

Supplementary Table 15. Association of known MS susceptibility variants with disability outcomes

SNV	Chr	position (bp)	EA	REF	ARMSS score			Confirmed disability worsening			Time to EDSS 6.0			Rate of EDSS worsening			R ²	Included in PRS?
					beta	s.e.	P	HR	s.e.	P	HR	s.e.	P	beta	s.e.	P		
rs3748817	1	2525665	C	T	-0.011	0.012	0.364	0.97	0.029	0.273	1.06	0.051	0.280	-2.9E-03	0.003	0.380	0.99	1
rs3007421	1	6530189	A	G	0.001	0.017	0.977	1.00	0.039	0.926	1.02	0.068	0.749	0.007	0.004	0.143	0.92	1
rs1801133	1	11856378	A	G	-0.001	0.012	0.919	1.00	0.029	0.953	0.92	0.053	0.119	-0.002	0.003	0.579	0.99	1
rs2639453	1	11982544	C	T	0.006	0.014	0.671	0.97	0.033	0.381	1.06	0.059	0.328	0.000	0.004	0.973	0.93	0
rs13551	1	24180962	C	T	-0.015	0.012	0.236	0.98	0.028	0.576	0.91	0.052	0.086	-0.003	0.003	0.405	0.96	1
rs7550552	1	25299602	T	C	-0.005	0.012	0.679	0.96	0.027	0.093	0.97	0.048	0.487	0.002	0.003	0.593	0.97	1
rs10914539	1	32715641	T	G	-0.012	0.015	0.406	0.98	0.041	0.570	1.02	0.071	0.741	7.7E-04	0.005	0.865	1.00	1
rs72922276	1	65429319	A	G	0.001	0.021	0.976	1.03	0.048	0.480	1.09	0.083	0.301	8.8E-03	0.005	0.109	0.97	1
rs12087340	1	85746993	T	C	0.011	0.019	0.579	1.01	0.045	0.805	0.99	0.080	0.943	-0.001	0.005	0.904	0.97	1
rs233100	1	85772009	A	G	-0.006	0.012	0.581	1.03	0.027	0.316	1.03	0.048	0.567	0.002	0.003	0.532	1.00	0
rs9887787	1	92222143	T	C	0.003	0.017	0.842	1.06	0.038	0.134	1.10	0.067	0.168	0.005	0.004	0.282	0.98	1
rs58394161	1	92939959	C	T	0.001	0.015	0.969	1.05	0.036	0.210	1.08	0.063	0.231	0.005	0.004	0.262	0.96	0
rs11577426	1	93160238	T	C	7.3E-03	0.013	0.568	1.02	0.030	0.526	1.09	0.052	0.079	0.004	0.003	0.276	0.99	1
rs10747454	1	93429247	G	T	0.009	0.015	0.567	1.02	0.036	0.505	0.96	0.063	0.523	0.005	0.004	0.234	0.94	0
rs12132283	1	1.01E+08	C	A	0.012	0.012	0.311	0.98	0.027	0.562	1.03	0.049	0.512	-0.001	0.003	0.664	0.94	1
rs11587215	1	1.01E+08	A	G	-8.1E-03	0.017	0.631	1.02	0.039	0.639	1.02	0.067	0.753	0.006	0.004	0.166	0.98	0
rs1335532	1	1.17E+08	G	A	-0.003	0.019	0.890	0.94	0.045	0.145	0.89	0.083	0.173	0.000	0.005	0.927	1.00	1
rs541503	1	1.2E+08	C	T	-0.007	0.012	0.547	1.01	0.028	0.652	1.03	0.049	0.494	0.002	0.003	0.516	0.99	1
rs113012729	1	1.55E+08	G	A	-0.050	0.030	0.096	0.94	0.069	0.340	0.98	0.123	0.837	0.004	0.008	0.648	0.96	1
rs3761959	1	1.58E+08	T	C	-0.010	0.012	0.386	0.99	0.027	0.620	0.95	0.048	0.263	-0.003	0.003	0.315	1.00	1
rs12086448	1	1.6E+08	G	A	-0.020	0.012	0.083	0.91	0.027	0.001	0.95	0.048	0.330	-0.006	0.003	0.070	0.96	1
rs6427540	1	1.61E+08	T	C	0.021	0.018	0.236	1.02	0.040	0.658	0.89	0.076	0.121	0.001	0.005	0.777	1.00	0
rs3766374	1	1.61E+08	A	G	0.002	0.013	0.877	1.07	0.029	0.022	1.02	0.053	0.764	0.008	0.003	0.025	0.99	1
rs1323292	1	1.93E+08	A	G	0.039	0.016	0.012	0.98	0.036	0.559	0.99	0.064	0.876	0.002	0.004	0.589	1.00	1
rs59655222	1	2.01E+08	C	T	0.015	0.013	0.253	1.02	0.031	0.433	1.05	0.055	0.367	-0.003	0.003	0.417	1.00	1
