



# Author Correction: Integrative genetic analysis illuminates ALS heritability and identifies risk genes

Correction to: *Nature Communications*  
<https://doi.org/10.1038/s41467-022-35724-1>,  
 published online 20 January 2023

<https://doi.org/10.1038/s41467-023-43710-4>

Published online: 04 December 2023



Salim Megat , Natalia Mora , Jason Sanogo, Olga Roman, Alberto Catanese , Najwa Ouali Alami, Axel Freischmidt, Xhuljana Mingaj, Hortense De Calbiac, François Muratet, Sylvie Dirrig-Grosch, Stéphane Dieterle, Nick Van Bakel, Kathrin Müller, Kirsten Sieverding, Jochen Weishaupt, Peter Munch Andersen , Markus Weber , Christoph Neuwirth , Markus Margelisch, Andreas Sommacal, Kristel R. Van Eijk, Jan H. Veldink , Project Mine Als Sequencing Consortium\*, Géraldine Lautrette, Philippe Couratier, Agnès Camuzat, Isabelle Le Ber, Maurizio Grassano, Adriano Chio, Tobias Boeckers , Albert C. Ludolph, Francesco Roselli, Deniz Yilmazer-Hanke, Stéphanie Millecamps , Edor Kabashi, Erik Storkebaum , Chantal Sellier & Luc Dupuis

The original version of this article contained errors in Table 2 in the variant\_location, cDNA\_change, protein\_change and dbSNPID columns. The correct version of Table 2 is:

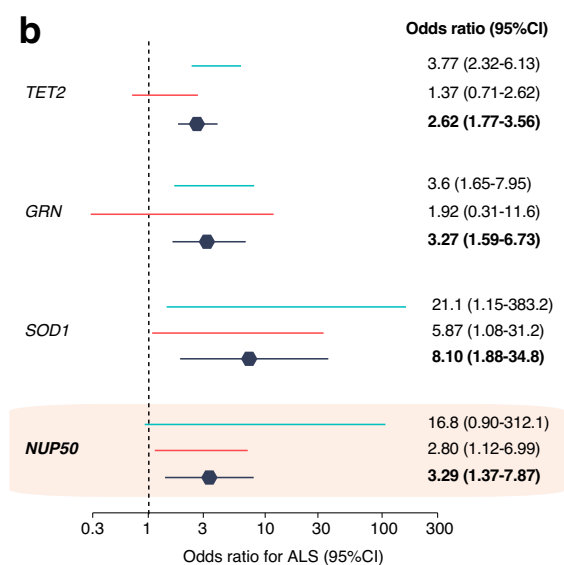
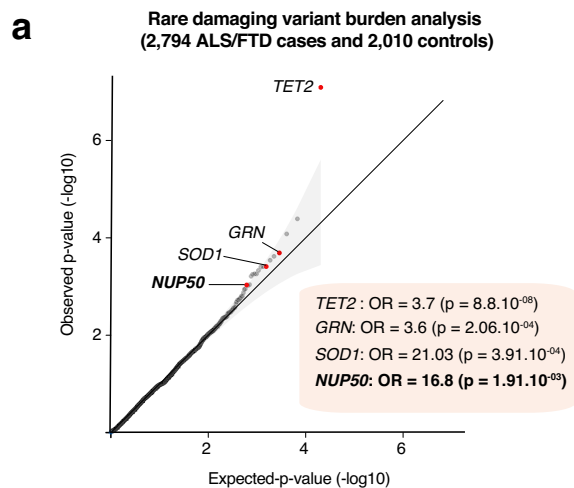
variant_type	variant_location	cDNA_change	protein_change	gnomAD_AF	ALS cases (n = 9390)	Control (n = 4594)	MVP	CADD	dbSNPID
missense_variant	22:g.45564104G>A	c.46G>A	p.Asp16Asn	0.000322851	11	2	0.87	26.5	rs200329756
frameshift_variant	22:g.45564091dupATAGGAATTG	c.35_45dupATAGGAATTGG	p.Asp16fs	NA	1	0	NA	NA	NA
structural	22:g.45564117A>G	c.59A>G	p.Glu20Gly	4.2e-06	3	0	0.84	26.3	rs1200142847
structural	22:g.45567544C>T	c.133C>T	p.Arg45Cys	9.68367e-05	9	0	0.89	28.1	rs113634721
missense_variant	22:g.45571835C>T	c.214C>T	p.Arg72Cys	3.23018e-05	1	0	0.81	23.6	rs781273344
splice_variant	22:g.45574119G>A	c.341G>A	p.Gly114Asp	0.000419897	3	0	0.73	24.2	rs148003438
missense_variant	22:g.45574245A>G	c.467A>G	p.Tyr156Cys	2.88367e-05	1	0	0.75	23	rs779406443
missense_variant	22:g.45574601A>G	c.823A>G	p.Lys275Glu	3.22768e-05	2	0	0.71	23.5	rs753113949
splice_acceptor	22:g.45567480G>C	c.70-1G>C	NA	3.9-06	1	0	NA	32	rs770658454
missense_variant	22:g.45574313C>G	c.535C>G	p.Pro179Ala	6.52768e-06	1	0	0.81	22.4	rs763689432
missense_variant	22:g.45580471C>T	c.1342C>T	p.Arg448Trp	6.52768e-05	1	0	0.91	24	rs77952476

