748
OFD1	0.480401863	0.898004	0.666052	1.210732
KRTAP5-9	0.480928592	0.898951	0.668471	1.208897
TMBIM1	0.481083026	1.111937	0.827738	1.493715
LACC1	0.481707444	1.111669	0.827747	1.492979
C1orf35	0.483185298	1.111115	0.827663	1.49164
SLC9C1	0.483248001	1.110787	0.828066	1.490036
ARL17A	0.483959548	0.900681	0.671989	1.2072
GPX4	0.484019738	0.900379	0.671108	1.207977
GAPVD1	0.485459632	0.900775	0.671581	1.208188
UBQLN2	0.485516754	1.11001	0.827849	1.488342
MDFIC	0.486105664	1.110126	0.827364	1.489526
VMA21	0.486432536	1.110018	0.827328	1.4893
TCN2	0.486538103	0.901117	0.672065	1.208235
TP53I11	0.486739403	0.900729	0.670868	1.209346
ANO6	0.487032524	1.110955	0.825724	1.494714
SSTR2	0.487265692	1.109773	0.827195	1.488881
THAP6	0.487558655	0.901472	0.672615	1.208197
PRR16	0.487972114	1.110159	0.826276	1.491576
CEP295	0.488151349	1.109682	0.826825	1.489304
DAZAP2	0.488615979	1.109073	0.827394	1.486648
STRN	0.48909451	1.112147	0.822941	1.50299
EBLN2	0.490397327	0.901369	0.67103	1.210774
SCO2	0.490925673	0.901976	0.672527	1.209707

PRKG1	0.49122816	0.90155	0.67117	1.211009
CHRNA10	0.491380956	0.902038	0.672497	1.209926
TMEM184C	0.491905344	1.108633	0.826159	1.487688
ANKRD36C	0.492560245	0.900941	0.668813	1.213634
PXT1	0.493552419	0.90096	0.66841	1.214416
HSPA4L	0.493711191	1.108335	0.825557	1.487974
COPS7B	0.493907825	0.901241	0.669053	1.214008
ZBTB37	0.493918471	0.90243	0.672466	1.211036
CENPS	0.494522228	1.109755	0.823127	1.496194
UQCRB	0.495492289	1.107405	0.825851	1.484946
GNB1	0.495865025	0.900235	0.66526	1.218205
ITPRIPL2	0.496758254	0.902564	0.671548	1.213051
ZFAND3	0.496903418	0.902911	0.672483	1.212295
THOC6	0.497565379	1.107454	0.824614	1.487307
TAS2R31	0.498092755	1.107084	0.824836	1.485914
ZNF45	0.498303935	1.107163	0.824606	1.48654
CTRL	0.498351881	1.106831	0.825047	1.484856
ADAT2	0.498355841	0.902749	0.671344	1.213917
AC012309.1	0.498499672	1.106395	0.825581	1.482725
HS1BP3	0.498941755	0.902831	0.67131	1.214199
ZZZ3	0.498958527	0.903528	0.673327	1.212433
ORC5	0.499255014	1.108035	0.822835	1.492088
MTOR	0.500243072	0.903356	0.672232	1.213944
WASL	0.500556609	0.903167	0.671538	1.214692
NDUFB7	0.500882775	0.903239	0.671596	1.214781
SPG11	0.501263475	1.106171	0.824339	1.484358
HIST1H1C	0.501794846	1.105827	0.824528	1.483095
PACRGL	0.502158703	0.904444	0.674517	1.212748
SDF2L1	0.502971556	1.1059	0.823757	1.484678
SWI5	0.50320465	1.105506	0.824191	1.482839
ANKRD23	0.503229802	0.903758	0.672016	1.215417
ZNF701	0.503542383	1.105891	0.823445	1.485217
CMTM3	0.504267348	1.105473	0.823635	1.483751
RAB23	0.504331683	1.106214	0.82253	1.487738
CAMSAP2	0.505485386	1.105753	0.822536	1.486487
ERGIC3	0.506087235	1.105651	0.822339	1.486568
STK17A	0.506596658	1.104519	0.823692	1.481089
T	0.507144381	0.905405	0.675022	1.214418
TARDBP	0.507358893	1.106294	0.820675	1.491317
ZNF81	0.507439839	0.904532	0.672313	1.216961
NR2C1	0.507727304	0.90469	0.672643	1.216789
L3MBTL1	0.508292555	0.905273	0.674095	1.215733
FBXO38	0.508320188	0.90503	0.673365	1.216397
ZNF593	0.508606383	0.905341	0.674147	1.21582

TMEM106C	0.508769676	1.105248	0.821386	1.48721
JPT2	0.508775624	1.105573	0.820908	1.488952
ADAMTSL1	0.50886055	0.905713	0.675127	1.215052
BTAFL1	0.50942745	0.905482	0.674181	1.21614
HIVEP2	0.509706097	1.103788	0.822989	1.480395
CDK19	0.50974844	0.905637	0.674487	1.216003
PFDN6	0.510060829	1.104202	0.822178	1.482965
SLAIN2	0.510396272	1.103983	0.822308	1.482145
COX17	0.510921239	1.103689	0.822442	1.481112
LAT	0.511724399	0.904487	0.670152	1.220762
KLHL5	0.512051695	1.103201	0.822517	1.479667
COPE	0.512639733	0.90643	0.675481	1.216341
TNFAIP6	0.512772485	1.104447	0.820255	1.487102
MT1H	0.51332435	1.103314	0.821619	1.481589
MYL6B	0.513725974	1.105574	0.81803	1.494192
CEP44	0.514131634	0.906226	0.674167	1.218162
GNRH1	0.51438087	0.906491	0.67484	1.21766
TOR1AIP2	0.514449246	1.102595	0.822045	1.478892
PDGFC	0.514821754	1.102577	0.821858	1.479179
MUL1	0.515065974	0.90731	0.676963	1.216036
NIN	0.515412706	0.906331	0.673873	1.218977
PGM3	0.516047587	1.103282	0.820094	1.484258
ICE2	0.516078997	0.90541	0.670809	1.222057
UNC119	0.516086046	1.102109	0.821834	1.47797
TRAPPC8	0.516174064	0.90708	0.675749	1.217601
TMEM110- MUSTN1	0.51618682	0.905654	0.671486	1.221484
TMEM200B	0.516592361	1.102047	0.821636	1.47816
MAP4	0.516710027	1.102193	0.821348	1.47907
ABCA1	0.516753671	0.906587	0.673999	1.219437
FMO4	0.516798624	0.905771	0.671542	1.221698
SON	0.517240171	1.101607	0.821928	1.476455
GALK2	0.517287917	0.906391	0.67316	1.220431
AL121594.3	0.517329696	0.907367	0.676062	1.217809
RGL3	0.517432807	0.907122	0.675278	1.218565
NDUFB11	0.517434482	1.103018	0.819685	1.484289
DLEU1	0.517458229	1.102319	0.820726	1.480527
RABGEF1	0.518143092	0.907888	0.677241	1.217085
MAZ	0.518661406	1.102213	0.820191	1.481208
ESR2	0.518665797	0.907167	0.674826	1.219503
MAP7D3	0.518700599	1.101314	0.821532	1.476379
MRPL43	0.518773291	0.908109	0.677608	1.217019
CUX1	0.519667616	0.908277	0.677691	1.217322
ASCC3	0.519669764	1.101052	0.821372	1.475965

GPR65	0.519955926	0.906822	0.673172	1.221569
KIAA0141	0.520065535	0.908188	0.67723	1.217908
POLG2	0.520296712	1.100818	0.821369	1.475341
ATM	0.520846644	0.907823	0.675759	1.219582
AGAP5	0.521311471	0.90799	0.676041	1.219522
SH3KBP1	0.521990041	1.100888	0.820282	1.477483
BCS1L	0.522284787	1.101247	0.81956	1.479751
APBA3	0.522665395	0.907781	0.674759	1.221276
IFNK	0.52267894	1.100993	0.81972	1.47878
TTN	0.523331444	0.908428	0.676395	1.220058
PDE6C	0.523397524	0.908253	0.675835	1.2206
MANF	0.52342948	0.909017	0.678137	1.218504
SLC25A2	0.523678991	0.908908	0.677687	1.219021
ZNF805	0.523999182	0.908045	0.674914	1.221705
MMP17	0.524447542	1.101068	0.818573	1.481055
PARD6B	0.52459379	0.909274	0.678361	1.21879
PPP4R2	0.525261972	1.10101	0.818186	1.481599
GPR4	0.525738085	1.099713	0.819923	1.474978
AC020915.1	0.526450512	0.909256	0.677412	1.220448
PTOV1	0.526454463	1.100129	0.818856	1.478018
STYXL1	0.526851576	1.09969	0.81931	1.476019
PTPN20	0.52723361	0.909204	0.676874	1.221277
TWISTNB	0.527704709	1.100249	0.817936	1.480004
BGLAP	0.528085004	0.909068	0.676048	1.222405
ANKRD50	0.528187736	0.909948	0.678689	1.220006
SEMA6B	0.528208166	1.098765	0.81997	1.47235
F8A1	0.528485743	1.099583	0.818521	1.477156
RIMS1	0.528600929	0.909187	0.676162	1.22252
COMTD1	0.529601068	1.098628	0.819373	1.473057
COL8A2	0.529879929	0.910006	0.67805	1.221313
ALG11	0.530371273	0.909846	0.67732	1.222199
ARHGAP42	0.530594196	1.098579	0.81887	1.473832
IRAK4	0.530725104	0.909969	0.677527	1.222157
CDKL4	0.531166233	0.910429	0.678725	1.221232
SRSF5	0.531799115	0.909847	0.676627	1.223453
PHPT1	0.531986875	1.097991	0.818989	1.472041
HNRNPDL	0.532693741	1.097998	0.818564	1.472824
RANBP2	0.532840231	0.9105	0.67813	1.222494
ITPA	0.533043419	1.097786	0.818698	1.472014
ZBTB41	0.533978084	1.098306	0.817316	1.4759
BST1	0.534964332	0.911063	0.678834	1.222738
LAMTOR2	0.535446005	1.097205	0.818219	1.471317
FCGR3B	0.535447524	0.910693	0.677452	1.224238
ATPIF1	0.537091192	0.911464	0.679038	1.223448

PROK2	0.537146351	0.910806	0.676965	1.225422
PRR22	0.537328136	1.097885	0.816008	1.477133
PRKD2	0.537462769	1.097508	0.816539	1.475157
ITCH	0.538353375	1.097717	0.81567	1.477291
DNAJC16	0.538571042	0.911766	0.67925	1.223875
TMEM159	0.53875058	1.09727	0.81616	1.475203
TAZ	0.538824448	0.910496	0.675169	1.227843
ARMCX6	0.539208207	0.911081	0.6768	1.226461
BLID	0.541335168	0.912768	0.681024	1.223372
ARFGEF2	0.541842366	0.912165	0.67888	1.225614
P3H3	0.542139347	1.095531	0.816998	1.469021
C3orf35	0.542536534	0.912765	0.68042	1.224449
MAT2A	0.542686694	0.912451	0.67936	1.225517
PEAK1	0.543176201	0.911832	0.677171	1.22781
XPO6	0.54336897	1.095359	0.816553	1.469361
LRRFIP1	0.543466347	1.095297	0.816596	1.469118
PLGLB1	0.543560288	0.912826	0.680104	1.225182
PAXBP1	0.544028029	0.913137	0.680851	1.224671
C19orf43	0.544268299	1.095975	0.814993	1.473828
OR4C6	0.544527218	0.912452	0.678446	1.227171
DICER1	0.545046678	0.91289	0.679566	1.226324
IFITM1	0.545065717	1.09521	0.815787	1.470341
PPRC1	0.547072304	1.094533	0.815721	1.468642
CEP192	0.547650124	0.913713	0.68087	1.226183
RWDD1	0.548531796	1.094593	0.814745	1.470562
F7	0.548645135	1.094337	0.815108	1.469222
ZCCHC6	0.548863454	1.093967	0.815602	1.467338
HIST1H4F	0.548889151	1.0947	0.814348	1.471569
CEP350	0.548892783	0.913972	0.681071	1.226517
GAB1	0.549736968	0.9143	0.681691	1.226279
PI4K2A	0.549743521	0.914541	0.682458	1.225548
MMAB	0.550180767	0.914581	0.682368	1.225818
AC135178.2	0.550873964	0.913496	0.678557	1.229778
LAYN	0.551061866	1.093355	0.815324	1.466195
USB1	0.55148377	1.093647	0.814572	1.468334
DUS4L	0.552394524	1.093631	0.814049	1.469234
SNRK	0.553310656	0.914631	0.68095	1.228504
RNF111	0.553311306	0.914345	0.680032	1.229392
ROMO1	0.553454885	0.91481	0.681452	1.22808
FBXL13	0.553573524	1.094623	0.811634	1.476279
AAAS	0.553958662	1.093545	0.813248	1.470451
CDK17	0.554305614	1.092718	0.814462	1.466039
PCDHGC3	0.554744711	0.915211	0.682086	1.228013
YAE1D1	0.555114216	1.092809	0.813816	1.467447

RPL36A	0.555408029	1.092356	0.814421	1.465141
CYHR1	0.555501762	1.092157	0.81471	1.464087
GTF2H2C	0.555613338	0.915646	0.683047	1.227451
ZGLP1	0.556353615	0.91451	0.679014	1.231683
TACSTD2	0.55658276	0.915028	0.680563	1.23027
RNASEH2C	0.556655896	1.0931	0.812373	1.470838
IRF9	0.556939571	1.094404	0.80994	1.478776
JUND	0.557094477	0.915335	0.681293	1.229777
FBXW12	0.557657008	1.091957	0.813753	1.465271
HIST1H1T	0.55774734	1.091794	0.813983	1.464422
PARP16	0.558110849	0.916104	0.683264	1.228292
RAB17	0.558311932	0.915517	0.681258	1.230329
ZEB1	0.558328221	0.91574	0.681971	1.229641
USP53	0.55859908	1.091524	0.813938	1.463776
STIM1	0.55881786	1.091596	0.813679	1.464437
GPATCH2	0.559196858	0.914594	0.67782	1.234077
RNF208	0.560203724	0.916328	0.682923	1.229506
BRD4	0.560429794	1.090972	0.813796	1.462555
AC087632.1	0.561285372	1.090707	0.813744	1.461934
TAOK1	0.561424741	0.91585	0.680738	1.232164
PMS2	0.561766198	0.914064	0.67477	1.238217
RPP21	0.561876668	0.916687	0.683233	1.22991
ATRAID	0.561960741	1.09226	0.810584	1.471817
7-Mar	0.561992345	0.91693	0.683969	1.22924
TNFAIP1	0.562289651	1.090732	0.813086	1.463186
NOXRED1	0.5624023	0.916276	0.681622	1.231712
ACSM6	0.563035105	0.916857	0.683194	1.230437
NME2	0.563284952	1.091	0.812	1.465864
TMEM214	0.563678823	1.090589	0.812492	1.463872
CEP85L	0.563761728	1.092155	0.809652	1.47323
ZDHHC12	0.563819683	1.091067	0.811552	1.466855
PARP4	0.563986964	0.917112	0.683539	1.230501
GSTP1	0.564716755	1.091148	0.810854	1.468334
CHCHD10	0.565537306	1.089946	0.812501	1.46213
DCTN5	0.566041334	0.917051	0.682274	1.232617
FUS	0.566140132	0.917879	0.684949	1.230023
DFNB59	0.566295006	0.917408	0.683315	1.231696
NAA38	0.56702405	1.090194	0.811139	1.465252
MRPS26	0.567061199	0.917513	0.683263	1.232072
EPHB4	0.567264693	1.089188	0.81281	1.459542
ZBTB45	0.567653334	1.09003	0.811046	1.464978
SGMS2	0.568594951	1.089035	0.812269	1.460103
CFAP54	0.568828669	0.918384	0.685224	1.230881
SLC30A4	0.569350514	1.088845	0.812148	1.459814

RAB8B	0.570135737	1.089743	0.810025	1.466053
NPIP4	0.570557698	0.918471	0.684611	1.232216
FAM186A	0.570717378	0.918475	0.684544	1.23235
GFM2	0.571073461	1.089302	0.810247	1.464465
C1orf100	0.571251635	1.088247	0.812071	1.458347
NDUFB1	0.571598817	1.088337	0.811689	1.459276
RHBDL1	0.57191349	0.918644	0.684477	1.232921
USP37	0.572441385	0.91814	0.682523	1.235095
GTPBP3	0.573386932	0.919044	0.685038	1.232985
MAP3K1	0.573489543	0.919083	0.685116	1.23295
MAPKAP1	0.573705221	1.087793	0.811388	1.458359
RFNG	0.573772844	0.918946	0.684509	1.233675
ZSCAN20	0.574717749	0.91946	0.685733	1.232852
FBXO40	0.574786756	0.919358	0.685353	1.23326
N4BP2	0.575928224	1.087652	0.810265	1.46
ZNF268	0.575948187	0.919469	0.685114	1.23399
TIA1	0.576123648	0.919442	0.684931	1.234247
GUCY1A3	0.57642224	0.91886	0.682819	1.236496
TSEN54	0.577024345	0.919286	0.68393	1.235635
ZBED6	0.578335291	0.918679	0.681193	1.238962
ABHD17A	0.579537209	0.919812	0.684364	1.236264
FAM217A	0.579645061	0.920337	0.686078	1.234582
PIK3C2A	0.580071982	0.920157	0.685244	1.235602
ACTL10	0.580340095	0.920801	0.687284	1.233661
HSBP1L1	0.580753746	0.920657	0.686575	1.234548
TMF1	0.580870246	0.92046	0.685844	1.235335
TMEM263	0.580934659	1.08616	0.809938	1.456584
C8orf82	0.581673444	0.919718	0.682901	1.23866
CYP2E1	0.582002243	0.920152	0.684192	1.237488
RASA2	0.582191229	0.919782	0.682837	1.238947
TAF1B	0.582546248	1.086354	0.808552	1.459604
PYGO1	0.582610042	1.086158	0.808885	1.458477
ECSIT	0.582654598	0.921017	0.686783	1.235138
CENPX	0.582884342	1.086303	0.808435	1.459677
CDH11	0.582943142	1.085759	0.809439	1.456405
SPRN	0.582980235	0.92118	0.687165	1.23489
SP3	0.583738049	0.920916	0.68586	1.236531
LZTS2	0.584465079	0.921218	0.686498	1.236191
COL27A1	0.585559515	0.920747	0.684301	1.238894
CSTB	0.586283214	1.08567	0.807491	1.45968
ZNF251	0.587395416	0.92203	0.687704	1.236199
SMGT1	0.587630809	0.921836	0.686908	1.23711
CCDC88A	0.587655488	1.084604	0.808687	1.45466
SST	0.588234284	0.922217	0.687894	1.236358

SMARCD1	0.58834311	1.084345	0.808754	1.453847
LY6G5B	0.588688367	0.920992	0.683434	1.241123
TARBP2	0.589531589	1.084301	0.808085	1.454931
SMIM26	0.589878577	1.084305	0.807855	1.455356
GMPPA	0.589952694	1.085476	0.805511	1.462748
PMF1	0.590162121	1.084015	0.808244	1.453877
TNRC6B	0.591326084	0.922595	0.687524	1.23804
CBWD6	0.591668095	1.083957	0.807394	1.455253
HK1	0.592208456	0.922488	0.686671	1.239291
BCLAF1	0.593436323	1.083209	0.807744	1.452614
UHRF1BP1L	0.594212343	1.083166	0.80733	1.453245
HIST1H4B	0.594405267	1.08282	0.807899	1.451293
GABPB2	0.594830105	1.08311	0.807044	1.453611
BTBD7	0.596135233	0.923507	0.688063	1.239516
SLC5A3	0.596611313	0.923911	0.689219	1.238522
RNF215	0.597112805	1.082188	0.807427	1.450448
STX10	0.597690511	0.923361	0.686691	1.2416
CNPY2	0.598650006	0.924031	0.688514	1.240111
IMP3	0.598654139	1.082334	0.806133	1.453169
GADD45GIP1	0.599311393	1.082174	0.806032	1.452921
UBR5	0.59958246	0.924223	0.688673	1.24034
SLC25A28	0.600252641	0.924313	0.688616	1.240682
AP001931.1	0.600760924	0.924186	0.687888	1.241657
KLF11	0.601477023	0.924891	0.68998	1.239778
ZNF688	0.601487825	0.92383	0.686222	1.243711
DDB1	0.601511755	1.082189	0.804564	1.455613
DDRGK1	0.602405969	0.924869	0.689386	1.240789
KLRC4-KLRK1	0.60244283	0.925072	0.690087	1.240073
TMED2	0.602709998	1.081316	0.805573	1.451443
ZNF771	0.603841255	1.081496	0.804459	1.453937
NPHP3	0.604175634	0.925028	0.68896	1.241982
NECAB3	0.604219954	0.925334	0.690028	1.240883
SUGP2	0.604733246	0.924002	0.684998	1.246396
CCDC12	0.605190632	0.925208	0.689034	1.242335
NUDT13	0.605942336	0.925556	0.689854	1.241791
CEP131	0.606012816	1.080586	0.804919	1.450664
ZBTB1	0.606177541	0.924963	0.687601	1.244263
TRIP11	0.606837692	1.080269	0.805039	1.449596
CYP39A1	0.606891185	0.925861	0.690411	1.241607
ZNF114	0.606914878	1.080216	0.805098	1.449348
HNRNPUL2	0.607183365	1.080598	0.804123	1.452131
POLR2J	0.607924236	1.080179	0.804511	1.450304
TNFRSF1A	0.608254103	1.080986	0.802598	1.455936
ATG4D	0.608830445	0.926038	0.689951	1.242909

HUS1	0.609589313	1.079382	0.805092	1.447121
PHACTR2	0.609674866	0.926601	0.691501	1.241631
BDP1	0.610053877	1.079313	0.804932	1.447222
MAP4K3	0.610149701	1.079615	0.804228	1.4493
ATR	0.610234214	1.079394	0.804639	1.447968
RWDD2A	0.610463775	0.926621	0.691127	1.242357
ARGLU1	0.611091	1.07971	0.803401	1.451047
CSNK1A1	0.612306354	1.078851	0.804423	1.446898
ZFP37	0.612329701	0.926779	0.690638	1.243661
HIST1H2BH	0.61336876	1.078723	0.803992	1.447331
MORC3	0.613581869	0.926908	0.69039	1.244455
RIN2	0.614149691	0.927346	0.691657	1.243348
LBHD1	0.614172548	0.926745	0.689458	1.245698
SNRNP35	0.614455842	1.078348	0.804074	1.446178
TPST1	0.614821354	1.078179	0.804194	1.445508
UCP3	0.614966636	0.927573	0.692019	1.243307
SPTY2D1-AS1	0.615318816	0.927256	0.690659	1.244903
SLC4A7	0.615554921	1.078617	0.802758	1.449271
ENOX2	0.615941714	1.078288	0.803208	1.447577
RAMP1	0.61617854	0.92719	0.68992	1.246058
TP53I13	0.616824808	1.077714	0.803863	1.444858
VPS13A	0.617288269	0.927377	0.689963	1.246485
NEK7	0.617891795	0.928006	0.691922	1.244643
JAK1	0.618646223	1.078025	0.80196	1.449122
VMAC	0.618734341	0.927016	0.687798	1.249435
AMOTL1	0.61913456	1.07734	0.803131	1.445172
GDF9	0.619159422	0.928466	0.692882	1.24415
AGAP9	0.619293906	1.077671	0.802298	1.447561
PRR14L	0.619716692	1.077209	0.803027	1.445006
STK36	0.619927234	0.928023	0.690802	1.246706
MTG1	0.620033285	0.928232	0.691512	1.245987
HIST1H3I	0.620184277	1.077504	0.802061	1.44754
CTNNAL1	0.620287467	1.07756	0.80187	1.448034
IDH3A	0.620522975	1.07723	0.802436	1.446128
OSBPL8	0.620697103	0.927339	0.687834	1.250241
AAK1	0.620710122	0.92764	0.688933	1.249056
LNPEP	0.621098928	0.928312	0.691185	1.246791
FBN1	0.621111765	1.077318	0.801845	1.447429
TAX1BP1	0.621120002	1.077196	0.802108	1.446627
ARSB	0.621716001	0.928885	0.692947	1.245156
FGF21	0.621718095	1.076879	0.802403	1.445245
NPRL3	0.621908172	1.077143	0.801689	1.447243
ANAPC11	0.622059859	1.077333	0.801165	1.448699
ZNF611	0.62212646	0.928422	0.69099	1.247437

KCNIP2	0.622731989	0.928958	0.692627	1.245928
QTRT1	0.622928987	0.928152	0.689519	1.249373
LIN7C	0.623252883	1.076351	0.802536	1.44359
SWSAP1	0.623854778	0.92835	0.689707	1.249565
RRNAD1	0.625081835	0.929348	0.692699	1.246843
ZNF562	0.625186817	0.928951	0.691157	1.248558
EDRF1	0.626755223	0.929619	0.692727	1.24752
AZIN1	0.626924844	1.076772	0.799079	1.450966
AL355102.2	0.627037518	0.929928	0.693719	1.246565
ZNF337	0.627039858	0.928233	0.687378	1.253483
ZRSR2	0.627845592	1.078782	0.793922	1.465851
ASXL2	0.629147062	0.929564	0.691099	1.250312
RBM25	0.629779173	1.075145	0.800797	1.443482
SLC25A10	0.630347846	0.928691	0.687098	1.255232
EPS8L2	0.630958231	0.930272	0.692688	1.249345
RPL38	0.63099717	1.075282	0.799642	1.445934
EDC3	0.631019746	1.075419	0.799313	1.446899
COG5	0.6311247	0.930448	0.693254	1.248797
AIDA	0.631169255	1.075075	0.799997	1.444738
RPN2	0.631378502	1.074871	0.800321	1.443604
NDUFA5	0.632199601	0.930749	0.693754	1.248706
TRMT1	0.633357379	1.07398	0.801007	1.439978
RABEP2	0.634596519	0.931099	0.693644	1.249841
CLK1	0.634964394	0.93062	0.691595	1.252255
HEXDC	0.635069665	0.930713	0.691888	1.251977
HDAC9	0.635327909	0.931349	0.694158	1.249587
PMF1-BGLAP	0.635688496	1.073544	0.800407	1.439887
ANKAR	0.635691456	0.931367	0.694009	1.249905
TTC37	0.635867133	1.073528	0.80032	1.440001
FAM46A	0.636031853	0.931133	0.692909	1.251261
FAM19A2	0.636678003	1.07343	0.799984	1.440344
CRTC3	0.63668983	0.931723	0.694772	1.249487
CNOT4	0.637819922	0.932016	0.695213	1.249479
CRACR2B	0.638500038	1.07374	0.797977	1.444799
TBC1D12	0.63872578	1.073405	0.798607	1.442759
AC244197.3	0.638730684	1.074652	0.795665	1.451461
PTDSS2	0.638976834	0.932272	0.695497	1.249655
NUP205	0.639061297	1.073369	0.798457	1.442935
TMEM140	0.63942508	1.072952	0.799187	1.440498
GABRR2	0.640087393	0.931843	0.693162	1.25271
TIFA	0.640109366	1.072578	0.799594	1.43876
PDE6A	0.641034498	1.072432	0.799292	1.438911
VPS16	0.641615568	1.072642	0.79838	1.44112
SFXN4	0.641811381	0.932709	0.69546	1.250892

TAF5L	0.642113141	0.932728	0.695349	1.251143
TMEM134	0.642239096	0.932831	0.695672	1.250838
ACVR1	0.64327967	1.072134	0.798422	1.439678
LENG1	0.643522288	0.932413	0.693256	1.254074
TMEM222	0.643655579	0.93299	0.695421	1.251716
SPTBN1	0.643786995	1.072006	0.79837	1.439428
C10orf35	0.644496813	0.932042	0.691206	1.256792
TRAPPC11	0.645026355	0.93346	0.696416	1.251189
FBRSL1	0.645142961	0.93295	0.694346	1.253547
PPAN	0.645205262	1.07156	0.79844	1.438105
MAN1A2	0.645613146	1.071454	0.798408	1.43788
MRPL58	0.646598893	0.933142	0.694193	1.25434
TSGA10IP	0.64719444	0.933849	0.696602	1.251896
ICMT	0.6482382	0.932127	0.689183	1.260711
YIPF4	0.648471192	0.934099	0.696796	1.25222
TES	0.648716285	1.071407	0.796301	1.441557
MITF	0.648797246	1.070825	0.797673	1.437514
ACSF3	0.649597993	0.934001	0.695704	1.253921
PRR25	0.64975122	1.072355	0.793223	1.449711
CRYBA1	0.650567106	0.933992	0.69506	1.255059
LRRC8E	0.650750075	0.934518	0.697033	1.252916
TMEM175	0.651153482	0.934231	0.695636	1.254659
NAXE	0.651635005	1.069776	0.798235	1.433688
EME2	0.652238542	1.071011	0.794722	1.443353
METTL26	0.65262811	0.933993	0.69376	1.257414
WDR92	0.653215803	0.934574	0.695699	1.255467
PLA2G6	0.653365745	0.934651	0.695914	1.255288
XAB2	0.653566452	0.934791	0.696345	1.254886
SDC4	0.653902226	1.069872	0.796356	1.437328
ZNF443	0.654109437	0.933947	0.692633	1.259336
PBOV1	0.654218772	1.070015	0.795767	1.438778
ZNHIT1	0.654313731	0.934871	0.696192	1.255377
WAPL	0.654603827	1.069801	0.796025	1.437736
TTC4	0.654610016	1.071996	0.790521	1.453694
PTGES2	0.655830322	1.069257	0.796502	1.435414
MIOS	0.656831914	1.068925	0.796615	1.434319
MACROD1	0.657483575	1.068992	0.795967	1.435667
KLHDC2	0.657875144	0.935372	0.695934	1.257191
VPS41	0.659934459	1.06832	0.79589	1.434001
XRN1	0.660041341	0.936044	0.69726	1.256603
U2AF1L5	0.660530801	0.936536	0.698947	1.254886
MRPL38	0.661068468	0.936215	0.697295	1.257
EFCAB2	0.661689814	1.067911	0.795653	1.43333
KRTAP5-1	0.66177603	0.936162	0.696616	1.258079

MRPS21	0.662048518	0.936386	0.697355	1.257348
TACR3	0.662135022	0.936586	0.698117	1.256513
SERINC1	0.662420071	0.936827	0.698918	1.255719
MET	0.663469936	1.067974	0.794171	1.436173
SMG8	0.663654915	0.936696	0.697579	1.257777
FASTK	0.663730757	0.936435	0.696462	1.259094
POLR2J2	0.664269196	0.937075	0.698738	1.256709
RAB7A	0.665076767	1.067298	0.794743	1.433324
TTC14	0.665751533	0.937063	0.697719	1.258511
CEP295NL	0.666137109	0.936772	0.696267	1.260352
CSNK1G1	0.66722134	1.066446	0.795391	1.429872
APLF	0.667314641	1.06664	0.794808	1.431441
SETX	0.667666976	0.937039	0.696358	1.260905
RSL24D1	0.668143021	1.067567	0.791726	1.439512
EP400NL	0.668253165	0.937808	0.699162	1.257913
GDAP2	0.66855718	1.066305	0.79477	1.430611
ZNF594	0.669234465	1.066108	0.794786	1.430054
ABL2	0.669562638	1.066114	0.794526	1.430536
TCF4	0.669693196	0.938195	0.699824	1.25776
CDK10	0.669793594	0.938001	0.698948	1.258816
PRKRIP1	0.669799615	0.937876	0.698421	1.259428
ZBTB25	0.670638645	0.938293	0.699605	1.258415
C17orf49	0.670951517	0.938347	0.699627	1.258522
HIST1H4J	0.671077045	1.065601	0.794764	1.428732
RPAP2	0.671597933	0.937477	0.695557	1.263538
PLXNB1	0.67174379	0.938104	0.698081	1.260655
ZDHHC4	0.67253432	1.065782	0.793174	1.432082
HIST1H3C	0.672855782	0.938558	0.699244	1.259777
NLRP6	0.673300088	1.065675	0.792882	1.432322
FBXW7	0.673343115	1.066448	0.790753	1.438264
NDUFA3	0.674216329	0.939054	0.700423	1.258985
WDR7	0.674403404	0.939095	0.700473	1.259007
SFRP1	0.674810526	1.064883	0.793891	1.428376
KDM6B	0.674902213	0.938692	0.698433	1.261599
FAM200B	0.675263682	0.939063	0.699757	1.260206
AL133352.1	0.675400427	0.938323	0.696539	1.264034
MRPL55	0.675995354	0.93923	0.699974	1.260265
AC005020.2	0.676762105	1.065206	0.791511	1.433541
OTUD4	0.676782927	0.939633	0.701154	1.259223
MOSPD3	0.677341329	0.93926	0.699194	1.261754
MYLK	0.679001401	0.938773	0.695987	1.266251
MKLN1	0.679068785	0.938806	0.696083	1.266167
GPAA1	0.679223345	0.9397	0.69979	1.261859
APBB2	0.679988578	0.939765	0.699543	1.262478

MTX1	0.680065462	1.06387	0.792668	1.42786
HSBP1	0.680385049	0.940014	0.70034	1.26171
ARHGAP17	0.680793757	0.940388	0.701667	1.260325
SYVN1	0.68174702	0.940334	0.700785	1.261767
TANGO6	0.681847505	0.940586	0.701805	1.260611
GNB2	0.682125865	0.93984	0.698398	1.26475
CCDC24	0.682637788	0.940414	0.700519	1.262462
NOTCH2NL	0.68273046	0.940627	0.701377	1.26149
RAB31	0.683143186	1.063193	0.792188	1.426907
CCZ1B	0.68340182	1.062774	0.793174	1.424012
CBWD3	0.683845862	0.940479	0.699966	1.263633
MSN	0.684371621	1.062745	0.792502	1.425141
MAP10	0.685064339	0.941085	0.701756	1.262037
PPP1R18	0.685445206	1.062362	0.792763	1.423644
PARP14	0.685721647	1.062767	0.791387	1.427208
NDUFS8	0.686179792	1.062907	0.790624	1.428962
NARFL	0.686832799	1.062652	0.790843	1.427879
DMXL2	0.687377519	0.941358	0.701338	1.26352
PRDM5	0.687457751	1.062219	0.791598	1.425355
CASTOR2	0.687588718	0.939343	0.69242	1.27432
RTEL1-	0.687907807	1.06343	0.787752	1.435584
TNFRSF6B				
HID1	0.68815129	1.062067	0.791492	1.425138
TULP4	0.688871545	1.06191	0.791378	1.424922
ELMO3	0.689388395	0.941882	0.702233	1.263315
AL161911.1	0.689854281	0.941968	0.702287	1.26345
USP25	0.689902118	1.061354	0.792182	1.421987
MYO5A	0.689911996	1.062295	0.789434	1.429468
HIST1H2BL	0.690545836	1.061345	0.791701	1.422826
ZNF195	0.690964075	0.942225	0.70264	1.263503
MDM4	0.691040981	0.942177	0.702375	1.263851
KCTD18	0.691489732	0.942328	0.702728	1.263623
PIIB	0.691493886	0.942196	0.702138	1.264328
GPR88	0.691625614	0.941673	0.699735	1.267264
TMEM238	0.693267557	0.942699	0.703118	1.263915
TAS2R43	0.693472488	0.942697	0.702965	1.264186
SH3D19	0.693516702	0.942764	0.703231	1.263886
AC055811.2	0.693547739	0.942438	0.70176	1.265661
CRYBG3	0.693662064	0.94256	0.702218	1.265161
USF1	0.69397496	1.060662	0.790989	1.422276
CDK5RAP3	0.694024084	1.060749	0.790694	1.423039
MAPK10	0.694088682	0.941823	0.698638	1.269657
PRRG4	0.694504975	0.942381	0.700823	1.2672
INAFM1	0.694591842	1.060858	0.789912	1.424741

LRP5L	0.69472883	1.061139	0.788968	1.4272
AHSA2	0.69482478	0.942562	0.701398	1.266645
INTS2	0.695029252	0.941962	0.69858	1.270138
USP38	0.695395385	1.060986	0.788885	1.42694
OSBPL11	0.695718	1.060803	0.789169	1.425934
GLI4	0.695900065	0.943001	0.702591	1.265672
PRPS1	0.69676623	0.943382	0.703684	1.264729
PIM1	0.696973568	1.060288	0.789697	1.423599
CORT	0.697590107	1.060142	0.789639	1.423311
C2CD4D	0.697711948	0.943311	0.702683	1.266338
CDC40	0.699878448	0.943366	0.701364	1.268869
STAG2	0.700020203	0.943886	0.703618	1.2662
DDX39A	0.700164924	1.059169	0.790504	1.419144
11-Sep	0.700455873	1.059274	0.789948	1.420424
TBL1XR1	0.701396914	1.059722	0.78781	1.425484
MAP7D1	0.701498395	0.944214	0.704038	1.266325
C5orf63	0.701564328	1.059416	0.788608	1.42322
FBXL3	0.701567968	0.944229	0.704053	1.266336
CLSTN1	0.702809897	0.94431	0.703519	1.267516
ARL2BP	0.703851483	0.944783	0.704923	1.266258
BSCL2	0.705034077	0.944681	0.703587	1.268389
POFUT1	0.705205121	1.059333	0.785853	1.427984
HIST1H2BE	0.705415728	1.058143	0.789382	1.418409
RPS28	0.705690344	0.944593	0.702694	1.269763
USP45	0.705797329	1.058127	0.789114	1.418848
MT-ND4	0.705953664	1.058312	0.788408	1.420617
AP5Z1	0.706168759	1.058267	0.788372	1.420559
SLFN12L	0.706301597	0.94395	0.699283	1.274221
SRCAP	0.706474192	0.944848	0.703292	1.269371
TMED4	0.707029401	1.05841	0.787209	1.423041
DDX18	0.707328587	0.944974	0.703239	1.269804
FIGNL1	0.707358764	1.058064	0.788021	1.420645
GNA12	0.707833865	1.057624	0.789011	1.417683
NARF	0.708813323	1.05746	0.788715	1.417776
SPDYA	0.709167137	0.945505	0.704336	1.269253
TMEM259	0.709538235	0.945654	0.704751	1.268904
CDKL5	0.709554509	1.057953	0.786534	1.423034
ZFYVE16	0.710064783	1.057215	0.788452	1.417592
ERLIN1	0.711256656	1.058261	0.784114	1.428258
DSE	0.712768487	1.057139	0.78642	1.421049
ZBED5	0.713350362	0.946333	0.705072	1.270149
NBPF12	0.714052502	0.946053	0.703217	1.272747
RNF113A	0.714087159	1.057013	0.785705	1.422004
IFI27L1	0.714652204	1.056375	0.787291	1.417427

BRD8	0.714722065	0.946586	0.705227	1.270549
UBL7	0.71610193	0.946781	0.7051	1.271302
M6PR	0.716529095	1.056202	0.786257	1.418826
SNRNP70	0.71670548	1.055932	0.786992	1.416775
GIGYF1	0.71726949	0.946928	0.704904	1.272049
CDK14	0.717458738	1.055575	0.787524	1.414862
NFKBIL1	0.71751156	0.947283	0.706416	1.27028
SLC39A3	0.718757764	1.055639	0.786199	1.417418
TOP2B	0.720103957	1.055041	0.787026	1.414326
ERVW-1	0.72022104	0.947485	0.705292	1.272844
CCDC159	0.72071512	0.947183	0.703456	1.275355
SPDYE3	0.720999694	1.057161	0.7792	1.434279
RPUSD1	0.721204834	1.055406	0.784854	1.419222
ZNF692	0.721941498	0.947876	0.705844	1.2729
STK25	0.722062134	1.055202	0.784793	1.418782
ARHGAP8	0.722337883	0.948249	0.707343	1.271202
CBLL1	0.722467898	1.05591	0.782062	1.42565
PRMT3	0.72272392	0.947561	0.703702	1.275926
C11orf65	0.723480045	0.948306	0.706731	1.272458
NCAPH2	0.723646061	1.054432	0.786004	1.414532
SPTY2D1	0.723773355	0.947934	0.704687	1.275146
ZNF264	0.724018037	0.947929	0.704468	1.275528
SLC9A6	0.724096214	1.054316	0.786008	1.414211
HIF1A	0.724224578	1.054652	0.784754	1.417375
TCEAL8	0.724397701	1.0548	0.784102	1.418952
LHX4	0.724940768	0.948307	0.705583	1.274528
KLF12	0.725001492	0.948556	0.706755	1.273084
KLC1	0.725612362	0.948612	0.706549	1.273606
RFK	0.725842053	1.053801	0.786238	1.412418
COX6C	0.726807202	1.053899	0.785051	1.414817
MT1G	0.727235969	1.053714	0.785312	1.41385
BTBD8	0.727454924	0.948525	0.704654	1.276797
WDR82	0.727483207	0.948926	0.706608	1.274342
ECI1	0.728417114	1.054015	0.783224	1.418429
RBBP8NL	0.72855472	0.948885	0.705551	1.276143
PDS5B	0.72900892	1.0532	0.785523	1.412092
CMTR2	0.72922146	0.949306	0.7071	1.274476
UTP20	0.729310538	0.949332	0.707157	1.274443
POMK	0.729404094	1.053733	0.78332	1.417496
EFNB2	0.729601631	1.053077	0.785426	1.411936
NDUFS7	0.729701373	0.949641	0.708381	1.27307
C8orf44	0.730463763	0.949591	0.707521	1.274484
STK4	0.730485575	1.053703	0.782455	1.418983
LTN1	0.730695281	0.949417	0.706465	1.275919

CRYGD	0.731021129	0.949768	0.707957	1.274173
PHACTR4	0.731129197	0.949642	0.707239	1.275128
NDUFV1	0.731581117	0.949568	0.706504	1.276255
B3GAT3	0.731953541	1.052539	0.785216	1.410871
ZNF358	0.732810326	1.052676	0.783966	1.413488
CTTNBP2NL	0.733164664	1.052548	0.784099	1.412905
PMVK	0.733601033	1.052478	0.783957	1.412972
TMEM60	0.733854329	1.052331	0.784248	1.412055
NRP2	0.73439447	1.052121	0.78451	1.411018
GALK1	0.734850696	1.052277	0.783541	1.413183
DNAH14	0.734924916	0.950385	0.707891	1.275948
ZNF800	0.735023861	0.950501	0.708394	1.275351
PQBP1	0.735047625	0.95017	0.706703	1.277514
ZNF460	0.735064254	0.950052	0.706094	1.278299
DAZAP1	0.735222667	1.051894	0.784573	1.410296
LRR39	0.736121251	1.051873	0.783834	1.411569
PLEKHA8	0.736501736	0.950822	0.708813	1.275459
SLC25A46	0.736662782	1.052188	0.782211	1.415346
SPATA25	0.736926659	1.051946	0.782839	1.413561
APBB3	0.737124989	0.950577	0.707056	1.27797
AL136295.4	0.737556413	0.951016	0.708938	1.275757
SCAF8	0.737746585	1.051431	0.78395	1.410176
HIST1H1B	0.73804512	0.950837	0.70762	1.277651
ZNF543	0.738622375	1.051335	0.783497	1.410735
ZNF35	0.738644959	1.051634	0.782393	1.413526
INPP4B	0.738806487	1.051246	0.783653	1.410212
SRRM2	0.73914077	0.951107	0.708089	1.277529
JMJD7	0.73924134	0.951099	0.707966	1.27773
TOR1A	0.739817135	1.051087	0.783306	1.410412
ZNF354B	0.741145542	1.051814	0.779418	1.419408
KCNJ13	0.74202808	1.050412	0.78375	1.407805
ZNF699	0.742268435	0.950748	0.703616	1.284682
IDS	0.742282231	1.050456	0.783355	1.40863
VAMP7	0.742459767	0.951937	0.709599	1.277036
CEPT1	0.742805925	1.050519	0.782635	1.410095
LRIT3	0.742857026	1.051021	0.780729	1.414889
BCAP29	0.743268786	1.051071	0.78016	1.416056
ZNF28	0.743458942	1.05013	0.783474	1.407543
CIZ1	0.743462317	0.952137	0.709799	1.277215
RNF207	0.746250104	0.952504	0.709353	1.279
SHQ1	0.746595247	0.952553	0.709316	1.2792
AFF4	0.747286235	0.953017	0.711173	1.277103
SF3B5	0.747605452	1.049506	0.781938	1.408633
ZNF267	0.747618588	1.049502	0.781944	1.40861

HYAL4	0.74801592	0.952803	0.709419	1.279686
NADSYN1	0.748271218	0.952738	0.708853	1.280532
ARHGEF12	0.748303527	1.04948	0.781377	1.409574
AKAP11	0.748687372	0.95299	0.709829	1.279448
PRPF39	0.749015686	1.049004	0.782518	1.406241
HEATR9	0.749123864	0.952739	0.708122	1.281856
PAN3	0.750929954	0.95353	0.710771	1.279203
ARL5A	0.751101018	0.95367	0.711371	1.278499
ZNF587	0.751550223	1.048537	0.781907	1.406088
CBL	0.751704308	0.953779	0.711431	1.278683
PPIP5K2	0.752046936	0.953678	0.710589	1.279925
TGM4	0.752611698	0.953592	0.709637	1.281413
NT5C	0.752777326	1.048376	0.781358	1.406643
RALY	0.753732679	0.953593	0.708653	1.283193
ZNF511	0.753762419	0.954176	0.711776	1.279128
PHKG2	0.753900252	0.953461	0.707795	1.284394
SIRT6	0.753992177	0.954133	0.711339	1.279797
DENND4C	0.754006337	0.954017	0.710699	1.280638
DHRS4L2	0.754492436	1.048139	0.780629	1.407321
SPARC	0.754883759	1.047859	0.781352	1.405266
PPP1R12A	0.755432852	1.048733	0.777381	1.414803
TBC1D14	0.75564309	1.047895	0.780474	1.406945
MFSD3	0.755692416	1.04791	0.780366	1.40718
HNRNPH1	0.756042209	1.04784	0.7803	1.407111
HIST1H3A	0.75726871	0.954767	0.711895	1.280497
SERINC3	0.757803635	0.954519	0.710059	1.28314
DUS1L	0.75783001	0.954853	0.711867	1.280779
UBE2L5P	0.757848099	1.047259	0.78085	1.40456
USP9X	0.758860439	1.046951	0.781092	1.403299
TXNRD2	0.759018623	1.047156	0.780113	1.405613
TRMT61A	0.760574286	0.955355	0.712173	1.281574
ANKRD16	0.761228568	1.0465	0.780584	1.403005
ZNF224	0.761263021	0.955538	0.712569	1.281353
ZNF736	0.761601147	0.955701	0.713173	1.280706
PTP4A2	0.761671924	1.047287	0.77695	1.411686
RPL37	0.76180839	1.046564	0.77975	1.404675
LCOR	0.762463625	0.955626	0.711971	1.282666
GNPTG	0.76288466	1.046512	0.778888	1.406092
ZNF346	0.763299154	1.046903	0.776875	1.410786
PTPRK	0.763385244	1.04647	0.778562	1.406566
C16orf72	0.763406359	1.046149	0.779858	1.403366
FNIP1	0.76381035	0.955955	0.712583	1.282446
LRRC40	0.764056899	0.955796	0.711466	1.284034
MFSD10	0.764282022	1.045986	0.779651	1.403305

TELO2	0.764399823	0.956004	0.712318	1.283056
TLN1	0.765030808	1.045974	0.77895	1.404533
CIR1	0.765276089	1.045618	0.780178	1.40137
TM2D3	0.765817896	1.045504	0.780109	1.401186
HIST1H2AB	0.766201485	1.045575	0.779428	1.402602
MPV17	0.76633744	1.045841	0.778181	1.405564
FBXL5	0.767518265	1.045868	0.776867	1.408013
EDF1	0.768303736	1.045151	0.779073	1.402104
GNRHR	0.768362231	1.045151	0.779013	1.402211
DNAH11	0.769734208	1.044883	0.778747	1.401971
TRMT2A	0.769794309	0.957242	0.714357	1.282709
EIF4A1	0.769941762	0.957054	0.713141	1.284392
ZNF669	0.77012484	0.957163	0.713596	1.283865
SLF2	0.770353102	1.044694	0.778921	1.40115
UBL5	0.770647382	0.95721	0.713373	1.284392
LPP	0.770809496	0.957326	0.71389	1.283774
C19orf60	0.770862729	1.044692	0.778405	1.402073
R3HCC1	0.770884632	0.957076	0.712377	1.285827
C19orf70	0.770889118	0.956866	0.711117	1.287446
FAM26E	0.771024541	0.957452	0.714415	1.283168
WDR90	0.771243858	1.044668	0.778114	1.402535
ALKBH7	0.772137257	1.044613	0.777425	1.403631
C1orf74	0.77220441	0.95754	0.713808	1.284494
CNNM4	0.773016733	0.957511	0.712868	1.286109
SOWAHB	0.773404128	1.044147	0.778122	1.40112
TM7SF2	0.773589724	0.957863	0.71437	1.284349
CAVIN1	0.773635457	0.957943	0.714796	1.2838
ARHGAP5	0.773772283	1.043891	0.778848	1.399128
ZNF410	0.773929258	0.957334	0.710971	1.289067
FBXO8	0.774263321	1.043904	0.778282	1.400181
ARHGAP29	0.774482098	0.958049	0.714605	1.284426
FRK	0.774608951	1.043819	0.778292	1.399934
MAGIX	0.774654925	0.957174	0.709338	1.291602
TRPV1	0.774687426	1.043829	0.778167	1.400188
ZNF514	0.775043483	0.958105	0.714396	1.284951
ELF4	0.775479614	1.043618	0.778264	1.399445
METTL14	0.775482058	1.043724	0.777794	1.400578
CENPT	0.776131112	0.958294	0.714466	1.285335
NBEAL2	0.776712562	0.958186	0.713267	1.287205
NOXA1	0.776729317	0.958301	0.713931	1.286318
ENO1	0.776855838	1.044194	0.774287	1.408187
MAP3K2	0.778079461	0.958698	0.714969	1.285513
PIDD1	0.778111893	0.958505	0.713791	1.287115
TRAPPC1	0.778158338	1.043317	0.776767	1.401336

NAA60	0.778519324	0.958426	0.712924	1.288469
SUV39H2	0.778752192	1.043163	0.776821	1.400825
POM121C	0.779052654	1.0428	0.778123	1.397505
DGAT2L6	0.77945616	1.042789	0.777742	1.398162
MICB	0.779818846	1.042782	0.777391	1.398773
CLASRP	0.780534783	1.042595	0.777466	1.398138
KAT2A	0.780877597	0.959091	0.714578	1.287273
ZC3H13	0.781207652	0.958927	0.713265	1.289199
CCDC130	0.781818494	0.958583	0.710599	1.293108
CDK5RAP1	0.78200714	1.042285	0.77729	1.397624
SEC24B	0.782011033	0.959128	0.713679	1.288993
NAA16	0.782380913	0.958978	0.712408	1.290889
IARS	0.783043415	1.042271	0.77624	1.399474
RNF25	0.783239774	1.042062	0.776979	1.397584
CD44	0.784152212	0.959435	0.713392	1.290336
INTS6	0.784486436	0.959717	0.714768	1.288609
DDOST	0.78528892	1.04197	0.775175	1.400588
ZNF205	0.785582294	1.041926	0.775058	1.400682
FAM208A	0.78568828	1.041493	0.776944	1.39612
SNRPB	0.78590862	1.042109	0.773851	1.40336
ZNF749	0.786085463	0.960049	0.715188	1.288743
IL5	0.786151935	0.95997	0.714635	1.289527
ATXN2L	0.786453668	1.041423	0.776431	1.396855
MOB2	0.788223777	0.960258	0.714299	1.290908
POU5F2	0.788806747	0.960212	0.713419	1.292378
ANKRD36	0.789117455	0.960661	0.715881	1.289138
DECR2	0.78911816	0.960597	0.715483	1.289683
HRC	0.789401674	0.960674	0.715674	1.289546
ACBD4	0.789765448	0.960688	0.715385	1.290104
C19orf66	0.789888128	1.041321	0.773104	1.402592
ZNF335	0.789988037	0.960711	0.715298	1.290323
SYPL1	0.790247362	1.040908	0.774657	1.398669
ZNF277	0.79045653	0.961084	0.717143	1.288002
ZNFX1	0.79051279	0.961004	0.716585	1.288791
RAB3GAP2	0.790800414	1.040428	0.776317	1.394393
CHTOP	0.791615254	1.040399	0.775547	1.395699
LMNTD2	0.791765302	0.96099	0.715209	1.291235
ZMIZ1	0.791872633	1.040431	0.775109	1.396573
SELENOO	0.792183059	1.040322	0.775282	1.395969
SNX19	0.793012869	1.040257	0.77466	1.396916
ANKRD31	0.793215622	0.961543	0.717177	1.289171
LRRC49	0.793458496	0.961525	0.716811	1.289782
PDCL2	0.793563873	1.040059	0.774992	1.395786
HECA	0.794041539	1.039983	0.774819	1.395893

METTL2A	0.794376194	0.96162	0.716456	1.290677
LINC01125	0.794453412	1.040391	0.772376	1.401406
KCNV2	0.794453672	1.039773	0.775373	1.394334
ZNRF2	0.794486627	0.961697	0.716829	1.290212
CDC42	0.794658816	1.03987	0.774667	1.395864
KIF2A	0.795191748	1.039647	0.77515	1.394395
CNN3	0.796869004	1.03937	0.774595	1.394651
PCNX1	0.797341356	1.03926	0.774595	1.394357
HIST1H2AG	0.798082879	0.962419	0.717651	1.29067
SLC25A34	0.798515289	0.961625	0.712071	1.298638
ANKS3	0.798595793	0.962285	0.716238	1.292856
INO80E	0.80000234	0.962708	0.717469	1.291774
COX6A1	0.800357604	1.039106	0.771863	1.398876
PFKFB2	0.801112676	0.963005	0.71821	1.291237
HYPK	0.801152018	0.962653	0.715865	1.294519
ULK1	0.801765782	1.038459	0.773468	1.394238
ATP5J2-PTCD1	0.801817647	1.038362	0.773901	1.393196
IRF3	0.802036643	0.96314	0.718092	1.291811
FAM135A	0.802161958	1.038808	0.771231	1.399221
MIGA2	0.802688779	0.962608	0.713881	1.297994
DIS3	0.802797022	1.038551	0.771783	1.39753
UBE3A	0.803628236	0.962828	0.714294	1.29784
LINC00998	0.804246276	1.037898	0.773409	1.392836
SRRM1	0.804393256	0.963517	0.718001	1.292985
TNFRSF18	0.804560292	0.963523	0.717862	1.293254
TIAF1	0.805631408	1.037774	0.772396	1.394331
KIAA1522	0.805706515	1.03766	0.7729	1.393114
ACRBP	0.805933109	1.037468	0.773626	1.391293
KIAA0825	0.805948121	1.037369	0.774122	1.390136
EPS15	0.805990414	0.963836	0.718365	1.293188
PDIA6	0.807190018	1.03788	0.769967	1.399014
RPS9	0.807625686	1.037067	0.773694	1.390095
CTR9	0.808187447	0.964307	0.719084	1.293158
POLRMT	0.808305924	1.036976	0.773359	1.390452
AFF1	0.80934725	0.96451	0.719151	1.293579
RBM12B	0.81056971	1.036746	0.771823	1.392602
SLC35F5	0.810617277	1.036474	0.773224	1.389349
SEC11A	0.811130343	0.964852	0.719467	1.29393
RPL7L1	0.811626471	0.964537	0.716739	1.298006
ATP10D	0.811641762	1.036279	0.773019	1.389195
BHMG1	0.811835934	1.036663	0.770713	1.394383
TAF6	0.812427358	1.036652	0.770035	1.395582
FLAD1	0.812762561	1.036017	0.773056	1.388426
CCDC126	0.814002917	1.035991	0.771663	1.390863

AP4E1	0.814226925	0.965152	0.717968	1.297435
USP15	0.815168596	0.965307	0.717953	1.297881
TMEM208	0.816019751	1.035685	0.770819	1.391563
DYRK1B	0.816195594	0.965685	0.719391	1.2963
ZNF236	0.816445096	1.035379	0.771977	1.388655
TBXA2R	0.816653949	1.035407	0.77156	1.38948
NCOA6	0.816699856	0.965818	0.719741	1.296029
IL13RA1	0.817056012	1.035243	0.771963	1.388316
ORAI2	0.817128231	0.965995	0.720483	1.295167
PBX3	0.818551633	1.034875	0.772134	1.38702
DPPA5	0.818895575	1.034868	0.771736	1.387717
CHMP4A	0.819035604	0.965946	0.717872	1.299747
TMEM262	0.819187199	0.966261	0.719937	1.296866
IL21	0.819859841	0.966383	0.720001	1.297077
TCTE3	0.823730521	1.034115	0.769801	1.389181
RAB14	0.82486959	1.033793	0.770179	1.387636
PTCH2	0.825789342	0.966703	0.715042	1.306936
SLC35B4	0.826335782	1.033384	0.770651	1.38569
EPCAM	0.826974323	1.033268	0.770496	1.385655
TRAF5	0.82720316	0.967577	0.719715	1.300801
CYP51A1	0.827259924	0.967874	0.721853	1.297744
SRRD	0.827655003	1.033108	0.770544	1.38514
PHF13	0.827720328	0.967906	0.721514	1.298439
UBALD1	0.827758363	0.967946	0.721769	1.298089
TSSC4	0.828284478	1.033118	0.769643	1.38679
GTPBP10	0.828692807	0.967614	0.718115	1.3038
AP002990.1	0.828857427	1.032885	0.770274	1.385029
RRAGC	0.828998127	0.967752	0.718753	1.303012
KIRREL	0.829005387	1.033029	0.769208	1.387335
INO80B	0.829031189	0.967809	0.719136	1.30247
PPDPF	0.829187141	0.967844	0.719205	1.302441
FN1	0.830484837	1.033042	0.767124	1.391138
ZC2HC1C	0.830530374	1.032482	0.770457	1.38362
ZNF12	0.831294783	0.968563	0.721947	1.299422
COQ4	0.831319709	1.032484	0.769376	1.385568
APPBP2	0.831588339	0.968579	0.721695	1.29992
MIER1	0.831610374	1.032475	0.769033	1.386162
RPLP1	0.831693485	0.96869	0.722406	1.298938
PTPN21	0.832089817	1.032211	0.769999	1.383715
NIT1	0.832158243	0.968604	0.721155	1.300961
BAG5	0.832271626	0.968797	0.722483	1.299087
BRWD1	0.832279674	1.03215	0.770116	1.383342
CLK3	0.832386547	1.032292	0.769098	1.385553
KIFC3	0.832392947	1.032209	0.769595	1.384437

CCSER1	0.832432596	0.968826	0.722495	1.299142
FRMD4B	0.832514496	1.032175	0.769638	1.384269
SIVA1	0.832797711	0.968803	0.721849	1.300243
MAN2A1	0.83294073	1.03201	0.770075	1.383041
CLEC18C	0.833134346	0.968843	0.721722	1.300578
ULBP3	0.83322457	1.032192	0.768563	1.386249
C12orf40	0.833325876	0.969007	0.722734	1.299198
PLSCR4	0.833715147	0.969	0.722179	1.300177
AC022400.6	0.833879733	0.968645	0.719234	1.304545
MMGT1	0.834386224	0.969212	0.722945	1.299368
MRPS25	0.834807145	0.969219	0.722449	1.300278
IQGAP1	0.836181456	1.031606	0.768112	1.385488
FUNDC2	0.836186468	1.031706	0.767474	1.386908
NAA10	0.836998316	1.031339	0.768653	1.383798
SLFN5	0.8372491	1.031443	0.767638	1.385906
WASHC1	0.837340279	1.031283	0.768528	1.383873
CHIC1	0.837591254	0.969586	0.721646	1.302712
XKR9	0.837666044	1.031301	0.767956	1.38495
SMURF1	0.837811958	1.031243	0.768114	1.384512
AGPAT1	0.837894806	0.969853	0.723345	1.300367
PBRM1	0.838156833	1.03099	0.76925	1.381787
DOCK10	0.838642789	0.969503	0.719583	1.306223
HDAC10	0.838706297	1.031029	0.768218	1.38375
SIAE	0.838953293	1.030887	0.768781	1.382356
HIST1H4K	0.839449977	1.030772	0.768818	1.381982
LINC00238	0.840132284	0.970159	0.722783	1.302201
CUEDC2	0.840814522	1.030676	0.767491	1.384112
DNAJB14	0.841112091	1.030445	0.768568	1.381553
CTSB	0.841152243	0.970303	0.722557	1.302996
NOL4L	0.841345825	0.97052	0.724036	1.300915
AC011498.1	0.841964334	0.970486	0.722921	1.30283
BBX	0.842215744	1.030408	0.767216	1.383888
GNG3	0.842238508	0.970398	0.721839	1.304546
PUS1	0.842405659	1.030203	0.768296	1.381392
MIB1	0.843025774	1.030153	0.767727	1.382281
CDK13	0.843414331	0.970859	0.72396	1.30196
DYNAP	0.843593268	0.970861	0.723727	1.302384
MAML2	0.843891379	0.970942	0.723976	1.302154
TCTN3	0.844324742	1.030268	0.765055	1.387418
RABGGTA	0.845287084	0.971015	0.722643	1.304754
NKX6-3	0.845597558	1.030097	0.764299	1.388332
TYSND1	0.845677854	0.971291	0.724366	1.302388
PP2D1	0.845948607	1.029792	0.765837	1.384721
SCAND1	0.846474609	1.029714	0.765575	1.384987

CFAP44	0.846523277	0.970987	0.72067	1.308249
CLDND2	0.846558568	1.02975	0.765208	1.385747
TRIM4	0.846927127	1.02948	0.766488	1.382709
PJA2	0.847120343	0.971624	0.725108	1.301948
GSDMD	0.847806739	0.97167	0.724523	1.303122
MFAP3	0.847844284	0.971324	0.721585	1.307497
EIF2B4	0.84809139	0.971429	0.722105	1.306837
CCDC71L	0.848191023	1.029207	0.766466	1.382013
BATF	0.849227695	0.971895	0.724391	1.303963
UCN	0.850406572	0.972187	0.725178	1.303333
RNF113B	0.850743455	1.02883	0.7652	1.383285
H1FX	0.850883845	1.028728	0.765698	1.382113
YTHDF3	0.851781687	0.972091	0.722364	1.308151
SFT2D2	0.852879696	1.028105	0.767035	1.378033
RBFA	0.853097003	0.972275	0.722006	1.309296
AC013394.1	0.85345807	1.028149	0.76582	1.380338
SLC30A6	0.853509734	1.028202	0.765363	1.381303
CALR	0.853702587	0.972702	0.724795	1.305401
TOGARAM1	0.853842707	0.972749	0.724997	1.305165
HIPK1	0.853879031	0.97286	0.725905	1.30383
MRPL23	0.85421794	1.027992	0.765761	1.380024
SPINT4	0.854347966	1.02817	0.764277	1.383182
ZNF134	0.854510532	1.027847	0.766351	1.37857
F11	0.855494445	0.972268	0.718343	1.315951
NSL1	0.856133657	1.027757	0.764441	1.381775
ERP29	0.856180446	1.02756	0.765806	1.378783
B3GNTL1	0.856359954	1.027494	0.766007	1.378245
NOTCH2	0.85636608	1.027596	0.765254	1.379873
TRAF2	0.856674247	0.973291	0.72553	1.305661
ZBED8	0.857114351	0.973263	0.724613	1.307236
RBM33	0.857502683	0.973406	0.725293	1.306395
SAMD1	0.857631069	1.027329	0.7652	1.379254
PET117	0.857854465	1.027199	0.765802	1.377821
ISPD	0.858136213	1.027084	0.766207	1.376784
MACC1	0.858289103	0.973597	0.725806	1.305985
C9orf172	0.858289242	0.973532	0.72522	1.306864
AGAP6	0.858814841	0.973642	0.725407	1.306824
HIST1H2AH	0.858827787	0.973779	0.726612	1.305024
IFNAR1	0.858918918	1.027005	0.76554	1.377771
KIAA0907	0.859121616	1.026906	0.765957	1.376754
TAS2R10	0.859340718	0.973701	0.725125	1.30749
C12orf10	0.859415645	1.027178	0.763444	1.382019
CXXC1	0.860196619	0.973704	0.723835	1.309829
CTDSPL2	0.860580363	1.027412	0.759773	1.38933

TRIM66	0.860582543	0.973894	0.724953	1.308319
RIC1	0.860602138	1.026851	0.763967	1.380193
C1orf56	0.860747657	0.973924	0.72497	1.30837
RPS20	0.861086243	1.026539	0.76554	1.37652
RPS15	0.861416236	1.026461	0.765594	1.376214
MDN1	0.861638954	0.974262	0.726658	1.306236
RSAD1	0.861709601	0.974307	0.726956	1.30582
EXOC4	0.862968137	0.97411	0.723175	1.312118
SERF2	0.863081864	0.974477	0.726373	1.307326
RAD9A	0.863809008	0.974625	0.726592	1.307329
MUTYH	0.863983016	0.974602	0.726103	1.308146
HSPG2	0.864065182	0.97469	0.726786	1.307153
KBTBD4	0.864548428	0.974766	0.726727	1.307463
CCDC7	0.865025515	0.974873	0.726961	1.307328
TTPAL	0.865067755	0.974957	0.727681	1.30626
OXLD1	0.865095796	0.974912	0.727214	1.306978
PAQR7	0.865861057	1.026238	0.759863	1.385992
ARID2	0.865874473	1.025591	0.764936	1.375066
TMEM160	0.867197101	1.02556	0.762938	1.378581
MOGS	0.868001481	0.975489	0.727989	1.307135
SUFU	0.869024508	1.024964	0.764585	1.374015
ATG4B	0.869380144	0.97568	0.727554	1.308426
ARHGEF5	0.869637067	1.024913	0.763943	1.375033
BBS10	0.869915495	0.97557	0.725611	1.311636
GPR107	0.870823516	1.024938	0.761656	1.37923
SGK494	0.870941883	0.975933	0.727417	1.309354
PCBD2	0.871650705	1.024481	0.763968	1.37383
PAN2	0.872352942	0.976106	0.726736	1.311045
TMEM225B	0.872693281	1.024453	0.762353	1.376665
RPL13	0.872807595	1.024315	0.763304	1.37458
MCRIP1	0.873365442	1.024203	0.763253	1.374369
FAM151B	0.873707155	0.976436	0.727691	1.31021
HIST1H3G	0.874238978	0.976493	0.727349	1.310978
TBC1D23	0.874806029	0.97644	0.725835	1.31357
IFT46	0.874821075	0.976621	0.727621	1.310832
TTLL3	0.874840161	0.976484	0.726214	1.313002
C2orf16	0.875032797	1.024039	0.761638	1.376842
IFT43	0.875636326	0.976699	0.726994	1.312173
USP34	0.875748297	0.976751	0.727324	1.311717
CFAP97	0.875869937	1.023592	0.763949	1.371479
ILK	0.876262822	0.976943	0.728363	1.310359
TIMM44	0.876725057	0.977094	0.729092	1.309454
SETD4	0.878085739	1.023337	0.762095	1.374131
PTPN14	0.878444015	1.023348	0.761335	1.375532

