

Condition	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	geneID
NR4A1 Medium	GO:0060078	regulation of postsynaptic membrane potential	16/559	156/21081	4.17528E-06	0.01652767	DVL1/PRKCZ/WNT7A/CHRNA9/GABRA2/CHRNA2/SHANK2/KCNA1/GABRA5/C15orf59/ABAT/GRIN2A/5E26/SH3GL1/SLC8A2/SHANK1
NR4A1 Medium	GO:0007613	memory	14/559	132/21081	1.12392E-05	0.016527667	PRKCZ/SLC6A1/ARC/RASGRF1/GRIN2A/JPH3/ITGA3/INSR/CIC/SLC8A2/SHANK1/SHISA7/COMT/PLA2G6
NR4A1 Medium	GO:0050808	synapse organization	30/559	479/21081	1.38226E-05	0.016527667	DVL1/IGSF21/EPHB2/PTPRF/BCAN/IGFN1/EPHA4/NGEF/SLC6A1/WNT7A/LAMB2/GABRA2/THBS2/ELFN1/SDK1/ADGRB1/ARC/ARHGAP22/SHANK2/ITGAM/PAFAH1B1/SEZ6/ITGA3/SDK2/C3/INSR/SLC8A2/SHANK1/SHISA7/NEFH
NR4A1 Medium	GO:0099565	chemical synaptic transmission, postsynaptic	13/559	118/21081	1.5261E-05	0.016527667	DVL1/PRKCZ/WNT7A/CHRNA9/CHRNA2/SHANK2/C15orf59/ABAT/GRIN2A/SEZ6/SH3GL1/SLC8A2/SHANK1
NR4A1 Medium	GO:0001505	regulation of neurotransmitter levels	20/559	261/21081	2.35584E-05	0.020411015	DVL1/SLC1A7/SNAP47/SLC6A1/WNT7A/CPLX1/GABRA2/CAMK2A/GRM4/SLC22A2/SLC22A3/GPER1/NC1/CHAT/SYT7/TRIM9/ABAT/SYT3/COMT/SYN3
NR4A1 Medium	GO:0006836	neurotransmitter transport	19/559	244/21081	3.00515E-05	0.021697193	DVL1/SLC1A7/SNAP47/SLC6A1/WNT7A/CPLX1/GABRA2/CAMK2A/GRM4/SLC22A2/SLC22A3/GPER1/IC1/NC1/CHAT/SYT7/TRIM9/SYT3/SYN3
NR4A1 Medium	GO:0097061	dendritic spine organization	11/559	94/21081	3.90279E-05	0.024152695	DVL1/EPHB2/EPHA4/NGEF/WNT7A/ARC/SHANK2/PAFAH1B1/ITGA3/INSR/SHANK1
NR4A1 Medium	GO:1904062	regulation of cation transmembrane transport	24/559	365/21081	4.63468E-05	0.025096777	KCNAB2/LRR38/EPHB2/GSTM2/DYSF/GPER1/HECW1/DPP6/ARC/KCNQ1/KCNC1/SHANK2/KCNA1/RASGRF1/CEMIP/GRIN2A/JPH3/CACNG1/DNM2/SHANK1/CACNG6/SHISA7/MIR133A2/PLA2G6
NR4A1 Medium	GO:0106027	neuron projection organization	11/559	102/21081	8.3244E-05	0.034504995	DVL1/EPHB2/EPHA4/NGEF/WNT7A/ARC/SHANK2/PAFAH1B1/ITGA3/INSR/SHANK1
NR4A1 Medium	GO:0060997	dendritic spine morphogenesis	9/559	69/21081	8.36198E-05	0.034504995	DVL1/EPHB2/EPHA4/NGEF/WNT7A/ARC/SHANK2/PAFAH1B1/SHANK1
NR4A1 Medium	GO:0008277	regulation of G protein-coupled receptor signaling pathway	14/559	159/21081	8.98194E-05	0.034504995	GNGA4/APELA/CAMK2A/GPER1/RGS3/GRK5/NECAB2/GNG7/C3/DNM2/CLK5/CLK6/CLK14/MIR133A2
NR4A1 Medium	GO:0045745	positive regulation of G protein-coupled receptor signaling pathway	6/559	29/21081	9.55817E-05	0.034504995	GPER1/NECAB2/C3/CLK5/CLK6/CLK14
NR4A1 Medium	GO:0046485	ether lipid metabolic process	5/559	19/21081	0.000110002	0.036656052	FAR1/PAFAH1B1/PLA2G4C/TMEM189/PLA2G6
NR4A1 Medium	GO:0050806	positive regulation of synaptic transmission	16/559	205/21081	0.000122053	0.037766797	DVL1/PRKCZ/EPHB2/KISS1/SNAP47/EPHA4/WNT7A/GPER1/ARC/SYT7/SHANK2/ABAT/GRIN2A/SLC8A2/SHANK1/SHISA7
