Supplementary Methods

Patient Selection. From January 2012 to October 2013, 69 adult patients operated on for high-grade glioma at Columbia University Medical Center (CUMC) were analyzed, including 49 primary GBM, 19 recurrent GBM and one primary anaplastic astrocytoma. All patients were enrolled under IRB protocol AAAJ-6163 or AAAA4666, as approved by the CUMC IRB committee, and all patient material was de-identified as specified by these protocols. Patients presenting for open surgical resection of lesions with the radiographic characteristics of GBM on MR imaging were considered eligible. An important inclusion criterion was the presence of FLAIR hyper-intense, non-contrast-enhancing (NE) tissue along the surgical trajectory between the planned craniotomy site and the gadolinium-enhancing border of the lesion. NE tissue outside of the planned surgical trajectory was not biopsied.

Immunohistochemistry and Microscopy. Formalin fixed, paraffin embedded tumor samples were sectioned at 5 microns and stained with hematoxylin and eosin (H&E). Histological analysis was performed by two board-certified neuropathologists (DP and PC). Samples were scored for the presence or absence of necrosis, microvascular proliferation, and mitotic figures. Chi-square analysis was performed to assess significant differences in the presence of these attributes between contrast enhancing (CE; n=105) and non-contrast enhancing (NE; n=86) samples (total n=191). The individual data for each sample is provided in supplementary table S5. Quantitative analysis of cell density was performed on all samples for which non-necrotic tissue filled at least one 400X field. To assess cellular density, H&E slides were scanned at low magnification for an area of highest cellular density and a representative photomicrograph was taken in this area at 400 x using an Olympus BX-43 light microscope outfitted with a DP-26 Olympus camera. The total cell count was obtained using ImageJ 1.46r software. A two-tailed Student's t-test was used to assess for a significant difference in cellularity between CE (n=87) and NE (n=80) samples (total n=167). Immunohistochemistry was performed using mouse anti-NeuN antibody (Millipore; dilution 1:1000) rabbit anti-OLIG2 (Chemicon, 1:500), mouse anti-GFAP (Chemicon, 1:1000), rat anti-CD44 (Calbiochem, 1:200), rabbit anti-IBA1 (Wako, 1:1000), rat anti-CD68 (AbD Serotec; 1:50) and mouse anti-SOX2 (Abcam; 1:5000). For the quantitative analysis in Figure 1, each slide was scanned at low magnification to select an area with the highest density of NeuN staining. A photomicrograph was taken of a representative 400x field in this area, and the total numbers of NeuN positive and negative nuclei were manually counted with the aid of the cell counter and grid macros in the ImageJ 1.46r software package. A two-tailed Student's t-test was used to assess for a significant difference in NeuN composition between CE and NE samples. We also performed a quantitative analysis of the labeling indices for OLIG2, NEUN, CD68 and SOX2 in normal (nonneoplastic) brain and non-enhancing regions of glioma samples. Each slide was scanned at low magnification to select the area with the highest density of staining for the respective marker. A representative 400x field was then manually counted by two independent observers (AD and MB) using a cell counter. Positive staining and total number of hematoxylin stained cells per field were counted and the labeling index was calculated as positive cells/total number of cells per 400x field x 100. A minimum of 100 cells per field was counted for each slide; if necessary, more than one field was counted to reach the minimum number of 100 cells. Counts from both observers were averaged for each sample and the final labeling index value was used for statistical analysis. Statistical analysis was performed using SPSS software, version 20.0 for Macintosh. A p value < 0.05 was considered statistically significant.

RNA Extraction, Sequencing and Analysis. We performed RNA-Seq on 92 flash frozen samples, which included 39 CE, 36 NE, and 17 NB. Only samples with an RNA Integrity Number (RIN) greater than 6 were used for RNA-seq. Genome-wide expression profiles were generated for each sample using RNA sequencing. For each sample, libraries were prepared using the Illumina TruSeq v2 RNA-Seq kit, and we obtained 15-30 million single-end, 100 base reads on an Illumina HiSeq 2000 sequencer. Raw reads from RNA-Seq experiments obtained from the Columbia Sulzberger Genome Center were mapped to the human transcriptome (hg19, Illumina iGenomes annotation) using Tophat 2(1). We used Cufflinks 2 to calculate expression levels for each gene as fragments per kilobase per million mapped reads (FPKM). For differential expression analysis, we computed read counts for reads that mapped uniquely to the transcriptome using HTSeq and used DESeq to calculate fold-changes and assess their statistical significance(2).

Computational Deconvolution of RNA-Seq Profiles. Our deconvolution strategy is an adaptation of the previously reported Population Specific Expression Analysis (PSEA) algorithm(3) with a few key modifications. For each sample *i* in our dataset, we write the expression level for a given gene *j* as follows:

$$G_{ij} = \sum_{k=1}^{N} C_{ik} g_{kj} + b \qquad (1)$$

where *N* is the number of cell types in the sample, C_{ik} is the fractional composition of a cell type *k* in a sample *i*, g_{kj} is the expression level of gene *j* in cell type *k*, and *b* is a background term that we assume is invariant across samples. Given the availability of *M* samples where *M* > *N* and experimental values for the fractional composition of each cell type, we can write an over-determined system of *M* equations like the one above and solve them to obtain *N* values corresponding to the expression of each gene in each cell type. Just as in PSEA, we obtain estimates of the fractional composition of each cell type using the expression data itself. The RNA expression levels of marker genes for each cell type serve as proxies for cellular composition. For example, if we re-write Equation 1 for a cell type-specific marker gene *j** that is expressed exclusively in a single cell type *k**, we obtain:

$$G_{ij*} = \sum_{k=1}^{N} C_{ik*} g_{k*j*} + b = C_{ik*} g_{k*j*} \qquad (2)$$

assuming that the background *b=0* for the marker gene. Hence, we can calculate the fractional composition of cell type *k** in sample *I* as $C_{ik*} = G_{ij*}/g_{k*j*}$. For simplicity of notation and because each marker gene is only expressed by a single cell type, we number the marker gene *j* for each cell type *k* as *j=k* and use Equation 2 to re-write Equation 1 as:

$$G_{ij} = \sum_{k=1}^{N} G_{ik} a_{kj} + b \qquad (3)$$

where $a_{kj} = g_{kj}/g_{kk}$ is the expression level of gene *j* in cell type *k* relative to that of the marker gene *k* for cell type *k*. We solve the corresponding system of equations subject to the constraint that a_{kj} be non-negative (a standard quadratic programming problem) using the MATLAB function *lsqnonneg*. Our approach deviates somewhat from the previously reported PSEA in two ways: 1) We attempt to estimate the absolute expression levels of each gene in each cell type g_{kj} after solving for the relative values a_{kj} and 2) We use an iterative procedure to improve our estimates of fractional composition until reaching convergence, when the sum of R^2 values differ by less than 0.000001 between iterations. For the first iteration, we seed the algorithm with cell type-specific marker genes and solve Equation 3. We then take the best-fit genes with $R^2 >$ 0.9 and calculate values for C_{ik} by taking advantage of the constraint that the sum of fractional compositions must equal one:

$$\sum_{k=1}^{N} C_{ik} = 1 \qquad (4)$$

allowing a direct estimate of the fractional composition of each cell type. These fractional compositions are then used to solve Equation 1 in subsequent iterations across the whole transcriptome. This process of iterative improvement continues until the overall fit no longer improves. We note that genes that are undetected (zero FPKM by RNA-Seq) and genes that are entirely assigned to the background term are not given a cell type assignment. We also note that similar algorithms for deconvolving expression data while simultaneously estimating fractional composition (i.e. "complete" deconvoution) have been reported previously (4). Hence, in addition to sharing aspects of PSEA(3), our strategy is closely related to the previously reported Digital Sorting Algorithm (DSA) (5) which exploits the same basic principles and assumptions.

In our specific implementation of the above algorithm for this data set, we used several carefully selected marker genes to define six major cellular populations found in glioma tissue. We used Olig2 expression levels across our samples as a proxy for the fractional composition of OPC-like transformed and recruited cells in the tumors, while Cd44 was used for reactive and transformed astrocytes in the tumors. In addition, we used Aqp4 for $Cd44^-$ astrocytes with an unreactive phenotype, Mal and Mog for oligodendrocytes, Rbfox3 and Neurod6 for neurons, and Aif1 and Cd68 for monocytes/microglia. The expression values used as input for deconvolution and for the seed genes were in FPKM as obtained using Cufflinks 2.0 (6) Values obtained from Cufflinks 2.0 were used directly with no additional pre-processing. Importantly, in all of the resulting heat maps throughout the text, the displayed values are the fraction of total expression of a given gene that is estimated to originate from a given cell type rather than the estimated expression levels for each cell type. This is so we can display a large number of genes with a wide range of expression levels on the same scale and emphasize our main point, which is the fractional contribution of each cell type to the expression of each gene.

Gene Ontology Analysis. For the gene ontology lists in Table S2, we took the 500 most highly expressed genes in the deconvolved profiles of each cell type from the NE tissue that had deconvolution purities > 0.5 (where more than 50% of the expression is attributed to the corresponding cell type) and assessed the enrichment of gene ontologies using FuncAssociate 2.0 (7). FuncAssociate uses Fisher's exact test to calculate a p-value for enrichment. For the gene ontology analysis shown in Fig 5., we used iPAGE, a mutual information-based algorithm for assessing gene ontology enrichment (8), to associate pathways with differentially expressed genes in the NE and normal (nonneoplastic) brain (NB) samples. Following differential expression analysis between the NE regions for each subtype and normal brain (NB), we took the adjusted p-values (p_{adj}) calculated using DESeq and used them to calculate $v = \pm(1- p_{adj})$. If a gene is more highly expressed in the NE samples than NB samples, $v > 0$. For each differential expression analysis, we ran iPAGE on the v-values separated into 20 bins and assessed the significance of association between each gene ontology and bin.

Supplementary References

1. Kim D*, et al.* (2013) TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome Biol.* 14(4).
2. Anders S & Huber W (2010) Differential expression analysis for sequence count data. *Genome Biol* 11(10):R106.
3. Kuhn A, Thu D, Waldvogel HJ, Faull RLM, & Luthi-Carter R (2011) Population-specific expression analysis (PSEA) reveals molecular changes in diseased brain. *nAture methods* 8(11):945-947.
4. Gaujoux R & Seoighe C (2013) CellMix: a comprehensive toolbox for gene expression deconvolution. *Bioinformatics* 29(17):2211-2212.
5. Zhong Y, Wan YW, Pang K, Chow LM, & Liu Z (2013) Digital sorting of complex tissues for cell type-specific gene expression profiles. *BMC bioinformatics* 14:89.
6. Trapnell C*, et al.* (2013) Differential analysis of gene regulation at transcript resolution with RNA-seq. *Nature biotechnology* 31(1):46-53.
7. Berriz GF, Beaver JE, Cenik C, Tasan M, & Roth FP (2009) Next generation software for functional trend analysis. *Bioinformatics* 25(22):3043-3044.
8. Goodarzi H, Elemento O, & Tavazoie S (2009) Revealing global regulatory perturbations across human cancers. *Molecular cell* 36(5):900-911.

Supplementary Figures

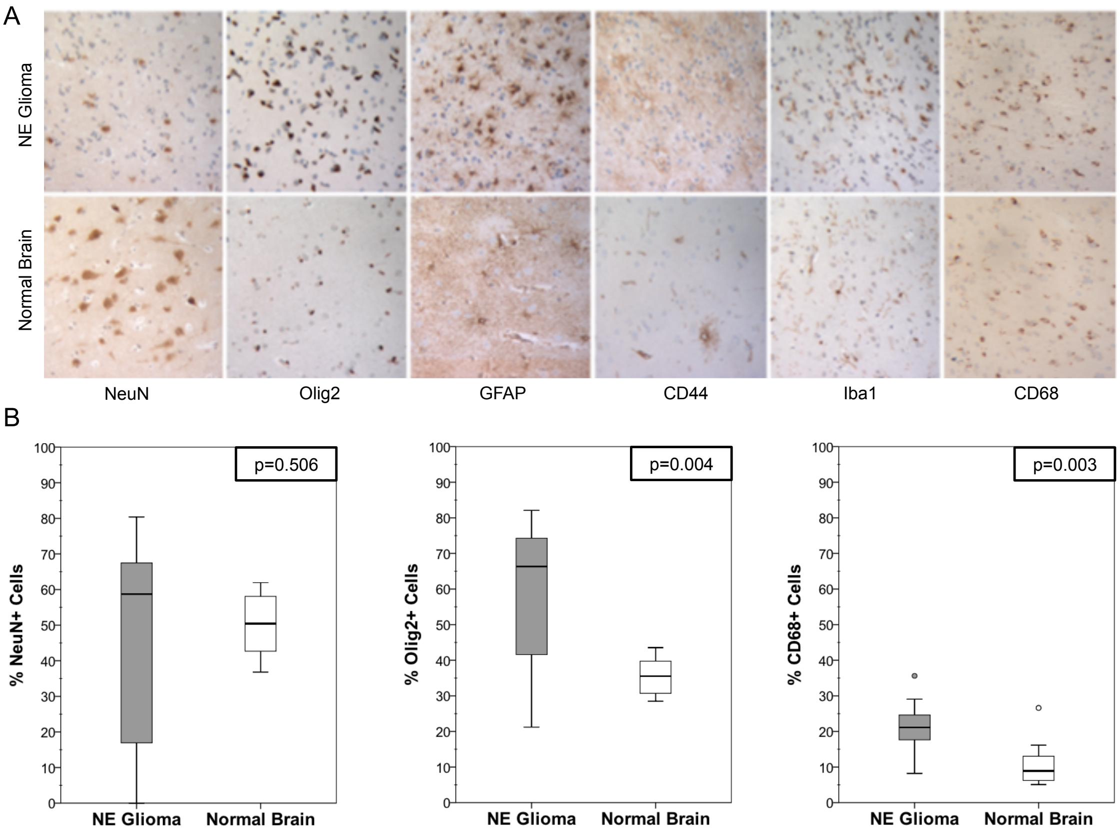

Fig S1. A) Immunohistochemical stains for cell type-specific markers show marked differences in the cellular composition of NE region of glioma samples compared to normal (nonneoplastic) brain. B) Quantitative analysis of Olig2 and CD68, but not NeuN, shows statistically significant differences in labeling index between NE regions and normal brain. A non-parametric Mann-Whitney U test was used to calculate p-values.

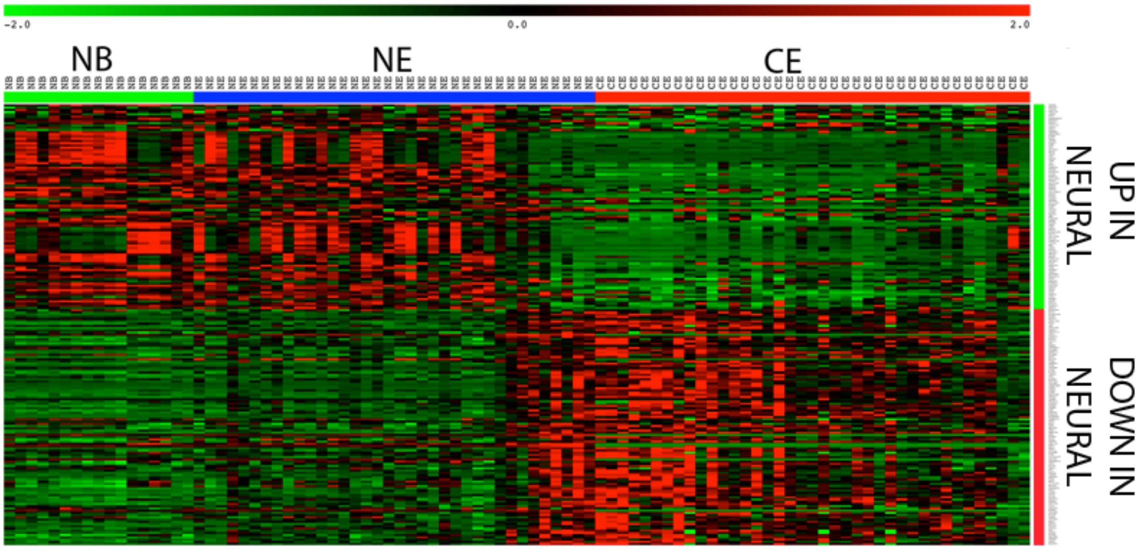

Fig. S2. Tissue samples from normal (nonneoplastic) brain (NB), non-enhancing regions of GBM (NE), and contrast-enhancing regions of GBM (CE) differ in the expression of Neural genes. NB and NE samples express higher levels of genes that are up in Neural GBM, and the CE samples express higher levels of genes that are down in Neural GBM.

