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**MAPT** expression and splicing is differentially regulated by brain region: relation to genotype and implication for tauopathies

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**INTRODUCTION**

The **MAPT** (microtubule-associated protein tau) locus is one of the most remarkable in neurogenetics due not only to its involvement in multiple neurodegenerative disorders, including progressive supranuclear palsy (PSP) (1,2), corticobasal degeneration (CBD) (3), Parkinson’s disease (PD) (4–6) and possibly Alzheimer’s disease (AD) (7,8), but also its genetic evolution and complex alternative splicing—features which are to some extent linked and so all the more intriguing (9–11). Therefore, obtaining robust information regarding the expression, splicing and genetic regulation of this gene within the human brain is of immense importance. In this study, we used 2011 brain samples originating from 439 individuals to provide the most reliable and coherent information on the regional expression, splicing and regulation of **MAPT** available to date. We found significant regional variation in mRNA expression and splicing of **MAPT** within the human brain. Furthermore, at the gene level, the regional distribution of mRNA expression and total tau protein expression levels were largely in agreement, appearing to be highly correlated. Finally and most importantly, we show that while the reported H1/H2 association with gene level expression is likely to be due to a technical artefact, this polymorphism is associated with the expression of exon 3-containing isoforms in human brain. These findings would suggest that contrary to the prevailing view, genetic risk factors for neurodegenerative diseases at the **MAPT** locus are likely to operate by changing mRNA splicing in different brain regions, as opposed to the overall expression of the **MAPT** gene.
The evolution of the MAPT locus has been extensively studied and it is well known that the gene sits within an inversion polymorphism on chromosome 17q21. While the majority of individuals inherit this region in the direct orientation, up to 25% of individuals of European-Caucasian descent have an ≏1.3–1.6 Mb region of linkage disequilibrium (LD) (13). This sequence appears, in Europeans at least, to descend from a single founder (13,14). The common haplotype clades marking the majority and inverted sequences are termed H1 and H2, respectively. It is not clear which of these sequences is the ancestral orientation because the polymorphism exists in other primate species and the rodent sequence is in the H2 orientation (9). It is worth noting that since this inversion polymorphism precludes recombination over a region of ≏1.3–1.6 Mb, haplotype-specific polymorphisms have arisen. Genetic studies, including genome-wide association, have demonstrated the importance of both the inversion polymorphism and haplotype-specific polymorphisms in disease. In fact, two distinct types of disease association have been demonstrated, of which the first is the association of the H1 haplotype with an increased risk of PD (odds ratio ≏1.7) (4–6), PSP (odds ratio 5.5) (1,2) and CBD (odds ratio ≏1.5) (2,15). The importance of tau, the protein product, in neurodegenerative disease was well recognized even before the advent of MAPT genetics. Tau is expressed throughout the adult human central nervous system and tau pathology, namely neurofibrillary tangles, is a notable pathological feature of a range of neurodegenerative disorders, including PSP, CBD (16) and AD (10). Interestingly, detailed investigation has demonstrated that neurofibrillary tangles in different diseases have a different isoform composition, suggesting that splicing is of key importance in the neuropathological process. Whereas the tangles found in PSP and CBD consist predominantly of 4R-tau (due to exon 10 inclusion), those found in AD contain both 3R- and 4R-tau (18,19). Furthermore, consistent with the findings on total tau, we have previously shown that regions of relatively high 4R-tau in PSP are more susceptible to tau-related pathology and neurodegeneration (16,17).

Understanding the expression, splicing and regulation of the mRNA and protein isoforms is of key importance to the field. At present, no robust and coherent study of this type has been performed. In order to address this, we used data from the UK Human Brain Expression Consortium (UKBEC), the largest exon-specific expression data set currently available (20), containing up to 10 distinct brain regions (including hippocampus and substantia nigra) sampled from 134 neuropathologically normal individuals (see details of the brains studied in Table 2 and Supplementary Material, Table S1) (20). In addition, expression QTL analysis was performed to understand the effects of both the H1 and H1c risk haplotypes on MAPT expression and splicing (Table 2). In order to increase statistical power, the latter was performed using a second data set originating from 390 neuropathologically normal individuals from the North American Brain Expression Consortium (NABEC) (see details of the brains studied in Table 2 and Supplementary Material, Table S1) (21).

