

Supplementary information

Systematic analysis of genetic variants in Han Chinese patients with sporadic Parkinson's disease

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Supplementary Table

dbSNP ID	Prediction ^a	Forward primer sequence ^b (5'→3')	Reverse primer sequence ^b (5'→3')	Product size	Extending primer sequence ^b (5'→3')
rs60003608	D/Pos/DC	acgttggatgTGGACGTCTGGAAAG CAAAC	acgttggatgTTGAACTCTCAACC TGCCTC	101 bp	GGAAAGCAAACCGGATGA
rs6788448	T/P/Po	acgttggatgCCTCCTTGATGAGCAG TTTC	acgttggatgTTGTGACAGAGTGA TCTGTG	105 bp	GTGATTTCTTTCTATAGGAGG TTAAT
rs35424709	D/P/Po	acgttggatgTTGTAGGCCAGTGCTA TGAC	acgttggatgAACTGCGTACTAAC CCTGTG	108 bp	TGTGTCGTGTAATCTGAAG
rs6350	T/Pos/DC	acgttggatgAGGTGGAGCTCATCCT TGTC	acgttggatgGAAAGTCGATCTTC TTGCC	126 bp	ccccaTTGTCAAGGAGCAGAA
rs13414223	T/Pos/Po	acgttggatgGTTTCTCAACTCATTG GATGC	acgttggatgTACCTCTAGTGTGTT TGCCG	94 bp	AGAAATATATTTGGAAGTAAT ACATAAT
rs10935014	T/Pos/DC	acgttggatgGTTGGAGGAGTCTTCT TGAG	acgttggatgGTTCTTCTCTAGGA GCTCAG	114 bp	ATTCTCTAGGCTTTCTTAGAA
rs79953286	T/Pos/Po	acgttggatgTAAAAAGGGTGATTG TGAC	acgttggatgACCTCCAGTTGGAA AGTAGG	126 bp	agGGGTGATTGTGACAAAAC T
rs2227851	D/P/DC	acgttggatgCCATCAAGAAGGAGA CCAAG	acgttggatgAAGGGACCATGCAG TTAAGG	102 bp	gcAGGAGACCAAGGTTCTCAA G
rs34086109	T/Pos/DC	acgttggatgTTCCTCTCCCAGACTC TCAC	acgttggatgGAGGAGCGGAGTA GAGAAC	111 bp	ccCCGGCATCCCGCCCA
rs1721100	-	acgttggatgGTGCGATAGTGACATT ATGG	acgttggatgATTCTTTCCAAATCC AGTC	138 bp	TCCCATCATAAAATAATGACC CAAG
rs1989754	-	acgttggatgCCACCCATATCTTCTT TCGC	acgttggatgTGCCTAGTTCTTCA GCCAAG	112 bp	CTTTGGAAATTGTGCAAC
rs34322892	D/Pos/DC	acgttggatgTCATTGTTTCAGAGGAC CATC	acgttggatgCCTGGCTTCATTGT GAAACG	108 bp	ctttCCGGCAGATCCACCC
rs34845648	T/Pos/DC	acgttggatgAAAGCTGAAGAGGAG	acgttggatgTATCAGTGATCACT	127 bp	CTACCAGCCAAAGTGC

