

DIPSorter User Manual

In combination with Biotype's Mentype® **DIPplex** PCR Amplification Kit
Software version: 1.0.2

DIPSorter

Bio **type**®

powered by Qualitype AG 2009

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1. Area of application

The software DIPSorter was developed as a utility application for the Mentype® **DIPplex** PCR Amplification Kit in order to resort genotype data of biallelic deletion/insertion markers, so called DIPs. It provides the import of **Genotype Table** text files exported from GeneMapper™ ID or Genotyper® software and displays them as sorted genotype tables. All arising data can be printed and exported to CSV- and PDF-files.

2. Setup

DIPSorter is offered as desktop application providing a graphical user interface.

2.1 System requirements

DIPSorter runs with the following Windows® operating systems:

Windows 32 Bit

- Windows 2000 Professional/Server
- Windows Server 2003
- Windows XP Home/Professional
- Windows Vista

Windows 64 Bit

- Windows Server 2003
- Windows XP
- Windows Vista

Minimum recommended system specification:

- PC with Microsoft Windows 2000, XP or Vista
- 512 MB RAM or higher
- approx. 300 MB free hard disc storage unit (without database)
- screen resolution of 1024 x 768 pixel

It is recommended to use more than 512 MB RAM.

2.2 Starting the setup

- Boot your operating system and close all active applications
- Boot the setup application called DIPSorterSetup.exe
- The setup program suggests a directory as destination folder. It is possible to change the directory but never install more than one product in the same directory
- To start the application afterwards, use the shortcut in the Windows® start menu which will be applied during the setup

2.3 The DIPSorter BINFILE

DIPSorter gets its information concerning all supported markers from parsing a file included in the software distribution for the Mentype® **DIPplex** PCR Amplification Kit, called DIPSorter BINFILE.

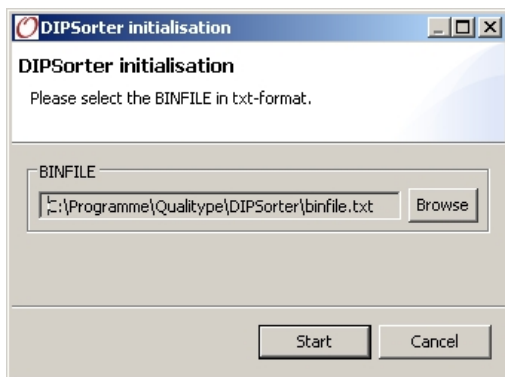


Fig.1 DIPSorter initialization with selected BINFILE

You can select another BINFILE in the initialization dialog. If you want to use the default one, simply press the start button.

3. DIPSorter

Fig. 2 shows the application after booting. You find the so called **Sample View** window on the left hand.

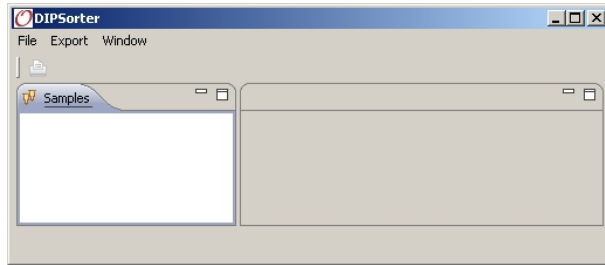


Fig. 2 Application after booting - Sample View

3.1 Expected file formats

DIPSorter expects genotype data in a specific .txt format, also known as GeneMapper™ ID or Genotyper® **Export Table** format. It consists of a header line, which is ignored by DIPSorter. Each subsequent line defines a list of alleles for a specific panel and a specific sample, named in the first three columns.

There are four lines per sample expected - one for each panel. The panel **dye order** is given as blue, green, yellow and red. The columns are solely delimited by a tabulator character (\t), field delimiters are not used. The order of columns is defined as follows:

Sample Name	Marker	Dye	Allele 1	Allele 2	...	Allele 20	...
-------------	--------	-----	----------	----------	-----	-----------	-----

Export Table from GeneMapper™ ID software

File Name	Sample Info	Category	Peak 1	Peak 2	...	Peak 20
-----------	-------------	----------	--------	--------	-----	---------

Export Table from Genotyper® software

Alleles for autosomal markers are defined as a string containing the name directly followed by a plus respectively minus sign. Double values are ignored (e.g. regarding two entries of D122-, the second one will be ignored). Gonosomal markers can be either X or Y.

