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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.

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

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]

Included if ≤3 pathogenic variants account for ≥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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