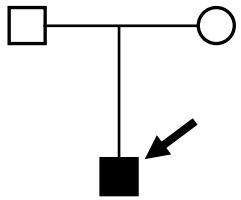
Supplementary Figure 1

Family 3 - RCD



[V1];[V4]

V1: c.1631A>G; p.(Lys544Arg)
V4: c.439G>T; p.(Ala147Ser)

Genotype Counts

		4-129920937-C-A		
		C/C	C/A	A/A
4-129864152-T-C	T/T	120,396	8	0
	T/C	2	0	0
	C/C	0	0	0

Samples consistent with variants appearing in isolation or on different haplotypes.
Samples consistent with variants appearing on the same haplotype.
Samples consistent with either co-occurrence pattern.

Based on their co-occurrence pattern in gnomAD, these variants are likely found on different haplotypes in most individuals in gnomAD.

Note Because no individual in gnomAD carries both variants, this table was computed based on the separate variant information and does not account for the possibility that some samples may not be covered at both variant sites.

Variant 1 (required)
4-129864152-T-C

Variant 2 (required)
4-129920937-C-A

Submit

Overview

Genetic ancestry group	Samples consistent with variants appearing in isolation or on different haplotypes	Samples consistent with variants appearing on the same haplotype	Samples consistent with either co-occurrence pattern	Likely co-occurrence pattern
African/African American	0	0	0	No prediction*
Admixed American	0	0	0	No prediction*
Ashkenazi Jewish	0	0	0	No prediction*
East Asian	10	0	0	Different haplotypes
European (Finnish)	0	0	0	No prediction*
European (non-Finnish)	0	0	0	No prediction*
Remaining individuals	0	0	0	No prediction*
South Asian	0	0	0	No prediction*
All	**10**	**0**	**0**	**Different haplotypes**

* A likely co-occurrence pattern cannot be calculated in some cases, such as when only one of the variants is observed in a genetic ancestry group, or when both variants are singletons and were seen in the same individual.

Haplotype Counts

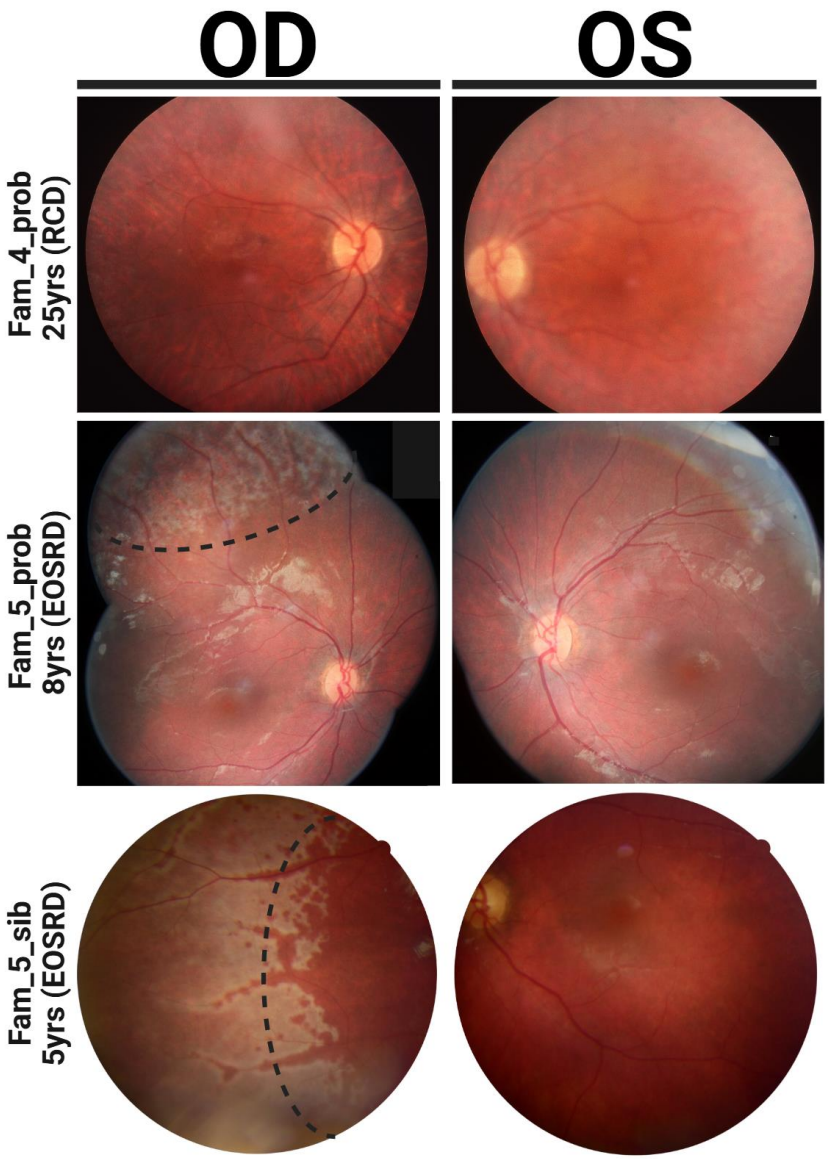
		4-129920937-C-A	
		C	A
4-129864152-T-C	T	240,802	8
	C	2	0

