Congenital Obesity Panel: Sequencing and CNV Analysis

Test Code: MM600
Turnaround time: 6 weeks
CPT Codes: 81406 x1, 81408 x1, 81403 x1, 81404 x1

Condition Description

Congenital obesity is the excessive accumulation and storage of fat in the body that is present during infancy and/or childhood. Obesity may be diagnosed as an isolated clinical finding or as a part of syndromic findings. Monogenic forms of childhood obesity are very rare. Mutations in only a few genes controlling appetite and metabolism are known to cause the development of severe obesity in early childhood. EGL offers testing for syndromic and nonsyndromic single-gene causes of congenital obesity; predisposition and susceptibility genes are not included in this testing.

Syndromic causes of congenital and early-onset obesity on this panel include:

- Albright hereditary osteodystrophy
- Alström syndrome
- Bardet-Biedl syndrome
- Borjeson-Forssman-Lehmann syndrome
- Cohen syndrome
- Schaaf-Yang syndrome (also called Prader-Willi-like syndrome)
- Leptin deficiency
- Leptin receptor deficiency
- MC4R (melanocortin 4 receptor) deficiency

References:


Genes

ALMS1, ARL6, BBS1, BBS10, BBS12, BBS2, BBS4, BBS5, BBS7, BBS9, CEP290, GNAS, LEP, LEPR, MAGEL2, MC4R, MKKS, MKS1, NROB2, NTRK2, PCSK1, PHF6, POMC, SDCCAG8, SIM1, TRIM32, TTC8, VPS13B, WDPCP

Indications

The test is indicated for:

- Individuals with a clinical or suspected diagnosis of congenital obesity.

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 mean 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

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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**