

Unique Combination of Clinical Features in a Large Cohort of 100 Patients With Retinitis Pigmentosa Caused by *FAM161A* Mutations

Avigail Beryozkin¹, Samer Khateb¹, Carlos Alberto Idrobo-Robalino ¹, Muhammad Imran Khan², Frans Cremers^{2,3}, Alexey Obolensky¹, Mor Hanany¹, Eedy Mezer⁴, Itay Chowers¹, Hadas Newman^{5,6}, Tamar Ben-Yosef⁷, Dror Sharon^{1*}, and Eyal Banin^{1*}

¹ Department of Ophthalmology, Hadassah-Hebrew University Medical Center, Jerusalem, Israel.

² Department of Human Genetics, Radboud University Medical Center, Nijmegen, The Netherlands.

³ Donders Institute for Brain, Cognition and Behaviour, Radboud University, Nijmegen, The Netherlands.

⁴ Alberto Moscona Department of Ophthalmology, Rambam Health Care Campus, Haifa, Israel.

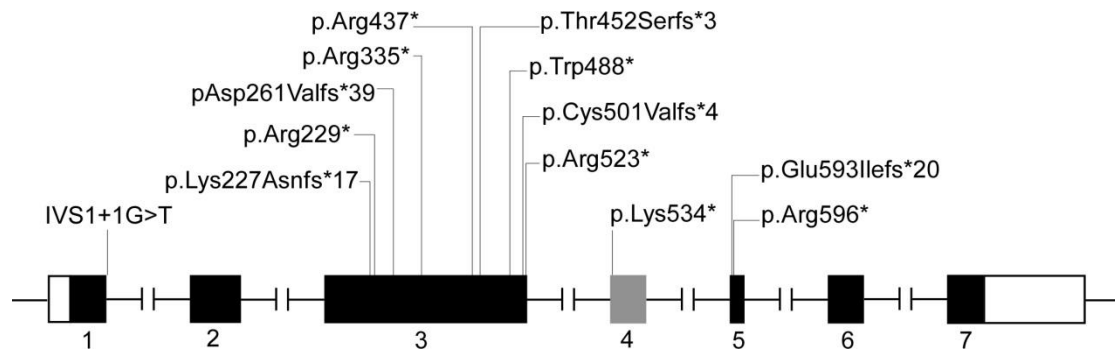
⁵ Sackler Faculty of Medicine, Tel-Aviv University, Tel-Aviv, Israel.

⁶ Department of Ophthalmology, Tel-Aviv Sourasky Medical Center, Tel-Aviv, Israel.

⁷ Rappaport Faculty of Medicine, Technion-Israel Institute of Technology, Haifa, Israel.

Supplementary Figure 1: Schematic representation of the *FAM161A*

pathogenic mutations that have been reported previously.



Supplementary Table S1: *FAM161A* mutations reported worldwide (based on NM_001201543)

#	Mutation Name	Location	Number of patients	Reference
1	c.183+1G>T (IVS1+1G>T)	Intron 1	1 compound heterozygous	1
2	c.678_681del, p.Lys227Asnfs*17	Exon 3	1 homozygous	2
3	c.685C>T, p.Arg229*	Exon 3	1 homozygous	3
4	c.728del, p.Asp261Valfs*39	Exon 3	1 homozygous	2
5	c.1003C>T, p.Arg335* (reported as c.1105C>T by ⁴)	Exon 3	2 homozygous	5
			3 homozygous	4
6	c.1309A>T, p.Arg437*	Exon 3	3 homozygous	3
			5 homozygous + 3 compound heterozygous	1
			6 homozygous	6
			1 homozygous + 1 compound heterozygous	7
			1 compound heterozygous	8
			1 compound heterozygous	9
7	c.1355_1356del, p.Thr452Serfs*3	Exon 3	26 homozygous + 5 compound heterozygous	10
			8 homozygous	11
			2 homozygous	12
8	c.1464G>A, p.Trp488*	Exon 3	1 homozygous	7
9	c.1501del, p.Cys501Valfs*4	Exon 3	1 compound heterozygous	1
			1 homozygous	13
			1 compound heterozygous	8
			1 homozygous	9
10	c.1567C>T, p.Arg523*	Exon 3	9 homozygous 5 compound heterozygous	10
			1 compound heterozygous	1
			1 compound heterozygous	7
			1 homozygous + 1 compound heterozygous	9
11	c.1600A>T, p.Lys534*	Exon 4	3 homozygous	14

