

GlbPSs 1.0 Manual Part 12: Documentation of `export_svars_02.0.pl`

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This tool enables you to have a look at the original sequence data and inferred alleles of a particular individual at a particular locus. It produces a FASTA file that contains the sequences of alleles and *svars*. The headers contain IDs, the inferred sequencing depths of alleles, the observed sequencing depths of *svars* and information about used and discarded *svars*. Use your favorite alignment or text editor to look at the file.

Usage

You must execute **indloc**, **poploc**, and **indpoploc** before you can use **export_svars**. The program needs two arguments: an individual ID and a locus ID (poplocID), for example:

```
export_svars_02.0.pl ind03 1068
or
perl export_svars_02.0.pl ind03 1068
```

The program produces one outfile in FASTA format in directory `export` in the main database directory. It creates this directory if it does not yet exist. The name of the outfile contains the individual ID and poplocID with extension `".fas"`, e.g. `ind03_1068.fas`. The program overwrites this file if it already exists.

The file contains sequences in this order: inferred alleles, used *svars*, discarded *svars*. The sequences are not merged, even when **poploc** has merged the allele sequences of this locus. The headers have the following fields, separated by `"_"`:

Inferred alleles:

```
popall_ID, inferred depth
```

The inferred depth can be a decimal. The program rounds the value to one decimal place when it is not an integer.

Used svars:

```
popall_ID, indloc_ID, indall_ID, svarID, "used", observed depth
```

Discarded svars:

```
"0", indloc_ID, "0", svarID, "discarded", observed depth
```