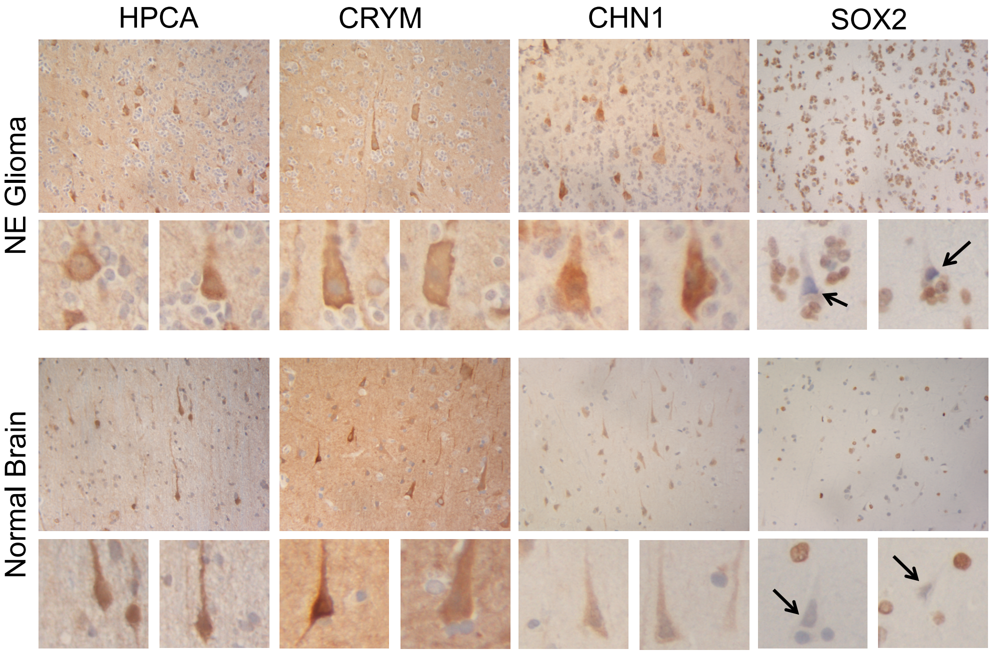

Fig S3. Immunohistochemical staining with HPCA, CRYM and CHN1 shows specific distribution within pyramidal neurons in both NE regions of GBM and in normal (nonneoplastic) brain samples. Comparable regions of the same sample are shown. HPCA, CRYM and CHN1 are Verhaak Neural Subtype classifier genes and are predicted by our computational algorithm to be highly selectively expressed in neurons, with cell-type purities of 96%, 94% and 92% respectively (Table S4). In contrast, SOX2 staining of the same NE glioma samples (upper panels) labels numerous infiltrating glioma cells, but not entrapped neurons (indicated with black arrows). Scattered SOX2+ cells are also seen in the normal brain samples (lower panels). The following antibodies were used: rabbit anti-HPCA (Abcam; 1:1000); mouse anti-CRYM (LifeSpan Biosciences; 1:1000); rabbit anti-CHN1 (Novus Biologicals; 1:500), mouse anti-SOX2 (Abcam; 1:5000).

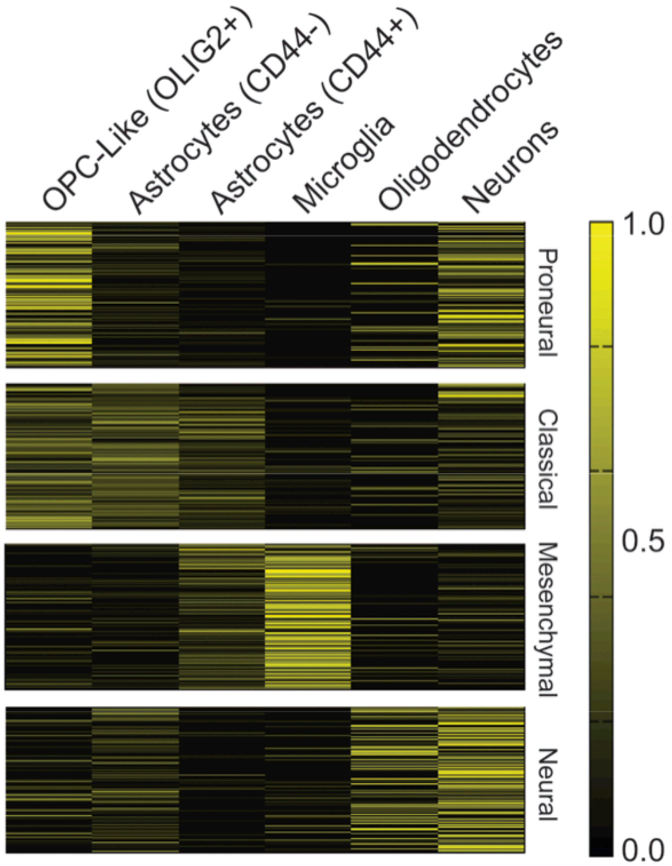

Fig S4. Heatmap showing the cell type-specific expression of Verhaak Classifier Genes derived from the deconvolution of the NE and NB samples. OPCs express the highest levels of Proneural genes. Classical genes are expressed by both astrocytes (CD44- and CD44+) as well as OPCs. Microglia, and to a lesser extent CD44+ astrocytes, express the highest levels of Mesenchymal genes. The expression of Neural genes are highest in neurons and oligodendrocytes. The list of Classifier genes and associated cell type-specific expression profiles are provided in Supplementary Table S4.

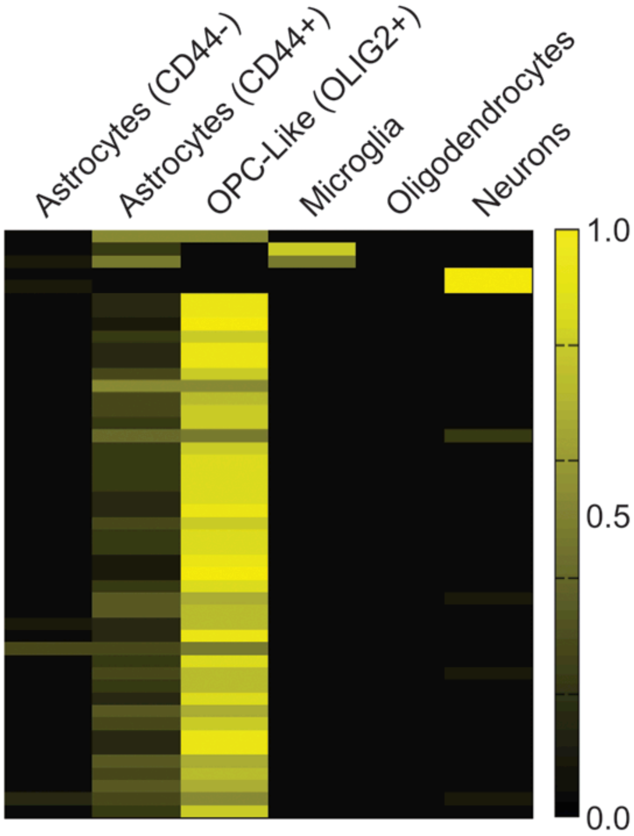

Fig. S5. OPC-like (OLIG2+) cells and CD44+ astrocytes are enriched in proliferation genes. These genes are derived from the iPAGE gene ontology (DNA-replication and M-phase and mitotic cell cycle). The heat map shows how the expression of these proliferation genes is distributed across different cell types, as determined by deconvolution of the NB and NE glioma samples.

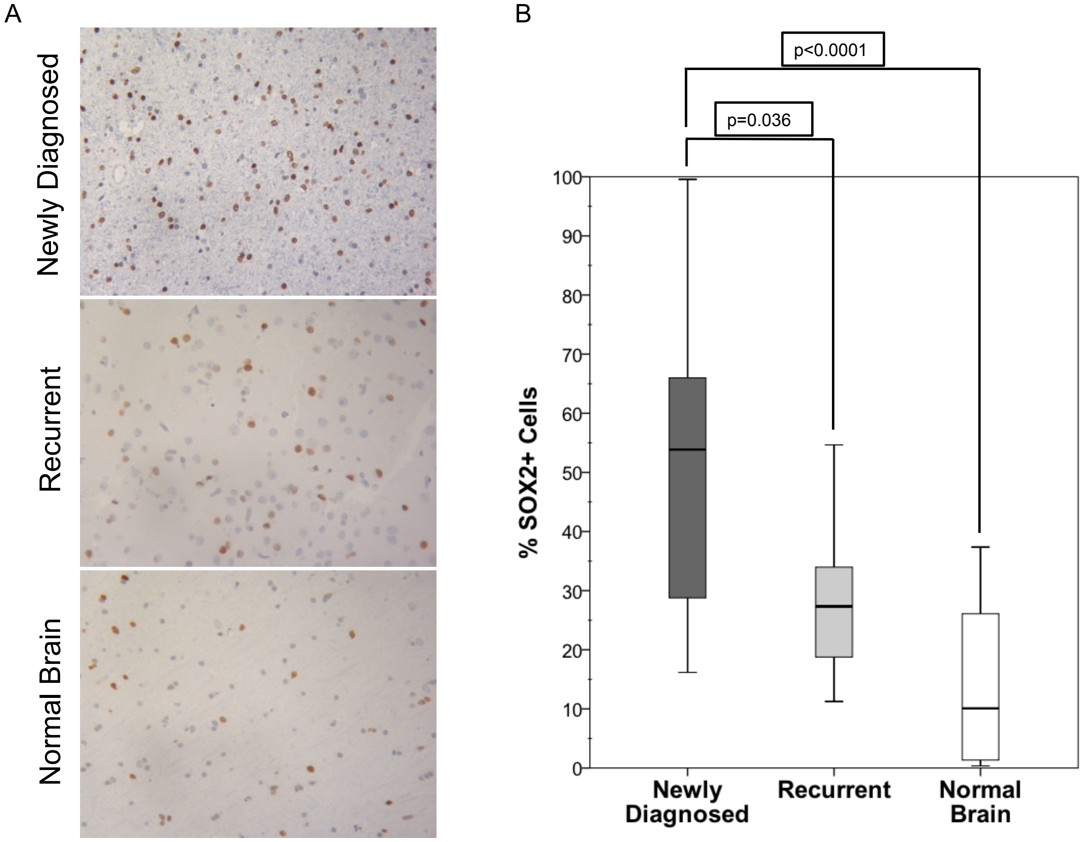

Fig. S6. A) Representative images of SOX2 immunohistochemical staining in the NE regions of newly diagnosed GBM, recurrent GBM and in normal (nonneoplastic) brain samples. B) SOX2 labeling indices are significantly different in NE regions of newly diagnosed GBM compared to equivalent areas in recurrent GBM specimens. SOX2 levels are not significantly different between NE regions of recurrent GBM and normal brain ($p=0.190$). For multiple comparisons, a one-way ANOVA with a Tamhane's T2 post-hoc test (equal variances not assumed) was used to calculate p-values. These findings are consistent with RNA-Seq differential expression analysis, which showed FDR-corrected p-values for Sox2 in newly diagnosed GBM vs. normal (nonneoplastic) brain of 1×10^{-12} and for newly diagnosed GBM vs. recurrent GBM of 1×10^{-8}.

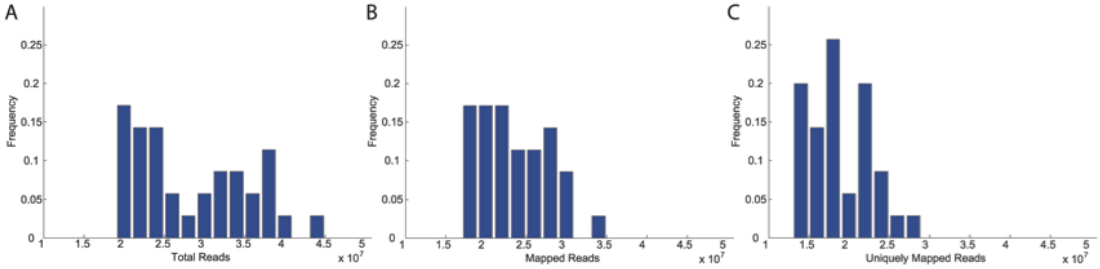

Fig. S7. Histograms showing A) the distribution of total reads, B) the distribution of mapped reads, and C) the distribution of reads uniquely mapped to the human transcriptome across all NE and NB samples included in this study. The medians for these three distributions are 26.9M (total reads), 22.6M (mapped reads), and 18.1M (uniquely mapped reads), respectively. The median fraction of reads that aligned was 80% (range 75%-92%) and the median fraction of mapped reads that aligned uniquely to the transcriptome was 80% (range 76%-83%).

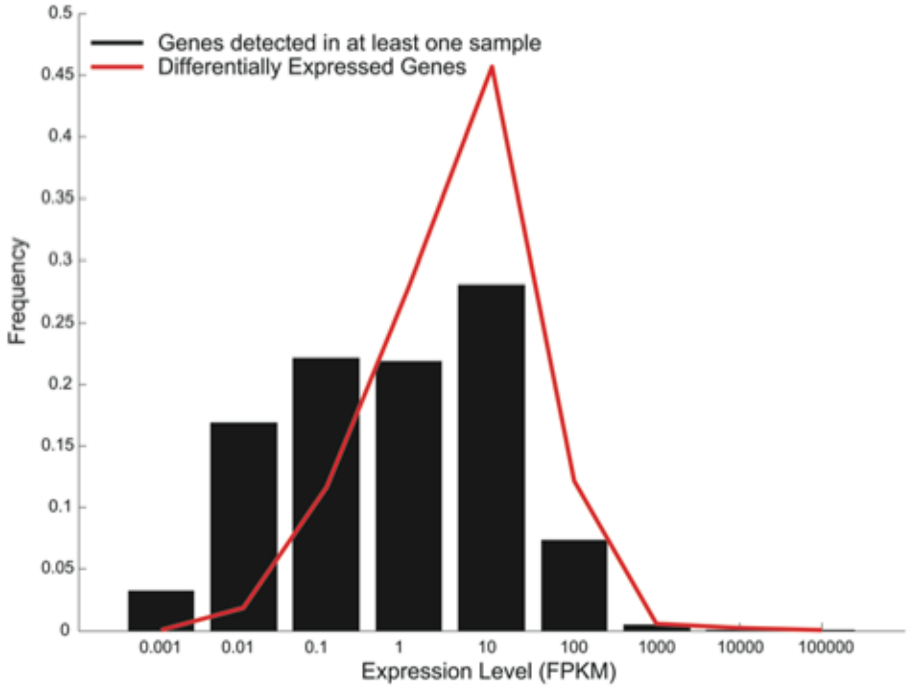

Fig. S8. Histograms showing the RNA abundance distributions for all genes detected in at least one nonneoplastic brain (NB) sample or NE sample from a Proneural GBM (black bars) and for genes that were found to be differentially expressed between these two sample sets (adjusted p-value < 0.05). Although the average expression level of the differentially expressed genes is higher than that of the whole transcriptome (50 FPKM vs. 21 FPKM), we can detect differential expression across a broad range of expression levels.

Age	Sex	Location	Primary or Recurrent	Adjuvant Therapy	EGFR Amplification	EGFRvIII	IDH1R132 Mutation	Subtype of CE Biopsy	Subtype of NE Biopsy
58	F	Left Temporal	Primary	N/A	Negative	Negative	Negative	Ⓟ	Ⓝ
76	M	Left Temporal	Primary	N/A	Negative	NT	Negative	Ⓟ	Ⓝ
65	M	Left Frontal	Primary	None	Negative	Negative	Positive	Ⓟ	Ⓟ
78	M	Left Frontal	Primary	N/A	Negative	Negative	Negative	Ⓟ	Ⓟ
59	F	Right Temporal	Primary	N/A	Negative	Negative	Negative	Ⓟ	Ⓟ
69	M	Left Parietal	Primary	N/A	Negative	Negative	Negative	Ⓟ	ⓅⓅ
38	F	Corpus Callosum	Primary	N/A	Negative	Negative	Negative	ⓅⓅⓅⓅ	ⓅⓃ
65	M	Left Occipital	Primary	N/A	Negative	Negative	Negative	Ⓒ	Ⓝ
64	M	Right Parietal	Primary	N/A	Positive	Positive	Negative	Ⓒ	Ⓝ
68	F	Left Temporal	Primary	N/A	Positive	Negative	Negative	Ⓒ	Ⓝ
57	M	Left Temporal	Primary	N/A	Positive	Negative	Negative	Ⓒ	Ⓜ
57	F	Left Frontal	Primary	N/A	Positive	Positive	Negative	ⒸⒸⒸ	ⒸⒸ
56	F	Right Temporal	Primary	N/A	Negative	Negative	Negative	ⓂⒸ	Ⓟ
69	F	Left Frontal	Primary	N/A	Negative	Negative	Negative	Ⓜ	ⓃⓃ
68	M	Left Parietal	Primary	N/A	Positive	Positive	Negative	ⓂⓂⓂ	ⓃⓃ
56	F	Splenium/ Bilateral Parietal	Primary	N/A	Negative	Negative	Negative	NS	Ⓝ
60	F	Left Temporal	Primary	N/A	Negative	Negative	Negative	NS	Ⓝ
81	M	Left Temporal	Primary	N/A	Negative	Negative	Negative	NS	Ⓝ
63	M	Right Temporal	Recurrent	Tmz, Rad	Positive	Negative	Negative	Ⓒ	NS
57	F	Right Frontal	Recurrent	Tmz, Rad, Bev	Positive	Positive	Negative	ⒸⒸ	NS
67	F	Right Temporal	Recurrent	Tmz, Rad	NT	Negative	NT	Ⓜ	Ⓜ
54	M	Left Temporal	Recurrent	Tmz, Rad, Vac	Negative	Negative	Negative	Ⓜ	Ⓝ
75	M	Left Temporal	Recurrent	Tmz, Rad	NT	Negative	NT	Ⓜ	Ⓝ
53	M	Left Parietal	Recurrent	Tmz, Rad	NT	Negative	Negative	ⓂⓂ	Ⓝ
57	M	Right Temporal	Recurrent	Tmz, Rad	Negative	Negative	Negative	ⓂⓂⓂⓂⓂⓂ	ⓃⓃⓃⓃⓃⓃ
53	M	Right Temporal	Recurrent	Tmz, Rad	Negative	Negative	Negative	Ⓝ	Ⓝ
44	M	Right Temporal	Recurrent	Tmz, Rad	Negative	Negative	Negative	Ⓝ	Ⓝ

Table S1. We performed RNA-Seq analysis on 75 glioma samples from 27 different glioma patients. These included 39 samples from the CE regions and 36 samples from the NE regions. NS=not sequenced. 9 patients had previous surgery for GBM and had received adjuvant therapy; Tmz-Temozolomide, Rad=Radiation, Bev=Bevacizamab, Vac=Vaccine therapy. Each sample was classified according to the Spearman correlation with the subtyped TCGA profiles from Verhaak et al., (2010).

