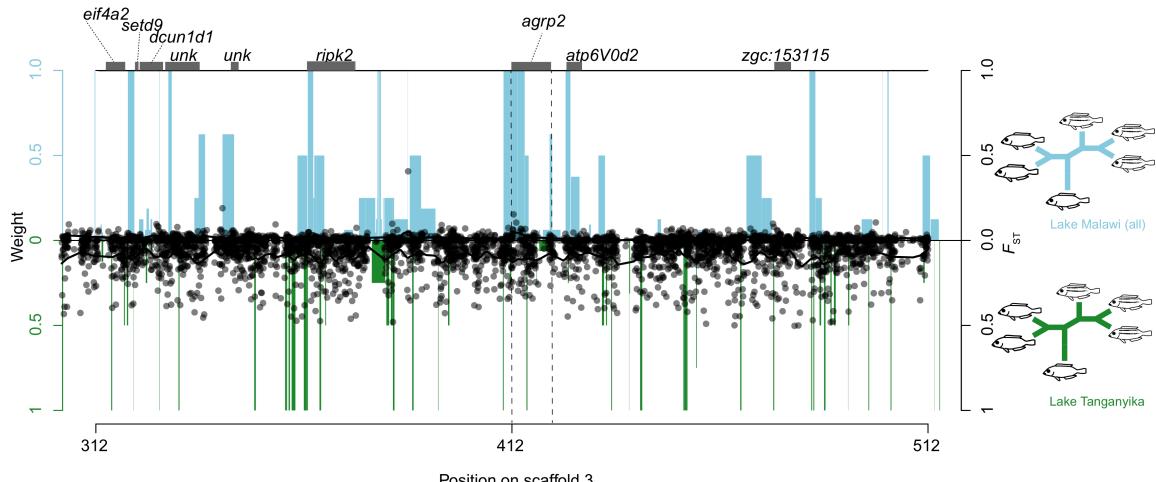


Supplementary Materials for

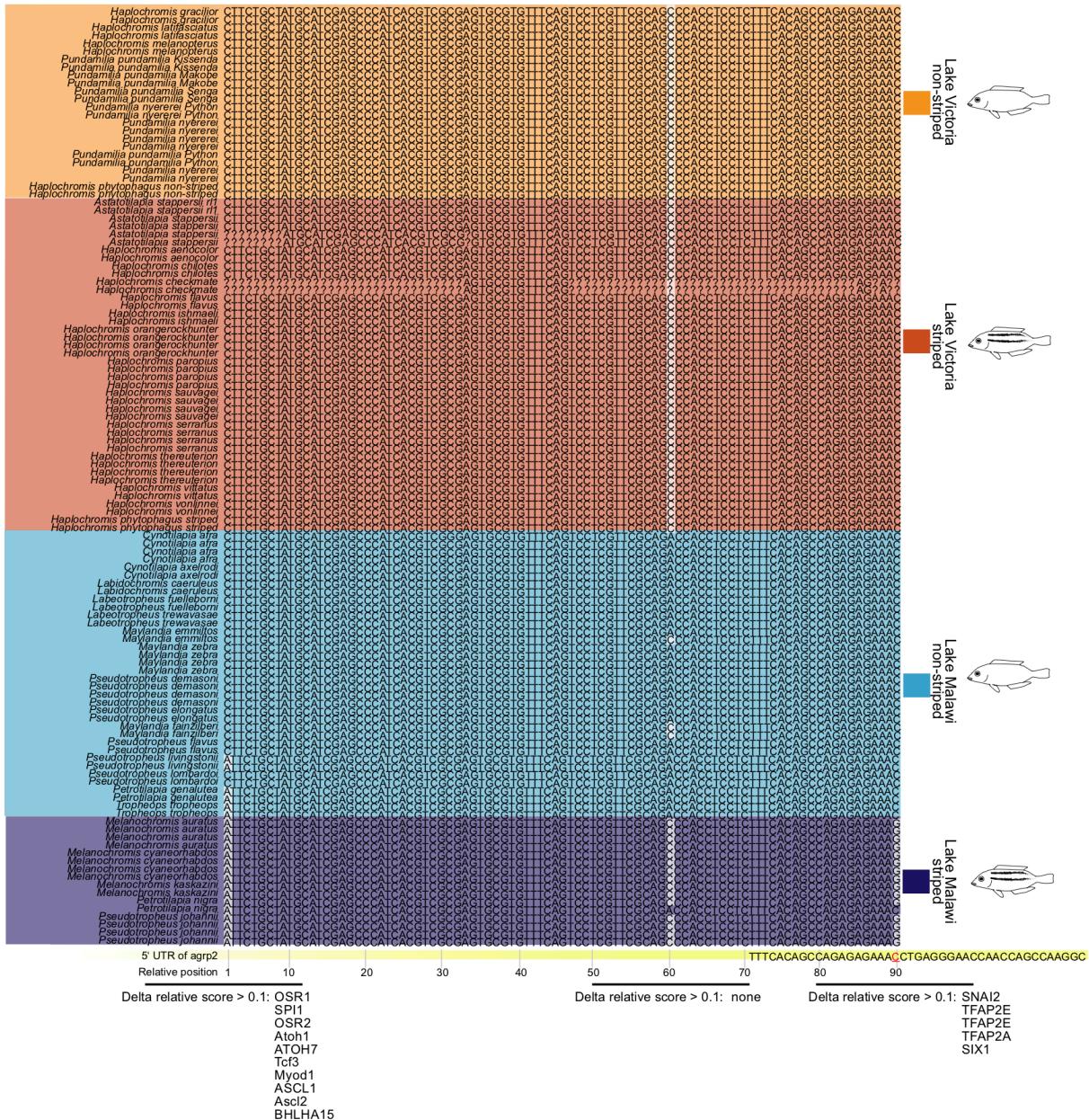
**Different sources of allelic variation drove repeated color pattern divergence in
cichlid fishes**

