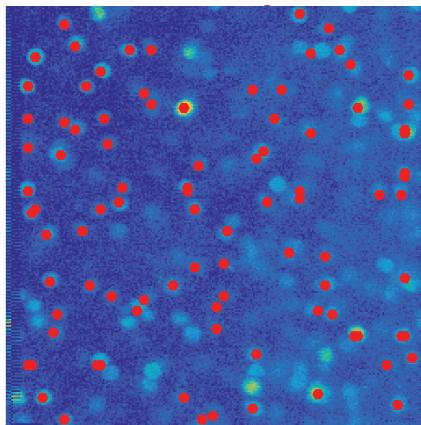
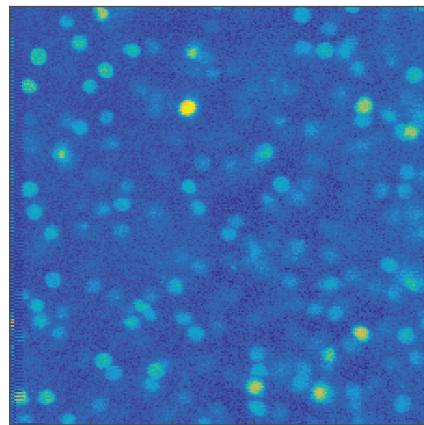


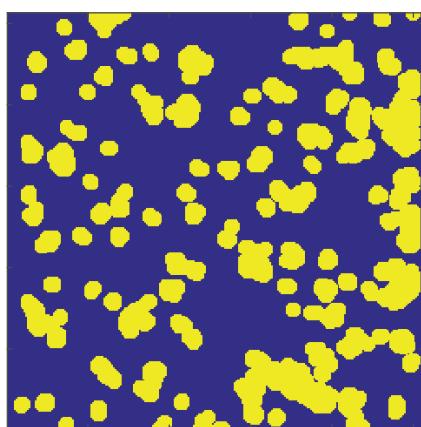
Original image (frame 30)



