Supplementary Information

Genome-Wide Association Study reveals genetic risk underlying Parkinson's disease

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Supplementary Note

Stage I Subjects
US cohort
The total number of cases and controls from the United States included in stage I of this project was 4,134, comprising 1,063 cases and 3,071 controls.
PD samples: 988 of the patients were derived from the NINDS-funded Neurogenetics Repository at the Coriell Institute for Medical research (Camden, NJ, USA, www.coriell.org). Samples from the precompiled panels NDPT001, NDPT005, NDPT007, NDPT014, NDPT015, NDPT016, NDPT017 and NDPT018, as well as 250 non-paneled samples, were included in the experiments. In addition, 75 PD cases collected by a movement disorders specialist in the Laboratory of Neurogenetics were also included (KG).
All patients were Caucasian individuals with idiopathic Parkinson's disease from the United States. The mean age at onset of the parkinsonian syndrome was 55.91 years, ranging from 7 to 98 years. Age at onset was defined as the time when symptom(s) of PD were first noted (including at least one: resting tremor, rigidity, bradykinesis, gait disorder, postural instability). Coriell Institute samples required complete NINDS Repository Clinical Data Elements, in order to be included. According to those criteria, all subjects had bradykinesia, and at least one of the following: muscular rigidity, 4-6 Hz resting tremor, postural instability (not caused by primary visual, vestibular, cerebellar, or proprioceptive dysfunction). None had exclusionary features. All had documentation of sustained, excellent response to anti-parkinsonian therapy.
Informed consent was obtained for every participant under locally approved protocols. All subjects were queried regarding family history of parkinsonism, dementia, tremor, gait disorders, and other neurological dysfunction. Subjects with and without family history of Parkinson's disease were included in this panel. However, patients with three or more relatives with parkinsonism or with an apparent Mendelian inheritance of PD were excluded.
Coriell Institute neurologically normal controls: Samples included in precompiled panels NDPT002, NDPT006, NDPT009, NDPT019, NDPT020, NDPT021, NDPT022, NDPT023 and NDPT024 were used for this study, leading to a total of 828 control individuals. All individuals are reported to be unrelated Caucasians free from any neurological disorders. All individuals were asked specifically regarding the following disorders: Alzheimer's disease, amyotrophic lateral sclerosis, ataxia, autism, bipolar disorder, cerebrovascular disease, dementia, dystonia, Parkinson's disease, and schizophrenia. None had any first-degree relative with a known primary neurological disorder. The mean age of participants was 58 years, ranging from 15 to 98 years. For more information about controls and PD cases from the Coriell institute see http://ccr.coriell.org.
CGEMS initiative controls: The Cancer Genetic Markers of Susceptibility initiative (CGEMS, Bethesda, USA, http://cgems.cancer.gov/) is a three-year, $14 million initiative aiming to identify genetic alterations that make individuals susceptible to prostate and breast cancer, funded by the National Cancer Institute. For this purpose they have collected not only cancer patients, but also 1,101 male

and 1,142 female controls. Genotyping data from all these 2,243 control samples was generously shared by the National Cancer Institute and included in our study.

German cohort
The German cohort consisted of 757 PD cases and 976 population based controls from the KORA and POPGEN surveys.
PD samples: The PD cases were collected by movement disorders specialists of the Universities of Munich and Tuebingen, who established the diagnosis according to the UK Brain Bank criteria[1]. The mean age at onset was 56 years, ranging from 28 to 86 years. Both patients with and without a reported family history of Parkinson's disease were included in this panel. However, cases showing clear evidence of dominant inheritance were excluded. In the German cohort 20% reported a family history of PD. All samples and data were collected with informed consent under locally approved protocols.
KORA survey controls: 488 control individuals were selected from the KORA survey (Cooperative Health Research in the Region of Augsburg, www.helmholtz-muenchen.de/kora), a population based study holding more that 18,000 individuals representative of the general population living in or near the region of Augsburg, Germany. All 488 samples were recruited from the KORA F3 survey in which a total of 3,006 subjects were studied in 2005. The age at sampling ranges from 34 to 84 years[2,3].
POPGEN survey controls: 488 healthy control individuals were collected by the 'Population Based Assessment of Genetic Risk Factors' (POPGEN) - Project (www.popgen.de), an on-going cross-sectional epidemiological survey of the population in the most northern part of Germany with Kiel Canal as the southern border. The region covers 1.1 Mio inhabitants. The control individuals were identified through the official population registry of the state of Schleswig-Holstein and were assessed by trained physicians to exclude neurological and other disorders in particular PD[4].

Stage II subjects
For our replication stage, we included a total of 8,208 Caucasian individuals (3,452 cases and 4,756controls), originally from the United Kingdom (824 cases and 7 controls), North America (1,528 cases and 2,044 controls) and Germany (1,100 cases and 2,168 controls). A brief description of these samples is listed below and in table 1 of the main text:

US cohort
Coriell PD samples: A total of 207 PD samples that where not available at the time of the Stage I genotyping execution where included in the replication stage. These included 140 males and 65 females from the United States. The age of PD onset ranges from 16 to 80 years with a mean of 54.6 years, defined as when symptom(s) of PD were first noted (including at least one: resting tremor, rigidity, bradykinesis, gait disorder, postural instability).
The Parkinson's Genes and Environment Study (*PAGE) samples:* These include 840 PD cases (643 males and 196 females) and 1700 controls (1329 males and 371 females) identified from a large population-based cohort. Cases were initially identified by self-reported with subsequent verification with patients treating neurologist. The age of onset ranges from 42 to 78 (average 65.8±7.4).
Washington University at St. Louis: Patients and spouse controls were recruited consecutively from the Movement Disorders Center at Washington University in St. Louis. PD diagnosis was made using the UK Brain Bank criteria[1]. All controls had normal neurologic examinations. This included 818 samples including 481 (299 males and 182 females) cases and 337 controls (118 males, 219 females).

UK cohort
824 cases were included, comprising 466 neuropathologically diagnosed PD cases and 358 clinically diagnosed PD cases. The male to female ratio was 3.5:1, age at onset ranged from 28:86 years (mean 59 years). Diagnosis was made using the UK Brain Bank criteria (Hughs et al, 1992). Additionally, 544 healthy controls were also collected. Male to female ratio was 0.57.

German cohort
1323 German controls were selected from the population-based KORA cohort described in stage I. Additionally, sample collection of 793 German controls was performed as part of the "Prospective validation of risk markers for the development of idiopathic Parkinson's disease (PRIPS)" study a longitudinal cohort study in Tuebingen. For this study participants were recruited using two main sources: advertisement in local newspapers, and employees from local companies. Inclusion criteria of this longitudinally designed study were age older than 50 years and no diagnosis of PD. Moreover, 62 German controls were either recruited as spouse controls or through advertisements in the clinic or local press at the movement disorder outpatient clinics at the Departments of Neurology at the

Universities of Luebeck, Germany. All underwent a detailed neurological and movement disorders examination.
607 patients with PD were recruited within the 'POPGEN Parkinson's Disease' - Project (POPGEN-PD). All patients were identified through the data-bases and charts office-based neurologists or neurological hospitals in the popgen region. Only patients fulfilling the British Brain Bank criteria[1] were included. They were contacted by mail and asked for their participation. The protocol was approved by the local ethical committees. 286 German sporadic and familial PD patients were recruited at two university clinics for neurology in Bochum and Tuebingen. All patients were evaluated by a neurologist experienced in movement disorders and were diagnosed as idiopathic PD, based on the UK Parkinson's disease brain bank criteria. 163 cases were collected by movement disorders specialists of the Universities of Munich and Tuebingen, who established the diagnosis according to the UK Brain Bank criteria[1]. Both patients with and without a reported family history of Parkinson's disease were included in this panel. However, cases showing clear evidence of dominant inheritance were excluded. 52 German patients were recruited at the movement disorder outpatient clinics at the Department of Neurology at the University of Luebeck, Germany. Consecutive patients willing to participate were included in the study. All patients underwent a detailed neurological and movement disorders examination.
All subjects gave written informed consent. The study including DNA collection was approved by the local ethical committees.

Stage I genotyping

US cohort
Genotyping of the DNA panels NDPT014, NDPT015, NDPT016, NDPT017, NDPT018, NDPT019, NDPT020, NDPT021, NDPT022, NDPT023, NDPT024, and those 252 non-paneled from the Coriell Institute was performed using HumanHap550 version 3 beadchips, attempting to genotype 555,363 SNPs. The samples collected by the Laboratory of Neurogenetics in Bethesda were assayed with HumanHap550 version 1 beadchips, attempting to genotype 561,467 SNPs. Samples from the Coriell Institute within DNA panels NDPT001, NDPT002, NDPT005, NDPT006, NDPT07 and NDPT009 had previously been genotyped with HumanHap300 beadchips[6]. For the present study these samples were additionally assayed with HumanHap240S beadchips, to provide (combined) the same genotype information as the HumanHap550 version 1 beadchips. The CGEMS controls were also genotyped with HumanHap300 and HumanHap240S beadchips. Using these genotyping platforms, 545,066 unique SNPs were genotyped for each sample of our cohort.

German cohort
Genotyping of all samples was performed with HumanHap550 version 1 beadchips, attempting to genotype 561,467 SNPs. Samples were assayed at three different sites (GSF, Munich, Germany; Illumina, SanDiego, USA; Dept. of Medical Genetics, Tuebingen, Germany). To assess the accuracy of genotyping, Eleven samples were genotyped in duplicates across all batches. The concordance rate of all duplicates was 99.99%, assuring high genotype accuracy.

Stage I quality control procedures
Although it provides the opportunity to scan the whole genome in a relative short period of time, the microarray based sequencing approach also has a major problem: the high rate of false positive results. Thus, eliminating any systematic bias like population stratification (existing when the case and control groups are not well-matched genetically or if several distinct, but unrecognized, sub-populations exist in a cohort) is required to minimize the rate of false positives. All statistical analyses were performed using PLINK[7].

US cohort
Low quality genotyping: Samples with call rates below 95% were repeated using fresh DNA aliquots and if the call rate persisted below this level, the samples were excluded from the analysis. Low-quality genotyping led us to repeat 57 individual samples, of which 41 were ultimately excluded from the analysis, including 16 cases and 25 controls.
Gender ambiguity: Individuals with gender ambiguity were flagged based on heterozygosity on chromosome X genotypes (inbreeding coefficient [F] in this chromosome). A male call is made if F is more than 0.8 and a female call if F is less than 0.2. Samples with an ambiguous F score or discrepancies between genotyped and reported sex, were considered as problematic. These samples were analyzed by visual examination of log R ratio and B allele frequency metrics with the Illumina Genome Viewer (IGV) tool within BeadStudio to rule out whether this discrepancy was caused

because of copy number variation or extended homozygosity in chromosome X. These analyses led to the exclusion of 15 samples, including 11 cases and 4 controls.
Population substructure: In an attempt to detect the presence of population substructure or ethnically mismatched individuals, pairwise Identity By State (IBS) distances were calculated. Consequently, IBS distance to its "nearest neighbor" was calculated for each individual in our cohort along with 30 trios from Yoruba (Nigeria), 45 unrelated individuals from the Tokyo area in Japan, 45 unrelated individuals from Beijing (China) and 30 US-resident trios with Northern and Western European ancestry from the Centre d'Etude du Polymorphisme Humain (CEPH, Paris, France); data downloaded from the HapMap website (www.hapmap.org). This distribution was standardized (by the sample mean and variance of nearest neighbor) and inspected for outliers. For this last purpose Multidimensional scaling (MDS) was performed. This analysis showed that except for three individuals with genetic background indicative of African ancestry. These samples were removed from further analysis. The remaining samples clearly shared Caucasian ancestry (supplementary figure 1).
Non-reported relatedness: The pairwise clustering based on IBS distances (see previous section) is useful for making estimations of pairwise Identity by Descent (IBD) to find pairs of individuals who look more similar than expected by chance, in a random sample. By estimating the probability of sharing 0, 1, or 2 alleles IBD for any two individuals, a proportion of IBD can be calculated (PI-HAT = P [IBD = 2] + 0.5 x P [IBD = 1]). Using 0.2 as a threshold for PI-HAT, 17 sample pairs were considered too similar to each other. Thus, one member of each pair was removed from further SNP association tests (11 cases and 6 controls). Additionally, PI-HAT data revealed 50 replicates within our dataset including 49 cases and one control. All these samples were also dropped from further analysis.
After this extensive quality-control phase, the final number of fully genotyped samples from the United States was 4,005 including 971 cases and 3,034 controls.
SNP quality control: Only those SNPs successfully genotyped in at least 95% of our final set of samples (18,579 SNPs removed) as well as those with a minimum allele frequency (MAF) above 5% (50,758 SNPs removed) and with no extreme departure from Hardy-Weinberg equilibrium (HWE) in controls ($p > 0.01$; 9,043 SNPs removed) were included in our Stage I statistical analyses. These procedures gave us a total of 474,995 SNPs in the US cohort.

German cohort
Low quality genotyping: Any sample with a call rate below 95% was excluded from the analysis. This led us to exclude 18 samples from the analysis (4 cases and 14 controls).
Gender ambiguity: Heterozygosity on chromosome X was used to detect gender discrepancies in our sample. Three individuals (2 cases and 1 control) were identified in which ambiguity could not be resolved, thus they were removed from further analysis. Moreover, we assessed the heterozygosity on all autosomes in our population. Excess of heterozygosity reflects genotyping error or contamination of the sample. We excluded 11 individuals (5 cases and 6 controls), which showed more than 4 standard deviations from the sample mean.
Population substructure: Population structure was assessed based upon the genome wide average proportion of alleles shared identical by state between two individuals. An agglomerative procedure is used to cluster the individuals into homogenous subsets. IBS distances were calculated between all study subjects and additional individuals, for whom genotype data was downloaded from the HapMap. These individuals originated from Nigeria, China, Japan and the United States with European ancestry. Visualization of sub-structuring in our population was done by the multi-dimensional scaling (MDS) approach, implemented in PLINK[7]. Inspection of the MDS plot (supplementary figure 2) led us to further exclude 6 individuals from our analysis (3 cases and 3 controls).
Non-reported relatedness: We excluded close relatives based on IBD estimates. Nine samples were identified as 1st and 2nd degree relatives and excluded from further analyses (1 case and 8 controls). After applying the stringent filtering criteria as described above, 1686 samples were included in the statistical analyses (742 cases and 944 controls).
SNP quality control: Only those SNPs genotyped in at least 95% of our final set of samples (5,387 SNPs removed) as well as those with a minimum allele frequency (MAF) above 5% (51,834 SNPs removed) and with no extreme departure from Hardy-Weinberg equilibrium (HWE) in controls ($p>0.01$; 5,685 SNPs removed) were included in our Stage I statistical analyses. These procedures gave us a total of 498,560 SNPs in the German cohort.

