ERRATUM

FREM1 Mutations Cause Bifid Nose, Renal Agenesis, and Anorectal Malformations Syndrome

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In our recent article on loss-of-function mutations in *FREM1*, the mutation-containing exons were inadvertently misnumbered. This occurred because of the inclusion of a noncoding exon that, although associated with the *QBRICK* transcript, is not present in the current RefSeq. Therefore, the Afghani mutation (cited as being in exon 12) is actually in exon 11, according to version NM_144966.4. Similarly, the Egyptian and Pakistani mutations reside in exons 16 and 24, respectively. The cDNA and protein nomenclature used in describing all mutations, as well as their locations along the FREM1 peptide, as given in Figure 1 and elsewhere, remain unchanged and accurate. The authors regret this oversight and appreciate the opportunity to amend the record.

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