

Supporting Information

Supplementary Figure S1: Pedigrees of the adRP families. Causative mutation in the *PRPF31* gene, cosegregation in available family members, results of the copy-number analysis of the minisatellite repeat element (MSR1) adjacent to the *PRPF31* promoter in available symptomatic and asymptomatic patients, and haplotype analysis in RP-0361 and RP-1599 families, are shown. m: mutated allele. +: wild-type allele. 3: 3-copy allele of the MSR1. 4: 4-copy allele of the MSR1. *: Hemizygous individuals for the MSR1. In blue 3 copies and in red 4 copies of the MSR1 allele. ND: no data. (-/-): no available data. Microsatellite markers inferred are shown in brackets.

Supplementary Figure S2: Long PCR validation of the tandem duplication in family RP-0932.

Electrophoresis results of the long PCR analysis are shown. Lambda DNA/HindIII was used as marker in a 1% agarose gel. Marker size in bp. A band of 8.6 kb, corresponding to the wild-type allele, is observed in patients III:1, IV:1, and control sample (WT). Patients III:1 and IV:1 have an upper band from 9.4 to 23.1 kb corresponding to the duplicated allele.

Supplementary Figure S3: Expression of the *PRPF31* gene in family RP-0932, in patients with duplication (III:1 and IV:1) and deletion (IV:12), respectively.

PRPF31 expression was decreased in patients compared to nine controls. Mean differences between both groups were significantly different (p -value <0.001), while mean differences between patients with duplication and patient with deletion were not significantly different (NS). Triplicate assays were performed twice.

Supplementary Figure S4. Haplotype analysis using six intragenic SNPs and five microsatellite markers flanking *PRPF31* in RP-0006 and RP-1609 families with the p.Glu181* causative mutation.

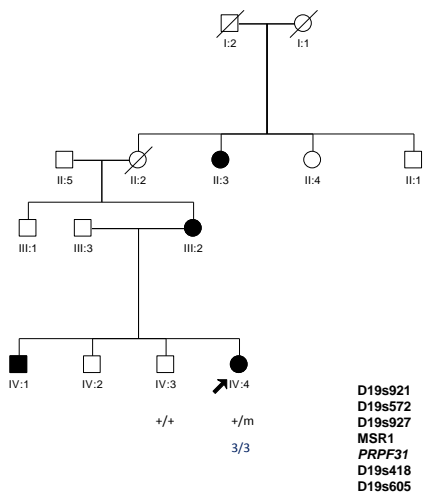
The analysis of the haplotypes showed a common region sharing a minimum of 1.2 Mb and a maximum of 1.4 Mb defined by the alleles located along the black bar (the marker D19S605 was not informative). Haplotypes suggest a founder effect.

Supplementary Table S1. Clinical features of 26 affected patients from 15 families characterized with a mutation in the *PRPF31* gene. Typical RP fundus: pale optic disc, narrowed retina vessels, and pigmentary changes (bone spicules). MA: macular alteration. y: years. NB: night blindness. VFC: visual field constriction. VA: visual acuity. BCVA: best corrected visual acuity. CF: counting finger. OD: right eye. OS: left eye. ERG: electroretinogram. NR: non-recordable. ND: no data available. Sco: scotopic. Pho: photopic. RA: reduced amplitude. Y: yes.

Supplementary Figure S1: Pedigrees of the adRP families.

