

Table S1. Results of genome-wide association studies of susceptibility to multiple sclerosis (relying on the data of the National Human Genome Research Institute (NHGRS) catalog [1])

Year	Genotyping platform (number of SNPs)	Initial sample size, ethnicity	Replication sample size, ethnicity	Locus	Gene(s)	SNP	p-value*	Reference
2007	Affymetrix (334 923)	931 trios , 2431 controls (British, Americans)	609 trios, 2322 MS patients, 2987 controls (British, Americans)	9q33	<i>DBC1</i>	rs10984447	$8 \times 10^{-6}$	[2]
				6p21.32	<i>HLA-DRA</i>	rs3135388	$9 \times 10^{-81}$	
				16p13.13	<i>KIAA0350 (CLEC16A)</i>	rs6498169	$4 \times 10^{-6}$	
				10p15.1	<i>IL2RA</i>	rs12722489	$3 \times 10^{-8}$	
				5p13.2	<i>IL7RA</i>	rs6897932	$3 \times 10^{-7}$	
				1p22.1	<i>RPL5</i>	rs6604026	$8 \times 10^{-6}$	
2007	Illumina (14 436)	994 MS patients, 1500 controls (British)	-	6p21.32	<i>HLA-DRB1</i>	H.n.	$<10^{-20}$	[3]#
2008	Affymetrix (428 867)	242 RRMS/SPMS patients, 242 controls (Spanish)	375 RRMS/SPMS patients , 375 controls (Spanish, Americans)	6p21.32	<i>HLA-DRB1</i>	rs3129934	$9 \times 10^{-11}$	[4]
				13	Intergenic	rs1327328	$5 \times 10^{-4}$	
2008	Affymetrix (~262 000)	45 MS patients, 195 controls (Danish isolate)	1) 490 MS patients, 426 controls (Danish), 2) 826 MS patients, 997 controls (Swedes), 3) 1318 trios (Canadians)	1p36.22	<i>KIF1B</i>	rs10492972	$2.5 \times 10^{-10}$	[5]
2009	Illumina (551 642)	978 MS patients, 883 controls (Americans, North Europeans)	-	6p21.3	<i>HLA-DRB1</i>	rs3129934	$<10^{-32}$	[6]
				13q31.3	<i>GPC5</i>	rs9523762	$1 \times 10^{-6}$	
				9p22.2	<i>SH3GL2</i>	rs1755289	$3 \times 10^{-6}$	
				8p23.2	<i>CSMD1</i>	rs1529316	$2 \times 10^{-6}$	
				12q12	<i>PDZRN4</i>	rs1458175	$2 \times 10^{-6}$	
				3q23	<i>SLC25A36</i>	rs908821	$3 \times 10^{-6}$	
				4q35.1	<i>MGC45800</i>	rs7672826	$8 \times 10^{-6}$	
				20p13	<i>C20orf46</i>	rs397020	$8 \times 10^{-7}$	
				2p25.1	<i>DDEF2</i>	rs1109670	$9 \times 10^{-6}$	
				3q24	<i>ZIC1</i>	rs1841770	$8 \times 10^{-6}$	
				2q14.2	<i>EN1</i>	rs651477	$7 \times 10^{-6}$	

