

Figure S1

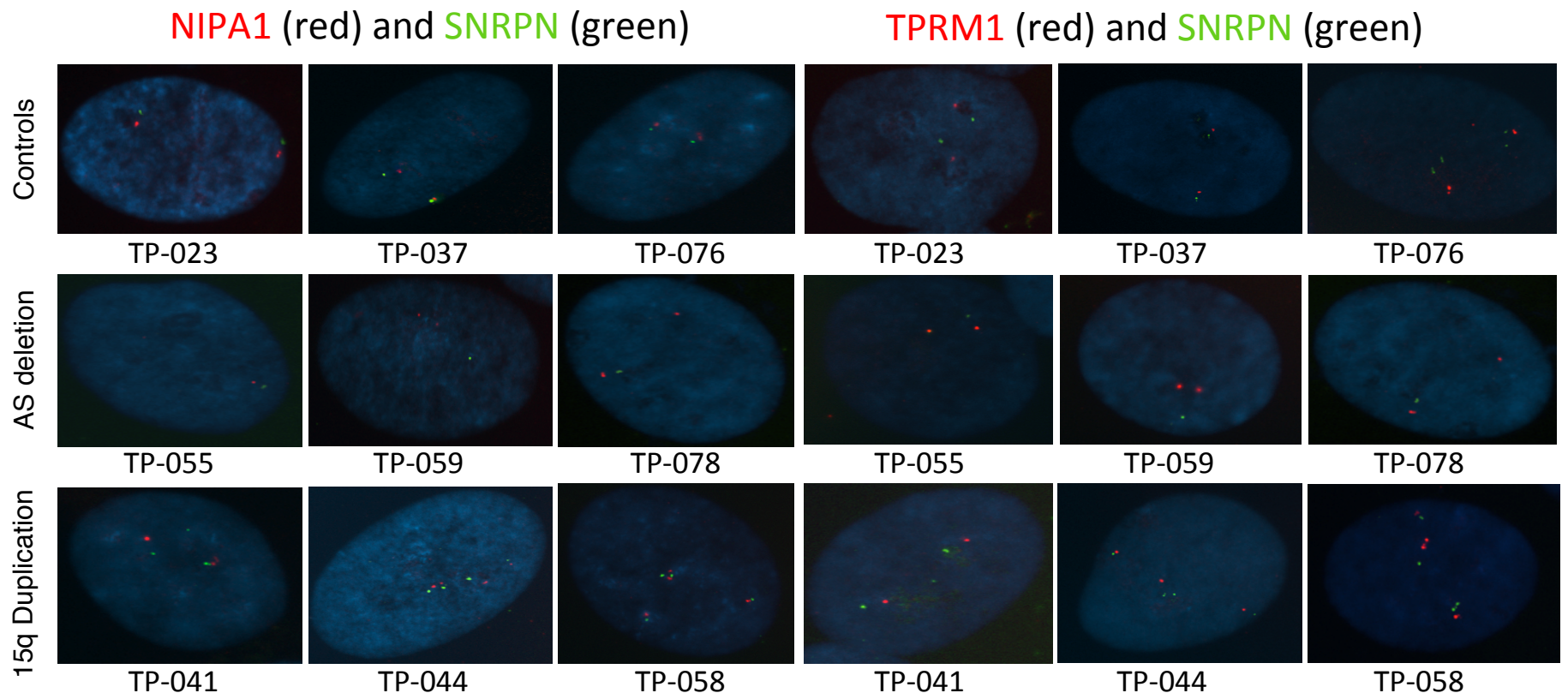


Figure S2

