Table S1. List of top 20 enriched genes in each of the unbiased groups in original pipeline.

OPC	Astrocytes	Endothelial	Fetal quiescent	Fetal replicating	Hybrid	Microglia	Neurons	oligodendrocytes
B2M	GPR98	B2M	DCX	SOX11	FGF12	B2M	MEG3	ENPP2
PIP4K2A	ATP1A2	NEAT1	SOX11	SYNE2	MEG3	HLA-DRA	SNAP25	TMEM144
PLP1	SLC1A3	KLF4	SOX4	EGR1	SCG2	SAT1	VSNL1	PLP1
APOD	SLC1A2	TIMP3	STMN2	MARCKS	ERBB4	LAPTM5	GABRB2	PIP4K2A
EGR1	ETNPPL	TACC1	TUBB	CREB5	TSPAN7	SPP1	SYT1	ERMN
FOS	GJA1	IFITM1	TUBA1A	TFAP2C	SOX2-OT	HLA-DPA1	SCN2A	TF
B3GNT7	AQP4	IFITM3	BCL11A	NNAT	SCG5	GPR183	SCG2	APOD
PDGFRA	F3	APOLD1	NREP	SOX4	GABRA1	OLR1	PNMA2	HHIP
MARCKS	PON2	FOS	MAP1B	FABP7	GAD1	CD74	GABRA1	SOX2-OT
SEMA5A	PREX2	ITIH5	NEUROD6	CENPF	DOCK10	CD53	SYNPR	MOG
LUZP2	SLCO1C1	ANXA2	SATB2	NFIA	CNTNAP2	ZFP36L2	GABRG2	UGT8
VCAN	SPARCL1	SPARC	DPYSL3	ITGB8	DLX6-AS1	PLEK	GABBR2	SLAIN1
ANXA5	LRRC16A	PTRF	STMN1	TNC	NRIP3	AIF1	SCG5	CNP
LHFPL3	GLUL	ATP1A2	MLLT11	EZR	PROX1	SRGN	NAP1L3	BCAS1
EDIL3	PPAP2B	DDX3Y	NNAT	NUSAP1	SNAP25	ITGAX	ALDOA	SPOCK3
PTPRZ1	NEAT1	GNG11	HN1	NHSL1	GPRASP1	A2M	PEG3	SPP1
CRISPLD2	BMPR1B	HLA-E	SRGAP1	MMS22L	NAP1L3	CCL4	FGF12	PCDH9
PCDH15	RYR3	SAT1	CXADR	GPR98	EDIL3	C3	GAD1	CNDP1
KLF4	ATP1B2	DUSP1	SLA	CENPU	REEP5	SGK1	NRIP3	CLDN11
DOCK10	SLC4A4	RBMS3	MARCKS	PHLDA1	SCN2A	MSR1	RTN1	CLDND1

* Genes ranked according to the enrichment score, from highest to the lowest.

Table S2. List of top 4 genes with the highest log-fold changes in each of the unbiased groups in original pipeline.