2009	Affymetrix & Illumina (~2.56 млн после импутации генотипов)	2624 MS patients, 7220 controls (Americans, North Europeans)	2215 MS patients, 2116 controls (Americans, North Europeans)	6p21.32	<i>HLA-DRB1</i>	rs3135388	$4 \times 10^{-225}$	[7]
				1p13.1	<i>CD58</i>	rs2300747	$3 \times 10^{-10}$	
				6p22.1	<i>HLA-B</i>	rs2523393	$1 \times 10^{-17}$	
				3q25.33	<i>IL12A</i>	rs4680534	$6 \times 10^{-6}$	
				10p15.1	<i>IL2RA</i>	rs2104286	$9 \times 10^{-8}$	
				12p13.31	<i>TNFRSF1A</i>	rs4149584	$5 \times 10^{-6}$	
				2q22.1	<i>CXCR4</i>	rs882300	$1 \times 10^{-7}$	
				12p13.31	<i>TNFRSF1A</i>	rs1800693	$2 \times 10^{-11}$	
				16p13.13	<i>CLEC16A</i>	rs11865121	$2 \times 10^{-7}$	
				5p13.2	<i>IL7R</i>	rs6897932	$2 \times 10^{-6}$	
				16q24.1	<i>IRF8</i>	rs17445836	$4 \times 10^{-9}$	
				11q12.2	<i>CD6</i>	rs17824933	$4 \times 10^{-9}$	
				5p13.1	<i>PTGER4</i>	rs6896969	$2 \times 10^{-7}$	
				12q24.31	<i>MPHOSPH9</i>	rs1790100	$7 \times 10^{-7}$	
				10q22.3	<i>ZMIZ1</i>	rs1250540	$2 \times 10^{-6}$	
				1q31	<i>RGS1</i>	rs2760524	$9.8 \times 10^{-6}$	
6q23	<i>OLIG3-TNFAIP3</i>	rs9321619	$1.7 \times 10^{-5}$					
2009	Illumina (302 098)	1618 MS patients, 3413 controls (Australians, New Zealanders, and Americans of European origin, British)	2256 MS patients, 2310 controls (Australians, New Zealanders of European origin)	10p15.1	<i>IL2RA</i>	rs2104286	$7.4 \times 10^{-6}$	[8]
				20q13.12	<i>CD40</i>	rs6074022	$1 \times 10^{-7}$	
				16p12.1	Intergenic	rs8049603	$1 \times 10^{-6}$	
				1p22.1	<i>EVI5, RPL5</i>	rs6604026	$2.5 \times 10^{-6}$	
				1p13.1	<i>CD58</i>	rs1335532	$9.6 \times 10^{-8}$	
				6p21.32	<i>HLA-DRB1</i>	rs9271366	$1 \times 10^{-184}$	
				8q24.21	<i>ASAP1 (DDEF1)</i>	rs6984045	$2 \times 10^{-6}$	
12q14.1	<i>METTL1, CYP27B1</i>	rs703842	$5 \times 10^{-11}$					
2010	Illumina (297 343)	68 MS patients, 136 controls (Finnish isolate)	4570 MS patients, 10143 controls (Finns, North Europeans, Americans)	17q21.2	<i>STAT3</i>	rs744166	$3 \times 10^{-10}$	[9]
				6p21.32	<i>HLA</i>	rs3135338	$2 \times 10^{-25}$	
2010	Affymetrix (6 607 266 после импутации генотипов)	882 RRMS patients, 872 controls (Sardinians)	1775 MS patients, 2005 controls (Sardinians)	6p21.32	<i>HLA-DRB, HLA-DQB1</i>	rs2040406	$1 \times 10^{-20}$	[10]
				3q13.11	<i>CBLB</i>	rs9657904	$2 \times 10^{-10}$	
2010	Illumina (~300 000)	590 MS patients, 825 controls (Europeans)	-	10q11.21	Intergenic	rs2503875	$2 \times 10^{-7}$	[11]
				19p13.2	<i>ZNF433</i>	rs3745672	$1 \times 10^{-6}$	
				9q34.2	<i>VAV2</i>	rs3780792	$1 \times 10^{-6}$	

