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CORRECTION

Correction: Pharmacogenomics of clinical response to Natalizumab in multiple sclerosis: a genome-wide multi-centric association study

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In the original version of this article, author's name Filippo Martinelli Boneschi was incorrectly written as Filippo Giovanni Martinelli Boneschi.

In Table 2, first two columns were missing. The Table 2 which previously appeared as

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Table 2 List of top-associated variants after meta-analysis. The list is obtained upon a clumping procedure (see *Methods* for details), filtered at $p < 5 \times 10^{-5}$. The effect allele is the minor allele

Position	Minor allele	Major allele	MAF	P	OR	SE	I^2	Gene	Genomic context	Distance to gene
187,410,850	T	C	0.268	1.328E−06	0.582	0.112	0	*F11-AS1*	ncRNA_intronic	
68,071,570	T	C	0.421	1.678E−06	1.538	0.090	0	*PIGH; ARG2*	Intergenic	Dist = 4552; Dist = 15,067
111,037,829	T	A	0.251	2.793E−06	0.596	0.111	13	*KLF4; ACTL7B*	Intergenic	Dist = 785,779; Dist = 579,040
20,863,249	G	A	0.057	4.804E−06	2.122	0.165	0	*GJB6; CRYL1*	Intergenic	Dist = 56,715; Dist = 114,557
98,275,102	C	G	0.429	6.938E−06	0.650	0.096	34	*LOC101927310; LINC00923*	Intergenic	Dist = 171,174; Dist = 10,744
47,775,385	A	G	0.230	1.187E−05	1.561	0.102	0	*SEMA6D*	Intronic	
21,728,917	A	G	0.142	1.191E−05	0.510	0.154	0	*ZNF385D*	Intronic	
187,402,360	A	G	0.480	1.233E−05	1.496	0.092	0	*F11-AS1*	ncRNA_intronic	
115,392,100	A	G	0.347	1.259E−05	1.476	0.089	0	*GAP43*	Intronic	
12,783,519	T	C	0.075	1.325E−05	1.934	0.151	0	*LINC00681; TRMT9B*	Intergenic	Dist = 107,719; Dist = 19,663
43,181,587	T	C	0.080	1.362E−05	1.918	0.150	0	*A4GALT; ARFGAP3*	Intergenic	Dist = 64,280; Dist = 10,922
79,303,163	G	A	0.430	1.475E−05	1.469	0.089	0	*WWOX; MAF*	Intergenic	Dist = 56,599; Dist = 324,572
98,347,870	C	G	0.429	1.494E−05	0.676	0.091	57	*LINC00923*	ncRNA_intronic	
27,204,531	C	T	0.095	2.087E−05	1.775	0.135	42	*ABI1; FAM238C*	Intergenic	Dist = 54,515; Dist = 15,604
47,746,678	C	G	0.075	2.692E−05	1.839	0.145	29	*STIL*	Exonic	
113,293,608	G	A	0.411	2.744E−05	1.461	0.090	0	*TUBGCP3; ATP11AUN*	Intergenic	Dist = 51,109; Dist = 7750
606,173	C	A	0.143	2.862E−05	1.646	0.119	0	*B4GALNT3*	Intronic	
83,766,280	A	C	0.114	2.909E−05	1.739	0.132	48	*DLG2*	Intronic	
236,647,736	T	C	0.233	2.939E−05	1.495	0.096	0	*EDARADD*	UTR3	NM_145861:c.*1787C>T; NM_080738:c.*1787C>T
93,450,212	A	G	0.295	3.023E−05	1.471	0.093	0	*RUNX1T1; LOC102724710*	Intergenic	Dist = 334,599; Dist = 127,459
4,314,917	A	G	0.220	3.087E−05	1.523	0.101	0	*CSMD1*	Intronic	
81,279,746	A	G	0.271	3.116E−05	1.479	0.094	6.4	*SPRY2; LINC00377*	Intergenic	Dist = 364,485; Dist = 312,780
111,023,899	T	C	0.404	3.369E−05	1.441	0.088	0	*KLF4; ACTL7B*	Intergenic	Dist = 771,849; Dist = 592,970
189,243,943	T	C	0.413	3.424E−05	1.433	0.087	0	*TPRG1; TP63*	Intergenic	Dist = 200,850; Dist = 70,592
114,813,313	C	T	0.267	3.459E−05	1.483	0.095	0	*TBX5*	Intronic	
110,446,839	G	A	0.413	3.508E−05	1.433	0.087	0	*IRS2; LINC00396*	Intergenic	Dist = 7909; Dist = 258,793
177,987,660	G	A	0.137	3.639E−05	1.617	0.116	0	*CRYZL2P*	ncRNA_intronic	
31,271,788	A	G	0.072	3.733E−05	1.845	0.148	60	*OVOS2*	ncRNA_intronic	
206,468,850	T	G	0.419	4.007E−05	1.433	0.088	0	*PARD3B*	Intronic	
54,692,961	G	A	0.116	4.025E−05	1.652	0.122	6.9	*TINAG; FAM83B*	Intergenic	Dist = 438,021; Dist = 18,608
141,938,633	C	T	0.069	4.217E−05	1.890	0.155	74	*MGAM2; MOXD2P*	Intergenic	Dist = 16,509; Dist = 1923

