Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease

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rsid	chrom	bp	w_i	$w_i^{missing}$
bias	-	-	-1.93614	-
rs823156	1	204031263	0.17978	0.29361
rs2117511	2	136179131	-0.19903	-0.04755
rs10513789	3	184242767	-0.20692	-0.08325
rs6599389	4	929113	0.22544	0.03374
rs11248060	4	954359	-0.18680	-0.32637
rs11724804	4	955779	-0.07805	-0.06768
rs4395500	4	13433745	-0.15007	-0.23841
rs6812193	4	77418010	0.17122	0.21732
rs11931074	4	90858538	-0.14634	-0.26935
rs356220	4	90860363	-0.11414	-0.14267
rs2736990	4	90897564	-0.13371	-0.14259
rs9366778	6	31377152	-0.12434	-0.10019
rs10886515	10	121333579	-0.15044	-0.08701
rs6589497	11	115128203	0.18249	0.04090
rs10878246	12	38918366	0.15039	0.05717
rs11868035	17	17655826	-0.15247	-0.09411
rs708382	17	39797870	0.12370	0.09699
rs12185268	17	41279463	0.17776	0.28040
rs12373139	17	41279910	-0.06829	-0.02925
rs11878694	19	6947509	0.20529	0.36115
rs1276377	20	55031299	-0.08092	-0.10845
rs331617	20	55073255	0.09799	0.05514

Table S5. Bias-corrected $E[FP] \leq 1$ model. This model, which achieves a covariate-adjusted AUC of 0.608 on the NINDS data, was obtained by training on the 23andMe cohort, using the subset of SNPs that were shared with the NINDS cohort. w_i refers to the weight for each SNP (i.e., the log odds ratio per copy of the alphabetically lesser allele), and w_i^{missing} is the weight used in the algorithm in the case of missing data for that SNP.