A cell-type-resolved directory of human brain reveals microRNAs and tRNA fragments associated with aging and Alzheimer's disease

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Abstract

Background: MicroRNAs (miRs) and transfer RNA fragments (tRFs) regulate diverse brain processes, from neurogenesis to neurological disease. While both these small RNA classes have been implicated in cell-type-specific regulation, most studies leaned on bulk measurements, due to technical limitations in detecting small RNAs using single-cell RNA sequencing. Consequently, the cell-type specificity of brain miRs and tRFs remains poorly characterized, limiting functional interpretation.

Results: To generate a comprehensive, cell-type-resolved atlas of miRs and tRFs from live human brain tissues, we isolated neurons, astrocytes, microglia, and oligodendrocytes from neurosurgery-derived fresh human brain samples and profiled their small RNAs by RNA-sequencing. This revealed pronounced cell-type-specific differences in miR and tRF levels, identified novel small RNA cell-type markers, and provided insight into the genetic regulation of miR cell-type specificity. Notably, neurons exhibited elevated levels of 5′ tRNA halves compared to glial cells, including enriched fragments derived from glycine, leucine and lysine tRNAs. Finally, our resource enabled assignment of cell-type origins to miRs associated with healthy brain aging and tRFs linked to Alzheimer's disease.

Conclusions: Highlighting the importance of cellular context for data interpretation, both human brain miRs and tRFs exhibit pronounced cell-type-specific differences associated with brain aging and neurodegenerative diseases. Combined with an accompanying statistical tool for miR cell-type enrichment analysis, this work provides a publicly available resource for resolving the cell-type origins of small RNAs in the human brain.

Key Words

Aging; Alzheimer's Disease; Human brain; Cell type atlas; Neurons; Glia; Small RNAs; MicroRNAs; tRNA fragments.

Background

MicroRNAs (miRs) are short non-coding RNA molecules, typically up to 22 nucleotides long, that may suppress gene expression through complementary binding to target mRNA transcripts[1,2]. Transfer RNA (tRNA) fragments (tRFs) are an additional species of short non-coding RNAs, 16-50 nucleotides long, that are generated by specific cleavage of precursors or mature tRNAs. They exert regulatory roles independently of their tRNA parent and can bind target mRNAs and interact directly with proteins[3]. miRs

are well-established regulators of key brain processes[4,5], including neurodevelopment[6–11], synaptic plasticity[12–14], apoptosis[15,16], neuroinflammation[17], neurodegeneration[18,19] and epilepsy[5,20]. tRFs have likewise been implicated in a growing number of neurological and neurodegenerative conditions[21,22], including Alzheimer's disease[23,24] (AD), Parkinson's disease[25] (PD), psychological stress[26], and neuronal ferroptosis[27]. However, despite extensive evidence for their involvement in brain function, the cell-type-specific expression of brain miRs and tRFs remains poorly characterized, limiting the functional interpretation of their regulatory roles in a cell type-specific manner.

While single-cell RNA sequencing (scRNA-seq) has revolutionized transcriptomics by enabling the study of gene regulation at the resolution level of the individual cell, small non-coding RNAs (sncRNAs) are rarely captured by scRNA-seq that measures only a fraction of the transcriptome, leaving many lowly expressed transcripts, including miRs, undetected[28]. Additionally, most scRNA-seq protocols rely on poly(T) priming to capture polyadenylated mRNAs, whereas most miRs and all tRFs are not polyadenylated[29]. Thus, sncRNA studies still tend to rely on bulk tissue samples that contain mixed combinations of cell types. Although several specialized protocols have been developed to measure miR expression at single-cell resolution, these approaches require dedicated methodology and are limited in the number of cells that can be profiled[30–34]. Currently, to the best of our knowledge, no human brain single-cell or cell-type-resolved miR datasets exist that simultaneously include all major brain cell types. That being said, miRs do display cell-type-specific expression across multiple tissues[35,36], including the brain[32]. Similarly, brain tRNA expression patterns have been shown to vary between cell types[37], although cell-type-specific regulation of tRFs remains largely unexplored.

To attempt filling this knowledge gap, we present the first cell-type-resolved atlas of miR and tRF expression patterns in live human brain, covering neurons, microglia, astrocytes and oligodendrocytes. To capture the transcriptome profiles of small RNAs in these populations we collected brain tissue samples obtained during neurosurgical procedures, isolated single nuclei with a surrounding perinuclear cytoplasmic fraction[38], separated them to cell types by fluorescence-activated cell sorting (FACS), and performed small RNA sequencing on each fraction separately. This procedure led to direct comparison of miR and tRF profiles across distinct brain cell populations, revealing both unique markers of individual cell types and shared transcripts co-expressed across cell types. We found that many cell-type-enriched miRs are associated with quantitative trait loci (miR-QTLs) located in the enhancer regions of the corresponding cell types, suggesting that miR-QTLs may contribute to the cell-type-associated differences in miR profiles. Additionally, we discovered that microglial miR genes tend to be located within microglia-specific regulatory genomic regions, potentially contributing to their cell-type-specific enrichment. The tRFs also differed between cell types, with nuclear 5'-tRFs derived from glycine, lysine, and leucine tRNAs significantly elevated in neurons compared to both microglia and astrocytes.

Owing to the wide age range of donors included in our atlas, we were able to identify age-associated miR profiles using bioIB[39], our recently developed method for elucidating maximally informative, signal-aware representations of high-dimensional transcriptomic data. We found that miR profiles that decrease with age consist of neuron-enriched miRs that target genes involved in nervous system development. In contrast, miR profiles that increase with age were enriched in both neurons and astrocytes, and their target genes associated with hallmark aging pathways. In parallel, analysis of an independent dataset of postmortem prefrontal cortex from Alzheimer's disease (AD) patients revealed elevated neuron-enriched 5′ tRNA halves in AD brains compared to controls. Together, these findings suggest that both miRs and tRFs participate in neuron-specific processes linked to brain aging and neurodegeneration.

Our study provides a unique resource for investigating cell-type-specific expression patterns and functions of miRs and tRFs from live human brain. To further enhance the study of brain miRs at cell-type resolution, we introduce a statistical tool that employs our data to quantify the degree of cell-type-specific marker enrichment in a given set of miRs. Both the dataset and tool are available for interactive usage on our website (https://brain-visualization.vercel.app/).

Results

Simultaneous FACS sorting of neurons, astrocytes and microglia from live human brain tissue

To establish a cell-type-resolved resource of sncRNAs, we separated cell types by fluorescence-activated cell sorting (FACS), followed by small RNA sequencing of the sorted populations (Figure 1a). 39 live human brain samples (17 females, 22 males; ages 37–85; Table 1) were obtained during neurosurgeries for removal of non-infiltrative brain tumors, including meningiomas and metastases (Supplementary Table 1). We followed the NuNeX protocol, in which samples were fixed briefly with formalin and then dissociated into suspensions of single nuclei that retained a perinuclear cytoplasmic layer[38] (Methods). Nuclei were stained with DAPI for the identification of single cells rather than debris or doublets (Figure 1b, c), and the preserved cytoplasmic fraction enabled the use of cell type-characteristic cytoplasmic markers to identify neurons (NeuN), astrocytes (GFAP) and microglia (IBA1).

Within the DAPI-positive population, manual gates for NeuN-, IBA1-, and GFAP-positive nuclei were defined using thresholds determined from non-stained controls of the same sample (Supplementary Figure 1a-f; Methods). To minimize overlap across populations, each sorting gate was refined in two stages by assessing its intersection with two other cell type populations (Figure 1b). In particular, NeuN (FITC) and IBA1 (Alexa 647) gates were first defined based on their overlap in the FITC vs the Alexa 647 space (Figure 1d) and then refined by excluding GFAP (Cy3)-positive events, yielding NeuN-clean and IBA1-clean populations (Figures 1e, f). Similarly, the initial GFAP (Cy3) gate was defined based on the overlap with the NeuN (FITC) signal (Figure 1e) and then refined by comparison to the IBA1 (Alexa 647)-associated signal (Figure 1f).

Total RNA was extracted from the sorted populations and used to validate their cell type identities by qPCR measurement of additional cell type markers. NeuN-positive nuclei expressed the neuronal markers SNAP25 and SYNPR (Figure 1g), GFAP-positive nuclei expressed the astrocytic markers AQP4 and ATP13A4 (Figure 1h), and IBA1-positive nuclei expressed the microglial markers ALOX5AP and CD74 (Figure 1i). None of these cell types significantly expressed markers specific to any other cell type that we tested. Hence, our gating strategy, combined with qPCR validation, enabled reliable assignment of neuronal, astrocytic and microglial identities to the FACS-sorted nuclei populations. Next, 66 samples with the highest RIN values were selected for small RNA-sequencing (24 NeuN-positive, 24 IBA1-positive, and 18 GFAP-positive; Table 1; Supplementary Table 1; Methods), yielding an atlas of cell-type-resolved miR and tRF profiles.

