

# WES MOVEMENT DISORDERS DG 2.18

<i>Gene</i>	<i>Median coverage</i>	<i>% covered &gt;10x</i>	<i>% covered &gt;20x</i>	<i>OMIM disease ID</i>
AARS2	131.5	100.0	99.4	615889
ABCB7	148.9	99.5	98.2	301310
ABCD1	78.1	75.8	71.6	300100
ABHD12	102.3	98.7	92.3	612674
ACTB	74.3	99.7	96.1	607371
ADAR	122.4	100.0	99.8	615010
ADCY5	132.5	95.1	91.2	606703
ADGRG1	163.9	100.0	100.0	606854
ADPRHL2	159.0	100.0	99.8	618170
AFG3L2	115.3	95.0	91.1	610246
AGTPBP1	144.2	96.0	94.1	618276
AIMP1	92.0	99.2	94.5	260600
ALDH18A1	142.2	100.0	99.9	601162;616603
ALDH3A2	138.4	95.3	94.6	270200
ALS2	176.4	100.0	99.9	607225
AMPD2	139.8	99.8	98.9	615809
ANO10	131.5	99.8	97.9	613728
ANO3	144.5	99.5	97.8	615034
AP4B1	151.8	99.9	98.7	614066
AP4E1	120.4	99.8	98.7	613744
AP4M1	145.6	99.9	98.9	612936
AP4S1	89.2	78.9	71.3	614067
APTX	122.6	94.9	92.5	208920
ARG1	164.4	100.0	100.0	207800
ARSA	126.4	100.0	99.8	250100

ARX	38.6	81.0	64.0	309510
ASPA	151.4	99.9	98.3	271900
ATCAY	166.3	100.0	99.8	601238
ATL1	180.1	100.0	99.7	182600
ATM	133.4	99.8	98.1	208900
ATP13A2	138.1	100.0	99.5	606693
ATP1A2	183.1	100.0	100.0	104290
ATP1A3	173.5	100.0	99.9	128235
ATP2B3	139.5	99.5	97.5	302500
ATP7B	146.0	99.9	99.2	277900
B4GALNT1	156.9	99.3	95.0	609195
BCAP31	80.0	92.6	83.2	300475
BCKDHA	200.1	99.9	99.2	248600
BCKDHB	146.8	99.5	94.4	248600
BCL11B	97.4	99.1	95.6	618092
BSCL2	113.7	100.0	100.0	270685
BTD	155.8	100.0	99.9	253260
C12orf65	122.8	99.8	98.5	615035
C19orf12	122.6	100.0	99.8	614298
CA8	126.5	99.6	97.3	613227
CACNA1A	97.0	95.1	91.9	108500
CACNA1E	142.9	100.0	99.9	618285
CACNA1G	151.8	100.0	99.6	616795
CACNB4	122.4	95.5	94.3	601949
CAMTA1	189.7	100.0	99.5	614756
CAPN1	170.9	100.0	100.0	616907
CCT5	146.2	100.0	99.7	256840
CHMP1A	131.9	100.0	99.8	614961
CLCN2	124.4	100.0	99.5	615651
CLCN4	117.3	99.9	98.9	300114

CLPB	142.9	100.0	99.9	616271
COASY	181.4	100.0	100.0	615643
COL4A1	115.6	98.7	97.4	175780
COL6A1	149.2	100.0	99.4	254090
COL6A2	161.0	100.0	99.8	254090
COL6A3	171.8	100.0	99.8	254090
COQ2	113.1	98.0	95.3	607426
COQ4	98.8	90.9	89.3	616276
COQ8A	164.9	100.0	99.5	607426
COQ9	79.4	100.0	97.9	607426
COX20	72.8	97.8	88.3	220110
CP	127.1	94.8	88.9	604290
CSF1R	125.5	99.9	99.3	221820
CSTB	85.0	99.6	89.8	254800
CYP27A1	180.7	98.9	96.7	213700
CYP2U1	160.0	94.8	91.5	615030
CYP7B1	131.5	98.0	92.8	270800
DARS2	151.1	100.0	99.3	611105
DBT	134.8	99.8	98.0	248600
DCAF17	107.3	98.9	93.3	241080
DCC	147.1	100.0	100.0	157600
DCTN1	126.0	100.0	98.8	168605
DDC	121.6	99.7	96.4	608643
DDHD1	164.0	97.9	95.8	609340
DDHD2	144.9	100.0	99.6	615033
DHDDS	93.1	99.0	95.0	617836
DLAT	111.4	100.0	99.7	245348
DLD	135.6	100.0	99.7	248600
DNAJC12	188.9	87.4	87.4	617384
DNAJC3	148.3	100.0	99.7	616192

