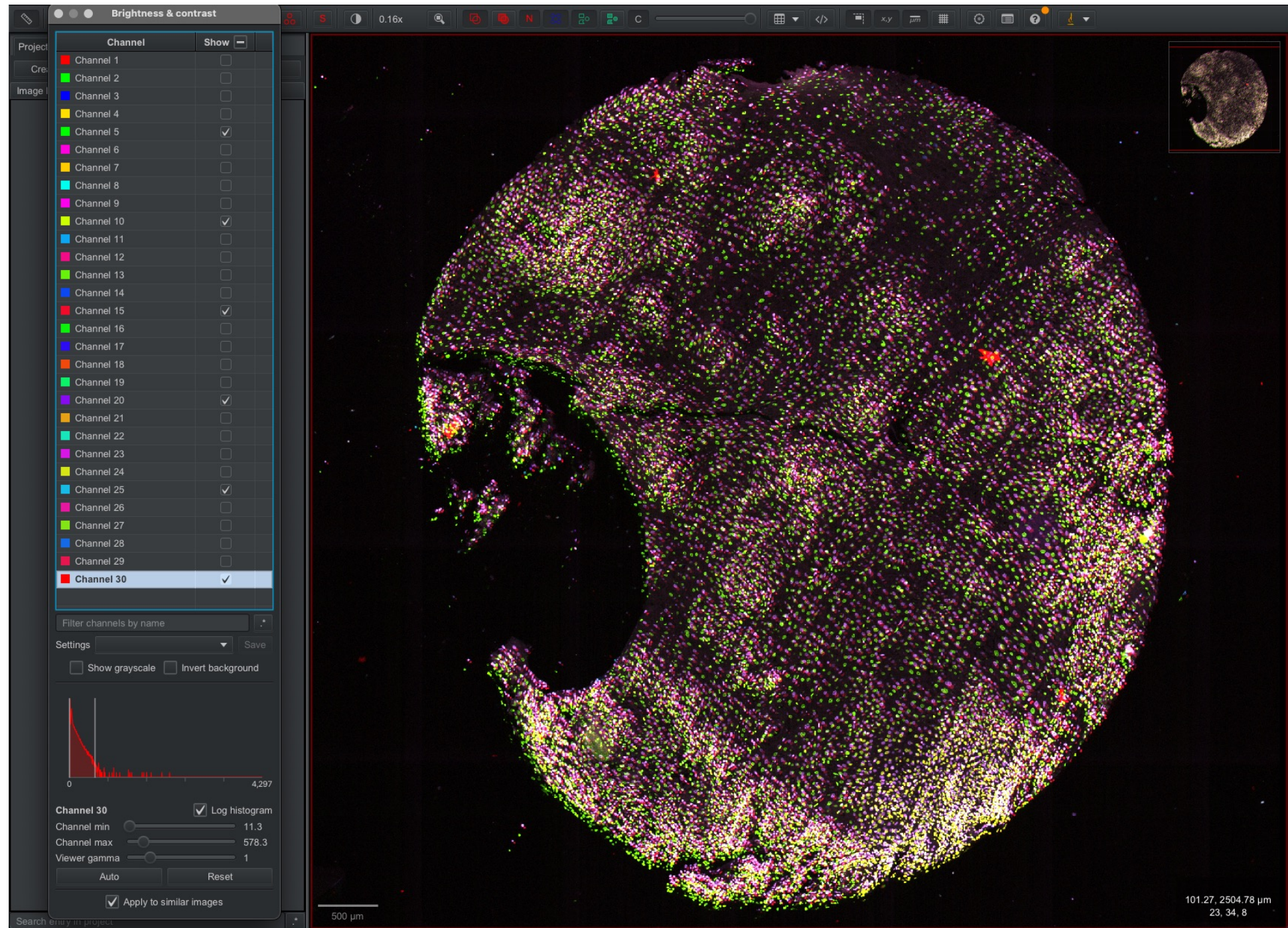


# Stitching, a story to understand it

HN46 Core 5

Baseline:  
Ashlar  
stitching and registration

Parameters:  
Max\_shift: 20um  
Sigma: 1



# BASELINE

Brightness & contrast

0.74x


Project

Channel	Show
Channel 1	<input type="checkbox"/>
Channel 2	<input type="checkbox"/>
Channel 3	<input type="checkbox"/>
Channel 4	<input type="checkbox"/>
Channel 5	<input checked="" type="checkbox"/>
Channel 6	<input type="checkbox"/>
Channel 7	<input type="checkbox"/>
Channel 8	<input type="checkbox"/>
Channel 9	<input type="checkbox"/>
Channel 10	<input checked="" type="checkbox"/>
Channel 11	<input type="checkbox"/>
Channel 12	<input type="checkbox"/>
Channel 13	<input type="checkbox"/>
Channel 14	<input type="checkbox"/>
Channel 15	<input checked="" type="checkbox"/>
Channel 16	<input type="checkbox"/>
Channel 17	<input type="checkbox"/>
Channel 18	<input type="checkbox"/>
Channel 19	<input type="checkbox"/>
Channel 20	<input checked="" type="checkbox"/>
Channel 21	<input type="checkbox"/>
Channel 22	<input type="checkbox"/>
Channel 23	<input type="checkbox"/>
Channel 24	<input type="checkbox"/>
Channel 25	<input checked="" type="checkbox"/>
Channel 26	<input type="checkbox"/>
Channel 27	<input type="checkbox"/>
Channel 28	<input type="checkbox"/>
Channel 29	<input type="checkbox"/>
Channel 30	<input checked="" type="checkbox"/>

Filter channels by name

Settings

Show grayscale  Invert background



Channel 30  Log histogram

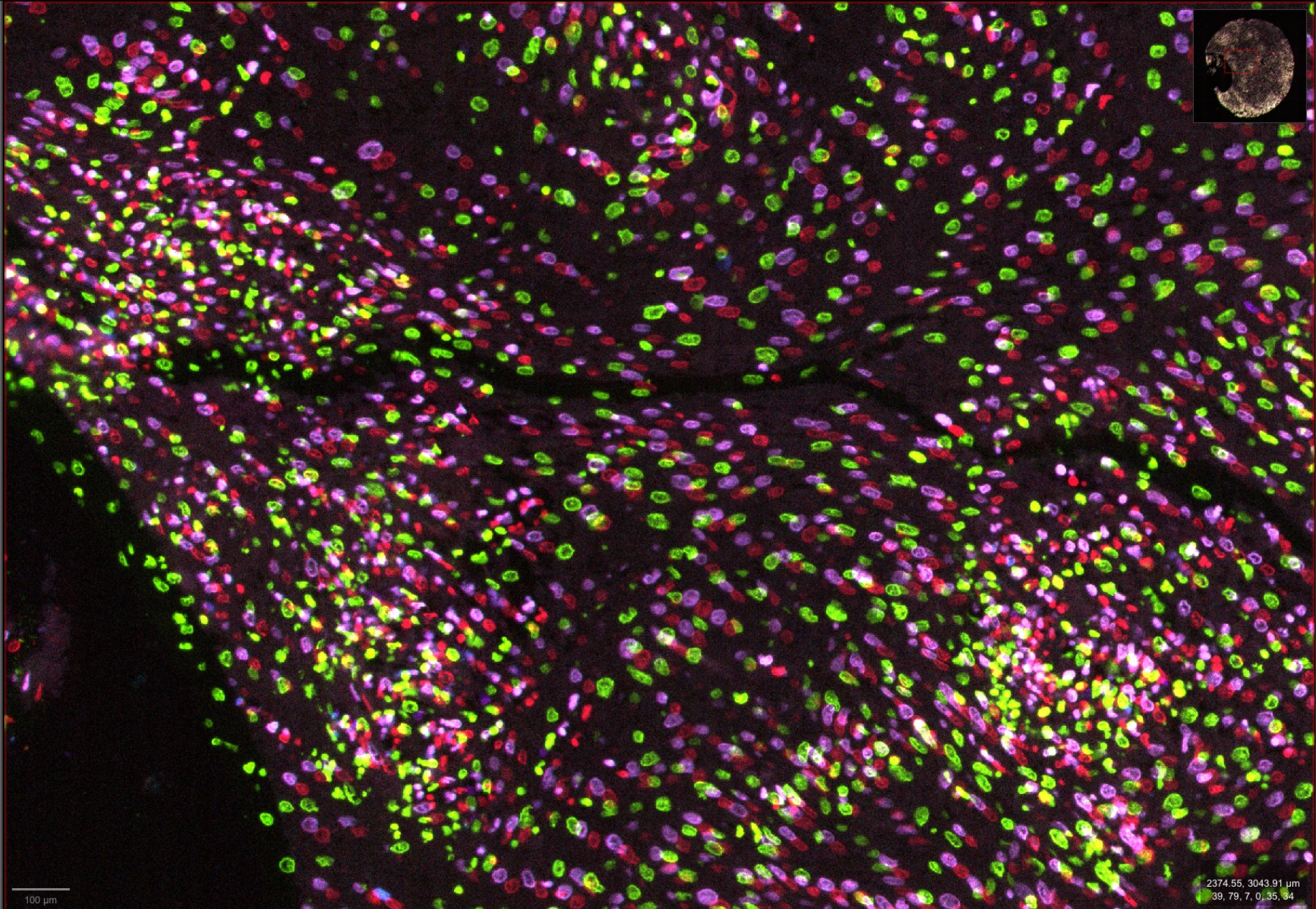
Channel min  11.3

Channel max  578.3

Viewer gamma  1

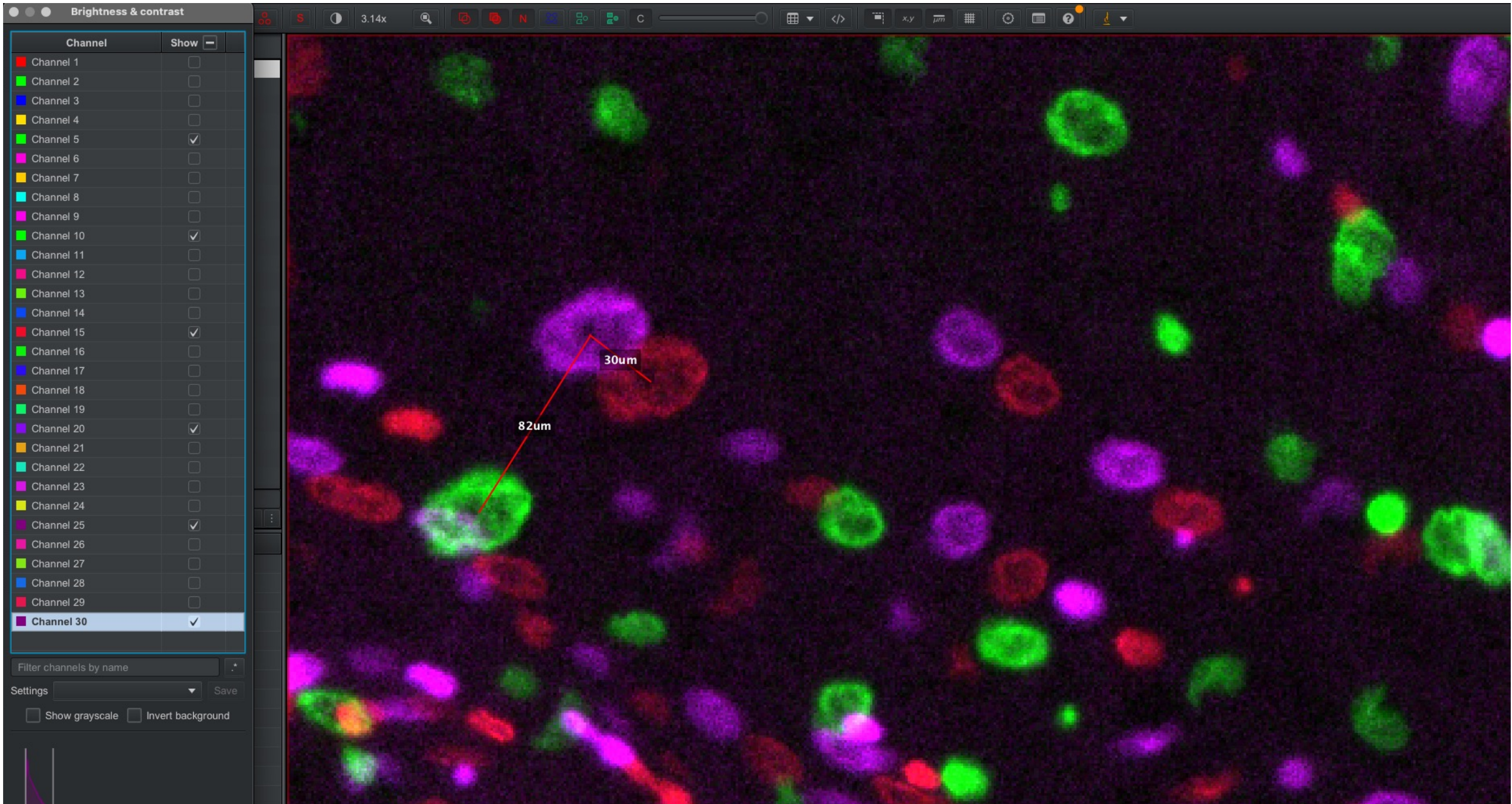
Auto Reset

Apply to similar images



2374.55, 3043.91 μm  
39, 79, 7, 0, 35, 34

# BASELINE

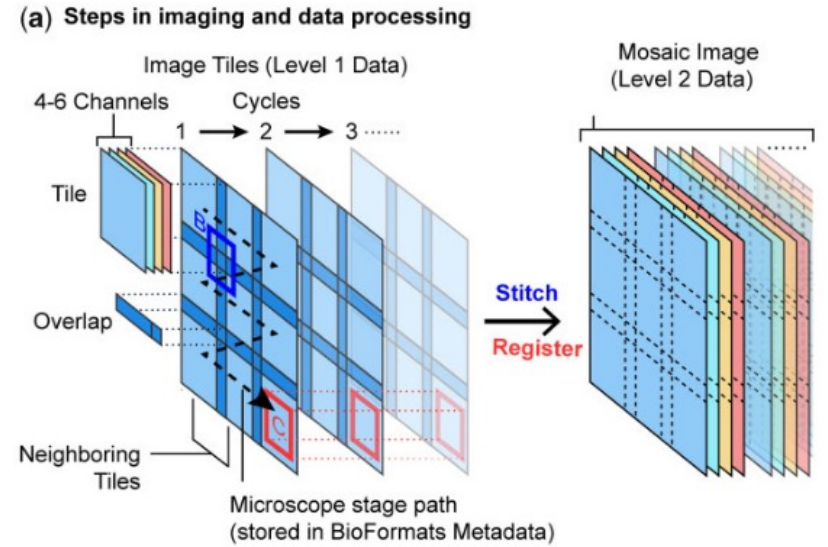


# Not good enough

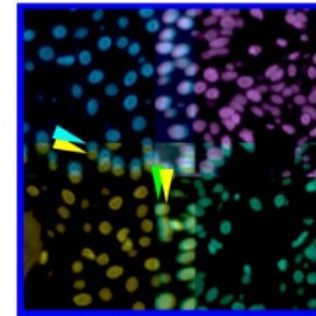
- BASELINE fails
- Stitching, registration, or both?

