

Supplemental Data

**Comprehensive Rare Variant Analysis via
Whole-Genome Sequencing to Determine the
Molecular Pathology of Inherited Retinal Disease**

Keren J. Carss, Gavin Arno, Marie Erwood, Jonathan Stephens, Alba Sanchis-Juan, Sarah Hull, Karyn Megy, Detelina Grozeva, Eleanor Dewhurst, Samantha Malka, Vincent Plagnol, Christopher Penkett, Kathleen Stirrups, Roberta Rizzo, Genevieve Wright, Dragana Josifova, Maria Bitner-Glindzicz, Richard H. Scott, Emma Clement, Louise Allen, Ruth Armstrong, Angela F. Brady, Jenny Carmichael, Manali Chitre, Robert H.H. Henderson, Jane Hurst, Robert E. MacLaren, Elaine Murphy, Joan Paterson, Elisabeth Rosser, Dorothy A. Thompson, Emma Wakeling, Willem H. Ouwehand, Michel Michaelides, Anthony T. Moore, NIHR-BioResource Rare Diseases Consortium, Andrew R. Webster, and F. Lucy Raymond

Supplemental tables, legends and references

Table S1: Genes that are associated with IRD. The list includes some genes associated with syndromic phenotypes and albinism.

This list has been curated according to previously described criteria.⁴ Associated disease information is from OMIM or the cited journal article.

Table S2: Patient and variant information.

Pathogenic variants in 722 patients with inherited retinal disease. Genomic coordinates refer to genome build GRCh37. WES = whole-exome sequencing, WGS = whole-genome sequencing, MEH = Moorfields Eye Hospital (London, UK), GOS = Great Ormond Street Hospital For Children (London, UK), CUH = Cambridge University Hospitals (Cambridge, UK), GUYS = Guy's And St Thomas' NHS Foundation Trust (London, UK), NWL = North West London Hospitals NHS Trust (London, UK), UCL = University College London Hospitals NHS Foundation Trust (London, UK), RP = retinitis pigmentosa, RD = retinal dystrophy, CRD = cone-rod dystrophy, Other = any phenotype with frequency of less than eight patients, CSNB = congenital stationary night blindness, Multiple = more than one phenotype including syndromic cases, LCA = Leber congenital amaurosis, FEVR = Familial exudative vitreoretinopathy.

Table S3: Supporting evidence for 19 novel biallelic candidate genes that may cause IRD.

Phenotype	Gene	Human Retina Expression* (ref 181)	Literature evidence for candidate gene for IRD	Reference	Strength of data
Multiple	<i>SCAPER</i>	yes	Rare variants identified in Parkinson's disease	182	Weak
RD	<i>FUT5</i>	yes	None	-	Weak
RD	<i>PODNL1</i>	yes	None	-	Weak
RP	<i>NAALADL1</i>	yes	None	-	Weak
CRD	<i>WASF3</i>	yes	Strong expression in brain	183	Moderate
Usher	<i>PLD4</i>	yes	Gene involved in the cerebellar cortex circuit development	184	Moderate
RP	<i>FAM71A</i>	no	None	-	Weak
Cone dystrophy	<i>POMZP3</i>	yes	None	-	Weak
RP	<i>IRX5</i>	yes	Required for retinal cone bipolar development in mouse	185	Strong
Stargardt	<i>ITIH2</i>	yes	Reduced expression in human retina in type 1 diabetic retinopathy	186	Moderate
RP	<i>SLC37A3</i>	yes	None	-	Weak
CRD	<i>NUMB</i>	yes	Required for the production of terminal asymmetric cell	187	Strong

			divisions in the developing mouse retina		
CRD	<i>FAM57B</i>	yes	None	-	Weak
RP	<i>FOXI2</i>	yes	Inhibition of gene in <i>gdf6a</i> (-/-) Zebrafish embryos reduces eye size	188	Moderate
RP	<i>CROCC</i>	yes	Mouse knock out shows photo-degeneration over time	189	Strong
RP	<i>CCZ1B</i>	yes	None	-	Weak
Other	<i>OR2M7</i>	no	None	-	Weak
RP	<i>PRTFDC1</i>	yes	None	-	Weak
RP	<i>UBAP1L</i>	yes	None	-	Weak

* The human retina expression was obtained from <https://oculargenomics.meei.harvard.edu/index.php/ret-trans/110-human-retinal-transcriptome>;
RD = retinal dystrophy, RP = retinitis pigmentosa, CRD = cone-rod dystrophy, Other = any phenotype with frequency of less than eight patients in the studied sample set.

Supplemental References

1. Khan, M.I., Ajmal, M., Micheal, S., Azam, M., Hussain, A., Shahzad, A., Venselaar, H., Bokhari, H., de Wijs, I.J., Hoefsloot, L.H., et al. (2013). Homozygosity mapping identifies genetic defects in four consanguineous families with retinal dystrophy from Pakistan. *Clin. Genet.* 84, 290–293.
2. Weston, M.D., Eudy, J.D., Fujita, S., Yao, S., Usami, S., Cremers, C., Greenberg, J., Ramesar, R., Martini, A., Moller, C., et al. (2000). Genomic structure and identification of novel mutations in *usherin*, the gene responsible for Usher syndrome type IIa. *Am. J. Hum. Genet.* 66, 1199–1210.
3. Eudy, J.D., Weston, M.D., Yao, S., Hoover, D.M., Rehm, H.L., Ma-Edmonds, M., Yan, D., Ahmad, I., Cheng, J.J., Ayuso, C., et al. (1998). Mutation of a gene encoding a protein with extracellular matrix motifs in Usher syndrome type IIa. *Science* 280, 1753–1757.
4. Rozet, J.M., Gerber, S., Souied, E., Perrault, I., Châtelain, S., Ghazi, I., Leowski, C., Dufier, J.L., Munnich, A., and Kaplan, J. Spectrum of ABCR gene mutations in autosomal recessive macular dystrophies. *Eur. J. Hum. Genet.* 6, 291–295.
5. Maugeri, A., van Driel, M.A., van de Pol, D.J., Klevering, B.J., van Haren, F.J., Tijmes, N., Bergen, A.A., Rohrschneider, K., Blankenagel, A., Pinckers, A.J., et al. (1999). The 2588G-->C mutation in the ABCR gene is a mild frequent founder mutation in the Western European population and allows the classification of ABCR mutations in patients with Stargardt disease. *Am. J. Hum. Genet.* 64, 1024–1035.
6. Bonnet, C., Grati, M., Marlin, S., Levilliers, J., Hardelin, J.-P., Parodi, M., Niasme-Grare, M., Zelenika, D., Délépine, M., Feldmann, D., et al. (2011). Complete exon sequencing of all known Usher syndrome genes greatly improves molecular diagnosis. *Orphanet J. Rare Dis.* 6, 21.
7. Maugeri, A., Klevering, B.J., Rohrschneider, K., Blankenagel, A., Brunner, H.G., Deutman, A.F., Hoyng, C.B., and Cremers, F.P. (2000). Mutations in the ABCA4 (ABCR) gene are the major cause of autosomal recessive cone-rod dystrophy. *Am. J. Hum. Genet.* 67, 960–966.

