Additional file legends

Additional file 1: Excel file

Sheet1: List of the 533 loss-of-function variants found in cave populations.

Sheet2: Correspondence between gene defined in Policarpo et al. 2021 and their annotation in the Ensembl database.

Sheet3: List of 12 genotyped loss-of-function variants. The last line written in orange correspond to a loss-of-function variant that did not pass our variant filters, as only one allele was found among 12 individual from Tinaja, but that we genotyped due to its location on the *per2* gene, often found as pseudogene in cave organisms.

Sheet4: Genotype and Phenotype score for each Toro individual

Additional file 2_Fig S1:

A: Distribution of each type of LoF variants in cave populations.

B: Frameshift sizes distribution.

Additional file 2_Fig S2:

Dotterplot between surface and cave genomes showing (A) *rgr2* and (B) *opn8* large deletions. (C) and (D) represent the coverage on these regions of one non-deleted individual, one heterozygous individual, and one homozygous deleted individual.

Additional file 2_Fig S3:

Comparison of LoF variant frequencies obtained in the WGS data and by genotyping with PCR followed by sanger sequencing or by identification in a 3% agarose gel.

Additional file 2_Fig S4:

Standard length and eye diameter measures on Toro individuals. Blue lines represent the standard length and red line the eye diameter.

Additional file 2_Fig S5:

For each LoF variant genotyped, the left panel show the corresponding genomic sequence extracted from the surface reference genome (GCA_000372685.2) as well as the primer sequences used (written in blue) and the position of the LoF variant (highlighted in red). Primer sequences in blue can be retrieved on the additional file 4_primer_list.
The right panel show examples of homozygous individuals without the LoF variant (wt/wt), heterozygous individuals (wt/-), and homozygous individuals with the LoF variant (-/-).

Additional file 2_Fig S6:

(A) Representation of deleted regions in the cave populations. Exons of genes are represented by blue squares, and exons amplified to genotype these deletions are indicated either with blue lines (exons used as control) or red lines (exons in the deleted regions). The deletion region in cave individuals is represented with dotted lines.
(B) The left panel show the expected gel pattern if an individual is not deleted. The right panel show a gel with homozygous deleted individuals (-) and with non-deleted individuals (+) for which we cannot differentiate between heterozygous or homozygous non-deleted.

Additional file 2_Table S1:

(A) GO-term enrichment analysis results with all human orthologous genes. Only significant GO-terms are shown.

(B) GO-term enrichment analysis results with all zebrafish orthologous genes, using the “GO Biological Process GeneRIF Predicted Z-score” database. The 25 top results are shown, but neither of those are significant.

(C) GO-term enrichment analysis results with all zebrafish orthologous genes, using the “Phenotype GeneRIF Predicted Z-score” database. The 25 top results are shown, but only the 21 first terms are significant.

Additional file 3: Excel file

Sheet1: List of SRA accession of each individual used in this study. For Chica individuals, reads were always downloaded in two distinct files and concatenated using the bash command “cat”.

Sheet2: Mean genome-wide coverage of genomic reads aligned against the surface reference genome (GCA_000372685.2) for each individual. These values were computed using SAMtools depth tool.

Additional file 4_primer_list: Excel file

Sheet1: List of primers used to amplify LoF variants and the method used to genotype these variants. The list of primers used to amplify control (non-deleted) and putatively deleted exons of *opn8* and *rgr2* are also described.