Combined cohort
Genotyping results obtained for both the US and the German populations were merged and a further quality control step was taken. This included the removal of SNPs that presented a MAF below 5% (589 SNPs removed), or a genotyping rate below 95% (42,169 SNPs removed) or extreme deviation from HWE ($p<0.01$) (2,463 SNPs removed). These filters were applied to the combined controls and flagged SNPs were removed from the complete combined cohort. This led us to obtain a total of

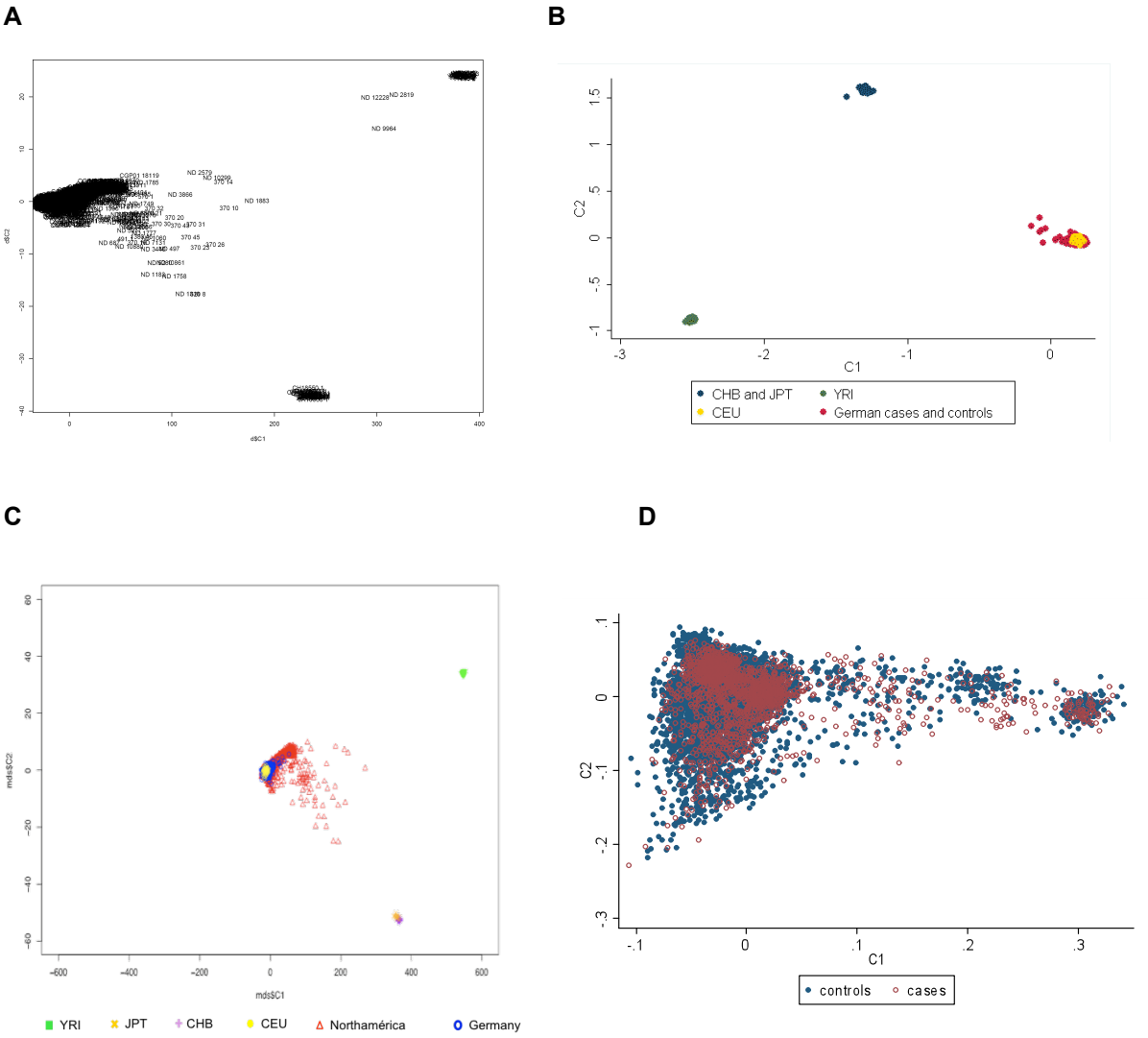
463,185 unique SNPs genotyped in 5,691 individuals (including 1,713 cases and 3,978 controls). Although the evidence generated so far supports the idea that population effects are unlikely to mask association or produce false positives when pooling white northern European and North American populations[8], we reassessed the effect of population structuring in our cohort. Therefore, pair wise Identity by State (IBS) distances were re-calculated for all 5,691 individuals in our cohort with the same procedure as mentioned above. This distribution was standardized (by the sample mean and variance of nearest neighbor) and inspected visually for outliers with a multidimensional scale plot (MDS). As expected, our observation showed that our cohort clearly shared common Caucasian ancestry as shown in supplementary figure 3. Hereafter, we describe the US and the German cohort as combined cohort.

Stage I secondary analyses
To further confirm that the potential population substructure detected (lambda = 1.17) was not biasing the results obtained in the stage I of our experiments, logistic regression models adjusted for the two principal components of the MDS values after pair-wise IBS were applied. To overcome the confounding of the clustering caused by LD, the components were based on a LD-pruned SNP dataset that was analyzed via MDS in cases and controls for US and German samples separately. This approach revealed a genomic inflation factor (based on median chi-squared) of 1.09116 in the German cohort (mean chi-squared statistic of 1.0992). For the US samples, the genomic inflation factor (based on median chi-squared) was 1.22095 and the mean chi-squared statistic was of 1.24298. The combined genomic inflation factor after genomic control from meta-analysis was 1.067. Application of this model had little effect on the rank order of SNPs carried forward to stage II analysis, although p values were slightly reduced they still remained highly significant. Supplementary table 6 shows the p values for SNPs carried forward to stage II at *SNCA*, *MAPT, LRRK2* and *PARK16* loci after this analysis.

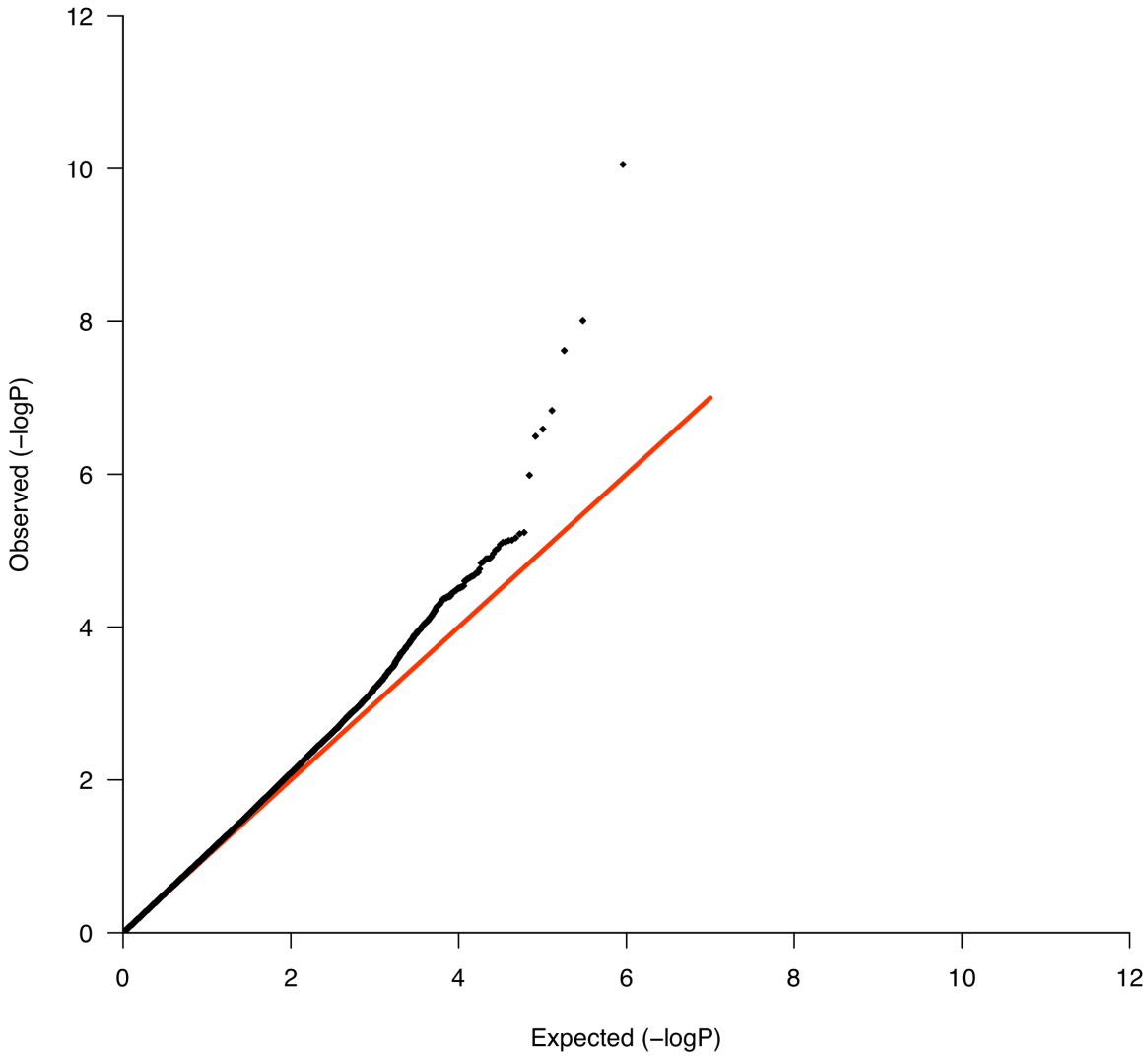
Stage II genotyping
GoldenGate genotyping
250 ng of DNA from each sample were activated through a chemical reaction with biotin. After purifying from excess biotin, assay oligonucleotides were added and hybridized to the DNA, and the mixture bound to streptavidin-conjugated paramagnetic particles (SA-PMPs). After the oligo hybridization, mis- and non-hybridized oligos were washed away and allele-specific extension (ASE) and ligation of the hybridized oligos was performed. The extended and ligated products formed synthetic templates that were then amplified through a PCR reaction. The strands containing the fluorescent signal in the PCR products were then isolated and hybridized to the VeraCode beads via an address sequence. After the hybridization, the VeraCode beads were washed and scanned in the BeadXpress Reader (Illumina). After scanning, raw data was imported into BeadStudio v3.1.12 (Illumina) for analysis and genotype calling.

eQTL analysis
Frozen tissue samples of the frontal cortex were obtained from 133 neurologically normal Caucasian subjects. 100-200mg aliquots of frozen tissue were sub-dissected from each of the samples and used for genotyping and expression assays. Genotyping was performed using Infinium HumanHap550 beadchips (Illumina Inc) followed by imputation to ~1.6 million SNPs after data cleaning, profiling of 22,000 mRNA transcripts was performed using HumanRef-8 Expression BeadChips (Illumina Inc) as previously described[31].
A regression analysis was performed on the expression intensities generated for mRNA. Gender, age, post-mortem interval, tissue source and hybridization batch were included as covariates. Residuals from the regression analysis for each probe were then used as the quantitative trait for that probe in genome-wide association analysis looking for quantitative trait loci, performed using the *assoc* function within PLINK, which correlates allele dosage with change in the trait [32]. To correct for the large number of SNPs tested per trait, a genome-wide empirical p-value was computed for the asymptotic p-value for each SNP using 1,000 permutations of sample-label swapping. To correct for the number of traits being tested per tissue region, a false discovery rate (FDR) threshold was determined based on the empirical p-values. Empirical p-values were allowed to exceed this threshold if the linkage disequilibrium r^2 was greater than or equal to 0.7 with a SNP with empirical values within the FDR threshold.

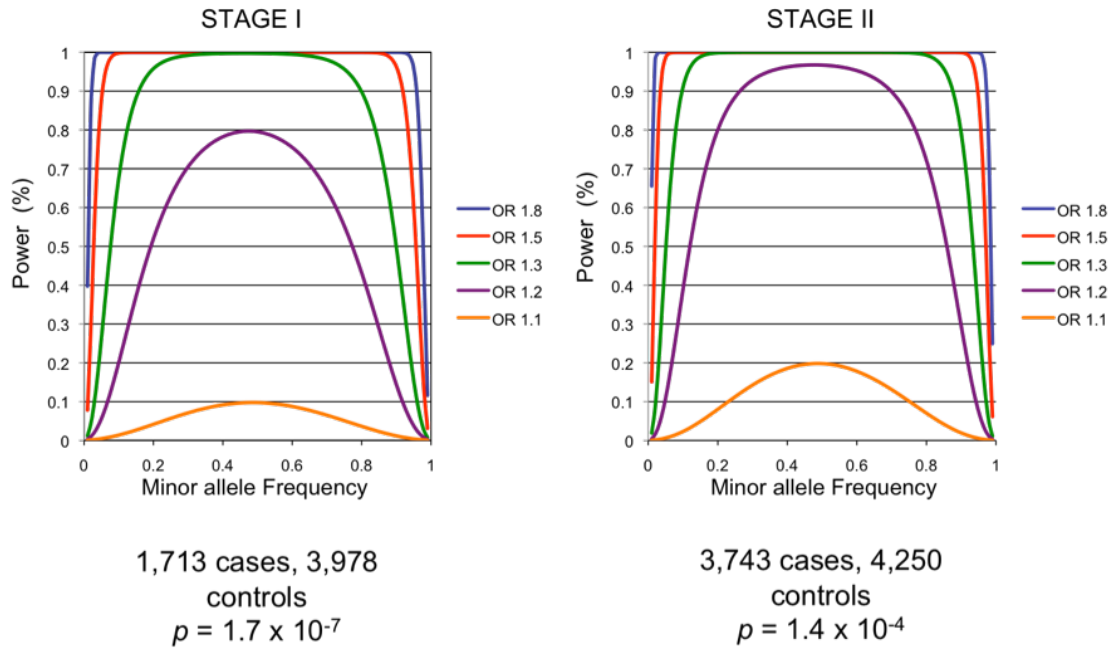
Supplementary Figures



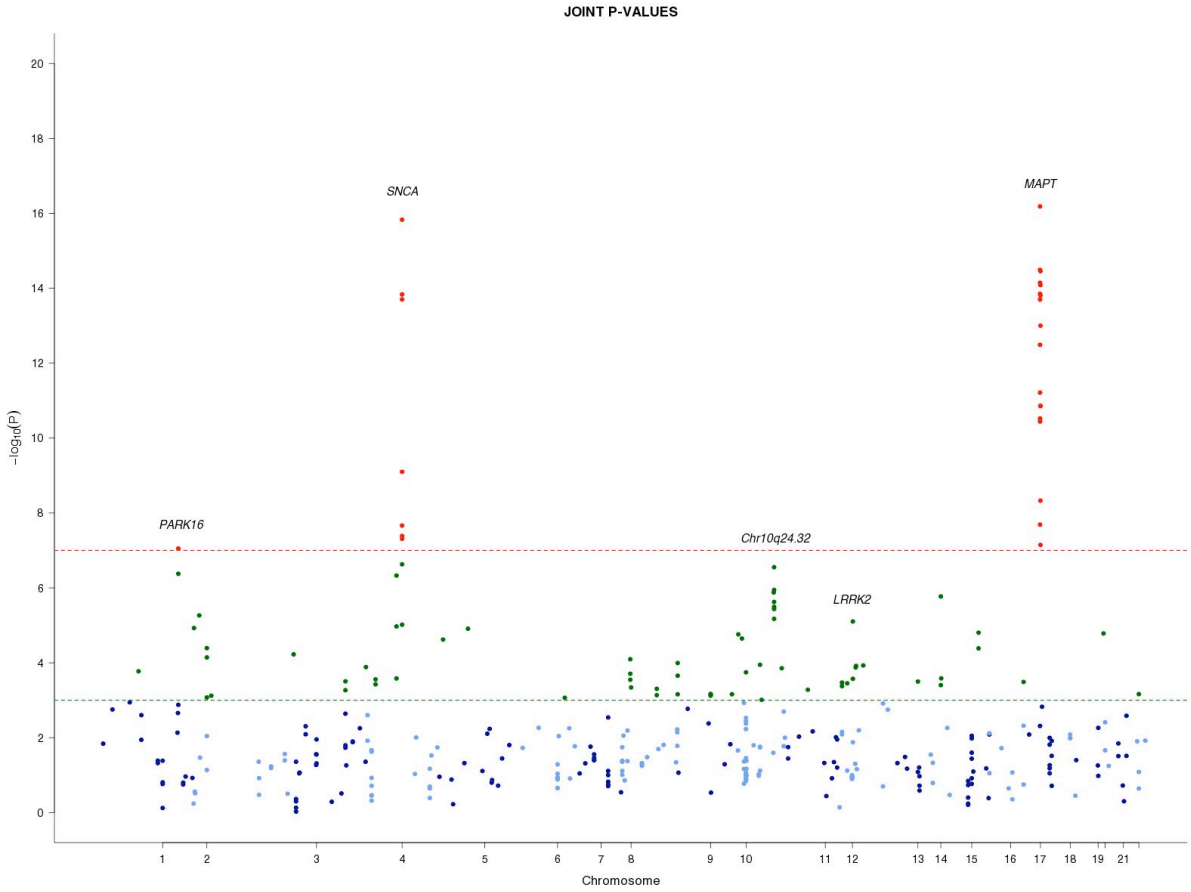
Supplementary figure 1: Multidimensional Scaling (MDS) plots for pair-wise Identity by State (IBS) showing the population substructure in our cohort. **A**: Population substructure of the US cohort clustered with HapMap phase II individuals. ND12228, ND2819 and ND9964 clearly shared African ancestry and thus, were removed from further analyses. **B**: Population substructure in the German cohort clustered with hapmap individuals. As clearly shown, there is near perfect overlapping with Caucasian ancestry. **C**: US-German combined cohort clustered with HapMap individuals. Most of our combined cohort subjects perfectly overlap with Caucasian ancestry. **D**: Combined US-German cohort. Cases and Controls are scattered in the same pattern.