Groups	Gene Names	Scores	Logfold changes	pvals	pvals_adj
OPC	GPRIN2	-3.86	13.59	0.0001	0.0013
OPC	AC104781.1	-3.92	12.35	0.0001	0.0011
OPC	RP11-195B17.1	-2.24	10.77	0.0255	0.0585
OPC	BNC2	-2.32	10.20	0.0208	0.0499
astrocytes	AC093157.1	-3.55	12.85	0.0004	0.0032
astrocytes	RP11-589N15.2	-2.88	10.85	0.0042	0.0186
astrocytes	MTCP1	-2.31	10.81	0.0211	0.0615
astrocytes	RP11-354P11.2	-2.18	8.62	0.0301	0.0806
endothelial	ACOT12	-2.89	12.15	0.0040	0.0175
endothelial	RP11-307I14.3	-2.45	11.45	0.0147	0.0488
endothelial	RP11-789C17.1	-2.66	11.37	0.0080	0.0311
endothelial	NOS2	-3.20	10.35	0.0015	0.0081
fetal_quiescent	NCLP1	-1.20	13.43	0.2298	0.3690
fetal_quiescent	HLX	-1.82	9.71	0.0693	0.1558
fetal_quiescent	SNORA45	-2.18	9.27	0.0300	0.0860
fetal_quiescent	RP11-337C18.7	-1.73	9.06	0.0851	0.1802
fetal_replicating	FOXQ1	-2.53	13.95	0.0117	0.0370
fetal_replicating	CYP24A1	-2.12	12.40	0.0345	0.0808
fetal_replicating	LAT2	-1.35	12.02	0.1797	0.2814
fetal_replicating	AC006116.17	-2.77	11.96	0.0059	0.0224
hybrid	RP11-345M22.1	-2.70	10.05	0.0073	0.0640
hybrid	XXbac-BPG181B23.7	-2.67	9.78	0.0079	0.0663
hybrid	RP11-12L8.2	-2.94	9.59	0.0034	0.0434
hybrid	RP11-461L13.4	-2.36	8.94	0.0190	0.1002
microglia	RP11-522L3.11	-2.76	12.64	0.0060	0.0201
microglia	CTD-2050B12.1	-2.58	11.85	0.0101	0.0291
microglia	SKA1	-2.61	11.59	0.0093	0.0276
microglia	RP11-269G24.8	-2.80	11.33	0.0053	0.0183
neurons	IL1RL1	-0.91	9.90	0.3626	0.6101
neurons	RP11-565J7.1	-1.19	9.34	0.2335	0.4947
neurons	ABO	-1.05	9.07	0.2925	0.5545
neurons	RP4-665J23.4	-1.41	8.38	0.1588	0.4090
oligodendrocytes	RPS10P16	-3.73	12.19	0.0002	0.0014
oligodendrocytes	RP11-627K11.3	-1.86	10.03	0.0636	0.1446
oligodendrocytes	SNORA1	-2.08	9.33	0.0384	0.1000
oligodendrocytes	RP1-30E17.2	-4.03	9.33	0.0001	0.0005

* Genes ranked according to the log-fold changes within each cluster, from highest to the lowest.

Table S3. List of top 20 enriched genes in each of the unbiased groups in original pipeline.

Cluster 0: Neurons	Cluster 1: Fetal replicating	Cluster 2: Fetal quiescent	Cluster 3: Astro-cytes	Cluster 4: Oligo-dendro-cytes	Cluster 5: Endo-thelial	Cluster 6: OPC	Cluster 7: Excitatory glutamin-ergic neurons	Cluster 8: Hybrid	Cluster 9: Microglia
MEG3	RPS27	TUBA1A	GJA1	PLP1	TNR	PROX1	CRYM	SLC17A7	MKI67
NRIP3	HNRNPH1	STMN2	ATP1A2	ERMN	PCDH15	LAMA3	TLE4	CHN1	BIRC5
SCG2	RPL34	MAP1B	SPARCL1	ENPP2	B3GNT7	NR4A1	XPR1	CA11	RRM2
ATP1B1	RPL21	NEUROD6	F3	TF	SEMA5A	VIP	SOX5	SV2B	CENPU
SYNPR	RPS19	TUBB	RANBP3L	TMEM144	PTPRZ1	KDM5D	LMO3	GABRA5	CASC5
GAD1	SOX4	SATB2	ATP1B2	SOX2-OT	OLIG1	TTTY15	LMO7	VSNL1	HIST1H1B
SNAP25	SOX11	CRMP1	ETNPPL	MOG	SOX6	TGFB2	AFF3	CAMK2A	NUSAP1
GABRA1	RPL39	DCX	AQP4	CLDND1	PDGFRA	RGS16	FBXW7	PHYHIP	HMGN2
ZNF385D	RPS11	TMSB15A	SLC1A3	UGT8	LHFPL3	CPNE6	EPHA7	SYN2	CENPF
SNHG14	RPS6	MLLT11	SLC1A2	SCD	LRRK2	NPTXR	NFIB	RYR2	RAD51AP1
NRXN3	RPL23	SLA	CLU	HHIP	LUZP2	KCNB1	KCTD12	ANO3	PTTG1
GABRB2	MARCKS	TMSB10	GPR98	CLDN11	MEGF11	NLGN4Y	SORCS1	C1orf115	FANCD2
DLX6-AS1	SYNE2	STMN1	SLCO1C1	PIP4K2A	VCAN	ARL4C	GRIK3	TSHZ2	ECT2
GAD2	RPS3A	MN1	GPR37L1	OPALIN	RAB31	NRIP3	SSBP2	KIAA1211L	HIST1H1E
GABRG2	WTAP	SRGAP1	LRRC16A	CNDP1	XYLT1	KCNJ3	BCL11A	HTR2A	HMGB1
NAP1L3	RPS18	PLXNA4	CST3	RNASE1	APOD	SYNPR	SOBP	MKL2	ANP32E
IGF1	EEF1A1	ZBTB18	AGT	CNP	LIMS2	ARNT2	BCL11B	TMEM155	HMGN2P5
GPRASP1	H3F3B	FABP7	FGFR3	SLC12A2	AFAP1L2	PDXK	KHDRBS3	NPTX1	HNRNPH1
GRIK2	RPL36A	NREP	MGST1	ANLN	PMP2	PPM1H	ADCY1	MFSD4	GMNN
AHI1	TMSB10	TUBB2B	SLC25A18	EVI2A	IL1RAP	CALN1	NREP	SYN1	MSI1

