

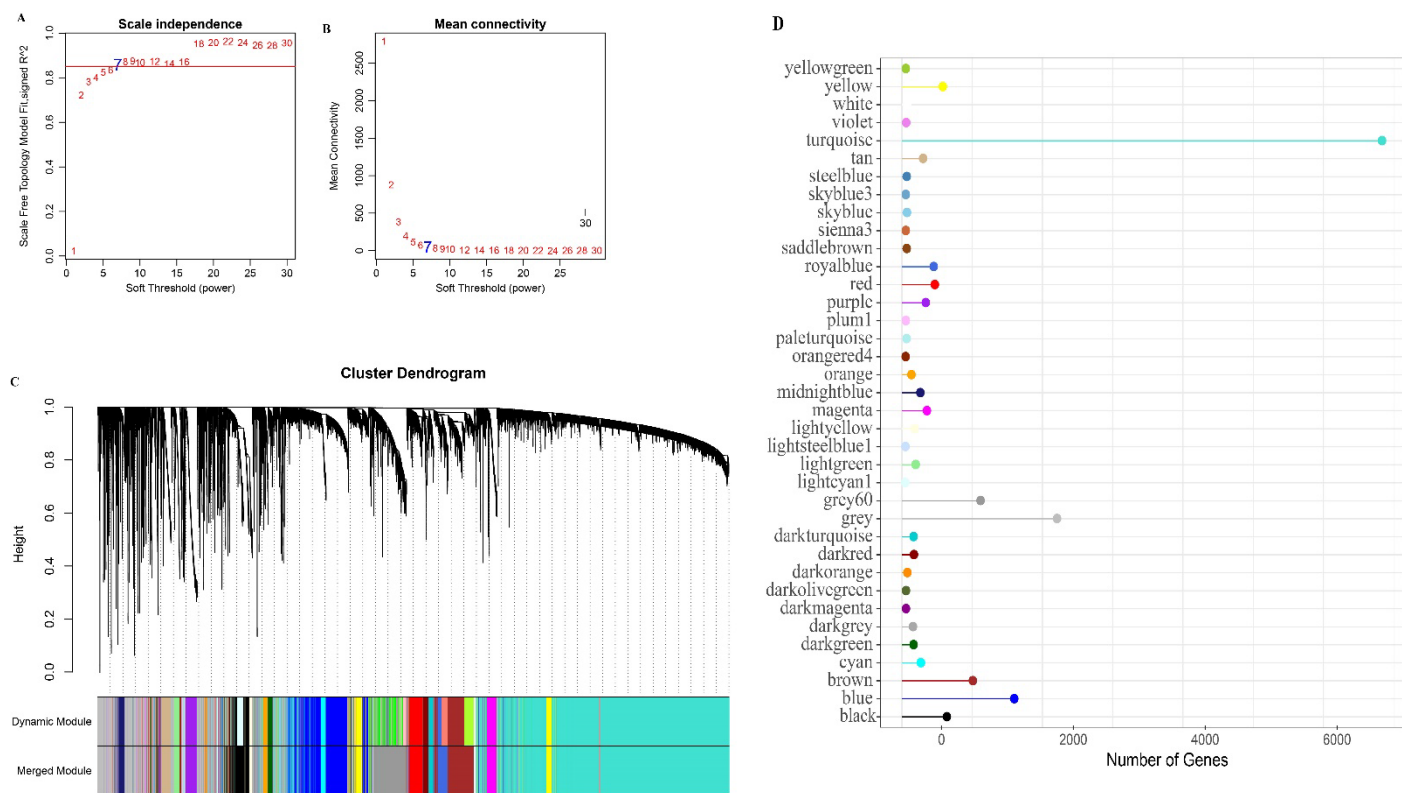


Figure S1 A-B, Network topology analysis with different soft-thresholding powers. C, Gene cluster dendrogram and the color of modules. D, Number of genes in every module.

Supplementary Table 1 Cox regression analysis of 78 hub genes in TCGA-PRAD patients

Tag	p.value	HR	Low 95%CI	High 95%CI
A2M	0.813494076	1.025699809	0.830743481	1.26640789
ABCA8	0.07363002	0.82747099	0.672420469	1.018273937
ABCC9	0.179563496	0.866983628	0.703856005	1.067918162
ABCG4	0.873120276	1.016177431	0.83451059	1.237391812
ACACB	0.560624583	0.940140069	0.763662639	1.157400276
ACOX2	0.002919004	0.721266225	0.581625184	0.894433361
ACSL4	0.756577898	0.968365077	0.790251991	1.186622663
ACSS3	0.01296481	0.759569538	0.61144719	0.943574348
ACTN1	0.48745009	0.931042162	0.760993029	1.139089943
ACY1	0.102839452	1.182189553	0.966834876	1.445512749
ADAM22	0.243060997	0.88401727	0.718738069	1.08730366
ADAM23	0.932773987	1.008801514	0.822964421	1.23660327
ADAMTS15	0.707773335	0.959632381	0.773636572	1.190344846
ADAMTS5	0.083779156	0.821985116	0.658210137	1.026510369
ADAMTS8	0.440525068	0.920868385	0.746827276	1.135468147
ADAMTS9	0.111521466	0.8400888	0.677834731	1.041181811
ADCY3	0.275511058	1.12485595	0.910451006	1.389751782
ADCY5	0.128374029	0.850459818	0.690205491	1.047922556
ADCY9	0.111579368	1.181719504	0.962035152	1.451569605
ADCYAP1R1	0.006622305	0.710243128	0.554814616	0.909214153
ADRA1A	0.001480509	0.678374981	0.534008312	0.861770509
ADRA1B	0.858772629	0.981037252	0.7945143	1.211348985
AGPAT4	0.821985672	0.975881414	0.788918	1.207152752
AHDC1	0.319575353	1.114427426	0.900325128	1.379444434
AHNAK2	0.039199899	0.801760592	0.64989217	0.989118004
AJAP1	0.003228637	0.70287263	0.555869175	0.888752168
ALDH1A2	0.000408412	0.687206186	0.558149075	0.846104318
ALDH1B1	0.947700419	1.007106402	0.815049763	1.244418869
ALDH1L2	0.125348959	0.839634111	0.671458672	1.049931246
ALPK1	0.186297961	0.870404642	0.708479043	1.069338957
AMOTL2	0.825028011	0.976630667	0.79193025	1.204408418
ANGPT1	0.00115739	0.706268178	0.57261846	0.871111873
ANGPTL1	0.000327326	0.669074362	0.537356346	0.833079398
ANK2	0.335825101	0.900888971	0.728386869	1.114244328
ANKRD33B	0.195711208	0.867850754	0.700165898	1.075694965
ANO1	0.858913222	0.98156967	0.799545527	1.20503334
ANO5	0.002147259	0.705268707	0.564301398	0.881450854
ANO6	0.043619276	0.813386261	0.66552112	0.994104002
ANP32E	0.152298856	1.168368995	0.944167256	1.445809628
AOC3	0.025796987	0.793174339	0.646983815	0.972397637
ARHGAP10	0.109398475	0.844161444	0.686039687	1.038727871
ARHGAP20	0.015370837	0.762573334	0.612462839	0.949474895
ARHGAP24	0.409274379	0.913845687	0.737797672	1.131901022
ARHGEF17	0.398010335	1.094769744	0.887429046	1.350553938

ARHGEF28	0.438175929	0.921772653	0.75022225	1.132550819
ARL10	0.625766292	1.054044514	0.853085521	1.30234286
ASAP1	0.504127566	1.073946418	0.871121031	1.32399617
ASPA	0.003844618	0.703744345	0.554569933	0.893045357
ATCAY	0.014104449	0.759332485	0.609478337	0.946031692
ATP10D	0.664448683	0.95601376	0.780179323	1.171477227
ATP1B2	0.078478101	0.82547547	0.666688196	1.022081619
ATP2B4	0.005990879	0.753243713	0.615418894	0.921934794
AVPR1A	0.067660733	0.819822499	0.662481247	1.014532762
B4GALNT1	0.783084937	0.970773119	0.78596729	1.199032657
BDNF	0.25850883	1.123726948	0.917877175	1.37574208
BEND6	0.324602528	0.901177599	0.732648386	1.108473152
BEST1	0.172110337	1.151772799	0.940332164	1.410757422
BHMT2	0.119651254	0.84892066	0.690686018	1.043406509
BMP4	0.798369276	1.027875626	0.832392892	1.269266368
BNC2	0.101980778	0.835597213	0.673766048	1.036298436
BNIP2	0.303686605	1.114143643	0.906760879	1.368956343
BOC	0.080686236	0.836491884	0.684632174	1.022035917
BTN2A1	0.037415274	1.258667313	1.013491871	1.56315354
C11orf95	0.010636235	1.343578612	1.071147478	1.685298733
C12orf75	0.623118591	0.949799552	0.773433107	1.166382949
C15orf41	0.008747531	0.74122716	0.592557288	0.927197614
C1QTNF7	0.220611049	0.873572456	0.70367425	1.084491632
C20orf194	0.2593274	0.89103435	0.729175115	1.08882242
C22orf23	0.812637227	0.974909251	0.790148964	1.202871978
C2orf88	0.000202724	0.627899999	0.491222742	0.802606181
C3orf70	0.006077311	0.751370255	0.612585003	0.92159824
C7	0.004189564	0.750468679	0.616599089	0.913402645
C7orf31	0.531528351	1.068714822	0.867861425	1.316052699
C8orf88	0.002830686	0.726152391	0.588565526	0.895902446
CACHD1	0.106031284	0.843278966	0.685806808	1.036909238
CACNA1C	0.166640666	0.863097157	0.700567096	1.063333842
CALD1	0.099393397	0.847419185	0.695945769	1.03186097
CALM1	0.253296972	0.891457855	0.731963438	1.085706015
CAMK1G	0.026479798	0.776805003	0.621488294	0.970937054
CAMK2G	0.199806412	0.875121359	0.713686524	1.073072514
CAMK4	0.177402327	0.86308784	0.696843416	1.068992837
CAP2	0.029199755	0.80732742	0.666056551	0.978561898
CAV1	0.03809069	0.801742756	0.650640708	0.987936105
CAV2	0.100601387	0.841380327	0.684631546	1.034017288
CBX7	0.595085606	0.943623462	0.761838584	1.168784644
CCDC178	0.001411407	0.681927341	0.539087417	0.86261501
CCDC181	0.998788414	0.999837051	0.81017682	1.233896235
CCDC69	0.057663062	0.817274633	0.6635705	1.006581555
CCDC80	0.566337846	0.941070743	0.764658923	1.158181925
CCDC82	0.354378364	1.106088091	0.89354779	1.369183471
CCDC85A	0.106578729	0.831725669	0.664956986	1.040319303

CCDC88A	0.589299683	0.945035233	0.769680356	1.160340892
CCDC89	0.377338657	0.908273996	0.733588401	1.124556564
CD200	0.650222722	1.051907443	0.845247354	1.309095217
CD99L2	0.196864436	0.880165788	0.725059156	1.068453253
CDC42EP3	0.004431264	0.744936192	0.608193685	0.912423039
CDC42EP4	0.030510227	0.802897912	0.658091162	0.979568022
CDH19	0.382211678	0.911207784	0.739674817	1.122519796
CDH23	0.617799914	1.052140563	0.861723096	1.284635132
CEACAM1	0.001419268	0.728395522	0.599546895	0.884935008
CELF2	0.013733182	0.784053138	0.646114383	0.951440394
CEP112	0.597520527	0.945167694	0.766639578	1.16526983
CEP68	0.989754442	0.998704089	0.819369452	1.217289534
CFH	0.693092746	0.959993157	0.783805544	1.175785077
CFL2	0.044314241	0.810062923	0.659726406	0.994657684
CHRD1	0.002380428	0.737272691	0.605665001	0.897478012
CHST3	0.193595575	0.871895692	0.709097739	1.072069556
CLDN11	0.347389186	0.903358961	0.730791406	1.116676259
CLIC4	0.287884477	0.899843138	0.740698387	1.093181363
CLIP3	0.141624619	0.853349172	0.690689713	1.054315412
CLIP4	0.133891004	0.856396624	0.699266208	1.048835434
CLMP	0.023298862	0.785286299	0.637284098	0.967660378
CLVS2	0.015161869	0.747397431	0.590879241	0.945375775
CNTN1	0.078657918	0.830479661	0.675176367	1.021505641
CNTNAP1	0.781053888	1.029525012	0.838545232	1.264000687
COL14A1	0.265734534	0.889267692	0.723227947	1.09342709
COL21A1	0.85079172	1.020603749	0.825223227	1.262242723
COL4A4	0.340735283	0.90348363	0.733225511	1.113276418
COL4A6	0.002531337	0.709510149	0.567829264	0.886542281
CORO1C	0.769407055	1.031897179	0.836498534	1.272939218
CORO2B	0.278896235	0.88992603	0.720576646	1.099075779
CPED1	0.062415616	0.827246522	0.677639092	1.009883899
CRIM1	0.957156926	0.994506653	0.813443721	1.215872048
CRISPLD2	0.0340677	0.798697176	0.648787138	0.983245723
CRTAP	0.263155933	0.894964082	0.736866484	1.08698214
CRTC3	0.408346384	1.092468417	0.885849195	1.347280384
CSRNP3	0.082201481	0.823844722	0.662134226	1.025049151
CTIF	0.507472279	1.074189414	0.869298183	1.327372956
CTTNBP2	0.159794501	0.85978668	0.696491708	1.061366743
CYB5R3	0.835376914	1.023158127	0.824456376	1.269748871
DAAM2	0.073127728	0.830732135	0.678226441	1.017530191
DAB2IP	0.135236468	1.176751662	0.950472698	1.456900841
DACT1	0.71690596	1.040557561	0.839337696	1.290017169
DBNDD2	0.7123224	0.960321006	0.774380065	1.190909318
DCBLD2	0.00213781	0.748364043	0.621947364	0.900476106
DCHS1	0.2633469	0.890089107	0.725815549	1.091542639
DCN	0.24093431	0.883498975	0.718282604	1.086717725
DDR2	0.05208327	0.815532377	0.663870993	1.001840818

DENND2C	0.417211852	0.918066441	0.746759366	1.128671469
DENND5A	0.092386261	1.21207601	0.968836563	1.516383992
DGKG	0.008631846	0.701060848	0.537830978	0.913830429
DIXDC1	0.027055753	0.798129839	0.653513155	0.974748917
DMC1	0.273833417	0.881611506	0.703498422	1.104819604
DNAJB4	0.136418394	0.853926447	0.693689963	1.051176196
DNAJB5	0.063485741	0.820215058	0.665308505	1.01118915
DNAJC18	0.898375306	1.013590711	0.823932908	1.246905082
DNM3	0.201463675	1.134541427	0.934774562	1.376999654
DPYD	0.853063326	0.981383543	0.804403732	1.19730133
DPYSL2	0.930215982	1.009442815	0.817954546	1.245759683
DPYSL3	0.17760156	0.869415703	0.709376961	1.06555993
DRD1	0.019283429	0.754786911	0.596336447	0.955338692
DRP2	0.477946512	0.925120535	0.746168603	1.146990105
DSE	0.680090942	0.957972846	0.781123462	1.174861617
DST	0.349394858	0.905322747	0.735068654	1.11501051
DSTN	0.032845464	0.809571982	0.666794131	0.98292226
DTX4	0.910786328	1.011826426	0.82373902	1.242860533
DUSP18	0.976242332	0.996883244	0.811745002	1.224246777
DUSP19	0.027976154	0.787562266	0.636481567	0.974504771
DUSP3	0.505589182	0.933847898	0.763423526	1.142317293
DYNC1I1	0.057394737	0.815921278	0.661488304	1.006408622
DYSF	0.44475683	0.922201955	0.74922578	1.1351137
DZIP1	0.706226773	0.960053977	0.776669128	1.186739122
EBF1	0.143866456	0.853967762	0.691039494	1.055310073
ECM2	0.834745101	1.02215085	0.831998354	1.255762532
EDIL3	0.584380127	0.942486403	0.762253537	1.16533486
EDNRA	0.094224148	0.840546845	0.685822755	1.030177248
EDNRB	0.063109171	0.815673732	0.657958188	1.011194402
EFEMP1	0.838211574	0.978430248	0.793642572	1.206242942
EFHD1	0.847033208	1.021251238	0.824789632	1.264509216
EGFLAM	0.502240963	0.931196988	0.756151625	1.146764486
EID3	0.226755001	0.880099594	0.715470993	1.082608942
EMILIN3	0.012185272	0.766127377	0.622068561	0.943547375
ENPEP	0.469528061	1.078114674	0.879315116	1.32185974
ENPP6	0.277021368	0.887545669	0.715775207	1.1005373
ENTPD1	0.36159564	1.101987223	0.894475171	1.357640635
EOGT	0.43151568	0.921794294	0.752511237	1.129158847
EPB41L1	0.905754445	0.987437958	0.80098266	1.217296916
EPB41L2	0.558228548	1.064426339	0.863658509	1.31186507
EPB41L3	0.647227533	0.952219402	0.772090454	1.174372491
EPHA3	0.189114955	0.872947759	0.712709851	1.06921181
EPM2A	0.058658972	0.827563511	0.680132034	1.006953549
EPS8	0.698584436	0.960932012	0.785402098	1.175691196
EVX2	0.017590098	0.728999718	0.56156772	0.94635174
EXT1	0.267021366	1.131136025	0.909949929	1.406086935
EYA1	0.001745775	0.70213963	0.562688127	0.876151525

EYA4	0.001785335	0.703751628	0.564528378	0.877309935
FAM107A	0.00010716	0.666777955	0.543154544	0.818538382
FAM124A	0.015562998	0.761765495	0.611038718	0.949672504
FAM162B	0.944001578	0.992396336	0.802028863	1.227948933
FAM184A	0.143410282	0.852836712	0.689066179	1.055530627
FAM83B	0.028353452	0.772175916	0.612822816	0.972965806
FAT4	0.058101514	0.811530724	0.653878927	1.007192753
FAXDC2	0.040636093	0.803386288	0.651480309	0.990712258
FBLIM1	0.306850121	0.897778427	0.730037894	1.104060641
FBXL7	0.699580451	1.043529481	0.840460098	1.295663863
FBXO30	0.199028804	0.876841625	0.717488602	1.07158669
FBXO32	0.502620617	0.932524248	0.760248543	1.143838394
FCHSD2	0.373556833	1.101468507	0.89027317	1.362764724
FERMT2	0.157560027	0.863129512	0.70376512	1.058581241
FEZ2	0.710150683	1.039483166	0.847477951	1.27498922
FGD6	0.557525724	1.064036602	0.86472169	1.309292807
FGF1	0.399278198	1.090895466	0.891104355	1.335480981
FGF10	0.009261536	0.750446759	0.604523397	0.931593948
FGFR1	0.241145118	0.883399154	0.717999149	1.0869011
FHL5	0.331053799	0.899357617	0.72617287	1.113845141
FHOD3	0.29786179	0.894516967	0.725176287	1.103401502
FILIP1	0.619076063	0.948255703	0.769056577	1.16921031
FILIP1L	0.735953303	0.963668295	0.777162464	1.194932366
FKBP7	0.093890188	0.842221914	0.688934215	1.029616089
FLNA	0.014176253	0.775707859	0.633224739	0.950251381
FLNC	0.004602034	0.747079604	0.610629555	0.914020507
FLRT2	0.013365183	0.75098786	0.598551813	0.942245522
FMO2	0.874009841	1.016680654	0.828667108	1.247351972
FNBP1	0.357580252	1.104789621	0.893460811	1.366103686
FOXC1	0.114897413	0.846844034	0.688730339	1.04125632
FOXF1	0.089061348	0.833060695	0.674905649	1.028277246
FOXF2	0.105842076	0.839091957	0.678373359	1.037887622
FOXO1	0.005669638	0.759783	0.625397852	0.923044756
FOXP2	0.034004129	0.782285095	0.623420242	0.98163314
FREM2	3.65E-05	0.6027972	0.474035762	0.766533865
FRMD3	0.650355581	0.95194047	0.769337699	1.17788412
FRMD6	0.009092086	0.768309444	0.63027951	0.936567653
FRY	0.053234135	1.228497738	0.997135265	1.51354259
FYCO1	0.269984998	0.894706354	0.734221847	1.090269193
FZD1	0.081002897	0.842344747	0.694697896	1.021371558
FZD10	0.962431037	0.994985708	0.807189555	1.226473452
FZD7	0.171897684	0.867394177	0.707256334	1.063790627
GAB2	0.23375909	1.136212737	0.920814436	1.401997333
GALNT5	0.002699405	0.701994771	0.55711134	0.88455686
GATM	0.617202492	0.948101365	0.769297463	1.168463751
GCNT4	0.174286652	0.860600227	0.693012156	1.068715381
GCOM1	0.100286517	0.821337521	0.649504187	1.038631215

GDNF	0.525847101	0.932047362	0.749913398	1.158416807
GFOD1	0.411008219	0.914979187	0.740311039	1.130858341
GFRA1	0.010056538	0.753843336	0.607900925	0.934823015
GIPC2	0.229354552	0.878191226	0.710571937	1.085350814
GJC1	0.711812351	0.960164114	0.773891122	1.19127239
GLDN	0.467124661	0.925584475	0.751442315	1.140083015
GLI2	0.612950532	0.947204277	0.767671234	1.168724192
GLI3	0.109237164	0.843646517	0.685174107	1.038771663
GLIS3	0.8462871	0.979514084	0.794558588	1.207523089
GLOD5	0.691185991	0.957750064	0.774021048	1.185090751
GNA14	0.727122498	0.963561588	0.782232916	1.186923888
GNAI2	0.14349085	1.186986758	0.94342148	1.493433839
GNAL	0.008401093	0.752997305	0.609772341	0.929863332
GNAO1	0.114416464	0.845677416	0.686793465	1.041317846
GNB5	0.36487301	1.103571533	0.891705927	1.365775523
GPM6B	0.031840613	0.798088494	0.649546393	0.980600078
GPR161	0.027642805	0.794398408	0.647257414	0.974988958
GPR20	0.95286707	1.006064939	0.823281022	1.229430334
GPRASP1	0.165802594	0.864264047	0.703145855	1.062300713
GPRC5B	0.072351757	0.829079648	0.675779869	1.017155281
GRIK3	0.303536574	0.892135836	0.717801625	1.108811017
GRK5	0.615984002	1.05582816	0.85387692	1.305543079
GXYLT2	0.812886226	0.974651071	0.787984664	1.205537054
HECTD2	0.329784781	0.902473306	0.734185931	1.109334888
HEG1	0.667113434	1.046366523	0.851113317	1.286412607
HEPH	0.293434223	0.892882304	0.722768315	1.103035084
HFE	0.039823313	0.806612905	0.657160878	0.990053425
HHIP	0.019123932	0.775741589	0.627288754	0.959326959
HIF3A	0.010421125	0.73896459	0.58627402	0.931422248
HLF	0.007819064	0.755144651	0.613976858	0.928770256
HMCN2	0.980085159	1.002595158	0.817986484	1.228867556
HOXA7	0.762052956	1.033138135	0.836584291	1.27587192
HOXD12	0.073324599	0.809761041	0.642772324	1.02013251
HOXD13	0.06943827	0.824834808	0.670010993	1.015434773
HPN	0.810107316	0.97401169	0.785751183	1.207378103
HRH2	0.030105269	0.786183967	0.63256362	0.977111566
HS3ST3A1	0.206639057	0.871768214	0.704536129	1.07869531
HS3ST3B1	0.268072154	0.889973381	0.724085104	1.09386675
HSD11B1	0.022331723	0.784508484	0.637053322	0.966094264
HSPA4L	0.084616509	0.82494005	0.662877675	1.026623933
ID4	0.548715272	0.937206323	0.758200042	1.158474866
IDS	0.342458815	1.105618734	0.898623197	1.360295159
IL33	0.288530346	0.894816867	0.728791246	1.098664712
IL6ST	0.011232067	0.786694977	0.653522343	0.947005093
ILK	0.692852524	0.95998281	0.78388614	1.175638843
INPP5B	0.017917141	1.282517715	1.043746919	1.575910462
INPP5F	0.783965068	0.972172028	0.794543249	1.189511652

