

Supplementary Table 5.
DEGs in MN cluster

gene	<i>p</i>	logFC	FDR	dysregulation
ENSG00000271774	0	3.467991	0	UP
HOXD3	0	1.623331	0	UP
PRKG1	0	4.526404	0	UP
RORA	0	4.596235	0	UP
TSHZ2	0	6.250553	0	UP
UTY	0	1.455885	0	UP
RPL39	4.6E-298	3.555133	9.4E-295	UP
MT-ND3	7.3E-291	1.41493	1.4E-287	UP
RPL41	9.6E-289	3.722881	1.8E-285	UP
RPS27	2.5E-255	2.934339	3.9E-252	UP
FGF13	1.7E-243	5.461438	2.3E-240	UP
ROBO2	2.1E-235	2.443094	2.7E-232	UP
RPL34	2.3E-232	3.132783	2.8E-229	UP
RPS18	3.6E-228	3.262647	4.1E-225	UP
KCNH5	3.9E-222	2.655989	4.2E-219	UP
LRRC7	2.2E-214	3.06327	2.2E-211	UP
RPL37A	6.6E-213	2.892168	6.4E-210	UP
RPS28	7.5E-207	2.980107	6.9E-204	UP
RPS21	2.3E-206	2.19815	2.1E-203	UP
ENSG00000288891	8.4E-206	1.20281	7.3E-203	UP
PLCB1	3E-202	3.046626	2.5E-199	UP
RPS15A	1.9E-192	2.870412	1.5E-189	UP
H19	2.4E-184	1.262077	1.8E-181	UP
RPL36A	1.4E-183	2.353552	9.8E-181	UP
RPL37	1.6E-164	2.438679	9.7E-162	UP
RPS23	7.6E-163	2.573831	4.5E-160	UP
B3GALT1	1E-162	1.44012	5.9E-160	UP
ENSG00000259481	4.8E-153	1.693724	2.7E-150	UP
RPL36	2.4E-152	2.043385	1.3E-149	UP
RPS19	2.9E-148	2.612099	1.5E-145	UP
RPS25	4E-146	2.359202	2.1E-143	UP

HTR4	3.6E-139	1.60315	1.9E-136	UP
RPS12	1E-134	2.403245	5.2E-132	UP
RPL35A	3.6E-134	2.292136	1.8E-131	UP
RAPGEF4	4.5E-129	2.378163	2.1E-126	UP
RPL28	1.1E-128	2.386149	5.1E-126	UP
RPS24	5.3E-128	2.385413	2.4E-125	UP
TPT1	4E-124	2.473884	1.7E-121	UP
RPL32	1.2E-123	2.315556	5.2E-121	UP
MGP	2.3E-118	1.554835	9E-116	UP
RPL26	3.2E-116	2.313	1.2E-113	UP
TRERF1	1.4E-115	1.488949	5E-113	UP
RPS29	8.6E-112	1.460693	2.9E-109	UP
RPL30	6.4E-111	2.187708	2.1E-108	UP
RPS13	5.9E-106	2.275667	1.8E-103	UP
RPS27A	6.6E-105	2.091255	2E-102	UP
COL1A1	1.2E-103	1.409423	3.5E-101	UP
NCKAP5	9.1E-103	2.01162	2.6E-100	UP
LUM	2.2E-102	1.363639	6.3E-100	UP
RPS15	9.2E-101	2.014417	2.58E-98	UP
RPLP2	8.9E-100	1.746576	2.45E-97	UP
RPS26	6.88E-94	1.313067	1.76E-91	UP
RPS6	6.15E-92	1.986705	1.53E-89	UP
RPL12	2.26E-91	1.879638	5.56E-89	UP
TCF25	7.62E-90	1.433532	1.83E-87	UP
SPOCK3	1.71E-89	1.800922	4.08E-87	UP
COL3A1	8.62E-89	1.839406	2.04E-86	UP
SQSTM1	2.06E-88	1.534294	4.8E-86	UP
PDZRN3	1.61E-86	2.014844	3.62E-84	UP
RPL17	1.2E-85	2.149222	2.64E-83	UP
RPL38	2.92E-85	1.014658	6.4E-83	UP
CDH13	2.85E-83	1.880599	6.18E-81	UP
SOX6	8.68E-82	1.041561	1.85E-79	UP
RPS8	5.03E-80	1.855227	1.06E-77	UP
RPL13	1.17E-79	1.837433	2.44E-77	UP
RPL10	4.74E-79	1.82849	9.73E-77	UP

TALAM1	7.27E-76	2.06619	1.43E-73	UP
LURAP1L	2.54E-75	1.128008	4.92E-73	UP
RPL21	6.29E-75	1.710994	1.21E-72	UP
RPL23A	3.54E-74	1.577475	6.77E-72	UP
RPL11	7.76E-69	1.837009	1.35E-66	UP
RPL35	1.98E-68	1.086502	3.37E-66	UP
RPLP1	1.27E-67	1.509002	2.16E-65	UP
SEZ6L	1.57E-66	1.012802	2.63E-64	UP
RPS11	5.01E-65	1.432169	8.16E-63	UP
RPL18A	3.81E-63	1.575263	5.95E-61	UP
ADARB2	6.09E-57	1.539728	8.45E-55	UP
ASAP1	5.7E-56	1.159831	7.83E-54	UP
RPL13A	8.12E-54	1.560135	1.07E-51	UP
RPL24	3.28E-53	1.455831	4.28E-51	UP
GLCCII	1.98E-52	1.447789	2.54E-50	UP
RPS3	1.02E-51	1.572154	1.29E-49	UP
RPS2	2.25E-51	1.950519	2.8E-49	UP
RPL29	2.44E-49	1.501866	2.84E-47	UP
DGKB	1.14E-48	1.062808	1.31E-46	UP
COL1A2	4.02E-47	1.163573	4.48E-45	UP
RPL22	7.82E-47	1.252889	8.6E-45	UP
RPS16	1.95E-46	1.548222	2.12E-44	UP
FAU	8.7E-46	1.385725	9.31E-44	UP
RPL19	1.43E-45	1.501341	1.51E-43	UP
RPL10A	4.5E-44	1.336506	4.57E-42	UP
ALK	5.02E-43	1.467517	4.93E-41	UP
CADM2	5.66E-43	1.499856	5.54E-41	UP
PTPRK	1.5E-39	1.021325	1.3E-37	UP
RPS10	2E-39	1.301089	1.72E-37	UP
RPS14	5.85E-39	1.271892	4.96E-37	UP
FMN1	1.21E-34	1.202259	9.31E-33	UP
ZEB2	1.57E-34	1.106207	1.21E-32	UP
RPS5	1.42E-33	1.112687	1.05E-31	UP
XYLT1	4E-33	1.319286	2.92E-31	UP
RPL6	2.75E-32	1.322423	1.93E-30	UP

RPLP0	7.83E-32	1.151083	5.41E-30	UP
RPS3A	3.46E-31	1.151762	2.33E-29	UP
RPL18	6.17E-31	1.401144	4.08E-29	UP
RPL8	3.21E-29	1.239473	1.99E-27	UP
RPL9	1.05E-25	1.058618	5.7E-24	UP
TMEM132C	4.25E-25	1.199456	2.22E-23	UP
PTPRR	3.36E-23	1.036285	1.65E-21	UP
AFP	8.32E-13	4.600555	2.27E-11	UP
MT-ND4	8.46E-09	1.218168	1.57E-07	UP
ANK3	0	-5.24214	0	DOWN
CNTNAP2	0	-6.14955	0	DOWN
DLGAP2	0	-3.53217	0	DOWN
DSCAM	0	-4.51269	0	DOWN
FHIT	0	-3.72888	0	DOWN
MARCHF1	0	-3.59889	0	DOWN
TCF4	0	-4.09214	0	DOWN
TTY14	0	-1.42433	0	DOWN
KC6	0	-1.73445	0	DOWN
LINC02315	1.8E-307	-2.12486	3.9E-304	DOWN
NCAM1	1.5E-275	-2.45953	2.7E-272	DOWN
TUBA1A	2.1E-248	-4.42852	3.1E-245	DOWN
TUBB2B	1.6E-245	-3.09597	2.3E-242	DOWN
ENSG00000286328	2.9E-237	-1.59015	3.9E-234	DOWN
GAP43	1.4E-233	-1.76021	1.8E-230	DOWN
RBMS3	2E-231	-1.03429	2.3E-228	DOWN
KCTD8	1.7E-222	-3.35244	1.9E-219	DOWN
ADGRL3	1.6E-221	-2.95036	1.6E-218	DOWN
STMN2	1.2E-214	-1.99872	1.2E-211	DOWN
GAL	4.6E-209	-1.92877	4.4E-206	DOWN
PPP2R2B	3.3E-203	-3.3127	2.8E-200	DOWN
NRXN1	3.5E-193	-3.27064	2.8E-190	DOWN
DLGAP1	1.4E-192	-2.14231	1.1E-189	DOWN
TMTC1	4.4E-190	-2.49897	3.3E-187	DOWN
PAK3	4E-180	-1.31054	2.8E-177	DOWN
FMN2	5.3E-178	-2.03936	3.7E-175	DOWN

