**Methods S1.**

# *Expression quantitative trait loci (eQTL) analysis*

We identified alias rsIDs for our significant SNPs at the *TP53INP1* and *IGHV1-67* loci using SNAP[1]. Further proxy SNPs in linkage disequilibrium (r2>0.8) were identified in the HapMap 1000 Genomes build (CEU population) with SNAP. SNP rsIDs and aliases were searched for primary SNPs and LD proxies against a collected database of expression SNP (eSNP) results, focusing only on brain tissue datasets. The collected eSNP results met criteria for statistical thresholds for association with gene transcript levels as described in the original papers.

Brain tissue results sources included the following: cortex [2–4], pre-frontal cortex [5–7], parietal lobe [8], frontal cortex [6,9], temporal cortex [4,6,9], hippocampus [6], thalamus [6], pons [9], cerebellum [4,6,8,9], and 3 additional large studies of brain regions including prefrontal cortex, visual cortex and cerebellum in Alzheimer’s disease cases and normal controles [10]. Additional eQTL data was integrated from ScanDB ([www.scandb.org](http://www.scandb.org)). Cerebellum and parietal lobe eQTL data was downloaded from ScanDB and cis-eQTLs were limited to those with P<1.0E-6 and trans-eQTLs with P<5.0E-8.

# *Methylation quantitative trait loci (meQTL) analysis*

Index SNPs and proxies were queried against previously published methylation QTLs (meQTLs). The meQTLs originated from cerebellum [9,11], frontal cortex [9], temporal cortex [9], and pons [9].

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