2011	Affymetrix & Illumina (2 529 394)	5545 MS patients, 12153 controls (Europeans)	-	6p21.32	<i>HLA-DQA1</i>	rs9271366	$4 \times 10^{-17}$	[12]
				6p21.32	<i>HLA-DRB1</i>	rs3129889	$1 \times 10^{-206}$	
				6p22.1	<i>HLA-B</i>	rs9260489	$1 \times 10^{-11}$	
				1p13.1	<i>CD58</i>	rs2300747	$6 \times 10^{-9}$	
				3p24.1	<i>EOMES</i>	rs170934	$2 \times 10^{-8}$	
				2p21	<i>THADA</i>	rs6718520	$3 \times 10^{-8}$	
				9p24.1	<i>MLANA</i>	rs2150702	$3 \times 10^{-8}$	
				10p15.1	<i>IL2RA</i>	rs12722489	$4 \times 10^{-8}$	
				17q21.2	<i>STAT3</i>	rs2293152	$4 \times 10^{-8}$	
				5q33.3	<i>IL12B</i>	rs2546890	$8 \times 10^{-8}$	
				17q21.32	<i>KPNB1, TBKBPI, TBX21</i>	rs8070463	$1 \times 10^{-7}$	
				3q13.33	<i>ILDRI, CD86</i>	rs2681424	$2 \times 10^{-7}$	
				19p13.11	<i>EPS15L1</i>	rs10411936	$2 \times 10^{-7}$	
				2p13.3	<i>PLEK, FBXO48, C2orf13</i>	rs7592330	$2 \times 10^{-7}$	
				10q22.3	<i>ZMIZ1</i>	rs1250542	$4.0 \times 10^{-7}$	
				6q25.3	<i>TAGAP</i>	rs1738074	$4.0 \times 10^{-7}$	
				16p13.13	<i>TNP2, PRM3, PRM2, PRM1, C16orf75</i>	rs7191700	$6.0 \times 10^{-7}$	
5q33.3	<i>IL12B</i>	rs10866713	$7.0 \times 10^{-7}$					
13q14.2	Intergenic	rs9596270	$7.0 \times 10^{-7}$					
20q13.12	<i>CD40</i>	rs6074022	$5.0 \times 10^{-6}$					
2011	Illumina (~660 000 SNP; 60 000 CNV)	9772 MS patients, 17376 controls (Europeans, Australians, New Zealanders of European origin, Americans)	4218 MS patients, 7296 controls from previous GWAS (Europeans)	6p21.32	<i>HLA-DRB1</i>	-	$1.0 \times 10^{-132}$	[13]
				6p21.3	<i>HLA-A</i>	-	$9 \times 10^{-23}$	
				1p21.2	<i>VCAM1</i>	rs11581062	$2.5 \times 10^{-10}$	
				1q31.2	<i>C1orf106</i>	rs7522462	$1.9 \times 10^{-9}$	
				1p22.3	<i>DDAHI</i>	rs233100	$1.0 \times 10^{-6}$	
				2p21	Intergenic	rs12466022	$6.2 \times 10^{-10}$	
				2p13.3	<i>PLEK</i>	rs7595037	$5.1 \times 10^{-11}$	
				2q13	<i>MERTK</i>	rs17174870	$1.3 \times 10^{-8}$	
				2q37.1	<i>SP140</i>	rs10201872	$1.8 \times 10^{-10}$	
				3p24.1	<i>EOMES</i>	rs11129295	$1.2 \times 10^{-9}$	
				3p24.1	Intergenic	rs669607	$1.9 \times 10^{-15}$	
3q13.33	<i>CD86</i>	rs9282641	$1.0 \times 10^{-11}$					

				3q13.33	<i>TIMMDC1</i> , <i>C3orf1</i> , <i>TMEM39A</i>	rs2293370	$3 \times 10^{-9}$
				4q24	<i>MANBA</i>	rs228614	$1.4 \times 10^{-7}$
				5q33.3	<i>IL12B</i>	rs2546890	$1.2 \times 10^{-11}$
				5q31.1	<i>TCF7</i>	rs756699	$6.2 \times 10^{-7}$
				5q31.3	<i>NDFIP1</i>	rs1062158	$2.3 \times 10^{-6}$
				5q35.3	<i>RGS14</i>	rs4075958	$4.9 \times 10^{-7}$
				6q15	<i>BACH2</i>	rs12212193	$3.8 \times 10^{-8}$
				6q22.33	<i>THEMIS</i>	rs802734	$5.5 \times 10^{-9}$
				6q23.3	<i>MYB</i>	rs11154801	$1.0 \times 10^{-13}$
				6q23.3	<i>IL22RA2</i>	rs17066096	$6.0 \times 10^{-13}$
				6q25.3	<i>TAGAP</i>	rs1738074	$6.8 \times 10^{-15}$
				6q23.3	<i>AHI1</i>	rs11154801	$1.0 \times 10^{-13}$
				7q36.1	<i>ZNF767</i>	rs354033	$4.7 \times 10^{-9}$
				8q24.21	<i>MYC</i> ( <i>MIR1204</i> - <i>MIR1205</i> )	rs4410871	$7.7 \times 10^{-9}$
				8q24.21	<i>PVT1</i> ( <i>MIR1208</i> - <i>MIR3686</i> )	rs2019960	$5.2 \times 10^{-9}$
				10q23.33	<i>HHEX</i>	rs7923837	$4.9 \times 10^{-9}$
				11q23.3	<i>CXCR5</i>	rs630923	$2.8 \times 10^{-7}$
				12p13.31	<i>CLECL1</i>	rs10466829	$1.4 \times 10^{-8}$
				14q24.1	<i>ZFP36L1</i>	rs4902647	$9.3 \times 10^{-12}$
				14q24.3	<i>BATF</i>	rs2300603	$2.0 \times 10^{-8}$
				14q31.3	<i>GALC</i>	rs2119704	$2.2 \times 10^{-10}$
				18q21.32	<i>MALT1</i>	rs7238078	$2.5 \times 10^{-9}$
				19p13.3	<i>TNFSF14</i>	rs1077667	$9.4 \times 10^{-14}$
				19p13.11	<i>MPV17L2</i>	rs874628	$1.3 \times 10^{-8}$
				19q13.33	<i>DKKL1</i>	rs2303759	$5.2 \times 10^{-9}$
				20q13.2	<i>CYP24A1</i>	rs2248359	$2.5 \times 10^{-11}$
				22q11.21	<i>MAPK1</i>	rs2283792	$4.7 \times 10^{-9}$
				22q13.33	<i>SCO2</i>	rs140522	$1.7 \times 10^{-8}$
				1p36.32	<i>MMEL1</i>	rs4648356	$3.1 \times 10^{-14}$
				1p22.1	<i>EVIS</i>	rs11810217	$6.5 \times 10^{-12}$
				1p13.1	<i>CD58</i>	rs1335532	$2.0 \times 10^{-9}$