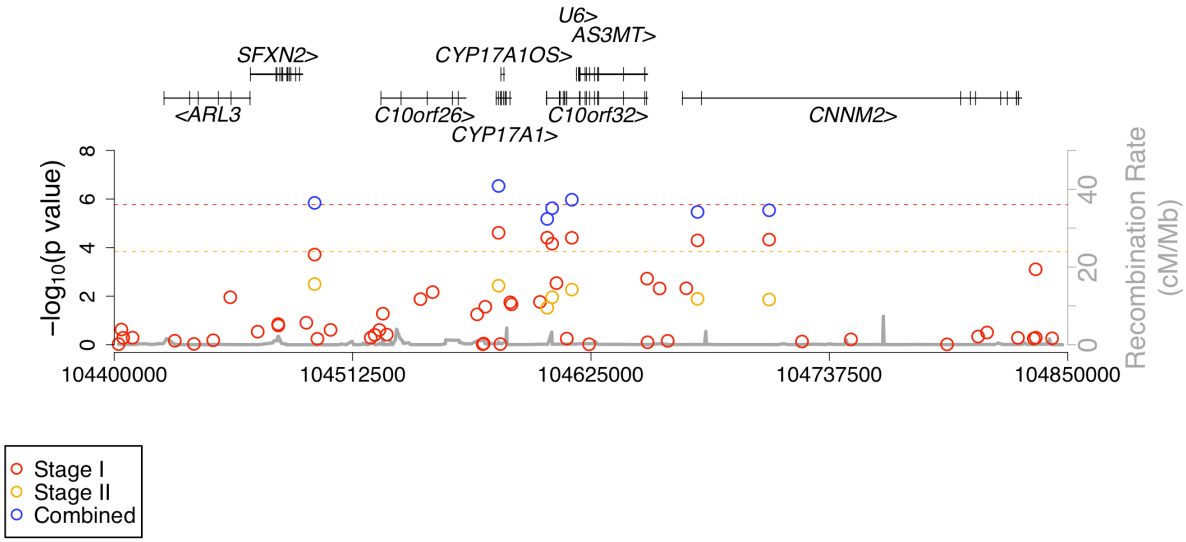
Supplementary figure 2: QQ plot showing the distribution of expected versus observed p values for the stage I combined German-North American cohort. This shows a slight deviation from the expected distribution (lambda = 1.17).



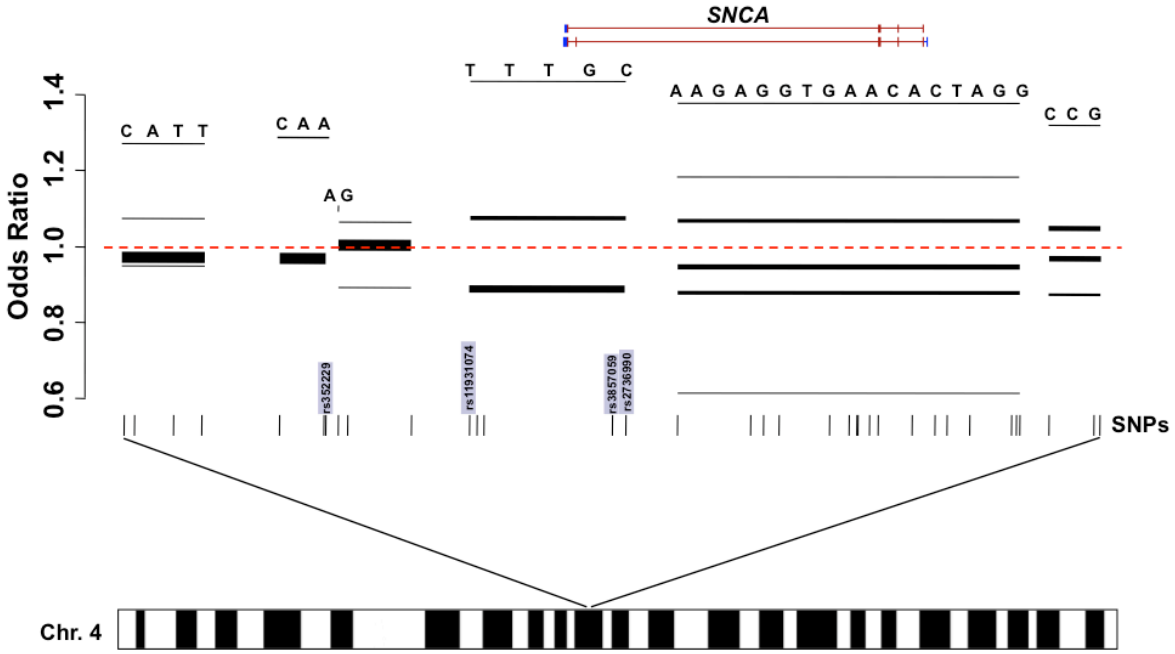
Supplementary figure 3: Power estimates for stage I (A) and stage II (B) of the study. Power on the y-axis is plotted against minor allele frequency with different thresholds for Odds ratio.



Supplementary figure 4: Graphical representation of p-values generated after combining stage I and stage II. In red SNPs surpassing Bonferroni correction; in green SNPs suggestive to be associated with PD.

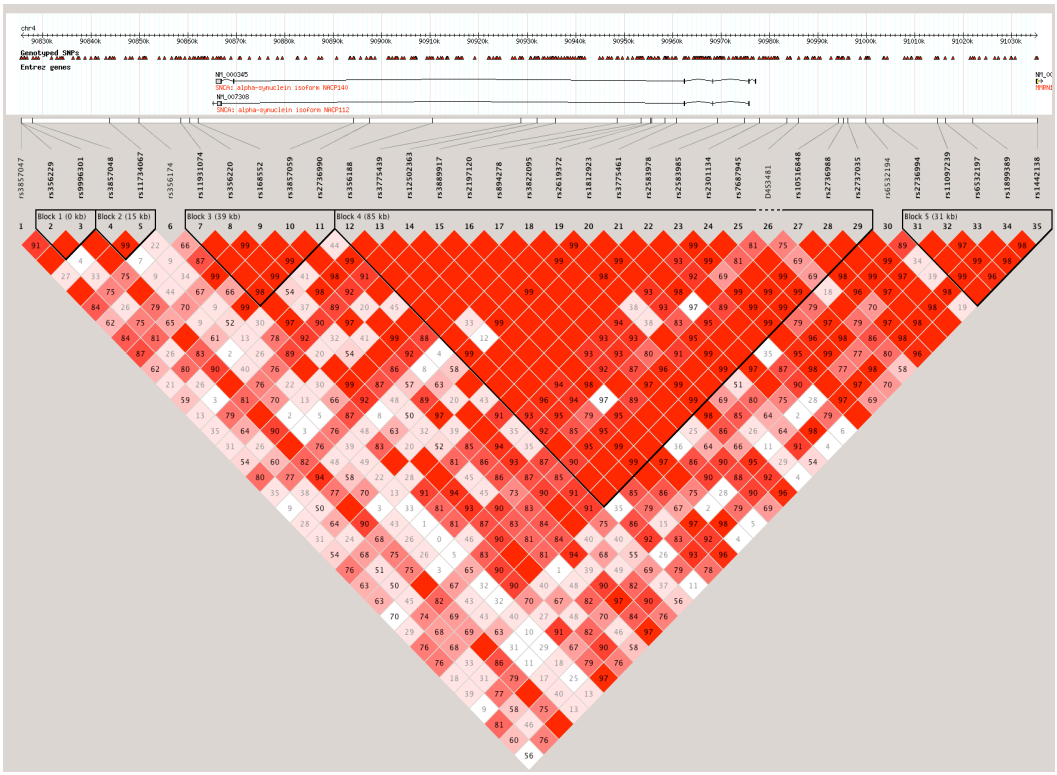


Supplementary figure 5: graphical representation of association p-values and recombination rates at the Chr10q24.32 showing suggestive association with PD. Individual stages and joint p-values are shown.

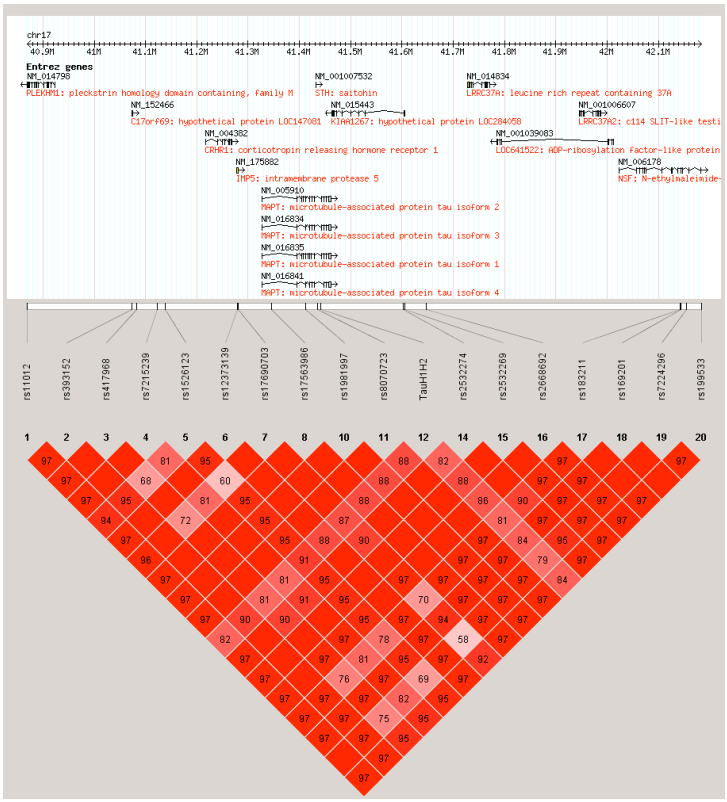


Supplementary figure 6: Odds ratio exerted by each of the haplotypes present in the two LD blocks identified across *SNCA locus*. Each haplotype is represented by a single line, which is wider according to the haplotype frequency. Those SNPS significantly associated with PD after stage II of our analyses are shaded in grey.

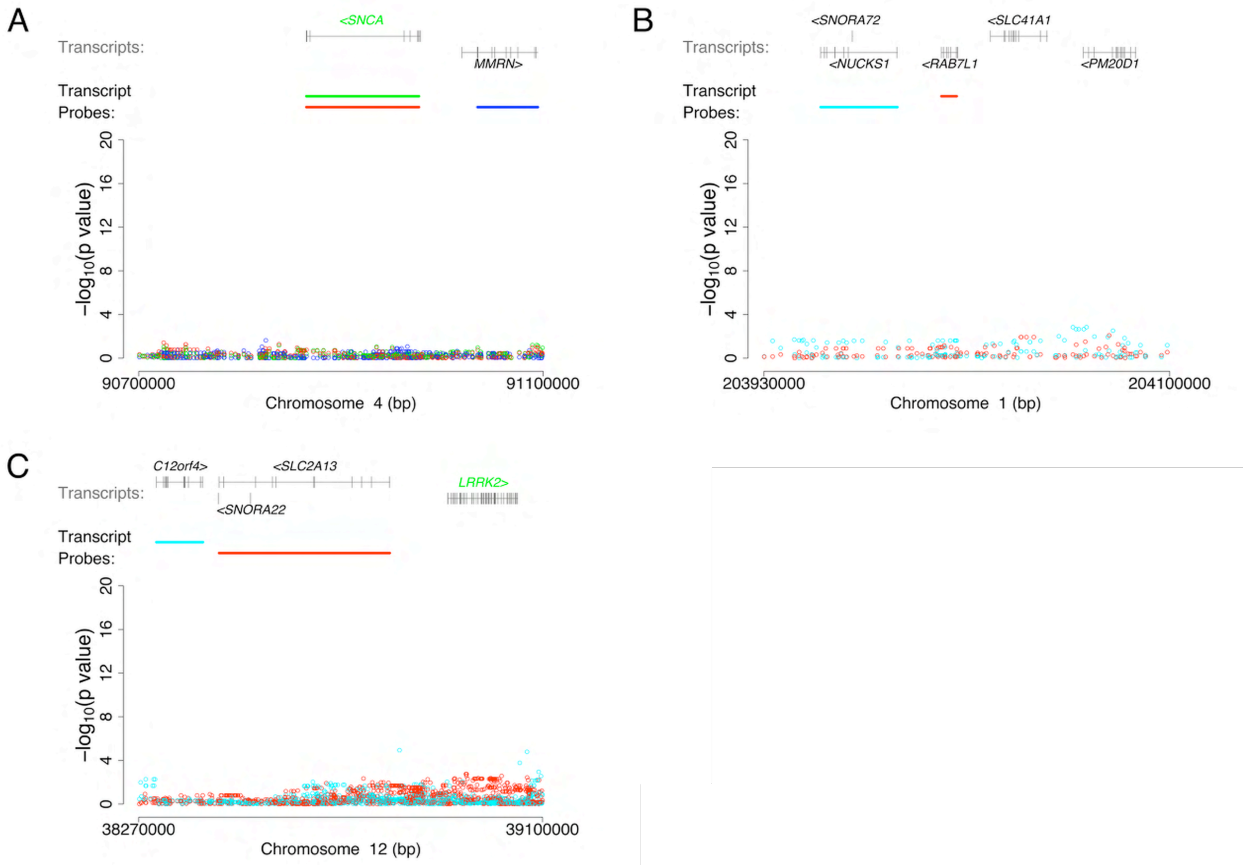
A



B



Supplementary figure 7: LD structure **A** across stage I American population in the SNCA locus. REP1 genotypes (D4S3481) have been included for these samples. **B** around *MAPT* H1/H2 polymorphism in the German cohort.



Supplementary figure 8: Expression quantitative trait loci across the *SNCA, PARK16* and *LRRK2* loci (A, B and C respectively), measured in 133 human frontal cortex samples; each plot A shows association between genotypes and transcript levels across the locus. In this analysis the allelic load at genotyped polymorphism across the locus is tested for association with transcript levels of each gene across the locus. The results of the analysis are shown as log transformed *p* values color-coded to match the transcript of interest.

Supplementary Tables

Supplementary table 1: SNPs selected for Stage II based on p value and predicted assay efficiency. Stage I, stage II and Joint p-values are shown.