## QC Metrics:

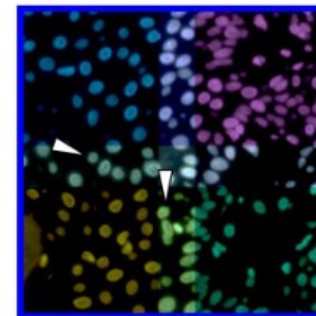
- Edge shift distance (tile shift)
- Edge Error probability (against MC)



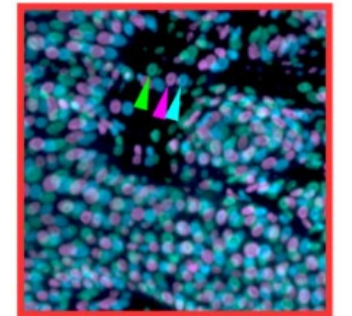
(b) Stitching four tiles



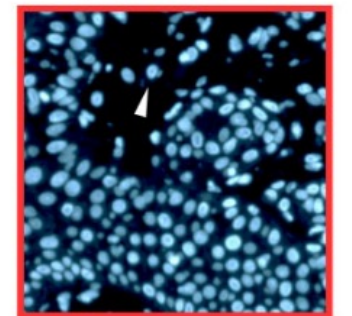
↓ Stitching



(c) Registering three cycles

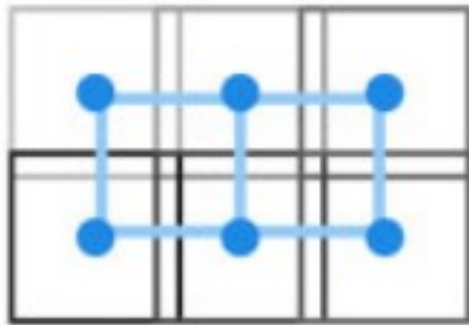


↓ Registration



# Stitching QC: what we want?

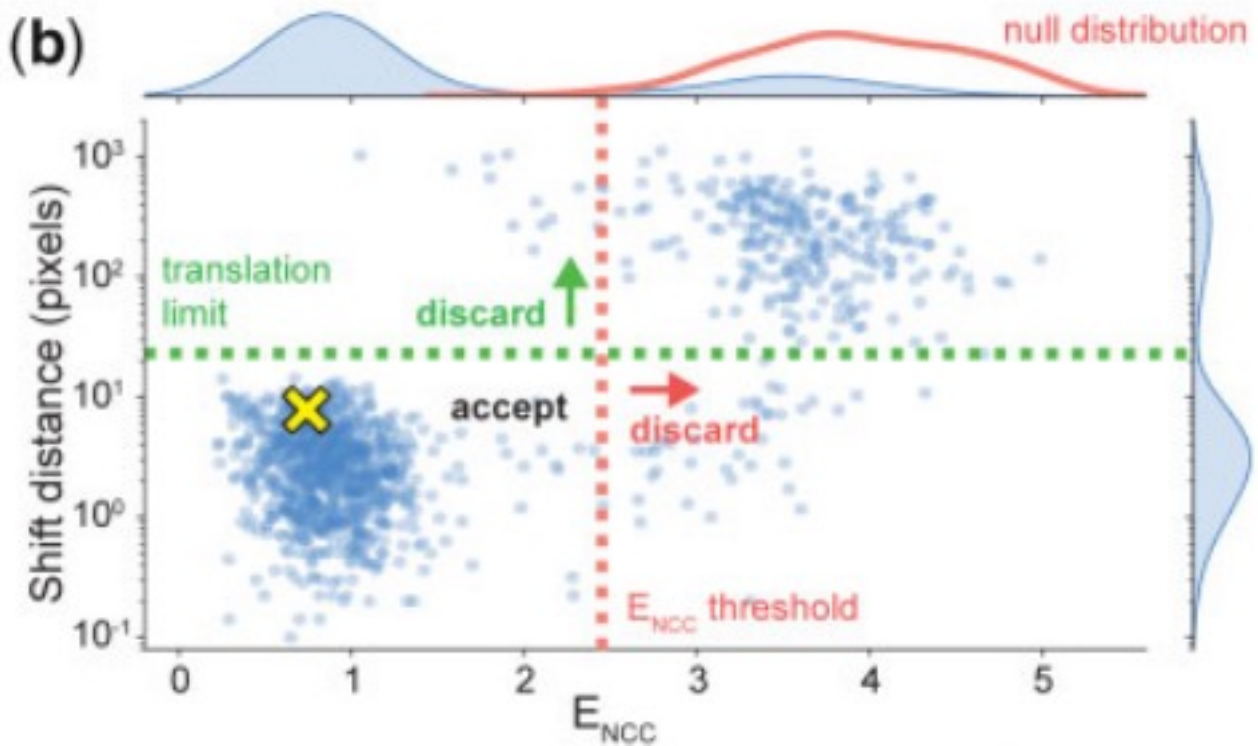
A1. Tile adjacency graph from stage positions



A2. Permutation test to find error threshold



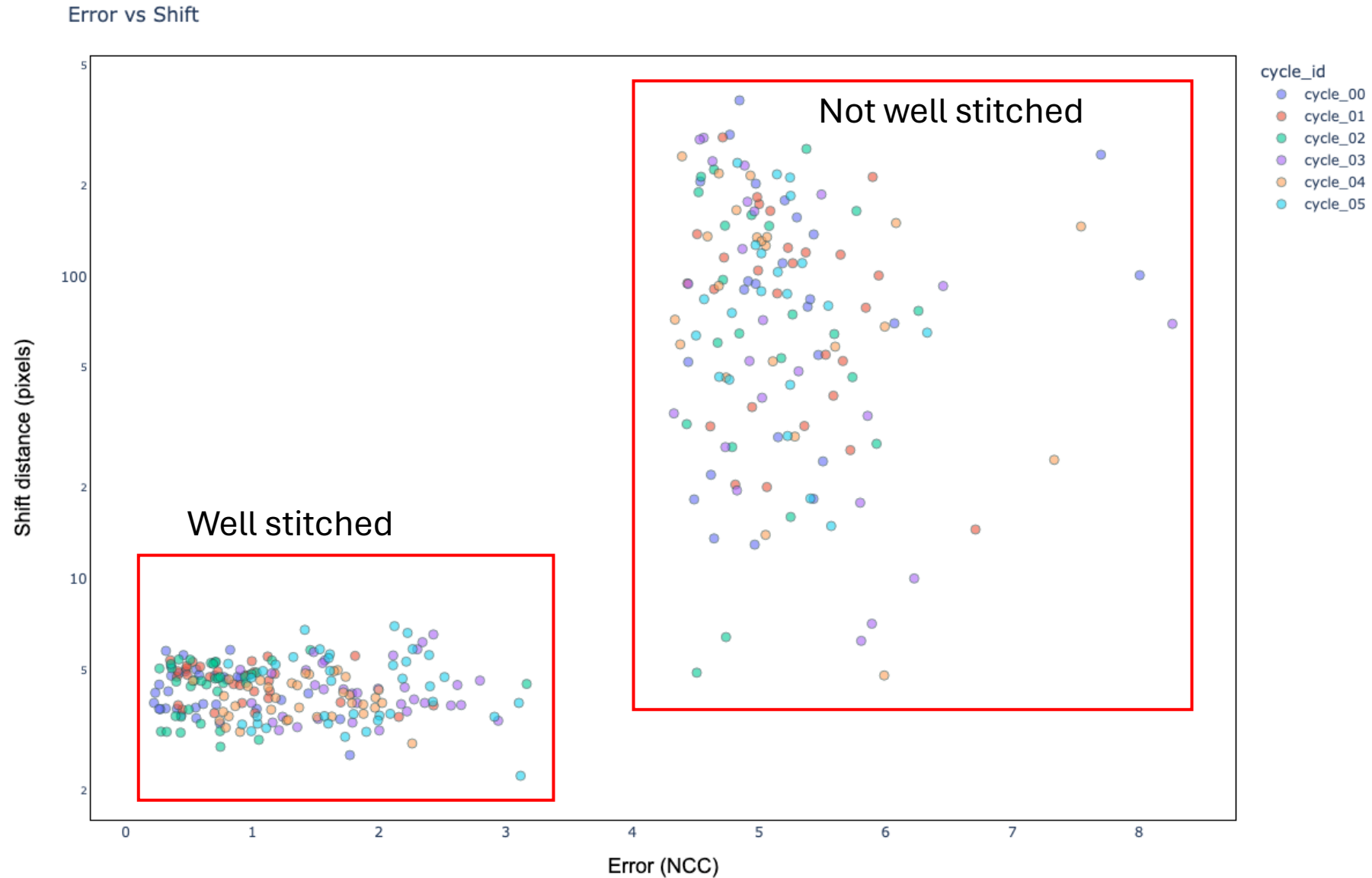
(b)



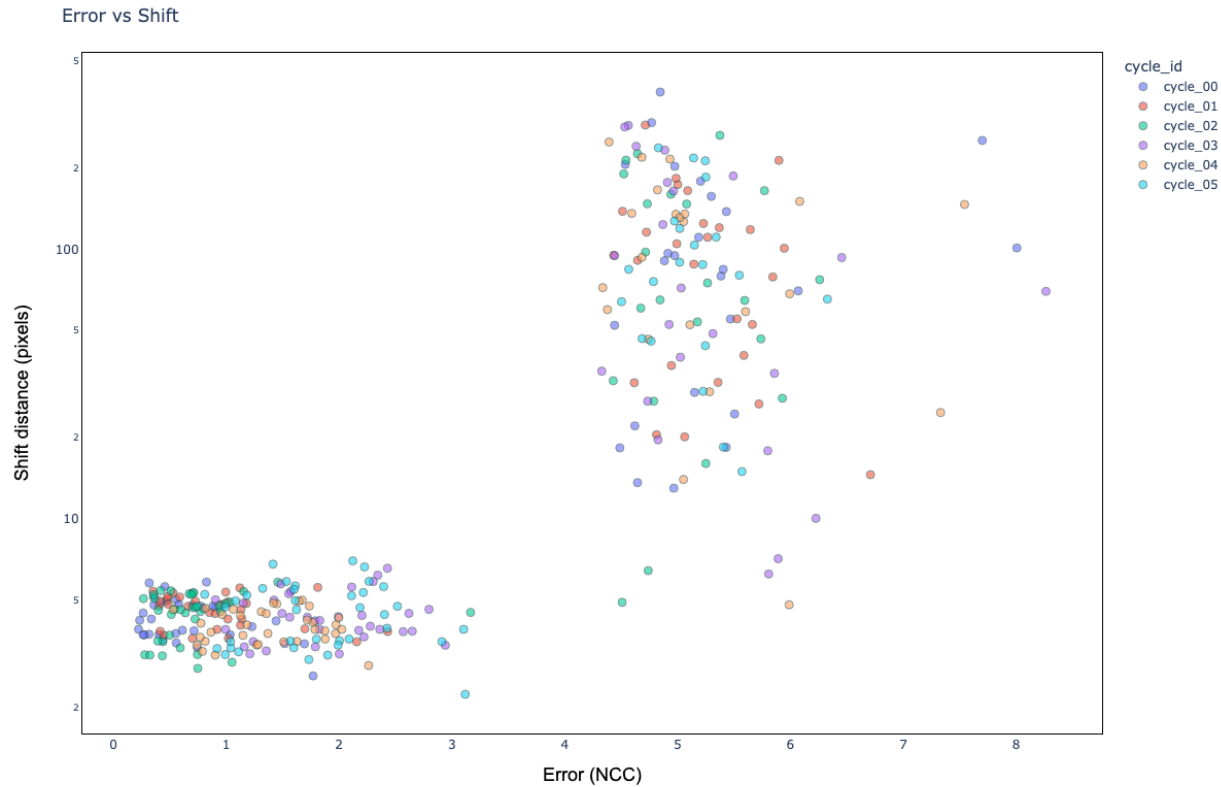
# BASELINE: Shift 25 Sigma 1

Ok,  
but not good enough

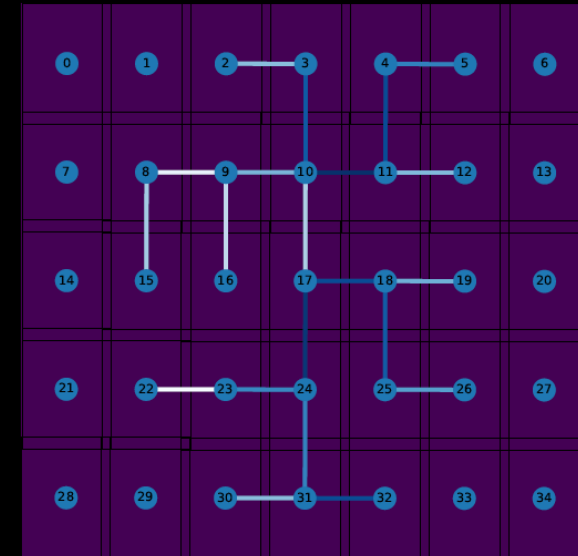
Consider that we  
expect tiles surrounding  
the core to fail at  
stitching



# BASELINE: Shift 25 Sigma 1



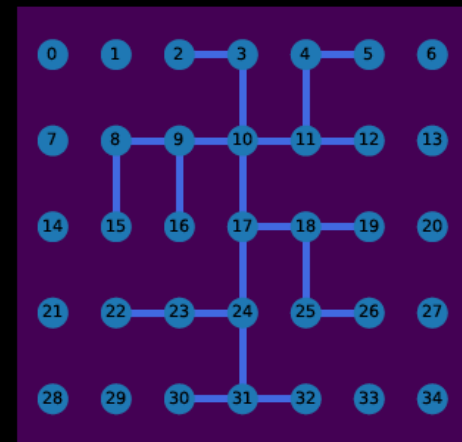
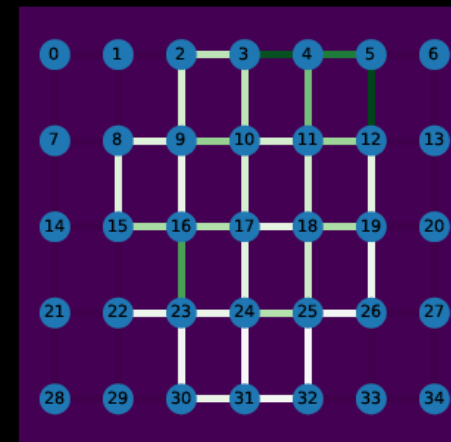
Edge Shifts for cycle 0, shift\_25\_sigma\_1



Edge Quality for cycle 0, shift\_25\_sigma\_1

Brighter = better quality

Spanning Tree

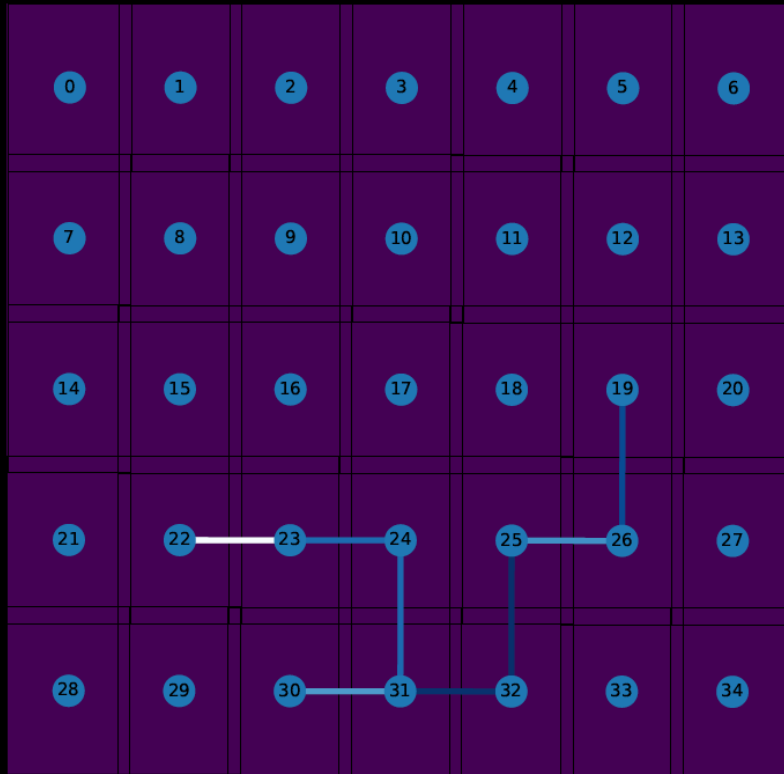




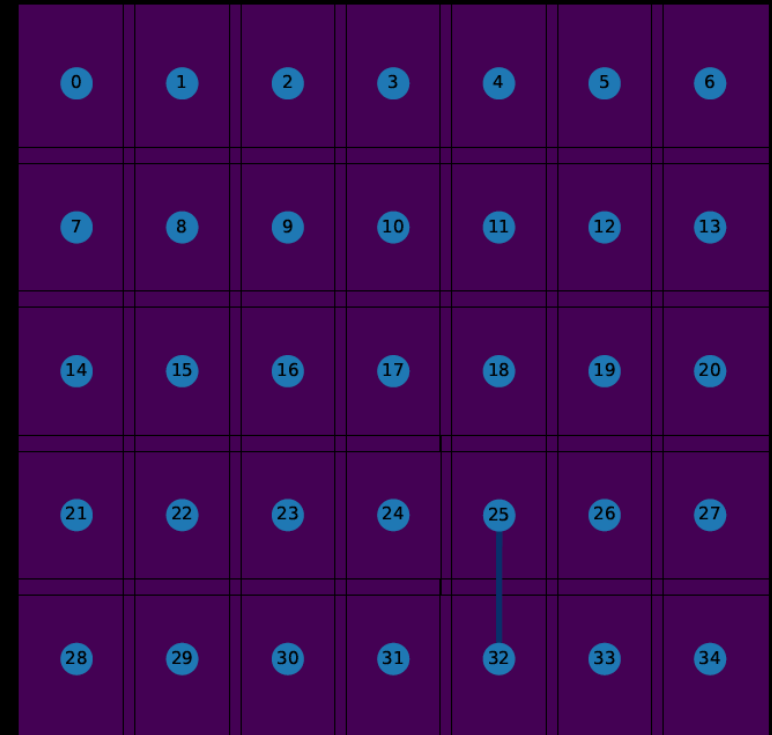
# Testing sigma changes

Conclusion:  
Sigma 0 does not work

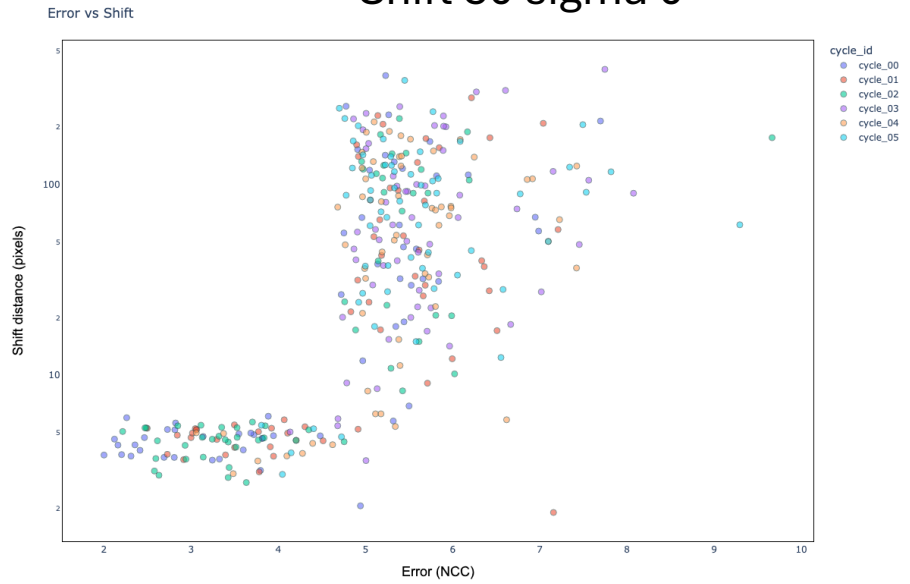
Edge Shifts for cycle 0, shift\_25\_sigma\_0



