

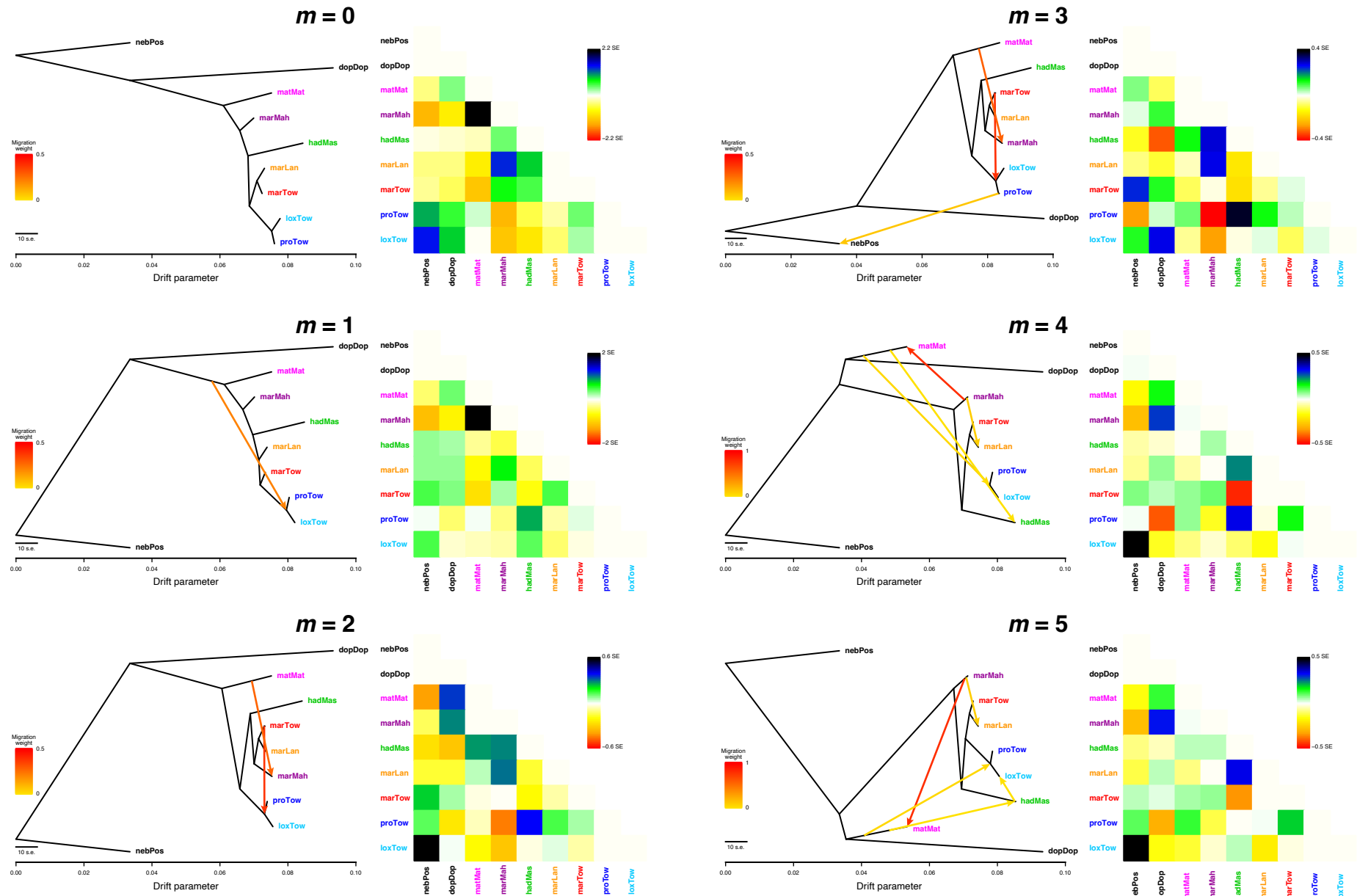


Fig. S3 Visualization of putative introgression inferred by TreeMix based on 3,947 SNPs. Maximum-likelihood trees are shown for models assuming zero to five migration events ($m = 0$ – 5). For each value of m , one representative maximum-likelihood tree from a single run is presented. Arrows indicate the inferred direction of gene flow, and color gradients represent migration weight. Heat maps display the residual covariance among population pairs given the migration events assumed in each model. loxTow: *O. loxolepis* in Lake Towuti; proTow: *O. profundicola* in Lake Towuti; marTow: *O. marmoratus* in Lake Towuti; marLan: *O. marmoratus* in Lake Lantoa; marMah: *O. marmoratus* in Lake Mahalona; hadMas: *O. hadiatyae* in Lake Masapi; matMat: *O. matanensis* in Lake Matano; nebPos: *O. nebulosus* in Lake Poso (outgroup); dopDop: *O. dopingdopingensis* in the Doping-doping River (outgroup)