Variant	Minor allele count and frequency	Major allele count and frequency	Genotype 1 count and frequency	Genotype 2 count and frequency	Genotype 3 count and frequency
rs1467967					
Pick's disease	G: 190 (28.1%)	A: 486 (71.9%)	AA: 176 (52.1%)	AG: 134 (39.6%)	GG: 28 (8.3%)
Controls	G: 849 (32.4%)	A: 1775 (67.6%)	AA: 603 (46.0%)	AG: 569 (43.4%)	GG: 140 (10.7%)
rs242557					
Pick's disease	A: 236 (34.9%)	G: 440 (65.1%)	GG: 146 (43.2%)	GA: 148 (43.8%)	AA: 44 (13.0%)
Controls	A: 965 (36.8%)	G: 1659 (63.2%)	GG: 548 (41.8%)	GA: 563 (42.9%)	AA: 201 (15.3%)
rs3785883					
Pick's disease	A: 114 (16.9%)	G: 562 (83.1%)	GG: 231 (68.3%)	GA: 100 (29.6%)	AA: 7 (2.1%)
Controls	A: 472 (18.0%)	G: 2152 (82.0%)	GG: 879 (67.0%)	GA: 394 (30.0%)	AA: 39 (3.0%)
rs2471738					
Pick's disease	T: 136 (20.1%)	C: 540 (79.9%)	CC: 215 (63.6%)	CT: 110 (32.5%)	TT: 13 (3.8%)
Controls	T: 542 (20.7%)	C: 2082 (79.3%)	CC: 842 (64.2%)	CT: 398 (30.3%)	TT: 72 (5.5%)
rs8070723					
Pick's disease	G: 196 (29.0%)	A: 480 (71.0%)	AA: 167 (49.4%)	AG: 146 (43.2%)	GG: 25 (7.4%)
Controls	G: 603 (23.0%)	A: 2021 (77.0%)	AA: 784 (59.8%)	AG: 453 (34.5%)	GG: 75 (5.7%)
rs7521					
Pick's disease	A: 278 (41.1%)	G: 398 (58.9%)	GG: 117 (34.6%)	GA: 164 (34.6%)	AA: 57 (16.9%)
Controls	A: 1223 (46.6%)	G: 1401 (53.4%)	GG: 385 (29.3%)	GA: 631 (48.1%)	AA: 296 (22.6%)

Supplementary Table 1: Genotype counts and frequencies of six common MAPT SNPs in Pick's disease cases and controls.

	Minor allele frequency		Association with Pick's disease	
Variant	Pick's disease patients (N=338)	Controls (N=1,312)	OR (95% CI)	P-value
rs1467967	28.1%	32.4%	0.83 (0.68, 1.00)	0.046
rs242557	34.9%	36.8%	0.94 (0.79, 1.12)	0.51
rs3785883	16.9%	18.0%	0.91 (0.72, 1.15)	0.42
rs2471738	20.1%	20.7%	0.96 (0.78, 1.18)	0.70
rs8070723	29.0%	23.0%	1.35 (1.12, 1.64)	0.0021
rs7521	41.1%	46.6%	0.81 (0.69, 0.96)	0.018

Supplementary Table 2: Associations between individual MAPT variants and risk of Pick's disease. ORs, 95% CIs, and p-values result from logistic regression models that were adjusted for age and sex. ORs correspond to each additional minor allele of the given variant. OR=odds ratio; CI=confidence interval.

		Association with age of disease onset		Association with disease duration	
Haplotype	Minor allele frequency (N=309)	β (95% CI)	P-value	β (95% CI)	P-value
rs1467967	28.8%	0.03 (-1.36, 1.41)	0.97	-0.11 (-0.80, 0.59)	0.76
rs242557	34.6%	-0.58 (-1.89, 0.72)	0.38	-0.42 (-1.07, 0.24)	0.22
rs3785883	16.8%	-0.33 (-2.05, 1.39)	0.71	0.08 (-0.79, 0.94)	0.86
rs2471738	19.9%	-0.16 (-1.73, 1.40)	0.84	0.01 (-0.77, 0.80)	0.98
rs8070723	29.6%	-0.54 (-1.94, 0.87)	0.45	0.25 (-0.46, 0.96)	0.50
rs7521	40.8%	1.11 (-0.18, 2.40)	0.091	-0.40 (-1.05, 0.26)	0.23

Supplementary Table 3: Associations of individual MAPT variants with age of disease onset and disease duration in Pick's disease subjects. β values, 95% CIs, and p-values result from linear regression models that were adjusted for sex and series (age of disease onset analysis) or sex, age of disease onset, and series (disease duration analysis). β values are interpreted as the change in the mean value of the given outcome (age of disease onset or disease duration) corresponding to each additional copy of the minor allele of the given variant. β=regression coefficient; CI=confidence interval.