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Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis

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Using the ImmunoChip custom genotyping array, we analyzed 14,498 subjects with multiple sclerosis and 24,091 healthy controls for 161,311 autosomal variants and identified 135 potentially associated regions ($P < 1.0 \times 10^{-4}$). In a replication phase, we combined these data with previous genome-wide association study (GWAS) data from an independent 14,802 subjects with multiple sclerosis and 26,703 healthy controls. In these 80,094 individuals of European ancestry, we identified 48 new susceptibility variants ($P < 5.0 \times 10^{-8}$), 3 of which we found after conditioning on previously identified variants. Thus, there are now 110 established multiple sclerosis risk variants at 103 discrete loci outside of the major histocompatibility complex. With high-resolution Bayesian fine mapping, we identified five regions where one variant accounted for more than 50% of the posterior probability of association. This study enhances the catalog of multiple sclerosis risk variants and illustrates the value of fine mapping in the resolution of GWAS signals.

Multiple sclerosis (MIM 126200) is an inflammatory demyelinating disorder of the central nervous system that is a common cause of chronic neurological disability[1,2]. It shows greatest prevalence among individuals of northern European ancestry[3] and is moderately heritable[4], with a sibling relative recurrence risk (λ_s) of ~6.3 (ref. 5). Aside from early success in demonstrating the important effects exerted by variants in the human leukocyte antigen (HLA) genes from the major histocompatibility complex (MHC)[6], there was little progress in unraveling the genetic architecture underlying susceptibility to multiple sclerosis before the advent of GWAS technology. Over the last decade, our consortium has performed several GWAS and meta-analyses in large cohorts[7–10], cumulatively identifying more than 50 non-MHC susceptibility alleles. As in other complex diseases, available data suggest that many additional susceptibility alleles remain to be identified[11].

The striking overlap in the genetic architectures underlying susceptibility to multiple autoimmune diseases[9,10,12,13] prompted the collaborative construction of the ImmunoChip (see **Supplementary Figs. 1** and **2** and the **Supplementary Note** for details on IMSGC-nominated content), an efficient genotyping platform designed to deeply interrogate 184 non-MHC loci with genome-wide significant associations to at least 1 autoimmune disease and to provide lighter coverage of other genomic regions with suggestive evidence of association[14]. Here we report a large-scale effort that leverages the ImmunoChip to detect association with multiple sclerosis susceptibility and to refine these associations via Bayesian fine mapping.

After performing stringent quality control, we report genotypes for 28,487 individuals of European ancestry (14,498 subjects with multiple sclerosis and 13,989 healthy controls) that are independent of the genotypes examined in previous GWAS efforts. We supplemented these data with genotypes from 10,102 independent control subjects provided by the International Inflammatory Bowel Disease Genetics Consortium (IIBDGC)[15], bringing the total number of subjects to 38,589 (14,498 subjects with multiple sclerosis and 24,091 healthy controls). We performed variant-level quality control, population outlier identification and subsequent case-control analysis in 11 country-organized strata. To account for within-stratum population stratification, we used the first five principal components as covariates in the association analysis. Per-stratum odds ratio (OR) and respective standard error (s.e.) estimates were then combined with an inverse variance meta-analysis under a fixed-effects model. In total, we tested 161,311 autosomal variants that passed quality control in at least 2 of the 11 strata (Online Methods). A Circos plot[16] summarizing the results from this discovery phase analysis is shown in **Figure 1**.

We defined an *a priori* significance threshold of $P < 1 \times 10^{-4}$ for the discovery phase and identified 135 statistically independent primary association signals, comprising 67 in the designated fine-mapping regions and 68 in less densely covered regions selected for deep replication of earlier GWAS signals. Using forward stepwise logistic regression, we identified a second statistically independent signal in 13 of these regions (secondary signals) and a third statistically independent signal in 2 regions (tertiary signals). A total of 48 of the 150 statistically independent association signals (**Supplementary Table 1**) reached genome-wide significance of $P < 5 \times 10^{-8}$ in the discovery phase alone. Next, we replicated our findings in 14,802 subjects with multiple sclerosis and 26,703 healthy controls with available GWAS data imputed using the 1000 Genomes Project European phase I (a) panel (Online Methods). Finally, we performed a joint analysis of the discovery and replication phases.

We identified 97 statistically independent SNPs meeting replication criteria (replication $P < 0.05$, joint $P < 5 \times 10^{-8}$ and joint $P <$ discovery P), comprising 93 primary signals (**Supplementary Figs. 3–95**) and 4 secondary signals. Of these signals, 48 are new

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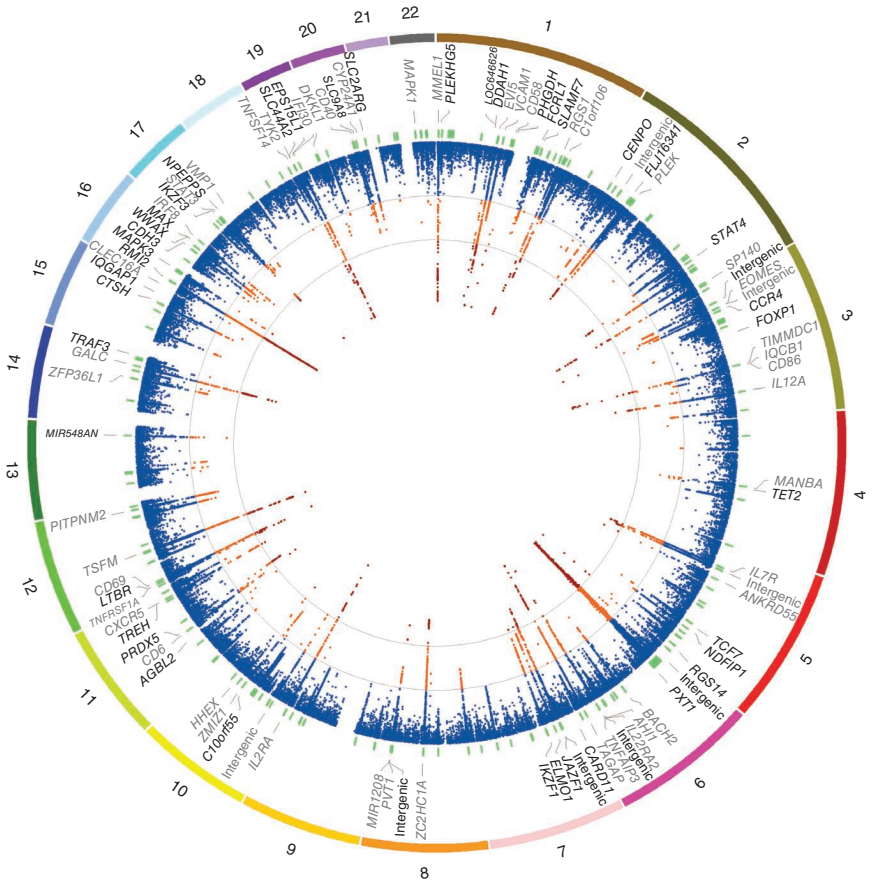

