WES HEREDITARY NEUROLOGICAL PAIN DISORDERS[1] DG 3.00

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ATL1	180.1	100.0	99.7	182600;613708
ATL3	147.6	99.8	98.3	615632
CABIN1	153.3	100.0	99.6	-
CLTCL1	113.0	98.6	98.2	-
COL6A5	163.1	99.9	99.5	-
COQ6	143.6	99.9	98.4	614650
DNM1L	139.3	99.9	98.5	614388
DNMT1	131.2	99.2	99.0	614116
DYNC1H1	157.5	99.9	99.4	158600;614228
ELP1	149.3	99.8	99.0	223900
FAAH	135.6	93.2	90.0	606581
FBLN5	121.2	91.8	91.8	-
FLVCR1	153.2	100.0	98.9	609033
GLA	81.9	91.1	88.2	301500
HCN1	151.2	98.5	98.2	615871;618482
HCN2	35.7	59.2	49.5	-
HCN3	147.6	99.9	98.5	-
HSPB1	55.8	98.8	91.6	606595;608634
KIF1A	114.7	97.4	95.2	614213;610357
LIFR	136.7	99.7	98.0	601559
LZTR1	136.8	100.0	99.9	615670
MME	138.2	99.8	98.7	617017;617018

MPZ	104.4	87.9	84.1	607677;118200;607791;607736
NAGLU	118.0	92.9	89.9	616491;252920
NGF	224.8	100.0	100.0	608654
NMNAT2	110.5	99.9	98.9	-
NTRK1	138.9	99.8	98.2	256800
PIEZO2	121.6	100.0	99.5	617146
PMP22	123.5	100.0	100.0	118220;118300;145900;162500;180800;139393
PRDM12	123.7	90.8	88.0	616488
RAB7A	151.4	100.0	99.9	600882
RETREG1	141.2	98.8	95.1	613115
SCN10A	148.7	100.0	99.6	615551
SCN11A	144.6	99.8	98.3	615548;615552
SCN1B	178.3	98.0	96.4	604233;615377;612838;617350
SCN2B	219.0	100.0	100.0	615378
SCN3A	173.5	99.8	99.2	617935;617938
SCN3B	151.4	100.0	100.0	613120
SCN4B	82.6	100.0	99.6	611819
SCN7A	126.5	98.3	93.3	-
SCN8A	189.5	100.0	99.8	614306;614558;618364;617080
SCN9A	163.1	99.3	97.9	133020;167400;243000
SEPTIN9	154.2	100.0	99.9	162100
SMARCB1	210.4	100.0	100.0	162091
SPTLC1	132.2	99.2	95.4	162400
SPTLC2	158.5	100.0	100.0	613640
TRPA1	99.7	96.1	89.8	615040
TRPM8	122.0	99.8	98.8	-
TRPV1	133.4	100.0	99.6	-
TRPV3	137.8	99.8	98.5	614594;616400
TRPV4	158.6	100.0	99.9	606071;600175;617383
TTR	151.6	94.6	94.6	115430;105210

WNK1	156.2	99.9	99.6	201300
ZFHX2	134.8	100.0	99.6	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.
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 10x describes the percentage of a gene's coding sequence that is covered at least 20x.
Genes with Median Coverage and % Covered 10x/20x denoting NC are non-coding genes for which coverage statistics could not be generated.
OMIM release used for OMIM disease identifiers and descriptions : October 1st, 2016.

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