rs9308424	1	2.13E+08	A	G	0.008	0.012	0.497	0.97	0.029	0.349	0.94	0.052	0.205	-0.002	0.003	0.487	0.98	1
rs1534422	2	12640741	A	G	0.021	0.012	0.070	1.02	0.027	0.436	0.98	0.049	0.675	8.4E-04	0.003	0.786	0.97	1
rs2082881	2	25038268	A	G	0.001	0.013	0.934	1.01	0.030	0.833	0.95	0.054	0.323	-0.003	0.003	0.405	0.96	1
rs10171296	2	30481309	G	A	0.003	0.015	0.855	1.01	0.036	0.679	1.07	0.063	0.271	0.002	0.004	0.677	0.98	1
rs17030410	2	43356490	G	T	-0.029	0.013	0.034	0.94	0.031	0.060	1.04	0.055	0.507	0.000	0.004	0.916	0.97	1
rs2278300	2	61176073	G	T	0.007	0.012	0.589	1.01	0.029	0.715	1.04	0.052	0.443	0.006	0.003	0.051	1.00	1
rs11673987	2	65597671	G	A	-0.013	0.012	0.273	1.00	0.028	0.902	0.93	0.050	0.154	0.000	0.003	0.917	0.99	1
rs3816281	2	68607947	T	G	0.025	0.013	0.049	1.03	0.030	0.366	1.06	0.053	0.246	0.003	0.003	0.325	1.00	1
rs12373588	2	1.12E+08	G	T	0.007	0.012	0.580	0.98	0.027	0.463	0.98	0.048	0.723	0.000	0.003	0.909	0.96	1
rs57116599	2	1.13E+08	A	G	-0.010	0.015	0.509	0.99	0.033	0.856	0.94	0.061	0.283	-0.004	0.004	0.281	0.96	0
rs11897084	2	1.37E+08	G	A	-0.004	0.013	0.779	0.98	0.030	0.579	0.99	0.054	0.844	-0.008	0.003	0.017	0.82	1
rs962052	2	1.52E+08	T	C	0.023	0.013	0.075	1.01	0.030	0.778	1.01	0.053	0.865	-2.1E-03	0.003	0.542	0.95	1
rs6738544	2	1.92E+08	C	A	0.004	0.012	0.730	1.03	0.027	0.332	0.91	0.048	0.059	0.000	0.003	0.978	1.00	1
rs6435203	2	2.05E+08	A	G	0.034	0.013	0.008	1.04	0.030	0.233	1.06	0.054	0.303	0.007	0.003	0.055	0.95	1
rs35540610	2	2.31E+08	C	T	6.5E-03	0.013	0.625	1.01	0.030	0.726	1.08	0.054	0.168	-0.002	0.003	0.638	0.99	1
rs12106877	3	18709522	C	T	0.017	0.012	0.150	0.99	0.027	0.609	0.99	0.049	0.807	1.5E-03	0.003	0.612	1.00	1
rs12330493	3	27791614	G	T	0.009	0.012	0.448	0.96	0.027	0.157	0.97	0.049	0.597	-0.006	0.003	0.069	0.97	1
rs438613	3	28072086	C	T	0.008	0.012	0.490	0.99	0.027	0.731	1.00	0.049	0.965	0.004	0.003	0.151	0.95	1
rs6550177	3	32979088	C	T	-0.003	0.012	0.796	0.96	0.027	0.102	1.05	0.049	0.283	-0.001	0.003	0.642	0.97	1
rs9878602	3	71535338	G	T	0.020	0.012	0.096	1.00	0.027	0.945	1.02	0.048	0.636	0.001	0.003	0.850	0.96	1
rs77958473	3	1.01E+08	C	T	0.013	0.025	0.595	1.07	0.055	0.235	0.95	0.100	0.584	0.011	0.006	0.102	0.95	1
rs771767	3	1.02E+08	G	A	0.008	0.013	0.515	0.98	0.029	0.584	0.99	0.052	0.868	0.004	0.003	0.187	1.00	0
rs2289746	3	1.05E+08	C	T	-0.010	0.013	0.445	0.99	0.029	0.778	0.96	0.050	0.430	-0.003	0.003	0.375	0.97	1
rs138433213	3	1.13E+08	G	T	0.077	0.057	0.174	1.07	0.134	0.610	0.92	0.231	0.733	0.004	0.016	0.816	0.96	1

rs9843355	3	1.19E+08	A	G	-0.016	0.016	0.296	0.98	0.037	0.551	1.02	0.065	0.707	0.004	0.004	0.349	0.98	1
rs12695416	3	1.22E+08	G	A	0.010	0.012	0.393	1.04	0.028	0.168	1.02	0.050	0.703	2.6E-03	0.003	0.410	0.97	1
rs2255214	3	1.22E+08	T	G	0.011	0.012	0.351	0.95	0.027	0.070	1.02	0.047	0.655	-0.001	0.003	0.763	0.99	1
rs9282641	3	1.22E+08	A	G	-0.014	0.021	0.511	0.94	0.050	0.213	0.87	0.089	0.113	0.005	0.005	0.410	1.00	0
