Alteration of the microRNA network during the progression of Alzheimer’s disease

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An overview of miRNAs altered in Alzheimer’s disease (AD) was established by profiling the hippocampus of a cohort of 41 late-onset AD (LOAD) patients and 23 controls, showing deregulation of 35 miRNAs. Profiling of miRNAs in the prefrontal cortex of a second independent cohort of 49 patients grouped by Braak stages revealed 41 deregulated miRNAs. We focused on miR-132-3p which is strongly altered in both brain areas. Downregulation of this miRNA occurs already at Braak stages III and IV, before loss of neuron-specific miRNAs. Next-generation sequencing confirmed a strong decrease of miR-132-3p and of three family-related miRNAs encoded by the same miRNA cluster on chromosome 17. Deregulation of miR-132-3p in AD brain appears to occur mainly in neurons displaying Tau hyper-phosphorylation. We provide evidence that miR-132-3p may contribute to disease progression through aberrant regulation of mRNA targets in the Tau network. The transcription factor (TF) FOXO1a appears to be a key target of miR-132-3p in this pathway.

INTRODUCTION

Alzheimer’s disease (AD) is a progressive age-related dementia characterized by amyloid plaques, neuronal tangles, neurofibrillary degeneration and vascular amyloidopathy in the brain.

The cause of early-onset AD (EOAD) is well known with mutations in the APP, PSEN1 and PSEN2 genes, contributing to the accumulation of amyloid plaques. In late-onset AD (LOAD), genome-wide association studies (GWAS) recently identified more than ten other loci [reviewed in (Tanzi, 2012)], suggesting the existence of additional molecular pathways contributing to the disease. MicroRNAs (miRNAs) are short ~22 nt RNA molecules that bind to the transcripts of protein-coding genes to direct their post-transcriptional repression and by that regulate important physiological and pathophysiological signalling pathways. Increasing evidence links aberrant expression of miRNAs to neurodegenerative disorders including AD [reviewed in (Lau & de Strooper, 2010)]. For instance, miR-29b was found to be downregulated in the anterior temporal cortex of a subgroup of AD patients with high BACE1 protein expression (Hebert et al, 2008) and decreased miR-107 was also observed in the temporal cortex of some AD cases (Wang et al, 2008). However, the small number of patients analyzed represents a major issue when identifying which miRNAs are deregulated during disease. Confounding factors, in particular the technologies used for miRNA profiling which provide deviating results (Pritchard et al, 2012), have to be considered as well.
A more systematic analysis of miRNAs is clearly needed to determine which miRNAs and molecular networks normally controlled by such miRNAs are affected during disease [reviewed in (Salta & De Strooper, 2012)]. We aimed here to determine miRNA alterations in LOAD by profiling two large and independent cohorts of patients using the nCounter system, a technology proven to reliably quantify miRNAs (Wyman et al, 2011). We found numerous changes in the expression of miRNAs in the hippocampus and prefrontal cortex of LOAD patients. Of importance, downregulation of miR-132-3p stands out by robustness and consistency. This observation was confirmed by real-time PCR on the two same brain areas initially investigated and for the temporal gyrus. In agreement, downregulation of miR-132-3p in the LOAD prefrontal cortex was also found by next-generation sequencing of miRNAs and by \textit{in situ} hybridization. We also provide initial identification of miR-132-3p targets of relevance to LOAD, thus offering novel insights into the pathogenesis of the disease.

**RESULTS**

**Deregulation of miRNAs in the hippocampus of LOAD patients**

We analyzed the miRNA expression profile of a first cohort made of 41 LOAD cases and 23 age-matched controls (clinical data in Supporting Information Table S1). The quality of the total RNA obtained from these \textit{post-mortem} samples was systematically assessed (Supporting Information Fig S1A). The RNA Integrity Number (RIN) values were relatively low, indicating fragmented total RNA. However, raw data analysis showed that global expression of miRNAs in the samples with lower (2 < RIN < 6) and higher RIN values (RIN > 6) was similar (Supporting Information Figs S1B and S2A), therefore indicating that miRNAs were relatively resistant to RNA degradation. Because of the discrete counting nature of the nCounter system used for miRNA profiling, positive skewness (Supporting Information Fig S2B) and overdispersion of the data (Supporting Information Fig S3B), a statistical model based on the negative binomial distribution as implemented in the DESeq package (Anders & Huber, 2010) was used to call differential miRNA expression. We found that 35 (5.5\%) of 641 tested miRNAs were differentially expressed between the LOAD cases and the control group [padj < 0.05, nbinomTest corrected for multiple testing by the Benjamini–Hochberg (BH) procedure]. Of interest, 20 miRNAs were downregulated and 15 were upregulated in the LOAD group when compared to the controls (Table 1 and Fig 1A). Notably, we identified miR-132-3p as the most significantly downregulated miRNA (padj = 1.57E–47) together with other brain-enriched miRNAs such as miR-128, miR-136-5p, miR-138-5p, miR-124-3p, miR-129-5p and miR-129-2-3p. Among the upregulated miRNAs in the LOAD group and with previous reported expression in the brain, we found miR-27a-3p, miR-142-3p, miR-92b-3p and miR-200a-3p (Table 1 and Fig 1A).

A supervised clustering based on Support Vector Machine (SVM) was built to evaluate whether the 35 differentially expressed miRNAs could be used to classify the hippocampus samples. After training with a subset consisting of 10 LOAD cases and 10 controls, the SVM classifier was tested on the 44 remaining samples including 31 LOAD cases and 13 controls. Among the 44 samples, three (X7H, X27H, X30H) LOAD cases were misclassified as controls whereas all the control samples were correctly assigned, resulting in a sensitivity of 90\% and a specificity of 100\% for this assay (Fig 1B). The receiver operating characteristic (ROC) curve further showed an area under the curve (AUC) of 0.96 (Fig 1C), confirming the potential application of these 35 miRNAs as markers of LOAD.

**Temporal analysis of miRNAs in the prefrontal cortex of LOAD patients**

We next studied 49 prefrontal cortex samples from a second cohort of clinically well-defined patients stratified according to the six classical Braak stages (BRI to VI) and of seven control samples (BR0) (clinical data in Supporting Information Table S2) (Boschers et al, 2010). The global cellular composition in this brain area remains well preserved over different Braak stages in comparison to the hippocampus.

Quality assessment showed excellent total RNA integrity for those samples when compared to those in the first cohort studied (Supporting Information Fig S1A). Global expression profile of miRNAs for the 49 prefrontal cortex samples was similar, irrespective of the Braak stages and of the quality of the RNA (Supporting Information Fig S1C). Skewness and overdispersion of the nCounter data were observed (Supporting Information Fig S3A and C). We therefore applied a general linear model (GLM) based on the negative binomial distribution to find differentially expressed miRNAs between any two Braak stages. In total, 41 (6.4\%) of 641 tested miRNAs were found to be changed [padj < 0.05, nbinomGLMTest after BH correction] (Table 2 and Fig 2A). The expression analysis of those 41 significantly altered miRNAs showed dynamic expression patterns that were characteristic of downregulated (clusters 1, 2 and 3) and upregulated (cluster 4) miRNAs (Fig 2B). Of importance, some of the miRNA changes were observed at early BRI and BRII stages. For instance, the eight miRNAs in cluster 1, including miR-132-3p, were upregulated between BRI and BRII, and then downregulated between BRII and BRVI. Cluster 2 was mainly characterized by a small loss between BRII and BRIV, followed by a steep decline between late BRV and BRVI stages. Eleven miRNAs such as miR-129-5p, miR-129-2-3p, miR-136-5p, miR-370, miR-409-5p and miR-487a belong to this cluster 2. Cluster 3 consisted of 10 miRNAs showing a gradual downregulation between BR0/BRII and BRVI. Lastly, cluster 4 was made of 12 upregulated miRNAs such as miR-27a-3p, miR-92b-3p and miR-200a-3p. The complete list of miRNAs in each of the four clusters is included in Table 2. In addition, a comparison of miRNAs found to be deregulated among any two Braak stages by the nbinomGLMTest implemented in DESeq to those found by two other popular algorithms, \textit{i.e.} edgeR and Voom + Limma, shows that 40 of 41 miRNAs found to be changed in the prefrontal cortex by DESeq were also called by at least one of the two other methods (Supporting Information Fig S4), therefore supporting the robustness of the analysis.