Figure 1 Discovery phase results. Circos plot showing primary association analysis of 161,311 autosomal variants in the discovery phase (14,498 cases and 24,091 healthy controls). The outermost track shows the numbered autosomal chromosomes. The second track indicates the gene closest to the most associated SNP meeting all replication criteria. Previously identified associations are indicated in gray. The third track indicates the physical position of the 184 fine-mapping intervals (green). The innermost track indicates $-\log(P)$ (two-sided) for each SNP (scaled from 0–12, which truncates the signal in several regions; **Supplementary Table 1**). Additionally, contour lines are given at the *a priori* discovery ($-\log(P) = 4$) and genome-wide significance ($-\log(P) = 7.3$) thresholds. Orange indicates $-\log(P) \geq 4$ and <7.3, and red indicates $-\log(P) \geq 7.3$. Details of the full discovery phase results can be found in ImmunoBase (see URLs).

to multiple sclerosis (**Table 1**), and 49 correspond to previously identified susceptibility loci for multiple sclerosis (**Table 2**). An additional 11 independent SNPs showed suggestive evidence of association (joint $P < 1 \times 10^{-6}$) (**Supplementary Table 2**).

The strongest newly associated SNP, rs12087340 (joint $P = 1.1 \times 10^{-20}$; OR = 1.21), lies between *BCL10* (encoding B cell CLL/lymphoma 10) and *DDAH1* (encoding dimethylarginine dimethylaminohylaminohydrolase 1). The protein encoded by *BCL10* contains a caspase recruitment domain (CARD) and has been shown to activate nuclear factor (NF)-κB signaling[17]. This signaling molecule has an important role in controlling gene expression in inflammation, immunity, cell proliferation and apoptosis. It has been pursued as a potential therapeutic target for multiple sclerosis[18]. BCL10 is also reported to interact with other CARD domain–containing proteins, including CARD11 (ref. 19). We additionally identified a new association for rs1843938 (joint $P = 1.2 \times 10^{-10}$; OR = 1.08), which is only 30 kb away from *CARD11*.

One newly associated SNP, rs2288904 (joint $P = 1.6 \times 10^{-11}$; OR = 1.10), was found within an exon, representing a missense variant in *SLC44A2* (encoding solute carrier family 44, member 2). Notably, this variant is also reported as a monocyte-specifc *cis*-acting expression quantitative trait locus (eQTL) for the antisense transcript of the nearby *ILF3* gene (encoding interleukin enhancer–binding factor 3)[20]. The ILF3 protein was first discovered as a subunit of a nuclear factor found in activated T cells, which is required for T cell expression of *IL2*, an important molecule that regulates many aspects of inflammation.

Of the 49 previously identified risk loci[9,10,21], 37 are in designated fine-mapping regions, and 23 of these 37 signals were localized to a single gene on the basis of genomic position (**Supplementary Table 3**). Although proximity does not necessarily indicate that these genes are functionally relevant, this observation nevertheless emphasizes the usefulness of dense mapping in localizing signals from a genome-wide screen. Our ImmunoChip analysis furthers the understanding of previously proposed secondary signals at three loci (**Supplementary Tables 4–6** and **Supplementary Note**); in particular, we showed that the effects of two previously proposed independent associations at the *IL2RA* locus[7,22] are driven by a single variant, rs2104286.

In an effort to define the functionally relevant variants underlying these associations, we further studied the regions surrounding the 97 associated SNPs using both Bayesian and frequentist approaches in 6,356 subjects with multiple sclerosis and 9,617 healthy controls from the UK (Online Methods)[23]. As determined by examining imputation quality, fine mapping was possible in 68 regions (**Supplementary Table 7**), including 66 of 93 primary (**Fig. 2a**) and 2 of 4 secondary signals. Eight of the 68 regions were fine mapped to high resolution (**Fig. 2b**, **Table 3** and **Supplementary Fig. 96**). One-third of the variants identified in these eight regions were imputed, indicating the value of imputation, even with dense genotyping coverage.

To assess whether functional annotation[24] provides clues about the molecular mechanisms associated with genetic risk, we considered the relationship of variants to annotated coding and regulatory features in these eight regions. Although we found no variants with missense or nonsense effects, there was a notable enrichment for variants with functional effects, including one variant known to affect splicing[25], three variants known to correlate with RNA or serum protein levels[22,26,27] and several variants overlapping transcription factor binding sites and DNase I hypersensitive sites[28,29]. Four of the 18 variants in the fine-mapped regions are within conserved regions (GERP > 2)[30]. The overall lack of functional annotation likely reflects the limited repertoire of reference expression and epigenomic profiles and suggests that the function of the variants may be specific to cell type or cell state, as has been reported for many eQTLs in immune cell types[20].

