Congenital Obesity: Sequencing Panel

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
- Alstrom 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:

6. OrphaNet available at [http://www.orpha.net/].

Genes

ALMS1, ARL6, BBS1, BBS10, BBS12, BBS2, BBS4, BBS5, BBS7, BBS9, CEP290, GNAS, LEP, LEPR, MAGEL2, MC4R, MKKS, MKS1, NR0B2, 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.

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. 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%.

Specimen Requirements