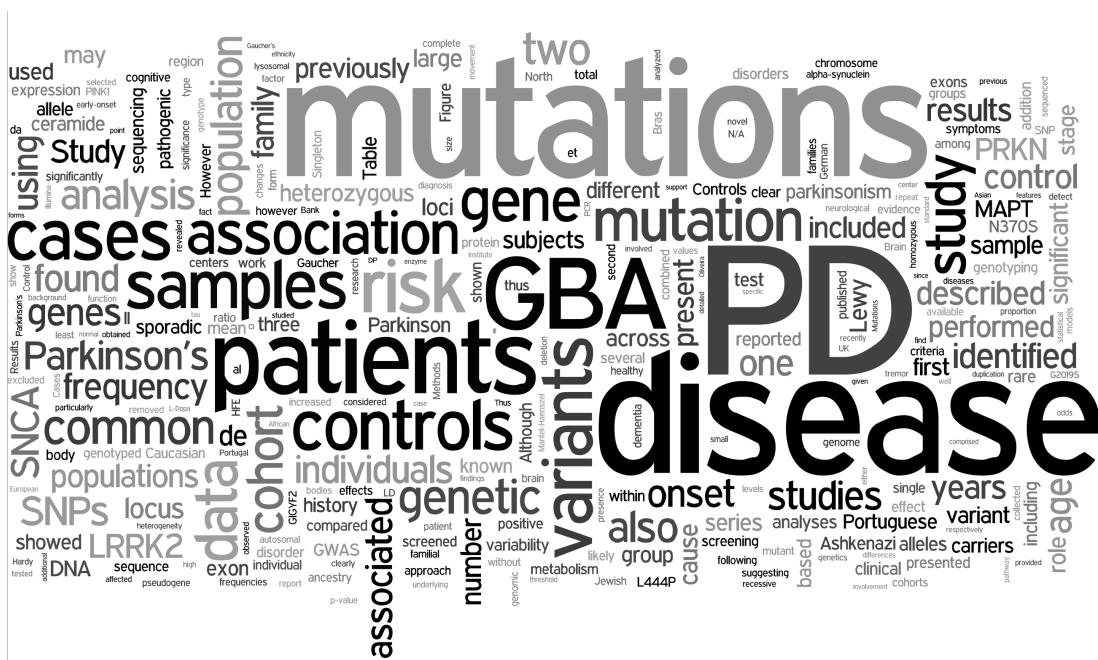


# The Genetic Architecture of Parkinson's Disease: Emphasis on Genetic Susceptibility

## **Supplementary Information**



# José Miguel Tomás Brás

# SUPPLEMENTARY INFORMATION

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Table 1: Variants found in PD cases and controls from the Portuguese series.  $\chi^2$  values, p values, odds ratios and 95% confident interval were calculated for each variant.\* These variants were described as pathogenic by Lautier and colleagues.

Exon	Variant	cDNA	Protein	Frequency affected %	Frequency unaffected %	CHISQ	p value	OR	C.I 95%
IVS3 5	rs1155646	-	-	0.322	0.322	3.84E-05	0.9951	1.001	0.7928-1.263
10	c.C129T	p.Y43Y	0	0.001	0.001	-	-	-	-
12	c.G56A	p.P189L	0	0.001	0.001	-	-	-	-
13	c.C924T	p.P308P	0	0.001	0.001	-	-	-	-
15	c.A1113T	p.D371E	0.004	0	-	-	-	-	-
15	c.C1397A	p.A466D	0	0.001	0.001	-	-	-	-
15	c.C1418T	p.P473L	0	0.001	0.001	-	-	-	-
15	c.T1433G*	p.N478T*	0	0.001	0.001	-	-	-	-
15	rs2289912	p.P481T	0.007	0.021	3.921	0.04768	0.3507	0.1187-1.037	-
15	c.T1444A	p.T482S	0.002	0	-	-	-	-	-
16	rs2305138	p.E539E	0.051	0.068	1.698	0.1925	0.7342	0.4606-1.17	-
17	c.G1779T	p.A593A	0.009	0.009	0.009129	0.9239	1.056	0.3438-3.245	-
23	c.C2470A	p.A824S	0.002	0	-	-	-	-	-
25	c.G2898T	p.S966S	0.004	0	-	-	-	-	-
26	rs3816334	p.Q1001Q	0.318	0.32	0.01092	0.9168	0.9877	0.7826-1.247	-
26	c.3004insCAGCAG	p.Q1002_Q1003insQQ	0	0.001	-	-	-	-	-
26	c.3127insCAG	p.Q1042_Q1043insQ	0	0.001	-	-	-	-	-
26	c.C3059T	p.T1020M	0	0.001	-	-	-	-	-
28	c.A3410T	p.E1137V	0	0.001	-	-	-	-	-
28	IVS28	rs2305137	-	0.33	0.33	0.0212	0.8842	0.9832	0.7832-1.234
29	c.A3575G	p.H1192R	0	0.002	-	-	-	-	-
29	c.3693_3695del3	p.Q1232del	0.395	0.407	0.1855	0.6667	0.9531	0.766-1.186	-
29	3693-	3693-	-	-	-	-	-	-	-
29	3694insCAGCAG	p.P1231_Q1232insQQ	0.006	0.009	0.4711	0.4925	0.6299	0.1664-2.385	-
29	c.3689insAGC	p.L1230_P1231insS	0	0.001	-	-	-	-	-
29	c.3689-3709del21	p.L1230_Q1233del	0.047	0.068	2.612	0.1061	0.6755	0.4187-1.09	-
29	3689-3708del24*	p.L1230_Q1237del*	0.006	0.01	0.7755	0.3785	0.5593	0.1508-2.075	-
29	rs12328151	p.P1238P	0.29	0.348	5.043	0.02473	0.767	0.6083-0.9671	-
30	c.A3812G	p.N1271S	0	0.002	-	-	-	-	-
30	c.A3816G	p.Q1272Q	0	0.001	-	-	-	-	-
30	c.G3837A	p.V1279V	0	0.001	-	-	-	-	-
31	rs34424361	p.S1306S	0	0.002	-	-	-	-	-