				1q31.2	<i>RGS1</i>	rs1323292	$2.3 \times 10^{-8}$	
				1q32.1	<i>KIF21B</i>	rs7522462	$9.2 \times 10^{-7}$	
				3q25.33	<i>IL12A</i>	rs2243123	$3.7 \times 10^{-6}$	
				5p13.2	<i>IL7R</i>	rs6897932	$1.7 \times 10^{-8}$	
				5p13.1	<i>PTGER4</i>	rs4613763	$6.9 \times 10^{-14}$	
				6q23.3	<i>OLIG3-TNFAIP3</i>	rs13192841	$2.3 \times 10^{-6}$	
				8q21.12	<i>IL7</i>	rs1520333	$6.1 \times 10^{-7}$	
				10p15.1	<i>IL2RA</i>	rs3118470	$2.0 \times 10^{-9}$	
				10q22.3	<i>ZMIZ1</i>	rs1250550	$6.3 \times 10^{-9}$	
				11q12.2	<i>CD6</i>	rs650258	$1.7 \times 10^{-9}$	
				12p13.31	<i>TNFRSF1A</i>	rs1800693	$1.8 \times 10^{-10}$	
				12q14.1	<i>CYP27B1</i>	rs12368653	$2.0 \times 10^{-7}$	
				16p13.13	<i>CLEC16A</i>	rs7200786	$6.3 \times 10^{-14}$	
				16q24.1	<i>IRF8</i>	rs13333054	$7.0 \times 10^{-8}$	
				17q21.2	<i>STAT3</i>	rs9891119	$4.6 \times 10^{-7}$	
				19p13.2	<i>TYK2</i>	rs8112449	$1.5 \times 10^{-6}$	
				20q13.12	<i>CD40</i>	rs2425752	$1.7 \times 10^{-6}$	
2012	Affymetrix (262 264)	296 MS patients, 801 controls (Spanish); some of previous GWAS data were included (meta-analysis)	2 785 MS patients, 2 940 controls (Europeans)	6p21	HLA	rs4959093§	$8.2 \times 10^{-34} ‡$	[14]
				5p13.1	<i>PTGER4</i>	rs9292777	$9.8 \times 10^{-9} ‡$	
				10p15.1	<i>IL2RA</i>	rs12722489	$2.1 \times 10^{-7} ‡$	
2012	Affymetrix (277 866)	197 PPMS patients, 234 controls (Italians)	379 PPMS patients, 398 controls (Europeans)	6p21	<i>HLA-DRB1, HLA-DQB</i>	rs3129934	$6.7 \times 10^{-16}$	[15]
				7q35	Intergenic	rs996343	$2.4 \times 10^{-5}$	

SNP – single nucleotide polymorphism; CNV – copy number variation.

RRMS – relapsing-remitting multiple sclerosis (MS); SPMS – secondary-progressive MS; PPMS – primary-progressive MS.

\* *P*-values obtained for combined first and second GWAS stage data are shown. For studies consisting of the replication stage only, we showed *p*-values obtained for the first stage.

# This GWAS results are not presented in the catalog.

§ 14 more SNPs in this locus are also reliably associated with MS according to this study.

‡ *p*-values obtained as a result of meta-analysis are shown.

