



# Corrigendum: Candidate Gene Resequencing in a Large Bicuspid Aortic Valve-Associated Thoracic Aortic Aneurysm Cohort: SMAD6 as an Important Contributor

## OPEN ACCESS

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## A corrigendum on

### Candidate Gene Resequencing in a Large Bicuspid Aortic Valve-Associated Thoracic Aortic Aneurysm Cohort: SMAD6 as an Important Contributor

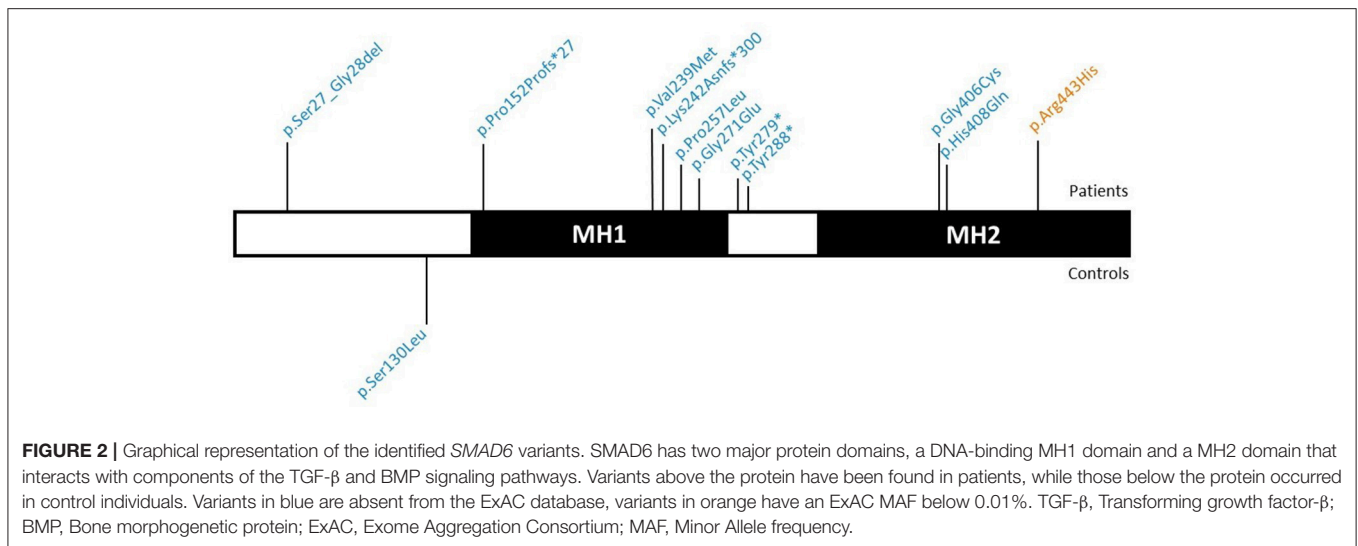
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In the original article, we noted two mutation annotation errors. The correction of these two mistakes does not change the scientific conclusions in any way. The authors apologize for these nomenclature errors. Please find below the corrected annotations of those two mutations:

(1) The correct RNA and protein annotations of the SMAD6 variant in P99 are c.455\_461del and p.Pro152Profs\*27, and not c.454\_461del and p.Gly166Valfs\*23.

(2) The correct RNA and protein annotations of the SMAD6 variant in P128 are c.74\_79del and p.Ser27\_Gly28del, and not c.73\_79del and p.Gly26\_Ser27del.

As a consequence, a correction has been made to RESULTS, Paragraphs 5 and 6:



The *SMAD6* c.726del variant leads to a frameshift (p.Lys242Asnfs\*300) and a predicted protein with a C-terminal extension due to loss of the intended stop codon. The c.455\_461del frameshift variant (p.Pro152Profs\*27) causes the introduction of a premature stop codon, most likely resulting in haploinsufficiency due to nonsense-mediated mRNA decay (NMD). Also the two nonsense variants (p.Tyr279\* and p.Tyr288\*) are predicted to lead to NMD. All of the missense variants cluster in the functionally important MH1 and MH2 domains (Makkar et al., 2009) (amino acids 148–275 and 331–496, respectively), which is not the case for the sole missense variant (p.Ser130Leu) found in a control individual (Figure 2). All but one (p.Arg443His) of the identified variants were absent in the ExAC control cohort (v0.3.1; Supplementary Table 2). Moreover, the missense variants in the patient cohort (7/7) are enriched in the MH1 and MH2 domains when compared to ExAC controls ( $n = 228/430$ ;  $p = 0.02$ ).

For two *SMAD6* mutation carriers (P89, p.Gly271Glu; P99, p.Pro152Profs\*27), gDNA of family members was available for

segregation analysis (Supplementary Figure 1). Although neither of these probands had a documented family history of BAV/TAA, a brother of P89 has been diagnosed with a sinus of Valsalva aneurysm (45 mm) and carried the *SMAD6* mutation. The mutation was also observed in an unaffected daughter (age 28) of the proband (Supplementary Figure 1). Three unaffected siblings at ages 54, 58, and 64 did not carry the mutation. No gDNA was available from a sister of P99 with unspecified aortic valve problems. The p.Pro152Profs\*27 mutation was found in an unaffected daughter (age 39) of P99 but was absent in his 37 year-old unaffected son (Supplementary Figure 1).

We also provide a corrected Figure 2 and Supplementary Table 2.

## SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <http://journal.frontiersin.org/article/10.3389/fphys.2017.00730/full#supplementary-material>

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**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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