8. Yang, Z., Chen, Y., Lillo, C., Chien, J., Yu, Z., Michaelides, M., Klein, M., Howes, K.A., Li, Y., Kaminoh, Y., et al. (2008). Mutant prominin 1 found in patients with macular degeneration disrupts photoreceptor disk morphogenesis in mice. *J. Clin. Invest.* 118, 2908–2916.
9. Allikmets, R., Shroyer, N.F., Singh, N., Seddon, J.M., Lewis, R.A., Bernstein, P.S., Peiffer, A., Zabriskie, N.A., Li, Y., Hutchinson, A., et al. (1997). Mutation of the Stargardt disease gene (ABCR) in age-related macular degeneration. *Science* 277, 1805–1807.
10. Fujinami, K., Zernant, J., Chana, R.K., Wright, G.A., Tsunoda, K., Ozawa, Y., Tsubota, K., Robson, A.G., Holder, G.E., Allikmets, R., et al. (2015). Clinical and molecular characteristics of childhood-onset Stargardt disease. *Ophthalmology* 122, 326–334.
11. Khan, S., Ullah, I., Irfanullah, Touseef, M., Basit, S., Khan, M.N., and Ahmad, W. (2013). Novel homozygous mutations in the genes ARL6 and BBS10 underlying Bardet-Biedl syndrome. *Gene* 515, 84–88.
12. Riazuddin, S.A., Zulfiqar, F., Zhang, Q., Yao, W., Li, S., Jiao, X., Shahzadi, A., Amer, M., Iqbal, M., Hussnain, T., et al. (2006). Mutations in the gene encoding the alpha-subunit of rod phosphodiesterase in consanguineous Pakistani families. *Mol. Vis.* 12, 1283–1291.
13. Adato, A., Vreugde, S., Joensuu, T., Avidan, N., Hamalainen, R., Belenkiy, O., Olender, T., Bonne-Tamir, B., Ben-Asher, E., Espinos, C., et al. (2002). USH3A transcripts encode clarin-1, a four-transmembrane-domain protein with a possible role in sensory synapses. *Eur. J. Hum. Genet.* 10, 339–350.
14. Breuer, D.K., Yashar, B.M., Filippova, E., Hiriyan, S., Lyons, R.H., Mears, A.J., Asaye, B., Acar, C., Vervoort, R., Wright, A.F., et al. (2002). A comprehensive mutation analysis of RP2 and RPGR in a North American cohort of families with X-linked retinitis pigmentosa. *Am. J. Hum. Genet.* 70, 1545–1554.
15. Tuson, M., Marfany, G., and González-Duarte, R. (2004). Mutation of CERKL, a novel human ceramide kinase gene, causes autosomal recessive retinitis pigmentosa (RP26). *Am. J. Hum. Genet.* 74, 128–138.
16. Vervoort, R., Lennon, A., Bird, A.C., Tulloch, B., Axton, R., Miano, M.G., Meindl, A., Meitinger, T., Ciccociola, A., and Wright, A.F. (2000). Mutational hot spot within a new RPGR exon in X-linked retinitis pigmentosa. *Nat. Genet.* 25, 462–466.
17. Mykytyn, K., Nishimura, D.Y., Searby, C.C., Shastri, M., Yen, H., Beck, J.S., Braun, T., Streb, L.M., Cornier, A.S., Cox, G.F., et al. (2002). Identification of the gene (BBS1) most commonly involved in Bardet-Biedl syndrome, a complex human obesity syndrome. *Nat. Genet.* 31, 435–438.
18. Cremers, F.P.M., Kimberling, W.J., Külm, M., de Brouwer, A.P., van Wijk, E., te Brinke, H., Cremers, C.W.R.J., Hoefsloot, L.H., Banfi, S., Simonelli, F., et al. (2007). Development of a genotyping microarray for Usher syndrome. *J. Med. Genet.* 44, 153–160.
19. Wang, F., Wang, H., Tuan, H.-F., Nguyen, D.H., Sun, V., Keser, V., Bowne, S.J., Sullivan, L.S., Luo, H., Zhao, L., et al. (2014). Next generation sequencing-based molecular diagnosis of retinitis pigmentosa: identification of a novel genotype-phenotype correlation and clinical refinements. *Hum. Genet.* 133, 331–345.
20. Nishiguchi, K.M., Tearle, R.G., Liu, Y.P., Oh, E.C., Miyake, N., Benaglio, P., Harper, S., Koskiniemi-Kuendig, H., Venturini, G., Sharon, D., et al. (2013). Whole genome sequencing in patients with retinitis pigmentosa reveals pathogenic DNA structural changes and NEK2 as a new disease gene. *Proc. Natl. Acad. Sci. U. S. A.* 110, 16139–16144.
21. Leroy, B.P., Aragon-Martin, J.A., Weston, M.D., Bessant, D.A., Willis, C., Webster, A.R., Bird, A.C., Kimberling, W.J., Payne, A.M., and Bhattacharya, S.S. (2001). Spectrum of mutations in USH2A in British patients with Usher syndrome type II. *Exp. Eye Res.* 72, 503–509.
22. van Wijk, E., Pennings, R.J.E., te Brinke, H., Claassen, A., Yntema, H.G., Hoefsloot, L.H., Cremers, F.P.M., Cremers, C.W.R.J., and Kremer, H. (2004). Identification of 51 novel exons of the Usher syndrome type 2A (USH2A) gene that encode multiple conserved functional domains and that are mutated in patients with Usher syndrome type II. *Am. J. Hum. Genet.* 74, 738–744.

23. Yan, D., Ouyang, X., Patterson, D.M., Du, L.L., Jacobson, S.G., and Liu, X.-Z. (2009). Mutation analysis in the long isoform of USH2A in American patients with Usher Syndrome type II. *J. Hum. Genet.* 54, 732–738.
24. Mackay, D.S., Borman, A.D., Sui, R., van den Born, L.I., Berson, E.L., Ocaka, L.A., Davidson, A.E., Heckenlively, J.R., Branham, K., Ren, H., et al. (2013). Screening of a large cohort of leber congenital amaurosis and retinitis pigmentosa patients identifies novel LCA5 mutations and new genotype-phenotype correlations. *Hum. Mutat.* 34, 1537–1546.
25. Ali, M., Ramprasad, V.L., Soumitra, N., Mohamed, M.D., Jafri, H., Rashid, Y., Danciger, M., McKibbin, M., Kumaramanickavel, G., and Inglehearn, C.F. (2008). A missense mutation in the nuclear localization signal sequence of CERKL (p.R106S) causes autosomal recessive retinal degeneration. *Mol. Vis.* 14, 1960–1964.
26. Lewis, R.A., Shroyer, N.F., Singh, N., Allikmets, R., Hutchinson, A., Li, Y., Lupski, J.R., Leppert, M., and Dean, M. (1999). Genotype/Phenotype analysis of a photoreceptor-specific ATP-binding cassette transporter gene, ABCR, in Stargardt disease. *Am. J. Hum. Genet.* 64, 422–434.
27. Zernant, J., Schubert, C., Im, K.M., Burke, T., Brown, C.M., Fishman, G.A., Tsang, S.H., Gouras, P., Dean, M., and Allikmets, R. (2011). Analysis of the ABCA4 gene by next-generation sequencing. *Invest. Ophthalmol. Vis. Sci.* 52, 8479–8487.
28. Henderson, R.H., Waseem, N., Searle, R., van der Spuy, J., Russell-Eggitt, I., Bhattacharya, S.S., Thompson, D.A., Holder, G.E., Cheetham, M.E., Webster, A.R., et al. (2007). An assessment of the apex microarray technology in genotyping patients with Leber congenital amaurosis and early-onset severe retinal dystrophy. *Invest. Ophthalmol. Vis. Sci.* 48, 5684–5689.
29. O’Sullivan, J., Mullaney, B.G., Bhaskar, S.S., Dickerson, J.E., Hall, G., O’Grady, A., Webster, A., Ramsden, S.C., and Black, G.C. (2012). A paradigm shift in the delivery of services for diagnosis of inherited retinal disease. *J Med Genet* 49, 322–326.
30. Huang, X.-F., Huang, F., Wu, K.-C., Wu, J., Chen, J., Pang, C.-P., Lu, F., Qu, J., and Jin, Z.-B. (2015). Genotype-phenotype correlation and mutation spectrum in a large cohort of patients with inherited retinal dystrophy revealed by next-generation sequencing. *Genet. Med.* 17, 271–278.
31. Li, L., Xiao, X., Li, S., Jia, X., Wang, P., Guo, X., Jiao, X., Zhang, Q., and Hejtmancik, J.F. (2011). Detection of variants in 15 genes in 87 unrelated Chinese patients with Leber congenital amaurosis. *PLoS One* 6, e19458.
32. Simpson, D.A., Clark, G.R., Alexander, S., Silvestri, G., and Willoughby, C.E. (2011). Molecular diagnosis for heterogeneous genetic diseases with targeted high-throughput DNA sequencing applied to retinitis pigmentosa. *J. Med. Genet.* 48, 145–151.
33. Eisenberger, T., Neuhaus, C., Khan, A.O., Decker, C., Preising, M.N., Friedburg, C., Bieg, A., Gliem, M., Charbel Issa, P., Holz, F.G., et al. (2013). Increasing the yield in targeted next-generation sequencing by implicating CNV analysis, non-coding exons and the overall variant load: The example of retinal dystrophies. *PLoS One* 8, e78496.
34. Consugar, M.B., Navarro-Gomez, D., Place, E.M., Bujakowska, K.M., Sousa, M.E., Fonseca-Kelly, Z.D.Z.D., Taub, D.G., Janessian, M., Wang, D.Y., Au, E.D., et al. (2015). Panel-based genetic diagnostic testing for inherited eye diseases is highly accurate and reproducible, and more sensitive for variant detection, than exome sequencing. *Genet. Med.* 17, 253–261.
35. Eksandh, L., Ekström, U., Abrahamson, M., Bauer, B., and Andréasson, S. (2001). Different clinical expressions in two families with Stargardt’s macular dystrophy (STGD1). *Acta Ophthalmol. Scand.* 79, 524–530.
36. Hichri, H., Stoetzel, C., Laurier, V., Caron, S., Sigaudy, S., Sarda, P., Hamel, C., Martin-Coignard, D., Gilles, M., Leheup, B., et al. (2005). Testing for triallelism: analysis of six BBS genes in a Bardet-Biedl syndrome family cohort. *Eur. J. Hum. Genet.* 13, 607–616.
37. Sundin, O.H., Yang, J.M., Li, Y., Zhu, D., Hurd, J.N., Mitchell, T.N., Silva, E.D., and Maumenee, I.H. (2000). Genetic basis of total colourblindness among the Pingelapese islanders. *Nat. Genet.* 25, 289–293.

