WES LONG QT SYNDROME [1] DG 3.5

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
CACNA1C	132.6	100.0	100.0	618447
CALM1	143.5	100.0	100.0	616247
CALM2	108.0	73.5	73.5	616249
CALM3	129.1	100.0	100.0	618782
KCNE1	237.9	100.0	100.0	613695
KCNE2	141.8	100.0	100.0	613693
KCNH2	137.1	100.0	100.0	613688
KCNQ1	123.7	100.0	100.0	192500
SCN5A	135.9	100.0	100.0	603830
TRDN	152.6	99.9	99.6	No OMIM phenotype

Gene symbols used follow HGCN guidelines: Gray KA, Yates B, Seal RL, Wright MW, Bruford EA. Nucleic Acids Res. 2015 Jan 43(Database issue):D1079-85.
TWIST is the default chemistry for all WES samples. Agilent V5 was the default chemistry until Q3 2021.
Median Coverage describes the average number of reads seen across 50 exomes.
Covered 10x describes the percentage of a gene's coding sequence that is covered at least 10x.
Covered 20x describes the percentage of a gene's coding sequence that is covered at least 20x.
Genes with no value for coverage are non protein coding genes.
Non protein coding genes are covered, but as coverage statistics are based on protein coding regions, statistics could not be generated.
OMIM release used for OMIM disease identifiers and descriptions: September 1st, 2021.

Ad 1. "No OMIM phenotype" signifies a gene without a current OMIM association Ad 2. OMIM phenotype descriptions between {} signify risk factors