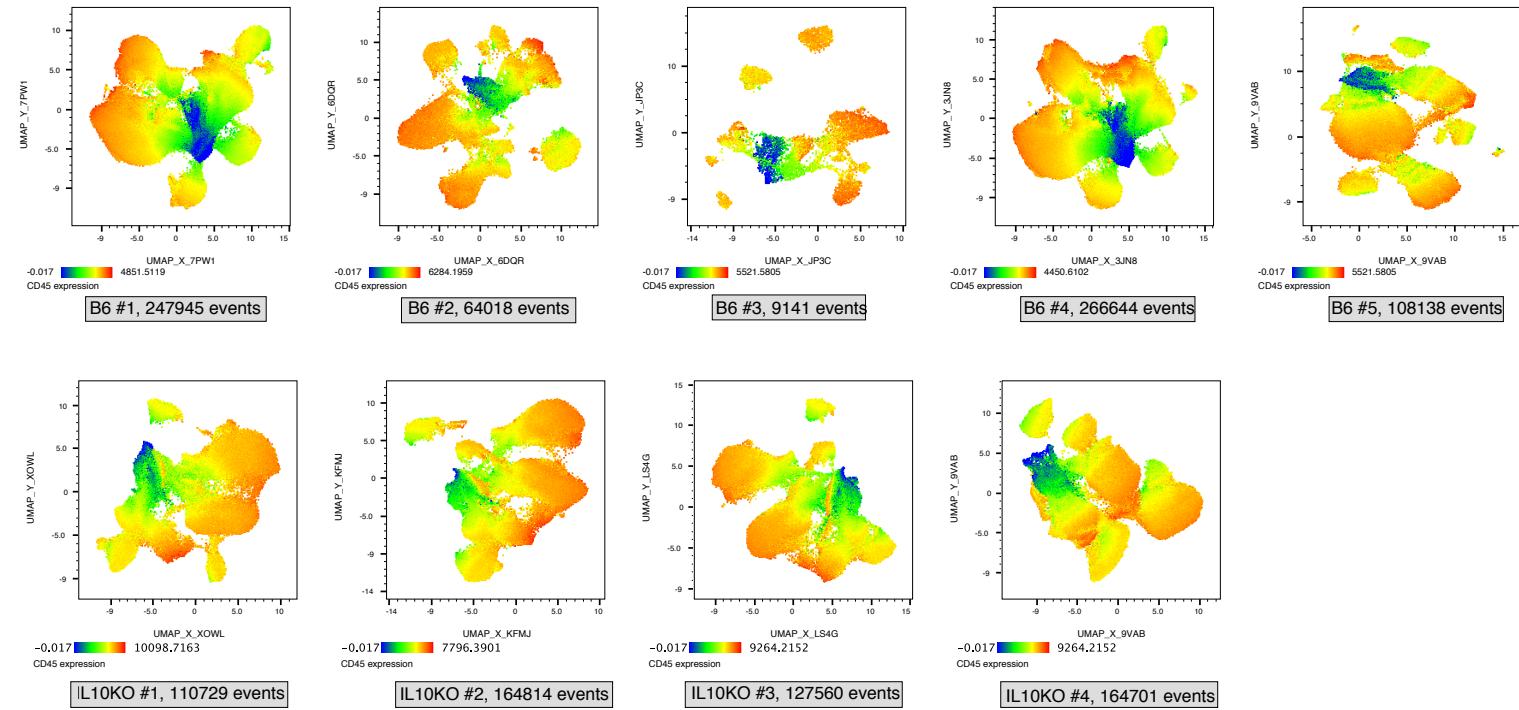


# Exploring the UMAP plugin in FlowJo

Abby Kimball, Clambey Lab 05/22/19

# All 9 UMAP plots

- Each file was analyzed separately, all events were included, all clustered on relevant markers, and distance function “Euclidean”, nearest neighbors: 15, and minimal distance: 0.5.

