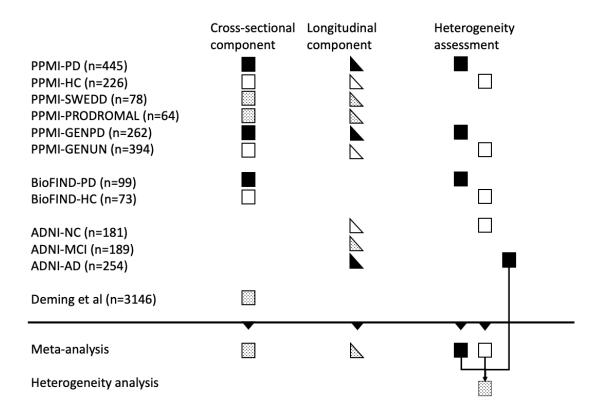
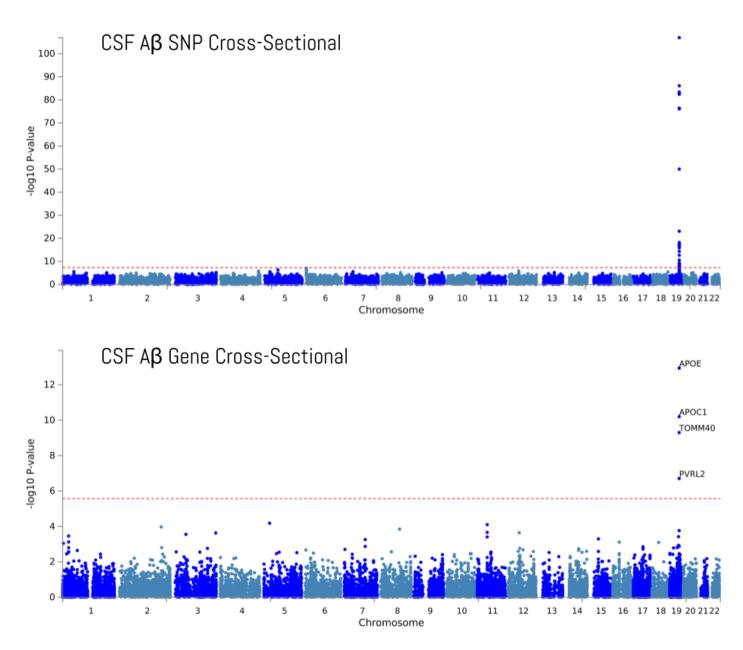
Supplemental Figure 1. Analysis overview

