Exome: Sanger Confirmation and Interpretation Only

Test Code: EXSAN  
Turnaround time: 11 weeks  
CPT Codes: 81417 x1

**Condition Description**

What is the Medical EmExome?
The human exome is the complete coding (exonic) region of the genome. It is estimated to encompass approximately 1-2% of the genome, yet contains approximately 85% of disease-causing pathogenic variants. Current off-the-shelf exome kits used for clinical exome sequencing cover 92% of the exome. Traditionally, gene discovery has been done in research laboratories; however, now with the ability to sequence nearly the entire coding region of the human genome, it is possible for clinical laboratories to use this information to identify a previously unrecognized cause of disease.

The Medical EmExome is the next level in clinical exome sequencing offered by Emory Genetics Laboratory (EGL). The exome sequencing design provides >97% coverage of 22,000 genes, with a mean read depth of 100X. Of the ~4600 disease-associated genes analyzed, 3000 have 100% coverage (≥20X) of all exons; twice the number of genes with complete coverage offered by competitors, making it the most comprehensive exome sequencing test available. This is also the highest coverage offered by any clinical exome sequencing performed in a CLIA-/CAP-certified laboratory.

The Medical EmExome also features the EmExome Boost Option (Medical EmExome Trios only), which allows clinicians to choose an EGL gene panel relevant to the patient’s phenotype to ensure coverage of ALL exons, at no additional cost. EGL is the first clinical laboratory to offer near complete coverage of all disease-associated genes with an exome boost option. A research protocol is also available for extended exome and genome testing for the discovery of novel disease genes.

What gene coverage levels can be expected?
The Exome Coverage Tool can be used to view typical depth of sequence coverage obtained by exome sequencing performed by EGL. To access this tool, please click [here](eglgenetics.com).

Will EGL re-analyze data?
Yes, upon request.

Will EGL release raw exome data?
Yes, upon request.

What options are available for Medical EmExome testing?

<table>
<thead>
<tr>
<th>Test Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>EXOMT</td>
<td>Medical EmExome: Clinical Exome Sequencing, Trios</td>
</tr>
<tr>
<td>EXOM</td>
<td>Medical EmExome: Clinical Exome Sequencing, Proband Only</td>
</tr>
<tr>
<td>EXOMA</td>
<td>Medical EmExome: Clinical Exome Sequencing, Additional Family Member (EXOMT should be order first or at the same time)</td>
</tr>
<tr>
<td>EXODD</td>
<td>Medical EmExome Array: Deletion/Duplication Analysis</td>
</tr>
<tr>
<td>EXSAN</td>
<td>Sanger Confirmation and Interpretation Only</td>
</tr>
<tr>
<td>EXINT</td>
<td>Interpretation Only (Exome or Genome)</td>
</tr>
</tbody>
</table>

How is the Medical EmExome performed?
Medical EmExome is performed on genomic DNA, using the Agilent V5 Plus designed to target the exome with greater coverage of known disease-associated genes. These targeted regions are then sequenced using the Illumina HiSeq 2500 sequencing system, with 100 basepair (bp) paired-end reads (similar to bidirectional Sanger sequencing) and an average coverage of 100X in the target region. (The target region includes the exon and 10 bp of flanking intronic region). The DNA sequence is mapped to, and analyzed in, comparison with the published human genome build UCSC hg19 reference sequence. The targeted coding exons and splice junctions of the known protein-coding RefSeq genes are assessed for the depth of coverage and data quality threshold values. The Medical EmExome bioinformatics analysis pipeline is used to compare sequence changes in the individual being tested to the reference sequence. All potential positive sequence variants in the proband are confirmed by conventional di-deoxy DNA sequence analysis (Sanger sequencing) using a separate DNA isolation.

The Medical EmExome also features the EmExome Boost Option (Medical EmExome Trios only), which allows clinicians to choose an EGL gene panel relevant to the patient’s phenotype to ensure coverage of ALL exons, at no additional cost.

Targeted sequencing of parental samples for the proband only option will be completed at no additional charge for exome sequencing only if needed (such as a variant of uncertain clinical significance).

The interpretation service is offered for exomes sequenced outside Emory, in either clinical or core laboratories. The exome data is mapped to, and analyzed in, comparison with the published human genome build UCSC hg19 reference sequence. The targeted coding exons and splice junctions of the known protein-coding RefSeq genes are assessed for the depth of coverage and data quality threshold values. The Medical EmExome bioinformatics analysis pipeline is used to compare sequence changes in the individual being tested to the reference sequence.

**Indications**

This service is offered for exomes sequenced outside Emory in either clinical or core research laboratories.

**Methodology**

Medical EmExome is performed on genomic DNA, using the Agilent V5 Plus designed to target the exome with greater coverage of known disease-associated genes. These targeted regions are then sequenced using the Illumina HiSeq 2500 sequencing system, with 100 basepair (bp) paired-end reads (similar to bidirectional Sanger sequencing) and an average coverage of 100X in the target region. (The target region includes the exon and 10 bp of flanking intronic region). The DNA sequence is mapped to, and analyzed in, comparison with the published human genome build UCSC hg19 reference sequence. The targeted coding exons and splice junctions of the known protein-coding RefSeq genes are assessed for the depth of coverage and data quality threshold values. The Medical EmExome bioinformatics analysis pipeline is used to compare sequence changes in the individual being tested to the reference sequence. All potential positive sequence variants in the proband are confirmed by conventional di-deoxy DNA sequence analysis (Sanger sequencing) using a separate DNA isolation.
bp of flanking intronic region). The DNA sequence is mapped to, and analyzed in, comparison with the published human genome build UCSC hg19 reference sequence. The targeted coding exons and splice junctions of the known protein-coding RefSeq genes are assessed for the depth of coverage and data quality threshold values. The Medical EmExome bioinformatics analysis pipeline is used to compare sequence changes in the individual being tested to the reference sequence. All potential positive sequence variants in the proband are confirmed by conventional di-deoxy DNA sequence analysis (Sanger sequencing) using a separate DNA isolation.

The Medical EmExome also features the EmExome Boost Option, which allows clinicians to choose an EGL gene panel relevant to the patient’s phenotype to ensure coverage of ALL exons, at no additional cost.

Targeted sequencing of parental samples for the proband only option will be completed at no additional charge for exome sequencing only if needed (such as a variant of uncertain clinical significance).

### Specimen Requirements

#### Additional Specimen Collection/Handling Instructions Required for this Test

Please send parental samples with the sample of the affected individual. If parental samples are not available, please notify the laboratory. No extra charge is applied for processing parental samples.

Please contact the lab before submitting any other specimen type.

**Type: Whole Blood**

Specimen Requirements:

In EDTA (purple top) or ACD (yellow top) tube: 5-10 ml for all ages

Specimen Collection and Shipping: Refrigerate until time of shipment. Ship sample within 5 days of collection at room temperature with overnight delivery.