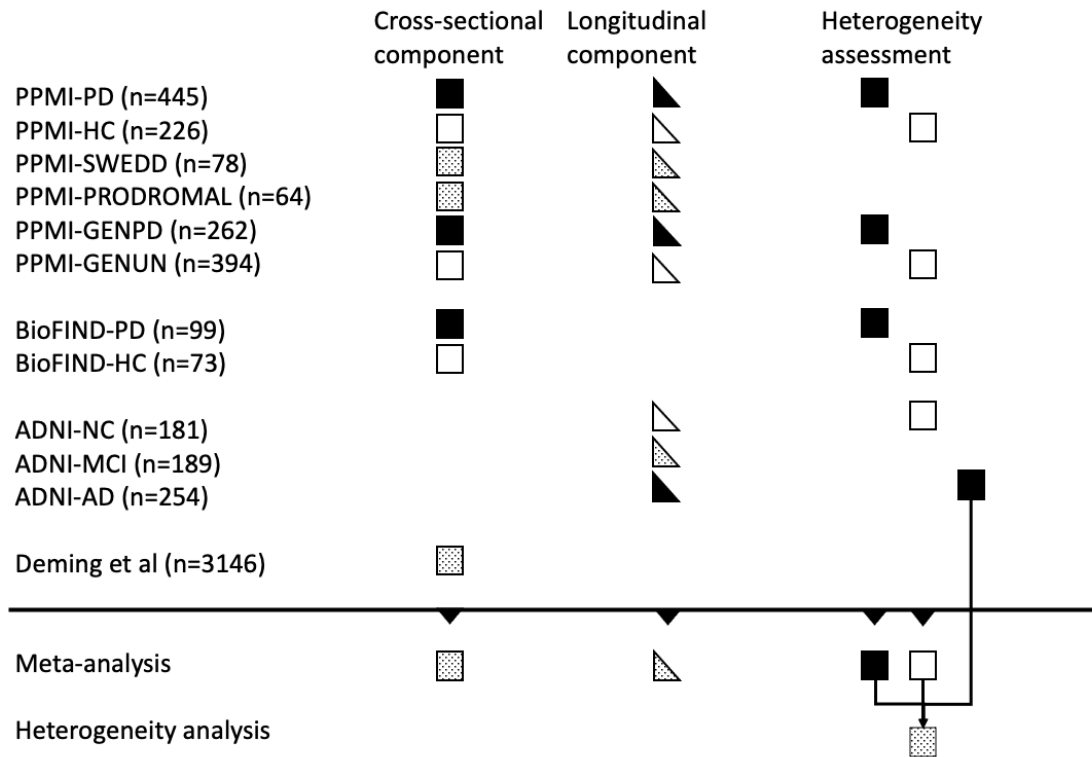


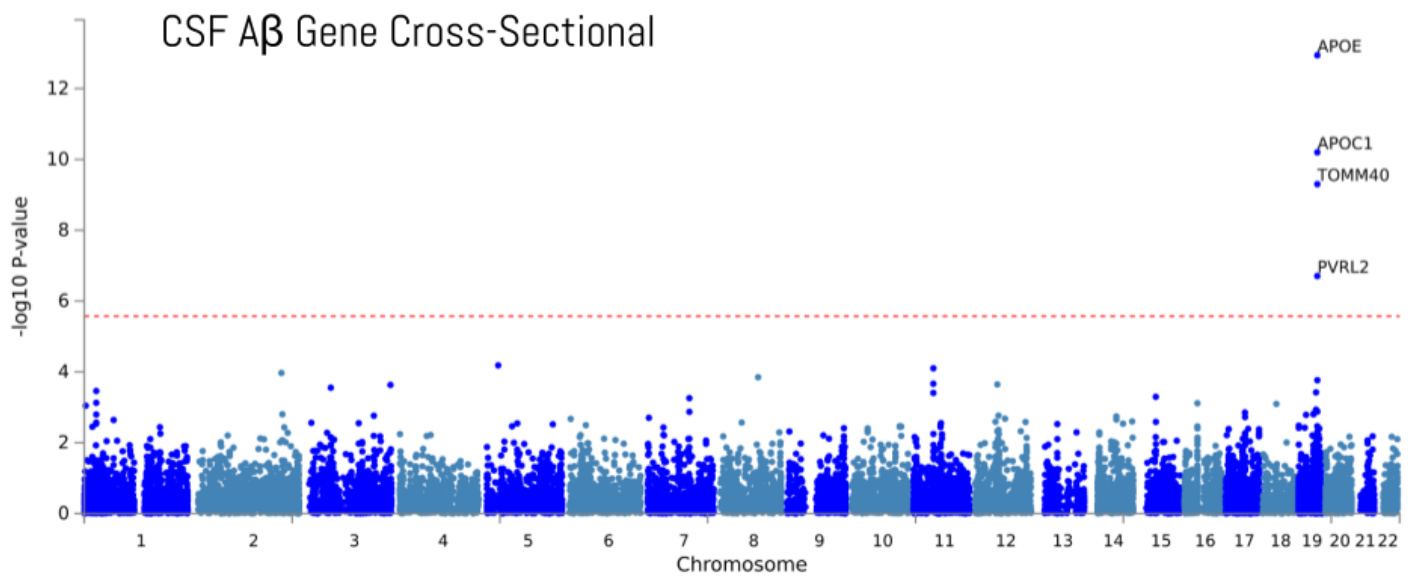
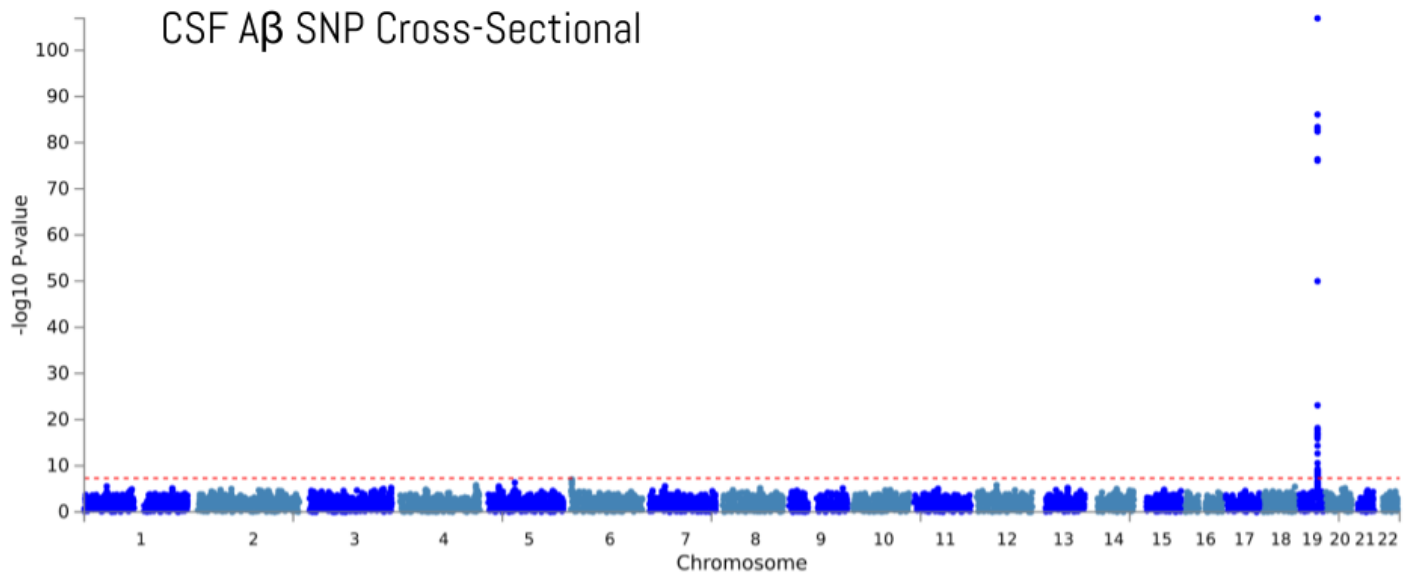
# Supplemental Figure 1. Analysis overview