locus					Stage I					Stage II				Stage I + II			
SNP ID	Chr.	Positon	Alleles (minor/ major)	Gene	MAF U	MAF A	p-value	cOR	quality filters	MAF U	MAF A	p-value	cOR	MAF U	MAF A	p-value	cOR
rs2736990	4	90897564	C/T	*SNCA*	0.46	0.52	5.69E-09	1.27	OK	0.46	0.51	5.52E-09	1.20	0.51	0.46	2.24E-16	1.23
rs3857059	4	90894261	G/A	*SNCA*	0.07	0.10	3.60E-08	1.58	OK	0.07	0.10	3.39E-08	1.43	0.10	0.07	3.74E-15	1.48
rs415430	17	42214305	G/A	*WNT3*	0.21	0.16	4.50E-08	0.76	Non concordant	NA	NA	NA	NA	NA	NA	NA	NA
rs11931074	4	90858538	T/G	*SNCA*	0.07	0.10	4.78E-08	1.58	OK	0.08	0.10	3.75E-08	1.42	0.10	0.07	1.62E-14	1.46
rs199533	17	42184098	T/C	*NSF*	0.20	0.16	5.05E-08	0.76	OK	0.20	0.17	7.95E-08	0.79	0.17	0.20	1.09E-14	0.78
rs356220	4	90860363	T/C	*SNCA*	0.38	0.43	6.99E-08	1.26	Bad cluster	NA	NA	NA	NA	NA	NA	NA	NA
rs169201	17	42145386	G/A	*NSF*	0.20	0.16	1.25E-07	0.76	OK	0.20	0.17	8.82E-08	0.79	0.17	0.20	4.39E-14	0.78
rs393152	17	41074926	G/A	*C17orf69*	0.22	0.18	1.42E-07	0.76	OK	0.22	0.18	1.69E-09	0.78	0.18	0.22	1.95E-16	0.77
rs12185268	17	41279463	G/A	*IMP5*	0.22	0.18	1.90E-07	0.77	MAF<0.05	NA	NA	NA	NA	NA	NA	NA	NA
rs1981997	17	41412603	A/G	*MAPT*	0.22	0.18	2.02E-07	0.77	OK	0.21	0.18	9.11E-08	0.80	0.18	0.22	3.55E-14	0.78
rs2532274	17	41602941	C/T	*KIAA1267*	0.22	0.18	2.22E-07	0.77	OK	0.22	0.19	1.64E-05	0.86	0.19	0.22	8.24E-11	0.83
rs2532269	17	41605885	G/A	*KIAA1267*	0.22	0.17	2.70E-07	0.77	OK	0.21	0.18	6.21E-07	0.81	0.18	0.22	5.62E-13	0.79
rs8070723	17	41436901	G/A	*MAPT*	0.22	0.18	3.36E-07	0.77	OK	0.21	0.18	9.20E-08	0.80	0.18	0.22	9.64E-14	0.79
rs17563986	17	41347100	G/A	*MAPT*	0.22	0.18	3.44E-07	0.77	OK	0.21	0.18	3.21E-08	0.79	0.18	0.22	1.67E-14	0.78
rs2668692	17	41648797	T/C	*LOC644246*	0.22	0.17	3.94E-07	0.77	OK	0.22	0.18	5.34E-08	0.79	0.18	0.22	7.87E-14	0.79
rs11648673	16	317795	A/G	*AXIN1*	0.28	0.23	4.77E-07	0.79	OK	0.27	0.27	0.62	1.03	0.26	0.27	5.38E-03	0.93
rs12373139	17	41279910	A/G	*IMP5*	0.22	0.18	4.91E-07	0.78	OK	0.21	0.18	1.24E-07	0.80	0.18	0.22	7.75E-14	0.79
rs239748	23	18793279	T/C	*LOC441484*	0.17	0.22	1.17E-06	1.44	Bad cluster	NA	NA	NA	NA	NA	NA	NA	NA
rs12431733	14	53360580	T/C	*BMP4*	0.44	0.49	1.52E-06	1.22	OK	0.46	0.48	0.05	1.06	0.48	0.45	2.54E-06	1.13
rs11591754	10	35247159	T/C	*LOC646213*	0.20	0.16	1.68E-06	0.78	OK	0.19	0.18	0.37	0.98	0.17	0.19	1.83E-04	0.90
rs7013027	8	2911376	A/G	*CSMD1*	0.46	0.51	1.85E-06	1.22	OK	0.49	0.48	0.15	0.95	0.49	0.48	0.07	1.05
rs11012	17	40869224	A/G	*LOC201175*	0.18	0.15	2.85E-06	0.78	OK	0.18	0.15	2.12E-05	0.84	0.15	0.18	8.04E-11	0.81
rs7004938	8	140328407	A/G	*COL22A1*	0.43	0.38	2.97E-06	0.82	Non concordant	NA	NA	NA	NA	NA	NA	NA	NA
rs10857899	1	111929241	A/G	*LOC643329*	0.46	0.41	3.06E-06	0.82	OK	0.45	0.45	0.85	1.00	0.43	0.45	2.39E-03	0.93
rs6542651	2	3737705	C/T	*LOC728597*	0.08	0.10	3.34E-06	1.38	OK	0.08	0.09	0.05	1.09	0.09	0.08	2.84E-05	1.18
rs2285459	16	30402913	A/G	*ITGAL*	0.45	0.40	3.38E-06	0.83	Bad cluster	NA	NA	NA	NA	NA	NA	NA	NA
rs13027881	2	6473384	A/G	*LOC391349*	0.15	0.11	3.76E-06	0.74	OK	0.13	0.14	0.04	1.08	0.13	0.14	0.16	0.94
rs2492448	10	35235412	A/G	*LOC646213*	0.30	0.26	3.84E-06	0.82	OK	0.29	0.29	0.92	1.00	0.28	0.30	4.19E-03	0.93
rs4957473	5	39378920	G/A	*C9*	0.39	0.34	4.24E-06	0.82	OK	0.36	0.39	1.85E-03	1.12	0.37	0.37	0.65	0.99
rs3775439	4	90928764	A/G	*SNCA*	0.12	0.15	4.43E-06	1.35	OK	0.13	0.15	1.48E-03	1.16	0.15	0.12	2.99E-08	1.23
rs6734894	2	6507379	A/G	*LOC391349*	0.15	0.11	4.63E-06	0.74	OK	0.13	0.14	0.04	1.08	0.13	0.14	0.20	0.95
rs4556079	8	140302117	C/T	*COL22A1*	0.29	0.25	4.79E-06	0.79	OK	0.27	0.28	0.39	1.04	0.27	0.28	0.03	0.94
rs2896905	12	38779683	A/G	*SLC2A13*	0.40	0.35	5.03E-06	0.82	OK	0.38	0.38	0.73	1.01	0.37	0.39	7.81E-03	0.93
rs11781101	8	140316844	C/T	*COL22A1*	0.43	0.38	5.31E-06	0.82	OK	0.42	0.42	0.77	1.01	0.41	0.42	0.01	0.94
rs11783351	8	140328721	T/C	*COL22A1*	0.43	0.39	5.51E-06	0.83	OK	0.42	0.42	0.78	1.01	0.41	0.42	0.01	0.94
rs817097	17	64889657	G/T	*MAP2K6*	0.35	0.31	6.22E-06	0.81	OK	0.35	0.35	0.96	0.99	0.33	0.35	8.08E-03	0.92
rs11644916	16	299568	A/G	*AXIN1*	0.29	0.25	6.24E-06	0.82	OK	0.28	0.29	0.17	1.06	0.27	0.28	0.08	0.96
rs2856336	12	11847265	C/A	*ETV6*	0.08	0.11	7.69E-06	1.38	OK	0.09	0.09	0.21	1.06	0.10	0.09	5.24E-04	1.16
rs764660	2	165921543	C/A	*TTC21B*	0.31	0.35	7.83E-06	1.20	Non concordant	NA	NA	NA	NA	NA	NA	NA	NA
rs11244079	9	135174347	A/G	*LOC653163*	0.07	0.05	8.66E-06	0.66	Bad cluster	NA	NA	NA	NA	NA	NA	NA	NA
rs2733333	15	55223218	A/G	*TCF12*	0.17	0.21	9.31E-06	1.23	OK	0.18	0.17	0.39	0.97	0.19	0.18	0.07	1.06
rs183211	17	42143493	A/G	*NSF*	0.24	0.20	1.05E-05	0.80	OK	0.23	0.20	3.88E-06	0.83	0.20	0.24	7.62E-11	0.82
rs11878803	19	57193133	A/G	*ZNF615*	0.07	0.09	1.07E-05	1.42	OK	0.07	0.07	0.65	1.03	0.08	0.07	6.81E-03	1.14
rs7176873	15	55136454	A/G	*TCF12*	0.17	0.21	1.15E-05	1.23	OK	0.18	0.17	0.50	0.97	0.18	0.18	0.05	1.06
rs17654531	1	111601208	G/A	*LOC728204*	0.11	0.09	1.16E-05	0.74	OK	0.11	0.11	0.85	0.99	0.10	0.11	5.95E-03	0.90
rs7923172	10	35349373	A/G	*CUL2*	0.34	0.38	1.43E-05	1.21	OK	0.36	0.35	0.15	0.96	0.36	0.35	0.09	1.05
rs4934704	10	35372170	T/C	*CUL2*	0.34	0.38	1.48E-05	1.21	OK	0.36	0.35	0.16	0.96	0.36	0.35	0.09	1.05
rs2116658	2	165874918	T/C	*SCN2A2*	0.31	0.35	1.48E-05	1.20	OK	0.32	0.31	0.28	0.96	0.32	0.32	0.09	1.04
rs163321	5	178679053	C/T	*ADAMTS2*	0.42	0.38	1.49E-05	0.82	OK	0.42	0.42	0.93	1.01	0.40	0.42	0.02	0.94
rs869714	1	165392874	C/T	*LOC391130*	0.51	0.47	1.54E-05	0.84	OK	0.49	0.51	0.20	1.04	0.49	0.50	0.10	0.96
rs1865648	15	45665913	T/G	*SEMA6D*	0.30	0.34	1.57E-05	1.22	OK	0.31	0.30	0.20	0.95	0.32	0.31	0.12	1.05
rs7175191	15	54973689	G/A	*LOC145783*	0.20	0.24	1.64E-05	1.21	OK	0.21	0.21	0.88	1.01	0.22	0.20	0.02	1.07
rs10827492	10	35469831	T/C	*CREM*	0.34	0.38	1.69E-05	1.21	OK	0.36	0.35	0.17	0.96	0.36	0.35	0.08	1.05
rs10505762	12	11881877	T/C	*ETV6*	0.14	0.17	1.72E-05	1.29	OK	0.15	0.15	0.99	0.99	0.16	0.15	0.01	1.09
rs13139027	4	4977067	A/G	*LDHAL1*	0.08	0.05	1.75E-05	0.69	OK	0.07	0.07	0.59	0.97	0.06	0.07	1.05E-03	0.85
rs2491015	10	70436819	T/C	*KIAA1279*	0.38	0.34	1.76E-05	0.84	OK	0.37	0.36	0.26	0.96	0.35	0.38	1.72E-04	0.91
rs4934540	10	35514705	C/T	*CREM*	0.34	0.38	1.83E-05	1.21	OK	0.36	0.35	0.14	0.95	0.36	0.35	0.10	1.05
rs10784359	12	38732017	T/C	*SLC2A13*	0.43	0.39	2.01E-05	0.83	Bad cluster	NA	NA	NA	NA	NA	NA	NA	NA
rs10437024	1	82673852	C/A	*LPHN2*	0.06	0.08	2.02E-05	1.44	OK	0.06	0.06	0.49	1.04	0.07	0.06	3.99E-03	1.16

rs2224437	14	28060178	T/C	*RPL26P3*	0.37	0.41	2.09E-05	1.20	OK	0.38	0.38	0.65	0.98	0.39	0.38	0.04	1.06
rs7099036	10	35389580	T/C	*CUL2*	0.34	0.38	2.13E-05	1.20	OK	0.36	0.35	0.14	0.95	0.36	0.35	0.10	1.05
rs11593858	10	35421379	A/G	*LOC729811*	0.34	0.38	2.14E-05	1.20	OK	0.36	0.35	0.16	0.96	0.36	0.35	0.09	1.05
rs12644119	4	90822442	A/C	*SNCA*	0.09	0.12	2.15E-05	1.35	OK	0.11	0.13	1.12E-03	1.16	0.12	0.10	6.12E-08	1.23
rs13025009	2	165878319	G/A	*SCN2A2*	0.20	0.24	2.16E-05	1.22	OK	0.22	0.21	0.05	0.95	0.22	0.21	0.31	1.04
rs3792738	5	76283540	A/C	*CRHBP*	0.07	0.09	2.19E-05	1.41	OK	0.07	0.08	0.03	1.13	0.08	0.07	1.09E-04	1.20
rs7920095	10	35343340	A/G	*CUL2*	0.34	0.38	2.20E-05	1.20	OK	0.37	0.36	0.30	0.97	0.37	0.35	0.03	1.06
rs7651825	3	14787122	A/G	*C3orf20*	0.45	0.40	2.20E-05	0.84	OK	0.43	0.42	0.11	0.96	0.41	0.44	3.91E-05	0.90
rs1635291	17	41107696	C/T	*C17orf69*	0.24	0.21	2.27E-05	0.82	Bad cluster	NA	NA	NA	NA	NA	NA	NA	NA
rs12768019	10	35429849	C/T	*LOC729811*	0.34	0.38	2.31E-05	1.20	OK	0.36	0.35	0.16	0.96	0.36	0.35	0.10	1.05
rs11595898	10	35366269	C/T	*CUL2*	0.34	0.38	2.31E-05	1.20	OK	0.36	0.35	0.13	0.95	0.36	0.35	0.11	1.05
rs17115100	10	104581383	T/G	*CYP17A1*	0.11	0.09	2.46E-05	0.75	OK	0.10	0.09	2.35E-03	0.85	0.09	0.11	7.44E-08	0.80
rs558076	17	64847377	T/C	*ABCA5*	0.30	0.26	2.53E-05	0.81	OK	0.28	0.28	0.84	1.02	0.27	0.29	0.01	0.94
rs4247113	17	228978	T/C	*RPH3AL*	0.06	0.08	2.62E-05	1.41	OK	0.06	0.07	0.35	1.05	0.07	0.06	1.88E-03	1.16
rs894278	4	90953558	G/T	*SNCA*	0.05	0.08	2.64E-05	1.47	OK	0.06	0.08	5.87E-05	1.31	0.08	0.06	9.01E-09	1.36
rs7527143	1	165393978	G/A	*LOC391130*	0.51	0.47	2.65E-05	0.84	OK	0.50	0.49	0.26	0.96	0.49	0.50	0.10	0.96
rs4934719	10	35416775	C/T	*LOC729811*	0.34	0.38	2.68E-05	1.20	IMISS>0.1	NA	NA	NA	NA	NA	NA	NA	NA
rs7844468	8	2916843	A/G	*CSMD1*	0.37	0.41	2.74E-05	1.19	OK	0.37	0.36	0.34	0.97	0.38	0.37	0.13	1.04
rs16977243	15	55181297	C/A	*TCF12*	0.17	0.20	2.74E-05	1.22	OK	0.18	0.17	0.09	0.92	0.18	0.18	0.26	1.02
rs2378554	9	82805138	C/T	*TLE1*	0.46	0.51	2.93E-05	1.19	OK	0.48	0.49	0.32	1.03	0.49	0.47	4.59E-04	1.09
rs7988279	13	78528580	T/G	*LOC390415*	0.46	0.42	3.05E-05	0.84	IMISS>0.1	NA	NA	NA	NA	NA	NA	NA	NA
rs1793949	12	46657862	T/C	*COL2A1*	0.45	0.41	3.14E-05	0.84	OK	0.44	0.43	0.15	0.95	0.42	0.45	2.07E-04	0.91
rs4603502	15	45661946	C/T	*SEMA6D*	0.30	0.34	3.15E-05	1.21	OK	0.32	0.31	0.18	0.95	0.32	0.31	0.16	1.04
rs4934724	10	35433675	T/C	*LOC729811*	0.34	0.38	3.21E-05	1.20	OK	0.36	0.35	0.13	0.95	0.36	0.35	0.13	1.05
rs1686103	2	36208125	T/G	*CRIM1*	0.34	0.38	3.26E-05	1.19	OK	0.35	0.35	0.56	0.96	0.36	0.35	0.04	1.05
rs1926554	10	35384975	A/G	*CUL2*	0.34	0.38	3.32E-05	1.20	OK	0.36	0.35	0.12	0.95	0.36	0.35	0.13	1.04
rs6992732	8	2911645	G/A	*CSMD1*	0.34	0.38	3.32E-05	1.20	OK	0.36	0.35	0.43	0.97	0.36	0.35	0.06	1.05
rs12834774	23	139529169	G/T	*LOC286411*	0.12	0.09	3.38E-05	0.68	HWE<10-7	NA	NA	NA	NA	NA	NA	NA	NA
rs2042079	2	16969333	A/G	*FAM49A*	0.24	0.28	3.40E-05	1.21	OK	0.24	0.26	0.01	1.10	0.27	0.24	1.20E-05	1.13
rs859522	7	38936691	G/A	*VPS41*	0.07	0.09	3.41E-05	1.38	OK	0.08	0.08	0.61	0.97	0.08	0.08	0.04	1.11
rs7215239	17	41123556	C/T	*C17orf69*	0.24	0.21	3.43E-05	0.82	OK	0.24	0.20	4.79E-07	0.81	0.21	0.24	1.67E-11	0.81
rs2708909	7	48018204	G/T	*SUNC1*	0.49	0.53	3.44E-05	1.18	OK	0.50	0.50	0.56	1.02	0.51	0.49	0.03	1.06
rs2666128	2	36199103	A/G	*CRIM1*	0.33	0.37	3.46E-05	1.19	OK	0.34	0.34	0.78	1.00	0.35	0.34	7.45E-03	1.07
rs1395993	3	21344590	C/T	*VENTXP7*	0.31	0.35	3.49E-05	1.19	OK	0.33	0.31	0.03	0.92	0.32	0.32	0.39	1.02
rs10849446	12	6349553	A/C	*SCNN1A*	0.43	0.39	3.66E-05	0.85	OK	0.40	0.42	7.06E-03	1.09	0.41	0.41	0.58	0.99
rs3824754	10	104604340	A/G	*C10orf32*	0.11	0.09	3.92E-05	0.76	OK	0.10	0.09	0.02	0.88	0.09	0.11	1.27E-06	0.81
rs11191425	10	104615960	T/C	*C10orf32*	0.11	0.09	3.96E-05	0.76	OK	0.10	0.09	3.42E-03	0.85	0.09	0.11	2.46E-07	0.80
rs12261843	10	35594060	G/T	*C10orf9*	0.28	0.31	4.05E-05	1.21	OK	0.30	0.29	0.43	0.99	0.30	0.29	0.04	1.07
rs11564162	12	38729159	G/A	*SLC2A13*	0.21	0.18	4.08E-05	0.78	OK	0.21	0.19	0.10	0.93	0.19	0.21	9.52E-05	0.87
rs4563067	17	69700141	G/A	*RPL38*	0.31	0.27	4.11E-05	0.82	OK	0.29	0.29	0.94	1.01	0.28	0.30	0.01	0.93
rs9458499	6	162633417	T/C	*PARK2*	0.25	0.29	4.27E-05	1.21	OK	0.26	0.26	0.97	1.00	0.27	0.26	0.02	1.07
rs6794137	3	134371136	G/A	*TMEM108*	0.21	0.17	4.27E-05	0.83	OK	0.20	0.21	0.08	1.07	0.20	0.20	0.26	0.97
rs9574355	13	78574175	T/C	*LOC390415*	0.47	0.43	4.28E-05	0.84	OK	0.46	0.47	0.13	1.05	0.46	0.47	0.24	0.97
rs6044224	20	16606300	G/A	*RPL7AL3*	0.46	0.42	4.37E-05	0.85	OK	0.44	0.44	0.80	0.99	0.44	0.45	3.90E-03	0.93
rs11778693	8	22518797	C/T	*KIAA1967*	0.33	0.37	4.45E-05	1.20	Bad cluster	NA	NA	NA	NA	NA	NA	NA	NA
rs2001893	10	35340629	T/C	*CUL2*	0.34	0.38	4.48E-05	1.20	HWE<10-7	NA	NA	NA	NA	NA	NA	NA	NA
rs207481	21	24133087	C/T	*TUBAP*	0.18	0.21	4.56E-05	1.24	OK	0.19	0.19	0.86	1.04	0.20	0.18	0.01	1.11
rs7707022	5	37802142	A/G	*WDR70*	0.29	0.33	4.58E-05	1.17	Non designable for Stage II	NA	NA	NA	NA	NA	NA	NA	NA
rs11183395	12	44890335	G/A	*SLC38A1*	0.34	0.30	4.59E-05	0.85	OK	0.33	0.34	0.55	1.02	0.32	0.34	0.05	0.95
rs9918939	9	82836491	C/T	*TLE1*	0.46	0.50	4.63E-05	1.18	OK	0.48	0.49	0.27	1.03	0.49	0.47	4.33E-04	1.09
rs935378	2	46962655	G/A	*MCFD2*	0.19	0.16	4.63E-05	0.80	OK	0.18	0.17	0.25	0.97	0.17	0.19	3.27E-04	0.90
rs1005511	11	57123232	A/G	*SERPING1*	0.32	0.36	4.68E-05	1.18	OK	0.33	0.34	0.25	1.04	0.35	0.33	6.39E-04	1.09
rs12413409	10	104709086	A/G	*CNNM2*	0.10	0.08	4.69E-05	0.75	OK	0.09	0.08	9.73E-03	0.86	0.08	0.10	6.85E-07	0.80
rs17071181	18	59307479	C/T	*SERPINB5*	0.06	0.08	4.86E-05	1.42	OK	0.07	0.06	0.05	0.90	0.07	0.06	0.37	1.07
rs12324092	15	54990533	A/G	*LOC145783*	0.16	0.19	4.97E-05	1.22	Non designable for Stage II	NA	NA	NA	NA	NA	NA	NA	NA
rs13085998	3	143746502	T/C	*ATR*	0.40	0.44	5.02E-05	1.19	OK	0.41	0.41	0.85	0.99	0.42	0.40	0.03	1.06
rs12411886	10	104675289	A/C	*CNNM2*	0.10	0.08	5.05E-05	0.75	OK	0.09	0.08	9.09E-03	0.86	0.08	0.10	7.79E-07	0.80
rs2227928	3	143764302	T/C	*ATR*	0.40	0.44	5.11E-05	1.19	OK	0.42	0.42	0.61	1.02	0.43	0.41	2.98E-03	1.08
rs10246477	7	83103936	A/G	*SEMA3E*	0.21	0.25	5.25E-05	1.20	OK	0.22	0.22	0.70	1.01	0.23	0.22	5.80E-03	1.08
rs12578421	12	11846605	G/A	*ETV6*	0.08	0.10	5.26E-05	1.34	OK	0.08	0.09	0.13	1.07	0.09	0.08	7.35E-04	1.15
rs1563863	8	2917883	C/A	*CSMD1*	0.37	0.41	5.39E-05	1.19	OK	0.39	0.38	0.79	0.99	0.39	0.38	0.03	1.06
rs1024889	3	70546020	G/A	*LOC654340*	0.32	0.36	5.46E-05	1.17	OK	0.32	0.32	0.94	1.00	0.33	0.32	0.03	1.06
rs10894203	11	129833092	G/A	*ADAMTS15*	0.49	0.45	5.46E-05	0.85	OK	0.48	0.48	0.54	1.02	0.47	0.48	0.06	0.96
rs3936503	10	35589263	A/G	*C10orf9*	0.31	0.35	5.50E-05	1.20	OK	0.33	0.32	0.29	0.98	0.33	0.32	0.08	1.06
rs8080993	17	13650646	G/A	*LOC644361*	0.29	0.33	5.53E-05	1.19	OK	0.30	0.30	0.94	1.01	0.31	0.29	0.02	1.07
rs9525776	13	42928966	A/G	*LOC647049*	0.35	0.39	5.53E-05	1.18	OK	0.37	0.37	0.45	0.97	0.38	0.36	0.05	1.05
rs7454430	6	123331736	A/G	*RLBP1L2*	0.27	0.23	5.54E-05	0.81	OK	0.25	0.25	0.81	0.99	0.25	0.26	4.24E-03	0.91
rs9924026	16	48147935	T/G	*ZNF423*	0.13	0.16	5.94E-05	1.27	OK	0.14	0.13	0.05	0.91	0.14	0.14	0.42	1.03
rs4843467	16	85441321	T/C	*LOC729979*	0.19	0.22	6.01E-05	1.26	OK	0.19	0.19	0.61	1.02	0.20	0.19	7.37E-03	1.10
rs1934828	13	75431142	G/A	*FLJ35379*	0.28	0.25	6.08E-05	0.83	Non	NA	NA	NA	NA	NA	NA	NA	NA