Table 1. Sample metadata

	Neurons (NEUN)	**Astrocytes (GFAP)**	**Microglia (IBA1)**	**Oligodendrocytes (OLIG2)**
Number of samples	24	18	24	14
Age (years)	62 ± 12 (37-75)	61 ± 14 (37-85)	60 ± 11 (41-75)	60 ± 13 (37-85)
Sex	8 females, 16 males	9 females, 9 males	10 females, 14 males	5 females, 9 males

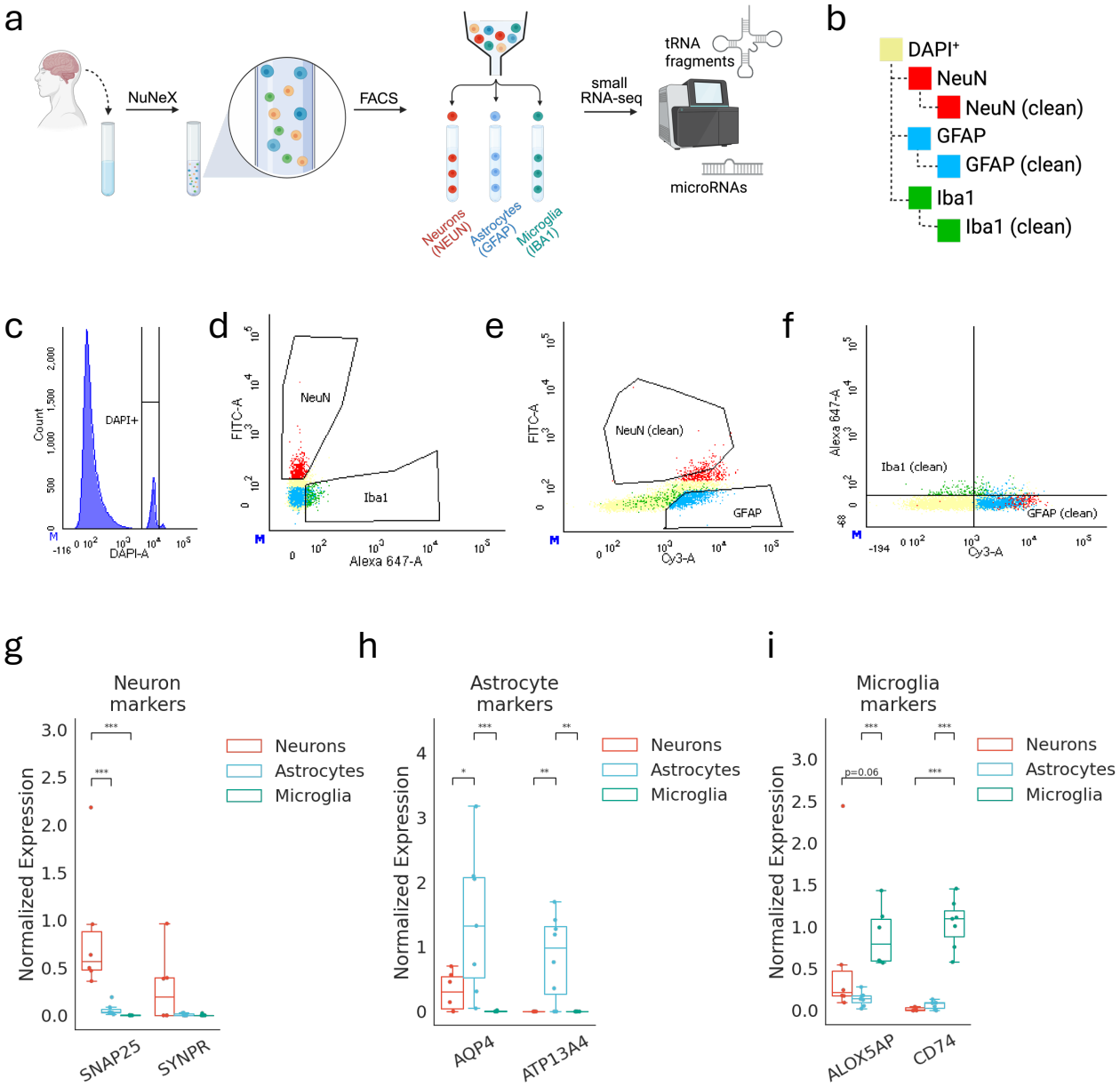

Figure 1. FACS sorting of neurons, astrocytes and microglia from live human brain tissues. a) Graphical representation of the pipeline used to produce the cell-type-resolved resource of small non-coding RNAs from live human brain. Created with BioRender. b) Scheme showing the FACS gate hierarchy: the primary parent gate is a DAPI-positive population; next, each cell-type-specific cellular population was identified via double gating, accessing its overlap with the two other cell types. Thus, NeuN-, GFAP-, and IBA1-positive gates included the refined daughter gates Neun-clean, GFAP-clean, and IBA1-clean. c) Histogram featuring the DAPI signal of FACS events, showing the defined DAPI-positive gate, separating single cells (middle peak) from debris (left peak, low signal levels) and doublets (right peak, higher signal level). d) Scatter plot showing Alexa 647 (IBA1) and FITC (NeuN) signals of the FACS events from the DAPI-positive gate shown in (c), with NeuN- and IBA1-positive gates. e) Scatter plot showing Cy3 (GFAP) and FITC (NeuN) signals of the DAPI-positive FACS events, with the refined NeuN-clean and GFAP-positive primary gates. f) Scatter plot showing the Cy3 (GFAP) and Alexa 647 (IBA1) signals of DAPI-positive FACS events, with the refined Iba1-clean and GFAP-clean gates ensuring minimal mutual overlap. g) Box plot showing qPCR-determined levels of SNAP25 and SYNPR in all three cell types, with neuronal levels set as controls. h) Box plot as in g for the astrocyte biomarkers AQP4 and ATP13A4, with astrocyte values set as controls. i) Box plot as in g for the microglial biomarkers ALOX5AP and CD74, with microglia values set as controls. All values were normalized to GAPDH and ACTB transcripts. Outliers

were removed for each gene's cell type box using the standard boxplot definition, excluding values lying below Q1 – 1.5×IQR or above Q3 + 1.5×IQR. *$p \leq 0.05$, **$p \leq 0.01$, ***$p \leq 0.001$; values with $0.05 < p < 0.15$ are labeled.

Characterizing the cell-type specificity of human brain miRs

We next leveraged our atlas to compare miR levels across brain cell types. To account for statistical dependencies in the data, such as repeated measurements from the same patient and global effects of batch, sex, age and pathology type, we used the dream framework[40]. This approach employs linear mixed-effects modeling to perform differential expression (DE) analysis while accommodating both fixed and random effects, such as cell type and patient ID, respectively. Variance partitioning revealed cell type as the strongest predictor of miR levels (mean explained variance 18.3%), followed by patient ID (mean explained variance 12%; Supplementary Figure 2a). By contrast, batch, pathology type, sex and age explained only minor fractions of variance (mean explained variances 3.0%, 0.7%, 0.5%, and 1.7%, respectively; Supplementary Figure 2a), highlighting the strong cell-type-specific regulation of miRs and validating that the tumor pathology had minimal influence on the miR profiles.

Importantly, the miR profiles clustered according to their cell type label: k-means clustering resulted in sample division that closely matched the annotated cell types (Figure 2a and Supplementary Figure 2b), yielding a normalized mutual information (NMI) score of 0.8 (Methods). In contrast, the NMI score between the k-means clusters and batch labels was 0.1, implying that the miR profiles clustered by cell type rather than by batch (Figure 2a, Supplementary Figure 2c). To identify cell-type-enriched miRs we performed DE analysis in three pairwise comparisons (neurons vs. microglia, neurons vs. astrocytes and microglia vs. astrocytes), correcting for batch, pathology type, sex, age and patient ID (Figure 2b; Supplementary Tables 2-4). Out of 280 miRs expressed above a defined threshold (Methods), 209 were significantly DE in one of the pairwise cell type comparisons (Figure 2b). Specifically, we identified 191 DE miRs between neurons and microglia,163 between neurons and astrocytes, 96 between microglia and astrocytes (Figure 2b).

To quantify overlaps between the DE miRs we performed three pairwise comparisons (Figure 2c): for each cell type we compared the miRs significantly elevated with those in the other two cell types. This yielded 82 miRs elevated in neurons, 115 in astrocytes, and 97 in microglia (Supplementary Table 5). Neurons and astrocytes featured elevated levels of 24 common miRs, compared to microglia; astrocytes and microglia featured elevated levels of 56 common miRs, compared to neurons, whereas neurons and microglia demonstrated increased levels of only 5 common miRs, compared to astrocytes (Supplementary table 5). After excluding these overlaps, we identified 53, 36, and 35 miRs uniquely enriched in neurons, microglia and astrocytes, respectively (Figure 2c).

The top miR markers for each cell type were defined as those with a log-fold change greater than 2 compared to both other cell types. We identified 23, 13 and 6 unique markers in neurons, microglia and astrocytes (Figure 2d; Supplementary Table 5; Methods). For neurons, the top 5 (by fold change) miRs were hsa-miR-935, hsa-129-2-3p, hsa-miR-7-5p, hsa-miR-137-3p and hsa-miR-124-3p (Figure 2e). Their neuronal identities are well supported in the literature: miR-7 regulates neuronal death and glutamatergic signaling[41,42]; miR-137 is critical for neural development[43]; and miR-935 and miR-129-2-3p are both elevated in epileptic brains and plasma[44]. Among astrocytic miRs, hsa-miR-92b-3p was enriched, and has previously been linked to astrocytes in murine brain[45] and shown to regulate glioblastoma development in the human brain[46] (Figure 2f). Top microglial miRs included the hsa-miR-142 family, previously associated with microglia in murine brain[45] and linked to neuroinflammation in murine models[47,48] (Figure 2g).

MiRs that are enriched in two cell types but depleted in the third are of particular interest as well, possibly pointing to shared cell-type functions (Supplementary Table 5). We found elevated levels of hsa-miR-9, a regulator of synaptic plasticity and memory[49], in both neurons and astrocytes (Supplementary Figure 2d). The hsa-miR-221/222 family, involved in neuroinflammation[50–52], was enriched both in neurons and

microglia (Supplementary Figure 2e). Finally, glial miRs enriched in both microglia and astrocytes relative to neurons included hsa-miR-32-5p, linked to neuroinflammation mediated by both glial types[53,54] (Supplementary Figure 2f).