Cell Type	N	X	LOD	P	P_adj	Attribute ID	Atrribute Name
OPC-like (olig2+)	80	196	1.442883392	5.97E-72	<0.001	GO:0005840	ribosome
OPC-like (olig2+)	111	477	1.113389768	2.96E-70	<0.001	GO:0006412	translation
OPC-like (olig2+)	62	334	0.941689266	9.75E-33	<0.001	GO:0008380	RNA splicing
OPC-like (olig2+)	44	580	0.475581402	3.96E-09	<0.001	GO:0006325	chromatin organization
OPC-like (olig2+)	69	1452	0.259302529	1.89E-05	0.038	GO:0007049	cell cycle
Astrocyte (CD44-)	132	3111	0.228057632	7.62E-07	0.002	GO:0044710	single-organism metabolic process
Astrocyte (CD44-)	113	2585	0.235449773	1.54E-06	0.002	GO:0044281	small molecule metabolic process
Astrocyte (CD44-)	59	1135	0.29931064	5.93E-06	0.018	GO:0005215	transporter activity
Astrocyte (CD44-)	48	880	0.318086198	1.37E-05	0.041	GO:0022857	transmembrane transporter activity
Astrocyte (CD44+)	17	72	1.043095319	1.38E-11	<0.001	GO:0006956	complement activation
Astrocyte (CD44+)	17	92	0.908928106	8.48E-10	<0.001	GO:0072376	protein activation cascade
Astrocyte (CD44+)	72	1284	0.342716095	2.52E-08	<0.001	GO:0006955	immune response
Astrocyte (CD44+)	69	1373	0.2870306	2.89E-06	0.007	GO:0006952	defense response
Astrocyte (CD44+)	95	2164	0.229901351	1.11E-05	0.034	GO:0005576	extracellular region
Microglia	158	1284	0.81400913	5.83E-60	<0.001	GO:0006955	immune response
Microglia	78	510	0.852025365	5.59E-35	<0.001	GO:0006954	inflammatory response
Microglia	59	388	0.833392802	2.30E-26	<0.001	GO:0031012	extracellular matrix
Microglia	87	867	0.642902457	2.87E-25	<0.001	GO:0016477	cell migration
Microglia	67	610	0.673162205	1.26E-21	<0.001	GO:0006935	chemotaxis
Oligodendrocyte	23	90	1.091229572	5.04E-16	<0.001	GO:0008366	axon ensheathment
Oligodendrocyte	22	87	1.084549462	2.80E-15	<0.001	GO:0042552	myelination
Oligodendrocyte	29	254	0.667558471	2.32E-10	<0.001	GO:0030424	axon
Oligodendrocyte	44	566	0.487434233	1.88E-09	<0.001	GO:0008610	lipid biosynthetic process
Oligodendrocyte	53	809	0.409137222	1.57E-08	<0.001	GO:0007010	cytoskeleton organization
Oligodendrocyte	30	435	0.423425548	8.66E-06	0.023	GO:0030695	GTPase regulator activity
Neuron	100	664	0.863391753	1.70E-44	<0.001	GO:0007268	synaptic transmission
Neuron	96	633	0.863435821	6.39E-43	<0.001	GO:0043005	neuron projection
Neuron	41	254	0.851040175	1.47E-19	<0.001	GO:0030424	axon
Neuron	38	307	0.713013509	2.60E-14	<0.001	GO:0030425	dendrite
Neuron	75	1099	0.441690746	1.47E-12	<0.001	GO:0006811	ion transport
Neuron	33	271	0.701802584	2.18E-12	<0.001	GO:0043025	neuronal cell body

Table S2. Gene ontologies for cell type-specific genes in NE regions of GBM. We took the top 500+ genes that showed purity of greater than 0.5 (ranked by FPKM levels distributed to the corresponding cell) and performed gene ontology analysis using FuncAssociate 2.0. Selected ontologies are shown. N= number of cell type-specific genes having the attribute, X= total number of genes having the attribute, LOD=logarithm (base 10) of the odds ratio, P= p-value, P adj= resampling adjusted p-value.

Classifier Genes	Cell Type	OPC-like (OLIG2+)	Astrocyte (CD44-)	Astrocyte (CD44+)	Microglia	Oligodendrocyte	Neuron
PDGFRA	OPC	0.90	0.00	0.10	0.00	0.00	0.00
RLBP1	OPC	0.26	0.45	0.00	0.01	0.00	0.27
LNX1	OPC	0.49	0.00	0.08	0.00	0.00	0.43
CSPG4	OPC	0.91	0.00	0.09	0.00	0.00	0.00
CDO1	OPC	0.00	0.17	0.55	0.00	0.00	0.28
NXPH1	OPC	0.60	0.03	0.10	0.00	0.00	0.27
OLFM2	OPC	0.29	0.26	0.09	0.00	0.00	0.35
CHRNA4	OPC	0.33	0.00	0.00	0.00	0.00	0.67
TACC2	OPC	0.63	0.00	0.00	0.00	0.00	0.37
RNF180	OPC	0.35	0.28	0.24	0.00	0.00	0.14
THSD7B	OPC	0.00	0.00	0.00	0.34	0.00	0.66
PTPRZ1	OPC	0.66	0.00	0.34	0.00	0.00	0.00
CSPG5	OPC	0.68	0.15	0.02	0.00	0.00	0.15
MATN4	OPC	0.87	0.00	0.11	0.00	0.00	0.02
SLITRK1	OPC	0.05	0.00	0.00	0.00	0.40	0.55
SPON1	OPC	0.20	0.51	0.00	0.00	0.00	0.29
MAP3K1	OPC	0.92	0.00	0.08	0.00	0.00	0.00
TMEM100	OPC	0.89	0.00	0.10	0.00	0.00	0.01
PCDH20	OPC	0.00	0.01	0.06	0.19	0.00	0.75
F2R	OPC	0.66	0.00	0.34	0.00	0.00	0.00
CHST11	OPC	0.79	0.00	0.14	0.00	0.00	0.07
OPRL1	OPC	0.00	0.13	0.01	0.02	0.00	0.84
EMID1	OPC	0.11	0.51	0.00	0.17	0.00	0.21
LRRTM3	OPC	0.35	0.10	0.05	0.00	0.00	0.50
ETV5	OPC	0.52	0.00	0.14	0.03	0.00	0.31
COL11A1	OPC	0.25	0.00	0.17	0.34	0.00	0.23
SLC35F1	OPC	0.41	0.00	0.13	0.00	0.00	0.45
DPYSL3	OPC	0.44	0.30	0.26	0.00	0.00	0.00
FSTL5	OPC	0.00	0.14	0.00	0.00	0.03	0.84
GFRA2	OPC	0.00	0.04	0.11	0.00	0.00	0.85
RRM2	OPC	0.74	0.00	0.26	0.00	0.00	0.00
CACNG4	OPC	0.92	0.00	0.08	0.00	0.00	0.00
SLC7A3	OPC	0.00	0.82	0.00	0.18	0.00	0.00
HES5	OPC	0.69	0.18	0.00	0.00	0.00	0.13
NETO1	OPC	0.36	0.00	0.00	0.00	0.00	0.64
KCND3	OPC	0.00	0.20	0.14	0.00	0.00	0.66
KCND2	OPC	0.74	0.00	0.00	0.00	0.00	0.26
DDAH1	OPC	0.08	0.45	0.00	0.00	0.00	0.47
CNTN6	OPC	0.13	0.05	0.00	0.05	0.00	0.77
CALCRL	OPC	0.60	0.28	0.12	0.00	0.00	0.00
LPHN3	OPC	0.43	0.13	0.11	0.00	0.00	0.33
SOX11	OPC	0.91	0.00	0.09	0.00	0.00	0.00
RPRM	OPC	0.53	0.14	0.00	0.00	0.00	0.33
ZBED4	OPC	0.77	0.00	0.11	0.00	0.00	0.12
LRP1	OPC	0.28	0.22	0.17	0.14	0.00	0.20
PRKG2	OPC	0.14	0.00	0.12	0.00	0.00	0.74
PTGFRN	OPC	0.50	0.10	0.25	0.01	0.00	0.14
INHBB	OPC	0.26	0.13	0.44	0.00	0.00	0.17
KLF12	OPC	0.54	0.02	0.07	0.00	0.00	0.36
GRIA3	OPC	0.23	0.22	0.04	0.00	0.00	0.50
PDZRN4	OPC	0.20	0.32	0.00	0.00	0.00	0.48
ZFP36L1	OPC	0.22	0.00	0.39	0.39	0.00	0.00
ENC1	OPC	0.00	0.19	0.01	0.00	0.00	0.80
PRRX1	OPC	0.08	0.09	0.53	0.26	0.00	0.03
SDC3	OPC	0.57	0.20	0.15	0.00	0.00	0.09
NTN1	OPC	0.62	0.04	0.32	0.02	0.00	0.00
CNTN4	OPC	0.00	0.12	0.00	0.00	0.00	0.88
LHFPL3	OPC	0.85	0.00	0.15	0.00	0.00	0.00
ZEB1	OPC	0.80	0.00	0.06	0.00	0.00	0.13
MEGF11	OPC	0.80	0.00	0.07	0.00	0.00	0.12
FNBP1L	OPC	0.31	0.28	0.19	0.00	0.00	0.23

DPP10	OPC	0.00	0.14	0.00	0.00	0.11	0.75
CPNE8	OPC	0.13	0.28	0.00	0.08	0.00	0.51
LRRFIP1	OPC	0.12	0.10	0.29	0.00	0.00	0.50
ADCYAP1R1	OPC	0.09	0.55	0.19	0.00	0.00	0.17
LRRTM4	OPC	0.21	0.00	0.10	0.00	0.00	0.69
TRIB2	OPC	0.91	0.00	0.05	0.00	0.00	0.04
SPSB4	OPC	0.96	0.00	0.04	0.00	0.00	0.00
FUT9	OPC	0.48	0.05	0.00	0.00	0.00	0.47
SPRED2	OPC	0.41	0.04	0.14	0.01	0.00	0.40
CDK6	OPC	0.64	0.21	0.13	0.02	0.00	0.00
FXYD6	OPC	0.42	0.17	0.05	0.00	0.00	0.36
MYT1	OPC	1.00	0.00	0.00	0.00	0.00	0.00
GPRASP1	OPC	0.00	0.08	0.00	0.00	0.00	0.92
GABRG1	OPC	0.00	0.26	0.00	0.00	0.21	0.53
OLFM3	OPC	0.00	0.07	0.00	0.00	0.00	0.93
RUNX1T1	OPC	0.00	0.19	0.03	0.00	0.00	0.78
RESP18	OPC	0.00	0.27	0.07	0.00	0.00	0.66
GFAP	astrocyte	0.00	0.53	0.04	0.31	0.12	0.00
AQP4	astrocyte	0.00	1.00	0.00	0.00	0.00	0.00
PLA2G7	astrocyte	0.00	0.37	0.00	0.48	0.14	0.01
SLC39A12	astrocyte	0.00	0.61	0.00	0.03	0.03	0.32
MLC1	astrocyte	0.17	0.60	0.07	0.00	0.00	0.16
DIO2	astrocyte	0.00	0.28	0.00	0.00	0.00	0.72
SLC14A1	astrocyte	0.00	0.47	0.12	0.00	0.35	0.06
ALDH1L1	astrocyte	0.00	0.85	0.00	0.00	0.00	0.15
ALDOC	astrocyte	0.28	0.27	0.00	0.00	0.00	0.45
TTPA	astrocyte	0.00	0.58	0.02	0.00	0.00	0.40
ACSBG1	astrocyte	0.01	0.64	0.00	0.00	0.10	0.25
CHRDL1	astrocyte	0.35	0.08	0.00	0.00	0.00	0.57
SLC4A4	astrocyte	0.11	0.55	0.03	0.00	0.00	0.30
SLC1A2	astrocyte	0.00	0.22	0.00	0.00	0.00	0.78
SLC25A18	astrocyte	0.00	0.65	0.00	0.00	0.00	0.35
SLC1A3	astrocyte	0.00	0.60	0.11	0.00	0.00	0.29
F3	astrocyte	0.06	0.41	0.16	0.22	0.00	0.15
PPP1R3G	astrocyte	0.00	0.60	0.00	0.00	0.00	0.39
FZD2	astrocyte	0.12	0.41	0.09	0.36	0.00	0.02
MERTK	astrocyte	0.00	0.30	0.00	0.57	0.00	0.13
GJB6	astrocyte	0.00	0.05	0.00	0.00	0.00	0.95
HAPLN1	astrocyte	0.20	0.29	0.24	0.00	0.00	0.28
RFX4	astrocyte	0.20	0.59	0.21	0.00	0.00	0.00
PAPSS2	astrocyte	0.25	0.00	0.02	0.55	0.00	0.19
SLC15A2	astrocyte	0.02	0.68	0.03	0.00	0.00	0.27
PPP1R3C	astrocyte	0.00	0.17	0.00	0.00	0.00	0.83
TLR3	astrocyte	0.00	0.36	0.22	0.40	0.00	0.02
ACOT11	astrocyte	0.00	0.51	0.07	0.02	0.00	0.40
ATP1A2	astrocyte	0.00	0.51	0.00	0.00	0.07	0.42
BMPR1B	astrocyte	0.00	0.68	0.11	0.00	0.00	0.21
PRODH	astrocyte	0.00	0.62	0.00	0.00	0.00	0.38
GLI3	astrocyte	0.08	0.28	0.43	0.00	0.00	0.20
TMEM47	astrocyte	0.00	0.64	0.06	0.00	0.00	0.30
SLC9A3R1	astrocyte	0.11	0.49	0.06	0.00	0.22	0.13
CTH	astrocyte	0.31	0.25	0.15	0.00	0.00	0.29
NTSR2	astrocyte	0.00	0.40	0.00	0.00	0.27	0.34
SLC7A10	astrocyte	0.00	0.14	0.00	0.00	0.00	0.86
VCAM1	astrocyte	0.00	0.00	0.80	0.20	0.00	0.00
FGFR3	astrocyte	0.00	0.56	0.00	0.00	0.01	0.43
CCDC80	astrocyte	0.01	0.42	0.10	0.47	0.00	0.00
ENTPD2	astrocyte	0.00	0.49	0.23	0.00	0.18	0.10
CYBRD1	astrocyte	0.00	0.18	0.15	0.33	0.16	0.18
KCNE1L	astrocyte	1.00	0.00	0.00	0.00	0.00	0.00
TNC	astrocyte	0.28	0.00	0.46	0.26	0.00	0.00
TLCD1	astrocyte	0.71	0.00	0.10	0.00	0.00	0.19
PBXIP1	astrocyte	0.00	0.67	0.06	0.04	0.04	0.18

