PRPH2 mutation update: *In silico* assessment of 245 reported and 7 novel variants in patients with retinal disease

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ABSTRACT

Mutations in *PRPH2*, encoding peripherin-2, are associated with the development of a wide variety of inherited retinal diseases (IRDs). To determine the causality of the many *PRPH2* variants that have been discovered over the last decades, we surveyed all published *PRPH2* variants up to July 2020, describing 720 index patients that in total carried 245 unique variants. In addition, we identified seven novel *PRPH2* variants in eight additional index patients. The pathogenicity of all variants was determined using the ACMG guidelines. With this, 107 variants were classified as pathogenic, 92 as likely pathogenic, one as benign, and two as likely benign. The remaining 50 variants were classified as variants of uncertain significance. Interestingly, of the in total 252 *PRPH2* variants, more than half (n=137) were missense variants. All variants were uploaded into the Leiden Open source Variation Database. Our study underscores the need of experimental assays for variants of unknown significance to improve pathogenicity classification, which is needed to better understand genotype-phenotype correlations, and in the long-term, hopefully also support the development of therapeutic strategies for patients with *PRPH2*-associated IRD.

1| INTRODUCTION

PRPH2, also known as retinal degeneration slow *(RDS)*, was first described in 1991 (Kajiwara et al., 1991). The gene encodes peripherin-2, a 346 amino-acid long glycoprotein that spans the membrane four times, and is located primarily in the rim regions of rod and cone outer segment (OS) discs and lamellae. Besides the four transmembrane domains, the protein contains a cytoplasmic (C) loop and two intra-discal (D1 and D2) loops (Travis, Brennan, Danielson, Kozak, & Sutcliffe, 1989; Travis et al., 1991; Travis, Groshan, Lloyd, & Bok, 1992). Its exact molecular function inside photoreceptor cells is not yet fully understood, but it is hypothesized that the protein plays an essential role in the initiation of OS disc formation, as well as in disc stabilization, maintenance, and disc size alignment, mainly by forming oligomers with other PRPH2 molecules and/or Retinal Outer Segment Membrane Protein 1 (ROM1) (Chakraborty et al., 2020; Zulliger, Conley, Mwoyosvi, Al-Ubaidi, & Naash, 2018). For instance*, Prph2*^{-/-} mice failed to initiate OS disc formation, whereas *Prph2* p.C150S^{+/-} mice did not support proper OS formation, interacted abnormally with Rom1, and showed reduced Prph2 protein levels (Zulliger et al., 2018). In addition, it was shown that in *Prph2* p.C213Y^{-/-} mice, mutant Prph2 could not oligomerize with ROM1 and was mislocalized, being retained in the inner segments (Chakraborty et al., 2020). Based on these studies, PRPH2 seems indeed to be critical for proper OS formation as well as for its function.

To date, over 200 different *PRPH2* variants have been described to be associated with the development of a wide variety of inherited retinal diseases (IRD) such as retinitis pigmentosa (RP), cone-rod dystrophy, and macular dystrophies. The group of *PRPH2*-associated macular dystrophies encompasses a wide variety of phenotypes, including pseudo-Stargardt pattern dystrophy, butterfly-shaped pigment dystrophy (BPD), adult-onset foveomacular vitelliform dystrophy (AOFVD), and central areolar choroidal dystrophy (CACD) (Boon et al., 2008; Boon et al., 2009; Boon, van Schooneveld, et al., 2007; Kersten et al., 2018). These macular dystrophy phenotypes, especially CACD, may be confused with geographic atrophy in age-related macular degeneration (AMD), and *PRPH2* mutations have been described in patients initially diagnosed with AMD (Boon et al., 2009; Kersten et al., 2018; Smailhodzic et al., 2011). *PRPH2* mutations are most frequently inherited in an autosomal dominant fashion, although autosomal recessive and sporadic cases have also been reported, as well as autosomal dominant cases with reduced penetrance (Alapati et al., 2014; Birtel et al., 2018; Boon et al., 2008; Boon et al., 2009; Coco, Tellería, Sanabria, Rodríguez-Rúa, & García, 2010; Dryja, Hahn, Kajiwara, & Berson, 1997; Khan, Al Rashaed, Neuhaus, Bergmann, & Bolz, 2016; Manes et al., 2015). Interestingly, heterozygous mutations in both *PRPH2* and *ROM1* can cause digenic RP (Kajiwara, Berson, & Dryja, 1994).

In this study, we performed a systematic analysis of all 245 *PRPH2* variants ever published in IRD patients. For this purpose, we collected all *PRPH2* variants published up to July 2020 that were associated with the development of IRD. In addition, we added *PRPH2* variants that were either identified via our routine diagnostics pipeline, or via a novel sequencing approach using molecular inversion probes (MIPs) (Hiatt, Pritchard, Salipante, O'Roak, & Shendure, 2013; Neveling et al., 2017; Weisschuh et al., 2018), seven of which have not been described before. All variants were classified for their pathogenicity using the American College of Medical Genetics and Genomics (ACMG) guidelines, after which they were uploaded into the Leiden Open source Variation Database (LOVD) for *PRPH2.* In addition, we attempted to establish genotype-phenotype correlations. There appears to be a high phenotypic variability between different families, as well as between members of the same family. For this reason, we discuss mechanisms by which this phenotypic variability might be explained.

By performing this study, we aim to shed light on how to experimentally assess the true causality of *PRPH2* variants in the future, as well as to explain the observed phenotypic variability within IRD patients. This will facilitate a better interpretation of the pathogenicity of variants that are identified in subjects with IRD, and in the long term, hopefully also support the development of therapeutic strategies for patients with *PRPH2*-associated IRD.

2| MATERIAL AND METHODS

2.1 Literature search

We collected all publications from up to July 2020 which report *PRPH2* variants in patients with inherited retinal disease. The following Pubmed search terms were used: *"(retinal+degeneration+slow+OR+PRPH2+OR+peripherin)+AND+*

(central+areolar+choroidal+dystrophy+OR+cacd+OR+vision+disorders+OR+retinal+dystrophy)+AND+(mutation+OR+variant+OR+mutations+OR+variants)". Additionally, the HGMD professional database was used to search for variants or articles that were possibly missed with our Pubmed queries. Variant detection, variant combinations, patient age, patient gender and age at onset, disease phenotype, segregation analysis, and allele frequencies (gnomAD) were collected. Obvious duplicates, in some cases following contact with the corresponding authors of the respective papers, were removed from the dataset.

2.2 Subjects

This study was approved by the institutional review boards of the Radboud University Medical Center (Radboudumc) and was conducted in adherence to the tenets of the

Declaration of Helsinki. All Sanger sequencing and/or whole (exome) sequencing data from the Radboudumc genome diagnostic laboratory were analysed in order to determine the causative genetic defects in patients with visual impairment. *PRPH2* variants were also identified by using a targeted sequencing approach based on molecular inversion probes (MIPs) (Hiatt et al., 2013; Neveling et al., 2017; Weisschuh et al., 2018). Single-molecule MIPs were synthesized to capture and sequence overlapping 110-nt segments of the three *PRPH2* protein-coding exons and flanking splice sites, similarly as described previously for the *ABCA4* gene (Khan et al., 2020). *PRPH2* variants identified with MIPs were validated with Sanger sequencing.

2.3 Variant Analysis

The cDNA was numbered as follows: the A of the ATG translation initiation codon of the *PRPH2* reference sequence (NM_000322) was reported as +1 while the initiation codon was reported as codon 1. Allele frequencies of *PRPH2* variants in control populations were extracted from the genome aggregation database (gnomAD: v2.1.1 and v3). This database contains both whole exome, and whole genome sequencing data obtained from 213,158 healthy individuals from all over the world (https://gnomad.broadinstitute.org/https://gnomad.broadinstitute.org/).

Next, we performed statistical analysis in order to compare allele frequencies in the index patient group to normal population (gnomAD). This enabled us to assess whether a specific variant is enriched in patient vs. control groups. For this purpose, the Fisher's Exact test was used. In order to only select true statistical significant findings, a correction by the false discovery rate (FDR) of Benjamini-Hochberg, classical one stage method with an error margin of 5%, was carried out (Benjamini, Drai, Elmer, Kafkafi, & Golani, 2001).

2.4 *In silico* predictions

For *PRPH2* missense variants, Polyphen-2 scores, Combined Annotation Dependent Depletion (CADD), and SIFT scores were obtained from http://genetics.bwh.harvard.edu/pph2/, http://cadd.gs.washington.edu/home (Kircher et al., 2014) and https://sift.bii.a-star.edu.sg/, respectively. For splice site variants, software to gather splicing scores available via Alamut Visual version 2.13 (Interactive Biosoftware, Rouen, France) was used.

