

Supplementary Table 1

cluster	gene	p_val	avg_log2FC	percentage_nuclei_EPO	percentage_nuclei_PL	p_val_adj
OPC	Atp2a2	1,54E-41	-0,599247729	0,141	0,378	4,97E-37
OPC	Unc80	8,75E-40	-0,776115464	0,171	0,442	2,82E-35
OPC	Csrnp3	1,98E-34	-0,634638154	0,127	0,351	6,40E-30
OPC	Rbfox2	4,79E-32	-0,495334102	0,25	0,489	1,55E-27
OPC	Myt1l	6,32E-32	-0,516097031	0,339	0,598	2,04E-27
OPC	Rgs7bp	8,53E-31	-0,60672112	0,216	0,458	2,75E-26
OPC	Sorbs2	2,78E-29	-0,519043872	0,318	0,561	8,96E-25
OPC	Nrcam	6,33E-29	-0,432638476	0,513	0,747	2,04E-24
OPC	Tafa2	1,06E-28	-0,552075731	0,442	0,686	3,41E-24
OPC	Asic2	1,12E-28	-0,483385956	0,606	0,823	3,63E-24
OPC	Ext1	1,80E-28	-0,373605199	0,428	0,665	5,82E-24
OPC	Mapk10	1,83E-28	-0,498253288	0,408	0,649	5,91E-24
OPC	Cacnb4	2,15E-28	-0,520452006	0,236	0,465	6,95E-24
OPC	Car10	1,00E-27	-0,754793647	0,246	0,472	3,23E-23
OPC	Erc2	1,32E-27	-0,690798712	0,289	0,515	4,25E-23
OPC	Rapgef2	4,46E-26	-0,424792635	0,246	0,453	1,44E-21
OPC	Gabrb1	3,96E-25	-0,298776602	0,515	0,732	1,28E-20
OPC	Cadps	3,67E-24	-0,275870856	0,608	0,807	1,19E-19
OPC	Arl15	4,21E-24	-0,426110803	0,489	0,708	1,36E-19
OPC	Tsc22d1	5,81E-24	-0,49354694	0,169	0,358	1,87E-19
OPC	Atp2b2	7,99E-24	-0,52960439	0,132	0,314	2,58E-19
OPC	Cd47	1,47E-23	-0,587878436	0,056	0,205	4,74E-19
OPC	Robo2	2,04E-23	-0,512319567	0,157	0,343	6,58E-19
OPC	Unc79	3,03E-23	-0,417680195	0,305	0,517	9,78E-19
OPC	Pcnp	3,37E-23	-0,503230249	0,025	0,144	1,09E-18
OPC	Gabrb2	3,98E-23	-0,468477466	0,156	0,334	1,29E-18
OPC	Lgi1	5,73E-23	-0,616662965	0,089	0,257	1,85E-18
OPC	Cntnap2	7,72E-23	-0,529353726	0,287	0,505	2,49E-18
OPC	Rabgap1l	2,20E-22	-0,261343467	0,481	0,68	7,12E-18
OPC	Brinp1	2,38E-22	-0,344495422	0,583	0,785	7,67E-18
OPC	Arfgef3	2,75E-22	-0,590152707	0,085	0,248	8,87E-18
OPC	Meg3	3,68E-22	-0,567197523	0,462	0,661	1,19E-17
OPC	Scn1a	4,62E-22	-0,519940744	0,206	0,403	1,49E-17
OPC	Cdh11	5,39E-22	-0,448315746	0,281	0,489	1,74E-17
OPC	Grm5	5,71E-22	-0,468952655	0,632	0,807	1,84E-17
OPC	Gpm6a	8,27E-22	-0,278887487	0,495	0,697	2,67E-17
OPC	Atxn1	3,65E-21	-0,389510012	0,391	0,601	1,18E-16
OPC	Vsnl1	5,82E-21	-0,563391899	0,091	0,249	1,88E-16
OPC	Mical2	1,21E-20	-0,514667932	0,036	0,158	3,90E-16
OPC	Grip1	3,68E-20	-0,440199661	0,438	0,645	1,19E-15
OPC	Nceh1	3,88E-20	-0,541542611	0,04	0,165	1,25E-15
OPC	Kcnp3	5,79E-20	0,490034658	0,755	0,711	1,87E-15
OPC	Gabrg3	8,73E-20	-0,594643131	0,265	0,46	2,82E-15
OPC	Large1	9,98E-20	-0,313864793	0,486	0,675	3,22E-15
OPC	Lrfn5	1,05E-19	-0,564819546	0,164	0,345	3,38E-15
OPC	Mapk1	1,55E-19	-0,504178431	0,133	0,301	5,02E-15
OPC	Stxbp6	1,73E-19	-0,359416664	0,199	0,361	5,57E-15
OPC	Rtn3	2,05E-19	-0,334927241	0,319	0,503	6,62E-15
OPC	Fam189a1	2,37E-19	-0,616362662	0,162	0,332	7,66E-15
OPC	Syt1	3,65E-19	-0,565149908	0,139	0,309	1,18E-14
OPC	Rab6a	7,32E-19	-0,542351964	0,087	0,231	2,36E-14
OPC	Rpl13	8,07E-19	-0,331994648	0,138	0,272	2,60E-14

OPC	Megf9	8,35E-19	-0,344359654	0,106	0,226	2,69E-14
OPC	Cacna2d3	3,09E-18	-0,530944776	0,285	0,444	9,98E-14
OPC	Samd12	3,13E-18	-0,352040351	0,435	0,632	1,01E-13
OPC	Flrt2	3,37E-18	-0,514132057	0,096	0,242	1,09E-13
OPC	Tenm2	3,99E-18	-0,503741943	0,319	0,516	1,29E-13
OPC	Gabbr2	4,08E-18	-0,543347591	0,134	0,298	1,32E-13
OPC	Trpm3	4,10E-18	-0,391589953	0,486	0,679	1,32E-13
OPC	Gria1	4,96E-18	-0,555965835	0,156	0,326	1,60E-13
OPC	Hdac9	1,06E-17	-0,524140129	0,381	0,569	3,43E-13
OPC	Raly1	1,18E-17	-0,505510069	0,491	0,675	3,80E-13
OPC	Phf20l1	1,58E-17	-0,3058743	0,379	0,559	5,10E-13
OPC	Lyst	1,88E-17	-0,363663616	0,145	0,285	6,07E-13
OPC	Gabrb3	2,25E-17	-0,525183413	0,141	0,301	7,25E-13
OPC	Frmpd4	2,53E-17	-0,577994876	0,111	0,261	8,17E-13
OPC	Scai	2,67E-17	-0,459041833	0,235	0,413	8,63E-13
OPC	Tafa1	2,82E-17	-0,563515419	0,197	0,367	9,10E-13
OPC	Lrrc7	4,07E-17	-0,437399204	0,534	0,713	1,31E-12
OPC	Pcsk2	4,07E-17	-0,470077532	0,184	0,352	1,31E-12
OPC	Dgkh	4,37E-17	-0,462284592	0,066	0,188	1,41E-12
OPC	Prr16	5,51E-17	-0,565385959	0,229	0,384	1,78E-12
OPC	Cap2	6,12E-17	-0,552328405	0,071	0,201	1,98E-12
OPC	Kmt2a	6,32E-17	-0,360750714	0,297	0,474	2,04E-12
OPC	Arhgef9	8,61E-17	-0,490361644	0,128	0,282	2,78E-12
OPC	Pde10a	1,13E-16	-0,29349485	0,429	0,609	3,63E-12
OPC	Ypel3	1,18E-16	-0,417732911	0,017	0,104	3,82E-12
OPC	Spock2	1,43E-16	-0,365265835	0,025	0,111	4,62E-12
OPC	Herc3	1,51E-16	-0,485109968	0,068	0,193	4,88E-12
OPC	Ube3a	1,86E-16	-0,369928955	0,289	0,465	6,01E-12
OPC	Kcnma1	1,98E-16	-0,445579985	0,472	0,65	6,40E-12
OPC	Stxbp5	2,53E-16	-0,311570494	0,193	0,335	8,17E-12
OPC	Gm2164	3,32E-16	0,395133813	0,54	0,504	1,07E-11
OPC	Pou3f1	3,85E-16	0,603837788	0,167	0,064	1,24E-11
OPC	330023F24Ri	4,09E-16	-0,376368796	0,114	0,241	1,32E-11
OPC	Eml6	6,29E-16	-0,329232662	0,4	0,579	2,03E-11
OPC	Ica1	6,88E-16	-0,489460069	0,215	0,384	2,22E-11
OPC	Celf2	8,00E-16	-0,416568513	0,474	0,653	2,58E-11
OPC	Etnk1	8,43E-16	-0,378022568	0,158	0,302	2,72E-11
OPC	Shank2	8,75E-16	-0,525005714	0,095	0,229	2,82E-11
OPC	Ssbp2	1,23E-15	-0,340692142	0,287	0,455	3,96E-11
OPC	Ptpn2	1,28E-15	-0,266138129	0,389	0,556	4,13E-11
OPC	030462N17Ri	2,92E-15	-0,373128955	0,06	0,16	9,42E-11
OPC	Abtb2	3,63E-15	0,366396459	0,568	0,553	1,17E-10
OPC	Rasal2	5,17E-15	-0,285119223	0,285	0,439	1,67E-10
OPC	Zwint	6,89E-15	-0,450378748	0,041	0,142	2,22E-10
OPC	Tspan5	7,17E-15	-0,387492666	0,167	0,312	2,31E-10
OPC	Celf1	1,21E-14	-0,306237474	0,222	0,365	3,90E-10
OPC	Ppp3ca	1,38E-14	-0,419211255	0,411	0,586	4,47E-10
OPC	Cdkl5	1,62E-14	-0,490135552	0,147	0,295	5,22E-10
OPC	Nedd4l	2,07E-14	-0,367325348	0,178	0,32	6,67E-10
OPC	Kcnh7	3,48E-14	-0,451926122	0,251	0,417	1,12E-09
OPC	Cacna2d1	3,50E-14	-0,430873917	0,264	0,431	1,13E-09
OPC	Snhg14	3,95E-14	-0,496805051	0,082	0,197	1,28E-09
OPC	Dmnl2	3,99E-14	-0,303433442	0,147	0,268	1,29E-09

OPC	Cstf3	4,30E-14	-0,382960724	0,208	0,358	1,39E-09
OPC	Kcnc2	4,37E-14	-0,485952785	0,164	0,312	1,41E-09
OPC	Tnp01	1,08E-13	0,250538488	0,507	0,518	3,48E-09
OPC	Mllt3	1,24E-13	-0,304189742	0,333	0,492	4,01E-09
OPC	Clip1	1,29E-13	-0,434345657	0,053	0,158	4,15E-09
OPC	Grina	1,30E-13	-0,383158799	0,097	0,211	4,21E-09
OPC	Nyap2	1,42E-13	-0,406911308	0,037	0,128	4,58E-09
OPC	AY036118	1,86E-13	-0,47637703	0,153	0,288	6,01E-09
OPC	Rps6ka3	2,06E-13	-0,342321042	0,157	0,286	6,66E-09
OPC	Sh3rf3	2,18E-13	-0,480459785	0,17	0,305	7,04E-09
OPC	Plekha5	2,54E-13	-0,301212204	0,369	0,53	8,18E-09
OPC	Trps1	2,86E-13	-0,281000647	0,459	0,624	9,24E-09
OPC	Immp2l	2,92E-13	-0,324979938	0,328	0,488	9,42E-09
OPC	Mbp	2,92E-13	0,333400833	0,234	0,229	9,42E-09
OPC	Neto1	3,47E-13	-0,332138022	0,345	0,508	1,12E-08
OPC	Ppfia2	3,68E-13	-0,413916926	0,44	0,603	1,19E-08
OPC	Nectin3	3,72E-13	-0,421373736	0,071	0,181	1,20E-08
OPC	Snhg11	4,38E-13	-0,397401632	0,33	0,494	1,42E-08
OPC	Rab31	6,79E-13	0,310802513	0,424	0,415	2,19E-08
OPC	Dnajc5	7,41E-13	-0,483605668	0,069	0,175	2,39E-08
OPC	Kif5c	9,46E-13	-0,419066369	0,113	0,237	3,06E-08
OPC	Dgki	1,21E-12	-0,276567602	0,412	0,567	3,90E-08
OPC	Sec61a2	1,44E-12	-0,395738835	0,135	0,263	4,64E-08
OPC	Cdh18	1,48E-12	-0,402235576	0,172	0,311	4,79E-08
OPC	Chrna7	1,78E-12	-0,356700744	0,027	0,105	5,75E-08
OPC	Nrg3	1,90E-12	-0,303669266	0,758	0,874	6,12E-08
OPC	Nebi	1,97E-12	-0,317587211	0,486	0,649	6,35E-08
OPC	Grin2a	2,04E-12	-0,474686174	0,059	0,156	6,57E-08
OPC	Esyt2	2,05E-12	-0,402329119	0,12	0,243	6,61E-08
OPC	Dlgap2	2,94E-12	-0,428359478	0,099	0,213	9,48E-08
OPC	Egfem1	3,13E-12	-0,328462868	0,493	0,655	1,01E-07
OPC	Cacna1a	3,16E-12	-0,3560307	0,575	0,707	1,02E-07
OPC	Lncpint	3,17E-12	-0,325354563	0,246	0,388	1,02E-07
OPC	Abhd17b	3,32E-12	0,386987313	0,494	0,439	1,07E-07
OPC	Sorbs1	3,72E-12	-0,313037302	0,352	0,498	1,20E-07
OPC	Clstn2	3,74E-12	-0,460353884	0,164	0,301	1,21E-07
OPC	Pip5k1b	4,31E-12	-0,417261062	0,08	0,188	1,39E-07
OPC	Atp6v0a1	4,33E-12	-0,290454109	0,27	0,411	1,40E-07
OPC	Slc4a10	4,35E-12	-0,407421887	0,168	0,303	1,40E-07
OPC	Map2k4	4,59E-12	-0,317579809	0,185	0,312	1,48E-07
OPC	Sulf2	5,06E-12	0,281504965	0,464	0,46	1,63E-07
OPC	Rimbp2	6,21E-12	-0,39388928	0,055	0,152	2,00E-07
OPC	Ryr3	6,37E-12	-0,464748322	0,099	0,215	2,06E-07
OPC	Cst3	6,75E-12	-0,364671701	0,201	0,337	2,18E-07
OPC	Iars	7,70E-12	0,302255853	0,146	0,124	2,48E-07
OPC	Dcaf6	8,71E-12	-0,367543712	0,253	0,4	2,81E-07
OPC	Akap6	9,45E-12	-0,260909577	0,546	0,7	3,05E-07
OPC	Dab1	9,55E-12	-0,323864385	0,465	0,624	3,08E-07
OPC	Epha3	1,08E-11	-0,417840967	0,047	0,138	3,47E-07
OPC	Lrrn2	1,25E-11	-0,351110118	0,086	0,189	4,03E-07
OPC	Shisa9	1,32E-11	-0,271103121	0,332	0,47	4,27E-07
OPC	Kalrn	1,50E-11	-0,379141304	0,2	0,336	4,84E-07
OPC	Gucy1b1	1,66E-11	-0,443925167	0,066	0,166	5,35E-07

OPC	Nr3c2	1,72E-11	-0,462488939	0,142	0,259	5,56E-07
OPC	Stxbp1	1,93E-11	-0,407520421	0,05	0,143	6,24E-07
OPC	Sec14l1	1,98E-11	-0,394805373	0,04	0,124	6,38E-07
OPC	Gm45159	1,98E-11	-0,32392961	0,041	0,123	6,39E-07
OPC	Cacna1b	2,02E-11	-0,331210785	0,035	0,112	6,53E-07
OPC	Rpl37a	2,24E-11	-0,391284191	0,031	0,111	7,23E-07
OPC	Kcnab1	2,25E-11	-0,435636568	0,182	0,319	7,26E-07
OPC	Cpne8	2,31E-11	-0,391817558	0,201	0,338	7,47E-07
OPC	Upp2	2,51E-11	-0,429034857	0,236	0,376	8,10E-07
OPC	C2cd5	2,62E-11	-0,352104761	0,259	0,404	8,45E-07
OPC	Atrnl1	2,69E-11	-0,412426147	0,121	0,24	8,67E-07
OPC	Epha5	2,71E-11	-0,380967774	0,475	0,587	8,75E-07
OPC	Eml5	2,93E-11	-0,332513241	0,297	0,441	9,45E-07
OPC	Slc16a7	3,00E-11	-0,397214289	0,088	0,193	9,69E-07
OPC	Cpeb1	4,70E-11	-0,331833227	0,088	0,185	1,52E-06
OPC	Mgat4c	5,07E-11	-0,442728777	0,154	0,282	1,64E-06
OPC	Gprasp1	5,35E-11	-0,367278853	0,184	0,314	1,73E-06
OPC	Hivep2	5,71E-11	-0,392589002	0,211	0,333	1,84E-06
OPC	Ckap5	5,95E-11	0,269710631	0,289	0,274	1,92E-06
OPC	Zfp804a	6,85E-11	-0,361780431	0,23	0,359	2,21E-06
OPC	Msra	6,86E-11	-0,339343546	0,189	0,314	2,21E-06
OPC	Snap91	7,69E-11	-0,35860155	0,367	0,51	2,48E-06
OPC	Arpp21	8,24E-11	-0,351889319	0,454	0,6	2,66E-06
OPC	Cspg5	8,48E-11	0,269421995	0,817	0,824	2,74E-06
OPC	Nell1	9,53E-11	-0,286031169	0,037	0,112	3,08E-06
OPC	Mvb12b	1,08E-10	0,270130384	0,275	0,254	3,50E-06
OPC	Phf20	1,23E-10	0,264690651	0,265	0,252	3,97E-06
OPC	Saraf	1,29E-10	-0,351570674	0,036	0,111	4,17E-06
OPC	Prpf4b	1,50E-10	0,268365332	0,613	0,609	4,86E-06
OPC	Cspg4	1,67E-10	0,264145962	0,499	0,49	5,41E-06
OPC	Orc4	1,74E-10	-0,277208148	0,121	0,218	5,62E-06
OPC	Mdh1	2,25E-10	-0,342783943	0,031	0,101	7,27E-06
OPC	Syndig1	2,31E-10	-0,362538034	0,029	0,101	7,44E-06
OPC	Prex1	2,52E-10	0,271509944	0,383	0,366	8,14E-06
OPC	Tardbp	3,11E-10	-0,342524647	0,111	0,217	1,00E-05
OPC	Tenm3	3,27E-10	-0,343604558	0,297	0,441	1,05E-05
OPC	Sobp	3,60E-10	-0,335691048	0,379	0,501	1,16E-05
OPC	Klc1	3,98E-10	-0,309282714	0,16	0,272	1,28E-05
OPC	Trpc5	4,13E-10	-0,354573431	0,035	0,112	1,33E-05
OPC	Zbtb16	4,22E-10	-0,329685255	0,074	0,163	1,36E-05
OPC	Arhgap31	4,65E-10	0,302383162	0,84	0,817	1,50E-05
OPC	Grin2b	4,73E-10	-0,426116894	0,068	0,161	1,53E-05
OPC	St6gal2	4,80E-10	-0,332356372	0,032	0,104	1,55E-05
OPC	Tusc3	5,35E-10	-0,36524131	0,067	0,153	1,73E-05
OPC	Hsp90b1	5,52E-10	-0,432585736	0,121	0,232	1,78E-05
OPC	Tpm1	5,85E-10	0,253627376	0,514	0,513	1,89E-05
OPC	Shisa6	6,40E-10	-0,401467729	0,098	0,203	2,07E-05
OPC	Kcnq5	6,45E-10	-0,370531415	0,42	0,549	2,08E-05
OPC	Chka	7,00E-10	-0,329067684	0,172	0,291	2,26E-05
OPC	Rsrc1	8,08E-10	0,31884816	0,409	0,375	2,61E-05
OPC	St7	8,69E-10	-0,32641516	0,236	0,363	2,81E-05
OPC	Sgk1	9,01E-10	0,268053877	0,396	0,385	2,91E-05
OPC	Armcx1	9,95E-10	-0,358914231	0,031	0,103	3,21E-05

OPC	Caml	1,02E-09	-0,357282452	0,055	0,141	3,30E-05
OPC	Fat3	1,06E-09	-0,321879999	0,578	0,693	3,43E-05
OPC	Unc13b	1,17E-09	-0,365745122	0,121	0,214	3,76E-05
OPC	Tmem59	1,19E-09	-0,312508202	0,074	0,16	3,83E-05
OPC	Fam171a1	1,34E-09	-0,386877103	0,045	0,121	4,34E-05
OPC	Glis3	1,55E-09	-0,292200563	0,052	0,126	5,01E-05
OPC	Ostf1	1,59E-09	0,277066543	0,262	0,245	5,14E-05
OPC	Mapk8	1,99E-09	-0,316187696	0,147	0,254	6,41E-05
OPC	Csnk2a2	2,13E-09	0,324796645	0,32	0,283	6,89E-05
OPC	Ppp1r16b	2,30E-09	0,260446827	0,279	0,262	7,42E-05
OPC	Arid1b	2,40E-09	-0,270196628	0,391	0,525	7,73E-05
OPC	Slc25a46	2,41E-09	-0,32103639	0,035	0,106	7,80E-05
OPC	Camkk2	2,42E-09	-0,304383229	0,039	0,112	7,81E-05
OPC	Gpr158	2,92E-09	-0,336881535	0,432	0,569	9,43E-05
OPC	Srebfb2	2,95E-09	0,268130297	0,168	0,152	9,52E-05
OPC	Kcnp4	3,49E-09	-0,35227199	0,456	0,589	0,00011271
OPC	Dtnb	4,04E-09	-0,336600494	0,306	0,438	0,000130362
OPC	Rheb	4,36E-09	-0,306294229	0,065	0,142	0,000140688
OPC	Grin1	5,72E-09	-0,259010556	0,052	0,123	0,00018458
OPC	Hecw1	6,03E-09	-0,332989773	0,074	0,16	0,000194652
OPC	Cacnb2	6,42E-09	-0,35470222	0,065	0,146	0,000207154
OPC	Fam49a	6,63E-09	-0,418706857	0,113	0,21	0,000213911
OPC	Ppm1h	6,85E-09	-0,422659869	0,186	0,304	0,000221111
OPC	Ccdc47	6,86E-09	-0,312466182	0,095	0,183	0,000221355
OPC	Adamts3	7,01E-09	-0,345616336	0,047	0,124	0,000226191
OPC	Clstn1	7,11E-09	-0,337352259	0,079	0,165	0,000229391
OPC	Cdr1os	7,74E-09	-0,328995956	0,083	0,173	0,000249845
OPC	Ywhag	7,83E-09	-0,328263115	0,059	0,139	0,000252802
OPC	Dync1i2	8,33E-09	-0,277830055	0,208	0,321	0,000269038
OPC	Scn8a	8,60E-09	-0,322033984	0,158	0,266	0,000277742
OPC	Gria3	8,98E-09	-0,351673195	0,414	0,55	0,000289986
OPC	Tank	9,61E-09	0,278229154	0,177	0,156	0,000310416
OPC	Pdzd4	9,62E-09	-0,348802934	0,093	0,187	0,000310576
OPC	Slc4a7	1,01E-08	-0,267682648	0,138	0,232	0,000325026
OPC	Pja2	1,14E-08	-0,304021849	0,176	0,286	0,00036861
OPC	Plxna2	1,35E-08	-0,376020321	0,169	0,283	0,000434813
OPC	Ahcyl2	1,36E-08	-0,309410341	0,089	0,174	0,000439445
OPC	mar/06	1,43E-08	-0,29163821	0,159	0,251	0,000461824
OPC	Plxna4	1,57E-08	-0,38206866	0,092	0,182	0,00050683
OPC	Arhgef25	1,58E-08	-0,320055943	0,036	0,104	0,000510507
OPC	.500004A13Ri	1,60E-08	0,25733241	0,337	0,32	0,00051523
OPC	Fam169a	1,65E-08	-0,336474998	0,057	0,13	0,000533878
OPC	Tenm1	1,79E-08	-0,2836667	0,577	0,704	0,000579062
OPC	Adamts17	1,88E-08	-0,262686654	0,057	0,129	0,000608546
OPC	Ndufaf4	2,10E-08	-0,276281553	0,035	0,1	0,000676465
OPC	Cdc42	2,10E-08	-0,313320707	0,164	0,271	0,000679503
OPC	Fam171b	2,16E-08	-0,334497635	0,171	0,279	0,00069734
OPC	Tenm4	2,23E-08	-0,311724966	0,059	0,133	0,000721109
OPC	Psmc6	2,34E-08	0,278533801	0,236	0,209	0,000756556
OPC	Cds2	2,40E-08	-0,344949941	0,094	0,184	0,000773875
OPC	Ksr2	2,46E-08	-0,298556785	0,087	0,172	0,000793589
OPC	Ralgapa2	2,95E-08	-0,311525756	0,302	0,431	0,000952416
OPC	Plp1	2,97E-08	0,259230817	0,329	0,317	0,000958722

OPC	Jakmip2	3,03E-08	-0,276349092	0,294	0,416	0,00097684
OPC	Slitrk1	3,13E-08	-0,299526158	0,049	0,123	0,001011091
OPC	Bicral	3,33E-08	-0,342394158	0,15	0,252	0,00107349
OPC	Dnajb4	3,49E-08	-0,283941093	0,045	0,113	0,001126763
OPC	Ppm1e	3,50E-08	-0,346569492	0,184	0,298	0,001129369
OPC	Fnbp1l	3,62E-08	-0,30893214	0,117	0,207	0,001170041
OPC	Rc3h2	3,83E-08	-0,28694198	0,192	0,299	0,00123677
OPC	Klhl7	4,45E-08	-0,312674121	0,171	0,278	0,00143629
OPC	Mmaa	4,91E-08	-0,333754585	0,048	0,119	0,001584586
OPC	Cacna1d	5,06E-08	-0,279852786	0,423	0,556	0,001633365
OPC	Arhgap26	5,06E-08	-0,369222052	0,169	0,276	0,001633901
OPC	Kctd16	5,08E-08	-0,373386456	0,133	0,233	0,001638681
OPC	Syn2	5,14E-08	-0,285752376	0,551	0,663	0,001659211
OPC	Gng2	5,27E-08	-0,320543587	0,111	0,201	0,001700589
OPC	Sipa1l1	5,63E-08	-0,260565302	0,241	0,352	0,001819056
OPC	Sybu	6,47E-08	-0,266238543	0,264	0,38	0,002089441
OPC	Chm	7,13E-08	-0,263455567	0,162	0,259	0,002301729
OPC	Syt16	7,21E-08	-0,37302983	0,231	0,342	0,00232838
OPC	Ryr2	7,74E-08	-0,361069742	0,08	0,163	0,002497337
OPC	Hnrnpd	8,01E-08	-0,265535324	0,116	0,203	0,002585318
OPC	Gnai1	8,63E-08	-0,254759069	0,111	0,193	0,002785321
OPC	Zc3h6	9,62E-08	-0,332449562	0,039	0,104	0,003106515
OPC	Otud4	1,01E-07	0,294975834	0,2	0,161	0,003261809
OPC	Nap1l1	1,07E-07	-0,312705638	0,079	0,161	0,003461952
OPC	Rapgef4	1,10E-07	-0,309656658	0,052	0,124	0,003553305
OPC	Asph	1,12E-07	-0,283991195	0,089	0,17	0,003621632
OPC	Klhl29	1,21E-07	-0,317424296	0,054	0,127	0,003893592
OPC	Ube2w	1,45E-07	-0,302314315	0,155	0,255	0,00467753
OPC	Mmp15	1,52E-07	0,348188674	0,215	0,166	0,004898135
OPC	Spata7	1,57E-07	-0,336803624	0,075	0,152	0,005060236
OPC	Nsg2	1,75E-07	-0,324896218	0,064	0,14	0,005640156
OPC	Chchd6	1,78E-07	-0,330483886	0,067	0,144	0,005740909
OPC	Mef2c	1,85E-07	-0,363972994	0,123	0,205	0,005966572
OPC	Trim9	2,22E-07	-0,281962119	0,294	0,412	0,007182519
OPC	Atp8a2	2,35E-07	-0,344978545	0,12	0,212	0,007593441
OPC	Uhrf1bp1l	2,46E-07	-0,332405001	0,076	0,155	0,007946648
OPC	Spock1	2,47E-07	-0,286352789	0,097	0,179	0,007959044
OPC	Dok6	2,50E-07	-0,301446028	0,405	0,531	0,008061706
OPC	Dnal1	2,68E-07	-0,313410312	0,056	0,127	0,008663047
OPC	Sacs	2,69E-07	-0,323849302	0,078	0,157	0,008678135
OPC	Erc1	2,83E-07	-0,347110279	0,19	0,294	0,009122328
OPC	Dync1i1	2,92E-07	-0,285479963	0,117	0,203	0,009420404
OPC	Cox7c	3,27E-07	-0,288542538	0,098	0,181	0,010563664
OPC	Tmx4	3,32E-07	-0,311740322	0,134	0,229	0,010720535
OPC	Trpc1	3,53E-07	-0,288696681	0,136	0,227	0,01138141
OPC	Atp2c1	3,68E-07	-0,252735231	0,254	0,356	0,01187406
OPC	Slc7a6	3,84E-07	-0,254829178	0,039	0,1	0,012387433
OPC	Snap25	4,45E-07	-0,283106425	0,079	0,15	0,014353048
OPC	Inpp4a	4,62E-07	-0,252489434	0,091	0,163	0,014901733
OPC	Klf3	4,77E-07	0,314614925	0,144	0,105	0,015395141
OPC	Socs7	4,99E-07	-0,2708508	0,059	0,122	0,016125311
OPC	Gm44257	5,56E-07	-0,296611307	0,053	0,123	0,017941574
OPC	Rab3c	5,68E-07	-0,290345362	0,258	0,363	0,018326656

OPC	Sptbn4	6,23E-07	-0,316922263	0,085	0,165	0,020117116
OPC	Lingo2	6,37E-07	-0,262056886	0,15	0,239	0,020576149
OPC	Mctp1	6,75E-07	-0,351890027	0,081	0,158	0,021795076
OPC	Mef2d	6,88E-07	0,287618661	0,164	0,127	0,022217233
OPC	Spaca6	6,90E-07	-0,273615126	0,053	0,12	0,022279701
OPC	i330434G04Ri	6,93E-07	-0,269102841	0,263	0,37	0,022361451
OPC	Jazf1	7,63E-07	-0,290420842	0,319	0,433	0,024638223
OPC	Nin	7,63E-07	-0,331775828	0,09	0,171	0,024643867
OPC	Scn3a	8,55E-07	-0,278347813	0,293	0,404	0,027608084
OPC	Ppp1r13b	8,73E-07	-0,334815409	0,08	0,156	0,028177279
OPC	Rph3a	8,89E-07	-0,275747594	0,056	0,123	0,028686607
OPC	Slc8a1	9,70E-07	-0,270444535	0,469	0,575	0,031310192
OPC	Luzp1	1,01E-06	-0,272551697	0,152	0,243	0,032701769
OPC	Cep128	1,07E-06	0,275770684	0,135	0,11	0,034694893
OPC	Sf3b2	1,15E-06	0,33766746	0,204	0,147	0,037046735
OPC	Shc4	1,17E-06	0,258558149	0,479	0,449	0,037656576
OPC	Lmtk2	1,22E-06	0,265094019	0,366	0,329	0,039290291
OPC	Brinp2	1,32E-06	-0,278113179	0,107	0,186	0,042725062
OPC	Vezf1	1,43E-06	0,260332617	0,178	0,149	0,046136499
OPC	Mbip	1,47E-06	-0,265288676	0,123	0,199	0,047304184
OPC	Cnot7	1,47E-06	-0,27335424	0,082	0,15	0,047521543
COP	Map2k4	7,31E-11	-0,685085373	0,129	0,403	2,36E-06
COP	Nap1l4	4,62E-10	0,42842813	0,238	0,247	1,49E-05
COP	Ext1	8,74E-09	-0,605310518	0,315	0,593	0,000282298
COP	Nectin3	2,39E-08	-0,561495521	0,073	0,263	0,000770363
COP	Mef2c	6,17E-08	-0,597162869	0,028	0,185	0,001992439
COP	Nap1l1	7,61E-08	-0,554429215	0,048	0,222	0,00245567
COP	AY036118	1,52E-07	-0,668748355	0,145	0,35	0,004896834
COP	Raly1	2,63E-07	-0,927929135	0,194	0,407	0,008493282
COP	Reep1	3,00E-07	-0,494269546	0,315	0,453	0,009682429
COP	Exoc6b	4,16E-07	0,311334934	0,649	0,72	0,013433016
COP	Safb	4,41E-07	0,353673432	0,27	0,28	0,014251408
COP	Atp2a2	5,23E-07	-0,590090644	0,085	0,267	0,016889096
COP	Oip5os1	7,12E-07	-0,357644183	0,02	0,128	0,022982154
COP	Ppp3ca	7,54E-07	-0,464747441	0,452	0,695	0,024345218
COP	Tardbp	1,30E-06	-0,482282793	0,133	0,329	0,041849876
NFOL	Sgk1	4,62E-10	0,683380496	0,137	0,025	1,49E-05
NFOL	Pdia6	6,50E-10	-0,49482408	0,01	0,1	2,10E-05
NFOL	Fgfr1op2	8,21E-10	-0,505883405	0,031	0,156	2,65E-05
NFOL	P4ha1	9,63E-10	-0,600759258	0,115	0,293	3,11E-05
NFOL	Arpp19	2,73E-09	-0,46527502	0,022	0,129	8,82E-05
NFOL	Fam171b	2,86E-09	-0,480945843	0,094	0,243	9,23E-05
NFOL	Ppp1r9a	4,82E-09	-0,473943114	0,262	0,465	0,000155495
NFOL	Faim2	5,35E-09	-0,524489534	0,022	0,122	0,00017262
NFOL	Lrrc4c	9,99E-09	-0,495903167	0,382	0,589	0,000322606
NFOL	Pnpla8	1,57E-08	-0,511699201	0,077	0,222	0,000507307
NFOL	Yipf5	1,66E-08	-0,579799843	0,05	0,18	0,000534477
NFOL	Dock3	3,93E-08	-0,312555884	0,43	0,624	0,001267452
NFOL	Tshz3	4,11E-08	-0,622661238	0,091	0,234	0,001327019
NFOL	Ncoa1	1,09E-07	0,559398189	0,394	0,257	0,003515532
NFOL	Hnrnpu	1,91E-07	-0,38549222	0,312	0,49	0,006164219
NFOL	Pnn	3,13E-07	0,272580484	0,44	0,436	0,010120163
NFOL	Fis1	3,79E-07	-0,418844917	0,017	0,102	0,012220329

NFOL	Ube2w	3,97E-07	-0,446607083	0,055	0,164	0,012827613
NFOL	Dlg2	4,14E-07	-0,401724778	0,591	0,757	0,013353968
NFOL	Clasp1	4,79E-07	-0,549626265	0,103	0,239	0,01545066
NFOL	Tra2b	5,05E-07	-0,404909127	0,19	0,346	0,016306741
NFOL	Zyg11b	1,33E-06	-0,499389985	0,05	0,16	0,042816023
MOL1	Lrrc4c	4,71E-59	-0,924410012	0,2	0,431	1,52E-54
MOL1	Tspan5	4,76E-46	-0,62823546	0,238	0,45	1,54E-41
MOL1	Ggnbp2	5,31E-45	-0,821032897	0,047	0,191	1,72E-40
MOL1	Tent2	6,98E-42	-0,741476603	0,037	0,163	2,25E-37
MOL1	Sgk1	3,29E-41	0,8427396	0,123	0,021	1,06E-36
MOL1	Dock3	3,29E-39	-0,464224416	0,266	0,453	1,06E-34
MOL1	Atf2	9,83E-38	-0,671022573	0,082	0,226	3,17E-33
MOL1	Ubr3	1,72E-34	-0,527570726	0,193	0,363	5,54E-30
MOL1	Rabep1	2,53E-34	-0,553704406	0,1	0,236	8,17E-30
MOL1	Arhgap32	1,21E-33	-0,664799785	0,114	0,266	3,89E-29
MOL1	Otud7a	3,23E-33	-0,448887438	0,236	0,406	1,04E-28
MOL1	Sptbn1	3,12E-32	-0,328274891	0,327	0,494	1,01E-27
MOL1	110051M20R	3,48E-32	-0,679437989	0,074	0,202	1,12E-27
MOL1	Tra2b	6,58E-32	-0,698922278	0,091	0,229	2,13E-27
MOL1	R3hdm2	2,24E-30	-0,644145888	0,111	0,254	7,22E-26
MOL1	Slc16a7	1,67E-29	-0,654767059	0,078	0,203	5,38E-25
MOL1	Pnpla8	2,00E-28	-0,578053439	0,023	0,109	6,46E-24
MOL1	Usp34	1,53E-27	-0,314115189	0,365	0,526	4,93E-23
MOL1	Chchd3	1,57E-27	-0,565788866	0,123	0,259	5,07E-23
MOL1	Senp7	2,22E-27	-0,614754354	0,098	0,227	7,17E-23
MOL1	Usp32	6,69E-27	-0,568887472	0,159	0,304	2,16E-22
MOL1	Pcmt1	5,91E-26	-0,485129524	0,133	0,261	1,91E-21
MOL1	Dgki	7,73E-26	-0,318438362	0,364	0,521	2,50E-21
MOL1	Mpc1	1,47E-25	-0,623849623	0,065	0,175	4,75E-21
MOL1	Ric8b	1,58E-25	-0,588445262	0,026	0,106	5,11E-21
MOL1	Tra2a	1,60E-25	-0,286128253	0,295	0,435	5,17E-21
MOL1	Brd9	1,60E-25	-0,414102831	0,205	0,344	5,17E-21
MOL1	Foxp1	2,39E-25	-0,260649512	0,35	0,496	7,71E-21
MOL1	Wasl	1,51E-24	-0,573767037	0,051	0,15	4,88E-20
MOL1	Dmxl1	1,75E-24	-0,392477632	0,264	0,413	5,63E-20
MOL1	Nalcn	5,01E-24	-0,445702596	0,197	0,336	1,62E-19
MOL1	Rlf	1,43E-23	-0,554302301	0,087	0,199	4,62E-19
MOL1	Abhd18	2,20E-23	-0,472292928	0,041	0,125	7,12E-19
MOL1	Senp5	2,98E-23	-0,551832265	0,035	0,12	9,63E-19
MOL1	Rmnd5a	4,64E-23	-0,59255635	0,059	0,157	1,50E-18
MOL1	Nrxn2	7,26E-23	-0,51429524	0,031	0,11	2,34E-18
MOL1	l632427E13Ri	4,06E-22	-0,427414514	0,142	0,256	1,31E-17
MOL1	Ppp1r9a	4,33E-22	-0,434912512	0,186	0,315	1,40E-17
MOL1	Rad23b	9,80E-22	-0,522301207	0,027	0,1	3,16E-17
MOL1	P4ha1	1,26E-21	-0,532641022	0,06	0,156	4,08E-17
MOL1	Reps2	1,90E-21	-0,454033273	0,073	0,167	6,13E-17
MOL1	Yipf5	1,95E-21	-0,558681811	0,048	0,136	6,28E-17
MOL1	Csnk1g3	2,05E-21	-0,561223683	0,079	0,173	6,62E-17
MOL1	Cspp1	3,57E-21	-0,498081757	0,106	0,215	1,15E-16
MOL1	Arhgap21	1,09E-20	-0,423005212	0,246	0,37	3,50E-16
MOL1	Chordc1	1,12E-20	-0,510710951	0,032	0,11	3,61E-16
MOL1	Ranbp2	1,16E-20	-0,440635146	0,045	0,124	3,74E-16
MOL1	Trip12	1,17E-20	-0,330221137	0,239	0,364	3,78E-16

MOL1	Hnrnpu	1,72E-20	-0,377414137	0,173	0,288	5,55E-16
MOL1	Ppp1r12a	3,02E-20	-0,308192294	0,291	0,422	9,76E-16
MOL1	Paip2	3,64E-20	-0,401807103	0,185	0,308	1,17E-15
MOL1	Mprip	3,85E-20	-0,525194004	0,111	0,222	1,24E-15
MOL1	Arfgef1	5,36E-20	-0,459993081	0,097	0,199	1,73E-15
MOL1	Clcn3	6,02E-20	-0,467409629	0,058	0,142	1,94E-15
MOL1	Cul3	7,79E-20	-0,445058012	0,047	0,125	2,52E-15
MOL1	Spred1	1,42E-19	-0,453074166	0,149	0,264	4,59E-15
MOL1	Atp2c1	2,65E-19	-0,382626778	0,259	0,392	8,54E-15
MOL1	Tlk1	3,05E-19	-0,511430616	0,094	0,198	9,84E-15
MOL1	Atp11b	5,34E-19	-0,529271755	0,065	0,157	1,72E-14
MOL1	Tef	5,94E-19	-0,363063867	0,037	0,102	1,92E-14
MOL1	Slc24a5	1,22E-18	0,530758838	0,152	0,086	3,94E-14
MOL1	Ecpas	1,73E-18	-0,494516722	0,094	0,194	5,57E-14
MOL1	Tcerg1	2,73E-18	-0,550613653	0,072	0,16	8,83E-14
MOL1	Eif4g3	2,86E-18	-0,394119183	0,136	0,238	9,23E-14
MOL1	Adam22	3,03E-18	-0,487043021	0,091	0,186	9,79E-14
MOL1	Ccnt2	6,40E-18	-0,349036232	0,16	0,262	2,07E-13
MOL1	Man1a	6,49E-18	-0,49761231	0,18	0,289	2,10E-13
MOL1	Nudcd3	6,60E-18	-0,477907924	0,151	0,26	2,13E-13
MOL1	Il1rapl1	1,08E-17	-0,377923215	0,45	0,579	3,49E-13
MOL1	Luc7l3	1,29E-17	-0,364941101	0,215	0,334	4,16E-13
MOL1	Ube2d3	2,56E-17	-0,47445908	0,139	0,24	8,27E-13
MOL1	Hectd4	2,80E-17	-0,481617709	0,075	0,166	9,05E-13
MOL1	Fth1	2,92E-17	-0,365163895	0,332	0,456	9,43E-13
MOL1	Zfp407	3,44E-17	-0,451993709	0,134	0,24	1,11E-12
MOL1	Prrc2b	6,37E-17	-0,433203995	0,085	0,171	2,06E-12
MOL1	Fam76b	6,97E-17	-0,502372999	0,05	0,127	2,25E-12
MOL1	Rab7	1,08E-16	-0,497842827	0,037	0,106	3,49E-12
MOL1	Ep300	1,16E-16	-0,387218615	0,104	0,193	3,75E-12
MOL1	Klhl24	1,30E-16	-0,483434631	0,054	0,132	4,20E-12
MOL1	Pls3	2,61E-16	-0,258828636	0,054	0,111	8,43E-12
MOL1	Phf14	2,82E-16	-0,297098177	0,234	0,341	9,11E-12
MOL1	Yme1l1	1,02E-15	-0,447501874	0,075	0,157	3,29E-11
MOL1	Oga	1,15E-15	-0,386948247	0,082	0,162	3,72E-11
MOL1	Ncor1	1,63E-15	-0,298424511	0,32	0,433	5,25E-11
MOL1	Arnt	1,75E-15	0,25220329	0,251	0,243	5,65E-11
MOL1	Gnaq	2,26E-15	-0,408208236	0,237	0,357	7,31E-11
MOL1	Cmss1	2,74E-15	-0,413446294	0,258	0,375	8,86E-11
MOL1	Kidins220	4,88E-15	-0,301066399	0,178	0,267	1,57E-10
MOL1	Rb1cc1	5,51E-15	-0,428392502	0,148	0,249	1,78E-10
MOL1	Mnat1	6,65E-15	-0,376663186	0,131	0,218	2,15E-10
MOL1	Psme4	6,77E-15	-0,263517706	0,212	0,307	2,19E-10
MOL1	Phactr1	7,43E-15	-0,300851155	0,409	0,513	2,40E-10
MOL1	Ssb	1,07E-14	-0,298054101	0,054	0,112	3,46E-10
MOL1	Uri1	1,16E-14	-0,411291756	0,042	0,106	3,73E-10
MOL1	Atxn7	1,59E-14	-0,364649066	0,066	0,135	5,12E-10
MOL1	Adipor2	2,23E-14	0,331466551	0,409	0,381	7,18E-10
MOL1	Top1	2,25E-14	-0,311987805	0,153	0,24	7,25E-10
MOL1	Fer	3,18E-14	-0,370808404	0,161	0,259	1,03E-09
MOL1	Psmb2	3,49E-14	-0,372037496	0,086	0,163	1,13E-09
MOL1	AY036118	3,63E-14	-0,451929653	0,064	0,137	1,17E-09
MOL1	Ppwd1	4,43E-14	-0,432658555	0,059	0,131	1,43E-09

MOL1	Lnpep	4,43E-14	-0,368712344	0,113	0,198	1,43E-09
MOL1	Mobp	4,61E-14	0,254011632	0,832	0,816	1,49E-09
MOL1	Slmap	5,17E-14	-0,390722148	0,066	0,139	1,67E-09
MOL1	Rfx7	5,88E-14	-0,311704153	0,134	0,218	1,90E-09
MOL1	Larp4b	5,99E-14	-0,33154103	0,134	0,215	1,93E-09
MOL1	Vps13b	6,14E-14	-0,262827841	0,239	0,335	1,98E-09
MOL1	Ints6	6,52E-14	-0,368381473	0,054	0,121	2,11E-09
MOL1	Chd4	8,97E-14	-0,345508958	0,196	0,297	2,89E-09
MOL1	Polb	1,08E-13	-0,31469626	0,065	0,129	3,49E-09
MOL1	Cdk8	1,17E-13	-0,459848932	0,121	0,21	3,76E-09
MOL1	Gm49797	1,23E-13	-0,428518534	0,068	0,142	3,96E-09
MOL1	Dnajc1	1,32E-13	-0,272179369	0,223	0,319	4,25E-09
MOL1	Oxr1	1,45E-13	-0,356675025	0,302	0,395	4,67E-09
MOL1	Slc8a1	1,50E-13	-0,29527388	0,635	0,737	4,83E-09
MOL1	Tuba1a	1,96E-13	-0,320762868	0,115	0,193	6,32E-09
MOL1	Klc1	1,98E-13	-0,384548141	0,18	0,276	6,39E-09
MOL1	Tmem132d	2,05E-13	-0,528927981	0,045	0,11	6,61E-09
MOL1	Pcdh15	3,18E-13	-0,475638155	0,083	0,16	1,03E-08
MOL1	Rsb1	3,40E-13	-0,25825033	0,052	0,1	1,10E-08
MOL1	Mdga2	5,29E-13	-0,267025756	0,593	0,7	1,71E-08
MOL1	Iqcb1	5,79E-13	-0,447284269	0,045	0,108	1,87E-08
MOL1	Zfp445	5,96E-13	-0,32292485	0,238	0,341	1,92E-08
MOL1	Spire1	6,10E-13	-0,349045064	0,117	0,198	1,97E-08
MOL1	Cpeb3	6,15E-13	-0,268448043	0,302	0,41	1,99E-08
MOL1	Fubp1	6,18E-13	-0,298273048	0,225	0,324	1,99E-08
MOL1	Fam171b	7,81E-13	-0,409260522	0,083	0,158	2,52E-08
MOL1	Vps50	8,52E-13	-0,417709775	0,089	0,165	2,75E-08
MOL1	Gria4	1,01E-12	-0,35705729	0,223	0,328	3,26E-08
MOL1	Chfr	1,29E-12	-0,409460981	0,079	0,153	4,16E-08
MOL1	Gm20732	1,34E-12	-0,415108818	0,059	0,128	4,33E-08
MOL1	Wdr33	1,39E-12	-0,280146679	0,236	0,329	4,50E-08
MOL1	Prr14	1,43E-12	-0,417884129	0,051	0,116	4,63E-08
MOL1	Ncoa5	1,66E-12	-0,356983942	0,051	0,113	5,35E-08
MOL1	Cplane1	1,90E-12	-0,392608065	0,065	0,134	6,14E-08
MOL1	Spock1	2,11E-12	-0,290919879	0,459	0,507	6,81E-08
MOL1	Rasa1	2,41E-12	-0,313143551	0,106	0,18	7,79E-08
MOL1	Rc3h2	2,76E-12	-0,40883878	0,068	0,138	8,92E-08
MOL1	Map3k2	2,96E-12	-0,31045187	0,073	0,136	9,55E-08
MOL1	Ice1	3,03E-12	-0,408546027	0,101	0,182	9,78E-08
MOL1	Dennd5b	3,68E-12	-0,365899929	0,198	0,274	1,19E-07
MOL1	Strn3	4,44E-12	-0,301779978	0,17	0,256	1,43E-07
MOL1	Cadm2	4,48E-12	-0,346688584	0,265	0,366	1,45E-07
MOL1	Ncald	7,39E-12	-0,423555556	0,051	0,115	2,39E-07
MOL1	Ptpm	8,56E-12	-0,380633221	0,054	0,115	2,76E-07
MOL1	Samd4	8,98E-12	0,298293825	0,416	0,386	2,90E-07
MOL1	Hsp90ab1	1,08E-11	0,444486415	0,188	0,117	3,48E-07
MOL1	Rap1gds1	1,21E-11	-0,272751828	0,212	0,297	3,91E-07
MOL1	Gsk3b	1,49E-11	-0,317937388	0,141	0,223	4,80E-07
MOL1	Nckap1	1,65E-11	-0,269623478	0,122	0,188	5,34E-07
MOL1	Cntn3	1,71E-11	-0,340052788	0,099	0,172	5,53E-07
MOL1	Sec61a2	1,81E-11	-0,261983724	0,121	0,191	5,85E-07
MOL1	Sertad2	2,07E-11	-0,308270232	0,059	0,106	6,67E-07
MOL1	Rcan2	4,52E-11	0,332670872	0,306	0,269	1,46E-06

MOL1	Trim33	4,65E-11	-0,314726462	0,059	0,117	1,50E-06
MOL1	Tmem135	4,88E-11	-0,37577581	0,087	0,159	1,58E-06
MOL1	Syt12	6,18E-11	0,290103777	0,636	0,586	2,00E-06
MOL1	Paxbp1	7,48E-11	-0,317705834	0,193	0,278	2,42E-06
MOL1	Rabl6	9,49E-11	-0,288955531	0,114	0,175	3,06E-06
MOL1	Fam135a	1,24E-10	-0,374943947	0,132	0,215	4,00E-06
MOL1	Rab14	1,35E-10	-0,366097341	0,049	0,105	4,37E-06
MOL1	Nsd2	1,37E-10	-0,32527176	0,076	0,139	4,41E-06
MOL1	2210408121Ril	1,46E-10	-0,299469442	0,106	0,174	4,70E-06
MOL1	Nova1	1,72E-10	-0,263977677	0,056	0,105	5,56E-06
MOL1	Rufy2	1,85E-10	-0,324285555	0,065	0,123	5,99E-06
MOL1	Rufy3	2,15E-10	-0,26398189	0,215	0,298	6,95E-06
MOL1	Bmt2	2,46E-10	-0,384191585	0,06	0,122	7,95E-06
MOL1	Ttc37	2,54E-10	-0,302012338	0,056	0,11	8,18E-06
MOL1	Ccser2	3,91E-10	-0,285306649	0,128	0,184	1,26E-05
MOL1	Plaa	4,51E-10	-0,334484925	0,055	0,109	1,46E-05
MOL1	Usp33	4,68E-10	-0,379541799	0,118	0,194	1,51E-05
MOL1	St13	5,35E-10	-0,325851037	0,072	0,133	1,73E-05
MOL1	Fam184a	5,45E-10	-0,271149875	0,056	0,103	1,76E-05
MOL1	Arid1a	6,03E-10	0,305555756	0,228	0,192	1,95E-05
MOL1	Mrps5	6,57E-10	-0,263226392	0,057	0,106	2,12E-05
MOL1	Btrc	7,94E-10	-0,255324079	0,093	0,152	2,56E-05
MOL1	Tubgcp5	9,36E-10	-0,351593132	0,06	0,115	3,02E-05
MOL1	Mbd5	1,02E-09	-0,278304101	0,132	0,196	3,30E-05
MOL1	Lrrtm3	1,28E-09	-0,281050294	0,384	0,451	4,13E-05
MOL1	Dcaf5	1,40E-09	-0,383065874	0,057	0,115	4,53E-05
MOL1	Gnb1	1,45E-09	-0,31296631	0,17	0,24	4,67E-05
MOL1	Mphosph8	1,71E-09	-0,302655652	0,079	0,138	5,52E-05
MOL1	Chtop	1,73E-09	-0,362543683	0,083	0,142	5,58E-05
MOL1	Dync1li1	1,73E-09	-0,324067491	0,077	0,136	5,60E-05
MOL1	Atp9b	1,79E-09	-0,265742468	0,144	0,215	5,77E-05
MOL1	Akap7	1,88E-09	-0,303162283	0,107	0,163	6,06E-05
MOL1	Erlec1	2,48E-09	-0,328402599	0,052	0,106	8,01E-05
MOL1	Sec24b	2,58E-09	-0,251259757	0,141	0,2	8,33E-05
MOL1	Kdm5b	2,93E-09	-0,277170969	0,066	0,116	9,47E-05
MOL1	Dcaf6	3,63E-09	-0,259550984	0,177	0,25	0,000117297
MOL1	Htt	6,43E-09	-0,261485938	0,108	0,169	0,000207512
MOL1	Zfand5	6,57E-09	-0,263857913	0,179	0,255	0,000212238
MOL1	Zkscan3	6,91E-09	-0,318399245	0,079	0,138	0,000222942
MOL1	Nfyc	7,33E-09	-0,259272208	0,098	0,157	0,00023662
MOL1	Fars2	7,43E-09	-0,302117931	0,108	0,169	0,000239969
MOL1	Stag1	8,51E-09	-0,258702341	0,237	0,321	0,000274846
MOL1	Smap1	9,51E-09	-0,303344128	0,061	0,114	0,000307165
MOL1	Serbp1	9,59E-09	-0,278353507	0,061	0,112	0,000309734
MOL1	Gon4l	1,04E-08	-0,318570534	0,061	0,114	0,000334929
MOL1	Ube3c	1,05E-08	-0,262551578	0,205	0,274	0,000339188
MOL1	Csmd2	1,11E-08	-0,275681174	0,153	0,223	0,000356827
MOL1	Prkca	1,24E-08	0,261752284	0,484	0,432	0,000400021
MOL1	Armc8	1,44E-08	-0,297591952	0,113	0,177	0,000464192
MOL1	Dnaja2	1,61E-08	-0,251613017	0,061	0,109	0,000519375
MOL1	Timm23	1,93E-08	-0,325537027	0,055	0,105	0,000624592
MOL1	Ralbp1	2,25E-08	-0,310092854	0,09	0,134	0,000726579
MOL1	Syne1	2,42E-08	-0,30755801	0,082	0,136	0,000781469

