Lysosomal Storage Disorders Panel: Sequencing and CNV Analysis

Test Code: MM120
Turnaround time: 6 weeks
CPT Codes: 81406 x1, 81404 x1, 81405 x1

Condition Description

Lysosomal storage disorders (LSDs) are a heterogeneous group of mostly autosomal recessive disorders with the exception of mucopolysaccharidosis type II (MPS II) also known as Hunter syndrome, Danon disease, and Fabry disease which show X-linked inheritance. LSDs comprise more than 50 metabolic disorders including defects in degradative and synthetic enzymes, lysosomal membrane defects, the neuronal ceroid lipofuscinoses (NCLs) and disorders of lysosome biogenesis and endosome–lysosome traffic.

Clinical and biochemical features continue to be used reliably to assign patients to this general disease category. Identification of the precise genetic defect is important, however, to permit carrier testing and early prenatal diagnosis. Molecular analysis is likely to expand the clinical spectrum of LSD and may also provide data relevant to prognosis and future therapeutic intervention. The overall incidence of LSDs as a group is estimated to be 1 in 5,000 births.

Although each LSD results from pathogenic variants in a different gene leading to a deficiency of enzyme activity or protein function, LSDs share one common biochemical characteristic: an accumulation of substrates within lysosomes. The particular substrates that are stored and the site(s) of storage vary. The substrate type is used to group the LSDs into broad categories, including the MPSs, the lipidoses, the glycogenoses, the oligosaccharidoses, and NCLs. Despite this categorization, many clinical similarities are observed between groups as well as within each group. Common clinical features of LSDs include coarse hair and facies, bone abnormalities, organomegaly, and central nervous system dysfunction.

References:

- OMIM

Genes

ADAMTS10, AGA, AP3B1, ARSA, ARSB, ARSAH1, ATP13A2, CLN3, CLN5, CLN6, CLN8, CTNS, CTSA, CTSD, CTSK, DNAJC5, FBN1, FUC1, GAA, GALC, GALNS, GBA, GLA, GLB1, GM2A, GNE, GNPTAB, GNPTG, GNS, GRN, GUSB, HEXA, HEXB, HGSNAT, HYAL1, IDS, IDUA, KCTD7, LAMP2, LIPA, LTBP2, LYST, MAN2B1, MANBA, MCOLN1, MFSD8, MYOSA, NAGA, NAGLU, NEU1, NPC1, NPC2, PPT1, PSAP, RAB27A, SGSH, SLC17A5, SMPD1, SUMF1, TPP1

Indications

This test is indicated for individuals:

- With clinical features such as bone abnormalities, organomegaly, central nervous system dysfunction and coarse hair and facies.
- In which NCLs are suspected (presenting with neurocognitive decline, blindness, seizures and premature death).
- Abnormal biochemical results suggestive of an LSD.

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

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

Analytical sensitivity for sequence variant detection is ~99%.

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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

Submit only 1 of the following specimen types

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.

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™ 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.

Related Tests

- Biochemical enzyme assay for lysosomal storage disorders
- Lysosomal Storage Disorders: Deletion/Duplication Panel