38. Dreyer, B., Brox, V., Tranebjaerg, L., Rosenberg, T., Sadeghi, A.M., Möller, C., and Nilssen, O. (2008). Spectrum of USH2A mutations in Scandinavian patients with Usher syndrome type II. *Hum. Mutat.* 29, 451.
39. Le Quesne Stabej, P., Saihan, Z., Rangesh, N., Steele-Stallard, H.B., Ambrose, J., Coffey, A., Emmerson, J., Haralambous, E., Hughes, Y., Steel, K.P., et al. (2012). Comprehensive sequence analysis of nine Usher syndrome genes in the UK National Collaborative Usher Study. *J. Med. Genet.* 49, 27–36.
40. Chiang, P.-W., Wang, J., Chen, Y., Fu, Q., Zhong, J., Chen, Y., Yi, X., Wu, R., Gan, H., Shi, Y., et al. (2012). Exome sequencing identifies NMNAT1 mutations as a cause of Leber congenital amaurosis. *Nat. Genet.* 44, 972–974.
41. Nishimura, D.Y., Baye, L.M., Perveen, R., Searby, C.C., Avila-Fernandez, A., Pereiro, I., Ayuso, C., Valverde, D., Bishop, P.N., Manson, F.D.C., et al. (2010). Discovery and functional analysis of a retinitis pigmentosa gene, C2ORF71. *Am. J. Hum. Genet.* 86, 686–695.
42. Klevering, B.J., Deutman, A.F., Maugeri, A., Cremers, F.P.M., and Hoyng, C.B. (2005). The spectrum of retinal phenotypes caused by mutations in the ABCA4 gene. *Graefes Arch. Clin. Exp. Ophthalmol. = Albr. von Graefes Arch. Für Klin. Und Exp. Ophthalmol.* 243, 90–100.
43. Fujinami, K., Zernant, J., Chana, R.K., Wright, G.A., Tsunoda, K., Ozawa, Y., Tsubota, K., Webster, A.R., Moore, A.T., Allikmets, R., et al. (2013). ABCA4 gene screening by next-generation sequencing in a British cohort. *Invest. Ophthalmol. Vis. Sci.* 54, 6662–6674.
44. McGee, T.L., Seyedahmadi, B.J., Sweeney, M.O., Dryja, T.P., and Berson, E.L. (2010). Novel mutations in the long isoform of the USH2A gene in patients with Usher syndrome type II or non-syndromic retinitis pigmentosa. *J. Med. Genet.* 47, 499–506.
45. Corton, M., Nishiguchi, K.M., Avila-Fernández, A., Nikopoulos, K., Riveiro-Alvarez, R., Tatu, S.D., Ayuso, C., and Rivolta, C. (2013). Exome sequencing of index patients with retinal dystrophies as a tool for molecular diagnosis. *PLoS One* 8, e65574.
46. Audo, I., Bujakowska, K., Orhan, E., Poloschek, C.M., Defoort-Dhellemmes, S., Drumare, I., Kohl, S., Luu, T.D., Lecompte, O., Zrenner, E., et al. (2012). Whole-exome sequencing identifies mutations in GPR179 leading to autosomal-recessive complete congenital stationary night blindness. *Am. J. Hum. Genet.* 90, 321–330.
47. Reuter, P., Koeppen, K., Ladewig, T., Kohl, S., Baumann, B., Wissinger, B., and Achromatopsia Clinical Study Group (2008). Mutations in CNGA3 impair trafficking or function of cone cyclic nucleotide-gated channels, resulting in achromatopsia. *Hum. Mutat.* 29, 1228–1236.
48. den Hollander, A.I., ten Brink, J.B., de Kok, Y.J., van Soest, S., van den Born, L.I., van Driel, M.A., van de Pol, D.J., Payne, A.M., Bhattacharya, S.S., Kellner, U., et al. (1999). Mutations in a human homologue of *Drosophila* crumbs cause retinitis pigmentosa (RP12). *Nat. Genet.* 23, 217–221.
49. Clark, G.R., Crowe, P., Muszynska, D., O'Prey, D., O'Neill, J., Alexander, S., Willoughby, C.E., McKay, G.J., Silvestri, G., and Simpson, D.A. (2010). Development of a diagnostic genetic test for simplex and autosomal recessive retinitis pigmentosa. *Ophthalmology* 117, 2169–2177.e3.
50. McLaughlin, M.E., Ehrhart, T.L., Berson, E.L., and Dryja, T.P. (1995). Mutation spectrum of the gene encoding the beta subunit of rod phosphodiesterase among patients with autosomal recessive retinitis pigmentosa. *Proc. Natl. Acad. Sci. U. S. A.* 92, 3249–3253.
51. Nakanishi, H., Ohtsubo, M., Iwasaki, S., Hotta, Y., Usami, S.-I., Mizuta, K., Mineta, H., and Minoshima, S. (2011). Novel USH2A mutations in Japanese Usher syndrome type 2 patients: marked differences in the mutation spectrum between the Japanese and other populations. *J. Hum. Genet.* 56, 484–490.
52. Seyedahmadi, B.J., Rivolta, C., Keene, J.A., Berson, E.L., and Dryja, T.P. (2004). Comprehensive screening of the USH2A gene in Usher syndrome type II and non-syndromic recessive retinitis pigmentosa. *Exp. Eye Res.* 79, 167–173.
53. Neidhardt, J., Glaus, E., Lorenz, B., Netzer, C., Li, Y., Schambeck, M., Wittmer, M., Feil, S., Kirschner-Schwabe, R., Rosenberg, T., et al. (2008). Identification of novel mutations in

- X-linked retinitis pigmentosa families and implications for diagnostic testing. *Mol. Vis.* 14, 1081–1093.
54. Bharadwaj, A.K., Kasztejna, J.P., Huq, S., Berson, E.L., and Dryja, T.P. (2000). Evaluation of the myosin VIIA gene and visual function in patients with Usher syndrome type I. *Exp. Eye Res.* 71, 173–181.
55. Liu, X.Z., Hope, C., Walsh, J., Newton, V., Ke, X.M., Liang, C.Y., Xu, L.R., Zhou, J.M., Trump, D., Steel, K.P., et al. (1998). Mutations in the myosin VIIA gene cause a wide phenotypic spectrum, including atypical Usher syndrome. *Am. J. Hum. Genet.* 63, 909–912.
56. Bitner-Glindzicz, M., Lindley, K.J., Rutland, P., Blaydon, D., Smith, V. V., Milla, P.J., Hussain, K., Furth-Lavi, J., Cosgrove, K.E., Shepherd, R.M., et al. (2000). A recessive contiguous gene deletion causing infantile hyperinsulinism, enteropathy and deafness identifies the Usher type 1C gene. *Nat. Genet.* 26, 56–60.
57. Riazuddin, S., Nazli, S., Ahmed, Z.M., Yang, Y., Zulfiqar, F., Shaikh, R.S., Zafar, A.U., Khan, S.N., Sabar, F., Javid, F.T., et al. (2008). Mutation spectrum of MYO7A and evaluation of a novel nonsyndromic deafness DFNB2 allele with residual function. *Hum. Mutat.* 29, 502–511.
58. Ebermann, I., Koenekoop, R.K., Lopez, I., Bou-Khzam, L., Pigeon, R., and Bolz, H.J. (2009). An USH2A founder mutation is the major cause of Usher syndrome type 2 in Canadians of French origin and confirms common roots of Quebecois and Acadians. *Eur. J. Hum. Genet.* 17, 80–84.
59. Baux, D., Larrieu, L., Blanchet, C., Hamel, C., Ben Salah, S., Vielle, A., Gilbert-Dussardier, B., Holder, M., Calvas, P., Philip, N., et al. (2007). Molecular and in silico analyses of the full-length isoform of usherin identify new pathogenic alleles in Usher type II patients. *Hum. Mutat.* 28, 781–789.
60. Vaché, C., Besnard, T., le Berre, P., García-García, G., Baux, D., Larrieu, L., Abadie, C., Blanchet, C., Bolz, H.J., Millan, J., et al. (2012). Usher syndrome type 2 caused by activation of an USH2A pseudoexon: implications for diagnosis and therapy. *Hum. Mutat.* 33, 104–108.
61. Payne, A.M., Morris, A.G., Downes, S.M., Johnson, S., Bird, A.C., Moore, A.T., Bhattacharya, S.S., and Hunt, D.M. (2001). Clustering and frequency of mutations in the retinal guanylate cyclase (GUCY2D) gene in patients with dominant cone-rod dystrophies. *J. Med. Genet.* 38, 611–614.
62. Bandah-Rozenfeld, D., Collin, R.W.J., Banin, E., van den Born, L.I., Coene, K.L.M., Siemiatkowska, A.M., Zelinger, L., Khan, M.I., Lefeber, D.J., Erdinest, I., et al. (2010). Mutations in IMPG2, encoding interphotoreceptor matrix proteoglycan 2, cause autosomal-recessive retinitis pigmentosa. *Am. J. Hum. Genet.* 87, 199–208.
63. Li, J.B., Gerdes, J.M., Haycraft, C.J., Fan, Y., Teslovich, T.M., May-Simera, H., Li, H., Blacque, O.E., Li, L., Leitch, C.C., et al. (2004). Comparative genomics identifies a flagellar and basal body proteome that includes the BBS5 human disease gene. *Cell* 117, 541–552.
64. Littink, K.W., van den Born, L.I., Koenekoop, R.K., Collin, R.W.J., Zonneveld, M.N., Blokland, E.A.W., Khan, H., Theelen, T., Hoyng, C.B., Cremers, F.P.M., et al. (2010). Mutations in the EYS gene account for approximately 5% of autosomal recessive retinitis pigmentosa and cause a fairly homogeneous phenotype. *Ophthalmology* 117, 2026–2033, 2033.e1–e7.
65. Zhao, C., Bellur, D.L., Lu, S., Zhao, F., Grassi, M.A., Bowne, S.J., Sullivan, L.S., Daiger, S.P., Chen, L.J., Pang, C.P., et al. (2009). Autosomal-dominant retinitis pigmentosa caused by a mutation in SNRNP200, a gene required for unwinding of U4/U6 snRNAs. *Am. J. Hum. Genet.* 85, 617–627.
66. McHenry, C.L., Liu, Y., Feng, W., Nair, A.R., Feathers, K.L., Ding, X., Gal, A., Vollrath, D., Sieving, P.A., and Thompson, D.A. (2004). MERTK arginine-844-cysteine in a patient with severe rod-cone dystrophy: loss of mutant protein function in transfected cells. *Invest. Ophthalmol. Vis. Sci.* 45, 1456–1463.
67. Stone, E.M., Cideciyan, A. V, Aleman, T.S., Scheetz, T.E., Sumaroka, A., Ehlinger, M.A., Schwartz, S.B., Fishman, G.A., Traboulsi, E.I., Lam, B.L., et al. (2011). Variations in NPHP5 in patients with nonsyndromic leber congenital amaurosis and Senior-Loken syndrome. *Arch. Ophthalmol.* (Chicago, Ill. 1960) 129, 81–87.

