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Supplemental Data

Association of Parkinson Disease with Structural and Regulatory Variants in the *HLA* Region

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Table S1. Accuracy of imputation.

Gene*allele	NGS		SNP2HLA			HLA*IMP			Gene*allele	NGS		SNP2HLA			HLA*IMP		
	N	freq.	N	SS	SP	N	SS	SP		N	freq.	N	SS	SP	N	SS	SP
*DRB1*01:01*	60	0.075	69	1.000	0.988	72	1.000	0.984	*DQA1*01:01*	102	0.128	102	1.000	1.000	102	1.000	1.000
*DRB1*01:02*	7	0.009	7	1.000	1.000	7	1.000	1.000	*DQA1*01:02*	146	0.183	147	1.000	0.998	149	1.000	0.995
*DRB1*01:03*	18	0.023	9	0.500	1.000	6	0.333	1.000	*DQA1*01:03*	48	0.060	48	1.000	1.000	48	1.000	1.000
*DRB1*03:01*	91	0.114	90	0.989	1.000	92	1.000	0.999	*DQA1*02:01*	108	0.136	107	0.991	1.000	124	0.981	0.972
*DRB1*04:01*	93	0.117	103	0.989	0.984	100	1.000	0.990	*DQA1*03:01*	155	0.195	155	1.000	1.000	139	0.890	0.998
*DRB1*04:02*	3	0.004	1	0.333	1.000	2	0.667	1.000	*DQA1*03:02*	0	0.000	0	NC	NC	2	NC	0.997
*DRB1*04:03*	4	0.005	9	0.500	0.991	2	0.250	0.999	*DQA1*04:01*	20	0.025	20	1.000	1.000	20	1.000	1.000
*DRB1*04:04*	29	0.036	27	0.724	0.992	31	0.897	0.993	*DQA1*05:01*	181	0.227	181	1.000	1.000	99	0.536	0.997
*DRB1*04:05*	5	0.006	3	0.600	1.000	1	0.200	1.000	*DQA1*05:05*	0	0.000	0	UD	UD	79	NC	0.896
*DRB1*04:06*	3	0.004	0	0.000	1.000	0	0.000	1.000	*DQA1*06:01*	2	0.003	2	1.000	1.000	0	0.000	1.000
*DRB1*04:07*	6	0.008	0	0.000	1.000	5	0.833	1.000	*DQA1*NA*	34	0.043	0	-	-	0	-	-
*DRB1*04:08*	2	0.003	2	0.500	0.999	0	0.000	1.000									
*DRB1*07:01*	113	0.142	113	1.000	1.000	117	1.000	0.994	*DQB1*02:01*	93	0.117	90	0.957	0.999	90	0.957	0.999
*DRB1*08:01*	20	0.025	2	0.100	1.000	21	1.000	0.999	*DQB1*02:02*	73	0.092	77	1.000	0.994	80	1.000	0.990
*DRB1*08:02*	0	0.000	1	NC	0.999	0	NC	NC	*DQB1*02:04*	1	0.001	0	0.000	1.000	0	0.000	1.000
*DRB1*08:03*	2	0.003	2	1.000	1.000	0	0.000	1.000	*DQB1*03:01*	154	0.193	158	1.000	0.994	159	1.000	0.994
*DRB1*08:04*	1	0.001	18	0.000	0.977	1	1.000	1.000	*DQB1*03:02*	79	0.099	79	1.000	1.000	79	1.000	1.000
*DRB1*09:01*	12	0.015	12	1.000	1.000	12	1.000	1.000	*DQB1*03:03*	47	0.059	47	1.000	1.000	47	1.000	1.000
*DRB1*10:01*	4	0.005	0	0.000	1.000	4	1.000	1.000	*DQB1*03:04*	1	0.001	0	0.000	1.000	0	0.000	1.000
*DRB1*11:01*	45	0.057	55	0.889	0.980	56	0.822	0.975	*DQB1*0319*	3	0.004	0	0.000	1.000	0	0.000	1.000
*DRB1*11:02*	4	0.005	5	1.000	0.999	0	0.000	1.000	*DQB1*04:02*	23	0.029	23	1.000	1.000	20	0.870	1.000
*DRB1*11:03*	5	0.006	1	0.000	0.999	1	0.000	0.999	*DQB1*05:01*	83	0.104	84	1.000	0.999	84	1.000	0.999
*DRB1*11:04*	9	0.011	6	0.444	0.997	7	0.333	0.995	*DQB1*05:02*	7	0.009	7	1.000	1.000	7	1.000	1.000
*DRB1*11:06*	0	0.000	1	NC	0.999	0	NC	NC	*DQB1*05:03*	25	0.031	25	1.000	1.000	25	1.000	1.000
*DRB1*11:28*	1	0.001	0	0.000	1.000	0	0.000	1.000	*DQB1*06:01*	5	0.006	5	1.000	1.000	5	1.000	1.000
*DRB1*12:01*	19	0.024	18	0.895	0.999	18	0.895	0.999	*DQB1*06:02*	105	0.132	104	0.990	1.000	107	0.990	0.996
*DRB1*13:01*	46	0.058	46	1.000	1.000	47	1.000	0.999	*DQB1*06:03*	46	0.058	46	1.000	1.000	43	0.935	1.000
*DRB1*13:02*	37	0.046	37	1.000	1.000	38	1.000	0.999	*DQB1*06:04*	25	0.031	25	1.000	1.000	25	1.000	1.000
*DRB1*13:03*	6	0.008	6	1.000	1.000	6	1.000	1.000	*DQB1*06:09*	10	0.013	10	1.000	1.000	10	1.000	1.000
*DRB1*13:05*	2	0.003	0	0.000	1.000	0	0.000	1.000	*DQB1*NA*	16	0.020	0	-	-	0	-	-
*DRB1*14:01*	27	0.034	12	0.444	1.000	27	1.000	1.000									

