

Lissencephaly Panel

Sequence Analysis and Exon-Level Deletion/Duplication Testing of 26 Genes

Panel Gene List

*ACTB**, *ACTG1*, *ARX**, *ATP6V0A2*, *B3GALNT2*, *B4GAT1****, *CIT*, *DCX*, *FKRP***, *FKTN*, *GMPPB*, *ISPD*, *KATNB1*, *LAMB1*, *LARGE1*, *NDE1*, *PAFAH1B1*, *POMGNT1**, *POMGNT2*, *POMT1*, *POMT2*, *RELN*, *TMEM5*, *TUBA1A**, *VLDLR*, *WDR62*

*Only large deletion/duplications may be detected for the *ACTB*, *ARX*, *POMGNT1* and *TUBA1A* genes

**No deletion/duplication analysis for the *B4GAT1* and *FKRP* genes

Clinical Features

Lissencephaly is characterized by a thickened cortex and the absence of folds or gyri (agyria) or the presence of abnormally wide gyri (pachygyria). Lissencephalies can present in different forms and with varying severity, ranging from complete agyria to mixed agyria and pachygyria, or simplified gyri with subcortical band heterotopia (double cortex). Pathogenic variants in distinct genes lead to overlapping forms of lissencephaly, including classic smooth lissencephaly, cobblestone lissencephaly, lissencephaly with agenesis of the corpus callosum, and lissencephaly with cerebellar hypoplasia. Subcortical band heterotopia is a mild form of lissencephaly characterized by normal gyri but the presence of an abnormal and often symmetric band of gray matter under the cortex. Lissencephalies uniformly cause developmental delay, epilepsy, and intellectual disability.¹ The spectrum of disorders associated with lissencephaly includes a group of congenital muscular dystrophies called the alpha-dystroglycanopathies including Walker-Warburg syndrome which is characterized by cobblestone lissencephaly, cerebellar abnormalities, eye defects, muscle weakness.^{2,3}

Genetics

The various forms of lissencephaly demonstrate clinical and genetic heterogeneity.^{1,2} Classic lissencephaly occurs as an autosomal dominant, autosomal recessive, or X-linked trait. *PAFAH1B1* (*LIS1*) is among the most prominent genes associated with lissencephaly. Loss of *PAFAH1B1* alone causes epilepsy and developmental delay, but with absence of severe dysmorphism. Deletion of this gene along with adjacent ones in the terminal end of the short arm of chromosome 17 causes Miller-Dieker syndrome, characterized by epilepsy, dysmorphic features, severe developmental delay and, occasionally, heart defects and omphalocele. Somatic mutations in *PAFAH1B1* and *DCX* have been described.^{4,5} Cobblestone lissencephaly and lissencephaly with cerebellar hypoplasia segregate as autosomal recessive disorders and lissencephaly with agenesis of the corpus callosum is an X-linked disorder. Lissencephaly can sometimes occur together with heterotopias or polymicrogyria, depending on the affected gene and the type of pathogenic variant.

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; however, technical limitations and inherent sequence properties effectively reduce this resolution for some genes. Alternative sequencing or copy number detection methods are used to analyze or confirm regions with inadequate sequence or copy number data by NGS. 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.

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. Specific information about the diagnostic yield for each gene in selected populations is summarized in the following table(s). 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. Gene specific exclusions for exon-level deletion/duplication testing for this panel are: *B4GAT1* and *FKRP* genes, no copy number testing, *ACTB*, *ARX*, *POMGNT1* and *TUBA1A* genes, only whole gene deletions or duplications may be detected.

