

Figure S1. MSP measurements and modeling of A1/A2 mixes of *Cichla monoculus*' photoreceptor absorption. Raw MSP records (*dashed grey lines*) and interpolating line through the data (*solid black lines*) are given. The best mix of A1 and A2 chromophores

(*in red*) is given together with the relative pure A1 (*in blue*) and corresponding pure A2 (*in cyan*) nomograms of reference (A,C,E,G, and I).

When no chromophore mixing is considered, the best A1 nomogram and best A2 nomogram fits are shown (B,D,F,H, and J), highlighting the significant improvement of fit when A1/A2 mixes are considered. In addition, the pure A1 λ_{\max} values used in the A1/A2 mixes in A,C,E,G, and I are in line with previous results in cichlids, while forcing fitting with pure A1 or pure A2 nomograms only (B,D,F,H, and J) leads to either poor fitting or fitting values that are far from accepted ranges for that pigment class.

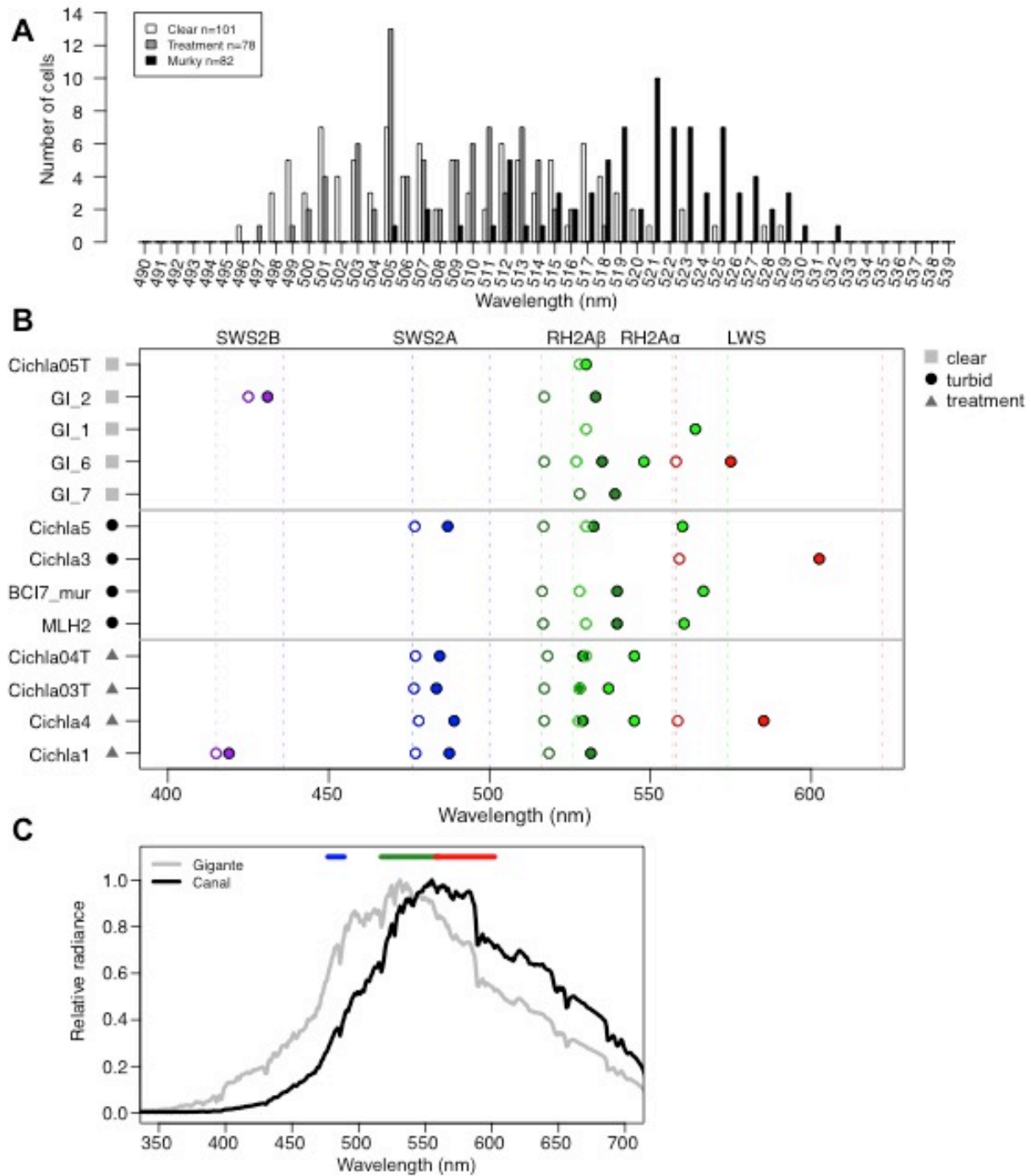


Figure S2. Rod and cone visual pigment peak sensitivities (λ_{\max}) measured in *C. monocolus* with micro-spectrophotometry. (A) Histogram showing the distribution of rod λ_{\max} from individuals collected at clear water sites, turbid water sites and individuals from turbid sites treated in clear water for six months. (B) Spectral sensitivities of visual pigments from wild-caught *C. monocolus* individuals. Filled circles denotes the maximum