DNAL4	80.8	100.0	98.9	616059
DNM1L	139.3	99.9	98.5	614388
DNMT1	131.2	99.2	99.0	604121
DPYS	137.1	100.0	99.9	222748
ECHS1	108.6	99.9	99.0	616277
EIF2B1	143.6	100.0	100.0	603896
EIF2B2	133.4	99.9	99.5	603896
EIF2B3	179.6	100.0	100.0	603896
EIF2B4	138.7	100.0	99.9	603896
EIF2B5	119.9	100.0	99.0	603896
ELOVL4	122.7	100.0	99.5	133190
ELOVL5	130.0	100.0	99.8	615957
ERLIN2	140.9	100.0	99.9	611225
ETHE1	96.2	99.9	97.4	602473
EXOSC3	125.9	99.5	94.9	614678
EXOSC5	161.4	100.0	100.0	-
FA2H	96.4	92.0	83.1	612319
FAM126A	146.4	100.0	99.4	610532
FAR1	84.8	97.6	92.8	616154
FARS2	206.7	100.0	100.0	614946
FBXO7	206.2	99.8	97.9	260300
FGF14	225.7	100.0	100.0	609307
FLVCR1	153.2	100.0	98.9	609033
FOLR1	130.7	100.0	100.0	613068
FRMD7	115.7	99.9	99.1	310700
FTL	144.1	98.5	89.4	606159
GALC	117.3	99.8	98.3	245200
GAN	177.4	100.0	99.6	256850
GBA	202.3	100.0	100.0	231000
GBA2	165.1	100.0	99.7	614409

GCDH	158.1	100.0	99.2	231670
GCH1	80.7	99.9	95.5	128230
GDAP2	130.1	100.0	99.2	618369
GFAP	104.1	91.8	89.7	203450
GJC2	37.0	78.2	58.7	613206
GLB1	89.8	99.9	97.4	230650
GNAL	135.5	96.8	93.4	615073
GOSR2	149.4	95.9	94.6	614018
GPR143	65.2	85.8	76.4	300814
GRID2	179.2	100.0	99.8	616204
GRIN1	164.3	100.0	100.0	614254
GRIN2B	174.2	99.8	99.2	613970;616139
GRM1	170.5	100.0	99.7	614831
HACE1	171.9	100.0	99.3	616756
HEXB	187.8	99.6	96.9	268800
HK1	140.2	100.0	100.0	618547
HPRT1	74.2	99.3	91.8	300322
HSD17B4	130.8	96.0	93.7	233400
HSPD1	91.9	98.8	93.7	605280
IBA57	117.3	93.7	90.1	616451
ISCA2	126.3	100.0	98.8	616370
ITPR1	152.5	100.0	99.9	606658
JAM3	149.8	100.0	99.9	613730
KATNB1	136.6	100.0	99.9	616212
KCNA1	166.8	100.0	99.9	160120
KCNA2	160.9	100.0	99.6	616366
KCNC1	157.1	100.0	100.0	616187
KCNC3	119.6	81.1	69.4	605259
KCND3	170.8	100.0	99.4	607346
KCNJ10	157.5	89.3	89.0	612780

KCNJ6	191.5	100.0	100.0	614098
KCNMA1	122.3	94.4	93.6	609446
KCTD7	163.6	95.0	95.0	611726
KIAA1161	188.1	100.0	100.0	618317
KIDINS220	167.4	100.0	100.0	617296
KIF1A	117.9	99.4	97.1	610357
KIF1C	157.4	100.0	100.0	611302
KIF5A	141.4	100.0	99.9	604187
KMT2B	146.9	95.8	94.0	617284
L1CAM	134.8	99.9	99.1	303350
LAMA1	142.0	100.0	99.7	615960
LAMB1	171.8	100.0	99.9	615191
LMNB1	116.4	99.9	98.9	169500
MAPK8IP3	163.6	100.0	99.6	618443
MARS2	170.6	100.0	100.0	611390
MECP2	149.7	100.0	98.7	19;300673
MECR	115.4	100.0	98.9	617282
MFF	101.3	94.3	89.9	617086
MICU1	126.1	98.9	95.2	615673
MLC1	103.0	100.0	99.0	604004
MMADHC	101.0	94.4	83.5	277410
MRE11	64.1	98.9	93.3	604391
MTHFR	117.2	97.3	96.0	236250
MTPAP	151.0	99.5	96.1	613672
MTTP	134.7	100.0	99.6	200100
NANS	114.3	100.0	99.9	610442
NEFL	153.5	99.9	98.2	607684
NEU1	146.4	99.7	97.7	256550
NEXMIF	153.1	100.0	99.5	300912
NF2	119.7	100.0	99.9	101000

