Expanding the Boundaries of RNA Sequencing as a Diagnostic Tool for Rare Mendelian Disease

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In the originally published version of this article, the 5' UTR variant of Family 5 was incorrectly described; the correct substitution is chr3:g.49761246G>A. Additionally, there were two instances of incorrect reference transcripts. The variant for family 8 correctly corresponds to GenBank: NM_133378.4. The variant for family 35 correctly corresponds to GenBank: NM_004006.2:c.93+1G>C. The article now appears correctly online. The authors regret these errors and any confusion that may have resulted.