### RESULTS

#### Regional distribution and splicing of MAPT mRNA expression in human brain

The frontal cortex (FCTX, n = 127), temporal cortex (TCTX, n = 119), occipital cortex (specifically primary visual cortex, OCTX, n = 129), hippocampus (HIPP, n = 122), thalamus (THAL, n = 124), cerebellum (CRBL, n = 130), substantia nigra (SNIG, n = 101), putamen (PUTM, n = 129), medulla (specifically inferior olivary nucleus, MEDU, n = 119) and intralobular white matter (WHMT, n = 131), originating from 134 individuals from the UKBEC, were profiled on 1231 Affymetrix Human Exon 1.0 ST arrays. The regional distribution of

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**Table 1. Semi-quantitative distribution of tangle pathology in human disease**

<table>
<thead>
<tr>
<th>Brain region</th>
<th>Alzheimer’s disease</th>
<th>Progressive supranuclear palsy</th>
<th>Corticobasal degeneration</th>
<th>Parkinson’s disease</th>
</tr>
</thead>
<tbody>
<tr>
<td>FCTX</td>
<td>3</td>
<td>2</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>TCTX</td>
<td>3</td>
<td>1</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>OCTX</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>WHMT</td>
<td>0</td>
<td>1</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>HIPP</td>
<td>3</td>
<td>2</td>
<td>2</td>
<td>2/3</td>
</tr>
<tr>
<td>PUTM</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>0</td>
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<tr>
<td>THAL</td>
<td>2</td>
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<tr>
<td>HYPO</td>
<td>1</td>
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<td>SNIG</td>
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<tr>
<td>MEDU</td>
<td>1</td>
<td>2</td>
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<td>0</td>
</tr>
<tr>
<td>CRBL</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>SPCO</td>
<td>0/1</td>
<td>2</td>
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<td>0</td>
</tr>
</tbody>
</table>

Semi-quantitative description of the distribution of tau pathology within the human brain in AD, PSP, CBD and PD. The data represent average severity of pathology in the following way: 0, none; 1, mild; 2, moderate; 3, severe [Tamas Revesz, derived from references (46–48)].
forms in this tissue (Fig. 2C). Alternate splicing of exon 2 in regions, suggesting higher expression of exon 6 containing iso-
of exon 6 in the cerebellum when compared with other brain tissue. Similarly, there was a relative increase in the expression of exon 2-containing isoforms specifically in this region when compared with other brain regions, suggesting lower expression of exon 2 in white matter all have lower levels of MAPT mRNA.

Regional distribution of MAPT mRNA expression at the gene level is shown in Figure 1. This demonstrated significant regional differences in MAPT mRNA expression with a 1.5-fold difference (paired t-test $P$-value $= 0.05$) between the frontal cortex, the highest MAPT expressing region, and the white matter, the lowest (Fig. 1). Regional differences in MAPT mRNA expression were confirmed on a subset of 12 individuals in 4 brain regions (CRBL, OCTX, PUTM and WHMT) using QuantiGene, which showed a similar pattern [please see Figure 5b in reference (20) for MAPT mRNA expression].

The unique design of the Affymetrix Exon arrays, with probe sets targeted against individual exons, also allowed us to investigate regional differences in MAPT mRNA splicing (alternative splicing $P$-value $< 1 \times 10^{-45}$, Fig. 2C). This demonstrated a relative reduction in the expression of exon 2 in white matter when compared with other brain regions, suggesting lower expression of exon 2-containing isoforms specifically in this tissue. Similarly, there was a relative increase in the expression of exon 6 in the cerebellum when compared with other brain regions, suggesting higher expression of exon 6 containing isoforms in this tissue (Fig. 2C). Alternate splicing of exon 2 in white matter was confirmed by TaqMan assays for 0N (E2$-3$), 1N (E2$+3$) and 2N (E2$+3$) transcripts (Supplementary Material, Fig. S1). These assays demonstrated a selective reduction of exon-2-containing transcripts (2N-tau and 1N-tau) in white matter, whereas 0N-tau isoforms, which do not contain exon 2 or 3, were unchanged between the selected regions.

