Online Supplementary Information

Supplementary Table S1. Primers for *PINK1* exons (5'-3')

PINK1(1A)FP	GCCCAGGACCAGTGATGTT
PINK1(1A)RP	AAGAAGCGGAGACGGTTAGG
PINK1(1B)FP	CTGGGTCGAGCGCTGCTG
PINK1(1B)RP	CCGCGCTTAGCTCCGTCCT
PINK1(2)FP	TCCCTTTTCTTGGGCCTTCC
PINK1(2)RP	GATGGGCATTTTGAGAACATCTCC
PINK1(3)FP	CTCAGCCTGCCAGTTAAGAC
PINK1(3)RP	AAATCCATCACCAACATTAAGCC
PINK1(4)FP	GTCAGTGCCAGTGTTGGTGTG
PINK1(4)RP	CTTCTCCGGAAGGGTGATG
PINK1(5)FP	CGTATTGGGAGTCGTCGAT
PINK1(5)RP	TTGTGTGCGGAGCTAAATAAA
PINK1(6)FP	GGCCAACACTGAGCCATTAG
PINK1(6)RP	AAGCAAAGTGGCAGGGAAG
PINK1(7)FP	GATTAGCCCATGGATCAGGT
PINK1(7)RP	AACCTGACCTTCACTCTGGAA
PINK1(8)FP	TCTAGCTACAGCTTCCCTTCCTGT
PINK1(8)RP	TGAACTCTCACTCAAGTTCTTCCATT

Supplementary Table S2. Primers for *DJ1* exons (5'-3')

DJ1(1)FP	CCTCTGACAACCCCAGTCC
DJ1(1)RP	GTCCAGCACAGGGACACC
DJ1(2)FP	TTTGGGGTATCTCAGGGTTG
DJ1(2)RP	GCGTTAAATGTGAGCAGTG
DJ1(3)FP	AGGGTGAGACCCCATCTCTC
DJ1(3)RP	GGGGAAGACATTCAAGCAAA
DJ1(4)FP	TTCCGTCATGTGGATACACC
DJ1(4)RP	CAGCCTCCTCCCGAAATATT
DJ1(5)FP	GCCTTGCTTGGGTTTAAGAA
DJ1(5)RP	ATCAAACCATCGAATGAAAGG
DJ1(6)FP	AAACATGGGCTTTTCTATATCTGCACT
DJ1(6)RP	CAGTAAGCCAAGATCACGCCACT
DJ1(7)FP	CACATAGCCCATTAGGATGTCA
DJ1(7)RP	AGCTGCAAATGAAGGTGATA

Supplementary Table S3. Exome sequencing statistics

Subject ID	II4	II5
Total reads	113,219,058	107,521,894
Total yield (bp)	11,435,124,858	10,859,711,294
Read length (bp)	101	101
Target regions (bp)	64,190,747	64,190,747
Average throughput depth of target regions	178.1	169.2
Mappable reads (=reads mapped to human genome)	77,742,112	69,579,491
Mappable yield (bp)	7,652,369,056	6,8,49,627,383
% Mappable reads (out of total reads)	68.70%	64.70%
On-target reads (=reads mapped to target regions)	58,803,203	52,004,764
On-target yield (bp)	4,678,327,999	4,124,980,529
% On-target reads (out of mappable reads)	75.60%	74.70%
% On-target reads (out of total reads)	51.90%	48.40%
% Coverage of target regions (more than 1X)	96.50%	96.50%
Number of on-target genotypes (more than 1X)	61,934,147	61,960,221
% Coverage of target regions (more than 10X)	93.90%	93.90%
Number of on-target genotypes (more than 10X)	60,257,749	60,304,932
Median read depth of target regions	65	59
Mean read depth of target regions	72.9	64.3

Supplementary Table S4. Variant prioritisation

Total variants (SNVs and indels) in both II4 &II5	2,701,114
Total unreported variants (after excluding variants reported in dbSNP135) in both II4 & II5	14,512
Total unreported homozygous in both II4 & II5	7,202
Total unreported homozygous shared between II4 & II5	1,142
Total unreported homozygous exonic shared between II4 & II5	347
After exclusion of variants with frequency >0.01 in 74 non-PD exomes, 144 control exomes, NHBLI6500 exomes, dbSNP138, 1000 genomes	17

SNVs- single nucleotide variants; indels- insertion deletions; II4 & II5- exome sequenced individuals

Supplementary Table S5. List of 17 prioritised variants screened by HaloPlex-targeted sequencing