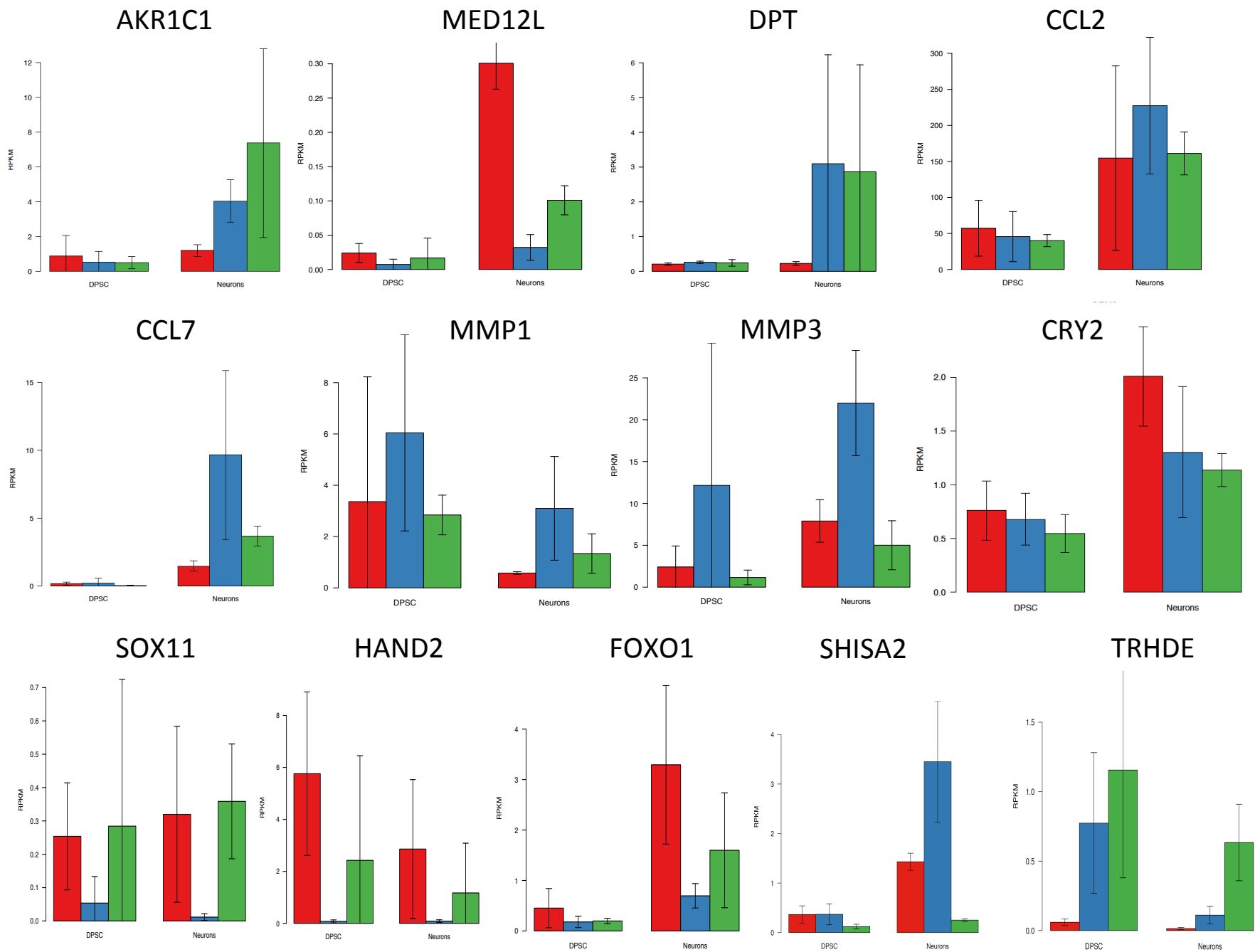
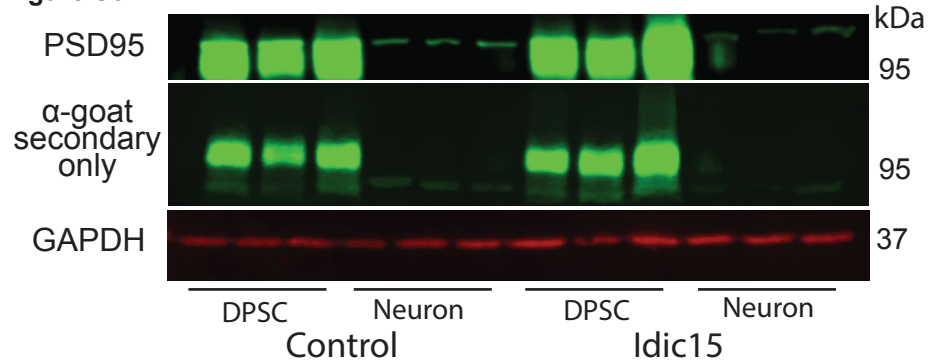