IQSEC3	0.027903975	0.766453125	0.604659264	0.971539557
IRAK3	0.177334723	0.865400012	0.701454831	1.067662731
ISL1	0.102197227	0.838253969	0.678394116	1.035783918
ITGA1	0.097487624	0.839434938	0.682471482	1.032498843
ITGA2	0.015497463	0.779396262	0.636960762	0.953682816
ITGA5	0.731949625	0.96357096	0.779232006	1.191518044
ITGA8	0.409221283	0.915601676	0.7426113	1.128889944
ITGA9	0.205239045	0.871556309	0.704562371	1.078130811
ITGB3	0.238276632	0.879424791	0.710327961	1.088775898
ITGB8	0.160706599	0.86270705	0.701853476	1.060425687
ITIH5	0.053439332	0.809957876	0.653986621	1.00312719
ITPRIP	0.514235937	0.931857306	0.75378501	1.151996959
ITSN1	0.402208581	0.917122571	0.749060849	1.122891166
JAK1	0.770757963	0.971104266	0.797280045	1.182825911
JAK2	0.926154158	0.990657665	0.812309752	1.208163027
JAM2	0.387903815	0.911889402	0.739624681	1.124276006
JAM3	0.001975433	0.735316879	0.605183558	0.89343292
JAZF1	0.05473303	0.81572967	0.662670904	1.004140805
JPH4	0.000240196	0.666374102	0.536585147	0.827556346
KANK1	0.498851387	0.932965592	0.76301644	1.140768075
KANK2	0.223191557	0.877407233	0.710900696	1.082912785
KATNAL1	0.579306225	0.943393516	0.767758582	1.159207264
KCNAB1	0.001898565	0.702328128	0.561943052	0.877784319
KCNIP1	0.000272151	0.647538351	0.512452879	0.818233117
KCNMA1	0.031118364	0.795243278	0.645696588	0.97942576
KCNQ4	0.336127864	1.110729152	0.896750725	1.375766102
KCNT2	0.712711568	0.961943987	0.782453546	1.182608524
KCTD10	0.538228862	1.068114003	0.865941041	1.317488686
KCTD14	0.001803451	0.701926633	0.562028959	0.876646995
KCTD9	0.136103124	0.864830202	0.714487396	1.04680822
KIAA1614	0.76480026	0.967482425	0.779094649	1.201423015
KLF8	0.383798711	0.908773135	0.732759308	1.127066694
KLHL13	0.107722302	0.842501692	0.683721675	1.038155039
KLHL14	0.052149987	0.800811936	0.639975535	1.002069176
KLHL29	0.087675218	1.19994672	0.973443822	1.479152776
KLHL33	0.104234849	0.833337611	0.66880687	1.038343961
KLHL4	0.154526429	0.842045737	0.66458316	1.066895861
KLHL42	0.301534184	0.902069324	0.741867848	1.096865252
KLHL5	0.703773594	0.961663952	0.786166276	1.17633837
KSR1	0.495403916	1.075461565	0.872491578	1.325648988
L1CAM	0.653161359	0.952843942	0.771835066	1.176302578
L3MBTL4	0.479374566	0.923169728	0.739735049	1.152091344
LAMA2	0.58420784	0.944680195	0.770491224	1.158248976
LAMA4	0.629982681	1.054140744	0.850623919	1.306350177
LAMB1	0.052905551	1.236714043	0.997339393	1.533541776
LCA5	0.208880549	0.878053854	0.716857036	1.075498366
LDLRAD2	0.908178232	1.012353149	0.821717505	1.247215608

LEPR	0.100297688	0.84357722	0.688683937	1.033307861
LGALS3	0.112516245	0.852674177	0.700323288	1.038168036
LGR6	0.040485704	0.780793726	0.616212056	0.98933287
LHFPL2	0.691212271	1.043342921	0.846256412	1.28632934
LIX1L	0.47776823	1.080078659	0.873148124	1.33605041
LMO3	0.041222288	0.792854958	0.634458955	0.990795353
LMO4	0.304640204	0.900700185	0.737666675	1.099766127
LONRF3	0.032196249	0.78477777	0.628690214	0.979617839
LPAR1	0.061910526	0.832148308	0.686159583	1.009197895
LPCAT2	0.649269097	0.954146321	0.77940161	1.16806944
LPIN1	0.433318632	1.086414548	0.882985943	1.336710487
LRCH2	0.010223388	0.761246279	0.618170817	0.937436517
LRFN1	0.007562513	1.334299741	1.079799882	1.648783102
LRP4	0.149273891	0.853913963	0.688967636	1.058350229
LRRK2	0.444504071	0.920774281	0.745186773	1.137735272
LSM11	0.346279622	0.904662599	0.734403283	1.114393737
LTBP1	0.960491009	0.994715408	0.806590189	1.22671805
LTBP4	0.131862596	0.852302732	0.692331348	1.049237405
LYVE1	0.335139956	0.901371335	0.729790325	1.113292758
MAMDC2	0.031649591	0.796790127	0.647676455	0.980234036
MAML2	0.020792698	0.784432952	0.638493605	0.963729395
MAMLD1	0.006772263	0.742504382	0.598562596	0.921061158
MAN1A1	0.344818164	0.907246717	0.741339979	1.11028223
MAP1A	0.028502858	0.792669844	0.6438669	0.975862375
MAP1LC3B	0.261149248	0.894388872	0.736167856	1.086615571
MAP3K12	0.003505089	1.372045398	1.109559299	1.69662728
MAP7D3	0.609119413	1.056928512	0.854825032	1.306814655
MAPKBP1	0.131508894	1.178926081	0.951887628	1.460116367
MAPRE2	0.147542328	0.863640726	0.708225671	1.053160503
MASP1	0.125083737	0.843043604	0.677791937	1.048585088
MATN2	0.116911963	0.853905812	0.700917308	1.040286962
MB21D2	0.177304008	1.148002851	0.939416905	1.402902737
MBNL1	0.218087774	0.882924579	0.724216866	1.07641212
MBNL2	0.0032875	0.749452924	0.61834054	0.908366262
MCC	0.152600259	0.861186502	0.70172426	1.056885494
MDFIC	0.042913827	0.810793945	0.661800024	0.993331516
MEIS1	0.123918111	0.846925492	0.685371456	1.04656064
MET	0.753584081	0.967433179	0.786764018	1.189590441
METTTL24	0.05724528	0.815381212	0.660682602	1.00630245
MICALL1	0.932892922	0.990873877	0.800465264	1.226575448
MICU3	0.584464675	0.943872726	0.767370027	1.160972792
MITF	0.108561066	0.847860455	0.69307497	1.037214416
MKX	0.41707045	0.918335306	0.747553377	1.128133134
MLPH	0.748273332	0.965187997	0.777375599	1.198375495
MOB3B	0.409352928	0.916613537	0.74534138	1.127242358
MPP2	0.013857296	0.763944815	0.616494519	0.946661588
MPRIP	0.00809844	1.34785419	1.080645303	1.681135255

MR1	0.050378528	0.81641224	0.666305946	1.000334681
MRAP2	0.002083619	0.732900537	0.601328384	0.893261005
MRAS	0.853158755	0.981024906	0.800898819	1.201662238
MRGPRE	0.143727208	0.849141917	0.681984087	1.057270997
MRVI1	0.037671577	0.801446685	0.650470128	0.987465469
MSRB3	0.050636691	0.815276438	0.664299485	1.000566288
MXRA7	0.143444693	0.853847632	0.690966009	1.055125388
MYH11	0.001351973	0.733563131	0.6069329	0.88661344
MYLK	0.003301055	0.743234752	0.609760753	0.905925634
MYOCD	0.000195045	0.668727868	0.541140974	0.826396415
MYOF	0.09501663	0.839933455	0.684400223	1.030812359
NACC2	0.518610708	0.935258381	0.763252465	1.146027402
NAP1L3	0.806581758	0.974619255	0.793336584	1.19732622
NAV2	0.535191302	0.935187162	0.756688325	1.155792945
NCAM1	0.062133823	0.810552607	0.650032533	1.010711765
NCKAP5L	0.428000023	1.091488147	0.879036094	1.355287209
NDNF	0.012902989	0.763237343	0.616828716	0.944397085
NECAB1	0.010218343	0.751162116	0.603814299	0.93446698
NEGR1	0.043200922	0.796037254	0.638109054	0.993051744
NEURL1B	0.65647578	0.9534766	0.772927333	1.176200644
NEXN	0.050625438	0.811713881	0.658505239	1.000568234
NHS	0.230463737	0.875883664	0.705307561	1.087712986
NID1	0.847026631	0.979625364	0.794751957	1.207503605
NID2	0.555720412	0.939473503	0.763285348	1.156330938
NKAPL	0.010510472	0.746640964	0.596912125	0.933927634
NLGN2	1.32E-05	1.700075833	1.339041283	2.158453122
NLGN3	0.052034965	0.81122423	0.656872699	1.001845187
NLGN4Y	0.018845497	0.786000455	0.642909101	0.960939446
NOTCH1	0.416468949	1.092743445	0.882285797	1.35340299
NPR2	0.551232458	0.937722348	0.75897321	1.158569487
NR2F1	0.626695843	0.951152628	0.777330391	1.163844012
NRG1	0.096389261	0.819420574	0.647955256	1.036259944
NRP2	0.645038709	1.051409739	0.849454369	1.301379426
NT5E	0.088343519	0.836689372	0.681564738	1.027120486
NTRK2	0.361093571	0.905074164	0.73067734	1.121095726
NTRK3	0.018141604	0.743503899	0.581443755	0.950733486
NUAK1	0.13038192	1.171684067	0.954220125	1.438707398
OGFRL1	0.336945013	0.906531859	0.7419847	1.107570022
OGN	0.004331962	0.74959441	0.614938474	0.913736582
OLFML1	0.051587466	0.81103319	0.656826872	1.001443247
OLFML2A	0.657359406	1.050517302	0.844946043	1.306103047
P2RY12	0.676599537	0.956840459	0.777688481	1.177262729
P4HA2	0.62427629	0.950770288	0.776861489	1.163610443
PAK3	0.005699538	0.726614701	0.579395581	0.911240854
PALLD	0.080876657	0.834981581	0.681925026	1.02239134
PAM	0.135336806	0.857143459	0.700149569	1.049339944
PAMR1	0.427015914	0.91880185	0.745540828	1.132328113

PAQR8	0.697737804	0.959962953	0.781089051	1.17980001
PARM1	0.000246832	0.707975429	0.588603158	0.851557115
PARVA	0.032847087	0.808064322	0.664412682	0.982774661
PBX1	0.051236706	0.82108943	0.673474344	1.001059445
PCDH10	0.131674531	0.852091224	0.692006257	1.049209378
PCDH18	0.008718599	0.757796625	0.615953824	0.932303207
PCDH19	0.718897826	1.038407883	0.845742769	1.274963229
PCDH7	0.012183575	0.762972309	0.617513649	0.942694539
PCDHB15	0.687322674	0.959167244	0.782937873	1.175063608
PCOLCE2	0.104208924	0.836578202	0.674569525	1.037495859
PCSK7	0.67174983	0.956468384	0.778513701	1.17510041
PCYT1B	0.010002059	0.738037809	0.5857281	0.929953349
PDE2A	0.115146467	0.842624431	0.680956622	1.042674245
PDE4A	0.560067611	0.93939266	0.761241725	1.159235682
PDE5A	0.006799857	0.752672974	0.612700308	0.924622689
PDE7B	0.959860706	0.994763362	0.810811792	1.220448636
PDGFC	0.04118887	0.813272116	0.666902123	0.991767025
PDZRN4	0.003637237	0.738685607	0.602286802	0.905974404
PEA15	0.069285839	1.23761248	0.983310435	1.55768168
PEAK1	0.494089568	0.92988847	0.755000589	1.145287275
PGAP1	0.054351203	0.816336087	0.663883505	1.003797506
PGR	0.023574114	0.778957389	0.627474662	0.967010543
PGRMC1	0.056123676	0.827389254	0.681193331	1.004961363
PHACTR2	0.061012938	0.827355118	0.678548343	1.008795465
PIEZO2	0.357906549	0.906244926	0.734680498	1.117873508
PIK3R1	0.016923185	0.787175685	0.646822665	0.957983685
PIP5K1C	0.57335431	1.064322631	0.856728501	1.322218954
PITPNC1	0.000528209	0.706373349	0.58031856	0.859809324
PITPNM2	0.971961983	1.003769088	0.813815889	1.238059363
PITPNM3	0.183470581	0.863350459	0.695278914	1.072050366
PLA2G4A	0.521167243	0.935986514	0.76470956	1.145625477
PLAG1	0.040438241	0.787626185	0.62684094	0.989652986
PLCD3	0.270967488	1.124352157	0.912586963	1.385257323
PLCE1	0.447011322	1.083025886	0.881772515	1.330212782
PLCL1	0.006249398	0.741978576	0.599087791	0.918950804
PLEKHA1	0.344334174	0.908617355	0.744937533	1.10826138
PLEKHA2	0.143423142	0.860786939	0.704183421	1.052217551
PLEKHG2	0.278950533	1.120500612	0.91193083	1.376772867
PLEKHG3	0.160656021	0.861411112	0.699346277	1.061032465
PLEKHH2	0.415623324	1.08700058	0.889199294	1.328802517
PLN	0.061922777	0.823109385	0.670962506	1.009756959
PLSCR4	0.233386871	0.885892414	0.725835345	1.081244353
PLXDC2	0.306404089	0.903114489	0.742905647	1.097872634
PNMA1	0.751169258	0.966835892	0.784908556	1.190930632
PNMA2	0.77633523	0.970419852	0.788852421	1.19377803
PPARGC1A	0.000574022	0.645011659	0.502551793	0.827855052
PPP1R12A	0.453367156	0.927524303	0.761931131	1.129106423

PPP1R12B	0.062614857	0.820407718	0.666089106	1.010478657
PPP1R3B	0.061869604	0.830293737	0.683049557	1.009279169
PPP2R2B	0.78340725	1.028401784	0.842246686	1.255701266
PRDM11	0.366127498	0.908970334	0.73902051	1.118002892
PRDM16	0.415250601	1.082681928	0.894332957	1.310697708
PRDM5	0.039339189	0.802451002	0.650887623	0.989306893
PRDM6	0.042220377	0.794321692	0.63607273	0.991941518
PRELP	0.712324361	1.041720971	0.838294023	1.294513085
PREX2	0.854608362	0.980863432	0.797724706	1.206046478
PRICKLE1	0.903343729	0.986868007	0.797265507	1.221561015
PRICKLE2	0.014614897	0.768915585	0.622696001	0.949470007
PRIMA1	0.051037366	0.81013485	0.655695617	1.000949919
PRKCB	0.087722175	0.82790118	0.666548434	1.028312916
PRKG1	0.378190983	0.909786619	0.737252904	1.122697094
PRNP	0.078668259	0.841641051	0.69450329	1.019951479
PRR36	0.174014942	1.167989352	0.933700419	1.461067273
PRSS12	0.13569553	0.846623821	0.68030248	1.053607647
PRTFDC1	0.734441314	0.962923847	0.774086621	1.197827621
PSIP1	0.756166163	0.968749774	0.792831315	1.183702139
PSTPIP2	0.021398949	0.791321496	0.6482856	0.965916426
PTCHD1	0.09414804	0.824930578	0.65849347	1.033435394
PTGER2	0.474345351	0.927870872	0.7558181	1.13908936
PTGER3	0.045045876	0.792631995	0.631498214	0.99488085
PTGFRN	0.955864486	0.994334341	0.813102998	1.215960075
PTGIS	0.004183354	0.740058619	0.602280599	0.909354811
PTPN14	0.240843688	0.882366233	0.715853955	1.087610349
PURG	0.650493493	0.950863739	0.764645628	1.182432511
QKI	0.167646098	1.15936156	0.939719768	1.430340483
RAB12	0.207568942	1.145130117	0.927523188	1.413789975
RAB9B	0.003308909	0.727129371	0.587861992	0.899389873
RARB	0.395150381	0.912739266	0.739514072	1.126541061
RASD2	0.053870911	0.827054583	0.681860669	1.00316577
RASGRF2	0.230349152	0.876861003	0.70742011	1.086886289
RBFOX2	0.610429657	0.948621573	0.774402222	1.162035521
RBMS1	0.635097601	0.952580603	0.779408768	1.164228378
RBMS2	0.542774897	1.066817012	0.866225758	1.313859033
RBMS3	0.022555723	0.784343664	0.636583596	0.966400937
RCAN2	0.511089751	0.932605828	0.757392504	1.148352572
RCBTB2	0.052030861	0.829505867	0.686949835	1.001645169
RECK	0.775935077	1.02992394	0.840670433	1.261782598
RELL1	0.946949714	0.99312859	0.810583487	1.216783232
RERG	0.429391711	0.919916765	0.747887641	1.131516029
RGL1	0.280641361	0.894016426	0.729384487	1.095808018
RGMA	0.278858402	0.893002522	0.727610354	1.095989771
RGN	0.140043185	0.851797098	0.688346538	1.054059629
RGS22	0.011040422	0.744284683	0.592683835	0.934663064
RGS7BP	0.002480107	0.717337556	0.57845172	0.88956978

RHOBTB2	0.815567297	0.975465908	0.791704257	1.201880283
RHOJ	0.760313792	1.033307126	0.837163269	1.275406668
RIMKLB	0.103870617	1.194887594	0.964137786	1.480863403
RIMS3	0.614030707	0.947860697	0.769780758	1.167137386
RMDN2	0.152013882	0.864095204	0.707557304	1.055265091
RNASEL	0.615531182	0.95060907	0.780095722	1.158393232
RNF152	0.351738857	0.907720711	0.740377755	1.112887148
RNF217	0.520822926	0.935247324	0.762392312	1.147293255
ROBO1	0.133327968	0.856559773	0.699778766	1.048466574
RSPO1	0.154647462	0.854539757	0.688215071	1.061061036
RSPO3	0.041832234	0.805339785	0.653782601	0.99203033
RSU1	0.110664691	0.857920286	0.710683557	1.035660963
RUNDC3B	0.205026458	0.874739956	0.711205636	1.075877289
RUNX2	0.869595219	0.982606914	0.796905407	1.211582126
RUSC2	0.600128234	1.060674888	0.851008746	1.321997247
SAMD10	0.38011265	1.102592806	0.886539329	1.371299454
SAMD14	0.495052609	1.077334255	0.869801824	1.33438338
SAMD4A	0.908825506	0.98797525	0.803206394	1.215248163
SCN2B	0.007649065	0.723627026	0.570531881	0.917803351
SCN4B	0.798196761	1.028682891	0.828201019	1.277695229
SCN5A	0.157367985	0.84440539	0.667945266	1.067483368
SCN7A	0.003368017	0.729001277	0.590154021	0.900515532
SDC3	0.259727966	1.133974081	0.911267337	1.411108645
SEC23A	0.621354721	0.950452997	0.776886268	1.162796844
SEMA3A	0.001179221	0.660846035	0.514521508	0.848783726
SFRP1	0.088744426	0.842619194	0.691821305	1.026286847
SFXN3	0.887062238	1.015359775	0.822739014	1.253077166
SGCB	0.359636053	0.911220955	0.746854712	1.111760581
SGCE	0.685136078	1.04468265	0.845699931	1.290483539
SH3BGRL	0.014996924	0.789985373	0.653318537	0.955241363
SH3PXD2A	0.67704563	1.045971369	0.846570589	1.292338901
SH3PXD2B	0.279539727	0.893676353	0.728943796	1.095636491
SHC3	0.558961542	0.934761269	0.745476583	1.172107413
SLC12A4	0.625676681	0.94893395	0.768731826	1.17137812
SLC16A2	0.06624998	0.827166263	0.675548462	1.012812649
SLC16A4	0.281655121	0.891175252	0.722555268	1.099145441
SLC16A7	0.428606776	0.918960548	0.745451047	1.132855728
SLC24A3	0.212642833	0.876093887	0.711551862	1.07868525
SLC25A45	0.003615673	1.347260094	1.102195908	1.646812286
SLC46A3	0.218450821	0.878299898	0.714311393	1.079936172
SLC47A1	0.207944759	0.871275366	0.703087199	1.079696464
SLC51B	0.00108504	0.706768884	0.57394258	0.870334896
SLC8A1	0.026471265	0.786068905	0.635527203	0.972270455
SLFN12	0.654504179	0.953857039	0.775580345	1.173112827
SLIT2	0.345139349	0.907266563	0.741290153	1.110405437
SLIT3	0.782129455	1.029669524	0.836958726	1.266752224
SLMAP	0.252485317	0.891688787	0.732724741	1.085139955

SMAD3	0.796211998	0.973596308	0.794662448	1.192820642
SMAD7	0.061422737	1.233279907	0.990014513	1.536320235
SNX7	0.561908955	0.941567466	0.768228228	1.154018117
SORBS1	0.013754907	0.778302885	0.637602345	0.950051997
SORCS1	0.132383858	0.84194302	0.672919642	1.053421544
SORCS2	0.053349538	0.809419173	0.65316328	1.003056076
SOX5	0.087988997	0.828294781	0.667107896	1.028427706
SP100	0.170179658	0.870561611	0.714129534	1.061260574
SPARCL1	0.130087329	0.852879541	0.694070106	1.048025991
SPATA18	0.005928449	0.749555766	0.610422439	0.920401692
SPOCK3	0.002009011	0.729316235	0.59694373	0.891042396
SPON1	0.024665699	0.786473835	0.637790113	0.969819193
SPRED1	0.960905743	0.994800486	0.807622912	1.225359005
SPRY2	0.150654032	0.871894133	0.723224862	1.051124511
SRD5A2	1.52E-06	0.608865515	0.497396917	0.745314661
SRF	0.486998226	0.927751323	0.750926933	1.146213406
SRPX	0.007401722	0.76162262	0.624014641	0.929575971
SSC5D	0.259394113	1.126787656	0.915692157	1.386547228
SSPN	0.017426494	0.791477226	0.652703602	0.959756
SSTR2	0.220544155	0.873257161	0.703036177	1.084692501
ST3GAL2	0.109057691	1.188567694	0.962191274	1.468204088
STAC	0.001754777	0.686647727	0.542578022	0.868971985
STARD8	0.080260177	0.830663736	0.674746757	1.022609201
STAT5B	0.235264313	0.887230913	0.728162884	1.081047538
STK32B	0.664648696	1.046419702	0.852336894	1.284696464
STOX2	0.024447648	0.770820824	0.614440774	0.967000837
STX2	0.002981233	1.380294317	1.115812248	1.707466831
STX7	0.610849966	0.950038218	0.779842685	1.157377806
SV2A	0.524956379	1.06765736	0.872519502	1.306437547
SVIL	0.048095294	0.818011528	0.670270098	0.998318233
SYNC	0.454518054	0.922881022	0.747835821	1.138898882
SYNE1	0.647008486	0.952704684	0.774278443	1.172247818
SYNM	0.00091053	0.714996974	0.586421337	0.871763424
SYNPO	0.958042837	0.994388426	0.806320481	1.226321747
SYNPO2	0.002836365	0.738183598	0.604781835	0.901010899
SYT11	0.941191057	1.007964732	0.816415588	1.24445554
TACC1	0.02775566	0.802719691	0.66003737	0.976246089
TAF3	0.061366548	0.82595397	0.676014219	1.009150312
TBC1D1	0.592167194	1.058504601	0.859704391	1.303275871
TBC1D2B	0.18454661	1.15085711	0.935159506	1.416306072
TBL1X	0.362398374	0.911712305	0.747266799	1.112346122
TCF21	0.044618325	0.80335395	0.64878317	0.994750788
TCF4	0.499960309	0.932618708	0.761512597	1.142171066
TEAD1	0.092057785	0.84390121	0.692686915	1.028125748
TENM3	0.019038706	0.771953385	0.621770264	0.958411913
TES	0.253385533	0.890133961	0.728988	1.086901937
TGFB2	0.219661814	0.879838782	0.717175838	1.079395376

