Peroxisome Disorders: Sequencing Panel

Test Code: MM140
Turnaround time: 6 weeks
CPT Codes: 81405 x1, 81479 x1

Condition Description

Peroxisomes are intracellular organelles with diverse cellular functions including biosynthesis, catabolism and detoxification of various compounds. Inborn errors of metabolism of peroxisomes function are roughly divided into peroxisome biogenesis disorders and single enzyme or transporter defects. This panel is designed for comprehensive testing for the following peroxisomal disorders:

1. Peroxisome biogenesis disorders, also called Zellweger syndrome spectrum (PBD, ZSS) that include Zellweger syndrome (ZS), neonatal adrenoleukodystrophy (NALD), and infantile Refsum disease (IRD).
2. X-linked adrenoleukodystrophy and adrenomyeloneuropathy.
3. Rhizomelic Chondrodysplasia Punctata, Types 1, 2, and 3.
4. Refsum Disease or phytanoyl-CoA hydroxylase deficiency.
5. Acyl-CoA oxidase (ACOX1) deficiency.
7. 2-Methylacyl-CoA racemase (AMACR) deficiency.
8. Acatalasaemia.
9. Hyperoxaluria Type 1 or alanine glyoxylate aminotransferase deficiency.
10. Mulibrey nanism.
11. Sterol carrier protein X (SCP2) deficiency.
12. DN1ML-related encephalopathy.
13. ABCD3-related congenital bile acid synthesis defect

Reference:


Genes

ABCD1, ABCD3, ACOX1, AGPS, AGXT, AMACR, CAT, DNM1L, GNPAT, HSD17B4, PEX1, PEX10, PEX11B, PEX12, PEX13, PEX14, PEX16, PEX19, PEX2, PEX26, PEX3, PEX5, PEX6, PEX7, PHYH, SCP2, TRIM37

Indications

This test is indicated for:

- Confirmation of a clinical/biochemical diagnosis of peroxisomal disorders.
- Carrier testing in adults with a family history of peroxisomal disorders.

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

Clinical Sensitivity: Pathogenic variants in the PEX genes account for ~95% of individuals with PBD, ZSS. Pathogenic variants in the promoter region, some pathogenic variants in the introns and other regulatory element pathogenic variants cannot be detected by this analysis. Large deletions will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient’s clinical and/or biochemical phenotype.

Analytical Sensitivity: ~99%

Specimen Requirements

Submit only 1 of the following specimen types.
Type: Whole Blood

Specimen Requirements:

In EDTA (purple top) tube:
Infants (2 years): 3-5 ml
Older Children & Adults: 5-10 ml

Specimen Collection and Shipping: Ship sample at room temperature with overnight delivery.

Type: Isolated DNA

Specimen Requirements:

In microtainer: 60 ug

Isolation using the Qiagen® Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping: Refrigerate until time of shipment in 100 ng/ul of TE buffer. Ship sample at room temperature with overnight delivery.

Related Tests

- Individual gene sequencing and deletion/duplication analysis are available for the following genes: ABCD1, PEX1, PEX2, PEX3, PEX5, PEX6, PEX12, PEX14, and PEX26
- Peroxisome Disorders: Deletion/Duplication Panel