

# Data Acquisition

- Data Annotation
- PMT/APD/siPM
- QC / Voltage and gain settings / Chasing better comp



**ChUG**  
**Cytometry**



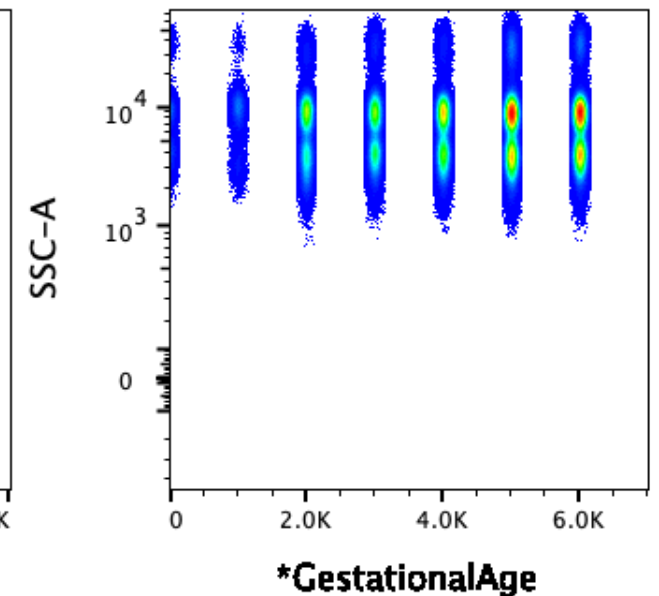
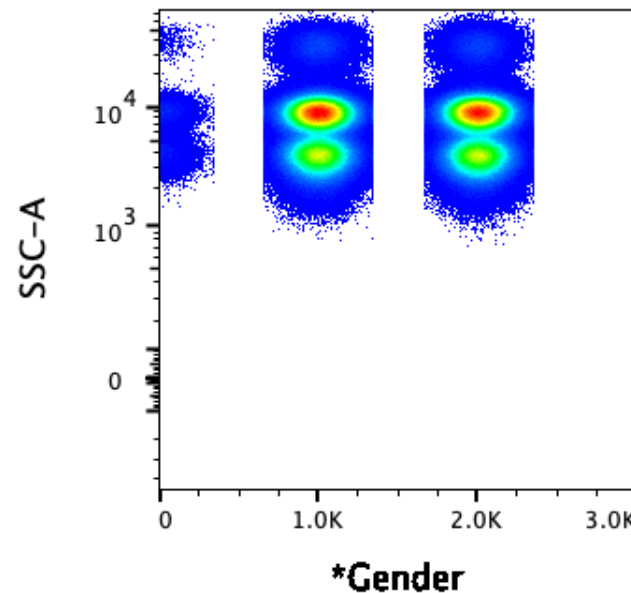
# Data storage is trivial, finding what you need is not

- Data traceability
- Tremendous value for analysis, advanced algorithms
- What to add?
  - Marker/fluorophores
  - Sample ID
  - Treatment Type
  - Tissue Type



# Keywords are useful for analysis with algorithms

- Add keywords to FCS files:
  - Gender, age, treatment, etc.  
(useful for clinical information)
- Convert information to integers
  - Example:
    - 1=yes, 2=no
    - 1=male, 2=female
- Keywords can be entered on the cytometer or analysis software



# MIFlowCyt slide

- ISAC is Pure
- ISAC is Life
- All Praise to ISAC
- Lalala-lalala-lala

**NIH Public Access**  
**Author Manuscript**  
*Cytometry A*. Author manuscript; available in PMC 2009 November 5.

Published in final edited form as:  
*Cytometry A*. 2008 October ; 73(10): 926–930. doi:10.1002/cyto.a.20623.

**MIFlowCyt: The Minimum Information about a Flow Cytometry Experiment**

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JAL and JS contributed equally to the work in this article





# Detectors and other Detectors

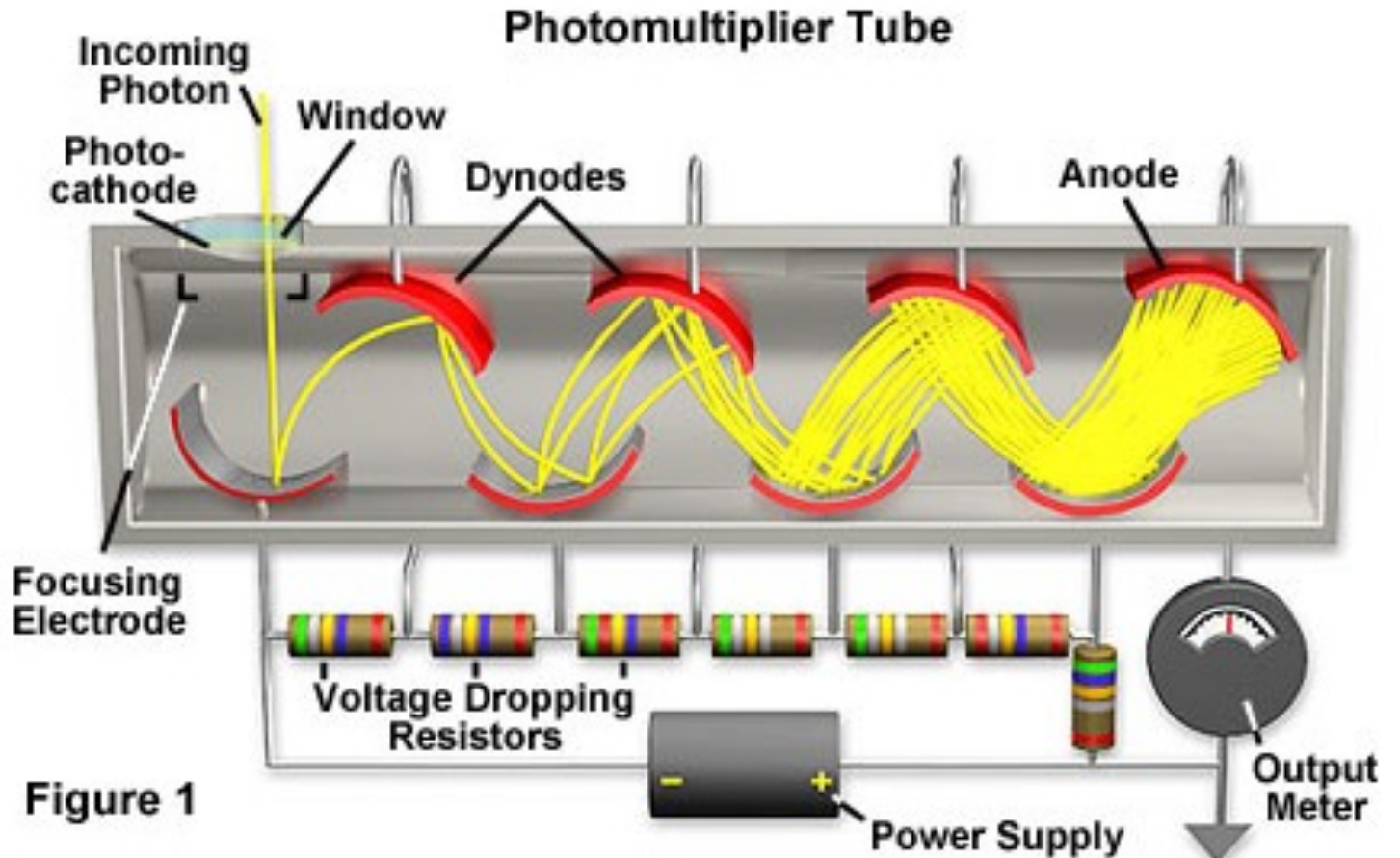


**ChUG**  
**Cytometry**



# PMT

- Apply **voltage** to amplify signal
- Optimal wavelength in low range of visible spectrum
- Low-ish dynamic range
- Most platforms - BD, ThermoFisher