Edge Shifts for cycle 1, shift\_25\_sigma\_0



## Shift 50 sigma 0



## Shift 50 sigma 1

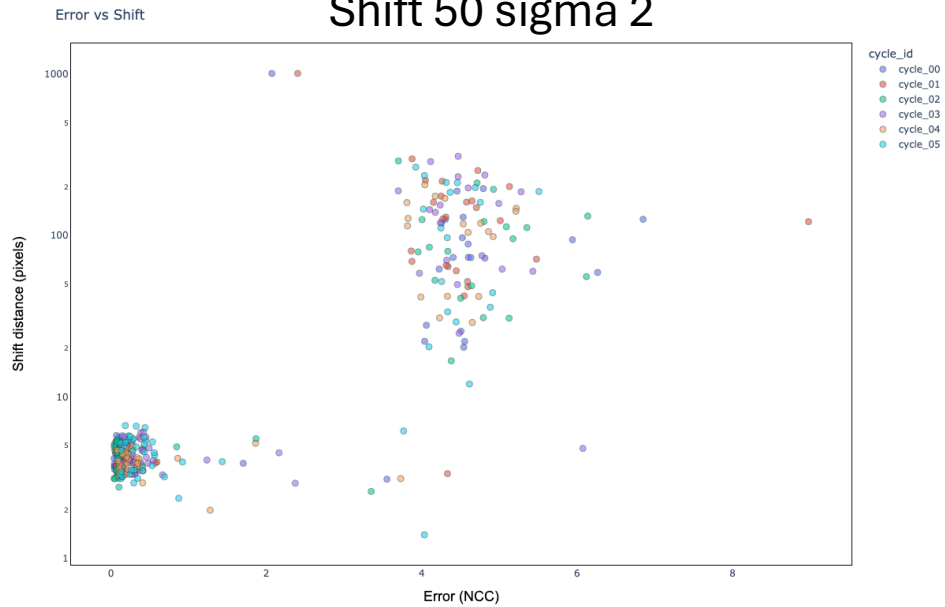


Question:  
What about different  
sigmas?

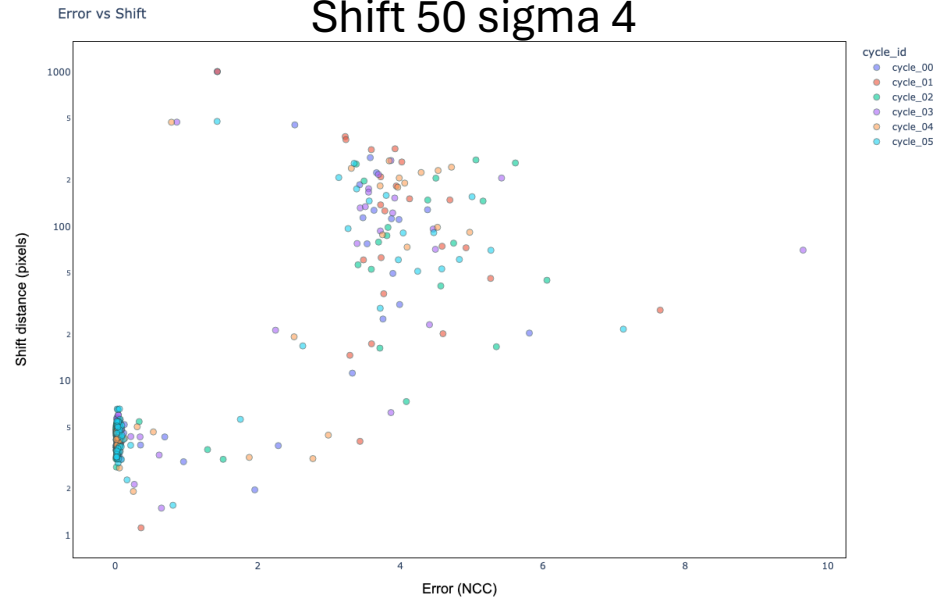
Tested:  
Sigmas 0,1,2,4

Conclusion:  
=>1 seems to be good  
enough

## Shift 50 sigma 2



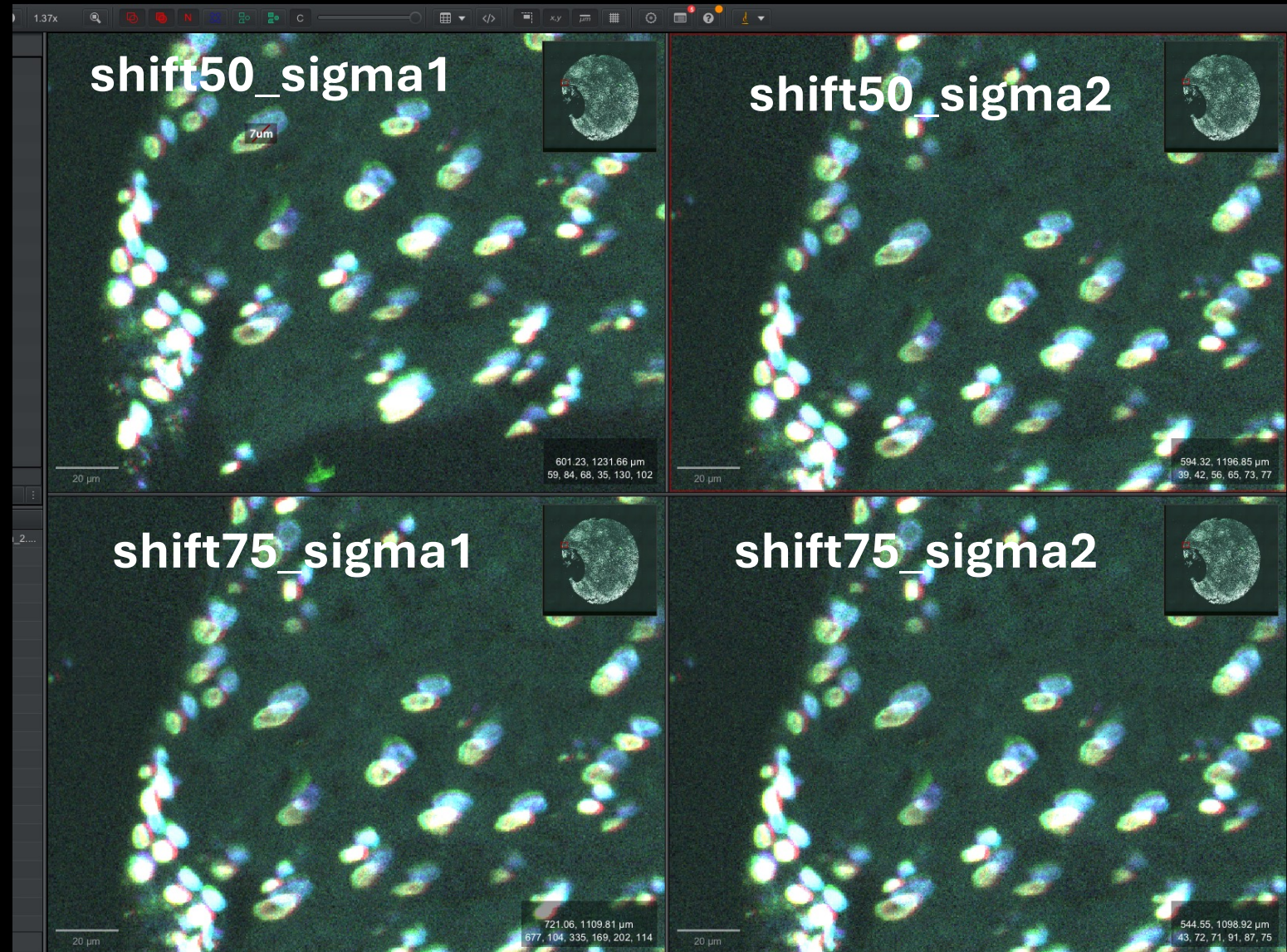
## Shift 50 sigma 4



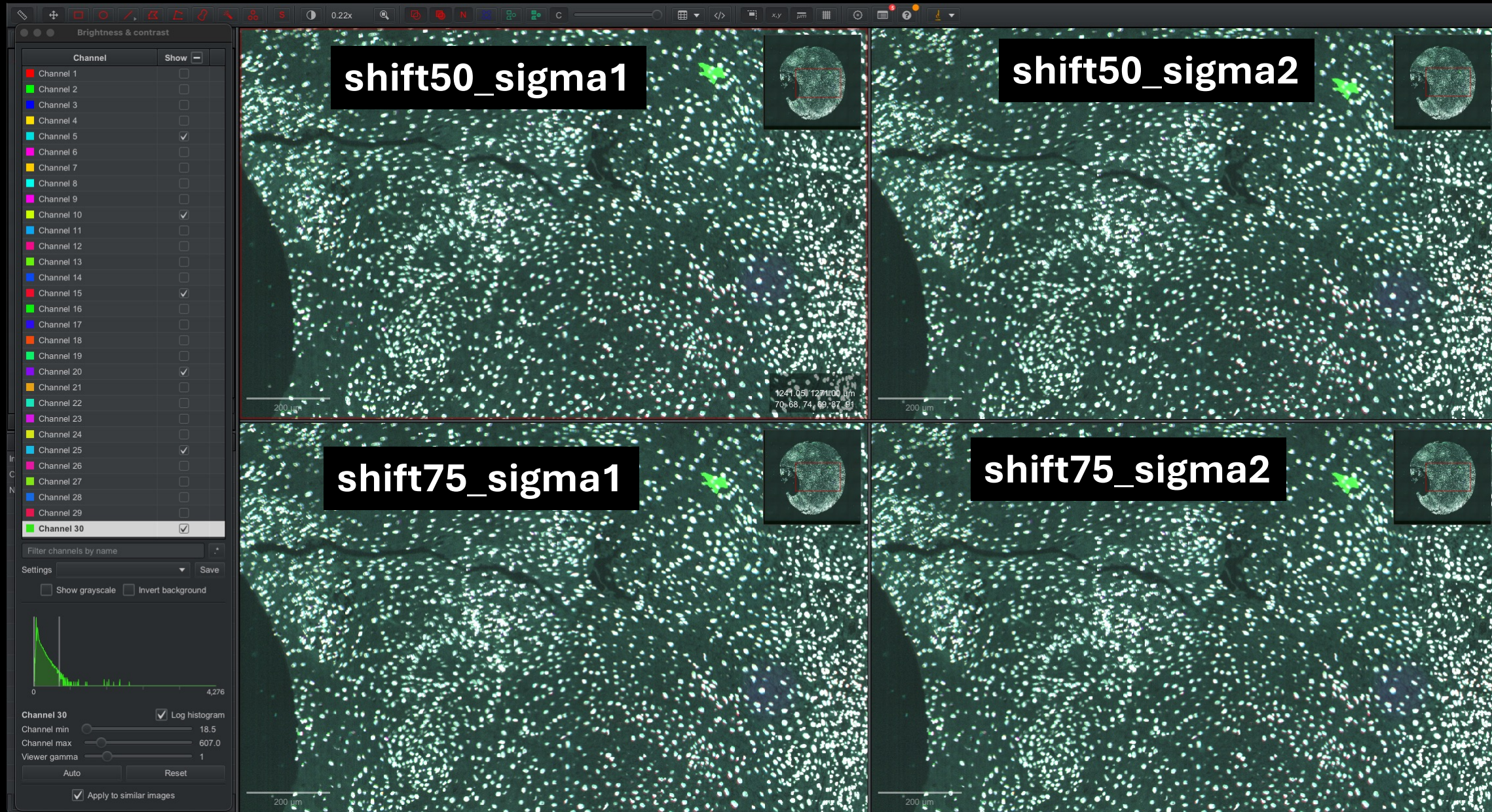
Question:  
Shift sigma changes

Conclusion:  
Shift must be at least 50  
Sigma must be at least 1

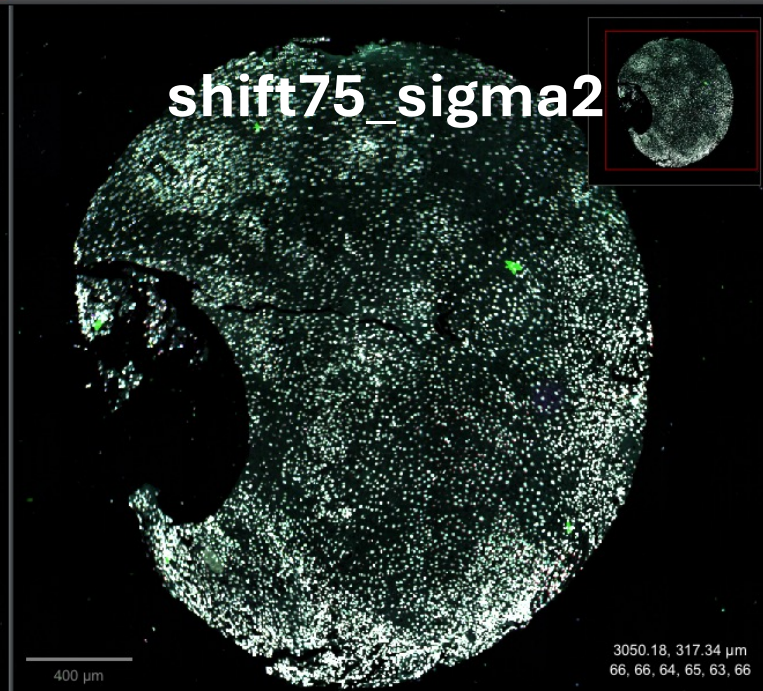
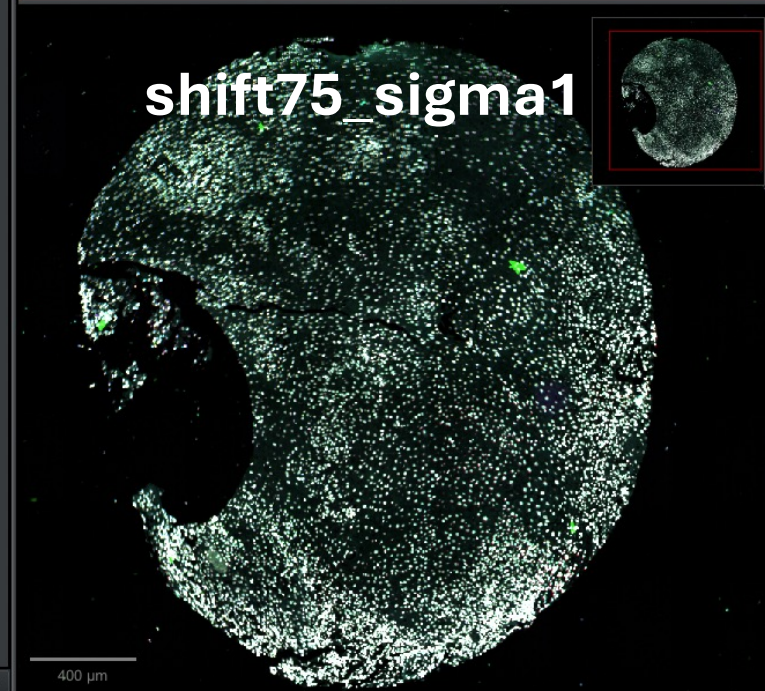
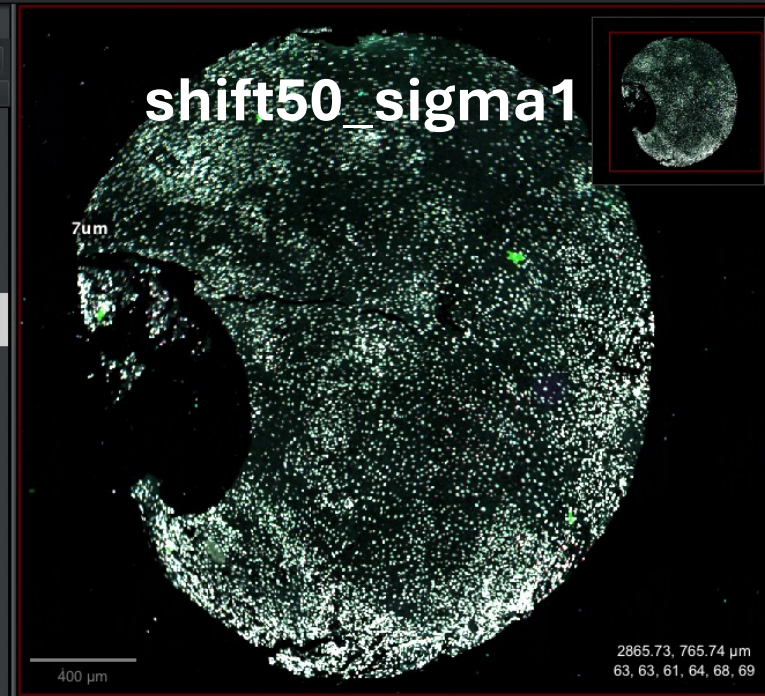
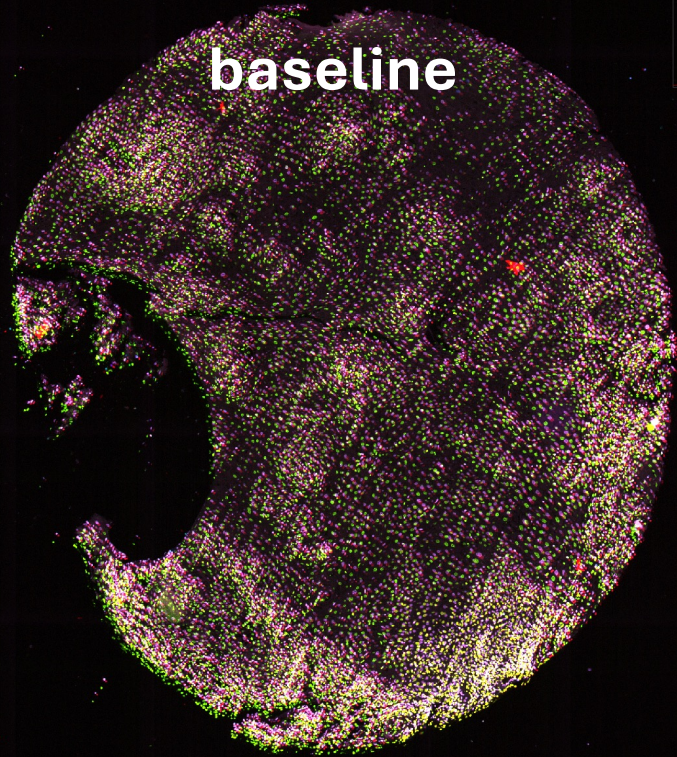
7um shift much better  
compared to 80/30um  
shifts seen before