**Table 2:** Variants found in PD cases and controls from the US series. Minor allele, frequency of the minor allele in cases and controls,  $\chi^2$  values, p values, odds ratios and 95% confident interval were calculated for each variant. \* This variant was described as pathogenic by Lautier and colleagues.

Exon	Variant	cDNA	Protein	Minor allele %	Frequency affected %	Frequency unaffected %	CHISQ	p value	OR	C.I.95%
IVS3	rs11555646	-	C	33.62	30.41	1.829	0.1763	1.16	0.9356 - 1.437	0.04694 - 5.731
7	c.322G>C	p.G108R	C	0.1202	0.2315	0.2973	0.5856	0.5187	-	-
12	c.894G>C	p.G298G	C	0.1351	0	-	-	-	-	-
14	c.1183T>A	p.S395T	A	0	0.1471	-	-	-	-	-
15	c.1358A>G	p.D453G	G	0.1241	0	-	-	-	-	-
15	c.1380G>C	p.Q460Q	C	0.1241	0	-	-	-	-	-
15	rs2289912	p.P481T	A	1.489	1.942	0.4951	0.4817	0.7632	0.3588 - 1.624	-
15	c.1467A>G	p.P489P	G	0.1241	0	-	-	-	-	-
16	rs2305138	p.E539E	A	4.4	6.824	4.186	0.04075	0.6284	0.4013 - 0.984	-
16	c.1620C>T	p.H540H	T	0	0.1312	-	-	-	-	-
17	c.1757T>C	p.M586T	C	0.1285	0	-	-	-	-	-
17	c.1779G>T	p.A593A	T	0.3856	0.5714	0.2699	0.6034	0.6735	0.1502 - 3.02	-
17	c.1793C>T	p.F598F	T	0.1285	0	-	-	-	-	-
17	c.1795C>T	p.Q599K	T	0.1285	0	-	-	-	-	-
18	c.1935C>T	p.H645H	T	0	0.1126	-	-	-	-	-
21	c.2186G>A	p.S729G	A	0.1229	0	-	-	-	-	-
21	c.2268A>G	p.A756A	G	0	0.1232	-	-	-	-	-
22	c.2332A>G	p.R778G	G	0.2445	0	-	-	-	-	-
24	c.2683A>G	p.R895G	G	0.2551	0	-	-	-	-	-
25	c.2898G>T	p.S966S	T	0.2924	0.7576	1.473	0.2248	0.3842	0.07728 - 1.91	-
25	c.2907A>G	p.E969E	G	0.1462	0	-	-	-	-	-
25	c.2945G>A	p.R982Q	A	0	0.1263	-	-	-	-	-
26	c.2985T>C	p.A995A	C	0	0.2375	-	-	-	-	-
26	rs3816334	p.Q1001Q	A	31.16	31.47	0.01905	0.8902	0.9855	0.8014 - 1.212	-
26	c.3045A>G	p.K1015K	G	0	0.2375	-	-	-	-	-
27	c.3167C>G	p.S1056C	G	0.2421	0	-	-	-	-	-
27	c.3174G>A	p.L1058L	A	0	0.1205	-	-	-	-	-
IVS28	rs2305137	-	G	35.99	33.46	1.113	0.2915	1.118	0.9084 - 1.377	-
29	c.3575A>G	p.H1192R	G	0.5195	0.1238	1.955	0.1621	4.214	0.47 - 37.79	-
29	c.3693_3695del3	p.Q1232del	W	47.53	50	0.9608	0.327	0.9059	0.7435 - 1.104	-
29	rs12328151	p.P1238P	A	29.15	30.74	0.4796	0.4886	0.9267	0.7472 - 1.149	-
29	c.3698_3709del21	p.L1230_Q1236del	M	5.829	5.693	0.01344	0.9077	1.025	0.6715 - 1.566	-
29	c.3693_3694insCAGCAG	p.P1231_Q1232insQ	M	0.3886	0.1238	1.097	0.295	3.148	0.3268 - 30.33	-
29	c.3689_3712del24*	p.L1230_Q1237del*	M	1.036	0.6188	0.8431	0.3585	1.682	0.5477 - 5.163	-
29	c.3711_3712insCAG	p.Q1237_P1238insQ	M	0	0.1188	-	-	-	-	-

