

CORRECTION

Correction: A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease

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In this article, the genetic variant *PNPLA3* p.I148M is misreported in several sentences as *PNPLA3* p.I48M. The variant *TM6SF2* p.E167K is misreported in one sentence as *TM6SF2* p.E40K.

In the Introduction, the third sentence of the second paragraph:

For example, *PNPLA3* p.I48M and *TM6SF2* p.E40K, although initially identified as associated with hepatic steatosis [9,10], strongly predispose to the development of alcoholic cirrhosis [11], non-alcoholic cirrhosis [12,13] and hepatitis C-related cirrhosis [14,15].

should read:

For example, *PNPLA3* p.I1148M and *TM6SF2* p.E167K, although initially identified as associated with hepatic steatosis [9,10], strongly predispose to the development of alcoholic cirrhosis [11], non-alcoholic cirrhosis [12,13] and hepatitis C-related cirrhosis [14,15].

In the Results, the fourth sentence of the first paragraph:

We examined the association of all-cause cirrhosis with six genetic variants previously reported to be associated with alcoholic or non-alcoholic cirrhosis: *PNPLA3* I48M, *TM6SF2* E167K, *MBOAT7* rs641738, *HSD17B13* rs72613567, *HFE* C282Y and *SERPINA1* E366K [11,16,18,19].

should read:

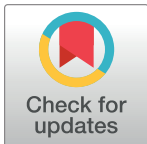
We examined the association of all-cause cirrhosis with six genetic variants previously reported to be associated with alcoholic or non-alcoholic cirrhosis: *PNPLA3* I148M, *TM6SF2* E167K, *MBOAT7* rs641738, *HSD17B13* rs72613567, *HFE* C282Y and *SERPINA1* E366K [11,16,18,19].

In the Methods, the first sentence of the first paragraph:

To examine whether known alcoholic and non-alcoholic cirrhosis variants associate with all-cause cirrhosis, we tested the association of six known cirrhosis variants (*PNPLA3* I48M, *TM6SF2* E167K, *MBOAT7* rs641738, *HSD17B13* rs72613567, *HFE* C282Y and *SERPINA1* E366K [11,16,18,19]) with all-cause cirrhosis in UK Biobank (hospitalization or death due to ICD codes K70.2, K70.3, K70.4, K74.0, K74.1, K74.2, K74.6, K76.6, or I85).

should read:

To examine whether known alcoholic and non-alcoholic cirrhosis variants associate with all-cause cirrhosis, we tested the association of six known cirrhosis variants (*PNPLA3* I148M,



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Table 1. DNA sequence variants associated with all-cause cirrhosis in the discovery analysis.

Model	Variant	CHR	EA	EAF	Gene	Annotation	OR	p-value
Additive	rs738409	22	G	26%	<i>PNPLA3</i>	Missense: p.I148M	1.47	2.2×10^{-67}
Additive	rs58542926	19	T	7%	<i>TM6SF2</i>	Missense: p.E167K	1.42	9.7×10^{-24}
Recessive	rs1800562	6	A	3%	<i>HFE</i>	Missense: p.C282Y	3.2	1.3×10^{-14}
Additive	rs72613567	4	TA	22%	<i>HSD17B13</i>	Splice Variant	0.82	4.5×10^{-8}
Additive	rs2642438	1	A	25%	<i>MARC1</i>	Missense: p.A165T	0.87	8.7×10^{-7}

CHR: chromosome, EA: effect allele, EAF: effect allele frequency

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TM6SF2 E167K, *MBOAT7* rs641738, *HSD17B13* rs72613567, *HFE* C282Y and *SERPINA1* E366K [11,16,18,19]) with all-cause cirrhosis in UK Biobank (hospitalization or death due to ICD codes K70.2, K70.3, K70.4, K74.0, K74.1, K74.2, K74.6, K76.6, or I85).

There is an error in [Table 1](#). The name p.I48M appears instead of p.I148M.

There is an error in the label of [S1 Fig](#). The name p.I48M appears instead of p.I148M. The authors have provided a corrected version here.

Supporting information

S1 Fig. Risk of alcoholic, non-alcoholic and hepatitis C cirrhosis associated with *PNPLA3* I148M, *TM6SF2* E167K and *HSD17B13*.

(PDF)

Reference

1. Emdin CA, Haas ME, Khera AV, Aragam K, Chaffin M, Klarin D, et al. (2020) A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. *PLoS Genet* 16(4): e1008629. <https://doi.org/10.1371/journal.pgen.1008629> PMID: 32282858