Notes

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GBS data Summary

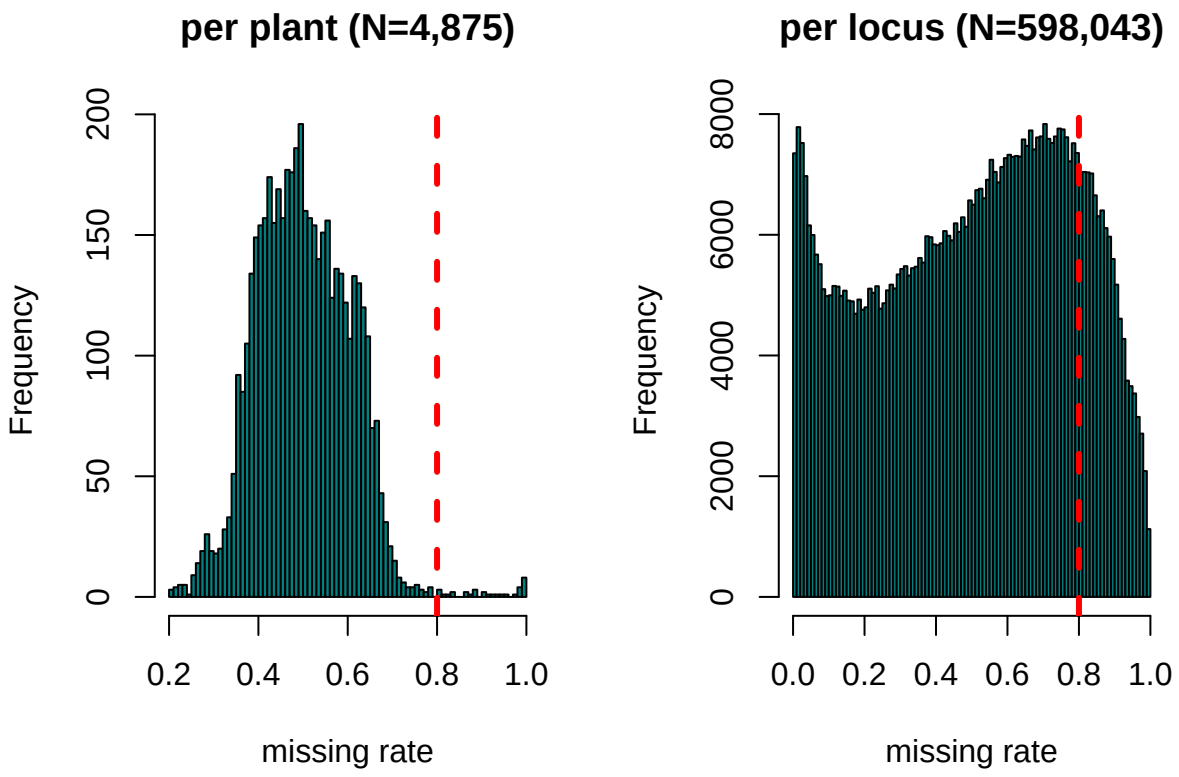
Loading HDF5 format GBS raw data

- loading in genotypes from HDF5 file `largedata/teo.h5`
- filtering biallelic loci: Removed `357,647` non-biallelic loci.
- data matrix dimension: [1:598043, 1:4875]

The missing rates were plotted as below for 598,043 SNPs of 4,875 plants (70/4,875 (1.4%) are founder lines). Note several plants have very high SNP missing rate, i.e. > 80%. Some of them even have a 100% missing rate. In addition, ~20% of them have very high (>80%) per locus missing rate.