Sabine Urban, Alexander Nater, Axel Meyer, and Claudius F. Kratochwil

Correspondence to: Claudius F. Kratochwil (claudius.kratochwil@uni-konstanz.de) or
Axel Meyer (axel.meyer@uni-konstanz.de)



1
 2 **Fig. S1. F_{ST} plot of all Lake Malawi and Lake Tanganyika species.** Association of
 3 stripes with genomic regions. Black dots represent midpoints of every associated region
 4 (F_{ST} value) and black lines are smoothed local regressions between striped and non-
 5 striped species from Lake Malawi (top) and Lake Tanganyika species (bottom). This is
 6 plotted together with topology weights for topologies in which striped and non-striped
 7 species are reciprocally monophyletic (blue bars Lake Malawi, green bars Lake
 8 Tanganyika). Each value is giving the proportionate contribution of a particular taxon tree
 9 to the full tree with values ranging from 0 to 1. An example for such a topology in which
 10 striped species are reciprocally monophyletic is provided at the right for both radiations.
 11



12

13 Fig. S2. The *de novo* mutations in Lake Malawi mbuna may alter *agrp2* expression.

14 Alignment of candidate region LM for Lake Malawi mbuna (blue), all Lake Victoria
 15 species as well as their ancestral lineages (orange). There are three SNPs within this 90
 16 bp region (highlighted in white) with one of them aligning to the 5'UTR of *agrp2* (yellow
 17 bar at the bottom). All TFBSs predicted by JASPAR for each variant +/-10 bp of this
 18 variant are given below (see also Table S2). While TFBSs for variants one and two
 19 (relative positions 1 and 60) are expressed in tissues such as the brain or gut (Table
 20 S2), predicted TFBSs at the third variant (relative position 90) are expressed in the
 21 neural crest, skin or in melanocytes (Table S2).

