

## Glycogen Storage Disorders - Muscle Panel: Sequencing and CNV Analysis

**Test Code:** MM152

**Turnaround time:** 6 weeks

**CPT Codes:** 81405 x1, 81406 x1

### Condition Description

Glycogen storage disorders (GSDs) are a group of inherited genetic defects of glycogen metabolism. Most of them have autosomal recessive inheritance, however there are a few exceptions. There are more than 20 subtypes classified by the specific enzyme deficiency, affected tissue, and disease phenotype. 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, as molecular analysis is likely to expand the clinical spectrum of GSDs, may provide data relevant to prognosis and future therapeutic intervention and is important for carrier testing and early prenatal diagnosis.

The overall incidence of GSDs as a group is estimated to be 1 in 20,000-43,000 births. GSDs primarily affect the liver, the muscle, or both. Although the phenotype range is broad, the majority of clinical manifestations are hepatomegaly, failure to thrive, hypoglycemia, hyperlactatemia, hyperuricemia, and hyperlipidemia. This GSD panel covers 15 genes in which pathogenic variants cause the muscle isoforms of GSD and disorders that have overlapping phenotype with GSDs.

References:

- Burwinkel et al. (2005), *Am J Hum Genet*, 76:1034-1049.
- Morris et al. (1995), *J Inherit Metab Dis*, 18:28-32.
- Santer, Steinmamm, and Schaub. (2002), *Curr Mol Med*, 2:213-227.

### Genes

[AGL](#), [ENO3](#), [GAA](#), [GBE1](#), [GYS1](#), [LAMP2](#), [PFKM](#), [PGAM2](#), [PGM1](#), [PHKB](#), [PRKAG2](#), [PYGM](#)

### Indications

This test is indicated for:

- Confirmation of a clinical diagnosis of glycogen storage disorders (GSDs).
- Carrier testing in adults with a family history of glycogen storage disorders (GSDs).

### 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%.

**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: 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 &amp; 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: 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: DNA, Isolated****Specimen Requirements:**

Microtainer

8µg

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**

- Pompe (dry blood spot - test code DZ; leukocytes - DW).
- Glycogen Storage Disorders- Muscle: Deletion/Duplication Panel