2.5 Variant pathogenicity classification

Pathogenicity of all reported and newly identified *PRPH2* variants was predicted using the ACMG guidelines (Richards et al., 2015). These guidelines enabled us to classify each variant into one of the following categories: pathogenic, likely pathogenic, benign, likely

benign, or of uncertain significance. In order to do so, we scored the variants based on the evidence of pathogenicity in different ACMG categories:

1. Pathogenic, very strong (PVS), for example, this variant is protein truncating.
2. Pathogenic, strong (PS), for example, this variant leads to the same amino acid being substituted compared to a previously described pathogenic variant.
3. Pathogenic, moderate (PM), for example, this variant is located in a mutational hot spot and/or well-established functional domain.
4. Pathogenic, supporting (PP), for example, multiple lines of computational evidence support the variant to be pathogenic.

The scores of each category are combined to come to the final classification in one of the five pathogenicity categories that are explained in more detail in Suppl. Table 1.

2.6 LOVD submission

The 245 reported, as well as the seven novel *PRPH2* variants were uploaded to the LOVD database, when available, together with patient data including the description of the phenotype, patient age, patient age of onset, and segregation information. Pathogenicity scores of all variants were based on the pathogenicity assessment as described in the "*In silico* predictions" section.

3| *PRPH2* VARIANTS

3.1 *PRPH2* mutation spectrum

We collected 245 *PRPH2* variants identified in 720 index patients that were described in 165 articles up to July 2020, as well as their phenotypic information (Abouelhoda, Faquih, El-Kalioby, & Alkuraya, 2016; Abu-Safieh et al., 2013; Ahmad, Ayyagari, & Zacks, 2010; Alapati et al., 2014; Anand et al., 2009; Anasagasti et al., 2013; Apfelstedt-Sylla et al., 1995; Arai et al., 2015; Avela et al., 2019; Avela et al., 2018; Ba-Abbad, Robson, MacPhee, Webster, & Michaelides, 2019; Ba-Abbad et al., 2014; Barbazetto et al., 2007; Bareil et al., 2000; Bareil, Hamel, Arnaud, Demaille, & Claustres, 1997; Bayés et al., 1996; Birtel et al., 2018; Boon et al., 2009; Boon, Klevering, et al., 2007; Boon, van Schooneveld, et al., 2007; Boulanger-Scemama et al., 2015; Budu et al., 2001; Carss et al., 2017; Cheng et al., 2019; Coco-Martin, Sanchez-Tocino, Desco, Usategui-Martín, & Tellería, 2020; Coco et al., 2010; Consugar et al., 2015; Coussa et al., 2015; Daftarian et al., 2019; de Breuk et al., 2020; de Sousa Dias et al., 2015; Donoso et al., 2003; Downes et al., 1999; Downs et al., 2007; Dryja et al., 1997; Duncan et al., 2011; Duncker et al., 2015; Ekström, Andréasson, et al., 1998; Ekström, Ponjavic, Abrahamson, et al., 1998; Ekström, Ponjavic, Andréasson, et al., 1998;

Essilfie, Sanfilippo, & Sarraf, 2018; Fakin, Zupan, Glavač, & Hawlina, 2012; Farrar et al., 1992; Farrar et al., 1991; Feist, White, Skalka, & Stone, 1994; Felbor, Schilling, & Weber, 1997; Fernandez-San Jose et al., 2015; Fishman et al., 1994; Fishman et al., 1997; Foote et al., 2019; Francis et al., 2005; Gamundi et al., 2007; Gao et al., 2019; Glöckle et al., 2014; Gocho et al., 2016; Gorin et al., 1995; Grover, Fishman, & Stone, 2002; Grüning et al., 1994; Hanany & Sharon, 2019; Hosono et al., 2018; Hoyng et al., 1996; Huang et al., 2013; Jacobson et al., 1996; Jacobson et al., 2016; Jespersgaard et al., 2019; Jin et al., 2008; Jones et al., 2017; Kajiwara et al., 1994; Kajiwara et al., 1991; Kajiwara, Sandberg, Berson, & Dryja, 1993; Kalyanasundaram, Black, O'Sullivan, & Bishop, 2009; Katagiri et al., 2018; Keen, Inglehearn, Kim, Bird, & Bhattacharya, 1994; Keilhauer, Meigen, Stöhr, & Weber, 2006; Keilhauer, Meigen, & Weber, 2006; Kemp et al., 1994; Kersten et al., 2018; Khan, 2019; Khan et al., 2016; Khoubian et al., 2005; Kikawa, Nakazawa, Chida, Shiono, & Tamai, 1994; Kim et al., 2012; Kim et al., 1995; Kitiratschky, Glöckner, & Kohl, 2011; Klevering et al., 2002; Kohl et al., 1997; Kohl et al., 2012; Lam, Vandenburgh, Sheffield, & Stone, 1995; Lee & Leys, 2020; Lee et al., 2015; Leroy, Kailasanathan, De Laey, Black, & Manson, 2007; Lim et al., 2009; Maertz, Gloeckle, Nentwich, & Rudolph, 2015; Manes et al., 2015; Martin-Merida et al., 2018; Meins et al., 1993; Meunier et al., 2011; Michaelides, Holder, Bradshaw, Hunt, & Moore, 2005; Miyata et al., 2018; Moshfeghi et al., 2006; Nakazawa et al., 1994; Nakazawa et al., 1996; Nakazawa, Wada, & Tamai, 1995; Nanda, McClements, Clouston, Shanks, & MacLaren, 2019; Neveling et al., 2012; Nichols, Drack, et al., 1993; Nichols, Sheffield, et al., 1993; Oishi et al., 2014; Pajic et al., 2006; Palma et al., 2019; Passerini, Sodi, Giambene, Menchini, & Torricelli, 2007; Patel et al., 2016; Payne, Downes, Bessant, Bird, & Bhattacharya, 1998; Poloschek et al., 2010; "Prevalence and architecture of de novo mutations in developmental disorders," 2017; Ramkumar et al., 2017; Reeves et al., 2020; Reig et al., 1995; Renner et al., 2009; Renner et al., 2004; Richards & Creel, 1995; Saga et al., 1993; Sallevelt et al., 2017; Schatz, Abrahamson, Eksandh, Ponjavic, & Andréasson, 2003; Schorderet, Bernasconi, Tiab, Favez, & Escher, 2014; Sears, Aaberg, Daiger, & Moshfeghi, 2001; Shankar et al., 2015; Shankar et al., 2016; Simonelli et al., 2007; Smailhodzic et al., 2011; Sohocki et al., 2001; Souied et al., 1998; Stone et al., 2017; Strafella et al., 2019; Strom et al., 2012; Sullivan et al., 2006; Sullivan et al., 2013; Sun et al., 2015; Testa et al., 2005; Trujillo et al., 1998; Trujillo et al., 2001; Trujillo Tiebas, Giménez Pardo, García Sandoval, & Ayuso García, 2002; Vaclavik, Tran, Gaillard, Schorderet, & Munier, 2012; Van Cauwenbergh et al., 2017; van Lith-Verhoeven et al., 2003; Wang et al., 2015; Wang et al., 2014; Wang et al., 2013; Wawrocka et al., 2018; Weleber, Carr, Murphey, Sheffield, & Stone, 1993; Wells et al., 1993; Wolock et al., 2019; Wroblewski et al., 1994a; Wroblewski et al., 1994b; Xiang, Yan, Song, & Zheng, 2012; Xu et al., 2014; Xue, Zhang, Wang, Liu, & Xu, 2014; Yanagihashi et al., 2003; Yang et al., 2000; Yang et al., 2004; Yang

et al., 2003; Yeoh et al., 2010; Yoon et al., 2015; Zaneveld et al., 2015; Zhang, Garibaldi, Li, Green, & Zack, 2002; Zhao et al., 2015; Zhou, Xiao, Li, Jia, & Zhang, 2018; Zhuk & Edwards, 2006). Additionally, 139 index cases from either the Radboudumc genome diagnostic laboratory or that were studied via MIPs analysis, carried *PRPH2* variants that were published before (Table 1). Finally, we also identified seven novel variants in eight additional index patients that, to our knowledge, were never identified (Table 1; variants depicted in bold lettering). Of the collective 252 *PRPH2* variants, 137 were missense, 85 were protein-truncating, 10 were splice site, 15 were in-frame amino acid changes, three were synonymous, and two were located in the 5' or 3' untranslated regions (UTRs) (Suppl. Figure 1A; Table 2). Of the in total 720 previously reported index patients, 686 patients carried heterozygous variants, 8 patients carried compound heterozygous variants, 14 patients carried homozygous variants, and 11 patients carried digenic variants. There was one patient that carried variants in three different genes (*PRPH2*, *ROM1*, *ABCA4*). The authors speculated trigenic inheritance, however it still needs to be elucidated to determine whether this case is truly trigenic. Of the 139 index cases identified by the Radboudumc genome diagnostic laboratory or our MIPs analysis, two patients carried homozygous variants while the remaining 137 index cases were all heterozygous carriers. Finally, the eight index patients carrying the seven novel *PRPH2* variants, were all heterozygous for the respective variants. All variants, together with a description of the phenotype and, when available, segregation analysis, were uploaded to the LOVD database (https://databases.lovd.nl/shared/genes/PRPH2).