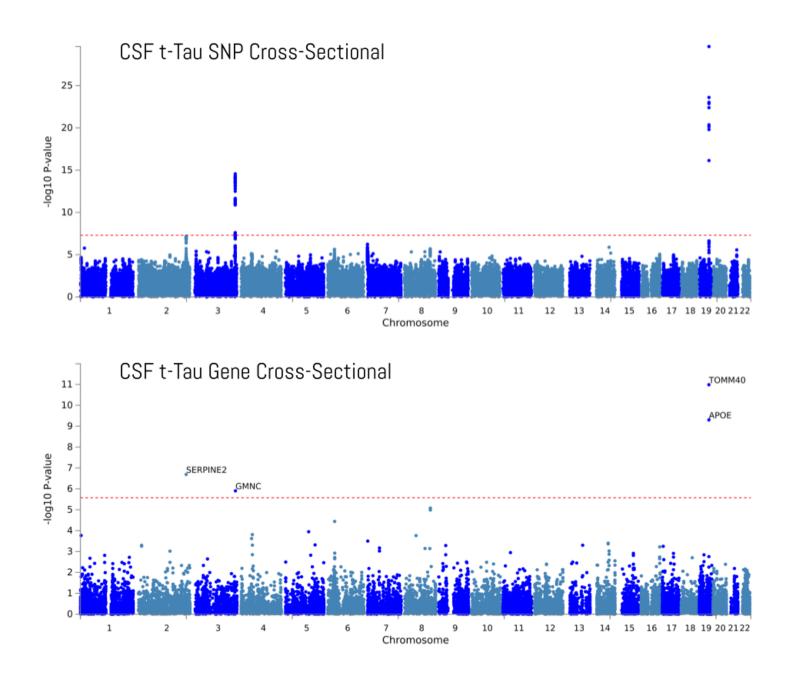


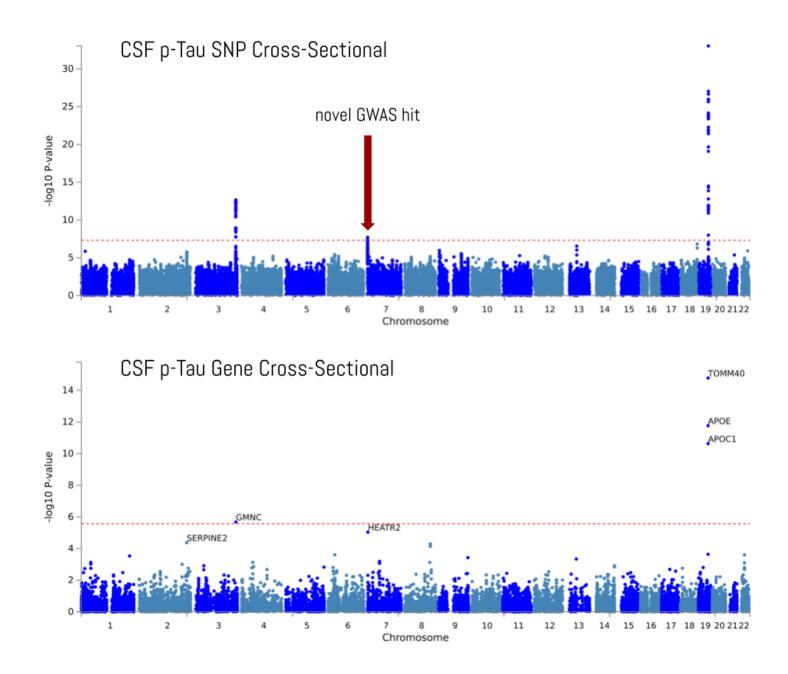
Individual arms were analyzed separately and then meta-analyzed. Squares represent the cross-sectional component analysis results while the triangles represent the longitudinal component (change over time) analysis results. The disease groups (either with Parkinson's disease or Alzheimer's disease) were 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







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

log CSF Aβ Cross-Sectional - rs769449 (chr19:44906745:G:A)

Study	N (obs)		Mean [95% C.I.]	P-value
BioFIND-PD	85.0 (85.0)		-0.15 [-0.30; 0.01]	0.070
BioFIND-Healthy-Control	63.0 (63.0)		-0.11 [-0.29; 0.07]	0.236
PPMI-SWEDD	55.0 (173.0)	•	0.03 [-0.20; 0.26]	0.800
PPMI-Prodromal	53.0 (225.0)		-0.22 [-0.43; 0.00]	0.050
PPMI-PD	378.0 (1919.0)	— •—	-0.17 [-0.27; -0.08]	4.274E-04
PPMI-Genetic-Cohort-Unaffected	265.0 (611.0)	— •	-0.13 [-0.24; -0.01]	0.037
PPMI-Healthy-Control	170.0 (851.0)	●	-0.25 [-0.39; -0.11]	3.650E-04
PPMI-Genetic-Cohort-PD	166.0 (423.0)		-0.21 [-0.43; 0.00]	0.055
Deming et. al.	3094.0 (3094.0)	•	-0.10 [-0.11; -0.09]	4.775E-94
METAL meta-analysis HetlSq=24.00; HetPVal=0.230	4329.0 (4329.0)	•	-0.10 [-0.11; -0.09]	1.13e-107
		0		