TGFBR3	0.028265995	0.795588401	0.648564752	0.975940954
THSD4	0.076077753	0.831910489	0.67884502	1.019489047
THSD7B	0.676398102	0.955943008	0.773648799	1.181191047
TIMP2	0.924112461	1.010362152	0.817253553	1.249100323
TIMP3	0.581594403	0.945067695	0.773020575	1.155406436
TINAGL1	0.586572551	1.062695935	0.853546722	1.323094121
TLN1	0.355580514	0.909875595	0.744661212	1.111745294
TLR3	0.151722448	0.860120138	0.69997565	1.056903412
TLR4	0.030253987	0.791678865	0.640885051	0.977952948
TMEM106A	0.935740333	1.008843088	0.814465236	1.24961058
TMEM108	0.39348191	0.905748254	0.72153829	1.136987337
TMEM109	0.588130167	1.062103928	0.854011282	1.320901465
TMEM132C	0.008990199	0.729483086	0.575761839	0.924245994
TMEM200B	0.311755678	0.896593791	0.725680521	1.107760788
TMEM200C	0.060469631	0.766185492	0.580200539	1.011788457
TMEM252	0.000249533	0.656897142	0.524612462	0.822538325
TMEM43	0.243455106	1.134161023	0.917912792	1.401354505
TMEM47	0.898625235	0.986624343	0.802010985	1.213733493
TMLHE	0.094423656	0.832447103	0.671467573	1.03202032
TMTC1	0.916460949	0.98899237	0.80421291	1.216227565
TNC	0.456384815	0.92421284	0.751106512	1.137214709
TNS1	0.024627849	0.794419822	0.649943089	0.971012484
TNS2	0.802121115	1.027745218	0.829715722	1.273038711
TNXB	0.888023604	1.01451794	0.830092386	1.23991819
TPBG	0.491439333	0.931406397	0.760722414	1.140386902
TRAF3IP2	0.006445055	0.755251391	0.617140311	0.92427063
TRANK1	0.796344392	1.027833811	0.834403129	1.266105443
TRHDE	0.042550696	0.78284122	0.617901406	0.991809325
TRIM34	0.9500346	0.993404028	0.807664943	1.221857616
TRIM6	0.240379561	0.884796889	0.721278832	1.085385428
TRIM61	0.460992725	0.920421819	0.738315609	1.14744469
TRIM9	0.555046285	0.934564317	0.746464851	1.170062411
TRPC1	0.843288924	1.021478249	0.827423347	1.261044684
TRPC4	0.015416765	0.772432936	0.626801969	0.951899753
TRPC6	0.617637396	0.94697287	0.764599536	1.172846142
TSHZ3	0.070345577	0.832364725	0.682354053	1.015354174
TSLP	0.113600983	0.832851094	0.664003379	1.044634661
TSPAN11	0.151684908	0.858086323	0.69607715	1.057802484
TSPAN18	0.074540983	0.828908497	0.674433129	1.018765638
TSPAN2	0.278474425	0.891663557	0.724669013	1.097140743
TTC23	0.98256903	0.997652722	0.808020737	1.231788874
TTC28	0.085372116	0.833769282	0.677788105	1.025646821
TTC39B	0.974897204	0.996797638	0.816285038	1.217228646
TTYH2	0.253500494	1.127151669	0.917822301	1.384223158
TVP23A	0.807150098	0.974211664	0.789857041	1.20159512
UBXN10	2.61E-05	0.608978849	0.483288844	0.767357333
UNC5B	0.557105192	1.065260879	0.862590613	1.315549605

USP11	0.221090331	1.145768396	0.921378512	1.42480555
USP44	0.340264359	0.901443273	0.728326426	1.115708487
UST	0.288038481	0.898319259	0.737089714	1.094815836
VCL	0.059490575	0.825840439	0.676809959	1.007686754
VSTM4	0.032302362	0.797005303	0.647499962	0.981030873
VWA5A	0.0845329	0.835969389	0.681994197	1.024707868
WDR1	0.733387741	0.96462998	0.78410016	1.186724663
WSCD2	0.098931913	0.831123241	0.667179297	1.035352632
WWC3	0.750121077	1.03464686	0.838995133	1.275924116
WWTR1	0.078626135	0.834126817	0.681476257	1.020971076
XKR5	0.045115273	0.780555072	0.6125609	0.994621466
YAP1	0.352106217	0.911736822	0.750484001	1.107637248
ZBTB47	0.512761014	1.071983072	0.870549352	1.320025917
ZCCHC24	0.256639377	0.888594684	0.724559416	1.089766408
ZEB1	0.138546628	0.856803227	0.698343406	1.051218877
ZEB2	0.800243936	0.97380301	0.79281004	1.196115405
ZFP92	0.996871162	0.999589112	0.813980716	1.227520964
ZNF185	0.002160721	0.721917184	0.58621892	0.889026953
ZNF366	0.923616818	1.0098963	0.825753487	1.235102912
ZNF385D	0.649358699	0.952940305	0.774140954	1.173036022
ZNF423	0.07952232	0.827774826	0.670127175	1.022509143
ZNF469	0.391897258	1.094415711	0.890197739	1.345482803
ZNF516	0.035534568	0.803520294	0.655272949	0.985306756
ZNF711	0.777245064	0.969236942	0.780582469	1.203486225
ZNF804A	0.093348019	0.827858903	0.663935832	1.032253917

Supplementary Table 2 Functional enrichment analysis in brown module

ID	description	pValue	FDR	qvalue	size	DB	enrichmentRatio
hsa04510	Focal adhesion	1.07E-12	2.99E-10	2.29E-10	38	pathway_KEGG	0.093137255
hsa04020	Calcium signaling pathway	1.78E-10	2.48E-08	1.90E-08	34	pathway_KEGG	0.083333333
hsa04360	Axon guidance	2.40E-09	2.23E-07	1.71E-07	31	pathway_KEGG	0.075980392
hsa04151	PI3K-Akt signaling pathway	2.72E-07	1.56E-05	1.19E-05	42	pathway_KEGG	0.102941176
hsa05414	Dilated cardiomyopathy (DCM)	3.20E-07	1.56E-05	1.19E-05	19	pathway_KEGG	0.046568627
hsa04713	Circadian entrainment	3.79E-07	1.56E-05	1.19E-05	19	pathway_KEGG	0.046568627
hsa04512	ECM-receptor interaction	3.91E-07	1.56E-05	1.19E-05	18	pathway_KEGG	0.044117647
hsa04024	cAMP signaling pathway	5.63E-07	1.96E-05	1.50E-05	30	pathway_KEGG	0.073529412
hsa04014	Ras signaling pathway	8.59E-07	2.42E-05	1.86E-05	31	pathway_KEGG	0.075980392
hsa04270	Vascular smooth muscle contraction	8.68E-07	2.42E-05	1.86E-05	22	pathway_KEGG	0.053921569
hsa04022	cGMP-PKG signaling pathway	1.25E-06	3.18E-05	2.43E-05	25	pathway_KEGG	0.06127451
hsa04015	Rap1 signaling pathway	3.08E-06	7.17E-05	5.49E-05	28	pathway_KEGG	0.068627451
hsa04810	Regulation of actin cytoskeleton	4.08E-06	8.77E-05	6.71E-05	28	pathway_KEGG	0.068627451
hsa05205	Proteoglycans in cancer	5.35E-06	0.00010659	8.16E-05	27	pathway_KEGG	0.066176471
hsa04390	Hippo signaling pathway	1.19E-05	0.000220883	0.000169173	22	pathway_KEGG	0.053921569
hsa05032	Morphine addiction	1.37E-05	0.000238193	0.00018243	16	pathway_KEGG	0.039215686
hsa04072	Phospholipase D signaling pathway	2.08E-05	0.000341957	0.000261903	21	pathway_KEGG	0.051470588
hsa05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	3.19E-05	0.000494874	0.00037902	14	pathway_KEGG	0.034313725
hsa05410	Hypertrophic cardiomyopathy (HCM)	4.87E-05	0.000715337	0.000547872	15	pathway_KEGG	0.036764706

hsa05146	Amoebiasis	5.90E-05	0.000823205	0.000630487	16	pathway_KEGG	0.039215686
hsa04261	Adrenergic signaling in cardiomyocytes	7.33E-05	0.000974175	0.000746114	20	pathway_KEGG	0.049019608
hsa04070	Phosphatidylinositol signaling system	0.000149668	0.001898059	0.001453711	15	pathway_KEGG	0.036764706
hsa05031	Amphetamine addiction AGE-RAGE signaling pathway in diabetic complications	0.000157403	0.001909366	0.001462371	12	pathway_KEGG	0.029411765
hsa04933	Cholinergic synapse	0.000167955	0.001944215	0.001489061	15	pathway_KEGG	0.036764706
hsa04725	Salivary secretion	0.000184329	0.001944215	0.001489061	16	pathway_KEGG	0.039215686
hsa04970	Melanogenesis	0.000186106	0.001944215	0.001489061	14	pathway_KEGG	0.034313725
hsa04916	Wnt signaling pathway	0.00018815	0.001944215	0.001489061	15	pathway_KEGG	0.036764706
hsa04310	Glutamatergic synapse	0.000198451	0.001977424	0.001514496	20	pathway_KEGG	0.049019608
hsa04724	Oxytocin signaling pathway	0.000227227	0.002186083	0.001674306	16	pathway_KEGG	0.039215686
hsa04921	Dopaminergic synapse	0.000310558	0.002888194	0.002212048	19	pathway_KEGG	0.046568627
hsa04728	Gastric acid secretion	0.000379242	0.003413182	0.002614133	17	pathway_KEGG	0.041666667
hsa04971	Aldosterone synthesis and secretion	0.000407246	0.003550679	0.002719441	12	pathway_KEGG	0.029411765
hsa04925	Cell adhesion molecules (CAMs)	0.000461102	0.003898408	0.002985764	14	pathway_KEGG	0.034313725
hsa04514	Hippo signaling pathway - multiple species	0.000527802	0.004254457	0.00325846	18	pathway_KEGG	0.044117647
hsa04392	MAPK signaling pathway	0.000533713	0.004254457	0.00325846	7	pathway_KEGG	0.017156863
hsa04010	EGFR tyrosine kinase inhibitor resistance	0.000582092	0.004511212	0.003455107	29	pathway_KEGG	0.071078431
hsa01521	Long-term depression	0.000662535	0.004995874	0.003826306	12	pathway_KEGG	0.029411765
hsa04730	Melanoma	0.000881516	0.006472182	0.004957	10	pathway_KEGG	0.024509804
hsa05218	Thyroid hormone signaling pathway	0.001049003	0.007504409	0.005747576	11	pathway_KEGG	0.026960784
hsa04919	Gastric cancer	0.001120588	0.007816103	0.0059863	15	pathway_KEGG	0.036764706
hsa05226		0.001654976	0.011261913	0.008625423	17	pathway_KEGG	0.041666667

hsa04611	Platelet activation	0.001707264	0.011341114	0.008686082	15	pathway_KEGG	0.036764706
hsa04540	Gap junction	0.001748437	0.011344507	0.008688681	12	pathway_KEGG	0.029411765
	Signaling pathways regulating pluripotency of						
hsa04550	stem cells	0.002205923	0.01398756	0.010712977	16	pathway_KEGG	0.039215686
hsa04924	Renin secretion	0.002630514	0.016309186	0.012491095	10	pathway_KEGG	0.024509804
hsa00230	Purine metabolism	0.002730267	0.016559662	0.012682933	15	pathway_KEGG	0.036764706
hsa04350	TGF-beta signaling pathway	0.003078191	0.018272664	0.01399491	12	pathway_KEGG	0.029411765
hsa05030	Cocaine addiction	0.003262505	0.01896331	0.014523871	8	pathway_KEGG	0.019607843
hsa04340	Hedgehog signaling pathway	0.003713427	0.021143797	0.016193891	8	pathway_KEGG	0.019607843
	Bacterial invasion of						
hsa05100	epithelial cells	0.004002975	0.022336598	0.017107449	10	pathway_KEGG	0.024509804
hsa05231	Choline metabolism in cancer	0.004351341	0.023804396	0.018231625	12	pathway_KEGG	0.029411765
hsa04911	Insulin secretion	0.004452077	0.023887106	0.018294972	11	pathway_KEGG	0.026960784
	Neuroactive ligand-receptor						
hsa04080	interaction	0.005021673	0.026434843	0.020246268	29	pathway_KEGG	0.071078431
hsa04727	GABAergic synapse	0.005790305	0.029916575	0.022912902	11	pathway_KEGG	0.026960784
	Human papillomavirus						
hsa05165	infection	0.006214577	0.031524852	0.02414467	28	pathway_KEGG	0.068627451
hsa04720	Long-term potentiation	0.007060678	0.035177307	0.026942061	9	pathway_KEGG	0.022058824
hsa05222	Small cell lung cancer	0.007426849	0.036352469	0.02784211	11	pathway_KEGG	0.026960784
	Parathyroid hormone						
	synthesis, secretion and						
hsa04928	action	0.008148852	0.039198786	0.030022085	12	pathway_KEGG	0.029411765
	urogenital system						
GO:0001655	development	3.36E-18	1.66E-14	1.26E-14	58	geneontology_Bio	0.066820276
GO:0072001	renal system development	4.56E-17	1.12E-13	8.56E-14	53	geneontology_Bio	0.061059908
GO:0001822	kidney development	4.51E-16	7.41E-13	5.65E-13	50	geneontology_Bio	0.057603687
GO:0031589	cell-substrate adhesion	1.58E-14	1.95E-11	1.49E-11	52	geneontology_Bio	0.059907834
GO:0034329	cell junction assembly	6.61E-13	5.48E-10	4.17E-10	39	geneontology_Bio	0.044930876

GO:0003012	muscle system process	7.64E-13	5.48E-10	4.17E-10	60	geneontology_Bio	0.069124424
GO:0034330	cell junction organization	7.78E-13	5.48E-10	4.17E-10	45	geneontology_Bio	0.051843318
GO:0061564	axon development	9.32E-13	5.56E-10	4.23E-10	59	geneontology_Bio	0.06797235
	extracellular matrix						
GO:0030198	organization	1.01E-12	5.56E-10	4.23E-10	50	geneontology_Bio	0.057603687
GO:0001823	mesonephros development	2.19E-12	1.08E-09	8.23E-10	26	geneontology_Bio	0.029953917
GO:0006936	muscle contraction	2.81E-12	1.26E-09	9.59E-10	50	geneontology_Bio	0.057603687
	kidney epithelium						
GO:0072073	development	4.35E-12	1.79E-09	1.36E-09	30	geneontology_Bio	0.034562212
	morphogenesis of a branching						
GO:0061138	epithelium	5.12E-12	1.94E-09	1.48E-09	34	geneontology_Bio	0.039170507
GO:0007411	axon guidance	7.41E-12	2.61E-09	1.99E-09	37	geneontology_Bio	0.042626728
GO:0097485	neuron projection guidance	9.91E-12	3.10E-09	2.36E-09	37	geneontology_Bio	0.042626728
	morphogenesis of a branching						
GO:0001763	structure	1.01E-11	3.10E-09	2.36E-09	35	geneontology_Bio	0.040322581
	cell morphogenesis involved						
GO:0048667	in neuron differentiation	2.73E-11	7.91E-09	6.03E-09	61	geneontology_Bio	0.070276498
	mesonephric epithelium						
GO:0072163	development	3.89E-11	1.01E-08	7.70E-09	24	geneontology_Bio	0.02764977
	mesonephric tubule						
GO:0072164	development	3.89E-11	1.01E-08	7.70E-09	24	geneontology_Bio	0.02764977
	extracellular structure						
GO:0043062	organization	7.64E-11	1.88E-08	1.43E-08	51	geneontology_Bio	0.05875576
GO:0007409	axonogenesis	1.34E-10	3.14E-08	2.39E-08	51	geneontology_Bio	0.05875576
	regulation of cellular						
	response to growth factor						
GO:0090287	stimulu	1.47E-10	3.29E-08	2.51E-08	41	geneontology_Bio	0.047235023
GO:0048565	digestive tract development	1.58E-10	3.39E-08	2.58E-08	27	geneontology_Bio	0.031105991
GO:0001657	ureteric bud development	2.01E-10	4.12E-08	3.14E-08	23	geneontology_Bio	0.026497696
GO:0007160	cell-matrix adhesion	2.32E-10	4.57E-08	3.48E-08	35	geneontology_Bio	0.040322581
GO:0030323	respiratory tube development	2.41E-10	4.57E-08	3.48E-08	31	geneontology_Bio	0.035714286

	branching morphogenesis of						
GO:0048754	an epithelial tube	3.52E-10	6.43E-08	4.89E-08	28	geneontology_Bio	0.032258065
GO:0050808	synapse organization	4.49E-10	7.91E-08	6.03E-08	50	geneontology_Bio	0.057603687
GO:0030900	forebrain development	5.24E-10	8.91E-08	6.78E-08	48	geneontology_Bio	0.055299539
	second-messenger-mediated						
GO:0019932	signaling	5.87E-10	9.45E-08	7.19E-08	47	geneontology_Bio	0.054147465
GO:0030324	lung development	5.94E-10	9.45E-08	7.19E-08	30	geneontology_Bio	0.034562212
GO:0060485	mesenchyme development	8.90E-10	1.37E-07	1.04E-07	38	geneontology_Bio	0.043778802
	regulation of actin filament-						
GO:0032970	based process	9.69E-10	1.45E-07	1.10E-07	45	geneontology_Bio	0.051843318
GO:0055123	digestive system development	1.04E-09	1.51E-07	1.15E-07	27	geneontology_Bio	0.031105991
GO:0060537	muscle tissue development	1.13E-09	1.59E-07	1.21E-07	49	geneontology_Bio	0.056451613
	cyclic-nucleotide-mediated						
GO:0019935	signaling	1.69E-09	2.31E-07	1.76E-07	29	geneontology_Bio	0.033410138
	regulation of small GTPase						
GO:0051056	mediated signal transduction	2.84E-09	3.79E-07	2.88E-07	42	geneontology_Bio	0.048387097
GO:0003205	cardiac chamber development	2.99E-09	3.88E-07	2.95E-07	29	geneontology_Bio	0.033410138
	respiratory system						
GO:0060541	development	3.87E-09	4.89E-07	3.72E-07	31	geneontology_Bio	0.035714286
GO:0003279	cardiac septum development	3.97E-09	4.89E-07	3.72E-07	23	geneontology_Bio	0.026497696
GO:0072006	nephron development	4.20E-09	5.05E-07	3.84E-07	26	geneontology_Bio	0.029953917
GO:0019933	cAMP-mediated signaling	4.90E-09	5.75E-07	4.38E-07	26	geneontology_Bio	0.029953917
GO:0001501	skeletal system development	6.68E-09	7.47E-07	5.69E-07	54	geneontology_Bio	0.062211982
GO:0060562	epithelial tube morphogenesis	6.74E-09	7.47E-07	5.69E-07	41	geneontology_Bio	0.047235023
	regulation of cytosolic						
GO:0051480	calcium ion concentration	6.82E-09	7.47E-07	5.69E-07	39	geneontology_Bio	0.044930876
GO:0035107	appendage morphogenesis	7.72E-09	8.04E-07	6.12E-07	26	geneontology_Bio	0.029953917
GO:0035108	limb morphogenesis	7.72E-09	8.04E-07	6.12E-07	26	geneontology_Bio	0.029953917
	positive regulation of						
	cytosolic calcium ion						
GO:0007204	concentrati	7.83E-09	8.04E-07	6.12E-07	36	geneontology_Bio	0.041474654

	mesenchymal cell						
GO:0048762	differentiation	8.22E-09	8.09E-07	6.16E-07	31	geneontology_Bio	0.035714286
	regulation of metal ion						
GO:0010959	transport	8.36E-09	8.09E-07	6.16E-07	45	geneontology_Bio	0.051843318
	negative regulation of cellular						
GO:0051271	component movement	8.36E-09	8.09E-07	6.16E-07	45	geneontology_Bio	0.051843318
GO:0050919	negative chemotaxis	1.28E-08	1.22E-06	9.28E-07	11	geneontology_Bio	0.012672811
	multicellular organismal						
GO:0035637	signaling	1.50E-08	1.40E-06	1.07E-06	30	geneontology_Bio	0.034562212
	cellular calcium ion						
GO:0006874	homeostasis	1.92E-08	1.75E-06	1.33E-06	45	geneontology_Bio	0.051843318
	striated muscle tissue						
GO:0014706	development	2.08E-08	1.81E-06	1.38E-06	45	geneontology_Bio	0.051843318
GO:0006816	calcium ion transport	2.09E-08	1.81E-06	1.38E-06	48	geneontology_Bio	0.055299539
	positive regulation of						
GO:0050769	neurogenesis	2.14E-08	1.81E-06	1.38E-06	51	geneontology_Bio	0.05875576
	embryonic limb						
GO:0030326	morphogenesis	2.17E-08	1.81E-06	1.38E-06	23	geneontology_Bio	0.026497696
	embryonic appendage						
GO:0035113	morphogenesis	2.17E-08	1.81E-06	1.38E-06	23	geneontology_Bio	0.026497696
	regulation of neuron						
GO:0010975	projection development	2.66E-08	2.15E-06	1.64E-06	51	geneontology_Bio	0.05875576
GO:0048736	appendage development	2.71E-08	2.15E-06	1.64E-06	28	geneontology_Bio	0.032258065
GO:0060173	limb development	2.71E-08	2.15E-06	1.64E-06	28	geneontology_Bio	0.032258065
	positive regulation of neuron						
GO:0045666	differentiation	3.03E-08	2.37E-06	1.80E-06	43	geneontology_Bio	0.049539171
	embryonic digestive tract						
GO:0048566	development	3.17E-08	2.44E-06	1.86E-06	12	geneontology_Bio	0.013824885
	regulation of cell-substrate						
GO:0010810	adhesion	3.88E-08	2.94E-06	2.24E-06	30	geneontology_Bio	0.034562212

