ALA 4.5 Estimating genetic relationships from molecular marker data.

Files:

QG_Mod4_ALA4.5_eval dist metrics.csv (note: .xlsx file also provided)
QG_Mod4_ALA4.5_eval dist metrics.xlsx
QG_Mod4_ALA4.5_dist eval.R

Goal:

Develop the ability to evaluate R functions based on known mathematical metrics.

Purpose:

Demonstrate and have the students participate in the evaluation of R "dist" functions using known genetic relationships.

ALA:

In ALAs from Chapter 3 and ALAs 4.2, 4.3, and 4.4 genetic diversity among the lines is based on pedigree information. Since the development of genome-wide molecular markers, it has become possible to determine realized relationships among lines, hybrids, individuals, etc.

The "dist" function in the R-code will determine the following distance metrics that can be used with clustering and dendrogram packages to visualize the relationships:

1. Euclidean:

   Usual distance between the two vectors (2 norm aka *L_2*), *sqrt(sum((x_i - y_i)^2))*.

2. Manhattan:

   Absolute distance between the two vectors (1 norm aka L1).

3. Canberra:

   ∑i|xi−yi|/(|xi|+|yi|). Terms with zero numerator and denominator are omitted from the sum and treated as if the values were missing. This is intended for non-negative values (e.g., counts), in which case the denominator can be written in various equivalent ways; Originally, R used xi+yi, then from 1998 to 2017, |xi+yi|, and then the correct |xi|+|yi|.

4. Binary (aka *asymmetric binary*):

   The vectors are regarded as binary bits, so non-zero elements are 'on' and zero elements are 'off'. The distance is the *proportion* of bits in which only one is on amongst those in which at least one is on.

5. Minkowski:

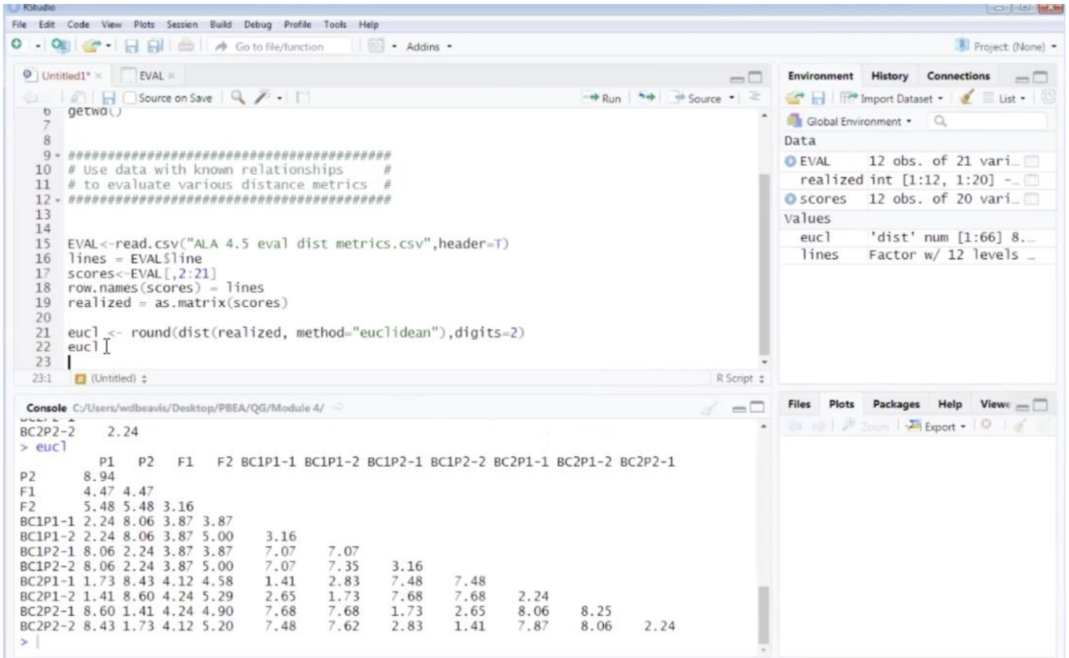
The p norm, the pth root of the sum of the pth powers of the differences of the components.

Ask students to consider which of these metrics provides the most accurate estimate of relationships among doubled haploid or recombinant inbred lines. Have them devise approaches to answer this question.

Provide a demonstration of how to evaluate metrics that you have never seen before by using a small data set consisting of a few individuals and a few markers.

For example, create a set of backcross series to each of the parents, such as found in “ALA 4.5 eval dist metrics.csv”.  Then observe the calculated distance measures and decide which most accurately reflects the true distances.