MOL1	Lrrc58	2,77E-08	-0,260405144	0,063	0,111	0,000894822
MOL1	Cdkl5	2,78E-08	-0,318141564	0,074	0,131	0,000897871
MOL1	Sumo1	2,97E-08	-0,371331246	0,057	0,11	0,000958884
MOL1	Oxct1	3,73E-08	-0,258765645	0,179	0,252	0,001204546
MOL1	Tor1aip2	4,23E-08	-0,337663019	0,059	0,106	0,001364144
MOL1	Dhdds	5,05E-08	-0,357537226	0,056	0,106	0,001629442
MOL1	Ckb	5,25E-08	-0,291771527	0,064	0,112	0,001694052
MOL1	130040H23Ri	5,94E-08	-0,257089136	0,061	0,108	0,001917098
MOL1	Fam171a1	6,24E-08	-0,326082451	0,093	0,148	0,002015892
MOL1	Ext1	8,26E-08	-0,287772965	0,068	0,118	0,002667905
MOL1	Fam117b	9,30E-08	0,271493723	0,193	0,149	0,003001014
MOL1	Baz1b	9,63E-08	-0,317443996	0,104	0,167	0,003109244
MOL1	Ythdc2	9,92E-08	-0,341210841	0,082	0,14	0,003202507
MOL1	Tmx3	1,17E-07	-0,286381558	0,055	0,103	0,00379318
MOL1	Ncoa1	1,21E-07	0,299587709	0,203	0,158	0,003909001
MOL1	Xpo4	1,41E-07	-0,274253465	0,078	0,129	0,004541634
MOL1	Clec16a	1,54E-07	-0,265516724	0,116	0,173	0,004970631
MOL1	Cpne1	1,62E-07	-0,252234625	0,073	0,117	0,00523957
MOL1	Fut8	2,09E-07	-0,261938568	0,115	0,172	0,006747028
MOL1	Hdlbp	2,14E-07	-0,289738191	0,079	0,131	0,006903656
MOL1	Ctdspl	2,22E-07	-0,312240935	0,074	0,126	0,007164511
MOL1	Gcc2	2,58E-07	-0,295399302	0,101	0,156	0,008327521
MOL1	Pcca	2,74E-07	-0,250246603	0,154	0,219	0,008851749
MOL1	Med13l	2,98E-07	-0,310000425	0,054	0,101	0,00961172
MOL1	Hira	3,21E-07	-0,264876441	0,08	0,128	0,010370717
MOL1	Srsf4	3,30E-07	-0,260909739	0,062	0,106	0,010640464
MOL1	Apoe	3,42E-07	-0,32893793	0,059	0,101	0,011039179
MOL1	H3f3a	4,22E-07	0,33928678	0,158	0,106	0,013621393
MOL1	Slc30a9	4,99E-07	-0,280839707	0,062	0,11	0,016117416
MOL1	Ubxn7	5,40E-07	0,251833845	0,16	0,134	0,017422396
MOL1	Cald1	5,97E-07	0,263385501	0,234	0,197	0,019264771
MOL1	Tecr	6,98E-07	-0,262884417	0,183	0,247	0,022525119
MOL1	Orc2	7,38E-07	-0,30563076	0,078	0,129	0,023818425
MOL1	R3hdm1	7,51E-07	-0,261072385	0,258	0,319	0,02424847
MOL1	Cenpc1	9,80E-07	-0,263594873	0,09	0,138	0,031645713
MOL1	Cacul1	1,23E-06	-0,253629547	0,077	0,123	0,039813072
MOL2	Lrrc4c	3,22E-46	-0,83615097	0,262	0,509	1,04E-41
MOL2	Tspan5	1,39E-44	-0,565159708	0,343	0,594	4,49E-40
MOL2	Pcmttd1	8,92E-37	-0,517506151	0,163	0,347	2,88E-32
MOL2	Ggnbp2	1,45E-36	-0,718372578	0,067	0,23	4,67E-32
MOL2	Faim2	4,25E-35	-0,637053544	0,006	0,102	1,37E-30
MOL2	Arhgap32	7,89E-35	-0,540665169	0,161	0,344	2,55E-30
MOL2	R3hdm2	8,93E-35	-0,694076278	0,119	0,3	2,88E-30
MOL2	Foxp1	2,07E-34	-0,350951922	0,409	0,612	6,69E-30
MOL2	Pnpla8	1,18E-31	-0,617311098	0,025	0,136	3,81E-27
MOL2	Tra2b	5,29E-31	-0,551989776	0,112	0,269	1,71E-26
MOL2	Ubr3	5,57E-31	-0,504210661	0,23	0,422	1,80E-26
MOL2	Tent2	1,50E-30	-0,575857447	0,054	0,182	4,85E-26
MOL2	Dock3	3,20E-29	-0,37802283	0,337	0,528	1,03E-24
MOL2	Rabep1	2,44E-28	-0,610504343	0,112	0,27	7,88E-24
MOL2	Csnk1g3	3,00E-28	-0,654696957	0,087	0,236	9,69E-24
MOL2	Nrxn2	7,08E-28	-0,617123777	0,041	0,158	2,29E-23
MOL2	Luc7l3	1,06E-26	-0,338819773	0,245	0,405	3,41E-22

MOL2	Wasl	5,06E-26	-0,648301006	0,063	0,193	1,63E-21
MOL2	Rmnd5a	8,43E-26	-0,545476755	0,069	0,192	2,72E-21
MOL2	Otud7a	1,27E-25	-0,451604596	0,352	0,528	4,09E-21
MOL2	Chordc1	1,52E-25	-0,519926485	0,035	0,138	4,89E-21
MOL2	Tra2a	1,82E-25	-0,310483509	0,339	0,506	5,88E-21
MOL2	Reps2	1,97E-25	-0,54871692	0,101	0,242	6,35E-21
MOL2	Hectd4	5,27E-25	-0,373925421	0,094	0,209	1,70E-20
MOL2	Atf2	1,04E-24	-0,523294738	0,123	0,269	3,37E-20
MOL2	Sgk1	1,37E-24	0,662278043	0,111	0,024	4,42E-20
MOL2	Senp7	2,05E-24	-0,455903565	0,144	0,288	6,62E-20
MOL2	Rad23b	4,45E-24	-0,514370137	0,03	0,127	1,44E-19
MOL2	Nalcn	5,03E-24	-0,471233861	0,203	0,366	1,62E-19
MOL2	Phf14	2,04E-23	-0,358209846	0,266	0,426	6,57E-19
MOL2	Usp32	3,42E-23	-0,453549855	0,198	0,356	1,10E-18
MOL2	110051M20Ri	6,12E-23	-0,473294366	0,112	0,244	1,98E-18
MOL2	Chfr	9,95E-23	-0,430353921	0,097	0,214	3,21E-18
MOL2	Mpc1	1,79E-22	-0,539218864	0,081	0,205	5,78E-18
MOL2	Adipor2	3,68E-22	0,447778174	0,542	0,506	1,19E-17
MOL2	Chchd3	4,79E-22	-0,435049335	0,171	0,316	1,55E-17
MOL2	Brd9	7,69E-22	-0,33484793	0,266	0,413	2,48E-17
MOL2	Rlf	1,05E-21	-0,513535584	0,113	0,244	3,40E-17
MOL2	Pdia3	1,18E-21	-0,557434277	0,03	0,123	3,81E-17
MOL2	Zfp407	1,58E-21	-0,367227581	0,163	0,293	5,09E-17
MOL2	Rc3h2	1,62E-21	-0,543165659	0,078	0,199	5,22E-17
MOL2	Spred1	1,81E-21	-0,428945147	0,156	0,293	5,83E-17
MOL2	Atp2c1	2,27E-21	-0,362261211	0,317	0,48	7,32E-17
MOL2	Slmap	2,55E-21	-0,448883991	0,075	0,182	8,25E-17
MOL2	Phactr1	2,81E-21	-0,417399036	0,474	0,633	9,08E-17
MOL2	Sec23a	3,62E-21	-0,496886407	0,019	0,1	1,17E-16
MOL2	Atp11b	6,63E-21	-0,544453811	0,07	0,187	2,14E-16
MOL2	Slc8a1	9,23E-21	-0,407935466	0,669	0,791	2,98E-16
MOL2	P4ha1	1,40E-20	-0,493320321	0,053	0,153	4,51E-16
MOL2	Pam	1,75E-20	-0,523305877	0,021	0,1	5,64E-16
MOL2	Tef	1,78E-20	-0,421243718	0,038	0,127	5,74E-16
MOL2	Top1	4,00E-20	-0,406823372	0,171	0,306	1,29E-15
MOL2	Smarcc1	4,41E-20	-0,484779909	0,039	0,132	1,42E-15
MOL2	Tlk1	7,15E-20	-0,537454712	0,113	0,243	2,31E-15
MOL2	Pea15a	1,64E-19	-0,480758866	0,022	0,101	5,28E-15
MOL2	Eif4g3	1,84E-19	-0,446277649	0,171	0,31	5,93E-15
MOL2	Cspp1	2,98E-19	-0,408741215	0,13	0,252	9,62E-15
MOL2	Lnpep	3,28E-19	-0,451686067	0,139	0,27	1,06E-14
MOL2	Cnot4	5,86E-19	-0,279558848	0,276	0,413	1,89E-14
MOL2	Smg1	6,18E-19	-0,466084018	0,094	0,206	1,99E-14
MOL2	Hnrnpu	6,36E-19	-0,276210237	0,205	0,325	2,05E-14
MOL2	Sema6d	7,53E-19	-0,253576855	0,385	0,533	2,43E-14
MOL2	I632427E13Ri	1,73E-18	-0,366992555	0,173	0,298	5,57E-14
MOL2	Actr2	3,15E-18	-0,46590274	0,03	0,113	1,02E-13
MOL2	Ppp1r9a	3,42E-18	-0,304036748	0,247	0,383	1,11E-13
MOL2	Gnaq	5,68E-18	-0,364644812	0,284	0,433	1,84E-13
MOL2	Dlg2	9,39E-18	-0,377400566	0,386	0,546	3,03E-13
MOL2	Srsf5	9,91E-18	-0,275594828	0,205	0,324	3,20E-13
MOL2	Fam171b	1,00E-17	-0,379768477	0,102	0,206	3,24E-13
MOL2	Slc16a7	1,76E-17	-0,451474329	0,122	0,243	5,67E-13

MOL2	Oxr1	2,22E-17	-0,438323099	0,33	0,455	7,17E-13
MOL2	Ice1	2,24E-17	-0,529060034	0,106	0,225	7,24E-13
MOL2	Ranbp2	5,54E-17	-0,429232621	0,056	0,147	1,79E-12
MOL2	Fubp1	5,67E-17	-0,27951011	0,25	0,377	1,83E-12
MOL2	Il1rapl1	6,81E-17	-0,346282245	0,538	0,68	2,20E-12
MOL2	Psmb1	7,27E-17	-0,473880816	0,036	0,119	2,35E-12
MOL2	Ric8b	8,28E-17	-0,470218779	0,044	0,132	2,67E-12
MOL2	Gmcl1	1,22E-16	-0,425459226	0,036	0,116	3,93E-12
MOL2	Mapk14	1,28E-16	-0,424339365	0,028	0,102	4,15E-12
MOL2	Senp5	1,99E-16	-0,461574073	0,05	0,139	6,42E-12
MOL2	Ankrd13c	2,00E-16	-0,277619147	0,061	0,134	6,46E-12
MOL2	Cplane1	2,33E-16	-0,380304047	0,08	0,174	7,51E-12
MOL2	Abhd18	2,36E-16	-0,437675267	0,06	0,152	7,60E-12
MOL2	Adam22	3,42E-16	-0,443255756	0,123	0,238	1,11E-11
MOL2	Zyg11b	4,87E-16	-0,430502214	0,03	0,105	1,57E-11
MOL2	Dmxl1	6,45E-16	-0,284888555	0,332	0,473	2,08E-11
MOL2	Fam76b	8,16E-16	-0,487867059	0,064	0,158	2,63E-11
MOL2	Mprp	9,35E-16	-0,396589102	0,157	0,277	3,02E-11
MOL2	Zfp148	1,36E-15	-0,466080674	0,062	0,154	4,38E-11
MOL2	Fer	1,48E-15	-0,39232922	0,187	0,311	4,77E-11
MOL2	Nsd3	1,69E-15	-0,274075813	0,301	0,432	5,44E-11
MOL2	Btrc	1,88E-15	-0,479475339	0,1	0,209	6,07E-11
MOL2	Clasp1	2,05E-15	-0,40247414	0,044	0,125	6,60E-11
MOL2	Clcn3	3,28E-15	-0,427254322	0,079	0,175	1,06E-10
MOL2	Shisa4	9,83E-15	0,332596533	0,555	0,525	3,17E-10
MOL2	Ash1l	1,01E-14	-0,257668371	0,308	0,434	3,25E-10
MOL2	Arfgef1	1,22E-14	-0,325876638	0,132	0,233	3,95E-10
MOL2	Kidins220	1,59E-14	-0,264418214	0,229	0,342	5,15E-10
MOL2	Pls3	2,04E-14	-0,279226758	0,057	0,125	6,59E-10
MOL2	Ext1	2,18E-14	-0,465004267	0,096	0,197	7,04E-10
MOL2	Ube2d3	2,21E-14	-0,392635196	0,164	0,281	7,12E-10
MOL2	Strbp	2,50E-14	-0,402438421	0,122	0,227	8,07E-10
MOL2	Yme1l1	3,93E-14	-0,360657573	0,094	0,187	1,27E-09
MOL2	Hsd17b12	4,07E-14	-0,38609624	0,035	0,104	1,31E-09
MOL2	Oga	4,49E-14	-0,316150309	0,104	0,193	1,45E-09
MOL2	Bmt2	4,73E-14	-0,363894064	0,07	0,155	1,53E-09
MOL2	Paip2	5,43E-14	-0,264320134	0,249	0,363	1,75E-09
MOL2	Atp9b	6,14E-14	-0,298664469	0,172	0,275	1,98E-09
MOL2	Ep300	6,94E-14	-0,370999652	0,12	0,219	2,24E-09
MOL2	Cntn3	7,04E-14	-0,379744028	0,255	0,367	2,27E-09
MOL2	Ppp1r12a	9,79E-14	-0,282003498	0,345	0,477	3,16E-09
MOL2	Cdkl5	1,11E-13	-0,343132369	0,098	0,188	3,59E-09
MOL2	Trim35	1,66E-13	0,2598967	0,562	0,555	5,35E-09
MOL2	Klhl24	1,68E-13	-0,437318699	0,065	0,152	5,41E-09
MOL2	Nckap1	1,79E-13	-0,260202869	0,155	0,248	5,77E-09
MOL2	Rab7	2,05E-13	-0,451193967	0,054	0,135	6,62E-09
MOL2	Fam135a	3,27E-13	-0,339202964	0,157	0,262	1,06E-08
MOL2	Cadm2	3,76E-13	-0,325479175	0,326	0,456	1,21E-08
MOL2	Man1a	4,43E-13	-0,454566973	0,143	0,248	1,43E-08
MOL2	Tcerg1	5,29E-13	-0,454895731	0,103	0,202	1,71E-08
MOL2	Rufy2	5,31E-13	-0,414846496	0,073	0,16	1,71E-08
MOL2	Dennd5b	6,19E-13	-0,396325714	0,224	0,338	2,00E-08
MOL2	Trappc6b	9,18E-13	-0,421693097	0,052	0,128	2,96E-08

MOL2	Dhx15	1,40E-12	-0,400639809	0,065	0,144	4,53E-08
MOL2	Zfp369	1,74E-12	-0,409599642	0,043	0,113	5,60E-08
MOL2	Polr3e	1,74E-12	0,329592748	0,193	0,175	5,63E-08
MOL2	Chd4	2,43E-12	-0,309190246	0,22	0,332	7,86E-08
MOL2	Dcaf5	2,60E-12	-0,344085173	0,073	0,152	8,40E-08
MOL2	Srgap1	2,67E-12	0,337343096	0,33	0,31	8,61E-08
MOL2	Dync1li1	2,77E-12	-0,42099388	0,077	0,161	8,94E-08
MOL2	Tuba1a	3,65E-12	-0,29039735	0,139	0,227	1,18E-07
MOL2	Akr1a1	3,69E-12	-0,296391572	0,056	0,12	1,19E-07
MOL2	Iqcb1	4,23E-12	-0,450276607	0,057	0,133	1,37E-07
MOL2	Syt11	4,25E-12	-0,287945245	0,406	0,524	1,37E-07
MOL2	Armc8	4,96E-12	-0,3243553	0,133	0,227	1,60E-07
MOL2	Epb41l1	5,39E-12	-0,378277642	0,057	0,133	1,74E-07
MOL2	Gnb1	5,54E-12	-0,294695367	0,192	0,297	1,79E-07
MOL2	130040H23Ri	6,03E-12	-0,336712918	0,061	0,134	1,95E-07
MOL2	Sertad2	6,23E-12	-0,411196346	0,065	0,145	2,01E-07
MOL2	Spire1	6,34E-12	-0,398990603	0,137	0,239	2,05E-07
MOL2	Arf4	6,43E-12	-0,355593799	0,046	0,115	2,08E-07
MOL2	Fam184a	7,52E-12	-0,259604875	0,044	0,101	2,43E-07
MOL2	Usp33	8,14E-12	-0,282127208	0,138	0,227	2,63E-07
MOL2	Sumo1	8,36E-12	-0,347794745	0,078	0,154	2,70E-07
MOL2	Ahcyl1	9,58E-12	-0,388317641	0,046	0,116	3,09E-07
MOL2	Nova1	1,02E-11	-0,251844301	0,056	0,115	3,29E-07
MOL2	Pdcd10	1,11E-11	-0,272534775	0,047	0,109	3,57E-07
MOL2	Smarca4	1,32E-11	-0,259826877	0,059	0,121	4,26E-07
MOL2	Psip1	1,39E-11	-0,255383788	0,171	0,261	4,48E-07
MOL2	Trim33	1,81E-11	-0,365670203	0,08	0,161	5,84E-07
MOL2	Baz1b	1,81E-11	-0,311610358	0,128	0,217	5,86E-07
MOL2	Rsb1l	2,11E-11	-0,264525409	0,117	0,197	6,80E-07
MOL2	Eml1	2,25E-11	0,328925036	0,525	0,487	7,26E-07
MOL2	Gm49797	2,26E-11	-0,320089919	0,091	0,168	7,29E-07
MOL2	Atxn10	2,48E-11	-0,26637725	0,049	0,109	8,00E-07
MOL2	Tor1aip2	2,66E-11	-0,415581204	0,06	0,137	8,60E-07
MOL2	Arid1a	2,97E-11	0,276172161	0,254	0,231	9,59E-07
MOL2	Pten	3,15E-11	-0,261746569	0,111	0,188	1,02E-06
MOL2	Ptpm	3,23E-11	-0,364119812	0,08	0,159	1,04E-06
MOL2	Tmem135	3,68E-11	-0,256332242	0,12	0,201	1,19E-06
MOL2	Mdn1	4,03E-11	-0,307606467	0,048	0,111	1,30E-06
MOL2	Rb1cc1	4,15E-11	-0,256689215	0,187	0,281	1,34E-06
MOL2	Rala	5,01E-11	-0,292841269	0,064	0,131	1,62E-06
MOL2	Gon4l	5,46E-11	-0,260688467	0,083	0,15	1,76E-06
MOL2	Gria4	5,81E-11	-0,314785049	0,251	0,364	1,88E-06
MOL2	Rab14	7,47E-11	-0,326154936	0,063	0,13	2,41E-06
MOL2	Ssb	1,01E-10	-0,345469989	0,057	0,127	3,24E-06
MOL2	Uri1	1,08E-10	-0,348711272	0,054	0,121	3,50E-06
MOL2	Fam171a1	1,17E-10	-0,36991405	0,147	0,244	3,79E-06
MOL2	Mnat1	1,23E-10	-0,355971184	0,155	0,252	3,98E-06
MOL2	Zfand5	1,40E-10	-0,261630699	0,198	0,294	4,52E-06
MOL2	Gm20732	1,50E-10	-0,302497507	0,065	0,133	4,85E-06
MOL2	R3hdm1	2,03E-10	-0,307530112	0,279	0,389	6,55E-06
MOL2	Rcan2	2,30E-10	0,343764876	0,329	0,297	7,41E-06
MOL2	Med13l	2,93E-10	-0,340046692	0,061	0,13	9,45E-06
MOL2	Rasa1	3,16E-10	-0,252708337	0,134	0,212	1,02E-05

MOL2	Cdk8	3,22E-10	-0,454366203	0,121	0,213	1,04E-05
MOL2	Prrc2b	3,44E-10	-0,322138347	0,114	0,198	1,11E-05
MOL2	Med13	4,01E-10	-0,303027171	0,163	0,251	1,29E-05
MOL2	Ube2g1	4,43E-10	-0,293593262	0,25	0,346	1,43E-05
MOL2	Selenot	5,07E-10	0,368762662	0,173	0,129	1,64E-05
MOL2	Dop1a	5,40E-10	-0,299703348	0,211	0,311	1,74E-05
MOL2	Map3k2	6,53E-10	-0,361199575	0,086	0,165	2,11E-05
MOL2	Srr	7,07E-10	-0,262835118	0,049	0,104	2,28E-05
MOL2	Pcdh15	1,01E-09	-0,46069252	0,094	0,176	3,27E-05
MOL2	Zmym5	1,22E-09	-0,295332415	0,046	0,105	3,94E-05
MOL2	Serbp1	1,46E-09	-0,350126078	0,073	0,146	4,71E-05
MOL2	Ldlrad4	1,69E-09	-0,337751162	0,13	0,215	5,44E-05
MOL2	Pum1	2,07E-09	-0,254799447	0,209	0,298	6,68E-05
MOL2	Yipf5	2,21E-09	-0,362903738	0,063	0,132	7,13E-05
MOL2	Mphosph8	2,22E-09	-0,349133637	0,099	0,176	7,16E-05
MOL2	Rbm33	3,09E-09	-0,256147789	0,157	0,237	9,98E-05
MOL2	Tubgcp5	3,15E-09	-0,2885294	0,067	0,13	0,00010167
MOL2	Angel2	3,27E-09	-0,314425362	0,056	0,117	0,000105602
MOL2	Ncald	4,16E-09	-0,337245744	0,073	0,139	0,000134366
MOL2	Vezt	4,53E-09	-0,250359761	0,067	0,126	0,0001462
MOL2	Plaa	4,54E-09	-0,286250767	0,073	0,138	0,000146729
MOL2	Pvt1	4,75E-09	0,259591622	0,218	0,198	0,000153221
MOL2	Larp4b	4,80E-09	-0,258166963	0,154	0,234	0,000155
MOL2	Nudcd3	5,11E-09	-0,338554538	0,187	0,278	0,000165026
MOL2	Prpf40a	5,35E-09	-0,289980809	0,245	0,344	0,000172763
MOL2	AY036118	5,49E-09	-0,383876876	0,064	0,127	0,000177302
MOL2	Ahctf1	6,60E-09	-0,345401709	0,052	0,115	0,00021298
MOL2	Kif3c	6,94E-09	0,268270176	0,254	0,231	0,000224176
MOL2	Wipf2	7,06E-09	-0,250670246	0,072	0,132	0,000228002
MOL2	Glul	7,54E-09	0,254475229	0,324	0,305	0,000243464
MOL2	Syne1	8,94E-09	-0,288872904	0,067	0,13	0,0002887
MOL2	Ythdf3	9,77E-09	-0,270829253	0,09	0,157	0,000315516
MOL2	Erlec1	9,94E-09	-0,30991859	0,065	0,128	0,000321062
MOL2	Setdb1	1,13E-08	-0,334859808	0,083	0,155	0,000365151
MOL2	Fut8	1,36E-08	-0,346414062	0,133	0,217	0,000438561
MOL2	Chm	1,43E-08	-0,275098955	0,084	0,149	0,000460656
MOL2	Cul3	1,48E-08	-0,299240736	0,086	0,154	0,000476781
MOL2	Polb	1,61E-08	-0,303361661	0,089	0,158	0,000520062
MOL2	Naa15	1,65E-08	0,295698802	0,197	0,162	0,000534168
MOL2	Ppip5k1	2,06E-08	-0,332985143	0,06	0,122	0,000665104
MOL2	Ppwd1	2,25E-08	-0,374843717	0,07	0,137	0,000725052
MOL2	Ncoa1	2,27E-08	0,316285156	0,244	0,195	0,000732271
MOL2	Grik1	3,36E-08	-0,284323137	0,285	0,378	0,001084888
MOL2	Rnf103	3,45E-08	-0,359272613	0,048	0,105	0,001113834
MOL2	Prr14	4,27E-08	-0,353043022	0,061	0,124	0,001379416
MOL2	Dip2c	4,53E-08	-0,325574692	0,098	0,171	0,001461022
MOL2	Xkr4	5,03E-08	-0,302316768	0,212	0,301	0,001625341
MOL2	Cmss1	5,12E-08	-0,256245637	0,291	0,388	0,001653994
MOL2	Tbce	5,28E-08	-0,328226705	0,11	0,186	0,001703291
MOL2	Lamc1	7,97E-08	-0,324276365	0,07	0,132	0,002573253
MOL2	Xpo4	9,14E-08	-0,294978431	0,094	0,159	0,002952183
MOL2	i330434G04Ri	9,60E-08	-0,29864731	0,062	0,121	0,003100293
MOL2	Dhdds	1,28E-07	-0,329641705	0,086	0,154	0,004132488

MOL2	Rsb1	1,36E-07	-0,259204297	0,059	0,108	0,004395029
MOL2	Pum2	1,59E-07	-0,269770364	0,165	0,245	0,005126964
MOL2	Chtop	1,59E-07	-0,250097487	0,102	0,165	0,005127932
MOL2	Vps50	1,61E-07	-0,250289043	0,128	0,198	0,005193094
MOL2	Tanc2	1,64E-07	-0,268205411	0,121	0,192	0,005295494
MOL2	2210408121Ril	2,13E-07	-0,300181428	0,133	0,208	0,006869534
MOL2	Galnt16	2,25E-07	0,349830043	0,148	0,099	0,007256833
MOL2	Sptlc1	2,53E-07	-0,25922058	0,066	0,12	0,008176094
MOL2	Wdr45b	3,25E-07	-0,275912544	0,061	0,114	0,010496944
MOL2	Ythdc2	3,25E-07	-0,268924093	0,115	0,185	0,010497184
MOL2	Nfib	3,45E-07	-0,255184947	0,162	0,238	0,011125513
MOL2	Ccdc59	3,66E-07	-0,345778291	0,056	0,107	0,011828944
MOL2	Itm2b	4,35E-07	-0,289877026	0,052	0,103	0,014056085
MOL2	Tmem132d	5,68E-07	-0,348037782	0,059	0,114	0,01834772
MOL2	Tecr	6,47E-07	-0,253203364	0,199	0,279	0,020874409
MOL2	Gcc2	7,92E-07	-0,307663585	0,131	0,2	0,02558473
MOL2	Uhrf2	1,15E-06	-0,263107037	0,108	0,172	0,036992453
MOL2	Ppp2r2c	1,20E-06	-0,291636527	0,146	0,215	0,038614502

Supplementary Table 2

cluster	geneSet	description	link	size	overlap	expect	enrichmentRatio	pValue	FDR	overlapId	userid
OPC	GO:0099177	regulation of trans-synaptic signaling	http://amigo.geneontology.org/amigo/term/GO:0099177	482	45	9,217916457	4,881797336	0	0	11441;11938;11941;12286;12287;12289;12296;12298;12552;12877;14677;14799;14810;14811;14812;15893;17260;18183;19055;20614;20910;20979;22249;22628;26413;29873;54195;56508;56839;64085;65945;72555;76089;78808;108071;111173;210274;214162;217692;244310;246317;319613;320127;327814;380702	Atp2a2;Cacnb4;Rapgef2;Atp2b2;Lgi1;Cdh11;Grm5;Mapk1;Syt1;Gria1;Kmt2a;Stxbp5;Ica1;Shank2;Ppp3ca;Neto1;Ppfi2;Dgki;Chrna7;Nrg3;Grin2a;Dlgap2;Cacna1a;Clstn2;Shisa9;Gucy1b1;Stxbp1;Cacna1b;Cpeb1;Cspg5;Grin2b;Shisa6;Unc13b;Grin1;Cacnb2;Clstn1;Ywhag;Cacna1d;Sipa1l1;Sybu;Gnai1;Rapgef4;Mef2c;Erc1;Snap25
OPC	GO:0050808	synapse organization	http://amigo.geneontology.org/amigo/term/GO:0050808	429	41	8,204328133	4,997362287	0	0	11418;11441;11941;12286;12296;12298;12540;13839;14810;14812;17260;19744;20411;20616;22215;22249;56508;64085;65945;76965;108071;111173;210274;217692;226016;234214;234267;236915;238205;238988;241514;242384;319504;319613;327814;333605;380702;382253;399558;433485;545156	Sorbs2;Nrcam;Asic2;Cacnb4;Erc2;Atp2b2;Grm5;Gpm6a;Lrfn5;Flrt2;Frmpd4;Arhgef9;Ube3a;Shank2;Cdkl5;Ppfi2;Chrna7;Cacna1a;Abhd17b;Sorbs1;Clstn2;Kalrn;Epha5;Zfp804a;Snap91;Syndig1;Grin2b;Shisa6;Unc13b;Rheb;Grin1;Cacnb2;Clstn1;Cdc42;Slitrk1;Sipa1l1;Sybu;Rapgef4;Mef2c;Erc1;Lingo2
OPC	GO:0042391	regulation of membrane potential	http://amigo.geneontology.org/amigo/term/GO:0042391	425	39	8,127830901	4,798328173	2,22E-16	6E-14	11418;11441;11938;12286;12289;12293;12296;12298;14400;14401;14402;14407;14799;14810;14811;14812;16531;17260;19055;20191;20238;20265;20269;20273;20541;22067;22249;52882;53623;56508;108071;170738;210274;214162;238161;246317;268345;319504;320127	Atp2a2;Rgs7bp;Nrcam;Asic2;Cacnb4;Gabrb1;Gabrb2;Scn1a;Grm5;Atxn1;Gabrg3;Gria1;Gabrb3;Kmt2a;Kcnma1;Shank2;Ppp3ca;Kcnh7;Cacna2d1;Kcnc2;Neto1;Dgki;Chrna7;Grin2a;Cacna1a;Akap6;Trpc5;Grin2b;Unc13b;Grin1;Cacnb2;Scn8a;Gria3;Cacna1d;Ryr2;Rapgef4;Mef2c;Scn3a;Slc8a1
OPC	GO:0050803	regulation of synapse structure or activity	http://amigo.geneontology.org/amigo/term/GO:0050803	264	31	5,048817313	6,140051834	4,441E-16	9E-14	11418;11441;12540;14810;14812;17260;19744;20411;20616;22215;56508;64085;65945;76965;210274;217692;26016;234214;234267;236915;238205;241514;242384;319504;319613;333605;380702;382253;399558;433485;545156	Sorbs2;Nrcam;Asic2;Gpm6a;Lrfn5;Flrt2;Frmpd4;Arhgef9;Ube3a;Shank2;Cdkl5;Chrna7;Abhd17b;Sorbs1;Clstn2;Kalrn;Zfp804a;Snap91;Syndig1;Grin2b;Shisa6;Rheb;Grin1;Clstn1;Cdc42;Slitrk1;Sipa1l1;Sybu;Rapgef4;Mef2c;Lingo2

OPC	GO:0099504	synaptic vesicle cycle	http://amigo.geneontology.org/amigo/term/GO:0099504	221	24	4,226472068	5,67849488	5,794E-12	9,4E-10	11441;11938;12286;12287;12289;12296;12298;13002;20614;20616;20910;20965;20979;22249;27062;29873;56508;78808;94090;111173;238988;320127;327814;433485	Atp2a2;Cacnb4;Erc2;Cadps;Syt1;Stxbp5;Ppfia2;Dnajc5;Dgki;Chrna7;Cacna1a;Stxbp1;Cacna1b;Snap91;Cspg5;Syndig1;Unc13b;Cacnb2;Cacna1d;Syn2;Rapgef4;Trim9;Erc1;Snap25
OPC	GO:0099003	vesicle-mediated transport in synapse	http://amigo.geneontology.org/amigo/term/GO:0099003	242	24	4,628082536	5,185732927	4,023E-11	5,4E-09	11441;11938;12286;12287;12289;12296;12298;16574;20614;20616;20910;20979;22249;26414;27062;29873;65945;74053;78808;94090;111173;238988;320127;327814	Atp2a2;Mapk10;Cacnb4;Erc2;Cadps;Grip1;Syt1;Stxbp5;Ppfia2;Kif5c;Dgki;Chrna7;Cacna1a;Stxbp1;Cacna1b;Snap91;Cspg5;Unc13b;Cacnb2;Clstn1;Cacna1d;Trim9;Erc1;Snap25
OPC	GO:0051648	vesicle localization	http://amigo.geneontology.org/amigo/term/GO:0051648	272	25	5,201811777	4,806017802	8,094E-11	9,4E-09	11441;11938;12286;12287;12289;12296;12298;13426;16574;20614;20616;20910;20965;20979;22249;27062;29873;78808;94090;111173;238988;319613;320127;327814;433485	Atp2a2;Cacnb4;Erc2;Cadps;Syt1;Stxbp5;Ppfia2;Kif5c;Dgki;Chrna7;Cacna1a;Stxbp1;Cacna1b;Snap91;Cspg5;Syndig1;Unc13b;Cacnb2;Cacna1d;Syn2;Sybu;Trim9;Erc1;Dync1i1;Snap25
OPC	GO:0006836	neurotransmitter transport	http://amigo.geneontology.org/amigo/term/GO:0006836	289	25	5,526925013	4,523310872	2,957E-10	2,7E-08	11441;11938;12286;12287;12289;12296;12298;15893;17260;19276;20614;20616;20910;20965;20979;22249;27062;29873;74136;78808;94090;111173;238988;320127;327814	Atp2a2;Cacnb4;Erc2;Cadps;Syt1;Stxbp5;Ica1;Ptprn2;Ppfia2;Dgki;Chrna7;Cacna1a;Stxbp1;Sec14l1;Cacna1b;Snap91;Cspg5;Unc13b;Cacnb2;Cacna1d;Syn2;Mef2c;Trim9;Erc1;Snap25
OPC	GO:0001505	regulation of neurotransmitter levels	http://amigo.geneontology.org/amigo/term/GO:0001505	361	28	6,903875189	4,05569325	3,04E-10	2,7E-08	11441;11938;11941;12286;12287;12289;12296;12298;12660;14811;15893;16423;17260;19276;20614;20616;20910;20965;20979;22249;27062;29873;78808;94090;111173;238988;320127;327814	Atp2a2;Cacnb4;Erc2;Cadps;Atp2b2;Cd47;Syt1;Stxbp5;Ica1;Ptprn2;Ppfia2;Dgki;Chrna7;Grin2a;Cacna1a;Stxbp1;Cacna1b;Snap91;Cspg5;Chka;Unc13b;Cacnb2;Cacna1d;Syn2;Mef2c;Trim9;Erc1;Snap25
OPC	GO:0016358	dendrite development	http://amigo.geneontology.org/amigo/term/GO:0016358	262	23	5,010568697	4,590297308	1,182E-09	9,6E-08	11441;12286;12540;13131;13839;14810;17260;19055;20393;22067;22215;26419;56508;74053;76089;93686;94253;210274;217692;239985;277360;382253;545156	Rbfox2;Rapgef2;Grip1;Ube3a;Shank2;Ppp3ca;Cdkl5;Chrna7;Cacna1a;Dab1;Kalrn;Epha5;Prex1;Trpc5;Sgk1;Mapk8;Arid1b;Grin1;Hecw1;Cdc42;Sipa1l1;Rapgef4;Mef2c
OPC	GO:0034765	regulation of ion transmembrane transport	http://amigo.geneontology.org/amigo/term/GO:0034765	439	30	8,395571213	3,573312552	1,431E-09	1,1E-07	11418;12286;12287;12289;12293;12294;12296;12298;16497;16531;17260;20191;20265;20269;20273;20541;22063;56461;65973;72555;80334;94253;108071;170738;210274;226922;238161;246317;268345;380702	Asic2;Cacnb4;Scn1a;Grm5;Kcnip3;Cacna2d3;Kcnma1;Shank2;Kcnh7;Cacna2d1;Kcnc2;Neto1;Cacna1a;Akap6;Shisa9;Cacna1b;Kcnab1;Shisa6;Kcnq5;Kcnip4;Hecw1;Cacnb2;Scn8a;Cacna1d;Ryr2;Asph;Mef2c;Trpc1;Scn3a;Slc8a1

OPC	GO:1990778	protein localization to cell periphery	http://amigo.geneontology.org/amigo/term/GO:1990778	324	25	6,196275793	4,034681611	3,197E-09	2,2E-07	12296;14677;14810;14811;20411;20614;20910;26414;56224;56374;56430;56461;56508;56839;58998;65945;67295;74053;74741;76089;80334;106572;241263;242274;545156	Mapk10;Rapgef2;Lgi1;Grip1;Kcnip3;Lrrc7;Tspan5;Clip1;Neto1;Grin2a;Sorbs1;Kctd5;Stxbp1;C2cd5;Tmem59;Gpr158;Kcnip4;Grin1;Cacnb2;Clstn1;Gnai1;Rapgef4;Snap25;Rab3c
OPC	GO:0035418	protein localization to synapse	http://amigo.geneontology.org/amigo/term/GO:0035418	82	13	1,568193256	8,289794608	4,705E-09	2,9E-07	11418;14810;14811;16574;20614;26414;56508;56839;65945;74053;226016;242274;545156	Asic2;Mapk10;Lgi1;Grip1;Lrrc7;Kif5c;Grin2a;Abhd17b;Kalrn;Grin1;Clstn1;Rapgef4;Snap25
OPC	GO:0035637	multicellular organismal signaling	http://amigo.geneontology.org/amigo/term/GO:0035637	134	16	2,562657272	6,243519246	5,52E-09	3,2E-07	11441;12286;12289;12293;12296;12298;14799;16531;20191;20265;20269;20273;20541;56508;80297;319504	Nrcam;Cacnb4;Scn1a;Gria1;Kcnma1;Cacna2d1;Chrna7;Cacna1a;Cacnb2;Scn8a;Cacna1d;Ryr2;Rapgef4;Sptbn4;Scn3a;Slc8a1
OPC	GO:0023061	signal release	http://amigo.geneontology.org/amigo/term/GO:0023061	492	30	9,409159537	3,188382542	1,992E-08	1,1E-06	11441;11938;12286;12287;12289;12296;12298;13839;15893;17260;19055;19276;20614;20616;20910;20965;20979;22249;26950;27062;29873;56508;78808;94090;111173;238988;319613;320127;327814;545156	Atp2a2;Cacnb4;Erc2;Cadps;Vsnl1;Syt1;Stxbp5;Ica1;Ptprn2;Ppp3ca;Ppfia2;Dgki;Chrna7;Cacna1a;Kalrn;Stxbp1;Cacna1b;Epha5;Snap91;Cspg5;Unc13b;Cacnb2;Cacna1d;Syn2;Sybu;Rapgef4;Mef2c;Trim9;Erc1;Snap25
OPC	GO:0051668	localization within membrane	http://amigo.geneontology.org/amigo/term/GO:0051668	171	17	3,270256668	5,198368729	2,982E-08	1,5E-06	12286;14812;16574;20411;20614;26414;56430;56508;56839;65945;74053;234214;236915;242274;246317;380702;545156	Sorbs2;Mapk10;Lgi1;Grip1;Lrrc7;Arhgef9;Clip1;Neto1;Kif5c;Cacna1a;Sorbs1;Kalrn;Grin2b;Shisa6;Clstn1;Rapgef4;Snap25
OPC	GO:0006887	exocytosis	http://amigo.geneontology.org/amigo/term/GO:0006887	357	24	6,827377957	3,515258735	9,434E-08	4,5E-06	11441;11938;12286;12287;12289;12296;12298;20614;20910;20979;22249;26950;27062;29873;56508;67295;78808;94090;106572;111173;238266;238988;320127;327814	Atp2a2;Cacnb4;Erc2;Cadps;Vsnl1;Syt1;Stxbp5;Ppfia2;Rab31;Dgki;Chrna7;Cacna1a;Stxbp1;Cacna1b;Cspg5;Unc13b;Cacnb2;Cacna1d;Syt16;Rapgef4;Trim9;Erc1;Snap25;Rab3c
OPC	GO:0007215	glutamate receptor signaling pathway	http://amigo.geneontology.org/amigo/term/GO:0007215	91	12	1,740312028	6,895315211	1,541E-07	7E-06	14799;14810;14811;14812;17260;53623;72555;108071;210274;246317;380702;545156	Grm5;Gria1;Shank2;Neto1;Grin2a;Shisa9;Kalrn;Grin2b;Shisa6;Grin1;Gria3;Mef2c
OPC	GO:0032409	regulation of transporter activity	http://amigo.geneontology.org/amigo/term/GO:0032409	247	19	4,723704076	4,022267206	2,796E-07	1,2E-05	11418;12286;12289;12293;12296;12298;16497;17260;20191;65973;72555;94253;108071;210274;214162;238161;246317;268345;380702	Asic2;Cacnb4;Grm5;Kmt2a;Shank2;Cacna2d1;Kcnc2;Neto1;Cacna1a;Akap6;Shisa9;Kcnab1;Shisa6;Hecw1;Cacnb2;Cacna1d;Ryr2;Asph;Mef2c

OPC	GO:0050890	cognition	http://amigo.geneontology.org/amigo/term/GO:0050890	309	21	5,909411173	3,553653551	5,178E-07	2,1E-05	11441;14799;14810;14811;14812;16497;17260;20238;20393;20614;56710;66797;80286;108071;109205;210274;214162;224938;246317;320127;545156	Cntnap2;Brinp1;Grm5;Atxn1;Gria1;Kmt2a;Shank2;Neto1;Dgki;Chrna7;Grin2a;Kalrn;Kcnab1;Sobp;Grin2b;Tusc3;Sgk1;Grin1;Pja2;Mef2c;Snap25
OPC	GO:0007214	gamma-aminobutyric acid signaling pathway	http://amigo.geneontology.org/amigo/term/GO:0007214	27	7	0,516356316	13,55653021	5,535E-07	2,1E-05	12286;12298;14400;14401;14402;14407;242425	Cacnb4;Gabbrb1;Gabbrb2;Gabbrg3;Gabbr2;Gabbrb3;Cacna1a
OPC	GO:0007626	locomotory behavior	http://amigo.geneontology.org/amigo/term/GO:0007626	235	18	4,49421238	4,005151176	6,176E-07	2,3E-05	11941;12286;12287;12298;13131;14810;14811;16531;20238;20265;20273;20614;26414;80297;94229;108071;109205;545156	Mapk10;Cacnb4;Atp2b2;Scn1a;Grm5;Atxn1;Kcnma1;Grin2a;Cacna1a;Slc4a10;Dab1;Kalrn;Cacna1b;Sobp;Grin1;Scn8a;Snap25;Sptbn4
OPC	GO:0030534	adult behavior	http://amigo.geneontology.org/amigo/term/GO:0030534	167	15	3,193759436	4,696659313	7,386E-07	2,6E-05	11441;12286;12298;13131;14810;16531;20238;20265;20273;66797;76965;80297;210274;217843;545156	Cacnb4;Unc79;Cntnap2;Scn1a;Atxn1;Kcnma1;Shank2;Chrna7;Cacna1a;Dab1;Kalrn;Grin1;Scn8a;Slitrk1;Sptbn4
OPC	GO:0106027	neuron projection organization	http://amigo.geneontology.org/amigo/term/GO:0106027	93	11	1,778560644	6,184776457	1,551E-06	5,2E-05	11441;12540;13839;14810;14812;22215;210274;217692;226016;241514;545156	Ube3a;Shank2;Chrna7;Abhd17b;Kalrn;Epha5;Zfp804a;Grin2b;Grin1;Cdc42;Sipa1l1
OPC	GO:0072511	divalent inorganic cation transport	http://amigo.geneontology.org/amigo/term/GO:0072511	450	25	8,605938601	2,90497076	1,802E-06	5,9E-05	11441;11938;11941;12286;12287;12289;12293;12294;12296;12298;14810;14811;14812;19055;20191;20192;20541;22063;22067;65973;67887;80286;234267;235574;238161	Atp2a2;Cacnb4;Atp2b2;Gpm6a;Cacna2d3;Ppp3ca;Cacna2d1;Chrna7;Grin2a;Cacna1a;Ryr3;Akap6;Cacna1b;Saraf;Trpc5;Grin2b;Tusc3;Grin1;Cacnb2;Cacna1d;Ryr2;Asph;Trpc1;Atp2c1;Slc8a1
OPC	GO:0055074	calcium ion homeostasis	http://amigo.geneontology.org/amigo/term/GO:0055074	482	26	9,217916457	2,820594016	1,917E-06	6E-05	11441;11938;11941;12286;12287;12289;12293;12296;12298;14799;14810;14811;14812;20191;20192;20541;22063;22067;65945;65973;66168;67163;108071;111173;235574;238161	Atp2a2;Cacnb4;Atp2b2;Grm5;Gria1;Cacna2d1;Grina;Chrna7;Grin2a;Cacna1a;Ryr3;Akap6;Cacna1b;Trpc5;Grin2b;Grin1;Cacnb2;Ccdc47;Clstn1;Cacna1d;Ryr2;Asph;Erc1;Trpc1;Atp2c1;Slc8a1
OPC	GO:0061564	axon development	http://amigo.geneontology.org/amigo/term/GO:0061564	458	25	8,758933065	2,854228913	2,472E-06	7,4E-05	12286;12552;13131;13839;14042;14810;16574;18080;18823;18845;20616;20910;22067;50769;56839;76965;78808;80297;217692;231876;243743;319504;382253;399558;545156	Nrcam;Ext1;Lgi1;Cdh11;Flrt2;Stxbp5;Cdkl5;Kif5c;Cacna1a;Dab1;Kalrn;Stxbp1;Epha5;Snap91;Trpc5;Grin1;Plxna2;Plxna4;Plp1;Slitrk1;Sipa1l1;Atp8a2;Sptbn4;Nin;Lmtk2
OPC	GO:0010959	regulation of metal ion transport	http://amigo.geneontology.org/amigo/term/GO:0010959	391	22	7,477604429	2,942118724	6,295E-06	0,00018	11941;12286;12287;12289;12293;12296;12298;14810;16497;20191;20393;20541;22063;56461;65973;67887;80297;80334;94253;238161;246317;268345	Cacnb4;Atp2b2;Kcnip3;Cacna2d1;Kcnc2;Neto1;Cacna1a;Akap6;Cacna1b;Kcnab1;Saraf;Sgk1;Kcnip4;Grin1;Hecw1;Cacnb2;Cacna1d;Ryr2;Asph;Trpc1;Sptbn4;Slc8a1

OPC	GO:0051656	establishment of organelle localization	http://amigo.geneontology.org/amigo/term/GO:0051656	456	24	8,720684449	2,752077562	7,363E-06	0,00021	11441;11938;12286;12287;12289;12296;12298;12540;13426;16574;20614;20616;20910;20979;22249;27062;29873;78808;94090;111173;238988;319613;320127;327814	Atp2a2;Cacnb4;Erc2;Cadps;Syty1;Stxbp5;Ppfia2;Kif5c;Dgki;Chrna7;Cacna1a;Stxbp1;Cacna1b;Snap91;Cspg5;Unc13b;Cacnb2;Cdc42;Cacna1d;Sybu;Trim9;Erc1;Dync1i1;Snap25
OPC	GO:0072503	cellular divalent inorganic cation homeostasis	http://amigo.geneontology.org/amigo/term/GO:0072503	491	25	9,390035229	2,662396827	8,381E-06	0,00023	11441;11938;11941;12286;12287;12289;12293;12296;12298;14799;14810;14811;14812;20191;20192;20541;22063;22067;65945;65973;66168;108071;111173;235574;238161	Atp2a2;Cacnb4;Atp2b2;Grm5;Gria1;Cacna2d1;Grina;Chrna7;Grin2a;Cacna1a;Ryr3;Akap6;Cacna1b;Trpc5;Grin2b;Grin1;Cacnb2;Clstn1;Cacna1d;Ryr2;Asph;Erc1;Trpc1;Atp2c1;Slc8a1
OPC	GO:0035249	synaptic transmission, glutamatergic	http://amigo.geneontology.org/amigo/term/GO:0035249	95	10	1,81680926	5,504155125	1,338E-05	0,00035	12286;12298;14810;17260;20910;20979;22249;108071;210274;320127	Cacnb4;Grm5;Syty1;Shank2;Dgki;Cacna1a;Stxbp1;Unc13b;Grin1;Mef2c
OPC	GO:0035690	cellular response to drug	http://amigo.geneontology.org/amigo/term/GO:0035690	361	20	6,903875189	2,89692375	2,1E-05	0,00053	11418;11441;11991;13010;13839;14677;17260;19055;20191;20192;20411;20541;22027;26413;26419;54195;214162;234214;268345;320472	Sorbs2;Asic2;Mapk1;Kmt2a;Ppp3ca;Kcnc2;Chrna7;Sorbs1;Ryr3;Cst3;Gucy1b1;Epha5;Hsp90b1;Mapk8;Ppm1e;Ryr2;Hnnpd;Gnai1;Mef2c;Slc8a1
OPC	GO:0015672	monovalent inorganic cation transport	http://amigo.geneontology.org/amigo/term/GO:0015672	488	24	9,332662305	2,57161346	2,26E-05	0,00056	11418;11938;11975;12289;12867;16497;16531;20265;20269;20273;20393;20541;20614;56461;80297;80334;94229;94253;170738;226922;235574;238161;246317;268345	Atp2a2;Asic2;Scn1a;Kcnip3;Kcnma1;Kcnh7;Kcnc2;Neto1;Atp6v0a1;Slc4a10;Akap6;Kcnab1;Kcnq5;Sgk1;Kcnip4;Hecw1;Scn8a;Cacna1d;Cox7c;Atp2c1;Snap25;Sptbn4;Scn3a;Slc8a1
OPC	GO:0050954	sensory perception of mechanical stimulus	http://amigo.geneontology.org/amigo/term/GO:0050954	176	13	3,365878208	3,86229067	3,389E-05	0,00081	11418;11941;12289;14401;14402;14811;14812;16531;17196;20265;20273;80297;109205	Asic2;Atp2b2;Gabbrb2;Scn1a;Gabbrb3;Kcnma1;Mbp;Grin2a;Sobp;Grin2b;Scn8a;Cacna1d;Sptbn4
OPC	GO:0019932	second-messenger-mediated signaling	http://amigo.geneontology.org/amigo/term/GO:0019932	408	21	7,802717665	2,691369969	3,873E-05	0,0009	11938;12289;13839;14677;14702;14810;14811;14812;19055;20191;20541;23984;54195;56508;65973;76089;108071;207565;238161;268345;333050	Atp2a2;Rapgef2;Grm5;Pde10a;Ppp3ca;Kcnc2;Grin2a;Akap6;Gucy1b1;Epha5;Grin2b;CaMKK2;Grin1;Ksr2;Cacna1d;Gng2;Ryr2;Gnai1;Rapgef4;Asph;Slc8a1
OPC	GO:0097366	response to bronchodilator	http://amigo.geneontology.org/amigo/term/GO:0097366	51	7	0,975339708	7,176986584	4,877E-05	0,0011	11991;14810;14811;19055;26419;54195;268345	Ppp3ca;Kcnc2;Grin2a;Gucy1b1;Mapk8;Grin1;Hnnpd
OPC	GO:0045666	positive regulation of neuron differentiation	http://amigo.geneontology.org/amigo/term/GO:0045666	420	21	8,032209361	2,614473684	5,886E-05	0,00127	12877;13131;17260;18080;18845;20393;20616;20979;22067;50769;56710;74053;76089;76965;210274;240843;241514;242274;243743;382253;545156	Rapgef2;Brinp1;Grip1;Syty1;Lrc7;Shank2;Cdkl5;Dab1;Kalrn;Cpeb1;Zfp804a;Snap91;Trpc5;Sgk1;Plxna2;Plxna4;Slitrk1;Mef2c;Atp8a2;Nin;Brinp2

OPC	GO:0099072	regulation of postsynaptic membrane neurotransmitter receptor levels	http://amigo.geneontology.org/amigo/term/GO:0099072	91	9	1,740312028	5,171486408	5,963E-05	0,00127	20614;26414;56508;56839;65945;74053;242274;380702;545156	Mapk10;Lgi1;Grip1;Lrrc7;Kalrn;Shisa6;Clstn1;Rapgef4;Snap25
OPC	GO:0050905	neuromuscular process	http://amigo.geneontology.org/amigo/term/GO:0050905	126	10	2,409662808	4,149958229	0,0001519	0,00316	11941;12286;14810;14811;14812;16531;20265;20273;50769;93686	Rbfox2;Atp2b2;Scn1a;Kcnma1;Grin2a;Cacna1a;Grin2b;Grin1;Scn8a;Atp8a2
OPC	GO:0060359	response to ammonium ion	http://amigo.geneontology.org/amigo/term/GO:0060359	128	10	2,447911424	4,085115132	0,000173	0,00351	11441;11991;14400;14401;14402;14810;20411;22215;26413;234214	Sorbs2;Gabrb1;Gabrb2;Mapk1;Gabrb3;Ube3a;Chrna7;Sorbs1;Grin1;Hnnpd
OPC	GO:0022604	regulation of cell morphogenesis	http://amigo.geneontology.org/amigo/term/GO:0022604	491	22	9,390035229	2,342909208	0,0001931	0,0038	12286;12540;13131;14810;18080;18845;19055;20393;20616;20979;22003;22067;22215;74053;76089;76965;94253;217692;243743;277360;382253;545156	Rapgef2;Grip1;Syt1;Ube3a;Ppp3ca;Cdkl5;Cacna1a;Dab1;Kalrn;Snap91;Prex1;Trpc5;Tpm1;Sgk1;Grin1;Hecw1;Plxna2;Plxna4;Cdc42;Slitrk1;Sipa11;Nin
OPC	GO:0043270	positive regulation of ion transport	http://amigo.geneontology.org/amigo/term/GO:0043270	298	16	5,699043785	2,80748852	0,0002031	0,0038	11418;11941;12289;12293;12296;12298;14810;14812;20191;20393;20910;22063;50769;65973;238161;268345	Asic2;Cacnb4;Atp2b2;Cacna2d1;Kcnc2;Akap6;Stxbp1;Grin2b;Sgk1;Grin1;Cacnb2;Cacna1d;Ryr2;Asph;Atp8a2;Trpc1
OPC	GO:0031644	regulation of neurological system process	http://amigo.geneontology.org/amigo/term/GO:0031644	156	11	2,983392048	3,687078273	0,0002051	0,0038	11441;14810;14811;22249;23966;56508;72555;210274;244310;246317;380702	Shank2;Neto1;Chrna7;Grin2a;Dlgap2;Shisa9;Shisa6;Unc13b;Grin1;Tenm4;Rapgef4
OPC	GO:0031346	positive regulation of cell projection organization	http://amigo.geneontology.org/amigo/term/GO:0031346	426	20	8,146955209	2,454904868	0,0002059	0,0038	12540;12877;14810;18080;18845;20393;20616;20979;22067;50769;74053;76089;76965;210274;234267;241514;242274;243743;382253;545156	Rapgef2;Gpm6a;Grip1;Syt1;Lrrc7;Shank2;Cdkl5;Kalrn;Cpeb1;Zfp804a;Snap91;Trpc5;Sgk1;Grin1;Plxna2;Plxna4;Cdc42;Slitrk1;Atp8a2;Nin
OPC	GO:0032386	regulation of intracellular transport	http://amigo.geneontology.org/amigo/term/GO:0032386	444	20	8,491192753	2,355381697	0,0003529	0,00637	11441;11938;12287;12289;12296;12298;12540;20910;20979;22249;23963;26413;29873;65973;74741;78808;111173;230908;320127;327814	Atp2a2;Cacnb4;Mapk1;Syt1;Stxbp5;Ppfia2;Dgki;Chrna7;Stxbp1;Cacna1b;C2cd5;Cspg5;Tardbp;Unc13b;Cacnb2;Tenm1;Cdc42;Cacna1d;Asph;Erc1
OPC	GO:0009582	detection of abiotic stimulus	http://amigo.geneontology.org/amigo/term/GO:0009582	116	9	2,218419728	4,056941924	0,0003833	0,00677	11418;11941;12298;14811;14812;20265;50769;110911;226025	Asic2;Cacnb4;Atp2b2;Scn1a;Trpm3;Grin2a;Grin2b;Cds2;Atp8a2
OPC	GO:0009581	detection of external stimulus	http://amigo.geneontology.org/amigo/term/GO:0009581	117	9	2,237544036	4,022267206	0,0004084	0,00706	11418;11941;12298;14811;14812;20265;50769;110911;226025	Asic2;Cacnb4;Atp2b2;Scn1a;Trpm3;Grin2a;Grin2b;Cds2;Atp8a2
OPC	GO:0043954	cellular component maintenance	http://amigo.geneontology.org/amigo/term/GO:0043954	73	7	1,396074484	5,01405912	0,0004802	0,00812	14810;14812;111173;210274;226016;238988;241514	Erc2;Shank2;Abhd17b;Zfp804a;Grin2b;Grin1;Erc1
OPC	GO:0051703	intraspecies interaction between organisms	http://amigo.geneontology.org/amigo/term/GO:0051703	53	6	1,013588324	5,919563059	0,0004996	0,00828	14810;20238;56710;66797;210274;545156	Cntnap2;Brinp1;Atxn1;Shank2;Kalrn;Grin1
OPC	GO:0051705	multi-organism behavior	http://amigo.geneontology.org/amigo/term/GO:0051705	74	7	1,415198792	4,946301565	0,0005219	0,00848	14810;14812;20238;56710;66797;210274;545156	Cntnap2;Brinp1;Atxn1;Shank2;Kalrn;Grin2b;Grin1
OPC	GO:0031503	protein-containing complex localization	http://amigo.geneontology.org/amigo/term/GO:0031503	236	13	4,513336688	2,880352364	0,0006264	0,00997	16574;20614;26414;56508;56839;65945;74053;238161;241694;242274;246317;380702;545156	Mapk10;Lgi1;Grip1;Lrrc7;Neto1;Kif5c;Akap6;Kalrn;Shisa6;Clstn1;Ralgapa2;Rapgef4;Snap25

