

# GeneLink: Importing Genotypes Quick Reference Guide

E-mail: [GeneLink@nhgri.nih.gov](mailto:GeneLink@nhgri.nih.gov)

December  
2004

## Lab Import

(for import from Linkage file see below)

### To Select a Start Panel:

1. Login to **GENELINK**.
2. Select a project from the drop-down list.
3. Click **SELECT PROJECT**. The privileges to which you have access will display on the left side of the screen.
4. Select **START PANEL** from the **IMPORT** menu.
5. Select the panel you want to start from the drop-down list.

1

### To Import a Table:

1. Select **IMPORT TABLE** from the **IMPORT** menu.
2. The **IMPORT TABLE** screen displays.
3. Select a **PANEL** from the drop-down list.
4. Enter the grid range in the **GRIDS** text boxes.
5. Enter the directory for the table in the **TABLE** text box, or click the **BROWSE** button search for the table.
6. To skip the header row upon import, select the **SKIP HEADER ROW** check box.
7. If this is a single table import and therefore will not be compared with a table imported by another user, select the **SINGLE TABLE IMPORT** check box.
8. Select **UPLOAD TABLE**.
9. The **IMPORT REPORT** displays.
10. To print the report, select the print icon on your web browser.
11. To go to the next step in the import process, duplicate checking, select either the **CHECK TABLE FOR DUPLICATES** link on the bottom of the report, or **CHECK TABLE FOR DUPLICATES** from the **IMPORT** menu.

2

### To Check Table for Duplicates:

1. Select **CHECK TABLE FOR DUPLICATES** from the **IMPORT** menu.
2. The check duplicate screen displays.
3. Select the table upload from the **UPLOAD** drop-down list and click **CHECK FOR DUPLICATES**.
4. If duplicates exist in the imported table, they will be displayed for your review.
5. To save the duplicate report, select **SAVE DUPLICATE REPORT**.
6. To cancel the upload without editing the duplicates, select **CANCEL UPLOAD**.
7. To continue with the upload, and in turn remove the duplicates, select **CONTINUE WITH UPLOAD**. If you select this option, the duplicates are removed and a confirmation message displays.

3

**Import Table**

FamID\MarkerName\Allele1\Allele2\Grid\Lane\n

Panel:  Grids:  -

Table:

Skip Header Row

This is a single table import. No one else will be importing this panel for these grids, so it will not need to be compared to another import by a different user.

**Import Report**

Username: lgilland  
Project Name: finalADD  
Import Date: 03/03/04  
# of Records Imported: 845  
# of Markers Imported: 13  
# of Individuals Imported: 64  
# markers x # individuals: 832  
Panel: P02.3  
Start Grid: 1  
End Grid: 1  
File Name: final Table P02.3 ADD emg

**Imported Individuals Without DNA**

---

None Found

**Individuals with DNA in the PEDIGREES table that are not imported**

---

None Found

[Check Table for Duplicates](#)

Uploader: lgilland Panel: P01.3  
Upload Date: Mar 1 2004 11:33AM Grids: 1 - 2

15 duplicates total

FamID	MarkerName	Allele1	Allele2	Duplicates	
134702	D1S4176	82	100	2	All match, 1 will be deleted
134702	D1S196	328	328	2	All match, 1 will be deleted
134702	D1S206	219	225	2	All match, 1 will be deleted
134702	D1S213	110	120	2	All match, 1 will be deleted
134702	D1S234	276	280	2	All match, 1 will be deleted
134702	D1S255	95	105	2	All match, 1 will be deleted
134702	D1S2667	144	148	2	All match, 1 will be deleted
134702	D1S2726	284	284	2	All match, 1 will be deleted
134702	D1S2785	181	185	2	All match, 1 will be deleted
134702	D1S2800	211	211	2	All match, 1 will be deleted
134702	D1S2836	249	253	2	All match, 1 will be deleted
134702	D1S2842	344	346	1 of 2	<input type="radio"/> delete this record.
134702	D1S2842	0	0	1 of 2	<input type="radio"/> delete this record.
134702	D1S2878	157	171	2	All match, 1 will be deleted
134702	D1S2890	213	217	2	All match, 1 will be deleted
134702	D1S450	332	340	2	All match, 1 will be deleted

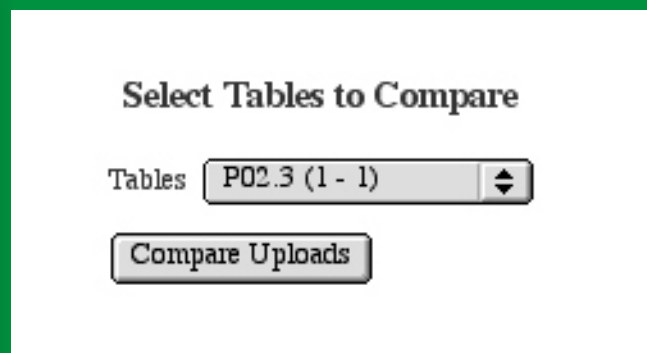
# GeneLink: Importing Genotypes Quick Reference Guide