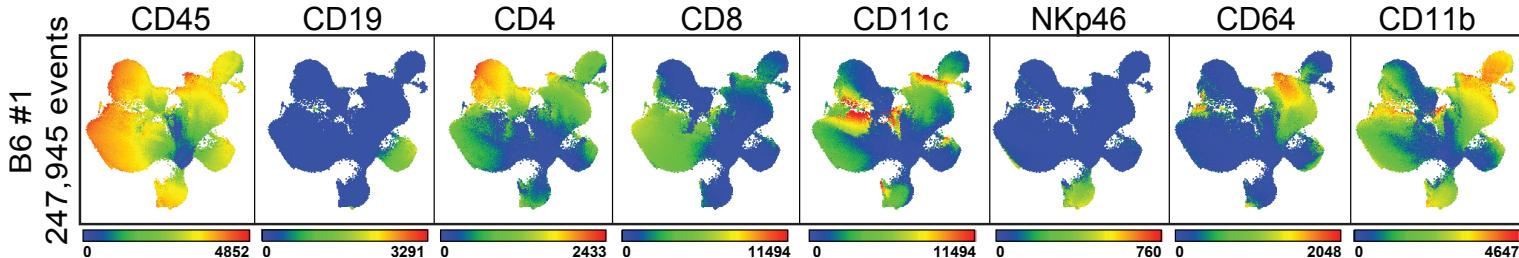


B6 #1 colored by lineage markers

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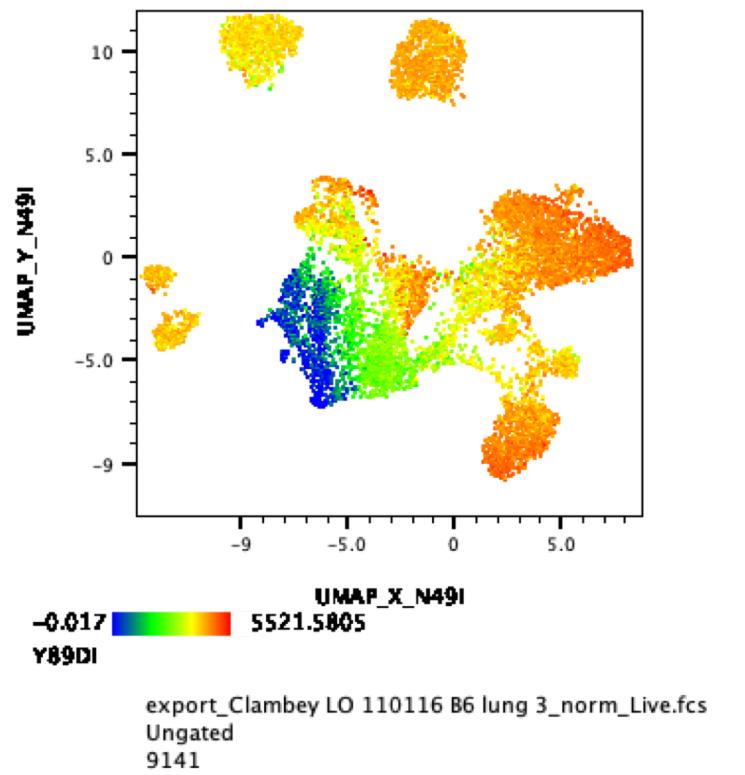
## UMAP in FlowJo\*

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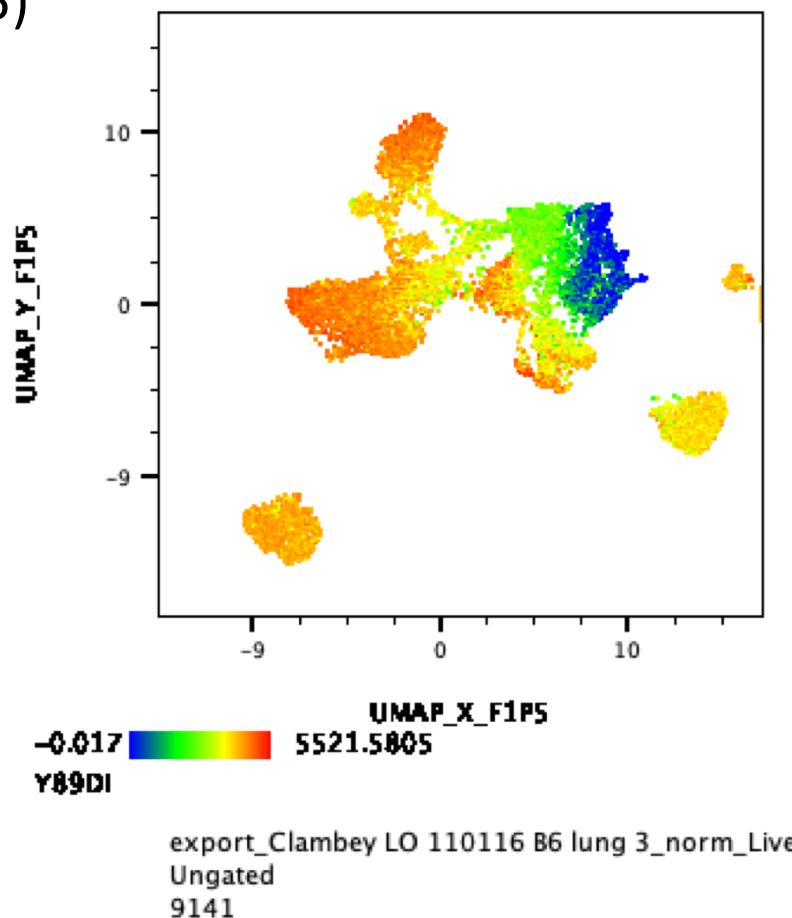