30	c.3806A>G	p.S1269G	G	0	0.1171	-	-	-	-
30	c.3808A>G	p.N1270D	G	0.2564	0	-	-	-	-
30	c.3814C>G	p.Q1272E	G	0	0.1404	-	-	-	-
31	rs34424361	p.S1306S	A	1.285	1.991	1.321	0.2503	0.6409	0.2984 - 1.377
31	c.3940A>G	p.I1314V	G	0.1168	0	-	-	-	-

**Table 3: Demographic data from the different centers**

Center Name	Sample Size (Number of AJ)	M:F ratio (unknown)	Mean Age Collection	N Mutations	% Mutations	Mutations Screened	Clinical Data Provided*
Brazil						N370S, L444P G377S	Limited
Patients	65	42:23	54.1	4	6.2%		
Controls	264	169:95	54.4	0	0%		
NYC, USA						Full sequencing	Full
Patients	275 (177)	171:104	65.6	34	12.4%		
Controls	140 (65)	73:67	62.8	3	2.14%		
France						N370S, L444P, D409H	Full
Patients	297	185:112	57.8	12	4.0%		
Controls	251	142:109	57.8	1	0.39%		
Haifa, IL						D409H, 84GG, V394L, IVS2+1, R496H	Partial
Patients	162 (162)	94:65 (3)	68.5	40	24.7%		
Controls	NP	NP	NP	NP	NP		
Italy						L444P, N370S	Full
Patients	395	244:151	66.5	11	2.8%		
Controls	483	180:303	56.9	1	0.21%		
Norway						L444P, N370S	Limited
Patients	311	186:123 (2)	NP	7	2.3%		
Controls	473	267:206	64.1	8	1.69%		
NHGRI, USA						Full sequencing	Partial
Patients	539	275:166 (98)	73.5	29	5.4%		
Controls	209 (1)	100:109	67.6	6	2.87%		
Portugal						Full sequencing	Limited
Patients	231	110:121	65.3.0	15	6.5%		
Controls	482	Unknown	65.5	6	1.24%		
Rostock, DE						Full sequencing	Partial
Patients	298	190:108	64.3	18	6.0%		
Controls	212	105:107	74.5	5	2.4%		
Singapore						L444P , N370S	Partial
Patients	329	170:158 (1)	70.3	8	2.4%		
Controls	201	99:102	64.2	0	0%		
Taiwan						L444, recNcil, R120W, some full sequencing	Full
Patients	559	304:255	69.1	22	3.9%		
Controls	377	198:179	60.5	4	1.06%		
Tel Aviv, IL						84GG, IVS2+1,	

*Supplementary Information*

					N370S, V394L, Limited D409H, L444P, R496H, RecTL
Patients	420 (419)	262:158	68.0	81	19.3%
Controls	321 (321)	159:162	65.3	13	4.05%
Japan				full sequencing	Limited
Patients	534	282:252	65.3	50	9.4%
Controls	546	294:252	44.8	2	0.37%
Tubingen, DE				L444P, N370S	Partial
Patients	377	222:155	64.8	12	3.2%
Controls	325	192:132	58.3	0	0%
Toronto, CA				N370S, K178T, L444P, 84GG, R329C, IVS2+1,recNcii I	Partial
Patients	88 (2)	51:37	55.0	5	5.7%
Controls	96	27:69	69.6	1	1.0%
Seattle, USA				N370S, L444P, recNcii	Full
Patients	811 (20)	607:204	66.9	24	2.9%
Controls	518	193:324	65.2	2	0.39%

