

WES MOVEMENT DISORDERS DG 3.5

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
AARS2	124.6	100.0	100.0	615889
ABCB7	119.3	99.8	99.3	301310
ABCD1	100.2	100.0	99.6	300100
ABHD12	130.6	100.0	100.0	612674
ACTB	238.4	100.0	100.0	607371
ADAR	130.7	100.0	100.0	615010
ADCY5	125.0	100.0	99.9	606703
ADGRG1	120.4	100.0	100.0	606854
ADPRS	126.6	100.0	100.0	618170
AFG3L2	134.1	100.0	100.0	610246
AGA	151.1	100.0	100.0	208400
AGTPBP1	150.3	100.0	100.0	618276
AIMP1	147.1	100.0	100.0	260600
ALDH18A1	131.6	100.0	100.0	601162;616603
ALDH3A2	137.0	93.5	93.5	270200
ALDH5A1	146.0	100.0	100.0	271980
ALS2	133.7	100.0	100.0	607225
AMPD2	126.3	100.0	100.0	615809
ANO10	135.8	100.0	100.0	613728
ANO3	151.8	100.0	100.0	615034
AP4B1	125.7	100.0	100.0	614066
AP4E1	149.7	100.0	100.0	613744
AP4M1	135.1	100.0	100.0	612936
AP4S1	130.2	87.4	87.4	614067
APTX	131.6	100.0	100.0	208920

ARG1	141.1	93.0	93.0	207800
ARSA	140.2	100.0	100.0	250100
ARX	109.5	99.0	96.7	309510
ASPA	143.1	100.0	100.0	271900
ATCAY	123.4	100.0	100.0	601238
ATL1	143.8	100.0	100.0	182600
ATM	151.7	100.0	100.0	208900
ATP13A2	129.6	100.0	100.0	606693
ATP1A2	132.9	100.0	100.0	104290
ATP1A3	138.8	100.0	100.0	128235
ATP2B3	99.7	100.0	99.8	302500
ATP7B	132.0	100.0	100.0	277900
B4GALNT1	145.1	100.0	100.0	609195
BCAP31	73.7	99.1	92.8	300475
BCKDHA	122.8	100.0	100.0	248600
BCKDHB	156.3	100.0	99.8	248600
BCL11B	135.2	99.9	99.6	618092
BRAT1	133.4	100.0	100.0	618056
BSCL2	125.5	100.0	100.0	270685
BTD	121.2	94.4	94.3	253260
C12orf65	113.7	100.0	100.0	615035
C19orf12	104.9	100.0	99.9	614298
CA8	131.0	100.0	100.0	613227
CACNA1A	141.5	100.0	100.0	108500
CACNA1E	131.6	100.0	100.0	618285
CACNA1G	133.6	100.0	100.0	616795
CACNB4	143.6	100.0	100.0	601949
CAMTA1	122.3	100.0	100.0	614756
CAPN1	120.8	100.0	100.0	616907
CCT5	138.6	100.0	100.0	256840

CHMP1A	128.4	100.0	100.0	614961
CLCN2	128.1	100.0	100.0	615651
CLCN4	97.0	100.0	100.0	300114
CLN5	135.3	83.1	83.0	256731
CLN6	141.1	100.0	100.0	601780
CLP1	134.0	100.0	100.0	615803
CLPB	120.8	100.0	100.0	616271
COASY	121.3	100.0	100.0	615643
COL4A1	136.3	100.0	100.0	175780
COL4A2	136.6	100.0	100.0	614483
COL6A1	129.9	100.0	100.0	254090
COL6A2	134.0	100.0	100.0	254090
COL6A3	129.6	100.0	100.0	254090
COQ2	141.3	96.3	96.3	607426
COQ4	143.7	100.0	100.0	616276
COQ8A	127.3	100.0	100.0	607426
COQ9	129.3	100.0	100.0	607426
COX20	151.6	100.0	100.0	220110
CP	143.5	100.0	100.0	604290
CSF1R	116.3	100.0	100.0	221820
CSTB	129.2	100.0	100.0	254800
CTBP1	185.9	100.0	99.5	617915
CTC1	120.1	100.0	100.0	612199
CTSD	143.8	100.0	100.0	610127
CTSF	114.0	100.0	100.0	615362
CWF19L1	131.4	100.0	100.0	616120
CYP27A1	136.9	100.0	100.0	213700
CYP2U1	149.8	100.0	100.0	615030
CYP7B1	158.7	100.0	100.0	270800
DARS1	151.9	100.0	100.0	615281