# Is UMAP reproducible?

- B6 #3 UMAP #1 (N49I)



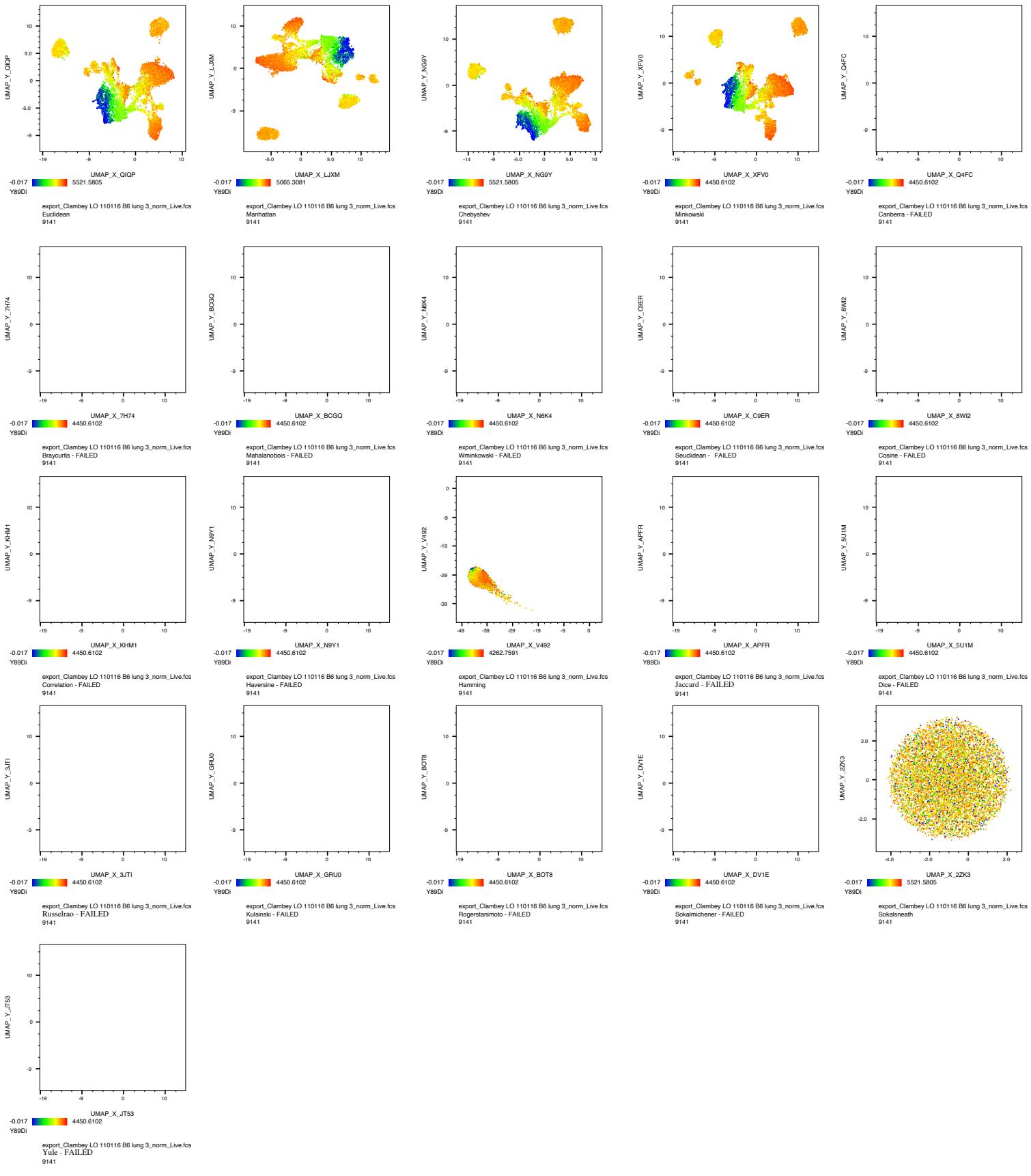
- B6 #3 UMAP #2 (F1P5)