OPC	GO:0003012	muscle system process	http://amigo.geneontology.org/amigo/term/GO:0003012	364	17	6,961248113	2,442090804	0,0006519	0,01018	11938;12289;12293;12296;16531;17260;19055;20191;20192;20265;20541;22003;26398;50769;72043;234214;238161	Atp2a2;Sorbs2;Scn1a;Kcnma1;Ppp3ca;Cacna2d1;Map2k4;Sulf2;Ryr3;Akap6;Tpm1;Cacnb2;Cacna1d;Ryr2;Mef2c;Atp8a2;Slc8a1
OPC	GO:0007264	small GTPase mediated signal transduction	http://amigo.geneontology.org/amigo/term/GO:0007264	468	20	8,950176145	2,234592892	0,0006865	0,01052	12540;12549;13131;19346;19744;52666;56508;67295;71302;76089;106572;215821;217692;236915;241694;277360;320127;320271;333050;545156	Rapgef2;Arfgef3;Rab6a;Scai;Arhgef9;Rab31;Dgki;Dab1;Karl;Prex1;Arhgap31;Rheb;Arhgef25;Cdc42;Ksr2;Ralgapa2;Arhgap26;Sipa1l1;Rapgef4;Rab3c
OPC	GO:0099601	regulation of neurotransmitter receptor activity	http://amigo.geneontology.org/amigo/term/GO:0099601	59	6	1,128334172	5,317573595	0,0008913	0,0134	17260;72555;210274;244310;246317;380702	Shank2;Neto1;Dlgap2;Shisa9;Shisa6;Mef2c
OPC	GO:0034764	positive regulation of transmembrane transport	http://amigo.geneontology.org/amigo/term/GO:0034764	218	12	4,169099144	2,878319652	0,0010125	0,01491	11418;12289;12293;12296;12298;20191;20411;22063;65973;74741;238161;268345	Asic2;Cacnb4;Cacna2d1;Kcnc2;Sorbs1;Akap6;C2cd5;Cacnb2;Cacna1d;Ryr2;Asph;Trpc1
OPC	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	http://amigo.geneontology.org/amigo/term/GO:0098742	249	13	4,761952693	2,729972522	0,0010285	0,01491	12552;13131;17196;23963;23966;58998;64085;65945;76965;235574;238205;319504;320865	Nrcam;Cdh11;Lrfrn5;Mbp;Netctn3;Cdh18;Clstn2;Dab1;Clstn1;Tenm1;Tenm4;Slitrk1;Atp2c1
OPC	GO:0033555	multicellular organismal response to stress	http://amigo.geneontology.org/amigo/term/GO:0033555	86	7	1,644690488	4,256119951	0,0012836	0,01829	12286;12287;14812;17260;19055;56461;56710	Brinp1;Kcnip3;Ppp3ca;Cacna1a;Cacna1b;Grin2b;Mef2c
OPC	GO:0019233	sensory perception of pain	http://amigo.geneontology.org/amigo/term/GO:0019233	140	9	2,67740312	3,361466165	0,0014816	0,02074	12286;12287;14810;14811;14812;20265;20269;26413;56461	Scn1a;Kcnip3;Mapk1;Grin2a;Cacna1a;Cacna1b;Grin2b;Grin1;Scn3a
OPC	GO:0071241	cellular response to inorganic substance	http://amigo.geneontology.org/amigo/term/GO:0071241	206	11	3,939607448	2,792156362	0,002069	0,02848	11991;14811;17260;20192;20979;26413;26419;54195;65973;66871;268345	Mapk1;Sytn1;Kcnc2;Grin2a;Ryr3;Gucy1b1;Cpne8;Mapk8;Hnrnpd;Asph;Mef2c
OPC	GO:0035640	exploration behavior	http://amigo.geneontology.org/amigo/term/GO:0035640	29	4	0,554604932	7,212341198	0,0021313	0,02884	56710;94229;210274;214162	Brinp1;Kmt2a;Shank2;Slc4a10
OPC	GO:0009612	response to mechanical stimulus	http://amigo.geneontology.org/amigo/term/GO:0009612	210	11	4,01610468	2,738972431	0,0024042	0,03173	11418;11941;14811;14812;20191;20265;20541;26398;26419;50769;66797	Asic2;Atp2b2;Cntnap2;Scn1a;Grin2a;Map2k4;Grin2b;Mapk8;Ryr2;Atp8a2;Slc8a1
OPC	GO:0010737	protein kinase A signaling	http://amigo.geneontology.org/amigo/term/GO:0010737	30	4	0,57372924	6,971929825	0,0024227	0,03173	14812;23984;224938;238161	Pde10a;Akap6;Grin2b;Pja2
OPC	GO:0071867	response to monoamine	http://amigo.geneontology.org/amigo/term/GO:0071867	31	4	0,592853548	6,747028862	0,0027404	0,03532	14702;20191;26413;238161	Mapk1;Akap6;Gng2;Ryr2
OPC	GO:0030048	actin filament-based movement	http://amigo.geneontology.org/amigo/term/GO:0030048	101	7	1,931555108	3,624022929	0,0032274	0,04095	12289;12293;12296;20191;20265;22003;238161	Scn1a;Cacna2d1;Akap6;Tpm1;Cacnb2;Cacna1d;Ryr2
MOL1	GO:0010498	proteasomal protein catabolic process	http://amigo.geneontology.org/amigo/term/GO:0010498	425	18	5,68337048	3,167134725	1,601E-05	0,013	11816;12234;15516;18786;19359;22218;26445;26554;56637;66105;66753;68477;68795;74125;74374;103554;230249;231600	Ubr3;Rmnd5a;Rad23b;Cul3;Ecpas;Ube2d3;Psmc4;Psmc2;Chfr;Hsp90ab1;Gsk3b;Plaa;Btrc;Erlec1;Armc8;Sumo1;Clec16a;Apoe

Supplementary Table 3

cluster	master_gene	genes	Active.in
OPC	Anxa2	Gm28590, Ccl7, Urah, 1700065J11Rik, Npr3, Tspan13, Slc6a20a, Gm48773, Bnc2, 4930553M12Rik, Egfros, Gm26544, Rspo2, 4933409G03Rik, Ttc22, 1700001L05Rik, A730004F24Rik, Gm42705, Foxc2, Gm2000	EPO
OPC	Bmp4	Trarg1, Arhgap24, Gm11738, Chd3, Vax2, Fyn, St6galnac2.1, Sh3rf1, Csgalnact1, Epb41l2, Gm13052, Pnoc, Bcas1, Fndc9, Rapgef1, Gm6408, Lta, Gm45335, Chn2, Cyfip2, BC048562	EPO
OPC	Dok7	Pcdh12, Gm45627, BC107364, Isl1, Krt26, Gm14210, Gm43701, Gm34150, Trim42	EPO
OPC	Gm44129	Gm34809, Ces1a, Platr12, Gm13442, Defb20, Plk2, Npy2r, Duox2, Dnajc22, Gm20139, 7420701I03Rik, Xlr4a, 4732419C18Rik, Gm26686, Sash3, Ankk1, CAAA01077340.1, 1700101I11Rik, Gm14137, A130030D18Rik, Gm13618	EPO
OPC	Mir142hg	Sult3a2, Gm21188, Gm27198, Gm4070, Clec2g, Gm48614, Gm47480, Lyz1, Csf2rb, Gm14262, Bco1, Asb10, Gm41307, 5830428M24Rik, C130050O18Rik, Fgr, Gm26995, Ripk3, Prkcd, Arhgap45, Gm10475	Placebo
OPC	Tnik	Prom1, Mical3, Sema6a, Fam214a, Ank3, Nckap5, Pip5k1b, Rras2, Lingo2, Gm36595, Creb5, Man1a, Onecut2, Cldn14, Aut2, Chsy3, 4930543I03Rik, Pcdh7, Prickle1, 9630013A20Rik, Gm26834, Hoxaas3, Ush1c, Cldn34c4, Gm37381, Sh3gl3, Cacnb4, 9630002D21Rik, Nfasc	Placebo
COP	Anxa2	Gm28590, Ccl7, Urah, 1700065J11Rik, Npr3, Tspan13, Slc6a20a, Gm48773, Bnc2, 4930553M12Rik, Egfros, Gm26544, Rspo2, 4933409G03Rik, Ttc22, 1700001L05Rik, A730004F24Rik, Gm42705, Foxc2, Gm2000	EPO
COP	Col1a2	Tspan13, Gm29478, Aldh1a2, Gm2000, Rspo2, Foxc2, Gm29418, Slc13a4, Gm49707, Gm28286, Sphk1, 4930540M03Rik, Ranbp3l, Slc22a6, Spp1, Isyna1, Egfros, Six1, Gm47109, mt-Nd4, Ccl7, Npr3 Gm15736, 4930470P17Rik, Gm48924, Gm11861, Tlr2, Gm37634, Gm20560, Cd37, Avpr1a, Gm34557, Cyp11b1, Agxt2, Cmk1r1, Gm15540, 4933409F18Rik, Themis2, Gm48021, Zbtb32, Gm37853, 4933428C19Rik	Placebo
COP	Inpp5d	Gm20560, Cd37, Avpr1a, Gm34557, Cyp11b1, Agxt2, Cmk1r1, Gm15540, 4933409F18Rik, Themis2, Gm48021, Zbtb32, Gm37853, 4933428C19Rik	Placebo
COP	Mir142hg	Sult3a2, Gm21188, Gm27198, Gm4070, Clec2g, Gm48614, Gm47480, Lyz1, Csf2rb, Gm14262, Bco1, Asb10, Gm41307, 5830428M24Rik, C130050O18Rik, Fgr, Gm26995, Ripk3, Prkcd, Arhgap45, Gm10475	EPO
COP	Mis18bp1	Depdc1a, Chn1os1, Gm20667, Ska1, Pimreg, Gm29520, D930020B18Rik, Zbtb32, Kel, Ccnb2, Shcbp1, Arap3, Gm40909, Ankle1, Hmnr, Platr22, Stoml3, Melk, Kif20b, Ly6a, Aspm	EPO
COP	Nkain2	Slc24a2, Map7, St18, Cdk19, Malat1, Dock10, Plp1, Mbp, D7Ertd443e, Fnbp1, St6galnac3, Aspa, Dip2b, Pde4b, Qk, Enpp2, Zfp536, Phlpp1, Maml2, Tubb4a, Tmeff2, Pcdh9, Mast3, Arhgef10, Ptprt, Rnf220, Trf, Ptprg, Mag, Atp8a1, Magi2, Pde8a, Plekhg1, Edil3, Klhl2, Gria2, Ppp2r3a, Ano4, Fa2h, Plxdc2, Sec14l5, Jakmip3, Rap1a, Tmod2, Exoc6b, Erbin, Frmd5, Bin1, Baz2b, Mast4	EPO

COP	Pcdh9	Ptprd, Tmeff2, Gm16110, Exoc6b, Nkain2, Mobp, Pde4b, Ano4, Tnfrsf8, 1700047M11Rik, Zfp536, Plekha1, Erbb4, Gm10863, Man1a, Ank3, Sytl2, Rnf220, Tspan2, Mbp, Synpr, Unc5c, Etd, Kcnmb3, Bin1, Daam1, Plp1, Opalin, Fscn3, Dock10, Lpar1, Gm4258, Dusp28, Ablim2, Phlpp1, Pak1, Acap2, Galnt15, Usp6nl, Ctpps, Malat1, Rilp, Phldb1, Ypel2, Clic4, Sh3gl3, Qk, Col13a1, Gm40557, Atp8a1	EPO
COP	Plcl1	Map7, Magi2, Malat1, Phlpp1, St18, Klhl2, St6galnac3, Slc24a2, Sept7, Nkain2, Dock10, Tcf12, Usp54, Cldn11, Arhgap23, Rtn4, Dip2a, Tulp4, Tmcc1, Myo6, Nbas, Pde4b, Mbnl2, Sept4	EPO
NFOL	Anln	Hapln2, Slco3a1, Akr1c14, Tmem117, Dgki, Selenop, Gm3512, Gm44864, Ctnna3, Apod, Spock3, A330049N07Rik, Crybg3, Zdhhc20, Gm28590, Gpr174, Usp31, Slc5a11, Klra2, Rasgrp3, Kctd3, Trf, Piezo2, 4930420G21Rik, Agmo, Rftn1, Myo1e, Gm44613, Gm47790	Placebo
NFOL	Carmil1	Cnksr3, Cemip2, Gm26834, Rras2, 1700008C04Rik, Sema4d, Nckap5, Abr, Cndp1, Cntn1, D430041D05Rik, Gm35229, Etv6, Dock6, Csn1s2a, Ptprb, Fam229a, 2610035D17Rik, 9630013A20Rik, Prok2, Alox5	EPO
NFOL	Cd180	Gm11361, Gm11816, Gm21188, Gm15232, Gm47564, 1700006J14Rik, Gm4070, Fyb, Gm48614, Gm28675, Gm29601, Cldn23, 2900052N01Rik, C3ar1, Olfr1443, Mc2r, Gm48422, Gm29654, Fgr, C130050O18Rik, Gm9869	EPO
NFOL	Gm42418	Cmss1, AY036118, Kctd12, Rbm38, Cdk8, 4930434F21Rik, Lars2, Ndn, Cbr2, Redrum, Gm47033, Gm26917, Trim10, Gm47914, Fgl2, 2900040C04Rik, Trim80, Gm35177, Gm46189, 6330409D20Rik, Rbfaos	Placebo
NFOL	Gm44129	Gm34809, Ces1a, Platr12, Gm13442, Defb20, Plk2, Npy2r, Duox2, Dnajc22, Gm20139, 7420701I03Rik, Xlr4a, 4732419C18Rik, Gm26686, Sash3, Ankk1, CAAA01077340.1, 1700101I11Rik, Gm14137, A130030D18Rik, Gm13618	Placebo
NFOL	Inpp5d	Gm15736, 4930470P17Rik, Gm48924, Gm11861, Tlr2, Gm37634, Gm20560, Cd37, Avpr1a, Gm34557, Cyp11b1, Agxt2, Cmkrlr1, Gm15540, 4933409F18Rik, Themis2, Gm48021, Zbtb32, Gm37853, 4933428C19Rik	EPO
NFOL	Kif20b	Mis18bp1, CAAA01077340.1, Shcbp1, Gm49046, Arap3, Pjvk, Gm1110, Melk, Gabrq, Synb, Pla2g2d, Ect2, Ankle1, Aspm, Depdc1a, Irgc1, Gm28054, Slc4a1, Gtse1, Troap, Gm36529	Placebo
NFOL	Mis18bp1	Depdc1a, Chn1os1, Gm20667, Ska1, Pimreg, Gm29520, D930020B18Rik, Zbtb32, Kel, Ccnb2, Shcbp1, Arap3, Gm40909, Ankle1, Hmnr, Platr22, Stoml3, Melk, Kif20b, Ly6a, Aspm	EPO
NFOL	Nxn	1700065J11Rik, Ccl7, A830031A19Rik, Egfros, Sphk1, Rplp1, Gm29418, Tspan13, Aldh1a2, Gm2000, 6030469F06Rik, Svp1, Gm6408, 2810433D01Rik, Gm29478, Slc22a6, Slc6a13, Zic4, Kdf1, Nxpe5, Ranbp3l, 2310014F06Rik, 1700001L05Rik, Slc6a20a	Placebo
NFOL	Ogfr	Gm31084, Gm11842, D830032E09Rik, Olfr204, Tbx1, 4930542C16Rik, Fcgr4, Vmn2r114, Tm4sf19, Gm36937, Hsd11b2, Gm47922, Hhipl2, Slfnl1, Gm12519, Gm33533, Gm11674, F730035M05Rik, Isx, Blk, Gm12863	Placebo

NFOL	Pik3r3	Gm36988, Frmd4a, Gm13187, Nfasc, Parvb, Tcf7l2, Tns3, Cadm2, Nhsl2, Kif19a, 9530059O14Rik, Tmem163, D430041D05Rik, Dock6, Ankrd44, Mpzl1, Tmem108, Bfsp2, Map1b, Uvrag, Dock4, Sema4d, Fam13c, Dusp15, Peli1, Etv6, Sema4a, Pdcd4, Sema5a, 9630013A20Rik, Rictor, Abr, Ptger1, Rassf10, Gm35501, Man1c1, Rnd2, Csad, Ctnnal1, Gm31822, Sirt2, Ptprj, Egflam, Mical3, Dynll2, 5830418P13Rik, Gm13175, Rhbdl2, Rinl, 1700042O10Rik	EPO
NFOL	Selenop	Pcdh12, Eras, Ott, Gm26995, Gm29946, Lect2, Gm41638, Gm47400, 1700061E18Rik, Fbxw27, Gm36667, Gm19569, C1rl, Gm8797, Gm27211, Gm45615, Htr3b, Ccdc144b, Gm15262, Gm47738	EPO
NFOL	Sema5a	Tcf7l2, Cadm2, Pde9a, 9530059O14Rik, Frmd4a, Tcf7l1, Nfasc, Etv6, Tmem163, Gm36988, Gm50138, Abr, Gm13187, D430041D05Rik, Cntn1, Nckap5, Tns3, Sema4a, Egflam, Dock4, Ccser2, Specc1, Parvb, Cnksr3, Itpr2, Rinl, Sema4d, Map1b, Rasgef1b, 2610035D17Rik, Tns1, Nhsl2, Large1, Lcorl, Sirt2, Pik3r3, Cdh11	EPO
NFOL	Sirt2	9530059O14Rik, Fyn, Tmem108, Ust, Bcas1, Epb41l2, Dock4, Kif19a, Dusp15, Map1b, Bcas1os2, Tns3, Tcf7l2, Arhgap35, Nfasc, Chn2, Rictor, Cdk14, Matn3, Otop1, Rinl, Enpp6, Bfsp2, Mical3, Ptprj, Csgalnact1, Ankrd44, Pcdh7, D630045J12Rik, Zdhhc14, Rapgef1, Gm26535, Arhgap5, Qk, Znrf1, Soga1, Camsap2, Ccser2, Arhgef10l, Pdcd4, Sh3rf1, Ptpro, Itpr2, Rasgef1b, Nhsl2	EPO
MOL1	Cd180	Gm11361, Gm11816, Gm21188, Gm15232, Gm47564, 1700006J14Rik, Gm4070, Fyb, Gm48614, Gm28675, Gm29601, Cldn23, 2900052N01Rik, C3ar1, Olfr1443, Mc2r, Gm48422, Gm29654, Fgr, C130050O18Rik, Gm9869	EPO
MOL1	Gm44129	Gm34809, Ces1a, Platr12, Gm13442, Defb20, Plk2, Npy2r, Duox2, Dnajc22, Gm20139, 7420701I03Rik, Xlr4a, 4732419C18Rik, Gm26686, Sash3, Ankk1, CAAA01077340.1, 1700101I11Rik, Gm14137, A130030D18Rik, Gm13618	EPO
MOL1	Mis18bp1	Depdc1a, Chn1os1, Gm20667, Ska1, Pimreg, Gm29520, D930020B18Rik, Zbtb32, Kel, Ccnb2, Shcbp1, Arap3, Gm40909, Ankle1, Hmnr, Platr22, Stoml3, Melk, Kif20b, Ly6a, Aspm	Placebo
MOL1	Slco1a4	Flt1, Klf2, Pltp, Lef1, Gm35190, Adgrl4, Cyrr1, Gm40658, Clec2d, Sox17, Ripor1, Egfl7, Cldn5, Gm46411, Prok1, Ccdc85b, Ddi1, Fli1, Ccdc141, Rsad2, Gm16282, Sgpp2, Gm34562, BB014433, Sod3	EPO
MOL2	Mir142hg	Sult3a2, Gm21188, Gm27198, Gm4070, Clec2g, Gm48614, Gm47480, Lyz1, Csf2rb, Gm14262, Bco1, Asb10, Gm41307, 5830428M24Rik, C130050O18Rik, Fgr, Gm26995, Ripk3, Prkcd, Arhgap45, Gm10475	Placebo
MOL2	Nfasc	Cnksr3, Tmem163, Mical3, 9530059O14Rik, Abr, Sema4d, Etv6, Prom1, Aut5, Frmd4a, Parvb, 9630013A20Rik, Tcf7l2, Bfsp2, Ablim2, Gm26834, Gm36988, Nckap5, Map1b, Kif19a, Ankrd44, Prickle1, Sirt2, Pik3r3, Map4k4, Gm13187, Grik2, Tns3, Dusp15, Ncor2, Pcyt2, Ank3, Tnik, Rnf122, Rictor, Specc1, Mbp, Rinl, Dock6, Peli1, D430041D05Rik, Tmem108, Slc22a23, Cemip2, Ccser2, Sema6a, 2610035D17Rik, Sema4a, Smurf1, Sh3gl3	EPO

MOL2	Slc4a4	Slc13a4, Gm2000, Zic4, Slc22a6, Mir22hg, Il13ra1, Gm15866, Gm29478, Cyb561, 1700065J11Rik, mt-Cytb, Npr3, Ccdc192, Anpep, Ccl7, 1700001L05Rik, Gm45237, Atp13a5, Tspan13, Slc6a20a	Placebo
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Supplementary Table 4

cluster	master_gene	ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count	Active.in
OPC	Anxa2	BP	GO:0035265	organ growth	3/11	220/28564	7,1E-05	0,019904	0,0066962	Bnc2/Rspo2/Foxc2	3	EPO
OPC	Anxa2	BP	GO:0120163	negative regulation of cold-induced thermogenesis	2/11	47/28564	0,00014	0,019904	0,0066962	Npr3/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0001974	blood vessel remodeling	2/11	61/28564	0,00024	0,019904	0,0066962	Npr3/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0030199	collagen fibril organization	2/11	61/28564	0,00024	0,019904	0,0066962	Anxa2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0007589	body fluid secretion	2/11	121/28564	0,00095	0,019904	0,0066962	Anxa2/Npr3	2	EPO
OPC	Anxa2	BP	GO:0061041	regulation of wound healing	2/11	137/28564	0,00122	0,019904	0,0066962	Anxa2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0120161	regulation of cold-induced thermogenesis	2/11	149/28564	0,00144	0,019904	0,0066962	Npr3/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0106106	cold-induced thermogenesis	2/11	152/28564	0,0015	0,019904	0,0066962	Npr3/Foxc2	2	EPO
OPC	Anxa2	BP	GO:1990845	adaptive thermogenesis	2/11	168/28564	0,00183	0,019904	0,0066962	Npr3/Foxc2	2	EPO
OPC	Anxa2	BP	GO:1903034	regulation of response to wounding	2/11	177/28564	0,00202	0,019904	0,0066962	Anxa2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0035296	regulation of tube diameter	2/11	179/28564	0,00207	0,019904	0,0066962	Npr3/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0097746	blood vessel diameter maintenance	2/11	179/28564	0,00207	0,019904	0,0066962	Npr3/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0035150	regulation of tube size	2/11	180/28564	0,00209	0,019904	0,0066962	Npr3/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0048754	branching morphogenesis of an epithelial tube	2/11	191/28564	0,00235	0,019904	0,0066962	Rspo2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0001659	temperature homeostasis	2/11	192/28564	0,00238	0,019904	0,0066962	Npr3/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0048771	tissue remodeling	2/11	212/28564	0,00289	0,020119	0,0067686	Npr3/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0061138	morphogenesis of a branching epithelium	2/11	229/28564	0,00336	0,021014	0,0070696	Rspo2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0003018	vascular process in circulatory system	2/11	240/28564	0,00368	0,021788	0,0073301	Npr3/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0001763	morphogenesis of a branching structure	2/11	249/28564	0,00395	0,022151	0,0074521	Rspo2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0033002	muscle cell proliferation	2/11	273/28564	0,00473	0,023644	0,0079544	Npr3/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0061448	connective tissue development	2/11	307/28564	0,00594	0,024874	0,0083685	Rspo2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0060485	mesenchyme development	2/11	310/28564	0,00605	0,024874	0,0083685	Bnc2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0030198	extracellular matrix organization	2/11	322/28564	0,00651	0,025541	0,0085929	Anxa2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0043062	extracellular structure organization	2/11	324/28564	0,00659	0,025541	0,0085929	Anxa2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0045229	external encapsulating structure organization	2/11	324/28564	0,00659	0,025541	0,0085929	Anxa2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0050878	regulation of body fluid levels	2/11	354/28564	0,00782	0,027902	0,0093871	Anxa2/Npr3	2	EPO
OPC	Anxa2	BP	GO:0042060	wound healing	2/11	392/28564	0,00952	0,029104	0,0097914	Anxa2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0060562	epithelial tube morphogenesis	2/11	397/28564	0,00975	0,029436	0,009903	Rspo2/Foxc2	2	EPO
OPC	Anxa2	BP	GO:0001503	ossification	2/11	427/28564	0,01122	0,031427	0,0105729	Rspo2/Foxc2	2	EPO
OPC	Anxa2	MF	GO:0008201	heparin binding	2/11	174/28171	0,00201	0,026963	0,0118557	Ccl7/Rspo2	2	EPO
OPC	Anxa2	MF	GO:0005539	glycosaminoglycan binding	2/11	235/28171	0,00363	0,027998	0,012311	Ccl7/Rspo2	2	EPO
OPC	Anxa2	MF	GO:1901681	sulfur compound binding	2/11	293/28171	0,00557	0,028848	0,0126845	Ccl7/Rspo2	2	EPO
OPC	Anxa2	MF	GO:0046873	metal ion transmembrane transporter activity	2/11	430/28171	0,01167	0,0461	0,0202706	Anxa2/Slc6a20a	2	EPO
OPC	Bmp4	BP	GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	3/16	103/28564	2,5E-05	0,02498	0,010946	Bmp4/Fyn/Sh3rf1	3	EPO
OPC	Bmp4	BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	3/16	169/28564	0,00011	0,02498	0,010946	Bmp4/Fyn/Sh3rf1	3	EPO
OPC	Bmp4	BP	GO:0032872	regulation of stress-activated MAPK cascade	3/16	203/28564	0,00018	0,02498	0,010946	Bmp4/Sh3rf1/Rapgef1	3	EPO

OPC	Bmp4	BP	GO:0070302	regulation of stress-activated protein kinase signaling cascade	3/16	206/28564	0,00019	0,02498	0,010946	Bmp4/Sh3rf1/Rapgef1	3	EPO
OPC	Bmp4	BP	GO:0001958	endochondral ossification	2/16	37/28564	0,00019	0,02498	0,010946	Bmp4/Csgalnact1	2	EPO
OPC	Bmp4	BP	GO:0036075	replacement ossification	2/16	37/28564	0,00019	0,02498	0,010946	Bmp4/Csgalnact1	2	EPO
OPC	Bmp4	BP	GO:0038179	neurotrophin signaling pathway	2/16	41/28564	0,00024	0,02498	0,010946	Rapgef1/Cyfip2	2	EPO
OPC	Bmp4	BP	GO:0010453	regulation of cell fate commitment	2/16	43/28564	0,00026	0,02498	0,010946	Bmp4/Chd3	2	EPO
OPC	Bmp4	BP	GO:0010976	positive regulation of neuron projection development	3/16	237/28564	0,00029	0,02498	0,010946	Bmp4/Fyn/Rapgef1	3	EPO
OPC	Bmp4	BP	GO:0097191	extrinsic apoptotic signaling pathway	3/16	242/28564	0,00031	0,02498	0,010946	Bmp4/Fyn/Sh3rf1	3	EPO
OPC	Bmp4	BP	GO:0042098	T cell proliferation	3/16	243/28564	0,00031	0,02498	0,010946	Bmp4/Fyn/Sh3rf1	3	EPO
OPC	Bmp4	BP	GO:0051403	stress-activated MAPK cascade	3/16	243/28564	0,00031	0,02498	0,010946	Bmp4/Sh3rf1/Rapgef1	3	EPO
OPC	Bmp4	BP	GO:2001234	negative regulation of apoptotic signaling pathway	3/16	246/28564	0,00033	0,02498	0,010946	Bmp4/Fyn/Sh3rf1	3	EPO
OPC	Bmp4	BP	GO:2000116	regulation of cysteine-type endopeptidase activity	3/16	251/28564	0,00034	0,02498	0,010946	Fyn/Sh3rf1/Cyfip2	3	EPO
OPC	Bmp4	BP	GO:0031098	stress-activated protein kinase signaling cascade	3/16	255/28564	0,00036	0,02498	0,010946	Bmp4/Sh3rf1/Rapgef1	3	EPO
OPC	Bmp4	BP	GO:0043547	positive regulation of GTPase activity	3/16	259/28564	0,00038	0,02498	0,010946	Arhgap24/Rapgef1/Chn2	3	EPO
OPC	Bmp4	BP	GO:0046580	negative regulation of Ras protein signal transduction	2/16	56/28564	0,00045	0,027674	0,0121263	Arhgap24/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0051058	negative regulation of small GTPase mediated signal transduction	2/16	63/28564	0,00056	0,03307	0,0144908	Arhgap24/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0060350	endochondral bone morphogenesis	2/16	69/28564	0,00068	0,035367	0,0154974	Bmp4/Csgalnact1	2	EPO
OPC	Bmp4	BP	GO:0043087	regulation of GTPase activity	3/16	353/28564	0,00093	0,035367	0,0154974	Arhgap24/Rapgef1/Chn2	3	EPO
OPC	Bmp4	BP	GO:0046651	lymphocyte proliferation	3/16	354/28564	0,00094	0,035367	0,0154974	Bmp4/Fyn/Sh3rf1	3	EPO
OPC	Bmp4	BP	GO:0032943	mononuclear cell proliferation	3/16	360/28564	0,00098	0,035367	0,0154974	Bmp4/Fyn/Sh3rf1	3	EPO
OPC	Bmp4	BP	GO:0052548	regulation of endopeptidase activity	3/16	368/28564	0,00105	0,035367	0,0154974	Fyn/Sh3rf1/Cyfip2	3	EPO
OPC	Bmp4	BP	GO:0045862	positive regulation of proteolysis	3/16	384/28564	0,00119	0,035367	0,0154974	Fyn/Sh3rf1/Cyfip2	3	EPO
OPC	Bmp4	BP	GO:0070661	leukocyte proliferation	3/16	396/28564	0,00129	0,035367	0,0154974	Bmp4/Fyn/Sh3rf1	3	EPO
OPC	Bmp4	BP	GO:0009798	axis specification	2/16	97/28564	0,00133	0,035367	0,0154974	Bmp4/Vax2	2	EPO
OPC	Bmp4	BP	GO:0090630	activation of GTPase activity	2/16	102/28564	0,00147	0,035367	0,0154974	Arhgap24/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0030900	forebrain development	3/16	416/28564	0,00149	0,035367	0,0154974	Bmp4/Vax2/Fyn	3	EPO
OPC	Bmp4	BP	GO:2001233	regulation of apoptotic signaling pathway	3/16	424/28564	0,00158	0,035367	0,0154974	Bmp4/Fyn/Sh3rf1	3	EPO
OPC	Bmp4	BP	GO:0009953	dorsal/ventral pattern formation	2/16	109/28564	0,00167	0,035367	0,0154974	Bmp4/Vax2	2	EPO
OPC	Bmp4	BP	GO:0060349	bone morphogenesis	2/16	111/28564	0,00173	0,035367	0,0154974	Bmp4/Csgalnact1	2	EPO
OPC	Bmp4	BP	GO:0045446	endothelial cell differentiation	2/16	116/28564	0,00189	0,035367	0,0154974	Bmp4/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0031346	positive regulation of cell projection organization	3/16	459/28564	0,00198	0,035367	0,0154974	Bmp4/Fyn/Rapgef1	3	EPO
OPC	Bmp4	BP	GO:0052547	regulation of peptidase activity	3/16	466/28564	0,00206	0,035367	0,0154974	Fyn/Sh3rf1/Cyfip2	3	EPO
OPC	Bmp4	BP	GO:0003158	endothelium development	2/16	135/28564	0,00255	0,035367	0,0154974	Bmp4/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0032874	positive regulation of stress-activated MAPK cascade	2/16	137/28564	0,00262	0,035367	0,0154974	Bmp4/Sh3rf1	2	EPO

OPC	Bmp4	BP	GO:0014013	regulation of gliogenesis	2/16	139/28564	0,0027	0,035367	0,0154974	Bmp4/Lta	2	EPO
OPC	Bmp4	BP	GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	2/16	139/28564	0,0027	0,035367	0,0154974	Bmp4/Sh3rf1	2	EPO
OPC	Bmp4	BP	GO:0008360	regulation of cell shape	2/16	141/28564	0,00277	0,035367	0,0154974	Fyn/Epb41l2	2	EPO
OPC	Bmp4	BP	GO:0046328	regulation of JNK cascade	2/16	152/28564	0,00321	0,035367	0,0154974	Sh3rf1/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:1900180	regulation of protein localization to nucleus	2/16	156/28564	0,00338	0,035367	0,0154974	Bmp4/Fyn	2	EPO
OPC	Bmp4	BP	GO:2001056	positive regulation of cysteine-type endopeptidase activity	2/16	158/28564	0,00347	0,035367	0,0154974	Fyn/Cyfp2	2	EPO
OPC	Bmp4	BP	GO:0007254	JNK cascade	2/16	179/28564	0,00442	0,035548	0,0155765	Sh3rf1/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0010950	positive regulation of endopeptidase activity	2/16	179/28564	0,00442	0,035548	0,0155765	Fyn/Cyfp2	2	EPO
OPC	Bmp4	BP	GO:0042552	myelination	2/16	180/28564	0,00447	0,035548	0,0155765	Fyn/Bcas1	2	EPO
OPC	Bmp4	BP	GO:0007272	ensheathment of neurons	2/16	183/28564	0,00462	0,035688	0,0156377	Fyn/Bcas1	2	EPO
OPC	Bmp4	BP	GO:0008366	axon ensheathment	2/16	183/28564	0,00462	0,035688	0,0156377	Fyn/Bcas1	2	EPO
OPC	Bmp4	BP	GO:0048592	eye morphogenesis	2/16	185/28564	0,00472	0,035688	0,0156377	Bmp4/Vax2	2	EPO
OPC	Bmp4	BP	GO:0043409	negative regulation of MAPK cascade	2/16	187/28564	0,00482	0,035688	0,0156377	Bmp4/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0045580	regulation of T cell differentiation	2/16	188/28564	0,00487	0,035688	0,0156377	Bmp4/Sh3rf1	2	EPO
OPC	Bmp4	BP	GO:0097553	calcium ion transmembrane import into cytosol	2/16	193/28564	0,00512	0,036085	0,0158119	Bmp4/Fyn	2	EPO
OPC	Bmp4	BP	GO:0042129	regulation of T cell proliferation	2/16	201/28564	0,00554	0,037623	0,0164856	Bmp4/Sh3rf1	2	EPO
OPC	Bmp4	BP	GO:1903169	regulation of calcium ion transmembrane transport	2/16	201/28564	0,00554	0,037623	0,0164856	Bmp4/Fyn	2	EPO
OPC	Bmp4	BP	GO:0010952	positive regulation of peptidase activity	2/16	203/28564	0,00565	0,037671	0,0165069	Fyn/Cyfp2	2	EPO
OPC	Bmp4	BP	GO:0001764	neuron migration	2/16	204/28564	0,0057	0,037671	0,0165069	Fyn/Sh3rf1	2	EPO
OPC	Bmp4	BP	GO:0046578	regulation of Ras protein signal transduction	2/16	204/28564	0,0057	0,037671	0,0165069	Arhgap24/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0031345	negative regulation of cell projection organization	2/16	219/28564	0,00654	0,039006	0,0170917	Arhgap24/Fyn	2	EPO
OPC	Bmp4	BP	GO:0051216	cartilage development	2/16	219/28564	0,00654	0,039006	0,0170917	Bmp4/Csgalnact1	2	EPO
OPC	Bmp4	BP	GO:0045619	regulation of lymphocyte differentiation	2/16	222/28564	0,00672	0,039006	0,0170917	Bmp4/Sh3rf1	2	EPO
OPC	Bmp4	BP	GO:0033157	regulation of intracellular protein transport	2/16	227/28564	0,00701	0,040383	0,017695	Bmp4/Fyn	2	EPO
OPC	Bmp4	BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	2/16	228/28564	0,00707	0,040383	0,017695	Bmp4/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0051056	regulation of small GTPase mediated signal transduction	2/16	236/28564	0,00756	0,041304	0,0180986	Arhgap24/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0002064	epithelial cell development	2/16	242/28564	0,00793	0,041712	0,0182776	Bmp4/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0050670	regulation of lymphocyte proliferation	2/16	260/28564	0,00911	0,043965	0,0192646	Bmp4/Sh3rf1	2	EPO
OPC	Bmp4	BP	GO:0090150	establishment of protein localization to membrane	2/16	260/28564	0,00911	0,043965	0,0192646	Trarg1/Fyn	2	EPO
OPC	Bmp4	BP	GO:0060348	bone development	2/16	262/28564	0,00924	0,043965	0,0192646	Bmp4/Csgalnact1	2	EPO
OPC	Bmp4	BP	GO:0032944	regulation of mononuclear cell proliferation	2/16	264/28564	0,00938	0,043965	0,0192646	Bmp4/Sh3rf1	2	EPO
OPC	Bmp4	BP	GO:0048705	skeletal system morphogenesis	2/16	264/28564	0,00938	0,043965	0,0192646	Bmp4/Csgalnact1	2	EPO
OPC	Bmp4	BP	GO:0002429	immune response-activating cell surface receptor signaling pathway	2/16	272/28564	0,00993	0,043965	0,0192646	Fyn/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0034599	cellular response to oxidative stress	2/16	276/28564	0,01021	0,043965	0,0192646	Bmp4/Fyn	2	EPO
OPC	Bmp4	BP	GO:0022604	regulation of cell morphogenesis	2/16	278/28564	0,01035	0,043965	0,0192646	Fyn/Epb41l2	2	EPO
OPC	Bmp4	BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	2/16	283/28564	0,01071	0,043965	0,0192646	Fyn/Rapgef1	2	EPO

OPC	Bmp4	BP	GO:0048863	stem cell differentiation	2/16	286/28564	0,01093	0,043965	0,0192646	Bmp4/Chd3	2	EPO
OPC	Bmp4	BP	GO:0070663	regulation of leukocyte proliferation	2/16	287/28564	0,011	0,043965	0,0192646	Bmp4/Sh3rf1	2	EPO
OPC	Bmp4	BP	GO:0060560	developmental growth involved in morphogenesis	2/16	290/28564	0,01122	0,044095	0,0193215	Bmp4/Cyfp2	2	EPO
OPC	Bmp4	BP	GO:0051924	regulation of calcium ion transport	2/16	292/28564	0,01137	0,044512	0,0195042	Bmp4/Fyn	2	EPO
OPC	Bmp4	BP	GO:0045165	cell fate commitment	2/16	303/28564	0,0122	0,045613	0,0199867	Bmp4/Chd3	2	EPO
OPC	Bmp4	BP	GO:0061448	connective tissue development	2/16	307/28564	0,01251	0,046052	0,0201792	Bmp4/Csgalnact1	2	EPO
OPC	Bmp4	BP	GO:0090596	sensory organ morphogenesis	2/16	319/28564	0,01346	0,048211	0,021125	Bmp4/Vax2	2	EPO
OPC	Bmp4	BP	GO:0090287	regulation of cellular response to growth factor stimulus	2/16	320/28564	0,01354	0,048334	0,0211792	Bmp4/Cyfp2	2	EPO
OPC	Bmp4	BP	GO:0034504	protein localization to nucleus	2/16	325/28564	0,01394	0,048789	0,0213784	Bmp4/Fyn	2	EPO
OPC	Bmp4	BP	GO:0002699	positive regulation of immune effector process	2/16	327/28564	0,0141	0,049197	0,0215573	Rapgef1/Lta	2	EPO
OPC	Bmp4	BP	GO:0070372	regulation of ERK1 and ERK2 cascade	2/16	329/28564	0,01427	0,049493	0,0216868	Bmp4/Rapgef1	2	EPO
OPC	Bmp4	BP	GO:0030217	T cell differentiation	2/16	331/28564	0,01443	0,049493	0,0216868	Bmp4/Sh3rf1	2	EPO
OPC	Bmp4	BP	GO:0048562	embryonic organ morphogenesis	2/16	334/28564	0,01468	0,049895	0,0218632	Bmp4/Vax2	2	EPO
OPC	Bmp4	BP	GO:1901653	cellular response to peptide	2/16	334/28564	0,01468	0,049895	0,0218632	Trarg1/Fyn	2	EPO
OPC	Bmp4	MF	GO:0030695	GTPase regulator activity	3/16	432/28171	0,00173	0,035449	0,0147155	Arhgap24/Rapgef1/ Chn2	3	EPO
OPC	Bmp4	MF	GO:0060589	nucleoside-triphosphatase regulator activity	3/16	432/28171	0,00173	0,035449	0,0147155	Arhgap24/Rapgef1/ Chn2	3	EPO
OPC	Bmp4	MF	GO:0005125	cytokine activity	2/16	231/28171	0,00745	0,035449	0,0147155	Bmp4/Lta	2	EPO
OPC	Bmp4	MF	GO:0005096	GTPase activator activity	2/16	241/28171	0,00808	0,035449	0,0147155	Arhgap24/Chn2	2	EPO
OPC	Bmp4	MF	GO:0001664	G protein-coupled receptor binding	2/16	328/28171	0,01456	0,041137	0,0170771	Fyn/Pnoc	2	EPO
OPC	Dok7	BP	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	2/4	192/28564	0,00027	0,0152	0,0018533	Dok7/Isl1	2	EPO
OPC	Dok7	BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	2/4	270/28564	0,00053	0,0152	0,0018533	Dok7/Isl1	2	EPO
OPC	Dok7	BP	GO:0018108	peptidyl-tyrosine phosphorylation	2/4	326/28564	0,00077	0,0152	0,0018533	Dok7/Isl1	2	EPO
OPC	Dok7	BP	GO:0018212	peptidyl-tyrosine modification	2/4	328/28564	0,00078	0,0152	0,0018533	Dok7/Isl1	2	EPO
OPC	Gm44129	BP	GO:0090394	negative regulation of excitatory postsynaptic potential	2/8	14/28564	6,2E-06	0,002663	0,0010108	Plk2/Npy2r	2	EPO
OPC	Gm44129	BP	GO:0015850	organic hydroxy compound transport	3/8	306/28564	6,6E-05	0,009614	0,0036497	Ces1a/Npy2r/Xlr4a	3	EPO
OPC	Gm44129	BP	GO:0014046	dopamine secretion	2/8	45/28564	6,8E-05	0,009614	0,0036497	Npy2r/Xlr4a	2	EPO
OPC	Gm44129	BP	GO:0015872	dopamine transport	2/8	61/28564	0,00012	0,01135	0,0043091	Npy2r/Xlr4a	2	EPO
OPC	Gm44129	BP	GO:0098815	modulation of excitatory postsynaptic potential	2/8	63/28564	0,00013	0,01135	0,0043091	Plk2/Npy2r	2	EPO
OPC	Gm44129	BP	GO:0050432	catecholamine secretion	2/8	76/28564	0,00019	0,012123	0,0046023	Npy2r/Xlr4a	2	EPO
OPC	Gm44129	BP	GO:0050805	negative regulation of synaptic transmission	2/8	77/28564	0,0002	0,012123	0,0046023	Plk2/Npy2r	2	EPO
OPC	Gm44129	BP	GO:0051937	catecholamine transport	2/8	93/28564	0,00029	0,014352	0,0054486	Npy2r/Xlr4a	2	EPO
OPC	Gm44129	BP	GO:0060079	excitatory postsynaptic potential	2/8	95/28564	0,0003	0,014352	0,0054486	Plk2/Npy2r	2	EPO
OPC	Gm44129	BP	GO:0015844	monoamine transport	2/8	113/28564	0,00043	0,01749	0,0066398	Npy2r/Xlr4a	2	EPO
OPC	Gm44129	BP	GO:0099565	chemical synaptic transmission, postsynaptic	2/8	116/28564	0,00045	0,01749	0,0066398	Plk2/Npy2r	2	EPO
OPC	Gm44129	BP	GO:0060078	regulation of postsynaptic membrane potential	2/8	132/28564	0,00058	0,020736	0,007872	Plk2/Npy2r	2	EPO
OPC	Gm44129	BP	GO:0031644	regulation of nervous system process	2/8	204/28564	0,00138	0,042137	0,0159968	Plk2/Npy2r	2	EPO
OPC	Gm44129	MF	GO:0004674	protein serine/threonine kinase activity	2/7	442/28171	0,0049	0,009423	0,0005221	Plk2/Ankk1	2	EPO

OPC	Mir142hg	BP	GO:0002443	leukocyte mediated immunity	4/11	480/28564	2,4E-05	0,010791	0,004459	Csf2rb/Fgr/Ripk3/Prkcd	4	Placebo
OPC	Mir142hg	BP	GO:0046777	protein autophosphorylation	3/11	242/28564	9,4E-05	0,021489	0,0088792	Fgr/Ripk3/Prkcd	3	Placebo
OPC	Mir142hg	BP	GO:0035306	positive regulation of dephosphorylation	2/11	60/28564	0,00024	0,022897	0,0094611	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0002449	lymphocyte mediated immunity	3/11	372/28564	0,00033	0,022897	0,0094611	Csf2rb/Ripk3/Prkcd	3	Placebo
OPC	Mir142hg	BP	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3/11	373/28564	0,00034	0,022897	0,0094611	Csf2rb/Ripk3/Prkcd	3	Placebo
OPC	Mir142hg	BP	GO:0042742	defense response to bacterium	3/11	386/28564	0,00037	0,022897	0,0094611	Lyz1/Fgr/Prkcd	3	Placebo
OPC	Mir142hg	BP	GO:2000379	positive regulation of reactive oxygen species metabolic process	2/11	78/28564	0,0004	0,022897	0,0094611	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0070661	leukocyte proliferation	3/11	396/28564	0,0004	0,022897	0,0094611	Csf2rb/Ripk3/Prkcd	3	Placebo
OPC	Mir142hg	BP	GO:0033674	positive regulation of kinase activity	3/11	440/28564	0,00055	0,024559	0,0101479	Fgr/Ripk3/Prkcd	3	Placebo
OPC	Mir142hg	BP	GO:0070301	cellular response to hydrogen peroxide	2/11	93/28564	0,00057	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0032147	activation of protein kinase activity	2/11	105/28564	0,00072	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0042542	response to hydrogen peroxide	2/11	120/28564	0,00094	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0035303	regulation of dephosphorylation	2/11	128/28564	0,00107	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0001776	leukocyte homeostasis	2/11	136/28564	0,0012	0,024559	0,0101479	Mir142hg/Ripk3	2	Placebo
OPC	Mir142hg	BP	GO:0034614	cellular response to reactive oxygen species	2/11	146/28564	0,00138	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:2000377	regulation of reactive oxygen species metabolic process	2/11	161/28564	0,00168	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0016064	immunoglobulin mediated immune response	2/11	165/28564	0,00176	0,024559	0,0101479	Csf2rb/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0019724	B cell mediated immunity	2/11	168/28564	0,00183	0,024559	0,0101479	Csf2rb/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:2001235	positive regulation of apoptotic signaling pathway	2/11	172/28564	0,00191	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0050830	defense response to Gram-positive bacterium	2/11	176/28564	0,002	0,024559	0,0101479	Lyz1/Fgr	2	Placebo
OPC	Mir142hg	BP	GO:0045834	positive regulation of lipid metabolic process	2/11	185/28564	0,00221	0,024559	0,0101479	Fgr/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0000302	response to reactive oxygen species	2/11	191/28564	0,00235	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0050866	negative regulation of cell activation	2/11	227/28564	0,0033	0,026304	0,0108689	Fgr/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0044242	cellular lipid catabolic process	2/11	230/28564	0,00338	0,026304	0,0108689	Bco1/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0072593	reactive oxygen species metabolic process	2/11	249/28564	0,00395	0,028382	0,0117274	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0001906	cell killing	2/11	250/28564	0,00398	0,028382	0,0117274	Lyz1/Ripk3	2	Placebo
OPC	Mir142hg	BP	GO:0002274	myeloid leukocyte activation	2/11	264/28564	0,00443	0,030607	0,0126468	Fgr/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0034599	cellular response to oxidative stress	2/11	276/28564	0,00483	0,031856	0,0131629	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0070663	regulation of leukocyte proliferation	2/11	287/28564	0,00521	0,031856	0,0131629	Csf2rb/Ripk3	2	Placebo
OPC	Mir142hg	BP	GO:0002703	regulation of leukocyte mediated immunity	2/11	310/28564	0,00605	0,033763	0,013951	Fgr/Ripk3	2	Placebo
OPC	Mir142hg	BP	GO:0018108	peptidyl-tyrosine phosphorylation	2/11	326/28564	0,00667	0,036221	0,0149668	Fgr/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0018212	peptidyl-tyrosine modification	2/11	328/28564	0,00675	0,036221	0,0149668	Fgr/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0016042	lipid catabolic process	2/11	342/28564	0,00732	0,036281	0,0149914	Bco1/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0016311	dephosphorylation	2/11	342/28564	0,00732	0,036281	0,0149914	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0062197	cellular response to chemical stress	2/11	347/28564	0,00753	0,036847	0,0152253	Ripk3/Prkcd	2	Placebo

OPC	Mir142hg	BP	GO:0046651	lymphocyte proliferation	2/11	354/28564	0,00782	0,037162	0,0153554	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0032943	mononuclear cell proliferation	2/11	360/28564	0,00808	0,03799	0,0156976	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0032956	regulation of actin cytoskeleton organization	2/11	362/28564	0,00817	0,038006	0,0157041	Fgr/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0045860	positive regulation of protein kinase activity	2/11	373/28564	0,00865	0,039065	0,0161418	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0048872	homeostasis of number of cells	2/11	391/28564	0,00947	0,040479	0,0167261	Mir142hg/Ripk3	2	Placebo
OPC	Mir142hg	BP	GO:0019216	regulation of lipid metabolic process	2/11	393/28564	0,00957	0,040479	0,0167261	Fgr/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0006979	response to oxidative stress	2/11	408/28564	0,01028	0,042442	0,0175373	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0032970	regulation of actin filament-based process	2/11	411/28564	0,01042	0,042442	0,0175373	Fgr/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:2001233	regulation of apoptotic signaling pathway	2/11	424/28564	0,01106	0,042946	0,0177456	Ripk3/Prkcd	2	Placebo
OPC	Mir142hg	BP	GO:0002697	regulation of immune effector process	2/11	472/28564	0,01358	0,048332	0,0199711	Fgr/Ripk3	2	Placebo
OPC	Mir142hg	MF	GO:0004715	non-membrane spanning protein tyrosine kinase activity	2/10	45/28171	0,00011	0,003675	0,0004689	Fgr/Prkcd	2	Placebo
OPC	Mir142hg	MF	GO:0004713	protein tyrosine kinase activity	2/10	132/28171	0,00096	0,008783	0,0011206	Fgr/Prkcd	2	Placebo
OPC	Mir142hg	MF	GO:0004674	protein serine/threonine kinase activity	2/10	442/28171	0,01017	0,018643	0,0023787	Ripk3/Prkcd	2	Placebo
OPC	Tnik	BP	GO:0045162	clustering of voltage-gated sodium channels	2/23	7/28564	1,3E-05	0,009198	0,0055114	Ank3/Nfasc	2	Placebo
OPC	Tnik	BP	GO:0099612	protein localization to axon	2/23	11/28564	3,4E-05	0,009671	0,0057943	Ank3/Nfasc	2	Placebo
OPC	Tnik	BP	GO:0007409	axonogenesis	5/23	498/28564	4,1E-05	0,009671	0,0057943	Sema6a/Ank3/Auts2/Prickle1/Nfasc	5	Placebo
OPC	Tnik	BP	GO:0045161	neuronal ion channel clustering	2/23	14/28564	5,6E-05	0,009931	0,0059503	Ank3/Nfasc	2	Placebo
OPC	Tnik	BP	GO:0019226	transmission of nerve impulse	3/23	101/28564	7,2E-05	0,010221	0,0061238	Ank3/Cacnb4/Nfasc	3	Placebo
OPC	Tnik	BP	GO:0051261	protein depolymerization	3/23	124/28564	0,00013	0,01566	0,0093828	Mical3/Nckap5/Sh3gl3	3	Placebo
OPC	Tnik	BP	GO:0032528	microvillus organization	2/23	27/28564	0,00022	0,021749	0,0130316	Tnik/Ush1c	2	Placebo
OPC	Tnik	BP	GO:0007043	cell-cell junction assembly	3/23	168/28564	0,00032	0,028725	0,0172112	Cldn14/Cldn34c4/Nfasc	3	Placebo
OPC	Tnik	BP	GO:0022411	cellular component disassembly	4/23	450/28564	0,00042	0,033387	0,0200044	Mical3/Nckap5/Prickle1/Sh3gl3	4	Placebo
OPC	Tnik	BP	GO:0034329	cell junction assembly	4/23	477/28564	0,00053	0,033428	0,0200292	Lingo2/Cldn14/Cldn34c4/Nfasc	4	Placebo
OPC	Tnik	BP	GO:0060219	camera-type eye photoreceptor cell differentiation	2/23	43/28564	0,00055	0,033428	0,0200292	Prom1/Ush1c	2	Placebo
OPC	Tnik	BP	GO:0045494	photoreceptor cell maintenance	2/23	45/28564	0,0006	0,033428	0,0200292	Prom1/Ush1c	2	Placebo
OPC	Tnik	BP	GO:1990138	neuron projection extension	3/23	209/28564	0,00061	0,033428	0,0200292	Sema6a/Auts2/Prickle1	3	Placebo
OPC	Tnik	BP	GO:0045806	negative regulation of endocytosis	2/23	50/28564	0,00074	0,037528	0,0224856	Ank3/Sh3gl3	2	Placebo
OPC	Tnik	BP	GO:0045216	cell-cell junction organization	3/23	230/28564	0,00081	0,038239	0,0229113	Cldn14/Cldn34c4/Nfasc	3	Placebo
OPC	Tnik	BP	GO:0032984	protein-containing complex disassembly	3/23	240/28564	0,00092	0,039634	0,0237475	Mical3/Nckap5/Sh3gl3	3	Placebo
OPC	Tnik	BP	GO:0001895	retina homeostasis	2/23	58/28564	0,001	0,039634	0,0237475	Prom1/Ush1c	2	Placebo

