**Supplementary File 2: Features used for the phagocytosis assay**

Names and descriptions of the features quantified by IDEAS software and used for clustering events based on cell morphology and function in the phagocytosis experiment. BF is Bright Field, CI is Cell Intrinsic, CF is Cell Function.

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| **ID** | **Feature Name\_**  **ImageMask\_Channel** | **CI or CF** | **Feature description** |
| 1 | Area\_AdaptiveErode\_BF | CI | Cell size |
| 2 | Area\_Intensity\_DHR | CF | Area of DHR staining above background |
| 3 | Area\_Intensity\_Bacteria | CF | Area of CTV staining above background |
| 4 | Area\_Intensity\_SSC | CI | Areas of SSC signal above background |
| 5 | Area\_Morphology\_Draq5 | CI | Area of DNA signal |
| 6 | Aspect.Ratio\_AdaptiveErode\_BF | CI | Aspect ratio of total cell area |
| 7 | Bright.Detail.Intensity.R3\_AdaptiveErode\_BF\_Bacteria | CF | Intensity of brightest staining areas |
| 8 | Bright.Detail.Intensity.R3\_AdaptiveErode\_BF\_BF | CI | Intensity of brightest staining areas |
| 9 | Bright.Detail.Intensity.R3\_AdaptiveErode\_BF\_DHR | CF | Intensity of brightest staining areas |
| 10 | Bright.Detail.Intensity.R3\_AdaptiveErode\_BF\_Draq5 | CI | Intensity of brightest staining areas |
| 11 | Bright.Detail.Intensity.R3\_AdaptiveErode\_BF\_SSC | CI | Intensity of brightest signal areas |
| 12 | Circularity\_AdaptiveErode\_BF | CI | Circularity of whole cell shape |
| 13 | Circularity\_Morphology\_Draq5 | CI | Circularity of nucleus |
| 14 | Contrast\_AdaptiveErode\_BF\_BF | CI | Large changes in pixel values - Granularity of signal |
| 15 | Contrast\_AdaptiveErode\_BF\_SSC | CI | Large changes in pixel values - Granularity of signal |
| 16 | Diameter\_AdaptiveErode\_BF | CI | Diameter of whole cell shape |
| 17 | Diameter\_Morphology\_Draq5 | CI | Diameter of nucleus |
| 18 | H.Energy.Mean\_AdaptiveErode\_BF\_BF | CI | Intensity concentration - Texture feature |
| 19 | H.Energy.Mean\_Intensity\_DHR\_DHR | CF | Intensity concentration - Texture feature |
| 20 | H.Energy.Mean\_Intensity\_Bacteria\_Bacteria | CF | Intensity concentration - Texture feature |
| 21 | H.Energy.Mean\_Morphology\_Draq5\_Draq5 | CI | Intensity concentration - Texture feature |
| 22 | H.Entropy.Mean\_AdaptiveErode\_BF\_BF | CI | Intensity concentration and randomness of signal - Texture feature |
| 23 | H.Entropy.Mean\_Intensity\_DHR\_DHR | CF | Intensity concentration and randomness of signal - Texture feature |
| 24 | H.Entropy.Mean\_Intensity\_Bacteria\_Bacteria | CF | Intensity concentration and randomness of signal - Texture feature |
| 25 | H.Entropy.Mean\_Morphology\_Draq5\_Draq5 | CI | Intensity concentration and randomness of signal - Texture feature |
| 26 | Intensity\_AdaptiveErode\_BF\_Bacteria | CF | Integrated intensity of signal within whole cell mask |
| 27 | Intensity\_AdaptiveErode\_BF\_DHR | CF | Integrated intensity of signal within whole cell mask |
| 28 | Intensity\_AdaptiveErode\_BF\_Draq5 | CI | Integrated intensity of signal within whole cell mask |
| 29 | Intensity\_AdaptiveErode\_BF\_SSC | CI | Integrated intensity of signal within whole cell mask - Cell granularity |
| 30 | Lobe.Count\_Morphology\_Draq5 | CI | Number of lobes of nucleus |
| 31 | Max.Pixel\_Intensity\_Bacteria | CF | Maximum pixel intensity within a whole cell mask |
| 32 | Max.Pixel\_Intensity\_SSC | CF | Maximum pixel intensity within a whole cell mask - Cell granularity |
| 33 | Max.Pixel\_Morphology\_Draq5 | CI | Maximum pixel intensity within a whole cell mask |
| 34 | Mean.Pixel\_Morphology\_Draq5 | CI | Mean pixel intensity within a whole cell mask |
| 35 | Shape.Ratio\_AdaptiveErode\_BF | CI | Minimum thickness divided by length - Cell shape |
| 36 | Std.Dev\_AdaptiveErode\_BF | CI | Standard deviation of BF signal - Cell granularity and variance in BF |