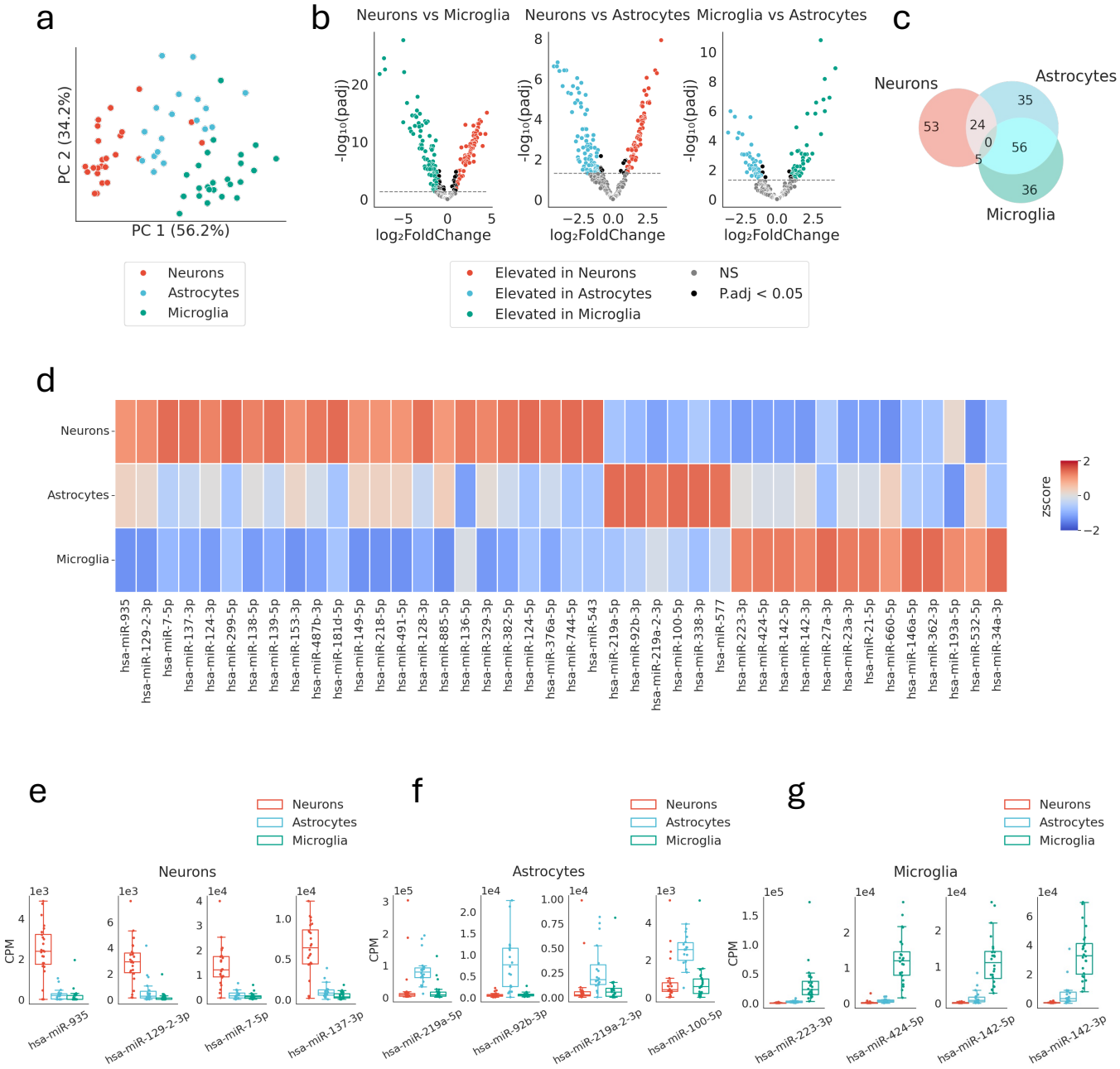

Figure 2. Cell-type-specificity of brain miRs. a) Scatter plot of Principal Component Analysis (PCA) applied to miR profiles of cell-type-specific populations. b) Volcano plots showing dream pairwise DE analysis, comparing each pair of cell types. c) Venn diagram showing the overlaps between the elevated miRs in each cell type. d) Heatmap of mean cell type z-scores of marker miRs for each cell type, defined as significantly DE miRs with a log-fold change greater than 2, relative to both other cell types (Methods). e) Box plot showing expression levels of the top five neuron-enriched miRs (Methods). f) Box plot as in f for astrocyte-enriched miRs. g) Box plot as in f for microglia-enriched miRs.

FACS isolation of oligodendrocytes derived from live human brain tissue

To enhance the depth of our cell-type-resolved atlas we also profiled sncRNAs from the fourth major brain cell type, oligodendrocytes. We used the well-established OLIG2 antibody, which requires an additional permeabilization step to allow antibody access to the nucleus. This necessitated separate staining and FACS sorting steps (Figure 3a; Methods). As in the original protocol (Figure 1), single cells were identified using DAPI (Supplementary Figure 3a), and OLIG2-positive nuclei were gated based on thresholds defined from non-stained controls (Supplementary Figure 3b, 3c; Methods). Altogether, we profiled miRs and tRFs from 14 sorted OLIG2-positive populations (5 females, 9 males; Table 1), using small RNA sequencing.

Similar to the other cell types, we used qPCR to measure enrichment of the oligodendrocyte biomarkers ENPP2 and MOBP in the OLIG2-positive fraction compared with neurons, microglia, and astrocytes (Figure 3b). However, the OLIG2-positive population also featured increased levels of the neuronal marker SNAP25, the astrocyte markers AQP4 and ATP13A4 and the microglial marker ALOX5AP (Supplementary Figure 3d-f). Therefore, the OLIG2-positive group represents a mixed, albeit oligodendrocyte-enriched population.

The mixed identity of the OLIG2-positive population justified a different statistical approach to identify the oligodendrocyte-enriched miRs. To find such miRs, we applied the dream framework[40] by comparing the OLIG2-positive population to the averaged profile of the three other cell types while correcting for batch, pathology type, sex, age and participant ID (Figure 3c; Supplementary Table 6; Methods). This analysis revealed 20 miRs that were significantly enriched in oligodendrocytes relative to all other cell types (Figures 3d). Notably, these included hsa-miR-219a and hsa-miR-338, both known to promote myelin repair[55], and hsa-miR-23, which enhances oligodendrocyte differentiation and myelin synthesis[56]. We also identified hsa-miR-181a-5p, previously implicated in oligodendrocyte maturation[57] and suggested as a potential epigenetic biomarker of multiple sclerosis[58]. To identify the oligodendrocyte miR markers we further excluded miRs with log-fold change lower than 2, as well as those that appeared as markers of other cell types. This resulted in two miRs that were uniquely enriched in the oligodendrocyte population: hsa-miR-181b-5p and hsa-miR-33b-5p (Figure 3e). The miR-33 family is associated with lipid metabolism in the brain[59], and the miR-181b family was implicated in myelin-assisted axon regeneration[60]. Altogether, we extracted the oligodendrocyte miR signature alongside neuron-, astrocyte-, and microglia-specific profiles, thereby extending our resource to encompass all four major brain cell types.