\* Clinical data: Limited-age, gender, ethnicity, Partial-age, gender, ethnicity, family history and some information on symptoms, Complete- data provided includes age, gender, ethnicity, duration, family history, presenting symptoms, prominent clinical findings, presence of dementia or dyskinesias, and scores on Hoehn and Yahr and/or Unified Parkinson Disease Rating scales

**Table 4: Variants found in GBA**

<i>Allele name</i> <sup>1</sup>	<i>cDNA</i> <sup>2</sup>	<i>Protein</i> <sup>3</sup>	<i>Exon</i>	<i>PD Subjects</i>		<i>Controls</i>	
				N	Carrier frequency <sup>4</sup>	N	Carrier frequency <sup>5</sup>
L444P	c.1448T>C	p.Leu483Pro	10	11	1.39%	0	0%
D443N*	c.1444G>A	p.Asp482Asn	10	1	0.13%	0	0%
R463C	c.1504C>T	p.Arg502Cys	10	3	0.38%	0	0%
	c.1448T>C	p.Leu483Pro,					
RecNcil	c.1483G>C	p.Ala495Pro,	10	2	0.25%	0	0%
	c.1497G>C	p.Val499Val					
RecA456P	c.1448T>C	p.Leu483Pro,	10	1	0.13%	0	0%
	c.1483G>C	p.Ala495Pro					
N370S	c.1226A>G	p.Asn409Ser	9	8	1.01%	1	0.39%
D409H	c.1342G>C	p.Asp448His	9	1	0.13%	0	0%
D380A	c.1256A>C	p.Asp419Ala	9	1	0.13%	0	0%
c.1263-1317 del55	c.1263-1317 del55	p.N421PfsX4	9	1	0.13%	0	0%
R257Q	c.887G>A	p.Arg296Gln	7	1	0.13%	1	0.39%
G193E*	c.695G>A	p.Gly232Glu	6	1	0.13%	0	0%
R131C	c.508C>T	p.Arg170Cys	5	1	0.13%	0	0%
K7E*	c.136A>G	p.Lys46Glu	3	1	0.13%	0	0%
V458L*†	c.1489G>T	p.Val497Leu	10	0	0%	1	0.39%

<sup>1</sup> Allele names follow the common nomenclature and apply to the processed protein, not including the 39-residue signal peptide

<sup>2</sup> cDNA sequence numbering starts with the adenine of the first translated ATG start codon (GenBank reference sequence NM\_001005749)

<sup>3</sup> Protein names are based on the primary translation product and include the 39-residue signal peptide

<sup>4</sup> Carrier frequency of GBA mutations among PD patients where the percentage of each mutation is shown in regard to the total number of screened PD patients (total N =700)

<sup>5</sup> Carrier frequency of GBA mutations among PD patients where the percentage of each mutation is shown in regard to the total number of screened controls (total N =257)

\*previously undescribed mutation

†change only found in the control group

Patient No.	Genotype	Clinical Diagnosis	Sex	AoO	AoD	L-Dopa	Fam Hist	First Symptom	Cognitive symptoms	Other non motor symptoms
1	L444P/wt	Familial PD	male	34	n/a	yes	yes	Tremor	Dementia, Confusion, Impaired memory	Frontal lobe dysfunction, Hallucinations
2	K7E/wt*	Familial PD	male	48	n/a	yes	yes	Decreased dexterity and stiffness in the left hand	None	
3	L444P/wt	Familial PD	female	43	n/a	yes	yes	Stiffness in the left arm, unilateral tremor on the left	None	
4	N370S/wt	Idiop. PD	male	57	n/a	yes	no	Bradykinesia	Cognitive deterioration	
5	N370S/wt	Idiop. PD	male	54	n/a	yes	no	Stiffness in the shoulder	None	Anxiety with panic attacks
6	L444P/wt	YOPD	male	41	n/a	yes	no	Bradykinesia	None	
7	N370S/wt	Idiop. PD	female	53	n/a	yes	no	Rigidity in the neck, Bradykinesia	Confusion, Impaired memory	Faint episodes with falls due to postural drops in B.P.
8	N370S/wt	Idiop. PD	male	57	n/a	yes	no	Resting tremor, Loss of dexterity in the left hand	none	REM sleep behavioural disorder, hallucinations anxiety attacks
9	D380A/wt	Idiop. PD	male	56	n/a	yes	no	Unilateral tremor on the left	none	REM sleep behavioural disorder
10	D443N/wt*	YOPD	male	43	n/a	yes	no	Unilateral tremor	frontal executive dysfunction, cognitive slowing	REM sleep behavioural disorder, visual disturbances
11	c.1263-1317 del	YOPD	male	26	n/a	yes	no	Tremor on the right, Bradykinesia on the left	none	
12	G193E/wt*	Idiop. PD †	male	49	62	yes	no	Back pain	yes	Hallucinations
13	R131C/wt	Idiop. PD †	male	56	65	yes	no	Bradykinesia, Lack of energy, Bradyphrenia	Dementia	Hallucinations, Depression