Figure S3



TRANSFAC: 15q Duplication Neurons

DOWN

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	
GCGSCMNTTT_UNKNOWN		64	-0.5094314	-1.8933098	0	0.02501921	0.017
V\$OCT1_06		226	-0.3933881	-1.7968041	0	0.02733338	0.035
V\$NKX61_01		198	-0.3649626	-1.6230397	0	0.13079427	0.23
V\$EN1_01		98	-0.4000299	-1.5965902	0.00420168	0.13397652	0.301
V\$CEBP_Q3		223	-0.3518449	-1.5878625	0	0.11962409	0.331
V\$HP1SITEFACTOR_Q6		208	-0.3452416	-1.5349915	0.0021645	0.18466899	0.516
V\$MYOGNF1_01		39	-0.4300448	-1.4831299	0.02626263	0.27976456	0.743
V\$GATA1_01		221	-0.322842	-1.4529176	0	0.33564568	0.85
V\$SOX9_B1		217	-0.3191878	-1.4236258	0.0046729	0.41007605	0.934
V\$SREBP_Q3		218	-0.3090884	-1.4095014	0.00888889	0.43028527	0.96
V\$OCT1_07		141	-0.3329824	-1.4077808	0.01545254	0.39733857	0.96
YGCANTGCR_UNKNOWN		119	-0.3381355	-1.4044033	0.02118644	0.380837	0.968
V\$DR3_Q4		124	-0.3318088	-1.3932549	0.01476793	0.39827082	0.981
MYAATNNNNNNNGGC_UNKNOWN		99	-0.3469147	-1.3911699	0.02296451	0.3774542	0.983
V\$VDR_Q3		192	-0.3127211	-1.3895535	0.00445434	0.35847512	0.985
V\$SRY_02		229	-0.3060061	-1.3804193	0.01106195	0.37415162	0.992
V\$AP3_Q6		217	-0.3025683	-1.3705543	0.00631579	0.3910617	0.993
V\$E2F_Q3		214	-0.3045821	-1.3676448	0.00909091	0.3813685	0.994
V\$EVI1_03		46	-0.3891891	-1.3647718	0.0533049	0.37119076	0.995
V\$SMAD3_Q6		203	-0.3031859	-1.3590547	0.01310044	0.3741324	0.997
V\$AML1_Q6		240	-0.2956955	-1.3540615	0.01809955	0.3729231	0.998
V\$NKX22_01		158	-0.317044	-1.3533521	0.02672606	0.3583222	0.998
V\$HFH1_01		215	-0.3021202	-1.3487269	0.0087146	0.36005485	0.998
V\$AML1_01		240	-0.2956955	-1.3477187	0.0137931	0.3483203	0.998
V\$FOXO1_02		215	-0.2949153	-1.3463267	0.00697674	0.33836308	0.998
V\$RP58_01		178	-0.3019264	-1.3356836	0.02252252	0.36630166	0.999
V\$CHX10_01		191	-0.298927	-1.333554	0.01492537	0.3599701	0.999
RRAGTTGT_UNKNOWN		230	-0.2960938	-1.3325471	0.01327434	0.3508565	0.999
V\$HIF1_Q3		208	-0.2936804	-1.3314378	0.015625	0.34252292	0.999
TGACGTCA_V\$ATF3_Q6		211	-0.2929922	-1.3294653	0.0046729	0.33794484	0.999
V\$MEIS1AHOXA9_01		97	-0.3268906	-1.3261049	0.02553191	0.3381378	1

UP

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	
V\$SRF_01		43	0.48542336	1.6573973	0.00718133	0.13352197	0.187
CCAWWNAAGG_V\$SRF_Q4		80	0.40319514	1.5448364	0.00567108	0.2478092	0.539
V\$TATA_01		193	0.30879465	1.3548863	0.01489758	1	0.999
V\$ISRE_01		225	0.30589628	1.3501171	0.01092896	1	0.999
V\$NFKAPPAB_01		217	0.30308276	1.3335816	0.02169982	1	0.999
V\$HOX13_01		40	0.39323503	1.32752	0.10242086	0.93175566	0.999
RGTTAMWNATT_V\$HNF1_01		53	0.37206316	1.3223978	0.06990291	0.8449261	0.999
V\$SRF_C		190	0.30571803	1.321815	0.02678572	0.74310005	0.999

