

Xantusia output from **populations** with -p 1 -r 0.5, then plink filters in order:

1. filter loci with less than 60% sequenced

Options in effect:

```
--ped Xr.ALL.new-z.ped
--map Xr.SBI.map
--geno 0.4
--out Xr.denovo-a
--recode
--noweb
```

Before frequency and genotyping pruning, there are 83445 SNPs
141 founders and 0 non-founders found
Total genotyping rate in remaining individuals is 0.301829
80300 SNPs failed missingness test (GENO > 0.4)
0 SNPs failed frequency test (MAF < 0)
After frequency and genotyping pruning, there are 3145 SNPs

2. filter individuals that have less than 50% data

Options in effect:

```
--ped Xr.denovo-a.ped
--map Xr.denovo-a.map
--mind 0.5
--out Xr.denovo-b
--recode
--noweb
```

Before frequency and genotyping pruning, there are 3145 SNPs
141 founders and 0 non-founders found
Writing list of removed individuals to [Xr.denovo-b.irem]
49 of 141 individuals removed for low genotyping (MIND > 0.5)
Total genotyping rate in remaining individuals is 0.815812
0 SNPs failed missingness test (GENO > 1)
0 SNPs failed frequency test (MAF < 0)
After frequency and genotyping pruning, there are 3145 SNPs

3. filter loci genotyped in less than 50% individuals and MAF < 0.02 in remaining individuals

Options in effect:

--ped Xr.denovo-b.ped

--map Xr.denovo-b.map

--geno 0.5

--maf 0.02

--out Xr.denovo-c

--recode

--noweb

Before frequency and genotyping pruning, there are 3145 SNPs

92 founders and 0 non-founders found

Total genotyping rate in remaining individuals is 0.815812

0 SNPs failed missingness test (GENO > 0.5)

2027 SNPs failed frequency test (MAF < 0.02)

After frequency and genotyping pruning, there are 1118 SNPs

Final genotyping rate:

Total genotyping rate in remaining individuals is 0.816938