# Visualizing. Seems good, but still a bit blurry.

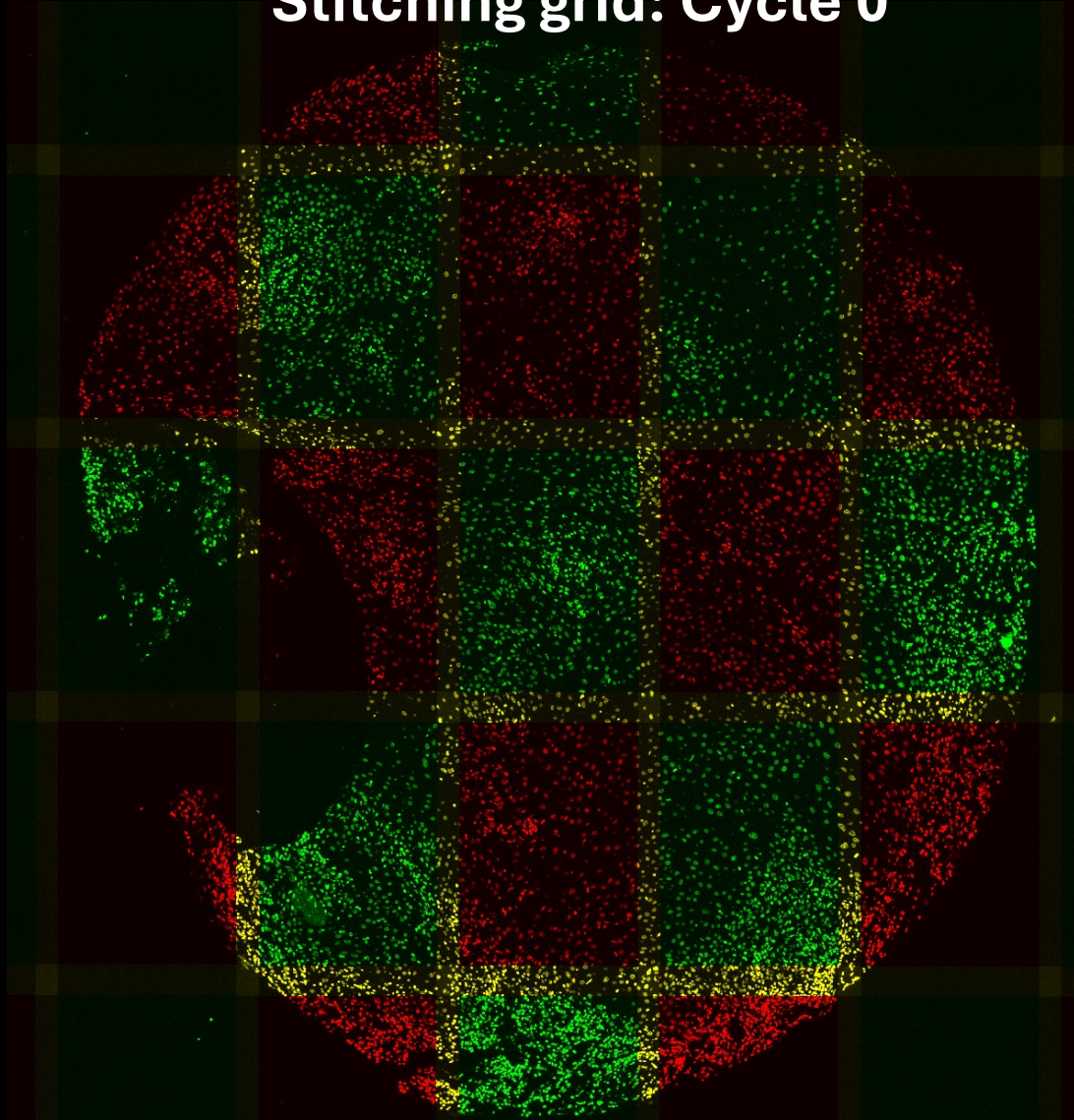


Visualizing.  
Still much  
better

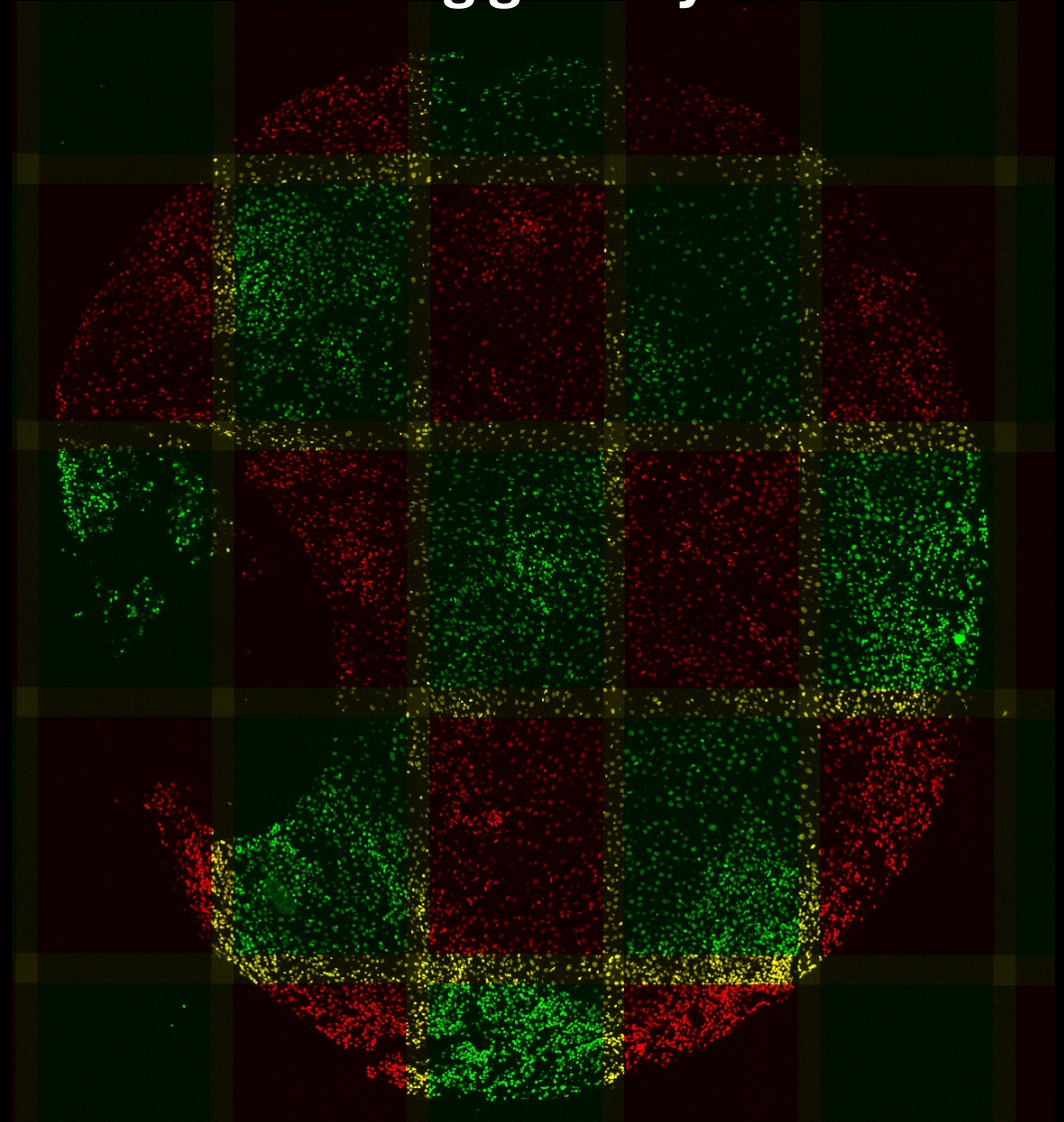


# Blurriness from stitching or registration? Stitching grids seem perfect...

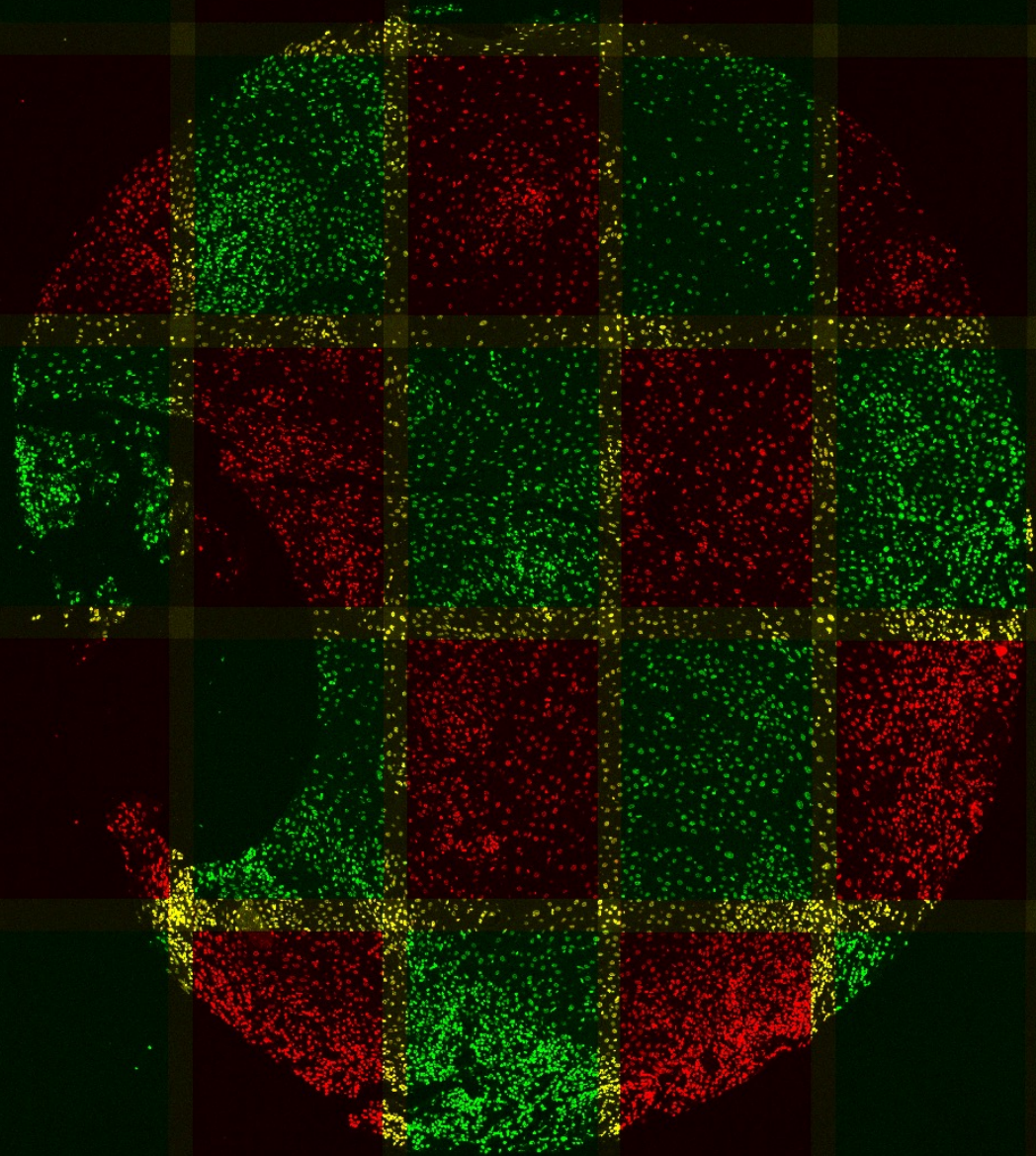
**Stitching grid: Cycle 0**



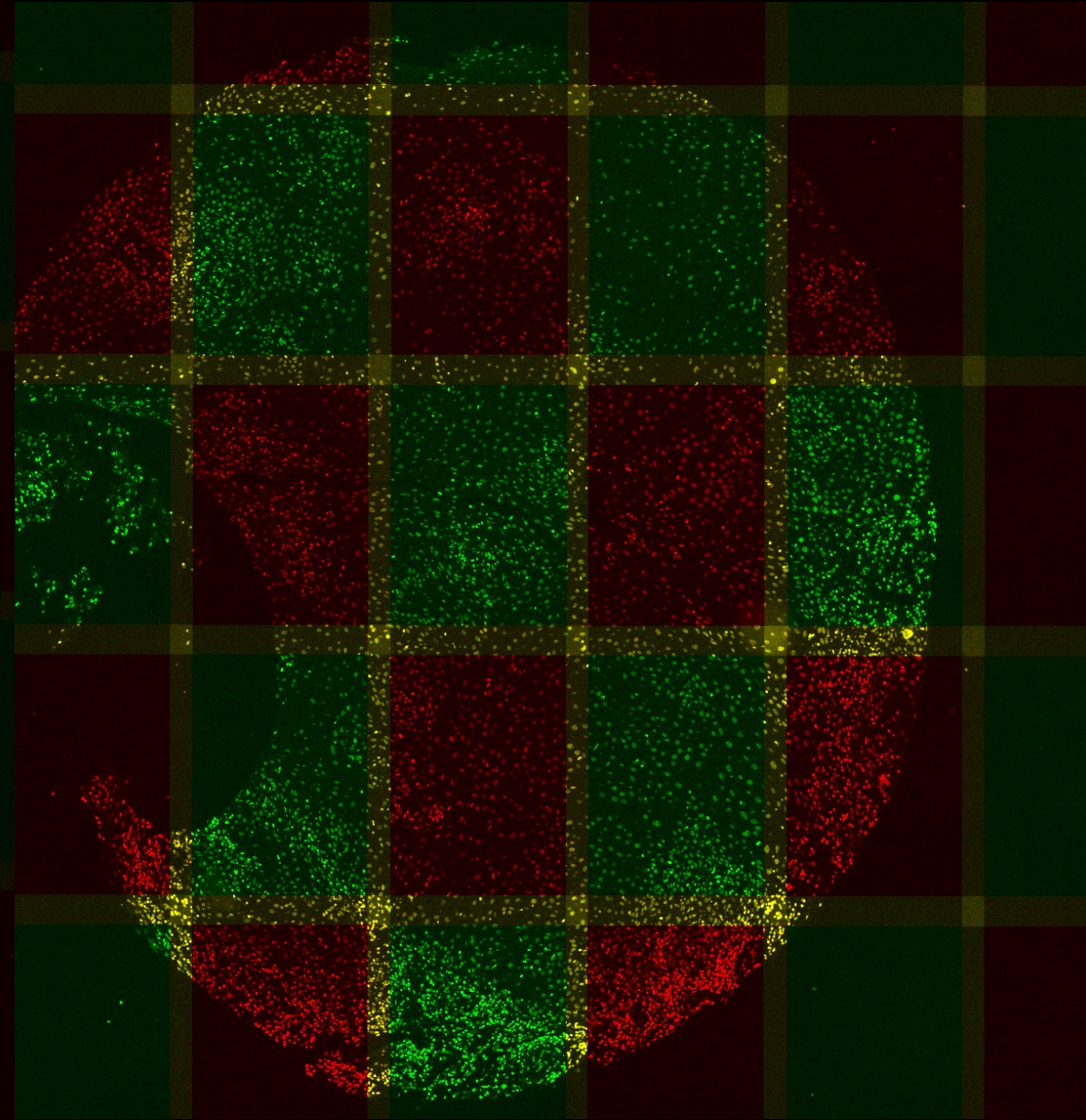
**Stitching grid: Cycle 1**



Stitching grid: Cycle 2



Stitching grid: Cycle 3



# Results from Stitching QC:

- Changing stitching parameters significantly improves output stack
  - 7um shifts still present
- Stitching seems perfect when checking the tile overlap

## **Conclusion:**

- After improving the stitching parameters, the problem lies in the registration, this should fix that 7um shifts



Question:

Passing shift and sigma values to registration process help?