rs9846396	3	1.41E+08	T	C	-0.018	0.012	0.127	1.01	0.027	0.679	0.94	0.049	0.210	-0.003	0.003	0.289	0.99	1
rs75029101	3	1.6E+08	A	G	-0.027	0.019	0.168	0.98	0.044	0.656	0.89	0.080	0.158	-0.006	0.005	0.268	0.98	0
rs1014486	3	1.6E+08	C	T	0.002	0.012	0.885	1.00	0.026	0.975	0.96	0.047	0.372	-0.004	0.003	0.187	0.99	1
rs10936599	3	1.69E+08	T	C	-0.014	0.014	0.302	0.92	0.032	0.005	0.91	0.056	0.108	-0.004	0.004	0.230	1.00	1
rs969625	3	1.88E+08	A	G	0.007	0.012	0.541	1.01	0.028	0.592	1.11	0.048	0.030	0.002	0.003	0.602	0.98	1
rs9839229	3	1.88E+08	C	T	-0.018	0.012	0.146	1.00	0.028	0.978	0.97	0.049	0.598	-4.2E-03	0.003	0.189	0.94	1
rs6832151	4	40303633	T	G	-0.005	0.012	0.698	1.02	0.029	0.577	1.00	0.051	0.970	0.004	0.003	0.246	1.00	1
rs17470892	4	48143201	C	T	-0.006	0.012	0.636	0.99	0.027	0.829	0.98	0.048	0.732	0.000	0.003	0.872	1.00	1
rs7665090	4	1.04E+08	G	A	0.000	0.012	0.997	1.01	0.026	0.708	1.06	0.047	0.226	0.000	0.003	0.973	1.00	1
rs2726518	4	1.06E+08	C	A	0.014	0.012	0.235	1.10	0.027	0.000	1.08	0.048	0.096	8.7E-04	0.003	0.775	0.99	1
rs7690934	4	1.09E+08	C	T	0.000	0.012	0.981	1.00	0.027	0.951	1.01	0.048	0.827	0.000	0.003	0.947	0.96	1
rs17051321	4	1.22E+08	T	C	-0.027	0.013	0.045	0.96	0.031	0.225	0.94	0.056	0.297	-0.001	0.003	0.791	0.99	1
rs13150896	4	1.64E+08	G	A	-0.016	0.012	0.176	0.98	0.027	0.480	0.99	0.047	0.855	-0.001	0.003	0.658	0.98	1
rs34681760	5	6712834	C	T	0.007	0.013	0.587	1.01	0.029	0.634	0.98	0.051	0.698	-0.001	0.003	0.684	0.98	1
rs11567694	5	35857704	G	A	0.010	0.014	0.471	1.00	0.031	0.937	1.06	0.056	0.276	-0.001	0.004	0.862	0.99	1
rs11740512	5	40424048	C	A	-0.014	0.016	0.374	1.00	0.036	0.920	0.94	0.067	0.393	-0.005	0.004	0.216	0.99	1
rs9292776	5	40437845	A	G	-0.006	0.012	0.585	1.04	0.027	0.192	0.96	0.048	0.359	0.003	0.003	0.354	0.98	0
rs71624119	5	55440730	A	G	0.017	0.014	0.214	1.06	0.031	0.045	1.09	0.056	0.120	0.004	0.004	0.244	1.00	1
rs32658	5	1.19E+08	T	G	-0.011	0.012	0.364	1.00	0.027	0.895	0.96	0.047	0.328	-0.002	0.003	0.597	0.96	1
rs756699	5	1.33E+08	T	C	0.000	0.017	0.994	0.96	0.039	0.246	0.99	0.070	0.882	0.003	0.004	0.442	0.94	1
rs2084007	5	1.34E+08	T	C	-0.012	0.012	0.283	0.97	0.027	0.228	0.97	0.047	0.478	-0.004	0.003	0.223	1.00	0
rs249677	5	1.42E+08	A	C	-0.008	0.012	0.508	0.98	0.028	0.490	0.99	0.051	0.784	-0.002	0.003	0.543	0.95	1
rs2546890	5	1.59E+08	G	A	-0.014	0.012	0.227	1.00	0.027	0.907	1.03	0.048	0.493	0.002	0.003	0.576	1.00	1
rs35716097	5	1.77E+08	T	C	-0.007	0.013	0.584	1.01	0.029	0.861	0.97	0.052	0.526	0.002	0.003	0.455	0.97	1
rs13193887	6	7128198	T	G	0.014	0.012	0.239	1.02	0.028	0.416	1.04	0.049	0.403	-0.002	0.003	0.491	0.96	1
rs17119	6	14719496	A	G	0.010	0.015	0.516	0.95	0.034	0.118	1.03	0.062	0.672	-0.009	0.004	0.026	1.00	1
rs719316	6	16672760	T	C	0.003	0.012	0.813	1.02	0.026	0.440	1.06	0.047	0.183	0.005	0.003	0.098	0.99	1
