

## PHENOTYPIC DATA

📄 Hover here for details

### Step 1: Select if file contains column names

- yes  
 no

### Step 2: Is the file comma separated

- yes  
 no

### Step 3: Code for missing value

### Step 4: Select phenotypic file

Select File

or enter file name (including full path)

### Step 5: Upload file



Loading Phenotype file ...

#### Summary of Phenotype File

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File name: /tmp/phenoex.dat

Number of individuals: 800

Number of columns: 4

First 5 rows of the phenotype file are

```
0.4175858 M OBT40 44.43333
0.6184936 M OBT40 38.93333
0.2972836 M OBT40 37.40000
0.7123469 M OBT40 41.20000
1.4439608 M OBT40 50.93333
```

Column classes are

|                |           |
|----------------|-----------|
| Bioch.HDL      | numeric   |
| Sex            | character |
| Batch          | character |
| Weight.Average | numeric   |

The phenotype file has been loaded.

## MAP DATA

📄 Hover here for details

### Step 1: Select if file contains column names

- yes  
 no

### Step 2: Is the file comma separated

- yes  
 no

### Step 3: Select map file

Select File

or enter file name (including full path)

### Step 4: Upload file



Loading map file ...

#### Summary of Map File

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File name: /tmp/mapex.dat

Number of marker loci: 70484

Number of columns: 3

Number of chromosomes: 19

First 5 markers of the map file are

```
M1C1 1 5151352
M6C1 1 5168874
M11C1 1 5181919
M16C1 1 5197376
M21C1 1 5213830
```

The map file has been loaded.