									concordant									
rs11642990	16	85467695	T/C	*LOC729979*	0.16	0.19	6.25E-05	1.26	OK	0.17	0.16	0.17	0.94	0.17	0.16	0.25	1.04
rs1449587	13	48311469	T/C	*LOC338099*	0.38	0.34	6.26E-05	0.84	OK	0.36	0.37	0.54	1.03	0.36	0.37	0.04	0.95
rs6599389	4	929113	A/G	*MGC4618*	0.07	0.09	6.28E-05	1.31	Non concordant	NA	NA	NA	NA	NA	NA	NA	NA
rs265120	1	215659568	C/T	*GPATCH2*	0.10	0.13	6.38E-05	1.31	OK	0.12	0.11	0.08	0.91	0.12	0.11	0.35	1.04
rs1498046	4	126152922	G/A	*LOC729377*	0.26	0.30	6.39E-05	1.18	OK	0.27	0.27	0.61	1.00	0.28	0.27	3.91E-03	1.07
rs1396003	3	21331410	T/C	*VENTXP7*	0.29	0.33	6.48E-05	1.19	OK	0.31	0.30	7.93E-03	0.91	0.31	0.30	0.60	1.01
rs17690703	17	41281077	T/C	*IMP5*	0.25	0.22	6.55E-05	0.83	OK	0.25	0.21	2.31E-08	0.80	0.21	0.25	9.45E-13	0.80
rs3740484	10	102737353	T/G	*MRPL43*	0.30	0.33	6.57E-05	1.20	OK	0.31	0.30	0.73	0.99	0.31	0.30	0.03	1.06
rs7183808	15	96641692	G/A	*FLJ39743*	0.36	0.40	6.61E-05	1.20	OK	0.37	0.36	0.05	0.94	0.37	0.37	0.45	1.03
rs636508	9	83582101	T/C	*TLE1*	0.25	0.21	6.65E-05	0.82	OK	0.23	0.24	0.09	1.08	0.23	0.24	0.22	0.97
rs6812193	4	77418010	T/C	*STBD1*	0.37	0.33	6.67E-05	0.86	OK	0.37	0.34	9.70E-04	0.91	0.34	0.37	4.20E-07	0.89
rs9530494	13	75434275	A/G	*FLJ35379*	0.28	0.25	6.82E-05	0.83	OK	0.27	0.26	0.19	0.96	0.26	0.28	2.81E-04	0.91
rs6959225	7	8499029	C/A	*NXPH1*	0.19	0.23	6.84E-05	1.24	Non concordant	NA	NA	NA	NA	NA	NA	NA	NA
rs8111509	19	57003307	C/T	*FPRL2*	0.28	0.31	6.84E-05	1.19	OK	0.29	0.28	0.41	0.96	0.29	0.28	0.08	1.04
rs7077361	10	15601549	C/T	*ITGA8*	0.13	0.11	6.88E-05	0.77	OK	0.13	0.12	8.10E-03	0.88	0.11	0.13	5.40E-06	0.84
rs9839984	3	162251606	T/C	*PPM1L*	0.34	0.37	6.92E-05	1.19	OK	0.35	0.35	0.98	1.03	0.36	0.34	0.01	1.08
rs4409766	10	104606653	C/T	*C10orf32*	0.11	0.09	6.92E-05	0.77	OK	0.10	0.09	7.99E-03	0.87	0.09	0.11	9.92E-07	0.82
rs2240914	9	131938127	T/C	*GPR107*	0.05	0.07	6.98E-05	1.38	OK	0.06	0.06	0.94	0.99	0.06	0.06	0.03	1.11
rs4661747	1	16612540	A/G	*SPATA21*	0.33	0.29	7.02E-05	0.84	OK	0.33	0.32	0.70	0.97	0.31	0.33	7.67E-03	0.92
rs4584384	1	152762321	T/C	*TDRD10*	0.36	0.40	7.09E-05	1.19	OK	0.38	0.38	0.44	0.98	0.39	0.37	0.06	1.05
rs807302	6	119968450	C/A	*LOC728727*	0.24	0.21	7.25E-05	0.80	OK	0.22	0.23	0.14	1.07	0.23	0.23	0.17	0.96
rs595046	21	43626445	A/G	*FLJ41733*	0.30	0.34	7.27E-05	1.20	OK	0.32	0.31	0.82	1.00	0.32	0.31	0.02	1.07
rs2686831	7	47959511	T/C	*PKD1L1*	0.47	0.51	7.31E-05	1.17	Bad cluster	NA	NA	NA	NA	NA	NA	NA	NA
rs6481928	10	35276450	G/A	*LOC646218*	0.25	0.21	7.31E-05	0.82	OK	0.24	0.24	0.64	1.00	0.23	0.24	5.77E-03	0.93
rs4242434	8	22557775	T/G	*BIN3*	0.32	0.36	7.31E-05	1.20	OK	0.32	0.34	0.09	1.06	0.34	0.32	1.99E-04	1.11
rs1580254	3	162249972	T/C	*PPM1L*	0.34	0.37	7.35E-05	1.18	OK	0.35	0.35	1.00	1.03	0.36	0.34	0.02	1.08
rs6582668	12	37052871	A/G	*ALG10B*	0.12	0.15	7.41E-05	1.28	OK	0.14	0.13	0.40	0.97	0.14	0.13	0.08	1.08
rs1526123	17	41139123	G/A	*C17orf69*	0.47	0.43	7.52E-05	0.85	OK	0.47	0.44	4.47E-04	0.89	0.44	0.47	1.28E-07	0.88
rs207521	21	24103584	G/A	*TUBAP*	0.18	0.21	7.53E-05	1.24	OK	0.19	0.18	0.92	1.02	0.19	0.18	0.03	1.09
rs12425761	12	114119258	C/T	*TBX3*	0.10	0.12	7.75E-05	1.28	OK	0.11	0.10	0.11	0.90	0.11	0.10	0.33	1.02
rs6780193	3	71988566	G/A	*PROK2*	0.29	0.26	7.93E-05	0.83	OK	0.28	0.28	0.76	1.00	0.27	0.29	0.02	0.93
rs16944593	12	113641262	A/C	*TBX3*	0.09	0.07	7.95E-05	0.78	OK	0.10	0.09	0.15	0.92	0.08	0.10	6.08E-04	0.87
rs11973020	7	25549191	C/T	*LOC646588*	0.35	0.39	7.98E-05	1.18	OK	0.34	0.34	0.90	0.99	0.36	0.35	0.06	1.05
rs417968	17	41084159	C/T	*C17orf69*	0.26	0.22	8.03E-05	0.83	OK	0.25	0.22	4.53E-07	0.82	0.22	0.26	5.50E-11	0.82
rs7436941	4	159654523	G/A	*RXFP1*	0.15	0.18	8.13E-05	1.31	OK	0.17	0.16	0.08	0.94	0.17	0.16	0.30	1.07
rs7911697	10	14525211	A/G	*FAM107B*	0.30	0.34	8.19E-05	1.19	OK	0.32	0.32	0.89	0.99	0.33	0.31	0.02	1.06
rs12255903	10	35269643	T/C	*LOC646218*	0.25	0.21	8.26E-05	0.83	OK	0.24	0.24	0.64	1.00	0.23	0.24	5.97E-03	0.93
rs7903802	10	12997566	T/C	*CCDC3*	0.14	0.17	8.38E-05	1.24	IMISS>0.1	NA	NA	NA	NA	NA	NA	NA	NA
rs9285433	6	119979004	G/A	*LOC728727*	0.28	0.24	8.40E-05	0.82	OK	0.26	0.27	0.14	1.07	0.26	0.27	0.16	0.97
rs699038	12	25050907	C/T	*LOC645177*	0.49	0.45	8.53E-05	0.85	OK	0.48	0.47	0.16	0.96	0.47	0.49	2.81E-04	0.91
rs7897198	10	35277737	T/C	*LOC646218*	0.25	0.21	8.55E-05	0.82	OK	0.24	0.24	0.76	1.01	0.23	0.24	7.84E-03	0.94
rs6446700	4	4962543	G/A	*LDHAL1*	0.49	0.45	8.56E-05	0.85	OK	0.50	0.50	0.45	1.02	0.48	0.50	0.01	0.94
rs2515501	8	6400033	T/C	*ANGPT2*	0.15	0.12	8.85E-05	0.78	OK	0.14	0.14	0.95	0.99	0.13	0.14	7.88E-03	0.90
rs7112698	11	129835261	G/A	*ADAMTS15*	0.39	0.35	8.96E-05	0.85	Non designable for Stage II	NA	NA	NA	NA	NA	NA	NA	NA
rs928939	12	11882934	A/G	*ETV6*	0.10	0.13	9.02E-05	1.28	OK	0.11	0.11	0.71	1.02	0.12	0.11	0.01	1.10
rs2387807	12	36733128	A/G	*LOC727847*	0.08	0.10	9.12E-05	1.33	OK	0.08	0.08	0.67	0.97	0.09	0.08	0.09	1.08
rs2794256	6	119985100	T/C	*LOC728727*	0.28	0.24	9.17E-05	0.82	OK	0.26	0.27	0.28	1.06	0.26	0.27	0.07	0.96
rs935920	2	35985642	G/T	*MRPL50P1*	0.36	0.33	9.24E-05	0.84	OK	0.35	0.34	0.03	0.94	0.17	0.15	6.65E-04	1.13
rs9480154	6	150652308	A/G	*RNU4P1*	0.06	0.08	9.25E-05	1.43	OK	0.06	0.06	0.28	0.94	0.06	0.06	0.22	1.08
rs7559362	2	196027545	G/A	*LOC391470*	0.43	0.47	9.26E-05	1.18	OK	0.45	0.44	0.43	0.97	0.45	0.44	0.06	1.05
rs2470179	15	49471703	C/T	*GLDN*	0.39	0.43	9.27E-05	1.17	Non designable for Stage II	NA	NA	NA	NA	NA	NA	NA	NA
rs12777747	10	123989646	G/A	*TACC2*	0.19	0.23	9.30E-05	1.21	OK	0.20	0.21	0.10	1.07	0.21	0.20	3.88E-04	1.11
rs1224671	15	45682835	A/G	*SEMA6D*	0.30	0.33	9.32E-05	1.19	OK	0.31	0.29	0.09	0.94	0.31	0.30	0.37	1.03
rs2708851	7	48052327	C/T	*LOC136288*	0.49	0.53	9.33E-05	1.17	OK	0.50	0.50	0.57	1.02	0.51	0.49	0.04	1.05
rs8014371	14	32579884	C/A	*NPAS3*	0.34	0.37	9.34E-05	1.19	OK	0.36	0.35	0.33	0.98	0.36	0.35	0.07	1.06
rs1605527	3	21351855	T/C	*VENTXP7*	0.07	0.09	9.41E-05	1.30	OK	0.07	0.07	0.71	0.97	0.08	0.07	0.06	1.07
rs6440096	3	143814050	G/A	*PLS1*	0.17	0.14	9.52E-05	0.79	OK	0.16	0.15	0.15	0.94	0.15	0.16	3.26E-04	0.88
rs7485262	12	37088013	C/T	*ALG10B*	0.08	0.11	9.54E-05	1.32	OK	0.10	0.09	0.27	0.94	0.10	0.09	0.11	1.07
rs13264187	8	22562043	T/C	*BIN3*	0.32	0.36	9.55E-05	1.20	OK	0.32	0.33	0.11	1.05	0.34	0.32	5.48E-04	1.10
rs560271	17	64870692	A/G	*ABCA5*	0.16	0.14	9.60E-05	0.77	Non designable for Stage II	NA	NA	NA	NA	NA	NA	NA	NA
rs748088	21	38320720	G/A	*DSCR4*	0.43	0.39	9.66E-05	0.86	OK	0.41	0.43	0.02	1.08	0.42	0.42	0.62	0.99
rs6596287	5	135507247	C/A	*SMAD5*	0.28	0.31	9.72E-05	1.21	OK	0.29	0.28	0.19	0.96	0.29	0.28	0.18	1.05
rs9544996	13	78590677	A/G	*RBM26*	0.43	0.39	9.82E-05	0.85	OK	0.42	0.43	0.19	1.05	0.42	0.43	0.19	0.97
rs7655536	4	77395792	C/T	*SCARB2*	0.19	0.22	9.86E-05	1.20	IMISS>0.1	NA	NA	NA	NA	NA	NA	NA	NA
rs662616	13	78593828	G/A	*RBM26*	0.08	0.10	1.01E-04	1.33	OK	0.08	0.08	0.54	0.98	0.08	0.08	0.06	1.11
rs359079	10	132035527	C/T	*LOC728497*	0.12	0.15	1.02E-04	1.25	OK	0.13	0.13	0.98	1.00	0.14	0.13	0.01	1.09

