

# WES MOVEMENT DISORDERS DG 2.14

<i>Gene</i>	<i>Median coverage</i>	<i>% covered &gt;10x</i>	<i>% covered &gt;20x</i>	<i>OMIM disease ID</i>
AARS2	126.2	100.0	99.3	615889
ABCB7	131.5	99.9	98.4	301310
ABCD1	76.0	74.7	68.0	300100
ABHD12	107.0	97.3	88.0	612674
ACTB	129.0	99.1	94.2	607371
ADAR	125.0	100.0	99.8	615010
ADCY5	129.2	92.3	89.1	606703
ADGRG1	149.7	100.0	100.0	606854
AFG3L2	121.0	91.9	84.9	610246
AIMP1	84.8	97.3	89.7	260600
ALDH18A1	131.1	100.0	99.9	601162;616603
ALDH3A2	125.7	95.3	94.6	270200
ALS2	170.2	99.9	99.2	607225
AMPD2	135.5	99.9	99.2	615809
ANO10	116.7	98.8	96.5	613728
ANO3	138.8	99.7	98.2	615034
AP4B1	147.4	100.0	99.8	614066
AP4E1	98.7	99.7	97.9	613744
AP4M1	127.2	99.1	96.4	612936
AP4S1	65.8	71.8	69.3	614067
APTX	118.9	94.2	91.1	208920
ARG1	167.8	100.0	100.0	207800
ARSA	97.8	100.0	99.7	250100
ARX	29.1	75.8	59.5	309510
ASPA	127.6	99.1	95.8	271900

ATCAY	146.1	100.0	99.7	601238
ATL1	161.0	99.7	97.9	182600
ATM	109.7	99.0	94.0	208900
ATP13A2	117.4	100.0	98.8	606693
ATP1A2	190.8	100.0	99.6	104290
ATP1A3	177.3	100.0	100.0	128235
ATP2B3	135.2	99.5	97.7	302500
ATP7B	168.9	100.0	99.8	277900
B4GALNT1	151.0	95.6	90.1	609195
BCAP31	70.6	93.1	82.5	300475
BCKDHA	171.5	100.0	99.5	248600
BCKDHB	112.6	88.9	81.3	248600
BSCL2	113.5	100.0	100.0	270685
C12orf65	88.2	97.3	91.9	615035
C19orf12	93.9	100.0	99.7	614298
CA8	114.6	96.8	93.0	613227
CACNA1A	87.8	92.7	89.1	108500
CACNA1E	139.3	99.8	99.3	-
CACNA1G	132.8	99.0	97.5	616795
CACNB4	106.1	96.3	94.6	601949
CAMTA1	185.9	99.6	98.8	614756
CAPN1	146.0	100.0	100.0	616907
CCT5	164.5	99.9	99.1	256840
CHMP1A	133.7	100.0	100.0	614961
CIZ1	152.8	98.9	95.4	614860
CLCN2	108.6	100.0	99.4	615651
CLPB	140.2	100.0	99.5	616271
COASY	168.5	100.0	100.0	615643
COL4A1	92.8	97.9	94.0	175780
COQ2	89.3	96.1	93.2	607426

COQ4	89.8	88.4	84.9	616276
COQ8A	134.3	100.0	99.1	607426
COQ9	91.4	99.9	96.6	607426
COX20	58.1	83.0	65.4	220110
CP	120.0	93.9	89.6	604290
CSF1R	139.5	99.5	98.4	221820
CSTB	82.5	97.1	82.7	254800
CYP27A1	175.1	98.3	96.1	213700
CYP2U1	119.2	93.7	91.2	615030
CYP7B1	93.2	94.7	87.7	270800
DBT	102.1	97.3	93.8	248600
DCAF17	91.9	95.6	89.3	241080
DCC	138.5	100.0	99.9	157600
DCTN1	131.6	99.7	98.3	168605
DDC	101.0	99.1	95.0	608643
DDHD1	141.8	97.1	94.8	609340
DDHD2	149.7	99.9	98.0	615033
DHDDS	93.5	97.8	94.8	617836
DLAT	91.6	99.1	96.0	245348
DLD	123.5	99.9	98.6	248600
DNAJC3	116.3	99.9	98.1	616192
DNAL4	72.6	99.3	93.5	616059
DNMT1	113.4	99.2	98.3	604121
DPYS	133.5	100.0	99.5	222748
ECHS1	112.8	99.8	97.8	616277
EIF2B1	149.9	100.0	100.0	603896
EIF2B2	131.9	100.0	99.5	603896
EIF2B3	163.8	100.0	100.0	603896
EIF2B4	146.0	100.0	99.5	603896
EIF2B5	128.0	99.6	97.9	603896

