Hemophagocytic Lymphohistiocytosis: Sequencing Panel

Test Code: MM640
Turnaround time: 6 weeks
CPT Codes: 81404 x1, 81479 x1

Condition Description

Hemophagocytic lymphohistiocytosis (HLH) is a rare autosomal recessive disorder, in which the immune system produces too many activated immune cells (histiocytes and T cells). Main clinical findings may include hepatosplenomegaly, cytopenia, prolonged fever, low or absent natural killer (NK)-cell activity, and neurological abnormalities such as hypotonia or hypertonia, convulsions, ataxia, coma, blindness, increased intracranial pressure, and neck stiffness. Liver dysfunction and bone marrow hemophagocytosis may also be present. The progression of disease and infection usually account for the majority of deaths in untreated individuals. The estimated prevalence of familial HLH is 1 in 50,000 births.

There are five subtypes of HLH. Types 2-5 are each caused by a mutation in a different gene: Type 2 (PRF1), Type 3 (UNC13D), Type 4 (STX11), and Type 5 (STXBP2). The genetic mechanism for type 1 has not been identified. Approximately, 40 to 60 percent of cases of familial HLH are caused in mutations in the PFR1 or UNC13D genes. The pathogenic variant p.Leu17ArgfsTer34 in PRF1 has been observed at a high frequency in individuals with familial HLH in the African American population.

This panel also includes genes that cause specific types of Hermansky-Pudlak, Chediak-Higashi, and lymphoproliferative syndromes due to overlapping of symptoms seen in individuals with these disorders and hemophagocytic lymphocytic syndrome.

References:

3. OMIM.

Genes

AP3B1, BLOC1S6, CD27, GATA2, ITK, LYST, MAGT1, NLRC4, PRF1, RAB27A, SH2D1A, SLC7A7, STX11, STXBP2, UNC13D, XIAP

Indications

This test is indicated for:

- Individuals with a clinical or suspected diagnosis of hemophagocytic lymphohistiocytosis.

Methodology

Next Generation Sequencing: In-solution hybridization of all coding exons is performed on the patient's genomic DNA. Although some deep intronic regions may also be analyzed, this assay is not meant to interrogate most promoter regions, deep intronic regions, or other regulatory elements, and does not detect single or multi-exon deletions or duplications. Direct sequencing of the captured regions is performed using next generation sequencing. The patient's gene sequences are then compared to a standard reference sequence. Potentially causative variants and areas of low coverage are Sanger-sequenced. Sequence variations are classified as pathogenic, likely pathogenic, benign, likely benign, or variants of unknown significance. Variants of unknown significance may require further studies of the patient and/or family members.

Detection

Next Generation Sequencing: Clinical Sensitivity: Unknown. Mutations in the promoter region, some mutations in the introns and other regulatory element mutations cannot be detected by this analysis. Large deletions/duplications will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical/biochemical phenotype.

Analytical Sensitivity: ~99%.

Specimen Requirements

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