Mentioned in the Text

TRANSFAC: AS Deletion Neurons

DOWN

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
V\$OCT1_07	144	-0.3807221	-1.5705194	0	0.7485122	0.407
V\$EVI1_03	49	-0.4583496	-1.5698875	0.01724138	0.37763244	0.41
V\$IRF_Q6	227	-0.3351715	-1.4980567	0	0.5593537	0.711
V\$ICSBP_Q6	231	-0.3313863	-1.4486657	0.002079	0.7329453	0.894
AGCYRWTTTC_UNKNOWN	113	-0.3535078	-1.4262518	0.01054852	0.747513	0.944
V\$MEIS1AHOXA9_01	100	-0.3584329	-1.4151071	0.02165354	0.7043254	0.965
V\$EVI1_06	18	-0.4935676	-1.3844324	0.10229645	0.84814113	0.99
V\$AML1_01	245	-0.3101316	-1.3788893	0.00410678	0.7864868	0.993
V\$HP1SITEFACTOR_Q6	211	-0.312507	-1.3728573	0.00976563	0.7419695	0.994
V\$AML1_Q6	245	-0.3101316	-1.3712174	0.00824742	0.6798666	0.994
V\$AMEF2_Q6	234	-0.3065637	-1.3519431	0.01207244	0.75519454	0.997
V\$HOX13_01	39	-0.4132153	-1.3484844	0.06614786	0.71743125	0.998
V\$CDPCR3HD_01	215	-0.3068185	-1.3481336	0.01810865	0.6646419	0.998
V\$POU3F2_01	86	-0.3556489	-1.3480694	0.04642166	0.6178575	0.998
CATTGTYV_V\$SOX9_B1	338	-0.2934313	-1.3464539	0.00390625	0.58556753	0.998
V\$E4BP4_01	208	-0.309348	-1.3416383	0.01782178	0.5763137	0.998
V\$HFH4_01	179	-0.315409	-1.3405806	0.02647658	0.5487232	0.999
V\$NKX61_01	202	-0.3068869	-1.3403333	0.01716738	0.5198254	0.999

UP

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
V\$PAX3_01	22	0.51021683	1.497745	0.04393305	0.8342927	0.708
V\$ALPHACP1_01	236	0.31215733	1.3771724	0.01639344	1	0.994
CCAATNNSNNGCG_UNKI	54	0.39008346	1.3762366	0.05761317	1	0.994

Mentioned in the Text

GO: 15q Duplication Neurons

DOWN

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
CHROMOSOME_ORGANIZATION_AND_BIOGENESIS	121	-0.4339858	-1.8201128	0	0.5585529	0.482
CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	26	-0.5826206	-1.7727206	0.00639659	0.47712943	0.678
ESTABLISHMENT_AND_OR_MAINTENANCE_OF_CHROMATIN_ARCHITECTURE	75	-0.4294769	-1.6466404	0.00635593	1	0.98
MACROMOLECULAR_COMPLEX_DISASSEMBLY	15	-0.6100932	-1.6214776	0.02114165	1	0.997
TRANSMEMBRANE_RECEPTOR_PROTEIN_PHOSPHATASE_ACTIVITY	18	-0.580447	-1.6134549	0.0210084	0.8977136	0.997
REGULATION_OF_ACTION_POTENTIAL	16	-0.5768601	-1.5918566	0.02459016	0.8929916	0.999
CHROMATIN_ASSEMBLY	16	-0.5808365	-1.5697571	0.03131524	0.90862095	1
GENERAL_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_ACTIVITY	32	-0.4683348	-1.541086	0.0190678	0.9858792	1
PORE_COMPLEX	36	-0.4601928	-1.5379628	0.02760085	0.89746743	1
DNA_PACKAGING	32	-0.4644173	-1.5290788	0.01898734	0.8651769	1
DENDRITE	15	-0.5660704	-1.51138	0.04462475	0.8930051	1
PEROXISOME_ORGANIZATION_AND_BIOGENESIS	16	-0.5441632	-1.4997828	0.06029106	0.89454967	1
PROTEIN_AMINO_ACID_DEPHOSPHORYLATION	59	-0.3967321	-1.4777185	0.02985075	0.97494745	1
SEQUENCE_SPECIFIC_DNA_BINDING	55	-0.4070704	-1.4746774	0.01918977	0.9252741	1
NUCLEAR_MEMBRANE	48	-0.4211148	-1.4667499	0.03416856	0.91236836	1
NUCLEAR_PORE	31	-0.440474	-1.4466326	0.04365904	0.9843774	1

