

# HNPD GENE PANEL DG 3.2.0 (58 genes)

Releasedate: 16-09-2021

<i>Gene</i>	<i>Agilent V5 covered &gt;10x</i>	<i>Agilent V5 covered &gt;20x</i>	<i>TWIST covered &gt;10x</i>	<i>TWIST covered &gt;20x</i>	<i>Associated Phenotype Description and OMIM disease ID</i>
ATL1	99,9	99,5	100	99,8	Spastic paraplegia 3A, autosomal dominant, 182600 Neuropathy, hereditary sensory, type ID, 613708
ATL3	99,6	97,6	100	99,9	Neuropathy, hereditary sensory, type IF, 615632
CABIN1	100	99,4	100	99,9	No OMIM disease ID
CACNA1A	93,1	88,4	100	99,9	Developmental and epileptic encephalopathy 42, 617106 Spinocerebellar ataxia 6, 183086 Episodic ataxia, type 2, 108500 Migraine, familial hemiplegic, 1, with progressive cerebellar ataxia, 141500 Migraine, familial hemiplegic, 1, 141500
CLTCL1	98,6	97,5	100	100	No OMIM disease ID
COL6A5	99,9	99,2	100	100	No OMIM disease ID
COMP	93,8	92,4	100	100	Pseudoachondroplasia, 177170 Carpal tunnel syndrome 2, 619161 Epiphyseal dysplasia, multiple, 1, 132400
COQ6	99,9	98,5	100	100	Coenzyme Q10 deficiency, primary, 6, 614650
DNM1L	99,6	98,3	100	100	Optic atrophy 5, 610708 Encephalopathy, lethal, due to defective mitochondrial peroxisomal fission 1, 614388
DNMT1	99,2	98,8	99,9	99,4	Neuropathy, hereditary sensory, type IE, 614116 Cerebellar ataxia, deafness, and narcolepsy, autosomal dominant, 604121
DYNC1H1	99,9	99,3	100	100	Spinal muscular atrophy, lower extremity-predominant 1, AD, 158600 Charcot-Marie-Tooth disease, axonal, type 20, 614228 Mental retardation, autosomal dominant 13, 614563
ELP1	99,8	98,9	100	100	Dysautonomia, familial, 223900
FAAH	94,3	90,3	100	100	No OMIM disease ID
FBLN5	91,8	91,7	91,8	91,8	Cutis laxa, autosomal recessive, type IA, 219100 Macular degeneration, age-related, 3, 608895 Neuropathy, hereditary, with or without age-related macular degeneration, 608895 ?Cutis laxa, autosomal dominant 2, 614434

FLVCR1	99,7	98,3	100	99,9	Ataxia, posterior column, with retinitis pigmentosa, 609033
GLA	91	85,9	91,3	91,3	Fabry disease, cardiac variant, 301500 Fabry disease, 301500
HCN1	98,4	98,3	98,5	98,4	Developmental and epileptic encephalopathy 24, 615871 Generalized epilepsy with febrile seizures plus, type 10, 618482
HCN2	59,8	47,7	84	76,9	Febrile seizures, familial, 2, 602477 Generalized epilepsy with febrile seizures plus, type 11, 602477
HCN3	99,9	98,5	100	100	No OMIM disease ID
HSPB1	99,1	92,1	100	100	Neuronopathy, distal hereditary motor, type IIB, 608634 Charcot-Marie-Tooth disease, axonal, type 2F, 606595
KIF1A	97,4	95,3	98	98	NESCAV syndrome, 614255 Neuropathy, hereditary sensory, type IIC, 614213 Spastic paraplegia 30, autosomal dominant, 610357 Spastic paraplegia 30, autosomal recessive, 610357
LIFR	99,3	97,8	100	99,9	Stuve-Wiedemann syndrome/Schwartz-Jampel type 2 syndrome, 601559
LZTR1	100	99,9	100	100	Noonan syndrome 2, 605275 Noonan syndrome 10, 616564
MME	99,7	98,6	98	97,9	?Spinocerebellar ataxia 43, 617018 Charcot-Marie-Tooth disease, axonal, type 2T, 617017
MPZ	85,6	81,9	100	100	Charcot-Marie-Tooth disease, type 2I, 607677 Dejerine-Sottas disease, 145900 Charcot-Marie-Tooth disease, type 1B, 118200 Roussy-Levy syndrome, 180800 Charcot-Marie-Tooth disease, dominant intermediate D, 607791 Hypomyelinating neuropathy, congenital, 2, 618184 Charcot-Marie-Tooth disease, type 2J, 607736
NAGLU	93,8	91,7	99,9	98,7	?Charcot-Marie-Tooth disease, axonal, type 2V, 616491 Mucopolysaccharidosis type IIIB (Sanfilippo B), 252920
NGF	100	100	100	100	Neuropathy, hereditary sensory and autonomic, type V, 608654
NMNAT2	100	98,8	100	100	No OMIM disease ID
NTRK1	99,9	98,5	100	100	Insensitivity to pain, congenital, with anhidrosis, 256800
PIEZO2	99,8	99,2	100	100	Arthrogryposis, distal, type 5, 108145 Arthrogryposis, distal, with impaired proprioception and touch, 617146 Arthrogryposis, distal, type 3, 114300 ?Marden-Walker syndrome, 248700

