



# Mentype<sup>®</sup> Nonaplex<sup>QS</sup>

PCR Amplification Kit

## Instructions for use

The Mentype<sup>®</sup> Nonaplex<sup>QS</sup> PCR Amplification Kit is a multiplex application for the Short Tandem Repeat (STR) loci, which belong to the German Forensic DNA Database and are recommended by EDNAP. In one PCR reaction, the eight polymorphic STR loci **D3S1358, D8S1179, D18S51, D21S11, FGA (FIBRA), SE33 (ACTBP2), TH01 (TC11),** and **vWA** as well as the gender-specific **Amelogenin** are amplified simultaneously.



100, 400, 1000



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Our Mentype® test kits guarantee the highest quality standards for clinics and research.

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### Warnings and safety instructions

The PCR Amplification Kit contains the following potentially hazardous chemicals:

Kit component	Chemical	Hazards
Primer mix, reaction mix and allelic ladder	Sodium azide NaN <sub>3</sub>	toxic if swallowed, develops toxic gases when it gets in contact with acids

Observe the Material Safety Data Sheets (MSDS) for all Biotype<sup>®</sup> products, which are available on request. Please contact the respective manufacturers for copies of the MSDS for any additionally needed reagents.

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## 1. Product description

The Mentype® **Nonaplex**<sup>QS</sup> PCR Amplification Kit is a multiplex application for the Short Tandem Repeat (STR) loci, which belong to the German Forensic DNA Database and are recommended by EDNAP. In one PCR reaction, the eight polymorphic STR loci **D3S1358, D8S1179, D18S51, D21S11, FGA (FIBRA), SE33 (ACTBP2), TH01 (TC11),** and **vWA** as well as the gender-specific **Amelogenin** are amplified simultaneously.

The test kit was developed for fast and reliable DNA genotyping of blood, buccal swabs and forensic stains. Moreover, a primer set for SE33 was included that addresses all known primer binding site mutations allowing the amplification of those alleles in samples containing this variants. The primers are fluorescence-labelled with **6-FAM** (Amelogenin, D8S1179, D21S11 and D18S51), **HEX** (TH01, D3S1358 and SE33) or **NED** (vWA and FGA).

As special feature, Mentype® **Nonaplex**<sup>QS</sup> contains an **internal PCR control** (Quality Sensor "QS") which provides helpful information on the efficiency of the PCR and on the presence of PCR inhibitors.

The detection limit of Mentype® **Nonaplex**<sup>QS</sup> PCR Amplification Kit is less than **100 pg genomic DNA**. However, it is recommended to use **0.2-1.0 ng DNA**.

The test kit was validated and evaluated using the GeneAmp® 9700 thermal cycler, ABI PRISM® 310 Genetic Analyzer, and ABI PRISM® 3100/3130 Genetic Analyzer.

**Table 1. Locus-specific information of Mentype® Nonaplex<sup>QS</sup>**

<b>Locus</b>	<b>GenBank® accession</b>	<b>Repeat motif of the reference allele</b>	<b>Reference allele</b>	<b>Allele range</b>
Amelogenin X	M55418			
Amelogenin Y	M55419			
D3S1358	11449919	TCTA [TCTG] <sub>2</sub> [TCTA] <sub>15</sub>	18	8-26
D8S1179	G08710	[TCTA] <sub>12</sub>	12	6-21.2
D18S51	L18333	[AGAA] <sub>13</sub>	13	5.3-42
D21S11	AP000433	[TCTA] <sub>4</sub> [TCTG] <sub>6</sub> [TCTA] <sub>3</sub> TA [TCTA] <sub>3</sub> TCA [TCTA] <sub>2</sub> TCCATA [TCTA] <sub>11</sub>	29	12-46
FGA (FIBRA)	M64982	[TTTC] <sub>3</sub> TTTTCTCT [CTTT] <sub>13</sub> CTCC [TTCC] <sub>2</sub>	21	12.2-51.2
SE33 (ACTBP2)	NG000840	[AAAG] <sub>9</sub> AA [AAAG] <sub>16</sub>	25.2	3-50
TH01 (TC11)	D00269	[TCAT] <sub>9</sub>	9	3-14
vWA	M25858	TCTA [TCTG] <sub>4</sub> [TCTA] <sub>13</sub>	18	10-26

Table 1 shows the STR loci with their repeat motifs and alleles that are concordant with the International Society for Forensic Genetics (ISFG) guidelines for the use of microsatellite markers (Bär et al., 1997). Allele ranges include all known alleles of the National Institute of Standards and Technology (NIST as at 12/2008) and of the current literature.

**Table 2. Chromosomal mapping of Mentype® Nonaplex<sup>OS</sup>**

<b>Locus</b>	<b>Chromosomal mapping</b>
Amelogenin X	Xp22.1-22.3
Amelogenin Y	Yp11.2
D3S1358	3p25.3
D8S1179	8q23.1-23.2
D18S51	18q21.3
D21S11	21q21.1
FGA (FIBRA)	4q28.2
SE33	6q14.2
TH01	11p15.5pter
vWA	12p13.31

**Content****Mentype® Nonaplex<sup>OS</sup> PCR Amplification Kit (100 Reactions)**

Nuclease-free water	3.0 mL
Reaction mix <b>A</b>	500 µL
Primer mix	250 µL
DNA polymerase	40 µL
Control DNA XY1 (2 ng/µL)	10 µL
DNA Size Standard 550 (ROX)	50 µL
Allelic ladder*	10 µL

\* Since January 2008 the allelic ladder Mentype® **Nonaplex<sup>OS</sup> extended** (Cat. No. 48-09330-0010) is additionally available (see page 27).

**Ordering information**

Mentype® <b>Nonaplex<sup>OS</sup></b>	100 reactions	Cat. No.	41-09330-0100
Mentype® <b>Nonaplex<sup>OS</sup></b>	400 reactions	Cat. No.	41-09330-0400
Mentype® <b>Nonaplex<sup>OS</sup></b>	1000 reactions	Cat. No.	41-09330-1000

**Storage**

Store all components at –20°C and avoid repeated thawing and freezing. Primer mix and allelic ladder must be stored protected from light. The DNA samples and post-PCR reagents (allelic ladder and DNA size standard) should be stored separately from the PCR reagents. The expiry date is indicated on the kit cover.

**Quality assurance**

All kit components undergo an intensive quality assurance process at Biotype Diagnostic GmbH. The quality of the test kits is permanently monitored in order to ensure unrestricted usability. Please contact us if you have any questions regarding quality assurance.

**Additionally required reagents**

Additional reagents are needed in order to use the Biotype<sup>®</sup> PCR Amplification Kit:

<b>Reagent</b>	<b>Supplier</b>	<b>Order number</b>
Hi-Di <sup>™</sup> Formamide, 25 mL	Applied Biosystems	4311320
Matrix Standards DS-30 for ABI PRISM <sup>®</sup> 310 Genetic Analyzer	Applied Biosystems	401546 and 402996 (NED)
Matrix Standards DS-30 for ABI PRISM <sup>®</sup> multi-capillary instruments	Applied Biosystems	4345827

## 2. PCR amplification

### Master mix preparation

The table below shows the volumes of all PCR reagents per 25  $\mu\text{L}$  reaction volume, including a sample volume of 1.0  $\mu\text{L}$  (template DNA). The number of reactions to be set up shall be determined taking into account positive and negative control reactions. Add one or two reactions to this number to compensate the pipetting error.