To assess to what extent changes in miRNAs could be explained by changes in the cell types over the disease, we analyzed the prefrontal cortex expression of miRNAs previously...
shown to be enriched in rodent neurons, astrocytes, oligodendrocytes and microglia, respectively (Jovicic et al., 2013; Lau et al., 2008). Neuron-enriched miRNAs were miR-124-3p, miR-127-3p, miR-128, miR-129-2-3p, miR-129-5p, miR-136-5p, miR-376a-3p and miR-495-3p. Of interest, downregulation of those neuronal miRNA markers was evident between BRV and BRVI stages (Fig 2C), supporting the idea of some neuronal loss at late stages of disease. In contrast, microglial-enriched miR-142-3p, miR-142-5p, miR-146a-5p, miR-150-5p and miR-223-3p were increased at late BRV and BRVI stages (Fig 2C). For oligodendrocytes, we recorded the level of miR-219-2-3p/miR-219-5p and the expression of miR-31-5p and miR-143-3p was monitored for astrocytes. Again, the oligodendrocyte-enriched miRNAs were increased between BRV and BRVI stages but no clear trend was found for the two astrocyte-enriched miRNAs (Fig 2C). More importantly, and in contrast to the late loss of neuronal miRNA markers, downregulation of miR-132-3p was remarkably strong at early and mid-stages of disease already. This difference in miR-132-3p expression was more pronounced than what was found for the other neuronal miRNAs, clearly indicating that downregulation of miR-132-3p cannot be explained by simple cell loss (Fig 2C, indicated by arrow). Overall, it seems likely that miRNAs that are already changing at early and mid Braak stages are linked to the disease process itself.

Table 1. Deregulated miRNAs in the hippocampus of LOAD patients

<table>
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<tr>
<th>miRNA</th>
<th>Control</th>
<th>LOAD</th>
<th>Fold Change</th>
<th>log2 Fold Change</th>
<th>pval</th>
<th>padj</th>
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<tr>
<td>hsa-miR-132-3p</td>
<td>4336</td>
<td>2541</td>
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<td>-0.76</td>
<td>6.35E-10</td>
<td>1.57E-07</td>
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<td>hsa-miR-128</td>
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<td>2443</td>
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<td>-0.71</td>
<td>1.42E-07</td>
<td>1.76E-05</td>
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<td>hsa-miR-23a-3p</td>
<td>1207</td>
<td>1876</td>
<td>1.55</td>
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<td>0.001193</td>
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<td>hsa-miR-455-5p</td>
<td>14</td>
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<td>3.51E-05</td>
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<td>hsa-miR-363-3p</td>
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<td>hsa-miR-127a-3p</td>
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<td>hsa-miR-370</td>
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<td>hsa-miR-487b</td>
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<td>1321</td>
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<td>hsa-let-7f-5p</td>
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<td>hsa-miR-433</td>
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<td>0.0072293</td>
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<td>hsa-miR-195-5p</td>
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<td>hsa-miR-127-3p</td>
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<td>1454</td>
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<td>0.53</td>
<td>-0.92</td>
<td>0.0021989</td>
<td>0.0209741</td>
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<tr>
<td>hsa-miR-487a</td>
<td>506</td>
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<td>hsa-miR-410</td>
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<td>0.65</td>
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<td>0.0389497</td>
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<tr>
<td>hsa-miR-199b-3p</td>
<td>88</td>
<td>138</td>
<td>1.57</td>
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<td>hsa-miR-425-5p</td>
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<td>hsa-miR-200a-3p</td>
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<td>0.0067664</td>
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</tr>
</tbody>
</table>

The name of the mature miRNAs is in accordance with the miRBase V19 nomenclature. Control: normalized counts for the control group; LOAD: normalized counts for the LOAD group; Fold Change and log2 Fold Change correspond to the difference between the LOAD and Control groups; pval: nominal p-value determined by the nbinomTest; padj: nominal p-value corrected for multiple testing by the BH procedure.
rather than being the result of simple alterations in cellular composition of the diseased brain, as this would have been reflected in much more dramatic expression changes of cell-type-enriched miRNAs. Because our main goal was to reliably identify individual miRNAs deregulated in the disease, we merged the hippocampus and prefrontal cortex data to obtain a ‘high-confidence’ list of miRNAs changed in these two brain areas. Although a vast

Figure 1.
majority of the 66 unique miRNA alterations appeared to be specific to one of the two brain regions investigated, an overlap of 10 miRNAs including miR-132-3p, miR-129-5p, miR-27a-3p, miR-92b-3p, miR-129-2-3p, miR-136-5p, miR-200a-3p, miR-370, miR-409-5p and miR-487a was found.

Deregulation of miR-132-3p in the hippocampus, prefrontal cortex and temporal gyrus of LOAD patients

The 10 miRNAs from the ‘high-confidence’ list were selected for technical validation by real-time PCR on the hippocampus of five LOAD cases (X1H, X14H, X29H, X32H, X9H) and five controls (X49H, X52H, X53H, X71H, X144H). We confirmed the upregulation of miR-92b-3p (padj < 0.05, ANOVA corrected for multiple testing by the BH procedure) and downregulation of miR-129-2-3p, miR-129-5p, miR-132-3p, miR-136-5p, miR-370, miR-409-5p and miR-487a in the five LOAD cases when compared to the control group (Fig 3A). Similarly to the nCounter data, miR-132-3p was the most significantly altered miRNA (padj = 2.88E-04). However, we did not confirm changes in the expression of miR-200a-3p (padj = 0.22) nor miR-27a-3p (padj = 0.90) (Fig 3A), therefore eight of 10 selected miRNAs were firmly validated by two assays.

For the prefrontal cortex samples, real-time PCR was performed for the 10 selected miRNAs on a first group consisting of four controls and two early-stage samples (BR0.2, BR0.4, BR0.5, BR0.7, BR1.2, BR1.3) and on a second group of six late-stage brain samples (BR5.7, BR6.2, BR6.3, BR6.4, BR6.5, BR6.7). Similar to the PCR validation of the hippocampus samples, we confirmed miR-132-3p as the most significantly downregulated miRNA in the prefrontal cortex (padj = 1.23E-03) (Fig 3B). In addition, miR-129-5p and miR-136-5p were also found to be differentially expressed, resulting in the validation of only three out of 10 miRNAs (Fig 3B). Such difference in the results, pending on sampling and/or techniques used, is an acknowledged concern in the field (Pritchard et al., 2012).

In addition to the hippocampus and prefrontal cortex areas, we aimed at biologically confirming the deregulation of the 10 miRNAs in a third brain region affected in LOAD. Real-time PCR was therefore performed on the temporal gyrus of a third cohort of eight LOAD individuals (five BRV and three BRVI patients) and eight apparently healthy individuals corresponding to non-demented cases (one BR0 and seven BR1 subjects) (clinical data in Supporting Information Table S3). There was no difference between the two groups for miR-129-5p, miR-136-5p and seven other miRNAs from the ‘high-confidence’ list (Fig 3C). Obviously, those miRNA changes were only seen in specific brain areas or picked by particular techniques, implying the importance of using orthogonal techniques when studying miRNA expression.

