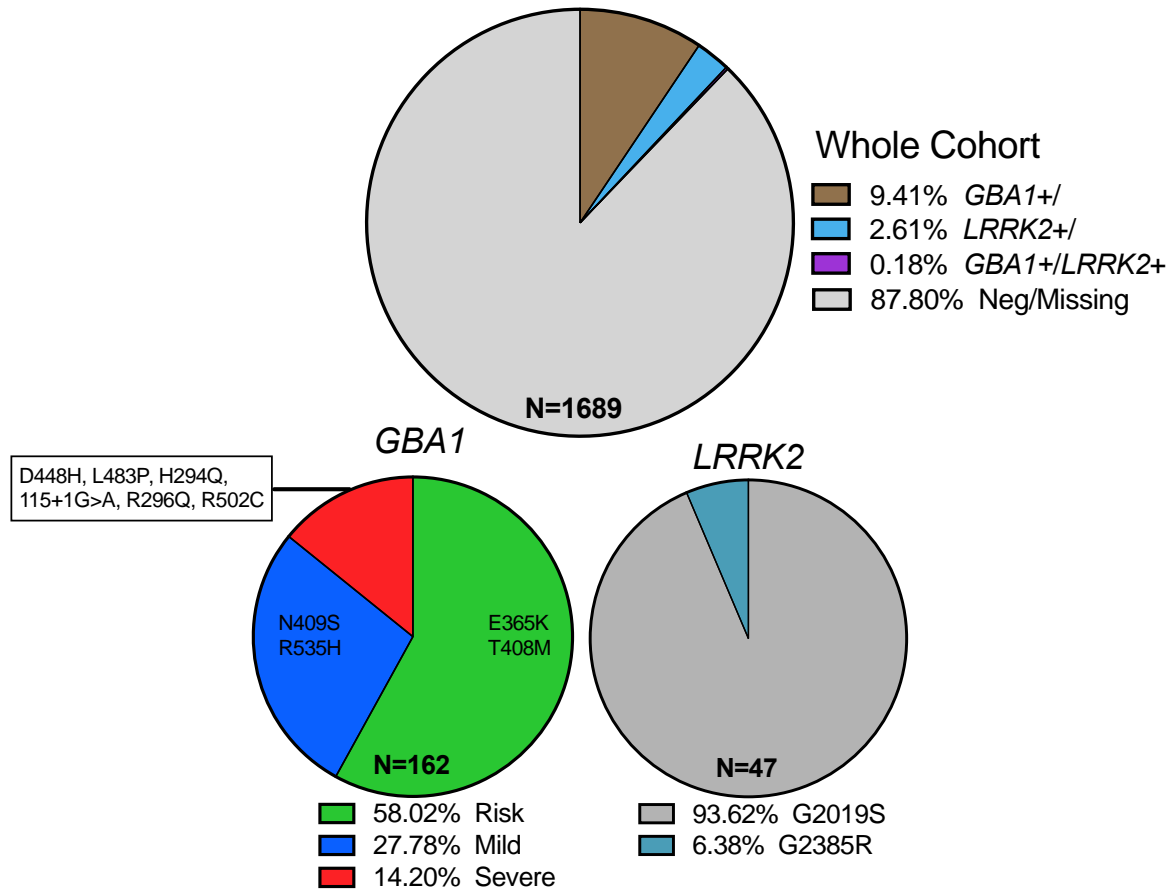


1 Supplement for “Genetic and phenotypic characterization of Parkinson’s disease at the clinic-  
 2 wide level” by Tropea et al. prepared for *NPJ Parkinson’s Disease*.  
 3  
 4

5 **Supplementary Table 1. *GBA1* and *LRRK2* variants included in testing.**  
 6

