WES HEREDITARY NEUROLOGICAL PAIN DISORDERS[1] DG 3.2

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ATL1	154.9	99.9	99.5	182600;613708
ATL3	126.1	99.6	97.6	615632
CABIN1	150.3	100.0	99.4	-
CACNA1A	85.3	93.1	88.4	-
CLTCL1	101.5	98.6	97.5	-
COL6A5	136.4	99.9	99.2	-
COMP	128.7	93.8	92.4	619161
COQ6	118.1	99.9	98.5	614650
DNM1L	118.8	99.6	98.3	614388
DNMT1	117.3	99.2	98.8	614116
DYNC1H1	140.2	99.9	99.3	158600;614228
ELP1	124.3	99.8	98.9	223900
FAAH	130.1	94.3	90.3	606581
FBLN5	103.8	91.8	91.7	No OMIM phenotype
FLVCR1	142.6	99.7	98.3	609033
GLA	72.8	91.0	85.9	301500
HCN1	133.8	98.4	98.3	615871;618482
HCN2	36.4	59.8	47.7	-
HCN3	148.5	99.9	98.5	-
HSPB1	60.0	99.1	92.1	606595;608634
KIF1A	116.1	97.4	95.3	614213;610357
LIFR	119.1	99.3	97.8	601559

LZTR1	141.0	100.0	99.9	615670
MME	109.8	99.7	98.6	617017;617018
MPZ	95.0	85.6	81.9	607677;118200;607791;607736
NAGLU	119.2	93.8	91.7	616491;252920
NGF	194.6	100.0	100.0	608654
NMNAT2	97.8	100.0	98.8	-
NTRK1	138.8	99.9	98.5	256800
PIEZO2	106.7	99.8	99.2	617146
PMP22	110.9	100.0	100.0	118220;118300;145900;162500;180800;139393
PRDM12	116.8	91.7	89.6	616488
RAB7A	131.7	100.0	100.0	600882
RETREG1	118.3	99.1	96.1	613115
SCN10A	127.0	99.9	98.5	615551
SCN11A	117.7	99.3	97.5	615548;615552
SCN1B	172.2	98.2	96.3	604233;615377;612838;617350
SCN2B	190.2	100.0	100.0	615378
SCN3A	150.4	99.8	99.1	617935;617938
SCN3B	143.0	100.0	100.0	613120
SCN4B	71.5	99.9	97.1	611819
SCN7A	99.6	97.7	91.2	-
SCN8A	168.5	100.0	99.5	614306;614558;618364;617080
SCN9A	137.8	99.1	97.0	133020;167400;243000
SEPTIN9	151.1	100.0	99.5	162100
SMARCB1	201.9	100.0	99.9	162091
SPTLC1	107.4	98.7	93.7	162400
SPTLC2	141.9	100.0	100.0	613640
TECPR2	140.7	100.0	100.0	No OMIM phenotype
TOR1A	127.6	91.3	91.3	No OMIM phenotype
TRPA1	89.1	96.4	89.9	615040
TRPM8	104.7	99.8	98.5	-

TRPV1	131.2	99.9	99.0	-
TRPV3	130.0	99.8	98.6	614594;616400
TRPV4	151.2	100.0	99.9	606071;600175;617383
TTR	128.3	94.6	94.6	115430;105210
WNK1	135.5	99.8	99.3	201300
ZFHX2	130.7	99.8	99.1	147430

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.