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GWAS of Parkinson's disease clinical biomarkers in 12 longitudinal patients' cohorts

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Abstract

Background: Several reports have identified different patterns of Parkinson's disease progression in individuals carrying missense variants in *GBA* or *LRRK2* genes. The overall contribution of genetic factors to the severity and progression of Parkinson's disease, however, has not been well studied.

Objectives: To test the association between genetic variants and the clinical features of Parkinson's disease on a genome-wide scale.

Methods: We accumulated individual data from 12 longitudinal cohorts in a total of 4,093 patients with 22,307 observations over a median of 3.81 years. Genome-wide associations were evaluated for 25 cross-sectional and longitudinal phenotypes. Specific variants of interest, including 90 recently-identified disease risk variants, were also investigated post-hoc for candidate associations with these phenotypes.

Results: Two variants were genome-wide significant. Rs382940(T>A), within the intron of *SLC44A1*, was associated with reaching Hoehn and Yahr stage 3 or higher faster (HR 2.04 [1.58, 2.62], P-value = 3.46E-8). Rs61863020(G>A), an intergenic variant and eQTL for *ADRA2A*, was associated with a lower prevalence of insomnia at baseline (OR 0.63 [0.52, 0.75], P-value = 4.74E-8). In the targeted analysis, we found nine associations between known Parkinson's risk variants and more severe motor/cognitive symptoms. Also, we replicated previous reports of *GBA* coding variants (rs2230288: p.E365K, rs75548401: p.T408M) being associated with greater motor and cognitive decline over time, and *APOE* E4 tagging variant (rs429358) being associated with greater cognitive deficits in patients.

Conclusions: We identified novel genetic factors associated with heterogeneity of Parkinson's disease. The results can be used for validation or hypothesis tests regarding Parkinson's disease.

Main text:**Introduction**

Parkinson's disease (PD) is clinically defined by its motor features of rigidity, bradykinesia, gait disturbance, and tremor. Although these prominent features are important for diagnosis, patients with PD also suffer from many non-motor features such as constipation, urinary incontinence, orthostatic hypotension, REM sleep behavior disorder (RBD), apathy, hyposmia, and cognitive impairment.¹ Moreover, patients develop motor complications, including wearing off and dyskinesia, as side effects of medication. The onset, intensity and progression of these different PD clinical features vary among individuals, and the mechanisms underlying this heterogeneity are not well understood.

Recent genome-wide studies have identified 90 common variants associated with the risk of PD, with an overall heritability estimated to be between 22-27%.^{2,3} While previous studies have indicated the importance of genetic contributions to disease risk, the contribution of genetic factors to PD progression and heterogeneity has not been well studied. Investigating genetic factors associated with disease progression and heterogeneity in disease presentation is an important step in elucidating the underlying molecular mechanisms and identifying better patient stratification in clinical trials.⁴

Longitudinal patient cohorts are powerful resources that can be used to explore the impact of genetics on the trajectory of PD-related phenotypes; the inherent precision of repeated measurements over time provides more power to detect these associations. However, the available number of participants in each study is usually not enough to conduct a genome-wide association study (GWAS). In this study, we accumulated 22,307 follow-up visits from 4,093 patients across 12 cohorts (Table 1) and performed meta-analyses of longitudinal GWAS on the progression markers of Parkinson's disease. Using the results from this meta-analysis, we evaluated how known risk variants, including the 90 recently identified variants for PD,³ *GBA* protein coding mutations, and *APOE* tagging variants were associated with the progression of phenotypes. To maximize the utility of this work to other researchers, we have made all results from this study publicly searchable and available for download.

[\(https://pdgenetics.shinyapps.io/pdprogmetagwasbrowser/\)](https://pdgenetics.shinyapps.io/pdprogmetagwasbrowser/)

Methods

Cohorts

Twelve longitudinal cohorts of PD patients recruited across North America, Europe and Australia were included in our study. The following observational studies were included: the Drug Interaction with Genes in Parkinson's Disease (DIGPD), the Harvard Biomarkers Study (HBS), the Oslo Parkinson's Disease study (partly including retrospective data), the Norwegian ParkWest study (PARKWEST), the Parkinson's Disease Biomarker Program (PDBP), the Parkinsonism Incidence and Cognitive and Non-motor heterogeneity In Cambridgeshire (PICNICS), the Parkinson's Progression Markers Initiative (PPMI), and the Profiling Parkinson's disease study (PROPARK). The four cohorts included were randomized clinical trials: the Deprenyl and Tocopherol Antioxidative Therapy of Parkinsonism (DATATOP), the NIH Exploratory Trials in Parkinson's Disease Large Simple Study 1 (NET-PD_LS1), the ParkFit study (PARKFIT), and the Parkinson Research Examination of CEP-1347 Trial study with its subsequent prospective study (PreCEPT/PostCEPT). More details of these cohorts are described in Appendix. Participants' information and genetic samples were obtained under appropriate written consent and with local institutional and ethical approvals.

Phenotyping

Each cohort had a different set of recorded biomarkers and phenotypes associated with Parkinson's disease. We selected the following continuous and binomial biomarkers based on their clinical importance and availability. For continuous outcomes, we collected the scores of Hoehn and Yahr staging scale (HY),⁵ total and sub-scores of the Unified Parkinson's Disease Rating Scale (UPDRS) or the Movement Disorder Society revised UPDRS version (MDS-UPDRS),⁶ Mini-Mental State Examination (MMSE), Montreal Cognitive Assessment (MoCA)⁷ and the modified Schwab and England Activities of Daily Living Scale (SEADL). With the exception of the subscores of UPDRS/MDS-UPDRS part 4, total scores and the subscores of UPDRS and MDS-UPDRS were normalized to the population-baseline mean and standard deviation and converted to Z values. The subscores of UPDRS/MDS-UPDRS part 4, measuring complication of treatment, were normalized to the mean and standard deviation of all observations because the score was 0 at the baseline for the de-novo PD

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3 cohorts. We also determined whether subjects were recorded as presenting the following
4 binomial outcomes during participant visits: constipation, cognitive impairment, depression,
5 daytime sleepiness, Hoehn and Yahr stage of 3 or worse (HY3), hyposmia, insomnia, motor
6 fluctuation, REM sleep behavior disorder (RBD), restless legs syndrome (RLS), and an
7 SEADL of 70 or less (SEADL70). Because study-specific criteria for these binomial
8 outcomes were not consistent amongst the studies, we tried to use the common criteria for
9 these binomial outcomes if we had access to the raw data from the studies. The details of the
10 definitions of binomial outcomes are provided in the Supplemental Table 1.
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20 **Genetics data**

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22 The genotyping was conducted with NeuroX, a targeted chip for neurodegenerative disease,⁸
23 for NET-PD_LS1, a part of DIGPD (DIGPD_neuroX), HBS, PDBP, and PRECEPT. The rest
24 of DIGPD (DIGPD_chip) were genotyped using Illumina Multi-Ethnic Genotyping Array.
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26 Participants in DATATOP, OSLO, PARKFIT, PARKWEST, PICNICS, and PROPARK
27 were genotyped using Illumina Infinium OmniExpress array. Whole genome sequencing data
28 was used for PPMI, with the detailed methods for genome sequencing provided on the PPMI
29 website (<https://www.ppmi-info.org/>).
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33 Variant inclusion criteria consisted of call rate > 0.95 , MAF > 0.01 , and Hardy-Weinberg
34 equilibrium test statistic $> 1E-4$. Participants were excluded due to the following criteria:
35 high-missingness ($> 5\%$ for genotyped variants), sex discordance, extreme heterozygosity (F
36 statistics > 0.15), Non-European ancestry confirmed by joint analysis with HapMap 3 data
37 using principal component (Outside of mean ± 6 SD in PC1 or PC2 for European reference
38 samples) (International HapMap 3 Consortium et al., 2010), and excessive relatedness
39 (pairwise kinships > 0.125). We used PLINK version 1.9 for the above filtering.⁹
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43 For all samples and variants passing quality control, imputation was conducted for
44 chromosome 1 to 22 using Minimac3 using the Haplotype Reference Consortium panel
45 (HRC r1.1) and Eagle v2.3 for phasing at the Michigan Imputation Server¹⁰, with the
46 exception of the whole genome sequenced PPMI dataset. SNPs with an imputation quality of
47 R2 less than 0.3 and MAF $< 1\%$ were excluded. After quality control, the number of variants
48 were approximately 2.6 - 2.9 million in NET-PD_LS1, DIGPD_neuroX, HBS, PDBP, and
49 PRECEPT; 7.7 - 7.8 million in PICNICS, PROPARK, PARKWEST, DATATOP, PARKFIT,
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DIGPD, and OSLO; and 8.6 million in PPMI. Note that the cohorts genotyped by NeuroX had relatively less genome coverage than others.

Cohort-level analyses

We conducted a separate GWAS for each cohort per phenotype of interest. In addition, DIGPD cohorts were analyzed separately according to the genotyping array used (DIGPD_neuroX cohort and DIGPD_chip cohort). Each outcome was analyzed by an additive model with covariates. For the binomial outcomes at baseline visit, when the outcomes were positive for more than 5% of participants and >20 counts, logistic regression analyses were conducted. Those without the binomial outcome at baseline were followed-up until either censored or the development of the outcome. If more than 20 events were observed during follow-ups, the outcome was analyzed using cox proportional hazard models with time-varying covariates. For the analysis of continuous traits, linear mixed models were used to evaluate the variants' association for the outcome. Age at diagnosis, year from diagnosis to the observation, and sex were adjusted for in all analyses. In addition, the following covariates were associated with the outcome of interest in a backwards stepwise manner: quadratic age, quadratic years from diagnosis, years of education, medication status (levodopa usage, dopamine agonist usage, using either dopamine agonist or levodopa), and a Hoehn and Yahr score of 2 or more at the first observation (except for the models regressing for Hoehn and Yahr score itself or UPDRS motor score). These covariates were selected per study using Akaike's Information Criteria (AIC) for logistic models and Cox survival models, and conditional AIC (cAIC) for linear mixed effect models. The cohort level analyses were conducted with R (version 3.5.0 <https://www.r-project.org/>) and rvttests.¹¹ R package 'cAIC4' was used to calculate cAIC.¹²

Meta-Analyses

The results from cohort-level analyses were combined using an inverse variance weighted fixed effect model. If the study-specific genomic inflation factor was more than 1.2, the study was excluded from the meta-analysis. Five of the 204 GWAS were excluded based on these criteria. For other cohorts, the overall alpha error was corrected using the genomic inflation factor before the meta-analysis. Meta-analyses were carried out with METAL.¹³ From the

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3 meta-analysis results, we only evaluated variants with $MAF > 0.05$ due to statistical power
4 constraints. We also excluded variants with minor allele frequency variability greater than
5 15% across cohorts. Further exclusions at the meta-analysis level include variants with
6 Cochran's Q-test for heterogeneity < 0.05 and a total participant $N < 1000$. The null
7 hypothesis was tested with a significance level of $5E-8$ on a two-sided test. For genome-wide
8 signals, additional visualization and functional analyses were conducted using LocusZoom,¹⁴
9 FUMA (<http://fuma.ctglab.nl/snp2gene/>, version 1.3.3d).¹⁵ FUMA is a web-based annotation
10 tool using MAGMA to conduct gene-based tests, a gene-set analysis and a tissue expression
11 analysis. We applied a default setting. Also, we explored in eQTLGen database
12 (<http://www.eqtlgen.org/>)¹⁶ and meta-analyzed expression data in the brain accessible from
13 the study by Qi et al.¹⁷
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24 Associations with the variants of interest, including the recently identified 90 risk variants for
25 PD, known *LRRK2* and *GBA* variants, and *APOE*, were extracted from the meta-analysis
26 results. We exploratory evaluated the associations of these variants and clinical features
27 based on the significance level of 0.05, applying the Bonferroni adjustment of a maximum of
28 25 tests per variant (raw P-value < 0.002).
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34 The summary of analytical processes is shown in figure 1.
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39 **Data availability**

40 The summary statistics of the meta-analysis results, including the ones which were not
41 evaluated in this manuscript, are publicly available for convenient browsing and
42 downloading. (<https://pdgenetics.shinyapps.io/pdprogmetagwasbrowser/>)
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50 **Results**

51 **Novel GWAS associations with PD progression markers**

52 The cohort characteristics are provided in Table 1. Overall, we analyzed 4,093 participants
53 with 22,307 longitudinal data points over a median of 3.81 years. These cohorts varied in the
54 years between enrollment and diagnosis, as well as follow-up durations. DATATOP,
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3 ParkWest, PPMI, and PreCEPT/PostCEPT enrolled untreated PD patients while others
4 enrolled both treated and untreated patients. Considering the difference in design and
5 recruitment strategies in the cohorts (Appendix), it is important to adjust for baseline
6 characteristics as well as the follow-up lengths per cohort-level. All cohort-specific models
7 for analysis are listed in Supplemental Table 2.
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11 In total, 204 GWAS were conducted and combined into 33 meta-analyses. Eight meta-
12 analyses were not evaluated because of the small number of total participants in the analyses
13 (N total <1000). Those excluded were baseline analyses for RBD, RLS and SEADL70; and
14 longitudinal analyses for constipation, daytime sleepiness, hyposmia, RBD, and RLS.
15 Therefore, we investigated 9 binomial traits at baseline, 7 binomial traits for survival, and 9
16 continuous traits over the follow-ups. The genomic inflation factor was the mean value of
17 0.993, SD of 0.023, and the range was [0.951, 1.031] across meta-analyses. The study
18 specific genomic inflation factors were provided in Supplemental Table 3.
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21 One association with the progression of PD was of genome-wide significance (P-value <
22 5.00E-08). The minor allele of rs382940 (chr9:108058562T>A), an intronic variant of
23 *SLC44A1*, was associated with a higher hazard ratio (HR) of reaching Hoehn and Yahr stage
24 3.0 or greater (HR 2.04 [1.58, 2.62], P-value = 3.46E-8 (Estimates in a random effect model,
25 1.97 [1.38, 2.81], P-value = 1.96E-4)). When considering the baseline observations, the
26 minor allele of rs61863020 (chr10:112956055G>A), an intergenic variant, was significantly
27 associated with the lower baseline OR of having insomnia (OR 0.63 [0.52, 0.75], P-value =
28 4.74E-8 (The same estimates and P-value in a random effect model)). Locus plots and forest
29 plots for these two associations are shown in Figure 2. Cochran's Q statistics, I-square and
30 forest plots all showed no evidence of heterogeneity for these associations. (Figure 2)
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45 To evaluate the potential molecular mechanism for the two genome-wide signals, we
46 explored eQTL datasets in blood and brain,^{16,17} and functional annotation of the GWAS
47 summary statistics using FUMA. Although it is in a regulatory region of *SLC44A1*, rs382940
48 itself was not reported to be an eQTL in blood or brain. Gene-based tests using the GWAS
49 summary statistics for reaching HY3 showed that *SLC44A1* was significant gene-wise (P-
50 value = 5.8E-07 < Bonferroni correction threshold = 2.7E-6, supplemental figure 1).
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55 Rs61863020 was a significant eQTL for *ADRA2A* (α -2A adrenergic receptor) (P-value =
56 7.2E-4, the Bonferroni corrected P-value = 6.5E-3, up-regulation for A allele) in the brain.
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3 In the meta-analysis results from the other clinical outcomes, rs382940 was associated with
4 higher scores in the UPDRS part 2 and part 3 (UPDRS2_scaled: 0.36 [0.15, 0.57], P-value =
5 8.21E-04; UPDRS3_scaled: 0.29 [0.14, 0.45], P-value = 2.18E-04). These findings are
6 consistent with the primary association of rs382940 and reaching HY3, which is a significant
7 motor milestone (bilateral signs on clinical examination and the emergence of postural
8 instability). Except for the association with having insomnia at baseline, rs61863020 was not
9 significantly associated with other clinical variables in this analysis after adjusting for 25
10 tests. Of note, the variant was not associated with the development of insomnia in the
11 survival analysis. This could be due to low power of the analysis (N=1,112) or the variant
12 may be important for the development of insomnia in an earlier phase of the disease.
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22 **Targeted assessment for the PD risk variants**

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24 Of the 90 risk variants from the recently published PD GWAS, rs34637584 (*LRRK2*
25 p.G2019S) and rs76763715 (*GBA* p.N370S) were not available in the meta-analyses because
26 of their minor allele frequency (MAF) < 0.01. The remaining 88 PD GWAS risk SNPs were
27 assessed in our 25 GWAS summary sets, resulting in evaluations of 2022 candidate
28 associations. 112 associations between known genetic risk variants and clinical markers had
29 raw p-values less than 0.05. After Bonferroni correction for all evaluated candidate
30 associations, nine surpassed the threshold of the analyses-wide significance for the maximum
31 of 25 analyses per variant (raw P-value < 0.002). The directions of these associations
32 generally indicated that having the higher risk allele was associated with more severe deficits
33 in both the cognitive and motor domains of PD, but not for sleeping problems. Having the
34 risk allele (A) of rs1293298 (intron variant of *CTSB*) was associated with a lower risk of
35 developing insomnia (HR 0.79 [0.69, 0.91], P-value = 1.2E-3), and the risk allele (A) of
36 rs6500328 (intron variant of *NOD2*) and (A) of rs76116224 (intergenic variant close to 3'
37 end of *KCNS3*) were associated with a lower prevalence of daytime sleepiness at baseline
38 (OR 0.76 [0.64, 0.90], P-value = 1.4E-3; OR 0.47 [0.32, 0.68], P-value = 8.4E-5;
39 respectively). Among the nine associations with analysis-wide significance, three were
40 significant after adjusting for 88 variants (raw P-value < 5.68E-4), and one among them had
41 test-wide significance (raw P-value < 2.47E-5). Figure 3 shows the strength of the
42 associations for the selected variants with associations of analyses-wide significance in at
43 least one analysis. This figure suggests that some risk variants were associated with specific
44 clinical features. For example, rs35749011 was associated with both the HR of cognitive
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3 impairment at test-wide significance (HR 2.45 [1.64, 3.65] for the minor allele, P-value =
4 1.1E-5) and lower MoCA score over time at analyses-wide significance (-1.16 [-1.89, -0.43],
5 P-value = 0.0018). Although it is an intergenic variant whose closest gene is *KRTCAP2*, the
6 variant is in high LD ($r^2 = 0.78$) with rs2230288 (*GBA* p.E365K),^{18,19} and has a similar
7 spectrum of phenotype associations as rs2230288. Other notable variants with variant-wide
8 significance were rs76904798, the intergenic variant close to the 5' end of *LRRK2*, for
9 reaching HY3 (HR 1.32 [1.14, 1.54] with the minor allele of T, P-value = 3.0E-4), and
10 rs76116224 and the baseline OR of having daytime sleepiness mentioned above. The detailed
11 information for all of the test results is provided as supplemental material. (Supplemental
12 Table 4 and Supplemental Figure 2)
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24 ***GBA* protein coding variants and APOE tagging variants**

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26 In the focused analyses for *GBA* coding variants, rs75548401, *GBA* p.T408M, was associated
27 with the faster development of HY3 (HR 2.35 [1.58, 3.49], P-value = 2.5E-5). rs2230288,
28 *GBA* p.E365K, was associated with the higher odds of having cognitive impairment at
29 baseline (OR 2.05 [1.33, 3.18], P-value = 1.3E-3), faster development of cognitive
30 impairment (HR 2.58 [1.71, 3.89] P-value = 5.5E-6), and lower MoCA score at the analysis-
31 wide significance (Beta -1.23 [-1.97, -0.50], P-value = 1.0E-3). We previously reported these
32 associations²⁰ and we were able to confirm them in our updated analysis with more stringent
33 multiple testing correction (FDR vs Bonferroni).
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40 The C allele of rs429358, the tagging variant for the *APOE* E4 allele, was associated with
41 lower MMSE (Beta -0.20 [-0.33, -0.07], P-value = 2.8E-3) and lower MoCA (Beta -0.52 [-
42 0.86, -0.17], P-value = 3.4E-3) as expected. Moreover, it was associated with higher UPDRS
43 part 1 scores (Beta 0.12 [0.04, 0.20] in Z score, P-value = 4.5E-3). We did not have enough
44 evidence to conclude that the *APOE* E4 allele was associated with the prevalence of cognitive
45 impairment at baseline (P-value = 0.4) or its development during follow-ups (P-value =
46 0.034). The T allele of rs7412 showed no association with these measurements, also
47 predicted as this variant tagging *APOE* E2.
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Discussion

We conducted GWAS using longitudinal data from multiple PD cohorts to investigate markers of PD progression and heterogeneity. Of the 25 meta-analyses that we evaluated, we identified two variant-phenotype associations with genome-wide significance.

We also evaluated the summary statistics to assess clinical value of the variants of interest.

One of our genome-wide hits, rs382940, in the intron of *SLC44A1*, was associated with a faster rate of progression to reach HY3. *SLC44A1*, soluble carrier 44A1, is also referred to as choline transporter-like protein 1 (CTL1). The gene is ubiquitously expressed in the brain, colon, thyroid and other organs and is involved in choline transport. No associations with PD and this variant or the gene itself have been reported so far although it has been studied in several vitro and vivo studies.^{21–24} Further investigation is warranted. The search of the Brain eQTL database suggested that another GWAS-signal, rs61863020, was associated with *ADRA2A* expression, a gene reported to be associated with arousal/sleep state.²⁵ *ADRA2A* is consistently expressed in locus coeruleus as well as nigral dopamine neurons and pyramidal neurons of the human brain (<http://www.humanbraincode.org/>).²⁶ The *ADRA2A*-encoded alpha2 adrenoreceptor modulates norepinephrine levels. In addition, norepinephrine²⁷ and its receptors^{28,29} have been linked to PD in multiple model systems.

Interestingly, neither of the variants were reported to be associated with the incidence of Parkinson's disease in the recent case-control analysis of PD.³ A case-control study cannot address some mechanisms which contribute to the heterogeneity of PD such as genetic effects only relevant to cases or interactions with PD treatments. The discrepancy between the case-control GWAS and our study may reflect this point.

In the targeted assessments, we confirmed the previous results of the associations between *GBA* risk variants and motor and cognitive aspects of PD.^{30–34} In contrast with *GBA* variants, association studies of *APOE* and cognitive function in PD have yielded mixed results previously.^{35–39} Our data supported the association of *APOE* and cognitive function on two measurements; MMSE and MoCA.

The strength of the current study is the hypothesis-free approach of GWAS, which can be powerful in identifying new associations and expanding our biological knowledge-base. While the associations here should be replicated and further investigated with vivo/vitro experiments, these findings suggest the prioritization of the two variants and loci for future validations. We have reported all of the summary results on our publicly accessible site to

benefit researchers so that they may conduct/replicate the analysis of variants of interest in their own research.

The major limitation of this study is the heterogeneity of the cohorts, which is apparent in several ways: baseline characteristics, definitions of binomial outcomes, patterns for clinical care over the course of follow-up, the platforms for genotyping/sequencing, and sample acquisition/enrollment practices. By meta-analyzing at the dataset-level and exercising careful quality control throughout, we tried to extract the most generalizable and reliable results across cohorts.

Another limitation is the power of the study. Although we have aggregated the largest collection of longitudinal data in PD genetics so far, more data would be needed to identify relatively small differences expected within PD patients compared to the case-vs-control setting. From the meta-analysis results, we estimated that if we had 30% more participants in the same setting, we would have had at least one variant of the genome-wide significance ($5E-8$) in 21 out of 25 phenotypes (Supplemental Table 5). Additionally, our study results can be a valuable resource for validation and hypothesis testing as we have shown in our targeted analysis. The study website aims to provide other researchers with a tool to explore variants of their interest easily for all included phenotypes.

(<https://pdgenetics.shinyapps.io/pdprogmetagwasbrowser/>)

In our survival analysis, we did not explicitly check the proportional hazard assumption. If a variant effect changed over time, the result would be interpreted as the average HR over time. Also, the result would be biased when one of the covariates violated the proportional hazard assumption in our model and it was also associated with the variant dosage. Replication is important in this regard as well.

Finally, the study participants were restricted to individuals with European ancestry. We are now striving to collect more data, including from populations that are under-represented in this study, to improve our understanding of this topic in future studies.

Conclusion

With 4,093 participants and 22,307 longitudinal data points over a median of 3.81 years, we performed 25 GWAS meta-analyses. We found two genome-wide significant signals: the rate to reach HY3 during the disease course and rs382940; and the prevalence of insomnia at baseline and rs61863020. We also conducted targeted assessments of previously published

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3 variants of interest using the GWAS results. These results provide valuable insights into how
4 genetic factors contribute to the heterogeneity of PD and disease progression.
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Supplementary Materials

Appendix: The description of study cohorts (A). IPDGC collaborators (B)

Supplemental table 1: Cohort specific definitions of binomial outcomes

Supplemental table 2: Analytical models per datasets

Supplemental table 3: The study-specific genomic inflation factors

Supplemental table 4: The meta-analysis results of the association between risk variants and the clinical features and progression of Parkinson's disease

Supplemental table 5: The estimated study size to detect at least one variant with genome-wide significance

Supplemental figure 1: Gene-based test for reaching Hoehn and Yahr stage 3 or higher

Supplemental figure 2: Heatmap for the meta-analysis results of the association between risk variants and the clinical features and progression of Parkinson's disease

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Figure legends

Figure 1: Graphical overview of the analysis strategy.

* DIGPD cohort was analyzed separately depending on the genotyping system.

Rsq, R square; MAF, Minor allele frequency; HWE, Hardy–Weinberg equilibrium test; OR, Odds ratio; HR, Hazard ratio; PC, Principal components; AAD, Age at diagnosis; YfD, Years from diagnosis to observation; HY score, the score on the Hoehn and Yahr scale;

Figure 2: Locuszoom plots and forest plots of the two genome-wide significant hits. A: The locus plot for rs382940 which is associated with HY3. B: The locus plot for rs61863020 which is associated with insomnia. C: The forest plot for rs382940. D: The forest plot for rs61863020.

Figure 3: Heatmap of the Parkinson's disease GWAS loci associated with progression markers

Cream, P-value > 0.05; light green, P-value < 0.05; green: P-value < 0.002; blue, P-value < 5.68E-4; dark blue, P-value < 2.47E-5).

CONST, constipation; COGi, cognitive impairment; DEPR, depression; HY3, Hoehn and Yahr score; INS, insomnia; MMSE, Mini-Mental State Examination; MOCA, Montreal Cognitive Assessment; SEADL70, the modified Schwab and England Activities of Daily Living Scale; SLEEP, daytime sleepiness; UPDRS, Unified Parkinson's Disease Rating Scale (UPDRS) or the Movement Disorder Society revised UPDRS, scaled at the baseline (UPDRS1-3) or during the course.

Suffix of 'base' indicates the logistic regression model at baseline, 'surv' for the survival analysis over the course, and 'cont' for the linear mixed effect model for continuous outcome analyzed by linear mixed model.

Figure 4: Heatmap of the GBA and APOE variants associated with progression markers

Cream, P-value > 0.05; light green, P-value < 0.05; green: Bonferroni corrected P-value < 0.05;

CONST, constipation; COGi, cognitive impairment; DEPR, depression; HY3, Hoehn and Yahr score; INS, insomnia; MMSE, Mini-Mental State Examination; MOCA, Montreal Cognitive Assessment; SEADL, the modified Schwab and England Activities of Daily Living Scale; SLEEP, daytime sleepiness; UPDRS, Unified Parkinson's Disease Rating Scale (UPDRS) or the Movement Disorder Society revised UPDRS, scaled at the baseline (UPDRS1-3) or during the course.

Suffix of 'base' indicates the logistic regression model at baseline, 'surv' for the survival

analysis over the course, and ‘cont’ for the linear mixed effect model for continuous outcome analyzed by linear mixed model.

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GWAS of Parkinson's disease clinical biomarkers in 12 longitudinal patients' cohorts

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Abstract

Background: Several reports have identified different patterns of Parkinson's disease progression in individuals carrying missense variants in *GBA* or *LRRK2* genes. The overall contribution of genetic factors to the severity and progression of Parkinson's disease, however, has not been well studied.

Objectives: To test the association between genetic variants and the clinical features ~~and~~ ~~progression~~ of Parkinson's disease on a genome-wide scale.

Methods: We accumulated individual data from 12 longitudinal cohorts in a total of 4,093 patients with 22,307 observations over a median of 3.81 years. Genome-wide associations were evaluated for 25 cross-sectional and longitudinal phenotypes. Specific variants of interest, including 90 recently-identified disease risk variants, were also investigated post-hoc for candidate associations with these phenotypes.

Results: Two variants were genome-wide significant. Rs382940(T>A), within the intron of *SLC44A1*, was associated with reaching Hoehn and Yahr stage 3 or higher faster (HR 2.04 [1.58, 2.62], P-value = 3.46E-8). Rs61863020(G>A), an intergenic variant and eQTL for *ADRA2A*, was associated with a lower prevalence of insomnia at baseline (OR 0.63 [0.52, 0.75], P-value = 4.74E-8). In the targeted analysis, we found nine associations between known Parkinson's risk variants and more severe motor/cognitive symptoms. Also, we replicated previous reports of *GBA* coding variants (rs2230288: p.E365K, rs75548401: p.T408M) being associated with greater motor and cognitive decline over time, and *APOE* E4 tagging variant (rs429358) being associated with greater cognitive deficits in patients.

Conclusions: We identified novel genetic factors associated with heterogeneity of Parkinson's disease. The results can be used for validation or hypothesis tests regarding ~~provide new insights into the pathogenesis of~~ Parkinson's disease.

Main text:**Introduction**

Parkinson's disease (PD) is clinically defined by its motor features of rigidity, bradykinesia, gait disturbance, and tremor. Although these prominent features are important for diagnosis, patients with PD also suffer from many non-motor features such as constipation, urinary incontinence, orthostatic hypotension, REM sleep behavior disorder (RBD), apathy, hyposmia, and cognitive impairment.¹ Moreover, patients develop motor complications, including wearing off and dyskinesia, as side effects of medication. The onset, intensity and progression of these different PD clinical features vary among individuals, and the mechanisms underlying this heterogeneity are not well understood.

Recent genome-wide studies have identified 90 common variants associated with the risk of PD, with an overall heritability estimated to be between 22-27%.^{2,3} While previous studies have indicated the importance of genetic contributions to disease risk, the contribution of genetic factors to PD progression and heterogeneity has not been well studied. Investigating genetic factors associated with disease progression and heterogeneity in disease presentation is an important step in elucidating the underlying molecular mechanisms and identifying better patient stratification in clinical trials.⁴

Longitudinal patient cohorts are powerful resources that can be used to explore the impact of genetics on the trajectory of PD-related phenotypes; the inherent precision of repeated measurements over time provides more power to detect these associations. However, the available number of participants in each study is usually not enough to conduct a genome-wide association study (GWAS). In this study, we accumulated 22,307 follow-up visits from 4,093 patients across 12 cohorts (Table 1) and performed meta-analyses of longitudinal GWAS on the progression markers of Parkinson's disease. Using the results from this meta-analysis, we evaluated how known risk variants, including the 90 recently identified variants for PD,³ *GBA* protein coding mutations, and *APOE* tagging variants were associated with the progression of phenotypes. To maximize the utility of this work to other researchers, we have made all results from this study publicly searchable and available for download.

[\(https://pdgenetics.shinyapps.io/pdprogmetagwasbrowser/\)](https://pdgenetics.shinyapps.io/pdprogmetagwasbrowser/)

Methods

Cohorts

Twelve longitudinal cohorts of PD patients recruited across North America, Europe and Australia were included in our study. The following observational studies were included: the Drug Interaction with Genes in Parkinson's Disease (DIGPD), the Harvard Biomarkers Study (HBS), the Oslo Parkinson's Disease study (partly including retrospective data), the Norwegian ParkWest study (PARKWEST), the Parkinson's Disease Biomarker Program (PDBP), the Parkinsonism Incidence and Cognitive and Non-motor heterogeneity In Cambridgeshire (PICNICS), the Parkinson's Progression Markers Initiative (PPMI), and the Profiling Parkinson's disease study (PROPARK). The four cohorts included were randomized clinical trials: the Deprenyl and Tocopherol Antioxidative Therapy of Parkinsonism (DATATOP), the NIH Exploratory Trials in Parkinson's Disease Large Simple Study 1 (NET-PD_LS1), the ParkFit study (PARKFIT), and the Parkinson Research Examination of CEP-1347 Trial study with its subsequent prospective study (PreCEPT/PostCEPT). More details of these cohorts are described in Appendix. Participants' information and genetic samples were obtained under appropriate written consent and with local institutional and ethical approvals.

