

Supplementary Figure 1. Linkage map with eye QTL. Figure adapted from Figure S1 produced by¹. Yellow: Markers present in the Astyanax mexicanus 1.0.2 genome assembly. Orange: Markers which we were unable to locate in the current draft genome. Blue: Locations of QTL for eye-size, lens length, or thickness of various eye layers. The linkage group number that is underlined and in bold in our key, is the linkage group represented in the Figure and corresponds to the linkage groups in ^{1,2}. We give the citation of the studies that contributed to each QTL and the names of the linkage groups in those studies, as naming of linkage groups is not consistent across studies. We detail cases below where other scaffolds with additional markers under the QTL (indicated by other maps) were also included, even if those particular markers are on displayed on this map. LG1: LG4³, LG5^{4,5}; TOP LG2: LG2¹, LG7⁴, LG2², LG8^{4,5}. **BOTTOM LG2**: LG6^{4,5}, also scaffolds including NYU27 and AM134b which are not on this map but were included in analysis because they are within the QTL. LG3: LG11⁴, also scaffolds including Am224A and Am205B which are not on this map but were included in analysis because they are within the QTL. LG4 Top QTL LG4², LG14⁴. LG4 Bottom QTL: LG13^{4,5}, so many markers were included because all were on the same scaffold. Scaffold containing NYU 24 was also under QTL, but not on map, and genes on that scaffold were included in the analysis. LG6: LG6². LG7: LG7¹, LG4^{4,5}. LG16: LG16², LG15⁴. LG17². LG17⁴. LG18: LG25⁴. LG21: LG27⁴, also included genes on scaffold containing marker 223C which is not on map displayed here but was under the QTL. LG23: LG194,5, LG24: LG241. Lastly, there is a QTL that is likely on LG10 on this linkage map that is localized to marker NYU14 and on LG20 in⁴⁵.



Supplementary Figure 2. Expression patterns of *otx2*. Whole gels showing semi quantitative RT-PCR (a) 18S rRNA and (b) *otx2* mRNA in surface fish (SF) and cavefish (CF) at 40 hours post-fertilization with size standards. Identical data to what is shown in Figure 4 but this figure includes the entire gel with a molecular weight scale.

SUPPLEMENTARY REFERENCES

- 1. O'Quin, K.E., Yoshizawa, M., Doshi, P. & Jeffery, W.R. Quantitative genetic analysis of retinal degeneration in the blind cavefish *Astyanax mexicanus*. *PLoS One* **8**, e57281 (2013).
- Yoshizawa, M., Yamamoto, Y., O'Quin, K.E. & Jeffery, W.R. Evolution of an adaptive behavior and its sensory receptors promotes eye regression in blind cavefish. *BMC Biol* 10, 108 (2012).
- 3. Gross, J.B. *et al.* Synteny and candidate gene prediction using an anchored linkage map of *Astyanax mexicanus*. *Proc Natl Acad Sci USA* **105**, 20106–20111 (2008).
- 4. Protas, M., Conrad, M., Gross, J.B., Tabin, C. & Borowsky, R. Regressive evolution in the Mexican cave tetra, *Astyanax mexicanus*. *Curr Biol* **17**, 452-454 (2007).
- 5. Protas, M. *et al.* Multi-trait evolution in a cave fish, *Astyanax mexicanus. Evol Dev* **10**, 196-209 (2008).