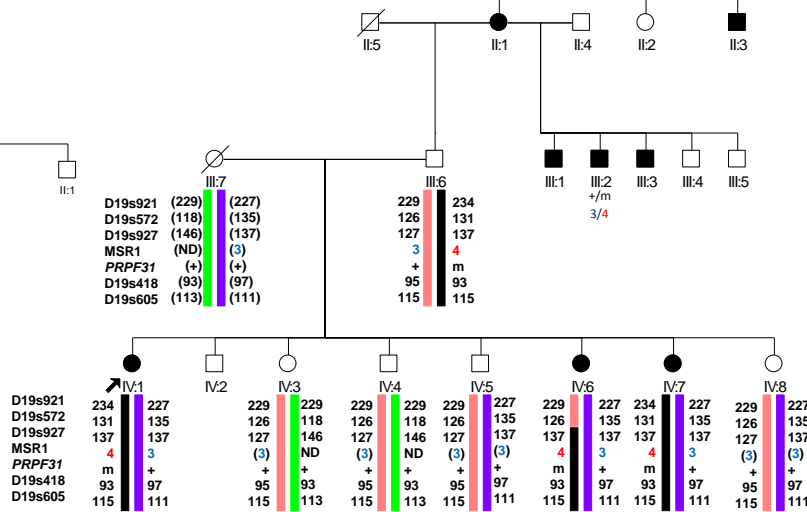
RP-0182

m: c.1146+2T>A



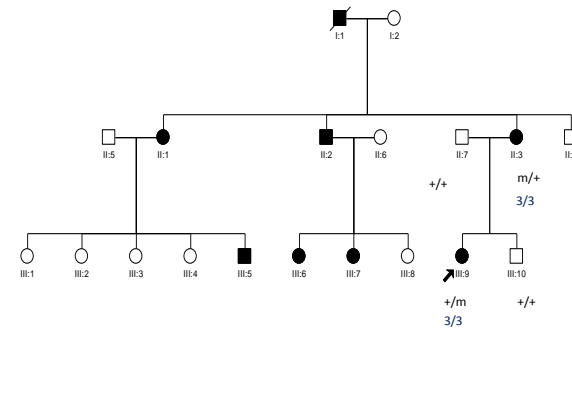
RP-0361

m: p.Ile110del



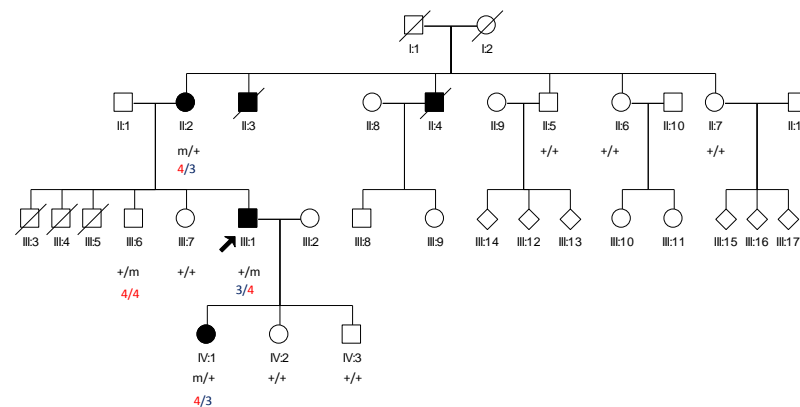
RP-0006

m: p.Glu181*