DMD	2.6E-175	-1.49553	1.7E-172	DOWN
SEMA6D	2E-169	-2.43098	1.3E-166	DOWN
MAGI2	2.4E-166	-3.81256	1.5E-163	DOWN
GULP1	6.8E-166	-1.79838	4.2E-163	DOWN
ST6GAL2	1.7E-133	-1.12853	8.2E-131	DOWN
MAP1B	6.1E-133	-1.62981	3E-130	DOWN
KCNH7	6.8E-133	-1.64391	3.3E-130	DOWN
BCL11B	1.7E-132	-1.58369	8E-130	DOWN
TRIM2	2.1E-131	-1.57032	1E-128	DOWN
ZMAT4	3.5E-129	-1.77316	1.6E-126	DOWN
SYT1	5.9E-128	-1.65034	2.6E-125	DOWN
TUBB	3.1E-122	-1.48929	1.2E-119	DOWN
TUBB3	1.5E-120	-1.99108	6E-118	DOWN
ACTB	1.9E-118	-2.42497	7.5E-116	DOWN
VIP	7.1E-117	-1.67446	2.7E-114	DOWN
ITGB8	4.7E-116	-1.03887	1.7E-113	DOWN
ACTG1	2E-114	-2.46695	7.1E-112	DOWN
NELL2	5.3E-113	-1.40276	1.9E-110	DOWN
CNTNAP4	7.5E-113	-2.52343	2.6E-110	DOWN
TMSB4X	3.4E-111	-2.14243	1.1E-108	DOWN
SCN9A	1.2E-109	-1.05768	3.9E-107	DOWN
OLFM3	2.6E-109	-2.23887	8.3E-107	DOWN
KCNMA1	7.1E-109	-1.74879	2.3E-106	DOWN
CASC15	1.5E-106	-2.93921	4.7E-104	DOWN
CCSER1	4.2E-106	-1.37388	1.3E-103	DOWN
SYN2	1.2E-104	-1.15244	3.6E-102	DOWN
ENSG00000287347	2.1E-103	-1.51628	6.1E-101	DOWN
UCHL1	1.8E-102	-1.45647	5.1E-100	DOWN
HDAC9	1.1E-100	-2.7736	3.15E-98	DOWN
STMN1	8.2E-100	-1.40212	2.27E-97	DOWN
ERBB4	1.03E-97	-1.09351	2.8E-95	DOWN
ZBTB20	1.06E-96	-3.35315	2.87E-94	DOWN
ENSG00000289605	1.7E-96	-2.35775	4.56E-94	DOWN
SLC8A1	6.83E-96	-1.57477	1.79E-93	DOWN
SEMA5A	1.04E-95	-1.9297	2.72E-93	DOWN

PCLO	2.21E-93	-1.53318	5.6E-91	DOWN
PLEKHA5	2.52E-93	-1.43078	6.36E-91	DOWN
BNC2	6.44E-90	-2.15874	1.55E-87	DOWN
EPHA7	8.45E-86	-1.91295	1.88E-83	DOWN
ROBO1	6.86E-84	-1.23916	1.5E-81	DOWN
PDE4B	4.66E-83	-2.1512	1.01E-80	DOWN
ST6GALNAC3	8.25E-80	-1.0527	1.73E-77	DOWN
MYT1L	1.55E-78	-1.60057	3.14E-76	DOWN
BASP1	1.7E-78	-1.01765	3.44E-76	DOWN
EML5	8.68E-77	-1.56035	1.73E-74	DOWN
MIAT	2.51E-71	-1.88963	4.61E-69	DOWN
EFNA5	3.27E-71	-1.5104	5.96E-69	DOWN
ARHGEF28	6.15E-71	-1.01629	1.11E-68	DOWN
KAZN	1.19E-70	-1.27625	2.12E-68	DOWN
MARCKSL1	6.36E-68	-1.03342	1.08E-65	DOWN
PTPRG	1.81E-67	-1.55788	3.04E-65	DOWN
ANK2	9.51E-65	-2.03531	1.54E-62	DOWN
ENOX1	4.58E-64	-2.03663	7.31E-62	DOWN
PHOX2A	8.93E-63	-1.05144	1.39E-60	DOWN
LDLRAD4	1.01E-60	-1.53541	1.51E-58	DOWN
DPYD	3.92E-60	-1.03882	5.8E-58	DOWN
MACROD2	5.05E-60	-1.41463	7.45E-58	DOWN
CALM1	2.54E-59	-1.17826	3.7E-57	DOWN
KCNQ5	2.7E-59	-1.18469	3.92E-57	DOWN
LHFPL3	2.54E-57	-1.76312	3.56E-55	DOWN
CCDC171	4.31E-57	-1.4376	6.03E-55	DOWN
DST	8.4E-57	-1.39167	1.16E-54	DOWN
CAMK4	1.91E-52	-1.19195	2.46E-50	DOWN
HS6ST3	6.82E-52	-1.48075	8.66E-50	DOWN
CD9	9.09E-52	-1.22072	1.15E-49	DOWN
NLGN4X	6.04E-51	-1.11091	7.45E-49	DOWN
MBNL2	1.32E-50	-1.01043	1.6E-48	DOWN
CCDC144NL-AS1	3.78E-50	-1.76939	4.56E-48	DOWN
NCAM2	4.64E-49	-1.89551	5.37E-47	DOWN
RYR2	1.36E-46	-1.19052	1.48E-44	DOWN

CHD7	1.12E-45	-1.26625	1.19E-43	DOWN
KALRN	7.35E-45	-1.32379	7.67E-43	DOWN
SORBS2	9.51E-45	-1.32158	9.87E-43	DOWN
RBP1	9.23E-44	-1.08991	9.3E-42	DOWN
MGAT4C	1.36E-43	-1.45091	1.36E-41	DOWN
LINC01122	1.51E-43	-1.14856	1.51E-41	DOWN
SCN1A-AS1	1.26E-42	-1.01484	1.22E-40	DOWN
RBMS3-AS2	9.15E-41	-1.37203	8.43E-39	DOWN
PTPRD	6.22E-40	-1.23728	5.49E-38	DOWN
XKR4	2.5E-38	-1.01427	2.08E-36	DOWN
RUNX1T1	1.05E-35	-1.24591	8.28E-34	DOWN
LINC03041	2.26E-34	-1.1232	1.72E-32	DOWN
JMJD1C	2.73E-34	-1.52377	2.07E-32	DOWN
ZFAND3	2.09E-32	-1.03111	1.48E-30	DOWN
CRACD	3.39E-32	-1.26959	2.36E-30	DOWN
LINC01619	3.52E-31	-1.3945	2.37E-29	DOWN
PHF14	6.82E-31	-1.16148	4.51E-29	DOWN
CLASP2	6.66E-30	-1.98293	4.24E-28	DOWN
ENSG00000257894	7.57E-29	-1.1647	4.63E-27	DOWN
UNC5C	3.24E-28	-1.33928	1.93E-26	DOWN
AGAP1	6.53E-26	-1.20533	3.58E-24	DOWN
TENM3	9E-24	-1.00658	4.49E-22	DOWN
PCDH9	2.87E-19	-1.03047	1.19E-17	DOWN
SOX4	5.75E-16	-1.07261	1.99E-14	DOWN
TRIO	4.75E-15	-1.03545	1.56E-13	DOWN
NREP	5.2E-07	-1.08336	7.65E-06	DOWN
MT-CO3	2.83E-05	-1.26116	0.000314	DOWN