		ACTCG	GGCCTC		
rs11538692	T/Pos/DC	acgttgatgACATCCGGCATTGTTA GCTC	acgttgatgTCAGGACGCACATC AATAGC	107 bp	AGCTCTGCTCAGCGT
rs77570025	T/B/DC	acgttgatgCAGTGGATCGTTACAT AGCC	acgttgatgCACACTCTGGCATT CTCTAC	129 bp	cctccCACCCTGTAATCTTGAT GA
rs2924835	D/B/Po	acgttgatgGGGTTTTGGTTGCTTA GGCG	acgttgatgAGCTCTCGGGCTTT TAAGAC	107 bp	TGGCCTGGAGAAGGATTCTG
rs3752321	D/Pos/DC	acgttgatgCCAGGGAGTTCGACA TTTTC	acgttgatgGTGTGACAGTCATT CCACAG	100 bp	GACATTTTCTACCAGTCCTAC
rs3764740	D/B/Po	acgttgatgCAGCAAGTTCTTCCAG TGTG	acgttgatgTCATGCTCAGACCT GTCGG	94 bp	ggaggGGA CT CAGACATGCTAC ATA
rs33949390	D/P/DC	acgttgatgGTTGTCCAAAACACCC TAAG	acgttgatgCTATTGGCAAAGCA ATCTGG	138 bp	AAGAAATTTTCCACATCTCT A
rs34410987	T/B/DC	acgttgatgGCCAGTCTCCTAAAAG GAAG	acgttgatgTCACGAGATCCACT ATTCAG	126 bp	GTGAGAAAGAGAGCAGTC
rs34594498	D/Pos/DC	acgttgatgAGCTCATAGGGAAGT GATGC	acgttgatgAAACATGGCCCACT GCTTAC	121 bp	ttgtAAGTTTTCCAGGCATCTG
rs74942016	D/Pos/Po	acgttgatgCATAACCGGCATCTGC ATCG	acgttgatgAAGCTGTCTCTGCA TGAAGG	120 bp	gccgTGTGGTCGGCATCATGTG T
rs61744200	T/P/DC	acgttgatgTGTTCTAGCTACAGCT TCCC	acgttgatgGGGCTAGAATATGT TCACCC	99 bp	caAGAGACCATCTGCCC
rs11570680	T/B/DC	acgttgatgGCTTCGACTGTGCCAT AGTG	acgttgatgGTCCTGGGCTCACC GACAT	105 bp	ttaTGCTGACCCACGGGGCCAA C
rs3758549	-	acgttgatgCCCCTTGCAAGAGATG ATAG	acgttgatgCTCCTAGGAGAAAA CCCATC	108 bp	TACCTGGAAGTGAGAATG
rs4919621	-	acgttgatgACTCTGACATGTGCTG ATCC	acgttgatgTGTTCTTTGGCACA CAGTGG	117 bp	ggCTACTTCCTGCCTCTATC
rs2254562	D/B/Po	acgttgatgCACCTTCCTTAGATCC AAGC	acgttgatgATTGGGCTTCTTATT TGAC	120 bp	CCAAGCAAATTTACTATTATT TGT

rs375681722	D/P/DC	acgttggatgTTGCTTAGCAGGAAGT GGTC	acgttggatgTGTCCCTCGACAACA ATGTGG	114 bp	AGGTGCGCATTGTC
rs538881762	D/P/DC	acgttggatgTCTGGGCAGGATTCAT ATTC	acgttggatgCCTTGCCTACAGGT CTAAAG	109 bp	AGGATTCATATTCATAACCCA
<i>TENM4</i> p.T1367N	T/P/DC	acgttggatgTACAGTGGACAAGTTT GGGC	acgttggatgTGAGATCATTAGAG CCGAGC	104 bp	tATCGATGCGTCTGATCATG
rs2076485	D/P/Po	acgttggatgTAAGACCAAGGTTCTT GTGC	acgttggatgGTAAGGTGGATGGT CTTCTC	114 bp	gggtATGGTCTTCTCTTTGTCA
rs7757931	D/B/Po	acgttggatgTAAGCTTTTTGACCCC TGCC	acgttggatgATGGCAGATTACGG CATCAG	107 bp	TGGTCACCTCCAATA
rs35693565	T/P/DC	acgttggatgACCCCTCAAGGCTACA TATC	acgttggatgCCACATTTTCGTGAG ATCCAG	95 bp	CCTTCTTCCTCCGG
rs62444122	T/Pos/Po	acgttggatgTTGCTTACCTTAAGCT GTCC	acgttggatgGCCTGGGATGTTTT TACTGC	113 bp	GTCCAATTTCTTTAAATTTAT AAACTT
rs199910950	D/P/DC	acgttggatgCCATTCCTTCCTTAAT ACGG	acgttggatgTTATGTGGTATTTTG TAGC	99 bp	tttGTAGCATTTATTACTGGCT T

Supplementary Table S1. Primer sequences designed by Sequenom Assay Design 3.1 software (Sequenom, San Diego, CA, USA). B: benign; D: damaging; DC: disease causing; P: probably damaging; Po: polymorphism; Pos: possibly damaging; T: tolerated. ^a Sorting Intolerant from Tolerant/Polymorphism Phenotyping version 2/MutationTaster prediction. ^b The lowercase letters in the primer sequences are 5'-end tags (forward and reverse primers) or nonhomologous sequences (extending primers) to increase the molecular weights.