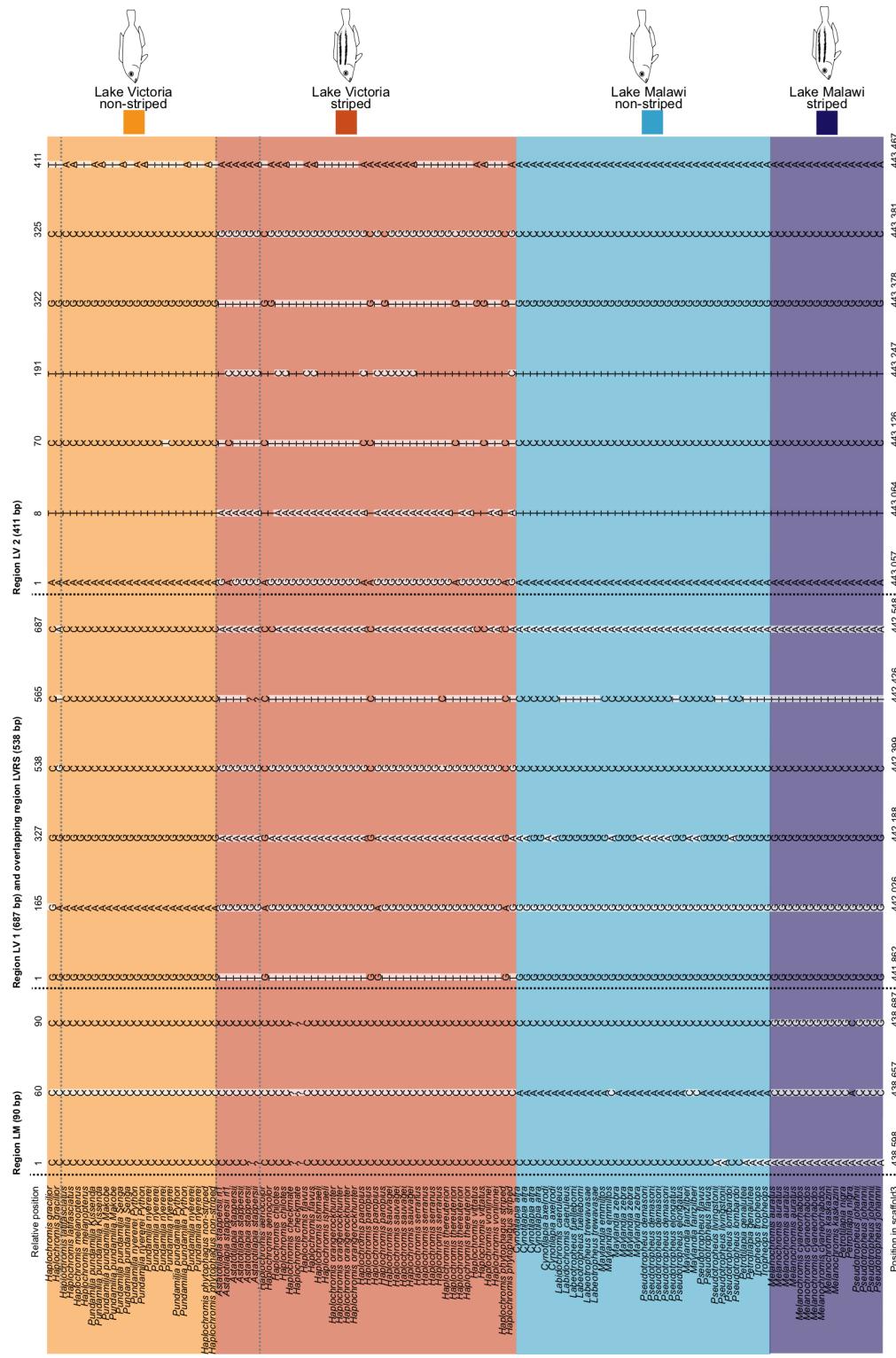


Fig. S3. Most variants within regions LM, LV 1, LV 2 and LVRS are not shared between Lakes Victoria and Malawi. Highly associated variants in region LM are unique in Lake Malawi and likely evolved de novo (see also Fig. 3, Fig. S2). For regions LV 1, LV 2 and LVRS the non-striped ancestral species *H. gracilior* is polymorphic for most variants which are highly differentiated between Lake Victoria striped and non-striped species. These results suggest that regulatory evolution via different routes lead to the repeated evolution of horizontal stripes in the two independent radiations of Lake Malawi and Lake Victoria cichlids.