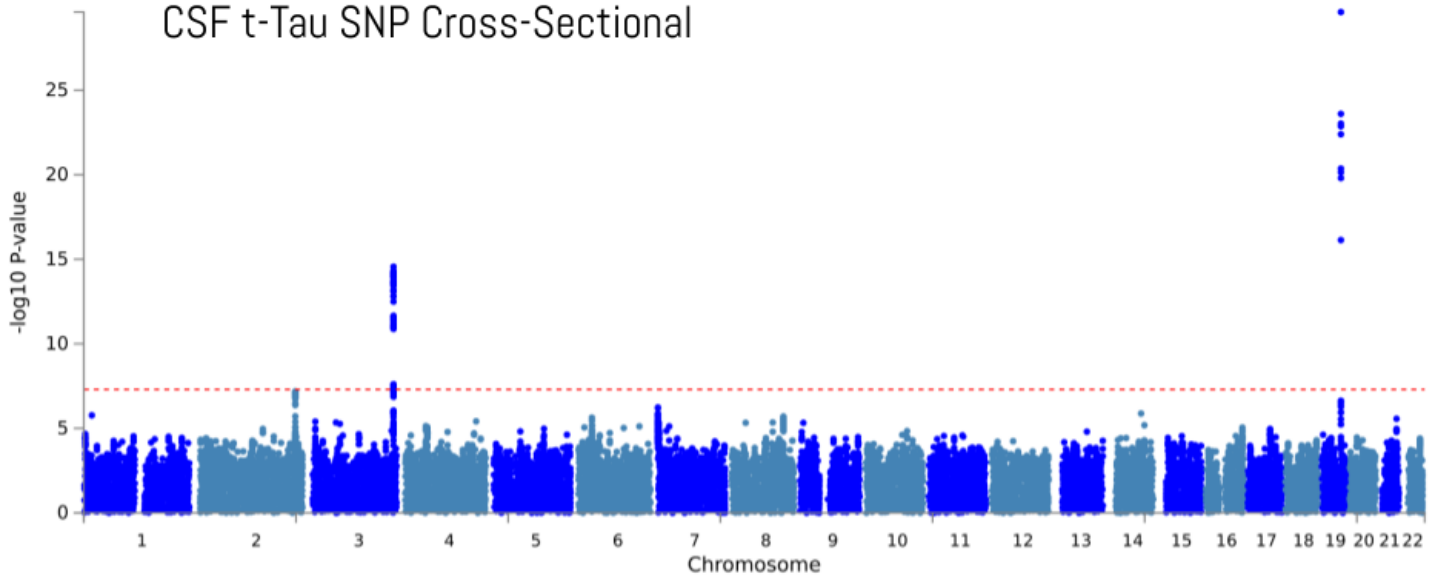
Individual arms were analyzed separately and then meta-analyzed. Squares represent the cross-sectional component analysis results while the triangles represent the longitudinal component (change over time) analysis results. The disease groups (either with Parkinson's disease or Alzheimer's disease) were filled with black while non-disease groups were unfilled. Dotted fills indicate the results from those with mixed/non-typical diseases. As shown in the reverse triangles we meta-analyzed cross-sectional component GWAS results and longitudinal component GWAS results retrospectively. In the heterogeneous analyses, we first meta-analyzed GWAS results per disease status for PD and HCs and then compared them.

PPMI, Parkinson's Progression Marker Initiative; BioFIND, the Fox Investigation for New Discovery of Biomarkers; ADNI, the Alzheimer's Disease Neuroimaging Initiative; PPMI-PD, PD patients in the PPMI study; PPMI-HC, healthy controls in the PPMI study; PPMI-SWEDD, those with scans without evidence of dopaminergic deficit in the PPMI study; PPMI-PRODROMAL, those with prodromal symptoms such as hyposmia, REM sleep behavior disorder, and image confirmed dopaminergic deficit in the PPMI study; PPMI\_GENPD, GBA/LRRK2/SNCA variant carriers of PD with Parkinson's disease; PPMI-GENUN, the unaffected GBA/LRRK2/SNCA variant carriers without PD; BioFIND-PD, cases in moderately advanced stages (BioFIND\_PD) in the BioFIND study; BioFIND-HC, healthy controls in the BioFIND study. ADNI-AD, those with dementia, (ADNI-AD) in the ADNI study; ADNI-MCI, those with mild cognitive impairment; and ADNI-NC, those with normal cognition (ADNI-NC).

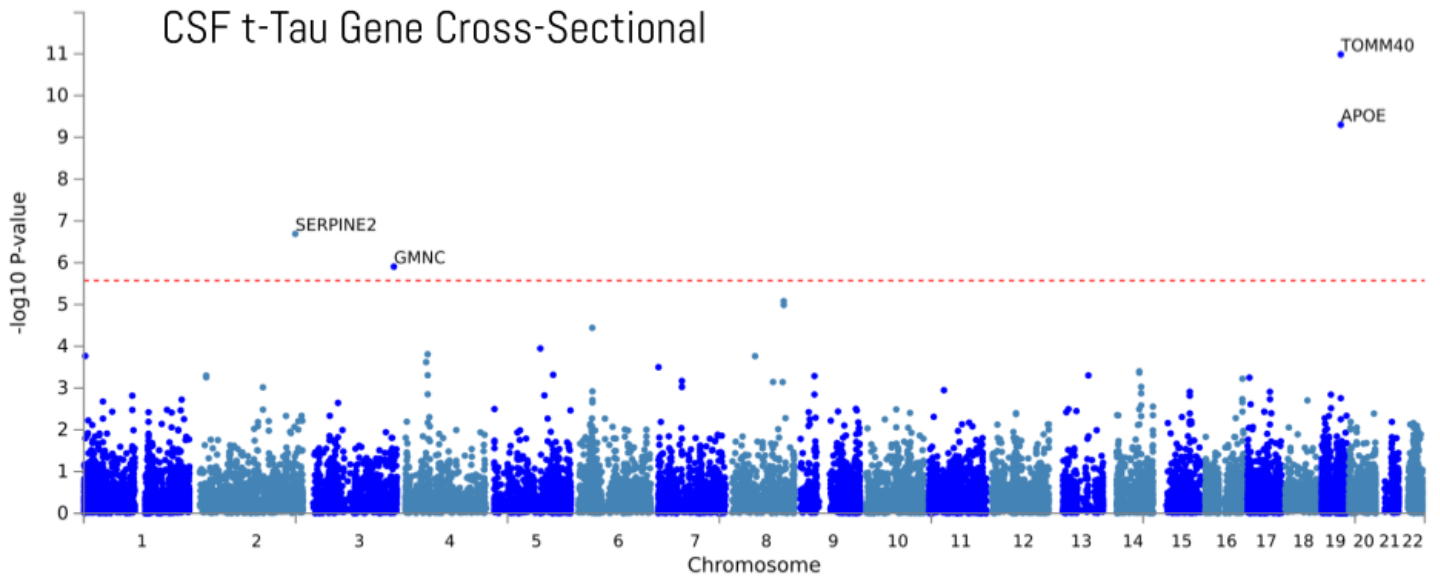
# Supplemental Figure 2. GWAS results for cross-sectional component