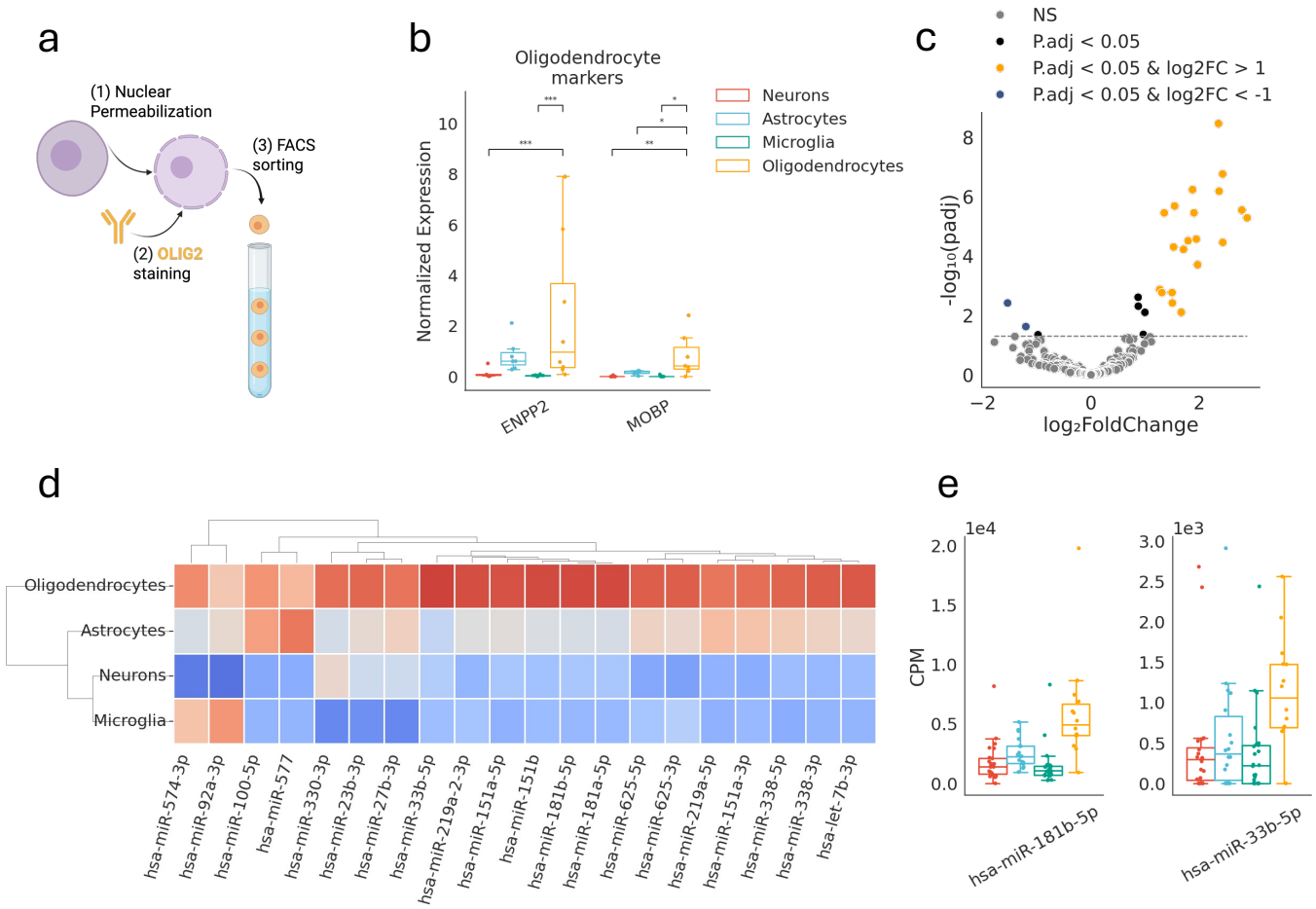

Figure 3. Identifying oligodendrocyte-enriched miRs. a) Graphical representation of the FACS sorting pipeline used to isolate oligodendrocytes from live human brain specimens. Created with BioRender. b) qPCR-measured levels of ENPP2 and MOBP, normalized to GADPH and ACTB transcripts, with oligodendrocyte levels set as controls. Outliers were removed within each gene's cell type box using the standard box plot definition, excluding values lying below Q1 – 1.5×IQR or above Q3 + 1.5×IQR. *p ≤ 0.05, **p ≤ 0.01, ***p ≤ 0.001. c) Volcano plot showing the DE oligodendrocyte miR signature compared to other cell type populations. d) Heatmap showing z-scores of 20 miRs significantly elevated in oligodendrocytes (log2 fold change > 1, adjusted p ≤ 0.05), compared to all other cell types. e) Boxplots showing the levels of two oligodendrocyte marker miRs (log2 fold change > 2; adjusted p ≤ 0.05; Methods). CPM - counts per million.

Cell-type-specific miRs are associated with cell-type-specific regulatory elements

Expression levels of miRs in the human brain were recently reported to be influenced by specific genetic variants, termed quantitative trait loci (miR-QTLs)[61]. We therefore hypothesized that cell-type-enriched miRs may be regulated by QTLs located within cell-type-specific promoter or enhancer regions (Figure 4a; Supplementary Table 7). Leveraging the previously annotated miR-QTLs[61], we identified 31 neuron-, 20 microglia-, 21 astrocyte-, and 4 oligodendrocyte-enriched miRs regulated by 152, 113, 108, and 39 QTLs, respectively. To examine whether these QTLs overlap with cell-type-specific regulatory regions we mapped their genomic coordinates to cell-type-specific promoter and enhancer annotations[62]. We then applied Fisher's exact test[63] to statistically evaluate the association between these cell-type-enriched miRs and their QTLs residing in cell-type-specific genomic regions. Neuronal miRs indeed showed significantly

enriched QTLs within neuron-specific enhancers ($p = 2 \times 10^{-5}$; Figure 4b, left panel) and a similar, though weaker, enrichment trend was observed between astrocytic miRs and miR-QTLs residing in astrocyte-specific enhancer regions ($p = 0.0575$; Figure 4b, right panel). The association between microglial miRs and miR-QTLs in microglia-specific enhancers, as well as between oligodendrocyte-enriched miRs and miR-QTLs in oligodendrocyte-specific enhancers, did not reach statistical significance (Supplementary Figure 4b; Supplementary Table 7). Similarly, no significant associations were observed between miR levels and cell-type-specific promoter regions (Supplementary Table 7). These results collectively suggest that miR-QTLs residing in cell-type-specific enhancer regions may contribute to the genetic regulation of cell-type-specific miR expression.

We next investigated whether the genomic loci of cell-type-enriched miRs overlap with cell-type-specific cis-regulatory (CRE) regions[64] (Figure 4c). Using a single-cell chromatin accessibility atlas of the adult human brain[64] we mapped the genomic coordinates of cell-type-enriched miRs to chromatin regions differentially accessible in diverse cell types, and quantified their associations using Fisher's exact test (Methods). Microglial miRs showed the strongest association within microglia-specific CRE regions ($p = 0.0012$; Figure 4d; Supplementary Figure 4d, Supplementary Table 8), suggesting that chromatin accessibility contributes to the cell-type-specificity of microglial miRs.

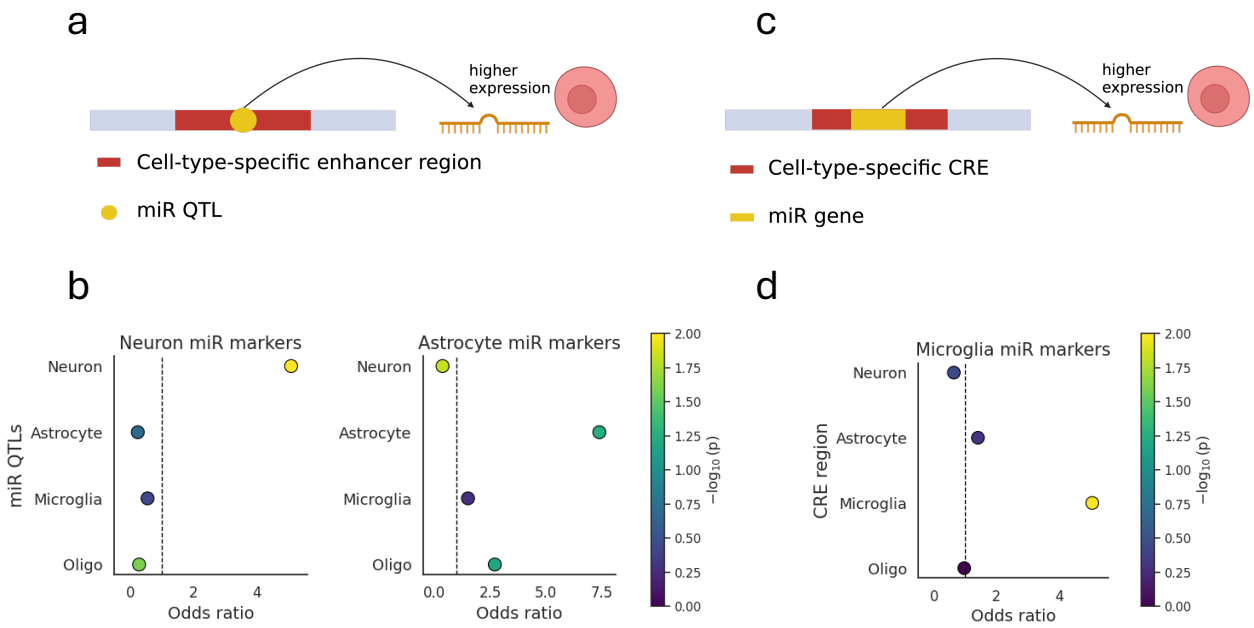

Figure 4. Cell-type-specific miRs are associated with cell-type-specific regulatory elements.

a) Schematic representation of a miR-QTL (yellow) residing within a cell-type-specific enhancer region (red), thereby contributing to the cell-type-specific expression of associated miRs. Created with BioRender. b) Dot plots showing Fisher's exact test results (alternative = two-sided) for the association between miRs enriched in neurons (left) and in astrocytes (right), and the associated miR-QTLs residing within cell-type-specific enhancer regions. Y-axis depicts cell type, X-axis positions reflect the odds ratio of each association, and dot colors depict $-\log_{10}$ p-values (unadjusted). c) Schematic representation of a miR gene (yellow) located within a cell-type-specific cis regulatory element (CRE) (red) that contributes to cell-type-specific expression of the miR. Created with BioRender. d) Dot plot showing Fisher's exact test results (alternative = two-sided) for the association between miRs enriched in microglia and the cell-type-specific cis-regulatory elements (CREs). Y-axis depicts cell type, X-axis positions reflect the odds ratio of each association, and dot colors depict $-\log_{10}$ p-values (unadjusted).

Measuring cell-type enrichment in candidate miR sets

By revealing the cell-type-specific miR markers, our atlas can serve to deconvolve cell-type-specific signals within a miR set of interest (Methods). Here, we provide a statistical framework that calculates the cell-type enrichment of a list of input miRs, such as a list of DE miRs from a bulk RNA-seq study. Specifically, we calculate the fraction of each cell type's marker miRs present in the input list and assess the significance of that association using Fisher's exact test with multiple comparison correction[63] (Figure 5a). To maximize coverage, we include overlapping markers; thus, if an input miR is enriched in more than one cell type, it contributes to the enrichment of each type.