NIPA1	191.5	100.0	100.0	600363
NKX2-1	57.4	98.6	85.6	610978
NKX6-2	81.3	89.0	81.8	617560
NOL3	87.7	93.7	84.2	614937
NPC1	136.4	99.6	98.7	257220
NPC2	160.5	100.0	99.6	607625
NT5C2	148.0	98.0	96.5	613162
NUP62	116.6	100.0	100.0	271930
OCLN	204.3	100.0	100.0	251290
OPA1	153.3	99.7	97.6	165500
OPHN1	104.2	99.5	97.6	300486
PACS2	155.5	99.3	96.2	618067
PANK2	185.6	100.0	99.3	234200
PAX6	141.4	100.0	100.0	206700
PCYT2	149.9	99.8	97.1	618770
PDE10A	134.7	81.2	80.5	616921;616922
PDE8B	110.4	99.9	99.7	609161
PDGFB	121.4	100.0	99.3	615483
PDGFRB	147.6	99.2	97.5	615007
PDHA1	102.0	99.4	97.1	312170
PDHX	159.4	99.9	99.4	245349
PDSS1	129.8	94.7	87.6	607426
PDSS2	125.9	99.8	97.1	607426
PDYN	138.2	100.0	100.0	131340
PEX10	101.8	96.8	89.7	202370
PEX2	158.8	100.0	100.0	614867
PEX7	135.9	87.8	80.7	266500
PHYH	89.1	100.0	99.6	266500
PIK3R5	126.8	100.0	99.9	615217
PLA2G6	120.6	99.9	98.3	612953

PLP1	141.7	100.0	99.2	312920
PMM2	145.4	100.0	100.0	212065
PMPCA	123.2	97.7	94.2	213200
PNKD	147.4	100.0	99.9	118800
PNKP	112.0	100.0	100.0	616267
PNPLA6	139.7	100.0	99.7	612020
POLG	111.6	100.0	99.3	607459
POLR1C	112.8	99.3	95.5	616494
POLR3A	136.9	100.0	99.7	607694
POLR3B	157.1	99.9	98.6	614381
PRF1	114.3	91.2	90.8	603553
PRICKLE1	118.6	100.0	100.0	612437
PRKCG	153.1	99.9	98.4	605361
PRKRA	175.9	100.0	99.4	612067
PRRT2	122.5	100.0	99.6	128200
PSAP	112.4	100.0	100.0	611722
PTS	118.8	99.9	99.1	261640
PUM1	148.2	100.0	99.9	617931
PYCR2	118.2	100.0	99.1	616420
QDPR	112.9	100.0	99.7	261630
RAB18	94.9	99.5	97.4	614222
RAB3GAP1	136.8	99.4	98.9	600118
RAB3GAP2	108.0	99.5	97.0	614225
RAD51	113.0	89.4	89.4	614508
RARS	114.8	94.2	91.6	616140
RARS2	122.7	100.0	99.8	611523
REEP1	82.5	78.7	76.1	610250
RNASEH2A	150.5	100.0	100.0	610333
RNASEH2B	126.7	96.0	92.5	610181
RNASEH2C	279.8	100.0	99.5	610329



RNF170	146.5	99.6	97.6	608984
RNF216	153.0	99.8	98.7	212840
RTN2	138.7	100.0	99.2	604805
RUBCN	114.6	99.4	97.5	615705
SACS	175.2	100.0	100.0	270550
SAMD9L	192.5	100.0	100.0	159550
SAMHD1	164.2	100.0	99.6	612952
SCN11A	144.6	99.8	98.3	615548
SCN1A	143.7	99.9	99.5	607208
SCN8A	189.5	100.0	99.8	614306
SEPSECS	192.2	100.0	100.0	613811
SERAC1	134.1	99.9	99.5	614739
SETX	182.3	100.0	99.8	606002
SGCE	120.2	98.7	94.0	159900
SIL1	157.6	99.2	96.7	248800
SLC12A6	146.8	100.0	100.0	218000
SLC16A2	71.9	99.2	93.7	300523
SLC19A3	160.1	100.0	99.8	607483
SLC1A3	120.2	100.0	99.9	612656
SLC20A2	121.1	100.0	99.2	213600
SLC25A15	176.5	99.8	98.1	238970
SLC2A1	164.9	92.8	92.8	612126
SLC30A10	168.1	100.0	100.0	613280
SLC33A1	156.2	99.9	98.9	612539
SLC39A14	109.2	100.0	99.4	617013
SLC52A2	170.8	100.0	100.0	614707
SLC52A3	125.5	100.0	100.0	211530
SLC6A3	147.6	100.0	100.0	613135
SLC9A1	164.0	100.0	100.0	616291
SMPD1	171.4	100.0	100.0	257200