	Target Gene	Coding	Protein	rs ID	GnomAD frequency	MIND frequency
	<i>LRRK2</i>	c.6055G>A	p.Gly2019Ser	rs34637584	0.000488	0.014123
	<i>LRRK2</i>	c.7153G>A	p.Gly2385Arg	rs34778348	0.001680	0.000901
	<i>LRRK2</i>	c.4309A>C	p.Asn1437His	rs74163686	Absent	Absent
	<i>LRRK2</i>	c.4321C>G	p.Arg1441Gly	rs33939927	0.000004	Absent
	<i>LRRK2</i>	c.4321C>T	p.Arg1441Cys	rs33939927	0.000012	Absent
	<i>LRRK2</i>	c.4322G>A	p.Arg1441His	rs34995376	0.000032	Absent
	<i>LRRK2</i>	c.5096A>G	p.Tyr1699Cys	rs35801418	Absent	Absent
	<i>LRRK2</i>	c.6059T>C	p.Ile2020Thr	rs35870237	Absent	Absent
Risk	<i>GBA1</i>	c.1093G>A	p.Glu365Lys	rs2230288	0.010730	0.016526
	<i>GBA1</i>	c.1223C>T	p.Thr408Met	rs75548401	0.006124	0.01262
Mild	<i>GBA1</i>	c.1226A>G	p.Asn409Ser	rs76763715	0.002235	0.012921
	<i>GBA1</i>	c.1604G>A	p.Arg535His	rs75822236	0.000169	0.000601
	<i>GBA1</i>	c.1304A>C	p.Asn435Thr	rs75385858	Absent	Absent
	<i>GBA1</i>	c.1342G>C	p.Asp448His	rs1064651	0.000135	0.001202
Severe	<i>GBA1</i>	c.1448T>C	p.Leu483Pro	rs421016	0.001226	0.003606
	<i>GBA1</i>	c.882T>G	p.His294Gln	rs367968666	0.000219	0.000901
	<i>GBA1</i>	c.115+1G>A		rs104886460	0.000071	0.000601
	<i>GBA1</i>	c.887G>A	p.Arg296Gln	rs78973108	0.000035	0.0003
	<i>GBA1</i>	c.1504C>T	p.Arg502Cys	rs80356771	0.000067	0.0003
	<i>GBA1</i>	c.475C>T	p.Arg159Trp	rs439898	Absent	Absent
	<i>GBA1</i>	c.680A>G	p.Asn227Ser	rs364897	0.000074	Absent
	<i>GBA1</i>	c.1297G>T	p.Val433Leu	rs80356769	0.000032	Absent

7  
 8 1 case identified as RecNcil (comprised of variants: p.L483P, p.A495P, and p.Val499=)  
 9  
 10