Component	Volume
Nuklease-free water	16.1 $\mu\text{L}$
Reaction mix <b>A*</b>	5.0 $\mu\text{L}$
Primer mix	2.5 $\mu\text{L}$
Multi Taq2 DNA Polymerase (hot start, 2.5 U/ $\mu\text{L}$ )	0.4 $\mu\text{L}$
Volume of master mix	24.0 $\mu\text{L}$

\* contains  $\text{Mg}^{2+}$ , dNTPs, BSA

All components should be mixed (vortex) and centrifuged for about 10 s before preparing the master mix. The DNA volume applied to the assay depends on its concentration. A volume of up to 5  $\mu\text{L}$  may be necessary for DNA trace templates. DNA volumes of more than 5  $\mu\text{L}$  are not recommended, because potential PCR inhibitors may interfere with the process. Fill up the final reaction volume to 25  $\mu\text{L}$  with nuclease-free water.

Generally, DNA templates shall be stored in nuclease-free water or in diluted TE buffer (10 mM Tris HCl, pH 8.0 and 1 mM EDTA), e.g. 0.1x TE buffer.

The primer mixes are adjusted for balanced peak heights at **30 PCR cycles** and **0.35 ng Control DNA XY1** in a reaction volume of 25  $\mu\text{L}$ . If more DNA template is introduced, higher peaks can be expected for small PCR fragments and relatively low peaks for large fragments. Reduce the amount of DNA template to correct this imbalance.

### Positive control

For the positive amplification control, dilute the Control DNA XY1 to 0.35 ng in the appropriate volume. Instead of the template DNA pipette the diluted Control DNA into a reaction tube containing the PCR master mix.

### Negative control

For the negative amplification control, pipette nuclease-free water instead of template DNA into a reaction tube containing the PCR master mix.



### PCR amplification parameter

Perform a “hot start” PCR in order to activate the Multi Taq2 DNA Polymerase and to prevent the formation of non-specific amplification products.

The number of cycles depends on the amount of DNA. 30 cycles are recommended for all samples. For critical stains (< 100 pg DNA), it is recommended to increase the number of PCR cycles from 30 to 34.

### Standard method

Recommended for all DNA samples

Temperature	Time	
94°C	4 min (hot start for activation of the Multi Taq2 DNA Polymerase)	
94°C	30 s	
60°C	120 s	<b>30 cycles</b>
72°C	75 s	
68°C	60 min	
10°C	∞	hold

### Optional

Recommended for stains with small amounts of DNA

Temperature	Time	
94°C	4 min (hot start for activation of the Multi Taq2 DNA Polymerase)	
94°C	30 s	
60°C	120 s	<b>34 cycles</b>
72°C	75 s	
68°C	60 min	
10°C	∞	hold

Too small amounts of DNA may result in allelic dropouts and imbalances of the peaks. Furthermore, unspecific amplification products could appear. With increasing numbers of cycles, there is the risk of cross contamination caused by minimal amounts of impurities.

### 3. Electrophoresis using the ABI PRISM® 310 Genetic Analyzer

For general instructions on instrument setup, matrix generation and application of the GeneScan® or GeneMapper™ ID software, refer to the *ABI PRISM® 310 Genetic Analyzer User's Manual*. Electrophoresis using the GeneScan® software is described below.

The virtual **filter set D** shall be used for combined application of the four fluorescent labels **6-FAM, HEX, NED, and ROX** (also called **DS-30**). Generally, Filter Sets A and F are suitable, too.

#### Material

Capillary	47 cm / 50 µm (green)
Polymer	POP-4 for 310 Genetic Analyzer
Buffer	10x Genetic Analyzer Buffer with EDTA

#### Matrix generation

Prior to conducting DNA fragment size analysis with the filter set D, a matrix with the four fluorescent labels 6-FAM, HEX, NED, and ROX must be generated. The suitable matrix standard **DS-30** is available from Applied Biosystems.

Colour	Matrix standard	Order number
Blue (B)	6-FAM	Applied Biosystems, 401546
Green (G)	HEX	Applied Biosystems, 401546
Yellow (Y)	NED	Applied Biosystems, 402996
Red (R)	ROX	Applied Biosystems, 401546

Four electrophoresis runs shall be conducted, one for each fluorescent label, 6-FAM, HEX, NED, and ROX, under the same conditions as for the samples and allelic ladders of the Biotype® test kit to generate suitable matrix files.

Matrix sample	Component	Volume
Matrix sample 1	Hi-Di™ Formamide	12.0 µL
	Matrix standard <b>6-FAM</b>	1.0 µL
Matrix sample 2	Hi-Di™ Formamide	12.0 µL
	Matrix standard <b>HEX</b>	1.0 µL
Matrix sample 3	Hi-Di™ Formamide	12.0 µL
	Matrix standard <b>NED</b>	1.0 µL
Matrix sample 4	Hi-Di™ Formamide	12.0 µL
	Matrix standard <b>ROX</b>	1.0 µL

- Denaturation for 3 min at 95°C
- Cool down to 4°C
- For analysis: load the samples on the tray

- Create a **Sample Sheet** and enter sample designation

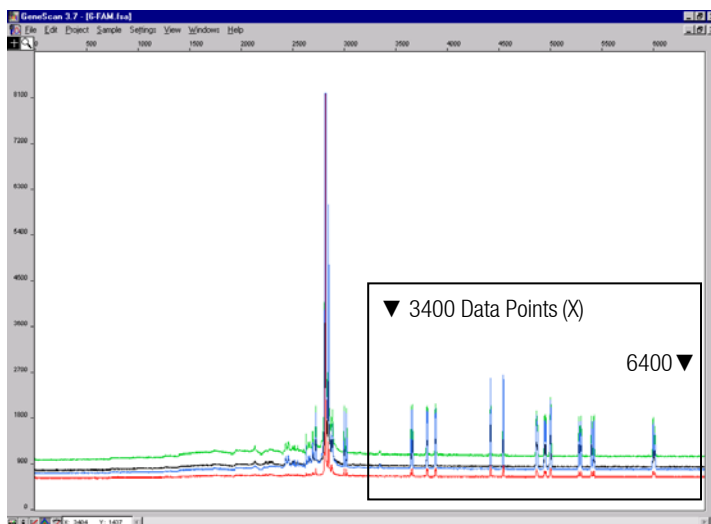
## Injection list for matrix generation

Parameter	Set up
Module File	GS STR POP-4 (1 mL) D
Matrix File	<b>NONE</b>
Size Standard*	<b>NONE</b>
Injection [s]	5
Injection [kV]	15.0
Run [kV]	15.0
Run [°C]	60
Run Time [min]	24

\* prepare matrix standards always **without DNA Size Standard (ROX)**

## Analysis of the matrix samples

- Run the GeneScan<sup>®</sup> software
- **File** → **New** → **Project** (open folder of current run) → **Add Sample Files**
- Select a matrix sample in the **Sample File** column
- **Sample** → **Raw Data**
- Check the matrix samples regarding a flat baseline. As shown in the figure below, there should be at least five peaks with peak heights about 1000-4000 (Y-axis) for each matrix sample (optimal range: 2000-4000)

