Supplementary Table 1: Number of patients with PD and number of controls according to series, country, and site

	Patients with PD				Controls		
Series	No. of patients	Age	Age at onset	No. (%) Male	No. of controls	Age	No. (%) Male
Caucasian series	5991				4331		
Australia – Queensland	923	72 ± 10 (38 - 106)	59 ± 11 (23 - 96)	570 (62%)	713	67 ± 10 (26 - 103)	257 (36%)
France – Lille	548	64 ± 10 (24 - 92)	55 ± 11 (24 - 86)	300 (55%)	143	65 ± 11 (35 - 89)	64 (45%)
Germany							
Frankfurt	232	72 ± 11 (27 - 94)	56 ± 11 (26 - 79)	119 (51%)	47	59 ± 10 (27 - 69)	30 (64%)
Luebeck	512	62 ± 12 (22 - 95)	45±12 (18 - 80)	297 (58%)	289	55 ± 14 (21 - 96)	137 (47%)
Tuebingen	330	53 ± 12 (18 - 81)	NA	193 (58%)	339	53 ± 12 (27 - 72)	187 (55%)
Greece							
Athens	134	73 ± 10 (35 - 93)	66 ± 11 (34 - 88)	78 (58%)	94	71 ± 10 (42 - 88)	42 (45%)
Thessaly	316	70 ± 9 (38 - 89)	65 ± 9 (30 - 86)	158 (50%)	311	70 ± 9 (35 - 90)	157 (50%)
Ireland – Dublin	360	67 ± 10 (37 - 94)	51 ± 10 (18 - 77)	211 (59%)	444	67±24 (23 - 104)	159 (36%)
Italy							
Mangone	185	72 ± 9 (44 - 98)	61 ± 9 (38 - 84)	100 (54%)	168	54 ± 9 (40 - 80)	77 (46%)
Milan	95	68 ± 9 (48 - 90)	62 ± 10 (37 - 90)	50 (53%)	102	62 ± 7 (42 - 76)	63 (62%)
Rome	189	68 ± 8 (47 - 92)	58 ± 8 (45 - 85)	96 (51%)	95	69 ± 10 (44 - 91)	43 (45%)
Norway - Trondheim	602	74 ± 11 (31 - 100)	59 ± 11 (28 - 88)	350 (58%)	526	71 ± 12 (44 - 107)	293 (56%)
Poland - Katowice	349	70 ± 11 (39 - 94)	57 ± 12 (25 - 81)	218 (62%)	340	64 ± 16 (23 - 98)	157 (46%)
Sweden – Stockholm	91	76 ± 9 (56 - 94)	66 ± 11 (39 - 90)	51 (56%)	180	74 ± 10 (53 - 96)	79 (44%)
United States							
Jacksonville, FL	377	71 ± 11 (35 - 91)	62 ± 12 (28 - 83)	209 (55%)	364	73 ± 11 (34 - 93)	189 (52%)
Rochester, MN	748	68 ± 9 (32 - 98)	64 ± 9 (23 - 88)	453 (61%)	176	60 ± 6 (43 - 77)	111 (63%)
Asian series	1351				938		
Japan – Tokyo	171	49±13 (22 - 88)	40±11 (21 - 80)	92 (54%)	90	57±16 (23 - 89)	42 (47%)
Korea							
Anyang Hallym	150	61±14 (20 - 89)	59±14 (20 - 89)	78 (52%)	144	52±6 (42 - 72)	16 (11%)
Seoul	661	65±9 (33 - 91)	55±9 (23 - 85)	292 (44%)	406	63±9 (37 - 85)	174 (43%)
Taiwan – Taipei	369	NA	58±11 (26 - 83)	210 (57%)	298	NA	90 (30%)

The sample median ± SD (minimum – maximum) is given for age and age at onset. Information was unavailable regarding age in the Caucasian series for 147 patients with PD (105 Luebeck, 39 Tuebingen, 1 Athens, 1 Trondheim, 1 Rochester) and 21 controls (12 Luebeck, 4 Tuebingen, 2 Milan, 2 Katowice, 1 Rochester). Information was unavailable regarding age in the Asian series for 371 patients with PD (2 Tokyo, 369 Taipei) and 298 controls (298 Taipei). Information was unavailable regarding age at onset for 723 patients in the Caucasian series (10 Queensland, 15 Frankfurt, 147 Luebeck, 330 Tuebingen, 2 Athens, 109 Dublin, 1 Rome, 90 Trondheim, 5 Katowice, 2 Stockholm, 4 Jacksonville, 8 Rochester) and 8 patients in the Asian series (8 Taipei).

Supplementary Table 2: Primer sequences

Gene	rs Number	PCR Primer Forward	PCR Primer Reverse	Extend Primer
SNCA	rs181489	ACGTTGGATGCTCTATTTTAGAATACAAAC	ACGTTGGATGCTGTAAGTGGAAAGTTATAG	TATAGATATTATCAAAGAACCAAGAA
SNCA	rs356219	ACGTTGGATGCATGGGTATACTGGTGGTTC	ACGTTGGATGATGTATAAGAAAACAAACAC	ataatAAAACAAACACAAAATTCCA
SNCA	rs11931074	ACGTTGGATGACAGTCAAATGGCAGCCTTC	ACGTTGGATGTCTTCCTCGGAAGAGATACC	AATTGTGAATATGTCTTTGACTG
SNCA	rs2583988	ACGTTGGATGACAACAGACCAATGTGAGAG	ACGTTGGATGGTTTGGAATCATGTTAAACG	gaagCATGTTAAACGTTTATAAGAAGT
LRRK2	rs7133914	ACGTTGGATGGGATTCTTGCCTGTCGTTTG	ACGTTGGATGTCGCTGCGTCATAAAATGGG	ttcTGAGTACTATAGAATTCCTCA

Supplementary Table 3a: Genotype counts and frequencies for each series

Variant/Series	Minor allele count, %	Major allele count, %	Minor-Minor genotype count, %	Heterozygous count, %	Major-Major count, %
SNCA rs181489					
Asian patients	T: 6 (0.2%)	C: 2650 (99.8%)	0 (0.0%)	6 (0.5%)	1322 (99.5%)
Asian controls	T: 1 (0.1%)	C: 1613 (99.9%)	0 (0.0%)	1 (0.1%)	806 (99.9%)
Caucasian patients	T: 4010 (34.7%)	C: 7546 (65.3%)	743 (12.9%)	2524 (43.7%)	2511 (43.5%)
Caucasian controls	T: 2468 (29.7%)	C: 5832 (70.3%)	369 (8.9%)	1730 (41.7%)	2051 (49.4%)
SNCA rs356219					
Asian patients	A: 957 (36.6%)	G: 1655 (63.4%)	169 (12.9%)	619 (47.4%)	518 (39.7%)
Asian controls	A: 826 (46.4%)	G: 956 (53.6%)	198 (22.2%)	430 (48.3%)	263 (29.5%)
Caucasian patients	G: 5007 (42.6%)	A: 6735 (57.4%)	1084 (18.5%)	2839 (48.4%)	1948 (33.2%)
Caucasian controls	G: 3273 (38.4%)	A: 5259 (61.6%)	630 (14.8%)	2013 (47.2%)	1623 (38.0%)
SNCA rs11931074					
Asian patients	G: 1012 (37.6%)	T: 1678 (62.4%)	184 (13.7%)	644 (47.9%)	517 (38.4%)
Asian controls	G: 868 (46.5%)	T: 998 (53.5%)	208 (22.3%)	452 (48.4%)	273 (29.3%)
Caucasian patients	T: 1089 (9.1%)	G: 10815 (90.9%)	48 (0.8%)	993 (16.7%)	4911 (82.5%)
Caucasian controls	T: 610 (7.1%)	G: 7992 (92.9%)	25 (0.6%)	560 (13.0%)	3716 (86.4%)
SNCA rs2583988					
Asian patients	T: 0 (0.0%)	C: 2660 (100.0%)	0 (0.0%)	0 (0.0%)	1330 (100.0%)
Asian controls	T: 1 (0.1%)	C: 1851 (99.9%)	0 (0.0%)	1 (0.1%)	925 (99.9%)
Caucasian patients	T: 3620 (30.5%)	C: 8234 (69.5%)	593 (10.0%)	2434 (41.1%)	2900 (48.9%)
Caucasian controls	T: 2270 (26.5%)	C: 6304 (73.5%)	333 (7.8%)	1604 (37.4%)	2350 (54.8%)
LRRK2 p.R1398H					
Asian patients	A: 284 (10.6%)	G: 2406 (89.4%)	23 (1.7%)	238 (17.7%)	1084 (80.6%)
Asian controls	A: 239 (12.8%)	G: 1623 (87.2%)	9 (1.0%)	221 (23.7%)	701 (75.3%)
Caucasian patients	A: 742 (6.3%)	G: 11046 (93.7%)	30 (0.5%)	682 (11.6%)	5182 (87.9%)
Caucasian controls	A: 617 (7.2%)	G: 7947 (92.8%)	15 (0.4%)	587 (13.7%)	3680 (85.9%)
MAPT rs1052553					
Asian patients	G: 5 (0.2%)	A: 2615 (99.8%)	0 (0.0%)	5 (0.4%)	1305 (99.6%)
Asian controls	G: 0 (0.0%)	A: 1852 (100%)	0 (0.0%)	0 (0.0%)	926 (100.0%)
Caucasian patients	G: 2111 (17.6%)	A: 9871 (82.4%)	218 (3.6%)	1675 (28.0%)	4098 (68.4%)
Caucasian controls	G: 1794 (20.7%)	A: 6868 (79.3%)	211 (4.9%)	1372 (31.7%)	2748 (63.4%)

Supplementary Table 3b: Genotype counts and frequencies for *SNCA* rs181489 for each site