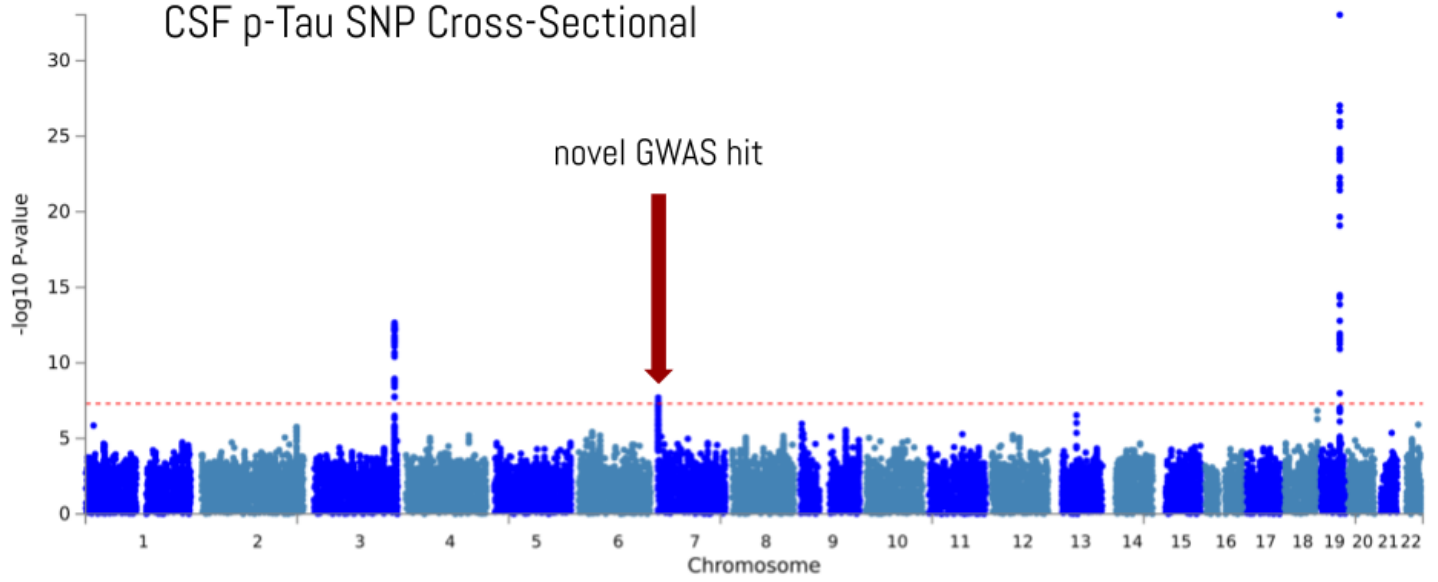
### CSF t-Tau SNP Cross-Sectional



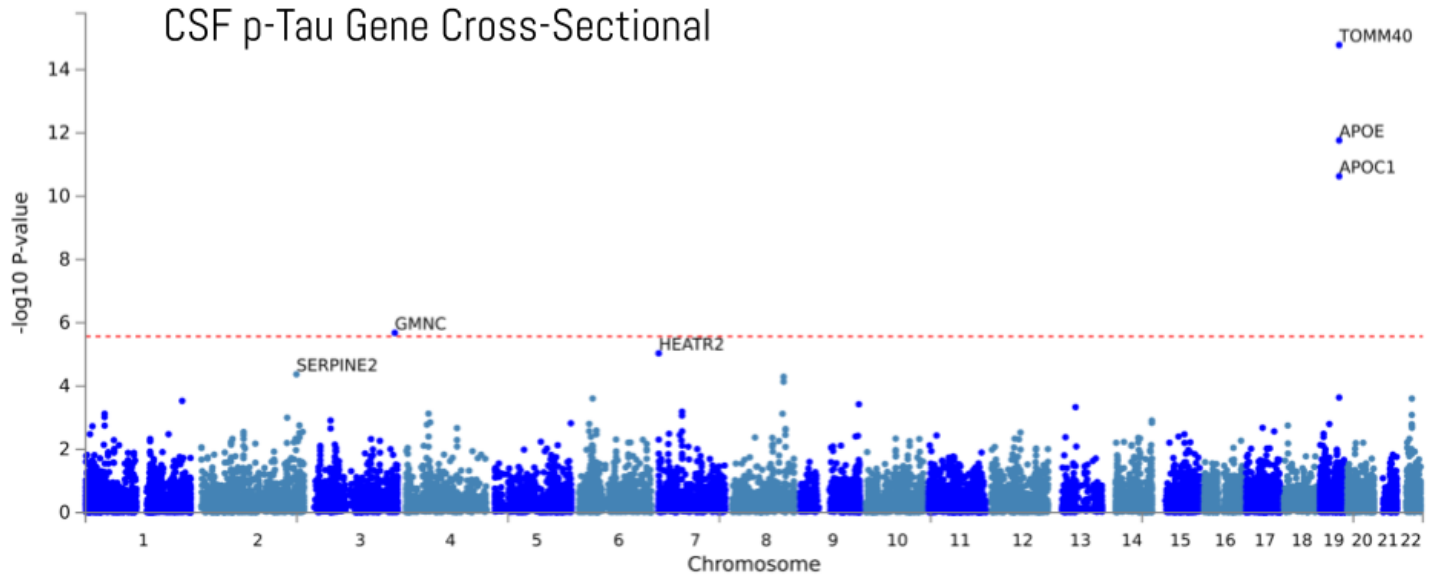
### CSF t-Tau Gene Cross-Sectional



### CSF p-Tau SNP Cross-Sectional

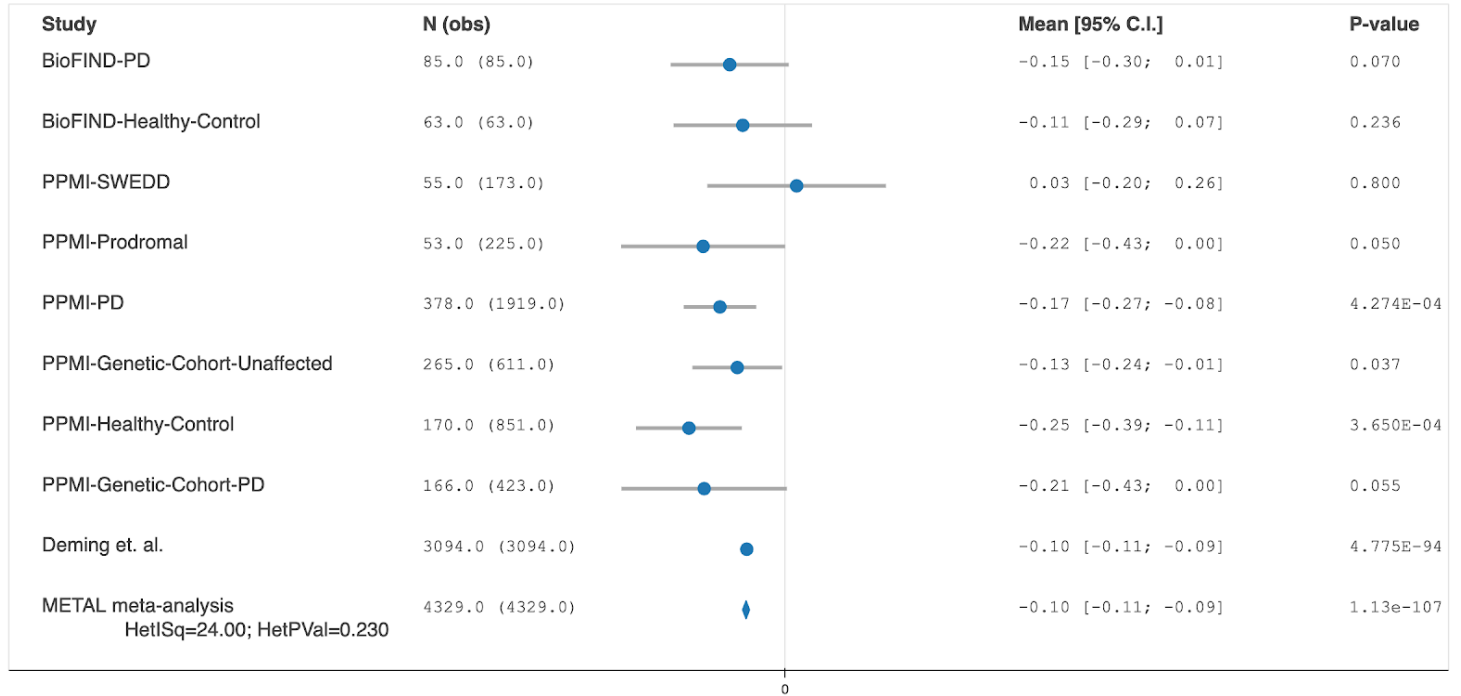