*DRB1*14:04*	0	0.000	15	NC	0.981	0	NC	NC		*DPB1*01:01*	33	0.041	33	1.000	1.000	63	1.000	0.961
*DRB1*15:01*	108	0.136	112	0.991	0.993	11:0	1.000	0.997		*DPB1*02:01*	98	0.123	102	1.000	0.994	91	0.867	0.991
*DRB1*15:02*	6	0.008	5	0.833	1.000	5	0.833	1.000		*DPB1*02:02*	5	0.006	5	1.000	1.000	3	0.000	0.996
*DRB1*15:03*	1	0.001	2	1.000	0.999	0	0.000	1.000		*DPB1*03:01*	71	0.089	70	0.958	0.997	79	0.958	0.985
*DRB1*16:01*	5	0.006	6	1.000	0.999	7	1.000	0.997		*DPB1*04:01*	370	0.465	371	0.984	0.984	382	0.989	0.962
*DRB1*16:04*	1	0.001	0	0.000	1.000	0	0.000	1.000		*DPB1*04:02*	95	0.119	95	0.989	0.999	104	1.000	0.987
*DRB1*NA*	1	0.001	0	-	-	0	-	-		*DPB1*05:01*	13	0.016	13	1.000	1.000	5	0.231	0.997
										*DPB1*05:02*	0	0.000	0	NC	NC	9	NC	0.989
*DRB3*00*	503	0.632				513	0.990	0.949		*DPB1*06:01*	10	0.013	12	0.900	0.996	0	0.000	1.000
*DRB3*01*	109	0.137				106	0.936	0.994		*DPB1*09:01*	3	0.004	1	0.333	1.000	9	0.000	0.989
*DRB3*02*	147	0.185				144	0.966	0.997		*DPB1*10:01*	15	0.019	14	0.933	1.000	7	0.000	0.991
*DRB3*03*	37	0.046				33	0.892	1.000		*DPB1*11:01*	17	0.021	17	1.000	1.000	18	1.000	0.999
										*DPB1*13:01*	18	0.023	18	1.000	1.000	19	1.000	0.999
*DRB4*00*	524	0.658	Not imputed			526	0.992	0.978		*DPB1*14:01*	11	0.014	14	1.000	0.996	0	0.000	1.000
*DRB4*01*	272	0.342				270	0.978	0.992		*DPB1*15:01*	6	0.008	6	1.000	1.000	0	0.000	1.000
										*DPB1*16:01*	5	0.006	5	1.000	1.000	0	0.000	1.000
*DRB5*00*	675	0.848				675	1.000	1.000		*DPB1*17:01*	12	0.015	11	0.917	1.000	6	0.333	0.997
*DRB5*01*	115	0.144				115	1.000	1.000		*DPB1*18:01*	1	0.001	1	1.000	1.000	0	0.000	1.000
*DRB5*02*	6	0.008				6	1.000	1.000		*DPB1*19:01*	5	0.006	5	1.000	1.000	0	0.000	1.000
										*DPB1*20:01*	1	0.001	0	0.000	1.000	0	0.000	1.000
										*DPB1*23:01*	6	0.008	2	0.000	0.997	1	0.000	0.999
										*DPB1*35:01*	1	0.001	1	0.000	0.999	0	0.000	1.000

Two imputation algorithms were applied to the exact same GWAS dataset for a side-by side comparison of two methods. A subset of data was *HLA* typed by deep sequencing allowing comparisons to the gold standard. Allele-specific sensitivity and specificity of two imputation algorithms as compared to next generation sequencing are shown for class II loci.

SNP2HLA[12] and HLA*IMP[13]: two imputation algorithms. N: number of alleles called by each technique (total across each locus = 796). Those called by imputation include true positives as well as any false positives. Even if both NGS and imputation show the same N, they may or not be perfect matches. SS: sensitivity is the ratio of true positives (N chromosomes called correctly by imputation as having the allele) to the number called by NGS. SP: specificity is the ratio of true negatives (N called correctly as allele absent by imputation) to the number of chromosomes called by NGS as not having the allele. NC: not calculated. UD: undetermined (*DQA1*05:01* splits into 05:01 and 05:05. HLA*IMP picked it up and since NGS did not, SS and SP of HLA*IMP is undetermined). NA: Not called by NGS. Each chromosome that had a no-call by NGS was tracked to the person, matched to the allele that was called by imputation, and was removed from SS and SP calculation.

Table S2. Association of PD with *HLA* haplotypes

	Frequency In NGRC		NGRC		Replication		Meta Analysis	
	PD	Cont	OR	P	OR	P	OR	P
Class I haplotypes								
*B*07:02_C*07:02*	0.15	0.13	1.21	6E-3	1.29	0.02	1.23	3E-4
*B*40:01_C*03:04*	0.05	0.06	0.79	0.03	0.71	0.03	0.76	2E-3
Class II haplotypes								
*DRB5*01_DRB1*15:01_DQA1*01:02_DQB1*06:02*	0.15	0.13	1.26	7E-4	1.27	0.02	1.27	5E-5
*DRB4*01_DRB1*04:04_DQA1*03:01_DQB1*03:02*	0.03	0.05	0.64	7E-4	0.65	0.02	0.64	4E-5
Extended haplotypes								
*B*07:02_C*07:02_DRB5*01_DRB1*15:01_DQA1*01:02_DQB1*06:02*	0.09	0.07	1.29	3E-3	1.38	0.02	1.32	2E-4
*B*40:01_C*03:04_DRB4*01_DRB1*04:04_DQA1*03:01_DQB1*03:02*	0.01	0.02	0.60	0.02	0.52	0.06	0.58	3E-3

Haplotypes were constructed with the 12 alleles that were associated with PD (Table 1).

Tests were conducted under additive model and adjusted for principal components 1 and 2.

P-values are two sided (including replication) uncorrected for multiple testing.

Table S3. Conditional analysis testing interdependence of alleles that form the "protective" haplotype (meta-analysis of NGRC and replication)

test	conditioned on	P	OR
*B*40:01*	unconditioned	2E-03	0.76
	*C*03:04*	0.36	1.15
	*DQA1*03:01*	0.01	0.79
	*DQB1*03:02*	0.01	0.80
	*DRB1*04:04*	0.03	0.82
	*DRB4*01*	5E-03	0.78
C*03:04	*B*40:01*	1E-03	0.66
	unconditioned	8E-06	0.72
	*DQA1*03:01*	3E-04	0.76
	*DQB1*03:02*	6E-04	0.77
	*DRB1*04:04*	2E-04	0.75
	*DRB4*01*	7E-05	0.74
DQA1*03:01	*B*40:01*	4E-06	0.78
	*C*03:04*	3E-05	0.79
	unconditioned	1E-06	0.77
	*DQB1*03:02*	0.02	0.83
	*DRB1*04:04*	7E-04	0.81
	*DRB4*01*	4E-03	0.81
*DQB1*03:02*	*B*40:01*	5E-05	0.76
	*C*03:04*	5E-04	0.79
	*DQA1*03:01*	0.20	0.88
	unconditioned	7E-06	0.74
	*DRB1*04:04*	0.01	0.81
	*DRB4*01*	0.01	0.80
DRB1*04:04	*B*40:01*	5E-04	0.68
	*C*03:04*	9E-04	0.70
	*DQA1*03:01*	0.03	0.77
	*DQB1*03:02*	0.06	0.79
	unconditioned	4E-05	0.65
	*DRB4*01*	3E-03	0.72
*DRB4*01*	*B*40:01*	1E-04	0.84
	*C*03:04*	4E-04	0.85
	*DQA1*03:01*	0.34	0.94
	*DQB1*03:02*	0.05	0.90
	*DRB1*04:04*	4E-03	0.87
	unconditioned	4E-05	0.83

Grey row: the allele in the left-hand column lost significance when conditioned on the allele in the second column.