Phenotyping

Each cohort had a different set of recorded biomarkers and phenotypes associated with Parkinson's disease. We selected the following continuous and binomial biomarkers based on their clinical importance and availability. For continuous outcomes, we collected the scores of Hoehn and Yahr staging scale (HY),⁵ total and sub-scores of the Unified Parkinson's Disease Rating Scale (UPDRS) or the Movement Disorder Society revised UPDRS version (MDS-UPDRS),⁶ Mini-Mental State Examination (MMSE), Montreal Cognitive Assessment (MoCA)⁷ and the modified Schwab and England Activities of Daily Living Scale (SEADL). With the exception of the subscores of UPDRS/MDS-UPDRS part 4, total scores and the subscores of UPDRS and MDS-UPDRS were normalized to the population-baseline mean and standard deviation and converted to Z values. The subscores of UPDRS/MDS-UPDRS part 4, measuring complication of treatment, were normalized to the mean and standard deviation of all observations because the score was 0 at the baseline for the de-novo PD

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3 cohorts. We also determined whether subjects were recorded as presenting the following
4 binomial outcomes during participant visits: constipation, cognitive impairment, depression,
5 daytime sleepiness, Hoehn and Yahr stage of 3 or worse (HY3), hyposmia, insomnia, motor
6 fluctuation, REM sleep behavior disorder (RBD), restless legs syndrome (RLS), and an
7 SEADL of 70 or less (SEADL70). Because study-specific criteria for these binomial
8 outcomes were not consistent amongst the studies, we tried to use the common criteria for
9 these binomial outcomes if we had access to the raw data from the studies. The details of the
10 definitions of binomial outcomes are provided in the Supplemental Table 1.
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20 **Genetics data**

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22 The genotyping was conducted with NeuroX, a targeted chip for neurodegenerative disease,⁸
23 for NET-PD_LS1, a part of DIGPD (DIGPD_neuroX), HBS, PDBP, and PRECEPT. The rest
24 of DIGPD (DIGPD_chip) were genotyped using Illumina Multi-Ethnic Genotyping Array.
25 Participants in DATATOP, OSLO, PARKFIT, PARKWEST, PICNICS, and PROPARK
26 were genotyped using Illumina Infinium OmniExpress array. Whole genome sequencing data
27 was used for PPMI, with the detailed methods for genome sequencing provided on the PPMI
28 website (<https://www.ppmi-info.org/>).
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33 Variant inclusion criteria consisted of call rate > 0.95 , MAF > 0.01 , and Hardy-Weinberg
34 equilibrium test statistic $> 1E-4$. Participants were excluded due to the following criteria:
35 high-missingness ($> 5\%$ for genotyped variants), sex discordance, extreme heterozygosity (F
36 statistics > 0.15), Non-European ancestry confirmed by joint analysis with HapMap 3 data
37 using principal component (Outside of mean ± 6 SD in PC1 or PC2 for European reference
38 samples) (International HapMap 3 Consortium et al., 2010), and excessive relatedness
39 (pairwise kinships > 0.125). We used PLINK version 1.9 for the above filtering.⁹
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45 For all samples and variants passing quality control, imputation was conducted for
46 chromosome 1 to 22 using Minimac3 using the Haplotype Reference Consortium panel
47 (HRC r1.1) and Eagle v2.3 for phasing at the Michigan Imputation Server¹⁰, with the
48 exception of the whole genome sequenced PPMI dataset. SNPs with an imputation quality of
49 R2 less than 0.3 and MAF $< 1\%$ were excluded. After quality control, the number of variants
50 were approximately 2.6 - 2.9 million in NET-PD_LS1, DIGPD_neuroX, HBS, PDBP, and
51 PRECEPT; 7.7 - 7.8 million in PICNICS, PROPARK, PARKWEST, DATATOP, PARKFIT,
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3 DIGPD, and OSLO; and 8.6 million in PPMI. Note that the cohorts genotyped by NeuroX
4 had relatively less genome coverage than others.
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10 **Cohort-level analyses**

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12 We conducted a separate GWAS for each cohort per phenotype of interest. In addition,
13 DIGPD cohorts were analyzed separately according to the genotyping array used
14 (DIGPD_neuroX cohort and DIGPD_chip cohort). Each outcome was analyzed by an
15 additive model with covariates. For the binomial outcomes at baseline visit, when the
16 outcomes were positive for more than 5% of participants and >20 counts, logistic regression
17 analyses were conducted. Those without the binomial outcome at baseline were followed-up
18 until either censored or the development of the outcome. If more than 20 events were
19 observed during follow-ups, the outcome was analyzed using cox proportional hazard models
20 with time-varying covariates. For the analysis of continuous traits, linear mixed models were
21 used to evaluate the variants' association for the outcome. Age at diagnosis, year from
22 diagnosis to the observation, and sex were adjusted for in all analyses. In addition, the
23 following covariates were associated with the outcome of interest in a backwards stepwise
24 manner: quadratic age, quadratic years from diagnosis, years of education, medication status
25 (levodopa usage, dopamine agonist usage, using either dopamine agonist or levodopa), and a
26 Hoehn and Yahr score of 2 or more at the first observation (except for the models regressing
27 for Hoehn and Yahr score itself or UPDRS motor score). These covariates were selected per
28 study using Akaike's Information Criteria (AIC) for logistic models and Cox survival
29 models, and conditional AIC (cAIC) for linear mixed effect models. The cohort level
30 analyses were conducted with R (version 3.5.0 <https://www.r-project.org/>) and rvttests.¹¹ R
31 package 'cAIC4' was used to calculate cAIC.¹²
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50 **Meta-Analyses**

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52 The results from cohort-level analyses were combined using an inverse variance weighted
53 fixed effect model. If the study-specific genomic inflation factor was more than 1.2, the study
54 was excluded from the meta-analysis. Five of the 204 GWAS were excluded based on these
55 criteria. For other cohorts, the overall alpha error was corrected using the genomic inflation
56 factor before the meta-analysis. Meta-analyses were carried out with METAL.¹³ From the
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3 meta-analysis results, we only evaluated variants with $MAF > 0.05$ due to statistical power
4 constraints. We also excluded variants with minor allele frequency variability greater than
5 15% across cohorts. Further exclusions at the meta-analysis level include variants with
6 Cochran's Q-test for heterogeneity < 0.05 and a total participant $N < 1000$. The null
7 hypothesis was tested with a significance level of $5E-8$ on a two-sided test. For genome-wide
8 signals, additional visualization and functional analyses were conducted using LocusZoom,¹⁴
9 FUMA (<http://fuma.ctglab.nl/snp2gene/>, version 1.3.3d).¹⁵ FUMA is a web-based annotation
10 tool using MAGMA to conduct gene-based tests, a gene-set analysis and a tissue expression
11 analysis. We applied a default setting. Also, we explored in eQTLGen database
12 (<http://www.eqtlgen.org/>)¹⁶ and meta-analyzed expression data in the brain accessible from
13 the study by Qi et al.¹⁷
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24 Associations with the variants of interest, including the recently identified 90 risk variants for
25 PD, known *LRRK2* and *GBA* variants, and *APOE*, were extracted from the meta-analysis
26 results. We exploratory evaluated the associations of these variants and clinical features
27 based on the significance level of 0.05, applying the Bonferroni adjustment of a maximum of
28 25 tests per variant (raw P-value < 0.002).
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34 The summary of analytical processes is shown in figure 1.
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39 **Data availability**

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41 The summary statistics of the meta-analysis results, including the ones which were not
42 evaluated in this manuscript, are publicly available for convenient browsing and
43 downloading. (<https://pdgenetics.shinyapps.io/pdprogmetagwasbrowser/>)
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50 **Results**

51 **Novel GWAS associations with PD progression markers**

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53 The cohort characteristics are provided in Table 1. Overall, we analyzed 4,093 participants
54 with 22,307 longitudinal data points over a median of 3.81 years. These cohorts varied in the
55 years between enrollment and diagnosis, as well as follow-up durations. DATATOP,
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3 ParkWest, PPMI, and PreCEPT/PostCEPT enrolled untreated PD patients while others
4 enrolled both treated and untreated patients. Considering the difference in design and
5 recruitment strategies in the cohorts (Appendix), it is important to adjust for baseline
6 characteristics as well as the follow-up lengths per cohort-level. All cohort-specific models
7 for analysis are listed in Supplemental Table 2.
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11 In total, 204 GWAS were conducted and combined into 33 meta-analyses. Eight meta-
12 analyses were not evaluated because of the small number of total participants in the analyses
13 (N total <1000). Those excluded were baseline analyses for RBD, RLS and SEADL70; and
14 longitudinal analyses for constipation, daytime sleepiness, hyposmia, RBD, and RLS.
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17 Therefore, we investigated 9 binomial traits at baseline, 7 binomial traits for survival, and 9
18 continuous traits over the follow-ups. The genomic inflation factor was the mean value of
19 0.993, SD of 0.023, and the range was [0.951, 1.031] across meta-analyses. The study
20 specific genomic inflation factors were provided in Supplemental Table 3.
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23 One association with the progression of PD was of genome-wide significance (P-value <
24 5.00E-08). The minor allele of rs382940 (chr9:108058562T>A), an intronic variant of
25 *SLC44A1*, was associated with a higher hazard ratio (HR) of reaching Hoehn and Yahr stage
26 3.0 or greater (HR 2.04 [1.58, 2.62], P-value = 3.46E-8 (Estimates in a random effect model,
27 1.97 [1.38, 2.81], P-value = 1.96E-4)). When considering the baseline observations, the
28 minor allele of rs61863020 (chr10:112956055G>A), an intergenic variant, was significantly
29 associated with the lower baseline OR of having insomnia (OR 0.63 [0.52, 0.75], P-value =
30 4.74E-8 (The same estimates and P-value in a random effect model)). Locus plots and forest
31 plots for these two associations are shown in Figure 2. Cochran's Q statistics, I-square and
32 forest plots all showed no evidence of heterogeneity for these associations. (Figure 2)
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44 To evaluate the potential molecular mechanism for the two genome-wide signals, we
45 explored eQTL datasets in blood and brain,^{16,17} and functional annotation of the GWAS
46 summary statistics using FUMA. Although it is in a regulatory region of *SLC44A1*, rs382940
47 itself was not reported to be an eQTL in blood or brain. Gene-based tests using the GWAS
48 summary statistics for reaching HY3 showed that *SLC44A1* was significant gene-wise (P-
49 value = 5.8E-07 < Bonferroni correction threshold = 2.7E-6, supplemental figure 1).
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52 Rs61863020 was a significant eQTL for *ADRA2A* (α -2A adrenergic receptor) (P-value =
53 7.2E-4, the Bonferroni corrected P-value = 6.5E-3, up-regulation for A allele) in the brain.
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3 In the meta-analysis results from the other clinical outcomes, rs382940 was associated with
4 higher scores in the UPDRS part 2 and part 3 (UPDRS2_scaled: 0.36 [0.15, 0.57], P-value =
5 8.21E-04; UPDRS3_scaled: 0.29 [0.14, 0.45], P-value = 2.18E-04). These findings are
6 consistent with the primary association of rs382940 and reaching HY3, which is a significant
7 motor milestone (bilateral signs on clinical examination and the emergence of postural
8 instability). Except for the association with having insomnia at baseline, rs61863020 was not
9 significantly associated with other clinical variables in this analysis after adjusting for 25
10 tests. Of note, the variant was not associated with the development of insomnia in the
11 survival analysis. This could be due to low power of the analysis (N=1,112) or the variant
12 may be important for the development of insomnia in an earlier phase of the disease.
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22 **Targeted assessment for the PD risk variants**

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24 Of the 90 risk variants from the recently published PD GWAS, rs34637584 (*LRRK2*
25 p.G2019S) and rs76763715 (*GBA* p.N370S) were not available in the meta-analyses because
26 of their minor allele frequency (MAF) < 0.01. The remaining 88 PD GWAS risk SNPs were
27 assessed in our 25 GWAS summary sets, resulting in evaluations of 2022 candidate
28 associations. 112 associations between known genetic risk variants and clinical markers had
29 raw p-values less than 0.05. After Bonferroni correction for all evaluated candidate
30 associations, nine surpassed the threshold of the analyses-wide significance for the maximum
31 of 25 analyses per variant (raw P-value < 0.002). The directions of these associations
32 generally indicated that having the higher risk allele was associated with more severe deficits
33 in both the cognitive and motor domains of PD, but not for sleeping problems. Having the
34 risk allele (A) of rs1293298 (intron variant of *CTSB*) was associated with a lower risk of
35 developing insomnia (HR 0.79 [0.69, 0.91], P-value = 1.2E-3), and the risk allele (A) of
36 rs6500328 (intron variant of *NOD2*) and (A) of rs76116224 (intergenic variant close to 3'
37 end of *KCNS3*) were associated with a lower prevalence of daytime sleepiness at baseline
38 (OR 0.76 [0.64, 0.90], P-value = 1.4E-3; OR 0.47 [0.32, 0.68], P-value = 8.4E-5;
39 respectively). Among the nine associations with analysis-wide significance, three were
40 significant after adjusting for 88 variants (raw P-value < 5.68E-4), and one among them had
41 test-wide significance (raw P-value < 2.47E-5). Figure 3 shows the strength of the
42 associations for the selected variants with associations of analyses-wide significance in at
43 least one analysis. This figure suggests that some risk variants were associated with specific
44 clinical features. For example, rs35749011 was associated with both the HR of cognitive
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3 impairment at test-wide significance (HR 2.45 [1.64, 3.65] for the minor allele, P-value =
4 1.1E-5) and lower MoCA score over time at analyses-wide significance (-1.16 [-1.89, -0.43],
5 P-value = 0.0018). Although it is an intergenic variant whose closest gene is *KRTCAP2*, the
6 variant is in high LD ($r^2 = 0.78$) with rs2230288 (*GBA* p.E365K),^{18,19} and has a similar
7 spectrum of phenotype associations as rs2230288. Other notable variants with variant-wide
8 significance were rs76904798, the intergenic variant close to the 5' end of *LRRK2*, for
9 reaching HY3 (HR 1.32 [1.14, 1.54] with the minor allele of T, P-value = 3.0E-4), and
10 rs76116224 and the baseline OR of having daytime sleepiness mentioned above. The detailed
11 information for all of the test results is provided as supplemental material. (Supplemental
12 Table 4 and Supplemental Figure 2)
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24 ***GBA* protein coding variants and APOE tagging variants**

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26 In the focused analyses for *GBA* coding variants, rs75548401, *GBA* p.T408M, was associated
27 with the faster development of HY3 (HR 2.35 [1.58, 3.49], P-value = 2.5E-5). rs2230288,
28 *GBA* p.E365K, was associated with the higher odds of having cognitive impairment at
29 baseline (OR 2.05 [1.33, 3.18], P-value = 1.3E-3), faster development of cognitive
30 impairment (HR 2.58 [1.71, 3.89] P-value = 5.5E-6), and lower MoCA score at the analysis-
31 wide significance (Beta -1.23 [-1.97, -0.50], P-value = 1.0E-3). We previously reported these
32 associations²⁰ (in press at *Neurology Genetics*) and we were able to confirm them in our
33 updated analysis with more stringent multiple testing correction (FDR vs Bonferroni).
34 The C allele of rs429358, the tagging variant for the *APOE* E4 allele, was associated with
35 lower MMSE (Beta -0.20 [-0.33, -0.07], P-value = 2.8E-3) and lower MoCA (Beta -0.52 [-
36 0.86, -0.17], P-value = 3.4E-3) as expected. Moreover, it was associated with higher UPDRS
37 part 1 scores (Beta 0.12 [0.04, 0.20] in Z score, P-value = 4.5E-3). We did not have enough
38 evidence to conclude that the *APOE* E4 allele was associated with the prevalence of cognitive
39 impairment at baseline (P-value = 0.4) or its development during follow-ups (P-value =
40 0.034). The T allele of rs7412 showed no association with these measurements, also
41 predicted as this variant tagging *APOE* E2.
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Discussion

We conducted GWAS using longitudinal data from multiple PD cohorts to investigate markers of PD progression and heterogeneity. Of the 25 meta-analyses that we evaluated, we identified two variant-phenotype associations with genome-wide significance.

We also evaluated the summary statistics to assess clinical value of the variants of interest. One of our genome-wide hits, rs382940, in the intron of *SLC44A1*, was associated with a faster rate of progression to reach HY3. *SLC44A1*, soluble carrier 44A1, is also referred to as choline transporter-like protein 1 (CTL1). The gene is ubiquitously expressed in the brain, colon, thyroid and other organs and is involved in choline transport. No associations with PD and this variant or the gene itself have been reported so far although it has been studied in several vitro and vivo studies.^{21–24} Further investigation is warranted. The search of the Brain eQTL database suggested that another GWAS-signal, rs61863020, was associated with *ADRA2A* expression, a gene reported to be associated with arousal/sleep state.²⁵ *ADRA2A* is consistently expressed in locus coeruleus as well as nigral dopamine neurons and pyramidal neurons of the human brain (<http://www.humanbraincode.org/>).²⁶ The *ADRA2A*-encoded alpha2 adrenoreceptor modulates norepinephrine levels. In addition, norepinephrine²⁷ and its receptors^{28,29} have been linked to PD in multiple model systems.

Interestingly, neither of the variants were reported to be associated with the incidence of Parkinson's disease in the recent case-control analysis of PD.³ A case-control study cannot address some mechanisms which contribute to the heterogeneity of PD such as genetic effects only relevant to cases or interactions with PD treatments. The discrepancy between the case-control GWAS and our study may reflect this point.

In the targeted assessments, we confirmed the previous results of the associations between *GBA* risk variants and motor and cognitive aspects of PD.^{30–34} In contrast with *GBA* variants, association studies of *APOE* and cognitive function in PD have yielded mixed results [previously](#).^{35–39} Our data supported the association of *APOE* and cognitive function on two measurements; MMSE and MoCA.

The strength of the current study is the hypothesis-free approach of GWAS, which can be powerful in identifying new associations and expanding our biological knowledge-base. While the associations here should be replicated and further investigated with vivo/vitro experiments, these findings suggest the prioritization of the two variants and loci for future validations. We have reported all of the summary results on our publicly accessible site to

benefit researchers so that they may conduct/replicate the analysis of variants of interest in their own research.

The major limitation of this study is the heterogeneity of the cohorts, which is apparent in several ways: baseline characteristics, definitions of binomial outcomes, patterns for clinical care over the course of follow-up, the platforms for genotyping/sequencing, and sample acquisition/enrollment practices. By meta-analyzing at the dataset-level and exercising careful quality control throughout, we tried to extract the most generalizable and reliable results across cohorts.

Another limitation is the power of the study. Although we have aggregated the largest collection of longitudinal data in PD genetics so far, more data would be needed to identify relatively small differences expected within PD patients compared to the case-vs-control setting. From the meta-analysis results, we estimated that if we had 30% more participants in the same setting, we would have had at least one variant of the genome-wide significance ($5E-810$) in 21 out of 25 phenotypes (Supplemental Table 5). Additionally, our study results can be a valuable resource for validation and hypothesis testing as we have shown in our targeted analysis. The study website aims to provide other researchers with a tool to explore variants of their interest easily for all included phenotypes. (<https://pdgenetics.shinyapps.io/pdprogmetagwasbrowser/>)

In our survival analysis, we did not explicitly check the proportional hazard assumption. If a variant effect changed over time, the result would be interpreted as the average HR over time. Also, the result would be biased when one of the covariates violated the proportional hazard assumption in our model and it was also associated with the variant dosage. Replication is important in this regard as well.

Finally, the study participants were restricted to individuals with European ancestry. We are now striving to collect more data, including from populations that are under-represented in this study, to improve our understanding of this topic in future studies.

Conclusion

With 4,093 participants and 22,307 longitudinal data points over a median of 3.81 years, we performed 25 GWAS meta-analyses. We found two genome-wide significant signals: the rate to reach HY3 during the disease course and rs382940; and the prevalence of insomnia at baseline and rs61863020. We also conducted targeted assessments of previously published

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3 variants of interest using the GWAS results. These results provide valuable insights into how
4 genetic factors contribute to the heterogeneity of PD and disease progression.
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11
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Supplementary Materials

Appendix: The description of study cohorts [\(A\)](#). [IPDGC collaborators \(B\)](#)

Supplemental table 1: Cohort specific definitions of binomial outcomes

Supplemental table 2: Analytical models per datasets

Supplemental table 3: The study-specific genomic inflation factors

Supplemental table 4: The meta-analysis results of the association between risk variants and the clinical features and progression of Parkinson's disease

Supplemental table 5: The estimated study size to detect at least one variant with genome-wide significance

Supplemental figure 1: Gene-based test for reaching Hoehn and Yahr stage 3 or higher

Supplemental figure 2: Heatmap for the meta-analysis results of the association between risk variants and the clinical features and progression of Parkinson's disease

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Figure legends

Figure 1: Graphical overview of the analysis strategy.

* DIGPD cohort was analyzed separately depending on the genotyping system.

Rsq, R square; MAF, Minor allele frequency; HWE, Hardy–Weinberg equilibrium test; OR, Odds ratio; HR, Hazard ratio; PC, Principal components; AAD, Age at diagnosis; YfD, Years from diagnosis to observation; HY score, the score on the Hoehn and Yahr scale;

Figure 2: Locuszoom plots and forest plots of the two genome-wide significant hits. A: The locus plot for rs382940 which is associated with HY3. B: The locus plot for rs61863020 which is associated with insomnia. C: The forest plot for rs382940. D: The forest plot for rs61863020.

Figure 3: Heatmap of the Parkinson's disease GWAS loci associated with progression markers

Cream, P-value > 0.05; light green, P-value < 0.05; green: P-value < 0.002; blue, P-value < 5.68E-4; dark blue, P-value < 2.47E-5).

CONST, constipation; COGi, cognitive impairment; DEPR, depression; HY3, Hoehn and Yahr score; INS, insomnia; MMSE, Mini-Mental State Examination; MOCA, Montreal Cognitive Assessment; SEADL70, the modified Schwab and England Activities of Daily Living Scale; SLEEP, daytime sleepiness; UPDRS, Unified Parkinson's Disease Rating Scale (UPDRS) or the Movement Disorder Society revised UPDRS, scaled at the baseline (UPDRS1-3) or during the course.

Suffix of 'base' indicates the logistic regression model at baseline, 'surv' for the survival analysis over the course, and 'cont' for the linear mixed effect model for continuous outcome analyzed by linear mixed model.

Figure 4: Heatmap of the GBA and APOE variants associated with progression markers

Cream, P-value > 0.05; light green, P-value < 0.05; green: Bonferroni corrected P-value < 0.05;

CONST, constipation; COGi, cognitive impairment; DEPR, depression; HY3, Hoehn and Yahr score; INS, insomnia; MMSE, Mini-Mental State Examination; MOCA, Montreal Cognitive Assessment; SEADL, the modified Schwab and England Activities of Daily Living Scale; SLEEP, daytime sleepiness; UPDRS, Unified Parkinson's Disease Rating Scale (UPDRS) or the Movement Disorder Society revised UPDRS, scaled at the baseline (UPDRS1-3) or during the course.

Suffix of 'base' indicates the logistic regression model at baseline, 'surv' for the survival

analysis over the course, and ‘cont’ for the linear mixed effect model for continuous outcome analyzed by linear mixed model.

Author Roles

1. Research project: A. Conception, B. Organization, C. Execution; 2. Statistical Analysis: A. Design, B. Execution, C. Review and Critique; 3. Manuscript Preparation: A. Writing of the first draft, B. Review and Critique;

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Table 1. Summary characteristics of 13 datasets (12 cohorts)

	DATATO P	DIGPD_ chip	DIGPD_ neuroX	HBS	NET- PD_LS1	OSLO	PARKFI T	PARKWE ST	PDBP	PICNICS	PPMI	PRECEPT /POSTCEP T	PROPAR K
n	428	108	235	503	340	318	332	147	515	117	441	318	291
Total number of visits	3,303	268	811	1,206	2,209	2,086	664	294	2,360	358	2,436	4,983	1,599
Number of visits per participants (Median [1Q, 3Q])	7 [6,8] 1.22 (0.41)	2 [1, 3.25] 1.52 (1.60)	4 [3, 4.5] 2.54 (1.30)	3 [2,3] 1.53 (0.84)	7 [6, 8] 12.08 4.47 (1.48)	6 [3, 10] 6.91 (6.91)	2 [2, 2] 1.97 (0.00)	2 [2,2] 3.04 (0.09)	5 [1, 7] 1.97 (1.73)	3 [2, 4] 3.03 (1.62)	6 [5, 7] 4.88 (2.05)	16 [14, 17] 6.78 (0.95)	6 [6, 6] 4.64 (1.13)
Follow up in years	58.73 (9.12)	59.04 (10.14)	60.44 (9.43)	62.27 (10.40)	60.84 (9.07)	54.43 (10.14)	60.85 (8.62)	67.16 (9.29)	58.59 (10.18)	68.95 (9.38)	61.05 (9.82)	59.45 (9.18)	53.11 (10.58)
Age at diagnosis	1.15 (1.16)	2.78 (1.56)	2.52 (1.57)	4.02 (4.62)	1.48 (0.97)	1.76 (4.69)	5.14 (4.40)	0.14 (0.12)	6.31 (5.44)	0.23 (0.48)	0.55 (0.54)	0.80 (0.84)	6.61 (4.67)
Year from diagnosis	142 (33.2)	44 (40.7)	91 (38.7)	174 (34.6)	122 (35.9)	106 (33.3)	109 (32.8)	55 (37.4)	202 (39.2)	43 (36.8)	159 (36.1)	105 (33.0)	105 (36.1)
Female (%)	197 (46.0)	68 (65.4)	151 (64.3)	420 (84.5)	-	22 (100.0)	314 (94.6)	85 (57.8)	426 (83.0)	62 (53.0)	242 (54.9)	198 (62.5)	271 (96.1)
Having HY2 or larger at baseline (%)	14.19 (3.29)	12.27 (2.92)	12.28 (3.17)	15.14 (1.72)	15.46 (2.23)	-	-	11.31 (3.24)	15.24 (4.56)	12.17 (2.89)	15.58 (2.98)	15.93 (3.15)	11.95 (4.10)
Years of education	142 (33.2)	64 (59.8)	161 (68.5)	353 (70.2)	171 (50.6)	-	-	0 (0.0)	409 (83.1)	35 (29.9)	185 (3 (0.9)	105 (0 (0.0)	105 (68.4)
Use of levodopa (%)	0 (0.0)	88 (81.5)	163 (69.4)	198 (39.4)	231 (68.3)	-	-	0 (0.0)	277 (56.3)	22 (18.8)	0 (0.0)	1 (0.3)	218 (74.9)
Use of agonist (%)	0 (0.0)	33 (30.8)	66 (28.4)	-	-	-	-	53 (36.1)	295 (63.6)	-	185 (44.6)	-	170 (63.7)
Hyposmia (%)	24 (5.6)	1 (0.9)	2 (0.9)	59 (11.9)	27 (7.9)	-	(16.6)	27 (18.4)	119 (23.2)	11 (9.4)	35 (7.9)	3 (0.9)	76 (27.1)
Cognitive impairment (%)	-	14 (13.1)	32 (13.6)	198 (39.9)	87 (25.7)	-	-	4 (2.7)	176 (37.3)	0 (0.0)	0 (0.0)	-	92 (32.3)
Motor fluctuations (%)	3 (0.7)	4 (3.7)	13 (5.5)	168 (33.8)	5 (1.5)	-	-	2 (1.4)	118 (25.0)	0 (0.0)	0 (0.0)	-	80 (27.8)
Dyskinesias (%)	11 (2.6)	29 (27.1)	77 (33.3)	28 (10.3)	31 (9.2)	-	-	20 (13.6)	107 (22.2)	26 (33.8)	141 (33.8)	72 (22.6)	48 (16.6)
Depression (%)	-	16 (15.7)	34 (14.5)	30 (10.4)	-	-	-	-	107 (24.4)	-	27 (0.65)	-	-
Restless legs syndrome (%)	9 (2.1)	17 (16.0)	48 (20.7)	-	-	-	-	17 (11.6)	255 (54.0)	27 (23.1)	149 (33.8)	-	137 (47.1)
Constipation (%)	-	-	-	-	-	-	-	-	217 (49.4)	-	104 (24.9)	-	-
REM sleep behavior disorder (%)	-	-	104 (44.3)	-	-	-	-	-	178 (49.4)	24 (20.5)	61 (14.7)	-	125 (43.0)
Daytime sleepiness (%)	3 (0.7)	51 (48.6)						23 (15.6)	(37.7)	(20.5)	(14.7)		

1	Insomnia (%)	11 (2.6)	31 (30.4)	86 (36.6)	170 (33.9)	-	-	-	45 (30.6)	332 (70.3)	59 (50.4)	109 (24.7)	-	83 (28.5)
2	Hoehn Yahr scale 3 or greater							17			12			115
3	(%)	0 (0.0)	2 (1.9)	3 (1.3)	59 (11.9)	10 (2.9)	0 (0.0)	(5.1)	11 (7.5)	81 (15.8)	(10.3)	2 (0.5)	0 (0.0)	(40.8)
4	SEADL 70 or less (%)	3 (0.7)	30 (30.0)	12 (5.1)	-	2 (0.6)	-	-	5 (3.4)	75 (15.9)	-	2 (0.5)	1 (0.3)	-
5		1.61	1.76	1.77	2.13		3.27	2.08	1.87	2.03	1.63	1.50	1.75	2.51
6	Hoehn Yahr scale	(0.53)	(0.56)	(0.54)	(0.63)	-	(0.55)	(0.33)	(0.58)	(0.73)	(0.66)	(0.50)	(0.48)	(0.79)
7		-0.07	0.08	-0.03	-0.00			-0.06	-0.02	-0.07	-0.01		0.02	
8	UPDRS_scaled	(0.98)	(1.00)	(0.96)	(1.00)	0.00 (1.01)	-	(0.96)	(1.01)	(1.01)	(0.98)	-	(1.00)	-
9			-0.10	-0.02	0.01				-0.03	0.03		0.00	-0.03	
10	UPDRS1_scaled	-	(0.99)	(0.90)	(1.01)	0.01 (1.06)	-	-	(1.00)	(1.01)	-	(4.31)	(0.96)	-
11			0.13	-0.06	0.00				-0.03	-0.00		0.00	-0.01	
12	UPDRS2_scaled	-	(1.01)	(0.98)	(1.00)	0.01 (0.98)	-	-	(1.00)	(1.01)	-	(4.19)	(1.00)	-
13			0.09	-0.02	-0.01		0.61		-0.01	-0.09		-0.00	0.04	
14	UPDRS3_scaled	-	(0.99)	(0.96)	(1.00)	0.00 (1.00)	(1.21)	-	(1.00)	(1.00)	-	(8.87)	(0.99)	-
15			-0.09	-0.17	-0.20				-0.25	-0.12				
16	UPDRS4_scaled	-	(1.55)	(0.81)	(0.86)	-0.33 (0.71)	-	-	(0.86)	(0.94)	-	-	-	-
17		29.01	28.59	28.21	28.39			28.09	27.86		28.70		29.28	27.05
18	MMSE	(1.32)	(1.66)	(1.75)	(2.17)	-	-	(1.61)	(2.29)	-	(1.44)	-	(1.08)	(2.50)
19		91.56	64.96	88.54		91.88			89.39	84.58		93.79	92.78	
20	SEADL	(6.49)	(41.02)	(14.94)	-	(5.84)	-	-	(7.42)	(14.84)	-	(6.11)	(5.26)	-

Continous variables were summarized in Mean (SD). MMSE, Mini Mental State Examination; Montreal Cognitive Assessment, SEADL, Schwab and England Activities of Daily Living Scale; UPDRS, Unified Parkinson Disease Rating Scale; MDS-UPDRS, Movement Disorder Society revised version of UPDRS.

Figure 1. Graphical overview of the analysis strategy.

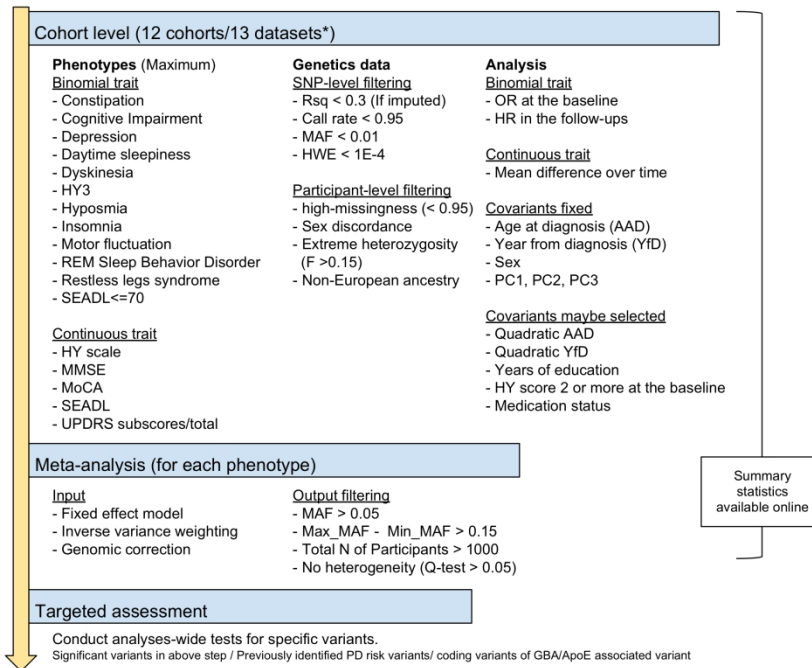


Figure1

Figure 2. LocusZoom plots and forest plots of the two genome-wide significant hits

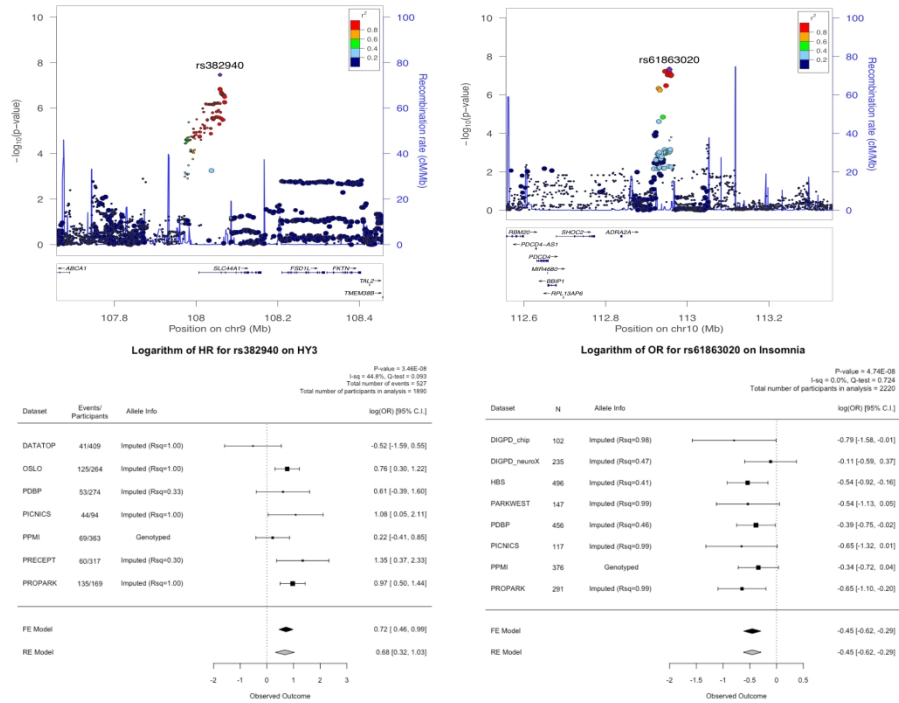


Figure2

Figure 3. Heatmap of the Parkinson's disease GWAS loci associated with progression markers.

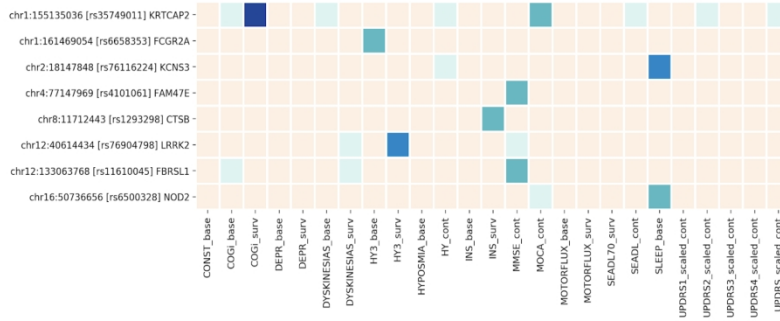


Figure3

Figure 4. Heatmap of the GBA and APOE variants associated with progression markers

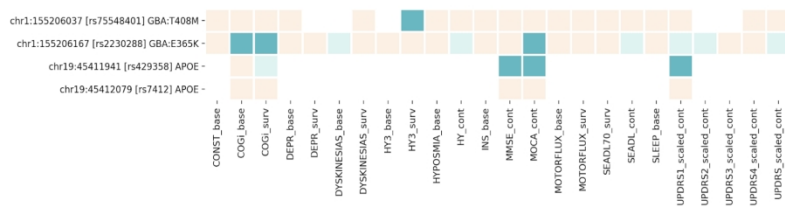
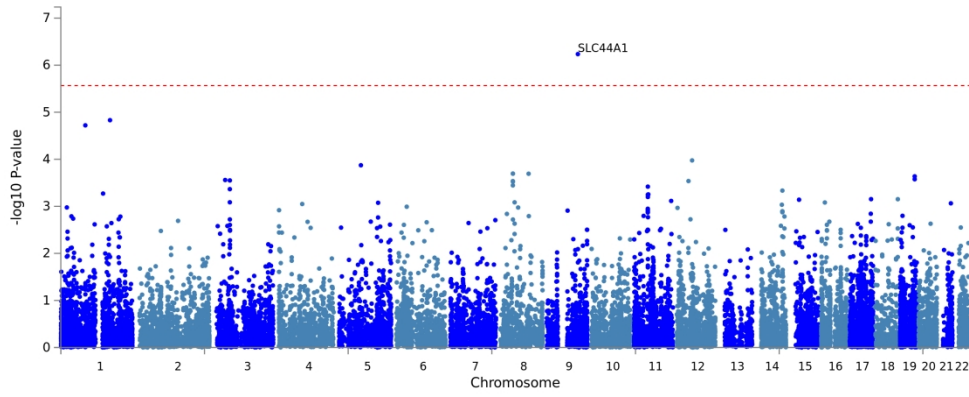
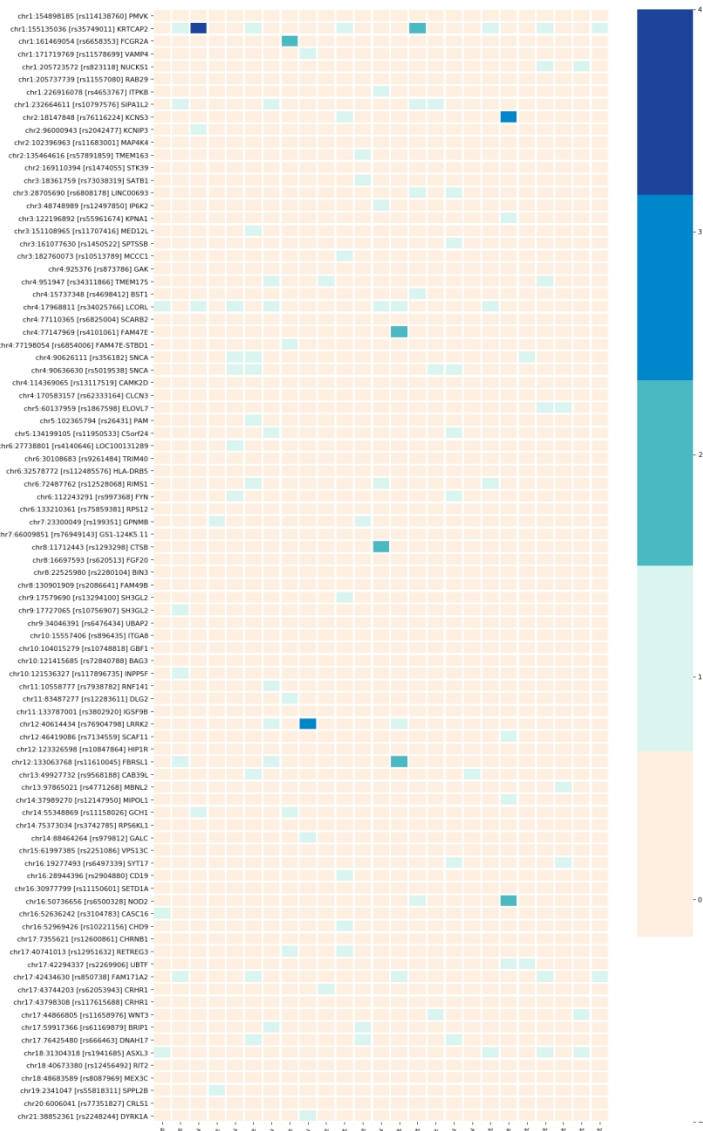


Figure3



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Supplementary Table 1. Cohort specific definitions of binomial outcomes

	DATATOP	DIGPD	HBS	NET-PD LS1	Oslo	ParkFit	ParkWest	PDBP	PICNICS	PPMI	εCEPT/ PostCEF	ProPark
hyposmia	-	NMS question-irc	-	-	-	-	"Is your sense of	UPSIT<21	-	UPSIT<21	UPSIT<21	study question
cognitive impairment	MMSE<27	DSM IV criteria	MMSE<27	SCOPA_COG<2-	-	MMSE<27	MMSE<27	MoCA<24	MDS dementia cr	MoCA<24	MMSE<27	SCOPA-COG value <23
motor fluctuations	-	Neurologist diagn	UPDRS4 Q32-Q	UPDRS4 off tim	-	-	UPDRS Q35 0/	MDS-UPDRS4	MDS-UPDRS 4.	MDS-UPDRS 4.	-	SPES/SCOPA item 20 >0
dyskinesia	Report of dyskine	Neurologist diagn	UPDRS4 Q36-Q	UPDRS4 dyskinc	-	-	UPDRS Q32 >/	MDS-UPDRS4	MDS-UPDRS 4.	MDS-UPDRS 4.	-	SPES/SCOPA item 18 >0
depression	Report of depress	Neurologist diagn	GDS15 >5	BDI>14	-	-	UPDRS 3 >/= 2	HDRS>9	Beck depression i	GDS15 >5	UPDRS item 3 >1	Beck DI score >14
restless legs syndrome	-	RLS criteria	Past medical histo	-	-	-	-	MSQ3 yes	-	RBDSQ, RLS ye-	-	-
constipation	Report of constip;	NMS question-irc	-	-	-	-	-	MDS-UPDRS1	MDS UPDRS ite	MDS-UPDRS1	MDS-UPDRS1	SCOPA-AUT item 5 >0
RBD	-	-	-	-	-	-	-	MSQ1 yes	-	RBDSQ>5	-	-
daytime sleepiess	Report of drowsii	Neurologist diagn	-	-	-	-	Epworth > 9	EPworth > 9	ESS>/=10 OR M	EPworth > 9	MDS-UPDRS1	SCOPA-SLEEP daytime sleepiness (section D) >4
insomnia	Report of insomn	Neurologist diagn	UPDRS4 Q41	-	-	-	"Do you have pre	UPDRS.Ins>0	MDS-UPDRS ite	MDS-UPDRS	Ir MDS-UPDRS	SCOPA-SLEEP Nighttime (section B) S >6

BDI, Beck's Depression Inventory; GDS, Geriatric Depression Scale; HDRS, Hamilton Depression Rating Scale; MMSE, the Mini-Mental State Examination; MoCA Montreal Cognitive Assessment; MSQ, Mayo Sleep Questionnaire; NMS, Non-motor Symptoms Questionnaire; RBD, REM sleep Behavior Disorder

