CORRECTION

Correction to: A multi-step genomic approach prioritized TBKBP1 gene as relevant for multiple sclerosis susceptibility

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The original version of this article unfortunately contained a mistake. The table 2 caption should read as

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Table 2 Association results in the replication sample. For each SNP, the association data in the replication cohort and results from the meta-analyses between discovery

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and replication cohorts (including and not including the NonIT-EUR cohort) are reported. Results for the genome-wide Italian approach are reported in the upper panel (A), while results for the approaches including the NonIT-EUR are reported in panel B (discovery sample derived from ITA_{GWAS} alone) and C (SNPs identified through the meta-analysis between ITA_{GWAS} and ITA_{iChip}). A1: reference allele (the same as defined in table 1); OR: odds ratio; L95: lower-bound of 95%-confidence interval; U95: upper bound of 95%-confidence interval; P: P-value of association; I^2: heterogeneity index. The SNPs with an association beyond the multiple testing correction (Bonferroni threshold of P-value: 1.7×10^{-3}, 3.6×10^{-3}, 6.25×10^{-3} respectively for A, B and C) are highlighted in bold. No significant association was found in the replication cohort for SNPs selected through the Italian genome-wide approach.

The original article has been corrected.