*C*03:04, DQA1*03:01* and *DRB1*04:04* had seemingly independent signals for association with PD

Table S4. Conditional analysis testing interdependence of PD-associated SNPs (Meta analysis of NGRC and replication)

Test	conditioned on	P	OR
rs2395163	unconditioned	2E-07	0.77
	rs3129882	5E-03	0.86
	rs41269955	4E-03	0.80
	rs660895	5E-04	0.78
	rs9268515	0.13	0.88
rs3129882	rs2395163	2E-06	1.23
	unconditioned	9E-11	1.30
	rs41269955	4E-08	1.27
	rs660895	1E-08	1.27
	rs9268515	7E-07	1.23
rs41269955/rs77539933	rs2395163	0.44	0.94
	rs3129882	0.02	0.88
	unconditioned	2E-05	0.81
	rs660895	0.03	0.83
	rs9268515	0.24	0.92
rs660895	rs2395163	0.87	0.99
	rs3129882	0.02	0.88
	rs41269955	0.66	0.96
	unconditioned	9E-05	0.82
	rs9268515	0.92	0.99
rs9268515	**rs2395163**	0.04	0.83
	rs3129882	3E-04	0.81
	rs41269955	2E-03	0.79
	rs660895	2E-04	0.75
	unconditioned	8E-08	0.75

Grey row: the SNP in the left-hand column lost significance when conditioned on the SNP in the second column.

rs2395163 and rs9268515 tag each other tightly.

rs3129882 is independent of all other SNPs.

Table S5. Association of SNPs with PD conditioned on classical variants (Extended version of Table 3 of the main manuscript)

	NGRC								Replication								Meta Analysis											
	rs3129882		rs9268515		rs41269955 [a]		rs660895		rs2395163		rs3129882		rs9268515		rs77539933 [a]		rs660895		rs2395163		rs3129882		rs9268515		rs41269955/ rs77539933		rs660895		rs2395163	
	OR	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**
Not conditioned	1.35	1E-9	0.74	5E-6	0.80	4E-4	0.83	2E-3	0.77	2E-5	1.20	0.01	0.75	5E-3	0.82	0.02	0.81	0.02	0.78	3E-3	1.30	9E-11	0.75	8E-8	0.81	2E-5	0.82	9E-5	0.77	2E-7
SNP association with PD conditioned on *HLA* alleles																														
*B*07:02*	1.33	2E-8	0.75	1E-5	0.80	8E-4	0.84	4E-3	0.78	5E-5	1.16	0.04	0.77	8E-3	0.84	0.04	0.82	0.02	0.79	6E-3	1.27	6E-9	0.76	3E-7	0.82	8E-5	0.83	2E-4	0.78	9E-7
*B*40:01*	1.34	2E-9	0.75	2E-5	0.81	1E-3	0.84	5E-3	0.78	4E-5	1.19	0.01	0.77	9E-3	0.83	0.02	0.82	0.03	0.79	6E-3	1.29	3E-10	0.76	5E-7	0.82	6E-5	0.83	4E-4	0.78	8E-7
*C*03:04*	1.33	6E-9	0.76	5E-5	0.82	2E-3	0.85	0.01	0.79	1E-4	1.17	0.02	0.80	0.03	0.84	0.03	0.84	0.06	0.81	0.01	1.28	1E-9	0.78	5E-6	0.83	2E-4	0.85	2E-3	0.80	5E-6
*C*07:02*	1.32	3E-8	0.75	2E-5	0.81	9E-4	0.84	4E-3	0.78	6E-5	1.17	0.03	0.76	7E-3	0.84	0.03	0.81	0.02	0.79	5E-3	1.27	7E-9	0.76	4E-7	0.82	8E-5	0.83	2E-4	0.78	1E-6
*DRB1*04:04*	1.32	1E-8	0.78	4E-4	0.85	0.03	0.89	0.07	0.81	1E-3	1.18	0.02	0.81	0.05	0.87	0.09	0.85	0.1	0.81	0.02	1.27	2E-9	0.79	6E-5	0.86	5E-3	0.87	0.02	0.81	5E-5
*DRB1*15:01*	1.33	2E-7	0.77	8E-5	0.83	4E-3	0.86	2E-2	0.80	3E-4	1.15	0.08	0.78	0.01	0.85	0.05	0.83	0.04	0.80	0.01	1.27	2E-7	0.77	3E-6	0.83	5E-4	0.85	2E-3	0.80	8E-6
*DRB4*01*	1.34	9E-8	0.76	4E-4	0.82	0.04	0.88	0.1	0.76	2E-3	1.12	0.1	0.83	0.1	1.14	0.4	0.91	0.4	0.86	0.2	1.26	2E-7	0.78	1E-4	0.89	0.2	0.89	0.07	0.79	1E-3
*DRB5*01*	1.33	3E-7	0.77	9E-5	0.83	4E-3	0.86	0.02	0.80	3E-4	1.15	0.08	0.78	0.01	0.85	0.06	0.83	0.04	0.80	0.01	1.27	2E-7	0.77	3E-6	0.83	5E-4	0.85	2E-3	0.80	8E-6
*DQA1*01:02*	1.35	1E-8	0.76	4E-5	0.82	2E-3	0.85	0.01	0.78	1E-4	1.15	0.06	0.78	0.01	0.85	0.06	0.84	0.05	0.80	0.01	1.28	1E-8	0.76	2E-6	0.83	4E-4	0.84	1E-3	0.79	5E-6
*DQA1*03:01*	1.30	3E-7	0.78	0.02	1.04	0.8	1.17	0.3	0.82	0.04	1.13	0.09	0.85	0.3	0.92	0.5	1.16	0.5	0.88	0.3	1.24	2E-7	0.80	0.01	0.95	0.6	1.17	0.2	0.84	0.03
*DQB1*03:02*	1.31	8E-8	0.79	2E-3	0.88	0.2	0.93	0.4	0.82	7E-3	1.15	0.05	0.83	0.1	0.89	0.2	0.91	0.4	0.84	0.1	1.26	3E-8	0.80	6E-4	0.88	0.06	0.92	0.2	0.82	2E-3
*DQB1*06:02*	1.33	3E-7	0.77	8E-5	0.83	4E-3	0.86	0.02	0.80	3E-4	1.15	0.08	0.78	0.01	0.85	0.05	0.83	0.04	0.80	0.01	1.26	2E-7	0.77	3E-6	0.83	5E-4	0.85	2E-3	0.80	8E-6
SNP association with PD conditioned on class I haplotypes																														
*B*07:02_C*07:02*	1.33	2E-8	0.75	1E-5	0.81	8E-4	0.84	4E-3	0.78	5E-5	1.16	0.03	0.77	8E-3	0.84	0.03	0.81	0.02	0.79	6E-3	1.27	6E-9	0.76	3E-7	0.82	8E-5	0.83	2E-4	0.78	9E-7
*B*40:01_C*03:04*	1.34	2E-9	0.75	2E-5	0.81	9E-4	0.84	5E-3	0.78	4E-5	1.19	0.01	0.77	9E-3	0.83	0.02	0.82	0.03	0.79	6E-3	1.29	3E-10	0.76	5E-7	0.82	6E-5	0.83	3E-4	0.78	8E-7
SNP association with PD conditioned on class II haplotypes																														
*DRB5*01_DRB1*15:01_DQA1*01:02_DQB1*06:02*																														
	1.33	3E-7	0.77	8E-5	0.83	4E-3	0.86	0.02	0.80	3E-4	1.15	0.08	0.78	0.01	0.85	0.05	0.83	0.04	0.80	0.01	1.27	2E-7	0.77	3E-6	0.83	5E-4	0.85	2E-3	0.80	8E-6
*DRB4*01_DRB1*04:04_DQA1*03:01_DQB1*03:02*																														
	1.32	1E-8	0.78	4E-4	0.85	2E-2	0.88	6E-2	0.81	9E-4	1.18	0.02	0.82	0.06	0.87	0.1	0.86	0.1	0.81	0.02	1.27	2E-9	0.79	6E-5	0.86	5E-3	0.87	0.02	0.81	5E-5
SNP association with PD conditioned on extended haplotypes																														
*B*07:02_C*07:02_DRB5*01_DRB1*15:01_DQA1*01:02_DQB1*06:02*																														
	1.33	5E-8	0.76	4E-5	0.82	2E-3	0.85	8E-3	0.79	1E-4	1.15	0.06	0.77	9E-3	0.85	0.04	0.82	0.03	0.79	7E-3	1.27	3E-8	0.76	1E-6	0.83	2E-4	0.84	6E-4	0.79	3E-6
*B*40:01_C*03:04_DRB4*01_DRB1*04:04_DQA1*03:01_DQB1*03:02*																														
	1.34	4E-9	0.76	5E-5	0.82	3E-3	0.85	0.01	0.79	1E-4	1.19	0.01	0.78	0.02	0.84	0.04	0.83	0.04	0.80	0.01	1.28	5E-10	0.77	3E-6	0.83	3E-4	0.84	1E-3	0.79	3E-6