68. Ávila-Fernández, A., Cantalapiedra, D., Aller, E., Vallespín, E., Aguirre-Lambán, J., Blanco-Kelly, F., Corton, M., Riveiro-Álvarez, R., Allikmets, R., Trujillo-Tiebas, M.J., et al. (2010). Mutation analysis of 272 Spanish families affected by autosomal recessive retinitis pigmentosa using a genotyping microarray. *Mol. Vis.* 16, 2550–2558.
69. Halford, S., Liew, G., Mackay, D.S., Sergouniotis, P.I., Holt, R., Broadgate, S., Volpi, E. V., Ocaka, L., Robson, A.G., Holder, G.E., et al. (2014). Detailed phenotypic and genotypic characterization of bietti crystalline dystrophy. *Ophthalmology* 121, 1174–1184.
70. Henderson, R.H., Li, Z., Abd El Aziz, M.M., Mackay, D.S., Eljinini, M.A., Zeidan, M., Moore, A.T., Bhattacharya, S.S., and Webster, A.R. (2010). Biallelic mutation of protocadherin-21 (PCDH21) causes retinal degeneration in humans. *Mol. Vis.* 16, 46–52.
71. Ducroq, D., Rozet, J.-M., Gerber, S., Perrault, I., Barbet, D., Hanein, S., Hakiki, S., Dufier, J.-L., Munnich, A., Hamel, C., et al. (2002). The ABCA4 gene in autosomal recessive cone-rod dystrophies. *Am. J. Hum. Genet.* 71, 1480–1482.
72. Zeitz, C., Robson, A.G., and Audo, I. (2015). Congenital stationary night blindness: an analysis and update of genotype-phenotype correlations and pathogenic mechanisms. *Prog. Retin. Eye Res.* 45, 58–110.
73. Morimura, H., Berson, E.L., and Dryja, T.P. (1999). Recessive mutations in the RLBP1 gene encoding cellular retinaldehyde-binding protein in a form of retinitis punctata albescens. *Invest. Ophthalmol. Vis. Sci.* 40, 1000–1004.
74. Valente, E.M., Silhavy, J.L., Brancati, F., Barrano, G., Krishnaswami, S.R., Castori, M., Lancaster, M.A., Boltshauser, E., Boccone, L., Al-Gazali, L., et al. (2006). Mutations in CEP290, which encodes a centrosomal protein, cause pleiotropic forms of Joubert syndrome. *Nat. Genet.* 38, 623–625.
75. Brancati, F., Barrano, G., Silhavy, J.L., Marsh, S.E., Travaglini, L., Bielas, S.L., Amorini, M., Zablocka, D., Kayserili, H., Al-Gazali, L., et al. (2007). CEP290 mutations are frequently identified in the oculo-renal form of Joubert syndrome-related disorders. *Am. J. Hum. Genet.* 81, 104–113.
76. Rivolta, C., Sweklo, E.A., Berson, E.L., and Dryja, T.P. (2000). Missense mutation in the USH2A gene: association with recessive retinitis pigmentosa without hearing loss. *Am. J. Hum. Genet.* 66, 1975–1978.
77. Morimura, H., Saindelle-Ribeau, F., Berson, E.L., and Dryja, T.P. (1999). Mutations in RGR, encoding a light-sensitive opsin homologue, in patients with retinitis pigmentosa. *Nat. Genet.* 23, 393–394.
78. Salvo, J., Lyubasyuk, V., Xu, M., Wang, H., Wang, F., Nguyen, D., Wang, K., Luo, H., Wen, C., Shi, C., et al. (2015). Next-generation sequencing and novel variant determination in a cohort of 92 familial exudative vitreoretinopathy patients. *Invest. Ophthalmol. Vis. Sci.* 56, 1937–1946.
79. Duno, M., Schwartz, M., Larsen, P.L., and Rosenberg, T. (2012). Phenotypic and genetic spectrum of Danish patients with ABCA4-related retinopathy. *Ophthalmic Genet.* 33, 225–231.
80. Rivera, A., White, K., Stöhr, H., Steiner, K., Hemmrich, N., Grimm, T., Jurklies, B., Lorenz, B., Scholl, H.P., Apfelstedt-Sylla, E., et al. (2000). A comprehensive survey of sequence variation in the ABCA4 (ABCR) gene in Stargardt disease and age-related macular degeneration. *Am. J. Hum. Genet.* 67, 800–813.
81. Stoetzel, C., Laurier, V., Davis, E.E., Muller, J., Rix, S., Badano, J.L., Leitch, C.C., Salem, N., Chouery, E., Corbani, S., et al. (2006). BBS10 encodes a vertebrate-specific chaperonin-like protein and is a major BBS locus. *Nat. Genet.* 38, 521–524.
82. Sohocki, M.M., Daiger, S.P., Bowne, S.J., Rodriguez, J.A., Northrup, H., Heckenlively, J.R., Birch, D.G., Mintz-Hittner, H., Ruiz, R.S., Lewis, R.A., et al. (2001). Prevalence of mutations causing retinitis pigmentosa and other inherited retinopathies. *Hum. Mutat.* 17, 42–51.
83. Webster, A.R., Héon, E., Lotery, A.J., Vandenberg, K., Casavant, T.L., Oh, K.T., Beck, G., Fishman, G.A., Lam, B.L., Levin, A., et al. (2001). An analysis of allelic variation in the ABCA4 gene. *Invest. Ophthalmol. Vis. Sci.* 42, 1179–1189.