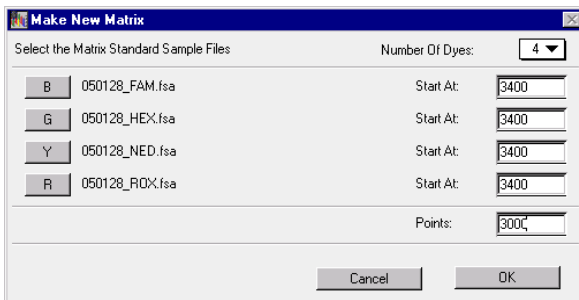


**Fig. 1** Electropherogram with raw data of the matrix standard 6-FAM

- Select analysis range with flat baseline and re-inject the matrix sample if necessary
- Note down start and end value (data points) of the analysis range, e.g. start value 3400, end value 6400
- Calculate the difference, e.g.  $6400 - 3400 = 3000$  data points

## Generation of a new matrix

- **File** → **New** → **Matrix**



**Fig. 2** Matrix sample selection

- Import matrix samples for all dyes (B, G, Y, R)
- Enter a **Start At** value, e.g. 3400
- Enter the calculated difference under **Points**, e.g. 3000
- Click on **OK** to calculate the new matrix

		Reactions			
		B	G	Y	R
B		1.0000	0.4164	0.0415	0.0012
G		0.8472	1.0000	0.8863	0.0107
Y		0.4509	0.4886	1.0000	0.0456
R		0.1273	0.1792	0.4964	1.0000

**Fig. 3** New matrix DS-30

- Save the matrix in the matrix folder: **File** → **Save as**, e.g. Matrix DS-30

## Matrix check

Check the new matrix with current samples.

- **File** → **New** → **Project** (open folder of the respective run) → **Add Sample Files**
- Select sample(s) in the **Sample File** column
- **Sample** → **Install New Matrix** (open matrix folder and select new matrix)
- Re-analyse your samples

There should be **no** pull-up peaks between the dye panels (B, G, Y, R) with the new matrix.

## Sample preparation

Component	Volume
Hi-Di™ Formamide	12.0 µL
DNA Size Standard 550 (ROX)	0.5 µL

prepare 12 µL of the mix (formamide + DNA size standard) for all samples  
add 1 µL PCR product (diluted if necessary) or allelic ladder

- Denaturation for 3 min at 95°C
- Cool down to 4°C
- For analysis: load the samples on the tray

## Signal intensities

Options to increase the signal intensity:

- Reduce the volume of the DNA Size Standard 550 (ROX) to peak heights of about 500 relative fluorescent units (RFU)
- Purify the PCR products before starting the analysis

## Setting up the GeneScan® software

- Create a **Sample Sheet** and enter sample designation

## Injection list

Parameter	Set up
Module File	GS STR POP-4 (1 mL) <b>D</b>
Matrix File	e.g. Matrix DS-30
Size Standard	e.g. SST-ROX_50-450bp
Injection [s]*	5
Injection [kV]	15.0
Run [kV]	15.0
Run [°C]	60
Run Time [min]**	<b>26</b>

\* Deviating from standard settings, the injection time may range between 1 and 10 s depending on the type of sample. If blood samples with very high signal intensities are recorded, a shorter injection time may be selected. For samples with low DNA content an injection time up to 10 s may be necessary.

\*\* Depending on the analysis conditions the run time for Mentype® **Nonaplex**<sup>DS</sup> was modified in order to analyse fragments with lengths of up to **450 bp**.

## Analysis parameter

The recommended analysis parameters are:

Analysis Range	Start: 2000 Stop: 10000
Data Processing	Baseline: Checked Multicomponent: Checked Smooth Options: Light
Peak Detection	Peak Amplitude Thresholds B:* Y:* G:* R:* Min. Peak Half Width: 2 pts Polynomial Degree: 3 Peak Window Size: 11 pts**
Size Call Range	Min: 50 Max: 550
Size Calling Method	Local Southern Method
Split Peak Correction	None

\* The peak amplitude threshold (cutoff value) corresponds to the minimum peak height that will be detected by the GeneScan<sup>®</sup> or GeneMapper<sup>™</sup> ID software. Thresholds are usually 50-200 RFU and should be determined individually by the laboratory. Recommendation: The minimal peak height should be three times as high as the background noise of the baseline.

\*\* Point alleles (i.e. alleles with at least 1 bp difference to the next integer allele) may occasionally not be distinguished. For improved peak detection, minimise the Peak Window Size further.

#### 4. Electrophoresis using the ABI PRISM® 3130/3130xl Genetic Analyzer

For detailed instructions on instrument setup, spectral calibration, or application of the ABI PRISM® Data Collection software version 3.0 and the GeneMapper™ ID software, refer to the *ABI PRISM® 3130/3130xl Genetic Analyzers Getting Started Guide*.

The system with 4 capillaries is named ABI 3130 (former ABI 3100-Avant), and the system with 16 capillaries is named ABI 3130xl (former ABI 3100).

The virtual **filter set D** shall be used for combined application of the four fluorescent labels **6-FAM**, **HEX**, **NED**, and **ROX** (also called **DS-30**).

##### Material

Capillary	36 cm Capillary Array for 3130/3130xl
Polymer	POP-4 Polymer for 3130
Buffer	10x Genetic Analyzer Buffer with EDTA

##### Spectral calibration / matrix generation

Prior to conducting DNA fragment size analysis, it is necessary to perform a spectral calibration with the four fluorescent labels 6-FAM, HEX, NED, and ROX for each analyzer. The calibration procedure creates a matrix which is used to correct the overlapping of fluorescence emission spectra of the dyes.

Spectral calibration comprises the following steps:

- Preparation the spectral calibration standards
- Loading the standards to the 96-well reaction plate (one sample per capillary)
- Creating the instrument protocol for spectral calibration (Protocol Manager)
- Defining the plate composition in the plate editor (Plate Manager)
- Performing a spectral calibration run and checking the matrix

## Setting up the spectral calibration standards

Example for 4 capillaries/ABI 3130

Component	Volume
Hi-Di™ Formamide	47.5 µL
Matrix standard DS-30	2.5 µL

- Load 12 µL of the mix to a 96-well reaction plate, e.g. position **A1-D1**
- Denaturation for 3 min at 95°C
- Cool down to 4°C

Example for 16 capillaries/ABI 3130xl

Component	Volume
Hi-Di™ Formamide	190.0 µL
Matrix standard DS-30	10.0 µL

- Load 12 µL of the mix to a 96-well reaction plate, e.g. position **A1-H1** and **A2-H2**
- Denaturation for 3 min at 95°C
- Cool down to 4°C

## Performing a spectral calibration run

- Place the 96-well plate on the autosampler tray
- In the **Protocol Manager** of the Data Collection software click **New** the window **Instrument Protocol** to open the **Protocol Editor** dialog box

## Instrument Protocol for spectral calibration

Protocol Editor	Set up
Name	User (e.g. Spectral36_POP4_DS30)
Type	SPECTRAL
Dye Set	D
Polymer*	User (e.g. POP4)
Array Length*	User (e.g. 36cm)
Chemistry	Matrix Standard
Run Module*	Default (e.g. Spect36_POP4_1)

\* Depends on the type of polymer and length of capillary used

- Select **OK** to complete the **Protocol Editor** dialog box
- In the **Plate Manager** of the Data Collection software click **New** to open the **New Plate Dialog** box

## Plate Editor for spectral calibration (I)

New Plate Dialog	Set up
Name	e.g. Spectral_DS-30_date
Application	Spectral Calibration
Plate Type	96-Well
Owner Name / Operator Name	...