### CSF p-Tau Gene Cross-Sectional

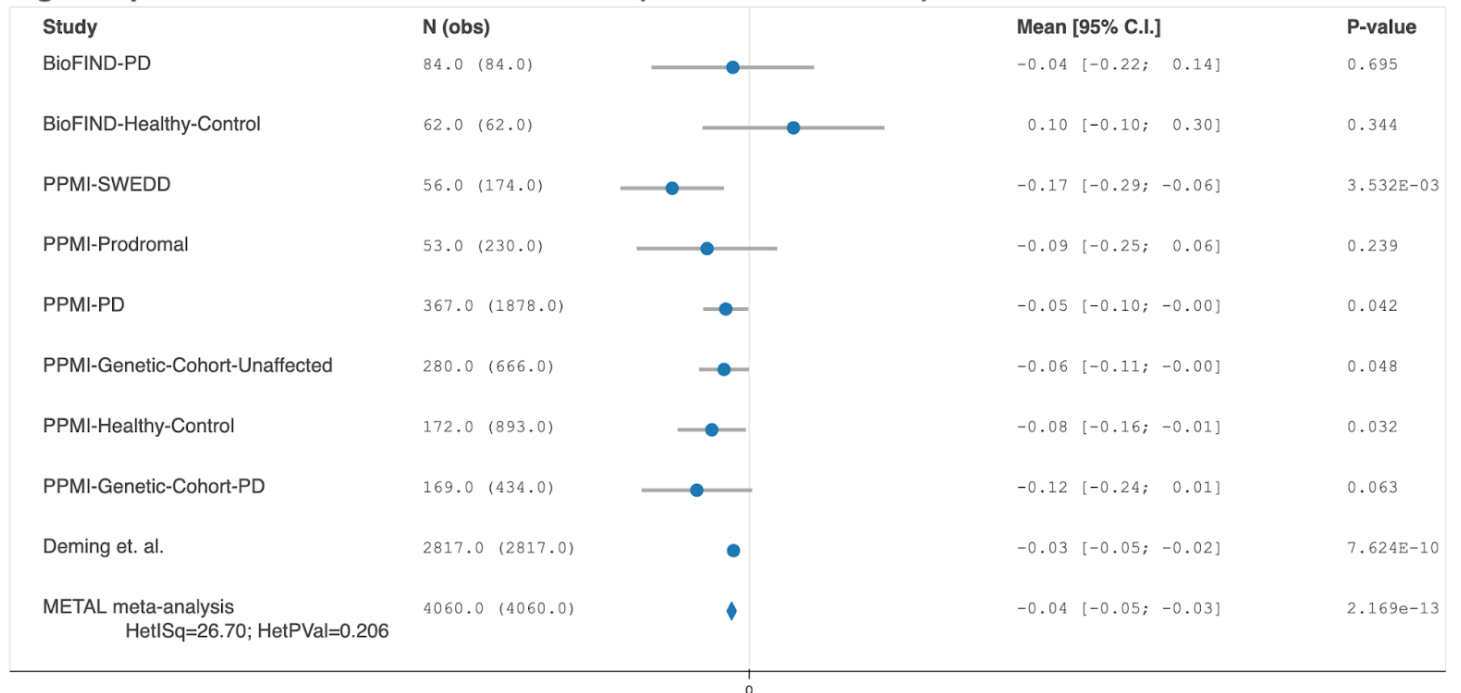


# Supplemental Figure 3. Forest plot for the GWAS loci - rs35055419 and rs769449

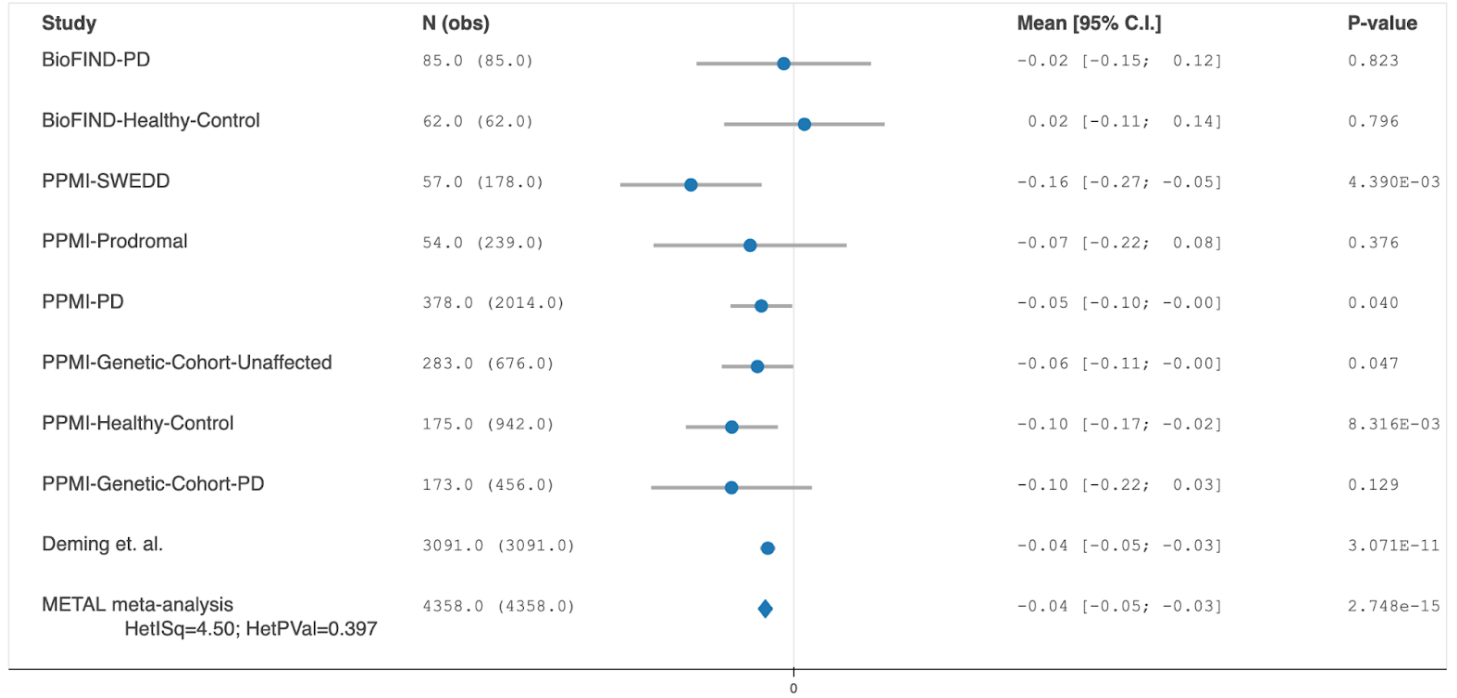