GRIN2C	astrocyte	0.00	0.40	0.00	0.00	0.10	0.50
ADHFE1	astrocyte	0.19	0.32	0.00	0.00	0.23	0.26
AGT	astrocyte	0.17	0.80	0.00	0.00	0.00	0.03
GLDC	astrocyte	0.60	0.13	0.17	0.00	0.00	0.10
SLC7A2	astrocyte	0.00	0.67	0.01	0.05	0.13	0.14
GJA1	astrocyte	0.00	0.68	0.00	0.08	0.08	0.16
PDK4	astrocyte	0.01	0.01	0.00	0.21	0.73	0.04
EGFR	astrocyte	0.00	0.15	0.85	0.00	0.00	0.00
SOX9	astrocyte	0.30	0.37	0.23	0.00	0.00	0.09
CLDN10	astrocyte	0.00	0.32	0.00	0.00	0.11	0.57
PLCD4	astrocyte	0.42	0.30	0.08	0.00	0.00	0.20
ID4	astrocyte	0.24	0.53	0.22	0.00	0.00	0.01
FMO1	astrocyte	0.10	0.26	0.00	0.36	0.00	0.27
EMP2	astrocyte	0.45	0.00	0.09	0.24	0.00	0.22
LONRF3	astrocyte	0.00	0.01	0.59	0.00	0.00	0.41
HTRA1	astrocyte	0.21	0.31	0.00	0.08	0.31	0.08
MGST1	astrocyte	0.00	0.13	0.55	0.00	0.17	0.15
THRSP	astrocyte	0.17	0.38	0.00	0.36	0.00	0.09
HSD11B1	astrocyte	0.00	0.20	0.00	0.00	0.37	0.43
LGI4	astrocyte	0.00	0.29	0.00	0.00	0.26	0.45
ITGB5	astrocyte	0.00	0.00	0.27	0.54	0.00	0.19
AIFM3	astrocyte	0.00	0.22	0.00	0.00	0.16	0.61
AXL	astrocyte	0.00	0.32	0.07	0.43	0.00	0.18
ADORA2B	astrocyte	0.28	0.20	0.07	0.00	0.00	0.45
CBR3	astrocyte	0.52	0.07	0.11	0.05	0.00	0.25
EPHX2	astrocyte	0.00	0.45	0.14	0.00	0.18	0.24
SLC27A1	astrocyte	0.13	0.23	0.02	0.01	0.62	0.00
SCARA3	astrocyte	0.15	0.35	0.24	0.11	0.00	0.15
NR2E1	astrocyte	0.04	0.43	0.22	0.00	0.00	0.31
LCN2	reactive astrocytes	0.00	0.00	0.00	0.82	0.00	0.18
CLCF1	reactive astrocytes	0.00	0.00	0.87	0.07	0.00	0.05
STEAP4	reactive astrocytes	0.00	0.00	0.00	0.93	0.00	0.07
TGM1	reactive astrocytes	0.00	0.22	0.00	0.35	0.01	0.42
S1PR3	reactive astrocytes	0.21	0.27	0.38	0.14	0.00	0.00
PTX3	reactive astrocytes	0.43	0.00	0.57	0.00	0.00	0.00
S100A10	reactive astrocytes	0.16	0.00	0.45	0.39	0.00	0.00
SPHK1	reactive astrocytes	0.13	0.00	0.05	0.82	0.00	0.00
TIMP1	reactive astrocytes	0.08	0.00	0.21	0.70	0.00	0.00
CD109	reactive astrocytes	0.00	0.17	0.47	0.06	0.12	0.19
PTGS2	reactive astrocytes	0.00	0.00	0.00	0.45	0.10	0.45
SERPING1	reactive astrocytes	0.00	0.00	0.59	0.27	0.00	0.14
EMP1	reactive astrocytes	0.00	0.00	0.31	0.69	0.00	0.00
SLC10A6	reactive astrocytes	0.00	0.00	0.24	0.24	0.41	0.10
TM4SF1	reactive astrocytes	0.74	0.00	0.09	0.17	0.00	0.00
B3GNT5	reactive astrocytes	0.25	0.00	0.71	0.00	0.00	0.03
HSPB1	reactive astrocytes	0.00	0.06	0.59	0.35	0.00	0.00
GBP2	reactive astrocytes	0.00	0.00	0.45	0.55	0.00	0.00
CD14	reactive astrocytes	0.00	0.00	0.13	0.87	0.00	0.00
FBLN5	reactive astrocytes	0.00	0.08	0.05	0.69	0.00	0.18
GALNTL2	reactive astrocytes	0.00	0.41	0.14	0.03	0.42	0.00
FKBP5	reactive astrocytes	0.00	0.00	0.05	0.87	0.04	0.05
IGFBP3	reactive astrocytes	0.56	0.00	0.44	0.00	0.00	0.00
KLF5	reactive astrocytes	0.00	0.03	0.25	0.00	0.00	0.72
CXCL10	reactive astrocytes	0.00	0.00	0.63	0.37	0.00	0.00
CD44	reactive astrocytes	0.00	0.00	1.00	0.00	0.00	0.00
HMOX1	reactive astrocytes	0.52	0.00	0.37	0.12	0.00	0.00
LGALS3	reactive astrocytes	0.07	0.04	0.38	0.29	0.00	0.21
OSMR	reactive astrocytes	0.09	0.01	0.50	0.35	0.00	0.05
PSMB8	reactive astrocytes	0.26	0.21	0.25	0.28	0.00	0.00
GAP43	reactive astrocytes	0.21	0.01	0.15	0.00	0.00	0.63
GDF15	reactive astrocytes	0.55	0.00	0.34	0.11	0.00	0.00
FLNC	reactive astrocytes	0.00	0.50	0.12	0.38	0.00	0.00
ANXA2	reactive astrocytes	0.00	0.00	0.74	0.26	0.00	0.00

SBNO2	reactive astrocytes	0.36	0.05	0.36	0.17	0.00	0.06
TUBB6	reactive astrocytes	0.29	0.00	0.36	0.35	0.00	0.00
SRGN	reactive astrocytes	0.00	0.00	0.06	0.85	0.00	0.09
ASNS	reactive astrocytes	0.31	0.15	0.14	0.00	0.00	0.40
SRXN1	reactive astrocytes	0.00	0.00	0.38	0.00	0.00	0.62
TNFRSF12A	reactive astrocytes	0.24	0.00	0.59	0.17	0.00	0.00
CTGF	reactive astrocytes	0.00	0.00	0.00	0.97	0.00	0.03
GCNT2	reactive astrocytes	0.74	0.00	0.13	0.04	0.00	0.09
AMIGO2	reactive astrocytes	0.00	0.06	0.57	0.00	0.00	0.37
CP	reactive astrocytes	0.00	0.03	0.18	0.57	0.22	0.00
HMGA1	reactive astrocytes	0.59	0.00	0.15	0.00	0.00	0.25
GADD45B	reactive astrocytes	0.00	0.00	0.05	0.77	0.00	0.18
ANXA3	reactive astrocytes	0.00	0.26	0.00	0.00	0.24	0.51
VGF	reactive astrocytes	0.64	0.00	0.07	0.00	0.00	0.29
ASPG	reactive astrocytes	0.00	0.00	0.00	0.00	0.00	1.00
VIM	reactive astrocytes	0.22	0.00	0.73	0.02	0.00	0.03
ODZ2	reactive astrocytes	0.00	0.11	0.01	0.00	0.00	0.88
AKAP12	reactive astrocytes	0.21	0.00	0.17	0.07	0.00	0.55
ICAM1	reactive astrocytes	0.12	0.00	0.15	0.69	0.00	0.04
IER3	reactive astrocytes	0.00	0.00	0.00	0.94	0.04	0.02
IFITM3	reactive astrocytes	0.00	0.35	0.11	0.53	0.00	0.00
SULF2	reactive astrocytes	0.73	0.00	0.12	0.04	0.00	0.12
HSPB6	reactive astrocytes	0.00	0.60	0.14	0.01	0.14	0.10
ENDOU	reactive astrocytes	0.00	0.51	0.00	0.00	0.17	0.33
SLC39A14	reactive astrocytes	0.23	0.00	0.53	0.00	0.00	0.25
TAPBP	reactive astrocytes	0.20	0.23	0.23	0.09	0.00	0.26
CRISPLD2	reactive astrocytes	0.00	0.00	0.00	0.71	0.13	0.16
GSR	reactive astrocytes	0.16	0.06	0.40	0.00	0.00	0.38
CXCL1	reactive astrocytes	0.00	0.00	0.00	0.95	0.05	0.00
GBP3	reactive astrocytes	0.12	0.44	0.44	0.00	0.00	0.00
TSPAN4	reactive astrocytes	0.13	0.00	0.18	0.51	0.00	0.18
OLFM1	reactive astrocytes	0.00	0.00	0.00	0.00	0.00	1.00
CHI3L1	reactive astrocytes	0.03	0.00	0.97	0.00	0.00	0.00
B2M	reactive astrocytes	0.07	0.16	0.19	0.57	0.00	0.01
C4B	reactive astrocytes	0.00	0.59	0.13	0.28	0.00	0.00
A2M	reactive astrocytes	0.21	0.00	0.24	0.45	0.00	0.10
SLC22A4	reactive astrocytes	0.14	0.33	0.21	0.29	0.00	0.03
NEK6	reactive astrocytes	0.31	0.14	0.38	0.00	0.00	0.17
SORBS1	reactive astrocytes	0.00	0.70	0.00	0.00	0.07	0.23
ENTPD1	microglia	0.28	0.12	0.09	0.39	0.00	0.12
MALAT1	microglia	0.20	0.16	0.27	0.20	0.16	0.00
CASP8	microglia	0.00	0.32	0.21	0.34	0.00	0.13
IKZF1	microglia	0.00	0.17	0.00	0.80	0.00	0.03
CD33	microglia	0.00	0.05	0.05	0.82	0.04	0.03
AIM2	microglia	0.00	0.00	0.52	0.37	0.00	0.11
CXorf21	microglia	0.00	0.00	0.00	0.99	0.01	0.00
SSH2	microglia	0.04	0.00	0.05	0.48	0.43	0.00
GAL3ST4	microglia	0.30	0.21	0.17	0.33	0.00	0.00
LAIR1	microglia	0.00	0.06	0.16	0.78	0.00	0.00
GTF2H2	microglia	0.22	0.29	0.19	0.29	0.00	0.00
SLCO2B1	microglia	0.00	0.16	0.00	0.71	0.03	0.10
ARAP3	microglia	0.61	0.10	0.22	0.00	0.00	0.07
IVNS1ABP	microglia	0.37	0.14	0.11	0.22	0.16	0.00
SLC29A3	microglia	0.13	0.21	0.00	0.26	0.25	0.15
CCR5	microglia	0.00	0.00	0.29	0.71	0.00	0.01
C1orf162	microglia	0.21	0.00	0.18	0.60	0.01	0.00
TMEM119	microglia	0.00	0.14	0.00	0.75	0.11	0.01
JUN	microglia	0.28	0.00	0.19	0.34	0.00	0.20
P2RY12	microglia	0.00	0.16	0.00	0.33	0.32	0.19
GNGT2	microglia	0.05	0.21	0.09	0.53	0.00	0.11
CX3CR1	microglia	0.00	0.39	0.00	0.38	0.17	0.06
PTGS1	microglia	0.04	0.28	0.04	0.60	0.00	0.04
DDX43	microglia	0.00	0.77	0.00	0.04	0.20	0.00

LYN	microglia	0.00	0.11	0.07	0.72	0.00	0.10
RNF41	microglia	0.00	0.02	0.07	0.02	0.00	0.89
ZNF839	microglia	0.27	0.13	0.12	0.00	0.29	0.20
RGS2	microglia	0.03	0.00	0.23	0.43	0.00	0.31
C3AR1	microglia	0.00	0.00	0.00	0.96	0.01	0.03
DRAM2	microglia	0.18	0.21	0.09	0.51	0.01	0.00
RGS1	microglia	0.00	0.00	0.16	0.79	0.01	0.04
IL1RL2	microglia	0.00	0.00	0.03	0.02	0.00	0.95
HPS3	microglia	0.11	0.27	0.16	0.46	0.00	0.00
PPP1R10	microglia	0.40	0.04	0.07	0.49	0.00	0.00
SCMH1	microglia	0.29	0.01	0.36	0.00	0.00	0.34
S1PR4	microglia	0.00	0.00	0.00	0.86	0.00	0.14
POU2F2	microglia	0.00	0.37	0.00	0.42	0.00	0.21
FOSB	microglia	0.00	0.00	0.00	0.60	0.00	0.40
SIGLEC8	microglia	0.00	0.29	0.00	0.58	0.13	0.00
ARHGDIB	microglia	0.15	0.05	0.06	0.71	0.00	0.02
EGR2	microglia	0.00	0.00	0.00	0.81	0.13	0.06
CMKLR1	microglia	0.00	0.00	0.00	0.96	0.00	0.04
EPB41L2	microglia	0.00	0.17	0.00	0.37	0.33	0.12
PHC3	microglia	0.38	0.00	0.12	0.35	0.00	0.16
PRPF38B	microglia	0.41	0.31	0.19	0.02	0.07	0.00
CCL4	microglia	0.00	0.00	0.00	0.80	0.20	0.00
FNBP1	microglia	0.00	0.10	0.00	0.00	0.88	0.02
SPAG7	microglia	0.45	0.10	0.00	0.15	0.00	0.30
ZDHHC24	microglia	0.13	0.28	0.06	0.23	0.14	0.17
MID1	microglia	0.31	0.24	0.29	0.00	0.00	0.16
TAGAP	microglia	0.00	0.00	0.06	0.94	0.00	0.00
PRG4	microglia	0.00	0.00	0.00	0.93	0.00	0.07
OSM	microglia	0.00	0.00	0.00	1.00	0.00	0.00
FGD2	microglia	0.00	0.17	0.00	0.66	0.13	0.04
CNOT2	microglia	0.54	0.18	0.24	0.00	0.04	0.00
CEP95	microglia	0.82	0.07	0.11	0.00	0.00	0.00
ACIN1	microglia	0.59	0.37	0.04	0.00	0.00	0.00
FAM166A	microglia	0.33	0.11	0.16	0.02	0.00	0.38
SLAMF8	microglia	0.00	0.00	0.20	0.79	0.00	0.01
C8orf4	microglia	0.18	0.00	0.73	0.00	0.00	0.09
SLC15A3	microglia	0.00	0.25	0.01	0.73	0.00	0.01
KCNRG	microglia	0.18	0.66	0.00	0.00	0.00	0.16
NPLOC4	microglia	0.00	0.00	0.69	0.00	0.29	0.02
TYROBP	microglia	0.00	0.08	0.04	0.88	0.01	0.00
IPCEF1	microglia	0.00	0.00	0.01	0.06	0.06	0.88
C1orf27	microglia	0.33	0.39	0.11	0.00	0.17	0.00
PTPN6	microglia	0.00	0.00	0.00	0.98	0.01	0.01
INPP5D	microglia	0.00	0.25	0.48	0.26	0.00	0.00
UBAP2L	microglia	0.46	0.20	0.18	0.00	0.00	0.16
TOR1AIP1	microglia	0.03	0.74	0.14	0.10	0.00	0.00
PCBP2	microglia	0.51	0.18	0.20	0.06	0.00	0.06
SNORA31	microglia	0.14	0.13	0.00	0.66	0.00	0.07
MOCS2	microglia	0.18	0.36	0.05	0.06	0.00	0.35
LY96	microglia	0.00	0.00	0.17	0.79	0.00	0.04
CNBP	microglia	0.70	0.08	0.21	0.01	0.00	0.00
PIK3CG	microglia	0.00	0.01	0.17	0.68	0.05	0.09
TNF	microglia	0.00	0.00	0.00	0.77	0.23	0.00
MOG	oligodendrocyte	0.00	0.06	0.00	0.05	0.89	0.00
MOBP	oligodendrocyte	0.08	0.00	0.00	0.02	0.90	0.00
ENPP6	oligodendrocyte	0.03	0.09	0.00	0.32	0.56	0.00
CLDN11	oligodendrocyte	0.02	0.00	0.00	0.08	0.90	0.00
MAG	oligodendrocyte	0.02	0.03	0.00	0.01	0.94	0.00
PLEKHH1	oligodendrocyte	0.00	0.06	0.00	0.00	0.94	0.00
FA2H	oligodendrocyte	0.04	0.00	0.00	0.00	0.95	0.00
SGK2	oligodendrocyte	0.00	0.15	0.00	0.07	0.77	0.01
IL23A	oligodendrocyte	0.61	0.00	0.12	0.13	0.00	0.14
MBP	oligodendrocyte	0.03	0.00	0.00	0.06	0.91	0.00