We applied this framework to a range of miR sets derived from small RNA-seq in studies of brain-related conditions and pathologies (Supplementary Table 9). The signature of 110 DE miRs identified in the AD study[65] showed significant enrichment for neuronal markers (Figure 5b). Similarly, 125 miRs altered in PD brains[66] were also enriched for neuronal markers (Figure 5c). This suggests that the miR signatures associated with neurodegeneration mainly reflect neuronal processes. In contrast, the 63 miRs associated with multiple sclerosis[67] (MS) were predominantly enriched in oligodendrocyte-specific miRs, but also showed significant contributions of astrocyte and microglia markers, consistent with the role of glial-driven neuroinflammation in MS[68] (Figure 5d). A curated set of 17 miRs functionally linked to oligodendrocyte differentiation was enriched for the oligodendrocyte and astrocyte signatures, further validating our framework[69] (Figure 5e). We also examined a murine aging-related miR study comprising 476 miRs[70], and although this set contained markers from all major brain cell types, only microglial enrichment was statistically significant, consistent with the original study that highlighted microglial miR involvement in brain aging[70] (Figure 5f). In summary, our cell-type-resolved brain miR atlas enabled the assignment of miR signatures to specific brain cell types, providing a powerful tool for interpreting bulk miR profiling studies.

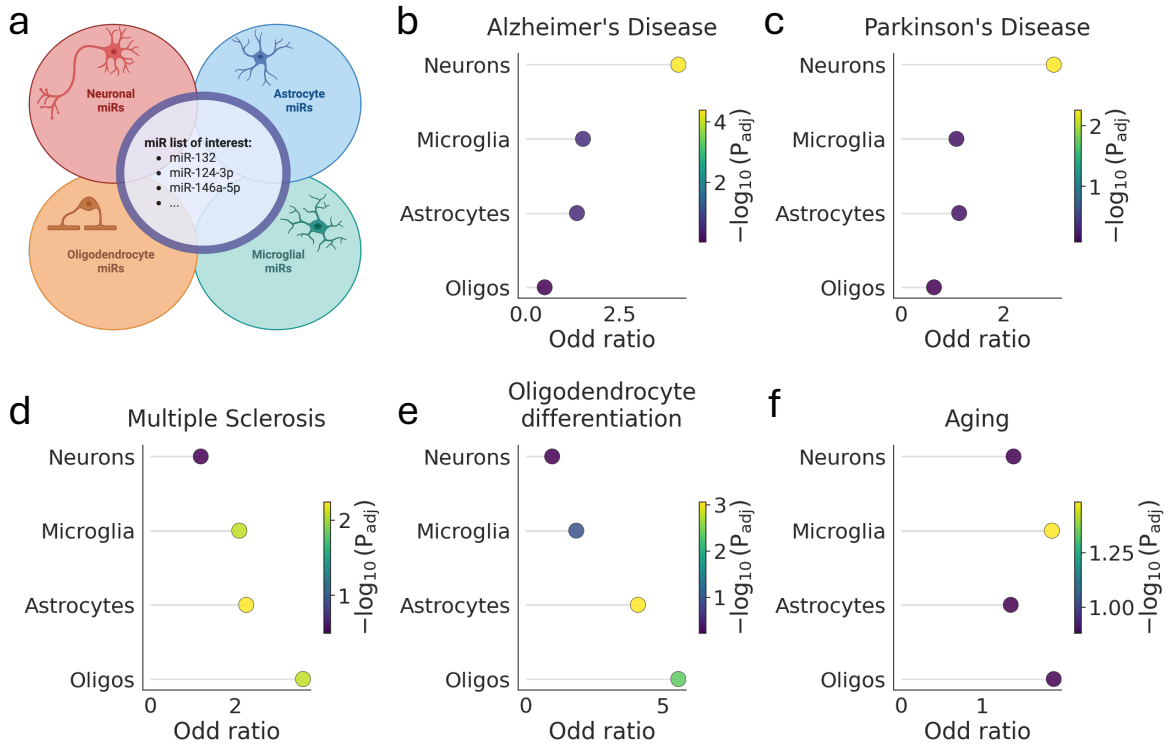

Figure 5. Measuring cell type enrichment in miR lists of interest. a) Graphical representation of the pipeline used to deconvolve miR lists of interest to specific cell type signals. Cell-type enrichment for a given list is calculated by applying the Fisher's exact test to the overlaps between the cell type miR markers identified in this study, and the input miR list. Thus, every analysis consists of four independent statistical tests (for the association with each of the four cell types), corrected for multiple comparisons. Created with BioRender. b-f) Fisher's exact test (*alternative* = *greater*) results for deconvolution of (b) AD[65], (c) PD[66], (d)

MS[67], (e) oligodendrocyte differentiation[69] and (f) brain aging[70] miR signatures. Reported *p*-values were adjusted for multiple testing using false discovery rate control.

Elucidating age-dependent miRs with bioIB

Although multiple miRs have been proposed as key regulators of aging-related processes in the mouse brain[70–72] , age-associated miR expression patterns in the human brain remain poorly characterized. Our cohort spans a wide age range (37 – 85 years of age) and is composed of individuals with no cognitive impairment, thus providing a unique opportunity to study miR dynamics during healthy aging of the brain. Previous studies have shown that miRs often change in coordinated clusters with correlated expression patterns[70,73]. We therefore hypothesized that analyzing age-associated miR clusters could reveal aging-related signatures. To this end, we employed bioIB[39], our recently developed framework for identifying maximally informative, signal-aware representations of high-dimensional data (Methods).

Samples were divided into two age groups: younger (<65 years) and older (≥65 years). To avoid bias arising from differential cell-type composition, we subsampled the data to include an equal number of samples from each of the four cell types in both age groups, selecting the six samples with the highest RNA integrity numbers (RINs) per cell type and age group. This resulted in a balanced dataset of 48 samples (six samples per cell type per age group). Using age group as the signal of interest, hierarchical bioIB partitioned miRs into three major metagenes: metagene 0, enriched in younger individuals; metagene 1, a neutral metagene; and metagene 2, enriched in older individuals (Figure 6a). Because metagene 1 did not show age-specific enrichment, subsequent analyses focused on the two age-associated metagenes.

BioIB enables direct mapping between each metagene and its representative miRs (Figure 6b; Supplementary Table 10). The top miR representing metagene 0 was hsa-miR-488-3p, recently implicated in regulating aging hallmark genes[74]. Another prominent member of this metagene, hsa-miR-193b-3p, has been shown to attenuate neuroinflammation[75,76]. In contrast, the top miRs representing metagene 2, hsa-miR-195-5p and hsa-miR-532-3p, have both been reported to exert neuroprotective effects in the context of brain injuiry[77–79].

Clustering samples based on the expression of metagenes 0 and 2 separated individuals primarily by age group (NMI = 0.35), rather than by cell type (NMI = 0.09), indicating that the identified metagenes capture age-related rather than cell-type-specific variation (Figure 6c; Methods). Consistent with this, metagene 0 exhibited a significant negative correlation with age (Spearman R = −0.39, adjusted p-value < 0.0001), contrasting metagene 2 that showed a significant positive correlation with age (Spearman R = 0.54, adjusted p-value < 0.0001) (Figure 6d, e).

For each metagene, we next defined the most representative miRs as those featuring metagene representation scores higher than 0.01, yielding 17 miRs for metagene 0 and 19 miRs for metagene 2 (Supplementary Table 10). Using these miR sets, we assessed cell-type enrichment with our deconvolution framework (Figure 5; Methods). Both metagenes appeared as significantly enriched for neuronal miRs, while metagene 2 also showed significant enrichment for astrocytic miRs (Figure 6f, g). Finally, for each metagene we extracted the predicted targets of its representative miRs using miRTarBase[80–82], and applied the Gene Ontology[83,84] (GO) enrichment analysis to elucidate the common targeted pathways (Methods; Supplementary Table 11). GO revealed shared enrichment for transcriptional regulation and central nervous system development processes (Figure 6h). Metagene 2, positively correlated with age, also included miRs targeting aging-related pathways such as telomere organization, DNA repair, and apoptosis[85]. Collectively, these results suggest that coordinated, cell-type-specific miR programs are associated with the healthy aging of the human brain.

