

# FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR TYPING

## GENEMAPPER ID – ANALYSIS METHOD EDITOR SETTINGS

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### Genemapper ID Analysis Method Editor Settings

#### Identifiler Analysis Settings:

Analysis Method Editor - HID

General | **Allele** | Peak Detector | Peak Quality | Quality Flags

Bin Set: Identifiler\_Bins

Use marker-specific stutter ratio if available

Marker Repeat Type :	Tri	Tetra	Penta	Hexa
Cut-off Value	0.0	0.1	0.0	0.0
MinusA Ratio	0.0	0.0	0.0	0.0
MinusA Distance	From 0.0	0.0	0.0	0.0
	To 0.0	0.0	0.0	0.0
Minus Stutter Ratio	0.0	0.0	0.0	0.0
Minus Stutter Distance	From 0.0	3.25	0.0	0.0
	To 0.0	4.75	0.0	0.0
Plus Stutter Ratio	0.0	0.0	0.0	0.0
Plus Stutter Distance	From 0.0	0.0	0.0	0.0
	To 0.0	0.0	0.0	0.0

Amelogenin Cutoff: 0.1

Range Filter... Factory Defaults

OK Cancel

Analysis Method Editor - HID

General | Allele | **Peak Detector** | Peak Quality | Quality Flags

Peak Detection Algorithm: Advanced

Ranges

Analysis: Partial Range Sizing: Partial Sizes

Start Pt: 2300 Start Size: 75

Stop Pt: 9000 Stop Size: 450

Smoothing and Baseline

Smoothing:  None  Light  Heavy

Baseline Window: 251 pts

Size Calling Method

2nd Order Least Squares  
 3rd Order Least Squares  
 Cubic Spline Interpolation  
 Local Southern Method  
 Global Southern Method

Peak Detection

Peak Amplitude Thresholds:

B: 75 R: 75

G: 75 O: 75

Y: 75

Min. Peak Half Width: 2 pts

Polynomial Degree: 3

Peak Window Size: 15 pts

Slope Threshold

Peak Start: 0.0

Peak End: 0.0

Factory Defaults

OK Cancel

Analysis Method Editor - HID

General | Allele | Peak Detector | **Peak Quality** | Quality Flags

Signal level

Homozygous min peak height: 75.0

Heterozygous min peak height: 75.0

Heterozygote balance

Min peak height ratio: 0.7

Peak morphology

Max peak width (basepairs): 1.5

Pull-up peak

Pull-up ratio: 0.05

Allele number

Max expected alleles: 2

Factory Defaults

OK Cancel

Analysis Method Editor - HID

General | Allele | Peak Detector | Peak Quality | **Quality Flags**

Quality weights are between 0 and 1.

Quality Flag Settings

Spectral Pull-up: 0.8 Control Concordance: 1.0

Broad Peak: 0.8 Low Peak Height: 0.3

Out of Bin Allele: 0.8 Off-scale: 0.8

Overlap: 0.8 Peak Height Ratio: 0.3

PQV Thresholds

Pass Range: Low Quality Range:

Sizing Quality: From 0.75 to 1.0 From 0.0 to 0.25

Genotype Quality: From 0.75 to 1.0 From 0.0 to 0.25

Factory Defaults

OK Cancel

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### MiniFiler Analysis Settings:

**Analysis Method Editor - HID**

General | **Allele** | Peak Detector | Peak Quality | Quality Flags

Bin Set: AmpFLSTR\_MiniFiler\_GS500\_Bins\_v1

Use marker-specific stutter ratio if available

Marker Repeat Type:	Tri	Tetra	Penta	Hexa
Cut-off Value	0.0	0.1	0.0	0.0
MinusA Ratio	0.0	0.0	0.0	0.0
MinusA Distance	From 0.0	0.0	0.0	0.0
	To 0.0	0.0	0.0	0.0
Minus Stutter Ratio	0.0	0.0	0.0	0.0
Minus Stutter Distance	From 0.0	3.25	0.0	0.0
	To 0.0	4.75	0.0	0.0
Plus Stutter Ratio	0.0	0.0	0.0	0.0
Plus Stutter Distance	From 0.0	0.0	0.0	0.0
	To 0.0	0.0	0.0	0.0

Amelogenin Cutoff: 0.1

Range Filter... Factory Defaults

OK Cancel

**Analysis Method Editor - HID**

General | Allele | **Peak Detector** | Peak Quality | Quality Flags

Peak Detection Algorithm: Advanced

**Ranges**

Analysis: Partial Range [dropdown] Sizing: Partial Sizes [dropdown]