12	c.1777_1778del, p.Glu593Ilefs*20 (reported as: p.R592FsX2)	Exon 5	5 homozygous	15
13	c.1786C>T, p.Arg596*	Exon 5	2 homozygous	10

References:

- 1 Van Schil, K. *et al.* A Nonsense Mutation in FAM161A Is a Recurrent Founder Allele in Dutch and Belgian Individuals With Autosomal Recessive Retinitis Pigmentosa. *Invest Ophthalmol Vis Sci* **56**, 7418-7426, doi:10.1167/iovs.15-17920 (2015).
- 2 Carss, K. J. *et al.* Comprehensive Rare Variant Analysis via Whole-Genome Sequencing to Determine the Molecular Pathology of Inherited Retinal Disease. *American journal of human genetics* **100**, 75-90, doi:10.1016/j.ajhg.2016.12.003 (2017).
- 3 Langmann, T. *et al.* Nonsense mutations in FAM161A cause RP28-associated recessive retinitis pigmentosa. *Am J Hum Genet* **87**, 376-381 (2010).
- 4 Duncan, J. L. *et al.* Ocular Phenotype of a Family with FAM161A-associated Retinal Degeneration. *Ophthalmic genetics*, 1-9, doi:10.3109/13816810.2014.929716 (2015).
- 5 Zobor, D., Balousha, G., Baumann, B. & Wissinger, B. Homozygosity mapping reveals new nonsense mutation in the FAM161A gene causing autosomal recessive retinitis pigmentosa in a Palestinian family. *Molecular vision* **20**, 178-182 (2014).
- 6 Rose, A. M. *et al.* Diverse clinical phenotypes associated with a nonsense mutation in FAM161A. *Eye* **29**, 1226-1232, doi:10.1038/eye.2015.93 (2015).
- 7 Ellingford, J. M. *et al.* Molecular findings from 537 individuals with inherited retinal disease. *Journal of medical genetics* **53**, 761-767, doi:10.1136/jmedgenet-2016-103837 (2016).
- 8 Wang, J. *et al.* Dependable and efficient clinical utility of target capture-based deep sequencing in molecular diagnosis of retinitis pigmentosa. *Investigative ophthalmology & visual science* **55**, 6213-6223, doi:10.1167/iovs.14-14936 (2014).
- 9 Jespersgaard, C. *et al.* Molecular genetic analysis using targeted NGS analysis of 677 individuals with retinal dystrophy. *Scientific reports* **9**, 1219, doi:10.1038/s41598-018-38007-2 (2019).
- 10 Bandah-Rozenfeld, D. *et al.* Homozygosity mapping reveals null mutations in FAM161A as a cause of autosomal-recessive retinitis pigmentosa. *Am J Hum Genet* **87**, 382-391 (2010).
- 11 Venturini, G. *et al.* Molecular genetics of FAM161A in North American patients with early-onset retinitis pigmentosa. *PLoS One* **9**, e92479, doi:10.1371/journal.pone.0092479 (2014).
- 12 Beryozkin, A. *et al.* Whole Exome Sequencing Reveals Mutations in Known Retinal Disease Genes in 33 out of 68 Israeli Families with Inherited Retinopathies. *Scientific reports* **5**, 13187, doi:10.1038/srep13187 (2015).
- 13 Glockle, N. *et al.* Panel-based next generation sequencing as a reliable and efficient technique to detect mutations in unselected patients with retinal dystrophies. *European journal of human genetics : EJHG* **22**, 99-104, doi:10.1038/ejhg.2013.72 (2014).
- 14 Maranhao, B. *et al.* Investigating the Molecular Basis of Retinal Degeneration in a Familial Cohort of Pakistani Decent by Exome Sequencing. *PloS one* **10**, e0136561, doi:10.1371/journal.pone.0136561 (2015).

- 15 Zhou, Y. *et al.* Whole-exome sequencing reveals a novel frameshift mutation in the FAM161A gene causing autosomal recessive retinitis pigmentosa in the Indian population. *Journal of human genetics* **60**, 625-630, doi:10.1038/jhg.2015.92 (2015).