14	N370S/wt	Idiop. PD <sup>†</sup>	male	69	79	yes	no	Subarachnoid hemorrhage	none
15	L444P/wt	Idiop. PD <sup>†</sup>	female	50	67	yes	no	Lethargy	none
16	RecA456P	Idiop. PD <sup>†</sup>	male	48	57	yes	no	Shuffling gait	Dementia
17	R463C/wt	Idiop. PD <sup>†</sup>	female	61	78	yes	no	Pain in the left shoulder,	none
								lower back pain	
18	R463C/wt	Idiop. PD <sup>†</sup>	male	35	51	yes	no	Tremor in the left hand	none
19	N370S/wt	Idiop. PD <sup>†</sup>	male	79	91	yes	no	Tremor, Bradykinesia	none
20	N370S/wt	Familial PD <sup>†</sup>	male	64	85	yes	yes	Stiffness in the left side	none
21	L444P/wt	Idiop. PD <sup>†</sup>	male	60	75	yes	no	Slowing down	Dementia
22	R463C/wt	Idiop. PD <sup>†</sup>	male	61	68	yes	no		Dementia
23	L444P/wt	Idiop. PD <sup>†</sup>	male	57	75	yes	no		Dementia
24	D409H/wt	Idiop. PD <sup>†</sup>	male	44	62	yes	no	Tremor	Dementia, Confusion
25	R257Q/wt	Idiop. PD <sup>†</sup>	male	58	66	yes	no		Dementia
26	L444P/wt	Idiop. PD <sup>†</sup>	male	58	65	yes	no	Akinesthesia, Rigidity	Dementia
27	RecNcil	YOPD <sup>†</sup>	female						
28	RecNcil	MSA <sup>†</sup>	female	58	64	no	no	Unusual gait	Cognitive impairment
29	L444P/wt	MSA <sup>†</sup>	male	52	59	no	no		Urinary urgency, Nocturia
30	L444P/wt	YOPD <sup>†</sup>	male	37	56	yes	no	Dragging of the left foot	Probably demented
31	L444P/wt								Depression
									Depression
32	N370S/wt	Idiop. PD <sup>†</sup>	male	68	82	yes	no	Impaired walking, Tremor	none
33	L444P/wt	Idiop. PD <sup>†</sup>	male	59	61	no	no	Unilateral tremor with	
								autonomic bulbar	
								involvement	

Table 5: Abbreviations: PD, Parkinson's Disease; MSA, Multiple System Atrophy; wt, wildtype; n/a, not applicable. \*previously undescribed mutations; † initial clinical diagnosis for pathologically proven PD cases

**Table 6: Most significant SNPs surpassing Bonferroni threshold for multiple testing in both stages, the 3 markers in the *LRRK2* locus and the additional loci in chromosomes 1 and 4.**

