

## FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR ANALYSIS

<b>Editing Codes</b>		
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**Artifacts listed below should be unlabeled using the comment “artifact” (code “a”)  
For additional detail on artifacts, refer to the STR Results Interpretation Manuals for each kit or  
relevant appendices.**

<b>Artifacts</b>
pull-ups or pull-down of peaks in any color caused by a very high peak of another color in the same basepair range of a sample
shoulder peaks approx. 1-4 bp bigger or smaller than main peak
split peak due to "N" bands
split peak due to matrix over-subtraction
stutter in non-mixtures <sup>1</sup>
peak classified as +/- 2 bp artifact <sup>2</sup>
kit-specific artifact <sup>3</sup>
labels placed on elevated baselines
spikes or peaks present in all colors in one sample
dye artifact occurring at a constant scan position
peak classified as primer front; low molecular weight artifacts appearing at the very beginning of a dye color
initial peak labels of range removed (use code “→”)

1. Stutter includes: Peaks in non-mixtures in a +/- 1 STR repeat positions for Identifiler®, Yfiler™ or peaks in a +/- 1 STR repeat position in a Fusion® and PowerPlex® Y23 exemplar sample or positive control. The height of the possible stutter peak must be compared to the height of the parent allelic peak to determine if it is reasonable to consider it as stutter. Refer to the appendices for stutter filter information for the relevant kit.
2. This edit is applicable for artifact peaks in the -2 bp position in Fusion® commonly seen in some locations such as D1S1656, D13S317, D18S51, D21S11, D7S820, D5S818, D12S391, and D19S433. For Yfiler™, this edit is applicable for artifacts in the +/-2 bp position at DYS19.
3. Refer to the appendix for each relevant kit for more information. **Promega can also verify if artifacts have been observed within other laboratories. Contact QA for assistance in this verification.**

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