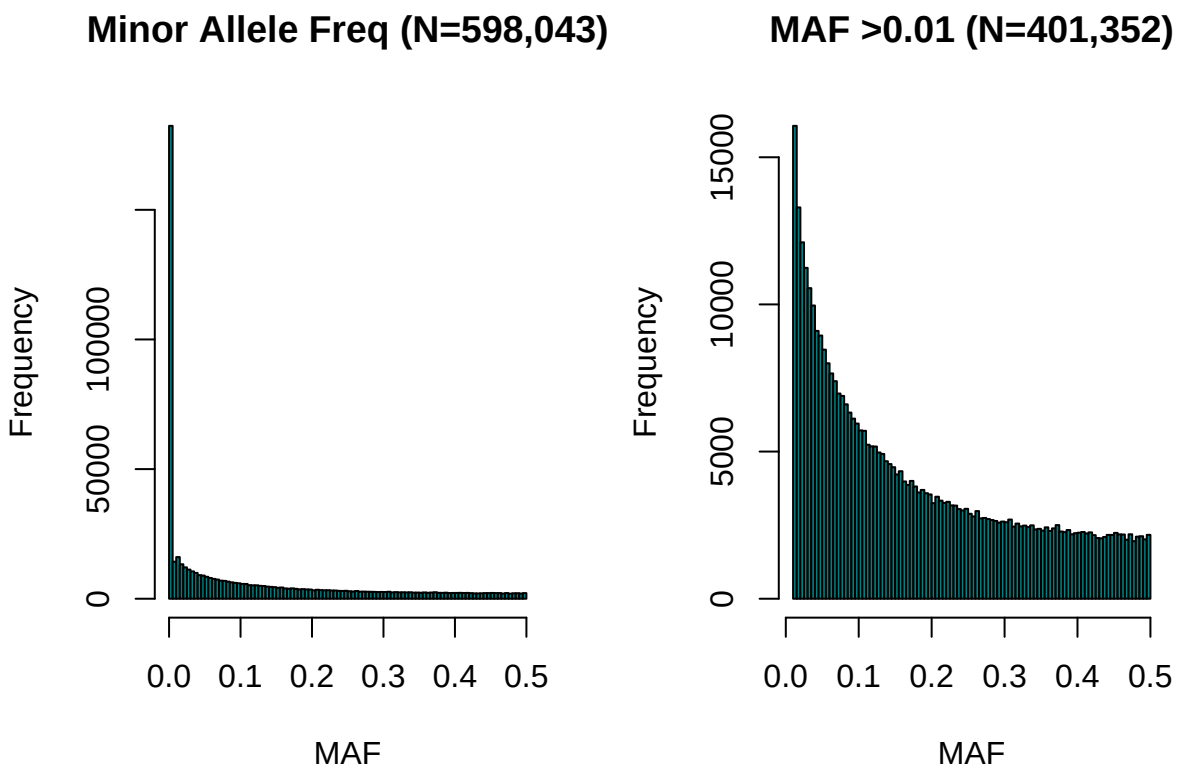
```
# source("../profiling/2.ci_data/2.A.1_vsb_hdf5.R")
info <- read.csv("../data/teo_info.csv")
imiss <- read.csv("../data/teo_imiss.csv")

par(mfrow=c(1,2))
hist(imiss$imiss, main="per plant (N=4,875)", col="#008080", breaks=100, xlab="missing rate")
abline(v=0.8, col="red", lty=2, lwd=3)
hist(info$lmiss, main="per locus (N=598,043)", col="#008080", breaks=100, xlab="missing rate")
abline(v=0.8, col="red", lty=2, lwd=3)
```



```
par(mfrow=c(1,2))
hist(info$maf, main="Minor Allele Freq (N=598,043)", col="#008080", breaks=100, xlab="MAF")
abline(v=0.8, col="red", lty=2, lwd=3)

hist(subset(info, maf>0.01)$maf, main="MAF >0.01 (N=401,352)", col="#008080", breaks=100, xlab="MAF")
abline(v=0.8, col="red", lty=2, lwd=3)
```



See above the MAF plots. Note 196665 SNPs have the MAF < 0.01.