Series	Country/Site	Disease group	Minor allele count, %	Major allele count, %	Minor-Minor count, %	Heterozygous count, %	Major-Major count, %
Caucasian	Australia – Queensland	PD	T: 593 (33.1%)	C: 1197 (66.9%)	98 (10.9%)	397 (44.4%)	400 (44.7%)
Caucasian	Australia – Queensland	Controls	T: 423 (30.9%)	C: 947 (69.1%)	58 (8.5%)	307 (44.8%)	320 (46.7%)
Caucasian	France – Lille	PD	T: 352 (33.1%)	C: 710 (66.9%)	57 (10.7%)	238 (44.8%)	236 (44.4%)
Caucasian	France – Lille	Controls	T: 83 (30.3%)	C: 191 (69.7%)	11 (8.0%)	61 (44.5%)	65 (47.4%)
Caucasian	Germany – Frankfurt	PD	T: 157 (35.0%)	C: 291 (65.0%)	19 (8.5%)	119 (53.1%)	86 (38.4%)
Caucasian	Germany – Frankfurt	Controls	T: 32 (39.0%)	C: 50 (61.0%)	7 (17.1%)	18 (43.9%)	16 (39.0%)
Caucasian	Germany – Luebeck	PD	T: 344 (36.4%)	C: 602 (63.6%)	85 (18.0%)	174 (36.8%)	214 (45.2%)
Caucasian	Germany – Luebeck	Controls	T: 157 (29.6%)	C: 373 (70.4%)	25 (9.4%)	107 (40.4%)	133 (50.2%)
Caucasian	Germany – Tuebingen	PD	T: 223 (34.1%)	C: 431 (65.9%)	39 (11.9%)	145 (44.3%)	143 (43.7%)
Caucasian	Germany – Tuebingen	Controls	T: 198 (29.3%)	C: 478 (70.7%)	29 (8.6%)	140 (41.4%)	169 (50.0%)
Caucasian	Greece – Athens	PD	T: 100 (39.4%)	C: 154 (60.6%)	17 (13.4%)	66 (52.0%)	44 (34.6%)
Caucasian	Greece – Athens	Controls	T: 57 (31.7%)	C: 123 (68.3%)	10 (11.1%)	37 (41.1%)	43 (47.8%)
Caucasian	Greece – Thessaly	PD	T: 215 (37.5%)	C: 359 (62.5%)	46 (16.0%)	123 (42.9%)	118 (41.1%)
Caucasian	Greece – Thessaly	Controls	T: 156 (29.2%)	C: 378 (70.8%)	17 (6.4%)	122 (45.7%)	128 (47.9%)
Caucasian	Ireland – Dublin	PD	T: 262 (38.1%)	C: 426 (61.9%)	58 (16.9%)	146 (42.4%)	140 (40.7%)
Caucasian	Ireland – Dublin	Controls	T: 232 (27.4%)	C: 614 (72.6%)	38 (9.0%)	156 (36.9%)	229 (54.1%)
Caucasian	Italy – Mangone	PD	T: 125 (34.7%)	C: 235 (65.3%)	20 (11.1%)	85 (47.2%)	75 (41.7%)
Caucasian	Italy – Mangone	Controls	T: 89 (26.6%)	C: 245 (73.4%)	9 (5.4%)	71 (42.5%)	87 (52.1%)
Caucasian	Italy – Milan	PD	T: 61 (37.2%)	C: 103 (62.8%)	8 (9.8%)	45 (54.9%)	29 (35.4%)
Caucasian	Italy – Milan	Controls	T: 39 (27.5%)	C: 103 (72.5%)	9 (12.7%)	21 (29.6%)	41 (57.7%)
Caucasian	Italy – Rome	PD	T: 144 (38.1%)	C: 234 (61.9%)	28 (14.8%)	88 (46.6%)	73 (38.6%)
Caucasian	Italy – Rome	Controls	T: 59 (31.1%)	C: 131 (68.9%)	8 (8.4%)	43 (45.3%)	44 (46.3%)
Caucasian	Norway – Trondheim	PD	T: 392 (32.6%)	C: 812 (67.4%)	80 (13.3%)	232 (38.5%)	290 (48.2%)
Caucasian	Norway – Trondheim	Controls	T: 340 (32.4%)	C: 708 (67.6%)	56 (10.7%)	228 (43.5%)	240 (45.8%)
Caucasian	Poland – Katowice	PD	T: 238 (34.1%)	C: 460 (65.9%)	47 (13.5%)	144 (41.3%)	158 (45.3%)
Caucasian	Poland – Katowice	Controls	T: 195 (29.0%)	C: 477 (71.0%)	30 (8.9%)	135 (40.2%)	171 (50.9%)
Caucasian	Sweden – Stockholm	PD	T: 50 (27.8%)	C: 130 (72.2%)	10 (11.1%)	30 (33.3%)	50 (55.6%)
Caucasian	Sweden – Stockholm	Controls	T: 102 (29.0%)	C: 250 (71.0%)	17 (9.7%)	68 (38.6%)	91 (51.7%)
Caucasian	United States - Jacksonville, FL	PD	T: 270 (36.0%)	C: 480 (64.0%)	50 (13.3%)	170 (45.3%)	155 (41.3%)
Caucasian	United States - Jacksonville, FL	Controls	T: 201 (27.9%)	C: 519 (72.1%)	32 (8.9%)	137 (38.1%)	191 (53.1%)
Caucasian	United States - Rochester, MN	PD	T: 484 (34.4%)	C: 922 (65.6%)	81 (11.5%)	322 (45.8%)	300 (42.7%)
Caucasian	United States - Rochester, MN	Controls	T: 105 (30.0%)	C: 245 (70.0%)	13 (7.4%)	79 (45.1%)	83 (47.4%)
Asian	Japan – Tokyo	PD	T: 0 (0.0%)	C: 338 (100.0%)	0 (0.0%)	0 (0.0%)	169 (100.0%)
Asian	Japan – Tokyo	Controls	T: 0 (0.0%)	C: 166 (100.0%)	0 (0.0%)	0 (0.0%)	83 (100.0%)
Asian	Korea - Anyang Hallym	PD	T: 3 (1.1%)	C: 281 (98.9%)	0 (0.0%)	3 (2.1%)	139 (97.9%)
Asian	Korea - Anyang Hallym	Controls	T: 1 (0.4%)	C: 279 (99.6%)	0 (0.0%)	1 (0.7%)	139 (99.3%)
Asian	Korea - Seoul – Cases	PD	T: 0 (0.0%)	C: 1300 (100.0%)	0 (0.0%)	0 (0.0%)	650 (100.0%)
Asian	Korea - Seoul - Controls	Controls	T: 0 (0.0%)	C: 794 (100.0%)	0 (0.0%)	0 (0.0%)	397 (100.0%)
Asian	Taiwan - Taipei - Cases	PD	T: 3 (0.4%)	C: 731 (99.6%)	0 (0.0%)	3 (0.8%)	364 (99.2%)
Asian	Taiwan - Taipei - Controls	Controls	T: 0 (0.0%)	C: 374 (100.0%)	0 (0.0%)	0 (0.0%)	187 (100.0%)

Supplementary Table 3c: Genotype counts and frequencies for *SNCA* rs356219 for each site

Series	Country/Site	Disease group	Minor allele count, %	Major allele count, %	Minor-Minor genotype count, %	Heterozygous count, %	Major-Major count, %
Caucasian	Australia – Queensland	PD	G: 749 (41.4%)	A: 1059 (58.6%)	147 (16.3%)	455 (50.3%)	302 (33.4%)
Caucasian	Australia – Queensland	Controls	G: 541 (39.0%)	A: 847 (61.0%)	102 (14.7%)	337 (48.6%)	255 (36.7%)
Caucasian	France – Lille	PD	G: 461 (42.1%)	A: 633 (57.9%)	93 (17.0%)	275 (50.3%)	179 (32.7%)
Caucasian	France – Lille	Controls	G: 110 (39.0%)	A: 172 (61.0%)	20 (14.2%)	70 (49.6%)	51 (36.2%)
Caucasian	Germany – Frankfurt	PD	G: 200 (43.5%)	A: 260 (56.5%)	36 (15.7%)	128 (55.7%)	66 (28.7%)
Caucasian	Germany – Frankfurt	Controls	G: 35 (39.8%)	A: 53 (60.2%)	7 (15.9%)	21 (47.7%)	16 (36.4%)
Caucasian	Germany – Luebeck	PD	G: 453 (45.0%)	A: 553 (55.0%)	110 (21.9%)	233 (46.3%)	160 (31.8%)
Caucasian	Germany – Luebeck	Controls	G: 212 (36.8%)	A: 364 (63.2%)	38 (13.2%)	136 (47.2%)	114 (39.6%)
Caucasian	Germany – Tuebingen	PD	G: 288 (43.8%)	A: 370 (56.2%)	69 (21.0%)	150 (45.6%)	110 (33.4%)
Caucasian	Germany – Tuebingen	Controls	G: 238 (35.1%)	A: 440 (64.9%)	41 (12.1%)	156 (46.0%)	142 (41.9%)
Caucasian	Greece – Athens	PD	G: 123 (46.6%)	A: 141 (53.4%)	28 (21.2%)	67 (50.8%)	37 (28.0%)
Caucasian	Greece – Athens	Controls	G: 73 (41.0%)	A: 105 (59.0%)	18 (20.2%)	37 (41.6%)	34 (38.2%)
Caucasian	Greece – Thessaly	PD	G: 260 (41.8%)	A: 362 (58.2%)	61 (19.6%)	138 (44.4%)	112 (36.0%)
Caucasian	Greece – Thessaly	Controls	G: 230 (37.1%)	A: 390 (62.9%)	36 (11.6%)	158 (51.0%)	116 (37.4%)
Caucasian	Ireland – Dublin	PD	G: 331 (47.0%)	A: 373 (53.0%)	76 (21.6%)	179 (50.9%)	97 (27.6%)
Caucasian	Ireland – Dublin	Controls	G: 406 (47.5%)	A: 448 (52.5%)	106 (24.8%)	194 (45.4%)	127 (29.7%)
Caucasian	Italy – Mangone	PD	G: 150 (41.0%)	A: 216 (59.0%)	27 (14.8%)	96 (52.5%)	60 (32.8%)
Caucasian	Italy – Mangone	Controls	G: 113 (34.0%)	A: 219 (66.0%)	22 (13.3%)	69 (41.6%)	75 (45.2%)
Caucasian	Italy – Milan	PD	G: 86 (46.7%)	A: 98 (53.3%)	20 (21.7%)	46 (50.0%)	26 (28.3%)
Caucasian	Italy – Milan	Controls	G: 70 (34.7%)	A: 132 (65.3%)	14 (13.9%)	42 (41.6%)	45 (44.6%)
Caucasian	Italy – Rome	PD	G: 166 (45.1%)	A: 202 (54.9%)	38 (20.7%)	90 (48.9%)	56 (30.4%)
Caucasian	Italy – Rome	Controls	G: 65 (35.3%)	A: 119 (64.7%)	10 (10.9%)	45 (48.9%)	37 (40.2%)
Caucasian	Norway – Trondheim	PD	G: 526 (43.8%)	A: 674 (56.2%)	124 (20.7%)	278 (46.3%)	198 (33.0%)
Caucasian	Norway – Trondheim	Controls	G: 430 (40.9%)	A: 622 (59.1%)	84 (16.0%)	262 (49.8%)	180 (34.2%)
Caucasian	Poland - Katowice	PD	G: 278 (40.8%)	A: 404 (59.2%)	64 (18.8%)	150 (44.0%)	127 (37.2%)
Caucasian	Poland - Katowice	Controls	G: 242 (35.8%)	A: 434 (64.2%)	40 (11.8%)	162 (47.9%)	136 (40.2%)
Caucasian	Sweden – Stockholm	PD	G: 68 (37.8%)	A: 112 (62.2%)	15 (16.7%)	38 (42.2%)	37 (41.1%)
Caucasian	Sweden – Stockholm	Controls	G: 130 (36.3%)	A: 228 (63.7%)	25 (14.0%)	80 (44.7%)	74 (41.3%)
Caucasian	United States - Jacksonville, FL	PD	G: 339 (45.3%)	A: 409 (54.7%)	80 (21.4%)	179 (47.9%)	115 (30.7%)
Caucasian	United States - Jacksonville, FL	Controls	G: 248 (34.8%)	A: 464 (65.2%)	44 (12.4%)	160 (44.9%)	152 (42.7%)
Caucasian	United States - Rochester, MN	PD	G: 529 (37.8%)	A: 869 (62.2%)	96 (13.7%)	337 (48.2%)	266 (38.1%)
Caucasian	United States - Rochester, MN	Controls	G: 130 (36.9%)	A: 222 (63.1%)	23 (13.1%)	84 (47.7%)	69 (39.2%)
Asian	Japan – Tokyo	PD	A: 111 (32.6%)	G: 229 (67.4%)	18 (10.6%)	75 (44.1%)	77 (45.3%)
Asian	Japan – Tokyo	Controls	A: 73 (44.0%)	G: 93 (56.0%)	14 (16.9%)	45 (54.2%)	24 (28.9%)
Asian	Korea - Anyang Hallym	PD	A: 92 (35.1%)	G: 170 (64.9%)	18 (13.7%)	56 (42.7%)	57 (43.5%)
Asian	Korea - Anyang Hallym	Controls	A: 106 (44.2%)	G: 134 (55.8%)	28 (23.3%)	50 (41.7%)	42 (35.0%)
Asian	Korea – Seoul	PD	A: 472 (36.4%)	G: 824 (63.6%)	78 (12.0%)	316 (48.8%)	254 (39.2%)
Asian	Korea – Seoul	Controls	A: 362 (45.5%)	G: 434 (54.5%)	88 (22.1%)	186 (46.7%)	124 (31.2%)
Asian	Taiwan – Taipei	PD	A: 282 (39.5%)	G: 432 (60.5%)	55 (15.4%)	172 (48.2%)	130 (36.4%)
Asian	Taiwan – Taipei	Controls	A: 285 (49.1%)	G: 295 (50.9%)	68 (23.4%)	149 (51.4%)	73 (25.2%)