OPC	Tnik	BP	GO:0007411	axon guidance	3/23	253/28564	0,00107	0,039634	0,0237475	Sema6a/Ank3/Nfasc	3	Placebo
OPC	Tnik	BP	GO:0097485	neuron projection guidance	3/23	254/28564	0,00108	0,039634	0,0237475	Sema6a/Ank3/Nfasc	3	Placebo
OPC	Tnik	BP	GO:0001754	eye photoreceptor cell differentiation	2/23	63/28564	0,00118	0,039634	0,0237475	Prom1/Ush1c	2	Placebo
OPC	Tnik	BP	GO:0042551	neuron maturation	2/23	63/28564	0,00118	0,039634	0,0237475	Ank3/Nfasc	2	Placebo
OPC	Tnik	BP	GO:0001894	tissue homeostasis	3/23	278/28564	0,0014	0,04304	0,0257881	Prom1/Prickle1/Ush1c	3	Placebo
OPC	Tnik	BP	GO:0060249	anatomical structure homeostasis	3/23	278/28564	0,0014	0,04304	0,0257881	Prom1/Prickle1/Ush1c	3	Placebo
OPC	Tnik	BP	GO:0048588	developmental cell growth	3/23	287/28564	0,00153	0,043545	0,0260906	Sema6a/Auts2/Prickle1	3	Placebo
OPC	Tnik	BP	GO:0060560	developmental growth involved in morphogenesis	3/23	290/28564	0,00158	0,043545	0,0260906	Sema6a/Auts2/Prickle1	3	Placebo
OPC	Tnik	BP	GO:0007422	peripheral nervous system development	2/23	75/28564	0,00166	0,043545	0,0260906	Onecut2/Nfasc	2	Placebo
OPC	Tnik	BP	GO:2001259	positive regulation of cation channel activity	2/23	75/28564	0,00166	0,043545	0,0260906	Ank3/Cacnb4	2	Placebo
OPC	Tnik	BP	GO:0072659	protein localization to plasma membrane	3/23	308/28564	0,00187	0,046188	0,0276742	Tnik/Ank3/Nfasc	3	Placebo
OPC	Tnik	BP	GO:0060042	retina morphogenesis in camera-type eye	2/23	82/28564	0,00198	0,046188	0,0276742	Prom1/Ush1c	2	Placebo
OPC	Tnik	BP	GO:0046530	photoreceptor cell differentiation	2/23	85/28564	0,00213	0,046188	0,0276742	Prom1/Ush1c	2	Placebo
OPC	Tnik	BP	GO:0003407	neural retina development	2/23	86/28564	0,00218	0,046188	0,0276742	Prom1/Ush1c	2	Placebo
OPC	Tnik	BP	GO:0070830	bicellular tight junction assembly	2/23	87/28564	0,00223	0,046188	0,0276742	Cldn14/Cldn34c4	2	Placebo
OPC	Tnik	BP	GO:0120192	tight junction assembly	2/23	93/28564	0,00254	0,047279	0,0283283	Cldn14/Cldn34c4	2	Placebo
OPC	Tnik	BP	GO:0043297	apical junction assembly	2/23	97/28564	0,00276	0,04907	0,0294011	Cldn14/Cldn34c4	2	Placebo
OPC	Tnik	BP	GO:0120193	tight junction organization	2/23	99/28564	0,00287	0,04907	0,0294011	Cldn14/Cldn34c4	2	Placebo
OPC	Tnik	BP	GO:0043010	camera-type eye development	3/23	378/28564	0,00335	0,04907	0,0294011	Prom1/Prickle1/Ush1c	3	Placebo
OPC	Tnik	BP	GO:1990778	protein localization to cell periphery	3/23	389/28564	0,00363	0,04907	0,0294011	Tnik/Ank3/Nfasc	3	Placebo
OPC	Tnik	BP	GO:0061326	renal tubule development	2/23	112/28564	0,00365	0,04907	0,0294011	Prom1/Prickle1	2	Placebo
OPC	Tnik	BP	GO:0031532	actin cytoskeleton reorganization	2/23	117/28564	0,00398	0,04907	0,0294011	Tnik/Auts2	2	Placebo
OPC	Tnik	CC	GO:0070160	tight junction	4/23	154/28585	6,6E-06	0,000445	0,0002466	Ank3/Cldn14/Cldn34c4/Nfasc	4	Placebo
OPC	Tnik	CC	GO:0043296	apical junction complex	4/23	169/28585	9,6E-06	0,000445	0,0002466	Ank3/Cldn14/Cldn34c4/Nfasc	4	Placebo
OPC	Tnik	CC	GO:0031254	cell trailing edge	2/23	12/28585	4,1E-05	0,001261	0,0006993	Pip5k1b/Prickle1	2	Placebo
OPC	Tnik	CC	GO:0033270	paranode region of axon	2/23	16/28585	7,4E-05	0,001547	0,0008578	Ank3/Nfasc	2	Placebo
OPC	Tnik	CC	GO:0005902	microvillus	3/23	106/28585	8,3E-05	0,001547	0,0008578	Prom1/Ush1c/Nfasc	3	Placebo
OPC	Tnik	CC	GO:0033268	node of Ranvier	2/23	20/28585	0,00012	0,001808	0,0010026	Ank3/Nfasc	2	Placebo

OPC	Tnik	CC	GO:0005923	bicellular tight junction	3/23	144/28585	0,00021	0,002736	0,0015173	Ank3/Cldn14/Cldn3 4c4	3	Placebo
OPC	Tnik	CC	GO:0043194	axon initial segment	2/23	29/28585	0,00025	0,002884	0,0015998	Ank3/Nfasc	2	Placebo
OPC	Tnik	CC	GO:0099092	postsynaptic density, intracellular component	2/23	42/28585	0,00052	0,005403	0,0029965	Tnik/Sh3gl3	2	Placebo
OPC	Tnik	CC	GO:0099091	postsynaptic specialization, intracellular component	2/23	50/28585	0,00074	0,006891	0,003822	Tnik/Sh3gl3	2	Placebo
OPC	Tnik	CC	GO:0098858	actin-based cell projection	3/23	232/28585	0,00083	0,007008	0,0038868	Prom1/Ush1c/Nfasc	3	Placebo
OPC	Tnik	CC	GO:0032420	stereocilium	2/23	58/28585	0,001	0,007719	0,004281	Prom1/Ush1c	2	Placebo
OPC	Tnik	CC	GO:0032421	stereocilium bundle	2/23	69/28585	0,00141	0,010058	0,0055784	Prom1/Ush1c	2	Placebo
OPC	Tnik	CC	GO:0005793	endoplasmic reticulum-Golgi intermediate compartment	2/23	79/28585	0,00184	0,012206	0,0067696	Prom1/Man1a	2	Placebo
OPC	Tnik	CC	GO:0001750	photoreceptor outer segment	2/23	86/28585	0,00217	0,012918	0,0071643	Prom1/Ush1c	2	Placebo
OPC	Tnik	CC	GO:0044304	main axon	2/23	87/28585	0,00222	0,012918	0,0071643	Ank3/Nfasc	2	Placebo
OPC	Tnik	CC	GO:0097733	photoreceptor cell cilium	2/23	117/28585	0,00397	0,020526	0,0113837	Prom1/Ush1c	2	Placebo
OPC	Tnik	CC	GO:0097731	9+0 non-motile cilium	2/23	131/28585	0,00495	0,021729	0,0120513	Prom1/Ush1c	2	Placebo
OPC	Tnik	CC	GO:0014069	postsynaptic density	3/23	442/28585	0,00517	0,021729	0,0120513	Tnik/Ank3/Sh3gl3	3	Placebo
OPC	Tnik	CC	GO:0032279	asymmetric synapse	3/23	462/28585	0,00584	0,021729	0,0120513	Tnik/Ank3/Sh3gl3	3	Placebo
OPC	Tnik	CC	GO:0005903	brush border	2/23	146/28585	0,00611	0,021854	0,0121204	Prom1/Ush1c	2	Placebo
OPC	Tnik	CC	GO:0099572	postsynaptic specialization	3/23	486/28585	0,00672	0,02231	0,0123735	Tnik/Ank3/Sh3gl3	3	Placebo
OPC	Tnik	CC	GO:0097730	non-motile cilium	2/23	168/28585	0,00801	0,025689	0,0142477	Prom1/Ush1c	2	Placebo
OPC	Tnik	CC	GO:0098862	cluster of actin-based cell projections	2/23	207/28585	0,01195	0,034719	0,0192558	Prom1/Ush1c	2	Placebo
OPC	Tnik	MF	GO:0030507	spectrin binding	2/23	34/28171	0,00035	0,023588	0,0133413	Ank3/Ush1c	2	Placebo
OPC	Tnik	MF	GO:0045296	cadherin binding	2/23	70/28171	0,00149	0,040898	0,0231318	Prom1/Ank3	2	Placebo
OPC	Tnik	MF	GO:0050839	cell adhesion molecule binding	3/23	305/28171	0,0019	0,040898	0,0231318	Prom1/Ank3/Nfasc	3	Placebo
OPC	Tnik	MF	GO:0051015	actin filament binding	2/23	221/28171	0,01391	0,049043	0,0277382	Mical3/Ush1c	2	Placebo
COP	Anxa2	BP	GO:0035265	organ growth	3/11	220/28564	7,1E-05	0,019904	0,0066962	Bnc2/Rspo2/Foxc2	3	EPO
COP	Anxa2	BP	GO:0120163	negative regulation of cold-induced thermogenesis	2/11	47/28564	0,00014	0,019904	0,0066962	Npr3/Foxc2	2	EPO
COP	Anxa2	BP	GO:0001974	blood vessel remodeling	2/11	61/28564	0,00024	0,019904	0,0066962	Npr3/Foxc2	2	EPO
COP	Anxa2	BP	GO:0030199	collagen fibril organization	2/11	61/28564	0,00024	0,019904	0,0066962	Anxa2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0007589	body fluid secretion	2/11	121/28564	0,00095	0,019904	0,0066962	Anxa2/Npr3	2	EPO
COP	Anxa2	BP	GO:0061041	regulation of wound healing	2/11	137/28564	0,00122	0,019904	0,0066962	Anxa2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0120161	regulation of cold-induced thermogenesis	2/11	149/28564	0,00144	0,019904	0,0066962	Npr3/Foxc2	2	EPO
COP	Anxa2	BP	GO:0106106	cold-induced thermogenesis	2/11	152/28564	0,0015	0,019904	0,0066962	Npr3/Foxc2	2	EPO
COP	Anxa2	BP	GO:1990845	adaptive thermogenesis	2/11	168/28564	0,00183	0,019904	0,0066962	Npr3/Foxc2	2	EPO
COP	Anxa2	BP	GO:1903034	regulation of response to wounding	2/11	177/28564	0,00202	0,019904	0,0066962	Anxa2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0035296	regulation of tube diameter	2/11	179/28564	0,00207	0,019904	0,0066962	Npr3/Foxc2	2	EPO
COP	Anxa2	BP	GO:0097746	blood vessel diameter maintenance	2/11	179/28564	0,00207	0,019904	0,0066962	Npr3/Foxc2	2	EPO
COP	Anxa2	BP	GO:0035150	regulation of tube size	2/11	180/28564	0,00209	0,019904	0,0066962	Npr3/Foxc2	2	EPO
COP	Anxa2	BP	GO:0048754	branching morphogenesis of an epithelial tube	2/11	191/28564	0,00235	0,019904	0,0066962	Rspo2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0001659	temperature homeostasis	2/11	192/28564	0,00238	0,019904	0,0066962	Npr3/Foxc2	2	EPO

COP	Anxa2	BP	GO:0048771	tissue remodeling	2/11	212/28564	0,00289	0,020119	0,0067686	Npr3/Foxc2	2	EPO
COP	Anxa2	BP	GO:0061138	morphogenesis of a branching epithelium	2/11	229/28564	0,00336	0,021014	0,0070696	Rspo2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0003018	vascular process in circulatory system	2/11	240/28564	0,00368	0,021788	0,0073301	Npr3/Foxc2	2	EPO
COP	Anxa2	BP	GO:0001763	morphogenesis of a branching structure	2/11	249/28564	0,00395	0,022151	0,0074521	Rspo2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0033002	muscle cell proliferation	2/11	273/28564	0,00473	0,023644	0,0079544	Npr3/Foxc2	2	EPO
COP	Anxa2	BP	GO:0061448	connective tissue development	2/11	307/28564	0,00594	0,024874	0,0083685	Rspo2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0060485	mesenchyme development	2/11	310/28564	0,00605	0,024874	0,0083685	Bnc2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0030198	extracellular matrix organization	2/11	322/28564	0,00651	0,025541	0,0085929	Anxa2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0043062	extracellular structure organization	2/11	324/28564	0,00659	0,025541	0,0085929	Anxa2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0045229	external encapsulating structure organization	2/11	324/28564	0,00659	0,025541	0,0085929	Anxa2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0050878	regulation of body fluid levels	2/11	354/28564	0,00782	0,027902	0,0093871	Anxa2/Npr3	2	EPO
COP	Anxa2	BP	GO:0042060	wound healing	2/11	392/28564	0,00952	0,029104	0,0097914	Anxa2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0060562	epithelial tube morphogenesis	2/11	397/28564	0,00975	0,029436	0,009903	Rspo2/Foxc2	2	EPO
COP	Anxa2	BP	GO:0001503	ossification	2/11	427/28564	0,01122	0,031427	0,0105729	Rspo2/Foxc2	2	EPO
COP	Anxa2	MF	GO:0008201	heparin binding	2/11	174/28171	0,00201	0,026963	0,0118557	Ccl7/Rspo2	2	EPO
COP	Anxa2	MF	GO:0005539	glycosaminoglycan binding	2/11	235/28171	0,00363	0,027998	0,012311	Ccl7/Rspo2	2	EPO
COP	Anxa2	MF	GO:1901681	sulfur compound binding	2/11	293/28171	0,00557	0,028848	0,0126845	Ccl7/Rspo2	2	EPO
COP	Anxa2	MF	GO:0046873	metal ion transmembrane transporter activity	2/11	430/28171	0,01167	0,0461	0,0202706	Anxa2/Slc6a20a	2	EPO
COP	Col1a2	BP	GO:0001503	ossification	5/15	427/28564	1,9E-06	0,001514	0,0005807	Col1a2/Rspo2/Foxc2/Ranbp3l/Spp1	5	Placebo
COP	Col1a2	BP	GO:0048762	mesenchymal cell differentiation	4/15	249/28564	7,1E-06	0,00279	0,0010702	Aldh1a2/Foxc2/Ranbp3l/Six1	4	Placebo
COP	Col1a2	BP	GO:0061053	somite development	3/15	96/28564	1,6E-05	0,003049	0,0011698	Aldh1a2/Foxc2/Six1	3	Placebo
COP	Col1a2	BP	GO:0060485	mesenchyme development	4/15	310/28564	1,7E-05	0,003049	0,0011698	Aldh1a2/Foxc2/Ranbp3l/Six1	4	Placebo
COP	Col1a2	BP	GO:0014033	neural crest cell differentiation	3/15	102/28564	1,9E-05	0,003049	0,0011698	Aldh1a2/Foxc2/Six1	3	Placebo
COP	Col1a2	BP	GO:0035282	segmentation	3/15	114/28564	2,7E-05	0,003105	0,0011913	Aldh1a2/Foxc2/Six1	3	Placebo
COP	Col1a2	BP	GO:0072001	renal system development	4/15	352/28564	2,8E-05	0,003105	0,0011913	Aldh1a2/Foxc2/Spp1/Six1	4	Placebo
COP	Col1a2	BP	GO:0030282	bone mineralization	3/15	134/28564	4,4E-05	0,003804	0,0014591	Col1a2/Rspo2/Spp1	3	Placebo
COP	Col1a2	BP	GO:0060562	epithelial tube morphogenesis	4/15	397/28564	4,4E-05	0,003804	0,0014591	Aldh1a2/Rspo2/Foxc2/Six1	4	Placebo
COP	Col1a2	BP	GO:0072189	ureter development	2/15	20/28564	4,9E-05	0,003804	0,0014591	Aldh1a2/Six1	2	Placebo
COP	Col1a2	BP	GO:0031214	biomineral tissue development	3/15	181/28564	0,00011	0,007653	0,002936	Col1a2/Rspo2/Spp1	3	Placebo

COP	Col1a2	BP	GO:0048754	branching morphogenesis of an epithelial tube	3/15	191/28564	0,00013	0,008225	0,0031553	Rspo2/Foxc2/Six1	3	Placebo
COP	Col1a2	BP	GO:0035115	embryonic forelimb morphogenesis	2/15	36/28564	0,00016	0,009592	0,0036796	Aldh1a2/Rspo2	2	Placebo
COP	Col1a2	BP	GO:0048771	tissue remodeling	3/15	212/28564	0,00017	0,009592	0,0036796	Foxc2/Spp1/Npr3	3	Placebo
COP	Col1a2	BP	GO:0001649	osteoblast differentiation	3/15	224/28564	0,0002	0,010528	0,0040389	Rspo2/Ranbp3l/Spp1	3	Placebo
COP	Col1a2	BP	GO:0061138	morphogenesis of a branching epithelium	3/15	229/28564	0,00022	0,010532	0,0040405	Rspo2/Foxc2/Six1	3	Placebo
COP	Col1a2	BP	GO:0035136	forelimb morphogenesis	2/15	47/28564	0,00027	0,011342	0,0043513	Aldh1a2/Rspo2	2	Placebo
COP	Col1a2	BP	GO:0120163	negative regulation of cold-induced thermogenesis	2/15	47/28564	0,00027	0,011342	0,0043513	Foxc2/Npr3	2	Placebo
COP	Col1a2	BP	GO:0001763	morphogenesis of a branching structure	3/15	249/28564	0,00028	0,011342	0,0043513	Rspo2/Foxc2/Six1	3	Placebo
COP	Col1a2	BP	GO:0060541	respiratory system development	3/15	270/28564	0,00035	0,013437	0,0051548	Aldh1a2/Rspo2/Six1	3	Placebo
COP	Col1a2	BP	GO:0033002	muscle cell proliferation	3/15	273/28564	0,00036	0,013437	0,0051548	Foxc2/Six1/Npr3	3	Placebo
COP	Col1a2	BP	GO:0048701	embryonic cranial skeleton morphogenesis	2/15	56/28564	0,00039	0,013861	0,0053174	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0048863	stem cell differentiation	3/15	286/28564	0,00041	0,013916	0,0053385	Aldh1a2/Foxc2/Six1	3	Placebo
COP	Col1a2	BP	GO:0003007	heart morphogenesis	3/15	291/28564	0,00043	0,013916	0,0053385	Aldh1a2/Foxc2/Six1	3	Placebo
COP	Col1a2	BP	GO:0001974	blood vessel remodeling	2/15	61/28564	0,00046	0,013916	0,0053385	Foxc2/Npr3	2	Placebo
COP	Col1a2	BP	GO:0030199	collagen fibril organization	2/15	61/28564	0,00046	0,013916	0,0053385	Col1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0046173	polyol biosynthetic process	2/15	64/28564	0,00051	0,014749	0,0056582	Sphk1/Isyna1	2	Placebo
COP	Col1a2	BP	GO:0048562	embryonic organ morphogenesis	3/15	334/28564	0,00065	0,01782	0,0068363	Aldh1a2/Foxc2/Six1	3	Placebo
COP	Col1a2	BP	GO:0001822	kidney development	3/15	336/28564	0,00066	0,01782	0,0068363	Foxc2/Spp1/Six1	3	Placebo
COP	Col1a2	BP	GO:0001756	somitogenesis	2/15	77/28564	0,00074	0,01919	0,0073619	Aldh1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0048844	artery morphogenesis	2/15	83/28564	0,00085	0,020348	0,007806	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0014855	striated muscle cell proliferation	2/15	84/28564	0,00088	0,020348	0,007806	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:1904888	cranial skeletal system development	2/15	84/28564	0,00088	0,020348	0,007806	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0003151	outflow tract morphogenesis	2/15	88/28564	0,00096	0,020348	0,007806	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0014032	neural crest cell development	2/15	89/28564	0,00098	0,020348	0,007806	Aldh1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0001656	metanephros development	2/15	91/28564	0,00103	0,020348	0,007806	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0035050	embryonic heart tube development	2/15	95/28564	0,00112	0,020348	0,007806	Aldh1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0048864	stem cell development	2/15	99/28564	0,00121	0,020348	0,007806	Aldh1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0030593	neutrophil chemotaxis	2/15	105/28564	0,00136	0,020348	0,007806	Spp1/Ccl7	2	Placebo
COP	Col1a2	BP	GO:0001657	ureteric bud development	2/15	107/28564	0,00141	0,020348	0,007806	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0048704	embryonic skeletal system morphogenesis	2/15	110/28564	0,00149	0,020348	0,007806	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0072163	mesonephric epithelium development	2/15	110/28564	0,00149	0,020348	0,007806	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0072164	mesonephric tubule development	2/15	110/28564	0,00149	0,020348	0,007806	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0019751	polyol metabolic process	2/15	111/28564	0,00152	0,020348	0,007806	Sphk1/Isyna1	2	Placebo

COP	Col1a2	BP	GO:0003002	regionalization	3/15	449/28564	0,00153	0,020348	0,007806	Aldh1a2/Foxc2/Six1	3	Placebo
COP	Col1a2	BP	GO:0001823	mesonephros development	2/15	113/28564	0,00157	0,020348	0,007806	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0060840	artery development	2/15	119/28564	0,00174	0,020348	0,007806	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0072009	nephron epithelium development	2/15	120/28564	0,00177	0,020348	0,007806	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0007389	pattern specification process	3/15	492/28564	0,00198	0,020348	0,007806	Aldh1a2/Foxc2/Six1	3	Placebo
COP	Col1a2	BP	GO:0071621	granulocyte chemotaxis	2/15	131/28564	0,00211	0,020348	0,007806	Spp1/Ccl7	2	Placebo
COP	Col1a2	BP	GO:1990266	neutrophil migration	2/15	132/28564	0,00214	0,020403	0,0078271	Spp1/Ccl7	2	Placebo
COP	Col1a2	BP	GO:2000027	regulation of animal organ morphogenesis	2/15	134/28564	0,0022	0,020762	0,0079649	Rspo2/Six1	2	Placebo
COP	Col1a2	BP	GO:0003014	renal system process	2/15	136/28564	0,00227	0,020931	0,0080299	Slc22a6/Npr3	2	Placebo
COP	Col1a2	BP	GO:0046165	alcohol biosynthetic process	2/15	142/28564	0,00247	0,020931	0,0080299	Sphk1/Isyna1	2	Placebo
COP	Col1a2	BP	GO:0030326	embryonic limb morphogenesis	2/15	144/28564	0,00254	0,020931	0,0080299	Aldh1a2/Rspo2	2	Placebo
COP	Col1a2	BP	GO:0035113	embryonic appendage morphogenesis	2/15	144/28564	0,00254	0,020931	0,0080299	Aldh1a2/Rspo2	2	Placebo
COP	Col1a2	BP	GO:0048706	embryonic skeletal system development	2/15	148/28564	0,00268	0,021159	0,0081172	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0120161	regulation of cold-induced thermogenesis	2/15	149/28564	0,00271	0,021226	0,0081429	Foxc2/Npr3	2	Placebo
COP	Col1a2	BP	GO:0106106	cold-induced thermogenesis	2/15	152/28564	0,00282	0,021853	0,0083837	Foxc2/Npr3	2	Placebo
COP	Col1a2	BP	GO:0072073	kidney epithelium development	2/15	155/28564	0,00293	0,022484	0,0086257	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0006820	monoatomic anion transport	2/15	159/28564	0,00308	0,022733	0,008721	Slc13a4/Slc22a6	2	Placebo
COP	Col1a2	BP	GO:0072006	nephron development	2/15	162/28564	0,0032	0,022733	0,008721	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0097530	granulocyte migration	2/15	162/28564	0,0032	0,022733	0,008721	Spp1/Ccl7	2	Placebo
COP	Col1a2	BP	GO:1990845	adaptive thermogenesis	2/15	168/28564	0,00343	0,023963	0,009193	Foxc2/Npr3	2	Placebo
COP	Col1a2	BP	GO:0120254	olefinic compound metabolic process	2/15	169/28564	0,00347	0,023963	0,009193	Aldh1a2/Sphk1	2	Placebo
COP	Col1a2	BP	GO:0071230	cellular response to amino acid stimulus	2/15	174/28564	0,00368	0,023963	0,009193	Col1a2/Six1	2	Placebo
COP	Col1a2	BP	GO:0035107	appendage morphogenesis	2/15	179/28564	0,00389	0,024454	0,0093814	Aldh1a2/Rspo2	2	Placebo
COP	Col1a2	BP	GO:0035108	limb morphogenesis	2/15	179/28564	0,00389	0,024454	0,0093814	Aldh1a2/Rspo2	2	Placebo
COP	Col1a2	BP	GO:0035296	regulation of tube diameter	2/15	179/28564	0,00389	0,024454	0,0093814	Foxc2/Npr3	2	Placebo
COP	Col1a2	BP	GO:0097746	blood vessel diameter maintenance	2/15	179/28564	0,00389	0,024454	0,0093814	Foxc2/Npr3	2	Placebo
COP	Col1a2	BP	GO:0035150	regulation of tube size	2/15	180/28564	0,00393	0,024454	0,0093814	Foxc2/Npr3	2	Placebo
COP	Col1a2	BP	GO:0045766	positive regulation of angiogenesis	2/15	181/28564	0,00397	0,024454	0,0093814	Foxc2/Sphk1	2	Placebo
COP	Col1a2	BP	GO:1904018	positive regulation of vasculature development	2/15	181/28564	0,00397	0,024454	0,0093814	Foxc2/Sphk1	2	Placebo
COP	Col1a2	BP	GO:0007219	Notch signaling pathway	2/15	184/28564	0,0041	0,025054	0,0096114	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0071356	cellular response to tumor necrosis factor	2/15	187/28564	0,00423	0,025144	0,009646	Sphk1/Ccl7	2	Placebo
COP	Col1a2	BP	GO:0016331	morphogenesis of embryonic epithelium	2/15	188/28564	0,00428	0,025144	0,009646	Aldh1a2/Six1	2	Placebo
COP	Col1a2	BP	GO:0071229	cellular response to acid chemical	2/15	188/28564	0,00428	0,025144	0,009646	Col1a2/Six1	2	Placebo
COP	Col1a2	BP	GO:0043200	response to amino acid	2/15	189/28564	0,00432	0,025216	0,0096735	Col1a2/Six1	2	Placebo
COP	Col1a2	BP	GO:0001659	temperature homeostasis	2/15	192/28564	0,00446	0,025808	0,0099009	Foxc2/Npr3	2	Placebo
COP	Col1a2	BP	GO:0034612	response to tumor necrosis factor	2/15	207/28564	0,00516	0,028065	0,0107667	Sphk1/Ccl7	2	Placebo
COP	Col1a2	BP	GO:0001101	response to acid chemical	2/15	211/28564	0,00535	0,028092	0,0107768	Col1a2/Six1	2	Placebo

COP	Col1a2	BP	GO:0048736	appendage development	2/15	211/28564	0,00535	0,028092	0,0107768	Aldh1a2/Rspo2	2	Placebo
COP	Col1a2	BP	GO:0060173	limb development	2/15	211/28564	0,00535	0,028092	0,0107768	Aldh1a2/Rspo2	2	Placebo
COP	Col1a2	BP	GO:0072330	monocarboxylic acid biosynthetic process	2/15	216/28564	0,0056	0,029072	0,011153	Aldh1a2/Sphk1	2	Placebo
COP	Col1a2	BP	GO:0035265	organ growth	2/15	220/28564	0,0058	0,029081	0,0111562	Rspo2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0008217	regulation of blood pressure	2/15	222/28564	0,00591	0,029081	0,0111562	Col1a2/Npr3	2	Placebo
COP	Col1a2	BP	GO:0030595	leukocyte chemotaxis	2/15	230/28564	0,00633	0,029099	0,0111633	Spp1/Ccl7	2	Placebo
COP	Col1a2	BP	GO:0009952	anterior/posterior pattern specification	2/15	233/28564	0,00649	0,029541	0,0113328	Aldh1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:1901617	organic hydroxy compound biosynthetic process	2/15	236/28564	0,00665	0,029541	0,0113328	Sphk1/Isyna1	2	Placebo
COP	Col1a2	BP	GO:0030324	lung development	2/15	239/28564	0,00681	0,029541	0,0113328	Aldh1a2/Rspo2	2	Placebo
COP	Col1a2	BP	GO:0003018	vascular process in circulatory system	2/15	240/28564	0,00687	0,029541	0,0113328	Foxc2/Npr3	2	Placebo
COP	Col1a2	BP	GO:0030323	respiratory tube development	2/15	242/28564	0,00698	0,029541	0,0113328	Aldh1a2/Rspo2	2	Placebo
COP	Col1a2	BP	GO:0097529	myeloid leukocyte migration	2/15	242/28564	0,00698	0,029541	0,0113328	Spp1/Ccl7	2	Placebo
COP	Col1a2	BP	GO:0042445	hormone metabolic process	2/15	246/28564	0,0072	0,029541	0,0113328	Aldh1a2/Spp1	2	Placebo
COP	Col1a2	BP	GO:0051259	protein complex oligomerization	2/15	254/28564	0,00766	0,03039	0,0116585	Col1a2/Aldh1a2	2	Placebo
COP	Col1a2	BP	GO:0048705	skeletal system morphogenesis	2/15	264/28564	0,00825	0,030448	0,011681	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0048738	cardiac muscle tissue development	2/15	276/28564	0,00899	0,03181	0,0122035	Aldh1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0014706	striated muscle tissue development	2/15	296/28564	0,01028	0,034062	0,0130674	Aldh1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0045165	cell fate commitment	2/15	303/28564	0,01075	0,03457	0,013262	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0045765	regulation of angiogenesis	2/15	305/28564	0,01089	0,03457	0,013262	Foxc2/Sphk1	2	Placebo
COP	Col1a2	BP	GO:0061448	connective tissue development	2/15	307/28564	0,01102	0,03457	0,013262	Rspo2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0060326	cell chemotaxis	2/15	308/28564	0,01109	0,03457	0,013262	Spp1/Ccl7	2	Placebo
COP	Col1a2	BP	GO:1901342	regulation of vasculature development	2/15	309/28564	0,01116	0,03457	0,013262	Foxc2/Sphk1	2	Placebo
COP	Col1a2	BP	GO:0046394	carboxylic acid biosynthetic process	2/15	310/28564	0,01123	0,03457	0,013262	Aldh1a2/Sphk1	2	Placebo
COP	Col1a2	BP	GO:0016053	organic acid biosynthetic process	2/15	313/28564	0,01144	0,03457	0,013262	Aldh1a2/Sphk1	2	Placebo
COP	Col1a2	BP	GO:0030198	extracellular matrix organization	2/15	322/28564	0,01207	0,035628	0,0136681	Col1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0043062	extracellular structure organization	2/15	324/28564	0,01222	0,035781	0,0137268	Col1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0045229	external encapsulating structure organization	2/15	324/28564	0,01222	0,035781	0,0137268	Col1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0006066	alcohol metabolic process	2/15	346/28564	0,01384	0,038255	0,0146757	Sphk1/Isyna1	2	Placebo
COP	Col1a2	BP	GO:0007517	muscle organ development	2/15	377/28564	0,01628	0,040173	0,0154116	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0043010	camera-type eye development	2/15	378/28564	0,01637	0,040247	0,0154402	Aldh1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0050900	leukocyte migration	2/15	386/28564	0,01703	0,041372	0,0158716	Spp1/Ccl7	2	Placebo
COP	Col1a2	BP	GO:1903532	positive regulation of secretion by cell	2/15	389/28564	0,01728	0,041443	0,0158989	Sphk1/Spp1	2	Placebo
COP	Col1a2	BP	GO:0048638	regulation of developmental growth	2/15	405/28564	0,01864	0,04338	0,0166419	Foxc2/Six1	2	Placebo
COP	Col1a2	BP	GO:0001654	eye development	2/15	426/28564	0,02049	0,046319	0,0177695	Aldh1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0050678	regulation of epithelial cell proliferation	2/15	427/28564	0,02058	0,046354	0,0177828	Aldh1a2/Six1	2	Placebo
COP	Col1a2	BP	GO:0019221	cytokine-mediated signaling pathway	2/15	429/28564	0,02077	0,046354	0,0177828	Sphk1/Ccl7	2	Placebo
COP	Col1a2	BP	GO:0150063	visual system development	2/15	429/28564	0,02077	0,046354	0,0177828	Aldh1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0048880	sensory system development	2/15	433/28564	0,02113	0,046834	0,0179669	Aldh1a2/Foxc2	2	Placebo
COP	Col1a2	BP	GO:0006869	lipid transport	2/15	447/28564	0,02242	0,048308	0,0185326	Slc22a6/Spp1	2	Placebo

COP	Col1a2	BP	GO:0051047	positive regulation of secretion	2/15	453/28564	0,02299	0,04912	0,0188438	Sphk1/Spp1	2	Placebo
COP	Col1a2	MF	GO:0031404	chloride ion binding	2/15	15/28171	2,8E-05	0,002242	0,0010487	Slc22a6/Npr3	2	Placebo
COP	Col1a2	MF	GO:0046332	SMAD binding	2/15	85/28171	0,00092	0,032211	0,0150694	Col1a2/Ranbp3l	2	Placebo
COP	Col1a2	MF	GO:0015103	inorganic anion transmembrane transporter activity	2/15	142/28171	0,00254	0,032211	0,0150694	Slc13a4/Slc22a6	2	Placebo
COP	Col1a2	MF	GO:0008201	heparin binding	2/15	174/28171	0,00378	0,032211	0,0150694	Rspo2/Ccl7	2	Placebo
COP	Col1a2	MF	GO:0005125	cytokine activity	2/15	231/28171	0,00655	0,032211	0,0150694	Spp1/Ccl7	2	Placebo
COP	Col1a2	MF	GO:0005539	glycosaminoglycan binding	2/15	235/28171	0,00677	0,032211	0,0150694	Rspo2/Ccl7	2	Placebo
COP	Col1a2	MF	GO:0015291	secondary active transmembrane transporter activity	2/15	262/28171	0,00835	0,032211	0,0150694	Slc13a4/Slc22a6	2	Placebo
COP	Col1a2	MF	GO:1901681	sulfur compound binding	2/15	293/28171	0,01035	0,032251	0,0150882	Rspo2/Ccl7	2	Placebo
COP	Inpp5d	BP	GO:0032695	negative regulation of interleukin-12 production	2/9	19/28564	1,5E-05	0,008367	0,002582	Tlr2/Cmklr1	2	Placebo
COP	Inpp5d	BP	GO:0002429	immune response-activating cell surface receptor signaling pathway	3/9	272/28564	6,9E-05	0,008497	0,0026222	Tlr2/Cmklr1/Themis2	3	Placebo
COP	Inpp5d	BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	3/9	283/28564	7,7E-05	0,008497	0,0026222	Tlr2/Cmklr1/Themis2	3	Placebo
COP	Inpp5d	BP	GO:0001818	negative regulation of cytokine production	3/9	296/28564	8,8E-05	0,008497	0,0026222	Inpp5d/Tlr2/Cmklr1	3	Placebo
COP	Inpp5d	BP	GO:0045429	positive regulation of nitric oxide biosynthetic process	2/9	50/28564	0,00011	0,008497	0,0026222	Tlr2/Agxt2	2	Placebo
COP	Inpp5d	BP	GO:1904407	positive regulation of nitric oxide metabolic process	2/9	52/28564	0,00012	0,008497	0,0026222	Tlr2/Agxt2	2	Placebo
COP	Inpp5d	BP	GO:0046651	lymphocyte proliferation	3/9	354/28564	0,00015	0,008497	0,0026222	Inpp5d/Cd37/Zbtb32	3	Placebo
COP	Inpp5d	BP	GO:0032943	mononuclear cell proliferation	3/9	360/28564	0,00016	0,008497	0,0026222	Inpp5d/Cd37/Zbtb32	3	Placebo
COP	Inpp5d	BP	GO:0032655	regulation of interleukin-12 production	2/9	62/28564	0,00017	0,008497	0,0026222	Tlr2/Cmklr1	2	Placebo
COP	Inpp5d	BP	GO:0032615	interleukin-12 production	2/9	64/28564	0,00018	0,008497	0,0026222	Tlr2/Cmklr1	2	Placebo
COP	Inpp5d	BP	GO:0006081	cellular aldehyde metabolic process	2/9	65/28564	0,00018	0,008497	0,0026222	Cyp11b1/Agxt2	2	Placebo
COP	Inpp5d	BP	GO:0002757	immune response-activating signaling pathway	3/9	391/28564	0,0002	0,008497	0,0026222	Tlr2/Cmklr1/Themis2	3	Placebo
COP	Inpp5d	BP	GO:0070661	leukocyte proliferation	3/9	396/28564	0,00021	0,008497	0,0026222	Inpp5d/Cd37/Zbtb32	3	Placebo
COP	Inpp5d	BP	GO:0002764	immune response-regulating signaling pathway	3/9	402/28564	0,00022	0,008497	0,0026222	Tlr2/Cmklr1/Themis2	3	Placebo
COP	Inpp5d	BP	GO:0045428	regulation of nitric oxide biosynthetic process	2/9	73/28564	0,00023	0,008497	0,0026222	Tlr2/Agxt2	2	Placebo
COP	Inpp5d	BP	GO:0080164	regulation of nitric oxide metabolic process	2/9	77/28564	0,00026	0,008864	0,0027353	Tlr2/Agxt2	2	Placebo
COP	Inpp5d	BP	GO:0006809	nitric oxide biosynthetic process	2/9	86/28564	0,00032	0,010224	0,0031552	Tlr2/Agxt2	2	Placebo
COP	Inpp5d	BP	GO:0046209	nitric oxide metabolic process	2/9	92/28564	0,00036	0,010224	0,0031552	Tlr2/Agxt2	2	Placebo
COP	Inpp5d	BP	GO:0002253	activation of immune response	3/9	482/28564	0,00037	0,010224	0,0031552	Tlr2/Cmklr1/Themis2	3	Placebo
COP	Inpp5d	BP	GO:2001057	reactive nitrogen species metabolic process	2/9	94/28564	0,00038	0,010224	0,0031552	Tlr2/Agxt2	2	Placebo
COP	Inpp5d	BP	GO:0050672	negative regulation of lymphocyte proliferation	2/9	96/28564	0,0004	0,010224	0,0031552	Inpp5d/Cd37	2	Placebo

COP	Inpp5d	BP	GO:0032945	negative regulation of mononuclear cell proliferation	2/9	97/28564	0,0004	0,010224	0,0031552	Inpp5d/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0070664	negative regulation of leukocyte proliferation	2/9	104/28564	0,00046	0,011237	0,0034677	Inpp5d/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0002702	positive regulation of production of molecular mediator of immune response	2/9	143/28564	0,00088	0,014932	0,0046079	Tlr2/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0006690	icosanoid metabolic process	2/9	147/28564	0,00092	0,014932	0,0046079	Tlr2/Avpr1a	2	Placebo
COP	Inpp5d	BP	GO:0050864	regulation of B cell activation	2/9	148/28564	0,00094	0,014932	0,0046079	Inpp5d/Themis2	2	Placebo
COP	Inpp5d	BP	GO:0097530	granulocyte migration	2/9	162/28564	0,00112	0,014932	0,0046079	Tlr2/Cmklr1	2	Placebo
COP	Inpp5d	BP	GO:0002687	positive regulation of leukocyte migration	2/9	164/28564	0,00115	0,014932	0,0046079	Tlr2/Cmklr1	2	Placebo
COP	Inpp5d	BP	GO:0032675	regulation of interleukin-6 production	2/9	170/28564	0,00123	0,014932	0,0046079	Inpp5d/Tlr2	2	Placebo
COP	Inpp5d	BP	GO:0051250	negative regulation of lymphocyte activation	2/9	172/28564	0,00126	0,014932	0,0046079	Inpp5d/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0019722	calcium-mediated signaling	2/9	179/28564	0,00137	0,015498	0,0047825	Avpr1a/Cmklr1	2	Placebo
COP	Inpp5d	BP	GO:0032635	interleukin-6 production	2/9	179/28564	0,00137	0,015498	0,0047825	Inpp5d/Tlr2	2	Placebo
COP	Inpp5d	BP	GO:0002695	negative regulation of leukocyte activation	2/9	204/28564	0,00177	0,016942	0,0052281	Inpp5d/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0002700	regulation of production of molecular mediator of immune response	2/9	208/28564	0,00184	0,016942	0,0052281	Tlr2/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0007204	positive regulation of cytosolic calcium ion concentration	2/9	218/28564	0,00201	0,017504	0,0054016	Avpr1a/Cmklr1	2	Placebo
COP	Inpp5d	BP	GO:0050866	negative regulation of cell activation	2/9	227/28564	0,00218	0,017504	0,0054016	Inpp5d/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0002685	regulation of leukocyte migration	2/9	236/28564	0,00236	0,017723	0,0054692	Tlr2/Cmklr1	2	Placebo
COP	Inpp5d	BP	GO:0097529	myeloid leukocyte migration	2/9	242/28564	0,00247	0,017723	0,0054692	Tlr2/Cmklr1	2	Placebo
COP	Inpp5d	BP	GO:0042098	T cell proliferation	2/9	243/28564	0,00249	0,017723	0,0054692	Cd37/Zbtb32	2	Placebo
COP	Inpp5d	BP	GO:0042180	cellular ketone metabolic process	2/9	244/28564	0,00251	0,017723	0,0054692	Avpr1a/Cyp11b1	2	Placebo
COP	Inpp5d	BP	GO:0050670	regulation of lymphocyte proliferation	2/9	260/28564	0,00285	0,018205	0,0056179	Inpp5d/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0002274	myeloid leukocyte activation	2/9	264/28564	0,00294	0,018337	0,0056586	Tlr2/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0032944	regulation of mononuclear cell proliferation	2/9	264/28564	0,00294	0,018337	0,0056586	Inpp5d/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0002573	myeloid leukocyte differentiation	2/9	277/28564	0,00323	0,019053	0,0058796	Inpp5d/Tlr2	2	Placebo
COP	Inpp5d	BP	GO:0070663	regulation of leukocyte proliferation	2/9	287/28564	0,00346	0,019053	0,0058796	Inpp5d/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0019932	second-messenger-mediated signaling	2/9	295/28564	0,00365	0,019257	0,0059426	Avpr1a/Cmklr1	2	Placebo
COP	Inpp5d	BP	GO:0046394	carboxylic acid biosynthetic process	2/9	310/28564	0,00402	0,020314	0,006269	Avpr1a/Agxt2	2	Placebo
COP	Inpp5d	BP	GO:0016053	organic acid biosynthetic process	2/9	313/28564	0,0041	0,02033	0,0062739	Avpr1a/Agxt2	2	Placebo
COP	Inpp5d	BP	GO:0042113	B cell activation	2/9	318/28564	0,00422	0,020573	0,0063486	Inpp5d/Themis2	2	Placebo
COP	Inpp5d	BP	GO:0002699	positive regulation of immune effector process	2/9	327/28564	0,00446	0,020666	0,0063774	Tlr2/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0050900	leukocyte migration	2/9	386/28564	0,00616	0,023771	0,0073358	Tlr2/Cmklr1	2	Placebo
COP	Inpp5d	BP	GO:1903532	positive regulation of secretion by cell	2/9	389/28564	0,00625	0,023771	0,0073358	Tlr2/Avpr1a	2	Placebo
COP	Inpp5d	BP	GO:0002440	production of molecular mediator of immune response	2/9	405/28564	0,00676	0,025054	0,0077314	Tlr2/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0051090	regulation of DNA-binding transcription factor activity	2/9	447/28564	0,00818	0,027395	0,008454	Tlr2/Cmklr1	2	Placebo
COP	Inpp5d	BP	GO:0051047	positive regulation of secretion	2/9	453/28564	0,00839	0,027722	0,008555	Tlr2/Avpr1a	2	Placebo
COP	Inpp5d	BP	GO:0002697	regulation of immune effector process	2/9	472/28564	0,00908	0,028577	0,0088188	Tlr2/Cd37	2	Placebo
COP	Inpp5d	BP	GO:0002443	leukocyte mediated immunity	2/9	480/28564	0,00938	0,028577	0,0088188	Inpp5d/Tlr2	2	Placebo
COP	Inpp5d	BP	GO:0030099	myeloid cell differentiation	2/9	482/28564	0,00946	0,028577	0,0088188	Inpp5d/Tlr2	2	Placebo

COP	Inpp5d	BP	GO:0002831	regulation of response to biotic stimulus	2/9	485/28564	0,00957	0,028614	0,0088301	Tlr2/Cd37	2	Placebo
COP	Inpp5d	MF	GO:0017046	peptide hormone binding	2/8	51/28171	8,9E-05	0,002785	0,0005278	Avpr1a/Cmklr1	2	Placebo
COP	Inpp5d	MF	GO:0042277	peptide binding	3/8	361/28171	0,00011	0,002785	0,0005278	Tlr2/Avpr1a/Cmklr1	3	Placebo
COP	Inpp5d	MF	GO:0033218	amide binding	3/8	450/28171	0,00021	0,00326	0,0006177	Tlr2/Avpr1a/Cmklr1	3	Placebo
COP	Inpp5d	MF	GO:0042562	hormone binding	2/8	87/28171	0,00026	0,00326	0,0006177	Avpr1a/Cmklr1	2	Placebo
COP	Mir142hg	BP	GO:0002443	leukocyte mediated immunity	4/11	480/28564	2,4E-05	0,010791	0,004459	Csf2rb/Fgr/Ripk3/Prkcd	4	EPO
COP	Mir142hg	BP	GO:0046777	protein autophosphorylation	3/11	242/28564	9,4E-05	0,021489	0,0088792	Fgr/Ripk3/Prkcd	3	EPO
COP	Mir142hg	BP	GO:0035306	positive regulation of dephosphorylation	2/11	60/28564	0,00024	0,022897	0,0094611	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0002449	lymphocyte mediated immunity	3/11	372/28564	0,00033	0,022897	0,0094611	Csf2rb/Ripk3/Prkcd	3	EPO
COP	Mir142hg	BP	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3/11	373/28564	0,00034	0,022897	0,0094611	Csf2rb/Ripk3/Prkcd	3	EPO
COP	Mir142hg	BP	GO:0042742	defense response to bacterium	3/11	386/28564	0,00037	0,022897	0,0094611	Lyz1/Fgr/Prkcd	3	EPO
COP	Mir142hg	BP	GO:2000379	positive regulation of reactive oxygen species metabolic process	2/11	78/28564	0,0004	0,022897	0,0094611	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0070661	leukocyte proliferation	3/11	396/28564	0,0004	0,022897	0,0094611	Csf2rb/Ripk3/Prkcd	3	EPO
COP	Mir142hg	BP	GO:0033674	positive regulation of kinase activity	3/11	440/28564	0,00055	0,024559	0,0101479	Fgr/Ripk3/Prkcd	3	EPO
COP	Mir142hg	BP	GO:0070301	cellular response to hydrogen peroxide	2/11	93/28564	0,00057	0,024559	0,0101479	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0032147	activation of protein kinase activity	2/11	105/28564	0,00072	0,024559	0,0101479	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0042542	response to hydrogen peroxide	2/11	120/28564	0,00094	0,024559	0,0101479	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0035303	regulation of dephosphorylation	2/11	128/28564	0,00107	0,024559	0,0101479	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0001776	leukocyte homeostasis	2/11	136/28564	0,0012	0,024559	0,0101479	Mir142hg/Ripk3	2	EPO
COP	Mir142hg	BP	GO:0034614	cellular response to reactive oxygen species	2/11	146/28564	0,00138	0,024559	0,0101479	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:2000377	regulation of reactive oxygen species metabolic process	2/11	161/28564	0,00168	0,024559	0,0101479	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0016064	immunoglobulin mediated immune response	2/11	165/28564	0,00176	0,024559	0,0101479	Csf2rb/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0019724	B cell mediated immunity	2/11	168/28564	0,00183	0,024559	0,0101479	Csf2rb/Prkcd	2	EPO
COP	Mir142hg	BP	GO:2001235	positive regulation of apoptotic signaling pathway	2/11	172/28564	0,00191	0,024559	0,0101479	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0050830	defense response to Gram-positive bacterium	2/11	176/28564	0,002	0,024559	0,0101479	Lyz1/Fgr	2	EPO
COP	Mir142hg	BP	GO:0045834	positive regulation of lipid metabolic process	2/11	185/28564	0,00221	0,024559	0,0101479	Fgr/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0000302	response to reactive oxygen species	2/11	191/28564	0,00235	0,024559	0,0101479	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0050866	negative regulation of cell activation	2/11	227/28564	0,0033	0,026304	0,0108689	Fgr/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0044242	cellular lipid catabolic process	2/11	230/28564	0,00338	0,026304	0,0108689	Bco1/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0072593	reactive oxygen species metabolic process	2/11	249/28564	0,00395	0,028382	0,0117274	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0001906	cell killing	2/11	250/28564	0,00398	0,028382	0,0117274	Lyz1/Ripk3	2	EPO
COP	Mir142hg	BP	GO:0002274	myeloid leukocyte activation	2/11	264/28564	0,00443	0,030607	0,0126468	Fgr/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0034599	cellular response to oxidative stress	2/11	276/28564	0,00483	0,031856	0,0131629	Ripk3/Prkcd	2	EPO

COP	Mir142hg	BP	GO:0070663	regulation of leukocyte proliferation	2/11	287/28564	0,00521	0,031856	0,0131629	Csf2rb/Ripk3	2	EPO
COP	Mir142hg	BP	GO:0002703	regulation of leukocyte mediated immunity	2/11	310/28564	0,00605	0,033763	0,013951	Fgr/Ripk3	2	EPO
COP	Mir142hg	BP	GO:0018108	peptidyl-tyrosine phosphorylation	2/11	326/28564	0,00667	0,036221	0,0149668	Fgr/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0018212	peptidyl-tyrosine modification	2/11	328/28564	0,00675	0,036221	0,0149668	Fgr/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0016042	lipid catabolic process	2/11	342/28564	0,00732	0,036281	0,0149914	Bco1/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0016311	dephosphorylation	2/11	342/28564	0,00732	0,036281	0,0149914	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0062197	cellular response to chemical stress	2/11	347/28564	0,00753	0,036847	0,0152253	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0046651	lymphocyte proliferation	2/11	354/28564	0,00782	0,037162	0,0153554	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0032943	mononuclear cell proliferation	2/11	360/28564	0,00808	0,03799	0,0156976	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0032956	regulation of actin cytoskeleton organization	2/11	362/28564	0,00817	0,038006	0,0157041	Fgr/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0045860	positive regulation of protein kinase activity	2/11	373/28564	0,00865	0,039065	0,0161418	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0048872	homeostasis of number of cells	2/11	391/28564	0,00947	0,040479	0,0167261	Mir142hg/Ripk3	2	EPO
COP	Mir142hg	BP	GO:0019216	regulation of lipid metabolic process	2/11	393/28564	0,00957	0,040479	0,0167261	Fgr/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0006979	response to oxidative stress	2/11	408/28564	0,01028	0,042442	0,0175373	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0032970	regulation of actin filament-based process	2/11	411/28564	0,01042	0,042442	0,0175373	Fgr/Prkcd	2	EPO
COP	Mir142hg	BP	GO:2001233	regulation of apoptotic signaling pathway	2/11	424/28564	0,01106	0,042946	0,0177456	Ripk3/Prkcd	2	EPO
COP	Mir142hg	BP	GO:0002697	regulation of immune effector process	2/11	472/28564	0,01358	0,048332	0,0199711	Fgr/Ripk3	2	EPO
COP	Mir142hg	MF	GO:0004715	non-membrane spanning protein tyrosine kinase activity	2/10	45/28171	0,00011	0,003675	0,0004689	Fgr/Prkcd	2	EPO
COP	Mir142hg	MF	GO:0004713	protein tyrosine kinase activity	2/10	132/28171	0,00096	0,008783	0,0011206	Fgr/Prkcd	2	EPO
COP	Mir142hg	MF	GO:0004674	protein serine/threonine kinase activity	2/10	442/28171	0,01017	0,018643	0,0023787	Ripk3/Prkcd	2	EPO
COP	Mis18bp1	BP	GO:0090306	meiotic spindle assembly	2/16	10/28564	1,3E-05	0,002984	0,0017928	Ccnb2/Aspm	2	EPO
COP	Mis18bp1	BP	GO:0045132	meiotic chromosome segregation	3/16	116/28564	3,5E-05	0,003768	0,0022642	Ccnb2/Ankle1/Aspm	3	EPO
COP	Mis18bp1	BP	GO:0000212	meiotic spindle organization	2/16	19/28564	5E-05	0,003768	0,0022642	Ccnb2/Aspm	2	EPO
COP	Mis18bp1	BP	GO:0007059	chromosome segregation	4/16	429/28564	7,9E-05	0,004471	0,0026865	Ska1/Ccnb2/Ankle1/Aspm	4	EPO
COP	Mis18bp1	BP	GO:0000280	nuclear division	4/16	456/28564	0,0001	0,004528	0,0027208	Ccnb2/Ankle1/Kif20b/Aspm	4	EPO
COP	Mis18bp1	BP	GO:0140013	meiotic nuclear division	3/16	210/28564	0,0002	0,006786	0,0040773	Ccnb2/Ankle1/Aspm	3	EPO
COP	Mis18bp1	BP	GO:0061351	neural precursor cell proliferation	3/16	212/28564	0,00021	0,006786	0,0040773	Shcbp1/Melk/Aspm	3	EPO
COP	Mis18bp1	BP	GO:1903046	meiotic cell cycle process	3/16	229/28564	0,00026	0,007448	0,0044753	Ccnb2/Ankle1/Aspm	3	EPO
COP	Mis18bp1	BP	GO:0098813	nuclear chromosome segregation	3/16	338/28564	0,00082	0,018697	0,0112338	Ccnb2/Ankle1/Aspm	3	EPO
COP	Mis18bp1	BP	GO:0051321	meiotic cell cycle	3/16	339/28564	0,00083	0,018697	0,0112338	Ccnb2/Ankle1/Aspm	3	EPO
COP	Mis18bp1	BP	GO:0051225	spindle assembly	2/16	123/28564	0,00212	0,03011	0,018091	Ccnb2/Aspm	2	EPO
COP	Mis18bp1	BP	GO:2000177	regulation of neural precursor cell proliferation	2/16	126/28564	0,00222	0,03011	0,018091	Shcbp1/Aspm	2	EPO

COP	Mis18bp1	BP	GO:0007127	meiosis I	2/16	133/28564	0,00247	0,03011	0,018091	Ccnb2/Ankle1	2	EPO
COP	Mis18bp1	BP	GO:0061982	meiosis I cell cycle process	2/16	136/28564	0,00258	0,03011	0,018091	Ccnb2/Ankle1	2	EPO
COP	Mis18bp1	BP	GO:0007292	female gamete generation	2/16	174/28564	0,00419	0,033785	0,0202992	Ccnb2/Aspm	2	EPO
COP	Mis18bp1	BP	GO:0051302	regulation of cell division	2/16	182/28564	0,00457	0,035604	0,0213925	Kif20b/Aspm	2	EPO
COP	Mis18bp1	BP	GO:0007051	spindle organization	2/16	189/28564	0,00492	0,036676	0,0220361	Ccnb2/Aspm	2	EPO
COP	Mis18bp1	BP	GO:0001764	neuron migration	2/16	204/28564	0,0057	0,039053	0,0234643	Kif20b/Aspm	2	EPO
COP	Mis18bp1	CC	GO:0005819	spindle	4/17	357/28585	5E-05	0,001652	0,0006851	Ska1/Hmmr/Kif20b/Aspm	4	EPO
COP	Mis18bp1	CC	GO:0072686	mitotic spindle	3/17	177/28585	0,00015	0,002457	0,0010188	Ska1/Kif20b/Aspm	3	EPO
COP	Mis18bp1	CC	GO:0097431	mitotic spindle pole	2/17	39/28585	0,00024	0,002679	0,0011107	Kif20b/Aspm	2	EPO
COP	Mis18bp1	CC	GO:0045171	intercellular bridge	2/17	98/28585	0,00153	0,012623	0,0052343	Ska1/Kif20b	2	EPO
COP	Mis18bp1	CC	GO:0005874	microtubule	3/17	441/28585	0,00211	0,013935	0,0057784	Ska1/Kif20b/Aspm	3	EPO
COP	Mis18bp1	CC	GO:0000922	spindle pole	2/17	144/28585	0,00326	0,016798	0,0069659	Kif20b/Aspm	2	EPO
COP	Mis18bp1	CC	GO:0030496	midbody	2/17	201/28585	0,00624	0,02562	0,0106241	Kif20b/Aspm	2	EPO
COP	Mis18bp1	CC	GO:0000775	chromosome, centromeric region	2/17	258/28585	0,01009	0,02562	0,0106241	Mis18bp1/Ska1	2	EPO
COP	Mis18bp1	CC	GO:0098687	chromosomal region	2/17	367/28585	0,01969	0,04536	0,0188096	Mis18bp1/Ska1	2	EPO
COP	Nkain2	BP	GO:0042063	gliogenesis	8/47	378/28564	1,8E-07	9,05E-05	5,837E-05	Plp1/Aspa/Enpp2/Arhgef10/Trf/Mag/Fa2h/Bin1	8	EPO
COP	Nkain2	BP	GO:0010001	glial cell differentiation	7/47	274/28564	3,1E-07	9,05E-05	5,837E-05	Plp1/Aspa/Enpp2/Arhgef10/Mag/Fa2h/Bin1	7	EPO
COP	Nkain2	BP	GO:0014015	positive regulation of gliogenesis	5/47	90/28564	3,8E-07	9,05E-05	5,837E-05	Aspa/Enpp2/Trf/Mag/Bin1	5	EPO
COP	Nkain2	BP	GO:0042552	myelination	6/47	180/28564	5E-07	9,05E-05	5,837E-05	Plp1/Mbp/Arhgef10/Trf/Mag/Fa2h	6	EPO
COP	Nkain2	BP	GO:0007272	ensheathment of neurons	6/47	183/28564	5,5E-07	9,05E-05	5,837E-05	Plp1/Mbp/Arhgef10/Trf/Mag/Fa2h	6	EPO
COP	Nkain2	BP	GO:0008366	axon ensheathment	6/47	183/28564	5,5E-07	9,05E-05	5,837E-05	Plp1/Mbp/Arhgef10/Trf/Mag/Fa2h	6	EPO
COP	Nkain2	BP	GO:0048709	oligodendrocyte differentiation	5/47	122/28564	1,7E-06	0,000245	0,0001582	Plp1/Aspa/Enpp2/Mag/Fa2h	5	EPO
COP	Nkain2	BP	GO:0045687	positive regulation of glial cell differentiation	4/47	56/28564	2,2E-06	0,000274	0,0001766	Aspa/Enpp2/Mag/Bin1	4	EPO
COP	Nkain2	BP	GO:0014013	regulation of gliogenesis	5/47	139/28564	3,3E-06	0,000362	0,0002338	Aspa/Enpp2/Trf/Mag/Bin1	5	EPO
COP	Nkain2	BP	GO:0050767	regulation of neurogenesis	7/47	480/28564	1,3E-05	0,001258	0,0008114	Mbp/Aspa/Dip2b/Enpp2/Trf/Mag/Bin1	7	EPO
COP	Nkain2	BP	GO:0022010	central nervous system myelination	3/47	30/28564	1,6E-05	0,001351	0,0008719	Plp1/Mag/Fa2h	3	EPO