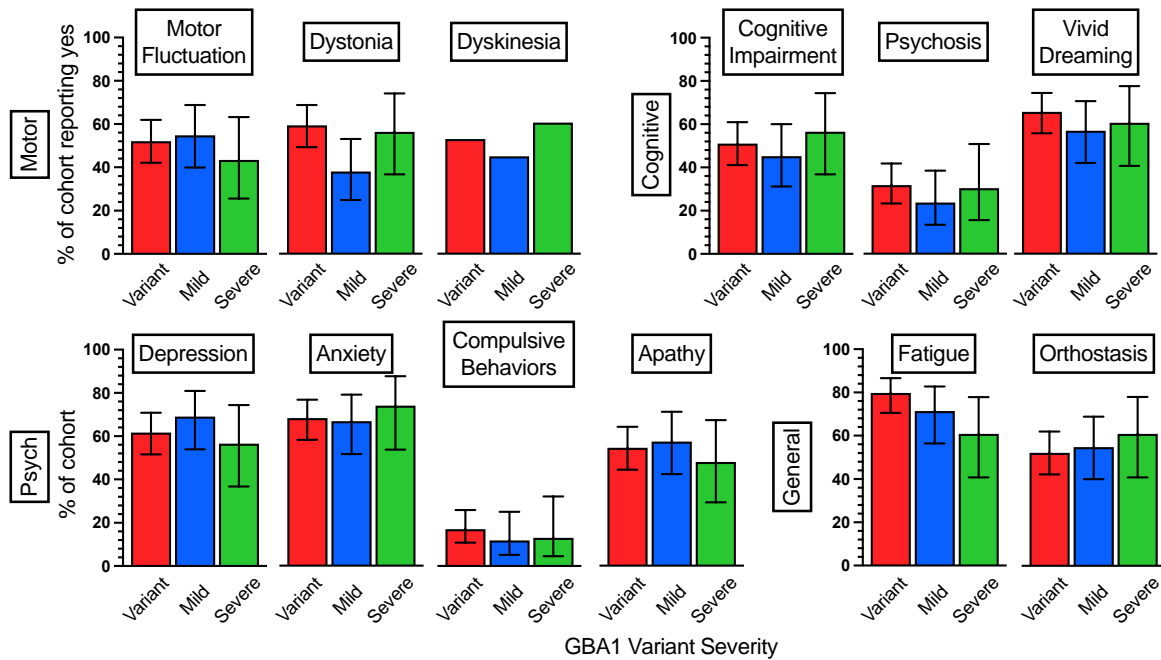
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**Supplemental Figure 1.** GBA1 and LRRK2 testing results in the Molecular Integration in Neurological Diagnosis Initiative Parkinson’s Disease Cohort.

1 **Supplemental Table 2. *GBA1* and *LRRK2* Testing Results.**  
 2

Target Gene	Variant	N (HET/HOM)
<i>LRRK2</i>	G2019S	41/3
	G2385R	3/0
<i>GBA1</i>	E365K	53/1
	T408M	40/1
	N409S	41/1
	R535H	2/0
	D448H	4/0
	L483P	12/0
	H294Q	3/0
	115+1G>A	2/0
	R296Q	1/0
	R502C	1/0
Complex	<i>GBA1</i> Rec1	1/0
	<i>LRRK2</i> G2019S HET/ <i>GBA1</i> N409S HET	2
	<i>LRRK2</i> G2019S HOM/ <i>GBA1</i> N409S HET	1
	<i>GBA1</i> H294Q HET/ <i>GBA1</i> D448H HET	1