3.2 Recurrent *PRPH2* variants

The most recurrent *PRPH2* variant amongst IRD patients, is p.R142W. This variant was reported in 95 out of 867 index patients, of which 93 were heterozygous carriers, and two were homozygous (Suppl. Table S2). The variant was exclusively reported in individuals with Caucasian ancestry, and in the Netherlands, this variant is mainly associated with the development of CACD. Analysis of single nucleotide polymorphisms (SNPs) in close proximity of the p.R142W variant in three Dutch families revealed the presence of a shared chromosomal segment of approximately 519 kb, strongly suggesting that this particular variant represents a founder mutation in the Netherlands (Boon et al., 2009). As mentioned in the introduction section, CACD may be confused with AMD, and besides retinal imaging modalities (optical coherence tomography and fundus autofluorescence), screening for the p.R142W may help to better discriminate between these two phenotypes (Kersten et al., 2018; Smailhodzic et al., 2011). One interesting observation in large Dutch CACD families harbouring this variant, is that there seems to be reduced penetrance (Boon et al., 2009). Within these families, some individuals were significantly less severely affected compared to

age-matched family members also carrying the variant. The molecular mechanisms behind this phenomenon still need to be elucidated. Possible explanations could be: (1) reduced expression of the mutant allele; (2) increased expression of the wild-type allele; (3) the influence of modifier alleles located in other genes; or (4) influence of environmental factors (e.g. smoking, nutrition).

Other recurrently reported variants (reported in >10 index patients) are p.R46*, p.Y141C, p.G148Afs*5, p.R172W, p.R172Q, p.L185P, p.R195L, p.G208D, p.P210R, p.P216S, p.P216L, p.Q239*, p.S289L, and c.828+3A>T. The p.R172W variant was reported in 60 index patients, and was mainly found in Caucasians with British ancestry. There was only one Japanese index patient carrying this variant. Of the in total 60 cases, 58 were heterozygous for this variant (Suppl. Table S2). Payne and colleagues performed haplotype analysis in multiple British families carrying the stand-alone p.R172W variant, and revealed that in Britain, this is a founder mutation (Payne et al., 1998). A German index patient carried an additional pathogenic heterozygous *ROM1* missense variant (p.R229H), and another patient carried two additional heterozygous missense variants, one in *ROM1* (p.R229H) and one in *ABCA4* (p.V2050L) (Suppl. Table S2) (Poloschek et al., 2010). The authors argued that the *ROM1* and *ABCA4* variants act as a moderator, worsening the pattern dystrophy phenotype compared to individuals that only carry the p.R172W variant in *PRPH2*. However, when applying the ACMG criteria to both the *ROM1* and *ABCA4* variants, the p.V2050L variant in *ABCA4* was classified as likely benign, which makes it unlikely to be a modifier that worsens the phenotype.

The splice site variant c.828+3A>T was recurrently found in 57 index patients. This variant is predicted to result in aberrant splicing of the *PRPH2* mRNA, and consequently in the formation of a non-functional truncated protein (Shankar et al., 2015; Shankar et al., 2016). The remaining 237 variants were reported in only a single or a few index patients, which clearly demonstrates the enormous allelic heterogeneity among patients with *PRPH2*-associated IRD.

4| PATHOGENICITY ASSESSMENT OF ALL *PRPH2* VARIANTS

The pathogenicity of all *PRPH2* variants was assessed using the ACMG classification system, as described in the Materials and Methods section. According to our analysis, 107 variants were classified as pathogenic, 92 as likely pathogenic, one as benign, and two as likely benign (Suppl. Figure S1B). The remaining 50 variants were classified as variants of uncertain significance. Of the collective 199 (likely) pathogenic variants, 93 were missense,

85 were protein-truncating, 8 were splice-site, and 13 were in-frame amino acid insertions/deletions (Figure 1A; Suppl. Table S2).

4.1 Missense variants

The vast majority of *PRPH2* variants reported in IRD patients represents missense variants. In total, 137 missense variants have been reported, corresponding to 605 alleles (Supp. Figure S1B; Table 2). Prior to assessing the pathogenicity of these variants, *in silico* predictions were performed using PolyPhen2, SIFT, and CADD. To consider a variant as pathogenic (supporting evidence; PP3), all three *in silico* prediction programmes should predict a damaging effect (Polyphen2; >1.5, SIFT; <0,05, CADD >15). When combining all information for the final ACMG pathogenicity assessment, of the 137 missense variants, 93 were classified as pathogenic/likely pathogenic (Figure 1B; Table 3; Suppl. Table S2). One variant was classified as likely benign. The remaining 43 were considered as variants of uncertain significance, mainly due to lack of family history and segregation analysis, or because the variant did not co-segregate with disease.

Next, we compared the position of (likely) pathogenic *PRPH2* missense variants relative to the protein structure of PRPH2, to identify regions that may be more prone to harbour disease-causing variants (Figure 1C). This analysis demonstrated that most missense variants (83 out of 93; Table 3; Figure 1C), are located within the D2 loop of the protein. It is hypothesized that the D2 loop is important for complex assembly with ROM1 and/or dimerization with other PRPH2 molecules, in order to both initiate and stabilize OS disc formation (Chakraborty, Conley, Zulliger, & Naash, 2016; Chakraborty, Ding, Conley, Fliesler, & Naash, 2009; Goldberg, Loewen, & Molday, 1998). Furthermore, the D2 loop contains numerous highly conserved cysteine residues (C165, C166, C213, C214, C222, C250) that form disulphide bonds in order to maintain the structure of the loop, and to regulate photoreceptor folding (Goldberg et al., 1998). For this reason, variants affecting amino acid residues within this loop will likely disrupt the structure or function of this loop, in turn interfering with PRPH2-PRPH2 and/or PRPH2-ROM1 interactions. Therefore, moderate evidence (PM1) was assigned if a variant was predicted to change the amino acid within this loop. Moderate evidence (PM1) was also assigned when missense variants were located in the one of the transmembrane domains, or in the C-terminus (Boon et al., 2008; Salinas, Baker, Gospe, & Arshavsky, 2013).

For most of the missense variants, patient ethnicity was not always mentioned in the studied papers, which made it difficult to determine whether some variants might be specific for patients of a particular ancestry. Papers that did mention the ethnicity showed that most variants were reported in patients from Caucasian or Asian ancestry. Some variants seem to be specific for a certain ethnicity; for instance, the p.C250G variant was exclusively reported

in patients with Asian ancestry, whereas p.R142W and p.R172Q were only identified in patients with Caucasian ancestry. The p.R172W variant was almost exclusively reported in Caucasians, but also reported once in a Japanese family (Nakazawa et al., 1995).

4.2 Protein-truncating variants

In total, 180 out of 891 *PRPH2* alleles (20.2%) can be considered as protein-truncating, represented by 85 unique variants (Table 2). Of these, 55 were frameshift, 27 were nonsense, two were fail-to-start, and one was a deletion of exon 1. Most of these variants are considered rare, and only four of them were present in the gnomAD database. We classified a protein-truncating variant as damaging if the variant induces a premature stop codon before amino acid 331, since the p.Q331* variant was reported to be pathogenic (Grover et al., 2002). Moreover, it was determined that the valine residue at position 332 is critical for targeting PRPH2 towards the OS of photoreceptor cells (Salinas et al., 2013). Based on this knowledge, we classified all protein-truncating variants as pathogenic or likely pathogenic. One aspect to take into account is that the annotations of p.Y140ins (1bp), p.S217_dup16bp, and p.224ins (37bp), as described in the original articles, are not correct. We used Alamut to check whether we were able to identify the correct cDNA annotation, but this could not be deduced. For this reason, we kept the protein annotation used in the corresponding articles and put a question mark for the cDNA change annotation, although each is categorized as protein-truncating variant. These variants are indicated in red in Suppl. Table S2.

