Supplemental Figure 2: Deep-intronic variants in intron 30 and 36 of the *ABCA4* gene. The genomic positions (hg19) of benign variants are shown in green, the positions of variants with unknown significance are indicated in red. Splicing patterns of retinal transcripts containing alternative exons 30.1, 36.01 or 36.1 are shown by black boxes and lines (RNA sequencing data were taken from Farkas et al., 2013 and Brandl et al., 2015).