RARS2	0.878686536	0.977448	0.729265	1.310092
AHNAK	0.879556502	0.977506	0.728314	1.311958
FDX2	0.880174782	1.022828	0.762694	1.371688
OLFML2A	0.881295569	1.022571	0.762891	1.370643
STK32C	0.881393847	0.977959	0.729742	1.310605
TROVE2	0.881482306	1.022788	0.760578	1.375394
PPCDC	0.881654741	0.977905	0.7287	1.312335
ELF1	0.882177687	0.977956	0.728283	1.313223
HIST2H3C	0.882209548	0.978101	0.729759	1.310955
AL138752.2	0.882853743	0.978033	0.727853	1.314206
GTF2IRD2	0.883859367	0.978205	0.727822	1.314723
MCC	0.884086534	1.022191	0.761005	1.373018
CPSF7	0.884541356	1.022054	0.76139	1.371957
STARD13	0.885067643	1.022054	0.760356	1.373822
B4GALT5	0.885681289	1.021749	0.76201	1.370021
QKI	0.887540601	0.978819	0.727519	1.316923
NDUFB8	0.888096749	1.021418	0.76034	1.372144
SPRED1	0.888293103	0.979092	0.72909	1.314819
GFER	0.888386392	1.021341	0.760499	1.37165
CXorf65	0.89009179	0.978911	0.723525	1.324443
NME1-NME2	0.890135813	1.020842	0.761806	1.367959
SPG7	0.890149477	0.979407	0.728988	1.315847
INO80D	0.890845734	1.020735	0.76141	1.368383
CLK2	0.891380061	0.979598	0.728727	1.316836
ERICH6B	0.892672147	0.979882	0.729395	1.316391
ARL16	0.893845583	0.980183	0.730513	1.315185
RPL37A	0.893861441	1.020162	0.760885	1.367788
BORCS6	0.893865361	0.979852	0.726605	1.321364
CLK4	0.894118304	0.980097	0.728948	1.317776
SLC25A11	0.894280183	1.020249	0.759099	1.371242
MED13	0.89453917	0.980104	0.728166	1.31921
PRSS48	0.894960213	0.980393	0.730703	1.315407
KHK	0.895440528	0.980553	0.731601	1.314219
ZNF845	0.895712698	1.019908	0.759548	1.369514
CCDC83	0.896285082	1.01972	0.760263	1.367724
RINT1	0.897006055	0.980538	0.728154	1.320401
SURF4	0.89795208	0.98098	0.731487	1.315569
EGFL7	0.898050927	1.019338	0.760448	1.366366
SFI1	0.898072594	1.01954	0.758253	1.370864
MFSD4B	0.898126747	0.981039	0.731834	1.315104
FGFBP3	0.899148522	0.981174	0.731303	1.31642
ATRX	0.899982627	1.019038	0.759395	1.367454
CCDC57	0.900780726	0.981442	0.731092	1.317519
ATP6V1A	0.901048475	1.018839	0.759162	1.367341

RAB24	0.90127071	1.018857	0.758463	1.368648
CHM	0.901372807	0.981582	0.73155	1.317071
CTNNA2	0.901438646	1.018774	0.758994	1.367468
FAM229A	0.901787879	0.98157	0.730479	1.318969
KLRC4	0.901798437	0.981579	0.730567	1.318834
PPP1R35	0.902068696	1.01873	0.758038	1.369076
D2HGDH	0.90222687	0.981778	0.732129	1.316554
CSAD	0.903098605	0.981763	0.730007	1.320342
MUS81	0.903715914	1.018244	0.759685	1.364803
ATP5G2	0.903766056	1.018336	0.758521	1.367147
COL10A1	0.904065982	0.982062	0.731652	1.318175
ZNF782	0.904933634	0.982165	0.731014	1.319603
ARHGAP12	0.905510829	0.98209	0.728713	1.323568
ANAPC15	0.906450019	1.017839	0.757889	1.366951
EXD3	0.907640549	0.982677	0.731478	1.320142
FAM160B2	0.907840031	1.017662	0.756609	1.368785
FKBP14	0.90840695	0.982943	0.733231	1.317698
ANKMY1	0.909318616	0.982995	0.731775	1.320461
ATP5H	0.909420923	1.017452	0.755214	1.370747
AGAP4	0.91010545	1.017039	0.758508	1.363689
CRYGS	0.910364645	1.017111	0.756985	1.366624
CDSN	0.910455646	1.016981	0.758346	1.363824
MDP1	0.910886245	0.983348	0.732824	1.319518
PEX11G	0.911342444	0.98351	0.733948	1.317929
SETD7	0.911428449	1.016846	0.757571	1.364856
SP4	0.912111083	1.016706	0.75757	1.364483
HEATR1	0.912605562	1.016845	0.754569	1.370284
STX16	0.913111555	0.983652	0.731576	1.322585
TRANK1	0.914097967	1.01651	0.75491	1.368764
ZNF444	0.914523196	1.016484	0.754124	1.37012
NCMAP	0.914569707	0.984002	0.732874	1.321182
CCER2	0.914826071	0.984038	0.732744	1.321514
ZNF8	0.914840611	0.984066	0.733111	1.320927
SPACA6	0.915168454	0.984187	0.734024	1.319609
SNX13	0.915261323	0.984181	0.73369	1.320191
TMPPE	0.916575769	0.984335	0.732546	1.322668
C1orf122	0.917383312	0.984436	0.731924	1.324063
UHMK1	0.917413394	1.015735	0.756171	1.364396
TMEM205	0.917458588	1.015712	0.756354	1.364005
SYCP3	0.917739619	0.984552	0.732711	1.322954
ORC3	0.917959572	0.984629	0.733276	1.322142
CMTM2	0.91863462	0.984852	0.734826	1.319951
CEP97	0.918765906	1.015553	0.754916	1.366175
ENGASE	0.919866307	1.015276	0.755633	1.364135

ANKRD36B	0.920862588	1.015043	0.75606	1.362739
KRTCAP2	0.922148861	1.014782	0.756072	1.362018
NDUFAF8	0.922790501	0.985589	0.734864	1.321857
EXT2	0.922812665	0.985544	0.73409	1.32313
MBD3	0.922825647	1.014679	0.755593	1.362603
TAS2R20	0.923029771	0.985623	0.734732	1.322186
STAU1	0.923099862	0.985545	0.733296	1.324565
QSER1	0.923370897	1.01459	0.755291	1.362908
ANKRD39	0.923551351	0.985633	0.733421	1.324577
ATP6V0A2	0.923675842	1.014481	0.755971	1.361391
B3GALNT2	0.923677402	0.985754	0.734997	1.322061
ZNF197	0.923890058	0.985835	0.735683	1.321044
U2AF1L4	0.924191796	1.014455	0.754837	1.363365
FBXW11	0.925004705	1.014316	0.75446	1.363673
IPO11	0.926238734	1.013999	0.755464	1.361011
FAM96B	0.926240283	0.986267	0.735954	1.321716
NOL12	0.926623669	0.986328	0.735836	1.322092
CCNL1	0.926867561	1.013823	0.756223	1.359172
WDR13	0.926947886	1.014065	0.752307	1.366901
C4orf45	0.927317296	1.013712	0.756541	1.358303
NOSIP	0.927708214	1.013651	0.756274	1.358621
CMTM6	0.927799232	0.98653	0.73573	1.322825
IFIT1B	0.927882527	0.986561	0.736002	1.322419
APITD1-CORT	0.927977974	0.986355	0.732236	1.328665
TMCC3	0.928709684	1.013468	0.756012	1.3586
ADAMTS13	0.928967871	0.986504	0.731735	1.329977
RAB5B	0.929188398	0.986805	0.736203	1.32271
HSPA8	0.929283881	0.986738	0.734772	1.325109
FAM160A2	0.929304785	1.01351	0.753496	1.363247
RBM14-RBM4	0.92932898	0.986734	0.734557	1.325485
AC023509.3	0.929371731	0.986773	0.735106	1.3246
ZNF407	0.930008507	0.986933	0.735902	1.323595
AL449266.1	0.930235998	1.01322	0.755115	1.359548
MAGT1	0.930498394	1.013209	0.754445	1.360726
CHST11	0.930739994	1.013083	0.7557	1.358126
FAM110A	0.931610237	0.987263	0.736688	1.323066
SLC50A1	0.931623067	1.012947	0.75505	1.358931
SRPK2	0.932644363	0.987221	0.732622	1.330296
APOL6	0.933327838	1.012627	0.754703	1.358698
NF2	0.933500155	0.987619	0.737064	1.323348
AHR	0.933511385	0.987559	0.73593	1.325227
MPHOSPH9	0.9337729	1.012699	0.751997	1.363783
FMO1	0.934403379	1.012446	0.754144	1.359219
SPOPL	0.934569528	0.987751	0.735982	1.325647

FAM3A	0.934819799	1.012312	0.755006	1.357308
WDR45	0.935097287	1.012405	0.752472	1.362127
RPLP2	0.93522716	1.012252	0.754647	1.357793
PARP10	0.935759482	0.988025	0.737131	1.324315
SGTB	0.936384666	0.988052	0.735509	1.327308
R3HDM2	0.936786952	1.012043	0.752861	1.360451
VPS28	0.936859705	1.011948	0.754282	1.357635
DEPDC7	0.937338085	1.011813	0.755008	1.355966
RABAC1	0.937664535	1.011807	0.753947	1.357859
NEURL4	0.938902927	0.988524	0.735877	1.327911
TRADD	0.938980411	0.988511	0.73534	1.328846
MBNL2	0.940036526	1.0113	0.754616	1.355297
MRPL57	0.940696024	1.011197	0.754113	1.355924
C20orf27	0.940893404	1.011124	0.754761	1.354562
LRRC45	0.941017291	1.011188	0.753077	1.357764
ATN1	0.941367419	0.989042	0.737392	1.326573
ANKIB1	0.941710686	0.98911	0.737526	1.326514
PRDX5	0.943179863	0.989364	0.737322	1.327564
CYP2R1	0.943197413	0.989368	0.737339	1.327543
CCDC14	0.944543616	0.989556	0.73615	1.330192
RB1	0.944592256	0.989647	0.737935	1.327219
DCAF8	0.945717804	0.989746	0.735647	1.331613
SLC35E1	0.946422017	1.01008	0.753906	1.353301
IGDCC4	0.946662173	1.010097	0.752557	1.355772
ZNF446	0.946905945	1.010091	0.751659	1.357375
KLHL7	0.946907464	0.990034	0.737268	1.32946
ILKAP	0.948061606	0.990297	0.738514	1.327922
RBM18	0.948278248	1.00975	0.753174	1.353731
ANKRD54	0.949179229	0.990523	0.739085	1.3275
FIS1	0.952352692	1.009029	0.751376	1.355033
USP47	0.952852337	0.991169	0.738655	1.330005
FAM222B	0.953241983	0.991128	0.735795	1.335065
CCDC84	0.953880416	0.991355	0.738641	1.33053
ANKZF1	0.955080575	1.008476	0.751841	1.352709
ZYG11B	0.955509683	0.991657	0.738822	1.331016
GLIPR1	0.956020883	0.991722	0.738054	1.332575
SMCHD1	0.956199429	0.991816	0.73974	1.329791
CERCAM	0.956679317	1.008197	0.750966	1.353538
AC011511.1	0.959178962	1.007736	0.750216	1.353654
MLANA	0.960071259	1.007547	0.750649	1.352364
TMEM161A	0.960157877	1.007509	0.751254	1.351171
NDUFA7	0.960573744	0.992623	0.740083	1.331336
IL27RA	0.961180116	1.007327	0.75076	1.351574
DHRS4	0.961640895	1.007248	0.750461	1.351899

IDO1	0.961927451	1.007144	0.751876	1.349078
ENOSF1	0.962166299	1.007142	0.750563	1.351433
FAAP100	0.962912822	0.993057	0.74033	1.332056
UTP23	0.962944294	1.00705	0.748757	1.354445
TMUB2	0.962977504	1.006965	0.751149	1.349904
RAB4B	0.963334832	0.99315	0.740854	1.331364
PYM1	0.963338484	0.99308	0.738566	1.3353
PYCR3	0.963382806	0.993118	0.739553	1.333621
PWWP2B	0.963580113	1.006873	0.750387	1.351028
DOCK7	0.963900813	1.006822	0.750027	1.351541
MZF1	0.964129141	1.0068	0.74934	1.352719
HOOK2	0.964590174	0.99322	0.735537	1.341178
FAM50A	0.96469672	1.006689	0.749341	1.352419
SPTAN1	0.964780474	0.993418	0.741024	1.331779
ATG16L2	0.9652958	0.993425	0.738026	1.337205
AKAP17A	0.965767496	0.993557	0.739599	1.334718
KPNA3	0.965825066	0.993531	0.738329	1.336944
GNAQ	0.965947053	0.993646	0.741539	1.331462
CHMP6	0.965964334	1.006414	0.750302	1.349949
OSTM1	0.966260742	1.00637	0.749842	1.350659
SPSB2	0.966918617	1.006246	0.749725	1.350537
ANKRD7	0.967423784	1.006148	0.749729	1.350268
TJP1	0.967683992	1.006136	0.748402	1.352628
AC072022.1	0.968550688	0.994052	0.738953	1.337217
ZMYM1	0.968752537	0.994081	0.738608	1.337916
ZNF92	0.969304439	0.994258	0.741516	1.333145
FOXO3	0.969511381	1.005738	0.75	1.348679
TACO1	0.970522692	0.994339	0.735797	1.343727
TEN1-CDK3	0.972256404	0.994802	0.741613	1.33443
DIP2A	0.972491741	0.994842	0.741503	1.334737
TMUB1	0.974186518	0.995137	0.740726	1.33693
AXL	0.974338281	1.004836	0.748922	1.348198
IKZF2	0.974762375	0.995279	0.74236	1.334365
FEM1C	0.974840334	0.995273	0.74141	1.33606
PYCR1	0.974992742	0.995325	0.742556	1.334137
PPP1R16A	0.975194102	1.004683	0.748401	1.348726
ZNF518A	0.975438104	0.995368	0.740653	1.337679
VPS50	0.975987873	1.004573	0.746373	1.352094
AASDH	0.976031909	0.995511	0.742303	1.335091
NDUFA1	0.976304929	1.004483	0.747745	1.349373
ANKRD61	0.976735834	1.004399	0.747817	1.349015
SCRG1	0.97761777	0.995661	0.734841	1.349056
GNA13	0.979860695	0.996217	0.742273	1.337041
DDX47	0.980490185	1.003673	0.748147	1.346473

TAS2R3	0.981069243	1.003571	0.747606	1.347173
CCDC97	0.981075943	0.996406	0.740021	1.341619
TIGD1	0.981188721	0.996434	0.740458	1.340902
KMT5C	0.981382523	1.003503	0.748121	1.346064
SYCE1L	0.981626816	1.003478	0.746767	1.348437
PANK3	0.981756725	1.003447	0.747148	1.347666
SAP25	0.983135756	0.996831	0.74266	1.337989
JTB	0.984297181	1.002984	0.745459	1.349473
SCYL2	0.985072101	0.997171	0.741085	1.341747
FAM193B	0.985142815	0.997184	0.741131	1.341702
TADA2A	0.98523205	1.002777	0.747606	1.345043
ZNF765	0.985870312	0.997345	0.743164	1.338464
PABPN1	0.986040282	1.002623	0.747623	1.3446
GALT	0.986217068	1.002619	0.745181	1.348994
ZBTB20	0.986661952	0.997498	0.743624	1.338044
CHKB	0.987064872	1.002436	0.746978	1.345259
KIAA1551	0.987408983	0.997638	0.743763	1.338171
NME7	0.988052575	0.997749	0.742891	1.34004
STAG1	0.988468304	0.997783	0.738476	1.348143
POP5	0.988807548	1.0021	0.747476	1.343461
TMEM91	0.988824099	0.9979	0.743578	1.339206
UNK	0.988966659	1.002104	0.743926	1.349883
GCC2	0.989518164	0.998029	0.743549	1.339605
ZBTB48	0.989573559	0.998039	0.743517	1.339689
HEXIM2	0.989920587	0.9981	0.74306	1.340677
WDR73	0.990131666	0.998145	0.743672	1.339693
TMEM39B	0.990451306	0.998196	0.742662	1.341654
HIST1H4L	0.990481103	1.001787	0.747132	1.343238
MBD6	0.991327442	0.998371	0.74408	1.339567
ASCL2	0.9918721	1.001528	0.746645	1.34342
MRPL24	0.993357692	0.998748	0.74362	1.341408
CNOT6L	0.993910384	1.001168	0.741898	1.351045
SLC38A10	0.994940199	1.000949	0.746523	1.342087
BBS4	0.995018993	0.999063	0.744412	1.340828
DAPP1	0.995020873	0.999062	0.744102	1.341383
TIMP3	0.995727583	0.999199	0.745074	1.339998
SPATA20	0.996121451	1.000726	0.746774	1.34104
TXNDC16	0.996410654	1.000675	0.745926	1.342425
HNRNPCL1	0.996436345	0.999331	0.744867	1.340724
AWAT1	0.997588214	0.999537	0.740464	1.349256
ULK4	0.998319706	1.000316	0.745152	1.342858
ARL6IP4	0.998470562	0.999713	0.745196	1.341158
CELF6	0.999761638	0.999955	0.745891	1.340558

Table S6. DEGs between low- and high-risk score phenotypes LUAD patients.

ID	log2FC	P value	FDR
SPAG11B	-6.69248	4.07E-28	1.19E-25
SPAG11A	-6.22762	1.41E-24	3.21E-22
GC	-6.13406	1.65E-30	6.10E-28
MSTN	-5.27982	1.13E-76	2.06E-72
ALB	-5.20768	7.00E-39	5.77E-36
LCN9	-5.13564	3.57E-28	1.06E-25
AFP	-4.95205	1.82E-30	6.51E-28
PRB4	-4.64341	4.47E-20	6.19E-18
SST	-4.52694	9.19E-21	1.40E-18
NEUROD4	-4.45957	1.67E-17	1.81E-15
PNLIP	-4.28956	4.44E-20	6.19E-18
SSX3	-4.18275	2.69E-20	3.87E-18
LIPF	-4.15985	6.27E-24	1.29E-21
TUNAR	-4.10292	8.79E-21	1.35E-18
G6PC	-4.07824	1.00E-17	1.11E-15
PRODH2	-3.93078	3.38E-19	4.41E-17
VSX2	-3.87062	9.29E-30	2.96E-27
PRAC1	-3.84558	1.45E-18	1.76E-16
SLC7A14	-3.84208	1.69E-34	8.29E-32
PRB1	-3.74922	7.60E-15	5.52E-13
TFAP2B	-3.72591	2.63E-24	5.74E-22
HDGFL1	-3.70399	2.36E-22	4.33E-20
GLRA4	-3.65273	1.74E-26	4.40E-24
BHMT	-3.61858	1.73E-38	1.26E-35
CYP11B1	-3.59924	3.84E-20	5.45E-18
HTR3B	-3.58026	1.05E-21	1.84E-19
CREB3L3	-3.57121	1.73E-38	1.26E-35
SLC17A6	-3.52355	7.28E-17	7.34E-15
LCN15	-3.50813	6.55E-21	1.04E-18
APOA1	-3.49083	1.38E-44	1.67E-41
CELA3A	-3.46507	8.97E-19	1.11E-16
SPIC	-3.41963	6.34E-30	2.09E-27
PRLHR	-3.29361	3.04E-17	3.23E-15
FOXI1	-3.26529	4.18E-25	9.73E-23
RHOXF2	-3.2331	1.11E-14	7.70E-13
RTP1	-3.20443	6.21E-21	1.01E-18
WFDC12	-3.16003	3.76E-22	6.76E-20
RHOXF2B	-3.0995	7.43E-13	3.63E-11
PAQR9	-3.06815	4.00E-13	2.07E-11
CDH22	-3.04471	3.93E-30	1.35E-27
GLYATL3	-3.03752	6.60E-14	3.91E-12
LGALS14	-3.00894	1.74E-13	9.56E-12

CALB1	-2.97239	5.05E-20	6.95E-18
GNRH2	-2.9712	1.32E-35	7.48E-33
REG1B	-2.96432	5.46E-13	2.75E-11
GFRA4	-2.96192	5.67E-17	5.78E-15
AC187653.1	-2.9185	4.53E-14	2.78E-12
APOA5	-2.89754	2.95E-24	6.38E-22
FABP7	-2.87293	3.51E-18	4.00E-16
PHOX2B	-2.83461	4.59E-13	2.35E-11
ALPI	-2.81794	1.40E-13	7.86E-12
PNMA6F	-2.80812	4.63E-14	2.83E-12
MORC1	-2.71985	3.35E-17	3.54E-15
PRH2	-2.71452	2.49E-35	1.37E-32
GIF	-2.71324	1.01E-14	7.13E-13
NEUROG3	-2.71195	1.23E-21	2.11E-19
KRT33A	-2.67986	3.19E-09	6.93E-08
UGT2A1	-2.65496	2.41E-14	1.55E-12
HTR3E	-2.61527	5.37E-18	6.05E-16
ACTL8	-2.56375	1.48E-12	6.86E-11
A4GNT	-2.54214	3.81E-25	8.98E-23
NLRP13	-2.53609	1.93E-10	5.77E-09
BPIFB4	-2.45806	1.23E-15	1.06E-13
WFDC5	-2.45466	2.39E-09	5.38E-08
CELA3B	-2.45331	2.06E-16	1.94E-14
CARTPT	-2.44233	8.49E-11	2.78E-09
CLCA1	-2.42543	3.31E-10	9.35E-09
CYP2B6	-2.41747	4.71E-15	3.52E-13
KRT31	-2.41213	2.18E-10	6.48E-09
KIR3DX1	-2.39021	1.72E-25	4.22E-23
HHATL	-2.37389	3.27E-16	2.97E-14
HMX3	-2.37012	1.42E-09	3.43E-08
MCCD1	-2.36778	2.52E-12	1.08E-10
CRH	-2.35741	1.75E-09	4.11E-08
PRB3	-2.34144	1.59E-29	4.97E-27
RERGL	-2.30095	2.76E-20	3.95E-18
NNAT	-2.29691	1.69E-24	3.79E-22
SOHLH1	-2.27501	6.31E-13	3.17E-11
CD177	-2.27443	3.58E-19	4.65E-17
CALML3	-2.23237	3.66E-12	1.52E-10
CDH16	-2.22896	3.45E-14	2.19E-12
OLIG3	-2.22537	2.90E-07	3.76E-06
F2	-2.19174	1.08E-10	3.43E-09
KLK14	-2.17615	4.42E-14	2.72E-12
VSTM2A	-2.17041	4.12E-10	1.13E-08
CCKAR	-2.13421	1.71E-09	4.04E-08

HRG	-2.11889	8.34E-14	4.81E-12
CPA1	-2.11358	2.61E-15	2.08E-13
KLK12	-2.10927	3.37E-10	9.49E-09
VTN	-2.09845	2.79E-15	2.20E-13
MYOD1	-2.08697	6.18E-08	9.67E-07
SLC7A3	-2.08458	1.55E-13	8.59E-12
HMP19	-2.07512	1.13E-10	3.59E-09
SERPINA6	-2.05879	8.64E-11	2.81E-09
MSMB	-2.03421	7.86E-13	3.79E-11
GLRA2	-2.02921	1.15E-12	5.38E-11
SNX31	-2.00713	9.76E-17	9.63E-15
TF	-2.00328	1.53E-13	8.54E-12
TNMD	-1.99729	1.93E-08	3.43E-07
CELF3	-1.97255	8.30E-13	3.97E-11
AQP2	-1.96857	2.00E-15	1.63E-13
FGF21	-1.96272	9.62E-09	1.87E-07
SLC14A2	-1.96212	2.22E-12	9.66E-11
NKX2-2	-1.95418	1.10E-06	1.19E-05
RET	-1.93715	6.94E-21	1.09E-18
XAGE5	-1.9238	1.94E-06	1.93E-05
TCHHL1	-1.92358	5.62E-07	6.62E-06
OTOS	-1.91993	1.35E-07	1.92E-06
SVOP	-1.90534	1.85E-12	8.30E-11
GFI1B	-1.89521	1.70E-23	3.39E-21
ATOH1	-1.88223	1.84E-06	1.85E-05
PRSS33	-1.88157	3.94E-10	1.09E-08
NKX2-4	-1.86869	3.31E-07	4.23E-06
DPPA5	-1.86078	5.76E-06	4.88E-05
C1orf64	-1.85294	4.64E-10	1.25E-08
KRTAP29-1	-1.83983	2.98E-12	1.25E-10
GABRA4	-1.82378	1.45E-09	3.50E-08
HEPACAM2	-1.79659	2.80E-10	8.06E-09
HRH3	-1.78647	1.52E-06	1.57E-05
SLC38A8	-1.78061	1.35E-10	4.23E-09
CEACAM7	-1.77218	3.50E-12	1.46E-10
PGC	-1.7721	5.44E-09	1.13E-07
NKX6-3	-1.76639	3.67E-15	2.81E-13
PRORY	-1.75461	9.61E-05	0.000546
BMX	-1.74245	1.67E-22	3.10E-20
CALY	-1.73415	1.67E-11	6.30E-10
TAS2R38	-1.73034	1.42E-08	2.61E-07
C6orf58	-1.72954	2.48E-17	2.68E-15
DCAF4L2	-1.72643	0.000212	0.001076
REG1A	-1.7155	7.65E-05	0.000448

TENM1	-1.71099	1.38E-15	1.17E-13
UGT3A1	-1.70796	8.75E-05	0.000503
TSPYL6	-1.70522	8.08E-11	2.67E-09
PIRT	-1.70346	1.45E-06	1.51E-05
SPATA16	-1.69926	5.57E-07	6.57E-06
KLRF2	-1.69486	1.16E-11	4.55E-10
TTR	-1.69009	7.94E-07	8.94E-06
KCNK10	-1.687	1.82E-12	8.21E-11
GRM4	-1.68485	2.41E-15	1.93E-13
TSPY2	-1.6824	0.000169	0.000891
MYT1	-1.67884	8.58E-13	4.10E-11
TBX10	-1.67166	6.16E-11	2.08E-09
EPHA5	-1.66704	8.02E-08	1.21E-06
PPY	-1.65592	5.08E-11	1.73E-09
AKR1C4	-1.6527	2.31E-08	4.00E-07
SI	-1.63252	8.69E-06	6.90E-05
SERPINA11	-1.63241	3.39E-07	4.32E-06
MYBPC1	-1.632	5.29E-08	8.43E-07
WIF1	-1.63188	6.69E-12	2.71E-10
LRRC74B	-1.63011	2.16E-12	9.41E-11
ZACN	-1.62233	2.28E-30	7.95E-28
SOX3	-1.61821	1.85E-06	1.86E-05
RETNLB	-1.61699	2.10E-10	6.26E-09
LRRTM3	-1.61148	1.10E-05	8.48E-05
KNG1	-1.60906	1.27E-07	1.82E-06
OBP2A	-1.60569	4.05E-08	6.71E-07
KRT38	-1.60154	1.14E-06	1.23E-05
KCNU1	-1.59814	7.91E-06	6.41E-05
AGXT	-1.59469	4.94E-08	7.93E-07
ATP12A	-1.59307	8.49E-11	2.78E-09
HTR3C	-1.5909	1.15E-11	4.50E-10
C14orf180	-1.58112	3.28E-13	1.73E-11
ETNPPL	-1.5739	4.23E-06	3.78E-05
RSPH6A	-1.56886	4.37E-10	1.19E-08
UNC13C	-1.5688	9.28E-15	6.60E-13
CFAP100	-1.56466	8.23E-16	7.25E-14
SEC14L3	-1.5589	1.83E-11	6.84E-10
LPA	-1.55003	5.33E-11	1.81E-09
TTLL8	-1.54474	6.98E-10	1.82E-08
HSD3B2	-1.54171	1.58E-09	3.77E-08
SLC39A5	-1.53345	1.72E-11	6.48E-10
STUM	-1.53314	2.71E-12	1.16E-10
TNNT3	-1.53249	1.67E-15	1.38E-13
APOA2	-1.53192	4.45E-06	3.92E-05

GAGE2A	-1.53181	0.001341	0.005096
STRA8	-1.52997	5.29E-06	4.54E-05
TRIM49	-1.52637	3.38E-06	3.11E-05
TRIM49C	-1.52573	1.38E-07	1.95E-06
CWH43	-1.52242	6.21E-09	1.26E-07
KRTAP16-1	-1.50509	2.05E-08	3.59E-07
DAPL1	-1.50508	1.32E-11	5.10E-10
PRR4	-1.5011	1.81E-20	2.68E-18
MUC6	-1.49733	3.00E-06	2.81E-05
CLVS2	-1.49517	0.00029	0.001395
VWA3A	-1.49366	1.57E-13	8.64E-12
FGFBP2	-1.48966	1.09E-19	1.49E-17
ASCL1	-1.48896	9.90E-06	7.77E-05
CDH9	-1.48365	9.34E-05	0.000533
TCEAL5	-1.48253	4.82E-10	1.30E-08
GLTPD2	-1.47789	2.17E-19	2.87E-17
INSRR	-1.47683	5.30E-13	2.67E-11
P2RY4	-1.46832	8.28E-14	4.80E-12
ANXA13	-1.45766	1.11E-08	2.11E-07
MAFA	-1.45603	8.65E-14	4.95E-12
ASGR2	-1.43857	7.98E-17	8.01E-15
PHGR1	-1.42986	3.57E-06	3.26E-05
TPH1	-1.42952	2.09E-19	2.79E-17
CHRD2	-1.42604	1.40E-15	1.19E-13
APOB	-1.419	3.62E-07	4.58E-06
MMP26	-1.41779	0.00017	0.000896
SLC17A4	-1.41037	2.14E-05	0.000152
ADAD2	-1.40917	4.71E-11	1.62E-09
GALR3	-1.40885	1.78E-09	4.17E-08
TRPM5	-1.40724	3.52E-11	1.25E-09
SMLR1	-1.40411	5.68E-07	6.68E-06
ITIH1	-1.40267	6.53E-15	4.80E-13
SPINK4	-1.39882	9.16E-05	0.000524
PGA5	-1.39705	3.07E-07	3.95E-06
KCNK16	-1.39617	2.65E-07	3.46E-06
PCDH8	-1.39237	0.000105	0.000589
SPINK1	-1.39055	5.10E-09	1.06E-07
LRRC26	-1.38972	3.23E-10	9.16E-09
SSX1	-1.38114	0.001728	0.006299
CPB1	-1.37345	2.10E-06	2.06E-05
ACTL6B	-1.37298	1.65E-05	0.000121
SERPINB12	-1.36551	2.73E-05	0.000187
RALYL	-1.36497	0.000532	0.002342
PROK1	-1.36047	6.94E-11	2.31E-09

CALCA	-1.35856	0.000426	0.001936
BPIFB2	-1.35464	1.40E-05	0.000105
KRTAP5-5	-1.35379	3.65E-05	0.00024
PRAP1	-1.35348	1.66E-07	2.30E-06
KLK13	-1.35071	3.90E-08	6.51E-07
BEX1	-1.34884	2.03E-07	2.75E-06
DNAAF1	-1.34803	4.13E-16	3.73E-14
MTTP	-1.34634	1.51E-11	5.75E-10
ADH7	-1.34473	6.94E-06	5.74E-05
HFE2	-1.3407	7.26E-12	2.94E-10
HOXB9	-1.33952	4.43E-06	3.91E-05
OBP2B	-1.3378	4.32E-07	5.33E-06
CLCNKA	-1.33452	3.40E-15	2.64E-13
MROH2B	-1.33418	6.57E-10	1.72E-08
SAGE1	-1.33065	0.000104	0.000585
PCP4	-1.32624	1.24E-08	2.31E-07
PROZ	-1.32619	6.56E-19	8.21E-17
POU3F3	-1.32536	0.000295	0.001416
UBE2U	-1.32298	4.56E-06	4.00E-05
ASPG	-1.31912	8.64E-10	2.20E-08
SLC22A10	-1.31854	2.46E-10	7.24E-09
ATP2B2	-1.31493	2.91E-11	1.04E-09
CHGB	-1.31062	1.17E-05	8.92E-05
GSTA3	-1.30913	8.61E-10	2.20E-08
GSTA2	-1.2894	1.93E-07	2.63E-06
GABRG3	-1.2865	8.12E-06	6.55E-05
TMEM229A	-1.28489	4.32E-05	0.000278
ACSM2B	-1.28197	3.33E-07	4.26E-06
HOXB1	-1.27681	2.47E-05	0.000172
TM4SF5	-1.27058	0.000523	0.00231
DLEC1	-1.26714	1.74E-16	1.65E-14
B3GALT2	-1.26624	1.13E-14	7.85E-13
CTNND2	-1.26539	3.66E-07	4.62E-06
CRISP2	-1.26503	1.92E-07	2.61E-06
KCNT1	-1.26407	4.21E-10	1.15E-08
SOST	-1.26406	2.13E-05	0.000151
CCDC154	-1.26001	6.05E-15	4.50E-13
AGTR2	-1.25772	7.65E-07	8.64E-06
AQP7	-1.25091	6.72E-15	4.91E-13
REG3A	-1.24622	0.006258	0.018321
VCX3B	-1.2452	5.56E-06	4.73E-05
SLC22A9	-1.24439	3.60E-07	4.56E-06
ENO3	-1.23786	1.11E-14	7.70E-13
CEACAM8	-1.23488	1.39E-07	1.97E-06

TTLL10	-1.22835	4.56E-13	2.35E-11
C9orf135	-1.2283	1.97E-08	3.49E-07
COL25A1	-1.22666	3.81E-06	3.45E-05
TDGF1	-1.22501	1.33E-09	3.24E-08
TTLL6	-1.22151	2.14E-13	1.16E-11
CTRB1	-1.22112	2.16E-07	2.90E-06
KCNE2	-1.21706	9.52E-17	9.44E-15
GALNTL5	-1.21685	2.52E-06	2.41E-05
A2ML1	-1.21463	1.63E-05	0.000119
CNGA3	-1.21335	2.69E-07	3.51E-06
CFAP73	-1.20576	2.13E-12	9.36E-11
PRMT8	-1.20569	1.56E-09	3.72E-08
SCGB1A1	-1.20416	5.13E-06	4.42E-05
AGXT2	-1.20357	0.000115	0.00064
GPR12	-1.20203	1.72E-05	0.000125
CYP17A1	-1.2017	2.19E-14	1.42E-12
SCGB3A2	-1.19854	1.48E-07	2.09E-06
LRFN2	-1.19518	2.97E-06	2.78E-05
GUCA2A	-1.1947	8.12E-06	6.55E-05
PSORS1C2	-1.19352	3.08E-08	5.22E-07
CCDC17	-1.19102	5.06E-14	3.08E-12
CLDN2	-1.18597	9.19E-07	1.02E-05
CNTN5	-1.18527	3.85E-09	8.21E-08
ADGRB1	-1.18375	2.10E-09	4.82E-08
APOH	-1.18062	2.29E-07	3.04E-06
KIR2DL1	-1.17819	0.000129	0.000705
STMN2	-1.17817	2.27E-07	3.03E-06
C10orf71	-1.17303	5.53E-05	0.000343
PCDH11Y	-1.17269	7.32E-06	6.00E-05
TMEM59L	-1.17163	3.85E-08	6.44E-07
EMX2	-1.16602	0.001313	0.005012
MCHR2	-1.16371	5.82E-05	0.000357
MYO18B	-1.16334	3.70E-06	3.36E-05
ALLC	-1.15964	2.24E-05	0.000158
STATH	-1.15933	0.000412	0.00188
NXF3	-1.15915	3.02E-10	8.61E-09
LINC01314	-1.15777	3.44E-11	1.22E-09
TSPY1	-1.1556	0.008994	0.024709
ST18	-1.15471	6.22E-09	1.27E-07
SLC7A9	-1.15452	2.36E-09	5.33E-08
ATP4B	-1.15429	8.59E-11	2.80E-09
DAZL	-1.15336	4.12E-07	5.12E-06
CDHR4	-1.15327	5.19E-08	8.28E-07
PNPLA7	-1.15233	1.77E-23	3.48E-21

POU5F1B	-1.14717	2.16E-14	1.40E-12
SCGB3A1	-1.14524	6.64E-06	5.53E-05
SLC16A11	-1.14033	2.79E-17	2.98E-15
SLCO1B1	-1.13622	0.000364	0.001686
PENK	-1.1361	1.98E-07	2.69E-06
APOC3	-1.13357	0.008762	0.02421
BPIFA1	-1.13262	0.000146	0.000785
GAD2	-1.12823	0.000169	0.000892
FAM83C	-1.12793	0.00075	0.00314
CFAP157	-1.12616	3.38E-18	3.93E-16
CHRNA9	-1.12399	4.76E-05	0.000303
HSD17B13	-1.11971	8.42E-09	1.66E-07
DNAI1	-1.11871	9.99E-09	1.93E-07
CACNG2	-1.11823	0.001012	0.004035
TMEM207	-1.11658	0.001636	0.006027
GAL	-1.11505	4.38E-06	3.88E-05
UGT2B28	-1.1137	0.000482	0.002153
CLEC18C	-1.11196	8.75E-07	9.73E-06
MAPK15	-1.10655	2.09E-16	1.97E-14
PMP2	-1.10424	7.23E-06	5.95E-05
ZPLD1	-1.10209	1.99E-08	3.52E-07
CFAP46	-1.10082	9.83E-10	2.47E-08
F7	-1.10061	2.83E-07	3.68E-06
ADCYAP1	-1.10054	1.21E-08	2.26E-07
CTRB2	-1.09975	8.98E-08	1.34E-06
GRIK1	-1.09855	3.87E-11	1.36E-09
SLC5A12	-1.09798	7.66E-07	8.65E-06
MSLNL	-1.0974	1.37E-06	1.44E-05
CFAP65	-1.09732	2.85E-09	6.29E-08
MAGEB17	-1.09647	2.62E-05	0.000181
TTLL9	-1.09081	1.70E-12	7.73E-11
TMEM190	-1.08932	3.50E-07	4.43E-06
LRRC71	-1.08544	7.83E-08	1.19E-06
CYP2C9	-1.08489	3.47E-07	4.41E-06
DNAI2	-1.08105	3.76E-07	4.72E-06
BSND	-1.0787	2.13E-07	2.87E-06
PHACTR3	-1.07723	1.58E-08	2.85E-07
KCNH6	-1.07676	7.38E-06	6.04E-05
OR2W3	-1.07634	2.01E-06	1.99E-05
ZMAT4	-1.07495	0.000284	0.001371
FRMPD2	-1.07464	1.37E-07	1.95E-06
WFDC6	-1.07383	3.33E-05	0.000223
CHAD	-1.07193	8.38E-10	2.14E-08
KRTAP9-1	-1.07095	4.95E-05	0.000311

GPR142	-1.06889	5.10E-06	4.40E-05
FGF17	-1.06681	9.70E-12	3.86E-10
TUBA4B	-1.06522	3.94E-08	6.57E-07
PEX5L	-1.06346	1.34E-07	1.91E-06
IFITM5	-1.06166	1.17E-05	8.95E-05
LGALS7B	-1.06028	7.65E-06	6.23E-05
SPOCK3	-1.05942	3.93E-06	3.54E-05
PAX2	-1.05559	0.001344	0.005105
SLC46A2	-1.05413	1.24E-09	3.04E-08
EFCAB8	-1.05315	4.23E-16	3.80E-14
SCN3A	-1.05152	1.69E-05	0.000123
MTMR7	-1.05135	3.86E-09	8.23E-08
NEB	-1.04893	2.75E-12	1.17E-10
ALDOB	-1.04881	5.18E-06	4.46E-05
MEP1B	-1.04754	8.53E-07	9.54E-06
VWA5B2	-1.03957	3.39E-08	5.70E-07
C1orf158	-1.03593	1.45E-05	0.000108
HHLA1	-1.03413	0.002248	0.00788
SLC17A2	-1.03409	0.006612	0.019162
C1orf194	-1.0337	6.17E-08	9.66E-07
PLA2G6	-1.02876	2.63E-28	7.94E-26
C1QTNF8	-1.02696	0.00017	0.000896
SH2D6	-1.02685	1.03E-13	5.84E-12
CSTL1	-1.02613	2.00E-05	0.000143
C11orf16	-1.02282	6.78E-09	1.37E-07
CCDC114	-1.02272	8.01E-13	3.85E-11
CPB2	-1.02022	1.23E-05	9.38E-05
SLC28A2	-1.01886	8.27E-05	0.000479
PTH2R	-1.0153	1.90E-06	1.90E-05
KRT76	-1.01464	0.005075	0.015443
COLEC11	-1.01369	3.31E-12	1.38E-10
CFAP74	-1.01271	8.88E-09	1.74E-07
EPPIN-	-1.0126	3.87E-05	0.000253
WFDC6			
C22orf15	-1.01249	8.79E-09	1.72E-07
SALL3	-1.01105	0.001322	0.005038
CHRM1	-1.01086	6.08E-07	7.07E-06
INS	-1.00933	0.00367	0.011833
FAM9B	-1.00875	0.000401	0.001837
ABCC12	-1.00782	3.10E-06	2.89E-05
ECEL1	-1.00689	2.69E-06	2.55E-05
SAG	-1.00623	4.05E-10	1.11E-08
AFM	-1.00491	0.000109	0.00061
TBC1D3E	-1.00196	1.65E-05	0.000121

TBPL2	-1.00028	9.31E-06	7.35E-05
C10orf90	1.000111	0.000104	0.000585
GREM1	1.001188	8.06E-11	2.67E-09
GPC6	1.001871	9.21E-15	6.58E-13
FOXL2NB	1.005385	0.000332	0.00157
MGARP	1.006075	5.10E-09	1.06E-07
KRT23	1.006381	4.94E-05	0.000311
PCDH7	1.006754	3.38E-13	1.77E-11
HIST2H2BF	1.007381	4.47E-11	1.54E-09
PDPN	1.007497	2.34E-16	2.18E-14
CD109	1.013963	3.15E-16	2.88E-14
TUSC5	1.015121	3.80E-06	3.44E-05
CES5A	1.019142	5.10E-05	0.00032
UGT1A1	1.020968	0.002136	0.007539
GCK	1.022258	3.84E-09	8.21E-08
CYP11A1	1.023846	1.03E-08	1.98E-07
GJB3	1.025314	5.90E-08	9.32E-07
FAM19A4	1.025576	3.06E-06	2.85E-05
LYPD3	1.026095	4.47E-10	1.22E-08
PITX3	1.026779	2.18E-08	3.79E-07
SPOCK1	1.029393	2.00E-09	4.62E-08
ADAMTSL1	1.029502	2.18E-15	1.77E-13
LRRC15	1.029905	1.11E-11	4.37E-10
CRB2	1.030894	2.94E-09	6.47E-08
KRT81	1.031209	0.000103	0.000582
AKR1B10	1.035629	0.000553	0.002423
SLC3A1	1.035903	1.22E-07	1.76E-06
KCNK12	1.038286	9.78E-10	2.47E-08
TAS2R50	1.03903	1.27E-07	1.83E-06
ONECUT3	1.039924	0.001181	0.00459
NETO1	1.042133	1.86E-08	3.30E-07
NCCRP1	1.047605	5.42E-07	6.43E-06
ANXA10	1.048814	0.000736	0.003096
TWIST1	1.049095	1.92E-11	7.15E-10
GJB2	1.049472	1.69E-12	7.72E-11
GALP	1.052444	0.000602	0.002608
PPP1R3A	1.053681	0.014757	0.03705
MYH13	1.055249	1.42E-09	3.44E-08
CALN1	1.058934	0.000447	0.002018
VIT	1.05972	1.14E-07	1.67E-06
EVX1	1.061185	0.00028	0.001359
EPGN	1.062635	7.37E-06	6.03E-05
SNAI2	1.065119	6.62E-21	1.04E-18
SYT9	1.06608	6.78E-07	7.76E-06

PROKR1	1.072008	2.84E-06	2.67E-05
HIST1H2BJ	1.077873	5.54E-12	2.27E-10
HS3ST3A1	1.078074	3.43E-18	3.96E-16
ESX1	1.078303	0.005259	0.015897
IFNE	1.078313	1.36E-05	0.000102
HCRTR2	1.084306	6.58E-08	1.02E-06
HTR7	1.085753	1.72E-18	2.07E-16
TRPA1	1.087272	3.59E-09	7.71E-08
STEAP1B	1.087904	3.67E-11	1.30E-09
GPR52	1.097414	3.90E-09	8.31E-08
SEZ6	1.100083	1.60E-05	0.000118
MME	1.104939	3.65E-14	2.28E-12
GPR78	1.106768	1.72E-10	5.24E-09
DCAF8L1	1.111681	0.001915	0.006873
REG4	1.11347	0.006124	0.017995
FAM83B	1.11842	2.92E-07	3.78E-06
LAMC2	1.120737	4.21E-17	4.34E-15
CDH12	1.121111	0.000114	0.000633
SCN5A	1.121598	1.23E-10	3.88E-09
SP7	1.121968	1.68E-07	2.33E-06
KCNA4	1.125319	1.72E-07	2.37E-06
TUBA3E	1.127709	0.000255	0.001255
TRPM8	1.132561	1.04E-06	1.14E-05
COL9A3	1.133224	5.09E-13	2.59E-11
KRT37	1.13906	0.000462	0.00208
S100A12	1.140587	3.48E-11	1.23E-09
TEX101	1.143628	8.44E-05	0.000487
SLC26A4	1.147033	1.75E-07	2.41E-06
ZBTB20	1.149122	6.12E-21	1.00E-18
SHCBP1L	1.150483	0.000116	0.000642
MUC22	1.151144	6.96E-09	1.40E-07
HIST1H2BG	1.15217	5.07E-09	1.06E-07
NPY5R	1.153554	6.68E-06	5.56E-05
OTOR	1.159016	4.73E-05	0.000301
KRT6C	1.160817	8.93E-05	0.000512
IDI2	1.160949	8.21E-07	9.21E-06
TRH	1.166972	2.07E-08	3.62E-07
HIST1H3D	1.16711	8.37E-11	2.75E-09
MGAT5B	1.168061	6.67E-12	2.71E-10
COL12A1	1.177001	1.18E-16	1.15E-14
ANXA8L1	1.177475	6.05E-10	1.60E-08
MDGA2	1.187091	0.00038	0.001754
ACP7	1.200472	1.78E-07	2.45E-06
COL11A2	1.200597	4.72E-09	9.94E-08

LVRN	1.205015	3.68E-10	1.03E-08
SH2D5	1.210226	4.63E-10	1.25E-08
SPATA22	1.210715	1.97E-07	2.68E-06
GPR1	1.210939	2.15E-14	1.40E-12
EREG	1.213307	5.81E-07	6.80E-06
KCNJ13	1.2148	1.56E-08	2.84E-07
C11orf87	1.216802	1.21E-08	2.25E-07
GADL1	1.217151	3.57E-09	7.68E-08
UGT2B11	1.217882	0.000491	0.00219
IGF2	1.2189	3.68E-07	4.64E-06
FOSL1	1.220886	1.61E-15	1.34E-13
FGF19	1.221154	0.000227	0.001138
STMN4	1.221817	1.27E-06	1.35E-05
ZNF460	1.222396	2.82E-22	5.12E-20
MYH8	1.226773	1.10E-09	2.72E-08
UCN3	1.227413	1.44E-05	0.000107
KCNG1	1.231954	5.34E-10	1.43E-08
COL11A1	1.232843	1.58E-10	4.88E-09
TAS2R46	1.232932	1.98E-08	3.49E-07
SERPINE2	1.250772	1.64E-21	2.79E-19
ODF3	1.259101	3.18E-07	4.08E-06
APCDD1L	1.260487	1.41E-11	5.41E-10
KRT6A	1.264108	7.55E-06	6.16E-05
HIST1H2BH	1.265812	1.30E-08	2.40E-07
CILP	1.266374	8.35E-16	7.32E-14
PSAPL1	1.268444	1.92E-06	1.91E-05
NPTX2	1.271052	2.10E-11	7.73E-10
PRSS48	1.272835	4.77E-09	9.99E-08
IGFL1	1.280273	1.23E-05	9.38E-05
CSMD3	1.290485	1.12E-07	1.63E-06
PRSS3	1.292473	4.40E-08	7.22E-07
HMGA2	1.294167	2.51E-07	3.31E-06
PNPLA5	1.299527	1.70E-05	0.000124
NPPB	1.30618	7.97E-05	0.000464
COLEC10	1.306751	1.23E-12	5.71E-11
ZBP2	1.307061	1.15E-05	8.81E-05
PNMA5	1.312601	1.98E-05	0.000141
HIST2H3C	1.313054	1.46E-08	2.67E-07
SPRR2F	1.327649	6.12E-05	0.000372
C6orf15	1.332835	3.30E-05	0.000221
CACNG8	1.34034	2.74E-15	2.17E-13
PADI3	1.344659	5.30E-05	0.00033
SLC39A2	1.346087	8.94E-11	2.90E-09
MRGPRX3	1.348373	5.37E-07	6.39E-06

HIST1H2AG	1.353335	3.00E-15	2.34E-13
SHISA9	1.365258	1.93E-05	0.000138
TAS2R13	1.368172	2.52E-12	1.08E-10
KRT34	1.372683	3.25E-06	3.00E-05
ADAMTS19	1.378831	6.14E-05	0.000373
FER1L6	1.380612	3.24E-06	2.99E-05
KCNK2	1.390279	2.63E-10	7.62E-09
DLK1	1.392734	0.001019	0.004059
IL1A	1.393311	7.33E-14	4.29E-12
SERPINB4	1.396613	4.53E-06	3.98E-05
EBF3	1.410522	2.93E-14	1.86E-12
GJA3	1.411431	4.58E-13	2.35E-11
LYPD4	1.416848	4.38E-06	3.88E-05
FETUB	1.418967	1.73E-06	1.75E-05
S100A2	1.419336	1.20E-14	8.25E-13
LEP	1.424375	2.60E-10	7.58E-09
TRPC5	1.424505	1.23E-10	3.88E-09
FSHB	1.434651	0.001529	0.005692
HIST1H3G	1.437739	1.37E-11	5.29E-10
SPRR1B	1.438871	1.87E-06	1.87E-05
CACNG1	1.440782	8.51E-11	2.78E-09
FRG2C	1.448479	5.28E-10	1.42E-08
CREG2	1.454556	4.27E-15	3.22E-13
C10orf99	1.455189	8.98E-05	0.000515
ASIC2	1.463528	5.89E-16	5.26E-14
TAC3	1.465495	5.03E-06	4.35E-05
SERPINB2	1.468237	3.96E-10	1.09E-08
MYH7	1.475643	8.01E-10	2.06E-08
ATCAY	1.478038	2.35E-08	4.07E-07
RBM46	1.478746	2.12E-06	2.08E-05
SORCS3	1.482301	1.17E-08	2.21E-07
PRSS38	1.484493	3.60E-05	0.000238
KIAA1549L	1.500063	2.56E-19	3.37E-17
CBLN1	1.509327	3.27E-09	7.10E-08
L1CAM	1.51688	6.98E-14	4.11E-12
SPRR1A	1.517442	5.18E-07	6.20E-06
AFF2	1.521474	2.88E-14	1.84E-12
RSPO3	1.525933	9.44E-15	6.69E-13
SFRP1	1.528729	1.56E-13	8.61E-12
S100A7A	1.535304	8.22E-05	0.000476
PRDM13	1.535833	6.01E-08	9.44E-07
SPRR2D	1.535871	5.70E-07	6.70E-06
MMP3	1.538878	1.25E-16	1.20E-14
SERPINB7	1.543104	6.66E-09	1.35E-07

OTOP1	1.54603	4.22E-05	0.000273
ANHX	1.553467	5.31E-05	0.000331
ADGRG7	1.559037	1.11E-05	8.58E-05
SLC12A3	1.569796	6.41E-21	1.03E-18
ANXA8	1.586405	3.37E-13	1.77E-11
RNASE7	1.588138	2.45E-10	7.22E-09
NLRP7	1.591998	1.67E-20	2.50E-18
PKHD1L1	1.592419	2.69E-18	3.14E-16
TEX37	1.592602	1.29E-07	1.84E-06
OTOP2	1.607961	4.62E-08	7.51E-07
TFF2	1.612974	0.000352	0.001646
TBX20	1.615061	1.33E-08	2.45E-07
CRISP3	1.617259	4.44E-07	5.44E-06
POU5F2	1.62126	3.69E-17	3.87E-15
PSG9	1.624172	1.47E-05	0.000109
CXorf67	1.628023	3.09E-07	3.97E-06
SLC35F4	1.642702	1.63E-13	8.99E-12
CA6	1.646551	1.28E-08	2.36E-07
NTSR2	1.659646	1.56E-06	1.61E-05
POU3F2	1.660338	3.91E-09	8.32E-08
C4orf26	1.669527	2.61E-18	3.07E-16
C21orf62	1.673564	1.16E-19	1.57E-17
LAMA1	1.680742	7.05E-22	1.25E-19
UMOD	1.683823	5.96E-05	0.000365
GRIA2	1.68614	8.62E-12	3.45E-10
TAAR1	1.687342	3.84E-07	4.81E-06
MFAP5	1.695146	1.74E-20	2.59E-18
TRIM48	1.697624	0.000943	0.003796
CRP	1.710791	1.00E-07	1.48E-06
TMEM196	1.71258	4.28E-06	3.81E-05
CLCA2	1.712977	8.22E-13	3.95E-11
FABP1	1.720206	5.82E-06	4.93E-05
MYRFL	1.720652	3.70E-19	4.77E-17
AC020914.1	1.728761	5.65E-05	0.000348
TAF7L	1.729953	9.41E-16	8.21E-14
GABRA2	1.73762	3.05E-09	6.67E-08
AMY1B	1.740269	3.19E-13	1.69E-11
AMBN	1.743825	7.00E-09	1.41E-07
HOXA13	1.745911	1.74E-07	2.40E-06
SLC6A2	1.763185	4.15E-08	6.85E-07
SSX5	1.778091	2.44E-05	0.00017
CALB2	1.797752	6.37E-19	8.03E-17
GLP2R	1.809323	3.02E-13	1.61E-11
CALML5	1.812213	2.89E-06	2.71E-05

C1orf94	1.816919	1.03E-08	1.98E-07
TAS2R30	1.819488	3.53E-15	2.72E-13
VAT1L	1.822406	1.85E-27	5.10E-25
PTF1A	1.822798	1.38E-06	1.45E-05
LIN28A	1.828588	6.64E-07	7.61E-06
SYNPR	1.845446	1.92E-12	8.58E-11
HIST1H2BF	1.84692	4.03E-15	3.05E-13
HIST1H2AM	1.847772	1.50E-22	2.81E-20
RHCG	1.849615	1.13E-12	5.31E-11
XAGE3	1.853257	2.77E-10	8.00E-09
PRDM9	1.853627	8.81E-07	9.79E-06
IFNK	1.859727	1.73E-11	6.52E-10
BRINP2	1.864816	1.96E-15	1.60E-13
QRFPR	1.898126	7.76E-13	3.78E-11
DPPA2	1.90494	4.65E-05	0.000296
SPRR3	1.908203	1.27E-08	2.35E-07
CLCA4	1.919147	6.55E-13	3.26E-11
SLC6A19	1.919249	2.60E-09	5.83E-08
MUCL1	1.926672	1.19E-11	4.63E-10
FAM25A	1.933002	1.76E-10	5.34E-09
COX8C	1.938966	1.25E-11	4.85E-10
UNC5D	1.939404	2.26E-09	5.14E-08
MAB21L2	1.959831	1.11E-20	1.68E-18
HIST1H2AI	1.977769	6.28E-24	1.29E-21
AC011473.4	1.981736	1.62E-08	2.93E-07
PRL	1.982104	1.22E-12	5.69E-11
KRT20	1.989628	7.74E-07	8.73E-06
DEFB4A	1.991773	5.50E-11	1.87E-09
GDPD2	1.999739	3.49E-23	6.82E-21
CASP14	2.005307	2.02E-06	2.00E-05
FOXR2	2.015221	4.80E-06	4.18E-05
SLC2A2	2.030918	7.86E-07	8.86E-06
4-Mar	2.0536	1.25E-22	2.36E-20
SNTG1	2.054831	1.72E-10	5.24E-09
MYL2	2.057731	1.21E-17	1.33E-15
NRSN1	2.06015	8.19E-10	2.10E-08
LY6G6C	2.077286	7.02E-21	1.09E-18
FLG2	2.09107	2.89E-16	2.65E-14
EIF4E1B	2.098323	2.16E-08	3.77E-07
UPK1B	2.100309	8.13E-10	2.09E-08
ADIPOQ	2.101804	2.69E-08	4.60E-07
PRG4	2.105794	1.84E-20	2.70E-18
SBSN	2.107693	2.87E-15	2.26E-13
IRX4	2.121078	1.26E-09	3.07E-08

FRG2	2.138547	1.23E-09	3.03E-08
HIST2H3D	2.155151	4.11E-26	1.02E-23
OR4A16	2.161786	1.80E-06	1.81E-05
S100G	2.165713	1.09E-11	4.30E-10
CYP4F8	2.178898	1.55E-10	4.80E-09
KRT6B	2.209629	1.91E-14	1.25E-12
TAC1	2.219817	1.40E-06	1.47E-05
CPA4	2.22626	1.00E-21	1.77E-19
HIST1H2AD	2.232277	1.59E-23	3.24E-21
GPR22	2.255659	9.25E-29	2.84E-26
MYPN	2.292308	1.80E-18	2.14E-16
GNAT3	2.296484	1.65E-08	2.98E-07
SCGB2A2	2.297483	3.98E-08	6.61E-07
RTL1	2.310606	1.31E-10	4.12E-09
CERS3	2.317011	1.11E-14	7.70E-13
HIST2H2AC	2.326725	5.10E-37	3.30E-34
CRCT1	2.368984	2.47E-09	5.54E-08
DGKK	2.422919	4.85E-17	4.97E-15
NLRP10	2.437979	1.61E-15	1.34E-13
TRIML2	2.441098	1.23E-16	1.19E-14
KRT9	2.449926	2.83E-16	2.60E-14
KCTD4	2.466558	1.35E-19	1.81E-17
TEX13B	2.48356	7.09E-13	3.49E-11
DSG3	2.526682	1.89E-15	1.55E-13
PSG6	2.530544	1.63E-09	3.86E-08
HIST1H3J	2.537458	7.42E-28	2.07E-25
OR6T1	2.574145	1.87E-10	5.64E-09
FBN2	2.576482	1.20E-36	7.50E-34
SPRR2A	2.583735	7.80E-13	3.78E-11
RPTN	2.59585	7.34E-13	3.59E-11
PI3	2.602239	3.36E-25	8.01E-23
KRTDAP	2.616466	1.09E-26	2.82E-24
SPRR2E	2.617226	3.82E-10	1.06E-08
GDF6	2.621342	1.75E-32	7.38E-30
ACTN3	2.629105	1.56E-33	7.28E-31
BARHL2	2.673426	7.33E-14	4.29E-12
BNC1	2.682063	5.73E-24	1.21E-21
KLK5	2.68488	1.54E-14	1.04E-12
HIST1H2BE	2.692981	1.06E-34	5.51E-32
HIST1H2BO	2.70863	2.23E-33	1.01E-30
SPANXC	2.728635	2.63E-10	7.62E-09
ARHGAP36	2.785425	1.53E-13	8.54E-12
PSG3	2.802646	7.39E-10	1.93E-08
HIST1H2BL	2.81833	3.59E-38	2.51E-35

CACNG7	2.837068	4.79E-21	7.90E-19
CRYGD	2.838592	4.44E-15	3.33E-13
S100A7	2.863991	1.50E-15	1.26E-13
LGI1	2.931928	2.22E-16	2.08E-14
IGDCC3	2.949042	2.60E-35	1.39E-32
RHAG	3.084487	3.46E-18	3.97E-16
FAM205C	3.094468	4.08E-27	1.11E-24
TMIGD1	3.101353	3.89E-17	4.06E-15
HIST1H3A	3.10194	6.69E-36	3.92E-33
DEFA6	3.120322	2.44E-11	8.87E-10
SLC1A6	3.132586	5.52E-28	1.56E-25
SPRR2B	3.14468	1.53E-12	7.05E-11
CT47B1	3.165251	2.24E-14	1.44E-12
KRT14	3.20082	5.67E-27	1.51E-24
HIST1H4E	3.207393	1.19E-33	5.66E-31
MMP27	3.238321	2.50E-16	2.31E-14
GPR26	3.261747	4.80E-18	5.44E-16
FAM9A	3.341902	1.10E-15	9.53E-14
RPE65	3.366252	2.52E-31	9.92E-29
NTSR1	3.382361	1.70E-32	7.36E-30
PRR9	3.399088	9.32E-19	1.15E-16
SPANXD	3.426647	1.30E-14	8.89E-13
MPC1L	3.446132	2.12E-21	3.57E-19
HIST1H2AL	3.472351	1.59E-38	1.25E-35
LCE3D	3.50116	6.94E-16	6.14E-14
CGB5	3.541396	2.65E-17	2.84E-15
HIST1H2BM	3.582988	1.20E-30	4.55E-28
ZP2	3.589383	5.13E-30	1.72E-27
SLC6A5	3.621523	2.00E-20	2.90E-18
SPANXB1	3.740972	3.93E-17	4.07E-15
HIST1H1D	3.917867	7.72E-45	1.00E-41
HSD3B1	3.939381	1.68E-23	3.39E-21
GSG1L2	3.99078	9.10E-23	1.74E-20
HIST1H3F	4.054512	1.83E-30	6.51E-28
SPRR2G	4.16961	1.17E-21	2.02E-19
HIST1H2AH	4.182647	4.78E-36	2.89E-33
FGF5	4.226851	2.21E-44	2.51E-41
HIST1H2AJ	4.249195	6.77E-45	9.45E-42
HIST1H1E	4.257372	3.44E-64	3.12E-60
HIST2H2AB	4.265461	2.48E-45	3.74E-42
HIST1H2AB	4.31505	5.03E-41	4.81E-38
PSG7	4.380681	2.53E-25	6.12E-23
HIST1H3B	4.392845	3.39E-48	6.15E-45
HIST1H3C	4.410661	6.02E-49	1.37E-45

HIST1H4A	4.454045	6.90E-43	6.96E-40
HIST1H4D	4.455757	3.30E-48	6.15E-45
DKK4	4.476173	4.72E-28	1.36E-25
HIST1H3I	4.497539	5.77E-39	4.98E-36
FGF3	4.566791	1.74E-31	7.01E-29
PSG4	4.567768	4.41E-20	6.19E-18
VGLL2	4.610676	3.67E-21	6.11E-19
HIST1H4B	4.801089	1.12E-52	3.38E-49
LGALS13	4.811191	9.91E-27	2.61E-24
CRISP1	4.848139	3.93E-24	8.39E-22
PSG8	4.992363	8.30E-25	1.91E-22
PSG1	5.074882	2.21E-24	4.89E-22
HIST1H2BI	5.077699	6.87E-43	6.96E-40
PSG2	5.116839	3.96E-31	1.53E-28
HIST1H4C	5.134759	3.98E-63	2.40E-59
ITLN1	5.189737	2.09E-51	5.41E-48
HIST1H1A	5.244349	6.60E-30	2.14E-27
NPY	5.397442	1.35E-26	3.44E-24
HIST1H1B	5.464045	2.94E-60	1.33E-56
HIST1H2BB	5.537647	8.89E-48	1.47E-44
DEFA5	5.739992	4.61E-19	5.85E-17
LRRC38	5.823485	7.27E-54	2.64E-50
HIST1H4L	5.950069	1.48E-34	7.46E-32
GCG	6.442577	1.52E-32	6.71E-30
PSG5	6.640979	5.45E-38	3.66E-35
PSG11	6.873113	3.23E-32	1.33E-29
HIST1H4F	7.013402	6.89E-40	6.25E-37

Table S7. Functional enrichment results of DEGs between low- and high-risk score phenotypes LUAD patients.