[a] Originally reported SNP could not be generated. Proxies that imputed best in NGRC (rs41269955) and replication (rs77539933) were in moderate LD with original SNP (r^2=0.75) and in complete LD with each other (D'=1, r^2=1). P values shown are two sided for all analyses (including replication) and not corrected for multiple testing. Tests were adjusted for principal components 1 and 2.

Table S6. Stratified analysis.

A	NGRC								Replication								Meta Analysis	
	N in Cases			N in Controls			OR	P	N in Cases			N in Controls			OR	P	OR	P
SNPs and *HLA* haplotypes	**0**	**1**	**2**	**0**	**1**	**2**			**0**	**1**	**2**	**0**	**1**	**2**				
Association of rs3129882_G vs. A allele with PD stratified by presence or absence of *B*07:02_C*07:02_DRB5*01_DRB1*15:01_DQA1*01:02_DQB1*06:02* haplotype																		
Irrespective of haplotype	434	790	341	726	948	310	1.35	1E-9	252	421	170	308	401	146	1.20	0.01	1.30	9E-11
Haplotype absent	434	638	224	726	772	204	1.33	1E-7	252	345	116	308	342	104	1.16	0.05	1.27	5E-8
Haplotype present	0	152	117	0	176	106	1.28	0.2	0	76	54	0	59	42	1.05	0.9	1.21	0.2
Test of association of *B*07:02_C*07:02_DRB5*01_DRB1*15:01_DQA1*01:02_DQB1*06:02* haplotype with PD stratified by SNP genotype																		
Irrespective of SNP	1296	257	12	1704	271	11	1.29	3E-3	713	124	6	755	97	4	1.38	0.02	1.32	2E-4
rs3129882_AA	434	0	0	726	0	0	-	-	252	0	0	308	0	0	-	-	-	-
rs3129882_AG	638	152	0	772	176	0	1.12	0.4	345	76	0	342	59	0	1.25	0.3	1.15	0.2
rs3129882_GG	224	105	12	204	95	11	1.06	0.7	116	48	6	104	38	4	1.22	0.4	1.11	0.4
Test of association of *B*40:01_C*03:04_DRB4*01_DRB1*04:04_DQA1*03:01_DQB1*03:02* haplotype with PD stratified by SNP genotype																		
Irrespective of SNP	1531	34	0	1914	71	1	0.60	0.02	831	12	0	832	24	0	0.52	0.06	0.58	3E-03
rs9268515_ GG	1118	3	0	1266	2	0	-	-	612	2	0	571	0	0	-	-	-	-
rs9268515_GC	377	25	0	589	57	0	0.69	0.1	171	6	0	201	17	0	0.39	0.06	0.61	0.03
rs9268515_CC	29	6	0	52	12	1	0.82	0.7	12	3	0	20	7	0	0.77	0.75	0.81	0.6
rs77539933_CC/rs41269955_GG	1086	0	0	1269	0	0	-	-	325	0	0	273	0	0	-	-	-	-
rs77539933_CT/rs41269955_GA	415	30	0	584	61	0	0.70	0.1	243	7	0	278	12	0	0.69	0.5	0.70	0.09
rs77539933_TT/rs41269955_AA	27	4	0	54	10	1	0.75	0.6	74	3	0	76	9	0	0.37	0.1	0.55	0.2
rs660895_AA	1046	0	0	1230	0	0	-	-	593	0	0	550	0	0	-	-	-	-
rs660895_AG	447	29	0	619	59	0	0.69	0.1	212	10	0	256	16	0	0.77	0.5	0.71	0.09
rs660895_GG	38	5	0	65	12	1	0.63	0.4	26	2	0	26	8	0	0.29	0.1	0.50	0.1
rs2395163_TT	1030	2	0	1162	2	0	-	-	562	2	0	520	0	0	-	-	-	-
rs2395163_TC	455	24	0	681	58	0	0.65	0.1	243	8	0	275	16	0	0.59	0.2	0.63	0.04
rs2395163_CC	45	8	0	71	11	1	1.01	1.0	26	2	0	37	8	0	0.42	0.3	0.82	0.6
Association of rs9268515_G vs. C allele with PD stratified by presence or absence of *B*40:01_C*03:04_DRB4*01_DRB1*04:04_DQA1*03:01_DQB1*03:02* haplotype																		
Irrespective of haplotype	1121	402	35	1268	646	65	0.74	5E-6	614	177	15	571	218	27	0.75	5E-3	0.75	8E-8
Haplotype absent	1118	377	29	1266	589	52	0.76	6E-5	612	171	12	571	201	20	0.79	0.03	0.77	4E-6
Haplotype present	3	25	6	2	57	13	0.74	0.5	2	6	3	0	17	7	0.34	0.2	0.62	0.3
Association of rs41269955_G vs. A / rs77539933_C vs.T allele with PD stratified by presence or absence of *B*40:01_C*03:04_DRB4*01_DRB1*04:04_DQA1*03:01_DQB1*03:02* haplotype																		
Irrespective of haplotype	1086	445	31	1269	645	65	0.80	4E-4	325	250	77	273	290	85	0.82	0.02	0.81	2E-5
Haplotype absent	1086	415	27	1269	584	54	0.82	3E-3	325	243	74	273	278	76	0.84	0.04	0.83	3E-4
Haplotype present	0	30	4	0	61	11	0.71	0.6	0	7	3	0	12	9	0.63	0.6	0.68	0.4
Association of rs660895_A vs. G allele with PD stratified by presence or absence of *B*40:01_C*03:04_DRB4*01_DRB1*04:04_DQA1*03:01_DQB1*03:02* haplotype																		
Irrespective of haplotype	1046	476	43	1230	678	78	0.83	2E-3	593	222	28	550	272	34	0.81	0.02	0.82	9E-5
Haplotype absent	1046	447	38	1230	619	65	0.85	0.01	593	212	26	550	256	26	0.84	0.05	0.84	1E-3
Haplotype present	0	29	5	0	59	13	0.75	0.6	0	10	2	0	16	8	0.48	0.4	0.66	0.4
Association of rs2395163_T vs. C allele with PD stratified by presence or absence of *B*40:01_C*03:04_DRB4*01_DRB1*04:04_DQA1*03:01_DQB1*03:02* haplotype																		
Irrespective of haplotype	1032	479	53	1164	739	83	0.77	2E-5	564	251	28	520	291	45	0.78	3E-3	0.77	2E-7
Haplotype absent	1030	455	45	1162	681	71	0.78	8E-5	562	243	26	520	275	37	0.81	0.02	0.79	4E-6
Haplotype present	2	24	8	2	58	12	1.25	0.6	2	8	2	0	16	8	0.28	0.1	0.88	0.7