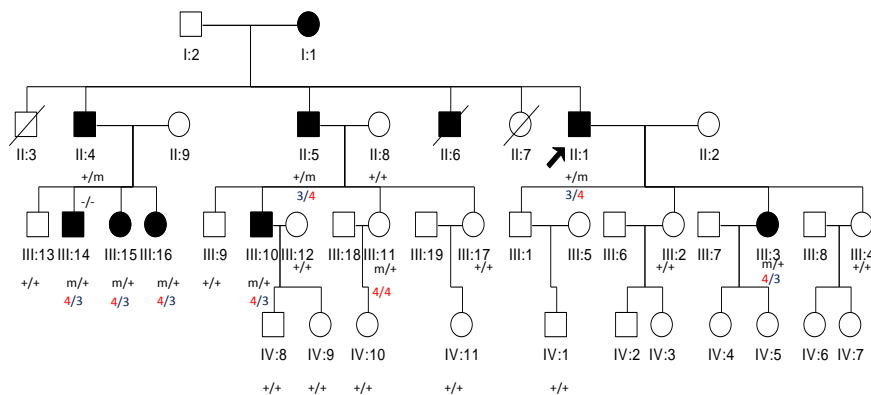
RP-0637

m: p.Thr258Aspfs*21



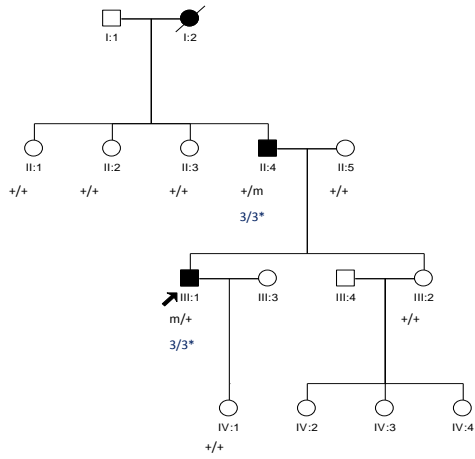
RP-0368

m: p.His276Glnfs*2



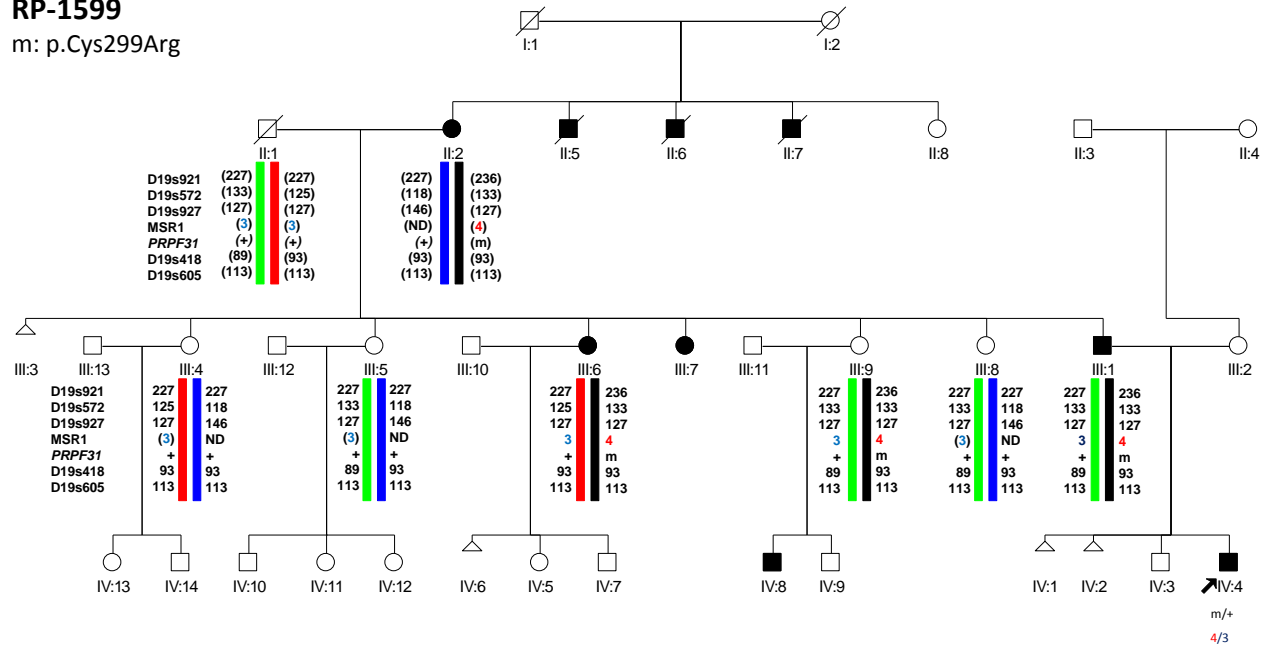
RP-0777