Enrichment of Down-regulated genes in MN cluster

pathway ID	description	GeneRatio	<i>p</i>	adjusted <i>p</i>	<i>q</i> -value	gene ID	count
GO:0007409	axonogenesis	23/104	2.89E-16	5.66559E-13	4.45E-13	ANK3/DSCAM/NCAM1/TUBB2B/GAP43/NRXN1/PAK3/SEMA6D/MAP1B/BCL11B/TUBB3/ACTB/ACTG1/UCHL1/STMN1/SEMA5A/EPHA7/ROBO1/EFNA5/ARHGEF28/KALRN/UNC5C/TRIO	23
GO:0007411	axon guidance	15/104	2.71E-12	1.77192E-09	1.39E-09	DSCAM/NCAM1/TUBB2B/GAP43/NRXN1/SEMA6D/BCL11B/TUBB3/SEMA5A/EPHA7/ROBO1/EFNA5/KALRN/UNC5C/TRIO	15
GO:0097485	neuron projection guidance	15/104	2.71E-12	1.77192E-09	1.39E-09	DSCAM/NCAM1/TUBB2B/GAP43/NRXN1/SEMA6D/BCL11B/TUBB3/SEMA5A/EPHA7/ROBO1/EFNA5/KALRN/UNC5C/TRIO	15
GO:0034329	cell junction assembly	18/104	3.87E-11	1.89339E-08	1.49E-08	CNTNAP2/DSCAM/GAP43/ADGRL3/NRXN1/MAP1B/ACTB/ACTG1/ERBB4/PCLO/EPHA7/EFNA5/ANK2/DST/CD9/NLGN4X/PTPRD/CLASP2	18
GO:0050808	synapse organization	17/104	1.16E-09	4.55016E-07	3.58E-07	ANK3/DSCAM/TUBA1A/GAP43/ADGRL3/NRXN1/PAK3/MAP1B/TUBB/ACTB/ACTG1/ERBB4/PCLO/EPHA7/EFNA5/NLGN4X/PTPRD	17

GO:0007416	synapse assembly	11/104	1.36E-08	4.43988E-06	3.49E-06	DSCAM/GAP43/ADGRL3/NRXN1/MAP1B/ERBB4/PCLO/EPHA7/EFNA5/NLGN4X/PTPRD	11
GO:0010880	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	6/104	1.59E-08	4.46369E-06	3.51E-06	DMD/SLC8A1/ANK2/CALM1/RYR2/CHD7	6
GO:0014808	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	6/104	4.13E-08	1.01047E-05	7.94E-06	DMD/SLC8A1/ANK2/CALM1/RYR2/CHD7	6
GO:1903514	release of sequestered calcium ion into cytosol by endoplasmic reticulum	6/104	4.9E-08	1.06727E-05	8.39E-06	DMD/SLC8A1/ANK2/CALM1/RYR2/CHD7	6
GO:0010881	regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	5/104	1.13E-07	2.20992E-05	1.74E-05	DMD/SLC8A1/ANK2/CALM1/RYR2	5

GO:0070296	sarcoplasmic reticulum calcium ion transport	6/104	1.25E-07	2.22951E-05	1.75E-05	DMD/SLC8A1/ANK2/CALM1/RYR2/CHD7	6
GO:0008038	neuron recognition	6/104	1.66E-07	2.70625E-05	2.13E-05	CNTNAP2/DSCAM/GAP43/SEMA5A/ROBO1/NCAM2	6
GO:0010975	regulation of neuron projection development	14/104	1.92E-07	2.75472E-05	2.17E-05	DSCAM/TUBB2B/STMN2/PAK3/SEMA6D/MAGI2/MAP1B/SEMA5A/EPHA7/ROBO1/EFNA5/PTPRG/PTPRD/TENM3	14
GO:0034765	regulation of monoatomic ion transmembrane transport	14/104	1.97E-07	2.75472E-05	2.17E-05	ANK3/GAL/DMD/KCNH7/TMSB4X/SCN9A/KCNMA1/SLC8A1/PDE4B/ANK2/CALM1/KCNQ5/RYR2/CHD7	14
GO:0050919	negative chemotaxis	6/104	2.17E-07	2.82879E-05	2.22E-05	SEMA6D/SEMA5A/EPHA7/ROBO1/EFNA5/UNC5C	6

GO:0010882	regulation of cardiac muscle contraction by calcium ion signaling	5/104	2.77E-07	3.39025E-05	2.67E-05	DMD/SLC8A1/ANK2/CALM1/RYR2	5
GO:0032414	positive regulation of ion transmembrane transporter activity	7/104	4.37E-07	5.03582E-05	3.96E-05	ANK3/GAL/DMD/TMSB4X/ANK2/CALM1/RYR2	7
GO:0032411	positive regulation of transporter activity	7/104	8.7E-07	9.47159E-05	7.45E-05	ANK3/GAL/DMD/TMSB4X/ANK2/CALM1/RYR2	7
GO:0050770	regulation of axonogenesis	8/104	2.52E-06	0.000259402	0.000204	DSCAM/PAK3/SEMA6D/MAP1B/SEMA5A/EPHA7/ROBO1/EFNA5	8
GO:0086001	cardiac muscle cell action potential	6/104	3.88E-06	0.000371685	0.000292	ANK3/DMD/SLC8A1/ANK2/CALM1/RYR2	6

GO:0048639	positive regulation of developmental growth	8/104	3.98E-06	0.000371685	0.000292	DSCAM/MAP1B/SYT1/ERBB4/SEMA5A/BASP1/EFNA5/CHD7	8
GO:0055117	regulation of cardiac muscle contraction	6/104	4.51E-06	0.00040191	0.000316	DMD/SLC8A1/PDE4B/ANK2/CALM1/RYR2	6
GO:2001257	regulation of cation channel activity	7/104	5.3E-06	0.000451465	0.000355	ANK3/GAL/DMD/TMSB4X/PDE4B/ANK2/CALM1	7
GO:0051279	regulation of release of sequestered calcium ion into cytosol	6/104	6.49E-06	0.000529492	0.000416	DMD/SLC8A1/ANK2/CALM1/RYR2/CHD7	6
GO:0022898	regulation of transmembrane transporter activity	9/104	6.97E-06	0.000546382	0.00043	ANK3/GAL/DMD/ACTB/TMSB4X/PDE4B/ANK2/CALM1/RYR2	9

GO:2001259	positive regulation of cation channel activity	5/104	7.26E-06	0.000546948	0.00043	ANK3/GAL/TMSB4X/ANK2/CALM1	5
GO:0032970	regulation of actin filament-based process	11/104	7.79E-06	0.00056531	0.000444	PAK3/ACTG1/TMSB4X/STMN1/SEMA5A/PDE4B/EFNA5/ANK2/RYR2/CRACD/CLASP2	11
GO:0048013	ephrin receptor signaling pathway	5/104	8.86E-06	0.00062021	0.000488	PAK3/EPHA7/EFNA5/ARHGEF28/KALRN	5
GO:1904062	regulation of monoatomic cation transmembrane transport	10/104	9.51E-06	0.000642423	0.000505	ANK3/GAL/DMD/TMSB4X/SLC8A1/PDE4B/ANK2/CALM1/RYR2/CHD7	10
GO:0099173	postsynapse organization	8/104	1.29E-05	0.000801979	0.00063	GAP43/NRXN1/PAK3/ACTB/ACTG1/EPHA7/NLGN4X/PTPRD	8

GO:1904064	positive regulation of cation transmembrane transport	7/104	1.3E-05	0.000801979	0.00063	ANK3/GAL/DMD/TMSB4X/ANK2/CALM1/RYR2	7
GO:0060485	mesenchyme development	10/104	1.32E-05	0.000801979	0.00063	NCAM1/SEMA6D/ERBB4/SEMA5A/BNC2/ROBO1/BASP1/LDLRAD4/CLASP2/SOX4	10
GO:0048638	regulation of developmental growth	10/104	1.35E-05	0.000801979	0.00063	DSCAM/SEMA6D/MAP1B/SYT1/ERBB4/SEMA5A/EPHA7/BASP1/EFNA5/CHD7	10
GO:0001508	action potential	7/104	1.63E-05	0.000940161	0.000739	ANK3/DMD/KCNH7/SLC8A1/ANK2/CALM1/RYR2	7
GO:0006942	regulation of striated muscle contraction	6/104	1.79E-05	0.001003904	0.000789	DMD/SLC8A1/PDE4B/ANK2/CALM1/RYR2	6

GO:0032409	regulation of transporter activity	9/104	1.9E-05	0.001035336	0.000814	ANK3/GAL/DMD/ACTB/TMSB4X/PDE4B/ ANK2/CALM1/RYR2	9
GO:0008037	cell recognition	7/104	2.3E-05	0.001212612	0.000953	CNTNAP2/DSCAM/GAP43/SEMA5A/ROB O1/CD9/NCAM2	7
GO:0009612	response to mechanical stimulus	8/104	2.35E-05	0.001212612	0.000953	CNTNAP2/TUBA1A/NRXN1/DMD/MAP1B/ /SCN9A/SLC8A1/RYR2	8
GO:0031346	positive regulation of cell projection organization	10/104	2.66E-05	0.001328412	0.001044	DSCAM/TUBB2B/STMN2/MAGI2/MAP1B/ SEMA5A/ROBO1/EFNA5/PTPRD/TENM3	10
GO:0034767	positive regulation of monoatomic ion transmembrane transport	7/104	2.72E-05	0.001328412	0.001044	ANK3/GAL/DMD/TMSB4X/ANK2/CALM1 /RYR2	7