To determine the Gene Ontology (GO) processes of the 97 associated variants, we used MetaCore from Thomson Reuters (Online Methods). We found that the majority of the 97 variants lie within 50 kb of genes having immunological function. Of the 86 unique genes

Table 1 Results for 48 new non-MHC variants associated with multiple sclerosis at a genome-wide significance level

				Discovery			Replication			Joint			
SNP	Chr.	Position[a]	RA	RAF	*P*	OR	RAF	*P*	OR	*P*	OR	Gene[b]	Function
rs3007421	1	6530189	A	0.12	9.6×10^{-7}	1.12	0.13	8.8×10^{-5}	1.10	4.7×10^{-10}	1.11	*PLEKHG5*	Intronic
rs12087340	1	85746993	A	0.09	5.1×10^{-12}	1.22	0.09	2.9×10^{-10}	1.20	1.1×10^{-20}	1.21	***BCL10***	Intergenic
rs11587876	1	85915183	A	0.79	8.4×10^{-8}	1.12	0.81	2.9×10^{-3}	1.06	4.4×10^{-9}	1.09	*DDAH1*	Intronic
rs666930	1	120258970	G	0.53	7.5×10^{-8}	1.09	0.53	1.3×10^{-5}	1.07	6.0×10^{-12}	1.08	*PHGDH*	Intronic
rs2050568	1	157770241	G	0.53	1.3×10^{-6}	1.08	0.54	2.3×10^{-5}	1.07	1.5×10^{-10}	1.08	*FCRL1*	Intronic
rs35967351	1	160711804	A	0.67	1.7×10^{-6}	1.09	0.68	5.9×10^{-6}	1.09	4.4×10^{-11}	1.09	***SLAMF7***	Intronic
rs4665719	2	25017860	G	0.25	6.8×10^{-6}	1.09	0.25	1.1×10^{-4}	1.08	3.1×10^{-9}	1.08	*CENPO*	Intronic
rs842639	2	61095245	A	0.65	1.7×10^{-9}	1.11	0.67	1.4×10^{-6}	1.09	2.0×10^{-14}	1.10	*FLJ16341*	Noncoding RNA
rs9967792	2	191974435	G	0.62	1.8×10^{-9}	1.11	0.64	1.2×10^{-4}	1.07	3.5×10^{-12}	1.09	***STAT4***	Intronic
rs11719975	3	18785585	C	0.27	5.4×10^{-6}	1.09	0.28	4.1×10^{-4}	1.07	1.1×10^{-8}	1.08		Intergenic
rs4679081	3	33013483	G	0.52	1.2×10^{-5}	1.08	0.55	3.7×10^{-4}	1.07	2.2×10^{-9}	1.07	***CCR4***	Intergenic
rs9828629	3	71530346	G	0.62	5.5×10^{-6}	1.08	0.64	8.5×10^{-6}	1.08	1.9×10^{-10}	1.08	***FOXP1***	Intronic
rs2726518	4	106173199	C	0.55	1.2×10^{-5}	1.09	0.58	4.7×10^{-4}	1.06	3.9×10^{-8}	1.07	***TET2***	Intronic
rs756699	5	133446575	A	0.87	3.0×10^{-6}	1.12	0.88	6.5×10^{-6}	1.11	8.8×10^{-11}	1.12	***TCF7***	Intergenic
None[c]	5	141506564	C	0.61	6.0×10^{-5}	1.07	0.62	1.5×10^{-5}	1.08	3.6×10^{-9}	1.07	*NDFIP1*	Intronic
rs4976646	5	176788570	G	0.34	1.0×10^{-12}	1.13	0.36	5.0×10^{-7}	1.10	4.4×10^{-18}	1.12	*RGS14*	Intronic
rs17119	6	14719496	A	0.81	1.9×10^{-6}	1.11	0.80	1.2×10^{-5}	1.10	1.0×10^{-10}	1.10		Intergenic
rs941816	6	36375304	G	0.18	4.5×10^{-9}	1.13	0.20	8.3×10^{-5}	1.08	3.9×10^{-12}	1.11	*PXT1*	Intronic
rs1843938	7	3113034	A	0.44	2.2×10^{-6}	1.08	0.44	1.1×10^{-5}	1.08	1.2×10^{-10}	1.08	***CARD11***	Intergenic
rs706015	7	27014988	C	0.18	1.3×10^{-9}	1.14	0.18	9.9×10^{-3}	1.06	1.1×10^{-9}	1.10		Intergenic
rs917116	7	28172739	C	0.20	2.1×10^{-8}	1.12	0.21	5.8×10^{-3}	1.06	3.3×10^{-9}	1.09	*JAZF1*	Intronic
rs60600003	7	37382465	C	0.10	2.5×10^{-8}	1.16	0.10	4.2×10^{-7}	1.14	6.0×10^{-14}	1.15	*ELMO1*	Intronic
rs201847125[d]	7	50325567	G	0.70	2.9×10^{-8}	1.11	0.70	6.7×10^{-5}	1.09	1.2×10^{-11}	1.10	***IKZF1***	Intergenic
rs2456449	8	128192981	G	0.36	2.2×10^{-8}	1.10	0.37	3.8×10^{-3}	1.05	1.8×10^{-9}	1.08		Intergenic
rs793108	10	31415106	A	0.50	5.6×10^{-8}	1.09	0.51	1.8×10^{-5}	1.07	6.1×10^{-12}	1.08		Intergenic
rs2688608	10	75658349	A	0.55	6.4×10^{-5}	1.07	0.56	2.0×10^{-4}	1.06	4.6×10^{-8}	1.07	*C10orf55*	Intergenic
rs7120737	11	47702395	G	0.15	7.6×10^{-8}	1.13	0.15	1.0×10^{-3}	1.08	1.0×10^{-9}	1.10	*AGBL2*	Intronic
rs694739	11	64097233	A	0.62	1.3×10^{-5}	1.08	0.62	3.8×10^{-5}	1.07	2.0×10^{-9}	1.07	***PRDX5***	Intergenic
rs9736016	11	118724894	T	0.63	2.2×10^{-8}	1.10	0.63	2.6×10^{-8}	1.10	3.0×10^{-15}	1.10	***CXCR5***	Intergenic
rs12296430	12	6503500	C	0.19	3.6×10^{-10}	1.14	0.21	1.7×10^{-5}	1.09	7.2×10^{-14}	1.12	***LTBR***	Intergenic
rs4772201	13	100086259	A	0.82	1.7×10^{-7}	1.12	0.83	1.1×10^{-4}	1.09	1.3×10^{-10}	1.10	*MIR548AN*	Intergenic
rs12148050	14	103263788	A	0.35	1.5×10^{-5}	1.08	0.36	4.3×10^{-9}	1.10	5.1×10^{-13}	1.09	***TRAF3***	Intronic
rs59772922	15	79207466	A	0.83	4.0×10^{-6}	1.11	0.83	5.4×10^{-4}	1.08	1.2×10^{-8}	1.09	***CTSH***	Intergenic
rs8042861	15	90977333	A	0.44	9.8×10^{-7}	1.08	0.45	3.4×10^{-4}	1.06	2.2×10^{-9}	1.07	*IQGAP1*	Intronic
rs6498184	16	11435990	G	0.81	2.1×10^{-10}	1.15	0.82	6.5×10^{-9}	1.14	7.4×10^{-18}	1.15	*RMI2*	Intergenic
rs7204270[e]	16	30156963	G	0.50	9.3×10^{-8}	1.09	0.49	3.7×10^{-5}	1.08	1.6×10^{-11}	1.09	***MAPK3***	Intergenic
rs1886700	16	68685905	A	0.14	8.8×10^{-6}	1.11	0.14	3.2×10^{-4}	1.08	1.3×10^{-8}	1.10	*CDH3*	Intronic
rs12149527	16	79110596	A	0.47	1.7×10^{-6}	1.08	0.47	4.3×10^{-6}	1.08	3.3×10^{-11}	1.08	*WWOX*	Intronic
rs7196953	16	79649394	A	0.29	2.6×10^{-5}	1.08	0.30	7.9×10^{-7}	1.09	1.0×10^{-10}	1.09	*MAF*	Intergenic
rs12946510	17	37912377	A	0.47	8.5×10^{-6}	1.08	0.48	8.0×10^{-5}	1.07	2.9×10^{-9}	1.07	***IKZF3***	Intergenic
rs4794058	17	45597098	A	0.50	1.6×10^{-5}	1.07	0.52	3.5×10^{-10}	1.11	1.0×10^{-13}	1.09	***NPEPPS***	Intergenic
rs2288904	19	10742170	G	0.77	9.6×10^{-10}	1.14	0.78	5.4×10^{-4}	1.07	1.6×10^{-11}	1.10	*SLC44A2*	Exonic
rs1870071	19	16505106	G	0.29	5.7×10^{-10}	1.12	0.30	4.6×10^{-7}	1.09	2.0×10^{-15}	1.10	*EPS15L1*	Intronic
rs17785991	20	48438761	A	0.35	6.4×10^{-7}	1.09	0.34	5.9×10^{-3}	1.05	4.2×10^{-8}	1.07	*SLC9A8*	Intronic
rs2256814	20	62373983	A	0.19	8.3×10^{-7}	1.11	0.21	6.4×10^{-4}	1.08	3.5×10^{-9}	1.09	*SLC2A4RG*	Intronic
Secondary													
rs7769192[f]	6	137962655	G	0.55	1.3×10^{-5}	1.08	0.54	5.1×10^{-5}	1.07	3.3×10^{-9}	1.08		Intergenic
rs533646[g]	11	118566746	G	0.68	3.6×10^{-7}	1.10	0.68	3.9×10^{-5}	1.08	7.6×10^{-11}	1.09	*TREH*	Intergenic
rs4780346[h]	16	11288806	A	0.23	6.8×10^{-6}	1.09	0.25	1.5×10^{-5}	1.09	4.4×10^{-10}	1.09	*CLEC16A*	Intergenic