84. Zeitz, C., van Genderen, M., Neidhardt, J., Luhmann, U.F.O., Hoeben, F., Forster, U., Wycisk, K., Mátyás, G., Hoyng, C.B., Riemsdag, F., et al. (2005). Mutations in GRM6 cause autosomal recessive congenital stationary night blindness with a distinctive scotopic 15-Hz flicker electroretinogram. *Invest. Ophthalmol. Vis. Sci.* 46, 4328–4335.
85. Schiaffino, M. V., Bassi, M.T., Galli, L., Renieri, A., Bruttini, M., De Nigris, F., Bergen, A.A., Charles, S.J., Yates, J.R., and Meindl, A. (1995). Analysis of the OA1 gene reveals mutations in only one-third of patients with X-linked ocular albinism. *Hum. Mol. Genet.* 4, 2319–2325.
86. Zernant, J., Collison, F.T., Lee, W., Fishman, G.A., Noupou, K., Yuan, B., Cai, C., Lupski, J.R., Yannuzzi, L.A., Tsang, S.H., et al. (2014). Genetic and clinical analysis of ABCA4-associated disease in African American patients. *Hum. Mutat.* 35, 1187–1194.
87. Strom, T.M., Nyakatura, G., Apfelstedt-Sylla, E., Hellebrand, H., Lorenz, B., Weber, B.H., Wutz, K., Gutwillinger, N., Rütger, K., Drescher, B., et al. (1998). An L-type calcium-channel gene mutated in incomplete X-linked congenital stationary night blindness. *Nat. Genet.* 19, 260–263.
88. Boycott, K.M., Maybaum, T.A., Naylor, M.J., Weleber, R.G., Robitaille, J., Miyake, Y., Bergen, A.A., Pierpont, M.E., Pearce, W.G., and Bech-Hansen, N.T. (2001). A summary of 20 CACNA1F mutations identified in 36 families with incomplete X-linked congenital stationary night blindness, and characterization of splice variants. *Hum. Genet.* 108, 91–97.
89. Pozo, M.G.-D., Bravo-Gil, N., Méndez-Vidal, C., Montero-de-Espinosa, I., Millán, J.M., Dopazo, J., Borrego, S., and Antiñolo, G. (2015). Re-evaluation casts doubt on the pathogenicity of homozygous USH2A p.C759F. *Am. J. Med. Genet. A* 167, 1597–1600.
90. Janecke, A.R., Meins, M., Sadeghi, M., Grundmann, K., Apfelstedt-Sylla, E., Zrenner, E., Rosenberg, T., and Gal, A. (1999). Twelve novel myosin VIIA mutations in 34 patients with Usher syndrome type I: confirmation of genetic heterogeneity. *Hum. Mutat.* 13, 133–140.
91. Jaijo, T., Aller, E., Beneyto, M., Najera, C., Graziano, C., Turchetti, D., Seri, M., Ayuso, C., Baiget, M., Moreno, F., et al. (2007). MYO7A mutation screening in Usher syndrome type I patients from diverse origins. *J. Med. Genet.* 44, e71.
92. Mears, A.J., Gieser, L., Yan, D., Chen, C., Fahrner, S., Hiriyanna, S., Fujita, R., Jacobson, S.G., Sieving, P.A., and Swaroop, A. (1999). Protein-truncation mutations in the RP2 gene in a North American cohort of families with X-linked retinitis pigmentosa. *Am. J. Hum. Genet.* 64, 897–900.
93. Neveling, K., Collin, R.W.J., Gilissen, C., van Huet, R.A.C., Visser, L., Kwint, M.P., Gijzen, S.J., Zonneveld, M.N., Wieskamp, N., de Ligt, J., et al. (2012). Next-generation genetic testing for retinitis pigmentosa. *Hum. Mutat.* 33, 963–972.
94. Vallespin, E., Cantalapiedra, D., Garcia-Hoyos, M., Riveiro, R., Villaverde, C., Trujillo-Tiebas, M.J., and Ayuso, C. (2006). Gene symbol: CRB1. Disease: Leber congenital amaurosis. Accession #Hd0510. *Hum. Genet.* 118, 774.
95. Hanein, S., Perrault, I., Gerber, S., Tanguy, G., Barbet, F., Ducroq, D., Calvas, P., Dollfus, H., Hamel, C., Lopponen, T., et al. (2004). Leber congenital amaurosis: comprehensive survey of the genetic heterogeneity, refinement of the clinical definition, and genotype-phenotype correlations as a strategy for molecular diagnosis. *Hum. Mutat.* 23, 306–317.
96. Otto, E.A., Loeys, B., Khanna, H., Hellemans, J., Sudbrak, R., Fan, S., Muerb, U., O’Toole, J.F., Helou, J., Attanasio, M., et al. (2005). Nephrocystin-5, a ciliary IQ domain protein, is mutated in Senior-Loken syndrome and interacts with RPGR and calmodulin. *Nat. Genet.* 37, 282–288.
97. Al-Magthteh, M., Gregory, C., Inglehearn, C., Hardcastle, A., and Bhattacharya, S. (1993). Rhodopsin mutations in autosomal dominant retinitis pigmentosa. *Hum. Mutat.* 2, 249–255.
98. Dryja, T.P., Hahn, L.B., Cowley, G.S., McGee, T.L., and Berson, E.L. (1991). Mutation spectrum of the rhodopsin gene among patients with autosomal dominant retinitis pigmentosa. *Proc. Natl. Acad. Sci. U. S. A.* 88, 9370–9374.

99. Bowne, S.J., Sullivan, L.S., Gire, A.I., Birch, D.G., Hughbanks-Wheaton, D., Heckenlively, J.R., and Daiger, S.P. (2008). Mutations in the TOPORS gene cause 1% of autosomal dominant retinitis pigmentosa. *Mol. Vis.* 14, 922–927.
100. Azam, M., Collin, R.W.J., Malik, A., Khan, M.I., Shah, S.T.A., Shah, A.A., Hussain, A., Sadeque, A., Arimadyo, K., Ajmal, M., et al. (2011). Identification of novel mutations in Pakistani families with autosomal recessive retinitis pigmentosa. *Arch. Ophthalmol.* (Chicago, Ill. 1960) 129, 1377–1378.
101. Weston, M.D., Luijendijk, M.W.J., Humphrey, K.D., Möller, C., and Kimberling, W.J. (2004). Mutations in the VLGR1 gene implicate G-protein signaling in the pathogenesis of Usher syndrome type II. *Am. J. Hum. Genet.* 74, 357–366.
102. Payne, A.M., Downes, S.M., Bessant, D.A., Taylor, R., Holder, G.E., Warren, M.J., Bird, A.C., and Bhattacharya, S.S. (1998). A mutation in guanylate cyclase activator 1A (GUCA1A) in an autosomal dominant cone dystrophy pedigree mapping to a new locus on chromosome 6p21.1. *Hum. Mol. Genet.* 7, 273–277.
103. Wissinger, B., Schaich, S., Baumann, B., Bonin, M., Jägle, H., Friedburg, C., Varsányi, B., Hoyng, C.B., Dollfus, H., Heckenlively, J.R., et al. (2011). Large deletions of the KCNV2 gene are common in patients with cone dystrophy with supernormal rod response. *Hum. Mutat.* 32, 1398–1406.
104. Le Saux, O., Beck, K., Sachsinger, C., Silvestri, C., Treiber, C., Göring, H.H.H., Johnson, E.W., De Paepe, A., Pope, F.M., Pasquali-Ronchetti, I., et al. (2001). A Spectrum of ABCC6 Mutations Is Responsible for Pseudoxanthoma Elasticum. *Am. J. Hum. Genet.* 69, 749–764.
105. Hu, X., Plomp, A., Wijnholds, J., Ten Brink, J., van Soest, S., van den Born, L.I., Leys, A., Peek, R., de Jong, P.T.V.M., and Bergen, A.A.B. (2003). ABCC6/MRP6 mutations: further insight into the molecular pathology of pseudoxanthoma elasticum. *Eur. J. Hum. Genet.* 11, 215–224.
106. Allikmets, R., Singh, N., Sun, H., Shroyer, N.F., Hutchinson, A., Chidambaram, A., Gerrard, B., Baird, L., Stauffer, D., Peiffer, A., et al. (1997). A photoreceptor cell-specific ATP-binding transporter gene (ABCR) is mutated in recessive Stargardt macular dystrophy. *Nat. Genet.* 15, 236–246.
107. Patiño, L.C., Battu, R., Ortega-Recalde, O., Nallathambi, J., Anandula, V.R., Renukaradhya, U., and Laissue, P. (2014). Exome sequencing is an efficient tool for variant late-infantile neuronal ceroid lipofuscinosis molecular diagnosis. *PLoS One* 9, e109576.
108. Liu, X., Xiao, J., Huang, H., Guan, L., Zhao, K., Xu, Q., Zhang, X., Pan, X., Gu, S., Chen, Y., et al. (2015). Molecular genetic testing in clinical diagnostic assessments that demonstrate correlations in patients with autosomal recessive inherited retinal dystrophy. *JAMA Ophthalmol.* 133, 427–436.
109. Beryozkin, A., Shevah, E., Kimchi, A., Mizrahi-Meissonnier, L., Khateb, S., Ratnapriya, R., Lazar, C.H., Blumenfeld, A., Ben-Yosef, T., Hemo, Y., et al. (2015). Whole Exome Sequencing Reveals Mutations in Known Retinal Disease Genes in 33 out of 68 Israeli Families with Inherited Retinopathies. *Sci. Rep.* 5, 13187.
110. Vozzi, D., Aaspöllu, A., Athanasakis, E., Berto, A., Fabretto, A., Licastro, D., Külm, M., Testa, F., Trevisi, P., Vahter, M., et al. (2011). Molecular epidemiology of Usher syndrome in Italy. *Mol. Vis.* 17, 1662–1668.
111. Briggs, C.E., Rucinski, D., Rosenfeld, P.J., Hirose, T., Berson, E.L., and Dryja, T.P. (2001). Mutations in ABCR (ABCA4) in patients with Stargardt macular degeneration or cone-rod degeneration. *Invest. Ophthalmol. Vis. Sci.* 42, 2229–2236.
112. Toomes, C., Bottomley, H.M., Jackson, R.M., Towns, K. V., Scott, S., Mackey, D.A., Craig, J.E., Jiang, L., Yang, Z., Trembath, R., et al. (2004). Mutations in LRP5 or FZD4 underlie the common familial exudative vitreoretinopathy locus on chromosome 11q. *Am. J. Hum. Genet.* 74, 721–730.
113. Rosenberg, T., Klie, F., Garred, P., and Schwartz, M. (2007). N965S is a common ABCA4 variant in Stargardt-related retinopathies in the Danish population. *Mol. Vis.* 13, 1962–1969.

