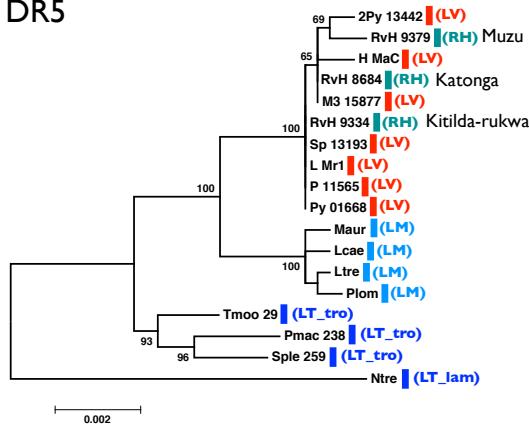


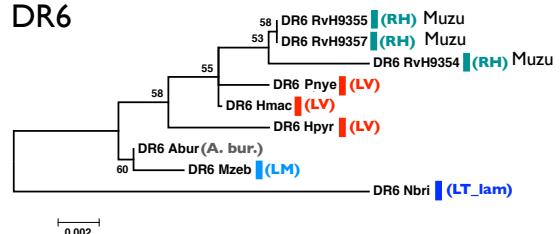
Figure S4. The origins of mutations in DRs. Three phylogenetic trees represent the accumulation of mutations in the common ancestral species of (A) Lake Victoria species, (B) Lake Victoria and riverine *Haplochromis* species, and (C) tribe Tropheini in Lake Tanganyika, Lakes Malawi, Victoria, and riverine *Haplochromis* species. The tree topologies constructed from sequences of each DR were consistent with (D) “Riverine origin” or (E) “Modern haplochromine origin.” Scale bars indicate the number of substitutions per site. (F) The LWS sequences were determined from three riverine species: *H. sp.* ‘katonga’ from Katonga, *H. sp.* ‘kitilda-rukwa’ from Kitilda-Rukwa, and *H. sp.* ‘muzu’ from Muzu.

D Riverine origin

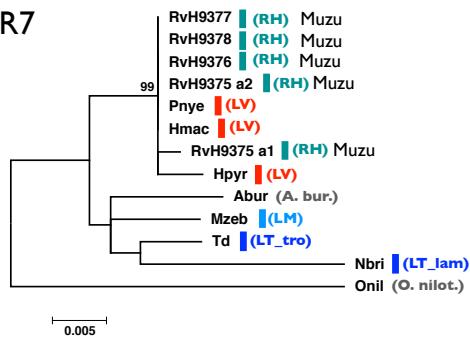
DR5



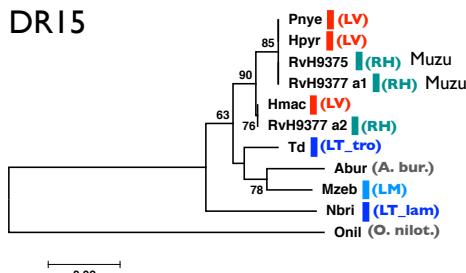
DR6



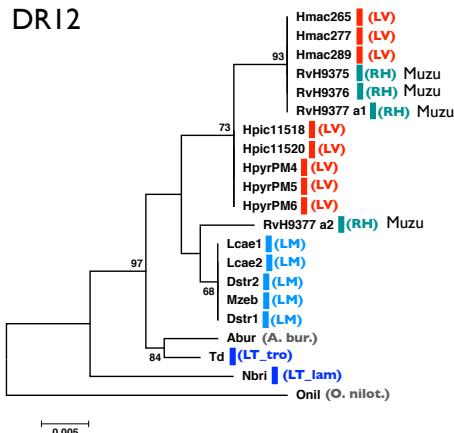
DR7



DR15



DR12



Lake Victoria (LV)
Riverine Haplochromis (RH)
Astatotilapia burtoni (A. bur.)
Lake Malawi (LM)
Lake Tanganyika Tropheini (LT_tro)
Lake Tanganyika Lamprologini (LT_lam)
Oreochromis niloticus (O. nilot.)