All listed signals had discovery $P \leq 1.0 \times 10^{-4}$, replication $P \leq 5.0 \times 10^{-2}$ and joint $P \leq 5.0 \times 10^{-8}$. All *P* values are two-sided. Chr., chromosome; RA, risk allele; RAF, risk allele frequency.
[a]Position is based on hg19 and dbSNP Build 137. [b]The nearest gene is listed if it lies within 50 kb of the signal. Bold font indicates genes that are part of the GO immune system process. [c]Proxy SNP rs1036207 ($r^2 = 0.99$) was used in replication. [d]Proxy SNP rs716719 ($r^2 = 1.00$) was used in replication. [e]The primary SNP was rs11865086 ($P = 1.77 \times 10^{-8}$) in the discovery phase, but this SNP (or a good proxy) was not available in replication, so the next best discovery SNP was used. [f]*P* values and OR values shown are after conditioning on rs67297943 (**Table 2**). [g]*P* values and OR values shown are after conditioning on rs9736016 (**Table 2**). [h]*P* values and OR values shown are after conditioning on rs12927355 (**Table 2**).

represented, 35 are linked to the GO immune system process (**Tables 1** and **2**). We did not see substantial over- or under-representation of certain GO processes when comparing the newly discovered and previously identified loci, but this may represent a limitation of the ImmunoChip in targeting genomic loci enriched for immunologically active genes, as more subtle distinctions between such loci might not be adequately captured by broad annotations such as GO processes.

Finally, we explored the overlap between our findings and those in other autoimmune diseases with reported ImmunoChip analyses. We calculated the percentage of multiple sclerosis signals (110 non-MHC; **Supplementary Table 8**) overlapping with those of other autoimmune diseases by requiring $r^2 \geq 0.8$ between the best variants reported in each study using SNAP[31]. In total, we found that ~22% of our signals overlapped at least one other autoimmune disease signal.

Table 2 Results for 49 known non-MHC variants associated with multiple sclerosis at genome-wide significance