114. Gamundi, M.J., Hernan, I., Martínez-Gimeno, M., Maseras, M., García-Sandoval, B., Ayuso, C., Antiñolo, G., Baiget, M., and Carballo, M. (2006). Three novel and the common Arg677Ter RP1 protein truncating mutations causing autosomal dominant retinitis pigmentosa in a Spanish population. *BMC Med. Genet.* 7, 35.
115. Boissy, R.E., Zhao, H., Oetting, W.S., Austin, L.M., Wildenberg, S.C., Boissy, Y.L., Zhao, Y., Sturm, R.A., Hearing, V.J., King, R.A., et al. (1996). Mutation in and lack of expression of tyrosinase-related protein-1 (TRP-1) in melanocytes from an individual with brown oculocutaneous albinism: a new subtype of albinism classified as "OCA3". *Am. J. Hum. Genet.* 58, 1145–1156.
116. Rozet, J.M., Gerber, S., Ghazi, I., Perrault, I., Ducroq, D., Souied, E., Cabot, A., Dufier, J.L., Munnich, A., and Kaplan, J. (1999). Mutations of the retinal specific ATP binding transporter gene (ABCR) in a single family segregating both autosomal recessive retinitis pigmentosa RP19 and Stargardt disease: evidence of clinical heterogeneity at this locus. *J. Med. Genet.* 36, 447–451.
117. McLaughlin, M.E., Sandberg, M.A., Berson, E.L., and Dryja, T.P. (1993). Recessive mutations in the gene encoding the beta-subunit of rod phosphodiesterase in patients with retinitis pigmentosa. *Nat. Genet.* 4, 130–134.
118. Chen, X., Sheng, X., Liu, X., Li, H., Liu, Y., Rong, W., Ha, S., Liu, W., Kang, X., Zhao, K., et al. (2014). Targeted next-generation sequencing reveals novel USH2A mutations associated with diverse disease phenotypes: implications for clinical and molecular diagnosis. *PLoS One* 9, e105439.
119. Xu, W., Dai, H., Lu, T., Zhang, X., Dong, B., and Li, Y. (2011). Seven novel mutations in the long isoform of the USH2A gene in Chinese families with nonsyndromic retinitis pigmentosa and Usher syndrome Type II. *Mol. Vis.* 17, 1537–1552.
120. Bader, I., Brandau, O., Achatz, H., Apfelstedt-Sylla, E., Hergersberg, M., Lorenz, B., Wissinger, B., Wittwer, B., Rudolph, G., Meindl, A., et al. (2003). X-linked retinitis pigmentosa: RPGR mutations in most families with definite X linkage and clustering of mutations in a short sequence stretch of exon ORF15. *Invest. Ophthalmol. Vis. Sci.* 44, 1458–1463.
121. Payne, A., Vithana, E., Khaliq, S., Hameed, A., Deller, J., Abu-Safieh, L., Kermani, S., Leroy, B.P., Mehdi, S.Q., Moore, A.T., et al. (2000). RP1 protein truncating mutations predominate at the RP1 adRP locus. *Invest. Ophthalmol. Vis. Sci.* 41, 4069–4073.
122. Janecke, A.R., Thompson, D.A., Utermann, G., Becker, C., Hübner, C.A., Schmid, E., McHenry, C.L., Nair, A.R., Rüschenhoff, F., Heckenlively, J., et al. (2004). Mutations in RDH12 encoding a photoreceptor cell retinol dehydrogenase cause childhood-onset severe retinal dystrophy. *Nat. Genet.* 36, 850–854.
123. Bonilha, V.L., Rayborn, M.E., Bell, B.A., Marino, M.J., Pauer, G.J., Beight, C.D., Chiang, J., Traboulsi, E.I., Hollyfield, J.G., and Hagstrom, S.A. (2015). Histopathological comparison of eyes from patients with autosomal recessive retinitis pigmentosa caused by novel EYS mutations. *Graefes Arch. Clin. Exp. Ophthalmol. = Albr. von Graefes Arch. Für Klin. Und Exp. Ophthalmol.* 253, 295–305.
124. Hřebíček, M., Mrázová, L., Seyrantepe, V., Durand, S., Roslin, N.M., Nosková, L., Hartmannová, H., Ivánek, R., Cízková, A., Poupětová, H., et al. (2006). Mutations in TMEM76* cause mucopolysaccharidosis IIIC (Sanfilippo C syndrome). *Am. J. Hum. Genet.* 79, 807–819.
125. Wissinger, B., Gamer, D., Jägle, H., Giorda, R., Marx, T., Mayer, S., Tippmann, S., Brogghammer, M., Jurklics, B., Rosenberg, T., et al. (2001). CNGA3 mutations in hereditary cone photoreceptor disorders. *Am. J. Hum. Genet.* 69, 722–737.
126. Inglehearn, C.F., Keen, T.J., Bashir, R., Jay, M., Fitzke, F., Bird, A.C., Crombie, A., and Bhattacharya, S. (1992). A completed screen for mutations of the rhodopsin gene in a panel of patients with autosomal dominant retinitis pigmentosa. *Hum. Mol. Genet.* 1, 41–45.
127. Li, Z., Sergouniotis, P.I., Michaelides, M., Mackay, D.S., Wright, G.A., Devery, S., Moore, A.T., Holder, G.E., Robson, A.G., and Webster, A.R. (2009). Recessive mutations of the gene TRPM1 abrogate ON bipolar cell function and cause complete congenital stationary night blindness in humans. *Am. J. Hum. Genet.* 85, 711–719.

128. Farrar, G.J., Kenna, P., Jordan, S.A., Kumar-Singh, R., Humphries, M.M., Sharp, E.M., Sheils, D., and Humphries, P. (1992). Autosomal dominant retinitis pigmentosa: a novel mutation at the peripherin/RDS locus in the original 6p-linked pedigree. *Genomics* 14, 805–807.
129. Watson, C.M., El-Asrag, M., Parry, D.A., Morgan, J.E., Logan, C. V, Carr, I.M., Sheridan, E., Charlton, R., Johnson, C.A., Taylor, G., et al. (2014). Mutation screening of retinal dystrophy patients by targeted capture from tagged pooled DNAs and next generation sequencing. *PLoS One* 9, e104281.
130. Cremers, F.P., van de Pol, D.J., van Driel, M., den Hollander, A.I., van Haren, F.J., Knoers, N. V, Tijmes, N., Bergen, A.A., Rohrschneider, K., Blankenagel, A., et al. (1998). Autosomal recessive retinitis pigmentosa and cone-rod dystrophy caused by splice site mutations in the Stargardt's disease gene ABCR. *Hum. Mol. Genet.* 7, 355–362.
131. Audo, I., Lancelot, M.-E., Mohand-Saïd, S., Antonio, A., Germain, A., Sahel, J.-A., Bhattacharya, S.S., and Zeitz, C. (2011). Novel C2orf71 mutations account for ~1% of cases in a large French arRP cohort. *Hum. Mutat.* 32, E2091–E2103.
132. Boon, C.J.F., van den Born, L.I., Visser, L., Keunen, J.E.E., Bergen, A.A.B., Booij, J.C., Riemsdijk, F.C., Florijn, R.J., and van Schooneveld, M.J. (2013). Autosomal recessive bestrophinopathy: differential diagnosis and treatment options. *Ophthalmology* 120, 809–820.
133. Yatsenko, A.N., Shroyer, N.F., Lewis, R.A., and Lupski, J.R. (2001). Late-onset Stargardt disease is associated with missense mutations that map outside known functional regions of ABCR (ABCA4). *Hum. Genet.* 108, 346–355.
134. Zhao, L., Wang, F., Wang, H., Li, Y., Alexander, S., Wang, K., Willoughby, C.E., Zaneveld, J.E., Jiang, L., Soens, Z.T., et al. (2015). Next-generation sequencing-based molecular diagnosis of 82 retinitis pigmentosa probands from Northern Ireland. *Hum. Genet.* 134, 217–230.
135. Miyagawa, M., Naito, T., Nishio, S., Kamatani, N., and Usami, S. (2013). Targeted exon sequencing successfully discovers rare causative genes and clarifies the molecular epidemiology of Japanese deafness patients. *PLoS One* 8, e71381.
136. Giebel, L.B., Strunk, K.M., King, R.A., Hanifin, J.M., and Spritz, R.A. (1990). A frequent tyrosinase gene mutation in classic, tyrosinase-negative (type IA) oculocutaneous albinism. *Proc. Natl. Acad. Sci. U. S. A.* 87, 3255–3258.
137. King, R.A., Pietsch, J., Fryer, J.P., Savage, S., Brott, M.J., Russell-Eggitt, I., Summers, C.G., and Oetting, W.S. (2003). Tyrosinase gene mutations in oculocutaneous albinism 1 (OCA1): definition of the phenotype. *Hum. Genet.* 113, 502–513.
138. Bowne, S.J., Daiger, S.P., Hims, M.M., Sohocki, M.M., Malone, K.A., McKie, A.B., Heckenlively, J.R., Birch, D.G., Inglehearn, C.F., Bhattacharya, S.S., et al. (1999). Mutations in the RP1 gene causing autosomal dominant retinitis pigmentosa. *Hum. Mol. Genet.* 8, 2121–2128.
139. Fishman, G.A., Stone, E.M., Grover, S., Derlacki, D.J., Haines, H.L., and Hockey, R.R. (1999). Variation of clinical expression in patients with Stargardt dystrophy and sequence variations in the ABCR gene. *Arch. Ophthalmol. (Chicago, Ill. 1960)* 117, 504–510.
140. Fujinami, K., Lois, N., Davidson, A.E., Mackay, D.S., Hogg, C.R., Stone, E.M., Tsunoda, K., Tsubota, K., Bunce, C., Robson, A.G., et al. (2013). A longitudinal study of stargardt disease: clinical and electrophysiologic assessment, progression, and genotype correlations. *Am. J. Ophthalmol.* 155, 1075–1088.e13.
141. Ba-Abbad, R., Robson, A.G., Yap, Y.C., Moore, A.T., Webster, A.R., and Holder, G.E. (2014). Prph2 mutations as a cause of electronegative ERG. *Retina* 34, 1235–1243.
142. Braun, T. a., Mullins, R.F., Wagner, A.H., Andorf, J.L., Johnston, R.M., Bakall, B.B., Deluca, A.P., Fishman, G. a., Lam, B.L., Weleber, R.G., et al. (2013). Non-exonic and synonymous variants in ABCA4 are an important cause of Stargardt disease. *Hum. Mol. Genet.* 22, 5136–5145.
143. Dreyer, B., Tranebjaerg, L., Rosenberg, T., Weston, M.D., Kimberling, W.J., and Nilssen, O. (2000). Identification of novel USH2A mutations: implications for the structure of USH2A protein. *Eur. J. Hum. Genet.* 8, 500–506.

