

Author Correction: A multi-ancestry genetic study of pain intensity in 598,339 veterans













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 Check for updates

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In the version of the article initially published, the pipeline for the cross-ancestry meta-analysis did not accurately code some SNPs such that they were not combined despite being the same polymorphism. To fix this, we correctly annotated the rsIDs for the summary statistics from each ancestry and meta-analyzed them based on the unique rsID for each polymorphism. We also corrected all downstream analyses that used the cross-ancestry meta-analysis data. Table 1 is a summary of the major changes which have been made to the main text and Fig. 1.

Item	Previous analyses (n)	Current analyses (n)
Autosomal SNPs included in meta-analyses	16,254,110	15,895,579
Genome-wide significant variants	4,416	4,364
Linkage disequilibrium clumped index variants	158	162
Independent loci	126	125
New pain loci	69	66
Exonic variants	5	4
Pleiotropic loci with immune traits	25	23
Gene-set analyses	Catecholamine uptake and startle response	Dopaminergic synaptic transmission and aryl hydrocarbon receptor complex

None of these changes changed any of our downstream analyses. These corrections have been made to the HTML and PDF versions of the article.

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A complete list of members and their affiliations is provided in the Supplementary Information.

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