UBE2A-related Syndromic XLMR: UBE2A Gene Deletion/Duplication

Test Code: DUBE2
Turnaround time: 2 weeks
CPT Codes: 81228 x1

Condition Description

Intellectual disability (ID) is a nonprogressive cognitive impairment affecting 1-3% of the Western population. It is estimated that up to 50% of moderate-severe cases have genetic causes and approximately 10% are due to X-linked intellectual disability disorders (XLID). XLID can be syndromic or nonsyndromic and is observed in all ethnic groups. More than 100 XLID syndromes have been described in the literature to date. Fragile X is the most common XLID syndrome (~1 in 4000 males) while others can be quite rare with only a few patients reported in the literature. Males can have moderate to severe intellectual disability depending on the syndrome, and carrier females can also be affected, but typically have milder clinical symptoms.

Rafaella et al. (2006) describe a family in which three males from two generations had syndromic intellectual disability. Chromosome analysis and fragile X testing were normal. In addition to intellectual disability, all three of the affected family members had hair whorls, up-slated palpebral fissures, large mouth with down-turned corners and thin lips, short, broad neck, low posterior hairline, widely spaced nipples, small penis, marked generalized hirsutism, dry skin, seizures, and severe speech impairment. Their carrier mothers were clinically unaffected with completely skewed X inactivation in leukocytes. A nonsense mutation in the UBE2A gene (Xq24-q25) was found in affected and carrier individuals and was absent in an unaffected female who had a random X inactivation pattern.

For patients with suspected UBE2A-Related Syndromic XLMR, sequence analysis is recommended as the first step in mutation identification. For patients in whom mutations are not identified by full gene sequencing, deletion/duplication analysis is appropriate.

References:

- OMIM #312180: UBE2A gene

Genes

UBE2A

Indications

This test is indicated for:

- Confirmation of a clinical diagnosis of UBE2A-Related Syndromic XLMR in an individual in whom sequence analysis was negative.
- Carrier testing in adults with a family history of UBE2A-Related Syndromic XLMR in whom sequence analysis was negative.

Methodology

DNA isolated from peripheral blood is hybridized to a CGH array to detect deletions and duplications. The targeted CGH array has overlapping probes which cover the entire genomic region.

Detection

Detection is limited to duplications and deletions. The CGH array will not detect point or intronic mutations. Results of molecular analysis must be interpreted in the context of the patient's clinical and/or biochemical phenotype.

Specimen Requirements

Submit only 1 of the following specimen types

Type: DNA, Isolated

Specimen Requirements:
Microtainer
3µg
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: Whole Blood (EDTA)

Specimen Requirements:
EDTA (Purple Top)
Infants and Young Children (2 years of age to 10 years old: 3-5 ml

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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.

Related Tests

- Sequence analysis of the *UBE2A* gene is available and is required before deletion/duplication analysis.
- Custom diagnostic mutation analysis (KM) is available to family members if mutations are identified by targeted mutation testing or sequencing analysis.
- Prenatal testing is available only for known familial mutations to individuals who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.
- X-Linked Intellectual Disability panels are available for 30, 60, and 90 genes.