UP

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
STRUCTURAL_CONSTITUENT_OF_RIBOSOME	79	0.60831857	2.3000758	0	0	0
CHEMOKINE_ACTIVITY	34	0.5833463	1.884044	0	0.13948384	0.228
CHEMOKINE_RECEPTOR_BINDING	34	0.5833463	1.8780724	0	0.10352428	0.246
LIPID_HOMEOSTASIS	15	0.6839274	1.8327537	0.00385356	0.1398569	0.406
CYTOKINE_ACTIVITY	81	0.47130308	1.8297948	0	0.11460169	0.409
G_PROTEIN_COUPLED_RECEPTOR_BINDING	44	0.5296605	1.8295625	0	0.09586461	0.409
RESPONSE_TO_OXIDATIVE_STRESS	43	0.5205627	1.7810241	0.00579151	0.15431596	0.611
CHEMICAL_HOMEOSTASIS	134	0.42244628	1.7672718	0	0.15933107	0.659
OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS	23	0.5848808	1.7657856	0.00773694	0.14387622	0.665
OXIDOREDUCTASE_ACTIVITY_GO_0016616	55	0.48507896	1.7547	0	0.14627519	0.711
RHO_GTPASE_ACTIVATOR_ACTIVITY	18	0.6055668	1.6716973	0.00968992	0.31963742	0.954
ELECTRON_CARRIER_ACTIVITY	77	0.43772656	1.6659968	0.0019084	0.30756313	0.963
REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	41	0.49528235	1.6654005	0.00180832	0.28580397	0.964
DEVELOPMENT_OF_PRIMARY_SEXUAL_CHARACTERISTICS	21	0.57378125	1.6525108	0.01142857	0.30238238	0.98
GROWTH_FACTOR_BINDING	27	0.5301724	1.6514517	0.00598802	0.2844534	0.98
OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DONORS	60	0.4556028	1.6512581	0	0.26723757	0.98
VESICLE_MEMBRANE	28	0.52973676	1.6331445	0.00369004	0.29772532	0.994
SECONDARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	44	0.4733048	1.6209818	0.00584795	0.3127635	0.995
RESPONSE_TO_EXTERNAL_STIMULUS	263	0.3569134	1.6198318	0	0.29943386	0.995
WOUND_HEALING	46	0.46991926	1.6192056	0.00948767	0.28596547	0.995
GTPASE_ACTIVATOR_ACTIVITY	58	0.44672424	1.6129533	0.00377359	0.2888022	0.997

Mentioned in the Text

Also of interest

GO: AS Deletion Neurons

DOWN

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
CYTOKINESIS	18	-0.6795768	-1.8728243	0.00206186	0.3198453	0.251
CELL_DIVISION	20	-0.6347529	-1.8209481	0	0.30862626	0.443
REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	16	-0.6616356	-1.7688583	0.00194932	0.38295674	0.646
CELL_CELL_ADHESION	79	-0.4531722	-1.7102556	0	0.5399729	0.859
CELLULAR_MORPHOGENESIS_DURING_DIFFERENTIATION	46	-0.4996825	-1.6966162	0.01022495	0.48838636	0.896
GROWTH_FACTOR_ACTIVITY	47	-0.4905852	-1.6842574	0.00202429	0.46317023	0.926
ANION_CHANNEL_ACTIVITY	18	-0.5992384	-1.6670983	0.00814664	0.4731243	0.96
LIGAND_GATED_CHANNEL_ACTIVITY	35	-0.5119488	-1.6586397	0.01077586	0.44763425	0.965
POSITIVE_REGULATION_OF_PROTEIN_AMINO_ACID_PHOSPHORYLATION	18	-0.5910826	-1.6436394	0.01052632	0.46002585	0.983
CHLORIDE_CHANNEL_ACTIVITY	18	-0.5992384	-1.6318763	0.01778656	0.45864907	0.99
CELLULAR_RESPIRATION	19	-0.5811528	-1.6277045	0.02620968	0.43265176	0.991
CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	26	-0.545148	-1.6260283	0.01361868	0.4017679	0.991
REGULATION_OF_PROTEIN_AMINO_ACID_PHOSPHORYLATION	28	-0.5269707	-1.6205647	0.00828157	0.39110622	0.992
NEURON_DEVELOPMENT	58	-0.4515381	-1.6056588	0.00788955	0.41111386	0.997
METALLOPEPTIDASE_ACTIVITY	46	-0.4605937	-1.5976261	0.00801603	0.41039008	0.998
POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	27	-0.5169987	-1.5852486	0.0244898	0.42801636	1
NEURITE_DEVELOPMENT	50	-0.4561331	-1.5704453	0.01039501	0.45334646	1
POSITIVE_REGULATION_OF_CELL_CYCLE	16	-0.5883299	-1.5534823	0.03017241	0.49400184	1
PEPTIDYL_TYROSINE_PHOSPHORYLATION	25	-0.5257874	-1.5464498	0.02345416	0.49399638	1
THIOLESTER_HYDROLASE_ACTIVITY	15	-0.5826979	-1.5402362	0.03250478	0.49413928	1
COLLAGEN	22	-0.5351812	-1.5391032	0.03386454	0.47478908	1
SULFURIC_ESTER_HYDROLASE_ACTIVITY	16	-0.5687776	-1.5352945	0.04	0.46625507	1
GLYCOLIPID_METABOLIC_PROCESS	16	-0.5713344	-1.5301486	0.03784861	0.46270463	1
CHROMOSOMEPERICENTRIC_REGION	31	-0.4808978	-1.5228419	0.03483607	0.47023144	1
REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	42	-0.445787	-1.5141118	0.02574257	0.48172045	1
AXONOGENESIS	41	-0.4501657	-1.5005414	0.02910603	0.5139358	1

