**UNEAK and post-processing step by step**

1. Run UNEAK pipeline

2. Run fasFilter.pl to get Query and Hit sequences

At command prompt ‘>’ type

**> perl fasFilter.pl HapMap.fas.txt out.txt out1.txt**

out.txt contains the Query and Hit – copy and paste and add to HapMap.hmc.txt in columns 2 and 3 using Excel

Go into HapMap.hmp.txt using Excel – copy column alleles to HapMap.hmc.txt column 4

3. At this point it may help to sort the file horizontally to get indivs in order

4. Run PairDuplicates.pl to sort out rev comp issues

**> perl PairDuplicates.pl HapMap.hmc.txt 281 HapMapPaired.txt**

Where 281 is the sample size and HapMapPaired.txt is the new outfile you want to create

5. Run UNEAKfilter1.pl to call genotypes and filter by obs het and number of missing data

**> perl UNEAKfilter1biall.pl HapMapPaired.txt 281 HapMapPairedFilt.txt 56 0.75**

Where 56 is the acceptable number of missing data per locus and 0.75 is the observed

heterozygosity threshold (loci with obs het higher than this assumed to be paralogs and are

removed).

6. Run MOD\_TO\_GENEPOP.pl to create genepop file

**> perl MOD\_TO\_GENEPOP.pl HapMapPairedFilt.txt 281 HapMapGENEPOP.txt**