Corrigendum to "comparative exome sequencing reveals novel candidate genes for retinitis pigmentosa" [EBioMedicine 56(2020) 102792] DOI: https://doi.org/10.1016/j.ebiom.2020.102792

*Zhen Yi,[1] Jiamin Ouyang,[1] Wenmin Sun,[1] Shiqiang Li Xueshan Xiao and Qingjiong Zhang **

State Key Laboratory of Ophthalmology, Zhongshan Ophthalmic Center, Sun Yat-sen University, 54 Xianlie Road, Guangzhou 510060, China

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The authors wish to correct the transcript numbering of *CCDC188*. The outdated transcript NM_001243537 was incorrectly used in the published paper. This should have been NM_001365892. The authors therefore update the description of the *CCDC188* mutation to c.937C>T (p.Arg313*).

The corrected Table 1, Figure 1, Supplementary Materials Table S7 and Fig. S2 are presented as below. Allele frequency in gnomAD was also updated according to NM_001365892 in Table 1 and Supplementary Materials Table S7. The revision does not change the conclusions of this paper.

The authors would like to apologise for any inconvenience caused.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.ebiom.2022.103913.

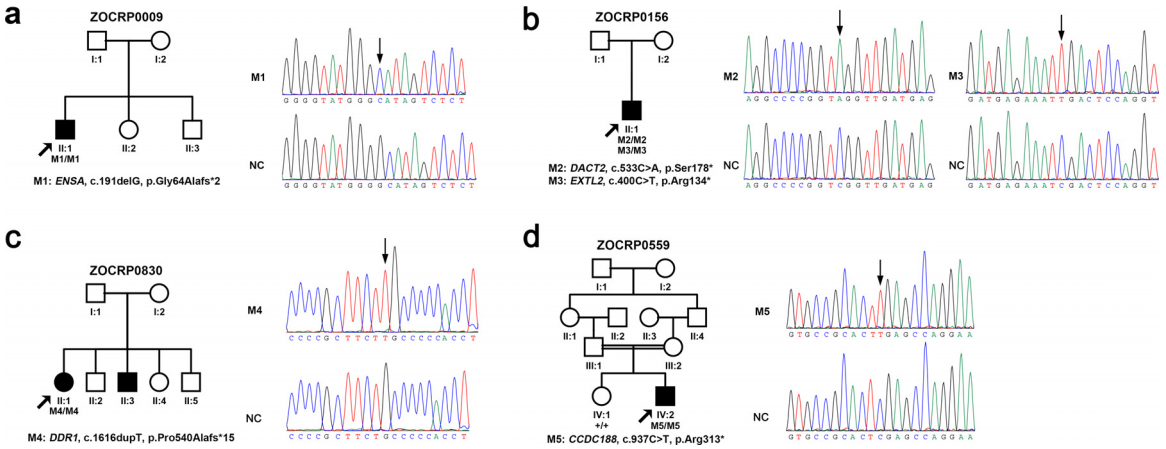

Figure 1. Pedigrees and sequences of the five homozygous loss-of-function variants in *ENSA*, *DACT2*, *EXTL2*, *DDR1*, and *CCDC188*. The genotypes of all probands and available family members are shown below each individual. The blackened symbols represent affected individuals. Mx, mutant alleles; +, wild-type allele.

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*Corresponding author.
E-mail address: zhangqji@mail.sysu.edu.cn (Q. Zhang).

[1] These authors contributed equally to this work.

Genes	Chromosome position	Reference transcript	Patient ID	Variant number	Nucleotide change	Amino acid Change	Expression & interaction[§]		Allele frequency in gnomAD		Allele frequency of other LoF variants	
							Retina	IRD genes	All	EA	control	gnomAD
ENSA	chr01: 150599935	NM_207168	ZOCRP0009	M1	c.191delG	p.Gly64Alafs*2	Ninth	OFD1	1/251460	1/18394	2/9456	22/282912
DACT2	chr06: 168710973	NM_214462	ZOCRP0156	M2	c.533C>A	p.Ser178*	Second	NA	NA	NA	4/9456	144/282912
EXTL2	chr01: 101343065	NM_001439	ZOCRP0156	M3	c.400C>T	p.Arg134*	Highest	NA	3/247450	3/18342	2/9456	37/282912
DDR1	chr06: 30864446	NM_001202523	ZOCRP0830	M4	c.1616dupT	p.Pro540Alafs*15	Fifth	CCT2, BBS10	NA	NA	0/9456	178/282912
CCDC188	chr22: 20136745	NM_001365892	ZOCRP0559	M5	c.937C>T	p.Arg313*	NA	NA	16/118792	0/10622	0/9456	62/282912

***Table 1*: Five homozygous rare variants in five novel candidate genes identified in four RP probands.**

Notes: EA, East Asian; gnomAD, genome aggregation database; IRD, inherited retinal degeneration; LoF, loss-of-function; M, mutation; NA, not available.

[§]Information based on GeneCards where expression in retina ranked by SAGE.

All these variants were not present in Exome Variant Server and 1000 Genomes.

No homozygous LoF variants in these five genes were found in 1000 Genomes.