NR4A1 Medium	GO:0060996	dendritic spine development	11/559	111/21081	0.00017855	0.043288035	DVL1/EPHB2/EPHA4/NGEF/WNT7A/CAMK2A/SDK1/ARC/SHANK2/PAFAH1B1/SHANK1
NR4A1 Medium	GO:0006662	glycerol ether metabolic process	5/559	21/21081	0.000184236	0.043288035	FAR1/PAFAH1B1/PLA2G4C/TMEM189/PLA2G6
NR4A1 Medium	GO:0071472	cellular response to salt stress	4/559	12/21081	0.00020436	0.044264306	XRCC5/EFHD1/AQP1/TRPV4
NR4A1 Medium	GO:0017158	regulation of calcium ion-dependent exocytosis	7/559	48/21081	0.000254585	0.049265159	ZP3/SYT13/SYT7/TRIM9/CACNA1H/SYT3/CACNA1I
NR4A1 Medium	GO:0070588	calcium ion transmembrane transport	21/559	335/21081	0.000261565	0.049265159	GSTM2/ANXA9/DYSF/CHRNA9/GPER1/TRPM6/NC1/TRPV4/CEMIP/CACNA1H/GRIN2A/PKD1L2/JPH3/CACNG1/CACNA1A/SLC8A2/TRPM4/CACNG6/MIR133A2/PLA2G6/CACNA1I
NR4A1 R848	GO:0019932	second-messenger-mediated signaling	22/295	494/21081	2.01271E-06	0.006662063	ADGRB2/EDN2/CASQ1/SELP/HDAC4/ADCY5/ADCYAP1R1/ADGRB1/UCN3/CALML5/INPP5A/GUCY1A2/DRD2/CMKLR1/NOS1/ADGRG5/MCSR/GALR1/GIPR/TRPM4/PDE9A/TRPM2
NR4A1 R848	GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	14/295	249/21081	1.19666E-05	0.019804761	ADGRB2/ADCY5/GRM4/GNA12/ADCYAP1R1/VIPR2/ADGRB1/UCN3/DRD2/NOS1/ADGRG5/MCSR/GALR1/GIPR
NR4A1 R848	GO:0014854	response to inactivity	4/295	14/21081	3.36721E-05	0.025309215	CASQ1/IL10/HDAC4/DRD2
NR4A1 R848	GO:0046879	hormone secretion	16/295	347/21081	3.37748E-05	0.025309215	POMC/ADCY5/CCKAR/UCN3/BAD/DRD2/TRPV4/SIRT4/HNF1A/AACS/GALR1/KCNG2/CACNA1A/GIPR/TRPM4/PLA2G6
NR4A1 R848	GO:0009914	hormone transport	16/295	356/21081	4.58777E-05	0.025309215	POMC/ADCY5/CCKAR/UCN3/BAD/DRD2/TRPV4/SIRT4/HNF1A/AACS/GALR1/KCNG2/CACNA1A/GIPR/TRPM4/PLA2G6
NR4A1 R848	GO:0035725	sodium ion transmembrane transport	11/295	183/21081	5.65879E-05	0.025712912	SCNN1D/SLC6A19/SLC20A2/WNK2/SLC3A2/SCNN1A/NOS1/CACNA1H/TRPM4/TRPM2/CACNA1I
NR4A1 R848	GO:0006814	sodium ion transport	13/295	253/21081	6.2146E-05	0.025712912	SCNN1D/SLC6A19/SLC20A2/WNK2/SLC3A2/DRD2/SCNN1A/NOS1/CACNA1H/SLC38A10/TRPM4/TRPM2/CACNA1I
NR4A1 R848	GO:0051480	regulation of cytosolic calcium ion concentration	16/295	373/21081	7.95074E-05	0.028327967	EDN2/CASQ1/ADCY5/ADCYAP1R1/FZD9/CDH23/DRD2/CMKLR1/TRPV4/NOS1/GALR1/CACNA1A/GIPR/TRPM4/TRPM2/PLA2G6
NR4A1 R848	GO:0050796	regulation of insulin secretion	11/295	204/21081	0.000149109	0.036061725	ADCY5/UCN3/BAD/DRD2/SIRT4/AACS/KCNG2/CACNA1A/GIPR/TRPM4/PLA2G6
NR4A1 R848	GO:0010759	positive regulation of macrophage chemotaxis	4/295	20/21081	0.000152527	0.036061725	PTK2/CMKLR1/TRPV4/IL34
