

Supplementary Tables

Table S1. Clinical data on 59 individuals with a *CACNA1F* mutation.

Individual #59 was excluded as this male had a *CABP4* mutation. BCVA = best corrected visual acuity, LogMar = Logarithm of Minimal angle of resolution, eq. sph.= equivalent sphere, D = diopters, P = light perception, -*High myopia prior to cataract operation, †Atypical course (severe retinal dystrophy), ‡ Progressive cone dystrophy, +/- = present/absent, nd = no data.

Table S2. Foveal Morphology in AED.

Cirrus and Spectralis grading of hypoplasia was masked. Agreement between modes for this subjective assessment was 100%. Also, in all cases where both eyes could be graded, there was symmetry. Y=yes, N=no, ND=no data, NA=image not analyzable

Table S3. Foveal Outer Segment Length in AED.

Mean \pm standard deviation outer segment length for CSNB2A was $41.65 \pm 4.99\mu\text{m}$, OD (n=48) and $42.07 \pm 5.65\mu\text{m}$, OS (n=48). For comparison, normal outer segment length is $46.04 \pm 4.34\mu\text{m}$. Normal data derived from Wilk et al.⁶ n=23 subjects; age (mean \pm standard deviation) = 30 ± 16 years; range 8-67 years. ND=no data, NA=image not analyzable. Subject #59 was not included in the calculation of the mean values.

Table S4. Subfoveal choroidal thickness in AED

Mean \pm standard deviation choroidal thickness for AED was $195.74 \pm 77.36\mu\text{m}$, OD (n=40) and $187.85 \pm 87.27\mu\text{m}$, OS (n=37). The values appear significantly below previously published normative data. ND=no data, NA=image not analyzable. Subject #59 was not included in the calculation of the mean values.

Table S5. *In silico* prediction of the pathogenicity of identified missense variants

^a SIFT (sift.jcvi.org/), the numbers in brackets are (score; median). ^b Polyphen2 (<http://genetics.bwh.harvard.edu/pph2/>), the number in brackets is the score using the HumVar model. AlignGVGD (<http://agvgd.iarc.fr/>), MutationTaster (<http://www.mutationtaster.org/>). ^c LuCAMP data are from exome sequencing of 2000 persons residing in Denmark (ref). ^d dbSNP is from version 142. ^e ESP is the Exome variant server (<http://evs.gs.washington.edu/EVS/>). ^f The class is based on an in house classification system based on mutation type, segregation data, population frequencies and functional studies.