## REFERENCES

1. <http://www.genome.gov/gwastudies/>
2. International Multiple Sclerosis Genetics Consortium, et al. 2007. Risk alleles for multiple sclerosis identified by a genomewide study. *N Engl J Med.* **357**, 851–862.
3. Wellcome Trust Case Control Consortium; Australo-Anglo-American Spondylitis Consortium (TASC), et al. 2007. Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nat Genet.* **39**, 1329-1337.
4. Comabella M., Craig D.W., Camiña-Tato M., Morcillo C., Lopez C., Navarro A., Rio J.; BiomarkerMS Study Group, Montalban X., Martin R. 2008. Identification of a novel risk locus for multiple sclerosis at 13q31.3 by a pooled genome-wide scan of 500,000 single nucleotide polymorphisms. *PLoS One.* **3**, e3490.
5. Aulchenko Y.S., Hoppenbrouwers I.A., Ramagopalan S.V., Broer L., Jafari N., Hillert J., Link J., Lundström W., Greiner E., Dessa Sadovnick A., Goossens D., Van Broeckhoven C., Del-Favero J., Ebers G.C., Oostra B.A., van Duijn C.M., Hintzen R.Q. 2008. Genetic variation in the KIF1B locus influences susceptibility to multiple sclerosis. *Nat Genet.* **40**, 1402-1403.
6. Baranzini S.E., Wang J., Gibson R.A., Galwey N., Naegelin Y., Barkhof F., Radue E.W., Lindberg R.L., Uitdehaag B.M., Johnson M.R., Angelakopoulou A., Hall L., Richardson J.C., Prinjha R.K., Gass A., Geurts J.J., Kragt J., Sombekke M., Vrenken H., Qualley P., Lincoln R.R., Gomez R., Caillier S.J., George M.F., Mousavi H., Guerrero R., Okuda D.T., Cree B.A., Green A.J., Waubant E., Goodin D.S., Pelletier D., Matthews P.M., Hauser S.L., Kappos L., Polman C.H., Oksenberg J.R. 2009. Genome-wide association analysis of susceptibility and clinical phenotype in multiple sclerosis. *Hum Mol Genet.* **18**, 767-778.
7. De Jager P.L., Jia X., Wang J., de Bakker P.I., Ottoboni L., Aggarwal N.T., Piccio L., Raychaudhuri S., Tran D., Aubin C., Briskin R., Romano S.; International MS Genetics Consortium, Baranzini S.E., McCauley J.L., Pericak-Vance M.A., Haines J.L., Gibson R.A., Naegelin Y., Uitdehaag B., Matthews P.M., Kappos L., Polman C., McArdle W.L., Strachan D.P., Evans D., Cross A.H., Daly M.J., Compston A., Sawcer S.J., Weiner H.L., Hauser S.L., Hafler D.A., Oksenberg J.R. 2009. Meta-analysis of genome scans and replication identify CD6, IRF8 and TNFRSF1A as new multiple sclerosis susceptibility loci. *Nat Genet.* **41**, 776-782.
8. Australia and New Zealand Multiple Sclerosis Genetics Consortium (ANZgene). 2009. Genome-wide association study identifies new multiple sclerosis susceptibility loci on chromosomes 12 and 20. *Nat Genet.* **41**, 824-828.
9. Jakkula E., Leppä V., Sulonen A.M., Varilo T., Kallio S., Kempainen A., Purcell S., Koivisto K., Tienari P., Sumelahti M.L., Elovaara I., Pirttilä T., Reunanen M., Aromaa A., Oturai A.B., Søndergaard H.B., Harbo H.F., Mero I.L., Gabriel S.B., Mirel D.B., Hauser S.L.,