m: del chr19:54602946 to chr19:54635178



RP-1599

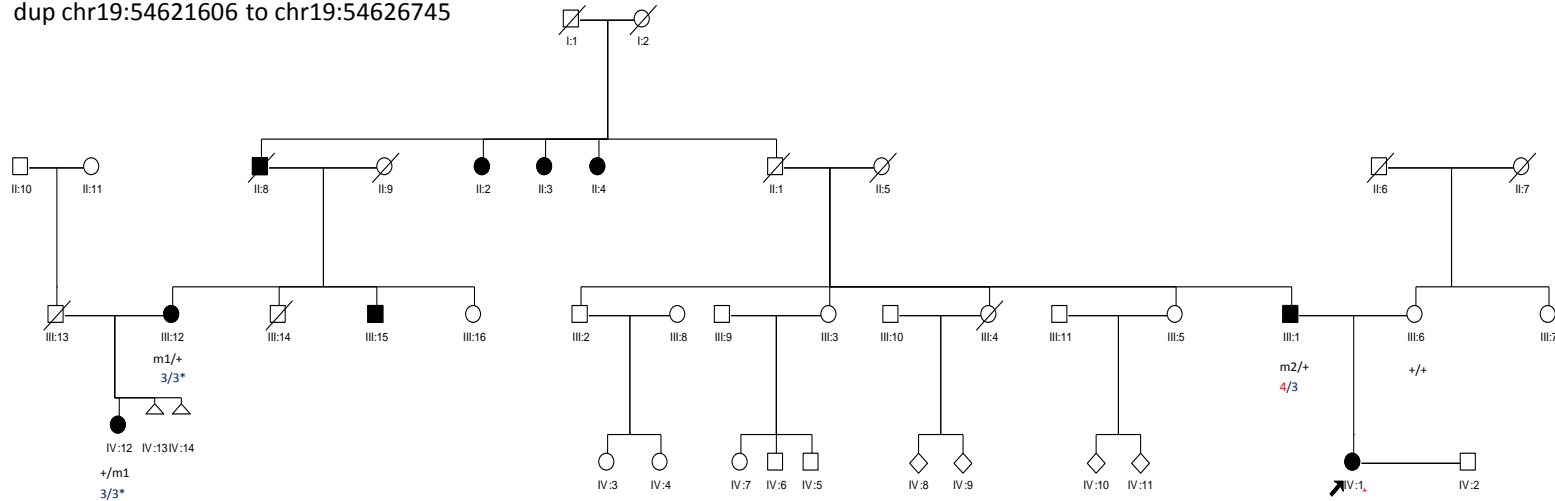
m: p.Cys299Arg



RP-0932

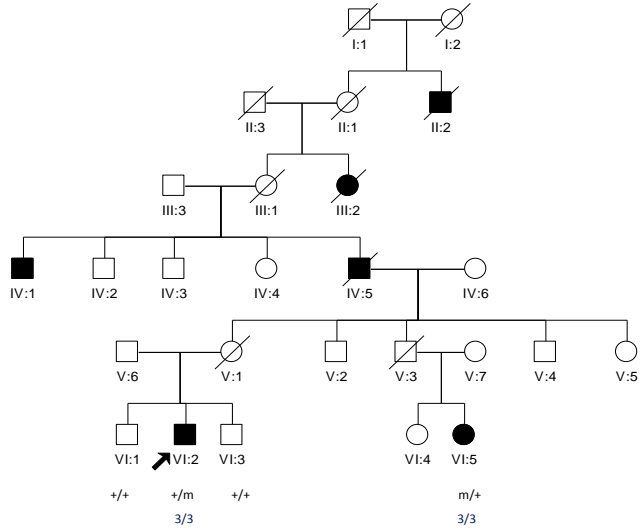
m1: del chr19:54602946 to chr19:54632693

