Preparing files:

1. An ancestral vcf: A vcf that has one ancestral sample only.
2. A target vcf: A vcf that you want to do the analysis (multiple samples).

\*\*All of the scripts in this analysis are local scripts, not server scripts. If you want to run it on a server, please use “create\_job.pl” or “vcf2thap\_qsub\_loop.pl”

Steps:

1. Run rehh\_new.pl

perl rehh.pl -vcf VCF\_FILE\/FOLDER -bp CHR\:POS -aid SAMPLE\_LIST\_FILE [-m METHOD][-syn][-list SAMPLE\_LIST\_FILE][-popi POP\_NAMES][-ebp EXTEND\_BP][-ka][-w WINDOW\_SIZE][-maf FLOAT][-bi][-o OUTPUT\_PATH][-sn SN][-ow][-exc][-local][-h]

Please run “perl rehh.pl” to see the detailed explanation of the functions.