If there are no peaks found within the allele ladder, the related value in the list of alleles is expected to be set to **OL** (off ladder).

Note: To ensure the right export format please use templates and table settings provided for the Mentype® **DIPplex** PCR Amplification Kit to analyse the samples within GeneMapper™ ID (-X) or Genotyper® software. We recommend settings of **Table for 20 Alleles** for GeneMapper™ ID (-X) and **Vertical Table for 20 Alleles** for Genotyper® software.

3.2 Importing data

In order to import samples, use the item **Import Sample file...** command in the file menu. Select the desired file and press **Finish**. All samples included in the data file will be imported. They are now visible in the **Sample View** window.

Note: The file type (either GeneMapper™ ID or Genetyper®) will be determined automatically. Importing will be aborted if the type could not be detected. DIPsorter software will not store the imported samples. Hence, the **Sample View** will be overwritten by importing a new sample file. Only the sorted genotype tables can be exported.

3.3 Viewing a genotype table

Double clicking a certain sample opens the **Sample Editor**. A sorted genotype table is presented for each sample. Heterozygote genotypes are displayed by two entries for allele 1 and allele 2, homozygote alleles are displayed by only one entry for either allele 1 or allele 2.

Name	Allele 1	Allele 2
HLD1XV	X	Y
HLD77	-	D77+
HLD45	D45-	-
HLD131	D131+	D131+
HLD79	D79-	-
HLD6	D6-	D6+
HLD111	D111+	-
HLD58	D58-	D58+
HLD56	D56-	-
HLD118	D118-	D118+
HLD92	-	D92+
HLD100	D100-	D100+

Off-Ladders per panel:		Non-value markers per panel:	
DIPplex_Blue:	1	DIPplex_Blue:	0
DIPplex_Green:	3	DIPplex_Green:	0
DIPplex_Yellow:	3	DIPplex_Yellow:	0
DIPplex_Red:	2	DIPplex_Red:	0
Sum:	9	Sum:	0

Fig.3 Genotype table

The number of off-ladder signals for each panel are counted and displayed in summary, as well as the number of markers for which no alleles were found. You can open more than one sample by simply double clicking on another sample in the **Sample View** window.

3.4 Comparing samples

You can compare two genotypes in DIPsorter by opening two samples and rearranging the editors.

At first, open two samples. As you can see in Fig. 4, they are represented as two tabs above the sample editor.

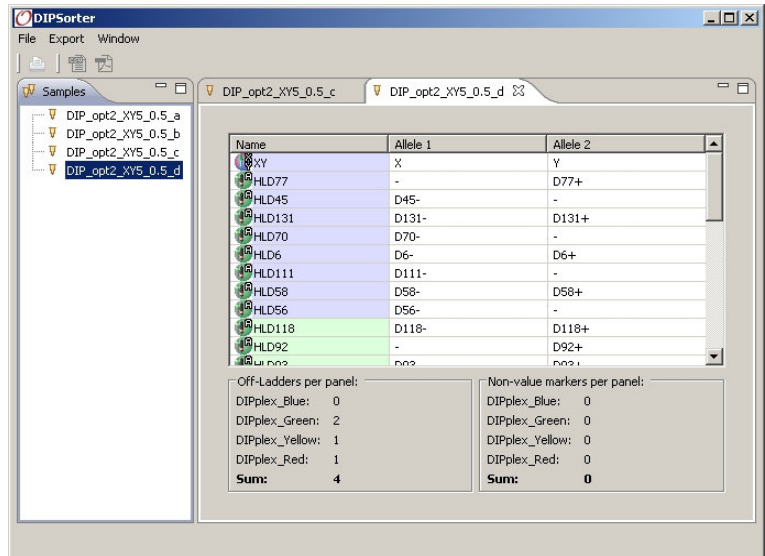


Fig. 4 Comparing samples

Now just click at one tab (the area containing the name of the sample above the editor), hold the left mouse button and move to the applications right border. Wait until the symbol turns into a black arrow pointing to the right and then release the button.