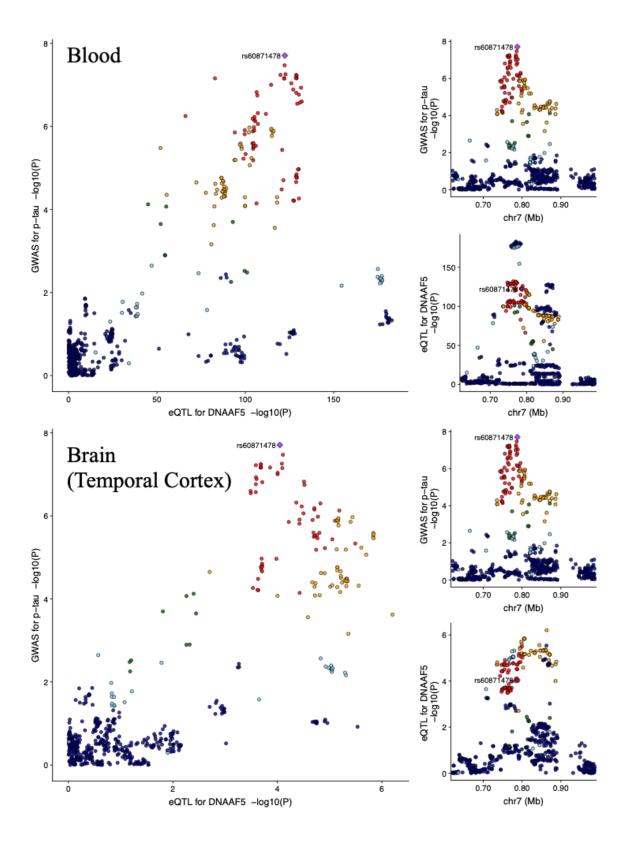
log CSF p-Tau Cross-Sectional - rs35055419 (chr3:190945768:T:C)

Study	N (obs)		Mean [95% C.I.]	P-value
BioFIND-PD	84.0 (84.0)		-0.04 [-0.22; 0.14]	0.695
BioFIND-Healthy-Control	62.0 (62.0)		0.10 [-0.10; 0.30]	0.344
PPMI-SWEDD	56.0 (174.0)	— •—	-0.17 [-0.29; -0.06]	3.532E-03
PPMI-Prodromal	53.0 (230.0)	●	-0.09 [-0.25; 0.06]	0.239
PPMI-PD	367.0 (1878.0)	-•-	-0.05 [-0.10; -0.00]	0.042
PPMI-Genetic-Cohort-Unaffected	280.0 (666.0)		-0.06 [-0.11; -0.00]	0.048
PPMI-Healthy-Control	172.0 (893.0)		-0.08 [-0.16; -0.01]	0.032
PPMI-Genetic-Cohort-PD	169.0 (434.0)		-0.12 [-0.24; 0.01]	0.063
Deming et. al.	2817.0 (2817.0)	•	-0.03 [-0.05; -0.02]	7.624E-10
METAL meta-analysis HetISq=26.70; HetPVal=0.206	4060.0 (4060.0)	•	-0.04 [-0.05; -0.03]	2 . 169e-13

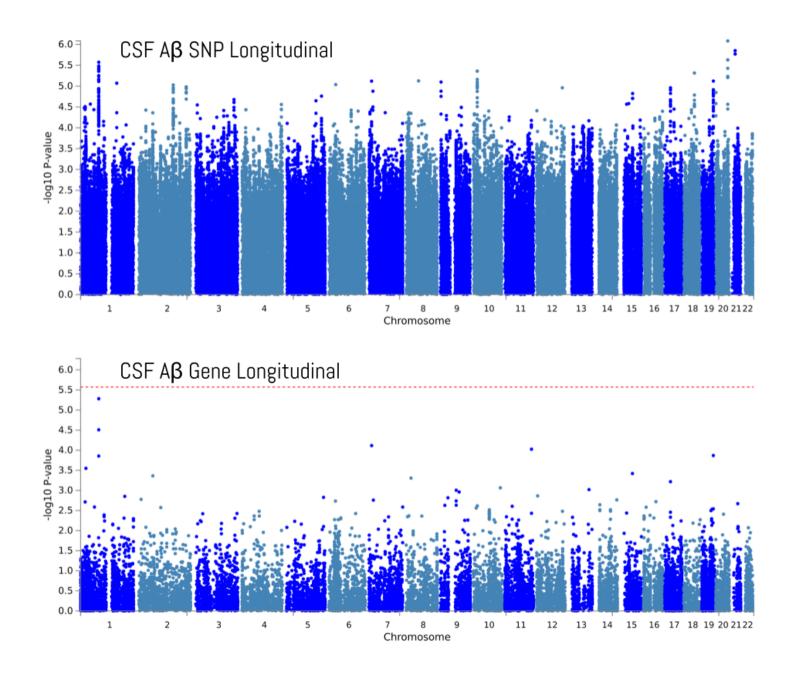
log CSF t-Tau Cross-Sectional - rs35055419 (chr3:190945768:T:C)