	small GTPase mediated						
GO:0007264	signal transduction	4.35E-08	3.25E-06	2.48E-06	51	geneontology_Bio	0.05875576
	negative regulation of cell						
GO:2000146	motility	4.48E-08	3.29E-06	2.51E-06	42	geneontology_Bio	0.048387097
	regulation of actin						
GO:0032956	cytoskeleton organization	4.54E-08	3.30E-06	2.51E-06	38	geneontology_Bio	0.043778802
	developmental growth						
GO:0060560	involved in morphogenesis	4.68E-08	3.34E-06	2.55E-06	31	geneontology_Bio	0.035714286
GO:0034333	adherens junction assembly	4.77E-08	3.36E-06	2.56E-06	19	geneontology_Bio	0.021889401
	regulation of cAMP-mediated						
GO:0043949	signaling	4.90E-08	3.40E-06	2.59E-06	14	geneontology_Bio	0.016129032
	regulation of membrane						
GO:0042391	potential	4.96E-08	3.40E-06	2.59E-06	44	geneontology_Bio	0.050691244
	positive regulation of						
GO:0010863	phospholipase C activity	5.12E-08	3.46E-06	2.63E-06	13	geneontology_Bio	0.014976959
	canonical Wnt signaling						
GO:0060070	pathway	5.24E-08	3.47E-06	2.65E-06	39	geneontology_Bio	0.044930876
	positive regulation of cell						
GO:0031346	projection organization	5.34E-08	3.47E-06	2.65E-06	43	geneontology_Bio	0.049539171
GO:0055074	calcium ion homeostasis	5.35E-08	3.47E-06	2.65E-06	45	geneontology_Bio	0.051843318
GO:0048880	sensory system development	6.20E-08	3.96E-06	3.02E-06	42	geneontology_Bio	0.048387097
	negative regulation of						
GO:0040013	locomotion	6.27E-08	3.96E-06	3.02E-06	44	geneontology_Bio	0.050691244
	regulation of canonical Wnt						
GO:0060828	signaling pathway	6.34E-08	3.96E-06	3.02E-06	35	geneontology_Bio	0.040322581
	adenylate cyclase-modulating						
GO:0007188	G protein-coupled receptor	7.05E-08	4.34E-06	3.31E-06	26	geneontology_Bio	0.029953917
	cellular divalent inorganic						
GO:0072503	cation homeostasis	7.26E-08	4.42E-06	3.36E-06	45	geneontology_Bio	0.051843318
GO:0048732	gland development	9.35E-08	5.62E-06	4.28E-06	47	geneontology_Bio	0.054147465

	regulation of phospholipase C						
GO:1900274	activity	9.52E-08	5.66E-06	4.31E-06	13	geneontology_Bio	0.014976959
GO:0007548	sex differentiation	1.02E-07	5.96E-06	4.54E-06	35	geneontology_Bio	0.040322581
	negative regulation of cell						
GO:0030336	migration	1.06E-07	6.16E-06	4.69E-06	40	geneontology_Bio	0.046082949
GO:0021537	telencephalon development	1.14E-07	6.52E-06	4.96E-06	33	geneontology_Bio	0.038018433
GO:0042692	muscle cell differentiation	1.17E-07	6.63E-06	5.05E-06	42	geneontology_Bio	0.048387097
GO:0060993	kidney morphogenesis	1.19E-07	6.67E-06	5.08E-06	19	geneontology_Bio	0.021889401
	cardiac septum						
GO:0060411	morphogenesis	1.21E-07	6.71E-06	5.11E-06	17	geneontology_Bio	0.019585253
	cellular metal ion						
GO:0006875	homeostasis	1.26E-07	6.91E-06	5.26E-06	50	geneontology_Bio	0.057603687
	cell-substrate junction						
GO:0007044	assembly	1.42E-07	7.68E-06	5.85E-06	19	geneontology_Bio	0.021889401
GO:0042476	odontogenesis	1.56E-07	8.35E-06	6.36E-06	22	geneontology_Bio	0.025345622
GO:0022612	gland morphogenesis	1.58E-07	8.35E-06	6.36E-06	21	geneontology_Bio	0.024193548
	regulation of cation						
GO:1904062	transmembrane transport	1.67E-07	8.70E-06	6.62E-06	38	geneontology_Bio	0.043778802
	positive regulation of MAPK						
GO:0043410	cascade	1.68E-07	8.70E-06	6.62E-06	52	geneontology_Bio	0.059907834
	regulation of Wnt signaling						
GO:0030111	pathway	2.18E-07	1.12E-05	8.53E-06	40	geneontology_Bio	0.046082949
	cardiac chamber						
GO:0003206	morphogenesis	2.39E-07	1.21E-05	9.20E-06	22	geneontology_Bio	0.025345622
GO:0007416	synapse assembly	2.40E-07	1.21E-05	9.20E-06	26	geneontology_Bio	0.029953917
	regulation of synapse						
GO:0050807	organization	2.43E-07	1.21E-05	9.22E-06	30	geneontology_Bio	0.034562212
	nephron epithelium						
GO:0072009	development	2.47E-07	1.22E-05	9.26E-06	20	geneontology_Bio	0.023041475
GO:0001656	metanephros development	3.04E-07	1.47E-05	1.12E-05	18	geneontology_Bio	0.020737327

	divalent inorganic cation						
GO:0072507	homeostasis	3.07E-07	1.47E-05	1.12E-05	45	geneontology_Bio	0.051843318
	regulation of ion						
GO:0034765	transmembrane transport	3.07E-07	1.47E-05	1.12E-05	48	geneontology_Bio	0.055299539
GO:0003231	cardiac ventricle development	3.16E-07	1.50E-05	1.14E-05	22	geneontology_Bio	0.025345622
GO:0150063	visual system development	3.21E-07	1.51E-05	1.15E-05	40	geneontology_Bio	0.046082949
GO:0070838	divalent metal ion transport	3.28E-07	1.51E-05	1.15E-05	48	geneontology_Bio	0.055299539
	cardiac muscle tissue						
GO:0048738	development	3.28E-07	1.51E-05	1.15E-05	30	geneontology_Bio	0.034562212
	regulation of synapse						
GO:0050803	structure or activity	3.63E-07	1.66E-05	1.26E-05	30	geneontology_Bio	0.034562212
GO:0016055	Wnt signaling pathway	3.77E-07	1.71E-05	1.30E-05	51	geneontology_Bio	0.05875576
GO:0003015	heart process	3.85E-07	1.72E-05	1.31E-05	35	geneontology_Bio	0.040322581
GO:0022029	telencephalon cell migration	3.89E-07	1.73E-05	1.32E-05	14	geneontology_Bio	0.016129032
GO:0042063	gliogenesis	4.18E-07	1.84E-05	1.40E-05	35	geneontology_Bio	0.040322581
	divalent inorganic cation						
GO:0072511	transport	4.25E-07	1.84E-05	1.40E-05	48	geneontology_Bio	0.055299539
GO:0198738	cell-cell signaling by wnt	4.27E-07	1.84E-05	1.40E-05	51	geneontology_Bio	0.05875576
	regulation of heart						
GO:0008016	contraction	4.72E-07	2.01E-05	1.53E-05	32	geneontology_Bio	0.036866359
	adherens junction						
GO:0034332	organization	4.73E-07	2.01E-05	1.53E-05	22	geneontology_Bio	0.025345622
	G protein-coupled receptor						
GO:0007187	signaling pathway, coupled to	4.76E-07	2.01E-05	1.53E-05	26	geneontology_Bio	0.029953917
GO:0060425	lung morphogenesis	4.97E-07	2.08E-05	1.58E-05	13	geneontology_Bio	0.014976959
	adenylate cyclase-activating						
GO:0007189	G protein-coupled receptor	5.05E-07	2.09E-05	1.59E-05	18	geneontology_Bio	0.020737327
	regulation of animal organ						
GO:2000027	morphogenesis	5.17E-07	2.12E-05	1.62E-05	32	geneontology_Bio	0.036866359
	regulation of muscle system						
GO:0090257	process	5.66E-07	2.29E-05	1.74E-05	32	geneontology_Bio	0.036866359

	ventricular septum						
GO:0003281	development	5.66E-07	2.29E-05	1.74E-05	16	geneontology_Bio	0.01843318
GO:0003401	axis elongation	5.85E-07	2.32E-05	1.77E-05	10	geneontology_Bio	0.011520737
	regulation of Ras protein						
GO:0046578	signal transduction	5.89E-07	2.32E-05	1.77E-05	29	geneontology_Bio	0.033410138
	regulation of transmembrane						
GO:0090092	receptor protein serine/thre	5.89E-07	2.32E-05	1.77E-05	29	geneontology_Bio	0.033410138
GO:0061326	renal tubule development	5.95E-07	2.33E-05	1.77E-05	18	geneontology_Bio	0.020737327
GO:0006939	smooth muscle contraction	6.13E-07	2.38E-05	1.81E-05	19	geneontology_Bio	0.021889401
GO:0001654	eye development	6.39E-07	2.43E-05	1.85E-05	39	geneontology_Bio	0.044930876
	regulation of animal organ						
GO:0003156	formation	6.39E-07	2.43E-05	1.85E-05	11	geneontology_Bio	0.012672811
	cyclic nucleotide metabolic						
GO:0009187	process	6.39E-07	2.43E-05	1.85E-05	11	geneontology_Bio	0.012672811
GO:0021885	forebrain cell migration	7.66E-07	2.88E-05	2.20E-05	14	geneontology_Bio	0.016129032
	reproductive structure						
GO:0048608	development	7.85E-07	2.93E-05	2.23E-05	45	geneontology_Bio	0.051843318
	regulation of calcium ion						
GO:0051924	transport	9.14E-07	3.39E-05	2.58E-05	31	geneontology_Bio	0.035714286
GO:0032835	glomerulus development	9.50E-07	3.48E-05	2.65E-05	14	geneontology_Bio	0.016129032
	reproductive system						
GO:0061458	development	9.53E-07	3.48E-05	2.65E-05	45	geneontology_Bio	0.051843318
GO:0001503	ossification	9.65E-07	3.50E-05	2.66E-05	42	geneontology_Bio	0.048387097
GO:0061333	renal tubule morphogenesis	9.84E-07	3.54E-05	2.70E-05	16	geneontology_Bio	0.01843318
GO:0007015	actin filament organization	1.28E-06	4.59E-05	3.49E-05	37	geneontology_Bio	0.042626728
GO:0060840	artery development	1.31E-06	4.64E-05	3.53E-05	18	geneontology_Bio	0.020737327
	cell-substrate adherens						
GO:0007045	junction assembly	1.40E-06	4.89E-05	3.73E-05	16	geneontology_Bio	0.01843318
GO:0048041	focal adhesion assembly	1.40E-06	4.89E-05	3.73E-05	16	geneontology_Bio	0.01843318
GO:0035265	organ growth	1.83E-06	6.36E-05	4.84E-05	25	geneontology_Bio	0.028801843

	calcium ion transport into						
GO:0060402	cytosol	1.87E-06	6.45E-05	4.91E-05	22	geneontology_Bio	0.025345622
	positive regulation of neuron						
GO:0010976	projection development	1.88E-06	6.45E-05	4.91E-05	32	geneontology_Bio	0.036866359
	glycosaminoglycan metabolic						
GO:0030203	process	2.05E-06	6.93E-05	5.28E-05	23	geneontology_Bio	0.026497696
GO:0072080	nephron tubule development	2.05E-06	6.93E-05	5.28E-05	17	geneontology_Bio	0.019585253
	regulation of blood						
GO:1903522	circulation	2.08E-06	6.96E-05	5.30E-05	34	geneontology_Bio	0.039170507
	mesenchymal cell						
GO:0014031	development	2.15E-06	7.12E-05	5.42E-05	14	geneontology_Bio	0.016129032
GO:0048546	digestive tract morphogenesis	2.15E-06	7.12E-05	5.42E-05	12	geneontology_Bio	0.013824885
GO:0010002	cardioblast differentiation	2.20E-06	7.24E-05	5.51E-05	8	geneontology_Bio	0.00921659
	calcium ion transmembrane						
GO:0070588	transport	2.24E-06	7.30E-05	5.56E-05	34	geneontology_Bio	0.039170507
	specification of animal organ						
GO:0010092	identity	2.27E-06	7.30E-05	5.56E-05	10	geneontology_Bio	0.011520737
	positive regulation of						
GO:0010922	phosphatase activity	2.27E-06	7.30E-05	5.56E-05	10	geneontology_Bio	0.011520737
	regulation of transmembrane						
GO:0022898	transporter activity	2.28E-06	7.31E-05	5.56E-05	30	geneontology_Bio	0.034562212
	positive regulation of						
GO:0010518	phospholipase activity	2.50E-06	7.96E-05	6.06E-05	13	geneontology_Bio	0.014976959
	nephron tubule						
GO:0072078	morphogenesis	2.53E-06	7.98E-05	6.08E-05	15	geneontology_Bio	0.017281106
	positive regulation of synapse						
GO:0051965	assembly	2.61E-06	8.19E-05	6.23E-05	14	geneontology_Bio	0.016129032
GO:0007272	ensheathment of neurons	2.68E-06	8.30E-05	6.32E-05	20	geneontology_Bio	0.023041475
GO:0008366	axon ensheathment	2.68E-06	8.30E-05	6.32E-05	20	geneontology_Bio	0.023041475
	regulation of synapse						
GO:0051963	assembly	2.72E-06	8.38E-05	6.38E-05	18	geneontology_Bio	0.020737327

GO:0001667	ameboidal-type cell migration	2.73E-06	8.38E-05	6.38E-05	45	geneontology_Bio	0.051843318
	regulation of transporter						
GO:0032409	activity	2.78E-06	8.46E-05	6.44E-05	31	geneontology_Bio	0.035714286
	outflow tract septum						
GO:0003148	morphogenesis	3.01E-06	9.09E-05	6.93E-05	9	geneontology_Bio	0.010368664
	mesonephric tubule						
GO:0072171	morphogenesis	3.15E-06	9.47E-05	7.21E-05	14	geneontology_Bio	0.016129032
	aminoglycan metabolic						
GO:0006022	process	3.18E-06	9.50E-05	7.23E-05	23	geneontology_Bio	0.026497696
	regulation of ion						
	transmembrane transporter						
GO:0032412	activity	3.37E-06	0.000100159	7.63E-05	29	geneontology_Bio	0.033410138
	nephron epithelium						
GO:0072088	morphogenesis	3.57E-06	0.000105384	8.02E-05	15	geneontology_Bio	0.017281106
GO:0050920	regulation of chemotaxis	3.71E-06	0.000108916	8.29E-05	25	geneontology_Bio	0.028801843
GO:0003007	heart morphogenesis	4.10E-06	0.000119749	9.12E-05	30	geneontology_Bio	0.034562212
GO:0060047	heart contraction	4.17E-06	0.000120929	9.21E-05	32	geneontology_Bio	0.036866359
	regulation of epithelial cell						
GO:0050678	proliferation	4.19E-06	0.000120929	9.21E-05	39	geneontology_Bio	0.044930876
GO:0072132	mesenchyme morphogenesis	4.29E-06	0.000122575	9.33E-05	12	geneontology_Bio	0.013824885
	regulation of calcium ion						
GO:0010522	transport into cytosol	4.33E-06	0.000122575	9.33E-05	17	geneontology_Bio	0.019585253
GO:0043583	ear development	4.35E-06	0.000122575	9.33E-05	27	geneontology_Bio	0.031105991
GO:0048863	stem cell differentiation	4.35E-06	0.000122575	9.33E-05	29	geneontology_Bio	0.033410138
	branching involved in ureteric						
GO:0001658	bud morphogenesis	4.61E-06	0.000129238	9.84E-05	13	geneontology_Bio	0.014976959
	cardiac muscle cell myoblast						
GO:0060379	differentiation	4.77E-06	0.000132667	0.00010102	6	geneontology_Bio	0.006912442
	embryonic organ						
GO:0048568	development	4.81E-06	0.000132667	0.00010102	42	geneontology_Bio	0.048387097

	negative regulation of						
GO:0051961	nervous system development	4.82E-06	0.000132667	0.00010102	33	geneontology_Bio	0.038018433
	negative regulation of cell						
GO:0010721	development	4.95E-06	0.000135507	0.000103182	35	geneontology_Bio	0.040322581
GO:0072028	nephron morphogenesis	4.98E-06	0.000135746	0.000103364	15	geneontology_Bio	0.017281106
GO:0001759	organ induction	5.13E-06	0.000138923	0.000105783	8	geneontology_Bio	0.00921659
GO:0048645	animal organ formation	5.60E-06	0.000151024	0.000114998	13	geneontology_Bio	0.014976959
	regulation of cell						
GO:0022604	morphogenesis	5.70E-06	0.000152787	0.000116341	43	geneontology_Bio	0.049539171
GO:0003151	outflow tract morphogenesis	5.86E-06	0.000156035	0.000118814	15	geneontology_Bio	0.017281106
	epithelial tube branching						
	involved in lung						
GO:0060441	morphogenesis	5.89E-06	0.000156035	0.000118814	9	geneontology_Bio	0.010368664
GO:0042552	myelination	6.30E-06	0.000166148	0.000126514	19	geneontology_Bio	0.021889401
	peptidyl-tyrosine						
GO:0018212	modification	6.86E-06	0.000179387	0.000136595	37	geneontology_Bio	0.042626728
	regulation of cardiac muscle						
GO:0055117	contraction	6.88E-06	0.000179387	0.000136595	15	geneontology_Bio	0.017281106
	regulation of MAP kinase						
GO:0043405	activity	7.00E-06	0.00018173	0.000138379	35	geneontology_Bio	0.040322581
	cytosolic calcium ion						
GO:0060401	transport	7.11E-06	0.000182134	0.000138687	22	geneontology_Bio	0.025345622
GO:0001508	action potential	7.12E-06	0.000182134	0.000138687	19	geneontology_Bio	0.021889401
	connective tissue						
GO:0061448	development	7.13E-06	0.000182134	0.000138687	29	geneontology_Bio	0.033410138
	membrane depolarization						
	during cardiac muscle cell						
GO:0086012	actio	7.53E-06	0.000191371	0.00014572	8	geneontology_Bio	0.00921659
	positive regulation of						
GO:0050772	axonogenesis	7.68E-06	0.000194181	0.00014786	14	geneontology_Bio	0.016129032

	pulmonary valve						
GO:0003184	morphogenesis	7.77E-06	0.000195379	0.000148772	7	geneontology_Bio	0.008064516
GO:0031099	regeneration	7.91E-06	0.000197443	0.000150344	25	geneontology_Bio	0.028801843
	Ras protein signal						
GO:0007265	transduction	8.03E-06	0.000197443	0.000150344	35	geneontology_Bio	0.040322581
GO:0051216	cartilage development	8.05E-06	0.000197443	0.000150344	24	geneontology_Bio	0.02764977
	positive regulation of Wnt						
GO:0030177	signaling pathway	8.05E-06	0.000197443	0.000150344	23	geneontology_Bio	0.026497696
	activation of phospholipase C						
GO:0007202	activity	8.05E-06	0.000197443	0.000150344	9	geneontology_Bio	0.010368664
GO:0007389	pattern specification process	8.33E-06	0.000202479	0.000154179	41	geneontology_Bio	0.047235023
	negative regulation of						
GO:0050768	neurogenesis	8.34E-06	0.000202479	0.000154179	31	geneontology_Bio	0.035714286
	actin filament bundle						
GO:0051017	assembly	8.83E-06	0.000213394	0.00016249	20	geneontology_Bio	0.023041475
	actin filament bundle						
GO:0061572	organization	9.88E-06	0.000237542	0.000180878	20	geneontology_Bio	0.023041475
	negative regulation of cAMP-						
GO:0043951	mediated signaling	1.08E-05	0.000258885	0.00019713	8	geneontology_Bio	0.00921659
	development of primary						
GO:0045137	sexual characteristics	1.12E-05	0.000267175	0.000203442	27	geneontology_Bio	0.031105991
	multicellular organismal						
GO:0048871	homeostasis	1.19E-05	0.000281535	0.000214376	45	geneontology_Bio	0.051843318
	regulation of cytoskeleton						
GO:0051493	organization	1.19E-05	0.000281535	0.000214376	45	geneontology_Bio	0.051843318
	cell communication involved						
GO:0086065	in cardiac conduction	1.21E-05	0.00028336	0.000215766	12	geneontology_Bio	0.013824885
	activation of protein kinase						
GO:0032147	activity	1.22E-05	0.000285215	0.000217178	33	geneontology_Bio	0.038018433
GO:0048678	response to axon injury	1.26E-05	0.000292771	0.000222932	14	geneontology_Bio	0.016129032

	odontogenesis of dentin-						
GO:0042475	containing tooth	1.27E-05	0.000293389	0.000223403	15	geneontology_Bio	0.017281106
GO:0045216	cell-cell junction organization	1.28E-05	0.000295715	0.000225174	19	geneontology_Bio	0.021889401
GO:0010001	glial cell differentiation	1.29E-05	0.000295822	0.000225255	26	geneontology_Bio	0.029953917
	regulation of phospholipase						
GO:0010517	activity	1.39E-05	0.000316957	0.000241349	13	geneontology_Bio	0.014976959
GO:0060675	ureteric bud morphogenesis	1.39E-05	0.000316957	0.000241349	13	geneontology_Bio	0.014976959
GO:0007517	muscle organ development	1.43E-05	0.000323839	0.000246589	40	geneontology_Bio	0.046082949
	regulation of muscle						
GO:0006937	contraction	1.44E-05	0.000324969	0.00024745	22	geneontology_Bio	0.025345622
	negative regulation of neuron						
GO:0045665	differentiation	1.48E-05	0.000330686	0.000251803	25	geneontology_Bio	0.028801843
GO:0002062	chondrocyte differentiation	1.60E-05	0.000356676	0.000271593	16	geneontology_Bio	0.01843318
GO:0090130	tissue migration	1.66E-05	0.000369404	0.000281284	37	geneontology_Bio	0.042626728
GO:0021543	pallium development	1.75E-05	0.000385593	0.000293612	22	geneontology_Bio	0.025345622
	regulation of cation channel						
GO:2001257	activity	1.75E-05	0.000385593	0.000293612	22	geneontology_Bio	0.025345622
GO:0060048	cardiac muscle contraction	2.01E-05	0.000438152	0.000333633	19	geneontology_Bio	0.021889401
GO:0001570	vasculogenesis	2.01E-05	0.000438152	0.000333633	14	geneontology_Bio	0.016129032
GO:0061337	cardiac conduction	2.09E-05	0.000453709	0.000345479	20	geneontology_Bio	0.023041475
	cell differentiation involved						
GO:0072202	in metanephros development	2.11E-05	0.000453709	0.000345479	8	geneontology_Bio	0.00921659
	membrane depolarization						
GO:0086010	during action potential	2.11E-05	0.000453709	0.000345479	8	geneontology_Bio	0.00921659
	coronary vasculature						
GO:0060976	development	2.13E-05	0.000457531	0.00034839	11	geneontology_Bio	0.012672811
GO:0010631	epithelial cell migration	2.26E-05	0.000483432	0.000368112	36	geneontology_Bio	0.041474654
	peripheral nervous system						
GO:0007422	development	2.30E-05	0.000489881	0.000373022	13	geneontology_Bio	0.014976959
GO:0051235	maintenance of location	2.44E-05	0.000516415	0.000393227	31	geneontology_Bio	0.035714286

GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecule	2.49E-05	0.000524413	0.000399317	27	geneontology_Bio	0.031105991
GO:0010769	regulation of cell morphogenesis involved in differentiation	2.60E-05	0.000545966	0.000415729	29	geneontology_Bio	0.033410138
GO:0007611	learning or memory	2.66E-05	0.000554963	0.00042258	28	geneontology_Bio	0.032258065
GO:1903510	mucopolysaccharide metabolic process	2.70E-05	0.000556777	0.000423961	17	geneontology_Bio	0.019585253
GO:0014033	neural crest cell differentiation	2.71E-05	0.000556777	0.000423961	13	geneontology_Bio	0.014976959
GO:0060193	positive regulation of lipase activity	2.71E-05	0.000556777	0.000423961	13	geneontology_Bio	0.014976959
GO:0090132	epithelium migration	2.71E-05	0.000556777	0.000423961	36	geneontology_Bio	0.041474654
GO:0060602	branch elongation of an epithelium	2.72E-05	0.000556777	0.000423961	7	geneontology_Bio	0.008064516
GO:0106070	regulation of adenylate cyclase-activating G protein-cou	2.73E-05	0.000556777	0.000423961	6	geneontology_Bio	0.006912442
GO:0010921	regulation of phosphatase activity	2.80E-05	0.000567776	0.000432336	22	geneontology_Bio	0.025345622
GO:0010717	regulation of epithelial to mesenchymal transition	2.95E-05	0.000595641	0.000453554	15	geneontology_Bio	0.017281106
GO:0003170	heart valve development	3.01E-05	0.000603867	0.000459818	12	geneontology_Bio	0.013824885
GO:0014032	neural crest cell development	3.01E-05	0.000603867	0.000459818	12	geneontology_Bio	0.013824885
GO:0048562	embryonic organ morphogenesis	3.11E-05	0.000621216	0.000473028	30	geneontology_Bio	0.034562212
GO:0046661	male sex differentiation	3.13E-05	0.000621216	0.000473028	21	geneontology_Bio	0.024193548
GO:0050770	regulation of axonogenesis	3.14E-05	0.000621216	0.000473028	20	geneontology_Bio	0.023041475
GO:0003179	heart valve morphogenesis	3.16E-05	0.000622948	0.000474347	11	geneontology_Bio	0.012672811
GO:0051146	striated muscle cell differentiation	3.22E-05	0.000631238	0.00048066	29	geneontology_Bio	0.033410138

GO:0048839	inner ear development peptidyl-tyrosine	3.23E-05	0.000631238	0.00048066	23	geneontology_Bio	0.026497696
GO:0018108	phosphorylation	3.28E-05	0.000637156	0.000485166	35	geneontology_Bio	0.040322581
GO:0003002	regionalization positive regulation of MAP	3.28E-05	0.000637156	0.000485166	33	geneontology_Bio	0.038018433
GO:0043406	kinase activity positive regulation of	3.31E-05	0.00063976	0.000487149	28	geneontology_Bio	0.032258065
GO:0050679	epithelial cell proliferation	3.62E-05	0.000697032	0.000530759	24	geneontology_Bio	0.02764977
GO:0030850	prostate gland development pulmonary valve	3.74E-05	0.000717592	0.000546415	10	geneontology_Bio	0.011520737
GO:0003177	development modulation of chemical	3.92E-05	0.000748284	0.000569785	7	geneontology_Bio	0.008064516
GO:0050804	synaptic transmission regulation of epithelial cell	4.14E-05	0.000788871	0.00060069	38	geneontology_Bio	0.043778802
GO:0010632	migration positive regulation of protein	4.16E-05	0.000788934	0.000600738	31	geneontology_Bio	0.035714286
GO:0071902	serine/threonine kinase a positive regulation of	4.21E-05	0.00079598	0.000606103	33	geneontology_Bio	0.038018433
GO:0045778	ossification regulation of trans-synaptic	4.36E-05	0.00082088	0.000625063	15	geneontology_Bio	0.017281106
GO:0099177	signaling transmembrane receptor	4.38E-05	0.00082088	0.000625063	38	geneontology_Bio	0.043778802
GO:0007178	protein serine/threonine kinase s	4.48E-05	0.000836895	0.000637258	33	geneontology_Bio	0.038018433
GO:0003197	endocardial cushion development	4.60E-05	0.000841257	0.00064058	10	geneontology_Bio	0.011520737
GO:0010463	mesenchymal cell proliferation	4.60E-05	0.000841257	0.00064058	10	geneontology_Bio	0.011520737
GO:0022602	ovulation cycle process ventricular septum	4.60E-05	0.000841257	0.00064058	10	geneontology_Bio	0.011520737
GO:0060412	morphogenesis	4.60E-05	0.000841257	0.00064058	10	geneontology_Bio	0.011520737

	regulation of actin filament						
GO:0110053	organization	4.60E-05	0.000841257	0.00064058	26	geneontology_Bio	0.029953917
GO:0001764	neuron migration	4.62E-05	0.000841257	0.00064058	20	geneontology_Bio	0.023041475
GO:0030168	platelet activation	4.62E-05	0.000841257	0.00064058	20	geneontology_Bio	0.023041475
	embryonic skeletal system						
GO:0048706	development	4.79E-05	0.000867512	0.000660572	17	geneontology_Bio	0.019585253
GO:0050673	epithelial cell proliferation	4.82E-05	0.000869999	0.000662466	40	geneontology_Bio	0.046082949
GO:0016358	dendrite development	5.01E-05	0.000901597	0.000686526	25	geneontology_Bio	0.028801843
GO:0014044	Schwann cell development	5.09E-05	0.000911909	0.000694378	8	geneontology_Bio	0.00921659
GO:0014037	Schwann cell differentiation	5.16E-05	0.000917721	0.000698804	9	geneontology_Bio	0.010368664
GO:0044091	membrane biogenesis	5.16E-05	0.000917721	0.000698804	9	geneontology_Bio	0.010368664
GO:0008406	gonad development	5.41E-05	0.000957032	0.000728737	25	geneontology_Bio	0.028801843
	skeletal system						
GO:0048705	morphogenesis	5.41E-05	0.000957032	0.000728737	24	geneontology_Bio	0.02764977
	neuron projection						
GO:0031102	regeneration	5.48E-05	0.000964762	0.000734623	11	geneontology_Bio	0.012672811
	regulation of striated muscle						
GO:0006942	contraction	5.61E-05	0.000983966	0.000749246	15	geneontology_Bio	0.017281106
GO:0048806	genitalia development	5.63E-05	0.000983966	0.000749246	10	geneontology_Bio	0.011520737
GO:0048864	stem cell development	5.83E-05	0.001015688	0.000773401	12	geneontology_Bio	0.013824885
GO:0050890	cognition	6.06E-05	0.001051888	0.000800966	30	geneontology_Bio	0.034562212
	adenylate cyclase-activating						
GO:0071880	adrenergic receptor signali	6.70E-05	0.001155524	0.00087988	6	geneontology_Bio	0.006912442
	G protein-coupled receptor						
GO:0086103	signaling pathway involved in	6.70E-05	0.001155524	0.00087988	6	geneontology_Bio	0.006912442
GO:0002027	regulation of heart rate	7.16E-05	0.001226581	0.000933986	15	geneontology_Bio	0.017281106
GO:0007043	cell-cell junction assembly	7.16E-05	0.001226581	0.000933986	15	geneontology_Bio	0.017281106
GO:0030539	male genitalia development	7.58E-05	0.001293514	0.000984953	7	geneontology_Bio	0.008064516
GO:0006941	striated muscle contraction	7.70E-05	0.001309243	0.00099693	21	geneontology_Bio	0.024193548
GO:0035904	aorta development	7.73E-05	0.00131028	0.00099772	11	geneontology_Bio	0.012672811

GO:0050918	positive chemotaxis	7.94E-05	0.001340903	0.001021038	12	geneontology_Bio	0.013824885
GO:0099173	postsynapse organization	8.03E-05	0.00135001	0.001027973	20	geneontology_Bio	0.023041475
	regulation of heart						
GO:2000826	morphogenesis	8.05E-05	0.00135001	0.001027973	9	geneontology_Bio	0.010368664
GO:0031103	axon regeneration	8.27E-05	0.001382335	0.001052586	10	geneontology_Bio	0.011520737
GO:0090596	sensory organ morphogenesis	8.51E-05	0.001417844	0.001079625	27	geneontology_Bio	0.031105991
	development of primary						
GO:0046545	female sexual characteristics	9.08E-05	0.001507193	0.00114766	15	geneontology_Bio	0.017281106
GO:0001659	temperature homeostasis	9.13E-05	0.001510107	0.00114988	21	geneontology_Bio	0.024193548
	positive regulation of						
	canonical Wnt signaling						
GO:0090263	pathway	9.18E-05	0.001513317	0.001152324	18	geneontology_Bio	0.020737327
	adenylate cyclase-activating						
GO:0086023	adrenergic receptor signali	9.55E-05	0.001570202	0.001195639	5	geneontology_Bio	0.005760369
	phosphatidylinositol-						
GO:0048015	mediated signaling	9.59E-05	0.001570779	0.001196078	20	geneontology_Bio	0.023041475
GO:0018209	peptidyl-serine modification	9.74E-05	0.001590798	0.001211322	27	geneontology_Bio	0.031105991
	positive regulation of ion						
GO:0043270	transport	9.92E-05	0.001614517	0.001229383	28	geneontology_Bio	0.032258065
GO:0048675	axon extension	0.000101923	0.001652922	0.001258626	15	geneontology_Bio	0.017281106
	morphogenesis of an						
GO:0060571	epithelial fold	0.000102574	0.001652922	0.001258626	7	geneontology_Bio	0.008064516
	cell communication by						
	electrical coupling involved						
GO:0086064	in ca	0.000102574	0.001652922	0.001258626	7	geneontology_Bio	0.008064516
GO:0043010	camera-type eye development	0.000106526	0.001711011	0.001302859	30	geneontology_Bio	0.034562212
	protein localization to cell						
GO:0034394	surface	0.000107369	0.001714819	0.001305758	11	geneontology_Bio	0.012672811
	extrinsic apoptotic signaling						
GO:0097191	pathway	0.000107459	0.001714819	0.001305758	24	geneontology_Bio	0.02764977

	activation of adenylate						
GO:0007190	cyclase activity	0.000109516	0.001730848	0.001317964	8	geneontology_Bio	0.00921659
	proximal/distal pattern						
GO:0009954	formation	0.000109516	0.001730848	0.001317964	8	geneontology_Bio	0.00921659
GO:0071709	membrane assembly	0.000109516	0.001730848	0.001317964	8	geneontology_Bio	0.00921659
	positive regulation of animal						
GO:0110110	organ morphogenesis	0.00011492	0.001810452	0.001378578	13	geneontology_Bio	0.014976959
	plasma membrane						
GO:0007009	organization	0.000116891	0.00183564	0.001397758	14	geneontology_Bio	0.016129032
GO:0046660	female sex differentiation	0.000120545	0.001887007	0.001436872	16	geneontology_Bio	0.01843318
	calcium ion transmembrane						
GO:0097553	import into cytosol	0.000122958	0.001918695	0.001461001	17	geneontology_Bio	0.019585253
	inositol lipid-mediated						
GO:0048017	signaling	0.00012419	0.001927593	0.001467776	20	geneontology_Bio	0.023041475
GO:0042445	hormone metabolic process	0.00012431	0.001927593	0.001467776	24	geneontology_Bio	0.02764977
GO:0051899	membrane depolarization	0.000130915	0.002023647	0.001540917	13	geneontology_Bio	0.014976959
	prostate gland epithelium						
GO:0060740	morphogenesis	0.000136541	0.002091227	0.001592376	7	geneontology_Bio	0.008064516
GO:0099068	postsynapse assembly	0.000136541	0.002091227	0.001592376	7	geneontology_Bio	0.008064516
	negative regulation of cell						
GO:0007162	adhesion	0.00013656	0.002091227	0.001592376	28	geneontology_Bio	0.032258065
	negative regulation of protein						
GO:0001933	phosphorylation	0.000137823	0.00210094	0.001599772	38	geneontology_Bio	0.043778802
GO:0031128	developmental induction	0.000138472	0.00210094	0.001599772	8	geneontology_Bio	0.00921659
	embryonic forelimb						
GO:0035115	morphogenesis	0.000138472	0.00210094	0.001599772	8	geneontology_Bio	0.00921659
GO:0021545	cranial nerve development	0.000141635	0.002135789	0.001626308	10	geneontology_Bio	0.011520737
	negative regulation of small						
GO:0051058	GTPase mediated signal tran	0.000141635	0.002135789	0.001626308	10	geneontology_Bio	0.011520737
GO:0032288	myelin assembly	0.000142924	0.002148653	0.001636103	6	geneontology_Bio	0.006912442

	chondroitin sulfate						
	proteoglycan metabolic						
GO:0050654	process	0.000148641	0.002216595	0.001687838	9	geneontology_Bio	0.010368664
GO:0099054	presynapse assembly	0.000148641	0.002216595	0.001687838	9	geneontology_Bio	0.010368664
	striated muscle cell						
GO:0014855	proliferation	0.000148792	0.002216595	0.001687838	13	geneontology_Bio	0.014976959
	regulation of protein						
	serine/threonine kinase						
GO:0071900	activity	0.000154948	0.002301355	0.001752379	42	geneontology_Bio	0.048387097
	AV node cell to bundle of His						
GO:0086067	cell communication	0.000157236	0.002328322	0.001772914	5	geneontology_Bio	0.005760369
	adenylate cyclase-inhibiting						
GO:0007193	G protein-coupled receptor	0.000162908	0.002397904	0.001825897	12	geneontology_Bio	0.013824885
GO:1990266	neutrophil migration	0.000162908	0.002397904	0.001825897	12	geneontology_Bio	0.013824885
	regulation of cell-matrix						
GO:0001952	adhesion	0.00016435	0.002411934	0.001836581	16	geneontology_Bio	0.01843318
	oligodendrocyte						
GO:0048709	differentiation	0.000166724	0.002432303	0.00185209	14	geneontology_Bio	0.016129032
GO:0060191	regulation of lipase activity	0.000166724	0.002432303	0.00185209	14	geneontology_Bio	0.016129032
	purine ribonucleotide						
GO:0009154	catabolic process	0.000179083	0.002589608	0.001971871	7	geneontology_Bio	0.008064516
	myelination in peripheral						
GO:0022011	nervous system	0.000179083	0.002589608	0.001971871	7	geneontology_Bio	0.008064516
	peripheral nervous system						
GO:0032292	axon ensheathment	0.000179083	0.002589608	0.001971871	7	geneontology_Bio	0.008064516
	homophilic cell adhesion via						
	plasma membrane adhesion						
GO:0007156	mo	0.000181023	0.002610006	0.001987404	17	geneontology_Bio	0.019585253
	regulation of cardiac						
GO:1903779	conduction	0.000186494	0.002677773	0.002039005	12	geneontology_Bio	0.013824885
GO:0007626	locomotory behavior	0.000186809	0.002677773	0.002039005	22	geneontology_Bio	0.025345622

	glycosaminoglycan						
GO:0006024	biosynthetic process	0.000197243	0.002819139	0.002146648	15	geneontology_Bio	0.017281106
	smoothened signaling						
GO:0007224	pathway	0.000198824	0.002833533	0.002157609	17	geneontology_Bio	0.019585253
	regulation of peptidyl-serine						
GO:0033135	phosphorylation	0.000200728	0.002852417	0.002171989	16	geneontology_Bio	0.01843318
	regulation of neurotransmitter						
GO:0001505	levels	0.000210381	0.002967842	0.002259879	31	geneontology_Bio	0.035714286
	neural precursor cell						
GO:0061351	proliferation	0.000210656	0.002967842	0.002259879	18	geneontology_Bio	0.020737327
	regulation of calcium ion						
GO:1903169	transmembrane transport	0.000210656	0.002967842	0.002259879	18	geneontology_Bio	0.020737327
	cardiac muscle cell action						
GO:0086001	potential	0.000212931	0.002991354	0.002277783	12	geneontology_Bio	0.013824885
	embryonic skeletal system						
GO:0048704	morphogenesis	0.000215564	0.00301973	0.00229939	13	geneontology_Bio	0.014976959
GO:0021795	cerebral cortex cell migration	0.00021666	0.003026488	0.002304536	9	geneontology_Bio	0.010368664
	aminoglycan biosynthetic						
GO:0006023	process	0.000218994	0.003050454	0.002322785	15	geneontology_Bio	0.017281106
GO:0097529	myeloid leukocyte migration	0.000220587	0.00306399	0.002333092	20	geneontology_Bio	0.023041475
	ribonucleotide catabolic						
GO:0009261	process	0.000231725	0.003185871	0.002425899	7	geneontology_Bio	0.008064516
GO:0060512	prostate gland morphogenesis	0.000231725	0.003185871	0.002425899	7	geneontology_Bio	0.008064516
	metanephric epithelium						
GO:0072207	development	0.000231725	0.003185871	0.002425899	7	geneontology_Bio	0.008064516
GO:0019226	transmission of nerve impulse	0.000232592	0.003185871	0.002425899	10	geneontology_Bio	0.011520737
	cell differentiation involved						
GO:0061005	in kidney development	0.000232592	0.003185871	0.002425899	10	geneontology_Bio	0.011520737
	contractile actin filament						
GO:0030038	bundle assembly	0.000233921	0.003186361	0.002426272	14	geneontology_Bio	0.016129032
GO:0043149	stress fiber assembly	0.000233921	0.003186361	0.002426272	14	geneontology_Bio	0.016129032

GO:0045165	cell fate commitment smooth muscle cell	0.000236985	0.003219211	0.002451286	25	geneontology_Bio	0.028801843
GO:0051145	differentiation positive regulation of muscle	0.000242495	0.003281272	0.002498542	12	geneontology_Bio	0.013824885
GO:1901863	tissue development negative regulation of transmembrane receptor	0.000242885	0.003281272	0.002498542	13	geneontology_Bio	0.014976959
GO:0090101	protein se negative regulation of Ras	0.000243902	0.003286018	0.002502156	16	geneontology_Bio	0.01843318
GO:0046580	protein signal transduction	0.00025932	0.003474754	0.00264587	9	geneontology_Bio	0.010368664
GO:0099172	presynapse organization positive regulation of cell-	0.00025932	0.003474754	0.00264587	9	geneontology_Bio	0.010368664
GO:0010811	substrate adhesion	0.000268781	0.003572156	0.002720038	15	geneontology_Bio	0.017281106
GO:0030278	regulation of ossification ventricular cardiac muscle	0.000268809	0.003572156	0.002720038	22	geneontology_Bio	0.025345622
GO:0003229	tissue development positive regulation of	0.000272106	0.003572156	0.002720038	10	geneontology_Bio	0.011520737
GO:0035306	dephosphorylation	0.000272106	0.003572156	0.002720038	10	geneontology_Bio	0.011520737
GO:0060021	roof of mouth development smooth muscle tissue	0.000273113	0.003572156	0.002720038	13	geneontology_Bio	0.014976959
GO:0048745	development axon extension involved in	0.000274558	0.003572156	0.002720038	6	geneontology_Bio	0.006912442
GO:0048846	axon guidance atrial cardiac muscle cell	0.000274558	0.003572156	0.002720038	6	geneontology_Bio	0.006912442
GO:0086014	action potential atrial cardiac muscle cell to	0.000274558	0.003572156	0.002720038	6	geneontology_Bio	0.006912442
GO:0086026	AV node cell signaling atrial cardiac muscle cell to	0.000274558	0.003572156	0.002720038	6	geneontology_Bio	0.006912442
GO:0086066	AV node cell communication neuron projection extension	0.000274558	0.003572156	0.002720038	6	geneontology_Bio	0.006912442
GO:1902284	involved in neuron projectio	0.000274558	0.003572156	0.002720038	6	geneontology_Bio	0.006912442

	central nervous system						
GO:0021954	neuron development	0.000275478	0.003574692	0.002721969	12	geneontology_Bio	0.013824885
	negative regulation of neuron						
GO:0010977	projection development	0.000286176	0.003703762	0.00282025	17	geneontology_Bio	0.019585253
GO:0003180	aortic valve morphogenesis	0.000296149	0.003822805	0.002910896	7	geneontology_Bio	0.008064516
GO:0021782	glial cell development	0.000297137	0.003825544	0.002912982	15	geneontology_Bio	0.017281106
	regulation of chondrocyte						
GO:0032330	differentiation	0.000308711	0.003964198	0.00301856	9	geneontology_Bio	0.010368664
GO:0019722	calcium-mediated signaling	0.000318863	0.004083925	0.003109727	21	geneontology_Bio	0.024193548
	regulation of Rho protein						
GO:0035023	signal transduction	0.000323684	0.004110206	0.003129739	16	geneontology_Bio	0.01843318
GO:0001755	neural crest cell migration	0.000324249	0.004110206	0.003129739	8	geneontology_Bio	0.00921659
	postsynaptic membrane						
GO:0001941	organization	0.000324249	0.004110206	0.003129739	8	geneontology_Bio	0.00921659
	semi-lunar valve						
GO:1905314	development	0.000324249	0.004110206	0.003129739	8	geneontology_Bio	0.00921659
GO:0021987	cerebral cortex development	0.000328031	0.004147492	0.003158131	15	geneontology_Bio	0.017281106
	regulation of adherens						
GO:1903391	junction organization	0.000346432	0.004368944	0.003326756	11	geneontology_Bio	0.012672811
	regulation of smoothened						
GO:0008589	signaling pathway	0.000352969	0.004440025	0.003380881	12	geneontology_Bio	0.013824885
GO:0061383	trabecula morphogenesis	0.000365624	0.004563012	0.003474531	9	geneontology_Bio	0.010368664
	cyclic nucleotide catabolic						
GO:0009214	process	0.000366448	0.004563012	0.003474531	5	geneontology_Bio	0.005760369
	regulation of macrophage						
GO:0010935	cytokine production	0.000366448	0.004563012	0.003474531	5	geneontology_Bio	0.005760369
GO:0046068	cGMP metabolic process	0.000366448	0.004563012	0.003474531	5	geneontology_Bio	0.005760369
GO:0046058	cAMP metabolic process	0.000368721	0.004579756	0.00348728	6	geneontology_Bio	0.006912442
	positive regulation of cell						
GO:0010770	morphogenesis involved in di	0.000371916	0.004607837	0.003508663	17	geneontology_Bio	0.019585253