Term	Count	%	P Value
GO:0005576~extracellular region	171	22.29465	5.81E-34
GO:0000786~nucleosome	41	5.345502	2.33E-31
GO:0005615~extracellular space	138	17.99218	1.90E-25
GO:0006334~nucleosome assembly	35	4.563233	1.32E-20
GO:0000788~nuclear nucleosome	19	2.477184	1.93E-14
GO:0000183~chromatin silencing at rDNA	17	2.216428	1.37E-13
GO:0032200~telomere organization	15	1.955671	1.98E-13
GO:0007218~neuropeptide signaling pathway	25	3.259452	5.89E-13
GO:0006335~DNA replication-dependent nucleosome assembly	15	1.955671	3.89E-12
GO:0008544~epidermis development	22	2.868318	7.43E-12
GO:0046982~protein heterodimerization activity	52	6.779661	8.05E-12
GO:0044267~cellular protein metabolic process	25	3.259452	2.10E-11
GO:0045814~negative regulation of gene expression, epigenetic	17	2.216428	3.28E-11
GO:0051290~protein heterotetramerization	15	1.955671	3.04E-10
GO:0045815~positive regulation of gene expression, epigenetic	17	2.216428	1.18E-09
GO:0000228~nuclear chromosome	16	2.08605	1.29E-09
GO:0010951~negative regulation of endopeptidase activity	23	2.998696	1.38E-09
GO:0005179~hormone activity	19	2.477184	1.23E-08
GO:0007586~digestion	16	2.08605	1.29E-08
GO:0004867~serine-type endopeptidase inhibitor activity	19	2.477184	2.06E-08
GO:0060968~regulation of gene silencing	8	1.043025	3.75E-08
GO:0007565~female pregnancy	18	2.346806	4.80E-08
GO:0019731~antibacterial humoral response	13	1.694915	7.28E-08
GO:0005887~integral component of plasma membrane	97	12.64668	1.35E-07
GO:0001533~cornified envelope	13	1.694915	1.58E-07
GO:0030216~keratinocyte differentiation	15	1.955671	1.16E-06
GO:0005198~structural molecule activity	27	3.520209	2.56E-06
GO:0018149~peptide cross-linking	12	1.564537	2.65E-06
GO:0031047~gene silencing by RNA	17	2.216428	5.97E-06
GO:0031492~nucleosomal DNA binding	11	1.434159	6.68E-06
GO:0007268~chemical synaptic transmission	26	3.389831	7.63E-06
GO:0006704~glucocorticoid biosynthetic process	6	0.782269	9.69E-06
GO:0031225~anchored component of membrane	17	2.216428	9.95E-06
GO:0007631~feeding behavior	10	1.303781	1.14E-05
GO:0031424~keratinization	11	1.434159	1.27E-05

GO:0042393~histone binding	17	2.216428	1.46E-05
GO:0006810~transport	32	4.172099	1.62E-05
GO:0045653~negative regulation of megakaryocyte differentiation	7	0.912647	4.20E-05
GO:0006342~chromatin silencing	10	1.303781	4.86E-05
GO:0005184~neuropeptide hormone activity	8	1.043025	1.03E-04
GO:0001523~retinoid metabolic process	11	1.434159	1.11E-04
GO:0042627~chylomicron	6	0.782269	1.45E-04
GO:0016233~telomere capping	7	0.912647	1.94E-04
GO:0070062~extracellular exosome	148	19.29596	2.03E-04
GO:0000784~nuclear chromosome, telomeric region	16	2.08605	2.04E-04
GO:0034220~ion transmembrane transport	21	2.73794	2.09E-04
GO:0019433~triglyceride catabolic process	7	0.912647	3.18E-04
GO:0005509~calcium ion binding	47	6.127771	3.40E-04
GO:0048265~response to pain	6	0.782269	3.67E-04
GO:0008201~heparin binding	17	2.216428	3.82E-04
GO:0006336~DNA replication-independent nucleosome assembly	7	0.912647	4.00E-04
GO:0006352~DNA-templated transcription, initiation	8	1.043025	4.06E-04
GO:0050830~defense response to Gram-positive bacterium	12	1.564537	4.41E-04
GO:0030300~regulation of intestinal cholesterol absorption	4	0.521512	5.52E-04
GO:0006508~proteolysis	36	4.693611	5.86E-04
GO:0007596~blood coagulation	18	2.346806	8.59E-04
GO:0034361~very-low-density lipoprotein particle	6	0.782269	9.20E-04
GO:0034774~secretory granule lumen	5	0.65189	9.47E-04
GO:1902476~chloride transmembrane transport	12	1.564537	9.52E-04
GO:0005232~serotonin-activated cation-selective channel activity	4	0.521512	9.91E-04
GO:0005578~proteinaceous extracellular matrix	23	2.998696	0.001074
GO:0008083~growth factor activity	16	2.08605	0.001272
GO:0051480~regulation of cytosolic calcium ion concentration	7	0.912647	0.00129
GO:0008284~positive regulation of cell proliferation	33	4.302477	0.001358
GO:0008289~lipid binding	15	1.955671	0.001799
GO:0006641~triglyceride metabolic process	7	0.912647	0.002093
GO:0007271~synaptic transmission, cholinergic	7	0.912647	0.002807
GO:0030279~negative regulation of ossification	5	0.65189	0.002838
GO:0030049~muscle filament sliding	7	0.912647	0.003225

GO:0042157~lipoprotein metabolic process	7	0.912647	0.003225
GO:0050832~defense response to fungus	6	0.782269	0.003471
GO:0003341~cilium movement	6	0.782269	0.003471
GO:0004983~neuropeptide Y receptor activity	4	0.521512	0.003822
GO:0042158~lipoprotein biosynthetic process	4	0.521512	0.004125
GO:0070653~high-density lipoprotein particle receptor binding	3	0.391134	0.004184
GO:0001580~detection of chemical stimulus involved in sensory perception of bitter taste	7	0.912647	0.0042
GO:0070093~negative regulation of glucagon secretion	3	0.391134	0.004413
GO:0072300~positive regulation of metanephric glomerulus development	3	0.391134	0.004413
GO:0010903~negative regulation of very-low-density lipoprotein particle remodeling	3	0.391134	0.004413
GO:0000790~nuclear chromatin	17	2.216428	0.004481
GO:0005796~Golgi lumen	11	1.434159	0.004788
GO:0050829~defense response to Gram-negative bacterium	8	1.043025	0.005223
GO:0005216~ion channel activity	7	0.912647	0.005314
GO:0005882~intermediate filament	12	1.564537	0.005315
GO:0051918~negative regulation of fibrinolysis	4	0.521512	0.005723
GO:0034080~CENP-A containing nucleosome assembly	7	0.912647	0.006047
GO:1904837~beta-catenin-TCF complex assembly	7	0.912647	0.006047
GO:0008202~steroid metabolic process	7	0.912647	0.006047
GO:0016324~apical plasma membrane	22	2.868318	0.006263
GO:0045095~keratin filament	11	1.434159	0.006383
GO:0009813~flavonoid biosynthetic process	5	0.65189	0.006677
GO:0071805~potassium ion transmembrane transport	12	1.564537	0.007537
GO:0004252~serine-type endopeptidase activity	19	2.477184	0.008497
GO:0007623~circadian rhythm	9	1.173403	0.008544
GO:0072221~metanephric distal convoluted tubule development	3	0.391134	0.008599
GO:0052696~flavonoid glucuronidation	5	0.65189	0.009481
GO:0030195~negative regulation of blood coagulation	4	0.521512	0.009901
GO:0004889~acetylcholine-activated cation-selective channel activity	5	0.65189	0.01015
GO:0031210~phosphatidylcholine binding	5	0.65189	0.01015
GO:0045211~postsynaptic membrane	17	2.216428	0.01028
GO:0007267~cell-cell signaling	19	2.477184	0.01059

GO:0034765~regulation of ion transmembrane transport	11	1.434159	0.011235
GO:0005267~potassium channel activity	6	0.782269	0.012241
GO:0008217~regulation of blood pressure	8	1.043025	0.012863
GO:0005499~vitamin D binding	3	0.391134	0.013257
GO:0006814~sodium ion transport	9	1.173403	0.013318
GO:0033038~bitter taste receptor activity	5	0.65189	0.013662
GO:0043234~protein complex	27	3.520209	0.013758
GO:0005892~acetylcholine-gated channel complex	5	0.65189	0.01393
GO:0051180~vitamin transport	3	0.391134	0.013963
GO:0014050~negative regulation of glutamate secretion	3	0.391134	0.013963
GO:0043025~neuronal cell body	22	2.868318	0.014534
GO:0036157~outer dynein arm	3	0.391134	0.01455
GO:0031012~extracellular matrix	21	2.73794	0.014792
GO:0033344~cholesterol efflux	5	0.65189	0.014958
GO:0002227~innate immune response in mucosa	5	0.65189	0.014958
GO:0033700~phospholipid efflux	4	0.521512	0.015462
GO:0010001~glial cell differentiation	4	0.521512	0.015462
GO:0005102~receptor binding	23	2.998696	0.015543
GO:0042166~acetylcholine binding	5	0.65189	0.015674
GO:0005254~chloride channel activity	7	0.912647	0.015892
GO:0008203~cholesterol metabolic process	8	1.043025	0.016223
GO:0045840~positive regulation of mitotic nuclear division	5	0.65189	0.017147
GO:0017127~cholesterol transporter activity	4	0.521512	0.017481
GO:0036158~outer dynein arm assembly	4	0.521512	0.018779
GO:0055102~lipase inhibitor activity	3	0.391134	0.019391
GO:0030020~extracellular matrix structural constituent conferring tensile strength	3	0.391134	0.019391
GO:0060228~phosphatidylcholine-sterol O-acyltransferase activator activity	3	0.391134	0.019391
GO:0004993~G-protein coupled serotonin receptor activity	5	0.65189	0.020231
GO:0022841~potassium ion leak channel activity	4	0.521512	0.020921
GO:0005788~endoplasmic reticulum lumen	15	1.955671	0.021319
GO:0031490~chromatin DNA binding	7	0.912647	0.021963
GO:0005249~voltage-gated potassium channel activity	7	0.912647	0.021963
GO:0030322~stabilization of membrane potential	4	0.521512	0.022457
GO:2000311~regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity	4	0.521512	0.022457

GO:0022008~neurogenesis	6	0.782269	0.02272
GO:0015020~glucuronosyltransferase activity	5	0.65189	0.022785
GO:0032281~AMPA glutamate receptor complex	5	0.65189	0.023699
GO:0032982~myosin filament	4	0.521512	0.023756
GO:0045909~positive regulation of vasodilation	5	0.65189	0.024867
GO:0030054~cell junction	28	3.650587	0.027256
GO:0004222~metalloendopeptidase activity	10	1.303781	0.027636
GO:0016323~basolateral plasma membrane	14	1.825293	0.027711
GO:0046326~positive regulation of glucose import	5	0.65189	0.027836
GO:0071639~positive regulation of monocyte chemotactic protein-1 production	3	0.391134	0.027843
GO:0072205~metanephric collecting duct development	3	0.391134	0.027843
GO:0061337~cardiac conduction	6	0.782269	0.029698
GO:0043691~reverse cholesterol transport	4	0.521512	0.030901
GO:0051412~response to corticosterone	4	0.521512	0.030901
GO:0005244~voltage-gated ion channel activity	5	0.65189	0.031578
GO:0015171~amino acid transmembrane transporter activity	6	0.782269	0.031709
GO:0045666~positive regulation of neuron differentiation	8	1.043025	0.03184
GO:0007399~nervous system development	19	2.477184	0.032336
GO:0016247~channel regulator activity	3	0.391134	0.034423
GO:0007605~sensory perception of sound	11	1.434159	0.034802
GO:0005230~extracellular ligand-gated ion channel activity	5	0.65189	0.034894
GO:0051781~positive regulation of cell division	6	0.782269	0.035024
GO:0006303~double-strand break repair via nonhomologous end joining	7	0.912647	0.035283
GO:0010898~positive regulation of triglyceride catabolic process	3	0.391134	0.03618
GO:0060012~synaptic transmission, glycinergic	3	0.391134	0.03618
GO:0060046~regulation of acrosome reaction	3	0.391134	0.03618
GO:0034380~high-density lipoprotein particle assembly	3	0.391134	0.03618
GO:0034366~spherical high-density lipoprotein particle	3	0.391134	0.037637
GO:0042632~cholesterol homeostasis	7	0.912647	0.037706
GO:0030574~collagen catabolic process	7	0.912647	0.037706
GO:0004869~cysteine-type endopeptidase inhibitor activity	5	0.65189	0.038403
GO:0007166~cell surface receptor signaling pathway	18	2.346806	0.03957

GO:0072562~blood microparticle	12	1.564537	0.040199
GO:0005201~extracellular matrix structural constituent	7	0.912647	0.04088
GO:0070588~calcium ion transmembrane transport	10	1.303781	0.042496
GO:0005215~transporter activity	14	1.825293	0.043938
GO:0034707~chloride channel complex	6	0.782269	0.044192
GO:0010873~positive regulation of cholesterol esterification	3	0.391134	0.045339
GO:0050796~regulation of insulin secretion	7	0.912647	0.045601
GO:0006865~amino acid transport	5	0.65189	0.04574
GO:0015276~ligand-gated ion channel activity	5	0.65189	0.046006
GO:0045861~negative regulation of proteolysis	4	0.521512	0.046241
GO:0042730~fibrinolysis	4	0.521512	0.046241
GO:0009235~cobalamin metabolic process	4	0.521512	0.046241
GO:0035902~response to immobilization stress	4	0.521512	0.046241
GO:0005104~fibroblast growth factor receptor binding	4	0.521512	0.048702
hsa05322:Systemic lupus erythematosus	39	5.084746	1.19E-23
hsa05034:Alcoholism	43	5.606258	9.29E-23
hsa04974:Protein digestion and absorption	17	2.216428	1.53E-07
hsa04080:Neuroactive ligand-receptor interaction	29	3.780965	1.82E-06
hsa05203:Viral carcinogenesis	21	2.73794	9.50E-05
hsa00140:Steroid hormone biosynthesis	10	1.303781	3.04E-04
hsa04972:Pancreatic secretion	12	1.564537	7.56E-04
hsa04742:Taste transduction	8	1.043025	0.001407
hsa00980:Metabolism of xenobiotics by cytochrome P450	10	1.303781	0.001858
hsa04950:Maturity onset diabetes of the young	6	0.782269	0.002629
hsa00982:Drug metabolism - cytochrome P450	9	1.173403	0.004058
hsa00830:Retinol metabolism	8	1.043025	0.010442
hsa03320:PPAR signaling pathway	8	1.043025	0.013279
hsa04975:Fat digestion and absorption	6	0.782269	0.015399
hsa04261:Adrenergic signaling in cardiomyocytes	12	1.564537	0.015874
hsa05202:Transcriptional misregulation in cancer	13	1.694915	0.025273
hsa05204:Chemical carcinogenesis	8	1.043025	0.03207
hsa00040:Pentose and glucuronate interconversions	5	0.65189	0.035348
hsa04913:Ovarian steroidogenesis	6	0.782269	0.037592
hsa04911:Insulin secretion	8	1.043025	0.042541
hsa04977:Vitamin digestion and absorption	4	0.521512	0.049281

Table S8. Survival analysis results of DEGs between low- and high-risk score phenotypes LUAD patients.

ID	Adjusted P λ	HR	Low 95%CI	High 95%CI
PRMT8	6.81E-05	0.541215	0.400091	0.732116
KRT9	8.91E-05	1.82798	1.351892	2.471729
GFI1B	0.000102667	0.547571	0.404072	0.742033
FETUB	0.00025968	1.746963	1.295009	2.356648
CYP17A1	0.000341603	0.576429	0.426398	0.779249
GJB2	0.000427435	1.725229	1.27369	2.336844
PITX3	0.000626607	1.718557	1.260049	2.343908
KRT6C	0.000945401	1.679071	1.234947	2.282915
C10orf99	0.001342806	1.634384	1.210456	2.206781
CES5A	0.001880827	1.605121	1.191047	2.163152
PKHD1L1	0.001932229	0.617756	0.455597	0.837631
GPR78	0.002448556	1.581614	1.175698	2.127674
APOB	0.002530709	1.581694	1.174567	2.129938
SLC14A2	0.002863376	0.634591	0.470632	0.85567
FOSL1	0.003120446	1.576892	1.165824	2.132902
CNGA3	0.003425329	0.641715	0.476787	0.863694
B3GALT2	0.003693919	0.643758	0.478178	0.866674
NTSR1	0.003760124	1.548159	1.151922	2.080693
SPOCK1	0.004187111	1.554464	1.149371	2.102332
KRT81	0.004220411	1.55227	1.148555	2.097891
HIST1H2BF	0.0051062	1.528887	1.135865	2.057899
PNPLA7	0.005294881	0.652668	0.483555	0.880926
PCDH7	0.006252861	1.511825	1.124164	2.033169
GJB3	0.006340542	1.520961	1.125515	2.055347
HOXA13	0.006711387	1.509717	1.120862	2.033476
CHAD	0.006871018	0.661203	0.489846	0.892503
CYP4F8	0.007779235	1.506862	1.114136	2.038023
GLRA4	0.00813889	0.670006	0.498038	0.901352
SPANXB1	0.009474888	1.483798	1.10131	1.999127
HOXB9	0.009597872	1.482116	1.100444	1.996165
DSG3	0.010287291	1.474474	1.096048	1.983558
KLK13	0.010441426	0.679794	0.505926	0.913415
TENM1	0.010620462	0.675092	0.499417	0.912563
LAMC2	0.011505187	1.468596	1.090058	1.978586
HIST1H4A	0.011687888	1.464335	1.08864	1.969683
ACP7	0.011756303	1.465147	1.088511	1.972103
EREG	0.011901895	1.473616	1.089339	1.993453
AFM	0.012848501	1.459239	1.083503	1.965272
EPGN	0.013172748	1.452666	1.081326	1.951529
C11orf16	0.013786216	0.687321	0.509995	0.926303
SPRR1B	0.014446689	1.454763	1.077322	1.964439

CLDN2	0.014909705	0.691895	0.514356	0.930716
SH2D5	0.015392859	1.449209	1.073476	1.956454
C10orf71	0.015397901	0.693844	0.516241	0.932548
TLL10	0.016384975	0.694604	0.515827	0.935342
KCNK16	0.017836572	0.697677	0.517969	0.939735
PRL	0.018278059	1.431354	1.062666	1.927957
MGAT5B	0.018602306	1.424734	1.060965	1.913227
NLRP10	0.01886138	1.431244	1.06108	1.930543
C14orf180	0.021167864	0.704985	0.523702	0.94902
STUM	0.021237913	0.706123	0.525183	0.949401
FRMPD2	0.021280194	0.70613	0.525143	0.949495
GAL	0.02134257	1.417673	1.053208	1.908262
SBSN	0.022495878	1.415573	1.050251	1.907969
RHCG	0.022623429	1.410519	1.049429	1.895854
EPPIN- WFDC6	0.022688694	0.70955	0.52821	0.953146
G6PC	0.022893756	1.417907	1.04957	1.915509
ZPBP2	0.023034412	0.707117	0.524448	0.95341
SLC22A10	0.023994377	0.707396	0.52375	0.955437
AMBN	0.024448287	1.406811	1.044982	1.893923
MMP3	0.026916705	1.398328	1.039042	1.88185
ZMAT4	0.02909918	1.389111	1.034029	1.866125
DAZL	0.029443743	0.721163	0.53734	0.967871
KRT76	0.029898005	1.388028	1.032448	1.866073
GPC6	0.030057219	1.388621	1.032194	1.868126
SERPINB4	0.031084042	1.383127	1.02993	1.857446
PI3	0.031092207	1.38488	1.030034	1.86197
GPR1	0.032377795	1.383963	1.027674	1.863776
KLK12	0.032393947	0.72575	0.541074	0.973458
OTOP2	0.032490713	1.384706	1.027521	1.866055
HS3ST3A1	0.033121303	1.37837	1.026035	1.851694
KIAA1549L	0.035502543	1.372514	1.02171	1.843766
KCNG1	0.036721149	1.368655	1.019553	1.837293
UPK1B	0.036751559	1.373113	1.019708	1.848999
F2	0.037993244	1.370908	1.017633	1.846823
BPIFB2	0.039957091	0.733282	0.545409	0.98587
CEACAM7	0.040540735	1.364302	1.013472	1.836578
CRP	0.04103548	1.360398	1.012613	1.82763
TEX13B	0.041392632	1.360987	1.012103	1.830135
PSG9	0.043214206	1.360924	1.009445	1.834784
HIST1H2BO	0.044662834	1.354779	1.007263	1.822191
PRDM9	0.04470821	1.352664	1.007162	1.816688
SPOCK3	0.045529138	1.354969	1.00606	1.824884
WFDC6	0.046033236	0.737529	0.546872	0.994654

LYPD3	0.046901303	1.361372	1.004236	1.845517
GNRH2	0.047292994	0.740186	0.549848	0.996412
CRB2	0.048194916	0.737425	0.545113	0.997585
EMX2	0.048969005	1.344806	1.00134	1.806084
KRT38	0.050916898	0.746355	0.556396	1.001167
CASP14	0.051095476	1.342601	0.998598	1.805108
PSG3	0.051664275	1.34659	0.997855	1.817203
COL12A1	0.05256155	1.341388	0.996754	1.805181
SPRR2E	0.053868531	1.340733	0.995134	1.806354
TRIML2	0.057648291	1.329445	0.990802	1.78383
ANXA13	0.058720724	1.327983	0.989597	1.782078
SLC6A19	0.058866658	1.331194	0.98934	1.791172
APOA1	0.059509952	0.753602	0.561511	1.011407
FAM83B	0.060346013	1.32662	0.98778	1.781691
ADGRB1	0.061292407	0.753741	0.560573	1.013472
MTMR7	0.062536389	0.755939	0.563136	1.014754
COL11A1	0.063591917	1.327306	0.984111	1.790186
FGF19	0.06517247	1.321297	0.982643	1.776663
SLC6A2	0.069037693	1.314847	0.97888	1.766124
SLC6A5	0.070834317	1.314085	0.97707	1.767344
PRSS33	0.07149065	0.760645	0.564902	1.024214
SLC16A11	0.072028936	0.7624	0.567309	1.024581
A2ML1	0.0728656	1.310136	0.975267	1.759987
CD109	0.075292709	1.31128	0.972757	1.76761
CREG2	0.075721972	1.317111	0.971883	1.784968
NLRP7	0.07613009	0.76127	0.563157	1.029077
KRT14	0.076240939	1.305424	0.972274	1.752728
CRH	0.079043864	1.302396	0.96982	1.74902
PNMA5	0.07932957	0.767696	0.571399	1.031427
LVRN	0.079495606	1.303117	0.969327	1.75185
HIST2H2AB	0.079768436	1.301984	0.969167	1.749091
HIST1H3J	0.081585013	1.300763	0.967562	1.748707
TWIST1	0.082089773	1.301464	0.967023	1.75157
C1orf94	0.08361294	1.296798	0.966058	1.740769
PSG5	0.084116739	1.30089	0.965186	1.753357
CCDC154	0.084608404	0.766287	0.566241	1.037006
TMEM59L	0.084745574	0.771482	0.574401	1.036185
NCCRP1	0.085524984	1.294833	0.96451	1.738284
HMGA2	0.086690243	1.294857	0.963452	1.740258
ECEL1	0.092384535	1.290266	0.95892	1.736106
RPTN	0.09270665	1.288399	0.958869	1.731179
HIST1H2AL	0.092786704	1.289638	0.958646	1.734911
PENK	0.093085884	0.775522	0.57642	1.043396
HIST1H4F	0.093608488	1.289813	0.95791	1.736716

TRH	0.095766065	0.777821	0.578742	1.045381
RPE65	0.098141473	1.284661	0.954708	1.728649
CELA3B	0.098749805	0.780046	0.580828	1.047593
SLC1A6	0.098796778	1.281063	0.954657	1.71907
SYT9	0.099230472	1.28041	0.954388	1.717801
MORC1	0.102191317	0.781424	0.581341	1.050371
MAFA	0.102391775	1.277963	0.952141	1.715281
TDGF1	0.102700217	0.782592	0.582999	1.050516
MYT1	0.104936987	0.783334	0.583106	1.052317
SPRR2D	0.105168817	1.279868	0.949587	1.725027
CPA4	0.105232434	1.277556	0.949895	1.718242
TMEM196	0.105465907	1.275844	0.949975	1.713498
MYL2	0.106287996	0.784463	0.584297	1.0532
DNAI2	0.10748428	0.784636	0.583995	1.054211
ATP4B	0.107861554	0.785681	0.585537	1.054237
ANXA10	0.108672229	1.272668	0.94793	1.708653
EBF3	0.108881662	0.785772	0.585189	1.055108
STEAP1B	0.111418673	1.272413	0.945812	1.711794
HIST1H4D	0.112714032	1.270508	0.945131	1.707901
TAS2R46	0.112946333	1.272278	0.94464	1.713555
TUNAR	0.113956004	0.788774	0.58773	1.05859
SLC38A8	0.114485589	0.78925	0.588271	1.058892
SPANXC	0.114766249	1.268587	0.943886	1.704985
MUCL1	0.116181829	1.26677	0.943134	1.701462
DNAAF1	0.116689626	0.789257	0.587234	1.060781
KRTAP16-1	0.117968778	0.791624	0.5906	1.061072
CTNND2	0.120639384	0.785589	0.579229	1.06547
UNC5D	0.120805089	1.26155	0.940647	1.69193
ABCC12	0.12123134	0.788313	0.583503	1.065011
LINC01314	0.121552885	0.78939	0.585159	1.064901
EVX1	0.12228204	1.261873	0.939487	1.694886
CACNG7	0.124196255	1.261743	0.938096	1.697049
HCRTR2	0.125297594	0.794199	0.591534	1.066298
CSMD3	0.125348262	1.258883	0.937838	1.689829
LIN28A	0.126368992	0.794438	0.591447	1.067098
MSTN	0.129215844	0.793899	0.589221	1.069674
HIST1H3D	0.129830245	1.256629	0.935067	1.688774
PAQR9	0.131826797	1.258039	0.933317	1.695738
CPA1	0.132076319	0.795421	0.59051	1.071437
SSX3	0.132686284	0.79711	0.593123	1.071251
FER1L6	0.133269257	1.25222	0.933599	1.679581
GDF6	0.133501931	1.252793	0.933304	1.681651
REG4	0.134339398	1.254321	0.932361	1.687459
CACNG1	0.136155298	0.797782	0.592713	1.073802

TRPA1	0.13728376	1.250954	0.931072	1.680737
GRIK1	0.138649928	1.248614	0.93068	1.675157
COLEC11	0.140159399	0.800957	0.596409	1.07566
RALYL	0.141477205	0.801494	0.596755	1.076475
HHLA1	0.142598502	1.247388	0.928258	1.676234
S100A7	0.144635704	1.245588	0.92732	1.673091
PRSS3	0.146025506	1.243863	0.926821	1.669358
DEFB4A	0.149227729	0.805254	0.59993	1.08085
TTLL8	0.149465031	0.805287	0.599884	1.08102
TRIM48	0.149836605	0.805681	0.600417	1.081119
CPB1	0.150401013	0.8042	0.597569	1.082282
KRT6A	0.153099514	1.253013	0.919543	1.707415
LRRC74B	0.153771256	0.807756	0.602381	1.083151
SSX1	0.154028774	1.23941	0.922669	1.664885
IFNK	0.154726473	1.240425	0.921923	1.668963
FAM9B	0.155957471	1.23725	0.922007	1.660278
SERPINB7	0.157445011	1.235797	0.921452	1.657378
ADH7	0.160316975	0.808782	0.601403	1.087669
TAC3	0.162254933	1.233357	0.919054	1.655147
RBM46	0.165221155	1.232099	0.917532	1.654512
GDPD2	0.165485636	1.231481	0.917553	1.652816
KRT6B	0.165526215	1.235128	0.916407	1.6647
GALP	0.166405863	1.230688	0.917212	1.651299
HIST1H1D	0.168677971	1.23054	0.915814	1.653423
KRTAP9-1	0.168723528	0.813321	0.605996	1.091578
SPRR3	0.169965089	1.230465	0.915021	1.654657
SNTG1	0.170052177	1.230357	0.915	1.654403
CLCNKA	0.1709448	0.812245	0.603122	1.093879
CARTPT	0.171591188	0.814042	0.606101	1.093323
SALL3	0.172234105	0.814976	0.607527	1.093261
HIST1H4E	0.172732127	1.226957	0.914407	1.646338
4-Mar	0.174851478	1.22631	0.913294	1.646606
CGB5	0.176000231	1.225093	0.912984	1.643898
SCGB3A2	0.17647035	0.814929	0.605681	1.096467
CFAP100	0.176958873	0.816008	0.607444	1.09618
PPY	0.177670298	0.816277	0.607642	1.096547
PTH2R	0.178457084	0.817619	0.609773	1.096312
HIST1H1E	0.179491	1.222716	0.911631	1.639955
LRRC26	0.180787866	0.818144	0.609777	1.097713
SAGE1	0.181359452	1.223039	0.91037	1.643095
LYPD4	0.182905333	1.223156	0.909377	1.645203
MRGPRX3	0.182933251	1.221135	0.910069	1.638524
BMX	0.183241647	0.817351	0.607311	1.100036
RHAG	0.183277211	1.22228	0.909456	1.642707

ADCYAP1	0.183547497	0.814715	0.602351	1.101949
SCGB3A1	0.187047291	0.819004	0.608793	1.1018
SPATA22	0.187410776	0.819427	0.609425	1.101793
ACTL8	0.188178867	1.219377	0.907504	1.638429
PSORS1C2	0.189920168	1.216652	0.907452	1.631208
VWA3A	0.191335061	0.819592	0.608126	1.104591
CHRM1	0.192552252	0.821954	0.612023	1.103893
RTL1	0.193185801	1.218391	0.904836	1.640604
NETO1	0.193783297	1.2167	0.905113	1.635551
S100A7A	0.193906339	1.21504	0.905668	1.630091
KCNK2	0.193919405	1.216337	0.905169	1.634475
GREM1	0.194440351	1.21757	0.904388	1.639204
HTR3E	0.194579365	0.823372	0.613853	1.104405
CFAP157	0.198807969	0.823059	0.611557	1.107708
RSPH6A	0.20025387	0.823902	0.612556	1.108167
KIR2DL1	0.200837276	0.824709	0.613841	1.108016
TAS2R13	0.200898632	0.825616	0.615526	1.107413
CDH12	0.201971502	1.212858	0.90172	1.631355
PSG1	0.202845897	1.210988	0.901951	1.625912
HIST2H2AC	0.203031189	1.211128	0.901786	1.626586
HIST1H2AI	0.204339867	1.209659	0.90161	1.622958
HRG	0.205361906	1.210536	0.900654	1.627036
KRT23	0.208162407	1.207648	0.900205	1.620091
GSTA2	0.208242694	0.826761	0.614752	1.111885
CNTN5	0.208543362	0.828488	0.617922	1.110807
AFF2	0.208984874	0.82851	0.617788	1.111107
SEC14L3	0.20925422	0.827064	0.614924	1.112389
GCG	0.209370166	1.208357	0.899207	1.623795
NPY5R	0.209529626	0.828353	0.617272	1.111616
KRT20	0.211203587	1.206824	0.898784	1.620439
RNASE7	0.211660169	1.205991	0.898873	1.618043
CYP11A1	0.212219709	0.829949	0.619255	1.112327
ZPLD1	0.212538308	1.205722	0.89848	1.618027
MCCD1	0.213425473	0.829502	0.61792	1.113532
HIST1H4C	0.218523581	0.831791	0.620309	1.115375
HIST1H2BI	0.220151509	0.831791	0.619665	1.116533
SNX31	0.220315678	1.201255	0.895969	1.610561
TAAR1	0.22059219	1.203357	0.894872	1.618185
TTLL9	0.222952712	1.201051	0.894559	1.612552
PCDH8	0.223590696	0.832704	0.620077	1.118242
PRR4	0.223880966	0.833007	0.620552	1.1182
DLK1	0.224205253	1.199834	0.8944	1.609573
TPH1	0.224963325	0.832594	0.61932	1.119312
KCNA4	0.225830225	0.83213	0.618075	1.120317

PRDM13	0.226035811	1.198445	0.894003	1.606561
VSX2	0.22608441	0.834225	0.622058	1.118757
ST18	0.226671925	0.833391	0.620199	1.119868
KLK5	0.229728412	1.196907	0.89264	1.604885
DLEC1	0.233309689	0.834384	0.619523	1.123762
HIST1H4L	0.234019101	1.195216	0.891041	1.603227
C9orf135	0.234954452	0.836253	0.622554	1.123307
APOA5	0.235203824	0.836628	0.623196	1.123155
TRPM5	0.236878121	0.837016	0.623308	1.123997
CLCA1	0.242596423	0.838845	0.624702	1.126395
NRSN1	0.24519151	1.190982	0.886924	1.599278
RERGL	0.245824711	0.839969	0.625687	1.127637
TUBA3E	0.246453628	1.189949	0.886757	1.596807
HIST2H2BF	0.247197855	1.189162	0.886752	1.594703
LRFN2	0.247406209	0.840587	0.626309	1.128175
RETNLB	0.248532826	1.190088	0.885536	1.599382
SNAI2	0.249082548	1.188061	0.886289	1.592584
DKK4	0.249503955	1.189929	0.885081	1.599774
CILP	0.249921464	1.188588	0.885553	1.595321
IFITM5	0.251160484	0.841873	0.627436	1.129597
LIPF	0.252212698	0.84223	0.627747	1.129995
ENO3	0.255265334	0.842707	0.627525	1.131676
AGTR2	0.25579125	0.842592	0.627087	1.132157
HIST1H2BG	0.256430825	1.186012	0.883353	1.59237
SCN5A	0.260187704	1.183591	0.882628	1.587179
GRM4	0.260653126	0.844972	0.630044	1.133219
IFNE	0.261618242	1.185066	0.881032	1.594018
HTR3C	0.261848439	0.844481	0.628575	1.134547
ALPI	0.262424101	1.183017	0.881732	1.587252
CACNG8	0.262689298	1.18223	0.882028	1.584607
GPR52	0.263772609	0.845501	0.629917	1.134867
GLTPD2	0.264564546	0.844746	0.62806	1.13619
ACTN3	0.264664045	0.845141	0.628831	1.135858
SPRR2A	0.264925851	1.185154	0.879168	1.597636
SLC2A2	0.265038761	1.181621	0.881099	1.584643
PSG4	0.266474831	1.184233	0.878838	1.595751
MAPK15	0.266522041	0.845661	0.629177	1.136632
KRTAP29-1	0.268370918	0.846846	0.6309	1.136707
S100A12	0.271654557	1.178978	0.879047	1.581244
SLC39A5	0.272184234	1.181869	0.877074	1.592584
CHRD2	0.272260525	0.847376	0.630485	1.138879
MPC1L	0.273449183	1.178703	0.878242	1.581958
CELF3	0.27729208	0.849263	0.632456	1.140391
HSD17B13	0.27881373	0.846375	0.625846	1.144611

CREB3L3	0.280686711	1.177142	0.875275	1.583118
ASPG	0.280897026	0.851072	0.63485	1.140937
C1orf64	0.281701566	0.850826	0.634021	1.141768
LAMA1	0.281710793	1.175923	0.875466	1.579496
FAM25A	0.281965776	1.176017	0.875272	1.5801
TEX101	0.283528138	0.85043	0.63248	1.143486
CTRB1	0.283590762	0.851316	0.634319	1.142545
LCE3D	0.284730745	1.174148	0.874942	1.575673
CDH16	0.285628084	1.173174	0.875068	1.572835
DEFA6	0.285950062	1.173651	0.874599	1.574958
SLC46A2	0.286986006	0.851766	0.633953	1.144416
VIT	0.287096295	1.173323	0.874193	1.57481
CEACAM8	0.288140556	0.852866	0.635834	1.143979
MDGA2	0.288459746	1.173368	0.873436	1.576296
APCDD1L	0.288482684	1.173144	0.873565	1.57546
C6orf58	0.291672127	1.172342	0.87237	1.575461
VWA5B2	0.291874499	1.172407	0.87222	1.575906
CALML5	0.293682157	1.171096	0.872097	1.572607
SH2D6	0.293784454	0.854371	0.636852	1.146185
CFAP65	0.29818285	0.854559	0.635544	1.149048
HIST1H2BB	0.30011815	0.85619	0.638299	1.14846
PGC	0.300163717	0.855363	0.636501	1.149481
GCK	0.3027193	0.856822	0.638655	1.149516
C11orf87	0.304663746	0.856847	0.637953	1.150847
MYH13	0.306461779	1.167478	0.867693	1.570838
CPB2	0.306728748	0.858019	0.639695	1.150856
PCP4	0.306969246	0.857849	0.639232	1.151233
C1orf158	0.307087947	0.857412	0.638234	1.151857
CXorf67	0.307303196	0.857234	0.637765	1.152227
HOXB1	0.307816593	0.858604	0.640547	1.150893
IGFL1	0.311282103	1.164856	0.86694	1.565149
SI	0.311646822	1.163789	0.867492	1.56129
DCAF4L2	0.31221447	1.163828	0.867165	1.561981
PSG8	0.312373213	1.164247	0.866788	1.563785
ITIH1	0.314912871	0.855951	0.631984	1.15929
LRRC15	0.3152925	1.163784	0.86557	1.564743
NNAT	0.315740946	0.858885	0.638072	1.156114
SLC28A2	0.317740577	0.860344	0.640498	1.15565
LCN15	0.319148434	1.161008	0.86552	1.557376
TBX20	0.319220578	1.161524	0.86511	1.559499
WFDC12	0.322903978	0.862062	0.642284	1.157044
TNNT3	0.323938231	0.862471	0.64279	1.15723
CA6	0.327360495	0.863514	0.64378	1.158246
SYNPR	0.32834604	0.862765	0.64172	1.15995

CRISP2	0.329018796	0.863907	0.644014	1.158882
UGT3A1	0.329144934	0.863899	0.643945	1.158982
KCNK10	0.33194417	0.863862	0.642765	1.161011
RHOXF2	0.332851681	0.865121	0.645245	1.159925
ADAMTSL1	0.333173432	0.864767	0.644318	1.16064
MAB21L2	0.334284356	0.864626	0.643564	1.161621
GADL1	0.335724026	0.865397	0.64474	1.161571
FAM9A	0.337154605	1.154958	0.860603	1.549992
MSMB	0.338720243	0.866281	0.645568	1.162454
L1CAM	0.340874657	1.15339	0.859883	1.547083
SERPINE2	0.341716051	1.153601	0.859275	1.548742
MYOD1	0.341900662	1.153742	0.859067	1.549495
KLK14	0.343040342	0.867648	0.646984	1.163572
TEX37	0.343777106	1.153711	0.858106	1.551147
VGLL2	0.344611447	1.152228	0.858852	1.545819
GLP2R	0.344663173	1.15301	0.858199	1.549096
MEP1B	0.345167821	0.868382	0.647829	1.164021
SLC12A3	0.348735648	0.86865	0.647038	1.166164
WFDC5	0.34911412	0.868865	0.647383	1.166119
CACNG2	0.34982038	1.15062	0.857426	1.544069
GSTA3	0.350483009	0.867926	0.644678	1.168483
PEX5L	0.351831768	1.149947	0.856926	1.543163
SVOP	0.35343816	1.148638	0.857169	1.539217
MYRFL	0.354680093	1.149342	0.855934	1.543328
MROH2B	0.356060777	0.868004	0.642629	1.172421
UNC13C	0.357031443	0.870595	0.648253	1.169196
MAGEB17	0.358128378	1.147374	0.855781	1.538323
OLIG3	0.358771134	0.871644	0.650012	1.168846
HHATL	0.359698412	0.871214	0.648638	1.170167
HIST1H2BJ	0.360137724	1.147222	0.85486	1.539572
LEP	0.360898218	1.146461	0.85511	1.537081
AGXT2	0.36277411	1.146182	0.85437	1.537662
AQP7	0.362973781	0.871421	0.647814	1.172211
LRRTM3	0.363543856	1.145545	0.854516	1.535691
TMEM229A	0.363964647	0.869822	0.643672	1.175429
ODF3	0.364859136	1.14559	0.85379	1.537118
TAC1	0.365272855	1.14512	0.853981	1.535515
MSLNL	0.365378625	1.147283	0.85205	1.544816
CHGB	0.365623123	0.872748	0.649874	1.172056
PRR9	0.366216359	1.145179	0.853436	1.536652
MUC22	0.366340712	0.873562	0.65151	1.171296
HSD3B1	0.367801234	1.1448	0.852937	1.536534
C10orf90	0.368630918	1.144235	0.852999	1.534907
KCNU1	0.372482508	1.143549	0.851588	1.535606

KIR3DX1	0.373718361	1.143008	0.851423	1.534451
UMOD	0.373769534	0.875044	0.652058	1.174285
KLRF2	0.373847498	1.144297	0.850201	1.540125
FOXL2NB	0.375893849	1.141503	0.85164	1.530023
MYO18B	0.379969244	0.876911	0.654047	1.175717
HIST1H2BM	0.382043995	1.139515	0.850245	1.527202
CALML3	0.3822489	0.877282	0.654023	1.176754
TCHHL1	0.383334732	1.139682	0.849413	1.529144
KCNH6	0.387448061	0.878627	0.655184	1.178271
CCDC17	0.388684188	0.877255	0.651343	1.181523
HMP19	0.389333737	1.138173	0.847678	1.528221
SLC35F4	0.390976221	1.13786	0.84711	1.528403
TRIM49	0.391306211	0.879301	0.655266	1.179934
TNMD	0.394556722	0.8802	0.65615	1.180756
HIST1H2AD	0.397369178	1.135281	0.846238	1.52305
ALB	0.397986525	1.134789	0.846397	1.521445
AFP	0.400925484	1.134438	0.845195	1.522667
SPANXD	0.404909052	1.133919	0.843604	1.524143
HIST1H2AJ	0.40720403	1.132352	0.843973	1.519268
FAM83C	0.407386207	1.133403	0.842809	1.524192
GPR142	0.407599863	1.134929	0.841147	1.531317
SLC39A2	0.410438066	1.131477	0.843156	1.518392
HIST1H2AM	0.410517454	1.131427	0.843166	1.518238
S100A2	0.412539861	1.131173	0.842356	1.519016
IDI2	0.413340131	0.882901	0.655117	1.189884
GPR22	0.413715065	0.884852	0.659891	1.186503
TAS2R50	0.414011503	1.129904	0.842895	1.514639
IRX4	0.41457362	1.129829	0.842676	1.514834
HIST2H3D	0.416152336	1.12939	0.8423	1.514331
GABRG3	0.418143717	1.13056	0.840005	1.521618
HEPACAM2	0.418190249	0.88484	0.657996	1.189888
MME	0.420966388	1.129412	0.839711	1.519061
CLCA4	0.421455812	0.886264	0.660263	1.189621
SOX3	0.422378956	1.129689	0.838656	1.521718
PRAP1	0.424215168	0.886899	0.660739	1.190471
ATCAY	0.425344319	1.127199	0.839753	1.513037
CYP2C9	0.426881095	1.126776	0.839393	1.512551
FAM205C	0.427030193	1.126437	0.839684	1.511117
EIF4E1B	0.43114315	1.12517	0.838883	1.50916
C6orf15	0.431503211	1.124998	0.838883	1.508697
GPR12	0.436579484	1.125246	0.835873	1.514797
CSTL1	0.437282464	0.889856	0.662895	1.194522
PIRT	0.439720381	1.122571	0.837221	1.505177
BPIFB4	0.444790035	0.891835	0.664915	1.196198

UGT2B11	0.446656133	1.121552	0.834659	1.507057
MFAP5	0.446795044	1.121272	0.834913	1.505846
TAS2R30	0.450115997	0.893345	0.666658	1.197113
TAS2R38	0.455205134	0.89443	0.667381	1.198721
IGF2	0.456415361	1.117919	0.833702	1.499029
TRIM49C	0.456486257	0.89421	0.66623	1.200203
OR2W3	0.456669742	1.118723	0.832585	1.5032
DAPL1	0.457221102	0.893611	0.664288	1.202098
FGF5	0.461615614	1.118883	0.829669	1.508915
PHGR1	0.462257974	1.116571	0.832176	1.498156
ATOH1	0.464826509	1.115401	0.832234	1.494915
TF	0.466023803	0.896663	0.66875	1.20225
NPTX2	0.467351223	1.115193	0.831114	1.496372
UGT2B28	0.470741864	0.896709	0.666789	1.20591
OR6T1	0.472705579	1.11346	0.830384	1.493037
NTSR2	0.475083375	1.1128	0.829931	1.49208
SLC17A6	0.47614531	0.898874	0.670403	1.205208
KRT31	0.476592084	1.113855	0.82772	1.498905
HTR7	0.479330571	0.898539	0.668037	1.208576
ADIPOQ	0.480733322	1.111163	0.828961	1.489435
TTR	0.481814159	0.900131	0.671399	1.206788
HMX3	0.48226904	0.900121	0.671166	1.20718
HDGFL1	0.483166783	0.900085	0.670661	1.207993
PNPLA5	0.48468276	1.111103	0.826843	1.493089
LCN9	0.486674606	0.901038	0.671778	1.208538
DCAF8L1	0.487661974	0.901406	0.67238	1.208443
SHISA9	0.488470053	1.109255	0.827228	1.487434
MYH8	0.489360356	1.109745	0.826061	1.490852
STMN2	0.49633664	1.107154	0.825727	1.484498
ARHGAP36	0.498928045	1.106981	0.82451	1.486224
MTPP	0.499955589	0.904133	0.674626	1.211717
INSRR	0.500067111	1.106262	0.824885	1.483618
ASGR2	0.50048176	1.106431	0.82441	1.48493
CCDC114	0.500995877	0.902931	0.670648	1.215668
QRFPR	0.50114566	0.904478	0.675083	1.211821
SLC7A3	0.503981373	0.904983	0.675252	1.212873
SLC5A12	0.5054073	0.904471	0.673086	1.215399
EPHA5	0.519029134	0.907667	0.676157	1.218445
FGFBP2	0.520171822	0.908291	0.677492	1.217715
SOHLH1	0.520592833	1.101381	0.820337	1.478708
COL25A1	0.521003785	0.908079	0.676454	1.219013
VCX3B	0.521544042	1.100536	0.821081	1.475103
TBPL2	0.522991041	0.908034	0.675368	1.220856
PRG4	0.524231397	0.909185	0.678263	1.218727

SHCBP1L	0.524534577	0.908903	0.677261	1.219774
NPPB	0.528369824	1.099527	0.818678	1.476722
ALDOB	0.528547957	0.910186	0.679247	1.219644
CTRB2	0.529340242	0.910009	0.678322	1.220833
FGF17	0.533618157	1.098544	0.817149	1.47684
TFF2	0.534176756	1.099221	0.815736	1.481222
P2RY4	0.537209206	1.097422	0.816828	1.474403
PRAC1	0.538682586	1.096285	0.817806	1.469591
KCNK12	0.539089709	1.09631	0.817524	1.470166
SPAG11A	0.540188929	0.912411	0.680468	1.223413
FRG2	0.543125554	0.912874	0.680473	1.224648
SCN3A	0.543478071	0.913132	0.681109	1.224195
LGALS7B	0.54412552	0.912845	0.679885	1.22563
KCNT1	0.545062319	0.911478	0.675114	1.230595
AKR1C4	0.546082039	1.094757	0.815938	1.468854
HSD3B2	0.548961823	0.914093	0.681421	1.226211
KRT34	0.549596006	1.095085	0.81327	1.474555
HIST1H3F	0.551086818	1.094119	0.814007	1.47062
TUSC5	0.552485207	0.914854	0.682081	1.227064
CLVS2	0.552902289	1.093213	0.814459	1.467373
SLC22A9	0.553951808	1.092437	0.81516	1.464031
F7	0.557307658	1.092208	0.813527	1.466354
APOH	0.564424325	0.916664	0.681843	1.232354
HIST1H3B	0.569269958	1.089296	0.811376	1.462413
TMIGD1	0.574132455	1.087832	0.81105	1.459069
COL9A3	0.574258313	1.087921	0.810807	1.459746
SPRR1A	0.574628862	1.088875	0.808807	1.465924
KRTDAP	0.575590025	0.918949	0.683559	1.235397
SAG	0.57982902	0.920069	0.685074	1.235672
HIST1H3C	0.583356509	0.920888	0.685968	1.23626
LRRC38	0.584231915	1.086762	0.806698	1.464056
ASCL1	0.584340338	0.920895	0.685464	1.237188
CYP2B6	0.58510476	0.921268	0.686325	1.236637
CRISP3	0.588068814	1.085216	0.80723	1.458931
SST	0.588234284	0.922217	0.687894	1.236358
INS	0.590962383	1.083628	0.808495	1.452389
PLA2G6	0.591169261	0.922366	0.686816	1.238701
SLC7A9	0.591430126	1.08377	0.807917	1.453808
VTN	0.594741057	0.922712	0.686056	1.241002
HIST1H2BL	0.59611186	1.082562	0.807318	1.451647
SCGB2A2	0.597101518	1.082191	0.807429	1.450453
KNG1	0.597923902	1.082014	0.807256	1.450288
C1QTNF8	0.599931506	0.924687	0.690117	1.238987
GSG1L2	0.601853339	1.082039	0.804648	1.455057

GAGE2A	0.601933874	0.924793	0.68938	1.240596
NKX2-2	0.60498023	1.080355	0.806077	1.447959
HIST1H4B	0.612158296	1.078704	0.804835	1.445767
PCDH11Y	0.612499802	0.926935	0.691107	1.243236
ESX1	0.618826383	1.077457	0.803082	1.445574
HIST1H3I	0.620184277	1.077504	0.802061	1.44754
CFAP73	0.621065812	1.077261	0.802	1.446999
NEUROG3	0.621305819	0.928528	0.691862	1.246149
AKR1B10	0.622340674	0.92786	0.688785	1.249916
KRT37	0.622456105	0.927827	0.688596	1.250172
CDH9	0.622784625	0.92896	0.692602	1.245978
HIST1H1A	0.625358451	0.928774	0.690395	1.24946
KCNE2	0.632966565	1.074637	0.799759	1.44399
GABRA4	0.635133367	0.931327	0.694192	1.249466
PRODH2	0.642282167	0.932904	0.69593	1.25057
PHACTR3	0.645906295	1.071399	0.798333	1.437865
SLC17A4	0.648936521	1.070582	0.798172	1.435964
ANHX	0.649318746	1.070261	0.798691	1.43417
BSND	0.650301098	0.93448	0.697162	1.252583
FRG2C	0.651580345	1.069802	0.798209	1.433804
PSG11	0.653016656	1.0698	0.797179	1.435652
NEB	0.653803052	1.069559	0.797213	1.434945
RSPO3	0.656910097	1.068623	0.797326	1.432232
HIST1H2BE	0.657025732	1.068679	0.797099	1.43279
ONECUT3	0.657742861	1.068984	0.7958	1.435947
CLCA2	0.658166275	1.06825	0.797365	1.431161
FGF3	0.658358888	1.070038	0.79266	1.44448
SPINK1	0.65865425	1.069732	0.79322	1.442635
UBE2U	0.661902282	0.93658	0.698244	1.256269
TM4SF5	0.664387297	1.067243	0.795399	1.431994
LRRC71	0.66460646	0.937015	0.69827	1.257389
PPP1R3A	0.667749212	0.937823	0.699554	1.257247
CCKAR	0.668276604	0.937991	0.699906	1.257065
SPAG11B	0.669824115	0.938232	0.699891	1.257738
HIST1H2AB	0.672373454	1.065497	0.794067	1.429709
OBP2B	0.674081847	0.938733	0.699158	1.260401
SLC3A1	0.674328927	0.938688	0.698802	1.260922
SPRR2G	0.674519417	1.065151	0.793379	1.430019
LPA	0.678033347	1.06407	0.793673	1.426588
GNAT3	0.678626173	0.939954	0.701281	1.259857
PROKR1	0.67880863	0.939621	0.699736	1.261746
PHOX2B	0.679782796	0.940079	0.70103	1.260643
CELA3A	0.683733548	0.940346	0.699468	1.264175
BRINP2	0.68522154	1.062402	0.792823	1.423644

APOC3	0.685738398	1.063799	0.788426	1.435351
PAX2	0.685933186	1.062357	0.792396	1.424289
MYPN	0.688859203	1.061825	0.791635	1.424233
IGDCC3	0.694296406	0.942809	0.702878	1.264642
CYP11B1	0.695112027	0.943045	0.703351	1.264424
CFAP46	0.696737597	0.943118	0.702519	1.266119
S100G	0.69841821	0.943101	0.701229	1.268401
PRB1	0.698602176	0.943735	0.703957	1.265184
PSG6	0.701193511	1.05914	0.789758	1.420405
HIST1H2BH	0.701417792	1.059161	0.789508	1.420914
TSPYL6	0.701486562	0.944195	0.703958	1.266416
LGALS14	0.701513593	1.059482	0.788446	1.423689
FOXI1	0.707871648	0.944604	0.701123	1.272641
ZBTB20	0.710299874	0.945772	0.704734	1.269252
SOST	0.710458002	1.05721	0.788139	1.418141
CBLN1	0.713454039	0.946415	0.70538	1.269815
TBX10	0.713483548	0.946121	0.703967	1.271571
TSPY1	0.717038985	1.05572	0.787402	1.415473
SPIC	0.719506486	1.055269	0.786782	1.415375
XAGE3	0.720614608	0.947746	0.706245	1.271827
ACTL6B	0.720901337	1.055174	0.785894	1.41672
TMEM207	0.721294379	1.05492	0.786403	1.415123
TRPM8	0.723099782	1.054354	0.786743	1.412993
PRH2	0.723297102	0.948258	0.706641	1.272491
FABP7	0.724930337	0.948621	0.707129	1.272585
OTOS	0.725833803	1.05438	0.784263	1.417531
AGXT	0.727349574	1.053588	0.785645	1.412912
REG3A	0.727825089	0.949326	0.708309	1.272353
HTR3B	0.728671479	0.949259	0.707304	1.273982
DPPA2	0.730889352	0.949829	0.708367	1.273599
LGALS13	0.732490304	1.052668	0.784284	1.412893
PRSS48	0.733469851	0.950098	0.707629	1.275649
CHRNA9	0.733901272	1.053311	0.780736	1.421049
GABRA2	0.736480518	1.051567	0.784608	1.409359
MGARP	0.738555834	0.951262	0.70937	1.275638
NKX2-4	0.740168497	1.050914	0.783616	1.40939
FBN2	0.742970814	1.05059	0.78222	1.411033
ALLC	0.743071449	1.051137	0.780099	1.416345
SMLR1	0.746258836	0.952769	0.710741	1.277214
CERS3	0.747713253	0.953057	0.711021	1.277484
DPPA5	0.748089233	0.953108	0.71097	1.277712
PMP2	0.750302039	0.953337	0.71028	1.279566
BARHL2	0.751205114	1.048731	0.781488	1.407362
CALCA	0.751563713	1.048654	0.781442	1.407238

BHMT	0.756117633	0.954504	0.711481	1.280537
SPRR2F	0.756805651	1.047903	0.779306	1.409075
DEFA5	0.757599607	0.954755	0.711538	1.281109
BPIFA1	0.75819504	1.04711	0.781105	1.403703
TMEM190	0.758654161	0.954932	0.711564	1.281536
UGT1A1	0.759821161	0.955136	0.711643	1.281941
GRIA2	0.762100055	0.955459	0.711137	1.283301
GIF	0.762558063	0.955846	0.713116	1.281198
SLC7A14	0.762694013	0.955569	0.711445	1.283462
SP7	0.763105983	0.955849	0.712634	1.282071
EFCAB8	0.76547738	0.955839	0.710399	1.286077
GAD2	0.768379303	0.956794	0.713117	1.283739
SORCS3	0.769062159	1.045171	0.778217	1.403699
AC187653.1	0.76937119	1.044849	0.779263	1.400951
PRLHR	0.771929381	0.957621	0.714541	1.283396
COLEC10	0.774553264	1.043772	0.778557	1.39933
BNC1	0.777245371	1.043221	0.77816	1.398567
AC011473.4	0.77890456	1.043019	0.7773	1.399574
CLEC18C	0.782189213	0.959327	0.7147	1.287686
GFRA4	0.78228776	0.959513	0.715724	1.286341
SERPINA6	0.783468502	0.95979	0.716231	1.286174
GLYATL3	0.78448088	0.959801	0.715286	1.287901
MYBPC1	0.787974128	1.041103	0.776256	1.396311
COL11A2	0.788965455	0.960572	0.715488	1.289608
POU3F3	0.79063368	1.040466	0.776324	1.394482
SERPINB12	0.793533263	1.040037	0.775136	1.395467
BEX1	0.797481424	1.039303	0.774225	1.395138
GJA3	0.798146095	1.038965	0.775133	1.392598
GUCA2A	0.799973183	0.96284	0.718358	1.290527
POU3F2	0.801251117	0.963095	0.718648	1.29069
APOA2	0.803058134	1.038176	0.773388	1.393621
TCEAL5	0.805341766	0.963876	0.719351	1.291522
POU5F2	0.807228912	0.963665	0.715833	1.297301
ATP2B2	0.809451951	1.037263	0.770443	1.396489
AQP2	0.80951141	1.037004	0.771745	1.393436
KRTAP5-5	0.809513726	0.9645	0.718893	1.294016
PROK1	0.811049955	1.036426	0.772952	1.389708
STRA8	0.81223466	1.036163	0.772916	1.38907
FGF21	0.813840209	0.965342	0.71974	1.294752
LY6G6C	0.816860558	0.96573	0.718929	1.297256
PRORY	0.818811737	0.966335	0.720906	1.295319
HRH3	0.819005554	1.034859	0.771645	1.387859
CFAP74	0.81929216	1.03468	0.772295	1.386209
IL1A	0.823811022	1.03392	0.770829	1.386807

C1orf194	0.82547136	0.967465	0.721042	1.298106
PROZ	0.831632164	0.968676	0.722375	1.298955
ASIC2	0.832109399	0.96884	0.72302	1.298237
GPR26	0.833163022	1.032536	0.766518	1.390876
FABP1	0.833611143	0.969074	0.72288	1.299114
FLG2	0.83381109	0.968836	0.720792	1.302239
WIF1	0.83399451	0.968842	0.720596	1.302609
RTP1	0.834444433	0.969278	0.723376	1.298769
TLL6	0.835354571	0.969374	0.722938	1.299814
C4orf26	0.839345835	1.031077	0.766997	1.386081
ZNF460	0.84001467	0.969913	0.720985	1.304788
SFRP1	0.8402409	1.03067	0.768352	1.382545
UGT2A1	0.841031771	1.030406	0.768942	1.380776
GLRA2	0.841275574	1.030499	0.76798	1.382755
ADAMTS19	0.844259728	1.030175	0.765769	1.385876
AMY1B	0.845073488	0.971153	0.724073	1.302546
HIST1H3A	0.845339085	0.971204	0.72412	1.302597
HIST1H1B	0.849415575	0.971756	0.722953	1.306184
REG1A	0.851027204	0.972169	0.724129	1.305172
CDH22	0.851812872	0.972498	0.7258	1.303048
TBC1D3E	0.85307886	1.028455	0.76423	1.384033
OTOP1	0.853172593	0.972719	0.725726	1.303774
PSG2	0.855777842	0.973202	0.726088	1.304419
PSAPL1	0.856564129	0.973223	0.725094	1.306264
MYH7	0.85769836	0.973307	0.724116	1.308251
DNAI1	0.858225689	1.027178	0.765365	1.378551
C21orf62	0.858836413	0.972933	0.719043	1.316468
HIST1H2AG	0.860205546	0.97398	0.72631	1.306104
FOXR2	0.860470285	1.026659	0.765629	1.376685
ZACN	0.865836879	0.975021	0.727053	1.30756
SEZ6	0.866727794	0.974854	0.724039	1.312554
DGKK	0.869459144	1.025007	0.763485	1.37611
UCN3	0.872021388	1.024651	0.761905	1.378006
SLCO1B1	0.873674691	1.024399	0.761046	1.378883
TSPY2	0.87378669	1.024055	0.763749	1.37308
ATP12A	0.873899041	0.97632	0.726208	1.312573
HIST1H3G	0.874238978	0.976493	0.727349	1.310978
TAF7L	0.875838079	0.976851	0.728171	1.310458
CALB2	0.876796197	1.023561	0.762522	1.373963
GC	0.877740545	0.977157	0.727956	1.311668
GALR3	0.878010848	1.023279	0.762744	1.372807
PGA5	0.878429178	1.023189	0.762754	1.372548
CWH43	0.883690221	1.022091	0.762698	1.369704
PRB4	0.88476415	1.021958	0.761846	1.370879

POU5F1B	0.886099618	1.022607	0.753121	1.388521
VSTM2A	0.887630623	1.021355	0.761883	1.369195
NPY	0.888444631	1.021182	0.761922	1.368659
HFE2	0.888783195	1.021396	0.759165	1.374206
TUBA4B	0.889703529	0.979415	0.729958	1.314121
ADGRG7	0.892169146	0.979912	0.730742	1.314043
CRCT1	0.894837648	1.019947	0.761012	1.366987
PRSS38	0.895775135	0.980542	0.730783	1.315662
PDPN	0.898043877	1.019498	0.758759	1.369837
SLC26A4	0.898450151	0.981051	0.731299	1.316099
NEUROD4	0.898529522	1.019239	0.760459	1.36608
CRISP1	0.901060704	1.018756	0.760046	1.365527
SLC17A2	0.902337004	1.018549	0.759439	1.366063
CALB1	0.904772459	0.98203	0.729637	1.321731
RET	0.90497498	0.982155	0.730795	1.319973
ACSM2B	0.905070081	1.018259	0.756332	1.370894
COX8C	0.910000334	1.017109	0.75792	1.364933
LGI1	0.912907033	0.983672	0.732369	1.321207
CALY	0.913960744	1.016358	0.757204	1.364208
ANXA8L1	0.91557778	0.984008	0.730377	1.325714
CDHR4	0.916730087	0.984495	0.734505	1.31957
AC020914.1	0.919328141	0.984984	0.734967	1.32005
ETNPPL	0.923637093	1.014489	0.755974	1.361406
SERPINB2	0.925199188	1.014142	0.756456	1.359607
OR4A16	0.927035533	0.986407	0.735946	1.322107
NXF3	0.928452584	0.986588	0.734739	1.324765
C22orf15	0.929164984	0.98678	0.735853	1.323274
KCTD4	0.931112698	1.012999	0.755858	1.357618
CT47B1	0.936547961	0.988145	0.73673	1.325358
TRPC5	0.936769192	1.012048	0.752831	1.360521
GALNTL5	0.937070452	1.011898	0.754427	1.357239
MMP27	0.938372439	0.988413	0.735575	1.328159
KRT33A	0.940374378	1.011247	0.754365	1.355605
PSG7	0.942388001	1.010871	0.753956	1.355332
NKX6-3	0.945201156	1.010532	0.749561	1.362363
MUC6	0.94655064	1.010167	0.75155	1.357776
SPRR2B	0.947654644	1.009885	0.752912	1.354563
ITLN1	0.947929298	0.990053	0.733432	1.336462
SERPINA11	0.948355181	1.009765	0.75251	1.354967
KCNJ13	0.948682445	0.990434	0.739095	1.327243
REG1B	0.948724984	1.009659	0.75324	1.353369
ANXA8	0.950206023	1.009377	0.753064	1.352929
MCHR2	0.950448577	1.00944	0.750561	1.357609
CRYGD	0.952700726	0.991145	0.738747	1.329775

ADAD2	0.955557262	0.991687	0.73938	1.33009
OBP2A	0.956325294	1.008233	0.751823	1.352093
A4GNT	0.9581905	1.008016	0.747872	1.358652
HIST2H3C	0.958384437	0.992234	0.740354	1.329809
RHOXF2B	0.959154816	1.007712	0.751007	1.352165
STMN4	0.960251764	1.007534	0.750011	1.353479
PTF1A	0.963426363	1.006877	0.751195	1.349586
NLRP13	0.965406089	0.993521	0.740624	1.332772
CALN1	0.969869958	0.994359	0.741409	1.333609
FAM19A4	0.973538403	1.005011	0.748017	1.350298
XAGE5	0.973828695	0.995108	0.742383	1.333866
PRB3	0.978937195	1.003976	0.747801	1.347909
VAT1L	0.981782787	0.996592	0.743475	1.335883
SSX5	0.982232635	1.003352	0.747398	1.346959
PNMA6F	0.982898795	1.003206	0.748623	1.344365
MMP26	0.983188728	0.996854	0.743612	1.33634
TFAP2B	0.986036309	0.997388	0.744161	1.336785
SCGB1A1	0.986256709	0.997425	0.743812	1.33751
SPATA16	0.988718878	1.002125	0.746658	1.345
HIST1H2AH	0.990699405	1.001743	0.747469	1.342516
OTOR	0.99158366	1.001588	0.745816	1.345076
FSHB	0.992523986	1.001402	0.746985	1.342471
CD177	0.994167339	1.001094	0.746745	1.342077
PNLIP	0.995361653	1.00087	0.746553	1.341821
PADI3	0.995584665	0.999172	0.74515	1.33979
STATH	0.995666651	1.000818	0.745009	1.344463
SPINK4	0.997713428	1.000429	0.745889	1.341834
ZP2	0.999488917	1.000096	0.745769	1.341156

Table S9. GSEA results between high-risk and low-risk phenotypes by using C5 reference gene set.

