Supplementary Table 9. MS severity genome-wide significant and suggestive variants in the discovery population

						Discovery						Replication						Meta-analysis				
Chr	SNV	position (bp)	EA	REF	gene(s)	n	EAF	beta	s.e.	P	R^2	n	EAF	beta	s.e.	P	R^2	EAF	beta	s.e.	P	effects
2	rs10191329	71676999	A	C	DYSF-ZNF638	12584	0.17	0.089	0.015	9.69E-09	0.97	9805	0.16	0.044	0.019	0.021	0.97	0.17	0.071	0.012	3.62E-09	++
1	rs149097173	172370873	T	C	DNM3-PIGC	12584	0.01	0.256	0.056	4.07E-06	0.94	9805	0.01	0.168	0.066	0.010	0.99	0.01	0.219	0.042	2.33E-07	++
13	rs2876767	82044107	C	T	-	12584	0.05	-0.137	0.026	8.76E-08	0.97	9805	0.05	-0.022	0.031	0.481	0.98	0.05	-0.091	0.020	4.67E-06	--
1	rs181310516	200217158	T	G	-	12584	0.01	-0.351	0.067	1.55E-07	0.77	9805	0.01	-0.050	0.077	0.517	0.81	0.01	-0.222	0.051	1.16E-05	--
3	rs147933117	24926166	A	C	RARB	12584	0.01	0.226	0.049	3.40E-06	0.94	9805	0.01	0.059	0.059	0.323	0.95	0.01	0.159	0.038	2.51E-05	++
14	rs194722	69320947	T	G	-	12584	0.20	-0.071	0.015	1.39E-06	0.93	9805	0.21	-0.011	0.017	0.525	0.95	0.20	-0.046	0.011	4.47E-05	--
3	rs12494504	2831218	A	G	CNTN4	12584	0.03	0.206	0.043	1.37E-06	0.74	9805	0.03	0.008	0.049	0.875	0.76	0.03	0.121	0.032	1.78E-04	++
7	rs112663015	37640233	A	G	-	12584	0.02	-0.223	0.049	4.24E-06	0.83	9805	0.02	-0.009	0.054	0.864	0.87	0.02	-0.128	0.036	3.92E-04	--
6	rs9397000	170164053	T	C	ERMARD	12584	0.04	-0.131	0.028	2.10E-06	0.99	9805	0.05	0.010	0.031	0.745	1.00	0.05	-0.069	0.021	8.48E-04	-+
6	rs61215450	148550897	A	G	-	12584	0.10	0.090	0.019	2.45E-06	0.97	9805	0.09	-0.015	0.024	0.533	0.99	0.10	0.049	0.015	1.01E-03	+-
14	rs4251626	54875607	G	A	CDKN3	12584	0.23	-0.065	0.014	3.52E-06	0.96	9805	0.23	0.008	0.017	0.619	0.96	0.23	-0.035	0.011	1.20E-03	-+
5	rs115687581	169785565	A	G	KCNIP1	12584	0.03	-0.159	0.034	2.94E-06	1.00	9805	0.03	0.023	0.040	0.565	0.98	0.03	-0.083	0.026	1.42E-03	-+

For non-replicated variants, we list the reported gene by the Ensembl Variant Effect Predictor (PMID 27268795). R^2 represents the Minimac4 imputation quality score.
Chr, chromosome; bp, base pair (GRCh37); EA, effect allele; REF, reference allele; EAF, effect allele frequency; s.e., standard error.