

Riboflavin Transporter Deficiency and Related Disorders Panel

Panel Gene List: *SLC52A1*, *SLC52A2*, *SLC52A3*, *SLC25A32*, *FLAD1*, *ETFDH*, *ETFA*, *ETFB*, *ACAD9*

Clinical Features:

Individuals with riboflavin transporter deficiency (also known as Brown-Vialetto-Van Laere syndrome and Fazio-Londe syndrome) typically present in infancy or childhood before age 8 years, but can also present as late as the third decade.² Symptoms may include motor neuronopathy (with muscle weakness and wasting and diaphragm paralysis causing respiratory insufficiency) cranial nerve deficits (sensorineural hearing loss, bulbar palsy, reduced vision and/or optic atrophy), gait ataxia, and feeding difficulties.¹ Infants left untreated typically become ventilator dependent and expire with the first few years of life. Some differences have been reported in the neurologic phenotype in individuals with riboflavin transporter deficiency due to variants in *SLC52A2* versus *SLC52A3*, in particular early onset weakness in the upper limbs and an ataxic gait in patients with *SLC52A2* variants.⁶ An improvement in clinical symptoms has been shown with high dose riboflavin supplementation.¹ Acylcarnitine profiles with the accumulation of short and medium chains are abnormal in 50-60% of individuals with riboflavin transporter deficiency and quickly normalize with riboflavin supplementation.

Some of the features of riboflavin transporter deficiency can overlap with those of other metabolic disorders such as multiple acyl-CoA dehydrogenase deficiency/glutaric acidemia type II (GAI), lipid storage myopathy due to flavin adenine dinucleotide synthetase deficiency, and mitochondrial complex I deficiency due to *ACAD9* deficiency.² The *SLC25A32* gene has been described in association with riboflavin-responsive exercise intolerance.⁷ Many individuals with GAI due to pathogenic variants in *ETFDH* and some with pathogenic variants in *FLAD1* and *ACAD9* genes have been reported to respond to riboflavin supplementation.^{3,4}

Genetics:

All of the disorders tested for in this panel are inherited in an autosomal recessive manner with the exception of riboflavin deficiency due to variants in *SLC52A1* for which only a single case has been reported.⁵

Clinical Test Sensitivity:

The clinical sensitivity of sequencing and deletion/duplication analysis of the genes included in this panel depends in part on the patient's clinical phenotype. In a large international study of patients with a phenotype of cranial neuropathies and sensorimotor neuropathy, with or without respiratory insufficiency, sequence analysis of *SLC52A2* detected pathogenic variants in 13/72

(18%).⁶ None of the other probands in this study had variants identified in the *SLC52A3* or *SLC52A1* genes.

Test Methods:

Using genomic DNA from the submitted specimen, the complete coding regions and splice site junctions of the genes on this panel are enriched using a proprietary targeted capture system developed by GeneDx for next-generation sequencing with CNV calling (NGS-CNV). The enriched targets are simultaneously sequenced with paired-end reads on an Illumina platform. Bi-directional sequence reads are assembled and aligned to reference sequences based on NCBI RefSeq transcripts and human genome build GRCh37/UCSC hg19. After gene specific filtering, data are analyzed to identify sequence variants and most deletions and duplications involving coding exons. Alternative sequencing or copy number detection methods are used to analyze regions with inadequate sequence or copy number data. Reportable variants include pathogenic variants, likely pathogenic variants and variants of uncertain significance. Likely benign and benign variants, if present, are not routinely reported but are available upon request.

The technical sensitivity of sequencing is estimated to be > 99% at detecting single nucleotide events. It will not reliably detect deletions greater than 20 base pairs, insertions or rearrangements greater than 10 base pairs, or low-level mosaicism. The copy number assessment methods used with this test cannot reliably detect copy number variants of less than 500 base pairs or mosaicism and cannot identify balanced chromosome aberrations. Assessment of exon-level copy number events is dependent on the inherent sequence properties of the targeted regions, including shared homology and exon size.

References:

1. Jaeger et al. (2016) J. Inherit. Metab. Dis. 39 (4):559-64 (PMID: 26973221)
2. Manole A, Houlden H. Riboflavin Transporter Deficiency Neuronopathy. 2015 Jun 11. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2018. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK299312/>
3. Olsen et al. (2016) Am. J. Hum. Genet. 98(6):1130-45 (PMID: 27259049)
4. Dewulf et al. (2016). Mol. Genet. Metab. 118(3):185-9 (PMID: 27233227)
5. Ho et al. (2011). Hum. Mutat. 32(1):E1976-84 (PMID: 21089064)
6. Foley et al. (2014) Brain: A Journal Of Neurology 137 (Pt 1):44-56 (PMID: 24253200)
7. Schiff et al., (2016) New Eng. J. Med. 374:795-797.