Table e-1. Cohort Clinical Characteristics

Cohort	BCM1	BCM2	UMB	PPMI	PDBP	PROPARK	PROBAND	OSLO
Subjects, n	199	83	375	307	429	136	1641	42
Male, n (%)	124 (62.3%)	56 (67.5%)	249 (66.4%)	210 (68.4%)	254 (59.2%)	94 (69.1%)	1,060 (64.6%)	31 (73.8%)
Age at evaluation, mean (SD)	60.6 (10.3)	62.5 (10.1)	66.7 (9.5)	63.7 (9.7)	64.6 (9.3)	64.9 (7.5)	67.6 (9.1)	65.6 (9.2)
Age at onset, mean (SD)	53.6 (9.8)	56.9 (10.0)	57.4 (10.5)	59.5 (9.8)	57.6 (11.2)	56.4 (8.9)	64.5 (9.6)	57.1 (9.7)
Disease duration, mean (SD)	5.2 (4.7)	4.4 (3.7)	4.8 (4.6)	1.9 (1.8)	6.9 (7.5)	8.5 (4.8)	3.2 (3.0)	8.5 (6.0)
TD subtype, n (%)	109 (54.8)	55 (66.3)	172 (45.9)	217 (70.7)	164 (38.2)	73 (53.7)	762 (46.4)	18 (42.9)
PIGD subtype, n (%)	72 (36.2)	25 (30.1)	169 (45.1)	55 (17.9)	217 (50.6)	47 (34.6)	659 (40.2)	15 (35.7)
Subtype ratio, mean (SD)	0.25 (0.9)	0.31 (0.9)	0.15 (1.1)	0.55 (0.9)	-0.1 (0.9)	0.22 (0.8)	0.02 (0.9)	0.21 (1.2)

BCM1: Baylor College of Medicine DNA bank with UPDRS; BCM2 = Baylor College of Medicine DNA bank with MDS-UPDRS; UMD = University of Maryland cohort; PPMI = Parkinson's Progression Markers Initiative; PDBP = Parkinson's Disease Biomarkers Program; PROPARK = Profiling Parkinson's disease (Netherlands); PROBAND = Tracking Parkinson's Study (United Kingdom); OSLO = University of Oslo (Norway). PIGD: Postural instability/gait difficulty PD motor subtype, TD: tremor-dominant PD motor subtype.

Table e-3. Top GWAS results for PD subtype (TD vs. PIGD)

chr: position	SNP	Gene	Allele	Freq	Effect	SE	P-value	I^2	HetP	Direction
1: 47557933	*rs116504637*	*CYP4Z1*	T/G	0.74	0.35	0.07	9.83E-07	12.9	0.33	+++++++-
5: 161678799	*rs11949046*	*GABRG2*	T/C	0.89	0.54	0.11	1.57E-06	31	0.21	++???+++
16: 19502663	*rs78926797*	*TMC5*	A/C	0.60	-0.3	0.06	2.08E-06	0	0.8	--------
6: 125107499	*rs6932127*	*NKAIN2*	T/C	0.89	-0.46	0.1	3.01E-06	20.7	0.27	--+-?---
11: 22583068	*rs55971529*	*FANCF*	A/G	0.97	-1.08	0.23	3.95E-06	51.6	0.1	+????---
1: 77190938	*rs988295487*	*ST6GALNAC3*	C/G	0.96	-0.84	0.18	4.98E-06	16.8	0.31	--???---
16: 82279626	*rs13330839*	*MPHOSPH6*	A/G	0.87	-0.47	0.1	7.00E-06	42.1	0.12	+++??---

The Allele column displays A1/A2, with A1 denoting the reference allele for the frequency (Freq) and effect. Direction of association shown (left to right) for BCM1, BCM2, OSLO, PDBP, PPMI, PROBAND, PROPARK, and UMD. For assessment of heterogeneity, the I^2 statistic and associated p-value (HetP) is provided.