Regional distribution of MAPT mRNA expression in human brain

The relationship between mRNA and protein expression is complex. However, establishing that relationship for MAPT is critical in interpreting reported expression quantitative trait loci, which have largely depended on mRNA expression levels alone. We assessed the regional variability in total tau protein expression levels in 5 brain regions (CRBL, FCTX, OCTX, PUTM and WHMT) in 12 individuals (Fig. 3A and B). This analysis showed that the frontal cortex has the highest tau protein levels with decreasing levels in the following order: frontal cortex > occipital cortex > white matter > putamen > cerebellum. Cerebellar tau protein levels were significantly lower than all other regions examined (Fig. 3B, $P < 0.01$) and tau protein levels in the putamen were significantly lower than the frontal cortex and occipital cortex ($P < 0.05$). These findings are largely in agreement with our mRNA expression results which showed that cortical regions express MAPT at the highest levels and the cerebellum, putamen and white matter all have lower levels of MAPT mRNA.

The levels of each individual isoform of tau protein were determined relative to total tau protein level for the same sample (Fig. 3C–H). We found 1N-tau protein isoforms formed the majority of total tau (~50%), followed by 0N-tau isoforms (~40%) with 2N-tau isoforms forming the lowest proportion of tau (~10%), and levels of 3R-tau and 4R-tau isoforms were approximately equal, in agreement with previous studies (22). Protein levels of the smallest tau isoform, 0N3R, were significantly lower in the cerebellum ($P < 0.05$) compared with other brain regions, but other tau isoforms were not found to vary significantly between brain regions. We also measured 3R- and 4R-tau protein levels in the same samples using sandwich ELISA assays (17,23). Both 3R- and 4R-tau are lowest in the cerebellum and white matter reflecting total transcript levels (Supplementary Material, Fig. S2). In conclusion, whereas MAPT gene-level expression and total tau protein expression follow similar trends between brain regions, the relationship between mRNA and protein isoforms could not be determined.
The effect of the H1/H2 haplotypes on MAPT mRNA expression and splicing

Previous studies have demonstrated the effects of the H1/H2 haplotypes on MAPT mRNA expression (6,21,24,25). However, there are large numbers of haplotype-specific polymorphisms at the MAPT locus (both SNP and insertion deletion polymorphisms), some of which have only recently been identified, and since expression probes have largely been designed against the H1 haplotype, these polymorphisms may have created false expression QTL results (26). This can occur because mRNA sequences transcribed from the H2 haplotype will depart from the H1 reference, due to both the presence of different nucleotides (i.e. SNPs) and the presence or absence of nucleotides (i.e. indels), and so are likely to exhibit a weaker binding affinity for the probes in question, which are a perfect match for mRNA sequences transcribed from the H1 haplotype. These polymorphisms may have created false expression QTL results (26). This can occur because mRNA sequences transcribed from the H2 haplotype will depart from the H1 reference, due to both the presence of different nucleotides (i.e. SNPs) and the presence or absence of nucleotides (i.e. indels), and so are likely to exhibit a weaker binding affinity for the probes in question, which are a perfect match for mRNA sequences transcribed from the H1 haplotype. These polymorphisms may have created false expression QTL results (26).

The most significant expression QTL identified was between SNP chr17:44357157 and exon 3 (Affymetrix probe set 3723712). Since this SNP is in strong LD with SNPs that tag the H1/H2 haplotypes, we used the better known H1/H2 tagging SNP, rs17665188 ($R^2 = 0.93$ with chr17:44357157) to demonstrate the effect of the H2 haplotype on exon 3 expression (as detected by Affymetrix probe set 3723712). The H2 haplotype was associated with higher expression of exon 3 in all brain regions (aveALL $P$-value $= 5.2 \times 10^{-13}$) except white matter (Fig. 4). The most significant association was observed in the frontal cortex ($P$-value $= 8.8 \times 10^{-9}$). In contrast to the alternate splicing of exon 10, the alternate splicing of exons 2 and 3, and more specifically the role of exon 3 has not been extensively studied. However, our data refine a previous report using cell lines (27) which suggested that H2 was associated with increased inclusion of exons 2 and 3, although we do not observe the former ($P > 1 \times 10^{-2}$ for all tissues for exon 2, as measured by Affymetrix probe set 3723710).