1. Euclidean distance

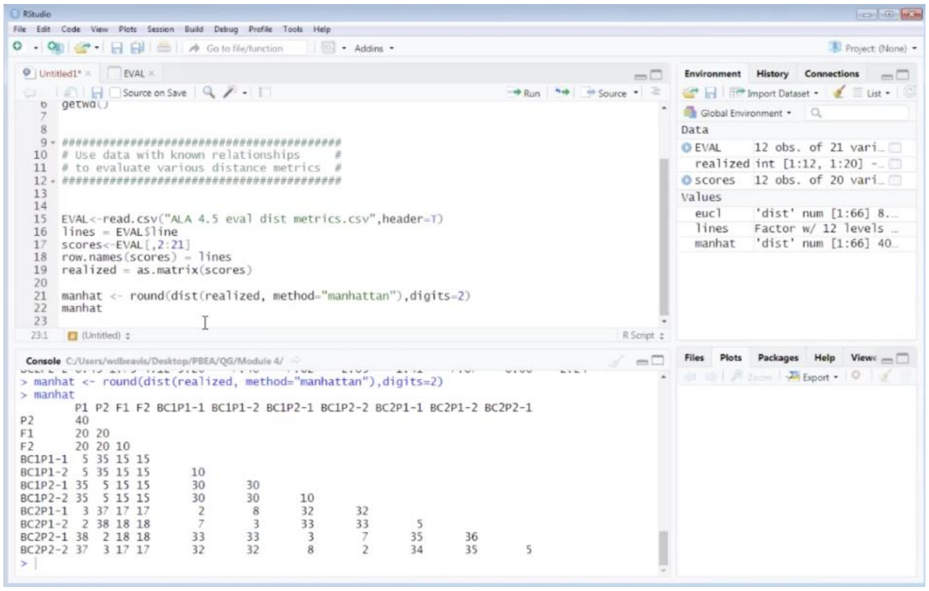


```
getwd()


###########################################
# Use data with known relationships      #
# to evaluate various distance metrics   #
###########################################


EVAL<-read.csv("ALA 4.5 eval dist metrics.csv",header=T)
lines = EVAL$line
scores<-EVAL[,2:21]
row.names(scores) = lines
realized = as.matrix(scores)

eucl <- round(dist(realized, method="euclidean"),digits=2)
eucl

```

```
BC2P2-2    2.24
> eucl
          P1   P2   F1   F2 BC1P1-1 BC1P1-2 BC1P2-1 BC1P2-2 BC2P1-1 BC2P1-2 BC2P2-1
P2      8.94
F1      4.47 4.47
F2      5.48 5.48 3.16
BC1P1-1 2.24 8.06 3.87 3.87
BC1P1-2 2.24 8.06 3.87 5.00    3.16
BC1P2-1 8.06 2.24 3.87 3.87    7.07    7.07
BC1P2-2 8.06 2.24 3.87 5.00    7.07    7.35    3.16
BC2P1-1 1.73 8.43 4.12 4.58    1.41    2.83    7.48    7.48
BC2P1-2 1.41 8.60 4.24 5.29    2.65    1.73    7.68    7.68    2.24
BC2P2-1 8.60 1.41 4.24 4.90    7.68    7.68    1.73    2.65    8.06    8.25
BC2P2-2 8.43 1.73 4.12 5.20    7.48    7.62    2.83    1.41    7.87    8.06    2.24
> 
```

```
Data
EVAL      12 obs. of 21 vari…
 realized int [1:12, 1:20] -…
scores    12 obs. of 20 vari…
Values
 eucl     'dist' num [1:66] 8.…
 lines    Factor w/ 12 levels …
```

2. Manhattan



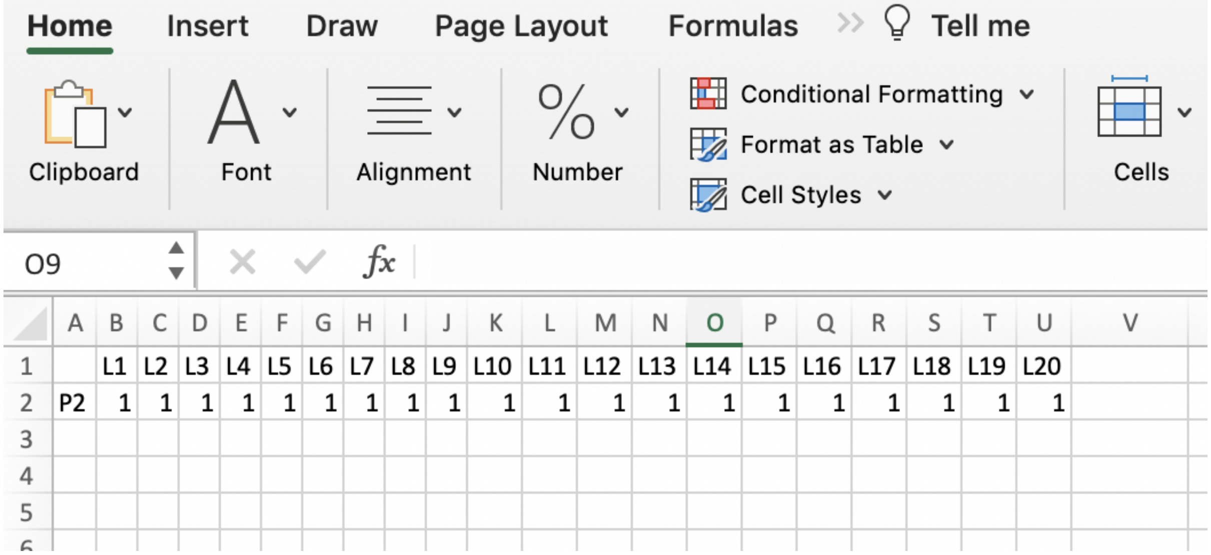
```
getwd()


###########################################
# Use data with known relationships      #
# to evaluate various distance metrics   #
###########################################


EVAL<-read.csv("ALA 4.5 eval dist metrics.csv",header=T)
lines = EVAL$line
scores<-EVAL[,2:21]
row.names(scores) = lines
realized = as.matrix(scores)

manhat <- round(dist(realized, method="manhattan"),digits=2)
manhat