E-mail: [GeneLink@nhgri.nih.gov](mailto:GeneLink@nhgri.nih.gov)

December  
2004

## To Check Table for Differences:

1. Select **CHECK TABLES FOR DIFFERENCES** from the **IMPORT** menu. **4**
2. If no differences exist, a message stating such will display.
3. If differences do indeed exist, an e-mail will be sent to the two users who imported the tables advising that the tables are ready for comparison.
4. If you receive this e-mail, upon selection of the **CHECK TABLE FOR DIFFERENCES** option from the **IMPORT** menu, you will be requested to select tables to compare.
5. Select the tables from the **TABLES** drop-down list and select **COMPARE UPLOADS**.
6. The **IMPORT COMPARISON** displays.
7. The differences are grouped in pairs. The user can now make adjustments as needed in the **ALLELE** text boxes as needed. **COMMENTS** can also be added.
8. When the adjustments are complete, select **UPDATE ROW**. That **MARKER** is removed from the **DIFFERENCES** list.
9. When all **MARKERS** have been updated, **GENELINK** will advise that the tables match.
10. If needed, a **DELETE** button is made available to delete an invalid table.



Import Comparison

	User	Date & Time	Panel	Grids	Rows
<input type="button" value="delete"/>	lgilland	Mar 3 2004 7:02PM	P02.3	(1 - 1)	832
<input type="button" value="delete"/>	pduggal	Mar 3 2004 7:07PM	P02.3	(1 - 1)	832

Total Differences: 1 Total Displayed: 1

Name	FamIndID	MarkerName	Allele1	Allele2	Grid	Lane	Comments	Select One
lgilland	1003	DIS207	160	169	ADD	31		<input type="radio"/> Keep this record
pduggal	1003	DIS207	165	169	ADD	31		<input type="radio"/> Keep this record
(new)	1003	DIS207			ADD	31		<input type="radio"/> Keep this record

## To View the Final Differences Report:

1. Select **VIEW FINAL DIFFERENCES REPORT** from the **IMPORT** menu. **5**
2. If differences were rectified, you will be able to view the report. Select an import from the drop-down list.
3. Select **GENERATE REPORT**.
4. The **DIFFERENCES REPORT** displays.

## To Move Final Table to Genotypes:

1. To finalize your table(s), select **MOVE FINAL TABLE TO GENOTYPES** from the **IMPORT** menu. **6**
2. The tables ready to be finalized display. Select the table from the drop-down list and click **FINALIZE DATA**.
3. If **GENELINK** is unable to finalize the data, a notification will display and **GENELINK** will allow you to correct the problem. Please note that in the example below, the data already exists in the final table. The data was reuploaded and **GENELINK** forces you to conduct a duplicate check to ensure that only one copy of the genotype data is stored in the database.
4. If no problems exist, or once the problems are rectified, the data will be finalized. If you attempt to select the table again from the **MOVE FINAL TABLE TO GENOTYPES** option, the table will no longer be available for selection.

# GeneLink Importing, continued

## *To Display Current Imports:*

1. To display imported tables that have not yet been finalized, select **DISPLAY CURRENT IMPORTS** from the **IMPORT** menu.
2. A table identifies the imported data that has not been finalized, by **PANEL**, **START GRID** number, **END GRID** number, **USER**, **DATE**, and **STATUS** for the data.

## *GeneLink Statuses, in order:*

<u>Status:</u>	<u>Description:</u>
Not Started	Lab work not yet started for this marker.
In Lab	Lab work in progress for this marker.
Genotypes Imported	One genotype data table is imported and awaiting second table from another user independently analyzing data for comparison and quality checks.
Single Table Imported	One genotype is imported and no comparison checks will be performed.
Waiting for Comparison	Two corresponding genotype tables analyzed and imported by different users are ready to be compared and quality checked for differences.
Compared and Ready	Two corresponding genotype data tables have been compared and are ready to be finalized and moved to the final genotypes table.
Ready to Finalize	A genotype table, which quality checks have been bypassed, is ready to be moved to the final genotypes table.
Ready to Export	Genotypes are ready to be exported for further analysis.

## *To Edit the Genotypes Imports Table:*

1. Select **EDIT GENOTYPE IMPORTS TABLE** from the **IMPORTS** menu.
2. If there are uploads available for editing, select the upload from the drop-down list and click **VIEW DATA**. Please note that the actions displayed are dependent upon your group's privileges.
3. To search for a record to view, select an item from the drop-down list and enter your search information in the **FOR** text box.
4. Select **SEARCH**.
5. To **MODIFY**, **DELETE**, or **INSERT** a record, select the appropriate action. Select an item from the drop-down list and enter the search information in the **FOR** text box.
6. Select **SEARCH**.
7. To sort the data, click on the column header once for ascending order, twice for descending order.
8. To **MODIFY** or **DELETE** a record, the table will display with a **MODIFY** button or **DELETE** button before each record. Select the **MODIFY** or **DELETE** button for the record you wish to perform such action.
9. To insert a record, select the **INSERT** button.
10. Enter the record data in the text boxes and select **INSERT RECORD**. To clear the information without inserting, select the **RESET** button.