- Click on **OK**. A new table in the **Plate Editor** opens automatically



## Plate Editor for spectral calibration (II)

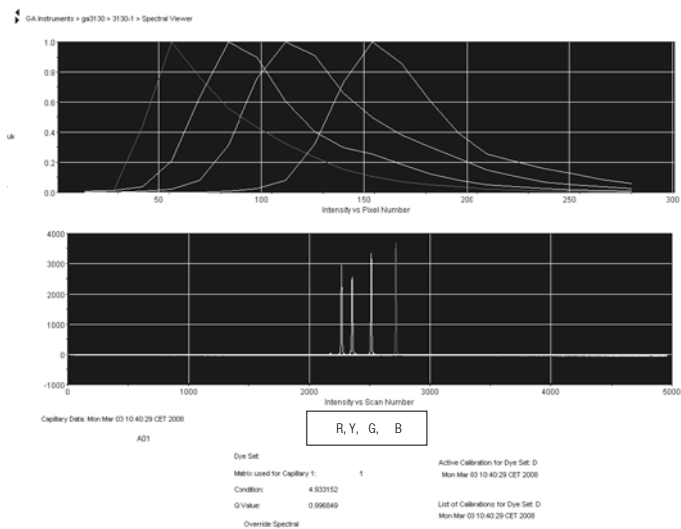
### Parameter

Sample Name  
Priority  
Instrument Protocol 1

### Set up

Type name for the matrix samples  
e.g. 100  
Spectral36\_POP4\_DS30 (setting described before)

- Click into the column header to select the entire column, select **Edit** → **Fill Down** to apply the information to all selected samples, and click on **OK**
- In the **Run Scheduler** click on **Find All**, select **Link** to link the reaction plate on the autosampler up with the newly created plate record (position A or B) and start the run



**Fig. 4** Electropherogram of spectral calibration with matrix standard DS-30 on an ABI 3130

## Matrix check

- The quality value (**Q value**) of each capillary must be greater than 0.95 and the condition number range (**C value**) must be between 1 and 20.
- Check the matrix samples for a flat baseline. As shown in the figure above, there should be four peaks with peak heights of about 1000-5000 (Y-axis) in each matrix sample (optimal range: 2000-4000)
- Check the new matrix with your current samples. There should be **no** pull-up peaks between the dye panels (B, G, Y, R) with the new matrix
- If calibration was not successful, use the optimised values and repeat the calibration run
- If all capillaries have passed the test, the last calibration file for the **Dye Set D** is activated automatically in the **Spectral Viewer**. **Rename** the calibration file (e.g. DS-30\_Date of calibration) using the respective button

## Sample preparation

Component	Volume
Hi-Di™ Formamide	12.0 µL
DNA Size Standard 550 (ROX)	0.5 µL

prepare 12 µL of the mix (formamide + DNA size standard) for all samples  
add 1 µL PCR product (diluted if necessary) or allelic ladder

- Denaturation for 3 min at 95°C
- Cool down to 4°C
- For analysis: load the samples on the tray

Since injections take place simultaneously on all capillaries, 4 or 16 samples must be pipetted on the plate of multi-capillary analysers. If fewer samples are analysed, the empty positions must be filled with 12 µL Hi-Di™ Formamide.

To ensure a reliable allelic assignment on multi-capillary analysers, several ladders should be run.

Room temperature may influence the performance of PCR products on multi-capillary instruments, so that shoulder peaks or split peaks occur especially at low temperatures. Pay attention to keeping ambient conditions as recommended by the instrument manufacturer.

## Signal intensities

Options to increase the signal intensity:

- Reduce the volume of the DNA Size Standard 550 (ROX) to peak heights of about 500 relative fluorescent units (RFU)
- Purify the PCR products before starting the analysis

## Setting up the GeneMapper™ ID software

Edit the Run Module as follows for the first run:

- In the **Module Manager** of the Data Collection software click on **New** to open the **Run Module Editor** dialog box

### Run Module 3kV\_10s\_450bp

Parameter	Set up
Oven Temperature [°C]	<i>Default</i>
Poly Fill Volume	<i>Default</i>
Current Stability [µA]	<i>Default</i>
PreRun Voltage [kV]	<i>Default</i>
PreRun Time [s]	<i>Default</i>
Injection Voltage [kV]	<b>3.0</b>
Injection Time [s]*	<b>10</b>
Voltage Number of Steps	<i>Default</i>
Voltage Step Interval	<i>Default</i>
Data Delay Time [s]	<i>Default</i>
Run Voltage [kV]	<i>Default</i>
Run Time [s]**	<b>1320</b>

\* Deviating from the standard settings, the injection time may range between 1 and 20 s depending on the type of sample. If samples with very high signal intensities are recorded, a shorter injection time may be selected. For samples with low DNA content an injection time of up to 20 s may be necessary.

\*\* Depending on the analysis conditions the run time for Mentype® Nonaplex<sup>DS</sup> was modified in order to be able to analyse fragments with lengths of up to **450 bp**.

- Click on **Save As**, enter the name of the new module (e.g. 3kV\_10s\_450bp) and confirm with **OK**
- Click on **Close** to exit the **Run Module Editor**

## Starting the run

- Place the prepared 96-well plate on the autosampler tray
- In the **Protocol Manager** of the Data Collection software, click on **New** in the **Instrument Protocol** window to open the **Protocol Editor** dialog box

### Instrument Protocol

Protocol Editor	Set up
Name	e.g. Run36_POP4_DS-30_22min
Type	REGULAR
Run Module*	3kV_10s_450bp
Dye Set	D

\* parameter see above

- Click on **OK** to exit the **Protocol Editor**

Prior to each run, it is necessary to create a plate definition as follows:

- In the **Plate Manager** of the Data Collection software click on **New** to open the **New Plate Dialog** box

### GeneMapper™ Plate Editor (I)

<b>New Plate Dialog</b>	<b>Set up</b>
Name	e.g. Plate_DS-30_Date
Application	select GeneMapper Application
Plate Type	96-Well
Owner Name / Operator Name	...

- Click **OK**. A new table in the **Pate Editor** opens automatically

### GeneMapper™ Plate Editor (II)

<b>Parameter</b>	<b>Set up</b>
Sample Name	Type name for the samples
Priority	e.g. 100 (Default)
Sample Type	Sample or Allelic Ladder
Size Standard	e.g. SST-ROX_50-450bp
Panel	e.g. Biotype_Panels_v3a (choose test kit)
Analysis Method	e.g. Analysis_HID_3130
SnP Set	-
User-defined 1-3	-
Results Group 1	(select results group)
Instrument Protocol 1	Run36_POP4_DS-30 (setting described earlier)

- Click into the column header to select the entire column, select **Edit** → **Fill Down** to apply the information to all selected samples and click on **OK**
- In the **Run Scheduler**, click on **Find All**, select **Link** to link the reaction plate on the autosampler up with the newly created plate record (position A or B) and start the run
- During the run, view **Error Status** in the **Event Log** or examine the quality of the raw data for each capillary in the **Capillaries Viewer** or the **Cap/Array Viewer**
- View data as overview in **Run History** or **Cap/Array Viewer** of the Data Collection software. Run data are saved in the **Run Folder** of the previously chosen **Result Group**

## Analysis parameter / analysis method

The recommended settings in the worksheet Peak Detector are:

Peak Detection Algorithm	Advanced
Ranges	Analysis: Partial Range Start Pt: 2000; Stop Pt: 10000 Sizing: All Sizes
Smoothing and Baselineing	Smoothing: Light Baseline Window: 51 pts
Size Calling Method	Local Southern Method
Peak Detection	Peak Amplitude Thresholds B:* Y:* G:* R:* Min. Peak Half Width: 2 pts Polynomial Degree: 3 Peak Window Size: 11 pts** Slope Thresholds: 0.0

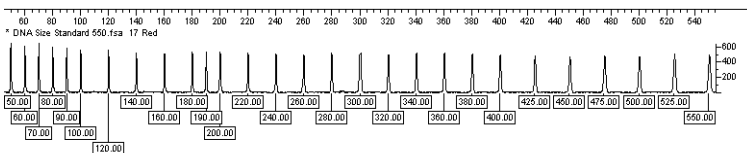
\* The peak amplitude threshold (cutoff value) corresponds to the minimum peak height that will be detected by the GeneMapper™ ID software. The thresholds are usually 50-200 RFU and should be determined individually by the laboratory. Recommendation: The minimal peak height should be three times as high as the background noise of the baseline.