COP	Nkain2	BP	GO:0032291	axon ensheathment in central nervous system	3/47	30/28564	1,6E-05	0,001351	0,0008719	Plp1/Mag/Fa2h	3	EPO
COP	Nkain2	BP	GO:0045685	regulation of glial cell differentiation	4/47	97/28564	2E-05	0,001513	0,0009761	Aspa/Enpp2/Mag/Bin1	4	EPO
COP	Nkain2	BP	GO:1990089	response to nerve growth factor	3/47	40/28564	4E-05	0,002601	0,001678	Magi2/Gria2/Rap1a	3	EPO
COP	Nkain2	BP	GO:1990090	cellular response to nerve growth factor stimulus	3/47	40/28564	4E-05	0,002601	0,001678	Magi2/Gria2/Rap1a	3	EPO
COP	Nkain2	BP	GO:0006470	protein dephosphorylation	5/47	243/28564	4,9E-05	0,003023	0,0019506	Phlpp1/Ptprt/Ptprg/Magi2/Ppp2r3a	5	EPO
COP	Nkain2	BP	GO:0021782	glial cell development	4/47	129/28564	6,1E-05	0,003537	0,0022821	Plp1/Arhgef10/Mag/Fa2h	4	EPO
COP	Nkain2	BP	GO:0014003	oligodendrocyte development	3/47	49/28564	7,3E-05	0,004	0,0025807	Plp1/Mag/Fa2h	3	EPO
COP	Nkain2	BP	GO:0006687	glycosphingolipid metabolic process	3/47	53/28564	9,2E-05	0,004796	0,0030943	Map7/St6galnac3/Fa2h	3	EPO
COP	Nkain2	BP	GO:0006665	sphingolipid metabolic process	4/47	147/28564	0,0001	0,00499	0,0032196	Map7/St6galnac3/Enpp2/Fa2h	4	EPO
COP	Nkain2	BP	GO:0038180	nerve growth factor signaling pathway	2/47	11/28564	0,00014	0,006786	0,0043783	Magi2/Rap1a	2	EPO
COP	Nkain2	BP	GO:0010977	negative regulation of neuron projection development	4/47	165/28564	0,00016	0,007078	0,0045671	Mbp/Dip2b/Ptprg/Mag	4	EPO
COP	Nkain2	BP	GO:0007009	plasma membrane organization	4/47	169/28564	0,00017	0,007126	0,004598	Tmeff2/Ano4/Fa2h/Bin1	4	EPO
COP	Nkain2	BP	GO:0050769	positive regulation of neurogenesis	5/47	318/28564	0,00017	0,007126	0,004598	Aspa/Enpp2/Trf/Mag/Bin1	5	EPO
COP	Nkain2	BP	GO:2000146	negative regulation of cell motility	5/47	325/28564	0,00019	0,007568	0,0048832	Tmeff2/Ptprt/Ptprg/Magi2/Frmd5	5	EPO
COP	Nkain2	BP	GO:0050771	negative regulation of axonogenesis	3/47	70/28564	0,00021	0,00803	0,0051813	Mbp/Dip2b/Mag	3	EPO
COP	Nkain2	BP	GO:0016311	dephosphorylation	5/47	342/28564	0,00024	0,00887	0,0057231	Phlpp1/Ptprt/Ptprg/Magi2/Ppp2r3a	5	EPO
COP	Nkain2	BP	GO:0048711	positive regulation of astrocyte differentiation	2/47	15/28564	0,00027	0,009392	0,0060602	Mag/Bin1	2	EPO
COP	Nkain2	BP	GO:0006643	membrane lipid metabolic process	4/47	191/28564	0,00028	0,009392	0,0060602	Map7/St6galnac3/Enpp2/Fa2h	4	EPO
COP	Nkain2	BP	GO:0040013	negative regulation of locomotion	5/47	360/28564	0,00031	0,009977	0,0064372	Tmeff2/Ptprt/Ptprg/Magi2/Frmd5	5	EPO
COP	Nkain2	BP	GO:0006677	glycosylceramide metabolic process	2/47	16/28564	0,00031	0,009977	0,0064372	St6galnac3/Fa2h	2	EPO
COP	Nkain2	BP	GO:0051962	positive regulation of nervous system development	5/47	379/28564	0,00039	0,011894	0,0076744	Aspa/Enpp2/Trf/Mag/Bin1	5	EPO
COP	Nkain2	BP	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	4/47	211/28564	0,0004	0,011894	0,0076744	Mbp/Ptprt/Mag/Magi2	4	EPO

COP	Nkain2	BP	GO:0031032	actomyosin structure organization	4/47	212/28564	0,00041	0,011894	0,0076744	Tmeff2/Arhgef10/Tmod2/Frmd5	4	EPO
COP	Nkain2	BP	GO:0035235	ionotropic glutamate receptor signaling pathway	2/47	19/28564	0,00045	0,012048	0,0077737	Plp1/Gria2	2	EPO
COP	Nkain2	BP	GO:0098696	regulation of neurotransmitter receptor localization to postsynaptic specialization membrane	2/47	19/28564	0,00045	0,012048	0,0077737	Magi2/Rap1a	2	EPO
COP	Nkain2	BP	GO:0031345	negative regulation of cell projection organization	4/47	219/28564	0,00046	0,012048	0,0077737	Mbp/Dip2b/Ptprg/Mag	4	EPO
COP	Nkain2	BP	GO:1902903	regulation of supramolecular fiber organization	5/47	394/28564	0,00046	0,012048	0,0077737	Tubb4a/Tmeff2/Arhgef10/Tmod2/Bin1	5	EPO
COP	Nkain2	BP	GO:0048708	astrocyte differentiation	3/47	93/28564	0,00049	0,012359	0,0079744	Plp1/Mag/Bin1	3	EPO
COP	Nkain2	BP	GO:0006664	glycolipid metabolic process	3/47	94/28564	0,0005	0,012433	0,0080221	Map7/St6galnac3/Fa2h	3	EPO
COP	Nkain2	BP	GO:1903509	liposaccharide metabolic process	3/47	95/28564	0,00052	0,012511	0,0080724	Map7/St6galnac3/Fa2h	3	EPO
COP	Nkain2	BP	GO:0032970	regulation of actin filament-based process	5/47	411/28564	0,00056	0,013201	0,0085178	Pde4b/Tmeff2/Arhgef10/Tmod2/Bin1	5	EPO
COP	Nkain2	BP	GO:0031643	positive regulation of myelination	2/47	26/28564	0,00084	0,019271	0,0124341	Trf/Mag	2	EPO
COP	Nkain2	BP	GO:0043547	positive regulation of GTPase activity	4/47	259/28564	0,00087	0,019271	0,0124341	Dock10/Arhgef10/Rap1a/Bin1	4	EPO
COP	Nkain2	BP	GO:0007015	actin filament organization	5/47	454/28564	0,00088	0,019271	0,0124341	Tmeff2/Arhgef10/Trf/Tmod2/Bin1	5	EPO
COP	Nkain2	BP	GO:0010959	regulation of metal ion transport	5/47	460/28564	0,00093	0,01999	0,012898	Nkain2/Plp1/Pde4b/Trf/Bin1	5	EPO
COP	Nkain2	BP	GO:1902473	regulation of protein localization to synapse	2/47	29/28564	0,00105	0,021962	0,0141706	Magi2/Rap1a	2	EPO
COP	Nkain2	BP	GO:0110053	regulation of actin filament organization	4/47	280/28564	0,00116	0,023279	0,0150204	Tmeff2/Arhgef10/Tmod2/Bin1	4	EPO
COP	Nkain2	BP	GO:0006688	glycosphingolipid biosynthetic process	2/47	31/28564	0,0012	0,023279	0,0150204	St6galnac3/Fa2h	2	EPO
COP	Nkain2	BP	GO:0071354	cellular response to interleukin-6	2/47	31/28564	0,0012	0,023279	0,0150204	St18/Ptprt	2	EPO
COP	Nkain2	BP	GO:0022011	myelination in peripheral nervous system	2/47	32/28564	0,00127	0,023279	0,0150204	Arhgef10/Fa2h	2	EPO
COP	Nkain2	BP	GO:0032292	peripheral nervous system axon ensheathment	2/47	32/28564	0,00127	0,023279	0,0150204	Arhgef10/Fa2h	2	EPO
COP	Nkain2	BP	GO:1902683	regulation of receptor localization to synapse	2/47	32/28564	0,00127	0,023279	0,0150204	Magi2/Rap1a	2	EPO
COP	Nkain2	BP	GO:1990806	ligand-gated ion channel signaling pathway	2/47	32/28564	0,00127	0,023279	0,0150204	Plp1/Gria2	2	EPO
COP	Nkain2	BP	GO:0048714	positive regulation of oligodendrocyte differentiation	2/47	33/28564	0,00135	0,023444	0,0151268	Aspa/Enpp2	2	EPO
COP	Nkain2	BP	GO:0070741	response to interleukin-6	2/47	33/28564	0,00135	0,023444	0,0151268	St18/Ptprt	2	EPO
COP	Nkain2	BP	GO:0045807	positive regulation of endocytosis	3/47	133/28564	0,00138	0,023444	0,0151268	Trf/Magi2/Bin1	3	EPO
COP	Nkain2	BP	GO:0099072	regulation of postsynaptic membrane neurotransmitter receptor levels	3/47	133/28564	0,00138	0,023444	0,0151268	Magi2/Rap1a/Erbin	3	EPO
COP	Nkain2	BP	GO:0014044	Schwann cell development	2/47	36/28564	0,00161	0,026949	0,0173885	Arhgef10/Fa2h	2	EPO

COP	Nkain2	BP	GO:0048710	regulation of astrocyte differentiation	2/47	37/28564	0,0017	0,027842	0,0179647	Mag/Bin1	2	EPO
COP	Nkain2	BP	GO:0030336	negative regulation of cell migration	4/47	312/28564	0,00172	0,027842	0,0179647	Tmeff2/Ptptrt/Ptprg /Magi2	4	EPO
COP	Nkain2	BP	GO:0086004	regulation of cardiac muscle cell contraction	2/47	39/28564	0,00189	0,030069	0,0194016	Pde4b/Bin1	2	EPO
COP	Nkain2	BP	GO:0038179	neurotrophin signaling pathway	2/47	41/28564	0,00209	0,031673	0,0204363	Magi2/Rap1a	2	EPO
COP	Nkain2	BP	GO:0099633	protein localization to postsynaptic specialization membrane	2/47	41/28564	0,00209	0,031673	0,0204363	Magi2/Rap1a	2	EPO
COP	Nkain2	BP	GO:0099645	neurotransmitter receptor localization to postsynaptic specialization membrane	2/47	41/28564	0,00209	0,031673	0,0204363	Magi2/Rap1a	2	EPO
COP	Nkain2	BP	GO:0014037	Schwann cell differentiation	2/47	43/28564	0,00229	0,03426	0,0221057	Arhgef10/Fa2h	2	EPO
COP	Nkain2	BP	GO:0070588	calcium ion transmembrane transport	4/47	339/28564	0,00233	0,03426	0,0221057	Slc24a2/Plp1/Pde4b /Bin1	4	EPO
COP	Nkain2	BP	GO:0051898	negative regulation of protein kinase B signaling	2/47	45/28564	0,00251	0,036399	0,023486	Phlpp1/Magi2	2	EPO
COP	Nkain2	BP	GO:0043087	regulation of GTPase activity	4/47	353/28564	0,00269	0,037941	0,0244805	Dock10/Arhgef10/R ap1a/Bin1	4	EPO
COP	Nkain2	BP	GO:0070371	ERK1 and ERK2 cascade	4/47	353/28564	0,00269	0,037941	0,0244805	Phlpp1/Trf/Pde8a/R ap1a	4	EPO
COP	Nkain2	BP	GO:1903115	regulation of actin filament-based movement	2/47	47/28564	0,00273	0,037986	0,0245099	Pde4b/Bin1	2	EPO
COP	Nkain2	BP	GO:0030517	negative regulation of axon extension	2/47	48/28564	0,00285	0,039039	0,0251891	Dip2b/Mag	2	EPO
COP	Nkain2	BP	GO:0050768	negative regulation of neurogenesis	3/47	173/28564	0,00291	0,039039	0,0251891	Mbp/Dip2b/Mag	3	EPO
COP	Nkain2	BP	GO:0032956	regulation of actin cytoskeleton organization	4/47	362/28564	0,00295	0,039039	0,0251891	Tmeff2/Arhgef10/T mod2/Bin1	4	EPO
COP	Nkain2	BP	GO:0007215	glutamate receptor signaling pathway	2/47	49/28564	0,00297	0,039039	0,0251891	Plp1/Gria2	2	EPO
COP	Nkain2	BP	GO:0051494	negative regulation of cytoskeleton organization	3/47	176/28564	0,00306	0,039685	0,0256061	Tubb4a/Tmeff2/Tm od2	3	EPO
COP	Nkain2	BP	GO:0051961	negative regulation of nervous system development	3/47	178/28564	0,00315	0,039917	0,0257557	Mbp/Dip2b/Mag	3	EPO
COP	Nkain2	BP	GO:1902904	negative regulation of supramolecular fiber organization	3/47	178/28564	0,00315	0,039917	0,0257557	Tubb4a/Tmeff2/Tm od2	3	EPO
COP	Nkain2	BP	GO:0045332	phospholipid translocation	2/47	52/28564	0,00333	0,041659	0,0268794	Atp8a1/Ano4	2	EPO
COP	Nkain2	BP	GO:0034204	lipid translocation	2/47	54/28564	0,00359	0,044148	0,0284856	Atp8a1/Ano4	2	EPO
COP	Nkain2	BP	GO:0050770	regulation of axonogenesis	3/47	187/28564	0,00362	0,044148	0,0284856	Mbp/Dip2b/Mag	3	EPO
COP	Nkain2	BP	GO:0048713	regulation of oligodendrocyte differentiation	2/47	57/28564	0,00399	0,048055	0,0310066	Aspa/Enpp2	2	EPO
COP	Nkain2	CC	GO:0044304	main axon	4/48	87/28585	1,4E-05	0,001314	0,0007743	Mbp/Tubb4a/Mag/ Bin1	4	EPO
COP	Nkain2	CC	GO:0033269	internode region of axon	2/48	4/28585	1,7E-05	0,001314	0,0007743	Mbp/Tubb4a	2	EPO
COP	Nkain2	CC	GO:0043209	myelin sheath	5/48	218/28585	3,2E-05	0,001712	0,0010089	Plp1/Mbp/Tubb4a/ Mag/Rap1a	5	EPO
COP	Nkain2	CC	GO:0043218	compact myelin	2/48	21/28585	0,00057	0,022583	0,0133062	Mbp/Mag	2	EPO

COP	Nkain2	CC	GO:0008021	synaptic vesicle	4/48	258/28585	0,00092	0,029367	0,0173036	Pde4b/Atp8a1/Gria2/Bin1	4	EPO
COP	Nkain2	CC	GO:0070382	exocytic vesicle	4/48	275/28585	0,00117	0,029647	0,0174686	Pde4b/Atp8a1/Gria2/Bin1	4	EPO
COP	Nkain2	CC	GO:0099572	postsynaptic specialization	5/48	486/28585	0,00131	0,029647	0,0174686	Pde4b/Ptprt/Magi2/Gria2/Erbin	5	EPO
COP	Nkain2	CC	GO:0030672	synaptic vesicle membrane	3/48	143/28585	0,0018	0,031769	0,0187184	Atp8a1/Gria2/Bin1	3	EPO
COP	Nkain2	CC	GO:0099501	exocytic vesicle membrane	3/48	143/28585	0,0018	0,031769	0,0187184	Atp8a1/Gria2/Bin1	3	EPO
COP	Nkain2	CC	GO:0030133	transport vesicle	4/48	368/28585	0,00336	0,046319	0,0272917	Pde4b/Atp8a1/Gria2/Bin1	4	EPO
COP	Nkain2	CC	GO:0030658	transport vesicle membrane	3/48	185/28585	0,00372	0,046319	0,0272917	Atp8a1/Gria2/Bin1	3	EPO
COP	Nkain2	CC	GO:0150034	distal axon	4/48	397/28585	0,0044	0,046319	0,0272917	Pcdh9/Gria2/Tmod2/Bin1	4	EPO
COP	Nkain2	CC	GO:0030017	sarcomere	3/48	200/28585	0,00463	0,046319	0,0272917	Pde4b/Tmod2/Bin1	3	EPO
COP	Nkain2	CC	GO:0098802	plasma membrane signaling receptor complex	3/48	201/28585	0,00469	0,046319	0,0272917	Plp1/Trf/Gria2	3	EPO
COP	Nkain2	CC	GO:0043197	dendritic spine	3/48	206/28585	0,00503	0,046319	0,0272917	Dock10/Pde4b/Gria2	3	EPO
COP	Nkain2	CC	GO:0044309	neuron spine	3/48	212/28585	0,00544	0,046319	0,0272917	Dock10/Pde4b/Gria2	3	EPO
COP	Nkain2	CC	GO:0030426	growth cone	3/48	213/28585	0,00551	0,046319	0,0272917	Pcdh9/Gria2/Tmod2	3	EPO
COP	Nkain2	CC	GO:0030427	site of polarized growth	3/48	221/28585	0,0061	0,046319	0,0272917	Pcdh9/Gria2/Tmod2	3	EPO
COP	Nkain2	CC	GO:0005905	clathrin-coated pit	2/48	71/28585	0,00637	0,046319	0,0272917	Fnbp1/Trf	2	EPO
COP	Nkain2	CC	GO:0030016	myofibril	3/48	225/28585	0,00641	0,046319	0,0272917	Pde4b/Tmod2/Bin1	3	EPO
COP	Nkain2	CC	GO:0014069	postsynaptic density	4/48	442/28585	0,00642	0,046319	0,0272917	Pde4b/Ptprt/Magi2/Gria2	4	EPO
COP	Nkain2	CC	GO:0032279	asymmetric synapse	4/48	462/28585	0,00748	0,047581	0,0280354	Pde4b/Ptprt/Magi2/Gria2	4	EPO
COP	Nkain2	CC	GO:0043292	contractile fiber	3/48	238/28585	0,00748	0,047581	0,0280354	Pde4b/Tmod2/Bin1	3	EPO
COP	Nkain2	CC	GO:0005770	late endosome	3/48	244/28585	0,00801	0,048971	0,0288542	Trf/Magi2/Rap1a	3	EPO
COP	Nkain2	MF	GO:0042578	phosphoric ester hydrolase activity	6/46	346/28171	2E-05	0,00407	0,0023776	Pde4b/Enpp2/Phlpp1/Ptprt/Ptprg/Pde8a	6	EPO
COP	Nkain2	MF	GO:0019911	structural constituent of myelin sheath	2/46	11/28171	0,00014	0,014213	0,0083031	Plp1/Mbp	2	EPO
COP	Nkain2	MF	GO:0004115	3',5'-cyclic-AMP phosphodiesterase activity	2/46	15/28171	0,00027	0,018014	0,0105237	Pde4b/Pde8a	2	EPO
COP	Nkain2	MF	GO:0008081	phosphoric diester hydrolase activity	3/46	86/28171	0,00038	0,018961	0,0110774	Pde4b/Enpp2/Pde8a	3	EPO
COP	Nkain2	MF	GO:0004114	3',5'-cyclic-nucleotide phosphodiesterase activity	2/46	24/28171	0,0007	0,027561	0,0161015	Pde4b/Pde8a	2	EPO

COP	Nkain2	MF	GO:0004112	cyclic-nucleotide phosphodiesterase activity	2/46	26/28171	0,00083	0,027561	0,0161015	Pde4b/Pde8a	2	EPO
COP	Pcdh9	CC	GO:0044291	cell-cell contact zone	4/44	90/28585	1,1E-05	0,001079	0,0005721	Pcdh9/Ank3/Opalin/Pak1	4	EPO
COP	Pcdh9	CC	GO:0030133	transport vesicle	6/44	368/28585	2E-05	0,001079	0,0005721	Pde4b/Syt12/Synpr/Bin1/Galnt15/Atp8a1	6	EPO
COP	Pcdh9	CC	GO:0030016	myofibril	5/44	225/28585	2,4E-05	0,001079	0,0005721	Pde4b/Ank3/Bin1/Ablim2/Pak1	5	EPO
COP	Pcdh9	CC	GO:0043292	contractile fiber	5/44	238/28585	3,2E-05	0,001079	0,0005721	Pde4b/Ank3/Bin1/Ablim2/Pak1	5	EPO
COP	Pcdh9	CC	GO:0030018	Z disc	4/44	131/28585	5E-05	0,001339	0,0007102	Pde4b/Ank3/Bin1/Pak1	4	EPO
COP	Pcdh9	CC	GO:0070382	exocytic vesicle	5/44	275/28585	6,3E-05	0,00142	0,000753	Pde4b/Syt12/Synpr/Bin1/Atp8a1	5	EPO
COP	Pcdh9	CC	GO:0031674	I band	4/44	145/28585	7,4E-05	0,00142	0,000753	Pde4b/Ank3/Bin1/Pak1	4	EPO
COP	Pcdh9	CC	GO:0001726	ruffle	4/44	154/28585	9,3E-05	0,001569	0,000832	Plekha1/Fscn3/Pak1/Acap2	4	EPO
COP	Pcdh9	CC	GO:0030017	sarcomere	4/44	200/28585	0,00025	0,003571	0,0018936	Pde4b/Ank3/Bin1/Pak1	4	EPO
COP	Pcdh9	CC	GO:0030426	growth cone	4/44	213/28585	0,00032	0,003571	0,0018936	Pcdh9/Unc5c/Fscn3/Pak1	4	EPO
COP	Pcdh9	CC	GO:0044304	main axon	3/44	87/28585	0,00033	0,003571	0,0018936	Ank3/Mbp/Bin1	3	EPO
COP	Pcdh9	CC	GO:0150034	distal axon	5/44	397/28585	0,00035	0,003571	0,0018936	Pcdh9/Unc5c/Bin1/Fscn3/Pak1	5	EPO
COP	Pcdh9	CC	GO:0043209	myelin sheath	4/44	218/28585	0,00035	0,003571	0,0018936	Mobp/Tspan2/Mbp/Plp1	4	EPO
COP	Pcdh9	CC	GO:0030427	site of polarized growth	4/44	221/28585	0,00037	0,003571	0,0018936	Pcdh9/Unc5c/Fscn3/Pak1	4	EPO
COP	Pcdh9	CC	GO:0031252	cell leading edge	5/44	412/28585	0,00042	0,003647	0,0019339	Plekha1/Unc5c/Fscn3/Pak1/Acap2	5	EPO
COP	Pcdh9	CC	GO:0033268	node of Ranvier	2/44	20/28585	0,00043	0,003647	0,0019339	Ank3/Bin1	2	EPO
COP	Pcdh9	CC	GO:0014069	postsynaptic density	5/44	442/28585	0,00057	0,004536	0,0024051	Pde4b/Erb4/Ank3/Pak1/Sh3gl3	5	EPO
COP	Pcdh9	CC	GO:0008021	synaptic vesicle	4/44	258/28585	0,00066	0,004955	0,0026272	Pde4b/Synpr/Bin1/Atp8a1	4	EPO
COP	Pcdh9	CC	GO:0032279	asymmetric synapse	5/44	462/28585	0,0007	0,004955	0,0026272	Pde4b/Erb4/Ank3/Pak1/Sh3gl3	5	EPO

COP	Pcdh9	CC	GO:0099572	postsynaptic specialization	5/44	486/28585	0,00088	0,005886	0,0031209	Pde4b/Erb4/Ank3/ Pak1/Sh3gl3	5	EPO
COP	Pcdh9	CC	GO:0043194	axon initial segment	2/44	29/28585	0,00092	0,005886	0,0031209	Ank3/Bin1	2	EPO
COP	Pcdh9	CC	GO:0098982	GABA-ergic synapse	3/44	134/28585	0,00116	0,007113	0,0037712	Erb4/Lpar1/Pak1	3	EPO
COP	Pcdh9	CC	GO:0030672	synaptic vesicle membrane	3/44	143/28585	0,0014	0,007859	0,004167	Synpr/Bin1/Atp8a1	3	EPO
COP	Pcdh9	CC	GO:0099501	exocytic vesicle membrane	3/44	143/28585	0,0014	0,007859	0,004167	Synpr/Bin1/Atp8a1	3	EPO
COP	Pcdh9	CC	GO:0045211	postsynaptic membrane	4/44	348/28585	0,002	0,010781	0,0057165	Erb4/Ank3/Lpar1/ Col13a1	4	EPO
COP	Pcdh9	CC	GO:0030027	lamellipodium	3/44	180/28585	0,00269	0,013968	0,0074061	Unc5c/Fscn3/Pak1	3	EPO
COP	Pcdh9	CC	GO:0030658	transport vesicle membrane	3/44	185/28585	0,00291	0,014532	0,0077051	Synpr/Bin1/Atp8a1	3	EPO
COP	Pcdh9	CC	GO:1990351	transporter complex	4/44	415/28585	0,00376	0,017687	0,0093778	Pde4b/Kcnmb3/Clic 4/Atp8a1	4	EPO
COP	Pcdh9	CC	GO:0098686	hippocampal mossy fiber to CA3 synapse	2/44	60/28585	0,00387	0,017687	0,0093778	Ptprd/Synpr	2	EPO
COP	Pcdh9	CC	GO:0043197	dendritic spine	3/44	206/28585	0,00393	0,017687	0,0093778	Pde4b/Dock10/Lpar 1	3	EPO
COP	Pcdh9	CC	GO:0044309	neuron spine	3/44	212/28585	0,00426	0,018545	0,0098326	Pde4b/Dock10/Lpar 1	3	EPO
COP	Pcdh9	CC	GO:0014704	intercalated disc	2/44	67/28585	0,0048	0,019078	0,0101152	Ank3/Pak1	2	EPO
COP	Pcdh9	CC	GO:0030315	T-tubule	2/44	70/28585	0,00523	0,020183	0,0107015	Ank3/Bin1	2	EPO
COP	Pcdh9	CC	GO:0098858	actin-based cell projection	3/44	232/28585	0,00547	0,020512	0,0108759	Unc5c/Fscn3/Clic4	3	EPO
COP	Pcdh9	CC	GO:0042734	presynaptic membrane	3/44	238/28585	0,00587	0,021417	0,0113554	Ptprd/Erb4/Lpar1	3	EPO
COP	Pcdh9	CC	GO:0015629	actin cytoskeleton	4/44	500/28585	0,00723	0,02501	0,0132606	Daam1/Fscn3/Ablim 2/Pak1	4	EPO
COP	Pcdh9	CC	GO:0030175	filopodium	2/44	100/28585	0,01042	0,034478	0,0182805	Unc5c/Fscn3	2	EPO
COP	Pcdh9	CC	GO:0034702	ion channel complex	3/44	301/28585	0,01113	0,034956	0,0185342	Pde4b/Kcnmb3/Clic 4	3	EPO
COP	Pcdh9	CC	GO:0005902	microvillus	2/44	106/28585	0,01164	0,035724	0,0189415	Fscn3/Clic4	2	EPO
COP	Pcdh9	CC	GO:0031594	neuromuscular junction	2/44	108/28585	0,01207	0,036197	0,0191921	Erb4/Ank3	2	EPO
COP	Pcdh9	CC	GO:0045178	basal part of cell	3/44	316/28585	0,01269	0,03723	0,0197398	Erb4/Ank3/Phldb1	3	EPO
COP	Pcdh9	CC	GO:0034399	nuclear periphery	2/44	134/28585	0,01815	0,049462	0,0262253	Rnf220/Clic4	2	EPO
COP	Pcdh9	MF	GO:0051020	GTPase binding	8/42	329/28171	2,7E-08	3,51E-06	1,817E-06	Sytl2/Bin1/Daam1/ Dock10/Pak1/Acap2 /Usp6nl/Rilp	8	EPO
COP	Pcdh9	MF	GO:0031267	small GTPase binding	7/42	290/28171	2,3E-07	1,49E-05	7,727E-06	Sytl2/Daam1/Dock1 0/Pak1/Acap2/Usp6 nl/Rilp	7	EPO
COP	Pcdh9	MF	GO:0019911	structural constituent of myelin sheath	3/42	11/28171	5E-07	2,22E-05	1,15E-05	Mobp/Mbp/Plp1	3	EPO
COP	Pcdh9	MF	GO:0043015	gamma-tubulin binding	2/42	35/28171	0,00125	0,038114	0,0197559	Pde4b/Pak1	2	EPO

COP	Pcdh9	MF	GO:0004721	phosphoprotein phosphatase activity	3/42	159/28171	0,00172	0,038114	0,0197559	Ptprd/Dusp28/Phlp p1	3	EPO
COP	Pcdh9	MF	GO:0042578	phosphoric ester hydrolase activity	4/42	346/28171	0,00173	0,038114	0,0197559	Ptprd/Pde4b/Dusp2 8/Phlpp1	4	EPO
COP	Pcdh9	MF	GO:0140303	intramembrane lipid transporter activity	2/42	46/28171	0,00215	0,040625	0,0210578	Ano4/Atp8a1	2	EPO
COP	Pcdh9	MF	GO:0005548	phospholipid transporter activity	2/42	60/28171	0,00364	0,048985	0,0253911	Ano4/Atp8a1	2	EPO
COP	Pcdh9	MF	GO:0003779	actin binding	4/42	447/28171	0,00435	0,048985	0,0253911	Bin1/Daam1/Fscn3/ Ablim2	4	EPO
COP	Pcdh9	MF	GO:0051015	actin filament binding	3/42	221/28171	0,00436	0,048985	0,0253911	Bin1/Fscn3/Ablim2	3	EPO
COP	Pcdh9	MF	GO:0017018	myosin phosphatase activity	2/42	72/28171	0,00519	0,048985	0,0253911	Dusp28/Phlpp1	2	EPO
COP	Pcdh9	MF	GO:0005543	phospholipid binding	4/42	480/28171	0,00559	0,048985	0,0253911	Syt12/Bin1/Lpar1/Ac ap2	4	EPO
COP	Pcdh9	MF	GO:0016791	phosphatase activity	3/42	259/28171	0,00677	0,048985	0,0253911	Ptprd/Dusp28/Phlp p1	3	EPO
COP	Pcdh9	MF	GO:0004722	protein serine/threonine phosphatase activity	2/42	86/28171	0,00733	0,048985	0,0253911	Dusp28/Phlpp1	2	EPO
COP	Pcdh9	MF	GO:0005254	chloride channel activity	2/42	86/28171	0,00733	0,048985	0,0253911	Ano4/Clic4	2	EPO
COP	Pcdh9	MF	GO:0004725	protein tyrosine phosphatase activity	2/42	91/28171	0,00817	0,048985	0,0253911	Ptprd/Dusp28	2	EPO
COP	Pcdh9	MF	GO:0005253	monoatomic anion channel activity	2/42	97/28171	0,00924	0,048985	0,0253911	Ano4/Clic4	2	EPO
COP	Plcl1	CC	GO:0014069	postsynaptic density	4/22	442/28585	0,00033	0,011051	0,0072853	Magi2/Rtn4/Myo6/ Pde4b	4	EPO
COP	Plcl1	CC	GO:0032279	asymmetric synapse	4/22	462/28585	0,00039	0,011051	0,0072853	Magi2/Rtn4/Myo6/ Pde4b	4	EPO
COP	Plcl1	CC	GO:0099572	postsynaptic specialization	4/22	486/28585	0,00047	0,011051	0,0072853	Magi2/Rtn4/Myo6/ Pde4b	4	EPO
COP	Plcl1	CC	GO:0043197	dendritic spine	3/22	206/28585	0,00051	0,011051	0,0072853	Dock10/Dip2a/Pde4 b	3	EPO
COP	Plcl1	CC	GO:0044309	neuron spine	3/22	212/28585	0,00056	0,011051	0,0072853	Dock10/Dip2a/Pde4 b	3	EPO
COP	Plcl1	CC	GO:0005635	nuclear envelope	3/22	440/28585	0,00449	0,044429	0,0292884	Phlpp1/Rtn4/Myo6	3	EPO
COP	Plcl1	CC	GO:0005923	bicellular tight junction	2/22	144/28585	0,00545	0,048838	0,0321952	Magi2/Cldn11	2	EPO
COP	Plcl1	CC	GO:0070160	tight junction	2/22	154/28585	0,00621	0,048838	0,0321952	Magi2/Cldn11	2	EPO
COP	Plcl1	CC	GO:0043296	apical junction complex	2/22	169/28585	0,00743	0,049017	0,0323129	Magi2/Cldn11	2	EPO
COP	Plcl1	MF	GO:0046332	SMAD binding	2/21	85/28171	0,00182	0,044679	0,024038	Magi2/Tcf12	2	EPO
COP	Plcl1	MF	GO:0008081	phosphoric diester hydrolase activity	2/21	86/28171	0,00186	0,044679	0,024038	Plcl1/Pde4b	2	EPO
COP	Plcl1	MF	GO:0042578	phosphoric ester hydrolase activity	3/21	346/28171	0,00207	0,044679	0,024038	Plcl1/Phlpp1/Pde4b	3	EPO
NFOL	Anln	CC	GO:0032045	guanyl-nucleotide exchange factor complex	2/23	19/28585	0,00011	0,008507	0,0054168	Dgki/Rasgrp3	2	Placebo
NFOL	Anln	CC	GO:0030864	cortical actin cytoskeleton	2/23	84/28585	0,00207	0,046853	0,0298351	Anln/Myo1e	2	Placebo
NFOL	Anln	CC	GO:0030863	cortical cytoskeleton	2/23	119/28585	0,00411	0,046853	0,0298351	Anln/Myo1e	2	Placebo
NFOL	Anln	CC	GO:0005912	adherens junction	2/23	153/28585	0,00669	0,046853	0,0298351	Ctnna3/Myo1e	2	Placebo

NFOL	AnIn	CC	GO:0019897	extrinsic component of plasma membrane	2/23	180/28585	0,00915	0,046853	0,0298351	Dgki/Trf	2	Placebo
NFOL	AnIn	CC	GO:0030135	coated vesicle	2/23	205/28585	0,01173	0,049996	0,0318366	Trf/Myo1e	2	Placebo
NFOL	AnIn	MF	GO:0003779	actin binding	3/23	447/28171	0,00555	0,044729	0,0180487	AnIn/Ctnna3/Myo1e	3	Placebo
NFOL	AnIn	MF	GO:0004497	monooxygenase activity	2/23	153/28171	0,00688	0,044729	0,0180487	Akr1c14/Agmo	2	Placebo
NFOL	AnIn	MF	GO:0005506	iron ion binding	2/23	170/28171	0,00843	0,044729	0,0180487	Trf/Agmo	2	Placebo
NFOL	AnIn	MF	GO:0051015	actin filament binding	2/23	221/28171	0,01391	0,049998	0,0201746	Ctnna3/Myo1e	2	Placebo
NFOL	AnIn	MF	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	2/23	230/28171	0,015	0,049998	0,0201746	Akr1c14/Agmo	2	Placebo
NFOL	Carmil1	BP	GO:0010765	positive regulation of sodium ion transport	2/15	43/28564	0,00023	0,040996	0,0220242	Cnksr3/Cntn1	2	EPO
NFOL	Carmil1	BP	GO:0043547	positive regulation of GTPase activity	3/15	259/28564	0,00031	0,040996	0,0220242	Sema4d/Abr/Dock6	3	EPO
NFOL	Carmil1	BP	GO:0043270	positive regulation of monoatomic ion transport	3/15	274/28564	0,00036	0,040996	0,0220242	Cnksr3/Cntn1/Alox5	3	EPO
NFOL	Carmil1	BP	GO:0008347	glial cell migration	2/15	71/28564	0,00063	0,040996	0,0220242	Rras2/Ptprb	2	EPO
NFOL	Carmil1	BP	GO:0043087	regulation of GTPase activity	3/15	353/28564	0,00076	0,040996	0,0220242	Sema4d/Abr/Dock6	3	EPO
NFOL	Carmil1	BP	GO:0001933	negative regulation of protein phosphorylation	3/15	354/28564	0,00077	0,040996	0,0220242	Cnksr3/Sema4d/Ptprb	3	EPO
NFOL	Carmil1	BP	GO:0042063	gliogenesis	3/15	378/28564	0,00093	0,040996	0,0220242	Rras2/Cntn1/Ptprb	3	EPO
NFOL	Carmil1	BP	GO:0042326	negative regulation of phosphorylation	3/15	405/28564	0,00113	0,040996	0,0220242	Cnksr3/Sema4d/Ptprb	3	EPO
NFOL	Carmil1	BP	GO:0002028	regulation of sodium ion transport	2/15	103/28564	0,00131	0,040996	0,0220242	Cnksr3/Cntn1	2	EPO
NFOL	Carmil1	BP	GO:0032102	negative regulation of response to external stimulus	3/15	429/28564	0,00134	0,040996	0,0220242	Sema4d/Abr/Alox5	3	EPO
NFOL	Carmil1	BP	GO:0031346	positive regulation of cell projection organization	3/15	459/28564	0,00162	0,040996	0,0220242	Carmil1/Sema4d/Cntn1	3	EPO
NFOL	Carmil1	BP	GO:0010563	negative regulation of phosphorus metabolic process	3/15	461/28564	0,00164	0,040996	0,0220242	Cnksr3/Sema4d/Ptprb	3	EPO
NFOL	Carmil1	BP	GO:0045936	negative regulation of phosphate metabolic process	3/15	461/28564	0,00164	0,040996	0,0220242	Cnksr3/Sema4d/Ptprb	3	EPO
NFOL	Carmil1	BP	GO:0051261	protein depolymerization	2/15	124/28564	0,00189	0,040996	0,0220242	Carmil1/Nckap5	2	EPO
NFOL	Carmil1	BP	GO:0032414	positive regulation of ion transmembrane transporter activity	2/15	132/28564	0,00214	0,040996	0,0220242	Cnksr3/Alox5	2	EPO
NFOL	Carmil1	BP	GO:0032411	positive regulation of transporter activity	2/15	140/28564	0,0024	0,040996	0,0220242	Cnksr3/Alox5	2	EPO
NFOL	Carmil1	BP	GO:0050728	negative regulation of inflammatory response	2/15	153/28564	0,00286	0,040996	0,0220242	Abr/Alox5	2	EPO
NFOL	Carmil1	BP	GO:0001935	endothelial cell proliferation	2/15	171/28564	0,00355	0,045084	0,0242208	Prok2/Alox5	2	EPO
NFOL	Cd180	BP	GO:0002757	immune response-activating signaling pathway	3/6	391/28564	4,9E-05	0,004826	0,0013264	Cd180/Fyb/C3ar1	3	EPO
NFOL	Cd180	BP	GO:0002764	immune response-regulating signaling pathway	3/6	402/28564	5,4E-05	0,004826	0,0013264	Cd180/Fyb/C3ar1	3	EPO
NFOL	Cd180	BP	GO:0002253	activation of immune response	3/6	482/28564	9,2E-05	0,005517	0,0015164	Cd180/Fyb/C3ar1	3	EPO

NFOL	Cd180	BP	GO:0007229	integrin-mediated signaling pathway	2/6	102/28564	0,00019	0,008444	0,0023208	Fyb/Fgr	2	EPO
NFOL	Cd180	BP	GO:0002429	immune response-activating cell surface receptor signaling pathway	2/6	272/28564	0,00132	0,027278	0,0074976	Fyb/C3ar1	2	EPO
NFOL	Cd180	BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	2/6	283/28564	0,00143	0,027278	0,0074976	Fyb/C3ar1	2	EPO
NFOL	Cd180	BP	GO:0002366	leukocyte activation involved in immune response	2/6	317/28564	0,00179	0,027278	0,0074976	Cd180/Fgr	2	EPO
NFOL	Cd180	BP	GO:0002263	cell activation involved in immune response	2/6	321/28564	0,00183	0,027278	0,0074976	Cd180/Fgr	2	EPO
NFOL	Cd180	BP	GO:0045088	regulation of innate immune response	2/6	385/28564	0,00262	0,027278	0,0074976	Cd180/Fgr	2	EPO
NFOL	Cd180	BP	GO:0002831	regulation of response to biotic stimulus	2/6	485/28564	0,00412	0,033305	0,0091541	Cd180/Fgr	2	EPO
NFOL	Gm44129	BP	GO:0090394	negative regulation of excitatory postsynaptic potential	2/8	14/28564	6,2E-06	0,002663	0,0010108	Plk2/Npy2r	2	Placebo
NFOL	Gm44129	BP	GO:0015850	organic hydroxy compound transport	3/8	306/28564	6,6E-05	0,009614	0,0036497	Ces1a/Npy2r/Xlr4a	3	Placebo
NFOL	Gm44129	BP	GO:0014046	dopamine secretion	2/8	45/28564	6,8E-05	0,009614	0,0036497	Npy2r/Xlr4a	2	Placebo
NFOL	Gm44129	BP	GO:0015872	dopamine transport	2/8	61/28564	0,00012	0,01135	0,0043091	Npy2r/Xlr4a	2	Placebo
NFOL	Gm44129	BP	GO:0098815	modulation of excitatory postsynaptic potential	2/8	63/28564	0,00013	0,01135	0,0043091	Plk2/Npy2r	2	Placebo
NFOL	Gm44129	BP	GO:0050432	catecholamine secretion	2/8	76/28564	0,00019	0,012123	0,0046023	Npy2r/Xlr4a	2	Placebo
NFOL	Gm44129	BP	GO:0050805	negative regulation of synaptic transmission	2/8	77/28564	0,0002	0,012123	0,0046023	Plk2/Npy2r	2	Placebo
NFOL	Gm44129	BP	GO:0051937	catecholamine transport	2/8	93/28564	0,00029	0,014352	0,0054486	Npy2r/Xlr4a	2	Placebo
NFOL	Gm44129	BP	GO:0060079	excitatory postsynaptic potential	2/8	95/28564	0,0003	0,014352	0,0054486	Plk2/Npy2r	2	Placebo
NFOL	Gm44129	BP	GO:0015844	monoamine transport	2/8	113/28564	0,00043	0,01749	0,0066398	Npy2r/Xlr4a	2	Placebo
NFOL	Gm44129	BP	GO:0099565	chemical synaptic transmission, postsynaptic	2/8	116/28564	0,00045	0,01749	0,0066398	Plk2/Npy2r	2	Placebo
NFOL	Gm44129	BP	GO:0060078	regulation of postsynaptic membrane potential	2/8	132/28564	0,00058	0,020736	0,007872	Plk2/Npy2r	2	Placebo
NFOL	Gm44129	BP	GO:0031644	regulation of nervous system process	2/8	204/28564	0,00138	0,042137	0,0159968	Plk2/Npy2r	2	Placebo
NFOL	Gm44129	MF	GO:0004674	protein serine/threonine kinase activity	2/7	442/28171	0,0049	0,009423	0,0005221	Plk2/Ankk1	2	Placebo
NFOL	Inpp5d	BP	GO:0032695	negative regulation of interleukin-12 production	2/9	19/28564	1,5E-05	0,008367	0,002582	Tlr2/Cmklr1	2	EPO
NFOL	Inpp5d	BP	GO:0002429	immune response-activating cell surface receptor signaling pathway	3/9	272/28564	6,9E-05	0,008497	0,0026222	Tlr2/Cmklr1/Themis2	3	EPO
NFOL	Inpp5d	BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	3/9	283/28564	7,7E-05	0,008497	0,0026222	Tlr2/Cmklr1/Themis2	3	EPO
NFOL	Inpp5d	BP	GO:0001818	negative regulation of cytokine production	3/9	296/28564	8,8E-05	0,008497	0,0026222	Inpp5d/Tlr2/Cmklr1	3	EPO
NFOL	Inpp5d	BP	GO:0045429	positive regulation of nitric oxide biosynthetic process	2/9	50/28564	0,00011	0,008497	0,0026222	Tlr2/Agxt2	2	EPO
NFOL	Inpp5d	BP	GO:1904407	positive regulation of nitric oxide metabolic process	2/9	52/28564	0,00012	0,008497	0,0026222	Tlr2/Agxt2	2	EPO
NFOL	Inpp5d	BP	GO:0046651	lymphocyte proliferation	3/9	354/28564	0,00015	0,008497	0,0026222	Inpp5d/Cd37/Zbtb32	3	EPO
NFOL	Inpp5d	BP	GO:0032943	mononuclear cell proliferation	3/9	360/28564	0,00016	0,008497	0,0026222	Inpp5d/Cd37/Zbtb32	3	EPO
NFOL	Inpp5d	BP	GO:0032655	regulation of interleukin-12 production	2/9	62/28564	0,00017	0,008497	0,0026222	Tlr2/Cmklr1	2	EPO
NFOL	Inpp5d	BP	GO:0032615	interleukin-12 production	2/9	64/28564	0,00018	0,008497	0,0026222	Tlr2/Cmklr1	2	EPO
NFOL	Inpp5d	BP	GO:0006081	cellular aldehyde metabolic process	2/9	65/28564	0,00018	0,008497	0,0026222	Cyp11b1/Agxt2	2	EPO

NFOL	Inpp5d	BP	GO:0002757	immune response-activating signaling pathway	3/9	391/28564	0,0002	0,008497	0,0026222	Tlr2/Cmk1r1/Themis2	3	EPO
NFOL	Inpp5d	BP	GO:0070661	leukocyte proliferation	3/9	396/28564	0,00021	0,008497	0,0026222	Inpp5d/Cd37/Zbtb32	3	EPO
NFOL	Inpp5d	BP	GO:0002764	immune response-regulating signaling pathway	3/9	402/28564	0,00022	0,008497	0,0026222	Tlr2/Cmk1r1/Themis2	3	EPO
NFOL	Inpp5d	BP	GO:0045428	regulation of nitric oxide biosynthetic process	2/9	73/28564	0,00023	0,008497	0,0026222	Tlr2/Agxt2	2	EPO
NFOL	Inpp5d	BP	GO:0080164	regulation of nitric oxide metabolic process	2/9	77/28564	0,00026	0,008864	0,0027353	Tlr2/Agxt2	2	EPO
NFOL	Inpp5d	BP	GO:0006809	nitric oxide biosynthetic process	2/9	86/28564	0,00032	0,010224	0,0031552	Tlr2/Agxt2	2	EPO
NFOL	Inpp5d	BP	GO:0046209	nitric oxide metabolic process	2/9	92/28564	0,00036	0,010224	0,0031552	Tlr2/Agxt2	2	EPO
NFOL	Inpp5d	BP	GO:0002253	activation of immune response	3/9	482/28564	0,00037	0,010224	0,0031552	Tlr2/Cmk1r1/Themis2	3	EPO
NFOL	Inpp5d	BP	GO:2001057	reactive nitrogen species metabolic process	2/9	94/28564	0,00038	0,010224	0,0031552	Tlr2/Agxt2	2	EPO
NFOL	Inpp5d	BP	GO:0050672	negative regulation of lymphocyte proliferation	2/9	96/28564	0,0004	0,010224	0,0031552	Inpp5d/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0032945	negative regulation of mononuclear cell proliferation	2/9	97/28564	0,0004	0,010224	0,0031552	Inpp5d/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0070664	negative regulation of leukocyte proliferation	2/9	104/28564	0,00046	0,011237	0,0034677	Inpp5d/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0002702	positive regulation of production of molecular mediator of immune response	2/9	143/28564	0,00088	0,014932	0,0046079	Tlr2/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0006690	icosanoid metabolic process	2/9	147/28564	0,00092	0,014932	0,0046079	Tlr2/Avpr1a	2	EPO
NFOL	Inpp5d	BP	GO:0050864	regulation of B cell activation	2/9	148/28564	0,00094	0,014932	0,0046079	Inpp5d/Themis2	2	EPO
NFOL	Inpp5d	BP	GO:0097530	granulocyte migration	2/9	162/28564	0,00112	0,014932	0,0046079	Tlr2/Cmk1r1	2	EPO
NFOL	Inpp5d	BP	GO:0002687	positive regulation of leukocyte migration	2/9	164/28564	0,00115	0,014932	0,0046079	Tlr2/Cmk1r1	2	EPO
NFOL	Inpp5d	BP	GO:0032675	regulation of interleukin-6 production	2/9	170/28564	0,00123	0,014932	0,0046079	Inpp5d/Tlr2	2	EPO
NFOL	Inpp5d	BP	GO:0051250	negative regulation of lymphocyte activation	2/9	172/28564	0,00126	0,014932	0,0046079	Inpp5d/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0019722	calcium-mediated signaling	2/9	179/28564	0,00137	0,015498	0,0047825	Avpr1a/Cmk1r1	2	EPO
NFOL	Inpp5d	BP	GO:0032635	interleukin-6 production	2/9	179/28564	0,00137	0,015498	0,0047825	Inpp5d/Tlr2	2	EPO
NFOL	Inpp5d	BP	GO:0002695	negative regulation of leukocyte activation	2/9	204/28564	0,00177	0,016942	0,0052281	Inpp5d/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0002700	regulation of production of molecular mediator of immune response	2/9	208/28564	0,00184	0,016942	0,0052281	Tlr2/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0007204	positive regulation of cytosolic calcium ion concentration	2/9	218/28564	0,00201	0,017504	0,0054016	Avpr1a/Cmk1r1	2	EPO
NFOL	Inpp5d	BP	GO:0050866	negative regulation of cell activation	2/9	227/28564	0,00218	0,017504	0,0054016	Inpp5d/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0002685	regulation of leukocyte migration	2/9	236/28564	0,00236	0,017723	0,0054692	Tlr2/Cmk1r1	2	EPO
NFOL	Inpp5d	BP	GO:0097529	myeloid leukocyte migration	2/9	242/28564	0,00247	0,017723	0,0054692	Tlr2/Cmk1r1	2	EPO
NFOL	Inpp5d	BP	GO:0042098	T cell proliferation	2/9	243/28564	0,00249	0,017723	0,0054692	Cd37/Zbtb32	2	EPO
NFOL	Inpp5d	BP	GO:0042180	cellular ketone metabolic process	2/9	244/28564	0,00251	0,017723	0,0054692	Avpr1a/Cyp11b1	2	EPO
NFOL	Inpp5d	BP	GO:0050670	regulation of lymphocyte proliferation	2/9	260/28564	0,00285	0,018205	0,0056179	Inpp5d/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0002274	myeloid leukocyte activation	2/9	264/28564	0,00294	0,018337	0,0056586	Tlr2/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0032944	regulation of mononuclear cell proliferation	2/9	264/28564	0,00294	0,018337	0,0056586	Inpp5d/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0002573	myeloid leukocyte differentiation	2/9	277/28564	0,00323	0,019053	0,0058796	Inpp5d/Tlr2	2	EPO

NFOL	Inpp5d	BP	GO:0070663	regulation of leukocyte proliferation	2/9	287/28564	0,00346	0,019053	0,0058796	Inpp5d/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0019932	second-messenger-mediated signaling	2/9	295/28564	0,00365	0,019257	0,0059426	Avpr1a/Cmk1r1	2	EPO
NFOL	Inpp5d	BP	GO:0046394	carboxylic acid biosynthetic process	2/9	310/28564	0,00402	0,020314	0,006269	Avpr1a/Agxt2	2	EPO
NFOL	Inpp5d	BP	GO:0016053	organic acid biosynthetic process	2/9	313/28564	0,0041	0,02033	0,0062739	Avpr1a/Agxt2	2	EPO
NFOL	Inpp5d	BP	GO:0042113	B cell activation	2/9	318/28564	0,00422	0,020573	0,0063486	Inpp5d/Themis2	2	EPO
NFOL	Inpp5d	BP	GO:0002699	positive regulation of immune effector process	2/9	327/28564	0,00446	0,020666	0,0063774	Tlr2/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0050900	leukocyte migration	2/9	386/28564	0,00616	0,023771	0,0073358	Tlr2/Cmk1r1	2	EPO
NFOL	Inpp5d	BP	GO:1903532	positive regulation of secretion by cell	2/9	389/28564	0,00625	0,023771	0,0073358	Tlr2/Avpr1a	2	EPO
NFOL	Inpp5d	BP	GO:0002440	production of molecular mediator of immune response	2/9	405/28564	0,00676	0,025054	0,0077314	Tlr2/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0051090	regulation of DNA-binding transcription factor activity	2/9	447/28564	0,00818	0,027395	0,008454	Tlr2/Cmk1r1	2	EPO
NFOL	Inpp5d	BP	GO:0051047	positive regulation of secretion	2/9	453/28564	0,00839	0,027722	0,008555	Tlr2/Avpr1a	2	EPO
NFOL	Inpp5d	BP	GO:0002697	regulation of immune effector process	2/9	472/28564	0,00908	0,028577	0,0088188	Tlr2/Cd37	2	EPO
NFOL	Inpp5d	BP	GO:0002443	leukocyte mediated immunity	2/9	480/28564	0,00938	0,028577	0,0088188	Inpp5d/Tlr2	2	EPO
NFOL	Inpp5d	BP	GO:0030099	myeloid cell differentiation	2/9	482/28564	0,00946	0,028577	0,0088188	Inpp5d/Tlr2	2	EPO
NFOL	Inpp5d	BP	GO:0002831	regulation of response to biotic stimulus	2/9	485/28564	0,00957	0,028614	0,0088301	Tlr2/Cd37	2	EPO
NFOL	Inpp5d	MF	GO:0017046	peptide hormone binding	2/8	51/28171	8,9E-05	0,002785	0,0005278	Avpr1a/Cmk1r1	2	EPO
NFOL	Inpp5d	MF	GO:0042277	peptide binding	3/8	361/28171	0,00011	0,002785	0,0005278	Tlr2/Avpr1a/Cmk1r1	3	EPO
NFOL	Inpp5d	MF	GO:0033218	amide binding	3/8	450/28171	0,00021	0,00326	0,0006177	Tlr2/Avpr1a/Cmk1r1	3	EPO
NFOL	Inpp5d	MF	GO:0042562	hormone binding	2/8	87/28171	0,00026	0,00326	0,0006177	Avpr1a/Cmk1r1	2	EPO
NFOL	Kif20b	BP	GO:0032954	regulation of cytokinetic process	2/15	3/28564	7,7E-07	0,000306	0,0001617	Kif20b/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0006979	response to oxidative stress	4/15	408/28564	4,9E-05	0,009811	0,0051765	Pjvk/Melk/Ect2/Slc4a1	4	Placebo
NFOL	Kif20b	BP	GO:0051302	regulation of cell division	3/15	182/28564	0,00011	0,010696	0,0056438	Kif20b/Ect2/Aspm	3	Placebo
NFOL	Kif20b	BP	GO:0000302	response to reactive oxygen species	3/15	191/28564	0,00013	0,010696	0,0056438	Pjvk/Ect2/Slc4a1	3	Placebo
NFOL	Kif20b	BP	GO:0061351	neural precursor cell proliferation	3/15	212/28564	0,00017	0,010696	0,0056438	Shcbp1/Melk/Aspm	3	Placebo
NFOL	Kif20b	BP	GO:0032506	cytokinetic process	2/15	38/28564	0,00018	0,010696	0,0056438	Kif20b/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0032467	positive regulation of cytokinesis	2/15	39/28564	0,00019	0,010696	0,0056438	Kif20b/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0034599	cellular response to oxidative stress	3/15	276/28564	0,00037	0,018488	0,0097551	Pjvk/Melk/Ect2	3	Placebo
NFOL	Kif20b	BP	GO:0098813	nuclear chromosome segregation	3/15	338/28564	0,00067	0,02657	0,0140193	Ect2/Ankle1/Aspm	3	Placebo
NFOL	Kif20b	BP	GO:0062197	cellular response to chemical stress	3/15	347/28564	0,00073	0,02657	0,0140193	Pjvk/Melk/Ect2	3	Placebo
NFOL	Kif20b	BP	GO:0000281	mitotic cytokinesis	2/15	77/28564	0,00074	0,02657	0,0140193	Kif20b/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0051781	positive regulation of cell division	2/15	84/28564	0,00088	0,028657	0,0151207	Kif20b/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0032465	regulation of cytokinesis	2/15	87/28564	0,00094	0,028657	0,0151207	Kif20b/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0036473	cell death in response to oxidative stress	2/15	101/28564	0,00126	0,030863	0,0162847	Pjvk/Melk	2	Placebo
NFOL	Kif20b	BP	GO:0061640	cytoskeleton-dependent cytokinesis	2/15	104/28564	0,00134	0,030863	0,0162847	Kif20b/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0007059	chromosome segregation	3/15	429/28564	0,00134	0,030863	0,0162847	Ect2/Ankle1/Aspm	3	Placebo
NFOL	Kif20b	BP	GO:0006821	chloride transport	2/15	108/28564	0,00144	0,030863	0,0162847	Gabrq/Slc4a1	2	Placebo