which replaces the previous incorrect version:

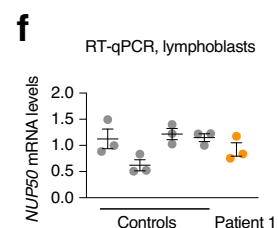
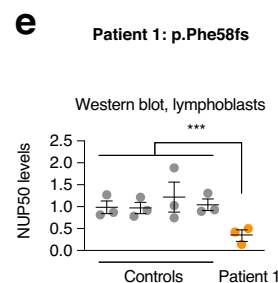
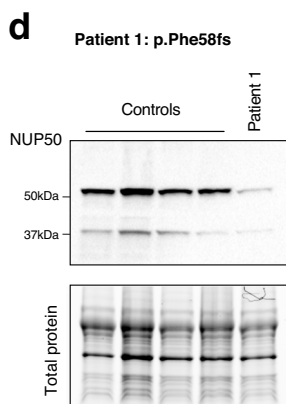
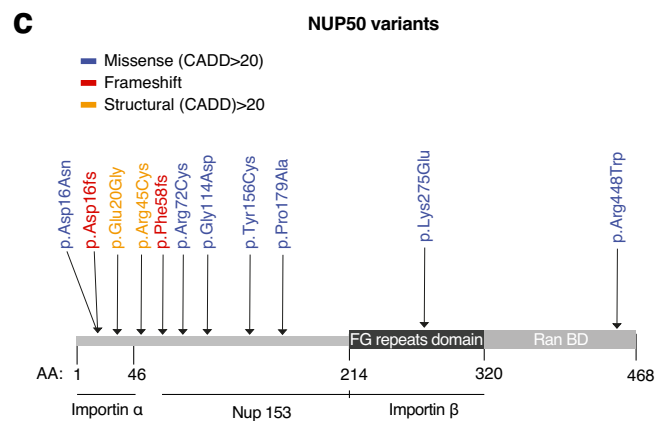
variant_type	variant_location	cDNA_change	protein_change	gnomAD_AF	ALS cases (n = 9390)	Control (n = 4594)	MVP	CADD	dbSNPID
missense_variant	22:g.45564104G>A	c.46G>A	p.Asp16Asn	0.000322851	11	2	0.88	26.5	rs200329756
frameshift_variant	22:g.45564091dupATAGGAATTG	c.35_45dupATAGGAATTGG	p.Asp16fs	NA	1	0	NA	NA	NA
structural	22:g.45564117A>G	c.59A>G	p.Gln20Cys	4.2e-06	3	0	0.86	26.3	rs1200142847
structural	22:g.45567544C>T	c.133C>T	p.Arg45Cys	9.68367e-05	9	0	0.89	28.1	rs113634721
missense_variant	22:g.45571835C>T	c.214C>T	p.Arg72Cys	3.23018e-05	1	0	0.81	23.6	rs781273344
splice_variant	22:g.45574119G>A	c.341G>A	p.Gly114Asp	0.000419897	3	0	0.74	24.2	rs148003438
missense_variant	22:g.45574245A>G	c.467A>G	p.Tyr156Cys	2.88367e-05	1	0	0.76	23	rs779406443
missense_variant	22:g.45574601A>G	c.823A>G	p.Lys275Glu	3.22768e-05	2	0	0.71	23.5	rs753113943
splice_acceptor	22:g.45567480G>C	c.70-1G>C	NA	3.9-06	1	0	NA	32	rs770658454
missense_variant	22:g.45178432C>G	c.734C>G	p.Pro179Ala	6.52768e-06	1	0	0.81	22.4	rs763689432
missense_variant	22:g.45184590C>T	c.1734C>G	p.Arg448Trp	6.52768e-05	1	0	0.91	24	rs77952476

In addition, the original version of Fig. 3c showed one variant (Lys275Glu) in an incorrect location and another variant (Arg448Trp) was missing. The correct version of Fig. 3 is:

\*A list of authors and their affiliations appears online.