NR4A1 R848	GO:0099601	regulation of neurotransmitter receptor activity	7/295	84/21081	0.000176618	0.038973616	SLURP1/SHANK2/NPTX1/SHANK1/SHISA7/DLGAP4/MAPK8IP2
NR4A1 R848	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	13/295	288/21081	0.000225649	0.041494299	SELP/IL10/CELSR3/FAT1/SDK1/CRB2/CDH23/CDHR1/IGSF9B/CDH5/MAG/CLDN14/ARVCF
NR4A2 Medium	GO:0086010	membrane depolarization during action potential	20/3033	38/21081	3.31817E-08	0.000164942	SLC8A1/SCN3A/SCN1A/SCN9A/SCN7A/SCN5A/CACNA1D/SLMAP/ANK2/CACNA2D1/KCNH2/CACNB2/SCN4B/SCN2B/MIR208A/HCN4/CACNA1H/KCNJ2/TRPM4/CACNA1I
NR4A2 Medium	GO:0050770	regulation of axonogenesis	58/3033	199/21081	5.53874E-08	0.000164942	EPHB2/MACF1/DAB1/TNR/CNTN2/SEMA4F/ZE2B/CHN1/BMPR2/MAP2/FN1/EPHA4/STK25/WNT7A/GOLGA4/TRAK1/SEMA3F/SEMA3B/ROBO1/PLXND1/SKIL/EPHB3/SLIT2/RUFY3/MAP1B/EFNA5/SEMA6A/TUBB2B/PLXNA4/KIF13B/PTK2/SEMA4D/OLFM1/NRP1/CXCL12/BRSK2/LRP4/PAK1/RAB21/PLXNC1/MP2/SIPA1L1/PSEN1/RAB11A/LINGO1/NTRK3/SEMA4B/MT3/IST1/PAFAH1B1/NTN1/CDH2/SEMA6B/P/TPRS/DNM2/BRSK1/ADNP/TIAM1
NR4A2 Medium	GO:0050808	synapse organization	112/3033	479/21081	7.5975E-08	0.000164942	EPHB2/PTPRF/TNR/IGFN1/NFASC/CNTN2/EGLN1/NRXN1/CHRNA1/NRP2/ERBB4/EPHA4/RAB17/KIF1A/SLC6A1/WNT7A/CX3CR1/DAG1/BSN/SEMA3F/ARF4/KALRN/PLXND1/PFN2/DHX36/SLITRK3/NLGN1/EPHB3/IL1RAP/OPA1/DOK7/GABRA2/REST/SEPT11/CDH9/GDNF/MAP1B/EFNA5/MYOT/PCDHGC5/SYNPO/GABRG2/LRFN2/ADGRF1/THBS2/ELFN1/SDK1/FNTA/SYBU/PTK2/ARHGAP39/SEMA4D/DAB2IP/CEL/CANB2/NRP1/ARHGAP22/ZNF365/SRGN/SPOCK2/INA/NEURL1/LRP4/NRXN2/CFL1/SPTBN2/SHANK2/VS1/M5/MTMR2/CNTN5/NECTIN1/DNM1/SLITRK6/FARP1/ACTN1/SLC8A3/SIPA1L1/PSEN1/UBE3A/GABRB3/MYO5A/NTRK3/ITGAM/PAFAH1B1/DLG4/MYH10/NTN1/SEZ6/NEUROD2/BAIAP2/AFG3L2/CDH2/CBLN2/PALM/PTPRS/C3/INSR/UNC13A/LRFN1/SLC8A2/PPFIA3/LRRC4B/SHISA7/ZMYND8/STAU1/ADNP/CB/LN4/APP/TIAM1/ITSN1/WRB/SEZ6L
NR4A2 Medium	GO:0007015	actin filament organization	109/3033	467/21081	1.24582E-07	0.000188126	ESPN/WNT4/MARCKSL1/RHOC/ACTN2/CDC42EP3/PRKCE/ALMS1/CAPG/RND3/NEB/CUL1/ESPN/ARPC4/CLASP2/VILL/XIRP1/TF/PFN2/SLIT2/KIAA1211/RUFY3/SHROOM3/ARFP1/SORBS2/FAT1/IQGAP2/FCHSD1/DPYSL3/SYNPO/CYFIP2/PHACTR1/CARMIL1/PACSIN1/MYO6/MARCKS/MICALL2/ELMO1/HIP1/CCL24/BAIAP2L1/ARPC1A/MET/MTPN/ACTR3B/BIN3/PTK2B/ARFGEF1/FAM49B/KANK1/JAK2/TPM2/FAM171A1/SVIL/NRP1/CXCL12/MCU/ADD3/SWAP70/MICAL2/USH1C/GAS2/CFL1/SPTBN2/ARRB1/MYO7A/P

							AK1/NOX4/RDX/EP58/AVIL/GAS2L3/WASHC3/HSP90B1/CORO1C/DIAPH3/SPTB/ACTN1/TGFB3/EVL/MY05A/TPM1/SMAD3/CORO2B/BBS4/PSTPIP1/PYCARD/ALOX15/MYO15A/TNFAIP1/SSH2/MYO1D/BAIAP2/ARHGAP28/FHOD3/PSTPIP2/ARHGFE18/KANK3/MYO1F/ICAM1/TPM4/GMFG/CCDC155/ARHGAP40/PREX1/MICAL3/GAS2L1/NF2/BAIAP2L2