Supplementary Table 3d: Genotype counts and frequencies for *SNCA* rs11931074 for each site

Series	Country/Site	Disease group	Minor allele count, %	Major allele count, %	Minor-Minor genotype count, %	Heterozygous count, %	Major-Major count, %
Caucasian	Australia – Queensland	PD	T: 150 (8.2%)	G: 1678 (91.8%)	6 (0.7%)	138 (15.1%)	770 (84.2%)
Caucasian	Australia – Queensland	Controls	T: 102 (7.2%)	G: 1310 (92.8%)	4 (0.6%)	94 (13.3%)	608 (86.1%)
Caucasian	France – Lille	PD	T: 96 (8.8%)	G: 998 (91.2%)	4 (0.7%)	88 (16.1%)	455 (83.2%)
Caucasian	France – Lille	Controls	T: 20 (7.0%)	G: 266 (93.0%)	1 (0.7%)	18 (12.6%)	124 (86.7%)
Caucasian	Germany – Frankfurt	PD	T: 45 (9.7%)	G: 419 (90.3%)	5 (2.2%)	35 (15.1%)	192 (82.8%)
Caucasian	Germany – Frankfurt	Controls	T: 5 (5.3%)	G: 89 (94.7%)	0 (0.0%)	5 (10.6%)	42 (89.4%)
Caucasian	Germany – Luebeck	PD	T: 81 (7.9%)	G: 941 (92.1%)	5 (1.0%)	71 (13.9%)	435 (85.1%)
Caucasian	Germany – Luebeck	Controls	T: 37 (6.4%)	G: 539 (93.6%)	1 (0.3%)	35 (12.2%)	252 (87.5%)
Caucasian	Germany – Tuebingen	PD	T: 62 (9.4%)	G: 598 (90.6%)	4 (1.2%)	54 (16.4%)	272 (82.4%)
Caucasian	Germany – Tuebingen	Controls	T: 43 (6.4%)	G: 633 (93.6%)	3 (0.9%)	37 (10.9%)	298 (88.2%)
Caucasian	Greece – Athens	PD	T: 21 (7.9%)	G: 245 (92.1%)	2 (1.5%)	17 (12.8%)	114 (85.7%)
Caucasian	Greece – Athens	Controls	T: 8 (4.4%)	G: 174 (95.6%)	0 (0.0%)	8 (8.8%)	83 (91.2%)
Caucasian	Greece – Thessaly	PD	T: 58 (9.3%)	G: 564 (90.7%)	0 (0.0%)	58 (18.6%)	253 (81.4%)
Caucasian	Greece – Thessaly	Controls	T: 52 (8.4%)	G: 566 (91.6%)	2 (0.6%)	48 (15.5%)	259 (83.8%)
Caucasian	Ireland – Dublin	PD	T: 68 (9.5%)	G: 646 (90.5%)	2 (0.6%)	64 (17.9%)	291 (81.5%)
Caucasian	Ireland – Dublin	Controls	T: 55 (6.2%)	G: 831 (93.8%)	3 (0.7%)	49 (11.1%)	391 (88.3%)
Caucasian	Italy – Mangone	PD	T: 26 (7.1%)	G: 342 (92.9%)	0 (0.0%)	26 (14.1%)	158 (85.9%)
Caucasian	Italy – Mangone	Controls	T: 28 (8.3%)	G: 308 (91.7%)	1 (0.6%)	26 (15.5%)	141 (83.9%)
Caucasian	Italy – Milan	PD	T: 25 (13.2%)	G: 165 (86.8%)	2 (2.1%)	21 (22.1%)	72 (75.8%)
Caucasian	Italy – Milan	Controls	T: 12 (6.0%)	G: 188 (94.0%)	0 (0.0%)	12 (12.0%)	88 (88.0%)
Caucasian	Italy – Rome	PD	T: 38 (10.2%)	G: 336 (89.8%)	3 (1.6%)	32 (17.1%)	152 (81.3%)
Caucasian	Italy – Rome	Controls	T: 14 (7.5%)	G: 172 (92.5%)	0 (0.0%)	14 (15.1%)	79 (84.9%)
Caucasian	Norway – Trondheim	PD	T: 136 (11.5%)	G: 1046 (88.5%)	5 (0.8%)	126 (21.3%)	460 (77.8%)
Caucasian	Norway – Trondheim	Controls	T: 82 (7.9%)	G: 956 (92.1%)	2 (0.4%)	78 (15.0%)	439 (84.6%)
Caucasian	Poland - Katowice	PD	T: 53 (7.6%)	G: 641 (92.4%)	2 (0.6%)	49 (14.1%)	296 (85.3%)
Caucasian	Poland - Katowice	Controls	T: 45 (6.6%)	G: 633 (93.4%)	3 (0.9%)	39 (11.5%)	297 (87.6%)
Caucasian	Sweden – Stockholm	PD	T: 18 (10.0%)	G: 162 (90.0%)	0 (0.0%)	18 (20.0%)	72 (80.0%)
Caucasian	Sweden – Stockholm	Controls	T: 28 (7.8%)	G: 332 (92.2%)	0 (0.0%)	28 (15.6%)	152 (84.4%)
Caucasian	United States - Jacksonville, FL	PD	T: 76 (10.1%)	G: 676 (89.9%)	3 (0.8%)	70 (18.6%)	303 (80.6%)
Caucasian	United States - Jacksonville, FL	Controls	T: 55 (7.6%)	G: 669 (92.4%)	4 (1.1%)	47 (13.0%)	311 (85.9%)
Caucasian	United States - Rochester, MN	PD	T: 136 (9.1%)	G: 1358 (90.9%)	5 (0.7%)	126 (16.9%)	616 (82.5%)
Caucasian	United States - Rochester, MN	Controls	T: 24 (6.9%)	G: 326 (93.1%)	1 (0.6%)	22 (12.6%)	152 (86.9%)
Asian	Japan – Tokyo	PD	G: 112 (33.1%)	T: 226 (66.9%)	19 (11.2%)	74 (43.8%)	76 (45.0%)
Asian	Japan – Tokyo	Controls	G: 86 (47.8%)	T: 94 (52.2%)	20 (22.2%)	46 (51.1%)	24 (26.7%)
Asian	Korea - Anyang Hallym	PD	G: 117 (39.8%)	T: 177 (60.2%)	26 (17.7%)	65 (44.2%)	56 (38.1%)
Asian	Korea - Anyang Hallym	Controls	G: 136 (47.9%)	T: 148 (52.1%)	33 (23.2%)	70 (49.3%)	39 (27.5%)
Asian	Korea – Seoul	PD	G: 486 (36.8%)	T: 836 (63.2%)	81 (12.3%)	324 (49.0%)	256 (38.7%)
Asian	Korea – Seoul	Controls	G: 367 (45.4%)	T: 441 (54.6%)	90 (22.3%)	187 (46.3%)	127 (31.4%)
Asian	Taiwan – Taipei	PD	G: 297 (40.4%)	T: 439 (59.6%)	58 (15.8%)	181 (49.2%)	129 (35.1%)
Asian	Taiwan - Taipei	Controls	G: 279 (47.0%)	T: 315 (53.0%)	65 (21.9%)	149 (50.2%)	83 (27.9%)

Supplementary Table 3e: Genotype counts and frequencies for *SNCA* rs2583988 for each site