3  
4



1  
2 **Supplemental Figure 2. Motor and Non-Motor Parkinson's Disease Symptoms by GBA1**  
3 **Variant Severity.** Responses groups as ever (currently or in the past) or never experiencing a  
4 symptom. Heterozygote and homozygote carriers are combined. Error bars represent 95%CI.  
5

```

1  R Code
2  #Loading Packages
3  library(readxl)
4  library(kableExtra)
5  library(vtable)
6  library(epiDisplay)
7  library(psych)
8  library(crosstable)
9  library(gmodels)
10
11  ###Summary statistics for the whole cohort
12  ###Data for Table 1 and Figure 2 (frequency of motor and non-motor symptoms)
13  sumtable(MINDFinal)
14  tab1(MINDFinal$Race)
15  sumtable(MINDFinal[MINDFinal$GBAYN == 0 & MINDFinal$LRRK2YN == 0, ])
16  tab1(MINDFinal[MINDFinal$GBAYN == 0 & MINDFinal$LRRK2YN == 0, ]$Race)
17  sumtable(MINDFinal[MINDFinal$GBAYN == 1 & MINDFinal$LRRK2YN == 0, ])
18  tab1(MINDFinal[MINDFinal$GBAYN == 1 & MINDFinal$LRRK2YN == 0, ]$Race)
19  sumtable(MINDFinal[MINDFinal$GBAYN == 0 & MINDFinal$LRRK2YN == 1, ])
20  tab1(MINDFinal[MINDFinal$GBAYN == 0 & MINDFinal$LRRK2YN == 1, ]$Race)
21
22  ###gene group comparisons
23  ###GBA
24  sumtable(MINDGBA)
25  table(MINDGBA$GBAYN, MINDGBA$Sex)
26  fisher.test(table(MINDGBA$GBAYN, MINDGBA$Sex))
27  table(MINDGBA$GBAYN, MINDGBA$Ethnicity)
28  table(MINDGBA$GBAYN, MINDGBA$Race)
29  describeBy(MINDGBA$AgeEnrollment, group=MINDGBA$GBAYN)
30  table(MINDGBA$GBAYN, MINDGBA$Onset)
31  kruskal.test(MINDGBA$AgeDiag, MINDGBA$GBAYN)
32  kruskal.test(MINDGBA$AgeEnrollment, MINDGBA$GBAYN)
33  fisher.test(table(MINDGBA$GBAYN, MINDGBA$Onset))
34  fisher.test(table(MINDGBA$GBAYN, MINDGBA$FHSum))
35
36  #LRRK2
37  sumtable(MINDLRRK2)
38  table(MINDLRRK2$LRRK2YN, MINDLRRK2$Sex)
39  fisher.test(table(MINDLRRK2$LRRK2YN, MINDLRRK2$Sex))
40  table(MINDLRRK2$LRRK2YN, MINDLRRK2$Ethnicity)
41  table(MINDLRRK2$LRRK2YN, MINDLRRK2$Race)
42  describeBy(MINDLRRK2$AgeEnrollment, group=MINDLRRK2$LRRK2YN)
43  table(MINDLRRK2$LRRK2YN, MINDLRRK2$Onset)
44  table(MINDLRRK2$LRRK2YN, MINDLRRK2$FHSum)
45  kruskal.test(MINDLRRK2$AgeDiag, MINDLRRK2$LRRK2YN)
46  kruskal.test(MINDLRRK2$AgeEnrollment, MINDLRRK2$LRRK2YN)
47  fisher.test(table(MINDLRRK2$LRRK2YN, MINDLRRK2$Onset))
48  fisher.test(table(MINDLRRK2$LRRK2YN, MINDLRRK2$FHSum))
49
50  ##p-value correction Table 1
51  #Sex

```

```

1 Sexgenepvalues = c(0.08123, 0.02407)
2 p.adjust(Sexgenepvalues, method = "BH")
3
4 #Age Diagnosis
5 GBADEMAGEpvalues = c(0.1077,0.3473)
6 p.adjust(GBADEMAGEpvalues, method = "BH")
7
8 #Age Enrollment
9 GBADEMenrollpvalues = c(0.02493,0.6828)
10 p.adjust(GBADEMenrollpvalues, method = "BH")
11
12 #Clinical Presentation
13 GBADEMPresentpvalues = c(0.4821,0.4158)
14 p.adjust(GBADEMPresentpvalues, method = "BH")
15
16 #1st degree fam
17 GBADEMFHpvalues = c(0.2258,0.00107)
18 p.adjust(GBADEMFHpvalues, method = "BH")
19
20
21 ###summary of clinical features
22 ###yes or no with comparisons
23 ###Sex
24 crosstable(MINDFinal, c(Dyskinesia1, Dystonia1, MotorFluc1, CognitiveImpair1,
25 CompulsiveBehav1, Depression1, Lightheaded1, Anxiety1, Fatigue1, Psychosis1,
26 DecreasedMot1, VivdDreaming1), test = TRUE, effect = TRUE, by = Sex01) %>%
27 as_flextable(keep_id=TRUE)
28
29 ###Sex-corrected pvalues
30 Sexpvalues = c(0.3232, 0.0034, 0.9887, 0.0003, 0.2111, 0.0254, 0.0341, 0.0002, 0.4032,
31 0.9756, 0.5116, 0.0040)
32 print("Sex")
33 p.adjust(Sexpvalues, method = "BH")
34
35 ###GBA
36 crosstable(MINDGBA, c(Dyskinesia1, Dystonia1, MotorFluc1, CognitiveImpair1,
37 CompulsiveBehav1, Depression1, Lightheaded1, Anxiety1, Fatigue1, Psychosis1,
38 DecreasedMot1, VivdDreaming1), test = TRUE, effect = TRUE, by = GBAYN) %>%
39 as_flextable(keep_id=TRUE)
40
41 ###GBA-corrected pvalues
42 GBApvalues = c(0.0529, 0.1556, 0.7982, 0.2553, 0.9666, 0.000033, 0.3559, 0.0060, 0.1004,
43 0.0135, 0.0537, 0.1708)
44 p.adjust(GBApvalues, method = "BH")
45
46
47 #GBASev
48 crosstable(MINDGBASev, c(Dyskinesia1, Dystonia1, MotorFluc1, CognitiveImpair1,
49 CompulsiveBehav1, Depression1, Lightheaded1, Anxiety1, Fatigue1, Psychosis1,
50 DecreasedMot1, VivdDreaming1), test = TRUE, effect = TRUE, by = GBASev) %>%
51 as_flextable(keep_id=TRUE)