DARS2	133.3	100.0	100.0	611105
DBT	142.4	100.0	100.0	248600
DCAF17	152.7	100.0	100.0	241080
DCC	142.6	100.0	100.0	157600
DCTN1	133.3	100.0	100.0	168605
DDC	130.7	100.0	100.0	608643
DDHD1	143.6	100.0	100.0	609340
DDHD2	138.3	100.0	100.0	615033
DHDDS	129.5	94.4	94.4	617836
DLAT	134.4	100.0	100.0	245348
DLD	155.9	100.0	100.0	248600
DNAJC12	145.0	100.0	100.0	617384
DNAJC3	144.9	100.0	100.0	616192
DNAL4	154.7	100.0	100.0	616059
DNM1L	142.0	100.0	100.0	614388
DNMT1	125.3	99.9	99.1	604121
DPYS	140.5	100.0	100.0	222748
DTYMK	132.0	100.0	100.0	No OMIM phenotype
EBF3	130.7	100.0	100.0	617330
ECHS1	133.3	100.0	100.0	616277
EIF2B1	136.0	100.0	100.0	603896
EIF2B2	127.5	100.0	100.0	603896
EIF2B3	127.9	100.0	100.0	603896
EIF2B4	138.2	100.0	100.0	603896
EIF2B5	132.6	100.0	100.0	603896
ELOVL4	151.2	100.0	100.0	133190
ELOVL5	129.4	100.0	100.0	615957
ERCC2	127.7	100.0	100.0	278730
ERCC4	143.3	100.0	100.0	278760
ERLIN2	129.7	100.0	100.0	611225

ETHE1	149.0	100.0	100.0	602473
EXOSC3	131.1	100.0	100.0	614678
EXOSC5	119.4	100.0	100.0	-
EXOSC8	147.9	100.0	100.0	616081
EXOSC9	145.9	100.0	100.0	618065
FA2H	135.3	100.0	100.0	612319
FAM126A	150.5	100.0	100.0	610532
FAR1	150.8	100.0	100.0	616154
FARS2	134.7	100.0	100.0	614946
FBXO7	138.4	100.0	100.0	260300
FGF14	145.5	100.0	100.0	609307
FICD	120.2	100.0	100.0	No OMIM phenotype
FLVCR1	145.8	100.0	100.0	609033
FOLR1	142.6	100.0	100.0	613068
FRMD5	131.5	100.0	100.0	-
FRMD7	111.4	99.9	99.2	310700
FTL	86.4	100.0	100.0	606159
GALC	146.4	100.0	100.0	245200
GAMT	127.9	100.0	100.0	612736
GAN	136.8	100.0	100.0	256850
GBA	136.2	100.0	100.0	231000
GBA2	128.8	100.0	100.0	614409
GBE1	156.7	100.0	99.9	263570
GCDH	118.6	100.0	100.0	231670
GCH1	163.0	100.0	100.0	128230
GDAP2	144.7	100.0	99.8	618369
GFAP	139.5	100.0	100.0	203450
GJC2	108.5	99.8	98.7	613206
GLB1	132.0	100.0	100.0	230650
GNAL	147.3	100.0	100.0	615073

