

# WES PARKINSON DISEASE DG 2.16

<i>Gene</i>	<i>Median coverage</i>	<i>% covered &gt;10x</i>	<i>% covered &gt;20x</i>	<i>OMIM disease ID</i>
ATP13A2	134.1	99.9	99.7	606693
ATP1A3	159.8	100.0	100.0	128235
C19orf12	104.2	100.0	99.8	614298
CHCHD2	69.7	99.9	93.7	616710
CHMP2B	90.2	99.5	97.7	614696
CSF1R	113.3	99.9	99.1	221820
DCTN1	112.6	99.9	99.2	168605
DNAJC6	126.5	99.9	99.0	615528
FBXO7	152.8	99.9	99.6	260300
FTL	145.2	99.7	96.7	606159
GBA	169.8	100.0	100.0	168600
GCH1	84.8	100.0	99.5	128230
GRN	174.1	100.0	100.0	607485
KIAA1161	250.0	100.0	100.0	618317
LRRK2	117.5	99.7	97.2	607060
MAPT	151.6	99.9	99.6	600274
PARK7	83.5	100.0	99.8	606324
PDGFB	115.4	100.0	100.0	615483
PDGFRB	126.6	99.7	98.0	615007
PINK1	87.3	96.4	90.7	605909
PLA2G6	111.9	99.8	98.2	612953
POLG	113.9	100.0	99.6	157640
PRKN	82.1	79.9	78.1	600116
PRKRA	190.7	100.0	100.0	612067
PSEN1	131.5	100.0	100.0	600274

SLC20A2	108.6	100.0	98.5	213600
SLC30A10	176.1	100.0	100.0	613280
SLC39A14	95.4	99.9	97.9	617013
SLC6A3	133.0	100.0	99.9	613135
SNCA	105.0	100.0	100.0	168601;605543
TAF1	86.8	99.1	95.5	314250
TH	96.3	100.0	98.2	605407
VPS13C	110.2	99.5	97.0	616840
VPS35	83.8	95.7	88.0	614203
WDR45	68.7	96.8	88.9	300894
XPR1	126.0	100.0	99.6	616413

*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*