However, we observed for a third time a significant downregulation of miR-132-3p (padj = 0.02) (Fig 3C). Overall, miR-132-3p was found to be downregulated in three different LOAD brain areas of three cohorts of patients using two different technologies, making this observation highly reproducible and robust.

We determined whether miR-132-3p deregulation in LOAD was the direct result of the inflammatory component of the disease by profiling its expression in another brain disorder characterized by neuroinflammation, i.e. multiple sclerosis (MS). Real-time PCR of the white matter of eight control subjects was compared to that of six MS samples with confirmed neuroinflammatory process (active lesions) and matched chronic lesions. We found that miR-132-3p was not differentially expressed between active lesions and controls (p = 0.83, post hoc Tukey’s after ANOVA corrected for multiple testing by the BH procedure) nor between chronic lesions and controls (padj = 0.10) (Fig 3D). Additionally, we found higher levels of miR-129-5p and miR-370 in the active and chronic lesions when compared to the controls (padj < 0.05). More specifically, downregulation of miR-92b-3p and miR-136-5p was only observed between chronic lesions and controls (Fig 3D). Overall, these data show that LOAD and MS share some altered miRNAs, but not miR-132-3p, therefore suggesting that deregulation of this miRNA in LOAD is unlikely a direct consequence of a general inflammatory process.

Deep-sequencing of miRNAs in the LOAD prefrontal cortex confirms the deregulation of miR-132-3p

The nCounter system used in our study turns out to have two major drawbacks. First, it covers only 641 well-expressed human miRNAs but not all the 2038 miRNAs found in the current...
version of miRBase (V19, August 2012). Moreover, RNA editing can modify the sequence of miRNAs and the nCounter system would have not detected such editing events. To address these two major issues, we expanded our initial profiling experiments by deep-sequencing miRNAs in the 12 prefrontal cortex samples previously used for real-time PCR validation. After lowering the stringency of detection to find miRNAs expressed at very low level (cut-off of 30 counts across the 12 libraries), 839 of 2038 miRNAs were called present with 85 of them differentially expressed between the two groups (padj < 0.001, nbinomTest corrected for multiple testing by the BH procedure) (Table 3). There were 50 and 35 miRNAs found to be, respectively, down and upregulated between LOAD subjects and controls (Fig 4A and B). Among those 85 miRNAs, 22 of them were not present in

| miRNA BR0 BRI BRII BRII BRIIV BRV BRVI pval padj Cluster |
|---|---|---|---|---|---|---|---|---|---|---|
| hsa-miR-132-3p 6405 5518 7889 5638 3387 3367 2409 7.377E-12 2.279E-09 1 |
| hsa-miR-127-5p 34 27 30 20 15 18 0 2.882E-10 3.98E-08 3 |
| hsa-miR-1321 16 11 25 8 0 2 2 3.864E-10 3.98E-08 1 |
| hsa-miR-210 19 38 22 28 8 5 0 6.376E-08 4.925E-06 3 |
| hsa-miR-214-3p 82 80 24 134 116 144 266 6.686E-07 4.132E-05 4 |
| hsa-miR-496 36 36 41 36 21 31 5 3.796E-06 0.0001955 2 |
| hsa-miR-1178-3p 20 19 16 5 15 7 0 2.605E-05 0.0010853 3 |
| hsa-miR-133b 18 13 21 6 3 7 1 |
| hsa-miR-337-3p 47 52 51 42 54 32 11 3.161E-05 0.0010853 2 |
| hsa-miR-1275 32 22 5 36 28 26 33 0.005612 0.0091191 4 |
| hsa-miR-551b-3p 43 45 41 28 24 38 10 0.0045750 0.0078541 3 |
| hsa-miR-129-5p 1140 1080 1199 1242 1184 1060 737 0.0029627 0.0281762 2 |
| hsa-miR-219-1-3p 12 19 14 5 1 4 4 0.0030901 0.0281762 3 |
| hsa-miR-409-5p 93 69 92 88 68 71 38 0.0044917 0.0408215 2 |
| hsa-miR-27a-3p 378 326 477 399 432 412 561 0.0046685 0.0412159 4 |
| hsa-miR-424-5p 123 99 87 125 100 119 180 0.0051385 0.0441053 4 |
| hsa-miR-487a 557 506 618 621 458 513 385 0.0053237 0.0444603 2 |
| hsa-miR-382-5p 49 62 51 56 42 56 38 0.0055054 0.0451577 3 |
| hsa-miR-92b-3p 1334 1357 1335 1490 1530 1658 1981 0.0061121 0.0484274 2 |
| hsa-miR-136-5p 1061 1241 1203 1242 1184 107 503 0.0063022 0.0488485 2 |
| hsa-miR-874 218 157 134 244 206 207 263 |

The values represent the mean of the normalized miRNA counts at each Braak stage for the significant miRNAs. pval: nominal p-value (nbinomGLMTest); padj: nominal p-value corrected for multiple testing using the BH procedure; Cluster: Fuzzy clustering of the significant miRNAs into four classes.
the nCounter design used for profiling the two large cohorts of patients, therefore representing a set of miRNAs meriting further investigation in the future (Supporting Information Table S4). From this limited list of 22 miRNAs, miR-132-3p and miR-212-3p are found in cluster together with miR-132-3p and miR-212-3p on the chromosome 17 of the human genome, between positions 1,953,200 and 1,953,700 (hg19 build). Of importance, the two miRNAs originating from the pre-miR-132 precursor i.e. miR-132-3p and miR-132-5p were both found to be downregulated (padj = 8.42E-15 and 1.95E-10, respectively). Moreover, miR-212-3p and miR-212-5p were also downregulated (padj = 3.04E-08 and 4.74E-07, respectively) (Table 3 and Fig 4C), showing that not only miR-132-3p but also the entire miR-132/-212 cluster was altered in the LOAD prefrontal cortex. Real-time PCR was also performed on the 12 prefrontal cortex samples to confirm alteration of the miR-132/-212 cluster, validating the downregulation of the four miRNAs (padj = 0.0005, ANOVA corrected by the BH procedure) (Fig 4D).

Because RNA editing can affect target recognition by the miRNAs, we surveyed adenosine to inosine (A-I) modification which is the main type of editing event described in the brain (Alon et al., 2012; Chiang et al., 2010). We detected 22 of the 29 known (A-I) RNA editing events in the 12 libraries. Two miRNAs were less edited in LOAD than in controls, on the borderline of significance level (miR-376c-3p and miR-1251 with padj = 0.05, Wilcoxon two-sample test corrected by BH procedure) (Fig 4E).

In addition, we characterized miR-132-3p isoforms in depth and found decreased mono-uridylation in LOAD (mean percent of controls = 1.52% of the total reads for miR-132-3p, mean percent of LOAD = 0.71%, p = 0.004, Wilcoxon two-sample test), increased miR-132-3p isoform lacking 1 nt at the 3’ end (mean percent of controls = 3.76% of the total reads for miR-132-3p,
mean percent of LOAD = 8.24%, \( p = 0.002 \), Wilcoxon two-sample test) and decreased miR-132-3p isoform lacking 1 nt at the 5' end (mean percent of controls = 2.31% of the total reads for miR-132-3p, mean percent of LOAD = 1.77%, \( p = 0.009 \), Wilcoxon two-sample test). Overall, these data show that miR-132-3p, in addition to being downregulated, is also differentially sequence-modified in LOAD. Whether such changes in the miR-132-3p sequence are biologically relevant to the disease remains to be determined.