GNAO1	124.2	100.0	100.0	617493
GOSR2	132.6	100.0	100.0	614018
GPR143	95.8	100.0	99.9	300814
GRID2	147.9	99.9	99.9	616204
GRIN1	126.3	100.0	100.0	614254
GRIN2B	126.3	99.9	99.8	616139;613970
GRM1	127.5	100.0	100.0	614831
GRN	136.9	100.0	100.0	614706
HACE1	153.1	100.0	100.0	616756
HEXB	154.1	100.0	100.0	268800
HK1	125.4	100.0	100.0	618547
HPCA	126.6	100.0	100.0	224500
HPDL	113.0	100.0	100.0	No OMIM phenotype
HPRT1	117.3	100.0	100.0	300322
HSD17B4	142.8	96.6	96.6	233400
HSPD1	152.4	100.0	100.0	605280
IBA57	149.2	100.0	100.0	616451
IRF2BPL	138.5	100.0	100.0	618088
ISCA2	161.7	100.0	100.0	616370
ITPR1	128.6	100.0	100.0	606658
JAM2	134.4	92.2	92.0	618824
JAM3	133.7	100.0	100.0	613730
KATNB1	136.3	100.0	100.0	616212
KCNA1	140.8	100.0	100.0	160120
KCNA2	134.9	100.0	100.0	616366
KCNC1	156.8	100.0	100.0	616187
KCNC3	116.7	99.7	98.3	605259
KCND3	122.7	100.0	100.0	607346
KCNJ10	131.0	100.0	100.0	612780
KCNJ6	129.7	100.0	100.0	614098

KCNMA1	140.0	100.0	99.9	609446
KCTD7	145.5	100.0	100.0	611726
KIDINS220	147.0	100.0	100.0	617296
KIF1A	122.6	100.0	100.0	610357
KIF1C	120.3	100.0	100.0	611302
KIF5A	120.8	100.0	100.0	604187
KMT2B	121.0	99.8	99.5	617284
L1CAM	98.5	100.0	99.9	303350
LAMA1	132.7	100.0	100.0	615960
LAMB1	130.1	100.0	100.0	615191
LMNB1	133.5	100.0	100.0	169500
MAG	124.9	100.0	100.0	616680
MAPK8IP3	138.7	100.0	100.0	618443
MARS2	121.8	100.0	100.0	611390
MECP2	88.9	100.0	99.7	300673
MECR	137.3	100.0	100.0	617282
MFF	138.1	100.0	100.0	617086
MFSD8	156.8	100.0	100.0	610951
MICU1	141.3	100.0	99.9	615673
MLC1	126.8	100.0	100.0	604004
MMADHC	138.3	89.3	89.3	277410
MRE11	155.3	100.0	100.0	604391
MTHFR	123.4	100.0	100.0	236250
MTPAP	134.7	100.0	100.0	613672
MTTP	144.6	100.0	100.0	200100
MYORG	120.9	100.0	100.0	618317
NANS	129.8	100.0	100.0	610442
NARS2	139.9	100.0	100.0	616239
NDUFS7	189.8	100.0	100.0	618224
NEFL	133.5	100.0	100.0	607684

NEU1	118.4	100.0	100.0	256550
NEXMIF	108.2	100.0	99.9	300912
NF2	123.1	100.0	100.0	101000
NGLY1	146.9	100.0	100.0	615273
NIPA1	142.4	100.0	100.0	600363
NKX2-1	158.3	100.0	100.0	610978
NKX6-2	158.6	100.0	100.0	617560
NOL3	170.9	100.0	100.0	614937
NPC1	133.9	100.0	100.0	257220
NPC2	136.1	100.0	100.0	607625
NPTX1	121.7	100.0	100.0	upcoming paper
NT5C2	139.1	100.0	100.0	613162
NUP62	116.5	100.0	100.0	271930
NUS1	154.9	100.0	100.0	617831
OCLN	129.7	100.0	100.0	251290
OPA1	148.0	100.0	100.0	165500
OPHN1	106.5	100.0	99.9	300486
PACS2	128.5	100.0	100.0	618067
PANK2	143.8	100.0	100.0	234200
PAX6	138.8	100.0	100.0	206700
PCYT2	125.3	100.0	100.0	618770
PDE10A	132.9	99.7	98.7	616922;616921
PDE8B	132.6	100.0	100.0	609161
PDGFB	127.0	100.0	100.0	615483
PDGFRB	124.3	100.0	100.0	615007
PDHA1	104.6	99.7	97.5	312170
PDHX	138.3	100.0	99.8	245349
PDSS1	148.8	100.0	100.0	607426
PDSS2	132.1	100.0	100.0	607426
PDYN	137.2	100.0	100.0	131340