GPR62	oligodendrocyte	0.01	0.06	0.00	0.00	0.92	0.00
TSPAN2	oligodendrocyte	0.12	0.00	0.31	0.29	0.00	0.28
MAL	oligodendrocyte	0.00	0.00	0.00	0.00	1.00	0.00
ERBB3	oligodendrocyte	0.11	0.03	0.00	0.00	0.86	0.00
ADAMTS4	oligodendrocyte	0.00	0.13	0.01	0.11	0.74	0.00
ELOVL7	oligodendrocyte	0.00	0.14	0.00	0.15	0.68	0.03
PPP1R14A	oligodendrocyte	0.02	0.00	0.00	0.08	0.90	0.00
PLP1	oligodendrocyte	0.00	0.03	0.00	0.10	0.87	0.00
PLXNB3	oligodendrocyte	0.27	0.05	0.03	0.00	0.66	0.00
GAL3ST1	oligodendrocyte	0.26	0.03	0.02	0.03	0.66	0.00
BCAS1	oligodendrocyte	0.18	0.00	0.00	0.03	0.78	0.01
SRPK3	oligodendrocyte	0.42	0.10	0.01	0.00	0.46	0.00
CPM	oligodendrocyte	0.30	0.31	0.22	0.10	0.06	0.00
EVI2A	oligodendrocyte	0.02	0.02	0.00	0.07	0.89	0.00
PLA2G4A	oligodendrocyte	0.23	0.09	0.25	0.31	0.00	0.12
GSN	oligodendrocyte	0.00	0.20	0.00	0.37	0.43	0.00
PRKCQ	oligodendrocyte	0.00	0.03	0.04	0.03	0.78	0.12
SEMA3D	oligodendrocyte	0.00	0.25	0.40	0.00	0.06	0.29
GALNT6	oligodendrocyte	0.00	0.22	0.00	0.00	0.78	0.00
PDLIM2	oligodendrocyte	0.26	0.27	0.05	0.22	0.00	0.20
RFFL	oligodendrocyte	0.06	0.20	0.08	0.04	0.62	0.00
GPR17	oligodendrocyte	0.83	0.00	0.17	0.00	0.00	0.00
HAPLN2	oligodendrocyte	0.07	0.10	0.00	0.00	0.83	0.00
GJB1	oligodendrocyte	0.00	0.05	0.00	0.15	0.80	0.00
SFT2D1	oligodendrocyte	0.12	0.12	0.06	0.08	0.63	0.00
LGI3	oligodendrocyte	0.00	0.02	0.00	0.00	0.76	0.21
NKX6-2	oligodendrocyte	0.00	0.18	0.00	0.02	0.80	0.00
SOX10	oligodendrocyte	0.60	0.00	0.00	0.04	0.35	0.00
ADSSL1	oligodendrocyte	0.21	0.08	0.09	0.09	0.53	0.00
SLC45A3	oligodendrocyte	0.00	0.17	0.00	0.08	0.75	0.00
ANLN	oligodendrocyte	0.00	0.14	0.00	0.05	0.80	0.00
TNNI1	oligodendrocyte	0.49	0.23	0.00	0.26	0.00	0.02
PLLP	oligodendrocyte	0.11	0.00	0.00	0.00	0.88	0.02
CYP27A1	oligodendrocyte	0.00	0.22	0.07	0.13	0.56	0.01
KNDC1	oligodendrocyte	0.00	0.19	0.00	0.00	0.00	0.81
DOCK10	oligodendrocyte	0.11	0.17	0.03	0.03	0.66	0.00
CHN2	oligodendrocyte	0.00	0.20	0.01	0.03	0.61	0.14
ST18	oligodendrocyte	0.00	0.16	0.00	0.06	0.79	0.00
MYO1D	oligodendrocyte	0.00	0.05	0.00	0.17	0.76	0.02
CPOX	oligodendrocyte	0.00	0.18	0.02	0.01	0.78	0.00
PPAP2C	oligodendrocyte	0.06	0.10	0.00	0.02	0.83	0.00
UNC5B	oligodendrocyte	0.00	0.25	0.02	0.15	0.57	0.00
DDC	oligodendrocyte	0.00	0.00	0.13	0.39	0.30	0.18
TRIM59	oligodendrocyte	0.18	0.09	0.04	0.00	0.69	0.00
PHLDB1	oligodendrocyte	0.10	0.05	0.01	0.00	0.84	0.00
BFSP2	oligodendrocyte	0.00	0.00	0.88	0.00	0.00	0.12
BMP4	oligodendrocyte	0.10	0.00	0.11	0.36	0.00	0.42
MATN1	oligodendrocyte	0.45	0.00	0.07	0.04	0.31	0.13
TMEFF2	oligodendrocyte	0.19	0.00	0.00	0.02	0.55	0.24
RNF122	oligodendrocyte	0.78	0.00	0.22	0.00	0.00	0.00
ICK	oligodendrocyte	0.49	0.00	0.05	0.03	0.40	0.04
ARPC1B	oligodendrocyte	0.00	0.00	0.20	0.75	0.00	0.05
NFASC	oligodendrocyte	0.00	0.26	0.04	0.00	0.59	0.11
CNTN1	oligodendrocyte	0.13	0.36	0.00	0.00	0.03	0.48
CLDN14	oligodendrocyte	0.05	0.00	0.00	0.32	0.62	0.00
SLC12A2	oligodendrocyte	0.00	0.27	0.00	0.00	0.70	0.04
LIMS2	oligodendrocyte	0.64	0.00	0.08	0.07	0.00	0.21
TMEM182	oligodendrocyte	0.29	0.13	0.58	0.00	0.00	0.00
DCT	oligodendrocyte	0.23	0.35	0.27	0.00	0.00	0.16
HHIP	oligodendrocyte	0.00	0.01	0.00	0.00	0.94	0.05
KCNA1	oligodendrocyte	0.00	0.00	0.00	0.00	0.00	1.00
TMEM63A	oligodendrocyte	0.00	0.19	0.00	0.00	0.81	0.00
TMEM141	oligodendrocyte	0.21	0.16	0.03	0.10	0.23	0.27

JOSD2	oligodendrocyte	0.14	0.11	0.05	0.11	0.53	0.07
TMEM163	oligodendrocyte	0.40	0.00	0.20	0.00	0.00	0.40
NEUROD6	neuron	0.00	0.00	0.00	0.00	0.00	1.00
GLRA2	neuron	0.00	0.24	0.02	0.00	0.00	0.73
PRDM8	neuron	0.00	0.09	0.00	0.00	0.01	0.89
SLA	neuron	0.00	0.00	0.05	0.89	0.00	0.05
CRH	neuron	0.01	0.00	0.00	0.00	0.00	0.99
GABRG2	neuron	0.00	0.10	0.00	0.00	0.00	0.90
HTR2C	neuron	0.00	0.01	0.00	0.13	0.00	0.86
HS3ST2	neuron	0.00	0.22	0.00	0.10	0.01	0.67
MAL2	neuron	0.00	0.05	0.00	0.00	0.00	0.95
GABRA5	neuron	0.00	0.06	0.00	0.04	0.05	0.85
NTS	neuron	0.36	0.00	0.64	0.00	0.00	0.00
GABRA1	neuron	0.00	0.04	0.00	0.00	0.00	0.96
SATB2	neuron	0.29	0.17	0.09	0.00	0.00	0.45
GPR88	neuron	0.00	0.34	0.04	0.02	0.00	0.60
SYT1	neuron	0.00	0.11	0.00	0.00	0.00	0.89
GDA	neuron	0.00	0.10	0.00	0.00	0.04	0.87
MYT1L	neuron	0.00	0.05	0.00	0.00	0.00	0.95
SLC17A6	neuron	0.00	0.05	0.00	0.00	0.00	0.95
NPAS4	neuron	0.00	0.21	0.00	0.00	0.03	0.76
CALB1	neuron	0.00	0.13	0.00	0.00	0.00	0.87
SLC12A5	neuron	0.00	0.09	0.00	0.00	0.00	0.91
EPHA7	neuron	0.00	0.27	0.04	0.00	0.00	0.69
VIP	neuron	0.00	0.10	0.00	0.00	0.00	0.90
MEF2C	neuron	0.00	0.12	0.02	0.00	0.00	0.86
SSTR2	neuron	0.00	0.26	0.00	0.01	0.00	0.73
PCSK2	neuron	0.00	0.00	0.00	0.00	0.00	1.00
SNAP25	neuron	0.00	0.05	0.00	0.00	0.00	0.95
SCG2	neuron	0.30	0.00	0.14	0.00	0.00	0.56
PGM2L1	neuron	0.00	0.05	0.16	0.00	0.00	0.79
PLCXD3	neuron	0.00	0.16	0.07	0.01	0.00	0.76
DLX1	neuron	0.00	0.49	0.00	0.19	0.00	0.32
VSNL1	neuron	0.00	0.04	0.00	0.00	0.00	0.96
SYT4	neuron	0.00	0.09	0.00	0.00	0.00	0.90
NRG3	neuron	0.00	0.30	0.00	0.00	0.01	0.69
ICAM5	neuron	0.00	0.26	0.00	0.00	0.00	0.74
KCNF1	neuron	0.30	0.11	0.06	0.00	0.00	0.53
CCK	neuron	0.00	0.13	0.00	0.00	0.00	0.87
TMEM130	neuron	0.00	0.12	0.00	0.00	0.00	0.88
CAMK4	neuron	0.00	0.02	0.00	0.00	0.00	0.98
ASPH	neuron	0.00	0.30	0.17	0.00	0.00	0.53
SLC6A7	neuron	0.00	0.05	0.00	0.00	0.00	0.95
ICA1L	neuron	0.00	0.34	0.10	0.00	0.00	0.56
MYO5B	neuron	0.19	0.02	0.34	0.00	0.00	0.45
NELL1	neuron	0.00	0.03	0.01	0.05	0.00	0.91
NEFM	neuron	0.00	0.00	0.00	0.00	0.00	1.00
NEFL	neuron	0.00	0.00	0.00	0.00	0.00	1.00
TTR	neuron	0.00	0.00	0.00	1.00	0.00	0.00
CDH8	neuron	0.00	0.04	0.00	0.01	0.08	0.87
SV2B	neuron	0.00	0.05	0.00	0.00	0.04	0.91
TRHDE	neuron	0.00	0.00	0.00	0.04	0.00	0.95
CAMK2B	neuron	0.00	0.14	0.00	0.00	0.00	0.86
RGS4	neuron	0.00	0.00	0.01	0.00	0.00	0.99
LPL	neuron	0.75	0.00	0.25	0.00	0.00	0.00
CACNA1B	neuron	0.00	0.14	0.00	0.00	0.00	0.86
KCNC2	neuron	0.00	0.05	0.00	0.00	0.00	0.95
TTC9	neuron	0.10	0.03	0.10	0.00	0.00	0.77
L1CAM	neuron	0.00	0.02	0.00	0.00	0.00	0.98
CLSTN2	neuron	0.00	0.22	0.09	0.03	0.00	0.65
NAPB	neuron	0.00	0.10	0.00	0.00	0.00	0.90
CYB561	neuron	0.00	0.19	0.10	0.04	0.00	0.68
CXADR	neuron	0.28	0.00	0.18	0.00	0.51	0.03

HPCA	neuron	0.00	0.04	0.01	0.00	0.00	0.96
CNKSR2	neuron	0.00	0.17	0.03	0.00	0.00	0.80
UNC13A	neuron	0.00	0.08	0.00	0.00	0.00	0.92
C1QTNF4	neuron	0.00	0.24	0.00	0.00	0.00	0.76
CBLN1	neuron	0.11	0.00	0.00	0.00	0.00	0.89
RHOV	neuron	0.00	0.04	0.01	0.00	0.00	0.95
EFNA3	neuron	0.13	0.14	0.00	0.00	0.00	0.73
HS6ST2	neuron	0.35	0.02	0.01	0.00	0.00	0.62
GRP	neuron	0.48	0.00	0.00	0.00	0.00	0.52
STX1A	neuron	0.01	0.06	0.00	0.06	0.00	0.87
KCNQ2	neuron	0.58	0.00	0.00	0.00	0.00	0.42
BCL11A	neuron	0.07	0.00	0.00	0.00	0.03	0.90
ELAVL2	neuron	0.00	0.05	0.00	0.00	0.00	0.95
NPTX1	neuron	0.00	0.08	0.00	0.00	0.00	0.92
ATP1A3	neuron	0.00	0.07	0.00	0.00	0.00	0.93
CALN1	neuron	0.00	0.13	0.00	0.00	0.06	0.81
ENO2	neuron	0.00	0.00	0.05	0.00	0.00	0.95
KCNV1	neuron	0.00	0.00	0.00	0.00	0.00	1.00
SERTAD4	neuron	0.00	0.26	0.02	0.00	0.04	0.68
SST	neuron	0.03	0.00	0.00	0.00	0.28	0.69

Table S3. We list cell type-specific genes, as reported in Cahoy *et al*., (2008), Zamanian, *et al.* (2012) and Chiu*, et al.* (2013), along with their fractional expression level in each of 6 cell types, as predicted by deconvolution of the RNA-seq data from NE glioma and nonneoplastic brain (NB) samples.

Classifier Genes	Subtype	OPC-like (OLIG2+)	Astrocyte (CD44-)	Astrocyte (CD44+)	Microglia	Oligodendrocyte	Neuron
ABAT	PN	0.21	0.23	0.08	0.00	0.00	0.49
ACTR1A	PN	0.15	0.22	0.00	0.00	0.21	0.42
ALCAM	PN	0.24	0.09	0.02	0.00	0.66	0.00
AMOTL2	PN	0.29	0.13	0.00	0.00	0.57	0.00
ARHGEF9	PN	0.00	0.09	0.02	0.00	0.00	0.88
ASCL1	PN	0.89	0.00	0.02	0.00	0.00	0.08
ATAD5	PN	0.77	0.01	0.15	0.00	0.00	0.08
ATP1A3	PN	0.00	0.07	0.00	0.00	0.00	0.93
BAI3	PN	0.05	0.21	0.00	0.00	0.00	0.74
BCAN	PN	0.62	0.28	0.09	0.00	0.00	0.00
BCL7A	PN	0.46	0.08	0.00	0.00	0.00	0.46
BCOR	PN	0.97	0.00	0.00	0.00	0.00	0.03
BEX1	PN	0.19	0.10	0.00	0.00	0.00	0.71
C1orf106	PN	0.89	0.00	0.11	0.00	0.00	0.00
C1orf61	PN	0.59	0.37	0.00	0.00	0.00	0.04
C1QL1	PN	0.98	0.00	0.02	0.00	0.00	0.00
CA10	PN	0.40	0.00	0.04	0.00	0.00	0.56
CASK	PN	0.59	0.08	0.22	0.01	0.00	0.09
CBX1	PN	0.66	0.11	0.10	0.00	0.00	0.13
CDC25A	PN	0.86	0.00	0.14	0.00	0.00	0.00
CDC7	PN	0.61	0.00	0.19	0.00	0.00	0.20
CDK5R1	PN	0.00	0.07	0.00	0.00	0.00	0.93
CDKN1B	PN	0.01	0.05	0.00	0.00	0.91	0.02
CHD7	PN	0.97	0.01	0.01	0.00	0.00	0.00
CKB	PN	0.11	0.39	0.00	0.00	0.00	0.50
CLASP2	PN	0.00	0.16	0.00	0.00	0.58	0.26
CLGN	PN	0.30	0.15	0.04	0.00	0.00	0.51
CNTN1	PN	0.13	0.36	0.00	0.00	0.03	0.48
CRB1	PN	0.37	0.43	0.05	0.00	0.00	0.15
CRMP1	PN	0.47	0.00	0.16	0.00	0.00	0.37
CSNK1E	PN	0.68	0.15	0.03	0.00	0.00	0.15
CSPG5	PN	0.68	0.15	0.02	0.00	0.00	0.15
CXXC4	PN	0.50	0.13	0.06	0.00	0.00	0.31
DBN1	PN	0.48	0.09	0.15	0.00	0.00	0.29
DCX	PN	0.88	0.00	0.07	0.00	0.00	0.05
DGKI	PN	0.37	0.00	0.10	0.00	0.00	0.53
DLL3	PN	0.98	0.02	0.00	0.00	0.00	0.00
DNM3	PN	0.00	0.08	0.00	0.00	0.50	0.42
DPF1	PN	0.37	0.02	0.08	0.00	0.00	0.53
DPP6	PN	0.23	0.18	0.15	0.00	0.00	0.45
DPYSL4	PN	0.58	0.14	0.00	0.00	0.00	0.28
DUSP26	PN	0.12	0.00	0.00	0.00	0.00	0.88
E2F3	PN	0.49	0.00	0.26	0.00	0.00	0.26
EPB41	PN	0.24	0.16	0.18	0.31	0.00	0.12
EPHB1	PN	0.63	0.13	0.03	0.00	0.00	0.21
ERBB3	PN	0.11	0.03	0.00	0.00	0.86	0.00
FAM110B	PN	0.47	0.00	0.16	0.00	0.00	0.37
FAM125B	PN	0.05	0.20	0.00	0.15	0.60	0.00
FBXO21	PN	0.35	0.12	0.07	0.00	0.00	0.46
FGF9	PN	0.00	0.19	0.00	0.00	0.00	0.81
FHOD3	PN	0.26	0.02	0.14	0.00	0.00	0.59
FLRT1	PN	0.39	0.01	0.03	0.00	0.23	0.34
FXYD6	PN	0.42	0.17	0.05	0.00	0.00	0.36
GABRA3	PN	0.26	0.00	0.04	0.00	0.00	0.70
GADD45G	PN	0.58	0.26	0.00	0.00	0.00	0.16
GNG4	PN	0.61	0.00	0.08	0.00	0.00	0.30
GPM6A	PN	0.17	0.24	0.07	0.00	0.00	0.53
GPR17	PN	0.83	0.00	0.17	0.00	0.00	0.00
GRIA2	PN	0.17	0.20	0.01	0.00	0.00	0.62
GRID2	PN	0.85	0.00	0.09	0.00	0.00	0.07
GSK3B	PN	0.37	0.08	0.12	0.00	0.00	0.44