\*\* Point alleles (i.e. alleles with at least 1 bp difference to the next integer allele) may occasionally not be distinguished. For improved peak detection, minimise the Peak Window Size further.

## 5. Analysis

For general instructions on automatic sample analysing, refer to the *GeneScan®* or *GeneMapper™ ID Software User's Manual*.

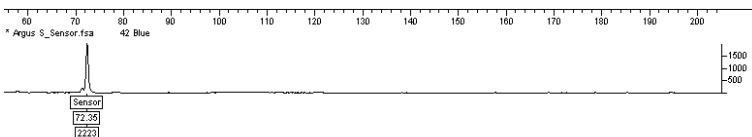
Finding the exact lengths of the amplified products depends on the device type, the conditions of electrophoresis, as well as the DNA size standard used. Due to the complexity of some loci, determining the size should be based on evenly distributed references. The DNA Size Standard 550 (ROX) shall thus be used with the following lengths of fragments: **50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 190, 200, 220, 240, 260, 280, 300, 320, 340, 360, 380, 400, 425, 450, 475, 500, 525, and 550 bp**.



**Fig. 5** Electropherogram of the DNA Size Standard 550 (ROX), fragments with lengths in bp

**Note:** The basic template files for the DNA Size Standard 550 (ROX) has to be adjusted to 450 bp within the GeneMapper™ ID software. The new template could be saved as e.g. SST-ROX\_50-450bp and used for further analyses.

As mentioned before, Mentype® **Nonaplex<sup>QS</sup>** contains an **internal PCR control** (Quality Sensor), which provides helpful information on the efficiency of the PCR and on presence of PCR inhibitors. A 6-FAM labelled **72 bp**-fragment is amplified independently of the DNA. The PCR control assay without DNA shows only the sensor fragment (Fig. 6) and indicates successful polymerase chain reaction.



**Fig. 6** Electropherogram of the 6-FAM labelled PCR control fragment (Quality Sensor). Fragment length in bp, signal intensities in peak height

## 6. Biotype Template Files

Allele allocation should be carried out with a suitable analysis software, e.g. GeneMapper™ ID or Genotyper® software in combination with the Mentype® Nonaplex<sup>QS</sup> template files from Biotype. Template files are available from our homepage or as CD-ROM on request.

Recommended Biotype® templates for GeneMapper™ ID/ID-X software are:

Panels	Biotype_Panels_v3a/v3X (choose kit)	or higher versions
BinSets	Biotype_Bins_v3a/v3X	or higher versions
Size Standard	SST-R0X_50-500bp (adjust up to 450bp, adjustment described earlier)	
Analysis Method	Analysis_HID_310	
	Analysis_HID_3130	
	Analysis_HID_310_50rfu	
	Analysis_HID_3130_50rfu	
Plot Settings	Plots_4dyes	
Table Settings	Table for 2 alleles	
	Table for 10 alleles	

Panels and BinSets always have to be used whereas the other template files are optional.

Additional Biotype® templates for GeneMapper™ ID-X Software:

Stutter*	Biotype_Stutter_v3X	or higher version
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\* When loading the above mentioned panels, the stutter settings will not be accepted. Thus, the stutter data has to be imported separately.

Recommended Biotype® template files for Genotyper® software are:

for standard allelic ladder	Nonaplex-QS_v1d	or higher versions
for extended allelic ladder	Nonaplex-QS-EXT_v0	or higher versions

### General procedure for the analysis

1. Check the DNA size standard
2. Check the allelic ladder
3. Check the positive control
4. Check the negative control
5. Analyse and interpret the sample data

## 7. Controls

The Control DNA XY1 of the test kit and other commercially available DNA from standard cell lines represent the following alleles:

**Table 3. Allele assignment of Mentype® Nonaplex<sup>OS</sup>**

Locus	Control DNA XY1	ATCC K-562	CCR 9947A	CCR 9948	CCR 3657
Amelogenin	X / Y	X / X	X / X	X / Y	X / Y
D3S1358	17 / 18	16 / 16	14 / 15	15 / 17	16 / 18
D8S1179	9 / 10	12 / 12	13 / 13	12 / 13	15 / 16
D18S51	12 / 14	15 / 16	15 / 19	15 / 18	12 / 20
D21S11	27 / 28	29 / 30 / 31	30 / 30	29 / 30	28 / 29
FGA	20 / 26	21 / 24	23 / 24	24 / 26	18 / 23
SE33	17 / 21.2	26.2 / 28.2	19 / 29.2	23.2 / 26.2	22.2 / 27.2
TH01	6 / 9.3	9.3 / 9.3	8 / 9.3	6 / 9.3	7 / 9.3
vWA	15 / 18	16 / 16	17 / 18	17 / 17	14 / 19

For further confirmation, the table above displays the alleles of the reference DNA purchased from ATCC (<http://atcc.org/Products/PurifiedDNA.cfm#celllines>) as well as three reference DNA purchased from Coriell Cell Repositories (CCR; <http://locus.umdj.edu/nigms/>) that is up to standard of Szibor et al. (2003).

### Lengths of fragments and alleles

**Table 4** to **table 9** show the fragment lengths of individual alleles that refer to the DNA Size Standard 550 (ROX). All analyses have been performed on an ABI PRISM® 310/3130 Genetic Analyzer with POP-4 polymer. Different analysis instruments, DNA size standards or polymers may result in different fragment lengths. In addition, a visual alignment with the allelic ladder is recommended.