Table e-4. Top GWAS results for tremor/PIGD subtype ratio

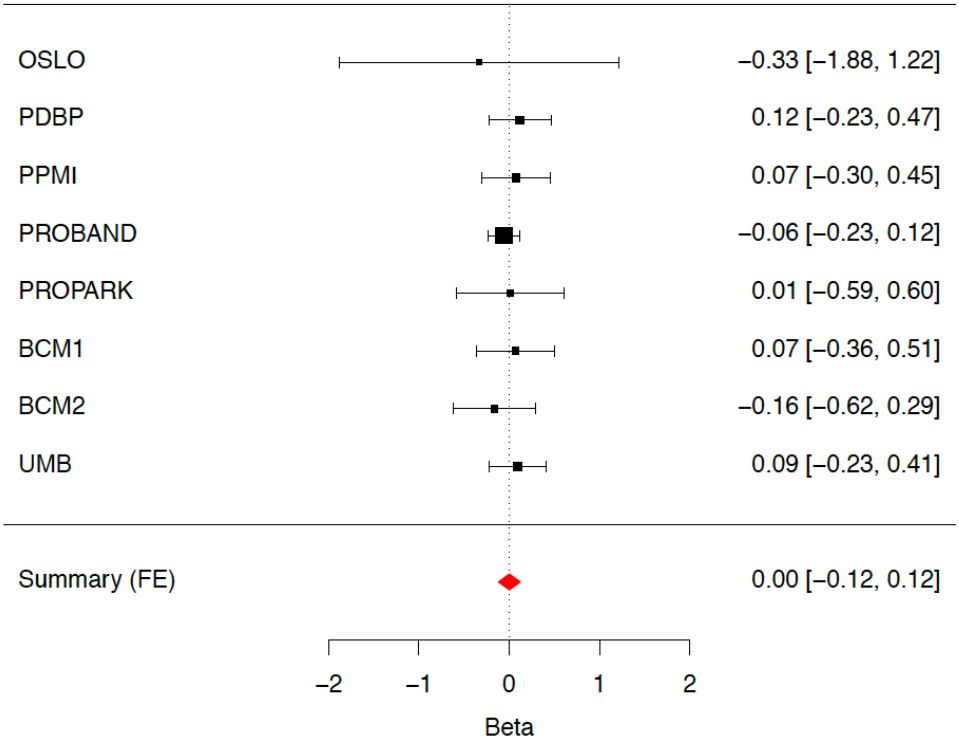
chr: position	SNP	Gene	Allele	Freq	Effect	SE	P-value	I^2	HetP	Direction
4: 5418485	*rs2301857*	*STK32B*	T/C	0.12	-0.19	0.04	6.60E-07	36	0.14	-+------
21: 20786475	*rs79890063*	none	A/C	0.12	-0.22	0.04	6.96E-07	0	0.58	--+??---
10: 103048995	*rs12242050*	*BTRC*	T/G	0.76	-0.14	0.03	8.44E-07	13.8	0.32	-++-----
4: 82616045	*rs6535273*	*RASGEF1B*	T/C	0.39	0.11	0.02	1.37E-06	0	0.96	+++++++++
8: 8387903	*rs10109703*	*SGK223*	A/C	0.64	-0.13	0.03	1.44E-06	16.5	0.31	---??---
13: 110127965	*rs17488950*	*LINC00676*	T/C	0.07	-0.27	0.06	1.46E-06	19.5	0.29	-+-??---
4: 86019236	*rs76377494*	*WDFY3-AS2*	T/C	0.07	-0.22	0.05	1.89E-06	0	0.6	--+-+---
22: 46008464	*rs9626407*	*FBLN1*	A/G	0.04	-0.35	0.07	1.97E-06	0	0.59	---??-+-
12: 62440045	*rs116917617*	*FAM19A2*	T/C	0.98	-0.46	0.1	2.11E-06	0	0.45	---??---
19: 14878196	*rs538015403*	*EMR3*	A/G	0.02	-0.41	0.09	2.56E-06	40	0.11	--------
7: 148211886	*rs2717804*	*C7orf33*	A/G	0.36	-0.12	0.03	2.67E-06	0	0.45	---??---
7: 5794044	*rs6958272*	*RNF216*	T/C	0.92	-0.22	0.05	3.01E-06	0	0.58	+--??---
16: 15972631	*rs11644635*	*FOPNL*	T/C	0.39	-0.13	0.03	3.14E-06	25.5	0.24	+++??---
4: 116121350	*rs2892663*	*NDST4*	T/C	0.5	0.1	0.02	5.73E-06	32.4	0.17	++++-+++
8: 22906180	*rs7834008*	*TNFRSF10B*	T/C	0.79	0.14	0.03	5.98E-06	26.2	0.22	++-+++++
5: 5224692	*rs2913614*	*ADAMTS16*	A/T	0.54	0.15	0.03	6.33E-06	0	0.42	+++??+++
2: 72300987	*rs143548133*	*CYP26B1*	T/C	0.01	0.57	0.13	7.02E-06	11.2	0.34	+--??+-+
6: 134657949	*rs9483680*	*SGK1*	A/C	0.9	-0.19	0.04	7.02E-06	0	0.76	-+-??---
11: 132873644	*rs2336592*	*OPCML*	C/G	0.63	-0.12	0.03	7.82E-06	0	0.61	---??---
1: 105497011	rs17015314	none	A/G	0.88	-0.17	0.04	7.90E-06	0	0.44	---??---
3: 75446661	rs113942635	FAM86DP	T/C	0.01	0.81	0.18	8.00E-06	0	0.5	--???+++
10: 56421400	rs117238693	PCDH15	T/C	0.98	0.43	0.1	8.04E-06	0	0.88	+-++?+++
11: 103916643	rs77942836	PDGFD	A/G	0.02	-0.53	0.12	8.11E-06	47	0.09	---??--+
2: 57141732	rs56242312	none	A/G	0.9	-0.19	0.04	8.18E-06	12.3	0.34	-++??---
19: 45887928	rs7257687	PPP1R13L	T/C	0.03	-0.30	0.07	8.30E-06	0	0.89	-++-----
13: 87927123	rs72636490	MIR4500HG	A/C	0.08	-0.21	0.05	8.59E-06	22.6	0.26	---??---
14: 47229012	rs75477320	RPL10L	T/C	0.13	0.16	0.04	9.07E-06	40.2	0.11	-+++++++
18: 5197857	rs80164227	C18orf42	A/G	0.97	-0.43	0.1	9.15E-06	8.9	0.34	+--??---
17: 72542970	rs118076379	CD300LD	A/G	0.01	0.59	0.13	9.49E-06	0	0.69	+++??+++
3: 142015590	rs1552340	XRN1	A/G	0.42	0.1	0.02	9.73E-06	41.8	0.1	+++--+++
7: 132040533	rs66792854	PLXNA4	A/G	0.06	0.25	0.06	9.96E-06	0	0.45	+++??+++