rs10122587	9	2681951	T/C	*KCNV2*	0.26	0.30	1.02E-04	1.20	OK	0.28	0.27	0.38	0.97	0.28	0.27	0.09	1.05
rs999826	5	67311112	T/C	*LOC643631*	0.23	0.20	1.03E-04	0.85	OK	0.22	0.22	0.48	1.03	0.22	0.23	0.05	0.96
rs11100188	4	159655208	T/G	*RXFP1*	0.15	0.18	1.03E-04	1.31	OK	0.17	0.16	0.07	0.94	0.17	0.16	0.31	1.07
rs7225002	17	41544850	G/A	*KIAA1267*	0.40	0.36	1.03E-04	0.85	OK	0.38	0.36	5.80E-04	0.89	0.36	0.39	8.40E-08	0.87
rs2168330	8	52111821	A/G	*SNTG1*	0.30	0.34	1.05E-04	1.18	IMISS>0.1	NA	NA	NA	NA	NA	NA	NA	NA
rs11136568	8	2922585	T/C	*CSMD1*	0.40	0.44	1.05E-04	1.18	OK	0.42	0.42	0.35	0.96	0.42	0.41	0.10	1.04
rs1542384	4	159664766	C/T	*RXFP1*	0.34	0.37	1.07E-04	1.20	OK	0.35	0.34	0.59	0.98	0.35	0.34	0.06	1.06
rs2000731	18	46150625	A/G	*C18orf24*	0.34	0.38	1.07E-04	1.18	OK	0.36	0.36	0.75	1.01	0.37	0.35	6.29E-03	1.08
rs305163	2	36221313	A/G	*CRIM1*	0.25	0.29	1.07E-04	1.19	Non concordant	NA	NA	NA	NA	NA	NA	NA	NA
rs3759407	12	46481336	T/C	*HDAC7A*	0.06	0.08	1.07E-04	1.38	OK	0.07	0.08	0.19	1.12	0.08	0.07	4.24E-04	1.22
rs12460684	19	1624793	G/A	*TCF3*	0.43	0.47	1.08E-04	1.18	Non concordant	NA	NA	NA	NA	NA	NA	NA	NA
rs12412945	10	54468113	T/C	*MBL2*	0.19	0.16	1.09E-04	0.80	OK	0.17	0.17	0.72	1.03	0.16	0.18	0.01	0.92
rs10064163	5	112007605	G/T	*APC*	0.40	0.44	1.11E-04	1.18	OK	0.41	0.41	0.91	1.01	0.42	0.40	0.03	1.07
rs7224296	17	42155230	G/A	*LOC644315*	0.27	0.24	1.13E-04	0.84	OK	0.27	0.24	3.35E-05	0.86	0.24	0.27	1.32E-08	0.85
rs1036745	13	78499702	C/T	*LOC390415*	0.06	0.08	1.13E-04	1.35	OK	0.07	0.07	0.83	1.00	0.07	0.07	0.05	1.11
rs11128994	3	21195185	G/A	*VENTXP7*	0.25	0.22	1.15E-04	0.85	OK	0.23	0.24	0.03	1.08	0.23	0.24	0.37	0.98
rs836109	11	34526784	C/A	*LOC729710*	0.12	0.15	1.16E-04	1.30	OK	0.13	0.13	0.95	1.00	0.14	0.13	0.02	1.10
rs11747238	5	4831369	G/A	*LOC340094*	0.21	0.24	1.16E-04	1.21	OK	0.22	0.22	0.41	0.95	0.23	0.22	0.07	1.05
rs4789632	17	69702146	T/C	*RPL38*	0.42	0.46	1.16E-04	1.17	OK	0.43	0.42	0.14	0.95	0.44	0.43	0.27	1.03
rs4823506	22	46643740	A/G	*RP11-191L9.1*	0.41	0.37	1.16E-04	0.85	OK	0.41	0.40	0.49	0.98	0.39	0.41	6.00E-03	0.93
rs6481654	10	30401130	G/A	*KIAA1462*	0.24	0.27	1.16E-04	1.19	OK	0.26	0.25	0.15	0.95	0.26	0.25	0.18	1.04
rs4142010	1	39938607	T/C	*HPCAL4*	0.10	0.12	1.16E-04	1.28	OK	0.10	0.11	0.26	1.10	0.11	0.10	2.63E-03	1.15
rs706858	6	120079876	G/A	*LOC728727*	0.43	0.39	1.17E-04	0.85	OK	0.41	0.41	0.53	1.03	0.40	0.42	0.06	0.96
rs11217299	11	98250101	A/G	*CNTN5*	0.35	0.31	1.17E-04	0.84	OK	0.34	0.34	0.49	1.02	0.33	0.34	0.06	0.95
rs11185726	9	136240925	C/T	*RXRA*	0.14	0.17	1.18E-04	1.27	OK	0.15	0.15	0.28	1.04	0.16	0.14	1.68E-03	1.12
rs10044636	5	150714711	A/C	*SLC36A2*	0.17	0.20	1.20E-04	1.23	OK	0.18	0.17	0.36	0.96	0.18	0.18	0.19	1.05
rs12361904	11	127208320	G/A	*LOC387820*	0.14	0.17	1.20E-04	1.28	OK	0.15	0.15	0.76	1.01	0.16	0.14	0.01	1.10
rs4508240	12	37186069	G/A	*CPNE8*	0.12	0.15	1.21E-04	1.27	OK	0.13	0.13	0.49	0.97	0.14	0.13	0.07	1.08
rs10515822	5	160512672	A/G	*GABRB2*	0.07	0.09	1.22E-04	1.27	OK	0.09	0.08	0.56	0.98	0.09	0.08	0.09	1.07
rs2686830	7	47957563	A/G	*PKD1L1*	0.47	0.51	1.23E-04	1.17	OK	0.49	0.49	0.65	0.99	0.50	0.48	0.04	1.05
rs11708730	3	72008678	C/T	*PROK2*	0.27	0.24	1.23E-04	0.83	OK	0.25	0.25	0.86	0.98	0.25	0.26	6.14E-03	0.92
rs974627	12	37205791	T/C	*CPNE8*	0.12	0.15	1.24E-04	1.27	OK	0.13	0.13	0.44	0.97	0.14	0.13	0.08	1.07
rs727549	7	83065910	G/A	*SEMA3E*	0.21	0.25	1.25E-04	1.19	OK	0.22	0.22	0.40	0.97	0.23	0.22	0.12	1.05
rs37391	5	123553864	G/A	*ZNF608*	0.33	0.30	1.27E-04	0.86	OK	0.32	0.31	0.74	1.00	0.31	0.32	5.28E-03	0.94
rs10839984	11	8137470	G/A	*RIC3*	0.25	0.21	1.27E-04	0.82	OK	0.23	0.24	0.84	1.00	0.23	0.24	0.02	0.92
rs1639304	7	83017558	G/A	*SEMA3E*	0.21	0.25	1.27E-04	1.19	OK	0.23	0.22	0.18	0.95	0.23	0.22	0.24	1.04
rs1693389	7	83014198	C/T	*SEMA3E*	0.21	0.25	1.27E-04	1.19	OK	0.23	0.22	0.22	0.96	0.23	0.22	0.18	1.04
rs6532197	4	91016324	G/A	*MMRN1*	0.07	0.09	1.28E-04	1.39	OK	0.07	0.09	4.19E-04	1.28	0.09	0.07	1.10E-07	1.32
rs10136071	14	32580195	T/G	*NPAS3*	0.35	0.39	1.32E-04	1.18	OK	0.38	0.36	0.10	0.95	0.37	0.37	0.21	1.04
rs2949065	2	36044594	C/T	*MRPL50P1*	0.37	0.33	1.32E-04	0.84	OK	0.35	0.34	0.04	0.94	0.33	0.36	3.61E-05	0.90
rs934397	2	237371678	T/C	*CXCR7*	0.23	0.19	1.32E-04	0.83	OK	0.21	0.22	0.11	1.06	0.21	0.22	0.27	0.97
rs4478801	1	152731196	G/A	*SHE*	0.37	0.40	1.33E-04	1.18	OK	0.38	0.38	0.49	0.98	0.39	0.38	0.07	1.05
rs9924308	16	30062241	A/G	*MAPK3*	0.48	0.44	1.34E-04	0.86	OK	0.46	0.46	0.81	1.01	0.45	0.47	0.01	0.94
rs972427	3	21339149	T/C	*VENTXP7*	0.29	0.32	1.35E-04	1.18	OK	0.32	0.29	2.35E-03	0.89	0.30	0.30	0.81	1.00
rs2681051	7	11615690	A/G	*KIAA0960*	0.30	0.26	1.35E-04	0.83	OK	0.28	0.29	0.31	1.04	0.28	0.29	0.12	0.96
rs8078967	17	41363929	T/C	*MAPT*	0.43	0.47	1.36E-04	1.17	OK	0.45	0.45	0.74	1.01	0.46	0.44	6.65E-03	1.07
rs7900480	10	35378705	A/G	*CUL2*	0.33	0.37	1.37E-04	1.19	OK	0.35	0.34	0.21	0.96	0.35	0.34	0.13	1.05
rs8034843	15	55368601	A/G	*TCF12*	0.17	0.20	1.37E-04	1.19	OK	0.18	0.18	0.98	1.00	0.19	0.18	0.02	1.07
rs12118128	1	221904876	C/T	*LOC388743*	0.07	0.10	1.37E-04	1.32	OK	0.09	0.08	0.16	0.92	0.09	0.08	0.21	1.06
rs643786	19	55547761	A/C	*NAPSA*	0.24	0.28	1.38E-04	1.21	OK	0.26	0.26	0.39	0.98	0.26	0.25	0.08	1.07
rs922687	15	71635861	A/C	*NPTN*	0.44	0.48	1.39E-04	1.17	OK	0.45	0.47	0.01	1.08	0.47	0.45	1.42E-05	1.12
rs11082819	18	46144485	C/T	*C18orf24*	0.34	0.37	1.41E-04	1.18	OK	0.36	0.36	0.64	1.02	0.36	0.35	4.88E-03	1.08
rs4697508	4	24576450	C/A	*DKFZp761B107*	0.23	0.26	1.42E-04	1.22	OK	0.24	0.25	0.24	1.03	0.25	0.24	6.17E-04	1.10
rs11595185	10	25231376	G/A	*PRTFDC1*	0.32	0.28	1.43E-04	0.84	OK	0.31	0.30	0.02	0.93	0.29	0.32	1.93E-05	0.89
rs11107270	12	92834257	G/A	*CRADD*	0.06	0.04	1.44E-04	0.70	MAF<0.05	NA	NA	NA	NA	NA	NA	NA	NA
rs1430961	4	90771943	C/T	*SNCA*	0.07	0.09	1.45E-04	1.34	OK	0.08	0.09	0.01	1.13	0.09	0.08	5.92E-06	1.21
rs1353615	7	83013723	A/C	*SEMA3E*	0.21	0.25	1.47E-04	1.19	OK	0.23	0.22	0.16	0.95	0.23	0.22	0.27	1.03
rs1950712	14	68550317	G/A	*RPS29P1*	0.08	0.06	1.47E-04	0.75	OK	0.08	0.07	0.59	0.95	0.07	0.08	3.23E-03	0.86
rs11852946	15	36975713	C/A	*FLJ35695*	0.10	0.13	1.48E-04	1.30	Non designable for Stage II	NA	NA	NA	NA	NA	NA	NA	NA
rs6473485	8	51979283	C/T	*SNTG1*	0.31	0.35	1.50E-04	1.17	OK	0.31	0.30	0.76	0.99	0.32	0.31	0.08	1.05
rs11656130	17	64912041	G/T	*MAP2K6*	0.45	0.41	1.50E-04	0.85	OK	0.45	0.45	0.83	1.01	0.44	0.45	0.05	0.95
rs1035833	2	230417442	C/T	*TRIP12*	0.28	0.32	1.52E-04	1.19	OK	0.30	0.30	0.81	1.00	0.30	0.29	0.03	1.07
rs4789636	17	69710434	T/C	*RPL38*	0.47	0.43	1.52E-04	0.86	OK	0.45	0.45	0.77	1.01	0.44	0.46	0.02	0.95
rs7589111	2	131887358	A/G	*LOC389043*	0.35	0.39	1.53E-04	1.18	Bad cluster	NA	NA	NA	NA	NA	NA	NA	NA
rs16925839	10	70277867	T/C	*STOX1*	0.48	0.52	1.53E-04	1.16	OK	0.49	0.48	0.40	0.97	0.50	0.49	0.10	1.04
rs12714369	2	3041245	A/G	*LOC729897*	0.50	0.47	1.56E-04	0.86	OK	0.48	0.50	0.03	1.07	0.49	0.49	0.47	0.98
rs4742236	9	676753	A/G	*ANKRD15*	0.14	0.17	1.56E-04	1.25	OK	0.15	0.15	0.12	1.09	0.16	0.14	4.88E-04	1.14
rs11222109	11	129841446	A/G	*ADAMTS15*	0.46	0.50	1.57E-04	1.17	OK	0.47	0.47	0.98	1.00	0.48	0.47	0.02	1.06