Position	Minor allele	Major allele	MAF	P	OR	SE	I^2	Gene	Genomic context	Distance to gene
81,959,114	T	C	0.499	4.222E−05	0.697	0.088	5.8	*ATP6AP1L; MIR3977*	Intergenic	Dist = 343,363; Dist = 176,860
158,058,545	T	C	0.436	4.257E−05	1.455	0.092	0	*ZDHHC14*	Intronic	
180,648,923	C	T	0.480	4.571E−05	0.699	0.088	0	*LINC01098; LINC00290*	Intergenic	Dist = 1,737,019; Dist = 1,336,320
83,182,354	A	G	0.299	4.605E−05	1.458	0.093	0	*DLG2*	Intronic	
10,732,844	G	A	0.050	4.841E−05	2.053	0.177	53	*TEKT5*	Intronic	
130,499,623	G	A	0.096	4.929E−05	1.749	0.138	42	*LINC01163; LINC02667*	Intergenic	Dist = 383,633; Dist = 211,474
156,675,608	A	C	0.135	4.934E−05	1.642	0.122	0	*GUCY1A1; GUCY1B1*	Intergenic	Dist = 17,399; Dist = 4565
50,679,081	T	G	0.372	4.966E−05	1.448	0.091	0	*DEFB112; TFAP2D*	Intergenic	Dist = 661,439; Dist = 2158

For each variant, the gene harboring it or nearest gene(s) are reported, together with its genomic context and distance in base-pairs from the nearest genes, as of ANNOVAR annotation

Abbreviations: MAF (Minor Allele Frequency), P (p value from fixed-effect meta-analysis), OR (odds ratio from fixed-effects meta-analysis), SE (standard error), I^2 (heterogeneity index)

but Table 2 should have appeared as shown below.

Table 2 List of top associated variants after meta-analysis

SNP	Chromosome	Position	Minor allele	Major allele	MAF	P	OR	SE	I^2	Gene	Genomic context	Distance to gene
rs11132400	4	187410850	T	C	0.268	1.328E−06	0.582	0.112	0	*F11-AS1*	ncRNA_intronic	
rs12885261	14	68071570	T	C	0.421	1.678E−06	1.538	0.090	0	*PIGH; ARG2*	Intergenic	dist = 4552; dist = 15,067
rs1323374	9	111037829	T	A	0.251	2.793E−06	0.596	0.111	13	*KLF4; ACTL7B*	Intergenic	dist = 785,779; dist = 579,040
rs61166479	13	20863249	G	A	0.057	4.804E−06	2.122	0.165	0	*GJB6; CRYL1*	Intergenic	dist = 56,715; dist = 114,557
rs1032954	15	98275102	C	G	0.429	6.938E−06	0.650	0.096	34	*LOC101927310; LINC00923*	Intergenic	dist = 171,174; dist = 10,744
rs75772884	15	47775385	A	G	0.230	1.187E−05	1.561	0.102	0	*SEMA6D*	Intronic	
rs34736466	3	21728917	A	G	0.142	1.191E−05	0.510	0.154	0	*ZNF385D*	Intronic	
rs12649886	4	187402360	A	G	0.480	1.233E−05	1.496	0.092	0	*F11-AS1*	ncRNA_intronic	
rs13073759	3	115392100	A	G	0.347	1.259E−05	1.476	0.089	0	*GAP43*	Intronic	
rs2977141	8	12783519	T	C	0.075	1.325E−05	1.934	0.151	0	*LINC00681; TRMT9B*	Intergenic	dist = 107,719; dist = 19,663
rs7286822	22	43181587	T	C	0.080	1.362E−05	1.918	0.150	0	*A4GALT; ARFGAP3*	Intergenic	dist = 64,280; dist = 10,922
rs9922330	16	79303163	G	A	0.430	1.475E−05	1.469	0.089	0	*WWOX; MAF*	Intergenic	dist = 56,599; dist = 324,572
rs72752604	15	98347870	C	G	0.429	1.494E−05	0.676	0.091	57	*LINC00923*	ncRNA_intronic	

Table 2 (continued)