## log CSF A $\beta$ Cross-Sectional - rs769449 (chr19:44906745:G:A)



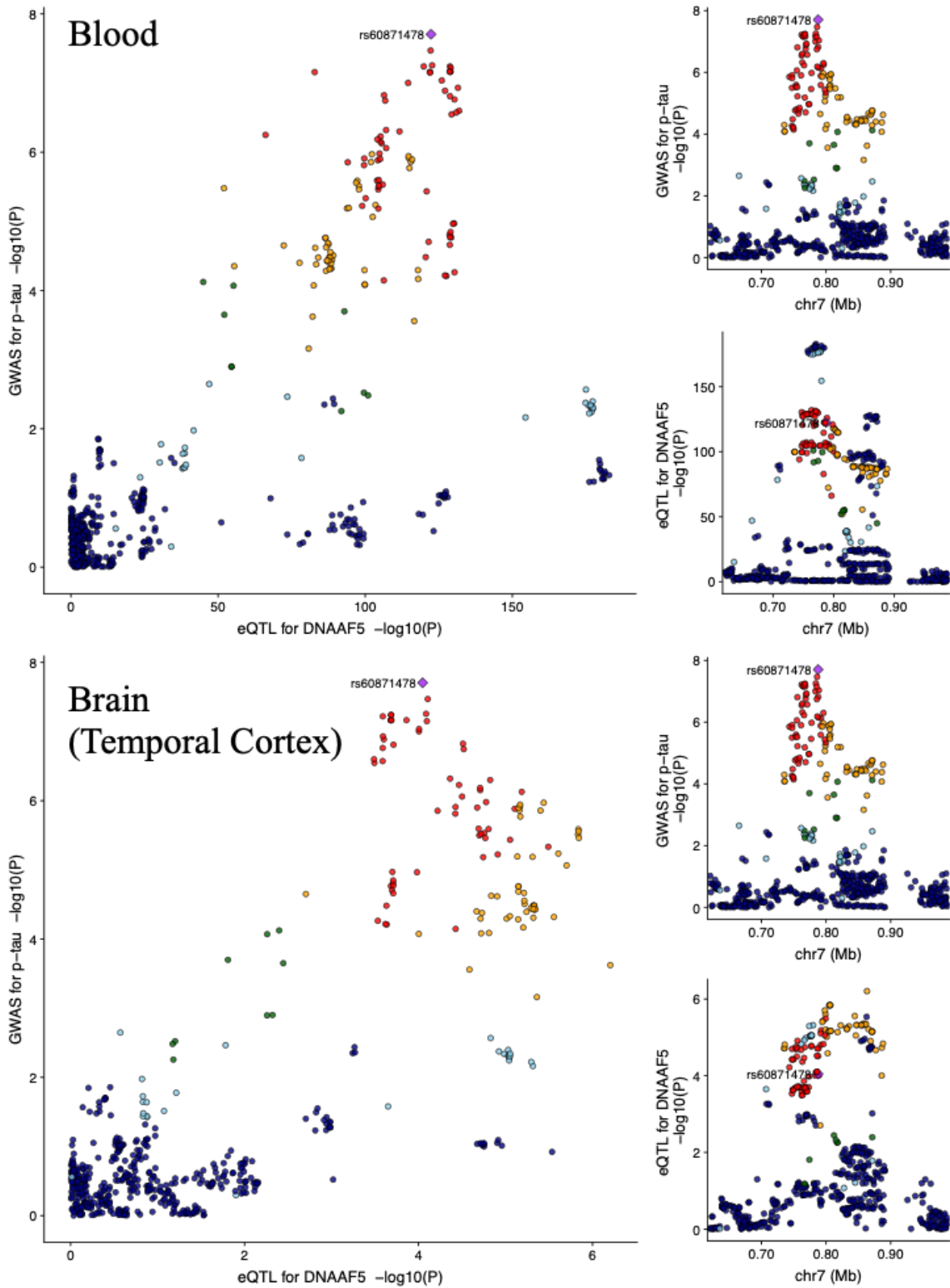
## log CSF p-Tau Cross-Sectional - rs35055419 (chr3:190945768:T:C)