In situ hybridization of miR-132-3p in the human prefrontal cortex

Given that miR-132-3p showed a negative correlation to the Braak stages (\( r = -0.63 \), Pearson’s correlation) and to the formation of Tau tangles in the prefrontal cortex (\( r = -0.63 \), Pearson’s correlation), ANCOVA analysis was done to determine whether downregulation of miR-132-3p in LOAD could be explained by additional covariates. The expression of miR-132-3p was related to the Braak stages as expected (\( p = 1.449 \times 10^{-6} \), ANCOVA F test) but not to sex (\( p = 0.20 \)) nor to APOE genotype (\( p = 0.50 \)) nor to age (\( p = 0.57 \)) (Fig 5A–C), therefore supporting a specific role for this miRNA in the disease.

We further determined the expression pattern of miR-132-3p in the prefrontal cortex of LOAD patients and controls using in situ hybridization. We first investigated whether miR-132-3p was expressed in a particular neuronal population. Virtually all neurons of the prefrontal cortex (94.3 ± 1.9%, \( n = 8 \) subjects, \( n = 98-219 \) neurons per subject) (Supporting Information Table

Figure 3. Technical and biological validation of miRNA deregulation in LOAD.

A. Validation of the LOAD hippocampus data. Five controls and five LOAD patients were analyzed to validate the 10 miRNAs found to be differentially expressed in both LOAD hippocampus and prefrontal cortex datasets. Fold changes obtained by real-time PCR were log2 transformed (Log2FC) and positive values represent upregulated miRNAs in LOAD whereas negative values correspond to downregulated miRNAs. The miRNAs are indicated at the bottom of the bar plot. Normalization was done with miR-9-5p. * \( \text{padj} < 0.05 \), ANOVA corrected for multiple testing by the BH procedure. Bars represent standard errors.

B. Validation of the LOAD prefrontal cortex data. Six controls/early-stage and six late-stage samples were selected to confirm expression changes of the 10 miRNAs shown in panel A. The fold changes obtained after real-time PCR between late-stage subjects and controls were log2 transformed. The three downregulated miRNAs (miR-132-3p, miR-129-5p and miR-136-5p) found to be differentially expressed between the two groups are indicated by ‘.’. * \( \text{padj} < 0.05 \), ANOVA corrected for multiple testing by the BH procedure. Normalization was done with miR-9-5p. Bars represent standard errors.

C. Biological validation in the LOAD temporal gyrus. The temporal gyr of eight healthy subjects and eight LOAD patients were analyzed for the expression of the 10 miRNAs found in panels A and B. The real-time PCR fold changes between LOAD and healthy subjects were log2 transformed. * \( \text{padj} < 0.05 \), ANOVA corrected for multiple testing by the BH procedure. Normalization was achieved using SNORD47. Bars represent standard errors.

D. Deregulation of miRNAs in multiple sclerosis (MS) patients. The active (MS.AL) and chronic (MS.CL) lesions of eight MS patients and the white matter of six controls (CT) were compared by real-time PCR for the expression of the 10 miRNAs initially found to be deregulated in both LOAD hippocampus and prefrontal cortex. Normalization was done with miR-9-5p. * \( \text{padj} < 0.05 \) (Post-hoc Tukey’s HSD after ANOVA with p values adjusted for multiple testing by BH correction). Bars represent standard errors.
Table 3. MiRNAs called differentially expressed by next-generation sequencing

<table>
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<tr>
<th>miRNA</th>
<th>Control</th>
<th>LOAD</th>
<th>Fold Change</th>
<th>log2 Fold Change</th>
<th>pval</th>
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</table>

(Continued)
were positive for miR-132-3p, suggesting a broad expression in neurons throughout this brain area. Interestingly, the miR-132-3p signal highly varied between different cortical layers (Fig 6A–D). Layer I was negative whilst a low-to-moderate staining intensity was observed in layers II and V. Of note, layers III/IV and VI contained neurons with highest levels of miR-132-3p. In agreement with the nCounter and real-time PCR data, neurons from layers III/IV and VI of a BRVI patient appeared to contain lower levels of miR-132-3p when compared to a BRI subject (Fig 6C and D). Although a more pronounced down-regulation of miR-132-3p was found in layers III/IV (Fig 6E–H), the laminar expression pattern was preserved in the BRVI sample (Fig 6C–D), suggesting that deregulation of miR-132-3p was not limited to a specific neuronal population in a defined cortical layer. As negative control, the absence of staining was verified using a scrambled probe (Fig 6I–J).

We also investigated a potential link between downregulation of miR-132-3p and presence of hyper-phosphorylated Tau in neuronal cells. In the prefrontal cortex of LOAD patients, Tau tangles are predominantly localized in layers III/IV and V neurons (Hof et al, 1990). By combining in situ hybridization and hyper-phosphorylated Tau immunostaining, we found several neurons in the layers III/IV and V of a BRV sample that were positive for both miR-132-3p and hyper-phosphorylated Tau (Fig 7A–G, indicated with arrows). Particularly in layers III/IV, miR-132-3p appeared to be decreased in neurons positive for hyper-phosphorylated Tau (Fig 7B, D and F). However, this expression change was less evident in layer V.

### Table 3. (Continued)

<table>
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<tr>
<th>miRNA</th>
<th>Control</th>
<th>LOAD</th>
<th>Fold Change</th>
<th>log2 Fold Change</th>
<th>pval</th>
<th>padj</th>
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Control: normalized counts for the control group; LOAD: normalized counts for the LOAD group; pval: nominal p-value determined by the nbinomTest; padj: nominal p-value corrected for multiple testing by the BH procedure.
neurons possibly because of the weaker staining obtained for the neurons of this cortical layer (Fig 7C, E and G). To establish if miR-132-3p was linked to the Tau pathology at the single-neuron level, we quantified miR-132-3p in tangle-positive [AT8(+)] and tangle-negative [AT8(–)] neurons. Of interest, miR-132-3p levels were significantly lower in AT8(+) neurons in both layers III and V, demonstrating a negative correlation between Tau hyper-phosphorylation and miR-132-3p expression on a single-neuron basis ($p = 0.0003$ and $0.0165$ for layers III and V respectively, paired Student’s $t$-test) (Fig 7J). Because layer V neurons are more prone to develop tangles than layer III neurons, we quantified the expression level of miR-132-3p in those layer V neurons and found it to be significantly lower when compared to layer III neurons ($p < 0.0001$, Mann–Whitney $U$ test) (Fig 7J). Overall, we established a correlation between Tau hyper-phosphorylation and miR-132-3p expression. Thus it appears that downregulation of miR-132-3p goes together with Tau hyper-phosphorylation, a major hallmark of LOAD. The question remains obviously whether there is also a functional relationship between the two.

