

Table 4: Prediction of AD and amyloid deposition risk with pathway-specific PRSs

Pathways	Number of Genes	AD (174) vs Controls (224)			Amyloid positive (357) vs negative (304)		
		Beta	p-value	p-value (no APOE region)	Beta	p-value	p-value (no APOE region)
protein-lipid complex assembly	20	0.87	3e-13	0.35	0.94	4e-21	0.4
regulation of beta-amyloid formation	10	0.79	1.1e-11	0.09	0.81	8.9e-17	0.47
protein-lipid complex	40	0.91	8.14e-14	5.5e-3	0.96	1.8e-21	7.9e-3
regulation of amyloid precursor protein catabolic process	12	0.79	1.1e-11	0.09	0.81	9.6e-17	0.49
tau protein binding	11	0.77	3.1e-11	0.39	0.82	4.8e-17	0.6
reverse cholesterol transport	17	0.84	2.4e-12	0.07	0.93	2.1e-19	0.03
protein-lipid complex subunit organization	35	0.92	8.e-14	0.03	0.97	9.67e-22	0.03
plasma lipoprotein particle assembly	18	0.89	2e-13	0.66	0.94	3.6e-21	0.98
activation of immune response	432	0.18	0.06	0.06	0.21	6.8e-3	0.01
Whole genome without all pathways	-	0.93	2.2e-14	-	0.38	9.1e-6	-

Legend: 1st column-name of pathways that were analysed, 2nd column- number of genes in each pathway, PRS pathways-specific effect sizes with p-values and p-values (no *APOE* region) of the models are presented in columns 3- 8 for AD vs controls and amyloid deposition status.

