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Supplemental Data

Autosomal-Recessive Posterior Microphthalmos Is Caused by Mutations in *PRSS56*, a Gene Encoding a Trypsin-Like Serine Protease

Andreas Gal, Isabella Rau, Leila El Matri, Hans-Jürgen Kreienkamp, Susanne Fehr, Karim Baklouti, Ibtissem Chouchane, Yun Li, Monika Rehbein, Josefine Fuchs, Hans C. Fledelius, Kaj Vilhelmsen, Daniel F. Schorderet, Francis L. Munier, Elsebet Ostergaard, Debra A. Thompson, and Thomas Rosenberg

Table S1. Single Nucleotide Polymorphisms (SNPs) Used to Map *PRSS56* in Two Faroese Families with Posterior Microphthalmos

Physical Location	Gene	Exon/Intron	Nucleotide changed	Alleles	SNP ID	Heterozygosity
232260537	*B3GNT7*	Intron 1	c.11+12	G/T	*rs4972989*	n. d.
232326417	*NCL*	Exon 3	c.447	A/G	*rs1131171*	0.486
233244930	*ALPP*	Exon 6	c.692	G/C	*rs1048988*	0.197
233347919	*ECEL1*	Intron 8	c.1507-30	G/C	*rs6750085*	0.500
233537125	*EFHD1*	Exon 3	c.557	G/A	*rs11550699*	0.460
233633460	*KCNJ13*	Exon 3	c.524	T/C	*rs1801251*	0.407

n.d., no data.

Table S2. Position and Size of *PRSS56* Exons and Sequence of Primers Used for PCR Amplification Thereof

Exon	Position (ATG = c.1 – c.3; TGA = c.1810 – c.1812)	Size (bp) Exon	Amplicon	Sequence (5'-3') of primers
1	c.-136 – c.97	233	421	TCCTAGGAGTTAAGGGCCAGGTG (F) AGGAGCCAAAGGTCCTTATGAGTG (R)
2	c.98 – c.205	108	216	AACCACGCATGATTGTGTGCC (F) AAGGGACAGAGGCAGCAGAATGG (R)
3	c.206 – c.256	51	1147	AGCAGTGAGACTCAAAGGTCTG (F) TCCCTACACTCTATTACCTCGGAC (R)
4	c.257 – c.446	190		
5	c.447 – c.546	100		
6	c.547 – c.706	160		
7	c.707 – c.849	143	334	AATGCTGCCTGCTCTTTCAAAGG (F) AGACAGACGTGGAAGGAAAAGAG (R)
8	c.850 – c.1012	163	1084	AGGCGTAAGGCAGGCGTCATAGG (F) AAGCGCTTCCGACCTCGTCCAG (R)
9	c.1013 – c.1186	174		
10	c.1187 – c.1351	165		
11	c.1352 – c.1414	63		
12	c.1415 – c.1521	107	233	AGGCCATCCTGAGGTGCTGGTGG (F) AGGCCATCGTGAAGGAGTCTGGAAG (R)
13	c.1522 – c.2022	501	451	TCTGGGGTTTCAACTCAGGAGTG (F) AGCCACTGGGGCAGCGACAGTTTG (R)

Table S3. Size of Amplicons and Sequence of Primers Used to Evaluate *PRSS56* Expression in Human and *Prss56* Expression in Mouse Eyes following Amplification of cDNA by Reverse Transcriptase-Coupled PCR

Gene transcript	Size (bp)	Sequence (5'-3') of primers
human *PRSS56* forward	416	TCGCACGAGTGCCGAGGATCT
human *PRSS56* reverse		CTCACCGGCGTCCACAGCTG
mouse *Prss56* forward_1	442	TTGCTTCGCCGGTGCCTCGAATG
mouse *Prss56* reverse_1		ACAGGTTAAAGGGCCCCCGGA
mouse *Prss56* forward_2	354/411*	GGCATCCACTGTACACGCGC
mouse *Prss56* reverse_2		ATTGCTTCGCCGGTGCCTCGAA
human *HPRT* forward	249	ACCCCACGAAGTGTTGGATA
human *HPRT* reverse		AAGCAGATGGCCACAGAACT
mouse *Hprt* forward	227	GCAAGCTTGCTGGTGAAAAGGAC
mouse *Hprt* reverse		GGCAACATCAACAGGACTCCTCGTA

*Using the second mouse primer combination, two apparent splice variants were detected; the longer variant differs from the database entry (XM_487606.5) as it includes an exon of 57 bases, coding for 19 additional amino acids. These residues are positioned between the signal peptide cleavage site, and the predicted proteolytic activation site of the mouse protein. In fact, the database entry for the human *PRSS56* mRNA also contains this exon. The sequence of the longer cDNA variant has been submitted to Genbank (accession number JF323950).