```

```
> manhat <- round(dist(realized, method="manhattan"),digits=2)
> manhat
        P1 P2 F1 F2 BC1P1-1 BC1P1-2 BC1P2-1 BC1P2-2 BC2P1-1 BC2P1-2 BC2P2-1
P2      40
F1      20 20
F2      20 20 10
BC1P1-1  5 35 15 15
BC1P1-2  5 35 15 15      10
BC1P2-1 35  5 15 15      30      30
BC1P2-2 35  5 15 15      30      30      10
BC2P1-1  3 37 17 17       2       8      32      32
BC2P1-2  2 38 18 18       7       3      33      33       5
BC2P2-1 38  2 18 18      33      33       3       7      35      36
BC2P2-2 37  3 17 17      32      32       8       2      34      35       5
> |
```

```
Data
EVAL       12 obs. of 21 vari…
realized   int [1:12, 1:20] -…
scores     12 obs. of 20 vari…
Values
eucl       'dist' num [1:66] 8.…
lines      Factor w/ 12 levels …
manhat     'dist' num [1:66] 40…
```

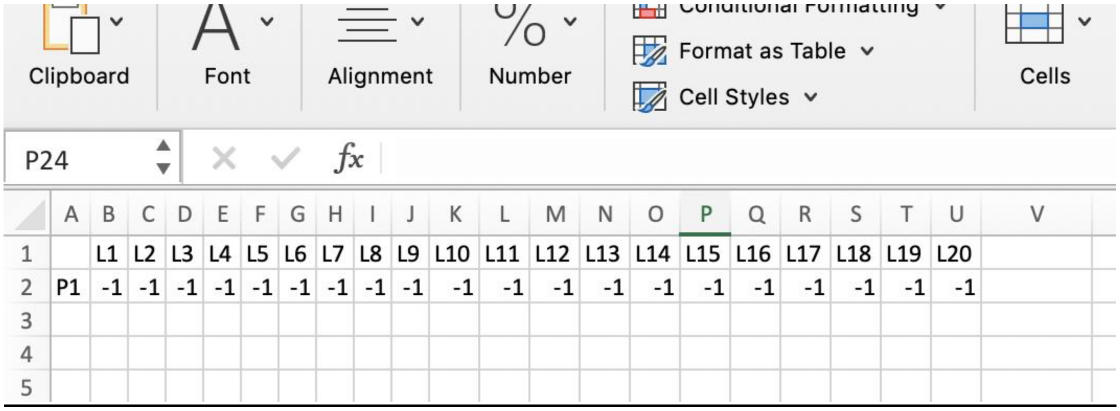
Note: Manhattan gives the most accurate sets of relationships based on what is known about the individuals.

There is always a reference line, in this case our reference line is Parent 2; 1 represents the homozygote for parent 2 at individual loci.



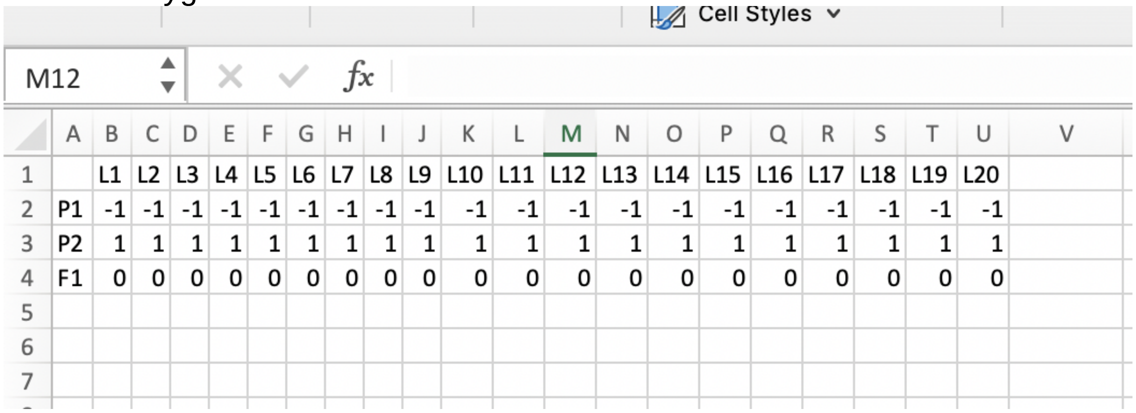
|   | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S | T | U | V |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 |  | L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | L10 | L11 | L12 | L13 | L14 | L15 | L16 | L17 | L18 | L19 | L20 |  |
| 2 | P2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |  |
| 3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

Next, to translate the information of unrelated line (P1) in relation to the reference line; -1 represents the homozygote for parent 1; which is the alternate allele of parent 2 at individual loci.