m2: dup chr19:54621606 to chr19:54626745

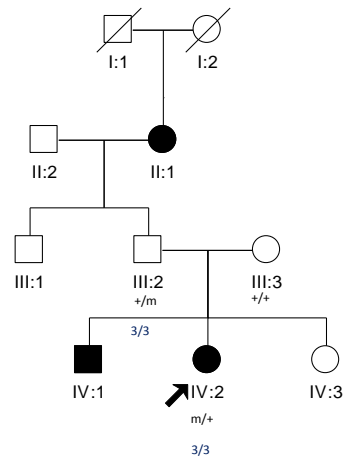


RP-1541

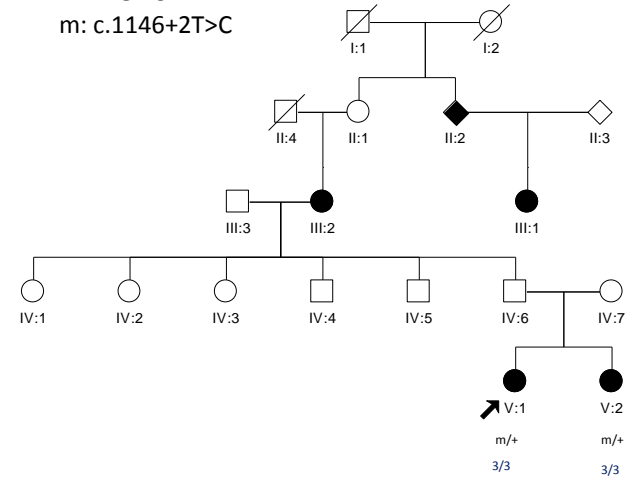
m: p.Gly314Argfs*10

**RP-1609**

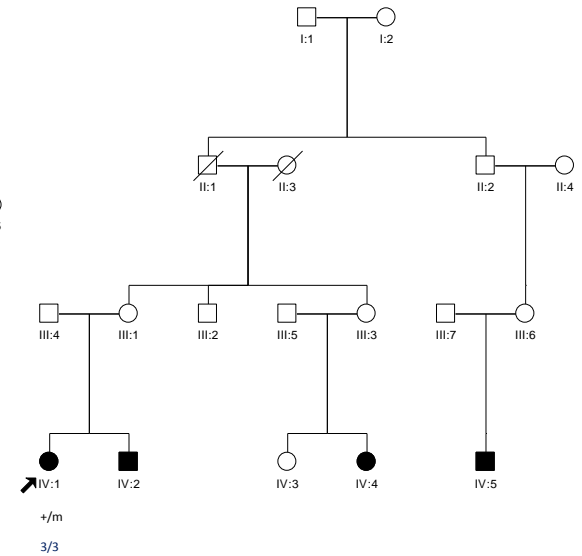
m: p.Glu181*

**RP-1970**

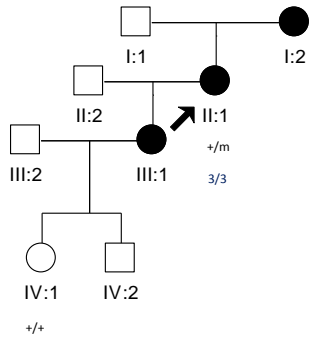
m: c.1146+2T>C

**RP-1318**

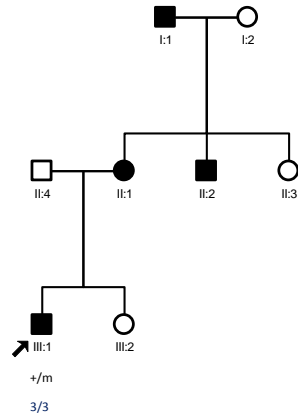
m: c.322+4_322+7del

**RP-2136**

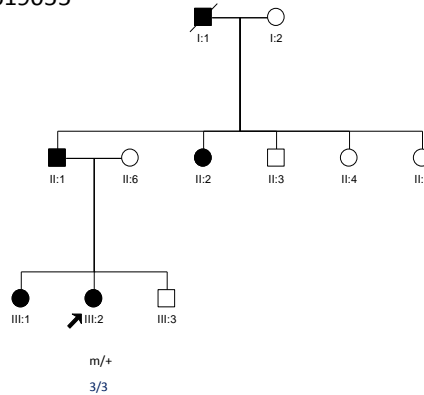