4.3 Splice variants

Variants that were known to affect the canonical di-nucleotides of the splice acceptor (AG) or splice donor (GT) site were assigned to be pathogenic (PVS1). For all non-canonical splice site variants, four different splice prediction tools in Alamut were used to predict pathogenicity. A variant was classified as pathogenic when an increase or decrease of >10% in splice scores was observed for all four programmes, as described previously (Messchaert, Haer-Wigman, Khan, Cremers, & Collin, 2018). Based on this, together with the ACMG classification, almost all splice variants were classified as (likely) pathogenic (Suppl. Table S2). There were two exceptions, namely c.581+4dupA and c.829-4C>G. For these variants, there was not enough robust evidence for their pathogenicity, and these were thus classified as variants of uncertain significance (Suppl. Table S2).

4.4 In-frame amino acid insertions/deletions

Of the 15 in-frame insertions/deletions, 13 were classified as pathogenic or likely pathogenic. All in-frame amino acid insertions/deletions were assigned with PM4, indicating they might affect normal protein length and function. In addition, none of these variants were present in

gnomAD indicating that these variants in fact might be disease-causing (Suppl. Table S2). Two variants, namely p.M67del and p.M67_G68delinsRHR, were classified as variants of uncertain significance.

4.5 Synonymous variants

Three synonymous variants were reported, namely p.Y101Y (c.303T>C), p.Y236Y (c.708T>C), and p.E335E (c.1005G>A). These variants were exclusively found in patients with macular dystrophy or pattern dystrophy. All variants were first classified as likely benign, due to the fact that *in silico* prediction programmes defined them as benign/tolerated. Moreover, no evidence for putative splice defects were predicted. However, the p.Y101Y (c.303T>C) and p.E335E (c.1005G>A) variants were not reported in the gnomAD database, indicating they are not commonly found in control individuals (Suppl. Table S2). For this reason, we classified these variants to be of uncertain significance. The p.Y236Y (c.708T>C) variant was reported in gnomAD, and statistical analysis showed that the variant was significantly enriched in the healthy control group when comparing to index patients. Therefore, this variant was classified as likely benign (Suppl. Table S2).

4.6 Digenic and trigenic variants

In section 3.2, it was shown that in a large German family segregating pattern dystrophy, p.R172W was present in patients that also carried a *ROM1* (p.R229H) and/or an *ABCA4* (p.V2050L) variant (Poloschek et al., 2010). When looking to the severity of each individual's phenotype, it appeared that patients carrying an additional *ROM1* (digenic carriers) variant were more severely affected compared to patients that only carried the *PRPH2* p.R172W variant. The phenotype was even more severe in patients carrying *PRPH2, ROM1* and *ABCA4* variants (trigenic carriers). The authors hypothesized that the additional *ROM1* and *ABCA4* variants function as genetic modifiers that worsen the pattern dystrophy phenotype. However, the p.V2050L variant in *ABCA4* was classified as likely benign, which makes it unlikely to be a modifier worsening the disease phenotype.

The p.L185P variant in *PRPH2* was also reported together with *ROM1* variants (p.G80G, p.G113E or p.L114L) in four large digenic RP families (Dryja et al., 1997; Kajiwara et al., 1994). In these families, individuals only carrying the p.L185P variant seemed to remain unaffected by disease, while individuals that also carried one of the *ROM1* variants showed clear phenotypic characteristics of RP. The p.L270del variant in *PRPH2* was found in combination with the p.M318Afs*17 variant in *ROM1* in another digenic RP patient (Dryja et al., 1997). Recently, *PRPH2* p.R46* in combination with the complex p.[(L2027F);(G1977S)] *ABCA4* variant, was identified in a patient with cone-rod dystrophy (Coco-Martin et al., 2020). Finally, the same group also reported a patient with pattern dystrophy carrying both

p.K154del in *PRPH2* and p.R2030Q in *ABCA4* (Coco-Martin et al., 2020). These findings indicate that besides digenic RP, cone-rod and pattern dystrophy also might be caused by digenic variants. However, mutations in IRD associated genes are relatively frequent. Nishiguchi and Rivolta screened high-quality genome sequences of control individuals from various ancestries, and estimated that ~one in 4–5 individuals from the general population carry variants that are associated with IRD (Nishiguchi & Rivolta, 2012). Furthermore, Hanany and colleagues created a database containing 276921 sequence variants that were identified in 187 autosomal recessive IRD genes, and found that 2.7 billion people worldwide (36% of the population) are being healthy carriers of at least one IRD variant (Hanany, Rivolta, & Sharon, 2020). Thus, patients may carry variants in multiple IRD genes without any clinical consequences. For this reason, caution is warranted, and studies of large cohorts are required to determine if the disease in a patient is truly inherited in a di-or trigenic fashion.

4.7 Reclassified variants

The evaluation of the pathogenicity for some variants resulted in a different outcome when compared to the original publication. This is partly due to the fact that more specific variant classification tools have become available. For example, the p.Y101Y (c.303T>C) and p.E335E (c.1005G>A) variants were previously classified to be benign by (Dryja et al., 1997), mainly since they do not change the amino acid sequence, and thus are predicted not to have a deleterious effects on the final protein. However, we have classified these variants as being of uncertain significance since they were not present in normal controls reported in gnomAD, and thus in fact may be disease-causing. Experimental assays are needed to truly determine the potential causality of these variants. Another example is the c.-11A>C variant, which is located in the 5' UTR region. This variant was classified as likely pathogenic because the it was not present in single nucleotide polymorphism databases, and was not found in 92 controls (Boon et al., 2007). However, we have classified the variant as benign, since when comparing the allele frequency in gnomAD to the allele frequency in the reported index patients, the variant was found to be enriched in the control population (gnomAD).

There were also some variants that were considered being of uncertain significance in initial publications, but were classified as (likely) pathogenic following our classification. For instance, the p.G167S variant was initially classified as being of uncertain significance (Meunier et al., 2011; Strom et al., 2012), but we classified the variant as pathogenic since it was located in the D2 loop (mutational hotspot; PM1), was absent in controls (gnomAD; PM2), was predicted to be damaging by all three *in silico* prediction programmes (PP3; Suppl. Table S2), and co-segregated with disease (PP1). Another mis-classified variant was p.G68R, originally considered to be of uncertain significance (Dryja et al., 1997), found in

patients that were suspected to have digenic RP. However, analysis of the segregation of *ROM1* alleles was uninformative. For this reason, the authors could not determine whether the p.G68R defect is pathogenic or that it represents a rare benign variant. Upon our pathogenicity classification, the variant was classified as likely pathogenic since it was significantly enriched in the patient population compared to controls (gnomAD; PS4), was located in the first TMD (PM1), and was predicted to be damaging by all three *in silico* prediction programmes (PP3; Suppl. Table S2). These findings demonstrate that pathogenicity classification tools have improved, enabling reclassification of certain variants that were reported many years ago.

5| GENOTYPE-PHENOTYPE CORRELATIONS

In order to define genotype-phenotype correlations, we collected information about disease phenotype, age at onset, and, when available, segregation data. However, most of the *PRPH2* variants show high phenotypic variability, both between different families and within the same family, which made it difficult to draw proper and well-defined conclusions regarding the relationship between *PRPH2* variants and disease phenotype. For instance, in an Italian family, the p.C165R variant resulted in clinically different phenotypes (fundus flavimaculatus or butterfly shaped pattern dystrophy) within the same family (Simonelli et al., 2007). The mechanism behind this intrafamilial phenotypic variability remains to be elucidated but the authors suggested the following explanation; since PRPH2 interacts with other adhesion proteins, the inheritance of genes encoding such proteins may - to some extent - explain the enormous phenotypic variability observed within families. A family described by Daftarian et al. carries both the p.Q239* and the p.I32V variant (Daftarian et al., 2019). The proband carried both variants in a homozygous state, indicating that these two variants are on the same allele, which resulted in the more severe phenotype Leber congenital amaurosis (LCA). Family members carrying the variants in a heterozygous state, developed much milder phenotypes with a later age of onset. The authors concluded that homozygous variants result in more severe phenotypes compared to heterozygous *PRPH2* variants. A family with even higher phenotypic variability is a large Dutch family (family E) described by Boon et al. Here, similarly-aged family members showed phenotypes ranging from retinitis pigmentosa, pseudo-Stargardt pattern dystrophy, to only mild foveal pigmentary changes, despite carrying the same frameshift mutation (p.G148Afs*5) (Boon, van Schooneveld, et al., 2007). The broad spectrum of phenotypical variability associated with *PRPH2* variants is further highlighted by a reduction in penetrance described in several papers. For example, Michaelides et al. described a five-generation family in which two individuals carrying the p.R172W mutation, a mother (49 years old) and her daughter (24 years old), had an entirely normal phenotype upon detailed testing (Michaelides et al., 2005). As previously mentioned, Boon et al. also described a normal phenotype in patients carrying

the p.R142W mutation, even up until the age of 64 years (Boon et al., 2009), illustrating the reduced penetrance for (at least some) *PRPH2* mutations. Another point to address is that we did not observe obvious indications that individuals with protein-truncating variants had a more severe phenotype than, for instance, individuals carrying missense variants or in-frame amino acid insertions/deletions. Finally, when looking at the location of likely pathogenic *PRPH2* variants, it was striking that variants associated with RP were almost exclusively found in the D2 loop (Figure 1C), suggesting that amino acid changes inside this loop may exert a pathophysiological mechanism that more often leads to RP, and not to any of the other phenotypes associated with PRPH2 variants. Taken together, additional genetic data from IRD patients would be of great help in order to determine genotype-phenotype correlations and to study the often observed intra- and inter-familiar phenotypic variability.

