

Species-Specific Markers Discovery in Tilapia

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Supplementary Information

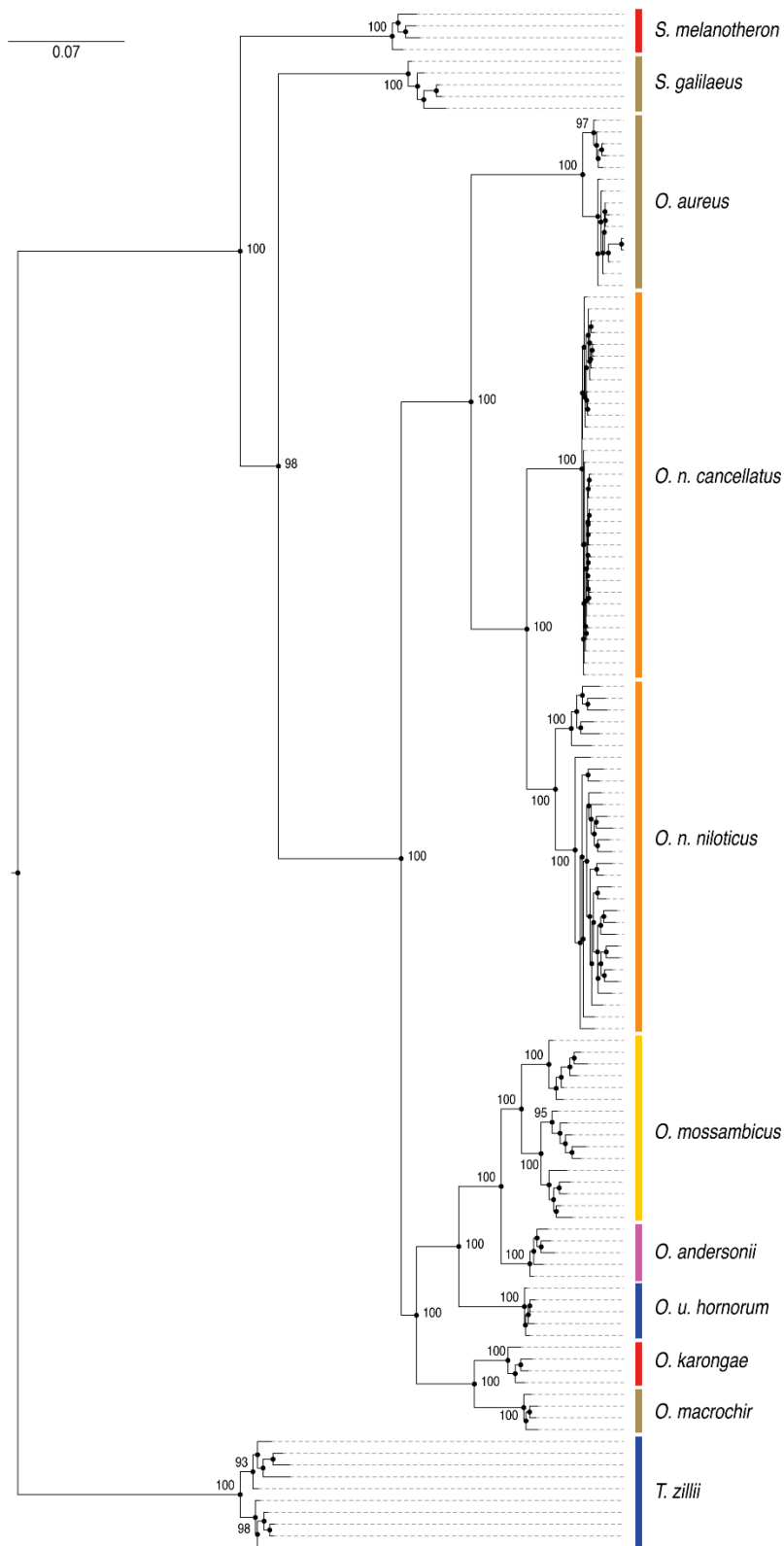


Figure S1. Phylogeny tree of tilapia species inferred from 1,371 common polymorphic SNP markers developed from *de novo*-based analysis (DBA) and rooted to *T. zillii*. All sequences were aligned, and the tree was constructed using RAxML (Randomized Axelerated Maximum Likelihood). The best ML bipartition tree is provided with bootstrap support when higher than 75%. STR, Stirling; AFI, Ein Feskha Israel; NSA, Natal South Africa.

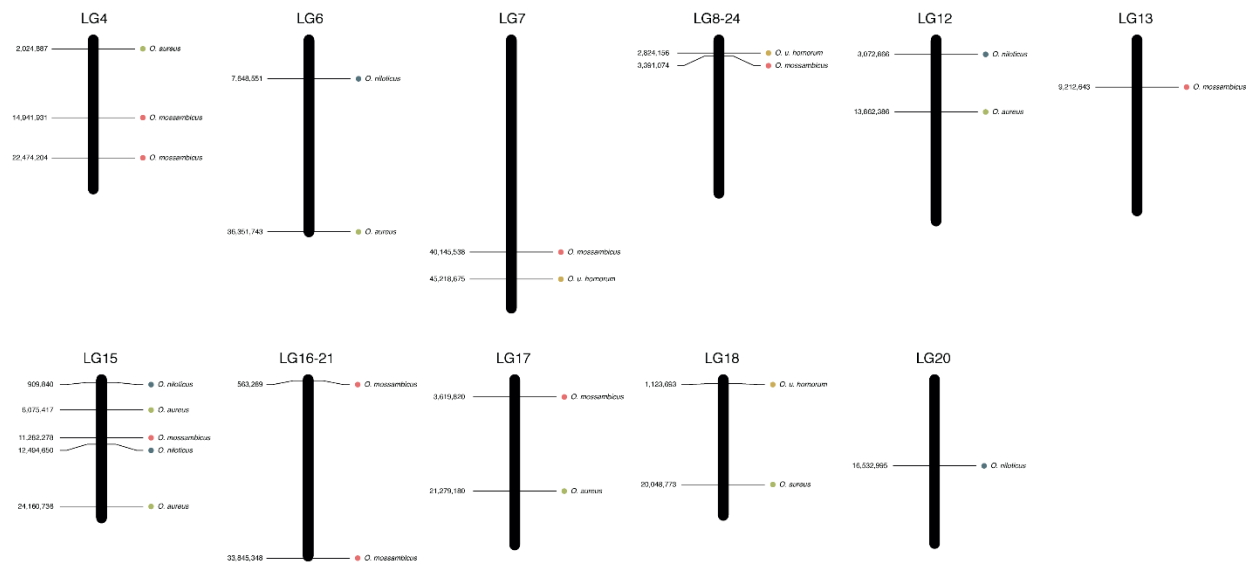


Figure S2. Distribution of 24 species-specific SNP markers (distinguishing among *O. aureus*, *O. mossambicus*, *O. niloticus* and *O. u. hornorum*) across the *O. niloticus* genome. LG: linkage group.