# B6 #3 UMAP iterations with all the possible distance functions

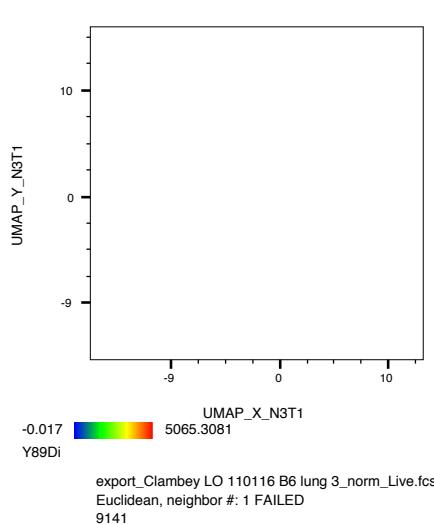
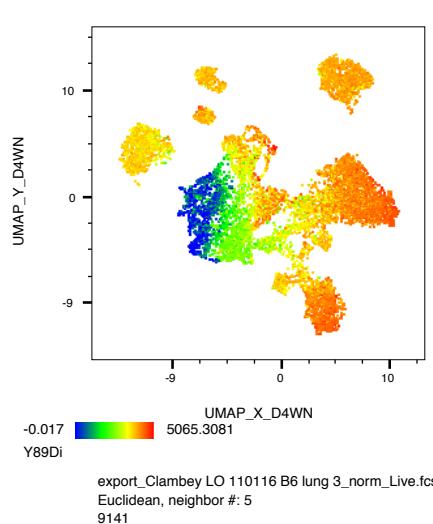
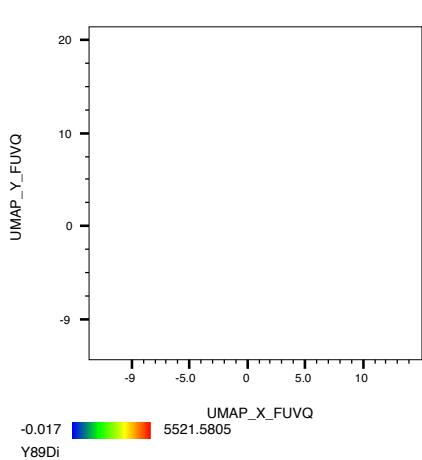
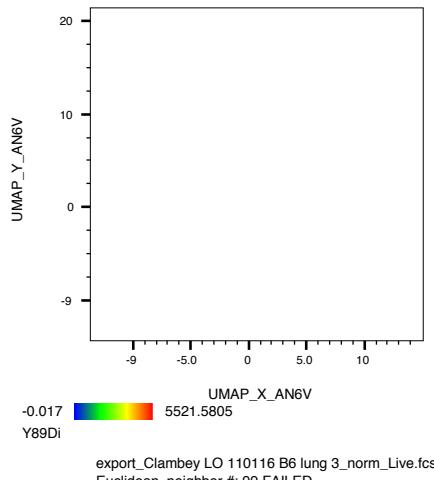
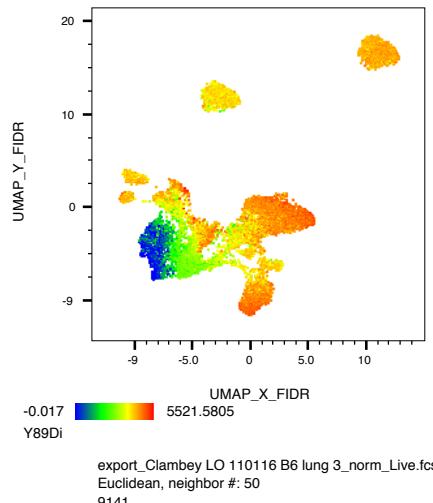
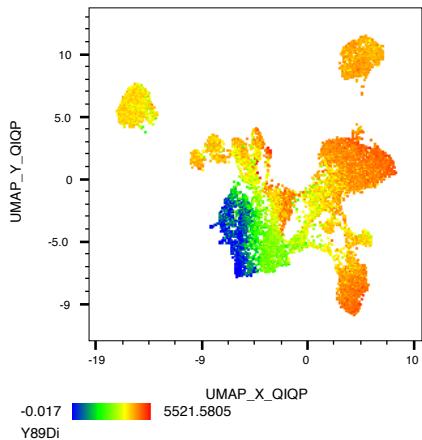
- Euclidean – QIQP
- Manhattan – LJXM
- Chebyshev – NG9Y
- Minkowski– XFVO
- Canberra – Q4FC **ERROR, FAILED**
- Braycurtis – 7H74 **ERROR, FAILED**
- Mahalanobois – BCGQ **ERROR, FAILED**
- Wminkowski – N6K4 **ERROR, FAILED**
- Seuclidean – C9ER **ERROR, FAILED**
- Cosine – 8WI2 **ERROR, FAILED**
- Correlation - KHM1 **ERROR, FAILED**
- Haversine - N9Y1 **ERROR, FAILED**
- Hamming – V492
- Jaccard – APFR **ERROR, FAILED**
- Dice – 5U1M **ERROR, FAILED**
- Russelrao – 3JTI **ERROR, FAILED**
- Kulsinski – GRU0 **ERROR, FAILED**
- Rogerstanimoto – BOT8 **ERROR, FAILED**
- Sokalmichener – DV1E **ERROR, FAILED**
- Sokalsneath – 2ZK3
- Yule – JT53 **ERROR, FAILED**