Series	Country/Site	Disease group	Minor allele count, %	Major allele count, %	Minor-Minor genotype count, %	Heterozygous count, %	Major-Major count, %
Caucasian	Australia – Queensland	PD	T: 522 (28.5%)	C: 1310 (71.5%)	70 (7.6%)	382 (41.7%)	464 (50.7%)
Caucasian	Australia – Queensland	Controls	T: 388 (27.6%)	C: 1018 (72.4%)	56 (8.0%)	276 (39.3%)	371 (52.8%)
Caucasian	France – Lille	PD	T: 348 (31.8%)	C: 746 (68.2%)	53 (9.7%)	242 (44.2%)	252 (46.1%)
Caucasian	France – Lille	Controls	T: 77 (26.9%)	C: 209 (73.1%)	8 (5.6%)	61 (42.7%)	74 (51.7%)
Caucasian	Germany – Frankfurt	PD	T: 135 (29.3%)	C: 325 (70.7%)	18 (7.8%)	99 (43.0%)	113 (49.1%)
Caucasian	Germany – Frankfurt	Controls	T: 29 (32.2%)	C: 61 (67.8%)	6 (13.3%)	17 (37.8%)	22 (48.9%)
Caucasian	Germany – Luebeck	PD	T: 345 (33.8%)	C: 677 (66.2%)	70 (13.7%)	205 (40.1%)	236 (46.2%)
Caucasian	Germany – Luebeck	Controls	T: 147 (25.5%)	C: 429 (74.5%)	22 (7.6%)	103 (35.8%)	163 (56.6%)
Caucasian	Germany – Tuebingen	PD	T: 195 (29.5%)	C: 465 (70.5%)	32 (9.7%)	131 (39.7%)	167 (50.6%)
Caucasian	Germany – Tuebingen	Controls	T: 180 (26.6%)	C: 496 (73.4%)	21 (6.2%)	138 (40.8%)	179 (53.0%)
Caucasian	Greece – Athens	PD	T: 81 (30.7%)	C: 183 (69.3%)	9 (6.8%)	63 (47.7%)	60 (45.5%)
Caucasian	Greece – Athens	Controls	T: 56 (29.8%)	C: 132 (70.2%)	9 (9.6%)	38 (40.4%)	47 (50.0%)
Caucasian	Greece – Thessaly	PD	T: 194 (31.4%)	C: 424 (68.6%)	35 (11.3%)	124 (40.1%)	150 (48.5%)
Caucasian	Greece – Thessaly	Controls	T: 164 (27.2%)	C: 438 (72.8%)	25 (8.3%)	114 (37.9%)	162 (53.8%)
Caucasian	Ireland – Dublin	PD	T: 233 (33.8%)	C: 457 (66.2%)	38 (11.0%)	157 (45.5%)	150 (43.5%)
Caucasian	Ireland – Dublin	Controls	T: 222 (25.7%)	C: 642 (74.3%)	33 (7.6%)	156 (36.1%)	243 (56.2%)
Caucasian	Italy – Mangone	PD	T: 116 (31.5%)	C: 252 (68.5%)	17 (9.2%)	82 (44.6%)	85 (46.2%)
Caucasian	Italy – Mangone	Controls	T: 74 (22.0%)	C: 262 (78.0%)	7 (4.2%)	60 (35.7%)	101 (60.1%)
Caucasian	Italy – Milan	PD	T: 52 (27.7%)	C: 136 (72.3%)	5 (5.3%)	42 (44.7%)	47 (50.0%)
Caucasian	Italy – Milan	Controls	T: 48 (23.5%)	C: 156 (76.5%)	7 (6.9%)	34 (33.3%)	61 (59.8%)
Caucasian	Italy – Rome	PD	T: 113 (29.9%)	C: 265 (70.1%)	18 (9.5%)	77 (40.7%)	94 (49.7%)
Caucasian	Italy – Rome	Controls	T: 44 (23.2%)	C: 146 (76.8%)	5 (5.3%)	34 (35.8%)	56 (58.9%)
Caucasian	Norway – Trondheim	PD	T: 367 (30.5%)	C: 835 (69.5%)	74 (12.3%)	219 (36.4%)	308 (51.2%)
Caucasian	Norway – Trondheim	Controls	T: 333 (31.7%)	C: 719 (68.3%)	57 (10.8%)	219 (41.6%)	250 (47.5%)
Caucasian	Poland - Katowice	PD	T: 195 (28.0%)	C: 501 (72.0%)	33 (9.5%)	129 (37.1%)	186 (53.4%)
Caucasian	Poland - Katowice	Controls	T: 155 (23.1%)	C: 517 (76.9%)	27 (8.0%)	101 (30.1%)	208 (61.9%)
Caucasian	Sweden – Stockholm	PD	T: 47 (25.8%)	C: 135 (74.2%)	5 (5.5%)	37 (40.7%)	49 (53.8%)
Caucasian	Sweden – Stockholm	Controls	T: 89 (24.9%)	C: 269 (75.1%)	15 (8.4%)	59 (33.0%)	105 (58.7%)
Caucasian	United States - Jacksonville, FL	PD	T: 246 (32.6%)	C: 508 (67.4%)	40 (10.6%)	166 (44.0%)	171 (45.4%)
Caucasian	United States - Jacksonville, FL	Controls	T: 168 (23.3%)	C: 554 (76.7%)	22 (6.1%)	124 (34.3%)	215 (59.6%)
Caucasian	United States - Rochester, MN	PD	T: 431 (29.8%)	C: 1015 (70.2%)	76 (10.5%)	279 (38.6%)	368 (50.9%)
Caucasian	United States - Rochester, MN	Controls	T: 96 (27.3%)	C: 256 (72.7%)	13 (7.4%)	70 (39.8%)	93 (52.8%)
Asian	Japan – Tokyo	PD	T: 0 (0.0%)	C: 340 (100.0%)	0 (0.0%)	0 (0.0%)	170 (100.0%)
Asian	Japan – Tokyo	Controls	T: 0 (0.0%)	C: 178 (100.0%)	0 (0.0%)	0 (0.0%)	89 (100.0%)
Asian	Korea - Anyang Hallym	PD	T: 0 (0.0%)	C: 294 (100.0%)	0 (0.0%)	0 (0.0%)	147 (100.0%)
Asian	Korea - Anyang Hallym	Controls	T: 0 (0.0%)	C: 284 (100.0%)	0 (0.0%)	0 (0.0%)	142 (100.0%)
Asian	Korea – Seoul	PD	T: 0 (0.0%)	C: 1302 (100.0%)	0 (0.0%)	0 (0.0%)	651 (100.0%)
Asian	Korea – Seoul	Controls	T: 0 (0.0%)	C: 802 (100.0%)	0 (0.0%)	0 (0.0%)	401 (100.0%)
Asian	Taiwan – Taipei	PD	T: 0 (0.0%)	C: 724 (100.0%)	0 (0.0%)	0 (0.0%)	362 (100.0%)
Asian	Taiwan – Taipei	Controls	T: 1 (0.2%)	C: 587 (99.8%)	0 (0.0%)	1 (0.3%)	293 (99.7%)

Supplementary Table 3f: Genotype counts and frequencies for LRRK2 p.R1398H for each site

Series	Country/Site	Disease group	Minor allele count, %	Major allele count, %	Minor-Minor genotype count, %	Heterozygous count, %	Major-Major count, %
Caucasian	Australia - Queensland	PD	A: 109 (5.9%)	G: 1729 (94.1%)	6 (0.7%)	97 (10.6%)	816 (88.8%)
Caucasian	Australia - Queensland	Controls	A: 104 (7.3%)	G: 1316 (92.7%)	5 (0.7%)	94 (13.2%)	611 (86.1%)
Caucasian	France - Lille	PD	A: 48 (4.4%)	G: 1034 (95.6%)	3 (0.6%)	42 (7.8%)	496 (91.7%)
Caucasian	France - Lille	Controls	A: 12 (4.3%)	G: 270 (95.7%)	0 (0.0%)	12 (8.5%)	129 (91.5%)
Caucasian	Germany - Frankfurt	PD	A: 20 (4.4%)	G: 438 (95.6%)	1 (0.4%)	18 (7.9%)	210 (91.7%)
Caucasian	Germany - Frankfurt	Controls	A: 5 (5.3%)	G: 89 (94.7%)	0 (0.0%)	5 (10.6%)	42 (89.4%)
Caucasian	Germany - Luebeck	PD	A: 62 (6.1%)	G: 958 (93.9%)	4 (0.8%)	54 (10.6%)	452 (88.6%)
Caucasian	Germany - Luebeck	Controls	A: 52 (9.2%)	G: 516 (90.8%)	0 (0.0%)	52 (18.3%)	232 (81.7%)
Caucasian	Germany - Tuebingen	PD	A: 46 (7.0%)	G: 608 (93.0%)	2 (0.6%)	42 (12.8%)	283 (86.5%)
Caucasian	Germany - Tuebingen	Controls	A: 51 (7.5%)	G: 627 (92.5%)	1 (0.3%)	49 (14.5%)	289 (85.3%)
Caucasian	Greece - Athens	PD	A: 7 (2.6%)	G: 259 (97.4%)	0 (0.0%)	7 (5.3%)	126 (94.7%)
Caucasian	Greece - Athens	Controls	A: 7 (3.8%)	G: 179 (96.2%)	0 (0.0%)	7 (7.5%)	86 (92.5%)
Caucasian	Greece - Thessaly	PD	A: 27 (4.3%)	G: 601 (95.7%)	0 (0.0%)	27 (8.6%)	287 (91.4%)
Caucasian	Greece - Thessaly	Controls	A: 35 (6.0%)	G: 553 (94.0%)	0 (0.0%)	35 (11.9%)	259 (88.1%)
Caucasian	Ireland - Dublin	PD	A: 39 (5.5%)	G: 673 (94.5%)	4 (1.1%)	31 (8.7%)	321 (90.2%)
Caucasian	Ireland - Dublin	Controls	A: 73 (8.2%)	G: 815 (91.8%)	3 (0.7%)	67 (15.1%)	374 (84.2%)
Caucasian	Italy - Mangone	PD	A: 26 (7.2%)	G: 336 (92.8%)	1 (0.6%)	24 (13.3%)	156 (86.2%)
Caucasian	Italy - Mangone	Controls	A: 24 (7.2%)	G: 310 (92.8%)	0 (0.0%)	24 (14.4%)	143 (85.6%)
Caucasian	Italy - Milan	PD	A: 11 (6.0%)	G: 171 (94.0%)	0 (0.0%)	11 (12.1%)	80 (87.9%)
Caucasian	Italy - Milan	Controls	A: 8 (4.1%)	G: 186 (95.9%)	0 (0.0%)	8 (8.2%)	89 (91.8%)
Caucasian	Italy - Rome	PD	A: 20 (5.5%)	G: 346 (94.5%)	0 (0.0%)	20 (10.9%)	163 (89.1%)
Caucasian	Italy - Rome	Controls	A: 13 (6.9%)	G: 175 (93.1%)	0 (0.0%)	13 (13.8%)	81 (86.2%)
Caucasian	Norway - Trondheim	PD	A: 102 (8.5%)	G: 1094 (91.5%)	0 (0.0%)	102 (17.1%)	496 (82.9%)
Caucasian	Norway - Trondheim	Controls	A: 83 (8.0%)	G: 961 (92.0%)	3 (0.6%)	77 (14.8%)	442 (84.7%)
Caucasian	Poland - Katowice	PD	A: 43 (6.2%)	G: 655 (93.8%)	1 (0.3%)	41 (11.7%)	307 (88.0%)
Caucasian	Poland - Katowice	Controls	A: 42 (6.2%)	G: 638 (93.8%)	2 (0.6%)	38 (11.2%)	300 (88.2%)
Caucasian	Sweden - Stockholm	PD	A: 15 (8.4%)	G: 163 (91.6%)	2 (2.2%)	11 (12.4%)	76 (85.4%)
Caucasian	Sweden - Stockholm	Controls	A: 36 (10.5%)	G: 308 (89.5%)	1 (0.6%)	34 (19.8%)	137 (79.7%)
Caucasian	United States - Jacksonville, FL	PD	A: 65 (8.8%)	G: 675 (91.2%)	4 (1.1%)	57 (15.4%)	309 (83.5%)
Caucasian	United States - Jacksonville, FL	Controls	A: 52 (7.2%)	G: 674 (92.8%)	0 (0.0%)	52 (14.3%)	311 (85.7%)
Caucasian	United States - Rochester, MN	PD	A: 102 (7.2%)	G: 1306 (92.8%)	2 (0.3%)	98 (13.9%)	604 (85.8%)
Caucasian	United States - Rochester, MN	Controls	A: 20 (5.7%)	G: 330 (94.3%)	0 (0.0%)	20 (11.4%)	155 (88.6%)
Asian	Japan - Tokyo	PD	A: 39 (11.4%)	G: 303 (88.6%)	4 (2.3%)	31 (18.1%)	136 (79.5%)
Asian	Japan - Tokyo	Controls	A: 16 (9.0%)	G: 162 (91.0%)	0 (0.0%)	16 (18.0%)	73 (82.0%)
Asian	Korea - Anyang Hallym	PD	A: 40 (13.4%)	G: 258 (86.6%)	5 (3.4%)	30 (20.1%)	114 (76.5%)
Asian	Korea - Anyang Hallym	Controls	A: 46 (16%)	G: 242 (84.0%)	1 (0.7%)	44 (30.6%)	99 (68.8%)
Asian	Korea - Seoul	PD	A: 142 (10.8%)	G: 1172 (89.2%)	9 (1.4%)	124 (18.9%)	524 (79.8%)
Asian	Korea - Seoul	Controls	A: 117 (14.5%)	G: 689 (85.5%)	6 (1.5%)	105 (26.1%)	292 (72.5%)
Asian	Taiwan - Taipei	PD	A: 63 (8.6%)	G: 673 (91.4%)	5 (1.4%)	53 (14.4%)	310 (84.2%)
Asian	Taiwan - Taipei	Controls	A: 60 (10.2%)	G: 530 (89.8%)	2 (0.7%)	56 (19.0%)	237 (80.3%)