144. Aguirre, J., Riveiro-Alvarez, R., Cantalapiedra, D., Vallespin, E., Avila-Fernandez, A., Trujillo-Tiebas, M.J., Villaverde-Montero, C., and Ayuso, C. (2008). Gene symbol: ABCA4. Disease: Macular dystrophy. *Hum. Genet.* 123, 544.
145. Fumagalli, A., Ferrari, M., Soriani, N., Gessi, A., Foglieni, B., Martina, E., Manitto, M.P., Brancato, R., Dean, M., Allikmets, R., et al. (2001). Mutational scanning of the ABCR gene with double-gradient denaturing-gradient gel electrophoresis (DG-DGGE) in Italian Stargardt disease patients. *Hum. Genet.* 109, 326–338.
146. Littink, K.W., Koenekoop, R.K., van den Born, L.I., Collin, R.W.J., Moruz, L., Veltman, J.A., Roosing, S., Zonneveld, M.N., Omar, A., Darvish, M., et al. (2010). Homozygosity mapping in patients with cone-rod dystrophy: novel mutations and clinical characterizations. *Invest. Ophthalmol. Vis. Sci.* 51, 5943–5951.
147. Jaakson, K., Zernant, J., Klm, M., Hutchinson, A., Tonisson, N., Glavac, D., Ravnik-Glavac, M., Hawlina, M., Meltzer, M.R., Caruso, R.C., et al. (2003). Genotyping microarray (gene chip) for the ABCR (ABCA4) gene. *Hum. Mutat.* 22, 395–403.
148. Papaioannou, M., Ockala, L., Bessant, D., Lois, N., Bird, A., Payne, A., and Bhattacharya, S. (2000). An analysis of ABCR mutations in British patients with recessive retinal dystrophies. *Invest. Ophthalmol. Vis. Sci.* 41, 16–19.
149. Mihalik, S.J., Morrell, J.C., Kim, D., Sacksteder, K.A., Watkins, P.A., and Gould, S.J. (1997). Identification of PAHX, a Refsum disease gene. *Nat. Genet.* 17, 185–189.
150. Jansen, G.A., Waterham, H.R., and Wanders, R.J.A. (2004). Molecular basis of Refsum disease: sequence variations in phytanoyl-CoA hydroxylase (PHYH) and the PTS2 receptor (PEX7). *Hum. Mutat.* 23, 209–218.
151. Cideciyan, A. V., Swider, M., Aleman, T.S., Tsybovsky, Y., Schwartz, S.B., Windsor, E.A.M., Roman, A.J., Sumaroka, A., Steinberg, J.D., Jacobson, S.G., et al. (2009). ABCA4 disease progression and a proposed strategy for gene therapy. *Hum. Mol. Genet.* 18, 931–941.
152. Miyamura, Y., Verma, I.C., Saxena, R., Hoshi, M., Murase, A., Nakamura, E., Kono, M., Suzuki, T., Yasue, S., Shibata, S.-I.I., et al. (2005). Five novel mutations in tyrosinase gene of Japanese and Indian patients with oculocutaneous albinism type I (OCA1). *J. Invest. Dermatol.* 125, 397–398.
153. Eisenberger, T., Slim, R., Mansour, A., Nauck, M., Nrnberg, G., Nrnberg, P., Decker, C., Dafinger, C., Ebermann, I., Bergmann, C., et al. (2012). Targeted next-generation sequencing identifies a homozygous nonsense mutation in ABHD12, the gene underlying PHARC, in a family clinically diagnosed with Usher syndrome type 3. *Orphanet J. Rare Dis.* 7, 59.
154. Indelman, M., Hamel, C.P., Bergman, R., Nischal, K.K., Thompson, D., Surget, M.-O., Ramon, M., Ganthos, H., Miller, B., Richard, G., et al. (2003). Phenotypic diversity and mutation spectrum in hypotrichosis with juvenile macular dystrophy. *J. Invest. Dermatol.* 121, 1217–1220.
155. Glckle, N., Kohl, S., Mohr, J., Scheurenbrand, T., Sprecher, A., Weisschuh, N., Bernd, A., Rudolph, G., Schubach, M., Poloschek, C., et al. (2014). Panel-based next generation sequencing as a reliable and efficient technique to detect mutations in unselected patients with retinal dystrophies. *Eur. J. Hum. Genet.* 22, 99–104.
156. Jaijo, T., Aller, E., Garca-Garca, G., Aparisi, M.J., Bernal, S., Avila-Fernndez, A., Barragn, I., Baiget, M., Ayuso, C., Antiolo, G., et al. (2010). Microarray-based mutation analysis of 183 Spanish families with Usher syndrome. *Invest. Ophthalmol. Vis. Sci.* 51, 1311–1317.
157. Pierce, E.A., Quinn, T., Meehan, T., McGee, T.L., Berson, E.L., and Dryja, T.P. (1999). Mutations in a gene encoding a new oxygen-regulated photoreceptor protein cause dominant retinitis pigmentosa. *Nat. Genet.* 22, 248–254.
158. Simonelli, F., Testa, F., de Crecchio, G., Rinaldi, E., Hutchinson, A., Atkinson, A., Dean, M., D’Urso, M., and Allikmets, R. (2000). New ABCR mutations and clinical phenotype in Italian patients with Stargardt disease. *Invest. Ophthalmol. Vis. Sci.* 41, 892–897.
159. Gonzlez-del Pozo, M., Borrego, S., Barragn, I., Pieras, J.I., Santoyo, J., Matamala, N., Naranjo, B., Dopazo, J., and Antiolo, G. (2011). Mutation screening of multiple genes in

Spanish patients with autosomal recessive retinitis pigmentosa by targeted resequencing. *PLoS One* 6, e27894.

160. Song, J., Smaoui, N., Ayyagari, R., Stiles, D., Benhamed, S., MacDonald, I.M., Daiger, S.P., Tumminia, S.J., Hejtmancik, F., and Wang, X. (2011). High-throughput retina-array for screening 93 genes involved in inherited retinal dystrophy. *Invest. Ophthalmol. Vis. Sci.* 52, 9053–9060.

161. Sohocki, M.M., Bowne, S.J., Sullivan, L.S., Blackshaw, S., Cepko, C.L., Payne, A.M., Bhattacharya, S.S., Khaliq, S., Qasim Mehdi, S., Birch, D.G., et al. (2000). Mutations in a new photoreceptor-pineal gene on 17p cause Leber congenital amaurosis. *Nat. Genet.* 24, 79–83.

162. Zhang, Q., Zulfiqar, F., Xiao, X., Riazuddin, S.A., Ahmad, Z., Caruso, R., MacDonald, I., Sieving, P., Riazuddin, S., and Hejtmancik, J.F. (2007). Severe retinitis pigmentosa mapped to 4p15 and associated with a novel mutation in the PROM1 gene. *Hum. Genet.* 122, 293–299.

163. Sergouniotis, P.I., Robson, A.G., Li, Z., Devery, S., Holder, G.E., Moore, A.T., and Webster, A.R. (2012). A phenotypic study of congenital stationary night blindness (CSNB) associated with mutations in the GRM6 gene. *Acta Ophthalmol.* 90, e192–e197.

164. Dryja, T.P., McGee, T.L., Hahn, L.B., Cowley, G.S., Olsson, J.E., Reichel, E., Sandberg, M.A., and Berson, E.L. (1990). Mutations within the rhodopsin gene in patients with autosomal dominant retinitis pigmentosa. *N. Engl. J. Med.* 323, 1302–1307.