# B6 #3 UMAP iterations with all the possible distance functions



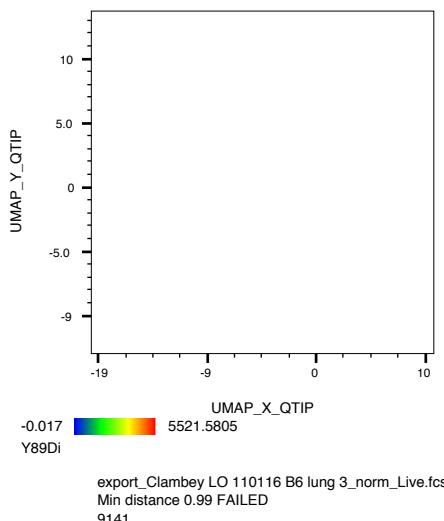
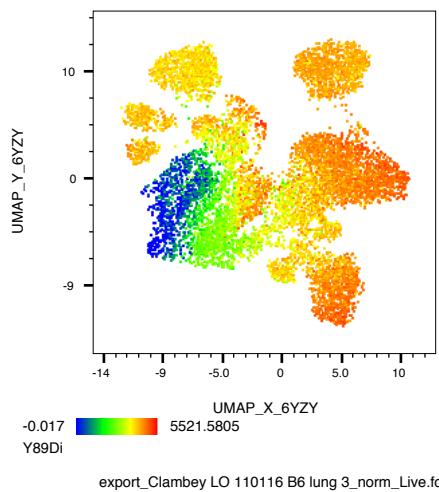
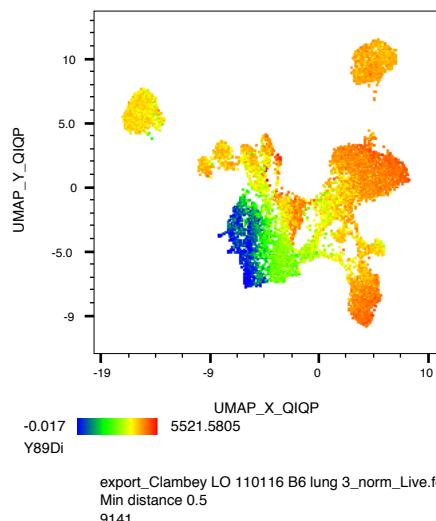
# B6 #1 UMAP iterations with various nearest neighbors #1-100