**miR-132-3p targets FOXO1a, a protein increased in the LOAD hippocampus**

The TargetScan algorithm version 6.2 predicts 407 miR-132-3p targets including several transcripts encoding proteins either directly involved in LOAD, i.e. MAPT (coding for Tau), or known regulators of Tau at the post-transcriptional level, i.e. EP300, SIRT1 and GSK3B. An additional salient feature is the prediction of six members of the Forkhead (FOX) transcription factor (TF) family: FOXA1, FOXN3, FOXO1, FOXO3, FOXP1 and FOXP2. Note that other target prediction tools have confirmed these predictions as well (Supporting Information Table S6). Of interest, when we analyzed published microarray data of prefrontal cortex samples from the same cohort of 49 patients analyzed here (Bossers et al, 2010), we found the enrichment of motifs for the FOX TF family in the promoter region [500 bases upstream the transcription start site (TSS)] of 882 upregulated transcripts (Table 4). We found the FOX motif as significantly enriched ($p$-value < 0.001), particularly as the 2nd strongest enriched motif from a large collection of more than 6000 position weight matrices (Herrmann et al, 2012) (shown in bold in Table 4). As control, we found no enrichment of any FOX motif in the promoters of 673 downregulated genes. Instead, CREB family motifs (CREB1 and ATF3) were enriched in this subset (Supporting Information Table S7). These predictions have been confirmed using another independent method for motif discovery (HOMER), and the FOX motifs remained enriched even within very large upstream sequences of 20 kb (Supporting Information Table S8).

Of interest, FOXO1a shows a preferential expression in the murine hippocampus (Hoekman et al, 2006). To determine whether miR-132-3p targets FOXO1a, a luciferase construct containing 2.5 kb of the 3’ Untranslated Region (3’UTR) of human FOXO1a (positions 874-3385 relative to the start of the 3’UTR) was co-transfected with miR-132-3p in HEK-293T cells. A 47% decrease of luciferase activity was observed in the presence of miR-132-3p when compared to the co-transfection of an irrelevant miRNA (Fig 8A). A double mutant containing two deletions corresponding to the miR-132-3p binding site predicted by TargetScan (position 2601: 5’-ACUGUUA-3’) and to a non-conserved binding site at position 2270 (5’-ACUGUUA-3’) was less responsive to miR-132-3p ($p < 0.01$, ANOVA corrected by BH procedure) (Fig 8A). In addition, we also tested the entire 3’UTR of EP300, SIRT1 and MAPT. A validated miR-132-3p target, i.e. TJAP1 (Cambronne et al, 2012), was included as positive control. Highest decreased luciferase activity was obtained for TJAP1 (65% decreased) followed by MAPT and SIRT1 (57%) (Fig 8A). Luciferase constructs containing deletion of the predicted binding sites were also less responsive to miR-132-3p than wild-type constructs ($p < 0.001$ for TJAP1 and SIRT1, $p < 0.01$ for EP300 and MAPT). Overall, a functional interaction with EP300 and SIRT1 was confirmed and in addition, two other transcripts (MAPT and FOXO1a) encoding for additional proteins of the Tau subnetwork were also found to interact with miR-132-3p, therefore adding evidence that this miRNA could be of relevance to LOAD. We also showed that FOXO1a was indeed increased in LOAD patients with low miR-132-3p level by comparing its expression in the hippocampus of 27 subjects including 13 selected controls and 14 LOAD patients. The controls showed 2.73-fold more miR-132-3p than the LOAD subjects (Fig 8B). Of importance, a 79% increase of FOXO1a was found in the LOAD group ($p = 0.002$, Welch two-sample $t$-test) (Fig 8C and D).

**DISCUSSION**

We show that the miR-132/-212 cluster is downregulated in LOAD. In particular, the highest expressed miRNA in this cluster i.e. miR-132-3p is downregulated in three different brain areas including the hippocampus, the prefrontal cortex and the temporal gyrus. Downregulation of miR-132-3p was consistently observed irrespective of the three quantitative methods used i.e. nCounter system, real-time PCR and deep-sequencing. A pioneer study done with a small cohort of subjects previously proposed miR-132-3p to be deregulated in the LOAD hippocampus and prefrontal cortex (Cogswell et al, 2008) (Supporting Information Fig S5A and B). While this work was under revision, decreased miR-132-3p was also found in the temporal cortex of a cohort of 29 patients and controls (Wong et al, 2013) and of a smaller group of eight AD versus eight controls (Hebert et al, 2013), demonstrating the robustness of our observation. Clearly, our work, in addition to these three studies, strongly puts miR-132-3p at the centre stage in the study of miRNAs in LOAD.

A major question of our study was to delineate to what extent miRNA changes accompany disease and disease progression. We attempted to obtain sufficiently large cohorts of LOAD patients and controls to address this question in a statistically sound way. While our work clearly demonstrates that miRNAs are altered in the brain of LOAD subjects, with 35 and 41 miRNAs significantly deregulated in the hippocampus and prefrontal cortex, respectively, we reveal that most of the recorded expression changes are brain area specific, with ten miRNAs deregulated in both regions. We also provide evidence
Figure 4.
that several of those miRNAs are changed according to the different Braak stages that characterize the progressive severity of the disease (Braak & Braak, 1991).

In the past years, profiling of miRNAs in four different brain regions of LOAD patients was attempted (Cogswell et al, 2008; Hebert et al, 2008; Nunez-Iglesias et al, 2010; Wang et al, 2011). However there is no overlap in the miRNAs identified as altered (Supporting Information Fig 5C). This clear lack of consensus could indeed be due to the small number of samples or the heterogeneity of the brain tissues studied. It should be noted that the well-known bias in the different technologies used for miRNA profiling could be a confounding factor as well (Pritchard et al, 2012). To tackle these caveats, we used a rather large number of patients in our study (n = 123 cases compared to 57 for the four previous reports combined together). Additionally, we carefully controlled several inter-individual covariates such as age, sex and post-mortem intervals. We also profiled several brain areas using different methodologies to reduce bias introduced by the techniques. We anticipate that, in the future, larger controlled studies with more subjects will be needed to fully capture miRNA changes in the LOAD brain. However, a major limiting factor to overcome is the availability of well-documented frozen brain samples.

Apart from brain area specific expression changes and methodology related considerations, another important question is to what extent recorded miRNA differences reflect disease related processes or more general alterations due to modifications of cellular composition in the affected brain regions. For instance, some of the miRNA changes may not solely be LOAD related but could simply reflect a more neuronal versus more glia-like profile. With regard to the hippocampus samples analyzed, we found increases of microglial-enriched miR-142-3p, miR-150-5p and miR-223-3p in the LOAD group. It is also impossible to exclude that loss of neurons contributes to decreased miRNA-132-3p in those samples. However, neuronal miRNAs decreased only (and relatively mildly) at late stages of disease in the prefrontal cortex, suggesting that neurodegeneration can be an explanation for loss of miRNAs at those late stages only. Several miRNAs, such as those found in cluster 1, and including miR-132-3p, emerged as being deregulated already at early Braak stages before the appearance of major neuronal loss. We also found that many of the downregulated genes in LOAD show a CREB motif in their promoter regions and given that miR-132-3p is regulated by CREB (Remenyi et al, 2010; Vo et al, 2005), it is likely that active downregulation of this miRNA is taking place during disease process. The specific deregulation pattern of miR-132-3p also supports the hypothesis that this miRNA plays a rather upstream role in the pathogenic cascade of AD.

In agreement, it is of interest to note that miRNA alterations can be observed rather early in the brain of mouse AD models as well. For example, the APPswe/PS1ΔE9 mouse model displays 37 miRNA alterations already at 3 months of age when there is no visible neuronal loss (Wang et al, 2009). We therefore hypothesize that part of the neuronal toxicity caused by Aβ species is mediated, or at least reflected, by changes in the expression of miRNAs. To support this view, hippocampal neurons treated with Aβ42 showed deregulation of 21 miRNAs (Schonrock et al, 2010). It remains to be determined whether miR-132-3p expression is also perturbed in the different mouse models of the disease. Although there was no difference observed for miR-132-3p in the APPswe/PS1ΔE9 mouse (Wang et al, 2009), a more recent study showed this miRNA to be downregulated in the double transgenic APP/PS1 mice at 6 months of age (Wong et al, 2013).