absorbance (λ_{\max}) determined by MSP whereas empty circles denote the estimated λ_{\max} assuming a pure A_1 chromophore. Dashed colored lines represent the ranges of each spectral/photoreceptor class when combined with A_1 (left) or A_2 (right line) chromophores, (purple: SWS2B, blue: SWS2A, darkgreen: RH2A β , lightgreen: RH2A α , and red: LWS). (C) Underwater light environment of Lake Gatun showing 1 meter-depth downward light intensity from clear and murky water localities (Gigante and Canal respectively). Color horizontal lines represent the spectral sensitivity range of the three main visual pigments (single cones: blue; double cones: red and green) measured by MSP in *C. monocolus*.

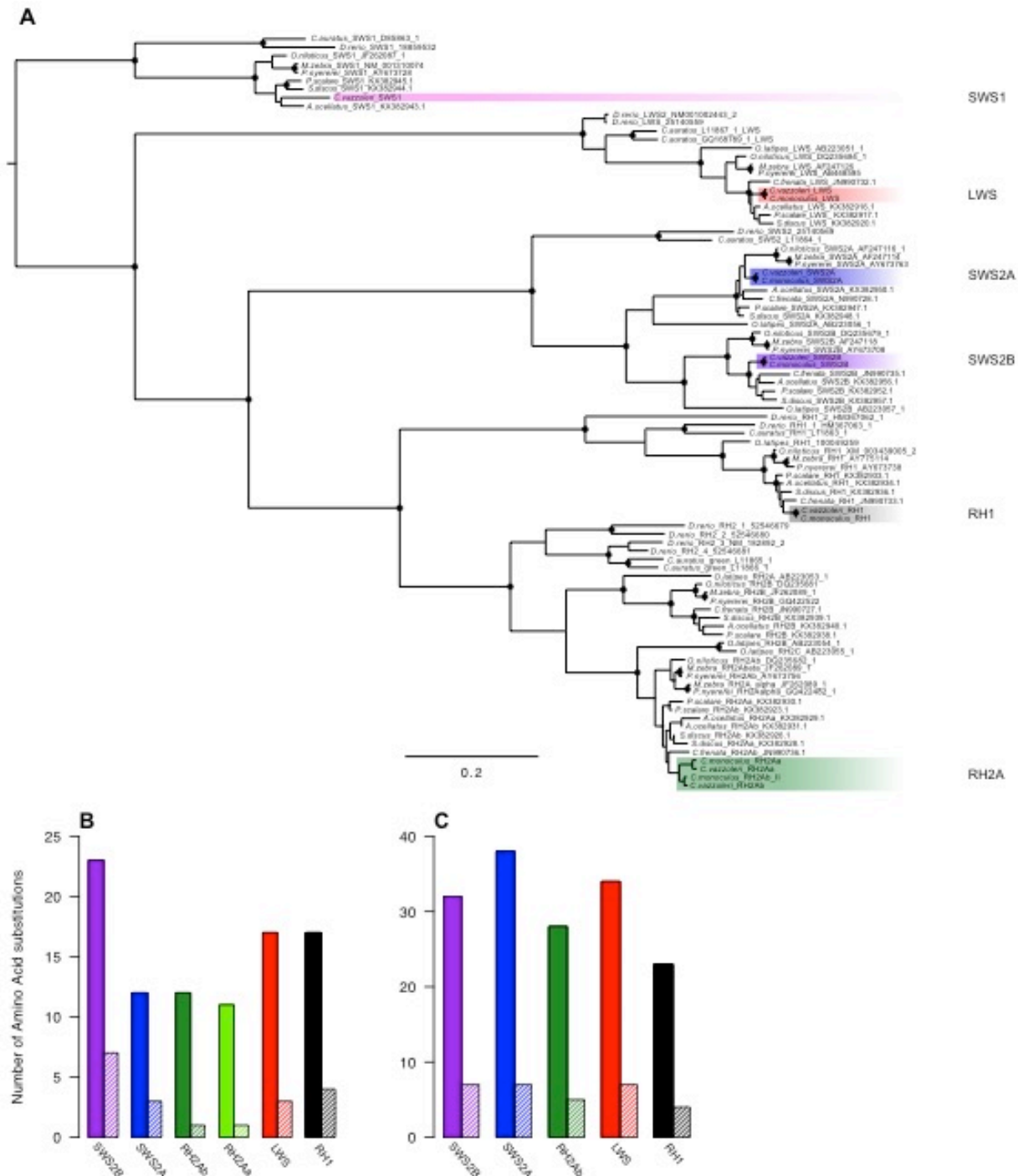


Figure S3. (A) Opsin maximum-likelihood phylogenetic tree of African (*O. niloticus*, *M. zebra*, *P. nyererei*) and Neotropical (*Cichla monoculus*, *C. vazzoleri*, *A. ocellatus*, *P. scalare*, *S. discus*, *C. frenata*) cichlids, with outgroups *D. rerio*, *O. latipes* and *C. auratus*. Color shades indicate the *Cichla* spp opsins. Black circles represent bootstrap support over 95%. (B & C) Amino acid substitution variation for each opsin between *C. monoculus* and *O. niloticus* (B) and between *C. monoculus* and other Neotropical cichlids (*C. frenata*, *S. discus*, *P. scalare*, and *A. ocellatus*) (C). Because there is no complete sequence for the RH2A α opsin available for all species, this was omitted in B

