

Biallelic Loss of Proprioception-Related *PIEZO2* Causes Muscular Atrophy with Perinatal Respiratory Distress, Arthrogryposis, and Scoliosis

Andrea Delle Vedove, Markus Storbeck, Raoul Heller, Irmgard Hölker, Malavika Hebbar, Anju Shukla, Olafur Magnusson, Sebahattin Cirak, Katta M. Girisha, Mary O'Driscoll, Bart Loeys, and Brunhilde Wirth*

(The American Journal of Human Genetics 99, 1206–1216; November 3, 2016)

In the original version of this article that appeared online, Figure 1 did not entirely correspond to the figure legend. Panel (D) was missing data of a breakpoint analysis performed for the deletion of the *PIEZO* exon and an exon in affected individual D-II. The agarose gel in (D) did not include the presence of the neighboring *PIEZO* exons. In (E), the graphical representation of *PIEZO* exons did not depict all exons. Reproduced here are the original and corrected panels (D) and (E). The corrected figure appears in print and online. The authors apologize for this error.

*Correspondence: brunhilde.wirth@uk-koeln.de

<http://dx.doi.org/10.1016/j.ajhg.2016.11.009>.

© 2016 American Society of Human Genetics.

Figure 1. Identification of Homozygous Frameshift Variants in *PIEZO2* in Ten Affected Individuals of Four Independent Families (corrected)

(A–D) Pedigrees and Sanger sequencing results of four independent families with homozygous frameshift mutations (A–C) or homozygous exon deletions (D) in *PIEZO2*. DNA was not available for individuals with gray outline. The unequivocal individual identifier is assembled of family, generation, and individual (e.g., A-III.1). Deletion of a genomic region comprising the *PIEZO2* exons 6 and 7 in individual D-II.2 (D) was confirmed by PCR analysis and by identification of the breakpoint region. *PIEZO2* exons 5, 6, 7, and 8 were amplified in multiplex with *RYR1* exon 93 as PCR-positive control. Breakpoint regions were identified by Sanger sequencing of a long-range PCR product amplified from the genomic region between exon 5 and exon 8.

(E) *PIEZO2* protein structure and mutations identified: homozygous loss-of-function mutations (black) and dominant gain-of-function mutations for DA3 (blue), DA5 (green), and MWKS (red) are given. Protein isoforms refer to UniProt entry Q9H515. Bright regions indicate putative transmembrane domains (approximated scale); blue regions indicate missing or inserted regions in different isoforms. The bottom line shows exons in which homozygous frameshift mutations were identified.