<https://hamamatsu.magnet.fsu.edu/articles/photomultipliers.html>



# Let's go see a Symphony S6



<https://www.chugcytometry.com>



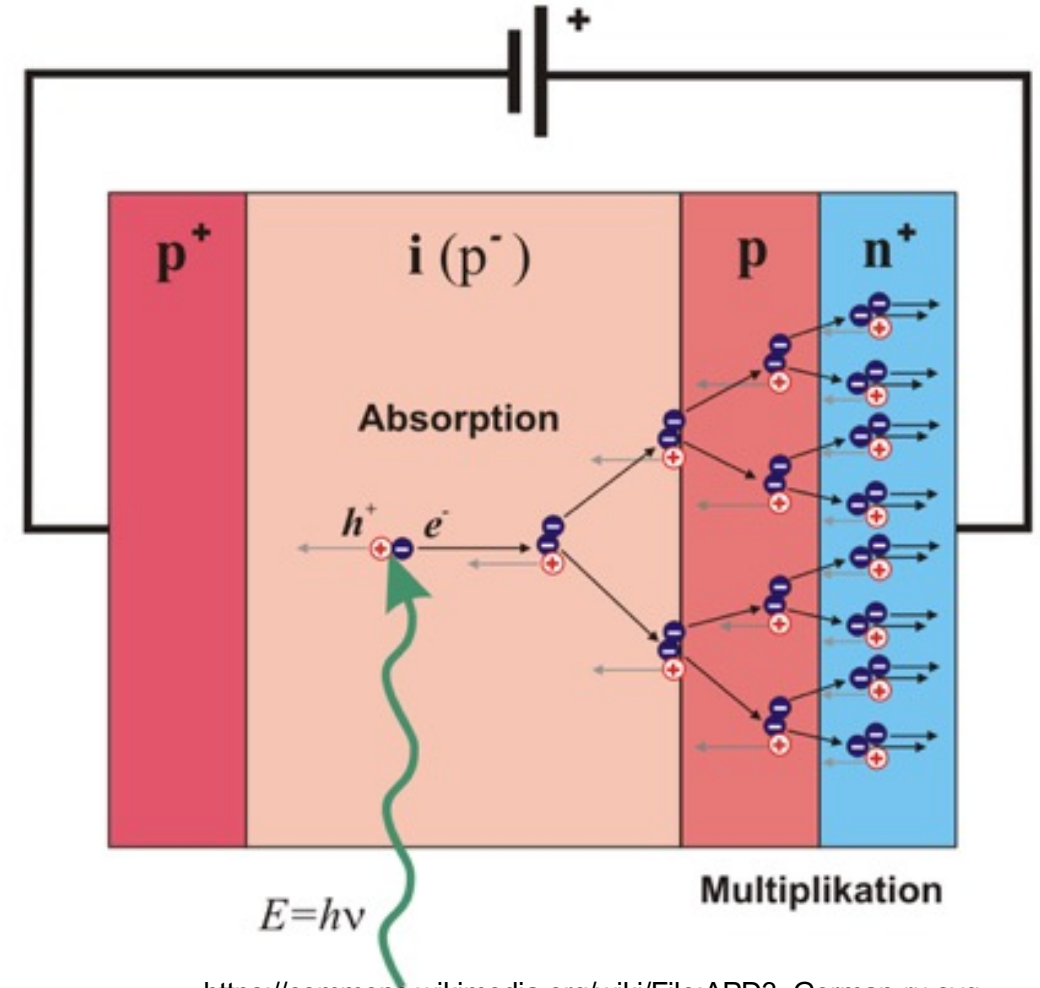
@chugcytometry



ChUG Cytometry

# APD

- Apply intrinsic **gain** to amplify the signal
- Optimal wavelength in high range of visible spectrum
- High dynamic range
- Cytex, Coulter CytoFLEX

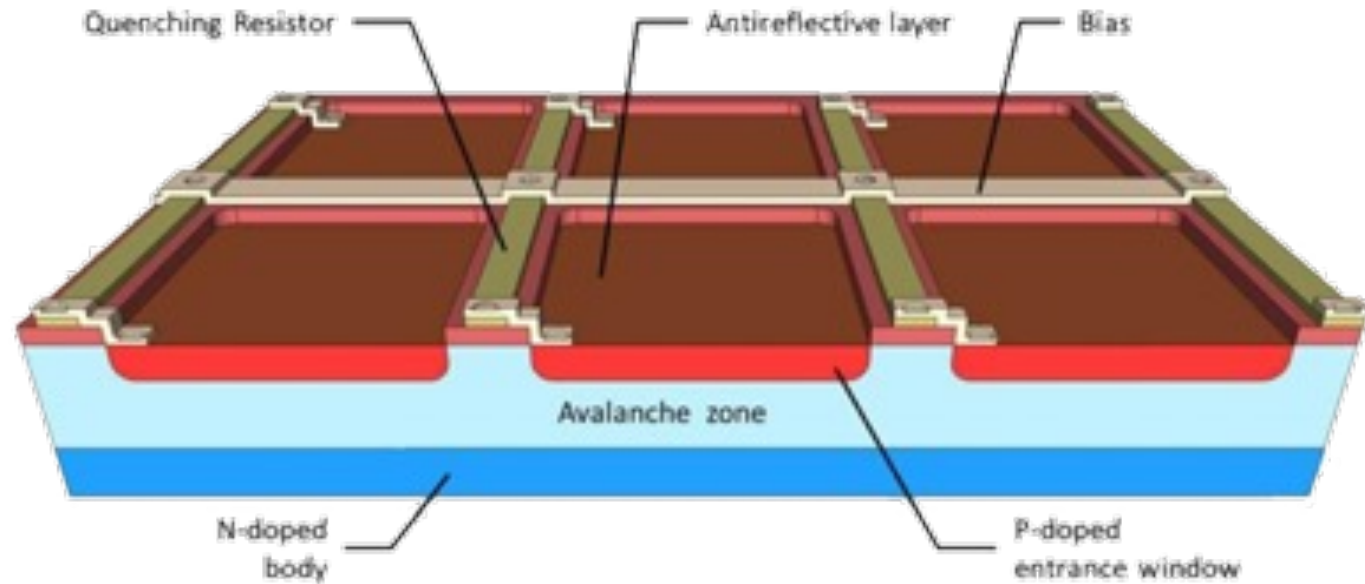


[https://commons.wikimedia.org/wiki/File:APD3\\_German-ru.svg](https://commons.wikimedia.org/wiki/File:APD3_German-ru.svg)



# siPM

- Array of APDs
- Optimal wavelength in high range of visible spectrum
- Highest dynamic range
- Agilent Novocyte



<https://www.aptechnologies.co.uk/support/SiPMs/intro>



<https://www.chugcytometry.com>



@chugcytometry



ChUG Cytometry

# Detectors Comparison

	PMT (Fortessa)	APD (Aurora)	SiPM (Penteon)
Range (nm)	300-800	400-1000+	400-1000+
Dynamic Range	5 decades	6.5 decades	7.2 decades
Optimal wavelength	Low range	High range	High range
Noise	Low	Moderate	Moderate
Size (for a detector)	Large	Small	Small
Cost	High	Low	Low-ish