The chosen editor is now placed to the right of the other open editor (see Fig. 5).

The screenshot shows the DIPSorter application with two open sample editors. The left editor is titled 'DIP_opt2_XY5_0.5_c' and the right is 'DIP_opt2_XY5_0.5_d'. Both editors display a table of markers with columns for Name, Allele 1, and Allele 2. Below each table is a summary table for 'Off-Ladders per panel' and 'Non-value markers per panel'.

Name	Allele 1	Allele 2
XY	X	Y
HLD77	-	D77+
HLD45	D45-	-
HLD131	D131-	D131+
HLD70	D70-	-
HLD6	D6-	D6+
HLD111	D111-	-
HLD58	D58-	D58+
HLD56	D56-	-
HLD118	D118-	D118+
HLD92	-	D92+
HLD93	D93-	D93+
HLD99	D99-	D99+
HLD88	D88-	D88+
HLD101	D101-	D101+
HLD67	-	D67+
HLD83	D83-	D83+
HLD114	D114-	-
HLD48	D48-	D48+
HLD124	D124-	D124+
HLD122	D122-	-
HLD125	D125-	-
HLD64	D64-	D64+
HLD81	D81-	D81+
HLD136	D136-	D136+
HLD133	D133-	D133+
HLD97	D97-	D97+
HLD40	D40-	D40+
HLD128	D128-	-
HLD39	D39-	D39+
HLD84	D84-	-

Off-Ladders per panel:		Non-value markers per	
DIPplex_Blue:	1	DIPplex_Blue:	0
DIPplex_Green:	3	DIPplex_Green:	0
DIPplex_Yellow:	3	DIPplex_Yellow:	0
DIPplex_Red:	2	DIPplex_Red:	0
Sum:	9	Sum:	0

Name	Allele 1	Allele 2
XY	X	Y
HLD77	-	D77+
HLD45	D45-	-
HLD131	D131-	D131+
HLD70	D70-	-
HLD6	D6-	D6+
HLD111	D111-	-
HLD58	D58-	D58+
HLD56	D56-	-
HLD118	D118-	D118+
HLD92	-	D92+
HLD93	D93-	D93+
HLD99	D99-	D99+
HLD88	D88-	D88+
HLD101	D101-	D101+
HLD67	-	D67+
HLD83	D83-	D83+
HLD114	D114-	-
HLD48	D48-	D48+
HLD124	D124-	D124+
HLD122	D122-	-
HLD125	D125-	-
HLD64	D64-	D64+
HLD81	D81-	D81+
HLD136	D136-	D136+
HLD133	D133-	D133+
HLD97	D97-	D97+
HLD40	D40-	D40+
HLD128	D128-	-
HLD39	D39-	D39+
HLD84	D84-	-

Off-Ladders per panel:		Non-value markers per	
DIPplex_Blue:	0	DIPplex_Blue:	0
DIPplex_Green:	2	DIPplex_Green:	0
DIPplex_Yellow:	1	DIPplex_Yellow:	0
DIPplex_Red:	1	DIPplex_Red:	0
Sum:	4	Sum:	0

Fig. 5 Two open sample editors for comparison

4. Exporting samples

DIPSorter basically provides two export file formats: PDF and CSV. For both you can choose whether you want to export a single sample or the complete database containing all imported samples.

4.1 Exporting a single sample

Open a sample by clicking on its item. Assure that the sample of the chosen editor is currently being processed (mind the colour scheme of the tab), click on the editor's canvas if in doubt. Now choose one of the icons at the tool bar:



- use this icon in order to export a sample to CSV-format



- use this icon for generating a PDF file

After clicking on one icon, you will be asked where to store the file.

4.2 Exporting all samples

Export all imported samples by choosing the **Export all samples to CSV ... / Export all samples to PDF...** command in the export menu.

4.3 Printing

To print the genotype table of a single sample, assure that the sample of the chosen editor is currently being processed (mind the colour scheme of the tab), click on the editor's canvas if in doubt and press the printer icon at the toolbar. Now you can send the genotype table to your printer by confirming your operating systems printer dialog.

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