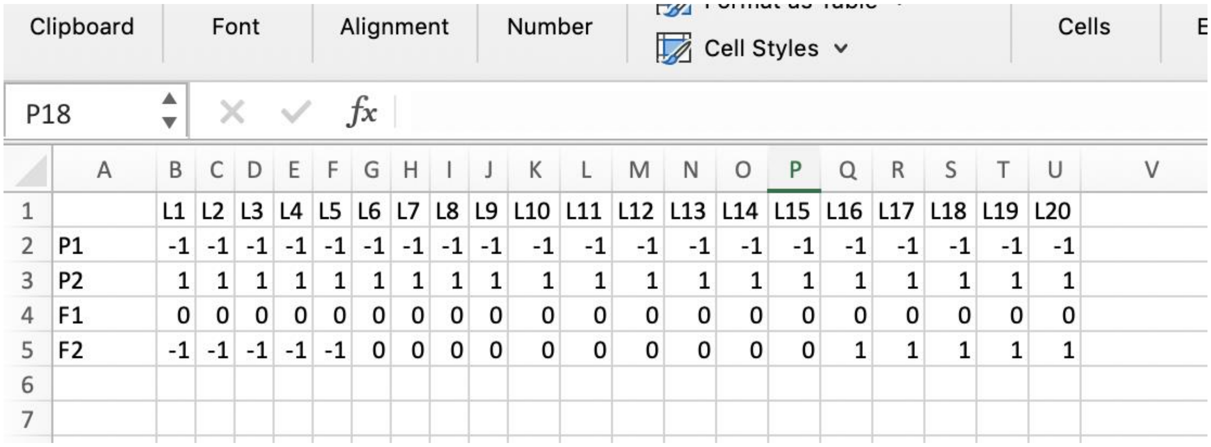
| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S | T | U | V |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | L10 | L11 | L12 | L13 | L14 | L15 | L16 | L17 | L18 | L19 | L20 | |
| 2 | P1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | |
| 3 | | | | | | | | | | | | | | | | | | | | | | |
| 4 | | | | | | | | | | | | | | | | | | | | | | |
| 5 | | | | | | | | | | | | | | | | | | | | | | |

Next, to translate the information of F1 in relation to the reference line; 0 represents the heterozygote at individual loci



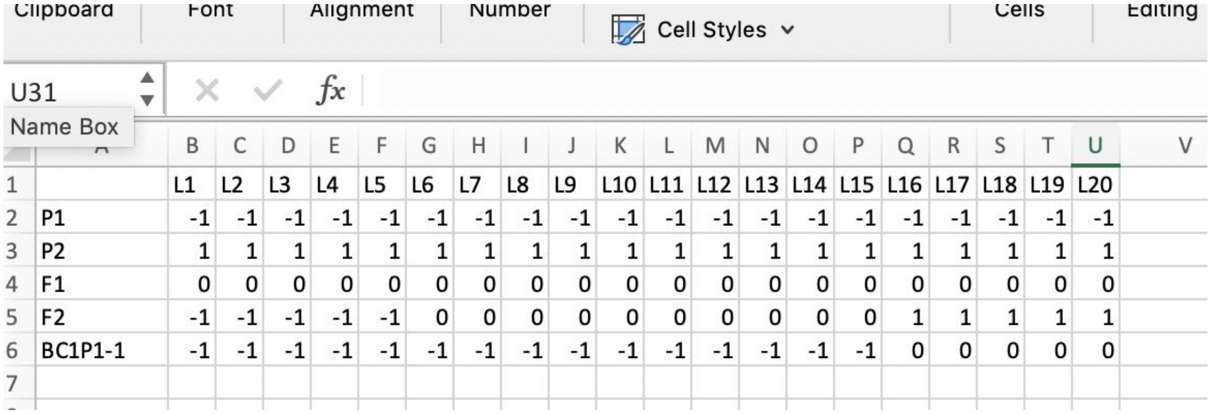
| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S | T | U | V |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | L10 | L11 | L12 | L13 | L14 | L15 | L16 | L17 | L18 | L19 | L20 | |
| 2 | P1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | |
| 3 | P2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| 4 | F1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| 5 | | | | | | | | | | | | | | | | | | | | | | |
| 6 | | | | | | | | | | | | | | | | | | | | | | |
| 7 | | | | | | | | | | | | | | | | | | | | | | |

Next, to translate the information of F2 in relation to the reference line; 1 represents the homozygote for parent 2 at individual loci -1 represents the homozygote for parent 1; 0 represent heterozygote at individual loci