UP

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
STEROID_METABOLIC_PROCESS	64	0.50926155	1.8503424	0	0.39164612	0.35
CHEMICAL_HOMEOSTASIS	136	0.44306058	1.8335853	0	0.23609515	0.4
OXIDOREDUCTASE_ACTIVITY_GO_0016616	55	0.49824286	1.7802109	0	0.31021947	0.619
OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONOR	23	0.6051666	1.7617718	0.0019685	0.28931224	0.699
OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DONORS	60	0.47402784	1.7153921	0	0.37308097	0.854
STEROID_BIOSYNTHETIC_PROCESS	22	0.57602483	1.66491	0.00804829	0.509658	0.957
NEGATIVE_REGULATION_OF_TRANSPORT	17	0.6166911	1.6592981	0.00744879	0.46184468	0.965
POTASSIUM_ION_TRANSPORT	49	0.47788802	1.6390767	0.0040568	0.4850235	0.98
VOLTAGE_GATED_POTASSIUM_CHANNEL_COMPLEX	37	0.49696887	1.6127906	0.02053388	0.5496902	0.996
OXIDOREDUCTASE_ACTIVITY_GO_0016705	31	0.51510423	1.6080852	0.01635992	0.51577073	0.997
REGULATION_OF_SECRETION	33	0.5096709	1.6061571	0.00590551	0.47715434	0.997
ATPASE_ACTIVITY_COUPLED_TO_TRANSMEMBRANE_MOVEMENT_OF_IOI	18	0.5774405	1.5980569	0.01953125	0.47134835	0.997
ION_HOMEOSTASIS	112	0.39221933	1.5854561	0.00398406	0.48894048	0.999
PROTEIN_PROCESSING	48	0.45572343	1.5844144	0.01214575	0.45853817	0.999
NEUROPEPTIDE_RECEPTOR_ACTIVITY	15	0.5987516	1.582735	0.03143419	0.4331638	0.999
CELLULAR_CATION_HOMEOSTASIS	93	0.40122604	1.5781736	0.0038835	0.42337033	0.999
OXYGEN_BINDING	19	0.5668802	1.5750759	0.02941177	0.40749937	0.999
NEUROPEPTIDE_BINDING	15	0.5987516	1.5654978	0.00976563	0.4164075	1
CARBOHYDRATE_TRANSPORT	16	0.58402526	1.5534754	0.03292181	0.4337085	1
RESPONSE_TO_NUTRIENT_LEVELS	28	0.5217431	1.5502299	0.02514507	0.4233382	1
SIGNAL_SEQUENCE_BINDING	15	0.5940841	1.549926	0.04743083	0.4040046	1
CARBOHYDRATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	15	0.5963993	1.5387459	0.03653846	0.42123857	1
VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVITY	33	0.4852749	1.535342	0.01945525	0.4140759	1

	Mentioned in the Text
	Also of interest

KEGG: 15q Duplication Neurons

DOWN

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
KEGG_NITROGEN_METABOLISM	21	-0.6195197	-1.8528584	0.0021692	0.04190687	0.05
KEGG_DORSO_VENTRAL_AXIS_FORMATION	23	-0.5353528	-1.5962297	0.02040816	0.31829458	0.535
KEGG_COLORECTAL_CANCER	61	-0.4084651	-1.5107552	0.01750547	0.4364343	0.796
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	68	-0.3824661	-1.4601109	0.0203252	0.48245612	0.911
KEGG_O_GLYCAN_BIOSYNTHESIS	26	-0.4429121	-1.376868	0.0755102	0.70290583	0.995
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	30	-0.4142374	-1.3466687	0.09052631	0.72519404	0.998
KEGG_PROSTATE_CANCER	86	-0.3274035	-1.3183947	0.0516129	0.74953264	1
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	24	-0.4263476	-1.2987518	0.12847966	0.73861414	1
KEGG_RENAL_CELL_CARCINOMA	68	-0.3336962	-1.2761695	0.08478261	0.75236195	1
KEGG_RNA_DEGRADATION	55	-0.3399249	-1.2471025	0.10775862	0.8043293	1
KEGG_MTOR_SIGNALING_PATHWAY	51	-0.3382346	-1.2241685	0.16059957	0.8366159	1
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	82	-0.307321	-1.2127756	0.15010571	0.8168095	1
KEGG_LYSINE_DEGRADATION	43	-0.3535678	-1.211876	0.1655914	0.757375	1
KEGG_CALCIIUM_SIGNALING_PATHWAY	158	-0.2761783	-1.2018442	0.09368192	0.7449851	1
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	40	-0.3439494	-1.1756773	0.22020201	0.8042487	1
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	46	-0.3187745	-1.1364563	0.22520661	0.9308508	1
KEGG_OOCYTE_MEIOSIS	104	-0.2766291	-1.1350114	0.18979591	0.88252515	1
KEGG_PEROXISOME	75	-0.2940089	-1.1291635	0.25211865	0.85886955	1
KEGG_CELL_ADHESION_MOLECULES_CAMS	108	-0.2709754	-1.1256946	0.21365638	0.82850426	1
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	96	-0.2784223	-1.124122	0.21318682	0.79267675	1