Table S6 Cont.

B	NGRC								Replication								Meta Analysis	
	N in Cases			N in Controls			OR	P	N in Cases			N in Controls			OR	P	OR	P
SNPs and *DRB1*04:04*	**0**	**1**	**2**	**0**	**1**	**2**			**0**	**1**	**2**	**0**	**1**	**2**				
Test of association of *DRB1*04:04* with PD stratified by SNP genotype																		
Irrespective of SNP	1467	98	0	1795	189	2	0.64	5E-04	794	48	1	781	73	2	0.67	0.03	0.65	4E-05
rs9268515_GG	1104	17	0	1241	27	0	0.73	0.32	608	6	0	562	9	0	0.64	0.41	0.71	0.20
rs9268515_GC	336	66	0	508	138	0	0.72	0.05	145	31	1	166	51	1	0.70	0.15	0.71	0.01
rs9268515_CC	21	14	0	39	24	2	0.87	0.74	10	5	0	15	11	1	0.43	0.24	0.74	0.38
rs77539933_CC/rs41269955_GG	1086	0	0	1269	0	0			325	0	0	273	0	0				
rs77539933_CT/rs41269955_GA	361	84	0	485	160	0	0.72	0.03	227	23	0	249	41	0	0.63	0.10	0.70	0.01
rs77539933_TT/rs41269955_AA	17	14	0	34	29	2	0.86	0.72	64	12	1	64	20	1	0.69	0.32	0.76	0.33
rs660895_AA	1046	0	0	1230	0	0			593	0	0	550	0	0				
rs660895_AG	395	81	0	520	158	0	0.69	0.01	181	41	0	212	60	0	0.81	0.36	0.72	0.01
rs660895_GG	26	17	0	45	31	2	0.77	0.49	20	7	1	19	13	2	0.65	0.36	0.72	0.27
rs2395163_TT	1022	10	0	1148	16	0	0.76	0.49	559	5	0	515	5	0	0.96	0.95	0.81	0.54
rs2395163_TC	411	68	0	594	145	0	0.70	0.03	212	38	1	234	56	1	0.80	0.32	0.73	0.02
rs2395163_CC	33	20	0	53	28	2	0.98	0.95	23	5	0	32	12	1	0.59	0.37	0.86	0.61
Association of rs9268515_G vs. C allele with PD stratified by presence or absence of *DRB1*04:04*																		
Irrespective of haplotype	1121	402	35	1268	646	65	0.74	5E-06	614	177	15	571	218	27	0.75	5E-03	0.75	8E-08
*DRB1*04:04* absent	1104	336	21	1241	508	39	0.77	3E-04	608	145	10	562	166	15	0.81	0.07	0.78	5E-05
*DRB1*04:04* present	17	66	14	27	138	26	0.93	0.76	6	32	5	9	52	12	0.56	0.17	0.83	0.35
Association of rs41269955_G vs. A / rs77539933_C vs.T allele with PD stratified by presence or absence of *DRB1*04:04*																		
Irrespective of haplotype	1086	445	31	1269	645	65	0.80	4E-04	325	250	77	273	290	85	0.82	0.02	0.81	2E-05
*DRB1*04:04* absent	1086	361	17	1269	485	34	0.85	0.03	325	227	64	273	249	64	0.86	0.08	0.85	5E-03
*DRB1*04:04* present	0	84	14	0	160	31	0.86	0.67	0	23	13	0	41	21	1.09	0.85	0.94	0.82
Association of rs660895_A vs. G allele with PD stratified by presence or absence of *DRB1*04:04*																		
Irrespective of haplotype	1046	476	43	1230	678	78	0.83	2E-03	593	222	28	550	272	34	0.81	0.02	0.82	9E-05
*DRB1*04:04* absent	1046	395	26	1230	520	45	0.88	0.06	593	181	20	550	212	19	0.85	0.11	0.87	0.01
*DRB1*04:04* present	0	81	17	0	158	33	0.98	0.96	0	41	8	0	60	15	0.82	0.69	0.93	0.80
Association of rs2395163_T vs. C allele with PD stratified by presence or absence of *DRB1*04:04*																		
Irrespective of haplotype	1032	479	53	1164	739	83	0.77	2E-05	564	251	28	520	291	45	0.78	3E-03	0.77	2E-07
*DRB1*04:04* absent	1022	411	33	1148	594	53	0.79	4E-04	559	212	23	515	234	32	0.82	0.03	0.80	4E-05
*DRB1*04:04* present	10	68	20	16	145	30	1.10	0.71	5	39	5	5	57	13	0.56	0.17	0.92	0.69

Table S6 Cont.

