How Did the Variant Get Its Name? Understanding Gene and Variant Nomenclature
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Genomics is foundational to precision oncology. Oncology nurses regularly review germline and somatic biomarker testing reports. The taxonomy and nomenclature of biomarker results have evolved. Accurate understanding and interpretation of germline and somatic genomic results are essential for safe patient care and patient education. This article reviews common variant nomenclature on genomic biomarker reports, including gene and variant location, coding data, information about protein function, and common DNA errors. This review includes examples of common variant types, such as insertions, deletions, duplications, and substitutions, and implications for nursing practice.

**AT A GLANCE**
- Germline and somatic biomarker test results include detailed information about altered genes, actionable variants, and DNA sequence and coding changes.
- Common types of DNA sequence changes include insertions, deletions, duplications, and substitution variants, which may or may not have implications for clinical care based on pathogenicity and actionability.
- Oncology nurses regularly encounter genomic biomarker reports and can explain the components and clinical implications of the reports to patients and families.

**Genomic Biomarker Test Report Terminology**
Biomarker test reports have extensive and specific information about the altered genes detected in an analysis. This nomenclature is presented in a standard format and provides detailed information about the variant and its location within the gene (den Dunnen, 2016). The information regarding location of a variant consists of a combination of numbers and letters in a specific order. To avoid confusion in this rapidly expanding and increasingly complex area, the Human Genome Variation Society (2020) maintains international standards for variant description (den Dunnen et al., 2022).