NR4A2 Medium	GO:0032535	regulation of cellular component size	98/3033	409/21081	1.44423E-07	0.000188126	ATP13A2/HP1BP3/MACF1/VAV3/TNR/CNTN2/ACTN2/CD42EP3/PRKCE/SEMA4F/CAPG/NEB/BMPR2/CREB1/MAP2/FN1/ARPC4/WNT7A/GOLGA4/VILL/SEMA3F/SEMA3B/SLC12A8/PFN2/SLIT2/KIAA1211/RUFY3/ARFIP1/MAP1B/IQGAP2/EFNA5/SEMA6A/FCHSD1/CYFIP2/CDHR2/CARMIL1/AQP1/CCL24/BAIAP2L1/ARPC1A/PLXNA4/MTPN/ACTR3B/PTK2B/RB1CC1/ARFGEF1/DEPTOR/FAM49B/KANK1/SEMA4D/VAV2/OLFM1/SVIL/NRP1/CXCL12/KCNMA1/ADD3/SWAP70/USH1C/CFL1/SPTBN2/PAK1/RDX/EP58/RARG/AVIL/RAB21/SPTB/EVL/AKT1/RAB11A/BBS4/NTRK3/SEMA4B/PYCARD/MT3/IST1/PAFAH1B1/RAP1GAP2/ALOX15/NTN1/SSH2/SLC9A3R1/RPTOR/BAIAP2/ARHGAP28/FHOD3/SEMA6B/PTPRS/PEX11G/KANK3/ICAM1/DNM2/GMFG/ARHGAP40/PREX1/ADNP/BAIAP2L2
NR4A2 Medium	GO:0007411	axon guidance	76/3033	297/21081	2.30966E-07	0.000248407	EPHA8/EPHB2/EPHA10/DAB1/NEXN/TNR/LHX4/NFASC/CNTN2/FEZ2/SOS1/NRXN1/SEMA4F/CHN1/BMPR2/NRP2/EPHA4/GBX2/CNTN4/CELSR3/DAG1/SEMA3F/SEMA3B/ROBO1/PLXND1/PIK3CB/EPHB3/SLIT2/APBB2/PALLD/TRIO/GDNF/FOXD1/EFNA5/SEMA6A/MYOT/SLIT3/TUBB2B/PLXNA4/MATN2/PTK2/NFI/B/SEMA4D/PTCH1/LHX3/NOTCH1/PRKCO/GATA3/NRP1/CXCL12/PAX6/SPTBN2/NECTIN1/PLXNC1/NTN4/MYCBP2/SPTB/NRXN3/EVL/NEO1/SEMA4B/MYH10/NTN1/LAMA1/PTPRM/LAMA3/SMAD4/EFNA2/S/EMA6B/PTPRA/GFRA4/VSTM2L/PLCG1/BMP7/LAMA5/APP
NR4A2 Medium	GO:0097485	neuron projection guidance	76/3033	298/21081	2.66981E-07	0.000248407	EPHA8/EPHB2/EPHA10/DAB1/NEXN/TNR/LHX4/NFASC/CNTN2/FEZ2/SOS1/NRXN1/SEMA4F/CHN1/BMPR2/NRP2/EPHA4/GBX2/CNTN4/CELSR3/DAG1/SEMA3F/SEMA3B/ROBO1/PLXND1/PIK3CB/EPHB3/SLIT2/APBB2/PALLD/TRIO/GDNF/FOXD1/EFNA5/SEMA6A/MYOT/SLIT3/TUBB2B/PLXNA4/MATN2/PTK2/NFI/B/SEMA4D/PTCH1/LHX3/NOTCH1/PRKCO/GATA3/NRP1/CXCL12/PAX6/SPTBN2/NECTIN1/PLXNC1/NTN4/MYCBP2/SPTB/NRXN3/EVL/NEO1/SEMA4B/MYH10/NTN1/LAMA1/PTPRM/LAMA3/SMAD4/EFNA2/S/EMA6B/PTPRA/GFRA4/VSTM2L/PLCG1/BMP7/LAMA5/APP
NR4A2 Medium	GO:0007163	establishment or maintenance of cell polarity	62/3033	230/21081	4.29139E-07	0.000349373	CLIC4/KIF2C/DOC7/GP5M2/RHOC/SNX27/LMNA/RAB10/CYP26B1/RND3/PARD3B/MAP2/STK25/WNT7A/CLASP2/ARF4/RUFY3/FAT1/ERBIN/MAP1B/CTNNA1/WWC1/DST/GJA1/KIF25/AQP1/PTK2B/ANK1/ARFGEF1/FAM49B/PTK2/DOCK8/KANK1/TEK/CRB2/MAPKAP1/GATA3/FRMD4A/ITGB1/BRSK2/INSC/PAX6/CKAP5/CFL1/TCIRG1/NUMA1/PAK1/AMOT1/JAM3/SPRY2/PAFAH1B1/LLGL1/BCAS3/SLC9A3R1/PFB1/LAMA1/MTCL1/MISP/SIPA1L3/BRSK1/PARVB/PARVG
NR4A2 Medium	GO:0035637	multicellular organismal signaling	58/3033	214/21081	8.22629E-07	0.000595309	NPPA/CASQ1/ATP1B1/TNR/NFASC/RYR2/KCNK3/SLC8A1/CALM2/KCNIP3/SCN3A/SCN1A/SCN9A/SCN7A/CHRNA1/SLC4A3/ATP2B2/SCN5A/CACNA1D/FGF12/ANK2/NUP155/PDE4D/GLRA1/GJA1/GPER1/CACNA2D1/AKAP9/CNTNAP2/KCNH2/CACNB2/KCNIP2/STIM1/SCN4B/SCN2B/JAM3/KCNMB4/MIR208A/SLC8A3/RYR3/HCN4/NTRK3/CACNA1H/OTOA/PAFAH1B1/ATP2A3/GJD3/CACNG4/CACNG1/KCNJ2/RYR1/ATP1A3/SLC8A2/TRPM4/MYH14/CACNG8/SOD1/CACNA1
