

Supplementary file 2. Filtering workflow

Parental filtering

mob mutants

```
for i in {1..5}
do
  ruby manage_vcf.rb Reads/m_mutants B.vcf B_chromosome$i $i cutting_vcf
  ruby manage_vcf.rb Reads/m_mutants C.vcf C_chromosome$i $i cutting_vcf
  ruby manage_vcf.rb Reads/m_mutants/parent parent.vcf chromosome$i $i cutting_vcf
done
for i in {1..5}
do
  ruby manage_vcf.rb Reads/m_mutants B_chromosome$i/chromosome$i.vcf interesting_$i
  ruby manage_vcf.rb Reads/m_mutants C_chromosome$i/chromosome$i.vcf interesting_$i
done
```

OCF2

```
unzip Reads/OCF2/OF_output25vcf.zip
unzip Reads/OCF2/Ler/OC_parent.vcf.zip
for i in {1..5}
do
  ruby manage_vcf.rb Reads/BCF2 OF/OF_output25.vcf OCF2_chromosome$i $i cutting_vcf
  ruby manage_vcf.rb Reads/OCF2/Ler OCF2/OCF2_parent/OC_output.vcf chromosome$i $i c
done
for i in {1..5}
do
  ruby manage_vcf.rb Reads/OCF2 OCF2_chromosome$i/chromosome$i.vcf interesting_$i $
done
```

BCF2

```
for i in {1..5}
do
  ruby manage_vcf.rb Reads/BCF2 BCF2.vcf BCF2_chromosome$i $i cutting_vcf
```

```

    ruby manage_vcf.rb Reads/Aw_sup1-2 BCF2_parent.vcf chromosome$i $i cutting_vcf
done
for i in {1..5}
do
    ruby manage_vcf.rb Reads/BCF2 BCF2_chromosome$i/chromosome$i.vcf interesting_$i $
done

```

sup1

```

unzip Reads/Aw_sup1-2/vcfs.zip
unzip Reads/Parental/vcfs.zip
for i in {1..5}
do
    ruby manage_vcf.rb Reads/Aw_sup1-2 vcfs/sup1.vcf sup1_chromosome$i $i cutting_vcf
    ruby manage_vcf.rb Reads/Aw_sup1-2 Parental/vcfs/colT.vcf Parental/colT_chromosome$i
    ruby manage_vcf.rb Reads/Aw_sup1-2 Parental/vcfs/WsT.vcf Parental/Ws_chromosome$i
done
for i in {1..5}
do
    ruby manage_vcf.rb Reads/Aw_sup1-2 sup1_chromosome$i/chromosome$i.vcf filter1_chromosome
done
for i in {1..5}
do
    ruby manage_vcf.rb Reads/Aw_sup1-2 filter1_chromosome$i/chromosome$i.vcf filter2_chromosome
done

```

Centromere filtering

```

for i in {1..5}
do
    ruby remove_cent.rb $i Aw_sup1-2/filter2_chromosome$i
    ruby remove_cent.rb $i BCF2/BCF2_chromosome$i
    ruby remove_cent.rb $i OCF2/OCF2_chromosome$i
    ruby remove_cent.rb $i B/B_chromosome$i
    ruby remove_cent.rb $i C/C_chromosome$i
done

```

SNP density analysis

```
for i in {1..5}; do ruby snp_density.rb $i BCF2 BCF2_chromosome$i interesting_$i BCF2;
for i in {1..5}; do ruby snp_density.rb $i OCF2 OCF2_chromosome$i Interesting_$i OCF2;
for i in {1..5}; do ruby snp_density.rb $i m_mutants B_chromosome$i interesting_$i mob;
for i in {1..5}; do ruby snp_density.rb $i m_mutants C_chromosome$i interesting_$i mob;
for i in {1..5}; do ruby snp_density.rb $i Aw_sup1-2 sup1_chromosome$i ../filter2_chro
```

Model genomes with real densities

```
ruby model_genome_real_hpc.rb No_centromere/2-5kb_contig/sup1_nocen_chr4_2kb 2000
ruby model_genome_real_hpc.rb No_centromere/2-5kb_contig/sup1_nocen_chr4_5kb 5000
ruby model_genome_real_hpc.rb No_centromere/10kb_contig/sup1_nocen_chr4_10kb 10000
```

```
ruby model_genome_real_hpc.rb No_centromere/2-5kb_contig/bcf2_nocen_ch2_2kb 2000 ara
ruby model_genome_real_hpc.rb No_centromere/2-5kb_contig/bcf2_nocen_ch5_5kb 5000 ara
ruby model_genome_real_hpc.rb No_centromere/10kb_contig/bcf2_nocen_ch5_10kb 10000 ara
```

```
ruby model_genome_real_hpc.rb No_centromere/2-5kb_contig/ocf2_nocen_chr3_2kb 2000
ruby model_genome_real_hpc.rb No_centromere/2-5kb_contig/ocf2_nocen_chr3_5kb 5000
ruby model_genome_real_hpc.rb No_centromere/10kb_contig/ocf2_nocen_chr3_10kb 10000
```

```
ruby model_genome_real_hpc.rb No_centromere/2-5kb_contig/C_nocen_chr5_2kb 2000 ara
ruby model_genome_real_hpc.rb No_centromere/2-5kb_contig/C_nocen_chr5_5kb 5000 ara
ruby model_genome_real_hpc.rb No_centromere/10kb_contig/C_nocen_chr5_10kb 10000 ara
```

```
ruby model_genome_real_hpc.rb No_centromere/2-5kb_contig/B_nocen_chr5_2kb 2000 ara
ruby model_genome_real_hpc.rb No_centromere/2-5kb_contig/B_nocen_chr5_5kb 5000 ara
ruby model_genome_real_hpc.rb No_centromere/10kb_contig/B_nocen_chr5_10kb 10000 ara
```