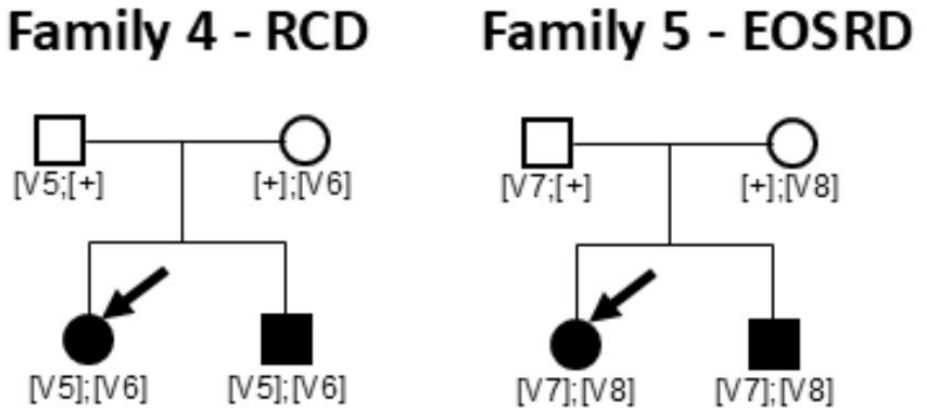
The estimated probability that these variants occur in different haplotypes is 100%.

Note Probability values are not well calibrated, particularly where both variants are extremely rare. Interpret with caution. Please see our blog post on variant co-occurrence for accuracy estimates and additional detail.

Supplementary Figure 1: Confirmation of the *trans* configuration of the *SCLT1* variants V1 and V4 in family 3 proband, according to the gnomAD v2 Variant Co-Occurrence tool.

