

Table 5: Prediction of amyloid deposition in individuals with MCI and of progression to AD in individuals with MCI and positive amyloid deposition with pathway-specific PRSs

Pathways	Amyloid positive (270) vs amyloid negative (171)			MCI and amyloid positive (AD (112) vs MCI (150))		
	Beta	P	P (no APOE region)	Beta	P	P (no APOE region)
protein-lipid complex assembly	1.11	1.92e-17	0.2	0.48	2.7e-4	0.81
regulation of beta-amyloid formation	0.95	7.6e-14	0.2	0.30	9e-3	0.11
protein-lipid complex	1.12	1.1e-17	3.1e-3	0.51	1.5e-4	0.23
regulation of amyloid precursor protein catabolic process	0.95	8.4e-14	0.2	0.3	9.4e-3	0.12
tau protein binding	0.99	2.2e-14	0.2	0.2	0.08	0.24
reverse cholesterol transport	1.05	1.9e-15	0.03	0.31	0.01	0.24
protein-lipid complex subunit organization	1.1	1.2e-17	0.05	0.51	1.9e-4	0.64
plasma lipoprotein particle assembly	1.09	3.4e-17	0.9	0.51	1e-4	0.31
activation of immune response	0.18	0.068	0.09	0.08	0.54	0.76
Whole genome PRS without pathways	0.36	2.1e-3	-	0.6	8.8e-5	-

Legend: 1st column-name of pathways that were analysed, PRS pathway-specific effect sizes with p-values and p-values (no *APOE* region) of the models are presented in columns 2- 7.