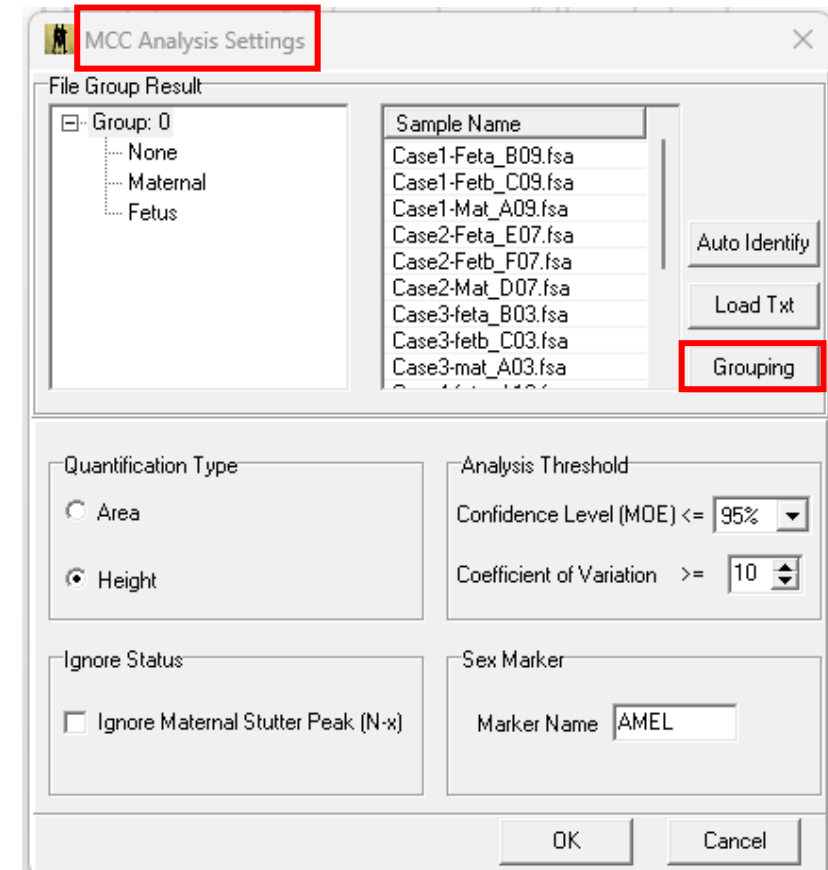
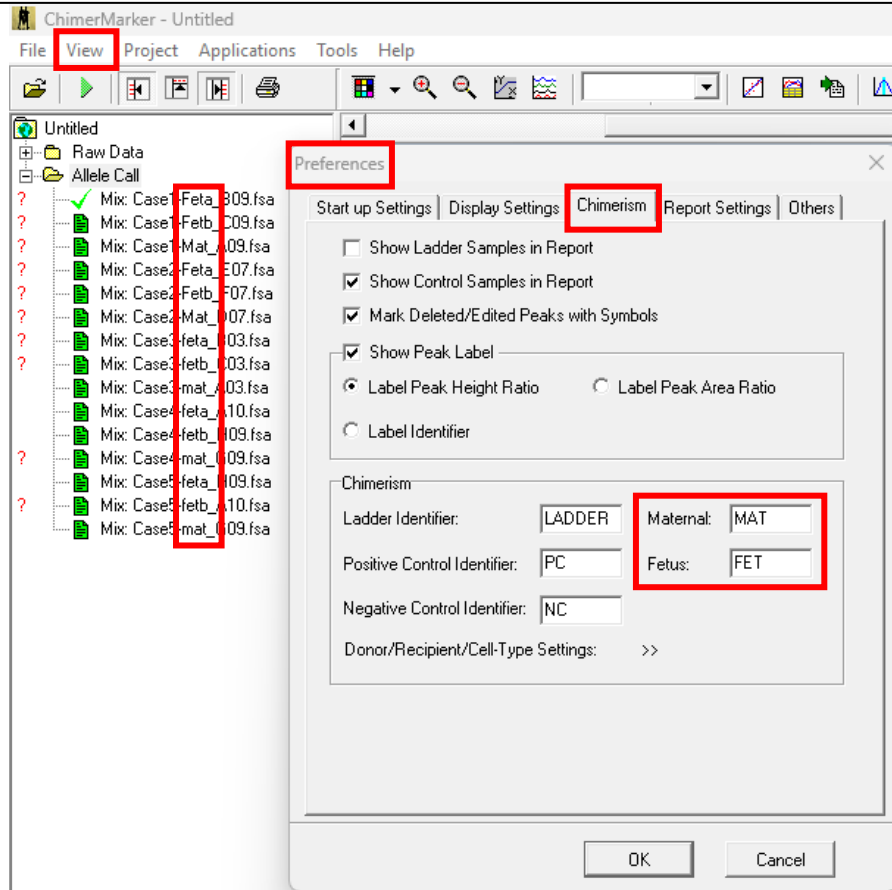