- Euclidean, neighbor #: 15 – QIQP
- Euclidean, neighbor #: 50 – FIDR
- Euclidean, neighbor #: 99 – AN6V **ERROR, FAILED**
- Euclidean, neighbor #: 0 – FUVQ **ERROR, FAILED**
- Euclidean, neighbor #: 5 – D4WN
- Euclidean, neighbor #: 1 – N3T1 **ERROR, FAILED**



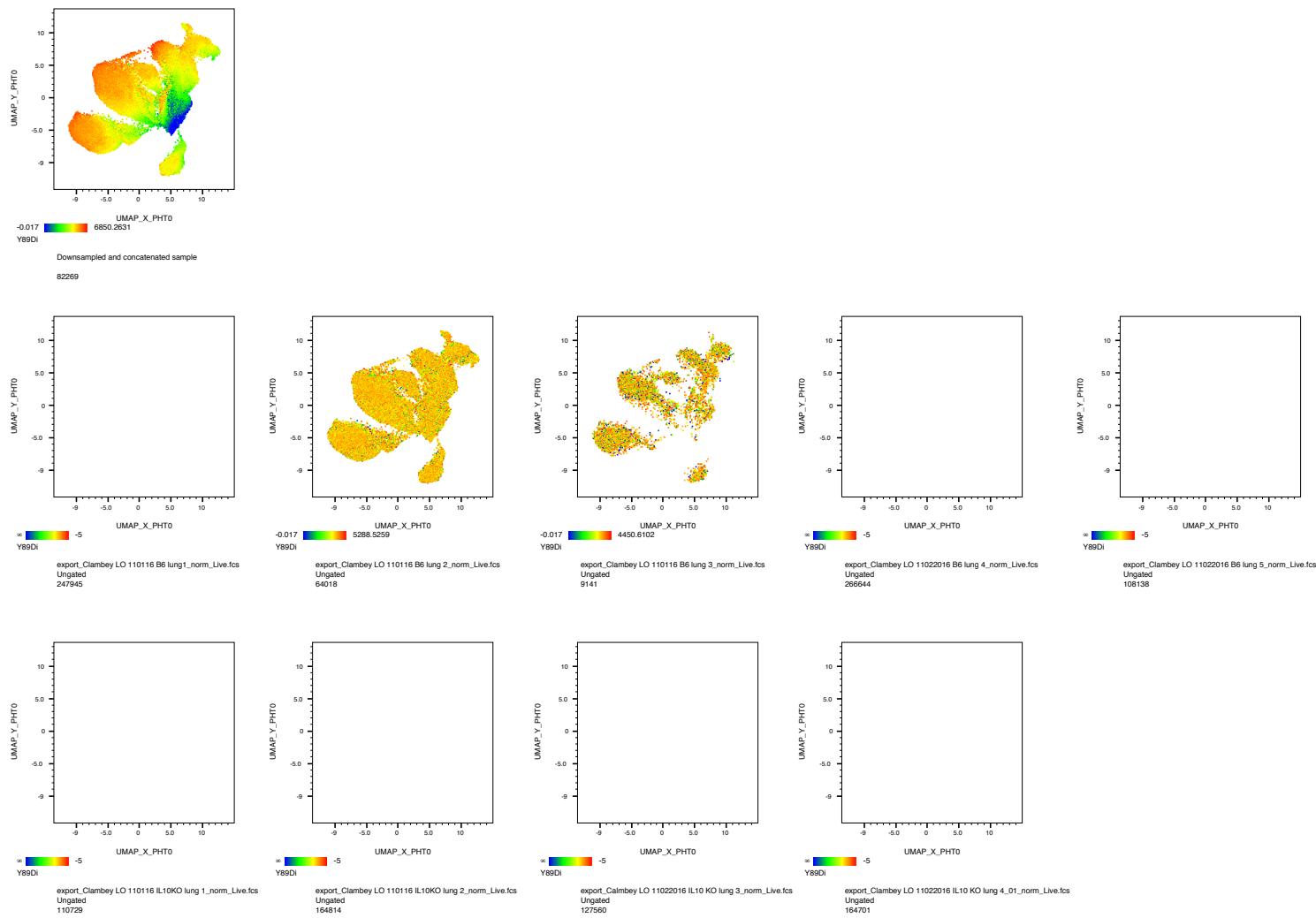
# B6 #1 UMAP iterations with various min distance value = 0.1-0.99