Supplementary Table S2: Clinical parameters of patients who participated in the study

Patient number (age)	Mutation 1	Mutation 2	Age of disease onset	Visual Acuity as Snellen ratio (age if differs from 1 st column) ^b	Refraction In diopters (age if differs from 1 st column) ^c	Cone flicker 30Hz (μV;msec) ^d	Mixed cone-rod response a wave: b wave (μV) ^d	Rod response (μV) ^d	ERM	Cataract (age at surgery, if performed)
MOL0053-2 (30) ^a	p.Arg523*	p.Arg523*	18	0.4	-6.50	ND	ND	ND	Yes	Yes
MOL0053-3 (44)	p.Arg523*	p.Arg523*	4	0.34	-7.00	NA	NA	NA	Yes	Yes
MOL0100-1 (10) ^a	p.Thr452Serfs*3	p.Thr452Serfs*3	10	1	-3.25	ND	ND	ND	Yes	No
MOL0100-2 (10) ^a	p.Thr452Serfs*3	p.Thr452Serfs*3	10	0.9	-6.00	ND	SR	ND	Yes	No
MOL0139-1 (10) ^a	p.Thr452Serfs*3	p.Thr452Serfs*3	Childhood	0.83	NA	33;39	80:258	216	Yes	No
MOL0139-2 (43) ^a	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	0.12	NA	SR	SR	SR	NA	NA
MOL0195-1 (29) ^a	p.Thr452Serfs*3	p.Arg523*	Teen years	1.25	-6.00	ND	ND	ND	Yes ^e	Yes (37)
MOL0228-1 (11)	p.Thr452Serfs*3	p.Thr452Serfs*3	11	0.63	High myopia	ND	ND	ND	NA	Yes
MOL0228-2 (27)	p.Thr452Serfs*3	p.Thr452Serfs*3	Teen years	0.45	-3.00	ND	ND	ND	NA	Yes (33)
MOL0228-3 (10)	p.Thr452Serfs*3	p.Thr452Serfs*3	10	0.5	-3.25	26;32	55:110	ND	Yes	Yes
MOL0276-1 (41) ^a	p.Arg523*	p.Arg523*	NA	0.9	NA	27;31	95:154	109	Yes	NA
MOL0276-2 (51) ^a	p.Arg523*	p.Arg523*	NA	0.05	-4.75	ND	ND	ND	Yes	Yes
MOL0284-1 (38) ^a	p.Thr452Serfs*3	p.Thr452Serfs*3	2	0.29	-12.00	ND	ND	ND	Yes	Yes (50)
MOL0286-1 (59) ^a	p.Thr452Serfs*3	p.Thr452Serfs*3	3	1.0	-1.75	22;35	67:154	65	Yes	Yes
MOL0303-1 (19) ^a	p.Thr452Serfs*3	p.Arg523*	18	1.0	NA	ND	ND	ND	NA	Yes
MOL0313-1 (35)	p.Thr452Serfs*3	p.Thr452Serfs*3	14	0.14	-6.00	ND	ND	ND	Yes	Yes
MOL0352-1 (78)	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	NA	NA	NA	NA	NA	NA	NA
MOL0446-1 (28) ^a	p.Thr452Serfs*3	p.Arg523*	Childhood	0.65	-9.00	ND	ND	ND	Yes	Yes
MOL0453-1 (43)	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	0.4	-3.75	ND	ND	ND	NA	NA