Grouping Samples for ChimerMarker's Maternal Cell Contamination Application

April 2025

1. When validating ChimerMarker for MCC analysis, go to *View*, *Preferences*, and select the *Chimerism* tab.
2. Then, enter in the abbreviations you use in the sample file names to identify maternal and fetal samples. *Note: It is helpful to separate different sections of the file name by using a "-", ".", or "_".*
3. Click *OK*.



4. After editing your samples. Go to *Applications* and select *Maternal Cell Contamination Analysis*.
5. You will first need to group your maternal and fetal samples.
6. Click *Grouping*.

7. When the “File Name Group Editor” window opens, there will be a few options available to group your samples.

Match by Sections

Automatically separates the sample filenames into groups based on the specified *Section Separators*.

Group Identification: Identifies how to match the filenames into groups based on the section entered into the *Compare by Section* field. The section of the filename specified will be highlighted red in the *File Name List*.

Control Identification: Identifies which section of the filename contains the reference vs. sample information based on the section number entered in the *Match to Identifier by Section* field. The section of the filename specified will be highlighted green in the *File Name List*.

Match by Fixed Position

Allows the user to manually identify the characters of the filename for grouping the samples. *Section Separators* like “_”, “-” are counted as individual characters.

Group Identification: Enter the number of the beginning and ending character to identify how to group the samples. The section of the filename specified will be highlighted red in the *File Name List*.

Control Identification: Enter the number of the beginning and ending character to identify which part of the filename contains the control identifier. The section of the filename specified will be highlighted green in the *File Name List*.

Match by Group Order

Allows the user to group samples that contain sequential identifiers.

Group Size: Enter the number of groups for the analysis.

File Name Group Editor

File Name List:

	1 (G)	2 (C)	3	4
1	Case1	Feta	B09	fsa
2	Case1	Fetb	C09	fsa
3	Case1	Mat	A09	fsa
4	Case2	Feta	E07	fsa
5	Case2	Fetb	F07	fsa
6	Case2	Mat	D07	fsa
7	Case3	feta	B03	fsa
8	Case3	fetb	C03	fsa
9	Case3	mat	A03	fsa
10	Case4	feta	A10	fsa
11	Case4	fetb	H09	fsa
12	Case4	mat	G09	fsa
13	Case5	feta	H09	fsa
14	Case5	fetb	A10	fsa
15	Case5	mat	G09	fsa

Matched Groups:

Match by Sections | Match by Fixed Position | Group By Order | Group By Run Date | Group By Cell Type

Group Identification:

Compare by Section: 1

Section Separators: ;_

Control Identification:

Match to Identifier by Section: 2

Control: Mat

Control Match Mode: ☐ Whole Words ☒ Include

Match Load File OK Cancel

8. Choose a grouping method.
9. If choosing *Match by Sections*, the *Group Identification* refers to the section containing a case number or name. The *Control Identification* refers to the section labeling the maternal and fetal abbreviations.
10. The maternal samples are the control samples. In this case, the maternal samples are identified by “Mat” in their name. If this abbreviation is case sensitive, you may select the checkbox.
11. For *Control Match Mode*, select *Whole Words* if the *Control Identification* needs to match exactly. If not, you can select *Include* instead.
12. Click *Match* to see the samples grouped in the *Matched Groups* window.
13. When grouping is complete, click *OK*.

