Supporting Information

Kauwe *et al.* 10.1073/pnas.0801227105

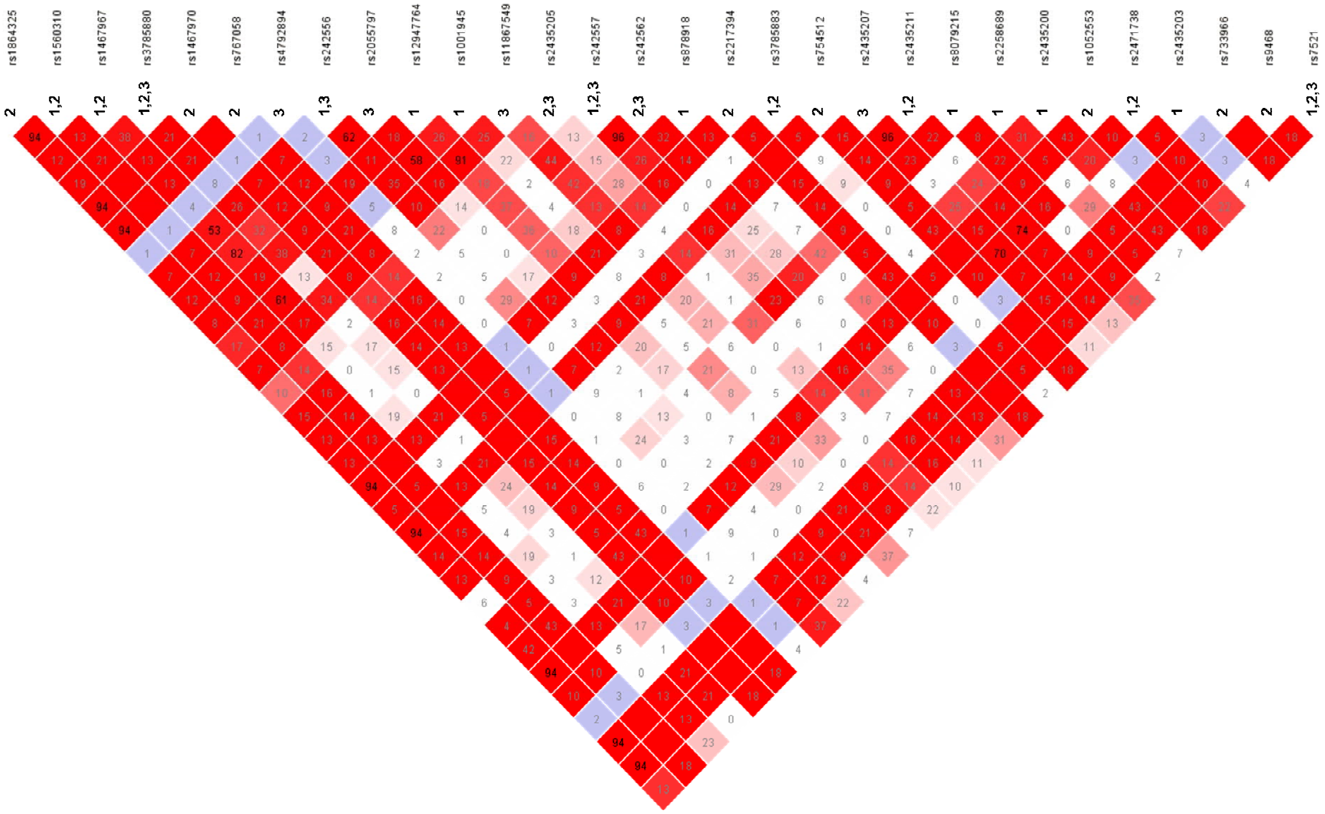

Fig. S1. LD plot of MAPT SNPs using CEPH data from HapMap. Coloring is the default D prime color scheme from Haploview. r^2 values are shown. This plot shows the overlap of SNPs between this study, the study by Pittman *et al.* (1), and the study by Rademakers *et al.* (2). SNPs from HapMap which are included in this manuscript are labeled with a ''1.'' SNPs from the Pittman *et al.* (1) manuscript are labeled with a ''2.'' SNPs from the Rademakers *et al.* (2) manuscript are labeled with a ''3.''

1. Pittman AM, *et al.* (2005) Linkage disequilibrium fine mapping and haplotype association analysis of the tau gene in progressive supranuclear palsy and corticobasal degeneration. *J Med Genet* 42:837–846.
2. Rademakers R, *et al.* (2005) High-density SNP haplotyping suggests altered regulation of tau gene expression in progressive supranuclear palsy. *Hum Mol Genet* 14:3281–3292.

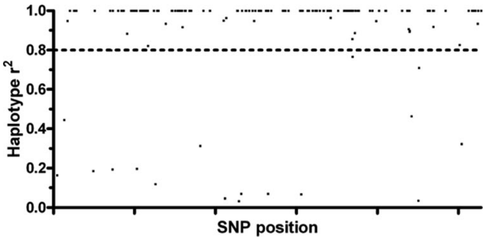

Fig. S2. *MAPT* diversity captured by our set of 21 tagging SNPs. Using CEPH data, we analyzed the maximum r^2 between each *MAPT* SNP in HapMap and our set of tagging SNPs in Haploview [Barrett JC, Fry B, Maller J, Daly MJ (2005) Haploview: Analysis and visualization of LD and haplotype maps. *Bioinformatics* 21:263–265.]. The *y* axis is the greatest r^2 between the SNP loci in HapMap and our tagging SNPs. The *x* axis is each SNP in HapMap sorted by position from the 5′ end of the *MAPT* gene. Of the 252 SNPs in HapMap 232 (92%) had an r^2 of >0.80 with one of our tagging SNPs. Just seven of the SNPs with an $r^2 < 0.8$ have a minor allele frequency >0.10.