Supplemental Table 2. Analytical models per datasets

DATASET	ANALYSIS	OUTCOME	MODEL
DATATOP	base	COGi	AAD+BLDDIAG+FEMALE+YEARS EDUC
DATATOP	cont	HY	AAD+FEMALE+YEARIDIAG
DATATOP	cont	MMSE	AAD+FEMALE+YEARS EDUC+YEARIDIAG+YEARIDIAGsq
DATATOP	cont	SEADL	AAD+FEMALE+YEARIDIAG+YEARIDIAGsq
DATATOP	cont	UPDRS_scaled	AAD+FEMALE+YEARS EDUC+YEARIDIAG+YEARIDIAGsq
DATATOP	surv	COGi	AAD+AADsq+BLDDIAG+BLDDIAGsq+FEMALE+YEARS EDUC
DATATOP	surv	HY3	AAD+BLDDIAG+BLDDIAGsq+FEMALE+firstHY2
DATATOP	surv	SEADL70	AAD+BLDDIAG+FEMALE+YEARS EDUC+firstHY2
DIGPD_chip	base	DEPR	AAD+BLDDIAG+BLDDIAGsq+LEVODOPA+FEMALE+YEARS EDUC
DIGPD_chip	base	HYPOSMIA	AAD+BLDDIAG+FEMALE+YEARS EDUC
DIGPD_chip	base	INS	AAD+BLDDIAG+FEMALE
DIGPD_chip	base	SEADL70	AAD+AADsq+BLDDIAG+BLDDIAGsq+FEMALE+YEARS EDUC
DIGPD_chip	base	SLEEP	AAD+BLDDIAG+DRT+FEMALE
DIGPD_chip	cont	HY	AAD+FEMALE+YEARS EDUC+YEARIDIAG+firstHY2
DIGPD_chip	cont	MMSE	AAD+FEMALE+YEARS EDUC+YEARIDIAG+firstHY2
DIGPD_chip	cont	SEADL	AAD+AADsq+AGONIST+LEVODOPA+FEMALE+YEARS EDUC+YEARIDIAG
DIGPD_chip	cont	UPDRS_scaled	AAD+AADsq+LEVODOPA+FEMALE+YEARS EDUC+YEARIDIAG+firstHY2
DIGPD_chip	cont	UPDRS1_scaled	AAD+AADsq+FEMALE+YEARIDIAG
DIGPD_chip	cont	UPDRS2_scaled	AAD+AADsq+LEVODOPA+FEMALE+YEARIDIAG+firstHY2
DIGPD_chip	cont	UPDRS3_scaled	AAD+AADsq+LEVODOPA+FEMALE+YEARS EDUC+YEARIDIAG
DIGPD_chip	cont	UPDRS4_scaled	AAD+FEMALE+YEARIDIAG
DIGPD_neuroX	base	CONST	AAD+AGONIST+BLDDIAG+BLDDIAGsq+FEMALE
DIGPD_neuroX	base	DEPR	AAD+BLDDIAG+FEMALE
DIGPD_neuroX	base	HYPOSMIA	AAD+BLDDIAG+FEMALE+YEARS EDUC
DIGPD_neuroX	base	INS	AAD+BLDDIAG+FEMALE
DIGPD_neuroX	base	MOTORFLUX	AAD+BLDDIAG+BLDDIAGsq+LEVODOPA+DRT+FEMALE
DIGPD_neuroX	base	RL	AAD+BLDDIAG+FEMALE
DIGPD_neuroX	base	SLEEP	AAD+BLDDIAG+BLDDIAGsq+FEMALE+firstHY2
DIGPD_neuroX	cont	HY	AAD+AGONIST+DRT+FEMALE+YEARS EDUC+YEARIDIAG+YEARIDIAGsq+firstHY2
DIGPD_neuroX	cont	MMSE	AAD+AGONIST+LEVODOPA+FEMALE+YEARS EDUC+YEARIDIAG+YEARIDIAGsq+firstHY2
DIGPD_neuroX	cont	SEADL	AAD+AGONIST+FEMALE+YEARIDIAG+YEARIDIAGsq
DIGPD_neuroX	cont	UPDRS_scaled	AAD+AADsq+LEVODOPA+FEMALE+YEARS EDUC+YEARIDIAG+YEARIDIAGsq+firstHY2
DIGPD_neuroX	cont	UPDRS1_scaled	AAD+FEMALE+YEARIDIAG+YEARIDIAGsq+firstHY2
DIGPD_neuroX	cont	UPDRS2_scaled	AAD+AADsq+FEMALE+YEARS EDUC+YEARIDIAG+YEARIDIAGsq+firstHY2
DIGPD_neuroX	cont	UPDRS3_scaled	AAD+AADsq+AGONIST+LEVODOPA+DRT+FEMALE+YEARIDIAG+YEARIDIAGsq
DIGPD_neuroX	cont	UPDRS4_scaled	AAD+AADsq+FEMALE+YEARIDIAG+YEARIDIAGsq
DIGPD_neuroX	surv	CONST	AAD+AADsq+BLDDIAG+LEVODOPA+FEMALE+YEARS EDUC+firstHY2
DIGPD_neuroX	surv	DEPR	AAD+BLDDIAG+FEMALE
DIGPD_neuroX	surv	DYSKINESIAS	AAD+BLDDIAG+LEVODOPA+FEMALE
DIGPD_neuroX	surv	HYPOSMIA	AAD+BLDDIAG+LEVODOPA+FEMALE+firstHY2
DIGPD_neuroX	surv	INS	AAD+AGONIST+BLDDIAG+BLDDIAGsq+FEMALE+YEARS EDUC
DIGPD_neuroX	surv	MOTORFLUX	AAD+BLDDIAG+LEVODOPA+FEMALE+firstHY2
DIGPD_neuroX	surv	RL	AAD+AGONIST+BLDDIAG+FEMALE
DIGPD_neuroX	surv	SLEEP	AAD+AGONIST+BLDDIAG+FEMALE+YEARS EDUC
HBS	base	COGi	AAD+AGONIST+BLDDIAG+LEVODOPA+FEMALE+YEARS EDUC
HBS	base	DEPR	AAD+AGONIST+BLDDIAG+LEVODOPA+FEMALE+firstHY2
HBS	base	DYSKINESIAS	AAD+BLDDIAG+LEVODOPA+FEMALE+YEARS EDUC+firstHY2
HBS	base	HY3	AAD+AGONIST+BLDDIAG+LEVODOPA+FEMALE+YEARS EDUC+firstHY2
HBS	base	INS	AAD+BLDDIAG+LEVODOPA+FEMALE+firstHY2
HBS	base	MOTORFLUX	AAD+BLDDIAG+BLDDIAGsq+LEVODOPA+FEMALE+firstHY2
HBS	base	RL	AAD+AADsq+AGONIST+BLDDIAG+FEMALE+YEARS EDUC+firstHY2
HBS	cont	HY	AAD+LEVODOPA+FEMALE+YEARIDIAG+YEARIDIAGsq+firstHY2
HBS	cont	MMSE	AAD+AADsq+AGONIST+FEMALE+YEARS EDUC+YEARIDIAG
HBS	cont	UPDRS_scaled	AAD+AGONIST+LEVODOPA+FEMALE+YEARIDIAG+YEARIDIAGsq
HBS	cont	UPDRS1_scaled	AAD+FEMALE+YEARIDIAG+firstHY2
HBS	cont	UPDRS2_scaled	AAD+LEVODOPA+DRT+FEMALE+YEARIDIAG+YEARIDIAGsq+firstHY2
HBS	cont	UPDRS3_scaled	AAD+AGONIST+LEVODOPA+FEMALE+YEARIDIAG+YEARIDIAGsq
HBS	cont	UPDRS4_scaled	AAD+LEVODOPA+FEMALE+YEARIDIAG+YEARIDIAGsq+firstHY2
HBS	surv	COGi	AAD+BLDDIAG+FEMALE+YEARS EDUC
HBS	surv	DEPR	AAD+BLDDIAG+BLDDIAGsq+LEVODOPA+FEMALE
HBS	surv	DYSKINESIAS	AAD+BLDDIAG+BLDDIAGsq+LEVODOPA+FEMALE
HBS	surv	HY3	AAD+BLDDIAG+DRT+FEMALE+firstHY2
HBS	surv	INS	AAD+BLDDIAG+FEMALE+firstHY2
HBS	surv	MOTORFLUX	AAD+BLDDIAG+DRT+FEMALE
NET-PD_L51	base	COGi	AAD+BLDDIAG+LEVODOPA+FEMALE+YEARS EDUC
NET-PD_L51	base	DEPR	AAD+BLDDIAG+FEMALE+YEARS EDUC
NET-PD_L51	base	MOTORFLUX	AAD+BLDDIAG+LEVODOPA+FEMALE
NET-PD_L51	cont	SEADL	AAD+AADsq+LEVODOPA+FEMALE+YEARS EDUC+YEARIDIAG+YEARIDIAGsq
NET-PD_L51	cont	UPDRS_scaled	AAD+AADsq+LEVODOPA+DRT+FEMALE+YEARS EDUC+YEARIDIAG+YEARIDIAGsq
NET-PD_L51	cont	UPDRS1_scaled	AAD+AADsq+FEMALE+YEARS EDUC+YEARIDIAG+YEARIDIAGsq
NET-PD_L51	cont	UPDRS2_scaled	AAD+AADsq+LEVODOPA+DRT+FEMALE+YEARS EDUC+YEARIDIAG+YEARIDIAGsq
NET-PD_L51	cont	UPDRS3_scaled	AAD+AADsq+LEVODOPA+DRT+FEMALE+YEARS EDUC+YEARIDIAG
NET-PD_L51	cont	UPDRS4_scaled	AAD+FEMALE+YEARIDIAG+YEARIDIAGsq
NET-PD_L51	surv	COGi	AAD+BLDDIAG+FEMALE
NET-PD_L51	surv	DEPR	AAD+BLDDIAG+BLDDIAGsq+FEMALE+YEARS EDUC
NET-PD_L51	surv	DYSKINESIAS	AAD+AADsq+BLDDIAG+LEVODOPA+FEMALE
NET-PD_L51	surv	HY3	AAD+BLDDIAG+FEMALE
NET-PD_L51	surv	MOTORFLUX	AAD+BLDDIAG+LEVODOPA+FEMALE
NET-PD_L51	surv	SEADL70	AAD+AADsq+BLDDIAG+LEVODOPA+FEMALE
OSLO	cont	HY	AAD+FEMALE+YEARIDIAG+YEARIDIAGsq
OSLO	cont	UPDRS3_scaled	AAD+AADsq+FEMALE+YEARIDIAG+YEARIDIAGsq
OSLO	surv	HY3	AAD+AADsq+FEMALE
PARKFIT	base	COGi	AAD+BLDDIAG+FEMALE
PARKFIT	cont	HY	AAD+AADsq+FEMALE+YEARIDIAG+YEARIDIAGsq+firstHY2
PARKFIT	cont	UPDRS_scaled	AAD+AADsq+FEMALE+YEARIDIAG+YEARIDIAGsq+firstHY2
PARKFIT	sngl	MMSE	AAD+FEMALE+YEARIDIAG
PARKWEST	base	COGi	AAD+AADsq+BLDDIAG+FEMALE+YEARS EDUC
PARKWEST	base	HYPOSMIA	AAD+BLDDIAG+FEMALE+firstHY2
PARKWEST	base	INS	AAD+BLDDIAG+FEMALE
PARKWEST	base	SLEEP	AAD+BLDDIAG+FEMALE
PARKWEST	cont	HY	AAD+AADsq+AGONIST+LEVODOPA+FEMALE+YEARS EDUC+YEARIDIAG+firstHY2
PARKWEST	cont	MMSE	AAD+AGONIST+FEMALE+YEARS EDUC+YEARIDIAG+YEARIDIAGsq
PARKWEST	cont	SEADL	AAD+AADsq+LEVODOPA+FEMALE+YEARS EDUC+YEARIDIAG+firstHY2
PARKWEST	cont	UPDRS_scaled	AAD+AGONIST+LEVODOPA+FEMALE+YEARS EDUC+YEARIDIAG+firstHY2
PARKWEST	cont	UPDRS1_scaled	AAD+LEVODOPA+FEMALE+YEARS EDUC+YEARIDIAG+firstHY2
PARKWEST	cont	UPDRS2_scaled	AAD+AADsq+LEVODOPA+FEMALE+YEARS EDUC+YEARIDIAG+firstHY2
PARKWEST	cont	UPDRS3_scaled	AAD+AGONIST+LEVODOPA+FEMALE+YEARS EDUC+YEARIDIAG+YEARIDIAGsq
PARKWEST	cont	UPDRS4_scaled	AAD+AGONIST+DRT+FEMALE+YEARIDIAG+firstHY2

1					
2	PARKWEST	surv	COGi	AAD+BLDDIAG+FEMALE+firstHY2	
3	PDBP	base	CONST	AAD+BLDDIAG+BLDDIAGsq+LEVODOPA+FEMALE+YEARS EDUC	
4	PDBP	base	COGi	AAD+BLDDIAG+DRT+FEMALE+YEARS EDUC	
5	PDBP	base	DEPR	AAD+BLDDIAG+FEMALE	
6	PDBP	base	DYSKINESIAS	AAD+AADsq+BLDDIAG+BLDDIAGsq+LEVODOPA+DRT+FEMALE+YEARS EDUC	
7	PDBP	base	HY3	AAD+AADsq+BLDDIAG+FEMALE+firstHY2	
8	PDBP	base	HYPOSMIA	AAD+BLDDIAG+FEMALE	
9	PDBP	base	INS	AAD+AADsq+AGONIST+BLDDIAG+LEVODOPA+FEMALE+YEARS EDUC	
10	PDBP	base	MOTORFLUX	AAD+BLDDIAG+LEVODOPA+FEMALE+firstHY2	
11	PDBP	base	RBD	AAD+AADsq+BLDDIAG+FEMALE+firstHY2+YEARS EDUC	
12	PDBP	base	RL	AAD+BLDDIAG+LEVODOPA+FEMALE	
13	PDBP	base	SEADL70	AAD+AADsq+BLDDIAG+BLDDIAGsq+LEVODOPA+DRT+FEMALE+firstHY2	
14	PDBP	base	SLEEP	AAD+AADsq+AGONIST+BLDDIAG+BLDDIAGsq+FEMALE	
15	PDBP	cont	HY	AAD+LEVODOPA+FEMALE+firstHY2+YEAR IDIAG	
16	PDBP	cont	MOCA	AAD+FEMALE+YEAR IDIAG+YEARS EDUC	
17	PDBP	cont	SEADL	AAD+AADsq+AGONIST+DRT+FEMALE+firstHY2+YEAR IDIAG+YEARS EDUC	
18	PDBP	cont	UPDRS_scaled	AAD+AADsq+AGONIST+DRT+FEMALE+firstHY2+YEAR IDIAG+YEAR IDIAGsq+YEARS EDUC	
19	PDBP	cont	UPDRS1_scaled	AAD+AGONIST+FEMALE+firstHY2+YEAR IDIAG+YEAR IDIAGsq+YEARS EDUC	
20	PDBP	cont	UPDRS2_scaled	AAD+AADsq+LEVODOPA+FEMALE+firstHY2+YEAR IDIAG+YEAR IDIAGsq+YEARS EDUC	
21	PDBP	cont	UPDRS3_scaled	AAD+AGONIST+DRT+FEMALE+YEAR IDIAG+YEAR IDIAGsq+YEARS EDUC	
22	PDBP	cont	UPDRS4_scaled	AAD+AADsq+FEMALE+firstHY2+YEAR IDIAG+YEAR IDIAGsq	
23	PDBP	surv	CONST	AAD+AADsq+AGONIST+BLDDIAG+LEVODOPA+FEMALE	
24	PDBP	surv	COGi	AAD+BLDDIAG+FEMALE+YEARS EDUC	
25	PDBP	surv	DEPR	AAD+AADsq+BLDDIAG+BLDDIAGsq+FEMALE+YEARS EDUC	
26	PDBP	surv	DYSKINESIAS	AAD+AADsq+BLDDIAG+DRT+FEMALE+firstHY2+YEARS EDUC	
27	PDBP	surv	HY3	AAD+BLDDIAG+FEMALE	
28	PDBP	surv	HYPOSMIA	AAD+BLDDIAG+FEMALE+firstHY2	
29	PDBP	surv	INS	AAD+BLDDIAG+FEMALE	
30	PDBP	surv	MOTORFLUX	AAD+BLDDIAG+LEVODOPA+DRT+FEMALE+firstHY2	
31	PDBP	surv	RBD	AAD+BLDDIAG+LEVODOPA+FEMALE	
32	PDBP	surv	RL	AAD+AGONIST+BLDDIAG+LEVODOPA+FEMALE+YEARS EDUC	
33	PDBP	surv	SEADL70	AAD+BLDDIAG+FEMALE+firstHY2	
34	PDBP	surv	SLEEP	AAD+AGONIST+BLDDIAG+DRT+FEMALE+YEARS EDUC	
35	PICNICS	base	CONST	AAD+BLDDIAG+LEVODOPA+FEMALE	
36	PICNICS	base	DEPR	AAD+AGONIST+BLDDIAG+FEMALE	
37	PICNICS	base	INS	AAD+BLDDIAG+LEVODOPA+FEMALE+YEARS EDUC	
38	PICNICS	base	SLEEP	AAD+BLDDIAG+LEVODOPA+DRT+FEMALE	
39	PICNICS	cont	HY	AAD+FEMALE+YEAR IDIAG+YEAR IDIAGsq+firstHY2	
40	PICNICS	cont	MMSE	AAD+AADsq+LEVODOPA+FEMALE+YEARS EDUC+YEAR IDIAG+firstHY2	
41	PICNICS	cont	MOCA	AAD+FEMALE+YEARS EDUC+YEAR IDIAG+YEAR IDIAGsq+firstHY2	
42	PICNICS	cont	UPDRS_scaled	AAD+FEMALE+YEARS EDUC+YEAR IDIAG+YEAR IDIAGsq+firstHY2	
43	PICNICS	surv	CONST	AAD+BLDDIAG+FEMALE	
44	PICNICS	surv	COGi	AAD+BLDDIAG+BLDDIAGsq+DRT+FEMALE	
45	PICNICS	surv	DEPR	AAD+AADsq+BLDDIAG+LEVODOPA+FEMALE+YEARS EDUC	
46	PICNICS	surv	HY3	AAD+BLDDIAG+BLDDIAGsq+DRT+FEMALE+firstHY2	
47	PICNICS	surv	INS	AAD+BLDDIAG+FEMALE+YEARS EDUC	
48	PICNICS	surv	MOTORFLUX	AAD+AGONIST+BLDDIAG+BLDDIAGsq+FEMALE+firstHY2	
49	PICNICS	surv	SLEEP	AAD+AGONIST+BLDDIAG+FEMALE	
50	PPMI	base	CONST	AAD+AADsq+BLDDIAG+FEMALE	
51	PPMI	base	COGi	AAD+AADsq+BLDDIAG+FEMALE+YEARS EDUC	
52	PPMI	base	HYPOSMIA	AAD+AADsq+BLDDIAG+FEMALE	
53	PPMI	base	INS	AAD+BLDDIAG+FEMALE	
54	PPMI	base	RBD	AAD+AADsq+BLDDIAG+FEMALE	
55	PPMI	base	SLEEP	AAD+BLDDIAG+FEMALE+YEARS EDUC	
56	PPMI	cont	HY	AAD+AADsq+FEMALE+MED+YEAR IDIAG+YEAR IDIAGsq	
57	PPMI	cont	MOCA	AAD+DRT+FEMALE+YEARS EDUC+YEAR IDIAG	
58	PPMI	cont	SEADL	AAD+DRT+FEMALE+LEVODOPA+YEARS EDUC+YEAR IDIAG+YEAR IDIAGsq	
59	PPMI	cont	UPDRS1	AAD+AGONIST+FEMALE+YEAR IDIAG	
60	PPMI	cont	UPDRS2	AAD+DRT+FEMALE+LEVODOPA+YEAR IDIAG+YEAR IDIAGsq	
61	PPMI	cont	UPDRS3	AAD+FEMALE+MED+YEAR IDIAG+YEAR IDIAGsq	
62	PPMI	surv	CONST	AAD+BLDDIAG+FEMALE	
63	PPMI	surv	COGi	AAD+BLDDIAG+FEMALE+firstHY2	
64	PPMI	surv	DYSKINESIAS	AAD+BLDDIAG+FEMALE+YEARS EDUC	
65	PPMI	surv	HY3	AAD+BLDDIAG+FEMALE+firstHY2	
66	PPMI	surv	INS	AAD+BLDDIAG+FEMALE	
67	PPMI	surv	MOTORFLUX	AAD+AADsq+BLDDIAG+FEMALE+YEARS EDUC	
68	PPMI	surv	RBD	AAD+BLDDIAG+FEMALE+YEARS EDUC+firstHY2	
69	PPMI	surv	SEADL70	AAD+AADsq+BLDDIAG+BLDDIAGsq+FEMALE	
70	PPMI	surv	SLEEP	AAD+BLDDIAG+BLDDIAGsq+FEMALE	
71	PRECEPT	base	DEPR	AAD+BLDDIAG+FEMALE+firstHY2	
72	PRECEPT	cont	HY	AAD+AADsq+AGONIST+FEMALE+YEARS EDUC+YEAR IDIAG+YEAR IDIAGsq+firstHY2	
73	PRECEPT	cont	MMSE	AAD+AADsq+AGONIST+FEMALE+YEARS EDUC+YEAR IDIAG	
74	PRECEPT	cont	MOCA	AAD+AADsq+FEMALE+YEARS EDUC+YEAR IDIAG+YEAR IDIAGsq+firstHY2	
75	PRECEPT	cont	SEADL	AAD+AADsq+AGONIST+LEVODOPA+DRT+FEMALE+YEARS EDUC+YEAR IDIAG+YEAR IDIAGsq+firstHY2	
76	PRECEPT	cont	UPDRS_scaled	AAD+AADsq+AGONIST+DRT+FEMALE+YEARS EDUC+YEAR IDIAG+YEAR IDIAGsq+firstHY2	
77	PRECEPT	cont	UPDRS1_scaled	AAD+AGONIST+DRT+FEMALE+YEARS EDUC+YEAR IDIAG+firstHY2	
78	PRECEPT	cont	UPDRS2_scaled	AAD+AADsq+AGONIST+LEVODOPA+DRT+FEMALE+YEARS EDUC+YEAR IDIAG+YEAR IDIAGsq+firstHY2	
79	PRECEPT	cont	UPDRS3_scaled	AAD+AADsq+AGONIST+LEVODOPA+DRT+FEMALE+YEARS EDUC+YEAR IDIAG+YEAR IDIAGsq	
80	PRECEPT	surv	CONST	AAD+BLDDIAG+FEMALE	
81	PRECEPT	surv	COGi	AAD+BLDDIAG+FEMALE+YEARS EDUC	
82	PRECEPT	surv	DEPR	AAD+BLDDIAG+FEMALE+YEARS EDUC	
83	PRECEPT	surv	DYSKINESIAS	AAD+AGONIST+BLDDIAG+LEVODOPA+FEMALE+firstHY2	
84	PRECEPT	surv	HY3	AAD+BLDDIAG+FEMALE+firstHY2	
85	PRECEPT	surv	HYPOSMIA	AAD+AADsq+BLDDIAG+LEVODOPA+FEMALE+firstHY2	
86	PRECEPT	surv	INS	AAD+BLDDIAG+FEMALE	
87	PRECEPT	surv	MOTORFLUX	AAD+AADsq+AGONIST+BLDDIAG+LEVODOPA+FEMALE	
88	PRECEPT	surv	SEADL70	AAD+AADsq+BLDDIAG+FEMALE+firstHY2	
89	PRECEPT	surv	SLEEP	AAD+BLDDIAG+LEVODOPA+FEMALE+firstHY2	
90	PROPARK	base	CONST	AAD+AGONIST+BLDDIAG+FEMALE	
91	PROPARK	base	COGi	AAD+BLDDIAG+FEMALE+YEARS EDUC+firstHY2	
92	PROPARK	base	DEPR	AAD+BLDDIAG+FEMALE	
93	PROPARK	base	DYSKINESIAS	AAD+AGONIST+BLDDIAG+LEVODOPA+FEMALE+YEARS EDUC	
94	PROPARK	base	HY3	AAD+BLDDIAG+BLDDIAGsq+FEMALE+firstHY2	
95	PROPARK	base	HYPOSMIA	AAD+BLDDIAG+LEVODOPA+FEMALE	
96	PROPARK	base	INS	AAD+AGONIST+BLDDIAG+LEVODOPA+FEMALE	
97	PROPARK	base	MOTORFLUX	AAD+AGONIST+BLDDIAG+LEVODOPA+DRT+FEMALE+YEARS EDUC	
98	PROPARK	base	SLEEP	AAD+AGONIST+BLDDIAG+LEVODOPA+FEMALE	
99	PROPARK	cont	HY	AAD+AGONIST+LEVODOPA+FEMALE+YEARS EDUC+YEAR IDIAG	
100	PROPARK	cont	MMSE	AAD+AGONIST+FEMALE+YEARS EDUC+YEAR IDIAG+YEAR IDIAGsq	
101	PROPARK	surv	CONST	AAD+AADsq+BLDDIAG+FEMALE+firstHY2	
102	PROPARK	surv	COGi	AAD+BLDDIAG+BLDDIAGsq+LEVODOPA+DRT+FEMALE+YEARS EDUC	
103	PROPARK	surv	DEPR	AAD+AADsq+BLDDIAG+FEMALE	
104	PROPARK	surv	DYSKINESIAS	AAD+BLDDIAG+BLDDIAGsq+LEVODOPA+DRT+FEMALE	
105	PROPARK	surv	HY3	AAD+AGONIST+BLDDIAG+FEMALE	
106	PROPARK	surv	INS	AAD+AADsq+BLDDIAG+BLDDIAGsq+DRT+FEMALE	
107	PROPARK	surv	MOTORFLUX	AAD+BLDDIAG+LEVODOPA+DRT+FEMALE	
108	PROPARK	surv	SLEEP	AAD+BLDDIAG+FEMALE	

base, logistic regression model at the baseline; surv, Cox survival model; cont, linear mixed effect model

Supplemental Table 3 Study specific genomic inflation factor (lambda)

Phenotype	Lambda
base_CONST	0.982
base_COGi	0.965
base_DEPR	0.980
base_DYSKINESIAS	0.960
base_HY3	0.969
base_HYPOSMIA	0.965
base_INS	0.969
base_MOTORFLUX	0.960
base_SLEEP	0.952
cont_HY	0.997
cont_MMSE	1.005
cont_MOCA	1.031
cont_SEADL	1.015
cont_UPDRS1_scaled	1.030
cont_UPDRS2_scaled	1.014
cont_UPDRS3_scaled	1.020
cont_UPDRS4_scaled	1.018
cont_UPDRS_scaled	1.000
surv_COGi	1.003
surv_DEPR	0.986
surv_DYSKINESIAS	1.014
surv_HY3	1.005
surv_INS	0.995
surv_MOTORFLUX	1.007
surv_SEADL70	0.997

base, logistic regression model at the baseline; surv, Cox survival model; cont, linear mixed effect model

CONST, constipation; COGi, cognitive impairment; INS, insomnia; SLEEP, daytime sleepiness; MOTORFLUX, motor fluctuations; HY3, Hoehn Yahr scale 3 or greater; RBD, REM sleep behavior disorder; DEPR, depression; MMSE, Mini Mental State Examination; Montreal Cognitive Assessment, SEADL, Schwab and England Activities of Daily Living Scale; UPDRS, Unified Parkinson Disease Rating Scale; MDS-UPDRS, Movement Disorder Society revised version of UPDRS.

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Supplemental Table 4 Risk associated variance and the results of meta-analysis

SNP	dbSNP	A1	A2	A1 Freq	FrqSE	Outcome	Analysis	N	Beta	SE	95% CI	Isq	Qtest	p	p<0.05	p<0.05/25	p<0.05/88	p<0.05/2022	NearGene	
1:155135036	rs35749011	a	g	0.0291	0.0119	COG1	COG1_surv	2244	0.895	0.203	2.45 [-1.64, 3.65]	0.00	0.794	1.06E-05	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0259	0.0067	MOCA	MOCA_cont	1074	-1.164	0.373	-1.16 [-1.89, -0.43]	0.00	0.490	1.80E-03	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0310	0.0131	COG1	COG1_cont	2859	0.678	0.220	1.97 [1.28, 3.03]	0.00	0.848	2.02E-03	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0289	0.0113	HY	HY_cont	3627	0.076	0.028	0.08 [0.02, 0.13]	0.00	0.531	7.10E-03	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0263	0.0080	SEADL	SEADL_cont	2218	-1.641	0.148	-1.64 [-3.11, -0.18]	0.00	0.441	2.82E-02	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0223	0.0076	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.212	0.099	0.21 [0.02, 0.41]	0.00	0.879	3.32E-02	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0288	0.0156	DYSKINESIAS	DYSKINESIAS_base	1232	0.643	0.307	1.90 [1.04, 3.47]	25.50	0.261	3.66E-02	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0265	0.0099	UPDRS_scaled	UPDRS_scaled_cont	2994	0.153	0.076	0.15 [0.00, 0.30]	0.00	0.855	4.50E-02	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0274	0.0139	INS	INS_base	2103	0.364	0.218	1.44 [0.94, 2.21]	0.00	0.493	9.48E-02	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0230	0.0075	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.157	0.099	0.16 [-0.04, 0.35]	0.00	0.704	1.15E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0346	0.0161	HY3	HY3_base	1289	0.440	0.315	1.55 [0.84, 2.88]	0.00	0.469	1.63E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0238	0.0119	MMSE	MMSE_cont	2114	-0.211	0.155	-0.21 [-0.52, 0.09]	0.00	0.850	1.74E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0244	0.0075	UPDRS3_scaled	UPDRS3_scaled_cont	2446	0.116	0.085	0.12 [-0.05, 0.28]	12.20	0.335	1.76E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0332	0.0158	DEPR	DEPR_surv	1314	0.301	0.229	1.35 [0.86, 2.12]	38.30	0.150	1.89E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0267	0.0092	HY3	HY3_surv	2582	0.212	0.192	1.24 [0.85, 1.80]	4.00	0.402	2.70E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0297	0.0140	SLEEP	SLEEP_base	1724	0.245	0.237	1.28 [0.80, 2.03]	7.00	0.375	3.00E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0298	0.0139	MOTORFLUX	MOTORFLUX_base	1803	0.247	0.250	1.28 [0.78, 2.09]	0.00	0.619	3.25E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0254	0.0088	DYSKINESIAS	DYSKINESIAS_surv	1656	0.170	0.183	1.19 [0.83, 1.70]	0.00	0.956	3.51E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0292	0.0137	HYPOSMIA	HYPOSMIA_base	1588	0.198	0.245	1.22 [0.75, 1.97]	0.00	0.657	4.19E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0243	0.0081	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.067	0.084	0.07 [-0.10, 0.23]	29.60	0.213	4.28E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0235	0.0058	SEADL70	SEADL70_surv	1277	0.203	0.292	1.23 [0.69, 2.17]	0.00	0.567	4.86E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0273	0.0082	MOTORFLUX	MOTORFLUX_surv	1709	0.034	0.153	1.03 [0.77, 1.40]	0.00	0.813	8.24E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0298	0.0145	CONST	CONST_base	1472	0.040	0.238	1.04 [0.65, 1.66]	0.00	0.729	8.65E-01	1	1	1	1	1	KRTPCAP2
1:155135036	rs35749011	a	g	0.0268	0.0132	DEPR	DEPR_base	1870	-0.003	0.302	1.00 [0.55, 1.80]	0.00	0.724	9.92E-01	1	1	1	1	1	KRTPCAP2
2:18147848	rs76116224	a	t	0.9045	0.0153	SLEEP	SLEEP_base	1033	-0.765	0.195	0.47 [0.32, 0.68]	0.00	0.453	8.41E-05	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9038	0.0145	HY	HY_cont	2574	-0.048	0.021	-0.05 [-0.09, -0.01]	0.00	0.513	2.11E-02	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9132	0.0094	SEADL70	SEADL70_surv	1100	-0.357	0.218	0.70 [0.46, 1.07]	0.00	0.702	1.01E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9049	0.0148	INS	INS_base	1529	-0.207	0.162	0.81 [0.59, 1.12]	45.70	0.101	2.01E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.8977	0.0094	UPDRS3_scaled	UPDRS3_scaled_cont	1389	-0.089	0.073	-0.09 [-0.23, 0.05]	55.80	0.060	2.22E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.8983	0.0131	UPDRS4_scaled	UPDRS4_scaled_cont	1091	0.091	0.081	0.09 [-0.07, 0.25]	0.00	0.425	2.59E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9010	0.0112	COG1	COG1_base	2369	-0.205	0.184	0.81 [0.57, 1.17]	0.00	0.708	2.63E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9062	0.0130	HY3	HY3_surv	1991	-0.138	0.126	0.87 [0.68, 1.12]	49.40	0.065	2.74E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.8983	0.0135	UPDRS1_scaled	UPDRS1_scaled_cont	1092	-0.107	0.102	-0.11 [-0.31, 0.09]	39.80	0.173	2.91E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9053	0.0186	UPDRS_scaled	UPDRS_scaled_cont	1941	-0.065	0.064	-0.06 [-0.19, 0.06]	36.20	0.152	3.14E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9117	0.0128	COG1	COG1_surv	1672	0.111	0.181	1.12 [0.78, 1.59]	0.00	0.590	5.38E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9036	0.0090	DYSKINESIAS	DYSKINESIAS_surv	1115	0.089	0.161	1.09 [0.80, 1.50]	0.00	0.475	5.79E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9039	0.0126	DEPR	DEPR_base	1119	-0.110	0.244	0.90 [0.56, 1.44]	0.00	0.713	6.53E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9132	0.0180	SEADL	SEADL_cont	1200	0.271	0.623	0.27 [-0.95, 1.49]	0.00	0.501	6.64E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9205	0.0174	MMSE	MMSE_cont	1565	0.046	0.109	0.05 [-0.17, 0.26]	0.00	0.984	6.70E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.8996	0.0128	UPDRS2_scaled	UPDRS2_scaled_cont	1087	0.032	0.100	0.03 [-0.17, 0.23]	0.00	0.648	7.53E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9019	0.0077	MOTORFLUX	MOTORFLUX_base	1112	-0.045	0.218	0.96 [0.62, 1.46]	0.00	0.684	8.36E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.8996	0.0173	UPDRS2_scaled	UPDRS2_scaled_cont	1087	0.032	0.100	0.03 [-0.17, 0.23]	0.00	0.648	7.53E-01	1	1	1	1	1	KCN53
2:18147848	rs76116224	a	t	0.9019	0.0077	MOTORFLUX	MOTORFLUX_base	1112	-0.045	0.218	0.96 [0.62, 1.46]	0.00	0.684	8.36E-01	1	1	1	1	1	KCN53
22:1814434	rs76904798	t	c	0.1552	0.0187	HY3	HY3_surv	2582	0.281	0.078	1.32 [1.14, 1.54]	17.90	0.283	3.01E-04	1	1	1	1	1	LRK2
22:1814434	rs76904798	t	c	0.1450	0.0114	DYSKINESIAS	DYSKINESIAS_surv	1856	0.179	0.078	1.20 [1.03, 1.39]	0.00	0.456	2.12E-02	1	1	1	1	1	LRK2
22:1814434	rs76904798	t	c	0.1553	0.0172	MMSE	MMSE_cont	2114	0.139	0.060	0.14 [0.02, 0.26]	0.00	0.936	2.12E-02	1	1	1	1	1	LRK2
22:1814434	rs76904798	t	c	0.1460	0.0158	HYPOSMIA	HYPOSMIA_base	1588	0.207	0.115	1.23 [0.98, 1.54]	0.00	0.566	7.05E-02	1	1	1	1	1	LRK2
22:1814434	rs76904798	t	c	0.1522	0.0165	HY	HY_cont	3627	0.020	0.012	0.02 [-0.00, 0.04]	14.40	0.303	1.02E-01	1	1	1	1	1	LRK2
22:1814434	rs76904798	t	c	0.1458	0.0153	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.064	0.040	-0.06 [-0.14, 0.01]	0.00	0.657	1.05E-01	1	1	1	1	1	LRK2
22:1814434	rs76904798	t	c	0.1472	0.0206	MOCA	MOCA_cont	1074	0.268	0.166	0.27 [-0.06, 0.59]	33.90	0.209	1.07E-01	1	1	1	1	1	LRK2
22:1814434	rs76904798	t	c	0.1540	0.0259	COG1	COG1_surv	2244	-0.145	0.104	0.87 [0.71, 1.06]	0.00	0.792	1.64E-01	1	1	1	1	1	LRK2
22:1814434	rs76904798	t	c	0.1508	0.0123	DEPR	DEPR_surv	1314	-0.122	0.108	0.88 [0.72, 1.09]	0.00	0.485	2.59E-01	1	1	1	1	1	LRK2
22:1814434	rs76904798	t	c	0.1521	0.0119	MOTORFLUX	MOTORFLUX_base	1803	0.120	0.110	1.13 [0.91, 1.40]	18.80	0.295	2.76E-01						