Start Pt: 2500 Start Size: 65

Stop Pt: 10000 Stop Size: 400

**Smoothing and Baselining**

Smoothing:  None  Light  Heavy

Baseline Window: 251 pts

**Peak Detection**

Peak Amplitude Thresholds:

B: 75 R: 75

G: 75 O: 75

Y: 75

Min. Peak Half Width: 2 pts

Polynomial Degree: 3

Peak Window Size: 15 pts

Slope Threshold

Peak Start: 0.0

Peak End: 0.0

**Size Calling Method**

2nd Order Least Squares

3rd Order Least Squares

Cubic Spline Interpolation

Local Southern Method

Global Southern Method

Factory Defaults

OK Cancel

**Analysis Method Editor - HID**

General | Allele | Peak Detector | **Peak Quality** | Quality Flags

**Signal level**

Homozygous min peak height: 75.0

Heterozygous min peak height: 75.0

**Heterozygote balance**

Min peak height ratio: 0.7

**Peak morphology**

Max peak width (basepairs): 1.5

**Pull-up peak**

Pull-up ratio: 0.05

**Allele number**

Max expected alleles: 2

Factory Defaults

OK Cancel

**Analysis Method Editor - HID**

General | Allele | Peak Detector | Peak Quality | **Quality Flags**

Quality weights are between 0 and 1.

**Quality Flag Settings**

Spectral Pull-up: 0.8 Control Concordance: 1.0

Broad Peak: 0.8 Low Peak Height: 0.3

Out of Bin Allele: 0.8 Off-scale: 0.8

Overlap: 0.8 Peak Height Ratio: 0.3

**PGV Thresholds**

Pass Range: Low Quality Range:

Sizing Quality: From 0.75 to 1.0 From 0.0 to 0.25

Genotype Quality: From 0.75 to 1.0 From 0.0 to 0.25

Factory Defaults

OK Cancel

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### Yfiler Analysis Settings:

Bin Set: AmpFLSTR\_Yfiler\_Binset\_v2

Use marker-specific stutter ratio if available

Marker Repeat Type :	Tri	Tetra	Penta	Hexa
Cut-off Value	0.08	0.08	0.08	0.08
MinusA Ratio	0.0	0.0	0.0	0.0
MinusA Distance	From 0.0	0.0	0.0	0.0
	To 0.0	0.0	0.0	0.0
Minus Stutter Ratio	0.0	0.0	0.0	0.0
Minus Stutter Distance	From 2.25	3.25	4.25	5.25
	To 3.75	4.75	5.75	6.75
Plus Stutter Ratio	0.0	0.0	0.0	0.0
Plus Stutter Distance	From 0.0	0.0	0.0	0.0
	To 0.0	0.0	0.0	0.0

Amelogenin Cutoff: 0.0

Range Filter... Factory Defaults

OK Cancel

Peak Detection Algorithm: Advanced

Analysis Ranges: Partial Range, Partial Sizes

Start Pt: 2500, Stop Pt: 10000, Start Size: 75, Stop Size: 400

Smoothing and Baseline: Smoothing (None, Light, Heavy), Baseline Window: 51 pts

Peak Detection: Peak Amplitude Thresholds (B: 75, R: 75, G: 75, O: 75, Y: 75), Min. Peak Half Width: 2 pts, Polynomial Degree: 3, Peak Window Size: 15 pts, Slope Threshold (Peak Start: 0.0, Peak End: 0.0)

Size Calling Method: 2nd Order Least Squares, 3rd Order Least Squares, Cubic Spline Interpolation, Local Southern Method, Global Southern Method

Factory Defaults

OK Cancel

Signal level: Homozygous min peak height: 75.0, Heterozygous min peak height: 75.0

Heterozygote balance: Min peak height ratio: 0.7

Peak morphology: Max peak width (basepairs): 1.5

Pull-up peak: Pull-up ratio: 0.05

Allele number: Max expected alleles: 2

Factory Defaults

OK Cancel

Quality weights are between 0 and 1.

Quality Flag Settings: Spectral Pull-up: 0.8, Broad Peak: 0.8, Out of Bin Allele: 0.8, Overlap: 0.8, Control Concordance: 1.0, Low Peak Height: 0.3, Off-scale: 0.8, Peak Height Ratio: 0.3

PQV Thresholds: Pass Range (0.75 to 1.0), Low Quality Range (0.0 to 0.25)

Sizing Quality: From 0.75 to 1.0, From 0.0 to 0.25

Genotype Quality: From 0.75 to 1.0, From 0.0 to 0.25

Factory Defaults

OK Cancel

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