Peroxisome Disorders Panel: Sequencing and CNV Analysis

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. DNM1L-related encephalopathy.
13. ABCD3-related congenital bile acid synthesis defect.

Reference:

Genes

ABCD1, ABCD3, ACOX1, AGPS, AGXT, AMACR, CAT, DNM1L, GNPAT, HSD17B4, PE1, PE10, PE11B, PE12, PE13, PE14, PE16, PE19, PE2, PE26, PE3, PE5, PE6, PE7, 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.

Copy Number Analysis: Comparative analysis of the NGS read depth (coverage) of the targeted regions of genes on this panel was performed to detect copy number variants (CNV). The accuracy of the detected variants is highly dependent on the size of the event, the sequence context and the coverage obtained for the targeted region. Due to these variables and limitations a minimum validated CNV size cannot be determined; however, single exon deletions and duplications are expected to be below the detection limit of this analysis.

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. Results of molecular analysis should be interpreted in the context of the patient's clinical and/or biochemical phenotype.

Analytical sensitivity for sequence variant detection is ~99%.

Copy Number Analysis: The sensitivity and specificity of this method for CNV detection is highly dependent on the size of the event, sequence context and depth of coverage for the region involved. The assay is highly sensitive for CNVs of 500 base pairs or larger and those containing at least 3 exons. Smaller (< 500 base pairs) CNVs and those that involving only 1 or 2 exons may or may not be detected depending on the sequence context, size of exon(s) involved and depth of coverage.

Specimen Requirements

Disclaimer: This information is confidential and subject to change without notice. It may not be reproduced in whole or part unless authorized in writing by an authorized EGL representative.
Submit only 1 of the following specimen types

Type: Whole Blood (EDTA)

Specimen Requirements:
EDTA (Purple Top)
Infants and Young Children (2 years of age to 10 years old): 3-5 ml
Older Children & Adults: 5-10 ml
Autopsy: 2-3 ml unclotted cord or cardiac blood

Specimen Collection and Shipping:
Ship sample at room temperature for receipt at EGL within 72 hours of collection. Do not freeze.

Type: DNA, Isolated

Specimen Requirements:
Microtainer
15µg
Isolation using the Perkin Elmer™Chemagen™ Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

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

Type: Saliva

Specimen Requirements:
Oragene™ Saliva Collection Kit
Oragene™ Saliva Collection Kit used according to manufacturer instructions. Please contact EGL for a Saliva Collection Kit for patients that cannot provide a blood sample.

Specimen Collection and Shipping:
Please do not refrigerate or freeze saliva sample. Please store and ship at room temperature.

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