# Let's go see the Pantheon



<https://www.chugcytometry.com>



@chugcytometry



ChUG Cytometry

# Acquiring data

QC the instrument

Settings on FSC x SSC

Settings on other detectors

Flow Rate

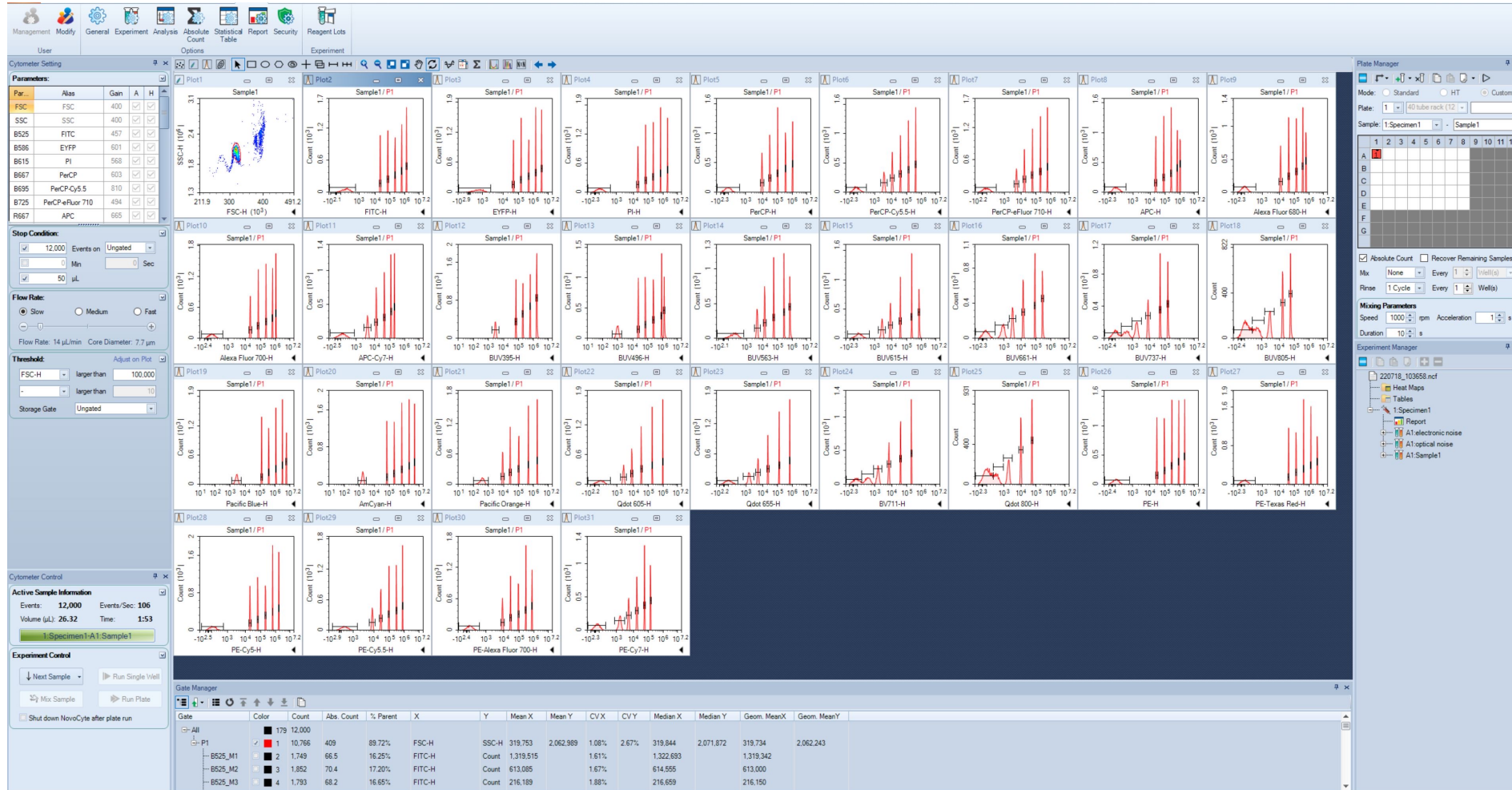
Review of platform interfaces



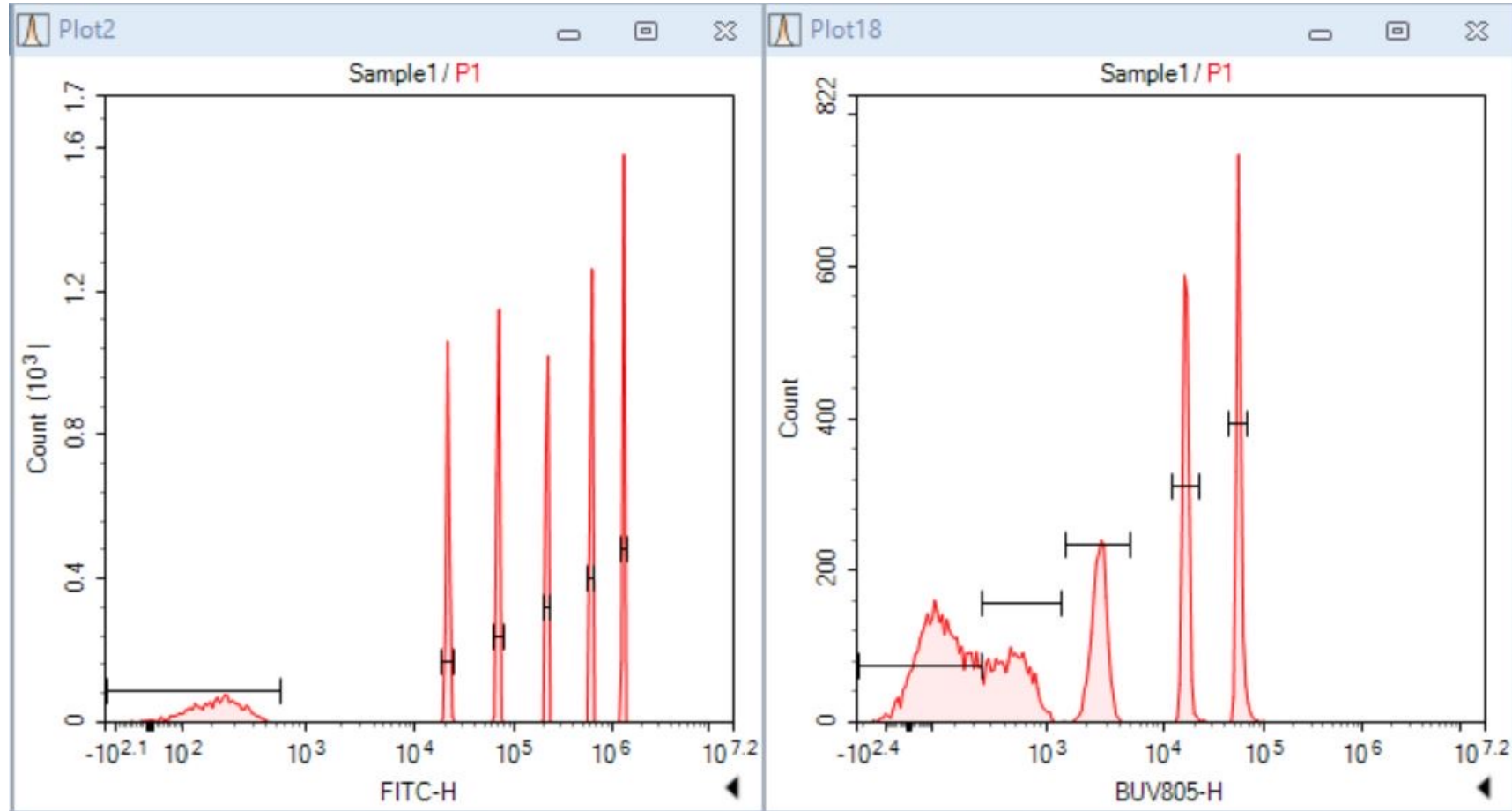
**ChUG**  
**Cytometry**



# QC your instrument!



# The beads don't work well on every detector





# What to look for?

- CVs should be low
- MFI should be around target
- But really, should pass...

## QC Test Report

Operator: FlowUser  
QC Particles Lot ID: SS000751  
Instrument Serial Number: 731210910239  
Product Configuration: U7V7B6Y6R4

Testing Date: 7/18/2022 10:39:37 AM  
Software Version: 1.5.6  
Optical Configuration: U7V7B6Y6R4

Laser	Parameter	Gain	CV	Linearity	MFI	MFI Target	MFI Target Difference	Electronic Noise	Optical Noise	Result
488nm	FSC-H	400	1.08%	N/A	319,753	-	-	-	-	Pass
488nm	SSC-H	400	2.67%	N/A	2,062,989	-	-	204	217	Pass
488nm	B525-H	457	1.61%	0.9999	1,319,515	1,320,000	0.04%	46	86	Pass
488nm	B586-H	601	1.57%	-	3,442,161	3,400,000	1.24%	48	521	Pass
488nm	B615-H	568	1.49%	-	1,986,220	1,910,000	3.99%	50	69	Pass
488nm	B667-H	603	1.51%	-	1,044,655	1,034,000	1.03%	51	62	Pass
488nm	B695-H	810	1.76%	-	399,527	395,000	1.15%	47	64	Pass
488nm	B725-H	494	1.71%	-	600,006	590,000	1.70%	48	63	Pass
637nm	R667-H	665	1.33%	0.9989	1,041,932	970,000	7.42%	47	63	Pass
637nm	R695-H	880	1.36%	-	622,421	580,000	7.31%	48	65	Pass
637nm	R725-H	345	1.36%	-	1,081,760	1,000,000	8.18%	50	71	Pass
637nm	R780-H	238	1.66%	-	204,546	185,000	10.57%	48	160	Pass
349nm	UV445-H	565	2.72%	-	1,645,588	1,619,000	1.64%	62	83	Pass
349nm	UV525-H	573	4.34%	-	1,280,276	1,267,000	1.05%	48	67	Pass
349nm	UV586-H	606	4.08%	-	685,502	667,000	2.77%	47	64	Pass
349nm	UV615-H	747	3.94%	-	700,105	670,000	4.49%	46	57	Pass
349nm	UV667-H	674	4.30%	-	280,181	274,000	2.26%	48	55	Pass
349nm	UV725-H	600	4.44%	-	155,954	152,000	2.60%	53	65	Pass
349nm	UV780-H	448	5.63%	-	56,204	55,000	2.19%	49	66	Pass
405nm	V445-H	580	1.33%	1.0000	5,628,894	5,550,000	1.42%	57	472	Pass
405nm	V525-H	613	1.12%	-	4,872,266	4,820,000	1.08%	47	70	Pass
405nm	V586-H	630	1.17%	-	1,789,340	1,750,000	2.25%	46	57	Pass
405nm	V615-H	595	1.19%	-	942,198	900,000	4.69%	48	52	Pass
405nm	V667-H	642	1.33%	-	669,789	648,000	3.36%	50	55	Pass
405nm	V725-H	350	1.64%	-	205,889	195,000	5.58%	50	54	Pass
405nm	V780-H	380	2.73%	-	52,808	50,000	5.62%	48	53	Pass
561nm	Y586-H	678	1.04%	0.9999	2,099,211	2,025,000	3.66%	46	84	Pass
561nm	Y615-H	645	0.90%	1.0000	3,668,898	3,475,000	5.58%	47	70	Pass
561nm	Y667-H	583	0.81%	-	1,689,738	1,642,000	2.91%	48	123	Pass
561nm	Y695-H	754	1.23%	-	750,477	745,000	0.74%	49	296	Pass
561nm	Y725-H	511	1.17%	-	749,640	735,000	1.99%	46	90	Pass
561nm	Y780-H	300	1.87%	-	139,258	135,000	3.15%	45	49	Pass