m: c.527+1G>T

**RP-2426**

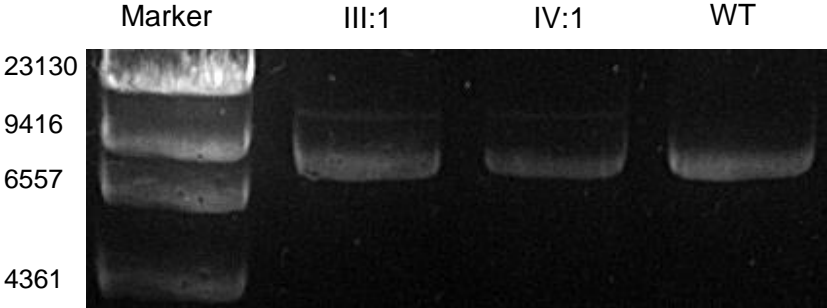
del chr19:54618828 to chr19:54619055

**RP-2496**

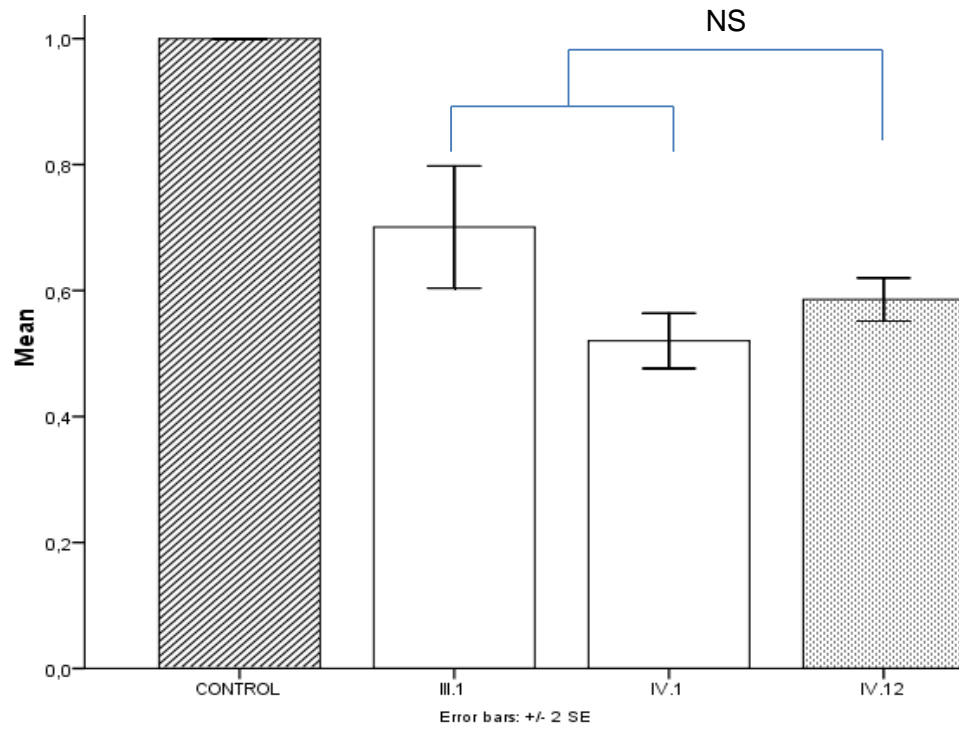
m: c.1074-1G>T



Supplementary Figure S2: Long-PCR validation of a tandem duplication in family RP-0932.



Supplementary Figure S3: Expression of the *PRPF31* gene in family RP-0932, in patients with duplication (III:1 and IV:1) and deletion (IV:12), respectively.