GO:0010644	cell communication by electrical coupling	4/104	2.78E-05	0.001328412	0.001044	ANK3/SLC8A1/CALM1/RYR2	4
GO:0061387	regulation of extent of cell growth	6/104	3.1E-05	0.001417171	0.001114	DSCAM/SEMA6D/MAP1B/SEMA5A/EPHA7/EFNA5	6
GO:0042391	regulation of membrane potential	11/104	3.11E-05	0.001417171	0.001114	ANK3/NRXN1/DMD/KCNH7/KCNMA1/SLC8A1/ANK2/CALM1/KCNQ5/NLGN4X/RYR2	11
GO:0032535	regulation of cellular component size	10/104	3.78E-05	0.001684289	0.001324	DSCAM/PAK3/SEMA6D/MAP1B/TMSB4X/KCNMA1/SEMA5A/EPHA7/EFNA5/CRACD	10
GO:0032412	regulation of monoatomic ion transmembrane transporter activity	8/104	4.19E-05	0.001786537	0.001404	ANK3/GAL/DMD/TMSB4X/PDE4B/ANK2/CALM1/RYR2	8

GO:0051261	protein depolymerization	6/104	4.2E-05	0.001786537	0.001404	STMN2/MAP1B/STMN1/SEMA5A/CRACD/CLASP2	6
GO:0005513	detection of calcium ion	3/104	4.47E-05	0.001862399	0.001464	SYT1/CALM1/RYR2	3
GO:0051651	maintenance of location in cell	8/104	5.03E-05	0.002011913	0.001582	ANK3/DMD/TMSB4X/SLC8A1/ANK2/CALM1/RYR2/CHD7	8
GO:1903169	regulation of calcium ion transmembrane transport	7/104	5.03E-05	0.002011913	0.001582	DMD/SLC8A1/PDE4B/ANK2/CALM1/RYR2/CHD7	7
GO:0048588	developmental cell growth	8/104	5.33E-05	0.002089308	0.001642	DSCAM/SEMA6D/MAP1B/SYT1/SEMA5A/EPHA7/EFNA5/SORBS2	8

GO:0031111	negative regulation of microtubule polymerization or depolymerization	4/104	5.56E-05	0.002137197	0.00168	STMN2/MAP1B/STMN1/CLASP2	4
GO:0060560	developmental growth involved in morphogenesis	8/104	6.17E-05	0.00228191	0.001794	DSCAM/SEMA6D/MAGI2/MAP1B/SYT1/SEMA5A/EPHA7/EFNA5	8
GO:0099068	postsynapse assembly	4/104	6.17E-05	0.00228191	0.001794	GAP43/NRXN1/NLGN4X/PTPRD	4
GO:0010959	regulation of metal ion transport	10/104	6.97E-05	0.002477358	0.001947	ANK3/GAL/DMD/VIP/SLC8A1/PDE4B/ANK2/CALM1/RYR2/CHD7	10
GO:0010649	regulation of cell communication by electrical coupling	3/104	7.05E-05	0.002477358	0.001947	ANK3/SLC8A1/CALM1	3

GO:0050772	positive regulation of axonogenesis	5/104	7.08E-05	0.002477358	0.001947	DSCAM/MAP1B/SEMA5A/ROBO1/EFNA5	5
GO:0008361	regulation of cell size	7/104	7.93E-05	0.002719592	0.002138	DSCAM/SEMA6D/MAP1B/KCNMA1/SEMA5A/EPHA7/EFNA5	7
GO:0050804	modulation of chemical synaptic transmission	11/104	8.05E-05	0.002719592	0.002138	DLGAP2/TUBB2B/NRXN1/DLGAP1/MAP1B/SYT1/CNTNAP4/EPHA7/NLGN4X/PTPRD/TRIO	11
GO:0099177	regulation of trans-synaptic signaling	11/104	8.2E-05	0.002722467	0.00214	DLGAP2/TUBB2B/NRXN1/DLGAP1/MAP1B/SYT1/CNTNAP4/EPHA7/NLGN4X/PTPRD/TRIO	11
GO:1901019	regulation of calcium ion transmembrane transporter activity	5/104	8.48E-05	0.00273132	0.002147	DMD/PDE4B/ANK2/CALM1/RYR2	5

GO:0045927	positive regulation of growth	8/104	8.63E-05	0.00273132	0.002147	DSCAM/MAP1B/SYT1/ERBB4/SEMA5A/BASP1/EFNA5/CHD7	8
GO:0007158	neuron cell-cell adhesion	3/104	8.64E-05	0.00273132	0.002147	NRXN1/NLGN4X/NCAM2	3
GO:0055001	muscle cell development	7/104	0.000103	0.003204363	0.002519	DMD/ACTG1/UCHL1/HDAC9/SLC8A1/ANK2/SORBS2	7
GO:0051209	release of sequestered calcium ion into cytosol	6/104	0.000107	0.003267407	0.002569	DMD/SLC8A1/ANK2/CALM1/RYR2/CHD7	6
GO:0007019	microtubule depolymerization	4/104	0.000109	0.00328606	0.002583	STMN2/MAP1B/STMN1/CLASP2	4

GO:0051283	negative regulation of sequestering of calcium ion	6/104	0.000111	0.003298859	0.002593	DMD/SLC8A1/ANK2/CALM1/RYR2/CHD7	6
GO:1901879	regulation of protein depolymerization	5/104	0.000113	0.003298914	0.002593	STMN2/MAP1B/SEMA5A/CRACD/CLASP 2	5
GO:0051282	regulation of sequestering of calcium ion	6/104	0.00012	0.003417258	0.002686	DMD/SLC8A1/ANK2/CALM1/RYR2/CHD7	6
GO:0060048	cardiac muscle contraction	6/104	0.00012	0.003417258	0.002686	DMD/SLC8A1/PDE4B/ANK2/CALM1/RYR 2	6
GO:0097553	calcium ion transmembrane import into cytosol	7/104	0.000141	0.00388012	0.00305	DMD/SCN9A/SLC8A1/ANK2/CALM1/RYR 2/CHD7	7

GO:0051208	sequestering of calcium ion	6/104	0.000141	0.00388012	0.00305	DMD/SLC8A1/ANK2/CALM1/RYR2/CHD7	6
GO:0071625	vocalization behavior	3/104	0.000148	0.003965997	0.003118	CNTNAP2/NRXN1/NLGN4X	3
GO:1901881	positive regulation of protein depolymerization	3/104	0.000148	0.003965997	0.003118	STMN2/SEMA5A/CRACD	3
GO:0030534	adult behavior	6/104	0.000152	0.004016619	0.003158	CNTNAP2/TUBA1A/NRXN1/UCHL1/NLGN4X/CHD7	6
GO:0046785	microtubule polymerization	5/104	0.000172	0.004486028	0.003527	TUBA1A/STMN2/MAP1B/STMN1/CLASP2	5

GO:1901888	regulation of cell junction assembly	7/104	0.000178	0.004588705	0.003607	CNTNAP2/NRXN1/ACTG1/EPHA7/EFNA5/PTPRD/CLASP2	7
GO:0043270	positive regulation of monoatomic ion transport	7/104	0.000183	0.004644906	0.003651	ANK3/GAL/DMD/TMSB4X/ANK2/CALM1/RYR2	7
GO:0051258	protein polymerization	8/104	0.000185	0.004644906	0.003651	TUBA1A/STMN2/PAK3/MAP1B/TMSB4X/STMN1/CRACD/CLASP2	8
GO:0034764	positive regulation of transmembrane transport	7/104	0.0002	0.004948364	0.00389	ANK3/GAL/DMD/TMSB4X/ANK2/CALM1/RYR2	7
GO:0086012	membrane depolarization during cardiac muscle cell action potential	3/104	0.000232	0.005682784	0.004467	ANK3/SLC8A1/ANK2	3