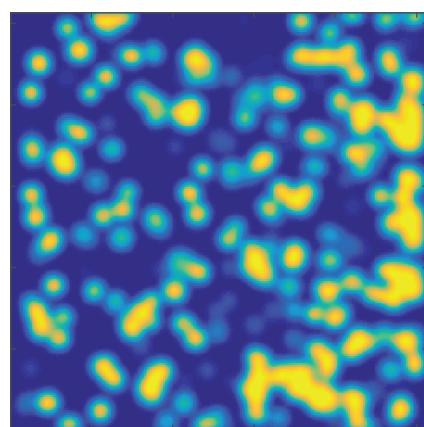
Filtered



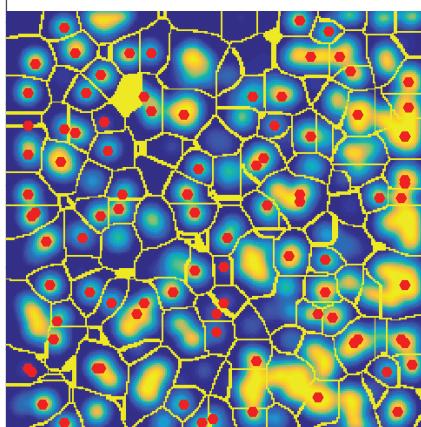
Thresholded



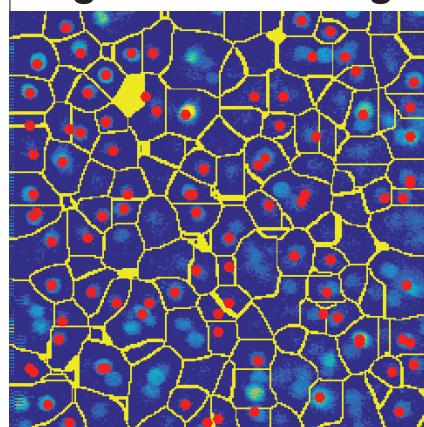
Convolved



Watershed detection

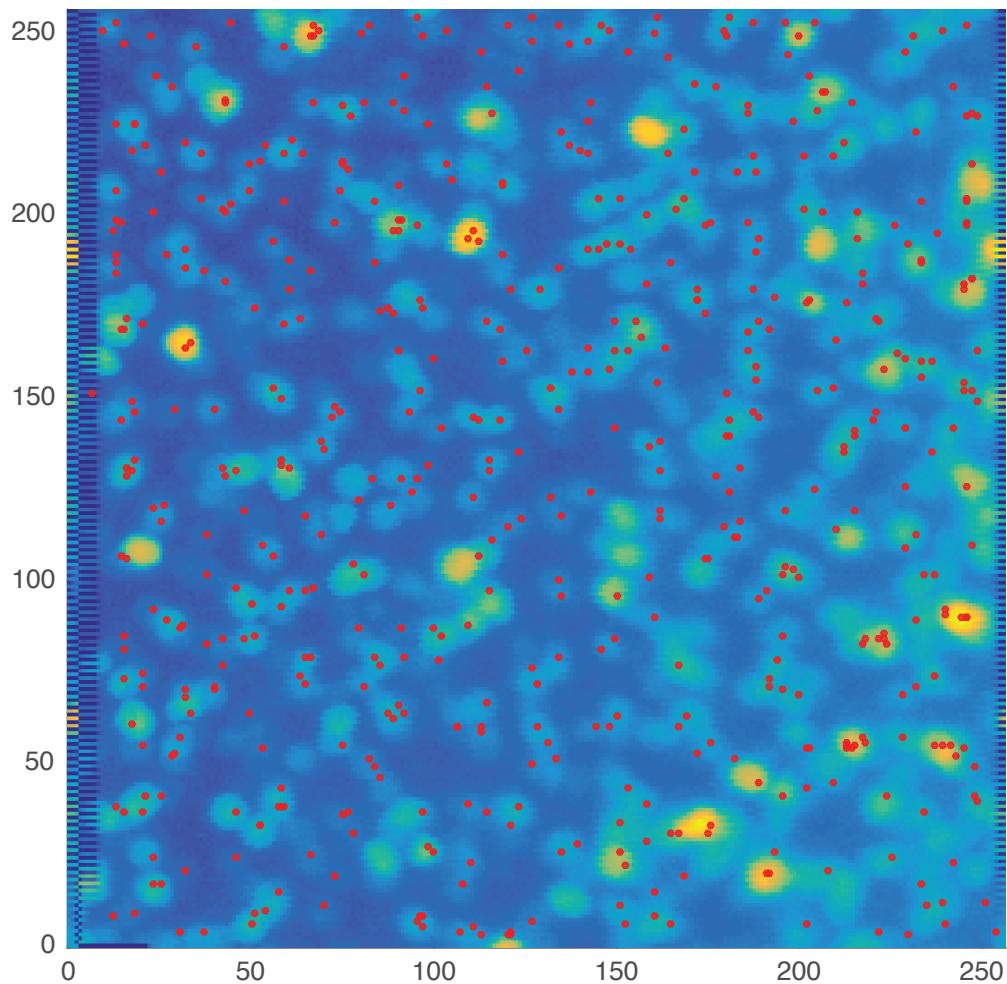


Alignment with original

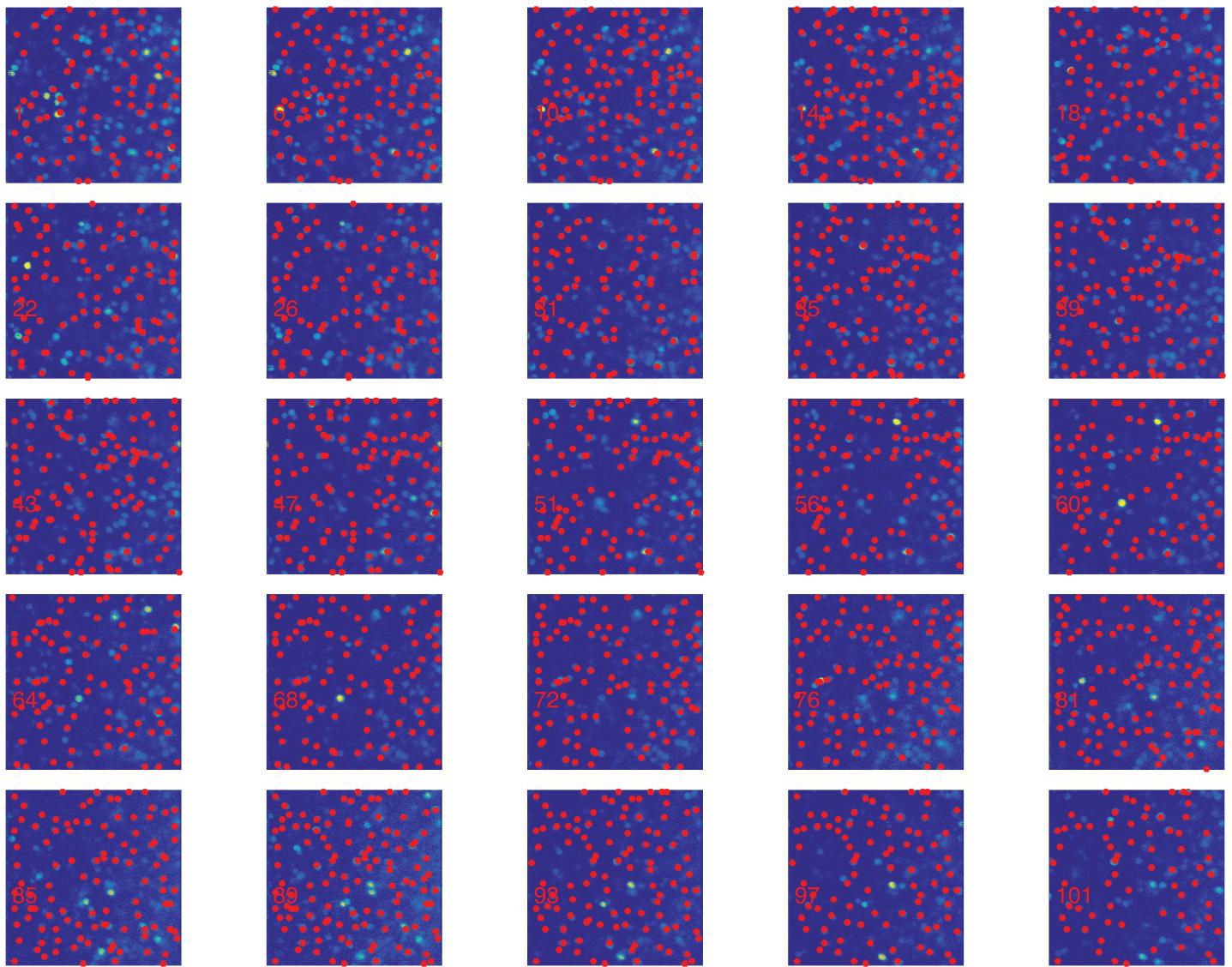


Cell identification process, for a single frame. Individual images are filtered and then thresholded. The thresholded stack is then convolved with a 3D Gaussian and treated as a watershed to segment the boundaries between cells (yellow lines). Cell bodies (red) are identified as the maximum amplitude within each cell.

