

**Plotting for change: an analytic framework to aid decisions on which lineages are candidate species in phylogenomic species discovery**

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**This Dryad Entry contains the following files:**

Resem\_raw.Rdata A binary file containing the raw SNP data used in subsequent analyses. Can be loaded into R using gl <- readRDS(file="Resem\_raw.Rdata").

FD\_analysis.r R script to undertake the fixed difference analysis on the SNP genotypes. Requires Resem\_raw.Rdata.

Smelt\_raw\_allozyme\_genotypes.xlsx A table of raw genotypes for the allozyme analysis. xlsx format.

refs.S7.relabel.nex Data file for the phylogenetic analysis of *S7* ribosomal protein gene. Nexus format.

refs.tropo.relabel.nex Data file for the phylogenetic analysis of *alpha-tropomyosin* gene. Nexus format.

refs.cytb.16s.relabel.nex Data file for the phylogenetic analysis of *cytochrome b* and *16s* mtDNA sequence. Nexus format.

retro.snp.raxml.12k.phy Concatenated sequence tags with the SNPs replaced by ambiguity codes and missing (null) tags replaced with the appropriate number of Ns. This file was used as input to RAxML to generate a maximum likelihood tree as a companion to the SDV Quartets tree.

svd\_448N\_11980L.nex Input file for the SVD quartets phylogenetic analysis undertaken with PAUP, Nexus format.

retro.12k.RAxML\_bips.nwk RAxML phylogenetic tree, SNP data (relaxed filtering). Newick format.

retro.4k.RAxML\_bips.nwk RAxML phylogenetic tree, SNP data (stringent filtering). Newick format.

svd12k.tre SVDquartets phylogenetic tree, SNP data (relaxed filtering). Nexus format.

svd4k.tre SVDquartets phylogenetic tree, SNP data (stringent filtering). Nexus format.