rs3819292	6	31322522	A	C	0.008	0.014	0.582	1.04	0.032	0.240	0.93	0.059	0.207	0.002	0.004	0.590	0.99	1
rs9266629	6	31346822	C	T	-0.016	0.015	0.290	0.96	0.035	0.235	0.95	0.062	0.404	0.001	0.004	0.840	1.00	1
rs3093982	6	31497244	G	A	-0.020	0.014	0.135	1.00	0.032	0.907	0.90	0.056	0.071	0.001	0.004	0.760	1.00	0
rs2523500	6	31518354	A	G	0.002	0.012	0.866	1.06	0.027	0.030	0.97	0.048	0.495	0.006	0.003	0.053	1.00	0
rs2844482	6	31539767	T	C	0.008	0.015	0.596	1.05	0.033	0.113	1.09	0.060	0.144	0.010	0.004	0.008	1.00	1
rs2229092	6	31540757	C	A	-0.017	0.022	0.447	0.99	0.049	0.899	1.08	0.085	0.368	0.007	0.006	0.194	1.00	0
rs3135388	6	32413051	G	A	-0.035	0.013	0.008	0.95	0.031	0.114	0.84	0.054	0.001	1.9E-03	0.003	0.586	1.00	1
rs9271366	6	32586854	A	G	-0.038	0.013	0.004	0.96	0.037	0.281	0.86	0.066	0.018	0.002	0.004	0.617	0.99	0
rs7454108	6	32681483	C	T	-0.019	0.020	0.338	1.06	0.043	0.152	0.99	0.080	0.941	0.001	0.005	0.832	1.00	0
rs3135024	6	33047466	C	T	0.010	0.013	0.452	0.99	0.031	0.721	0.97	0.055	0.600	-0.003	0.003	0.411	0.99	0
rs11751659	6	33081632	G	A	0.013	0.017	0.439	1.10	0.039	0.015	1.02	0.068	0.777	0.003	0.005	0.517	1.00	0
rs9277626	6	33081823	G	A	0.032	0.013	0.011	1.00	0.030	0.932	0.96	0.054	0.476	0.001	0.003	0.834	1.00	0
rs879036	6	36349890	C	T	-0.012	0.018	0.504	0.98	0.040	0.643	0.92	0.071	0.269	-0.002	0.005	0.635	0.76	1
rs72928038	6	90976768	A	G	0.005	0.015	0.770	1.03	0.043	0.488	0.95	0.076	0.464	1.9E-03	0.005	0.698	0.93	1
rs11542663	6	1.19E+08	C	A	-0.010	0.013	0.428	1.08	0.029	1.0E-02	0.99	0.053	0.924	0.002	0.003	0.467	0.96	1
rs802725	6	1.28E+08	G	T	-0.019	0.013	0.146	1.01	0.030	0.682	0.97	0.053	0.590	-0.001	0.003	0.816	0.99	1
rs9321490	6	1.35E+08	C	T	0.001	0.014	0.921	1.01	0.031	0.777	0.95	0.055	0.383	-0.006	0.004	0.116	0.95	1
rs12206850	6	1.36E+08	C	T	0.006	0.012	0.588	1.00	0.027	0.937	1.02	0.049	0.753	8.4E-03	0.003	0.007	0.98	1
rs17066096	6	1.37E+08	G	A	0.006	0.013	0.641	1.08	0.030	0.009	1.06	0.054	0.259	0.008	0.003	0.016	1.00	1
rs35858108	6	1.38E+08	T	C	0.007	0.012	0.585	1.07	0.028	0.025	1.02	0.051	0.679	0.005	0.003	0.139	0.99	1
rs17780429	6	1.38E+08	A	G	0.003	0.017	0.855	0.98	0.040	0.656	0.98	0.073	0.824	-0.006	0.004	0.219	0.98	0
rs12206238	6	1.44E+08	T	C	-0.014	0.022	0.517	0.93	0.052	0.187	0.99	0.093	0.872	0.000	0.006	0.996	0.96	1

rs212397	6	1.59E+08	A	C	0.019	0.013	0.132	1.02	0.029	0.524	1.01	0.052	0.814	-0.001	0.003	0.858	0.96	1
rs6952809	7	2448493	C	T	0.006	0.012	0.623	1.03	0.028	0.246	1.07	0.051	0.165	0.004	0.003	0.179	1.00	1
rs10951042	7	3139417	C	T	0.000	0.012	0.978	1.02	0.027	0.558	0.96	0.048	0.357	-0.002	0.003	0.517	0.98	1
rs706015	7	27014988	G	T	-0.006	0.015	0.697	0.92	0.035	0.020	0.91	0.062	0.133	-0.003	0.004	0.486	0.98	1
rs10245867	7	28142186	T	G	0.006	0.012	0.595	1.01	0.027	0.787	1.01	0.049	0.869	-0.001	0.003	0.753	0.99	1
rs60600003	7	37382465	G	T	-0.010	0.018	0.582	1.04	0.042	0.346	1.11	0.073	0.161	-0.002	0.005	0.619	0.97	1