1	6:72487762	rs12528068	t	c	0.2920	0.0195	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.003	0.028	0.00	[-0.05, 0.06]	54.30	0.053	9.21E-01	0	0	0	0	RIMS1
2	6:72487762	rs12528068	t	c	0.2906	0.0097	MOTORFLUX	MOTORFLUX_base	1803	-0.008	0.092	0.99	[0.83, 1.19]	0.00	0.591	9.33E-01	0	0	0	0	RIMS1
3	6:72487762	rs12528068	t	c	0.2937	0.0136	INS	INS_base	2220	-0.002	0.078	1.00	[0.86, 1.16]	22.60	0.250	9.80E-01	0	0	0	0	RIMS1
1	1.23266461	rs10797576	t	c	0.1416	0.0080	MOTORFLUX	MOTORFLUX_base	1803	0.337	0.114	1.40	[1.12, 1.75]	0.00	0.943	3.01E-03	0	0	0	0	SIPAIL2
2	1.23266461	rs10797576	t	c	0.1371	0.0119	COGI	COGI_base	2859	0.349	0.118	1.42	[1.12, 1.79]	4.40	0.396	3.16E-03	0	0	0	0	SIPAIL2
4	1.23266461	rs10797576	t	c	0.1482	0.0136	DYSKINESIAS	DYSKINESIAS_surv	1856	0.189	0.080	1.21	[1.03, 1.41]	0.00	0.640	1.75E-02	0	0	0	0	SIPAIL2
5	1.23266461	rs10797576	t	c	0.1408	0.0148	MOCA	MOCA_cont	1074	-0.383	0.175	-0.38	[-0.73, -0.04]	0.00	0.762	2.88E-02	0	0	0	0	SIPAIL2
1	1.23266461	rs10797576	t	c	0.1390	0.0144	CONST	CONST_base	1472	0.152	0.122	1.16	[0.92, 1.48]	0.00	0.566	2.14E-01	0	0	0	0	SIPAIL2
2	1.23266461	rs10797576	t	c	0.1381	0.0178	SLEEP	SLEEP_base	1724	0.133	0.121	1.14	[0.90, 1.45]	0.00	0.546	2.70E-01	0	0	0	0	SIPAIL2
6	1.23266461	rs10797576	t	c	0.1479	0.0182	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.035	0.035	0.03	[-0.03, 0.10]	0.00	0.591	3.28E-01	0	0	0	0	SIPAIL2
1	1.23266461	rs10797576	t	c	0.1399	0.0034	DYSKINESIAS	DYSKINESIAS_base	1232	-0.119	0.146	0.89	[0.67, 1.18]	0.00	0.996	4.14E-01	0	0	0	0	SIPAIL2
7	1.23266461	rs10797576	t	c	0.1379	0.0037	HY3	HY3_base	1289	-0.136	0.173	0.87	[0.62, 1.23]	34.00	0.220	4.31E-01	0	0	0	0	SIPAIL2
1	1.23266461	rs10797576	t	c	0.1360	0.0210	UPDRS_scaled	UPDRS_scaled_cont	2994	0.023	0.034	0.02	[-0.04, 0.09]	0.00	0.944	5.00E-01	0	0	0	0	SIPAIL2
8	1.23266461	rs10797576	t	c	0.1361	0.0217	HY	HY_cont	3627	0.008	0.013	0.01	[-0.02, 0.03]	0.00	0.414	5.25E-01	0	0	0	0	SIPAIL2
1	1.23266461	rs10797576	t	c	0.1440	0.0175	INS	INS_surv	1112	0.057	0.095	1.06	[0.88, 1.27]	16.00	0.311	5.47E-01	0	0	0	0	SIPAIL2
1	1.23266461	rs10797576	t	c	0.1408	0.0187	UPDRS3_scaled	UPDRS3_scaled_cont	2446	0.021	0.037	0.02	[-0.05, 0.09]	0.00	0.951	5.75E-01	0	0	0	0	SIPAIL2
9	1.23266461	rs10797576	t	c	0.1415	0.0198	COGI	COGI_surv	2244	0.057	0.111	1.06	[0.85, 1.32]	33.20	0.152	6.07E-01	0	0	0	0	SIPAIL2
1	1.23266461	rs10797576	t	c	0.1392	0.0168	HY3	HY3_surv	2582	0.048	0.094	1.05	[0.87, 1.26]	0.00	0.079	6.10E-01	0	0	0	0	SIPAIL2
1	1.23266461	rs10797576	t	c	0.1410	0.0162	HYPOSIMIA	HYPOSIMIA_base	1588	0.049	0.116	1.05	[0.84, 1.32]	15.10	0.317	6.71E-01	0	0	0	0	SIPAIL2
11	1.23266461	rs10797576	t	c	0.1297	0.0192	MMSE	MMSE_cont	2114	-0.027	0.066	-0.03	[-0.16, 0.10]	0.00	0.787	6.87E-01	0	0	0	0	SIPAIL2
1	1.23266461	rs10797576	t	c	0.1428	0.0201	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.013	0.042	-0.01	[-0.09, 0.07]	29.00	0.207	7.57E-01	0	0	0	0	SIPAIL2
12	1.23266461	rs10797576	t	c	0.1393	0.0173	INS	INS_base	2220	-0.028	0.102	0.97	[0.80, 1.19]	0.00	0.498	7.86E-01	0	0	0	0	SIPAIL2
1	1.23266461	rs10797576	t	c	0.1446	0.0200	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.006	0.041	0.01	[-0.08, 0.09]	0.00	0.502	8.88E-01	0	0	0	0	SIPAIL2
13	1.23266461	rs10797576	t	c	0.1459	0.0118	SEADL70	SEADL70_surv	1683	-0.016	0.135	0.98	[0.76, 1.28]	13.60	0.327	9.05E-01	0	0	0	0	SIPAIL2
1	1.23266461	rs10797576	t	c	0.1379	0.0149	DEPR	DEPR_surv	1314	0.009	0.118	1.01	[0.80, 1.27]	37.90	0.154	9.42E-01	0	0	0	0	SIPAIL2
14	1.23266461	rs10797576	t	c	0.1393	0.0129	MOTORFLUX	MOTORFLUX_surv	1709	-0.005	0.072	0.99	[0.86, 1.15]	0.00	0.442	9.44E-01	0	0	0	0	SIPAIL2
1	1.23266461	rs10797576	t	c	0.1369	0.0172	DEPR	DEPR_base	2138	0.007	0.133	1.01	[0.78, 1.31]	0.00	0.569	9.60E-01	0	0	0	0	SIPAIL2
15	1.23266461	rs10797576	t	c	0.1351	0.0165	SEADL	SEADL_cont	2218	-0.012	0.344	-0.01	[-0.69, 0.66]	0.00	0.473	9.73E-01	0	0	0	0	SIPAIL2
1	1.23266461	rs34025766	a	t	0.1636	0.0118	DYSKINESIAS	DYSKINESIAS_surv	1856	0.224	0.077	1.25	[1.08, 1.45]	32.30	0.182	3.30E-03	0	0	0	0	LCORL
16	1.23266461	rs34025766	a	t	0.1598	0.0093	SEADL	SEADL_cont	2218	-0.758	0.312	-0.76	[-1.37, -0.15]	13.20	0.327	1.52E-02	0	0	0	0	LCORL
1	1.23266461	rs34025766	a	t	0.1645	0.0096	CONST	CONST_base	1472	0.271	0.116	1.31	[1.05, 1.64]	48.60	0.100	1.90E-02	0	0	0	0	LCORL
17	1.23266461	rs34025766	a	t	0.1581	0.0127	MMSE	MMSE_cont	2114	-0.129	0.060	-0.13	[-0.25, -0.01]	0.00	0.874	3.27E-02	0	0	0	0	LCORL
1	1.23266461	rs34025766	a	t	0.1617	0.0190	INS	INS_surv	1112	0.173	0.084	1.19	[1.01, 1.40]	0.00	0.648	3.83E-02	0	0	0	0	LCORL
18	1.23266461	rs34025766	a	t	0.1604	0.0189	COGI	COGI_surv	2244	0.201	0.098	1.22	[1.01, 1.48]	29.00	0.187	4.03E-02	0	0	0	0	LCORL
1	1.23266461	rs34025766	a	t	0.1601	0.0128	DEPR	DEPR_surv	1314	0.200	0.099	1.22	[1.01, 1.48]	0.00	0.904	4.38E-02	0	0	0	0	LCORL
19	1.23266461	rs34025766	a	t	0.1536	0.0222	HY	HY_cont	3627	0.022	0.012	0.02	[-0.00, 0.05]	33.60	0.122	6.29E-02	0	0	0	0	LCORL
1	1.23266461	rs34025766	a	t	0.1660	0.0106	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.062	0.037	0.06	[-0.01, 0.14]	0.00	0.541	9.60E-02	0	0	0	0	LCORL
20	1.23266461	rs34025766	a	t	0.1643	0.0078	SEADL70	SEADL70_surv	1683	0.129	0.118	1.14	[0.90, 1.43]	8.70	0.357	2.77E-01	0	0	0	0	LCORL
1	1.23266461	rs34025766	a	t	0.1574	0.0202	UPDRS_scaled	UPDRS_scaled_cont	2994	0.031	0.032	0.03	[-0.03, 0.09]	14.10	0.313	3.34E-01	0	0	0	0	LCORL
21	1.23266461	rs34025766	a	t	0.1685	0.0079	DYSKINESIAS	DYSKINESIAS_surv	1232	0.124	0.131	1.13	[0.87, 1.46]	0.00	0.558	3.47E-01	0	0	0	0	LCORL
1	1.23266461	rs34025766	a	t	0.1634	0.0149	MOTORFLUX	MOTORFLUX_surv	1709	-0.060	0.065	0.94	[0.83, 1.07]	0.00	0.718	3.53E-01	0	0	0	0	LCORL
22	1.23266461	rs34025766	a	t	0.1518	0.0221	HY3	HY3_surv	2582	0.068	0.087	1.07	[0.90, 1.27]	43.70	0.076	4.37E-01	0	0	0	0	LCORL
1	1.23266461	rs34025766	a	t	0.1659	0.0111	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.027	0.037	0.03	[-0.05, 0.10]	30.80	0.193	4.65E-01	0	0	0	0	LCORL
23	1.23266461	rs34025766	a	t	0.1638	0.0091	DEPR	DEPR_base	2138	0.082	0.119	1.09	[0.86, 1.37]	0.00	0.681	4.91E-01	0	0	0	0	LCORL
1	1.23266461	rs34025766	a	t	0.1644	0.0108	SLEEP	SLEEP_base	1724	0.040	0.116	1.04	[0.83, 1.30]	26.30	0.228	7.30E-01	0	0	0	0	LCORL
24	1.23266461	rs34025766	a	t	0.1643	0.0124	HYPOSIMIA	HYPOSIMIA_base	1588	-0.035	0.108	0.97	[0.78, 1.19]	0.00	0.547	7.44E-01	0	0	0	0	LCORL
1	1.23266461	rs34025766	a	t	0.1571	0.0194	COGI	COGI_base	2859	-0.033	0.121	0.97	[0.76, 1.23]	27.90	0.206	7.87E-01	0	0	0	0	LCORL
25	1.23266461	rs34025766	a	t	0.1675	0.0073	MOTORFLUX	MOTORFLUX_base	1803	0.025	0.106	1.03	[0.83, 1.26]	0.00	0.906	8.14E-01	0	0	0	0	LCORL
1	1.23266461	rs34025766	a	t	0.1585	0.0239	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.007	0.034	-0.01	[-0.07, 0.06]	33.40	0.162	8.47E-01	0	0	0	0	LCORL
26	1.23266461	rs34025766	a	t	0.1675	0.0104	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.005	0.032	0.01	[-0.06, 0.07]	0.00	0.925	8.71E-01	0	0	0	0	LCORL
1	1.23266461	rs34025766	a	t	0.1632	0.0107	HY3	HY3_base	1289	-0.024	0.157	0.98	[0.72, 1.33]	0.00	0.960	8.77E-01	0	0	0	0	LCORL
27	1.23266461	rs34025766	a	t	0.1657	0.0123	INS	INS_base	2220	-0.015	0.095	0.99	[0.82, 1.19]	48.40	0.060	8.79E-01	0	0	0	0	LCORL
28	19:2341047	rs55818311	t	c	0.6692	0.0131	DEPR	DEPR_base	2138	0.287	0.101	1.33	[1.09, 1.62]	0.00	0.701	4.49E-03	0	0	0	0	SPPL2B
1	19:2341047	rs55818311	t	c	0.6744	0.0188	COGI	COGI_base	2859	0.154	0.095	1.17	[0.97, 1.40]	1.00	0.421	1.04E-01	0	0	0	0	SPPL2B
1	19:2341047	rs55818311	t	c	0.6784	0.0154	INS	INS_surv	1112	-0.107	0.072	0.90	[0.78, 1.03]	0.00	0.550	1.36E-01	0	0	0	0	SPPL2B
29	19:2341047	rs55818311	t	c	0.6614	0.0103	MMSE	MMSE_cont	2114	-0.067	0.050	-0.07	[-0.16, 0.03]	0.00	0.628	1.80E-01	0	0	0	0	SPPL2B
1	19:2341047	rs55818311	t	c	0.6673	0.0181	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.037	0.034	0.04	[-0.03, 0.10]	11.60	0.341	2.71E-01	0	0	0	0	SPPL2B
30	19:2341047	rs55818311	t	c	0.6766	0.0149	CONST	CONST_base	1472	0.078	0.091	1.08	[0.90, 1.29]	0.00	0.745	3.92E-01	0	0	0	0	SPPL2B
1	19:2341047	rs55818311	t	c	0.6671	0.0199	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.023	0.029	-0.02	[-0.08, 0.03]	0.00	0.691	4.26E-01	0	0	0	0	SPPL2B
31	19:2341047	rs55818311	t	c	0.6																

1	9:17727065	rs10756907	a	g	0.7601	0.0166	MOCA	MOCA_cont	1074	-0.116	0.140	-0.12 [-0.39, 0.16]	43.70	0.149	4.07E-01	0	0	0	0	SH3GL2
2	9:17727065	rs10756907	a	g	0.7511	0.0212	HYPOSMIA	HYPOSMIA_base	1588	0.057	0.092	1.06 [0.88, 1.27]	33.10	0.188	5.33E-01	0	0	0	0	SH3GL2
	9:17727065	rs10756907	a	g	0.7520	0.0226	DEPR	DEPR_base	2138	0.064	0.106	1.07 [0.87, 1.31]	23.40	0.243	5.46E-01	0	0	0	0	SH3GL2
3	9:17727065	rs10756907	a	g	0.7446	0.0262	UPDRS3_scaled	UPDRS3_scaled_cont	2446	0.017	0.030	0.02 [-0.04, 0.07]	0.00	0.617	5.74E-01	0	0	0	0	SH3GL2
	9:17727065	rs10756907	a	g	0.7621	0.0142	SEADL70	SEADL70_surv	1683	-0.029	0.105	0.97 [0.79, 1.19]	0.00	0.672	7.85E-01	0	0	0	0	SH3GL2
4	9:17727065	rs10756907	a	g	0.7752	0.0154	DYSKINESIAS	DYSKINESIAS_base	1232	-0.022	0.120	0.98 [0.77, 1.24]	0.00	0.781	8.53E-01	0	0	0	0	SH3GL2
	9:17727065	rs10756907	a	g	0.7565	0.0215	UPDRS_scaled	UPDRS_scaled_cont	2994	0.005	0.027	0.00 [-0.05, 0.06]	9.50	0.355	8.55E-01	0	0	0	0	SH3GL2
5	9:17727065	rs10756907	a	g	0.7606	0.0286	INS	INS_surv	1112	-0.014	0.078	0.99 [0.85, 1.15]	47.10	0.093	8.55E-01	0	0	0	0	SH3GL2
	9:17727065	rs10756907	a	g	0.7507	0.0233	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.004	0.029	-0.00 [-0.06, 0.05]	0.00	0.791	9.01E-01	0	0	0	0	SH3GL2
6	9:17727065	rs10756907	a	g	0.7679	0.0186	MOTORFLUX	MOTORFLUX_base	1803	-0.007	0.095	0.99 [0.82, 1.20]	0.00	0.976	9.46E-01	0	0	0	0	SH3GL2
	13:49927732	rs9568188	t	c	0.7423	0.0204	DYSKINESIAS	DYSKINESIAS_base	1232	-0.307	0.117	0.74 [0.58, 0.93]	12.70	0.318	8.91E-03	0	0	0	0	CAB39L
7	13:49927732	rs9568188	t	c	0.7471	0.0080	SEADL70	SEADL70_surv	1683	-0.220	0.100	0.80 [0.66, 0.98]	0.00	0.585	2.82E-02	0	0	0	0	CAB39L
	13:49927732	rs9568188	t	c	0.7482	0.0249	UPDRS2_scaled	UPDRS2_scaled_cont	2103	-0.062	0.034	-0.06 [-0.13, 0.00]	33.40	0.173	6.82E-02	0	0	0	0	CAB39L
8	13:49927732	rs9568188	t	c	0.7434	0.0236	MMSE	MMSE_cont	2114	0.092	0.051	0.09 [-0.01, 0.19]	0.00	0.826	7.36E-02	0	0	0	0	CAB39L
	13:49927732	rs9568188	t	c	0.7479	0.0241	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.035	0.029	-0.03 [-0.09, 0.02]	0.00	0.937	2.33E-01	0	0	0	0	CAB39L
9	13:49927732	rs9568188	t	c	0.7451	0.0290	DEPR	DEPR_base	2138	-0.114	0.104	0.89 [0.73, 1.09]	0.00	0.574	2.74E-01	0	0	0	0	CAB39L
	13:49927732	rs9568188	t	c	0.7470	0.0176	COGi	COGi_surv	2244	-0.087	0.084	0.92 [0.78, 1.08]	0.00	0.758	2.99E-01	0	0	0	0	CAB39L
10	13:49927732	rs9568188	t	c	0.7489	0.0251	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.034	0.034	0.03 [-0.03, 0.10]	43.60	0.100	3.13E-01	0	0	0	0	CAB39L
	13:49927732	rs9568188	t	c	0.7470	0.0247	DYSKINESIAS	DYSKINESIAS_surv	1856	0.062	0.067	1.06 [0.93, 1.21]	6.50	0.378	3.56E-01	0	0	0	0	CAB39L
11	13:49927732	rs9568188	t	c	0.7409	0.0284	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.021	0.030	-0.02 [-0.08, 0.04]	0.00	0.866	4.78E-01	0	0	0	0	CAB39L
	13:49927732	rs9568188	t	c	0.7556	0.0077	MOCA	MOCA_cont	1074	-0.100	0.141	-0.10 [-0.38, 0.18]	0.00	0.802	4.79E-01	0	0	0	0	CAB39L
12	13:49927732	rs9568188	t	c	0.7410	0.0251	CONST	CONST_base	1472	-0.062	0.097	0.94 [0.78, 1.14]	0.00	0.512	5.21E-01	0	0	0	0	CAB39L
	13:49927732	rs9568188	t	c	0.7431	0.0210	MOTORFLUX	MOTORFLUX_base	1803	0.058	0.096	1.06 [0.88, 1.28]	26.10	0.247	5.46E-01	0	0	0	0	CAB39L
13	13:49927732	rs9568188	t	c	0.7355	0.0278	HYPOSMIA	HYPOSMIA_base	1588	-0.052	0.092	0.95 [0.79, 1.14]	0.00	0.651	5.70E-01	0	0	0	0	CAB39L
	13:49927732	rs9568188	t	c	0.7298	0.0275	HY3	HY3_surv	2582	-0.038	0.072	0.96 [0.84, 1.11]	5.00	0.394	5.94E-01	0	0	0	0	CAB39L
14	13:49927732	rs9568188	t	c	0.7420	0.0174	MOTORFLUX	MOTORFLUX_surv	1709	-0.028	0.055	0.97 [0.87, 1.08]	0.00	0.969	6.13E-01	0	0	0	0	CAB39L
	13:49927732	rs9568188	t	c	0.7438	0.0237	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.012	0.027	-0.01 [-0.07, 0.04]	5.70	0.389	6.47E-01	0	0	0	0	CAB39L
15	13:49927732	rs9568188	t	c	0.7404	0.0276	HY	HY_cont	3627	-0.003	0.010	-0.00 [-0.02, 0.02]	40.00	0.074	7.32E-01	0	0	0	0	CAB39L
	13:49927732	rs9568188	t	c	0.7369	0.0194	SLEEP	SLEEP_base	1724	0.025	0.095	1.03 [0.85, 1.23]	0.00	0.611	7.92E-01	0	0	0	0	CAB39L
16	13:49927732	rs9568188	t	c	0.7347	0.0206	COGi	COGi_base	2859	-0.019	0.098	0.98 [0.81, 1.19]	0.00	0.816	8.48E-01	0	0	0	0	CAB39L
	13:49927732	rs9568188	t	c	0.7313	0.0253	HY3	HY3_base	1289	0.019	0.132	1.02 [0.79, 1.32]	0.00	0.581	8.86E-01	0	0	0	0	CAB39L
17	13:49927732	rs9568188	t	c	0.7472	0.0222	INS	INS_surv	1112	0.011	0.077	1.01 [0.87, 1.18]	0.00	0.426	8.91E-01	0	0	0	0	CAB39L
	13:49927732	rs9568188	t	c	0.7496	0.0158	SEADL	SEADL_cont	2218	0.014	0.273	0.01 [-0.52, 0.55]	0.00	0.855	9.60E-01	0	0	0	0	CAB39L
18	13:49927732	rs9568188	t	c	0.7475	0.0204	DEPR	DEPR_surv	1314	-0.003	0.088	1.00 [0.84, 1.19]	0.00	0.759	9.76E-01	0	0	0	0	CAB39L
	13:49927732	rs9568188	t	c	0.7417	0.0255	INS	INS_base	2220	-0.001	0.082	1.00 [0.85, 1.17]	36.60	0.137	9.93E-01	0	0	0	0	CAB39L
19	3:48748989	rs12497850	t	g	0.6440	0.0143	INS	INS_surv	1112	-0.175	0.067	0.84 [0.74, 0.96]	6.30	0.376	9.44E-03	0	0	0	0	IP6K2
	3:48748989	rs12497850	t	g	0.6408	0.0134	MOCA	MOCA_cont	1074	0.237	0.123	0.24 [-0.01, 0.48]	0.00	0.447	5.51E-02	0	0	0	0	IP6K2
20	3:48748989	rs12497850	t	g	0.6399	0.0174	HY3	HY3_base	1289	0.182	0.121	1.20 [0.95, 1.52]	2.60	0.358	1.32E-01	0	0	0	0	IP6K2
	3:48748989	rs12497850	t	g	0.6598	0.0174	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.034	0.026	0.03 [-0.02, 0.09]	0.00	0.497	2.03E-01	0	0	0	0	IP6K2
21	3:48748989	rs12497850	t	g	0.6550	0.0195	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.034	0.030	0.03 [-0.02, 0.09]	27.20	0.221	2.58E-01	0	0	0	0	IP6K2
	3:48748989	rs12497850	t	g	0.6495	0.0239	HYPOSMIA	HYPOSMIA_base	1588	-0.088	0.084	0.92 [0.78, 1.08]	0.00	0.754	2.92E-01	0	0	0	0	IP6K2
22	3:48748989	rs12497850	t	g	0.6446	0.0235	COGi	COGi_base	2859	-0.093	0.090	0.91 [0.76, 1.09]	0.00	0.667	2.99E-01	0	0	0	0	IP6K2
	3:48748989	rs12497850	t	g	0.6423	0.0119	DYSKINESIAS	DYSKINESIAS_surv	1856	0.048	0.059	1.05 [0.93, 1.18]	0.00	0.491	4.16E-01	0	0	0	0	IP6K2
23	3:48748989	rs12497850	t	g	0.6270	0.0271	HY3	HY3_surv	2582	-0.047	0.063	0.95 [0.84, 1.08]	0.00	0.914	4.58E-01	0	0	0	0	IP6K2
	3:48748989	rs12497850	t	g	0.6444	0.0226	HY	HY_cont	3627	0.006	0.009	0.01 [-0.01, 0.02]	12.80	0.320	5.08E-01	0	0	0	0	IP6K2
24	3:48748989	rs12497850	t	g	0.6488	0.0164	DYSKINESIAS	DYSKINESIAS_base	1232	-0.069	0.105	0.93 [0.76, 1.15]	0.00	0.797	5.11E-01	0	0	0	0	IP6K2
	3:48748989	rs12497850	t	g	0.6316	0.0147	DEPR	DEPR_surv	1314	-0.048	0.078	0.95 [0.82, 1.11]	0.00	0.857	5.38E-01	0	0	0	0	IP6K2
25	3:48748989	rs12497850	t	g	0.6438	0.0212	SLEEP	SLEEP_base	1724	0.047	0.086	1.05 [0.89, 1.24]	0.00	0.920	5.88E-01	0	0	0	0	IP6K2
	3:48748989	rs12497850	t	g	0.6470	0.0239	UPDRS_scaled	UPDRS_scaled_cont	2994	0.012	0.024	0.01 [-0.04, 0.06]	0.00	0.813	6.34E-01	0	0	0	0	IP6K2
26	3:48748989	rs12497850	t	g	0.6508	0.0191	SEADL	SEADL_cont	2218	0.094	0.239	0.09 [-0.38, 0.56]	0.00	0.492	6.94E-01	0	0	0	0	IP6K2
	3:48748989	rs12497850	t	g	0.6386	0.0153	DEPR	DEPR_base	2138	-0.030	0.092	0.97 [0.81, 1.16]	0.00	0.523	7.48E-01	0	0	0	0	IP6K2
27	3:48748989	rs12497850	t	g	0.6453	0.0210	MMSE	MMSE_cont	2114	0.010	0.045	0.01 [-0.08, 0.10]	19.70	0.274	8.22E-01	0	0	0	0	IP6K2
	3:48748989	rs12497850	t	g	0.6563	0.0197	UPDRS2_scaled	UPDRS2_scaled_cont	2103	-0.005	0.030	-0.01 [-0.06, 0.05]	6.10	0.381	8.64E-01	0	0	0	0	IP6K2
28	3:48748989	rs12497850	t	g	0.6414	0.0149	CONST	CONST_base	1472	-0.015	0.088	0.99 [0.83, 1.17]	28.90	0.229	8.68E-01	0	0	0	0	IP6K2
	3:48748989	rs12497850	t	g	0.6494	0.0147	MOTORFLUX	MOTORFLUX_base	1803	-0.014	0.085	0.99 [0.84, 1.16]	0.00	0.715	8.69E-01	0	0	0	0	IP6K2
29	3:48748989	rs12497850	t	g	0.6416	0.0205	MOTORFLUX	MOTORFLUX_surv	1709	0.003	0.050	1.00 [0.91, 1.11]	0.00	0.521	9.49E-01	0	0	0	0	IP6K2
	3:48748989	rs12497850	t	g	0.6538	0.0188	UPDRS3_scaled	UPDRS3_scaled_cont	2446	0.001	0.027	0.00 [-0.05, 0.05]	0.00	0.928	9.75E-01	0	0	0	0	IP6K2
30	3:48748989	rs12497850	t	g	0.6511	0.0226	INS	INS_base	2220	-0.002	0.073	1.00 [0.86, 1.15]	0.00	0.671	9.77E-01	0	0	0	0	IP6K2
	3:48748989	rs12497850	t	g	0.6506	0.0118	SEADL70	SEADL70_surv	1683	0.000	0.094	1.00 [0.83, 1.20]	0.00	0.632	9.97E-01	0	0	0	0	IP6K2
31	7:23300049	rs199351	a	c	0.6076	0.0192	DEPR	DEPR_base	2138	-0.242	0.093	0.79 [0.65, 0.94]	8.60	0.364	9.65E-03	0	0	0	0	GNPMB
	7:23300049	rs199351	a	c	0.6086	0.0191	INS	INS_base												

1	17:44866805	rs11658976	a	g	0.5919	0.0241	INS	INS_base	2220	0.090	0.070	1.09 [0.95, 1.26]	0.00	0.440	2.03E-01	0	0	0	0	0	WNT3
2	17:44866805	rs11658976	a	g	0.5925	0.0279	HYPOSOMIA	HYPOSOMIA_base	1588	-0.096	0.080	0.91 [0.78, 1.06]	29.20	0.216	2.27E-01	0	0	0	0	0	WNT3
3	17:44866805	rs11658976	a	g	0.5801	0.0182	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.038	0.033	0.04 [-0.03, 0.10]	0.00	0.662	2.47E-01	0	0	0	0	0	WNT3
4	17:44866805	rs11658976	a	g	0.5973	0.0628	DEPR	DEPR_base	2138	0.092	0.089	1.10 [0.92, 1.31]	0.00	0.619	3.03E-01	0	0	0	0	0	WNT3
5	17:44866805	rs11658976	a	g	0.6053	0.0232	HY3	HY3_base	1289	-0.112	0.115	0.89 [0.71, 1.12]	63.50	0.064	3.29E-01	0	0	0	0	0	WNT3
6	17:44866805	rs11658976	a	g	0.5946	0.0245	COGI	COGI_base	2859	-0.071	0.085	0.93 [0.79, 1.10]	0.00	0.701	4.02E-01	0	0	0	0	0	WNT3
7	17:44866805	rs11658976	a	g	0.5789	0.0186	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.027	0.033	0.03 [-0.04, 0.09]	0.00	0.833	4.17E-01	0	0	0	0	0	WNT3
8	17:44866805	rs11658976	a	g	0.5917	0.0093	SEADL70	SEADL70_surv	1683	-0.074	0.101	1.08 [0.88, 1.31]	0.00	0.612	4.63E-01	0	0	0	0	0	WNT3
9	17:44866805	rs11658976	a	g	0.5905	0.0036	MOCA	MOCA_cont	1074	-0.090	0.133	-0.09 [-0.35, 0.17]	0.00	0.968	4.96E-01	0	0	0	0	0	WNT3
10	17:44866805	rs11658976	a	g	0.5769	0.0208	MMSE	MMSE_cont	2114	0.030	0.048	0.03 [-0.06, 0.12]	0.00	0.718	5.33E-01	0	0	0	0	0	WNT3
11	17:44866805	rs11658976	a	g	0.6036	0.0322	HY3	HY3_surv	2582	0.041	0.069	1.04 [0.91, 1.19]	11.20	0.342	5.53E-01	0	0	0	0	0	WNT3
12	17:44866805	rs11658976	a	g	0.5794	0.0185	SEADL	SEADL_cont	2218	-0.146	0.256	-0.15 [-0.65, 0.35]	0.00	0.810	5.67E-01	0	0	0	0	0	WNT3
13	17:44866805	rs11658976	a	g	0.5949	0.0258	SLEEP	SLEEP_base	1724	-0.044	0.081	0.96 [0.82, 1.12]	0.00	0.777	5.86E-01	0	0	0	0	0	WNT3
14	17:44866805	rs11658976	a	g	0.5923	0.0250	COGI	COGI_surv	2244	-0.039	0.080	0.96 [0.82, 1.12]	0.00	0.604	6.28E-01	0	0	0	0	0	WNT3
15	17:44866805	rs11658976	a	g	0.5820	0.0209	UPDRS_scaled	UPDRS_scaled_cont	2994	0.012	0.026	0.01 [-0.04, 0.06]	0.00	0.905	6.48E-01	0	0	0	0	0	WNT3
16	17:44866805	rs11658976	a	g	0.5970	0.0172	DYSKINESIAS	DYSKINESIAS_surv	1856	0.030	0.067	1.03 [0.90, 1.17]	28.60	0.210	6.53E-01	0	0	0	0	0	WNT3
17	17:44866805	rs11658976	a	g	0.5869	0.0217	HY	HY_cont	3627	0.003	0.010	0.00 [-0.02, 0.02]	18.70	0.260	7.26E-01	0	0	0	0	0	WNT3
18	17:44866805	rs11658976	a	g	0.5924	0.0152	MOTORFLUX	MOTORFLUX_surv	1709	-0.017	0.055	0.98 [0.88, 1.09]	32.70	0.179	7.51E-01	0	0	0	0	0	WNT3
19	17:44866805	rs11658976	a	g	0.6017	0.0288	DEPR	DEPR_surv	1314	0.013	0.089	1.01 [0.85, 1.21]	0.00	0.737	8.85E-01	0	0	0	0	0	WNT3
20	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
21	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
22	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
23	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
24	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
25	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
26	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
27	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
28	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
29	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
30	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
31	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
32	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
33	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
34	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
35	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
36	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
37	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
38	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
39	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
40	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
41	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
42	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
43	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
44	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
45	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
46	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
47	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
48	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
49	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
50	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
51	17:44866805	rs11658976	a	g	0.5993	0.0192	CONST	CONST_base	1472	0.002	0.084	1.00 [0.85, 1.18]	18.00	0.396	9.85E-01	0	0	0	0	0	WNT3
52	17:44866805	rs11658976	a	g	0.5807	0.0171	UPDRS2_scaled	UPDRS2_scaled_cont	2446	-0.001	0.029	-0.00 [-0.06, 0.06]	0.00	0.927	9.74E-01	0	0	0	0	0	WNT3
53	17:44866805	rs1																			