	cell communication by						
GO:0010644	electrical coupling	0.000374197	0.004624472	0.003521329	7	geneontology_Bio	0.008064516
GO:0035329	hippo signaling	0.000393469	0.00485049	0.003693432	8	geneontology_Bio	0.00921659
	negative regulation of						
GO:0050805	synaptic transmission	0.000395489	0.004851137	0.003693925	11	geneontology_Bio	0.012672811
	cardiac muscle cell						
GO:0086003	contraction	0.000395489	0.004851137	0.003693925	11	geneontology_Bio	0.012672811
	proteoglycan metabolic						
GO:0006029	process	0.000398162	0.004871806	0.003709663	12	geneontology_Bio	0.013824885
	negative regulation of						
GO:0042326	phosphorylation	0.000413836	0.005051053	0.003846152	39	geneontology_Bio	0.044930876
	positive regulation of small						
GO:0051057	GTPase mediated signal tran	0.000425757	0.005170958	0.003937454	10	geneontology_Bio	0.011520737
GO:0070527	platelet aggregation	0.000425757	0.005170958	0.003937454	10	geneontology_Bio	0.011520737
	regulation of						
GO:0035303	dephosphorylation	0.000436086	0.005283396	0.004023071	22	geneontology_Bio	0.025345622
	epithelial to mesenchymal						
GO:0001837	transition	0.000440693	0.005326123	0.004055606	17	geneontology_Bio	0.019585253
	negative regulation of cell						
GO:0031345	projection organization	0.000444961	0.005364551	0.004084867	19	geneontology_Bio	0.021889401
GO:0070509	calcium ion import	0.000450242	0.005414986	0.00412327	11	geneontology_Bio	0.012672811
	regulation of anatomical						
GO:0090066	structure size	0.000460717	0.005527488	0.004208936	38	geneontology_Bio	0.043778802
GO:0021772	olfactory bulb development	0.000467867	0.00559964	0.004263876	7	geneontology_Bio	0.008064516
	chondroitin sulfate metabolic						
GO:0030204	process	0.000474237	0.005648466	0.004301055	8	geneontology_Bio	0.00921659
	positive regulation of bone						
GO:0030501	mineralization	0.000474237	0.005648466	0.004301055	8	geneontology_Bio	0.00921659
GO:0035051	cardiocyte differentiation	0.000483526	0.005745226	0.004374734	18	geneontology_Bio	0.020737327
GO:0030318	melanocyte differentiation	0.000486355	0.005751121	0.004379223	6	geneontology_Bio	0.006912442

	adrenergic receptor signaling						
GO:0071875	pathway	0.000486355	0.005751121	0.004379223	6	geneontology_Bio	0.006912442
GO:0002040	sprouting angiogenesis	0.000504613	0.005952749	0.004532753	20	geneontology_Bio	0.023041475
	phospholipase C-activating G						
GO:0007200	protein-coupled receptor si	0.0005112	0.006016055	0.004580958	11	geneontology_Bio	0.012672811
GO:0045927	positive regulation of growth	0.000551262	0.00647208	0.0049282	26	geneontology_Bio	0.029953917
	positive regulation of						
GO:0050921	chemotaxis	0.000552581	0.00647216	0.004928261	16	geneontology_Bio	0.01843318
	regulation of synaptic						
GO:0048167	plasticity	0.000556752	0.006490176	0.00494198	19	geneontology_Bio	0.021889401
	negative regulation of						
	canonical Wnt signaling						
GO:0090090	pathway	0.000556752	0.006490176	0.00494198	19	geneontology_Bio	0.021889401
GO:0030593	neutrophil chemotaxis	0.000563723	0.006497682	0.004947696	10	geneontology_Bio	0.011520737
GO:0045445	myoblast differentiation	0.000564092	0.006497682	0.004947696	12	geneontology_Bio	0.013824885
GO:0106106	cold-induced thermogenesis	0.000564327	0.006497682	0.004947696	17	geneontology_Bio	0.019585253
	regulation of cold-induced						
GO:0120161	thermogenesis	0.000564327	0.006497682	0.004947696	17	geneontology_Bio	0.019585253
	negative regulation of cellular						
GO:0090288	response to growth facto	0.000564959	0.006497682	0.004947696	18	geneontology_Bio	0.020737327
	regulation of developmental						
GO:0048638	growth	0.000565812	0.006497682	0.004947696	30	geneontology_Bio	0.034562212
	vascular endothelial growth						
GO:0038084	factor signaling pathway	0.000567938	0.006497682	0.004947696	8	geneontology_Bio	0.00921659
GO:0048286	lung alveolus development	0.000567938	0.006497682	0.004947696	8	geneontology_Bio	0.00921659
GO:0003382	epithelial cell morphogenesis	0.000579317	0.006582057	0.005011944	7	geneontology_Bio	0.008064516
	regulation of release of						
	sequestered calcium ion into						
GO:0010880	cy	0.000579317	0.006582057	0.005011944	7	geneontology_Bio	0.008064516
GO:0021988	olfactory lobe development	0.000579317	0.006582057	0.005011944	7	geneontology_Bio	0.008064516

	positive regulation of						
GO:0048639	developmental growth	0.000581233	0.006588646	0.005016961	20	geneontology_Bio	0.023041475
	regulation of actin filament						
GO:0032231	bundle assembly	0.000588842	0.006659593	0.005070983	13	geneontology_Bio	0.014976959
GO:0048813	dendrite morphogenesis	0.0006018	0.006790561	0.00517071	16	geneontology_Bio	0.01843318
	positive regulation of						
	peptidyl-tyrosine						
GO:0050731	phosphorylation	0.000623183	0.007015789	0.005342211	20	geneontology_Bio	0.023041475
	regulation of stress fiber						
GO:0051492	assembly	0.000630914	0.00703522	0.005357007	12	geneontology_Bio	0.013824885
	semaphorin-plexin signaling						
GO:0071526	pathway	0.000631253	0.00703522	0.005357007	6	geneontology_Bio	0.006912442
	metanephric tubule						
GO:0072170	development	0.000631253	0.00703522	0.005357007	6	geneontology_Bio	0.006912442
	metanephric nephron						
GO:0072243	epithelium development	0.000631253	0.00703522	0.005357007	6	geneontology_Bio	0.006912442
	positive regulation of calcium						
GO:0051928	ion transport	0.000632043	0.00703522	0.005357007	15	geneontology_Bio	0.017281106
	regulation of focal adhesion						
GO:0051893	assembly	0.000645465	0.007152331	0.005446181	10	geneontology_Bio	0.011520737
	regulation of cell-substrate						
GO:0090109	junction assembly	0.000645465	0.007152331	0.005446181	10	geneontology_Bio	0.011520737
GO:0008585	female gonad development	0.000652553	0.007197465	0.005480549	13	geneontology_Bio	0.014976959
	regulation of supramolecular						
GO:1902903	fiber organization	0.000653842	0.007197465	0.005480549	29	geneontology_Bio	0.033410138
	regulation of sodium ion						
GO:0002028	transport	0.000653917	0.007197465	0.005480549	11	geneontology_Bio	0.012672811
GO:0016049	cell growth	0.000658033	0.007226643	0.005502766	39	geneontology_Bio	0.044930876
	neurotransmitter metabolic						
GO:0042133	process	0.000662378	0.007258186	0.005526785	17	geneontology_Bio	0.019585253
GO:0035136	forelimb morphogenesis	0.000676049	0.007391568	0.00562835	8	geneontology_Bio	0.00921659

	regulation of sodium ion						
GO:1902305	transmembrane transport	0.000686495	0.007489179	0.005702676	9	geneontology_Bio	0.010368664
	regulation of calcium ion						
	transmembrane transporter						
GO:1901019	acti	0.000704247	0.007665877	0.005837224	12	geneontology_Bio	0.013824885
GO:0003176	aortic valve development	0.000710861	0.007670148	0.005840476	7	geneontology_Bio	0.008064516
	negative regulation of						
	epithelial to mesenchymal						
GO:0010719	transit	0.000710861	0.007670148	0.005840476	7	geneontology_Bio	0.008064516
	heart trabecula						
GO:0061384	morphogenesis	0.000710861	0.007670148	0.005840476	7	geneontology_Bio	0.008064516
	cell-cell signaling involved in						
GO:0086019	cardiac conduction	0.000710861	0.007670148	0.005840476	7	geneontology_Bio	0.008064516
GO:0048545	response to steroid hormone	0.000713907	0.007686186	0.005852689	33	geneontology_Bio	0.038018433
GO:0021536	diencephalon development	0.000736847	0.007886323	0.006005084	11	geneontology_Bio	0.012672811
	macrophage cytokine						
GO:0010934	production	0.000737294	0.007886323	0.006005084	5	geneontology_Bio	0.005760369
	morphogenesis of an						
GO:0060572	epithelial bud	0.000737294	0.007886323	0.006005084	5	geneontology_Bio	0.005760369
	positive regulation of						
GO:0010634	epithelial cell migration	0.000743005	0.007913083	0.00602546	19	geneontology_Bio	0.021889401
	positive regulation of protein						
GO:0051897	kinase B signaling	0.000743005	0.007913083	0.00602546	19	geneontology_Bio	0.021889401
GO:0000187	activation of MAPK activity	0.000774674	0.008232582	0.006268744	17	geneontology_Bio	0.019585253
	positive regulation of striated						
GO:0045844	muscle tissue developmen	0.000784579	0.008302053	0.006321644	12	geneontology_Bio	0.013824885
	positive regulation of muscle						
GO:0048636	organ development	0.000784579	0.008302053	0.006321644	12	geneontology_Bio	0.013824885
GO:0048747	muscle fiber development	0.000795052	0.00839486	0.006392312	9	geneontology_Bio	0.010368664
	atrioventricular valve						
GO:0003181	morphogenesis	0.000807479	0.008453674	0.006437096	6	geneontology_Bio	0.006912442

	endocardial cushion						
GO:0003272	formation	0.000807479	0.008453674	0.006437096	6	geneontology_Bio	0.006912442
	regulation of cardiac muscle						
GO:0010881	contraction by regulation o	0.000807479	0.008453674	0.006437096	6	geneontology_Bio	0.006912442
	regulation of endothelial cell						
GO:2001026	chemotaxis	0.000807479	0.008453674	0.006437096	6	geneontology_Bio	0.006912442
GO:0021675	nerve development	0.000828324	0.008653531	0.006589278	11	geneontology_Bio	0.012672811
	positive regulation of cardiac						
GO:0055025	muscle tissue development	0.000838395	0.008740223	0.006655529	10	geneontology_Bio	0.011520737
	regulation of peptidyl-						
GO:0050730	tyrosine phosphorylation	0.000857975	0.008925478	0.006796354	24	geneontology_Bio	0.02764977
	regulation of vascular						
	endothelial growth factor						
GO:0030947	recepto	0.000864966	0.00897926	0.006837307	7	geneontology_Bio	0.008064516
	substrate adhesion-dependent						
GO:0034446	cell spreading	0.000872421	0.009037619	0.006881745	12	geneontology_Bio	0.013824885
GO:0099504	synaptic vesicle cycle	0.000883899	0.009137329	0.006957669	18	geneontology_Bio	0.020737327
	actomyosin structure						
GO:0031032	organization	0.000949782	0.009797854	0.00746063	18	geneontology_Bio	0.020737327
	glutamate receptor signaling						
GO:0007215	pathway	0.00096831	0.009968135	0.007590291	12	geneontology_Bio	0.013824885
	central nervous system						
GO:0021953	neuron differentiation	0.000980523	0.01007283	0.007670011	19	geneontology_Bio	0.021889401
GO:1901654	response to ketone	0.000997101	0.010198599	0.007765779	20	geneontology_Bio	0.023041475
GO:0060004	reflex	0.001003107	0.010198599	0.007765779	5	geneontology_Bio	0.005760369
	cell proliferation involved in						
GO:0061323	heart morphogenesis	0.001003107	0.010198599	0.007765779	5	geneontology_Bio	0.005760369
	regulation of cell proliferation						
GO:2000136	involved in heart morph	0.001003107	0.010198599	0.007765779	5	geneontology_Bio	0.005760369
GO:2000811	negative regulation of anoikis	0.001003107	0.010198599	0.007765779	5	geneontology_Bio	0.005760369

	negative regulation of cytokine production involved in i	0.001019355	0.010321227	0.007859154	6	geneontology_Bio	0.006912442
GO:0002719	regulation of ryanodine-sensitive calcium-release						
GO:0060314	channel	0.001019355	0.010321227	0.007859154	6	geneontology_Bio	0.006912442
GO:0048844	artery morphogenesis	0.001039612	0.010504765	0.007998911	11	geneontology_Bio	0.012672811
	dopamine receptor signaling pathway						
GO:0007212	salivary gland morphogenesis	0.001044247	0.010508532	0.008001779	7	geneontology_Bio	0.008064516
GO:0007435	phosphatidylinositol 3-kinase signaling	0.001044247	0.010508532	0.008001779	7	geneontology_Bio	0.008064516
GO:0014065	mammary gland development	0.001063096	0.010633113	0.008096642	16	geneontology_Bio	0.01843318
GO:0030879	development of primary male sexual characteristics	0.001063096	0.010633113	0.008096642	16	geneontology_Bio	0.01843318
GO:0046546	cellular response to vascular endothelial growth factor	0.001076334	0.01074373	0.008180872	10	geneontology_Bio	0.011520737
GO:0035924	epithelial cell differentiation involved in kidney development	0.001103057	0.010966075	0.008350178	8	geneontology_Bio	0.00921659
GO:0035850	purine-containing compound catabolic process	0.001103057	0.010966075	0.008350178	8	geneontology_Bio	0.00921659
GO:0072523	regulation of phosphoprotein phosphatase activity	0.001123057	0.011142444	0.008484474	14	geneontology_Bio	0.016129032
GO:0043666	regulation of muscle tissue development	0.001128797	0.011154506	0.008493659	17	geneontology_Bio	0.019585253
GO:1901861	adaptive thermogenesis	0.001128797	0.011154506	0.008493659	17	geneontology_Bio	0.019585253
GO:1990845	homotypic cell-cell adhesion	0.001160848	0.011448287	0.00871736	11	geneontology_Bio	0.012672811
GO:0034109	negative regulation of production of molecular mediator	0.001251461	0.012219709	0.009304764	7	geneontology_Bio	0.008064516
GO:0002701							

	endocardial cushion						
GO:0003203	morphogenesis	0.001251461	0.012219709	0.009304764	7	geneontology_Bio	0.008064516
	release of sequestered calcium ion into cytosol by						
GO:0014808	sarco	0.001251461	0.012219709	0.009304764	7	geneontology_Bio	0.008064516
	mesodermal cell						
GO:0048333	differentiation	0.001251461	0.012219709	0.009304764	7	geneontology_Bio	0.008064516
	negative regulation of animal						
GO:0110111	organ morphogenesis	0.001251461	0.012219709	0.009304764	7	geneontology_Bio	0.008064516
	positive regulation of cell						
GO:0045785	adhesion	0.001270171	0.012341441	0.009397457	33	geneontology_Bio	0.038018433
	atrioventricular valve						
GO:0003171	development	0.001271436	0.012341441	0.009397457	6	geneontology_Bio	0.006912442
GO:0060914	heart formation	0.001271436	0.012341441	0.009397457	6	geneontology_Bio	0.006912442
	regulation of body fluid						
GO:0050878	levels	0.001286224	0.012460455	0.009488081	40	geneontology_Bio	0.046082949
	regulation of release of sequestered calcium ion into						
GO:0051279	cy	0.001293485	0.012506228	0.009522935	11	geneontology_Bio	0.012672811
	regulation of extent of cell						
GO:0061387	growth	0.00130999	0.012641019	0.009625573	12	geneontology_Bio	0.013824885
	regulation of transforming						
GO:0017015	growth factor beta receptor s	0.00133359	0.012747462	0.009706625	14	geneontology_Bio	0.016129032
	actin-mediated cell						
GO:0070252	contraction	0.00133359	0.012747462	0.009706625	14	geneontology_Bio	0.016129032
	cyclic nucleotide biosynthetic						
GO:0009190	process	0.001333947	0.012747462	0.009706625	5	geneontology_Bio	0.005760369
	embryonic digestive tract						
GO:0048557	morphogenesis	0.001333947	0.012747462	0.009706625	5	geneontology_Bio	0.005760369
	cyclic purine nucleotide						
GO:0052652	metabolic process	0.001333947	0.012747462	0.009706625	5	geneontology_Bio	0.005760369

GO:0060326	cell chemotaxis	0.001337879	0.012760314	0.009716411	24	geneontology_Bio	0.02764977
	negative regulation of cell-						
GO:0010812	substrate adhesion	0.001366795	0.012987635	0.009889506	10	geneontology_Bio	0.011520737
GO:0086016	AV node cell action potential	0.001374066	0.012987635	0.009889506	4	geneontology_Bio	0.004608295
	AV node cell to bundle of His						
GO:0086027	cell signaling	0.001374066	0.012987635	0.009889506	4	geneontology_Bio	0.004608295
	negative regulation of						
	adenylate cyclase-activating						
GO:0106072	G pr	0.001374066	0.012987635	0.009889506	4	geneontology_Bio	0.004608295
	cardiac muscle cell action						
GO:0086002	potential involved in contrac	0.001377516	0.012987635	0.009889506	9	geneontology_Bio	0.010368664
	regulation of glutamate						
GO:1900449	receptor signaling pathway	0.001377516	0.012987635	0.009889506	9	geneontology_Bio	0.010368664
GO:0007612	learning	0.001441247	0.013536078	0.01030712	16	geneontology_Bio	0.01843318
	cellular component assembly						
GO:0010927	involved in morphogenesis	0.001443921	0.013536078	0.01030712	12	geneontology_Bio	0.013824885
GO:0014909	smooth muscle cell migration	0.001443921	0.013536078	0.01030712	12	geneontology_Bio	0.013824885
	regulation of heart rate by						
GO:0086091	cardiac conduction	0.001489503	0.013899299	0.010583697	7	geneontology_Bio	0.008064516
	release of sequestered						
	calcium ion into cytosol by						
GO:1903514	endop	0.001489503	0.013899299	0.010583697	7	geneontology_Bio	0.008064516
	positive regulation of						
	biomineral tissue						
GO:0070169	development	0.001491123	0.013899299	0.010583697	8	geneontology_Bio	0.00921659
	positive regulation of						
GO:0032103	response to external stimulus	0.001506763	0.014018584	0.010674527	28	geneontology_Bio	0.032258065
GO:0042698	ovulation cycle	0.001534262	0.01422076	0.010828475	10	geneontology_Bio	0.011520737
	cardiac muscle cell						
GO:0060038	proliferation	0.001534262	0.01422076	0.010828475	10	geneontology_Bio	0.011520737

	negative regulation of Wnt						
GO:0030178	signaling pathway	0.001549092	0.014331281	0.010912632	20	geneontology_Bio	0.023041475
	regulation of morphogenesis						
GO:0060688	of a branching structure	0.001566783	0.014392441	0.010959202	9	geneontology_Bio	0.010368664
	regulation of the force of						
GO:0002026	heart contraction	0.001568497	0.014392441	0.010959202	6	geneontology_Bio	0.006912442
	negative regulation of						
	peptidyl-serine						
GO:0033137	phosphorylation	0.001568497	0.014392441	0.010959202	6	geneontology_Bio	0.006912442
	regulation of adenylate						
GO:0045761	cyclase activity	0.001568497	0.014392441	0.010959202	6	geneontology_Bio	0.006912442
	formation of primary germ						
GO:0001704	layer	0.001576134	0.014392441	0.010959202	14	geneontology_Bio	0.016129032
	regulation of						
	phosphatidylinositol 3-kinase						
GO:0014066	signaling	0.001576134	0.014392441	0.010959202	14	geneontology_Bio	0.016129032
	regulation of cellular						
	response to transforming						
GO:1903844	growth f	0.001576134	0.014392441	0.010959202	14	geneontology_Bio	0.016129032
GO:0043087	regulation of GTPase activity	0.001653855	0.015074227	0.011478352	34	geneontology_Bio	0.039170507
GO:0016311	dephosphorylation	0.001678359	0.01526935	0.01162693	37	geneontology_Bio	0.042626728
GO:0033002	muscle cell proliferation	0.0017173	0.015572477	0.011857747	23	geneontology_Bio	0.026497696
	T cell differentiation in						
GO:0033077	thymus	0.001717994	0.015572477	0.011857747	10	geneontology_Bio	0.011520737
	positive regulation of						
	vascular endothelial growth						
GO:0030949	facto	0.001738798	0.015674614	0.011935521	5	geneontology_Bio	0.005760369
GO:0060039	pericardium development	0.001738798	0.015674614	0.011935521	5	geneontology_Bio	0.005760369
	regulation of epithelial cell						
GO:2000696	differentiation involved i	0.001738798	0.015674614	0.011935521	5	geneontology_Bio	0.005760369

	negative regulation of						
GO:0009895	catabolic process	0.00175725	0.015812041	0.012040165	26	geneontology_Bio	0.029953917
GO:0046209	nitric oxide metabolic process	0.001767904	0.015878938	0.012091104	11	geneontology_Bio	0.012672811
GO:0007405	neuroblast proliferation	0.00177636	0.015925872	0.012126842	9	geneontology_Bio	0.010368664
	positive regulation of						
GO:0050806	synaptic transmission	0.001794114	0.016055853	0.012225817	16	geneontology_Bio	0.01843318
	regulation of muscle						
GO:0043502	adaptation	0.001827297	0.016323191	0.012429383	13	geneontology_Bio	0.014976959
GO:0055001	muscle cell development	0.001848559	0.016483262	0.01255127	17	geneontology_Bio	0.019585253
	integrin-mediated signaling						
GO:0007229	pathway	0.00191507	0.01692712	0.012889248	12	geneontology_Bio	0.013824885
	regulation of actomyosin						
GO:0110020	structure organization	0.00191507	0.01692712	0.012889248	12	geneontology_Bio	0.013824885
	regulation of cardiac muscle						
GO:0010882	contraction by calcium ion	0.0019155	0.01692712	0.012889248	6	geneontology_Bio	0.006912442
	forebrain neuron						
GO:0021884	development	0.0019155	0.01692712	0.012889248	6	geneontology_Bio	0.006912442
GO:0085029	extracellular matrix assembly	0.0019155	0.01692712	0.012889248	6	geneontology_Bio	0.006912442
GO:0048588	developmental cell growth	0.001927223	0.017000244	0.012944929	21	geneontology_Bio	0.024193548
	regulation of endothelial cell						
GO:0010594	migration	0.001979416	0.017332648	0.013198039	22	geneontology_Bio	0.025345622
	peptidyl-serine						
GO:0018105	phosphorylation	0.001979416	0.017332648	0.013198039	22	geneontology_Bio	0.025345622
	ventricular cardiac muscle						
GO:0055010	tissue morphogenesis	0.001980211	0.017332648	0.013198039	8	geneontology_Bio	0.00921659
	pathway-restricted SMAD						
GO:0060389	protein phosphorylation	0.001980211	0.017332648	0.013198039	8	geneontology_Bio	0.00921659
	regulation of cell						
	communication by electrical						
GO:0010649	coupling	0.001982481	0.017332648	0.013198039	4	geneontology_Bio	0.004608295
GO:0007431	salivary gland development	0.002070282	0.018068246	0.013758164	7	geneontology_Bio	0.008064516