rs921911	7	50241812	G	A	-0.018	0.015	0.251	0.94	0.037	0.072	0.95	0.065	0.408	-0.005	0.004	0.256	1.00	1
rs28625973	7	50334208	G	A	0.008	0.013	0.535	0.98	0.030	0.593	1.09	0.054	0.128	0.001	0.003	0.868	0.99	1
rs3801275	7	1.06E+08	C	T	0.010	0.021	0.644	1.01	0.048	0.859	1.07	0.085	0.410	-0.001	0.005	0.870	0.94	1
rs4728142	7	1.29E+08	A	G	-0.001	0.011	0.936	1.01	0.027	0.765	1.00	0.047	0.968	0.003	0.003	0.354	1.00	1
rs10271373	7	1.39E+08	C	A	-0.027	0.012	0.022	1.00	0.026	0.887	1.01	0.047	0.835	0.002	0.003	0.562	0.97	1
rs735120	7	1.49E+08	T	C	0.010	0.014	0.467	1.00	0.031	0.893	0.95	0.057	0.406	0.001	0.004	0.704	0.96	1
rs6999228	8	79557844	G	A	0.001	0.012	0.926	1.00	0.029	0.954	1.07	0.053	0.230	0.001	0.003	0.704	1.00	1
rs78456818	8	95826590	C	T	-0.013	0.023	0.583	0.95	0.054	0.366	1.06	0.091	0.492	-0.004	0.006	0.470	1.00	1
rs2445610	8	1.28E+08	G	A	0.007	0.012	0.543	1.05	0.027	0.096	0.98	0.050	0.653	-0.001	0.003	0.801	0.98	1
rs4410871	8	1.29E+08	C	T	-0.012	0.013	0.337	0.96	0.030	0.160	0.96	0.052	0.462	-0.007	0.003	0.034	1.00	1
rs16902700	8	1.29E+08	A	G	-0.003	0.014	0.808	1.00	0.032	0.928	1.10	0.055	0.073	2.1E-03	0.004	0.555	0.98	1
rs7014582	8	1.45E+08	G	A	-0.010	0.012	0.385	1.00	0.027	0.924	1.02	0.048	0.659	0.003	0.003	0.302	1.00	1
rs4743150	9	1.01E+08	T	C	0.014	0.014	0.323	0.99	0.034	0.777	1.02	0.058	0.720	-0.005	0.004	0.210	1.00	1
rs2104286	10	6099045	C	T	0.005	0.014	0.714	1.01	0.032	0.702	1.09	0.055	0.100	0.002	0.004	0.661	0.99	1
rs62626325	10	6121285	A	G	0.025	0.016	0.115	1.03	0.037	0.362	1.07	0.063	0.270	0.004	0.004	0.388	0.99	0
rs1399180	10	8098719	C	T	0.011	0.016	0.489	0.97	0.037	0.422	0.94	0.065	0.328	-0.004	0.004	0.372	0.87	1
rs793108	10	31415106	T	C	-0.003	0.011	0.809	0.99	0.026	0.681	0.98	0.047	0.733	-0.001	0.003	0.808	1.00	1
rs224032	10	64521829	A	G	0.002	0.011	0.840	1.02	0.027	0.400	1.06	0.047	0.241	0.001	0.003	0.630	0.98	1
rs17741873	10	75653800	T	G	0.008	0.015	0.592	1.00	0.034	0.996	1.09	0.059	0.149	5.5E-03	0.004	0.151	1.00	1
rs1250568	10	81045280	C	T	0.010	0.012	0.387	1.01	0.027	0.680	0.94	0.049	0.209	1.5E-03	0.003	0.614	0.98	1
rs7923837	10	94481917	A	G	-0.001	0.012	0.918	1.03	0.027	0.225	0.97	0.049	0.475	-0.003	0.003	0.364	1.00	1
rs1059091	11	309127	G	A	-0.004	0.012	0.753	0.98	0.034	0.578	0.97	0.060	0.616	-0.001	0.004	0.721	1.00	1
rs11023242	11	14529099	T	C	0.026	0.017	0.130	1.01	0.039	0.875	1.03	0.071	0.650	0.002	0.004	0.707	0.98	1
rs116970203	11	14876718	A	G	0.001	0.035	0.978	1.01	0.080	0.939	1.08	0.142	0.594	-0.013	0.009	0.158	0.95	1
rs3931757	11	36437982	T	C	-0.015	0.018	0.400	0.95	0.039	0.204	0.89	0.070	0.082	-0.003	0.004	0.469	0.91	1
rs2957873	11	47249294	A	G	0.008	0.014	0.571	0.97	0.033	0.398	0.93	0.059	0.206	-1.0E-04	0.004	0.978	0.98	1
rs506616	11	60835043	T	G	-0.011	0.013	0.402	0.98	0.030	0.538	1.07	0.052	0.170	0.000	0.003	0.910	0.96	1
rs694739	11	64097233	G	A	0.010	0.012	0.392	0.98	0.028	0.403	0.97	0.050	0.574	0.001	0.003	0.654	1.00	1