Sum stack vs. identified centers

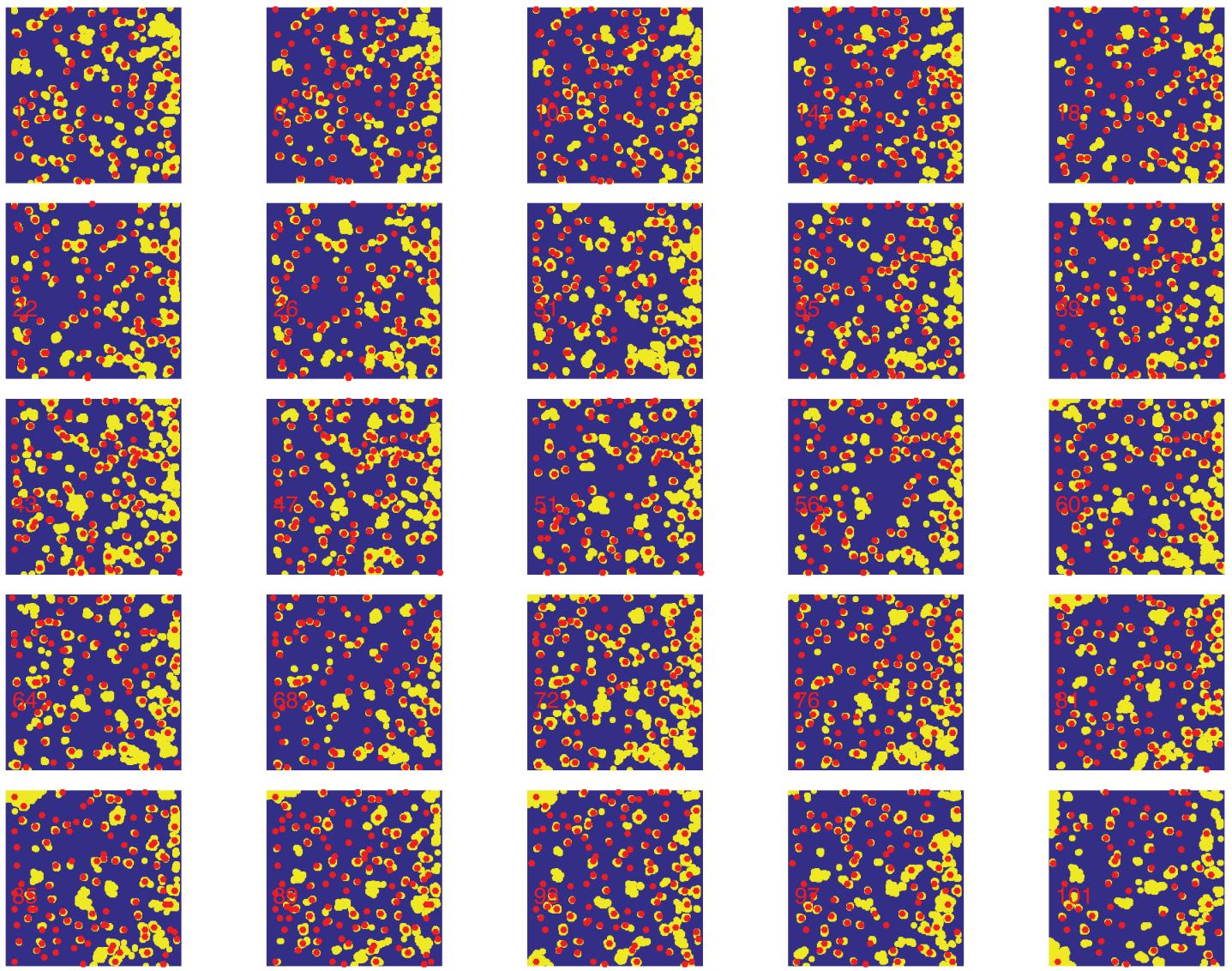


All identified cell bodies are shown (red dots) overlayed on the sum of the full stack (image). Most obvious cell bodies are identified, although there are some exceptions.



Montage of all frames (5 μ m intervals) showing overlapping identified cell bodies. For each frame, cells that are nearby in Z are shown (+/- 10 μ m). This is a wide range, so each point is replicated over ~4 slices.

For this figure, we are showing the thresholded data derived from each slice.



Montage of all frames (5 μ m intervals) showing overlapping identified cell bodies. For each frame, cells that are nearby in Z are shown (+/- 10 μ m). This is a wide range, so each point is replicated over ~4 slices.

For this figure, we are showing the thresholded data derived from each slice.