MOL1073-1 (43)	p.Thr452Serfs*3	p.Thr452Serfs*3	30	0.63	-4.50	NA	NA	NA	Yes	Yes (34)
MOL1073-2	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	NA	NA	NA	NA	NA	NA	NA
MOL1073-3	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	NA	NA	NA	NA	NA	NA	NA
MOL1160-1 (61)	p.Thr452Serfs*3	p.Thr452Serfs*3	18	0.2	-3.75	ND	ND	ND	Yes	Yes (65)
MOL1200-1 (29)	p.Thr452Serfs*3	p.Thr452Serfs*3	30	1.0	NA	ND	ND	ND	Yes	Yes
MOL1209-1 (18)	p.Thr452Serfs*3	p.Thr452Serfs*3	10	0.8	NA	10:26	3:36	ND	Yes	No
MOL1221-1	p.Arg523*	p.Arg523*	NA	NA	NA	NA	NA	NA	NA	NA
MOL1289-1 (9)	p.Thr452Serfs*3	p.Thr452Serfs*3	9	0.5	-9.75	ND	ND	ND	Yes	NA
MOL1294-1 (31)	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	1.0	NA	NA	NA	NA	NA	NA
MOL1300-1 (9)	p.Arg523*	p.Arg523*	Childhood	0.45	-1.50	ND	ND	ND	NA	NA
MOL1300-2 (19)	p.Arg523*	p.Arg523*	Childhood	0.1	-4.00	ND	ND	ND	NA	NA
MOL1300-3 (9)	p.Arg523*	p.Arg523*	Childhood	0.43	-1.25	ND	ND	ND	NA	NA
MOL1335-1	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	NA	High myopia	NA	NA	NA	NA	Yes
MOL1335-2	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	NA	NA	NA	NA	NA	NA	NA
MOL1350-1 (69)	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	0.0001	NA	ND	ND	ND	Yes	NA
MOL1365-1 (82)	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	NA	NA	NA	NA	NA	NA	NA
MOL1380-1 (47)	p.Thr452Serfs*3	p.Thr452Serfs*3	Childhood	0.33	-4.00	ND	ND	ND	Yes	Yes (63)
MOL1387-1 (17)	p.Thr452Serfs*3	p.Thr452Serfs*3	Childhood	0.65	NA	9:40	38:58	ND	Yes	NA
MOL1392-1 (43)	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	0.8	NA	13:36	ND	ND	Yes	Yes
MOL1426-1 (40)	p.Thr452Serfs*3	p.Arg523*	18	0.3	-3.50	21:31	27:41	ND	Yes	Yes
MOL1504-1 (20)	p.Thr452Serfs*3	p.Thr452Serfs*3	6	1	-4.75	10:43	29:77	64	Yes	NA
MOL1545-1 (19)	p.Arg523*	p.Arg523*	Childhood	0.45	-5.75	ND	ND	ND	No	No
MOL1545-2 (14)	p.Arg523*	p.Arg523*	Childhood	0.44	-7.75	ND	ND	ND	No	No
MOL1545-4 (7)	p.Arg523*	p.Arg523*	5	0.5	-6.75	SR	SR	SR	No	No
MOL1649-1 (62)	p.Thr452Serfs*3	p.Thr452Serfs*3	60	0.8	-0.75	11:40	ND	ND	Yes	Yes
MOL1666-1 (45)	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	NA	NA	ND	ND	ND	NA	NA
MOL1666-2 (38)	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	NA	NA	ND	ND	ND	NA	NA
MOL1668-1 (5)	p.Thr452Serfs*3	p.Arg523*	NA	NA	NA	14:33	ND	ND	NA	NA
MOL1750-1 (15)	p.Thr452Serfs*3	p.Thr452Serfs*3	Childhood	0.8	-7.50	ND	ND	ND	Yes	No
MOL1765-1 (20)	p.Thr452Serfs*3	p.Thr452Serfs*3	20	0.8	NA	27:44	ND	ND	Yes	No
MOL1773-1 (39)	p.Thr452Serfs*3	p.Arg523*	Childhood	0.8	NA	ND	ND	ND	Yes	Yes
MOL1779-1 (18)	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	0.8	NA	ND	ND	ND	NA	NA
MOL1793-1 (62)	p.Thr452Serfs*3	p.Thr452Serfs*3	7	0.06	-8.00	ND	ND	ND	Yes	Yes
MOL1831-1 (86)	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	0.0001	High myopia	ND	ND	ND	Yes	Yes