165. Feldhammer, M., Durand, S., Mrázová, L., Boucher, R.-M., Laframboise, R., Steinfeld, R., Wraith, J.E., Michelakakis, H., van Diggelen, O.P., Hrebíček, M., et al. (2009). Sanfilippo syndrome type C: mutation spectrum in the heparan sulfate acetyl-CoA: alpha-glucosaminide N-acetyltransferase (HGSNAT) gene. *Hum. Mutat.* 30, 918–925.

166. Testa, F., Rossi, S., Sodi, A., Passerini, I., Di Iorio, V., Della Corte, M., Banfi, S., Surace, E.M., Menchini, U., Auricchio, A., et al. (2012). Correlation between photoreceptor layer integrity and visual function in patients with Stargardt disease: implications for gene therapy. *Invest. Ophthalmol. Vis. Sci.* 53, 4409–4415.

167. Boulanger-Scemama, E., El Shamieh, S., Démontant, V., Condroyer, C., Antonio, A., Michiels, C., Boyard, F., Saraiva, J.-P., Letexier, M., Souied, E., et al. (2015). Next-generation sequencing applied to a large French cone and cone-rod dystrophy cohort: mutation spectrum and new genotype-phenotype correlation. *Orphanet J. Rare Dis.* 10, 85.

168. Pras, E., Abu, A., Rotenstreich, Y., Avni, I., Reish, O., Morad, Y., Reznik-Wolf, H., and Pras, E. (2009). Cone-rod dystrophy and a frameshift mutation in the PROM1 gene. *Mol. Vis.* 15, 1709–1716.

169. Chakarova, C.F., Papaioannou, M.G., Khanna, H., Lopez, I., Waseem, N., Shah, A., Theis, T., Friedman, J., Maubaret, C., Bujakowska, K., et al. (2007). Mutations in TOPORS cause autosomal dominant retinitis pigmentosa with perivascular retinal pigment epithelium atrophy. *Am. J. Hum. Genet.* 81, 1098–1103.

170. Coppieters, F., Van Schil, K., Bauwens, M., Verdin, H., De Jaegher, A., Syx, D., Sante, T., Lefever, S., Abdelmoula, N.B., Depasse, F., et al. (2014). Identity-by-descent-guided mutation analysis and exome sequencing in consanguineous families reveals unusual clinical and molecular findings in retinal dystrophy. *Genet. Med.* 16, 671–680.

171. Kohl, S., Christ-Adler, M., Apfelstedt-Sylla, E., Kellner, U., Eckstein, A., Zrenner, E., and Wissinger, B. (1997). RDS/peripherin gene mutations are frequent causes of central retinal dystrophies. *J. Med. Genet.* 34, 620–626.

172. Lorenz, B., Poliakov, E., Schambeck, M., Friedburg, C., Preising, M.N., and Redmond, T.M. (2008). A comprehensive clinical and biochemical functional study of a novel RPE65 hypomorphic mutation. *Invest. Ophthalmol. Vis. Sci.* 49, 5235–5242.

173. Gu, S.M., Thompson, D.A., Srikumari, C.R., Lorenz, B., Finckh, U., Nicoletti, A., Murthy, K.R., Rathmann, M., Kumaramanickavel, G., Denton, M.J., et al. (1997). Mutations in RPE65 cause autosomal recessive childhood-onset severe retinal dystrophy. *Nat. Genet.* 17, 194–197.

174. Neveling, K., Feenstra, I., Gilissen, C., Hoefsloot, L.H., Kamsteeg, E.-J., Mensenkamp, A.R., Rodenburg, R.J.T., Yntema, H.G., Spruijt, L., Vermeer, S., et al. (2013). A post-hoc

comparison of the utility of sanger sequencing and exome sequencing for the diagnosis of heterogeneous diseases. *Hum. Mutat.* 34, 1721–1726.

175. Bech-Hansen, N.T., Naylor, M.J., Maybaum, T.A., Pearce, W.G., Koop, B., Fishman, G.A., Mets, M., Musarella, M.A., and Boycott, K.M. (1998). Loss-of-function mutations in a calcium-channel alpha1-subunit gene in Xp11.23 cause incomplete X-linked congenital stationary night blindness. *Nat. Genet.* 19, 264–267.

176. McKie, A.B., McHale, J.C., Keen, T.J., Tartelin, E.E., Goliath, R., van Lith-Verhoeven, J.J., Greenberg, J., Ramesar, R.S., Hoyng, C.B., Cremers, F.P., et al. (2001). Mutations in the pre-mRNA splicing factor gene *PRPC8* in autosomal dominant retinitis pigmentosa (RP13). *Hum. Mol. Genet.* 10, 1555–1562.

177. Khan, A.O., Eisenberger, T., Nagel-Wolfrum, K., Wolfrum, U., and Bolz, H.J. (2015). *C21orf2* is mutated in recessive early-onset retinal dystrophy with macular staphyloma and encodes a protein that localises to the photoreceptor primary cilium. *Br. J. Ophthalmol.* 99, 1725–1731.

178. Sullivan, L.S., Koboldt, D.C., Bowne, S.J., Lang, S., Blanton, S.H., Cadena, E., Avery, C.E., Lewis, R.A., Webb-Jones, K., Wheaton, D.H., et al. (2014). A dominant mutation in hexokinase 1 (HK1) causes retinitis pigmentosa. *Investig. Ophthalmol. Vis. Sci.* 55, 7147–7158.

179. Hull, S., Owen, N., Islam, F., Tracey-White, D., Plagnol, V., Holder, G.E., Michaelides, M., Carss, K., Raymond, F.L., Rozet, J.-M., et al. (2016). Nonsyndromic Retinal Dystrophy due to Bi-Allelic Mutations in the Ciliary Transport Gene *IFT140*. *Investig. Ophthalmology Vis. Sci.* 57, 1053.

180. Wright, C.F., Fitzgerald, T.W., Jones, W.D., Clayton, S., McRae, J.F., van Kogelenberg, M., King, D. a, Ambridge, K., Barrett, D.M., Bayzeturina, T., et al. (2014). Genetic diagnosis of developmental disorders in the DDD study: a scalable analysis of genome-wide research data. *Lancet* 6736, 1–10.

181. Farkas, M.H., Grant, G.R., White, J.A., Sousa, M.E., Consugar, M.B., Pierce, E.A. (2013). Transcriptome analyses of the human retina identify unprecedented transcript diversity and 3.5 Mb of novel transcribed sequence via significant alternative splicing and novel genes. *BMC Genomics* 14, 486.

182. Quadri, M., Yang, X., Cossu, G., Olgiati, S., Saddi, V. M., Breedveld, G. J., Ouyang, L., Hu, J., Xu, N., Graafland, J., et al. (2015). An exome study of Parkinson's disease in Sardinia, a Mediterranean genetic isolate. *Neurogenetics.* 16, 55-64.

183. Suetsugu, S., Miki, H., Takenawa, T. (1999). Identification of two human *WAVE/SCAR* homologues as general actin regulatory molecules which associate with the Arp2/3 complex. *Biochem. Biophys. Res. Commun.* 260, 296-302.

184. Furuichi, T., Shiraishi-Yamaguchi, Y., Sato, A., Sadakata, T., Huang, J., Shinoda, Y., Hayashi, K., Mishima, Y., Tomomura, M., Nishibe, H., Yoshikawa, F. (2011). Systematizing and cloning of genes involved in the cerebellar cortex circuit development. *Neurochem. Res.* 36, 1241-1252.

185. Cheng, C. W., Chow, R. L., Lebel, M., Sakuma, R., Cheung, H. O., Thanabalasingham, V., Zhang, X., Bruneau, B. G., Birch, D. G., Hui, C. C. (2005). The Iroquois homeobox gene, *Irx5*, is required for retinal cone bipolar cell development. *Dev. Biol.* 287, 48-60.

186. Garcia-Ramirez, M., Canals, F., Hernandez, C., Colome, N., Ferrer, C., Carrasco, E. Garcia-Arumi, J., Simo, R. (2007). Proteomic analysis of human vitreous fluid by fluorescence-based difference gel electrophoresis (DIGE): a new strategy for identifying potential candidates in the pathogenesis of proliferative diabetic retinopathy. *Diabetologia.* 50, 1294-303.

187. Kechad, A., Jolicoeur, C., Tufford, A., Mattar, P., Chow, R. W., Harris, W. A., Cayouette, M. (2012). *Numb* is required for the production of terminal asymmetric cell divisions in the developing mouse retina. *J. Neurosci.* 32, 17197-210.

188. French, C. R., Stach, T. R., March, L. D., Lehmann, O. J., Waskiewicz, A. J. (2013). Apoptotic and proliferative defects characterize ocular development in a microphthalmic BMP model. *Invest. Ophthalmol. Vis. Sci.*, 54, 4636-47.

189. Yang, J., Gao, J., Adamian, M., Wen, X. H., Pawlyk, B., Zhang, L., Sanderson, M. J., Zuo, J., Makino, C. L., Li, T. (2005) The ciliary rootlet maintains long-term stability of sensory cilia. *Mol. Cell Biol.* 25, 4129-37.