Gene	Protein	Inheritance	Disease Associations
<i>ACTB</i> *	Actin, Beta	AD	80% of Baraitser-Winter syndrome ⁶
<i>ACTG1</i>	Actin, Gamma-1	AD	20% of Baraitser-Winter syndrome ⁶
<i>ARX</i> *	Aristaless-related homeobox protein	XL	70-95% of XLAG7, ⁸ 3-10% in XLID ^{9,10}
<i>ATP6V0A2</i>	Lysosomal H(+)-ATPase V0 subunit A2	AR	21-24% of autosomal recessive cutis laxatype II ^{11,12}
<i>B3GALNT2</i>	Beta-1,3-N-Acetylgalactosaminyltransferase 2	AR	Rare in alpha-dystroglycanopathies ¹³ Rare in congenital muscular dystrophy ¹⁴
<i>B4GAT1</i> (<i>B3GNT1</i>)**	Beta-1,4-Glucuronyltransferase 1	AR	Rare in alpha-dystroglycanopathies ^{15,16}
<i>CIT</i>	Citron rho-interacting serine/threonine kinase	AR	Rare in MCPH17, ^{18,19}
<i>DCX</i>	Doublecortin	XL	Up to 100% XL lissencephaly 10% of classic lissencephaly 85% females and ~30% males with SBH ^{1,8,20}
<i>FKRP</i> **	Fukutin-related protein	AR	~2% of cobblestone lissencephaly ^{3,21} 9% of alpha-dystroglycanopathies ²² 6% of limb-girdle MD ²³ 2.5% of congenital muscular dystrophy ¹⁴
<i>FKTN</i>	Fukutin	AR	~7% of alpha-dystroglycanopathies ²⁴ Rare in congenital muscular dystrophy ¹⁴ 1.5% of limb-girdle MD ²⁵ Does not include the Japanese founder mutation in the 3' UTR ²⁶

<i>GMPPB</i>	GDP-Mannose Pyrophosphorylase B	AR	Rare in alpha-dystroglycanopathies ^{27,28} Rare in congenital muscular dystrophy ¹⁴
<i>ISPD</i>	Isoprenoid synthase domain-containing protein	AR	~6% of cobblestone lissencephaly ²⁴ ~30% of Walker-Warburg syndrome and ~11% of alpha-dystroglycanopathies ^{29,30} Rare in LGMD31
<i>KATNB1</i>	Katanin regulatory subunit B1	AR	<1% of MCD ^{32,33}
<i>LAMB1</i>	Laminin, Beta-1	AR	Rare in cobblestone lissencephaly ³⁴
<i>LARGE1</i>	Like-glycosyltransferase	AR	2-5% of cobblestone lissencephaly ^{3,21} ~1% of alpha-dystroglycanopathies ^{22,24}
<i>NDE1</i>	nudE neurodevelopment protein 1	AR	Rare ^{35,36,37}
<i>PAFAH1B1 (LIS1)</i>	Platelet-Activating Factor Acetylhydrolase 1b, Regulatory Subunit 1	AD	~40-65% of classic lissencephaly ^{1,38}
<i>POMGNT1*</i>	Protein O-Mannose Beta 1-2-N-Acetylglucosaminyltransferase	AR	11-18% of cobblestone lissencephaly ^{3,21} 8-10% of alpha-dystroglycanopathies ^{22,24}
<i>POMGNT2</i>	Protein O-Mannose Beta-1,4-N-Acetylglucosaminyltransferase 2	AR	Rare in alpha-dystroglycanopathies ³⁹
<i>POMT1</i>	Protein O-Mannosyltransferase 1	AR	27-34% of cobblestone lissencephaly ^{3,21} 9-21% of alpha-dystroglycanopathies ^{22,24}
<i>POMT2</i>	Protein O-Mannosyltransferase 2	AR	8-11% of cobblestone lissencephaly ^{3,21} 9-11% of alpha-dystroglycanopath ^{22,24}
<i>RELN</i>	Reelin	AR	Rare ^{40,41}
<i>TMEM5</i>	Transmembrane protein 5	AR	~6% of cobblestone lissencephaly ²¹ Rare in alpha-dystroglycanopathies ⁴²
<i>TUBA1A*</i>	Tubulin, Alpha-1A	AD	1% of classic lissencephaly 30% of lissencephaly with cerebellar hypoplasia ^{43,44}
<i>VLDLR</i>	Very low density lipoprotein receptor	AR	Rare cerebellar hypoplasia with simplified gyri ^{45,46}
<i>WDR62</i>	WD repeat-containing protein 62	AR	Unknown ⁴⁷

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