It is also likely that several miRNA changes recorded in our human brain samples are related to some neuroinflammatory changes occurring during disease, for instance reflected in the enrichment of microglial-specific miRNAs at late stages of disease i.e. increased miR-142-3p, miR-150-5p and miR-223-3p. Deregulation of miR-132-3p was not however observed in the small group of MS patients analyzed, in agreement with a

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**Figure 4. Deep-sequencing of miRNAs in LOAD prefrontal cortex.**

A. Downregulated miRNAs in the LOAD prefrontal cortex. Prefrontal cortex of 12 subjects was profiled by next-generation sequencing of miRNAs. The six controls/early-stages (CT = BR0.2, BR0.4, BR0.5, BR0.7, BR1.2, BR1.3 samples) and six late-stages (LOAD = BR5.7, BR6.2, BR6.3, BR6.4, BR6.5, BR6.7 samples) were compared and heatmap and cluster dendrogram of the 50 most significantly downregulated miRNAs (padj < 0.001, nbinomTest after BH adjustment) are shown. Green = controls/early-stages (CT) and brown = LOAD patients. Blue: low expression, red: high expression.

B. Upregulated miRNAs in the LOAD prefrontal cortex. Next-generation sequencing of miRNAs of the 12 prefrontal cortex samples shown in panel A revealed 35 upregulated miRNAs (padj < 0.001, nbinomTest after BH adjustment). Hierarchical clustering of upregulated miRNAs shows separation of the LOAD group and controls. Green = controls/early-stages (CT) and brown = LOAD individuals. Blue: low expression, red: high expression.

C. Normalized counts for the four miRNAs in the miR-132-2/121 cluster. Normalized reads corresponding to the miRNAs found in the miR-132-2/121 cluster and obtained from the 12 sequencing libraries are represented on a logarithm scale. Pairwise comparisons of the two arms (5p and 3p) of each miRNA precursor (pre-miR-132 and pre-miR-212) are shown for the two groups (CT = controls/early-stages represented in green and LOAD = Alzheimer’s subjects shown in brown). The expression level of miR-132-3p, miR-132-5p, miR-212-3p and miR-212-5p was, respectively, 4.02, 3.68, 3.22 and 3.61 times lower in the LOAD group compared to the CT group. * * * padj < 0.001, nbinomTest after BH adjustment.

D. Validation of the four miRNAs in the miR-132-2/121 cluster. Real-time PCR for miR-132-3p, miR-132-5p, miR-212-3p and miR-212-5p was performed on the 12 prefrontal cortex samples used in panels A, B and C. Fold changes between the LOAD group and controls were log2 transformed. The log2 fold changes (Log2FC) obtained for miR-132-3p, miR-132-5p, miR-212-3p and miR-212-5p were −1.67, −1.82, −1.83 and −2.03, respectively. * * * padj < 0.001, ANOVA corrected by BH procedure.

E. A-I RNA editing events in the LOAD prefrontal cortex. For each miRNA known to be (A-I) edited, the percentage of editing events at each known position was calculated by dividing the number of reads containing the edited base by the total number of reads corresponding to the miRNA. The six controls/early-stages (CT) libraries are indicated by blue circles and the six LOAD libraries are represented by red crosses. The number in parenthesis indicates the position on the miRNA where the editing event occurs, with the first nucleotide at the 5′ end of the miRNA being the position 1. The last number at the right side of the parenthesis corresponds to the p value adjusted for multiple testing using the BH procedure (padj, Wilcoxon two-sample test).
Effect of the age on miR-132-3p downregulation. All the 49 patients were grouped into bins of 10 years, from 50 to 100 years old. For the five different bins, we found no significant difference in the downregulation of miR-132-3p (ANCOVA, \( p = 0.57 \)).

Effect of the sex on miR-132-3p downregulation. For the males and the females in the cohort of 49 patients analyzed for the expression of miR-132-3p in the prefrontal cortex, there was no significant difference in the downregulation of miR-132-3p during disease progression (ANCOVA, \( p = 0.20 \)).

Figure 5. Downregulation of miR-132-3p is specifically related to disease progression.

A. Effect of the APOE genotype on miR-132-3p downregulation. The normalized expression level of miR-132-3p in the prefrontal cortex as determined by the nCounter system was plotted against the controls (0) and the six Braak stages (1–6) for which the APOE genotyping was made. The ANCOVA model was used to assess the effect of the different APOE genotypes. For the five genotypes present in the 49 samples i.e. APOE 32, 33, 42, 43 and 44, there was no significant difference in the downregulation of miR-132-3p (ANCOVA, \( p = 0.50 \)). Note that APOE42 was found for two patients only.

B. Effect of the age on miR-132-3p downregulation. All the 49 patients were grouped into bins of 10 years, from 50 to 100 years old. For the five different bins, we found no significant difference in the downregulation of miR-132-3p (ANCOVA, \( p = 0.57 \)).

C. Effect of the sex on miR-132-3p downregulation. For the males and the females in the cohort of 49 patients analyzed for the expression of miR-132-3p in the prefrontal cortex, there was no significant difference in the downregulation of miR-132-3p during disease progression (ANCOVA, \( p = 0.20 \)).

previous study done with a larger cohort of 30 MS patients/control subjects (Junker et al, 2009). Thus, alteration of miR-132-3p is not systematically observed in a neuroinflammatory context although it has been shown that miR-132-3p mediates anti-inflammatory signalling (Shaked et al, 2009). The targeting of acetylcholinesterase by miR-132-3p may be indeed relevant for the association of the enzyme activity with amyloid load in LOAD (Alkalay et al, 2013; Berson et al, 2008), as well as with the anxiety phenotype and RNA metabolism impairment that are characteristic of the disease (Berson et al, 2012; Shaltiel et al, 2013).

The deregulation of miR-132-3p might be particularly relevant to LOAD at several additional levels. For instance, miR-132-3p has been involved in modulating synaptic activity and plasticity (Wanet et al, 2012). Furthermore, miR-132-3p regulates neuronal outgrowth in response to neurotrophins (Vo et al, 2005), mediates integration of newborn neurons in the adult hippocampus and dentate gyrus (Luikart et al, 2011; Magill et al, 2010), and shapes synaptic structure (Edbauer et al, 2010) and plasticity in the visual cortex (Mellios et al, 2011; Tognini et al, 2011). This brings us to the question which molecular targets of miR-132-3p are relevant to LOAD. We analyzed deregulated transcripts in the LOAD prefrontal cortex samples and identified several miR-132-3p targets including Tau, EP300 and SIRT1, the latter being post-translational regulators of Tau (Min et al, 2010) and FOXO1a. These targets were confirmed using luciferase assays and we further demonstrated upregulation of FOXO1a protein in AD hippocampus samples, in agreement with previous works showing that the FOXO1a transcript is upregulated in function of the severity of the disease (Blalock et al, 2004; Gomez Ravetti et al, 2010; Liang et al, 2012), but see (Broner et al, 2009). During the revision of the manuscript, a study proposed miR-132-3p to regulate another member of the FOX family of TFs, i.e. FOX3a, which is increased in LOAD and in turn transcriptionally activates pro-apoptotic genes (Wong et al, 2013). Thus, evidence increases that FOXs and the FOXOs in particular, may be regulating important molecular pathways relevant to LOAD. Intriguingly, we found that not only miR-132-3p regulates FOXs but also many of the predicted miR-132-3p targets show in their promoter regions an enrichment of motifs for this family of TFs. We estimate the number of such co-regulation events mediated by miR-132-3p and the FOXs to be up to 311 out of 407 (81.3%) predicted targets (Supporting Information Fig S6).

