set.seed**(**7**)**

nindi **<-** 19

library**(**MoBPS**)** # MoBPS is available at https://github.com/tpook92/

# Alternatively use devtools::install\_github("tpook92/MoBPS", subdir="pkg") to install

# Generate a base-population with 50k SNPs, 3 Morgan genome,

# Fully homozygous individuals,

# All plants are stored as male individuals (sex=0)

population **<-** creating.diploid**(**nindi**=**nindi, nsnp**=**50000, sex.quota **=** 0,

chromosome.length **=** 3, dataset**=**"homorandom"**)**

# Simulate matings between all founders

population **<-** breeding.diploid**(**population, breeding.size**=**c**(**nindi**\*(**nindi**-**1**)/**2,0**)**,

selection.size**=**c**(**nindi,0**)**,

breeding.all.combination **=** **TRUE**,

mutation.rate**=**10**^-**4**)**

# Simulation of 4 generations of random mating of the prior generation

**for(**index **in** 1**:**4**){**

population **<-** breeding.diploid**(**population, breeding.size**=**c**(**nindi**\*(**nindi**-**1**)/**2,0**)**,

selection.size**=**c**(**nindi**\*(**nindi**-**1**)/**2,0**)**,

same.sex.activ **=** **TRUE**, same.sex.sex**=**0,

mutation.rate**=**10**^-**4**)**

**}**

# Simulation of 10 generations of self-fertilization

# Only one offspring per plant

**for(**index **in** 1**:**10**){**

population **<-** breeding.diploid**(**population, breeding.size**=**c**(**nindi**\*(**nindi**-**1**)/**2,0**)**,

selection.size**=**c**(**nindi**\*(**nindi**-**1**)/**2,0**)**,

selfing.mating**=TRUE**, selfing.sex**=**0,

max.offspring **=** 1, mutation.rate**=**10**^-**4**)**

**}**

# Derive haplotypes of last generation and founders

# Founders are doubled haploid (only one haplotype by plant needed)

haplos **<-** get.haplo**(**population, gen**=**16**)**

founderhaplo **<-** get.haplo**(**population, gen**=**1**)[**,1**:**nindi**\***2**]**

# Derivation of the haplotype library

library**(**HaploBlocker**)**

blockl **<-** block\_calculation**(**haplos, target\_coverage **=** 0.95**)**

# Extract points of recombination for final generation in MoBPS:

recombination **<-** get.recombi**(**population, gen**=**16**)**

# Compare founder haplotypes to haplotype blocks:

start **<-** blockl**[[**1**]][[**2**]]$**snp

end **<-** blockl**[[**1**]][[**3**]]$**snp

concordance **<-** colMeans**(**founderhaplo**[**start**:**end,**]==**blockl**[[**1**]][[**7**]]$**snp**)**