1	2:135464616	rs57891859	a	g	0.7270	0.0188	SLEEP	SLEEP_base	1724	-0.023	0.096	0.98 [0.81, 1.18]	0.00	0.506	8.13E-01	0	0	0	0	0	TMEM163
2	2:135464616	rs57891859	a	g	0.7349	0.0119	HY3	HY3_base	1289	0.032	0.141	1.03 [0.78, 1.36]	62.70	0.068	8.19E-01	0	0	0	0	0	TMEM163
2	2:135464616	rs57891859	a	g	0.7207	0.0164	INS	INS_surv	1112	0.015	0.071	1.02 [0.88, 1.17]	0.00	0.861	8.31E-01	0	0	0	0	0	TMEM163
3	2:135464616	rs57891859	a	g	0.7353	0.0175	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.004	0.030	-0.00 [-0.06, 0.05]	10.10	0.351	8.88E-01	0	0	0	0	0	TMEM163
3	2:135464616	rs57891859	a	g	0.7279	0.0103	MOTORFLUX	MOTORFLUX_base	1803	0.009	0.094	1.01 [0.84, 1.21]	0.00	0.454	9.22E-01	0	0	0	0	0	TMEM163
4	3:122196892	rs55961674	t	c	0.1708	0.0163	SLEEP	SLEEP_base	1724	0.267	0.107	1.31 [1.06, 1.61]	0.00	0.768	1.30E-02	0	0	0	0	0	KPNA1
3	3:122196892	rs55961674	t	c	0.1662	0.0156	COGI	COGI_base	2859	-0.185	0.118	0.83 [0.66, 1.05]	0.00	0.902	1.17E-01	0	0	0	0	0	KPNA1
5	3:122196892	rs55961674	t	c	0.1641	0.0184	HY3	HY3_surv	2582	0.129	0.087	1.14 [0.96, 1.35]	30.60	0.174	1.35E-01	0	0	0	0	0	KPNA1
3	3:122196892	rs55961674	t	c	0.1800	0.0101	MOCA	MOCA_cont	1074	-0.183	0.160	-0.18 [-0.50, 0.13]	47.50	0.126	2.54E-01	0	0	0	0	0	KPNA1
6	3:122196892	rs55961674	t	c	0.1774	0.0170	INS	INS_base	2220	0.082	0.091	1.09 [0.91, 1.30]	0.00	0.719	3.68E-01	0	0	0	0	0	KPNA1
3	3:122196892	rs55961674	t	c	0.1769	0.0173	DYSKINESIAS	DYSKINESIAS_base	1232	-0.120	0.135	0.89 [0.68, 1.16]	0.00	0.848	3.76E-01	0	0	0	0	0	KPNA1
7	3:122196892	rs55961674	t	c	0.1738	0.0201	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.028	0.032	-0.03 [-0.09, 0.03]	0.00	0.536	3.81E-01	0	0	0	0	0	KPNA1
3	3:122196892	rs55961674	t	c	0.1814	0.0280	INS	INS_surv	1112	0.067	0.088	1.07 [0.90, 1.27]	0.00	0.841	4.46E-01	0	0	0	0	0	KPNA1
8	3:122196892	rs55961674	t	c	0.1718	0.0096	SEADL70	SEADL70_surv	1683	0.085	0.122	1.09 [0.86, 1.38]	4.80	0.379	4.87E-01	0	0	0	0	0	KPNA1
3	3:122196892	rs55961674	t	c	0.1862	0.0233	DEPR	DEPR_surv	1314	0.067	0.105	1.07 [0.87, 1.31]	0.00	0.784	5.23E-01	0	0	0	0	0	KPNA1
9	3:122196892	rs55961674	t	c	0.1778	0.0229	DYSKINESIAS	DYSKINESIAS_surv	1856	-0.050	0.079	0.95 [0.81, 1.11]	0.00	0.833	5.29E-01	0	0	0	0	0	KPNA1
3	3:122196892	rs55961674	t	c	0.1794	0.0158	MMSE	MMSE_cont	2114	0.036	0.058	0.04 [-0.08, 0.15]	0.00	0.860	5.36E-01	0	0	0	0	0	KPNA1
10	3:122196892	rs55961674	t	c	0.1706	0.0215	MOTORFLUX	MOTORFLUX_surv	1709	-0.041	0.068	0.96 [0.84, 1.10]	0.00	0.575	5.42E-01	0	0	0	0	0	KPNA1
3	3:122196892	rs55961674	t	c	0.1742	0.0148	COGI	COGI_surv	2244	0.059	0.098	1.06 [0.87, 1.29]	0.00	0.769	5.49E-01	0	0	0	0	0	KPNA1
11	3:122196892	rs55961674	t	c	0.1684	0.0161	HY3	HY3_base	1289	0.080	0.153	1.08 [0.80, 1.46]	0.00	0.560	6.04E-01	0	0	0	0	0	KPNA1
3	3:122196892	rs55961674	t	c	0.1711	0.0159	HYPOSIMIA	HYPOSIMIA_base	1588	-0.049	0.103	0.95 [0.78, 1.16]	0.00	0.556	6.32E-01	0	0	0	0	0	KPNA1
12	3:122196892	rs55961674	t	c	0.1741	0.0214	HY	HY_cont	3627	-0.005	0.012	-0.00 [-0.03, 0.02]	10.70	0.340	6.90E-01	0	0	0	0	0	KPNA1
3	3:122196892	rs55961674	t	c	0.1774	0.0174	SEADL	SEADL_cont	2218	0.110	0.311	0.11 [-0.50, 0.72]	0.00	0.815	7.23E-01	0	0	0	0	0	KPNA1
13	3:122196892	rs55961674	t	c	0.1746	0.0194	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.011	0.035	-0.01 [-0.08, 0.06]	42.10	0.098	7.48E-01	0	0	0	0	0	KPNA1
3	3:122196892	rs55961674	t	c	0.1704	0.0141	CONST	CONST_base	1472	-0.022	0.111	0.98 [0.79, 1.21]	0.00	0.976	8.40E-01	0	0	0	0	0	KPNA1
14	3:122196892	rs55961674	t	c	0.1789	0.0193	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.005	0.034	-0.00 [-0.07, 0.06]	0.00	0.842	8.91E-01	0	0	0	0	0	KPNA1
3	3:122196892	rs55961674	t	c	0.1802	0.0185	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.003	0.039	0.00 [-0.07, 0.08]	34.90	0.162	9.49E-01	0	0	0	0	0	KPNA1
15	3:122196892	rs55961674	t	c	0.1750	0.0171	MOTORFLUX	MOTORFLUX_base	1803	0.006	0.108	1.01 [0.81, 1.24]	4.40	0.381	9.53E-01	0	0	0	0	0	KPNA1
3	3:122196892	rs55961674	t	c	0.1813	0.0183	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.002	0.039	0.00 [-0.07, 0.08]	0.00	0.603	9.55E-01	0	0	0	0	0	KPNA1
16	10:121536327	rs117896735	a	g	0.0219	0.0050	COGI	COGI_base	2483	0.700	0.283	2.01 [1.16, 3.50]	0.00	0.435	1.32E-02	0	0	0	0	0	INPP5F
10:121536327	rs117896735	a	g	0.0234	0.0035	MOTORFLUX	MOTORFLUX_surv	1709	0.290	0.162	1.34 [0.97, 1.83]	48.40	0.071	7.39E-02	0	0	0	0	0	INPP5F	
17	10:121536327	rs117896735	a	g	0.0264	0.0056	MOCA	MOCA_cont	1074	-0.500	0.415	-0.50 [-1.31, 0.31]	46.60	0.132	2.29E-01	0	0	0	0	0	INPP5F
10:121536327	rs117896735	a	g	0.0273	0.0087	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.094	0.082	0.09 [-0.07, 0.25]	0.00	0.487	2.47E-01	0	0	0	0	0	INPP5F	
18	10:121536327	rs117896735	a	g	0.0275	0.0103	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.108	0.104	0.11 [-0.10, 0.31]	0.00	0.915	3.00E-01	0	0	0	0	0	INPP5F
10:121536327	rs117896735	a	g	0.0182	0.0018	DYSKINESIAS	DYSKINESIAS_base	1232	-0.346	0.356	0.71 [0.35, 1.42]	6.50	0.343	3.31E-01	0	0	0	0	0	INPP5F	
19	10:121536327	rs117896735	a	g	0.0256	0.0070	DEPR	DEPR_base	2138	-0.307	0.351	0.74 [0.37, 1.46]	0.00	0.911	3.82E-01	0	0	0	0	0	INPP5F
10:121536327	rs117896735	a	g	0.0232	0.0073	SLEEP	SLEEP_base	1724	0.219	0.270	1.25 [0.73, 2.11]	0.00	0.860	4.17E-01	0	0	0	0	0	INPP5F	
20	10:121536327	rs117896735	a	g	0.0209	0.0039	CONST	CONST_base	1472	0.239	0.296	1.27 [0.71, 2.27]	25.00	0.255	4.19E-01	0	0	0	0	0	INPP5F
10:121536327	rs117896735	a	g	0.0239	0.0037	INS	INS_surv	1112	-0.162	0.212	0.85 [0.56, 1.29]	0.00	0.662	4.44E-01	0	0	0	0	0	INPP5F	
21	10:121536327	rs117896735	a	g	0.0276	0.0110	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.065	0.091	0.07 [-0.11, 0.24]	41.10	0.131	4.75E-01	0	0	0	0	0	INPP5F
10:121536327	rs117896735	a	g	0.0254	0.0036	SEADL	SEADL_cont	2112	-0.512	0.798	-0.51 [-2.08, 1.05]	0.00	0.732	5.22E-01	0	0	0	0	0	INPP5F	
22	10:121536327	rs117896735	a	g	0.0233	0.0031	DYSKINESIAS	DYSKINESIAS_surv	1856	0.124	0.193	1.13 [0.77, 1.65]	0.00	0.601	5.23E-01	0	0	0	0	0	INPP5F
10:121536327	rs117896735	a	g	0.0292	0.0066	HY3	HY3_surv	2582	-0.118	0.196	0.89 [0.60, 1.31]	0.00	0.973	5.48E-01	0	0	0	0	0	INPP5F	
23	10:121536327	rs117896735	a	g	0.0227	0.0068	HYPOSIMIA	HYPOSIMIA_base	1588	0.156	0.261	1.17 [0.70, 1.95]	16.50	0.307	5.50E-01	0	0	0	0	0	INPP5F
10:121536327	rs117896735	a	g	0.0286	0.0098	HY	HY_cont	3627	-0.017	0.029	-0.02 [-0.07, 0.04]	0.00	0.591	5.51E-01	0	0	0	0	0	INPP5F	
24	10:121536327	rs117896735	a	g	0.0221	0.0066	INS	INS_base	2220	-0.127	0.236	0.88 [0.55, 1.40]	0.00	0.582	5.91E-01	0	0	0	0	0	INPP5F
10:121536327	rs117896735	a	g	0.0220	0.0044	SEADL70	SEADL70_surv	1683	0.134	0.324	1.14 [0.61, 2.16]	0.00	0.804	6.78E-01	0	0	0	0	0	INPP5F	
25	10:121536327	rs117896735	a	g	0.0233	0.0039	COGI	COGI_surv	2075	0.113	0.273	1.12 [0.66, 1.91]	0.00	0.983	6.80E-01	0	0	0	0	0	INPP5F
10:121536327	rs117896735	a	g	0.0252	0.0044	DEPR	DEPR_surv	1314	-0.066	0.277	0.94 [0.54, 1.61]	0.00	0.964	8.11E-01	0	0	0	0	0	INPP5F	
26	10:121536327	rs117896735	a	g	0.0182	0.0023	MOTORFLUX	MOTORFLUX_base	1803	-0.067	0.296	0.94 [0.52, 1.67]	0.00	0.884	8.21E-01	0	0	0	0	0	INPP5F
10:121536327	rs117896735	a	g	0.0277	0.0105	UPDRS2_scaled	UPDRS2_scaled_cont	2103	-0.016	0.104	-0.02 [-0.22, 0.19]	0.00	0.698	8.78E-01	0	0	0	0	0	INPP5F	
27	10:121536327	rs117896735	a	g	0.0297	0.0101	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.012	0.088	-0.01 [-0.18, 0.16]	0.00	0.713	8.97E-01	0	0	0	0	0	INPP5F
10:121536327	rs117896735	a	g	0.0289	0.0078	MMSE	MMSE_cont	2114	0.014	0.143	0.01 [-0.27, 0.29]	0.00	0.931	9.21E-01	0	0	0	0	0	INPP5F	
28	13:97865021	rs4771268	t	c	0.2272	0.0185	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.075	0.030	-0.07 [-0.13, -0.02]	0.00	0.486	1.34E-02	0	0	0	0	0	MBNL2
13:97865021	rs4771268	t	c	0.2390	0.0098	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.051	0.029	-0.05 [-0.11, 0.00]	0.00	0.601	7.29E-02	0	0	0	0	0	MBNL2	
29	13:97865021	rs4771268	t	c	0.2336	0.0133	DYSKINESIAS	DYSKINESIAS_surv	1856	-0.112	0.068	0.89 [0.78, 1.02]	0.00	0.831	1.02E-01	0	0	0	0	0	MBNL2
13:97865021	rs4771268	t	c	0.2284	0.0159	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.044	0.027	-0.04 [-0.10, 0.01]	0.00	0.443	1.10E-01	0	0	0	0	0	MBNL2	
30	13:97865021	rs4771268	t	c	0.2198	0.0142	MMSE	MMSE_cont	2114	0.079	0.051	0.08 [-0.02, 0.18]	0.00	0.912	1.25E-01	0	0	0	0	0	MBNL2
13:97865021	rs4771268	t	c	0.2258	0.0119	HY3	HY3_base	1289	-0.19												

1	4:90626111	rs356182	a	g	0.5804	0.0238	COGi	COGi_surv	2244	-0.051	0.075	0.95	[0.82, 1.10]	23.30	0.236	4.98E-01	0	0	0	0	SNCA
2	4:90626111	rs356182	a	g	0.5852	0.0172	UPDRS_scaled	UPDRS_scaled_cont	2994	0.015	0.024	0.02	[-0.03, 0.06]	0.00	0.914	5.22E-01	0	0	0	0	SNCA
3	4:90626111	rs356182	a	g	0.5853	0.0121	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.016	0.025	-0.02	[-0.07, 0.03]	0.00	0.505	5.32E-01	0	0	0	0	SNCA
4	4:90626111	rs356182	a	g	0.5978	0.0155	CONST	CONST_base	1472	0.040	0.086	1.04	[0.88, 1.23]	24.50	0.258	6.39E-01	0	0	0	0	SNCA
5	4:90626111	rs356182	a	g	0.5740	0.0222	SEADL	SEADL_cont	2218	-0.086	0.235	-0.09	[-0.55, 0.37]	0.00	0.591	7.14E-01	0	0	0	0	SNCA
6	4:90626111	rs356182	a	g	0.6000	0.0184	SLEEP	SLEEP_surv	1724	0.029	0.085	1.03	[0.87, 1.22]	0.00	0.596	7.32E-01	0	0	0	0	SNCA
7	4:90626111	rs356182	a	g	0.5778	0.0227	HY3	HY3_surv	2582	-0.019	0.064	0.98	[0.87, 1.11]	29.80	0.181	7.68E-01	0	0	0	0	SNCA
8	4:90626111	rs356182	a	g	0.5820	0.0176	HY	HY_cont	3627	0.002	0.009	0.00	[-0.02, 0.02]	0.00	0.890	8.06E-01	0	0	0	0	SNCA
9	4:90626111	rs356182	a	g	0.5879	0.0160	SEADL70	SEADL70_surv	1683	-0.022	0.093	0.98	[0.82, 1.17]	45.60	0.119	8.15E-01	0	0	0	0	SNCA
10	4:90626111	rs356182	a	g	0.5973	0.0195	HY3	HY3_base	1289	0.019	0.117	1.02	[0.81, 1.28]	0.00	0.840	8.69E-01	0	0	0	0	SNCA
11	4:90626111	rs356182	a	g	0.6055	0.0167	INS	INS_base	2220	-0.009	0.071	0.99	[0.86, 1.14]	0.00	0.604	8.95E-01	0	0	0	0	SNCA
12	4:15737348	rs4698412	a	g	0.5809	0.0264	MOCA	MOCA_cont	1074	-0.285	0.117	-0.28	[-0.51, -0.06]	0.00	0.527	1.45E-02	0	0	0	0	BST1
13	4:15737348	rs4698412	a	g	0.5705	0.0164	UPDRS2_scaled	UPDRS2_scaled_cont	2103	-0.040	0.029	-0.04	[-0.10, 0.02]	0.00	0.584	1.63E-01	0	0	0	0	BST1
14	4:15737348	rs4698412	a	g	0.5681	0.0263	COGi	COGi_surv	2244	0.101	0.074	1.11	[0.96, 1.28]	0.00	0.930	1.74E-01	0	0	0	0	BST1
15	4:15737348	rs4698412	a	g	0.5697	0.0153	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.038	0.029	-0.04	[-0.09, 0.02]	0.00	0.761	1.81E-01	0	0	0	0	BST1
16	4:15737348	rs4698412	a	g	0.5643	0.0203	HY3	HY3_base	1289	-0.138	0.116	0.87	[0.69, 1.09]	10.50	0.327	2.33E-01	0	0	0	0	BST1
17	4:15737348	rs4698412	a	g	0.5601	0.0181	CONST	CONST_base	1472	-0.102	0.086	0.90	[0.76, 1.07]	0.00	0.548	2.36E-01	0	0	0	0	BST1
18	4:15737348	rs4698412	a	g	0.5583	0.0154	MOTORFLUX	MOTORFLUX_base	1803	-0.077	0.081	0.93	[0.79, 1.09]	12.50	0.334	3.46E-01	0	0	0	0	BST1
19	4:15737348	rs4698412	a	g	0.5817	0.0208	SEADL	SEADL_cont	2112	0.215	0.229	0.22	[-0.23, 0.66]	0.00	0.861	3.48E-01	0	0	0	0	BST1
20	4:15737348	rs4698412	a	g	0.5698	0.0159	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.023	0.026	-0.02	[-0.07, 0.03]	0.00	0.809	3.68E-01	0	0	0	0	BST1
21	4:15737348	rs4698412	a	g	0.5571	0.0168	HYPOSOMIA	HYPOSOMIA_base	1588	-0.069	0.081	0.93	[0.80, 1.09]	41.70	0.128	3.94E-01	0	0	0	0	BST1
22	4:15737348	rs4698412	a	g	0.5600	0.0146	INS	INS_base	2220	0.055	0.071	1.06	[0.92, 1.21]	12.10	0.336	4.35E-01	0	0	0	0	BST1
23	4:15737348	rs4698412	a	g	0.5757	0.0150	HY3	HY3_surv	2582	-0.046	0.063	0.96	[0.84, 1.08]	0.00	0.471	4.71E-01	0	0	0	0	BST1
24	4:15737348	rs4698412	a	g	0.5600	0.0164	DYSKINESIAS	DYSKINESIAS_base	1232	-0.069	0.102	0.93	[0.76, 1.14]	0.00	0.381	5.01E-01	0	0	0	0	BST1
25	4:15737348	rs4698412	a	g	0.5677	0.0222	INS	INS_surv	1112	0.043	0.064	1.04	[0.92, 1.18]	0.00	0.732	5.02E-01	0	0	0	0	BST1
26	4:15737348	rs4698412	a	g	0.5798	0.0127	HY	HY_cont	3627	0.006	0.009	0.01	[-0.01, 0.02]	0.00	0.612	5.12E-01	0	0	0	0	BST1
27	4:15737348	rs4698412	a	g	0.5625	0.0153	SEADL70	SEADL70_surv	1683	-0.050	0.092	0.95	[0.79, 1.14]	0.00	0.938	5.85E-01	0	0	0	0	BST1
28	4:15737348	rs4698412	a	g	0.5822	0.0086	M MSE	M MSE_cont	2114	-0.020	0.044	-0.02	[-0.11, 0.07]	2.80	0.408	6.56E-01	0	0	0	0	BST1
29	4:15737348	rs4698412	a	g	0.5741	0.0193	DYSKINESIAS	DYSKINESIAS_surv	1856	0.025	0.057	1.03	[0.92, 1.15]	0.00	0.808	6.56E-01	0	0	0	0	BST1
30	4:15737348	rs4698412	a	g	0.5734	0.0153	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.007	0.023	-0.01	[-0.05, 0.04]	27.20	0.194	7.78E-01	0	0	0	0	BST1
31	4:15737348	rs4698412	a	g	0.5588	0.0182	SLEEP	SLEEP_base	1724	0.021	0.085	1.02	[0.86, 1.21]	0.00	0.623	8.09E-01	0	0	0	0	BST1
32	4:15737348	rs4698412	a	g	0.5767	0.0272	DEPR	DEPR_surv	1314	-0.017	0.077	0.98	[0.84, 1.14]	44.10	0.111	8.24E-01	0	0	0	0	BST1
33	4:15737348	rs4698412	a	g	0.5648	0.0205	COGi	COGi_base	2859	-0.019	0.087	0.98	[0.83, 1.16]	0.00	0.441	8.25E-01	0	0	0	0	BST1
34	4:15737348	rs4698412	a	g	0.5659	0.0156	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.002	0.025	-0.00	[-0.05, 0.05]	0.00	0.501	9.27E-01	0	0	0	0	BST1
35	4:15737348	rs4698412	a	g	0.5663	0.0173	DEPR	DEPR_base	2138	-0.003	0.091	1.00	[0.83, 1.19]	17.00	0.296	9.70E-01	0	0	0	0	BST1
36	17:42294337	rs2269906	a	c	0.6706	0.0216	SLEEP	SLEEP_base	1724	-0.217	0.089	0.80	[0.68, 0.96]	0.00	0.636	1.46E-02	0	0	0	0	UBTF
37	17:42294337	rs2269906	a	c	0.6617	0.0210	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.086	0.036	-0.09	[-0.16, -0.02]	38.40	0.136	1.56E-02	0	0	0	0	UBTF
38	17:42294337	rs2269906	a	c	0.6672	0.0172	CONST	CONST_base	1472	-0.171	0.090	0.84	[0.71, 1.01]	0.00	0.473	5.74E-02	0	0	0	0	UBTF
39	17:42294337	rs2269906	a	c	0.6544	0.0228	SEADL	SEADL_cont	2218	0.514	0.271	0.51	[-0.02, 1.05]	24.50	0.234	5.76E-02	0	0	0	0	UBTF
40	17:42294337	rs2269906	a	c	0.6608	0.0213	UPDRS2_scaled	UPDRS2_scaled_cont	2103	-0.067	0.035	-0.07	[-0.14, 0.00]	0.00	0.779	6.03E-02	0	0	0	0	UBTF
41	17:42294337	rs2269906	a	c	0.6591	0.0200	INS	INS_surv	1112	-0.138	0.074	0.87	[0.75, 1.01]	10.90	0.346	6.28E-02	0	0	0	0	UBTF
42	17:42294337	rs2269906	a	c	0.6687	0.0215	DEPR	DEPR_base	2138	-0.172	0.095	0.84	[0.70, 1.01]	0.00	0.923	6.90E-02	0	0	0	0	UBTF
43	17:42294337	rs2269906	a	c	0.6720	0.0254	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.049	0.028	-0.05	[-0.10, 0.01]	0.00	0.961	8.08E-02	0	0	0	0	UBTF
44	17:42294337	rs2269906	a	c	0.6662	0.0212	HYPOSOMIA	HYPOSOMIA_base	1588	0.129	0.085	1.14	[0.96, 1.35]	0.00	0.976	1.30E-01	0	0	0	0	UBTF
45	17:42294337	rs2269906	a	c	0.6562	0.0202	MOTORFLUX	MOTORFLUX_base	1803	-0.117	0.086	0.89	[0.75, 1.05]	4.00	0.384	1.76E-01	0	0	0	0	UBTF
46	17:42294337	rs2269906	a	c	0.6728	0.0268	HY	HY_cont	3627	-0.010	0.010	-0.01	[-0.03, 0.01]	0.00	0.963	3.27E-01	0	0	0	0	UBTF
47	17:42294337	rs2269906	a	c	0.6645	0.0223	MOTORFLUX	MOTORFLUX_surv	1709	-0.050	0.057	0.95	[0.85, 1.06]	0.00	0.949	3.81E-01	0	0	0	0	UBTF
48	17:42294337	rs2269906	a	c	0.6654	0.0246	HY3	HY3_base	1289	-0.099	0.122	0.91	[0.71, 1.15]	2.70	0.358	4.17E-01	0	0	0	0	UBTF
49	17:42294337	rs2269906	a	c	0.6533	0.0230	DYSKINESIAS	DYSKINESIAS_base	1232	-0.086	0.107	0.92	[0.74, 1.13]	36.30	0.208	4.22E-01	0	0	0	0	UBTF
50	17:42294337	rs2269906	a	c	0.6694	0.0191	M MSE	M MSE_cont	2114	-0.035	0.050	-0.03	[-0.13, 0.06]	30.80	0.182	4.85E-01	0	0	0	0	UBTF
51	17:42294337	rs2269906	a	c	0.6482	0.0291	MOCA	MOCA_cont	1074	-0.091	0.143	-0.09	[-0.37, 0.19]	0.00	0.590	5.25E-01	0	0	0	0	UBTF
52	17:42294337	rs2269906	a	c	0.6591	0.0244	INS	INS_base	2220	0.038	0.074	1.04	[0.90, 1.20]	0.00	0.577	6.12E-01	0	0	0	0	UBTF
53	17:42294337	rs2269906	a	c	0.6682	0.0247	COGi	COGi_base	2859	-0.047	0.093	0.95	[0.80, 1.15]	15.80	0.306	6.15E-01	0	0	0	0	UBTF
54	17:42294337	rs2269906	a	c	0.6731	0.0192	DEPR	DEPR_surv	1314	-0.044	0.092	0.96	[0.80, 1.15]	44.10	0.111	6.34E-01	0	0	0	0	UBTF
55	17:42294337	rs2269906	a	c	0.6623	0.0125	SEADL70	SEADL70_surv	1683	-0.042	0.108	0.96	[0.78, 1.18]	4.50	0.381	6.94E-01	0	0	0	0	UBTF
56	17:42294337	rs2269906	a	c	0.6758	0.0219	HY3	HY3_surv	2582	-0.025	0.069	0.98	[0.85, 1.12]	0.00	0.827	7.14E-01	0	0	0	0	UBTF
57	17:42294337	rs2269906	a	c	0.6605	0.0213	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.011	0.031	-0.01	[-0.07, 0.05]	0.00	0.557	7.17E-01	0	0	0	0	UBTF
58	17:42294337	rs2269906	a	c	0.6628	0.0230	DYSKINESIAS	DYSKINESIAS_surv	1856	0.022	0.070	1.02	[0.89, 1.17]	25.30	0.236	7.52E-01	0	0	0	0	UBTF
59	17:42294337	rs2269906	a	c	0.6643	0.0172	COGi	COGi_surv	2244	-0.024	0.085	0.98	[0.83, 1.15]	0.00	0.464	7.75E-01	0	0	0	0	UBTF
60	17:42294337	rs2269906	a	c	0.6645	0.0204	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.006	0.0										

1	17:76425480	rs666463	a	t	0.8331	0.0149	MMSE	MMSE_cont	2114	-0.116	0.060	-0.12 [-0.23, 0.00]	41.50	0.102	5.46E-02	0	0	0	0	0	DNAH17
2	17:76425480	rs666463	a	t	0.8227	0.0124	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.051	0.033	0.05 [-0.01, 0.12]	0.00	0.513	1.20E-01	0	0	0	0	0	DNAH17
2	17:76425480	rs666463	a	t	0.8346	0.0159	DEPR	DEPR_base	2138	-0.164	0.121	0.85 [0.67, 1.08]	40.90	0.106	1.75E-01	0	0	0	0	0	DNAH17
3	17:76425480	rs666463	a	t	0.8283	0.0088	MOTORFLUX	MOTORFLUX_base	1803	0.134	0.108	1.14 [0.93, 1.41]	0.00	0.617	2.12E-01	0	0	0	0	0	DNAH17
3	17:76425480	rs666463	a	t	0.8365	0.0139	INS	INS_surv	1112	0.098	0.087	1.10 [0.93, 1.31]	0.00	0.505	2.60E-01	0	0	0	0	0	DNAH17
4	17:76425480	rs666463	a	t	0.8272	0.0157	SEADL70	SEADL70_surv	1683	0.131	0.123	1.14 [0.90, 1.45]	43.00	0.135	2.86E-01	0	0	0	0	0	DNAH17
4	17:76425480	rs666463	a	t	0.8190	0.0210	HY3	HY3_surv	2582	-0.064	0.078	0.94 [0.81, 1.09]	0.00	0.665	4.14E-01	0	0	0	0	0	DNAH17
5	17:76425480	rs666463	a	t	0.8397	0.0278	DEPR	DEPR_surv	1314	0.088	0.109	1.09 [0.88, 1.35]	0.00	0.965	4.19E-01	0	0	0	0	0	DNAH17
5	17:76425480	rs666463	a	t	0.8310	0.0204	MOCA	MOCA_cont	1074	-0.114	0.164	-0.11 [-0.44, 0.21]	45.10	0.141	4.89E-01	0	0	0	0	0	DNAH17
6	17:76425480	rs666463	a	t	0.8258	0.0082	COGI	COGI_base	2859	0.072	0.111	1.07 [0.86, 1.34]	0.00	0.745	5.16E-01	0	0	0	0	0	DNAH17
6	17:76425480	rs666463	a	t	0.8289	0.0196	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.025	0.039	-0.03 [-0.10, 0.05]	16.00	0.308	5.19E-01	0	0	0	0	0	DNAH17
7	17:76425480	rs666463	a	t	0.8247	0.0205	DYSKINESIAS	DYSKINESIAS_surv	1856	0.046	0.075	1.05 [0.90, 1.21]	0.00	0.847	5.38E-01	0	0	0	0	0	DNAH17
7	17:76425480	rs666463	a	t	0.8267	0.0173	COGI	COGI_surv	2244	0.050	0.097	1.05 [0.87, 1.27]	0.00	0.648	6.07E-01	0	0	0	0	0	DNAH17
8	17:76425480	rs666463	a	t	0.8272	0.0073	CONST	CONST_base	1472	0.036	0.109	1.04 [0.84, 1.28]	37.50	0.171	7.42E-01	0	0	0	0	0	DNAH17
8	17:76425480	rs666463	a	t	0.8256	0.0088	SLEEP	SLEEP_base	1724	-0.026	0.108	0.97 [0.79, 1.20]	0.00	0.864	8.07E-01	0	0	0	0	0	DNAH17
9	17:76425480	rs666463	a	t	0.8249	0.0090	HYPOSMIA	HYPOSMIA_base	1588	-0.022	0.102	0.98 [0.80, 1.19]	0.00	0.481	8.32E-01	0	0	0	0	0	DNAH17
9	17:76425480	rs666463	a	t	0.8269	0.0159	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.003	0.035	-0.00 [-0.07, 0.06]	17.80	0.290	9.30E-01	0	0	0	0	0	DNAH17
10	17:42434630	rs850738	a	g	0.5920	0.0205	MMSE	MMSE_cont	2114	0.109	0.045	0.11 [0.02, 0.20]	44.30	0.083	1.67E-02	0	0	0	0	0	FAM171A2
10	17:42434630	rs850738	a	g	0.5854	0.0268	COGI	COGI_base	2859	-0.207	0.087	0.81 [0.69, 0.96]	0.00	0.905	1.72E-02	0	0	0	0	0	FAM171A2
11	17:42434630	rs850738	a	g	0.5964	0.0192	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.050	0.024	-0.05 [-0.10, -0.00]	0.00	0.597	3.57E-02	0	0	0	0	0	FAM171A2
11	17:42434630	rs850738	a	g	0.5851	0.0279	DYSKINESIAS	DYSKINESIAS_base	1232	-0.215	0.104	0.81 [0.66, 0.99]	0.00	0.595	3.80E-02	0	0	0	0	0	FAM171A2
12	17:42434630	rs850738	a	g	0.5970	0.0148	UPDRS2_scaled	UPDRS2_scaled_cont	2103	-0.059	0.029	-0.06 [-0.12, -0.00]	0.00	0.578	4.63E-02	0	0	0	0	0	FAM171A2
12	17:42434630	rs850738	a	g	0.5976	0.0239	COGI	COGI_surv	2244	-0.132	0.077	0.88 [0.75, 1.02]	0.00	0.697	8.54E-02	0	0	0	0	0	FAM171A2
13	17:42434630	rs850738	a	g	0.5871	0.0255	MOTORFLUX	MOTORFLUX_base	1803	-0.128	0.082	0.88 [0.75, 1.03]	30.80	0.216	1.18E-01	0	0	0	0	0	FAM171A2
13	17:42434630	rs850738	a	g	0.5946	0.0170	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.041	0.026	-0.04 [-0.09, 0.01]	0.00	0.663	1.20E-01	0	0	0	0	0	FAM171A2
14	17:42434630	rs850738	a	g	0.5908	0.0269	MOTORFLUX	MOTORFLUX_surv	1709	-0.074	0.050	0.93 [0.84, 1.02]	0.00	0.907	1.35E-01	0	0	0	0	0	FAM171A2
14	17:42434630	rs850738	a	g	0.5939	0.061	DYSKINESIAS	DYSKINESIAS_surv	1856	-0.087	0.060	0.92 [0.82, 1.03]	0.00	0.938	1.44E-01	0	0	0	0	0	FAM171A2
15	17:42434630	rs850738	a	g	0.5866	0.0213	HY	HY_cont	3627	-0.012	0.009	-0.01 [-0.03, 0.01]	0.00	0.591	1.96E-01	0	0	0	0	0	FAM171A2
15	17:42434630	rs850738	a	g	0.5955	0.0144	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.032	0.026	-0.03 [-0.08, 0.02]	0.00	0.689	2.12E-01	0	0	0	0	0	FAM171A2
16	17:42434630	rs850738	a	g	0.5965	0.0137	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.034	0.030	-0.03 [-0.09, 0.02]	0.00	0.554	2.42E-01	0	0	0	0	0	FAM171A2
16	17:42434630	rs850738	a	g	0.5885	0.0290	HYPOSMIA	HYPOSMIA_base	1588	-0.094	0.082	0.91 [0.78, 1.07]	13.70	0.327	2.48E-01	0	0	0	0	0	FAM171A2
17	17:42434630	rs850738	a	g	0.5975	0.0130	SEADL	SEADL_cont	2218	0.252	0.240	0.25 [-0.22, 0.72]	2.30	0.412	2.94E-01	0	0	0	0	0	FAM171A2
17	17:42434630	rs850738	a	g	0.5869	0.0351	INS	INS_surv	1112	-0.058	0.066	0.94 [0.83, 1.08]	0.20	0.415	3.86E-01	0	0	0	0	0	FAM171A2
18	17:42434630	rs850738	a	g	0.5874	0.0321	CONST	CONST_base	1472	0.068	0.086	1.07 [0.90, 1.27]	0.00	0.448	4.33E-01	0	0	0	0	0	FAM171A2
18	17:42434630	rs850738	a	g	0.5697	0.0417	HY3	HY3_surv	2582	-0.045	0.066	0.96 [0.84, 1.09]	0.00	0.776	4.95E-01	0	0	0	0	0	FAM171A2
19	17:42434630	rs850738	a	g	0.6009	0.0225	MOCA	MOCA_cont	1074	-0.075	0.123	-0.07 [-0.32, 0.17]	0.00	0.821	5.45E-01	0	0	0	0	0	FAM171A2
19	17:42434630	rs850738	a	g	0.6032	0.0158	SEADL70	SEADL70_surv	1683	-0.051	0.096	0.95 [0.79, 1.15]	0.00	0.506	5.96E-01	0	0	0	0	0	FAM171A2
20	17:42434630	rs850738	a	g	0.5874	0.0381	DEPR	DEPR_surv	1314	-0.032	0.081	0.97 [0.83, 1.13]	41.30	0.130	6.91E-01	0	0	0	0	0	FAM171A2
20	17:42434630	rs850738	a	g	0.5904	0.0273	DEPR	DEPR_base	2138	-0.001	0.091	1.00 [0.84, 1.19]	27.90	0.205	9.92E-01	0	0	0	0	0	FAM171A2
21	4:90636630	rs5019538	a	g	0.6699	0.0086	MOTORFLUX	MOTORFLUX_base	1803	-0.196	0.083	0.82 [0.70, 0.97]	46.30	0.114	1.80E-02	0	0	0	0	0	SNCA
21	4:90636630	rs5019538	a	g	0.6691	0.0131	MOTORFLUX	MOTORFLUX_surv	1709	-0.114	0.051	0.89 [0.81, 0.98]	0.00	0.888	2.37E-02	0	0	0	0	0	SNCA
22	4:90636630	rs5019538	a	g	0.6709	0.0097	DYSKINESIAS	DYSKINESIAS_base	1232	-0.229	0.103	0.80 [0.65, 0.97]	14.30	0.311	2.54E-02	0	0	0	0	0	SNCA
22	4:90636630	rs5019538	a	g	0.6593	0.0095	DEPR	DEPR_surv	1314	0.169	0.082	1.18 [1.01, 1.39]	0.00	0.712	3.99E-02	0	0	0	0	0	SNCA
23	4:90636630	rs5019538	a	g	0.6574	0.0110	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.058	0.030	0.06 [-0.00, 0.12]	0.00	0.875	5.52E-02	0	0	0	0	0	SNCA
23	4:90636630	rs5019538	a	g	0.6674	0.0095	CONST	CONST_base	1472	0.142	0.088	1.15 [0.97, 1.37]	0.00	0.578	1.07E-01	0	0	0	0	0	SNCA
24	4:90636630	rs5019538	a	g	0.6694	0.0138	DEPR	DEPR_base	2138	0.138	0.095	1.15 [0.95, 1.38]	0.00	0.954	1.45E-01	0	0	0	0	0	SNCA
24	4:90636630	rs5019538	a	g	0.6659	0.0098	COGI	COGI_base	2859	0.114	0.090	1.12 [0.94, 1.34]	0.00	0.495	2.05E-01	0	0	0	0	0	SNCA
25	4:90636630	rs5019538	a	g	0.6672	0.0088	DYSKINESIAS	DYSKINESIAS_surv	1856	-0.064	0.059	0.94 [0.84, 1.05]	0.00	0.854	2.82E-01	0	0	0	0	0	SNCA
25	4:90636630	rs5019538	a	g	0.6587	0.0114	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.023	0.026	-0.02 [-0.07, 0.03]	0.00	0.507	3.72E-01	0	0	0	0	0	SNCA
26	4:90636630	rs5019538	a	g	0.6518	0.0190	MMSE	MMSE_cont	2114	-0.042	0.047	-0.04 [-0.13, 0.05]	0.00	0.544	3.73E-01	0	0	0	0	0	SNCA
26	4:90636630	rs5019538	a	g	0.6564	0.0170	HY	HY_cont	3627	0.007	0.009	0.01 [-0.01, 0.03]	0.00	0.414	4.37E-01	0	0	0	0	0	SNCA
27	4:90636630	rs5019538	a	g	0.6698	0.0129	SLEEP	SLEEP_base	1724	0.066	0.087	1.07 [0.90, 1.27]	0.00	0.636	4.53E-01	0	0	0	0	0	SNCA
27	4:90636630	rs5019538	a	g	0.6570	0.0171	UPDRS_scaled	UPDRS_scaled_cont	2994	0.017	0.025	0.02 [-0.03, 0.07]	0.00	0.478	4.78E-01	0	0	0	0	0	SNCA
28	4:90636630	rs5019538	a	g	0.6661	0.0092	HY3	HY3_base	1289	-0.076	0.117	0.93 [0.74, 1.17]	4.20	0.352	5.14E-01	0	0	0	0	0	SNCA
28	4:90636630	rs5019538	a	g	0.6569	0.0106	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.017	0.030	0.02 [-0.04, 0.08]	0.00	0.469	5.62E-01	0	0	0	0	0	SNCA
29	4:90636630	rs5019538	a	g	0.6417	0.0167	MOCA	MOCA_cont	1074	-0.066	0.124	-0.07 [-0.31, 0.18]	0.00	0.831	5.95E-01	0	0	0	0	0	SNCA
29	4:90636630	rs5019538	a	g	0.6599	0.0135	SEADL70	SEADL70_surv	1683	0.044	0.097	1.04 [0.86, 1.26]	0.00	0.435	6.52E-01	0	0	0	0	0	SNCA
30	4:90636630	rs5019538	a	g	0.6582	0.0175	COGI	COGI_surv	2244	0.027	0.078	1.03 [0.88, 1.20]	0.00	0.472	7.28E-01	0	0	0	0	0	SNCA
30	4:90636630	rs5019538	a	g	0.6690	0.0105	HYPOSMIA	HYPOSMIA_base	1588	-0.0											