MOL1833-1 (30)	p.Thr452Serfs*3	p.Arg523*	10	0.45	-8.00	ND	ND	ND	NA	NA
TB21-R28 (24) ^a	p.Thr452Serfs*3	p.Thr452Serfs*3	12	0.001	NA	30;28	ND	ND	Yes	Yes
TB21-R27 (34)	p.Thr452Serfs*3	p.Thr452Serfs*3	34	0.31	-9.65	ND	ND	ND	NA	Yes
TB21-R29	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	NA	NA	NA	NA	NA	NA	NA
TB21-R20 (63) ^a	p.Thr452Serfs*3	p.Thr452Serfs*3	50	0.3	NA	ND	ND	ND	Yes ^e	Yes
TB65-U52 (27)	p.Thr452Serfs*3	p.Thr452Serfs*3	Childhood	0.8	NA	ND	ND	ND	Yes	Yes
TB65-U61	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	NA	NA	NA	NA	NA	NA	NA
TB112-835522 (64)	p.Thr452Serfs*3	p.Thr452Serfs*3	40	0.001	-4.50	ND	ND	ND	Yes	Yes (68)
TB155-R417 (52)	p.Thr452Serfs*3	p.Thr452Serfs*3	20	0.05	NA	9;39	22:16	ND	Yes	Yes
TB190-R476 (52)	p.Thr452Serfs*3	p.Thr452Serfs*3	45	0.28	NA	SR	SR	SR	Yes ^e	Yes
TB190-R477 (24)	p.Thr452Serfs*3	p.Thr452Serfs*3	20	NA	NA	ND	ND	ND	Yes	No
TB195-R492 (65)	p.Thr452Serfs*3	p.Thr452Serfs*3	17	NA	NA	NA	NA	NA	NA	NA
TB205-R515 (56)	p.Thr452Serfs*3	p.Thr452Serfs*3	40	NA	NA	NA	NA	NA	NA	NA
TB250-R582 (33)	p.Thr452Serfs*3	p.Arg523*	20	0.58	-8.00	ND	ND	ND	Yes	No
TB332-R710 (39)	p.Thr452Serfs*3	p.Thr452Serfs*3	29	NA	NA	ND	ND	ND	NA	NA
TB346-R732 (51)	p.Thr452Serfs*3	p.Thr452Serfs*3	Childhood	NA	NA	NA	NA	NA	NA	NA
TB370-R760 (44)	p.Thr452Serfs*3	p.Thr452Serfs*3	24	0.6	-6.00	9;41	44:117	16	Yes	Yes
TB379-R777 (58)	p.Thr452Serfs*3	p.Thr452Serfs*3	Childhood	0.0001	NA	ND	ND	ND	Yes	Yes (57)
TB490-R940 (56)	p.Thr452Serfs*3	p.Thr452Serfs*3	NA	NA	NA	51;38	81:90	ND	Yes	NA
TB525-R994 (17)	p.Thr452Serfs*3	p.Arg523*	8	0.4	-15.00	ND	ND	ND	No	No
TB525-R995 (21)	p.Thr452Serfs*3	p.Arg523*	14	0.7	-10.00	ND	ND	ND	No	Yes
TB539-R1015 (69)	p.Thr452Serfs*3	p.Thr452Serfs*3	20	0.35	-3.00	ND	ND	ND	Yes	Yes
TB712-R1292 (31)	p.Thr452Serfs*3	p.Thr452Serfs*3	7	0.66	-5.25	11;37	SR	ND	Yes	No
TB790-R1390 (32)	p.Thr452Serfs*3	p.Thr452Serfs*3	32	0.75	-2.75	ND	ND	ND	Yes	No
TB836-R1466 (4)	p.Thr452Serfs*3	p.Thr452Serfs*3	4	0.01	NA	ND	ND	ND	No	No
TB840-R1474 (36)	p.Thr452Serfs*3	p.Thr452Serfs*3	10	0.5	-10.00	ND	ND	ND	Yes	Yes (45)

ND - non-detectable, SR- severely reduced, NA- not available

a - Clinical data regarding these patients were previously published⁹

b - Best corrected visual acuity is presented as an average of the two eyes, in decimal values. In order to provide numerical values for low VA, the following conversions were made: NLP (no light perception) = 0; LP (light perception) = 0.0001; HM (hand movement) = 0.001; FC (finger counting) = 0.01.

c - Refraction is presented as average spherical equivalent of both eyes, in diopters

d - Full field ERG testing performed according to ISCEV standard; average of the values recorded in the two eyes are shown for each of the main stimulus conditions. Limits of normal are as follows: 30Hz Cone Flicker: lower threshold of normal for amplitude-60 μ V; upper limit for implicit time- 33msec; Mixed cone-rod response- lower threshold of normal for b wave amplitude- 400 μ V; for a-wave- 100 μ V; Rod response- lower threshold of normal for amplitude- 200 μ V.

e - Macular edema

Supplementary Table S3: Statistical analysis of BCVA in patients with *FAM161A* genotypes