* Genes ranked according to the enrichment score, from highest to the lowest.

Table S4. List of top 4 genes with the highest log-fold changes in each unbiased groups in alt pipeline.

Groups	Gene	Scores	Logfold changes	pvals	pvals_adj
0	CLEC4GP1	2.9	28.4	0.003736797	0.03492771
0	SYNPR	11.56	6.68	6.928347E-31	4.84527E-27
0	DLX6-AS1	11	6.52	3.93898E-28	1.059495E-24
0	GAD1	11.51	6.51	1.118388E-30	6.517779E-27
1	C1QA	2.8	8.2	0.005103787	0.03695674
1	CCL4L1	2.72	5.32	0.006459913	0.04476492
1	ITGAX	3.13	5.1	0.001766284	0.01547136
1	HLA-DRB5	2.82	5.08	0.004763082	0.0349676
2	NEUROD6	10.44	7.73	1.681449E-25	1.192519E-21
2	SATB2	10.38	7.66	3.112163E-25	1.813717E-21
2	SOX11	8.84	7.07	9.734009E-19	1.418205E-15
2	DCX	9.69	6.87	3.341846E-22	1.460679E-18
3	AQP4	10.78	10.25	4.314934E-27	1.803165E-23
3	ETNPPL	10.8	9.99	3.276555E-27	1.636733E-23
3	GJA1	11.04	9.43	2.384792E-28	4.854448E-24
3	ATP1A2	11.03	8.99	2.776588E-28	4.854448E-24
4	PLP1	10.69	12.62	1.192003E-26	1.267383E-22
4	ERMN	10.65	11.54	1.673953E-26	1.267383E-22
4	OPALIN	10.39	10.74	2.715056E-25	6.781241E-22
4	CNDP1	10.36	10.59	3.584712E-25	8.356441E-22
5	PDGFRA	7.17	8.3	7.588648E-13	3.316903E-09
5	B3GNT7	7.86	8.1	3.784685E-15	4.411303E-11
5	TNR	8.1	8.06	5.702448E-16	1.993975E-11
5	PCDH15	7.87	8.01	3.460263E-15	4.411303E-11
6	RP11-301G23.1	3.07	8.51	0.002160042	0.0469715
6	VIP	5.9	7.18	3.684578E-09	2.642733E-05
6	PROX1	6.23	6.41	4.678244E-10	1.635842E-05
6	SYNPR	5.49	5.96	3.952401E-08	7.625774E-05
7	CRYM	6.83	7.61	8.713221E-12	3.046752E-07
7	GRIK3	5.8	6.6	6.439995E-09	1.73221E-05
7	HS3ST4	4.04	6.56	5.282098E-05	0.01348169
7	KLHL1	5.46	6.35	4.716855E-08	6.597371E-05
8	AC018799.1	4.21	8.66	2.607201E-05	0.004300284
8	ANO3	5.58	8.44	02.4521E-08	7.567851E-05
8	COL22A1	3.72	8.33	0.0001993453	0.01505509
8	GPR88	3.74	8.15	0.0001850385	0.01445003
9	CDK1	4.55	13.54	5.316958E-06	0.005173608
9	RRM2	5.12	12.67	3.0505E-07	0.001548173
9	CASC5	5.12	12.45	3.099268E-07	0.001548173
9	AURKB	3.99	12.34	6.707081E-05	0.02750308

* Genes ranked according to the log-fold changes within each cluster, from highest to the lowest.

^ The group assignment: 0: Neurons; 1: Fetal replicating; 2: Fetal quiescent; 3: Astrocytes; 4: Oligodendrocytes; 5: Endothelial; 6: OPC; 7: Excitatory glutaminergic neurons; 8: Hybrid; 9: Microglia