Results:

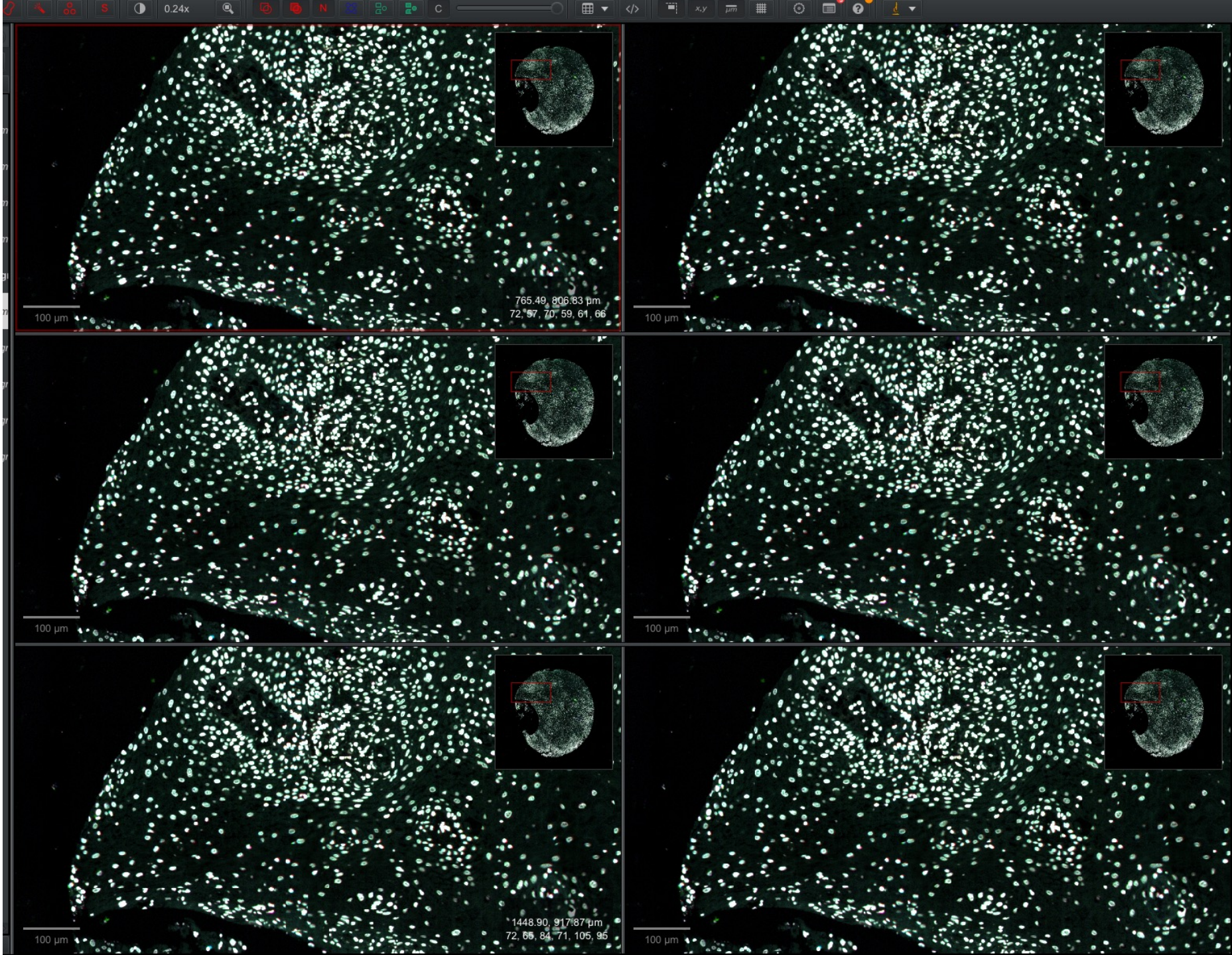
Blurriness is gone, stitching and registration seem perfect.

Conclusion:

Registration was causing the issue, not stitching.

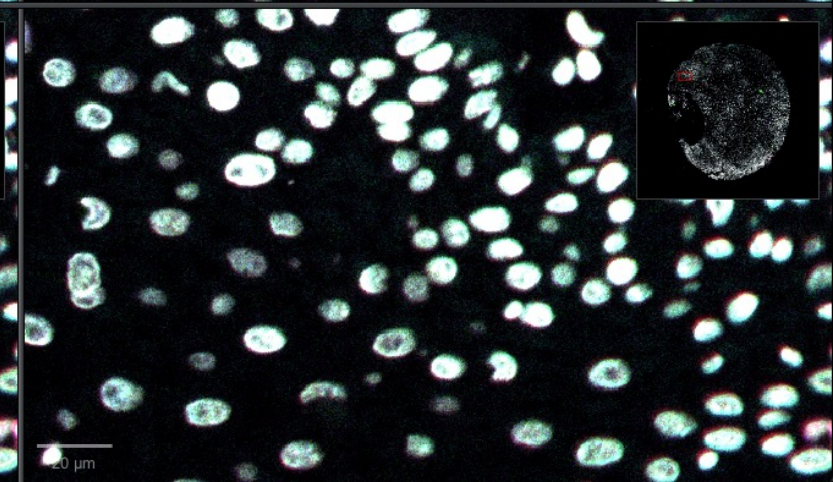
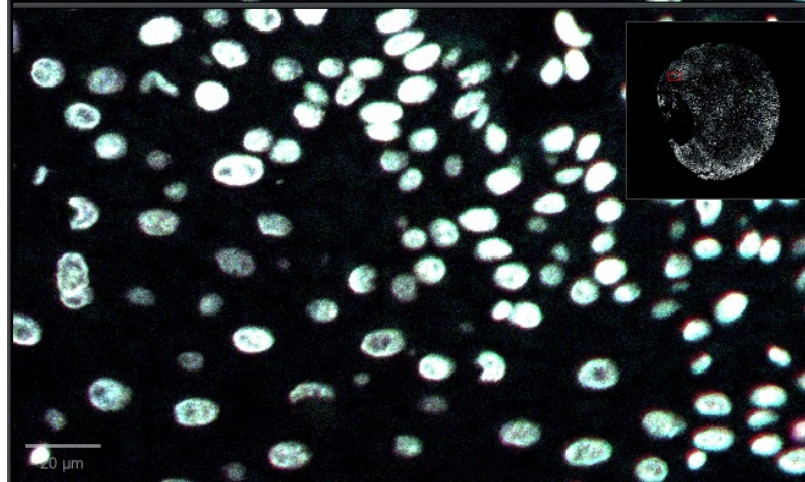
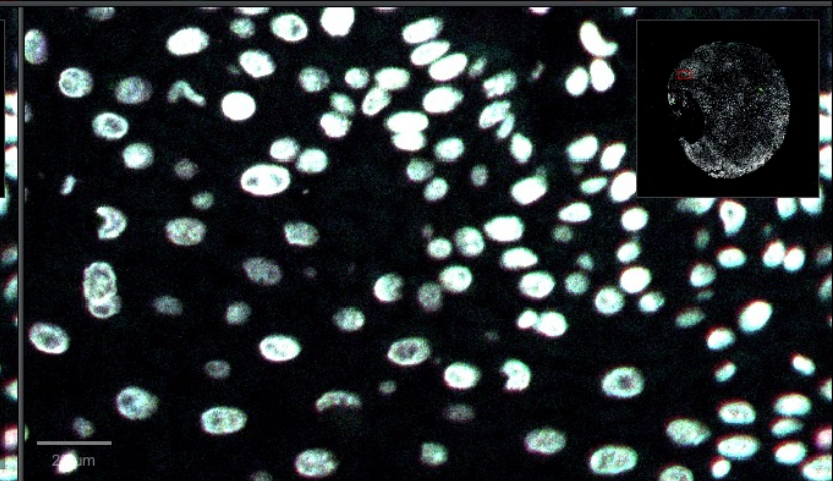
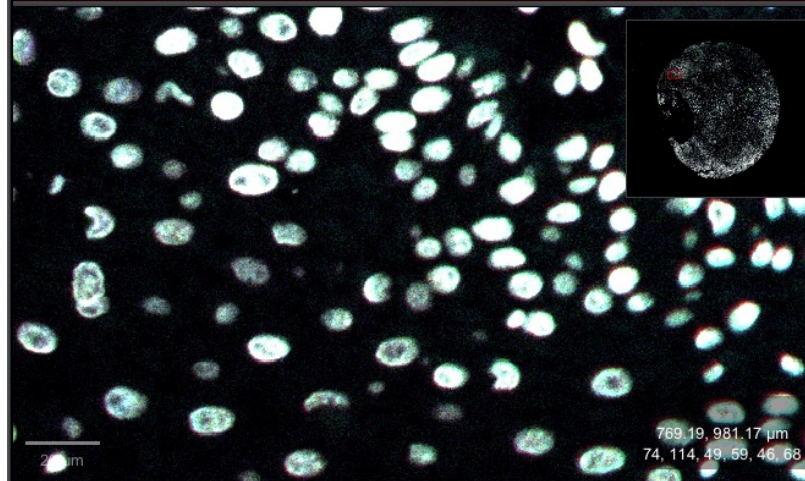
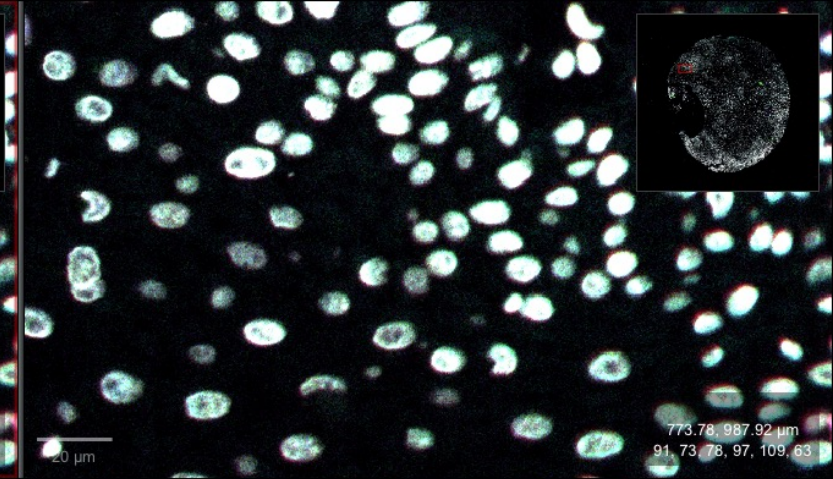
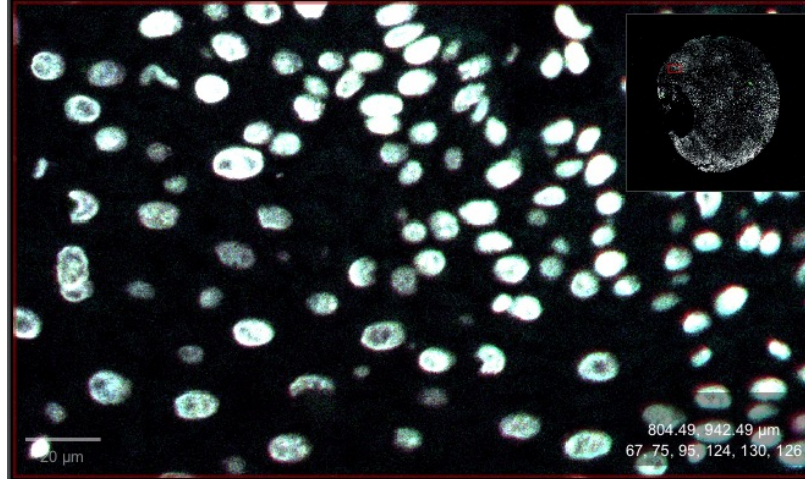
Shift 50 Sigma 1	Shift 50 Sigma 2
Shift 100 Sigma 1	Shift 100 Sigma 2
Shift 150 Sigma 1	Shift 150 Sigma 2

Also: Increasing shift greatly does not cause artefacts



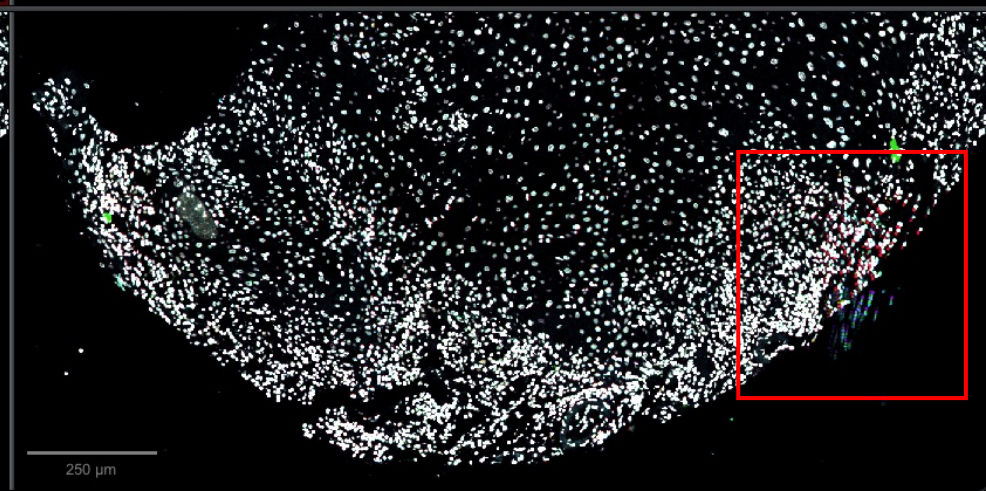
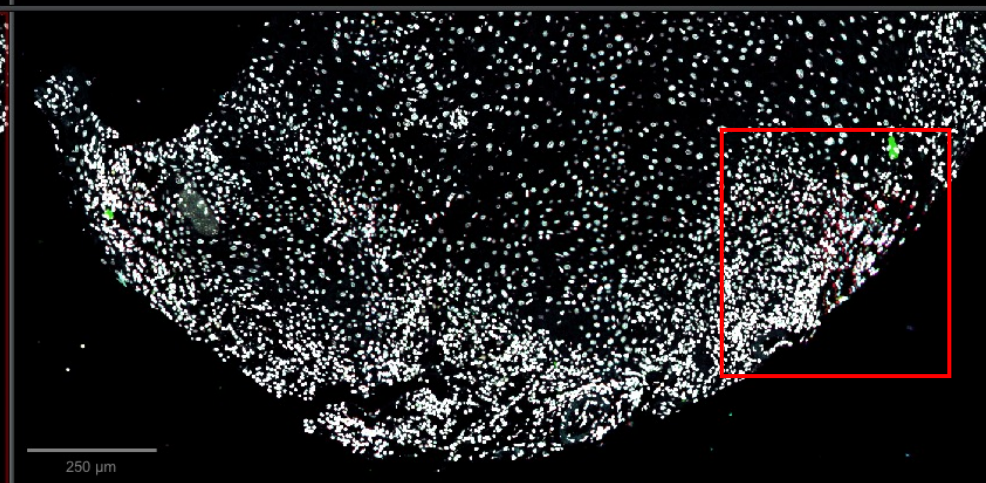
# Same but closer