The effect of the H1c haplotype (tagged by rs242557) on MAPT mRNA expression

Although ideally we would have liked to determine the effect of the H1c haplotype on both MAPT mRNA expression and splicing, we were insufficiently powered to run such a conditional analysis using the available exon-specific expression data generated using the Affymetrix exon arrays (UKBEC...
Therefore, in order to address this issue, we used expression data originating from 390 individuals (frontal the cortex and cerebellum samples only) generated by the North American Brain Expression Consortium using the Illumina HumanHT-12 v3 Expression BeadChips. This Illumina expression array contains four probes mapping to the \textit{MAPT} gene, of which only two are robustly detected in human brain, ILMN\_2310814 and ILMN\_1710903. As previously
of the H1/H2 and H1c haplotypes on MAPT mRNA expression and splicing are as accurate as possible. Thus, we have been able to demonstrate, firstly, the significant regional variation in MAPT mRNA expression and splicing, validated using Quantigene and TaqMan assays, and secondly that at the gene-level MAPT mRNA expression and total tau protein are highly correlated. Finally and most importantly, we have shown that while the effect of the reported H1/H2 effect on MAPT mRNA gene-level expression is likely to be a technical artefact, this polymorphism is associated with the expression of exon 3-containing isoforms in human brain. These findings would suggest that contrary to the present, prevailing view genetic risk factors for neurodegenerative diseases at the MAPT locus are likely to operate by changing the balance of mRNA splicing in different brain regions, as opposed to the overall expression of the MAPT gene.

Profiling mRNA and protein expression in human brain demonstrated significant regional variation. We found that MAPT mRNA expression was 2.0-fold higher in the neocortex, when compared with white matter and cerebellum. Total tau protein expression level had a similar regional pattern of expression to that for mRNA. Since the frontal and temporal cortices are among the brain regions most affected by tangle pathology in AD, these findings support the concept that despite high ubiquitous expression of MAPT in the human brain, regional variation in basal MAPT expression might predispose some brain regions to tangle pathology and explain the regional specificity of disease in AD at least.

Analogous profiling of MAPT mRNA splicing and protein isoform expression was more complex. While we were able to demonstrate region-biased splicing of exon 2 containing mRNA isoforms and validate these findings using TaqMan assays, we were unable to replicate this observation at the protein level. The only significant regional difference in tau protein isoform expression was the reduced levels of ON3R in the cerebellum when compared with other regions. This finding is in agreement with previous studies that have observed decreased ON3R in the cerebellum of control (22) and PSP (28) patients. However, the absence of any clear relationship between mRNA splicing and tau protein isoform production is difficult to interpret. One possible reason for this is that altered splicing of exon 2 would be ‘shared’ across four tau protein isoforms (1N3R, 1N4R, 2N3R and 2N4R), thus a sizeable change would be needed to allow detection by a semi-quantitative technique such as western blotting.

Finally and most importantly, we investigated the effects of the H1/H2 and H1c haplotypes on MAPT mRNA expression and splicing. In the case of the former, we had sufficient statistical power to use the exon-specific and region-wide expression data provided by the UK Human Brain Expression Consortium. Thus, we were able to assess for the first time the effect of the H1/H2 inversion polymorphism on MAPT splicing, and do this in 10 brain regions (including highly clinically relevant regions such as the hippocampus and substantia nigra). These data show that the under-represented, protective H2 haplotype is associated, in all grey matter brain regions, with more expression of exon 3 and that this effect is most prominent in cortical regions. This finding is consistent with previous allele-specific expression studies (27).

DISCUSSION

This study, based on multiple analyses with a minimum of 780 brain samples used in any single analysis (originating from 390 individuals), provides the most robust and coherent information on the regional mRNA expression, splicing and regulation of MAPT available to date. Rigorous quality-control steps have been used to ensure that, in particular, the effects described, in order to avoid the detection of false QTLs arising from the presence of genetic polymorphisms within the probe sequences used for MAPT mRNA expression detection, we checked both Illumina probes for SNPs and indels using the most recent release of the 1000 Genomes Project (March 2012: Integrated Phase I haplotype release version 3). This rigorous quality-control process allowed us to identify a 2 bp deletion (rs67759530, MAF = 23% in Europeans) in the target sequence of Illumina probe, ILMN_1710903, specifically within the MAPT H2 haplotype.

However, removal of H2 haplotype-carrying individuals did allow us to use data generated by both MAPT probes to investigate the effects of rs242557 in the remaining 222 H1/H1 individuals. This SNP defines the H1c sub-haplotype within the H1 clade and has also been shown to be a significant risk SNP for PSP (risk allele = A, P-value = 9.5 x 10^{-18} from the relevant GWAS) (2). In fact, we found that the H1c haplotype (tagged by rs242557) was not significantly associated with increased mRNA expression of MAPT, as measured with Illumina probes ILMN_1710903 (P = 0.957 in the frontal cortex, P = 0.825 in the cerebellum) and ILMN_2310814 (P = 0.975 in the frontal cortex, P = 0.768 in the cerebellum).