PEX10	124.7	100.0	100.0	202370
PEX2	165.5	100.0	100.0	614867
PEX7	139.0	91.2	91.2	266500
PHYH	144.6	100.0	100.0	266500
PIGG	129.4	100.0	100.0	616917
PIK3R5	111.5	100.0	100.0	615217
PLA2G6	126.8	100.0	99.9	612953
PLP1	95.9	99.9	98.9	312920
PMM2	145.7	100.0	100.0	212065
PMP22	160.7	100.0	100.0	145900
PMPCA	124.2	100.0	100.0	213200
PNKD	121.0	100.0	100.0	118800
PNKP	120.5	100.0	100.0	616267
PNPLA6	123.9	100.0	100.0	612020
POLG	138.3	100.0	100.0	607459
POLR1C	117.4	83.3	83.2	616494
POLR3A	123.2	100.0	100.0	607694
POLR3B	141.2	100.0	99.9	614381
PPT1	138.1	90.3	90.3	256730
PRF1	136.5	100.0	100.0	603553
PRICKLE1	125.3	100.0	100.0	612437
PRKCG	122.9	100.0	100.0	605361
PRKN	129.3	91.9	91.1	600116
PRKRA	223.2	100.0	100.0	612067
PRRT2	120.6	100.0	100.0	128200
PSAP	136.2	100.0	100.0	611722
PTRH2	156.6	100.0	100.0	No OMIM phenotype
PTS	155.2	100.0	100.0	261640
PUM1	124.1	100.0	100.0	617931
PYCR2	137.4	100.0	100.0	616420

QDPR	140.2	100.0	100.0	261630
RAB18	160.5	100.0	100.0	614222
RAB3GAP1	142.2	99.0	99.0	600118
RAB3GAP2	148.2	100.0	100.0	614225
RAD51	113.1	89.3	89.3	614508
RARS1	131.7	94.4	94.3	616140
RARS2	144.1	100.0	100.0	611523
REEP1	136.5	100.0	100.0	610250
RNASEH2A	131.4	100.0	100.0	610333
RNASEH2B	146.8	91.4	91.4	610181
RNASEH2C	147.6	100.0	100.0	610329
RNF170	141.9	100.0	100.0	608984
RNF216	129.5	100.0	100.0	212840
RTN2	117.8	100.0	100.0	604805
RUBCN	128.3	100.0	100.0	615705
SACS	151.3	100.0	100.0	270550
SAMD9L	152.6	100.0	100.0	159550
SAMHD1	149.8	100.0	100.0	612952
SCN11A	136.5	100.0	99.9	615548
SCN1A	165.6	100.0	100.0	607208
SCN2A	167.7	100.0	100.0	618924
SCN8A	131.2	100.0	100.0	614306
SEPSECS	141.0	100.0	100.0	613811
SERAC1	147.5	100.0	100.0	614739
SETX	144.1	100.0	100.0	606002
SGCE	142.8	90.7	90.0	159900
SIL1	134.7	100.0	100.0	248800
SLC12A6	136.2	100.0	100.0	218000
SLC16A2	123.0	100.0	99.9	300523
SLC19A3	137.6	99.6	98.4	607483