Supplementary Table 3g: Genotype counts and frequencies for *MAPT* rs1052553 for each site

Series	Country/Site	Disease group	Minor allele count, %	Major allele count, %	Minor-Minor genotype count, %	Heterozygous count, %	Major-Major count, %
Caucasian	Australia - Queensland	PD	G: 360 (19.5%)	A: 1486 (80.5%)	41 (4.4%)	278 (30.1%)	604 (65.4%)
Caucasian	Australia - Queensland	Controls	G: 344 (24.1%)	A: 1082 (75.9%)	40 (5.6%)	264 (37.0%)	409 (57.4%)
Caucasian	France - Lille	PD	G: 223 (20.3%)	A: 873 (79.7%)	31 (5.7%)	161 (29.4%)	356 (65.0%)
Caucasian	France - Lille	Controls	G: 59 (20.6%)	A: 227 (79.4%)	7 (4.9%)	45 (31.5%)	91 (63.6%)
Caucasian	Germany - Frankfurt	PD	G: 70 (15.1%)	A: 394 (84.9%)	4 (1.7%)	62 (26.7%)	166 (71.6%)
Caucasian	Germany - Frankfurt	Controls	G: 16 (17.0%)	A: 78 (83.0%)	0 (0.0%)	16 (34.0%)	31 (66.0%)
Caucasian	Germany - Luebeck	PD	G: 172 (16.8%)	A: 852 (83.2%)	18 (3.5%)	136 (26.6%)	358 (69.9%)
Caucasian	Germany - Luebeck	Controls	G: 110 (19.0%)	A: 468 (81.0%)	14 (4.8%)	82 (28.4%)	193 (66.8%)
Caucasian	Germany - Tuebingen	PD	G: 113 (17.1%)	A: 547 (82.9%)	9 (2.7%)	95 (28.8%)	226 (68.5%)
Caucasian	Germany - Tuebingen	Controls	G: 134 (19.8%)	A: 544 (80.2%)	14 (4.1%)	106 (31.3%)	219 (64.6%)
Caucasian	Greece - Athens	PD	G: 37 (13.8%)	A: 231 (86.2%)	3 (2.2%)	31 (23.1%)	100 (74.6%)
Caucasian	Greece - Athens	Controls	G: 37 (19.7%)	A: 151 (80.3%)	5 (5.3%)	27 (28.7%)	62 (66.0%)
Caucasian	Greece - Thessaly	PD	G: 121 (19.1%)	A: 511 (80.9%)	12 (3.8%)	97 (30.7%)	207 (65.5%)
Caucasian	Greece - Thessaly	Controls	G: 117 (18.8%)	A: 505 (81.2%)	11 (3.5%)	95 (30.5%)	205 (65.9%)
Caucasian	Ireland - Dublin	PD	G: 115 (16.0%)	A: 605 (84.0%)	12 (3.3%)	91 (25.3%)	257 (71.4%)
Caucasian	Ireland - Dublin	Controls	G: 196 (22.1%)	A: 692 (77.9%)	23 (5.2%)	150 (33.8%)	271 (61.0%)
Caucasian	Italy - Mangone	PD	G: 86 (23.2%)	A: 284 (76.8%)	8 (4.3%)	70 (37.8%)	107 (57.8%)
Caucasian	Italy - Mangone	Controls	G: 84 (25.0%)	A: 252 (75.0%)	10 (6.0%)	64 (38.1%)	94 (56.0%)
Caucasian	Italy - Milan	PD	G: 38 (20.0%)	A: 152 (80.0%)	4 (4.2%)	30 (31.6%)	61 (64.2%)
Caucasian	Italy - Milan	Controls	G: 60 (29.4%)	A: 144 (70.6%)	16 (15.7%)	28 (27.5%)	58 (56.9%)
Caucasian	Italy - Rome	PD	G: 91 (24.1%)	A: 287 (75.9%)	15 (7.9%)	61 (32.3%)	113 (59.8%)
Caucasian	Italy – Rome	Controls	G: 49 (25.8%)	A: 141 (74.2%)	5 (5.3%)	39 (41.1%)	51 (53.7%)
Caucasian	Norway - Trondheim	PD	G: 179 (14.9%)	A: 1025 (85.1%)	16 (2.7%)	147 (24.4%)	439 (72.9%)
Caucasian	Norway - Trondheim	Controls	G: 191 (18.2%)	A: 861 (81.8%)	18 (3.4%)	155 (29.5%)	353 (67.1%)
Caucasian	Poland – Katowice	PD	G: 95 (13.6%)	A: 603 (86.4%)	6 (1.7%)	83 (23.8%)	260 (74.5%)
Caucasian	Poland – Katowice	Controls	G: 100 (14.7%)	A: 580 (85.3%)	15 (4.4%)	70 (20.6%)	255 (75.0%)
Caucasian	Sweden – Stockholm	PD	G: 27 (14.8%)	A: 155 (85.2%)	2 (2.2%)	23 (25.3%)	66 (72.5%)
Caucasian	Sweden – Stockholm	Controls	G: 51 (14.2%)	A: 309 (85.8%)	3 (1.7%)	45 (25.0%)	132 (73.3%)
Caucasian	United States - Jacksonville, FL	PD	G: 143 (19.0%)	A: 611 (81.0%)	15 (4.0%)	113 (30.0%)	249 (66.0%)
Caucasian	United States - Jacksonville, FL	Controls	G: 173 (23.8%)	A: 555 (76.2%)	20 (5.5%)	133 (36.5%)	211 (58.0%)
Caucasian	United States - Rochester, MN	PD	G: 241 (16.1%)	A: 1255 (83.9%)	22 (2.9%)	197 (26.3%)	529 (70.7%)
Caucasian	United States - Rochester, MN	Controls	G: 73 (20.7%)	A: 279 (79.3%)	10 (5.7%)	53 (30.1%)	113 (64.2%)
Asian	Japan – Tokyo	PD	G: 0 (0.0%)	A: 338 (100.0%)	0 (0.0%)	0 (0.0%)	169 (100.0%)
Asian	Japan – Tokyo	Controls	G: 0 (0.0%)	A: 178 (100.0%)	0 (0.0%)	0 (0.0%)	89 (100.0%)
Asian	Korea - Anyang Hallym	PD	G: 1 (0.4%)	A: 281 (99.6%)	0 (0.0%)	1 (0.7%)	140 (99.3%)
Asian	Korea - Anyang Hallym	Controls	G: 0 (0.0%)	A: 270 (100.0%)	0 (0.0%)	0 (0.0%)	135 (100.0%)
Asian	Korea – Seoul	PD	G: 1 (0.1%)	A: 1269 (99.9%)	0 (0.0%)	1 (0.2%)	634 (99.8%)
Asian	Korea – Seoul	Controls	G: 0 (0.0%)	A: 810 (100.0%)	0 (0.0%)	0 (0.0%)	405 (100.0%)
Asian	Taiwan – Taipei	PD	G: 3 (0.4%)	A: 727 (99.6%)	0 (0.0%)	3 (0.8%)	362 (99.2%)
Asian	Taiwan – Taipei	Controls	G: 0 (0.0%)	A: 594 (100.0%)	0 (0.0%)	0 (0.0%)	297 (100.0%)