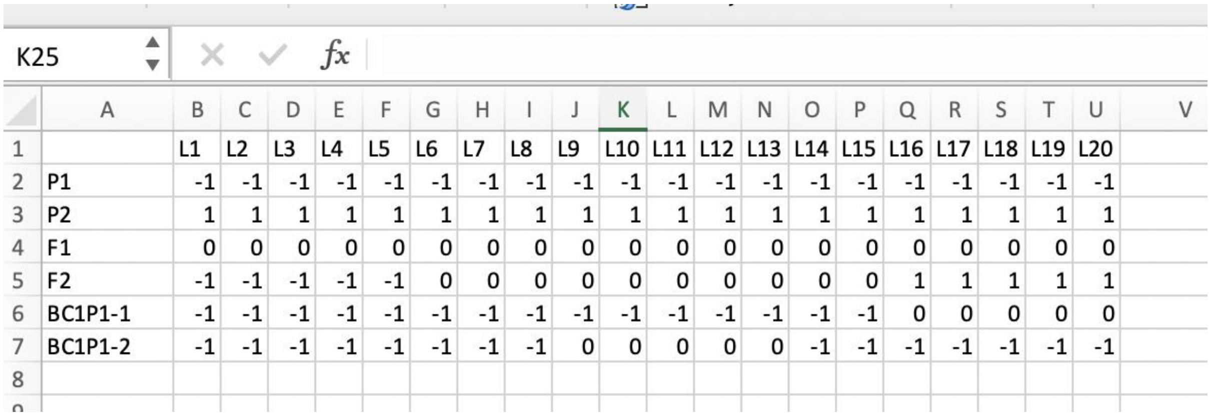
| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S | T | U | V |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | L10 | L11 | L12 | L13 | L14 | L15 | L16 | L17 | L18 | L19 | L20 | |
| 2 | P1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | |
| 3 | P2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| 4 | F1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| 5 | F2 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | |
| 6 | | | | | | | | | | | | | | | | | | | | | | |
| 7 | | | | | | | | | | | | | | | | | | | | | | |

Next, to translate the information of BC1P1-1 in relation to the reference line; 1 represents the homozygote for parent 2 at individual loci; -1 represents the homozygote for parent 1; 0 represent heterozygote at individual loci



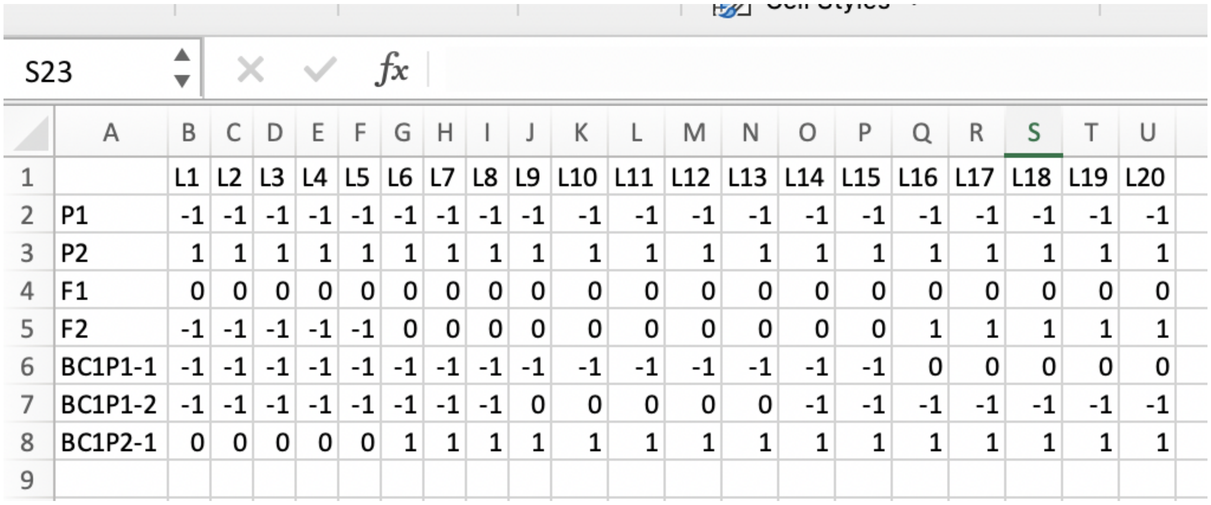
| | L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | L10 | L11 | L12 | L13 | L14 | L15 | L16 | L17 | L18 | L19 | L20 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| P1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |
| P2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| F1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| F2 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 |
| BC1P1-1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 |

Next, to translate the information of BC1P1-2 in relation to the reference line; 1 represents the homozygote for parent 2 at individual loci; -1 represents the homozygote for parent 1; 0 represent heterozygote at individual loci