1	5:60137959	rs1867598	a	g	0.8909	0.0123	MOTORFLUX	MOTORFLUX_surv	1709	0.008	0.077	1.01 [0.87, 1.17]	31.50	0.188	9.20E-01	0	0	0	0	ELOVL7
2	1.226916078	rs4653767	t	c	0.7302	0.0150	INS	INS_surv	1112	0.168	0.076	1.18 [1.02, 1.37]	0.00	0.551	2.71E-02	0	0	0	0	ITPKB
	1.226916078	rs4653767	t	c	0.7288	0.0140	HY3	HY3_surv	2582	-0.100	0.071	0.90 [0.79, 1.04]	20.70	0.259	1.56E-01	0	0	0	0	ITPKB
3	1.226916078	rs4653767	t	c	0.7331	0.0150	COGI	COGI_base	2859	-0.131	0.098	0.88 [0.72, 1.06]	0.00	0.748	1.79E-01	0	0	0	0	ITPKB
	1.226916078	rs4653767	t	c	0.7232	0.0173	MOTORFLUX	MOTORFLUX_base	1803	-0.102	0.091	0.90 [0.76, 1.08]	0.00	0.908	2.58E-01	0	0	0	0	ITPKB
4	1.226916078	rs4653767	t	c	0.7293	0.0179	SEADL	SEADL_cont	2218	-0.258	0.261	-0.26 [-0.77, 0.25]	22.30	0.252	3.23E-01	0	0	0	0	ITPKB
	1.226916078	rs4653767	t	c	0.7261	0.0190	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.024	0.029	-0.02 [-0.08, 0.03]	42.50	0.095	4.01E-01	0	0	0	0	ITPKB
5	1.226916078	rs4653767	t	c	0.7244	0.0190	DYSKINESIAS	DYSKINESIAS_base	1232	-0.088	0.114	0.92 [0.73, 1.15]	6.90	0.341	4.44E-01	0	0	0	0	ITPKB
	1.226916078	rs4653767	t	c	0.7260	0.0170	MNSE	MNSE_cont	2114	-0.035	0.050	-0.03 [-0.13, 0.06]	0.00	0.676	4.87E-01	0	0	0	0	ITPKB
6	1.226916078	rs4653767	t	c	0.7233	0.0100	SEADL70	SEADL70_surv	1683	0.066	0.105	1.07 [0.87, 1.31]	33.70	0.196	5.27E-01	0	0	0	0	ITPKB
	1.226916078	rs4653767	t	c	0.7390	0.0113	CONST	CONST_base	1472	0.048	0.098	1.05 [0.87, 1.27]	0.00	0.444	6.23E-01	0	0	0	0	ITPKB
7	1.226916078	rs4653767	t	c	0.7330	0.0189	COGI	COGI_surv	2244	0.036	0.085	1.04 [0.88, 1.22]	0.00	0.687	6.70E-01	0	0	0	0	ITPKB
	1.226916078	rs4653767	t	c	0.7289	0.0191	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.011	0.026	-0.01 [-0.06, 0.04]	44.10	0.065	6.89E-01	0	0	0	0	ITPKB
8	1.226916078	rs4653767	t	c	0.7236	0.0191	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.013	0.032	-0.01 [-0.08, 0.05]	33.70	0.171	6.91E-01	0	0	0	0	ITPKB
	1.226916078	rs4653767	t	c	0.7415	0.0186	MOCA	MOCA_cont	1074	0.053	0.137	0.05 [-0.22, 0.32]	0.00	0.743	7.02E-01	0	0	0	0	ITPKB
9	1.226916078	rs4653767	t	c	0.7266	0.0066	MOTORFLUX	MOTORFLUX_surv	1709	0.020	0.054	1.02 [0.92, 1.13]	0.00	0.890	7.07E-01	0	0	0	0	ITPKB
	1.226916078	rs4653767	t	c	0.7323	0.0104	DEPR	DEPR_base	2138	-0.035	0.102	0.97 [0.79, 1.18]	0.00	0.603	7.31E-01	0	0	0	0	ITPKB
10	1.226916078	rs4653767	t	c	0.7334	0.0174	HY3	HY3_base	1289	-0.041	0.132	0.96 [0.74, 1.24]	0.00	0.647	7.59E-01	0	0	0	0	ITPKB
	1.226916078	rs4653767	t	c	0.7415	0.0155	SLEEP	SLEEP_base	1724	-0.026	0.095	0.97 [0.81, 1.17]	0.00	0.644	7.86E-01	0	0	0	0	ITPKB
11	1.226916078	rs4653767	t	c	0.7232	0.0197	UPDRS2_scaled	UPDRS2_scaled_cont	2103	-0.008	0.032	-0.01 [-0.07, 0.05]	0.00	0.458	8.03E-01	0	0	0	0	ITPKB
	1.226916078	rs4653767	t	c	0.7313	0.0206	INS	INS_base	2220	0.019	0.080	1.02 [0.87, 1.19]	6.60	0.380	8.17E-01	0	0	0	0	ITPKB
12	1.226916078	rs4653767	t	c	0.7233	0.0196	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.006	0.028	-0.01 [-0.06, 0.05]	0.00	0.854	8.19E-01	0	0	0	0	ITPKB
	1.226916078	rs4653767	t	c	0.7398	0.0132	HYPOSMIA	HYPOSMIA_base	1588	0.014	0.091	1.01 [0.85, 1.21]	0.00	0.552	8.77E-01	0	0	0	0	ITPKB
13	1.226916078	rs4653767	t	c	0.7330	0.0191	HY	HY_cont	3627	-0.001	0.010	-0.00 [-0.02, 0.02]	8.20	0.365	9.19E-01	0	0	0	0	ITPKB
	17:40741013	rs12951632	t	c	0.7403	0.0083	HY3	HY3_base	1289	-0.287	0.131	0.75 [0.58, 0.97]	0.00	0.431	2.78E-02	0	0	0	0	RETREG3
14	17:40741013	rs12951632	t	c	0.7471	0.0196	HY	HY_cont	3627	-0.021	0.010	-0.02 [-0.04, -0.00]	41.90	0.062	3.47E-02	0	0	0	0	RETREG3
	17:40741013	rs12951632	t	c	0.7499	0.0159	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.042	0.029	-0.04 [-0.10, 0.02]	0.00	0.518	1.49E-01	0	0	0	0	RETREG3
15	17:40741013	rs12951632	t	c	0.7561	0.0117	MNSE	MNSE_cont	2114	0.059	0.052	0.06 [-0.04, 0.16]	10.00	0.353	2.55E-01	0	0	0	0	RETREG3
	17:40741013	rs12951632	t	c	0.7523	0.0122	MOCA	MOCA_cont	1074	-0.153	0.140	-0.15 [-0.43, 0.12]	43.60	0.150	2.75E-01	0	0	0	0	RETREG3
16	17:40741013	rs12951632	t	c	0.7493	0.0212	HY3	HY3_surv	2582	-0.068	0.071	0.93 [0.81, 1.07]	0.00	0.486	3.42E-01	0	0	0	0	RETREG3
	17:40741013	rs12951632	t	c	0.7508	0.0176	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.026	0.027	-0.03 [-0.08, 0.03]	0.00	0.962	3.42E-01	0	0	0	0	RETREG3
17	17:40741013	rs12951632	t	c	0.7565	0.0158	UPDRS2_scaled	UPDRS2_scaled_cont	2103	-0.031	0.033	-0.03 [-0.10, 0.03]	0.00	0.483	3.53E-01	0	0	0	0	RETREG3
	17:40741013	rs12951632	t	c	0.7411	0.0148	CONST	CONST_base	1472	0.091	0.099	1.10 [0.90, 1.33]	0.00	0.624	3.54E-01	0	0	0	0	RETREG3
18	17:40741013	rs12951632	t	c	0.7457	0.0182	SLEEP	SLEEP_base	1724	0.086	0.096	1.09 [0.90, 1.32]	0.00	0.495	3.70E-01	0	0	0	0	RETREG3
	17:40741013	rs12951632	t	c	0.7436	0.0092	DYSKINESIAS	DYSKINESIAS_base	1232	-0.086	0.117	0.92 [0.73, 1.15]	0.00	0.442	4.63E-01	0	0	0	0	RETREG3
19	17:40741013	rs12951632	t	c	0.7578	0.0175	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.018	0.029	-0.02 [-0.07, 0.04]	0.00	0.800	5.37E-01	0	0	0	0	RETREG3
	17:40741013	rs12951632	t	c	0.7578	0.0139	SEADL	SEADL_cont	2218	-0.160	0.272	-0.16 [-0.69, 0.37]	0.00	0.707	5.57E-01	0	0	0	0	RETREG3
20	17:40741013	rs12951632	t	c	0.7585	0.0163	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.018	0.033	-0.02 [-0.08, 0.05]	0.00	0.914	5.91E-01	0	0	0	0	RETREG3
	17:40741013	rs12951632	t	c	0.7583	0.0189	DEPR	DEPR_base	2138	-0.047	0.104	0.95 [0.78, 1.17]	0.00	0.891	6.50E-01	0	0	0	0	RETREG3
21	17:40741013	rs12951632	t	c	0.7485	0.0178	COGI	COGI_surv	2244	0.033	0.085	1.03 [0.88, 1.22]	0.00	0.763	6.96E-01	0	0	0	0	RETREG3
	17:40741013	rs12951632	t	c	0.7411	0.0129	COGI	COGI_base	2859	-0.031	0.098	0.97 [0.80, 1.17]	0.00	0.637	7.49E-01	0	0	0	0	RETREG3
22	17:40741013	rs12951632	t	c	0.7539	0.0200	MOTORFLUX	MOTORFLUX_surv	1709	0.013	0.055	1.01 [0.91, 1.13]	0.00	0.489	8.10E-01	0	0	0	0	RETREG3
	17:40741013	rs12951632	t	c	0.7571	0.0188	DEPR	DEPR_surv	1314	-0.020	0.088	0.98 [0.82, 1.17]	0.00	0.949	8.22E-01	0	0	0	0	RETREG3
23	17:40741013	rs12951632	t	c	0.7544	0.0160	SEADL70	SEADL70_surv	1683	-0.020	0.104	0.98 [0.80, 1.20]	30.80	0.216	8.48E-01	0	0	0	0	RETREG3
	17:40741013	rs12951632	t	c	0.7508	0.0169	MOTORFLUX	MOTORFLUX_base	1803	-0.009	0.094	0.99 [0.82, 1.19]	29.50	0.225	9.20E-01	0	0	0	0	RETREG3
24	17:40741013	rs12951632	t	c	0.7566	0.0182	DYSKINESIAS	DYSKINESIAS_surv	1856	-0.002	0.066	1.00 [0.88, 1.14]	0.00	0.480	9.75E-01	0	0	0	0	RETREG3
	17:40741013	rs12951632	t	c	0.7477	0.0160	INS	INS_base	2220	0.002	0.081	1.00 [0.86, 1.17]	19.70	0.274	9.79E-01	0	0	0	0	RETREG3
25	17:40741013	rs12951632	t	c	0.7527	0.0171	INS	INS_surv	1112	-0.002	0.075	1.00 [0.86, 1.16]	26.20	0.238	9.81E-01	0	0	0	0	RETREG3
	17:40741013	rs12951632	t	c	0.7436	0.0167	HYPOSMIA	HYPOSMIA_base	1588	-0.002	0.091	1.00 [0.84, 1.19]	40.00	0.139	9.86E-01	0	0	0	0	RETREG3
26	5:134199105	rs11950533	a	c	0.0987	0.0110	MOTORFLUX	MOTORFLUX_surv	1709	-0.185	0.085	0.83 [0.70, 0.98]	0.00	0.681	2.98E-02	0	0	0	0	C5orf24
	5:134199105	rs11950533	a	c	0.0955	0.0114	DYSKINESIAS	DYSKINESIAS_surv	1856	-0.228	0.105	0.80 [0.65, 0.98]	38.40	0.136	3.00E-02	0	0	0	0	C5orf24
27	5:134199105	rs11950533	a	c	0.0904	0.0110	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.085	0.045	-0.09 [-0.17, 0.00]	0.00	0.940	5.65E-02	0	0	0	0	C5orf24
	5:134199105	rs11950533	a	c	0.1050	0.0025	HY3	HY3_base	1289	-0.371	0.211	0.69 [0.46, 1.04]	0.00	0.796	7.87E-02	0	0	0	0	C5orf24
28	5:134199105	rs11950533	a	c	0.0939	0.0133	UPDRS3_scaled	UPDRS3_scaled_cont	2446	0.069	0.044	0.07 [-0.02, 0.16]	1.10	0.421	1.20E-01	0	0	0	0	C5orf24
	5:134199105	rs11950533	a	c	0.0990	0.0136	CONST	CONST_base												

1	3:18361759	rs73038319	a	c	0.9581	0.0092	MOTORFLUX	MOTORFLUX_base	1803	0.051	0.212	1.05 [0.69, 1.60]	41.00	0.148	8.10E-01	0	0	0	0	0	SATB1
2	3:18361759	rs73038319	a	c	0.9572	0.0076	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.012	0.062	0.01 [-0.11, 0.13]	0.00	0.939	8.42E-01	0	0	0	0	0	SATB1
3	3:18361759	rs73038319	a	c	0.9515	0.0098	COGI	COGI_base	2148	0.032	0.169	1.03 [0.74, 1.44]	0.00	0.939	8.49E-01	0	0	0	0	0	SATB1
3	3:18361759	rs73038319	a	c	0.9504	0.0120	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.011	0.061	-0.01 [-0.13, 0.11]	27.60	0.209	8.63E-01	0	0	0	0	0	SATB1
3	3:18361759	rs73038319	a	c	0.9493	0.0087	HY3	HY3_base	2582	0.024	0.147	1.02 [0.77, 1.37]	0.00	0.490	8.69E-01	0	0	0	0	0	SATB1
4	3:18361759	rs73038319	a	c	0.9527	0.0099	HY3	HY3_base	1289	-0.038	0.258	0.96 [0.58, 1.60]	0.00	0.824	8.83E-01	0	0	0	0	0	SATB1
4	3:18361759	rs73038319	a	c	0.9502	0.0047	MOCA	MOCA_cont	1026	-0.039	0.285	-0.04 [-0.60, 0.52]	0.00	0.667	8.92E-01	0	0	0	0	0	SATB1
5	3:18361759	rs73038319	a	c	0.9526	0.0084	COGI	COGI_base	2859	-0.027	0.197	0.97 [0.66, 1.43]	0.00	0.634	8.92E-01	0	0	0	0	0	SATB1
5	3:18361759	rs73038319	a	c	0.9444	0.0083	DEPR	DEPR_surv	1177	-0.010	0.186	0.99 [0.69, 1.43]	0.00	0.937	9.58E-01	0	0	0	0	0	SATB1
6	6:27738801	rs4140646	a	g	0.2512	0.0209	DEPR	DEPR_surv	1314	-0.186	0.090	0.83 [0.70, 0.99]	0.00	0.845	3.93E-02	0	0	0	0	0	LOC100131289
6	6:27738801	rs4140646	a	g	0.2371	0.0268	COGI	COGI_surv	2244	-0.159	0.088	0.85 [0.72, 1.01]	0.00	0.503	7.03E-02	0	0	0	0	0	LOC100131289
7	6:27738801	rs4140646	a	g	0.2465	0.0244	HY3	HY3_surv	2582	-0.104	0.073	0.90 [0.78, 1.04]	14.10	0.317	1.51E-01	0	0	0	0	0	LOC100131289
7	6:27738801	rs4140646	a	g	0.2309	0.0131	SEADL	SEADL_cont	2218	-0.342	0.272	-0.34 [-0.88, 0.19]	0.00	0.824	2.09E-01	0	0	0	0	0	LOC100131289
8	6:27738801	rs4140646	a	g	0.2310	0.0168	UPDRS3_scaled	UPDRS3_scaled_cont	2446	0.037	0.030	0.04 [-0.02, 0.10]	47.60	0.064	2.16E-01	0	0	0	0	0	LOC100131289
8	6:27738801	rs4140646	a	g	0.2396	0.0200	SLEEP	SLEEP_base	1724	0.113	0.096	1.12 [0.93, 1.35]	0.00	0.549	2.40E-01	0	0	0	0	0	LOC100131289
9	6:27738801	rs4140646	a	g	0.2341	0.0294	HY3	HY3_base	1289	0.152	0.140	1.16 [0.89, 1.53]	43.40	0.171	2.76E-01	0	0	0	0	0	LOC100131289
9	6:27738801	rs4140646	a	g	0.2284	0.0187	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.035	0.034	-0.03 [-0.10, 0.03]	9.00	0.360	3.14E-01	0	0	0	0	0	LOC100131289
10	6:27738801	rs4140646	a	g	0.2364	0.0248	UPDRS_scaled	UPDRS_scaled_cont	2994	0.026	0.028	0.03 [-0.03, 0.08]	7.70	0.371	3.40E-01	0	0	0	0	0	LOC100131289
10	6:27738801	rs4140646	a	g	0.2401	0.0227	MOTORFLUX	MOTORFLUX_surv	1709	-0.053	0.057	0.95 [0.85, 1.06]	0.00	0.633	3.46E-01	0	0	0	0	0	LOC100131289
11	6:27738801	rs4140646	a	g	0.2270	0.0112	SEADL70	SEADL70_surv	1683	0.091	0.102	1.10 [0.90, 1.34]	0.00	0.913	3.72E-01	0	0	0	0	0	LOC100131289
11	6:27738801	rs4140646	a	g	0.2407	0.0208	DEPR	DEPR_base	2138	-0.089	0.108	0.91 [0.74, 1.13]	19.60	0.274	4.09E-01	0	0	0	0	0	LOC100131289
12	6:27738801	rs4140646	a	g	0.2300	0.0270	INS	INS_base	2220	0.068	0.083	1.07 [0.91, 1.26]	0.00	0.578	4.15E-01	0	0	0	0	0	LOC100131289
12	6:27738801	rs4140646	a	g	0.2270	0.0203	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.022	0.035	0.02 [-0.05, 0.09]	0.00	0.776	5.17E-01	0	0	0	0	0	LOC100131289
13	6:27738801	rs4140646	a	g	0.2248	0.0245	MOTORFLUX	MOTORFLUX_base	1803	-0.058	0.098	0.94 [0.78, 1.14]	44.40	0.126	5.53E-01	0	0	0	0	0	LOC100131289
13	6:27738801	rs4140646	a	g	0.2340	0.0285	INS	INS_surv	1112	-0.038	0.075	0.96 [0.83, 1.11]	0.00	0.824	6.10E-01	0	0	0	0	0	LOC100131289
14	6:27738801	rs4140646	a	g	0.2256	0.0189	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.015	0.030	0.01 [-0.04, 0.07]	9.00	0.358	6.17E-01	0	0	0	0	0	LOC100131289
14	6:27738801	rs4140646	a	g	0.2337	0.0253	COGI	COGI_base	2859	-0.050	0.104	0.95 [0.78, 1.17]	44.10	0.085	6.29E-01	0	0	0	0	0	LOC100131289
15	6:27738801	rs4140646	a	g	0.2329	0.0163	MOCA	MOCA_cont	1074	-0.063	0.140	-0.06 [-0.34, 0.21]	0.00	0.997	6.52E-01	0	0	0	0	0	LOC100131289
15	6:27738801	rs4140646	a	g	0.2378	0.0213	CONST	CONST_base	1472	0.033	0.098	1.03 [0.85, 1.25]	31.20	0.213	7.34E-01	0	0	0	0	0	LOC100131289
16	6:27738801	rs4140646	a	g	0.2329	0.0151	DYSKINESIAS	DYSKINESIAS_surv	1856	-0.022	0.069	0.98 [0.85, 1.12]	45.90	0.086	7.45E-01	0	0	0	0	0	LOC100131289
16	6:27738801	rs4140646	a	g	0.2371	0.0185	HYPOSMIA	HYPOSMIA_base	1588	-0.011	0.094	0.99 [0.82, 1.19]	0.00	0.826	9.11E-01	0	0	0	0	0	LOC100131289
17	6:27738801	rs4140646	a	g	0.2300	0.0279	MMSE	MMSE_cont	2114	0.003	0.053	0.00 [-0.10, 0.11]	0.00	0.767	9.49E-01	0	0	0	0	0	LOC100131289
17	16:52969426	rs10221156	a	g	0.0793	0.0095	HY	HY_cont	2077	-0.045	0.022	-0.05 [-0.09, -0.00]	0.00	0.951	3.93E-02	0	0	0	0	0	CHD9
18	16:52969426	rs10221156	a	g	0.0834	0.0149	INS	INS_base	1033	0.156	0.196	1.17 [0.80, 1.71]	38.60	0.164	4.27E-01	0	0	0	0	0	CHD9
18	16:52969426	rs10221156	a	g	0.0787	0.0144	SLEEP	SLEEP_base	1033	-0.175	0.221	0.84 [0.54, 1.29]	14.10	0.325	4.27E-01	0	0	0	0	0	CHD9
19	16:52969426	rs10221156	a	g	0.0869	0.0118	COGI	COGI_surv	1132	-0.122	0.200	0.88 [0.60, 1.31]	25.80	0.249	5.40E-01	0	0	0	0	0	CHD9
19	16:52969426	rs10221156	a	g	0.0825	0.0067	MMSE	MMSE_cont	1066	-0.031	0.102	-0.03 [-0.23, 0.17]	0.00	0.863	7.61E-01	0	0	0	0	0	CHD9
20	16:52969426	rs10221156	a	g	0.0852	0.0134	HY3	HY3_surv	1299	-0.017	0.137	0.98 [0.75, 1.29]	0.00	0.975	9.03E-01	0	0	0	0	0	CHD9
20	16:52969426	rs10221156	a	g	0.0784	0.0140	COGI	COGI_base	1538	-0.011	0.235	0.99 [0.62, 1.57]	23.50	0.264	9.63E-01	0	0	0	0	0	CHD9
21	16:52969426	rs10221156	a	g	0.0770	0.0075	UPDRS_scaled	UPDRS_scaled_cont	1108	0.000	0.073	-0.00 [-0.14, 0.14]	0.00	0.985	9.99E-01	0	0	0	0	0	CHD9
21	16:52636242	rs3104783	a	c	0.4252	0.0193	CONST	CONST_base	1472	-0.172	0.086	0.84 [0.71, 1.00]	0.00	0.977	4.55E-02	0	0	0	0	0	CASC16
22	16:52636242	rs3104783	a	c	0.4280	0.0308	HY3	HY3_base	1289	-0.148	0.119	0.86 [0.68, 1.09]	24.40	0.267	2.17E-01	0	0	0	0	0	CASC16
22	16:52636242	rs3104783	a	c	0.4403	0.0238	MOTORFLUX	MOTORFLUX_base	1803	0.102	0.083	1.11 [0.94, 1.30]	0.00	0.514	2.18E-01	0	0	0	0	0	CASC16
23	16:52636242	rs3104783	a	c	0.4253	0.0251	SLEEP	SLEEP_base	1724	0.094	0.084	1.10 [0.93, 1.29]	0.00	0.566	2.64E-01	0	0	0	0	0	CASC16
23	16:52636242	rs3104783	a	c	0.4360	0.0204	DEPR	DEPR_base	2138	-0.096	0.090	0.91 [0.76, 1.08]	0.00	0.792	2.88E-01	0	0	0	0	0	CASC16
24	16:52636242	rs3104783	a	c	0.4394	0.0265	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.021	0.025	0.02 [-0.03, 0.07]	5.50	0.382	4.09E-01	0	0	0	0	0	CASC16
24	16:52636242	rs3104783	a	c	0.4380	0.0130	SEADL70	SEADL70_surv	1683	0.066	0.090	1.07 [0.89, 1.27]	16.40	0.310	4.68E-01	0	0	0	0	0	CASC16
25	16:52636242	rs3104783	a	c	0.4226	0.0256	HYPOSMIA	HYPOSMIA_base	1588	-0.055	0.082	0.95 [0.81, 1.11]	0.00	0.451	4.98E-01	0	0	0	0	0	CASC16
25	16:52636242	rs3104783	a	c	0.4346	0.0285	INS	INS_base	2220	-0.044	0.071	0.96 [0.83, 1.10]	13.10	0.328	5.32E-01	0	0	0	0	0	CASC16
26	16:52636242	rs3104783	a	c	0.4343	0.0217	INS	INS_surv	1112	0.034	0.064	1.03 [0.91, 1.17]	0.00	0.747	5.96E-01	0	0	0	0	0	CASC16
26	16:52636242	rs3104783	a	c	0.4433	0.0243	UPDRS_scaled	UPDRS_scaled_cont	2994	0.012	0.024	0.01 [-0.03, 0.06]	0.00	0.463	6.17E-01	0	0	0	0	0	CASC16
27	16:52636242	rs3104783	a	c	0.4330	0.0246	DEPR	DEPR_surv	1314	0.025	0.078	1.03 [0.88, 1.19]	0.00	0.767	7.50E-01	0	0	0	0	0	CASC16
28	16:52636242	rs3104783	a	c	0.4256	0.0342	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.008	0.026	-0.01 [-0.06, 0.04]	0.00	0.826	7.70E-01	0	0	0	0	0	CASC16
28	16:52636242	rs3104783	a	c	0.4216	0.0285	HY3	HY3_surv	2582	-0.018	0.061	0.98 [0.87, 1.11]	33.10	0.153	7.75E-01	0	0	0	0	0	CASC16
28	16:52636242	rs3104783	a	c	0.4358	0.0293	HY	HY_cont	3627	-0.002	0.009	-0.00 [-0.02, 0.02]	31.60	0.138	8.01E-01	0	0	0	0	0	CASC16
29	16:52636242	rs3104783	a	c	0.4394	0.0262	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.006	0.029	0.01 [-0.05, 0.06]	0.00	0.578	8.25E-01	0	0	0	0	0	CASC16
29	16:52636242	rs3104783	a	c	0.4325	0.0239	SEADL	SEADL_cont	2218	-0.051	0.234	-0.05 [-0.51, 0.41]	0.00	0.975	8.26E-01	0	0	0	0	0	CASC16
30	16:52636242	rs3104783	a	c	0.4373	0.0284	COGI	COGI_base	2859	0.018	0.088	1.02 [0.86, 1.21]	38.10	0.126	8.40E-01	0	0	0	0	0	

1	1:171719769	rs11578699	t	c	0.1853	0.0182	INS	INS_base	2220	0.106	0.091	1.11 [0.93, 1.33]	0.00	0.472	2.42E-01	0	0	0	0	0	0	VAMP4
2	1:171719769	rs11578699	t	c	0.1944	0.0211	SEADL70	SEADL70_surv	1683	-0.122	0.121	0.88 [0.70, 1.12]	0.00	0.945	3.11E-01	0	0	0	0	0	0	VAMP4
3	1:171719769	rs11578699	t	c	0.1849	0.0191	HY	HY_cont	3627	0.010	0.011	0.01 [-0.01, 0.03]	0.00	0.698	3.85E-01	0	0	0	0	0	0	VAMP4
4	1:171719769	rs11578699	t	c	0.1868	0.0254	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.024	0.033	-0.02 [-0.09, 0.04]	22.30	0.252	4.61E-01	0	0	0	0	0	0	VAMP4
5	1:171719769	rs11578699	t	c	0.1825	0.0168	SLEEP	SLEEP_base	1724	0.078	0.108	1.08 [0.88, 1.33]	0.00	0.915	4.07E-01	0	0	0	0	0	0	VAMP4
6	1:171719769	rs11578699	t	c	0.1877	0.0237	SEADL	SEADL_cont	2218	-0.207	0.297	-0.21 [-0.79, 0.38]	0.00	0.442	4.87E-01	0	0	0	0	0	0	VAMP4
7	1:171719769	rs11578699	t	c	0.1803	0.0185	MMSE	MMSE_cont	2114	-0.037	0.057	-0.04 [-0.15, 0.08]	35.30	0.146	5.23E-01	0	0	0	0	0	0	VAMP4
8	1:171719769	rs11578699	t	c	0.1902	0.0188	DEPR	DEPR_base	2138	0.064	0.113	1.07 [0.85, 1.33]	7.70	0.371	5.71E-01	0	0	0	0	0	0	VAMP4
9	1:171719769	rs11578699	t	c	0.1887	0.0115	DYSKINESIAS	DYSKINESIAS_base	1232	0.062	0.131	1.06 [0.82, 1.38]	0.00	0.845	6.36E-01	0	0	0	0	0	0	VAMP4
10	1:171719769	rs11578699	t	c	0.1818	0.0114	CONST	CONST_base	1472	-0.044	0.110	0.96 [0.77, 1.19]	0.00	0.775	6.88E-01	0	0	0	0	0	0	VAMP4
11	1:171719769	rs11578699	t	c	0.1833	0.0191	COGI	COGI_base	2859	0.040	0.113	1.04 [0.83, 1.30]	3.60	0.403	7.23E-01	0	0	0	0	0	0	VAMP4
12	1:171719769	rs11578699	t	c	0.1822	0.0128	HY3	HY3_base	1289	0.053	0.150	1.05 [0.79, 1.41]	0.00	0.952	7.24E-01	0	0	0	0	0	0	VAMP4
13	1:171719769	rs11578699	t	c	0.1928	0.0220	UPDRS2_scaled	UPDRS2_scaled_cont	2103	-0.012	0.037	-0.01 [-0.08, 0.06]	0.00	0.693	7.46E-01	0	0	0	0	0	0	VAMP4
14	1:171719769	rs11578699	t	c	0.1939	0.0219	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.009	0.037	-0.01 [-0.08, 0.06]	18.10	0.292	8.08E-01	0	0	0	0	0	0	VAMP4
15	1:171719769	rs11578699	t	c	0.1828	0.0152	DEPR	DEPR_surv	1314	0.019	0.099	1.02 [0.84, 1.24]	0.00	0.683	8.50E-01	0	0	0	0	0	0	VAMP4
16	1:171719769	rs11578699	t	c	0.1952	0.0178	MOTORFLUX	MOTORFLUX_base	1803	0.017	0.105	1.02 [0.83, 1.25]	42.60	0.137	8.76E-01	0	0	0	0	0	0	VAMP4
17	1:171719769	rs11578699	t	c	0.1844	0.0196	COGI	COGI_surv	2244	-0.009	0.096	0.99 [0.82, 1.20]	6.70	0.380	9.23E-01	0	0	0	0	0	0	VAMP4
18	1:171719769	rs11578699	t	c	0.1848	0.0224	UPDRS_scaled	UPDRS_scaled_cont	2994	0.003	0.030	0.00 [-0.06, 0.06]	0.00	0.851	9.28E-01	0	0	0	0	0	0	VAMP4
19	6:30108683	rs9261484	t	c	0.2458	0.0127	HY3	HY3_base	1289	0.261	0.133	1.30 [1.00, 1.68]	0.00	0.536	5.01E-02	0	0	0	0	0	0	TRIM40
20	6:30108683	rs9261484	t	c	0.2403	0.0286	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.064	0.033	0.06 [-0.00, 0.13]	0.00	0.703	5.25E-02	0	0	0	0	0	0	TRIM40
21	6:30108683	rs9261484	t	c	0.2411	0.0202	COGI	COGI_surv	2244	0.147	0.083	1.16 [0.98, 1.36]	0.00	0.593	7.84E-02	0	0	0	0	0	0	TRIM40
22	6:30108683	rs9261484	t	c	0.2339	0.0083	SEADL70_surv	SEADL70_surv	1683	0.165	0.102	1.18 [0.96, 1.44]	0.00	0.930	1.08E-01	0	0	0	0	0	0	TRIM40
23	6:30108683	rs9261484	t	c	0.2386	0.0260	SLEEP	SLEEP_base	1724	-0.151	0.097	0.86 [0.71, 1.04]	0.00	0.901	1.18E-01	0	0	0	0	0	0	TRIM40
24	6:30108683	rs9261484	t	c	0.2353	0.0104	MOCA	MOCA_cont	1074	-0.209	0.137	-0.21 [-0.48, 0.06]	0.00	0.778	1.28E-01	0	0	0	0	0	0	TRIM40
25	6:30108683	rs9261484	t	c	0.2392	0.0260	SEADL	SEADL_cont	2218	-0.375	0.269	-0.37 [-0.90, 0.15]	0.00	0.541	1.64E-01	0	0	0	0	0	0	TRIM40
26	6:30108683	rs9261484	t	c	0.2381	0.0220	DEPR	DEPR_surv	1314	0.112	0.091	1.12 [0.94, 1.34]	47.80	0.088	2.17E-01	0	0	0	0	0	0	TRIM40
27	6:30108683	rs9261484	t	c	0.2451	0.0270	INS	INS_base	2220	-0.076	0.080	0.93 [0.79, 1.09]	0.00	0.527	3.46E-01	0	0	0	0	0	0	TRIM40
28	6:30108683	rs9261484	t	c	0.2293	0.0143	MOTORFLUX	MOTORFLUX_surv	1709	-0.052	0.058	0.95 [0.85, 1.06]	0.00	0.679	3.67E-01	0	0	0	0	0	0	TRIM40
29	6:30108683	rs9261484	t	c	0.2439	0.0151	MOTORFLUX	MOTORFLUX_base	1803	0.084	0.094	1.09 [0.90, 1.31]	0.00	0.421	3.73E-01	0	0	0	0	0	0	TRIM40
30	6:30108683	rs9261484	t	c	0.2502	0.0346	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.025	0.029	-0.03 [-0.08, 0.03]	0.00	0.621	3.81E-01	0	0	0	0	0	0	TRIM40
31	6:30108683	rs9261484	t	c	0.2371	0.0115	DYSKINESIAS	DYSKINESIAS_surv	1856	0.051	0.068	1.05 [0.92, 1.20]	0.00	0.836	4.57E-01	0	0	0	0	0	0	TRIM40
32	6:30108683	rs9261484	t	c	0.2515	0.0103	DYSKINESIAS	DYSKINESIAS_base	1232	-0.064	0.118	0.94 [0.74, 1.18]	0.00	0.915	5.90E-01	0	0	0	0	0	0	TRIM40
33	6:30108683	rs9261484	t	c	0.2356	0.0276	HY	HY_cont	3627	0.004	0.010	0.00 [-0.02, 0.02]	0.00	0.610	6.72E-01	0	0	0	0	0	0	TRIM40
34	6:30108683	rs9261484	t	c	0.2428	0.0285	HYPOSMIA	HYPOSMIA_base	1588	0.035	0.092	1.04 [0.87, 1.24]	0.00	0.937	6.99E-01	0	0	0	0	0	0	TRIM40
35	6:30108683	rs9261484	t	c	0.2397	0.0133	INS	INS_surv	1112	-0.025	0.074	0.98 [0.84, 1.13]	37.90	0.153	7.35E-01	0	0	0	0	0	0	TRIM40
36	6:30108683	rs9261484	t	c	0.2344	0.0140	CONST	CONST_base	1472	0.024	0.098	1.02 [0.85, 1.24]	0.00	0.649	8.09E-01	0	0	0	0	0	0	TRIM40
37	6:30108683	rs9261484	t	c	0.2305	0.0235	MMSE	MMSE_cont	2114	-0.011	0.052	-0.01 [-0.11, 0.09]	0.00	0.993	8.30E-01	0	0	0	0	0	0	TRIM40
38	6:30108683	rs9261484	t	c	0.2351	0.0167	DEPR	DEPR_base	2138	0.020	0.103	1.02 [0.83, 1.25]	2.60	0.410	8.49E-01	0	0	0	0	0	0	TRIM40
39	6:30108683	rs9261484	t	c	0.2449	0.0233	COGI	COGI_base	2859	-0.018	0.099	0.98 [0.81, 1.19]	0.00	0.964	8.53E-01	0	0	0	0	0	0	TRIM40
40	6:30108683	rs9261484	t	c	0.2414	0.0285	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.006	0.033	0.01 [-0.06, 0.07]	37.20	0.145	8.63E-01	0	0	0	0	0	0	TRIM40
41	6:30108683	rs9261484	t	c	0.2373	0.0285	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.003	0.029	-0.00 [-0.06, 0.05]	15.90	0.311	9.04E-01	0	0	0	0	0	0	TRIM40
42	6:30108683	rs9261484	t	c	0.2431	0.0303	HY3	HY3_surv	2582	0.008	0.072	1.01 [0.87, 1.16]	11.70	0.337	9.13E-01	0	0	0	0	0	0	TRIM40
43	6:30108683	rs9261484	t	c	0.2384	0.0146	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.001	0.027	-0.00 [-0.05, 0.05]	12.80	0.326	9.62E-01	0	0	0	0	0	0	TRIM40
44	10:15557406	rs896435	t	c	0.7000	0.0126	MOTORFLUX	MOTORFLUX_base	1803	0.172	0.089	1.19 [1.00, 1.41]	0.00	0.649	5.29E-02	0	0	0	0	0	0	ITGA8
45	10:15557406	rs896435	t	c	0.6981	0.0292	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.031	0.027	0.03 [-0.02, 0.08]	0.00	0.684	2.43E-01	0	0	0	0	0	0	ITGA8
46	10:15557406	rs896435	t	c	0.6970	0.0267	COGI	COGI_surv	2244	-0.087	0.078	0.92 [0.79, 1.07]	29.10	0.186	2.62E-01	0	0	0	0	0	0	ITGA8
47	10:15557406	rs896435	t	c	0.6950	0.0229	COGI	COGI_base	2859	0.101	0.093	1.11 [0.92, 1.33]	0.00	0.680	2.80E-01	0	0	0	0	0	0	ITGA8
48	10:15557406	rs896435	t	c	0.6940	0.0253	SLEEP	SLEEP_base	1724	-0.071	0.090	0.93 [0.78, 1.11]	0.00	0.444	4.30E-01	0	0	0	0	0	0	ITGA8
49	10:15557406	rs896435	t	c	0.6971	0.0296	UPDRS2_scaled	UPDRS2_scaled_cont	2103	-0.023	0.031	-0.02 [-0.08, 0.04]	36.70	0.149	4.65E-01	0	0	0	0	0	0	ITGA8
50	10:15557406	rs896435	t	c	0.6846	0.0196	SEADL	SEADL_cont	2218	0.179	0.248	1.18 [-0.31, 0.67]	0.00	0.936	4.71E-01	0	0	0	0	0	0	ITGA8
51	10:15557406	rs896435	t	c	0.7088	0.0163	HY3	HY3_base	1289	0.082	0.127	1.09 [0.85, 1.39]	0.00	0.795	5.15E-01	0	0	0	0	0	0	ITGA8
52	10:15557406	rs896435	t	c	0.6938	0.0258	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.016	0.025	-0.02 [-0.06, 0.03]	44.50	0.063	5.29E-01	0	0	0	0	0	0	ITGA8
53	10:15557406	rs896435	t	c	0.6927	0.0277	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.014	0.028	-0.01 [-0.07, 0.04]	48.60	0.058	6.26E-01	0	0	0	0	0	0	ITGA8
54	10:15557406	rs896435	t	c	0.6990	0.0169	MOTORFLUX	MOTORFLUX_surv	1709	0.022	0.053	1.02 [0.92, 1.13]	0.00	0.610	6.78E-01	0	0	0	0	0	0	ITGA8
55	10:15557406	rs896435	t	c	0.6904	0.0280	HYPOSMIA	HYPOSMIA_base	1588	0.032	0.086	1.03 [0.87, 1.22]	0.00	0.490	7.14E-01	0	0	0	0	0	0	ITGA8
56	10:15557406	rs896435	t	c	0.7064	0.0203	INS	INS_surv	1112	-0.027	0.074	0.97 [0.84, 1.13]	0.00	0.908	7.22E-01	0	0	0	0	0	0	ITGA8
57	10:15557406	rs896435	t	c	0.6949	0.0142	SEADL70	SEADL70_surv	1683	0.033	0.098	1.03 [0.85, 1.25]	0.00	0.674	7.35E-01	0	0	0	0	0	0	ITGA8
58	10:15557406	rs896435	t	c	0.7048	0.0201	DYSKINESIAS															