	vascular process in						
GO:0003018	circulatory system	0.002113938	0.018416657	0.014023464	17	geneontology_Bio	0.019585253
GO:0060348	bone development	0.002118054	0.018419973	0.014025989	19	geneontology_Bio	0.021889401
GO:0001707	mesoderm formation	0.002138835	0.01856795	0.014138667	10	geneontology_Bio	0.011520737
GO:1990138	neuron projection extension	0.002216617	0.019197091	0.01461773	16	geneontology_Bio	0.01843318
	positive regulation of phosphoprotein phosphatase activi						
GO:0032516	metanephric nephron tubule development	0.002226878	0.019197091	0.01461773	5	geneontology_Bio	0.005760369
GO:0072234	positive regulation of stem cell differentiation	0.002226878	0.019197091	0.01461773	5	geneontology_Bio	0.005760369
GO:2000738	exocrine system development	0.002226878	0.019197091	0.01461773	5	geneontology_Bio	0.005760369
GO:0035272	substrate-dependent cell migration	0.00226796	0.019517124	0.014861421	8	geneontology_Bio	0.00921659
GO:0006929	endocrine system development	0.00231758	0.019909383	0.015160108	6	geneontology_Bio	0.006912442
GO:0035270	regulation of striated muscle tissue development	0.002347132	0.02012819	0.01532672	14	geneontology_Bio	0.016129032
GO:0016202	positive regulation of transmembrane receptor protein se	0.002374664	0.020265393	0.015431194	16	geneontology_Bio	0.01843318
GO:0090100	reactive nitrogen species metabolic process	0.002375461	0.020265393	0.015431194	11	geneontology_Bio	0.012672811
GO:2001057	purine nucleotide catabolic process	0.002375461	0.020265393	0.015431194	11	geneontology_Bio	0.012672811
GO:0006195	neurotrophin signaling pathway	0.002419416	0.020533807	0.015635579	7	geneontology_Bio	0.008064516
GO:0038179	positive regulation of cardiac muscle cell proliferation	0.002419416	0.020533807	0.015635579	7	geneontology_Bio	0.008064516

	embryonic digit						
GO:0042733	morphogenesis	0.002542494	0.021541303	0.016402743	9	geneontology_Bio	0.010368664
	sodium ion transmembrane						
GO:0035725	transport	0.0025512	0.021577984	0.016430674	13	geneontology_Bio	0.014976959
	positive regulation of						
	epithelial to mesenchymal						
GO:0010718	transit	0.002587506	0.021847592	0.016635968	8	geneontology_Bio	0.00921659
	cardiac ventricle						
GO:0003208	morphogenesis	0.002638892	0.022205421	0.016908439	10	geneontology_Bio	0.011520737
GO:0048332	mesoderm morphogenesis	0.002638892	0.022205421	0.016908439	10	geneontology_Bio	0.011520737
GO:0008584	male gonad development	0.00265296	0.022285767	0.016969619	15	geneontology_Bio	0.017281106
GO:0001649	osteoblast differentiation	0.002685258	0.02251872	0.017147002	21	geneontology_Bio	0.024193548
	regulation of extrinsic						
GO:2001236	apoptotic signaling pathway	0.002718957	0.022762612	0.017332715	16	geneontology_Bio	0.01843318
	neurotransmitter biosynthetic						
GO:0042136	process	0.002732269	0.022828018	0.017382519	12	geneontology_Bio	0.013824885
	regulation of skeletal muscle						
GO:0014842	satellite cell proliferati	0.002754547	0.022828018	0.017382519	4	geneontology_Bio	0.004608295
GO:0021554	optic nerve development	0.002754547	0.022828018	0.017382519	4	geneontology_Bio	0.004608295
	regulation of cell fate						
GO:0042659	specification	0.002754547	0.022828018	0.017382519	4	geneontology_Bio	0.004608295
	negative regulation of						
GO:0043116	vascular permeability	0.002754547	0.022828018	0.017382519	4	geneontology_Bio	0.004608295
	regulation of nephron tubule						
GO:0072182	epithelial cell differentia	0.002754547	0.022828018	0.017382519	4	geneontology_Bio	0.004608295
GO:1901214	regulation of neuron death	0.002768343	0.022903855	0.017440265	27	geneontology_Bio	0.031105991
	positive regulation of						
GO:0051491	filopodium assembly	0.002780008	0.022961841	0.017484419	6	geneontology_Bio	0.006912442
	retinal ganglion cell axon						
GO:0031290	guidance	0.002807552	0.023150569	0.017628127	5	geneontology_Bio	0.005760369
GO:0006813	potassium ion transport	0.002846628	0.023415105	0.017829559	19	geneontology_Bio	0.021889401

	synaptic transmission,						
GO:0035249	glutamatergic	0.002849131	0.023415105	0.017829559	9	geneontology_Bio	0.010368664
	long-term synaptic						
GO:0060291	potentiation	0.002921793	0.023972318	0.018253852	10	geneontology_Bio	0.011520737
	positive regulation of Ras						
GO:0046579	protein signal transduction	0.002941183	0.024068258	0.018326906	8	geneontology_Bio	0.00921659
GO:0009581	detection of external stimulus	0.002943249	0.024068258	0.018326906	14	geneontology_Bio	0.016129032
GO:0007613	memory	0.002992746	0.024311749	0.018512314	13	geneontology_Bio	0.014976959
	release of sequestered						
GO:0051209	calcium ion into cytosol	0.002992746	0.024311749	0.018512314	13	geneontology_Bio	0.014976959
	negative regulation of						
GO:0051283	sequestering of calcium ion	0.002992746	0.024311749	0.018512314	13	geneontology_Bio	0.014976959
GO:0060419	heart growth	0.002992746	0.024311749	0.018512314	13	geneontology_Bio	0.014976959
	regulation of morphogenesis						
GO:1905330	of an epithelium	0.003076032	0.024947229	0.018996203	18	geneontology_Bio	0.020737327
	regulation of neuron						
GO:0043523	apoptotic process	0.003097747	0.025082083	0.019098889	20	geneontology_Bio	0.023041475
	regulation of muscle organ						
GO:0048634	development	0.003103639	0.025088596	0.019103848	16	geneontology_Bio	0.01843318
GO:0097530	granulocyte migration	0.003236059	0.026031362	0.019821723	12	geneontology_Bio	0.013824885
	positive regulation of axon						
GO:0045773	extension	0.003251941	0.026031362	0.019821723	7	geneontology_Bio	0.008064516
	sarcoplasmic reticulum						
GO:0070296	calcium ion transport	0.003251941	0.026031362	0.019821723	7	geneontology_Bio	0.008064516
	metanephric nephron						
GO:0072210	development	0.003251941	0.026031362	0.019821723	7	geneontology_Bio	0.008064516
	inorganic cation import						
GO:0098659	across plasma membrane	0.003251941	0.026031362	0.019821723	7	geneontology_Bio	0.008064516
	inorganic ion import across						
GO:0099587	plasma membrane	0.003251941	0.026031362	0.019821723	7	geneontology_Bio	0.008064516

	cellular potassium ion						
GO:0071804	transport	0.003269733	0.026089084	0.019865675	15	geneontology_Bio	0.017281106
	potassium ion transmembrane						
GO:0071805	transport	0.003269733	0.026089084	0.019865675	15	geneontology_Bio	0.017281106
	positive regulation of sodium						
GO:0010765	ion transport	0.003308174	0.026268284	0.020002128	6	geneontology_Bio	0.006912442
GO:0035767	endothelial cell chemotaxis	0.003308174	0.026268284	0.020002128	6	geneontology_Bio	0.006912442
	regulation of presynapse						
GO:0099174	organization	0.003308174	0.026268284	0.020002128	6	geneontology_Bio	0.006912442
GO:0001558	regulation of cell growth	0.003323829	0.026350159	0.020064472	32	geneontology_Bio	0.036866359
	regulation of protein kinase B						
GO:0051896	signaling	0.003339565	0.026432419	0.02012711	22	geneontology_Bio	0.025345622
	calcium ion regulated						
GO:0017156	exocytosis	0.003405665	0.026869336	0.020459802	14	geneontology_Bio	0.016129032
	regulation of postsynaptic						
GO:0060078	membrane potential	0.003405665	0.026869336	0.020459802	14	geneontology_Bio	0.016129032
GO:0033622	integrin activation	0.003490257	0.027352818	0.020827952	5	geneontology_Bio	0.005760369
	positive regulation of cAMP-						
GO:0043950	mediated signaling	0.003490257	0.027352818	0.020827952	5	geneontology_Bio	0.005760369
GO:0098810	neurotransmitter reuptake	0.003490257	0.027352818	0.020827952	5	geneontology_Bio	0.005760369
	regulation of non-canonical						
GO:2000050	Wnt signaling pathway	0.003490257	0.027352818	0.020827952	5	geneontology_Bio	0.005760369
	regulation of sequestering of						
GO:0051282	calcium ion	0.003494682	0.027352818	0.020827952	13	geneontology_Bio	0.014976959
	regulation of cardiac muscle						
GO:0055024	tissue development	0.003514716	0.02746603	0.020914159	12	geneontology_Bio	0.013824885
	nitric oxide biosynthetic						
GO:0006809	process	0.003560006	0.02773205	0.021116721	10	geneontology_Bio	0.011520737
GO:0060415	muscle tissue morphogenesis	0.003560006	0.02773205	0.021116721	10	geneontology_Bio	0.011520737
GO:0002576	platelet degranulation	0.003658188	0.028407124	0.02163076	14	geneontology_Bio	0.016129032
GO:0007498	mesoderm development	0.003658188	0.028407124	0.02163076	14	geneontology_Bio	0.016129032

GO:0003128	heart field specification	0.003709787	0.028538156	0.021730535	4	geneontology_Bio	0.004608295
	skeletal muscle satellite cell						
GO:0014841	proliferation	0.003709787	0.028538156	0.021730535	4	geneontology_Bio	0.004608295
	regulation of skeletal muscle						
GO:0014857	cell proliferation	0.003709787	0.028538156	0.021730535	4	geneontology_Bio	0.004608295
	embryonic skeletal joint						
GO:0072498	development	0.003709787	0.028538156	0.021730535	4	geneontology_Bio	0.004608295
	regulation of transcription						
	from RNA polymerase II						
GO:1901213	promo	0.003709787	0.028538156	0.021730535	4	geneontology_Bio	0.004608295
	regulation of Wnt signaling						
GO:2000095	pathway, planar cell polarit	0.003709787	0.028538156	0.021730535	4	geneontology_Bio	0.004608295
	regulation of cardiac muscle						
GO:0086004	cell contraction	0.0037423	0.028743427	0.021886839	7	geneontology_Bio	0.008064516
	proteoglycan biosynthetic						
GO:0030166	process	0.003760582	0.028762214	0.021901145	8	geneontology_Bio	0.00921659
	positive regulation of heart						
GO:0060421	growth	0.003760582	0.028762214	0.021901145	8	geneontology_Bio	0.00921659
GO:0042471	ear morphogenesis	0.003770115	0.028762214	0.021901145	13	geneontology_Bio	0.014976959
GO:0002064	epithelial cell development	0.00377391	0.028762214	0.021901145	19	geneontology_Bio	0.021889401
	positive regulation of						
GO:0034764	transmembrane transport	0.00377391	0.028762214	0.021901145	19	geneontology_Bio	0.021889401
GO:0050931	pigment cell differentiation	0.003907553	0.029734793	0.022641721	6	geneontology_Bio	0.006912442
GO:0008306	associative learning	0.003918089	0.029769023	0.022667785	10	geneontology_Bio	0.011520737
	cellular response to retinoic						
GO:0071300	acid	0.003947145	0.029897652	0.02276573	9	geneontology_Bio	0.010368664
	cranial skeletal system						
GO:1904888	development	0.003947145	0.029897652	0.02276573	9	geneontology_Bio	0.010368664
GO:0023061	signal release	0.003967755	0.030007671	0.022849505	34	geneontology_Bio	0.039170507
GO:0043542	endothelial cell migration	0.003990221	0.03013136	0.022943688	24	geneontology_Bio	0.02764977

	regulation of cell junction						
GO:1901888	assembly	0.004095358	0.030877999	0.02351222	11	geneontology_Bio	0.012672811
GO:0014812	muscle cell migration	0.004130037	0.03109193	0.023675119	12	geneontology_Bio	0.013824885
GO:0050900	leukocyte migration	0.004163287	0.03129446	0.023829337	36	geneontology_Bio	0.041474654
	establishment or maintenance						
GO:0007163	of cell polarity	0.004208336	0.031584937	0.024050523	17	geneontology_Bio	0.019585253
GO:0001945	lymph vessel development	0.004284425	0.031882843	0.024277365	5	geneontology_Bio	0.005760369
	positive regulation of						
	synaptic transmission,						
GO:0051968	glutamater	0.004284425	0.031882843	0.024277365	5	geneontology_Bio	0.005760369
	regulation of metanephros						
GO:0072215	development	0.004284425	0.031882843	0.024277365	5	geneontology_Bio	0.005760369
	regulation of vascular						
	endothelial growth factor						
GO:1900746	signali	0.004284425	0.031882843	0.024277365	5	geneontology_Bio	0.005760369
GO:0010761	fibroblast migration	0.004286823	0.031882843	0.024277365	7	geneontology_Bio	0.008064516
	mammary gland						
GO:0060443	morphogenesis	0.004286823	0.031882843	0.024277365	7	geneontology_Bio	0.008064516
	negative regulation of cell						
GO:0010771	morphogenesis involved in di	0.00430406	0.03196283	0.024338271	10	geneontology_Bio	0.011520737
	cellular hormone metabolic						
GO:0034754	process	0.004373706	0.032321781	0.024611596	13	geneontology_Bio	0.014976959
GO:0051208	sequestering of calcium ion	0.004373706	0.032321781	0.024611596	13	geneontology_Bio	0.014976959
GO:0015844	monoamine transport	0.004378615	0.032321781	0.024611596	9	geneontology_Bio	0.010368664
	regulation of cartilage						
GO:0061035	development	0.004378615	0.032321781	0.024611596	9	geneontology_Bio	0.010368664
GO:0043393	regulation of protein binding	0.004489785	0.033092866	0.025198744	20	geneontology_Bio	0.023041475
	Rho protein signal						
GO:0007266	transduction	0.004535818	0.033282917	0.025343459	16	geneontology_Bio	0.01843318
	phosphatidylinositol						
GO:0046488	metabolic process	0.004535818	0.033282917	0.025343459	16	geneontology_Bio	0.01843318

	sensory perception of						
GO:0050954	mechanical stimulus	0.004535818	0.033282917	0.025343459	16	geneontology_Bio	0.01843318
	striated muscle cell						
GO:0055002	development	0.004556412	0.033384348	0.025420694	15	geneontology_Bio	0.017281106
GO:0007340	acrosome reaction	0.004583684	0.033435127	0.02545936	6	geneontology_Bio	0.006912442
	neurotrophin TRK receptor						
GO:0048011	signaling pathway	0.004583684	0.033435127	0.02545936	6	geneontology_Bio	0.006912442
	apoptotic process involved in						
GO:1902742	development	0.004583684	0.033435127	0.02545936	6	geneontology_Bio	0.006912442
GO:0001708	cell fate specification	0.004719385	0.034374132	0.02617437	10	geneontology_Bio	0.011520737
	cellular response to						
	transforming growth factor						
GO:0071560	beta sti	0.004728399	0.03438899	0.026185684	21	geneontology_Bio	0.024193548
GO:0098900	regulation of action potential	0.004746031	0.03446639	0.026244621	8	geneontology_Bio	0.00921659
	actin filament-based						
GO:0030048	movement	0.004825323	0.034830899	0.026522178	14	geneontology_Bio	0.016129032
GO:0006821	chloride transport	0.004849817	0.034830899	0.026522178	11	geneontology_Bio	0.012672811
	negative regulation of neuron						
GO:0043524	apoptotic process	0.004857521	0.034830899	0.026522178	15	geneontology_Bio	0.017281106
	skeletal muscle cell						
GO:0014856	proliferation	0.004866861	0.034830899	0.026522178	4	geneontology_Bio	0.004608295
	detection of temperature						
	stimulus involved in sensory						
GO:0050961	pe	0.004866861	0.034830899	0.026522178	4	geneontology_Bio	0.004608295
	detection of temperature						
	stimulus involved in sensory						
GO:0050965	pe	0.004866861	0.034830899	0.026522178	4	geneontology_Bio	0.004608295
GO:0051923	sulfation	0.004866861	0.034830899	0.026522178	4	geneontology_Bio	0.004608295
	venous blood vessel						
GO:0060841	development	0.004866861	0.034830899	0.026522178	4	geneontology_Bio	0.004608295

	nephron tubule epithelial cell						
GO:0072160	differentiation	0.004866861	0.034830899	0.026522178	4	geneontology_Bio	0.004608295
	positive regulation of						
GO:2001028	endothelial cell chemotaxis	0.004866861	0.034830899	0.026522178	4	geneontology_Bio	0.004608295
	autonomic nervous system						
GO:0048483	development	0.004889157	0.03493976	0.026605071	7	geneontology_Bio	0.008064516
	central nervous system						
	projection neuron						
GO:0021952	axonogenesis	0.005199411	0.036820791	0.028037392	5	geneontology_Bio	0.005760369
GO:0031069	hair follicle morphogenesis	0.005199411	0.036820791	0.028037392	5	geneontology_Bio	0.005760369
	regulation of activin receptor						
GO:0032925	signaling pathway	0.005199411	0.036820791	0.028037392	5	geneontology_Bio	0.005760369
	glomerulus vasculature						
GO:0072012	development	0.005199411	0.036820791	0.028037392	5	geneontology_Bio	0.005760369
	regulation of cellular						
	response to vascular						
GO:1902547	endothelial	0.005199411	0.036820791	0.028037392	5	geneontology_Bio	0.005760369
GO:2000209	regulation of anoikis	0.005199411	0.036820791	0.028037392	5	geneontology_Bio	0.005760369
GO:0055017	cardiac muscle tissue growth	0.00521211	0.036820791	0.028037392	12	geneontology_Bio	0.013824885
	regulation of synaptic vesicle						
GO:0098693	cycle	0.00521211	0.036820791	0.028037392	12	geneontology_Bio	0.013824885
GO:0035282	segmentation	0.005266214	0.037149788	0.028287909	11	geneontology_Bio	0.012672811
	carbohydrate derivative						
GO:1901136	catabolic process	0.005302716	0.037333861	0.028428072	17	geneontology_Bio	0.019585253
	positive regulation of protein						
GO:0061098	tyrosine kinase activity	0.00530745	0.037333861	0.028428072	8	geneontology_Bio	0.00921659
	regulation of mesenchymal						
GO:0010464	cell proliferation	0.005342135	0.037364634	0.028451504	6	geneontology_Bio	0.006912442
	central nervous system						
GO:0021955	neuron axonogenesis	0.005342135	0.037364634	0.028451504	6	geneontology_Bio	0.006912442
GO:0060428	lung epithelium development	0.005342135	0.037364634	0.028451504	6	geneontology_Bio	0.006912442

GO:0097009	energy homeostasis	0.005342135	0.037364634	0.028451504	6	geneontology_Bio	0.006912442
GO:0003014	renal system process	0.005422778	0.037874957	0.028840093	13	geneontology_Bio	0.014976959
GO:0030509	BMP signaling pathway	0.005512521	0.038447302	0.029275908	14	geneontology_Bio	0.016129032
GO:0050922	negative regulation of chemotaxis	0.005552991	0.03867486	0.029449183	7	geneontology_Bio	0.008064516
GO:0014902	myotube differentiation	0.005619112	0.03908017	0.029757808	12	geneontology_Bio	0.013824885
GO:0014068	positive regulation of phosphatidylinositol 3-kinase sig	0.005644101	0.039143549	0.029806069	10	geneontology_Bio	0.011520737
GO:0030510	regulation of BMP signaling pathway	0.005644101	0.039143549	0.029806069	10	geneontology_Bio	0.011520737
GO:1990823	response to leukemia inhibitory factor	0.005710342	0.039491858	0.030071291	11	geneontology_Bio	0.012672811
GO:1990830	cellular response to leukemia inhibitory factor	0.005710342	0.039491858	0.030071291	11	geneontology_Bio	0.012672811
GO:0045444	fat cell differentiation	0.005772693	0.039867153	0.030357061	20	geneontology_Bio	0.023041475
GO:0043500	muscle adaptation	0.005814062	0.040040695	0.030489206	13	geneontology_Bio	0.014976959
GO:0055007	cardiac muscle cell differentiation	0.005814062	0.040040695	0.030489206	13	geneontology_Bio	0.014976959
GO:0007596	blood coagulation	0.005879636	0.040435823	0.030790078	27	geneontology_Bio	0.031105991
GO:0007369	gastrulation	0.005931159	0.040733347	0.031016629	17	geneontology_Bio	0.019585253
GO:0048644	muscle organ morphogenesis	0.006156558	0.042064562	0.03203029	10	geneontology_Bio	0.011520737
GO:0042472	inner ear morphogenesis	0.006183439	0.042064562	0.03203029	11	geneontology_Bio	0.012672811
GO:0120034	positive regulation of plasma membrane bounded cell proj	0.006183439	0.042064562	0.03203029	11	geneontology_Bio	0.012672811
GO:0003230	cardiac atrium development	0.006188481	0.042064562	0.03203029	6	geneontology_Bio	0.006912442
GO:2000310	regulation of NMDA receptor activity	0.006188481	0.042064562	0.03203029	6	geneontology_Bio	0.006912442
GO:0030902	hindbrain development	0.0062275	0.042064562	0.03203029	15	geneontology_Bio	0.017281106
GO:0003222	ventricular trabecula myocardium morphogenesis	0.006243383	0.042064562	0.03203029	4	geneontology_Bio	0.004608295

	response to follicle-						
GO:0032354	stimulating hormone	0.006243383	0.042064562	0.03203029	4	geneontology_Bio	0.004608295
GO:0055119	relaxation of cardiac muscle	0.006243383	0.042064562	0.03203029	4	geneontology_Bio	0.004608295
GO:0072189	ureter development	0.006243383	0.042064562	0.03203029	4	geneontology_Bio	0.004608295
	metanephric glomerulus						
GO:0072224	development	0.006243383	0.042064562	0.03203029	4	geneontology_Bio	0.004608295
GO:0097091	synaptic vesicle clustering	0.006243383	0.042064562	0.03203029	4	geneontology_Bio	0.004608295
GO:0021544	subpallium development	0.006244425	0.042064562	0.03203029	5	geneontology_Bio	0.005760369
	ionotropic glutamate receptor						
GO:0035235	signaling pathway	0.006244425	0.042064562	0.03203029	5	geneontology_Bio	0.005760369
GO:0007219	Notch signaling pathway	0.006267336	0.042087992	0.032048131	17	geneontology_Bio	0.019585253
	negative regulation of BMP						
GO:0030514	signaling pathway	0.006282045	0.042087992	0.032048131	7	geneontology_Bio	0.008064516
GO:0055078	sodium ion homeostasis	0.006282045	0.042087992	0.032048131	7	geneontology_Bio	0.008064516
GO:0060324	face development	0.006282045	0.042087992	0.032048131	7	geneontology_Bio	0.008064516
	response to transforming						
GO:0071559	growth factor beta	0.006301371	0.042160192	0.032103108	21	geneontology_Bio	0.024193548
	fibroblast growth factor						
GO:0008543	receptor signaling pathway	0.006508627	0.043429011	0.033069257	12	geneontology_Bio	0.013824885
	peptidyl-threonine						
GO:0018210	modification	0.006508627	0.043429011	0.033069257	12	geneontology_Bio	0.013824885
	positive regulation of actin						
GO:0032233	filament bundle assembly	0.006580861	0.043733458	0.03330108	8	geneontology_Bio	0.00921659
	mechanoreceptor						
GO:0042490	differentiation	0.006580861	0.043733458	0.03330108	8	geneontology_Bio	0.00921659
	regulation of cardiac muscle						
GO:0060043	cell proliferation	0.006580861	0.043733458	0.03330108	8	geneontology_Bio	0.00921659
	regulation of epithelial cell						
GO:0030856	differentiation	0.006614472	0.043897658	0.033426111	15	geneontology_Bio	0.017281106
	regulation of ERK1 and						
GO:0070372	ERK2 cascade	0.006638181	0.043995796	0.033500839	23	geneontology_Bio	0.026497696

	regulation of protein						
GO:0035304	dephosphorylation	0.006688692	0.044197688	0.033654571	14	geneontology_Bio	0.016129032
GO:0097479	synaptic vesicle localization	0.006688692	0.044197688	0.033654571	14	geneontology_Bio	0.016129032
	regulation of cytokine						
	production involved in						
GO:0002718	immune res	0.006704496	0.044197688	0.033654571	10	geneontology_Bio	0.011520737
	extrinsic apoptotic signaling						
GO:0008625	pathway via death domain r	0.006704496	0.044197688	0.033654571	10	geneontology_Bio	0.011520737
	regulation of plasma						
	membrane bounded cell						
GO:0120032	projection as	0.006845607	0.045067672	0.034317024	16	geneontology_Bio	0.01843318
	steroid hormone mediated						
GO:0043401	signaling pathway	0.006986035	0.045869692	0.034927727	17	geneontology_Bio	0.019585253
GO:0051099	positive regulation of binding	0.006986035	0.045869692	0.034927727	17	geneontology_Bio	0.019585253
	positive regulation of ion						
GO:0034767	transmembrane transport	0.007020505	0.04603472	0.035053389	15	geneontology_Bio	0.017281106
	negative regulation of cold-						
GO:0120163	induced thermogenesis	0.007080053	0.046302046	0.035256946	7	geneontology_Bio	0.008064516
	regulation of actin filament-						
GO:1903115	based movement	0.007080053	0.046302046	0.035256946	7	geneontology_Bio	0.008064516
	regulation of bone						
GO:0030500	mineralization	0.00711347	0.046367188	0.035306548	9	geneontology_Bio	0.010368664
	negative regulation of MAP						
GO:0043407	kinase activity	0.00711347	0.046367188	0.035306548	9	geneontology_Bio	0.010368664
	regulation of cell fate						
GO:0010453	commitment	0.007128277	0.046367188	0.035306548	6	geneontology_Bio	0.006912442
	detection of mechanical						
GO:0050982	stimulus	0.007128277	0.046367188	0.035306548	6	geneontology_Bio	0.006912442
GO:0007599	hemostasis	0.00713703	0.046367188	0.035306548	27	geneontology_Bio	0.031105991
GO:0042446	hormone biosynthetic process	0.007289501	0.047171299	0.035918843	10	geneontology_Bio	0.011520737
GO:0055006	cardiac cell development	0.007289501	0.047171299	0.035918843	10	geneontology_Bio	0.011520737