				Discovery			Replication			Joint			
SNP	Chr.	Position[a]	RA	RAF	*P*	OR	RAF	*P*	OR	*P*	OR	Gene[b]	Function
rs3748817	1	2525665	A	0.64	1.3×10^{-12}	1.14	0.65	1.2×10^{-15}	1.15	1.3×10^{-26}	1.14	*MMEL1*	Intronic
rs41286801	1	92975464	A	0.14	7.9×10^{-16}	1.20	0.16	2.1×10^{-12}	1.17	1.4×10^{-26}	1.19	*EVI5*	3′ UTR
rs7552544[c]	1	101240893	A	0.56	3.7×10^{-6}	1.08	0.43	3.3×10^{-12}	1.12	1.9×10^{-16}	1.10	***VCAM1***	Intergenic
rs6677309	1	117080166	A	0.88	1.5×10^{-28}	1.34	0.88	4.1×10^{-16}	1.24	5.4×10^{-42}	1.29	***CD58***	Intronic
rs1359062	1	192541472	C	0.82	1.8×10^{-13}	1.18	0.83	2.1×10^{-8}	1.13	4.8×10^{-20}	1.15	***RGS1***	Intergenic
rs55838263	1	200874728	A	0.71	1.4×10^{-9}	1.12	0.71	3.9×10^{-11}	1.13	4.0×10^{-19}	1.13	*C1orf106*	Intronic
rs2163226	2	43361256	A	0.71	7.0×10^{-8}	1.10	0.73	3.8×10^{-10}	1.14	2.1×10^{-16}	1.12		Intergenic
rs7595717	2	68587477	A	0.26	3.3×10^{-7}	1.10	0.27	6.8×10^{-8}	1.10	1.2×10^{-13}	1.10	***PLEK***	Intergenic
rs9989735	2	231115454	C	0.18	7.8×10^{-14}	1.17	0.19	6.8×10^{-11}	1.14	4.2×10^{-23}	1.16	*SP140*	Intronic
rs2371108	3	27757018	A	0.38	2.1×10^{-6}	1.08	0.39	5.8×10^{-11}	1.12	1.5×10^{-15}	1.10	***EOMES***	downstream
rs1813375	3	28078571	A	0.47	5.7×10^{-18}	1.15	0.49	4.4×10^{-16}	1.15	1.9×10^{-32}	1.15		Intergenic
rs1131265	3	119222456	C	0.80	2.0×10^{-15}	1.19	0.81	4.8×10^{-10}	1.14	1.4×10^{-23}	1.17	*TIMMDC1*	Exonic
rs1920296[c]	3	121543577	C	0.64	6.8×10^{-15}	1.14	0.64	5.5×10^{-9}	1.10	6.5×10^{-22}	1.12	*IQCB1*	Intronic
rs2255214[c]	3	121770539	C	0.52	5.3×10^{-13}	1.13	0.52	3.3×10^{-13}	1.13	1.2×10^{-24}	1.13	***CD86***	Intergenic
rs1014486	3	159691112	G	0.43	1.2×10^{-9}	1.11	0.44	1.4×10^{-10}	1.11	1.1×10^{-18}	1.11	***IL12A***	Intergenic
rs7665090	4	103551603	G	0.52	2.4×10^{-6}	1.08	0.53	5.0×10^{-4}	1.13	1.0×10^{-8}	1.09	*MANBA*	Intergenic
rs6881706	5	35879156	C	0.72	4.9×10^{-9}	1.12	0.73	1.7×10^{-9}	1.12	4.3×10^{-17}	1.12	***IL7R***	Intergenic
rs6880778	5	40399096	G	0.60	1.7×10^{-8}	1.10	0.61	3.9×10^{-13}	1.13	8.1×10^{-20}	1.12		Intergenic
rs71624119	5	55440730	G	0.76	2.7×10^{-9}	1.12	0.76	1.9×10^{-5}	1.09	3.4×10^{-13}	1.11	*ANKRD55*	Intronic
rs72928038	6	90976768	A	0.17	7.6×10^{-7}	1.11	0.19	9.0×10^{-11}	1.17	1.5×10^{-15}	1.14	*BACH2*	Intronic
rs11154801	6	135739355	A	0.37	2.3×10^{-9}	1.11	0.37	1.0×10^{-12}	1.13	1.8×10^{-20}	1.12	*AHI1*	Intronic
rs17066096	6	137452908	G	0.23	5.9×10^{-12}	1.14	0.25	4.1×10^{-13}	1.15	1.6×10^{-23}	1.14	*IL22RA2*	Intergenic
rs67297943	6	138244816	A	0.78	4.8×10^{-8}	1.12	0.80	2.5×10^{-6}	1.11	5.5×10^{-13}	1.11	***TNFAIP3***	Intergenic
rs212405	6	159470559	T	0.62	1.4×10^{-15}	1.15	0.64	1.8×10^{-7}	1.10	8.0×10^{-21}	1.12	*TAGAP*	Intergenic
rs1021156	8	79575804	A	0.24	5.6×10^{-10}	1.12	0.26	2.1×10^{-8}	1.11	8.5×10^{-17}	1.11	*ZC2HC1A*	Intergenic
rs4410871	8	128815029	G	0.72	2.0×10^{-9}	1.12	0.72	3.4×10^{-8}	1.11	4.3×10^{-16}	1.11	*MIR1204*	Intergenic
rs759648	8	129158945	C	0.31	2.8×10^{-6}	1.09	0.31	3.7×10^{-5}	1.08	5.0×10^{-10}	1.08	*MIR1208*	Intergenic
rs2104286	10	6099045	A	0.72	7.6×10^{-23}	1.21	0.73	3.6×10^{-26}	1.23	2.3×10^{-47}	1.22	***IL2RA***	Intronic
rs1782645	10	81048611	A	0.43	4.3×10^{-7}	1.09	0.41	6.2×10^{-10}	1.11	2.5×10^{-15}	1.10	*ZMIZ1*	Intronic
rs7923837	10	94481917	G	0.61	4.6×10^{-9}	1.11	0.62	2.0×10^{-9}	1.11	4.3×10^{-17}	1.11	***HHEX***	Intergenic
rs34383631	11	60793330	A	0.40	5.7×10^{-10}	1.11	0.39	4.5×10^{-15}	1.15	3.7×10^{-23}	1.13	*CD6*	Intergenic
rs1800693	12	6440009	G	0.40	6.9×10^{-16}	1.14	0.41	1.0×10^{-13}	1.14	6.7×10^{-28}	1.14	*TNFRSF1A*	Intronic
rs11052877	12	9905690	G	0.36	5.4×10^{-9}	1.10	0.38	1.2×10^{-5}	1.08	5.6×10^{-13}	1.09	***CD69***	3′ UTR
rs201202118[d]	12	58182062	A	0.67	7.4×10^{-13}	1.14	0.67	1.6×10^{-10}	1.12	9.0×10^{-22}	1.13	*TSFM*	Intronic
rs7132277	12	123593382	A	0.19	1.9×10^{-6}	1.10	0.19	1.4×10^{-8}	1.13	1.9×10^{-13}	1.12	*PITPNM2*	Intronic
rs2236262	14	69261472	A	0.50	1.2×10^{-5}	1.08	0.50	3.8×10^{-8}	1.09	2.5×10^{-12}	1.08	***ZFP36L1***	Intronic
rs74796499	14	88432328	C	0.95	8.5×10^{-11}	1.31	0.95	4.5×10^{-11}	1.33	2.4×10^{-20}	1.32	*GALC*	Intronic
rs12927355	16	11194771	G	0.68	8.2×10^{-27}	1.21	0.69	4.3×10^{-21}	1.18	6.4×10^{-46}	1.20	*CLEC16A*	Intronic
rs35929052	16	85994484	G	0.89	3.3×10^{-7}	1.14	0.88	3.6×10^{-6}	1.15	5.9×10^{-12}	1.15	***IRF8***	Intergenic
rs4796791	17	40530763	A	0.36	1.8×10^{-8}	1.10	0.36	1.2×10^{-13}	1.14	3.7×10^{-20}	1.12	*STAT3*	Intronic
rs8070345	17	57816757	A	0.45	5.4×10^{-16}	1.14	0.46	1.9×10^{-9}	1.10	2.2×10^{-23}	1.12	*VMP1*	Intronic
rs1077667	19	6668972	G	0.79	3.5×10^{-13}	1.16	0.79	8.4×10^{-13}	1.16	1.7×10^{-24}	1.16	***TNFSF14***	Intronic
rs34536443	19	10463118	C	0.95	1.2×10^{-8}	1.28	0.96	2.9×10^{-7}	1.30	1.8×10^{-14}	1.29	***TYK2***	Exonic
rs11554159	19	18285944	G	0.73	2.6×10^{-13}	1.15	0.74	1.4×10^{-12}	1.15	1.9×10^{-24}	1.15	***IFI30***	Exonic
rs8107548	19	49870643	G	0.25	2.0×10^{-6}	1.09	0.26	2.5×10^{-10}	1.13	5.7×10^{-15}	1.11	*DKKL1*	Intronic
rs4810485	20	44747947	A	0.25	1.8×10^{-5}	1.08	0.25	1.4×10^{-12}	1.14	7.7×10^{-16}	1.11	***CD40***	Intronic
rs2248359	20	52791518	G	0.60	9.8×10^{-5}	1.07	0.62	8.2×10^{-11}	1.12	2.0×10^{-13}	1.09	*CYP24A1*	Intergenic
rs2283792	22	22131125	C	0.51	1.1×10^{-6}	1.08	0.53	5.4×10^{-11}	1.11	5.5×10^{-16}	1.10	***MAPK1***	Intronic
Secondary													
rs523604[e]	11	118755738	A	0.53	2.5×10^{-7}	1.09	0.54	4.0×10^{-9}	1.11	6.2×10^{-15}	1.10	***CXCR5***	Intronic

