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 mutations cannot be detected by this analysis. Large deletions/duplications will not be detected by this analysis. Results of molecular analysis
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.

**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 a syndrome, and carrier females can also be affected, but typically have milder clinical
symptoms.

A majority of individuals with XLID are non-syndromic with no other features to assist in diagnosis. Because of the number of genes involved, it is very
difficult to identify which X-linked gene may be responsible for the phenotype in any given patient. Simultaneous testing of all known XLID genes in a
single study provides a significant diagnostic advantage over single gene sequencing. Additional benefits for the patient and families include:

- Providing information for recurrence risk and family planning and allowing for presymptomatic support
- Helping physicians determine appropriate follow-up testing and develop a health maintenance plan
- Predicting better patient prognostic value
- Assisting researchers in the understanding of the molecular basis of disease in the hope for treatments and cures
- Assessing the possibility of therapy for some forms of XLID

Testing includes trinucleotide repeat analysis for the **FMRI** (test code: MFRA) and **AFF2/FMRE** (test code: FRAXE) genes.

**Genes**

ACS4L, AFF2, AP1S2, ARHGEF9, ARX, ATP6AP2, ATP7A, ATRX, BCOR, BRWD3, CASK, CCDC22, CDK16, CDKL5, CLIC2, CNKSR2, CUL4B,
DOX, DKK1, DLD3, DMD, FANCB, FG01, FLNA, FMR1, FRMDP4, FTSJ1, GDI1, GK, GPC3, GRIA3, HCCS, HCFC1, HPRT1, HSD17B10, HUWE1,
IDS, IGGBP1, IL1RAPL1, IQSEC2, KDM5C, KIAA0222, KLF8, L1CAM, LAMP2, MAOA, MBTPS2, MECP2, MED12, MID1, NAA10, NDP, NDUFA1,
NHS, NLGN3, NLGN4X, NSDH1, OCR1, QDF1, OPHN1, QTG, PAK3, PCDH19, PDHA1, PGK1, PHF5, PHF8, PLP1, PORCN, PGBP1, PRPS1,
PTCH1D1, RAB3B, RBM10, RPL10, RPS6KA3, SHROOM4, SLC16A2, SLC9A6, SMC1A, SMS, SOX3, SYN1, SYNGAP1, SYP, TIMM8A, TSPAN7,
UBE2A, UPF3B, ZDHHC15, ZDHHC3, ZNF711

**Indications**

This test is indicated for:

- Individuals with a clinical and family history consistent with an X-linked intellectual disability disorder after fragile X testing and genomic array
  testing are normal.
- Carrier testing in adult females with a family history of X-linked intellectual disability.

**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%.

**FRAXE:** Normal: Approximately 6-35 CCG repeats. Affected: Approximately >200 CCG repeats and methylation of expanded allele.

**MFRA:**
Normal: Approximately 5-44 CGG repeats.
Intermediate: Approximately 54-65 unmethylated CGG repeats.
Premutation: Approximately 55-200 CGG repeats and methylation of expanded allele.
Affected: Over 200 CGG repeats and methylation of expanded allele.

**Reference Range**
Next Generation Sequencing: N/A.


MFRAX:
Normal: Approximately 5-44 CGG repeats.
Intermediate: Approximately 54-45 unmethylated CGG repeats.
Premutation: Approximately 55-200 CGG repeats and methylation of expanded allele.
Affected: Over 200 CGG repeats and methylation of expanded allele.

**Specimen Requirements**

Submit only 1 of the following specimen types

* Preferred specimen type: Whole Blood

**Type: Whole Blood**

Specimen Requirements:

In EDTA (purple top) or ACD (yellow top) tube:

- Infants (2 years): 3-5 ml
- Older Children & Adults: 5-10 ml

Specimen Collection and Shipping: Refrigerate until time of shipment. Ship sample within 5 days of collection 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**

- The Autism Panel is available to detect the most common known genetic causes of autism/ID. The autism panel includes testing for fragile X syndrome and chromosome microarray analysis (using oligonucleotide array) and is recommended before XLID gene sequencing panel testing.
- Testing is also available for individual XLID genes that have specific phenotypes.
- Prenatal testing is available for couples 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: Deletion/Duplication Panel.