Supplementary Table 4: Single variant associations with PD

	Caucasian series (5991 PD, 4331 controls)			Asian series (1351 PD, 938 controls)		
Variant & Genotype/Model	Sample Frequency	OR (95% CI)	P-value	Sample Frequency	OR (95% CI)	P-value
SNCA rs181489						
Genotype						
CC	46.0%	1.00 (reference)	---	---	---	---
CT	42.8%	1.16 (1.06 - 1.26)	0.0012	---	---	---
TT	11.2%	1.67 (1.45 - 1.92)	1.4E-12	---	---	---
Additive		1.24 (1.17 - 1.32)	6.7E-12		---	---
Dominant	MAF: 32.6%	1.25 (1.15 - 1.35)	2.1E-7	---	---	---
Recessive		1.56 (1.36 - 1.78)	1.5E-10		---	---
SNCA rs356219[1]						
Genotype						
AA	35.2%	1.00 (reference)	---	16.7%	1.00 (reference)	---
AG	47.9%	1.17 (1.07 - 1.28)	7.0E-4	47.7%	1.66 (1.30 - 2.11)	4.0E-5
GG	16.9%	1.50 (1.33 - 1.70)	6.9E-11	35.5%	2.26 (1.75 - 2.92)	3.4E-10
Additive		1.21 (1.15 - 1.29)	9.1E-11		1.48 (1.31 - 1.68)	5.9E-10
Dominant	MAF: 40.8%	1.25 (1.15 - 1.36)	3.9E-7	MAF: 40.6%	1.88 (1.50 - 2.37)	4.5E-08
Recessive		1.37 (1.23 - 1.53)	2.0E-8		1.56 (1.30 - 1.87)	1.9E-06
SNCA rs11931074[1]						
Genotype						
GG	84.1%	1.00 (reference)	---	17.2%	1.00 (reference)	---
GT	15.1%	1.37 (1.22 - 1.54)	1.0E-7	48.1%	1.59 (1.26 - 2.01)	9.5E-5
TT	0.7%	1.38 (0.84 - 2.30)	0.21	34.7%	2.09 (1.63 - 2.68)	5.1E-9
Additive		1.34 (1.20 - 1.49)	1.1E-7		1.43 (1.26 - 1.61)	9.7E-9
Dominant	MAF: 8.3%	1.37 (1.22 - 1.53)	5.7E-8	MAF: 41.3%	1.78 (1.43 - 2.22)	2.8E-7
Recessive		1.31 (0.80 - 2.17)	0.28		1.49 (1.25 - 1.78)	1.4E-5
SNCA rs2583988[1]						
Genotype						
CC	51.4%	1.00 (reference)	---	---	---	---
CT	39.5%	1.22 (1.12 - 1.33)	7.70E-6	---	---	---
TT	9.1%	1.43 (1.24 - 1.67)	2.20E-6	---	---	---
Additive		1.21 (1.13 - 1.28)	5.9E-9		---	---
Dominant	MAF: 28.8%	1.25 (1.16 - 1.36)	5.0E-8	---	---	---
Recessive		1.32 (1.14 - 1.52)	1E-4		---	---
MAPT rs1052553						
Genotype[2]						
GG	4.2%	1.00 (reference)	---	---	---	---
GA	29.5%	1.21 (0.98 - 1.49)	0.077	---	---	---
AA	66.3%	1.49 (1.22 - 1.82)	0.00012	---	---	---
Additive		1.23 (1.14 - 1.32)	2.2E-8		---	---
Dominant	MAF: 18.9%	1.39 (1.14 - 1.70)	0.0012	---	---	---
Recessive		1.26 (1.16 - 1.37)	1.09E-7		---	---
LRRK2 p.R1398H						
Dominant	MAF: 6.7%			MAF: 11.5%		
GG	87.1%	1.00 (reference)	---	78.4%	1.00 (reference)	---
GA/AA	12.5%	0.87 (0.78 - 0.99)	0.028	21.6%	0.73 (0.60 - 0.90)	0.0026

ORs and p-values result from fixed-effects logistic regression models adjusted for site. For genotype models, ORs and p-values are given in comparison to the reference category of homozygotes of the major allele (*SNCA*, *LRRK2*) or minor allele (*MAPT*). For additive models, ORs and p-values correspond to an additional minor allele (*SNCA*, *LRRK2*) or major allele (*MAPT*). For dominant models, ORs and p-values correspond to presence of the minor allele (*SNCA*, *LRRK2*) or major allele (*MAPT*). For recessive models, ORs and p-values correspond to presence of two copies of the minor allele (*SNCA*, *LRRK2*) or major allele (*MAPT*). [1]The minor allele differed between the Caucasian and Asian series' for *SNCA* rs356219 and rs11931074; for easier interpretation of results, odds ratio estimates for these two *SNCA* variants correspond to the minor allele in the overall patient-control series of Caucasian and Asian individuals (rs356219: G; rs11931074: T), which is the major allele in the smaller Asian series. [2]The A allele for *MAPT* rs1052553 corresponds to the H1 haplotype. OR=odds ratio. CI=confidence interval. MAF=minor allele frequency. --- indicates a variant observed at a frequency too low in the given series to allow for association analysis.

Supplementary Table 5: Interactions of LRRK2 p.R1398H with *SNCA* and *MAPT* variants in regard to susceptibility to PD in the Caucasian series under a dominant model

			Test of association		
Variant/Genotype	LRRK2 p.R1398H	Sample genotype count and frequency	OR (95% CI)	P-value	Test of interaction
SNCA rs181489					
CC	GG	3908 (39.9%)	1.00 (reference)	N/A	OR: 1.13 95% CI: 0.88 - 1.44 P=0.33
CC	GA or AA	599 (6.1%)	0.82 (0.69 - 0.98)	0.030	
CT or TT	GG	4603 (47.0%)	1.23 (1.12 - 1.34)	6.3E-06	
CT or TT	GA or AA	678 (6.9%)	1.14 (0.96 - 1.35)	0.13	
SNCA rs356219					
AA	GG	3087 (30.9%)	1.00 (reference)	N/A	OR: 1.09 95% CI: 0.85 - 1.41 P=0.49
AA	GA or AA	440 (4.4%)	0.82 (0.67 - 1.01)	0.060	
AG or GG	GG	5618 (56.2%)	1.23 (1.12 - 1.35)	9.0E-06	
AG or GG	GA or AA	847 (8.5%)	1.10 (0.94 - 1.29)	0.22	
SNCA rs11931074					
GG	GG	7443 (73.6%)	1.00 (reference)	N/A	OR: 1.12 95% CI: 0.81 - 1.54 P=0.50
GG	GA or AA	1061 (10.5%)	0.85 (0.74 - 0.97)	0.017	
GT or TT	GG	1359 (13.4%)	1.34 (1.18 - 1.52)	3.4E-06	
GT or TT	GA or AA	244 (2.4%)	1.27 (0.97 - 1.67)	0.080	
SNCA rs2583988					
CC	GG	4495 (44.6%)	1.00 (reference)	N/A	OR: 1.13 95% CI: 0.89 - 1.44 P=0.32
CC	GA or AA	677 (6.7%)	0.82 (0.69 - 0.97)	0.019	
CT or TT	GG	4280 (42.5%)	1.24 (1.13 - 1.35)	2.2E-06	
CT or TT	GA or AA	617 (6.1%)	1.14 (0.96 - 1.36)	0.13	
MAPT rs1052553[1]					
GG	GG	364 (3.6%)	1.00 (reference)	N/A	OR: 1.65 95% CI: 0.91 - 3.05 P=0.10
GG	GA or AA	58 (0.6%)	0.54 (0.03 - 0.97)	0.040	
GA or AA	GG	8498 (83.5%)	1.27 (1.02 - 1.58)	0.029	
GA or AA	GA or AA	1256 (12.3%)	1.14 (0.89 - 1.45)	0.29	

ORs and p-values result from fixed-effects logistic regression models. For tests of association, the two given variants were combined into one variable, and the model was adjusted for site. For tests of interaction, models were adjusted for each of the two variants, their interaction, and site. Dominant models refer to the characterization of *SNCA* and *MAPT* variants; only dominant models were considered for LRRK2 p.R1398H due to the small number of rare homozygotes for this variant. Interaction ORs under a dominant model are interpreted as the multiplicative increase in the effect of the minor allele for LRRK2 p.R1398H on PD corresponding to presence of the risk allele for *SNCA* and *MAPT* variants, or alternatively as the multiplicative increase in the effect of presence of the risk allele for *SNCA* and *MAPT* variants on PD corresponding to presence of the minor allele for LRRK2 p.R1398H. OR=odds ratio. CI=confidence interval. [1]The A allele for *MAPT* rs1052553 corresponds to the H1 haplotype.

Supplementary Table 6: Interactions of LRRK2 p.R1398H with *SNCA* and *MAPT* variants in regard to susceptibility to PD in the Caucasian series under a recessive model

			Test of association		
Variant/Genotype	LRRK2 p.R1398H	Sample genotype count and frequency	OR (95% CI)	P-value	Test of interaction
SNCA rs181489					
CC or CT	GG	7544 (77.1%)	1.00 (reference)	N/A	
CC or CT	GA or AA	1141 (11.7%)	0.88 (0.77 - 1.00)	0.051	OR: 0.96
TT	GG	967 (9.9%)	1.55 (1.34 - 1.79)	4.0E-9	95% CI: 0.65 - 1.44 P=0.86
TT	GA or AA	136 (1.4%)	1.31 (0.93 - 1.88)	0.13	
SNCA rs356219					
AA or AG	GG	7229 (72.3%)	1.00 (reference)	N/A	
AA or AG	GA or AA	1068 (10.7%)	0.90 (0.79 - 1.03)	0.14	OR: 0.80
GG	GG	1476 (14.8%)	1.40 (1.24 - 1.58)	3.5E-8	95% CI: 0.58 - 1.11 P=0.18
GG	GA or AA	219 (2.2%)	1.02 (0.77 - 1.34)	0.91	
SNCA rs11931074					
GG or GT	GG	8743 (86.5%)	1.00 (reference)	N/A	
GG or GT	GA or AA	1293 (12.8%)	0.88 (0.78 - 0.99)	0.039	OR: 0.52
TT	GG	59 (0.6%)	1.41 (0.81 - 2.52)	0.24	95% CI: 0.14 - 1.96
TT	GA or AA	12 (0.1%)	0.64 (0.19 - 2.14)	0.46	P=0.33
SNCA rs2583988					
CC or CT	GG	7975 (79.2%)	1.00 (reference)	N/A	
CC or CT	GA or AA	1177 (11.7%)	0.87 (0.76 - 0.98)	0.027	OR: 0.99
TT	GG	800 (7.9%)	1.31 (1.13 - 1.54)	0.0006	95% CI: 0.65 - 1.52 P=0.97
TT	GA or AA	117 (1.2%)	1.13 (0.78 - 1.66)	0.53	
MAPT rs1052553[1]					
GG or GA	GG	2981 (29.3%)	1.00 (reference)	N/A	
GG or GA	GA or AA	456 (4.5%)	0.89 (0.72 - 1.09)	0.25	OR: 0.98
AA	GG	5881 (57.8%)	1.25 (1.14 - 1.38)	1.55E-06	95% CI: 0.76 - 1.26
AA	GA or AA	858 (8.4%)	1.09 (0.93 - 1.28)	0.28	P=0.88

ORs and p-values result from fixed-effects logistic regression models. For tests of association, the two given variants were combined into one variable, and the model was adjusted for site. For tests of interaction, models were adjusted for each of the two variants, their interaction, and site. Recessive models refer to the characterization of *SNCA* and *MAPT* variants; only dominant models were considered for LRRK2 p.R1398H due to the small number of rare homozygotes for this variant. Interaction ORs under a recessive model are interpreted as the multiplicative increase in the effect of the minor allele for LRRK2 p.R1398H on PD corresponding to presence of two risk alleles for *SNCA* and *MAPT* variants, or alternatively as the multiplicative increase in the effect presence of two risk alleles for *SNCA* and *MAPT* variants on PD corresponding to presence of the minor allele for LRRK2 p.R1398H. OR=odds ratio. CI=confidence interval. [1]The A allele for *MAPT* rs1052553 corresponds to the H1 haplotype.