GO:0002027	regulation of heart rate	5/104	0.000252	0.006016288	0.004729	DMD/SLC8A1/ANK2/CALM1/RYR2	5
GO:0051960	regulation of nervous system development	10/104	0.000252	0.006016288	0.004729	DSCAM/NRXN1/SEMA6D/MAP1B/SEMA5A/EPHA7/ROBO1/EFNA5/CHD7/PTPRD	10
GO:0006935	chemotaxis	10/104	0.000261	0.006150296	0.004835	DSCAM/TUBB2B/SEMA6D/TMSB4X/SEMA5A/EPHA7/ROBO1/PDE4B/EFNA5/UNC5C	10
GO:0042330	taxis	10/104	0.00027	0.006287032	0.004942	DSCAM/TUBB2B/SEMA6D/TMSB4X/SEMA5A/EPHA7/ROBO1/PDE4B/EFNA5/UNC5C	10
GO:0051494	negative regulation of cytoskeleton organization	6/104	0.000286	0.006592744	0.005183	STMN2/MAP1B/TMSB4X/STMN1/CRACD/CLASP2	6

GO:0086065	cell communication involved in cardiac conduction	4/104	0.000294	0.00669461	0.005263	SLC8A1/ANK2/CALM1/RYR2	4
GO:1902903	regulation of supramolecular fiber organization	9/104	0.0003	0.006761291	0.005315	STMN2/PAK3/MAP1B/ACTG1/TMSB4X/STMN1/SEMA5A/CRACD/CLASP2	9
GO:0050767	regulation of neurogenesis	9/104	0.000306	0.006811414	0.005355	DSCAM/SEMA6D/MAP1B/SEMA5A/EPHA7/ROBO1/EFNA5/CHD7/PTPRD	9
GO:1902904	negative regulation of supramolecular fiber organization	6/104	0.000326	0.007143444	0.005616	STMN2/MAP1B/TMSB4X/STMN1/CRACD/CLASP2	6
GO:1902414	protein localization to cell junction	5/104	0.000328	0.007143444	0.005616	NRXN1/ACTB/ACTG1/ERBB4/PCLO	5

GO:0071709	membrane assembly	4/104	0.000335	0.007210606	0.005668	ANK3/NRXN1/NLGN4X/PTPRD	4
GO:0035994	response to muscle stretch	3/104	0.000342	0.007213696	0.005671	DMD/SLC8A1/RYR2	3
GO:0086064	cell communication by electrical coupling involved in cardiac conduction	3/104	0.000342	0.007213696	0.005671	SLC8A1/CALM1/RYR2	3
GO:0006937	regulation of muscle contraction	6/104	0.000358	0.007467239	0.00587	DMD/SLC8A1/PDE4B/ANK2/CALM1/RYR2	6
GO:0006813	potassium ion transport	7/104	0.000377	0.007778067	0.006114	ANK3/GAL/KCNH7/VIP/KCNMA1/ANK2/KCNQ5	7

GO:0007026	negative regulation of microtubule depolymerization	3/104	0.000386	0.007868224	0.006185	STMN2/MAP1B/CLASP2	3
GO:0050807	regulation of synapse organization	7/104	0.000406	0.00820498	0.00645	TUBA1A/NRXN1/PAK3/TUBB/EPHA7/EFNA5/PTPRD	7
GO:0032984	protein-containing complex disassembly	7/104	0.000416	0.008262124	0.006495	STMN2/MAP1B/STMN1/SEMA5A/CALM1/CRACD/CLASP2	7
GO:0030900	forebrain development	9/104	0.000418	0.008262124	0.006495	CNTNAP2/TUBA1A/TUBB2B/BCL11B/ERBB4/SEMA5A/ROBO1/CHD7/PCDH9	9
GO:0044091	membrane biogenesis	4/104	0.000429	0.008379945	0.006588	ANK3/NRXN1/NLGN4X/PTPRD	4

GO:0098698	postsynaptic specialization assembly	3/104	0.000432	0.008379945	0.006588	GAP43/NRXN1/PTPRD	3
GO:0050803	regulation of synapse structure or activity	7/104	0.00047	0.008991947	0.007069	TUBA1A/NRXN1/PAK3/TUBB/EPHA7/EFNA5/PTPRD	7
GO:0051924	regulation of calcium ion transport	7/104	0.000481	0.008991947	0.007069	DMD/SLC8A1/PDE4B/ANK2/CALM1/RYR2/CHD7	7
GO:0086010	membrane depolarization during action potential	3/104	0.000482	0.008991947	0.007069	ANK3/SLC8A1/ANK2	3
GO:1903779	regulation of cardiac conduction	3/104	0.000482	0.008991947	0.007069	SLC8A1/ANK2/RYR2	3

GO:0048857	neural nucleus development	4/104	0.000511	0.009447153	0.007427	ACTB/BASP1/PHOX2A/CALM1	4
GO:0098901	regulation of cardiac muscle cell action potential	3/104	0.000535	0.009802724	0.007706	ANK2/CALM1/RYR2	3
GO:0032956	regulation of actin cytoskeleton organization	8/104	0.000554	0.010055657	0.007905	PAK3/ACTG1/TMSB4X/STMN1/SEMA5A/EFNA5/CRACD/CLASP2	8
GO:0006941	striated muscle contraction	6/104	0.000577	0.010372805	0.008154	DMD/SLC8A1/PDE4B/ANK2/CALM1/RYR2	6
GO:0031114	regulation of microtubule depolymerization	3/104	0.000593	0.010425569	0.008196	STMN2/MAP1B/CLASP2	3

GO:1901021	positive regulation of calcium ion transmembrane transporter activity	3/104	0.000593	0.010425569	0.008196	ANK2/CALM1/RYR2	3
GO:0043244	regulation of protein-containing complex disassembly	5/104	0.000596	0.010425569	0.008196	STMN2/MAP1B/SEMA5A/CRACD/CLASP2	5
GO:1901880	negative regulation of protein depolymerization	4/104	0.000604	0.010467916	0.008229	STMN2/MAP1B/CRACD/CLASP2	4
GO:0048488	synaptic vesicle endocytosis	4/104	0.000637	0.010949365	0.008607	SYT1/ACTB/ACTG1/NLGN4X	4
GO:0140238	presynaptic endocytosis	4/104	0.000672	0.011444356	0.008997	SYT1/ACTB/ACTG1/NLGN4X	4

GO:0051235	maintenance of location	8/104	0.00071	0.011989551	0.009425	ANK3/DMD/TMSB4X/SLC8A1/ANK2/CALM1/RYR2/CHD7	8
GO:0070588	calcium ion transmembrane transport	8/104	0.000737	0.012335579	0.009697	DMD/SCN9A/SLC8A1/PDE4B/ANK2/CALM1/RYR2/CHD7	8
GO:0110053	regulation of actin filament organization	7/104	0.000791	0.013125199	0.010318	PAK3/ACTG1/TMSB4X/STMN1/SEMA5A/CRACD/CLASP2	7
GO:0099504	synaptic vesicle cycle	6/104	0.0008	0.013177658	0.010359	SYT1/ACTB/ACTG1/SYN2/PCLO/NLGN4X	6
GO:0021537	telencephalon development	7/104	0.000843	0.013758775	0.010816	CNTNAP2/TUBA1A/TUBB2B/BCL11B/ERBB4/ROBO1/CHD7	7

GO:0048841	regulation of axon extension involved in axon guidance	3/104	0.000859	0.013915179	0.010939	DSCAM/SEMA6D/SEMA5A	3
GO:0031109	microtubule polymerization or depolymerization	5/104	0.000878	0.014099896	0.011084	TUBA1A/STMN2/MAP1B/STMN1/CLASP2	5
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	7/104	0.000898	0.014297584	0.01124	DSCAM/ADGRL3/ROBO1/EFNA5/PTPRD/TENM3/PCDH9	7
GO:0032271	regulation of protein polymerization	6/104	0.000935	0.014442882	0.011354	STMN2/PAK3/MAP1B/TMSB4X/STMN1/C RACD	6
GO:0021772	olfactory bulb development	3/104	0.000936	0.014442882	0.011354	ERBB4/ROBO1/CHD7	3

GO:0086004	regulation of cardiac muscle cell contraction	3/104	0.000936	0.014442882	0.011354	PDE4B/ANK2/RYR2	3
GO:1901385	regulation of voltage-gated calcium channel activity	3/104	0.000936	0.014442882	0.011354	DMD/PDE4B/CALM1	3
GO:0032272	negative regulation of protein polymerization	4/104	0.000999	0.015165208	0.011922	STMN2/TMSB4X/STMN1/CRACD	4
GO:0043242	negative regulation of protein-containing complex disassembly	4/104	0.000999	0.015165208	0.011922	STMN2/MAP1B/CRACD/CLASP2	4
GO:0008016	regulation of heart contraction	6/104	0.001033	0.015569574	0.012239	DMD/SLC8A1/PDE4B/ANK2/CALM1/RYR2	6