NR4A2 Medium	GO:0010769	regulation of cell morphogenesis involved in differentiation	79/3033	331/21081	2.65093E-06	0.001726552	EPHB2/MACF1/DAB1/TNR/CNTN2/SEMA4F/ZEB2/CHN1/BMPR2/MAP2/FN1/EPHA4/KIF1A/STK25/WNT7A/GOLGA4/TRAK1/SEMA3F/SEMA3B/ROBO1/KALRN/PLXND1/DHX36/SKIL/NLGN1/EPHB3/OPA1/SLIT2/RUFY3/MAP1B/EFNA5/SEMA6A/TUBB2B/CARMIL1/HECW1/CUX1/PLXNA4/DOCK5/KIF13B/PTK2/KA NK1/SEMA4D/OLFM1/NRP1/CXCL12/BRSK2/LRP4/CFL1/PAK1/DNM1L/RAB21/PLXNC1/CORO1C/MYCBP2/SIPA1L1/PSEN1/UBE3A/RAB11A/PARP6/LINGO1/CHRNA3/NTRK3/SEMA4B/MT3/IST1/PAFAH1B1/NTN1/BAIAP2/P4HB/CDH2/SEMA6B/PTPRS/DNM2/ANKRD27/BRSK1/PREX1/ADNP/TIAM1/FBLN1
NR4A2 Medium	GO:0048738	cardiac muscle tissue development	63/3033	248/21081	3.11643E-06	0.001845208	TP73/NPPA/TGFB3/LMNA/TNNT2/EGLN1/ACTN2/RYR2/HNRNP/SLC8A1/MEIS1/NEB/XIRP2/CREB1/EBB4/HEG1/C3orf58/PDGFR/FGF2/SORBS2/JARID2/PI16/GJA1/FGFR1/MIR204/RXRA/NOTCH1/ITGB1/SOX6/CSRP3/WT1/FGF3/PAK1/TENM4/NOX4/LRRC10/FGF9/MIR17HG/MIR208A/MYH6/MYH7/SAV1/BMP4/YY1/DLL4/ALDH1A2/TPM1/AKAP13/MESP1/NPRL3/MYLK3/NDRG4/ZFPM1/KDM6B/MYH10/RAR A/KAT2A/FHOD3/SMAD4/PPP1R13L/JPH2/BMP7/MYO18B
NR4A2 Medium	GO:1990778	protein localization to cell periphery	85/3033	366/21081	3.62196E-06	0.001965819	EPHB2/MACF1/TMEM59/GPSM2/RAB13/ATP1B1/NFASC/ACTN2/RAB10/PRKCE/ASB3/KCNIP3/DPP10/GRIP2/CLASP2/GOLGA4/DAG1/SLMAP/CPLX1/GAK/WDR19/MAPK10/ANK2/FCHO2/PACSIN1/MRAP2/EPB41L2/AFDN/GPER1/ADAM22/TSPAN33/DPP6/ANK1/IKKBK/EFR3A/PTCH1/STXB1/SEC16A/ABCA2/CACNB2/ITGB1/TSPAN15/ARL3/DCHS1/CSRP3/STX3/PACS1/NUMA1/RDX/PDZ3/GRIP1/CLIP1/RILPL1/TMED2/GAS6/NUMB/TTC7B/AKT1/PACS2/EHD4/MYO5A/RAB11A/NUBP1/STX1B/ATP2C2/TUSCS/RABEP1/DLG4/RAMP2/SKAP1/CACNG4/SLC9A3R1/RAB40B/EPB41L3/RAB12/CDH2/PALM/MISP/AKT2/EHD2/CACNG8/SMAD4/DNM2/PPP1R13L/JAG1/BMP7
NR4A2 Medium	GO:0048839	inner ear development	55/3033	212/21081	6.58016E-06	0.003061184	EPHB2/KCNQ4/PRRX1/KCNK3/PAX8/EPHA4/GBX2/TMIE/LRIG1/MCM2/OPA1/ADGRV1/DCANP1/MYO6/AHI1/DNA5/BMPER/FGFR1/CALB1/OC90/TMC1/LHX3/NOTCH1/GATA3/MYO3A/HMX2/DCHS1/USH1C/MYO7A/COL2A1/LRIG3/SLC17A8/FGF9/ATP8A2/SPRY2/SLITRK6/BMP4/TGFB3/ESRRB/JAG2/GABRB3/NTRK3/PAFAH1B1/DVL2/NTN1/MYO15A/NAGLU/SLC9A3R1/USH1G/TTC39G/ATP8B1/HPN/JAG1/SOD1/WRB
NR4A2 Medium	GO:0003205	cardiac chamber development	48/3033	179/21081	9.58808E-06	0.003902946	TGFB3/TNNT2/EGLN1/RYR2/LTBP1/SOS1/PAX8/XIRP2/BMPR2/NRP2/SCN5A/ROBO1/HEG1/PLXND1/SLIT2/ANK2/ADAMTS6/NDST1/SLIT3/MSX2/ADGRG6/DNAH11/NOS3/TEK/RXRA/NOTCH1/GATA3/NRP1/PDE2A/MIR17HG/MYH6/MYH7/SAV1/BMP4/HIF1A/DLL4/TPM1/MESP1/NPRL3/DCTNS5/ZFPM1/MYH10/RARA/SMAD4/DNM2/PPP1R13L/JAG1/BMP7
NR4A2 Medium	GO:0007605	sensory perception of sound	44/3033	161/21081	1.32136E-05	0.005062351	ESPN/KCNQ4/CD14A/OTOF/ESPNL/OTOS/GRM7/ATP2B2/TMIE/CACNA1D/LRIG1/WFS1/HEXB/ADGRV1/ALDH7A1/MYO6/DFNA5/ATP6V0A4/FGFR1/TMC1/MYO3A/USH1C/NAV2/MYO7A/CNTNS5/COL2A1/EPYC/SLC17A8/SRRM4/SPRY2/SLITRK6/GABRB3/OTOA/MYO15A/SLC9A3R1/USH1G/LOXHD1/ATP8B1/ICAM1/HPN/MYH14/SOD1/WRB/TMPRSS3