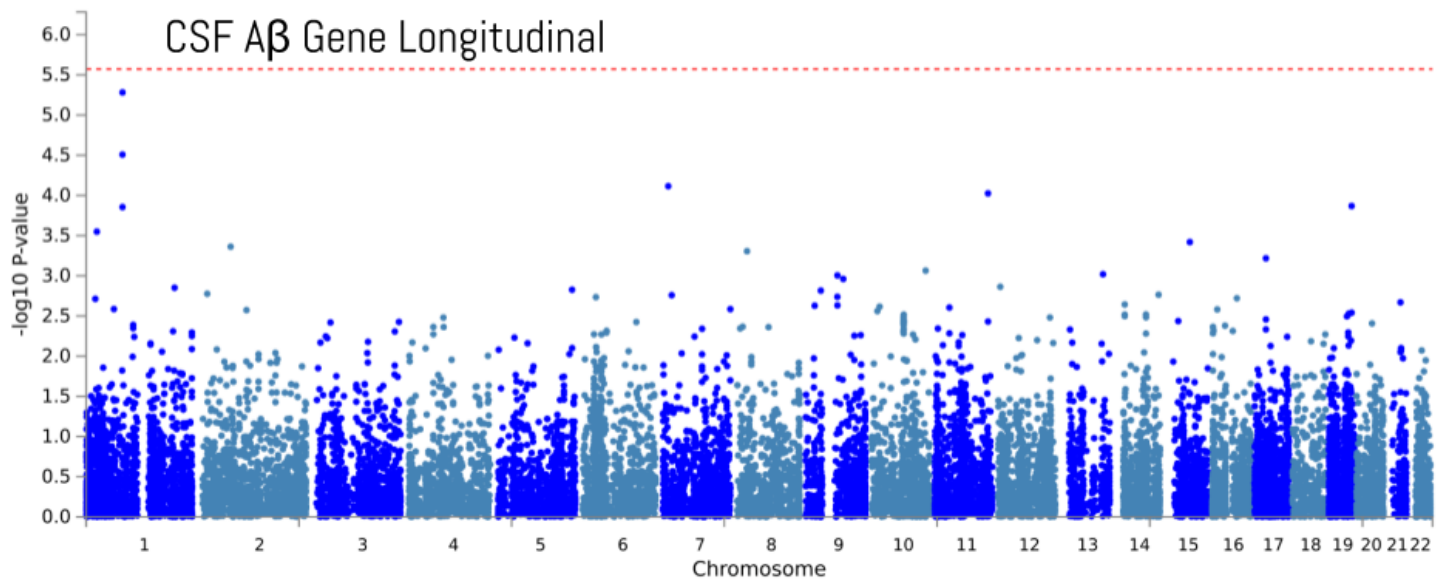
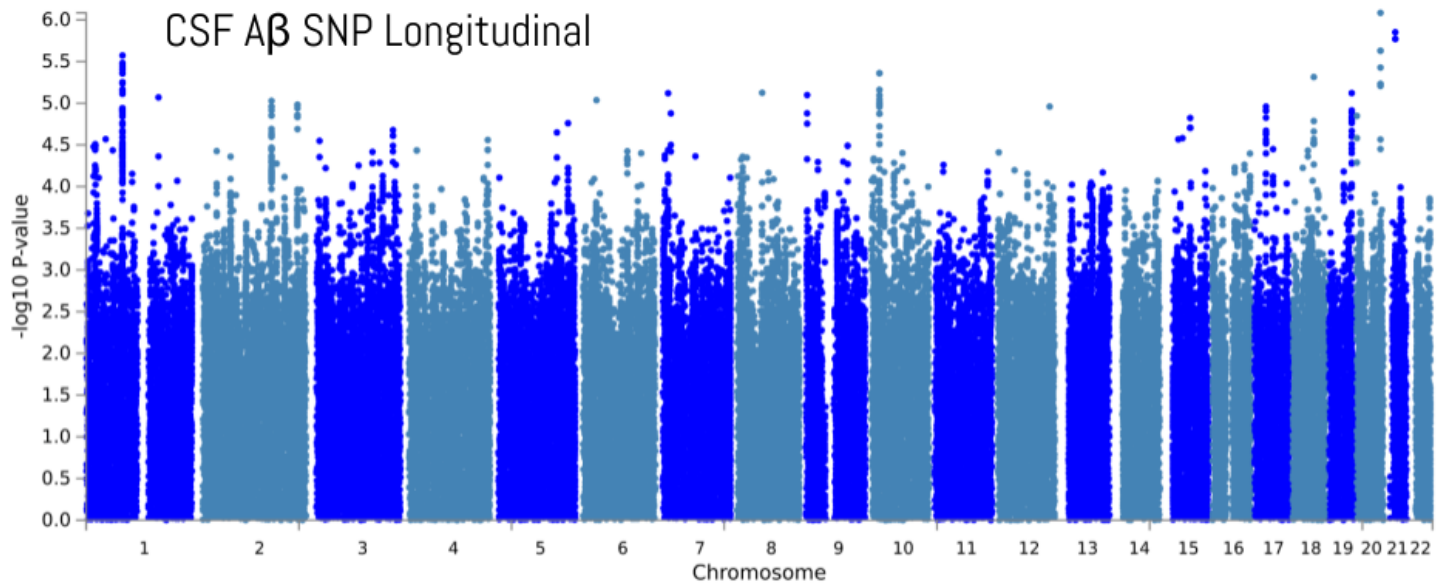
### log CSF t-Tau Cross-Sectional - rs35055419 (chr3:190945768:T:C)