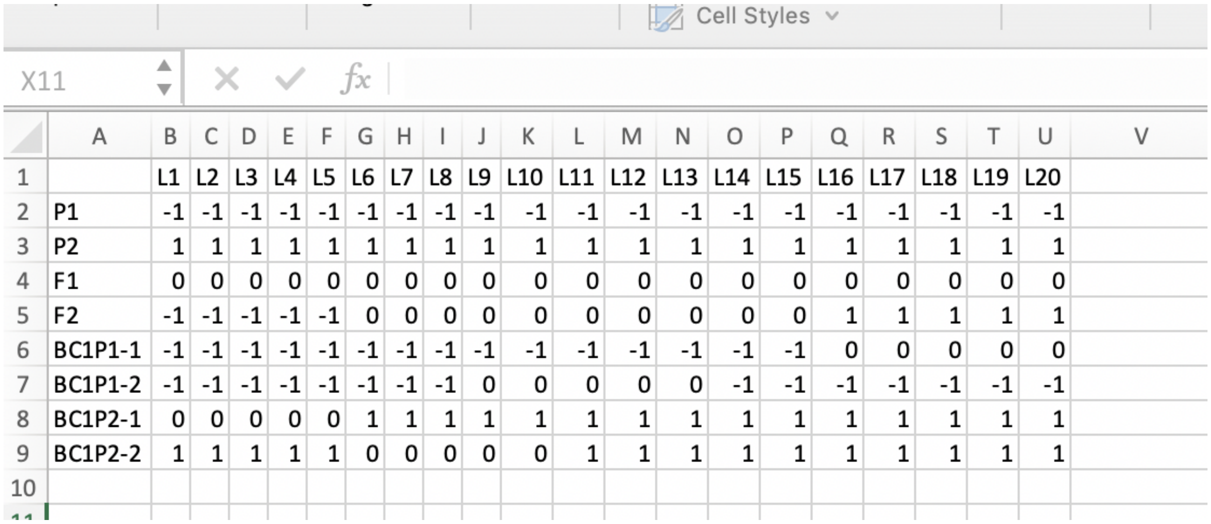
| | L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | L10 | L11 | L12 | L13 | L14 | L15 | L16 | L17 | L18 | L19 | L20 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| P1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |
| P2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| F1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| F2 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 |
| BC1P1-1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 |
| BC1P1-2 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |

Next, to translate the information of BC1P2-1 in relation to the reference line; 1 represents the homozygote for parent 2 at individual loci; 0 represent heterozygote at individual loci.



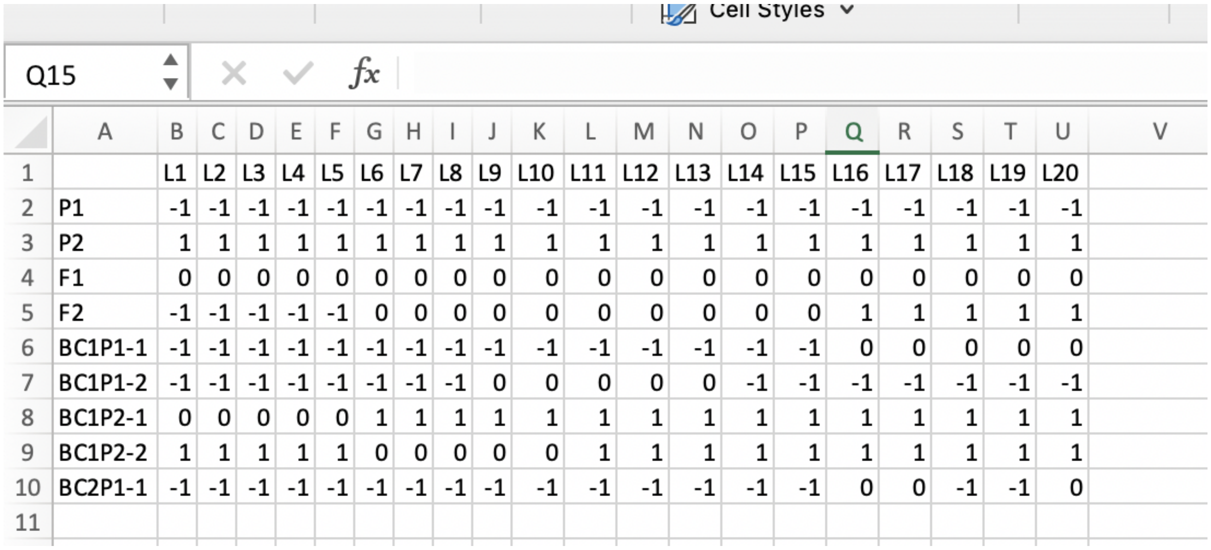
| | L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | L10 | L11 | L12 | L13 | L14 | L15 | L16 | L17 | L18 | L19 | L20 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| P1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |
| P2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| F1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| F2 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 |
| BC1P1-1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 |
| BC1P1-2 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |
| BC1P2-1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

Next, to translate the information of BC1P2-2 in relation to the reference line; 1 represents the homozygote for parent 2 at individual loci; 0 represent heterozygote at individual loci.