Chromosome	Position	Reference/Alternative Allele	Gene	Region, change	Effect on amino acid	OMIM ID, name (associated diseases)
Chr1	22446108	CTTTTTT/+++++++T	WNT4	3UTR	none	158330, Mullerian Aplasia and Hyperandrogenism
Chr1	101441384	GTTTTTTTTTTTTTTTTTTTTTTTTTT/GTTTTTTTTTTTTTTTTTTT------/GTTTTTTTTTTTTTTTTTTTTTTT----	SLC30A7	3UTR	none	none
Chr1	234565176	C/T	TARBP1	Exonic, missense	NM_005646 (30Exons):exon16:c.G2857A:p.V953M	none
Chr6	90374283	A/G	MDN1	Exonic, missense	NM_014611(102Exons):exon85:c.T14159C:p.I4720T	none
Chr7	21598500	A/G	DNAH11	Exonic, missense	NM_001277115(82Exons):exon3:c.A576G:p.I192M	611884, Ciliary Dyskinesia, Primary, 7; CILD7
Chr7	100637547	G/A	MUC12	Exonic, missense	NM_001164462(12Exons):exon2:c.G3703A:p.A1235T	none
Chr7	131241029	GGCGAC/GGGGCGACGGCGAC	PODXL	Exonic, frameshift	NM_001018111(9Exons):exon1:c.89_90insGTCGCCCC:p.S31insfs; NM_005397.3(8Exons):exon1:c.89_90insGTCGCCCC:p.S31insfs	none
Chr8	7787850	C/T	ZNF705B	5UTR	none	none
Chr10	17841713	T/A	TMEM236	3UTR	none	none
Chr10	75434095	T/A	AGAP5	3UTR	none	none
Chr10	5682135	C/G	ASB13	3UTR	none	none
Chr10	86274785	C/T	CCSER2	3UTR	none	none
Chr16	129266	GTTT/++++T	MPG	5UTR	none	none
Chr16	10624465	GCA/+++CA	EMP2	3UTR	none	none
Chr16	30505559	C/T	ITGAL	Exonic, missense	NM_001114380(29Exons):exon10:c.C991T:p.R331W; NM_002209(31Exons):exon12:c.C1240T:p.R414W	none
Chr21	9569365	TACACA/TACA--	unknown	unknown	none	none
Chr21	9418848	A/G	unknown	unknown	none	none

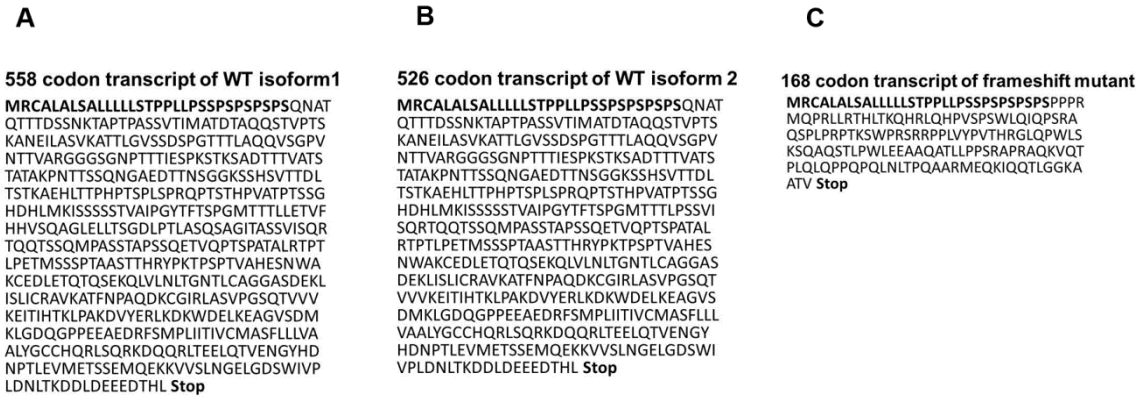
Supplementary Table S6. Primers for *PODXL* exons (5'-3')

PODXL(1)FP	GGACGGGCCAGGAGTAG
PODXL(1)RP	CATGCAAACCCACTTAGCAC
PODXL(2A)FP	CCCATTCTCCACAAAAAGGA
PODXL(2A)RP	GTGAGGGGTCGTCAGATGTT
PODXL(2B)FP	AGGCAACCCTACTACCACCA
PODXL(2B)RP	AAGGCATGAGCCTTTTCAGA
PODXL(3)FP	CCGTCTCTGTGGGAGGTAAG
PODXL(3)RP	GGGTAAGTGCTGCTCAAAGC
PODXL(4)FP	GGGCTTTGAGCAGCACTTAC
PODXL(4)RP	ATGGGAAAGGACCACTTCCT
PODXL(5)FP	GGAGGCAGGTTCTAGCACAG
PODXL(5)RP	GGGTGTGGCTTGACAGTTCT
PODXL(6)FP	CCCGAGAGACACTCAGGAGA
PODXL(6)RP	ATGGGAAGTGGCAGAGAACA
PODXL(7)FP	CCTTGTGGGAGGTCTGGTTA
PODXL(7)RP	CCTGCTCCCTTTCCTCTTCT
PODXL(8C)FP	AGAATGACCACCAGGAGCAG
PODXL(8C)RP	CTTCAGGTCTCGGCAATCTC

Supplementary Table S7. Primers for site directed mutagenesis (5'-3')

P429T PODXL FP	GACCGCTTCAGCATGACCCTCATCATCACCA
P429T PODXL RP	TGGTGATGATGAGGGTCATGCTGAAGCGGTC
S373N PODXL FP	GCATCTGTTCCAGGAAATCAGACCGTGGTCG
S373N PODXL RP	CGACCACGGTCTGATTTCCTGGAACAGATGC
R294Q PODXL FP	AGCATCAACTACCCACCAATACCCCAAAACACCTT
R294Q PODXL RP	AAGGTGTTTTGGGGTATTGGTGGGTAGTTGATGCT

Supplementary Figure S1. Comparison of transcripts from two isoforms of wildtype and mutant alleles of *PODXL*



Amino acids in bold, in line 1 are common across all three transcripts