GO:0007015	actin filament organization	9/104	0.001061	0.015858138	0.012466	PAK3/FMN2/ACTG1/TMSB4X/STMN1/SEMA5A/MARCKSL1/CRACD/CLASP2	9
GO:0010977	negative regulation of neuron projection development	5/104	0.001069	0.015858138	0.012466	STMN2/SEMA6D/SEMA5A/EPHA7/PTPRG	5
GO:0036465	synaptic vesicle recycling	4/104	0.001095	0.015884077	0.012487	SYT1/ACTB/ACTG1/NLGN4X	4
GO:0021988	olfactory lobe development	3/104	0.001103	0.015884077	0.012487	ERBB4/ROBO1/CHD7	3
GO:0043243	positive regulation of protein-containing complex disassembly	3/104	0.001103	0.015884077	0.012487	STMN2/SEMA5A/CRACD	3

GO:0045773	positive regulation of axon extension	3/104	0.001103	0.015884077	0.012487	DSCAM/MAP1B/SEMA5A	3
GO:0051962	positive regulation of nervous system development	7/104	0.001124	0.01606681	0.01263	DSCAM/NRXN1/MAP1B/SEMA5A/ROBO1/EFNA5/PTPRD	7
GO:0035633	maintenance of blood-brain barrier	3/104	0.001192	0.016498157	0.012969	DMD/ACTB/ACTG1	3
GO:0048846	axon extension involved in axon guidance	3/104	0.001192	0.016498157	0.012969	DSCAM/SEMA6D/SEMA5A	3
GO:0060563	neuroepithelial cell differentiation	3/104	0.001192	0.016498157	0.012969	MAP1B/TUBB/SOX4	3

GO:1902284	neuron projection extension involved in neuron projection guidance	3/104	0.001192	0.016498157	0.012969	DSCAM/SEMA6D/SEMA5A	3
GO:0045216	cell-cell junction organization	6/104	0.001196	0.016498157	0.012969	CNTNAP2/ACTB/ACTG1/ANK2/CD9/NLG N4X	6
GO:0051592	response to calcium ion	5/104	0.001212	0.016596729	0.013047	TUBA1A/SYT1/KCNMA1/CALM1/RYR2	5
GO:0071805	potassium ion transmembrane transport	6/104	0.001284	0.017471118	0.013734	ANK3/GAL/KCNH7/KCNMA1/ANK2/KCN Q5	6
GO:0097090	presynaptic membrane organization	2/104	0.001315	0.01752885	0.01378	NLGN4X/PTPRD	2

GO:0097104	postsynaptic membrane assembly	2/104	0.001315	0.01752885	0.01378	NRXN1/NLGN4X	2
GO:0098598	learned vocalization behavior or vocal learning	2/104	0.001315	0.01752885	0.01378	CNTNAP2/NRXN1	2
GO:0099003	vesicle-mediated transport in synapse	6/104	0.001378	0.018233592	0.014334	SYT1/ACTB/ACTG1/SYN2/PCLO/NLGN4X	6
GO:0023061	signal release	9/104	0.001421	0.018688123	0.014691	GAL/NRXN1/SYT1/VIP/SYN2/PCLO/EFNA5/CHD7/SOX4	9
GO:1903115	regulation of actin filament-based movement	3/104	0.001489	0.0194453	0.015286	PDE4B/ANK2/RYR2	3

GO:0003357	noradrenergic neuron differentiation	2/104	0.001602	0.019978715	0.015706	PHOX2A/SOX4	2
GO:0021889	olfactory bulb interneuron differentiation	2/104	0.001602	0.019978715	0.015706	ERBB4/ROBO1	2
GO:0071313	cellular response to caffeine	2/104	0.001602	0.019978715	0.015706	SLC8A1/RYR2	2
GO:0071872	cellular response to epinephrine stimulus	2/104	0.001602	0.019978715	0.015706	PDE4B/RYR2	2
GO:0071895	odontoblast differentiation	2/104	0.001602	0.019978715	0.015706	MAP1B/TUBB	2

GO:0086070	SA node cell to atrial cardiac muscle cell communication	2/104	0.001602	0.019978715	0.015706	ANK2/RYR2	2
GO:1901841	regulation of high voltage-gated calcium channel activity	2/104	0.001602	0.019978715	0.015706	PDE4B/CALM1	2
GO:0030901	midbrain development	4/104	0.001611	0.019978715	0.015706	ACTB/BASP1/PHOX2A/CALM1	4
GO:0001738	morphogenesis of a polarized epithelium	4/104	0.001678	0.020539371	0.016146	MAGI2/ACTB/ACTG1/ERBB4	4
GO:0030516	regulation of axon extension	4/104	0.001678	0.020539371	0.016146	DSCAM/SEMA6D/MAP1B/SEMA5A	4

GO:0099084	postsynaptic specialization organization	3/104	0.00171	0.020807029	0.016357	GAP43/NRXN1/PTPRD	3
GO:0007043	cell-cell junction assembly	5/104	0.001775	0.021461404	0.016871	CNTNAP2/ACTB/ACTG1/ANK2/CD9	5
GO:0050920	regulation of chemotaxis	6/104	0.001803	0.021673754	0.017038	DSCAM/TUBB2B/SEMA6D/TMSB4X/SEMA5A/ROBO1	6
GO:0021762	substantia nigra development	3/104	0.001828	0.021701508	0.01706	ACTB/BASP1/CALM1	3
GO:0071526	semaphorin-plexin signaling pathway	3/104	0.001828	0.021701508	0.01706	NCAM1/SEMA6D/SEMA5A	3

GO:0050890	cognition	7/104	0.001869	0.022008581	0.017301	CNTNAP2/TUBA1A/NRXN1/VIP/CAMK4/ NLGN4X/CHD7	7
GO:0007044	cell-substrate junction assembly	4/104	0.001887	0.022008581	0.017301	ACTG1/EFNA5/DST/CLASP2	4
GO:0031110	regulation of microtubule polymerization or depolymerization	4/104	0.001887	0.022008581	0.017301	STMN2/MAP1B/STMN1/CLASP2	4
GO:0031223	auditory behavior	2/104	0.001915	0.022071319	0.017351	CNTNAP2/NRXN1	2
GO:0033605	positive regulation of catecholamine secretion	2/104	0.001915	0.022071319	0.017351	SYT1/VIP	2

GO:0034109	homotypic cell-cell adhesion	4/104	0.001961	0.022468138	0.017663	ANK3/ACTB/ACTG1/CD9	4
GO:0070507	regulation of microtubule cytoskeleton organization	5/104	0.001981	0.022566761	0.01774	STMN2/MAP1B/STMN1/EFNA5/CLASP2	5
GO:0061337	cardiac conduction	4/104	0.002037	0.023066654	0.018133	SLC8A1/ANK2/CALM1/RYR2	4
GO:0030307	positive regulation of cell growth	5/104	0.002091	0.023407398	0.018401	DSCAM/MAP1B/SYT1/SEMA5A/EFNA5	5
GO:0050905	neuromuscular process	5/104	0.002091	0.023407398	0.018401	CNTNAP2/TUBA1A/NRXN1/DMD/UCHL1	5

GO:0030072	peptide hormone secretion	6/104	0.002183	0.024301937	0.019104	GAL/VIP/PCLO/EFNA5/CHD7/SOX4	6
GO:0099054	presynapse assembly	3/104	0.002211	0.02439454	0.019177	PCLO/NLGN4X/PTPRD	3
GO:0042692	muscle cell differentiation	8/104	0.002225	0.02439454	0.019177	DMD/ACTG1/UCLH1/HDAC9/SLC8A1/ANK2/CD9/SORBS2	8
GO:0050769	positive regulation of neurogenesis	6/104	0.002229	0.02439454	0.019177	DSCAM/MAP1B/SEMA5A/ROBO1/EFNA5/PTPRD	6
GO:0030836	positive regulation of actin filament depolymerization	2/104	0.002255	0.024411124	0.01919	SEMA5A/CRACD	2

GO:0031115	negative regulation of microtubule polymerization	2/104	0.002255	0.024411124	0.01919	STMN2/STMN1	2
GO:0060047	heart contraction	6/104	0.002275	0.024491821	0.019253	DMD/SLC8A1/PDE4B/ANK2/CALM1/RYR2	6
GO:0003205	cardiac chamber development	5/104	0.002384	0.025525759	0.020066	ROBO1/ANK2/RYR2/CHD7/SOX4	5
GO:0002790	peptide secretion	6/104	0.002419	0.025754138	0.020246	GAL/VIP/PCLO/EFNA5/CHD7/SOX4	6
GO:0043266	regulation of potassium ion transport	4/104	0.002447	0.02576784	0.020256	ANK3/GAL/VIP/ANK2	4

