Supplementary Material

Genetics Contributes to Concomitant Pathology and Clinical Presentation in Dementia with Lewy Bodies

Supplementary Table 1. Cohort characteristics controls

	Controls LASA (n=1648)	Controls ADC (n=867)	Controls NBB (n=37)
Female (n. %)	876 (53.2)	345 (39.1%)	21 (58.3%)
Age	62.8 (6.4)	59.8 (8.9)	81.5 (11.2)
MMSE	27.9 (2.1)	28.2 (1.7)	-
CSF biomarkers§			
$A\beta_{1-42}$ (pg/ml)	-	1087 (236)	-
tau (pg/ml)	-	282 (159)	-
p-tau (pg/ml)	-	47.6 (21)	-

Data are presented as mean (SD) or n (%). ADC, Amsterdam Dementia Cohort; CSF, cerebrospinal fluid; GDS, Geriatric Depression Scale; LASA, Longitudinal Aging Study Amsterdam; MMSE, Mini-Mental State Examination; NBB, Netherlands Brain Bank; p-tau, tau phosphorylated at threonine 181.

Supplementary Table 2. Variants included in the AD polygenic risk score. The reported was extracted from the GWAS for AD and the sign of the effect was corrected that is matched the Effect_allele of the HRC reference panel. MAF, minor allele frequency; Rsq, Imputation quality. See Excel file.

Supplementary Table 3. Variants included in the PD polygenic risk score. Variants included in the PD polygenic risk score. The reported was extracted from the GWAS for AD and the sign of the effect was corrected that is matched the Effect_allele of the HRC reference panel. See Excel file.

Supplementary Table 4. Allele counts and frequencies in all groups

Gene (variant position)	Non risk allele / risk allele	Group	Frequency non-risk allele	Frequency risk allele	N total	No risk allele (%)	One risk alleles (%)	Two risk alleles (%)
APOE (19.45411941)	T / C	DLB-All	66.1	33.9	190	83 (43.7)	85 (44.7)	22 (11.6)
		DLB-AD	58.5	41.5	82	27 (32.9)	42 (51.2)	13 (15.9)
		DLB-pure	77.1	22.9	72	42 (58.3)	27 (37.5)	3 (4.2)
		Controls	82.7	17.3	2552	1746 (68.4)	729 (28.6)	77 (3)
		Controls LASA	84	16	1648	1158 (70.3)	453 (27.5)	37 (2.2)
		Controls ADC	80.2	19.8	867	562 (64.8)	266 (30.7)	39 (4.5)
		Controls NBB	82.9	17.1	35	24 (68.6)	10 (28.6)	1 (2.9)
GBA (1:155206167)	C / G	DLB-All	90.5	9.5	190	158 (83.2)	28 (14.7)	4 (2.1)
		DLB-AD	93.9	6.1	82	72 (87.8)	10 (12.2)	0 (0)
		DLB-pure	83.3	16.7	72	52 (72.2)	16 (22.2)	4 (5.6)
		Controls	97.9	2.1	2552	2448 (95.9)	100 (3.9)	4 (0.2)
		Controls LASA	97.8	2.2	1648	1579 (95.8)	67 (4.1)	2 (0.1)
		Controls ADC	97.9	2.1	867	833 (96.1)	32 (3.7)	2 (0.2)
		Controls NBB	98.6	1.4	35	34 (97.1)	1 (2.9)	0 (0)
SNCA (4:90756550)	C / G	DLB-All	36.6	63.4	190	28 (14.7)	83 (43.7)	79 (41.6)
		DLB-AD	37.8	62.2	82	13 (15.9)	36 (43.9)	33 (40.2)
		DLB-pure	36.1	63.9	72	13 (18.1)	26 (36.1)	33 (45.8)
		Controls	44	56	2552	504 (19.7)	1240 (48.6)	808 (31.7)
		Controls LASA	43.7	56.3	1648	328 (19.9)	785 (47.6)	535 (32.5)
		Controls ADC	44.9	55.1	867	170 (19.6)	438 (50.5)	259 (29.9)
		Controls NBB	38.6	61.4	35	5 (14.3)	17 (48.6)	13 (37.1)

Controls ADC, Controls from Amsterdam Dementia Cohort; *APOE*, Apolipoprotein E; *GBA*, Glucocerebrosidase; Controls LASA, Controls from Longitudinal Aging of Amsterdam Study; Controls NBB, controls from Netherlands Brain Bank; *SNCA*, Alpha-synuclein.

Supplementary Table 5. Single variant associations of the variants included in the AD polygenic risk score. The effect is reported for the effect allele, this is not necessarily the minor allele. See Excel file.

Supplementary Table 6. Single variant associations of the variants included in the PD polygenic risk score. The effect is reported for the effect allele, this is not necessarily the minor allele. See Excel file.

Supplementary Table 7. Interaction effect of genetic variants with presence of amyloid pathology.

Association with	Gene or PRS	Beta	p	p_{fdr}	N
Age	*APOE*	0.10	0.957	0.985	154
	GBA	1.69	0.508	0.854	154
	SNCA	-1.04	0.500	0.854	154
	AD-PRS	1.78	0.136	0.794	154
	PD-PRS	2.65	0.019	0.169	154
MMSE	*APOE*	-0.48	0.683	0.888	153
	GBA	1.29	0.479	0.854	153
	SNCA	2.54	0.011	0.127	153
	AD-PRS	-2.29	0.004	0.081	153
	PD-PRS	0.11	0.882	0.935	153
Parkinsonism	*APOE*	0.04	0.736	0.902	149
	GBA	-0.13	0.485	0.854	149
	SNCA	-0.10	0.336	0.854	149
	AD-PRS	-0.03	0.685	0.888	149
	PD-PRS	-0.08	0.321	0.854	149
Hallucinations	*APOE*	0.08	0.526	0.854	152
	GBA	0.00	0.997	0.997	152
	SNCA	0.08	0.480	0.854	152
	AD-PRS	-0.06	0.450	0.854	152
	PD-PRS	-0.05	0.574	0.854	152
Fluctuations	*APOE*	0.03	0.747	0.902	132
	GBA	0.10	0.557	0.854	132
	SNCA	-0.02	0.840	0.935	132
	AD-PRS	-0.19	0.005	0.081	132
	PD-PRS	0.11	0.082	0.574	132
REM sleep	*APOE*	-0.04	0.774	0.904	116
	GBA	0.13	0.549	0.854	116
	SNCA	0.09	0.470	0.854	116
	AD-PRS	-0.09	0.348	0.854	116
	PD-PRS	-0.02	0.863	0.935	116
mortality	*APOE*	0.17	0.618	0.865	153
	GBA	-0.26	0.585	0.854	153
	SNCA	0.16	0.582	0.854	153
	AD-PRS	0.21	0.343	0.854	153
	PD-PRS	0.12	0.572	0.854	153

p is the p-value for the interaction between the variant and concomitant AD pathology. p_{fdr} is the fdr adjusted p-value. *APOE*, Apolipoprotein E; *GBA*, Glucocerebrosidase; MMSE, Mini-Mental State Examination; RBD, rapid eye movement (REM) sleep behavior disorder; *SNCA*, Alpha-synuclein.