NFOL	Kif20b	BP	GO:0000280	nuclear division	3/15	456/28564	0,00159	0,030863	0,0162847	Kif20b/Ankle1/Aspm	3	Placebo
NFOL	Kif20b	BP	GO:0045132	meiotic chromosome segregation	2/15	116/28564	0,00166	0,030863	0,0162847	Ankle1/Aspm	2	Placebo
NFOL	Kif20b	BP	GO:0042542	response to hydrogen peroxide	2/15	120/28564	0,00177	0,030863	0,0162847	Ect2/Slc4a1	2	Placebo
NFOL	Kif20b	BP	GO:2000177	regulation of neural precursor cell proliferation	2/15	126/28564	0,00195	0,030863	0,0162847	Shcbp1/Aspm	2	Placebo
NFOL	Kif20b	BP	GO:0090316	positive regulation of intracellular protein transport	2/15	145/28564	0,00257	0,032034	0,0169027	Kif20b/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0034614	cellular response to reactive oxygen species	2/15	146/28564	0,00261	0,032034	0,0169027	Pjvk/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0015698	inorganic anion transport	2/15	150/28564	0,00275	0,032034	0,0169027	Gabrq/Slc4a1	2	Placebo
NFOL	Kif20b	BP	GO:0006820	monoatomic anion transport	2/15	159/28564	0,00308	0,032034	0,0169027	Gabrq/Slc4a1	2	Placebo
NFOL	Kif20b	BP	GO:0000910	cytokinesis	2/15	176/28564	0,00376	0,034716	0,0183176	Kif20b/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0032388	positive regulation of intracellular transport	2/15	187/28564	0,00423	0,038186	0,0201485	Kif20b/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0042129	regulation of T cell proliferation	2/15	201/28564	0,00487	0,041142	0,0217084	Pla2g2d/Slc4a1	2	Placebo
NFOL	Kif20b	BP	GO:0001764	neuron migration	2/15	204/28564	0,00501	0,041283	0,0217827	Kif20b/Aspm	2	Placebo
NFOL	Kif20b	BP	GO:0140013	meiotic nuclear division	2/15	210/28564	0,0053	0,041283	0,0217827	Ankle1/Aspm	2	Placebo
NFOL	Kif20b	BP	GO:0033157	regulation of intracellular protein transport	2/15	227/28564	0,00617	0,043772	0,023096	Kif20b/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:1903046	meiotic cell cycle process	2/15	229/28564	0,00627	0,043772	0,023096	Ankle1/Aspm	2	Placebo
NFOL	Kif20b	BP	GO:0042098	T cell proliferation	2/15	243/28564	0,00704	0,047715	0,0251763	Pla2g2d/Slc4a1	2	Placebo
NFOL	Kif20b	BP	GO:0045664	regulation of neuron differentiation	2/15	244/28564	0,00709	0,047715	0,0251763	Ect2/Aspm	2	Placebo
NFOL	Kif20b	BP	GO:0043547	positive regulation of GTPase activity	2/15	259/28564	0,00796	0,049603	0,0261728	Arap3/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0050670	regulation of lymphocyte proliferation	2/15	260/28564	0,00801	0,049603	0,0261728	Pla2g2d/Slc4a1	2	Placebo
NFOL	Kif20b	BP	GO:0090068	positive regulation of cell cycle process	2/15	262/28564	0,00813	0,049603	0,0261728	Kif20b/Ect2	2	Placebo
NFOL	Kif20b	BP	GO:0032944	regulation of mononuclear cell proliferation	2/15	264/28564	0,00825	0,049603	0,0261728	Pla2g2d/Slc4a1	2	Placebo
NFOL	Kif20b	CC	GO:0005938	cell cortex	4/17	300/28585	2,5E-05	0,001525	0,0007757	Pjvk/Melk/Ect2/Slc4a1	4	Placebo
NFOL	Kif20b	CC	GO:0072686	mitotic spindle	3/17	177/28585	0,00015	0,003653	0,0018583	Kif20b/Ect2/Aspm	3	Placebo
NFOL	Kif20b	CC	GO:0030496	midbody	3/17	201/28585	0,00022	0,003653	0,0018583	Kif20b/Ect2/Aspm	3	Placebo
NFOL	Kif20b	CC	GO:0097431	mitotic spindle pole	2/17	39/28585	0,00024	0,003653	0,0018583	Kif20b/Aspm	2	Placebo
NFOL	Kif20b	CC	GO:0005819	spindle	3/17	357/28585	0,00115	0,01384	0,0070416	Kif20b/Ect2/Aspm	3	Placebo
NFOL	Kif20b	CC	GO:0005874	microtubule	3/17	441/28585	0,00211	0,016827	0,0085611	Kif20b/Aspm/Gtse1	3	Placebo
NFOL	Kif20b	CC	GO:0030863	cortical cytoskeleton	2/17	119/28585	0,00224	0,016827	0,0085611	Pjvk/Slc4a1	2	Placebo
NFOL	Kif20b	CC	GO:0000922	spindle pole	2/17	144/28585	0,00326	0,019436	0,0098886	Kif20b/Aspm	2	Placebo
NFOL	Kif20b	MF	GO:0005096	GTPase activator activity	3/17	241/28171	0,00038	0,026935	0,0157966	Arap3/Ect2/Depdc1a	3	Placebo
NFOL	Kif20b	MF	GO:0030695	GTPase regulator activity	3/17	432/28171	0,00208	0,031637	0,0185538	Arap3/Ect2/Depdc1a	3	Placebo
NFOL	Kif20b	MF	GO:0060589	nucleoside-triphosphatase regulator activity	3/17	432/28171	0,00208	0,031637	0,0185538	Arap3/Ect2/Depdc1a	3	Placebo
NFOL	Kif20b	MF	GO:0015108	chloride transmembrane transporter activity	2/17	120/28171	0,00235	0,031637	0,0185538	Gabrq/Slc4a1	2	Placebo
NFOL	Kif20b	MF	GO:0008509	monoatomic anion transmembrane transporter activity	2/17	140/28171	0,00318	0,031637	0,0185538	Gabrq/Slc4a1	2	Placebo

NFOL	Kif20b	MF	GO:0015103	inorganic anion transmembrane transporter activity	2/17	142/28171	0,00327	0,031637	0,0185538	Gabrq/Slc4a1	2	Placebo
NFOL	Mis18bp1	BP	GO:0090306	meiotic spindle assembly	2/16	10/28564	1,3E-05	0,002984	0,0017928	Ccnb2/Aspm	2	EPO
NFOL	Mis18bp1	BP	GO:0045132	meiotic chromosome segregation	3/16	116/28564	3,5E-05	0,003768	0,0022642	Ccnb2/Ankle1/Aspm	3	EPO
NFOL	Mis18bp1	BP	GO:0000212	meiotic spindle organization	2/16	19/28564	5E-05	0,003768	0,0022642	Ccnb2/Aspm	2	EPO
NFOL	Mis18bp1	BP	GO:0007059	chromosome segregation	4/16	429/28564	7,9E-05	0,004471	0,0026865	Ska1/Ccnb2/Ankle1/Aspm	4	EPO
NFOL	Mis18bp1	BP	GO:0000280	nuclear division	4/16	456/28564	0,0001	0,004528	0,0027208	Ccnb2/Ankle1/Kif20b/Aspm	4	EPO
NFOL	Mis18bp1	BP	GO:0140013	meiotic nuclear division	3/16	210/28564	0,0002	0,006786	0,0040773	Ccnb2/Ankle1/Aspm	3	EPO
NFOL	Mis18bp1	BP	GO:0061351	neural precursor cell proliferation	3/16	212/28564	0,00021	0,006786	0,0040773	Shcbp1/Melk/Aspm	3	EPO
NFOL	Mis18bp1	BP	GO:1903046	meiotic cell cycle process	3/16	229/28564	0,00026	0,007448	0,0044753	Ccnb2/Ankle1/Aspm	3	EPO
NFOL	Mis18bp1	BP	GO:0098813	nuclear chromosome segregation	3/16	338/28564	0,00082	0,018697	0,0112338	Ccnb2/Ankle1/Aspm	3	EPO
NFOL	Mis18bp1	BP	GO:0051321	meiotic cell cycle	3/16	339/28564	0,00083	0,018697	0,0112338	Ccnb2/Ankle1/Aspm	3	EPO
NFOL	Mis18bp1	BP	GO:0051225	spindle assembly	2/16	123/28564	0,00212	0,03011	0,018091	Ccnb2/Aspm	2	EPO
NFOL	Mis18bp1	BP	GO:2000177	regulation of neural precursor cell proliferation	2/16	126/28564	0,00222	0,03011	0,018091	Shcbp1/Aspm	2	EPO
NFOL	Mis18bp1	BP	GO:0007127	meiosis I	2/16	133/28564	0,00247	0,03011	0,018091	Ccnb2/Ankle1	2	EPO
NFOL	Mis18bp1	BP	GO:0061982	meiosis I cell cycle process	2/16	136/28564	0,00258	0,03011	0,018091	Ccnb2/Ankle1	2	EPO
NFOL	Mis18bp1	BP	GO:0007292	female gamete generation	2/16	174/28564	0,00419	0,033785	0,0202992	Ccnb2/Aspm	2	EPO
NFOL	Mis18bp1	BP	GO:0051302	regulation of cell division	2/16	182/28564	0,00457	0,035604	0,0213925	Kif20b/Aspm	2	EPO
NFOL	Mis18bp1	BP	GO:0007051	spindle organization	2/16	189/28564	0,00492	0,036676	0,0220361	Ccnb2/Aspm	2	EPO
NFOL	Mis18bp1	BP	GO:0001764	neuron migration	2/16	204/28564	0,0057	0,039053	0,0234643	Kif20b/Aspm	2	EPO
NFOL	Mis18bp1	CC	GO:0005819	spindle	4/17	357/28585	5E-05	0,001652	0,0006851	Ska1/Hmmr/Kif20b/Aspm	4	EPO
NFOL	Mis18bp1	CC	GO:0072686	mitotic spindle	3/17	177/28585	0,00015	0,002457	0,0010188	Ska1/Kif20b/Aspm	3	EPO
NFOL	Mis18bp1	CC	GO:0097431	mitotic spindle pole	2/17	39/28585	0,00024	0,002679	0,0011107	Kif20b/Aspm	2	EPO
NFOL	Mis18bp1	CC	GO:0045171	intercellular bridge	2/17	98/28585	0,00153	0,012623	0,0052343	Ska1/Kif20b	2	EPO
NFOL	Mis18bp1	CC	GO:0005874	microtubule	3/17	441/28585	0,00211	0,013935	0,0057784	Ska1/Kif20b/Aspm	3	EPO
NFOL	Mis18bp1	CC	GO:0000922	spindle pole	2/17	144/28585	0,00326	0,016798	0,0069659	Kif20b/Aspm	2	EPO
NFOL	Mis18bp1	CC	GO:0030496	midbody	2/17	201/28585	0,00624	0,02562	0,0106241	Kif20b/Aspm	2	EPO
NFOL	Mis18bp1	CC	GO:0000775	chromosome, centromeric region	2/17	258/28585	0,01009	0,02562	0,0106241	Mis18bp1/Ska1	2	EPO
NFOL	Mis18bp1	CC	GO:0098687	chromosomal region	2/17	367/28585	0,01969	0,04536	0,0188096	Mis18bp1/Ska1	2	EPO
NFOL	Nxn	BP	GO:0072337	modified amino acid transport	2/15	46/28564	0,00026	0,046746	0,0244325	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	BP	GO:0089718	amino acid import across plasma membrane	2/15	55/28564	0,00038	0,046746	0,0244325	Slc6a13/Slc6a20a	2	Placebo

NFOL	Nxn	BP	GO:0046942	carboxylic acid transport	3/15	367/28564	0,00085	0,046746	0,0244325	Slc22a6/Slc6a13/Slc6a20a	3	Placebo
NFOL	Nxn	BP	GO:0015849	organic acid transport	3/15	369/28564	0,00087	0,046746	0,0244325	Slc22a6/Slc6a13/Slc6a20a	3	Placebo
NFOL	Nxn	BP	GO:0003333	amino acid transmembrane transport	2/15	99/28564	0,00121	0,046746	0,0244325	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	BP	GO:0015711	organic anion transport	3/15	437/28564	0,00141	0,046746	0,0244325	Slc22a6/Slc6a13/Slc6a20a	3	Placebo
NFOL	Nxn	BP	GO:1905039	carboxylic acid transmembrane transport	2/15	143/28564	0,0025	0,046746	0,0244325	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	BP	GO:1903825	organic acid transmembrane transport	2/15	144/28564	0,00254	0,046746	0,0244325	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	BP	GO:0035725	sodium ion transmembrane transport	2/15	166/28564	0,00335	0,046746	0,0244325	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	BP	GO:0006865	amino acid transport	2/15	167/28564	0,00339	0,046746	0,0244325	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	BP	GO:0120254	olefinic compound metabolic process	2/15	169/28564	0,00347	0,046746	0,0244325	Sphk1/Aldh1a2	2	Placebo
NFOL	Nxn	MF	GO:0005283	amino acid:sodium symporter activity	2/15	23/28171	6,7E-05	0,004402	0,0013306	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	MF	GO:0005416	amino acid:monoatomic cation symporter activity	2/15	28/28171	9,9E-05	0,004402	0,0013306	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	MF	GO:0072349	modified amino acid transmembrane transporter activity	2/15	35/28171	0,00016	0,004402	0,0013306	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	MF	GO:0005343	organic acid:sodium symporter activity	2/15	37/28171	0,00017	0,004402	0,0013306	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	MF	GO:0008514	organic anion transmembrane transporter activity	3/15	238/28171	0,00025	0,005077	0,0015344	Slc22a6/Slc6a13/Slc6a20a	3	Placebo
NFOL	Nxn	MF	GO:0015291	secondary active transmembrane transporter activity	3/15	262/28171	0,00033	0,005607	0,0016948	Slc22a6/Slc6a13/Slc6a20a	3	Placebo
NFOL	Nxn	MF	GO:0015370	solute:sodium symporter activity	2/15	79/28171	0,0008	0,011488	0,0034723	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	MF	GO:0015171	amino acid transmembrane transporter activity	2/15	88/28171	0,00099	0,012455	0,0037644	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	MF	GO:0022804	active transmembrane transporter activity	3/15	414/28171	0,00126	0,014108	0,0042639	Slc22a6/Slc6a13/Slc6a20a	3	Placebo
NFOL	Nxn	MF	GO:0015294	solute:monoatomic cation symporter activity	2/15	108/28171	0,00148	0,014457	0,0043696	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	MF	GO:0015103	inorganic anion transmembrane transporter activity	2/15	142/28171	0,00254	0,014457	0,0043696	Slc22a6/Slc6a13	2	Placebo
NFOL	Nxn	MF	GO:0015293	symporter activity	2/15	146/28171	0,00268	0,014457	0,0043696	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	MF	GO:0015081	sodium ion transmembrane transporter activity	2/15	158/28171	0,00313	0,014457	0,0043696	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	MF	GO:0046943	carboxylic acid transmembrane transporter activity	2/15	171/28171	0,00365	0,014457	0,0043696	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	MF	GO:0005342	organic acid transmembrane transporter activity	2/15	172/28171	0,00369	0,014457	0,0043696	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	MF	GO:0022853	active monoatomic ion transmembrane transporter activity	2/15	225/28171	0,00623	0,018929	0,0057211	Slc6a13/Slc6a20a	2	Placebo
NFOL	Nxn	MF	GO:0046873	metal ion transmembrane transporter activity	2/15	430/28171	0,0214	0,037264	0,0112627	Slc6a13/Slc6a20a	2	Placebo
NFOL	Ogfr	BP	GO:0048771	tissue remodeling	2/9	212/28564	0,00191	0,033302	0,0123473	Tbx1/Fcgr4	2	Placebo
NFOL	Pik3r3	BP	GO:0043491	protein kinase B signaling	6/41	209/28564	5,2E-07	0,000598	0,00038	Pik3r3/Tcf7l2/Sema5a/Rictor/Sirt2/Ptprj	6	EPO

NFOL	Pik3r3	BP	GO:0061387	regulation of extent of cell growth	5/41	129/28564	1,1E-06	0,000659	0,0004187	Map1b/Sema4d/Sema4a/Sema5a/Rnd2	5	EPO
NFOL	Pik3r3	BP	GO:0048588	developmental cell growth	6/41	287/28564	3,3E-06	0,000918	0,000583	Tmem108/Map1b/Sema4d/Sema4a/Sema5a/Rnd2	6	EPO
NFOL	Pik3r3	BP	GO:0060560	developmental growth involved in morphogenesis	6/41	290/28564	3,5E-06	0,000918	0,000583	Tmem108/Map1b/Sema4d/Sema4a/Sema5a/Rnd2	6	EPO
NFOL	Pik3r3	BP	GO:0001558	regulation of cell growth	7/41	464/28564	4E-06	0,000918	0,000583	Map1b/Sema4d/Sema4a/Sema5a/Rictor/Rnd2/Ptprj	7	EPO
NFOL	Pik3r3	BP	GO:0050767	regulation of neurogenesis	7/41	480/28564	5E-06	0,000955	0,0006066	Map1b/Sema4d/Sema4a/Sema5a/Rassf10/Rnd2/Sirt2	7	EPO
NFOL	Pik3r3	BP	GO:0050770	regulation of axonogenesis	5/41	187/28564	7,1E-06	0,00113	0,0007178	Map1b/Sema4d/Sema4a/Sema5a/Rnd2	5	EPO
NFOL	Pik3r3	BP	GO:0048843	negative regulation of axon extension involved in axon guidance	3/41	27/28564	7,8E-06	0,00113	0,0007178	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:1905702	regulation of inhibitory synapse assembly	2/41	4/28564	1,2E-05	0,00122	0,0007754	Sema4d/Sema4a	2	EPO
NFOL	Pik3r3	BP	GO:1990138	neuron projection extension	5/41	209/28564	1,2E-05	0,00122	0,0007754	Tmem108/Map1b/Sema4d/Sema4a/Sema5a	5	EPO
NFOL	Pik3r3	BP	GO:0030307	positive regulation of cell growth	5/41	210/28564	1,2E-05	0,00122	0,0007754	Map1b/Sema4d/Sema5a/Rictor/Rnd2	5	EPO
NFOL	Pik3r3	BP	GO:0050772	positive regulation of axonogenesis	4/41	102/28564	1,4E-05	0,00122	0,0007754	Map1b/Sema4d/Sema5a/Rnd2	4	EPO
NFOL	Pik3r3	BP	GO:0048841	regulation of axon extension involved in axon guidance	3/41	33/28564	1,5E-05	0,00122	0,0007754	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0008361	regulation of cell size	5/41	218/28564	1,5E-05	0,00122	0,0007754	Map1b/Sema4d/Sema4a/Sema5a/Rnd2	5	EPO
NFOL	Pik3r3	BP	GO:0051962	positive regulation of nervous system development	6/41	379/28564	1,6E-05	0,001225	0,0007781	Map1b/Sema4d/Sema4a/Sema5a/Rassf10/Rnd2	6	EPO
NFOL	Pik3r3	BP	GO:0048846	axon extension involved in axon guidance	3/41	37/28564	2,1E-05	0,001291	0,0008204	Sema4d/Sema4a/Sema5a	3	EPO

NFOL	Pik3r3	BP	GO:1902284	neuron projection extension involved in neuron projection guidance	3/41	37/28564	2,1E-05	0,001291	0,0008204	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0030516	regulation of axon extension	4/41	114/28564	2,2E-05	0,001291	0,0008204	Map1b/Sema4d/Sema4a/Sema5a	4	EPO
NFOL	Pik3r3	BP	GO:0032535	regulation of cellular component size	6/41	404/28564	2,3E-05	0,001291	0,0008204	Map1b/Sema4d/Sema4a/Sema5a/Rictor/Rnd2	6	EPO
NFOL	Pik3r3	BP	GO:0048638	regulation of developmental growth	6/41	405/28564	2,3E-05	0,001291	0,0008204	Tcf7l2/Map1b/Sema4d/Sema4a/Sema5a/Rnd2	6	EPO
NFOL	Pik3r3	BP	GO:0032984	protein-containing complex disassembly	5/41	240/28564	2,4E-05	0,001291	0,0008204	Kif19a/Map1b/Uvrag/Sema5a/Mical3	5	EPO
NFOL	Pik3r3	BP	GO:0051897	positive regulation of protein kinase B signaling	4/41	120/28564	2,7E-05	0,001364	0,0008665	Tcf7l2/Sema5a/Rictor/Ptprj	4	EPO
NFOL	Pik3r3	BP	GO:0048762	mesenchymal cell differentiation	5/41	249/28564	2,8E-05	0,001364	0,0008665	Tcf7l2/Sema4d/Sema4a/Pdcd4/Sema5a	5	EPO
NFOL	Pik3r3	BP	GO:0048709	oligodendrocyte differentiation	4/41	122/28564	2,8E-05	0,001364	0,0008665	Tcf7l2/Dusp15/Sirt2/Ptprj	4	EPO
NFOL	Pik3r3	BP	GO:0051261	protein depolymerization	4/41	124/28564	3E-05	0,001395	0,0008866	Kif19a/Map1b/Sema5a/Mical3	4	EPO
NFOL	Pik3r3	BP	GO:0048640	negative regulation of developmental growth	4/41	129/28564	3,5E-05	0,001566	0,0009953	Tcf7l2/Sema4d/Sema4a/Sema5a	4	EPO
NFOL	Pik3r3	BP	GO:0045926	negative regulation of growth	5/41	267/28564	3,9E-05	0,001671	0,0010615	Tcf7l2/Sema4d/Sema4a/Sema5a/Ptprj	5	EPO
NFOL	Pik3r3	BP	GO:0030517	negative regulation of axon extension	3/41	48/28564	4,5E-05	0,001869	0,0011876	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0071526	semaphorin-plexin signaling pathway	3/41	50/28564	5,1E-05	0,002041	0,0012968	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0048675	axon extension	4/41	144/28564	5,4E-05	0,002086	0,0013252	Map1b/Sema4d/Sema4a/Sema5a	4	EPO
NFOL	Pik3r3	BP	GO:0007409	axonogenesis	6/41	498/28564	7,3E-05	0,002716	0,0017256	Nfasc/Map1b/Sema4d/Sema4a/Sema5a/Rnd2	6	EPO
NFOL	Pik3r3	BP	GO:0048713	regulation of oligodendrocyte differentiation	3/41	57/28564	7,6E-05	0,002719	0,0017275	Tcf7l2/Dusp15/Sirt2	3	EPO

NFOL	Pik3r3	BP	GO:0060485	mesenchyme development	5/41	310/28564	7,9E-05	0,002719	0,0017275	Tcf7l2/Sema4d/Sema4a/Pdcd4/Sema5a	5	EPO
NFOL	Pik3r3	BP	GO:0050922	negative regulation of chemotaxis	3/41	58/28564	8E-05	0,002719	0,0017275	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0050769	positive regulation of neurogenesis	5/41	318/28564	8,9E-05	0,002945	0,0018714	Map1b/Sema4d/Sema5a/Rassf10/Rnd2	5	EPO
NFOL	Pik3r3	BP	GO:0045927	positive regulation of growth	5/41	323/28564	9,6E-05	0,003081	0,0019576	Map1b/Sema4d/Sema5a/Rictor/Rnd2	5	EPO
NFOL	Pik3r3	BP	GO:0001755	neural crest cell migration	3/41	63/28564	0,0001	0,003199	0,0020329	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0050768	negative regulation of neurogenesis	4/41	173/28564	0,00011	0,003332	0,0021171	Sema4d/Sema4a/Sema5a/Sirt2	4	EPO
NFOL	Pik3r3	BP	GO:0090497	mesenchymal cell migration	3/41	65/28564	0,00011	0,003332	0,0021171	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0051896	regulation of protein kinase B signaling	4/41	176/28564	0,00012	0,003403	0,0021623	Tcf7l2/Sema5a/Rictor/Ptprj	4	EPO
NFOL	Pik3r3	BP	GO:0051961	negative regulation of nervous system development	4/41	178/28564	0,00012	0,003468	0,0022033	Sema4d/Sema4a/Sema5a/Sirt2	4	EPO
NFOL	Pik3r3	BP	GO:0050771	negative regulation of axonogenesis	3/41	70/28564	0,00014	0,003858	0,0024515	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0043087	regulation of GTPase activity	5/41	353/28564	0,00015	0,003907	0,0024825	Tns3/Dock6/Sema4d/Rictor/Abr	5	EPO
NFOL	Pik3r3	BP	GO:0048672	positive regulation of collateral sprouting	2/41	13/28564	0,00016	0,004068	0,0025846	Sema4d/Rnd2	2	EPO
NFOL	Pik3r3	BP	GO:0040013	negative regulation of locomotion	5/41	360/28564	0,00016	0,004091	0,0025992	Sema4d/Sema4a/Sema5a/Abr/Ptprj	5	EPO
NFOL	Pik3r3	BP	GO:0030308	negative regulation of cell growth	4/41	208/28564	0,00022	0,005614	0,0035674	Sema4d/Sema4a/Sema5a/Ptprj	4	EPO
NFOL	Pik3r3	BP	GO:0048639	positive regulation of developmental growth	4/41	220/28564	0,00028	0,006803	0,0043227	Map1b/Sema4d/Sema5a/Rnd2	4	EPO
NFOL	Pik3r3	BP	GO:0014032	neural crest cell development	3/41	89/28564	0,00029	0,006872	0,0043667	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:1904862	inhibitory synapse assembly	2/41	18/28564	0,0003	0,007022	0,0044619	Sema4d/Sema4a	2	EPO
NFOL	Pik3r3	BP	GO:0002237	response to molecule of bacterial origin	5/41	414/28564	0,0003	0,007022	0,0044619	Peli1/Pdcd4/Abr/Ptger1/Sirt2	5	EPO
NFOL	Pik3r3	BP	GO:0007163	establishment or maintenance of cell polarity	4/41	228/28564	0,00032	0,00718	0,004562	Frmd4a/Parvb/Map1b/Rictor	4	EPO

NFOL	Pik3r3	BP	GO:0043542	endothelial cell migration	4/41	230/28564	0,00033	0,007243	0,004602	Pik3r3/Tns3/Sema4a/Sema5a	4	EPO
NFOL	Pik3r3	BP	GO:0006029	proteoglycan metabolic process	3/41	94/28564	0,00034	0,007243	0,004602	Tcf7l2/Man1c1/Egflam	3	EPO
NFOL	Pik3r3	BP	GO:0050920	regulation of chemotaxis	4/41	232/28564	0,00034	0,007243	0,004602	Sema4d/Sema4a/Sema5a/Ptprj	4	EPO
NFOL	Pik3r3	BP	GO:0007264	small GTPase mediated signal transduction	5/41	428/28564	0,00035	0,00738	0,0046894	Tns3/Dock6/Dock4/Rnd2/Ctnnal1	5	EPO
NFOL	Pik3r3	BP	GO:0032102	negative regulation of response to external stimulus	5/41	429/28564	0,00036	0,00738	0,0046894	Sema4d/Sema4a/Sema5a/Abr/Sirt2	5	EPO
NFOL	Pik3r3	BP	GO:0045685	regulation of glial cell differentiation	3/41	97/28564	0,00037	0,007454	0,0047363	Tcf7l2/Dusp15/Sirt2	3	EPO
NFOL	Pik3r3	BP	GO:0048864	stem cell development	3/41	99/28564	0,00039	0,007777	0,0049419	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0014033	neural crest cell differentiation	3/41	102/28564	0,00043	0,008345	0,0053022	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0022411	cellular component disassembly	5/41	450/28564	0,00045	0,008566	0,0054429	Kif19a/Map1b/Uvrag/Sema5a/Mical3	5	EPO
NFOL	Pik3r3	BP	GO:0007411	axon guidance	4/41	253/28564	0,00047	0,00888	0,0056422	Nfasc/Sema4d/Sema4a/Sema5a	4	EPO
NFOL	Pik3r3	BP	GO:0097485	neuron projection guidance	4/41	254/28564	0,00048	0,00888	0,0056422	Nfasc/Sema4d/Sema4a/Sema5a	4	EPO
NFOL	Pik3r3	BP	GO:0048670	regulation of collateral sprouting	2/41	23/28564	0,0005	0,009131	0,0058021	Sema4d/Rnd2	2	EPO
NFOL	Pik3r3	BP	GO:0001667	ameboidal-type cell migration	5/41	470/28564	0,00054	0,009783	0,0062161	Pik3r3/Tns3/Sema4d/Sema4a/Sema5a	5	EPO
NFOL	Pik3r3	BP	GO:1904035	regulation of epithelial cell apoptotic process	3/41	115/28564	0,00061	0,010752	0,0068319	Tcf7l2/Pdcd4/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0010001	glial cell differentiation	4/41	274/28564	0,00063	0,011084	0,0070428	Tcf7l2/Dusp15/Sirt2/Ptprj	4	EPO
NFOL	Pik3r3	BP	GO:1901890	positive regulation of cell junction assembly	3/41	127/28564	0,00081	0,013917	0,0088432	Sema4d/Sema4a/Ptprj	3	EPO
NFOL	Pik3r3	BP	GO:0071695	anatomical structure maturation	4/41	305/28564	0,00095	0,016033	0,0101873	Nfasc/Bfsp2/Sema4d/Sirt2	4	EPO
NFOL	Pik3r3	BP	GO:0048668	collateral sprouting	2/41	33/28564	0,00103	0,017242	0,0109559	Sema4d/Rnd2	2	EPO
NFOL	Pik3r3	BP	GO:0008360	regulation of cell shape	3/41	141/28564	0,00109	0,017918	0,0113853	Parvb/Sema4d/Sema4a	3	EPO
NFOL	Pik3r3	BP	GO:0010721	negative regulation of cell development	4/41	318/28564	0,0011	0,017918	0,0113853	Sema4d/Sema4a/Sema5a/Sirt2	4	EPO

NFOL	Pik3r3	BP	GO:0010631	epithelial cell migration	4/41	327/28564	0,00122	0,019584	0,0124437	Pik3r3/Tns3/Sema4a/Sema5a	4	EPO
NFOL	Pik3r3	BP	GO:0090132	epithelium migration	4/41	329/28564	0,00125	0,019713	0,0125261	Pik3r3/Tns3/Sema4a/Sema5a	4	EPO
NFOL	Pik3r3	BP	GO:0090130	tissue migration	4/41	331/28564	0,00128	0,019713	0,0125261	Pik3r3/Tns3/Sema4a/Sema5a	4	EPO
NFOL	Pik3r3	BP	GO:1904019	epithelial cell apoptotic process	3/41	149/28564	0,00128	0,019713	0,0125261	Tcf7l2/Pdcd4/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0016311	dephosphorylation	4/41	342/28564	0,00144	0,021876	0,0139	Tns3/Sema4d/Dusp15/Ptprj	4	EPO
NFOL	Pik3r3	BP	GO:0030010	establishment of cell polarity	3/41	163/28564	0,00166	0,024835	0,0157803	Frmd4a/Map1b/Rictor	3	EPO
NFOL	Pik3r3	BP	GO:0010977	negative regulation of neuron projection development	3/41	165/28564	0,00172	0,025385	0,0161301	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0050919	negative chemotaxis	2/41	43/28564	0,00175	0,025523	0,0162173	Sema4d/Sema4a	2	EPO
NFOL	Pik3r3	BP	GO:0050918	positive chemotaxis	2/41	45/28564	0,00191	0,027582	0,0175257	Sema5a/Ptprj	2	EPO
NFOL	Pik3r3	BP	GO:0042063	gliogenesis	4/41	378/28564	0,00208	0,029329	0,0186361	Tcf7l2/Dusp15/Sirt2/Ptprj	4	EPO
NFOL	Pik3r3	BP	GO:0043114	regulation of vascular permeability	2/41	47/28564	0,00209	0,029329	0,0186361	Abr/Ptprj	2	EPO
NFOL	Pik3r3	BP	GO:0021700	developmental maturation	4/41	381/28564	0,00214	0,02969	0,0188657	Nfasc/Bfsp2/Sema4d/Sirt2	4	EPO
NFOL	Pik3r3	BP	GO:0042552	myelination	3/41	180/28564	0,0022	0,030197	0,0191877	Nfasc/Tcf7l2/Sirt2	3	EPO
NFOL	Pik3r3	BP	GO:1905521	regulation of macrophage migration	2/41	49/28564	0,00227	0,030208	0,0191948	Abr/Ptprj	2	EPO
NFOL	Pik3r3	BP	GO:1902905	positive regulation of supramolecular fiber organization	3/41	182/28564	0,00227	0,030208	0,0191948	Map1b/Sema5a/Rictor	3	EPO
NFOL	Pik3r3	BP	GO:0007272	ensheathment of neurons	3/41	183/28564	0,00231	0,030208	0,0191948	Nfasc/Tcf7l2/Sirt2	3	EPO
NFOL	Pik3r3	BP	GO:0008366	axon ensheathment	3/41	183/28564	0,00231	0,030208	0,0191948	Nfasc/Tcf7l2/Sirt2	3	EPO
NFOL	Pik3r3	BP	GO:0046854	phosphatidylinositol phosphate biosynthetic process	2/41	50/28564	0,00236	0,030539	0,0194047	Pik3r3/Uvrag	2	EPO
NFOL	Pik3r3	BP	GO:0032496	response to lipopolysaccharide	4/41	394/28564	0,00241	0,030913	0,0196428	Peli1/Pdcd4/Abr/Ptger1	4	EPO
NFOL	Pik3r3	BP	GO:2000351	regulation of endothelial cell apoptotic process	2/41	52/28564	0,00255	0,032272	0,0205057	Pdcd4/Sema5a	2	EPO
NFOL	Pik3r3	BP	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	3/41	192/28564	0,00264	0,033101	0,0210326	Sema4d/Rictor/Ptprj	3	EPO
NFOL	Pik3r3	BP	GO:0008154	actin polymerization or depolymerization	3/41	197/28564	0,00284	0,034166	0,0217094	Sema5a/Rictor/Mical3	3	EPO
NFOL	Pik3r3	BP	GO:0007019	microtubule depolymerization	2/41	55/28564	0,00284	0,034166	0,0217094	Kif19a/Map1b	2	EPO
NFOL	Pik3r3	BP	GO:0045773	positive regulation of axon extension	2/41	55/28564	0,00284	0,034166	0,0217094	Map1b/Sema5a	2	EPO
NFOL	Pik3r3	BP	GO:0072577	endothelial cell apoptotic process	2/41	55/28564	0,00284	0,034166	0,0217094	Pdcd4/Sema5a	2	EPO
NFOL	Pik3r3	BP	GO:1901861	regulation of muscle tissue development	2/41	56/28564	0,00295	0,034867	0,0221551	Tcf7l2/Sirt2	2	EPO

NFOL	Pik3r3	BP	GO:0051099	positive regulation of binding	3/41	200/28564	0,00296	0,034867	0,0221551	Tcf7l2/Tns3/Sirt2	3	EPO
NFOL	Pik3r3	BP	GO:0051495	positive regulation of cytoskeleton organization	3/41	204/28564	0,00313	0,036494	0,0231885	Map1b/Sema5a/Rictor	3	EPO
NFOL	Pik3r3	BP	GO:0030042	actin filament depolymerization	2/41	59/28564	0,00327	0,037654	0,0239259	Sema5a/Mical3	2	EPO
NFOL	Pik3r3	BP	GO:0030166	proteoglycan biosynthetic process	2/41	60/28564	0,00338	0,038532	0,0244837	Tcf7l2/Man1c1	2	EPO
NFOL	Pik3r3	BP	GO:0045017	glycerolipid biosynthetic process	3/41	213/28564	0,00354	0,039986	0,0254073	Pik3r3/Tcf7l2/Uvrag	3	EPO
NFOL	Pik3r3	BP	GO:0045599	negative regulation of fat cell differentiation	2/41	62/28564	0,0036	0,040294	0,025603	Tcf7l2/Sirt2	2	EPO
NFOL	Pik3r3	BP	GO:0031345	negative regulation of cell projection organization	3/41	219/28564	0,00382	0,040639	0,0258228	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	BP	GO:0031641	regulation of myelination	2/41	64/28564	0,00383	0,040639	0,0258228	Tcf7l2/Sirt2	2	EPO
NFOL	Pik3r3	BP	GO:0031346	positive regulation of cell projection organization	4/41	459/28564	0,00417	0,040639	0,0258228	Map1b/Sema4d/Sema5a/Rnd2	4	EPO
NFOL	Pik3r3	BP	GO:1905517	macrophage migration	2/41	67/28564	0,00419	0,040639	0,0258228	Abr/Ptprj	2	EPO
NFOL	Pik3r3	BP	GO:0048469	cell maturation	3/41	227/28564	0,00423	0,040639	0,0258228	Nfasc/Bfsp2/Sirt2	3	EPO
NFOL	Pik3r3	BP	GO:1904036	negative regulation of epithelial cell apoptotic process	2/41	71/28564	0,00469	0,043773	0,0278139	Tcf7l2/Sema5a	2	EPO
NFOL	Pik3r3	BP	GO:0050679	positive regulation of epithelial cell proliferation	3/41	237/28564	0,00477	0,043773	0,0278139	Tcf7l2/Sema5a/Rictor	3	EPO
NFOL	Pik3r3	BP	GO:0034329	cell junction assembly	4/41	477/28564	0,00477	0,043773	0,0278139	Nfasc/Sema4d/Sema4a/Ptprj	4	EPO
NFOL	Pik3r3	BP	GO:0071868	cellular response to monoamine stimulus	2/41	72/28564	0,00482	0,043773	0,0278139	Ptger1/Sirt2	2	EPO
NFOL	Pik3r3	BP	GO:0071870	cellular response to catecholamine stimulus	2/41	72/28564	0,00482	0,043773	0,0278139	Ptger1/Sirt2	2	EPO
NFOL	Pik3r3	BP	GO:0003018	vascular process in circulatory system	3/41	240/28564	0,00493	0,044451	0,0282448	Dock4/Abr/Ptprj	3	EPO
NFOL	Pik3r3	BP	GO:1901888	regulation of cell junction assembly	3/41	242/28564	0,00505	0,045134	0,0286785	Sema4d/Sema4a/Ptprj	3	EPO
NFOL	Pik3r3	BP	GO:0007422	peripheral nervous system development	2/41	75/28564	0,00522	0,045599	0,0289744	Nfasc/Sirt2	2	EPO
NFOL	Pik3r3	BP	GO:0071867	response to monoamine	2/41	75/28564	0,00522	0,045599	0,0289744	Ptger1/Sirt2	2	EPO
NFOL	Pik3r3	BP	GO:0071869	response to catecholamine	2/41	75/28564	0,00522	0,045599	0,0289744	Ptger1/Sirt2	2	EPO
NFOL	Pik3r3	BP	GO:0021536	diencephalon development	2/41	76/28564	0,00536	0,046196	0,0293536	Tcf7l2/Sema5a	2	EPO
NFOL	Pik3r3	BP	GO:0051965	positive regulation of synapse assembly	2/41	80/28564	0,00592	0,047384	0,0301083	Sema4d/Sema4a	2	EPO
NFOL	Pik3r3	BP	GO:0043547	positive regulation of GTPase activity	3/41	259/28564	0,00609	0,048444	0,0307817	Dock6/Sema4d/Abr	3	EPO
NFOL	Pik3r3	CC	GO:0033010	paranodal junction	2/41	8/28585	5,6E-05	0,005925	0,0031772	Nfasc/Sirt2	2	EPO
NFOL	Pik3r3	CC	GO:0033270	paranode region of axon	2/41	16/28585	0,00024	0,009434	0,0050587	Nfasc/Sirt2	2	EPO
NFOL	Pik3r3	CC	GO:0044304	main axon	3/41	87/28585	0,00027	0,009434	0,0050587	Nfasc/Map1b/Sirt2	3	EPO
NFOL	Pik3r3	CC	GO:0005942	phosphatidylinositol 3-kinase complex	2/41	30/28585	0,00085	0,022556	0,0120956	Pik3r3/Uvrag	2	EPO
NFOL	Pik3r3	CC	GO:0005875	microtubule associated complex	3/41	148/28585	0,00126	0,026442	0,0141797	Kif19a/Map1b/Dynll2	3	EPO

NFOL	Pik3r3	CC	GO:0005769	early endosome	4/41	347/28585	0,00152	0,026442	0,0141797	Tmem163/Tmem108/Uvrag/Rnd2	4	EPO
NFOL	Pik3r3	CC	GO:0097386	glial cell projection	2/41	43/28585	0,00175	0,026442	0,0141797	Nfasc/Sirt2	2	EPO
NFOL	Pik3r3	CC	GO:0030496	midbody	3/41	201/28585	0,003	0,035037	0,0187882	Uvrag/Sirt2/Mical3	3	EPO
NFOL	Pik3r3	CC	GO:0005874	microtubule	4/41	441/28585	0,0036	0,035037	0,0187882	Kif19a/Map1b/Sirt2/Dynll2	4	EPO
NFOL	Pik3r3	CC	GO:0014069	postsynaptic density	4/41	442/28585	0,00363	0,035037	0,0187882	Tmem108/Map1b/Abr/Dynll2	4	EPO
NFOL	Pik3r3	CC	GO:0032279	asymmetric synapse	4/41	462/28585	0,00425	0,035037	0,0187882	Tmem108/Map1b/Abr/Dynll2	4	EPO
NFOL	Pik3r3	CC	GO:0099572	postsynaptic specialization	4/41	486/28585	0,00508	0,03793	0,0203397	Tmem108/Map1b/Abr/Dynll2	4	EPO
NFOL	Pik3r3	CC	GO:0015629	actin cytoskeleton	4/41	500/28585	0,00562	0,03793	0,0203397	Parvb/Tns3/Dynll2/Rinl	4	EPO
NFOL	Pik3r3	MF	GO:0030215	semaphorin receptor binding	3/40	22/28171	4E-06	0,000493	0,0002742	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	MF	GO:0045499	chemorepellent activity	3/40	29/28171	9,4E-06	0,000581	0,0003231	Sema4d/Sema4a/Sema5a	3	EPO
NFOL	Pik3r3	MF	GO:0005085	guanyl-nucleotide exchange factor activity	4/40	203/28171	0,0002	0,006273	0,0034896	Dock6/Dock4/Abr/Rinl	4	EPO
NFOL	Pik3r3	MF	GO:0045295	gamma-catenin binding	2/40	15/28171	0,0002	0,006273	0,0034896	Tcf7l2/Ptprj	2	EPO
NFOL	Pik3r3	MF	GO:0030695	GTPase regulator activity	5/40	432/28171	0,00035	0,007184	0,0039961	Tns3/Dock6/Dock4/Abr/Rinl	5	EPO
NFOL	Pik3r3	MF	GO:0060589	nucleoside-triphosphatase regulator activity	5/40	432/28171	0,00035	0,007184	0,0039961	Tns3/Dock6/Dock4/Abr/Rinl	5	EPO
NFOL	Pik3r3	MF	GO:0008574	plus-end-directed microtubule motor activity	2/40	26/28171	0,00063	0,010986	0,0061114	Kif19a/Dynll2	2	EPO
NFOL	Sema5a	BP	GO:0007409	axonogenesis	7/32	498/28564	1,1E-06	0,001019	0,0006333	Sema5a/Nfasc/Cntn1/Sema4a/Sema4d/Map1b/Cdh11	7	EPO
NFOL	Sema5a	BP	GO:0048843	negative regulation of axon extension involved in axon guidance	3/32	27/28564	3,7E-06	0,001019	0,0006333	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0048841	regulation of axon extension involved in axon guidance	3/32	33/28564	6,8E-06	0,001019	0,0006333	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:1905702	regulation of inhibitory synapse assembly	2/32	4/28564	7,3E-06	0,001019	0,0006333	Sema4a/Sema4d	2	EPO
NFOL	Sema5a	BP	GO:0030516	regulation of axon extension	4/32	114/28564	7,9E-06	0,001019	0,0006333	Sema5a/Sema4a/Sema4d/Map1b	4	EPO
NFOL	Sema5a	BP	GO:0007411	axon guidance	5/32	253/28564	8,7E-06	0,001019	0,0006333	Sema5a/Nfasc/Cntn1/Sema4a/Sema4d	5	EPO

NFOL	Sema5a	BP	GO:0097485	neuron projection guidance	5/32	254/28564	8,8E-06	0,001019	0,0006333	Sema5a/Nfasc/Cntn1/Sema4a/Sema4d	5	EPO
NFOL	Sema5a	BP	GO:0048846	axon extension involved in axon guidance	3/32	37/28564	9,7E-06	0,001019	0,0006333	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:1902284	neuron projection extension involved in neuron projection guidance	3/32	37/28564	9,7E-06	0,001019	0,0006333	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0001667	ameboidal-type cell migration	6/32	470/28564	1,2E-05	0,001022	0,0006358	Sema5a/Tns3/Sema4a/Sema4d/Tns1/Pik3r3	6	EPO
NFOL	Sema5a	BP	GO:0048640	negative regulation of developmental growth	4/32	129/28564	1,3E-05	0,001022	0,0006358	Sema5a/Tcf7l2/Sema4a/Sema4d	4	EPO
NFOL	Sema5a	BP	GO:0061387	regulation of extent of cell growth	4/32	129/28564	1,3E-05	0,001022	0,0006358	Sema5a/Sema4a/Sema4d/Map1b	4	EPO
NFOL	Sema5a	BP	GO:0048675	axon extension	4/32	144/28564	2E-05	0,001445	0,0008987	Sema5a/Sema4a/Sema4d/Map1b	4	EPO
NFOL	Sema5a	BP	GO:0030517	negative regulation of axon extension	3/32	48/28564	2,1E-05	0,001445	0,0008987	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0071526	semaphorin-plexin signaling pathway	3/32	50/28564	2,4E-05	0,001526	0,0009491	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0050922	negative regulation of chemotaxis	3/32	58/28564	3,8E-05	0,0021	0,0013058	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0050768	negative regulation of neurogenesis	4/32	173/28564	4,1E-05	0,0021	0,0013058	Sema5a/Sema4a/Sema4d/Sirt2	4	EPO
NFOL	Sema5a	BP	GO:0051961	negative regulation of nervous system development	4/32	178/28564	4,6E-05	0,0021	0,0013058	Sema5a/Sema4a/Sema4d/Sirt2	4	EPO
NFOL	Sema5a	BP	GO:0040013	negative regulation of locomotion	5/32	360/28564	4,7E-05	0,0021	0,0013058	Sema5a/Abr/Sema4a/Sema4d/Cdh11	5	EPO
NFOL	Sema5a	BP	GO:0042552	myelination	4/32	180/28564	4,8E-05	0,0021	0,0013058	Tcf7l2/Nfasc/Cntn1/Sirt2	4	EPO
NFOL	Sema5a	BP	GO:0001755	neural crest cell migration	3/32	63/28564	4,8E-05	0,0021	0,0013058	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0007272	ensheathment of neurons	4/32	183/28564	5,1E-05	0,0021	0,0013058	Tcf7l2/Nfasc/Cntn1/Sirt2	4	EPO
NFOL	Sema5a	BP	GO:0008366	axon ensheathment	4/32	183/28564	5,1E-05	0,0021	0,0013058	Tcf7l2/Nfasc/Cntn1/Sirt2	4	EPO
NFOL	Sema5a	BP	GO:0090497	mesenchymal cell migration	3/32	65/28564	5,3E-05	0,002101	0,0013067	Sema5a/Sema4a/Sema4d	3	EPO

NFOL	Sema5a	BP	GO:0050770	regulation of axonogenesis	4/32	187/28564	5,5E-05	0,002101	0,0013067	Sema5a/Sema4a/Sema4d/Map1b	4	EPO
NFOL	Sema5a	BP	GO:0050771	negative regulation of axonogenesis	3/32	70/28564	6,6E-05	0,002422	0,0015061	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0048638	regulation of developmental growth	5/32	405/28564	8,2E-05	0,002788	0,0017335	Sema5a/Tcf7l2/Sema4a/Sema4d/Map1b	5	EPO
NFOL	Sema5a	BP	GO:0043491	protein kinase B signaling	4/32	209/28564	8,5E-05	0,002788	0,0017335	Sema5a/Tcf7l2/Sirt2/Pik3r3	4	EPO
NFOL	Sema5a	BP	GO:1990138	neuron projection extension	4/32	209/28564	8,5E-05	0,002788	0,0017335	Sema5a/Sema4a/Sema4d/Map1b	4	EPO
NFOL	Sema5a	BP	GO:0008361	regulation of cell size	4/32	218/28564	0,0001	0,003171	0,001972	Sema5a/Sema4a/Sema4d/Map1b	4	EPO
NFOL	Sema5a	BP	GO:0032102	negative regulation of response to external stimulus	5/32	429/28564	0,00011	0,003291	0,0020462	Sema5a/Abr/Sema4a/Sema4d/Sirt2	5	EPO
NFOL	Sema5a	BP	GO:0043542	endothelial cell migration	4/32	230/28564	0,00012	0,003655	0,0022725	Sema5a/Tns3/Sema4a/Pik3r3	4	EPO
NFOL	Sema5a	BP	GO:0014032	neural crest cell development	3/32	89/28564	0,00014	0,003902	0,0024265	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0048762	mesenchymal cell differentiation	4/32	249/28564	0,00017	0,004645	0,0028884	Sema5a/Tcf7l2/Sema4a/Sema4d	4	EPO
NFOL	Sema5a	BP	GO:0034329	cell junction assembly	5/32	477/28564	0,00018	0,004645	0,0028884	Nfasc/Sema4a/Sema4d/Tns1/Cdh11	5	EPO
NFOL	Sema5a	BP	GO:0050767	regulation of neurogenesis	5/32	480/28564	0,00018	0,004645	0,0028884	Sema5a/Sema4a/Sema4d/Map1b/Sirt2	5	EPO
NFOL	Sema5a	BP	GO:1904862	inhibitory synapse assembly	2/32	18/28564	0,00018	0,004645	0,0028884	Sema4a/Sema4d	2	EPO
NFOL	Sema5a	BP	GO:0048864	stem cell development	3/32	99/28564	0,00019	0,004645	0,0028884	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0014033	neural crest cell differentiation	3/32	102/28564	0,0002	0,00482	0,0029969	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0050772	positive regulation of axonogenesis	3/32	102/28564	0,0002	0,00482	0,0029969	Sema5a/Sema4d/Map1b	3	EPO
NFOL	Sema5a	BP	GO:0045926	negative regulation of growth	4/32	267/28564	0,00022	0,00505	0,0031404	Sema5a/Tcf7l2/Sema4a/Sema4d	4	EPO
NFOL	Sema5a	BP	GO:0048863	stem cell differentiation	4/32	286/28564	0,00028	0,006339	0,0039416	Sema5a/Tcf7l1/Sema4a/Sema4d	4	EPO
NFOL	Sema5a	BP	GO:0048588	developmental cell growth	4/32	287/28564	0,00029	0,006339	0,0039416	Sema5a/Sema4a/Sema4d/Map1b	4	EPO

NFOL	Sema5a	BP	GO:0060560	developmental growth involved in morphogenesis	4/32	290/28564	0,0003	0,006444	0,004007	Sema5a/Sema4a/Sema4d/Map1b	4	EPO
NFOL	Sema5a	BP	GO:0048709	oligodendrocyte differentiation	3/32	122/28564	0,00034	0,007256	0,0045116	Tcf7l2/Cntn1/Sirt2	3	EPO
NFOL	Sema5a	BP	GO:0032288	myelin assembly	2/32	25/28564	0,00036	0,007286	0,0045305	Nfasc/Cntn1	2	EPO
NFOL	Sema5a	BP	GO:0051261	protein depolymerization	3/32	124/28564	0,00036	0,007286	0,0045305	Sema5a/Nckap5/Map1b	3	EPO
NFOL	Sema5a	BP	GO:0060485	mesenchyme development	4/32	310/28564	0,00038	0,007603	0,0047279	Sema5a/Tcf7l2/Sema4a/Sema4d	4	EPO
NFOL	Sema5a	BP	GO:0021782	glial cell development	3/32	129/28564	0,00041	0,007846	0,0048788	Tcf7l2/Cntn1/Sirt2	3	EPO
NFOL	Sema5a	BP	GO:0010721	negative regulation of cell development	4/32	318/28564	0,00042	0,007885	0,0049032	Sema5a/Sema4a/Sema4d/Sirt2	4	EPO
NFOL	Sema5a	BP	GO:0001578	microtubule bundle formation	3/32	131/28564	0,00042	0,007885	0,0049032	Nckap5/Ccser2/Map1b	3	EPO
NFOL	Sema5a	BP	GO:0010631	epithelial cell migration	4/32	327/28564	0,00047	0,008583	0,0053371	Sema5a/Tns3/Sema4a/Pik3r3	4	EPO
NFOL	Sema5a	BP	GO:0090132	epithelium migration	4/32	329/28564	0,00048	0,008617	0,0053579	Sema5a/Tns3/Sema4a/Pik3r3	4	EPO
NFOL	Sema5a	BP	GO:0090130	tissue migration	4/32	331/28564	0,00049	0,008652	0,0053799	Sema5a/Tns3/Sema4a/Pik3r3	4	EPO
NFOL	Sema5a	BP	GO:0008360	regulation of cell shape	3/32	141/28564	0,00053	0,009063	0,0056357	Sema4a/Parvb/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0043087	regulation of GTPase activity	4/32	353/28564	0,00063	0,01062	0,0066035	Abr/Tns3/Sema4d/Rasgef1b	4	EPO
NFOL	Sema5a	BP	GO:0051962	positive regulation of nervous system development	4/32	379/28564	0,00082	0,013567	0,0084358	Sema5a/Sema4a/Sema4d/Map1b	4	EPO
NFOL	Sema5a	BP	GO:0010977	negative regulation of neuron projection development	3/32	165/28564	0,00083	0,013567	0,0084358	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0032535	regulation of cellular component size	4/32	404/28564	0,00104	0,016581	0,0103099	Sema5a/Sema4a/Sema4d/Map1b	4	EPO
NFOL	Sema5a	BP	GO:0010765	positive regulation of sodium ion transport	2/32	43/28564	0,00107	0,016581	0,0103099	Cntn1/Cnksr3	2	EPO
NFOL	Sema5a	BP	GO:0050919	negative chemotaxis	2/32	43/28564	0,00107	0,016581	0,0103099	Sema4a/Sema4d	2	EPO
NFOL	Sema5a	BP	GO:0014003	oligodendrocyte development	2/32	49/28564	0,00138	0,021156	0,013155	Tcf7l2/Cntn1	2	EPO
NFOL	Sema5a	BP	GO:0051099	positive regulation of binding	3/32	200/28564	0,00144	0,02173	0,0135119	Tcf7l2/Tns3/Sirt2	3	EPO
NFOL	Sema5a	BP	GO:0030308	negative regulation of cell growth	3/32	208/28564	0,00162	0,023848	0,0148286	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0031346	positive regulation of cell projection organization	4/32	459/28564	0,00166	0,023848	0,0148286	Sema5a/Cntn1/Sema4d/Map1b	4	EPO
NFOL	Sema5a	BP	GO:0030307	positive regulation of cell growth	3/32	210/28564	0,00166	0,023848	0,0148286	Sema5a/Sema4d/Map1b	3	EPO