NR4A2 Medium	GO:0048864	stem cell development	28/3033	86/21081	1.55786E-05	0.005340197	PEF1/KLHL12/SEMA4F/ZEB2/NRP2/ERBB4/FN1/HTR2B/GBX2/WNT7A/SEMA3F/SEMA3B/GDNF/SEMA6A/TCOF1/SEMA4D/NRP1/CFL1/CORO1C/BMP4/HIF1A/ALDH1A2/SEMA4B/MSI2/SEMA6B/JAG1/BMP7/LAMA5

NR4A2 Medium	GO:007272	ensheathment of neurons	40/3033	144/21081	2.11937E-05	0.005386406	NFASC/CNTN2/DEGS1/EIF2B4/NAB1/PIKFYVE/DAG1/ANK2/HEXB/SERINC5/ID4/PPARD/ADGRG6/ADAM22/TG/ABCA2/SBF2/MYRF/TENM4/MTMR2/IAM3/CD9/RARG/RNF10/SLC8A3/EIF2B2/AKT1/MYO5A/NTRK3/FA2H/TMEM98/RARA/EPB41L3/AFG3L2/ZNF24/AKT2/PRX/ATRN/CST7/SOD1
NR4A2 Medium	GO:008366	axon ensheathment	40/3033	144/21081	2.11937E-05	0.005386406	NFASC/CNTN2/DEGS1/EIF2B4/NAB1/PIKFYVE/DAG1/ANK2/HEXB/SERINC5/ID4/PPARD/ADGRG6/ADAM22/TG/ABCA2/SBF2/MYRF/TENM4/MTMR2/IAM3/CD9/RARG/RNF10/SLC8A3/EIF2B2/AKT1/MYO5A/NTRK3/FA2H/TMEM98/RARA/EPB41L3/AFG3L2/ZNF24/AKT2/PRX/ATRN/CST7/SOD1
NR4A2 Medium	GO:0046434	organophosphate catabolic process	42/3033	154/21081	2.16742E-05	0.005386406	ACOT7/PLA2G5/INPP5B/XDH/INPP1/IDH1/ENTPD3/ABHD6/NUDT9/PDE5A/ENPP6/PDE4D/NUDT12/HI1NT1/NUDT3/NT5E/ENPP1/NUDT1/ENPP2/NUDT13/NT5C2/INPP5A/SMPD1/PDE2A/MTMR2/ACAT1/PLA2G4E/PLA2G4D/PLA2G4F/DUT/NUDT7/PLCG2/NT5M/CNP/IMPA2/PDE4C/APOC1/ABHD12/PLCG1/NTSR1/PDE9A/PLA2G6
NR4A2 Medium	GO:0001755	neural crest cell migration	21/3033	57/21081	2.18941E-05	0.005386406	SEMA4F/ZEB2/NRP2/ERBB4/FN1/HTR2B/GBX2/SEMA3F/SEMA3B/GDNF/SEMA6A/SEMA4D/NRP1/CFL1/CORO1C/BMP4/HIF1A/SEMA4B/SEMA6B/BMP7/LAMA5
NR4A2 R848	GO:0099565	chemical synaptic transmission, postsynaptic	18/892	118/21081	2.31635E-06	0.005725192	PRKCZ/RAB3GAP1/WNT7A/RIMS1/SHANK2/IGSF9B/CHRN4/GRIN2A/CHRNA4/SH3GL1/GRIK5/SLC8A2/SHANK1/CHRNA4
NR4A2 R848	GO:0060079	excitatory postsynaptic potential	17/892	108/21081	2.8296E-06	0.005725192	PRKCZ/RAB3GAP1/WNT7A/RIMS1/SHANK2/CHRN4/GRIN2A/CHRNA4/SH3GL1/GRIK5/SLC8A2/SHANK1/CHRNA4
NR4A2 R848	GO:0006814	sodium ion transport	28/892	253/21081	3.54063E-06	0.005725192	SLC6A9/SLC5A9/SLC4A5/SERPINE2/SLC6A1/SLC6A20/SLC6A19/HECW1/SLC13A4/WNK2/TRPM5/NOS1/ATP12A/SLC24A1/CACNA1H/SLC6A2/CACNA1G/SCN4A/ATP4A/ATP1A3/SLC8A2/TRPM4/SLC4A11/BP1FA1/CACNA1
NR4A2 R848	GO:0035725	sodium ion transmembrane transport	22/892	183/21081	1.04268E-05	0.012645091	SLC6A9/SLC4A5/SLC6A1/SLC6A20/SLC6A19/HECW1/WNK2/TRPM5/NOS1/ATP12A/SLC24A1/CACNA1H/SLC6A2/CACNA1G/SCN4A/ATP4A/ATP1A3/SLC8A2/TRPM4/SLC4A11/BP1FA1/CACNA1
NR4A2 R848	GO:0042391	regulation of membrane potential	40/892	473/21081	2.73052E-05	0.015772972	PRKCZ/KCNAB2/ACTN2/RAB3GAP1/BOK/WNT7A/CACNA1D/HTR3C/RIMS1/FZD9/DLD/KCNQ3/KCNK9/KCNQ1/KCNK1/SHANK2/IGSF9B/CHRN4/CACNA1H/GRIN2A/WWP2/CHRNA4/SH3GL1/GRIK5/SLC8A2/TRPM4/MYH14/SHANK1/CHRNA4/CACNA1
