Supplementary Table 3. Previously reported genome-wide significant signals stratified by family history

				Original report			NGRC All-PD			Familial-PD			Sporadic-PD		
Chr	Gene	SNP [Ref]	BP	OR	SE	P	OR	SE	P	OR	SE	P	OR	SE	P
1	*GBA*	rs2230288 [1]	155206167	0.02	1.71	5E-8	1.57	0.27	9E-3	1.94	0.49	8E-3	1.49	0.27	0.03
1	*PARK16*	rs708723 [2]	205739266	0.44	0.91	1E-12	0.88	0.04	6E-3	0.85	0.07	0.04	0.89	0.05	0.02
2	*STK39*	rs2102808 [3]	169117025	0.13	1.28	2E-11	1.20	0.08	8E-3	1.31	0.14	0.01	1.17	0.09	0.03
3	*NMD3*	rs34016896 [2]	160992864	0.31	1.14	2E-8	1.10	0.06	0.05	0.98	0.08	0.83	1.15	0.06	0.01
3	*MCCC1/LAMP3*	rs10513789 [4]	182760073	0.20	0.80	3E-10	0.95	0.06	0.40	1.00	0.10	1.00	0.93	0.06	0.25
3	*MCCC1/LAMP3*	rs11711441 [3]	182821275	0.14	0.82	1E-8	0.91	0.06	0.17	0.90	0.11	0.39	0.90	0.07	0.16
4	*GAK/DGKQ*	rs11248051 [5]	858332	0.11	1.46	3E-9	1.32	0.10	3E-4	1.14	0.15	0.32	1.38	0.11	8E-5
4	*GAK/DGKQ*	rs11248060 [1]	964359	0.12	1.35	2E-9	1.23	0.09	5E-3	1.05	0.13	0.72	1.29	0.10	1E-3
4	*BST1*	rs11724635 [3]	15737101	0.45	0.87	2E-8	0.89	0.04	0.01	0.95	0.07	0.53	0.86	0.04	3E-3
4	*SCARB2*	rs6812193 [4]	77198986	0.37	0.84	8E-10	0.96	0.05	0.42	1.02	0.08	0.79	0.95	0.05	0.36
4	*SNCA*	rs356219 [3]	90637601	0.39	1.30	1E-26	1.37	0.07	1E-10	1.39	0.11	3E-5	1.36	0.07	4E-9
4	*SNCA*	rs356220 [5]	90641340	0.40	1.38	3E-11	1.38	0.07	3E-11	1.40	0.11	2E-5	1.37	0.07	1E-9
4	*SNCA*	rs2736990 [6]	90678541	0.49	1.23	2E-16	1.30	0.06	5E-8	1.37	0.10	5E-5	1.28	0.06	1E-6
4	*SNCA*	rs356198 [1]	90682504	0.18	0.82	5E-9	0.79	0.05	1E-4	0.76	0.08	0.01	0.78	0.05	3E-4
6	*HLA*	rs2395163 [1]	32387809	0.20	0.81	3E-11	0.80	0.05	2E-4	0.87	0.09	0.16	0.78	0.05	9E-5
6	*HLA*	rs3129882 [5]	32409530	0.43	1.26	2E-10	1.31	0.06	3E-8	1.12	0.09	0.15	1.38	0.07	5E-10
7	*GPNMB*	rs156429 [2]	23306020	0.40	0.89	3E-10	0.91	0.04	0.04	0.87	0.07	0.09	0.91	0.05	0.07
8	*FGF20*	rs591323 [2]	16697091	0.27	0.88	7E-11	0.92	0.05	0.13	0.90	0.08	0.22	0.93	0.05	0.19
8	*MMP16*	rs60298754 [2]	89373041	0.02	1.38	2E-9	1.04	0.16	0.78	1.15	0.28	0.58	1.00	0.17	0.98
10	*ITGA8*	rs7077361 [7]	15561543	0.12	0.88	2E-8	0.94	0.07	0.39	1.00	0.11	0.99	0.93	0.07	0.33
12	*LRRK2*	rs1491942 [3]	40620808	0.21	1.19	3E-8	1.22	0.07	6E-4	1.37	0.12	6E-4	1.17	0.07	9E-3
16	*STX1B*	rs4889603 [2]	30982225	0.41	1.12	3E-12	1.01	0.05	0.90	1.07	0.08	0.40	0.99	0.05	0.91
17	*MAPT*	rs2942168 [3]	43714850	0.22	0.76	4E-19	0.76	0.05	5E-6	0.64	0.07	2E-5	0.79	0.05	3E-4
18	*RIT2*	rs12456492 [1]	40673380	0.34	1.19	2E-10	1.09	0.06	0.10	1.22	0.10	0.02	1.06	0.06	0.28

Included in this table are results of prior GWAS that reached genome-wide significance in whites of European decent, and for which data (genotyped or imputed) were available in NGRC GWAS. BP=position in Build 37. All analyses are adjusted for age, sex, PC1, and PC2.

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