

WES MOVEMENT DISORDERS DG 2.16

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
AARS2	122.7	100.0	99.8	615889
ABCB7	126.2	99.9	98.6	301310
ABCD1	87.4	77.2	75.0	300100
ABHD12	93.1	100.0	98.9	612674
ACTB	80.5	100.0	99.7	607371
ADAR	109.2	99.9	99.3	615010
ADCY5	131.8	97.8	94.7	606703
ADGRG1	147.2	100.0	100.0	606854
ADPRHL2	163.8	100.0	100.0	618170
AFG3L2	98.3	95.9	86.1	610246
AGTPBP1	116.9	98.7	95.1	618276
AIMP1	79.4	99.1	92.4	260600
ALDH18A1	113.7	100.0	99.8	601162;616603
ALDH3A2	113.5	95.3	94.3	270200
ALS2	145.1	100.0	99.8	607225
AMPD2	132.3	100.0	99.9	615809
ANO10	106.0	98.9	96.3	613728
ANO3	118.3	99.5	97.7	615034
AP4B1	121.0	99.9	98.4	614066
AP4E1	106.6	99.8	98.8	613744
AP4M1	129.3	99.7	98.1	612936
AP4S1	66.2	78.5	71.3	614067
APTX	96.3	94.1	91.3	208920
ARG1	159.1	100.0	100.0	207800
ARSA	138.5	100.0	100.0	250100

ARX	49.3	87.3	79.2	309510
ASPA	116.1	99.7	96.9	271900
ATCAY	152.7	100.0	99.7	601238
ATL1	134.7	99.9	99.0	182600
ATM	110.9	99.6	97.2	208900
ATP13A2	134.1	99.9	99.7	606693
ATP1A2	161.7	100.0	99.5	104290
ATP1A3	159.8	100.0	100.0	128235
ATP2B3	123.0	99.6	97.5	302500
ATP7B	128.7	99.9	99.1	277900
B4GALNT1	151.2	99.8	97.9	609195
BCAP31	73.4	93.2	78.3	300475
BCKDHA	176.9	100.0	99.8	248600
BCKDHB	123.3	98.6	92.8	248600
BSCL2	105.2	100.0	100.0	270685
C12orf65	110.4	100.0	99.6	615035
C19orf12	104.2	100.0	99.8	614298
CA8	107.5	99.7	97.6	613227
CACNA1A	92.4	97.8	94.7	108500
CACNA1E	120.9	99.8	99.2	618285
CACNA1G	148.6	100.0	99.8	616795
CACNB4	97.8	97.2	95.5	601949
CAMTA1	179.5	100.0	99.7	614756
CAPN1	162.5	100.0	100.0	616907
CCT5	117.9	99.9	98.9	256840
CHMP1A	123.2	100.0	99.8	614961
CLCN2	115.1	100.0	99.7	615651
CLCN4	105.7	99.9	98.9	300114
CLPB	125.6	99.8	97.9	616271
COASY	172.7	100.0	100.0	615643

COL4A1	95.7	99.6	97.3	175780
COQ2	103.5	97.6	97.1	607426
COQ4	105.0	91.3	90.2	616276
COQ8A	161.8	100.0	99.9	607426
COQ9	73.8	100.0	98.1	607426
COX20	66.2	96.4	85.3	220110
CP	100.6	93.1	87.4	604290
CSF1R	113.3	99.9	99.1	221820
CSTB	70.0	99.3	90.9	254800
CYP27A1	173.0	100.0	99.7	213700
CYP2U1	134.3	98.4	95.5	615030
CYP7B1	103.8	99.6	96.6	270800
DBT	109.9	99.6	96.9	248600
DCAF17	90.4	99.9	97.9	241080
DCC	118.6	100.0	99.8	157600
DCTN1	112.6	99.9	99.2	168605
DDC	97.9	99.5	95.0	608643
DDHD1	161.6	99.9	98.4	609340
DDHD2	129.6	100.0	99.5	615033
DHDDS	81.0	97.1	93.8	617836
DLAT	100.2	99.8	99.2	245348
DLD	119.2	99.9	99.7	248600
DNAJC3	137.4	100.0	99.7	616192
DNAL4	69.9	99.9	95.3	616059
DNMT1	114.3	99.2	98.7	604121
DPYS	117.5	100.0	99.8	222748
ECHS1	103.8	100.0	99.7	616277
EIF2B1	121.7	100.0	99.9	603896
EIF2B2	109.7	99.4	92.4	603896
EIF2B3	134.7	100.0	100.0	603896