Supplementary Figure 2



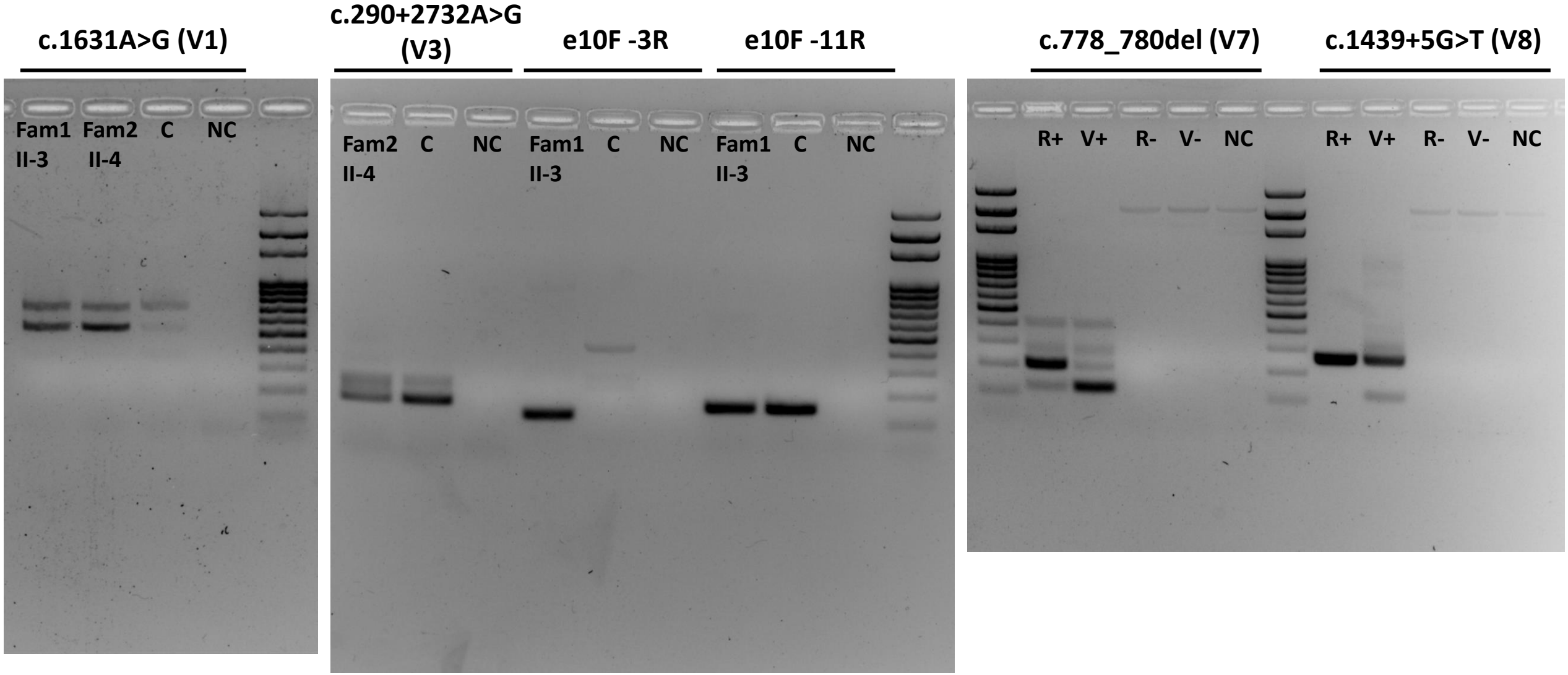


V5: c.671T>G; p.(Leu224Arg)
V6: c.1706G>A; p.(Ser569Asn)

V7: c.778_780del; p.(Glu260del)
V8: c.1439+5G>T

Supplementary Figure 2: Fundus pictures of family 4 proband and family 5 affected siblings. Family 5 siblings exhibit numerous mottled and whitish lesions in the peripheral retina, highlighted as areas behind the dashed line.

Supplementary Figure 3



Supplementary Figure 3: Uncropped and unprocessed scans of gel blots showed in Figure 3. C, control; NC, negative control; R, reference splicing construct; V, mutant splicing construct; +, RT+; -, RT-.

Supplementary Figure 4

Supplementary Figure 4: Structural modeling of wild-type SCLT1 and SCLT1 exon 3-10 duplication. To evaluate the structural changes caused by the in-frame exon 3-10 duplication in *SCLT1*, we performed structural modeling using the AlphaFold Server3 (https://alphafoldserver.com). (A) Structural model of wild-type SCLT1 with the exon 3-10 regions highlighted in blue (B) AlphaFold predicts increased intra-protein interactions in the *SCLT1* exon 3-10 duplication variant. The wild-type elongated linker protein is predicted to become shortened due to the exon 3-10 duplication, potentially leading to a loss of function. The duplicated exon 3-10 regions are highlighted in green.