rs3823906	7	83067501	C/A	*SEMA3E*	0.21	0.24	1.59E-04	1.19	OK	0.22	0.22	0.34	0.97	0.23	0.22	0.16	1.04
rs7251728	19	62492200	A/G	*ZNF460*	0.38	0.34	1.60E-04	0.86	Non concordant	NA	NA	NA	NA	NA	NA	NA	NA
rs12624568	20	2187669	T/C	*TGM3*	0.08	0.11	1.60E-04	1.33	Non designable for Stage II	NA	NA	NA	NA	NA	NA	NA	NA
rs6044218	20	16605508	G/A	*RPL7AL3*	0.47	0.43	1.60E-04	0.86	OK	0.45	0.45	0.80	1.01	0.45	0.46	0.02	0.95
rs11602361	11	122068548	A/G	*STS-1*	0.36	0.39	1.64E-04	1.17	OK	0.38	0.37	0.66	0.99	0.38	0.37	0.04	1.06
rs1782322	10	70156331	C/A	*CCAR1*	0.47	0.43	1.65E-04	0.86	OK	0.45	0.45	0.84	1.01	0.44	0.46	0.02	0.94
rs700802	9	78424532	G/A	*KIAA0367*	0.22	0.19	1.66E-04	0.82	OK	0.21	0.20	0.41	0.99	0.20	0.21	2.33E-03	0.92
rs1147255	12	125968187	T/C	*LOC121296*	0.09	0.07	1.66E-04	0.75	OK	0.09	0.08	0.18	0.93	0.08	0.09	7.29E-04	0.86
rs12817211	12	48865665	T/C	*LIMA1*	0.23	0.19	1.66E-04	0.83	OK	0.21	0.21	0.34	1.05	0.21	0.22	0.07	0.96
rs13076171	3	71988841	G/A	*PROK2*	0.51	0.47	1.66E-04	0.86	OK	0.48	0.49	0.42	1.03	0.48	0.49	0.05	0.95
rs2686821	7	47941607	G/A	*PKD1L1*	0.48	0.52	1.67E-04	1.16	OK	0.49	0.49	0.66	0.99	0.50	0.49	0.04	1.05
rs333917	17	64863054	G/A	*ABCA5*	0.32	0.28	1.67E-04	0.83	OK	0.31	0.31	0.59	1.03	0.30	0.31	0.07	0.95
rs11226125	11	103418178	T/C	*PDGFD*	0.48	0.44	1.68E-04	0.86	OK	0.45	0.47	0.04	1.07	0.46	0.47	0.37	0.98
rs10826765	10	30447990	C/T	*KIAA1462*	0.31	0.34	1.70E-04	1.17	OK	0.32	0.32	0.52	0.98	0.33	0.31	0.07	1.05
rs12130076	1	238984728	G/A	*LOC645939*	0.13	0.16	1.71E-04	1.24	OK	0.14	0.13	0.32	0.94	0.14	0.14	0.16	1.04
rs6079575	20	14755599	A/G	*C20orf133*	0.06	0.04	1.71E-04	0.72	MAF<0.05	NA	NA	NA	NA	NA	NA	NA	NA
rs1438339	3	29457050	T/C	*RBMS3*	0.18	0.21	1.73E-04	1.22	OK	0.18	0.18	0.69	0.98	0.19	0.18	0.07	1.06
rs7164298	15	55370593	G/A	*TCF12*	0.17	0.20	1.73E-04	1.19	OK	0.18	0.17	0.31	0.95	0.18	0.18	0.19	1.03
rs10826764	10	30447878	A/G	*KIAA1462*	0.34	0.38	1.74E-04	1.17	OK	0.35	0.35	0.72	0.98	0.36	0.35	0.04	1.05
rs7678831	4	159660989	G/T	*RXFP1*	0.19	0.22	1.74E-04	1.27	OK	0.21	0.20	0.05	0.94	0.20	0.20	0.41	1.06
rs2317515	8	137044531	T/C	*KHDRBS3*	0.50	0.46	1.75E-04	0.86	OK	0.49	0.49	0.85	1.01	0.48	0.49	0.04	0.95
rs9957722	18	46100998	T/C	*CXXC1*	0.41	0.45	1.76E-04	1.17	OK	0.42	0.43	0.64	1.02	0.43	0.42	7.31E-03	1.07
rs681210	21	43603771	T/C	*FLJ41733*	0.31	0.35	1.77E-04	1.18	OK	0.33	0.33	0.43	1.05	0.34	0.32	2.25E-03	1.10
rs3924079	5	117871768	T/C	*DTWD2*	0.18	0.15	1.80E-04	0.84	HWE<10-7	NA	NA	NA	NA	NA	NA	NA	NA
rs9988732	10	30438875	A/G	*KIAA1462*	0.39	0.43	1.80E-04	1.17	OK	0.40	0.41	0.28	1.04	0.42	0.40	1.72E-03	1.08
rs699052	12	25077644	T/G	*LOC645177*	0.32	0.35	1.81E-04	1.17	OK	0.33	0.32	0.40	0.97	0.33	0.32	0.11	1.04
rs4505549	2	195996381	T/C	*LOC391470*	0.37	0.41	1.82E-04	1.18	OK	0.38	0.38	0.61	0.98	0.39	0.38	0.08	1.05
rs1443562	8	92997929	T/C	*MRPS16P1*	0.30	0.33	1.86E-04	1.21	OK	0.31	0.31	0.94	0.99	0.31	0.30	0.03	1.07
rs997120	22	31438536	T/C	*SYN3*	0.10	0.12	1.87E-04	1.28	OK	0.10	0.11	0.22	1.07	0.11	0.10	1.48E-03	1.14
rs7813504	8	88868935	G/T	*SOX5P*	0.19	0.22	1.87E-04	1.17	OK	0.20	0.21	0.20	1.06	0.22	0.20	6.33E-04	1.10
rs4534200	9	25642508	C/T	*TUSC1*	0.49	0.45	1.87E-04	0.86	OK	0.50	0.49	0.18	0.96	0.47	0.49	1.85E-03	0.93
rs787274	9	114590184	A/C	*SNX30*	0.07	0.10	1.87E-04	1.36	Bad cluster	NA	NA	NA	NA	NA	NA	NA	NA
rs1481088	15	71629314	A/G	*NPTN*	0.46	0.50	1.89E-04	1.17	OK	0.47	0.49	0.03	1.07	0.49	0.47	4.11E-05	1.11
rs6851219	4	77398854	T/C	*SCARB2*	0.09	0.12	1.90E-04	1.28	OK	0.09	0.11	0.02	1.13	0.11	0.09	4.69E-05	1.18
rs2141202	23	144519417	T/G	*LOC347422*	0.48	0.51	1.91E-04	1.26	HWE<10-7	NA	NA	NA	NA	NA	NA	NA	NA
rs4784045	16	57094125	G/A	*NDRG4*	0.43	0.39	1.91E-04	0.85	OK	0.41	0.42	0.53	1.02	0.41	0.42	0.08	0.96
rs3764941	5	135497426	C/A	*SMAD5*	0.28	0.31	1.91E-04	1.20	OK	0.29	0.28	0.20	0.96	0.29	0.29	0.22	1.05
rs4965303	15	98641293	C/T	*ADAMTS17*	0.19	0.22	1.92E-04	1.21	OK	0.20	0.20	0.73	1.00	0.20	0.19	0.01	1.07
rs2243988	21	35124310	T/C	*RUNX1*	0.42	0.39	1.92E-04	0.87	OK	0.39	0.40	0.13	1.06	0.40	0.41	0.14	0.97
rs13273663	8	51712711	T/C	*SNTG1*	0.37	0.40	1.93E-04	1.17	Non designable for Stage II	NA	NA	NA	NA	NA	NA	NA	NA
rs999867	10	104494554	A/G	*SFXN2*	0.10	0.08	1.94E-04	0.77	OK	0.09	0.08	4.07E-03	0.84	0.08	0.10	5.65E-07	0.80
rs11705555	22	26536912	C/A	*MN1*	0.23	0.27	1.94E-04	1.18	OK	0.25	0.25	1.00	1.01	0.25	0.24	0.02	1.08
rs9619283	22	31363048	A/G	*SYN3*	0.13	0.16	1.95E-04	1.25	OK	0.15	0.14	0.36	0.95	0.15	0.14	0.13	1.05
rs1882832	14	74870997	T/C	*FOS*	0.41	0.38	1.95E-04	0.86	OK	0.39	0.41	0.07	1.07	0.40	0.40	0.28	0.98
rs2736050	8	15718351	A/G	*LOC137012*	0.39	0.42	1.96E-04	1.16	OK	0.39	0.40	0.65	1.02	0.41	0.39	0.01	1.06
rs4775330	15	59022174	A/G	*RORA*	0.32	0.29	1.96E-04	0.85	OK	0.32	0.32	0.70	1.01	0.31	0.32	0.07	0.96
rs12172730	1	104913058	A/G	*LOC642337*	0.09	0.07	1.98E-04	0.75	OK	0.09	0.08	0.04	0.87	0.08	0.09	4.87E-05	0.82
rs9288651	2	230439641	T/C	*TRIP12*	0.29	0.32	1.98E-04	1.18	OK	0.30	0.30	0.70	1.00	0.31	0.29	0.05	1.06
rs1108089	1	221907077	C/T	*LOC388743*	0.09	0.11	1.98E-04	1.28	Bad cluster/stage I	NA	NA	NA	NA	NA	NA	NA	NA
rs1533969	2	36036959	A/G	*MRPL50P1*	0.15	0.17	1.98E-04	1.23	OK	0.15	0.16	0.16	1.08	0.33	0.36	2.14E-05	0.90
rs2710697	12	53684257	T/C	*NEUROD4*	0.12	0.09	1.99E-04	0.80	OK	0.11	0.11	0.40	0.96	0.10	0.12	3.25E-03	0.90
rs7622285	3	146367022	G/A	*GM2AP*	0.29	0.32	2.01E-04	1.20	OK	0.29	0.29	0.83	0.99	0.30	0.29	0.06	1.06
rs1863985	16	57181595	A/C	*CNOT1*	0.11	0.14	2.01E-04	1.24	OK	0.13	0.12	0.06	0.91	0.12	0.12	0.52	1.02
rs10908183	11	68962197	A/G	*LOC390218*	0.20	0.23	2.01E-04	1.19	OK	0.20	0.21	0.61	1.03	0.22	0.20	0.02	1.08
rs1662694	17	64869168	G/A	*ABCA5*	0.32	0.28	2.07E-04	0.83	OK	0.31	0.31	0.71	1.02	0.30	0.31	0.05	0.95
rs10854627	22	31433918	G/A	*SYN3*	0.08	0.11	2.07E-04	1.30	IMISS>0.1	NA	NA	NA	NA	NA	NA	NA	NA
rs2102480	3	87657428	C/T	*LOC643766*	0.08	0.11	2.07E-04	1.54	Non designable for Stage II	NA	NA	NA	NA	NA	NA	NA	NA
rs13081379	3	193918614	A/G	*FGF12*	0.19	0.16	2.07E-04	0.80	OK	0.18	0.18	0.89	1.00	0.18	0.19	0.04	0.93
rs7767977	6	5530769	G/A	*FARS2*	0.16	0.19	2.08E-04	1.25	Non designable for Stage II	NA	NA	NA	NA	NA	NA	NA	NA
rs2009817	8	15721394	T/C	*LOC137012*	0.39	0.42	2.09E-04	1.16	OK	0.39	0.39	0.86	1.00	0.40	0.39	0.08	1.05
rs9374809	6	119977195	G/T	*LOC728727*	0.29	0.26	2.10E-04	0.83	OK	0.27	0.28	0.32	1.05	0.27	0.28	0.07	0.95
rs10504370	8	65150536	C/T	*LOC729415*	0.06	0.08	2.14E-04	1.32	OK	0.06	0.06	0.99	1.00	0.07	0.06	0.04	1.10
rs4340037	11	8084734	C/A	*TUB*	0.24	0.21	2.14E-04	0.83	OK	0.23	0.23	0.64	1.01	0.22	0.23	0.04	0.93
rs6800573	3	143828507	T/C	*PLS1*	0.16	0.13	2.17E-04	0.80	OK	0.16	0.15	0.12	0.93	0.14	0.16	3.50E-04	0.88
rs4669060	2	6429026	C/A	*LOC391349*	0.19	0.16	2.18E-04	0.82	Non	NA	NA	NA	NA	NA	NA	NA	NA

									concordant								
rs903056	3	14785294	G/A	*C3orf20*	0.45	0.49	2.18E-04	1.17	Bad cluster	NA	NA	NA	NA	NA	NA	NA	NA
rs880183	19	2000314	A/G	*MKNK2*	0.26	0.29	2.19E-04	1.19	OK	0.28	0.28	0.59	0.98	0.28	0.27	0.04	1.06
rs1491923	12	38877384	C/T	*LRRK2*	0.31	0.34	2.20E-04	1.20	OK	0.31	0.33	0.01	1.10	0.33	0.31	1.55E-05	1.14
rs2487707	10	70435098	T/G	*KIAA1279*	0.49	0.46	2.24E-04	0.86	OK	0.48	0.48	0.96	1.00	0.47	0.49	0.02	0.94
rs264122	5	129675680	T/C	*CHSY-2*	0.32	0.35	2.25E-04	1.17	OK	0.32	0.33	0.55	1.02	0.34	0.32	6.81E-03	1.08
rs1223271	20	13244912	A/G	*C20orf82*	0.15	0.12	2.28E-04	0.81	OK	0.14	0.13	0.01	0.89	0.13	0.15	4.85E-06	0.85
rs11248060	4	954359	T/C	*DGKQ*	0.12	0.14	2.28E-04	1.24	OK	0.12	0.13	0.07	1.10	0.13	0.12	4.03E-04	1.14
rs6800015	3	180262240	C/T	*ZMAT3*	0.26	0.23	2.30E-04	0.83	OK	0.26	0.25	0.50	0.96	0.24	0.26	5.31E-03	0.91
rs17275640	1	176155379	T/C	*SEC16B*	0.13	0.16	2.31E-04	1.22	Bad cluster	NA	NA	NA	NA	NA	NA	NA	NA
rs2169166	8	105999385	A/G	*LOC644103*	0.31	0.27	2.33E-04	0.84	OK	0.29	0.29	0.91	0.99	0.29	0.30	0.01	0.93
rs7666265	4	77395305	A/G	*SCARB2*	0.19	0.22	2.33E-04	1.19	OK	0.19	0.20	0.07	1.05	0.21	0.19	5.52E-04	1.09
rs2586469	17	45682246	C/T	*LOC729160*	0.22	0.19	2.35E-04	0.83	OK	0.22	0.21	0.12	0.94	0.20	0.22	5.25E-04	0.90
rs6903627	6	120169406	T/C	*LOC728727*	0.16	0.19	2.36E-04	1.21	OK	0.17	0.17	0.79	1.00	0.18	0.17	0.05	1.07
rs4517741	15	90711310	G/A	*ST8SIA2*	0.14	0.16	2.37E-04	1.21	OK	0.15	0.14	0.53	0.96	0.15	0.14	0.09	1.05
rs7920137	10	73806703	G/A	*CBARA1*	0.41	0.44	2.38E-04	1.15	OK	0.42	0.43	0.28	1.04	0.43	0.41	1.96E-03	1.08
rs10765137	10	129278636	C/T	*DOCK1*	0.40	0.36	2.39E-04	0.86	OK	0.40	0.39	0.60	0.98	0.38	0.40	0.01	0.94
rs9377145	6	148961594	C/T	*SASH1*	0.18	0.21	2.41E-04	1.22	OK	0.19	0.19	0.80	1.02	0.20	0.19	9.94E-03	1.10
rs2962101	5	35171498	C/T	*PRLR*	0.11	0.13	2.43E-04	1.28	OK	0.11	0.11	0.27	0.94	0.11	0.11	0.26	1.05
rs11766212	7	47910478	T/C	*PKD1L1*	0.38	0.35	2.43E-04	0.86	IMISS>0.1	NA	NA	NA	NA	NA	NA	NA	NA
rs9299039	9	680460	T/C	*ANKRD15*	0.25	0.22	2.44E-04	0.84	OK	0.23	0.22	0.26	0.95	0.22	0.24	4.12E-04	0.89
rs473532	2	165021032	A/G	*GRB14*	0.33	0.37	2.44E-04	1.17	OK	0.34	0.34	0.73	0.99	0.35	0.34	0.05	1.05
rs1369642	15	45692185	G/A	*SEMA6D*	0.34	0.38	2.44E-04	1.17	OK	0.35	0.34	0.07	0.93	0.35	0.35	0.48	1.01
rs2512139	11	117320774	A/G	*TMPRSS13*	0.38	0.34	2.45E-04	0.86	OK	0.37	0.38	0.67	1.02	0.36	0.38	0.08	0.96
rs13437473	6	72711578	T/C	*RIMS1*	0.07	0.09	2.46E-04	1.29	OK	0.08	0.08	0.69	1.02	0.09	0.08	0.01	1.11
rs356229	4	90825620	G/A	*SNCA*	0.36	0.40	2.46E-04	1.16	OK	0.36	0.40	2.59E-06	1.17	0.40	0.36	2.28E-09	1.17
rs7671488	4	122618788	C/T	*LOC729112*	0.46	0.43	2.49E-04	0.86	OK	0.45	0.46	0.25	1.04	0.45	0.46	0.17	0.97
rs398293	9	118023823	A/C	*PAPPA*	0.39	0.43	2.49E-04	1.16	OK	0.41	0.40	0.85	1.00	0.41	0.40	0.04	1.06
rs9846960	3	143790760	G/A	*ATR*	0.42	0.46	2.50E-04	1.17	OK	0.43	0.43	0.86	1.00	0.44	0.43	0.02	1.06
rs10520381	4	178769035	A/G	*LOC285500*	0.18	0.15	2.52E-04	0.82	OK	0.18	0.18	0.75	0.98	0.17	0.18	0.01	0.91
rs2051569	22	31355180	A/C	*SYN3*	0.30	0.34	2.52E-04	1.17	OK	0.32	0.31	0.12	0.95	0.32	0.31	0.30	1.03
rs9593152	13	75495388	G/A	*FLJ35379*	0.29	0.33	2.52E-04	1.15	OK	0.30	0.30	0.71	0.99	0.31	0.30	0.05	1.05
rs2616510	8	89087241	C/A	*MMP16*	0.19	0.22	2.53E-04	1.26	OK	0.20	0.21	0.14	1.05	0.22	0.20	5.79E-04	1.12
rs7625872	3	45132572	A/C	*CDCP1*	0.15	0.12	2.54E-04	0.82	OK	0.13	0.13	0.86	1.02	0.13	0.14	5.37E-03	0.93
rs4769388	13	24393134	A/G	*CENPJ*	0.31	0.28	2.55E-04	0.85	OK	0.31	0.31	0.96	1.02	0.30	0.31	0.03	0.95
rs4505777	4	164419696	G/A	*LOC133332*	0.18	0.15	2.60E-04	0.82	OK	0.17	0.17	0.78	1.00	0.16	0.17	0.03	0.92
rs6427069	1	165391458	C/T	*LOC391130*	0.39	0.35	2.60E-04	0.86	OK	0.37	0.37	0.83	1.02	0.36	0.38	0.03	0.95
rs207465	21	24120442	G/T	*TUBAP*	0.35	0.39	2.60E-04	1.17	IMISS>0.1	NA	NA	NA	NA	NA	NA	NA	NA
rs16959883	15	45698555	T/C	*SEMA6D*	0.30	0.33	2.60E-04	1.18	OK	0.31	0.29	0.07	0.93	0.31	0.30	0.48	1.02
rs1881925	3	110444079	C/T	*DPPA2*	0.47	0.51	2.62E-04	1.16	OK	0.49	0.48	0.06	0.94	0.49	0.48	0.42	1.02
rs1484127	8	51888207	A/G	*SNTG1*	0.32	0.35	2.63E-04	1.17	OK	0.32	0.31	0.85	0.99	0.33	0.32	0.07	1.04
rs13192471	6	32779081	C/T	*HLA-DQB1*	0.14	0.16	2.65E-04	1.22	OK	0.14	0.14	0.83	1.02	0.15	0.14	0.02	1.09
rs1613367	11	104416241	G/T	*COPI*	0.40	0.44	2.65E-04	1.16	IMISS>0.1	NA	NA	NA	NA	NA	NA	NA	NA
rs26286	5	14219402	T/G	*TRIO*	0.45	0.49	2.67E-04	1.16	OK	0.47	0.49	0.04	1.07	0.49	0.46	5.38E-05	1.11
rs11136092	8	22522433	G/T	*KIAA1967*	0.32	0.36	2.68E-04	1.18	OK	0.33	0.34	0.14	1.05	0.35	0.33	8.06E-04	1.10
rs996243	6	137895153	A/C	*LOC391040*	0.26	0.22	2.68E-04	0.85	OK	0.26	0.25	0.09	0.94	0.24	0.26	6.53E-04	0.91
rs7094852	10	129223387	C/T	*DOCK1*	0.25	0.28	2.69E-04	1.19	OK	0.26	0.27	0.24	1.07	0.27	0.26	1.96E-03	1.11
rs2150279	14	53343338	C/T	*BMP4*	0.40	0.44	2.69E-04	1.17	OK	0.41	0.42	0.15	1.05	0.43	0.41	6.43E-04	1.09
rs1868108	3	162073563	G/A	*PPM1L*	0.31	0.34	2.70E-04	1.18	Non concordant	NA	NA	NA	NA	NA	NA	NA	NA
rs7854502	9	686683	A/G	*ANKRD15*	0.46	0.42	2.71E-04	0.86	OK	0.45	0.43	0.09	0.95	0.43	0.45	1.61E-04	0.91
rs19334	8	9047316	T/C	*PPP1R3B*	0.30	0.34	2.73E-04	1.19	OK	0.33	0.32	0.20	0.95	0.32	0.32	0.18	1.03
rs2046065	12	65458480	T/C	*GRIP1*	0.44	0.40	2.74E-04	0.86	OK	0.44	0.42	0.06	0.94	0.41	0.44	2.69E-04	0.91
rs925030	8	25298518	A/C	*DOCK5*	0.41	0.37	2.74E-04	0.85	OK	0.40	0.39	0.07	0.94	0.38	0.41	3.14E-04	0.91
rs9842991	3	70554058	A/G	*LOC654340*	0.31	0.35	2.75E-04	1.16	OK	0.31	0.31	0.91	1.00	0.32	0.31	0.06	1.05
rs9876540	3	45137320	T/C	*CDCP1*	0.14	0.12	2.76E-04	0.81	OK	0.13	0.12	0.80	1.02	0.12	0.13	4.27E-03	0.92
rs6480643	10	74204180	T/C	*CCDC109A*	0.31	0.35	2.76E-04	1.15	Bad cluster/stage I	NA	NA	NA	NA	NA	NA	NA	NA
rs9489765	6	120038756	C/T	*LOC728727*	0.43	0.40	2.80E-04	0.86	OK	0.42	0.42	0.57	1.02	0.41	0.43	0.07	0.96
rs10996742	10	67294261	G/A	*CTNNA3*	0.19	0.16	2.81E-04	0.81	OK	0.18	0.18	0.40	1.03	0.18	0.18	0.11	0.94
rs2896159	7	114989770	C/T	*TFEC*	0.31	0.35	2.82E-04	1.17	OK	0.34	0.33	0.06	0.94	0.33	0.33	0.33	1.03
rs10996743	10	67294317	A/G	*CTNNA3*	0.19	0.16	2.82E-04	0.81	OK	0.18	0.18	0.44	1.02	0.18	0.18	0.09	0.94
rs1453815	4	24566751	C/T	*DKFZp761B107*	0.23	0.26	2.83E-04	1.20	OK	0.24	0.25	0.22	1.04	0.25	0.24	8.57E-04	1.10
rs11096577	2	19114014	G/A	*FLJ41481*	0.15	0.18	2.84E-04	1.20	OK	0.17	0.16	0.80	1.00	0.17	0.16	0.04	1.07
rs7024926	9	82766092	A/C	*TLE1*	0.42	0.46	2.85E-04	1.16	OK	0.44	0.45	0.18	1.04	0.45	0.43	4.81E-04	1.09
rs2878172	14	54443420	G/A	*GCH1*	0.43	0.39	2.85E-04	0.87	OK	0.42	0.41	0.12	0.95	0.40	0.42	4.71E-04	0.92
rs10510622	3	29670592	C/T	*RBMS3*	0.18	0.21	2.85E-04	1.16	OK	0.18	0.18	0.65	0.97	0.19	0.18	0.10	1.03
rs4422788	8	51843584	C/T	*SNTG1*	0.32	0.35	2.86E-04	1.16	OK	0.32	0.32	0.88	0.99	0.33	0.32	0.07	1.05
rs6050867	20	25678968	C/T	*LOC728882*	0.09	0.11	2.86E-04	1.26	OK	0.09	0.09	0.66	0.99	0.10	0.09	0.12	1.07
rs187286	1	215659907	G/A	*GPATCH2*	0.10	0.13	2.87E-04	1.26	OK	0.12	0.11	0.13	0.93	0.12	0.11	0.37	1.04
rs1027493	1	165399506	A/G	*LOC391130*	0.33	0.37	2.87E-04	1.17	OK	0.35	0.33	0.03	0.92	0.35	0.34	0.65	1.01
rs11240572	1	204074636	A/C	*PM20D1*	0.04	0.02	1.30E-04	0.63	add. SNP	0.04	0.03	1.81E-03	0.72	0.03	0.04	6.11E-07	0.67
rs823128	1	203980001	G/A	*NUCKS1*	0.04	0.03	1.93E-04	0.64	add. SNP	0.04	0.03	1.96E-04	0.68	0.03	0.04	7.29E-08	0.66