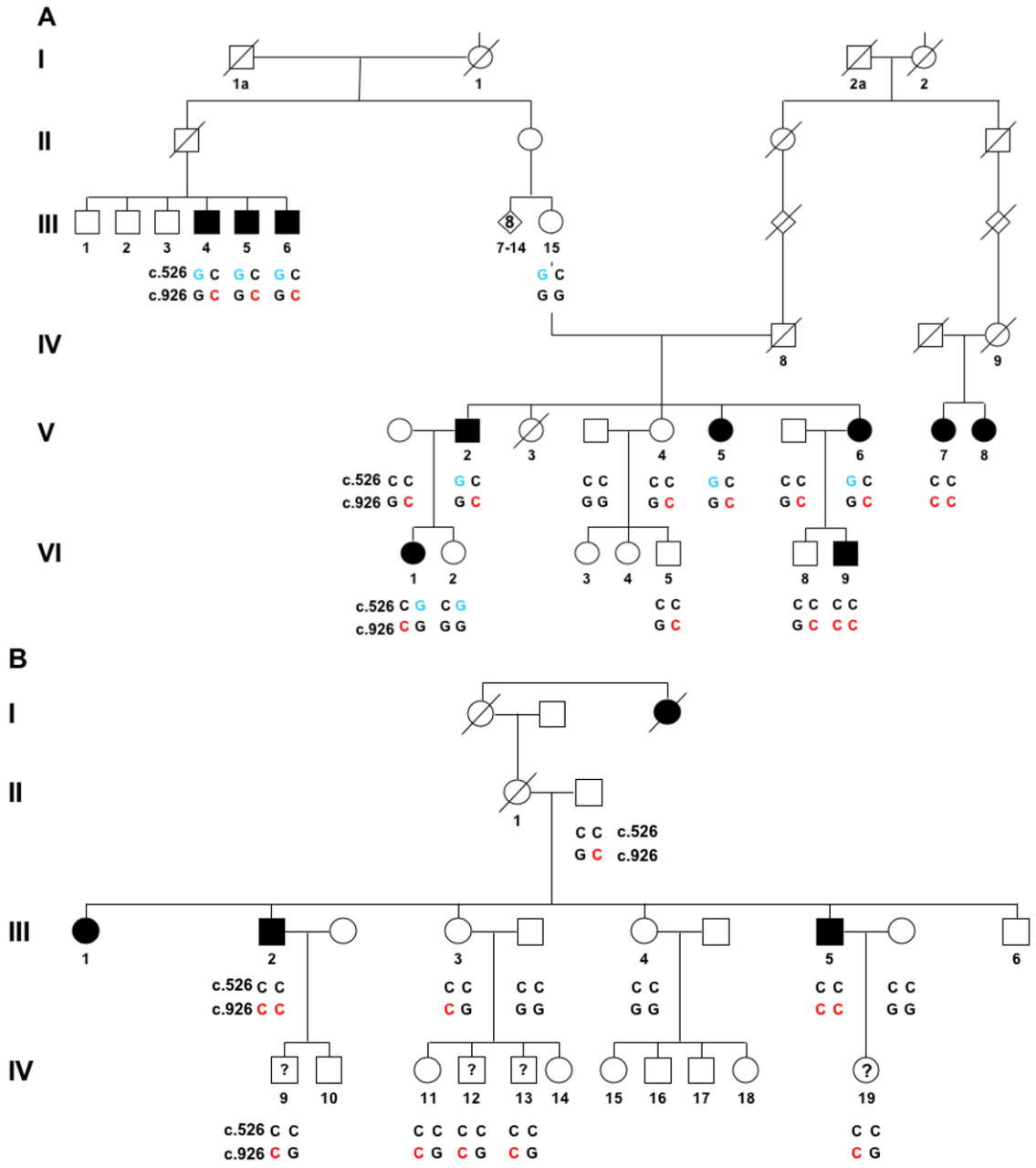

Figure S1. Pedigrees of Two Large Families with arMCOP from the Faroe Islands
Families HOP00201 (A) and HOP00202 were published by Fuchs *et al.*[1] as Families 1 and 2, respectively. Generation and individual numbers shown in the figure are the same as in the original paper. Genotypes for nucleotides c.526 (exon 5; first line) and c.926 (exon 8; second line) of *PRSS56* are shown below the corresponding pedigree symbols, with the mutant nucleotide in color. ?: MCOP phenotype is not defined due to young age.