GO:0071621	granulocyte chemotaxis	0.007289501	0.047171299	0.035918843	10	geneontology_Bio	0.011520737
GO:0002683	negative regulation of immune system process	0.007327074	0.047352295	0.036056663	34	geneontology_Bio	0.039170507
GO:0009952	anterior/posterior pattern specification	0.00736955	0.047564465	0.036218222	17	geneontology_Bio	0.019585253
GO:0050817	coagulation	0.007413437	0.047633011	0.036270416	27	geneontology_Bio	0.031105991
GO:0060037	pharyngeal system development	0.00742847	0.047633011	0.036270416	5	geneontology_Bio	0.005760369
GO:0061437	renal system vasculature development	0.00742847	0.047633011	0.036270416	5	geneontology_Bio	0.005760369
GO:0061440	kidney vasculature development	0.00742847	0.047633011	0.036270416	5	geneontology_Bio	0.005760369
GO:0099560	synaptic membrane adhesion	0.00742847	0.047633011	0.036270416	5	geneontology_Bio	0.005760369
GO:0051384	response to glucocorticoid	0.007578309	0.048530705	0.03695397	14	geneontology_Bio	0.016129032
GO:0060491	regulation of cell projection assembly	0.007655801	0.048963368	0.037283424	16	geneontology_Bio	0.01843318
GO:0015850	organic hydroxy compound transport	0.00769431	0.04914591	0.037422422	20	geneontology_Bio	0.023041475
GO:0043266	regulation of potassium ion transport	0.007789201	0.049559422	0.037737292	11	geneontology_Bio	0.012672811
GO:0050848	regulation of calcium- mediated signaling	0.007789201	0.049559422	0.037737292	11	geneontology_Bio	0.012672811
GO:0099175	regulation of postsynapse organization	0.007789201	0.049559422	0.037737292	11	geneontology_Bio	0.012672811
GO:0006704	glucocorticoid biosynthetic process	0.007855776	0.049790269	0.037913072	4	geneontology_Bio	0.004608295
GO:0048339	paraxial mesoderm development	0.007855776	0.049790269	0.037913072	4	geneontology_Bio	0.004608295
GO:0060438	trachea development	0.007855776	0.049790269	0.037913072	4	geneontology_Bio	0.004608295
GO:0014910	regulation of smooth muscle cell migration	0.007913175	0.049961419	0.038043395	10	geneontology_Bio	0.011520737

	maintenance of protein						
GO:0045185	location	0.007913175	0.049961419	0.038043395	10	geneontology_Bio	0.011520737
	neuron projection						
GO:0106027	organization	0.007913175	0.049961419	0.038043395	10	geneontology_Bio	0.011520737
GO:0031012	extracellular matrix	7.61E-18	3.51E-15	2.68E-15	71	geneontology_Cel	0.078366446
	collagen-containing						
GO:0062023	extracellular matrix	3.16E-16	7.29E-14	5.58E-14	62	geneontology_Cel	0.068432671
GO:0044449	contractile fiber part	1.05E-11	1.62E-09	1.24E-09	35	geneontology_Cel	0.038631347
GO:0005912	adherens junction	2.11E-11	2.07E-09	1.58E-09	61	geneontology_Cel	0.067328918
GO:0030016	myofibril	2.24E-11	2.07E-09	1.58E-09	35	geneontology_Cel	0.038631347
GO:0043292	contractile fiber	2.93E-11	2.25E-09	1.72E-09	36	geneontology_Cel	0.039735099
GO:0030055	cell-substrate junction	1.27E-10	8.35E-09	6.39E-09	52	geneontology_Cel	0.057395143
GO:0030018	Z disc	1.86E-10	9.47E-09	7.24E-09	24	geneontology_Cel	0.026490066
GO:0005925	focal adhesion	2.06E-10	9.47E-09	7.24E-09	51	geneontology_Cel	0.056291391
GO:0031674	I band	2.41E-10	9.47E-09	7.24E-09	25	geneontology_Cel	0.027593819
GO:0042383	sarcolemma	2.42E-10	9.47E-09	7.24E-09	26	geneontology_Cel	0.028697572
	cell-substrate adherens						
GO:0005924	junction	2.46E-10	9.47E-09	7.24E-09	51	geneontology_Cel	0.056291391
GO:0030017	sarcomere	2.91E-10	1.03E-08	7.88E-09	31	geneontology_Cel	0.034216336
GO:0005604	basement membrane	1.05E-08	3.45E-07	2.64E-07	20	geneontology_Cel	0.022075055
GO:0005901	caveola	3.13E-08	9.12E-07	6.97E-07	18	geneontology_Cel	0.01986755
GO:0044853	plasma membrane raft	3.16E-08	9.12E-07	6.97E-07	21	geneontology_Cel	0.023178808
GO:0097060	synaptic membrane	3.53E-08	9.57E-07	7.32E-07	46	geneontology_Cel	0.050772627
GO:0098857	membrane microdomain	5.00E-08	1.28E-06	9.80E-07	39	geneontology_Cel	0.043046358
GO:0098589	membrane region	1.28E-07	3.10E-06	2.37E-06	39	geneontology_Cel	0.043046358
GO:0045121	membrane raft	1.35E-07	3.11E-06	2.38E-06	38	geneontology_Cel	0.041942605
GO:0005911	cell-cell junction	3.69E-07	8.09E-06	6.19E-06	45	geneontology_Cel	0.049668874
GO:0043034	costamere	8.42E-07	1.76E-05	1.35E-05	8	geneontology_Cel	0.008830022
	transmembrane transporter						
GO:1902495	complex	1.12E-06	2.24E-05	1.71E-05	33	geneontology_Cel	0.036423841

GO:0045211	postsynaptic membrane	1.35E-06	2.59E-05	1.98E-05	35	geneontology_Cel	0.038631347
GO:0034702	ion channel complex	1.46E-06	2.69E-05	2.06E-05	31	geneontology_Cel	0.034216336
	plasma membrane protein						
GO:0098797	complex	1.65E-06	2.87E-05	2.20E-05	46	geneontology_Cel	0.050772627
GO:1990351	transporter complex	1.68E-06	2.87E-05	2.20E-05	33	geneontology_Cel	0.036423841
GO:0043235	receptor complex	2.14E-06	3.53E-05	2.70E-05	34	geneontology_Cel	0.037527594
GO:0030315	T-tubule	4.34E-06	6.91E-05	5.28E-05	12	geneontology_Cel	0.013245033
GO:0015629	actin cytoskeleton	6.66E-06	0.000102332	7.83E-05	43	geneontology_Cel	0.047461369
GO:0098978	glutamatergic synapse	8.62E-06	0.000128178	9.80E-05	37	geneontology_Cel	0.040838852
GO:0098982	GABA-ergic synapse	1.09E-05	0.000156474	0.000119691	14	geneontology_Cel	0.015452539
GO:0032279	asymmetric synapse	1.72E-05	0.000239649	0.000183314	32	geneontology_Cel	0.035320088
	intrinsic component of						
GO:0098936	postsynaptic membrane	1.89E-05	0.000256931	0.000196534	18	geneontology_Cel	0.01986755
GO:0031252	cell leading edge	2.57E-05	0.000339035	0.000259337	38	geneontology_Cel	0.041942605
GO:0098984	neuron to neuron synapse	2.79E-05	0.000357187	0.000273222	33	geneontology_Cel	0.036423841
GO:0099572	postsynaptic specialization	2.97E-05	0.000370491	0.000283399	33	geneontology_Cel	0.036423841
GO:0014069	postsynaptic density	3.28E-05	0.000398288	0.000304662	31	geneontology_Cel	0.034216336
	intrinsic component of						
GO:0099240	synaptic membrane	4.62E-05	0.0005461	0.000417727	21	geneontology_Cel	0.023178808
GO:0031256	leading edge membrane	5.17E-05	0.000596356	0.000456169	20	geneontology_Cel	0.022075055
GO:0043197	dendritic spine	5.73E-05	0.00064458	0.000493057	19	geneontology_Cel	0.020971302
GO:0034703	cation channel complex	7.43E-05	0.000815363	0.000623694	22	geneontology_Cel	0.024282561
GO:0044309	neuron spine	7.64E-05	0.000819547	0.000626894	19	geneontology_Cel	0.020971302
GO:0005614	interstitial matrix	9.60E-05	0.00098576	0.000754035	5	geneontology_Cel	0.005518764
GO:0098793	presynapse	9.62E-05	0.00098576	0.000754035	40	geneontology_Cel	0.04415011
GO:0060077	inhibitory synapse	1.00E-04	0.001001821	0.00076632	6	geneontology_Cel	0.006622517
GO:0033267	axon part	0.00012114	0.001188204	0.00090889	34	geneontology_Cel	0.037527594
	integral component of						
GO:0099055	postsynaptic membrane	0.000135792	0.00130417	0.000997595	16	geneontology_Cel	0.017660044

	integral component of						
GO:0099699	synaptic membrane	0.000144439	0.001358906	0.001039464	19	geneontology_Cel	0.020971302
GO:0043025	neuronal cell body	0.000205619	0.001895811	0.001450158	40	geneontology_Cel	0.04415011
GO:0045178	basal part of cell	0.000261578	0.002364458	0.001808639	9	geneontology_Cel	0.009933775
GO:0043198	dendritic shaft	0.000267374	0.002370372	0.001813162	8	geneontology_Cel	0.008830022
	plasma membrane receptor						
GO:0098802	complex	0.000453449	0.003944152	0.00301699	18	geneontology_Cel	0.01986755
GO:0008305	integrin complex	0.00047108	0.004021629	0.003076254	7	geneontology_Cel	0.007726269
	intrinsic component of						
	postsynaptic density						
GO:0099146	membrane	0.000692225	0.005802107	0.004438192	9	geneontology_Cel	0.009933775
GO:0031253	cell projection membrane	0.000817012	0.006725758	0.005144717	29	geneontology_Cel	0.03200883
	intrinsic component of						
	postsynaptic specialization						
GO:0098948	membr	0.000836388	0.006764469	0.005174329	11	geneontology_Cel	0.01214128
	protein complex involved in						
GO:0098636	cell adhesion	0.000870763	0.006921063	0.005294111	7	geneontology_Cel	0.007726269
GO:0032280	symmetric synapse	0.001379646	0.010779947	0.008245878	4	geneontology_Cel	0.004415011
GO:0032587	ruffle membrane	0.001458496	0.011206112	0.008571863	12	geneontology_Cel	0.013245033
	extracellular matrix						
GO:0044420	component	0.001734452	0.013107909	0.0100266	8	geneontology_Cel	0.008830022
GO:0005938	cell cortex	0.001801715	0.013396621	0.010247444	22	geneontology_Cel	0.024282561
GO:0009925	basal plasma membrane	0.001926389	0.013519944	0.010341777	6	geneontology_Cel	0.006622517
GO:0044291	cell-cell contact zone	0.001935608	0.013519944	0.010341777	10	geneontology_Cel	0.011037528
GO:0033270	paranode region of axon	0.001990438	0.013519944	0.010341777	4	geneontology_Cel	0.004415011
	spanning component of						
GO:0089717	membrane	0.001990438	0.013519944	0.010341777	4	geneontology_Cel	0.004415011
GO:0034707	chloride channel complex	0.001994425	0.013519944	0.010341777	8	geneontology_Cel	0.008830022
	integral component of						
	postsynaptic density						
GO:0099061	membrane	0.001994425	0.013519944	0.010341777	8	geneontology_Cel	0.008830022

	postsynaptic density						
GO:0098839	membrane	0.002023592	0.013519944	0.010341777	9	geneontology_Cel	0.009933775
	integral component of postsynaptic specialization						
GO:0099060	membra	0.002157077	0.014205893	0.010866478	10	geneontology_Cel	0.011037528
GO:0002102	podosome	0.002330633	0.015132703	0.011575421	6	geneontology_Cel	0.006622517
GO:0014704	intercalated disc	0.00260579	0.016684296	0.012762277	8	geneontology_Cel	0.008830022
	postsynaptic specialization						
GO:0099634	membrane	0.002892886	0.018268775	0.013974289	11	geneontology_Cel	0.01214128
GO:0043204	perikaryon	0.003442034	0.021442941	0.016402296	14	geneontology_Cel	0.015452539
GO:0044304	main axon	0.003976893	0.024444636	0.018698375	9	geneontology_Cel	0.009933775
GO:0016323	basolateral plasma membrane	0.004264528	0.025867727	0.019786936	19	geneontology_Cel	0.020971302
GO:0150034	distal axon	0.004502851	0.026958629	0.020621397	23	geneontology_Cel	0.025386313
GO:0030027	lamellipodium	0.005487158	0.03243051	0.024806989	18	geneontology_Cel	0.01986755
	dystrophin-associated						
GO:0016010	glycoprotein complex	0.006267281	0.036115206	0.027625514	4	geneontology_Cel	0.004415011
GO:0090665	glycoprotein complex	0.006267281	0.036115206	0.027625514	4	geneontology_Cel	0.004415011
GO:0005788	endoplasmic reticulum lumen	0.007804979	0.043797693	0.03350206	25	geneontology_Cel	0.027593819
	platelet alpha granule						
GO:0031092	membrane	0.007885485	0.043797693	0.03350206	4	geneontology_Cel	0.004415011
GO:0097440	apical dendrite	0.007885485	0.043797693	0.03350206	4	geneontology_Cel	0.004415011
GO:0030427	site of polarized growth	0.008176728	0.044874661	0.034325862	16	geneontology_Cel	0.017660044
	extracellular matrix structural						
GO:0005201	constituent	3.57E-10	2.50E-07	2.09E-07	30	geneontology_Mol	0.034682081
GO:0003779	actin binding	1.07E-09	3.76E-07	3.15E-07	48	geneontology_Mol	0.055491329
GO:0005539	glycosaminoglycan binding	1.85E-09	4.31E-07	3.61E-07	33	geneontology_Mol	0.038150289
GO:0005178	integrin binding	1.02E-08	1.78E-06	1.49E-06	23	geneontology_Mol	0.026589595
GO:0050840	extracellular matrix binding	1.42E-08	1.98E-06	1.66E-06	14	geneontology_Mol	0.016184971
GO:0008201	heparin binding	4.55E-07	5.31E-05	4.45E-05	24	geneontology_Mol	0.027745665

	transmembrane receptor						
GO:0019199	protein kinase activity	6.85E-07	6.85E-05	5.74E-05	15	geneontology_Mol	0.01734104
	passive transmembrane						
GO:0022803	transporter activity	2.68E-06	0.000234288	0.000196238	41	geneontology_Mol	0.047398844
GO:0015267	channel activity	6.05E-06	0.00047087	0.000394398	40	geneontology_Mol	0.046242775
GO:1901681	sulfur compound binding	8.27E-06	0.000579243	0.000485171	28	geneontology_Mol	0.032369942
GO:0005216	ion channel activity	1.34E-05	0.000854293	0.000715551	36	geneontology_Mol	0.041618497
GO:0016247	channel regulator activity	2.30E-05	0.001300778	0.001089524	19	geneontology_Mol	0.021965318
	substrate-specific channel						
GO:0022838	activity	2.42E-05	0.001300778	0.001089524	36	geneontology_Mol	0.041618497
	transmembrane receptor						
	protein tyrosine kinase						
GO:0004714	activity	2.78E-05	0.001388917	0.001163348	11	geneontology_Mol	0.012716763
GO:0043236	laminin binding	3.03E-05	0.001415075	0.001185258	8	geneontology_Mol	0.009248555
GO:0005518	collagen binding	4.93E-05	0.002155589	0.001805509	12	geneontology_Mol	0.013872832
GO:0044325	ion channel binding	7.98E-05	0.003284344	0.002750947	17	geneontology_Mol	0.019653179
GO:0005261	cation channel activity	0.000104531	0.004065101	0.003404904	28	geneontology_Mol	0.032369942
GO:0017166	vinculin binding	0.000121491	0.004475971	0.003749046	5	geneontology_Mol	0.005780347
GO:0097110	scaffold protein binding	0.000142743	0.004852588	0.004064498	11	geneontology_Mol	0.012716763
GO:0008013	beta-catenin binding	0.000145578	0.004852588	0.004064498	13	geneontology_Mol	0.015028902
GO:0022839	ion gated channel activity	0.000243558	0.00774956	0.006490985	28	geneontology_Mol	0.032369942
GO:0022836	gated channel activity	0.00025912	0.007886268	0.00660549	28	geneontology_Mol	0.032369942
	transforming growth factor						
GO:0005160	beta receptor binding	0.000360772	0.010522529	0.008813607	6	geneontology_Mol	0.006936416
	growth factor receptor						
GO:0070851	binding	0.000426621	0.011945388	0.010005385	16	geneontology_Mol	0.01849711
GO:0050998	nitric-oxide synthase binding	0.000463049	0.01246671	0.010442041	5	geneontology_Mol	0.005780347
	cell adhesion molecule						
GO:0050839	binding	0.000675564	0.01751462	0.01467014	39	geneontology_Mol	0.045086705
GO:0001540	amyloid-beta binding	0.000878578	0.021219628	0.017773433	11	geneontology_Mol	0.012716763

	calcium ion transmembrane						
GO:0015085	transporter activity	0.000879099	0.021219628	0.017773433	14	geneontology_Mol	0.016184971
GO:0051015	actin filament binding	0.000987277	0.023036469	0.019295208	17	geneontology_Mol	0.019653179
GO:0045499	chemorepellent activity	0.001099688	0.024055666	0.020148881	4	geneontology_Mol	0.004624277
	transmembrane receptor						
	protein serine/threonine						
GO:0070696	kinase b	0.001099688	0.024055666	0.020148881	4	geneontology_Mol	0.004624277
	protein tyrosine kinase						
GO:0004713	activity	0.001150309	0.024400502	0.020437714	15	geneontology_Mol	0.01734104
	phosphorus-oxygen lyase						
GO:0016849	activity	0.001259506	0.025931005	0.021719654	5	geneontology_Mol	0.005780347
	fibroblast growth factor						
GO:0005104	receptor binding	0.001325005	0.026500096	0.022196321	6	geneontology_Mol	0.006936416
GO:0060090	molecular adaptor activity	0.001581452	0.028535806	0.02390142	22	geneontology_Mol	0.025433526
	intracellular calcium						
	activated chloride channel						
GO:0005229	activit	0.001658657	0.028535806	0.02390142	4	geneontology_Mol	0.004624277
GO:0031005	filamin binding	0.001658657	0.028535806	0.02390142	4	geneontology_Mol	0.004624277
	intracellular chloride channel						
GO:0061778	activity	0.001658657	0.028535806	0.02390142	4	geneontology_Mol	0.004624277
	ionotropic glutamate receptor						
GO:0004970	activity	0.001671383	0.028535806	0.02390142	5	geneontology_Mol	0.005780347
GO:0009975	cyclase activity	0.001671383	0.028535806	0.02390142	5	geneontology_Mol	0.005780347
GO:0005262	calcium channel activity	0.001819486	0.03032476	0.025399837	12	geneontology_Mol	0.013872832
	phosphoric diester hydrolase						
GO:0008081	activity	0.001932224	0.031454807	0.026346357	11	geneontology_Mol	0.012716763
GO:0030165	PDZ domain binding	0.002143742	0.034104991	0.028566135	11	geneontology_Mol	0.012716763
	protein tyrosine kinase						
GO:1990782	binding	0.002373671	0.036923766	0.030927125	11	geneontology_Mol	0.012716763
	sodium channel regulator						
GO:0017080	activity	0.002473871	0.037315216	0.031255001	6	geneontology_Mol	0.006936416

	receptor tyrosine kinase						
GO:0030971	binding	0.00250545	0.037315216	0.031255001	9	geneontology_Mol	0.010404624
GO:0001653	peptide receptor activity	0.002837247	0.04085257	0.034217867	13	geneontology_Mol	0.015028902
	voltage-gated ion channel						
GO:0005244	activity	0.002918041	0.04085257	0.034217867	17	geneontology_Mol	0.019653179
GO:0022832	voltage-gated channel activity	0.002918041	0.04085257	0.034217867	17	geneontology_Mol	0.019653179
GO:0042056	chemoattractant activity	0.002986768	0.040994858	0.034337047	6	geneontology_Mol	0.006936416
GO:0008083	growth factor activity	0.003405528	0.045299242	0.037942373	16	geneontology_Mol	0.01849711
GO:0019838	growth factor binding	0.0034298	0.045299242	0.037942373	14	geneontology_Mol	0.016184971