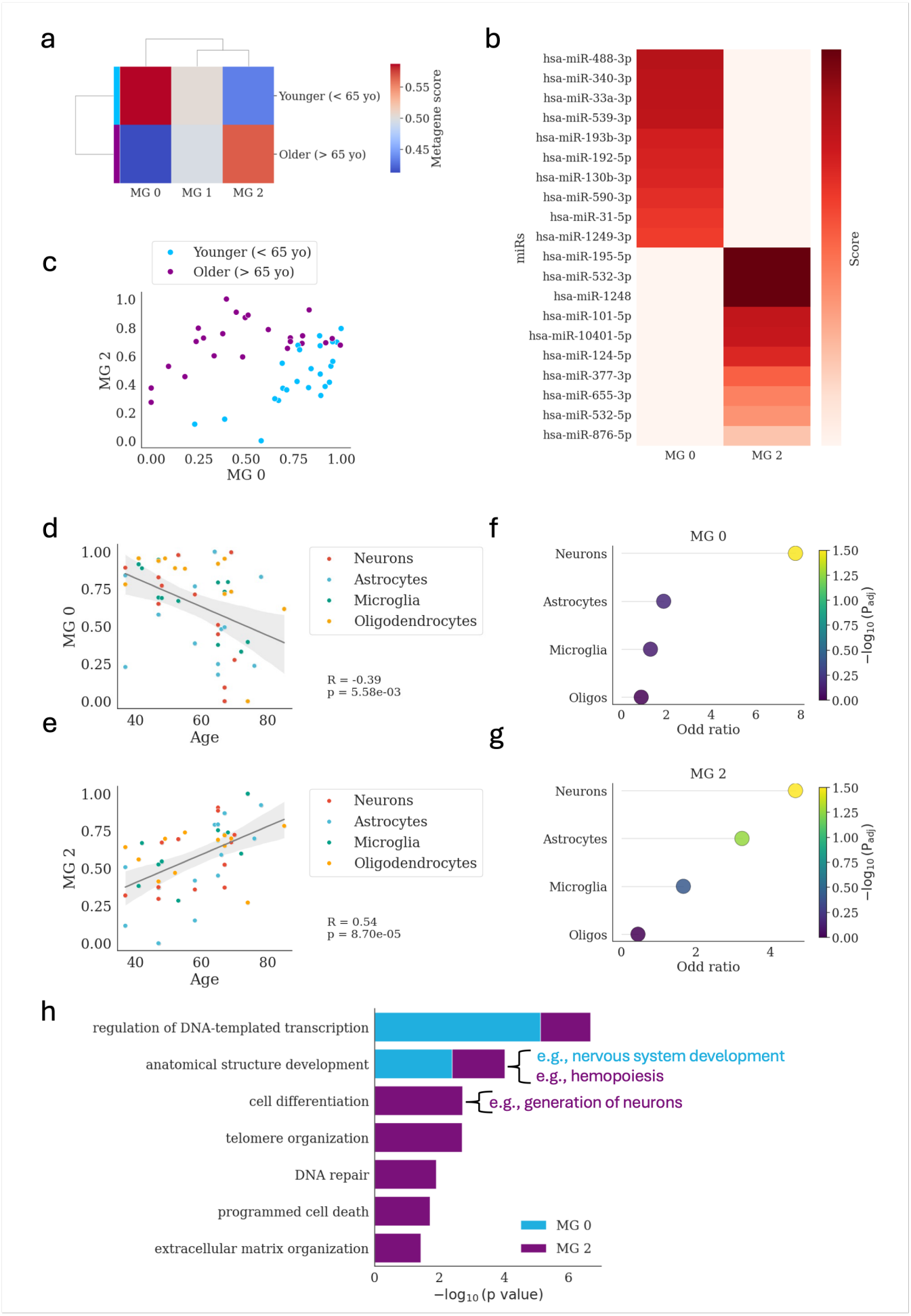
a
Younger (< 65 yo)
Older (> 65 yo)
MG 0
MG 1
MG 2
0.55
0.50
0.45
Metagene score
b
hsa-miR-488-3p
hsa-miR-340-3p
hsa-miR-33a-3p
hsa-miR-539-3p
hsa-miR-193b-3p
hsa-miR-192-5p
hsa-miR-130b-3p
hsa-miR-590-3p
hsa-miR-31-5p
hsa-miR-1249-3p
hsa-miR-195-5p
hsa-miR-532-3p
hsa-miR-1248
hsa-miR-101-5p
hsa-miR-10401-5p
hsa-miR-124-5p
hsa-miR-377-3p
hsa-miR-655-3p
hsa-miR-532-5p
hsa-miR-876-5p
miRs
MG 0
MG 2
Score
c
Younger (< 65 yo)
Older (> 65 yo)
MG 2
MG 0
d
MG 0
Age
Neurons
Astrocytes
Microglia
Oligodendrocytes
R = -0.39
p = 5.58e-03
e
MG 2
Age
Neurons
Astrocytes
Microglia
Oligodendrocytes
R = 0.54
p = 8.70e-05
f
MG 0
Neurons
Astrocytes
Microglia
Oligos
Odd ratio
−log10 (Padj)
g
MG 2
Neurons
Astrocytes
Microglia
Oligos
Odd ratio
−log10 (Padj)
h
regulation of DNA-templated transcription
anatomical structure development
cell differentiation
telomere organization
DNA repair
programmed cell death
extracellular matrix organization
e.g., nervous system development
e.g., hemopoiesis
e.g., generation of neurons
MG 0
MG 2
−log10 (p value)

Figure 6. Determining age-dependent miRs with bioIB. a) Heatmap showing bioIB metagene scores across age groups. Scores are normalized within each metagene, with higher values indicating higher relative metagene expression in the corresponding age group. Metagene 0 is enriched in younger individuals (bioIB metagene score = 0.6 in the younger group); metagene 1 is a neutral metagene (score = 0.5 in both groups); metagene 2 is enriched in older individuals (score = 0.6 in the older group). b) Heatmap showing bioIB metagene scores for the top 10 representative miRs per metagene. Scores are normalized within each metagene, with higher values indicating a stronger contribution of a given miR to that metagene. c) Scatter plot of samples included in the bioIB analysis (younger, n = 24; older, n = 24), showing normalized expression of metagene 0 (x-axis) versus metagene 2 (y-axis). Points are colored by age group. d) Scatter plot showing normalized metagene 0 expression as a function of age, with points colored by the cell-type origin of each sample. Shaded region indicates the 95% confidence interval of the regression fit (bootstrap-estimated). e) Same as (d) for metagene 2. f) Dot plot showing cell-type enrichment in the list of representative miRs for metagene 0. g) Same as (f) for metagene 2. h) Bar plot showing the top GO Slim categories enriched among predicted targets of miRs representing each bioIB metagene. Enrichment p-values (X-axis) correspond to the lowest adjusted p-value among GO terms mapping to each GO Slim category.

Cell-type specificity of tRFs

Transfer RNA fragments (tRFs) are a recently re-identified family of sncRNAs which have been implicated in various neurological conditions[21,22]. Once considered to be inert degradation products of tRNAs, tRFs are now recognized as independent regulators that act either by interacting with target RNAs, in a manner similar to that of microRNAs[26,86,87], and/or by directly binding proteins[27,88]. Using our cell-type-resolved sncRNA atlas, we were able to characterize the cell-type specificity of brain expression profiles of tRFs in addition to those of miRs.

tRFs exhibit strong sequence similarity: fragments derived from the same tRNA share most of their sequence, such that even those originating from different tRNAs exhibit similarity due to high conservation in the tRNA genes themselves[89]. We therefore analyzed tRFs at the level of families, defined by genome of origin (nuclear or mitochondrial), amino acid identity of the parent tRNA, and cleavage type[26] (Figure 6a). Collapsing raw tRF counts into family sums reduced noise and increased the variance explained by the cell type factor (Supplementary Figure 5a, b). However, unlike miR profiles, tRFs expression profiles displayed a stronger batch effect, requiring more rigorous correction with ComBat-seq[90] (Supplementary Figure 5b; Methods).

To determine the cell-type specificity of each tRF family, we conducted pairwise DE analyses between three cell type pairs (neurons vs. astrocytes, neurons vs. microglia, and astrocytes vs. microglia) using the Mann–Whitney non-parametric test after batch correction. Neurons exhibited the most distinct tRF profiles (Figure 6b), with 14 enriched tRF families (Figure 6c, 6d, 6e) compared to 4 in microglia (Figure 6c) and none in astrocytes (Figure 6d), resulting in 18 cell-type-enriched families (Figure 6e, Supplementary table 12). Ten out of those 14 tRF families elevated in neurons represented the 5’ half of their nuclear-encoded tRNA of origin (5’-halves or 5’-tRFs; Figure 6c, 6d, 6e). By contrast, all 4 microglia-enriched families were derived from the 3’ halves of mitochondrial-transcribed tRNAs (Figure 6c, 6d, 6e). Overall, tRF profiles showed a weaker cell-type effect than that of miRs, with an NMI of 0.04 between k-means clusters and cell type labels, compared to 0.8 for miRs (Supplementary Figure 5c).

We next compared the mean tRF family levels for each cleavage type, identifying a significant elevation of 5’-tRF and 5’-half families in neurons compared to both microglia and astrocytes (Figure 6f). Specifically, the Nuc-Gly-5′-half, Nuc-Leu-5′-half, and Nuc-Lys-5′-half families were significantly upregulated in neurons relative to both astrocytes and microglia (Figure 6g), highlighting them as candidates for neuron-specific tRF markers.

Comparison of tRF family profiles between the oligodendrocyte-enriched population and other cell types identified four significantly enriched families; however, the effect sizes were small (Supplementary Table 13; Supplementary Figure 5d). Notably, the tRF families with the highest log fold change were derived from mitochondrial tRNAs, potentially reflecting differences in the oligodendrocyte isolation protocol, which required a nucleus permeabilization step (Methods).

To seek cell-type-specific signals in bulk tRF profiles, we re-aligned a small RNA dataset of postmortem prefrontal cortex (PFC) samples from AD patients and age-matched controls (n=6 each group)[73] to the tRF reference database[91]. Performing DE analysis using DESeq2[92] (Figure 6h) identified nuclear 5'-derived tRNA halves as being enriched in neurons in our atlas and consistently upregulated in AD, with 72% of expressed 5'-tRNA-halves significantly elevated in AD (Figure 6h; Supplementary Table 14). In particular, the neuron-enriched Nuc-Gly-5'-, Nuc-Leu-5'- and Nuc-Lys-5'-halves were all upregulated, potentially reflecting a neuron-specific process linked to AD pathology (Figure 6i).