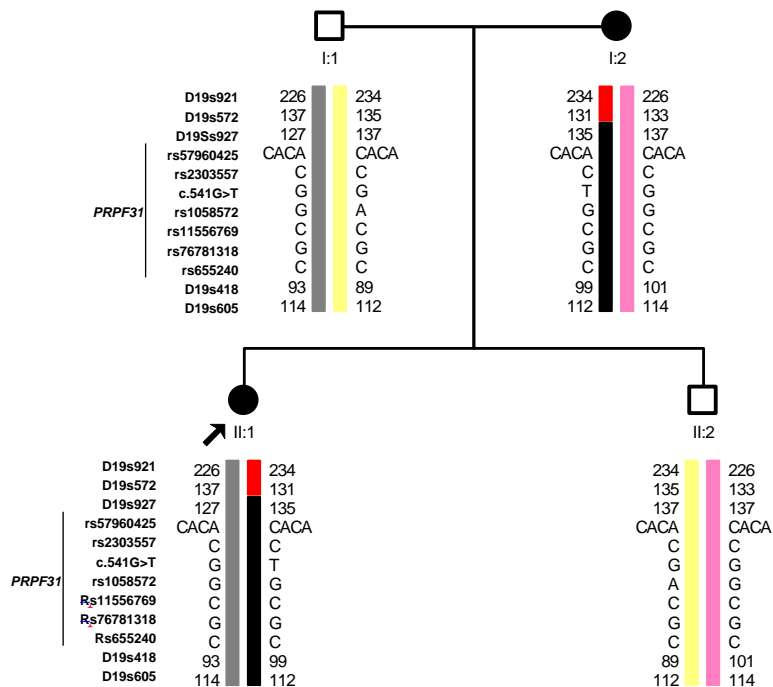


Supplementary Figure S4. Haplotype analysis using six intragenic SNPs and five microsatellite markers flanking *PRPF31* in RP-0006 and RP-1609 families with the p.Glu181* causative mutation.

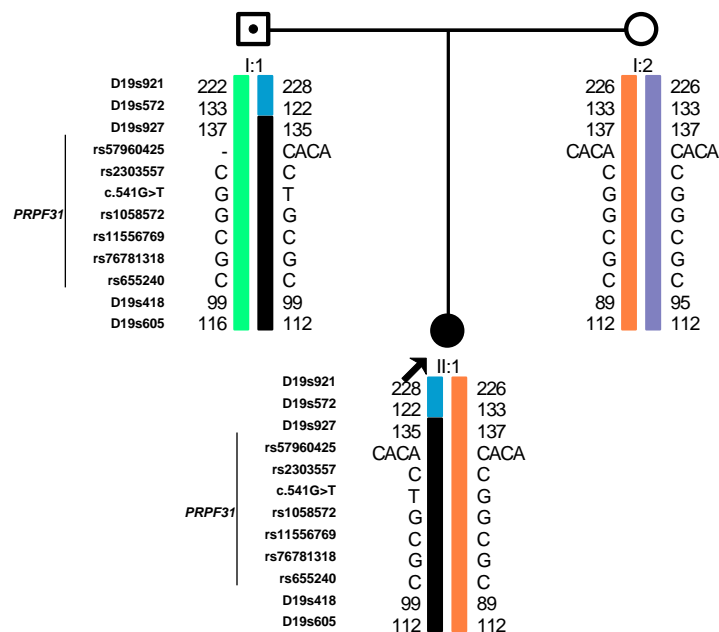
Markers/ SNPs	Start (Mb)
D19s921	53.3
D19s572	53.6
D19s927	53.8
rs57960425	c.528-78_528-75delCACAA
rs2303557	c.528-31C>T
c.541G>T	p.Glu181*
rs1058572	c.564G>A
rs11556769	c.735C>T
rs76781318	c.855+40G>A
rs655240	c.1148-9T>C
D19s418	55.0
D19s605	55.2

1.2 Mb
1.4 Mb

RP-0006



RP-1609



Supplementary Table S1. Clinical features of 26 affected patients from 15 families characterized with mutation in the *PRPF31* gene.