C	NGRC								Replication								Meta Analysis	
SNPs and *C*03:04*	N in Cases			N in Controls			OR	P	N in Cases			N in Controls			OR	P	OR	P
	0	1	2	0	1	2			0	1	2	0	1	2				
Test of association of *C*03:04* with PD stratified by SNP genotype																		
Irrespective of SNP	1354	202	9	1634	337	15	0.76	2E-03	748	92	3	707	142	7	0.63	6E-04	0.72	8E-06
rs9268515_GG	1005	113	3	1121	143	4	0.90	0.39	558	55	1	503	65	3	0.75	0.12	0.85	0.11
rs9268515_GC	319	80	3	465	175	6	0.70	0.01	147	28	2	154	60	4	0.54	0.01	0.65	5E-04
rs9268515_CC	24	8	3	42	18	5	1.02	0.95	8	7	0	13	14	0	0.82	0.77	0.98	0.94
rs77539933_CC/rs41269955_GG	975	109	2	1119	146	4	0.86	0.24	301	24	0	250	22	1	0.86	0.61	0.86	0.20
rs77539933_CT/rs41269955_GA	353	86	6	467	170	8	0.74	0.03	217	32	1	234	55	1	0.67	0.09	0.72	0.01
rs77539933_TT/rs41269955_AA	23	7	1	43	19	3	0.80	0.61	61	15	1	67	16	2	1.04	0.91	0.94	0.81
rs660895_AA	951	93	2	1089	136	5	0.78	0.07	545	47	1	480	66	4	0.62	0.01	0.72	3E-03
rs660895_AG	368	103	5	494	177	7	0.83	0.15	183	37	2	204	65	3	0.67	0.06	0.78	0.03
rs660895_GG	35	6	2	51	24	3	0.57	0.16	20	8	0	23	11	0	1.03	0.96	0.69	0.26
rs2395163_TT	924	105	3	1025	135	4	0.87	0.29	513	50	1	455	62	3	0.70	0.06	0.81	0.05
rs2395163_TC	391	85	3	551	182	6	0.72	0.02	214	36	1	222	66	3	0.58	0.01	0.68	9E-04
rs2395163_CC	38	12	3	58	20	5	0.97	0.93	21	6	1	30	14	1	0.90	0.83	0.95	0.85
Association of rs9268515_G vs. C allele with PD stratified by presence or absence of *C*03:04*																		
Irrespective of haplotype	1121	402	35	1268	646	65	0.74	5E-06	614	177	15	571	218	27	0.75	5E-03	0.75	8E-08
*C*03:04 absent*	1005	319	24	1121	465	42	0.79	2E-03	558	147	8	503	154	13	0.84	0.13	0.81	5E-04
*C*03:04 present*	116	83	11	147	181	23	0.66	6E-03	56	30	7	68	64	14	0.70	0.09	0.67	1E-03
Association of rs41269955_G vs. A / rs77539933_C vs.T allele with PD stratified by presence or absence of *C*03:04*																		
Irrespective of haplotype	1086	445	31	1269	645	65	0.80	4E-04	325	250	77	273	290	85	0.82	0.02	0.81	2E-05
*C*03:04 absent*	975	353	23	1119	467	43	0.85	0.02	301	217	61	250	234	67	0.83	0.04	0.84	2E-03
*C*03:04 present*	111	92	8	150	178	22	0.71	0.02	24	33	16	23	56	18	0.89	0.63	0.76	0.03
Association of rs660895_A vs. G allele with PD stratified by presence or absence of *C*03:04*																		
Irrespective of haplotype	1046	476	43	1230	678	78	0.83	2E-03	593	222	28	550	272	34	0.81	0.02	0.82	9E-05
*C*03:04 absent*	951	368	35	1089	494	51	0.87	0.04	545	183	20	480	204	23	0.82	0.05	0.85	0.01
*C*03:04 present*	95	108	8	141	184	27	0.78	0.10	48	39	8	70	68	11	0.96	0.87	0.84	0.15
Association of rs2395163_T vs. C allele with PD stratified by presence or absence of *C*03:04*																		
Irrespective of haplotype	1032	479	53	1164	739	83	0.77	2E-05	564	251	28	520	291	45	0.78	3E-03	0.77	2E-07
*C*03:04 absent*	924	391	38	1025	551	58	0.80	1E-03	513	214	21	455	222	30	0.82	0.04	0.81	1E-04
*C*03:04 present*	108	88	15	139	188	25	0.73	0.03	51	37	7	65	69	15	0.75	0.16	0.74	0.01

The 0, 1, 2 sub-header under case and control columns denote the number of subjects with 0, 1 or 2 copies of SNP minor allele or the haplotype, whichever is being tested. Association tests were done under an additive model, thus the OR represents the change in risk for each added copy of SNP minor allele or haplotype. SNP frequencies were high enough to stratify by 3 genotypes. Haplotypes were not common; hence they were stratified as being present (1 or 2 copies) or absent (0 copy). Two individuals had imputed haplotypes but did not have the SNP genotype; they appear in unstratified haplotype tests only. We did not calculate OR and P if a class had N<5.

Table S7. Association of *HLA* alleles with PD conditioned on SNPs (Extended version of Table 4 of the main manuscript)

