# WES HEREDITARY NEUROLOGICAL PAIN DISORDERS[1] DG 3.1

| 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 | - |
| CACNA1A | 95.0 | 93.2 | 90.0 | PMID: 33413531;31928344 |
| 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 | No OMIM phenotype |
| 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 |

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| 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 |
| TOR1A | 142.1 | 91.3 | 91.2 | No OMIM phenotype |
| 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 |

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|---|---|---|---|---|
| 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*