EIF2B4	122.0	100.0	99.6	603896
EIF2B5	103.1	100.0	99.6	603896
ELOVL4	104.4	99.9	99.1	133190
ELOVL5	105.7	100.0	99.1	615957
ERLIN2	115.3	100.0	99.2	611225
EXOSC3	125.1	96.4	87.8	614678
FA2H	92.7	98.8	92.5	612319
FAM126A	125.4	100.0	99.4	610532
FAR1	73.7	97.2	91.8	616154
FARS2	161.9	100.0	100.0	614946
FBXO7	152.8	99.9	99.6	260300
FGF14	214.2	100.0	100.0	609307
FLVCR1	146.1	99.9	99.2	609033
FOLR1	107.4	100.0	99.9	613068
FRMD7	101.0	99.8	97.8	310700
FTL	145.2	99.7	96.7	606159
GALC	102.9	99.8	98.8	245200
GAN	142.2	99.9	99.4	256850
GBA	169.8	100.0	100.0	231000
GBA2	141.5	100.0	99.6	614409
GCDH	145.9	100.0	99.1	231670
GCH1	84.8	100.0	99.5	128230
GDAP2	118.2	99.9	99.3	618369
GFAP	103.7	91.9	91.4	203450
GJC2	45.3	92.6	75.4	613206
GLB1	82.6	99.7	95.4	230650
GNAL	130.2	99.4	96.5	615073
GOSR2	102.6	95.8	93.7	614018
GPR143	59.5	91.0	79.1	300814
GRID2	146.8	99.9	99.4	616204

GRIN1	166.1	100.0	99.9	614254
GRIN2B	158.0	99.8	99.0	613970;616139
GRM1	156.6	100.0	99.9	614831
HACE1	136.2	99.9	99.1	616756
HEXB	163.0	99.7	98.5	268800
HPRT1	59.8	98.3	88.2	300322
HSD17B4	109.4	96.3	93.6	233400
HSPD1	74.3	98.1	92.5	605280
IBA57	137.4	99.3	95.9	616451
ISCA2	105.1	99.8	95.8	616370
ITPR1	131.2	100.0	99.7	606658
KATNB1	154.2	100.0	100.0	616212
KCNA1	150.1	100.0	100.0	160120
KCNA2	126.3	100.0	99.7	616366
KCNC1	170.9	100.0	100.0	616187
KCNC3	112.7	90.4	72.9	605259
KCND3	162.0	99.9	99.2	607346
KCNJ10	148.6	89.2	88.1	612780
KCNJ6	157.2	100.0	99.9	614098
KCNMA1	102.3	94.8	93.4	609446
KCTD7	154.9	95.0	95.0	611726
KIAA1161	250.0	100.0	100.0	618317
KIDINS220	137.5	100.0	99.8	617296
KIF1A	115.0	99.7	97.6	610357
KIF1C	147.7	100.0	99.4	611302
KIF5A	116.0	100.0	99.9	604187
KMT2B	141.1	96.9	93.5	617284
L1CAM	126.6	99.9	98.6	303350
LAMA1	116.0	100.0	99.5	615960
LAMB1	142.9	100.0	99.7	615191