Figure S4. continued

E Modern haplochromines origin

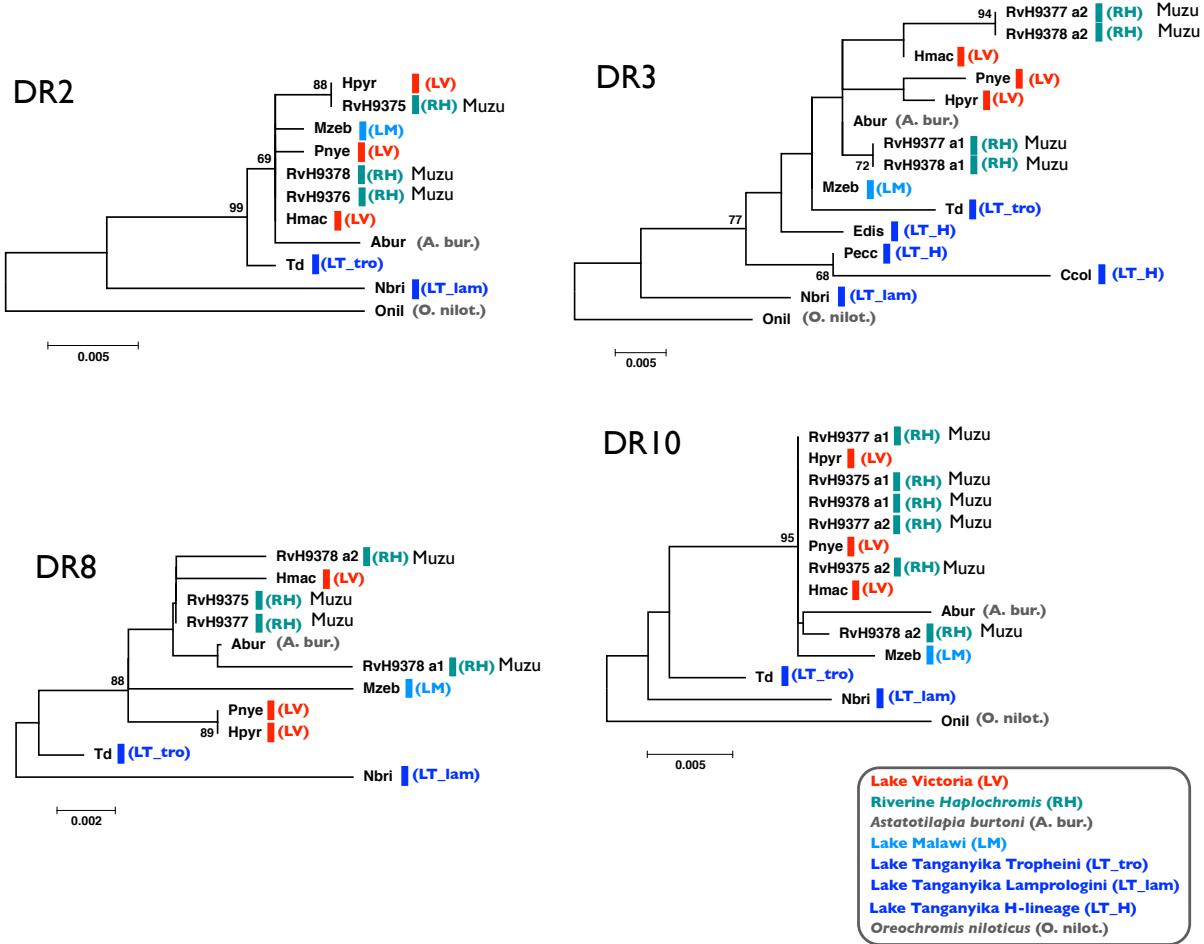


Figure S4. continued

E Modern haplochromines origin

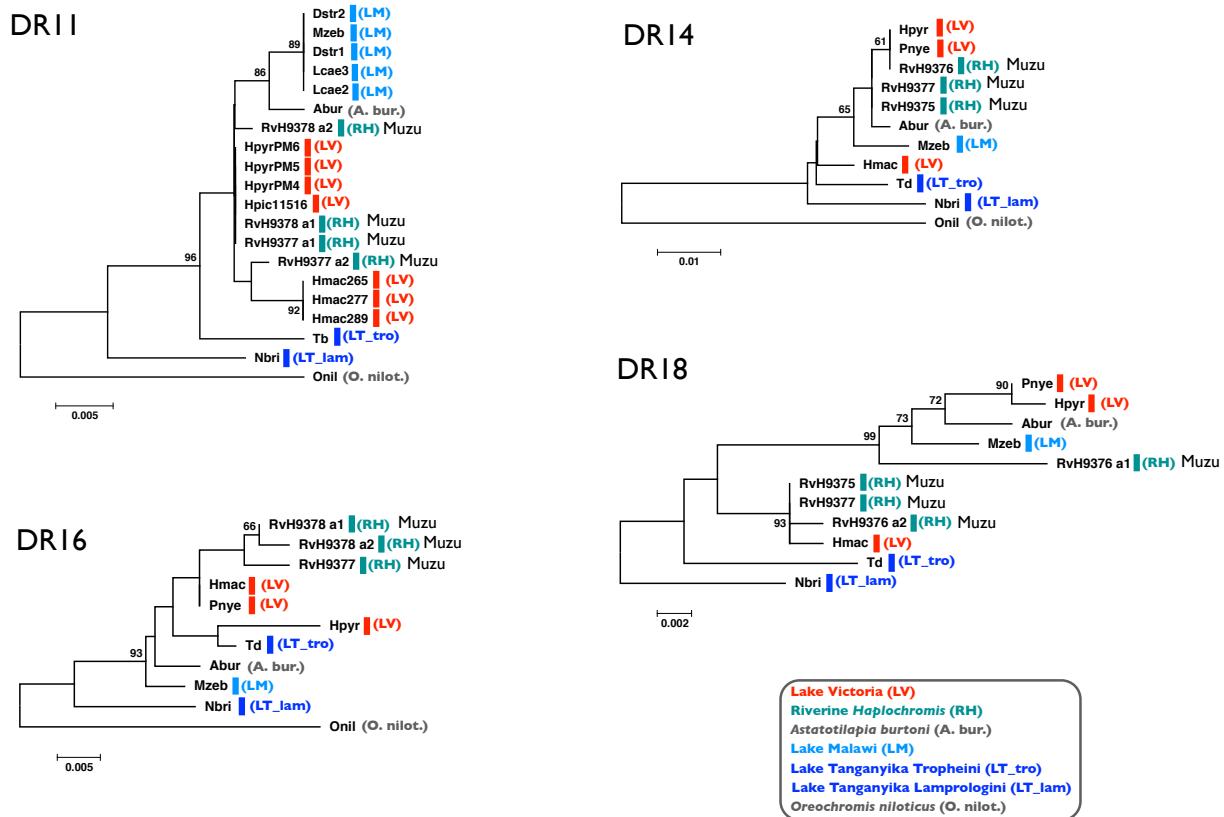
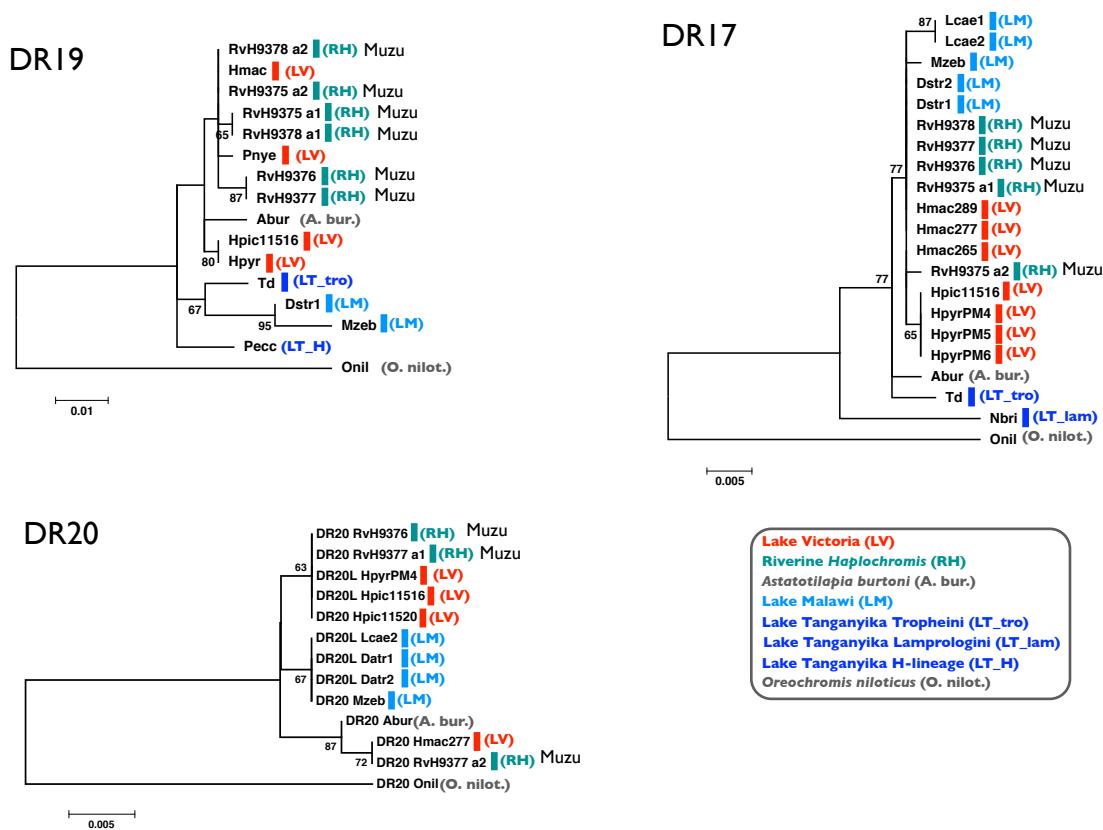


Figure S4. continued

E Modern haplochromines origin



Lake Victoria (LV)
Riverine Haplochromis (RH)
Astatotilapia burtoni (A. bur.)
Lake Malawi (LM)
Lake Tanganyika Tropheini (LT_tro)
Lake Tanganyika Lamprologini (LT_jam)
Lake Tanganyika H-lineage (LT_H)
Oreochromis niloticus (O. nilot.)

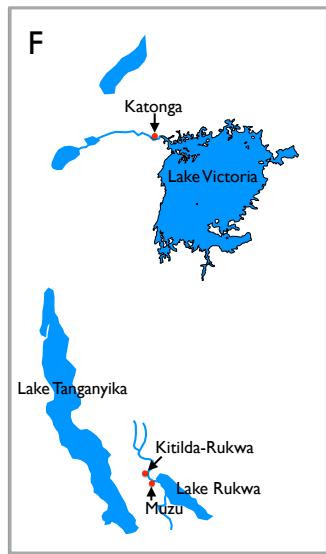


Figure S4. continued