	NGRC												Replication												Meta analysis									
	Not conditioned		rs3129882		rs9268515		rs41269955[a]		rs660895		rs2395163		Not conditioned		rs3129882		rs9268515		rs77539933[a]		rs660895		rs2395163		Not conditioned		rs3129882		rs9268515		rs41269955/ rs77539933		rs660895		rs2395163	
	OR	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**
***HLA* allele association with PD conditioned on SNP**																																				
*B*07:02*	1.20	8E-3	1.09	0.2	1.18	0.02	1.18	0.02	1.18	0.02	1.17	0.03	1.31	0.01	1.25	0.04	1.33	9E-3	1.24	0.08	1.30	0.01	1.29	0.02	1.23	3E-4	1.13	0.04	1.22	8E-4	1.20	3E-3	1.21	8E-4	1.20	1E-3
*B*40:01*	0.79	0.02	0.82	0.07	0.83	0.08	0.82	0.07	0.82	0.06	0.82	0.07	0.71	0.03	0.74	0.05	0.74	0.06	0.87	0.5	0.73	0.05	0.73	0.05	0.76	2E-3	0.79	9E-3	0.80	0.01	0.83	0.05	0.79	8E-3	0.79	9E-3
*C*03:04*	0.76	2E-3	0.81	0.02	0.81	0.02	0.80	0.02	0.79	0.01	0.80	0.02	0.63	6E-4	0.65	2E-3	0.67	4E-3	0.78	0.1	0.66	2E-3	0.66	2E-3	0.72	8E-6	0.75	2E-4	0.77	5E-4	0.80	4E-3	0.75	1E-4	0.76	3E-4
*C*07:02*	1.22	3E-3	1.11	0.1	1.20	7E-3	1.20	6E-3	1.21	5E-3	1.19	0.01	1.25	0.03	1.19	0.1	1.27	0.02	1.21	0.1	1.24	0.03	1.23	0.05	1.23	2E-4	1.13	0.03	1.22	5E-4	1.21	1E-3	1.22	5E-4	1.20	1E-3
*DRB1*04:04*	0.64	5E-4	0.71	8E-3	0.75	0.03	0.73	0.03	0.71	0.01	0.75	0.03	0.67	0.03	0.70	0.05	0.70	0.09	0.65	0.05	0.77	0.2	0.77	0.2	0.65	4E-5	0.71	1E-3	0.73	7E-3	0.71	4E-3	0.73	6E-3	0.75	0.01
*DRB1*15:01*	1.26	9E-4	1.04	0.6	1.18	0.02	1.20	9E-3	1.21	7E-3	1.18	0.02	1.26	0.02	1.15	0.2	1.20	0.09	1.13	0.3	1.22	0.06	1.21	0.07	1.26	6E-5	1.07	0.3	1.19	4E-3	1.18	6E-3	1.21	1E-3	1.19	3E-3
*DRB4*01*	0.85	3E-3	0.98	0.8	0.97	0.6	0.96	0.6	0.91	0.2	1.01	0.9	0.80	4E-3	0.84	0.05	0.87	0.1	0.68	0.03	0.84	0.08	0.88	0.3	0.83	4E-5	0.93	0.2	0.93	0.2	0.91	0.2	0.89	0.03	0.97	0.6
*DRB5*01*	1.25	8E-4	1.04	0.6	1.18	0.02	1.20	8E-3	1.21	6E-3	1.18	0.02	1.25	0.03	1.13	0.3	1.18	0.1	1.14	0.2	1.20	0.07	1.19	0.08	1.25	5E-5	1.07	0.3	1.18	4E-3	1.18	4E-3	1.21	1E-3	1.18	3E-3
*DQA1*01:02*	1.15	0.02	0.99	0.9	1.07	0.3	1.09	0.1	1.10	0.1	1.07	0.3	1.22	0.02	1.14	0.2	1.16	0.1	1.12	0.3	1.17	0.08	1.16	0.1	1.17	1E-3	1.04	0.5	1.10	0.06	1.10	0.07	1.12	0.02	1.10	0.06
*DQA1*03:01*	0.77	1E-4	0.87	0.04	0.94	0.5	0.75	0.2	0.66	9E-3	0.92	0.5	0.76	3E-3	0.80	0.02	0.85	0.3	0.80	0.1	0.65	0.06	0.85	0.3	0.77	1E-6	0.84	3E-3	0.91	0.3	0.79	0.04	0.66	1E-3	0.90	0.2
*DQB1*03:02*	0.75	3E-4	0.84	0.03	0.87	0.1	0.84	0.1	0.80	0.04	0.88	0.2	0.73	7E-3	0.77	0.03	0.80	0.1	0.80	0.1	0.80	0.2	0.84	0.3	0.74	7E-6	0.82	3E-3	0.85	0.03	0.82	0.03	0.80	0.01	0.87	0.08
*DQB1*06:02*	1.26	7E-4	1.05	0.5	1.19	0.01	1.21	7E-3	1.22	5E-3	1.19	0.01	1.27	0.02	1.15	0.2	1.20	0.08	1.14	0.3	1.22	0.06	1.21	0.07	1.26	4E-5	1.08	0.2	1.19	3E-3	1.19	4E-3	1.22	8E-4	1.19	2E-3
Class I haplotype association with PD conditioned on SNP																																				
*B*07:02_C*07:02*	1.21	6E-3	1.09	0.2	1.18	0.02	1.19	0.01	1.19	0.01	1.18	0.02	1.29	0.02	1.23	0.06	1.32	0.01	1.23	0.1	1.28	0.02	1.27	0.03	1.23	3E-4	1.13	0.04	1.22	8E-4	1.20	3E-3	1.21	9E-4	1.20	2E-3
*B*40:01_C*03:04*	0.79	0.03	0.83	0.08	0.84	0.1	0.83	0.08	0.82	0.07	0.83	0.08	0.71	0.03	0.73	0.05	0.74	0.06	0.87	0.5	0.73	0.05	0.73	0.05	0.76	2E-3	0.80	0.01	0.80	0.02	0.84	0.06	0.79	9E-3	0.80	0.01
Class II haplotype association with PD conditioned on SNP																																				
*DRB5*01_DRB1*15:01_DQA1*01:02_DQB1*06:02*																																				
	1.26	7E-4	1.04	0.6	1.19	0.02	1.21	8E-3	1.22	6E-3	1.19	0.02	1.27	0.02	1.15	0.2	1.20	0.09	1.14	0.3	1.22	0.06	1.21	0.07	1.27	5E-5	1.08	0.3	1.19	3E-3	1.19	4E-3	1.22	8E-4	1.20	2E-3
*DRB4*01_DRB1*04:04_DQA1*03:01_DQB1*03:02*																																				
	0.64	7E-4	0.71	0.01	0.75	0.04	0.73	0.03	0.71	0.02	0.75	0.04	0.65	0.02	0.68	0.04	0.67	0.06	0.62	0.04	0.74	0.1	0.75	0.1	0.64	4E-5	0.70	1E-3	0.73	7E-3	0.70	3E-3	0.72	5E-3	0.75	0.01
Extended haplotype association with PD conditioned on SNP																																				
*B*07:02_C*07:02_DRB5*01_DRB1*15:01_DQA1*01:02_DQB1*06:02*																																				
	1.29	3E-3	1.08	0.4	1.22	0.03	1.24	0.02	1.24	0.01	1.22	0.03	1.38	0.02	1.26	0.1	1.34	0.04	1.27	0.1	1.34	0.03	1.33	0.04	1.32	2E-4	1.13	0.1	1.25	3E-3	1.25	4E-3	1.27	1E-3	1.25	3E-3
*B*40:01_C*03:04_DRB4*01_DRB1*04:04_DQA1*03:01_DQB1*03:02*																																				
	0.60	0.02	0.68	0.07	0.75	0.2	0.71	0.1	0.69	0.08	0.72	0.1	0.52	0.06	0.55	0.1	0.59	0.2	0.54	0.1	0.61	0.2	0.62	0.2	0.58	3E-3	0.64	0.02	0.71	0.06	0.66	0.03	0.67	0.03	0.70	0.05

[a] Originally reported SNP could not be generated (see methods). Proxies that imputed best in NGRC (rs41269955) and replication (rs77539933) are in moderate LD with original SNP (r^2=0.75) and in complete LD with each other (D'=1, r^2=1). P values shown are two sided for all analyses (even replication) and not corrected for multiple testing. Tests were adjusted for principal components 1 and 2.

