

Haplotype	Frequency PPMI (n=725)	Frequency Coriell (n=1118)	Frequency All (n=1842)	Reported Frequency
1	23%	29%	27%	28%
2	40%	21%	28%	33%
3	6%	10%	8%	8%
4	31%	40%	37%	31%

Supplementary table 1: Allele frequencies for each CT-rich SNCA haplotype split up by cohort.

Expression Dataset	Cohort	N	Variant ID	AF	P-nominal	FDR	Slope	Slope SE
Bulk RNA (SNCA)	NABEC	202	Haplotype 1	0.205	5.60E-01	9.05E-01	-0.057	0.098
			Haplotype 2	0.418	2.45E-01	7.44E-01	0.094	0.081
			Haplotype 3	0.094	4.54E-01	9.05E-01	0.114	0.152
			Haplotype 4	0.282	1.98E-01	7.44E-01	-0.124	0.096
			rs356182 (PD)	0.349	6.24E-01	9.05E-01	-0.042	0.086
			rs5019538 (PD)	0.291	8.52E-01	9.33E-01	-0.017	0.092
			rs2289728 (PD)	0.094	5.68E-01	9.05E-01	0.086	0.150
			rs7680557 (LBD)	0.500	2.26E-01	7.44E-01	0.099	0.082

Supplementary table 2: NABEC RNA-seq QTL results. AF= haplotype allele frequency, P-nominal = nominal p-value, FDR= false discovery rate, SE= standard error

Expression Dataset	Cohort	Variant ID	AF	P-nominal	FDR	Slope	Slope SE
Bulk RNA (<i>SNCA</i>)	PPMI	Haplotype 1	0.225	3.07E-03	1.23E-02	0.201	0.068
		Haplotype 2	0.401	3.09E-02	4.95E-02	-0.127	0.059
		Haplotype 3	0.052	1.36E-02	3.62E-02	0.301	0.122
		Haplotype 4	0.323	5.46E-02	7.28E-02	-0.137	0.071
		rs356182 (PD)	0.384	4.65E-01	4.65E-01	-0.042	0.058
		rs5019538 (PD)	0.324	2.35E-02	4.70E-02	-0.132	0.058
		rs2298728 (PD)	0.059	6.36E-04	5.09E-03	0.399	0.116
		rs7680557 (LBD)	0.490	3.35E-01	3.82E-01	-0.053	0.055

Supplementary table 3: PPMI RNA-seq QTL results. AF= haplotype allele frequency, P-nominal = nominal p-value, FDR= false discovery rate, SE= standard error

Study	Cases (N)	Controls (N)	Total (N)	Female case (%)	Female control (%)	Case age at baseline/onset (mean , SD in years)	Control age at baseline (mean, SD in years)
PPMI	629	265	894	40.00	42.00	61.7, 9.83	60.3, 10.5
Coriell	746	694	1440	48.00	50.00	68.8, 6.2	71.6, 7.3
NABEC	NA	204	204	NA	35.00	NA	40.08, 26.65

Supplementary table 4: Clinical and demographic characteristics of samples included in long-read and transcriptomic analyses. SD: standard deviation; NA: Not available

PCR1

Reagent	Volume
H2O	5 μ L
REDTaq Readymix PCR Reaction Mix	12.5 μ L
FW Primer (5 μ M) 5' GTTGGAACTCTCCCAGACACT 3'	2.5 μ L
RV Primer (5 μ M) 5' CAAGCATACCCTTGCCCTGA 3'	2.5 μ L
Control DNA (10ng/ μ L)	2.5 μ L

Protocol

94.0 °C, 3:00 minutes
94.0 °C, 1:00 minutes (x30)
55.1 °C, 0:30 minutes (x30)
72.0 °C, 1:00 minutes (x30)
72.0 °C, 10:00 minutes

PCR2

Reagent	Volume
H2O	16µL
KAPA HIFI	5µL
dNTPs	0.75µL
FW Primer (10µM) 5' GCAGTCGAACATGTAGCTGACTCAGGTCACGTTGGAACTCTCCCAGACAC 3'	0.75µL
RV Primer (10µM) 5' TGGATCACTTGTGCAAGCATCACATCGTAGCAAGCATACCCTTGCCCTGA 3'	0.75µL
Polymerase	0.75 µL
PCR1 Product (1:200 dilution)	1µL

Protocol

95.0 °C, 0:30 minutes (x10)
57 °C, 0:30 minutes (x10)
72.0 °C, 1:00 minutes (x10)

PCR3

Reagent	Volume
H2O	14µL
KAPA HIFI	5µL
dNTPs	0.75µL
1 uM Unique Barcoding Primers (FW+RV)	3.75µL
Polymerase	0.5 µL
PCR2 Product (1:20 dilution)	1µL

Protocol
95.0 °C, 0:30 minutes (x15)
57 °C, 0:30 minutes (x15)
72.0 °C, 1:00 minutes (x15)

Supplementary table 5: PCR CT-rich SNCA amplification protocol description

Haplotype	Flank Allele Length (bp)	
	Greater Than	Less Than
1	223	227
2	NA	224
3	226	291
4	290	NA

Supplementary table 6: TRGT flanking bins

Haplotype 1

[illegible]

Haplotype 2

[illegible]

Haplotype 3

3' TACTTTTTTCTTCCTTTCTTTCTTTTCTTTTCTTTCTTTCTTTCTTTCTCCTTT[23bp]CCTTTCTTTCTT
TTCCCTTCCTTCCTTCCTTTCTCCCTTCCTTCCTTCCTCCCTCTCTCCCTCCCTTCCTTCCTCCCTTTCTTTCTTTCTCTTTTTCTTTCTTGCTTCCTTCCTC
CTTCTTTCTTTTCTTTCTTTTCTTTTCTTTGCCAAAGTGTTATTC 5'

Haplotype 4

[illegible]

Supplementary Figure 1: Sequences for the CT-rich *SNCA* haplotype. Haplotype 1 is the reference sequence corresponding to chr4:89821175-89821400 on the minus strand.