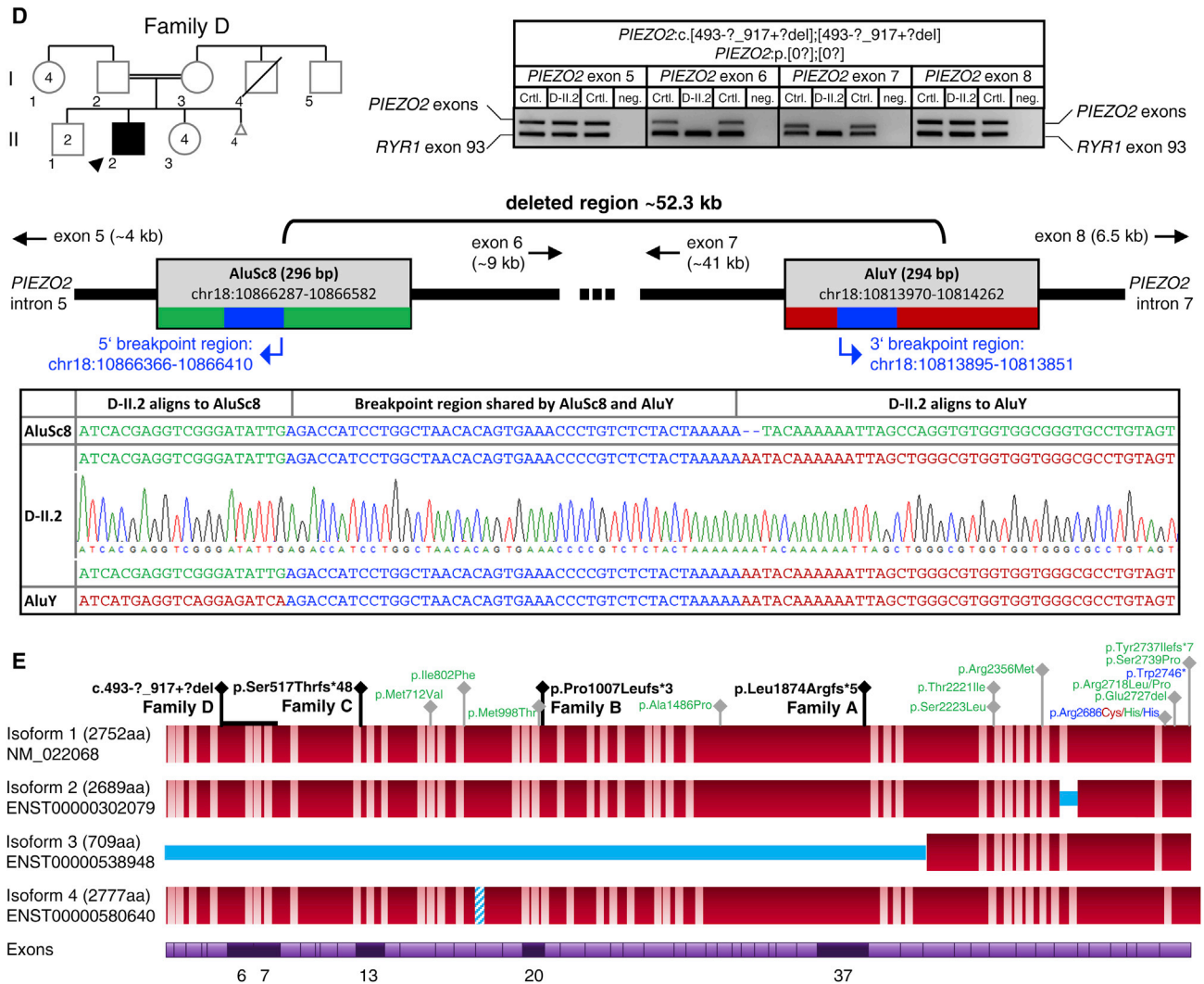


Figure 1. Identification of Homozygous Frameshift Variants in *PIEZO2* in Ten Affected Individuals of Four Independent Families (original)

(A–D) Pedigrees and Sanger sequencing results of four independent families with homozygous frameshift mutations (A–C) or homozygous exon deletions (D) in *PIEZO2*. DNA was not available for individuals with gray outline. The unequivocal individual identifier is assembled of family, generation, and individual (e.g., A-III.1). Deletion of a genomic region comprising the *PIEZO2* exons 6 and 7 in individual D-II.2 (D) was confirmed by PCR analysis and by identification of the breakpoint region. *PIEZO2* exons 5, 6, 7, and 8 were amplified in multiplex with *RYR1* exon 93 as PCR-positive control. Breakpoint regions were identified by Sanger sequencing of a long-range PCR product amplified from the genomic region between exon 5 and exon 8.

(E) *PIEZO2* protein structure and mutations identified: homozygous loss-of-function mutations (black) and dominant gain-of-function mutations for DA3 (blue), DA5 (green), and MWKS (red) are given. Protein isoforms refer to UniProt entry Q9H515. Bright regions indicate putative transmembrane domains (approximated scale); blue regions indicate missing or inserted regions in different isoforms. The bottom line shows exons in which homozygous frameshift mutations were identified.