NAME	SIZ E	ES	NES	NOM p-val	FDR q- val
HP_OSTEOLYSIS_INVOLVING_BONES_OF_THE_UPPER_LIMBS	21	0.7975	2.3049	<0.01	0.0098
		92	66		65
GOBP_EPHRIN_RECEPTOR_SIGNALING_PATHWAY	86	0.6079	2.3105	<0.01	0.0158
		66	38		57
GOCC_CELL_SUBSTRATE_JUNCTION	422	0.4992	2.1387	<0.01	0.0444
		06	45		49
HP_DERMAL_ATROPHY	79	0.5656	2.1712	<0.01	0.0480
		07	85		37
GOBP_MORPHOGENESIS_OF_AN_EPITHELIAL_SHEET	55	0.5789	2.0623	<0.01	0.0489
		89	58		05
GOBP_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	108	0.5211	2.0708	<0.01	0.0491
		39	78		63
HP_ATROPHIC_SCARS	30	0.7941	2.1403	<0.01	0.0491
		26	55		84
GOBP_CELL_ADHESION_MEDIATED_BY_INTEGRIN	69	0.6030	2.1249	<0.01	0.0493
		9	82		23
HP_FACIAL_EDEMA	67	0.5459	2.0662	<0.01	0.0503
		19	22		09
GOBP_ENDODERMAL_CELL_DIFFERENTIATION	43	0.6857	2.1868	<0.01	0.0503
		38	01		44
HP_HYPEREXTENSIBLE_SKIN	61	0.6161	2.0623	<0.01	0.0510
			7		31
HP_LONG_NOSE	31	0.6249	2.0582	0.001912	0.0513
		78	82		7
GOMF_COLLAGEN_BINDING	67	0.6524	2.0711	0.001938	0.0514
		79	69		48

HP_FRAGILE_SKIN	30	0.7620	2.1160	<0.01	0.0515
		95	67		97
GOBP_SUBSTRATE_DEPENDENT_CELL_MIGRATION	23	0.7022	2.1453	<0.01	0.0525
		37	79		47
GOBP_ENDODERM_FORMATION	52	0.6366	2.1095	0.002012	0.0531
		54	83		67
HP_ABNORMALLY_LAX_OR_HYPEREXTENSIBLE_SKIN	137	0.5010	2.0724	<0.01	0.0532
		47	41		81
HP_ABNORMAL_CEREBRAL_ARTERY_MORPHOLOGY	59	0.6089	2.0489	0.006085	0.0538
		14	77		72
HP_ABNORMAL_CAROTID_ARTERY_MORPHOLOGY	65	0.5999	2.0511	<0.01	0.0545
		19	23		61
GOBP_POSITIVE_REGULATION_OF_LAMELLIPODIUM_ORGANIZATION	36	0.6068	2.0448	<0.01	0.0549
		53	82		41
GOBP_FC_RECEPTOR_MEDIATED_STIMULATORY_SIGNALING_PATHWAY	84	0.5666	2.0426	<0.01	0.0553
		22	5		65
GOMF_INTEGRIN_BINDING	135	0.5606	2.0731	<0.01	0.0555
		54	43		02
GOBP_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	90	0.5676	2.1500	<0.01	0.0557
		89	18		48
GOBP_EPIBOLY	32	0.6372	2.0768	0.002075	0.0561
		45	09		08
GOBP_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	47	0.5815	2.0789	<0.01	0.0569
		25	44		37
HP_ECHOLALIA	36	0.6015	2.0834	0.001953	0.0572
		1	38		98
GOBP_FORMATION_OF_PRIMARY_GERM_LAYER	108	0.5428	2.0925	<0.01	0.0585
		69	45		25
GOBP_RESPONSE_TO_AMYLOID_BETA	44	0.6158	2.0864	<0.01	0.0586
		68	7		38

HP_OSTEOLYSIS	74	0.5483	2.0955	<0.01	0.0605
		96	36		34
GOBP_CORTICAL_CYTOSKELETON_ORGANIZATION	58	0.5242	2.0349	<0.01	0.0613
		56	93		43
GOCC_LAMELLIPODIUM_MEMBRANE	22	0.7062	2.0325	<0.01	0.0615
		11	24		55
GOBP_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYSIS	42	0.5638	2.0304	<0.01	0.0618
		72	55		59
HP_ABSCESS	48	0.5908	2.0275	<0.01	0.0628
		21	33		26
GOBP_POSITIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	48	0.5967	2.0189	0.006303	0.0656
		47	13		47
GOBP_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	117	0.4608	2.0093	0.002	0.0659
		67	75		63
GOBP_CELLULAR_RESPONSE_TO_AMYLOID_BETA	35	0.6268	2.0028	<0.01	0.0662
		39	54		09
GOBP_NEGATIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	21	0.6953	2.0163	0.002146	0.0663
		01	52		89
GOMF_EXTRACELLULAR_MATRIX_BINDING	53	0.6063	2.0040	0.003876	0.0665
		53	64		79
GOBP_EXTERNAL_ENCAPSULATING_STRUCTURE_ORGANIZATION	386	0.5240	2.0059	<0.01	0.0668
		44	61		3
GOMF_CADHERIN_BINDING	313	0.4914	2.0102	0.004	0.0668
		54	94		48
GOBP_POSITIVE_REGULATION_OF_CELL_SUBSTRATE_ADHESION	118	0.5157	2.0120	<0.01	0.0668
		76	53		56
GOBP_POSITIVE_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	27	0.6204	2.0219	<0.01	0.0671
		42	5		19
GOBP_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	148	0.4494	2.0191	<0.01	0.0672
		95	04		57

GOBP_CELLULAR_RESPONSE_TO_MECHANICAL_STIMULUS	73	0.5314	2.0070	<0.01	0.0674
		24	54		09
HP_PROPTOSIS	229	0.4723	1.9998	<0.01	0.0677
		41			87
GOCC_PODOSOME	28	0.6749	2.0128	<0.01	0.0679
		36	87		59
GOBP_ENTRY_INTO_HOST	151	0.4702	1.9762	0.00211	0.0687
		15	23		12
GOBP_CELL_SUBSTRATE_JUNCTION_ORGANIZATION	106	0.5364	1.9942	<0.01	0.0687
		88	75		44
GOBP_RESPONSE_TO_X_RAY	31	0.6193	1.9784	<0.01	0.0689
		31	85		89
HP_SCALING_SKIN	30	0.6168	1.9891	<0.01	0.0693
		12	35		17
GOCC_LAMELLIPODIUM	192	0.4657	1.9820	0.001984	0.0694
		41	15		38
HP_PREMATURE_LOSS_OF_TEETH	46	0.5510	1.9766	<0.01	0.0695
		56	54		18
GOBP_BASEMENT_MEMBRANE_ORGANIZATION	30	0.6398	1.9898	0.00202	0.0700
		65	09		09
HP_REDUNDANT_SKIN	65	0.5227	1.9841	<0.01	0.0700
		54	07		44
GOBP_RESPONSE_TO_INTERLEUKIN_12	49	0.5828	1.9943	0.001923	0.0700
		94	95		8
HP_ABNORMAL_ARTERIAL_PHYSIOLOGY	125	0.4902	1.9785	0.002037	0.0701
		73	21		32
GOBP_REGULATION_OF_MONOOXYGENASE_ACTIVITY	57	0.5009	1.9793	<0.01	0.0704
		64	61		33
HP_ABNORMAL_ELASTICITY_OF_SKIN	181	0.4568	1.9866	<0.01	0.0704
		08	88		92

HP_DILATATION_OF_THE_CEREBRAL_ARTERY	38	0.6698	1.9821	0.005792	0.0705
		53	37		95
GOBP_REGULATION_OF_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	97	0.4769	1.9904	0.004	0.0706
		58	73		05
HP_SUBCUTANEOUS_NODULE	84	0.4919	1.9847	<0.01	0.0709
		51	65		87
GOBP_POSITIVE_REGULATION_OF_LAMELLIPODIUM_ASSEMBLY	28	0.6358	1.9944	<0.01	0.0715
		4	52		29
HP_CORNEAL_SCARRING	15	0.6834	1.9722	0.002083	0.0718
		7	09		51
GOBP_GASTRULATION	167	0.4604	1.9666	<0.01	0.0733
		79	55		43
GOBP_COLLAGEN_FIBRIL_ORGANIZATION	52	0.7031	1.9670	0.003883	0.0741
		98	13		34
GOBP_ENDODERM_DEVELOPMENT	75	0.537	1.9674	0.001984	0.0748
			8		83
GOBP_REGULATION_OF_CELL_SUBSTRATE_ADHESION	207	0.4795	1.9598	<0.01	0.0779
		35	56		84
GOBP_MOVEMENT_IN_HOST_ENVIRONMENT	173	0.4536	1.9566	0.002119	0.0796
		72	37		4
GOBP_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA_DEATH_DOMAIN_RECEPTORS	55	0.5091	1.9537	<0.01	0.0816
		63	75		4
GOBP_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	46	0.5586	1.9515	<0.01	0.0828
		6	34		66
GOMF_LAMININ_BINDING	28	0.6241	1.9502	0.00207	0.0829
		73	31		96
GOBP_FC_RECEPTOR_SIGNALING_PATHWAY	176	0.4846	1.9470	0.002	0.0853
		23	19		37
GOMF_CELL_ADHESION_MEDIATOR_ACTIVITY	58	0.5244	1.9455	<0.01	0.0860
		59			34

GOBP_POSITIVE_REGULATION_OF_NEURON_DEATH	89	0.4695	1.9283	0.001953	0.0938
		6	55		14
HP_JUVENILE_ASEPTIC_NECROSIS	29	0.5998	1.9339	0.004024	0.0940
		04	71		02
HP_ALOPECIA_OF_SCALP	25	0.6437	1.9288	<0.01	0.0943
		81	54		97
GOBP_POSITIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	146	0.4760	1.9307	0.001992	0.0946
		28	48		27
HP_AVASCULAR_NECROSIS	70	0.4882	1.9201	<0.01	0.0946
		05	82		7
HP_ABNORMAL_MITRAL_VALVE_MORPHOLOGY	111	0.5006	1.9344	0.002033	0.0947
		78	85		54
HP_PREMATURE_LOSS_OF_PRIMARY_TEETH	21	0.6211	1.9209	<0.01	0.0949
		49	04		49
HP_PREMATURELY_AGED_APPEARANCE	121	0.4655	1.9314	0.002033	0.0950
		88	72		94
GOCC_FILOPODIUM_MEMBRANE	18	0.6764	1.9290	<0.01	0.0953
		96	37		76
GOBP_BIOLOGICAL_PROCESS_INVOLVED_IN_INTERACTION_WITH_HOST	215	0.4237	1.9349	<0.01	0.0953
		09	17		96
GOBP_REGULATION_OF_LAMELLIPODIUM_ASSEMBLY	38	0.5708	1.9173	<0.01	0.0956
		39	12		82
GOBP_MYD88_INDEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	34	0.5926	1.9210	0.002033	0.0958
		19	21		66
GOBP_POSITIVE_REGULATION_OF_FIBROBLAST_PROLIFERATION	45	0.5431	1.9124	0.004008	0.0959
		46	81		64
GOBP_PORE_COMPLEX_ASSEMBLY	20	0.6694	1.9354	0.002096	0.0959
		33	81		65
GOCC_COSTAMERE	18	0.6780	1.9220	0.001996	0.0960
		84	91		33

GOBP_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_POLARITY	210	0.4283	1.9252	<0.01	0.0962
		74	78		51
GOMF_PHOSPHOPROTEIN_BINDING	87	0.4705	1.9132	0.001996	0.0962
		63	28		55
GOBP_HOMOTYPIC_CELL_CELL_ADHESION	85	0.4875	1.9176	<0.01	0.0962
		91	51		73
HP_MITRAL_VALVE_PROLAPSE	88	0.5254	1.9138	0.006098	0.0966
		16	21		57
GOBP_ENTRY_OF_BACTERIUM_INTO_HOST_CELL	15	0.7362	1.9241	<0.01	0.0967
		27	7		92
GOBP_WOUND_HEALING	487	0.4265	1.9223	<0.01	0.0969
		51	46		89
GOBP_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	92	0.4756	1.9142	0.003968	0.0971
		69	65		37
GOMF_PROTEASE_BINDING	128	0.4661	1.9229	<0.01	0.0974
		26	95		05
GOBP_REGULATION_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	188	0.4199	1.9143	0.001996	0.0979
		13	98		59
GOBP_ASTROCYTE_ACTIVATION	22	0.6432	1.9071	0.004032	0.0988
		14	11		23
GOBP_ANGIOGENESIS_INVOLVED_IN_WOUND_HEALING	24	0.6316	1.9048	0.003937	0.0991
		84	69		54
HP_ANKYLOSIS	20	0.6341	1.9040	0.002037	0.0991
		84	83		84
GOBP_FIBROBLAST_MIGRATION	41	0.5246	1.9071	0.001992	0.0997
		57	43		92
GOMF_EPHRIN_RECEPTOR_BINDING	27	0.5906	1.9050	<0.01	0.1000
		46	86		12
HP_ABNORMALITY_OF_BLADDER_MORPHOLOGY	55	0.5391	1.9022	0.008163	0.1001
		32	09		84

GOBP_REGULATION_OF_FIBROBLAST_MIGRATION	33	0.5534	1.9074	0.005964	0.1004
		78	36		06
GOBP_TYPE_I_INTERFERON_PRODUCTION	123	0.4746	1.8999	0.002049	0.1017
		62	8		47
GOBP_REGULATION_OF_LAMELLIPODIUM_ORGANIZATION	50	0.5323	1.8982	0.003984	0.1028
		5	43		7
GOBP_CORTICAL_ACTIN_CYTOSKELETON_ORGANIZATION	38	0.5491	1.8960	0.004132	0.1034
		98	7		
HP_BOWING_OF_THE_LEGS	179	0.4302	1.8965	0.001996	0.1038
		1	19		52
GOBP_CARDIAC_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	30	0.6010	1.8939	0.001869	0.1042
		02	02		49
HP_DELAYED_CRANIAL_SUTURE_CLOSURE	61	0.5037	1.8944	0.002016	0.1044
		99	41		82
GOMF_G_PROTEIN_BETA_GAMMA_SUBUNIT_COMPLEX_BINDING	18	0.6331	1.8926	<0.01	0.1045
		76	66		1
GOMF_FIBRONECTIN_BINDING	26	0.6719	1.8912	0.00823	0.1053
		74	08		44
GOBP_POSITIVE_REGULATION_OF_T_CELL_MIGRATION	29	0.6207	1.8886	0.002012	0.1069
		53	41		63
HP_APLASIA_HYPOPLASIA_OF_THE_SKIN	163	0.4269	1.8892	0.001992	0.1070
		67	36		8
GOBP_CELL_SUBSTRATE_ADHESION	345	0.4468	1.8863	<0.01	0.1085
		54	3		79
HP_HALLUX_VALGUS	55	0.5030	1.8832	0.005837	0.1092
		6	38		04
HP_ABNORMALITY_OF_SUBCUTANEOUS_FAT_TISSUE	44	0.5299	1.8837	<0.01	0.1096
		99	46		98
GOBP_PHAGOCYTOSIS	265	0.4713	1.8844	0.006	0.1098
		66	16		12

GOBP_REGULATION_OF_VASCULATURE_DEVELOPMENT	261	0.4442	1.8816	<0.01	0.1102
		71	12		95
HP_MUTISM	52	0.4908	1.8798	0.00198	0.1106
		87	9		18
HP_ARTERIOVENOUS_MALFORMATION	53	0.5568	1.8802	0.006122	0.1109
		67	91		43
GOBP_MEMBRANE_PROTEIN_PROTEOLYSIS	60	0.4839	1.8790	0.003922	0.1110
		47	03		46
GOBP_CELLULAR_RESPONSE_TO_ABIOTIC_STIMULUS	313	0.3817	1.8776	<0.01	0.1117
		83	12		36
GOBP_REGULATION_OF_LEUKOCYTE_ADHESION_TO_VASCULAR_ENDOTHELIAL_CELL	27	0.6081	1.8767	0.002045	0.1118
		45	78		66
GOBP_MAINTENANCE_OF_PROTEIN_LOCATION	91	0.4425	1.8751	<0.01	0.1120
		27	9		56
GOBP_NEGATIVE_REGULATION_OF_EXOCYTOSIS	29	0.5819	1.8735	0.006012	0.1121
		78	25		95
GOBP_PLACENTA_DEVELOPMENT	131	0.4347	1.8757	<0.01	0.1122
		03	41		96
GOCC_ACTIN_FILAMENT_BUNDLE	67	0.5548	1.8737	0.008097	0.1127
		14	52		99
GOBP_ASTROCYTE_DEVELOPMENT	39	0.5589	1.8715	0.005976	0.1136
		6	1		17
GOBP_LEUKOCYTE_ADHESION_TO_VASCULAR_ENDOTHELIAL_CELL	44	0.5702	1.8654	0.004115	0.1138
		76	2		29
HP_BLADDER_DIVERTICULUM	22	0.6874	1.8664	0.014199	0.1144
		2	41		77
HP_PALPEBRAL_EDEMA	35	0.5572	1.8655	0.001961	0.1145
		55	49		49
GOBP_RESPONSE_TO_PLATELET_DERIVED_GROWTH_FACTOR	17	0.6523	1.8695	<0.01	0.1150
		79	02		55

HP_LIPOATROPHY	69	0.4926	1.8666	0.004246	0.1151
		44	09		53
GOCC_BASEMENT_MEMBRANE	92	0.5314	1.8671	<0.01	0.1154
		39	03		74
GOBP_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	210	0.3890	1.8519	0.004115	0.1161
		48	91		19
GOBP_REGULATION_OF_LYMPHOCYTE_CHEMOTAXIS	25	0.6467	1.8673	0.005814	0.1161
		66	2		52
GOBP_FIBROBLAST_PROLIFERATION	78	0.4519	1.8533	0.002028	0.1161
		8	28		66
GOBP_POSITIVE_REGULATION_OF_CELL_SUBSTRATE_JUNCTION_ORGANIZATION	30	0.5932	1.8678	0.004008	0.1164
		24	21		81
GOBP_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	143	0.4438	1.8523	0.001984	0.1165
		94	22		53
GOCC_FILOPODIUM	98	0.4613	1.8510	<0.01	0.1166
		57	54		39
HP_CUTIS_LAXA	95	0.4520	1.8490	0.004228	0.1167
		92	95		5
GOBP_LABYRINTHINE_LAYER_MORPHOGENESIS	19	0.6274	1.8533	0.004124	0.1168
		58	75		86
GOCC_SITE_OF_DOUBLE_STRAND_BREAK	63	0.5329	1.8564	0.004065	0.1168
		95	53		92
HP_ANKLE_FLEXION_CONTRACTURE	41	0.5254	1.8539	0.004024	0.1170
		09	44		25
GOBP_VASCULOGENESIS	76	0.5159	1.8426	0.003984	0.1170
		77	14		25
GOCC_RUFFLE	173	0.4396	1.8501	0.001976	0.1170
		4	1		99
HP_OSTEOARTHRITIS	52	0.5319	1.8544	0.009881	0.1172
		23	34		28

GOBP_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEGRIN	47	0.5278	1.8555	0.009728	0.1172
		11	95		33
GOBP_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	103	0.4998	1.8568	0.00409	0.1172
		42	17		57
GOBP_MODULATION_OF_PROCESS_OF_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERACTION	94	0.4358	1.8481	<0.01	0.1172
		93	96		79
GOBP_REGULATION_OF_T_CELL_MIGRATION	42	0.5584	1.8417	0.003883	0.1172
		01	45		89
GOBP_POSITIVE_REGULATION_OF_CELL_ADHESION	414	0.4464	1.8492	0.004115	0.1173
		7			42
GOBP_MUSCLE_CELL_MIGRATION	76	0.4875	1.8428	0.001961	0.1174
		51	78		28
HP_POOR_WOUND_HEALING	22	0.6892	1.8547	0.013972	0.1175
		87	99		67
GOBP_POSITIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	56	0.5193	1.8610	0.002058	0.1177
		59	1		66
GOBP_POSITIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	49	0.5010	1.8432	<0.01	0.1178
		23	49		06
GOBP_REGULATION_OF_LYMPHOCYTE_MIGRATION	62	0.5410	1.8569	0.003891	0.1178
		53	98		93
GOBP_NEGATIVE_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	79	0.4731	1.8573	0.004065	0.1181
		12	53		97
HP_FACIAL_ASYMMETRY	122	0.4955	1.8612	0.004141	0.1183
		65	3		28
GOBP_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	86	0.5003	1.8433	0.004032	0.1183
		65	62		41
GOBP_EPIDERMAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	119	0.4307	1.8444	0.002058	0.1184
		32	03		34
GOBP_NEGATIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	99	0.4314	1.8599	0.002028	0.1184
		06	38		92

GOBP_GLIAL_CELL_MIGRATION	47	0.5159	1.8459	0.007767	0.1187
		35	35		02
GOCC_FICOLIN_1_RICH_GRANULE	182	0.4735	1.8435	<0.01	0.1188
		92	09		64
GOCC_MEMBRANE_MICRODOMAIN	316	0.4184	1.8574	0.002024	0.1188
		52	81		66
GOMF_EXOGENOUS_PROTEIN_BINDING	77	0.4849	1.8445	0.002016	0.1188
		38	89		76
GOCC_GTPASE_COMPLEX	32	0.5328	1.8581	0.006342	0.1189
		19	67		02
GOBP_REGULATION_OF_ERBB_SIGNALING_PATHWAY	91	0.4398	1.8463	0.00404	0.1190
		03	45		06
GOBP_WOUND_HEALING_SPREADING_OF_EPIDERMAL_CELLS	18	0.6957	1.8585	0.00625	0.1191
		07	57		88
GOBP_CELLULAR_RESPONSE_TO_HEAT	114	0.4906	1.8446	0.001923	0.1194
		43	5		89
HP_SHALLOW_ORBITS	24	0.5592	1.8375	0.001996	0.1207
		02	56		3
GOMF_PROTEOGLYCAN_BINDING	36	0.6084	1.8380	0.002053	0.1209
		25	57		76
HP_LIPODYSTROPHY	105	0.4364	1.8336	<0.01	0.1237
		98	69		29
GOBP_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	166	0.4306	1.8343	<0.01	0.1237
		95	32		48
GOBP_POSITIVE_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	21	0.6194	1.8317	<0.01	0.1247
		95	06		27
GOBP_MUCOPOLYSACCHARIDE_METABOLIC_PROCESS	112	0.4647	1.8310	0.004065	0.1248
		45	3		77
GOBP_POST_ANAL_TAIL_MORPHOGENESIS	15	0.6456	1.8303	0.003824	0.1249
		48	89		93

GOBP_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	66	0.4348	1.8025	0.004115	0.1252
		25	32		81
GOBP_REGULATION_OF_RECEPTOR_BINDING	23	0.5762	1.8016	0.008163	0.1252
		66	32		96
GOCC_FICOLIN_1_RICH_GRANULE_LUMEN	124	0.4992	1.8317	0.00198	0.1254
		26	07		36
HP_TISSUE_ISCHEMIA	96	0.4535	1.8027	0.008316	0.1255
		46	62		45
GOBP_SEMI_LUNAR_VALVE_DEVELOPMENT	41	0.5750	1.7999	0.002053	0.1255
		65	27		99
GOBP_TISSUE_MIGRATION	292	0.4102	1.8016	0.005917	0.1258
		3	61		07
GOBP_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	44	0.5310	1.8030	0.015873	0.1258
		82	01		37
GOBP_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	109	0.4963	1.8005	0.007984	0.1259
		99	68		51
GOBP_REGULATION_OF_CELL_MATRIX_ADHESION	118	0.4568	1.8000	0.001996	0.1260
		75	2		26
GOBP_POSITIVE_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION	23	0.6149	1.8035	0.010142	0.1262
		1	84		34
GOBP_POSITIVE_REGULATION_OF_CELL_MATRIX_ADHESION	53	0.5007	1.8030	0.002037	0.1263
		37	16		55
GOBP_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	16	0.6525	1.8192	0.005917	0.1265
		19	66		19
GOBP_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	101	0.4526	1.8266	0.003937	0.1265
		76	97		35
HP_PROSTATE_NEOPLASM	30	0.5641	1.8180	0.006012	0.1265
		4	3		71
GOBP_MODULATION_BY_HOST_OF_SYMBIONT_PROCESS	60	0.4381	1.8041	0.009398	0.1266
		73	32		6

GOBP_MUSCLE_CELL_PROLIFERATION	172	0.4388	1.8185	0.004098	0.1266
		8	29		85
GOBP_NEGATIVE_REGULATION_OF_BIOMINERALIZATION	26	0.5807	1.8036	0.009785	0.1266
		74	76		92
GOMF_CELL_CELL_ADHESION_MEDIATOR_ACTIVITY	49	0.4996	1.8043	0.001961	0.1269
		92	91		59
GOBP_INTERFERON_BETA_PRODUCTION	50	0.5199	1.8269	0.00996	0.1269
		1	99		62
GOBP_AMINOGLYCAN_BIOSYNTHETIC_PROCESS	114	0.4684	1.8193	0.001996	0.1270
		57	97		21
GOBP_LAMELLIPODIUM_ASSEMBLY	69	0.4655	1.8139	0.005894	0.1271
		27	18		77
GOBP_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	93	0.4139	1.8073	<0.01	0.1273
		92	06		44
GOBP_RESPONSE_TO_VITAMIN_D	31	0.5316	1.8077	0.003899	0.1274
		99	44		4
GOBP_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	64	0.4801	1.8044	0.004065	0.1274
		63	63		47
GOBP_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	22	0.5705	1.8247	0.002066	0.1274
		22	85		75
HP_THORACOLUMBAR_SCOLIOSIS	26	0.6063	1.8066	0.002008	0.1275
		1	61		42
GOBP_POSITIVE_REGULATION_OF_CYTOSKELETON_ORGANIZATION	210	0.3904	1.8194	0.003883	0.1275
		78	86		52
GOCC_COLLAGEN_CONTAINING_EXTRACELLULAR_MATRIX	405	0.4697	1.8270	0.011858	0.1275
		87	35		79
GOBP_CELLULAR_RESPONSE_TO_IONIZING_RADIATION	63	0.4813	1.8139	0.009901	0.1277
		28	18		97
HP_SOFT_SKIN	34	0.5966	1.8046	0.018939	0.1278
		26	29		08

GOBP_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	57	0.4936	1.8197	0.003937	0.1278
		34	51		91
GOBP_REGULATION_OF_INNATE_IMMUNE_RESPONSE	299	0.4432	1.8058	0.007828	0.1279
		66	81		07
GOBP_POSITIVE_REGULATION_OF_PEPTIDYL_THREONINE_PHOSPHORYLATION	30	0.5505	1.8049	<0.01	0.1279
		65	65		67
GOBP_RESPONSE_TO_GAMMA_RADIATION	51	0.5003	1.8077	0.005848	0.1279
		78	89		71
HP_RENAL_DUPLICATION	24	0.5527	1.7963	0.01002	0.1280
		61	53		18
GOBP_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	119	0.4094	1.7976	<0.01	0.1280
		29	43		22
HP_ABNORMALITY_OF_HAND_JOINT_MOBILITY	29	0.5946	1.8272	0.009862	0.1280
		66	36		68
GOBP_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYSIS	23	0.5902	1.8248	0.002123	0.1280
		92	55		85
HP_AORTIC_ANEURYSM	136	0.4431	1.7949	0.00396	0.1282
		53	33		19
GOBP_CARDIAC_MUSCLE_CELL_PROLIFERATION	44	0.5582	1.7956	0.006036	0.1282
		99	97		62
GOBP_NEGATIVE_REGULATION_OF_ERBB_SIGNALING_PATHWAY	51	0.4739	1.8051	0.002049	0.1282
		67	63		66
GOCC_ACTIN_CYTOSKELETON	480	0.3903	1.8083	0.004016	0.1282
		02	83		72
HP_OCULOMOTOR_NERVE_PALSY	25	0.5851	1.7952	0.006329	0.1282
		63	76		82
GOBP_CELLULAR_RESPONSE_TO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_STIMULUS	59	0.5156	1.7965	0.006148	0.1283
		2	59		15
HP_ABNORMAL_PROSTATE_MORPHOLOGY	38	0.5161	1.8199	0.01004	0.1283
		79	32		27

HP_MICROGLOSSIA	16	0.6371	1.8079	0.007605	0.1283
		96	53		34
HP_SOFT_TISSUE_SARCOMA	114	0.4206	1.8139	0.001965	0.1284
		69	21		11
GOBP_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	54	0.5084	1.7967	0.00823	0.1285
		81	26		58
GOBP_CELLULAR_RESPONSE_TO_VITAMIN	29	0.5484	1.8212	0.003899	0.1286
		38	13		08
HP_ACROCYANOSIS	16	0.6261	1.8142	0.00202	0.1286
		25	89		33
HP_LARGE_EARLOBE	20	0.6065	1.8206	0.005747	0.1286
		26	51		54
GOBP_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	143	0.4253	1.8233	0.007663	0.1287
		09	42		46
HP_IRREGULAR_HYPERPIGMENTATION	135	0.4220	1.8084	<0.01	0.1288
		73	44		06
GOBP_CELLULAR_RESPONSE_TO_ACID_CHEMICAL	64	0.4629	1.8093	0.006073	0.1288
		61	11		65
GOBP_BASEMENT_MEMBRANE_ASSEMBLY	15	0.6693	1.8145	0.01227	0.1289
		03	5		08
GOBP_EXTRACELLULAR_MATRIX_DISASSEMBLY	79	0.5001	1.8200	0.007968	0.1289
		25	13		3
HP_ABNORMAL_HEART_VALVE_MORPHOLOGY	275	0.4117	1.8096	0.005941	0.1289
		1	87		51
GOBP_AMEBOIDAL_TYPE_CELL_MIGRATION	396	0.4003	1.8214	<0.01	0.1290
		37	79		5
GOMF_GROWTH_FACTOR_RECEPTOR_BINDING	138	0.4217	1.8154	<0.01	0.1291
		63	49		
HP_RECURRENT_BACTERIAL_SKIN_INFECTIONS	24	0.6721	1.8149	0.008368	0.1291
		89	33		02

HP_PALMAR_HYPERHIDROSIS	17	0.7148	1.8104	0.003953	0.1291
		2	26		65
HP_ABNORMAL_ATRIOVENTRICULAR_VALVE_MORPHOLOGY	130	0.4527	1.8085	0.003937	0.1291
		82	97		72
GOBP_REGULATION_OF_PRESYNAPSE_ORGANIZATION	30	0.5632	1.8099	0.003883	0.1292
		33	57		08
GOMF_NUCLEAR_IMPORT_SIGNAL_RECEPTOR_ACTIVITY	20	0.6613	1.8217	0.003906	0.1293
		25	63		79
GOBP_POSITIVE_REGULATION_OF_LYMPHOCYTE_MIGRATION	36	0.5933	1.8221	0.006	0.1295
		07	02		67
GOBP_ACTIN_POLYMERIZATION_OR_DEPOLYMERIZATION	202	0.3962	1.8105	0.001938	0.1296
		84	37		65
GOBP_CELL_JUNCTION_DISASSEMBLY	20	0.6664	1.8114	0.01	0.1296
		86	19		89
GOBP_SMOOTH_MUSCLE_CELL_MIGRATION	63	0.4953	1.7932	0.003953	0.1298
		49	06		29
HP_PNEUMOTHORAX	40	0.5579	1.8105	0.018036	0.1302
		5	74		57
GOBP_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	29	0.5727	1.7872	0.011881	0.1304
		11	84		95
GOBP_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	122	0.4290	1.7897	0.001984	0.1304
		38	85		98
HP_ABNORMALITY_OF_THE_CALF	229	0.3882	1.7687	0.004008	0.1305
		45	19		69
HP_CONVEX_NASAL_RIDGE	64	0.5214	1.7893	0.002075	0.1306
		04	11		09
GOBP_POSITIVE_REGULATION_OF_MONOOXYGENASE_ACTIVITY	32	0.5077	1.7682	0.010183	0.1306
		66	9		35
GOBP_SMOOTH_MUSCLE_CELL_PROLIFERATION	125	0.4330	1.7678	0.004065	0.1306
		01	95		58

GOBP_OSSIFICATION	369	0.3901	1.7874	<0.01	0.1307
		33	5		22
GOBP_EPITHELIAL_CELL_PROLIFERATION	370	0.3803	1.7916	<0.01	0.1307
		55	93		48
HP_SKIN_NODULE	102	0.4331	1.7903	<0.01	0.1307
		87	47		97
HP_ABNORMAL_ADIPOSE_TISSUE_MORPHOLOGY	189	0.3872	1.7866	<0.01	0.1308
		31	58		26
GOBP_LAMELLIPODIUM_ORGANIZATION	85	0.4469	1.7907	0.003922	0.1308
		42	6		31
HP_ABNORMALITY_OF_TIBIA_MORPHOLOGY	80	0.4380	1.7911	<0.01	0.1308
		19	38		76
GOMF_ACTIN_BINDING	423	0.3929	1.7919	0.004024	0.1309
		24	7		43
GOBP_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	214	0.4279	1.7687	0.012097	0.1309
		34	41		46
GOBP_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	23	0.5701	1.7898	0.002008	0.1309
		18	39		51
GOBP_NUCLEOTIDE_BINDING_OLIGOMERIZATION_DOMAIN_CONTAINING_2_SIGNALING_PATHWAY	15	0.6920	1.7861	0.01004	0.1309
		05	6		63
HP_TIBIAL_BOWING	30	0.5352	1.7707	0.010101	0.1310
		89	16		69
GOBP_REGULATION_OF_T_CELL_CHEMOTAXIS	15	0.6588	1.7875	0.001931	0.1311
		41	77		17
GOCC_EXTRINSIC_COMPONENT_OF_CYTOPLASMIC_SIDE_OF_PLASMA_MEMBRANE	97	0.4124	1.7688	0.002	0.1311
		88	94		26
GOBP_CARDIAC_RIGHT_VENTRICLE_MORPHOGENESIS	19	0.6203	1.7639	0.008097	0.1312
		52	08		5
GOBP_MAINTENANCE_OF_LOCATION	305	0.3643	1.7766	0.00202	0.1312
		13	02		95

GOBP_TRANSFORMING_GROWTH_FACTOR_BETA_PRODUCTION	41	0.5129	1.7881	0.017822	0.1313
		83	91		29
GOBP_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA_STIMULUS	120	0.4343	1.7708	0.005929	0.1313
		16	54		47
GOMF_STRUCTURAL_CONSTITUENT_OF_CYTOSKELETON	95	0.4486	1.7645	0.001992	0.1313
		99	63		64
HP_FEMORAL_BOWING	36	0.5175	1.7700	0.006303	0.1313
		83	35		89
GOBP_REGULATION_OF_NITRIC_OXIDE_METABOLIC_PROCESS	54	0.4820	1.7877	0.004032	0.1314
		71	4		08
GOBP_OVULATION	15	0.6370	1.7693	0.014141	0.1314
		94	49		63
GOBP_POSITIVE_REGULATION_OF_LYMPHOCYTE_CHEMOTAXIS	19	0.6353	1.7689	0.007843	0.1314
		67	47		91
GOBP_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	188	0.4160	1.7696	0.003899	0.1315
		91	75		14
GOBP_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION	45	0.5492	1.7640	0.022312	0.1315
		63	07		88
HP_ABNORMALITY_OF_THE_ACETABULUM	68	0.4652	1.7843	0.00404	0.1316
		09	41		35
GOCC_POSTSYNAPTIC_CYTOSOL	16	0.6360	1.7646	0.01145	0.1316
		05	42		74
GOBP_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	35	0.5491	1.7766	0.003883	0.1316
		45	8		86
GOBP_RENAL_FILTRATION	22	0.6093	1.7708	0.006061	0.1317
		8	55		83
GOBP_CHONDROCYTE_DEVELOPMENT	27	0.5794	1.7649	0.01227	0.1317
		6	15		94
HP_ESOPHAGITIS	26	0.5341	1.7749	0.004057	0.1318
		34	79		48

HP_INTRACRANIAL_HEMORRHAGE	125	0.4157	1.7603	0.00202	0.1318
		16	79		64
HP_UNERUPTED_TOOTH	16	0.6507	1.7771	0.006085	0.1318
		86	59		86
HP_GINGIVAL_OVERGROWTH	95	0.4423	1.7665	0.006036	0.1319
		33	81		02
HP_AORTIC_ROOT_ANEURYSM	72	0.4979	1.7625	0.013672	0.1319
		64	8		29
GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_ADHESION_TO_VASCULAR_ENDOTHELIAL_CELL	20	0.6225	1.7849	0.016563	0.1319
		76	34		35
GOBP_POSITIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	173	0.4033	1.7651	0.001901	0.1319
		25	39		35
GOBP_NEGATIVE_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	23	0.5531	1.7618	0.002037	0.1319
		23	38		58
GOBP_CYTOPLASMIC_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	69	0.4589	1.7654	0.00211	0.1319
		74	23		93
GOBP_CELL_MATRIX_ADHESION	220	0.4397	1.7844	0.006198	0.1319
		8	59		97
GOMF_CYTOKINE_RECEPTOR_BINDING	233	0.4164	1.7608	0.008097	0.1320
		82	84		4
GOBP_VASCULAR_WOUND_HEALING	16	0.6428	1.7752	0.01002	0.1320
		87	01		4
HP ABDOMINAL_AORTIC_ANEURYSM	18	0.6733	1.7657	0.016393	0.1320
		53	92		41
GOBP_POSITIVE_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	42	0.4968	1.7777	0.004024	0.1320
		59	31		51
GOBP_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	110	0.4545	1.7709	0.012024	0.1320
		65	75		59
GOBP_MODULATION_OF_PROCESS_OF_OTHER_ORGANISM	118	0.4142	1.7605	<0.01	0.1321
		05	14		03

HP_GENU_VALGUM	118	0.4328	1.7767	0.00813	0.1321
		48	18		19
GOBP_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	199	0.4185	1.7610	0.002041	0.1321
		73	98		43
HP_ABNORMALITY_OF_THE_KNEE	310	0.3828	1.7754	0.003984	0.1321
		45	71		48
GOBP_RESPONSE_TO_VIRUS	325	0.4001	1.7627	0.008048	0.1321
		11	61		83
GOBP_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	125	0.3953	1.7772	0.003937	0.1321
		67	64		98
HP_ABNORMALITY_OF_THE_HALLUX	161	0.4107	1.7619	0.005882	0.1322
		4	1		99
GOCC_REGION_OF_CYTOSOL	21	0.5890	1.7735	0.003984	0.1323
		01	93		
GOBP_POSITIVE_REGULATION_OF_TRANSCRIPTION_REGULATORY_REGION_DNA_BINDING	22	0.5411	1.7742	0.004032	0.1323
		72	89		07
GOBP_POSITIVE_REGULATION_OF_CELL_DIVISION	77	0.4470	1.7659	0.004175	0.1323
		25	31		18
GOBP_ERBB_SIGNALING_PATHWAY	140	0.4049	1.7718	0.004057	0.1323
		89	18		26
GOBP_RESPONSE_TO_DSRNA	38	0.5006	1.7711	0.008214	0.1323
			03		6
GOBP_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA	242	0.4133	1.7790	0.001938	0.1323
		56	61		62
GOBP_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	94	0.4449	1.7612	0.006148	0.1324
		1	1		04
GOCC_ACTIN_FILAMENT	112	0.4494	1.7793	0.002053	0.1324
		65	83		34
GOCC_CELL_LEADING_EDGE	405	0.3827	1.7777	0.001938	0.1324
		84	8		73

GOBP_VIRAL_LIFE_CYCLE	337	0.3746	1.7738	0.002041	0.1325
		03	05		05
GOMF_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT_CONFERRING_TENSILE_STRENGTH	41	0.6542	1.7720	0.023346	0.1325
		33	14		31
GOBP_CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS	294	0.3662	1.7819	<0.01	0.1326
		74	04		06
GOBP KERATINOCYTE MIGRATION	18	0.6126	1.7712	0.011811	0.1326
		29	27		41
GOBP_ENDOTHELIAL_CELL_MIGRATION	206	0.4172	1.7799	0.005837	0.1326
		19	79		67
HP_DEVIATION_OF_THE_HALLUX	81	0.4575	1.7803	0.008	0.1326
		1	38		89
GOMF_METALLOENDOPEPTIDASE_ACTIVITY	104	0.4432	1.7830	0.004082	0.1327
		91	65		34
HP_SLENDER_LONG_BONE	39	0.4974	1.7779	0.008247	0.1327
		33	27		87
GOBP_TISSUE_REMODELING	160	0.4420	1.7809	0.004049	0.1328
		36	39		03
GOCC_ACTOMYOSIN	68	0.5209	1.7805	0.006048	0.1328
		42	98		38
GOBP_LEUKOCYTE_TETHERING_OR_ROLLING	30	0.5890	1.7720	0.010183	0.1328
		01	97		5
GOBP_MACROPHAGE_DIFFERENTIATION	45	0.5349	1.7793	0.021368	0.1329
		06	97		13
HP_ABNORMAL_AORTIC_VALVE_CUSP_MORPHOLOGY	83	0.4730	1.7820	0.013514	0.1329
		83	74		56
GOBP_POSITIVE_REGULATION_OF_PROTEIN_CONTAINING_COMPLEX_ASSEMBLY	244	0.3692	1.7780	0.003984	0.1331
		6	07		35
GOBP_BIOLOGICAL_PROCESS_INVOLVED_IN_INTERACTION_WITH_SYMBIONT	84	0.4411	1.7810	0.004073	0.1332
		77	11		11

GOBP_RESPONSE_TO_VITAMIN	85	0.4255	1.7721	<0.01	0.1332
		79	63		43
GOCC_PHAGOCYTTIC_VESICLE	133	0.4659	1.7822	0.008147	0.1332
		71	34		93
GOBP_POSITIVE_REGULATION_OF_FOCAL_ADHESION_ASSEMBLY	25	0.5808	1.7724	0.016	0.1334
		19	19		01
GOBP_REGULATION_OF_VASCULAR_ASSOCIATED_SMOOTH_MUSCLE_CELL_PROLIFERATION	50	0.5016	1.7575	0.010309	0.1338
		06	61		82
GOMF_GDP DISSOCIATION INHIBITOR ACTIVITY	16	0.6104	1.7577	0.00813	0.1340
		47	98		06
GOBP_REGULATION_OF_CELL_SUBSTRATE_JUNCTION_ORGANIZATION	69	0.4900	1.7579	0.007843	0.1342
		83	12		2
GOBP_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	394	0.4137	1.7560	0.00404	0.1351
		98	86		81
HP_LYMPHEDEMA	60	0.4560	1.7541	0.004107	0.1367
		56	18		31
GOBP_TOLL LIKE RECEPTOR 4 SIGNALING PATHWAY	39	0.5364	1.7543	0.007968	0.1368
		84	83		54
HP_SHOULDER_DISLOCATION	16	0.6509	1.7501	0.02	0.1368
		57	53		91
GOMF_ACTIN_FILAMENT_BINDING	201	0.4090	1.7536	0.006024	0.1369
		63	29		27
GOBP_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	27	0.5484	1.7511	0.017647	0.1369
		58	08		69
HP_KNEE_FLEXION_CONTRACTURE	70	0.4399	1.7517	0.006452	0.1369
		36			73
GOBP_MESODERM_MORPHOGENESIS	64	0.4644	1.7522	0.002004	0.1369
		51	99		88
HP_PATELLAR_DISLOCATION	48	0.4999	1.7490	0.015686	0.1370
		17	97		73

GOCC_PROTEIN_COMPLEX_INVOLVED_IN_CELL_ADHESION	36	0.6024	1.7493	0.032	0.1371
		51	87		39
GOCC_COLLAGEN_TRIMER	84	0.5383	1.7512	0.027668	0.1371
		88	47		63
GOBP_LYMPH_NODE_DEVELOPMENT	17	0.6148	1.7502	0.008264	0.1371
		83	67		85
GOMF_NUCLEAR_LOCALIZATION_SEQUENCE_BINDING	25	0.6337	1.7496	0.015968	0.1372
		04	16		05
GOBP_STRIATED_MUSCLE_CELL_PROLIFERATION	57	0.5046	1.7505	0.006098	0.1372
		6	41		66
GOBP_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	174	0.3879	1.7517	0.002024	0.1373
		54	31		26
HP_HYDROURETER	65	0.4899	1.7523	0.00994	0.1373
		57	45		56
GOBP_REGULATION_OF_CELL_SHAPE	146	0.4126	1.7525	0.003953	0.1374
		62	6		42
GOBP_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	47	0.5122	1.7479	0.011834	0.1376
		35	17		27
GOBP_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	53	0.5192	1.7526	0.018072	0.1377
		83	78		12
GOMF_CXCR_CHEMOKINE_RECEPTOR_BINDING	17	0.6589	1.7479	0.014493	0.1379
		02	6		78
GOBP_INTEGRIN_ACTIVATION	25	0.5981	1.7459	0.01232	0.1384
		21	5		84
GOBP_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	222	0.4046	1.7454	0.00996	0.1386
		17	99		37
HP_ABNORMALITY_OF_THE_PERIORBITAL_REGION	201	0.3834	1.7459	0.006122	0.1388
		4	55		66
GOBP_REGULATION_OF_EXTRACELLULAR_MATRIX_DISASSEMBLY	16	0.6342	1.7462	0.02	0.1389
		2			28

HP_ABNORMALITY_OF_THE_PHALANGES_OF_THE_HALLUX	37	0.5197	1.7462	0.010204	0.1392
		01	95		12
HP_PERIAURICULAR_SKIN_PITS	44	0.4824	1.7446	0.014286	0.1393
		18	71		24
GOBP_POSITIVE_REGULATION_OF_PROTEIN_POLYMERIZATION	127	0.3911	1.7439	0.00813	0.1397
		08	39		33
HP_TRANSIENT_ISCHEMIC_ATTACK	54	0.4964	1.7433	0.018	0.1400
		16	99		29
HP_DESCENDING_THORACIC_AORTA_ANEURYSM	16	0.6972	1.7347	0.018036	0.1400
		77	44		6
GOMF_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT	164	0.5279	1.7429	0.021869	0.1401
		71	23		88
GOMF_PROTEIN_PHOSPHORYLATED_AMINO_ACID_BINDING	56	0.4745	1.7390	0.011976	0.1403
		28	34		09
HP_JOINT_SUBLUXATION	19	0.6431	1.7347	0.021696	0.1403
		15	8		75
GOBP_T_CELL_MIGRATION	63	0.5260	1.7424	0.021912	0.1404
		17	38		32
HP_URINARY_RETENTION	21	0.5698	1.7373	0.012097	0.1404
		1	78		48
HP_ABNORMAL_MITRAL_VALVE_PHYSIOLOGY	130	0.3889	1.7365	0.009747	0.1404
		75	19		71
GOBP_CELLULAR_RESPONSE_TO_CHEMICAL_STRESS	326	0.3566	1.7376	<0.01	0.1405
		25	01		19
HP_UPPER_EXTREMITY_JOINT_DISLOCATION	87	0.4818	1.7392	0.014085	0.1405
		36	31		26
GOCC_SITE_OF_DNA_DAMAGE	83	0.4935	1.7419	0.012097	0.1405
		68	38		97
HP_ABNORMALITY_OF_THE_CARPAL_BONES	76	0.4566	1.7394	0.016032	0.1406
		73	36		09

GOBP_POSITIVE_REGULATION_OF_VASCULAR_ASSOCIATED_SMOOTH_MUSCLE_CELL_PROLIFERATION	32	0.5117	1.7403	0.012685	0.1406
		58	86		42
GOBP_REGULATION_OF_ACTIN_FILAMENT_ORGANIZATION	256	0.3847	1.7348	0.006	0.1406
		98	31		86
HP_COXA_VARA	54	0.4877	1.7330	0.014	0.1406
		53	63		89
HP_RECTAL_PROLAPSE	27	0.5532	1.7415	0.016563	0.1407
		79	99		03
GOBP_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERATION	36	0.5590	1.7377	0.010204	0.1407
		13	56		04
HP_DYSTROPHIC_FINGERNAILS	31	0.5254	1.7366	0.01341	0.1407
		42	06		16
GOBP_ASTROCYTE_DIFFERENTIATION	69	0.4543	1.7350	0.006276	0.1408
		59	05		5
GOBP_BLOOD_VESSEL_REMODELING	40	0.5024	1.7405	0.004008	0.1408
		18	51		53
GOBP_CENTRAL_NERVOUS_SYSTEM_PROJECTION_NEURON_AXONOGENESIS	26	0.5469	1.7395	0.017442	0.1409
		75	11		12
GOBP_SYNAPTIC_MEMBRANE_ADHESION	25	0.5576	1.7331	0.016097	0.1409
		25	68		15
GOBP_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_SIGNALING_PATHWAY	40	0.5140	1.7352	0.014583	0.1409
		79	28		24
GOBP_NECROPTOTIC_PROCESS	36	0.5091	1.7367	0.012605	0.1409
		5	21		41
GOBP_RAS_PROTEIN_SIGNAL_TRANSDUCTION	332	0.3699	1.7407	0.001957	0.1409
		71	88		43
HP_BOWING_OF_THE_ARM	24	0.5524	1.7358	0.018405	0.1409
		18	37		75
GOBP_RESPONSE_TO_INTERLEUKIN_1	195	0.4277	1.7336	0.002012	0.1409
		56	3		97

GOMF_GROWTH_FACTOR_BINDING	130	0.4470	1.7378	0.013699	0.1410
		25	16		09
HP_NARROW_NOSE	18	0.6284	1.7410	0.005747	0.1410
		64	21		23
GOBP_RECEPTOR_CATABOLIC_PROCESS	36	0.5017	1.7324	0.0125	0.1410
		25	84		84
GOBP_ENDOTHELIAL_CELL_PROLIFERATION	140	0.4150	1.7332	0.003846	0.1411
		59	7		56
GOBP_REGULATION_OF_CELL_SIZE	170	0.3860	1.7353	0.007752	0.1411
		43	27		76
HP_JOINT_HYPERFLEXIBILITY	173	0.4344	1.7379	0.008247	0.1412
		85	35		23
GOBP_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	80	0.4395	1.7395	0.004115	0.1412
		95	19		61
HP_PAPULE	76	0.4530	1.7306	0.012146	0.1414
		23	95		65
GOBP_REGULATION_OF_CELL_AGING	46	0.4892	1.7308	0.003976	0.1416
		89	35		58
HP_ABNORMAL_INTRAOCULAR_PRESSURE	27	0.5419	1.7308	0.01002	0.1420
		69	36		14
HP_SUBCUTANEOUS_HEMORRHAGE	206	0.4099	1.7313	0.010309	0.1421
		53	4		7
HP_PROMINENT_NOSE	73	0.4625	1.7308	0.008163	0.1423
		8	39		68
GOBP_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS	367	0.3693	1.7293	0.00396	0.1424
		38	96		3
GOBP_CELLULAR_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	191	0.4346	1.7287	0.01217	0.1424
		34	75		76
GOCC_CELL_CELL_CONTACT_ZONE	68	0.4319	1.7296	0.01006	0.1425
		84	01		04

HP_HYPEREXTENSIBILITY_OF_THE_KNEE	27	0.5358	1.7289	0.016162	0.1425
		75	66		92
GOBP_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_HEART_DEVELOPMENT	27	0.5525	1.7281	0.013889	0.1428
		01	85		26
HP_ABNORMAL_DIAPHYSIS_MORPHOLOGY	254	0.3732	1.7270	0.006122	0.1432
		21	75		17
GOBP_PLATELET_ACTIVATION	155	0.4262	1.7255	0.00998	0.1432
		74	09		45
HP_LOW_HANGING_COLUMELLA	22	0.5743	1.7250	0.013592	0.1433
		44	91		32
HP_ABNORMAL_PATELLA_MORPHOLOGY	89	0.4804	1.7255	0.014199	0.1435
		92	74		04
GOBP_OSTEOBLAST_DIFFERENTIATION	200	0.3917	1.7259	<0.01	0.1435
		87	36		09
GOBP_ACTIN_FILAMENT_ORGANIZATION	412	0.3658	1.7270	0.005917	0.1435
		62	81		57
HP_ABNORMAL_ATRIOVENTRICULAR_VALVE_PHYSIOLOGY	155	0.3813	1.7273	0.008048	0.1435
		93	34		76
HP_ABNORMAL_SENSORY_NERVE_CONDUCTION_VELOCITY	19	0.5673	1.7261	0.005929	0.1436
		85	82		23
GOBP_NEGATIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	212	0.3836	1.7263	<0.01	0.1436
		84	98		56
GOCC_VESICLE_LUMEN	323	0.3982	1.7245	<0.01	0.1436
		47	49		83
GOBP_AGING	278	0.3616	1.7238	<0.01	0.1438
		43	52		29
GOBP_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	411	0.4019	1.7241	0.019881	0.1438
		83	5		85
HP_ABNORMAL_SPINAL_MENINGEAL_MORPHOLOGY	21	0.6485	1.7233	0.019685	0.1440
		03	73		41

GOBP_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	474	0.3932	1.7229	0.009862	0.1442
		15	6		04
GOBP_LEUKOCYTE_MIGRATION	431	0.4153	1.7217	0.013889	0.1451
		35	39		43
GOBP_PROTEIN_K48_LINKED_UBIQUITINATION	60	0.4697	1.7217	0.006135	0.1454
		37	89		17
HP_ABNORMAL_ORAL_MUCOSA_MORPHOLOGY	277	0.3784	1.7199	0.010395	0.1466
		66	19		8
GOBP_NEGATIVE_REGULATION_OF_CELL_SUBSTRATE_ADHESION	60	0.4690	1.7195	0.011673	0.1467
		9	86		23
GOBP_NEGATIVE_REGULATION_OF_CELL_ADHESION	268	0.4057	1.7201	0.014433	0.1468
		74	07		43
HP_ABNORMALITY_OF_EPIDERMAL_MORPHOLOGY	68	0.4770	1.7190	0.009843	0.1470
		1	38		11
GOMF_DISORDERED_DOMAIN_SPECIFIC_BINDING	30	0.4850	1.7185	0.007752	0.1472
		12	96		66
GOBP_OSTEOCLAST_DEVELOPMENT	16	0.6152	1.7180	0.025743	0.1476
		72	32		65
GOBP_NEGATIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	20	0.5951	1.7164	0.019646	0.1491
		52	14		81
GOBP_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	333	0.4057	1.7149	0.007937	0.1492
		41	92		61
HP_DELAYED_CLOSURE_OF_THE_ANTERIOR_FONTANELLE	25	0.5183	1.7164	0.015656	0.1494
		97	74		41
GOCC_TERTIARY_GRANULE_MEMBRANE	71	0.5141	1.7141	0.034623	0.1495
		04	65		18
GOBP_REGULATION_OF_SUPRAMOLECULAR_FIBER_ORGANIZATION	347	0.3587	1.7150	0.004016	0.1495
		7	23		47
HP_SPINAL_RIGIDITY	52	0.4726	1.7155	0.005964	0.1496
		33	26		33

GOBP_REGULATION_OF_ENDOCYTOSIS	198	0.3715	1.7152	0.003883	0.1496
		57	18		65
GOBP_COAGULATION	311	0.3900	1.7141	<0.01	0.1498
		81	67		51
GOMF_GDP_BINDING	72	0.4677	1.7155	0.005988	0.1499
		47	57		42
GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION	226	0.4408	1.7135	0.012	0.1499
		08	39		62
HP_STRIAE_DISTENSAE	20	0.5944	1.7124	0.022774	0.1500
		38	04		66
GOBP_POSITIVE_REGULATION_OF_STRESS_FIBER_ASSEMBLY	51	0.4478	1.7126	0.00396	0.1500
		94	34		77
GOBP_MAINTENANCE_OF_LOCATION_IN_CELL	200	0.3594	1.7120	0.002037	0.1502
		27	15		08
GOBP_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	179	0.3868	1.7105	0.003868	0.1502
		28	66		71
HP_ABNORMAL_AORTIC_VALVE_MORPHOLOGY	136	0.4162	1.7127	0.004016	0.1502
		2	73		72
HP_ABNORMALITY_OF_THE_HUMERORADIAL_JOINT	43	0.4997	1.7129	0.011905	0.1503
		79	79		64
HP_INCREASED_BONE_MINERAL_DENSITY	92	0.3976	1.7106	0.007663	0.1505
		48	17		72
GOBP_MYELOID_LEUKOCYTE_DIFFERENTIATION	197	0.4110	1.7108	0.014344	0.1506
		1	02		4
HP_ABNORMAL_FALLOPIAN_TUBE_MORPHOLOGY	27	0.5659	1.7108	0.01992	0.1509
		64	36		12
GOBP_POSITIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	78	0.4751	1.7109	0.014315	0.1510
		87	64		91
HP_DIAPHRAGMATIC_WEAKNESS	15	0.6464	1.7096	0.011605	0.1511
		76			21

GOBP_POSITIVE_REGULATION_OF_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	19	0.5811	1.7091	0.013807	0.1513
		43	75		11
GOCC_PLATELET_ALPHA_GRANULE_MEMBRANE	16	0.6330	1.7080	0.025	0.1513
		13	06		98
GOBP_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	144	0.3966	1.7088	0.005941	0.1514
		13	28		21
HP_NAIL_DYSPLASIA	148	0.4015	1.7084	0.009862	0.1514
		25	94		77
GOBP_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_ACTIVITY	46	0.4569	1.7080	0.008529	0.1517
		79	23		13
GOBP_NEGATIVE_REGULATION_OF_ANOIKIS	17	0.5950	1.7069	0.015564	0.1524
		77	16		27
GOBP_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	56	0.4955	1.7001	0.02454	0.1534
		95	11		54
GOCC_CLATHRIN_COAT_OF_COATED_PIT	16	0.6098	1.7001	0.020367	0.1537
		07	54		38
GOBP_EMBRYONIC_PLACENTA_MORPHOGENESIS	23	0.5447	1.7055	0.020325	0.1537
		08	49		9
GOBP_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	150	0.4240	1.7049	0.011952	0.1538
		99	67		53
GOBP_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	27	0.5367	1.6989	0.005859	0.1539
		16	87		17
HP_PREMATURE_SKIN_WRINKLING	50	0.4584	1.7046	0.009785	0.1539
		51	29		53
GOBP_T_CELL_CHEMOTAXIS	24	0.6133	1.7001	0.02045	0.1540
		45	91		03
GOBP_CELLULAR_EXTRAVASATION	69	0.5041	1.7043	0.030992	0.1540
		1	21		19
GOBP_LEUKOCYTE_CELL_CELL_ADHESION	344	0.4417	1.7051	0.028283	0.1540
		17	08		27

GOCC_PLASMA_MEMBRANE_RAFT	110	0.4232	1.6991	0.01341	0.1540
		14	51		27
HP_FRAGILE_NAILS	31	0.5283	1.7029	0.008114	0.1540
		61	96		42
HP_MALE_REPRODUCTIVE_SYSTEM_NEOPLASM	58	0.4554	1.6958	0.012048	0.1540
		92	2		48
GOCC_CLEAVAGE_FURROW	49	0.4729	1.6986	0.012245	0.1540
		09	17		48
GOBP_REGULATION_OF_BONE_MINERALIZATION	71	0.4418	1.7040	0.007843	0.1540
		36	55		54
GOCC_CUL3_RING_UBIQUITIN_LIGASE_COMPLEX	35	0.4706	1.7031	0.012766	0.1541
		77	75		63
GOBP_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	472	0.3465	1.6959	0.002	0.1541
		42	46		86
GOBP_ENDOTHELIAL_CELL_DEVELOPMENT	66	0.4599	1.7033	0.019841	0.1542
		44	81		14
GOCC_EXTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	164	0.3728	1.6992	<0.01	0.1542
		66	8		25
GOBP_CEREBRAL_CORTEX_RADIALY_ORIENTED_CELL_MIGRATION	28	0.5182	1.7002	0.009225	0.1543
		05	12		02
GOBP_PROTEOGLYCAN_METABOLIC_PROCESS	86	0.4496	1.7004	0.021912	0.1543
		31	25		92
HP_DEVIATION_OF_TOES	132	0.4176	1.7035	0.014286	0.1544
		25	01		54
GOBP_POSITIVE_REGULATION_OF_DNA_BINDING	53	0.4398	1.6959	0.002016	0.1544
		07	69		71
HP_PROGRESSIVE_PROXIMAL_MUSCLE_WEAKNESS	16	0.6084	1.6980	0.012	0.1544
		15	04		97
HP_POOR_APPETITE	32	0.4820	1.6935	0.018109	0.1545
		65	65		25

GOMF_CADHERIN_BINDING_INVOLVED_IN_CELL_CELL_ADHESION	18	0.6255	1.6966	0.027778	0.1545
		51	5		84
GOBP_MULTI_ORGANISM_LOCALIZATION	65	0.4932	1.6938	0.011976	0.1545
		79	28		87
HP_PATCHY_HYPOPIGMENTATION_OF_HAIR	17	0.5627	1.6968	0.022312	0.1546
		39	57		48
GOBP_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	189	0.3984	1.7004	0.003906	0.1547
		93	28		1
GOBP_RESPONSE_TO_HEPATOCYTE_GROWTH_FACTOR	18	0.5699	1.6939	0.013699	0.1547
		68	55		37
GOBP_CHONDROITIN_SULFATE_BIOSYNTHETIC_PROCESS	25	0.5775	1.6941	0.023392	0.1547
		31	75		64
GOBP_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_DNA_DAMAGE	98	0.3988	1.6959	0.003854	0.1547
		79	94		71
HP_PULMONARY_ARTERY_DILATATION	28	0.5385	1.6969	0.022774	0.1547
		47	98		8
GOBP_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	174	0.4064	1.6961	0.010183	0.1548
		16	71		62
GOBP_POSITIVE_REGULATION_OF_MACROPHAGE_ACTIVATION	24	0.5818	1.7005	0.015779	0.1548
		14	3		87
GOBP_POSITIVE_REGULATION_OF_AXON_EXTENSION	38	0.4984	1.6971	0.015717	0.1548
		25	65		95
HP_ABNORMALITY_OF_MALE_INTERNAL_GENITALIA	56	0.4323	1.6943	0.008247	0.1549
		43	21		1
GOBP_REGULATION_OF_EXTRACELLULAR_MATRIX_ASSEMBLY	15	0.6311	1.6947	0.026104	0.1550
		46	42		52
HP_ABNORMAL_RECTUM_MORPHOLOGY	97	0.3889	1.6944	0.012	0.1550
		83	5		93
GOBP_MACROPHAGE_ACTIVATION	94	0.4894	1.7006	0.018182	0.1551
		57	1		11

HP_ABNORMALITY_OF_UPPER_LIMB_JOINT	442	0.3643	1.6916	0.005976	0.1551
		28	76		16
HP_THORACIC_AORTIC_ANEURYSM	98	0.4467	1.6972	0.023483	0.1551
		31	05		5
GOBP_REGULATION_OF_ACTIN_FILAMENT_LENGTH	174	0.3748	1.7015	0.007843	0.1551
			92		99
GOBP_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	241	0.4221	1.6917	0.008065	0.1553
		95	77		04
GOBP_POSITIVE_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY	142	0.4053	1.7017	0.001931	0.1553
		74	2		82
HP_INGUINAL_HERNIA	233	0.3958	1.7006	0.015779	0.1554
		11	28		2
GOBP_REGULATION_OF_PHAGOCYTOSIS	89	0.4835	1.6919	0.026694	0.1554
		46	03		31
GOBP_MESENCHYMAL_CELL_DIFFERENTIATION	219	0.3885	1.6920	0.013566	0.1554
		19	96		82
HP_ABNORMALITY_OF_THE_CEREBRAL_VASCULATURE	263	0.3647	1.6892	0.002066	0.1555
		71	87		36
GOCC_SARCOLEMMMA	133	0.4033	1.6904	0.004082	0.1555
		46	74		85
HP_BRUISING_SUSCEPTIBILITY	135	0.4208	1.6924	0.017928	0.1556
		31	63		1
GOBP_STRESS_FIBER_ASSEMBLY	99	0.4240	1.6906	0.008114	0.1556
		64	54		35
HP_DEATH_IN_EARLY_ADULTHOOD	29	0.5291	1.7006	0.024641	0.1557
		37	51		4
GOBP_REGULATION_OF_CYTOSKELETON_ORGANIZATION	484	0.3398	1.6921	0.003861	0.1557
		34	38		41
GOBP_REGULATION_OF_CELLULAR_COMPONENT_SIZE	355	0.3505	1.7009	0.002016	0.1557
		05	1		44

HP_FIBROUS_TISSUE_NEOPLASM	69	0.4317	1.6896	0.011719	0.1557
		01	08		66
GOBP_BIOMINERALIZATION	148	0.3895	1.6893	0.003937	0.1557
		25	26		85
GOBP_POSITIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	161	0.3930	1.6860	0.001988	0.1557
		39	02		87
GOBP_REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	489	0.3433	1.6907	0.003929	0.1558
		8	68		21
GOCC_HOST_CELLULAR_COMPONENT	59	0.5049	1.6900	0.012	0.1558
		53	15		22
GOBP_NEGATIVE_REGULATION_OF_KINASE_ACTIVITY	246	0.3421	1.6897	0.001988	0.1558
		4	5		64
GOBP_POSITIVE_REGULATION_OF_PROTEIN_BINDING	82	0.4020	1.6856	0.00818	0.1558
		83	74		7
HP_SUBARACHNOID_HEMORRHAGE	30	0.5900	1.6860	0.035644	0.1560
		88	32		54
HP_ABNORMAL_SHARPEY_FIBER_MORPHOLOGY	22	0.5337	1.6865	0.009901	0.1562
		45	5		92
GOBP_MYELOID_LEUKOCYTE_CYTOKINE_PRODUCTION	26	0.5237	1.6837	0.027778	0.1563
		82	57		12
GOBP_NEGATIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA_DEATH_DOMAIN_RECE PTORS	38	0.4802	1.6860	0.01227	0.1563
		88	46		36
HP_DISPROPORTIONATE_SHORT_TRUNK_SHORT_STATURE	23	0.5147	1.6876	0.008247	0.1563
		03	85		42
HP_ABNORMALITY_OF_THE_FOREARM	201	0.4039	1.6817	0.004024	0.1563
		2	77		86
GOBP_NEGATIVE_REGULATION_OF_CELL_MATRIX_ADHESION	36	0.5077	1.6866	0.022587	0.1564
		24	95		
HP_HYPERKERATOSIS	236	0.3808	1.6820	0.007937	0.1564
		22	24		07

HP_DISPROPORTIONATE_TALL_STATURE	53	0.4837	1.6841	0.018672	0.1564
		22			29
HP_HOARSE_VOICE	72	0.4144	1.6861	0.012072	0.1564
		67	6		54
HP_PEPTIC_ULCER	24	0.5340	1.6838	0.020408	0.1564
		11	56		57
GOBP_NEGATIVE_CHEMOTAXIS	45	0.4801	1.6834	0.006085	0.1564
		8	11		57
GOBP_AORTIC_VALVE_MORPHOGENESIS	31	0.5622	1.6877	0.016194	0.1565
		14	61		61
GOBP_POSITIVE_REGULATION_OF_ENDOCYTOSIS	97	0.4033	1.6867	0.008081	0.1566
		96	59		17
HP_ABNORMAL_METATARSAL_MORPHOLOGY	119	0.4138	1.6846	0.008247	0.1566
		35	61		31
GOBP_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	17	0.6165	1.6820	0.031683	0.1566
		2	61		39
HP_FLEXION_CONTRACTURE_OF_DIGIT	283	0.3735	1.6848	0.010204	0.1566
		08	6		44
GOBP_HETEROTYPIC_CELL_CELL_ADHESION	59	0.4807	1.6794	0.029703	0.1566
		55	4		54
HP_VASCULAR_DILATATION	181	0.4033	1.6878	0.006135	0.1566
		18	93		71
HP_ARTERIAL_STENOSIS	84	0.4253	1.6841	0.010246	0.1566
		19	19		99
HP_ISCHEMIC_STROKE	24	0.6086	1.6813	0.044266	0.1567
		06	03		04
HP_SOMATIC_MUTATION	158	0.3943	1.6871	0.005929	0.1567
		82	65		24
GOBP_POSITIVE_REGULATION_OF_PROTEIN_DEPHOSPHORYLATION	45	0.4600	1.6869	0.010482	0.1567
		4	07		25

GOBP_REGULATION_OF_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	36	0.5063	1.6796	0.019608	0.1567
		26	14		29
GOBP_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	161	0.4000	1.6824	0.009843	0.1568
		21	12		26
GOBP_TELENCEPHALON_GLIAL_CELL_MIGRATION	21	0.5488	1.6826	0.007547	0.1568
		12			35
GOBP_NEGATIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	275	0.3363	1.6821	0.00202	0.1568
		23	32		5
GOBP_REGULATION_OF_DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	32	0.4985	1.6797	0.012658	0.1568
		33	24		58
HP_ABNORMAL_SCLERA_MORPHOLOGY	97	0.4248	1.6879	0.025292	0.1568
		63	68		76
GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_OR_POLYSACCHARIDE_ANTIGEN_VIA_MHC_CLASS_II	99	0.4343	1.6828	0.013889	0.1568
		56	12		89
GOBP_RESPONSE_TO_HEAT	155	0.4167	1.6841	0.005814	0.1568
		53	89		98
GOBP_AXONAL_FASCICULATION	18	0.5695	1.6799	0.025048	0.1569
		51	05		28
HP_ABNORMALITY_OF_THE_WRIST	123	0.4159	1.6808	0.012121	0.1569
		43	62		78
HP_ABNORMAL_PUPIL_MORPHOLOGY	48	0.4444	1.6800	0.013917	0.1569
		58	85		95
HP_ASCENDING_AORTIC_DISSECTION	21	0.6379	1.6804	0.03006	0.1571
		69	76		07
GOBP_CELL_AGING	98	0.4139	1.6801	0.005976	0.1572
		79	04		6
HP_BLUE_SCLERAE	77	0.4511	1.6733	0.039761	0.1573
		49	81		6
GOBP_INTERLEUKIN_2_PRODUCTION	59	0.5032	1.6764	0.045726	0.1573
		26	31		91

HP_ABNORMALITY_OF_THE_ANKLES	124	0.3857	1.6765	0.008032	0.1574
		32	86		2
GOBP_PLATELET_AGGREGATION	62	0.4525	1.6767	0.017751	0.1574
		27	75		47
GOBP_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	465	0.3236	1.6783	0.002049	0.1575
		14	84		02
GOBP_CELLULAR_PROTEIN_CONTAINING_COMPLEX_LOCALIZATION	19	0.5495	1.6777	0.029412	0.1575
		65	13		21
HP_NAIL_DYSTROPHY	110	0.4174	1.6774	0.007984	0.1575
		96	23		38
HP_HIATUS_HERNIA	27	0.5344	1.6778	0.011788	0.1575
		44	83		89
GOCC_COMPLEX_OF_COLLAGEN_TRIMERS	20	0.7201	1.6734	0.027397	0.1575
		39	15		95
HP_FOLLICULAR_HYPERKERATOSIS	19	0.6410	1.6769	0.031746	0.1576
		78	04		06
HP_ULNAR_DEVIATION_OF_THE_HAND_OR_OF_FINGERS_OF_THE_HAND	45	0.4810	1.6725	0.003976	0.1576
		68	03		44
HP_LIMB_PAIN	29	0.5126	1.6780	0.015534	0.1576
		35	2		89
HP_STILLBIRTH	24	0.5088	1.6784	0.014141	0.1577
		87	03		56
GOBP_LENS_FIBER_CELL_DIFFERENTIATION	30	0.5065	1.6734	0.010121	0.1577
		2	86		79
GOBP_REGULATION_OF_CELL_CELL_ADHESION	415	0.3988	1.6737	0.024	0.1578
		24	16		06
GOBP_CELLULAR_RESPONSE_TO_VITAMIN_D	21	0.5317	1.6727	0.021154	0.1578
		69	6		19
GOBP_CELLULAR_RESPONSE_TO_GAMMA_RADIATION	26	0.5340	1.6769	0.014257	0.1578
		94	31		56

