Severe Congenital Neutropenia Gene Set

Genomic profiling for congenital neutropenia

Next-generation sequencing for efficient, cost-effective and robust germline variant detection

Concise, expert interpretations by board-certified clinical genomicists, reported back to the ordering physician

Professional consultation available to physicians in result interpretation, and other technical and clinical considerations

Testing covered by most insurance; preauthorization performed by GPS

Clinical utility

The SCN Gene Set is designed to identify genetic mutations in individuals with symptoms consistent with Severe Congenital Neutropenia.

Many times, patients present with a variety of related phenotypes making diagnosis challenging. Targeted next-generation sequencing provides clinicians with a powerful tool to analyze multiple genes with clinical relevance to enhance the diagnostic yield of testing.

Identification of a pathogenic mutation can often be used to make a more definitive diagnosis, allowing for more appropriate patient management. It also enables tailored genetic counseling in both the patient and at-risk family members.

Over time, such analyses have the potential for genotype-phenotype correlations to be drawn and may enable disease-specific therapies.
Indications for testing

Indications for testing include symptoms of congenital neutropenia, a family history of neutropenia, recurrent childhood infection, osteopenia, osteoporosis, childhood leukemia, childhood MDS, recurrent fever, recurrent sinusitis and recurrent gingivitis.

Genes tested

AP3B1, CSF3R, CXCR2, CXCR4, ELANE, G6PC3, GATA2, GF1, HAX1, JAGN1, KRAS, LAMTOR2, LYST, NRAS, RAB27A, RUNX1, SBDS, SLC37A4, SRP54, TAZ, TCIRG1, USB1, VPS13B, VPS45 and WAS.

Testing methodology

Tests are performed using targeted hybridization capture coupled with next-generation sequencing (NGS) in our CAP/CLIA labs for comprehensive coverage of all coding exons of ordered genes.

Types of variation detected include single nucleotide variants (SNVs) and small insertions and deletions (indels).

Results and interpretation

DNA sequence data are analyzed by GPS’ clinically validated bioinformatics pipeline to identify and annotate genetic variants associated with severe congenital neutropenia.

Variants are interpreted by a board-certified clinical genomics in the context of the patient’s disease. Those that are most likely to account for the observed clinical phenotype based on evidence from the medical literature are highlighted.

Results are returned to the ordering physician in a concise report.

Turnaround time

The turnaround time for testing and interpretation of sequencing results is four to six weeks from the time a specimen arrives. If performed, deletion/duplication analysis may take an additional six weeks.