Family	PRPF31 mutation	ID Patient	First symptoms and course (Age)			Age at	BCVA	Visual Field	ERG	Fundus aspect	Additional findings
			NB	VFC	VA loss	Ophthalmic Examination					
RP-0006	c.541 G>T	VI:5	8	9	no	44y	0.2/0.3	Tubular	NR	Typical RP	Bilateral Cataracts (42y)
		VII:9	5	Y	Y	19y	0.5/0.5	Tubular	NR	Typical RP	
RP-0182	c.1146+2T>A	IV:4	7	Y	Y	40y	0.3/0.3	Tubular	NA	Typical RP	Bilateral Cataracts (38y)
RP-0361	c.328 G>del	IV:1	14	14	20	27y	0.9/0.9	Tubular + peripheral islands	NR	Typical RP	
		IV:6	14	14	20	27y	0.7/0.7	Tubular	NA	Typical RP	
		IV:7	Y	Y	Y	24y	0.7/0.6	Tubular	NA	Typical RP	
RP-0368	c.828 G>del	II:1	20	20	Y	56y	NA	NA	NA	NA	Cataract (56y)
		III:3	Y	Y	no	39y	1/0.6	Tubular	NA	Typical RP	
RP-0637	c.770dup	II:2	18	40	50	64y	CF/CF	Tubular	NR	Typical RP + MA	Photophobia. Dyschromatopsia. OS cataract (65y)
		III:1	10	20	35	40y	0.7/0.7	Tubular + peripheral islands	NR	Typical RP	OS Cataract (38y)
		IV:1	NA	NA	NA	16y	0.7/1	Peripheral constriction + diffuse loss	NA	Cystoid macular oedema	
RP-0777	del chr19:54602946-54635178	III:1	27	32	no	37y	0.7/0.8	Tubular	NR	Typical RP	
RP-0932	dup chr19:54621606-54626745	III:1	Y	Y	Y	at old age	NA	NA	NA	NA	Dyschromatopsia. Bilateral cataracts (25y). OS vitrectomized
		IV:1	5	7	20	30y	0.2/0.2	Tubular	NA	Typical RP + MA	Bilateral cataracts (50y)
		III:12	Y	14	13	51y	0.125/0.125	Tubular	NA	Typical RP + MA	
RP-0932	del chr19:54602946-54632693	IV:12	Y	17	no	28y	0.8/0.8	Tubular	NA	Typical RP	
RP-1541	c.939dup	IV:2	6	20	39	38y	0.1/0.1	NA	NA	Typical RP	Cataract (21y)
RP-1599	c.895T>C	III:6	Y	7	7	43y	0.1/0.05	Tubular	NA	Typical RP	Cataract (30y)
		IV:4	3	5	6	15y	0.8/0.6	NA	NA	Typical RP	
RP-1609	c.541G>T	IV:2	6	22	25	23y	0.8/0.7	Tubular	SCO:NR. Pho: RA	Peripheral pigmentary changes	Photophobia. Dyschromatopsia
		V:1	14	12	no	16y	NA	Peripheral constriction 30°	SCO:NR. Pho: RA	NA	Hypermetropia. Astigmatism
RP-1970	c.1146+2T>C	V:2	13	no	no	14y	1.0/1.0	Peripheral constriction 30°	SCO:NR. Pho: RA	Pigmentary changes + narrowed vessels	
RP-2136	c.527+1G>T	II:1	Y	Y	Y	41y	0.2/0.2	Tubular	NR	Typical RP	
RP-2426	del chr19:54618828-54619055	III:1	NA	NA	NA	37y	0.8/0.8	Tubular	NA	Typical RP	
RP-2496	c.10 G>T	III:2	20	30	35	36y	0.6/0.8	Tubular	NA	Typical RP	Photophobia
RP-1318	c.322+ G>del	III:1	9	9	16	NA	NA	NA	NA	NA	