HP_ULNAR_DEVIATION_OF_THE_HAND	15	0.6103	1.6725	0.01217	0.1578
		53	24		83
HP_AORTIC_REGURGITATION	73	0.4091	1.6737	0.020619	0.1580
		94	45		28
HP_ABNORMAL_PROXIMAL_PHALANX_MORPHOLOGY_OF_THE_HAND	24	0.5421	1.6744	0.010183	0.1582
		92	55		62
HP_LEIOMYOSARCOMA	27	0.5135	1.6740	0.008247	0.1582
		87	41		66
GOBP_CYTOPLASMIC_SEQUESTERING_OF_PROTEIN	22	0.5332	1.6737	0.008565	0.1582
		51	81		73
GOBP_REGULATION_OF_COAGULATION	70	0.4744	1.6744	0.012195	0.1584
		9	96		75
HP_URETHRAL_STENOSIS	39	0.4956	1.6740	0.020492	0.1584
		26	77		94
HP_ARNOLD_CHIARI_MALFORMATION	67	0.4638	1.6702	0.018595	0.1586
		03	57		67
HP_THIN_SKIN	74	0.4067	1.6745	0.007937	0.1587
		84	02		48
GOBP_GLOMERULAR_MESANGIUM_DEVELOPMENT	15	0.6654	1.6710	0.026423	0.1588
		13	12		39
GOBP_REGULATION_OF_EXTENT_OF_CELL_GROWTH	102	0.4057	1.6703	0.009506	0.1588
		27	1		87
GOBP_REGULATION_OF_BIOMINERALIZATION	89	0.4167	1.6693	0.009921	0.1588
		83	98		89
GOBP_NIK_NF_KAPPAB_SIGNALING	164	0.4113	1.6705	0.008299	0.1589
		9	16		6
HP_ARTHROPATHY	42	0.5087	1.6750	0.044444	0.1589
		23	34		68
GOMF_NUCLEOCYTOPLASMIC_CARRIER_ACTIVITY	30	0.5854	1.6745	0.015656	0.1590
		66	07		14

GOBP_CHONDROCYTE_DIFFERENTIATION	97	0.4426	1.6706	0.017613	0.1590
		99	69		18
HP_ABNORMALITY_OF_THE_INTERNAL_AUDITORY_CANAL	18	0.5800	1.6697	0.018036	0.1590
		07	22		51
GOBP_EMBRYONIC_PLACENTA_DEVELOPMENT	77	0.4289	1.6710	0.001992	0.1590
		44	51		62
GOBP_FOCAL_ADHESION_ASSEMBLY	85	0.4500	1.6694	0.023622	0.1591
		52	41		19
GOBP_INTERFERON_ALPHA_PRODUCTION	28	0.5700	1.6746	0.022044	0.1591
		94	6		27
GOMF_PHOSPHOTYROSINE_RESIDUE_BINDING	44	0.4904	1.6687	0.032454	0.1594
		7	19		05
GOBP-NLS_BEARING_PROTEIN_IMPORT_INTO_NUCLEUS	19	0.6331	1.6660	0.028283	0.1601
		68	02		08
GOBP_POSITIVE_REGULATION_OF_BINDING	165	0.3714	1.6661	0.004107	0.1601
		95	75		17
HP_JOINT_HYPERMOBILITY	299	0.3971	1.6657	0.01217	0.1601
		4	27		41
GOBP_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY	40	0.5035	1.6661	0.023762	0.1603
		28	94		71
GOBP_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	52	0.4771	1.6662	0.023529	0.1605
		39	88		31
HP_OSTEOPENIA	225	0.3559	1.6670	0.009597	0.1606
		86	68		25
GOBP_INTERLEUKIN_1_PRODUCTION	102	0.4538	1.6666	0.029354	0.1606
		49	26		68
GOBP_REGULATION_OF_CELL_MORPHOGENESIS	298	0.3564	1.6663	0.007828	0.1606
		39	92		8
GOBP_RESPONSE_TO_IONIZING_RADIATION	137	0.4075	1.6671	0.021611	0.1607
		08	97		53

GOBP_NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	24	0.5426	1.6641	0.027559	0.1608
		11	59		16
GOBP_NEGATIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	20	0.5266	1.6644	0.014374	0.1608
		22	92		53
GOBP_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	325	0.3838	1.6672	0.011561	0.1609
		95	81		18
GOBP_REGULATION_OF_WOUND_HEALING	121	0.4196	1.6666	0.01227	0.1609
		51	37		29
GOBP_REGULATION_OF_ANOIKIS	23	0.5238	1.6642	0.018939	0.1610
		02	09		05
GOBP_INTERLEUKIN_17_PRODUCTION	35	0.5210	1.6645	0.032819	0.1610
		12	7		29
GOBP_REACTIVE_NITROGEN_SPECIES_METABOLIC_PROCESS	69	0.4244	1.6638	0.01002	0.1610
		68	17		36
GOBP_NEGATIVE_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	22	0.5665	1.6624	0.043478	0.1611
		17	27		25
HP_ABNORMALITY_OF_THE_RADIAL_HEAD	38	0.5128	1.6646	0.028	0.1612
		31	21		53
GOBP_REGULATION_OF_PROTEIN_POLYMERIZATION	214	0.3499	1.6621	0.009823	0.1612
		92	05		69
HP_ABNORMAL_PHALANGEAL_JOINT_MORPHOLOGY_OF_THE_HAND	189	0.3712	1.6624	0.010438	0.1613
		31	77		22
GOBP_ACTIN_FILAMENT_DEPOLYMERIZATION	57	0.4527	1.6632	0.016227	0.1613
		79	81		91
GOBP_DENDRITIC_SPINE_DEVELOPMENT	97	0.4053	1.6626	0.013944	0.1613
		97	15		98
GOBP_AXON_EXTENSION	113	0.4067	1.6630	0.007533	0.1614
			37		06
GOBP_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	60	0.4332	1.6617	0.010081	0.1614
		6	3		88

GOBP_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	269	0.4332	1.6626	0.034553	0.1615
		08	9		64
GOBP_SPROUTING_ANGIOGENESIS	119	0.4293	1.6608	0.01996	0.1620
		94	29		04
GOBP_ACTIN_FILAMENT_BUNDLE_ORGANIZATION	151	0.3941	1.6609	0.011858	0.1620
		66	93		75
GOBP_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	326	0.3535	1.6587	<0.01	0.1626
		22	43		35
HP_PHONOPHOBIA	15	0.6206	1.6593	0.044534	0.1626
		18	07		92
GOBP_POSITIVE_REGULATION_OF_VASOCONSTRICTION	29	0.5139	1.6570	0.018	0.1627
		21	33		17
HP_LIMITED_HIP_MOVEMENT	54	0.4620	1.6575	0.012048	0.1627
		11	92		26
GOBP_POSITIVE_REGULATION_OF_PHOSPHATASE_ACTIVITY	33	0.5187	1.6588	0.03055	0.1627
		17	57		72
GOBP_MYD88_DEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	35	0.5137	1.6600	0.021611	0.1627
		3	25		81
GOCC_CELL_CORTEX	278	0.3463	1.6577	0.00969	0.1628
		67	17		21
GOBP_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	175	0.3512	1.6571	<0.01	0.1628
		49	03		64
GOCC_ADHERENS_JUNCTION	169	0.3893	1.6578	0.008065	0.1629
		86	26		39
HP_ABNORMAL_STOMACH_MORPHOLOGY	245	0.3500	1.6593	0.006173	0.1629
		79	08		45
HP_ABNORMALITY_OF_THE_PLANTAR_SKIN_OF_FOOT	84	0.4414	1.6572	0.025194	0.1629
		6	14		55
GOBP_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	34	0.4937	1.6588	0.02863	0.1629
		39	97		67

GOBP_T_HELPER_1_CELL_DIFFERENTIATION	18	0.5965	1.6594	0.032787	0.1629
		87	58		9
HP_JOINT_CONTRACTURE_OF_THE_HAND	222	0.3646	1.6563	0.008247	0.1629
		72	09		95
GOBP_CHEMOKINE_PRODUCTION	89	0.4504	1.6581	0.017787	0.1630
		39	5		44
GOBP_VESICLE_DOCKING_INVOLVED_IN_EXOCYTOSIS	44	0.4568	1.6596	0.011742	0.1630
		12	22		66
GOBP_BONE_MINERALIZATION	108	0.4025	1.6564	0.009843	0.1630
		31	79		68
HP_DYSTROPHIC_TOENAIL	21	0.5541	1.6578	0.029412	0.1631
		55	62		46
HP_CONTRACTURES_OF_THE_JOINTS_OF_THE_UPPER_LIMBS	265	0.3562	1.6558	0.010331	0.1633
		6	36		67
GOBP_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	30	0.5779	1.6555	0.02863	0.1634
		27	41		4
GOBP_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	62	0.4532	1.6542	0.031434	0.1641
		58	28		72
HP_CARIOUS_TEETH	138	0.3765	1.6542	0.016097	0.1643
		48	86		61
GOBP_REGULATION_OF_PROTEIN_CONTAINING_COMPLEX_ASSEMBLY	423	0.3246	1.6535	<0.01	0.1644
		18	71		73
GOBP_POSITIVE_REGULATION_OF_CHEMOTAXIS	138	0.4236	1.6536	0.032787	0.1645
		68	74		97
GOCC_PLATELET_ALPHA_GRANULE	89	0.4412	1.6543	0.014553	0.1646
		15			05
HP_ABNORMAL_SHOULDER_MORPHOLOGY	87	0.4198	1.6525	0.01833	0.1654
		08	94		59
GOMF_WIDE_PORE_CHANNEL_ACTIVITY	28	0.5082	1.6514	0.027723	0.1665
		27	38		48

GOBP_POSITIVE_REGULATION_OF_INTERFERON_BETA_PRODUCTION	33	0.4963	1.6509	0.015534	0.1665
		18	74		97
HP_PES_VALGUS	37	0.4710	1.6505	0.018367	0.1665
		02	26		98
GOBP_SALIVARY_GLAND_DEVELOPMENT	31	0.5043	1.6505	0.026915	0.1667
		86	78		99
HP_BLOODY_DIARRHEA	34	0.4884	1.6510	0.02994	0.1668
		55	09		18
HP_ABNORMALITY_OF_THE_ANTERIOR_FONTANELLE	96	0.3956	1.6500	0.020161	0.1669
		33	74		24
HP_PROLONGED_BLEEDING_TIME	43	0.4878	1.6494	0.033531	0.1671
		27	78		95
GOBP_PROTEIN_LOCALIZATION_TO_NUCLEUS	271	0.3691	1.6496	0.004016	0.1672
		07	51		74
HP_CUTIS_MARMORATA	70	0.4364	1.6454	0.013133	0.1673
		83	84		9
GOBP_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	96	0.4154	1.6455	0.016327	0.1675
		02	85		32
GOBP_CRANIAL_SKELETAL_SYSTEM_DEVELOPMENT	63	0.4506	1.6459	0.019881	0.1675
		82	79		59
GOMF_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_ACTIVITY	36	0.5306	1.6457	0.03125	0.1676
		28	07		39
GOBP_MONONUCLEAR_CELL_MIGRATION	180	0.4411	1.6441	0.035433	0.1676
		58	31		57
GOMF_PEPTIDASE_ACTIVATOR_ACTIVITY	43	0.4436	1.6468	0.016807	0.1677
		7	31		12
HP_STENOSIS_OF_THE_EXTERNAL_AUDITORY_CANAL	26	0.5075	1.6460	0.029821	0.1677
		95	09		84
GOBP_NEUROTRANSMITTER_RECEPTOR_LOCALIZATION_TO_POSTSYNAPTIC_SPECIALIZATION_MEMBRANE	19	0.5525	1.6442	0.016461	0.1678
		61	14		16

HP_RADIAL_BOWING	17	0.5687	1.6465	0.037344	0.1678
		8	32		74
GOBP_DETECTION_OF_BIOTIC_STIMULUS	35	0.5457	1.6468	0.038153	0.1679
		35	59		36
GOBP_PRESYNAPSE_ORGANIZATION	49	0.4608	1.6469	0.013359	0.1680
		66	95		12
GOBP_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	247	0.3658	1.6460	0.014228	0.1680
		36	23		2
GOBP_CELL_CHEMOTAXIS	283	0.3952	1.6442	0.029586	0.1680
			24		5
GOBP_L_Glutamate_IMPORT_ACROSS_PLASMA_MEMBRANE	15	0.5914	1.6461	0.033543	0.1680
		74	78		6
GOBP_REGULATION_OF_KERATINOCYTE_PROLIFERATION	34	0.4884	1.6483	0.015355	0.1680
		97	92		7
HP_HEREDITARY_NONPOLYPOSIS_COLORECTAL_CARCINOMA	30	0.5077	1.6470	0.010352	0.1681
		87	85		39
GOMF_GENERAL_TRANSCRIPTION_INITIATION_FACTOR_BINDING	45	0.4793	1.6443	0.020284	0.1681
		85	59		42
HP_CORNEAL_OPACITY	223	0.3513	1.6484	0.00216	0.1682
		3	64		4
GOBP_REGULATION_OF_CELLULAR_RESPONSE_TO_HEAT	78	0.4843	1.6480	0.019763	0.1682
		31	19		55
GOBP_PROTEIN_K63_LINKED_UBIQUITINATION	56	0.4235	1.6475	0.007752	0.1683
		06	71		15
GOBP_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZATION	92	0.3886	1.6445	0.006061	0.1683
		4	96		18
GOCC_CELL_CELL_JUNCTION	472	0.3446	1.6471	0.003914	0.1683
		93	3		49
GOBP_POSITIVE_REGULATION_OF_MACROAUTOPHAGY	57	0.4268	1.6443	0.019231	0.1683
		62	78		73

HP_THIN_RIBS	43	0.4530	1.6421	0.010288	0.1684
		1	22		95
GOBP_CELL_JUNCTION_ASSEMBLY	414	0.3624	1.6475	0.00998	0.1685
		61	97		4
GOBP_L_Glutamate_Transmembrane_Transport	25	0.4969	1.6384	0.027613	0.1685
		47	95		41
HP_PLANTAR_HYPERKERATOSIS	47	0.5148	1.6428	0.047431	0.1685
		38	78		56
GOBP_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	87	0.4084	1.6471	0.011605	0.1685
		09	79		71
GOBP_CELLULAR_RESPONSE_TO_LIPOPROTEIN_PARTICLE_STIMULUS	30	0.5293	1.6426	0.028283	0.1686
		02	37		19
GOMF_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_BINDING	15	0.6426	1.6422	0.042945	0.1686
		59	36		23
GOMF_SUMO_BINDING	15	0.5767	1.6386	0.015748	0.1686
		86	07		46
GOCC_AZUROPHIL_Granule_Lumen	89	0.4217	1.6389	0.021654	0.1686
		71	64		83
GOBP_INTERLEUKIN_1_BETA_PRODUCTION	88	0.4573	1.6407	0.033465	0.1687
		79	42		01
GOBP_NEGATIVE_REGULATION_OF_CHEMOTAXIS	57	0.4389	1.6381	0.017717	0.1687
		02	57		07
GOBP_EMBRYO_IMPLANTATION	44	0.4486	1.6417	0.011742	0.1687
		18	35		36
GOCC_VACUOLAR_LUMEN	167	0.4148	1.6429	0.019763	0.1687
		45	18		4
GOBP_REGULATION_OF_AXONOGENESIS	149	0.3840	1.6415	0.015414	0.1687
		48	38		41
HP_ABNORMAL_UPPER_LIMB_BONE_MORPHOLOGY	392	0.3636	1.6422	0.011881	0.1687
		95	89		89

GOBP_B_CELL_HOMEOSTASIS	27	0.5549	1.6386	0.036885	0.1688
		81	78		1
GOBP_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	27	0.5305	1.6408	0.028866	0.1688
		18	73		15
HP_ABNORMALITY_OF_CRANIAL_SUTURES	278	0.3605	1.6378	0.00409	0.1688
		25	58		73
GOBP_TOLL_LIKE_RECEPTOR_2_SIGNALING_PATHWAY	17	0.5996	1.6411	0.03666	0.1688
		77	91		83
HP_INSOMNIA	41	0.4579	1.6390	0.018789	0.1688
		45	03		92
GOBP_CARTILAGE_DEVELOPMENT	170	0.4027	1.6409	0.017928	0.1689
			94		07
GOBP_POSITIVE_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	17	0.5891	1.6429	0.026316	0.1689
		47	42		44
HP_ABNORMALITY_OF_FEMUR_MORPHOLOGY	231	0.3753	1.6398	0.013889	0.1690
		94	44		79
GOBP_COLLAGEN_METABOLIC_PROCESS	101	0.4405	1.6390	0.031809	0.1690
		79	47		93
GOBP_CARDIAC_ATRIUM_MORPHOGENESIS	27	0.5238	1.6396	0.028902	0.1691
		04	42		03
GOBP_REGULATION_OF_CHEMOTAXIS	212	0.3942	1.6391	0.026694	0.1692
		19	02		67
GOBP_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	261	0.3846	1.6398	0.011881	0.1692
		63	86		87
GOMF_HISTONE_KINASE_ACTIVITY	15	0.6260	1.6392	0.028112	0.1693
		8	03		95
HP_APHASIA	70	0.4149	1.6366	0.014	0.1694
		56	06		08
GOBP_EXTRACELLULAR_MATRIX_ASSEMBLY	44	0.5116	1.6398	0.041667	0.1695
		96	99		12

HP_EXTERNAL_EAR_MALFORMATION	82	0.4381	1.6366	0.020325	0.1695
		28	79		62
GOMF_TBP_CLASS_PROTEIN_BINDING	26	0.5321	1.6370	0.014228	0.1696
		5	21		67
GOBP_EPITHELIAL_CELL_APOPTOTIC_PROCESS	101	0.3945	1.6367	0.006369	0.1696
		51	82		82
GOBP_NEURON_PROJECTION_EXTENSION_INVOLVED_IN_NEURON_PROJECTION_GUIDANCE	37	0.4906	1.6323	0.025794	0.1699
		23	81		18
GOBP_RUFFLE_ORGANIZATION	53	0.4300	1.6321	0.020576	0.1699
		31	18		6
HP_ABNORMALITY_OF_THE_MAXILLA	130	0.3945	1.6315	0.013917	0.1699
		51	08		86
GOBP_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	266	0.3355	1.6316	0.004124	0.1699
		94	94		96
HP_PES_PLANUS	286	0.3680	1.6318	0.009804	0.1701
		02	13		01
HP_ARTHRITIS	186	0.3838	1.6324	0.018557	0.1701
		07	25		09
GOBP_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	37	0.4759	1.6325	0.018828	0.1701
		86	57		81
GOBP_MAINTENANCE_OF_PROTEIN_LOCATION_IN_CELL	63	0.3980	1.6357	0.010438	0.1703
		72	43		14
HP_EXOSTOSES	20	0.5440	1.6326	0.028056	0.1703
		16	28		35
HP_PROMINENT_SUPERFICIAL_BLOOD_VESSELS	26	0.4958	1.6335	0.022634	0.1703
		95	87		37
GOBP_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_SIGNALING_PATHWAY	40	0.4921	1.6329	0.033058	0.1703
		88	9		81
GOBP_ACTIN_FILAMENT_SEVERING	16	0.5616	1.6336	0.01992	0.1704
		38	94		32

GOBP_MESENCHYME_DEVELOPMENT	272	0.3756	1.6327	0.015686	0.1704
		66	1		92
GOBP_NEURAL_CREAST_CELL_DIFFERENTIATION	88	0.4030	1.6338	0.016064	0.1705
		66	05		33
GOBP_MODULATION_BY_VIRUS_OF_HOST_PROCESS	29	0.4885	1.6353	0.025391	0.1705
		51	78		47
HP_HETEROCHROMIA_IRIDIS	19	0.5363	1.6329	0.024291	0.1706
		02	9		17
GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN	187	0.4382	1.6338	0.020284	0.1706
		07	96		64
GOBP_REGULATION_OF_EPIDERMAL_GROWTH_FACTOR_ACTIVATED_RECEPTOR_ACTIVITY	30	0.4603	1.6331	0.029586	0.1706
		08	17		7
GOBP_POSITIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	53	0.4139	1.6349	0.006122	0.1708
		27	69		12
GOBP_CELLULAR_RESPONSE_TO_NUTRIENT	40	0.4469	1.6339	0.017787	0.1708
		86	47		29
GOBP_REGULATION_OF_ACTOMYOSIN_STRUCTURE_ORGANIZATION	91	0.4052	1.6345	0.01417	0.1709
		93	87		9
GOBP_NON_CANONICAL_WNT_SIGNALING_PATHWAY	151	0.3820	1.6341	0.00998	0.171
		97	68		
HP_ASCENDING_TUBULAR_AORTA_ANEURYSM	16	0.5681	1.6339	0.029412	0.1710
		75	56		51
GOBP_NEGATIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	72	0.3900	1.6342	0.006173	0.1711
		36	66		04
GOCC_INTERCALATED_DISC	48	0.4389	1.6296	0.018595	0.1711
		33	63		06
GOBP_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	226	0.3648	1.6297	0.006211	0.1713
		11	06		
GOBP_POSITIVE_REGULATION_OF_CELLULAR_EXTRAVASATION	16	0.5795	1.6298	0.034694	0.1714
		66	35		39

GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	132	0.4207	1.6292	0.036	0.1714
		92	22		77
GOBP_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	289	0.3385	1.6290	0.004024	0.1715
		26	1		26
GOBP_CELLULAR_RESPONSE_TO_OSMOTIC_STRESS	39	0.4330	1.6300	0.014706	0.1716
		58	44		04
GOBP_OSTEOCLAST_DIFFERENTIATION	89	0.4458	1.6286	0.018072	0.1717
		33	52		51
GOCC_MIDBODY	181	0.3777	1.6260	0.017928	0.1719
		8	81		45
GOBP_ANATOMICAL_STRUCTURE_ARRANGEMENT	15	0.5902	1.6252	0.031746	0.1719
		05	91		94
HP_JOINT_LAXITY	200	0.3725	1.6254	0.014463	0.1720
		5	16		25
GOBP_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	319	0.3265	1.6258	0.005952	0.1720
		63	01		52
GOBP_ENDOCARDIAL_CUSHION_FORMATION	24	0.5741	1.6261	0.037549	0.1721
		29	1		45
GOBP_REGULATION_OF_TYPE_I_INTERFERON_MEDIATED_SIGNALING_PATHWAY	33	0.4662	1.6254	0.021696	0.1721
		63	92		73
GOBP_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	129	0.3757	1.6261	0.005747	0.1723
		13	15		75
GOBP_VASCULAR_ENDOTHELIAL_CELL_PROLIFERATION	19	0.5159	1.6246	0.020408	0.1723
		7	38		97
GOBP_RESPONSE_TO_TUMOR_NECROSIS_FACTOR	301	0.3658	1.6262	0.010204	0.1724
		19	42		7
GOBP_NEGATIVE_REGULATION_OF_PHAGOCYTOSIS	20	0.5915	1.6243	0.032854	0.1725
		09	31		48
GOBP_POSITIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR_ACTIVITY	158	0.3706	1.6263	0.020921	0.1726
		53	07		

GOBP_NEURON_RECOGNITION	45	0.4686	1.6246	0.034951	0.1726
		83	39		24
HP_ABNORMALITY_OF_CHROMOSOME_STABILITY	48	0.5297	1.6224	0.048096	0.1726
		87	83		95
GOBP_REGULATION_OF_RESPONSE_TO_WOUNDING	150	0.3933	1.6226	0.010309	0.1727
		75	4		19
GOBP_MEMBRANE_FISSION	15	0.5811	1.6236	0.024242	0.1727
		08	4		26
GOBP_INTERLEUKIN_6_MEDIATED_SIGNALING_PATHWAY	22	0.5483	1.6265	0.04	0.1727
		97	83		5
GOBP_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	93	0.3917	1.6263	0.013487	0.1727
		17	29		97
GOBP_REPRODUCTIVE_SYSTEM_DEVELOPMENT	388	0.3324	1.6237	0.003914	0.1728
		36	23		6
GOBP_MEMBRANE_PROTEIN_INTRACELLULAR_DOMAIN_PROTEOLYSIS	20	0.5445	1.6266	0.033465	0.1728
		99	71		62
GOBP_POSITIVE_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	300	0.3266	1.6272	0.002	0.1728
		23	09		65
GOCC_SPECIFIC_GRANULE	157	0.4106	1.6226	0.031496	0.1729
		13	65		24
GOBP_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	172	0.3963	1.6269	0.028866	0.1729
		77	53		55
HP_ELBOW_FLEXION_CONTRACTURE	72	0.4060	1.6275	0.017964	0.1729
		04	15		74
HP_TEMPORAL_CORTICAL_ATROPHY	19	0.5254	1.6230	0.022312	0.1729
		32	22		88
GOBP_ESTABLISHMENT_OF_TISSUE_POLARITY	121	0.4161	1.6272	0.025692	0.1730
		91	89		04
GOBP_MORPHOGENESIS_OF_A_POLARIZED_EPITHELIUM	142	0.3958	1.6231	0.017964	0.1730
		43	93		07

GOBP_POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	180	0.3693	1.6267	0.006237	0.1730
		89	1		49
GOBP_NEGATIVE_REGULATION_OF_JNK_CASCADE	36	0.4438	1.6213	0.012146	0.1733
		83	45		97
HP_APLASIA_HYPOPLASIA_OF_THE_EYELID	33	0.4847	1.6214	0.02863	0.1735
		75	1		58
GOMF_EPIDERMAL_GROWTH_FACTOR_RECEPTOR_BINDING	33	0.4629	1.6204	0.028261	0.1736
		31	16		82
GOBP_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	75	0.4180	1.6214	0.031434	0.1736
		02	94		85
GOBP_REGULATION_OF_CELLULAR_EXTRAVASATION	33	0.5039	1.6206	0.042084	0.1737
		02	62		95
GOBP_NEURON_PROJECTION_ORGANIZATION	89	0.4005	1.6204	0.007905	0.1738
		17	59		43
GOBP_REGULATION_OF_RECEPTOR_RECYCLING	22	0.4918	1.6206	0.028747	0.1740
		51	76		08
HP_ABNORMAL_BLEEDING	430	0.3426	1.6199	0.004149	0.1740
		79	06		74
GOBP_POSITIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	61	0.4214	1.6193	0.011673	0.1744
		35	74		67
GOBP_REPLICATIVE_SENESCENCE	16	0.5494	1.6155	0.039139	0.1746
		36	69		52
GOBP_AMINOGLYCAN_METABOLIC_PROCESS	169	0.3861	1.6167	0.01848	0.1746
		21	67		88
GOBP_REGULATION_OF_PROTEIN_IMPORT	59	0.4169	1.6156	0.014493	0.1747
		59	97		19
GOBP_POSITIVE_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	94	0.3965	1.6158	0.011742	0.1747
		5	56		3
HP_PSEUDOEPHYSSES	15	0.5962	1.6168	0.033195	0.1748
		77	2		45

HP_ONYCHOGRYPOSIS	22	0.5973	1.6162	0.039526	0.1748
		29	43		96
GOCC_ENDOPLASMIC_RETICULUM_LUMEN	299	0.3902	1.6151	0.034979	0.1749
		16	98		06
GOBP_NEURAL_CREAST_CELL_MIGRATION	54	0.4272	1.6158	0.013699	0.1749
		08	69		38
GOBP_MEMBRANE_INVAGINATION	71	0.4374	1.6163	0.027368	0.1749
		03	47		79
GOMF_CHEMOKINE_RECEPTOR_BINDING	56	0.5004	1.6168	0.041096	0.1749
		52	73		81
HP_ABNORMALITY_OF_THE_ULNA	135	0.4108	1.6159	0.012195	0.1750
		06	82		24
GOBP_BLASTOCYST_GROWTH	19	0.5849	1.6169	0.018519	0.1751
		87	48		05
GOBP_MAINTENANCE_OF_CELL_POLARITY	18	0.5371	1.6186	0.014085	0.1751
		05	54		54
GOBP_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	75	0.4156	1.6139	0.011719	0.1751
		97	66		69
GOBP_PYRUVATE_METABOLIC_PROCESS	143	0.3958	1.6137	0.01004	0.1751
		68	44		95
GOBP_MODULATION_BY_SYMBIONT_OF_HOST_PROCESS	35	0.4581	1.6146	0.029644	0.1751
		75	33		96
GOBP_POSITIVE_REGULATION_OF_MACROPHAGE_MIGRATION	24	0.5579	1.6140	0.043651	0.1752
		51	59		6
GOBP_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	173	0.3596	1.6169	0.006073	0.1753
		02	61		2
GOCC_SECRETORY_GRANULE_MEMBRANE	290	0.3795	1.6146	0.031683	0.1753
		44	8		44
GOBP_HEART_VALVE_DEVELOPMENT	60	0.4841	1.6183	0.028	0.1753
		77	05		82

GOBP_REGULATION_OF_EARLY_ENDOSOME_TO_LATE_ENDOSOME_TRANSPORT	17	0.5798	1.6142	0.038855	0.1753
		73	92		99
HP_WORMIAN_BONES	46	0.4637	1.6140	0.017578	0.1754
		71	75		57
GOBP_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	26	0.5799	1.6170	0.041754	0.1754
		82	16		81
HP_MILD_SHORT_STATURE	20	0.5493	1.6174	0.032946	0.1756
		1	25		23
HP_CUPPED_RIBS	20	0.5433	1.6172	0.033597	0.1756
		1	21		49
GOBP_POSITIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	41	0.4714	1.6132	0.018443	0.1756
		82	01		6
GOBP_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	130	0.3853	1.6170	0.004167	0.1756
		1	22		96
GOBP_REGULATION_OF_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	26	0.4858	1.6175	0.020202	0.1757
		66	07		45
GOBP_RECEPTOR_METABOLIC_PROCESS	162	0.3604	1.6178	0.015936	0.1758
		11	22		01
GOBP_POSITIVE_REGULATION_OF_INTERLEUKIN_17_PRODUCTION	18	0.5940	1.6175	0.03861	0.1759
		61	32		39
GOBP_RESPONSE_TO_OSMOTIC_STRESS	81	0.3805	1.6124	0.01232	0.1761
		58	76		16
HP_ABNORMALITY_OF_THE_ELBOW	230	0.3788	1.6125	0.01626	0.1762
		66	66		29
GOBP_NEGATIVE_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	45	0.4193	1.6104	0.010101	0.1763
		91	16		41
GOBP_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	328	0.3533	1.6104	0.003802	0.1764
		29	91		64
GOBP_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA_DEATH_DOMAIN_RECEPTORS	79	0.3858	1.6105	0.012605	0.1766
		39	1		61

GOBP_ARP2_3_COMPLEX_MEDIATED_ACTIN_NUCLEATION	35	0.4681	1.6118	0.024145	0.1767
		05	17		01
GOBP_MICROTUBULE_ORGANIZING_CENTER_LOCALIZATION	30	0.4931	1.6105	0.02766	0.1768
		18	43		39
GOBP_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	119	0.3980	1.6096	0.014286	0.1768
		56	59		63
GOBP_CELL_CYCLE_G1_S_PHASE_TRANSITION	260	0.3898	1.6097	0.042339	0.1769
		18	27		86
GOMF_GAP_JUNCTION_CHANNEL_ACTIVITY	19	0.5502	1.6105	0.040404	0.1770
		31	48		46
GOCC_CONNEXIN_COMPLEX	19	0.5502	1.6105	0.040404	0.1772
		31	48		63
HP_CHROMOSOME_BREAKAGE	28	0.5664	1.6090	0.038697	0.1773
		1	8		56
GOBP_POSITIVE_REGULATION_OF_AXONOGENESIS	77	0.4123	1.6106	0.020952	0.1773
		68	1		99
GOCC_SITE_OF_POLARIZED_GROWTH	183	0.3736	1.6109	0.01232	0.1774
		05	66		09
HP_OVARIAN_NEOPLASM	64	0.4358	1.6088	0.033195	0.1774
		63	31		64
GOBP_IMMUNE_RESPONSE_REGULATING_SIGNALING_PATHWAY	388	0.3882	1.6107	0.029528	0.1774
		85	33		66
GOBP_DENDRITIC_CELL_MIGRATION	29	0.5752	1.6111	0.046875	0.1774
		28	05		75
GOBP_DEFENSE_RESPONSE_TO_VIRUS	235	0.3861	1.6081	0.025105	0.1778
		26	96		22
GOCC_PHOSPHATASE_COMPLEX	50	0.4451	1.6082	0.031936	0.1779
		59	79		28
HP_ABNORMALITY_OF_THE_ZYGOMATIC_BONE	221	0.3612	1.6076	0.011858	0.1783
		63	42		67

GOBP_RESPONSE_TO_MECHANICAL_STIMULUS	197	0.3558	1.6064	0.004032	0.1789
		29	35		69
HP_ALOPECIA	188	0.3600	1.6037	0.005929	0.1790
		8	73		69
GOBP_POSITIVE_REGULATION_OF_DEPHOSPHORYLATION	58	0.4254	1.6065	0.016701	0.1790
		84	24		88
GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	84	0.4239	1.6066	0.014085	0.1791
		05	6		35
GOCC_TRANS_GOLGI_NETWORK_TRANSPORT_VESICLE	30	0.4739	1.6038	0.03937	0.1791
		54	75		44
HP_ABNORMALITY_OF_THE_GASTRIC_MUCOSA	33	0.4722	1.6044	0.031056	0.1791
		8	08		5
GOBP_POSITIVE_REGULATION_OF_VIRAL_LIFE_CYCLE	32	0.4734	1.6044	0.038855	0.1793
		39	18		57
HP_RAYNAUD_PHENOMENON	20	0.5323	1.6040	0.016563	0.1793
		71	12		83
GOBP_REGULATION_OF_MYELINATION	41	0.4342	1.6044	0.028986	0.1794
		46	77		95
HP_PERSEVERATION	18	0.5286	1.6052	0.031068	0.1795
		01	95		56
HP_ECCHYMOSES	42	0.4480	1.6057	0.028112	0.1796
		95	65		03
HP_FEMORAL_HERNIA	17	0.5621	1.6044	0.040619	0.1797
		83	82		04
GOCC_CELL_DIVISION_SITE	58	0.4321	1.6049	0.037924	0.1797
		75	48		5
GOBP_PLATELET_DEGRANULATION	125	0.4085	1.6053	0.026639	0.1797
		03	05		54
GOBP_CELL_MIGRATION_INVOLVED_IN_HEART_DEVELOPMENT	17	0.5870	1.6045	0.030426	0.1798
		88	41		28

GOBP_PROTEIN_KINASE_B_SIGNALING	243	0.3501	1.6054	0.00404	0.1798
		98	12		45
GOCC_CYTOPLASMIC_SIDE_OF_MEMBRANE	185	0.3329	1.6028	0.006073	0.1800
		01	2		12
GOBP_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	110	0.4126	1.6025	0.022222	0.1802
		23	11		12
HP_DEEP_PHILTRUM	51	0.4513	1.6006	0.025641	0.1818
		52	16		75
GOCC_CAVEOLA	79	0.4121	1.6006	0.025	0.1820
		15	7		32
GOBP_POSITIVE_REGULATION_OF_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	40	0.4621	1.6002	0.024242	0.1821
		62	4		27
HP_JOINT_DISLOCATION	339	0.3536	1.5998	0.013725	0.1821
		61	53		67
GOBP_REGULATION_OF_LEUKOCYTE_MIGRATION	199	0.404	1.6000	0.045635	0.1822
			14		03
GOBP_CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS	227	0.3282	1.5983	0.001942	0.1822
		5	17		4
GOBP_ORGANELLE_MEMBRANE_FUSION	105	0.3642	1.5984	0.01833	0.1822
		75	61		54
HP_PAIN_IN_HEAD_AND_NECK_REGION	32	0.4601	1.5990	0.033268	0.1823
		94	92		04
GOBP_MESODERM_DEVELOPMENT	113	0.3852	1.5994	0.01227	0.1824
		61	46		63
GOBP_NEGATIVE_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	29	0.4436	1.5985	0.027132	0.1825
		85	98		13
GOBP_REGULATION_OF_JUN_KINASE_ACTIVITY	82	0.3774	1.5992	0.007767	0.1825
		51	48		16
GOBP_NEGATIVE_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	130	0.3474	1.5986	0.007859	0.1826
		66	58		57

HP_ABNORMALITY_OF_THE_TARSAL_BONES	104	0.3846	1.5976	0.017408	0.1827
		39	89		52
HP_ABNORMAL_BRAIN_POSITRON_EMISSION_TOMOGRAPHY	28	0.4666	1.5966	0.02381	0.1829
		6	82		99
GOBP_POSITIVE_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	65	0.4212	1.5973	0.02268	0.1830
		06	23		32
GOBP_BRANCHING_INVOLVED_IN_BLOOD_VESSEL_MORPHOGENESIS	31	0.4897	1.5962	0.032064	0.1831
		15			62
HP_ASYMMETRIC_GROWTH	45	0.4378	1.5966	0.032653	0.1832
		63	89		06
HP_LIMITED_ELLOW_MOVEMENT	121	0.3786	1.5966	0.013861	0.1834
		89	99		01
HP_ABNORMAL_AORTIC_VALVE_PHYSIOLOGY	131	0.3664	1.5955	0.027368	0.1836
		85	33		26
HP_ABNORMALITY_OF_BONE_MINERAL_DENSITY	500	0.3111	1.5955	0.005917	0.1837
		3	97		38
GOBP_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	267	0.3327	1.5946	0.01833	0.1840
		1	62		32
GOBP_POSITIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	94	0.4137	1.5946	0.039526	0.1842
		01	77		34
GOMF_HYALURONIC_ACID_BINDING	20	0.5591	1.5947	0.040404	0.1843
		53	52		47
GOBP_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	494	0.3316	1.5937	0.007952	0.1849
		26	66		42
GOBP_POSITIVE_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYSIS	15	0.5668	1.5928	0.039583	0.1853
		36	43		23
HP_ABNORMALITY_OF_PRIMARY_TEETH	58	0.4210	1.5930	0.014	0.1854
		77	89		39
HP_WEIGHT_LOSS	271	0.3350	1.5928	0.002	0.1854
		89	78		94

HP_ABNORMAL_UTERUS_MORPHOLOGY	123	0.4036	1.5924	0.030801	0.1855
		68	79		41
HP_VERTEBRAL_COMPRESSION_FRACTURES	28	0.4998	1.5918	0.030738	0.1862
			01		04
HP_MICRONODULAR_CIRRHOSIS	20	0.5394	1.5914	0.03252	0.1864
		47	76		31
GOMF_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	38	0.4649	1.5903	0.03666	0.1875
		69	74		62
GOBP_BLOOD_VESSEL_ENDOTHELIAL_CELL_PROLIFERATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	22	0.5167	1.5897	0.025794	0.1881
		78	09		41
GOBP_POSTSYNAPSE_ORGANIZATION	156	0.3658	1.5895	0.017613	0.1882
		47	1		08
GOBP_POSITIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	54	0.4545	1.5890	0.039014	0.1885
		01	94		14
GOBP_NEGATIVE_REGULATION_OF_BONE_MINERALIZATION	17	0.5550	1.5879	0.032064	0.1891
		55	97		42
GOCC_EARLY_ENDOSOME_MEMBRANE	153	0.3537	1.5883	0.012024	0.1891
		98	55		47
GOBP_REGULATION_OF_WNT_SIGNALING_PATHWAY	350	0.3358	1.5877	0.005929	0.1891
		58	99		69
GOBP_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	59	0.4249	1.5881	0.037475	0.1892
		73	12		13
GOBP_POSITIVE_REGULATION_OF_CHEMOKINE_PRODUCTION	58	0.4643	1.5884	0.04175	0.1892
		04			87
GOBP_POSITIVE_REGULATION_OF_INTERFERON_ALPHA_PRODUCTION	22	0.5527	1.5868	0.031683	0.1902
		82	12		81
GOBP_ALANINE_TRANSPORT	15	0.5635	1.5866	0.037383	0.1903
		72	25		28
GOCC_CLATHRIN_COAT	44	0.4379	1.5855	0.023904	0.1912
		03	68		12

GOBP_CEREBRAL_CORTEX_DEVELOPMENT	102	0.3919	1.5853	0.019417	0.1913
		54			52
GOBP_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	90	0.3945	1.5838	0.03252	0.1916
		58	03		22
HP_SCARRING	156	0.3490	1.5847	0.008114	0.1916
		49	69		36
GOBP_LEUKOCYTE_APOPTOTIC_PROCESS	99	0.3995	1.5839	0.042169	0.1916
		42	52		43
GOCC_ENDOLYSOSOME	23	0.5275	1.5831	0.035644	0.1916
		02	14		97
HP_DENTAL_CROWDING	84	0.4189	1.5848	0.028169	0.1917
		54	67		23
HP_CACHEXIA	60	0.4068	1.5833	0.02621	0.1918
		13	52		02
GOBP_GLAND_MORPHOGENESIS	109	0.3871	1.5839	0.01833	0.1918
		57	94		08
HP_SELECTIVE_TOOTH_AGENESIS	29	0.4787	1.5831	0.034483	0.1918
		73	77		26
GOBP_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	229	0.3609	1.5825	0.011696	0.1918
		47	9		86
GOBP_REGULATION_OF_MACROPHAGE_DIFFERENTIATION	20	0.5374	1.5834	0.046122	0.1919
		06	17		27
HP_LONG_TOE	30	0.4942	1.5840	0.040404	0.192
		03	06		
GOBP_REGULATION_OF_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	97	0.3790	1.5826	0.023952	0.1920
		75	18		63
GOBP_INTERLEUKIN_6_PRODUCTION	129	0.4278	1.5822	0.039841	0.1920
		43	81		9
GOBP_POSITIVE_REGULATION_OF_ERBB_SIGNALING_PATHWAY	39	0.4556	1.5842	0.018256	0.1921
		96	01		96

HP_DECREASED_MUSCLE_MASS	51	0.4268	1.5812	0.031579	0.1922
		45	25		88
HP_BLADDER_NEOPLASM	35	0.4531	1.5813	0.026316	0.1923
		69	54		75
GOBP_NEGATIVE_REGULATION_OF_AXON_EXTENSION	43	0.4238	1.5806	0.028056	0.1925
		41	92		78
GOBP_REGULATION_OF_STEM_CELL_PROLIFERATION	37	0.4340	1.5808	0.028902	0.1926
		84	14		25
HP_ABNORMALITY_OF_THE_GINGIVA	191	0.3508	1.5801	0.017928	0.1927
		77	07		08
HP_APLASIA_HYPOPLASIA_OF_THE ABDOMINAL_WALL_MUSCULATURE	34	0.4613	1.5803	0.02045	0.1928
		4	06		46
GOBP_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	142	0.4104	1.5801	0.044807	0.1929
		7	14		08
GOBP_NEGATIVE_REGULATION_OF_AXONOGENESIS	65	0.3960	1.5788	0.01992	0.1940
		52	26		51
GOBP_MODULATION_BY_SYMBIONT_OF_ENTRY_INTO_HOST	46	0.4627	1.5779	0.031983	0.1947
		85	69		52
GOBP_RESPONSE_TO_AMPHETAMINE	30	0.4627	1.5780	0.01581	0.1948
		25	29		81
HP_ABNORMALITY_OF_THE_SYNOVIA	299	0.3496	1.5776	0.015504	0.1949
		04	43		91
HP_ABSENT_EARLOBE	15	0.6120	1.5774	0.044922	0.1950
		21	45		41
GOCC_ENDOCYTIC_VESICLE	299	0.3623	1.5769	0.030675	0.1950
		59	27		57
GOBP_ACTIVATION_OF_MAPKK_ACTIVITY	50	0.4322	1.5761	0.022044	0.1954
		14	4		64
HP_INCREASED_INTRACRANIAL_PRESSURE	75	0.3925	1.5762	0.014056	0.1955
		11	4		7

HP_ABNORMAL_CORTICAL_BONE_MORPHOLOGY	67	0.3977	1.5763	0.032129	0.1956
		07	14		75
GOBP_REGULATION_OF_MAP_KINASE_ACTIVITY	298	0.3198	1.5737	0.003984	0.1962
		71	9		16
HP_ABNORMAL_RIGHT_VENTRICULAR_FUNCTION	18	0.5348	1.5742	0.031712	0.1962
		01	22		39
GOBP_CENTRAL_NERVOUS_SYSTEM_NEURON_AXONOGENESIS	35	0.4638	1.5738	0.03675	0.1963
		65	64		17
GOBP_AXON_DEVELOPMENT	495	0.3369	1.5740	0.01145	0.1963
		81	17		2
HP_SKIN_ULCER	111	0.3882	1.5752	0.040816	0.1964
		93	01		31
HP_ABNORMAL_ESOPHAGUS_MORPHOLOGY	171	0.3646	1.5742	0.014493	0.1964
		45	3		43
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	122	0.4070	1.5746	0.042424	0.1965
		18	21		56
GOBP_POSITIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	34	0.4515	1.5747	0.017682	0.1966
		67	22		51
GOBP_NUCLEOTIDE_PHOSPHORYLATION	126	0.3842	1.5743	0.010504	0.1966
		31	89		69
HP_PECTUS_EXCAVATUM	246	0.3669	1.5732	0.030426	0.1967
		94	5		18
GOBP_POSITIVE_REGULATION_OF_NITRIC_OXIDE_METABOLIC_PROCESS	36	0.4595	1.5747	0.042683	0.1967
		88	88		85
GOBP_SPINDLE_LOCALIZATION	51	0.4681	1.5728	0.040241	0.1968
		77	77		07
GOBP_KERATINOCYTE_PROLIFERATION	45	0.4432	1.5725	0.027397	0.1968
		73	04		66
GOBP_NEURON_DEATH	329	0.3182	1.5720	0.004024	0.1969
		72	92		42

GOBP_REGULATION_OF_MEMBRANE_INVAGINATION	16	0.5773	1.5728	0.038855	0.1969
		31	93		91
GOBP_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	118	0.4107	1.5718	0.038314	0.1970
		73	41		58
HP_ABNORMALITY_OF_DENTAL_STRUCTURE	272	0.3353	1.5710	0.008081	0.1975
		8	16		45
GOBP_CHONDROITIN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	42	0.4578	1.5711	0.031683	0.1975
		73	62		58
GOBP_CELL_CELL_JUNCTION_ORGANIZATION	200	0.3579	1.5703	0.013972	0.1978
		23	53		5
GOBP_NEGATIVE_REGULATION_OF_MAPK_CASCADE	162	0.3311	1.5706	0.010142	0.1978
		57	16		65
HP_MICRODONTIA	109	0.3658	1.5704	0.01996	0.1979
		61	47		4
HP_RENAL_CELL_CARCINOMA	69	0.3855	1.5699	0.027723	0.1982
		32	28		1
GOBP_RESPONSE_TO_NUTRIENT	160	0.3486	1.5695	0.008282	0.1985
		56	27		53
GOBP_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	28	0.4785	1.5679	0.026531	0.1987
		82	74		42
HP_FINE_HAIR	64	0.4127	1.5687	0.033932	0.1987
		56	58		43
HP_LIMITED_ELBOW_EXTENSION	34	0.4777	1.5677	0.035088	0.1988
		62	49		22
GOBP_PEPTIDYL_TYROSINE_MODIFICATION	356	0.3378	1.5688	0.014199	0.1988
		27	25		75
GOBP_POSITIVE_REGULATION_OF_PROTEOLYSIS	349	0.3167	1.5679	0.005976	0.1989
		24	82		33
HP_HYPERLORDOSIS	173	0.3710	1.5688	0.019841	0.1990
		84	59		4

GOBP_EXOCRINE_SYSTEM_DEVELOPMENT	40	0.4499	1.5672	0.026971	0.1990
		6	57		47
HP_DYSPHASIA	53	0.4059	1.5679	0.023529	0.1991
		09	88		33
HP_ABNORMAL_HEART_VALVE_PHYSIOLOGY	291	0.3281	1.5673	0.01	0.1991
		25	14		8
GOBP_FIBROBLAST_APOPTOTIC_PROCESS	20	0.5185	1.5668	0.046967	0.1992
		22	91		96
GOBP_GRANULOCYTE_CHEMOTAXIS	120	0.4167	1.5679	0.049603	0.1993
		36	97		21
GOBP_RESPONSE_TO_ACID_CHEMICAL	112	0.3551	1.5664	0.011561	0.1993
		39	21		25
GOBP_RAC_PROTEIN_SIGNAL_TRANSDUCTION	38	0.4401	1.5666	0.036961	0.1993
		03	82		67
GOBP_NEGATIVE_REGULATION_OF_WOUND_HEALING	69	0.4428	1.5664	0.024341	0.1994
		19	9		61
GOBP_NEGATIVE_REGULATION_OF_PHOSPHORYLATION	373	0.3082	1.5661	0.002004	0.1994
		53	75		83
GOBP_CELL_DEATH_IN_RESPONSE_TO_OXIDATIVE_STRESS	78	0.3708	1.5655	0.01	0.2001
		49	04		85
HP_ABNORMALITY_OF_THE_METAPHYSIS	200	0.3397	1.5647	0.01165	0.2006
		38	26		22
GOMF_PHOSPHATIDYLINOSITOL_3_KINASE_BINDING	32	0.4970	1.5650	0.049808	0.2006
		43	17		46
HP_BONE_CYST	28	0.4486	1.5648	0.034261	0.2007
		47	08		
GOBP_ENDOTHELIUM_DEVELOPMENT	125	0.4067	1.5643	0.041257	0.2008
		9	89		8
GOBP_POSITIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	61	0.4116	1.5639	0.034413	0.2010
		61	5		54

GOBP_CEREBRAL_CORTEX_CELL_MIGRATION	38	0.4403	1.5639	0.024482	0.2012
		28	53		53
GOBP_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	68	0.4256	1.5634	0.039448	0.2012
		29	42		8
GOCC_PLATELET_ALPHA_GRANULE_LUMEN	66	0.4375	1.5629	0.03112	0.2015
		61	56		02
GOCC_EARLY_ENDOSOME	364	0.3223	1.5626	0.007968	0.2016
		22	87		64
HP_THICKENED_SKIN	394	0.3226	1.5621	0.008016	0.2021
		61	73		68
GOBP_MEMBRANE_BIOGENESIS	40	0.4193	1.5616	0.041494	0.2024
		7	56		14
HP_ABNORMAL_UMBILICUS_MORPHOLOGY	253	0.3645	1.5607	0.026	0.2026
		76	04		09
HP_DIMINISHED_MOTIVATION	76	0.3808	1.5613	0.022358	0.2026
		66	09		5
HP_ABNORMAL_CRANIAL_NERVE_PHYSIOLOGY	282	0.3154	1.5610	<0.01	0.2026
		89	03		62
HP_LACK_OF_SKIN_ELASTICITY	41	0.4437	1.5603	0.040856	0.2026
		62	43		65
HP_PORENCEPHALIC_CYST	25	0.4781	1.5601	0.047431	0.2027
		51	03		49
GOCC_AZUROPHIL_GRANULE	150	0.3883	1.5610	0.039063	0.2028
		75	6		01
GOBP_CARDIAC_VENTRICLE_DEVELOPMENT	109	0.4024	1.5603	0.027944	0.2028
		1	84		12
GOBP_REGULATION_OF_POSTSYNAPSE_ORGANIZATION	84	0.3886	1.5593	0.015564	0.2032
		95	92		49
GOCC_ENDOLYSOSOME_MEMBRANE	15	0.5623	1.5580	0.035639	0.2032
		18	12		51

GOBP_RESPONSE_TO_TEMPERATURE_STIMULUS	220	0.3397	1.5581	0.015209	0.2032
		69	62		61
HP_TALL_STATURE	173	0.3726	1.5594	0.017751	0.2033
		96	81		43
GOMF_GTPASE_BINDING	214	0.3407	1.5582	0.024096	0.2033
		35	46		69
GOBP_CELL_CELL_SIGNALING_BY_WNT	496	0.3181	1.5588	0.013725	0.2033
		81	2		94
HP_PROTRUDING_EAR	161	0.3729	1.5586	0.033333	0.2034
		86	67		25
GOBP_DENDRITIC_SPINE_MORPHOGENESIS	59	0.4093	1.5589	0.022	0.2034
		71	17		58
GOBP_PROTEIN_POLYMERIZATION	282	0.3162	1.5583	0.01581	0.2034
		43	01		94
GOBP_POSITIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	26	0.4865	1.5575	0.03252	0.2035
		35	79		83
HP_ABNORMALITY_OF_THE_COLUMELLA	51	0.4364	1.5561	0.04931	0.2046
		3	15		48
GOBP_ACTIVATION_OF_INNATE_IMMUNE_RESPONSE	139	0.4016	1.5562	0.02994	0.2046
		06	36		72
HP_ABNORMALITY_OF_LIMB_EPIPHYSIS_MORPHOLOGY	98	0.3896	1.5559	0.039419	0.2047
		41	04		35
GOBP_NEGATIVE_REGULATION_OF_PLATELET_ACTIVATION	17	0.5568	1.5565	0.037549	0.2047
		19	08		66
GOBP_PLACENTA_BLOOD_VESSEL_DEVELOPMENT	28	0.4658	1.5562	0.033865	0.2048
		77	4		63
HP_PSORIASIFORM_DERMATITIS	25	0.5088	1.5549	0.045175	0.2056
		14	3		25
GOBP_NEGATIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION	466	0.2971	1.5537	0.008163	0.2063
		63	38		56

HP_METATARSUS_ADDUCTUS	42	0.4432	1.5537	0.043738	0.2065
		64	6		21
GOBP_SPHINGOLIPID_MEDIATED_SIGNALING_PATHWAY	15	0.5381	1.5533	0.042945	0.2067
		37	07		17
GOBP_POSITIVE_REGULATION_OF_PLASMA_MEMBRANE_BOUNDED_CELL_PROJECTION_ASSEMBLY	102	0.3615	1.5522	0.020243	0.2077
		86	97		25
GOBP_HEART_GROWTH	80	0.4076	1.5514	0.018036	0.2079
		92	13		2
HP_DYSCALCULIA	21	0.4951	1.5514	0.039848	0.2080
		06	89		07
GOBP_CRANIAL_NERVE_MORPHOGENESIS	24	0.5111	1.5516	0.045455	0.2082
		23	38		03
GOBP_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_GROWTH	23	0.4997	1.5510	0.033058	0.2082
		76	22		56
GOBP_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	271	0.3618	1.5499	0.041584	0.2093
		41	29		05
HP_ABNORMALITY_OF_THE_CALCANEUS	27	0.4717	1.5499	0.035382	0.2094
		95	68		55
GOBP_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	181	0.3754	1.5493	0.042424	0.2098
		81	74		99
HP_ABNORMALITY_OF_THE ABDOMINAL_WALL	432	0.3414	1.5491	0.016032	0.2099
		2	92		42
GOBP_REGULATION_OF_CELL_DEVELOPMENT	462	0.3209	1.5484	0.007519	0.2103
		19	52		52
GOCC_RECYCLING_ENDOSOME_MEMBRANE	83	0.3823	1.5480	0.01626	0.2104
		51	86		01
GOBP_RESPONSE_TO_INTERLEUKIN_6	41	0.4415	1.5482	0.032854	0.2104
		83	09		53
HP_APLASIA_HYPOPLASIA_OF_THE_FIBULA	25	0.4924	1.5450	0.04499	0.2108
		04	86		28

GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	90	0.4097	1.5451	0.044715	0.2109
		08	12		98
GOBP_BONE_DEVELOPMENT	187	0.3619	1.5452	0.025391	0.2110
		57	18		77
HP_ABNORMAL_AUDITORY_EVOKED_POTENTIALS	16	0.5346	1.5459	0.032454	0.2111
		85	13		35
GOBP_PINOCYTOSIS	22	0.4924	1.5460	0.047431	0.2111
		81	31		67
GOBP_REGULATION_OF_NEURON_PROJECTION_REGENERATION	28	0.4651	1.5455	0.041237	0.2111
		87	85		85
GOBP_MYELOID_CELL_DEVELOPMENT	65	0.4078	1.5473	0.035573	0.2112
		34	69		19
GOBP_NEGATIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	47	0.4319	1.5445	0.047619	0.2112
		85	98		73
HP_DECREASED_SKULL_OSSIFICATION	31	0.4487	1.5460	0.028986	0.2113
		93	47		42
GOBP_CONNECTIVE_TISSUE_DEVELOPMENT	223	0.3704	1.5470	0.024242	0.2113
		56	51		48
GOBP_NEGATIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS	47	0.4125	1.5453	0.02834	0.2113
		51	04		61
HP_LIMITATION_OF_JOINT_MOBILITY	357	0.3275	1.5461	0.014028	0.2116
		2	28		32
HP_URETHRAL_OBSTRUCTION	49	0.4352	1.5464	0.044968	0.2117
		9	98		1
GOBP_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	15	0.5704	1.5433	0.047525	0.2117
		57	11		73
GOBP_HYALURONAN_METABOLIC_PROCESS	37	0.4503	1.5433	0.043197	0.2118
		54	92		6
GOBP_GLOMERULAR_EPITHELIAL_CELL_DIFFERENTIATION	20	0.5195	1.5434	0.042194	0.2119
		59	94		18

HP_ABNORMALITY_OF_CORNEAL_SIZE	146	0.3621	1.5437	0.020284	0.2120
		51	1		27
HP_EXCESSIVE_WRINKLED_SKIN	33	0.4451	1.5435	0.028112	0.2120
		36	33		53
HP_APLASIA_HYPOPLASIA_INVOLVING_THE_METACARPAL_BONES	113	0.3798	1.5427	0.031496	0.2123
		56	03		77
HP_APLASIA_HYPOPLASIA_OF_THE_CLAVICLES	47	0.4060	1.5412	0.025862	0.2123
		21	29		94
HP_CARDIOVASCULAR_CALCIFICATION	32	0.4370	1.5412	0.031983	0.2125
		81	82		24
GOBP_ARTERY_DEVELOPMENT	86	0.4226	1.5416	0.044747	0.2126
		27	28		11
GOBP_REGULATION_OF_BINDING	344	0.3110	1.5404	0.006048	0.2126
		58	58		63
GOBP_MESODERMAL_CELL_DIFFERENTIATION	29	0.4786	1.5418	0.02621	0.2127
		56	57		21
HP_ABNORMAL_FEMORAL_NECK_HEAD_MORPHOLOGY	156	0.3683	1.5423	0.030242	0.2127
		7	06		36
GOBP_AMYLOID_PRECURSOR_PROTEIN_METABOLIC_PROCESS	69	0.3684	1.5421	0.017787	0.2127
		45	31		63
GOBP_INFLAMMATORY_CELL_APOPTOTIC_PROCESS	19	0.4930	1.5393	0.027888	0.2127
		53	65		79
GOBP_NEGATIVE_REGULATION_OF_LOCOMOTION	294	0.3423	1.5419	0.034951	0.2127
		79	69		79
GOBP_SECRETORY_GRANULE_ORGANIZATION	32	0.4247	1.5388	0.018828	0.2128
		35	68		61
GOBP_NEGATIVE_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS	483	0.2948	1.5395	<0.01	0.2128
		86	75		79
GOBP_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	85	0.3858	1.5377	0.021654	0.2129
		22	34		18

GOBP_ACTOMYOSIN_STRUCTURE_ORGANIZATION	182	0.3670	1.5378	0.027944	0.2129
		92	45		73
GOBP_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	274	0.3262	1.5375	0.018672	0.2129
		87	5		91
GOMF_PEPTIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	35	0.4517	1.5395	0.027668	0.2130
		68	93		49
GOBP_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	103	0.3800	1.5398	0.02834	0.2130
		13	59		52
HP_ABNORMALITY_OF_SKULL_OSSIFICATION	37	0.4278	1.5399	0.03006	0.2130
		61	93		53
GOBP_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	86	0.4148	1.5397	0.042596	0.2130
		65	06		64
GOBP_REGULATION_OF_PEPTIDYL_THREONINE_PHOSPHORYLATION	46	0.4180	1.5372	0.027668	0.2131
		19	89		23
HP_ABNORMAL_TRICUSPID_VALVE_PHYSIOLOGY	55	0.4140	1.5380	0.025641	0.2131
		28	06		66
HP_STROKE	134	0.3535	1.5389	0.00996	0.2131
		61	43		7
GOBP_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	17	0.5707	1.5381	0.044118	0.2131
		4	47		76
GOMF_TRANSMEMBRANE_RECEPTOR_PROTEIN_KINASE_ACTIVITY	79	0.4106	1.5364	0.038536	0.2136
		25	88		58
HP_PLATYSPONDYLY	108	0.3821	1.5358	0.033543	0.2140
		41	51		98
GOBP_REGULATION_OF_BODY_FLUID_LEVELS	460	0.3264	1.5359	0.016162	0.2142
		5	03		24
HP_OLIGODONTIA	46	0.4334	1.5354	0.04466	0.2143
		8	73		86
GOMF_INSULIN_LIKE_GROWTH_FACTOR_BINDING	23	0.4968	1.5350	0.045726	0.2147
		53	13		69

GOBP_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	57	0.4304	1.5347	0.03125	0.2148
		05	19		
GOMF_ATPASE_BINDING	83	0.3703	1.5341	0.029644	0.2151
		08	64		4
HP_ABNORMALITY_OF_THE_METACARPAL_BONES	183	0.3543	1.5342	0.023622	0.2152
		62	54		23
GOBP_ESTABLISHMENT_OF_CELL_POLARITY	135	0.3598	1.5335	0.029703	0.2154
		81	04		1
GOBP_REGULATION_OF_HEART_GROWTH	61	0.4100	1.5332	0.019802	0.2154
		21	11		37
GOBP_POSITIVE_REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTION	32	0.4717	1.5329	0.047438	0.2154
		27	25		38
HP_COXA_VALGA	82	0.3997	1.5333	0.037475	0.2154
		45	03		94
GOCC_GAP_JUNCTION	29	0.4665	1.5325	0.049281	0.2157
		66	8		15
GOBP_REGULATION_OF_ORGAN_GROWTH	85	0.3962	1.5213	0.024096	0.2159
		89	07		62
HP_ADDUCTED_THUMB	82	0.3726	1.5231	0.025591	0.2159
		74	6		78
HP_HYPOPLASIA_OF_TEETH	79	0.3879	1.5213	0.035417	0.2161
		38	31		
HP_LOWER_EXTREMITY_JOINT_DISLOCATION	262	0.3461	1.5247	0.027344	0.2161
		86	44		46
GOBP_RESPONSE_TO_INCREASED_OXYGEN_LEVELS	29	0.4386	1.5251	0.030675	0.2161
		12	9		46
GOBP_NEGATIVE_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	125	0.3401	1.5207	0.027668	0.2161
		74	3		62
GOBP_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	95	0.3419	1.5233	0.011834	0.2161
		45	06		68

HP_DENTAL_MALOCCLUSION	109	0.3679	1.5197	0.026531	0.2162
		55	49		36
GOBP_POSITIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	187	0.3348	1.5192	0.020492	0.2162
		47	24		38
GOBP_POSITIVE_REGULATION_OF_MAPK_CASCADE	497	0.3142	1.5213	0.02	0.2162
		3	48		4
GOMF_PROTEIN_TYROSINE_SERINE_THREONINE_PHOSPHATASE_ACTIVITY	41	0.3867	1.5244	0.021611	0.2162
		69	01		56
HP_ORTHOSTATIC_HYPOTENSION	39	0.4182	1.5245	0.037109	0.2163
		69	03		15
HP_METAPHYSEAL_IRREGULARITY	43	0.3955	1.5227	0.032075	0.2163
		43	67		21
GOBP_NEGATIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	93	0.3933	1.5305	0.04175	0.2163
		39	49		31
HP_ANONYCHIA	60	0.4135	1.5233	0.03719	0.2163
		58	23		35
GOBP_NEURON_PROJECTION_GUIDANCE	272	0.3504	1.5254	0.029126	0.2163
		31	41		37
HP_CORNEAL_DYSTROPHY	29	0.4492	1.5315	0.040816	0.2163
		9	37		55
GOMF_GTPASE_ACTIVITY	294	0.3152	1.5194	0.006173	0.2163
		06	04		62
GOBP_MEMBRANE_FUSION	160	0.3280	1.5278	0.018711	0.2163
		16	39		69
GOBP_ORGAN_GROWTH	144	0.3765	1.5192	0.025292	0.2163
		53	64		69
GOBP_DETECTION_OF_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTION_OF_PAIN	24	0.4831	1.5213	0.046784	0.2163
		64	77		72
GOCC_FLEMMING_BODY	34	0.4565	1.5199	0.049407	0.2163
		9	34		75

GOBP_POSITIVE_REGULATION_OF_GLYCOLYTIC_PROCESS	23	0.4898	1.5234	0.039448	0.2163
		68	21		9
GOBP_NEURON_PROJECTION_EXTENSION	161	0.3522	1.5307	0.024436	0.2164
		87	83		03
HP_PROXIMAL_AMYOTROPHY	39	0.4343	1.5238	0.041096	0.2164
		84	37		37
GOBP_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	414	0.3132	1.5281	0.017045	0.2164
		03	84		76
GOBP_RECEPTOR_MEDIATED_ENDOCYTOSIS	261	0.3414	1.5234	0.018219	0.2164
		5	94		82
HP KERATOSIS PILARIS	20	0.5227	1.5317	0.039683	0.2164
		79	35		93
HP_FLARED_ILIAC_WINGS	21	0.5030	1.5254	0.042084	0.2164
		88	64		99
GOBP_NEGATIVE_REGULATION_OF_BINDING	151	0.3197	1.5214	0.018036	0.2165
		96	09		12
GOCC_CORTICAL_ACTIN_CYTOSKELETON	75	0.3899	1.5271	0.038618	0.2165
		62	82		33
GOBP_REGULATION_OF_PROTEIN_CONTAINING_COMPLEX_DISASSEMBLY	115	0.3614	1.5220	0.032258	0.2165
		31	5		56
GOBP_CELLULAR_RESPONSE_TO_RADIATION	179	0.3368	1.5296	0.01833	0.2165
		86	26		69
GOBP_LABYRINTHINE_LAYER_DEVELOPMENT	42	0.4222	1.5255	0.046185	0.2165
		52	62		77
GOBP_NEGATIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	52	0.3867	1.5275	0.036145	0.2165
		03	49		97
GOBP_RHO_PROTEIN_SIGNAL_TRANSDUCTION	131	0.3733	1.5274	0.040385	0.2165
		41	19		98
GOBP_CELLULAR_RESPONSE_TO_VIRUS	60	0.3904	1.5202	0.043912	0.2165
		76	82		99

HP_ABNORMALITY_OF_THE_ILIUM	88	0.3633	1.5216	0.026415	0.2166
		92	97		38
GOBP_REGULATION_OF_RAS_PROTEIN_SIGNAL_TRANSDUCTION	187	0.3551	1.5288	0.028846	0.2166
		26	85		63
HP_APLASIA_HYPOPLASIA_OF_THE_HUMERUS	25	0.4719	1.5234	0.036437	0.2166
		72	94		65
HP_ABNORMAL_STERNUM_MORPHOLOGY	372	0.3349	1.5287	0.02994	0.2166
		32	4		74
GOBP_RUFFLE_ASSEMBLY	41	0.4123	1.5214	0.039419	0.2166
		82	19		86
HP_CEREBRAL_HEMORRHAGE	59	0.3923	1.5259	0.022403	0.2166
		93	4		92
GOBP_MODULATION_BY_HOST_OF_VIRAL_PROCESS	29	0.4339	1.5260	0.041068	0.2166
		17	77		95
GOBP_RESPONSE_TO_OXYGEN_LEVELS	369	0.3152	1.5294	0.006173	0.2166
		78	05		98
GOBP_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY	166	0.3828	1.5292	0.039832	0.2167
		17	5		15
GOBP_SIGNAL_TRANSDUCTION_IN_RESPONSE_TO_DNA_DAMAGE	125	0.3743	1.5261	0.042254	0.2167
		78	86		39
GOCC_ENDOCYTIC_VESICLE_MEMBRANE	157	0.3740	1.5283	0.043738	0.2167
		31	85		77
HP_METAPHYSEAL_WIDENING	80	0.3831	1.5309	0.043222	0.2167
		39	37		78
GOBP_CARDIAC_VENTRICLE_MORPHOGENESIS	66	0.4251	1.5264	0.036217	0.2167
		24	22		8
GOBP_VASOCONSTRICTION	76	0.4028	1.5284	0.02863	0.2168
		37	94		23
GOBP_POSITIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	225	0.3212	1.5297	0.005941	0.2168
		68	12		31