In conclusion, we provide strong evidence for meaningful changes in miRNA expression during LOAD and downregulation of miR-132-3p as the most salient feature. Recently, alteration of miR-132-3p expression has also been reported in several other neurodegenerative diseases including schizophrenia, progressive supranuclear palsy, Huntington’s disease and frontotemporal lobar degeneration with TDP-43 inclusions (FTLD-TDP) (Chen-Plotkin et al, 2012; Johnson et al, 2008; Miller et al, 2012; Smith et al, 2011). Our work thus clearly indicates that miRNAs such as miR-132-3p deserve further functional exploration to deepen our understanding of molecular mechanisms driving not only LOAD but also other neurodegenerative disorders. It is not unlikely that future studies might reveal part of those common molecular pathways that are relevant to these conditions.

MATERIALS AND METHODS

Participants and study design

Frozen prefrontal cortex and hippocampus samples were obtained from the Netherlands Brain Bank (Amsterdam, The Netherlands) and the MRC London Brain Bank (London, UK), respectively. The prefrontal...
Figure 6. Characterization of miR-132-3p expression in LOAD prefrontal cortex.

A-D. miR-132-3p is expressed in a layer-specific manner. Thionine staining (A) and in situ hybridization for miR-132-3p (B) in consecutive prefrontal cortex sections of a LOAD patient (BRVI) reveals that miR-132-3p is predominantly expressed in cortical layers III/IV and VI whereas layer I is devoid of signal. In cortical layers II and V, a low-to-moderate expression of miR-132-3p is seen. The same layer-specific expression pattern is observed in a BRI subject (C and I) and in another LOAD patient (BRVI) (D). Note the overall decrease of the miR-132-3p signal in the LOAD sample.

E-H. miR-132-3p is constrained to neuronal structures in the prefrontal cortex. Layer III/IV neurons (E, G) express higher levels of miR-132-3p than layer VI neurons (F, H). There is apparent overall decrease in the intensity of the signal in LOAD neurons (G, H) compared to the BRI subject (E, F).

I,J. Negative control staining with a scrambled probe. To verify the specificity of the miR-132-3p LNA probe, we hybridized consecutive tissue sections of an early-stage patient with the miR-132-3p probe (I) or with a scrambled probe (J). The section hybridized with the scrambled probe was completely devoid of staining whilst intense staining with the miR-132-3p probe was obtained. Scale bars in B, D and J represent 0.25 mm. Scale bar in H represents 50 μm.
The cortex collection was made of 49 samples covering the six Braak stages ($n = 7$ samples for each stage) and of seven additional controls. To avoid effect of potential confounding factors, the samples were carefully matched for sex, age, post-mortem interval and pH of the cerebrospinal fluid (CSF). The 64 hippocampus samples were made of 23 controls and 41 LOAD cases. All samples were collected according to the legislation and ethical boards of the two Brain Banks. The samples from the temporal lobe of LOAD patients were also obtained from the...
Total RNA isolation and nCounter hybridization

Prefrontal cortex samples were snap-frozen in liquid nitrogen and grey matter was dissected in a cryostat. Frozen hippocampus samples were directly dissected on dry-ice. Total RNA was extracted using TRIzol (Invitrogen, Carlsbad, CA, USA) and purified on mirVana columns (Ambion, Austin, TX). The active and chronic lesions of six MS patients and the white matter of normal appearance of eight control subjects were also dissected and snap-frozen in TRIzol. The total RNA quality was assessed on Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA). Medium-throughput profiling of miRNAs was performed with the nCounter Human miRNA Expression Assay Kit version 1 (Nanostring Technologies, Seattle, WA, USA). Briefly, 100 ng of total RNA was annealed to the nCounter miRNA Tag reagent, hybridized to the Reporter CodeSet and run on a nCounter Prep Station (VIB microarray facility, Leuven).

nCounter analysis

All R packages were downloaded from the Bioconductor (http://www.bioconductor.org) and the Comprehensive R Archive Network (CRAN) (http://cran.r-project.org) repositories. The nCounter definition file from the nCounter Human miRNA assay Kit version 1 was re-annotated to match the human miRNAs found in the most recent version of miRBase (V19, August 2012). For the hippocampus samples, the nCounter data were background subtracted using the library NanoStringNorm (version 2.1.1.4) and a filtering step was applied to keep mean counts > 20, followed by testing for differential expression using the nbimomTest (library DESeq, version 1.12.0) and corrected for multiple testing using the BH false discovery rate (FDR) controlling procedure. For the hierarchical clustering of hippocampus miRNAs, data were clustered following Spearman’s correlation and average linkage method (library gplots, version 2.15.1). The SVM classification of the hippocampus samples was performed using a linear kernel with a gamma = 0.01 and cost = 1 (library e1071, version 1.6-1). The sensitivity or true positive rate (TPR) was defined as TPR = True Positive/(True Positive + False Negative). The specificity or true negative rate (TNR) was calculated as followed: TNR = True Negative/(True Negative + False Positive). The ROC was determined using the library ROC (version 1.0-5).

The nCounter data obtained from the prefrontal cortex samples were similarly processed except that filtering was set to keep > 10 mean counts and differential expression between any two Braak stages was assessed using ANOVADEV (fitNbinomGLMs in the library DESeq). p-values were corrected for multiple testing using the BH procedure. Hierarchical clustering of prefrontal cortex miRNAs was performed.

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There were 882 genes upregulated between BRI and BRVI stages. Motif ids were obtained from the JASPAR, TRANSFAC and Yetfasco database. Transcription Factor: TF predicted to bind to the motif; NA: motifs not annotated; Targets: number of upregulated genes containing the motif inside 500 bp upstream the transcription start site.
Profiling of microRNAs in Alzheimer’s disease

Real-time PCR

To validate miRNA changes, total RNA of five controls and five LOAD hippocampus samples was reverse transcribed using the miRCURY LNA Universal RT kit (Exiqon, Denmark). The reverse transcription mix contained 4 μl of total RNA (200 ng), 4 μl of 5x reaction buffer, 2 μl of enzyme mix and 10 μl of water. The reactions were incubated at 42°C for 1 h followed by inactivation at 95°C for 5 min. The samples were diluted 20× and 4 μl of diluted product was assessed in a PCR reaction mix containing 5 μl of SYBR Green master mix and 1 μl of miRNA specific primers (Exiqon). Real-time PCR was performed on 96-well plates using the LightCycler 480 Real-Time PCR system (Roche, Indianapolis, IN, USA). The PCR conditions were 95°C, 10 s and 60°C, 1 min. The crossing point (Cp) was determined by using the second derivative method and data were normalized with miR-9-5p. Fold changes and statistical significance were calculated using one-way ANOVA. Validation of the 12 prefrontal cortex samples and analysis of the 14 MS samples were performed similarly using miR-9-5p as normalizer and ANOVA followed by post-hoc Tukey’s HSD for the comparison of multiple MS groups. Correction for multiple testing was done using the BH procedure. The validation of the temporal lobe of eight LOAD patients and eight controls was done after extracting the RNA using the miRNeasy Mini Kit (Qiagen, Venlo, The Netherlands). The cDNA was prepared using the qScript microRNA cDNA Synthesis Kit (Quanta BioSciences, Gaithersburg, MD, USA) and semi-quantitative PCR was performed using Quanta miR primers and PerfeCta SYBR Green FastMix, Low ROX (Quanta BioSciences). Light emission was measured using the Bio-Rad CFX96TM Real-Time PCR Detection System (Bio-Rad). Normalization was achieved using SNORD47.