- Kappos L., Polman C., De Jager P.L., Hafler D.A., Daly M.J., Palotie A., Saarela J., Peltonen L. 2010. Genome-wide association study in a high-risk isolate for multiple sclerosis reveals associated variants in STAT3 gene. *Am J Hum Genet.* **86**, 285-291.
10. Sanna S., Pitzalis M., Zoledziewska M., Zara I., Sidore C., Murru R., Whalen M.B., Busonero F., Maschio A., Costa G., Melis M.C., Deidda F., Poddie F., Morelli L., Farina G., Li Y., Dei M., Lai S., Mulas A., Cuccuru G., Porcu E., Liang L., Zavattari P., Moi L., Deriu E., Urru M.F., Bajorek M., Satta M.A., Cocco E., Ferrigno P., Sotgiu S., Pugliatti M., Traccis S., Angius A., Melis M., Rosati G., Abecasis G.R., Uda M., Marrosu M.G., Schlessinger D., Cucca F. 2010. Variants within the immunoregulatory CBLB gene are associated with multiple sclerosis. *Nat Genet.* **42**, 495-497.
11. Nischwitz S., Cepok S., Kroner A., Wolf C., Knop M., Müller-Sarnowski F., Pfister H., Roeske D., Rieckmann P., Hemmer B., Ising M., Uhr M., Bettecken T., Holsboer F., Müller-Myhsok B., Weber F. 2010. Evidence for VAV2 and ZNF433 as susceptibility genes for multiple sclerosis. *J Neuroimmunol.* **227**, 162-166.
12. Patsopoulos N.A.; Bayer Pharma MS Genetics Working Group; Steering Committees of Studies Evaluating IFN $\beta$ -1b and a CCR1-Antagonist; ANZgene Consortium; GeneMSA; International Multiple Sclerosis Genetics Consortium, Esposito F., Reischl J., Lehr S., Bauer D., Heubach J., Sandbrink R., Pohl C., Edan G., Kappos L., Miller D., Montalbán J., Polman C.H., Freedman M.S., Hartung H.P., Arnason B.G., Comi G., Cook S., Filippi M., Goodin D.S., Jeffery D., O'Connor P., Ebers G.C., Langdon D., Reder A.T., Traboulsee A., Zipp F., Schimrigk S., Hillert J., Bahlo M., Booth D.R., Broadley S., Brown M.A., Browning B.L., Browning S.R., Butzkueven H., Carroll W.M., Chapman C., Foote S.J., Griffiths L., Kermodé A.G., Kilpatrick T.J., Lechner-Scott J., Marriott M., Mason D., Moscato P., Heard R.N., Pender M.P., Perreau V.M., Perera D., Rubio J.P., Scott R.J., Slee M., Stankovich J., Stewart G.J., Taylor B.V., Tubridy N., Willoughby E., Wiley J., Matthews P., Boneschi F.M., Compston A., Haines J., Hauser S.L., McCauley J., Ivinson A., Oksenberg J.R., Pericak-Vance M., Sawcer S.J., De Jager P.L., Hafler D.A., de Bakker P.I. 2011. Genome-wide meta-analysis identifies novel multiple sclerosis susceptibility loci. *Ann Neurol.* **70**, 897-912.
13. International Multiple Sclerosis Genetics Consortium; Wellcome Trust Case Control Consortium 2. 2011. Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. *Nature.* **476**, 214-219.
14. Matesanz F., González-Pérez A., Lucas M., Sanna S., Gayán J., Urcelay E., Zara I., Pitzalis M., Cavanillas M.L., Arroyo R., Zoledziewska M., Marrosu M., Fernández O., Leyva L., Alcina A., Fedetz M., Moreno-Rey C., Velasco J., Real L.M., Ruiz-Peña J.L., Cucca F., Ruiz A.,



Izquierdo G. 2012. Genome-wide association study of multiple sclerosis confirms a novel locus at 5p13.1. *PLoS One*. **7**, e36140.

15. Martinelli-Boneschi F., Esposito F., Brambilla P., Lindström E., Lavorgna G., Stankovich J., Rodegher M., Capra R., Ghezzi A., Coniglio G., Colombo B., Sorosina M., Martinelli V., Booth D., Bang Oturai A., Stewart G., Harbo H.F., Kilpatrick T.J., Hillert J., Rubio J.P., Abderrahim H., Wojcik J., Comi G. 2012. A genome-wide association study in progressive multiple sclerosis. *Mult Scler*. **18**, 1384-1394.

