

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	Sizing
Partial Range	Partial Sizes
Start Pt: 2300	Start Size: 75
Stop Pt: 9000	Stop Size: 450

Smoothing and Baselining

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: (highlighted green)

Low Quality Range: (highlighted red)

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 Partial Sizes

Start Pt: 2500 Start Size: 65

Stop Pt: 10000 Stop Size: 400

Smoothing and Baselining

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

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:

Analysis Method Editor - HID

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

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	From 0.0	From 0.0	From 0.0
	To 0.0	To 0.0	To 0.0	To 0.0
Minus Stutter Ratio	0.0	0.0	0.0	0.0
Minus Stutter Distance	From 2.25	From 3.25	From 4.25	From 5.25
	To 3.75	To 4.75	To 5.75	To 6.75
Plus Stutter Ratio	0.0	0.0	0.0	0.0
Plus Stutter Distance	From 0.0	From 0.0	From 0.0	From 0.0
	To 0.0	To 0.0	To 0.0	To 0.0

Amelogenin Cutoff: 0.0

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: 2500 Start Size: 75

Stop Pt: 10000 Stop Size: 400

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

Smoothing and Baseline

Smoothing: None Light Heavy

Baseline Window: 51 pts

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

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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