

# FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR TYPING

GENEMAPPER ID – QUALITY FLAGS		
DATE EFFECTIVE 06-20-2016	APPROVED BY NUCLEAR DNA TECHNICAL LEADER	PAGE 1 OF 4

## Quality Flags

The **Pass** (green square) symbol indicates that no problem exists. The **Check** (yellow triangle) symbol appears when there are problematic components such as missing size standards, or off-scale data. The **Low Quality** (red octagon) symbol appears when the result falls below the defined threshold.

Whether you identify a size standard problem or not, proceed to the sizing section of the manual to individually check each size standard.

The following flags are visible in the **Project Window** with the “**Samples**” tab selected:

Quality Flag in “Samples” tab	Code
<b>Sizing Quality Override</b> – This check box marks the samples that have had the size standard quality score overridden. This box can also be used to indicate if the size standard has been reviewed.	<b>SQO</b>
<b>Sample File Not Found</b> – if the software cannot locate the .fsa files that correspond to a project, a yellow “check” flag is displayed. Re-import the run into the GeneMapper® <i>ID</i> software.	<b>SFNF</b>
<b>Size Standard Not Found</b> – A yellow “check” flag is displayed when no size standard is found in the sample. If a size standard has failed, it will be assigned an SQ value of 0.0 and “no sizing data” will be displayed in the “samples plot” window.	<b>SNF</b>

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DATE EFFECTIVE 06-20-2016	APPROVED BY NUCLEAR DNA TECHNICAL LEADER	PAGE 2 OF 4

<p><b>Off scale</b> – This flag directs your attention to overblown peaks whose height [RFU] exceeds the range of the collection instrument.</p>	<b>OS</b>
<p><b>Sizing Quality</b> – Values closest to 1.0 are denoted by a green “pass” flag. Questionable data is within the range of 0.25 and 0.75, and indicated with a yellow “check” flag. Low quality data is within the range of 0.0 – 0.25 and denoted by a red flag. If the RFU of the size standard falls below our detection threshold, it will be assigned an SQ value of 0.0, and the corresponding sample will display “no sizing data” in the “samples plot” window.</p>	<b>SQ</b>

These flags are intended to draw your attention to samples that have analysis problems. These flags do not replace our method for editing samples. Each sample must still be viewed and edited. If you identify a problem in a sample that can be edited, proceed to the editing section of this manual.

The following flags are visible in the **Plot View** with the “**Genotypes**” tab selected:

Quality Flag in “Genotypes” tab	Code
<p><b>Allele Display Overflow</b> – This check box indicates that there are more alleles at this locus than are displayed in the current window view.</p>	<b>ADO</b>
<p><b>Allele Edit</b> – This box is checked when the allelic calls have been edited by the analyst in the plot view page.</p>	<b>AE</b>

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DATE EFFECTIVE 06-20-2016	APPROVED BY NUCLEAR DNA TECHNICAL LEADER	PAGE 3 OF 4
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Quality Flag in “Genotypes” tab	Code
<b>Off scale</b> – This flag directs your attention to overblown peaks whose height [RFU] exceeds the range of the collection instrument for each locus.	<b>OS</b>
<b>Out of bin allele</b> – Displays a yellow “check” flag when peaks are outside of the bin boundary. These peaks are called OL.	<b>BIN</b>
<b>Peak Height Ratio</b> – Displays a yellow “check” flag if the ratio between the lower allele height and the higher allele height are below 70%. This value can be set in the Analysis Methods Peak Quality window.	<b>PHR</b>
<b>Allele Number</b> – This flag is a useful indicator of mixture samples, locus dropout, and extraneous alleles in the positive and negative controls. A yellow “check” flag is displayed when the number of alleles exceeds the number of expected alleles at a locus for the individual, or if no alleles are found. This number can be set in the Analysis Methods Peak Quality window.	<b>AN</b>
<b>Control Concordance</b> – Serves as quality assurance during STR analysis. A yellow “check” flag appears when the designated control sample (positive or negative) does not exactly match the defined alleles at each locus.	<b>CC</b>

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DATE EFFECTIVE 06-20-2016	APPROVED BY NUCLEAR DNA TECHNICAL LEADER	PAGE 4 OF 4
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Quality Flag in “Genotypes” tab	Code
<b>Overlap</b> – It is possible to have two allele size ranges that overlap, therefore a yellow “check” flag is displayed when a peak in the overlapped region is called twice.	<b>OVL</b>