## *To View the Markers Table:*

1. Select **MARKERS TABLE** from the **IMPORT** menu.
2. Depending upon your privileges, the **SEARCH**, **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, and **EXPORT** options will be available for selection. **SEARCH** is selected by default.
3. To **SEARCH**, select a field from the drop-down list.
4. Enter a word or phrase into the text box to refine your query. If you do not want this word or phrase returned in your results, select the exclude check box.
5. Select the number of display rows from the drop-down list.
6. Select the order, **ASCENDING** or **DESCENDING**, from the drop-down list.
7. Identify the field for which you wish to order your search results. For example, if you select **ASCENDING** by **MARKERNAME**, **ASCENDING** by **DYE**, and **ASCENDING** by **PANEL**, the results will display in ascending order according to the following fields, in order of priority: **MARKERNAME**, **DYE**, and **PANEL**.
8. Select the **SEARCH** button.
9. The results display in table format. The query is located on the top of the screen for editing, if necessary.
10. To adjust the order of the data displayed, the column headers are links that allow you to identify ascending and descending order. Select the column header again to sort in descending order.
11. To **MODIFY**, **DELETE**, **INSERT**, **IMPORT**, or **EXPORT**, select the appropriate action link.
12. Follow steps 3-10 to continue with the selected action.

## Import Genotypes from Linkage file

Select the families table, import, import multiple genotypes:

To upload the multiple genotypes the file must be in a similar format as the example below. The first line must be the header. The head and the columns must have the same file delimiter. Can be delimited either by tab, space, comma, pipe, or colon. You cannot have a space in any of the values of header labels if you are using space delimitation to parse.

The first column in your file must be FamilyID. The second column must be the IndividualID. You must specify which column the Marker Data will start (for the example below it's 8) and you can have as many markers as you want as long as the allele columns are labeled the same and next to each other in sets of two (example: D21s1 D21s1 D21S2 D21S2 D21s3 D21s3). After the header, the file can then list the data.

The DNA check in Pedigrees is optional, if checked any FamIndID that has "N" in the DNA field in Pedigrees will not be loaded. Also if any of the FamIndID's do not exist for that project in the Pedigrees table, the program will not load your data until you resolve the problem. If the toggle is checked off, input file will be allowed to load FamIndID's that exist in Pedigrees table regardless of what the value is for DNA.

Example Format for Input File (space delimited):

FamID IndID FatherID MotherID Sex StatusBroad LiabilityClass D21s1 D21s1 D21S2 D21S2 D21s3 D21s3 D21s4 D21s4 D21s5 D21s5

```
0025 11 21 22 1 0 6 0 0 0 0 0 0 0 0 0 0
0025 12 21 22 1 0 1 0 0 0 0 0 0 0 0 0 0
0025 13 21 22 1 0 6 0 0 0 0 0 0 0 0 0 0
0025 14 10 17 1 2 3 5 5 5 6 1 8 1 4 0 0
0025 15 10 17 2 2 3 5 5 5 6 1 8 1 1 0 0
0025 16 20 19 1 2 3 5 8 3 3 1 3 1 5 2 3
0025 17 0 0 2 0 5 4 5 5 6 1 1 1 4 3 3
0025 18 23 22 2 0 7 0 0 0 0 0 0 0 0 0 0
0025 19 23 22 2 0 7 5 5 3 6 3 8 4 5 2 3
0025 20 0 0 1 0 6 8 8 3 4 1 3 1 8 3 3
```

### Multiple Genotype Import Data

**NOTE:** The data file for the **GENOTYPES** table must follow this format. It needs to be a delimited text file, and cannot be an Excel Workbook.

[Click here](#) for directions and format your upload.

Data File:

Number that Column Marker Data Starts On:

Check for existence of DNA in Pedigrees Table:

File Delimiter:

*NOTE: This software/database is "United States Government Work" under the terms of the United States Copyright Act. It was written as part of the authors' official duties for the United States Government and thus cannot be copyrighted. This software/database is freely available to the public for use without a copyright notice. Restrictions cannot be placed on its present or future use.*

*Although all reasonable efforts have been taken to ensure the accuracy and reliability of the software and data, the National Human Genome Research Institute (NHGRI) and the U.S. Government does not and cannot warrant the performance or results that may be obtained by using this software or data. NHGRI and the U.S. Government disclaims all warranties as to performance, merchantability or fitness for any particular purpose.*

*In any work or product derived from this material, proper attribution of the authors as the source of the software or data should be made, using <http://research.nhgri.nih.gov/apps/genelink> as the citation.*