PMP22	100	100	100	100	Charcot-Marie-Tooth disease, type 1A, 118220 Roussy-Levy syndrome, 180800 Charcot-Marie-Tooth disease, type 1E, 118300 ?Neuropathy, inflammatory demyelinating, 139393 Neuropathy, recurrent, with pressure palsies, 162500 Dejerine-Sottas disease, 145900
PRDM12	91,7	89,6	92,8	91	Neuropathy, hereditary sensory and autonomic, type VIII, 616488
RAB7A	100	100	100	100	Charcot-Marie-Tooth disease, type 2B, 600882
RETREG1	99,1	96,1	100	100	Neuropathy, hereditary sensory and autonomic, type IIB, 613115
SCN10A	99,9	98,5	100	100	Episodic pain syndrome, familial, 2, 615551
SCN11A	99,3	97,5	100	100	Episodic pain syndrome, familial, 3, 615552 Neuropathy, hereditary sensory and autonomic, type VII, 615548
SCN1B	98,2	96,3	99,7	98,9	Generalized epilepsy with febrile seizures plus, type 1, 604233 Developmental and epileptic encephalopathy 52, 617350 Cardiac conduction defect, nonspecific, 612838 Atrial fibrillation, familial, 13, 615377 Brugada syndrome 5, 612838
SCN2B	100	100	100	100	Atrial fibrillation, familial, 14, 615378
SCN3A	99,8	99,1	100	100	Epilepsy, familial focal, with variable foci 4, 617935 Developmental and epileptic encephalopathy 62, 617938
SCN3B	100	100	100	100	Atrial fibrillation, familial, 16, 613120 Brugada syndrome 7, 613120
SCN4B	99,9	97,1	100	100	Atrial fibrillation, familial, 17, 611819 Long QT syndrome 10, 611819
SCN7A	97,7	91,2	100	99,9	No OMIM disease ID
SCN8A	100	99,5	100	100	?Myoclonus, familial, 2, 618364 Seizures, benign familial infantile, 5, 617080 Cognitive impairment with or without cerebellar ataxia, 614306 Developmental and epileptic encephalopathy 13, 614558
SCN9A	99,1	97	100	100	Erythralgia, primary, 133020 Insensitivity to pain, congenital, 243000 Small fiber neuropathy, 133020 Paroxysmal extreme pain disorder, 167400 Neuropathy, hereditary sensory and autonomic, type IID, 243000
SEPTIN9	100	99,5	100	100	Amyotrophy, hereditary neuralgic, 162100

SMARCB1	100	99,9	100	100	Rhabdoid tumors, somatic, 609322 Coffin-Siris syndrome 3, 614608
SPTLC1	98,7	93,7	100	100	Neuropathy, hereditary sensory and autonomic, type IA, 162400
SPTLC2	100	100	100	99,9	Neuropathy, hereditary sensory and autonomic, type IC, 613640
TECPR2	100	100	100	100	Spastic paraplegia 49, autosomal recessive, 615031
TOR1A	91,3	91,3	91,7	91,3	Arthrogryposis multiplex congenita 5, 618947 Dystonia-1, torsion, 128100
TRPA1	96,4	89,9	100	99,9	?Episodic pain syndrome, familial, 1, 615040
TRPM8	99,8	98,5	100	100	No OMIM disease ID
TRPV1	99,9	99	100	100	No OMIM disease ID
TRPV3	99,8	98,6	97,1	97,1	?Palmoplantar keratoderma, nonepidermolytic, focal 2, 616400 Olmsted syndrome 1, 614594
TRPV4	100	99,9	100	100	Spondylometaphyseal dysplasia, Kozlowski type, 184252 Digital arthropathy-brachydactyly, familial, 606835 SED, Maroteaux type, 184095 Metatropic dysplasia, 156530 Scapuloperoneal spinal muscular atrophy, 181405 Hereditary motor and sensory neuropathy, type IIc, 606071 ?Avascular necrosis of femoral head, primary, 2, 617383 Neuronopathy, distal hereditary motor, type VIII, 600175 Parastremmatic dwarfism, 168400 Brachyolmia type 3, 113500
TTR	94,6	94,6	94,6	94,6	Amyloidosis, hereditary, transthyretin-related, 105210 Carpal tunnel syndrome, familial, 115430
WNK1	99,8	99,3	100	100	Neuropathy, hereditary sensory and autonomic, type II, 201300 Pseudohypoaldosteronism, type IIC, 614492
ZFHX2	99,8	99,1	100	100	?Marsili syndrome, 147430

Gene symbols used follow HGNC guidelines: Gray KA, Yates B, Seal RL, Wright MW, Bruford EA. Nucleic Acids Res. 2015 Jan 43(Database issue):D1079-85.

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Agilent V5 is the default chemistry, and used for all exome analyses apart from the (in-house) TURBO/RAPID WES route.

TWIST is the chemistry used for (in-house) TURBO/RAPID WES analysis.

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 coverage denoting NC 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 16th , 2021.*

*This list is accurate for panel version DG 3.2.0*

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

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