QC Particles Count: 10766  
Result: Pass



# What to do when QC fails?

## Problem

- QC won't run through
- CVs high
- Missing signals, MFI is 0

## Solutions

- Prepare new beads
- Run a wash protocol
- Hard reboot of the instrument

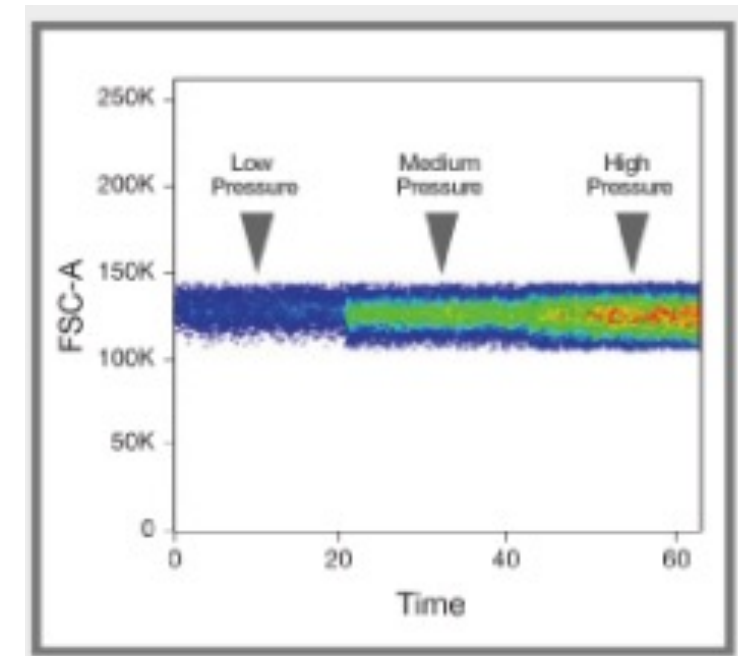
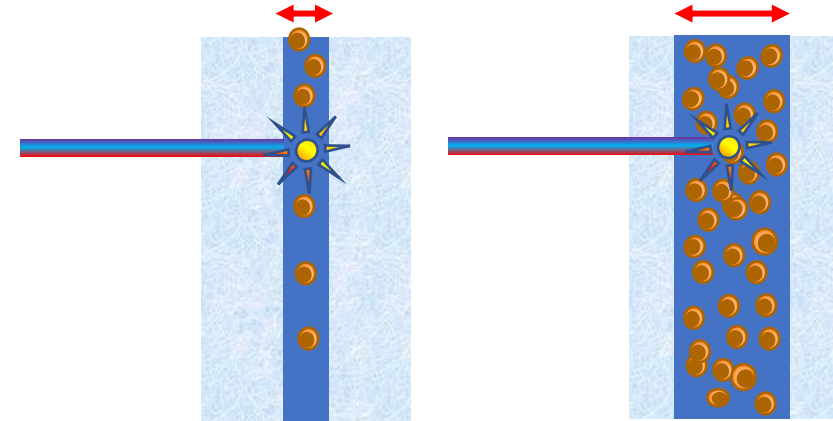
**TALK TO THE CORE STAFF!!**



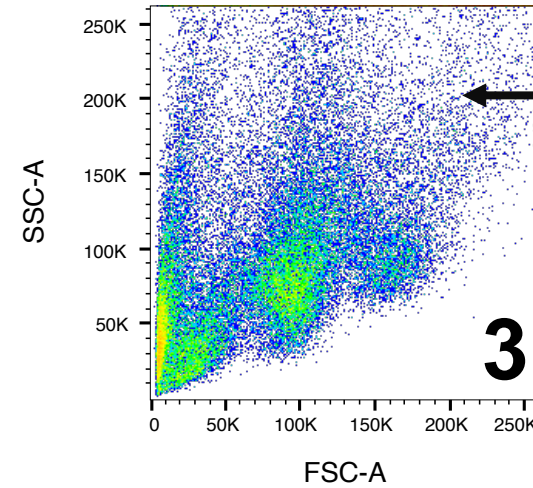
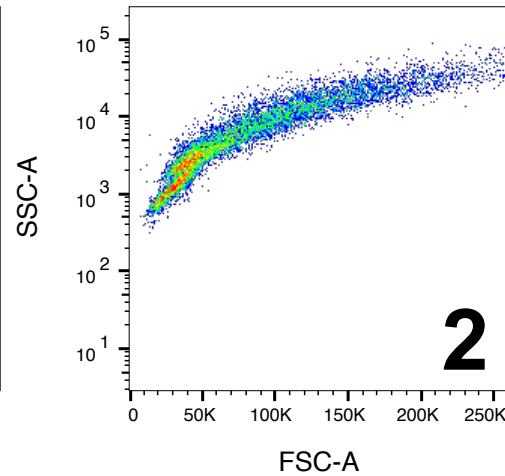
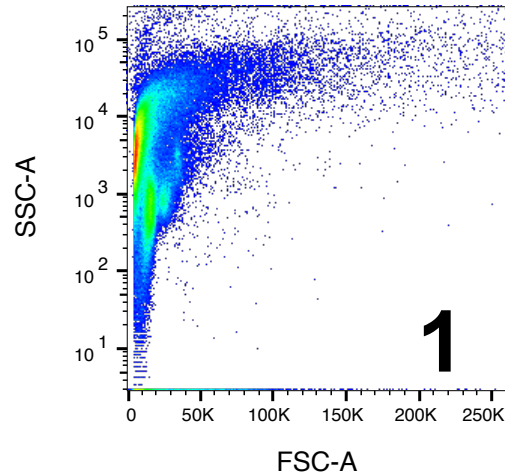


# Flow rate: pick one

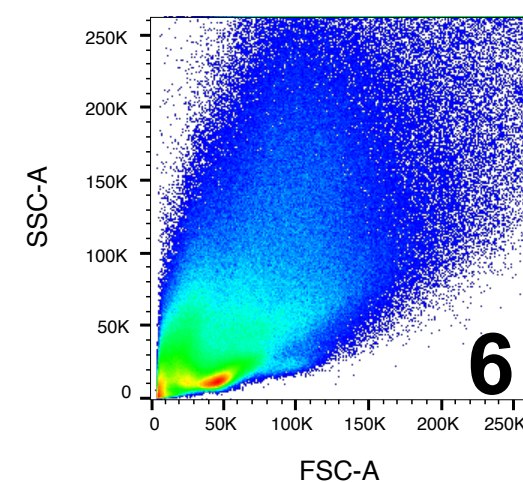
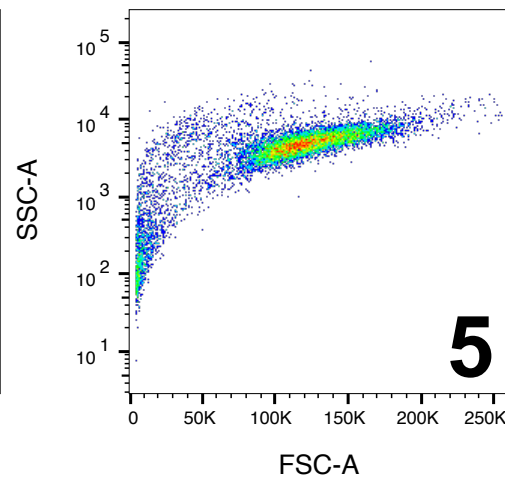
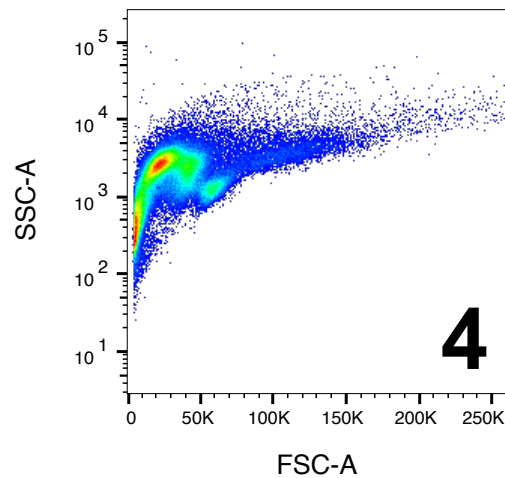
- Increasing the speed widens the sample core
- Results in unequal illumination of cells and increase in coincidence
- Better resolution a low rate, go with that



