

## FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR ANALYSIS

<b>ReRun Codes</b>		
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### SAMPLE COMMENTS INDEX

Code Groups	Parameters for Rerun	insert sample status code (if applicable)	insert system code	insert rerun code (if applicable)	insert realiquot code (if applicable)
<b>A) Sample Status Code</b>	All peak labels removed.	**			
	Peak(s) within basepair range affected by overblown peak(s). Labels removed.*	*			
	Sample chart shows OL/OB allele	^			
	No or poor size standard	#			
	Excessive elevated baseline	^^			
	Excessive spikes	##			
	Migration shift	+			
<b>B) System Code</b>	<b>Identifiler®</b>		<b>I</b>		
	<b>Minifiler®</b>		<b>F</b>		
	<b>Yfiler®</b>		<b>M</b>		
	<b>PowerPlex Fusion®</b>		<b>U</b>		
	<b>Do Not Rerun</b>		<b>N/A</b>		
<b>C) Rerun Code</b>	Normal			<b>no code</b>	
	High			<b>R</b>	
<b>D) Realiquot Code</b>	1/5 dilution				<b>D.2</b>
	1/10 dilution				<b>D.1</b>
	1/20 dilution				<b>D.05</b>
	1/100 dilution				<b>D.01</b>
	Re-aliquot 1 ul				<b>1ul</b>
	Re-aliquot 2 ul				<b>2ul</b>

If multiple rerun codes apply, place a comma between each in the sample comments (i.e. an YF system sample's chart shows OL/OB alleles and some unlabeled peaks just below 75 RFU threshold that could be part of the contributor's profile, to schedule the sample for rerun normal and high, enter “^M,MR” in the sample comments)

\*Not for use with Fusion®

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