

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

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

Top_SNP, the SNP with the smallest p-value;

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

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

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

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

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