

(A) Dataset with only tetraploid samples

```
#define OUTFILE output_4x.txt //(str) name of output data file
#define INFILE input_4x.txt //(str) name of input data file
#define NUMINDS 749
#define NUMLOCI 298
#define LABEL 1
#define POPDATA 1
#define POPFLAG 0
#define LOCDATA 0
#define PHENOTYPE 0
#define MARKERNAMES 0
#define MAPDISTANCES 0
#define ONEROWPERIND 0
#define PHASEINFO 0
#define PHASED 0
#define RECESSIVEALLELES 1
#define EXTRACOLS 0
#define MISSING -9
#define PLOIDY 4
#define MAXPOPS 43
#define BURNIN 10000
#define NUMREPS 500000
#define NOADMIX 0
#define LINKAGE 0
#define USEPOPINFO 0
#define LOCPRIOR 0
#define INFERALPHA 1
#define ALPHA 1.0
#define POPALPHAS 0
#define UNIFPRIORALPHA 1
#define ALPHAMAX 10.0
#define ALPHAPROPSD 0.025
#define FREQSCORR 1
#define ONEFST 0
#define FPRIORMEAN 0.01
#define FPRIORS 0.05
#define INFERLAMBDA 0
#define LAMBDA 1.0
#define COMPUTEPROB 1
#define PFROMPOPFLAGONLY 0
#define ANCESTDIST 0
#define STARTATPOPINFO 0
#define METROFREQ 10
#define UPDATEFREQ 1
```

(B) Dataset with only diploid samples

```
#define OUTFILE output_dipl_2x.txt //(str) name of output data file
#define INFILE dipl_input_2x.txt //(str) name of input data file
#define NUMINDS 163
#define NUMLOCI 298
```

```
#define LABEL 1
#define POPDATA 1
#define POPFLAG 0
#define LOCDATA 0
#define PHENOTYPE 0
#define MARKERNAMES 0
#define MAPDISTANCES 0
#define ONEROWPERIND 0
#define PHASEINFO 0
#define PHASED 0
#define RECESSIVEALLELES 1
#define EXTRACOLS 0
#define MISSING -9
#define PLOIDY 2
#define MAXPOPS 11
#define BURNIN 10000
#define NUMREPS 500000
#define NOADMIX 0
#define LINKAGE 0
#define USEPOPINFO 0
#define LOCPRIOR 0
#define INFERALPHA 1
#define ALPHA 1.0
#define POPALPHAS 0
#define UNIFPRIORALPHA 1
#define ALPHAMAX 10.0
#define ALPHAPROPSD 0.025
#define FREQSCORR 1
#define ONEFST 0
#define FPRIORMEAN 0.01
#define FPRIORS 0.05
#define INFERLAMBDA 0
#define LAMBDA 1.0
#define COMPUTEPROB 1
#define PFROMPOPFLAGONLY 0
#define ANCESTDIST 0
#define STARTATPOPINFO 0
#define METROFREQ 10
#define UPDATEFREQ 1
```

(C) Whole dataset disregarding cytotype.

```
#define OUTFILE output_all.txt //(str) name of output data file
#define INFILE all_input_all.txt //(str) name of input data file
#define NUMINDS 1009
#define NUMLOCI 298
#define LABEL 1
#define POPDATA 1
#define POPFLAG 0
#define LOCDATA 0
#define PHENOTYPE 0
#define MARKERNAMES 0
```

```
#define MAPDISTANCES 0
#define ONEROWPERIND 0
#define PHASEINFO 0
#define PHASED 0
#define RECESSIVEALLELES 1
#define EXTRACOLS 0
#define MISSING -9
#define PLOIDY 2
#define MAXPOPS 56
#define BURNIN 10000
#define NUMREPS 500000
#define NOADMIX 0
#define LINKAGE 0
#define USEPOPINFO 0
#define LOCPRIOR 0
#define INFERALPHA 1
#define ALPHA 1.0
#define POPALPHAS 0
#define UNIFPRIORALPHA 1
#define ALPHAMAX 10.0
#define ALPHAPROPSD 0.025
#define FREQSCORR 1
#define ONEFST 0
#define FPRIORMEAN 0.01
#define FPRIORS 0.05
#define INFERLAMBDA 0
#define LAMBDA 1.0
#define COMPUTEPROB 1
#define PFROMPOPFLAGONLY 0
#define ANCESTDIST 0
#define STARTATPOPINFO 0
#define METROFREQ 10
#define UPDATEFREQ 1
```