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Cluster Counting

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Protocol status: Working

We use this protocol and it's working

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Abstract

Used for counting clusters labeled for pSer129 alpha-synuclein in mouse upper gastrointestinal tract (intestine). Sections should be stained, mounted, and imaged with high resolution (2048 x 2048 scanning).

- 1 Stain structures for pSer129 and scan with high-resolution (pixel size of 6.25 μ m).
- 2 Import the images into ImageJ.
- 3 Convert to grayscale.
- 4 Adjust signal intensity to a standardized threshold of 95%. (All thresholds, exposure settings, and laser intensities were applied consistently across all scans).
- 5 Employ the "Process - Binary - Convert to Mask" function.
The mask function can be determined using the default method against a black background.
- 6 Apply a watershed filter to select clusters with similar distribution.
- 7 Execute the "Analyze Particles" function.
Size range: 0 to infinity
Display and summarize results.
This will extract all clusters including their coordinates and areas.
- 8 To extract clusters with a size equal to or smaller than 1 pixel (6.25 μ m²) and clusters identified as artifacts (>15000 μ m²), use the Excel COUNTIF function, count the number of small clusters (6.25 to 50 pixels), medium-sized clusters (50 to 200 pixels), and large clusters (>200 pixels).
- 9 Determine relative density of clusters for the amount of tissue area analyzed.