6| DISCUSSION

6.1 Improvement of *in silico* analysis
Before classifying the pathogenicity of *PRPH2* missense variants according to ACMG, *in silico* predictions were performed using Polyphen-2, SIFT, and CADD. Polyphen2 is a software programme and is accessible via a Web server. The programme predicts the possible effects of non-synonymous single nucleotide variants (SNVs) on the stability and function of human proteins. It uses both structural and comparative evolutionary considerations. These properties are then combined in order to estimate the probability of a particular missense variant being damaging to the protein of interest (Adzhubei, Jordan, & Sunyaev, 2013). SIFT uses datasets of functionally related protein sequences that are obtained via a protein database. The algorithm scans each position in the sequence of interest, after which the probabilities for all possible 20 amino acids at that position is calculated, resulting in one final SIFT score (Kumar, Henikoff, & Ng, 2009). The CADD *in silico* prediction software is also available via a webserver. The programme integrates multiple lineages of data including genomic features within the surrounding sequence of interest, gene model annotations, evolutionary data from multiple species, epigenetic measurements, as well as functional predictions. In contrast to many other *in silico* prediction programmes, CADD is not limited to the number of genomic variants of which either a pathogenic or benign status is already known (Rentzsch, Witten, Cooper, Shendure, & Kircher, 2019). Instead, CADD bases its score on less biased and much larger data sets, and thus might have an advantage over Polyphen2 and SIFT.

Some missense variants, including p.A2S, p.K15R, p.R123W, p.S125L, p.E127G, p.R142Q, p.R172Q, p.D186N, p.D194E, p.I196F, p.P216L, p.A252P, p.W316G, and p.A337T, gave

contradictory outcomes upon *in silico* pathogenicity predictions. Whilst different algorithms may rely on the same type of data to predict pathogenicity, it is known that for some genes, similar algorithms can have a significantly different outcome (Richards et al., 2015). Only when all of the *in silico* programs used give the same prediction output, the evidence can be counted as supporting (PP3) (Richards et al., 2015). Based on this, the *in silico* predictions for the aforementioned variants were not considered to be of supporting evidence (PP3). It would therefore be very helpful if there were more experimental data available that could show whether these variants have a deleterious effect on normal protein morphology and/or function. This will be explained in more detail in the next section.

6.2 Experimental assessment of variants of unknown significance

Approximately one-third of the missense variants were classified as variants of unknown significance (Figure 1B). This was due to the fact that these variants did not robustly meet important ACMG pathogenicity criteria. Furthermore, two splice-site, two in-frame amino acid insertions/deletions, two synonymous variants, and one 3' UTR variant also needed to be classified as variants of uncertain significance for the same reasons as for the missense variants. Experimental models would be of great help to classify such variants. However, experimental data are extremely limited. This is mainly due to the fact that *PRPH2* expression is highly retina-specific. This makes it difficult to use widely used immortalized lymphoblastoid, skin fibroblast, or blood cell lines. However, depending on the type and location of each variant, this issue may be circumvented. For instance, when studying missense variants, one could clone the coding region of *PRPH2* (~1.1 kb) into specific expression vectors to create a *PRPH2* wildtype vector. Next, site-directed mutagenesis can be applied to insert the desired mutation. Wildtype and mutant vectors can be transfected into widely-used cell lines to study, for example, expression patterns (western blots) or interacting proteins (yeast-two-hybrid, co-immunoprecipitation), and compare mutant and wild-type conditions. These vectors can even be administered to neonatal mice in order to study *in vivo* localization of wild type or mutant PRPH2. Chakraborty and colleagues created vectors containing wild-type *PRPH2* or the *PRPH2* p.C213Y variant, and electroporated these into neonatal mice. Four weeks after injection, retinas were collected and it was seen that the p.C213Y construct mislocalized to the inner segments and perinuclear region (Chakraborty et al., 2020). Another research group showed that constructs containing the p.P210L and p.C214S missense variants mislocalized to the inner segments upon administration to wildtype mice (Becirovic et al., 2016). Interestingly, results differed between rods and cones, indicating that PRPH2 might have a different function in the two different photoreceptor cell types.

Secondly, when one wants to study splice site variants, midi- or minigene splice assays can be used as described previously (Sangermano et al., 2018). Mini- or midigenes represent

plasmids in which the desired *PRPH2* splice site variant can be cloned between two exons of interest. The plasmids are transfected into e.g. HEK293T cells, and splice effects can be analysed using RT-PCR in order to determine whether there are differences between RNAs transcribed from wild-type and mutant minigenes. Becirovic and colleagues constructed *PRPH2* wild-type minigenes as well as minigenes containing the IRD-associated p.R195L, p.S198R, p.V209I, p.P210L, p.S212T, p.C214S, p.R220W, p.R220Q, p.W246R, and p.G249S missense variants (Becirovic et al., 2016). RT-PCR analysis of *PRPH2* transcripts in murine retinas transduced with the wild-type or the mutant *PRPH2* minigene, identified three different *PRPH2* splice isoforms in rods and cones. These splice isoforms consisted of the unspliced transcript, a transcript in which intron 1 was retained, and the correctly spliced *PRPH2*. The p.G249S variant created a new splice donor site, resulting in aberrant splicing of the protein. This suggests that also point mutations in coding regions might affect splicing (Becirovic et al., 2016).

Finally, for studying all types of variants, one could ideally make use of induced pluripotent stem cell (iPSC) technology. In short, somatic cells are extracted from *PRPH2*-associated IRD patients or from healthy controls, which can then be reprogrammed towards iPSCs. Next these iPSCs can be differentiated towards retina-like cells thus carrying the variant of interest (Giacalone et al., 2016; Öner, 2018), after which a variety of functional studies can be performed, including expression (western blot), localization (immunohistochemistry), and morphological (microscopy) studies. A drawback of this approach is that it is very labour- and time-consuming, as well as expensive.

Taken together, these experimental studies are crucial to improve the classification of *PRPH2* variants in order to will aid in the molecular diagnostics of IRDs.

6.3 Development of therapeutic strategies for *PRPH2*-associated IRD

A proper classification of possible disease-causing variants is of great importance, not only to determine the true causal genetic defect in IRD patients, but also for developing therapeutic strategies. *PRPH2* has been a target for gene therapy for over two decades now, mainly due to the disease burden associated with variants in this gene, as well as the availability of several extremely well-characterized animal models mimicking important phenotypic characteristics of patient with *PRPH2*-associated IRD (Conley & Naash, 2014). Currently, at least three therapeutic strategies can be distinguished: (1) gene replacement therapy; (2) gene knock-down therapy; and (3) delivery of neurotrophic factors. To develop such therapeutic strategies, it is important to not only know the genetic defect but also the underlying pathophysiological mechanism (e.g. dominant-negative vs. haploinsufficiency).

6.3.1 Gene replacement therapy

The first proof-of-principle studies regarding gene replacement therapy attempted to correct IRD phenotypes in *Prph2$^{-/-}$* and *Prph2$^{+/-}$* mice. For this purpose, a wild-type *Prph2* transgene was delivered, and the results were highly promising since in *Prph2$^{-/-}$* mice, the structure of the OS of rod photoreceptor cells was preserved (Travis et al., 1992). Furthermore, in *Prph2$^{+/-}$* mice, the expression of a wildtype *Prph2* transgene rescued rod and cone OS structure and function (Nour, Ding, Stricker, Fliesler, & Naash, 2004). In mice harbouring the recurrent p.R172W variant - that is considered a dominant-negative variant -, expression of wildtype PRPH2 also caused structural and functional improvements (Conley, Nour, Fliesler, & Naash, 2007; Nour, Fliesler, & Naash, 2008).