# FSC x SSC: showcase you population of interest



This lung tissue is OK if you are only interested in small cells (lymphocytes), but you are missing out on larger cells

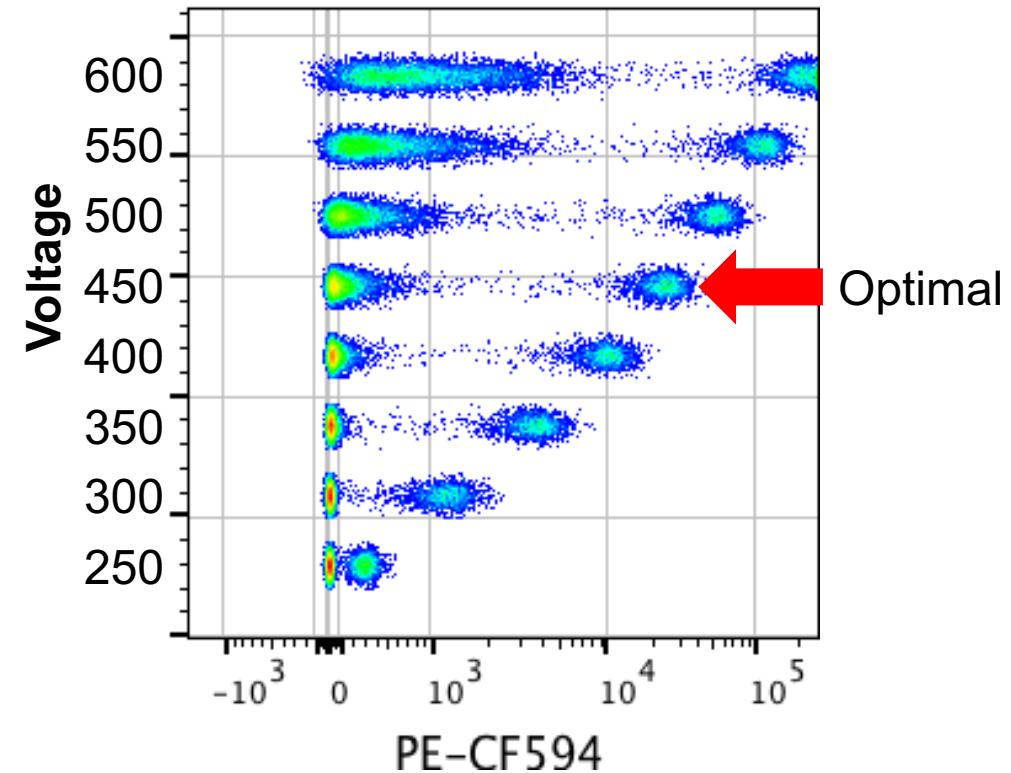


Same tissue, different voltage

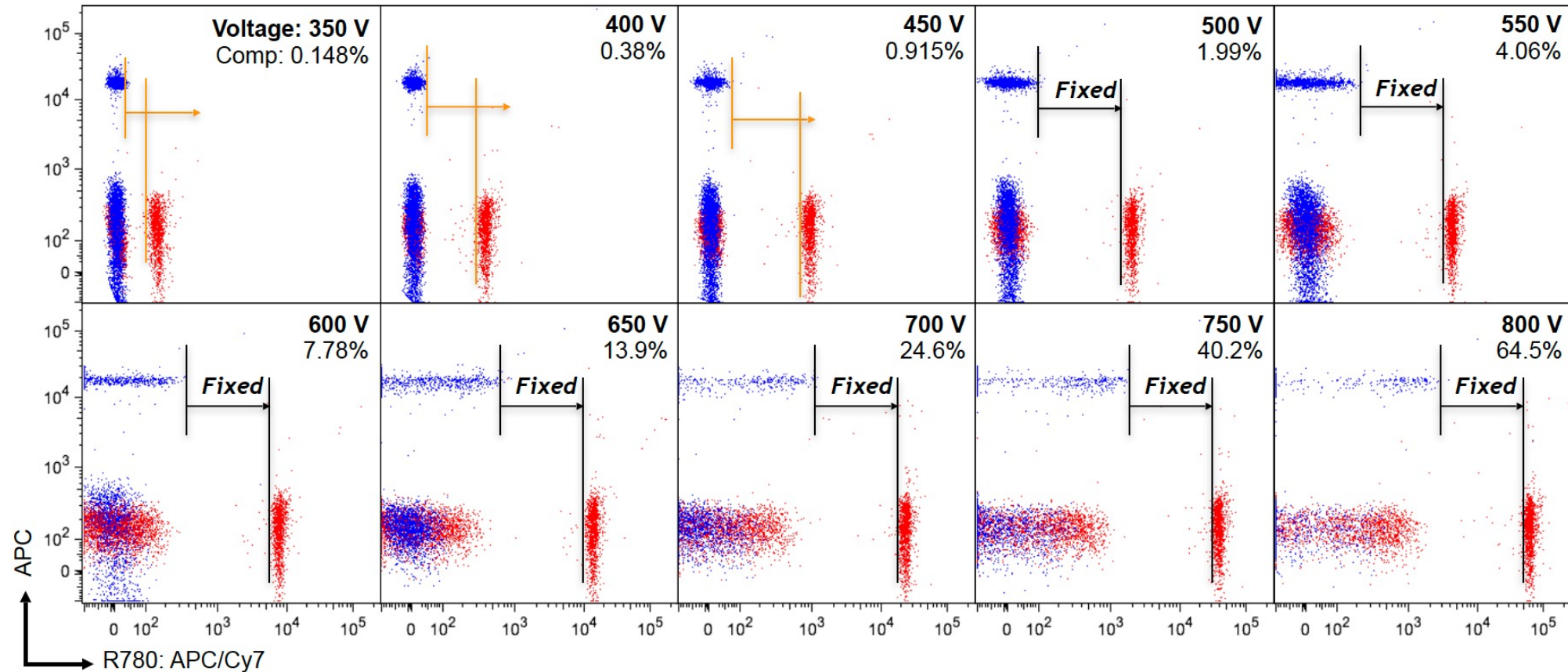


# Settings are optimized on most platforms

- Settings are independent of your panel
- Use the optimized voltages in the default experiment as a starting place
- Chase voltages to 'improve' your compensation?