GSTA4	PN	0.45	0.11	0.06	0.00	0.00	0.37
HDAC2	PN	0.66	0.00	0.15	0.06	0.00	0.13
HMGB3	PN	0.82	0.00	0.09	0.00	0.00	0.09
HN1	PN	0.72	0.00	0.15	0.00	0.00	0.13
HOXD3	PN	0.95	0.00	0.05	0.00	0.00	0.00
HRASLS	PN	0.75	0.00	0.18	0.00	0.00	0.07
ICK	PN	0.49	0.00	0.05	0.03	0.40	0.04
IL1RAPL1	PN	0.00	0.00	0.00	0.00	0.88	0.12
KIF21B	PN	0.41	0.16	0.03	0.00	0.00	0.41
KLRC3	PN	1.00	0.00	0.00	0.00	0.00	0.00
KLRC4	PN	1.00	0.00	0.00	0.00	0.00	0.00
KLRK1	PN	1.00	0.00	0.00	0.00	0.00	0.00
LPHN3	PN	0.43	0.13	0.11	0.00	0.00	0.33
LRP6	PN	0.53	0.19	0.11	0.00	0.17	0.00
LRRTM4	PN	0.21	0.00	0.10	0.00	0.00	0.69
MAP2	PN	0.21	0.14	0.02	0.00	0.00	0.63
MAPT	PN	0.00	0.20	0.00	0.00	0.16	0.64
MARCKS	PN	0.68	0.06	0.18	0.00	0.00	0.08
MARCKSL1	PN	0.61	0.01	0.02	0.01	0.36	0.00
MAST1	PN	0.00	0.16	0.00	0.00	0.00	0.84
MATR3	PN	0.25	0.12	0.06	0.00	0.00	0.57
MCM10	PN	0.96	0.00	0.04	0.00	0.00	0.00
MLLT11	PN	0.19	0.09	0.04	0.00	0.00	0.68
MMP15	PN	0.72	0.00	0.18	0.00	0.00	0.10
MMP16	PN	0.95	0.00	0.02	0.00	0.00	0.03
MPPED2	PN	0.65	0.00	0.01	0.00	0.00	0.35
MTSS1	PN	0.57	0.00	0.00	0.24	0.19	0.00
MYB	PN	0.99	0.00	0.00	0.00	0.00	0.01
MYO10	PN	0.40	0.51	0.00	0.00	0.09	0.00
MYT1	PN	1.00	0.00	0.00	0.00	0.00	0.00
NCALD	PN	0.14	0.00	0.07	0.00	0.00	0.79
NCAM1	PN	0.00	0.40	0.07	0.00	0.42	0.11
NKX2-2	PN	0.78	0.00	0.00	0.20	0.01	0.00
NLGN3	PN	0.57	0.23	0.04	0.02	0.00	0.15
NOL4	PN	0.18	0.11	0.06	0.00	0.00	0.64
NR0B1	PN	0.92	0.00	0.08	0.00	0.00	0.00
NRXN1	PN	0.00	0.22	0.00	0.00	0.00	0.78
NRXN2	PN	0.00	0.00	0.00	0.00	0.00	1.00
OLIG2	PN	1.00	0.00	0.00	0.00	0.00	0.00
P2RX7	PN	0.25	0.12	0.02	0.00	0.61	0.00
PAFAH1B3	PN	0.57	0.14	0.12	0.00	0.00	0.17
PAK3	PN	0.00	0.05	0.01	0.00	0.00	0.94
PAK7	PN	0.09	0.07	0.00	0.00	0.00	0.85
PCDH11X	PN	0.00	0.11	0.00	0.00	0.00	0.89
PCDH11Y	PN	0.00	0.19	0.00	0.00	0.00	0.81
PDE10A	PN	0.54	0.00	0.00	0.00	0.00	0.46
PELI1	PN	0.54	0.03	0.00	0.43	0.00	0.00
PFN2	PN	0.25	0.18	0.04	0.00	0.00	0.54
PHF16	PN	0.61	0.24	0.01	0.11	0.04	0.00
PLCB4	PN	0.03	0.00	0.07	0.00	0.00	0.90
PODXL2	PN	0.52	0.05	0.03	0.00	0.00	0.40
PPM1D	PN	0.71	0.00	0.10	0.15	0.04	0.00
PPM1E	PN	0.14	0.05	0.12	0.00	0.00	0.69
PURG	PN	0.40	0.31	0.01	0.00	0.00	0.28
RAB33A	PN	0.41	0.00	0.00	0.00	0.40	0.20
RAD21	PN	0.67	0.13	0.08	0.00	0.12	0.00
RALGPS1	PN	0.00	0.23	0.00	0.00	0.42	0.35
RALGPS2	PN	0.38	0.00	0.16	0.11	0.00	0.35
RAP2A	PN	0.48	0.00	0.10	0.00	0.00	0.41
RBPJ	PN	0.26	0.01	0.06	0.00	0.67	0.00
REEP1	PN	0.16	0.00	0.13	0.00	0.00	0.70
RUFY3	PN	0.00	0.25	0.41	0.00	0.13	0.21
SATB1	PN	0.32	0.03	0.00	0.00	0.00	0.64

SCG3	PN	0.28	0.00	0.00	0.00	0.00	0.71
SCN3A	PN	0.43	0.00	0.08	0.00	0.00	0.49
SEC61A2	PN	0.00	0.11	0.00	0.00	0.37	0.52
SEZ6L	PN	0.32	0.19	0.00	0.00	0.00	0.48
SLC1A1	PN	0.48	0.00	0.09	0.00	0.00	0.43
SLCO5A1	PN	0.98	0.00	0.02	0.00	0.00	0.00
SORCS3	PN	0.34	0.01	0.04	0.00	0.00	0.62
SOX10	PN	0.60	0.00	0.00	0.04	0.35	0.00
SOX11	PN	0.91	0.00	0.09	0.00	0.00	0.00
SOX2	PN	0.57	0.09	0.31	0.00	0.00	0.03
SOX4	PN	0.93	0.00	0.07	0.00	0.00	0.00
SPTBN2	PN	0.00	0.04	0.00	0.00	0.00	0.96
SRGAP3	PN	0.00	0.13	0.05	0.00	0.00	0.82
STMN1	PN	0.16	0.06	0.00	0.00	0.41	0.36
STMN4	PN	0.14	0.00	0.00	0.00	0.62	0.24
TAF5	PN	0.79	0.00	0.00	0.00	0.00	0.21
TMCC1	PN	0.50	0.08	0.23	0.08	0.00	0.10
TMEFF1	PN	0.06	0.06	0.00	0.00	0.80	0.08
TMEM35	PN	0.05	0.10	0.01	0.00	0.00	0.84
TOP2B	PN	0.61	0.18	0.04	0.00	0.00	0.17
TOPBP1	PN	0.54	0.11	0.19	0.00	0.00	0.16
TOX3	PN	0.68	0.00	0.19	0.00	0.00	0.14
TSPAN3	PN	0.28	0.45	0.11	0.00	0.00	0.16
TTYH1	PN	0.44	0.35	0.00	0.00	0.06	0.15
VAX2	PN	0.97	0.00	0.03	0.00	0.00	0.00
VEZF1	PN	0.51	0.11	0.08	0.07	0.23	0.00
WASF1	PN	0.18	0.02	0.02	0.00	0.00	0.78
YPEL1	PN	0.31	0.04	0.00	0.00	0.00	0.66
ZEB2	PN	0.11	0.07	0.02	0.05	0.75	0.00
ZNF184	PN	0.24	0.14	0.11	0.00	0.00	0.51
ZNF248	PN	0.09	0.00	0.00	0.00	0.01	0.89
ZNF286A	PN	0.79	0.11	0.10	0.00	0.00	0.00
ZNF510	PN	0.34	0.16	0.13	0.00	0.00	0.37
ZNF643	PN	0.47	0.02	0.09	0.00	0.00	0.41
ZNF711	PN	0.55	0.10	0.08	0.00	0.00	0.26
ZNF804A	PN	0.11	0.12	0.08	0.00	0.00	0.69
ABCD2	CL	0.00	0.37	0.02	0.00	0.00	0.62
ACSBG1	CL	0.01	0.64	0.00	0.00	0.10	0.25
ACSL3	CL	0.21	0.30	0.11	0.00	0.00	0.37
ADAM19	CL	0.37	0.32	0.15	0.00	0.00	0.16
AKT2	CL	0.67	0.20	0.07	0.00	0.00	0.06
ANXA5	CL	0.24	0.17	0.31	0.27	0.00	0.01
APBA3	CL	0.58	0.22	0.13	0.02	0.06	0.00
ARNTL	CL	0.00	0.32	0.17	0.00	0.00	0.51
B3GALT1	CL	0.03	0.32	0.07	0.00	0.00	0.58
BLM	CL	0.67	0.10	0.23	0.00	0.00	0.01
BTBD2	CL	0.30	0.15	0.05	0.00	0.00	0.50
CALM1	CL	0.00	0.08	0.03	0.00	0.00	0.89
CAMK2B	CL	0.00	0.14	0.00	0.00	0.00	0.86
CC2D1A	CL	0.32	0.25	0.06	0.00	0.00	0.36
CD151	CL	0.26	0.19	0.41	0.07	0.00	0.06
CD3EAP	CL	0.34	0.21	0.13	0.00	0.00	0.32
CD97	CL	0.23	0.17	0.12	0.32	0.17	0.00
CDH2	CL	0.30	0.18	0.29	0.00	0.00	0.22
CDH4	CL	0.00	0.24	0.23	0.00	0.02	0.52
CDH6	CL	0.34	0.20	0.23	0.00	0.00	0.22
CDK6	CL	0.64	0.21	0.13	0.02	0.00	0.00
CLIP2	CL	0.57	0.16	0.16	0.00	0.00	0.11
CREB5	CL	0.35	0.15	0.11	0.00	0.39	0.00
DAG1	CL	0.32	0.32	0.21	0.00	0.00	0.15
DENND2A	CL	0.44	0.28	0.25	0.00	0.00	0.02
DLC1	CL	0.00	0.43	0.00	0.07	0.44	0.05
DMWD	CL	0.29	0.28	0.14	0.00	0.00	0.29

DOCK6	CL	0.58	0.13	0.09	0.10	0.00	0.10
EGFR	CL	0.00	0.15	0.85	0.00	0.00	0.00
ELOVL2	CL	0.14	0.57	0.15	0.00	0.00	0.14
EPHB4	CL	0.26	0.38	0.36	0.00	0.00	0.00
ERCC2	CL	0.40	0.21	0.12	0.00	0.00	0.27
EXTL3	CL	0.31	0.17	0.21	0.00	0.00	0.31
EYA2	CL	0.16	0.41	0.27	0.00	0.00	0.16
FGFR3	CL	0.00	0.56	0.00	0.00	0.01	0.43
FZD3	CL	0.24	0.27	0.14	0.00	0.00	0.35
FZD7	CL	0.00	0.16	0.77	0.00	0.00	0.07
GALNT4	CL	0.15	0.41	0.27	0.11	0.06	0.00
GAS1	CL	1.00	0.00	0.00	0.00	0.00	0.00
GJA1	CL	0.00	0.68	0.00	0.08	0.08	0.16
GLG1	CL	0.19	0.49	0.18	0.00	0.14	0.00
GLI2	CL	0.18	0.09	0.64	0.00	0.00	0.09
GNAS	CL	0.29	0.12	0.07	0.00	0.00	0.52
GNG7	CL	0.15	0.12	0.00	0.10	0.40	0.23
GPR56	CL	0.41	0.45	0.12	0.00	0.00	0.02
GRIK1	CL	0.00	0.38	0.11	0.00	0.00	0.50
GRIK5	CL	0.22	0.28	0.16	0.00	0.00	0.35
GSTK1	CL	0.17	0.21	0.48	0.03	0.00	0.11
HMG20B	CL	0.45	0.31	0.15	0.08	0.00	0.00
HS3ST3B1	CL	0.00	0.15	0.81	0.00	0.00	0.04
HSPBP1	CL	0.35	0.20	0.08	0.01	0.00	0.36
ILK	CL	0.13	0.06	0.34	0.34	0.00	0.13
IRF3	CL	0.29	0.30	0.10	0.21	0.00	0.10
IRS2	CL	0.09	0.06	0.46	0.00	0.00	0.39
ITGA7	CL	0.17	0.44	0.33	0.00	0.00	0.06
ITGB8	CL	0.25	0.51	0.23	0.00	0.02	0.00
JAG1	CL	0.61	0.00	0.34	0.00	0.00	0.06
JUND	CL	0.35	0.00	0.04	0.00	0.55	0.05
KCNF1	CL	0.30	0.11	0.06	0.00	0.00	0.53
KEAP1	CL	0.44	0.29	0.14	0.01	0.08	0.04
KIAA0355	CL	0.30	0.17	0.16	0.06	0.31	0.00
KLHDC8A	CL	0.44	0.36	0.21	0.00	0.00	0.00
KLHL25	CL	0.54	0.34	0.08	0.00	0.00	0.05
KLHL4	CL	0.19	0.27	0.13	0.03	0.37	0.00
LAMB2	CL	0.28	0.43	0.28	0.01	0.00	0.00
LFNG	CL	0.36	0.41	0.23	0.00	0.00	0.00
LHFP	CL	0.16	0.27	0.17	0.17	0.00	0.23
LMO2	CL	0.37	0.29	0.17	0.10	0.00	0.07
LRFN3	CL	0.35	0.16	0.13	0.00	0.00	0.37
LRP10	CL	0.12	0.40	0.09	0.39	0.00	0.00
LRP5	CL	0.75	0.18	0.05	0.00	0.00	0.02
MAB21L1	CL	0.25	0.35	0.24	0.00	0.00	0.16
MCC	CL	0.22	0.40	0.19	0.00	0.00	0.19
MEGF8	CL	0.23	0.28	0.08	0.00	0.00	0.41
MEIS1	CL	0.25	0.25	0.04	0.00	0.46	0.00
MEOX2	CL	0.17	0.51	0.32	0.00	0.00	0.00
MLC1	CL	0.17	0.60	0.07	0.00	0.00	0.16
MYO5C	CL	0.00	0.51	0.20	0.12	0.00	0.16
NDP	CL	0.02	0.65	0.01	0.00	0.19	0.12
NES	CL	0.53	0.10	0.37	0.00	0.00	0.00
NPAS3	CL	0.41	0.41	0.08	0.00	0.00	0.10
NPEPL1	CL	0.33	0.42	0.23	0.02	0.00	0.00
NR2E1	CL	0.04	0.43	0.22	0.00	0.00	0.31
NR2F6	CL	0.34	0.13	0.16	0.00	0.00	0.37
OSBPL3	CL	0.02	0.28	0.55	0.00	0.00	0.15
PCSK5	CL	0.00	0.30	0.17	0.34	0.00	0.19
PDGFA	CL	0.35	0.00	0.11	0.01	0.53	0.00
PEPD	CL	0.19	0.31	0.08	0.24	0.15	0.03
PIPOX	CL	0.07	0.73	0.20	0.00	0.00	0.00
PLA2G5	CL	0.00	0.36	0.48	0.00	0.00	0.16