UP

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
KEGG_RIBOSOME	86	0.6251042	2.4255242	0	0	0
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	59	0.5316615	1.9352894	0	0.00627027	0.011
KEGG_OXIDATIVE_PHOSPHORYLATION	109	0.45912483	1.842193	0	0.02433797	0.06
KEGG_PARKINSONS_DISEASE	108	0.4482542	1.8021054	0	0.03072979	0.099
KEGG_FRUCTOSE_AND_MANNANOSE_METABOLISM	32	0.53406686	1.7226743	0.00380952	0.05994333	0.224
KEGG_BUTANOATE_METABOLISM	33	0.5276093	1.6830931	0.0094697	0.07439231	0.319
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	43	0.44892675	1.5230733	0.02480916	0.2722843	0.803
KEGG_GRAFT_VERSUS_HOST_DISEASE	18	0.54067326	1.5114006	0.03944773	0.26209706	0.835
KEGG_STEROID_BIOSYNTHESIS	17	0.5389776	1.5104612	0.05343511	0.23531026	0.838
KEGG_GLYCOLYSIS_GLUONEOGENESIS	56	0.4155577	1.5070602	0.01541426	0.21801564	0.846
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	197	0.34570226	1.502887	0.0017762	0.20495717	0.857
KEGG_HUNTINGTONS_DISEASE	164	0.35330614	1.5002633	0.00170068	0.19295803	0.868
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	42	0.4381724	1.4954516	0.0310219	0.18418214	0.873
KEGG_GALACTOSE_METABOLISM	24	0.49400884	1.493101	0.03180914	0.17509758	0.877
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	50	0.4093204	1.453237	0.0323741	0.22599593	0.95
KEGG_BLADDER_CANCER	41	0.42557076	1.4399163	0.04323308	0.23295492	0.961
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	44	0.41345498	1.4374782	0.03551402	0.22274841	0.962
KEGG_FATTY_ACID_METABOLISM	41	0.42373234	1.4245584	0.04036697	0.23309301	0.976
KEGG_TYROSINE_METABOLISM	34	0.43931115	1.4240425	0.05323194	0.22209801	0.976
KEGG_ALZHEIMERS_DISEASE	147	0.33042386	1.4001417	0.01094891	0.25217772	0.985
KEGG_P53_SIGNALING_PATHWAY	64	0.37650755	1.3924896	0.03690037	0.25440663	0.988
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	57	0.38298565	1.3846358	0.04752852	0.25584307	0.991
KEGG_GAP_JUNCTION	83	0.35940734	1.3708907	0.02573529	0.2696298	0.995
KEGG_PRIMARY_IMMUNODEFICIENCY	24	0.44865113	1.357959	0.07339449	0.28243303	0.998
KEGG_STEROID_HORMONE_BIOSYNTHESIS	34	0.41790196	1.3535304	0.08914729	0.27886382	0.998
KEGG_LYSOSOME	116	0.3170462	1.28857	0.07191781	0.41091797	1
KEGG_CHEMOKINE_SIGNALING_PATHWAY	164	0.30074504	1.2801428	0.03723404	0.41790593	1