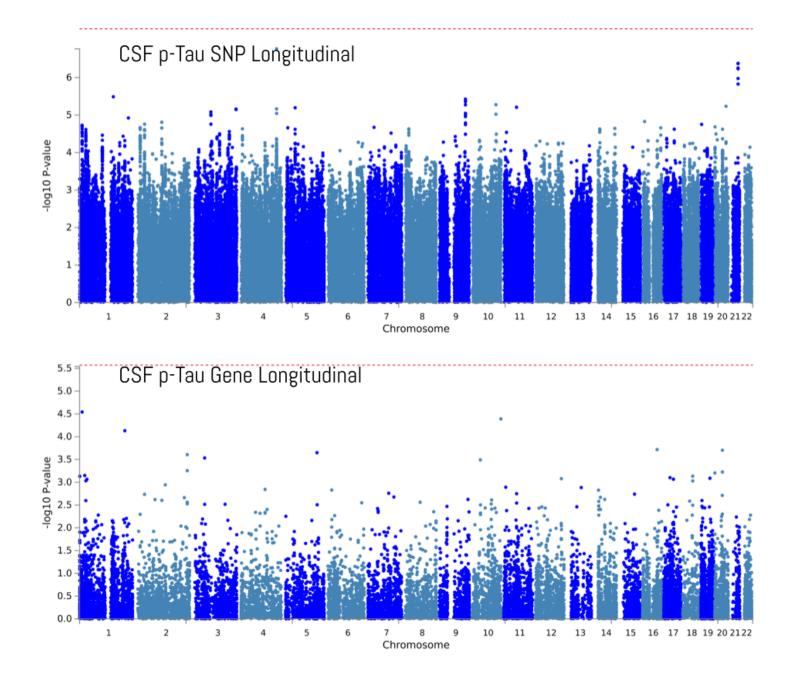
Study	N (obs)		Mean [95% C.I.]	P-value
BioFIND-PD	85.0 (85.0)		-0.02 [-0.15; 0.12]	0.823
BioFIND-Healthy-Control	62.0 (62.0)	•	0.02 [-0.11; 0.14]	0.796
PPMI-SWEDD	57.0 (178.0)	●	-0.16 [-0.27; -0.05]	4.390E-03
PPMI-Prodromal	54.0 (239.0)		-0.07 [-0.22; 0.08]	0.376
PPMI-PD	378.0 (2014.0)		-0.05 [-0.10; -0.00]	0.040
PPMI-Genetic-Cohort-Unaffected	283.0 (676.0)		-0.06 [-0.11; -0.00]	0.047
PPMI-Healthy-Control	175.0 (942.0)	_	-0.10 [-0.17; -0.02]	8.316E-03
PPMI-Genetic-Cohort-PD	173.0 (456.0)		-0.10 [-0.22; 0.03]	0.129
Deming et. al.	3091.0 (3091.0)	•	-0.04 [-0.05; -0.03]	3.071E-11
METAL meta-analysis HetlSq=4.50; HetPVal=0.397	4358.0 (4358.0)	•	-0.04 [-0.05; -0.03]	2.748e-15
		0		