rs531612	11	65705432	T	C	0.014	0.012	0.219	0.98	0.026	0.454	1.01	0.048	0.830	0.001	0.003	0.738	0.99	1
rs4409785	11	95311422	C	T	0.019	0.014	0.179	1.02	0.034	0.589	1.20	0.058	0.002	0.003	0.004	0.406	1.00	1
rs72981578	11	95420123	T	C	0.022	0.018	0.227	0.95	0.041	0.190	1.02	0.072	0.735	0.005	0.005	0.269	0.83	1
rs585039	11	1.19E+08	A	C	-0.005	0.013	0.688	1.01	0.029	0.606	1.00	0.052	0.925	-0.001	0.003	0.876	0.97	0
rs12365699	11	1.19E+08	A	G	0.000	0.016	0.993	0.97	0.037	0.419	0.97	0.067	0.603	-0.005	0.004	0.280	0.96	1
rs6589706	11	1.19E+08	G	A	0.006	0.012	0.585	1.07	0.027	0.016	1.11	0.048	0.030	0.004	0.003	0.170	0.94	1
rs77841686	11	1.19E+08	A	G	0.037	0.039	0.347	1.14	0.088	0.145	1.26	0.150	0.130	0.016	0.011	0.124	0.92	0
rs11605422	11	1.23E+08	T	C	-0.024	0.012	0.048	0.95	0.028	0.091	0.92	0.050	0.089	-0.006	0.003	0.054	0.98	1
rs3809006	11	1.28E+08	T	C	-0.005	0.012	0.642	1.02	0.027	0.462	1.00	0.047	0.992	0.000	0.003	0.897	0.98	1
rs1800693	12	6440009	C	T	-0.006	0.012	0.600	1.02	0.027	0.423	1.09	0.047	0.073	0.003	0.003	0.307	1.00	1
rs767455	12	6450945	C	T	-0.003	0.012	0.805	1.03	0.026	0.302	1.07	0.047	0.146	0.003	0.003	0.312	1.00	0
rs2364482	12	6502131	G	T	0.013	0.015	0.366	1.07	0.033	0.048	0.98	0.059	0.759	0.000	0.004	0.948	0.90	1
rs3764021	12	9833628	T	C	0.013	0.011	0.254	1.02	0.026	0.353	1.03	0.047	0.569	0.009	0.003	0.003	1.00	0
rs10877012	12	58162085	T	G	0.003	0.013	0.821	1.00	0.029	0.885	0.98	0.053	0.746	-3.3E-03	0.003	0.325	1.00	1
rs61708525	12	94661453	G	A	-0.024	0.013	0.065	0.97	0.030	0.269	0.90	0.055	0.064	-0.007	0.003	0.031	0.96	1
rs3184504	12	1.12E+08	C	T	-0.004	0.011	0.735	0.99	0.026	0.670	0.91	0.047	0.040	-0.004	0.003	0.234	1.00	1
rs883263	12	1.23E+08	G	A	0.009	0.013	0.505	0.99	0.031	0.696	1.05	0.055	0.408	-0.005	0.004	0.121	0.97	1
rs9591325	13	50811220	C	T	-0.025	0.024	0.300	0.99	0.056	0.928	1.00	0.098	0.993	0.003	0.006	0.678	1.00	1
rs9562970	13	51002615	A	G	0.005	0.018	0.799	0.99	0.042	0.873	0.99	0.072	0.902	0.002	0.005	0.652	1.00	1

rs4772201	13	1E+08	G	A	-0.013	0.016	0.425	0.95	0.037	0.147	0.96	0.067	0.498	-0.005	0.004	0.205	0.99	1
rs4468527	14	52325131	G	A	-0.033	0.018	0.058	1.05	0.041	0.200	0.99	0.071	0.838	-0.006	0.005	0.217	0.92	1
rs8022092	14	69265564	A	C	-0.012	0.012	0.297	0.96	0.027	0.138	0.94	0.048	0.191	2.0E-03	0.003	0.513	0.96	1
rs175706	14	75976200	A	G	-0.008	0.012	0.483	0.98	0.027	0.576	0.99	0.048	0.775	-0.006	0.003	0.066	0.93	1
rs117822168	14	88504511	A	G	0.003	0.031	0.934	0.97	0.074	0.650	0.92	0.137	0.528	1.9E-03	0.008	0.821	0.98	1
rs10141746	14	1.03E+08	G	A	-0.021	0.013	0.097	0.99	0.028	0.728	0.91	0.051	0.057	-4.1E-04	0.003	0.901	0.96	1
rs8006649	14	1.03E+08	G	A	-0.014	0.012	0.242	0.97	0.028	0.291	0.97	0.048	0.542	-2.5E-03	0.003	0.421	0.95	1
rs10152892	15	79231203	C	A	0.018	0.015	0.222	1.00	0.034	0.908	1.01	0.060	0.868	0.004	0.004	0.291	0.98	1