LMNB1	118.4	100.0	99.7	169500
MARS2	178.4	100.0	100.0	611390
MECP2	124.8	100.0	98.5	19;300673
MECR	108.2	100.0	99.7	617282
MICU1	103.3	98.8	96.5	615673
MLC1	96.7	100.0	99.9	604004
MMADHC	81.2	92.7	79.5	277410
MRE11	49.7	97.3	86.0	604391
MTHFR	114.9	98.2	96.4	236250
MTPAP	122.3	99.0	93.2	613672
MTPP	114.7	99.9	99.4	200100
NANS	97.2	99.9	98.4	610442
NEFL	178.7	99.8	97.8	607684
NEU1	141.3	99.3	96.4	256550
NEXMIF	132.0	100.0	99.5	300912
NF2	94.2	100.0	99.6	101000
NIPA1	156.7	100.0	99.9	600363
NKX2-1	88.8	100.0	99.7	610978
NKX6-2	122.9	98.1	91.2	617560
NOL3	112.8	99.6	96.3	614937
NPC1	117.8	100.0	99.2	257220
NPC2	124.7	100.0	99.9	607625
NT5C2	121.2	97.9	96.3	613162
NUP62	111.8	100.0	100.0	271930
OCLN	173.9	100.0	100.0	251290
OPA1	124.7	99.7	97.4	165500
PANK2	154.1	100.0	100.0	234200
PAX6	116.5	100.0	99.8	206700
PDE10A	107.6	81.4	80.4	616921;616922
PDE8B	99.7	99.9	98.9	609161

PDGFB	115.4	100.0	100.0	615483
PDGFRB	126.6	99.7	98.0	615007
PDHA1	85.3	98.9	95.4	312170
PDHX	129.0	99.9	99.5	245349
PDSS1	104.8	96.7	87.7	607426
PDSS2	112.9	99.6	96.1	607426
PDYN	121.8	100.0	100.0	131340
PEX10	113.3	99.9	97.4	202370
PEX2	134.9	100.0	100.0	614867
PEX7	111.0	91.2	89.3	266500
PHYH	74.0	99.9	96.9	266500
PIK3R5	120.7	100.0	99.9	615217
PLA2G6	111.9	99.8	98.2	612953
PLP1	112.8	99.7	97.7	312920
PMM2	127.7	100.0	99.7	212065
PMPCA	108.1	99.1	95.9	213200
PNKD	126.8	100.0	99.8	118800
PNKP	109.0	100.0	99.9	616267
PNPLA6	137.9	99.9	99.5	612020
POLG	113.9	100.0	99.6	607459
POLR1C	98.3	98.9	94.9	616494
POLR3A	116.8	100.0	99.9	607694
POLR3B	129.8	99.7	98.2	614381
PRF1	138.1	91.2	90.6	603553
PRICKLE1	100.0	100.0	99.8	612437
PRKCG	129.8	100.0	99.3	605361
PRKRA	190.7	100.0	100.0	612067
PRRT2	111.8	100.0	99.0	128200
PSAP	98.1	100.0	99.3	611722
PUM1	126.9	100.0	99.5	617931

PYCR2	116.5	99.7	96.9	616420
RAB18	83.4	99.7	97.2	614222
RAB3GAP1	121.7	99.4	98.9	600118
RAB3GAP2	91.6	99.7	96.9	614225
RAD51	100.6	89.4	89.4	614508
RARS	93.4	93.6	90.0	616140
RARS2	104.0	100.0	99.4	611523
REEP1	71.5	78.6	76.2	610250
RNASEH2A	129.8	100.0	99.7	610333
RNASEH2B	100.8	98.9	95.2	610181
RNASEH2C	281.7	100.0	100.0	610329
RNF170	126.6	99.7	97.7	608984
RNF216	125.0	99.9	98.1	212840
RTN2	140.8	99.9	98.7	604805
RUBCN	99.3	99.9	99.1	615705
SACS	150.4	100.0	99.9	270550
SAMD9L	171.8	100.0	100.0	159550
SAMHD1	133.4	99.8	98.5	612952
SCN11A	122.1	99.3	97.1	615548
SCN8A	154.3	100.0	99.7	614306
SEPSECS	159.6	100.0	99.6	613811
SERAC1	111.0	99.7	99.0	614739
SETX	151.6	100.0	99.6	606002
SGCE	97.7	96.0	92.3	159900
SIL1	129.5	98.9	96.2	248800
SLC12A6	118.9	100.0	99.9	218000
SLC16A2	63.3	98.7	91.0	300523
SLC19A3	134.6	100.0	99.9	607483
SLC1A3	99.5	100.0	99.8	612656
SLC20A2	108.6	100.0	98.5	213600