1	20:6006041	rs77351827	t	c	0.1329	0.0083	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.062	0.043	0.06 [-0.02, 0.15]	0.00	0.449	1.50E-01	0	0	0	0	CRLS1
2	20:6006041	rs77351827	t	c	0.1300	0.0092	HYPOSIMIA	HYPOSIMIA_base	1588	-0.151	0.116	0.86 [0.68, 1.08]	34.90	0.175	1.92E-01	0	0	0	0	CRLS1
3	20:6006041	rs77351827	t	c	0.1315	0.0060	DEPR	DEPR_surv	1314	0.139	0.115	1.15 [0.92, 1.44]	38.20	0.152	2.28E-01	0	0	0	0	CRLS1
4	20:6006041	rs77351827	t	c	0.1313	0.0038	INS	INS_surv	1112	-0.117	0.100	0.89 [0.73, 1.08]	0.00	0.665	2.41E-01	0	0	0	0	CRLS1
5	20:6006041	rs77351827	t	c	0.1342	0.0085	COGI	COGI_base	2712	0.119	0.122	1.13 [0.89, 1.43]	0.00	0.668	3.31E-01	0	0	0	0	CRLS1
6	20:6006041	rs77351827	t	c	0.1335	0.0085	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.034	0.037	-0.03 [-0.11, 0.04]	38.30	0.151	3.59E-01	0	0	0	0	CRLS1
7	20:6006041	rs77351827	t	c	0.1311	0.0056	MOTORFLUX	MOTORFLUX_base	1803	-0.104	0.115	0.90 [0.72, 1.13]	0.00	0.439	3.67E-01	0	0	0	0	CRLS1
8	20:6006041	rs77351827	t	c	0.1330	0.0073	HY3	HY3_base	1289	0.139	0.157	1.15 [0.84, 1.56]	0.00	0.943	3.76E-01	0	0	0	0	CRLS1
9	20:6006041	rs77351827	t	c	0.1307	0.0073	MMSE	MMSE_cont	2114	-0.058	0.066	-0.06 [-0.19, 0.07]	0.00	0.765	3.81E-01	0	0	0	0	CRLS1
10	20:6006041	rs77351827	t	c	0.1315	0.0069	CONST	CONST_base	1472	0.105	0.121	1.11 [0.88, 1.41]	0.00	0.898	3.88E-01	0	0	0	0	CRLS1
11	20:6006041	rs77351827	t	c	0.1325	0.0095	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.035	0.043	0.03 [-0.05, 0.12]	15.50	0.311	4.16E-01	0	0	0	0	CRLS1
12	20:6006041	rs77351827	t	c	0.1303	0.0087	SLEEP	SLEEP_base	1724	0.097	0.121	1.10 [0.87, 1.40]	0.00	0.719	4.21E-01	0	0	0	0	CRLS1
13	20:6006041	rs77351827	t	c	0.1367	0.0094	MOTORFLUX	MOTORFLUX_surv	1709	0.048	0.071	1.05 [0.91, 1.21]	0.00	0.614	5.01E-01	0	0	0	0	CRLS1
14	20:6006041	rs77351827	t	c	0.1312	0.0071	INS	INS_base	2220	0.061	0.101	1.06 [0.87, 1.30]	38.40	0.124	5.48E-01	0	0	0	0	CRLS1
15	20:6006041	rs77351827	t	c	0.1299	0.0090	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.023	0.039	-0.02 [-0.10, 0.05]	0.00	0.736	5.51E-01	0	0	0	0	CRLS1
16	20:6006041	rs77351827	t	c	0.1311	0.0059	DEPR	DEPR_base	2138	0.065	0.128	1.07 [0.83, 1.37]	13.30	0.326	6.11E-01	0	0	0	0	CRLS1
17	20:6006041	rs77351827	t	c	0.1317	0.0043	HY3	HY3_surv	2582	-0.028	0.096	0.97 [0.81, 1.17]	0.00	0.633	7.67E-01	0	0	0	0	CRLS1
18	20:6006041	rs77351827	t	c	0.1276	0.0081	SEADL	SEADL_cont	2218	0.105	0.356	0.11 [-0.59, 0.80]	5.60	0.387	7.92E-01	0	0	0	0	CRLS1
19	20:6006041	rs77351827	t	c	0.1325	0.0074	DYSKINESIAS	DYSKINESIAS_surv	1856	-0.023	0.085	0.98 [0.83, 1.16]	0.00	0.473	7.92E-01	0	0	0	0	CRLS1
20	20:6006041	rs77351827	t	c	0.1341	0.0055	MOCA	MOCA_cont	1074	0.040	0.180	0.04 [-0.31, 0.39]	17.90	0.301	8.25E-01	0	0	0	0	CRLS1
21	20:6006041	rs77351827	t	c	0.1318	0.0058	DYSKINESIAS	DYSKINESIAS_base	1232	0.025	0.143	1.03 [0.77, 1.36]	60.50	0.080	8.63E-01	0	0	0	0	CRLS1
22	20:6006041	rs77351827	t	c	0.1337	0.0100	UPDRS_scaled	UPDRS_scaled_cont	2994	0.005	0.035	0.00 [-0.06, 0.07]	0.00	0.909	8.97E-01	0	0	0	0	CRLS1
23	20:6006041	rs77351827	t	c	0.1334	0.0107	HY	HY_cont	3627	0.001	0.013	0.00 [-0.02, 0.03]	0.00	0.946	9.29E-01	0	0	0	0	CRLS1
24	8:16697593	rs620513	t	g	0.1305	0.0072	COGI	COGI_surv	2244	0.005	0.118	1.00 [0.80, 1.27]	0.00	0.632	9.69E-01	0	0	0	0	CRLS1
25	8:16697593	rs620513	t	g	0.2631	0.0109	CONST	CONST_base	1472	0.187	0.100	1.21 [0.99, 1.47]	0.00	0.439	6.24E-02	0	0	0	0	FGF20
26	8:16697593	rs620513	t	g	0.2637	0.0053	HY3	HY3_base	1289	0.219	0.137	1.24 [0.95, 1.63]	0.00	0.460	1.11E-01	0	0	0	0	FGF20
27	8:16697593	rs620513	t	g	0.2524	0.0203	HY3	HY3_surv	2582	-0.093	0.074	0.91 [0.79, 1.05]	17.00	0.291	2.10E-01	0	0	0	0	FGF20
28	8:16697593	rs620513	t	g	0.2550	0.0201	COGI	COGI_surv	2244	0.101	0.086	1.11 [0.93, 1.31]	0.00	0.576	2.41E-01	0	0	0	0	FGF20
29	8:16697593	rs620513	t	g	0.2583	0.0131	DEPR	DEPR_base	2138	0.101	0.104	1.11 [0.90, 1.36]	0.00	0.679	3.34E-01	0	0	0	0	FGF20
30	8:16697593	rs620513	t	g	0.2393	0.0148	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.030	0.034	0.03 [-0.04, 0.10]	49.30	0.066	3.75E-01	0	0	0	0	FGF20
31	8:16697593	rs620513	t	g	0.2609	0.0121	SLEEP	SLEEP_base	1724	0.078	0.098	1.08 [0.89, 1.31]	0.00	0.958	4.25E-01	0	0	0	0	FGF20
32	8:16697593	rs620513	t	g	0.2482	0.0117	SEADL	SEADL_cont	2112	0.174	0.270	0.17 [-0.36, 0.70]	0.00	0.517	5.19E-01	0	0	0	0	FGF20
33	8:16697593	rs620513	t	g	0.2376	0.0133	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.019	0.030	-0.02 [-0.08, 0.04]	0.00	0.721	5.22E-01	0	0	0	0	FGF20
34	8:16697593	rs620513	t	g	0.2397	0.0143	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.018	0.030	-0.02 [-0.08, 0.04]	2.60	0.410	5.49E-01	0	0	0	0	FGF20
35	8:16697593	rs620513	t	g	0.2604	0.0088	HYPOSIMIA	HYPOSIMIA_base	1588	-0.057	0.096	0.94 [0.78, 1.14]	33.90	0.182	5.51E-01	0	0	0	0	FGF20
36	8:16697593	rs620513	t	g	0.2463	0.0151	MOTORFLUX	MOTORFLUX_surv	1709	0.034	0.059	1.03 [0.92, 1.16]	0.00	0.587	5.62E-01	0	0	0	0	FGF20
37	8:16697593	rs620513	t	g	0.2501	0.0127	DYSKINESIAS	DYSKINESIAS_surv	1856	0.040	0.070	1.04 [0.91, 1.19]	25.60	0.234	5.70E-01	0	0	0	0	FGF20
38	8:16697593	rs620513	t	g	0.2627	0.0111	INS	INS_base	2220	0.047	0.083	1.05 [0.89, 1.23]	4.10	0.399	5.73E-01	0	0	0	0	FGF20
39	8:16697593	rs620513	t	g	0.2397	0.0139	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.019	0.034	0.02 [-0.05, 0.09]	17.30	0.298	5.77E-01	0	0	0	0	FGF20
40	8:16697593	rs620513	t	g	0.2634	0.0374	INS	INS_surv	1112	0.014	0.077	1.01 [0.87, 1.18]	0.00	0.733	8.55E-01	0	0	0	0	FGF20
41	8:16697593	rs620513	t	g	0.2453	0.0129	DEPR	DEPR_surv	1314	0.016	0.089	1.02 [0.85, 1.21]	9.40	0.356	8.55E-01	0	0	0	0	FGF20
42	8:16697593	rs620513	t	g	0.2582	0.0087	MOTORFLUX	MOTORFLUX_base	1803	0.013	0.096	1.01 [0.84, 1.22]	0.00	0.618	8.90E-01	0	0	0	0	FGF20
43	8:16697593	rs620513	t	g	0.2471	0.0223	UPDRS_scaled	UPDRS_scaled_cont	2994	0.002	0.027	0.00 [-0.05, 0.05]	0.00	0.494	9.54E-01	0	0	0	0	FGF20
44	8:16697593	rs620513	t	g	0.2495	0.0148	SEADL70	SEADL70_surv	1683	0.006	0.110	1.01 [0.81, 1.25]	0.00	0.408	9.56E-01	0	0	0	0	FGF20
45	8:16697593	rs620513	t	g	0.2497	0.0187	HY	HY_cont	3627	0.000	0.010	0.00 [-0.02, 0.02]	11.60	0.331	9.79E-01	0	0	0	0	FGF20
46	17:43798308	rs117615688	a	g	0.0484	0.0073	HY3	HY3_base	1289	-0.605	0.330	0.55 [0.29, 1.04]	0.00	0.751	6.69E-02	0	0	0	0	CRRH1
47	17:43798308	rs117615688	a	g	0.0510	0.0062	COGI	COGI_base	2450	0.340	0.200	1.40 [0.95, 2.08]	10.10	0.352	8.92E-02	0	0	0	0	CRRH1
48	17:43798308	rs117615688	a	g	0.0540	0.0090	CONST	CONST_base	1335	-0.341	0.211	0.71 [0.47, 1.08]	0.00	0.788	1.07E-01	0	0	0	0	CRRH1
49	17:43798308	rs117615688	a	g	0.0497	0.0052	SEADL	SEADL_cont	2218	0.891	0.563	0.89 [-0.21, 2.00]	0.00	0.726	1.14E-01	0	0	0	0	CRRH1
50	17:43798308	rs117615688	a	g	0.0557	0.0146	SLEEP	SLEEP_base	1724	0.309	0.196	1.36 [0.93, 2.00]	10.70	0.348	1.15E-01	0	0	0	0	CRRH1
51	17:43798308	rs117615688	a	g	0.0503	0.0031	DEPR	DEPR_surv	1314	0.276	0.179	1.32 [0.93, 1.87]	21.80	0.270	1.22E-01	0	0	0	0	CRRH1
52	17:43798308	rs117615688	a	g	0.0584	0.0140	HYPOSIMIA	HYPOSIMIA_base	1588	0.247	0.186	1.28 [0.89, 1.84]	54.40	0.052	1.84E-01	0	0	0	0	CRRH1
53	17:43798308	rs117615688	a	g	0.0517	0.0089	MOTORFLUX	MOTORFLUX_surv	1709	-0.123	0.122	0.88 [0.70, 1.12]	0.00	0.658	3.13E-01	0	0	0	0	CRRH1
54	17:43798308	rs117615688	a	g	0.0519	0.0049	MOTORFLUX	MOTORFLUX_base	1803	0.188	0.199	1.21 [0.82, 1.78]	16.70	0.308	3.43E-01	0	0	0	0	CRRH1
55	17:43798308	rs117615688	a	g	0.0597	0.0128	INS	INS_base	2220	0.154	0.173	1.17 [0.83, 1.64]	41.50	0.102	3.74E-01	0	0	0	0	CRRH1
56	17:43798308	rs117615688	a	g	0.0519	0.0146	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.053	0.061	-0.05 [-0.17, 0.07]	2.90	0.398	3.80E-01	0	0	0	0	CRRH1
57	17:43798308	rs117615688	a	g	0.0524	0.0104	HY	HY_cont	3627	0.017	0.021	0.02 [-0.02, 0.06]	14.40	0.304	4.23E-01	0	0	0	0	CRRH1
58	17:43798308	rs117615688	a	g	0.0548	0.0079	INS	INS_surv	1112	0.107	0.152	1.11 [0.83, 1.50]	0.00	0.672	4.83E-01	0	0	0	0	CRRH1
59	17:43798308	rs117615688	a	g	0.0501	0.0150	UPDRS3_scaled	UPDRS3_scaled_cont	2446	0.038	0.066	0.04 [-0.09, 0.17]	0.00	0.772	5.59E-01	0	0	0	0	CRRH1
60	17:43798308	rs117615688	a	g	0.0522	0.0133	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.036	0.070	0.04 [-0.10, 0.17]	0.00	0.637	6.09E-01	0	0	0	0	CRRH1
61	17:43798308	rs117615688	a																	

1	10:121415685	rs72840788	a	g	0.2287	0.0106	DYSKINESIAS	DYSKINESIAS_base	1232	-0.057	0.119	0.94 [0.75, 1.19]	59.70	0.084	6.34E-01	0	0	0	0	BAG3
2	10:121415685	rs72840788	a	g	0.2307	0.0105	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.016	0.034	-0.02 [-0.08, 0.05]	0.00	0.693	6.44E-01	0	0	0	0	BAG3
3	10:121415685	rs72840788	a	g	0.2328	0.0135	SLEEP	SLEEP_base	1724	-0.032	0.097	0.97 [0.80, 1.17]	0.00	0.920	7.38E-01	0	0	0	0	BAG3
4	10:121415685	rs72840788	a	g	0.2243	0.0144	SEADL	SEADL_cont	2218	-0.084	0.275	-0.08 [-0.62, 0.45]	6.60	0.379	7.59E-01	0	0	0	0	BAG3
5	10:121415685	rs72840788	a	g	0.2314	0.0120	CONST	CONST_base	1472	-0.028	0.100	1.03 [0.84, 1.25]	10.80	0.344	7.82E-01	0	0	0	0	BAG3
6	10:121415685	rs72840788	a	g	0.2292	0.0160	DYSKINESIAS	DYSKINESIAS_surv	1856	-0.016	0.068	0.98 [0.86, 1.13]	11.40	0.343	8.15E-01	0	0	0	0	BAG3
7	10:121415685	rs72840788	a	g	0.2153	0.0140	M MSE	M MSE_cont	2114	-0.010	0.053	-0.01 [-0.11, 0.10]	0.00	0.875	8.59E-01	0	0	0	0	BAG3
8	10:121415685	rs72840788	a	g	0.2346	0.0212	HY3	HY3_surv	2582	-0.012	0.072	0.99 [0.86, 1.14]	31.70	0.165	8.71E-01	0	0	0	0	BAG3
9	10:121415685	rs72840788	a	g	0.2306	0.0139	COGi	COGi_base	2859	0.013	0.102	1.01 [0.83, 1.24]	17.60	0.291	8.96E-01	0	0	0	0	BAG3
10	10:121415685	rs72840788	a	g	0.2279	0.0133	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.002	0.028	-0.00 [-0.06, 0.05]	0.00	0.762	9.36E-01	0	0	0	0	BAG3
11	10:121415685	rs72840788	a	g	0.2285	0.0139	INS	INS_base	2220	0.000	0.084	1.00 [0.85, 1.18]	26.30	0.219	9.97E-01	0	0	0	0	BAG3
12	17:7355621	rs12600861	a	c	0.6426	0.0238	SEADL	SEADL_cont	2218	-0.429	0.244	-0.43 [-0.91, 0.05]	0.90	0.423	7.91E-02	0	0	0	0	CHRNBI
13	17:7355621	rs12600861	a	c	0.6329	0.0298	HY	HY_cont	3627	0.013	0.009	0.01 [-0.00, 0.03]	0.00	0.637	1.42E-01	0	0	0	0	CHRNBI
14	17:7355621	rs12600861	a	c	0.6479	0.0185	MOCA	MOCA_cont	1074	-0.179	0.124	-0.18 [-0.42, 0.06]	23.40	0.271	1.50E-01	0	0	0	0	CHRNBI
15	17:7355621	rs12600861	a	c	0.6359	0.0299	UPDRS_scaled	UPDRS_scaled_cont	2994	0.034	0.024	0.03 [-0.01, 0.08]	0.00	0.739	1.54E-01	0	0	0	0	CHRNBI
16	17:7355621	rs12600861	a	c	0.6452	0.0141	DYSKINESIAS	DYSKINESIAS_base	1232	0.108	0.105	1.11 [0.91, 1.37]	46.80	0.153	3.07E-01	0	0	0	0	CHRNBI
17	17:7355621	rs12600861	a	c	0.6417	0.0211	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.028	0.030	0.03 [-0.03, 0.09]	38.40	0.136	3.45E-01	0	0	0	0	CHRNBI
18	17:7355621	rs12600861	a	c	0.6383	0.0178	HY3	HY3_base	1289	-0.085	0.117	0.92 [0.73, 1.16]	0.00	0.444	4.71E-01	0	0	0	0	CHRNBI
19	17:7355621	rs12600861	a	c	0.6409	0.0144	MOTORFLUX	MOTORFLUX_base	1803	-0.059	0.084	0.94 [0.80, 1.11]	0.00	0.458	4.81E-01	0	0	0	0	CHRNBI
20	17:7355621	rs12600861	a	c	0.6411	0.0185	DYSKINESIAS	DYSKINESIAS_surv	1856	0.041	0.059	1.04 [0.93, 1.17]	28.00	0.215	4.87E-01	0	0	0	0	CHRNBI
21	17:7355621	rs12600861	a	c	0.6402	0.0220	HY3	HY3_surv	2582	-0.039	0.064	0.96 [0.85, 1.09]	13.80	0.320	5.47E-01	0	0	0	0	CHRNBI
22	17:7355621	rs12600861	a	c	0.6420	0.0258	SLEEP	SLEEP_base	1724	0.050	0.085	1.05 [0.89, 1.24]	0.00	0.999	5.62E-01	0	0	0	0	CHRNBI
23	17:7355621	rs12600861	a	c	0.6380	0.0254	DEPR	DEPR_surv	1314	0.045	0.079	1.05 [0.90, 1.22]	0.00	0.800	5.69E-01	0	0	0	0	CHRNBI
24	17:7355621	rs12600861	a	c	0.6461	0.0196	CONST	CONST_base	1472	-0.049	0.087	0.95 [0.80, 1.13]	0.00	0.485	5.75E-01	0	0	0	0	CHRNBI
25	17:7355621	rs12600861	a	c	0.6499	0.0177	MOTORFLUX	MOTORFLUX_surv	1709	0.027	0.051	1.03 [0.93, 1.14]	0.00	0.713	5.91E-01	0	0	0	0	CHRNBI
26	17:7355621	rs12600861	a	c	0.6531	0.0217	M MSE	M MSE_cont	2114	-0.023	0.047	-0.02 [-0.11, 0.07]	0.00	0.524	6.18E-01	0	0	0	0	CHRNBI
27	17:7355621	rs12600861	a	c	0.6333	0.0311	COGi	COGi_base	2859	-0.036	0.089	0.96 [0.81, 1.15]	41.00	0.105	6.84E-01	0	0	0	0	CHRNBI
28	17:7355621	rs12600861	a	c	0.6415	0.0213	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.012	0.030	0.01 [-0.05, 0.07]	0.00	0.540	6.91E-01	0	0	0	0	CHRNBI
29	17:7355621	rs12600861	a	c	0.6374	0.0223	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.008	0.027	-0.01 [-0.06, 0.04]	0.00	0.916	7.52E-01	0	0	0	0	CHRNBI
30	17:7355621	rs12600861	a	c	0.6518	0.0207	COGi	COGi_surv	2244	-0.023	0.076	0.98 [0.84, 1.14]	0.00	0.672	7.67E-01	0	0	0	0	CHRNBI
31	17:7355621	rs12600861	a	c	0.6570	0.0167	SEADL70	SEADL70_surv	1683	-0.026	0.096	0.97 [0.81, 1.18]	0.00	0.910	7.88E-01	0	0	0	0	CHRNBI
32	17:7355621	rs12600861	a	c	0.6437	0.0183	DEPR	DEPR_base	2138	0.022	0.093	1.02 [0.85, 1.23]	16.40	0.301	8.10E-01	0	0	0	0	CHRNBI
33	17:7355621	rs12600861	a	c	0.6425	0.0279	HYPOSMIA	HYPOSMIA_base	1588	-0.013	0.083	0.99 [0.84, 1.16]	0.00	0.897	8.71E-01	0	0	0	0	CHRNBI
34	17:7355621	rs12600861	a	c	0.6443	0.0237	INS	INS_base	2220	0.003	0.072	1.00 [0.87, 1.16]	0.00	0.639	9.63E-01	0	0	0	0	CHRNBI
35	17:7355621	rs12600861	a	c	0.6558	0.0200	INS	INS_surv	1112	0.001	0.067	1.00 [0.88, 1.14]	0.00	0.780	9.87E-01	0	0	0	0	CHRNBI
36	16:30977799	rs11150601	a	g	0.6731	0.0194	INS	INS_surv	1112	-0.123	0.071	0.88 [0.77, 1.01]	46.40	0.097	8.01E-02	0	0	0	0	SETDIA
37	16:30977799	rs11150601	a	g	0.6503	0.0272	HY3	HY3_surv	2582	-0.105	0.064	0.90 [0.79, 1.02]	0.00	0.899	1.02E-01	0	0	0	0	SETDIA
38	16:30977799	rs11150601	a	g	0.6542	0.0186	UPDRS2_scaled	UPDRS2_scaled_cont	2103	-0.049	0.030	-0.05 [-0.11, 0.01]	0.00	0.750	1.06E-01	0	0	0	0	SETDIA
39	16:30977799	rs11150601	a	g	0.6540	0.0263	INS	INS_base	2220	-0.119	0.074	0.89 [0.77, 1.03]	25.10	0.229	1.07E-01	0	0	0	0	SETDIA
40	16:30977799	rs11150601	a	g	0.6536	0.0190	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.046	0.030	-0.05 [-0.11, 0.01]	0.00	0.954	1.29E-01	0	0	0	0	SETDIA
41	16:30977799	rs11150601	a	g	0.6544	0.0231	HY	HY_cont	3627	-0.012	0.009	-0.01 [-0.03, 0.01]	15.80	0.289	1.86E-01	0	0	0	0	SETDIA
42	16:30977799	rs11150601	a	g	0.6603	0.0188	HYPOSMIA	HYPOSMIA_base	1588	-0.110	0.084	0.90 [0.76, 1.06]	0.00	0.953	1.88E-01	0	0	0	0	SETDIA
43	16:30977799	rs11150601	a	g	0.6439	0.0144	SEADL70	SEADL70_surv	1683	-0.118	0.098	1.12 [0.93, 1.36]	0.00	0.925	2.27E-01	0	0	0	0	SETDIA
44	16:30977799	rs11150601	a	g	0.6518	0.0169	COGi	COGi_base	2859	0.106	0.092	1.11 [0.93, 1.33]	40.00	0.112	2.49E-01	0	0	0	0	SETDIA
45	16:30977799	rs11150601	a	g	0.6534	0.0203	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.026	0.026	-0.03 [-0.08, 0.03]	0.00	0.828	3.25E-01	0	0	0	0	SETDIA
46	16:30977799	rs11150601	a	g	0.6480	0.0151	MOTORFLUX	MOTORFLUX_base	1803	0.083	0.086	1.09 [0.92, 1.29]	0.00	0.836	3.38E-01	0	0	0	0	SETDIA
47	16:30977799	rs11150601	a	g	0.6571	0.0185	DEPR	DEPR_surv	1314	-0.069	0.080	0.93 [0.80, 1.09]	4.90	0.385	3.85E-01	0	0	0	0	SETDIA
48	16:30977799	rs11150601	a	g	0.6476	0.0259	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.021	0.025	-0.02 [-0.07, 0.03]	0.00	0.935	3.85E-01	0	0	0	0	SETDIA
49	16:30977799	rs11150601	a	g	0.6526	0.0287	SLEEP	SLEEP_base	1724	-0.075	0.087	0.93 [0.78, 1.10]	22.70	0.256	3.86E-01	0	0	0	0	SETDIA
50	16:30977799	rs11150601	a	g	0.6451	0.0287	DEPR	DEPR_base	2138	-0.057	0.093	0.94 [0.79, 1.13]	0.00	0.565	5.38E-01	0	0	0	0	SETDIA
51	16:30977799	rs11150601	a	g	0.6544	0.0148	HY3	HY3_base	1289	0.063	0.122	1.07 [0.84, 1.35]	0.00	0.840	6.04E-01	0	0	0	0	SETDIA
52	16:30977799	rs11150601	a	g	0.6534	0.0268	M MSE	M MSE_cont	2114	0.024	0.046	0.02 [-0.07, 0.11]	0.00	0.964	6.06E-01	0	0	0	0	SETDIA
53	16:30977799	rs11150601	a	g	0.6483	0.0175	MOTORFLUX	MOTORFLUX_surv	1709	0.019	0.051	1.02 [0.92, 1.13]	47.20	0.078	7.06E-01	0	0	0	0	SETDIA
54	16:30977799	rs11150601	a	g	0.6521	0.0273	CONST	CONST_base	1472	-0.029	0.090	0.97 [0.81, 1.16]	0.00	0.435	7.45E-01	0	0	0	0	SETDIA
55	1																			

1	9:34046391	rs6476434	t	c	0.7220	0.0156	INS	INS_surv	1112	-0.084	0.072	0.92	[0.80, 1.06]	0.00	0.809	2.45E-01	0	0	0	0	0	UBAP2
2	9:34046391	rs6476434	t	c	0.7275	0.0110	CONST	CONST_base	1472	0.105	0.095	1.11	[0.92, 1.34]	0.00	0.467	2.67E-01	0	0	0	0	0	UBAP2
3	9:34046391	rs6476434	t	c	0.7321	0.0081	HY3	HY3_base	1289	-0.119	0.129	0.89	[0.69, 1.14]	0.00	0.415	3.55E-01	0	0	0	0	0	UBAP2
4	9:34046391	rs6476434	t	c	0.7080	0.0143	MOCA	MOCA_cont	1074	0.119	0.134	0.12	[-0.14, 0.38]	0.00	0.805	3.77E-01	0	0	0	0	0	UBAP2
5	9:34046391	rs6476434	t	c	0.7234	0.0183	HY3	HY3_surv	2582	-0.059	0.071	0.94	[0.82, 1.08]	0.00	0.905	4.02E-01	0	0	0	0	0	UBAP2
6	9:34046391	rs6476434	t	c	0.7166	0.0152	HY	HY_cont	3627	0.007	0.010	0.01	[-0.01, 0.03]	25.10	0.197	4.58E-01	0	0	0	0	0	UBAP2
7	9:34046391	rs6476434	t	c	0.7270	0.0101	HYPOSMIA	HYPOSMIA_base	1588	0.062	0.091	1.06	[0.89, 1.27]	2.10	0.403	4.95E-01	0	0	0	0	0	UBAP2
8	9:34046391	rs6476434	t	c	0.7252	0.0094	INS	INS_base	2220	0.050	0.078	1.05	[0.90, 1.23]	0.00	0.501	5.20E-01	0	0	0	0	0	UBAP2
9	9:34046391	rs6476434	t	c	0.7097	0.0121	SEADL70	SEADL70_surv	1683	0.053	0.106	1.05	[0.86, 1.30]	0.00	0.510	6.14E-01	0	0	0	0	0	UBAP2
10	9:34046391	rs6476434	t	c	0.7101	0.0152	MMSE	MMSE_cont	2114	0.020	0.048	0.02	[-0.07, 0.11]	15.60	0.307	6.77E-01	0	0	0	0	0	UBAP2
11	9:34046391	rs6476434	t	c	0.7285	0.0100	SLEEP	SLEEP_base	1724	0.036	0.094	1.04	[0.86, 1.25]	27.40	0.220	6.99E-01	0	0	0	0	0	UBAP2
12	9:34046391	rs6476434	t	c	0.7132	0.0145	COGI	COGI_surv	2244	0.032	0.084	1.03	[0.88, 1.22]	2.90	0.410	7.08E-01	0	0	0	0	0	UBAP2
13	9:34046391	rs6476434	t	c	0.7277	0.0076	MOTORFLUX	MOTORFLUX_base	1803	-0.031	0.092	0.97	[0.81, 1.16]	0.00	0.417	7.32E-01	0	0	0	0	0	UBAP2
14	9:34046391	rs6476434	t	c	0.7070	0.0110	SEADL	SEADL_cont	2218	0.050	0.258	0.05	[-0.46, 0.56]	20.00	0.271	8.47E-01	0	0	0	0	0	UBAP2
15	9:34046391	rs6476434	t	c	0.7219	0.0175	DEPR	DEPR_surv	1314	0.014	0.090	1.01	[0.85, 1.21]	0.00	0.741	8.76E-01	0	0	0	0	0	UBAP2
16	9:34046391	rs6476434	t	c	0.7223	0.0060	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.003	0.028	0.00	[-0.05, 0.06]	43.30	0.116	9.09E-01	0	0	0	0	0	UBAP2
17	6:32578772	rs112485576	a	c	0.1439	0.0185	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.070	0.040	0.07	[-0.01, 0.15]	8.10	0.367	8.23E-02	0	0	0	0	0	HLA-DRB5
18	6:32578772	rs112485576	a	c	0.1450	0.0185	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.062	0.040	0.06	[-0.02, 0.14]	0.00	0.743	1.23E-01	0	0	0	0	0	HLA-DRB5
19	6:32578772	rs112485576	a	c	0.1436	0.0185	UPDRS3_scaled	UPDRS3_scaled_cont	2994	0.049	0.033	0.05	[-0.02, 0.11]	0.00	0.889	1.33E-01	0	0	0	0	0	HLA-DRB5
20	6:32578772	rs112485576	a	c	0.1484	0.0183	INS	INS_base	2220	-0.136	0.099	0.87	[0.72, 1.06]	0.00	0.548	1.72E-01	0	0	0	0	0	HLA-DRB5
21	6:32578772	rs112485576	a	c	0.1455	0.0182	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.045	0.035	0.04	[-0.02, 0.11]	0.00	0.851	2.00E-01	0	0	0	0	0	HLA-DRB5
22	6:32578772	rs112485576	a	c	0.1444	0.0161	DEPR	DEPR_base	2138	0.135	0.125	1.14	[0.90, 1.46]	0.00	0.878	2.80E-01	0	0	0	0	0	HLA-DRB5
23	6:32578772	rs112485576	a	c	0.1432	0.0174	COGI	COGI_surv	2244	0.106	0.104	1.11	[0.91, 1.36]	37.50	0.119	3.09E-01	0	0	0	0	0	HLA-DRB5
24	6:32578772	rs112485576	a	c	0.1514	0.0100	MOTORFLUX	MOTORFLUX_base	1803	-0.104	0.113	0.90	[0.72, 1.12]	0.00	0.687	3.57E-01	0	0	0	0	0	HLA-DRB5
25	6:32578772	rs112485576	a	c	0.1495	0.0141	COGI	COGI_base	2859	-0.106	0.124	0.90	[0.71, 1.15]	0.00	0.736	3.92E-01	0	0	0	0	0	HLA-DRB5
26	6:32578772	rs112485576	a	c	0.1421	0.0080	MOTORFLUX	MOTORFLUX_surv	1709	0.049	0.071	1.05	[0.91, 1.21]	0.00	0.575	4.86E-01	0	0	0	0	0	HLA-DRB5
27	6:32578772	rs112485576	a	c	0.1380	0.0027	HY	HY_cont	3627	-0.007	0.013	-0.01	[-0.03, 0.02]	0.00	0.901	5.78E-01	0	0	0	0	0	HLA-DRB5
28	6:32578772	rs112485576	a	c	0.1487	0.0108	HY3	HY3_base	1289	0.080	0.159	1.08	[0.79, 1.48]	28.00	0.249	6.17E-01	0	0	0	0	0	HLA-DRB5
29	6:32578772	rs112485576	a	c	0.1405	0.0099	DYSKINESIAS	DYSKINESIAS_surv	1856	-0.039	0.084	0.96	[0.82, 1.13]	0.00	0.603	6.47E-01	0	0	0	0	0	HLA-DRB5
30	6:32578772	rs112485576	a	c	0.1453	0.0209	HYPOSMIA	HYPOSMIA_base	1588	0.052	0.115	1.05	[0.84, 1.32]	0.00	0.768	6.51E-01	0	0	0	0	0	HLA-DRB5
31	6:32578772	rs112485576	a	c	0.1454	0.0201	SLEEP	SLEEP_base	1724	0.044	0.120	1.04	[0.83, 1.32]	19.50	0.281	7.16E-01	0	0	0	0	0	HLA-DRB5
32	6:32578772	rs112485576	a	c	0.1412	0.0244	SEADL	SEADL_cont	2218	0.119	0.337	0.12	[-0.54, 0.78]	0.00	0.970	7.23E-01	0	0	0	0	0	HLA-DRB5
33	6:32578772	rs112485576	a	c	0.1408	0.0151	MMSE	MMSE_cont	2114	-0.020	0.063	-0.02	[-0.14, 0.10]	0.00	0.768	7.55E-01	0	0	0	0	0	HLA-DRB5
34	6:32578772	rs112485576	a	c	0.1417	0.0070	SEADL70	SEADL70_surv	1683	0.031	0.128	1.03	[0.80, 1.33]	33.90	0.195	8.07E-01	0	0	0	0	0	HLA-DRB5
35	6:32578772	rs112485576	a	c	0.1406	0.0131	INS	INS_surv	1112	0.022	0.095	1.02	[0.85, 1.23]	0.00	0.912	8.18E-01	0	0	0	0	0	HLA-DRB5
36	6:32578772	rs112485576	a	c	0.1488	0.0160	HY3	HY3_surv	2582	0.019	0.086	1.02	[0.86, 1.21]	0.00	0.647	8.23E-01	0	0	0	0	0	HLA-DRB5
37	6:32578772	rs112485576	a	c	0.1338	0.0269	MOCA	MOCA_cont	1074	0.029	0.174	0.03	[-0.31, 0.37]	3.20	0.377	8.68E-01	0	0	0	0	0	HLA-DRB5
38	6:32578772	rs112485576	a	c	0.1489	0.0197	UPDRS3_scaled	UPDRS3_scaled_cont	2446	0.005	0.036	0.00	[-0.06, 0.07]	20.00	0.271	8.90E-01	0	0	0	0	0	HLA-DRB5
39	6:32578772	rs112485576	a	c	0.1443	0.0143	CONST	CONST_base	1472	0.015	0.121	1.02	[0.80, 1.29]	0.00	0.781	9.02E-01	0	0	0	0	0	HLA-DRB5
40	6:32578772	rs112485576	a	c	0.1372	0.0082	DEPR	DEPR_surv	1314	0.000	0.113	1.00	[0.80, 1.25]	0.00	0.904	9.98E-01	0	0	0	0	0	HLA-DRB5
41	10:104015279	rs10748818	a	g	0.8586	0.0126	DEPR	DEPR_base	2138	0.232	0.134	1.26	[0.97, 1.64]	0.00	0.987	8.39E-02	0	0	0	0	0	GBF1
42	10:104015279	rs10748818	a	g	0.8543	0.0115	HY3	HY3_surv	2582	-0.145	0.085	0.87	[0.73, 1.02]	0.00	0.511	8.88E-02	0	0	0	0	0	GBF1
43	10:104015279	rs10748818	a	g	0.8454	0.0163	DYSKINESIAS	DYSKINESIAS_base	1232	0.223	0.143	1.25	[0.94, 1.66]	0.00	0.732	1.19E-01	0	0	0	0	0	GBF1
44	10:104015279	rs10748818	a	g	0.8517	0.0197	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.053	0.041	0.05	[-0.03, 0.13]	0.00	0.826	1.87E-01	0	0	0	0	0	GBF1
45	10:104015279	rs10748818	a	g	0.8500	0.0173	DYSKINESIAS	DYSKINESIAS_surv	1856	0.108	0.083	1.11	[0.95, 1.31]	43.10	0.103	1.93E-01	0	0	0	0	0	GBF1
46	10:104015279	rs10748818	a	g	0.8530	0.0158	HY	HY_cont	3627	0.016	0.012	0.02	[-0.01, 0.04]	0.00	0.555	1.94E-01	0	0	0	0	0	GBF1
47	10:104015279	rs10748818	a	g	0.8623	0.0102	SLEEP	SLEEP_base	1724	0.157	0.123	1.17	[0.92, 1.49]	26.20	0.228	2.01E-01	0	0	0	0	0	GBF1
48	10:104015279	rs10748818	a	g	0.8488	0.0213	UPDRS3_scaled	UPDRS3_scaled_cont	2446	0.037	0.036	0.04	[-0.03, 0.11]	13.60	0.324	2.98E-01	0	0	0	0	0	GBF1
49	10:104015279	rs10748818	a	g	0.8468	0.0235	MOCA	MOCA_cont	1074	0.161	0.166	0.16	[-0.16, 0.49]	23.20	0.272	3.31E-01	0	0	0	0	0	GBF1
50	10:104015279	rs10748818	a	g	0.8550	0.0068	SEADL70	SEADL70_surv	1683	-0.117	0.123	0.89	[0.70, 1.13]	23.50	0.264	3.41E-01	0	0	0	0	0	GBF1
51	10:104015279	rs10748818	a	g	0.8500	0.0191	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.032	0.035	0.03	[-0.04, 0.10]	8.10	0.365	3.67E-01	0	0	0	0	0	GBF1
52	10:104015279	rs10748818	a	g	0.8531	0.0185	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.035	0.041	0.04	[-0.04, 0.11]	7.40	0.372	3.87E-01	0	0	0	0	0	GBF1
53	10:104015279	rs10748818	a	g	0.8515	0.0147	COGI	COGI_surv	2244	-0.085	0.104	0.92	[0.75, 1.13]	0.00	0.873	4.18E-01	0	0	0	0	0	GBF1
54	10:104015279	rs10748818	a	g	0.8485	0.0155	MOTORFLUX	MOTORFLUX_base	1803	0.088	0.114	0.99	[0.87, 1.37]	23.50	0.265	4.42E-01	0	0	0	0	0	GBF1
55	10:104015279	rs10748818	a	g	0.8523	0.0140	COGI	COGI_base	2859	-0.087	0.120	0.92	[0.72, 1.16]	25.30	0.227	4.71E-01	0	0	0	0	0	GBF1
56	10:104015279	rs10748818	a	g	0.8525	0.0187	SEADL	SEADL_cont	2218	0.233	0.325	0.23	[-0.40, 0.87]	11.90	0.399	4.73E-01	0	0	0	0	0	GBF1
57	10:104015279	rs10748818	a	g	0.8525	0.0157	INS	INS_surv	1112	-0.057	0.092	0.94	[0.79, 1.13]	4.90	0.339	5.35E-01	0	0	0			