GO:0150115	cell-substrate junction organization	4/104	0.002447	0.02576784	0.020256	ACTG1/EFNA5/DST/CLASP2	4
GO:0090257	regulation of muscle system process	6/104	0.002468	0.02585786	0.020327	DMD/SLC8A1/PDE4B/ANK2/CALM1/RYR2	6
GO:0007638	mechanosensory behavior	2/104	0.002622	0.026891741	0.02114	CNTNAP2/NRXN1	2
GO:0071415	cellular response to purine-containing compound	2/104	0.002622	0.026891741	0.02114	SLC8A1/RYR2	2
GO:0071871	response to epinephrine	2/104	0.002622	0.026891741	0.02114	PDE4B/RYR2	2

GO:0099150	regulation of postsynaptic specialization assembly	2/104	0.002622	0.026891741	0.02114	GAP43/PTPRD	2
GO:1901890	positive regulation of cell junction assembly	4/104	0.002812	0.028696052	0.022558	CNTNAP2/NRXN1/EFNA5/PTPRD	4
GO:0003015	heart process	6/104	0.002891	0.029090016	0.022868	DMD/SLC8A1/PDE4B/ANK2/CALM1/RYR2	6
GO:0031103	axon regeneration	3/104	0.002954	0.029090016	0.022868	GAP43/MAP1B/NREP	3
GO:0035176	social behavior	3/104	0.002954	0.029090016	0.022868	CNTNAP2/NRXN1/NLGN4X	3

GO:0099172	presynapse organization	3/104	0.002954	0.029090016	0.022868	PCLO/NLGN4X/PTPRD	3
GO:0001764	neuron migration	5/104	0.002987	0.029090016	0.022868	TUBA1A/TUBB2B/ADGRL3/MAP1B/UNC5C	5
GO:0035265	organ growth	5/104	0.002987	0.029090016	0.022868	ERBB4/BNC2/BASP1/NLGN4X/SORBS2	5
GO:0003279	cardiac septum development	4/104	0.003009	0.029090016	0.022868	ROBO1/ANK2/CHD7/SOX4	4
GO:0031000	response to caffeine	2/104	0.003014	0.029090016	0.022868	SLC8A1/RYR2	2

GO:0051284	positive regulation of sequestering of calcium ion	2/104	0.003014	0.029090016	0.022868	CALM1/RYR2	2
GO:2000651	positive regulation of sodium ion transmembrane transporter activity	2/104	0.003014	0.029090016	0.022868	ANK3/DMD	2
GO:2001028	positive regulation of endothelial cell chemotaxis	2/104	0.003014	0.029090016	0.022868	TMSB4X/SEMA5A	2
GO:1903522	regulation of blood circulation	6/104	0.003062	0.029408632	0.023119	DMD/SLC8A1/PDE4B/ANK2/CALM1/RYR2	6
GO:1990138	neuron projection extension	5/104	0.003134	0.029950102	0.023544	DSCAM/SEMA6D/MAP1B/SYT1/SEMA5A	5

GO:0010720	positive regulation of cell development	8/104	0.003174	0.030181696	0.023726	DSCAM/MAP1B/ACTB/SEMA5A/ROBO1/EFNA5/PTPRD/SOX4	8
GO:0006816	calcium ion transport	8/104	0.003217	0.030448715	0.023936	DMD/SCN9A/SLC8A1/PDE4B/ANK2/CALM1/RYR2/CHD7	8
GO:0051703	biological process involved in intraspecies interaction between organisms	3/104	0.00329	0.030666805	0.024108	CNTNAP2/NRXN1/NLGN4X	3
GO:0006936	muscle contraction	7/104	0.003299	0.030666805	0.024108	DMD/KCNMA1/SLC8A1/PDE4B/ANK2/CALM1/RYR2	7
GO:0015833	peptide transport	6/104	0.003303	0.030666805	0.024108	GAL/VIP/PCLO/EFNA5/CHD7/SOX4	6

GO:0048762	mesenchymal cell differentiation	6/104	0.003303	0.030666805	0.024108	NCAM1/SEMA6D/ERBB4/SEMA5A/LDLR AD4/CLASP2	6
GO:0097091	synaptic vesicle clustering	2/104	0.003433	0.031720245	0.024936	SYN2/PCLO	2
GO:0003012	muscle system process	8/104	0.003536	0.032521177	0.025565	DMD/KCNMA1/SLC8A1/PDE4B/ANK2/CA LM1/RYR2/SORBS2	8
GO:0051963	regulation of synapse assembly	4/104	0.003653	0.033444813	0.026291	NRXN1/EPHA7/EFNA5/PTPRD	4
GO:1901016	regulation of potassium ion transmembrane transporter activity	3/104	0.003835	0.034834909	0.027384	ANK3/GAL/ANK2	3

GO:0055119	relaxation of cardiac muscle	2/104	0.003876	0.034834909	0.027384	SLC8A1/PDE4B	2
GO:0061548	ganglion development	2/104	0.003876	0.034834909	0.027384	TUBB3/UNC5C	2
GO:0098974	postsynaptic actin cytoskeleton organization	2/104	0.003876	0.034834909	0.027384	ACTB/ACTG1	2
GO:0031102	neuron projection regeneration	3/104	0.004028	0.036029754	0.028324	GAP43/MAP1B/NREP	3
GO:0007611	learning or memory	6/104	0.00411	0.036596404	0.028769	CNTNAP2/TUBA1A/NRXN1/VIP/CAMK4/ NLGN4X	6

GO:0031099	regeneration	5/104	0.004132	0.036622844	0.02879	GAP43/MAP1B/ERBB4/CD9/NREP	5
GO:0031345	negative regulation of cell projection organization	5/104	0.004224	0.036965516	0.029059	STMN2/SEMA6D/SEMA5A/EPHA7/PTPRG	5
GO:0001755	neural crest cell migration	3/104	0.004227	0.036965516	0.029059	SEMA6D/ERBB4/SEMA5A	3
GO:0098900	regulation of action potential	3/104	0.004227	0.036965516	0.029059	ANK2/CALM1/RYR2	3
GO:0031644	regulation of nervous system process	4/104	0.004258	0.037070698	0.029142	DLGAP2/NRXN1/DLGAP1/NLGN4X	4

GO:0048675	axon extension	4/104	0.004517	0.039156018	0.030781	DSCAM/SEMA6D/MAP1B/SEMA5A	4
GO:0031113	regulation of microtubule polymerization	3/104	0.004642	0.039887813	0.031356	STMN2/MAP1B/STMN1	3
GO:0090497	mesenchymal cell migration	3/104	0.004642	0.039887813	0.031356	SEMA6D/ERBB4/SEMA5A	3
GO:0032516	positive regulation of phosphoprotein phosphatase activity	2/104	0.004839	0.040513215	0.031848	MAGI2/CALM1	2
GO:0086014	atrial cardiac muscle cell action potential	2/104	0.004839	0.040513215	0.031848	ANK2/RYR2	2

GO:0086026	atrial cardiac muscle cell to AV node cell signaling	2/104	0.004839	0.040513215	0.031848	ANK2/RYR2	2
GO:0086066	atrial cardiac muscle cell to AV node cell communication	2/104	0.004839	0.040513215	0.031848	ANK2/RYR2	2
GO:1900242	regulation of synaptic vesicle endocytosis	2/104	0.004839	0.040513215	0.031848	ACTB/ACTG1	2
GO:1902307	positive regulation of sodium ion transmembrane transport	2/104	0.004839	0.040513215	0.031848	ANK3/DMD	2
GO:0051893	regulation of focal adhesion assembly	3/104	0.005082	0.042005819	0.033021	ACTG1/EFNA5/CLASP2	3

GO:0051965	positive regulation of synapse assembly	3/104	0.005082	0.042005819	0.033021	NRXN1/EFNA5/PTPRD	3
GO:0090109	regulation of cell-substrate junction assembly	3/104	0.005082	0.042005819	0.033021	ACTG1/EFNA5/CLASP2	3
GO:1903131	mononuclear cell differentiation	8/104	0.005125	0.042184843	0.033162	BCL11B/ACTB/ITGB8/HDAC9/CAMK4/CHD7/PHF14/SOX4	8
GO:0003215	cardiac right ventricle morphogenesis	2/104	0.005358	0.043027614	0.033825	CHD7/SOX4	2
GO:0043011	myeloid dendritic cell differentiation	2/104	0.005358	0.043027614	0.033825	ITGB8/CAMK4	2