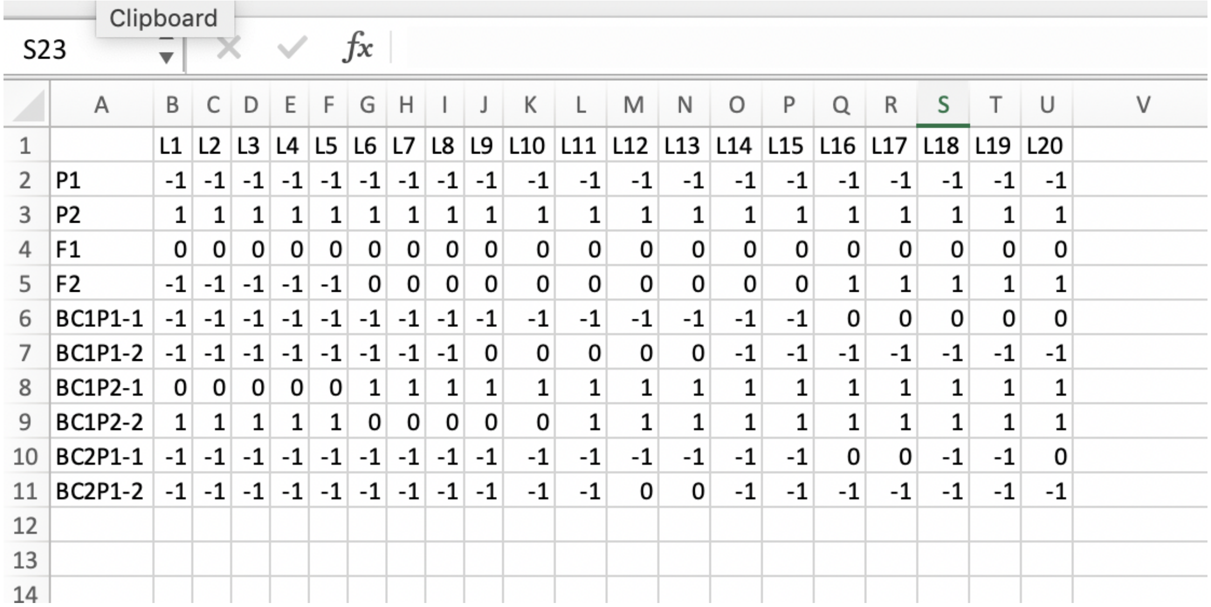
| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S | T | U | V |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | L10 | L11 | L12 | L13 | L14 | L15 | L16 | L17 | L18 | L19 | L20 | |
| 2 | P1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | |
| 3 | P2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| 4 | F1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| 5 | F2 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | |
| 6 | BC1P1-1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | |
| 7 | BC1P1-2 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | |
| 8 | BC1P2-1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| 9 | BC1P2-2 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| 10 | | | | | | | | | | | | | | | | | | | | | | |

Next, to translate the information of BC2P1-1 in relation to the reference line; 1 represents the homozygote for parent 2 at individual loci; -1 represents the homozygote for parent 1; 0 represent heterozygote at individual loci



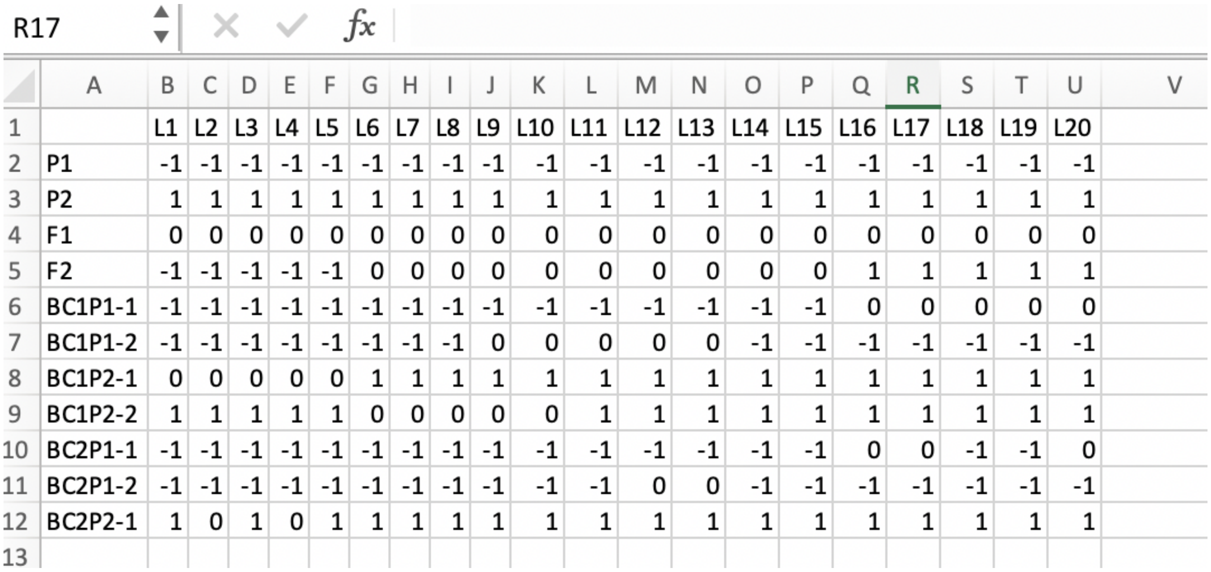
| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S | T | U | V |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | L10 | L11 | L12 | L13 | L14 | L15 | L16 | L17 | L18 | L19 | L20 | |
| 2 | P1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | |
| 3 | P2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| 4 | F1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |
| 5 | F2 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | |
| 6 | BC1P1-1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | |
| 7 | BC1P1-2 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | |
| 8 | BC1P2-1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| 9 | BC1P2-2 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| 10 | BC2P1-1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | -1 | -1 | 0 | |
| 11 | | | | | | | | | | | | | | | | | | | | | | |

Next, to translate the information of BC2P1-2 in relation to the reference line; 1 represents the homozygote for parent 2 at individual loci; -1 represents the homozygote for parent 1; 0 represent heterozygote at individual loci.