All listed signals had discovery $P \leq 1.0 \times 10^{-4}$, replication $P \leq 5.0 \times 10^{-2}$ and joint $P \leq 5.0 \times 10^{-8}$. All *P* values are two-sided. Chr., chromosome; RA, risk allele; RAF, risk allele frequency. [a]Position is based on hg19 and dbSNP Build 137. [b]The nearest gene is listed if it lies within 50 kb of the signal. Bold font indicates genes that are part of GO immune system process. [c]These three SNPs were not primary in the 2011 GWAS[9] (two were secondary, and the third was tertiary in that study). [d]A proxy SNP (rs10431552; $r^2 = 0.99$) was used in replication. [e]The *P* values and OR values shown are after conditioning on rs9736016 and rs533646 (**Table 1**).

More specifically, ~9.1% overlapped signals in inflammatory bowel disease, ~7.3% overlapped signals in ulcerative colitis, ~9.1% overlapped signals in Crohn's disease[15], ~9.1% overlapped signals in primary biliary cirrhosis[32,33], ~4.5% overlapped signals in celiac disease[34], ~4.5% overlapped signals in rheumatoid arthritis[35], ~0.9% overlapped signals in psoriasis[36], and ~2.7% overlapped signals in autoimmune thyroid disease[37]. We report at seven loci the same top variant seen in primary biliary cirrhosis. We also note that our best *TYK2* variant (rs34536443)[38] is also the most associated *TYK2* variant for primary biliary cirrhosis, psoriasis and rheumatoid arthritis. Lastly, variants have been reported for autoimmune thyroid disease, celiac disease, primary biliary cirrhosis and rheumatoid arthritis that have pairwise $r^2 \geq 0.8$ with the multiple sclerosis risk variant near *MMEL1* (**Supplementary Table 8**)[39].

In summary, we have identified 48 new susceptibility variants for multiple sclerosis. These newly discovered loci expand our understanding

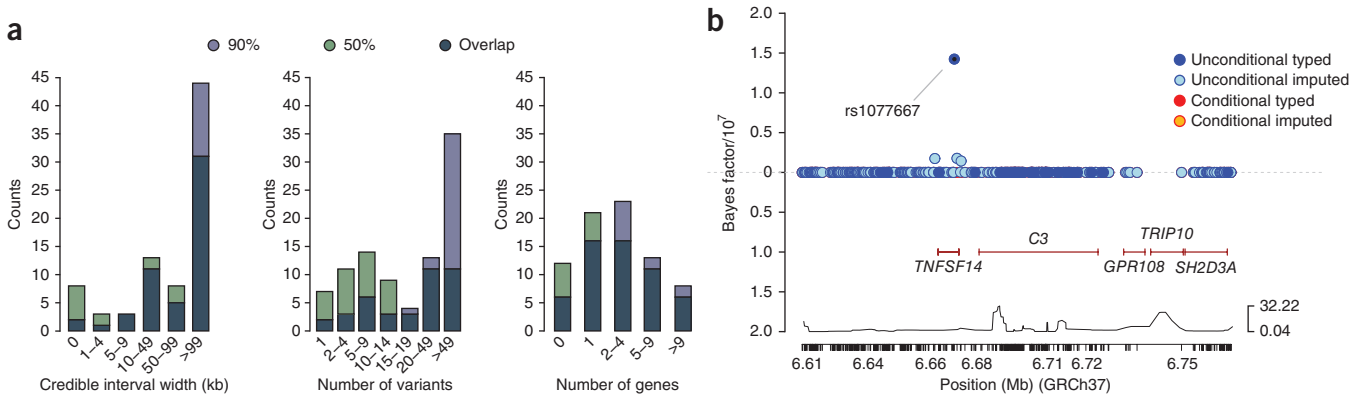

Figure 2 Bayesian fine mapping within primary regions of association. (**a**) Summary of the extent of fine mapping across 66 regions in 6,356 subjects with multiple sclerosis and 9,617 healthy controls from the UK, showing the physical extent of the number of variants and the number of genes spanned by the posterior 90% and 50% credible sets. (**b**) Details of fine mapping in the region encompassing *TNFSF14*. Bayes factors summarizing evidence for association of the SNPs before conditioning on the lead SNP (rs1077667) are shown above the *x* axis (blue markers), and the Bayes factors after conditioning are shown below the *x* axis.