The Allele column displays A1/A2, with A1 denoting the reference allele for the frequency (Freq) and effect. Direction of association shown (left to right) for BCM1, BCM2, OSLO, PDBP, PPMI, PROBAND, PROPARK, and UMD. For assessment of heterogeneity, the I^2 statistic and associated p-value (HetP) is provided.

Table e-5. ET-risk variant associations with PD motor subtype.

					Subtype (TD vs. PIGD)			Subtype Ratio		
chr: position	SNP	Gene	Allele	Freq	Effect	SE	P	Effect	SE	P
4: 5128159	rs10937625	*STK32B*	T/C	0.75	0.02	0.07	0.79	-0.01	0.03	0.78
4: 24362541	rs17590046	*PPARGC1A*	T/C	0.8	-0.08	0.08	0.3	-0.02	0.03	0.52
10: 68845715	rs12764057	*CTNNA3*	T/G	0.62	0.06	0.07	0.35	-0.04	0.03	0.14
10: 68850419	rs10822974	*CTNNA3*	A/G	0.54	0.06	0.06	0.31	-0.05	0.03	0.07
10: 68917164	rs7903491	*CTNNA3*	A/G	0.45	0.09	0.06	0.16	-0.04	0.03	0.14

Figure e-1. PD genetic risk score association with motor subtype (TD vs. PIGD).



Meta-analysis evaluating for potential association of our genetic risk score and categorically determined PD motor subtypes in all available cohorts. The error bars represent 95% confidence intervals. The size of the black squares represents the effect size from each cohort. The combined estimate for all cohorts is represented by the red diamond with the width of the diamond representing the 95% confidence interval bounds. The summary effect = 0.00157 (p=0.979).