Figure 4. The effect of the H1/H2 haplotypes (tagged by rs17665188) on the expression of MAPT exon 3: MAPT exon 3 expression (Affymetrix probe set 3723712) stratified by genotype at rs17665188 in 134 brain samples for 10 brain regions. Increased exon 3 expression was associated with the homozygous major allele (CC). A similar association pattern was observed in all brain regions except for white matter (P < 0.03).
no association was seen in white matter, where in fact there was a trend in the opposite direction ($P = 0.03$). These data suggest that the inclusion of exon 3 in grey matter is protective in PSP, CBD and PD. Since several physiological roles for the amino-terminal inserts coded by exons 2 and 3 have been suggested, these might help explain this finding. For example, it has been suggested that the amino-terminal inserts could regulate the spacing between microtubules (29,30). Alternatively, has been suggested that the amino-terminal inserts could regulate the spacing between microtubules (29,30). Alternatively, since the amino-terminal region of tau has also been shown to interact with the plasma membrane where it can, in turn, interact with src-family kinases, it could be involved in signal transduction (31,32). Moreover, it has been recently shown that the exon 2- and 10-encoded inserts increase aggregation propensity, whereas the exon 3-encoded insert decreases aggregation (33). The latter could in part explain the protective function of H2 with its increased inclusion of exon 3. Interestingly, this function has recently been shown to be important in mediating amyloid-beta toxicity in a mouse model of AD (34).

Although we would have liked to run a similar exon-specific analysis to investigate the effects of the H1c haplotype (tagged by rs242557) on $\text{MAPT}$ expression, the sample numbers available within the UK Human Brain Expression Consortium were insufficient ($n = 74$). Consequently, we used brain mRNA expression data (the frontal cortex and cerebellum) generated from the Illumina HT12-v3 Expression Beadchips and provided by the North American Brain Expression Consortium ($n = 222$). Using the most recent release of the 1000 Genomes project (Interim phase I haplotypes, June 2011), quality-control procedures identified a 2-bp deletion (rs67759530) in the target sequence of ILMN_1710903 within the H2 haplotype. It is now well recognized that such sequence polymorphisms can result in hybridization artefacts, which in turn cause reporting of false cis-acting expression QTLs (35,36). Since the signals produced by Illumina probe, ILMN_1710903, in mixed H1/H2 sample sets are responsible for the widely reported cis-acting $\text{MAPT}$ expression QTL (characterized by lower expression of $\text{MAPT}$ in H2 individuals) (6,21,24), this finding, combined with our own inability to replicate such a result using a different platform, would suggest that this gene-level mRNA expression QTL is a technical artefact. However, restricting our analysis to H1 homozygotes, we were still able to use this powerful data set to explore the impact of the H1c haplotype on gene expression. Unfortunately, this analysis did not demonstrate a significant association between the H1c haplotype (tagged by rs242557) and $\text{MAPT}$ mRNA expression, as measured with Illumina probes ILMN_1710903 and ILMN_2310814. This does not preclude the possibility that this haplotype could affect $\text{MAPT}$ mRNA splicing.

In summary, in this paper, we use the largest exon-specific and gene-level human brain expression data sets available to study the regional expression, splicing and regulation of $\text{MAPT}$ mRNA. In addition, for providing valuable baseline information regarding regional differences in $\text{MAPT}$ mRNA and protein isoform expression, we demonstrate the importance of exon-specific analyses in the study of neurodegenerative diseases. We found that the H1/H2 inversion polymorphism was associated with the expression of exon-3-containing mRNA transcripts, not gene-level expression. While recognition of this underlying complexity may complicate studies, it is a necessary complication, which may hold the key to explaining how a single locus can give rise to at least four human diseases, all with distinct clinical and pathological features.