- Min distance = 0.5: – QIQP
- Min distance = 0.1: – 6YZY
- Min distance = 0.99: – QTIP \*ERROR\*



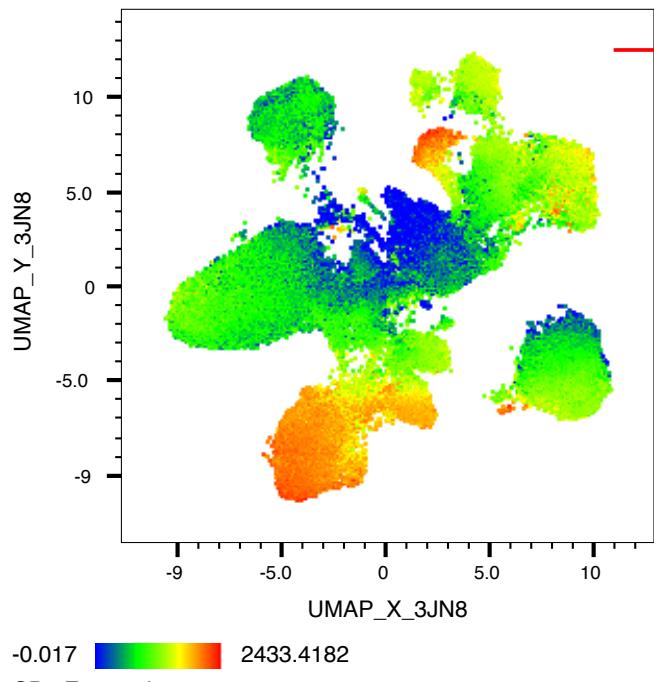
# How can you make a common UMAP plot between samples?

- I tried concatenating all of the available events (1,263,690 events total) and running a UMAP on it, but after 2 hours of crunching it froze and then crashed my computer.
- I downsampled each of the 9 files (9,141 events from each), concatenated, and then ran a UMAP analysis (82,269 events). I then applied this UMAP (PHT0) to all of the 9 samples. This only worked for samples with less than the concatenated # of events (i.e. B6 #2 & #3)

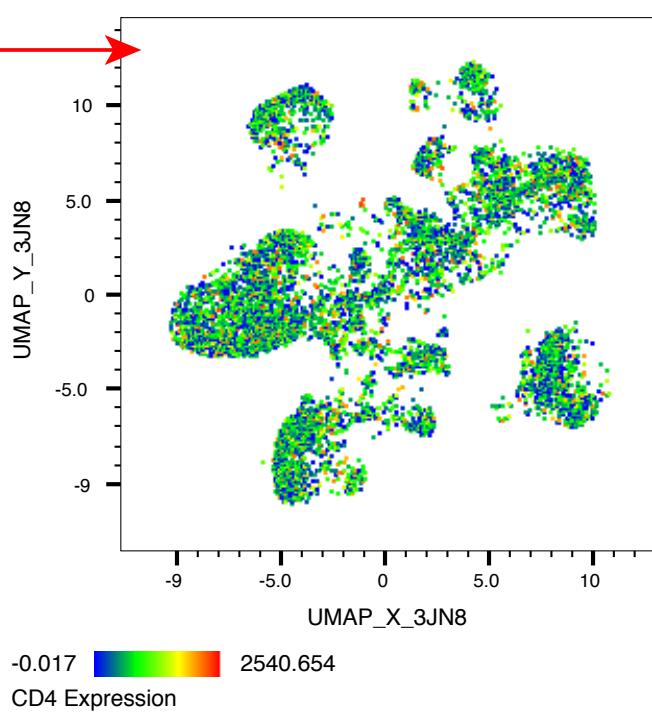


# Can you apply a UMAP generated by one sample to another sample?

UMAP Analysis 3JN8 was calculated using 64,018 events from B6 #2.  
The UMAP axes were then applied to B6 #3.