HP_VASCULAR_SKIN_ABNORMALITY	482	0.3052	1.5290	0.006012	0.2168
		65	19		32
GOBP_ANATOMICAL_STRUCTURE_REGRESSION	16	0.5291	1.5179	0.045872	0.2175
		92	68		76
HP_ABNORMAL_FORM_OF_THE_VERTEBRAL_BODIES	281	0.3328	1.5167	0.019608	0.2182
		12	74		09
HP_ABNORMAL_METACARPAL_MORPHOLOGY	145	0.3602	1.5169	0.035503	0.2183
		08	82		08
HP_HYPERPIGMENTATION_OF_THE_SKIN	219	0.3291	1.5161	0.012048	0.2185
		56	37		12
GOBP_MYELOID_CELL_DIFFERENTIATION	378	0.3226	1.5155	0.014831	0.2187
		64	69		85
GOBP_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	182	0.3622	1.5139	0.023952	0.2202
		07	66		17
HP_ABNORMAL_DELIVERY	70	0.4024	1.5134	0.023669	0.2202
		91	48		21
HP_ABNORMALITY_OF_THE_PHALANGES_OF_THE_TOES	118	0.3720	1.5128	0.030181	0.2202
		61	53		53
GOBP_RESPONSE_TO_FIBROBLAST_GROWTH_FACTOR	135	0.3439	1.5129	0.021611	0.2202
		08	9		56
HP_MEMORY_IMPAIRMENT	119	0.3365	1.5139	0.013834	0.2203
		25	97		63
GOBP_PROTEIN_DEPOLYMERIZATION	107	0.3834	1.5135	0.034836	0.2204
		96	6		39
GOBP_HEPARAN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	31	0.4490	1.5136	0.049713	0.2204
		77	47		82
GOBP_CELLULAR_SENESCENCE	64	0.3959	1.5123	0.025948	0.2207
		06	62		3
HP_ABNORMAL_VASCULAR_PHYSIOLOGY	239	0.3257	1.5121	0.028	0.2208
		65	74		02

HP_RECURRENT_URINARY_TRACT_INFECTIONS	112	0.3685	1.5087	0.043121	0.2210
		51	45		33
GOBP_BONE_REMODELING	88	0.3886	1.5093	0.040777	0.2211
		66	34		1
GOBP_REGULATION_OF_TUBE_SIZE	122	0.3722	1.5089	0.03617	0.2212
		36	98		11
GOBP_FOREBRAIN_CELL_MIGRATION	51	0.4082	1.5094	0.035019	0.2212
		87	69		98
GOBP_REGULATION_OF_ATP_METABOLIC_PROCESS	107	0.3707	1.5115	0.022495	0.2213
		32	15		52
GOMF_GLUTAMATE_RECEPTOR_BINDING	40	0.4191	1.5090	0.041833	0.2213
		43	13		62
HP_ABNORMAL_SYSTEMIC_ARTERIAL_MORPHOLOGY	423	0.3108	1.5113	0.016293	0.2213
		69	74		8
HP_ABNORMAL_NASOLACRIMAL_SYSTEM_MORPHOLOGY	57	0.4032	1.5095	0.041096	0.2214
		49	73		92
GOBP_POSITIVE_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	41	0.4250	1.5073	0.047431	0.2214
		68	12		98
GOBP_PEPTIDYL_TYROSINE_DEPHOSPHORYLATION	99	0.3426	1.5110	0.021505	0.2215
		99	89		72
HP_COLORECTAL_POLYPOSIS	23	0.4806	1.5073	0.046185	0.2215
		44	79		79
GOBP_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	146	0.3626	1.5076	0.031185	0.2215
		35	51		84
HP_GASTROINTESTINAL_OBSTRUCTION	59	0.3670	1.5096	0.039683	0.2215
		82	34		97
HP_DIFFICULTY_RUNNING	37	0.4053	1.5097	0.020964	0.2216
		86	37		32
GOBP_REGULATION_OF_OSSIFICATION	106	0.3720	1.5067	0.03	0.2216
		76	94		4

GOMF_PROTEIN_TYROSINE_PHOSPHATASE_ACTIVITY	97	0.3396	1.5068	0.025316	0.2217
		21	65		07
GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	113	0.3878	1.5099	0.04277	0.2217
		98	12		44
GOBP_AMYLOID_PRECURSOR_PROTEIN_CATABOLIC_PROCESS	53	0.3800	1.5099	0.023438	0.2218
		24	9		19
GOMF_SH3_DOMAIN_BINDING	127	0.3555	1.5079	0.036145	0.2218
		69	49		87
GOBP_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	93	0.3885	1.5105	0.033203	0.2219
		69	53		42
HP NEOPLASM OF THE SKIN	177	0.3235	1.5100	0.018145	0.2219
		09	05		69
GOBP_BARBED_END_ACTIN_FILAMENT_CAPPING	25	0.4662	1.5101	0.048421	0.2219
		49	22		84
GOBP_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	44	0.4074	1.5053	0.044534	0.2232
		48	59		5
GOBP_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	84	0.3623	1.5050	0.017928	0.2235
		72	1		58
GOMF_METALLOPEPTIDASE_ACTIVITY	178	0.3335	1.5043	0.019881	0.2238
		64	98		43
GOBP_ARTERY_MORPHOGENESIS	61	0.4302	1.5041	0.049904	0.2239
		91	8		54
GOBP_NEURON_APOPTOTIC_PROCESS	220	0.3161	1.5022	0.007874	0.2239
		68	44		74
HP_ABNORMALITY_OF_EARLOBE	81	0.3955	1.5024	0.043564	0.2239
		04	83		93
HP_OPEN_BITE	48	0.4083	1.5039	0.044625	0.2240
		43	74		47
GOBP_NEGATIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	28	0.4505	1.5025	0.035857	0.2240
		67	31		92

GOCC_Glutamatergic_Synapse	301	0.3307	1.5028	0.024145	0.2241
		34	61		56
GOBP_Regulation_of_Phosphoprotein_Phosphatase_Activity	113	0.3317	1.5029	0.022222	0.2242
		57	6		08
HP_Abnormal_Scalp_Morphology	322	0.3173	1.5032	0.024194	0.2243
		03	57		35
GOBP_Cellular_Response_to_Drug	61	0.3826	1.5029	0.024194	0.2243
		25	88		49
HP_Sarcoma	164	0.3328	1.5029	0.031809	0.2245
		55	96		11
GOBP_Developmental_Growth_Involved_in_Morphogenesis	220	0.3341	1.5004	0.020873	0.2251
		32	66		41
GOBP_Regulation_of_Tissue_Remodeling	73	0.3985	1.5004	0.039293	0.2252
		57	85		95
GOBP_Negative_Regulation_of_Intrinsic_Apoptotic_Signaling_Pathway	90	0.3705	1.5001	0.043137	0.2254
		68	63		08
HP_Disproportionate_Short_Limb_Short_Stature	85	0.3725	1.4983	0.038697	0.2264
		1	52		82
GOMF_Phosphatidylinositol_Phosphate_Binding	163	0.3240	1.4988	0.021526	0.2265
		71	3		28
GOBP_Protein_De phosphorylation	311	0.2984	1.4986	0.010267	0.2265
		99	81		39
GOBP_Positive_Regulation_of_Cell_Development	280	0.3149	1.4983	0.009416	0.2266
		12	55		52
HP_Abnormal_Uvea_Morphology	468	0.2984	1.4984	0.008097	0.2267
		23	37		1
GOBP_Negative_Regulation_of_Response_to_External_Stimulus	339	0.3352	1.4977	0.040816	0.2270
		27	07		12
HP_Misalignment_of_Teeth	284	0.3449	1.4977	0.02988	0.2270
		7	95		65

HP_DISPROPORTIONATE_SHORT_STATURE	111	0.3556	1.4961	0.034	0.2280
		9	49		64
HP_ABNORMALITY_OF_THE_SPINAL_CORD	280	0.3432	1.4955	0.042	0.2283
		25	94		99
GOBP_REGULATION_OF_SPROUTING_ANGIOGENESIS	34	0.4334	1.4953	0.048356	0.2285
		46	81		15
GOBP_RECEPTOR_RECYCLING	29	0.4180	1.4944	0.048682	0.2290
		71	4		3
HP_ABNORMALLY_LARGE_GLOBE	38	0.4331	1.4936	0.044355	0.2293
		54	72		88
GOCC_PLASMA_MEMBRANE_SIGNALING_RECEPTOR_COMPLEX	181	0.3592	1.4934	0.033663	0.2295
		52	28		44
GOBP_POSITIVE_CHEMOTAXIS	60	0.4110	1.4938	0.043568	0.2297
		49	14		13
HP_ABNORMALITY_IRIS_MORPHOLOGY	363	0.3101	1.4925	0.020161	0.2297
		13	64		96
GOBP_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	146	0.3235	1.4930	0.022727	0.2298
		44	19		82
HP_SPINA_BIFIDA_OCCULTA	69	0.3979	1.4925	0.043738	0.2299
		36	75		54
GOBP_EPITHELIAL_CELL_DEVELOPMENT	201	0.3225	1.4921	0.020367	0.2301
			86		16
HP_ABNORMALITY_OF_THE_BLADDER	412	0.3143	1.4916	0.026316	0.2301
		02	29		54
HP_PULMONARY_ARTERY_STENOSIS	57	0.3715	1.4908	0.034979	0.2306
		4	77		81
GOBP_REGULATION_OF_DNA_BINDING	114	0.3489	1.4901	0.029167	0.2314
		17	59		65
GOBP_POSITIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	331	0.3107	1.4898	0.021359	0.2315
		21	86		24

GOBP_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	70	0.3913	1.4886	0.04918	0.2324
		3	21		03
GOBP_JNK_CASCADE	187	0.3118	1.4887	0.01833	0.2325
		77	25		99
GOBP_REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	208	0.3425	1.4868	0.021739	0.2327
		12	48		39
HP_ABNORMAL_AORTIC_MORPHOLOGY	309	0.3241	1.4871	0.026477	0.2328
		76	21		72
GOBP_ORGANELLE_FUSION	140	0.3244	1.4879	0.032389	0.2329
		22	73		11
GOBP_EXOCYTIC_PROCESS	76	0.3629	1.4869	0.029412	0.2329
		32	57		11
GOCC_CLATHRIN_COATED_VESICLE	186	0.3360	1.4873	0.03012	0.2331
		58	1		18
HP_PALMOPLANTAR KERATODERMA	146	0.3663	1.4871	0.035433	0.2331
		1	8		42
GOMF_GUANYL_NUCLEOTIDE_BINDING	363	0.2961	1.4873	0.006048	0.2332
		68	88		03
GOBP_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	111	0.3542	1.4843	0.026157	0.2342
		19	51		2
HP_ABNORMAL_MORPHOLOGY_OF_THE_RADIUS	53	0.3880	1.4849	0.037113	0.2342
		92	95		35
GOBP_REGULATION_OF_CELL_DIVISION	159	0.3359	1.4843	0.02935	0.2343
		15	78		56
GOBP_ACTIN_CYTOSKELETON_REORGANIZATION	101	0.3679	1.4844	0.049801	0.2343
		55	75		95
GOBP_RESPONSE_TO_PROGESTERONE	43	0.3887	1.4834	0.02439	0.2345
		75	76		44
HP_ABNORMALITY_OF_THE_UVULA	153	0.3708	1.4830	0.047525	0.2348
		61	82		68

HP_KYPHOSCOLIOSIS	164	0.3310	1.4829	0.025097	0.2349
		6	06		19
GOCC_MEMBRANE_COAT	90	0.3737	1.4827	0.048387	0.2349
		82	43		69
GOBP_POSITIVE_REGULATION_OF_NEUROGENESIS	210	0.3220	1.4811	0.028409	0.2361
		47	26		41
GOBP_CELL_CELL_JUNCTION_ASSEMBLY	140	0.3413	1.4803	0.028398	0.2367
		74	04		18
GOBP_REGULATION_OF_FAT_CELL_DIFFERENTIATION	122	0.3499	1.4777	0.017893	0.2393
		05	84		46
GOBP_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	155	0.3462	1.4778	0.030801	0.2394
		23	53		29
GOBP_RESPONSE_TO_OXIDATIVE_STRESS	419	0.2926	1.4772	0.015267	0.2397
		94	03		33
HP_UNDERDEVELOPED_NASAL_ALAE	78	0.3786	1.4743	0.038229	0.2401
		93	66		08
GOBP_CANONICAL_WNT_SIGNALING_PATHWAY	319	0.3133	1.4765	0.019493	0.2401
		24	38		31
HP_LOW_POSTERIOR_HAIRLINE	92	0.3682	1.4765	0.040856	0.2402
		86	64		63
GOBP_NEGATIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	77	0.3689	1.4739	0.032	0.2402
		08	68		82
GOMF_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ACTIVITY	61	0.4008	1.4745	0.045977	0.2403
		93	08		9
GOBP_POSITIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	115	0.3454	1.4739	0.023061	0.2404
		89	86		22
GOBP_STEM_CELL_DIFFERENTIATION	243	0.3244	1.4731	0.031873	0.2405
		16	98		04
GOBP_NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	129	0.3289	1.4724	0.017717	0.2410
		08	47		13

GOBP_REGULATION_OF_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	83	0.3566	1.4716	0.041257	0.2416
		69	51		
HP_MIGRAINE	97	0.3320	1.4717	0.018109	0.2416
		35	54		36
GOBP_POSITIVE_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	60	0.3736	1.4710	0.0375	0.2417
		97	07		84
GOBP_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_CELL_DEATH	58	0.3676	1.4710	0.029703	0.2419
		92	08		52
GOBP_REGULATION_OF_JNK_CASCADE	127	0.3237	1.4690	0.026694	0.2421
		02	63		62
GOBP_RESPONSE_TO_HYDROGEN_PEROXIDE	127	0.3282	1.4690	0.022044	0.2422
		49	81		99
HP_OSTEOMYELITIS	50	0.3890	1.4698	0.042169	0.2423
		65	78		2
GOBP_RESPONSE_TO_PEPTIDE	489	0.2926	1.4699	0.014085	0.2423
		59	77		62
HP_ABNORMALITY_OF_HAIR_TEXTURE	151	0.3411	1.4700	0.045098	0.2423
		09	95		73
GOMF_PROTEIN_KINASE_C_BINDING	54	0.3735	1.4692	0.034413	0.2424
		18	27		08
GOBP_SKELETAL_SYSTEM_DEVELOPMENT	461	0.3274	1.4702	0.042389	0.2424
		19	78		59
GOBP_REGULATION_OF_PROTEIN_DEPHOSPHORYLATION	136	0.3178	1.4694	0.026	0.2424
		78	19		78
GOBP_POSITIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	77	0.3595	1.4692	0.036609	0.2425
		44	32		69
HP_MIDFACE_RETRUSION	251	0.3328	1.4682	0.038685	0.2426
		19	66		33
GOMF_UBIQUITIN_LIKE_PROTEIN_LIGASE_BINDING	304	0.3180	1.4677	0.023622	0.2428
		23	46		32

GOBP_POSITIVE_REGULATION_OF_CELL_GROWTH	147	0.3162	1.4656	0.019084	0.2431
		41	86		92
GOBP_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	99	0.3456	1.4653	0.020492	0.2434
		86	72		68
GOBP_POSITIVE_REGULATION_OF_JUN_KINASE_ACTIVITY	67	0.3735	1.4651	0.044625	0.2436
		54	4		12
GOCC_RECYCLING_ENDOSOME	179	0.3109	1.4614	0.030303	0.2439
		91	64		2
GOBP_ZINC_ION_TRANSPORT	27	0.4522	1.4644	0.042885	0.2439
		71	11		5
HP_LIMB_JOINT_CONTRACTURE	339	0.3046	1.4622	0.023256	0.2441
		47	07		98
HP_APLASIA_HYPOPLASIA_INVOLVING_THE_NOSE	93	0.3636	1.4630	0.042718	0.2442
		98	41		
HP_CRANIOSYNOSTOSIS	147	0.3452	1.4639	0.049383	0.2442
		99	03		08
GOBP_REGULATION_OF_MORPHOGENESIS_OF_AN_EPITHELIUM	60	0.3878	1.4630	0.035857	0.2443
		97	52		51
HP_LONG_FINGERS	229	0.3387	1.4606	0.04829	0.2444
		87	27		1
GOBP_GLIOGENESIS	270	0.3157	1.4633	0.030426	0.2444
		54	2		81
GOBP_REGULATION_OF_OSTEOLAST_DIFFERENTIATION	111	0.3641	1.4598	0.02924	0.2446
		12	92		05
HP_HERNIA	459	0.3203	1.4595	0.043738	0.2449
		17	07		96
GOBP_CELL_GROWTH	445	0.2862	1.4586	0.011673	0.2454
		64	96		83
HP_SKELETAL_DYSPLASIA	168	0.3235	1.4579	0.031683	0.2459
		31	1		23

GOBP_INOSITOL_LIPID_MEDIATED_SIGNALING	186	0.3393	1.4571	0.036511	0.2460
		09	98		87
GOCC_COATED_VESICLE_MEMBRANE	175	0.3372	1.4574	0.038934	0.2460
		07	23		96
GOBP_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	208	0.3000	1.4568	0.00996	0.2463
		29	5		79
GOCC_SPECIFIC_GRANULE_LUMEN	61	0.3942	1.4565	0.049116	0.2466
		9	54		47
GOBP_DEVELOPMENTAL_CELL_GROWTH	210	0.3199	1.4556	0.030303	0.2467
		56	41		82
GOBP_NEGATIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	53	0.3590	1.4551	0.025692	0.2468
		64	45		49
GOBP_PALLIUM_DEVELOPMENT	147	0.3436	1.4545	0.040541	0.2468
		42	11		81
GOCC_COATED_VESICLE	284	0.3199	1.4542	0.041152	0.2469
		74	54		09
GOBP_POSITIVE_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	51	0.3830	1.4552	0.03861	0.2469
		68	05		12
GOBP_CELLULAR_RESPONSE_TO_RETINOIC_ACID	62	0.3578	1.4552	0.034483	0.2470
		22	47		24
GOBP_NEGATIVE_REGULATION_OF_CELL_GROWTH	177	0.3111	1.4561	0.013972	0.2470
		98	74		29
GOBP_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	63	0.3855	1.4557	0.043388	0.2470
		89	99		52
HP_APLASIA_HYPOPLASIA_OF_THE_EYEBROW	153	0.3263	1.4536	0.036893	0.2474
		96	62		41
HP_GENU_VARUM	47	0.3917	1.4525	0.043564	0.2481
		32	74		69
GOCC_EXCITATORY_SYNAPSE	45	0.4274	1.4523	0.045098	0.2482
		21	07		1

GOMF_MOLECULAR_ADAPTOR_ACTIVITY	312	0.2868	1.4516	0.016495	0.2486
		03	4		35
GOBP_CELLULAR_RESPONSE_TO_UV	85	0.3446	1.4514	0.047131	0.2487
		69	71		12
HP_APLASIA_HYPOPLASIA_INVOLVING_THE_VERTEBRAL_COLUMN	61	0.3595	1.4512	0.035928	0.2488
		04	5		56
GOBP_NUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS	149	0.3320	1.4505	0.02521	0.2492
		74	09		19
HP_MORPHOLOGICAL_ABNORMALITY_OF_THE_INNER_EAR	58	0.3871	1.4505	0.042636	0.2492
		39	92		72
HP_PECTUS_CARINATUM	135	0.3343	1.4502	0.046371	0.2493
		58	91		65

Table S10. GSEA results between high-risk and low-risk phenotypes by using C2 reference gene set.

NAME	SI	ES	NE	NO	FD
	Z		S	M	R q-
	E			p-	val
				val	
GRUETZMANN_PANCREATIC_CANCER_UP	34	0.57	2.31	<0.0	0.00
	9	822	464	1	184
		2	9		
REACTOME_SIGNALING_BY_MET	79	0.63	2.34	<0.0	0.00
		754	101	1	189
		2	1		8
REACTOME_MET_PROMOTES_CELL_MOTILITY	41	0.76	2.28	<0.0	0.00
		429	574	1	279
		7	9		6
PASINI_SUZ12_TARGETS_DN	30	0.59	2.29	<0.0	0.00
	4	810	334	1	304
		1	1		9
CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN	43	0.62	2.27	<0.0	0.00
	8	125	988	1	320
		9	1		6
HUANG_DASATINIB_SENSITIVITY_UP	78	0.76	2.23	<0.0	0.00
		033	485	1	373
		2	8		5
REACTOME_EPH_EPHRIN_SIGNALING	92	0.59	2.23	0.00	0.00
		770	825	198	400
		3	8	8	2
SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN	31	0.77	2.25	<0.0	0.00
		581	083	1	405
		5	7		
MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_DN	21	0.58	2.22	<0.0	0.00
	8	320	849	1	418
		2	9		8
SENESE_HDAC3_TARGETS_UP	46	0.53	2.22	<0.0	0.00
	7	943	570	1	421
			9		1
RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN	37	0.59	2.23	<0.0	0.00
	0	240	855	1	431
		3	3		
REACTOME_EPHB_MEDIATED_FORWARD_SIGNALING	42	0.69	2.25	<0.0	0.00
		489	159	1	45
		1	8		
SENESE_HDAC1_TARGETS_UP	42	0.55	2.23	<0.0	0.00
	3	572	949	1	457
		7	1		5

BROWNE_HCMV_INFECTION_2HR_DN	46	0.66	2.24	<0.0	0.00
		893	102	1	488
		8	5		9
BURTON_ADIPOGENESIS_7	48	0.67	2.25	<0.0	0.00
		091	775	1	489
		4			4
VANTVEER_BREAST_CANCER_ESR1_DN	21	0.58	2.26	<0.0	0.00
		8	319	707	1
		2			1
SENESE_HDAC2_TARGETS_UP	10	0.62	2.20	<0.0	0.00
		8	258	434	1
			8		2
WATANABE_RECTAL_CANCER_RADIOOTHERAPY_RESPONSIVE_DN	91	0.58	2.19	<0.0	0.00
		485	743	1	601
		6	6		9
TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NOR MAL_UP	72	0.68	2.19	<0.0	0.00
		073	235	1	605
		8	6		1
REACTOME_SIGNALING_BY_PDGF	58	0.67	2.18	<0.0	0.00
		932	883	1	618
		6	5		9
FOSTER_TOLERANT_MACROPHAGE_DN	39	0.50	2.18	<0.0	0.00
		5	422	487	1
		7	1		3
REN_ALVEOLAR_RHABDOMYOSARCOMA_DN	40	0.60	2.18	0.00	0.00
		4	595	110	210
		6	1	1	5
PID_AVB3_INTEGRIN_PATHWAY	74	0.66	2.17	<0.0	0.00
		595	771	1	720
		3	6		6
WIEDERSCHAIN_TARGETS_OF_BMI1_AND_PCGF2	57	0.67	2.17	<0.0	0.00
		121	315	1	754
		4	3		
REACTOME_COLLAGEN_FORMATION	90	0.67	2.16	0.00	0.00
		403	558	198	771
		2	3		4
REACTOME_RHOJ_GTPASE_CYCLE	55	0.59	2.16	<0.0	0.00
		182	583	1	793
		3	5		8
PEDERSEN_TARGETS_OF_611CTF_ISOFORM_OF_ERBB2	72	0.65	2.14	<0.0	0.00
		484	713	1	934
		1	8		4

HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_1_DN	35	0.66	2.14	<0.0	0.00
		983	788	1	948
		8	3		1
REACTOME_PARASITE_INFECTION	59	0.61	2.12	<0.0	0.00
		089	248	1	972
		3	5		7
WP_FOCAL_ADHESION	19	0.54	2.11	<0.0	0.00
		6	468	977	1
		1	2		1
REACTOME_FLT3_SIGNALING_IN_DISEASE	28	0.65	2.14	<0.0	0.00
		819	843	1	975
		3	1		3
KEGG_RENAL_CELL_CARCINOMA	70	0.53	2.12	<0.0	0.00
		623	078	1	983
		7	6		8
REACTOME_ASSEMBLY_OF_COLLAGEN_FIBRILS_AND_OTHER_MULTIMERIC_STRUCTURES	61	0.72	2.12	<0.0	0.00
		911	275	1	986
		5	9		9
VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP	16	0.70	2.13	<0.0	0.00
		5	641	852	1
		4	1		4
MCBRYAN_PUBERTAL_TGFB1_TARGETS_UP	16	0.54	2.12	<0.0	0.01
		6	024	276	1
		9	8		8
WP_HEPATITIS_C_AND_HEPATOCELLULAR_CARCINOMA	49	0.60	2.14	<0.0	0.01
		651	257	1	016
		3	8		1
GERHOLD_ADIPOGENESIS_DN	60	0.61	2.13	<0.0	0.01
		815	857	1	022
		5	8		4
JI_RESPONSE_TO_FSH_DN	52	0.66	2.12	<0.0	0.01
		115	309	1	026
		1	5		3
KEGG_FOCAL_ADHESION	19	0.56	2.11	<0.0	0.01
		7	487	267	1
		7	2		4
PID_PDGFRB_PATHWAY	12	0.54	2.12	<0.0	0.01
		9	708	976	1
		7	7		8
RIGGI_EWING_SARCOMA_PROGENITOR_DN	18	0.57	2.11	<0.0	0.01
		3	891	645	1
		8	9		2

HOSHIDA_LIVER_CANCER_SUBCLASS_S1	23	0.58	2.11	<0.0	0.01
	0	887	354	1	038
		5	9		3
SENESE_HDAC1_AND_HDAC2_TARGETS_UP	22	0.53	2.13	<0.0	0.01
	5	536	971	1	041
		5	6		4
RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POORLY_UP	12	0.50	2.13	<0.0	0.01
	0	464	015	1	041
		9	8		5
IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_UP	12	0.51	2.11	<0.0	0.01
	4	726	416	1	047
		5	2		
NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_UP	27	0.56	2.12	<0.0	0.01
	1	127	318	1	050
		4	8		2
SIG_REGULATION_OF_THE_ACTIN_CYTOSKELETON_BY_RHO_GTPASES	35	0.65	2.13	<0.0	0.01
		342	039	1	052
		8	8		2
RIEGE_DELTANP63_DIRECT_TARGETS_UP	13	0.57	2.11	<0.0	0.01
	4	700	475	1	062
		6	4		5
KIM_WT1_TARGETS_UP	21	0.54	2.12	0.00	0.01
	4	186	679	204	064
		3	3	1	3
REACTOME_RHOF_GTPASE_CYCLE	42	0.64	2.12	<0.0	0.01
		543	483	1	064
		5	2		8
KEGG_SMALL_CELL_LUNG_CANCER	84	0.54	2.13	<0.0	0.01
		070	299	1	066
		2	9		8
WOOD_EBV_EBNA1_TARGETS_DN	47	0.60	2.10	0.00	0.01
		514	737	210	070
		7	1	5	5
PID_INTEGRIN_A4B1_PATHWAY	33	0.65	2.12	0.00	0.01
		907	320	209	072
			3	2	1
AZARE_NEOPLASTIC_TRANSFORMATION_BY_STAT3_UP	12	0.56	2.10	<0.0	0.01
	2	736	561	1	075
		9	5		8
ROZANOV_MMP14_TARGETS_SUBSET	33	0.80	2.13	0.00	0.01
		110	105	205	077
		6	1	3	1

REACTOME_NON_INTEGRIN_MEMBRANE_ECM_INTERACTIONS	59	0.72	2.10	0.00	0.01
		048	821	201	080
		6	8	6	7
PID_S1P_S1P3_PATHWAY	29	0.68	2.10	<0.0	0.01
		799	039	1	087
		6	7		9
DANG_REGULATED_BY_MYC_DN	24	0.51	2.09	0.00	0.01
	2	147	901	200	090
		9	8	8	6
TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORM AL_UP	47	0.71	2.09	<0.0	0.01
		360	631	1	093
		6	4		
RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP	33	0.46	2.10	<0.0	0.01
	2	888	865	1	095
		1	7		6
WP_PRIMARY_FOCAL_SEGMENTAL_GLOMERULOSCLEROSIS_FSGS	71	0.58	2.09	<0.0	0.01
		880	368	1	098
		5	5		9
BRUECKNER_TARGETS_OF_MIRLET7A3_DN	74	0.62	2.10	<0.0	0.01
		283	097	1	099
			9		2
PID_INTEGRIN1_PATHWAY	66	0.71	2.09	<0.0	0.01
		465	675	1	103
		8	4		4
JECHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP	66	0.66	2.09	<0.0	0.01
		353	432	1	106
		7	5		
PID_ERBB1_RECEPTOR_PROXIMAL_PATHWAY	35	0.65	2.10	<0.0	0.01
		122	170	1	111
		3	7		
CHIARADONNA NEOPLASTIC_TRANSFORMATION_CDC25_UP	12	0.53	2.08	<0.0	0.01
	1	539	753	1	122
		5	4		1
SHIN_B_CELL_LYMPHOMA_CLUSTER_8	36	0.67	2.10	0.00	0.01
		110	232	204	125
		6	3	5	2
PID_LYMPH_ANGIOGENESIS_PATHWAY	25	0.73	2.08	<0.0	0.01
		162	882	1	130
		7	1		7
CROMER_TUMORIGENESIS_UP	57	0.70	2.08	0.00	0.01
		998	795	206	134
		7	8	2	6

RUTELLA_RESPONSE_TO_HGF_UP	41	0.49	2.08	<0.0	0.01
	4	855	898	1	142
		9	8		2
REACTOME_SIGNALING_BY_EGFR	50	0.59	2.08	<0.0	0.01
		675	935	1	144
		4	2		4
REACTOME_MET_ACTIVATES_PTK2_SIGNALING	30	0.77	2.07	0.00	0.01
		252	691	4	167
		7	7		8
WANG_SMARCE1_TARGETS_UP	28	0.55	2.08	<0.0	0.01
	1	760	067	1	169
		6	8		2
RODRIGUES_THYROID_CARCINOMA_DN	76	0.56	2.07	<0.0	0.01
		143	920	1	178
			2		6
AMIT_SERUM_RESPONSE_240_MCF10A	54	0.62	2.07	<0.0	0.01
		726	697	1	182
		5	8		
PID_INTEGRIN3_PATHWAY	42	0.70	2.07	<0.0	0.01
		017	467	1	182
		3	7		5
APRELIKOVA_BRCA1_TARGETS	45	0.60	2.08	<0.0	0.01
		065	073	1	184
		4	5		2
REACTOME_RHO_GTPASES_ACTIVATE_WASPS_AND_WAVES	36	0.63	2.08	<0.0	0.01
		604	29	1	184
		6			4
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_UP	13	0.52	2.07	<0.0	0.01
	0	438	767	1	185
		2	5		
VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1	37	0.66	2.08	<0.0	0.01
		914	324	1	194
		7			2
REACTOME_SYNDECAN_INTERACTIONS	27	0.83	2.08	<0.0	0.01
		317	379	1	196
		7	5		3
REACTOME_SIGNALING_BY_FLT3_ITD_AND_TKD_MUTANTS	16	0.75	2.08	<0.0	0.01
		367	084	1	199
		5	2		5
REACTOME_EPH_EPHRIN_MEDIATED_REPULSION_OF_CELLS	51	0.59	2.08	0.00	0.01
		518	094	196	211
			1	9	4

ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF	47	0.46	2.07	<0.0	0.01
	4	960	033	1	246
		2	9		2
LU_TUMOR_ENDOTHELIAL_MARKERS_UP	22	0.78	2.07	<0.0	0.01
		251	063	1	250
		9	2		2
REACTOME_FCGAMMA_RECEPTOR_FCGR_DEPENDENT_PHAGOCY TOSIS	86	0.55	2.07	<0.0	0.01
		204	076	1	258
			6		8
KIM_WT1_TARGETS_8HR_UP	16	0.53	2.06	<0.0	0.01
	5	337	562	1	312
		9	3		9
PID_CXCR4_PATHWAY	10	0.57	2.06	0.00	0.01
	0	633	604	202	315
		5	7		6
LU_TUMOR_VASCULATURE_UP	29	0.71	2.06	0.00	0.01
		205	201	221	325
		5	7	2	1
REACTOME_RHOQ_GTPASE_CYCLE	59	0.58	2.05	<0.0	0.01
		296	988	1	326
		5	5		3
BLANCO_MELO_RESPIRATORY_SYNCYTIAL_VIRUS_INFECTION_A 594_CELLS_UP	27	0.59	2.06	0.00	0.01
	8	436	086	403	328
		6	3	2	1
GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP	69	0.59	2.06	0.00	0.01
		646	323	200	331
		7	4	4	3
BIOCARTA_P38MAPK_PATHWAY	36	0.56	2.05	<0.0	0.01
		093	138	1	375
			1		8
PHONG_TNF_RESPONSE_VIA_P38_PARTIAL	15	0.51	2.04	0.00	0.01
	9	604	812	203	382
			3	7	4
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	34	0.70	2.05	0.00	0.01
	0	369	150	206	388
		5	6	2	5
SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP	29	0.59	2.04	0.00	0.01
	9	177	846	210	388
		4	6	5	8
KARAKAS_TGFB1_SIGNALING	18	0.75	2.05	<0.0	0.01
		414	573	1	389
		7	7		

PID_INSULIN_PATHWAY	44	0.58	2.05	<0.0	0.01
		739	221	1	391
		5	9		7
PID_UPA_UPAR_PATHWAY	42	0.66	2.05	<0.0	0.01
		252	438	1	396
			2		4
SESTO_RESPONSE_TO_UV_C8	69	0.58	2.05	<0.0	0.01
		815	353	1	396
		9	8		4
REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	29	0.65	2.04	0.00	0.01
		390	846	196	400
		5	9	9	8
IKEDA_MIR30_TARGETS_UP	11	0.57	2.05	<0.0	0.01
	5	464	260	1	402
		3	6		3
WP_REGULATION_OF_MICROTUBULE_CYTOSKELETON	46	0.59	2.04	0.00	0.01
		714	873	193	411
		9	3	8	8
REACTOME_RAC3_GTPASE_CYCLE	91	0.53	2.04	<0.0	0.01
		98	621	1	421
			9		
PHONG_TNF_RESPONSE_NOT_VIA_P38	33	0.47	2.04	<0.0	0.01
	3	690	297	1	422
		4	3		8
HE_PTEN_TARGETS_UP	17	0.71	2.02	<0.0	0.01
		318	980	1	426
		5	7		9
REACTOME_RAC2_GTPASE_CYCLE	87	0.54	2.04	<0.0	0.01
		611	345	1	429
			8		
VANHARANTA_UTERINE_FIBROID_UP	43	0.63	2.04	0.00	0.01
		529	196	392	430
		4	7	2	1
BLANCO_MELO_BETA_INTERFERON_TREATED_BRONCHIAL_EPITHELIAL_CELLS_UP	35	0.54	2.03	0.00	0.01
	5	198	005	201	430
		4	8	2	8
PID_AVB3_OPN_PATHWAY	31	0.64	2.04	<0.0	0.01
		523	464	1	430
		7	7		9
KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_UP	12	0.49	2.04	<0.0	0.01
	8	448	092	1	434
		9	7		3

PID_ARF6_TRAFFICKING_PATHWAY	49	0.57	2.03	<0.0	0.01
		366	025	1	439
		5	8		9
KUNINGER_IGF1_VS_PDGF_B_TARGETS_DN	45	0.59	2.03	<0.0	0.01
		013	125	1	445
		7	1		4
SASSON_RESPONSE_TO_FORSKOLIN_DN	85	0.53	2.03	<0.0	0.01
		490	163	1	451
		2	1		1
JIANG_TIP30_TARGETS_UP	44	0.57	2.03	0.00	0.01
		034	027	206	451
		8	9	2	4
REACTOME_EXTRA_NUCLEAR_ESTROGEN_SIGNALING	75	0.50	2.03	<0.0	0.01
		664	195	1	454
		8	6		4
ZHAN_MULTIPLE_MYELOMA_CD2_DN	45	0.57	2.03	<0.0	0.01
		035	209	1	464
		4	2		2
MEBARKI_HCC_PROGENITOR_WNT_UP	17	0.57	2.02	0.00	0.01
		7	222	751	200
		6	2	4	3
PID_A6B1_A6B4_INTEGRIN_PATHWAY	46	0.60	2.03	0.00	0.01
		499	786	203	467
			3	7	1
WP_TGFBETA_SIGNALING_PATHWAY	13	0.50	2.03	<0.0	0.01
		2	308	341	1
		2	2		3
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NOR MAL_UP	66	0.78	2.03	<0.0	0.01
		278	251	1	470
		3	7		7
WP_SMALL_CELL_LUNG_CANCER	95	0.49	2.03	<0.0	0.01
		592	670	1	475
			6		6
REACTOME_CTLA4_INHIBITORY_SIGNALING	21	0.64	2.03	<0.0	0.01
		599	807	1	476
			9		3
BIOCARTA_ATM_PATHWAY	20	0.67	2.03	<0.0	0.01
		847	358	1	477
		5	2		5
HINATA_NFKB_TARGETS_KERATINOCYTE_UP	84	0.61	2.03	0.00	0.01
		241	395	202	489
		2	7	4	

RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_D N	10	0.59	2.03	<0.0	0.01
	6	601	362	1	490
		8	1		1
LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_UP	81	0.58	2.03	<0.0	0.01
		086	448	1	490
		5	7		5
GU_PDEF_TARGETS_DN	39	0.62	2.03	<0.0	0.01
		488	498	1	498
		2	6		3
REACTOME_SEMA3A_PAK_DEPENDENT_AXON_REPULSION	16	0.70	2.02	<0.0	0.01
		946	233	1	568
		6			2
GU_PDEF_TARGETS_UP	70	0.63	2.02	0.00	0.01
		688	249	207	574
			3	5	6
KEGG_ECM_RECEPTOR_INTERACTION	83	0.65	2.02	<0.0	0.01
		063	145	1	576
		2	5		7
BIOCARTA_P53HYPOXIA_PATHWAY	21	0.65	2.01	0.00	0.01
		110	979	202	585
		4	9	8	8
ONDER_CDH1_TARGETS_1_DN	16	0.52	2.02	<0.0	0.01
	4	399	053	1	591
			2		9
PID_CDC42_PATHWAY	69	0.55	2.02	<0.0	0.01
		083	000	1	592
		7	9		2
COULOUARN_TEMPORAL_TGFB1_SIGNATURE_UP	10	0.50	2.01	<0.0	0.01
	7	597	758	1	610
		6	5		9
PID_S1P_META_PATHWAY	21	0.66	2.01	<0.0	0.01
		291	769	1	617
		9	5		7
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	20	0.48	2.01	<0.0	0.01
	7	532	495	1	643
			2		2
BURTON_ADIPOGENESIS_PEAK_AT_8HR	38	0.59	2.01	<0.0	0.01
		254	510	1	652
		5	7		9
GENTILE_UV_RESPONSE_CLUSTER_D8	37	0.63	2.00	<0.0	0.01
		538	950	1	760
		6	6		4

CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_UP	13	0.54	2.00	<0.0	0.01
	1	981	772	1	779
		1			
HARRIS_HYPOXIA	81	0.55	2.00	0.00	0.01
		879	789	203	784
		2	4	7	8
WP_FAS_LIGAND_FASL_PATHWAY_AND_STRESS_INDUCTION_OF_HEAT_SHOCK_PROTEINS_HSP_REGULATION	42	0.59	2.00	0.00	0.01
		251	596	207	817
		5	8	5	1
WANG_METHYLATED_IN_BREAST_CANCER	35	0.66	2.00	0.00	0.01
		795	506	614	827
		8	1	8	5
ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP	21	0.52	2.00	0.00	0.01
	7	999	355	596	851
		7	2	4	3
WU_CELL_MIGRATION	17	0.52	2.00	<0.0	0.01
	7	594	258	1	868
		9			4
PID_SYNDECAN_1_PATHWAY	46	0.67	2.00	0.00	0.01
		575	122	603	888
		3	8	6	6
KANG_AR_TARGETS_UP	17	0.75	1.99	0.00	0.01
		925	999	393	907
		6	4	7	5
SESTO_RESPONSE_TO_UV_C5	46	0.66	1.99	<0.0	0.01
		226	807	1	933
		2	1		7
WP_NEURAL_CREST_CELL_MIGRATION_DURING_DEVELOPMENT	40	0.58	1.99	<0.0	0.01
		432	568	1	945
		7	1		
HINATA_NFKB_TARGETS_FIBROBLAST_UP	81	0.54	1.99	<0.0	0.01
		732	640	1	946
		5	8		7
HUMMERICH_SKIN_CANCER_PROGRESSION_UP	87	0.56	1.99	<0.0	0.01
		649	698	1	946
		4	8		7
REACTOME_INTERLEUKIN_12_SIGNALING	46	0.58	1.99	<0.0	0.01
		066	502	1	953
		9	3		4
VERHAAK_GLIOBLASTOMA_MESENCHYMAL	21	0.63	1.99	0.00	0.01
	5	668	713	608	954
		6	1	5	9

PID_VEGFR1_PATHWAY	26	0.65	1.99	<0.0	0.01
		053	269	1	955
			8		6
JOHNSTONE_PARVB_TARGETS_1_DN	59	0.58	1.99	0.00	0.01
		854	406	409	956
		9	1		1
PID_SYNDECAN_4_PATHWAY	31	0.62	1.99	<0.0	0.01
		089	300	1	959
		5	9		
DITTMER_PTHLH_TARGETS_DN	70	0.54	1.99	<0.0	0.01
		057	228	1	961
		8	3		2
HENDRICKS_SMARCA4_TARGETS_UP	52	0.64	1.99	<0.0	0.01
		425	161	1	961
		1	5		9
REACTOME_TRANSLOCATION_OF_SLC2A4_Glut4_TO_THE_PLASMA_MEMBRANE	71	0.51	1.99	<0.0	0.01
		064	332	1	963
		3	4		
CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP	58	0.59	1.99	0.00	0.01
		288	426	208	965
		1	7	8	
PID_MET_PATHWAY	79	0.53	1.98	<0.0	0.01
		943	984	1	997
		5	4		3
PID_EPHB_FWD_PATHWAY	40	0.60	1.98	0.00	0.02
		719	831	199	031
		4	6	2	9
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	29	0.54	1.98	0.00	0.02
		9	859	724	402
		6	6	4	4
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	89	0.53	1.98	0.00	0.02
		956	641	386	051
		1	6	1	5
SWEET_KRAS_TARGETS_UP	77	0.60	1.98	0.00	0.02
		922	416	210	090
		3	6	1	2
PID_GLYPICAN_1PATHWAY	27	0.64	1.98	<0.0	0.02
		123	459	1	091
			9		6
REACTOME_SIGNALING_BY_VEGF	10	0.49	1.98	<0.0	0.02
		5	557	299	1
		2	3		107

WP_VIRAL_ACUTE_MYOCARDITIS	86	0.50	1.98	<0.0	0.02
		986	077	1	108
		2			6
WP_NEURAL_CREST_CELL_MIGRATION_IN_CANCER	43	0.57	1.98	<0.0	0.02
		062	240	1	118
		4	1		7
WP_MIR5093P_ALTERATION_OF_YAP1ECM_AXIS	17	0.83	1.97	0.00	0.02
		877	963	203	120
		1	4	7	6
OSMAN_BLADDER_CANCER_UP	38	0.49	1.98	<0.0	0.02
		5	685	118	1
		6	3		6
PID_CXCR3_PATHWAY	43	0.55	1.98	<0.0	0.02
		757	077	1	120
		7	8		9
BURTON_ADIPOGENESIS_8	79	0.58	1.97	0.00	0.02
		393	903	409	122
		1	2		3
CHICAS_RB1_TARGETS_GROWING	23	0.55	1.97	0.00	0.02
		9	141	765	613
		2	2	5	8
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NOR MAL_DN	71	0.68	1.98	0.00	0.02
		049	146	607	127
		8		3	1
LINDSTEDT_DENDRITIC_CELL_MATURATION_A	61	0.60	1.97	0.00	0.02
		463	693	581	131
			2	4	
WP_ANGIOGENESIS	24	0.68	1.97	<0.0	0.02
		373	79	1	131
		2			3
KEGG_PANCREATIC_CANCER	70	0.51	1.97	<0.0	0.02
		234	630	1	139
		3	3		1
GHANDHI_BYSTANDER_IRRADIATION_UP	77	0.55	1.97	0.00	0.02
		896	806	208	139
		5	6	3	3
PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP	20	0.61	1.97	0.00	0.02
		2	091	496	202
		4	1	8	8
VERRECCHIA_EARLY_RESPONSE_TO_TGFB1	54	0.65	1.97	0.00	0.02
		219	285	424	178
		9	1	6	5

HOELZEL_NF1_TARGETS_UP	13	0.48	1.97	<0.0	0.02
	2	014	306	1	184
		6	1		7
POOLA_INVASIVE_BREAST_CANCER_UP	26	0.60	1.97	0.00	0.02
	6	169	332	403	188
		1	1	2	4
PID_NETRIN_PATHWAY	32	0.58	1.97	0.00	0.02
		675	336	407	196
		2	8	3	6
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	84	0.63	1.97	<0.0	0.02
		633	357	1	200
		1	8		4
WP_EBOLA_VIRUS_PATHWAY_ON_HOST	12	0.54	1.97	<0.0	0.02
	8	530	068	1	209
		9	9		9
REACTOME_CLATHRIN_MEDIATED_ENDOCYTOSIS	14	0.46	1.97	<0.0	0.02
	4	737	074	1	221
		2	4		
GENTILE_UV_RESPONSE_CLUSTER_D6	33	0.61	1.96	<0.0	0.02
		491	936	1	228
		7	2		
WP_TOLLLIKE_RECEPTOR_SIGNALING_PATHWAY	90	0.52	1.97	0.00	0.02
		532	081	561	229
		3	6	8	6
WP_PATHOGENIC_ESCHERICHIA_COLI_INFECTIION	55	0.55	1.96	0.00	0.02
		469	732	423	240
		2	7	7	4
PID_S1P_S1P1_PATHWAY	21	0.65	1.96	0.00	0.02
		375	672	212	240
		7	6	8	9
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTIION	55	0.55	1.96	0.00	0.02
		469	732	423	252
		2	7	7	
BAELDE_DIABETIC_NEPHROPATHY_DN	42	0.44	1.96	<0.0	0.02
	2	613	810	1	253
			2		4
GOLDRATH_ANTIGEN_RESPONSE	34	0.51	1.96	<0.0	0.02
	5	129	764	1	253
		7	3		9
REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES	49	0.41	1.96	<0.0	0.02
	9	640	473	1	274
		7			6

REACTOME_COLLAGEN_DEGRADATION	64	0.64	1.96	0.00	0.02
		776	395	818	275
		2	6		6
BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_UP	10	0.50	1.96	0.00	0.02
	8	053	284	206	276
		7	3	2	6
REACTOME_RHOG_GTPASE_CYCLE	73	0.52	1.96	<0.0	0.02
		354	433	1	276
		9	8		7
ALONSO_METASTASIS_EMT_UP	35	0.60	1.96	0.00	0.02
		810	474	806	286
		1	2	5	2
NUTT_GBM_VS_AO_GLIOMA_UP	46	0.60	1.96	0.00	0.02
		570	289	197	287
		6	4	6	
PID_TCPTP_PATHWAY	42	0.60	1.96	0.00	0.02
		460	316	389	287
		8	9	1	9
DURCHDEWALD_SKIN_CARCINOGENESIS_DN	26	0.47	1.96	<0.0	0.02
	0	226	136	1	303
		1			9
ELVIDGE_HYPOXIA_BY_DMOG_UP	13	0.50	1.96	0.00	0.02
	0	511	155	207	311
		6	3		8
REACTOME_ECM_PROTEOGLYCANS	76	0.66	1.95	<0.0	0.02
		227	985	1	325
		9	9		5
SASSON_RESPONSE_TO_GONADOTROPHINS_DN	86	0.51	1.95	<0.0	0.02
		152	913	1	342
		2			6
RAGHAVACHARI_PLATELET_SPECIFIC_GENES	67	0.55	1.95	0.00	0.02
		117	668	203	392
		2	3	7	3
REACTOME_SIGNALING_BY_FLT3_FUSION_PROTEINS	19	0.69	1.95	<0.0	0.02
		268	530	1	405
		3	1		8
REACTOME_INTERLEUKIN_12_FAMILY_SIGNALING	56	0.54	1.95	<0.0	0.02
		369	545	1	410
		6	1		2
WP_MFAP5_EFFECT_ON_PERMEABILITY_AND_MOTILITY_OF_ENDOTHELIAL_CELLS_VIA_CYTOSKELETON_REARRANGEMENT	18	0.69	1.95	<0.0	0.02
		899	481	1	413
		9	6		

DESERT_STEM_CELL_HEPATOCELLULAR_CARCINOMA_SUBCLASS _UP	23	0.54	1.95	0.00	0.02
	6	425	245	211	463
		7	3		8
ROY_WOUND_BLOOD_VESSEL_UP	48	0.66	1.95	0.00	0.02
		013	012	423	512
		1	1	7	6
SIMBULAN_UV_RESPONSE_NORMAL_DN	33	0.60	1.95	0.00	0.02
		819	015	202	523
		2	6		9
WINTER_HYPOXIA_METAGENE	23	0.46	1.94	0.00	0.02
	3	857	773	403	537
		2	2	2	7
REACTOME_COLLAGEN_BIOSYNTHESIS_AND_MODIFYING_ENZY MES	67	0.64	1.94	0.00	0.02
		434	901	608	537
		4	8	5	8
HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_UP	61	0.53	1.94	<0.0	0.02
		592	699	1	548
		4	1		3
DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP	24	0.47	1.94	<0.0	0.02
	6	588	777	1	549
			7		5
PID_BETA_CATENIN_NUC_PATHWAY	72	0.49	1.94	<0.0	0.02
		498	653	1	550
		6	6		4
KEGG_PATHWAYS_IN_CANCER	32	0.41	1.94	<0.0	0.02
	3	791	611	1	552
		2	7		9
REACTOME_CELL_CELL_COMMUNICATION	12	0.49	1.94	0.00	0.02
	5	259	463	203	559
		2	3	3	3
VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_UP	15	0.52	1.94	<0.0	0.02
	9	359	425	1	559
		9			9
REACTOME_INLB_MEDIATED_ENTRY_OF_LISTERIA_MONOCYTOG ENES_INTO_HOST_CELL	15	0.70	1.94	<0.0	0.02
		461	777	1	561
		7	9		3
KHETCHOUMIAN_TRIM24_TARGETS_UP	46	0.64	1.94	0.00	0.02
		239	475	200	567
		7	5	4	4
GEISS_RESPONSE_TO_DSRNA_UP	39	0.60	1.94	0.00	0.02
		564	324	598	573
		4		8	4

RUIZ_TNC_TARGETS_DN	14	0.62	1.94	0.01	0.02
	1	755	498	041	575
		8	9	7	7
PID_ER_NONGENOMIC_PATHWAY	40	0.55	1.94	0.00	0.02
		993	268	193	581
		2	8	4	7
MORI_SMALL_PRE_BII_LYMPHOCYTE_DN	76	0.49	1.94	0.00	0.02
		083	166	204	595
		5	7	9	4
XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP	15	0.73	1.94	<0.0	0.02
		701	200	1	596
		3	3		
FRIDMAN_IMMORTALIZATION_DN	31	0.63	1.93	0.00	0.02
		056	996	202	635
		5	9	4	7
PID_PI3KCI_AKT_PATHWAY	35	0.58	1.93	<0.0	0.02
		697	783	1	666
		6	3		2
PID_FAK_PATHWAY	59	0.57	1.93	0.00	0.02
		838	729	411	668
		9	3	5	2
REACTOME_CONSTITUTIVE_SIGNALING_BY_LIGAND_RESPONSIV E_EGFR_CANCER_VARIANTS	19	0.64	1.93	<0.0	0.02
		273	812	1	67
		7	6		
WP_ASSOCIATION_BETWEEN_PHYSICOCHEMICAL_FEATURES_AN D_TOXICITY_ASSOCIATED_PATHWAYS	65	0.49	1.93	0.00	0.02
		453	559	197	680
		4	1	6	8
PID_ECADHERIN_NASCENT_AJ_PATHWAY	39	0.58	1.93	0.00	0.02
		526	590	203	685
			6	7	4
PETROVA_PROX1_TARGETS_DN	56	0.61	1.93	<0.0	0.02
		047	517	1	687
		2			
BIOCARTA_HCMV_PATHWAY	17	0.68	1.93	<0.0	0.02
		056	619	1	687
		8			6
WP_TYPE_2_PAPILLARY_RENAL_CELL_CARCINOMA	34	0.52	1.93	0.00	0.02
		663	259	213	695
		4	2	2	9
PLASARI_TGFB1_TARGETS_10HR_UP	19	0.49	1.93	0.00	0.02
		2	099	360	411
		8	6	5	3

REACTOME_RHO_GTPASE_EFFECTORS	25	0.49	1.93	0.00	0.02
	9	128	273	653	704
		4	8	6	1
MEBARKI_HCC_PROGENITOR_WNT_UP_BLOCKED_BY_FZD8CRD	11	0.53	1.93	<0.0	0.02
	2	463	299	1	708
		7			7
ZHU_SKIL_TARGETS_UP	19	0.70	1.93	0.00	0.02
		689	196	383	710
		1		9	4
ZHENG_GLIOBLASTOMA_PLASTICITY_UP	24	0.47	1.93	0.00	0.02
	4	849	370	608	711
			5	5	4
WP_G13_SIGNALING_PATHWAY	39	0.55	1.93	0.00	0.02
		520	132	196	712
		2	6	9	6
HOWLIN_CITED1_TARGETS_1_DN	37	0.60	1.93	<0.0	0.02
		991	393	1	713
		7	5		2
MARTINEZ_RESPONSE_TO TRABECTEDIN_DN	26	0.51	1.93	0.00	0.02
	1	048	029	209	733
			8	6	3
BLANCO_MELO_BRONCHIAL_EPITHELIAL_CELLS_INFLUENZA_A_I NFECTIION_UP	12	0.53	1.92	0.00	0.02
	5	03	881	193	735
			6	4	
WP_VEGFAVEGFR2_SIGNALING_PATHWAY	42	0.43	1.92	<0.0	0.02
	5	464	972	1	740
		4	5		7
KEGG_AXON_GUIDANCE	12	0.46	1.92	0.00	0.02
	8	428	894	196	742
		7	6	1	8
IKEDA_MIR1_TARGETS_UP	54	0.59	1.92	0.00	0.02
		119	921	207	747
		6	5		5
HOLLERN_EMT_BREAST_TUMOR_UP	13	0.59	1.92	<0.0	0.02
	9	385	621	1	806
			2		5
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	45	0.54	1.92	0.00	0.02
	3	331	482	798	806
		5	6	4	9
KOKKINAKIS_METHIONINE_DEPRIVATION_96HR_UP	11	0.47	1.92	0.00	0.02
	6	505	575	199	807
			4	2	5

PID_INTEGRIN5_PATHWAY	16	0.75	1.92	<0.0	0.02
		558	495	1	815
		6	3		5
REACTOME_NEPHRIN_FAMILY_INTERACTIONS	21	0.68	1.92	0.00	0.02
		304	520	379	816
		3	6	5	3
REACTOME_CONSTITUTIVE_SIGNALING_BY_EGFRVIII	15	0.70	1.92	<0.0	0.02
		230	346	1	821
		8	2		6
STREICHER_LSM1_TARGETS_DN	19	0.65	1.92	0.00	0.02
		350	349	199	832
		7	9	6	7
KIM_LIVER_CANCER_POOR_SURVIVAL_UP	22	0.68	1.92	0.00	0.02
		110	223	616	851
		3	5		5
REACTOME_REGULATION_OF_SIGNALING_BY_CBL	22	0.64	1.92	0.00	0.02
		300	144	189	867
		2	8	8	2
REACTOME_GENE_AND_PROTEIN_EXPRESSION_BY_JAK_STAT_SIGNALING_AFTER_INTERLEUKIN_12_STIMULATION	37	0.59	1.91	<0.0	0.02
		773	741	1	970
		7	1		6
LAIHO_COLORECTAL_CANCER_SERRATED_UP	10	0.57	1.91	0.00	0.02
		8	676	795	425
		6	8	5	8
HAHTOLA_SEZARY_SYNDROM_UP	96	0.48	1.91	<0.0	0.02
		714	745	1	981
		6			6
BERENJENO_TRANSFORMED_BY_RHOA_REVERSIBLY_DN	28	0.65	1.91	<0.0	0.02
		000	650	1	982
		5	3		6
WP_REGULATION_OF_ACTIN_CYTOSKELETON	14	0.45	1.91	<0.0	0.02
		8	706	657	1
		5			8
WP_MIRNA_TARGETS_IN_ECM_AND_MEMBRANE_RECEPTORS	22	0.89	1.91	<0.0	0.03
		578	509	1	023
		4	5		2
SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN	29	0.44	1.91	<0.0	0.03
		3	541	470	1
		1	2		3
NEMETH_INFLAMMATORY_RESPONSE_LPS_UP	85	0.53	1.91	0.00	0.03
		999	386	613	043
		4		5	9

WP_HIPPOMERLIN_SIGNALING_DYSREGULATION	11	0.47	1.91	<0.0	0.03
	8	135	12	1	112
		1			1
REACTOME_RHOH_GTPASE_CYCLE	37	0.53	1.91	0.00	0.03
		751	122	197	122
		2	7	6	5
PID_P38_ALPHA_BETA_PATHWAY	30	0.55	1.91	0.00	0.03
		623	024	616	133
		7	3		6
KAN_RESPONSE_TO_ARSENIC_TRIOXIDE	12	0.49	1.90	<0.0	0.03
	1	745	947	1	145
		6	9		5
WEST_ADRENOCORTICAL_TUMOR_UP	28	0.53	1.90	0.00	0.03
	8	778	432	632	153
			1	9	3
GYORFFY_MITOXANTRONE_RESISTANCE	34	0.55	1.90	<0.0	0.03
		398	886	1	156
		2	8		7
GEORGES_CELL_CYCLE_MIR192_TARGETS	59	0.63	1.90	0.01	0.03
		391	444	252	162
			7	6	4
HAN_JNK_SINGALING_UP	34	0.59	1.90	<0.0	0.03
		984	471	1	166
		8	2		8
JOHNSTONE_PARVB_TARGETS_2_DN	32	0.50	1.90	<0.0	0.03
	3	660	824	1	170
		6	1		4
WP_FOCAL_ADHESIONPI3KAKTMTORSIGNALING_PATHWAY	29	0.42	1.90	<0.0	0.03
	8	455	483	1	173
		9	2		8
PETROVA_ENDOTHELIUM_LYMPHATIC_VS_BLOOD_DN	16	0.51	1.90	0.00	0.03
	0	393	499	210	178
		8	6	5	
LE_SKI_TARGETS_UP	17	0.71	1.90	0.00	0.03
		287	560	207	186
		8	4		8
BUFFA_HYPOXIA_METAGENE	50	0.69	1.90	0.00	0.03
		511	528	845	188
			7	7	3
BIOCARTA_G1_PATHWAY	28	0.61	1.90	<0.0	0.03
		869	508	1	188
		8	6		3

KRIEG_HYPOXIA_VIA_KDM3A	52	0.55	1.90	<0.0	0.03
		807	275	1	193
			6		4
DOANE_BREAST_CANCER_CLASSES_DN	32	0.60	1.90	0.00	0.03
		659	607	202	194
		7	7		3
WESTON_VEGFA_TARGETS_6HR	48	0.57	1.90	0.00	0.03
		505	562	811	197
		2	5	4	7
ZHU_CMV_ALL_DN	11	0.52	1.90	0.01	0.03
	5	811	620	252	202
		1	4	6	2
REACTOME_EGFR_DOWNREGULATION	31	0.58	1.90	0.00	0.03
		136	627	195	211
			3	7	1
ZHENG_FOXP3_TARGETS_IN_THYMUS_UP	19	0.51	1.90	0.00	0.03
	3	474	654	198	216
		3	8		7
BURTON_ADIPOGENESIS_2	71	0.49	1.90	0.00	0.03
		130	163	393	228
		8	2	7	9
BIOCARTA_NDKDYNAMIN_PATHWAY	17	0.66	1.90	<0.0	0.03
		728	015	1	258
		5			9
REACTOME_SIGNALING_BY_SCF_KIT	43	0.54	1.90	0.00	0.03
		925	026	597	266
		3	5	6	5
JACKSON_DNMT1_TARGETS_UP	80	0.49	1.89	<0.0	0.03
		053	743	1	332
		7	2		2
SIG_CHEMOTAXIS	45	0.52	1.89	0.00	0.03
		523	763	191	337
		6	2	6	4
ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN	10	0.49	1.89	0.00	0.03
	2	301	693	409	343
		3	8		
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	14	0.53	1.89	0.00	0.03
	0	309	602	801	361
		8		6	1
PID_VEGFR1_2_PATHWAY	69	0.50	1.89	0.00	0.03
		448	559	404	368
		3	7	9	

PETRETTO_CARDIAC_HYPERTROPHY	34	0.65	1.89	0.00	0.03
		553	528	814	371
		8		7	
MARKEY_RB1_CHRONIC_LOF_UP	11	0.49	1.89	0.00	0.03
	1	460	411	202	406
		1	6	8	1
RASHI_RESPONSE_TO_IONIZING_RADIATION_4	46	0.51	1.89	0.00	0.03
		949	311	209	417
		1	6	2	6
ZHU_CMV_24_HR_DN	81	0.57	1.89	0.00	0.03
		600	343	441	421
		2	4	5	5
REACTOME_ELASTIC_FIBRE_FORMATION	44	0.65	1.89	0.01	0.03
		585	266	810	424
		2	3	9	6
XU_HGF_SIGNALING_NOT_VIA_AKT1_48HR_UP	34	0.55	1.89	0.00	0.03
		876	197	396	439
		9	2		1
KANG_AR_TARGETS_DN	18	0.71	1.89	0.00	0.03
		683	124	613	441
		7	2	5	2
BIOCARTA_GCR_PATHWAY	17	0.66	1.89	0.00	0.03
		618	070	192	449
		9	3	7	2
LINDGREN_BLADDER_CANCER_HIGH_RECURRENCE	48	0.63	1.89	0.01	0.03
		180	132	010	45
		7	1	1	
PID_SYNDECAN_2_PATHWAY	33	0.58	1.89	0.00	0.03
		000	152	401	451
		8	8	6	8
WP_PDGF_PATHWAY	40	0.53	1.88	0.00	0.03
		553	885	626	477
			7	3	7
WP_HEPATITIS_B_INFECTIION	13	0.44	1.88	<0.0	0.03
	8	208	897	1	485
		7	6		
WP_OXIDATIVE_DAMAGE	40	0.54	1.88	0.00	0.03
		769	922	404	489
		6	7		8
WOO_LIVER_CANCER_RECURRENCE_UP	10	0.48	1.88	0.00	0.03
	3	996	629	208	523
		3	9	3	5

PID_PTP1B_PATHWAY	51	0.55	1.88	<0.0	0.03
		767	654	1	528
		3			5
DIRMEIER_LMP1_RESPONSE_LATE_UP	54	0.54	1.88	0.00	0.03
		683	554	814	531
		4	3	7	2
WP_RANKLRANK_RECEPTOR_ACTIVATOR_OF_NFKB_LIGAND_SIGNALING_PATHWAY	55	0.48	1.88	<0.0	0.03
		025	580	1	532
		4	3		8
PID_INTEGRIN_A9B1_PATHWAY	25	0.63	1.88	0.00	0.03
		253	673	410	537
			5	7	5
PID_RAC1_PATHWAY	53	0.52	1.88	0.00	0.03
		019	700	211	540
		9	3		2
WP_NETRINUNC5B_SIGNALING_PATHWAY	49	0.51	1.88	<0.0	0.03
		926	418	1	568
			7		7
REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS	18	0.76	1.88	0.00	0.03
		345	388	206	570
		2	5	2	9
RODWELL_AGING_KIDNEY_NO_BLOOD_UP	20	0.50	1.88	0.00	0.03
		9	146	259	418
			2	3	4
					8
PID_ERBB1_DOWNSTREAM_PATHWAY	10	0.48	1.88	0.00	0.03
		5	547	109	213
			7	3	2
					2
JEON_SMAD6_TARGETS_UP	24	0.67	1.88	0.00	0.03
		232	010	801	655
		5	3	6	
ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_UP	17	0.42	1.88	0.00	0.03
		5	024	038	192
			9	4	3
					3
WINTER_HYPOXIA_UP	93	0.57	1.87	0.01	0.03
		815	882	709	665
			3	4	
SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_UP	18	0.68	1.87	0.00	0.03
		749	957	198	665
			4	4	3
GROSS_HYPOXIA_VIA_ELK3_DN	14	0.46	1.88	0.00	0.03
		7	430	041	411
			3	8	5
					1

WP_EGFEGFR_SIGNALING_PATHWAY	16	0.45	1.87	0.00	0.03
	2	164	885	191	675
		2	5	6	1
DANG_MYC_TARGETS_DN	30	0.59	1.87	0.00	0.03
		455	758	612	677
		3	8	2	2
KANG_IMMORTALIZED_BY_TERT_UP	87	0.46	1.87	0.00	0.03
		428	798	206	685
		3	2	6	4
BIOCARTA_FAS_PATHWAY	30	0.60	1.87	0.00	0.03
		251	759	414	688
		6	8	1	5
GENTILE_UV_HIGH_DOSE_DN	28	0.44	1.87	<0.0	0.03
	0	872	684	1	700
		3	5		8
WIERENGA_STAT5A_TARGETS_GROUP2	53	0.56	1.87	0.00	0.03
		948	621	603	711
		1	1	6	8
REACTOME_SIGNALING_BY_ERBB2_ECD_MUTANTS	16	0.66	1.87	<0.0	0.03
		332	552	1	726
		9	3		1
VERRECCHIA_RESPONSE_TO_TGFB1_C5	21	0.63	1.87	0.01	0.03
		195	19	209	766
		3		7	1
AMIT_EGF_RESPONSE_60_HELA	44	0.55	1.87	0.00	0.03
		787	223	396	768
		8	5	8	
REACTOME_DEREGULATED_CDK5_TRIGGERS_MULTIPLE_NEURO DEGENERATIVE_PATHWAYS_IN_ALZHEIMER_S_DISEASE_MODELS	22	0.62	1.87	<0.0	0.03
		444	287	1	768
		5	1		1
NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP	85	0.64	1.87	0.01	0.03
		266	339	464	774
			6	4	7
PID_IL3_PATHWAY	24	0.57	1.87	0.00	0.03
		402	296	787	777
		8	4	4	6
MEBARKI_HCC_PROGENITOR_WNT_UP_CTNNB1_INDEPENDENT	22	0.74	1.87	0.00	0.03
		973	226	603	778
		4	3	6	8
CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_DN	51	0.57	1.87	0.01	0.03
		201	347	247	780
		6	3	4	9