### MATERIALS AND METHODS

#### Collection and dissection of post-mortem human brain tissue analysed using Affymetrix Exon 1.0 ST Arrays

Brain and CNS tissue originating from 134 control individuals was collected by the Medical Research Council (MRC) Sudden Death Brain and Tissue Bank, Edinburgh, UK (37), and the Sun Health Research Institute (SHRI) an affiliate of Sun Health Corporation, USA (38). In all cases, control status was confirmed by histology performed on sections prepared from paraffin-embedded brain tissue blocks and the diagnosis was determined by a consultant neuropathologist. A detailed description of the samples used in the study, tissue processing and dissection is provided in Trabzuni et al. (20). All samples had fully informed consent for retrieval and were authorized for ethically approved scientific investigation (Research Ethics Committee number 10/H0716/3).

#### RNA isolation and processing of brain samples analysed using Affymetrix Exon 1.0 ST Arrays

Total RNA was isolated from human post-mortem brain tissues using the miRNeasy 96-well kit (Qiagen, UK). The quality of total RNA was evaluated by the 2100 Bioanalyzer (Agilent) and RNA 6000 Nano Kit (Agilent) before processing with the Ambion® WT Expression Kit and Affymetrix GeneChip Whole Transcript Sense Target Labeling Assay, and hybridization to the Affymetrix Exon 1.0 ST Arrays following the manufacturers’ protocols. Hybridized arrays were scanned on an Affymetrix GeneChip® Scanner 3000 7G and visually inspected for hybridization artefacts. Further details regarding RNA isolation, quality control and processing are reported in Trabzuni et al. (20).

#### Analysis of Affymetrix Exon Array Data

All arrays were pre-processed using RNA quantile normalization with background correction and probe set summarization with median polish in Affymetrix Power Tools 1.14.3 (http://www.affymetrix.com/partners_programs/programs/developer/tools/powertools.affx). After re-mapping the Affymetrix probe sets onto human genome build 19 (GRCh37) as documented in the NetAffx annotation file (HuEx-1.0-st-v2 Probe set Annotations, Release 31), we restricted analysis to 294 943 probe sets that: (i) had gene annotation, (ii) contained at least three probes, (iii) were unaffected by SNPs both genotyped and imputed on the basis of 1000 Genomes Release (May 2011), and (iv) uniquely hybridized. Since most exons are represented by only one probe set, we used the probe set signal intensity as a synonym of exon expression level, unless explicitly mentioned. The transcript-level expression for 23 960 genes was estimated using the 90% Winsorized mean of the corresponding probe sets. Regional differences in gene-level expression and splicing were investigated using Partek’s mixed-model ANOVA and
alternative splicing ANOVA, which looks for a significant interaction between brain region and exon-specific expression (Partek Genomics Suite v6.6). In all analysis, we corrected for gender and batch effects [date of hybridization and brain bank), as investigated in detail (20)].

Direct RNA quantification with branched DNA, QuantiGene® 2.0 Assay
CRBL, OCTX, PUTM and WHMT samples from 12 individuals were analysed using the QuantiGene® (QG) platform for validation of exon array results. We selected RPLP0 and UBC as housekeeping genes as they showed relatively low variability in expression levels (i.e. low coefficient of variation) in all brain regions in our data set (20).

Quantitative RT–PCR
MAPT gene expression for CRBL, OCTX and WHMT was quantified by TaqMan real-time PCR (Invitrogen, UK). The MAPT transcript-specific assays used were Hs00902188, Hs00902978 and Hs00902314 (Invitrogen). Real-time quantification was carried out on the Stratagene MX3000P system. All runs were performed in technical triplicates and were normalized to the geometric mean of three housekeeping genes, PPIA, BACT and HPRT. The relative expression values were calculated using the ΔΔCT method.

Collection, RNA isolation and processing of brain samples analysed using Illumina Human HT-12 v3 expression BeadChip arrays
Cerebellar and frontal cortex samples originating from 390 control individuals were collected as previously described (6,21,39). It is worth noting that 85 individuals had also been analysed as part of the Affymetrix exon array data set. Total RNA was extracted from sub-dissected samples (100–200 mg) of human post-mortem brain tissue using either Qiagen’s miRNeasy Kit (Qiagen) or using a glass-Teflon homogenizer and 1 ml TRIzol (Invitrogen, Carlsbad, CA, USA) according to the manufacturers’ instructions. RNA was biotinylated and amplified using the Illumina® TotalPrep-96 RNA Amplification Kit and directly hybridized onto HumanHT-12 v3 Expression BeadChips (Illumina Inc., USA) in accordance with the manufacturer’s instructions.