SLC1A3	141.1	100.0	100.0	612656
SLC20A2	117.3	100.0	100.0	213600
SLC25A15	132.1	100.0	100.0	238970
SLC2A1	126.1	100.0	100.0	612126
SLC30A10	144.7	100.0	100.0	613280
SLC33A1	133.1	100.0	100.0	612539
SLC39A14	112.6	93.6	93.6	617013
SLC52A2	172.5	100.0	100.0	614707
SLC52A3	133.0	100.0	100.0	211530
SLC6A3	113.2	100.0	100.0	613135
SLC9A1	123.4	100.0	100.0	616291
SMDT1	125.9	100.0	100.0	No OMIM phenotype
SMPD1	139.2	100.0	100.0	257200
SNCA	132.0	100.0	100.0	605543
SNORD118				614561
SNX14	152.5	100.0	100.0	616354
SOX10	142.9	100.0	100.0	611584
SPART	142.0	100.0	100.0	275900
SPAST	148.3	100.0	100.0	182601
SPG11	138.5	100.0	100.0	604360
SPG21	134.6	100.0	100.0	248900
SPG7	136.4	100.0	100.0	607259
SPR	154.1	100.0	100.0	612716
SPTAN1	120.8	100.0	100.0	pending
SPTBN2	124.6	100.0	99.8	600224
STUB1	140.6	100.0	100.0	615768
SUMF1	133.3	100.0	100.0	272200
SUOX	130.2	100.0	100.0	272300
SYNE1	135.9	99.8	99.5	610743
TAF1	100.3	100.0	99.9	314250

TANGO2	123.0	100.0	100.0	616878
TBC1D20	121.7	100.0	100.0	615663
TBC1D23	147.2	100.0	100.0	617695
TBCD	131.3	100.0	100.0	617193
TDP1	136.8	100.0	100.0	607250
TDP2	146.1	100.0	100.0	616949
TECPR2	117.7	100.0	100.0	615031
TENM4	126.4	100.0	100.0	616736
TGM6	124.6	100.0	100.0	613908
TH	142.0	100.0	100.0	605407
THAP1	128.2	100.0	100.0	602629
TIMM8A	80.5	100.0	99.5	304700
TMEM106B	165.3	100.0	100.0	617964
TMEM240	135.0	100.0	100.0	607454
TMEM67	147.4	99.5	97.5	216360
TOE1	117.1	100.0	100.0	614969
TOR1A	132.3	91.2	90.6	128100
TPP1	133.0	100.0	100.0	609270
TREM2	135.7	100.0	100.0	221770
TREX1	142.6	100.0	100.0	225750
TRIT1	130.8	100.0	100.0	617873
TRPM3	134.1	100.0	100.0	-
TSEN15	156.6	100.0	100.0	617026
TSEN2	136.8	100.0	100.0	612389
TSEN54	126.3	100.0	100.0	277470
TTBK2	140.9	100.0	100.0	604432
TTC19	154.4	100.0	100.0	615157
TTPA	147.4	100.0	100.0	277460
TUBA1A	199.9	100.0	100.0	611603
TUBB	153.2	99.6	98.8	615771

TUBB4A	255.0	98.9	95.9	128101;612438
TUBG1	157.4	100.0	100.0	615412
TWNK	117.5	100.0	100.0	609286
TYROBP	151.3	100.0	100.0	221770
UBAP1	130.0	100.0	100.0	618418
UBTF	125.9	100.0	100.0	617672
UCHL1	154.7	100.0	100.0	615491
VAMP1	124.2	100.0	100.0	108600
VAR2	126.1	100.0	100.0	615917
VCP	126.6	100.0	100.0	167320
VLDLR	135.3	100.0	100.0	224050
VPS11	120.2	100.0	100.0	616683
VPS13A	155.0	100.0	100.0	200150
VPS13D	128.8	100.0	100.0	607317
VPS16	137.6	100.0	100.0	-
VPS37A	145.4	100.0	100.0	614898
VPS53	126.4	100.0	100.0	615851
VRK1	160.5	100.0	99.8	607596
WASHC5	137.3	100.0	100.0	603563
WDR26	136.2	100.0	100.0	617616
WDR45	105.6	100.0	100.0	300894
WDR73	115.6	100.0	100.0	251300
WDR81	119.5	100.0	100.0	610185
WFS1	129.4	100.0	100.0	222300
WVOX	134.1	100.0	100.0	614322
XK	96.8	100.0	99.9	300842
XPA	180.2	100.0	100.0	278700
XPR1	137.5	100.0	100.0	616413
XRCC1	123.3	100.0	100.0	617633
ZC4H2	97.2	100.0	99.9	314580

ZFYVE26	132.1	100.0	100.0	270700
ZFYVE27	124.4	100.0	100.0	610244

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