GAL_LEUKEMIC_STEM_CELL_DN	22	0.46	1.87	0.00	0.03
	7	403	401	2	782
		6	3		1
WP_RAC1PAK1P38MMP2_PATHWAY	68	0.48	1.87	0.00	0.03
		977	368	205	784
		1	6	3	2
PID_ANGIOPOIETIN_RECEPTOR_PATHWAY	49	0.54	1.86	0.00	0.03
		887	972	391	822
		7		4	6
LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN	13	0.48	1.87	0.00	0.03
	4	730	003	407	830
		2	6	3	8
WIERENGA_STAT5A_TARGETS_UP	19	0.43	1.86	0.00	0.03
	5	420	980	404	831
		6	4	9	5
ELVIDGE_HYPOXIA_UP	16	0.46	1.86	0.00	0.03
	7	370	876	210	846
		2	6	1	7
BROWNE_HCMV_INFECTION_20HR_DN	92	0.48	1.86	0.00	0.03
		367	882	196	855
		6	7	5	5
PID_NECTIN_PATHWAY	30	0.61	1.86	0.00	0.03
		92	743	596	868
			6	4	6
KIM_GLIS2_TARGETS_UP	82	0.64	1.86	0.00	0.03
		69	745	421	879
			1	1	4
WP_THYMIC_STROMAL_LYMPHOPOIETIN_TSLP_SIGNALING_PATHWAY	47	0.52	1.86	0.00	0.03
		938	773	598	879
		4	6	8	9
GALINDO_IMMUNE_RESPONSE_TO_ENTEROTOXIN	80	0.56	1.86	0.01	0.03
		170	658	590	888
		7	3	5	9
SCHOEN_NFKB_SIGNALING	32	0.61	1.86	0.00	0.03
		661	498	793	931
		6	8	7	
REACTOME_SIGNALING_BY_INTERLEUKINS	43	0.42	1.86	0.00	0.03
	7	263	523	406	932
		3	8	5	7
WP_SENESCENCE_AND_AUTOPHAGY_IN_CANCER	10	0.46	1.86	0.00	0.03
	4	403	530	411	941
			5	5	2

FRIDMAN_SENESCENCE_UP	75	0.51	1.86	0.00	0.03
		359	354	410	973
		6	9	7	9
REACTOME_SIGNAL_TRANSDUCTION_BY_L1	21	0.61	1.86	0.00	0.03
		850	312	401	979
		1	8	6	
WP_MET_IN_TYPE_1_PAPILLARY_RENAL_CELL_CARCINOMA	59	0.50	1.86	0.00	0.03
		234	223	196	990
		5	1	1	8
BECKER_TAMOXIFEN_RESISTANCE_DN	52	0.52	1.86	0.00	0.03
		917	244	209	993
		8	4	6	9
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_17	19	0.63	1.86	0.00	0.04
		756	173	607	000
		6	4	3	9
CLASPER_LYMPHATIC_VESSELS_DURING_METASTASIS_DN	35	0.74	1.86	0.00	0.04
		352	136	634	005
		6	1	2	8
WP_COPPER_HOMEOSTASIS	50	0.49	1.86	<0.0	0.04
		629	026	1	045
		9			5
PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_UP	30	0.58	1.85	0.00	0.04
		358	901	194	095
		3	1	9	7
AZARE_STAT3_TARGETS	24	0.64	1.85	0.00	0.04
		712	829	594	113
		9	5	1	7
REACTOME_RHOD_GTPASE_CYCLE	51	0.52	1.85	0.00	0.04
		304	761	609	128
		7	7	8	
LINDVALL_IMMORTALIZED_BY_TERT_DN	70	0.53	1.85	0.00	0.04
		272	533	823	212
		3	6		2
WP_INTERFERON_TYPE_I_SIGNALING_PATHWAYS	54	0.49	1.85	0.00	0.04
		545	388	191	267
		3		2	4
SARTIPY_NORMAL_AT_INSULIN_RESISTANCE_UP	29	0.60	1.85	0.00	0.04
		785	129	429	282
		2	2	2	4
CHIBA_RESPONSE_TO_TSA_DN	21	0.65	1.85	0.00	0.04
		463	32	816	288
		2		3	9

CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN	91	0.52	1.85	0.00	0.04
		413	131	823	292
		3	1		2
BONCI_TARGETS_OF_MIR15A_AND_MIR16_1	90	0.48	1.85	<0.0	0.04
		216	142	1	300
		3	2		8
WP_TYPE_I_COLLAGEN_SYNTHESIS_IN_THE_CONTEXT_OF_OSTEOGENESIS_IMPERFECTA	33	0.58	1.85	0.01	0.04
		563	158	185	307
		2	7	8	6
KEGG_MELANOMA	70	0.48	1.85	<0.0	0.04
		051	180	1	310
		7	4		1
GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_DN	25	0.66	1.85	0.00	0.04
		919	199	803	312
				2	7
TOOKER_GEMCITABINE_RESISTANCE_DN	11	0.48	1.85	<0.0	0.04
		9	347	208	1
		4	6		9
YANG_BREAST_CANCER_ESR1_BULK_DN	22	0.60	1.85	0.00	0.04
		493	211	601	328
			2	2	3
REACTOME_NEGATIVE_REGULATORS_OF_DDX58_IFIH1_SIGNALING	34	0.55	1.84	0.00	0.04
		844	956	202	331
		4	9	8	5
REACTOME_SIGNALLING_TO_RAS	20	0.60	1.84	0.01	0.04
		837	876		339
		7	5		7
LINDVALL_IMMORTALIZED_BY_TERT_UP	62	0.49	1.84	0.00	0.04
		546	884	396	349
			1		5
SANA_TNF_SIGNALING_UP	82	0.57	1.84	0.02	0.04
		986	796	381	354
		2	6		8
PID_S1P_S1P2_PATHWAY	24	0.59	1.84	0.01	0.04
		900	764	386	356
		3	6	1	6
DE_YY1_TARGETS_DN	92	0.52	1.84	<0.0	0.04
		712	801	1	363
		9			8
SIG_INSULIN_RECEPTOR_PATHWAY_IN_CARDIAC_MYOCYTES	51	0.50	1.84	0.00	0.04
		201	695	383	365
		8	6	1	2

YANG_BREAST_CANCER_ESR1_LASER_DN	46	0.54	1.84	0.00	0.04
		013	707	197	372
		4		2	4
BIOCARTA_RAC1_PATHWAY	21	0.61	1.84	0.00	0.04
		376	592	392	390
		1	4	9	8
REACTOME_FLT3_SIGNALING	38	0.57	1.84	0.01	0.04
		154	594	789	402
		3	8	3	4
REACTOME_THE_NLRP3_INFLAMMASOME	16	0.69	1.84	0.00	0.04
		548	524	194	407
		2	1	9	6
TARTE_PLASMA_CELL_VS_PLASMABLAST_DN	29	0.53	1.84	0.01	0.04
		7	631	445	687
		3	7	8	4
REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_A ND_MAPK	18	0.60	1.84	0.00	0.04
		301	394	779	439
		2	5	7	1
REACTOME_LAMININ_INTERACTIONS	30	0.68	1.84	0.00	0.04
		703	292	990	450
			3	1	2
PID_PDGFR_A_PATHWAY	22	0.62	1.84	0.00	0.04
		611	332	386	454
		5	7	8	6
BIOCARTA_GSK3_PATHWAY	20	0.62	1.84	0.00	0.04
		771	298	194	459
		9	1	2	4
WP_GASTRIN_SIGNALING_PATHWAY	11	0.46	1.83	0.00	0.04
		4	088	996	618
		8	4	6	4
BASAKI_YBX1_TARGETS_UP	28	0.55	1.84	0.03	0.04
		0	692	044	151
		5	6	3	
LU_EZH2_TARGETS_DN	37	0.42	1.83	<0.0	0.04
		7	147	998	1
		3	8		3
LU_TUMOR_ANGIOGENESIS_UP	25	0.59	1.83	0.00	0.04
		672	922	621	56
		9	1	1	
WP_PROLACTIN_SIGNALING_PATHWAY	76	0.48	1.83	0.00	0.04
		075	628	204	688
		4	4	5	

KEGG_CHRONIC_MYELOID_LEUKEMIA	73	0.47	1.83	0.00	0.04
		378	565	396	702
		9	7		8
VERRECCHIA_RESPONSE_TO_TGFB1_C2	21	0.73	1.83	0.00	0.04
		189	537	419	704
		1	8	3	1
REACTOME_SIGNALING_BY_ERBB4	57	0.46	1.83	<0.0	0.04
		543	119	1	713
		5	2		5
SERVITJA_ISLET_HNF1A_TARGETS_UP	16	0.49	1.83	0.00	0.04
		3	520	092	4
		9	9		3
AMIT_SERUM_RESPONSE_480_MCF10A	35	0.56	1.83	0.00	0.04
		622	045	419	716
		6	3	3	3
ELVIDGE_HIF1A_TARGETS_UP	66	0.52	1.83	0.00	0.04
		016	124	409	722
		5	9	8	
ANASTASSIOU_MULTICANCER_INVASIVENESS_SIGNATURE	64	0.82	1.83	0.00	0.04
		974	006	819	722
		6	1	7	8
SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP	22	0.62	1.83	0.00	0.04
		369	214	813	723
		8	1		9
FLECHNER_PBL_KIDNEY_TRANSPLANT_OK_VS_DONOR_DN	38	0.51	1.83	0.00	0.04
		886	141	396	725
		6	9		5
KAPOSI_LIVER_CANCER_MET_UP	18	0.66	1.82	0.00	0.04
		074	949	403	726
		9	1	2	8
BURTON_ADIPOGENESIS_PEAK_AT_16HR	41	0.63	1.83	0.03	0.04
		386	047	042	727
		4	5	6	8
THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP	76	0.50	1.83	0.00	0.04
		366	164	204	728
		4	3	5	3
ZHENG_BOUND_BY_FOXP3	47	0.43	1.82	0.00	0.04
		5	682	885	578
		4			1
SESTO_RESPONSE_TO_UV_C2	53	0.55	1.83	0.00	0.04
		708	226	808	730
		1	4	1	6

REACTOME_RHO_GTPASE_CYCLE	44	0.39	1.82	0.00	0.04
	0	872	908	785	731
		3	2	9	9
WILSON_PROTEASES_AT_TUMOR_BONE_INTERFACE_UP	20	0.66	1.83	0.00	0.04
		275	247	204	733
		9		5	4
WP_HEAD_AND_NECK_SQUAMOUS_CELL_CARCINOMA	73	0.46	1.82	0.00	0.04
		986	956	391	735
		7	1	4	8
WANG_RESPONSE_TO_BEXAROTENE_DN	29	0.57	1.83	0.00	0.04
		237	168	795	739
		6	4	2	4
AMIT_EGF_RESPONSE_240_HELA	58	0.53	1.82	0.01	0.04
		183	841	061	741
		7	5	6	3
CLASPER_LYMPHATIC_VESSELS_DURING_METASTASIS_UP	20	0.65	1.83	0.01	0.04
		046	248	207	744
		9	2	2	5
HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_2_UP	56	0.49	1.82	<0.0	0.04
		212	809	1	747
		8	9		3
WANG_SMARCE1_TARGETS_DN	36	0.43	1.83	0.00	0.04
		6	165	255	437
		2	8	6	4
PARK_APL_PATHOGENESIS_DN	48	0.53	1.82	0.00	0.04
		702	761	798	755
		5	6	4	8
PECE_MAMMARY_STEM_CELL_DN	13	0.45	1.83	0.00	0.04
		6	454	257	199
		6	3	6	6
PID_ERBB1_INTERNALIZATION_PATHWAY	41	0.52	1.83	0.00	0.04
		508	366	808	765
		9	1	1	9
THUM_SYSTOLIC_HEART_FAILURE_UP	40	0.46	1.83	0.00	0.04
		1	528	275	209
		8	6	6	4
KEGG_ADHERENS_JUNCTION	73	0.50	1.83	0.00	0.04
		160	321	795	772
		4	1	2	3
BLANCO_MELO_HUMAN_PARAINFLUENZA_VIRUS_3_INFECTION_A594_CELLS_UP	19	0.57	1.83	0.02	0.04
		3	696	290	788
		8	2	8	2

AMIT_EGF_RESPONSE_480_HELA	15	0.50	1.82	0.01	0.04
	9	001	599	244	774
		7	1	8	6
REACTOME_RHOV_GTPASE_CYCLE	33	0.59	1.82	0.01	0.04
		866	545	757	775
		7	2	8	6
KIM_WT1_TARGETS_12HR_DN	20	0.42	1.82	0.00	0.04
	7	776	610	207	780
			7		4
WP_SPINAL_CORD_INJURY	11	0.46	1.82	<0.0	0.04
	6	298	496	1	783
		7	9		7
MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP	24	0.65	1.82	0.00	0.04
		918	548	423	784
		4	7	7	9
HOSHIDA_LIVER_CANCER_SURVIVAL_UP	72	0.47	1.82	0.00	0.04
		967	512	396	785
		9	8		8
REACTOME_SIGNALING_BY_KIT_IN_DISEASE	20	0.61	1.82	0.00	0.04
		699	620	776	787
		8	6	7	1
REACTOME_RHOU_GTPASE_CYCLE	34	0.55	1.82	0.01	0.04
		029	654	711	792
		1	1		2
URS_ADIPOCYTE_DIFFERENTIATION_DN	31	0.59	1.82	0.01	0.04
		591	621	972	796
		7	9	4	2
DUTERTRE ESTRADIOL_RESPONSE_24HR_DN	49	0.42	1.82	0.00	0.04
	6	573	442	384	799
		5	7	6	6
WP_PI3KAKT_SIGNALING_PATHWAY	32	0.39	1.82	<0.0	0.04
	1	731	288	1	820
			7		5
GROSS_HYPOXIA_VIA_ELK3_AND_HIF1A_UP	13	0.43	1.82	0.00	0.04
	7	841	234	410	822
		5	3	7	1
REACTOME_CELL_JUNCTION_ORGANIZATION	90	0.47	1.82	0.00	0.04
		475	256	823	823
		6			8
PID_NFKAPPAB_CANONICAL_PATHWAY	22	0.63	1.82	0.00	0.04
		825	354	204	826
		6	9	9	8

REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	10	0.47	1.82	0.00	0.04
	7	777	327	988	827
		9	5	1	1
SESTO_RESPONSE_TO_UV_C1	69	0.52	1.82	0.01	0.04
		487	289	106	831
		8	5	2	2
ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION	12	0.57	1.82	0.01	0.04
	2	444	138	207	846
		4	8	2	7
WP_SARSCOV2_INNATE_IMMUNITY_EVASION_AND_CELLSPECIFIC_IMMUNE_RESPONSE	66	0.50	1.82	0.00	0.04
		920	155	950	849
		2	2	6	6
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_CYAN_UP	16	0.64	1.81	0.00	0.04
		916	942	978	904
		6	8	5	6
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_UP	15	0.46	1.81	0.00	0.04
	2	797	99	204	907
		9		1	2
CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_DN	16	0.48	1.81	0.00	0.04
	5	278	951	617	911
		7	1	3	5
PID_ILK_PATHWAY	45	0.53	1.81	0.00	0.04
		743	879	413	92
				2	
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	11	0.48	1.81	0.00	0.04
	1	795	843	206	924
		8	4	6	5
VERRECCHIA_RESPONSE_TO_TGFB1_C1	19	0.63	1.81	0.01	0.04
		863	664	656	942
		6		3	8
WP_HUMAN_THYROID_STIMULATING_HORMONE_TSH_SIGNALING_PATHWAY	65	0.46	1.81	0.00	0.04
		195	680	789	944
		3	6		4
REACTOME_CARGO_RECOGNITION_FOR_CLATHRIN_MEDIATED_ENDOCYTOSIS	10	0.44	1.81	<0.0	0.04
	4	220	687	1	952
		7	6		
MITSIADES_RESPONSE_TO_APLIDIN_DN	24	0.56	1.81	0.01	0.04
	3	378	762	898	952
			5	7	6
LIEN_BREAST_CARCINOMA_METAPLASTIC	33	0.68	1.81	0.01	0.04
		671	694	840	960
			7	5	8

MARCHINI TRABECTEDIN RESISTANCE_DN	45	0.54	1.81	0.00	0.04
		947	611	604	961
		2	5	8	1
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	95	0.45	1.81	0.00	0.04
		414	586	773	962
		7	4	7	1
BERENJENO_TRANSFORMED_BY_RHOA_FOREVER_DN	29	0.58	1.81	0.01	0.04
		312	548	026	966
		3	4	7	6
LINDGREN_BLADDER_CANCER_CLUSTER_2B	37	0.53	1.81	0.01	0.04
		5	076	696	006
			6		5
JOHANSSON_GLIOMAGENESIS_BY_PDGF_UP	57	0.52	1.81	<0.0	0.04
		614	410	1	977
		6	8		2
WP_PHOTODYNAMIC_THERAPYINDUCED_API_SURVIVAL_SIGNALING	50	0.48	1.81	0.00	0.04
		302	421	202	985
		3	4		1
LIM_MAMMARY_LUMINAL_MATURE_DN	92	0.54	1.81	0.01	0.04
		514	444	833	987
		9			1
LU_IL4_SIGNALING	89	0.50	1.81	0.00	0.04
		111	452	408	992
		5	6	2	8
SASAI_RESISTANCE_TO NEOPLASTIC TRANSFORMATION	48	0.58	1.81	0.02	0.04
		828	351	653	996
		7	4	1	1
BORCZUK_MALIGNANT_MESOTHELIOMA_UP	29	0.53	1.81	0.01	0.04
		8	221	462	882
		7	5	8	3
GILDEA_METASTASIS	28	0.63	1.81	0.00	0.05
		832	280	204	012
		3	8	1	7
SEMENZA_HIF1_TARGETS	36	0.58	1.81	0.01	0.05
		330	232	052	026
		4	5	6	6
WILCOX_RESPONSE_TO_PROGESTERONE_DN	60	0.54	1.81	0.01	0.05
		505	085	222	071
		9	1		1
CROONQUIST_NRAS_SIGNALING_UP	37	0.63	1.81	0.00	0.05
		636	097	784	076
			5	3	4

BROCKE_APOPTOSIS_REVERSED_BY_IL6	14	0.45	1.80	0.00	0.05
	2	971	982	851	107
		9	4	1	6
KARLSSON_TGFB1_TARGETS_UP	12	0.53	1.80	0.01	0.05
	0	472	932	452	121
		8	6	3	1
GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_UP	55	0.54	1.80	0.01	0.05
		594	898	035	124
		7	1	2	3
ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN	45	0.52	1.80	0.00	0.05
		282	875	390	125
		2	9	6	4
BIOCARTA_CTCF_PATHWAY	24	0.61	1.80	0.00	0.05
		130	825	792	137
		5	8	1	5
LEE_CALORIE_RESTRICTION_NEOCORTEX_DN	58	0.46	1.80	<0.0	0.05
		798	735	1	173
		9	5		3
REACTOME_SIGNALLING_TO_ERKS	33	0.53	1.80	0.00	0.05
		149	572	808	182
		3	1	1	3
YOSHIMURA_MAPK8_TARGETS_DN	35	0.39	1.80	<0.0	0.05
	6	696	635	1	184
		2	5		3
ZHAN_EARLY_DIFFERENTIATION_GENES_DN	42	0.53	1.80	0.01	0.05
		592	687	207	184
		9	2	2	3
REACTOME_L1CAM_INTERACTIONS	12	0.44	1.80	0.00	0.05
	0	661	661	390	184
			9	6	5
LY_AGING_OLD_DN	54	0.65	1.80	0.01	0.05
		358	575	257	191
		3		9	8
MARKEY_RB1_ACUTE_LOF_DN	22	0.50	1.80	0.01	0.05
	5	904	365	408	207
		6	9	5	5
LIANG_SILENCED_BY_METHYLATION_2	52	0.54	1.80	0.01	0.05
		977	456	642	209
		6	2	7	4
WP_EGFR_TYROSINE_KINASE_INHIBITOR_RESISTANCE	84	0.45	1.80	0.00	0.05
		613	380	386	209
		2	5	8	6

GENTILE_UV_RESPONSE_CLUSTER_D5	35	0.55	1.80	0.00	0.05
		472	475	406	210
			1	5	6
YIH_RESPONSE_TO_ARSENITE_C4	17	0.61	1.80	0.00	0.05
		136	397	386	211
		5	4	1	6
LINDGREN_BLADDER_CANCER_CLUSTER_1_DN	36	0.42	1.80	0.01	0.05
	8	169	496	010	211
			3	1	7
LIM_MAMMARY_STEM_CELL_UP	46	0.48	1.80	0.02	0.05
	5	800	416	626	214
		5	7	3	1
SEIDEN_ONCOGENESIS_BY_MET	88	0.56	1.80	0.01	0.05
		490	332	257	214
		4	5	9	4
BIOCARTA_CREB_PATHWAY	21	0.60	1.80	0.00	0.05
		627	289	417	229
		6	7	5	2
GHANDHI_DIRECT_IRRADIATION_UP	98	0.48	1.80	0.00	0.05
		363	224	203	240
		5	1	7	1
WP_APOPTOSIS_MODULATION_BY_HSP70	19	0.60	1.80	0.00	0.05
		150	164	207	243
		4	8		2
SASAKI_ADULT_T_CELL_LEUKEMIA	15	0.45	1.80	0.00	0.05
	9	616	229	835	248
		3	7	1	2
MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN	49	0.42	1.80	0.00	0.05
	7	231	170	202	251
		6	8		7
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIGNALING_PATHWAYS	56	0.51	1.80	0.00	0.05
		260	077	616	275
		4	2		6
WP_PHOTODYNAMIC_THERAPYINDUCED_HIF1_SURVIVAL_SIGNALING	37	0.52	1.80	0.01	0.05
		835	042	434	282
		3	1	4	9
SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP	15	0.48	1.79	0.01	0.05
	7	169	957	397	313
		1		2	7
ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF	21	0.48	1.79	0.01	0.05
	3	247	843	636	339
		7	2		7

BIOCARTA_MET_PATHWAY	33	0.55	1.79	0.00	0.05
		037	862	400	344
		5		8	4
LEI_MYB_TARGETS	31	0.42	1.79	0.00	0.05
	1	072	862	203	355
		7	7	7	3
PID_LYSOPHOSPHOLIPID_PATHWAY	65	0.49	1.79	0.01	0.05
		083	723	652	358
		4	5	9	5
JISON_SICKLE_CELL_DISEASE_UP	17	0.48	1.79	0.00	0.05
	8	722	740	209	359
		1	2	2	
ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_DN	20	0.59	1.79	<0.0	0.05
		830	698	1	360
		4	1		3
WINZEN_DEGRADED_VIA_KHSRP	96	0.48	1.79	0.00	0.05
		551	742	854	368
		3	2	7	6
YANAGIHARA_ESX1_TARGETS	28	0.56	1.79	0.01	0.05
		414	761	178	368
		2	7	8	7
BROWNE_HCMV_INFECTION_12HR_DN	94	0.46	1.79	<0.0	0.05
		469	525	1	430
		8	7		9
BOQUEST_STEM_CELL_UP	25	0.52	1.79	0.01	0.05
	4	785	386	642	488
		4	7	7	7
REACTOME_SIGNAL_AMPLIFICATION	33	0.52	1.79	0.00	0.05
		263	184	659	541
		2	1	3	5
HAHTOLA_MYCOSIS_FUNGOIDES_UP	15	0.64	1.79	0.01	0.05
		951	187	028	551
			7	8	3
REACTOME_LISTERIA_MONOCYTOGENES_ENTRY_INTO_HOST_CELLS	20	0.62	1.79	0.01	0.05
		312	204	028	552
		7	6	8	1
JINESH_BLEBBISHIELD_TO_IMMUNE_CELL_FUSION_PBSHMS_UP	36	0.40	1.79	0.00	0.05
	5	419	068	392	554
		4	1	2	3
OSADA_ASCL1_TARGETS_DN	24	0.61	1.79	0.00	0.05
		972	218	976	557
		6	2	6	1

OKUMURA_INFLAMMATORY_RESPONSE_LPS	17	0.39	1.79	<0.0	0.05
	2	391	079	1	560
		3	8		2
MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN	19	0.68	1.78	0.01	0.05
		644	995	268	561
		9	9	5	2
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	10	0.49	1.79	0.01	0.05
	9	739	226	046	563
		6	9		8
BARIS_THYROID_CANCER_DN	58	0.47	1.79	0.00	0.05
		730	090	195	567
		3	8	7	7
WP_APOPTOSISRELATED_NETWORK_DUE_TO_ALTERED_NOTCH3_IN_OVARIAN_CANCER	53	0.47	1.78	0.00	0.05
		686	965	408	567
		2	2	2	9
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_DN	20	0.66	1.78	0.00	0.05
		899	938	414	568
		9	2	1	7
SMIRNOV_RESPONSE_TO_IR_2HR_UP	51	0.49	1.78	0.01	0.05
		364	997	523	570
				8	9
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	81	0.53	1.79	0.00	0.05
		230	104	860	571
		7	1	2	5
NGUYEN_NOTCH1_TARGETS_DN	78	0.45	1.78	0.00	0.05
		911	876	829	573
		1	6	9	1
SCHRAETS_MLL_TARGETS_DN	34	0.58	1.79	0.01	0.05
		264	006	397	578
			3	2	2
BROWNE_HCMV_INFECTION_8HR_UP	98	0.41	1.78	<0.0	0.05
		759	883	1	581
		9	9		2
WP_PATHWAYS_IN_CLEAR_CELL_RENAL_CELL_CARCINOMA	83	0.47	1.78	0.00	0.05
		181	751	430	597
		1	3	1	5
WANG_CLIM2_TARGETS_DN	17	0.46	1.78	0.00	0.05
	2	086	775	619	597
		5	9	8	7
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	25	0.41	1.78	<0.0	0.05
	7	863	794	1	599
		8	7		4

IKEDA_MIR133_TARGETS_UP	43	0.55	1.78	0.01	0.05
		018	728	446	600
		2	7	3	7
BIOCARTA_G2_PATHWAY	24	0.62	1.78	0.01	0.05
		200	641	458	603
		2	4	3	9
FOURNIER_ACINAR_DEVELOPMENT_LATE_2	27	0.53	1.78	0.02	0.05
	6	864	675	719	606
			4	7	9
HELLEBREKERS_SILENCED_DURING_TUMOR_ANGIOGENESIS	76	0.49	1.78	0.00	0.05
		547	603	806	609
		7	9	5	8
WP_ALPHA_6_BETA_4_SIGNALING_PATHWAY	33	0.57	1.78	0.01	0.05
		332	652	646	611
		7	4	1	
REACTOME_ACTIVATION_OF_IRF3_IRF7_MEDIATED_BY_TBK1_IK K_EPSILON	17	0.60	1.78	0.00	0.05
		843	691	409	611
		4	7		6
MANALO_HYPOXIA_UP	19	0.44	1.78	0.01	0.05
	9	349	542	050	624
			9	4	8
REACTOME_CD28_CO_STIMULATION	33	0.51	1.78	0.00	0.05
		616	506	575	633
		4	9	8	4
KIM_HYPOXIA	17	0.67	1.78	0.02	0.05
		438	466	066	642
		8	6	1	7
REACTOME_NEGATIVE_REGULATION_OF_MET_ACTIVITY	21	0.57	1.78	0.00	0.05
		260	441	388	646
		6	7	3	7
MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP	25	0.40	1.78	0.00	0.05
	6	632	407	200	652
		6	9	4	2
REACTOME_SIGNALING_BY_EGFR_IN_CANCER	25	0.55	1.78	0.00	0.05
		741	323	590	654
		1	2	6	7
RIGGINS_TAMOXIFEN_RESISTANCE_DN	21	0.43	1.78	<0.0	0.05
	6	440	292	1	658
		7	7		3
IGLESIAS_E2F_TARGETS_UP	14	0.51	1.78	0.01	0.05
	3	325	352	492	659
		1	8	5	6

WP_CANONICAL_AND_NONCANONICAL_TGFB_SIGNALING	17	0.67	1.78	0.00	0.05
		293	331	617	660
		8		3	1
PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_7	36	0.38	1.78	0.00	0.05
	9	668	059	208	664
		9	3	3	6
LI_CISPLATIN_RESISTANCE_UP	25	0.55	1.78	0.00	0.05
		477	137	840	666
			4	3	5
LEI_HOXC8_TARGETS_DN	17	0.64	1.78	0.01	0.05
		077	356	037	669
		2	7	3	1
WP_PANCREATIC_ADENOCARCINOMA_PATHWAY	89	0.44	1.78	<0.0	0.05
		028	110	1	670
		8	2		6
DAUER_STAT3_TARGETS_UP	47	0.54	1.78	0.01	0.05
		575	211	247	670
		4	4	4	6
POS_HISTAMINE_RESPONSE_NETWORK	29	0.53	1.78	<0.0	0.05
		600	227	1	671
		9	6		9
JAEGER_METASTASIS_UP	43	0.59	1.78	0.02	0.05
		363	061	365	674
		3	1	6	7
GROSS_HYPOXIA_VIA_ELK3_AND_HIF1A_DN	10	0.42	1.78	0.00	0.05
	2	510	138	616	676
		6	2		7
BURTON_ADIPOGENESIS_9	82	0.44	1.78	0.00	0.05
		848	240	603	677
		5	5	6	6
PID_ERBB4_PATHWAY	38	0.51	1.78	0.00	0.05
		900	145	550	682
		3	5	5	7
HOLLERN_SOLID_NODULAR_BREAST_TUMOR_DN	30	0.60	1.78	0.01	0.05
		210	064	587	683
		8	1	3	6
GRABARCZYK_BCL11B_TARGETS_UP	73	0.47	1.78	0.01	0.05
		973	147	616	692
		1	3	2	5
CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP	17	0.55	1.77	0.02	0.05
	4	657	929	959	715
			9	8	2

SIG_PIP3_SIGNALING_IN_CARDIAC_MYOCYTES	67	0.46	1.77	0.00	0.05
		095	877	192	729
		8	2	7	1
REACTOME_NEGATIVE_REGULATION_OF_THE_PI3K_AKT_NETWORK	11	0.42	1.77	<0.0	0.05
	2	577	852	1	729
		4	6		6
TSAL_RESPONSE_TO_IONIZING_RADIATION	14	0.43	1.77	0.00	0.05
	7	892	601	8	806
		4			3
LANG_MYB_FAMILY_TARGETS	29	0.55	1.77	0.00	0.05
		606	672	404	808
		8	4	9	1
KAYO_CALORIE_RESTRICTION_MUSCLE_UP	93	0.47	1.77	0.00	0.05
		017	635	592	816
		9	9	9	6
WP_INTEGRATED_CANCER_PATHWAY	44	0.52	1.77	0.01	0.05
		826	535	840	817
		7	3	5	2
MEBARKI_HCC_PROGENITOR_WNT_UP_CTNNB1_DEPENDENT	78	0.53	1.77	0.00	0.05
		781	320	840	820
		3	3	3	7
PID_DELTA_NP63_PATHWAY	46	0.50	1.77	0.00	0.05
		382	546	196	823
		8		1	2
ELVIDGE_HIF1A_TARGETS_DN	89	0.46	1.77	0.01	0.05
		755	604	455	823
		9	5	3	5
GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_DN	37	0.50	1.77	0.00	0.05
		704	496	414	829
		9	3	1	6
MCCABE_HOXC6_TARGETS_DN	19	0.62	1.77	0.02	0.05
		105	478	357	829
				6	6
REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE	35	0.58	1.77	0.01	0.05
		100	322	364	830
		9	8	5	1
BIOCARTA_GLEEVEC_PATHWAY	23	0.55	1.77	0.00	0.05
		813	341	988	830
		2		1	2
REACTOME_RHO_GTPASES_ACTIVATE_FORMINS	13	0.53	1.77	0.03	0.05
	7	303	375	983	833
		4	2	2	6

SCHAEFFER_PROSTATE_DEVELOPMENT_12HR_DN	51	0.52	1.77	0.00	0.05
		231	354	213	833
		7	1	2	8
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	44	0.60	1.77	0.04	0.05
	1	125	386	086	837
		9	4		8
MARZEC_IL2_SIGNALING_UP	11	0.44	1.77	0.00	0.05
	4	027	43	635	840
		7		6	5
HOWLIN_PUBERTAL_MAMMARY_GLAND	65	0.49	1.77	0.00	0.05
		559	135	798	842
		8	5	4	2
GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP	23	0.62	1.77	0.01	0.05
		760	105	632	845
		5		7	6
LI_CISPLATIN_RESISTANCE_DN	33	0.55	1.77	0.00	0.05
		226	087	413	846
		2	2	2	5
PID_EPHA2_FWD_PATHWAY	19	0.59	1.77	0.01	0.05
		417	147	192	847
		9	4	8	2
KYNG_DNA_DAMAGE_DN	17	0.40	1.77	<0.0	0.05
	7	996	388	1	847
		4	6		3
SAKAI_CHRONIC_HEPATITIS_VS_LIVER_CANCER_UP	80	0.51	1.77	0.01	0.05
		411	228	411	848
		8	6	3	2
GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_UP	97	0.44	1.77	0.00	0.05
		974	184	595	848
		2	6	2	5
SYED ESTRADIOL_RESPONSE	18	0.59	1.77	0.01	0.05
		443	160	268	849
		1	7	5	8
HAHTOLA_MYCOSIS_FUNGOIDES_CD4_UP	59	0.54	1.77	0.01	0.05
		041	186	848	857
		7	9		5
GROSS_HYPOXIA_VIA_ELK3_ONLY_UP	33	0.53	1.77	0.01	0.05
		933	230	212	857
		3	5	1	7
REACTOME_MOLECULES_ASSOCIATED_WITH_ELASTIC_FIBRES	37	0.61	1.77	0.02	0.05
		988	031	941	864
		6	3	2	8

HORIUCHI_WTAP_TARGETS_DN	30	0.52	1.77	0.02	0.05
	3	524	001	916	870
		9		7	7
WP_TGFB_SIGNALING_IN_THYROID_CELLS_FOR_EPITHELIALMES ENCHYMAL_TRANSITION	18	0.60	1.76	0.00	0.05
		915	904	418	895
			5	4	9
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_C A2	13	0.45	1.76	0.00	0.05
	0	423	881	398	897
		3	2	4	2
MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_DN	56	0.65	1.76	0.02	0.05
		767	907	851	905
		6	9	3	9
PID_AJDISS_2PATHWAY	48	0.49	1.76	0.00	0.05
		424	819	632	918
		8	5	9	4
IVANOVA_HEMATOPOIESIS_MATURE_CELL	27	0.38	1.76	0.00	0.05
	9	380	763	202	928
		4	2	4	1
DITTMER_PTHLH_TARGETS_UP	10	0.46	1.76	0.01	0.05
	7	337	775	470	931
		2	5	6	
LENAOUR_DENDRITIC_CELL_MATURATION_DN	12	0.47	1.76	0.02	0.05
	6	361	717	012	943
		3	1	1	4
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR _WALL	13	0.46	1.76	0.00	0.05
	5	979	650	779	969
		1	9	7	4
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	62	0.49	1.76	0.00	0.06
		866	488	996	042
		6	4		6
WP_MIRNAS_INVOLVEMENT_IN_THE_IMMUNE_RESPONSE_IN_SEP SIS	37	0.55	1.76	0.02	0.06
		952	443	191	057
			3	2	1
REACTOME_INTERLEUKIN_3_INTERLEUKIN_5_AND_GM-CSF_SIGN ALING	47	0.54	1.76	0.02	0.06
		311	364	941	068
			4	2	6
REACTOME_GAP_JUNCTION_TRAFFICKING_AND_REGULATION	49	0.49	1.76	0.01	0.06
		367	400	431	069
		3	9	5	5
BIOCARTA_ARF_PATHWAY	17	0.59	1.76	0.00	0.06
		029	380	795	069
		6	9	2	9

CHEN_LVAD_SUPPORT_OF_FAILING_HEART_DN	42	0.52	1.76	0.00	0.06
		615	339	984	073
			8	3	
WP_IL7_SIGNALING_PATHWAY	25	0.56	1.76	0.02	0.06
		274	265	290	105
		4	9	1	2
BIOCARTA_ECM_PATHWAY	19	0.62	1.76	0.00	0.06
		443	234	609	113
			6	8	6
PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_6	28	0.54	1.76	0.00	0.06
		318	162	616	147
		6	6		2
OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_UP	21	0.40	1.76	0.00	0.06
		3	908	089	609
			3	3	8
					3
SMIRNOV_RESPONSE_TO_IR_6HR_DN	11	0.48	1.76	0.01	0.06
		0	112	098	417
			7	1	
					9
BURTON_ADIPOGENESIS_3	10	0.62	1.76	0.04	0.06
		2	166	017	303
			6	9	3
					1
WESTON_VEGFA_TARGETS	92	0.46	1.76	0.01	0.06
			019	025	050
				2	4
					9
PID_FCER1_PATHWAY	59	0.50	1.75	0.01	0.06
			315	975	848
			2	5	
					7
REACTOME_BASIGIN_INTERACTIONS	25	0.54	1.75	0.00	0.06
			353	766	809
			6	2	7
					4
EPPERT_PROGENITOR	13	0.51	1.75	0.02	0.06
			3	086	769
				9	1
					4
					6
PID_ECADHERIN_KERATINOCYTE_PATHWAY	21	0.59	1.75	0.01	0.06
			399	842	956
			4		9
					2
RICKMAN_HEAD_AND_NECK_CANCER_C	10	0.49	1.75	0.00	0.06
			5	245	778
				6	2
					6
					5
REACTOME_THE_ROLE_OF_NEF_IN_HIV_1_REPLICATION_AND_DISEASE_PATHOGENESIS	28	0.58	1.75	0.01	0.06
			975	813	796
				8	4
					2

PID_NFAT_TFPATHWAY	44	0.54	1.75	0.01	0.06
		272	797	818	243
			2	2	6
REACTOME_ACTIVATION_OF_BAD_AND_TRANSLOCATION_TO_MI TOCHONDRIA	15	0.64	1.75	0.00	0.06
		985	709	823	247
		7	3		
RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP	40	0.42	1.75	0.01	0.06
	2	889	588		295
		9	5		3
REACTOME_RHO_GTPASES_ACTIVATE_PAKS	21	0.60	1.75	0.01	0.06
		111	454	649	351
		1	2	5	2
KIM_MYCL1_AMPLIFICATION_TARGETS_DN	18	0.58	1.75	0.01	0.06
		582	409	026	368
			5	7	5
CROONQUIST_STROMAL_STIMULATION_UP	53	0.57	1.75	0.01	0.06
		706	359	840	382
		6	1	5	7
REACTOME_RECYCLING_PATHWAY_OF_L1	48	0.49	1.75	0.00	0.06
		701	318	779	392
		7	7	7	
REACTOME_GAB1_SIGNALOSOME	17	0.63	1.75	0.01	0.06
		543	291	727	396
		5	6	4	7
ZHU_CMV_ALL_UP	10	0.46	1.75	0.01	0.06
	5	937	251	875	407
		5	6		6
KATSANOUELAVL1_TARGETS_DN	14	0.39	1.75	0.00	0.06
	2	824	109	199	439
		2	9	6	
LANDIS_ERBB2_BREAST_TUMORS_324_DN	15	0.43	1.75	0.01	0.06
	0	702	118	446	443
		8	1	3	3
BLANCO_MELO_COVID19_BRONCHIAL_EPITHELIAL_CELLS_SARS_ COV_2_INFECTION_UP	14	0.50	1.75	0.01	0.06
	2	209	132	673	447
		5	2	6	6
BILD_HRAS_ONCOGENIC_SIGNATURE	23	0.42	1.74	0.01	0.06
	8	983	920	629	489
			1	3	6
PROVENZANI_METASTASIS_DN	13	0.45	1.74	0.00	0.06
	8	108	930	207	495
		1	5		

REACTOME_REGULATION_OF_HSF1_MEDIATED_HEAT_SHOCK_RE SPONSE	80	0.50	1.74	0.01	0.06
		022	931	440	505
		9		3	2
WEIGEL_OXIDATIVE_STRESS_BY_TBH_AND_H2O2	35	0.51	1.74	0.01	0.06
		469	852	197	506
		5	9	6	2
PID_PI3K_PLC_TRK_PATHWAY	36	0.50	1.74	0.00	0.06
		713	868	6	508
		6	5		3
PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_4	10	0.42	1.74	0.00	0.06
		5	994	942	408
		9	1	2	2
LINDSTEDT_DENDRITIC_CELL_MATURATION_C	61	0.46	1.74	0.01	0.06
		716	947	405	518
		2	7	6	1
LAU_APOPTOSIS_CDKN2A_UP	55	0.47	1.74	0.01	0.06
		264	799	422	524
		4	9	8	2
PID_INTEGRIN_CS_PATHWAY	26	0.66	1.74	0.01	0.06
		150	712	033	559
		5	3	1	6
HUANG_FOXA2_TARGETS_DN	38	0.56	1.74	0.02	0.06
		895	661	429	566
		4	3	1	9
QI_PLASMACYTOMA_DN	94	0.43	1.74	0.00	0.06
		302	677	988	567
		2	9	1	8
NABA_COLLAGENS	44	0.63	1.74	0.03	0.06
		530	441	180	641
		7	8	9	4
LANDIS_BREAST_CANCER_PROGRESSION_DN	71	0.50	1.74	0.02	0.06
		190	462	916	649
		1	1	7	
BIOCARTA_PDGF_PATHWAY	28	0.54	1.74	0.01	0.06
		517	477	176	651
		7	5	5	1
REACTOME_COLLAGEN_CHAIN_TRIMERIZATION	44	0.63	1.74	0.03	0.06
		530	441	180	652
		7	8	9	
WP_NANOPARTICLEMEDIATED_ACTIVATION_OF_RECEPTOR_SIGN ALING	28	0.54	1.74	0.01	0.06
		808	349	030	688
		4	2	9	6

PID_GMCSF_PATHWAY	35	0.52	1.74	0.01	0.06
		842	246	018	730
		2	7	3	5
LU_AGING_BRAIN_UP	25	0.41	1.74	<0.0	0.06
	4	408	176	1	743
		4	7		9
MAHADEVAN_IMATINIB_RESISTANCE_UP	20	0.61	1.74	0.00	0.06
		001	181	795	751
		9		2	6
GROSS_HYPOXIA_VIA_HIF1A_DN	10	0.42	1.74	0.00	0.06
	4	875	131	818	753
			6		7
MCCABE_HOXC6_TARGETS_CANCER_DN	20	0.60	1.74	0.01	0.06
		418	081	290	76
			5	3	
HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP	23	0.42	1.74	0.01	0.06
	8	046	099	844	762
		3	4	3	8
PID_EPHRINB_REV_PATHWAY	30	0.54	1.73	0.01	0.06
		211	932	431	804
			3	5	8
PID_INSULIN_GLUCOSE_PATHWAY	26	0.51	1.73	0.00	0.06
		581	946	967	806
		6	8	1	5
SUNG_METASTASIS_STROMA_DN	52	0.55	1.73	0.02	0.06
		184	875	719	835
		7		7	
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_16	78	0.48	1.73	0.02	0.06
		448	852	414	836
		4	3	5	
AMIT_EGF_RESPONSE_480_MCF10A	43	0.50	1.73	0.00	0.06
		726	814	873	85
		1	8	4	
PUJANA_BREAST_CANCER_LIT_INT_NETWORK	10	0.52	1.73	0.03	0.06
	0	187	784	205	855
		3	7	1	7
TAVOR_CEBPA_TARGETS_UP	49	0.51	1.73	0.00	0.06
		485	754	630	863
			9	3	
LINSLEY_MIR16_TARGETS	20	0.41	1.73	0.01	0.06
	3	656	715	030	865
		9	7	9	

REACTOME_PROGRAMMED_CELL_DEATH	19	0.42	1.73	0.01	0.06
	9	863	642	646	866
		6	1	1	5
SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS	37	0.53	1.73	0.00	0.06
		712	593	202	872
		5	3	4	
REACTOME_SIGNALING_BY_ERBB2_IN_CANCER	26	0.53	1.73	0.00	0.06
		620	719	784	874
		3	8	3	1
REACTOME_DDX58_IFIH1_MEDIATED_INDUCATION_OF_INTERFERON_ALPHA_BETA	68	0.45	1.73	0.00	0.06
		386	644	622	876
		7	5	4	
WP_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_IN_COLORECTAL_CANCER	15	0.40	1.73	0.00	0.06
	7	263	662	211	876
		1	7	4	4
SUNG_METASTASIS_STROMA_UP	10	0.44	1.73	0.01	0.06
	6	701	473	048	876
		2	8	2	4
WP_SIGNALING_OF_HEPATOCYTE_GROWTH_FACTOR_RECEPTOR	34	0.52	1.73	0.00	0.06
		816	505	821	877
		6	4	4	
YAMAZAKI_TCEB3_TARGETS_UP	16	0.41	1.73	0.01	0.06
	2	200	542	810	878
		5	9	9	9
FARMER_BREAST_CANCER_CLUSTER_3	16	0.61	1.73	0.01	0.06
		596	563	255	879
		9	5	2	2
WP_P38_MAPK_SIGNALING_PATHWAY	34	0.49	1.73	0.00	0.06
		368	676	399	880
		2	4	2	5
TANG_SENESCENCE_TP53_TARGETS_DN	53	0.65	1.73	0.04	0.06
		952	520	925	880
		8	7	1	7
TIEN_INTESTINE_PROBIOTICS_6HR_DN	16	0.41	1.73	0.00	0.06
	7	140	596	816	881
		9	2	3	8
MATSUDA_NATURAL_KILLER_DIFFERENTIATION	46	0.35	1.73	<0.0	0.06
	4	747	476	1	884
		4	8		7
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM2	16	0.38	1.73	0.00	0.06
	3	747	348	421	892
		6	4	9	2

LEE_LIVER_CANCER_SURVIVAL_DN	17	0.52	1.73	0.03	0.06
	1	866	371	219	892
			2	3	2
REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIUM_MOBILIZATION	16	0.64	1.73	0.01	0.06
		042	386	323	894
		7	6	3	3
SHAFFER_IRF4_TARGETS_IN_ACTIVATED_B_LYMPHOCYTE	76	0.49	1.73	0.01	0.06
		394	288	684	897
		9	6	2	6
PID_NOTCH_PATHWAY	58	0.46	1.73	0.01	0.06
		309	399	244	898
		1	9	8	
VETTER_TARGETS_OF_PRKCA_AND_ETS1_UP	16	0.61	1.73	0.02	0.06
		954	319	020	898
		1	3	2	7
FARMER_BREAST_CANCER_CLUSTER_4	19	0.89	1.73	0.00	0.06
		044	297	626	901
		8	7	3	6
REACTOME_INTERLEUKIN_10_SIGNALING	45	0.61	1.73	0.01	0.06
		420	406	584	904
		9	2	2	1
BLANCO_MELO_COVID19_SARS_COV_2_INFECTION_CALU3_CELLS_UP	31	0.46	1.73	0.04	0.06
	2	867	198	069	937
		1	5	8	
VETTER_TARGETS_OF_PRKCA_AND_ETS1_DN	16	0.61	1.73	0.01	0.06
		719	178	419	939
		5		9	6
PID_NEPHRIN_NEPH1_PATHWAY	29	0.51	1.73	0.00	0.06
		688	158	982	940
		8		3	7
NEWMAN_ERCC6_TARGETS_DN	36	0.58	1.73	0.02	0.06
		335	085	028	959
		4	9	4	1
PID_PRL_SIGNALING_EVENTS_PATHWAY	23	0.55	1.73	0.00	0.06
		905	044	635	971
		9	8	6	2
REACTOME_RHOB_GTPASE_CYCLE	70	0.47	1.73	0.02	0.06
		408	000	204	981
		5	4	4	6
PODAR_RESPONSE_TO_ADAPHOSTIN_UP	13	0.44	1.73	0.02	0.06
	7	135	010	235	986
		7	1	8	2

GENTILE_UV_LOW_DOSE_DN	63	0.51	1.72	0.01	0.06
		565	955	825	996
		3	1	6	9
HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_UP	67	0.47	1.72	0.01	0.07
		496	830	2	051
		8	1		
NAKAMURA_ADIPOGENESIS_EARLY_DN	34	0.60	1.72	0.02	0.07
		366	810	953	054
		6	3	6	
PID_SHP2_PATHWAY	57	0.47	1.72	0.01	0.07
		694	728	234	092
		4	1	6	3
WANG_LMO4_TARGETS_DN	34	0.41	1.72	0.00	0.07
		3	256	656	416
		5		7	2
STEIN_ESRRA_TARGETS_RESPONSIVE_TO_ESTROGEN_DN	41	0.60	1.72	0.04	0.07
		074	455	948	226
		6	4	5	2
BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN	16	0.49	1.72	0.03	0.07
		5	635	397	564
		3	9	4	3
BROWNE_HCMV_INFECTION_24HR_DN	13	0.43	1.72	0.01	0.07
		9	590	353	411
		5	1	3	1
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM1	25	0.36	1.72	0.00	0.07
		6	505	314	200
		2	6	8	2
OISHI_CHOLANGIOMA_STEM_CELL_LIKE_DN	26	0.44	1.72	0.02	0.07
		6	683	271	454
		2	9		1
PID_EPO_PATHWAY	33	0.54	1.72	0.02	0.07
		35	232	559	302
			4	1	7
PID_HIF1_TFPATHWAY	66	0.45	1.72	0.00	0.07
		694	055	623	387
		4	5	7	
GROSS_HYPOXIA_VIA_ELK3_UP	20	0.38	1.72	0.00	0.07
		4	556	027	814
		5	7	7	2
HOOI_ST7_TARGETS_UP	88	0.43	1.71	0.00	0.07
		326	975	821	416
		8		4	3

NADLER_OBESITY_UP	60	0.58	1.71	0.03	0.07
		190	923	434	421
		7	3	3	
BRUNO_HEMATOPOIESIS	64	0.46	1.71	0.00	0.07
		248	930	632	427
		2	3	9	7
BILANGES_SERUM_SENSITIVE_VIA_TSC2	28	0.58	1.71	0.03	0.07
		649	88	131	437
		3		1	
REACTOME_SIGNALING_BY_PDGFR_IN_DISEASE	20	0.60	1.71	0.02	0.07
		211	850	385	440
		5	2	7	9
WP_MAMMARY_GLAND_DEVELOPMENT_PATHWAY_EMBRYONIC_DEVELOPMENT_STAGE_1_OF_4	15	0.61	1.71	0.01	0.07
		322	796	417	445
		8	4		
PID_IFNG_PATHWAY	40	0.49	1.71	0.01	0.07
		833	758	354	447
					1
STAMBOLSKY_TARGETS_OF_MUTATED_TP53_UP	46	0.48	1.71	0.00	0.07
		144	812	213	447
		2	7	7	1
PID_ANTHRAX_PATHWAY	17	0.58	1.71	0.00	0.07
		078	691	992	449
		5	4	1	6
BIOCARTA_NKCELLS_PATHWAY	20	0.64	1.71	0.02	0.07
		910	763	702	453
		9	7	7	2
TOMIDA_METASTASIS_UP	25	0.59	1.71	0.01	0.07
		174	666	649	453
		9	2	5	3
WP_HOSTPATHOGEN_INTERACTION_OF_HUMAN_CORONA_VIRUS_ES_INTERFERON_INDUCITION	33	0.54	1.71	0.02	0.07
		970	724	952	454
		2	7	8	3
ONDER_CDH1_SIGNALING_VIA_CTNNB1	83	0.49	1.71	0.02	0.07
		169	815	004	455
		8	4		2
REACTOME_POTENTIAL_THERAPEUTICS_FOR_SARS	81	0.40	1.71	0.00	0.07
		154	698	396	456
		1	8	8	8
LEE_LIVER_CANCER_DENA_UP	59	0.46	1.71	0.00	0.07
		074	6	849	483
		3		3	5

REACTOME_SYNTHESIS_OF_ACTIVE_UBIQUITIN_ROLES_OF_E1_A ND_E2_ENZYMES	30	0.58	1.71	0.01	0.07	850	567	486	491
						5	9	2	5
PID_ATF2_PATHWAY	58	0.45	1.71	0.01	0.07	259	500	388	497
						4	6	9	3
REACTOME_CROSSLINKING_OF_COLLAGEN_FIBRILS	18	0.70	1.71	0.02	0.07	308	510	745	501
						8	9	1	9
WP_GLUCOCORTICOID_RECEPTOR_PATHWAY	70	0.47	1.71	0.01	0.07	750	519	229	506
						3	5	5	
WP_ENDOCHONDRAL_OSSIFICATION_WITH_SKELETAL_DYSPLASI AS	63	0.47	1.71	0.01	0.07	815	443	209	515
							6	7	3
WP_ENDOCHONDRAL_OSSIFICATION	63	0.47	1.71	0.01	0.07	815	443	209	526
							6	7	
WP_INTEGRINMEDIATED_CELL_ADHESION	10	0.44	1.71	0.00	0.07	1	674	293	806
							5	7	5
									4
WP_REGULATION_OF_TOLLLIKE_RECEPTOR_SIGNALING_PATHW AY	12	0.43	1.71	0.02	0.07	5	566	260	564
							8	6	1
									2
LIANG_SILENCED_BY_METHYLATION_UP	29	0.55	1.71	0.01	0.07	150	186	252	608
							6	1	6
									4
REACTOME_RAF_INDEPENDENT_MAPK1_3_ACTIVATION	23	0.52	1.71	0.03	0.07	062	204	131	609
							8	8	5
									2
REACTOME_GLYCOLYSIS	68	0.49	1.71	0.01	0.07	918	217	663	613
							9	9	2
									2
PID_IL2_PI3K_PATHWAY	34	0.52	1.71	0.00	0.07	060	119	790	615
							2	8	5
									4
REACTOME_FC_EPSILON_RECEPTOR_FCERI_SIGNALING	13	0.43	1.71	0.00	0.07	0	622	133	838
							3	9	6
									3
LI_WILMS_TUMOR_VS_FETAL_KIDNEY_2_DN	48	0.52	1.71	0.02	0.07	811	152	240	617
							3	9	3

LIAO_HAVE_SOX4_BINDING_SITES	41	0.47	1.71	0.00	0.07
		795	226	808	620
			1	1	5
WP_GASTRIC_CANCER_NETWORK_2	31	0.56	1.71	0.02	0.07
		929	024	510	667
		3	2	5	
REACTOME_GAP_JUNCTION_ASSEMBLY	36	0.50	1.70	0.00	0.07
		503	948	635	696
		1	2	6	
REACTOME_NEUTROPHIL_DEGRANULATION	46	0.42	1.70	0.01	0.07
	9	176	963	844	697
		8	3	3	1
ALONSO_METASTASIS_NEURAL_UP	18	0.57	1.70	0.02	0.07
		998	898	045	703
		2	3		2
REACTOME_DISEASES_OF_SIGNAL_TRANSDUCTION_BY_GROWTH_FACTOR_RECEPTORS_AND_SECOND_MESSENGERS	38	0.35	1.70	<0.0	0.07
	9	774	909	1	706
					7
WP_CELL_MIGRATION_AND_INVASION_THROUGH_P75NTR	30	0.51	1.70	0.01	0.07
		005	854	244	722
		7	3	8	2
MARKS_HDAC_TARGETS_DN	15	0.63	1.70	0.01	0.07
		607	814	498	730
		4	7	9	4
REACTOME_SEMAPHORIN_INTERACTIONS	64	0.45	1.70	0.02	0.07
		835	741	385	737
		1	2	7	8
DELYS_THYROID_CANCER_UP	43	0.41	1.70	0.02	0.07
	6	865	722	424	742
		8	7	2	
OLSSON_E2F3_TARGETS_DN	32	0.55	1.70	0.02	0.07
		097	698	760	747
		2	5	1	5
HAN_JNK_SINGALING_DN	39	0.50	1.70	0.00	0.07
		944	760	406	748
		7	6	5	5
KIM_WT1_TARGETS_12HR_UP	16	0.42	1.70	0.01	0.07
	3	059	586	642	759
		5	4	7	6
YAGI_AML_FAB_MARKERS	18	0.37	1.70	<0.0	0.07
	9	484	662	1	761
		2	8		5

XU_HGF_SIGNALING_NOT_VIA_AKT1_6HR	25	0.59	1.70	0.03	0.07
		763	595	386	765
		1	5	5	7
DUNNE_TARGETS_OF_AML1_MTG8_FUSION_DN	19	0.57	1.70	0.02	0.07
		359	536	357	770
		6	5	6	1
TAKAO_RESPONSE_TO_UVB_RADIATION_DN	96	0.43	1.70	0.02	0.07
		721	604	479	771
		7	4	3	8
CUI_TCF21_TARGETS_UP	35	0.53	1.70	0.03	0.07
		789	624	312	773
			6	6	6
BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN	46	0.51	1.70	0.03	0.07
		664	478	061	774
		7		2	1
TSAI_RESPONSE_TO_RADIATION_THERAPY	30	0.57	1.70	0.02	0.07
		309	511	686	775
		8	7		
WP_ONCOSTATIN_M_SIGNALING_PATHWAY	64	0.46	1.70	0.02	0.07
		311	546	173	775
		6	6	9	1
REACTOME_MYD88_INDEPENDENT_TLR4_CASCADE	97	0.42	1.70	0.00	0.07
		72	488	206	778
			6	6	
WP_TYPE_I_INTERFERON_INDUCTION_AND_SIGNALING_DURING_SARSCOV2_INFECTION	29	0.53	1.70	0.03	0.07
		923	430	468	792
		9	4	2	8
PID_RET_PATHWAY	39	0.48	1.70	0.01	0.07
		614	378	026	809
			8	7	8
HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_DN	22	0.56	1.70	0.00	0.07
		174	243	992	836
		4	5	1	1
SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_UP	70	0.52	1.70	0.02	0.07
		356	306	564	836
		8		1	2
MURAKAMI_UV_RESPONSE_6HR_DN	21	0.56	1.70	0.00	0.07
		744	253	603	839
		3	7	6	6
KEGG_GLIOMA	65	0.44	1.70	0.00	0.07
		215	273	582	842
			8	5	1

GHO_ATF5_TARGETS_DN	16	0.62	1.70	0.01	0.07
		985	308	829	845
		1	7	3	
WHITFIELD_CELL_CYCLE_M_G1	12	0.44	1.70	0.02	0.07
	0	271	190	254	863
		1	3	1	1
WP_ARYL_HYDROCARBON_RECEPTOR_NETPATH	46	0.46	1.70	0.01	0.07
		308	143	237	875
		3	4	1	3
BIOCARTA_INTEGRIN_PATHWAY	34	0.53	1.70	0.02	0.07
		650	128	028	875
		1	2	4	6
PID_RHOA_PATHWAY	43	0.47	1.70	0.00	0.07
		570	093	803	887
		2		2	7
AMIT_SERUM_RESPONSE_60_MCF10A	56	0.49	1.70	0.02	0.07
		124	076	777	889
		4	3	8	6
KEGG_APOPTOSIS	84	0.43	1.69	0.01	0.07
		183	954	012	942
		5	2	1	9
REACTOME_ANCHORING_FIBRIL_FORMATION	15	0.70	1.69	0.01	0.07
		062	961	744	946
			6	2	9
THUM_MIR21_TARGETS_HEART_DISEASE_UP	17	0.76	1.69	0.04	0.07
		575	879	322	961
		7	3	2	9
WP_TCELL_ANTIGEN_RECEPTOR_TCR_SIGNALING_PATHWAY	88	0.48	1.69	0.03	0.07
		569	842	853	962
		5	1	6	5
WILLIAMS_ESR1_TARGETS_UP	26	0.55	1.69	0.01	0.07
		001	905	851	963
		1	6	9	4
GNATENKO_PLATELET_SIGNATURE	38	0.57	1.69	0.02	0.07
		212	887	355	966
		7	2	5	8
TSENG_IRS1_TARGETS_UP	10	0.42	1.69	0.00	0.07
	9	499	851	207	969
		5	7	9	4
GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_DN	84	0.50	1.69	0.01	0.07
		295	800	825	976
			5	6	2

DORSEY_GAB2_TARGETS	30	0.55	1.69	0.01	0.07
		230	766	375	986
		1	7	2	7
BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP	41	0.39	1.69	0.00	0.07
	4	438	742	808	989
		1	8	1	1
JINESH_BLEBBISHIELD_TRANSFORMED_STEM_CELL_SPHERES_UP	16	0.42	1.69	0.02	0.08
	7	177	668	249	024
		3		5	6
BIOCARTA_BCELLSURVIVAL_PATHWAY	15	0.59	1.69	0.01	0.08
		077	627	222	034
		2	8		6
DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTIION_UP	28	0.42	1.69	0.01	0.08
	4	133	601	616	040
		1		2	9
BURTON_ADIPOGENESIS_11	51	0.48	1.69	0.01	0.08
		859	491	730	088
		5	2	8	6
PLASARI_TGFB1_TARGETS_10HR_DN	24	0.39	1.69	0.00	0.08
	7	985	500	790	092
		7	8	5	7
LEE_LIVER_CANCER_MYC_E2F1_UP	56	0.44	1.69	0.00	0.08
		804	465	608	095
		4	6	5	4
BIOCARTA_CASPASE_PATHWAY	22	0.58	1.69	0.01	0.08
		129	430	378	095
		2	9		8
NABA_BASEMENT_MEMBRANES	40	0.59	1.69	0.02	0.08
		050	376	822	097
		1	3	6	6
HASLINGER_B_CLL_WITH_11Q23_DELETION	22	0.59	1.69	0.01	0.08
		170	408	688	099
		6	4	6	8
MATTHEWS_AP1_TARGETS	17	0.58	1.69	0.02	0.08
		644	389	424	100
			7	2	4
LIU_TARGETS_OF_VMYB_VS_CMYB_DN	41	0.49	1.69	0.01	0.08
		366	347	209	101
		4		7	1
WP_PLATELETMEDIATED_INTERACTIONS_WITH_VASCULAR_AND_CIRCULATING_CELLS	17	0.72	1.69	0.00	0.08
		751	436	609	103
		4	1	8	2

NAKAYAMA_FRA2_TARGETS	46	0.45	1.69	0.00	0.08
		074	261	608	141
		1		5	3
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TURQUOISE_UP	79	0.46	1.69	0.02	0.08
		598	214	178	145
		5	6	2	4
RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN	24	0.37	1.69	0.01	0.08
		2	481	184	224
		1	8	5	9
REACTOME_APOPTOSIS	17	0.42	1.69	0.02	0.08
		0	978	222	714
			8		3
ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP	14	0.52	1.69	0.04	0.08
		2	512	115	208
		8	4	4	1
BYSTROEM_CORRELATED_WITH_IL5_DN	57	0.50	1.69	0.01	0.08
			349	072	593
			9	2	6
BIOCARTA_CELLCYCLE_PATHWAY	23	0.59	1.69	0.02	0.08
			711	073	049
			5	8	2
BERENJENO_ROCK_SIGNALING_NOT_VIA_RHOA_DN	47	0.51	1.69	0.02	0.08
			490	014	459
			8	4	4
JI_CARCIANOGENESIS_BY_KRAS_AND_STK11_DN	17	0.70	1.69	0.03	0.08
			810	024	557
			4	6	3
WP_IL3_SIGNALING_PATHWAY	48	0.48	1.68	0.03	0.08
			734	983	495
			5	4	1
MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_UP	16	0.38	1.68	0.00	0.08
			7	644	941
			9	7	625
WP_LEPTIN_SIGNALING_PATHWAY	76	0.43	1.68	0.00	0.08
			203	909	990
				1	7
RODWELL_AGING_KIDNEY_UP	45	0.46	1.68	0.04	0.08
			7	287	86
			3		233
				9	251
BURTON_ADIPOGENESIS_PEAK_AT_0HR	60	0.49	1.68	0.02	0.08
			813	822	510
			8	6	5
				5	7

MCDOWELL_ACUTE_LUNG_INJURY_UP	45	0.51	1.68	0.03	0.08
		606	692	006	317
		7	9		
REACTOME_SIGNALING_BY_NTRKS	13	0.39	1.68	0.01	0.08
	3	881	703	992	320
		1	8		3
PID_FOXM1_PATHWAY	39	0.56	1.68	0.04	0.08
		024	710	402	327
		9	1	5	1
WP_INTEGRATED_BREAST_CANCER_PATHWAY	15	0.39	1.68	0.00	0.08
	2	940	592	207	357
		7	5		3
ENK_UV_RESPONSE_KERATINOCYTE_DN	46	0.41	1.68	0.01	0.08
	7	800	567	652	364
		8	2	9	
BIOCARTA_PTEN_PATHWAY	18	0.62	1.68	0.01	0.08
		064	497	821	392
		2	7	9	
REACTOME_OVARIAN_TUMOR_DOMAIN_PROTEASES	38	0.47	1.68	0.01	0.08
		889	312	361	408
		9	9	9	
WP_MAPK_SIGNALING_PATHWAY	24	0.35	1.68	0.00	0.08
	2	973	330	584	409
		8	6	8	5
REACTOME_RHO_GTPASES_ACTIVATE_PKNS	34	0.50	1.68	0.01	0.08
		431	361	039	416
		9	2	5	9
BIOCARTA_IL1R_PATHWAY	30	0.52	1.68	0.02	0.08
		218	333	863	417
		1	2		1
HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_DN	10	0.40	1.68	0.00	0.08
	0	840	342	824	421
		3		7	5
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_DN	29	0.59	1.68	0.03	0.08
		738	362	883	426
		2	3	5	9
PID_AURORA_A_PATHWAY	31	0.55	1.68	0.03	0.08
		652	387	036	433
		1	8	4	2
LY_AGING_PREMATURE_DN	29	0.62	1.68	0.03	0.08
		606	417	711	434
		6	8	3	5

WP_PDGFREBETA_PATHWAY	29	0.52	1.68	0.02	0.08
		894	363	307	436
		1	5	7	2
XU_GH1_AUTOCRINE_TARGETS_DN	12	0.39	1.68	0.01	0.08
	4	180	119	268	474
		7	5	5	4
SAGIV_CD24_TARGETS_DN	45	0.50	1.68	0.02	0.08
		402	128	725	479
		1		4	4
PID_KIT_PATHWAY	52	0.47	1.68	0.02	0.08
		445	134	772	486
		2		3	5
SEIDEN_MET_SIGNALING	19	0.59	1.68	0.02	0.08
		506	146	434	489
		5	5	1	8
REACTOME_CD209_DC_SIGN_SIGNALING	20	0.55	1.68	0.02	0.08
		555	154	254	493
		2	9	1	8
SENESE_HDAC1_AND_HDAC2_TARGETS_DN	21	0.39	1.68	0.01	0.08
	2	969	010	2	526
		6	5		9
WP_MAMMARY_GLAND_DEVELOPMENT_PATHWAY_PREGNANCY _AND_LACTATION_STAGE_3_OF_4	31	0.48	1.67	0.00	0.08
		373	990	625	529
		3	6		7
AMIT_EGF_RESPONSE_240_MCF10A	21	0.57	1.67	0.00	0.08
		270	935	416	542
		2	9	7	3
REACTOME_SIGNALING_BY_HIPPO	20	0.60	1.67	0.02	0.08
		820	915	312	544
		5	3	1	4
WU_HBX_TARGETS_1_DN	22	0.51	1.67	0.02	0.08
		781	936	2	552
		9	3		8
LEONARD_HYPOXIA	40	0.53	1.67	0.02	0.08
		739	747	454	597
		8	9		7
WP_HYPERTROPHY_MODEL	18	0.59	1.67	0.03	0.08
		362	753	157	604
		2	4	9	7
NAKAMURA_ADIPOGENESIS_LATE_DN	34	0.57	1.67	0.03	0.08
		368	714	571	610
		4	6	4	6