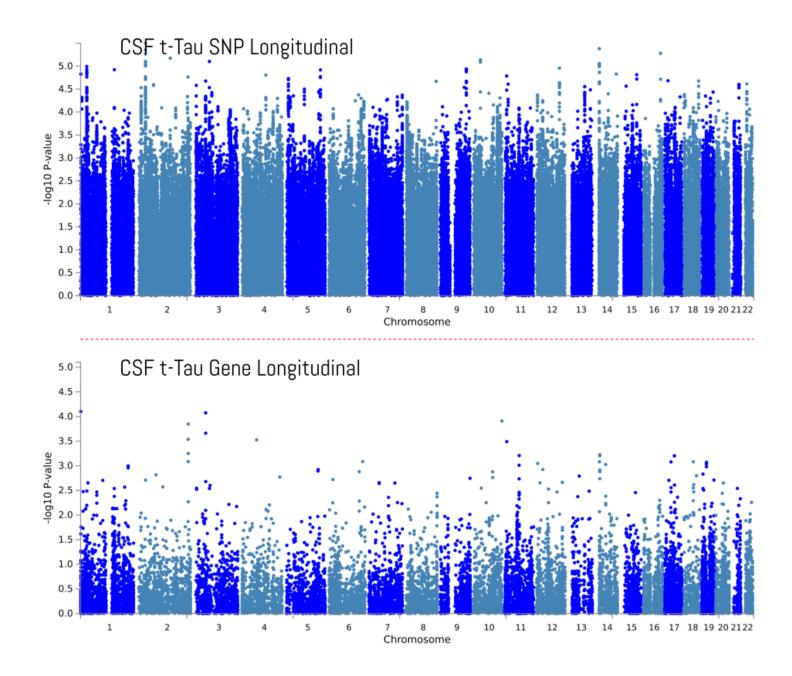
Supplemental Figure 4. Co-localization plots for the chromosome 7 and



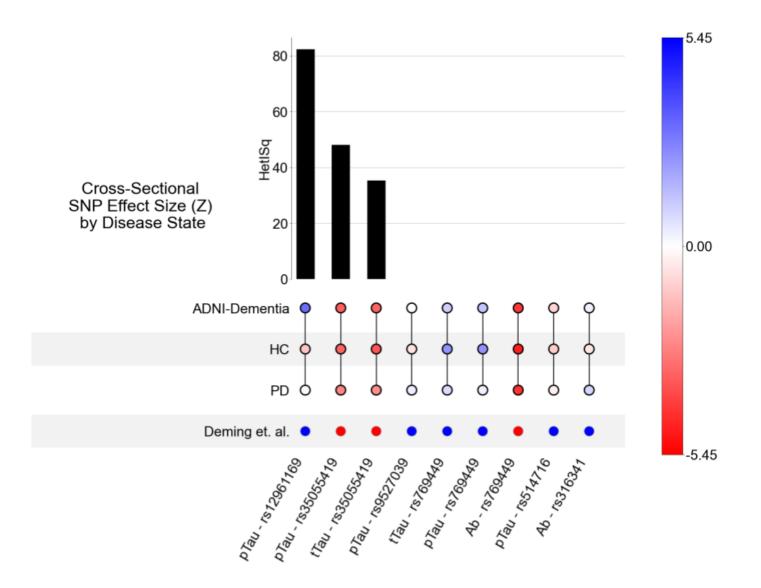
Supplemental Figure 5. GWAS results for longitudinal component







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_β (rs185031519) was not identified in the current dataset.

Supplemental Figure 7. Forest plot for SNP - rs12961169

Study	N (obs)		Mean [95% C.I.]	P-value
ADNI-Dementia	181.0 (432.0)	•	0.16 [0.06; 0.27]	1.826E-03
PD	620.0 (2396.0) —	•	-0.00 [-0.06; 0.05]	0.870
нс	680.0 (1992.0)	-	-0.03 [-0.08; 0.02]	0.206
METAL meta-analysis HetISq=82.40; HetPVal=0.00	1481.0 (4820.0))3	•	0.00 [-0.03; 0.04]	0.922
		0		

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