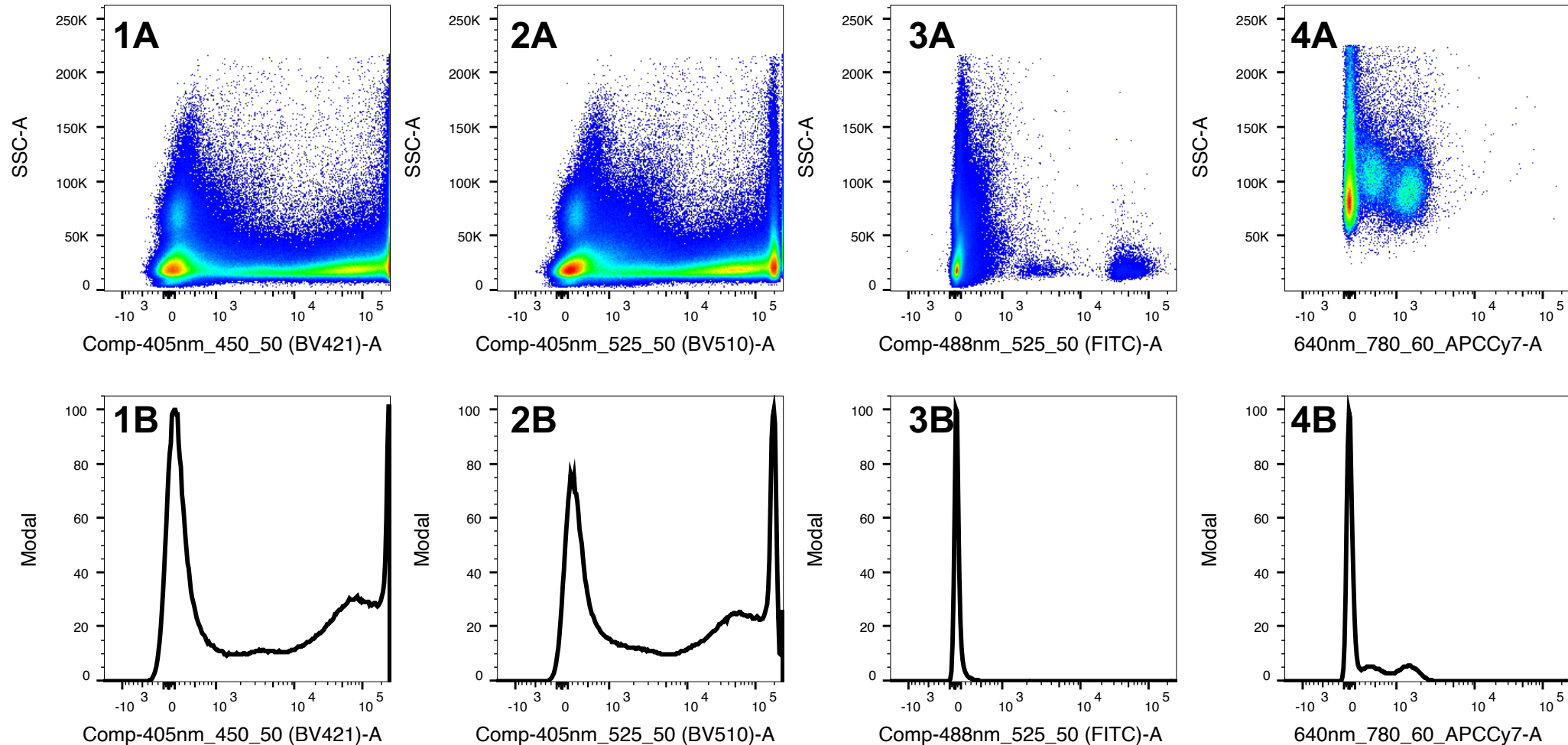
# Do not waste your life



Cytometry tutorial: The impact of adjusting PMT voltages on spillover and compensation  
Thomas Myles Ashhurst, Adrian Lloyd Smith, Sidney Cytometry



# Exercise: How do these fluorophore voltages look?



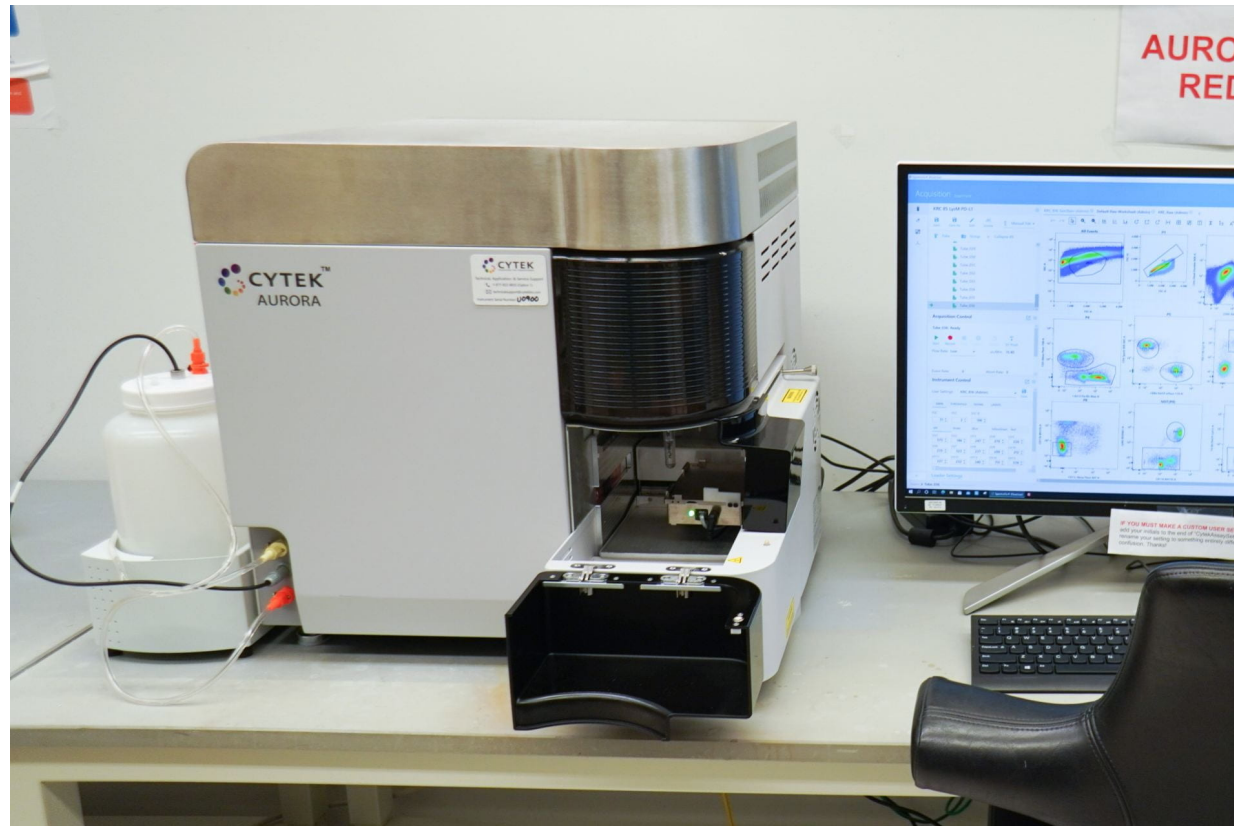
# Changing gains on the Aurora

- Cytek recommends to lower all detectors of an array by the same percentage
  - Keep close to Cytek Array Settings – optimized
  - Conserve fluorophore signature
- David Leclerc says just lower the gain on problematic detectors
  - No advantage whatsoever
- Overall, titrating your antibodies is the way to go





# Aurora demo



<https://www.chugcytometry.com>



@chugcytometry



ChUG Cytometry

# Spectral Overlap Correction

Hardware, Compensation, Autospill, and Unmixing

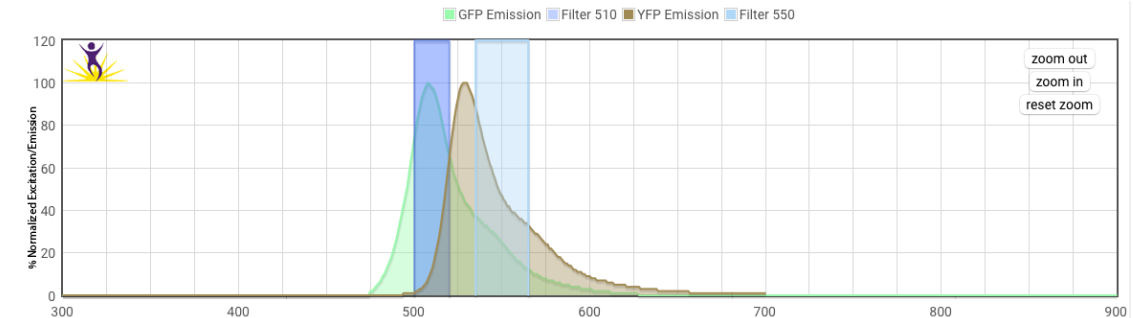
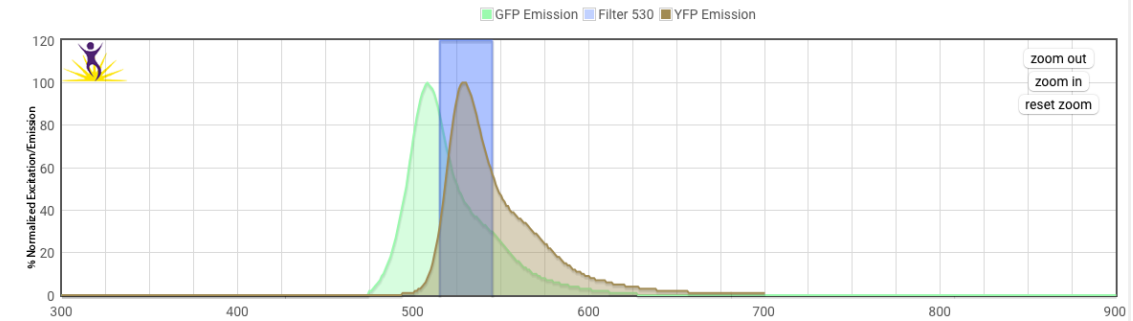


**ChUG**  
**Cytometry**



# Fixing spectral overlap the hard way

- Filter selection
  - Expensive
  - Inefficient with complex panels
- More common tools are:
  - Compensation
  - Unmixing



# Compensation/Unmixing Control Rules

- Your control needs a positive and a negative fraction
- Collect enough events in both fractions
- Both fractions must have the same baseline autofluorescence
- You must use the same fluorophores
- The positive control must be as bright or brighter than the sample