SNCA	124.1	100.0	100.0	605543
SNORD118				614561
SNX14	95.2	99.6	95.9	616354
SOX10	70.3	99.9	97.9	611584
SPART	153.2	99.7	96.8	275900
SPAST	111.5	99.8	98.7	182601
SPG11	135.0	100.0	99.3	604360
SPG21	152.3	99.4	96.8	248900
SPG7	124.3	94.9	92.6	607259
SPR	170.3	99.8	96.3	612716
SPTBN2	120.5	100.0	99.3	600224
STUB1	152.7	100.0	98.7	615768
SUMF1	104.0	97.5	90.8	272200
SUOX	189.7	100.0	100.0	272300
SYNE1	146.5	98.3	98.0	610743
TAF1	108.9	99.8	97.7	314250
TANGO2	133.1	100.0	99.3	616878
TBC1D20	127.7	94.2	94.2	615663
TBC1D23	113.4	99.7	97.2	617695
TBCD	147.0	96.2	94.4	617193
TDP1	123.5	99.9	99.5	607250
TDP2	198.6	100.0	99.4	616949
TECPR2	151.5	100.0	100.0	615031
TENM4	128.3	100.0	99.6	616736
TGM6	140.8	99.7	97.3	613908
TH	88.5	99.3	96.1	605407
THAP1	182.6	100.0	100.0	602629
TIMM8A	58.8	98.0	90.1	304700
TMEM106B	148.7	99.9	98.8	617964
TMEM240	125.3	100.0	100.0	607454

TMEM67	96.9	99.5	95.0	216360
TOE1	170.4	100.0	100.0	614969
TOR1A	166.2	100.0	99.9	128100
TPP1	146.7	100.0	100.0	609270
TREM2	127.3	100.0	99.8	221770
TREX1	244.5	100.0	100.0	225750
TRPM3	134.3	100.0	99.5	-
TSEN2	119.0	100.0	99.6	612389
TSEN54	113.9	96.3	94.3	277470
TTBK2	134.6	99.8	97.6	604432
TTC19	89.7	81.5	73.8	615157
TTPA	129.1	94.7	87.1	277460
TUBA1A	77.0	99.9	97.0	611603
TUBB	125.1	97.3	93.9	615771
TUBB4A	76.9	95.9	94.0	128101;612438
TUBG1	178.8	100.0	100.0	615412
TWNK	202.8	100.0	100.0	609286
TYROBP	98.7	100.0	100.0	221770
UBAP1	151.0	98.8	93.4	618418
UBTF	129.1	100.0	99.4	617672
VAMP1	153.2	100.0	100.0	108600
VAR2	139.2	100.0	99.4	615917
VCP	122.7	100.0	99.2	167320
VLDLR	157.4	100.0	99.8	224050
VPS13A	92.6	99.4	95.6	200150
VPS13D	171.0	100.0	99.7	607317
VPS16	163.6	100.0	100.0	-
VPS37A	70.6	91.3	78.2	614898
VPS53	133.5	91.5	90.7	615851
VRK1	156.9	99.7	98.5	607596

WASHC5	164.8	100.0	99.8	603563
WDR26	119.5	99.0	96.6	617616
WDR45	77.0	96.4	89.7	300894
WDR73	180.8	100.0	100.0	251300
WDR81	175.2	100.0	100.0	610185
WVOX	138.2	100.0	100.0	614322
XK	83.0	99.8	98.1	300842
XPR1	152.8	100.0	99.9	616413
XRCC1	130.5	100.0	98.8	617633
ZC4H2	87.8	100.0	99.0	314580
ZFYVE26	116.7	100.0	99.1	270700
ZFYVE27	122.0	100.0	100.0	610244
ZNF592	151.9	100.0	99.6	606937

*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.*

*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*