ELOVL4	91.9	99.9	98.0	133190
ELOVL5	120.9	100.0	99.8	615957
ERLIN2	156.0	100.0	99.3	611225
EXOSC3	88.5	97.3	89.4	614678
FA2H	94.1	87.9	79.9	612319
FAM126A	125.2	97.3	95.2	610532
FAR1	80.4	96.3	92.4	616154
FARS2	207.7	100.0	100.0	614946
FBXO7	189.4	98.5	93.3	260300
FGF14	190.1	100.0	99.7	609307
FLVCR1	139.5	99.2	95.8	609033
FOLR1	150.4	100.0	100.0	613068
FRMD7	114.2	99.9	98.8	310700
FTL	147.7	99.0	93.2	606159
GALC	100.6	98.9	94.6	245200
GAN	190.0	100.0	99.9	256850
GBA	240.3	100.0	100.0	231000
GBA2	176.2	99.9	99.3	614409
GCDH	147.6	99.9	99.1	231670
GCH1	74.4	97.0	86.5	128230
GDAP2	131.1	99.7	97.2	-
GFAP	102.6	91.7	90.3	203450
GJC2	41.9	68.9	58.6	613206
GLB1	94.3	99.6	97.0	230650
GNAL	134.9	94.5	91.6	615073
GOSR2	127.2	95.9	95.0	614018
GPR143	61.5	85.3	75.5	300814
GRID2	175.4	100.0	99.9	616204
GRIN1	150.7	100.0	99.5	614254
GRIN2B	189.4	99.9	99.3	613970;616139

GRM1	185.8	100.0	99.9	614831
HEXB	129.7	99.4	94.0	268800
HPRT1	58.2	96.0	84.8	300322
HSD17B4	95.1	93.9	90.8	233400
HSPD1	96.5	98.3	93.2	605280
IBA57	113.3	93.3	89.5	616451
ITPR1	161.4	100.0	99.9	606658
KATNB1	141.7	100.0	100.0	616212
KCNA1	167.0	100.0	99.7	160120
KCNA2	157.7	100.0	99.9	616366
KCNC1	199.2	100.0	100.0	616187
KCNC3	144.0	68.5	59.0	605259
KCND3	182.5	99.9	99.1	607346
KCNJ10	213.4	89.3	89.1	612780
KCNJ6	156.6	100.0	99.9	614098
KCNMA1	120.4	94.4	93.2	609446
KCTD7	166.7	95.0	95.0	611726
KIDINS220	155.4	99.9	99.5	617296
KIF1A	114.0	99.2	96.1	610357
KIF1C	121.3	99.9	99.1	611302
KIF5A	136.1	100.0	99.9	604187
KMT2B	120.3	94.0	91.2	617284
L1CAM	133.3	99.8	98.4	303350
LAMA1	137.5	100.0	99.6	615960
LAMB1	169.8	100.0	99.6	615191
LMNB1	123.3	99.9	99.1	169500
MARS2	173.2	100.0	100.0	611390
MECP2	87.3	99.1	93.1	19;300673
MECR	108.1	98.8	96.1	617282
MICU1	134.2	96.0	88.8	615673