rs708730	1	202509437	G/A	*SLC41A1*	0.17	0.15	2.66E-03	0.85	add. SNP	0.17	0.16	0.10	0.94	0.16	0.17	1.59E-03	0.90
rs823156	1	204031263	G/A	*SLC41A1*	0.18	0.16	4.31E-03	0.85	add. SNP	0.17	0.16	0.06	0.93	0.16	0.18	7.60E-04	0.89
rs12502586	4	15335662	A/G	*BST1*	0.10	0.12	6.51E-03	1.20	add. SNP	0.10	0.10	0.89	1.00	0.11	0.10	0.07	1.08
rs947211	1	202484322	A/G	*SLC41A1*	0.24	0.22	0.01	0.88	add. SNP	0.24	0.23	0.26	0.96	0.23	0.24	0.01	0.93
rs12646913	4	15348374	G/A	*BST1*	0.08	0.07	0.04	0.85	add. SNP	0.08	0.07	0.32	0.97	0.07	0.08	0.03	0.92
rs4698412	4	15346446	G/A	*BST1*	0.44	0.43	0.08	0.93	add. SNP	0.45	0.43	0.14	0.95	0.43	0.44	0.03	0.94
rs11931532	4	15334864	C/T	*BST1*	0.03	0.03	0.58	0.94	add. SNP	0.03	0.03	0.55	0.93	0.03	0.03	0.44	0.94
rs12645693	4	15338632	A/G	*BST1*	0.03	0.03	0.63	0.95	add. SNP	0.03	0.03	0.49	0.92	0.03	0.03	0.44	0.94
rs4538475	4	15347035	G/A	*BST1*	0.16	0.16	0.76	1.01	add. SNP	0.17	0.16	0.17	0.95	0.16	0.16	0.27	0.98
rs7672311	4	15340788	A/G	*BST1*	NA	NA	NA	NA	add. SNP	0.08	0.08	0.57	0.99	NA	NA	NA	NA

Table displaying the 396 SNPs with lowest p value following a trend mode of association after our Stage I analysis. For Stage II, 10 of the 384 most associated SNPs, were predicted to originate an inefficient assay with GoldenGate technology and 2 couldn't be clustered properly. These twelve SNPs were removed from further analysis and were substituted with the next most associated ones according to a trend mode of association (shaded). 345 of this final list of 384 passed our MAF, HWE and missingness filters.
Additionally the 12 SNPs are included at the bottom of the list, which were genotyped in stage II, to replicate the Asian risk loci on chromosome 1 and 4.

Position from NCBI genome build 36; chr. = Chromosome; MAF U = minor allele frequency in controls; MAF A = minor allele frequency in cases; cOR = common Odds ratio; Het = heterozygote; Hom = minor allele homozygote; CI = confidence interval.

Supplementary table 2: Additional Odds ratios for the top three SNPs of the 2 loci that surpass Bonferroni threshold for multiple testing in both stages and the top three SNPs in the *LRRK2* locus and the additional loci in chromosomes 1 and 4.

locus			Alleles	Stage I		Stage II		Stage I and II combined	
SNP	Chr.	Position	(minor/ major)	OR het. (95%CI)	OR hom. (95%CI)	OR het. (95%CI)	OR hom. (95%CI)	OR het. (95%CI)	OR hom. (95%CI)
Genome-wide significant loci									
rs393152	17	41074926	G/A	0.75 (0.66 - 0.84)	0.67 (0.45 - 0.89)	0.79 (0.72-0.87)	0.59 (0.46-0.76)	0.77 (0.71-0.83)	0.59 (0.49-0.71)
rs199533	17	42184098	T/C	0.71 (0.62 - 0.81)	0.71 (0.47 - 0.96)	0.82 (0.74-0.90)	0.59 (0.45-0.76)	0.77 (0.72-0.84)	0.61 (0.49-0.74)
rs17563986	17	41347100	C/T	0.75 (0.66 - 0.84)	0.69 (0.46 - 0.92)	0.82 (0.75-0.91)	0.58 (0.45-0.73)	0.79 (0.73-0.85)	0.60 (0.49-0.72)
rs2736990	4	90897564	C/T	1.17 (1.07 - 1.27)	1.45 (1.34 - 1.56)	1.30 (1.16-1.44)	1.45 (1.28-1.64)	1.25 (1.15-1.36)	1.51 (1.37-1.66)
rs3857059	4	90894261	G/A	1.35 (1.24 - 1.46)	4.39 (3.94 - 4.84)	1.31 (1.16-1.47)	3.44 (1.88-6.29)	1.34 (1.22-1.47)	3.57 (2.33-5.47)
rs11931074	4	90858538	T/G	1.35 (1.23 - 1.46)	4.39 (3.94 - 4.84)	1.31 (1.16-1.48)	3.13 (1.73-5.67)	1.33 (1.21-1.46)	3.31 (2.18-5.03)
Other loci									
rs823128	1	203980001	C/T	0.64 (0.50-0.82)	0.38 (0.08-1.68)	0.68 (0.54-0.84)	0.51 (0.13-1.96)	0.66 (0.56-0.77)	0.42 (0.16-1.12)
rs11240572	1	204074636	T/G	0.65 (0.50-0.83)	0.13 (0.01-2.30)	0.73 (0.59-0.90)	0.40 (0.08-1.97)	0.69 (0.59-0.81)	0.23 (0.05-1.00)
rs823156	1	204031263	C/T	0.86 (0.75-0.97)	0.72 (0.50-1.02)	0.89 (0.79-1.00)	0.93 (0.69-1.24)	0.87 (0.80-0.95)	0.84 (0.67-1.05)
rs12646913	4	15348374	G/A	0.86 (0.73-1.01)	0.66 (0.28-1.54)	0.87 (0.75-1.01)	1.69 (0.91-3.15)	0.86 (0.77-0.96)	1.21 (0.76-1.94)
rs4698412	4	15346446	G/A	0.98 (0.86-1.11)	0.85 (0.72-1.01)	0.94 (0.84-1.05)	0.90 (0.78-1.04)	0.96 (0.88-1.04)	0.89 (0.80-0.99)
rs12502586	4	15335662	A/G	1.19 (1.03-1.37)	1.48 (0.91-2.40)	1.02 (0.90-1.16)	0.93 (0.58-1.51)	1.09 (0.99-1.20)	1.14 (0.81-1.60)
rs11564162	12	38729159	C/T	0.89 (0.79-1.01)	0.44 (0.31-0.63)	0.96 (0.88-1.06)	0.80 (0.64-1.01)	0.93 (0.86-1.00)	0.67 (0.55-0.80)
rs2896905	12	38779683	T/C	0.84 (0.74-0.95)	0.67 (0.56-0.80)	1.03 (0.94-1.14)	1.01 (0.88-1.16)	0.95 (0.88-1.03)	0.86 (0.77-0.96)
rs1491923	12	38877384	C/T	1.07 (0.95-1.21)	1.52 (1.26-1.84)	1.04 (0.95-1.14)	1.25 (1.07-1.46)	1.06 (0.98-1.14)	1.35 (1.20-1.52)

Position from NCBI genome build 36; chr. = Chromosome; OR = Odds ratio; Het = heterozygote; Hom = minor allele homozygote; CI = confidence interval.

Supplementary table 3: Additive minor allele dosages for each SNP within each of the *SNCA* and *MAPT* loci in combined German and US samples were used in the conditional models to test for possible independence of association with PD. Shown are the results of this analysis.

Conditional logistic regression at SNCA					
CHR	SNP	BP	minor allele	OR	P
4	rs1430961	90771943	C	0.9198	0.5581
4	rs12644119	90822442	A	1.164	0.2612
4	rs356229	90825620	G	1.001	0.9834
4	rs11931074	90858538	T	0.7196	0.72
4	rs3857059	90894261	G	2.196	0.3987
4	rs2736990	90897564	C	1.21	0.003432
4	rs3775439	90928764	A	0.9394	0.5558
4	rs894278	90953558	G	0.8577	0.4264
4	rs6532197	91016324	G	0.9382	0.6937

Supplementary table 4: SNPs at the SNCA locus in PD, Controls and MSA. Comparing 92 pathologically proven MSA cases genotyped at the same markers and previously reported by us[14] with the current data shows a difference between the PD and MSA risk SNPs, rs2736990 being the most significant PD associated SNP and not significantly associated with MSA. Further the most highly associated marker with MSA (rs11931074) is significantly different between PD and MSA ($p=7x10^{-4}$).

		Minor Allele Frequency			P values		
SNP	Allele	PD	MSA	CON	PD vs Con	MSA vs Con	MSA vs PD
rs1430961	C	0.093	0.11	0.082	0.0191	0.1741	0.4283
rs12644119	A	0.124	0.163	0.108	0.0016	0.0178	0.1193
rs356229	G	0.402	0.359	0.363	1.12E-06	0.8937	0.2371
rs11931074	T	0.098	0.174	0.076	7.87E-07	8.91E-07	7.00E-04
rs3857059	G	0.098	0.152	0.075	6.46E-07	1.00E-04	0.0152
rs2736990	T	0.509	0.473	0.46	2.90E-09	0.7379	0.3365
rs3775439	A	0.145	0.217	0.13	0.007	5.00E-04	0.0062
rs894278	G	0.074	0.103	0.06	4.00E-04	0.0146	0.1392
rs6532197	G	0.089	0.141	0.076	0.0027	0.001	0.0148

Supplementary table 5: expression quantitative trait analysis of most significant disease associated SNPs at the *SNCA*, *MAPT*, *LRRK2* and *PARK16* loci. Shown are the association p values between allele load each SNP and the expression levels of the most proximal transcripts.

CHR	SNP	Transcript	Illumina Probe ID	*p* value
4	rs2736990	*SNCA*	1110228	0.3479
4	rs2736990	*SNCA*	6840092	0.5497
4	rs2736990	*MMRN1*	940328	0.8847
17	rs393152	*STH*	1050195	0.3241
17	rs393152	*ARL17P1*	1780139	0.0002787
17	rs393152	*NSF*	2030397	0.03584
17	rs393152	*KIAA1267*	2320280	0.07785
17	rs393152	*LOC474170*	2490142	0.1312
17	rs393152	*C17orf69*	3120403	0.6945
17	rs393152	*ARHGAP27*	3120647	0.9138
17	rs393152	*WNT3*	3780440	0.1844
17	rs393152	*NSF*	3830040	0.00311
17	rs393152	*LRRC37A*	4390484	$1.70x10^{-13}$

17	rs393152	*CRHR1*	4880730	0.6454
17	rs393152	*PLEKHM1*	6760575	0.5906
17	rs393152	*MAPT*	7400379	$4.11x10^{-6}$
1	rs823128	*RAB7L1*	1820082	0.126
1	rs823128	*NUCKS1*	4730386	0.813
12	rs1491923	*SLC2A13*	4730132	0.1398
12	rs1491923	*C12orf40*	7380202	0.4383
12	rs1491923	*LRRK2*	not detected	NA

Supplementary table 6: Adjusted p values from the addition models of association applied.

MarkerName	chr	*bp*	P.value
rs2736990	4	*90897564*	2.40E-08
rs356220	4	*90860363*	1.47E-07
rs3857059	4	*90894261*	2.57E-07
rs11931074	4	*90858538*	3.19E-07
rs3775439	4	*90928764*	7.70E-06
rs12644119	4	*90822442*	4.15E-05
rs894278	4	*90953558*	8.41E-05
rs356229	4	*90825620*	0.0001322
rs199533	17	*42184098*	5.78E-06
rs415430	17	*42214305*	1.09E-05
rs169201	17	*42145386*	1.21E-05
rs393152	17	*41074926*	2.50E-05
rs12185268	17	*41279463*	3.00E-05
rs1981997	17	*41412603*	3.07E-05
rs2668692	17	*41648797*	6.52E-05
rs2896905	12	*38779683*	2.14E-05
rs10784359	12	*38732017*	4.57E-05
rs6582668	12	*37052871*	4.83E-05
rs11564162	12	*38729159*	6.28E-05
rs4508240	12	*37186069*	0.0001047
rs2387807	12	*36733128*	0.0001072
rs974627	12	*37205791*	0.0001294
rs823128	1	203980001	0.0003834
rs823156	1	204031263	0.008226
rs11240572	1	204074636	0.0001927