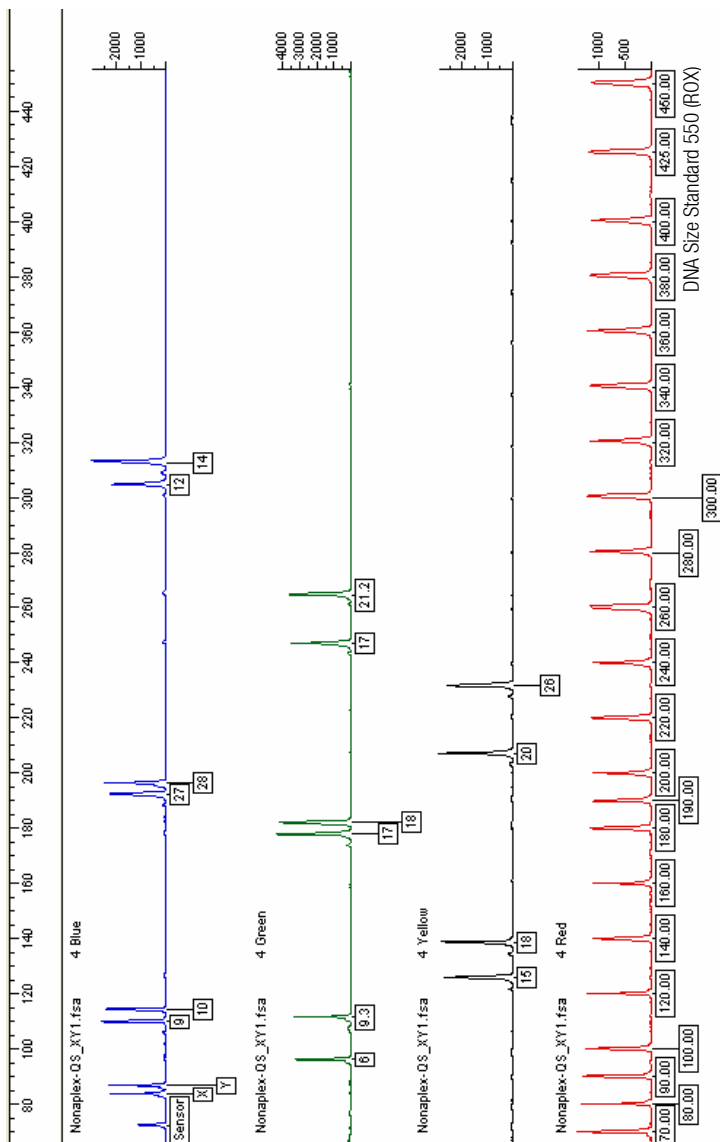
### Scaling

Horizontal: 75-455 bp (with Quality Sensor 65-455 bp)

Vertical: Depending on signal intensity



Figure 7



**Fig. 7** Electropherogram of the Mentype® **Nonaplex**<sup>OS</sup> using 500 pg Control DNA XY1. The **Quality Sensor (QS)** is shown at 72 bp. Analysis was performed on an ABI PRISM® 310 Genetic Analyzer with the DNA Size Standard 550 (ROX). Allele assignment was performed using the Genotype® software and the Mentype® **Nonaplex**<sup>OS</sup> template file.

Figure 8

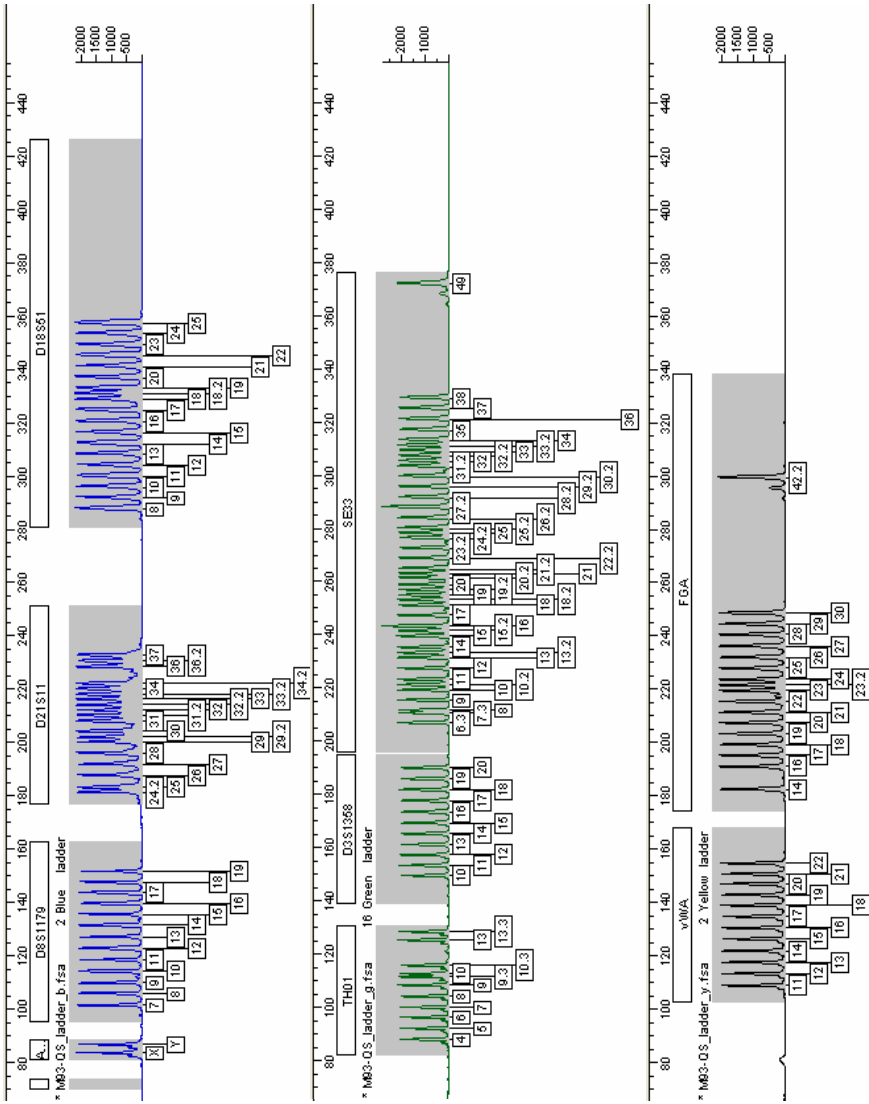


Fig. 8 Electropherogram of the allelic ladder Mentype® Nonplex<sup>OS</sup> analysed on an ABI PRISM® 310 Genetic Analyzer. Allele assignment was performed using the Genotyper® software and the Mentype® Nonplex<sup>OS</sup> template files.

**Table 4. Fragment lengths of the allelic ladder Mentype® Nonaplex<sup>QS</sup> analysed on an ABI PRISM® 310/3130 Genetic Analyzer (blue panel)**

Marker/ allele	Size [bp]*	Further alleles**	Marker/ allele	Size [bp]*	Further alleles**	Marker/ allele	Size [bp]*	Further alleles**
<b>PCR control</b>	<b>6-FAM</b>		<b>D21S11</b>	<b>6-FAM</b>		<b>D18S51</b>	<b>6-FAM</b>	
Quality Sensor	72		24.2	181	23.2, 24	8	288	7
			25	183	25.2	9	292	9.2
<b>Amelogen in</b>	<b>6-FAM</b>		26	188	26.2	10	296	10.2
X	83		27	192		11	300	11.2
Y	86		28	196	28.2, 28.3	12	304	12.2
			29	200		13	308	13.2
<b>D8S1179</b>	<b>6-FAM</b>		29.2	202	29.3	14	312	14.2
7	101		30	204	30.2	15	316	
8	106		31	208		16	320	16.2
9	110		31.2	210		17	325	17.2, 17.3
10	114		32	212		18	329	
11	118		32.2	214		18.2	331	
12	123		33	216	33.1	19	333	19.2
13	127		33.2	218		20	337	
14	131		34	220	34.1	21	341	21.2
15	135		34.2	222	35, 35.2	22	345	
16	140		36	228		23	349	23.1
17	144		36.2	230		24	353	
18	148		37	232	37.2, 38, 38.2, 39	25	357	26, 27, 28, 29
19	152	20						

**Table 5. Fragment lengths of the allelic ladder Mentype® Nonaplex<sup>OS</sup> analysed on an ABI PRISM® 310/3130 Genetic Analyzer (green panel)**