MLC1	103.4	100.0	99.8	604004
MMADHC	77.0	89.3	75.0	277410
MRE11	51.2	95.3	82.3	604391
MTHFR	126.1	98.4	97.2	236250
MTPAP	109.6	98.9	93.5	613672
MTTP	132.4	99.9	98.8	200100
NANS	106.1	100.0	99.9	610442
NEFL	164.6	99.7	98.1	607684
NEXMIF	139.2	99.9	99.0	300912
NF2	100.2	100.0	99.9	101000
NIPA1	174.3	99.9	99.1	600363
NKX2-1	52.0	96.6	83.3	610978
NKX6-2	52.0	79.0	74.5	617560
NOL3	76.3	93.5	83.9	614937
NPC1	147.9	99.2	97.8	257220
NPC2	140.7	100.0	99.9	607625
NT5C2	125.3	97.1	92.7	613162
NUP62	111.6	100.0	99.9	271930
OCLN	220.7	100.0	100.0	251290
OPA1	122.5	99.1	94.1	165500
PANK2	146.6	99.3	93.1	234200
PAX6	119.9	100.0	99.9	206700
PDE10A	119.8	81.2	80.8	616921;616922
PDE8B	111.0	99.9	98.9	609161
PDGFB	95.1	100.0	100.0	615483
PDGFRB	147.1	99.1	96.5	615007
PDHA1	109.8	98.1	92.1	312170
PDHX	132.5	98.9	94.6	245349
PDSS1	116.7	88.8	78.7	607426
PDSS2	126.8	96.5	93.5	607426

PDYN	107.1	100.0	99.9	131340
PEX10	111.8	96.1	90.1	202370
PEX2	147.1	100.0	100.0	614867
PEX7	113.5	89.6	82.0	266500
PHYH	74.6	97.5	90.8	266500
PIK3R5	110.1	100.0	99.8	615217
PLA2G6	117.5	99.9	98.4	612953
PLP1	129.2	100.0	99.4	312920
PMM2	141.1	99.9	99.4	212065
PMPCA	120.8	99.4	96.8	213200
PNKD	99.8	100.0	99.2	118800
PNKP	93.0	99.8	97.7	616267
PNPLA6	122.1	99.7	98.5	612020
POLG	114.4	100.0	99.5	607459
POLR1C	117.0	99.7	96.1	616494
POLR3A	137.4	100.0	99.9	607694
POLR3B	146.4	99.9	98.5	614381
PRF1	122.5	91.2	90.8	603553
PRICKLE1	117.3	100.0	100.0	612437
PRKCG	116.1	99.0	94.5	605361
PRKRA	179.6	99.8	98.4	612067
PRRT2	78.9	99.9	98.4	128200
PSAP	114.4	99.9	99.0	611722
PUM1	158.0	100.0	99.9	617931
PYCR2	127.6	100.0	97.6	616420
RAB18	82.7	97.1	86.4	614222
RAB3GAP1	124.2	99.4	98.8	600118
RAB3GAP2	94.1	98.4	93.9	614225
RAD51	123.2	89.4	89.4	614508
RARS	86.4	92.7	85.9	616140

RARS2	107.2	100.0	99.1	611523
REEP1	78.3	76.3	75.7	610250
RNASEH2A	142.1	100.0	99.9	610333
RNASEH2B	103.8	93.2	87.5	610181
RNASEH2C	209.2	100.0	99.9	610329
RNF170	147.1	98.3	91.2	608984
RNF216	137.1	99.8	98.6	212840
RTN2	104.8	99.2	96.7	604805
RUBCN	104.1	98.0	97.5	615705
SACS	154.5	100.0	99.7	270550
SAMD9L	165.7	100.0	99.9	159550
SAMHD1	127.9	99.6	96.6	612952
SCN11A	138.1	99.2	97.6	615548
SCN8A	198.3	100.0	99.7	614306
SEPSECS	159.3	100.0	100.0	613811
SERAC1	112.5	98.8	94.6	614739
SETX	163.2	99.9	99.1	606002
SGCE	88.9	93.7	90.0	159900
SIL1	154.4	99.8	98.0	248800
SLC12A6	141.8	100.0	99.9	218000
SLC16A2	60.3	92.8	82.1	300523
SLC19A3	186.4	100.0	99.9	607483
SLC1A3	121.9	100.0	99.8	612656
SLC20A2	119.0	99.7	97.3	213600
SLC25A15	192.5	98.8	95.0	238970
SLC2A1	190.1	92.9	92.8	612126
SLC30A10	164.4	100.0	100.0	613280
SLC33A1	140.9	96.8	90.1	612539
SLC39A14	107.7	99.8	97.9	617013
SLC52A2	177.6	100.0	100.0	614707