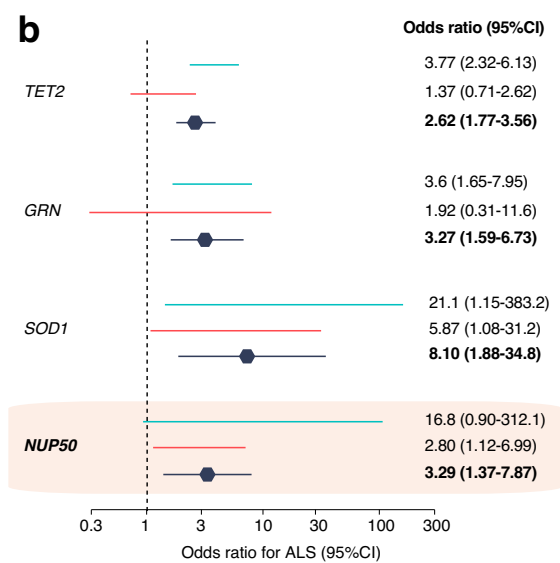
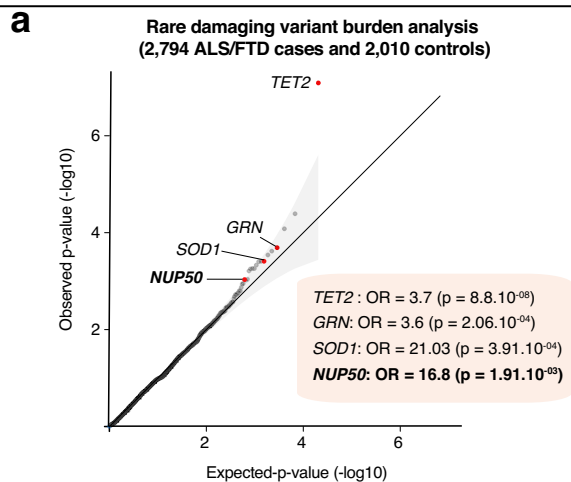


Replication (6,596 ALS cases and 2,584 controls)  
 Discovery (2,794 ALS/FTD cases and 2,010 controls)  
 ● Inverse variance-weighted meta-analysis



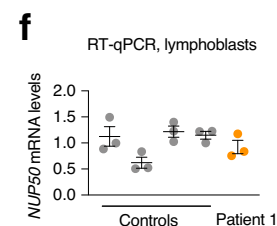
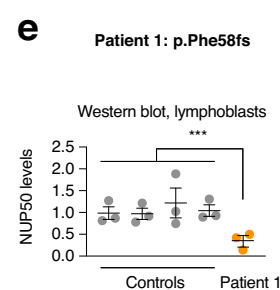
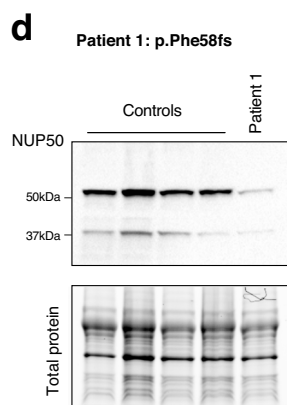
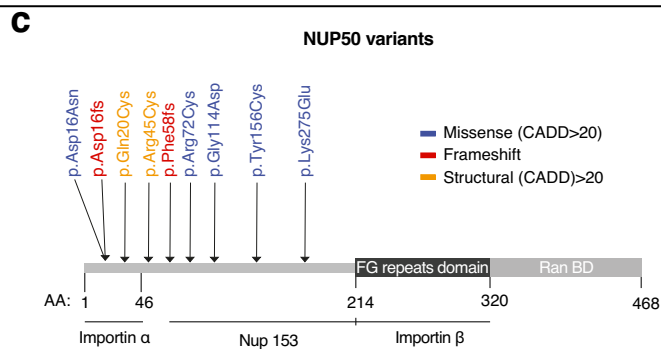
which replaces the previous incorrect version:

# Corrections & amendments



Replication (6,596 ALS cases and 2,584 controls)  
 Discovery (2,794 ALS/FTD cases and 2,010 controls)  
 ● Inverse variance-weighted meta-analysis

This has been corrected in both the PDF and HTML versions of the Article.



**Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this license, visit <http://creativecommons.org/licenses/by/4.0/>.

© The Author(s) 2023