| representation of second allele | characters have not been tested. |

- You will need to save your input file as a plain text file (either .txt or .csv), in order to upload it correctly. To do this, you may use the "Save As" function in Excel to save a spreadsheet in a "tab-delimited" or "comma-delimited" file format.

- Select the correct file type, and then click on "Select Input File" to upload the file.

- *The pedigree information displayed in the Pedigree Browser will not appear exactly the same as the input file*. The pedigree shown in the Pedigree Browser has been built using input file contents that may be used to produce other columns of information displayed. Input file processing will include:

  - A check for the 4 required fields: Ego ID, Sire ID, Dam ID, and Sex.

  - A check for either Age or Birth information.

  - A new row entry will be added for any Sire or Dam that do not already have their own row as an Ego.

  - Animals will be checked to ensure that their sex is consistent throughout the file.

  - Duplicate rows will be removed.

  - If Death or Departure date columns have been included, an "Exit" column will be built. Otherwise, Exit date assignment will be skipped if an Exit date column was provided in the input file.

  - If Birth dates have been included, age will be calculated as (Birth Date - Exit Date) / 365.25. If no Death, Departure, or Exit dates are provided, it is assumed that the ego is still alive, and Age will be calculated as (Birth Date - Today's Date) / 365.25. Age calculation will be skipped if an Age information column is included in the input file.

  - Generation numbers will be added to each ego.

  - Families (Pedigrees) will be numbered and this information will be added to each ego.

Genotype File Format Details:

The following columns names are reserved and will be recognized:

Columns *id*, *first_name*, and *second_name* are required columns.

Columns *first* and *second* will be automatically generated and cannot be present.

- Use the Allowable Names listed in the table below. Allowable Name case and order are not significant. The Allowable Name listed for each column is the name used internally and is the name used in examples and output.

- Genotype data can be supplied within the pedigree file or in this genotype file. Only two additional columns (*first* and *second* are required when the genotypes are provided within the pedigree file. See table above for a description. The genotype file columns are described below.

Allowable Name	Description of Information	Data Format
id	ID: Unique animal identifier	Alphanumeric characters (no symbols)
allele_1	Allele 1: Alphanumeric representation of first allele	Currently limited to alphanumeric values, underscores, spaces and dashes.
allele_2	Allele 2: Alphanumeric representation of second allele	Currently limited to alphanumeric values, underscores, spaces and dashes. Other characters have not been tested.

- You will need to save your genotype file as a plain text file (either .txt or .csv), in order to upload it correctly. To do this, you may use the "Save As" function in Excel to save a spreadsheet in a "tab-delimited" or "comma-delimited" file format.

- Select the correct file type, and then click on "Select Genotype File" to upload the file.