NFOL	Sema5a	BP	GO:0001558	regulation of cell growth	4/32	464/28564	0,00172	0,023904	0,0148639	Sema5a/Sema4a/Sema4d/Map1b	4	EPO
NFOL	Sema5a	BP	GO:0007019	microtubule depolymerization	2/32	55/28564	0,00174	0,023904	0,0148639	Nckap5/Map1b	2	EPO
NFOL	Sema5a	BP	GO:0045773	positive regulation of axon extension	2/32	55/28564	0,00174	0,023904	0,0148639	Sema5a/Map1b	2	EPO
NFOL	Sema5a	BP	GO:1901861	regulation of muscle tissue development	2/32	56/28564	0,0018	0,024419	0,0151836	Tcf7l2/Sirt2	2	EPO
NFOL	Sema5a	BP	GO:0048713	regulation of oligodendrocyte differentiation	2/32	57/28564	0,00187	0,024619	0,0153082	Tcf7l2/Sirt2	2	EPO
NFOL	Sema5a	BP	GO:0031345	negative regulation of cell projection organization	3/32	219/28564	0,00187	0,024619	0,0153082	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0048639	positive regulation of developmental growth	3/32	220/28564	0,0019	0,024619	0,0153082	Sema5a/Sema4d/Map1b	3	EPO
NFOL	Sema5a	BP	GO:0007163	establishment or maintenance of cell polarity	3/32	228/28564	0,0021	0,026883	0,0167159	Frmd4a/Parvb/Map1b	3	EPO
NFOL	Sema5a	BP	GO:0050920	regulation of chemotaxis	3/32	232/28564	0,0022	0,027501	0,0171006	Sema5a/Sema4a/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0045599	negative regulation of fat cell differentiation	2/32	62/28564	0,0022	0,027501	0,0171006	Tcf7l2/Sirt2	2	EPO
NFOL	Sema5a	BP	GO:0031641	regulation of myelination	2/32	64/28564	0,00235	0,028898	0,0179691	Tcf7l2/Sirt2	2	EPO
NFOL	Sema5a	BP	GO:0032984	protein-containing complex disassembly	3/32	240/28564	0,00243	0,029497	0,0183415	Sema5a/Nckap5/Map1b	3	EPO
NFOL	Sema5a	BP	GO:1904036	negative regulation of epithelial cell apoptotic process	2/32	71/28564	0,00288	0,03455	0,0214835	Sema5a/Tcf7l2	2	EPO
NFOL	Sema5a	BP	GO:0043547	positive regulation of GTPase activity	3/32	259/28564	0,00301	0,034974	0,0217472	Abr/Sema4d/Rasgef1b	3	EPO
NFOL	Sema5a	BP	GO:0007422	peripheral nervous system development	2/32	75/28564	0,00321	0,034974	0,0217472	Nfasc/Sirt2	2	EPO
NFOL	Sema5a	BP	GO:0021536	diencephalon development	2/32	76/28564	0,00329	0,034974	0,0217472	Sema5a/Tcf7l2	2	EPO
NFOL	Sema5a	BP	GO:0010001	glial cell differentiation	3/32	274/28564	0,00353	0,036325	0,022587	Tcf7l2/Cntn1/Sirt2	3	EPO
NFOL	Sema5a	BP	GO:0051965	positive regulation of synapse assembly	2/32	80/28564	0,00364	0,037025	0,0230227	Sema4a/Sema4d	2	EPO
NFOL	Sema5a	BP	GO:0022604	regulation of cell morphogenesis	3/32	278/28564	0,00367	0,037025	0,0230227	Sema4a/Parvb/Sema4d	3	EPO
NFOL	Sema5a	BP	GO:0035019	somatic stem cell population maintenance	2/32	88/28564	0,00438	0,042412	0,0263723	Tcf7l2/Tcf7l1	2	EPO
NFOL	Sema5a	BP	GO:0060070	canonical Wnt signaling pathway	3/32	305/28564	0,00475	0,044192	0,0274788	Sema5a/Tcf7l2/Tcf7l1	3	EPO
NFOL	Sema5a	BP	GO:0071695	anatomical structure maturation	3/32	305/28564	0,00475	0,044192	0,0274788	Nfasc/Sema4d/Sirt2	3	EPO
NFOL	Sema5a	BP	GO:0006029	proteoglycan metabolic process	2/32	94/28564	0,00498	0,04587	0,0285225	Tcf7l2/Egflam	2	EPO
NFOL	Sema5a	BP	GO:1901879	regulation of protein depolymerization	2/32	95/28564	0,00509	0,046075	0,02865	Sema5a/Map1b	2	EPO
NFOL	Sema5a	BP	GO:0045685	regulation of glial cell differentiation	2/32	97/28564	0,0053	0,046075	0,02865	Tcf7l2/Sirt2	2	EPO
NFOL	Sema5a	BP	GO:0050769	positive regulation of neurogenesis	3/32	318/28564	0,00534	0,046075	0,02865	Sema5a/Sema4d/Map1b	3	EPO
NFOL	Sema5a	BP	GO:0007044	cell-substrate junction assembly	2/32	99/28564	0,00551	0,046075	0,02865	Tns1/Cdh11	2	EPO

NFOL	Sema5a	BP	GO:0045927	positive regulation of growth	3/32	323/28564	0,00557	0,046075	0,02865	Sema5a/Sema4d/M ap1b	3	EPO
NFOL	Sema5a	BP	GO:0002028	regulation of sodium ion transport	2/32	103/28564	0,00595	0,048643	0,0302463	Cntn1/Cnksr3	2	EPO
NFOL	Sema5a	CC	GO:0033010	paranodal junction	2/32	8/28585	3,4E-05	0,002857	0,0016401	Nfasc/Sirt2	2	EPO
NFOL	Sema5a	CC	GO:1990907	beta-catenin-TCF complex	2/32	13/28585	9,4E-05	0,002857	0,0016401	Tcf7l2/Tcf7l1	2	EPO
NFOL	Sema5a	CC	GO:0043209	myelin sheath	4/32	218/28585	0,0001	0,002857	0,0016401	Nfasc/Cntn1/Itpr2/S irt2	4	EPO
NFOL	Sema5a	CC	GO:0044304	main axon	3/32	87/28585	0,00013	0,002857	0,0016401	Nfasc/Map1b/Sirt2	3	EPO
NFOL	Sema5a	CC	GO:0033270	paranode region of axon	2/32	16/28585	0,00014	0,002857	0,0016401	Nfasc/Sirt2	2	EPO
NFOL	Sema5a	CC	GO:0043204	perikaryon	3/32	154/28585	0,00068	0,01119	0,0064247	Pde9a/Map1b/Sirt2	3	EPO
NFOL	Sema5a	CC	GO:0005925	focal adhesion	3/32	174/28585	0,00097	0,013184	0,0075696	Tns3/Parvb/Tns1	3	EPO
NFOL	Sema5a	CC	GO:0097386	glial cell projection	2/32	43/28585	0,00107	0,013184	0,0075696	Nfasc/Sirt2	2	EPO
NFOL	Sema5a	CC	GO:0030055	cell-substrate junction	3/32	188/28585	0,00121	0,013274	0,0076212	Tns3/Parvb/Tns1	3	EPO
NFOL	Sema5a	CC	GO:0015629	actin cytoskeleton	4/32	500/28585	0,00226	0,022334	0,0128234	Tns3/Specc1/Parvb/ Rinl	4	EPO
NFOL	Sema5a	MF	GO:0030215	semaphorin receptor binding	3/32	22/28171	2E-06	0,000198	0,0001063	Sema5a/Sema4a/Se ma4d	3	EPO
NFOL	Sema5a	MF	GO:0045499	chemorepellent activity	3/32	29/28171	4,8E-06	0,000234	0,0001255	Sema5a/Sema4a/Se ma4d	3	EPO
NFOL	Sema5a	MF	GO:0005085	guanyl-nucleotide exchange factor activity	4/32	203/28171	8E-05	0,002324	0,0012484	Abr/Dock4/Rinl/Ras gef1b	4	EPO
NFOL	Sema5a	MF	GO:0030695	GTPase regulator activity	5/32	432/28171	0,00012	0,002324	0,0012484	Abr/Tns3/Dock4/Ri nl/Rasgef1b	5	EPO
NFOL	Sema5a	MF	GO:0060589	nucleoside-triphosphatase regulator activity	5/32	432/28171	0,00012	0,002324	0,0012484	Abr/Tns3/Dock4/Ri nl/Rasgef1b	5	EPO
NFOL	Sema5a	MF	GO:0098632	cell-cell adhesion mediator activity	2/32	33/28171	0,00065	0,010546	0,0056637	Nfasc/Cntn1	2	EPO
NFOL	Sema5a	MF	GO:0098631	cell adhesion mediator activity	2/32	43/28171	0,0011	0,01535	0,0082438	Nfasc/Cntn1	2	EPO
NFOL	Sema5a	MF	GO:0005096	GTPase activator activity	3/32	241/28171	0,00255	0,03128	0,0167993	Abr/Dock4/Rinl	3	EPO
NFOL	Sema5a	MF	GO:0050839	cell adhesion molecule binding	3/32	305/28171	0,00494	0,037025	0,0198846	Nfasc/Cntn1/Cdh11	3	EPO
NFOL	Sema5a	MF	GO:0008013	beta-catenin binding	2/32	99/28171	0,00566	0,037025	0,0198846	Tcf7l2/Tcf7l1	2	EPO
NFOL	Sema5a	MF	GO:0042578	phosphoric ester hydrolase activity	3/32	346/28171	0,007	0,040343	0,0216667	Pde9a/Tns3/Tns1	3	EPO
NFOL	Sema5a	MF	GO:0015631	tubulin binding	3/32	388/28171	0,00957	0,049874	0,0267852	Ccser2/Map1b/Sirt2	3	EPO
NFOL	Sirt2	BP	GO:0042552	myelination	5/42	180/28564	6,6E-06	0,002723	0,0017188	Sirt2/Fyn/Bcas1/Tcf 7l2/Nfasc	5	EPO
NFOL	Sirt2	BP	GO:0007272	ensheathment of neurons	5/42	183/28564	7,2E-06	0,002723	0,0017188	Sirt2/Fyn/Bcas1/Tcf 7l2/Nfasc	5	EPO

NFOL	Sirt2	BP	GO:0008366	axon ensheathment	5/42	183/28564	7,2E-06	0,002723	0,0017188	Sirt2/Fyn/Bcas1/Tcf7l2/Nfasc	5	EPO
NFOL	Sirt2	BP	GO:0043087	regulation of GTPase activity	6/42	353/28564	1,2E-05	0,003108	0,0019618	Tns3/Arhgap35/Chn2/Rictor/Rapgef1/Rasgef1b	6	EPO
NFOL	Sirt2	BP	GO:0043491	protein kinase B signaling	5/42	209/28564	1,4E-05	0,003108	0,0019618	Sirt2/Tcf7l2/Rictor/Ptprj/Rapgef1	5	EPO
NFOL	Sirt2	BP	GO:1905451	positive regulation of Fc-gamma receptor signaling pathway involved in phagocytosis	2/42	5/28564	2,1E-05	0,003995	0,002522	Ptprj/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:0048709	oligodendrocyte differentiation	4/42	122/28564	3,1E-05	0,004596	0,0029008	Sirt2/Dusp15/Tcf7l2/Ptprj	4	EPO
NFOL	Sirt2	BP	GO:0051261	protein depolymerization	4/42	124/28564	3,3E-05	0,004596	0,0029008	Kif19a/Map1b/Mical3/Camsap2	4	EPO
NFOL	Sirt2	BP	GO:0007264	small GTPase mediated signal transduction	6/42	428/28564	3,6E-05	0,004596	0,0029008	Dock4/Tns3/Arhgap35/Rapgef1/Arhgap5/Rasgef1b	6	EPO
NFOL	Sirt2	BP	GO:0060369	positive regulation of Fc receptor mediated stimulatory signaling pathway	2/42	7/28564	4,4E-05	0,005025	0,0031717	Ptprj/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:1905449	regulation of Fc-gamma receptor signaling pathway involved in phagocytosis	2/42	8/28564	5,9E-05	0,005826	0,0036773	Ptprj/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:0007019	microtubule depolymerization	3/42	55/28564	7,4E-05	0,005826	0,0036773	Kif19a/Map1b/Camsap2	3	EPO
NFOL	Sirt2	BP	GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	2/42	9/28564	7,5E-05	0,005826	0,0036773	Ptprj/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	2/42	9/28564	7,5E-05	0,005826	0,0036773	Ptprj/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:0046580	negative regulation of Ras protein signal transduction	3/42	56/28564	7,8E-05	0,005826	0,0036773	Tns3/Arhgap35/Rapgef1	3	EPO
NFOL	Sirt2	BP	GO:0048713	regulation of oligodendrocyte differentiation	3/42	57/28564	8,2E-05	0,005826	0,0036773	Sirt2/Dusp15/Tcf7l2	3	EPO
NFOL	Sirt2	BP	GO:1990264	peptidyl-tyrosine dephosphorylation involved in inactivation of protein kinase activity	2/42	10/28564	9,4E-05	0,006316	0,0039868	Ptprj/Ptpro	2	EPO
NFOL	Sirt2	BP	GO:0051058	negative regulation of small GTPase mediated signal transduction	3/42	63/28564	0,00011	0,006985	0,0044091	Tns3/Arhgap35/Rapgef1	3	EPO
NFOL	Sirt2	BP	GO:0051896	regulation of protein kinase B signaling	4/42	176/28564	0,00013	0,007785	0,0049137	Tcf7l2/Rictor/Ptprj/Rapgef1	4	EPO
NFOL	Sirt2	BP	GO:0007265	Ras protein signal transduction	5/42	340/28564	0,00014	0,00783	0,0049424	Tns3/Arhgap35/Rapgef1/Arhgap5/Rasgef1b	5	EPO

NFOL	Sirt2	BP	GO:0060368	regulation of Fc receptor mediated stimulatory signaling pathway	2/42	14/28564	0,00019	0,010301	0,0065023	Ptprrj/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:0038094	Fc-gamma receptor signaling pathway	2/42	15/28564	0,00022	0,011335	0,0071549	Ptprrj/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:1902903	regulation of supramolecular fiber organization	5/42	394/28564	0,00027	0,013433	0,0084792	Map1b/Arhgap35/Rictor/Camsap2/Arhgef10l	5	EPO
NFOL	Sirt2	BP	GO:0002431	Fc receptor mediated stimulatory signaling pathway	2/42	17/28564	0,00028	0,013433	0,0084792	Ptprrj/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:0007163	establishment or maintenance of cell polarity	4/42	228/28564	0,00035	0,015548	0,009814	Ust/Map1b/Arhgap35/Rictor	4	EPO
NFOL	Sirt2	BP	GO:0038093	Fc receptor signaling pathway	2/42	20/28564	0,00039	0,015548	0,009814	Ptprrj/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:0043116	negative regulation of vascular permeability	2/42	20/28564	0,00039	0,015548	0,009814	Arhgap35/Ptprrj	2	EPO
NFOL	Sirt2	BP	GO:0045721	negative regulation of gluconeogenesis	2/42	20/28564	0,00039	0,015548	0,009814	Tcf7l2/Soga1	2	EPO
NFOL	Sirt2	BP	GO:0045685	regulation of glial cell differentiation	3/42	97/28564	0,0004	0,015548	0,009814	Sirt2/Dusp15/Tcf7l2	3	EPO
NFOL	Sirt2	BP	GO:0032984	protein-containing complex disassembly	4/42	240/28564	0,00042	0,016075	0,0101468	Kif19a/Map1b/Mical3/Camsap2	4	EPO
NFOL	Sirt2	BP	GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	3/42	103/28564	0,00047	0,01734	0,010945	Fyn/Tcf7l2/Sh3rf1	3	EPO
NFOL	Sirt2	BP	GO:0060828	regulation of canonical Wnt signaling pathway	4/42	250/28564	0,00049	0,017574	0,0110929	Tcf7l2/Cdk14/Rapgef1/Ptpro	4	EPO
NFOL	Sirt2	BP	GO:0043547	positive regulation of GTPase activity	4/42	259/28564	0,00056	0,019461	0,0122841	Arhgap35/Chn2/Rapgef1/Rasgef1b	4	EPO
NFOL	Sirt2	BP	GO:0035024	negative regulation of Rho protein signal transduction	2/42	25/28564	0,00062	0,020761	0,0131048	Tns3/Arhgap35	2	EPO
NFOL	Sirt2	BP	GO:0010001	glial cell differentiation	4/42	274/28564	0,0007	0,02265	0,0142969	Sirt2/Dusp15/Tcf7l2/Ptprrj	4	EPO
NFOL	Sirt2	BP	GO:0051897	positive regulation of protein kinase B signaling	3/42	120/28564	0,00074	0,023304	0,0147094	Tcf7l2/Rictor/Ptprrj	3	EPO
NFOL	Sirt2	BP	GO:0007409	axonogenesis	5/42	498/28564	0,00079	0,024288	0,0153311	Ust/Map1b/Arhgap35/Nfasc/Ptpro	5	EPO
NFOL	Sirt2	BP	GO:0031109	microtubule polymerization or depolymerization	3/42	131/28564	0,00095	0,028462	0,0179654	Kif19a/Map1b/Camsap2	3	EPO
NFOL	Sirt2	BP	GO:2000178	negative regulation of neural precursor cell proliferation	2/42	32/28564	0,00102	0,028791	0,0181731	Sirt2/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:0090090	negative regulation of canonical Wnt signaling pathway	3/42	135/28564	0,00104	0,028791	0,0181731	Tcf7l2/Rapgef1/Ptpro	3	EPO
NFOL	Sirt2	BP	GO:0060070	canonical Wnt signaling pathway	4/42	305/28564	0,00104	0,028791	0,0181731	Tcf7l2/Cdk14/Rapgef1/Ptpro	4	EPO
NFOL	Sirt2	BP	GO:0007266	Rho protein signal transduction	3/42	138/28564	0,0011	0,029925	0,018889	Tns3/Arhgap35/Arhgap5	3	EPO
NFOL	Sirt2	BP	GO:0035335	peptidyl-tyrosine dephosphorylation	2/42	34/28564	0,00115	0,03039	0,0191823	Ptprrj/Ptpro	2	EPO

NFOL	Sirt2	BP	GO:0008360	regulation of cell shape	3/42	141/28564	0,00117	0,03039	0,0191823	Fyn/Epb41l2/Arhgap35	3	EPO
NFOL	Sirt2	BP	GO:0030111	regulation of Wnt signaling pathway	4/42	321/28564	0,00125	0,031675	0,0199936	Tcf7l2/Cdk14/Rapgef1/Ptpro	4	EPO
NFOL	Sirt2	BP	GO:0007026	negative regulation of microtubule depolymerization	2/42	36/28564	0,00129	0,031897	0,0201335	Map1b/Camsap2	2	EPO
NFOL	Sirt2	BP	GO:1901653	cellular response to peptide	4/42	334/28564	0,00145	0,034805	0,021969	Fyn/Otop1/Ptprj/Soga1	4	EPO
NFOL	Sirt2	BP	GO:0031114	regulation of microtubule depolymerization	2/42	39/28564	0,00151	0,034805	0,021969	Map1b/Camsap2	2	EPO
NFOL	Sirt2	BP	GO:0071320	cellular response to cAMP	2/42	39/28564	0,00151	0,034805	0,021969	Rapgef1/Itpr2	2	EPO
NFOL	Sirt2	BP	GO:0016311	dephosphorylation	4/42	342/28564	0,00158	0,034805	0,021969	Dusp15/Tns3/Ptprj/Ptpro	4	EPO
NFOL	Sirt2	BP	GO:1990089	response to nerve growth factor	2/42	40/28564	0,00159	0,034805	0,021969	Tmem108/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:1990090	cellular response to nerve growth factor stimulus	2/42	40/28564	0,00159	0,034805	0,021969	Tmem108/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:0038179	neurotrophin signaling pathway	2/42	41/28564	0,00167	0,035866	0,0226387	Tmem108/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:0030010	establishment of cell polarity	3/42	163/28564	0,00178	0,037517	0,0236809	Ust/Map1b/Rictor	3	EPO
NFOL	Sirt2	BP	GO:0030178	negative regulation of Wnt signaling pathway	3/42	168/28564	0,00194	0,040102	0,0253126	Tcf7l2/Rapgef1/Ptpro	3	EPO
NFOL	Sirt2	BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	3/42	169/28564	0,00197	0,040102	0,0253126	Fyn/Tcf7l2/Sh3rf1	3	EPO
NFOL	Sirt2	BP	GO:0051898	negative regulation of protein kinase B signaling	2/42	45/28564	0,00201	0,040113	0,0253196	Ptprj/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:0043114	regulation of vascular permeability	2/42	47/28564	0,00219	0,042965	0,0271198	Arhgap35/Ptprj	2	EPO
NFOL	Sirt2	BP	GO:0042063	gliogenesis	4/42	378/28564	0,00227	0,043859	0,0276841	Sirt2/Dusp15/Tcf7l2/Ptprj	4	EPO
NFOL	Sirt2	BP	GO:0031111	negative regulation of microtubule polymerization or depolymerization	2/42	49/28564	0,00238	0,045099	0,0284667	Map1b/Camsap2	2	EPO
NFOL	Sirt2	BP	GO:1902905	positive regulation of supramolecular fiber organization	3/42	182/28564	0,00243	0,045435	0,0286788	Map1b/Rictor/Arhgef10l	3	EPO
NFOL	Sirt2	BP	GO:0050770	regulation of axonogenesis	3/42	187/28564	0,00263	0,048264	0,0304646	Ust/Map1b/Arhgap35	3	EPO
NFOL	Sirt2	BP	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	3/42	192/28564	0,00283	0,049674	0,0313548	Fyn/Rictor/Ptprj	3	EPO
NFOL	Sirt2	BP	GO:0032535	regulation of cellular component size	4/42	404/28564	0,00289	0,049674	0,0313548	Map1b/Arhgap35/Rictor/Arhgap5	4	EPO
NFOL	Sirt2	BP	GO:2000378	negative regulation of reactive oxygen species metabolic process	2/42	55/28564	0,00298	0,049674	0,0313548	Sirt2/Fyn	2	EPO
NFOL	Sirt2	BP	GO:0008154	actin polymerization or depolymerization	3/42	197/28564	0,00304	0,049674	0,0313548	Arhgap35/Rictor/Mical3	3	EPO
NFOL	Sirt2	BP	GO:1901861	regulation of muscle tissue development	2/42	56/28564	0,00309	0,049674	0,0313548	Sirt2/Tcf7l2	2	EPO
NFOL	Sirt2	BP	GO:0051099	positive regulation of binding	3/42	200/28564	0,00318	0,049674	0,0313548	Sirt2/Tns3/Tcf7l2	3	EPO
NFOL	Sirt2	BP	GO:0010677	negative regulation of cellular carbohydrate metabolic process	2/42	57/28564	0,0032	0,049674	0,0313548	Tcf7l2/Soga1	2	EPO

NFOL	Sirt2	BP	GO:0031113	regulation of microtubule polymerization	2/42	57/28564	0,0032	0,049674	0,0313548	Map1b/Camsap2	2	EPO
NFOL	Sirt2	BP	GO:0030900	forebrain development	4/42	416/28564	0,00321	0,049674	0,0313548	Fyn/Tmem108/Tcf7l2/Arhgap35	4	EPO
NFOL	Sirt2	BP	GO:0006111	regulation of gluconeogenesis	2/42	58/28564	0,00331	0,049674	0,0313548	Tcf7l2/Soga1	2	EPO
NFOL	Sirt2	BP	GO:0046578	regulation of Ras protein signal transduction	3/42	204/28564	0,00336	0,049674	0,0313548	Tns3/Arhgap35/Rapgef1	3	EPO
NFOL	Sirt2	BP	GO:0051495	positive regulation of cytoskeleton organization	3/42	204/28564	0,00336	0,049674	0,0313548	Map1b/Rictor/Arhgef10l	3	EPO
NFOL	Sirt2	BP	GO:0032271	regulation of protein polymerization	3/42	206/28564	0,00345	0,049674	0,0313548	Map1b/Rictor/Camsap2	3	EPO
NFOL	Sirt2	BP	GO:0030166	proteoglycan biosynthetic process	2/42	60/28564	0,00354	0,049674	0,0313548	Tcf7l2/Csgalnact1	2	EPO
NFOL	Sirt2	BP	GO:0051591	response to cAMP	2/42	61/28564	0,00366	0,049674	0,0313548	Rapgef1/Itpr2	2	EPO
NFOL	Sirt2	BP	GO:0043254	regulation of protein-containing complex assembly	4/42	435/28564	0,00376	0,049674	0,0313548	Sirt2/Map1b/Rictor/Camsap2	4	EPO
NFOL	Sirt2	BP	GO:0031122	cytoplasmic microtubule organization	2/42	62/28564	0,00377	0,049674	0,0313548	Kif19a/Camsap2	2	EPO
NFOL	Sirt2	BP	GO:0045599	negative regulation of fat cell differentiation	2/42	62/28564	0,00377	0,049674	0,0313548	Sirt2/Tcf7l2	2	EPO
NFOL	Sirt2	BP	GO:0045912	negative regulation of carbohydrate metabolic process	2/42	63/28564	0,00389	0,049674	0,0313548	Tcf7l2/Soga1	2	EPO
NFOL	Sirt2	BP	GO:0031641	regulation of myelination	2/42	64/28564	0,00402	0,049674	0,0313548	Sirt2/Tcf7l2	2	EPO
NFOL	Sirt2	BP	GO:0008361	regulation of cell size	3/42	218/28564	0,00404	0,049674	0,0313548	Map1b/Arhgap35/Arhgap5	3	EPO
NFOL	Sirt2	BP	GO:0009991	response to extracellular stimulus	4/42	447/28564	0,00414	0,049674	0,0313548	Sirt2/Tcf7l2/Arhgap35/Rictor	4	EPO
NFOL	Sirt2	BP	GO:1901652	response to peptide	4/42	447/28564	0,00414	0,049674	0,0313548	Fyn/Otop1/Ptprj/Soga1	4	EPO
NFOL	Sirt2	BP	GO:0016051	carbohydrate biosynthetic process	3/42	220/28564	0,00415	0,049674	0,0313548	Tcf7l2/Csgalnact1/Soga1	3	EPO
NFOL	Sirt2	BP	GO:0032869	cellular response to insulin stimulus	3/42	221/28564	0,0042	0,049674	0,0313548	Otop1/Ptprj/Soga1	3	EPO
NFOL	Sirt2	BP	GO:0022411	cellular component disassembly	4/42	450/28564	0,00424	0,049674	0,0313548	Kif19a/Map1b/Mical3/Camsap2	4	EPO
NFOL	Sirt2	BP	GO:0048008	platelet-derived growth factor receptor signaling pathway	2/42	66/28564	0,00427	0,049674	0,0313548	Ptprj/Rapgef1	2	EPO
NFOL	Sirt2	BP	GO:0007015	actin filament organization	4/42	454/28564	0,00437	0,049674	0,0313548	Arhgap35/Rictor/Mical3/Arhgef10l	4	EPO
NFOL	Sirt2	BP	GO:0016055	Wnt signaling pathway	4/42	458/28564	0,00451	0,049703	0,031373	Tcf7l2/Cdk14/Rapgef1/Ptpro	4	EPO
NFOL	Sirt2	BP	GO:0048469	cell maturation	3/42	227/28564	0,00453	0,049703	0,031373	Sirt2/Nfasc/Bfsp2	3	EPO
NFOL	Sirt2	BP	GO:0031346	positive regulation of cell projection organization	4/42	459/28564	0,00455	0,049703	0,031373	Fyn/Map1b/Arhgap35/Rapgef1	4	EPO
NFOL	Sirt2	BP	GO:0198738	cell-cell signaling by wnt	4/42	460/28564	0,00458	0,049703	0,031373	Tcf7l2/Cdk14/Rapgef1/Ptpro	4	EPO

NFOL	Sirt2	CC	GO:0097386	glial cell projection	3/42	43/28585	3,5E-05	0,003345	0,0021002	Sirt2/Fyn/Nfasc	3	EPO
NFOL	Sirt2	CC	GO:0033010	paranodal junction	2/42	8/28585	5,9E-05	0,003345	0,0021002	Sirt2/Nfasc	2	EPO
NFOL	Sirt2	CC	GO:0033270	paranode region of axon	2/42	16/28585	0,00025	0,008176	0,0051339	Sirt2/Nfasc	2	EPO
NFOL	Sirt2	CC	GO:0044304	main axon	3/42	87/28585	0,00029	0,008176	0,0051339	Sirt2/Map1b/Nfasc	3	EPO
NFOL	Sirt2	CC	GO:0014069	postsynaptic density	5/42	442/28585	0,00046	0,010463	0,0065695	Fyn/Tmem108/Bcas1/Map1b/Ptpro	5	EPO
NFOL	Sirt2	CC	GO:0032279	asymmetric synapse	5/42	462/28585	0,00056	0,010657	0,0066914	Fyn/Tmem108/Bcas1/Map1b/Ptpro	5	EPO
NFOL	Sirt2	CC	GO:0099572	postsynaptic specialization	5/42	486/28585	0,0007	0,01141	0,0071639	Fyn/Tmem108/Bcas1/Map1b/Ptpro	5	EPO
NFOL	Sirt2	CC	GO:0015629	actin cytoskeleton	5/42	500/28585	0,0008	0,01141	0,0071639	Fyn/Epb41l2/Tns3/Arhgap35/Rinl	5	EPO
NFOL	Sirt2	CC	GO:0005874	microtubule	4/42	441/28585	0,00394	0,038599	0,0242355	Sirt2/Kif19a/Map1b/Camsap2	4	EPO
NFOL	Sirt2	CC	GO:0043209	myelin sheath	3/42	218/28585	0,00403	0,038599	0,0242355	Sirt2/Nfasc/Itpr2	3	EPO
NFOL	Sirt2	MF	GO:0030695	GTPase regulator activity	9/42	432/28171	1,2E-08	9,28E-07	5,177E-07	Dock4/Tns3/Arhgap35/Chn2/Rinl/Rapgef1/Arhgap5/Arhgef10l/Rasgef1b	9	EPO
NFOL	Sirt2	MF	GO:0060589	nucleoside-triphosphatase regulator activity	9/42	432/28171	1,2E-08	9,28E-07	5,177E-07	Dock4/Tns3/Arhgap35/Chn2/Rinl/Rapgef1/Arhgap5/Arhgef10l/Rasgef1b	9	EPO
NFOL	Sirt2	MF	GO:0005096	GTPase activator activity	6/42	241/28171	1,5E-06	7,52E-05	4,191E-05	Dock4/Arhgap35/Chn2/Rinl/Arhgap5/Arhgef10l	6	EPO
NFOL	Sirt2	MF	GO:0005085	guanyl-nucleotide exchange factor activity	5/42	203/28171	1,3E-05	0,000478	0,0002667	Dock4/Rinl/Rapgef1/Arhgef10l/Rasgef1b	5	EPO
NFOL	Sirt2	MF	GO:0015631	tubulin binding	6/42	388/28171	2,3E-05	0,000684	0,0003816	Sirt2/Fyn/Kif19a/Map1b/Camsap2/Ccs2	6	EPO
NFOL	Sirt2	MF	GO:0042578	phosphoric ester hydrolase activity	5/42	346/28171	0,00016	0,004003	0,0022322	Dusp15/Tns3/Enpp6/Ptprj/Ptpro	5	EPO
NFOL	Sirt2	MF	GO:0045295	gamma-catenin binding	2/42	15/28171	0,00023	0,004855	0,0027074	Tcf7l2/Ptprj	2	EPO
NFOL	Sirt2	MF	GO:0004725	protein tyrosine phosphatase activity	3/42	91/28171	0,00034	0,006449	0,0035966	Dusp15/Ptprj/Ptpro	3	EPO
NFOL	Sirt2	MF	GO:0016791	phosphatase activity	4/42	259/28171	0,00059	0,009961	0,0055554	Dusp15/Tns3/Ptprj/Ptpro	4	EPO

NFOL	Sirt2	MF	GO:0008017	microtubule binding	4/42	269/28171	0,00068	0,01033	0,0057607	Kif19a/Map1b/Camsap2/Ccser2	4	EPO
NFOL	Sirt2	MF	GO:0030507	spectrin binding	2/42	34/28171	0,00118	0,016212	0,0090414	Epb41l2/Camsap2	2	EPO
NFOL	Sirt2	MF	GO:0004721	phosphoprotein phosphatase activity	3/42	159/28171	0,00172	0,021686	0,0120938	Dusp15/Ptprrj/Ptpro	3	EPO
NFOL	Sirt2	MF	GO:0045296	cadherin binding	2/42	70/28171	0,00491	0,049472	0,0275901	Ptprrj/Ptpro	2	EPO
MOL1	Cd180	BP	GO:0002757	immune response-activating signaling pathway	3/6	391/28564	4,9E-05	0,004826	0,0013264	Cd180/Fyb/C3ar1	3	EPO
MOL1	Cd180	BP	GO:0002764	immune response-regulating signaling pathway	3/6	402/28564	5,4E-05	0,004826	0,0013264	Cd180/Fyb/C3ar1	3	EPO
MOL1	Cd180	BP	GO:0002253	activation of immune response	3/6	482/28564	9,2E-05	0,005517	0,0015164	Cd180/Fyb/C3ar1	3	EPO
MOL1	Cd180	BP	GO:0007229	integrin-mediated signaling pathway	2/6	102/28564	0,00019	0,008444	0,0023208	Fyb/Fgr	2	EPO
MOL1	Cd180	BP	GO:0002429	immune response-activating cell surface receptor signaling pathway	2/6	272/28564	0,00132	0,027278	0,0074976	Fyb/C3ar1	2	EPO
MOL1	Cd180	BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	2/6	283/28564	0,00143	0,027278	0,0074976	Fyb/C3ar1	2	EPO
MOL1	Cd180	BP	GO:0002366	leukocyte activation involved in immune response	2/6	317/28564	0,00179	0,027278	0,0074976	Cd180/Fgr	2	EPO
MOL1	Cd180	BP	GO:0002263	cell activation involved in immune response	2/6	321/28564	0,00183	0,027278	0,0074976	Cd180/Fgr	2	EPO
MOL1	Cd180	BP	GO:0045088	regulation of innate immune response	2/6	385/28564	0,00262	0,027278	0,0074976	Cd180/Fgr	2	EPO
MOL1	Cd180	BP	GO:0002831	regulation of response to biotic stimulus	2/6	485/28564	0,00412	0,033305	0,0091541	Cd180/Fgr	2	EPO
MOL1	Gm44129	BP	GO:0090394	negative regulation of excitatory postsynaptic potential	2/8	14/28564	6,2E-06	0,002663	0,0010108	Plk2/Npy2r	2	EPO
MOL1	Gm44129	BP	GO:0015850	organic hydroxy compound transport	3/8	306/28564	6,6E-05	0,009614	0,0036497	Ces1a/Npy2r/Xlr4a	3	EPO
MOL1	Gm44129	BP	GO:0014046	dopamine secretion	2/8	45/28564	6,8E-05	0,009614	0,0036497	Npy2r/Xlr4a	2	EPO
MOL1	Gm44129	BP	GO:0015872	dopamine transport	2/8	61/28564	0,00012	0,01135	0,0043091	Npy2r/Xlr4a	2	EPO
MOL1	Gm44129	BP	GO:0098815	modulation of excitatory postsynaptic potential	2/8	63/28564	0,00013	0,01135	0,0043091	Plk2/Npy2r	2	EPO
MOL1	Gm44129	BP	GO:0050432	catecholamine secretion	2/8	76/28564	0,00019	0,012123	0,0046023	Npy2r/Xlr4a	2	EPO
MOL1	Gm44129	BP	GO:0050805	negative regulation of synaptic transmission	2/8	77/28564	0,0002	0,012123	0,0046023	Plk2/Npy2r	2	EPO
MOL1	Gm44129	BP	GO:0051937	catecholamine transport	2/8	93/28564	0,00029	0,014352	0,0054486	Npy2r/Xlr4a	2	EPO
MOL1	Gm44129	BP	GO:0060079	excitatory postsynaptic potential	2/8	95/28564	0,0003	0,014352	0,0054486	Plk2/Npy2r	2	EPO
MOL1	Gm44129	BP	GO:0015844	monoamine transport	2/8	113/28564	0,00043	0,01749	0,0066398	Npy2r/Xlr4a	2	EPO
MOL1	Gm44129	BP	GO:0099565	chemical synaptic transmission, postsynaptic	2/8	116/28564	0,00045	0,01749	0,0066398	Plk2/Npy2r	2	EPO
MOL1	Gm44129	BP	GO:0060078	regulation of postsynaptic membrane potential	2/8	132/28564	0,00058	0,020736	0,007872	Plk2/Npy2r	2	EPO
MOL1	Gm44129	BP	GO:0031644	regulation of nervous system process	2/8	204/28564	0,00138	0,042137	0,0159968	Plk2/Npy2r	2	EPO
MOL1	Gm44129	MF	GO:0004674	protein serine/threonine kinase activity	2/7	442/28171	0,0049	0,009423	0,0005221	Plk2/Ankk1	2	EPO
MOL1	Mis18bp1	BP	GO:0090306	meiotic spindle assembly	2/16	10/28564	1,3E-05	0,002984	0,0017928	Ccnb2/Aspm	2	Placebo
MOL1	Mis18bp1	BP	GO:0045132	meiotic chromosome segregation	3/16	116/28564	3,5E-05	0,003768	0,0022642	Ccnb2/Ankle1/Aspm	3	Placebo
MOL1	Mis18bp1	BP	GO:0000212	meiotic spindle organization	2/16	19/28564	5E-05	0,003768	0,0022642	Ccnb2/Aspm	2	Placebo
MOL1	Mis18bp1	BP	GO:0007059	chromosome segregation	4/16	429/28564	7,9E-05	0,004471	0,0026865	Ska1/Ccnb2/Ankle1/Aspm	4	Placebo
MOL1	Mis18bp1	BP	GO:0000280	nuclear division	4/16	456/28564	0,0001	0,004528	0,0027208	Ccnb2/Ankle1/Kif20b/Aspm	4	Placebo

MOL1	Mis18bp1	BP	GO:0140013	meiotic nuclear division	3/16	210/28564	0,0002	0,006786	0,0040773	Ccnb2/Ankle1/Aspm	3	Placebo
MOL1	Mis18bp1	BP	GO:0061351	neural precursor cell proliferation	3/16	212/28564	0,00021	0,006786	0,0040773	Shcbp1/Melk/Aspm	3	Placebo
MOL1	Mis18bp1	BP	GO:1903046	meiotic cell cycle process	3/16	229/28564	0,00026	0,007448	0,0044753	Ccnb2/Ankle1/Aspm	3	Placebo
MOL1	Mis18bp1	BP	GO:0098813	nuclear chromosome segregation	3/16	338/28564	0,00082	0,018697	0,0112338	Ccnb2/Ankle1/Aspm	3	Placebo
MOL1	Mis18bp1	BP	GO:0051321	meiotic cell cycle	3/16	339/28564	0,00083	0,018697	0,0112338	Ccnb2/Ankle1/Aspm	3	Placebo
MOL1	Mis18bp1	BP	GO:0051225	spindle assembly	2/16	123/28564	0,00212	0,03011	0,018091	Ccnb2/Aspm	2	Placebo
MOL1	Mis18bp1	BP	GO:2000177	regulation of neural precursor cell proliferation	2/16	126/28564	0,00222	0,03011	0,018091	Shcbp1/Aspm	2	Placebo
MOL1	Mis18bp1	BP	GO:0007127	meiosis I	2/16	133/28564	0,00247	0,03011	0,018091	Ccnb2/Ankle1	2	Placebo
MOL1	Mis18bp1	BP	GO:0061982	meiosis I cell cycle process	2/16	136/28564	0,00258	0,03011	0,018091	Ccnb2/Ankle1	2	Placebo
MOL1	Mis18bp1	BP	GO:0007292	female gamete generation	2/16	174/28564	0,00419	0,033785	0,0202992	Ccnb2/Aspm	2	Placebo
MOL1	Mis18bp1	BP	GO:0051302	regulation of cell division	2/16	182/28564	0,00457	0,035604	0,0213925	Kif20b/Aspm	2	Placebo
MOL1	Mis18bp1	BP	GO:0007051	spindle organization	2/16	189/28564	0,00492	0,036676	0,0220361	Ccnb2/Aspm	2	Placebo
MOL1	Mis18bp1	BP	GO:0001764	neuron migration	2/16	204/28564	0,0057	0,039053	0,0234643	Kif20b/Aspm	2	Placebo
MOL1	Mis18bp1	CC	GO:0005819	spindle	4/17	357/28585	5E-05	0,001652	0,0006851	Ska1/Hmmr/Kif20b/Aspm	4	Placebo
MOL1	Mis18bp1	CC	GO:0072686	mitotic spindle	3/17	177/28585	0,00015	0,002457	0,0010188	Ska1/Kif20b/Aspm	3	Placebo
MOL1	Mis18bp1	CC	GO:0097431	mitotic spindle pole	2/17	39/28585	0,00024	0,002679	0,0011107	Kif20b/Aspm	2	Placebo
MOL1	Mis18bp1	CC	GO:0045171	intercellular bridge	2/17	98/28585	0,00153	0,012623	0,0052343	Ska1/Kif20b	2	Placebo
MOL1	Mis18bp1	CC	GO:0005874	microtubule	3/17	441/28585	0,00211	0,013935	0,0057784	Ska1/Kif20b/Aspm	3	Placebo
MOL1	Mis18bp1	CC	GO:0000922	spindle pole	2/17	144/28585	0,00326	0,016798	0,0069659	Kif20b/Aspm	2	Placebo
MOL1	Mis18bp1	CC	GO:0030496	midbody	2/17	201/28585	0,00624	0,02562	0,0106241	Kif20b/Aspm	2	Placebo
MOL1	Mis18bp1	CC	GO:0000775	chromosome, centromeric region	2/17	258/28585	0,01009	0,02562	0,0106241	Mis18bp1/Ska1	2	Placebo
MOL1	Mis18bp1	CC	GO:0098687	chromosomal region	2/17	367/28585	0,01969	0,04536	0,0188096	Mis18bp1/Ska1	2	Placebo
MOL1	Slco1a4	BP	GO:1903671	negative regulation of sprouting angiogenesis	2/21	14/28564	4,7E-05	0,008698	0,004622	Flt1/Klf2	2	EPO
MOL1	Slco1a4	BP	GO:0045765	regulation of angiogenesis	4/21	305/28564	6,6E-05	0,008698	0,004622	Flt1/Klf2/Cldn5/Prok1	4	EPO
MOL1	Slco1a4	BP	GO:0016525	negative regulation of angiogenesis	3/21	108/28564	6,7E-05	0,008698	0,004622	Flt1/Klf2/Cldn5	3	EPO
MOL1	Slco1a4	BP	GO:1901342	regulation of vasculature development	4/21	309/28564	7E-05	0,008698	0,004622	Flt1/Klf2/Cldn5/Prok1	4	EPO
MOL1	Slco1a4	BP	GO:2000181	negative regulation of blood vessel morphogenesis	3/21	110/28564	7E-05	0,008698	0,004622	Flt1/Klf2/Cldn5	3	EPO
MOL1	Slco1a4	BP	GO:1901343	negative regulation of vasculature development	3/21	111/28564	7,2E-05	0,008698	0,004622	Flt1/Klf2/Cldn5	3	EPO
MOL1	Slco1a4	BP	GO:0060033	anatomical structure regression	2/21	19/28564	8,7E-05	0,009024	0,0047953	Flt1/Lef1	2	EPO
MOL1	Slco1a4	BP	GO:0002040	sprouting angiogenesis	3/21	128/28564	0,00011	0,009959	0,0052923	Flt1/Klf2/Lef1	3	EPO
MOL1	Slco1a4	BP	GO:0001936	regulation of endothelial cell proliferation	3/21	154/28564	0,00019	0,014404	0,0076544	Flt1/Egfl7/Prok1	3	EPO
MOL1	Slco1a4	BP	GO:1905562	regulation of vascular endothelial cell proliferation	2/21	29/28564	0,00021	0,014404	0,0076544	Flt1/Prok1	2	EPO

MOL1	Slco1a4	BP	GO:0101023	vascular endothelial cell proliferation	2/21	30/28564	0,00022	0,014404	0,0076544	Flt1/Prok1	2	EPO
MOL1	Slco1a4	BP	GO:0050678	regulation of epithelial cell proliferation	4/21	427/28564	0,00024	0,014404	0,0076544	Flt1/Egfl7/Prok1/Sgpp2	4	EPO
MOL1	Slco1a4	BP	GO:0001935	endothelial cell proliferation	3/21	171/28564	0,00026	0,014404	0,0076544	Flt1/Egfl7/Prok1	3	EPO
MOL1	Slco1a4	BP	GO:0030099	myeloid cell differentiation	4/21	482/28564	0,00038	0,019705	0,0104714	Klf2/Lef1/Clec2d/Fli1	4	EPO
MOL1	Slco1a4	BP	GO:1903670	regulation of sprouting angiogenesis	2/21	41/28564	0,00041	0,019998	0,010627	Flt1/Klf2	2	EPO
MOL1	Slco1a4	BP	GO:0001569	branching involved in blood vessel morphogenesis	2/21	45/28564	0,0005	0,022594	0,0120069	Flt1/Lef1	2	EPO
MOL1	Slco1a4	BP	GO:0003018	vascular process in circulatory system	3/21	240/28564	0,0007	0,029626	0,0157437	Klf2/Cldn5/Sod3	3	EPO
MOL1	Slco1a4	BP	GO:0030522	intracellular receptor signaling pathway	3/21	261/28564	0,00089	0,035667	0,0189541	Flt1/Klf2/Rsad2	3	EPO
MOL1	Slco1a4	BP	GO:0001818	negative regulation of cytokine production	3/21	296/28564	0,00128	0,048547	0,0257984	Flt1/Klf2/Lef1	3	EPO
MOL1	Slco1a4	MF	GO:0008013	beta-catenin binding	2/21	99/28171	0,00246	0,038635	0,0138866	Lef1/Sox17	2	EPO
MOL1	Slco1a4	MF	GO:0005319	lipid transporter activity	2/21	176/28171	0,00754	0,038635	0,0138866	Slco1a4/Pltp	2	EPO
MOL2	Mir142hg	BP	GO:0002443	leukocyte mediated immunity	4/11	480/28564	2,4E-05	0,010791	0,004459	Csf2rb/Fgr/Ripk3/Prkcd	4	Placebo
MOL2	Mir142hg	BP	GO:0046777	protein autophosphorylation	3/11	242/28564	9,4E-05	0,021489	0,0088792	Fgr/Ripk3/Prkcd	3	Placebo
MOL2	Mir142hg	BP	GO:0035306	positive regulation of dephosphorylation	2/11	60/28564	0,00024	0,022897	0,0094611	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0002449	lymphocyte mediated immunity	3/11	372/28564	0,00033	0,022897	0,0094611	Csf2rb/Ripk3/Prkcd	3	Placebo
MOL2	Mir142hg	BP	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3/11	373/28564	0,00034	0,022897	0,0094611	Csf2rb/Ripk3/Prkcd	3	Placebo
MOL2	Mir142hg	BP	GO:0042742	defense response to bacterium	3/11	386/28564	0,00037	0,022897	0,0094611	Lyz1/Fgr/Prkcd	3	Placebo
MOL2	Mir142hg	BP	GO:2000379	positive regulation of reactive oxygen species metabolic process	2/11	78/28564	0,0004	0,022897	0,0094611	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0070661	leukocyte proliferation	3/11	396/28564	0,0004	0,022897	0,0094611	Csf2rb/Ripk3/Prkcd	3	Placebo
MOL2	Mir142hg	BP	GO:0033674	positive regulation of kinase activity	3/11	440/28564	0,00055	0,024559	0,0101479	Fgr/Ripk3/Prkcd	3	Placebo
MOL2	Mir142hg	BP	GO:0070301	cellular response to hydrogen peroxide	2/11	93/28564	0,00057	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0032147	activation of protein kinase activity	2/11	105/28564	0,00072	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0042542	response to hydrogen peroxide	2/11	120/28564	0,00094	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0035303	regulation of dephosphorylation	2/11	128/28564	0,00107	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0001776	leukocyte homeostasis	2/11	136/28564	0,0012	0,024559	0,0101479	Mir142hg/Ripk3	2	Placebo
MOL2	Mir142hg	BP	GO:0034614	cellular response to reactive oxygen species	2/11	146/28564	0,00138	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:2000377	regulation of reactive oxygen species metabolic process	2/11	161/28564	0,00168	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0016064	immunoglobulin mediated immune response	2/11	165/28564	0,00176	0,024559	0,0101479	Csf2rb/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0019724	B cell mediated immunity	2/11	168/28564	0,00183	0,024559	0,0101479	Csf2rb/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:2001235	positive regulation of apoptotic signaling pathway	2/11	172/28564	0,00191	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0050830	defense response to Gram-positive bacterium	2/11	176/28564	0,002	0,024559	0,0101479	Lyz1/Fgr	2	Placebo
MOL2	Mir142hg	BP	GO:0045834	positive regulation of lipid metabolic process	2/11	185/28564	0,00221	0,024559	0,0101479	Fgr/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0000302	response to reactive oxygen species	2/11	191/28564	0,00235	0,024559	0,0101479	Ripk3/Prkcd	2	Placebo

MOL2	Mir142hg	BP	GO:0050866	negative regulation of cell activation	2/11	227/28564	0,0033	0,026304	0,0108689	Fgr/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0044242	cellular lipid catabolic process	2/11	230/28564	0,00338	0,026304	0,0108689	Bco1/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0072593	reactive oxygen species metabolic process	2/11	249/28564	0,00395	0,028382	0,0117274	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0001906	cell killing	2/11	250/28564	0,00398	0,028382	0,0117274	Lyz1/Ripk3	2	Placebo
MOL2	Mir142hg	BP	GO:0002274	myeloid leukocyte activation	2/11	264/28564	0,00443	0,030607	0,0126468	Fgr/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0034599	cellular response to oxidative stress	2/11	276/28564	0,00483	0,031856	0,0131629	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0070663	regulation of leukocyte proliferation	2/11	287/28564	0,00521	0,031856	0,0131629	Csf2rb/Ripk3	2	Placebo
MOL2	Mir142hg	BP	GO:0002703	regulation of leukocyte mediated immunity	2/11	310/28564	0,00605	0,033763	0,013951	Fgr/Ripk3	2	Placebo
MOL2	Mir142hg	BP	GO:0018108	peptidyl-tyrosine phosphorylation	2/11	326/28564	0,00667	0,036221	0,0149668	Fgr/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0018212	peptidyl-tyrosine modification	2/11	328/28564	0,00675	0,036221	0,0149668	Fgr/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0016042	lipid catabolic process	2/11	342/28564	0,00732	0,036281	0,0149914	Bco1/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0016311	dephosphorylation	2/11	342/28564	0,00732	0,036281	0,0149914	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0062197	cellular response to chemical stress	2/11	347/28564	0,00753	0,036847	0,0152253	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0046651	lymphocyte proliferation	2/11	354/28564	0,00782	0,037162	0,0153554	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0032943	mononuclear cell proliferation	2/11	360/28564	0,00808	0,03799	0,0156976	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0032956	regulation of actin cytoskeleton organization	2/11	362/28564	0,00817	0,038006	0,0157041	Fgr/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0045860	positive regulation of protein kinase activity	2/11	373/28564	0,00865	0,039065	0,0161418	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0048872	homeostasis of number of cells	2/11	391/28564	0,00947	0,040479	0,0167261	Mir142hg/Ripk3	2	Placebo
MOL2	Mir142hg	BP	GO:0019216	regulation of lipid metabolic process	2/11	393/28564	0,00957	0,040479	0,0167261	Fgr/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0006979	response to oxidative stress	2/11	408/28564	0,01028	0,042442	0,0175373	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0032970	regulation of actin filament-based process	2/11	411/28564	0,01042	0,042442	0,0175373	Fgr/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:2001233	regulation of apoptotic signaling pathway	2/11	424/28564	0,01106	0,042946	0,0177456	Ripk3/Prkcd	2	Placebo
MOL2	Mir142hg	BP	GO:0002697	regulation of immune effector process	2/11	472/28564	0,01358	0,048332	0,0199711	Fgr/Ripk3	2	Placebo
MOL2	Mir142hg	MF	GO:0004715	non-membrane spanning protein tyrosine kinase activity	2/10	45/28171	0,00011	0,003675	0,0004689	Fgr/Prkcd	2	Placebo
MOL2	Mir142hg	MF	GO:0004713	protein tyrosine kinase activity	2/10	132/28171	0,00096	0,008783	0,0011206	Fgr/Prkcd	2	Placebo
MOL2	Mir142hg	MF	GO:0004674	protein serine/threonine kinase activity	2/10	442/28171	0,01017	0,018643	0,0023787	Ripk3/Prkcd	2	Placebo
MOL2	Nfasc	BP	GO:1990138	neuron projection extension	8/44	209/28564	1E-09	1,39E-06	8,53E-07	Sema4d/Auts2/Map1b/Prickle1/Tmem108/Sema6a/Sema4a/Smurf1	8	EPO
MOL2	Nfasc	BP	GO:0007409	axonogenesis	10/44	498/28564	3,5E-09	2,37E-06	1,453E-06	Nfasc/Sema4d/Auts2/Map1b/Prickle1/Ank3/Mbp/Sema6a/Sema4a/Smurf1	10	EPO
MOL2	Nfasc	BP	GO:0048588	developmental cell growth	8/44	287/28564	1,2E-08	4,53E-06	2,779E-06	Sema4d/Auts2/Map1b/Prickle1/Tmem108/Sema6a/Sema4a/Smurf1	8	EPO

MOL2	Nfasc	BP	GO:0060560	developmental growth involved in morphogenesis	8/44	290/28564	1,3E-08	4,53E-06	2,779E-06	Sema4d/Auts2/Map1b/Prickle1/Tmem108/Sema6a/Sema4a/Smurf1	8	EPO
MOL2	Nfasc	BP	GO:0048675	axon extension	6/44	144/28564	8,9E-08	2,44E-05	1,497E-05	Sema4d/Auts2/Map1b/Sema6a/Sema4a/Smurf1	6	EPO
MOL2	Nfasc	BP	GO:0022411	cellular component disassembly	8/44	450/28564	3,8E-07	8,15E-05	5,004E-05	Mical3/Nckap5/Map1b/Kif19a/Prickle1/Map4k4/Smurf1/Sh3gl3	8	EPO
MOL2	Nfasc	BP	GO:0050770	regulation of axonogenesis	6/44	187/28564	4,2E-07	8,15E-05	5,004E-05	Sema4d/Map1b/Mbp/Sema6a/Sema4a/Smurf1	6	EPO
MOL2	Nfasc	BP	GO:0050767	regulation of neurogenesis	8/44	480/28564	6,3E-07	0,000107	6,566E-05	Sema4d/Map1b/Sirt2/Tnik/Mbp/Sema6a/Sema4a/Smurf1	8	EPO
MOL2	Nfasc	BP	GO:0030516	regulation of axon extension	5/44	114/28564	8,9E-07	0,000135	8,298E-05	Sema4d/Map1b/Sema6a/Sema4a/Smurf1	5	EPO
MOL2	Nfasc	BP	GO:0007163	establishment or maintenance of cell polarity	6/44	228/28564	1,3E-06	0,000168	0,0001029	Frmd4a/Parvb/Map1b/Prickle1/Ank3/Rictor	6	EPO
MOL2	Nfasc	BP	GO:0051261	protein depolymerization	5/44	124/28564	1,3E-06	0,000168	0,0001029	Mical3/Nckap5/Map1b/Kif19a/Sh3gl3	5	EPO
MOL2	Nfasc	BP	GO:0061387	regulation of extent of cell growth	5/44	129/28564	1,6E-06	0,000187	0,0001147	Sema4d/Map1b/Sema6a/Sema4a/Smurf1	5	EPO
MOL2	Nfasc	BP	GO:0050771	negative regulation of axonogenesis	4/44	70/28564	4,2E-06	0,000439	0,0002693	Sema4d/Mbp/Sema6a/Sema4a	4	EPO
MOL2	Nfasc	BP	GO:0010977	negative regulation of neuron projection development	5/44	165/28564	5,5E-06	0,000535	0,0003287	Sema4d/Map4k4/Mbp/Sema6a/Sema4a	5	EPO
MOL2	Nfasc	BP	GO:0050768	negative regulation of neurogenesis	5/44	173/28564	6,9E-06	0,000629	0,0003863	Sema4d/Sirt2/Mbp/Sema6a/Sema4a	5	EPO
MOL2	Nfasc	BP	GO:0051961	negative regulation of nervous system development	5/44	178/28564	7,9E-06	0,000677	0,0004159	Sema4d/Sirt2/Mbp/Sema6a/Sema4a	5	EPO
MOL2	Nfasc	BP	GO:0048843	negative regulation of axon extension involved in axon guidance	3/44	27/28564	9,7E-06	0,000782	0,0004803	Sema4d/Sema6a/Sema4a	3	EPO