Supplementary Table 7: Interactions of LRRK2 p.R1398H with SNCA and MAPT variants in regard to susceptibility to PD when adjusting for age and gender in addition to site.

	Caucasian series		Asian series	
Interaction between LRRK2 p.R1398H and:	Interaction OR (95% CI)	P-value	Interaction OR (95% CI)	P-value
SNCA rs181489				
Additive model	1.06 (0.88 – 1.28)	0.54	---	---
Dominant model	1.12 (0.87 – 1.44)	0.36	---	---
Recessive model	0.97 (0.65 – 1.46)	0.88	---	---
Genotype model [1]	NA	0.12	---	---
SNCA rs356219				
Additive model	0.96 (0.80 – 1.15)	0.64	0.94 (0.65 – 1.33)	0.72
Dominant model	1.06 (0.82 – 1.38)	0.64	0.95 (0.56 – 1.59)	0.84
Recessive model	0.78 (0.56 – 1.09)	0.14	0.90 (0.47 – 1.72)	0.76
Genotype model [1]	NA	0.34	NA	0.96
SNCA rs11931074				
Additive model	1.03 (0.76 – 1.39)	0.87	0.89 (0.63 – 1.26)	0.52
Dominant model	1.08 (0.78 – 1.50)	0.64	0.84 (0.50 – 1.41)	0.52
Recessive model	0.49 (0.13 – 1.82)	0.28	0.91 (0.49 – 1.70)	0.78
Genotype model [1]	NA	0.60	NA	0.93
SNCA rs2583988				
Additive model	1.07 (0.88 – 1.29)	0.51	---	---
Dominant model	1.10 (0.86 – 1.42)	0.43	---	---
Recessive model	1.04 (0.67 – 1.60)	0.87	---	---
Genotype model [1]	NA	0.66	---	---
MAPT rs1052553				
Additive model	1.04 (0.84 – 1.29)	0.74	---	---
Dominant model	1.67 (0.91 – 3.11)	0.10	---	---
Recessive model	0.96 (0.74 – 1.25)	0.77	---	---
Genotype model [1]	NA	0.34	---	---

ORs, 95% CIs, and p-values result from fixed-effects logistic regression models adjusted for age, gender, and site. OR=odds ratio. CI=confidence interval. --- indicates a variant observed at a frequency too low in the given series to allow for association analysis.
[1]Tests of interaction under a genotype model do not produce a single interaction OR, and therefore only a p-value is given.

Supplementary Table 8: Interactions of LRRK2 p.R1398H with *SNCA* and *MAPT* variants in regard to susceptibility to PD utilizing a random effects model, and tests for heterogeneity of interaction effects between sites

	Caucasian series (5991 PD, 4331 controls)				Asian series (1351 PD, 938 controls)			
	Evaluation of between-site heterogeneity in interaction ORs		Evaluation of gene-gene interaction		Evaluation of between-site heterogeneity in interaction ORs		Evaluation of gene-gene interaction	
Interaction between LRRK2 p.R1398H and:	I^2 (95% CI)[1]	P-value	Interaction OR (95% CI)	P-value	I^2 (95% CI)[1]	P-value	Interaction OR (95% CI)	P-value
SNCA rs181489								
Additive model	25% (0% – 59%)	0.18	1.07 (0.84 – 1.34)	0.59	---	---	---	---
Dominant model	31% (0% - 62%)	0.11	1.15 (0.83 – 1.58)	0.40	---	---	---	---
SNCA rs356219								
Additive model	0% (0% - 47%)	0.57	0.98 (0.82 – 1.17)	0.83	50% (0% - 84%)	0.11	1.03 (0.64 – 1.67)	0.89
Dominant model[2]	0% (0% - 52%)	0.45	1.11 (0.85 – 1.44)	0.45	55% (0% - 85%)	0.084	1.02 (0.49 – 2.10)	0.96
SNCA rs11931074								
Additive model	0% (0% - 24%)	0.86	0.91 (0.66 – 1.25)	0.56	48% (0% - 83%)	0.12	1.13 (0.72 – 1.77)	0.60
Dominant model[2]	0% (0% - 15%	0.90	0.97 (0.70 – 1.36)	0.88	46% (0% - 82%)	0.14	1.22 (0.64 – 2.34)	0.54
SNCA rs2583988								
Additive model	0% (0% - 42%)	0.68	1.07 (0.88 – 1.29)	0.50	---	---	---	---
Dominant model	0% (0% - 22%)	0.87	1.14 (0.88 – 1.46)	0.32	---	---	---	---
MAPT rs1052553								
Additive model	36% (0% - 65%)	0.075	1.01 (0.75 – 1.36)	0.95	---	---	---	---
Recessive model[3]	30% (0% - 62%)	0.13	0.95 (0.69 – 1.33)	0.78	---	---	---	---

Interaction ORs and p-values result from random effects models. Heterogeneity p-values result from chi-square tests based on the Q statistic, where the test is for differences in interaction ORs between sites. [1]The I^2 statistic is a measure of the proportion of variation in interaction ORs between sites that is due to heterogeneity beyond chance [25] [2]The minor allele differed between the Caucasian and Asian series' for *SNCA* rs356219 and rs11931074, although the risk allele was the same; in the Asian series, recessive models rather than dominant models were considered for these two variants due to the small number of homozygotes of the protective allele for individual sites in that series. [3]For *MAPT* rs1052553, a recessive model rather than a dominant model was considered due to the small number of homozygotes of the protective allele for individual sites. --- indicates a variant observed at a frequency too low in the given series to allow for association analysis.

Supplementary Table 9: Interactions of LRRK2 p.R1398H with *SNCA* and *MAPT* variants in regard to susceptibility to PD in the Caucasian series, separately for each country

			Interaction between LRRK2 p.R1398H and:									
	Sample size		*SNCA* rs181489		*SNCA* rs356219		*SNCA* rs11931074		*SNCA* rs2583988		*MAPT* rs1052553	
Country	Patients with PD	Controls	OR (95% CI)	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value
Additive model												
Australia	923	713	0.82 (0.52, 1.29)	0.39	0.93 (0.60, 1.44)	0.74	1.88 (0.88. 4.18)	0.11	0.96 (0.61, 1.51)	0.86	1.11 (0.68, 1.86)	0.68
France	548	143	0.56 (0.16, 1.89)	0.36	0.92 (0.28, 3.05)	0.90	---	---	0.51 (0.17, 1.51)	0.22	0.27 (0.04, 1.02)	0.097
Germany	1074	675	1.33 (0.84, 2.10)	0.22	1.23 (0.80, 1.89)	0.35	0.79 (0.39, 1.62)	0.52	1.23 (0.79, 1.94)	0.37	1.50 (0.90, 2.54)	0.13
Greece	450	405	0.63 (0.29, 1.35)	0.24	0.62 (0.30, 1.77)	0.20	0.48 (0.09, 2.09)	0.34	1.05 (0.52, 2.15)	0.89	0.41 (0.16, 1.06)	0.069
Ireland	360	444	2.25 (1.18, 4.51)	0.012	0.72 (0.39, 1.29)	0.27	1.07 (0.31, 3.61)	0.91	1.85 (0.92, 3.88)	0.092	0.98 (0.46, 2.19)	0.96
Italy	469	365	0.82 (0.43, 1.61)	0.56	1.15 (0.61, 2.24)	0.67	1.49 (0.51, 4.75)	0.48	0.96 (0.48, 1.95)	0.90	1.72 (0.83, 3.73)	0.15
Norway	602	526	1.21 (0.75, 1.97)	0.43	1.26 (0.79, 2.01)	0.33	1.07 (0.52, 2.24)	0.85	1.30 (0.80, 2.13)	0.29	1.10 (0.62, 1.96)	0.75
Poland	349	340	1.12 (0.55, 2.33)	0.76	1.30 (0.63, 2.72)	0.48	1.01 (0.26, 4.04)	0.99	1.16 (0.59, 2.37)	0.67	0.88 (0.37, 2.04)	0.76
Sweden	91	180	0.63 (0.21, 1.69)	0.38	0.57 (0.20, 1.56)	0.28	0.50 (0.08, 2.55)	0.42	0.60 (0.17, 1.87)	0.40	0.47 (0.12, 1.92)	0.29
United States	1,125	540	1.22 (0.75, 2.02)	0.43	0.91 (0.58, 1.44)	0.69	0.58 (0.28, 1.24)	0.15	0.96 (0.58, 1.61)	0.88	1.03 (0.60, 1.76)	0.93
Overall Caucasian	5,991	4,331	1.06 (0.88, 1.28)	0.52	0.98 (0.82, 1.17)	0.81	1.06 (0.79, 1.43)	0.69	1.07 (0.89, 1.29)	0.47	1.05 (0.85, 1.30)	0.65
Dominant model[1]												
Australia	923	713	0.96 (0.52, 1.77)	0.89	1.31 (0.68, 2.58)	0.42	1.83 (0.83, 4.17)	0.14	1.00 (0.55, 1.82)	0.99	1.08 (0.58, 2.00)	0.81
France	548	143	0.67 (0.15, 2.61)	0.57	0.92 (0.17, 3.96)	0.91	---	---	0.71 (0.18, 2.72)	0.62	0.24 (0.03, 1.09)	0.093
Germany	1074	675	1.34 (0.74, 2.42)	0.34	1.23 (0.67, 2.27)	0.50	0.97 (0.42, 2.27)	0.94	1.55 (0.87, 2.79)	0.14	1.26 (0.69, 2.30)	0.46
Greece	450	405	0.34 (0.12, 0.92)	0.034	0.36 (0.13, 0.96)	0.043	0.46 (0.09, 2.03)	0.32	0.86 (0.32, 2.27)	0.75	0.32 (0.11, 0.88)	0.028
Ireland	360	444	2.97 (1.19, 7.80)	0.022	0.81 (0.32, 2.11)	0.66	0.98 (0.28, 3.32)	0.97	1.76 (0.69, 4.64)	0.24	0.92 (0.38, 2.31)	0.85
Italy	469	365	1.02 (0.43, 2.45)	0.96	1.32 (0.54, 3.28)	0.54	1.44 (0.46, 4.88)	0.54	1.05 (0.44, 2.53)	0.91	1.78 (0.74, 4.33)	0.20
Norway	602	526	1.25 (0.66, 2.38)	0.50	1.55 (0.78, 3.06)	0.21	1.16 (0.55, 2.52)	0.70	1.18 (0.62, 2.25)	0.60	1.17 (0.59, 2.33)	0.65
Poland	349	340	1.71 (0.66, 4.52)	0.27	2.03 (0.75, 5.69)	0.17	0.95 (0.24, 3.86)	0.94	1.67 (0.66, 4.35)	0.29	0.96 (0.33, 2.78)	0.94
Sweden	91	180	0.69 (0.16, 2.83)	0.61	0.84 (0.19, 4.07)	0.82	0.50 (0.08, 2.55)	0.42	0.61 (0.14, 2.51)	0.50	0.58 (0.12, 2.96)	0.50
United States	1,125	540	1.26 (0.66, 2.40)	0.48	0.88 (0.45, 1.68)	0.69	0.66 (0.30, 1.49)	0.31	1.02 (0.54, 1.95)	0.95	0.88 (0.46, 1.69)	0.70
Overall Caucasian	5,991	4,331	1.13 (0.88, 1.44)	0.33	1.09 (0.85, 1.41)	0.49	1.12 (0.81, 1.54)	0.50	1.13 (0.89, 1.44)	0.32	0.98 (0.76, 1.26)	0.88