Table S2. New loci associated with MS, according to study on the ImmunoChip platform, Illumina.\*

Chromosome	Locus	Gene(s)	SNP	<i>p</i> -value
1	1p36.31	<i>PLEKHG5</i>	rs3007421	$4.7 \times 10^{-10}$
	1p22.3	<i>BCL10</i>	rs12087340	$1.1 \times 10^{-20}$
		<i>DDAH1</i>	rs11587876	$4.4 \times 10^{-9}$
	1p12	<i>PHGDH</i>	rs666930	$6.0 \times 10^{-12}$
	1q21-q22	<i>FCRL1</i>	rs2050568	$1.5 \times 10^{-10}$
1q23.1-q24.1	<i>SLAMF7</i>	rs35967351	$4.4 \times 10^{-11}$	
2	2p23.3	<i>CENPO</i>	rs4665719	$3.1 \times 10^{-9}$
	2p16.1	<i>FLJ16341</i>	rs842639	$2.0 \times 10^{-14}$
	2q32.2-q32.3	<i>STAT4</i>	rs9967792	$3.5 \times 10^{-12}$
3	3p24.3	-	rs11719975	$1.1 \times 10^{-8}$
	3p24	<i>CCR4</i>	rs4679081	$2.2 \times 10^{-9}$
	3p14.1	<i>FOXP1</i>	rs9828629	$1.9 \times 10^{-10}$
4	4q24	<i>TET2</i>	rs2726518	$3.9 \times 10^{-8}$
5	5q31.1	<i>TCF7</i>	rs756699	$8.8 \times 10^{-11}$
	5q31.3	<i>NDFIP1</i>	NA	$3.6 \times 10^{-9}$
	5q35.3	<i>RGS14</i>	rs4976646	$4.4 \times 10^{-18}$
6	6p23	-	rs17119	$1.0 \times 10^{-10}$
	6p21.31	<i>PXT1</i>	rs941816	$3.9 \times 10^{-12}$
7	7p22	<i>CARD11</i>	rs1843938	$1.2 \times 10^{-10}$
	7p15.2	-	rs706015	$1.1 \times 10^{-9}$
	7p15.2-p15.1	<i>JAZF1</i>	rs917116	$3.3 \times 10^{-9}$
	7p14.1	<i>ELMO1</i>	rs60600003	$6.0 \times 10^{-14}$
	7p12.2	<i>IKZF1</i>	rs201847125	$1.2 \times 10^{-11}$
8	H.n.	-	rs2456449	$1.8 \times 10^{-9}$
10	10p11.22	-	rs793108	$6.1 \times 10^{-12}$
	10q22.2	<i>C10orf55</i>	rs2688608	$4.6 \times 10^{-8}$
11	11p11.2	<i>AGBL2</i>	rs7120737	$1.0 \times 10^{-9}$
	11q13	<i>PRDX5</i>	rs694739	$2.0 \times 10^{-9}$
	11q23.3	<i>CXCR5</i>	rs9736016	$3.0 \times 10^{-15}$
12	12p13	<i>LTBR</i>	rs12296430	$7.2 \times 10^{-14}$
13	13q32.3	<i>MIR548AN-TM9SF2</i>	rs4772201	$1.3 \times 10^{-10}$
14	14q32.32	<i>TRAF3</i>	rs12148050	$5.1 \times 10^{-13}$
15	15q25.1	<i>CTSH</i>	rs59772922	$1.2 \times 10^{-8}$
	15q26.1	<i>IQGAP1</i>	rs8042861	$2.2 \times 10^{-9}$
16	16p13.13	<i>RMI2</i>	rs6498184	$7.4 \times 10^{-18}$
	16p11.2	<i>MAPK3</i>	rs7204270	$1.6 \times 10^{-11}$
	16q22.1	<i>CDH3</i>	rs1886700	$1.3 \times 10^{-8}$
	16q23.3-q24.1	<i>WWOX</i>	rs12149527	$3.3 \times 10^{-11}$
	16q22-q23	<i>MAF</i>	rs7196953	$1.0 \times 10^{-10}$
17	17q21	<i>IKZF3</i>	rs12946510	$2.9 \times 10^{-9}$
		<i>NPEPPS</i>	rs4794058	$1.0 \times 10^{-13}$
19	19p13.1	<i>SLC44A2</i>	rs2288904	$1.6 \times 10^{-11}$
	19p13.11	<i>EPS15L1</i>	rs1870071	$2.0 \times 10^{-15}$
20	20q13.13	<i>SLC9A8</i>	rs17785991	$4.2 \times 10^{-8}$
	20q13.33	<i>SLC2A4RG</i>	rs2256814	$3.5 \times 10^{-9}$

\* reference: International Multiple Sclerosis Genetics Consortium (IMSGC), Beecham A.H., et al. 2013. Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. *Nat Genet.* **45**, 1353-1360.

Discovery dataset consisted of independent samples of 14 498 MS patients and 24 091 controls of European origin. Replication dataset included previous GWAS data (14 802 MS patients and 26 703 controls).