Spinal Muscular Atrophy (SMA) is the second most common lethal, autosomal recessive disorder in Caucasians, with an incidence of approximately 1/6,000 births. SMN1 is deleted in about 95% of individuals with SMA. This carrier assay tests for the common deletion only; other pathogenic variants will not be detected.

Approximately 5-8% of carrier individuals will have a normal SMN1 copy number of two, but both copies will be on the same chromosome (in cis) with a deletion on the second chromosome. This assay will not detect these carrier individuals. This assay will not report SMN2 copy number.

Although a positive test result should not affect the health of the individual, she could be at a 25% risk for passing that condition on to her children depending on the carrier status of the partner. In addition to the specific pathogenic variants identified by the panel, EGL Genetics also offers single-gene, full gene sequencing for genes on the panel, which can be utilized to screen partners of positive carriers. Knowing about these risks ahead of time can help couples make decisions about testing options prior to and during pregnancy, and can help healthcare providers be more readily prepared to offer appropriate follow-up care at delivery.

### Genes

- ABCG8, ASPA, BCKDHB, BLM, CFTR, CLRN1, DLD, ELP1, FANCC, FKTN, FMR1, G6PC, GBA, HEXA, MCOLN1, NEB, PCDH15, SMN1, SMPD1, TMEM216

### Indications

Appropriate for:

- Carrier testing in individuals of Ashkenazi Jewish descent.

### 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. Only known pathogenic variants will be reported.

#### Fragile X Syndrome Repeat Analysis:
Both normal CGG repeat tracts and expanded CGG repeat tracts are detected by PCR amplification, using a CGG repeat-specific probe, and capillary electrophoresis. Expanded CGG repeat tracts will be reflexed to a gene specific PCR and sized by agarose gel electrophoresis. Expanded CGG tracts, which are detected with this assay, will be called intermediate. Severe cases result from tracts greater than 200 repeats, which are not detected by this assay. Cases with 55-200 repeats are called premutation alleles and may expand in subsequent generations to full mutation, especially when passed from mother to child. Alleles over 200 repeats are full mutations and will cause fragile X syndrome in males.

Please note this panel will be performed and reported on both male and female specimens. Because of the nature of X-linked inheritance, this test, if positive, may be diagnostic for male patients in rare cases. If you do not wish to have X-linked conditions assessed in male patients, please contact the laboratory.

### Fragile X Syndrome

Fragile X syndrome is characterized by moderate intellectual disability in affected males. Affected females may show mild intellectual disability. It has a prevalence of 1/4000 to 1/6000 in the general population, and is a leading genetic cause of intellectual disability. Fragile X syndrome is associated with a triplet (CGG) repeat expansion in the promoter of the FMR1 gene on the X chromosome. CGG expansion leads to methylation and subsequent inactivation of the FMR1 gene. Normal alleles have ~5-44 repeats. Intermediate alleles have ~45-54 repeats and may expand in subsequent generations to premutation alleles. Alleles with ~55-200 repeats are called premutation alleles and may expand in subsequent generations to full mutations, especially when passed from mother to child. Alleles over ~200 repeats are full mutations and will cause fragile X syndrome in males.

Click [here](#) for a complete list of conditions.

Note that the quoted detection rates and residual carrier risks are directly applicable only to persons of Ashkenazi Jewish descent. The carrier detection rate in persons from other ethnic backgrounds is likely to be significantly lower.
gel electrophoresis.

**Spinal Muscular Atrophy (SMA) Testing:** SMN1 gene deletions were quantified by multiplex ligation polymerase chain reaction amplification (MLPA) of exons 7 and 8. Gene dosage ratios of SMN1 are calculated relative to the average of 16 reference loci and are expressed as gene dosage, and/or copy number. Diploid gene dose or 2 copies of SMN1 indicates normal (not affected) status, 1x gene dosage or 1 copy of the SMN1 gene most likely indicates carrier status and deletions (less than 0.1x) of SMN1 or 0 copies of the SMN1 gene designates affected status. This carrier assay tests for the common SMN1 deletion only; other pathogenic variants will not be detected. SMN2 copy number is not assessed.

**Detection**

**Next Generation Sequencing:** Next Generation Sequencing: Clinical Sensitivity: See results report. Pathogenic variants in regions other than the targeted area, including 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%.

**For Fragile X Syndrome Repeat Analysis:** All cases of fragile X syndrome caused by CGG expansion will be detected by this assay. Rare cases of fragile X syndrome caused by other pathogenic variants in the FMR1 gene will not be detected by this assay.

**For Spinal Muscular Atrophy (SMA) Testing:** Deletions of the SMN1 gene are found in approximately 95% of individuals with SMA. This carrier assay tests for the common SMN1 deletion only; other pathogenic variants will not be detected. Approximately 5-8% of carrier individuals will have a normal SMN1 copy number of two, but both copies will be on the same chromosome (in cis) with a deletion on the second chromosome. This assay will not detect these carrier individuals. SMN2 copy number is not assessed.

**Reference Range**

**For Fragile X Testing:**
- Normal: Approximately 5-44 CGG repeats.
- Intermediate: Approximately 45-54 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

**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 20µg
- 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.

**Related Tests**

- Ashkenazi Jewish Carrier Screen: Targeted Mutation Panel
- Pan-Ethnic Carrier Screen: Gene Sequencing Panel
- ACOG/ACMG Carrier Screen: Gene Sequencing Panel