Supplementary data for "No evidence for shared genetic basis of common variants in multiple sclerosis and amyotrophic lateral sclerosis"

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Supplementary Table 1. Polygenic risk model excluding the HLA region

A. Polygenic score based on MS data in ALS

Model	P-value	# SNPs	Nagelkerke r^2 corrected for baseline[a]
<5E-8	0.341	4	9.4E-05
<5E-7	0.446	8	6.0E-05
<5E-6	0.481	23	5.2E-05
<5E-5	0.512	87	4.5E-05
<5E-4	0.727	518	1.3E-05
<5E-3	0.405	3314	7.2E-05
<0.05	0.623	22116	2.5E-05
<0.1	0.732	29682	1.2E-05
<0.2	0.928	66084	9.0E-07
<0.3	0.652	88914	2.1E-05
<0.4	0.380	108424	8.0E-05
<0.5	0.338	125353	9.5E-05

[a]Baseline: PC1-3, dummy coded cohorts

A. Polygenic score based on ALS data in MS

Model	P-value	# SNPs	Nagelkerke r^2 corrected for baseline[b]
<5E-8	0.843	3	4.5E-06
<5E-7	0.785	4	8.4E-06
<5E-6	0.500	7	5.2E-05
<5E-5	0.452	49	6.4E-05
<5E-4	0.882	388	2.5E-06
<5E-3	0.597	3066	3.2E-05
<0.05	0.029	22274	5.4E-04
<0.1	0.050	38850	4.4E-04
<0.2	0.038	66630	4.9E-04
<0.3	0.052	89464	4.3E-04
<0.4	0.041	108697	4.7E-04
<0.5	0.061	125179	4.0E-04

[b]Baseline: PC1-5, dummy coded cohorts

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