A. Analysis of Covariance including all 3 <i>FAM161A</i> genotypes. Tests of Between-Subjects Effects						
Dependent Variable:	Average VA Snellen					
Source	Type III Sum of Squares	df	Mean Square	F	Sig.	
Corrected Model	14.659 ^a	5	2.932	42.181	0.000	
Intercept	20.045	1	20.045	288.402	0.000	
Genotype	2.303	2	1.151	16.565	p<0.001	
AGE (years)	7.013	1	7.013	100.902	p<0.001	
Genotype * AGE (years)	1.700	2	0.850	12.228	p<0.001	
Error	25.021	360	0.070			
Total	122.967	366				
Corrected Total	39.680	365				
a. R Squared = .369 (Adjusted R Squared = .361)						
B. Analysis of Covariance, comparing homozygotes for Frameshift versus Compound heterozygotes: Tests of Between-Subjects Effects						
Dependent Variable:	Average VA Snellen					
Source	Type III Sum of Squares	df	Mean Square	F	Sig.	

Corrected Model	10.509 ^a	3	3.503	46.114	0.000	
Intercept	18.794	1	18.794	247.417	0.000	
Genotype	1.336	1	1.336	17.593	p<0.001	
AGE (years)	7.209	1	7.209	94.903	p<0.001	
Genotype * AGE (years)	1.660	1	1.660	21.853	p<0.001	
Error	22.940	302	0.076			
Total	116.164	306				
Corrected Total	33.449	305				

a. R Squared = .314 (Adjusted R Squared = .307)

C. Analysis of Covariance, comparing homozygotes Frameshift versus homozygotes Nonsense: Tests of Between-Subjects Effects

Dependent Variable:	Average VA Snellen					
Source	Type III Sum of Squares	df	Mean Square	F	Sig.	
Corrected Model	10.216 ^a	3	3.405	52.424	0.000	
Intercept	13.647	1	13.647	210.102	0.000	
Genotype	0.735	1	0.735	11.313	0.001	
AGE (years)	2.706	1	2.706	41.653	p<0.001	
Genotype * AGE (years)	0.004	1	0.004	0.061	0.805	

Error	19.876	306	0.065			
Total	102.982	310				
Corrected Total	30.092	309				

a. R Squared = .339 (Adjusted R Squared = .333)

D. Analysis of Covariance, comparing Compound heterozygotes versus homozygotes Nonsense: Tests of Between-Subjects Effects

Dependent Variable:	Average VA Snellen					
Source	Type III Sum of Squares	df	Mean Square	F	Sig.	
Corrected Model	5.924 ^a	3	1.975	30.606	0.000	
Intercept	10.400	1	10.400	161.201	0.000	
Genotype	2.294	1	2.294	35.555	p<0.001	
AGE (years)	4.633	1	4.633	71.809	p<0.001	
Genotype * AGE (years)	1.199	1	1.199	18.590	p<0.001	
Error	7.226	112	0.065			
Total	26.788	116				
Corrected Total	13.149	115				

a. R Squared = .450 (Adjusted R Squared = .436)

Generalized Linear Model with repeated measurements: Tests of Model Effects						
Source	Type III					
	Wald Chi-Square	df	Sig.			
(Intercept)	73.401	1	0.000			
Genotype	15.578	2	p<0.001			
AGE (years)	46.579	1	p<0.001			
Mutation Type * AGE (years)	8.638	2	0.013			
Dependent Variable: Average VA Snellen						
Model: (Intercept), Mutation Type, AGE (years), Mutation Type * AGE (years)						

Supplementary Table S4: Statistical analysis of VF in patients with *FAM161A* mutations versus patients with mutations in other RP-causing genes.

A. Pearson Correlation:						
		Visual Field Area (cm2)				
Age	Pearson Correlation	-0.129				
	Sig. (2-tailed)	0.185				
	N	108				
Spearman's rho:						
		Visual Field Area (cm2)				
Age	Correlation Coefficient	-0.088				
	Sig. (2-tailed)	0.366				
	N	108				
Pearson Correlation: Different genes						
Gene name			Visual Field Area (cm2)			
MAK	Age	Pearson Correlation	-.724**			
		Sig. (2-tailed)	0.000			
		N	27			

RPGR	Age	Pearson Correlation	-.580*			
		Sig. (2-tailed)	0.048			
		N	12			
DHDDS	Age	Pearson Correlation	-0.245			
		Sig. (2-tailed)	0.442			
		N	12			
FAM161A	Age	Pearson Correlation	0.194			
		Sig. (2-tailed)	0.149			
		N	57			

** . Correlation is significant at the 0.01 level (2-tailed).

* . Correlation is significant at the 0.05 level (2-tailed).