MOL2	Nfasc	BP	GO:1905702	regulation of inhibitory synapse assembly	2/44	4/28564	1,4E-05	0,001055	0,000648	Sema4d/Sema4a Abr/Sema4d/Map4k	2	EPO
MOL2	Nfasc	BP	GO:0043087	regulation of GTPase activity	6/44	353/28564	1,6E-05	0,001168	0,000717	4/Tns3/Rictor/Dock 6	6	EPO
MOL2	Nfasc	BP	GO:0048841	regulation of axon extension involved in axon guidance	3/44	33/28564	1,8E-05	0,001232	0,0007566	Sema4d/Sema6a/Se ma4a	3	EPO
MOL2	Nfasc	BP	GO:0008361	regulation of cell size	5/44	218/28564	2,1E-05	0,00134	0,0008226	Sema4d/Map1b/Se ma6a/Sema4a/Smu rf1	5	EPO
MOL2	Nfasc	BP	GO:0031345	negative regulation of cell projection organization	5/44	219/28564	2,2E-05	0,00134	0,0008226	Sema4d/Map4k4/M bp/Sema6a/Sema4a	5	EPO
MOL2	Nfasc	BP	GO:0048846	axon extension involved in axon guidance	3/44	37/28564	2,6E-05	0,001456	0,000894	Sema4d/Sema6a/Se ma4a	3	EPO
MOL2	Nfasc	BP	GO:1902284	neuron projection extension involved in neuron projection guidance	3/44	37/28564	2,6E-05	0,001456	0,000894	Sema4d/Sema6a/Se ma4a	3	EPO
MOL2	Nfasc	BP	GO:0031532	actin cytoskeleton reorganization	4/44	117/28564	3,2E-05	0,001712	0,0010514	Auts2/Parvb/Tnik/Ri ctor	4	EPO
MOL2	Nfasc	BP	GO:0032984	protein-containing complex disassembly	5/44	240/28564	3,3E-05	0,001712	0,0010514	Mical3/Nckap5/Ma p1b/Kif19a/Sh3gl3	5	EPO
MOL2	Nfasc	BP	GO:0032535	regulation of cellular component size	6/44	404/28564	3,5E-05	0,001712	0,0010514	Sema4d/Map1b/Ric tor/Sema6a/Sema4 a/Smurf1	6	EPO
MOL2	Nfasc	BP	GO:0048638	regulation of developmental growth	6/44	405/28564	3,5E-05	0,001712	0,0010514	Sema4d/Tcf7l2/Ma p1b/Sema6a/Sema4 a/Smurf1	6	EPO
MOL2	Nfasc	BP	GO:0050919	negative chemotaxis	3/44	43/28564	4E-05	0,001869	0,0011479	Sema4d/Sema6a/Se ma4a	3	EPO
MOL2	Nfasc	BP	GO:0007411	axon guidance	5/44	253/28564	4,3E-05	0,001869	0,0011479	Nfasc/Sema4d/Ank 3/Sema6a/Sema4a	5	EPO
MOL2	Nfasc	BP	GO:0097484	dendrite extension	3/44	44/28564	4,3E-05	0,001869	0,0011479	Auts2/Tmem108/S murf1	3	EPO
MOL2	Nfasc	BP	GO:0097485	neuron projection guidance	5/44	254/28564	4,4E-05	0,001869	0,0011479	Nfasc/Sema4d/Ank 3/Sema6a/Sema4a	5	EPO
MOL2	Nfasc	BP	GO:0048640	negative regulation of developmental growth	4/44	129/28564	4,7E-05	0,001942	0,0011926	Sema4d/Tcf7l2/Sem a6a/Sema4a	4	EPO
MOL2	Nfasc	BP	GO:0045162	clustering of voltage-gated sodium channels	2/44	7/28564	4,8E-05	0,00195	0,0011973	Nfasc/Ank3	2	EPO
MOL2	Nfasc	BP	GO:0030517	negative regulation of axon extension	3/44	48/28564	5,6E-05	0,002196	0,0013486	Sema4d/Sema6a/Se ma4a	3	EPO

MOL2	Nfasc	BP	GO:0071526	semaphorin-plexin signaling pathway	3/44	50/28564	6,4E-05	0,002324	0,0014269	Sema4d/Sema6a/Sema4a	3	EPO
MOL2	Nfasc	BP	GO:0120180	cell-substrate junction disassembly	2/44	8/28564	6,5E-05	0,002324	0,0014269	Prickle1/Map4k4	2	EPO
MOL2	Nfasc	BP	GO:0120181	focal adhesion disassembly	2/44	8/28564	6,5E-05	0,002324	0,0014269	Prickle1/Map4k4	2	EPO
MOL2	Nfasc	BP	GO:0022604	regulation of cell morphogenesis	5/44	278/28564	6,7E-05	0,002352	0,0014444	Sema4d/Parvb/Tnik/Sema4a/Smurf1	5	EPO
MOL2	Nfasc	BP	GO:0001558	regulation of cell growth	6/44	464/28564	7,4E-05	0,002546	0,0015632	Sema4d/Map1b/Rictor/Sema6a/Sema4a/Smurf1	6	EPO
MOL2	Nfasc	BP	GO:0001667	ameboidal-type cell migration	6/44	470/28564	8E-05	0,002665	0,0016367	Sema4d/Pik3r3/Map4k4/Tns3/Sema6a/Sema4a	6	EPO
MOL2	Nfasc	BP	GO:0007019	microtubule depolymerization	3/44	55/28564	8,5E-05	0,002755	0,0016919	Nckap5/Map1b/Kif19a	3	EPO
MOL2	Nfasc	BP	GO:0048713	regulation of oligodendrocyte differentiation	3/44	57/28564	9,4E-05	0,002995	0,0018391	Tcf7l2/Sirt2/Dusp15	3	EPO
MOL2	Nfasc	BP	GO:0050922	negative regulation of chemotaxis	3/44	58/28564	9,9E-05	0,003083	0,0018933	Sema4d/Sema6a/Sema4a	3	EPO
MOL2	Nfasc	BP	GO:0071695	anatomical structure maturation	5/44	305/28564	0,0001	0,003153	0,0019359	Nfasc/Sema4d/Bfsp2/Sirt2/Ank3	5	EPO
MOL2	Nfasc	BP	GO:0060485	mesenchyme development	5/44	310/28564	0,00011	0,003328	0,0020436	Sema4d/Tcf7l2/Prickle1/Sema6a/Sema4a	5	EPO
MOL2	Nfasc	BP	GO:0030010	establishment of cell polarity	4/44	163/28564	0,00012	0,00338	0,0020753	Frmd4a/Map1b/Prickle1/Rictor	4	EPO
MOL2	Nfasc	BP	GO:0045599	negative regulation of fat cell differentiation	3/44	62/28564	0,00012	0,003405	0,002091	Tcf7l2/Sirt2/Ncor2	3	EPO
MOL2	Nfasc	BP	GO:0010721	negative regulation of cell development	5/44	318/28564	0,00013	0,003405	0,002091	Sema4d/Sirt2/Mbp/Sema6a/Sema4a	5	EPO
MOL2	Nfasc	BP	GO:0099612	protein localization to axon	2/44	11/28564	0,00013	0,003405	0,002091	Nfasc/Ank3	2	EPO
MOL2	Nfasc	BP	GO:0001755	neural crest cell migration	3/44	63/28564	0,00013	0,003405	0,002091	Sema4d/Sema6a/Sema4a	3	EPO
MOL2	Nfasc	BP	GO:0090497	mesenchymal cell migration	3/44	65/28564	0,00014	0,003666	0,0022509	Sema4d/Sema6a/Sema4a	3	EPO
MOL2	Nfasc	BP	GO:0035022	positive regulation of Rac protein signal transduction	2/44	12/28564	0,00015	0,003912	0,0024021	Auts2/Tns3	2	EPO
MOL2	Nfasc	BP	GO:0042552	myelination	4/44	180/28564	0,00017	0,004307	0,0026449	Nfasc/Tcf7l2/Sirt2/Mbp	4	EPO
MOL2	Nfasc	BP	GO:0007272	ensheathment of neurons	4/44	183/28564	0,00018	0,004425	0,0027172	Nfasc/Tcf7l2/Sirt2/Mbp	4	EPO

MOL2	Nfasc	BP	GO:0008366	axon ensheathment	4/44	183/28564	0,00018	0,004425	0,0027172	Nfasc/Tcf7l2/Sirt2/Mbp	4	EPO
MOL2	Nfasc	BP	GO:0030032	lamellipodium assembly	3/44	73/28564	0,0002	0,00464	0,0028489	Auts2/Parvb/Abli2	3	EPO
MOL2	Nfasc	BP	GO:0046579	positive regulation of Ras protein signal transduction	3/44	73/28564	0,0002	0,00464	0,0028489	Auts2/Map4k4/Tns3	3	EPO
MOL2	Nfasc	BP	GO:0045161	neuronal ion channel clustering	2/44	14/28564	0,00021	0,004836	0,0029693	Nfasc/Ank3	2	EPO
MOL2	Nfasc	BP	GO:0051057	positive regulation of small GTPase mediated signal transduction	3/44	80/28564	0,00026	0,00588	0,0036106	Auts2/Map4k4/Tns3	3	EPO
MOL2	Nfasc	BP	GO:0051962	positive regulation of nervous system development	5/44	379/28564	0,00028	0,006376	0,0039149	Sema4d/Map1b/Tnfr/Sema4a/Smurf1	5	EPO
MOL2	Nfasc	BP	GO:0021700	developmental maturation	5/44	381/28564	0,00029	0,006426	0,003946	Nfasc/Sema4d/Bfsp2/Sirt2/Ank3	5	EPO
MOL2	Nfasc	BP	GO:0043491	protein kinase B signaling	4/44	209/28564	0,0003	0,006527	0,004008	Tcf7l2/Sirt2/Pik3r3/Rictor	4	EPO
MOL2	Nfasc	BP	GO:0030307	positive regulation of cell growth	4/44	210/28564	0,00031	0,006541	0,0040162	Sema4d/Map1b/Rictor/Smurf1	4	EPO
MOL2	Nfasc	BP	GO:2000651	positive regulation of sodium ion transmembrane transporter activity	2/44	17/28564	0,00031	0,006541	0,0040162	Cnksr3/Ank3	2	EPO
MOL2	Nfasc	BP	GO:0030705	cytoskeleton-dependent intracellular transport	4/44	213/28564	0,00032	0,006695	0,004111	Map1b/Prickle1/Ank3/Tmem108	4	EPO
MOL2	Nfasc	BP	GO:1904862	inhibitory synapse assembly	2/44	18/28564	0,00035	0,007103	0,0043613	Sema4d/Sema4a	2	EPO
MOL2	Nfasc	BP	GO:0014032	neural crest cell development	3/44	89/28564	0,00035	0,007103	0,0043613	Sema4d/Sema6a/Sema4a	3	EPO
MOL2	Nfasc	BP	GO:0097581	lamellipodium organization	3/44	91/28564	0,00038	0,007472	0,004588	Auts2/Parvb/Abli2	3	EPO
MOL2	Nfasc	BP	GO:0048469	cell maturation	4/44	227/28564	0,00041	0,008031	0,0049313	Nfasc/Bfsp2/Sirt2/Ank3	4	EPO
MOL2	Nfasc	BP	GO:0045685	regulation of glial cell differentiation	3/44	97/28564	0,00045	0,008756	0,0053766	Tcf7l2/Sirt2/Dusp15	3	EPO
MOL2	Nfasc	BP	GO:0048864	stem cell development	3/44	99/28564	0,00048	0,009166	0,0056282	Sema4d/Sema6a/Sema4a	3	EPO
MOL2	Nfasc	BP	GO:0032102	negative regulation of response to external stimulus	5/44	429/28564	0,0005	0,009329	0,0057284	Abr/Sema4d/Sirt2/Sema6a/Sema4a	5	EPO
MOL2	Nfasc	BP	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	5/44	430/28564	0,00051	0,009329	0,0057284	Prickle1/Sirt2/Rnf122/Peli1/Smurf1	5	EPO
MOL2	Nfasc	BP	GO:0019226	transmission of nerve impulse	3/44	101/28564	0,00051	0,009329	0,0057284	Nfasc/Grik2/Ank3	3	EPO
MOL2	Nfasc	BP	GO:0014033	neural crest cell differentiation	3/44	102/28564	0,00053	0,009352	0,0057425	Sema4d/Sema6a/Sema4a	3	EPO

MOL2	Nfasc	BP	GO:0050772	positive regulation of axonogenesis	3/44	102/28564	0,00053	0,009352	0,0057425	Sema4d/Map1b/Smurf1	3	EPO
MOL2	Nfasc	BP	GO:1902307	positive regulation of sodium ion transmembrane transport	2/44	23/28564	0,00057	0,009946	0,0061074	Cnksr3/Ank3	2	EPO
MOL2	Nfasc	BP	GO:0048762	mesenchymal cell differentiation	4/44	249/28564	0,00058	0,009946	0,0061074	Sema4d/Tcf7l2/Sema6a/Sema4a	4	EPO
MOL2	Nfasc	BP	GO:0090288	negative regulation of cellular response to growth factor stimulus	3/44	106/28564	0,00059	0,009946	0,0061074	Tcf7l2/Sema6a/Smurf1	3	EPO
MOL2	Nfasc	BP	GO:2000060	positive regulation of ubiquitin-dependent protein catabolic process	3/44	106/28564	0,00059	0,009946	0,0061074	Prickle1/Sirt2/Smurf1	3	EPO
MOL2	Nfasc	BP	GO:0043547	positive regulation of GTPase activity	4/44	259/28564	0,00067	0,011199	0,0068766	Abr/Sema4d/Map4k4/Dock6	4	EPO
MOL2	Nfasc	BP	GO:0031346	positive regulation of cell projection organization	5/44	459/28564	0,00068	0,011199	0,0068766	Sema4d/Auts2/Map1b/Tnik/Smurf1	5	EPO
MOL2	Nfasc	BP	GO:0150146	cell junction disassembly	2/44	26/28564	0,00074	0,011989	0,0073616	Prickle1/Map4k4	2	EPO
MOL2	Nfasc	BP	GO:0045926	negative regulation of growth	4/44	267/28564	0,00076	0,012155	0,0074633	Sema4d/Tcf7l2/Sema6a/Sema4a	4	EPO
MOL2	Nfasc	BP	GO:0035020	regulation of Rac protein signal transduction	2/44	28/28564	0,00085	0,013593	0,0083466	Auts2/Tns3	2	EPO
MOL2	Nfasc	BP	GO:0001894	tissue homeostasis	4/44	278/28564	0,00088	0,013618	0,0083618	Prom1/Prickle1/Tns3/Mbp	4	EPO
MOL2	Nfasc	BP	GO:0060249	anatomical structure homeostasis	4/44	278/28564	0,00088	0,013618	0,0083618	Prom1/Prickle1/Tns3/Mbp	4	EPO
MOL2	Nfasc	BP	GO:0048709	oligodendrocyte differentiation	3/44	122/28564	0,00089	0,013618	0,0083618	Tcf7l2/Sirt2/Dusp15	3	EPO
MOL2	Nfasc	BP	GO:0048863	stem cell differentiation	4/44	286/28564	0,00097	0,014818	0,0090987	Sema4d/Prickle1/Sema6a/Sema4a	4	EPO
MOL2	Nfasc	BP	GO:1901890	positive regulation of cell junction assembly	3/44	127/28564	0,001	0,014958	0,009185	Sema4d/Map4k4/Sema4a	3	EPO
MOL2	Nfasc	BP	GO:0001578	microtubule bundle formation	3/44	131/28564	0,00109	0,015836	0,0097242	Nckap5/Map1b/Ccser2	3	EPO
MOL2	Nfasc	BP	GO:0031109	microtubule polymerization or depolymerization	3/44	131/28564	0,00109	0,015836	0,0097242	Nckap5/Map1b/Kif19a	3	EPO
MOL2	Nfasc	BP	GO:1903052	positive regulation of proteolysis involved in protein catabolic process	3/44	131/28564	0,00109	0,015836	0,0097242	Prickle1/Sirt2/Smurf1	3	EPO
MOL2	Nfasc	BP	GO:0008360	regulation of cell shape	3/44	141/28564	0,00134	0,019363	0,0118895	Sema4d/Parvb/Sema4a	3	EPO
MOL2	Nfasc	BP	GO:0007162	negative regulation of cell adhesion	4/44	318/28564	0,00144	0,020321	0,0124777	Sema4d/Mbp/Peli1/Sema6a	4	EPO
MOL2	Nfasc	BP	GO:0050769	positive regulation of neurogenesis	4/44	318/28564	0,00144	0,020321	0,0124777	Sema4d/Map1b/Tnik/Smurf1	4	EPO

MOL2	Nfasc	BP	GO:0090287	regulation of cellular response to growth factor stimulus	4/44	320/28564	0,00147	0,020581	0,0126373	Tcf7l2/Tmem108/Sema6a/Smurf1	4	EPO
MOL2	Nfasc	BP	GO:0045927	positive regulation of growth	4/44	323/28564	0,00153	0,021081	0,0129443	Sema4d/Map1b/Rictor/Smurf1	4	EPO
MOL2	Nfasc	BP	GO:0010631	epithelial cell migration	4/44	327/28564	0,0016	0,021615	0,0132721	Pik3r3/Map4k4/Tns3/Sema4a	4	EPO
MOL2	Nfasc	BP	GO:0016358	dendrite development	4/44	327/28564	0,0016	0,021615	0,0132721	Sema4d/Map1b/Prickle1/Tnik	4	EPO
MOL2	Nfasc	BP	GO:0090132	epithelium migration	4/44	329/28564	0,00163	0,021735	0,0133461	Pik3r3/Map4k4/Tns3/Sema4a	4	EPO
MOL2	Nfasc	BP	GO:0045598	regulation of fat cell differentiation	3/44	152/28564	0,00167	0,021735	0,0133461	Tcf7l2/Sirt2/Ncor2	3	EPO
MOL2	Nfasc	BP	GO:0046328	regulation of JNK cascade	3/44	152/28564	0,00167	0,021735	0,0133461	Map4k4/Grik2/Tnik	3	EPO
MOL2	Nfasc	BP	GO:0090130	tissue migration	4/44	331/28564	0,00167	0,021735	0,0133461	Pik3r3/Map4k4/Tns3/Sema4a	4	EPO
MOL2	Nfasc	BP	GO:0060325	face morphogenesis	2/44	42/28564	0,00192	0,024779	0,0152149	Tcf7l2/Prickle1	2	EPO
MOL2	Nfasc	BP	GO:0010765	positive regulation of sodium ion transport	2/44	43/28564	0,00201	0,025719	0,0157925	Cnksr3/Ank3	2	EPO
MOL2	Nfasc	BP	GO:2000058	regulation of ubiquitin-dependent protein catabolic process	3/44	168/28564	0,00222	0,028087	0,0172461	Prickle1/Sirt2/Smurf1	3	EPO
MOL2	Nfasc	BP	GO:0040013	negative regulation of locomotion	4/44	360/28564	0,00226	0,028408	0,0174435	Abr/Sema4d/Sema6a/Sema4a	4	EPO
MOL2	Nfasc	BP	GO:0060323	head morphogenesis	2/44	48/28564	0,0025	0,031099	0,019096	Tcf7l2/Prickle1	2	EPO
MOL2	Nfasc	BP	GO:0007254	JNK cascade	3/44	179/28564	0,00265	0,032412	0,0199023	Map4k4/Grik2/Tnik	3	EPO
MOL2	Nfasc	BP	GO:0010970	transport along microtubule	3/44	179/28564	0,00265	0,032412	0,0199023	Map1b/Ank3/Tmem108	3	EPO
MOL2	Nfasc	BP	GO:0045806	negative regulation of endocytosis	2/44	50/28564	0,00271	0,032813	0,0201482	Ank3/Sh3gl3	2	EPO
MOL2	Nfasc	BP	GO:0016601	Rac protein signal transduction	2/44	51/28564	0,00282	0,033819	0,0207663	Auts2/Tns3	2	EPO
MOL2	Nfasc	BP	GO:0045862	positive regulation of proteolysis	4/44	384/28564	0,00286	0,033974	0,020861	Prickle1/Sirt2/Mbp/Smurf1	4	EPO
MOL2	Nfasc	BP	GO:1903531	negative regulation of secretion by cell	3/44	188/28564	0,00305	0,035939	0,0220676	Abr/Frmd4a/Map4k4	3	EPO
MOL2	Nfasc	BP	GO:0045773	positive regulation of axon extension	2/44	55/28564	0,00327	0,03823	0,0234747	Map1b/Smurf1	2	EPO
MOL2	Nfasc	BP	GO:1901861	regulation of muscle tissue development	2/44	56/28564	0,00339	0,039272	0,0241143	Tcf7l2/Sirt2	2	EPO
MOL2	Nfasc	BP	GO:0019228	neuronal action potential	2/44	57/28564	0,00351	0,040318	0,024757	Grik2/Ank3	2	EPO
MOL2	Nfasc	BP	GO:0051099	positive regulation of binding	3/44	200/28564	0,00363	0,041028	0,0251927	Tcf7l2/Sirt2/Tns3	3	EPO
MOL2	Nfasc	BP	GO:0030514	negative regulation of BMP signaling pathway	2/44	58/28564	0,00363	0,041028	0,0251927	Tcf7l2/Smurf1	2	EPO
MOL2	Nfasc	BP	GO:0032872	regulation of stress-activated MAPK cascade	3/44	203/28564	0,00378	0,042387	0,0260273	Map4k4/Grik2/Tnik	3	EPO
MOL2	Nfasc	BP	GO:0046578	regulation of Ras protein signal transduction	3/44	204/28564	0,00383	0,042625	0,026173	Auts2/Map4k4/Tns3	3	EPO

MOL2	Nfasc	BP	GO:2000649	regulation of sodium ion transmembrane transporter activity	2/44	60/28564	0,00388	0,042651	0,026189	Cnksr3/Ank3	2	EPO
MOL2	Nfasc	BP	GO:0070302	regulation of stress-activated protein kinase signaling cascade	3/44	206/28564	0,00394	0,042651	0,026189	Map4k4/Grik2/Tnik	3	EPO
MOL2	Nfasc	BP	GO:0030308	negative regulation of cell growth	3/44	208/28564	0,00405	0,042651	0,026189	Sema4d/Sema6a/Sema4a	3	EPO
MOL2	Nfasc	BP	GO:0001503	ossification	4/44	427/28564	0,00417	0,042651	0,026189	Sema4d/Tcf7l2/Prickle1/Smurf1	4	EPO
MOL2	Nfasc	BP	GO:0007264	small GTPase mediated signal transduction	4/44	428/28564	0,0042	0,042651	0,026189	Auts2/Map4k4/Tns3/Dock6	4	EPO
MOL2	Nfasc	BP	GO:0042551	neuron maturation	2/44	63/28564	0,00427	0,042651	0,026189	Nfasc/Ank3	2	EPO
MOL2	Nfasc	BP	GO:0098815	modulation of excitatory postsynaptic potential	2/44	63/28564	0,00427	0,042651	0,026189	Grik2/Tmem108	2	EPO
MOL2	Nfasc	BP	GO:0045017	glycerolipid biosynthetic process	3/44	213/28564	0,00432	0,042651	0,026189	Tcf7l2/Pik3r3/Pcyt2	3	EPO
MOL2	Nfasc	BP	GO:0010171	body morphogenesis	2/44	64/28564	0,0044	0,042651	0,026189	Tcf7l2/Prickle1	2	EPO
MOL2	Nfasc	BP	GO:0031641	regulation of myelination	2/44	64/28564	0,0044	0,042651	0,026189	Tcf7l2/Sirt2	2	EPO
MOL2	Nfasc	BP	GO:0060324	face development	2/44	64/28564	0,0044	0,042651	0,026189	Tcf7l2/Prickle1	2	EPO
MOL2	Nfasc	BP	GO:0051048	negative regulation of secretion	3/44	218/28564	0,00461	0,042651	0,026189	Abr/Frmd4a/Map4k4	3	EPO
MOL2	Nfasc	BP	GO:0048639	positive regulation of developmental growth	3/44	220/28564	0,00473	0,043012	0,0264106	Sema4d/Map1b/Smurf1	3	EPO
MOL2	Nfasc	BP	GO:0099111	microtubule-based transport	3/44	220/28564	0,00473	0,043012	0,0264106	Map1b/Ank3/Tmem108	3	EPO
MOL2	Nfasc	BP	GO:0007018	microtubule-based movement	4/44	443/28564	0,00475	0,043012	0,0264106	Map1b/Kif19a/Ank3/Tmem108	4	EPO
MOL2	Nfasc	BP	GO:0098930	axonal transport	2/44	67/28564	0,00481	0,043304	0,0265902	Ank3/Tmem108	2	EPO
MOL2	Nfasc	BP	GO:1903050	regulation of proteolysis involved in protein catabolic process	3/44	225/28564	0,00504	0,04502	0,0276438	Prickle1/Sirt2/Smurf1	3	EPO
MOL2	Nfasc	BP	GO:0043542	endothelial cell migration	3/44	230/28564	0,00535	0,047536	0,0291888	Pik3r3/Tns3/Sema4a	3	EPO
MOL2	Nfasc	BP	GO:0050920	regulation of chemotaxis	3/44	232/28564	0,00548	0,048374	0,0297036	Sema4d/Sema6a/Sema4a	3	EPO
MOL2	Nfasc	BP	GO:1902305	regulation of sodium ion transmembrane transport	2/44	72/28564	0,00554	0,04854	0,0298055	Cnksr3/Ank3	2	EPO
MOL2	Nfasc	BP	GO:0051056	regulation of small GTPase mediated signal transduction	3/44	236/28564	0,00575	0,049848	0,0306086	Auts2/Map4k4/Tns3	3	EPO
MOL2	Nfasc	BP	GO:0007422	peripheral nervous system development	2/44	75/28564	0,00599	0,049848	0,0306086	Nfasc/Sirt2	2	EPO
MOL2	Nfasc	BP	GO:0034329	cell junction assembly	4/44	477/28564	0,00615	0,049848	0,0306086	Nfasc/Sema4d/Map4k4/Sema4a	4	EPO

MOL2	Nfasc	BP	GO:1901888	regulation of cell junction assembly	3/44	242/28564	0,00616	0,049848	0,0306086	Sema4d/Map4k4/Sema4a	3	EPO
MOL2	Nfasc	CC	GO:0044304	main axon	5/44	87/28585	2,3E-07	3,49E-05	2,154E-05	Nfasc/Map1b/Sirt2/Ank3/Mbp	5	EPO
MOL2	Nfasc	CC	GO:0033270	paranode region of axon	3/44	16/28585	1,9E-06	0,000143	8,801E-05	Nfasc/Sirt2/Ank3	3	EPO
MOL2	Nfasc	CC	GO:0014069	postsynaptic density	7/44	442/28585	4,7E-06	0,000239	0,0001472	Abr/Map1b/Grik2/Ank3/Tnik/Tmem108/Sh3gl3	7	EPO
MOL2	Nfasc	CC	GO:0032279	asymmetric synapse	7/44	462/28585	6,3E-06	0,000239	0,0001474	Abr/Map1b/Grik2/Ank3/Tnik/Tmem108/Sh3gl3	7	EPO
MOL2	Nfasc	CC	GO:0099572	postsynaptic specialization	7/44	486/28585	8,7E-06	0,000266	0,0001639	Abr/Map1b/Grik2/Ank3/Tnik/Tmem108/Sh3gl3	7	EPO
MOL2	Nfasc	CC	GO:0099092	postsynaptic density, intracellular component	3/44	42/28585	3,7E-05	0,000949	0,0005848	Abr/Tnik/Sh3gl3	3	EPO
MOL2	Nfasc	CC	GO:0099091	postsynaptic specialization, intracellular component	3/44	50/28585	6,3E-05	0,001225	0,0007548	Abr/Tnik/Sh3gl3	3	EPO
MOL2	Nfasc	CC	GO:0033010	paranodal junction	2/44	8/28585	6,4E-05	0,001225	0,0007548	Nfasc/Sirt2	2	EPO
MOL2	Nfasc	CC	GO:0015629	actin cytoskeleton	6/44	500/28585	0,00011	0,001886	0,0011623	Auts2/Parvb/Abli2/Tns3/Specc1/Rin1	6	EPO
MOL2	Nfasc	CC	GO:0033268	node of Ranvier	2/44	20/28585	0,00043	0,006571	0,0040497	Nfasc/Ank3	2	EPO
MOL2	Nfasc	CC	GO:0043218	compact myelin	2/44	21/28585	0,00048	0,006596	0,0040651	Sirt2/Mbp	2	EPO
MOL2	Nfasc	CC	GO:0043194	axon initial segment	2/44	29/28585	0,00092	0,011598	0,0071481	Nfasc/Ank3	2	EPO
MOL2	Nfasc	CC	GO:0043204	perikaryon	3/44	154/28585	0,00173	0,018753	0,0115583	Map1b/Sirt2/Grik2	3	EPO
MOL2	Nfasc	CC	GO:0070160	tight junction	3/44	154/28585	0,00173	0,018753	0,0115583	Nfasc/Frmd4a/Ank3	3	EPO
MOL2	Nfasc	CC	GO:0097386	glial cell projection	2/44	43/28585	0,00201	0,020356	0,012546	Nfasc/Sirt2	2	EPO
MOL2	Nfasc	CC	GO:0043296	apical junction complex	3/44	169/28585	0,00225	0,021378	0,0131764	Nfasc/Frmd4a/Ank3	3	EPO
MOL2	Nfasc	CC	GO:0005925	focal adhesion	3/44	174/28585	0,00244	0,021854	0,0134697	Parvb/Map4k4/Tns3	3	EPO
MOL2	Nfasc	CC	GO:0030055	cell-substrate junction	3/44	188/28585	0,00304	0,025681	0,0158282	Parvb/Map4k4/Tns3	3	EPO
MOL2	Nfasc	CC	GO:0043209	myelin sheath	3/44	218/28585	0,0046	0,0322	0,0198461	Nfasc/Sirt2/Mbp	3	EPO
MOL2	Nfasc	CC	GO:0005874	microtubule	4/44	441/28585	0,00466	0,0322	0,0198461	Nckap5/Map1b/Kif19a/Sirt2	4	EPO
MOL2	Nfasc	CC	GO:0001750	photoreceptor outer segment	2/44	86/28585	0,0078	0,047407	0,0292189	Prom1/Map1b	2	EPO
MOL2	Nfasc	MF	GO:0030215	semaphorin receptor binding	3/44	22/28171	5,4E-06	0,000767	0,0005193	Sema4d/Sema6a/Sema4a	3	EPO

MOL2	Nfasc	MF	GO:0045499	chemorepellent activity	3/44	29/28171	1,3E-05	0,000903	0,0006113	Sema4d/Sema6a/Sema4a	3	EPO
MOL2	Nfasc	MF	GO:0015631	tubulin binding	5/44	388/28171	0,00034	0,016078	0,010888	Map1b/Kif19a/Sirt2/Map4k4/Ccser2	5	EPO
MOL2	Nfasc	MF	GO:0008017	microtubule binding	4/44	269/28171	0,00082	0,029221	0,0197889	Map1b/Kif19a/Map4k4/Ccser2	4	EPO
MOL2	Slc4a4	BP	GO:0003014	renal system process	3/14	136/28564	3,7E-05	0,005978	0,0030066	Slc22a6/Npr3/Anpep	3	Placebo
MOL2	Slc4a4	BP	GO:0006820	monoatomic anion transport	3/14	159/28564	5,9E-05	0,005978	0,0030066	Slc4a4/Slc13a4/Slc22a6	3	Placebo
MOL2	Slc4a4	BP	GO:0097254	renal tubular secretion	2/14	39/28564	0,00016	0,01107	0,0055679	Slc22a6/Anpep	2	Placebo
MOL2	Slc4a4	BP	GO:0007588	excretion	2/14	54/28564	0,00031	0,015966	0,0080307	Slc22a6/Anpep	2	Placebo
MOL2	Slc4a4	BP	GO:0015711	organic anion transport	3/14	437/28564	0,00114	0,038233	0,0192304	Slc4a4/Slc22a6/Slc6a20a	3	Placebo
MOL2	Slc4a4	BP	GO:0035725	sodium ion transmembrane transport	2/14	166/28564	0,00292	0,04231	0,0212811	Slc4a4/Slc6a20a	2	Placebo
MOL2	Slc4a4	CC	GO:0016323	basolateral plasma membrane	2/13	258/28585	0,00593	0,049098	0,0313783	Slc4a4/Slc22a6	2	Placebo
MOL2	Slc4a4	CC	GO:0009925	basal plasma membrane	2/13	292/28585	0,00753	0,049098	0,0313783	Slc4a4/Slc22a6	2	Placebo
MOL2	Slc4a4	CC	GO:0045178	basal part of cell	2/13	316/28585	0,00877	0,049098	0,0313783	Slc4a4/Slc22a6	2	Placebo
MOL2	Slc4a4	MF	GO:0022804	active transmembrane transporter activity	5/13	414/28171	7,8E-07	5,71E-05	1,563E-05	Slc4a4/Slc13a4/Slc22a6/Atp13a5/Slc6a20a	5	Placebo
MOL2	Slc4a4	MF	GO:0022853	active monoatomic ion transmembrane transporter activity	4/13	225/28171	2,7E-06	9,77E-05	2,677E-05	Slc4a4/Slc13a4/Atp13a5/Slc6a20a	4	Placebo
MOL2	Slc4a4	MF	GO:0015291	secondary active transmembrane transporter activity	4/13	262/28171	4,9E-06	0,000109	2,974E-05	Slc4a4/Slc13a4/Slc22a6/Slc6a20a	4	Placebo
MOL2	Slc4a4	MF	GO:0015370	solute:sodium symporter activity	3/13	79/28171	5,9E-06	0,000109	2,974E-05	Slc4a4/Slc13a4/Slc6a20a	3	Placebo
MOL2	Slc4a4	MF	GO:0015294	solute:monoatomic cation symporter activity	3/13	108/28171	1,5E-05	0,000222	6,096E-05	Slc4a4/Slc13a4/Slc6a20a	3	Placebo
MOL2	Slc4a4	MF	GO:0031404	chloride ion binding	2/13	15/28171	2,1E-05	0,00025	6,857E-05	Slc22a6/Npr3	2	Placebo
MOL2	Slc4a4	MF	GO:0005452	solute:inorganic anion antiporter activity	2/13	17/28171	2,7E-05	0,000278	7,609E-05	Slc4a4/Slc22a6	2	Placebo
MOL2	Slc4a4	MF	GO:0015103	inorganic anion transmembrane transporter activity	3/13	142/28171	3,5E-05	0,000305	8,343E-05	Slc4a4/Slc13a4/Slc22a6	3	Placebo
MOL2	Slc4a4	MF	GO:0015293	symporter activity	3/13	146/28171	3,8E-05	0,000305	8,343E-05	Slc4a4/Slc13a4/Slc6a20a	3	Placebo
MOL2	Slc4a4	MF	GO:0015081	sodium ion transmembrane transporter activity	3/13	158/28171	4,8E-05	0,000347	9,501E-05	Slc4a4/Slc13a4/Slc6a20a	3	Placebo
MOL2	Slc4a4	MF	GO:0008514	organic anion transmembrane transporter activity	3/13	238/28171	0,00016	0,001062	0,0002908	Slc4a4/Slc22a6/Slc6a20a	3	Placebo

MOL2	Slc4a4	MF	GO:0015297	antiporter activity	2/13	97/28171	0,00089	0,005061	0,0013867	Slc4a4/Slc22a6	2	Placebo
MOL2	Slc4a4	MF	GO:0046873	metal ion transmembrane transporter activity	3/13	430/28171	0,0009	0,005061	0,0013867	Slc4a4/Slc13a4/Slc6a20a	3	Placebo
MOL2	Slc4a4	MF	GO:0042277	peptide binding	2/13	361/28171	0,01164	0,026542	0,0072719	Npr3/Anpep	2	Placebo
MOL2	Slc4a4	MF	GO:0033218	amide binding	2/13	450/28171	0,01768	0,033086	0,0090645	Npr3/Anpep	2	Placebo

Supplementary Table 5

Behavioral test	Variable	Control - mean	Control - SEM	Control - n	Knock-out - mean	Knock-out - SEM	Knock-out - n	Statistical test	Effect	p-value
Health Status	Body weight [g] pre transponder surgery - 28 weeks	24.57	0.39	15	24.82	0.54	13	t	N/A	0.7101
Health Status	Body weight [g] pre perfusion - 50 weeks	26.35	0.42	14	26.56	0.53	13	t	N/A	0.7571
Locomotor activity	IntelliCage - total corner visits [#]	248.1	15.69	8	321.5	23.83	8	U	N/A	0.026
Locomotor activity	IntelliCage - total corner visits in dark phase [#]	223.3	12.93	8	282.4	18.64	8	U	N/A	0.0379
Locomotor activity	Complex Running Wheels - average distance per night [km]	4.76	0.63	11	3.6	0.64	11	U	N/A	0.2426
Locomotor activity	Complex Running Wheels - average time per night [h]	4.38	0.54	11	3.42	0.59	11	t	N/A	0.2404
Exploration	Elevated Plus Maze - total distance [m]	1.42	0.067	16	1.25592	0.096	13	t	N/A	0.1643
Exploration	Open Field Test - total distance [m]	2.84	0.23	16	2.38	0.21	13	t	N/A	0.1533
Exploration	Tripartite Chamber Test - total distance [m]	3.69	0.23	16	3.63	0.36	13	U	N/A	0.1437
Exploration	Social IntelliCage Paradigm - total exploration time [min]	32.25	1.28	9	31.38	1.22	8	t	N/A	0.6333
Elevated Plus Maze	Latency to enter an open arm [s]	57.74	12.84	16	40.91	9.53	13	U	N/A	0.7257
Elevated Plus Maze	Latency to enter an closed arm [s]	53.72	8.95	16	65.35	7.84	13	t	N/A	0.3665
Elevated Plus Maze	Time in the open arms [s]	17.63	3.98	16	35.48	7.34	13	U	N/A	0.0499
Light-Dark Box	Latency to enter light [s]	78.94	15.36	16	131.23	14.13	13	U	N/A	0.0257
Open Field Test	Escape latency [s]	27.88	8.46	16	62.46	17.05	13	U	N/A	0.1536
Open Field Test	Time spent in peripheral zone [#]	391.3	4.67	16	393.55	4.66	13	t	N/A	0.7390

Behavioral test	Variable	Control - mean	Control - SEM	Control - n	Knock-out - mean	Knock-out - SEM	Knock-out - n	Statistical test	Effect	p-value
Open Field Test	Time spent in intermediate zone [#]	24.85	4.03	16	19.74	3.23	13	t	N/A	0.3475
Open Field Test	Time spent in center zone [#]	3.83	0.84	16	6.68	1.98	13	U	N/A	0.4682
Open Field Test	Time in each zone	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Genotype	0.9988
Open Field Test	Time in each zone	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Zone	< 0.0001
Open Field Test	Time in each zone	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	GxZ	0.4690
Grip Strength Test	Grip Strength [AU]	55.15	2.28	16	52.51	2.98	13	t	N/A	0.4811
RotaRod	Latency to fall off [s] - trial 1	119.27	14.67	15	149.09	21.21	11	t	N/A	0.2432
RotaRod	Latency to fall off [s] - trial 2	158.33	19.8	15	179.27	16.39	11	t	N/A	0.4473
RotaRod	Trial 1 vs. trial 2	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Genotype	0.2309
RotaRod	Trial 1 vs. trial 2	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Trial	0.0390
RotaRod	Trial 1 vs. trial 2	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	GxT	0.2309
Beam Balance	Escape latency [s] - 25mm	21.19	4.23	16	24	4.71	13	U	N/A	0.3678
Beam Balance	Escape latency [s] - 10mm	18.25	3.69	16	14.77	3.14	13	U	N/A	0.5972
Beam Balance	Escape latency [s] - 8mm	27.94	4.22	16	29.54	5.12	13	U	N/A	0.9825
Beam Balance	Beam thickness	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Genotype	0.9208
Beam Balance	Beam thickness	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Thickness	< 0.0001
Beam Balance	Beam thickness	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	GxT	0.6797
Bar Test	Time immobile [s]	0.36	0.09	8	0.3	0.06	9	U	N/A	0.5630
Hurdle Test	Trial 1 - Executive function [s/#]	8.69	0.9	15	22.56	4.81	12	Welch t	N/A	0.0152
Hurdle Test	Trial 2 - Executive function [s/#]	3.5	0.42	15	3.82	0.24	12	U	N/A	0.0832

Behavioral test	Variable	Control - mean	Control - SEM	Control - n	Knock-out - mean	Knock-out - SEM	Knock-out - n	Statistical test	Effect	p-value
Hurdle Test	Trial 1 vs. trial 2	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Genotype	0.0035
Hurdle Test	Trial 1 vs. trial 2	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Trial	< 0.0001
Hurdle Test	Trial 1 vs. trial 2	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	GxT	0.0028
Hurdle Test	Trial 3 - Executive function [s/#]	2.65	0.27	13	3.57	0.6	13	Welch t	N/A	0.1859
Hurdle Test	Trial 4 - Executive function [s/#]	1.56	0.14	13	1.77	0.18	13	t	N/A	0.3554
Hurdle Test	Trial 3 vs. trial 4	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Genotype	0.6876
Hurdle Test	Trial 3 vs. trial 4	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Trial	< 0.0001
Hurdle Test	Trial 3 vs. trial 4	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	GxT	0.8770
Puzzle Box	Habituation - Average escape latency open door [s]	50.58	16.78	16	60.97	22.98	13	U	N/A	0.8094
Puzzle Box	Challenge 1 - Average escape latency gateway [s]	18.86	4.32	16	20.16	4.63	13	U	N/A	0.9828
Puzzle Box	Challenge 2 - Average escape latency bedding [s]	50.73	7.47	16	36.61	10.03	13	U	N/A	0.1006
Puzzle Box	Challenge 3 - Average escape latency tissue plug [s]	171.52	26.42	16	165.33	22.96	13	t	N/A	0.8645
Puzzle Box	Challenge 4 - Average escape latency nesting material [s]	170.29	17.26	16	150.76	16.97	13	t	N/A	0.4329
Puzzle Box	Challenges	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Genotype	0.1495
Puzzle Box	Challenges	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Challenge	< 0.0001
Puzzle Box	Challenges	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	GxC	0.3602

Behavioral test	Variable	Control - mean	Control - SEM	Control - n	Knock-out - mean	Knock-out - SEM	Knock-out - n	Statistical test	Effect	p-value
Tripartite Chamber Test	Empty Cage - time spent with insert [s]	155.38	7.32	16	159.66	13.10	13	t	N/A	0.7669
Tripartite Chamber Test	Stimulus - time spent with insert [s]	246.79	9.40	16	249.79	13.48	13	t	N/A	0.8526
Tripartite Chamber Test	Empty Cage vs. stimulus - time	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Genotype	0.5921
Tripartite Chamber Test	Empty Cage vs. stimulus - time	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Cage	< 0.0001
Tripartite Chamber Test	Empty Cage vs. stimulus - time	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	GxCa	0.8471
Tripartite Chamber Test	Empty Cage - visits to insert [#]	19.25	0.92	16	16.85	1.73	13	U	N/A	0.1388
Tripartite Chamber Test	Stimulus - visits to insert [#]	25.25	2.45	16	27.46	3.18	13	U	N/A	0.7751
Tripartite Chamber Test	Empty Cage vs. stimulus - visits [#]	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Genotype	0.2135
Tripartite Chamber Test	Empty Cage vs. stimulus - visits [#]	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Cage	< 0.0001
Tripartite Chamber Test	Empty Cage vs. stimulus - visits [#]	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	GxCa	0.0053
Tripartite Chamber Test	Empty Cage - latency to insert [s]	78.71	20.28	16	82.91	28.25	13	U	N/A	0.9650
Tripartite Chamber Test	Stimulus - latency to insert [s]	43.13	12.21	16	47.11	14.02	13	U	N/A	0.8460
Tripartite Chamber Test	Empty Cage vs. stimulus - latency [s]	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Genotype	0.8748
Tripartite Chamber Test	Empty Cage vs. stimulus - latency [s]	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Cage	0.2186
Tripartite Chamber Test	Empty Cage vs. stimulus - latency [s]	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	GxCa	0.6454
Morris Water Maze	Visible day 1 - escape latency [s]	15.4	3.33	14	15.77	3.42	11	U	N/A	>0.9999
Morris Water Maze	Visible day 2 - escape latency [s]	6.28	0.98	14	7.91	1.57	11	U	N/A	>0.9999
Morris Water Maze	Visible day 1 -. Visible day 2	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Genotype	0.3457
Morris Water Maze	Visible day 1 -. Visible day 2	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Day	0.0007

Behavioral test	Variable	Control - mean	Control - SEM	Control - n	Knock-out - mean	Knock-out - SEM	Knock-out - n	Statistical test	Effect	p-value
Morris Water Maze	Visible day 1 -. Visible day 2	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	GxD	0.7290
Morris Water Maze	Hidden day 1 - escape latency [s]	49.73	4.63	14	59.40	6.41	11	U	N/A	0.6462
Morris Water Maze	Hidden day 2 - escape latency [s]	27.69	4.61	14	33.92	5.40	11	U	N/A	0.3944
Morris Water Maze	Hidden day 3 - escape latency [s]	17.60	2.18	14	30.93	7.94	11	U	N/A	0.1453
Morris Water Maze	Hidden day 4 - escape latency [s]	19.26	3.28	14	31.02	7.27	11	U	N/A	0.2766
Morris Water Maze	Hidden day 5 - escape latency [s]	19.86	2.17	14	21.40	2.86	11	U	N/A	>0.9999
Morris Water Maze	Hidden day 6 - escape latency [s]	26.39	4.35	14	20.51	4.63	11	U	N/A	>0.9999
Morris Water Maze	Hidden day 7 - escape latency [s]	19.98	3.78	14	15.93	2.11	11	U	N/A	>0.9999
Morris Water Maze	Hidden day 8 - escape latency [s]	21.50	5.16	14	19.94	5.03	11	U	N/A	>0.9999
Morris Water Maze	Hidden day 1 - Hidden day 8	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Genotype	0.3471
Morris Water Maze	Hidden day 1 - Hidden day 8	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Day	< 0.0001
Morris Water Maze	Hidden day 1 - Hidden day 8	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	GxD	0.2496
Morris Water Maze	Probe trial 1 - time in TQ [s]	32.94	2.73	14	37.84	3.05	11	U	N/A	0.32
Morris Water Maze	Reversal day 1 - escape latency [s]	25.7710714	4.39	14	27.98545455	7.311363352	11	U	N/A	>0.9999
Morris Water Maze	Reversal day 2 - escape latency [s]	19.5408929	2.01	14	21.31659091	4.40626521	11	U	N/A	>0.9999
Morris Water Maze	Reversal day 3 - escape latency [s]	12.8160714	2.06	14	19.46431818	4.209560994	11	U	N/A	0.3922
Morris Water Maze	Reversal day 4 - escape latency [s]	14.0983929	3.18	14	12.44068182	3.083554897	13	U	N/A	>0.9999
Morris Water Maze	Reversal day 1 - Reversal day 4	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Genotype	0.9587
Morris Water Maze	Reversal day 1 - Reversal day 4	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Day	0.0003

Behavioral test	Variable	Control - mean	Control - SEM	Control - n	Knock-out - mean	Knock-out - SEM	Knock-out - n	Statistical test	Effect	p-value
Morris Water Maze	Reversal day 1 - Reversal day 4	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	GxD	0.3485
Morris Water Maze	Probe trial 2 - time in TQ [s]	48.46	2.27	14	42.21	3.50	11	t	N/A	0.39
IntelliCage (spatial memory)	Place Learning - cognition error	0.45	0.03	8	0.39	0.26	8	t	N/A	0.0993
IntelliCage (spatial memory)	Reversal Learning - cognition error	0.64	0.02	8	0.58	0.14	8	t	N/A	0.0418
IntelliCage (spatial memory)	Multiple Reversal Learning - cognition error	0.62	0.02	8	0.60	0.28	8	t	N/A	0.4795
IntelliCage - Episodic-like memory (What- where-when memory)	Phase 1 Acquisition - cognition error	0.51	0.04	8	0.45	0.43	8	U	N/A	0.2786
IntelliCage - Episodic-like memory (What- where-when memory)	Phase 1 Retrieval - cognition error	0.64	0.03	8	0.62	0.37	8	t	N/A	0.6007
IntelliCage - Episodic-like memory (What- where-when memory)	Phase 2 Acquisition - cognition error	0.68	0.02	7	0.62	0.39	8	t	N/A	0.2053
IntelliCage - Episodic-like memory (What- where-when memory)	Phase 2 Retrieval - cognition error	0.70	0.02	7	0.69	0.24	8	U	N/A	0.7789
IntelliCage - Patrolling (working memory)	Clockwise 1 - cognition error	0.35	0.01	7	0.31	0.19	8	t	N/A	0.0186
IntelliCage - Patrolling (working memory)	Clockwise 2 - cognition error	0.37	0.02	7	0.31	0.17	8	t	N/A	0.0118

Behavioral test	Variable	Control - mean	Control - SEM	Control - n	Knock-out - mean	Knock-out - SEM	Knock-out - n	Statistical test	Effect	p-value
IntelliCage - Patrolling (working memory)	Counter-Clockwise 1 - cognition error	0.64	0.01	7	0.57	0.17	8	t	N/A	0.0001
IntelliCage - Patrolling (working memory)	Counter-Clockwise 2 - cognition error	0.65	0.01	7	0.57	0.15	8	t	N/A	0.0001
Social IntelliCage Paradigm - pheromone test	Habituation - Time in target cage [s]	15.29	1.02	9	14.21	0.52	8	t	N/A	0.3760
Social IntelliCage Paradigm - pheromone test	Test phase - Time in target cage [s]	28.16	1.51	9	23.14	3.38	8	t	N/A	0.1779
Social IntelliCage Paradigm - pheromone test	Habituation vs. test	N/A	N/A	N/A	N/A	N/A	N/A	U	N/A	0.0003
Pre-pulse Inhibition	Pre-pulse Inhibition at 70dB [%]	19.64	6.32	14	22.76	4.67	13	t	N/A	0.6986
Pre-pulse Inhibition	Pre-pulse Inhibition at 75dB [%]	46.31	4.57	14	32.95	7.64	13	t	N/A	0.1393
Pre-pulse Inhibition	Pre-pulse Inhibition at 80dB [%]	50.81	4.5	14	37.21	6.10	13	t	N/A	0.0820
Pre-pulse Inhibition	PPI 70-80dB	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Genotype	0.9995
Pre-pulse Inhibition	PPI 70-80dB	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Intensity	0.0010
Pre-pulse Inhibition	PPI 70-80dB	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	GxI	0.4437
Hearing test	Hearing at 65dB [AU]	2.74	0.19	14	3.06	0.27	13	t	N/A	0.3363
Hearing test	Hearing at 68dB [AU]	2.61	0.16	14	3.35	0.33	13	Welch t	N/A	0.0571
Hearing test	Hearing at 71dB [AU]	2.65	0.18	14	2.86	0.18	13	U	N/A	0.3822
Hearing test	Hearing at 74dB [AU]	3.06	0.36	14	3.20	0.18	13	U	N/A	0.1522
Hearing test	Hearing at 77dB [AU]	3.23	0.25	14	3.79	0.33	13	t	N/A	0.1875
Hearing test	Hearing at 80dB [AU]	3.9	0.31	14	4.46	0.36	13	t	N/A	0.2419
Hearing test	Hearing at 83dB [AU]	4.55	0.42	14	5.35	0.61	13	t	N/A	0.2846
Hearing test	Hearing at 86dB [AU]	5.25	0.48	14	5.80	0.62	13	t	N/A	0.4863
Hearing test	Hearing at 89dB [AU]	5.57	0.41	14	5.88	0.40	13	t	N/A	0.5980
Hearing test	Hearing at 92dB [AU]	6.1	0.42	14	6.03	0.63	13	t	N/A	0.9318
Hearing test	Hearing at 95dB [AU]	7.24	0.5	14	7.51	0.66	13	t	N/A	0.7418

Behavioral test	Variable	Control - mean	Control - SEM	Control - n	Knock-out - mean	Knock-out - SEM	Knock-out - n	Statistical test	Effect	p-value
Hearing test	Hearing at 98dB [AU]	8.46	0.89	14	8.57	0.80	13	U	N/A	0.9430
Hearing test	Hearing at 101dB [AU]	11.27	1.02	14	9.54	1.15	13	U	N/A	0.1820
Hearing test	Hearing at 104dB [AU]	11.9	1.41	14	11.57	2.17	13	U	N/A	0.2588
Hearing test	Hearing at 107dB [AU]	14.73	1.77	14	11.51	1.47	13	U	N/A	0.2020
Hearing test	Hearing at 110dB [AU]	16.14	2.01	14	10.80	0.99	13	t	N/A	0.0285
Hearing test	Hearing at 113dB [AU]	18.42	2.9	14	12.02	2.30	13	U	N/A	0.0091
Hearing test	Hearing at 116dB [AU]	17.63	3.06	14	14.60	2.31	13	U	N/A	0.5826
Hearing test	Hearing at 120dB [AU]	19.28	2.66	14	14.97	1.76	13	U	N/A	0.2020
Hearing test	Hearing 65-120dB	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Genotype	0.6325
Hearing test	Hearing 65-120dB	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Intensity	< 0.0001
Hearing test	Hearing 65-120dB	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	GxI	0.0010
Mental Time Travel - Episodic-like memory (What-where-when memory)	Day 5-8 average - visits to punished corner [%]	17.24	2.44	7	19.93	2.40	8	t	N/A	>0.9999
Mental Time Travel - Episodic-like memory (What-where-when memory)	Day 5-8 average - visits to recent corner [%]	22.33	2.07	7	21.38	3.44	8	t	N/A	>0.9999
Mental Time Travel - Episodic-like memory (What-where-when memory)	Day 5-8 average - visits to intermediate corner [%]	31.77	2.97	7	26.37	2.67	8	t	N/A	>0.9999

Behavioral test	Variable	Control - mean	Control - SEM	Control - n	Knock-out - mean	Knock-out - SEM	Knock-out - n	Statistical test	Effect	p-value
Mental Time Travel - Episodic-like memory (What-where-when memory)	Day 5-8 average - visits to safe corner [%]	28.88	3.02	7	32.33	4.19	8	t	N/A	0.8965
Mental Time Travel - Episodic-like memory (What-where-when memory)	Day 5-8 visits per corner	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Genotype	0.9995
Mental Time Travel - Episodic-like memory (What-where-when memory)	Day 5-8 visits per corner	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	Corner	0.0010
Mental Time Travel - Episodic-like memory (What-where-when memory)	Day 5-8 visits per corner	N/A	N/A	N/A	N/A	N/A	N/A	Two-way ANOVA	GxCo	0.4437
Fear Conditioning	Time freezing at baseline [s]	6.13	2.3	14	14.47	3.28	13	U	N/A	0.0740
Fear Conditioning	Time freezing at context [s]	85.06	4.48	14	95.77	6.04	13	U	N/A	0.1279
Fear Conditioning	Time freezing at pre-cue [s]	12.00	2.5	14	28.62	5.47	13	Welch t	N/A	0.0133
Fear Conditioning	Time freezing at cue [s]	86.86	5.39	14	95.11	6.85	13	U	N/A	0.1040
Fear Conditioning	Freezing per phase	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Genotype	0.0143
Fear Conditioning	Freezing per phase	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	Phase	< 0.0001
Fear Conditioning	Freezing per phase	N/A	N/A	N/A	N/A	N/A	N/A	Two-way Friedman	GxP	0.8972
Complex Running Wheels (3w)	Average Velocity [m/s]	0.28	0.01	11	0.27	0.02	11	t	N/A	0.6615
Complex Running Wheels (3w)	Maximal Velocity [m/s]	0.41	0.02	11	0.38	0.02	11	U	N/A	0.3000