SLC25A15	146.8	97.9	93.6	238970
SLC2A1	148.9	92.8	92.8	612126
SLC30A10	176.1	100.0	100.0	613280
SLC33A1	132.0	99.7	97.7	612539
SLC39A14	95.4	99.9	97.9	617013
SLC52A2	185.4	100.0	100.0	614707
SLC52A3	118.8	100.0	99.8	211530
SLC6A3	133.0	100.0	99.9	613135
SLC9A1	142.4	100.0	100.0	616291
SMPD1	146.4	100.0	99.2	257200
SNCA	105.0	100.0	100.0	605543
SNORD118				614561
SNX14	84.1	99.0	95.4	616354
SOX10	88.2	100.0	99.1	611584
SPART	132.6	99.8	98.2	275900
SPAST	95.4	99.8	97.7	182601
SPG11	116.1	99.7	98.4	604360
SPG21	120.6	99.7	96.8	248900
SPG7	115.2	99.3	96.4	607259
SPR	145.7	100.0	99.8	612716
SPTBN2	126.2	100.0	99.7	600224
STUB1	173.9	100.0	99.5	615768
SUMF1	89.7	99.7	96.8	272200
SUOX	167.2	100.0	100.0	272300
SYNE1	121.6	98.3	97.8	610743
TAF1	86.8	99.1	95.5	314250
TANGO2	127.3	100.0	100.0	616878
TBC1D20	115.7	96.3	93.8	615663
TBC1D23	92.7	99.2	95.4	617695
TBCD	136.2	98.2	94.3	617193

TDP1	103.9	99.9	99.5	607250
TDP2	173.0	99.9	99.4	616949
TECPR2	137.2	100.0	100.0	615031
TENM4	119.9	100.0	99.6	616736
TGM6	130.2	99.9	98.7	613908
TH	96.3	100.0	98.2	605407
THAP1	141.3	100.0	100.0	602629
TIMM8A	46.3	94.6	79.9	304700
TMEM106B	121.4	99.7	98.9	617964
TMEM240	163.9	100.0	100.0	607454
TMEM67	83.1	99.1	94.6	216360
TOE1	141.1	100.0	99.8	614969
TOR1A	142.4	100.0	100.0	128100
TPP1	123.7	100.0	99.9	609270
TREM2	127.0	100.0	99.9	221770
TREX1	233.4	100.0	100.0	225750
TSEN2	95.6	99.9	98.9	612389
TSEN54	114.4	99.4	96.8	277470
TTBK2	108.4	99.9	96.8	604432
TTC19	83.4	97.0	82.6	615157
TTPA	109.2	97.6	92.5	277460
TUBA1A	77.6	99.8	97.1	611603
TUBB4A	101.2	97.1	95.6	128101;612438
TUBG1	154.3	100.0	100.0	615412
TWNK	159.6	100.0	100.0	609286
TYROBP	83.3	100.0	100.0	221770
UBAP1	126.1	99.0	96.0	618418
VAMP1	135.4	100.0	100.0	108600
VCP	100.3	100.0	99.2	167320
VLDLR	141.4	100.0	99.9	224050

VPS13A	78.2	99.2	95.3	200150
VPS13D	138.0	100.0	99.7	607317
VPS37A	64.3	91.3	79.3	614898
VPS53	111.3	91.1	89.6	615851
VRK1	129.6	99.8	98.7	607596
WASHC5	134.2	99.9	99.5	603563
WDR26	98.2	99.5	97.4	617616
WDR45	68.7	96.8	88.9	300894
WDR73	153.2	100.0	99.9	251300
WDR81	184.8	100.0	100.0	610185
WWOX	116.1	100.0	99.9	614322
XK	85.4	100.0	99.4	300842
XPR1	126.0	100.0	99.6	616413
XRCC1	111.4	99.9	99.1	617633
ZC4H2	72.4	99.8	95.9	314580
ZFYVE26	104.8	99.9	98.7	270700
ZFYVE27	110.4	100.0	100.0	610244
ZNF592	142.8	100.0	100.0	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