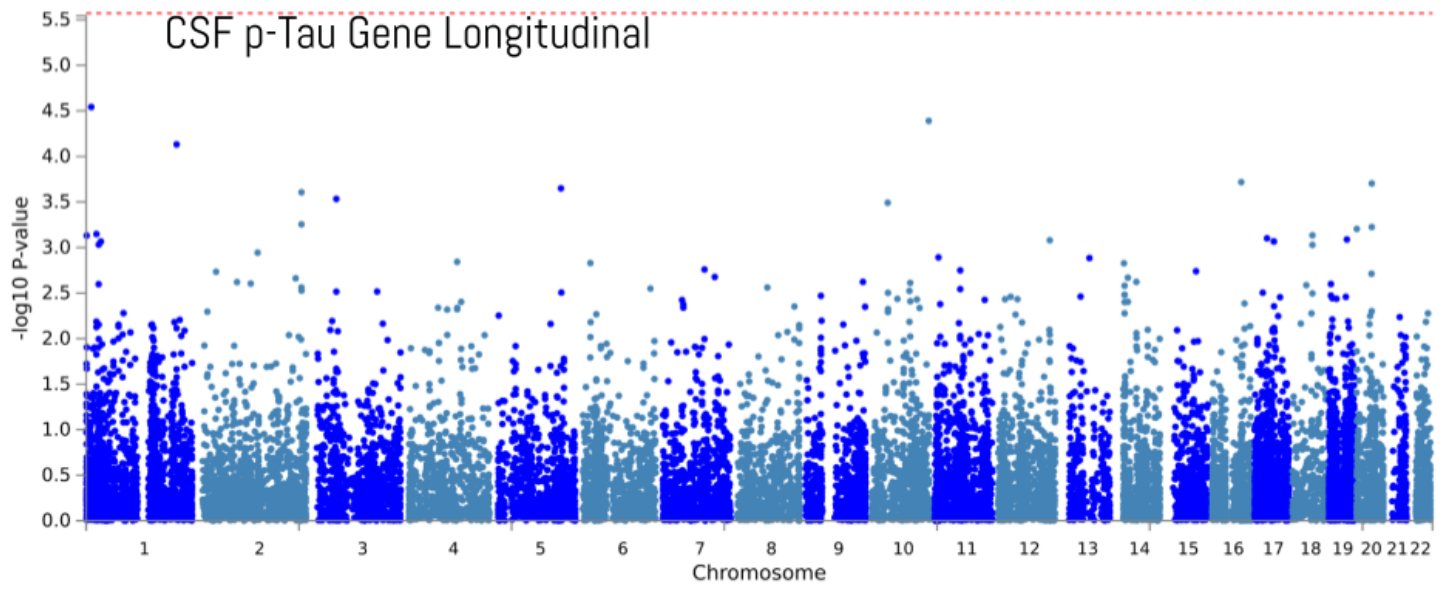
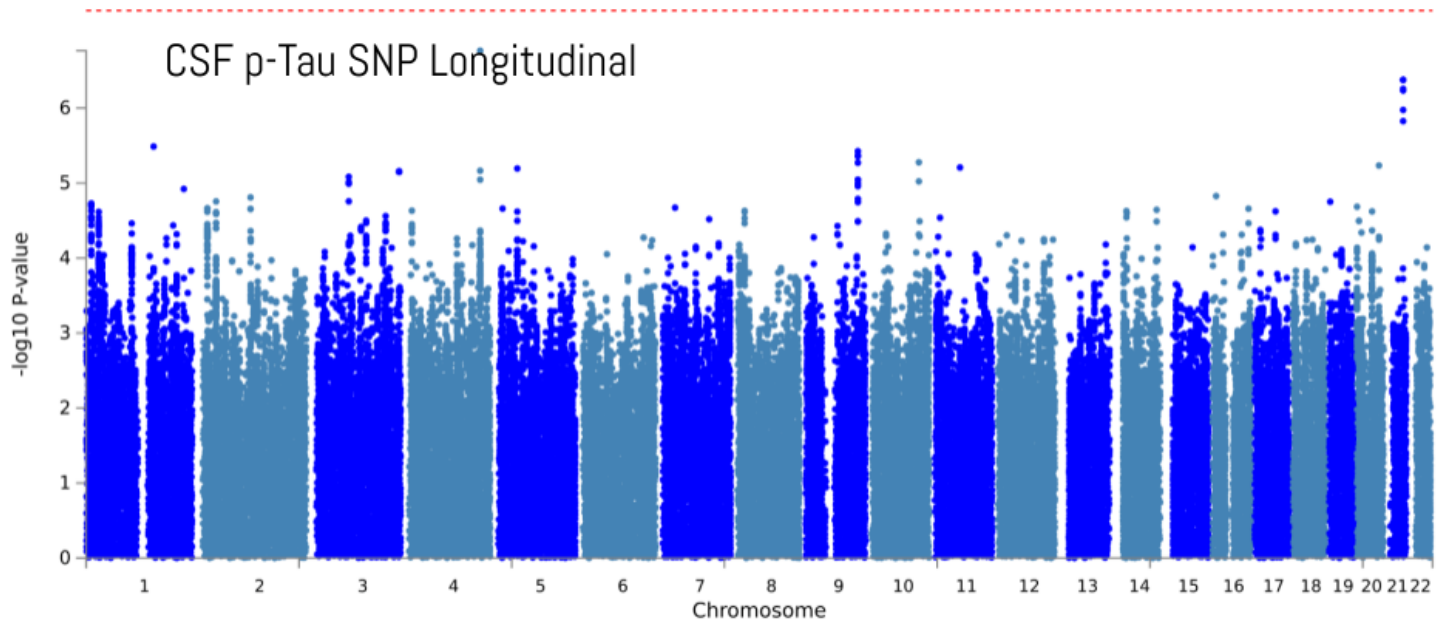
# Supplemental Figure 4. Co-localization plots for the chromosome 7 and



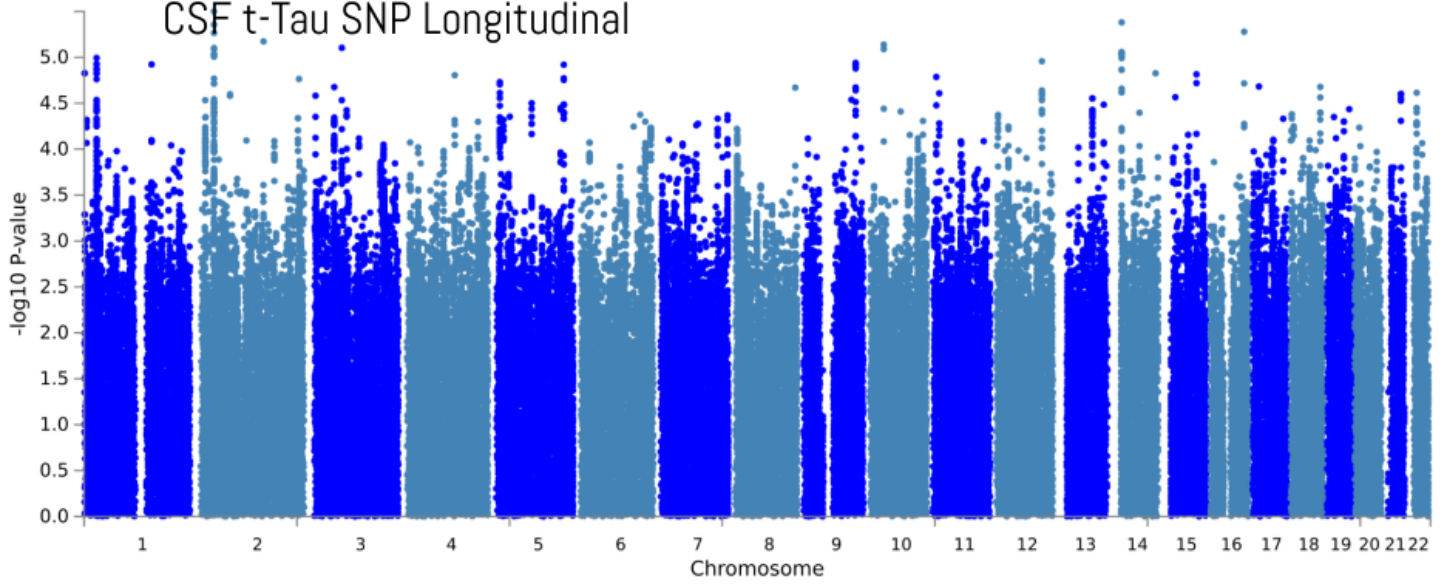
# Supplemental Figure 5. GWAS results for longitudinal component