Mentioned in the Text

KEGG: AS Deletion Neurons

DOWN

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
KEGG_LONG_TERM_DEPRESSION	62	-0.4619342	-1.6945065	0	0.4060894	0.284
KEGG_ALZHEIMERS_DISEASE	145	-0.3698002	-1.5450963	0.0021322	0.82666373	0.747
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	38	-0.4680263	-1.5383085	0.02282158	0.5832817	0.764
KEGG_SMALL_CELL_LUNG_CANCER	83	-0.396	-1.5047491	0.0087146	0.5771273	0.856
KEGG_CALCIIUM_SIGNALING_PATHWAY	159	-0.3523216	-1.4686618	0.01434426	0.6066712	0.922
KEGG_LYSINE_DEGRADATION	44	-0.4264061	-1.4446168	0.02589642	0.60743296	0.953
KEGG_PARKINSONS_DISEASE	108	-0.357089	-1.4245723	0.01026694	0.6023005	0.973
KEGG_PRION_DISEASES	31	-0.4528733	-1.4236437	0.06746032	0.53044367	0.973
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	102	-0.3595672	-1.4170115	0.01207244	0.49426493	0.978
KEGG_MELANOGENESIS	92	-0.3574246	-1.397897	0.03067485	0.5071475	0.985
KEGG_ALANINE_ASPARTATE_AND_Glutamate_METABOLISM	30	-0.4466879	-1.3961729	0.07489879	0.46770537	0.986
KEGG_ECM_RECEPTOR_INTERACTION	79	-0.365923	-1.3891255	0.03151261	0.45221663	0.987
KEGG_SELENOAMINO_ACID_METABOLISM	24	-0.4673972	-1.373588	0.08033827	0.46872815	0.99
KEGG_LONG_TERM_POTENTIATION	62	-0.3726961	-1.3586869	0.04990403	0.4833538	0.993
KEGG_GLIOMA	62	-0.3725277	-1.3579254	0.0491453	0.4530296	0.993
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	46	-0.392426	-1.3503655	0.06378601	0.44834524	0.995
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	15	-0.5100718	-1.3433353	0.14609054	0.44290158	0.997
KEGG_SPHINGOLIPID_METABOLISM	35	-0.4174554	-1.3421384	0.09696969	0.42120445	0.997
KEGG_RENIN_ANGIOTENSIN_SYSTEM	15	-0.4954344	-1.3377883	0.11195446	0.41043818	0.998
KEGG_NOTCH_SIGNALING_PATHWAY	43	-0.3982469	-1.3349452	0.0724346	0.39750975	0.998
KEGG_VIBRIO_CHOLERAEE_INFECTION	53	-0.3761694	-1.3150212	0.10240964	0.4308302	1

UP

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
KEGG_STEROID_BIOSYNTHESIS	17	0.79428303	2.1545434	0	7.91E-04	0.001
KEGG_FRUCTOSE_AND_MANNULOSE_METABOLISM	33	0.60110503	1.8836194	0.00192308	0.01389321	0.037
KEGG_STEROID_HORMONE_BIOSYNTHESIS	40	0.54847443	1.8275898	0	0.01820514	0.071
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	15	0.6516438	1.7261577	0.01145038	0.04510398	0.21
KEGG_PENTULOSE_PHOSPHATE_PATHWAY	25	0.5772126	1.683968	0.0113852	0.05559753	0.301
KEGG_GLYCOLYSIS_GLUCONOGENESIS	58	0.45955414	1.6402068	0.00393701	0.07311387	0.438
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	57	0.4583219	1.6067728	0.00401606	0.08702132	0.559
KEGG_RNA_POLYMERASE	29	0.5114668	1.5849962	0.00578035	0.09407733	0.637
KEGG_BASAL_TRANSCRIPTION_FACTORS	33	0.48395783	1.5266265	0.03428571	0.13768664	0.802
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	22	0.46971262	1.3734919	0.09942639	0.3916363	0.997
KEGG_RIBOSOME	86	0.35412627	1.372683	0.0368217	0.35812816	0.997
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	37	0.41842628	1.3668619	0.07677165	0.34231362	0.998
KEGG_PPAR_SIGNALING_PATHWAY	62	0.3655422	1.3473259	0.06262231	0.3612048	0.999
KEGG_GLYCEROLIPID_METABOLISM	47	0.38226116	1.3127617	0.06967213	0.42007983	1
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	42	0.38038158	1.2725906	0.10836502	0.5034263	1
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	21	0.40839535	1.1981012	0.21301775	0.73112905	1
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_S	20	0.42574117	1.1892812	0.2267658	0.7216315	1
KEGG_STARCH_AND_SUCROSE_METABOLISM	40	0.353763	1.1885904	0.18958333	0.6851217	1
KEGG_THYROID_CANCER	28	0.38601628	1.1878542	0.21359223	0.65200734	1
KEGG_PROTEASOME	41	0.35376793	1.1820115	0.20292504	0.63990986	1

Mentioned in the Text

Also of interest