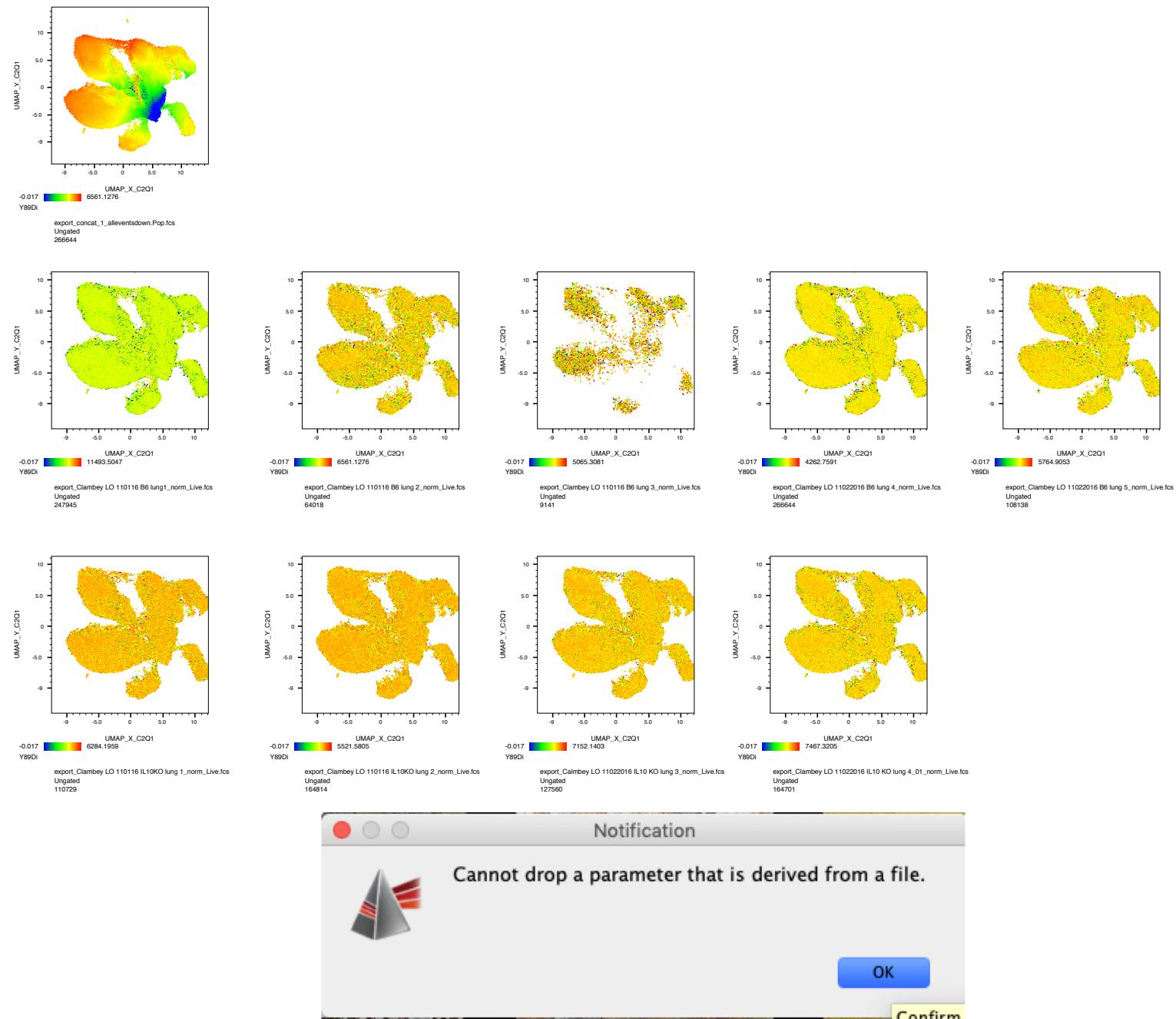
B6 #2, 64018 events



B6 #3, 9141 events

# How can you make a common UMAP plot between samples?

- I concatenated all of the available events (1,263,690 events total) and then downsampled to 266644 events (# of events that are the same as the highest sample) and then ran a UMAP and applied that UMAP to all of the files. It “worked”, but it doesn’t look right. Also note that I always get this warning, so I don’t think this is a viable option.



# Analysis Time

- Doing over 1 million events took over 2 hours and froze and ultimately crashed my computer.
- 10k events took under a minute