Parentage Infomation

```
# source("../profiling/2.ci_data/2.B.1_cj_parentage.R")
pinfo <- read.table("../data/parentage_sum.txt", header=TRUE)
#dim(pinfo) 68,5
subset(pinfo, !is.na(WGS))
```

```
##           sid                   founder nselfer nox WGS
## 5  PC_I11_ID2 PC_I11_ID2_mrg:250276264      43 126 yes
## 7  PC_I50_ID2 PC_I50_ID2_mrg:250276265      55 101 yes
## 10 PC_I55_ID2 PC_I55_ID2_mrg:250276267      81  94 yes
## 12 PC_I58_ID2 PC_I58_ID2_mrg:250276268      30 105 yes
## 16 PC_J07_ID2 PC_J07_ID2_mrg:250276269      40  92 yes
## 22 PC_J14_ID2 PC_J14_ID2_mrg:250276270      60  63 yes
## 23 PC_J48_ID2 PC_J48_ID2_mrg:250276262      46 101 yes
## 29 PC_K55_ID2 PC_K55_ID2_mrg:250276291      47 135 yes
## 31 PC_L06_ID2 PC_L06_ID2_mrg:250276271      24  98 yes
```

```
## 35 PC_L12_ID2 PC_L12_ID2_mrg:250276272      61  57 yes
## 38 PC_L48_ID2 PC_L48_ID2_mrg:250276273      48  78 yes
## 44 PC_N03_ID2 PC_N03_ID2_mrg:250276274      14 107 yes
## 47 PC_N07_ID2 PC_N07_ID2_mrg:250276276      38  95 yes
## 50 PC_N10_ID2 PC_N10_ID2_mrg:250276277      45  47 yes
## 54 PC_N14_ID2 PC_N14_ID2_mrg:250276278      58  85 yes
## 58 PC_N57_ID2 PC_N57_ID2_mrg:250276279      45 116 yes
## 60 PC_N58_ID2 PC_N58_ID2_mrg:250276280      46 141 yes
## 63 PC_O08_ID2 PC_O08_ID2_mrg:250276281      62  97 yes
## 66 PC_O51_ID2 PC_O51_ID2_mrg:250276282      97  13 yes
```

```
subset(pinfo, nox < 30)
```

```
##           sid                   founder nselfer nox  WGS
## 4  PC_I11_ID1   PC_I11_ID1_1:250276201      NA   7 <NA>
## 9  PC_I53_ID1   PC_I53_ID1_1:250276206      NA   4 <NA>
## 13 PC_J01_ID1   PC_J01_ID1_1:250276209      NA   1 <NA>
## 15 PC_J07_ID1   PC_J07_ID1_1:250276211      NA  28 <NA>
## 21 PC_J14_ID1   PC_J14_ID1_1:250276217      NA  16 <NA>
## 28 PC_K55_ID1   PC_K55_ID1_1:250276224      NA   4 <NA>
## 33 PC_L10_ID1   PC_L10_ID1_1:250276228      NA   6 <NA>
## 37 PC_L48_ID1   PC_L48_ID1_1:250276231      NA  19 <NA>
## 49 PC_N10_ID1   PC_N10_ID1_1:250276243      NA   2 <NA>
## 53 PC_N14_ID1   PC_N14_ID1_1:250276247      NA   1 <NA>
## 56 PC_N56_ID1   PC_N56_ID1_1:250276250      NA  15 <NA>
## 57 PC_N57_ID1   PC_N57_ID1_1:250276251      NA   5 <NA>
## 61 PC_N60_ID1   PC_N60_ID1_1:250276255      NA   3 <NA>
## 62 PC_O08_ID1   PC_O08_ID1_1:250276256      NA  12 <NA>
## 64 PC_O10_ID1   PC_O10_ID1_1:250276258      NA  15 <NA>
## 65 PC_O51_ID1   PC_O51_ID1_1:250276259      NA   5 <NA>
## 66 PC_O51_ID2 PC_O51_ID2_mrg:250276282      97  13  yes
## 67 PC_O59_ID1   PC_O59_ID1_1:250276261      NA  29 <NA>
```

We calculated the number of selfers and the number of outcrossers associated with the founder lines. In total, 68 unique founder lines were involved in the crosses. Among them, 49 founder lines had selfing families; and ten smallest family size were 3, 7, 12, 14, 15, 16, 18, 20, 22, 24.

WGS of 19 *Teosintes*

```
# source("../profiling/2.ci_data/2.B.2_cj_wgsdata.R")
```

Comparing GBS vs. WGS

```
par(mfrow=c(1,2))
hist(lmiss1, main="WGS (N=301,249)", ylim=c(0, 70000), col="#008080", breaks=50, xlab="missing rate")
#abline(v=0.8, col="red", lty=2, lwd=3)
```

```r
hist(lmiss2, main="GBS (N=301,249)", ylim=c(0, 70000), col="#008080", breaks=50, xlab="missing rate")
#abline(v=0.8, col="red", lty=2, lwd=3)

par(mfrow=c(1,2))
hist(imiss1, main="WGS (N=19)",  col="#008080",  xlab="missing rate")
#abline(v=0.8, col="red", lty=2, lwd=3)
hist(imiss2, main="GBS (N=19)",  col="#008080",  xlab="missing rate")
#abline(v=0.8, col="red", lty=2, lwd=3)

par(mfrow=c(1,2))
hist(maf1, main="WGS (N=301,249)",  col="#008080",  xlab="MAF")
#abline(v=0.8, col="red", lty=2, lwd=3)
hist(maf2, main="GBS (N=301,249)",  col="#008080",  xlab="MAF")
#abline(v=0.8, col="red", lty=2, lwd=3)
```