SNP	Chromosome	Position	Minor allele	Major allele	MAF	P	OR	SE	I^2	Gene	Genomic context	Distance to gene
rs1815323	10	27204531	C	T	0.095	2.087E−05	1.775	0.135	42	*ABI1; FAM238C*	Intergenic	dist = 54,515; dist = 15,604
rs10789505	1	47746678	C	G	0.075	2.692E−05	1.839	0.145	29	*STIL*	Exonic	
rs9577824	13	113293608	G	A	0.411	2.744E−05	1.461	0.090	0	*TUBGCP3; ATP11AUN*	Intergenic	dist = 51,109; dist = 7750
rs2159600	12	606173	C	A	0.143	2.862E−05	1.646	0.119	0	*B4GALNT3*	Intronic	
rs12806160	11	83766280	A	C	0.114	2.909E−05	1.739	0.132	48	*DLG2*	Intronic	
rs6428955	1	236647736	T	C	0.233	2.939E−05	1.495	0.096	0	*EDARADD*	UTR3	NM_145861:c.*1787C > T; NM_080738:c.*1787C > T
rs1072934	8	93450212	A	G	0.295	3.023E−05	1.471	0.093	0	*RUNX1T1; LOC102724710*	Intergenic	dist = 334,599; dist = 127,459
rs1217680	8	4314917	A	G	0.220	3.087E−05	1.523	0.101	0	*CSMD1*	Intronic	
rs12428095	13	81279746	A	G	0.271	3.116E−05	1.479	0.094	6.4	*SPRY2; LINC00377*	Intergenic	dist = 364,485; dist = 312,780
rs10739255	9	111023899	T	C	0.404	3.369E−05	1.441	0.088	0	*KLF4; ACTL7B*	Intergenic	dist = 771,849; dist = 592,970
rs6803844	3	189243943	T	C	0.413	3.424E−05	1.433	0.087	0	*TPRG1; TP63*	Intergenic	dist = 200,850; dist = 70,592
rs7960396	12	114813313	C	T	0.267	3.459E−05	1.483	0.095	0	*TBX5*	Intronic	
rs1414319	13	110446839	G	A	0.413	3.508E−05	1.433	0.087	0	*IRS2; LINC00396*	Intergenic	dist = 7909; dist = 258,793
rs7537568	1	177987660	G	A	0.137	3.639E−05	1.617	0.116	0	*CRYZL2P*	ncRNA_intronic	
rs112417083	12	31271788	A	G	0.072	3.733E−05	1.845	0.148	60	*OVOS2*	ncRNA_intronic	
rs13031793	2	206468850	T	G	0.419	4.007E−05	1.433	0.088	0	*PARD3B*	Intronic	
rs9475026	6	54692961	G	A	0.116	4.025E−05	1.652	0.122	6.9	*TINAG; FAM83B*	Intergenic	dist = 438,021; dist = 18,608
rs59801030	7	141938633	C	T	0.069	4.217E−05	1.890	0.155	74	*MGAM2; MOXD2P*	Intergenic	dist = 16,509; dist = 1923
rs10040233	5	81959114	T	C	0.499	4.222E−05	0.697	0.088	5.8	*ATP6AP1L; MIR3977*	Intergenic	dist = 343,363; dist = 176,860
rs618823	6	158058545	T	C	0.436	4.257E−05	1.455	0.092	0	*ZDHHC14*	Intronic	
rs4444875	4	180648923	C	T	0.480	4.571E−05	0.699	0.088	0	*LINC01098; LINC00290*	Intergenic	dist = 1,737,019; dist = 1,336,320
rs2068076	11	83182354	A	G	0.299	4.605E−05	1.458	0.093	0	*DLG2*	Intronic	
rs76674464	16	10732844	G	A	0.050	4.841E−05	2.053	0.177	53	*TEKT5*	Intronic	
rs12265034	10	130499623	G	A	0.096	4.929E−05	1.749	0.138	42	*LINC01163; LINC02667*	Intergenic	dist = 383,633; dist = 211,474
rs6838876	4	156675608	A	C	0.135	4.934E−05	1.642	0.122	0	*GUCY1A1; GUCY1B1*	Intergenic	dist = 17,399; dist = 4565
rs1923523	6	50679081	T	G	0.372	4.966E−05	1.448	0.091	0	*DEFB112; TFAP2D*	Intergenic	dist = 661,439; dist = 2158

The list is obtained upon a clumping procedure (see Methods for details), filtered at $p < 5 \times 10^{-5}$. The effect allele is the minor allele

For each variant, the gene harboring it or nearest gene(s) are reported, together with its genomic context and distance in base-pairs from the nearest genes, as of ANNOVAR annotation

MAF (Minor Allele Frequency), P (p-value from fixed-effect meta-analysis), OR (odds ratio from fixed-effects meta-analysis), SE (standard error), I^2 (heterogeneity index)