Deep-sequencing of miRNAs

Deep-sequencing of miRNAs from 12 prefrontal cortex samples was performed after reverse transcription of the total RNA and ligation of 5´ and 3´ adaptors using the TruSeq Small RNA Sample Preparation Kit (Illumina, San Diego, CA, USA). After gel purification, the PCR products were sequenced for 35 cycles on an Illumina HiSeq 2000 system (CMC Genomics Core, UZ Leuven). The adaptor (5´-TGAAATTCTCGGGTGCGCACAGG-3´) was trimmed from the raw sequencing reads using Flicker 3.0 (Illumina) and manual filtering steps were performed to remove low quality reads and reads containing ambiguous nucleotides. Reads longer than 15 nucleotides were mapped to the hg19 build genome using the short-read aligner Bowtie2 (version 2.0.2) and allowing one mismatch, the PCR products were sequenced for 35 cycles on an Illumina HiSeq 2000 system (CMC Genomics Core, UZ Leuven). The adaptor (5´-TGAAATTCTCGGGTGCGCACAGG-3´) was trimmed from the raw sequencing reads using Flicker 3.0 (Illumina) and manual filtering steps were performed to remove low quality reads and reads containing ambiguous nucleotides. Reads longer than 15 nucleotides were mapped to the hg19 build genome using the short-read aligner Bowtie2 (version 2.0.2) and allowing one

by 45 cycles at 95°C, 10 s and 60°C, 1 min. The crossing point (Cp) was determined by using the second derivative method and data were normalized with miR-9-5p. Fold changes and statistical significance were calculated using one-way ANOVA. Validation of the 12 prefrontal cortex samples and analysis of the 14 MS samples were performed similarly using miR-9-5p as normalizer and ANOVA followed by post-hoc Tukey’s HSD for the comparison of multiple MS groups. Correction for multiple testing was done using the BH procedure. The validation of the temporal lobe of eight LOAD patients and eight controls was done after extracting the RNA using the miRNeasy Mini Kit (Qiagen, Venlo, The Netherlands). The cDNA was prepared using the qScript microRNA cDNA Synthesis Kit (Quanta BioSciences, Gaithersburg, MD, USA) and semi-quantitative PCR was performed using Quanta miR primers and PerfeCta SYBR Green FastMix, Low ROX (Quanta BioSciences). Light emission was measured using the Bio-Rad CFX96TM Real-Time PCR Detection System (Bio-Rad). Normalization was achieved using SNORD47.

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The paper explained

PROBLEM:
Alzheimer’s disease (AD) is the most common form of dementia. While most of ongoing research is focused on the contribution of Tau and the amyloid β- (Aβ) protein, other molecular pathways are involved in the neurodegenerative process underlying the disorder. Recently, microRNAs have been recognized as important regulators of gene expression and their aberrant expression could lead to perturbation of cellular homeostasis and ultimately to neurodegeneration. However, little is known about the global expression pattern of microRNAs in the brain of patients and the molecular networks potentially regulated by such microRNAs. Moreover, reproducibility of recorded alterations is a major issue.

RESULTS:
In our study, we found deregulation of a small subset of microRNAs in the hippocampus and prefrontal cortex of AD patients. We established miR-132-3p as being the most altered microRNA during disease. Downregulation of miR-132-3p in neuronal cells was inversely correlated with the appearance of the hyper-phosphorylated form of Tau. Additional analysis of miR-132-3p targets points to the FOX transcription factors (TFs) as regulated by and sharing a common subset of targets with this microRNA.

IMPACT:
Our results provide the first large scale analysis of microRNAs altered in AD. When the disease worsens, neuronal cells show lower amount of miR-132-3p and hyper-phosphorylated Tau accumulates in these cells, therefore establishing the down-regulation of miR-132-3p as a new marker of AD and potentially other neurodegenerative disorders.
Furthermore, each neuron was classified as AT8(+) or AT8(−). Finally, the average miR-132-3p intensity of AT8(+) and AT8(−) neurons was calculated separately for layers III and V. Statistical significance was determined with a paired Student’s t-test. For the comparison of miR-132-3p levels between cortical layers, the miR-132-3p expression levels were estimated by measuring the average fluorescence intensity in miR-132-3p positive neurons as described above.

**Regulatory analysis**
Differentially expressed transcripts between BRI and BRVI stages were determined with Limma. Detection of enriched TFs on protein coding genes was performed on 500 bp promoter sequences of 882 upregulated genes between BRVI and BRI stages (FDR < 0.05) with the parameters for a motif collection of 6683 position weight matrices using an empirical p-value (Herrmann et al., 2012). The results were confirmed using Hypergeometric Optimization of Motif EnRichment (HOMER) Suite version 4.2 (Heinz et al., 2010). The program findMotifs.pl was run on a regulatory region of 20 kb centred around the TSS and all the other parameters were used as default to detect the significant motifs from their in-house motif library (1865 motifs).

**Luciferase assays**
The 3’UTRs were cloned by PCR using the Phusion enzyme kit (NEB, Ipswich, MA, USA) and human brain cDNA as template (Clontech, Mountain View, CA, USA). For MAPT cloning, PCR was performed using a 201 kb P1-derived artificial chromosome (PAC) containing the human MAPT gene (Pookraj et al., 2001). The sequences of the PCR primers used for cloning can be found in Supporting Information Table S9. Briefly, PCR products were cut with Asc I and Xho I restriction enzymes and cloned into the pSICHECK3 vector, a derivative of the pSICHECK2 plasmid. All plasmids were verified using Hypergeometric Optimization of Motif EnRichment (HOMER) Suite version 4.2. The program findMotifs.pl was run on a regulatory region of 20 kb centred around the TSS and all the other parameters were used as default to detect the significant motifs from their in-house motif library (1865 motifs).

**Western-blot**
Primary antibody against FOXO1a (C29H4) was from Cell Signalling Technology (Danvers, MA, USA). Primary antibody against GAPDH (SG4) was obtained from Hy-Test (Turku, Finland). Protein extracts from human hippocampus were obtained after cell lysis in RIPA buffer and sonication. After determining the protein concentration, twenty micrograms of proteins were resolved on Bis-Tris gels (Invitrogen) and transferred onto nylon membranes. After blocking with 5% non-fat milk in TBS/Tween-20, blots were incubated overnight with the different primary antibodies. After several consecutive washes in TBS/Tween-20, membranes were incubated with anti-rabbit-HRP conjugated secondary antibody (for FOXO1a) or anti-mouse-HRP secondary antibody (for GAPDH) and developed using the Western Lighting Plus-ECL chemiluminescent reagent (Perkin-Elmer).

**Author contributions**
PL and BDS conceived the study, performed data analysis and wrote the manuscript. KB obtained samples from the Netherlands Brain Bank, performed in situ experiments, helped in the nCounter data analysis and the writing of the manuscript under the supervision of JV and DS. RJ and SA performed deep-sequencing data, RNA editing and regulatory analyses. CSF performed real-time PCR and Western-blot experiments. ES performed luciferase assays. SB, RR, DG and HS acquired temporal gyrus samples from the Netherlands Brain Bank and analyzed real-time PCR data. AT collected samples from the London Brain Bank. AS, SP and TA analyzed miR-132-3p targets. TA supervised deep-sequencing experiment. All co-authors provided discussion, data interpretation and contributed to the final version of the manuscript.

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Supporting Information is available at EMBO Molecular Medicine Online.

The authors declare that they have no conflict of interest.

**References**
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