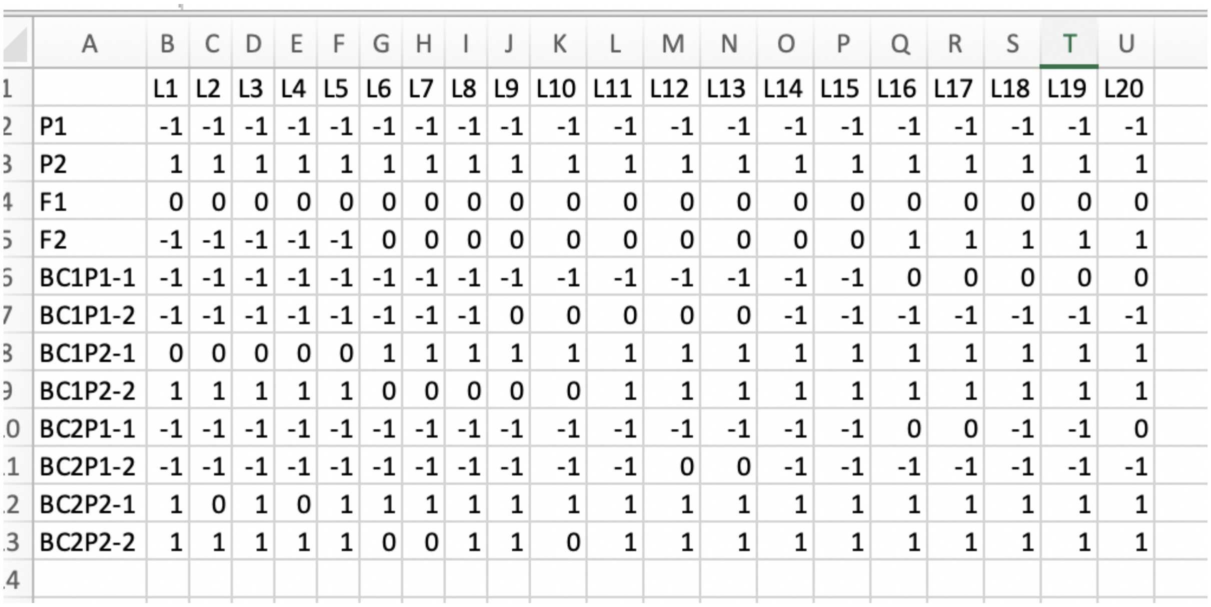
| | L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | L10 | L11 | L12 | L13 | L14 | L15 | L16 | L17 | L18 | L19 | L20 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| P1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |
| P2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| F1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| F2 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 |
| BC1P1-1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 |
| BC1P1-2 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |
| BC1P2-1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| BC1P2-2 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| BC2P1-1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | -1 | -1 | 0 |
| BC2P1-2 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |

Next, to translate the information of BC2P2-1 in relation to the reference line; 1 represents the homozygote for parent 2 at individual loci; -1 represents the homozygote for parent 1; 0 represent heterozygote at individual loci.



| | L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | L10 | L11 | L12 | L13 | L14 | L15 | L16 | L17 | L18 | L19 | L20 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| P1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |
| P2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| F1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| F2 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 |
| BC1P1-1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 |
| BC1P1-2 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |
| BC1P2-1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| BC1P2-2 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| BC2P1-1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | -1 | -1 | 0 |
| BC2P1-2 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |
| BC2P2-1 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

Next, to translate the information of BC2P2-2 in relation to the reference line; 1 represents the homozygote for parent 2 at individual loci; -1 represents the homozygote for parent 1; 0 represent heterozygote at individual loci.



| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S | T | U |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | L10 | L11 | L12 | L13 | L14 | L15 | L16 | L17 | L18 | L19 | L20 |
| 2 | P1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |
| 3 | P2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 4 | F1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | F2 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 |
| 6 | BC1P1-1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 |
| 7 | BC1P1-2 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | 0 | 0 | 0 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |
| 8 | BC1P2-1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 9 | BC1P2-2 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 10 | BC2P1-1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | -1 | -1 | 0 |
| 11 | BC2P1-2 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | -1 | 0 | 0 | -1 | -1 | -1 | -1 | -1 | -1 | -1 |
| 12 | BC2P2-1 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 13 | BC2P2-2 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 14 | | | | | | | | | | | | | | | | | | | | | |

Save this final file as "QG_Mod4_ALA4.5_eval dist metrics.csv" (provided).