6.3.2 Gene knock-down therapy

As some mutations in *PRPH2*-associated IRD are believed to act in a dominant-negative manner, such as p.R172W (Conley et al., 2007), and the fact that gene replacement did not completely correct the dominant phenotype in mice carrying this specific variant, alternative approaches are needed in order to eliminate the mutant allele. One such approach is the gene-knockdown approach. For *PRPH2*, the usage of shRNA to knock-down the mutant allele, seems to be the most promising. For example, an shRNAs that was shown to knock-down *Prph2 in vitro*, was packaged into an rAAV vector. Upon injection into the subretinal space of wildtype mice, wildtype Prph2 levels were reduced by 75% (Petrs-Silva et al., 2012). Next, they created a vector containing wild-type *Prph2* that was proven to be resistant to the aforementioned shRNA. Co-delivery of these vectors resulted in the rescue of functional defects caused by the shRNA knockdown and partial recovery of total Prph2 levels (Petrs-Silva et al., 2012). Similarly, using electroporation instead of a virus, co-injection of both an shRNA vector that is able to knock-down both wildtype and mutant *Prph2* and an shRNA-resistant copy of wild-type *Prph2* resulted in degradation of endogenous *Prph2* and stabilized expression of the exogenously delivered Prph2 in mouse retinal explants (Palfi et al., 2006). Although the efficacy of this kind of therapy has not yet been evaluated in IRD disease models, these studies show that allele-independent knockdown in combination with gene supplementation represents a potential therapy to counteract genetic defects in *PRPH2*-associated diseases.

6.3.3 Delivery of neurotrophic factors

Unlike gene replacement and gene-knock down therapies, also more general therapeutic strategies are considered, e.g. the delivery of neurotrophic factors. An advantage of such a strategy is that it can be applied to multiple genetic subtypes of IRD. The first proof-of principle came from a mouse study, in which ciliary neurotrophic factor (CNTF) was injected into the intravitreal space of *Prph2$^{-/-}$* mice (Cayouette, Behn, Sendtner, Lachapelle, & Gravel,

1998), and lead to an improvement in OS structure. However, at the functional level, only a small improvement in rods, and no improvement in cones, was observed. In a similar study performed by another group, CTNF was delivered to p.P216L $Prph2^{+/-}$ mice. These mice showed improved OS structure, but the authors also observed dose-dependent abnormalities in photoreceptor nuclei as well as a decrease in both rod and cone function (Bok et al., 2002). Follow-up studies revealed that CNTF alters retinal signalling pathways. Furthermore, they observed a down-regulation of critical phototransduction genes, such as cone opsins (Rhee et al., 2007). Although these adverse findings have led to the preclusion to use CNTF to treat $PRPH2$-associated IRD, other neurotrophic factors were investigated. For example, lentiviruses carrying either fibroblast growth factor-2 (FGF-2) or human pigment epithelial-derived factor (PEDF) were reported to significantly improve both scotopic a- and b-waves in $Prph2^{-/-}$ mice. However, these agents did not restore photoreceptor survival (Miyazaki et al., 2008). Other non-traditional neurotrophic factors, such as hormones, also have been shown to result in neuroprotection. Administration of some of these agents, including erythropoietin (hormone) (Rex et al., 2004; Rex, Wong, Kodali, & Merry, 2009), and nilvadipine (calcium channel blocker) (Takeuchi, Nakazawa, & Mizukoshi, 2008), significantly improved photoreceptor function in $Prph2^{-/-}$ and $Prph2^{+/-}$ mouse models. However, more studies are required to determine both the safety and efficacy of such particular therapeutic approaches.

7| CONCLUDING REMARKS

Taken together, in this study, we describe 245 reported and seven novel $PRPH2$ variants identified in 891 alleles in 867 index cases, and uploaded these to the LOVD database for $PRPH2$, which thus far only included 76 variants. This study thereby provides an important step towards a complete overview of all $PRPH2$ variants in a single database. A continuous addition of genetic data from newly identified patients with $PRPH2$ variants is of great importance for a more robust classification of pathogenic variants. Furthermore, additional data regarding phenotypes might aid the identification of genotype-phenotype correlations. Our analysis resulted in the *in silico* classification of all the 245 reported, as well as the seven novel identified $PRPH2$ variants. More importantly, our study illustrates the need of experimental assays to identify the true causality of the many $PRPH2$ variants that are now still assigned to be variants of uncertain significance. This will help to improve molecular diagnostics and, in the long-term, hopefully also support the development of therapeutic strategies for patients with $PRPH2$-associated IRD.

Disclosure statement

The authors declare no conflict of interest.

Data sharing statement

All mutation data are uploaded into the Leiden Open Variation Database. Other data that support the findings of this study are available from the corresponding author upon reasonable request.

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TABLES

Table 1. Previously unreported *PRPH2* variants identified in index cases by MIPs or the Radboudumc genome diagnostic laboratory

PID	cDNA change	Protein change	Type of mutation	Identified by	Phenotype
1	c.2T>C	p.?	Fail-to-start	MIPs	Pseudo-STGD
2	c.63G>A	p.W21*	Nonsense	Exome seq.	MD/ PD
3	c.63G>A	p.W21*	Nonsense	Sanger seq.	MD/ PD
4	c.63G>A	p.W21*	Nonsense	Sanger seq.	MD/ PD
5	c.94A>G	p.I32V	Missense	MIPs	AMD
6	c.112G>T	p.G38*	Nonsense	MIPs	Pseudo-STGD
7	c.122T>C	p.L41P	Missense	Sanger seq.	MD/ PD
8	c.133C>T	p.L45F	Missense	MIPs	AMD
9	c.136C>T	p.R46*	Nonsense	MIPs	Pseudo-STGD
10	**c.209dup**	**p.S71lfs*106**	**Frameshift**	**MIPs**	**Pseudo-STGD**
11	c.253G>A	p.A85T	Missense	Sanger seq.	MD/ PD
12	c.271T>A	p.Y91N	Missense	MIPs	Pseudo-STGD
13	c.281G>A	p.W94*	Nonsense	MIPs	Pseudo-STGD
14	c.303C>G	p.Y101*	Nonsense	Exome seq.	MD/ PD
15	c.367C>T	p.R123W	Missense	Exome seq.	RP
16	c.377T>C	p.L126P	Missense	Exome seq.	RP
17	**c.415_417del**	**p.k139del**	**Deletion**	**MIPs**	**Pseudo-STGD**
18	**c.415_417del**	**p.k139del**	**Deletion**	**MIPs**	**Pseudo-STGD**
19	**c.423C>A**	**p.Y141***	**Nonsense**	**MIPs**	**Pseudo-STGD**
20	c.424C>T	p.Rr142W	Missense	MIPs	Pseudo-STGD
21	c.424C>T	p.R142W	Missense	Exome seq.	MD
22	c.424C>T	p.R142W	Missense	Exome seq.	RD
23	c.424C>T	p.R142W	Missense	Exome seq.	RCD
24	c.424C>T	p.R142W	Missense	Exome seq.	MD
25	c.424C>T	p.R142W	Missense	Exome seq.	MD
26	c.424C>T	p.R142W	Missense	Exome seq.	MD
27	c.424C>T	p.R142W	Missense	Exome seq.	MD
28	c.424C>T	p.R142W	Missense	Exome seq.	MD
29	c.424C>T	p.R142W	Missense	Exome seq.	MD
30	c.424C>T	p.R142W	Missense	Exome seq.	CACD
31	c.424C>T	p.R142W	Missense	Exome seq.	MD/ CD
32	c.424C>T	p.R142W	Missense	Exome seq.	MD
33	c.424C>T	p.R142W	Missense	Exome seq.	MD/ PD