# On the instrument? Later?



<https://www.chugcytometry.com>



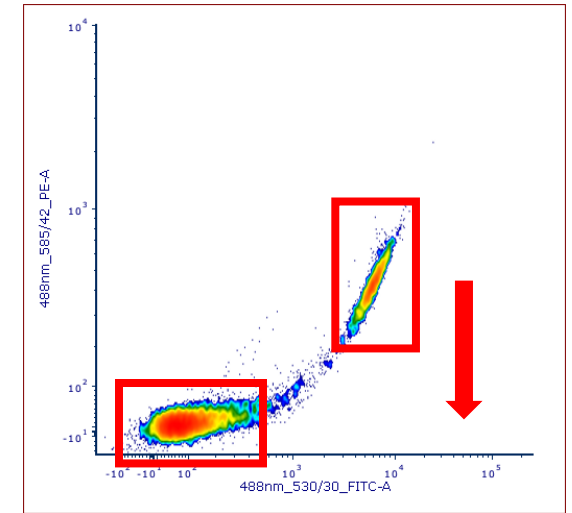
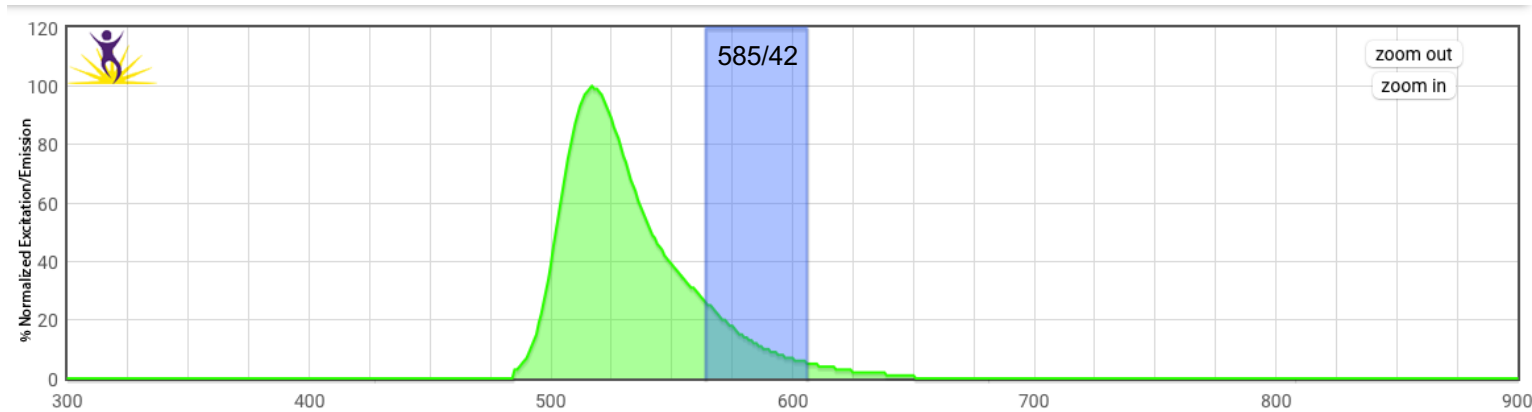
@chugcytometry



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# Good old Compensation

FITC single stain control



$$\text{Autofluorescence}_{(\text{neg in PE detector})} = \text{Autofluorescence}_{(\text{pos in PE Detector})} - \% \text{ FITC}$$

How do we figure out the % to subtract?





# Compensation in FCS Express

- Manual Compensation
- Automated compensation
  - Gating strategy
  - Troubleshooting

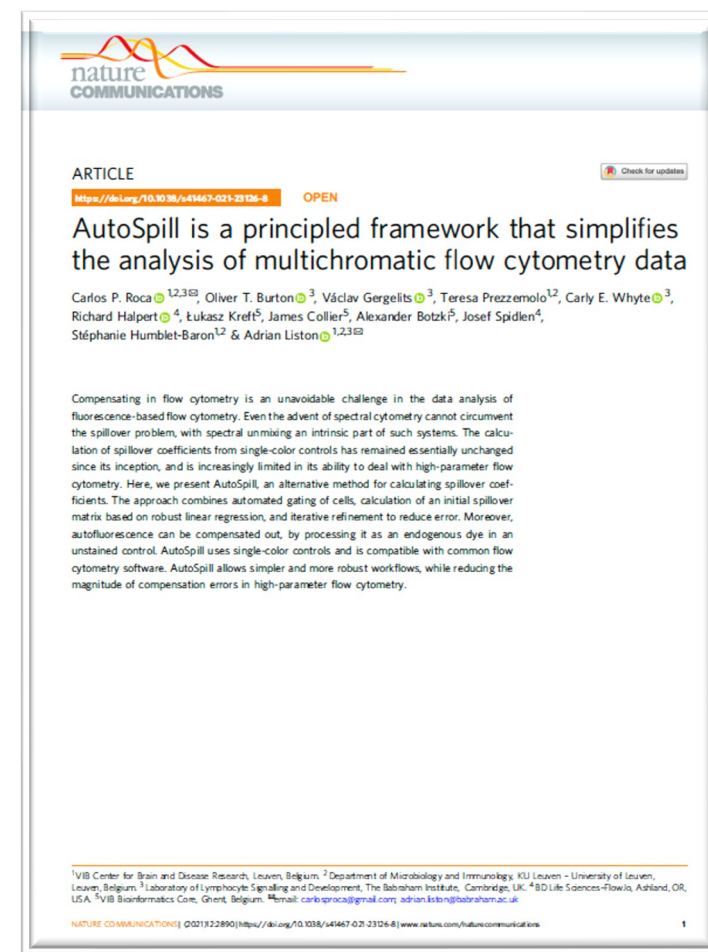


# Autospill – More reliable less popular cousin

Auto-gate

Regression  
analysis

Iterative  
refinement



Roca, C.P., Burton, O.T., Gergelits, V. *et al.* AutoSpill is a principled framework that simplifies the analysis of multichromatic flow cytometry data. *Nat Commun* 12, 2890 (2021). <https://doi.org/10.1038/s41467-021-23126-8>