Table 3 Results for 18 variants from the 8 regions with consistent high-resolution fine mapping

Gene	SNP	Chr.	Position[a]	Posterior	GERP	Functional annotation[b]
IL2RA	rs2104286	10	6099045	0.93	−0.47	Intronic, correlates with soluble IL-2RA levels
TNFSF14	rs1077667	19	6668972	0.74	−3.89	Intronic, TFBS or DNase I peak, correlates with serum levels of TNFSF14
TNFRSF1A	rs1800693	12	6440009	0.69	2.53	Intronic, causes splicing defect and truncated soluble TNFRSF1A
	rs4149580[c]	12	6446990	0.10	2.06	intronic
IL12A	rs1014486	3	159691112	0.67	0.24	–
STAT4	rs78712823	2	191958581	0.59	−3.98	Intronic
TNFAIP3	rs632574	6	137959118	0.27	−1.15	–
	rs498549[c]	6	137984935	0.20	0.52	–
	rs651973	6	137996134	0.17	2.41	Downstream of RP11-95M15.1 lincRNA gene
	rs536331	6	137993049	0.15	0.19	Upstream of RP11-95M15.1 lincRNA gene
CD58	rs35275493[c]	1	117095502	0.24	0.75	Intronic (insertion)
	rs10754324[c]	1	117093035	0.22	0.32	Intronic
	rs6677309	1	117080166	0.21	−1.18	Intronic, TFBS or DNase I peak
	rs1335532	1	117100957	0.17	−1.32	Intronic
CD6	rs34383631	11	60793330	0.20	1.66	–
	rs4939490[c]	11	60793651	0.14	−0.53	–
	rs4939491[c]	11	60793722	0.14	−0.37	–
	rs4939489	11	60793648	0.10	3.25	–

All listed variants have posterior probability ≥0.1 in regions where ≤5 variants explain the top 50% of the posterior probability, and the top SNP from the frequentist analysis resides in the 90% confidence interval; SNPs are ordered by maximum posterior probability within each region. Posterior probability is the probability of any variant driving association[23]. GERP denotes Genomic Evolutionary Rate Profiling. Chr., chromosome; TFBS, transcription factor binding site; lncRNA, long noncoding RNA.

[a]Position is based on hg19 and dbSNP Build 137. [b]Functional data are from VEP, the eQTL browser, Fairfax *et al.*[20], PubMed searches and the 1000 Genomes Project. Minus signs indicate intergenic signals with no additional annotation and no reported regulatory consequence. [c]Imputed variant.

of the immune system processes implicated in multiple sclerosis. We estimate that the 110 established non-MHC risk variants explain 20% of the sibling recurrence risk, 28% when including the already identified MHC effects[9] (**Supplementary Note**). Additionally, we have identified five previously associated regions (*TNFSF14*, *IL2RA*, *TNFRSF1A*, *IL12A* and *STAT4*) where consistent high-resolution fine mapping implicated one variant that accounted for more than 50% of the posterior probability of association. Our study further implicates NF-κB in multiple sclerosis pathobiology[18], emphasizes the value of dense fine mapping in large follow-up data sets and exposes the urgent need for functional annotation in relevant tissues. Understanding the implicated networks and their relationship to environmental risk factors will promote the development of rational therapies and may enable the development of preventive strategies.

URLs. ImmunoBase, http://www.immunobase.org/; eQTL browser, http://eqtl.uchicago.edu/; MetaCore, https://portal.genego.com/.

METHODS

Methods and any associated references are available in the online version of the paper.

Note: Any Supplementary Information and Source Data files are available in the online version of the paper.

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AUTHOR CONTRIBUTIONS

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The authors declare no competing financial interests.

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ONLINE METHODS

ImmunoChip data (discovery set). Details of case ascertainment, processing and genotyping for the discovery phase are provided in the **Supplementary Note** (see also **Supplementary Table 9**). All cases and controls involved in this study gave valid informed consent in accordance with approval from the relevant local ethical committees or institutional review boards (IRBs). The investigators were not blinded to allocation during experiments and outcome assessment. Genotype calling for all samples was performed using Opticall[40]. Samples that performed poorly or were determined to be related were removed (**Supplementary Table 10**). Data were organized into 11 country-level strata: ANZ (Australia and New Zealand), Belgium, Denmark, Finland, France, Germany, Italy, Norway, Sweden, the UK and the United States. SNP-level quality control (**Supplementary Table 11**) and population outlier identification using principal-components analysis (**Supplementary Fig. 97**) were carried out in each stratum separately. No statistical method was used to predetermine sample size.

Discovery set analysis. We applied logistic regression, assuming a per-allelic genetic model for each data set, including the first five principal components as covariates to correct for population stratification (**Supplementary Table 12** lists the genomic inflation factors for each data set, λ). We then performed an inverse variance meta-analysis of the 11 strata under a fixed-effects model, as implemented in PLINK[41]. To be more conservative and account for any residual inflation in the test statistic, we applied the genomic control equivalent to the per-SNP standard error in each stratum. Specifically, we corrected the standard errors for SNPs by multiplying them by the square root of the raw genomic inflation factor, λ, for each data set if λ was >1.

Within the designated fine-mapping intervals, we applied a forward stepwise logistic regression to identify statistically independent effects. The primary SNP in each interval was included as a covariate, and association analysis was repeated for the remaining SNPs. This process was repeated until no SNPs reached the minimum level of significance ($P < 1 \times 10^{-4}$). Outside of the designated fine-mapping intervals, all SNPs having association $P < 1 \times 10^{-4}$ were identified and grouped into sets on the basis of being separated by a physical distance of less than 2 Mb, and a similar stepwise regression model was applied. Any SNPs that entered the model with association $P < 1 \times 10^{-4}$ after conditioning were considered to be statistically independent primary signals.

In addition, because of the close physical proximity of some fine-mapping intervals and SNP sets, independence was tested for all identified signals within 2 Mb of one another. Forest and cluster plots (**Supplementary Fig. 98**) of all independent SNPs were examined, and a SNP was excluded if cluster plots were unsatisfactory. If a SNP was excluded, forward stepwise logistic regression within the corresponding fine-mapping interval or SNP set was repeated after removal of the SNP. During this process, 17 additional SNPs were excluded on the basis of cluster or forest plot review.