PMP22	CL	0.01	0.10	0.05	0.19	0.64	0.00
POFUT1	CL	0.31	0.23	0.26	0.10	0.00	0.11
POMT2	CL	0.83	0.05	0.08	0.01	0.03	0.00
PRKD2	CL	0.47	0.17	0.23	0.04	0.00	0.09
PRPF31	CL	0.46	0.24	0.15	0.01	0.00	0.15
PTPN14	CL	0.00	0.40	0.12	0.00	0.00	0.47
PTPRA	CL	0.11	0.32	0.06	0.04	0.07	0.41
QTRT1	CL	0.40	0.40	0.10	0.00	0.00	0.10
RASGRP1	CL	0.07	0.25	0.05	0.00	0.00	0.64
RBCK1	CL	0.38	0.27	0.13	0.16	0.01	0.06
RBM42	CL	0.62	0.20	0.12	0.04	0.00	0.01
RFX2	CL	0.00	0.49	0.39	0.00	0.00	0.12
RFXANK	CL	0.43	0.31	0.14	0.07	0.00	0.05
RGS12	CL	0.28	0.33	0.09	0.00	0.00	0.31
RIN1	CL	0.00	0.31	0.12	0.12	0.00	0.45
SARS2	CL	0.37	0.23	0.15	0.02	0.00	0.23
SCAMP4	CL	0.28	0.27	0.18	0.09	0.19	0.00
SEMA6A	CL	0.26	0.22	0.04	0.00	0.47	0.00
SEMA6D	CL	0.21	0.24	0.05	0.00	0.26	0.23
SHOX2	CL	0.03	0.21	0.76	0.00	0.00	0.00
SIPA1L1	CL	0.00	0.30	0.28	0.00	0.00	0.42
SLC12A4	CL	0.36	0.39	0.23	0.00	0.00	0.02
SLC2A10	CL	0.10	0.30	0.46	0.07	0.00	0.06
SLC4A4	CL	0.11	0.55	0.03	0.00	0.00	0.30
SLC6A11	CL	0.16	0.38	0.01	0.00	0.00	0.45
SLC6A9	CL	0.23	0.27	0.13	0.00	0.37	0.00
SMO	CL	0.40	0.23	0.37	0.00	0.00	0.00
SNTA1	CL	0.00	0.51	0.00	0.00	0.13	0.35
SOCS2	CL	0.17	0.16	0.67	0.00	0.00	0.00
SOX9	CL	0.30	0.37	0.23	0.00	0.00	0.09
SPRY2	CL	0.56	0.01	0.12	0.11	0.00	0.21
SSH3	CL	0.00	0.21	0.03	0.08	0.69	0.00
TBX2	CL	0.48	0.17	0.24	0.00	0.00	0.11
TEAD3	CL	0.32	0.28	0.25	0.07	0.00	0.08
TGFB3	CL	0.22	0.23	0.06	0.00	0.50	0.00
TGIF2	CL	0.37	0.39	0.24	0.00	0.00	0.00
TLE2	CL	0.59	0.04	0.10	0.00	0.00	0.27
TMED1	CL	0.33	0.27	0.09	0.22	0.00	0.08
TMEM147	CL	0.40	0.26	0.09	0.12	0.00	0.13
TMEM161A	CL	0.43	0.23	0.11	0.07	0.00	0.16
TRIB2	CL	0.91	0.00	0.05	0.00	0.00	0.04
TRIP6	CL	0.11	0.43	0.38	0.07	0.01	0.00
VAV3	CL	0.18	0.27	0.24	0.00	0.00	0.31
VPS16	CL	0.45	0.26	0.08	0.08	0.00	0.13
WSCD1	CL	0.90	0.00	0.10	0.00	0.00	0.00
ZFHX4	CL	0.17	0.40	0.13	0.00	0.30	0.00
ZNF134	CL	0.40	0.19	0.19	0.00	0.00	0.23
ZNF20	CL	0.62	0.10	0.18	0.00	0.00	0.10
ZNF211	CL	0.47	0.28	0.12	0.00	0.00	0.14
ZNF227	CL	0.60	0.17	0.12	0.02	0.00	0.10
ZNF235	CL	0.47	0.30	0.11	0.00	0.00	0.12
ZNF264	CL	0.73	0.00	0.23	0.00	0.04	0.00
ZNF304	CL	0.31	0.21	0.19	0.00	0.00	0.30
ZNF419	CL	0.37	0.34	0.13	0.00	0.00	0.16
ZNF446	CL	0.48	0.27	0.10	0.00	0.04	0.12
ZNF45	CL	0.46	0.25	0.13	0.07	0.00	0.08
ZNF606	CL	0.59	0.20	0.17	0.00	0.00	0.04
ZNF671	CL	0.37	0.23	0.11	0.03	0.00	0.25
ZNF8	CL	0.52	0.02	0.19	0.00	0.00	0.27
ACPP	MS	0.24	0.15	0.40	0.07	0.10	0.04
ACSL1	MS	0.00	0.00	0.00	0.42	0.58	0.00
ADAM12	MS	0.08	0.00	0.43	0.50	0.00	0.00
AIM1	MS	0.00	0.00	0.44	0.36	0.00	0.21

ALDH3B1	MS	0.00	0.15	0.26	0.51	0.08	0.00
ALOX5	MS	0.00	0.08	0.03	0.80	0.08	0.00
AMPD3	MS	0.00	0.26	0.03	0.16	0.55	0.00
ANXA1	MS	0.00	0.00	0.98	0.00	0.00	0.02
ANXA2	MS	0.00	0.00	0.74	0.26	0.00	0.00
ANXA4	MS	0.00	0.18	0.28	0.14	0.31	0.09
ARHGAP29	MS	0.00	0.00	0.27	0.28	0.00	0.45
ARPC1B	MS	0.00	0.00	0.20	0.75	0.00	0.05
ARSJ	MS	0.26	0.28	0.38	0.00	0.00	0.08
ASL	MS	0.14	0.21	0.21	0.23	0.00	0.22
BATF	MS	0.00	0.00	0.00	0.99	0.00	0.01
BDKRB2	MS	0.00	0.00	0.57	0.00	0.17	0.25
BLVRB	MS	0.00	0.17	0.15	0.41	0.00	0.27
BNC2	MS	0.00	0.00	0.21	0.73	0.00	0.06
C1orf38	MS	0.00	0.00	0.00	0.62	0.32	0.06
C1orf54	MS	0.29	0.39	0.11	0.18	0.00	0.03
C5AR1	MS	0.00	0.00	0.28	0.70	0.00	0.03
CASP1	MS	0.06	0.20	0.30	0.44	0.00	0.00
CASP4	MS	0.00	0.00	0.28	0.68	0.00	0.04
CASP5	MS	0.00	0.02	0.38	0.59	0.00	0.01
CASP8	MS	0.00	0.32	0.21	0.34	0.00	0.13
CAST	MS	0.00	0.15	0.29	0.37	0.19	0.01
CCDC109B	MS	0.26	0.13	0.45	0.14	0.00	0.03
CCR5	MS	0.00	0.00	0.29	0.71	0.00	0.01
CD14	MS	0.00	0.00	0.13	0.87	0.00	0.00
CD2AP	MS	0.00	0.00	0.65	0.18	0.00	0.17
CD4	MS	0.00	0.02	0.04	0.85	0.00	0.08
CDCP1	MS	0.19	0.00	0.25	0.55	0.00	0.01
CEBPB	MS	0.02	0.00	0.15	0.66	0.00	0.17
CHI3L1	MS	0.03	0.00	0.97	0.00	0.00	0.00
CLCF1	MS	0.00	0.00	0.87	0.07	0.00	0.05
CLEC2B	MS	0.14	0.00	0.15	0.63	0.00	0.07
CNN2	MS	0.00	0.00	0.00	1.00	0.00	0.00
COL1A1	MS	0.00	0.00	0.00	1.00	0.00	0.00
COL1A2	MS	0.00	0.00	0.00	1.00	0.00	0.00
COL5A1	MS	0.00	0.00	0.00	0.98	0.00	0.02
COL8A2	MS	0.00	0.00	0.06	0.94	0.00	0.00
COPZ2	MS	0.00	0.09	0.20	0.65	0.01	0.05
CSTA	MS	0.00	0.00	0.45	0.55	0.00	0.00
CTSB	MS	0.00	0.04	0.16	0.59	0.00	0.21
CTSC	MS	0.00	0.00	0.04	0.96	0.00	0.00
CTSZ	MS	0.00	0.00	0.08	0.80	0.00	0.12
CYBRD1	MS	0.00	0.18	0.15	0.33	0.16	0.18
DAB2	MS	0.00	0.00	0.04	0.91	0.00	0.05
DCBLD2	MS	0.16	0.00	0.53	0.10	0.00	0.22
DOK3	MS	0.01	0.03	0.30	0.54	0.00	0.13
DSC2	MS	0.00	0.12	0.15	0.56	0.00	0.17
DSE	MS	0.00	0.00	0.36	0.48	0.00	0.16
EFEMP2	MS	0.18	0.19	0.22	0.25	0.00	0.16
EHD2	MS	0.27	0.08	0.31	0.17	0.00	0.17
ELF4	MS	0.11	0.00	0.10	0.79	0.00	0.00
EMP3	MS	0.10	0.15	0.46	0.29	0.00	0.00
ENG	MS	0.36	0.00	0.08	0.42	0.00	0.14
FCGR2A	MS	0.00	0.00	0.17	0.83	0.00	0.00
FCGR2B	MS	0.00	0.00	0.56	0.44	0.00	0.00
FES	MS	0.00	0.13	0.12	0.54	0.00	0.20
FHL2	MS	0.00	0.00	0.00	0.40	0.00	0.60
FHOD1	MS	0.08	0.00	0.17	0.66	0.00	0.09
FMNL1	MS	0.00	0.00	0.04	0.40	0.00	0.56
FNDC3B	MS	0.32	0.01	0.28	0.28	0.00	0.11
FOLR2	MS	0.00	0.00	0.00	0.96	0.00	0.04
FURIN	MS	0.00	0.06	0.17	0.31	0.00	0.46
FXYD5	MS	0.13	0.00	0.01	0.87	0.00	0.00

GCNT1	MS	0.00	0.00	0.60	0.00	0.00	0.40
GLT25D1	MS	0.28	0.09	0.18	0.36	0.00	0.08
GNA15	MS	0.00	0.00	0.04	0.69	0.00	0.27
GRN	MS	0.14	0.16	0.19	0.46	0.00	0.05
HEXA	MS	0.17	0.14	0.19	0.46	0.00	0.04
HEXB	MS	0.13	0.00	0.20	0.48	0.00	0.19
HFE	MS	0.00	0.10	0.33	0.30	0.08	0.18
HK3	MS	0.00	0.00	0.10	0.81	0.00	0.09
ICAM3	MS	0.12	0.10	0.03	0.53	0.00	0.23
IFI30	MS	0.00	0.00	0.31	0.69	0.00	0.00
IGFBP6	MS	0.44	0.00	0.10	0.17	0.00	0.29
IL15RA	MS	0.08	0.00	0.34	0.43	0.00	0.15
IL1R1	MS	0.00	0.00	0.00	0.91	0.00	0.09
IL4R	MS	0.00	0.00	0.00	0.96	0.00	0.04
IQGAP1	MS	0.00	0.17	0.22	0.22	0.39	0.00
ITGA4	MS	0.35	0.00	0.51	0.03	0.00	0.10
ITGA5	MS	0.37	0.00	0.18	0.45	0.00	0.00
ITGAM	MS	0.00	0.10	0.04	0.64	0.13	0.09
ITGB2	MS	0.00	0.11	0.12	0.74	0.00	0.03
KYNU	MS	0.00	0.00	0.27	0.70	0.00	0.02
LAIR1	MS	0.00	0.06	0.16	0.78	0.00	0.00
LAMB1	MS	0.00	0.00	0.16	0.66	0.00	0.18
LAPTM5	MS	0.00	0.11	0.08	0.81	0.00	0.00
LCP1	MS	0.00	0.00	0.01	0.94	0.00	0.05
LCP2	MS	0.00	0.00	0.18	0.68	0.00	0.13
LGALS1	MS	0.13	0.12	0.07	0.52	0.00	0.15
LGALS3	MS	0.07	0.04	0.38	0.29	0.00	0.21
LHFPL2	MS	0.13	0.07	0.06	0.67	0.00	0.06
LILRB2	MS	0.00	0.00	0.15	0.77	0.00	0.08
LILRB3	MS	0.00	0.00	0.14	0.86	0.00	0.00
LOX	MS	0.19	0.00	0.53	0.28	0.00	0.00
LRRFIP1	MS	0.12	0.10	0.29	0.00	0.00	0.50
LTBP1	MS	0.00	0.03	0.37	0.56	0.00	0.04
LTBP2	MS	0.00	0.00	0.00	1.00	0.00	0.00
LY75	MS	0.00	0.00	0.04	0.93	0.00	0.03
LY96	MS	0.00	0.00	0.17	0.79	0.00	0.04
MAFB	MS	0.00	0.00	0.09	0.79	0.00	0.12
MAN1A1	MS	0.00	0.14	0.07	0.41	0.00	0.38
MAN2A1	MS	0.00	0.25	0.07	0.00	0.68	0.00
MAN2B1	MS	0.31	0.07	0.15	0.47	0.00	0.00
MAPK13	MS	0.00	0.02	0.05	0.34	0.00	0.59
MFSD1	MS	0.00	0.22	0.14	0.57	0.00	0.07
MGAT1	MS	0.22	0.02	0.14	0.51	0.00	0.11
MGST2	MS	0.00	0.26	0.05	0.60	0.00	0.08
MRC2	MS	0.17	0.00	0.59	0.24	0.00	0.00
MS4A4A	MS	0.00	0.00	0.06	0.94	0.00	0.00
MSR1	MS	0.02	0.00	0.38	0.60	0.00	0.00
MVP	MS	0.10	0.10	0.16	0.30	0.34	0.00
MYH9	MS	0.00	0.12	0.09	0.79	0.00	0.00
MYO1F	MS	0.02	0.10	0.06	0.81	0.00	0.00
NCF2	MS	0.01	0.00	0.00	0.91	0.03	0.05
NCF4	MS	0.00	0.00	0.00	0.98	0.00	0.02
NOD2	MS	0.58	0.00	0.26	0.16	0.00	0.00
NPC2	MS	0.05	0.12	0.15	0.65	0.02	0.00
NRP1	MS	0.24	0.00	0.38	0.12	0.00	0.26
P4HA2	MS	0.00	0.00	0.24	0.43	0.00	0.33
PDPN	MS	0.13	0.16	0.72	0.00	0.00	0.00
PHF11	MS	0.00	0.28	0.06	0.19	0.46	0.01
PLAU	MS	0.00	0.00	0.15	0.85	0.00	0.00
PLAUR	MS	0.00	0.00	0.26	0.74	0.00	0.00
PLK3	MS	0.00	0.00	0.31	0.62	0.00	0.07
PLS3	MS	0.00	0.09	0.21	0.11	0.53	0.06
POLD4	MS	0.13	0.13	0.05	0.63	0.05	0.00

PROCR	MS	0.09	0.00	0.11	0.80	0.00	0.00
PTGER4	MS	0.00	0.08	0.16	0.77	0.00	0.00
PTPN22	MS	0.00	0.00	0.21	0.67	0.00	0.12
PTPN6	MS	0.00	0.00	0.00	0.98	0.01	0.01
PTPRC	MS	0.00	0.00	0.13	0.74	0.00	0.14
PTRF	MS	0.00	0.00	0.30	0.49	0.20	0.00
PYGL	MS	0.37	0.00	0.48	0.15	0.00	0.00
RAB11FIP1	MS	0.00	0.19	0.00	0.41	0.00	0.40
RAB27A	MS	0.00	0.00	0.24	0.67	0.00	0.09
RAB32	MS	0.05	0.25	0.18	0.51	0.00	0.02
RABGAP1L	MS	0.00	0.16	0.00	0.18	0.05	0.61
RAC2	MS	0.00	0.00	0.04	0.88	0.00	0.08
RBKS	MS	0.00	0.21	0.08	0.17	0.19	0.35
RBMS1	MS	0.18	0.00	0.20	0.43	0.00	0.20
RELB	MS	0.27	0.00	0.19	0.41	0.00	0.13
RHOG	MS	0.07	0.13	0.04	0.19	0.58	0.01
RRAS	MS	0.00	0.05	0.26	0.70	0.00	0.00
RUNX2	MS	0.00	0.00	0.00	0.81	0.02	0.17
S100A11	MS	0.04	0.00	0.12	0.85	0.00	0.00
S100A13	MS	0.00	0.45	0.12	0.06	0.19	0.18
S100A4	MS	0.00	0.00	0.14	0.86	0.00	0.00
SAT1	MS	0.17	0.00	0.12	0.57	0.00	0.14
SCPEP1	MS	0.00	0.14	0.07	0.58	0.00	0.22
SEC24D	MS	0.21	0.00	0.18	0.41	0.00	0.20
SERPINA1	MS	0.05	0.00	0.29	0.66	0.00	0.00
SERPINE1	MS	0.00	0.00	0.22	0.78	0.00	0.00
SFT2D2	MS	0.00	0.00	0.37	0.55	0.08	0.00
SH2B3	MS	0.17	0.00	0.10	0.57	0.00	0.15
SHC1	MS	0.12	0.00	0.29	0.44	0.00	0.15
SIGLEC7	MS	0.00	0.00	0.27	0.73	0.00	0.00
SIGLEC9	MS	0.00	0.00	0.11	0.89	0.00	0.00
SLAMF8	MS	0.00	0.00	0.20	0.79	0.00	0.01
SLC10A3	MS	0.12	0.00	0.32	0.39	0.01	0.16
SLC11A1	MS	0.00	0.00	0.06	0.94	0.00	0.00
SLC16A3	MS	0.23	0.00	0.31	0.46	0.00	0.00
SP100	MS	0.13	0.02	0.20	0.60	0.00	0.05
SQRDL	MS	0.00	0.00	0.17	0.76	0.00	0.07
SRPX2	MS	0.00	0.00	0.43	0.57	0.00	0.00
ST14	MS	0.18	0.00	0.37	0.45	0.00	0.00
STAB1	MS	0.00	0.01	0.14	0.86	0.00	0.00
STAT6	MS	0.00	0.14	0.00	0.50	0.00	0.36
STXBP2	MS	0.07	0.15	0.00	0.77	0.00	0.02
SWAP70	MS	0.00	0.00	0.26	0.62	0.08	0.04
SYNGR2	MS	0.07	0.09	0.01	0.27	0.55	0.00
SYPL1	MS	0.05	0.24	0.24	0.00	0.46	0.00
TCIRG1	MS	0.00	0.00	0.12	0.86	0.00	0.02
TEC	MS	0.00	0.00	0.05	0.61	0.00	0.33
TES	MS	0.23	0.00	0.19	0.49	0.00	0.10
TGFBI	MS	0.00	0.00	0.34	0.66	0.00	0.00
TGFBR2	MS	0.00	0.00	0.01	0.89	0.00	0.09
TGOLN2	MS	0.00	0.17	0.18	0.17	0.24	0.24
THBD	MS	0.00	0.00	0.30	0.62	0.00	0.08
THBS1	MS	0.00	0.00	0.09	0.87	0.00	0.04
TIMP1	MS	0.08	0.00	0.21	0.70	0.00	0.00
TLR2	MS	0.00	0.12	0.06	0.81	0.00	0.01
TLR4	MS	0.00	0.36	0.15	0.22	0.15	0.13
TMBIM1	MS	0.00	0.21	0.14	0.23	0.40	0.03
TNFAIP3	MS	0.10	0.00	0.07	0.77	0.00	0.06
TNFAIP8	MS	0.00	0.00	0.35	0.53	0.00	0.11
TNFRSF11A	MS	0.00	0.00	0.25	0.24	0.00	0.50
TNFRSF1A	MS	0.22	0.12	0.36	0.24	0.00	0.06
TNFRSF1B	MS	0.05	0.00	0.09	0.78	0.00	0.07
TRADD	MS	0.15	0.14	0.12	0.18	0.36	0.05