rs7183707	15	90883733	T	G	0.013	0.012	0.290	1.01	0.029	0.726	1.04	0.053	0.430	0.000	0.003	0.950	1.00	1
rs108990	16	1065433	C	T	0.000	0.015	0.996	1.00	0.034	0.971	1.12	0.059	0.046	0.005	0.004	0.217	0.96	1
rs1985372	16	11114839	T	C	0.012	0.012	0.312	1.05	0.027	0.107	1.05	0.049	0.327	0.006	0.003	0.053	0.98	0
rs12708716	16	11179873	G	A	0.004	0.012	0.768	1.04	0.028	0.194	1.03	0.051	0.557	0.005	0.003	0.117	1.00	1
rs12928822	16	11403893	T	C	-0.024	0.016	0.148	0.97	0.038	0.354	0.99	0.067	0.892	0.004	0.004	0.393	1.00	0
rs36090551	16	11443873	T	G	0.013	0.013	0.291	1.03	0.029	0.324	1.00	0.052	0.936	-0.003	0.003	0.340	0.98	1
rs4609871	16	29932064	T	C	-1.8E-02	0.012	0.139	1.01	0.027	0.627	0.98	0.049	0.663	0.000	0.003	0.972	0.92	1
rs9937051	16	57106671	T	C	2.2E-02	0.015	0.146	0.96	0.034	0.232	1.02	0.061	0.718	7.7E-03	0.004	0.047	0.96	1
rs12925972	16	79111297	C	T	-0.007	0.012	0.555	0.95	0.028	0.047	0.94	0.049	0.175	-0.006	0.003	0.039	0.93	1
rs17797448	16	79348278	T	C	1.7E-03	0.022	0.940	0.93	0.052	0.176	0.95	0.091	0.558	-3.5E-03	0.006	0.556	0.98	1
rs7196953	16	79649394	G	A	0.004	0.014	0.786	1.01	0.030	0.812	1.03	0.054	0.561	0.000	0.003	0.922	0.83	1
rs35703946	16	86021505	A	G	0.021	0.018	0.246	0.97	0.043	0.417	0.94	0.077	0.422	0.002	0.005	0.650	0.93	1
rs2306593	17	34866546	T	C	0.003	0.012	0.822	0.97	0.027	0.192	1.02	0.047	0.632	-0.001	0.003	0.865	0.96	1
rs9909593	17	37970149	G	A	0.022	0.012	0.053	0.99	0.026	0.676	1.07	0.047	0.170	-0.003	0.003	0.312	0.98	1
rs883871	17	38252660	A	G	0.011	0.017	0.513	0.99	0.038	0.759	1.01	0.067	0.917	0.004	0.004	0.399	0.99	1
rs17886724	17	40496163	G	A	0.015	0.012	0.219	1.04	0.027	0.146	0.99	0.050	0.776	0.003	0.003	0.405	0.97	1
rs7216796	17	43392208	A	G	-0.013	0.012	0.251	0.95	0.027	0.052	0.99	0.048	0.786	0.000	0.003	0.976	0.97	1
rs11079784	17	45702280	C	T	0.004	0.012	0.737	1.00	0.027	0.993	0.92	0.048	0.080	0.001	0.003	0.728	0.96	1
rs8070345	17	57816757	C	T	-0.004	0.012	0.735	1.02	0.027	0.447	0.96	0.048	0.431	0.002	0.003	0.620	0.94	1
rs9913257	17	73320893	T	C	-0.002	0.013	0.895	0.99	0.031	0.808	0.98	0.055	0.765	-0.002	0.003	0.480	0.92	1
rs9947399	18	56271544	A	G	-0.007	0.012	0.575	1.01	0.027	0.707	1.01	0.048	0.904	-0.001	0.003	0.664	1.00	1
rs4545915	18	56422868	G	A	0.006	0.014	0.665	1.01	0.032	0.674	0.99	0.057	0.799	0.000	0.004	0.924	0.96	1
rs1610555	18	67543147	T	G	-0.005	0.012	0.669	1.04	0.027	0.181	1.04	0.049	0.377	0.002	0.003	0.607	0.97	1
rs2992	19	4443046	C	T	-0.002	0.013	0.851	0.97	0.030	0.350	0.98	0.054	0.644	-0.006	0.003	0.093	0.93	1
rs1077667	19	6668972	T	C	-0.002	0.015	0.914	1.06	0.035	0.109	0.92	0.063	0.194	-0.001	0.004	0.899	0.99	1
rs1051738	19	10577843	A	C	0.005	0.016	0.774	1.00	0.036	0.946	0.91	0.064	0.156	0.000	0.004	0.990	0.97	1
rs12460421	19	10981352	G	A	-0.001	0.012	0.925	1.01	0.027	0.697	1.05	0.049	0.315	0.002	0.003	0.445	0.95	0
rs1870071	19	16505106	C	T	-0.007	0.013	0.598	0.97	0.029	0.289	1.10	0.051	0.052	-0.001	0.003	0.718	0.96	1