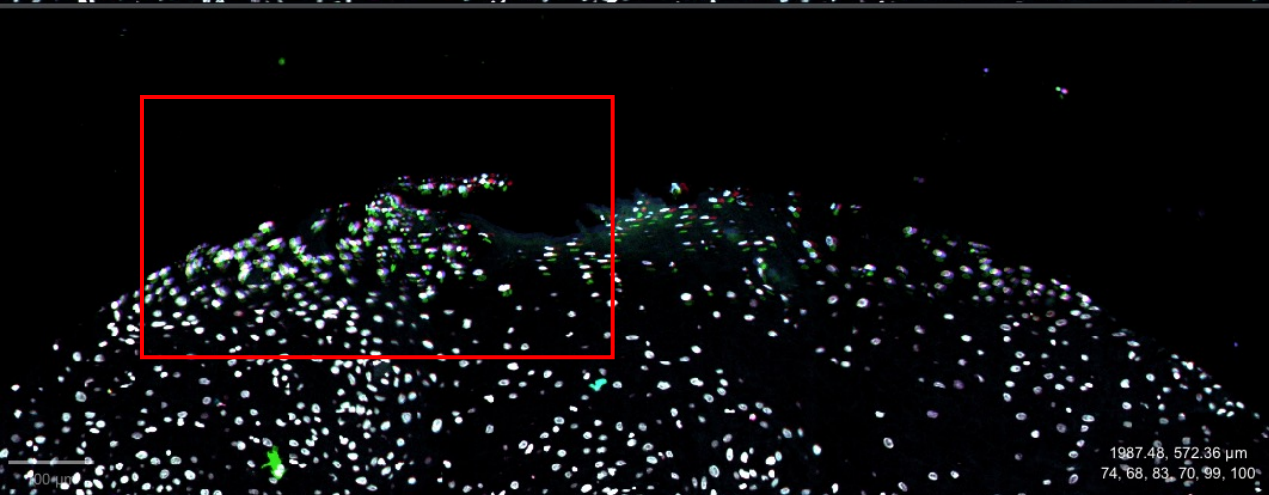
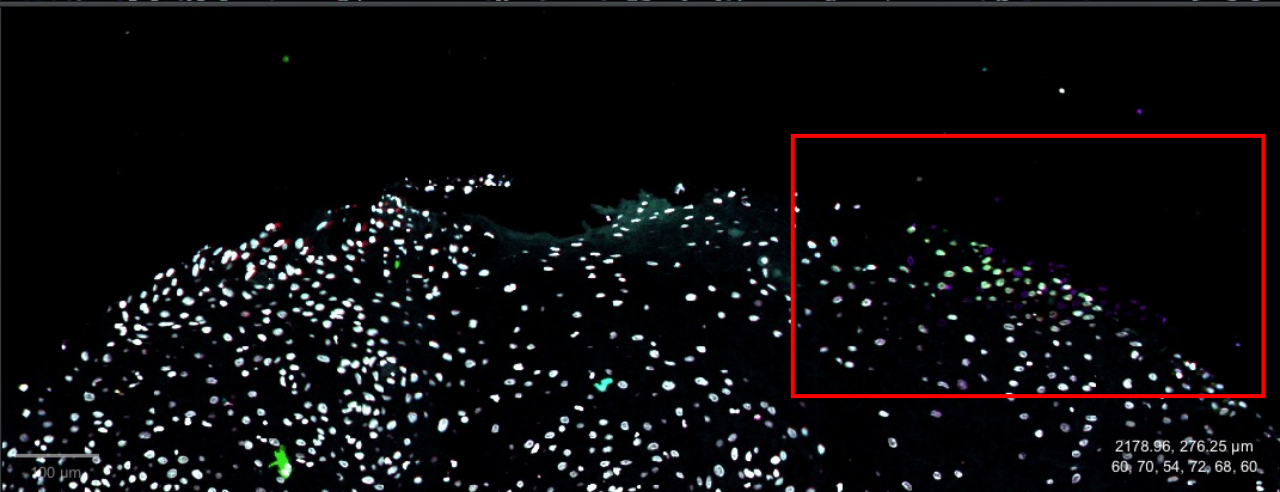
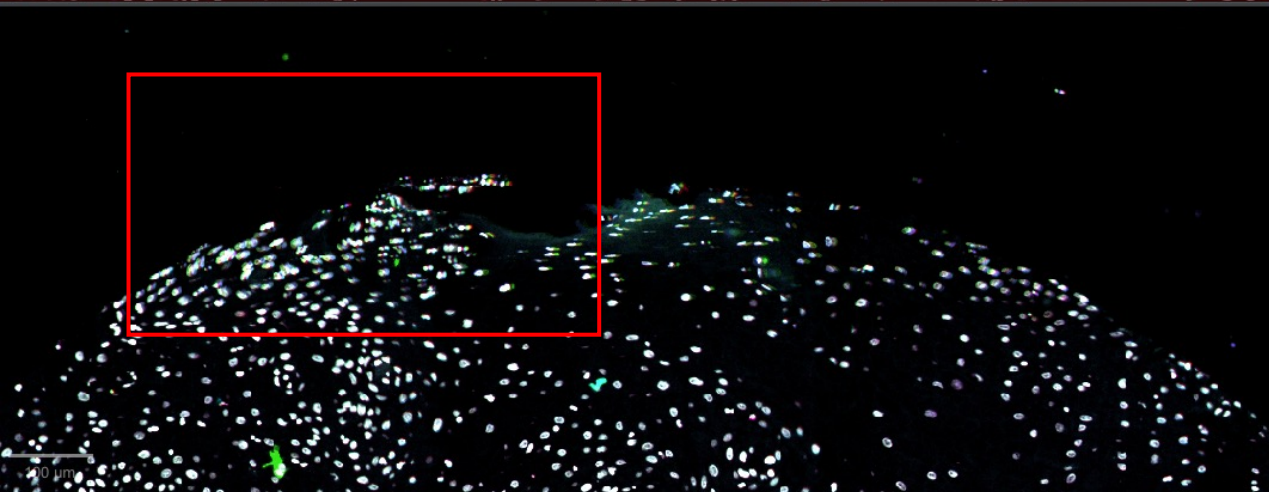
Shift 50 Sigma 1	Shift 50 Sigma 2
Shift 100 Sigma 1	Shift 100 Sigma 2
Shift 150 Sigma 1	Shift 150 Sigma 2



# Still small issues with specific tiles

Shift 50 Sigma 1	Shift 50 Sigma 2
Shift 100 Sigma 1	Shift 100 Sigma 2
Shift 150 Sigma 1	Shift 150 Sigma 2





# Why are some tiles misbehaving?

I don't know, but I have a hypothesis:

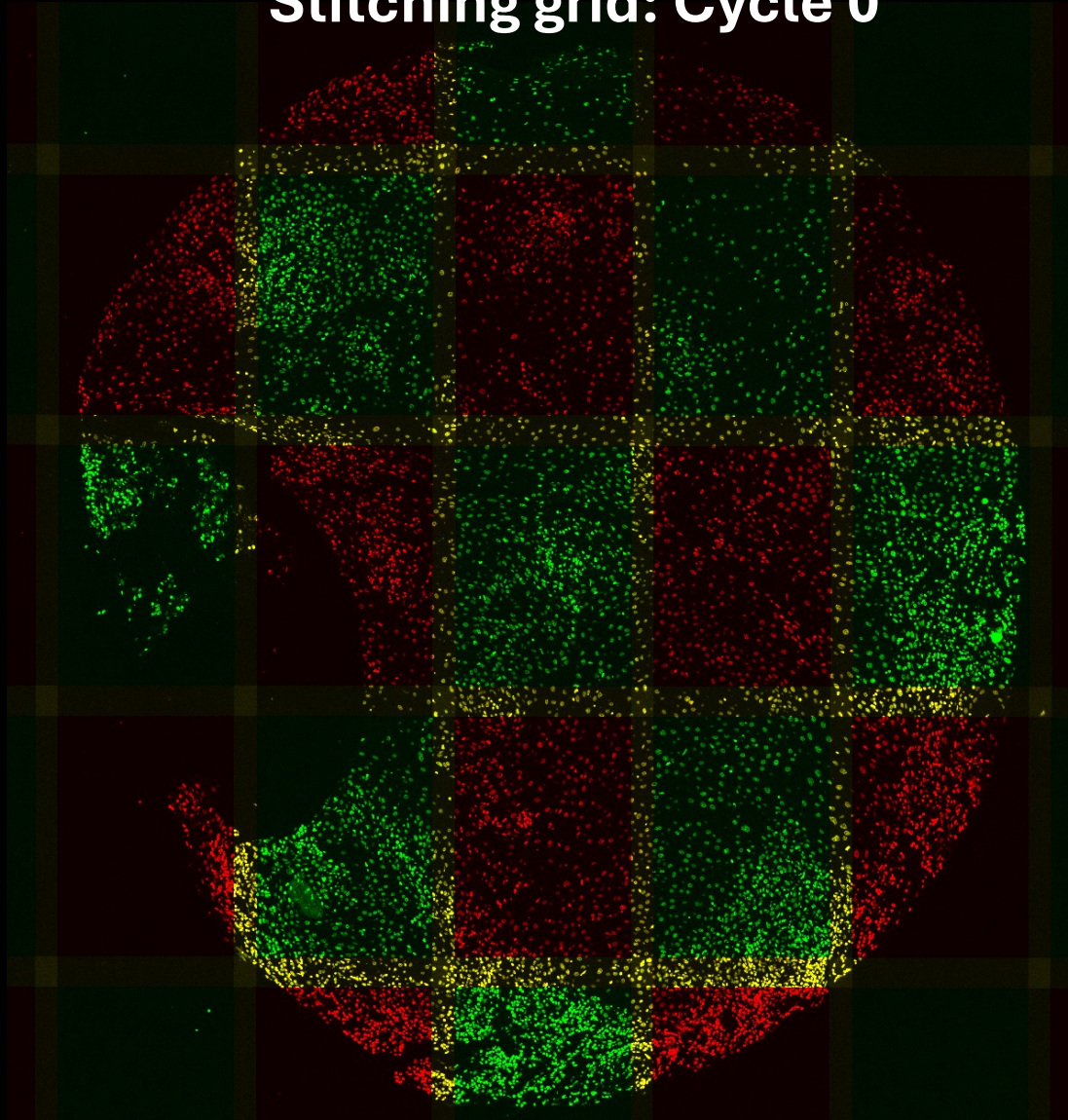
Tissue positioning on tiles changes through cycles, and sometimes there are large discrepancies that the math can't deal with.

What do I mean with discrepancies?

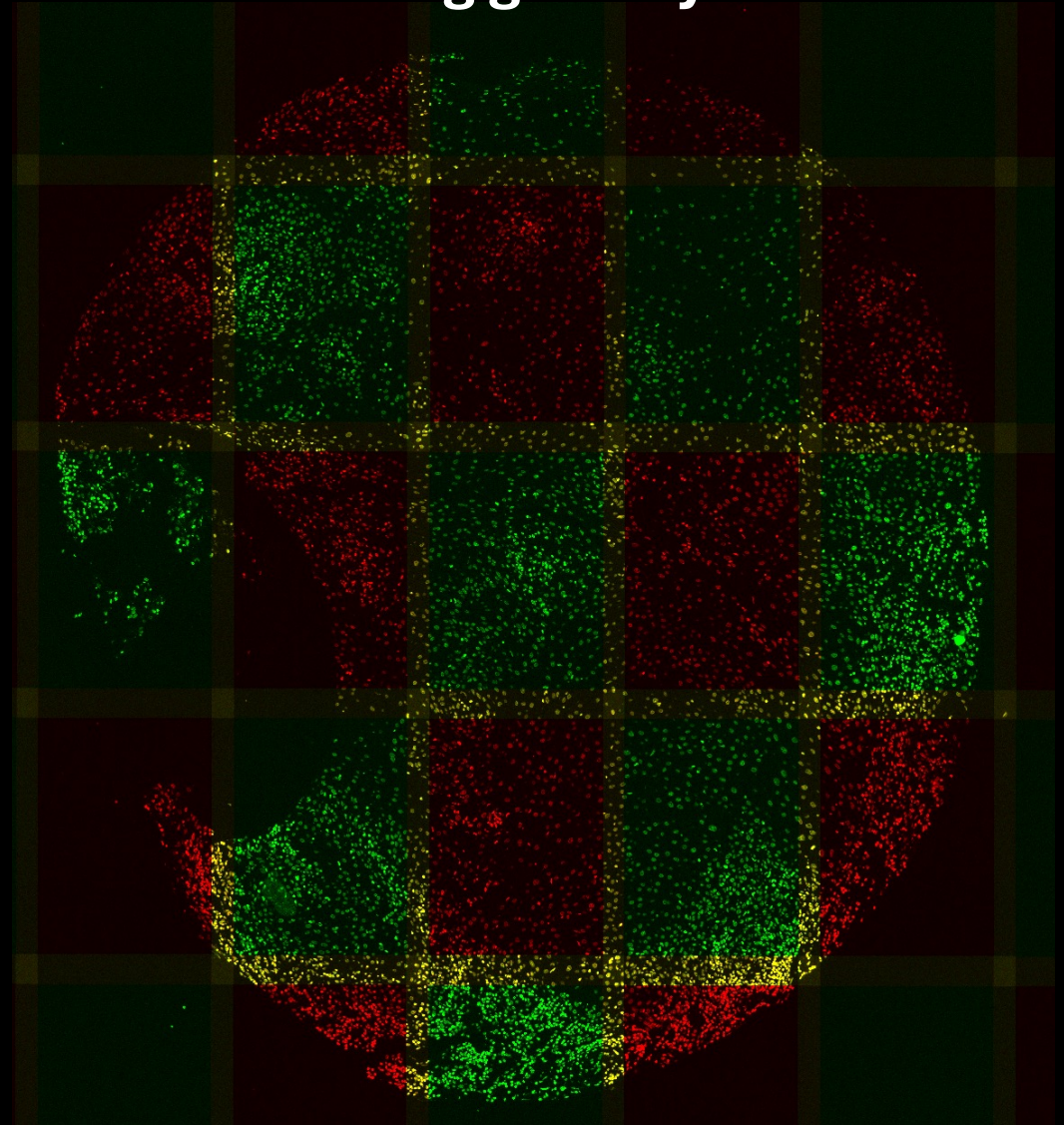
Look at this images again:

Look at the top tiles and the bottom right tiles

**Stitching grid: Cycle 0**

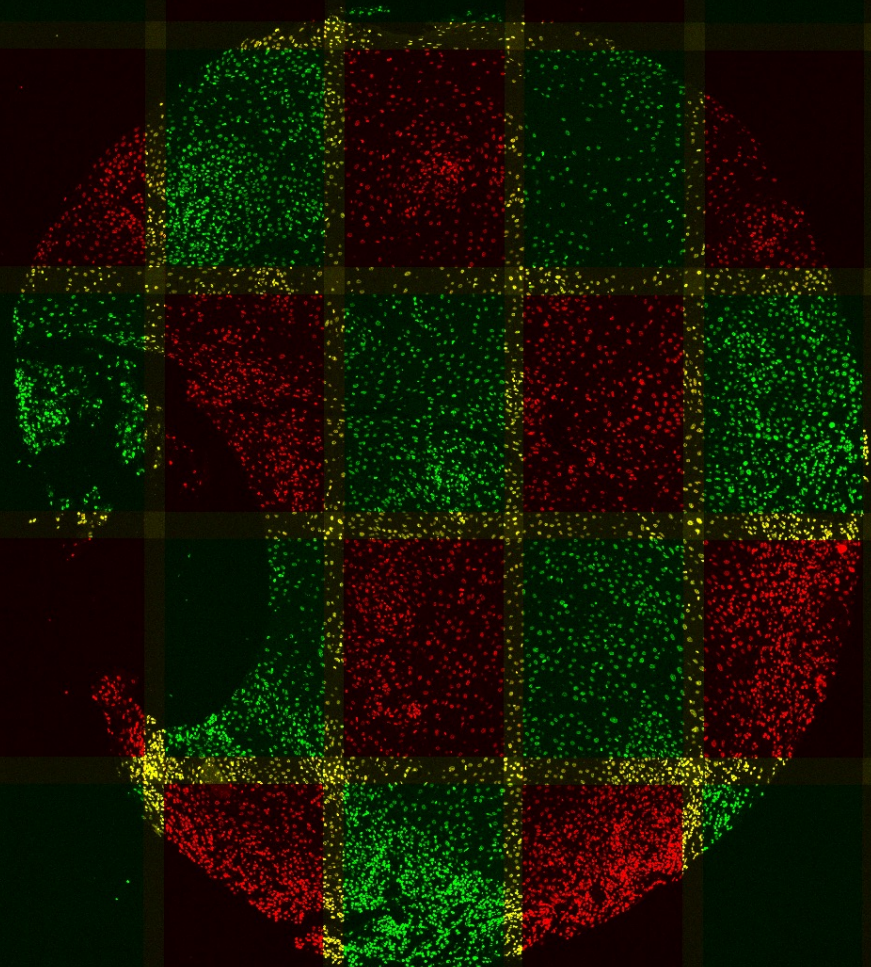


**Stitching grid: Cycle 1**

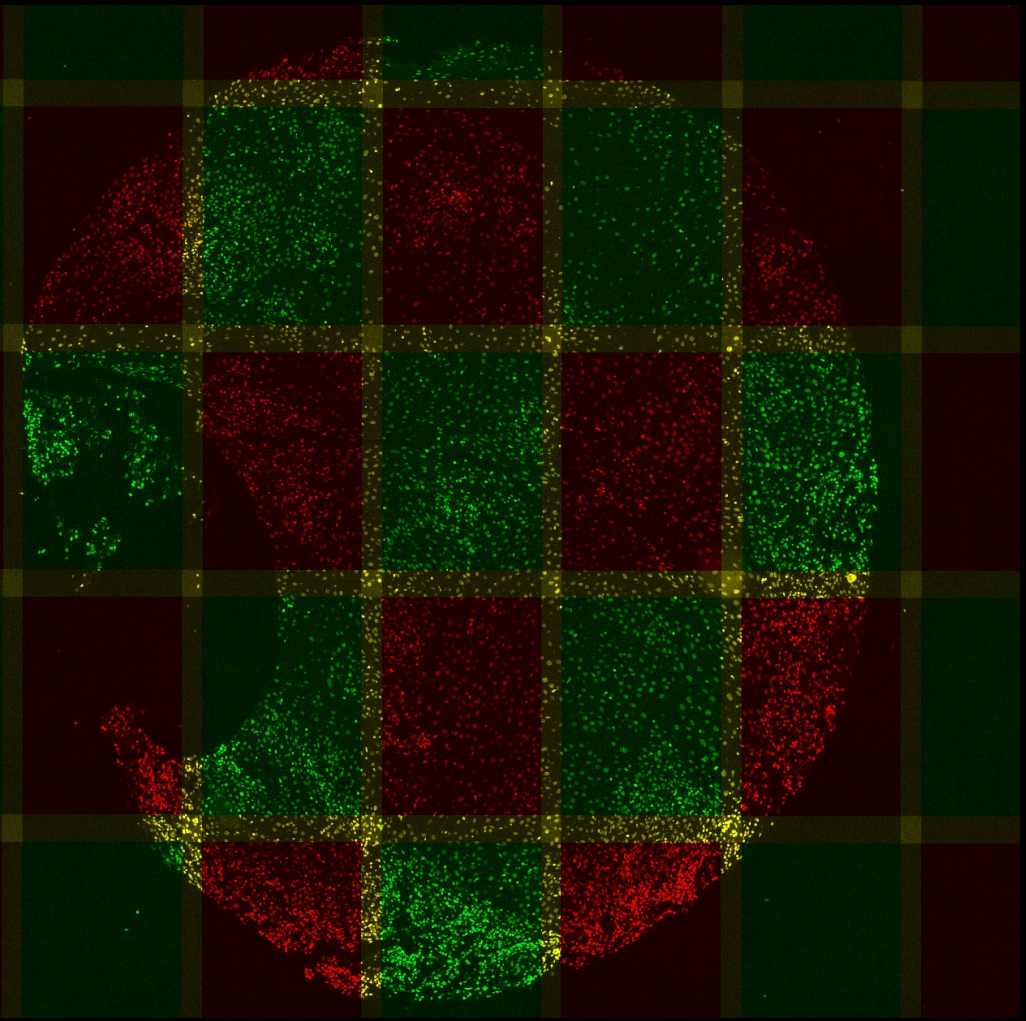


# Look again.

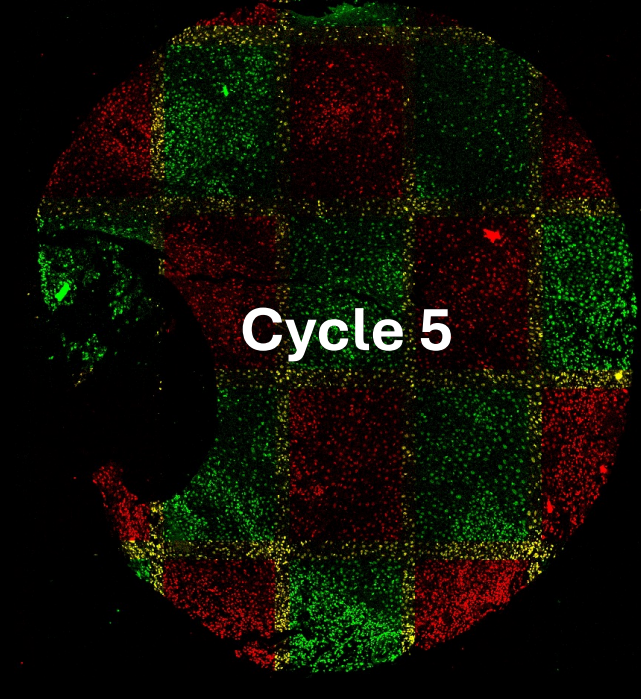
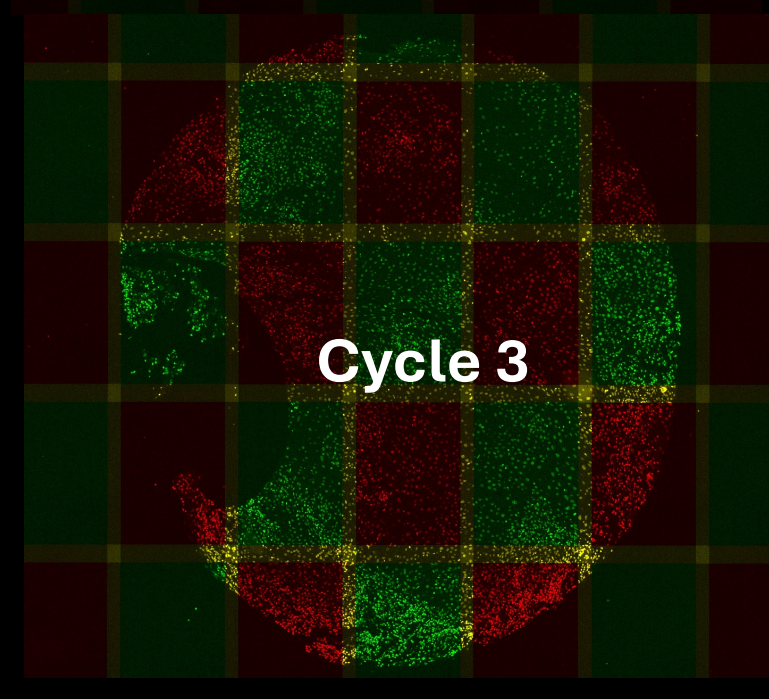
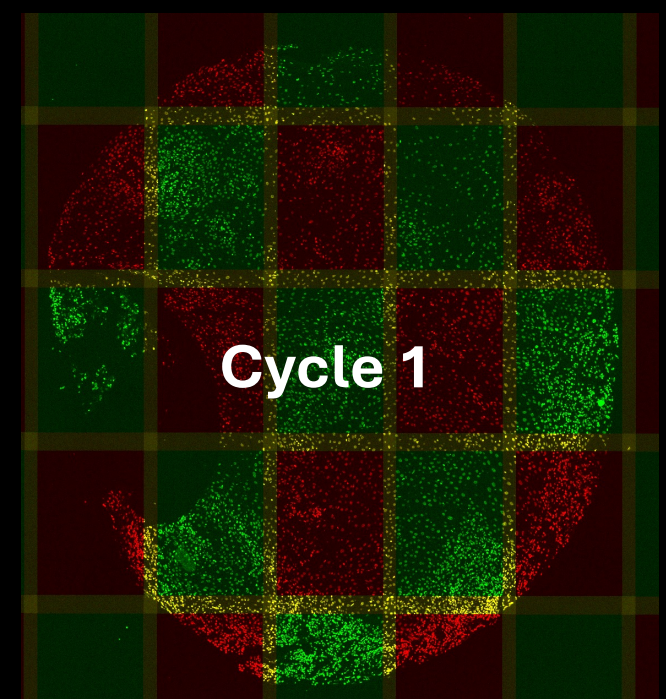
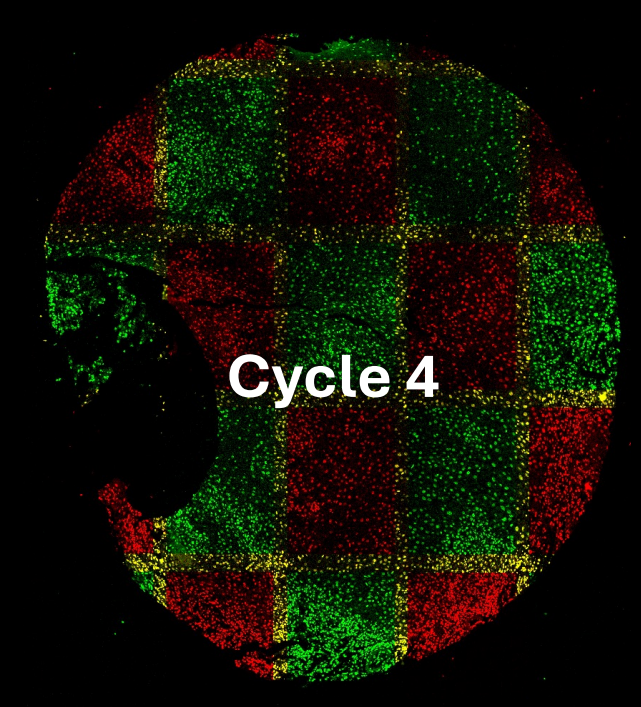
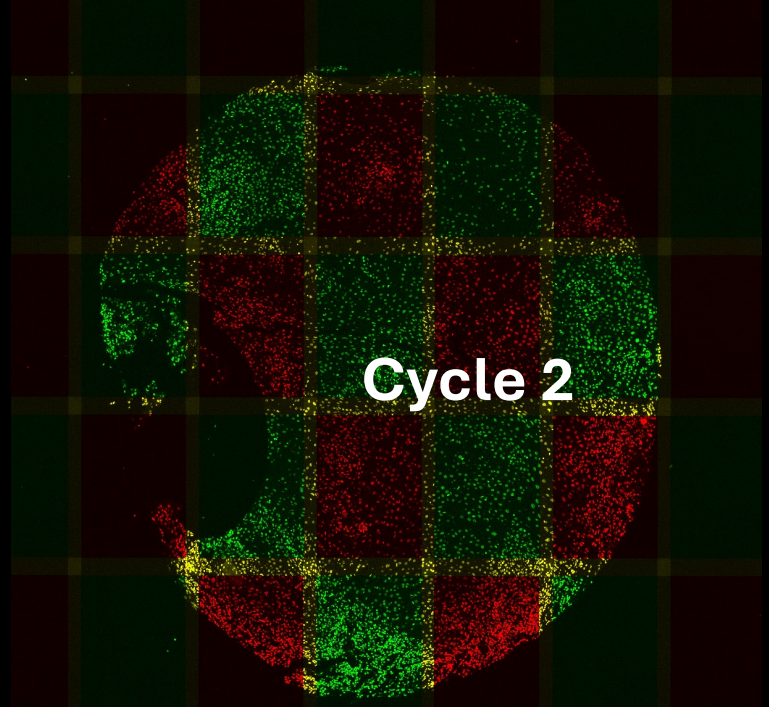
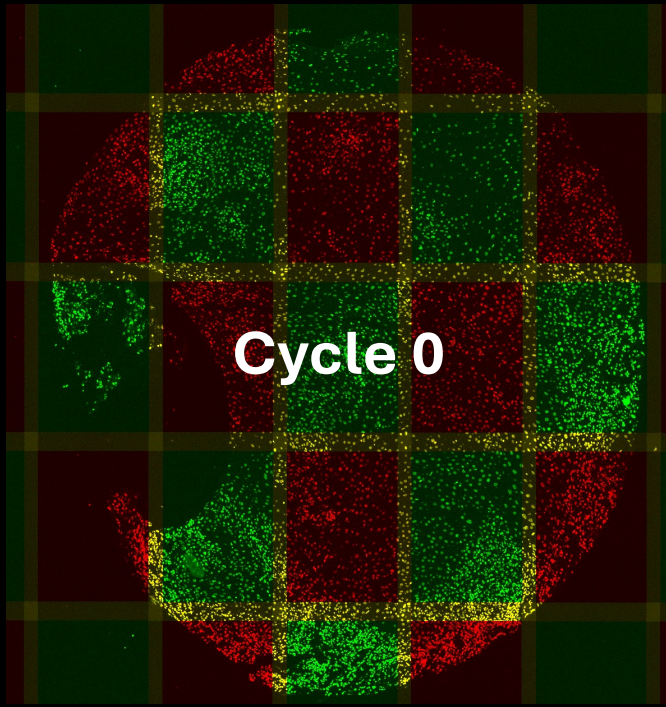
See how there is much less tissue on those tiles compared to before



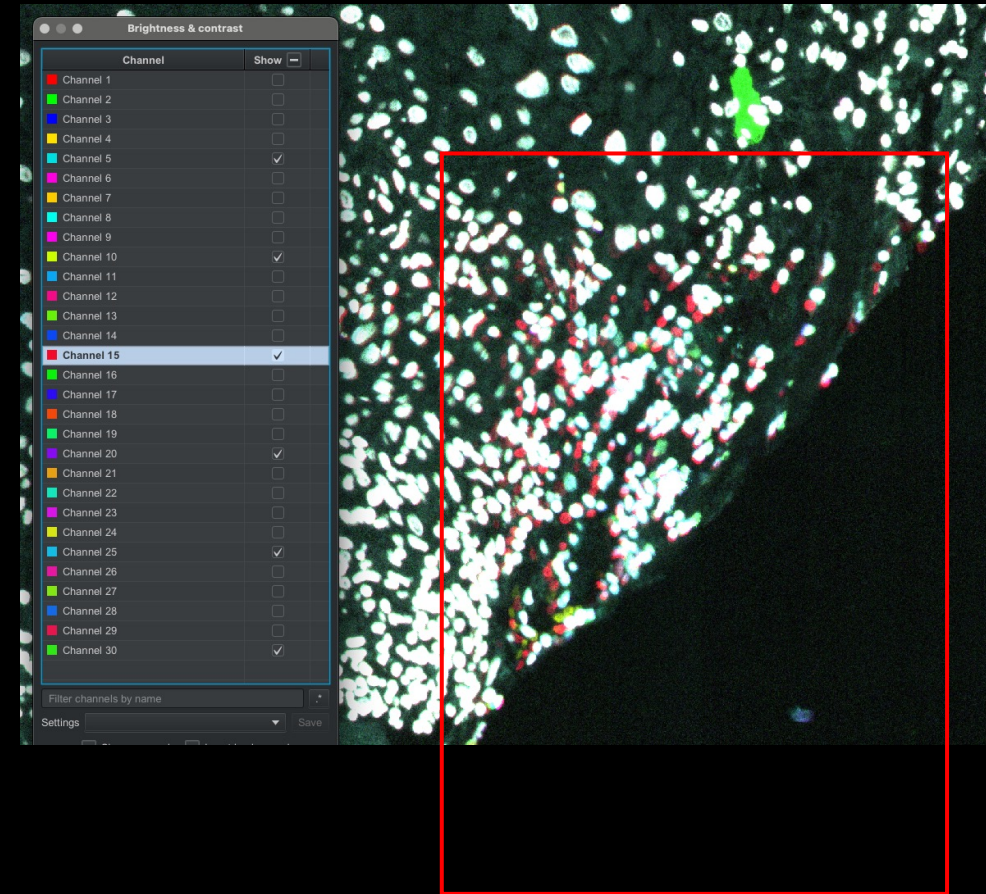
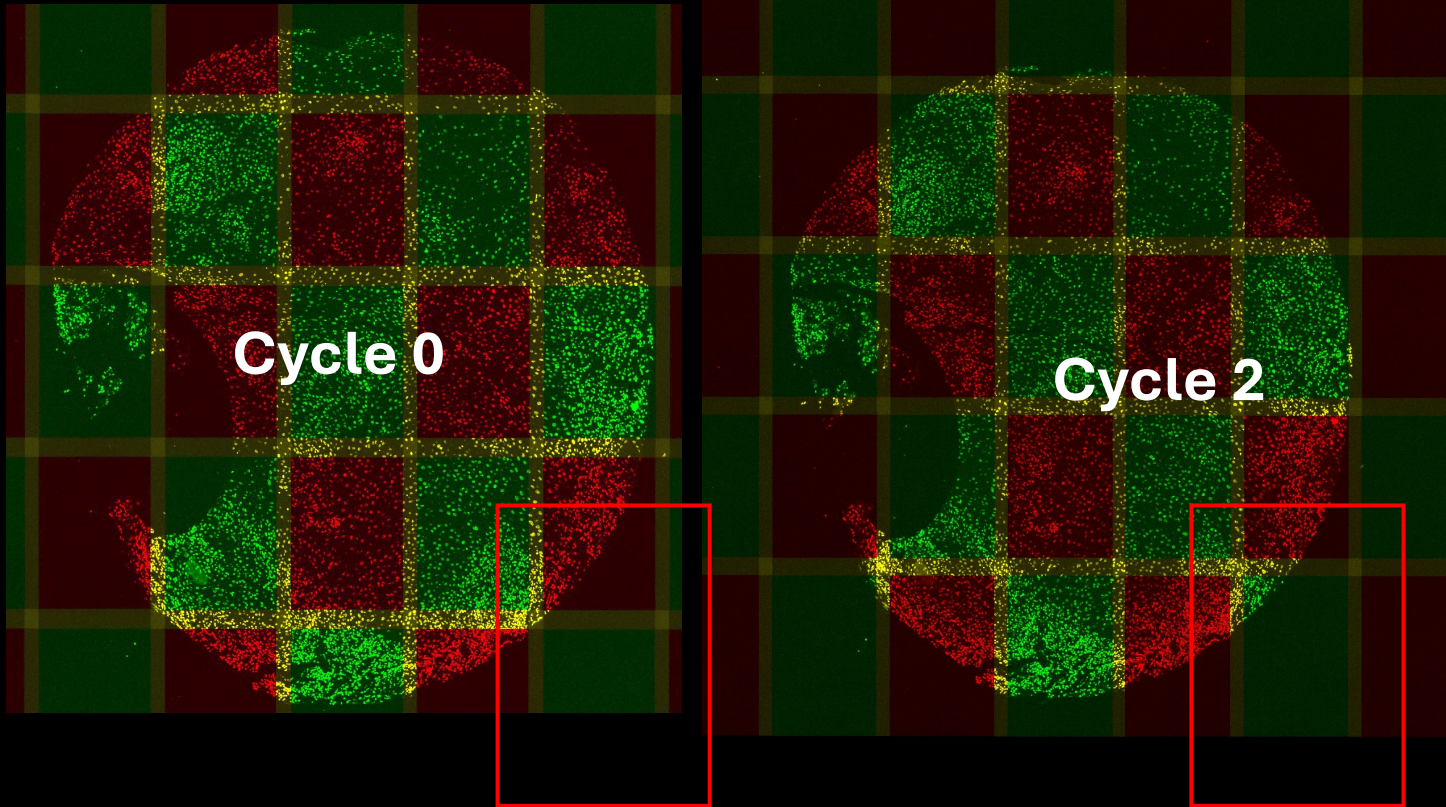
**Stitching grid: Cycle 2**