Replication set. The replication phase included GWAS data organized into 15 strata. Within each stratum, poorly performing samples (call rate < 95%, sex discordance or excess heterozygosity) and poorly performing SNPs (Hardy-Weinberg equilibrium $P < 1 \times 10^{-6}$, minor allele frequency (MAF) < 1% or call rate < 95%) were removed. Principal-components analysis was performed to identify population outliers for each stratum, and the genomic control inflation factor was < 1.1 for each. Data included in the final discovery and replication analyses are summarized in **Supplementary Tables 13** and **14**. All samples used in the replication set were unrelated to those in the discovery set, as verified by identity-by-descent analysis.

We attempted replication of all non-MHC independent signals that reached discovery $P < 1 \times 10^{-4}$ in a meta-analysis set of GWAS. Each data set was imputed with the 1000 Genomes Project European phase I (a) panel using BEAGLE[42] to maximize the overlap between the ImmunoChip SNP content and the GWAS data. Post-imputation genotypic probabilities were used in a logistic regression model, for each stratum, to estimate SNP effect sizes and *P* values. By using the post-imputation genotypic probabilities, we penalized SNPs that did not have good imputation quality, thus ensuring a conservative analysis. Furthermore, we accounted for population stratification in each data set by including the first five principal components in the logistic model. We then performed meta-analysis of the effect sizes and respective standard errors of the 15 strata using a fixed-effects, inverse variance method. We applied the genomic control equivalent to the per-SNP standard error in each stratum, controlling for the respective genomic inflation factor, λ (**Supplementary Table 14**).

To replicate the primary SNPs with identified signal in the discovery phase, we determined the replication effect sizes and respective standard errors. For the secondary and tertiary SNPs, we fitted the same exact models as in the discovery phase for each data set. We then performed fixed-effects meta-analysis to estimate an effect size that corresponded to the same logistic model. In the case that a SNP was not present in the replication set, we replaced it with a perfectly tagging SNP, i.e., a SNP that had r^2 and D′ values equal to 1. If a perfectly tagging SNP was not available, we selected a SNP that had equivalent MAF and the highest possible r^2 and D′ values. Estimation of r^2 and D′ values for this objective were based on data from ImmunoChip control samples.

Joint analysis (discovery and replication sets). We performed meta-analysis of the effect sizes and respective standards errors from the discovery and replication phases under a fixed-effects model. A SNP was considered to have replicated when all three of the following criteria were met: (i) replication $P < 5.0 \times 10^{-2}$; (ii) joint $P < 5 \times 10^{-8}$; and (iii) the joint *P* value was more statistically significant than the discovery *P* value. SNPs that reached $P < 1 \times 10^{-6}$ but did not pass the genome-wide significance threshold were defined as having suggestive signals if criteria (i) and (iii) were met.

Fine mapping of association signals. To fine map association signals, we used a combination of imputation and Bayesian methodology[23]. Around each of the 97 associated SNPs, we isolated 2 Mb of sequence in the discovery and replication phase UK data as well as in the European samples from Phase 1 of the 1000 Genomes Project[28]. Forming the single largest cohort, only UK samples were considered to minimize the effects of differential imputation quality between populations of different ancestry. In addition to the previous quality control, SNPs with failed alignment or difference in MAF > 10% between the typed cohorts and the 1000 Genomes Project samples, MAF < 1% or Hardy-Weinberg equilibrium $P < 1.0 \times 10^{-4}$ were removed.

Imputation was performed separately for the UK discovery and replication cohorts on each 2-Mb region using the default settings of IMPUTEv2 (refs. 43,44). Missing genotypes for the genotyped SNPs were not imputed, and any imputed SNP that failed to reach the Hardy-Weinberg equilibrium and MAF thresholds was subsequently removed. We carried out frequentist and Bayesian association tests on all SNPs in each cohort separately, assuming additivity, using the default settings of SNPTESTv2 (ref. 45). Frequentist fixed-effects meta-analysis was carried out using the software META[46]. Bayesian meta-analysis was carried out using an independence prior (near-identical results were obtained using a fixed-effects Bayesian meta-analysis).

To identify regions where reliable fine mapping could be achieved, we used the information score (INFO, obtained from IMPUTEv2) as determined from the 1000 Genomes Project samples. Specifically, we measured the fraction of variants having both $r^2 > 0.5$ and $r^2 > 0.8$ with the primary associated variant and having greater than 50% and 80% INFO scores, respectively. Regions where any SNP with $r^2 > 0.5$ had INFO < 50% were excluded. We also excluded regions where the top hit from imputation had an INFO score less than 80%. Regions were considered to be fine mapped with high quality when all variants with $r^2 > 0.8$ had an INFO score of at least 80%. Within these regions, we excluded variants where the inferred direction of association was opposite between the UK discovery and replication cohorts.

To measure the posterior probability that any single variant drives association, we calculated the Bayes factor. Under the assumption that there is a single causal variant in the region, the Bayes factor is proportional to the probability that the variant drives the association[23]. We identified the smallest set of variants that contained 90% and 50% of the posterior probability. We called a region successfully and consistently fine mapped it if there were at most five variants in the 50% confidence interval and the top SNP from the frequentist analysis was contained in the 90% confidence interval. For these regions, we annotated variants with information about evolutionary conservation, predicted coding consequences, regulation, published associations to expression

or DNase I hypersensitive sites using ANNOVAR[47], VEP[24] and the eQTL browser, a recent study of expression in immune cells[20] and other literature.

GO classification. To determine the GO processes in which our 97 associated variants were involved, we used MetaCore from Thomson Reuters. We annotated the processes for the unique genes within 50 kb of the variants.

Cross-disease comparisons. To explore the potential overlap with variants identified across other autoimmune diseases, we calculated the percentage overlap of reported variants found in other ImmunoChip reports to our ImmunoChip results. The top variants reported as either newly discovered or previously known in other ImmunoChip reports were compared with the 110 variants representing both our new and previous discoveries in multiple sclerosis. For a signal to be considered to be overlapping, we required $r^2 \geq 0.8$ using the Pairwise LD function of the SNAP tool in European samples[31].

Secondary analyses. We performed a severity-based analysis of the Multiple Sclerosis Severity Score (MSSS) in cases only from the discovery phase (**Supplementary Fig. 99**). In addition, a transmission disequilibrium test was performed in 633 trios to test for transmission of the 97 identified risk alleles (**Supplementary Fig. 100**). Details are given in the **Supplementary Note**.

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