rs11554159	19	18285944	A	G	-0.017	0.013	0.209	0.95	0.031	0.134	1.07	0.054	0.212	-0.003	0.004	0.386	1.00	1
rs7260482	19	45143942	C	A	0.001	0.013	0.958	1.00	0.030	0.910	0.99	0.054	0.832	0.000	0.003	0.993	0.95	1
rs307896	19	47661493	A	G	0.002	0.015	0.905	0.98	0.032	0.566	0.99	0.057	0.797	-0.004	0.004	0.298	0.82	1
rs8107548	19	49870643	C	T	0.039	0.013	0.002	1.04	0.029	0.179	1.02	0.053	0.706	0.004	0.003	0.211	0.98	1
rs6072343	20	39968188	A	G	0.012	0.017	0.479	0.99	0.037	0.843	1.05	0.065	0.429	0.003	0.004	0.483	0.94	1
rs4812773	20	42579148	C	T	-0.002	0.013	0.870	0.96	0.030	0.180	0.97	0.054	0.524	-0.001	0.003	0.786	0.95	1
rs6032662	20	44734310	T	C	0.002	0.013	0.863	1.03	0.030	0.397	1.09	0.053	0.122	-0.003	0.003	0.386	0.98	1
rs2616277	20	52745040	T	C	-0.008	0.016	0.600	0.98	0.036	0.666	0.91	0.065	0.171	-0.001	0.004	0.750	0.93	0
rs2248359	20	52791518	T	C	-0.025	0.012	0.036	0.95	0.028	0.042	0.93	0.050	0.160	0.002	0.003	0.485	1.00	1
rs1151625	20	62369997	T	C	-0.020	0.023	0.378	0.92	0.054	0.112	0.96	0.097	0.687	0.002	0.006	0.772	0.98	1
rs9808753	21	34787312	G	A	0.028	0.017	0.100	1.03	0.038	0.374	1.16	0.066	0.022	-0.002	0.004	0.703	0.98	1
rs1041796	21	39852472	C	T	0.029	0.017	0.096	1.05	0.039	0.230	1.06	0.070	0.437	0.000	0.004	0.976	0.96	1
rs2283792	22	22131125	G	T	0.006	0.011	0.588	0.99	0.026	0.604	0.98	0.048	0.749	0.005	0.003	0.069	1.00	1
rs2027982	22	31593435	C	T	-0.003	0.012	0.800	1.03	0.027	0.354	1.01	0.049	0.765	0.001	0.003	0.754	0.97	1
rs4821544	22	37258503	C	T	-0.019	0.014	0.181	0.99	0.031	0.666	0.98	0.056	0.669	0.006	0.004	0.115	0.84	1
rs2413436	22	37312561	G	A	-0.004	0.012	0.732	0.98	0.027	0.504	1.01	0.049	0.875	-0.001	0.003	0.682	0.96	0
rs137956	22	40293463	T	C	-0.022	0.012	0.060	0.98	0.027	0.445	0.99	0.049	0.848	0.001	0.003	0.797	0.92	1

rs361725	22	50971047	C	T	0.006	0.012	0.589	1.02	0.028	0.421	1.05	0.049	0.342	-0.004	0.003	0.226	0.97	1
----------	----	----------	---	---	-------	-------	-------	------	-------	-------	------	-------	-------	--------	-------	-------	------	---

Associations with ARMSS score (rank-based inverse normal transformed) were assessed as part of the GWAS, with $P < 5E-8$ considered significant and $P < 5E-6$ considered suggestive. For all other outcomes, a candidate variant approach was employed and the significance threshold was corrected for the number of variants tested ($P < 0.05/209$ or $2.4E-4$)

MHC variants were defined as those on chromosome 6 between positions 24Mbps to 35Mbps (GRCh37). R^2 represents the Minimac4 imputation quality score.

Variants retained in the construction of the susceptibility PRS following LD clumping ($r^2 < 0.01$) are marked in the last column (1 = yes, 0 = no)

CHR, chromosome; bp; base pair (GRCh37); EA, effect allele; REF, reference allele; s.e., standard error; HR, hazard ratio; PRS, polygenic risk score