

Supplementary table 1

MS study cohort

	Case	Controls
Gender (n)		
Female	1900	1929
Male	926	904
No details	50	77
Female to male ratio	2.1	2.1
Age (years)		
Age at onset		
Mean \pm SD	30 \pm 9.7	
Range	6-68	
Age at analysis		
Mean \pm SD	36 \pm 12.3	38 \pm 12.3
Range	13-85	10-90
Disease course no. (%)		
RR	2047 (75.2)	
SP	472 (17.3)	
PP	158 (5.8)	
PR	13 (0.4)	
CIS	32 (1)	
No details	154	

Abbreviations: RR, relapsing-remitting; SP, secondary-progressive; PP, primary-progressive; PR, progressive-relapsing; CIS, clinically isolated syndrome.

Supplementary table 2

Coordinates and oligonucleotides used for PCR amplification of the clones assayed for allele-specific regulatory sequences.

Fragment	Coordinates (NCBI36/hg18)	Size	Primers
I	56432826-56433210	383	Forward GGAGTTGGGGTACCAGAGGT Reverse GGCCTCAGGTCTTTGCATTA
II	56444040-56444493	453	Forward GGTCAAGGGGAGTGTTTGAA Reverse CTACCCCTCAGCCACTGTTC
III	56451121-56451516	395	Forward CAAAAGAGGGCCTGAGTGT Reverse GGCCTCATGATGGTCCTATG
IV	56451404-56453283	1879	Forward AAAGGGAGGAGGGTTTCTCA Reverse AGACTGGGCCCAAAGTTCTC
V	56462202-56463817	1615	Forward GCCTCTTCCTGAGCCTCTT Reverse AAATAAAATAGCCGGGTGTCG
VI	56464042-56465447	1405	Forward ATTCTGAGAAATGGCGTCGT Reverse AGGAGATGACAGGTCCATGC

Supplementary table 3.

SNP captured by the Tag-SNP assay

Test	Alleles Captured
rs1678542(1)	rs11172254,rs10783832,rs775322,rs1284464, rs11172247,rs1678542
rs2888334	rs2888334,rs10876994,rs2306390,rs775251
rs775249	rs775249,rs775250,rs775246
rs1678536	rs1678536
rs7313599	rs7313599
rs1078109	rs1078109
rs7305391	rs7305391,rs8873,rs1545783,rs812315
rs1564374	rs1564374,rs2277324
rs11172290	rs2277323,rs12320537,rs11172290,rs774897,rs12322482, rs715930,rs774899
rs3825078	rs3825078,rs1082502,rs10877001,rs810204, rs1678504,rs1871417,rs2640629,rs774890,rs1678516, rs1678540,rs10877008,rs10783844,rs7314152,rs4760168, rs1678514,rs2640631,rs2277322,rs1678520,rs7979246,rs2640637, rs1689595,rs1628552,rs7976852,rs1689585,rs1689592,rs774887, rs10083154,rs1629032, rs10876993 (2)
rs701006	rs701006
rs2301551	rs2301551
rs12307841	rs12307841,rs4760169
rs12368653(3)	rs12368653
rs1048691	rs1048691
rs6581155	rs6581155,rs10747783,rs923829,rs10431552,rs2072052, rs2291617,rs4646536,rs724834,rs2069502,rs10877013, rs10877011,rs701008,rs8181644,rs10877019,rs11172335, rs703842(4) ,rs10877015,rs11172333

Bold indicate the SNPs reported to be associated in this region to different diseases by GWAS

- (1) Variant reported associated with RA by Raychaudhuri S et al. [13]
- (2) Variant reported associated with RA and CD by Zhernakova A et al..[14] The LD between rs10876993 and rs3825078 is $r^2=0.95$
- (3) Variant reported associated with MS by Sawcer S et al. [8]
- (4) Variant reported associated with MS by ANZgene.[12] The LD between rs6581155 and rs703842 is $r^2=1$.