```

```

1
2 ###GBA-corrected pvalues
3 GBApvalues = c(0.0529, 0.1556, 0.7982, 0.2553, 0.9666, 0.000033, 0.3559, 0.0060, 0.1004,
4 0.0135, 0.0537, 0.1708)
5 p.adjust(GBApvalues, method = "BH")
6
7 ###LRRK2
8 crosstable(MINDLRRK2, c(Dyskinesia1, Dystonia1, MotorFluc1, CognitiveImpair1,
9 CompulsiveBehav1, Depression1, Lightheaded1, Anxiety1, Fatigue1, Psychosis1,
10 DecreasedMot1, VivdDreaming1), test = TRUE, effect = TRUE, by = LRRK2YN) %>%
11 as_flextable(keep_id=TRUE)
12
13 ###LRRK2-corrected pvalues
14 LRRK2pvalues = c(0.2862, 0.1306, 0.8173, 0.0706, 0.0256, 0.3801, 0.0697, 0.5110, 0.4933,
15 0.4095, 0.4150, 0.0141)
16 print("LRRK2")
17 p.adjust(LRRK2pvalues, method = "BH")
18
19 ###adjusted pvalues
20 GBApvalues = c(0.054, 0.157, 0.803, 0.277, 1, 0, 0.36, 0.007, 0.105, 0.015, 0.055, 0.17)
21 print("GBA")
22 p.adjust(GBApvalues, method = "BH")
23
24 LRRK2pvalues = c(0.356, 0.168, 0.879, 0.09, 0.033, 0.443, 0.091, 0.539, 0.297, 0.572, 0.445,
25 0.02)
26 print("LRRK2")
27 p.adjust(LRRK2pvalues, method = "BH")
28
29 Sexpvalues = c(0.333, 0.004, 1, 0, 0.231, 0.026, 0.033, 0, 0.411, 0.951, 0.542,0.004)
30 print("Sex")
31 p.adjust(Sexpvalues, method = "BH")
32
33 MedSexpvalues = c(0.006, 0.078, 0.562, 0.262, 0.305, 0.346, 0.00000556, 0.359, 0.291, 0.041)
34 print("Meds.Sex")
35 p.adjust(MedSexpvalues, method = "BH")
36
37 MedGBApvalues = c(0.087, 0.189, 0.701, 0.217, 0.525, 1, 0.066, 0.259, 0.354, 0.385)
38 print("Meds.GBA")
39 p.adjust(MedGBApvalues, method = "BH")
40
41 MedLRRK2pvalues = c(0.513, 0.234, 0.279, 1, 0.343, 0.256, 0.175, 1, 0.009, 0.819)
42 print("Meds.LRRK2")
43 p.adjust(MedLRRK2pvalues, method = "BH")
44
45
46
47
48

```