locus	Alleles		Stage I				Stage II				stage I + II combined				OR hom. (95%CI)		
	SNP	Chr.	Position	(minor/ major)	MAF_U	MAF_A	p-value	cOR	(95%CI)	MAF_U	MAF_A	p value	cOR	(95%CI)	OR hom. (95%CI)	OR het. (95%CI)	
rs393152	17	41074926	G/A	0.22	0.18	1.42E-07	0.76	0.75(0.66 0.67)(0.45 - 0.89)	0.22	0.18	2.29E-10	0.77	0.78(0.71 - 0.64)(0.47 - 0.81)	0.22	0.18	5.14E-17	0.77(0.71 - 0.65)(0.52 - 0.82)
rs2736990	4	90897564	G/A	0.46	0.52	5.68E-09	1.27	1.17(1.07 1.45)(1.34 - 1.27)	0.46	0.51	5.39E-09	1.21	1.28(1.2 - 1.23)(1.14 - 1.32)	0.46	0.51	2.69E-16	1.23(1.18 - 1.31)(1.24 - 1.38)
rs199533	17	42184098	A/C	0.20	0.16	5.05E-08	0.75	0.71(0.62 0.71)(0.47 - 0.81)	0.20	0.17	1.26E-08	0.79	0.81(0.74 - 0.61)(0.43 - 0.79)	0.20	0.16	3.06E-15	0.77(0.72 - 0.65)(0.51 - 0.83)
rs17563986	17	41347100	A/G	0.22	0.18	3.44E-07	0.77	0.75(0.66 0.69)(0.46 - 0.84)	0.21	0.18	4.93E-09	0.79	0.81(0.74 - 0.62)(0.45 - 0.88)	0.22	0.18	3.42E-15	0.78(0.73 - 0.65)(0.52 - 0.84)
rs169201	17	42145386	T/G	0.20	0.16	1.25E-07	0.75	0.72(0.63 0.72)(0.49 - 0.81)	0.20	0.17	1.40E-08	0.79	0.81(0.74 - 0.6(0.42 - 0.78)	0.20	0.16	7.51E-15	0.78(0.72 - 0.65)(0.5 - 0.83)
rs1981997	17	41412603	A/C	0.22	0.18	2.02E-07	0.76	0.74(0.65 0.71)(0.48 - 0.83)	0.21	0.18	1.46E-08	0.79	0.82(0.75 - 0.63)(0.46 - 0.89)	0.22	0.18	7.70E-15	0.78(0.73 - 0.67)(0.53 - 0.83)
rs8070723	17	41436801	T/C	0.22	0.18	3.36E-07	0.77	0.74(0.66 0.71)(0.48 - 0.83)	0.22	0.18	1.47E-08	0.80	0.81(0.74 - 0.64)(0.48 - 0.88)	0.22	0.18	1.50E-14	0.78(0.73 - 0.68)(0.54 - 0.83)
rs3857059	4	90894261	G/A	0.07	0.10	3.60E-08	1.49	1.35(1.24 4.39)(3.94 - 1.46)	0.08	0.10	1.85E-07	1.34	1.28(1.19 - 3.27)(2.84 - 3.71)	0.07	0.10	1.52E-14	1.40(1.25 - 3.61)(3.3 - 3.92)
rs2668692	17	41648797	G/A	0.22	0.17	3.94E-07	0.77	0.74(0.65 0.71)(0.49 - 0.83)	0.22	0.18	8.32E-09	0.79	0.82(0.75 - 0.62)(0.45 - 0.88)	0.22	0.18	7.79(0.73 - 0.66)(0.52 - 0.84)	0.78(0.73 - 0.66)(0.52 - 0.84)
rs11931074	4	90858538	A/G	0.07	0.10	4.78E-08	1.49	1.35(1.23 4.39)(3.94 - 1.46)	0.08	0.10	2.03E-07	1.34	1.28(1.2 - 1.37)(2.56 - 3.4)	0.07	0.10	2.02E-14	1.40(1.25 - 3.43)(3.13 - 3.74)