Table S8. eQTL data: Association of PD-associated SNPs with expression of genes in the *HLA*-region (Extended version of Table 6 of main text.)

SNP	Gene	P	Probe	Specificity	Browser	Source	Method	Population	Tissue
rs3129882	*DRA*	1E-5 7E-4	ILMN_2157441	unique	Genevar	Nica[23]	Illumina whole genome expression HumHT-12v3	MuTHER twins UK Cauc	Lymphoblasts
	DRA	4E-5	--	unique	eqtl	Montgomery[24]	RNA-Seq	HapMap CEU	Lymphoblasts
	DRB5	9E-5	--	unique	eqtl	Montgomery[24]	RNA-Seq	HapMap CEU	Lymphoblasts
	DQB1	3E-14	Probe cluster	unique	SCAN	Gamazon [25]	Affymetrix Human Exon 1.0 ST Array	HapMap CEU	Lymphoblasts
	DQA2	2E-7	GI_11095446-S	100% *DQA2,* 88% *DQA1*	eqtl	Stranger [26]	Illumina Sentrix Hum-6 Expression BeadChip v1	HapMaP mixed 4 populations	Lymphoblasts
	DRB5	9E-9	ILMN_1697499	100% *DRB5,* 92% *DRB1,* 88% *DRB3*	Genevar	Stranger[29]	Illumina Sentrix Hum-6 Expression BeadChip v2	HapMap CEU	Lymphoblasts
	DRB5	4E-5 9E-5	ILMN_1697499	100% *DRB5,* 92% *DRB1,* 88% *DRB3*	Genevar	Dimas[30]	Illumina Human WG-6 v3	Western European	Lymphoblasts, T cells
	DQB2	3E-14	Probe cluster	Unknown	SCAN	Gamazon[25]	Affymetrix Human Exon 1.0 ST Array	HapMap CEU	Lymphoblasts
	DRB1	3E-14	Probe cluster	Unknown	SCAN	Gamazon[25]	Affymetrix Human Exon 1.0 ST Array	HapMap CEU	Lymphoblasts
	DRB3,4,5	3E-14	Probe cluster	Unknown	SCAN	Gamazon[25]	Affymetrix Human Exon 1.0 ST Array	HapMap CEU	Lymphoblasts
rs2395163	*DQA1*	5E-14, 5E-13	ILMN_1791534	unique	Genevar	Nica[23]	Illumina whole genome expression HumHT-12v3	MuTHER twins UK Cauc	Lymphoblasts
	DQA2	1E-6	--	unique	eqtl	Montgomery[24]	RNA-Seq	HapMap CEU	Lymphoblasts
	DRB1	5E-16	ILMN_1715169	100% *DRB*1, 94% *DRB4*, 92% *DRB5*, 82% *DRB3*	eqtl	Zeller[27]	Illumina whole genome expression HumHT-12v3	German	Monocytes
	DQA1	2E-79	ILMN_1808405	100% *DQA1,* 98% *DQA2* , 74% *DOA*	eqtl	Zeller[27]	Illumina whole genome expression HumHT-12v3	German	Monocytes
	DQA1	6E-6	GI_18426974-S	100% *DQA1,* 94% *DQA2*	eqtl	Veyrieras[28]	Illumina Sentrix Hum-6 Expression BeadChip v1	HapMaP mixed 4 populations	Lymphoblasts
	DQA2	9E-15	GI_11095446-S	100% *DQA2,* 88% *DQA1*	eqtl	Stranger[26]	Illumina Sentrix Hum-6 Expression BeadChip v1	HapMaP mixed 4 populations	Lymphoblasts
	DQB1	2E-30	ILMN_1661266	100% *DQB1,* 86% *DQB2,* 74% *DRB5*	eqtl	Zeller[27]	Illumina whole genome expression HumHT-12v3	German	Monocytes
	DRB5	1E-14	ILMN_1697499	100% *DRB5,* 92% *DRB1*, 88% *DRB3*	eqtl	Zeller[27]	Illumina whole genome expression HumHT-12v3	German	Monocytes
	DRB5	3E-6	ILMN_1697499	100% *DRB5,* 92% *DRB1,* 88% *DRB3*	Genevar	Stranger[29]	Illumina Sentrix Hum-6 Expression BeadChip v2	HapMap CEU	Lymphoblasts
rs660895	*DQA1*	2E-17 1E-13	ILMN_1791534	unique	Genevar	Nica[23]	Illumina whole genome expression HumHT-12v3	MuTHER twins UK Cauc	Lymphoblasts
	DQA2	6E-7	--	unique	eqtl	Montgomery[24]	RNA-Seq	HapMap CEU	Lymphoblasts
	AIF1	3E-5	ILMN_1792473	unique	Genevar	Grundberg[31]	Illumina whole genome expression HumHT-12v3	MuTHER twins UK Cauc	Lymphoblasts
	DQA1	6E-11	GI_18426974-S	100% *DQA1*, 94% *DQA2*	eqtl	Veyrieras[28]	Illumina Sentrix Hum-6 Expression BeadChip v1	HapMaP mixed	Lymphoblasts
	DQA2	1E-21	GI_11095446-S	100% *DQA2,* 88% *DQA1*	eqtl	Stranger[26]	Illumina Sentrix Hum-6 Expression BeadChip v1	HapMaP mixed 4 populations	Lymphoblasts
	DRB5	4E-7	ILMN_1697499	100% *DRB5,* 92%*DRB1,* 88%*DRB3*	Genevar	Stranger[29]	Illumina Sentrix Hum-6 Expression BeadChip v2	HapMap CEU	Lymphoblasts

Each PD-associated SNP was tested for association with expression of genes within 1 Mb of the SNP using three publically available databases (Browser). SNP-gene associations that passed Bonferroni-corrected significance (P) are shown. Rows that have two P values denote independent confirmation in co-twins or in two different tissues. We went back to the original data (Source column),

identified the probe that was used (Probe column) and determined specificity of each probe to the identified gene and its allelic variants. Specificity denotes if the probe hybridized with only one gene or with multiple genes. Unique denotes when probe hybridized with one gene only with 100% sequence match. % denotes the nucleotide match between the probe (usually 50 nucleotides) and the targeted sequences. Except in one case, the probes were against a functionally non-polymorphic gene (ex. *DRA*) or the 3'UTR and therefore allele-specificity was not of relevance. In the one exception (see rs2395163, *DQB1*, Zeller, 2010[27]) where the probe mapped to exon 4, it was a 100% match to all *DQB1*02* alleles, 98% to *DQB1*03* and *DQB1*04* alleles, 82%-92% to *DQB1*06* alleles, and 82%-88% to *DQB1*05* alleles.