WES NEUROLOGICAL PAIN DISORDERS[1] DG 3.5

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ATL1	143.8	100.0	100.0	182600;613708
ATL3	134.9	100.0	100.0	615632
CABIN1	118.1	100.0	100.0	-
CACNA1A	141.5	100.0	100.0	-
CACNA1H	148.3	100.0	100.0	No OMIM phenotype
CLTCL1	122.9	100.0	100.0	-
COL6A5	146.0	100.0	99.9	-
COMP	135.9	100.0	100.0	619161
COQ6	146.6	100.0	100.0	614650
DNM1L	142.0	100.0	100.0	614388
DNMT1	125.3	99.9	99.1	614116
DYNC1H1	125.6	100.0	100.0	158600;614228
ELP1	140.0	100.0	100.0	223900
FAAH	128.7	100.0	100.0	606581
FBLN5	117.6	91.8	91.8	No OMIM phenotype
FBN2	141.3	100.0	100.0	No OMIM phenotype
FLVCR1	145.8	100.0	100.0	609033
GLA	95.1	90.9	90.9	301500
HCN1	142.0	99.9	99.7	615871;618482
HCN2	112.7	94.4	92.1	-
HCN3	126.1	100.0	100.0	-
HSPB1	156.1	100.0	100.0	606595;608634
KCNQ3	134.7	100.0	100.0	No OMIM phenotype
KIF1A	122.6	100.0	100.0	614213;610357
LIFR	153.9	100.0	100.0	601559

LZTR1	134.2	100.0	100.0	615670
MME	148.7	97.6	97.4	617017;617018
MPZ	119.2	100.0	100.0	607677;118200;607791;607736
NAGLU	132.5	100.0	100.0	616491;252920
NGF	149.1	100.0	100.0	608654
NMNAT2	125.1	100.0	100.0	-
NTRK1	130.0	100.0	100.0	256800
PIEZO2	133.8	100.0	100.0	617146
PMP22	160.7	100.0	100.0	118220;118300;145900;162500;180800;139393
PRDM12	115.3	95.7	92.4	616488
RAB7A	127.7	100.0	100.0	600882
RETREG1	160.3	100.0	100.0	613115
SCN10A	127.9	100.0	100.0	615551
SCN11A	136.5	100.0	99.9	615548;615552
SCN1B	110.6	100.0	100.0	604233;615377;612838;617350
SCN2B	105.9	100.0	100.0	615378
SCN3A	160.9	100.0	100.0	617935;617938
SCN3B	113.4	100.0	100.0	613120
SCN4B	118.2	100.0	100.0	611819
SCN7A	159.3	100.0	100.0	-
SCN8A	131.2	100.0	100.0	614306;614558;618364;617080
SCN9A	157.6	100.0	99.9	133020;167400;243000
SEPTIN9	119.1	100.0	100.0	162100
SMARCB1	118.8	100.0	100.0	162091
SPTLC1	143.5	100.0	100.0	162400
SPTLC2	136.6	100.0	100.0	613640
TECPR2	117.7	100.0	100.0	No OMIM phenotype
TOR1A	132.3	91.2	90.6	No OMIM phenotype
TRPA1	152.3	100.0	100.0	615040
TRPM7	149.1	100.0	100.0	No OMIM phenotype

TRPM8	140.2	100.0	100.0	-
TRPV1	117.7	100.0	100.0	-
TRPV3	120.1	100.0	100.0	614594;616400
TRPV4	122.4	100.0	100.0	606071;600175;617383
TTR	142.6	90.7	90.7	115430;105210
WNK1	134.9	100.0	100.0	201300
ZFHX2	114.9	100.0	100.0	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.

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