rs12373139	17	41279910	A/G	0.22	0.18	4.91E-07	0.77	0.75(0.66 0.71)(0.48 - 0.84)	0.21	0.18	2.02E-08	0.80	0.82(0.75 - 0.64)(0.47 - 0.89)	0.22	0.18	2.15E-14	0.78(0.73 - 0.67)(0.54 - 0.84)
rs2532269	17	41605885	A/C	0.22	0.17	2.70E-07	0.76	0.74(0.65 0.71)(0.48 - 0.83)	0.21	0.18	8.06E-08	0.80	0.83(0.77 - 0.61)(0.44 - 0.9)	0.22	0.18	1.71E-14	0.78(0.74 - 0.65)(0.52 - 0.85)
rs17690703	17	41281077	A/G	0.25	0.22	6.55E-05	0.83	0.8(0.71 0.79)(0.61 - 0.88)	0.25	0.21	2.93E-09	0.80	0.81(0.74 - 0.65)(0.49 - 0.88)	0.25	0.21	1.78E-13	0.80(0.75 - 0.69)(0.58 - 0.85)
rs7215239	17	41123556	G/A	0.24	0.21	3.43E-05	0.81	0.79(0.71 0.77)(0.58 - 0.88)	0.24	0.20	1.12E-07	0.81	0.84(0.78 - 0.65)(0.5 - 0.91)	0.24	0.21	7.30E-12	0.81(0.77 - 0.69)(0.57 - 0.88)
rs183211	17	42143493	A/G	0.24	0.20	1.05E-05	0.80	0.8(0.71 0.79)(0.61 - 0.89)	0.23	0.20	5.44E-07	0.82	0.83(0.77 - 0.7(0.55 - 0.9)	0.23	0.20	1.04E-13	0.79(0.74 - 0.65)(0.52 - 0.85)
rs2532274	17	41602941	G/A	0.22	0.18	2.22E-07	0.76	0.75(0.66 0.68)(0.46 - 0.83)	0.22	0.19	3.36E-06	0.83	0.8(0.73 - 0.84)(0.69 - 0.87)	0.22	0.19	2.10E-11	0.81(0.72 - 0.81)(0.58 - 0.83)
rs417968	17	41084159	G/A	0.26	0.22	8.03E-05	0.83	0.82(0.73 0.75)(0.57 - 0.91)	0.26	0.22	2.11E-07	0.82	0.85(0.78 - 0.67)(0.53 - 0.92)	0.26	0.22	3.42E-11	0.82(0.78 - 0.7(0.59 - 0.88)
rs11012	17	40869224	A/G	0.18	0.15	2.85E-06	0.77	0.75(0.65 0.73)(0.46 - 0.84)	0.18	0.15	6.01E-06	0.82	0.81(0.74 - 0.77)(0.58 - 0.88)	0.18	0.15	4.23E-11	0.80(0.78 - 0.77)(0.52 - 0.83)
rs356229	4	90825620	G/A	0.36	0.40	2.46E-04	1.17	1.2(1.11 - 1.21)(1.08 - 1.29)	0.36	0.40	1.25E-06	1.18	1.19(1.12 - 1.24)(1.14 - 1.26)	0.36	0.40	8.36E-10	1.17(1.14 - 1.23)(1.16 - 1.31)
rs7224296	17	42155230	T/C	0.27	0.24	1.13E-04	0.83	0.82(0.73 0.78)(0.61 - 0.9)	0.27	0.24	1.06E-05	0.85	0.86(0.8 - 0.76)(0.63 - 0.93)	0.27	0.24	5.22E-09	0.85(0.79 - 0.77)(0.57 - 0.89)
rs894278	4	90953558	A/G	0.05	0.08	2.64E-05	1.41	1.32(1.19 3.74)(3.18 - 4.31)	0.06	0.07	2.93E-04	1.26	1.23(1.14 - 2.22)(1.68 - 2.75)	0.06	0.07	2.12E-08	1.32(1.2 - 2.72)(2.33 - 3.1)
rs1526123	17	41139123	T/G	0.47	0.43	7.52E-05	0.85	0.88(0.78 0.78)(0.66 - 0.9)	0.47	0.44	1.00E-04	0.88	0.9(0.83 - 0.83)(0.74 - 0.97)	0.47	0.43	2.50E-03	0.87(0.83 - 0.81)(0.74 - 0.94)