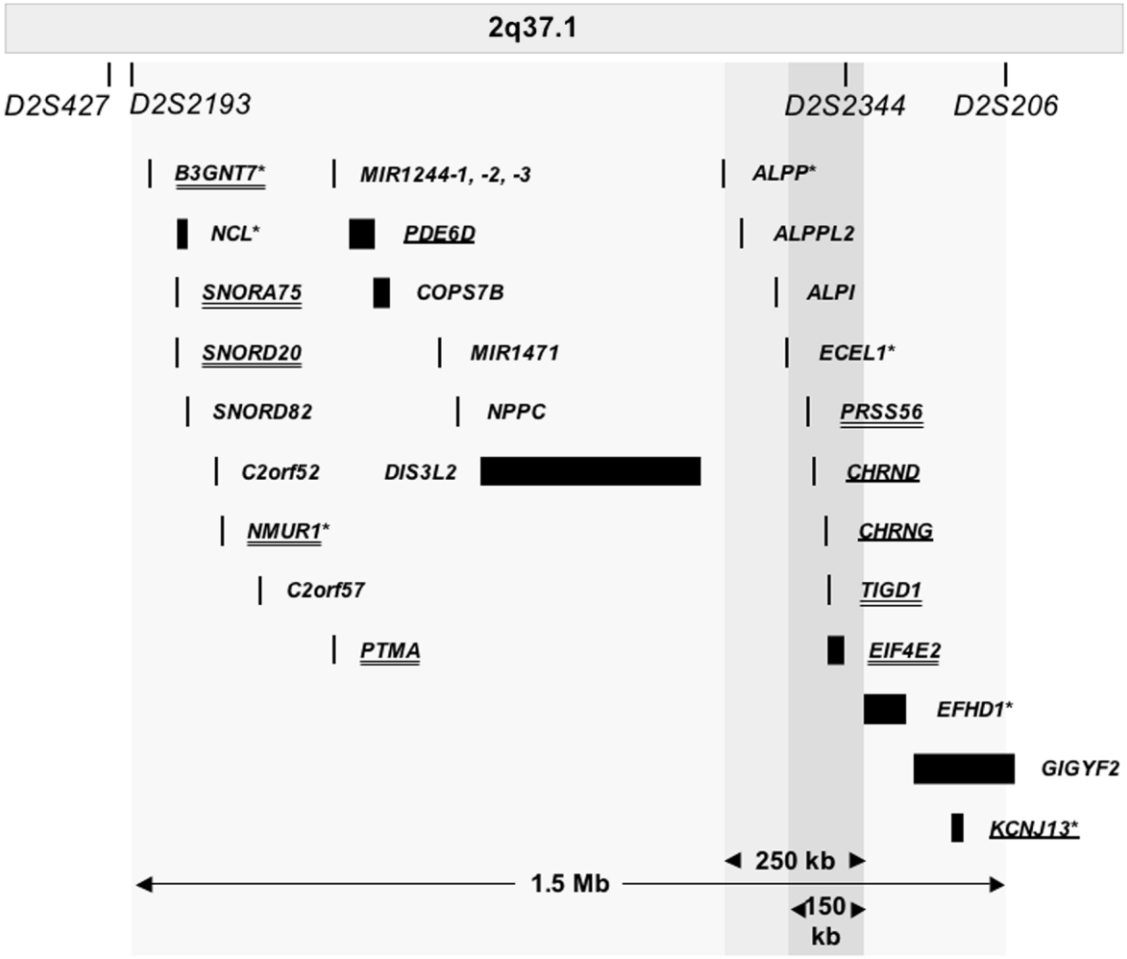

Figure S2. Physical Map and Relative Position of the Genes Mapped in the 1.5 Mb Genomic Region Defined to Harbour the *PRSS56* Gene by Linkage Analysis

Candidate genes excluded by missing co-segregation of SNP alleles with the disease phenotype are marked by asterisk. Genes sequenced in this study (double underlined) or by Hmani-Aifa et al.[2] (underlined) are also shown. For more details see text.