NR4A2 R848	GO:0098659	inorganic cation import across plasma membrane	15/892	104/21081	3.14201E-05	0.015772972	SLC6A1/SLC12A9/KCNK9/WNK2/TRPV4/ATP12A/SLC24A1/SLC12A4/TRPV3/ATP4A/ATP1A3/SLC8A2/TRPM4/SLC12A5/KCNJ4
NR4A2 R848	GO:0099587	inorganic ion import across plasma membrane	15/892	104/21081	3.14201E-05	0.015772972	SLC6A1/SLC12A9/KCNK9/WNK2/TRPV4/ATP12A/SLC24A1/SLC12A4/TRPV3/ATP4A/ATP1A3/SLC8A2/TRPM4/SLC12A5/KCNJ4
NR4A2 R848	GO:0050808	synapse organization	40/892	479/21081	3.62662E-05	0.015772972	IGSF21/PTPRF/IGFN1/NGEF/RAB17/KIF1A/SLC6A1/WNT7A/PLXNB1/SEMA3F/EPH1/DOK7/THBS2/ELF1/N1/SDK1/CAMK2B/FZD9/SEMA3E/ADGRB1/SEMA4D/ANAPC2/SHANK2/IGSF9B/ACTN1/DLG4/SEZ6/SXK2/BAIAP2/C3/INSR/ARHGAP33/LRFN1/SLC8A2/LRRC4B/SHANK1/SHISA7/SYNDIG1/SEZ6L/WNT7B/NB2
NR4A2 R848	GO:0050770	regulation of axonogenesis	22/892	199/21081	3.88586E-05	0.015772972	STK25/WNT7A/PLXNB1/SEMA3F/PLXNA1/FSTL4/LIMK1/SEMA3E/DPYSL2/SEMA4D/OLFM1/ANAPC2/SHANK2/BRSK2/LRP1/LINGO1/RND2/STK11/SEMA6B/MEGF8/CDH4/PLXNB2
NR4A2 R848	GO:0031646	positive regulation of nervous system process	12/892	71/21081	3.91909E-05	0.015772972	PRKCZ/WNT7A/RIMS1/SHANK2/IGSF9B/CHRN4/DLG4/BAIAP2/SHANK1/CST7/S100B/SOX10
NR4A2 R848	GO:0007018	microtubule-based movement	34/892	385/21081	4.56399E-05	0.015814237	PRKCZ/NPHP4/CELSR2/KIF21B/KIF1A/MAP4/HTT/BLOC1S4/KIF25/DNAF5/NME8/HSPB1/LRRC6/WDR34/CFAP46/TRIP11/KLC1/SPG11/BBS4/AP3B2/MAPK8IP3/DRC7/DNAH2/KPNB1/TTL6/KIF19/QRICH2/DNAH17/STK11/MAP1S/SEMG1/PLTP/SUN2/CACNA1I
NR4A2 R848	GO:0032535	regulation of cellular component size	35/892	409/21081	6.72901E-05	0.021761611	ATP13A2/ACTN2/WNT7A/VILL/SEMA3F/FSTL4/CDHR2/ELN/LIMK1/SEMA3E/SLC12A9/DPYSL2/SEMA4D/AV2/OLFM1/ANAPC2/SHTN1/LIMA1/LRP1/TRPV4/EVL/BBS4/SLC12A4/RND2/RPTOR/BAIAP2/FHOD3/SEMA6B/KANK3/SPTBN4/MEGF8/ARHGAP40/SLC12A5/CDH4/WNT7B
NR4A2 R848	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	27/892	288/21081	0.000100529	0.03047915	IGSF21/PTPRF/CELSR2/IGFN1/PTPN23/FAT1/CDHR2/SDK1/CLDN3/CLDN15/CRB2/CDH23/CDHR1/DCHS1/ROBO4/IGSF9B/PKD1/CDH5/SDK2/LRRC4B/VSTM2L/CDH4/ITGB2/ARVCF/SCARF2/CELSR1/PLXNB2
NR4A2 R848	GO:0006836	neurotransmitter transport	24/892	244/21081	0.000115261	0.031062777	SLC6A9/SLC1A7/GLUL/SNAP47/OTOF/RAB3GAP1/GAD1/SLC6A1/WNT7A/CACNA1D/GRM4/RIMS1/ICA1/NCS1/CHAT/RPH3A/NOS1/APBA2/CHRN4/SLC6A2/PIP5K1C/GRIK5/NAPA/CHRNA4
NR4A2 R848	GO:0007163	establishment or maintenance of cell polarity	23/892	230/21081	0.000123938	0.03138716	PRKCZ/SNX27/PARD3B/STK25/WNT7A/MAP4/EPH1/HTT/FAT1/KIF25/CDK5RAP2/CRB2/SHTN1/BRSK2/CDC42BPB/PKD1/CDH5/RND2/FSCN2/STK11/SIPA1L3/PARVB/WNT7B