SLC52A3	119.6	100.0	100.0	211530
SLC6A3	145.7	100.0	99.8	613135
SLC9A1	160.9	100.0	100.0	616291
SMPD1	123.5	99.6	97.9	257200
SNCA	129.8	100.0	100.0	605543
SNORD118				614561
SNX14	70.1	95.2	82.9	616354
SOX10	65.8	98.2	91.3	611584
SPART	132.4	99.8	98.2	275900
SPAST	63.8	93.1	81.9	182601
SPG11	129.2	99.2	96.9	604360
SPG21	121.4	98.6	94.8	248900
SPG7	119.2	93.3	92.4	607259
SPR	166.5	98.9	90.0	612716
SPTBN2	118.0	99.9	99.3	600224
STUB1	176.1	100.0	98.9	615768
SUMF1	103.3	98.6	91.1	272200
SUOX	212.6	100.0	100.0	272300
SYNE1	136.6	98.2	97.6	610743
TAF1	112.4	99.4	96.6	314250
TANGO2	145.3	100.0	100.0	616878
TBC1D20	145.7	94.2	94.1	615663
TBC1D23	86.0	95.7	91.5	617695
TDP1	122.9	98.7	95.3	607250
TDP2	165.1	99.9	98.8	616949
TECPR2	161.1	100.0	99.9	615031
TENM4	160.8	99.9	99.2	616736
TGM6	149.7	99.7	98.0	613908
TH	68.2	97.6	88.7	605407
THAP1	122.0	100.0	100.0	602629

TIMM8A	46.0	94.5	78.8	304700
TMEM106B	120.2	99.8	96.4	617964
TMEM240	112.2	99.8	97.4	607454
TMEM67	72.9	93.3	83.4	216360
TOE1	165.1	100.0	100.0	614969
TOR1A	185.0	100.0	99.8	128100
TPP1	146.3	100.0	100.0	609270
TREM2	149.0	99.9	99.6	221770
TREX1	242.4	100.0	100.0	225750
TSEN2	123.8	100.0	99.8	612389
TSEN54	82.9	95.9	92.9	277470
TTBK2	123.2	100.0	98.9	604432
TTC19	92.1	80.6	72.5	615157
TTPA	101.5	83.6	76.6	277460
TUBA1A	113.2	99.9	97.8	611603
TUBB4A	121.2	96.0	95.3	128101;612438
TUBG1	164.2	100.0	100.0	615412
TWNK	178.8	100.0	100.0	609286
TYROBP	95.2	100.0	99.9	221770
VAMP1	131.5	100.0	100.0	108600
VCP	144.8	99.9	99.5	167320
VLDLR	200.9	99.9	99.4	224050
VPS13A	69.5	95.3	85.3	200150
VPS13D	158.6	99.9	99.4	-
VPS37A	73.6	86.6	66.4	614898
VPS53	129.2	91.4	90.4	615851
VRK1	124.8	97.5	94.2	607596
WASHC5	146.6	99.6	98.1	603563
WDR45	75.0	97.4	90.1	300894
WDR73	138.9	100.0	100.0	251300

WDR81	163.3	99.9	99.4	610185
WVOX	130.9	100.0	99.7	614322
XK	96.8	99.9	99.1	300842
XPR1	131.7	100.0	99.8	616413
XRCC1	106.6	99.7	97.5	617633
ZC4H2	78.6	99.8	98.1	314580
ZFYVE26	120.3	99.9	99.4	270700
ZFYVE27	118.3	100.0	100.0	610244
ZNF592	150.1	100.0	99.9	606937

*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 20x 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*