TRIM22	MS	0.01	0.40	0.27	0.29	0.00	0.03
TRIM38	MS	0.00	0.08	0.00	0.92	0.00	0.00
TRPM2	MS	0.00	0.13	0.00	0.30	0.00	0.57
UAP1	MS	0.27	0.06	0.20	0.22	0.00	0.25
UCP2	MS	0.26	0.09	0.06	0.59	0.00	0.00
VAMP5	MS	0.13	0.18	0.10	0.51	0.00	0.07
VDR	MS	0.00	0.00	0.23	0.71	0.00	0.06
WIPF1	MS	0.08	0.05	0.09	0.25	0.53	0.00
WWTR1	MS	0.22	0.15	0.22	0.40	0.00	0.00
YAP1	MS	0.00	0.44	0.39	0.00	0.00	0.17
ZNF217	MS	0.03	0.00	0.48	0.49	0.00	0.00
ACSL4	NL	0.00	0.00	0.06	0.11	0.24	0.60
ACYP2	NL	0.01	0.31	0.00	0.00	0.45	0.23
ADD3	NL	0.00	0.46	0.00	0.00	0.39	0.15
AGTPBP1	NL	0.00	0.00	0.01	0.00	0.75	0.24
AGXT2L1	NL	0.06	0.39	0.00	0.00	0.19	0.35
AKR7A3	NL	0.01	0.51	0.13	0.00	0.14	0.21
ANKRD46	NL	0.00	0.15	0.04	0.00	0.00	0.80
ANKS1B	NL	0.00	0.15	0.00	0.00	0.56	0.29
ANXA3	NL	0.00	0.26	0.00	0.00	0.24	0.51
ANXA7	NL	0.00	0.32	0.00	0.06	0.24	0.38
ARRB1	NL	0.00	0.25	0.00	0.09	0.19	0.47
ATP5F1	NL	0.31	0.25	0.11	0.06	0.00	0.26
ATP5L	NL	0.35	0.12	0.07	0.17	0.00	0.29
ATRNL1	NL	0.00	0.03	0.04	0.00	0.00	0.92
BASP1	NL	0.12	0.01	0.00	0.00	0.00	0.86
BCAS1	NL	0.18	0.00	0.00	0.03	0.78	0.01
BEST1	NL	0.00	0.25	0.00	0.18	0.57	0.00
CA4	NL	0.00	0.13	0.00	0.00	0.00	0.87
CALM2	NL	0.00	0.08	0.00	0.00	0.52	0.40
CAMK2G	NL	0.00	0.26	0.00	0.00	0.00	0.74
CASQ1	NL	0.14	0.17	0.04	0.00	0.00	0.65
CCDC121	NL	0.00	0.35	0.20	0.00	0.45	0.00
CCK	NL	0.00	0.13	0.00	0.00	0.00	0.87
CDC42	NL	0.33	0.00	0.18	0.26	0.04	0.19
CDR1	NL	0.02	0.00	0.00	0.00	0.56	0.43
CHN1	NL	0.00	0.08	0.00	0.00	0.00	0.92
CLCA4	NL	0.00	0.23	0.00	0.00	0.77	0.00
COX5B	NL	0.16	0.24	0.00	0.02	0.08	0.50
CPNE6	NL	0.00	0.32	0.00	0.00	0.08	0.60
CRBN	NL	0.00	0.21	0.04	0.00	0.19	0.56
CRYL1	NL	0.00	0.35	0.01	0.10	0.45	0.09
CRYM	NL	0.00	0.05	0.00	0.00	0.00	0.94
CRYZL1	NL	0.00	0.19	0.06	0.00	0.28	0.47
CUTC	NL	0.08	0.22	0.00	0.01	0.69	0.00
DHRS9	NL	0.00	0.11	0.00	0.36	0.50	0.03
DYNC1I1	NL	0.00	0.19	0.00	0.00	0.07	0.74
EDIL3	NL	0.00	0.10	0.00	0.00	0.83	0.06
ENPP4	NL	0.00	0.18	0.00	0.00	0.72	0.11
EPB41L3	NL	0.00	0.05	0.00	0.00	0.55	0.41
EVI2A	NL	0.02	0.02	0.00	0.07	0.89	0.00
FAM49B	NL	0.16	0.00	0.07	0.33	0.07	0.37
FBXO3	NL	0.00	0.35	0.11	0.00	0.00	0.55
FEZF2	NL	0.00	0.20	0.00	0.00	0.17	0.62
FHIT	NL	0.13	0.00	0.00	0.22	0.65	0.00
FUT9	NL	0.48	0.05	0.00	0.00	0.00	0.47
FXYD1	NL	0.00	0.33	0.00	0.00	0.25	0.41
GABARAPL2	NL	0.10	0.32	0.00	0.00	0.40	0.19
GABRB2	NL	0.00	0.00	0.00	0.00	0.00	1.00
GNAI1	NL	0.13	0.00	0.01	0.00	0.70	0.16
GPR22	NL	0.00	0.11	0.00	0.00	0.00	0.89
GRM1	NL	0.00	0.24	0.00	0.00	0.00	0.76
GRM3	NL	0.00	0.04	0.00	0.01	0.66	0.29

GUK1	NL	0.10	0.23	0.00	0.00	0.21	0.46
HPCA	NL	0.00	0.04	0.01	0.00	0.00	0.96
HPCAL4	NL	0.00	0.20	0.00	0.00	0.00	0.80
HPRT1	NL	0.00	0.02	0.04	0.00	0.00	0.94
IMPA1	NL	0.00	0.32	0.34	0.00	0.04	0.30
KCNJ3	NL	0.00	0.08	0.00	0.00	0.00	0.92
KCNK1	NL	0.00	0.30	0.00	0.00	0.08	0.62
KIAA1598	NL	0.00	0.01	0.00	0.00	0.98	0.01
LYRM1	NL	0.13	0.13	0.14	0.00	0.16	0.43
MAGEH1	NL	0.39	0.02	0.00	0.07	0.18	0.33
MAT2B	NL	0.00	0.00	0.10	0.15	0.00	0.75
MBP	NL	0.03	0.00	0.00	0.06	0.91	0.00
MDH1	NL	0.00	0.09	0.00	0.00	0.00	0.91
MMD	NL	0.22	0.00	0.01	0.23	0.01	0.52
MORF4L2	NL	0.19	0.00	0.13	0.03	0.00	0.65
MRPL49	NL	0.24	0.26	0.20	0.01	0.00	0.28
MSRB2	NL	0.00	0.16	0.01	0.17	0.32	0.34
MYBPC1	NL	0.00	0.61	0.00	0.04	0.19	0.16
NANOS1	NL	0.69	0.00	0.07	0.00	0.00	0.23
NDRG2	NL	0.00	0.24	0.00	0.00	0.46	0.30
NDUFS3	NL	0.34	0.20	0.05	0.09	0.00	0.33
NSL1	NL	0.44	0.21	0.04	0.09	0.21	0.00
NTSR2	NL	0.00	0.40	0.00	0.00	0.27	0.34
PARP8	NL	0.21	0.10	0.11	0.27	0.00	0.31
PDE6D	NL	0.58	0.09	0.03	0.11	0.05	0.16
PEX11B	NL	0.29	0.17	0.01	0.00	0.00	0.52
PEX19	NL	0.00	0.41	0.00	0.16	0.10	0.32
PGBD5	NL	0.00	0.13	0.00	0.00	0.06	0.81
POPDC3	NL	0.00	0.00	0.00	0.12	0.48	0.40
PPA1	NL	0.00	0.01	0.00	0.00	0.46	0.52
PPFIA2	NL	0.00	0.00	0.00	0.00	0.51	0.49
PPP1R1A	NL	0.00	0.35	0.00	0.00	0.25	0.40
PPP2R5A	NL	0.24	0.37	0.00	0.00	0.29	0.10
PRPSAP2	NL	0.43	0.19	0.07	0.07	0.24	0.00
REPS2	NL	0.00	0.10	0.00	0.00	0.27	0.63
RND1	NL	0.10	0.11	0.00	0.00	0.00	0.78
ROGDI	NL	0.00	0.03	0.00	0.02	0.75	0.20
SAR1A	NL	0.60	0.00	0.00	0.35	0.00	0.04
SCHIP1	NL	0.22	0.24	0.00	0.00	0.36	0.18
SEPP1	NL	0.00	0.24	0.00	0.21	0.55	0.00
SEPW1	NL	0.18	0.10	0.00	0.06	0.39	0.27
SERPINI1	NL	0.00	0.08	0.00	0.04	0.24	0.64
SGK3	NL	0.00	0.16	0.12	0.00	0.73	0.00
SH3GL2	NL	0.00	0.10	0.00	0.00	0.00	0.90
SH3GL3	NL	0.00	0.04	0.00	0.00	0.78	0.18
SIRT5	NL	0.00	0.29	0.02	0.00	0.00	0.69
SLC16A7	NL	0.14	0.00	0.00	0.45	0.00	0.40
SLC30A10	NL	0.00	0.24	0.00	0.00	0.00	0.76
SLC31A2	NL	0.00	0.07	0.00	0.14	0.79	0.00
SLCO1A2	NL	0.00	0.08	0.00	0.00	0.87	0.06
SNCG	NL	0.00	0.23	0.00	0.00	0.00	0.77
SNX11	NL	0.16	0.17	0.00	0.49	0.06	0.11
SPAST	NL	0.48	0.09	0.00	0.00	0.41	0.02
TCEAL1	NL	0.01	0.26	0.06	0.00	0.00	0.66
TCEAL2	NL	0.17	0.05	0.00	0.00	0.00	0.78
THTPA	NL	0.34	0.26	0.00	0.05	0.03	0.33
TMEM144	NL	0.00	0.18	0.00	0.02	0.80	0.00
TPM3	NL	0.05	0.00	0.19	0.32	0.00	0.44
TSNAX	NL	0.00	0.33	0.03	0.19	0.00	0.45
TTC1	NL	0.18	0.06	0.03	0.17	0.15	0.41
TTPA	NL	0.00	0.58	0.02	0.00	0.00	0.40
UGT8	NL	0.09	0.06	0.00	0.10	0.75	0.00
UROS	NL	0.00	0.13	0.00	0.04	0.16	0.67

USP33	NL	0.00	0.06	0.18	0.00	0.00	0.76
VIP	NL	0.00	0.10	0.00	0.00	0.00	0.90
VSX1	NL	0.00	0.00	0.00	0.06	0.51	0.42
YPEL5	NL	0.00	0.10	0.05	0.12	0.00	0.74
ZNF323	NL	0.00	0.46	0.01	0.00	0.00	0.54

Table S4. We list the Verhaak Classifier Genes along with their fractional expression level in each of 6 cell types, as predicted by deconvolution of the RNA-seq data from NE glioma and nonneoplastic brain (NB) samples.

HISTO ID#	MRI REGION	NECROSIS	MVP	MITS
1	CE	1	0	1
2	CE	1	0	1
3	CE	0	0	0
4	CE	1	0	0
5	CE	0	0	1
6	CE	1	0	0
7	CE	1	1	1
8	CE	1	0	0
9	CE	1	0	0
10	CE	1	1	1
11	CE	0	0	1
12	CE	0	0	1
13	CE	0	1	1
14	CE	0	0	0
15	CE	0	1	1
16	CE	0	0	0
17	CE	1	0	0
18	CE	0	0	0
19	CE	0	0	0
20	CE	0	0	0
21	CE	0	0	0
22	CE	1	0	0
23	CE	1	0	0
24	CE	1	0	0
25	CE	1	0	1
26	CE	1	1	1
27	CE	0	1	1
28	CE	1	0	1
29	CE	1	1	1
30	CE	1	0	1
31	CE	0	1	1
32	CE	0	0	0
33	CE	0	1	1
34	CE	0	1	1
35	CE	0	1	1
36	CE	0	0	1
37	CE	1	0	1
38	CE	1	0	1
39	CE	0	0	1
40	CE	1	0	0
41	CE	0	0	0
42	CE	0	1	1
43	CE	0	1	1
44	CE	0	0	1
45	CE	1	0	1
46	CE	1	1	1
47	CE	1	1	1
48	CE	1	0	0
49	CE	0	0	0
50	CE	1	1	1
51	CE	1	1	1
52	CE	0	1	1
53	CE	1	0	0
54	CE	1	1	1

55	CE	1	1	1
56	CE	1	0	0
57	CE	1	1	1
58	CE	1	0	0
59	CE	0	1	1
60	CE	0	1	1
61	CE	1	1	1
62	CE	0	1	1
63	CE	1	1	1
64	CE	1	0	0
65	CE	0	0	0
66	CE	0	1	1
67	CE	1	1	1
68	CE	1	0	0
69	CE	1	0	1
70	CE	1	0	1
71	CE	1	0	0
72	CE	0	1	1
73	CE	1	0	0
74	CE	1	0	0
75	CE	1	0	0
76	CE	1	1	1
77	CE	1	1	1
78	CE	0	0	0
79	CE	0	0	0
80	CE	1	0	1
81	CE	1	1	1
82	CE	0	1	1
83	CE	1	1	1
84	CE	1	1	1
85	CE	1	1	1
86	CE	1	0	0
87	CE	1	1	1
88	CE	0	1	1
89	CE	1	0	0
90	CE	1	1	1
91	CE	0	0	0
92	CE	1	1	1
93	CE	1	1	1
94	CE	1	1	1
95	CE	1	1	1
96	CE	1	1	1
97	CE	0	0	1
98	CE	0	1	1
99	CE	1	1	1
100	CE	1	0	0
101	CE	1	0	0
102	CE	1	1	1
103	CE	1	1	1
104	CE	1	1	1
105	CE	1	1	1
106	NE	0	0	0
107	NE	0	0	0
108	NE	0	0	0
109	NE	0	0	0
110	NE	0	0	0

111	NE	0	0	0
112	NE	0	0	1
113	NE	0	0	0
114	NE	0	0	0
115	NE	0	0	1
116	NE	0	0	0
117	NE	0	0	0
118	NE	0	0	0
119	NE	0	1	1
120	NE	0	0	0
121	NE	0	0	0
122	NE	0	0	0
123	NE	1	1	1
124	NE	0	0	0
125	NE	0	0	0
126	NE	0	0	0
127	NE	0	0	0
128	NE	0	0	0
129	NE	0	0	0
130	NE	0	0	0
131	NE	0	0	0
132	NE	0	0	1
133	NE	0	0	0
134	NE	0	0	0
135	NE	0	0	1
136	NE	0	0	0
137	NE	1	0	0
138	NE	0	0	1
139	NE	0	0	0
140	NE	0	0	0
141	NE	1	1	1
142	NE	0	0	0
143	NE	0	0	0
144	NE	0	0	0
145	NE	0	0	1
146	NE	0	1	1
147	NE	0	1	1
148	NE	0	0	0
149	NE	0	0	0
150	NE	0	0	1
151	NE	0	1	1
152	NE	0	0	0
153	NE	0	0	0
154	NE	0	0	1
155	NE	0	0	0
156	NE	0	0	1
157	NE	0	0	0
158	NE	0	0	0
159	NE	1	1	1
160	NE	1	0	0
161	NE	1	0	1
162	NE	0	0	0
163	NE	0	0	0
164	NE	0	0	0
165	NE	0	0	1
166	NE	0	1	1

167	NE	0	0	0
168	NE	0	0	1
169	NE	0	1	1
170	NE	0	0	0
171	NE	0	0	1
172	NE	0	0	0
173	NE	0	0	0
174	NE	0	0	0
175	NE	1	0	0
176	NE	0	0	1
177	NE	0	0	0
178	NE	1	0	0
179	NE	0	0	0
180	NE	0	0	0
181	NE	0	0	1
182	NE	0	0	1
183	NE	0	0	0
184	NE	0	0	0
185	NE	0	0	0
186	NE	0	0	0
187	NE	0	0	0
188	NE	0	0	1
189	NE	0	0	0
190	NE	0	0	0
191	NE	0	0	0

Table S5. The histological features of GBM tabulated for each glioma specimen in this study.