WP_SEROTONIN_RECEPTOR_467_AND_NR3C_SIGNALING	19	0.53	1.67	0.01	0.08
		971	762	138	611
		2	9	5	
ONDER_CDH1_TARGETS_2_UP	24	0.46	1.67	0.03	0.08
	8	707	782	534	612
			3	3	5
WAMUNYOKOLI_OVARIAN_CANCER_LMP_DN	19	0.47	1.67	0.03	0.08
	2	006	680	732	619
		6	8	8	6
TOMLINS_PROSTATE_CANCER_DN	38	0.53	1.67	0.02	0.08
		417	568	291	668
		4	3	7	8
SESTO_RESPONSE_TO_UV_C3	19	0.59	1.67	0.04	0.08
		585	513	140	691
			3	8	8
WP_IL1_AND_MEGAKARYOCYTES_IN_OBESITY	24	0.59	1.67	0.02	0.08
		095	276	240	692
			9	3	2
BIOCARTA_EDG1_PATHWAY	22	0.54	1.67	0.01	0.08
		594	255	165	694
		6			9
ENGELMANN_CANCER_PROGENITORS_UP	47	0.44	1.67	0.00	0.08
		108	280	595	698
		2	1	2	9
AMIT_EGF_RESPONSE_120_MCF10A	41	0.50	1.67	0.02	0.08
		196	435	922	702
		5	7	8	
YU_BAP1_TARGETS	29	0.56	1.67	0.04	0.08
		052	366	742	702
		8	5	3	9
ALFANO_MYC_TARGETS	23	0.37	1.67	0.00	0.08
	3	830	478	421	704
		3		1	1
REACTOME_RAC1_GTPASE_CYCLE	18	0.41	1.67	0.02	0.08
	1	506	402	539	705
		4	5	1	1
WP_OVERVIEW_OF_NANOPARTICLE_EFFECTS	19	0.56	1.67	0.01	0.08
		140	444	829	706
		1	1	3	3
BLANCO_MELO_COVID19_SARS_COV_2_INFECTION_A594_CELLS_UP	78	0.44	1.67	0.01	0.08
		632	283	556	706
		8	8	4	3

REACTOME_SIGNALING_BY_CYTOSOLIC_FGFR1_FUSION_MUTANTS	17	0.60	1.67	0.02	0.08
		824	378	303	707
			8	3	2
KANNAN_TP53_TARGETS_DN	22	0.53	1.67	0.02	0.08
		509	288	032	711
		6	8	5	8
WANG_CISPLATIN_RESPONSE_AND_XPC_DN	21	0.36	1.67	0.00	0.08
	4	532	407	618	711
		8		6	9
BIOCARTA_MAPK_PATHWAY	81	0.40	1.67	0.01	0.08
		860	454	378	712
		3	1		1
WP_IL5_SIGNALING_PATHWAY	40	0.48	1.67	0.02	0.08
		659	300	381	715
		3	5		4
STEIN_ESRRA_TARGETS_RESPONSIVE_TO_ESTROGEN_UP	29	0.50	1.67	0.01	0.08
		588	027	626	822
			3		
PID_EPHA_FWDPATHWAY	34	0.49	1.67	0.02	0.08
		296	004	434	829
		4	6	1	7
WP_INFLAMMATORY_RESPONSE_PATHWAY	30	0.61	1.66	0.04	0.08
		758	906	564	862
		2	5	3	5
WP_OVERVIEW_OF_INTERFERONSMEDIATED_SIGNALING_PATHWAY	22	0.60	1.66	0.04	0.08
		990	931	452	863
		5	9	7	1
BROWN_MYELOID_CELL_DEVELOPMENT_UP	15	0.47	1.66	0.04	0.08
	9	844	878	466	867
		4	5		6
VALK_AML_CLUSTER_11	37	0.52	1.66	0.02	0.08
		389	908	040	870
		6	7	8	8
PID_NFAT_3PATHWAY	53	0.45	1.66	0.01	0.08
		014	835	768	877
		5	7	2	
ANDERSEN_CHOLANGIOCARCINOMA_CLASS2	17	0.47	1.66	0.04	0.08
	4	898	772	516	886
		8	1	1	5
REACTOME_PURINERGIC_SIGNALING_IN_LEISHMANIASIS_INFECTION	26	0.57	1.66	0.02	0.08
		089	782	766	890
		6	6	8	8

WEINMANN_ADAPTATION_TO_HYPOXIA_DN	38	0.50	1.66	0.02	0.08
		473	742	164	891
			4	5	8
HOFFMANN_PRE_BI_TO_LARGE_PRE_BII_LYMPHOCYTE_DN	75	0.43	1.66	0.01	0.08
		335	783	408	900
		5	8	5	1
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_UP	20	0.40	1.66	0.01	0.08
	1	780	709	935	900
		2	8	5	7
NAKAMURA_ADIPOGENESIS_LATE_UP	94	0.39	1.66	0.01	0.08
		434	656	016	926
		9	9	3	4
VANTVEER_BREAST_CANCER_POOR_PROGNOSIS	46	0.49	1.66	0.04	0.08
		292	633	008	931
		1			
DAVIES_MULTIPLE_MYELOMA_VS_MGUS_DN	26	0.60	1.66	0.04	0.08
		445	576	101	96
		9	2	6	
HASLINGER_B_CLL_WITH_13Q14_DELETION	24	0.50	1.66	0.01	0.08
		348	547	789	963
		4	1	3	7
CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP	23	0.37	1.66	0.01	0.09
	2	161	462	414	008
		8	5	1	
FOSTER_TOLERANT_MACROPHAGE_UP	16	0.39	1.66	0.01	0.09
	2	903	292	224	060
		6	4	5	4
MCCLUNG_DELTA_FOSB_TARGETS_2WK	45	0.47	1.66	0.01	0.09
		168	293	024	070
		5	1	6	1
DER_IFN_BETA_RESPONSE_UP	10	0.47	1.66	0.04	0.09
	2	423	344	208	076
			2	4	
REACTOME_RHOC_GTPASE_CYCLE	73	0.45	1.66	0.02	0.09
		262	325	505	079
		4	1	2	2
SERVITJA_LIVER_HNF1A_TARGETS_UP	13	0.37	1.66	0.01	0.09
	3	779	294	443	079
		7	9	3	6
PID_TXA2PATHWAY	56	0.50	1.66	0.03	0.09
		275	296	869	088
		7	4	7	7

REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	24	0.51	1.66	0.01	0.09
		047	155	882	142
		4	5	8	5
WONG_PROTEASOME_GENE_MODULE	49	0.56	1.66	0.03	0.09
		100	061	917	149
		4	2	5	
BIOCARTA_FMLP_PATHWAY	34	0.48	1.66	0.00	0.09
		916	124	824	151
			8	7	8
REACTOME_SIGNALING_BY_NTRK2_TRKB	25	0.52	1.66	0.02	0.09
		672	081	028	157
		1	1	4	9
REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	31	0.47	1.66	0.01	0.09
		582	083	138	166
		6	6	5	8
BIOCARTA_IL2RB_PATHWAY	37	0.51	1.66	0.03	0.09
		143	006	660	173
		4	8	9	5
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	12	0.38	1.65	0.01	0.09
		6	534	972	737
		6	7	5	
ZHONG_SECRETOME_OF_LUNG_CANCER_AND_FIBROBLAST	13	0.45	1.65	0.02	0.09
		1	281	922	880
		3	8	7	6
REACTOME_ATTENUATION_PHASE	27	0.55	1.65	0.03	0.09
		983	952	036	186
		8	5	4	8
WP_SIMPLIFIED_DEPICTION_OF_MYD88_DISTINCT_INPUTOUTPUT_PATHWAY	18	0.61	1.65	0.04	0.09
		648	930	572	190
			6	6	4
REACTOME_EPHRIN_SIGNALING	19	0.57	1.65	0.03	0.09
		870	857	137	218
		8	1	3	2
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX2	11	0.44	1.65	0.02	0.09
		8	391	827	254
		9		1	8
SCHAEFFER_SOX9_TARGETS_IN_PROSTATE_DEVELOPMENT_DN	45	0.52	1.65	0.02	0.09
		174	783	249	246
		1	7	5	3
WP_INTERACTIONS_BETWEEN_IMMUNE_CELLS_AND_MICRORNAS_IN_TUMOR_MICROENVIRONMENT	28	0.62	1.65	0.03	0.09
		204	727	495	265
		2	5	1	8

ZHAN_MULTIPLE_MYELOMA_MF_UP	47	0.45	1.65	0.01	0.09
		072	671	976	293
		1	2	3	
BIOCARTA_EGF_PATHWAY	27	0.51	1.65	0.02	0.09
		079	627	339	310
		5		2	5
WP_PHOTODYNAMIC_THERAPYINDUCED_NFKB_SURVIVAL_SIGN ALING	35	0.53	1.65	0.02	0.09
		721	599	941	318
			5	2	3
NAKAMURA_CANCER_MICROENVIRONMENT_DN	40	0.59	1.65	0.04	0.09
		644	534	602	347
		8	8	5	4
ZHU_CMV_24_HR_UP	82	0.44	1.65	0.03	0.09
		999	480	080	368
		6	2	1	8
LIU_VMYB_TARGETS_UP	12	0.38	1.65	<0.0	0.09
		0	132	347	1
			8	1	410
					6
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM3	75	0.42	1.65	0.01	0.09
		793	305	043	414
		7		8	8
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	11	0.47	1.65	0.04	0.09
		7	228	319	150
			3	5	2
					2
IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_DN	10	0.44	1.65	0.02	0.09
		6	644	372	966
			1	8	1
					7
PHONG_TNF_RESPONSE_VIA_P38_COMPLETE	22	0.37	1.65	0.00	0.09
		1	538	350	617
			5	7	3
KEGG_P53_SIGNALING_PATHWAY	67	0.42	1.65	0.00	0.09
			408	374	823
			8	9	7
REACTOME_P130CAS_LINKAGE_TO_MAPK_SIGNALING_FOR_INTE GRINS	15	0.58	1.65	0.03	0.09
			746	248	734
			9	3	4
					8
GOZGIT_ESR1_TARGETS_UP	13	0.39	1.65	0.01	0.09
		7	317	198	010
			1	7	1
					7
ZHANG_PROLIFERATING_VS_QUIESCENT	48	0.50	1.65	0.02	0.09
			792	175	760
			7	5	1
					3

BIOCARTA_HIVNEF_PATHWAY	56	0.44	1.65	0.01	0.09
		260	145	956	477
		5		9	
DEN_INTERACT_WITH_LCA5	26	0.57	1.65	0.02	0.09
		931	100	697	478
			8	1	5
PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP	12	0.41	1.65	0.01	0.09
		5	476	108	367
			4	2	2
					7
GAVIN_FOXP3_TARGETS_CLUSTER_T4	88	0.42	1.65	0.01	0.09
		732	112	222	492
			9	3	
					3
KENNY_CTNNB1_TARGETS_UP	49	0.43	1.64	0.01	0.09
		152	965	807	534
			8	5	2
					1
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_YELLOW_UP	29	0.54	1.64	0.01	0.09
		827	995	639	537
			4	5	3
					1
CHEN_ETV5_TARGETS_SERTOLI	25	0.60	1.64	0.04	0.09
		716	972	061	540
			1	6	9
					3
CAIRO_LIVER_DEVELOPMENT_UP	16	0.40	1.64	0.02	0.09
		1	618	869	748
			4	4	4
					1
NEWMAN_ERCC6_TARGETS_UP	24	0.52	1.64	0.02	0.09
		812	873	714	555
			4	3	
					5
KUMAR_AUTOPHAGY_NETWORK	64	0.39	1.64	0.00	0.09
		609	874	617	565
			2		3
					9
PETROVA_ENDOTHELIUM_LYMPHATIC_VS_BLOOD_UP	12	0.40	1.64	0.02	0.09
		9	753	874	083
			9	3	3
					3
WP_NUCLEOTIDEBINDING_OLIGOMERIZATION_DOMAIN_NOD_PATHWAY	40	0.49	1.64	0.02	0.09
		690	718	554	604
			6	1	
					7
WP_TOLLLIKE_RECEPTOR_SIGNALING_RELATED_TO_MYD88	31	0.54	1.64	0.03	0.09
		589	730	762	607
			6	8	4
					5
WP_RELATIONSHIP_BETWEEN_INFLAMMATION_COX2_AND_EGFR	25	0.49	1.64	0.01	0.09
		198	744	380	610
			5	2	7
					3

CHEBOTAEV_GR_TARGETS_DN	12	0.39	1.64	0.00	0.09
	0	300	670	609	625
		6	5	8	7
CHANG_IMMORTALIZED_BY_HP31_DN	59	0.45	1.64	0.01	0.09
		711	626	239	634
			3	7	2
REACTOME_HS_GAG_BIOSYNTHESIS	31	0.51	1.64	0.03	0.09
		422	589	024	638
		5	9	6	1
REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM	50	0.48	1.64	0.03	0.09
		609	632	441	640
		2	4	7	6
NAM_FXYD5_TARGETS_DN	18	0.60	1.64	0.03	0.09
		321	591	171	648
		8	8	2	5
PID_AMB2_NEUTROPHILS_PATHWAY	40	0.53	1.64	0.04	0.09
		059	552	040	650
		1	5	4	5
DELACROIX_RAR_TARGETS_DN	24	0.51	1.64	0.02	0.09
		622	517	330	655
		5	9	1	2
REACTOME_CELLULAR_RESPONSE_TO_HEAT_STRESS	99	0.44	1.64	0.03	0.09
		852	484	673	655
		3	7	5	5
JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_UP	47	0.46	1.64	0.02	0.09
		748	386	371	660
		8	8	5	2
DUTERTRE ESTRADIOL_RESPONSE_6HR_UP	22	0.41	1.64	0.04	0.09
	1	515	429	375	660
		6			8
BIOCARTA_HIF_PATHWAY	15	0.58	1.64	0.01	0.09
		377	524	906	661
		5		8	3
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_DN	42	0.48	1.64	0.03	0.09
		474	400	082	661
		9	7	9	6
REACTOME_SMOOTH_MUSCLE_CONTRACTION	34	0.58	1.64	0.04	0.09
		517	436	384	666
		4	7	1	9
WP_ZINC_HOMEOSTASIS	34	0.50	1.64	0.02	0.09
		263	449	851	667
		6	5	3	6

MEBARKI_HCC_PROGENITOR_WNT_UP_CTNNB1_DEPENDENT_BLOCKED_BY_FZD8CRD	43	0.52	1.64	0.02	0.09
		202	358	731	668
		9		1	9
SASSON_RESPONSE_TO_GONADOTROPHINS_UP	84	0.41	1.64	0.01	0.09
		277	180	369	773
		8	3	9	
IWANAGA_CARCINOGENESIS_BY_KRAS_PTEN_DN	34	0.33	1.64	0.00	0.09
	1	989	189	392	776
		2	9	9	1
REACTOME_DISEASES_ASSOCIATED_WITH_GLYCOSAMINOGLYCAN_METABOLISM	41	0.53	1.64	0.04	0.09
		431	043	117	851
		9	7	6	7
SCIEN_INVESDED_TARGETS_OF_TP53_AND_TP73_DN	30	0.48	1.64	0.02	0.09
		334	015	306	858
		5	5	1	3
REACTOME_PI3K_AKT_SIGNALING_IN_CANCER	10	0.39	1.63	0.01	0.09
	4	086	977	132	874
		7	8	1	6
REACTOME_SIGNALING_BY_ERBB2	50	0.43	1.63	0.01	0.09
		762	931	596	886
		5	8	8	8
QI_HYPOXIA_TARGETS_OF_HIF1A_AND_FOXA2	34	0.50	1.63	0.03	0.09
		728	932	379	896
		9	7	7	7
KOINUMA_COLON_CANCER_MSI_UP	16	0.61	1.63	0.02	0.09
		703	895	898	902
		2		6	2
WP_SIGNAL_TRANSDUCTION_THROUGH_IL1R	32	0.49	1.63	0.03	0.09
		779	842	549	925
		7	5	1	6
REACTOME_OTHER_SEMAPHORIN_INTERACTIONS	19	0.59	1.63	0.03	0.09
		91	743	187	929
			6	3	5
LIU_SOX4_TARGETS_UP	13	0.39	1.63	0.01	0.09
	2	208	723	626	932
		4	1		8
WEST_ADRENOCORTICAL_TUMOR_MARKERS_UP	22	0.62	1.63	0.03	0.09
		072	802	958	933
			3	3	
JOSEPH_RESPONSE_TO_SODIUM_BUTYRATE_DN	59	0.43	1.63	0.00	0.09
		359	768	818	933
		4	9		8

LINDSTEDT_DENDRITIC_CELL_MATURATION_D	62	0.51	1.63	0.03	0.09
		032	774	353	940
		6	9	1	7
HUPER_BREAST_BASAL_VS_LUMINAL_UP	52	0.54	1.63	0.02	0.09
		370	803	272	942
		8	2	7	6
WP_NEOVASCULARISATION_PROCESSES	37	0.49	1.63	0.03	0.09
		483	628	151	979
		9	8	3	2
KAMIKUBO_MYELOID_MN1_NETWORK	19	0.53	1.63	0.02	0.10
		667	585	310	001
		1		9	
GENTILE_UV_RESPONSE_CLUSTER_D4	53	0.47	1.63	0.03	0.10
		966	327	696	147
		9	2	1	
BIOCARTA_TFF_PATHWAY	23	0.52	1.63	0.02	0.10
		186	294	012	152
		3		1	2
REACTOME_METAL_ION_SLC_TRANSPORTERS	26	0.50	1.63	0.02	0.10
		511	294	144	162
		8	3	2	6
ONDER_CDH1_TARGETS_2_DN	45	0.38	1.63	0.01	0.10
		9	917	251	391
		2	8	7	1
REACTOME_SIGNALING_BY_ERYTHROPOIETIN	25	0.54	1.63	0.04	0.10
		242	169	699	212
		8	1	2	2
REACTOME_RHO_GTPASES_ACTIVATE_IQGAPS	31	0.50	1.63	0.01	0.10
		732	106	863	235
		1	3	4	9
DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_DN	83	0.47	1.63	0.04	0.10
		600	113	271	241
		7	4	8	9
BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_UP	37	0.32	1.62	0.00	0.10
		0	795	993	191
		7	7	6	9
PID_FGF_PATHWAY	54	0.45	1.62	0.01	0.10
		202	966	568	303
		3	2	6	8
NAKAMURA_METASTASIS_MODEL_UP	42	0.48	1.62	0.03	0.10
		291	796	893	365
		8	5	4	1

PID_FRA_PATHWAY	37	0.49	1.62	0.02	0.10
		347	864	970	369
				3	4
YAMASHITA_METHYLATED_IN_PROSTATE_CANCER	61	0.46	1.62	0.01	0.10
		262	817	425	369
		5	6	7	7
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	63	0.45	1.62	0.03	0.10
		690	802	071	371
		1			1
PID_IL2_1PATHWAY	55	0.45	1.62	0.04	0.10
		593	830	251	371
		3	1		1
CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP	25	0.59	1.62	0.03	0.10
		710	569	917	505
		5	9	5	6
NAKAMURA_METASTASIS_MODEL_DN	42	0.45	1.62	0.02	0.10
		977	476	258	545
		7	5	7	9
WP_TNF_RELATED_WEAK_INDUCER_OF_APOPTOSIS_TWEAK_SIGNALLING_PATHWAY	42	0.45	1.62	0.03	0.10
		331	488	168	549
		3	1	3	
PID_ALK1_PATHWAY	25	0.52	1.62	0.03	0.10
		265	388	563	550
		9	3	9	8
REACTOME_SIGNALING_BY_FGFR1_IN_DISEASE	36	0.49	1.62	0.01	0.10
		206	334	785	574
		6	5	7	
KEGG_PROSTATE_CANCER	89	0.40	1.62	0.00	0.10
		469	273	779	604
		2	6	7	4
IVANOVSKA_MIR106B_TARGETS	86	0.42	1.62	0.01	0.10
		773	229	984	605
		1	7	1	4
HAHTOLA_CTCL_CUTANEOUS	24	0.54	1.62	0.02	0.10
		708	242	898	608
		8		6	3
TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_TOP20_DN	19	0.52	1.62	0.02	0.10
		818	250	6	611
		9	8		6
GENTILE_UV_RESPONSE_CLUSTER_D1	17	0.54	1.62	0.03	0.10
		396	158	265	642
		5	8	3	9

SA_MMP_CYTOKINE_CONNECTION	15	0.67	1.62	0.03	0.10
		675	088	434	660
		6	3	3	9
PID_IL1_PATHWAY	34	0.49	1.62	0.02	0.10
		453	031	674	677
			5	9	
BIOCARTA_PYK2_PATHWAY	27	0.48	1.61	0.02	0.10
		075	974	395	682
		8	6	2	5
KEGG_MAPK_SIGNALING_PATHWAY	26	0.34	1.61	0.00	0.10
		1	101	937	400
			1	5	8
					4
PID_P38_MK2_PATHWAY	21	0.53	1.61	0.03	0.10
		903	976	042	692
		7	6	6	5
VERNELL_RETINOBLASTOMA_PATHWAY_DN	20	0.52	1.61	0.03	0.10
		317	990	578	694
		3	9	9	2
FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN	43	0.39	1.61	0.03	0.10
		6	970	91	557
			8		3
					2
WANG_ESOPHAGUS_CANCER_VS_NORMAL_DN	99	0.40	1.61	0.01	0.10
		678	875	761	698
		6	1	3	7
CHUNG_BLISTER_CYTOTOXICITY_UP	13	0.42	1.61	0.04	0.10
		2	655	879	142
			2		707
NABA_ECM_REGULATORS	22	0.39	1.61	0.01	0.10
		8	925	801	260
			7	4	5
					7
REACTOME_INTERFERON_SIGNALING	18	0.42	1.61	0.03	0.10
		6	867	827	703
			2	4	7
GABRIELY_MIR21_TARGETS	28	0.48	1.61	0.04	0.10
		4	255	802	696
			2	5	7
					4
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	12	0.40	1.61	0.02	0.10
		2	067	829	316
			2	7	6
					6
PID_API1_PATHWAY	69	0.42	1.61	0.03	0.10
		329	683	6	760
		4	4		1

WP_FGF23_SIGNALLING_IN_HYPOPHOSPHATEMIC_RICKETS_AND_RELATED_DISORDERS	20	0.52	1.61	0.01	0.10
		45	694	825	765
			2	6	1
CERVERA_SDHB_TARGETS_2	11	0.40	1.61	0.01	0.10
	0	174	633	434	787
		4	9	4	4
REACTOME_INFLAMMASOMES	21	0.58	1.61	0.04	0.10
		016	572	8	805
		8	7		4
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_1	49	0.36	1.61	0.02	0.10
	6	160	499	484	848
		8	2	5	
FERRANDO_HOX11_NEIGHBORS	23	0.59	1.61	0.03	0.10
		156	449	846	867
			5	2	9
REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	12	0.41	1.61	0.02	0.10
	4	515	374	419	904
		4	3	4	9
JACKSON_DNMT1_TARGETS_DN	21	0.58	1.61	0.02	0.10
		950	389	947	905
		3	6	4	8
DAZARD_UV_RESPONSE_CLUSTER_G6	14	0.46	1.61	0.04	0.10
	1	165	348	563	911
		7	7	5	4
LAMB_CCND1_TARGETS	19	0.54	1.61	0.03	0.10
		888	234	125	975
			7		3
PID_TOLL_ENDOGENOUS_PATHWAY	24	0.55	1.61	0.04	0.10
		032	120	661	983
		9	1		3
PID_SYNDECAN_3_PATHWAY	17	0.52	1.61	0.03	0.10
		425	125	118	989
		1	5	9	9
LENAOUR_DENDRITIC_CELL_MATURATION_UP	11	0.43	1.61	0.03	0.10
	4	069	155	536	990
		3	1	3	2
WP_HAIR_FOLLICLE_DEVELOPMENT_ORGANOGENESIS_PART_2_OF_3	32	0.50	1.61	0.03	0.10
		596	138	765	991
		6	2	7	
BIOCARTA_AKT_PATHWAY	22	0.51	1.61	0.03	0.10
		468	197	632	991
		5	4	9	8

GROSS_HIF1A_TARGETS_DN	26	0.52	1.61	0.04	0.10
		779	175	040	995
				4	3
HORIUCHI_WTAP_TARGETS_UP	28	0.37	1.61	0.01	0.11
	6	272	156	593	
		5	6	6	
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP	17	0.37	1.61	0.01	0.11
	6	416	069	603	009
		5	1	2	5
ZHONG_SECRETOME_OF_LUNG_CANCER_AND_ENDOTHELIUM	68	0.44	1.61	0.03	0.11
		815	001	440	051
		7	1	9	
PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_3	18	0.54	1.60	0.04	0.11
		161	974	339	058
			4	3	8
SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP	38	0.39	1.60	0.00	0.11
	6	037	853	809	099
		9	2	7	3
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREY_D N	74	0.40	1.60	0.01	0.11
		528	863	878	103
		9	4	9	5
KIM_PTEN_TARGETS_UP	18	0.54	1.60	0.02	0.11
		654	816	674	103
		3	5	9	5
PID_TGFBR_PATHWAY	53	0.45	1.60	0.04	0.11
		170	824	790	108
		6	4	4	9
REACTOME_ESTROGEN_DEPENDENT_NUCLEAR_EVENTS_DOWNS TREAM_OF_ESR_MEMBRANE_SIGNALING	24	0.50	1.60	0.02	0.11
		553	750	584	109
		7	6	5	2
BIOCARTA_FCER1_PATHWAY	39	0.46	1.60	0.02	0.11
		826	766	352	109
		4	4	9	3
DESERT_EXTRACELLULAR_MATRIX_HEPATOCELLULAR_CARCIN OMA_SUBCLASS_UP	22	0.55	1.60	0.04	0.11
		971	874	268	116
		9	4	3	9
REACTOME_NOD1_2_SIGNALING_PATHWAY	36	0.47	1.60	0.03	0.11
		779	711	042	118
		2	3	6	1
SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_UP	27	0.51	1.60	0.03	0.11
		999	682	055	130
		8	1		7

HAN_SATB1_TARGETS_UP	41	0.32	1.60	0.00	0.11
	1	528	665	618	131
		3	6	6	
NEMETH_INFLAMMATORY_RESPONSE_LPS_DN	29	0.48	1.60	0.02	0.11
		373	639	474	138
		4	2	2	8
CHEN_LUNG_CANCER_SURVIVAL	27	0.52	1.60	0.03	0.11
		606	612	671	145
		4	1	7	7
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	13	0.40	1.60	0.02	0.11
	2	376	593	505	149
		6	1	2	8
REACTOME_GLYCOGEN_SYNTHESIS	16	0.58	1.60	0.02	0.11
		586	578	766	150
		8	4		8
WP_AGERAGE_PATHWAY	66	0.42	1.60	0.02	0.11
		928	265	024	197
		8	7	3	7
COATES_MACROPHAGE_M1_VS_M2_UP	83	0.41	1.60	0.02	0.11
		492	230	222	204
		4	9	2	
HUTTMANN_B_CLL_POOR_SURVIVAL_DN	57	0.44	1.60	0.01	0.11
		573	288	988	205
		6	1	1	
KEGG_GAP_JUNCTION	86	0.39	1.60	0.02	0.11
		798	236	231	210
		4		2	8
GRESHOCK_CANCER_COPY_NUMBER_UP	31	0.36	1.60	0.01	0.11
	6	381	292	603	212
		2	7	2	7
REACTOME_ESR_MEDIATED_SIGNALING	16	0.36	1.60	0.00	0.11
	1	221	166	6	218
		7	6		
KANG_DOXORUBICIN_RESISTANCE_DN	19	0.60	1.60	0.04	0.11
		663	455	590	219
		4	9	8	6
BIOCARTA_CHEMICAL_PATHWAY	18	0.53	1.60	0.03	0.11
		197	442	333	223
		9	2	3	5
HONRADO_BREAST_CANCER_BRCA1_VS_BRCA2	16	0.59	1.60	0.04	0.11
		087	421	040	227
		4	4	4	9

RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP	27	0.49	1.60	0.02	0.11
		905	405	631	228
		7	7	6	2
WP_CHEMOKINE_SIGNALING_PATHWAY	16	0.40	1.60	0.04	0.11
	2	690	338	536	233
		2	3	1	6
PID_THROMBIN_PAR1_PATHWAY	43	0.47	1.60	0.03	0.11
		208	319	174	235
		8	4	6	
PID_CASPASE_PATHWAY	51	0.43	1.60	0.01	0.11
		780	349	666	237
		2	6	7	9
PID_REELIN_PATHWAY	28	0.51	1.60	0.02	0.11
		180	361	725	238
		6	9	4	9
REACTOME_RHOA_GTPASE_CYCLE	14	0.38	1.60	0.02	0.11
	8	671	375	653	239
		7	6	1	3
REACTOME_N_GLYCAN_ANTENNAE_ELONGATION	15	0.57	1.60	0.03	0.11
		673	051	292	242
		2		2	2
ISSAEVA_MLL2_TARGETS	59	0.44	1.60	0.02	0.11
		508	100	626	256
		7	5	3	4
BIOCARTA_STATHMIN_PATHWAY	19	0.56	1.60	0.04	0.11
		841	069	842	261
		7	7	1	3
WANG_NEOPLASTIC_TRANSFORMATION_BY_CCND1_MYC	22	0.55	1.60	0.03	0.11
		312	081	455	262
		9	9	3	4
PUIFFE_INVASION_INHIBITED_BY_ASCITES_UP	72	0.43	1.59	0.03	0.11
		524	976	105	290
		1	8	6	2
ZWANG_CLASS_2_TRANSIENTLY_INDUCED_BY_EGF	47	0.44	1.59	0.02	0.11
		211	962	816	290
		8	2	9	3
WIERENGA_STAT5A_TARGETS_GROUP1	12	0.37	1.59	0.01	0.11
	2	126	942	785	291
		8	2	7	9
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_RECRUITING_THEM_TO_CLATHRIN_ADAPTERS	21	0.55	1.59	0.04	0.11
		710	920	715	295
		7	6	1	1

GRYDER_PAX3FOXO1_ENHANCERS_KO_DOWN	42	0.35	1.59	0.01	0.11
	6	724	883	268	300
		6	6	5	5
GENTILE_UV_RESPONSE_CLUSTER_D2	37	0.47	1.59	0.02	0.11
		729	849	231	317
		4	5	2	1
WP_REGULATION_OF_APOPTOSIS_BY_PARATHYROID_HORMONER ELATED_PROTEIN	22	0.51	1.59	0.03	0.11
		502	821	368	325
		1	6	4	5
GRYDER_PAX3FOXO1_TOP_ENHANCERS	42	0.35	1.59	0.01	0.11
	6	776	784	229	341
		9	5	5	
STEIN_ESRRA_TARGETS_DN	97	0.38	1.59	0.01	0.11
		183	691	603	343
		7	8	2	1
REACTOME_CDC42_GTPASE_CYCLE	15	0.39	1.59	0.02	0.11
	8	983	694	907	351
			9		2
THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN	22	0.34	1.59	0.01	0.11
	4	651	696	771	360
		9	4	7	4
PID_NCADHERIN_PATHWAY	33	0.49	1.59	0.02	0.11
		356	714	579	378
		5	6	4	9
REACTOME_RUNX2_REGULATES_OSTEOLAST_DIFFERENTIATIO N	23	0.50	1.59	0.03	0.11
		308	598	346	387
		9	1	5	3
WP_LTF_DANGER_SIGNAL_RESPONSE_PATHWAY	18	0.59	1.59	0.04	0.11
		652	565	417	399
		1	2	7	
PID_P38_ALPHA_BETA_DOWNSTREAM_PATHWAY	38	0.43	1.59	0.01	0.11
		960	524	663	420
		8	3	2	5
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREEN_ UP	27	0.51	1.59	0.04	0.11
		278	454	466	433
			7		9
PID_LIS1_PATHWAY	28	0.50	1.59	0.04	0.11
		008	472	268	443
		9	8	3	6
KYNG_DNA_DAMAGE_BY_4NQO_OR_UV	59	0.40	1.59	0.01	0.11
		699	392	361	446
		4	9	9	9

SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_UP	15	0.38	1.59	0.02	0.11
	4	431	362	886	458
		6	7	6	5
REACTOME_RND3_GTPASE_CYCLE	42	0.46	1.59	0.03	0.11
		695	328	571	472
		4	9	4	
MARTIN_NFKB_TARGETS_UP	44	0.43	1.59	0.01	0.11
		378	237	181	515
			9	1	3
WP_MBDNF_AND_PROBDNF_REGULATION_OF_GABA_NEUROTRANSMISSION	37	0.46	1.59	0.02	0.11
		394	219	348	518
		3	1	3	5
BASSO_HAIRY_CELL_LEUKEMIA_UP	77	0.45	1.59	0.03	0.11
		273	139	232	567
		5	6	3	2
BIOCARTA_RACCYCD_PATHWAY	26	0.50	1.58	0.02	0.11
		777	977	070	634
		9	5	4	2
MCBRYAN_PUBERTAL_BREAST_6_7WK_UP	18	0.38	1.59	0.02	0.11
	2	603	027	892	638
		8	6	6	9
LANDIS_ERBB2_BREAST_TUMORS_65_DN	39	0.47	1.58	0.03	0.11
		281	987	534	646
		9	7	3	6
REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS_PARS	32	0.44	1.58	0.02	0.11
		599	998	301	649
		9	7	3	
BOYLAN_MULTIPLE_MYELOMA_D_UP	84	0.38	1.58	0.01	0.11
		312	938	004	650
		1	9		4
QI_HYPOXIA	13	0.37	1.58	0.01	0.11
	1	436	869	859	652
		9		5	2
PID_TELOMERASE_PATHWAY	67	0.43	1.58	0.02	0.11
		534	895	922	652
		6	9	8	6
PID_BCR_5PATHWAY	63	0.46	1.58	0.04	0.11
		305	918	426	655
		8	8	6	9
RASHI_RESPONSE_TO_IONIZING_RADIATION_2	12	0.39	1.58	0.03	0.11
	0	507	897	592	662
		1	2	8	7

SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP	39	0.48	1.58	0.03	0.11
		268	741		694
		5	4		1
IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR	49	0.36	1.58	0.02	0.11
	2	013	762	725	699
		8		4	8
SENESE_HDAC2_TARGETS_DN	11	0.39	1.58	0.02	0.11
	7	650	700	658	712
		8	8	5	
REACTOME_CONSTITUTIVE_SIGNALING_BY_ABERRANT_PI3K_IN_CANCER	77	0.42	1.58	0.02	0.11
		438	619	339	732
		4	9	2	6
BIOCARTA_RAS_PATHWAY	22	0.52	1.58	0.03	0.11
		784	603	673	737
		3	3	5	2
REACTOME_MAPK_FAMILY_SIGNALING_CASCADES	31	0.31	1.58	<0.0	0.11
	8	94	626	1	737
			1		7
WILLERT_WNT_SIGNALING	21	0.49	1.58	0.03	0.11
		875	650	426	741
		8	8	1	3
DAZARD_RESPONSE_TO_UV_SCC_DN	11	0.42	1.58	0.03	0.11
	1	110	580	976	745
		5	7	1	
BIOCARTA_MCALPAIN_PATHWAY	18	0.55	1.58	0.02	0.11
		448	536	755	747
			1	9	1
GUO_HEX_TARGETS_UP	77	0.39	1.58	0.03	0.11
		716	559	162	750
		5	1	1	8
HALMOS_CEBPA_TARGETS_UP	46	0.44	1.58	0.03	0.11
		998	400	012	753
		5	6		8
MOHANKUMAR_HOXA1_TARGETS_UP	39	0.38	1.58	0.04	0.11
	3	615	537	554	756
			2	9	6
REACTOME_C_TYPE_LECTIN_RECEPTORS_CLRS	13	0.40	1.58	0.04	0.11
	8	295	406	468	759
		8	9	1	3
WP_PROSTAGLANDIN_SYNTHESIS_AND_REGULATION	45	0.46	1.58	0.04	0.11
		264	461	526	762
		3	3	7	2

REACTOME_DEFECTIVE_B4GALT7_CAUSES_EDS_PROGEROID_TYP E	20	0.58	1.58	0.04	0.11
		074	417	030	762
		5	8	7	8
BALDWIN_PRKCI_TARGETS_UP	37	0.46	1.58	0.01	0.11
		066	433	871	771
		7	9	1	7
TSENG_ADIPOGENIC_POTENTIAL_DN	47	0.48	1.58	0.04	0.11
		546	350	294	782
		1	4	5	2
GAJATE_RESPONSE_TO TRABECTEDIN_DN	17	0.57	1.58	0.04	0.11
		097	277	791	818
			7	7	
MARKS_HDAC_TARGETS_UP	21	0.50	1.58	0.03	0.11
		651	158	238	823
			2	9	1
WP_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPAT HY	73	0.44	1.58	0.03	0.11
		919	169	534	826
		6	9	3	4
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	24	0.42	1.58	0.04	0.11
		3	302	186	911
				3	6
				6	7
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPA THY_ARVC	73	0.44	1.58	0.03	0.11
		919	169	534	836
		6	9	3	8
DOUGLAS_BMI1_TARGETS_DN	30	0.34	1.58	0.01	0.11
		6	804	193	222
				6	2
					3
TIEN_INTESTINE_PROBIOTICS_2HR_DN	88	0.41	1.58	0.03	0.11
		878	086	238	867
			7	5	9
				9	7
TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_DN	30	0.34	1.58	0.01	0.11
		3	384	044	394
				2	4
				4	6
KEGG_ENDOMETRIAL_CANCER	52	0.43	1.57	0.04	0.11
		156	971	016	934
			8	1	1
				1	3
REACTOME_TOLL_LIKE_RECEPTOR_9_TLR9_CASCADE	94	0.38	1.57	0.02	0.11
		845	879	494	951
			3	9	8
				8	3
REACTOME_METABOLISM_OF_CARBOHYDRATES	28	0.34	1.57	0.01	0.11
		6	414	854	829
				6	3
				3	7

HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_UP	17	0.36	1.57	0.02	0.11
	4	224	896	697	960
		7	3	1	2
KEGG_ERBB_SIGNALING_PATHWAY	87	0.38	1.57	0.02	0.11
		846	905	824	963
		5	4	9	2
ROZANOV_MMP14_TARGETS_UP	25	0.36	1.57	0.02	0.11
	4	924	803	325	969
		2	4	6	4
WP_NOTCH_SIGNALING_PATHWAY_NETPATH	61	0.42	1.57	0.03	0.11
		040	809	505	973
		4	9	2	8
BOYLAN_MULTIPLE_MYELOMA_C_DN	55	0.40	1.57	0.01	0.11
		842	818	380	977
		6	1	7	9
BIOCARTA_TID_PATHWAY	19	0.53	1.57	0.03	0.11
		38	753	564	986
			1	4	1
REACTOME_NETRIN_1_SIGNALING	48	0.42	1.57	0.03	0.11
		976	706	036	992
		4		4	6
WP_ALZHEIMERS_DISEASE	80	0.38	1.57	0.01	0.11
		017	723	408	998
			8	5	4
PARENT_MTOR_SIGNALING_DN	44	0.43	1.57	0.03	0.12
		590	706	929	002
		9	1	3	9
DOANE_BREAST_CANCER_ESR1_DN	46	0.46	1.57	0.02	0.12
		938	651	429	010
		6	1	1	5
BIOCARTA_IGF1R_PATHWAY	22	0.50	1.57	0.04	0.12
		478	606	621	026
		5	3	8	8
WP_FIBRIN_COMPLEMENT_RECEPTOR_3_SIGNALING_PATHWAY	41	0.48	1.57	0.03	0.12
		529	315	854	150
		2	4		7
HOFMANN_CELL_LYMPHOMA_UP	44	0.45	1.57	0.03	0.12
		984	357	010	171
		9	2	8	1
LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_UP	73	0.40	1.57	0.01	0.12
		165	242	192	185
		2	3	8	6

WANG_RESPONSE_TO_FORSKOLIN_UP	22	0.52	1.57	0.04	0.12
		669	225	106	189
		7	5	8	7
WP_STRUCTURAL_PATHWAY_OF_INTERLEUKIN_1_IL1	49	0.42	1.57	0.03	0.12
		181	064	272	250
		9	9		9
WP_IL6_SIGNALING_PATHWAY	43	0.44	1.57	0.02	0.12
		221	071	395	255
		9		2	7
IGARASHI_ATF4_TARGETS_DN	96	0.40	1.57	0.03	0.12
		861	077	340	260
			5	3	7
GERY_CEBP_TARGETS	12	0.38	1.57	0.03	0.12
	4	539	008	455	263
		1	6	3	2
REACTOME_RAB_GEF5_EXCHANGE_GTP_FOR_GDP_ON_RABS	89	0.37	1.57	0.01	0.12
		228	094	417	266
		8	5		5
GRAHAM_CML QUIESCENT_VS_NORMAL_DIVIDING_UP	53	0.43	1.56	0.04	0.12
		910	917	417	308
		3	8	7	4
NAKAMURA_METASTASIS	46	0.45	1.56	0.04	0.12
		135	866	106	325
		5		8	6
MCBRYAN_PUBERTAL_BREAST_6_7WK_DN	77	0.38	1.56	0.01	0.12
		830	658	859	378
		3	6	5	5
KORKOLA_TERATOMA	41	0.45	1.56	0.04	0.12
		64	726	408	382
			9	8	5
ZHOU_TNF_SIGNALING_4HR	49	0.47	1.56	0.04	0.12
		601	753	329	383
		3	6		9
PID_P73PATHWAY	78	0.40	1.56	0.01	0.12
		809	631	508	389
			6	6	2
REACTOME_ONCOGENIC_MAPK_SIGNALING	81	0.38	1.56	0.03	0.12
		920	670	719	390
		8	6		3
MILI_PSEUDOPODIA_CHEMOTAXIS_DN	41	0.34	1.56	0.03	0.12
	4	250	538	225	411
		3	4	8	1

LA_MEN1_TARGETS	25	0.48	1.56	0.04	0.12
		142	573	233	411
		5	9	9	8
KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP	51	0.40	1.56	0.01	0.12
		894	428	875	477
		8	3		4
REACTOME_ZINC_TRANSPORTERS	17	0.53	1.56	0.04	0.12
		748	353	271	486
		7	9	8	
WP_TGFBETA_RECEPTOR_SIGNALING	54	0.44	1.56	0.03	0.12
		514	365	688	486
		3	8	5	4
JAZAG_TGFB1_SIGNALING_UP	10	0.36	1.56	0.02	0.12
	1	754	257	714	536
		6	6		5
REACTOME_APOPTOTIC_FACTOR_MEDIATED_RESPONSE	18	0.51	1.56	0.04	0.12
		811	117	781	548
		6	3	7	2
CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN	24	0.49	1.56	0.03	0.12
		014	160	711	556
		3	1	3	
BAE_BRCA1_TARGETS_DN	30	0.46	1.56	0.03	0.12
		105	046	080	578
		1	5	1	9
YORDY_RECIPROCAL_REGULATION_BY_ETS1_AND_SP100_DN	67	0.38	1.55	0.00	0.12
		895	928	580	628
			2	3	2
BROWNE_HCMV_INFECTION_8HR_DN	43	0.43	1.55	0.04	0.12
		827	894	2	644
		5			2
NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_UP	29	0.47	1.55	0.04	0.12
		910	779	621	697
		5	4	8	7
SASSON_RESPONSE_TO_FORSKOLIN_UP	86	0.38	1.55	0.01	0.12
		669	755	930	705
		1	5	5	5
NGUYEN_NOTCH1_TARGETS_UP	27	0.45	1.55	0.03	0.12
		551	716	777	724
		6	5	3	4
WESTON_VEGFA_TARGETS_12HR	25	0.50	1.55	0.04	0.12
		662	670	838	726
		6	6	7	7

REACTOME_SIGNALING_BY_TGFB_FAMILY_MEMBERS	99	0.40	1.55	0.02	0.12
		442	631	407	737
		9			6
ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION	87	0.38	1.55	0.02	0.12
		494	595	263	744
		8	8	4	1
BIOCARTA_TNFR1_PATHWAY	29	0.48	1.55	0.02	0.12
		159	634	439	745
		5			6
SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_DN	31	0.45	1.55	0.03	0.12
		746	508	073	781
		5	7	8	3
BIOCARTA_PTDINS_PATHWAY	23	0.48	1.55	0.04	0.12
		214	512	854	788
		9	5	4	8
PID_MYC_REPRESS_PATHWAY	63	0.38	1.55	0.02	0.12
		755	452	061	803
		9	2	9	6
WP_MELANOMA	68	0.38	1.55	0.01	0.12
		575	431	178	810
			5	8	6
REACTOME_TRAF6_MEDIATED_INDUCION_OF_TAK1_COMPLEX_WITHIN_TLR4_COMPLEX	16	0.53	1.55	0.04	0.12
		204	382	271	817
		9	4	8	5
LI_PROSTATE_CANCER_EPIGENETIC	32	0.45	1.55	0.02	0.12
		543	341	863	827
		6	4		7
GENTILE_UV_RESPONSE_CLUSTER_D7	36	0.43	1.55	0.02	0.12
		656	291	605	834
		9	1	2	
WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP	12	0.40	1.55	0.04	0.12
	0	154	300	508	838
		5	3	2	3
HOLLERN_MICROACINAR_BREAST_TUMOR_DN	15	0.54	1.55	0.03	0.12
		009	269	522	841
		2	6	5	1
WP_IL17_SIGNALING_PATHWAY	30	0.46	1.55	0.03	0.12
		438	216	787	861
		9	6	9	4
DELPUECH_FOXO3_TARGETS_UP	64	0.42	1.54	0.03	0.12
		682	932	497	874
		1	9	9	5

LEE_AGING_MUSCLE_DN	41	0.42	1.54	0.02	0.12
		356	943	988	874
		3	8		9
BOYALT_LIVER_CANCER_SUBCLASS_G2	28	0.45	1.55	0.02	0.12
		174	053	994	877
			3		7
LEE_NEURAL_CRESCENT_STEM_CELL_UP	14	0.41	1.55	0.03	0.12
	3	010	179	490	881
		6	3	8	3
WP_IL9_SIGNALING_PATHWAY	16	0.57	1.55	0.04	0.12
		079	027	845	886
		3	7		4
BENPORATH_OCT4_TARGETS	27	0.33	1.55	0.02	0.12
	9	516	078	642	888
		2	9	3	9
GAUSSMANN_MLL_AF4_FUSION_TARGETS_A_UP	18	0.34	1.55	0.01	0.12
	8	468	104	024	889
		1	5	6	
COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_DN	28	0.47	1.55	0.04	0.12
		369	154	99	890
		5	4		7
MOHANKUMAR_HOXA1_TARGETS_DN	15	0.35	1.55	0.01	0.12
	5	943	121	639	897
		8	7	3	3
HUANG_GATA2_TARGETS_DN	68	0.39	1.55	0.02	0.12
		882	125	966	904
		6	9	1	2
LIN_TUMOR_ESCAPE_FROM_IMMUNE_ATTACK	19	0.52	1.54	0.03	0.12
		186	846	909	913
		9	1	5	6
WP_TNF_ALPHA_SIGNALING_PATHWAY	90	0.37	1.54	0.03	0.12
		620	786	073	938
		9	1	8	8
MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_DN	24	0.49	1.54	0.04	0.12
		404	718	703	940
		1	7	5	9
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	72	0.43	1.54	0.03	0.12
		235	729	695	941
			8	7	8
DASU_IL6_SIGNALING_UP	58	0.44	1.54	0.04	0.12
		316	731	733	960
		9	5	7	2

REACTOME_ERK_MAPK_TARGETS	22	0.48	1.54	0.04	0.12
		437	738	789	965
		2	9	3	9
KYNG_DNA_DAMAGE_BY_GAMMA_AND_UV_RADIATION	74	0.37	1.54	0.02	0.13
		508	497	589	064
		3	7	6	8
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_15	33	0.43	1.54	0.02	0.13
		522	501	669	071
		4	5	4	1
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLACK_UP	33	0.43	1.54	0.02	0.13
		789	474	734	071
		8		4	7
WP_PI3KAKTMTOR_VITD3_SIGNALLING	22	0.50	1.54	0.04	0.13
		511	182	761	223
		8	4	9	7
DELASERNA_MYOD_TARGETS_DN	56	0.39	1.54	0.03	0.13
		609	144	048	241
		9	8	8	2
PEART_HDAC_PROLIFERATION_CLUSTER_UP	51	0.44	1.54	0.04	0.13
		065	074	210	250
		8		5	4
REACTOME KERATAN_SULFATE_BIOSYNTHESIS	28	0.48	1.54	0.04	0.13
		153	077	526	258
		6		7	8
REACTOME_SIGNALING_BY_WNT	26	0.33	1.54	0.01	0.13
		4	659	032	619
		2	1	4	2
REACTOME_LEISHMANIA_INFECTION	23	0.35	1.54	0.02	0.13
		5	576	036	092
		6	1	1	5
WP_NRF2ARE_REGULATION	23	0.49	1.53	0.03	0.13
		212	988	8	283
HOLLMANN_APOPTOSIS_VIA_CD40_DN	24	0.34	1.53	0.02	0.13
		6	648	960	296
		3	5	5	3
BIOCARTA_CARDIACEGF_PATHWAY	18	0.53	1.53	0.04	0.13
		462	965	408	291
			1	8	7
COLINA_TARGETS_OF_4EBP1_AND_4EBP2	35	0.34	1.53	0.02	0.13
		1	090	907	505
		7	6	2	7
WANG_RESPONSE_TO_ANDROGEN_UP	28	0.49	1.53	0.04	0.13
		231	817	989	356
		3		6	3

WP_NONGENOMIC_ACTIONS_OF_125_DIHYDROXYVITAMIN_D3	70	0.40	1.53	0.03	0.13
		261	821	937	362
		8	3		7
WP_MIRNA_REGULATION_OF_P53_PATHWAY_IN_PROSTATE_CANCER	24	0.47	1.53	0.04	0.13
		387	731	098	402
		6	1	4	5
GUO_HEX_TARGETS_DN	64	0.39	1.53	0.02	0.13
		720	685	510	414
		3	6	5	1
BREUHAHN_GROWTH_FACTOR_SIGNALING_IN_LIVER_CANCER	15	0.53	1.53	0.04	0.13
		453	535	743	471
		6	9	1	4
CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_DN	13	0.38	1.53	0.04	0.13
		9	735	537	313
			5	7	2
ZWANG_EGF_PERSISTENTLY_UP	29	0.46	1.53	0.04	0.13
		296	497	888	490
		6	1		4
WP_MECHANOREGULATION_AND_PATHOLOGY_OF_YAPTAZ_VIA_HIPPO_AND_NONHIPPO_MECHANISMS	47	0.42	1.53	0.03	0.13
		301	546	789	495
		8	3	5	6
PID_P75_NTR_PATHWAY	68	0.38	1.53	0.01	0.13
		61	439	867	528
				2	4
WP_CARDIAC_HYPERTROPHIC_RESPONSE	55	0.39	1.53	0.02	0.13
		227	220	584	632
		7	4	5	2
WP_EXTRACELLULAR_VESICLEMEDIATED_SIGNALING_IN_RECIPIENT_CELLS	30	0.45	1.53	0.04	0.13
		513	18	417	651
		2		7	
BOYLAN_MULTIPLE_MYELOMA_D_CLUSTER_DN	36	0.42	1.53	0.03	0.13
		418	054	673	676
		9	5	5	7
PID_SMAD2_3NUCLEAR_PATHWAY	81	0.38	1.53	0.01	0.13
		711	121	972	689
		5	2	4	9
PID_HIF2PATHWAY	34	0.43	1.53	0.04	0.13
		236	093	814	701
		9	5		4
KEGG_BLADDER_CANCER	42	0.40	1.52	0.01	0.13
		005	961	593	712
		1	5	6	8

WP_HIPPOYAP_SIGNALING_PATHWAY	23	0.47	1.52	0.04	0.13
		164	964	106	720
		4	3	8	2
LIN_NPAS4_TARGETS_UP	16	0.34	1.52	0.00	0.13
	3	036	967	809	727
			4	7	4
KEGG_PRION_DISEASES	34	0.46	1.52	0.03	0.13
		260	892	563	748
		4	9	9	9
KEGG_COLORECTAL_CANCER	62	0.38	1.52	0.04	0.13
		404	834	838	769
		1	6	7	4
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_UP	82	0.39	1.52	0.02	0.13
		624	738	729	810
		6	4		3
REACTOME_SIGNALING_BY_FGFR3	40	0.42	1.52	0.02	0.13
		010	746	381	814
		8			4
SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_DN	44	0.33	1.52	0.02	0.13
	2	986	536	032	873
		9	9	5	
MA_MYELOID_DIFFERENTIATION_DN	42	0.41	1.52	0.04	0.13
		934	508	024	876
		8	2	1	7
GOTTWEIN_TARGETS_OF_KSHV_MIR_K12_11	62	0.37	1.52	0.02	0.13
		923	518	760	877
		3		1	6
PILON_KLF1_TARGETS_UP	46	0.32	1.52	0.01	0.13
	7	891	567	829	881
		2	2	3	4
ZHAN_MULTIPLE_MYELOMA_CD1_AND_CD2_DN	51	0.40	1.52	0.04	0.13
		511	571	321	887
		5	7		8
SCHRAETS_MLL_TARGETS_UP	33	0.47	1.52	0.04	0.13
		496	598	980	889
		7	7	1	3
ABDELMOHSEN_ELAVL4_TARGETS	16	0.55	1.52	0.04	0.13
		463	574	130	895
		7	1	4	9
GAVIN_FOXP3_TARGETS_CLUSTER_P7	89	0.39	1.52	0.03	0.13
		453	334	883	930
		3	7	5	8

WP_ENDOMETRIAL_CANCER	63	0.39	1.52	0.03	0.13
		648	231	869	998
		7	5	7	5
CHANG_IMMORTALIZED_BY_HP31_UP	68	0.39	1.52	0.02	0.14
		989	185	868	018
		8	7	9	3
ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP	40	0.31	1.52	0.01	0.14
		8	863	122	361
		7	1	9	5
GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP	17	0.36	1.52	0.02	0.14
		6	041	066	723
		5	6	7	1
WP_NONSMALL_CELL_LUNG_CANCER	72	0.37	1.52	0.02	0.14
		089	016	549	086
		3	8		8
BIOCARTA_PPARA_PATHWAY	51	0.41	1.51	0.03	0.14
		176	960	877	108
		5	6	6	2
WP_ERBB_SIGNALING_PATHWAY	91	0.37	1.51	0.03	0.14
		217	895	383	139
		5	3	5	
SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_UP	65	0.38	1.51	0.02	0.14
		167	796	371	184
		8	9	5	2
DOANE_RESPONSE_TO_ANDROGEN_DN	23	0.32	1.51	0.02	0.14
		6	280	699	195
		9	3	6	7
REACTOME_INTRACELLULAR_SIGNALING_BY_SECOND_MESSENGERS	30	0.31	1.51	0.01	0.14
		4	584	587	449
		5	2	3	7
YANG_BREAST_CANCER_ESR1_DN	24	0.48	1.51	0.04	0.14
		657	590	931	294
			6		8
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	67	0.37	1.51	0.03	0.14
		998	401	711	375
		9	8	3	9
WP_NOVEL_INTRACELLULAR_COMPONENTS_OF_RIGILIKE_RECEPTOR_RLR_PATHWAY	58	0.39	1.51	0.04	0.14
		168	301	117	425
		3	2	6	1
REACTOME_SARS_COV_INFECTIONS	14	0.33	1.51	0.01	0.14
		6	684	313	232
		2	3		6

HEIDENBLAD_AMPLICON_12P11_12_UP	36	0.42	1.51	0.04	0.14
		848	151	627	506
				8	2
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	82	0.40	1.51	0.04	0.14
		943	122	048	509
		2		6	7
HUANG_FOXA2_TARGETS_UP	46	0.40	1.51	0.03	0.14
		852	027	869	546
		5	7	7	4
VALK_AML_CLUSTER_12	29	0.44	1.50	0.04	0.14
		112	569	684	840
		3		3	3
KYNG_DNA_DAMAGE_BY_GAMMA_RADIATION	74	0.35	1.50	0.01	0.14
		480	444	768	908
		3	6	2	7
WP_LUNG_FIBROSIS	62	0.42	1.50	0.04	0.14
		791	450	590	914
		8	5	8	1
SMIRNOV_RESPONSE_TO_IR_6HR_UP	16	0.33	1.50	0.01	0.14
		3	436	417	836
				1	7
					5
CHESLER_BRAIN_HIGHEST_GENETIC_VARIANCE	35	0.41	1.50	0.03	0.14
		747	212	813	995
		6	6	6	7
BIOCARTA_NFAT_PATHWAY	49	0.40	1.50	0.03	0.15
		744	214	585	004
		2	7	7	5
WP_IL1_SIGNALING_PATHWAY	55	0.39	1.50	0.04	0.15
		440	176	444	014
		1	6	4	2
WP_INTERLEUKIN11_SIGNALING_PATHWAY	44	0.39	1.50	0.04	0.15
		677	115	618	015
		9		5	6
PID_THROMBIN_PAR4_PATHWAY	15	0.54	1.50	0.04	0.15
		468	223	646	017
		4	8	5	3
BROWNE_HCMV_INFECTION_16HR_UP	21	0.36	1.50	0.04	0.15
		8	038	046	382
				5	052
				5	1
VALK_AML_WITH_CEBPA	35	0.41	1.50	0.03	0.15
		174	019	073	052
				4	8
					3

PID_P53_DOWNSTREAM_PATHWAY	13	0.34	1.49	0.02	0.15
	5	433	939	982	055
		6		1	1
FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	61	0.38	1.49	0.04	0.15
		331	948	192	058
		8	9	9	8
SAFFORD_T_LYMPHOCYTE_ANERGY	87	0.35	1.49	0.02	0.15
		232	997	165	062
		2		4	3
FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_DN	26	0.44	1.49	0.04	0.15
		280	835	474	104
		5		7	8
VANASSE_BCL2_TARGETS_DN	58	0.41	1.49	0.03	0.15
		260	645	869	170
		2	4	7	8
KYNG_DNA_DAMAGE_BY_UV	53	0.37	1.49	0.03	0.15
		142	655	742	171
		1	4	2	4
WP_CHROMOSOMAL_AND_MICROSATELLITE_INSTABILITY_IN_CO LORECTAL_CANCER	73	0.37	1.49	0.04	0.15
		789	666	914	182
			2	5	1
LIU_BREAST_CANCER	28	0.43	1.49	0.04	0.15
		518	507	444	184
		5	2	4	4
WP_SIGNALING_PATHWAYS_IN_GLIOBLASTOMA	82	0.38	1.49	0.04	0.15
		654	491	457	186
		5		4	3
WP_THE_OVERLAP_BETWEEN_SIGNAL_TRANSDUCTION_PATHWA YS_THAT_CONTRIBUTE_TO_A_RANGE_OF_LMNA_LAMINOPATHIE S	55	0.38	1.49	0.02	0.15
		973	610	345	189
		7	3	4	4
WP_REGUCALCIN_IN_PROXIMAL_TUBULE_EPITHELIAL_KIDNEY_ CELLS	32	0.42	1.49	0.04	0.15
		692	668	710	190
		4	9	9	3
NAKAMURA_ADIPOGENESIS_EARLY_UP	56	0.41	1.49	0.04	0.15
		176	36	790	192
		6		4	7
PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_UP	56	0.42	1.49	0.03	0.15
		013	592	854	193
		1	6		6
REACTOME_SLC_TRANSPORTER_DISORDERS	96	0.37	1.49	0.01	0.15
		212	576	227	196
		8	6		4

WEI_MIR34A_TARGETS	14	0.35	1.49	0.03	0.15
	2	492	179	917	280
		4	6	5	6
WP_VITAMIN_D_RECEPTOR_PATHWAY	16	0.34	1.49	0.03	0.15
	6	591	144	643	289
		8	8	7	2
STAMBOLSKY_RESPONSE_TO_VITAMIN_D3_UP	79	0.38	1.49	0.04	0.15
		055	152	125	293
		2		7	4
BENPORATH_NOS_TARGETS	17	0.33	1.49	0.01	0.15
	1	761	111	863	309
		9	3	4	2
FARMER_BREAST_CANCER_BASAL_VS_LULMINAL	31	0.32	1.48	0.02	0.15
	7	529	728	647	447
		6	6	7	3
UDAYAKUMAR_MED1_TARGETS_DN	22	0.32	1.48	0.03	0.15
	8	039	733	326	453
		6	1	8	7
WP_IL18_SIGNALING_PATHWAY	26	0.32	1.48	0.03	0.15
	5	123	649	441	494
		3	4	3	2
WP_ARYL_HYDROCARBON_RECEPTOR_PATHWAY	45	0.41	1.48	0.04	0.15
		096	243	480	755
		4	2	7	3
MCBRYAN_PUBERTAL_BREAST_3_4WK_UP	20	0.32	1.47	0.02	0.15
	1	419	918	574	954
		7	6	3	7
MCBRYAN_PUBERTAL_BREAST_4_5WK_UP	25	0.32	1.47	0.04	0.16
	8	538	441	356	180
		5	2	4	1
BILBAN_B_CLL_LPL_UP	59	0.38	1.47	0.03	0.16
		818	272	968	282
		3	9	3	2
BREDEMEYER_RAG_SIGNALING_VIA_ATM_NOT_VIA_NFKB_UP	50	0.37	1.47	0.04	0.16
		488	236	471	305
		4	1	5	1
KAYO_AGING_MUSCLE_UP	22	0.30	1.46	0.00	0.16
	1	597	950	583	459
		2	5	7	2
WP_RAS_AND_BRADYKININ_PATHWAYS_IN_COVID19	29	0.47	1.46	0.04	0.16
		088	682	780	544
		5	5	9	5

WANG_TUMOR_INVASIVENESS_DN	20	0.33	1.46	0.03	0.16
	2	888	697	974	552
		8	5	9	
WP_BLADDER_CANCER	40	0.38	1.46	0.04	0.16
		249	652	288	558
		2	6	5	1
CHIARETTI_T_ALL_REFRACTORY_TO_THERAPY	25	0.44	1.46	0.04	0.16
		480	576	517	584
		6	9	5	2
REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	13	0.34	1.46	0.04	0.16
	8	788	475	602	630
		9	6	5	2
GRABARCZYK_BCL11B_TARGETS_DN	59	0.37	1.46	0.04	0.16
		800	414	291	655
		7	3	8	2
GREGORY_SYNTHETIC_LETHAL_WITH_IMATINIB	13	0.32	1.46	0.02	0.16
	9	070	416	024	663
		6	9	3	1
RIZKI_TUMOR_INVASIVENESS_3D_DN	25	0.29	1.45	0.00	0.16
	2	768	989	819	835
		7	1	7	4
OUILLETTE_CLL_13Q14_DELETION_DN	52	0.35	1.45	0.02	0.16
		395	888	947	887
		4	1	4	1
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	37	0.32	1.45	0.04	0.17
	0	284	534	517	097
		6	5	5	7
MARTORIATI_MDM4_TARGETS_FETAL_LIVER_UP	22	0.31	1.45	0.04	0.17
	7	761	356	042	197
		8	2	6	8
KONDO_EZH2_TARGETS	21	0.34	1.45	0.04	0.17
	4	335	288	098	224
			9	4	7
REACTOME_FGFR1_MUTANT_RECEPTOR_ACTIVATION	29	0.45	1.45	0.04	0.17
		996	220	382	272
		8	5	5	2
RADMACHER_AML_PROGNOSIS	77	0.36	1.44	0.04	0.17
		003	970	733	408
		6	1	7	3
REACTOME_SIGNALING_BY_PTK6	54	0.37	1.44	0.04	0.17
		343	904	554	448
		2	4	9	2

WP_DNA_DAMAGE_RESPONSE_ONLY_ATM_DEPENDENT	11	0.33	1.44	0.03	0.17
	0	910	622	578	584
		4	1	5	8
AMUNDSON_RESPONSE_TO_ARSENITE	20	0.31	1.44	0.02	0.17
	5	240	567	857	602
		1	4	1	7
RAO_BOUND_BY_SALL4	21	0.31	1.43	0.03	0.17
	8	449	887	448	939
		8	9	3	9
WP_FRAGILE_X_SYNDROME	12	0.33	1.43	0.04	0.17
	0	954	783	863	992
		2	3	8	2
KEGG_ENDOCYTOSIS	18	0.32	1.43	0.04	0.18
	1	030	288	826	317
		4	2	3	4
HOWLIN_CITED1_TARGETS_1_UP	32	0.41	1.43	0.04	0.18
		158	134	142	415
YAGI_AML_WITH_T_8_21_TRANSLOCATION	35	0.29	1.43	0.02	0.18
	3	380	040	584	439
		6	5	5	5
OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_DN	25	0.30	1.42	0.03	0.18
	9	299	811	4	494
		1	8		7
WP_RAS_SIGNALING	18	0.31	1.42	0.03	0.18
	1	834	835	944	515
		5	3	8	6
IWANAGA_CARCIANOGENESIS_BY_KRAS_PTEN_UP	17	0.30	1.42	0.02	0.18
	9	504	658	708	565
		6	8	3	1
YAGI_AML_SURVIVAL	11	0.31	1.42	0.03	0.18
	8	598	405	024	692
		8	3	2	5
PID_CMYB_PATHWAY	81	0.34	1.42	0.04	0.18
		707	079	819	817
		9	3	3	3
FIRESTEIN_PROLIFERATION	16	0.30	1.42	0.04	0.18
	2	606	058	527	825
		9	6	6	7
KIM_WT1_TARGETS_8HR_DN	11	0.30	1.41	0.03	0.18
	9	834	810	976	951
		9	9	1	2
KYNG_DNA_DAMAGE_UP	19	0.29	1.41	0.02	0.19
	8	869	483	631	062
			7	6	3

ZHOU_INFLAMMATORY_RESPONSE_FIMA_UP	45	0.28	1.41	0.01	0.19
	4	951	338	956	158
		7	6	9	3
HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP	42	0.28	1.40	0.02	0.19
	5	263	609	490	530
			2	4	8
ZHOU_INFLAMMATORY_RESPONSE_LPS_UP	35	0.29	1.40	0.03	0.19
	5	466	329	867	652
		4	3	4	4
BOYLAN_MULTIPLE_MYELOMA_PCA3_UP	78	0.33	1.40	0.04	0.19
		698	180	592	706
			1	9	4
KOYAMA_SEMA3B_TARGETS_DN	34	0.28	1.40	0.03	0.19
	1	934	155	726	709
		2	4	7	2
SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_1	39	0.29	1.39	0.03	0.20
	6	604	321	339	161
		9	8	9	2
RAO_BOUND_BY_SALL4_ISOFORM_B	49	0.28	1.38	0.03	0.20
	2	600	219	340	762
		1	5	3	6
HAN_SATB1_TARGETS_DN	37	0.27	1.36	0.04	0.22
	2	628	118	621	120
			9	8	2
BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_D	26	0.26	1.35	0.01	0.22
	4	383	810	458	315
		2	7	3	5
ZHANG_BREAST_CANCER_PROGENITORS_DN	13	0.28	1.35	0.04	0.22
	0	591	729	008	32
		7	6	4	
BROWNE_HCMV_INFECTION_30MIN_DN	13	0.29	1.34	0.03	0.22
	4	344	754	527	996
		3	4		3
CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN	45	0.67	2.38	<0.0	<0.0
	1	168	971	1	1
		5	9		