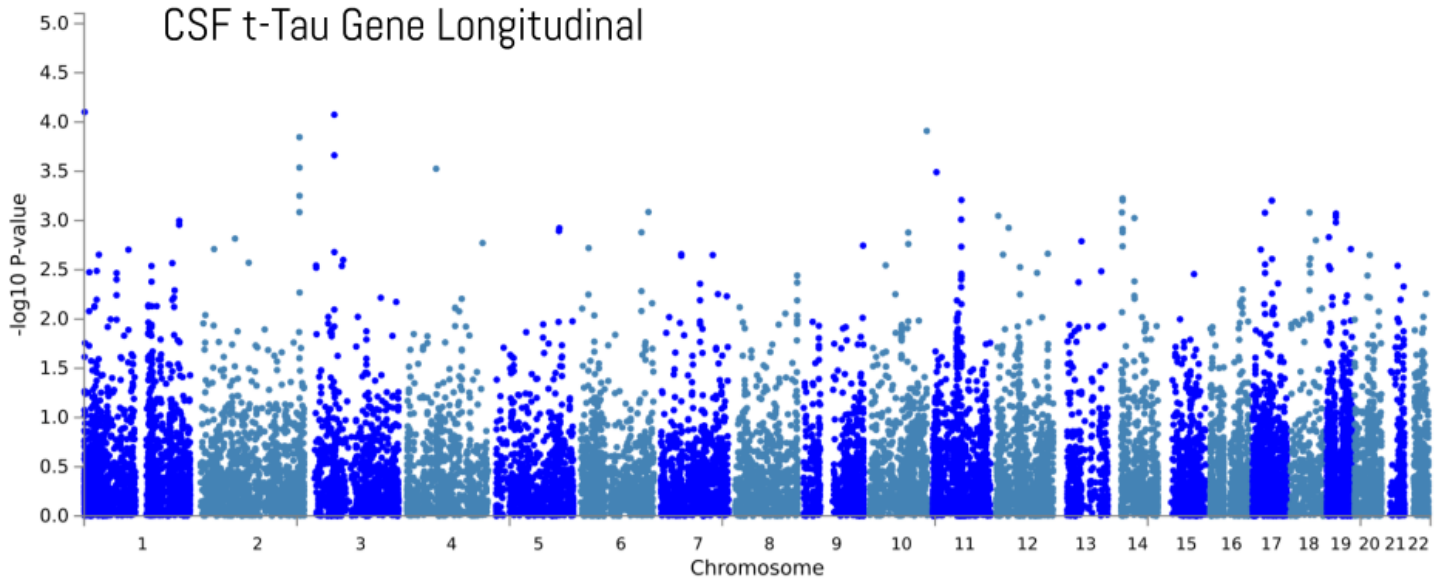




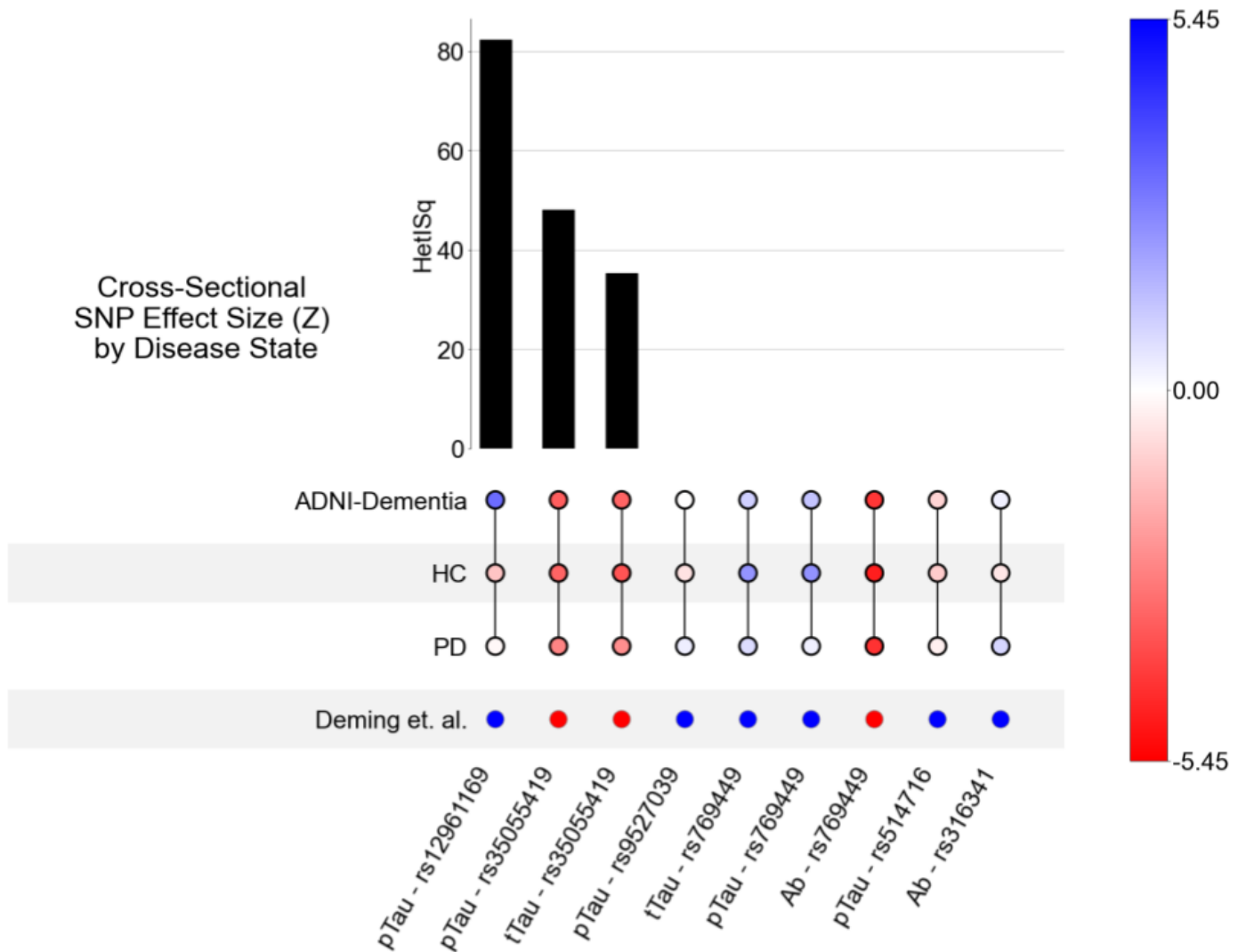
CSF t-Tau SNP Longitudinal



CSF t-Tau Gene Longitudinal



# Supplemental Figure 6. UpSet plots per disease status for the association previously reported by Deming et al.



One reported loci at 1p32.3 for A $\beta$  (rs185031519) was not identified in the current dataset.

# Supplemental Figure 7. Forest plot for SNP - rs12961169

## log CSFp-tau Cross-Sectional - rs12961169 (chr18:79621649:C:T)