GO:0099188	postsynaptic cytoskeleton organization	2/104	0.005358	0.043027614	0.033825	ACTB/ACTG1	2
GO:0003206	cardiac chamber morphogenesis	4/104	0.005359	0.043027614	0.033825	ROBO1/RYR2/CHD7/SOX4	4
GO:0003231	cardiac ventricle development	4/104	0.005359	0.043027614	0.033825	ROBO1/RYR2/CHD7/SOX4	4
GO:0021987	cerebral cortex development	4/104	0.005359	0.043027614	0.033825	CNTNAP2/TUBA1A/TUBB2B/ROBO1	4
GO:0010927	cellular component assembly involved in morphogenesis	4/104	0.005509	0.044050104	0.034628	ACTG1/ANK2/CD9/CLASP2	4

GO:0035904	aorta development	3/104	0.005546	0.044162125	0.034717	ROBO1/CHD7/SOX4	3
GO:0050771	negative regulation of axonogenesis	3/104	0.005787	0.045508116	0.035775	SEMA6D/SEMA5A/EPHA7	3
GO:0007413	axonal fasciculation	2/104	0.0059	0.045508116	0.035775	SEMA5A/NCAM2	2
GO:0048670	regulation of collateral sprouting	2/104	0.0059	0.045508116	0.035775	EPHA7/EFNA5	2
GO:0061318	renal filtration cell differentiation	2/104	0.0059	0.045508116	0.035775	MAGI2/BASP1	2

GO:0072112	podocyte differentiation	2/104	0.0059	0.045508116	0.035775	MAGI2/BASP1	2
GO:0097107	postsynaptic density assembly	2/104	0.0059	0.045508116	0.035775	NRXN1/PTPRD	2
GO:0106030	neuron projection fasciculation	2/104	0.0059	0.045508116	0.035775	SEMA5A/NCAM2	2
GO:1901018	positive regulation of potassium ion transmembrane transporter activity	2/104	0.0059	0.045508116	0.035775	GAL/ANK2	2
GO:0019722	calcium-mediated signaling	5/104	0.006147	0.047219661	0.03712	DMD/SLC8A1/ANK2/CALM1/RYR2	5

GO:0001667	ameboidal-type cell migration	8/104	0.00621	0.047333243	0.037209	SEMA6D/TMSB4X/HDAC9/ERBB4/SEMA5A/ROBO1/PTPRG/CLASP2	8
GO:0016049	cell growth	8/104	0.00621	0.047333243	0.037209	DSCAM/SEMA6D/MAP1B/SYT1/SEMA5A/EPHA7/EFNA5/SORBS2	8
GO:0150116	regulation of cell-substrate junction organization	3/104	0.006288	0.047741443	0.03753	ACTG1/EFNA5/CLASP2	3
GO:0021756	striatum development	2/104	0.006467	0.04835689	0.038014	CNTNAP2/BCL11B	2
GO:0048485	sympathetic nervous system development	2/104	0.006467	0.04835689	0.038014	PHOX2A/SOX4	2

GO:0072311	glomerular epithelial cell differentiation	2/104	0.006467	0.04835689	0.038014	MAGI2/BASP1	2
GO:0150105	protein localization to cell-cell junction	2/104	0.006467	0.04835689	0.038014	ACTB/ACTG1	2
GO:0030705	cytoskeleton-dependent intracellular transport	5/104	0.006518	0.048551878	0.038167	TUBA1A/MAP1B/TUBB/UCHL1/DST	5

Enrichment of Up-regulated genes in MN cluster

pathway ID	description	GeneRatio	<i>p</i>	adjusted <i>p</i>	<i>q</i> -value	gene ID	count
GO:0002181	cytoplasmic translation	61/104	3.3E-104	4.858E-101	4.8E-101	RPL39/RPL41/RPS27/RPL34/RPS18/RPL37A/RPS28/RPS21/RPS15A/RPL36A/RPL37/RPS23/RPL36/RPS19/RPS25/RPS12/RPL35A/RPL28/RPS24/RPL32/RPL26/RPS29/RPL30/RPS13/RPS27A/RPS15/RPLP2/RPS26/RPS6/RPL12/RPL17/RPL38/RPS8/RPL13/RPL10/RPL21/RPL23A/RPL11/RPL35/RPLP1/RPS11/RPL18A/RPL13A/RPL24/RPS3/RPS2/RPL29/RPL22/RPS16/FAU/RPL19/RPL10A/RPS10/RPS14/RPS5/RPL6/RPLP0/RPS3A/RPL18/RPL8/RPL9	61
GO:0042254	ribosome biogenesis	29/104	2.95E-27	2.2031E-24	2.17E-24	RPS27/RPS28/RPS21/RPS15A/RPS23/RPS19/RPS25/RPS12/RPL35A/RPS24/RPL26/RPS13/RPS15/RPS6/RPL38/RPS8/RPL10/RPL23A/RPL11/RPL35/RPS11/RPL24/RPS16/RPL10A/RPS14/RPS5/RPL6/RPLP0/RPS3A	29
GO:0042274	ribosomal small subunit biogenesis	19/104	4.43E-24	2.2048E-21	2.17E-21	RPS27/RPS28/RPS21/RPS15A/RPS23/RPS19/RPS25/RPS12/RPS24/RPS13/RPS15/RPS6/RPL38/RPS8/RPS11/RPS16/RPS14/RPS5/RPS3A	19

GO:0042255	ribosome assembly	13/104	2.08E-17	7.7541E-15	7.64E-15	RPS27/RPS28/RPS19/RPS15/RPL38/RPL10/RPL23A/RPL11/RPL24/RPS14/RPS5/RPL6/RPLP0	13
GO:0006364	rRNA processing	16/104	1.03E-13	3.0628E-11	3.02E-11	RPS27/RPS28/RPS21/RPS19/RPS25/RPL35A/RPS24/RPL26/RPS15/RPS6/RPS8/RPL11/RPL35/RPS16/RPL10A/RPS14	16
GO:0042273	ribosomal large subunit biogenesis	11/104	3.53E-13	8.7742E-11	8.65E-11	RPL35A/RPL26/RPL38/RPL10/RPL23A/RPL11/RPL35/RPL24/RPL10A/RPL6/RPLP0	11
GO:0016072	rRNA metabolic process	16/104	1.21E-12	2.5783E-10	2.54E-10	RPS27/RPS28/RPS21/RPS19/RPS25/RPL35A/RPS24/RPL26/RPS15/RPS6/RPS8/RPL11/RPL35/RPS16/RPL10A/RPS14	16

GO:0000028	ribosomal small subunit assembly	7/104	6.01E-12	1.1208E-09	1.1E-09	RPS27/RPS28/RPS19/RPS15/RPL38/RPS14/RPS5	7
GO:0022618	protein-RNA complex assembly	14/104	4.32E-11	7.1635E-09	7.06E-09	RPS27/RPS28/RPS19/RPS15/RPL38/RPL10/RPL23A/RPL11/RPL13A/RPL24/RPS14/RPS5/RPL6/RPLP0	14
GO:0071826	protein-RNA complex organization	14/104	6.75E-11	1.007E-08	9.93E-09	RPS27/RPS28/RPS19/RPS15/RPL38/RPL10/RPL23A/RPL11/RPL13A/RPL24/RPS14/RPS5/RPL6/RPLP0	14
GO:0000027	ribosomal large subunit assembly	7/104	7.6E-11	1.0311E-08	1.02E-08	RPL38/RPL10/RPL23A/RPL11/RPL24/RPL6/RPLP0	7

GO:0034470	ncRNA processing	17/104	2.7E-10	3.364E-08	3.32E-08	RPS27/RPS28/RPS21/H19/RPS19/RPS25/RPL35A/RPS24/RPL26/RPS15/RPS6/RPS8/RPL11/RPL35/RPS16/RPL10A/RPS14	17
GO:0140694	non-membrane-bounded organelle assembly	15/104	6.75E-09	7.7576E-07	7.65E-07	RPS27/RPS28/RPS23/RPS19/RPS15/RPL38/RPL10/RPL23A/RPL11/RPL24/RPS3/RPS14/RPS5/RPL6/RPLP0	15
GO:0030490	maturation of SSU-rRNA	6/104	4.51E-07	4.8084E-05	4.74E-05	RPS28/RPS21/RPS19/RPS8/RPS16/RPS14	6
GO:1901798	positive regulation of signal transduction by p53 class mediator	4/104	2.14E-05	0.00212686	0.002096	RPL37/RPL26/RPS15/RPL11	4

GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU- rRNA, 5.8S rRNA, LSU- rRNA)	4/104	4.48E-05	0.00417833	0.004118	RPS21/RPS19/RPS8/RPS16	4
GO:0030199	collagen fibril organization	4/104	0.000455	0.03999043	0.039417	COL1A1/LUM/COL3A1/COL1A2	4