

This populations.plink_readme.txt file was generated on 2022-01-15 by Martha Burford Reiskind

General Information

1. **Title of the journal article that uses this data set:** Resolving the phylogenetic relationship among recently diverged members of the rockfish subgenus *Sebastosomus* (MPE-D-21-00445R1)
2. **Author Information for the data file**
 - a. **Principal Investigator Contact Information**

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 - b. **Co-investigator Contact Information**

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SHARING/ACCESS INFORMATION

1. **Licenses/restrictions on the data:** None
2. **Links to publications that cite or use the data:** Molecular Phylogenetics and Evolution MPE-D-21-00445R1
3. **Links to other publicly accessible locations of the data:** None
4. **Links/relationships to ancillary data sets:** None
5. **Was the data derived from another source?** No
6. **Recommended citation for this dataset:** link to the DOI for the manuscript (will update when published)

DATA & FILE OVERVIEW

1. **File list:**
 - a. populations.plink.map and populations.plink.ped. These PLINK files were generated using STACKs *denovo* and *population* pipelines details are found in Dryad account software section: <https://doi.org/10.5061/dryad.6t1g1jx1n>
 - b. Gzip raw fq files & population map (popmap.txt) for individuals.
2. **Relationship between files:** both PLINK files were generated together from the same *population* pipeline on STACKs as one of two output files. The Gzip raw fq files underwent process radtag to rename the raw sequence reads per individual. Quality control phred scores of 30 and trimming of sequences to 90bps.
3. **No additional data was collected**

4. **Are there multiple versions of the data set?** No

METHODOLOGICAL INFORMATION

1. **Description of methods used for collection/generation of the data:** These data files were used to generate data for the following manuscript Wallace et al. 2022. Resolving the phylogenetic relationship among recently diverged members of the rockfish subgenus *Sebastosomus*. *Molecular Phylogenetics and Evolution* MPE-D-00445R1 (DOI will be included after manuscript is published)
2. **Methods for processing the data:** These data files are the raw plink files, how they were generated and how they were later processed is described in the software section of this DRYAD account: <https://doi.org/10.5061/dryad.6t1g1jx1n>. The raw sequence reads were generated as described in the manuscript and above.
3. **Software specific information:** The PLINK files were generated STACKS v.1.24, and downstream analyses were generated in PLINK v.1.19 <http://pngu.mgh.harvard.edu/purcell/plink/>
4. **People involved in process analysis and/or submission:** Martha Burford Reiskind, Andres Aguilar, Emma Wallace, and Emily Reed.

DATA SPECIFIC INFORMATION FOR: populations.plink.ped and populations.plink.map

1. **Number of Loci:** Number of variant loci (**i**) = 86,100 loci
2. **Number of Individuals:** 85 individuals, see methods section for the one individual removed in the final data set due to missing data.
3. **Headers:** Species, Individuals, Loci 1 to **i**