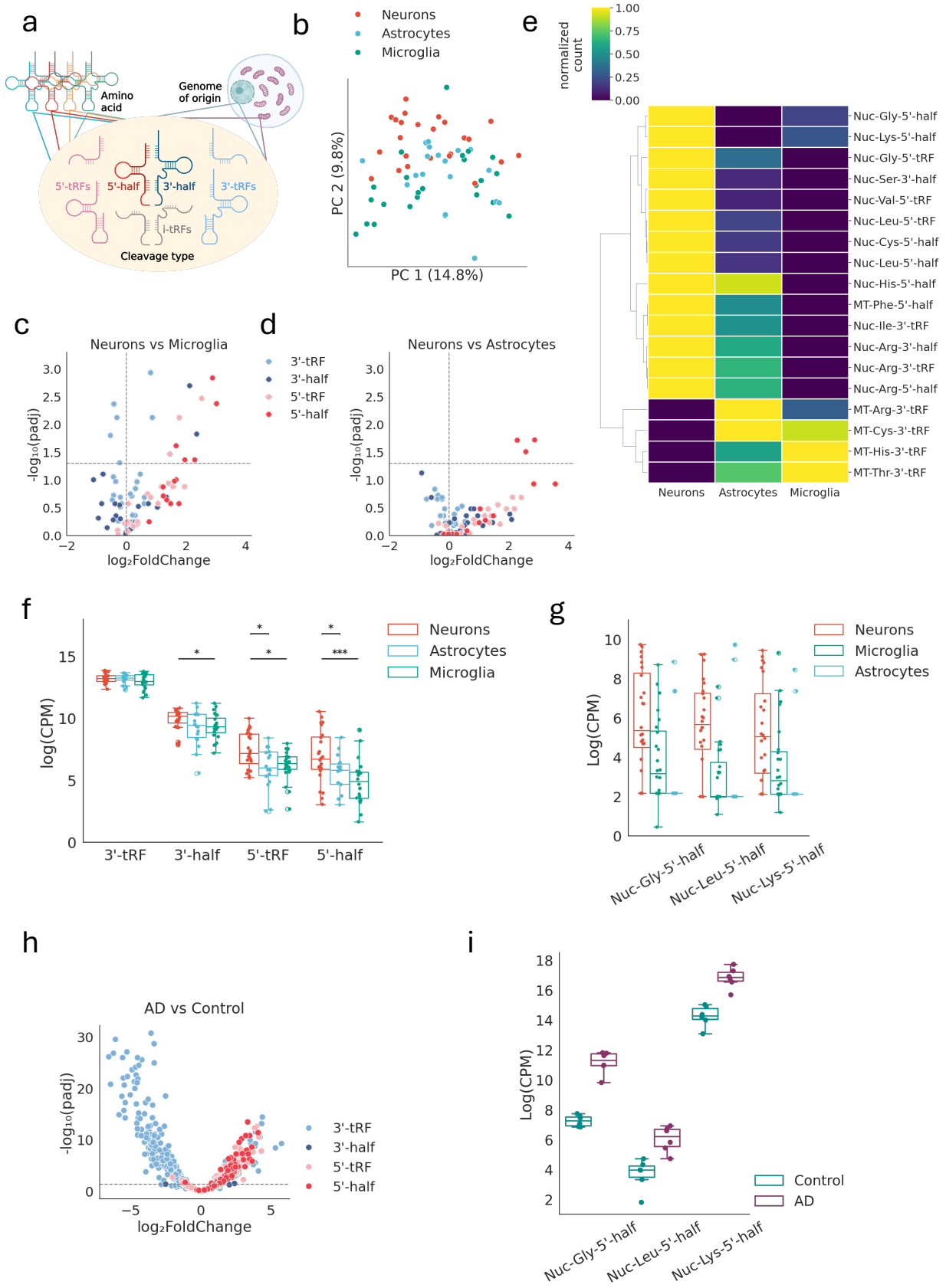

Figure 6. Cell-type specificity of tRF families. a) Graphical representation of the three elements defining tRF families. Created with BioRender. b) Scatter plot of Principal Component Analysis (PCA) applied to tRF family profiles of the three cell populations. c-d) Volcano plots showing the tRF family DE analysis, colored by tRFs cleavage type, comparing (c) neuronal and microglial profiles; and (d) neuronal and astrocytic

profiles. e) Heatmap showing the mean normalized scores of statistically significantly altered tRF families across three distinct cell type populations. f) Box plot of the patient-wise average levels of tRF families, grouped by cleavage type. Significance was determined using the Mann-Whitney non-parametric test. *$p \leq 0.05$, **$p \leq 0.01$, ***$p \leq 0.001$. g) Same as (f) showing the levels of tRF families upregulated in neurons compared to astrocytes and microglia, grouped by cleavage type and amino acid. h) Volcano plot showing DE analysis of AD samples vs. healthy age-matched controls, colored by tRF cleavage type. i) Box plot showing the expression levels of neuron-enriched tRF families in AD samples and age-matched controls.

Discussion

In this study we have established the first cell-type-resolved atlas of miR and tRF expression profiles in the live human brain. Importantly, identifying both unique and shared miR markers across four major brain cell types revealed that the brain miR profiles are highly cell-type-specific. Furthermore, based on association tests we propose that miR cell-type specificity may be regulated by miR-QTLs and by miR genes residing within cell-type-associated genomic regions such as cell-type-specific enhancers and other cis-regulatory elements. Using our atlas, we were also able to identify cell-type-enriched miR profiles that are associated with aging. These included miRs with reported neuroprotective functions that target genes involved in hallmark aging-related processes.

We have also introduced a statistical framework for cell-type enrichment analysis of miR lists of interest. Since no robust, commercial scRNA-seq technology currently enables the capture of small RNA profiles, most studies of brain small RNAs are based on bulk RNA-seq. In this context, our atlas offers an opportunity to deconvolve cell-type signals from bulk-derived miR profiles. Once scalable single-cell small RNA sequencing becomes feasible, our resource may also serve as a reference resource for cell type annotation, providing validated miR markers for neuronal and glial populations.

While miRs are encoded by their own genes, tRFs are generated by the cleavage of tRNAs that are ubiquitous and essential to all cells for survival. It is therefore biologically reasonable that tRFs exhibit a less pronounced cell-type effect than miRs. Nevertheless, we found that neurons exhibit distinct tRF signatures compared to both astrocytes and microglia, which could be explained by cell-type-specific tRF production or degradation rates that are affected by DE profiles of the corresponding ribonucleases. Notably, neurons are particularly enriched in nuclear tRF families aligned to the 5’ side of their tRNAs of origin, and we identified three distinct tRF families as candidate markers: Nuc-Gly-5’-half, Nuc-Leu-5’-half and Nuc-Lys-5’-half. Moreover, these families are also robustly elevated in AD, suggesting that they may reflect a neuron-specific response to AD pathology. Interestingly, Nuc-Lys-5’-half was recently reported to regulate neuronal ferroptosis in the context of botulinum intoxication[27].

Our atlas was generated from fresh human brain tissue, which, on the one hand, represents its unique strength by avoiding postmortem transcriptional artifacts. On the other hand, a potential limitation of our study is the possible influence of tumor-related processes on the small RNA profiles. To minimize this effect, we obtained specimens only during resections of non-invasive brain tumors. All the tumors resected were non-infiltrative and external to the brain, originating from the meninges in meningioma or from non-neural tissue in metastases. Accordingly, our previous work on this cohort[93] demonstrated that these samples are transcriptionally closer to postmortem human brain tissues than to tumor-associated profiles, suggesting minimal contamination. Additionally, our statistical analysis demonstrated minimal effect of the tumor pathology on both miR and tRF profiles.

In summary, this study represents an effort to decipher the small RNA landscape of human brain cells. Future work could extend this atlas to finer cellular states such as neuronal subtypes[32] or disease-associated glial populations[94–96], and integrate emerging single-cell small-RNA sequencing technologies to achieve higher resolution. Both our cell-type-resolved miR and tRF atlases, and the miR cell-type

deconvolution tool are publicly available for interactive exploration on our portal (https://brain-visualization.vercel.app/).

Conclusions

This work introduces the first cell-type-resolved atlas of miRs and tRFs in the human brain. We show that miR cell-type specificity is partially genetically regulated, through the enrichment of miR-QTLs and miR genes within cell-type-specific regulatory regions. Leveraging this atlas, we identify coordinated, cell-type-dependent changes in miRs across neurological diseases and during healthy brain aging, as well as a coordinated alteration of neuron-enriched tRFs in Alzheimer's disease. Both the atlas and the accompanying statistical framework for miR cell-type enrichment analysis are publicly available to the scientific community.

Methods

Tissue samples

Biopsies were extracted during resection operations of non-neural pathologies such as meningiomas and metastases, with exclusion of patients who were operated on for neural pathologies (e.g., gliomas). Tissue samples were fixed in 4% formaldehyde (Sigma-Aldrich, HT501128) for 30 minutes, washed with PBS (Merck, D8537) and stored at 4°C in RNA*later*® (Merck, R0901) for 1-3 days until homogenization.

NuNeX

Brain sections (average size of 3 x 5 mm) were homogenized in 5 mL nuclear isolation buffer (10mM Tris pH 8.0, 25 mM KCl, 5 mM $MgCl_2$, 0.1% Triton, 250 mM sucrose, 1 mM DTT) containing RNase inhibitor (1:100, NEB, M0314) and Protease Inhibitor Cocktail (1:00, Cell Signaling Technology, 5871), using a Dounce tissue grinder (Sigma-Aldrich, D9063). The homogenate was passed through a 40 µm cell strainer (Corning, 352340) and pelleted by centrifugation at 900 *g* for 5 min. Cells (nuclei with attached perinuclear cytoplasm) were resuspended in 1 mL staining buffer (PBS containing 0.8% BSA, RNase Inhibitor as above) and stored in Eppendorf test tubes at -80°C until FACS sorting.

Immunostaining of neurons, astrocytes and microglia

Samples were incubated for 20 minutes in 20 µL of Fc block (Invitrogen,14-9161-73) in staining buffer. Primary antibodies were then added for 30 minutes as follows: labelled anti-NeuN for neurons (1:500; Alexa Fluor™488 conjugated, Merck, MAB377X), anti-GFAP for astrocytes (1:1000; Invitrogen, 14-9892-80), and anti-Iba1 for microglia (1:500; Abcam, ab178846). Cells were pelleted by centrifugation at 900 *g* for 5 minutes, resuspended in staining buffer and incubated for 30 minutes with secondary antibodies for neurons (1:500; Alexa Fluor™ 647 conjugated, Jackson ImmunoResearch, 711-605-152) and astrocytes (1:500; Cy3-conjugated; Jackson ImmunoResearch, 115-165-072). Cells were pelleted again as above and resuspended in staining buffer containing DAPI (1µg/mL; Santa Cruz, sc-3598). All steps were performed on ice or at 4°C.