1	18:40673380	rs12456492	a	g	0.6428	0.0173	DEPR	DEPR_base	2138	-0.111	0.093	0.89	[0.75, 1.07]	13.40	0.325	2.30E-01	0	0	0	0	RIT2
2	18:40673380	rs12456492	a	g	0.6338	0.0123	UPDRS2_scaled	UPDRS2_scaled_cont	2103	-0.032	0.030	-0.03	[-0.09, 0.03]	0.00	0.486	2.90E-01	0	0	0	0	RIT2
3	18:40673380	rs12456492	a	g	0.6498	0.0196	COGI	COGI_base	2859	0.086	0.091	1.09	[0.91, 1.30]	0.00	0.903	3.44E-01	0	0	0	0	RIT2
4	18:40673380	rs12456492	a	g	0.6530	0.0176	SLEEP	SLEEP_base	1724	-0.081	0.086	0.92	[0.78, 1.09]	7.90	0.368	3.48E-01	0	0	0	0	RIT2
5	18:40673380	rs12456492	a	g	0.6577	0.0185	CONST	CONST_base	1472	0.082	0.089	1.09	[0.91, 1.29]	34.00	0.195	3.57E-01	0	0	0	0	RIT2
6	18:40673380	rs12456492	a	g	0.6551	0.0202	HYPOSIMIA	HYPOSIMIA_base	1588	-0.074	0.084	0.93	[0.79, 1.09]	51.10	0.069	3.81E-01	0	0	0	0	RIT2
7	18:40673380	rs12456492	a	g	0.6343	0.0127	UPDRS1_scaled	UPDRS1_scaled_cont	2111	-0.024	0.030	-0.02	[-0.08, 0.04]	21.30	0.267	4.31E-01	0	0	0	0	RIT2
8	18:40673380	rs12456492	a	g	0.6538	0.0108	DYSKINESIAS	DYSKINESIAS_base	1232	0.078	0.108	1.08	[0.87, 1.34]	0.00	0.628	4.73E-01	0	0	0	0	RIT2
9	18:40673380	rs12456492	a	g	0.6441	0.0321	MOCA	MOCA_cont	1074	-0.090	0.127	-0.09	[-0.34, 0.16]	0.00	0.426	4.76E-01	0	0	0	0	RIT2
10	18:40673380	rs12456492	a	g	0.6452	0.0258	COGI	COGI_surv	2244	0.054	0.079	1.06	[0.90, 1.23]	0.00	0.570	4.99E-01	0	0	0	0	RIT2
11	18:40673380	rs12456492	a	g	0.6387	0.0170	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.015	0.024	-0.02	[-0.06, 0.03]	0.00	0.657	5.33E-01	0	0	0	0	RIT2
12	18:40673380	rs12456492	a	g	0.6469	0.0228	HY	HY_cont	3627	-0.005	0.009	-0.00	[-0.02, 0.01]	0.00	0.662	6.13E-01	0	0	0	0	RIT2
13	18:40673380	rs12456492	a	g	0.6574	0.0172	INS	INS_base	2220	-0.036	0.073	0.96	[0.84, 1.11]	0.00	0.511	6.25E-01	0	0	0	0	RIT2
14	18:40673380	rs12456492	a	g	0.6477	0.0113	HY3	HY3_base	1289	0.059	0.121	1.06	[0.84, 1.34]	0.00	0.957	6.28E-01	0	0	0	0	RIT2
15	18:40673380	rs12456492	a	g	0.6352	0.0136	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.011	0.026	-0.01	[-0.06, 0.04]	32.60	0.191	6.84E-01	0	0	0	0	RIT2
16	18:40673380	rs12456492	a	g	0.6355	0.0240	DEPR	DEPR_surv	1314	-0.028	0.084	0.97	[0.83, 1.15]	26.80	0.233	7.38E-01	0	0	0	0	RIT2
17	18:40673380	rs12456492	a	g	0.6387	0.0281	SEADL70	SEADL70_surv	1683	-0.017	0.094	0.98	[0.82, 1.18]	55.60	0.061	8.55E-01	0	0	0	0	RIT2
18	18:40673380	rs12456492	a	g	0.6335	0.0260	SEADL	SEADL_cont	2218	-0.042	0.243	-0.04	[-0.52, 0.43]	0.00	0.854	8.63E-01	0	0	0	0	RIT2
19	18:40673380	rs12456492	a	g	0.6402	0.0129	HY3	HY3_surv	2582	-0.011	0.066	0.99	[0.87, 1.13]	36.10	0.130	8.67E-01	0	0	0	0	RIT2
20	18:40673380	rs12456492	a	g	0.6425	0.0216	DYSKINESIAS	DYSKINESIAS_surv	1856	-0.009	0.059	0.99	[0.88, 1.11]	0.00	0.992	8.82E-01	0	0	0	0	RIT2
21	18:40673380	rs12456492	a	g	0.6326	0.0128	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.003	0.027	-0.00	[-0.06, 0.05]	10.80	0.346	9.04E-01	0	0	0	0	RIT2
22	18:40673380	rs12456492	a	g	0.6580	0.0221	INS	INS_surv	1112	-0.005	0.070	0.99	[0.87, 1.14]	0.00	0.938	9.38E-01	0	0	0	0	RIT2
23	8:22525980	rs2280104	t	c	0.6456	0.0186	MOTORFLUX	MOTORFLUX_base	1803	-0.005	0.084	1.00	[0.84, 1.17]	0.00	0.774	9.55E-01	0	0	0	0	RIT2
24	8:22525980	rs2280104	t	c	0.3768	0.0166	MOCA	MOCA_cont	1074	-0.205	0.123	-0.20	[-0.45, 0.04]	0.00	0.448	9.58E-02	0	0	0	0	GIN3
25	8:22525980	rs2280104	t	c	0.3801	0.0057	CONST	CONST_base	1472	-0.137	0.087	0.87	[0.74, 1.03]	0.00	0.967	1.17E-01	0	0	0	0	GIN3
26	8:22525980	rs2280104	t	c	0.3745	0.0236	DYSKINESIAS	DYSKINESIAS_surv	1856	0.080	0.060	1.08	[0.96, 1.22]	0.00	0.696	1.79E-01	0	0	0	0	GIN3
27	8:22525980	rs2280104	t	c	0.3603	0.0184	SEADL	SEADL_cont	2218	-0.320	0.240	-0.32	[-0.79, 0.15]	15.70	0.307	1.83E-01	0	0	0	0	GIN3
28	8:22525980	rs2280104	t	c	0.3772	0.0235	COGI	COGI_base	2859	0.118	0.089	1.13	[0.95, 1.34]	0.00	0.813	1.83E-01	0	0	0	0	GIN3
29	8:22525980	rs2280104	t	c	0.3745	0.0062	DYSKINESIAS	DYSKINESIAS_base	1232	0.122	0.102	1.13	[0.92, 1.38]	0.00	0.713	2.33E-01	0	0	0	0	GIN3
30	8:22525980	rs2280104	t	c	0.3752	0.0181	COGI	COGI_surv	2244	0.086	0.073	1.09	[0.94, 1.26]	22.00	0.248	2.42E-01	0	0	0	0	GIN3
31	8:22525980	rs2280104	t	c	0.3638	0.0229	SEADL70	SEADL70_surv	1683	0.109	0.095	1.12	[0.93, 1.34]	40.10	0.154	2.52E-01	0	0	0	0	GIN3
32	8:22525980	rs2280104	t	c	0.3771	0.0254	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.023	0.029	0.02	[-0.03, 0.08]	0.00	0.709	4.42E-01	0	0	0	0	GIN3
33	8:22525980	rs2280104	t	c	0.3679	0.0155	MOTORFLUX	MOTORFLUX_base	1803	-0.064	0.083	0.94	[0.80, 1.10]	0.00	0.429	4.44E-01	0	0	0	0	GIN3
34	8:22525980	rs2280104	t	c	0.3752	0.0275	UPDRS4_scaled	UPDRS4_scaled_cont	1798	-0.017	0.025	-0.02	[-0.07, 0.03]	0.00	0.705	5.12E-01	0	0	0	0	GIN3
35	8:22525980	rs2280104	t	c	0.3696	0.0184	DEPR	DEPR_surv	1314	0.044	0.080	1.05	[0.89, 1.22]	12.70	0.334	5.80E-01	0	0	0	0	GIN3
36	8:22525980	rs2280104	t	c	0.3858	0.0325	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.013	0.026	-0.01	[-0.06, 0.04]	0.00	0.880	6.20E-01	0	0	0	0	GIN3
37	8:22525980	rs2280104	t	c	0.3816	0.0206	HYPOSIMIA	HYPOSIMIA_base	1588	-0.039	0.082	0.96	[0.82, 1.13]	53.50	0.056	6.38E-01	0	0	0	0	GIN3
38	8:22525980	rs2280104	t	c	0.3807	0.0299	UPDRS_scaled	UPDRS_scaled_cont	2994	-0.010	0.024	-0.01	[-0.06, 0.04]	0.00	0.482	6.96E-01	0	0	0	0	GIN3
39	8:22525980	rs2280104	t	c	0.3829	0.0210	SLEEP	SLEEP_base	1724	0.024	0.085	1.02	[0.87, 1.21]	37.10	0.145	7.81E-01	0	0	0	0	GIN3
40	8:22525980	rs2280104	t	c	0.3779	0.0070	HY3	HY3_base	1289	0.027	0.116	1.03	[0.82, 1.29]	0.00	0.798	8.17E-01	0	0	0	0	GIN3
41	8:22525980	rs2280104	t	c	0.3727	0.0250	DEPR	DEPR_base	2138	0.017	0.091	1.02	[0.85, 1.22]	0.00	0.875	8.52E-01	0	0	0	0	GIN3
42	8:22525980	rs2280104	t	c	0.3781	0.0184	INS	INS_base	2220	-0.012	0.071	0.99	[0.86, 1.14]	0.00	0.969	8.62E-01	0	0	0	0	GIN3
43	8:22525980	rs2280104	t	c	0.3841	0.0071	INS	INS_surv	1112	-0.007	0.067	0.99	[0.87, 1.13]	0.00	0.806	9.12E-01	0	0	0	0	GIN3
44	8:22525980	rs2280104	t	c	0.3896	0.0274	HY	HY_cont	3627	0.000	0.009	-0.00	[-0.02, 0.02]	25.90	0.190	9.84E-01	0	0	0	0	GIN3
45	8:22525980	rs2280104	t	c	0.3728	0.0198	MOTORFLUX	MOTORFLUX_surv	1709	-0.001	0.050	1.00	[0.91, 1.10]	0.00	0.777	9.85E-01	0	0	0	0	GIN3
46	8:22525980	rs2280104	t	c	0.3737	0.0265	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.000	0.029	-0.00	[-0.06, 0.06]	0.00	0.806	9.93E-01	0	0	0	0	GIN3
47	8:22525980	rs2280104	t	c	0.3712	0.0211	MMSE	MMSE_cont	2114	0.000	0.046	-0.00	[-0.09, 0.09]	0.00	0.475	9.95E-01	0	0	0	0	GIN3
48	11:133787001	rs3802920	t	g	0.2152	0.0183	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.048	0.030	0.05	[-0.01, 0.11]	47.20	0.092	1.06E-01	0	0	0	0	IGSF9B
49	11:133787001	rs3802920	t	g	0.2189	0.0163	COGI	COGI_base	2859	0.155	0.101	1.17	[0.96, 1.42]	0.00	0.586	1.26E-01	0	0	0	0	IGSF9B
50	11:133787001	rs3802920	t	g	0.2157	0.0143	DYSKINESIAS	DYSKINESIAS_surv	1856	0.087	0.067	1.09	[0.96, 1.24]	0.00	0.802	1.91E-01	0	0	0	0	IGSF9B
51	11:133787001	rs3802920	t	g	0.2153	0.0119	MOTORFLUX	MOTORFLUX_surv	1709	-0.059	0.058	0.94	[0.84, 1.06]	0.00	0.568	3.10E-01	0	0	0	0	IGSF9B
52	11:133787001	rs3802920	t	g	0.2053	0.0157	SEADL	SEADL_cont	2218	-0.283	0.281	-0.28	[-0.83, 0.27]	0.00	0.729	3.15E-01	0	0	0	0	IGSF9B
53	11:133787001	rs3802920	t	g	0.2199	0.0205	HYPOSIMIA	HYPOSIMIA_base	1588	-0.094	0.094	0.91	[0.76, 1.09]	0.00	0.861	3.17E-01	0	0	0	0	IGSF9B</

1	14:75373034	rs3742785	a	c	0.7821	0.0134	HYPOSIMIA	HYPOSIMIA_base	1588	-0.038	0.096	0.96[0.80,1.16]	2.80	0.399	6.97E-01	0	0	0	0	0	RPS6KL1
2	14:75373034	rs3742785	a	c	0.7791	0.0201	DEPR	DEPR_surv	1314	-0.037	0.107	0.96[0.78,1.19]	0.00	0.917	7.34E-01	0	0	0	0	0	RPS6KL1
3	14:75373034	rs3742785	a	c	0.7877	0.0125	INS	INS_surv	1112	-0.029	0.087	0.97[0.82,1.15]	0.00	0.818	7.45E-01	0	0	0	0	0	RPS6KL1
4	14:75373034	rs3742785	a	c	0.7806	0.0196	MOCA	MOCA_cont	1074	-0.049	0.166	-0.05[-0.37,0.28]	43.50	0.150	7.70E-01	0	0	0	0	0	RPS6KL1
5	14:75373034	rs3742785	a	c	0.7837	0.0118	COGI	COGI_base	2859	-0.024	0.107	0.98[0.79,1.20]	0.00	0.870	8.21E-01	0	0	0	0	0	RPS6KL1
6	14:75373034	rs3742785	a	c	0.7810	0.0135	SLEEP	SLEEP_base	1724	-0.018	0.102	0.98[0.80,1.20]	0.00	0.907	8.61E-01	0	0	0	0	0	RPS6KL1
7	14:75373034	rs3742785	a	c	0.7838	0.0126	MMSE	MMSE_cont	2114	-0.007	0.057	-0.01[-0.12,0.10]	0.00	0.878	8.98E-01	0	0	0	0	0	RPS6KL1
8	14:75373034	rs3742785	a	c	0.7916	0.0037	SEADL70	SEADL70_surv	1683	-0.014	0.121	0.99[0.78,1.25]	0.00	0.998	9.07E-01	0	0	0	0	0	RPS6KL1
9	14:75373034	rs3742785	a	c	0.7834	0.0140	CONST	CONST_base	1472	-0.012	0.104	0.99[0.81,1.21]	0.00	0.412	9.09E-01	0	0	0	0	0	RPS6KL1
10	1:154898185	rs114138760	c	g	0.0194	0.0036	DEPR	DEPR_surv	1177	0.407	0.270	1.50[0.89,2.55]	0.00	0.998	1.31E-01	0	0	0	0	0	PMVK
11	1:154898185	rs114138760	c	g	0.0164	0.0037	MOTORFLUX	MOTORFLUX_surv	1709	0.271	0.186	1.31[0.91,1.89]	0.00	0.543	1.45E-01	0	0	0	0	0	PMVK
12	1:154898185	rs114138760	c	g	0.0156	0.0033	CONST	CONST_base	1355	0.501	0.355	1.65[0.82,3.31]	44.60	0.144	1.58E-01	0	0	0	0	0	PMVK
13	1:154898185	rs114138760	c	g	0.0153	0.0034	DEPR	DEPR_base	1683	0.579	0.422	1.78[0.78,4.08]	17.50	0.300	1.70E-01	0	0	0	0	0	PMVK
14	1:154898185	rs114138760	c	g	0.0142	0.0035	UPDRS2_scaled	UPDRS2_scaled_cont	1956	-0.137	0.133	-0.14[-0.40,0.12]	0.00	0.689	3.04E-01	0	0	0	0	0	PMVK
15	1:154898185	rs114138760	c	g	0.0178	0.0051	HY3	HY3_surv	1498	0.235	0.279	1.26[0.73,2.19]	41.90	0.142	4.00E-01	0	0	0	0	0	PMVK
16	1:154898185	rs114138760	c	g	0.0137	0.0041	DYSKINESIAS	DYSKINESIAS_base	1232	0.375	0.482	1.45[0.57,3.74]	0.00	0.846	4.37E-01	0	0	0	0	0	PMVK
17	1:154898185	rs114138760	c	g	0.0148	0.0035	MOTORFLUX	MOTORFLUX_base	1803	0.259	0.352	1.30[0.65,2.58]	0.00	0.928	4.61E-01	0	0	0	0	0	PMVK
18	1:154898185	rs114138760	c	g	0.0149	0.0029	DYSKINESIAS	DYSKINESIAS_surv	1656	0.165	0.233	1.18[0.75,1.86]	0.00	0.756	4.81E-01	0	0	0	0	0	PMVK
19	1:154898185	rs114138760	c	g	0.0154	0.0029	SEADL	SEADL_cont	1836	-0.694	1.020	-0.69[-2.69,1.31]	0.00	0.765	4.96E-01	0	0	0	0	0	PMVK
20	1:154898185	rs114138760	c	g	0.0164	0.0046	HY3	HY3_base	1289	-0.374	0.557	0.69[0.23,2.05]	0.00	0.870	5.02E-01	0	0	0	0	0	PMVK
21	1:154898185	rs114138760	c	g	0.0163	0.0034	SLEEP	SLEEP_base	1460	-0.240	0.374	0.79[0.38,1.64]	0.00	0.706	5.22E-01	0	0	0	0	0	PMVK
22	1:154898185	rs114138760	c	g	0.0143	0.0035	HY	HY_cont	3060	-0.026	0.040	-0.03[-0.10,0.05]	0.00	0.745	5.24E-01	0	0	0	0	0	PMVK
23	1:154898185	rs114138760	c	g	0.0141	0.0031	INS	INS_base	1854	0.181	0.320	1.20[0.64,2.24]	23.70	0.263	5.72E-01	0	0	0	0	0	PMVK
24	1:154898185	rs114138760	c	g	0.0160	0.0039	COGI	COGI_surv	2030	0.103	0.313	1.11[0.60,2.05]	0.00	0.975	7.41E-01	0	0	0	0	0	PMVK
25	1:154898185	rs114138760	c	g	0.0150	0.0034	UPDRS1_scaled	UPDRS1_scaled_cont	1964	-0.039	0.128	-0.04[-0.29,0.21]	34.10	0.180	7.62E-01	0	0	0	0	0	PMVK
26	1:154898185	rs114138760	c	g	0.0148	0.0036	UPDRS3_scaled	UPDRS3_scaled_cont	1997	-0.036	0.125	-0.04[-0.28,0.21]	0.00	0.465	7.74E-01	0	0	0	0	0	PMVK
27	1:154898185	rs114138760	c	g	0.0150	0.0033	COGI	COGI_base	2219	0.112	0.435	1.12[0.48,2.62]	0.00	0.890	7.97E-01	0	0	0	0	0	PMVK
28	1:154898185	rs114138760	c	g	0.0140	0.0033	UPDRS4_scaled	UPDRS4_scaled_cont	1651	0.027	0.114	0.03[-0.20,0.25]	0.00	0.671	8.10E-01	0	0	0	0	0	PMVK
29	1:154898185	rs114138760	c	g	0.0137	0.0033	UPDRS4_scaled	UPDRS4_scaled_cont	2730	0.025	0.110	0.03[-0.19,0.24]	16.40	0.301	8.20E-01	0	0	0	0	0	PMVK
30	1:154898185	rs114138760	c	g	0.0154	0.0028	MOCA	MOCA_cont	1026	-0.103	0.519	-0.10[-1.12,0.91]	14.60	0.310	8.42E-01	0	0	0	0	0	PMVK
31	1:154898185	rs114138760	c	g	0.0141	0.0040	MMSE	MMSE_cont	1850	-0.040	0.203	-0.04[-0.44,0.36]	42.00	0.125	8.44E-01	0	0	0	0	0	PMVK
32	1:154898185	rs114138760	c	g	0.0158	0.0034	HYPOSIMIA	HYPOSIMIA_base	1334	-0.034	0.386	0.97[0.45,2.06]	0.00	0.522	9.29E-01	0	0	0	0	0	PMVK
33	1:154898185	rs114138760	c	g	0.0142	0.0020	SEADL70	SEADL70_surv	1683	-0.014	0.375	0.99[0.47,2.06]	0.00	0.959	9.70E-01	0	0	0	0	0	PMVK
34	1:23326598	rs10847864	t	g	0.3732	0.0205	INS	INS_surv	1112	0.097	0.067	1.10[0.97,1.26]	0.00	0.618	1.48E-01	0	0	0	0	0	HIP1R
35	1:23326598	rs10847864	t	g	0.3696	0.0237	SLEEP	SLEEP_base	1724	0.118	0.087	1.13[0.95,1.33]	0.00	0.425	1.72E-01	0	0	0	0	0	HIP1R
36	1:23326598	rs10847864	t	g	0.3770	0.0204	SEADL70	SEADL70_surv	1683	-0.124	0.094	0.88[0.73,1.06]	0.00	0.872	1.90E-01	0	0	0	0	0	HIP1R
37	1:23326598	rs10847864	t	g	0.3878	0.0222	SEADL	SEADL_cont	2112	0.308	0.240	0.31[-0.16,0.78]	37.80	0.141	1.99E-01	0	0	0	0	0	HIP1R
38	1:23326598	rs10847864	t	g	0.3810	0.0263	HY	HY_cont	3627	-0.011	0.009	-0.01[-0.03,0.01]	0.00	0.959	2.06E-01	0	0	0	0	0	HIP1R
39	1:23326598	rs10847864	t	g	0.3738	0.0226	INS	INS_base	2220	0.089	0.073	1.09[0.95,1.26]	8.30	0.366	2.25E-01	0	0	0	0	0	HIP1R
40	1:23326598	rs10847864	t	g	0.3780	0.0266	UPDRS3_scaled	UPDRS3_scaled_cont	2446	-0.030	0.027	-0.03[-0.08,0.02]	0.00	0.506	2.65E-01	0	0	0	0	0	HIP1R
41	1:23326598	rs10847864	t	g	0.3784	0.0267	UPDRS4_scaled	UPDRS4_scaled_cont	1798	0.025	0.026	0.02[-0.03,0.08]	43.30	0.117	3.39E-01	0	0	0	0	0	HIP1R
42	1:23326598	rs10847864	t	g	0.3795	0.0291	COGI	COGI_surv	2244	-0.071	0.079	0.93[0.80,1.09]	34.90	0.139	3.67E-01	0	0	0	0	0	HIP1R
43	1:23326598	rs10847864	t	g	0.3662	0.0206	HYPOSIMIA	HYPOSIMIA_base	1588	-0.072	0.083	0.93[0.79,1.10]	0.00	0.615	3.91E-01	0	0	0	0	0	HIP1R
44	1:23326598	rs10847864	t	g	0.3619	0.0116	HY3	HY3_base	1289	-0.109	0.123	0.90[0.71,1.15]	0.00	0.466	4.11E-01	0	0	0	0	0	HIP1R
45	1:23326598	rs10847864	t	g	0.3855	0.0286	MOCA	MOCA_cont	1074	0.071	0.123	0.88[-0.16,0.32]	7.90	0.354	5.22E-01	0	0	0	0	0	HIP1R
46	1:23326598	rs10847864	t	g	0.3638	0.0165	COGI	COGI_base	2859	0.046	0.089	1.05[0.88,1.25]	0.00	0.972	6.09E-01	0	0	0	0	0	HIP1R
47	1:23326598	rs10847864	t	g	0.3845	0.0228	DEPR	DEPR_base	2138	-0.047	0.094	0.95[0.79,1.15]	14.00	0.321	6.21E-01	0	0	0	0	0	HIP1R
48	1:23326598	rs10847864	t	g	0.3698	0.0208	CONST	CONST_base	1472	-0.037	0.088	0.96[0.81,1.15]	0.00	0.831	6.74E-01	0	0	0	0	0	HIP1R
49	1:23326598	rs10847864	t	g	0.3834	0.0275	UPDRS1_scaled	UPDRS1_scaled_cont	2111	0.007	0.030	0.01[-0.05,0.07]	49.10	0.067	8.09E-01	0	0	0	0	0	HIP1R
50	1:23326598	rs10847864	t	g	0.3877	0.0319	DEPR	DEPR_surv	1314	0.018	0.080	1.02[0.87,1.19]	20.20	0.281	8.23E-01	0	0	0	0	0	HIP1R
51	1:23326598	rs10847864	t	g	0.3687	0.0127	DYSKINESIAS	DYSKINESIAS_base	1232	0.016	0.107	1.02[0.82,1.25]	59.30	0.086	8.79E-01	0	0	0	0	0	HIP1R
52	1:23326598	rs10847864	t	g	0.3733	0.0259	HY3	HY3_surv	2582	0.010	0.066	1.01[0.89,1.15]	44.10	0.074	8.79E-01	0	0	0	0	0	HIP1R
53	1:23326598	rs10847864	t	g	0.3816	0.0227	MOTORFLUX	MOTORFLUX_surv	1709	0.006	0.050	1.01[0.91,1.11]	0.00	0.940	9.07E-01	0	0	0	0	0	HIP1R
54	1:23326598	rs10847864	t	g	0.3738	0.0162	MOTORFLUX	MOTORFLUX_base	1803	0.009	0.086	1.01[0.85,1.19]	0.00	0.568	9.21E-01	0	0	0	0	0	HIP1R
55	1:23326598	rs10847864	t	g	0.3944	0.0218	MMSE	MMSE_cont	2114	0.001	0.045	0.00[-0.09,0.09]	21.50	0.259	9.90E-01	0	0	0	0	0	HIP1R
56	1:23326598	rs10847864	t	g	0.3816	0.0285	UPDRS2_scaled	UPDRS2_scaled_cont	2103	0.000	0.030	-0.00[-0.06,0.06]	15.90	0.309	9.93E-01	0	0	0	0	0	HIP1R
57	1:23326598	rs10847864	t	g	0.3806	0.0285	UPDRS4_scaled	UPDRS4_scaled_cont	2994	0.000	0.024	-0.00[-0.05,0.05]	0.00	0.442	9.96E-01	0	0	0	0	0	HIP1R
58	1:205737739	rs11557080	a	g	0.1349	0.0111	COGI	COGI_surv	2244	-0.164	0.115	0.85[0.68,1.06]	0.00	0.945	1.54E-01	0	0	0	0	0	RAB29
59	1:205737739	rs11557080	a	g	0.1443	0.0245	DEPR	DEPR_base	2138	-0.175	0.134	0.84[0.6									

Supplemental Table 5 The Estimated Study Size to Detect at Least One Variant with Genome-wide Significance

Phenotype	Top_SNP	A1	A2	MAF	BETA	SE	P	N	N_Multiplier	N_required	Sig_in_1.3_larger_N
base_HYPOSMIA	1:56034603	C	A	0.119	0.570	0.118	1.49E-06	1588	1.30	2064	TRUE
base_MOTORFLUX	2:170778662	C	G	0.143	0.734	0.162	6.08E-06	1568	1.48	2325	FALSE
base_SLEEP	17:27353069	A	G	0.188	0.592	0.118	5.56E-07	1724	1.20	2062	TRUE
base_HY3	2:232324780	A	G	0.349	0.610	0.122	5.71E-07	1289	1.20	1545	TRUE
base_CONST	2:18336194	A	G	0.269	0.479	0.097	8.59E-07	1472	1.24	1825	TRUE
base_INS	10:112956055	A	G	0.318	-0.455	0.083	4.74E-08	2220	1.00	2212	TRUE
base_DYSKINESIAS	1:182045339	C	G	0.066	0.898	0.212	2.25E-05	1232	1.70	2100	FALSE
base_DEPR	17:33680811	A	C	0.164	0.554	0.114	1.22E-06	2138	1.28	2730	TRUE
base_COGi	8:116961224	A	G	0.080	1.013	0.190	9.77E-08	1538	1.05	1612	TRUE
cont_HY	10:27370747	G	A	0.063	0.098	0.020	8.68E-07	3627	1.24	4501	TRUE
cont_SEADL	11:88031232	C	T	0.299	1.469	0.281	1.74E-07	2218	1.09	2424	TRUE
cont_UPDRS	6:25370200	T	G	0.050	0.486	0.101	1.41E-06	1792	1.29	2318	TRUE
cont_UPDRS4_scaled	10:90420315	T	G	0.240	0.201	0.041	1.14E-06	1798	1.27	2283	TRUE
cont_UPDRS2_scaled	19:17340155	A	G	0.074	0.294	0.060	9.66E-07	2301	1.25	2881	TRUE
cont_MMSE	6:2977327	A	G	0.056	-0.709	0.135	1.51E-07	1066	1.08	1153	TRUE
cont_UPDRS3_scaled	5:60307904	G	A	0.409	0.149	0.031	1.09E-06	2822	1.27	3570	TRUE
cont_UPDRS_scaled	12:129483261	T	C	0.139	-0.298	0.058	2.96E-07	1108	1.14	1261	TRUE
cont_MOCA	14:54619316	C	T	0.188	-0.937	0.199	2.61E-06	1074	1.37	1468	FALSE
surv_SEADL70	22:50944128	A	G	0.288	0.488	0.103	2.03E-06	1683	1.34	2249	FALSE
surv_MOTORFLUX	8:142310903	T	G	0.134	0.431	0.087	6.21E-07	1709	1.21	2062	TRUE
surv_HY3	9:108058562	A	T	0.075	0.711	0.129	3.46E-08	1890	0.98	1844	TRUE
surv_INS	2:241442030	T	C	0.060	0.703	0.144	9.75E-07	1112	1.25	1393	TRUE
surv_DYSKINESIAS	12:121627464	A	T	0.068	0.509	0.100	3.76E-07	1856	1.16	2151	TRUE
surv_DEPR	14:52568619	C	T	0.095	0.640	0.127	4.66E-07	1395	1.18	1645	TRUE
surv_COGi	21:17309623	G	C	0.083	0.912	0.170	7.76E-08	1132	1.03	1167	TRUE

Top_SNP, the SNP with the smallest p-value;

Multiplier, Multiplier of the N to have enough power to detect the Top_SNP at the significance level of 5E-8;

N_required, The total number required to detect the Top_SNP at the significance level of 5E-8;

Sig_in_1.3_larger_N, Whether or not obtaining at least one genome-wide significant variant for that phenotype if the N was 1.3 times larger;

base, logistic regression model at the baseline; surv, Cox survival model; cont, linear mixed effect model

CONST, constipation; COGi, cognitive impairment; INS, insomnia; SLEEP, daytime sleepiness; MOTORFLUX, motor fluctuations; HY3, Hoehn Yahr scale 3 or greater; RBD, REM sleep behavior disorder; DEPR, depression; MMSE, Mini Mental State Examination; Montreal Cognitive Assessment, SEADL, Schwab and England Activities of Daily Living Scale; UPDRS, Unified Parkinson Disease Rating Scale; MDS-UPDRS, Movement Disorder Society revised version of UPDRS."

Appendix A: The description of study cohorts

Deprenyl and Tocopherol Antioxidative Therapy of Parkinsonism (DATATOP) was a randomized clinical trial conducted between September 1987 and November 1989 at 28 sites across US and Canada. The primary objective was to test the efficacy of deprenyl and/or tocopherol. 800 patients with Parkinson's disease diagnosed within 5 years and not requiring symptomatic treatment were observed for up to 2 years.¹ The study was supported by a Public Health Service grant (NS24778) from the National Institute of Neurological Disorders and Stroke; by grants from the General Clinical Research Centers Program of the National Institutes of Health at Columbia University (RR00645), the University of Virginia (RR00847), the University of Pennsylvania (RR00040), the University of Iowa (RR00059), Ohio State University (RR00034), Massachusetts General Hospital (RR01066), the University of Rochester (RR00044), Brown University (RR02038), Oregon Health Sciences University (RR00334), Baylor College of Medicine (RR00350), the University of California, San Diego (RR00827), Johns Hopkins University (RR00035), the University of Michigan (RR00042), and Washington University (RR00036); the Parkinson's Disease Foundation at Columbia-Presbyterian Medical Center, New York; the National Parkinson Foundation, Miami; the Parkinson Foundation of Canada, Toronto; the United Parkinson Foundation, Chicago; the American Parkinson's Disease Association, New York; and the University of Rochester, Rochester, N.Y.

Drug Interaction with Genes in Parkinson's Disease (DIGPD) is a cohort with 413 patients with Parkinson's disease diagnosed by UK Parkinson's disease society brain bank clinical diagnostic (UKPDSBB) criteria with disease duration less than 5 years at the entry.² It is an ongoing study since 2009, and the participants are followed for up to 7 years at eight sites in France. (Corvol et al., in press in *Neurology*). DNA samples were collected from all of them. DIGPD is sponsored by Assistance Publique Hôpitaux de Paris, funded by a grant from the French Ministry of Health (PHRC 2008, AOM08010) and a grant from the Agence Nationale pour la Sécurité des Médicaments (ANSM 2013).

Harvard Biomarkers Study (HBS) is a longitudinal case-control study. More than 2,700 individuals with early-stage PD, patients with memory impairment, and controls without

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3 neurological disease were enrolled and longitudinally phenotyped since 2008.³ HBS was
4 supported by the Harvard NeuroDiscovery Center, MJFF, NINDS U01NS082157,
5 U01NS100603, and the Massachusetts Alzheimer's Disease Research Center NIA
6 P50AG005134.
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10 NIH Exploratory Trials in Parkinson's Disease Large Simple Study 1 (NET-PD LS1) was a
11 randomized study conducted between March 2007 and September 2013 to determine if the
12 nutritional supplement creatine slows the clinical progression of Parkinson's disease over time.
13 1741 patients from 50 sites in the US and Canada participated.⁴ They were within 5 years from
14 diagnosis. The plan was for them to be followed for at least 5 years, but the study ended early for
15 futility based on an interim analysis at which point the median follow-up time was 4 years.
16 Financial support for the LS-1 study was provided by National Institute of Neurological
17 Disorders and Stroke (NINDS) grant U01NS43128.
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24 Oslo PD study[Citation error] (Oslo) is an ongoing study since 2007, with 317 patients
25 diagnosed with ULPDSBB criteria with modification of allowing family history. The participants
26 are being followed up to 6 years in prospective (30 years in retrospective) at Oslo University
27 Hospital in Norway.⁵ Oslo PD is supported by the Research Council of Norway and South-
28 Eastern Norway Regional Health Authority.
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32 ParkFit cohort was originally a randomized trial evaluating a multifaceted behavioural change
33 programme to increase physical activities in patients with Parkinson's disease.⁶ The study
34 conducted from September 2008 to February 2012 at a single center in the Netherlands, with 586
35 patients with Parkinson's disease diagnosed by UKPDSBB, with Hoehn Yahr stage 3 or lower,
36 and with sedentary lifestyle at the entry. They were followed up for 2 years. The primary
37 objective was concluded as not significant⁶. ParkFit is supported by ZonMw (the Netherlands
38 Organization for Health Research and Development (75020012)) and the Michael J Fox
39 Foundation for Parkinson's research, VGZ (health insurance company), GlaxoSmithKline, and
40 the National Parkinson Foundation.
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48 The Norwegian ParkWest study (ParkWest) is an ongoing prospective longitudinal multicenter
49 cohort study of patients with incident Parkinson's disease from Western and Southern Norway,
50 designed to study the incidence, neurobiology and prognosis of PD.⁷ Between November 1st
51 2004 and 31st of August 2006, all new cases of Parkinson Disease within the study area (Sogn
52 and Fjordane, Hordaland, Rogaland and Aust-Agder) were recruited, and since the start of the
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3 study 212 of these patients and their age-/sex-matched control group were followed. The
4 Norwegian ParkWest study is supported by the Research Council of Norway, the Western
5 Norway Regional Health Authority, Stavanger University Hospital Research Funds, and the
6 Norwegian Parkinson's Disease Association.
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10 The National Institute of Neurological Disorders and Stroke (NINDS) Parkinson's Disease
11 Biomarker Program (PDBP) is aiming to discover new diagnostic and progression biomarkers
12 for Parkinson's disease.⁸ It is a combined cohort of 9 PDBP-funded research studies. The
13 members have various stages of Parkinson's disease and recruited throughout the United States.
14
15 Parkinsonism: Incidence and Cognitive and Non-motor heterogeneity In Cambridgeshire
16 (PICNICS) is a population-based longitudinal study of 282 incident PD cases recruited between
17 2008 and 2013 with ongoing follow-up at 18 month intervals.^{9,10} PD cases were diagnosed based
18 on the UKPDSBB criteria, and followed up at a single center in the UK. PICNICS has received
19 funding from the Cure Parkinson's Trust, the Van Geest Foundation and is supported by the the
20 National Institute of Health Research Cambridge Biomedical Research Centre.
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27 Parkinson's progression markers initiative (PPMI) is an ongoing study started on July 2010,
28 enrolling 424 patients with Parkinson's disease diagnosed within 2 years from the study entry
29 date.¹¹ The study sites are located in 33 sites across the US, Europe, Israel and Australia¹¹. PPMI
30 is supported by the Michael J Fox Foundation for Parkinson's Research.
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34 Parkinson Research Examination of CEP1348 Trial (PreCEPT) is a clinical trial of the mixed
35 lineage kinase inhibitor CEP-1357,4 sponsored by Cephalon, Inc. (West Chester, PA) and H.
36 Lundbeck A/S (Valby-Copenhagen, Denmark). The study was conducted at 65 sites in North
37 America. The trial enrolled 806 early, untreated PD patients within one year from the onset. The
38 original trial was started in April 2002 and terminated in August 2005 due to the futility, but the
39 participants were continuously followed-up in the prospective observational study (PostCEPT).¹²
40
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3 Profiling Parkinson's disease study (ProPark) is an ongoing study started from May 2003.
4 Initially, 420 patients recruited in several sites in the Netherlands by March 2006.¹³ Patients were
5 diagnosed with UKPDSBB criteria and in various disease durations at the enrollment. They are
6 evaluated annually with the SCOPA scale. This study is funded by the Alkemade-Keuls
7 Foundation, Stichting Parkinson Fonds, Parkinson Vereniging, The Netherlands Organisation for
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