Marker/ allele	Size [bp]*	Further alleles**	Marker/ allele	Size [bp]*	Further alleles**	Marker/ allele	Size [bp]*	Further alleles**
<b>TH01</b>	<b>HEX</b>		<b>SE33</b>	<b>HEX</b>		<b>SE33</b>	<b>HEX</b>	
4	88	3	6.3	207	4.2, 5.3	24.2	276	24
5	92		7.3	211	7	25	278	
6	96	6.3	8	212	8.2	25.2	280	
7	100	7.3	9	216	9.2	26.2	284	26
8	104	8.3	10	219		<b>27.2†</b>	288	27
9	108	9.1	10.2	221		28.2	291	28, 28.3
9.3	111		11	223	11.2	29.2	295	29
10	112		12	227	12.2	30.2	299	30
10.3	116	11	13	231		31.2	303	31
13	125		13.2	233	13.3	32	305	
13.3	128		14	235	14.2, 14.3	32.2	307	
			15	239		33	309	
<b>D3S1358</b>	<b>HEX</b>		15.2	241		33.2	311	
10	149	8, 9	<b>16†</b>	243	16.2, 16.3	34	313	34.2
11	153		17	247	17.2, 17.3	35	317	35.2
12	157		18	251		36	321	36.2
13	161		18.2	253	18.3	37	325	37.2
14	165		19	255		38	329	39, 42
15	169		19.2	257		49	372	
16	173		20	259	20.1			
17	178		20.2	261				
18	182		21	263				
19	186		21.2	265				
20	190	21	22.2	269	22			
			23.2	272	23			

† For a better orientation, these alleles are heightened within the allelic ladder

**Table 6. Fragment lengths of the allelic ladder Mentype® Nonaplex<sup>QS</sup> analysed on an ABI PRISM® 310/3130 Genetic Analyzer (yellow panel)**

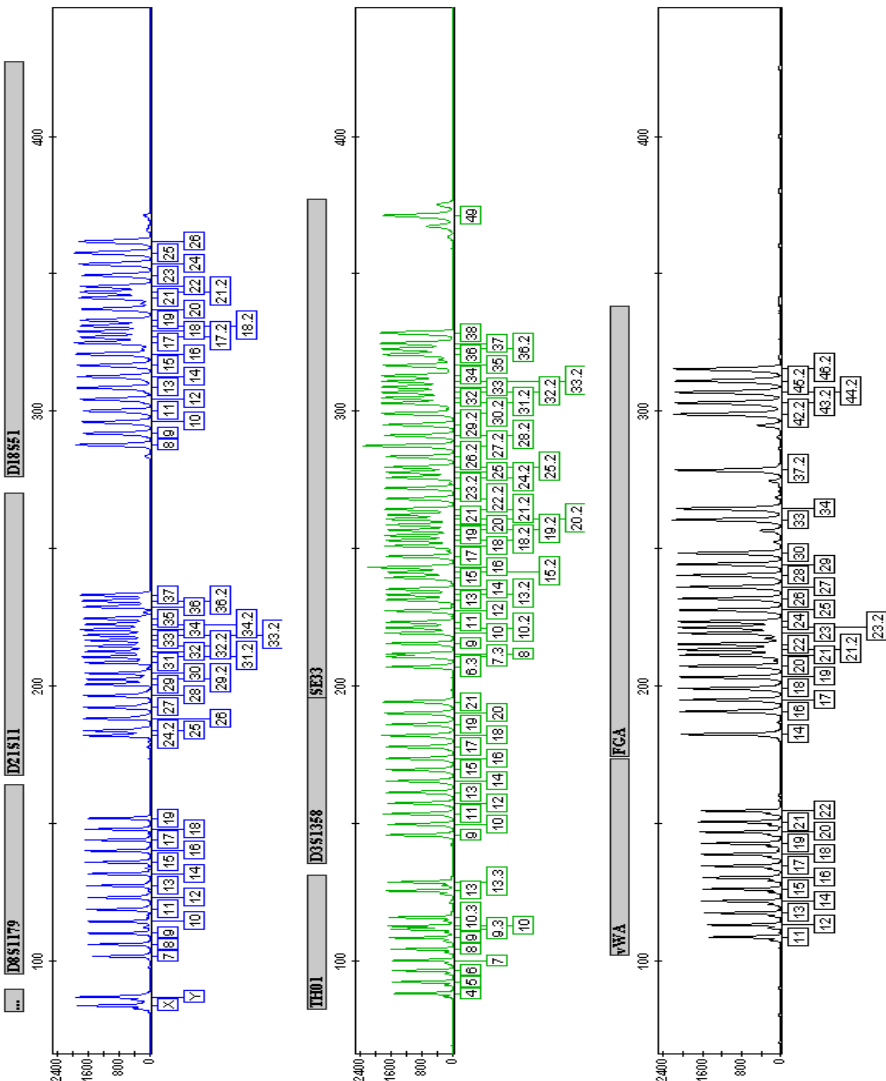
Marker/ allele	Size [bp]*	Further alleles**	Marker/ allele	Size [bp]*	Further alleles**
<b>vWA</b>	<b>NED</b>		<b>FGA</b>	<b>NED</b>	
11	108	10	14	182	15
12	113		16	191	16.1
13	117		17	195	
14	122		18	199	18.2
15	126		19	203	19.2
16	130		20	207	20.2
17	134		21	211	21.2
18	138		22	215	22.2
19	142		23	219	
20	146		23.2	221	23.3
21	150		24	223	24.1, 24.2
22	154	23, 24	25	227	25.2
			26	231	26.2
			27	235	
			28	240	
			29	244	
			30	248	30.2, 31, 31.2, 32.2, 33, 33.2, 34, 37.2
			42.2	299	43.2, 44.2, 45.2, 46.2, 47.2, 48.2, 50.2, 51.2

\* rounded to integer

\*\* The "off-ladder" alleles of Biotype's DNA pool are allocated with the actual Biotype® template files for GeneMapper™ ID or Genotyper® software. For further alleles see amongst others [http://www.cstl.nist.gov/biotech/strbase/str\\_fact.htm](http://www.cstl.nist.gov/biotech/strbase/str_fact.htm)

**Figure 9**

Since January 2008 the allelic ladder Mentype® **Nonplex**<sup>OS</sup> extended (Cat. No. 48-09330-0010) is additionally available.



**Fig. 9** Electropherogram of the allelic ladder Mentype® **Nonplex**<sup>OS</sup> extended analysed on an ABI PRISM® 310 Genetic Analyzer. Allele assignment was performed using the Genotyper® software and the Mentype® **Nonplex**<sup>OS</sup> extended template files.