Analysis of Illumina HT-12 v3 expression BeadChip Array Data
Expression data were analysed using the Gene Expression Module 3.2.7 within Illumina® BeadStudio. Raw intensity values for each probe were transformed using the cubic spline normalization method and then log2 transformed for mRNA analysis. We re-mapped the annotation for probes according to ReMOAT (40) on the human genome build 19 and then restricted the analysis to genes that were reliable, uniquely hybridized and were associated with gene descriptions. In our analysis, we used analysed data generated by the following two probes: ILMN_1710903 and ILMN_2310814.

DNA extraction, genotyping and imputation
Genomic DNA was extracted from sub-dissected samples (100–200 mg) of human post-mortem brain tissue using either Qiagen’s DNeasy Tissue Kit (Qiagen) or standard phenol–chloroform DNA extraction protocol. Genotyping was performed using the Illumina Infinium Omni1-Quad BeadChip or Illumina Infinium HumanHap550 v3 (Illumina). In the case of samples analysed on the Affymetrix exon arrays, genotyping was also performed using the ImmunoChip, a custom genotyping array designed for the fine-mapping of auto-immune disorders (6). In all cases, the BeadChips were scanned using an iScan (Illumina) with an AutoLoader (Illumina). GenomeStudio v.1.8.X (Illumina) was used for analysing the data and generating SNP calls. After standard quality controls, both genotype data sets were combined and imputed using MaCh (41,42) and minimac (http://genome.sph.umich.edu/wiki/Minimac) using the 1000 Genomes (Interim phase I haplotypes, June 2011). We used the resulting ~5.8 million SNPs with good post-imputation quality (Rsq > 0.50) and MAF of at least 5% in subsequent analyses. The selection of individuals with the H1/H1 status was based on SNPs rs1800547 and rs1052553.

Expression QTL analysis
We tested the association between given SNPs and expression profiles using the R package MatrixEQTL (http://www.bio.unc.edu/research/genomic_software/Matrix_eQTL/) and Revolution R (43). We assumed an additive genetic model for each SNP (1 degree-of-freedom trend test) without additional covariates.

Protein extraction and western blot analysis
Brain tissue was homogenized in 10 mM Tris–HCl (pH 7.4), 0.8 M NaCl, 1 mM EDTA, 10% sucrose and protease inhibitor tablets (Roche). Homogenates were clarified by centrifugation at 10 000g (av) for 10 min at 4°C prior to aliquoting and storage at −80°C. Protein concentrations were measured by BCA assay and equal amounts of protein were dephosphorylated using λ protein phosphatase (NEB) as described previously (44). Briefly, proteins were incubated with λ protein phosphatase at a final concentration of 40 U/μl for 3 h at 30°C. Dephosphorylation reactions were stopped by the addition of LDS buffer (Invitrogen) followed by heating at 100°C for 10 min. Samples were centrifuged at 10 000g (av) prior to separation on 10% Bis–Tris gels alongside recombinant tau protein ladder (Sigma). Proteins were transferred to nitrocellulose membrane and probed with rabbit polyclonal antibody to total tau (DAKO) and mouse monoclonal to actin (Sigma). Blots were visualized and quantified using an Odyssey Infrared imaging system (LI-COR Biosciences). The levels of total tau in each brain region were normalized to actin, and the levels of individual tau isoforms were calculated as a percentage of total tau for the same sample.

Tau isoform sandwich ELISA
Sandwich ELISAs for 3R- and 4R-tau were carried out as previously described (17). Briefly, microtitre plates were coated
with 150 μl of 10 μg ml$^{-1}$ of capture antibody (RD3 or RD4) (45) in coating buffer (150 μl, sodium tetraborate buffer, pH 9.4). The plate was washed and 150 μl of diluted buffer was added into the plate after which 25 μl of diluted supernatants obtained from the brain homogenates (1 in 1000 and 1 in 150 for 3R- and 4R-tau ELISAs, respectively) were added in duplicates to the blocked plates previously coated with RD3 or RD4 antibodies. The plates were incubated at RT for 2 h, washed and 150 μl affinity-purified sheep anti-tau-HRP conjugates, diluted to 1 in 1000 and 1 in 3500 for 3R- and 4R-tau assays, was added, respectively, and incubated for 1 h on a shaker. After washing, the plates were developed with tetramethylbenzidine substrate as previously described. The isoform composition in each sample region is expressed as ng per mg of total brain protein.

**SUPPLEMENTARY MATERIAL**

Supplementary Material is available at HMG online.

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