B. Spearman's rho: Different genes

Gene name			Visual Field Area (cm2)			
MAK	Age	Correlation Coefficient	-.788**			
		Sig. (2-tailed)	0.000			
		N	27			
RPGR	Age	Correlation Coefficient	-0.453			

		Sig. (2-tailed)	0.140			
		N	12			
DHDDS	Age	Correlation Coefficient	0.007			
		Sig. (2-tailed)	0.983			
		N	12			
FAM161A	Age	Correlation Coefficient	0.011			
		Sig. (2-tailed)	0.936			
		N	57			

** . Correlation is significant at the 0.01 level (2-tailed).

C. Analysis of Covariance: Tests of Between-Subjects Effects

Dependent Variable:	Visual Field Area (cm2)					
Source	Type III Sum of Squares	df	Mean Square	F	Sig.	
Corrected Model	61105.896 ^a	7	8729.414	17.846	0.000	
Intercept	26487.945	1	26487.945	54.152	0.000	
Gene	46682.434	3	15560.811	31.812	p<0.001	
Age	9090.285	1	9090.285	18.584	p<0.001	
Gene * age	29128.015	3	9709.338	19.850	p<0.001	

Error	48914.320	100	489.143			
Total	151717.967	108				
Corrected Total	110020.215	107				

a. R Squared = .555 (Adjusted R Squared = .524)

D. Analysis of Covariance, FAM161A vs. MAK

Dependent Variable:	Visual Field Area (cm2)					
Source	Type III Sum of Squares	df	Mean Square	F	Sig.	
Corrected Model	54104.895 ^a	3	18034.965	42.450	0.000	
Intercept	46564.430	1	46564.430	109.602	0.000	
Gene	43283.565	1	43283.565	101.879	p<0.001	
Age	21710.042	1	21710.042	51.100	p<0.001	
Gene * age	26086.272	1	26086.272	61.401	p<0.001	
Error	33988.090	80	424.851			
Total	115112.313	84				
Corrected Total	88092.985	83				

a. R Squared = .614 (Adjusted R Squared = .600)

E. Analysis of Covariance, FAM161A vs. RPGR

Dependent Variable:	Visual Field Area (cm2)					
Source	Type III Sum of Squares	df	Mean Square	F	Sig.	
Corrected Model	7332.330 ^a	3	2444.110	10.390	0.000	
Intercept	7983.718	1	7983.718	33.938	0.000	
Gene	6937.289	1	6937.289	29.490	p<0.001	
Age	4379.930	1	4379.930	18.619	p<0.001	
Gene * age	5278.146	1	5278.146	22.437	p<0.001	
Error	15290.850	65	235.244			
Total	28478.345	69				

a. R Squared = .324 (Adjusted R Squared = .293)

F. Analysis of Covariance, FAM161A vs. DHDDS

Dependent Variable:	Visual Field Area (cm2)					
Source	Type III Sum of Squares	df	Mean Square	F	Sig.	
Corrected Model	5992.598 ^a	3	1997.533	12.756	0.000	
Intercept	1617.701	1	1617.701	10.330	0.002	

Gene	1311.998	1	1311.998	8.378	0.005	
Age	223.810	1	223.810	1.429	0.236	
Gene * age	397.653	1	397.653	2.539	0.116	
Error	10178.794	65	156.597			
Total	24215.869	69				
Corrected Total	16171.392	68				
a. R Squared = .371 (Adjusted R Squared = .342)						

Supplementary Table S5: Sequence of primers used in this study

	Forward	Reverse
Ex 3a	TGAGCATGGTGGCACAAG	GCTGACCTACAAGGCAGAGG
Ex 3b	TGCATCTGTCTTTCTCCCC	TCTTAGAATACCCTCTGACAAAATATC
Ex 4	ATCCCATGTTAAATCTTTGC	GAAAACCAGTGGTCTGGAG