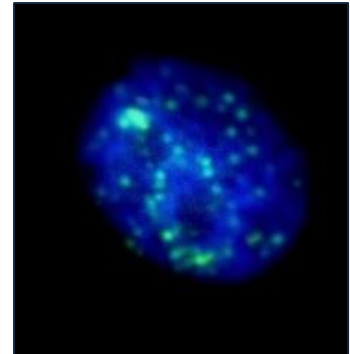


## Nuclei Real Dot Count (1F)

### General Purpose

The Nuclei Real Dot Count analysis algorithm is to be used in an end point assay, where cell nuclei are counted in a first fluorescence image (based e.g. on DAPI staining) and further stained sub structures (e.g. DNA string breaks with  $\gamma$ H2AX-staining) in a second fluorescence image. The stained sub structures are counted and analyzed on each cell nucleus area and their number and average intensities are stored as additional cell nuclei attributes.



Short Note  
SN-F225-XVII-05

### Result Table

• <i>Dot Count</i>	<i>Number of recognized sub structures</i>
• <i>Nuclei Count</i>	<i>Number of recognized cell nuclei</i>
• <i>Nuclei Dot positive</i>	<i>Number of cell nuclei, that own at least the desired number of sub structures („Dots“)</i>
• <i>Nuclei Dot positive percent</i>	<i>Percentage ratio of Nuclei Dot positive counts with respect to the Nuclei Count</i>
• <i>Cell Area Count Fluo 1</i>	<i>Number of recognized sub structures in the first additional fluorescence image</i>
• <i>Avg Nucleus Fluorescence Intensity BC</i>	<i>Average fluorescence intensity of a cell nucleus over background level</i>
• <i>Avg Fluo CH1 Intensity BC</i>	<i>Average fluorescence intensity of the cell sub structures in the first additional fluorescence image over background level</i>
• <i>Avg Nucleus Size</i>	<i>Average Size of a cell nucleus</i>
• <i>Sum of Nuclei Sizes</i>	<i>Total area of all recognized cell nuclei</i>

### Example

Two labeled DAPI stained cell nuclei in a  $\gamma$ H2AX assay: One with some identified double DNA string breaks (green labeled nucleus) and one without (red labeled nucleus).

