CORRECTION | Genetics inMedicine

**Correction:** Interpretation of mitochondrial tRNA variants

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The original version of this Article contained an error in the spelling of "Criteria for mt-tRNA variants" in the top right column header of Table **2**, which was incorrectly given as "mt-mRNA." This has now been corrected in both the PDF and HTML versions of the Article.

**Table 2** Criteria for the classification of benign variants.

| Evidence | ACMG criteria | Criteria for mt-tRNA variants |
|---|---|---|
| **Stand-alone** | **BA1** Allele frequency is above 5% in Exome Sequencing Project, 1000 Genomes, or ExAC. | **BA1** Top-level haplogroup defining variants. |
| **Strong** | **BS1** Allele frequency is greater than expected for disorder. | **BS1** Reported in public databases (e.g., MitoMap or mtDB) or literatures as polymorphism. |
| | **BS2** Observed in healthy adult individual for a recessive (homozygous), dominant (heterozygous), or X-linked (hemizygous) disorder with full penetrance expected at an early age. | **BS2** Found homoplasmic in more than three unrelated healthy adults. |
| | **BS3** Well-established in vitro or in vivo functional studies shows no damaging effect on protein function or splicing. | **BS3** Not applicable. |
| | **BS4** Lack of segregation in affected members of a family. | **BS4** Homoplasmy in both probands and at least 2 asymptomatic matrilineal family members. |
| **Supporting** | **BP1** Missense variant in a gene for which primarily truncating variants are known to cause disease. | **BP1** Not applicable. |
| | **BP2** Observed in *trans* with a pathogenic variant for a fully penetrant dominant gene/disorder; or observed in *cis* with a pathogenic variant in any inheritance pattern. | **BP2** Not applicable. |
| | **BP3** In-frame deletions/insertions in a repetitive region without a known function. | **BP3** Not applicable. |
| | **BP4** Multiple lines of computational evidence suggest no impact on gene or gene product. | **BP4** The MitoTIP prediction score is <10. |
| | **BP5** Variant found in a case with an alternate molecular basis for disease. | **BP5** In the presence of a known pathogenic genetic cause unless there is evidence of more than one disease and clinically explained. |
| | **BP6** Reputable source recently reports variant as benign but the evidence is not available to the laboratory to perform an independent evaluation. | **BP6** Found to be homoplasmic more than once in asymptomatic adults in private reputable laboratory databases. |
| | **BP7** A synonymous (silent) variant for which splicing prediction algorithms predict no impact to the splice consensus sequence nor the creation of a new splice site AND the nucleotide is not highly conserved. | **BP7** Not applicable. |

The ACMG criteria are listed on the left column and the new criteria for mt-tRNA variants are on the right.

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