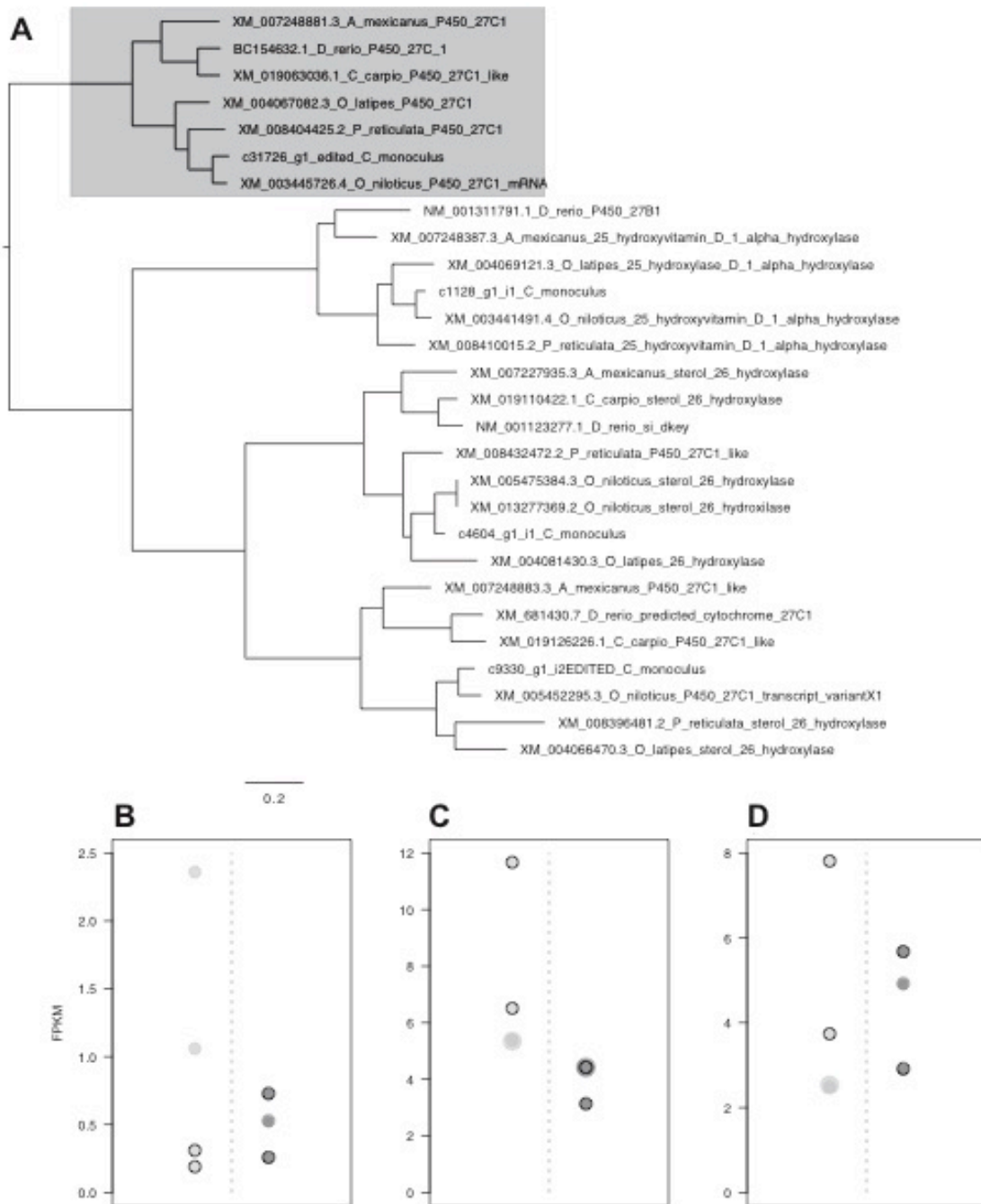


Figure S4. (A) Phylogenetic tree of different genes from the teleost P450 superfamily, which were also found in *C. monoculus* transcriptome. The Cyp27c1 gene clade is shaded in gray. (B) Gene expression of the other three P450 genes found in the transcriptomes of *C. monoculus*. (B) alpha hydroxylase, (C) sterol 26 hydroxylase, (D) P450 27C1 like. Light grey circles denote samples from clear waters whereas darker circles denote samples from murky water sites. Black borders denote duplicates from a single fish and bigger circles are used to indicate overlapping data points. Gene expression values are based on FPKM counts

Table S1

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References

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