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Author Correction: Positive selection acts on regulatory genetic variants in populations of European ancestry that affect ALDH2 gene expression

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Correction to: *Scientific Reports* <https://doi.org/10.1038/s41598-022-08588-0>, published online 16 March 2022

The original version of this Article contained a repeated error, where gene name “SH2B3” was incorrectly given as “SH2B2”. As a result of this error, in the Introduction,

“This region, approximately 0.6 Mbp in size (according to the human reference genome), encompasses in addition to *ALDH2* the genes *CUX2*, *FAM109A*, *SH2B2*, *ATXN2*, *BRAP*, *ACAD10* and *MAPKAPK5*, as well as the uncharacterized transcript ENST00000546840.3 (UniProt F8VP50—Aldedh domain-containing protein), which partially overlaps with the genes *ACAD10* and *ALDH2*. High F_{ST} values at linked sites at the *ALDH2* locus point to some form of selection for this genomic region³⁶.”

now reads:

“This region, approximately 0.6 Mbp in size (according to the human reference genome), encompasses in addition to *ALDH2* the genes *CUX2*, *FAM109A*, *SH2B3*, *ATXN2*, *BRAP*, *ACAD10* and *MAPKAPK5*, as well as the uncharacterized transcript ENST00000546840.3 (UniProt F8VP50—Aldedh domain-containing protein), which partially overlaps with the genes *ACAD10* and *ALDH2*. High F_{ST} values at linked sites at the *ALDH2* locus point to some form of selection for this genomic region³⁶.”

And, in the Results section, under the subheading ‘Positive selection acts on regulatory variants of *ALDH2*’,

“We also obtained *cis*-eQTLs (1970 in total) for the other protein-coding genes located in this genomic region (*CUX2*, *FAM109A*, *SH2B2*, *ATXN2*, *BRAP*, *ACAD10*, *MAPKAPK5*) (Supplementary Table 3).”

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“We also obtained *cis*-eQTLs (1970 in total) for the other protein-coding genes located in this genomic region (*CUX2*, *FAM109A*, *SH2B3*, *ATXN2*, *BRAP*, *ACAD10*, *MAPKAPK5*) (Supplementary Table 3).”

The original Article has been corrected.

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