ABSTRACT: Background: It has been shown that mRNA levels of many human transcripts are under genetic control. We postulate that some Alzheimer’s disease (AD) susceptibility variants confer disease risk via influencing gene expression in the brain. If correct, such variants will associate with both mRNA levels in the brain and disease risk. **Objective:** To investigate cis-SNP/mRNA level associations of 13 AD candidate genes in the cerebellum and temporal cortex of pathologically-confirmed AD patients and controls with other neurologic diseases. **Methods:** Using quantitative PCR, we measured mRNA levels of 13 AD candidate genes in the cerebellum of 197 AD patients vs. 177 non-AD controls, and in the temporal cortex of 184 ADs vs. 185 non-ADs. We obtained cis-SNP genotypes that reside within the genes’ 5’/3’ flanking regions from the genome-wide association study of these subjects performed on the Illumina Human1M platform (Carrasquillo et al., 2009). The cis-SNP/mRNA associations for each brain region and diagnostic group were obtained via multivariate linear regression analyses within PLINK, using age, gender, and APOE genotypes as covariates. When cases and controls were analyzed together, diagnosis was also included as an additional covariate. **Results:** There were 256 cis-SNP/mRNA associations detected in the cerebellum of ADs vs non-ADs and 247 in the combined group with nominal p-values of 0.05 to 3.06x10^-10. There were 164 cis-SNP/mRNA associations detected in the temporal cortex of ADs, 178 in non-ADs and 191 in the combined group with nominal p-values of 0.05 to 2.14x10^-9. There were 7 genes with cis-SNP/mRNA associations in the ADs with nominal p<0.01 in both the cerebellum and the temporal cortex, and consistent direction of association with the minor allele. There were 3 such genes detected in the controls and five in the combined groups. Comparison of cis-SNP/mRNA associations in the ADs vs. non-ADs vs. combined ADs+non-ADs, revealed consistent associations in 4 genes in the cerebellum, where IDE cis-SNP/mRNA associations were the strongest and reached genome-wide significance in the ADs and combined subjects. Our findings on IDE cis-SNP/mRNA associations in the cerebellum and temporal cortex are published (Zou et al., 2010). In the temporal cortex, two genes showed consistent and nominally significant associations in ADs, non-ADs and combined ADs+non-ADs. Although not reaching study-wide significance after stringent Bonferroni correction, the strongest cis-SNP/mRNA association in the temporal cortex occurred for GSTO2 previously implicated in AD as a candidate gene (Li et al., 2003) that may harbor e-SNPs with influence on its expression in the brain (Webster et al., 2009). **Conclusions:** These results suggest that there may exist variants in AD candidate genes that influence brain gene expression. Some of these variants appear to have brain-region and disease-specific effects whereas others may be more ubiquitous. Our top cis-SNP/mRNA hit in the temporal cortex, GSTO2, merits additional follow-up studies based on our data and previous publications to further delineate the role of GSTO2 e-SNPs in brain gene expression and AD risk. (*Equal contribution*).