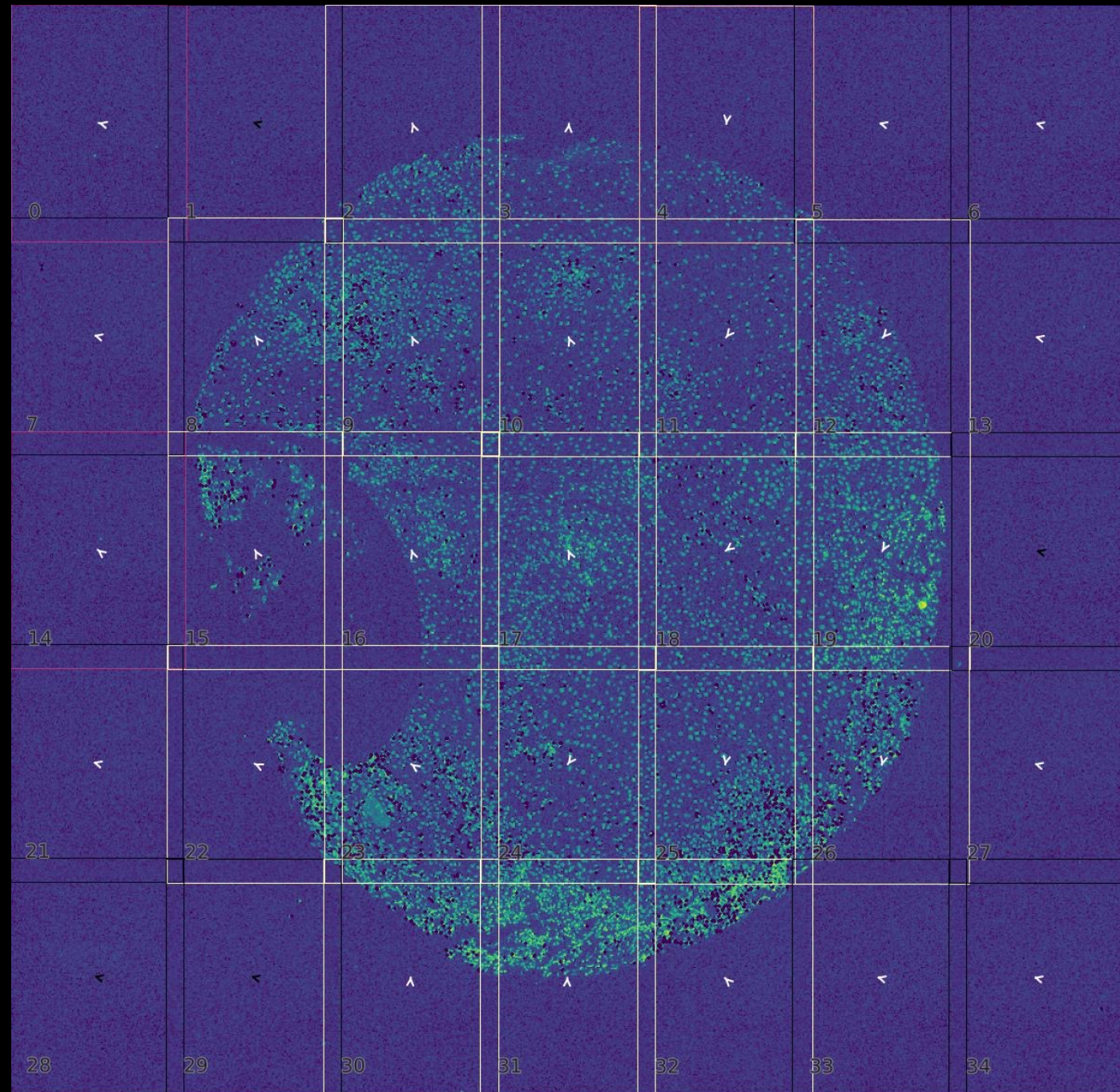
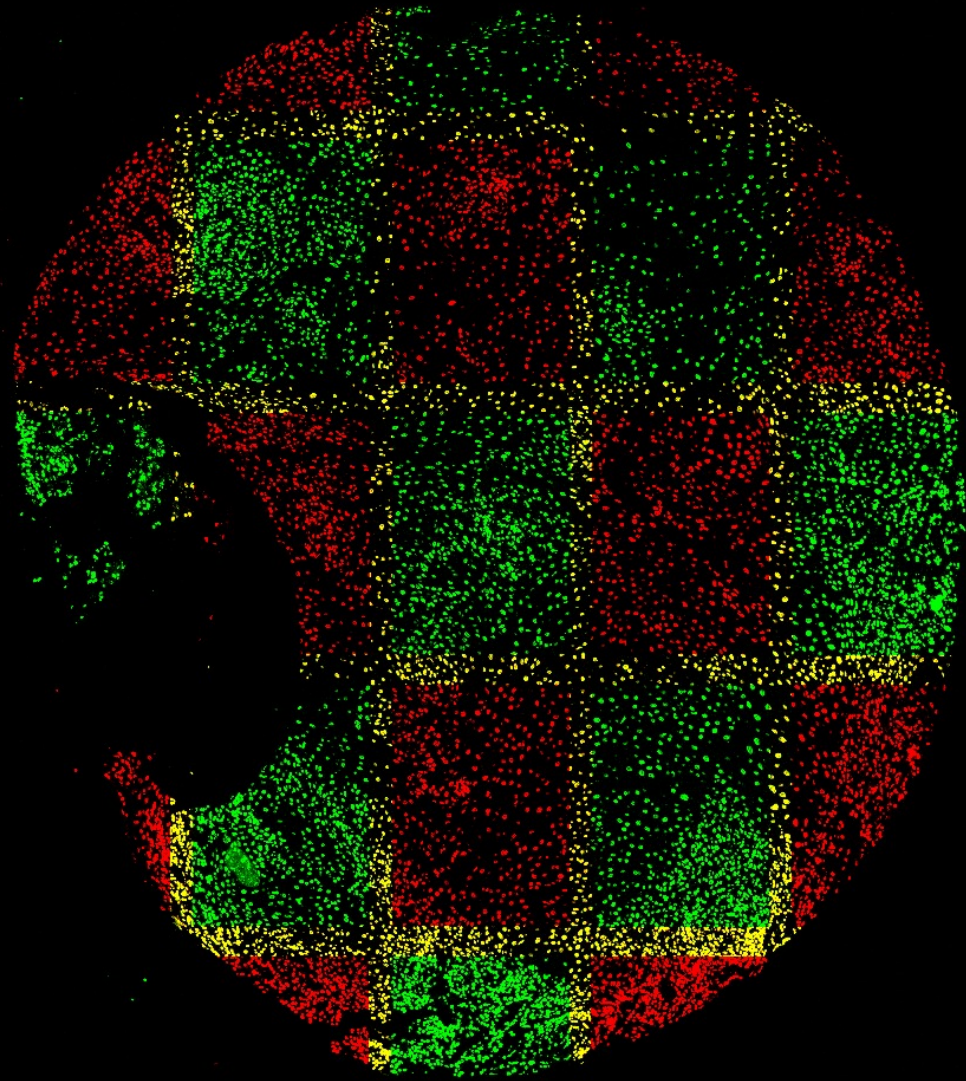
**Stitching grid: Cycle 3**







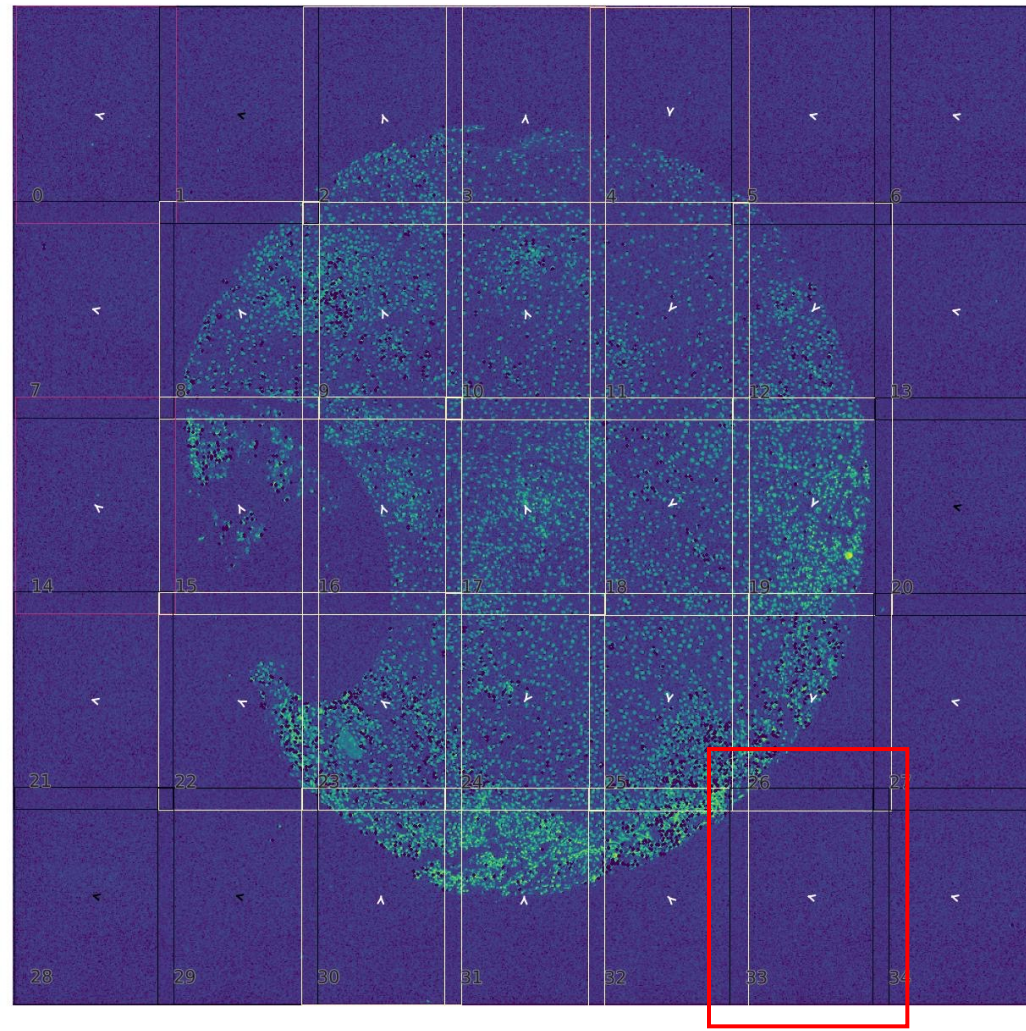
Hypothesis:  
This difference is causing a mistake in registration



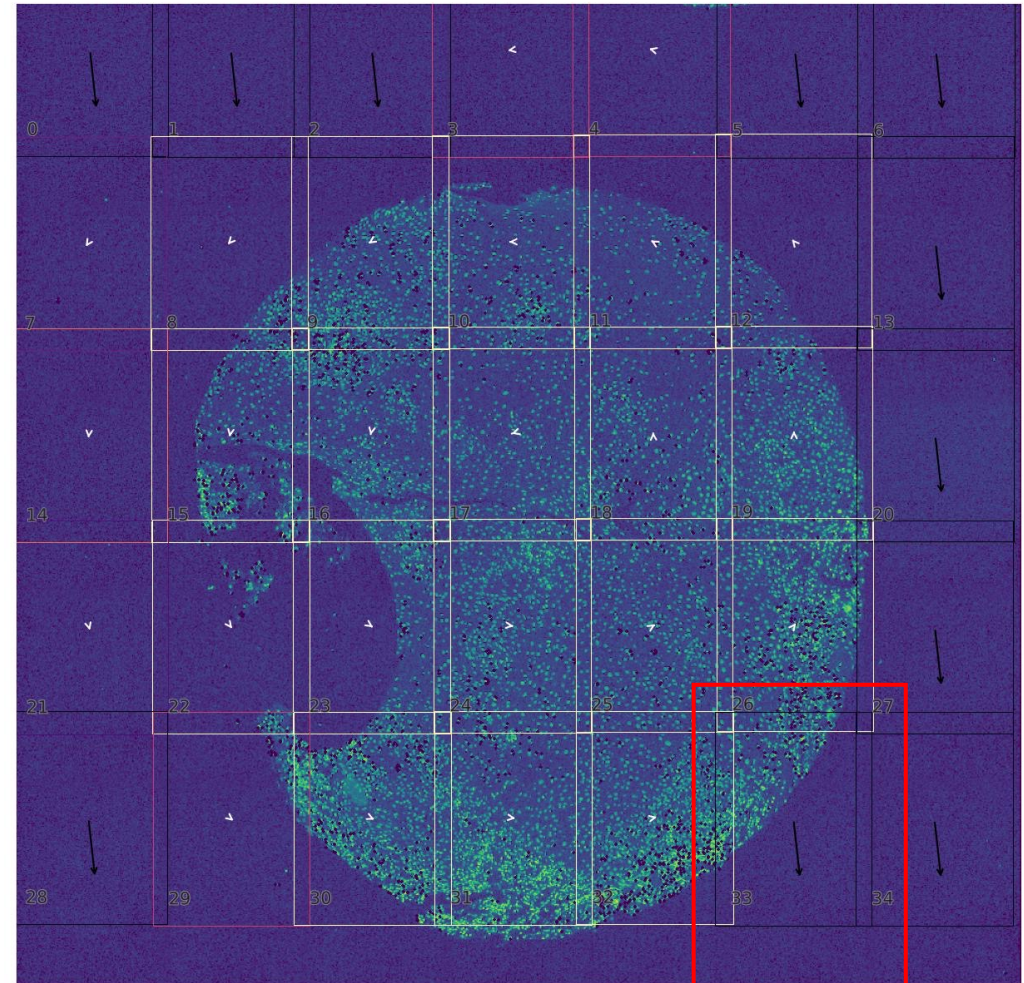
I double checked by measuring the registration shift per cycle.  
Remember this is always done again a single cycle as reference, here cycle 0.

Black arrows mean too much error and will not register

## Cycle 0-1



## Cycle 0-2



# Conclusion

- Increasing sigma and max\_shift parameters significantly improves the stitching and registration.
- Small shifts still exists in specific tiles, most likely due to slide shifts between cycles, which leads to inconsistent tissue amounts for the same tile.

## Next steps:

- Stitch and register whole TMA slides with new parameters (hopefully it scales up well)
- Allowing much better segmentation, quantification, and analysis.