ORs and p-values result from fixed-effects logistic regression models adjusted for each of the two variants, their interaction, and site for countries with more than one site. Interaction ORs under an additive model are interpreted as the multiplicative increase in the effect of the minor allele for LRRK2 p.R1398H on PD corresponding to each additional risk allele for *SNCA* and *MAPT* variants, or alternatively as the as the multiplicative increase in the effect of each additional risk allele for *SNCA* and *MAPT* variants on PD corresponding to presence of the minor allele for LRRK2 p.R1398H. Interaction ORs under a dominant model are interpreted as the multiplicative increase in the effect of the minor allele for LRRK2 p.R1398H on PD corresponding to presence of the risk allele for *SNCA* and *MAPT* variants, or alternatively as the as the multiplicative increase in the effect of presence of the risk allele for *SNCA* and *MAPT* variants on PD corresponding to presence of the minor allele for LRRK2 p.R1398H. [1]Models for *MAPT* rs1052553 are recessive models rather than dominant models due to the small number of homozygotes of the minor allele for this variant in individual sites; the minor allele was the reference allele for *MAPT* rs1052553, and therefore a recessive model compares homozygotes of the major (risk) allele with the other two genotypes. OR=odds ratio. CI=confidence interval. --- indicates a country where the risk allele was not present in either patients with PD or controls.

Supplementary Table 10: Three-way interactions between LRRK2 p.R1398H, *SNCA* variants, and *MAPT* rs1052553 in regard to susceptibility to PD in the Caucasian series

				Test of association		
SNCA Variant/Genotype	*MAPT* rs1052553 genotype[1]	LRRK2 p.R1398H genotype	Sample genotype count and frequency	OR (95% CI)	P-value	Test of interaction
SNCA rs181489						
CC	GG or GA	GG	1335 (13.6%)	1.00 (reference)	N/A	
CC	GG or GA	GA or AA	214 (2.2%)	0.81 (0.60 - 1.09)	0.17	
CC	AA	GG	2573 (26.3%)	1.19 (1.04 - 1.37)	0.011	
CC	AA	GA or AA	385 (3.9%)	0.99 (0.78 - 1.26)	0.95	P=0.80
CT or TT	GG or GA	GG	1528 (15.6%)	1.16 (1.00 - 1.35)	0.053	
CT or TT	GG or GA	GA or AA	231 (2.4%)	1.11 (0.83 - 1.48)	0.48	
CT or TT	AA	GG	3075 (31.4%)	1.51 (1.32 - 1.72)	2.3E-9	
CT or TT	AA	GA or AA	447 (4.6%)	1.38 (1.10 - 1.72)	0.0051	
SNCA rs356219						
AA	GG or GA	GG	1066 (10.7%)	1.00 (reference)	N/A	
AA	GG or GA	GA or AA	156 (1.6%)	0.86 (0.61 - 1.22)	0.41	
AA	AA	GG	2021 (20.2%)	1.26 (1.08 - 1.47)	0.0038	
AA	AA	GA or AA	284 (2.8%)	1.00 (0.77 - 1.32)	0.97	P=0.96
AG or GG	GG or GA	GG	1846 (18.5%)	1.23 (1.05 - 1.43)	0.011	
AG or GG	GG or GA	GA or AA	290 (2.9%)	1.11 (0.85 - 1.46)	0.43	
AG or GG	AA	GG	3772 (37.8%)	1.54 (1.34 - 1.78)	2.2E-9	
AG or GG	AA	GA or AA	557 (5.6%)	1.38 (1.11 - 1.71)	0.0032	
SNCA rs11931074						
GG	GG or GA	GG	2517 (24.9%)	1.00 (reference)	N/A	
GG	GG or GA	GA or AA	371 (3.7%)	0.88 (0.70 - 1.10)	0.27	
GG	AA	GG	4926 (48.7%)	1.26 (1.14 - 1.40)	4.7E-6	
GG	AA	GA or AA	690 (6.8%)	1.06 (0.89 - 1.26)	0.52	P=0.88
GT or TT	GG or GA	GG	446 (4.4%)	1.43 (1.16 - 1.77)	0.0009	
GT or TT	GG or GA	GA or AA	81 (0.8%)	1.22 (0.77 - 1.94)	0.40	
GT or TT	AA	GG	913 (9.0%)	1.64 (1.39 - 1.93)	2.8E-9	
GT or TT	AA	GA or AA	163 (1.6%)	1.65 (1.18 - 2.33)	0.0039	
SNCA rs2583988						
CC	GG or GA	GG	1526 (15.2%)	1.00 (reference)	N/A	
CC	GG or GA	GA or AA	251 (2.5%)	0.81 (0.62 - 1.07)	0.14	
CC	AA	GG	2969 (29.5%)	1.18 (1.04 - 1.35)	0.0095	
CC	AA	GA or AA	426 (4.2%)	0.98 (0.79 - 1.23)	0.88	P=0.63
CT or TT	GG or GA	GG	1426 (14.2%)	1.15 (0.99 - 1.34)	0.068	
CT or TT	GG or GA	GA or AA	199 (2.0%)	1.20 (0.88 - 1.63)	0.25	
CT or TT	AA	GG	2854 (28.3%)	1.52 (1.33 - 1.73)	3.2E-10	
CT or TT	AA	GA or AA	418 (4.2%)	1.32 (1.06 - 1.66)	0.015	

ORs and p-values result from fixed-effects logistic regression models. For tests of association, the three given variants were combined into one variable, and the model was adjusted for site. For tests of interaction, the fixed-effects logistic regression model was adjusted for site, and the p-value given tested for any interaction (pair-wise or three-way) between the three given variants. Rare homozygotes were collapsed with heterozygotes in order to avoid extremely rare three-variant genotype combinations. [1]The A allele for *MAPT* rs1052553 corresponds to the H1 haplotype. OR=odds ratio. CI=confidence interval.

Supplementary Table 11: Interactions of LRRK2 p.R1398H with *SNCA* and *MAPT* variants in regard to susceptibility to PD in the Asian series, separately for each country

			Interaction between LRRK2 p.R1398H and:			
			SNCA rs356219		*SNCA* rs11931074	
Country	Patients with PD	Controls	OR (95% CI)	P-value	OR (95% CI)	P-value
Additive model						
Japan	171	90	0.45 (0.15, 1.24)	0.13	0.47 (0.18, 1.20)	0.12
Korea	811	550	1.24 (0.85, 1.82)	0.27	1.34 (0.92, 1.96)	0.13
Taiwan	369	298	1.41 (0.77, 2.62)	0.27	1.50 (0.84, 2.76)	0.18
Overall Asian	1,351	938	1.17 (0.87, 1.59)	0.30	1.25 (0.93, 1.69)	0.14
Recessive model[1]						
Japan	171	90	0.25 (0.06, 1.04)	0.056	0.30 (0.08, 1.19)	0.084
Korea	811	550	1.42 (0.81, 2.51)	0.22	1.61 (0.92, 2.83)	0.096
Taiwan	369	298	1.58 (0.65, 3.94)	0.32	1.73 (0.73, 4.17)	0.21
Overall Asian	1,351	938	1.22 (0.78, 1.92)	0.38	1.39 (0.90, 2.17)	0.14

ORs and p-values result from fixed-effects logistic regression models adjusted for each of the two variants, their interaction, and site for countries with more than one site. Interaction ORs under an additive model are interpreted as the multiplicative increase in the effect of the minor allele for LRRK2 p.R1398H on PD corresponding to each additional risk allele for *SNCA* variants, or alternatively as the as the multiplicative increase in the effect of each additional risk allele for *SNCA* variants on PD corresponding to presence of the minor allele for LRRK2 p.R1398H. Interaction ORs under a recessive model are interpreted as the multiplicative increase in the effect of the minor allele for LRRK2 p.R1398H on PD corresponding to presence of two risk alleles for *SNCA* variants, or alternatively as the as the multiplicative increase in the effect of presence of two risk alleles for *SNCA* variants on PD corresponding to presence of the minor allele for LRRK2 p.R1398H. [1]Recessive models rather than dominant models are displayed in the Asian series due to the small number of homozygotes of the protective allele for *SNCA* variants in that series; in the Asian series, recessive models for *SNCA* variants compare homozygotes of the major (risk) allele with the other two genotypes. OR=odds ratio. CI=confidence interval.

Supplementary Text: Genetic Epidemiology of Parkinson's Disease (GEO-PD) Consortium

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