rs12644119	4	90322442	T/G	0.09	0.12	2.15E-05	1.32	1.27 (1.16 2.13 (1.78 - 1.37) 2.49)	0.11	0.12	1.81E-03	1.17	1.19 (1.12 - 1.14 (0.87 - 1.27) 1.41)	0.10	0.12	4.64E-03	1.24	1.24 (1.18 - 1.46 (1.25 - 1.3) 1.68)
rs3775439	4	90928764	G/A	0.12	0.15	4.43E-06	1.32	1.23 (1.13 2.18 (1.9 - 1.33) 2.46)	0.13	0.15	2.72E-03	1.15	1.15 (1.07 - 1.29 (1.05 - 1.22) 1.52)	0.12	0.15	5.48E-03	1.22	1.19 (1.13 - 1.59 (1.41 - 1.25) 1.77)
rs7225002	17	41544850	T/C	0.40	0.36	1.03E-04	0.85	0.86 (0.77 0.78 (0.65 - 0.94) 0.91)	0.38	0.36	4.30E-04	0.89	0.89 (0.82 - 0.85 (0.75 - 0.96) 0.94)	0.39	0.36	6.91E-03	0.87	0.87 (0.82 - 0.81 (0.73 - 0.93) 0.89)
rs823128	1	203980001	G/A	0.04	0.03	1.90E-04	0.64	0.64 (0.50 - 0.38 (0.08 - 0.82) 1.68)	0.04	0.03	0.005017	0.69	0.7 (0.55 - 0.46 (-0.47 - 0.84) 1.4)	0.04	0.03	1.32E-07	0.66	0.67 (0.56 - 0.41 (-0.28 - 1.11) 1.11)
rs11240572	1	204074636	A/C	0.04	0.02	1.30E-04	0.63	0.65 (0.50 - 0.13 (0.01 - 0.83) 2.30)	0.04	0.03	0.01495	0.72	0.73 (0.59 - 0.31 (-0.79 - 0.88) 1.4)	0.04	0.03	4.83E-07	0.68	0.7 (0.59 - 0.2 (-0.84 - 0.81) 1.25)
rs823156	1	204031263	G/A	0.18	0.16	4.31E-03	0.85	0.86 (0.75 - 0.72 (0.50 - 0.97) 1.02)	0.17	0.16	0.08966	0.92	0.9 (0.82 - 0.96 (0.76 - 0.98) 1.16)	0.18	0.16	0.00142	0.89	0.88 (0.82 - 0.88 (0.72 - 0.94) 1.03)
rs708730	1	204044403	G/A	0.17	0.15	2.66E-03	0.85	0.84 (0.74 - 0.73 (0.50 - 0.96) 1.06)	0.17	0.16	0.07048	0.93	0.9 (0.83 - 0.99 (0.78 - 0.98) 1.2)	0.17	0.16	0.002157	0.90	0.88 (0.82 - 0.91 (0.74 - 0.94) 1.07)
rs947211	1	204049288	A/G	0.24	0.22	0.014	0.88	0.89 (0.79 - 0.77 (0.59 - 1.01) 1.00)	0.24	0.23	0.2093	0.94	0.91 (0.84 - 1.0 (0.84 - 0.98) 1.15)	0.24	0.23	0.007107	0.92	0.9 (0.85 - 0.92 (0.8 - 0.96) 1.04)
rs12646913	4	15348374	G/A	0.08	0.07	0.041	0.85	0.86 (0.73 - 0.66 (0.28 - 1.01) 1.54)	0.08	0.07	0.09085	0.92	0.87 (0.77 - 1.46 (1.05 - 0.97) 1.87)	0.08	0.07	0.02208	0.89	0.86 (0.78 - 1.15 (0.32 - 1.04) 1.47)
rs4698412	4	15346446	G/A	0.44	0.43	0.085	0.93	0.98 (0.86 - 0.85 (0.72 - 1.11) 1.01)	0.45	0.43	0.03925	0.95	0.96 (0.88 - 0.92 (0.82 - 1.03) 1.02)	0.45	0.43	0.02379	0.94	0.97 (0.91 - 0.9 (0.82 - 1.02) 0.98)
rs12502586	4	15335632	A/G	0.10	0.12	6.50E-03	1.20	1.19 (1.03 - 1.48 (0.91 - 1.37) 2.40)	0.10	0.10	0.99882	0.99	1.02 (0.94 - 0.77 (0.45 - 1.11) 1.09)	0.10	0.11	0.1217	1.07	1.09 (1.02 - 1.01 (0.78 - 1.15) 1.25)
rs4538475	4	15347035	G/A	0.16	0.16	0.76	1.01	0.93 (0.82 - 1.19 (0.84 - 1.06) 1.69)	0.17	0.16	0.1584	0.93	0.89 (0.81 - 1.02 (0.82 - 0.97) 1.22)	0.16	0.16	0.1953	0.95	0.95 (0.85 - 1.11 (0.36 - 0.97) 1.27)
rs12645693	4	15338632	A/G	0.03	0.03	0.63	0.95	0.94 (0.73 - 0.99 (0.26 - 1.20) 3.84)	0.03	0.03	0.3403	0.91	0.92 (0.77 - 0.69 (-0.3 - 1.06) 1.68)	0.03	0.03	0.3494	0.93	0.94 (0.83 - 0.8 (0.11 - 1.05) 1.49)
rs11931532	4	15334864	C/T	0.03	0.03	0.58	0.94	0.93 (0.73 - 1.00 (0.26 - 1.19) 3.87)	0.03	0.03	0.3794	0.92	0.94 (0.8 - 0.46 (-0.68 - 1.08) 1.61)	0.03	0.03	0.3517	0.93	0.94 (0.83 - 0.67 (-0.07 - 1.05) 1.41)
rs7672311	4	15340788	A/G	NA	NA	NA	NA	NA	0.08	0.08	0.1253	0.95	0.92 (0.82 - 1.33 (0.9 - 1.02) 1.75)	0.08	0.08	0.4813	0.95	0.92 (0.82 - 1.33 (0.9 - 1.02) 1.75)
rs11564162	12	38729159	G/A	0.21	0.18	4.00E-05	0.78	0.89 (0.79 - 0.44 (0.31 - 1.01) 0.63)	0.20	0.21	0.94	0.97 (0.9 - 0.83 (0.67 - 1.04) 0.99)	0.21	0.19	2.76E-05	0.86	0.94 (0.88 - 0.69 (0.56 - 0.99) 0.82)	
rs2896905	12	38779683	A/G	0.40	0.35	5.03E-06	0.82	0.84 (0.74 - 0.67 (0.56 - 0.95) 0.80)	0.38	0.38	0.62	1.02	1.04 (0.97 - 1.0 (0.9 - 1.11) 1.1)	0.39	0.37	3.30E-03	0.92	0.96 (0.9 - 0.89 (0.31 - 1.01) 0.96)
rs1491923	12	38877384	C/T	0.31	0.34	2.20E-04	1.20	1.07 (0.95 - 1.52 (1.26 - 1.21) 1.84)	0.31	0.33	7.12E-03	1.10	1.05 (0.99 - 1.22 (1.11 - 1.12) 1.33)	0.31	0.34	2.10E-05	1.14	1.06 (1.01 - 1.31 (1.23 - 1.12) 1.4)