Immunostaining of oligodendrocytes

For oligodendrocyte isolation, nuclei were fixed and permeabilized using a specialized kit (Invitrogen, 00-5523-00), according to the manufacturer's protocol. Anti-OLIG2 (1:100; Invitrogen, P21954) was then added in staining buffer (PBS, 0.8% BSA, RNase Inhibitor) for 1 hour. Following centrifugation and resuspension in staining buffer, cells were incubated with a secondary antibody (1:200; Alexa Fluor™ 647 conjugated, Jackson ImmunoResearch, 711-605-152) for 30 minutes. Cells were pelleted again as above and resuspended in staining buffer containing DAPI (1µg/mL; Santa Cruz, sc-3598). All steps were performed on ice or at 4°C.

FACS-sorting

NeuN-, GFAP-, Iba1-, and OLIG2-positive cells were sorted through an 85 µm nozzle with an approximate flow rate of 8,000 events/s. Sorted populations (> 1,000 cells) were collected into tubes containing 500 µL

staining buffer. Samples were collected with BD FACSAria III (BD Biosciences) and analyzed using the FCS Express 7 Software (*De Novo* Software).

RNA extraction

Cells were centrifuged at 900 *g* for 5 minutes, resuspended in 100 µL PKD buffer (RNeasy FFPE Kit, Qiagen, 73504) and RNA was extracted (RNeasy FFPE Kit) according to manufacturer's instructions. Concentration and RIN values were determined (Bioanalyzer 6000, Agilent Technologies), with concentrations between 0.1-12.1 ng/µL and RIN between 1.2 and 7.4. The RIN range most likely reflects varying amounts of rRNA present in the samples, in addition to possible cleavage due to the formaldehyde fixation, and not low RNA quality due to degradation.

RT-qPCR

Synthesis of cDNA from lncRNA and mRNA was done using qScript™ cDNA Synthesis Kit (Quantabio, 95047) and qPCR was done using PerfeCTa® SYBR® Green FastMix® (Quantabio, 95072) with human-specific forward and reverse primers (Supplementary Table 15). The CFX384 Touch Real-Time PCR System (Bio-Rad) was used for quantification and the CFX Maestro software (Bio-Rad v4.1.2433.1219) for extracting Cq values. The reference genes were β-actin and GAPDH. All primers were human-specific.

RNA sequencing and alignment

Libraries for short RNA sequencing were constructed in two batches from 500 pg (Batch 1) and 1000 pg (Batch 2) total RNA, using the D-Plex Small RNA-seq Kit for Illumina (Diagenode, C05030001) and Single Indexes for Illumina - Set #B (Diagenode, C05030011). The small RNA fraction was separated (Invitrogen, G401004) and verified (TapeStation, Agilent Technologies), then sequenced (Illumina, 20046810 or 20046811) using the NextSeq 2000 System (Illumina) at the Center for Genomic Technologies, the Hebrew University of Jerusalem. Small RNA was aligned to miRBase 22.1 (Kozomara et al, 2019; Griffiths-Jones et al, 2007) using miRDeep (Friedländer et al, 2008) and to the tRNA transcriptome using MINTmap (Loher et al, 2017) to MINTbase v2.0 (Pliatsika et al, 2016).

MicroRNA DE analysis

Raw read counts were preprocessed using DESeq2 (Love et al., 2014). Library size normalization factors were estimated using the estimateSizeFactors function to correct for sequencing depth across samples. Lowly expressed genes were filtered out by requiring counts per million (CPM) > 1 in at least 50% of samples. For the retained genes, normalized expression values were transformed as $\log_2$ (CPM + 1).
To quantify the contribution of biological and technical factors to expression variability we used the variancePartition framework (Hoffman & Schadt, 2016). Variance components were estimated using the linear mixed model with the formula $\sim(1|ID) + (1|Sex) + (1|Batch) + (1|Cell.type) + Age$, allowing estimation of the proportion of variance explained by donor identity, sex, batch, cell type, and age.
DE analysis was then performed using the dream framework implemented in variancePartition, which models both fixed and random effects. The DE model was defined as $\sim 0 + Cell.Type + Batch + Sex + Age + (1|ID)$. Pairwise contrasts were computed to compare Neurons vs Microglia, Microglia vs Astrocytes, and Neurons vs Astrocytes. To identify oligodendrocyte-enriched fragments, a specific contrast comparing oligodendrocytes against all other cell types combined was constructed using the same model formulation: $Cell.typeOligodendrocytes - \frac{1}{3}(Cell.typeNeurons + Cell.typeMicroglia + Cell.typeAstrocytes)$. Model fitting was performed with dream (Hoffman & Roussos, 2021) and limma's eBayes functions (Ritchie et al, 2015).

MiR mapping to cell-type-specific miR-QTLs and CREs

Annotated miR-QTLs were derived (Vattathil et al, 2025) and the cell-type-specific enhancer and promoter region annotation were determined (Nott et al, 2019). To map miR genes to cell-type-specific CREs we retrieved the genomic coordinates of all annotated miRs from miRbase 22.1 (Kozomara et al, 2019; Griffiths-Jones et al, 2007). For each miR we then extracted its chromosomal position and extended the genomic interval by 500 bases upstream and downstream, to account for minor positional uncertainty and local regulatory proximity. Each extended miR interval was then intersected with the set of open chromatin

regions defined as candidate CREs (Li et al., 2023). Four major brain cell classes (neurons, astrocytes, microglia and oligodendrocytes) were defined based on the provided cell type hierarchical taxonomy (Li et al, 2023) and all corresponding fine-grained cell types were grouped under these classes.

Cell type signal deconvolution

To infer the cellular enrichment of bulk-derived miR lists we implemented a reference-based deconvolution approach based on our cell-type-specific atlas. This was done by computing the overlap between the lists of input miRs and cell-type specific miR markers and calculating the fraction of cell-type-specific marker miRs detected in the input. To statistically assess whether an observed overlap exceeded random expectation we applied Fisher's exact test. For each cell type, a 2 × 2 contingency table was constructed representing: (i) the number of overlapping miRs between the input and the cell type markers, (ii) the number of miRs present in the input but not among that cell type markers, (iii) the number of miRs specific to the cell type but absent from the input, and (iv) the remaining background miRs not belonging to either set. One-sided Fisher's exact tests (alternative = 'greater') were used to identify significant cell type enrichments. Resulting *p*-values were corrected for multiple testing using the false discovery rate (FDR) method, yielding adjusted *p*-values.

Elucidating age-dependent miRs with bioIB

The log-normalized miR count matrix was stored as an AnnData object. Hierarchical bioIB[39] (described in detail in our recent paper, reference 39) was then applied using the bioIB.compress() function, with age bin (younger vs. older) specified as the signal of interest and parameters set to $\beta = 1000$, num_betas = 40, and bulk = True. For calculating the normalized mutual information (NMI) scores between metagene-based clustering and true labels of the age group (younger vs. older) and cell types, the data was clustered to 4 clusters based on the metagene profiles, using k-means. Predicted miR target genes were obtained from miRTarBase[80–82]. Gene Ontology (GO) enrichment analysis was performed using gseapy with the GO_Biological_Process_2025 library[83,84]. Significant GO terms (adjusted $p \leq 0.05$) were further filtered to retain categories with at least three target genes. For improved interpretability, enriched GO terms were subsequently summarized using GO Slim subsets.

tRF statistical analysis

The tRFs were divided into families defined by genome origin (nuclear/mitochondrial), associated amino acid, side (5' or 3') of the tRNA of origin to which the tRF was aligned, and cleavage type (tRNA half, cleaved at the anticodon loop, or tRF, cleaved elsewhere). The counts of all single tRFs in each family were summed. Batch correction was performed using pyComBat (Behdenna et al, 2023). Pairwise statistical comparisons were performed between each pair of the three cell types (neurons, astrocytes, and microglia) using the non-parametric Mann–Whitney U test. The resulting *p*-values were adjusted for multiple comparisons using the Benjamini–Hochberg FDR correction ($\alpha = 0.05$). Comparisons with adjusted $p < 0.05$ were considered statistically significant.

Comparing tRF profiles between AD and control brain samples

Raw fastq files from short RNA-Seq of Alzheimer's disease subjects and controls were downloaded from the GEO database (accession number GSE48552) and aligned to the tRNA transcriptome using MINTmap (Loher et al, 2017) to MINTbase v2.0 (Pliatsika et al, 2016). DE analysis was performed using the DESeq2 package (Love et al, 2014) on tRFs with median expression above 10 counts per million (CPM).

Declarations

Ethics approval and consent to participate

This study, including acquisition of cortical brain samples, was approved by the Rambam Medical Center institutional review board and by the national ethical review board (IRB protocol RMB-0713-19). All patients signed informed consent forms.

Consent for publication

Not applicable.

Availability of data and materials
Raw and processed data generated in this study are available in GEO under accession number GSE314790. In addition, both the atlas and the miR cell-type deconvolution framework are available on our website for interactive exploration (https://brain-visualization.vercel.app/).

Competing interests
The authors declare that they have no competing interests.

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Authors' contributions
S.D.: conceptualization, data curation, formal analysis, investigation, methodology, visualization, writing – original draft; L.L. and I.Z.: investigation; O.A.: software; E.R.B: data curation, project administration and writing – original draft; D.G.: data curation and project administration; A.T.: methodology; M.N.: supervision and writing – original draft; I.P. and H.S.: funding acquisition, supervision and writing – original and finalized drafts.

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