34	c.424C>T	p.R142W	Missense	Exome seq.	MD
35	c.424C>T	p.R142W	Missense	Exome seq.	MD
36	c.424C>T	p.R142W	Missense	Exome seq.	CACD
37	c.424C>T	p.R142W	Missense	Exome seq.	MD
38	c.424C>T	p.R142W	Missense	Exome seq.	RD
39	c.424C>T	p.R142W	Missense	Sanger seq.	CACD
40	c.424C>T	p.R142W	Missense	Sanger seq.	CACD
41	c.424C>T	p.R142W	Missense	Sanger seq.	MD/ PD
42	c.424C>T	p.R142W	Missense	Sanger seq.	CACD
43	c.424C>T	p.R142W	Missense	Sanger seq.	CACD
44	c.424C>T	p.R142W	Missense	Sanger seq.	CACD
45	c.424C>T	p.R142W	Missense	Sanger seq.	CACD
46	c.424C>T	p.R142W	Missense	Sanger seq.	CACD
47	c.424C>T	p.R142W	Missense	Sanger seq.	MD/ PD
48	c.424C>T	p.R142W	Missense	Sanger seq.	MD/ PD
49	c.424C>T	p.R142W	Missense	Sanger seq.	CACD
50	c.424C>T	p.R142W	Missense	Sanger seq.	CACD
51	c.424C>T	p.R142W	Missense	Sanger seq.	CACD
52	c.424C>T	p.R142W	Missense	Sanger seq.	MD/ PD
53	c.424C>T	p.R142W	Missense	Sanger seq.	CACD
54	c.424C>T	p.R142W	Missense	Sanger seq.	CACD
55	c.433_434del	p.D145Hfs*31	Frameshift	Sanger seq.	CACD
56	c.441del	p.G148Afs*5	Frameshift	MIPs	Pseudo-STGD
57	c.441del	p.G148Afs*5	Frameshift	MIPs	Pseudo-STGD
58	c.441del	p.G148Afs*5	Frameshift	Sanger seq.	MD/ PD
59	c.441del	p.G148Afs*5	Frameshift	Sanger seq.	MD/ PD
60	c.441del	p.G148Afs*5	Frameshift	Exome seq.	MD
61	c.458A>G	p.K153R	Missense	Asper	RP
62	c.469G>A	p.D157N	Missense	MIPs	Pseudo-STGD
63	c.499G>A	p.G167S	Missense	Sanger seq.	MD/ PD
64	c.499G>A	p.G167S	Missense	MIPs	Pseudo-STGD
65	c.505_507del	p.N169del	Deletion	Sanger seq.	MD/ PD
66	c.505_507del	p.N169del	Deletion	Exome seq.	RP
67	c.514C>T	p.R172W	Missense	MIPs	Pseudo-STGD
68	c.514C>T	p.R172W	Missense	MIPs	Pseudo-STGD
69	c.514C>T	p.R172W	Missense	MIPs	Pseudo-STGD
70	c.514C>T	p.R172W	Missense	Asper	RD
71	c.514C>T	p.R172W	Missense	Sanger seq.	MD/ PD

72	c.514C>T	p.R172W	Missense	Sanger seq.	MD/ PD
73	c.514C>T	p.R172W	Missense	Exome seq.	CD
74	c.514C>T	p.R172W	Missense	Exome seq.	MD
75	c.514C>T	p.R172W	Missense	Exome seq.	MD
76	c.515G>A	p.R172Q	Missense	MIPs	Pseudo-STGD
77	c.515G>A	p.R172Q	Missense	Exome seq.	MD
78	c.515G>A	p.R172Q	Missense	MIPs	Pseudo-STGD
79	c.520T>A	p.W174R	Missense	Sanger seq.	MD/ PD
80	c.520T>A	p.W174R	Missense	Exome seq.	MD
81	c.522G>C	p.W174C	Missense	MIPs	Pseudo-STGD
82	**c.581+1G>A**	**p.?**	**Splice site**	**MIPs**	**Pseudo-STGD**
83	c.581+4dup	p.?	Splice site	Sanger seq.	?
84	c.582-1G>A	p.?	Splice site	MIPs	Pseudo-STGD
85	c.582-1G>A	p.?	Splice site	Sanger seq.	CACD
86	c.582-2A>T	p.?	Splice site	Sanger seq.	CACD
87	**c.582_828del**	**p.D194Efs*2**	**Frameshift**	**MIPs**	**Pseudo-STGD**
88	c.583C>T	p.R195*	Nonsense	MIPs	Pseudo-STGD
89	c.583C>T	p.R195*	Nonsense	MIPs	Pseudo-STGD
90	c.584G>T	p.R195L	Missense	MIPs	Pseudo-STGD
91	c.584G>A	p.R195Q	Missense	Sanger seq.	CACD
92	c.584G>A	p.R195Q	Missense	MIPs	Pseudo-STGD
93	c.614T>C	p.L205P	Missense	Sanger seq.	CACD
94	c.623G>A	p.G208D	Missense	MIPs	Pseudo-STGD
95	c.623G>A	p.G208D	Missense	Sanger seq.	MD/ PD
96	c.623G>A	p.G208D	Missense	Sanger seq.	MD/ PD
97	c.623G>A	p.G208D	Missense	MIPs	AMD
98	c.628C>T	p.P210S	Missense	MIPs	Pseudo-STGD
99	c.633C>A	p.F211L	Missense	Asper	RP
100	c.646C>T	p.P216S	Missense	Asper	RP
101	c.646C>T	p.P216S	Missense	Exome seq.	RCD
102	c.646C>T	p.P216S	Missense	Exome seq.	RP
103	c.646C>T	p.P216S	Missense	Exome seq.	RP
104	c.646C>T	p.P216S	Missense	Sanger seq.	RP
105	c.646C>T	p.P216S	Missense	Exome seq.	RP
106	c.656C>G	p.P219R	Missense	Sanger seq.	CACD
107	c.657_662del	p.R220_P221del	Deletion	Sanger seq.	MD/ PD
108	c.658C>T	p.R220W	Missense	Sanger seq.	MD/ PD
109	c.658del	p.R220fs*34	Frameshift	Exome seq.	RCD/ CRD
110	c.658del	p.R220fs*34	Frameshift	Sanger seq.	MD/ PD

111	c.659G>A	p.R220Q	Missense	Sanger seq.	MD/ PD
112	c.665G>A	p.C222Y	Missense	MIPs	CRD
113	c.715C>T	p.Q239*	Missense	MIPs	AMD
114	c.736T>C	p.W246R	Missense	MIPs	AMD
115	c.746del	p.G249Afs*7	Frameshift	Exome seq.	MD/ PD
116	c.749G>A	p.C250Y	Missense	MIPs	Pseudo-STGD
117	c.754G>C	p.A252P	Missense	MIPs	AMD
118	c.781C>T	p.L261F	Missense	MIPs	AMD
119	**c.809_810del**	**p.L270Pfs*30**	**Frameshift**	**MIPs**	**Pseudo-STGD**
120	c.850C>T	p.R284C	Missense	MIPs	AMD
121	c.866C>T	p.S289L	Missense	MIPs	AMD
122	c.866C>T	p.S289L	Missense	MIPs	AMD
123	c.866C>T	p.S289L	Missense	MIPs	AMD
124	c.866C>T	p.S289L	Missense	MIPs	AMD
125	c.866C>T	p.S289L	Missense	MIPs	AMD
126	c.866C>T	p.S289L	Missense	MIPs	AMD
127	c.866C>T	p.S289L	Missense	MIPs	AMD
128	c.866C>T	p.S289L	Missense	MIPs	AMD
129	c.866C>T	p.S289L	Missense	MIPs	AMD
130	c.866C>T	p.S289L	Missense	MIPs	AMD
131	c.866C>T	p.S289L	Missense	MIPs	AMD
132	c.866C>T	p.S289L	Missense	MIPs	AMD
133	c.866C>T	p.S289L	Missense	MIPs	AMD
134	c.866C>T	p.S289L	Missense	MIPs	AMD
135	c.866C>T	p.S289L	Missense	MIPs	AMD
136	c.866C>T	p.S289L	Missense	MIPs	AMD
137	c.866C>T	p.S289L	Missense	MIPs	AMD
138	c.866C>T	p.S289L	Missense	Sanger seq.	MD/ PD
139	c.923T>A	p.L308Q	Missense	MIPs	AMD
140	c.923T>A	p.L308Q	Missense	MIPs	AMD
141	c.938C>T	p.P313L	Missense	MIPs	AMD
142	c.938C>T	p.P313L	Missense	MIPs	AMD
143	c.938C>T	p.P313L	Missense	MIPs	AMD
144	c.828+1G>A	p.?	Splice site	Sanger seq.	MD/ PD
145	**c.829-3_829-1del**	**p.?**	**Splice site**	**MIPs**	**Pseudo-STGD**
146	c.897_898del	p.S301Rfs*90	Frameshift	Exome seq.	MD
147	c.946T>G	p.W316G	Missense	Exome seq.	MD/ PD

Novel variants identified via MIPs are depicted in bold. Abbreviations phenotypes: CACD = Central areolar choroidal dystrophy; CD = Cone dystrophy; CRD = Cone-rod dystrophy; MD = Macular dystrophy; PD = pattern

dystrophy; Pseudo-STGD = pseudo-Stargardt disease; RD = Retinal dystrophy; RP = Retinitis pigmentosa; RCD = Rod-cone dystrophy.

