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Resources for Genetics Professionals – Genetic Disorders Associated with Founder Variants Common in the Gitxsan Population

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A founder variant is a pathogenic variant observed at high frequency in a specific population due to the presence of the variant in a single ancestor or small number of ancestors. The presence of a founder variant can affect the approach to molecular genetic testing. When one or more founder variants account for a large percentage of all pathogenic variants found in a population, testing for the founder variant(s) may be performed first.

The table below includes common founder variants – here defined as **three or fewer variants that account for** >**50% of the pathogenic variants identified in a single gene in individuals of a specific ancestry** – in individuals of Gitxsan ancestry. Note: Pathogenic variants that are common worldwide due to a DNA sequence hot spot are not considered founder variants and thus are not included.

Gene	Disorder	MOI	DNA Nucleotide Change	Predicted Protein Change	% of Pathogenic Variants in Gene ¹	Carrier Frequency	Ethnicity	Reference Sequences	References
ANK2	Long QT syndrome 4 (OMIM 600919)	AD	c.1937C>T	p.Ser646Phe	<100%	NA	Gitxsan	NM_001148.6 NP_001139.3	Swayne et al [2017]
KCNQ1	Long QT syndrome 1 (OMIM 192500)	AD	c.613G>A	p.Val205Met	<100%	NA	Gitxsan	NM_000218.3 NP_000209.2	Arbour et al [2008], Jackson et al [2014]

Table. Genetic Disorders Associated with Founder Variants Common in the Gitxsan Population

Included if \leq 3 pathogenic variants account for \geq 50% of variants identified in a specific ethnic group

AD = autosomal dominant; MOI = mode of inheritance; NA = not applicable

1. This percentage does not account for the possibility of rare *de novo* pathogenic variants occurring in this population.

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