Medical EmExome: Clinical Exome Sequencing, Proband Only

Test Code: EXOME
Turnaround time: 8 weeks
CPT Codes: 81415 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 EGL Genetics (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 (720X) 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 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.

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

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

What options are available for Medical EmExome testing?
EXOMT - Medical EmExome: Clinical Exome Sequencing, Trios
EXOME - Medical EmExome: Clinical Exome Sequencing, Proband Only
EXOMA - Medical EmExome: Clinical Exome Sequencing, Additional Family Member (EXOMT should be order first or at the same time)
EXODD - Medical EmExome Array: Deletion/Duplication Analysis
EXSAN - Sanger Confirmation and Interpretation Only
EXINT - Interpretation Only (Exome or Genome)
EXOMR - Medical EmExome: Clinical Exome Rereanalysis

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. 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.

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

The EmExome is indicated when there is a suspicion of a genetic etiology contributing to the proband’s manifestations.

Methodology

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### Detection

Unknown

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<th>Specimen Requirements</th>
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**Additional Specimen Collection/Handling Instructions Required for this Test**

Please send samples from parents at the time of sending 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.

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: 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.

#### Type: Saliva

Specimen Requirements:

NGSwab is accepted for this testing. NGSwab utilizes Oragene’s OCD-100 kit to collect high quality DNA from saliva. For more information, click [here](#)

Specimen Collection and Shipping: Do not expose specimen to heat or direct sunlight. Keep the specimen dry. Ship sample at room temperature with overnight delivery.

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<th>Special Instructions</th>
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Please submit medical records or clinic summary notes, and a signed consent form when ordering exome testing. Testing will not be initiated until these documents are received.