The screenshot shows the 'File Name Group Editor' window. The 'File Name List' on the left contains 15 rows of file names with columns for Case, Section, Abbreviation, and File Name. The 'Matched Groups' on the right shows the result of the matching process, with columns for Group, Control, and Matched File Name. The bottom section contains configuration options for the matching process.

File Name List:

	1 (G)	2 (C)	3	4
1	Case1	Feta	B09	fsa
2	Case1	Fetb	C09	fsa
3	Case1	Mat	A09	fsa
4	Case2	Feta	E07	fsa
5	Case2	Fetb	F07	fsa
6	Case2	Mat	D07	fsa
7	Case3	feta	B03	fsa
8	Case3	fetb	C03	fsa
9	Case3	mat	A03	fsa
10	Case4	feta	A10	fsa
11	Case4	fetb	H09	fsa
12	Case4	mat	G09	fsa
13	Case5	feta	H09	fsa
14	Case5	fetb	A10	fsa
15	Case5	mat	G09	fsa

Matched Groups:

	1 (Control)	2	3
1	Case1-Mat_A09.fsa	Case1-Fetb_C09.fsa	Case1-Feta_B09.fsa
2	Case2-Mat_D07.fsa	Case2-Fetb_F07.fsa	Case2-Feta_E07.fsa
3	Case3-mat_A03.fsa	Case3-fetb_C03.fsa	Case3-feta_B03.fsa
4	Case4-mat_G09.fsa	Case4-fetb_H09.fsa	Case4-feta_A10.fsa
5	Case5-mat_G09.fsa	Case5-fetb_A10.fsa	Case5-feta_H09.fsa

Configuration:

Match by Sections | Match by Fixed Position | Group By Order | Group By Run Date | Group By Cell Type

Group Identification: Compare by Section

Control Identification: Match to Identifier by Section

Section Separators:

Control Mat ☐ Case Sensitive

Control Match Mode: ☐ Whole Words ☒ Include

14. In the Maternal Cell Application Analysis window, you should see the samples grouped on the left with an “F” in front of the fetal sample names and an “M” in front of the maternal sample names. If that is not the case, confirm the steps in this guide were completed successfully and contact tech_support@softgenetics.com.

Maternal Cell Contamination Analysis

File Tool

Group: 1

- ✓ F: Case1-Feta_B09.fsa
- F: Case1-Fetb_C09.fsa
- M: Case1-Mat_A09.fsa

Group: 2

- F: Case2-Feta_E07.fsa
- F: Case2-Fetb_F07.fsa
- M: Case2-Mat_D07.fsa

Group: 3

- F: Case3-feta_B03.fsa
- F: Case3-fetb_C03.fsa
- M: Case3-mat_A03.fsa

Group: 4

- F: Case4-feta_A10.fsa
- F: Case4-fetb_H09.fsa
- M: Case4-mat_G09.fsa

Group: 5

- F: Case5-feta_H09.fsa
- F: Case5-fetb_A10.fsa
- M: Case5-mat_G09.fsa

Marker Name	Fetus Genotype	Maternal Genotype	# of Shared allele	Ignored	%MCC
D8S1179	16	14,16	1	No	NI
D21S11	28.2,30.2	28.2	1	No	NI
D7S820	11,12	12	1	No	NI
CSF1PO	10	10,11	1	No	NI
D3S1358	16,17,18	16,17	2	No	9%
TH01	7,8	7,8	2	No	NI
D13S317	12,13	12,13	2	No	NI
D16S539	10,12	10,12	2	No	NI
D2S1338	17,21	21	1	No	NI
D19S433	13,14,16.2	13,14	2	Yes(User)	10%
vWA	16,18	16,19	1	No	NI
TPOX	8,9	8	1	No	NI
D18S51	20,21	17,20	1	No	NI
AMEL	X,Y	X	1	No	NI
D5S818	10,11,12	11,12	2	No	6%
FGA	26	26	1	No	NI
Average MCC:	7%				
Coefficient of Variation:	28%				
St. Dev:	2				
MOE:	19% (95%)				
Number of Informative Loci:	2				
Gender:	XY				
Peak Ratio of Amelogenin:	0.95				