

Table 1: Top 2 genes with highest logfoldchanges in each group of genes (original pipeline)

	group	names	scores	logfoldchanges	pvals	pvals_adj
3057	OPC	CTC-365E16.1	-2.744038	15.860168	6.345860e-03	0.025368
868	OPC	AC074391.1	0.393595	12.640070	6.983024e-01	0.756967
6219	astrocytes	RP11-337C18.7	-1.668066	14.325747	9.619690e-02	0.192734
7486	astrocytes	MYBPC3	-3.158101	13.549382	1.715677e-03	0.010945
8858	endothelial	RPL31P52	0.696653	13.485387	4.972563e-01	0.629849
11720	endothelial	FIBIN	-4.294025	11.916581	2.253567e-05	0.000348
14759	fetal_quiescent	HMGA1P7	-2.011036	15.701316	4.520428e-02	0.128787
14157	fetal_quiescent	RNA5SP295	-1.472998	10.959235	1.418024e-01	0.269971
19084	fetal_replicating	AKAP17BP	-2.610420	14.402124	9.401144e-03	0.036940
19237	fetal_replicating	OLFML3	-2.836706	11.595176	4.795499e-03	0.022918
22979	hybrid	DDX43	-2.005920	10.107913	4.556738e-02	0.153087
23381	hybrid	NEUROD4	-2.342430	9.539777	1.968379e-02	0.104423
27795	microglia	LHX6	-5.318503	12.736008	1.760014e-07	0.000004
26168	microglia	RP11-565F19.2	-1.959648	12.445036	5.088430e-02	0.101271
29592	neurons	RP11-107M16.2	0.477371	11.338261	6.338657e-01	0.772301
30758	neurons	KRT18P11	-1.249004	11.260698	2.124464e-01	0.432901
35227	oligodendrocytes	RP11-122C21.1	-2.835732	14.881016	4.812472e-03	0.021341
35024	oligodendrocytes	MIR1285-1	-2.494510	11.308447	1.304645e-02	0.046444

Table 2: Top 2 genes with highest logfoldchanges in each group of genes (Alternative pipeline)

	group	names	scores	logfoldchanges	pvals	pvals_adj
2	0	SYNPR	11.990235	7.121284	3.997681e-33	6.231852e-29
4	0	DLX6-AS1	11.618639	7.104732	3.313721e-31	3.099390e-27
46837	1	C1QA	2.838698	8.291865	4.529795e-03	4.596233e-02
46820	1	ITGAX	3.192155	5.197433	1.412155e-03	1.757808e-02
93535	2	NEUROD6	10.638222	7.729523	1.978700e-26	2.035180e-22
93537	2	SATB2	10.569890	7.656928	4.109767e-26	3.203289e-22
140315	3	AQP4	10.505355	9.732701	8.161556e-26	2.120463e-22
140304	3	ETNPPL	11.040619	9.699903	2.433512e-28	1.625794e-24
187064	4	PLP1	10.700719	12.617879	1.009918e-26	1.969928e-22
187066	4	ERMN	10.655007	11.401220	1.652323e-26	1.969928e-22
233839	5	RGS4	6.773355	7.562348	1.258299e-11	5.355934e-08
233830	5	VSNL1	7.979712	7.059061	1.466755e-15	6.859426e-11
280596	6	TNR	7.893887	7.957314	2.929182e-15	1.369861e-10
280603	6	PDGFRA	6.905768	7.921408	4.993247e-12	2.918927e-08
327362	7	CRYM	6.587894	7.252936	4.461095e-11	2.086276e-06
327506	7	HS3ST4	3.909808	6.375838	9.236946e-05	2.492753e-02
374193	8	AQP4	4.218843	6.725787	2.455594e-05	1.730878e-02
374128	8	PROX1	5.078102	6.214446	3.812234e-07	9.994545e-03
420917	9	CDK1	5.404496	13.838960	6.499080e-08	1.266400e-04
420979	9	AURKB	4.423233	12.705043	9.723481e-06	5.226762e-03

Table3: Top 2 genes with highest logfoldchanges in each group of genes (Original pipeline neuron walk community)

	group	names	scores	logfoldchanges	pvals	pvals_adj
132	2	NCOA3	4.604604	12.489227	7.554121e-02	2.405771e-01
116	2	LDOC1L	5.333736	11.876977	5.750017e-02	2.037207e-01
6257	4	PGK1	-0.083735	10.068966	9.334613e-01	9.833671e-01
7629	4	GBP3	-1.469138	8.980725	1.488053e-01	6.537288e-01
9448	5	GDF11	0.276875	10.108558	7.845588e-01	9.101610e-01
9535	5	APOOL	0.200493	9.292867	8.433015e-01	9.375225e-01
14793	6	BCL11A	-1.382740	17.125774	1.996888e-01	5.504861e-01
14063	6	NR2C1	-0.512931	12.142733	6.219659e-01	8.529526e-01
19633	7	RP11-301G7.1	-3.582349	14.621448	7.794909e-04	8.597993e-03
17163	7	C22orf23	0.353680	13.635322	7.554395e-01	8.486369e-01
20911	8	RP11-472I20.1	0.482619	14.652143	6.456734e-01	8.177907e-01
22981	8	RP11-517P14.7	-1.887542	12.730510	6.294162e-02	2.510135e-01
25163	11	ZNF19	0.151327	13.351387	8.863317e-01	9.479483e-01
24397	11	RP11-484D2.2	0.830440	12.167615	4.090952e-01	7.193598e-01
31950	12	KBTBD7	-8.107540	13.796643	2.035421e-12	1.628337e-10
29939	12	NR2C1	-1.159490	12.246593	4.474976e-01	7.142820e-01
35676	13	RP11-517P14.7	-3.872727	12.299545	3.505967e-04	5.389820e-03
32053	13	SRGN	1.410486	12.191781	1.774776e-01	3.820832e-01