NR4A2 R848	GO:0010769	regulation of cell morphogenesis involved in differentiation	29/892	331/21081	0.000184786	0.040745315	NGEF/KIF1A/STK25/WNT7A/PLXNB1/SEMA3F/PLXNA1/FSTL4/HECW1/CAMK2B/LIMK1/SEMA3E/DPYSL2/SEMA4D/OLFM1/ANAPC2/SHTN1/BRSK2/LRP1/LINGO1/RND2/BAIAP2/STK11/SEMA6B/ARHGAP33/MEGF8/CDH4/FBLN1/PLXNB2
NR4A2 R848	GO:0055075	potassium ion homeostasis	7/892	31/21081	0.000255792	0.049380046	SLC12A9/ATP12A/SLC12A4/ATP4A/ATP1A3/SLC12A5/UPK3A
NR4A2 R848	GO:0070509	calcium ion import	13/892	99/21081	0.000272724	0.049380046	PSEN2/DYSF/CACNA1D/GCK/TRPV4/SLC24A1/CACNA1H/TRPV3/CACNA1G/CACNA1A/SLC8A2/SEMG1/CACNA1I
NR4A2 R848	GO:0048167	regulation of synaptic plasticity	21/892	213/21081	0.000291381	0.049380046	PRKCZ/SNAP47/RAB3GAP1/SERPINE2/SORCS2/RIMS1/CAMK2B/ADGRB1/ANAPC2/RIN1/SHANK2/SLC24A1/RASGRF1/GRIN2A/JPH3/DLG4/BAIAP2/SLC8A2/SHANK1/SHISA7/S100B
NR4A2 R848	GO:0030198	extracellular matrix organization	35/892	442/21081	0.000302319	0.049380046	HSPG2/PXDN/COL6A3/FBLN2/COL7A1/ADAMT512/FGFR4/COL23A1/SMOC2/ELN/PLOD3/COL22A1/COL27A1/COL13A1/TLL2/COL17A1/MMP21/CAPN1/MMP8/PHLDB1/LRP1/MMP17/ITGA11/COL5A3/NCAN/ERCC2/KLK2/KLK4/KLK7/LAMA5/ITGB2/COL18A1/COL6A1/COL6A2/FBLN1
NR4A3 Medium	GO:0050808	synapse organization	21/295	479/21081	4.40688E-06	0.013150124	C1QB/CNTN2/NGEF/KIF1A/WNT7A/LAMB2/MDGA1/THBS2/FZD9/ADGRB1/SNCG/SLIT1/SHANK2/ACTN1/NTRK3/ITGAM/DLG4/C3/LRRC4B/SHISA7/SEZ6L
NR4A3 R848	GO:0007215	glutamate receptor signaling pathway	12/514	104/21081	8.77741E-06	0.036399903	PINK1/GRM4/GRM8/GRID1/DAGLA/SHANK2/RASGRF1/GRIN2A/DLG4/UNC13A/CACNG7/SHISA7
NR4A3 R848	GO:0030198	extracellular matrix organization	26/514	442/21081	3.62071E-05	0.047141539	HSPG2/OPTC/CAPN2/PXDN/FBLN2/DSP/CLKB1/FGFR4/SMOC2/ELN/COL22A1/COL27A1/COL5A1/COL17A1/PHLDB1/MMP17/PECAM1/COL5A3/COMP/NCAN/CAPNS1/KLK7/ITGB2/COL18A1/COL6A1/COL6A2
NR4A3 R848	GO:0043062	extracellular structure organization	26/514	443/21081	3.76066E-05	0.047141539	HSPG2/OPTC/CAPN2/PXDN/FBLN2/DSP/CLKB1/FGFR4/SMOC2/ELN/COL22A1/COL27A1/COL5A1/COL17A1/PHLDB1/MMP17/PECAM1/COL5A3/COMP/NCAN/CAPNS1/KLK7/ITGB2/COL18A1/COL6A1/COL6A2
NR4A3 R848	GO:0048168	regulation of neuronal synaptic plasticity	8/514	56/21081	6.00751E-05	0.047141539	CAMK2A/CAMK2B/RASGRF1/DLG4/UNC13A/PPIA3/SHISA7/SYNGR1

NR4A3 R848	GO:0048167	regulation of synaptic plasticity	16/514	213/21081	7.24467E-05	0.047141539	PRKCZ/FAM107A/SORCS2/CAMK2A/CAMK2B/ADGRB1/SHANK2/RASGRF1/GRIN2A/DLG4/BAIAP2/UNC13A/PPFIA3/SHISA7/YTHDF1/SYNGR1
NR4A3 R848	GO:0003382	epithelial cell morphogenesis	7/514	43/21081	7.40484E-05	0.047141539	FLNB/COL22A1/RILPL1/CCDC88C/PECAM1/SIPA1L3/COL18A1
NR4A3 R848	GO:0001505	regulation of neurotransmitter levels	18/514	261/21081	7.95734E-05	0.047141539	SLC1A7/OTOF/GAD1/PER2/CACNA1D/CPLX1/CAMK2A/GRM4/SLC1A2/DAGLA/PDE1B/RPH3A/NOS1/PI5K1C/STXBP2/UNC13A/PPFIA3/SYT3