Table 2. Distribution of *PRPH2* variants found in IRD patients

Variant type	Number of unique variants	Number of alleles
Missense	137	605
Protein-truncating	85	180
Splice site	10	77
In-frame amino acid insertions/deletions	15	24
Synonymous	3	3
5'- or 3'-UTR	2	2
Total	**252**	**891**

Table 3. Likely pathogenic and pathogenic missense variants

cDNA change	Protein change	Heterozygous	Compound heterozygous	Homozygous	Digenic	Trigenic	Protein domain
c.38G>A	p.R13Q	2	0	0	0	0	N-terminus
c.80C>T	p.S27F	1	0	0	0	0	1st TMD
c.202G>C	p.G68R	2	0	0	0	0	2nd TMD
c.271T>A	p.Y91N	1	2	0	0	0	C-loop
c.271T>C	p.Y91H	1	0	0	0	0	C-loop
c.367C>T	p.R123W	2	0	0	0	0	D2-loop
c.374C>T	p.S125L	1	0	0	0	0	D2-loop
c.377T>C	p.L126P	3	0	0	0	0	D2-loop
c.377T>G	p.L126R	2	0	0	0	0	D2-loop
c.380A>G	p.E127G	2	0	0	0	0	D2-loop
c.389T>C	p.L130P	6	0	0	0	0	D2-loop
c.421T>C	p.Y141H	2	0	0	0	0	D2-loop
c.422A>G	p.Y141C	24	0	0	0	0	D2-loop
c.424C>T	p.R142W	93	0	2	0	0	D2-loop
c.425G>A	p.R142Q	2	0	0	0	0	D2-loop
c.457A>G	p.K153E	1	0	0	0	0	D2-loop
c.458A>G	p.K153R	3	0	0	0	0	D2-loop
c.464C>T	p.T155I	0	0	0	1	0	D2-loop
c.469G>A	p.D157N	5	0	0	0	0	D2-loop
c.494G>T	p.C165F	1	0	0	0	0	D2-loop
c.494G>A	p.C165Y	4	0	0	0	0	D2-loop
c.493T>C	p.C165R	1	0	0	0	0	D2-loop
c.499G>A	p.G167S	10	0	0	0	0	D2-loop
c.500G>A	p.G167D	3	0	0	0	0	D2-loop
c.515G>A	p.R172Q	13	0	0	0	0	D2-loop
c.514C>G	p.R172G	1	0	0	0	0	D2-loop
c.514C>T	p.R172W	58	0	0	1	1	D2-loop
c.518A>T	p.D173V	4	0	0	0	0	D2-loop
c.520T>A	p.W174R	2	0	0	0	0	D2-loop
c.533A>G	p.Q178R	2	0	0	0	0	D2-loop
c.536G>T	p.W179L	1	0	0	0	0	D2-loop
c.535T>C	p.W179R	4	0	0	0	0	D2-loop
c.537G>T	p.W179C	1	0	0	0	0	D2-loop
c.551A>C	p.Y184S	1	0	0	0	0	D2-loop
c.554T>C	p.L185P	6	0	2	4	0	D2-loop
c.582T>A	p.D194E	1	0	0	0	0	D2-loop
c.583C>G	p.R195G	1	0	0	0	0	D2-loop

c.584G>A	p.R195Q	6	0	0	0	0	D2-loop
c.584G>T	p.R195L	12	0	0	0	0	D2-loop
c.587T>A	p.I196N	1	0	0	0	0	D2-loop
c.589A>G	p.K197E	2	0	0	0	0	D2-loop
c.592A>C	p.S198R	1	0	0	0	0	D2-loop
c.594C>G	p.S198R	3	0	0	0	0	D2-loop
c.599T>A	p.V200E	1	0	0	0	0	D2-loop
c.599T>G	p.V200G	1	0	0	0	0	D2-loop
c.623G>A	p.G208D	12	0	1	0	0	D2-loop
c.625G>A	p.V209I	2	0	0	0	0	D2-loop
c.625G>T	p.V209F	1	0	0	0	0	D2-loop
c.626T>A	p.V209D	2	0	0	0	0	D2-loop
c.628C>T	p.P210S	2	0	0	0	0	D2-loop
c.629C>G	p.P210R	20	0	1	0	0	D2-loop
c.629C>T	p.P210L	2	0	0	0	0	D2-loop
c.631T>C	p.F211L	6	0	0	0	0	D2-loop
c.634A>G	p.S212G	7	0	0	0	0	D2-loop
c.635G>C	p.S212T	4	0	0	0	0	D2-loop
c.636 T>A	p.C213S	2	0	0	0	0	D2-loop
c.637T>C	p.C213R	1	0	1	0	0	D2-loop
c.638G>T	p.C213F	1	0	0	0	0	D2-loop
c.638G>A	p.C213Y	6	0	0	0	0	D2-loop
c.639C>G	p.C213W	3	0	0	0	0	D2-loop
c.641G>A	p.C214Y	2	0	0	0	0	D2-loop
c.641G>C	p.C214S	1	0	0	0	0	D2-loop
c.643A>T	p.N215Y	1	0	0	0	0	D2-loop
c.646C>T	p.P216S	21	0	0	0	0	D2-loop
c.646C>G	p.P216A	1	0	0	0	0	D2-loop
c.647C>G	p.P216R	1	0	0	0	0	D2-loop
c.656C>G	p.P219R	2	0	0	0	0	D2-loop
c.658C>T	p.R220W	8	0	0	0	0	D2-loop
c.659G>A	p.R220Q	3	0	1	0	0	D2-loop
c.659G>C	p.R220P	2	0	0	0	0	D2-loop
c.664T>C	p.C222R	2	0	0	0	0	D2-loop
c.665G>C	p.C222S	2	0	0	0	0	D2-loop
c.665G>A	p.C222Y	2	0	0	0	0	D2-loop
c.668T>A	p.I223N	1	0	0	0	0	D2-loop
c.683C>T	p.T228I	5	0	0	0	0	D2-loop
c.730A>C	p.N244H	1	0	0	0	0	D2-loop

c.732C>A	p.N244K	2	0	0	0	0	D2-loop
c.732C>G	p.N244K	1	0	0	0	0	D2-loop
c.736T>C	p.W246R	2	0	0	0	0	D2-loop
c.738G>C	p.W246C	1	0	0	0	0	D2-loop
c.745G>A	p.G249S	1	0	0	0	0	D2-loop
c.748T>C	p.C250R	1	0	0	0	0	D2-loop
c.748T>G	p.C250G	3	1	0	1	0	D2-loop
c.748T>A	p.C250S	1	0	0	0	0	D2-loop
c.749G>A	p.C250Y	2	0	0	0	0	D2-loop
c.749G>T	p.C250F	1	0	0	0	0	D2-loop
c.758C>A	p.A253E	1	0	0	0	0	D2-loop
c.761T>A	p.L254Q	5	0	1	0	0	D2-loop
c.797G>A	p.G266D	4	0	0	0	0	4th TMD
c.802G>A	p.V268I	1	0	0	0	0	4th TMD
c.850C>T	p.R284C	1	0	0	0	0	C-terminus
c.923T>A	p.L308Q	2	0	0	0	0	C-terminus
c.946T>G	p.W316G	5	0	0	0	0	C-terminus

1st TMD = first transmembrane domain, 2nd TMD = second transmembrane domain, 4th TMD = fourth transmembrane domain, C-loop = cytoplasmic loop, D2-loop = second intradiscal loop. Novel missense variants are depicted in bold.

FIGURE LEGENDS

Figure 1. A| Pie-chart showing the distribution of (likely) pathogenic *PRPH2* variants in IRD patients B| Pie-chart showing the ACMG pathogenicity assessment of missense variants. About two-third of the missense variants was classified as pathogenic or likely pathogenic. **C| Location likely pathogenic missense variants relative to the protein structure.** The vast majority of the likely pathogenic missense variants are located in the D2 loop. AMD = Age-related macular degeneration; AVMD = Adult vitelliform macular dystrophy; CACD = central areolar choroidal dystrophy; CD = Cone dystrophy; CRD = Cone-rod dystrophy; EOHM = Early-onset high myopia; PD = pattern dystrophy; RP = Retinitis pigmentosa.