**Table 7. Fragment lengths of the allelic ladder Mentype® Nonaplex<sup>QS</sup> extended analysed on an ABI PRISM® 310/3130 Genetic Analyzer (blue panel)**

Marker/ allele	Size [bp]*	Further alleles**	Marker/ allele	Size [bp]*	Further alleles**	Marker/ allele	Size [bp]*	Further alleles**
<b>PCR control</b>	<b>6-FAM</b>		<b>D21S11</b>	<b>6-FAM</b>		<b>D18S51</b>	<b>6-FAM</b>	
Quality Sensor	72		24.2	181	23.2, 24	8	288	7
			25	183	25.2	9	292	9.2
<b>Amelogen in</b>	<b>6-FAM</b>		26	188	26.2	10	296	10.2
X	83		27	192		11	300	11.2
Y	86		28	196	28.2, 28.3	12	304	12.2
			29	200		13	308	13.2
<b>D8S1179</b>	<b>6-FAM</b>		29.2	202	29.3	14	312	14.2
7	101		30	204	30.2	15	316	
8	106		31	208		16	320	16.2
9	110		31.2	210		17	325	
10	114		32	212		<b>17.2<sup>†</sup></b>	327	17.3
11	118		32.2	214		18	329	
12	123		33	216	33.1	18.2	331	
13	127		33.2	218		19	333	19.2
14	131		34	220	34.1	20	337	
15	135		34.2	222		21	341	
16	140		<b>35<sup>†</sup></b>	224	35.2	<b>21.2<sup>†</sup></b>	343	
17	144		36	228		22	345	
18	148		36.2	230		23	349	23.1
19	152	20	37	232	37.2, 38, 38.2, 39	24	353	
						25	357	
						<b>26<sup>†</sup></b>	361	27, 28, 29

**Table 8. Fragment lengths of the allelic ladder Mentype® Nonaplex<sup>OS</sup> extended analysed on an ABI PRISM® 310/3130 Genetic Analyzer (green panel)**

Marker/ allele	Size [bp]*	Further alleles**	Marker/ allele	Size [bp]*	Further alleles**	Marker/ allele	Size [bp]*	Further alleles**
<b>TH01</b>	<b>HEX</b>		<b>SE33</b>	<b>HEX</b>		<b>SE33</b>	<b>HEX</b>	
4	88	3	6.3	207	4.2, 5.3	25	278	
5	92		7.3	211	7	25.2	280	
6	96	6.3	8	212	8.2	26.2	284	26
7	100	7.3	9	216	9.2	<b>27.2†</b>	288	27
8	104	8.3	10	219		28.2	291	28, 28.3
9	108	9.1	10.2	221		29.2	295	29
9.3	111		11	223	11.2	30.2	299	30
10	112		12	227	12.2	31.2	303	31
10.3	116	11	13	231		32	305	
13	125		13.2	233	13.3	32.2	307	
13.3	128		14	235	14.2, 14.3	33	309	
			15	239		33.2	311	
			15.2	241		34	313	34.2
<b>D3S1358</b>	<b>HEX</b>		<b>16†</b>	243	16.2, 16.3	35	317	35.2
<b>9†</b>	145	8	17	247	17.2, 17.3	36	321	
10	149		18	251		<b>36.2†</b>	323	
11	153		18.2	253	18.3	37	325	37.2
12	157		19	255		38	329	39, 42
13	161		19.2	257		49	372	
14	165		20	259	20.1			
15	169		20.2	261				
16	173		21	263				
17	178		21.2	265				
18	182		22.2	269	22			
19	186		23.2	272	23			
20	190		24.2	276	24			
<b>21†</b>	194							

† For a better orientation, these alleles are heightened within the allelic ladder



**Table 9. Fragment lengths of the allelic ladder Mentype® Nonaplex<sup>QS</sup> extended analysed on an ABI PRISM® 310/3130 Genetic Analyzer (yellow panel)**

Marker/ allele	Size [bp]*	Further alleles**	Marker/ allele	Size [bp]*	Further alleles**
<b>vWA</b>	<b>NED</b>		<b>FGA</b>	<b>NED</b>	
11	108	10	14	182	15
12	113		16	191	16.1
13	117		17	195	
14	122		18	199	18.2
15	126		19	203	19.2
16	130		20	207	20.2
17	134		21	211	
18	138		<b>21.2†</b>	213	
19	142		22	215	22.2
20	146		23	219	
21	150		23.2	221	23.3
22	154	23, 24	24	223	24.1, 24.2
			25	227	25.2
			26	231	26.2
			27	235	
			28	240	
			29	244	
			30	248	30.2, 31, 31.2
			<b>33†</b>	260	32.2, 33.2
			<b>34†</b>	264	
			<b>37.2†</b>	278	
			42.2	299	
			<b>43.2†</b>	303	
			<b>44.2†</b>	307	
			<b>45.2†</b>	311	
			<b>46.2†</b>	315	47.2, 48.2, 50.2, 51.2

\* rounded to integer

\*\* The "off-ladder" alleles of Biotype's DNA pool are allocated with the actual Biotype® template files for GeneMapper™ ID or Genotyper® software. For further alleles see amongst others [http://www.cstl.nist.gov/biotech/strbase/str\\_fact.htm](http://www.cstl.nist.gov/biotech/strbase/str_fact.htm)

† These alleles are not included in the Mentype® Nonaplex<sup>QS</sup> allelic ladder.

## 8. Interpretation of results

As mentioned above, post PCR analysis and automatic allele assignment with suitable analysis software ensure a precise and reliable discrimination of alleles.

### Pull-up peaks

Pull-up peaks may occur if peak heights are outside the linear detection range (>3000 RFU), or if an incorrect matrix was applied. They appear at positions of specific peaks in other colour channels, typically with lower signal intensities. Peak heights should not exceed 3000 RFU in order to prevent pull-up peaks.

### Stutter peaks

The occurrence of stutter peaks depends on the sequence of the repeat structure and the number of alleles. n-4 peaks are caused by a loss of a repeat unit during amplification of tetranucleotide STR motives, caused by slippage effects of the Taq DNA Polymerase. Interpretation of those peaks should be done in accordance with the Template Files of the Genotyper<sup>®</sup> and GeneMapper<sup>™</sup> ID software.

### Template-independent addition of nucleotides

Because of its terminal transferase activity, the Taq DNA Polymerase tends to add an adenosine radical at the 3'-end of the amplified DNA fragments. The artefact peak is one base shorter than expected (-1 peaks). All Biotype<sup>®</sup> primers are designed to minimise these artefacts. Artefact formation is further reduced by the final extension step of the PCR protocol at 68°C for 60 minutes. Peak height of the artefact correlates with the amount of DNA. Laboratories should define their own limits for analysis of the peaks.

### Quality Sensor to check the PCR results

Mentype<sup>®</sup> Nonaplex<sup>QS</sup> contains an internal PCR check (Quality Sensor), which provides helpful information on the efficiency of the PCR and on presence of PCR inhibitors (see Fig. 6). Complete sensor failure indicates total inhibition of the PCR or errors in the assay. If the sensor signal is amplified in presence of DNA either in the negative control or in the positive control, the PCR is not inhibited. Samples with sufficient DNA and without inhibiting substances result in the DNA profile according to the kit and the sensor fragment. Reduced sensor peak heights in forensic samples indicate partial PCR inhibition. If only the Quality Sensor is amplified, the sample contains very little or degraded DNA.

### Artefacts

Room temperature may influence the performance of PCR products on multi-capillary instruments, so that shoulder peaks or split peaks occur. If shoulder or split peaks appear, we recommend injecting the sample again.

## 9. References

**Bär W, Brinkmann B, Budowle B, Carracedo A, Gill P, Lincoln P, Mayr W, Olaisen B (1997)** DNA recommendations. Further report of the DNA Commission of the ISFG regarding the use of short tandem repeat systems. *Int. J. Legal Med.* 110: 175-176.

**Szibor R, Edelmann J, Hering S, Plate I, Wittig H, Roewer L, Wiegand P, Cali F, Romano V, Michael M (2003)** Cell line DNA typing in forensic genetics – the necessity of reliable standards. *Forensic Sci. Int.* 138 37-43.