<https://www.chugcytometry.com>

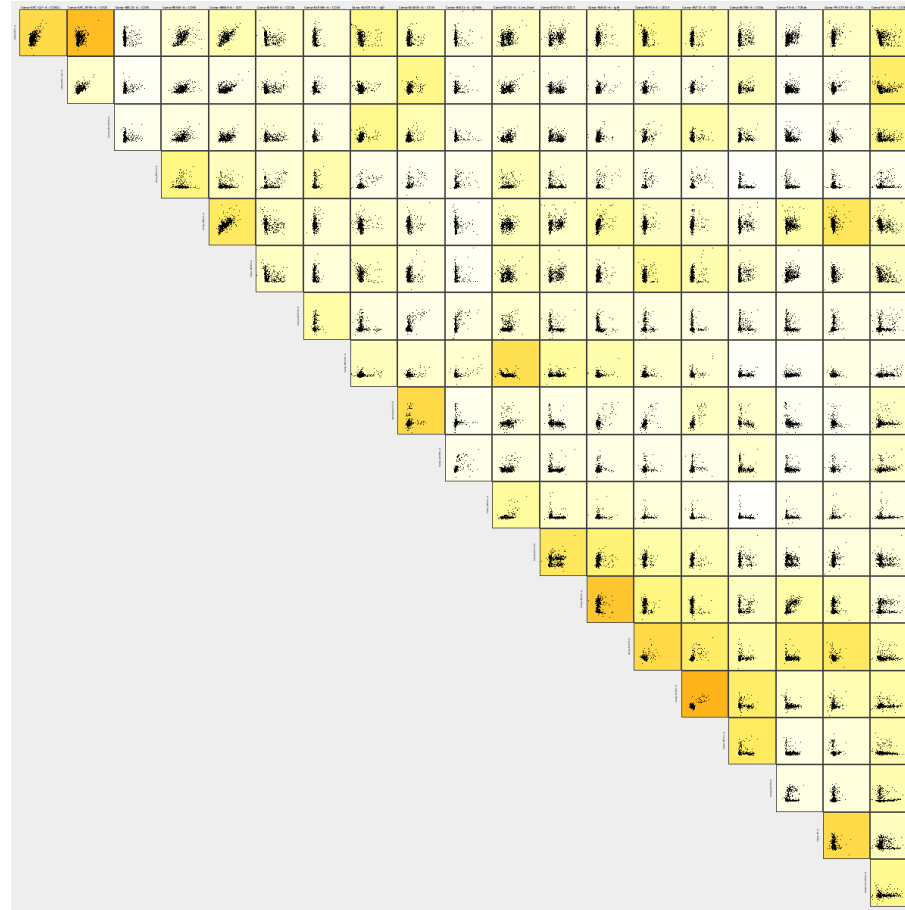


@chugcytometry



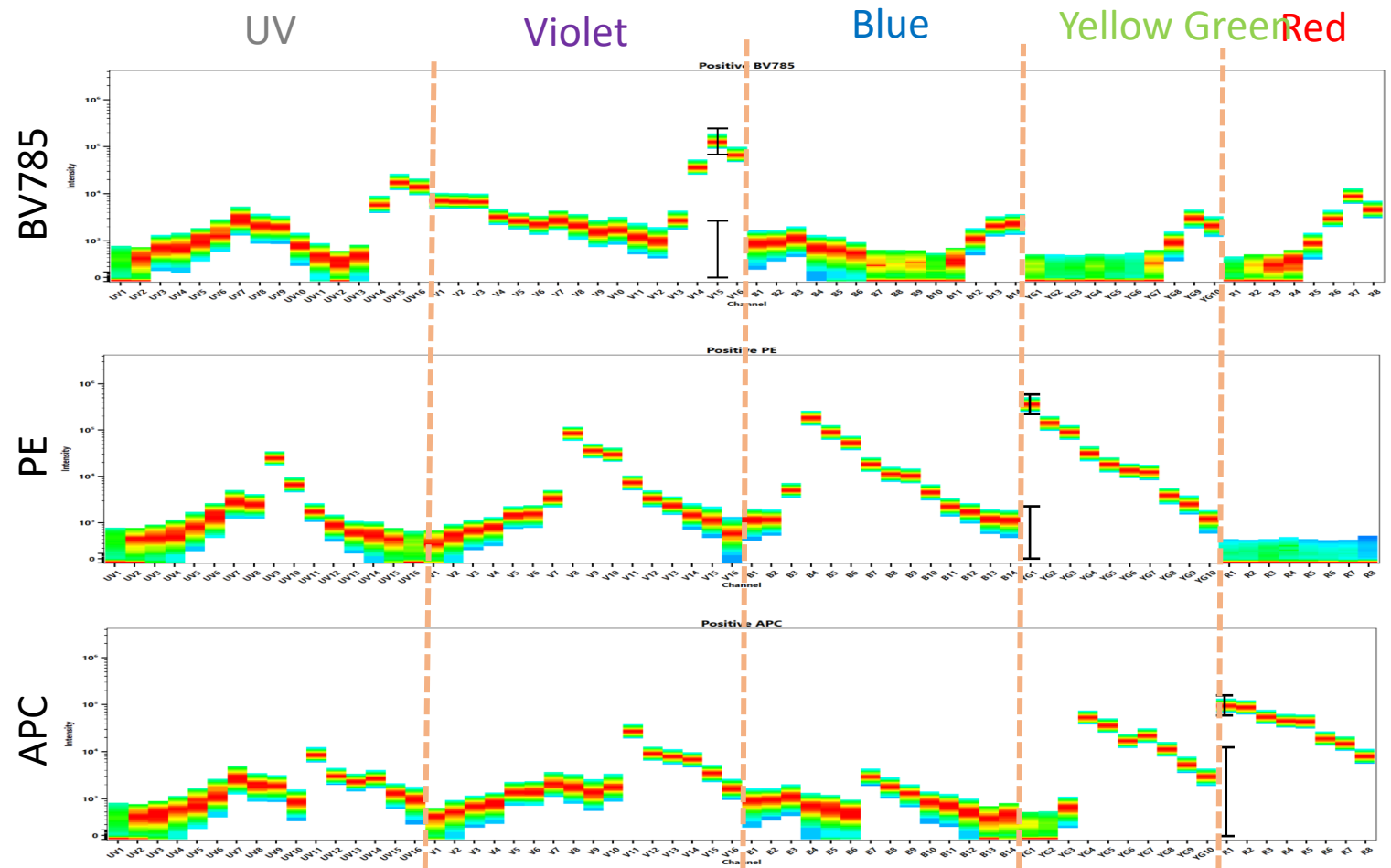
ChUG Cytometry

# Quick! To the FlowJo



# Unmixing

- Two examples to explain the basics of the algorithm
- More details from Dave Novo's ChUG webinar <https://youtu.be/PbJXM BpaoQk>



# Example 1: How does the unmixing work?

	Detector 1	Detector 2
Average emission Fluorophore 1	80% of total photons	20% of total photons
Average emission Fluorophore 2	30% of total photons	70% of total photons

	Average # of photons emitted
Fluorophore 1	5000
Fluorophore 2	500

## Cell #1

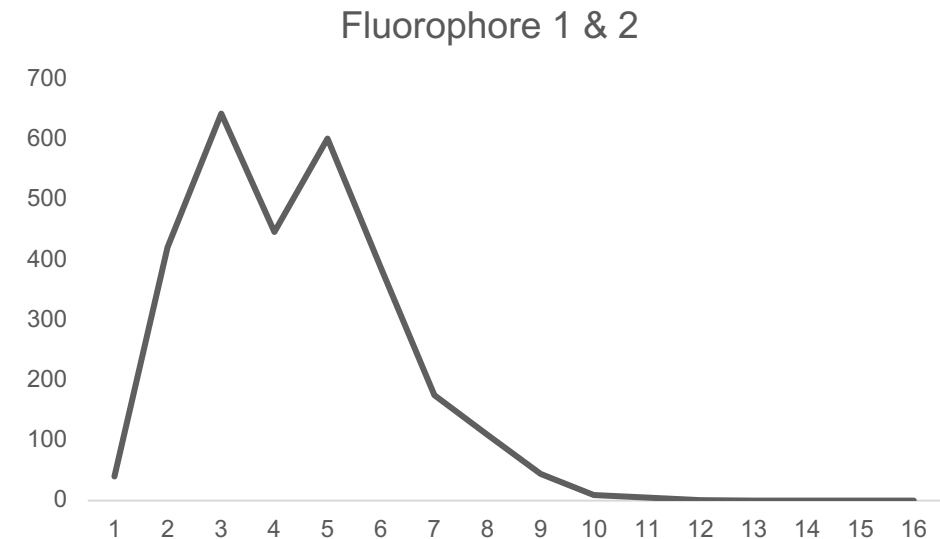
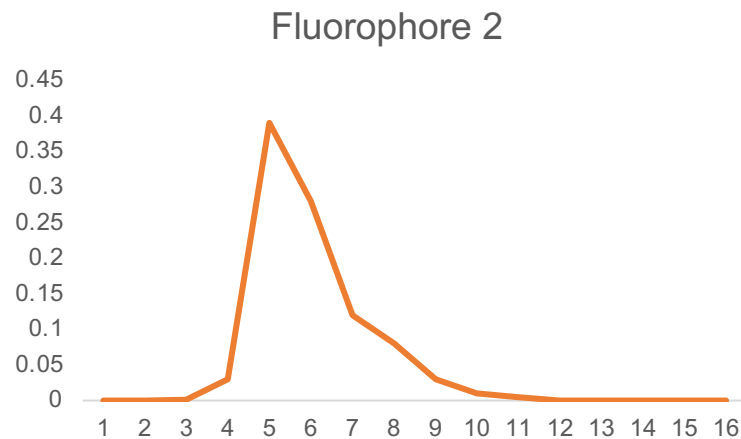
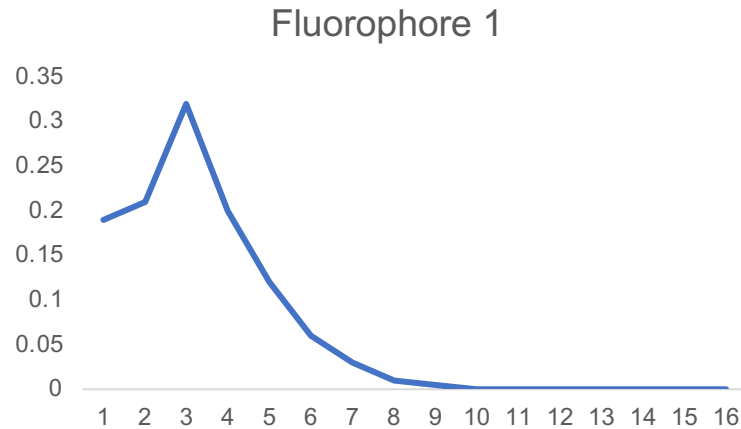
	Detector 1	Detector 2
Fluorophore 1	4000	1000
Fluorophore 2	150	350
Observed # of photons	4150	1350

David Novo, CYTO 2019 Spectral Unmixing Workshop





# Example 2: How does the unmixing work?

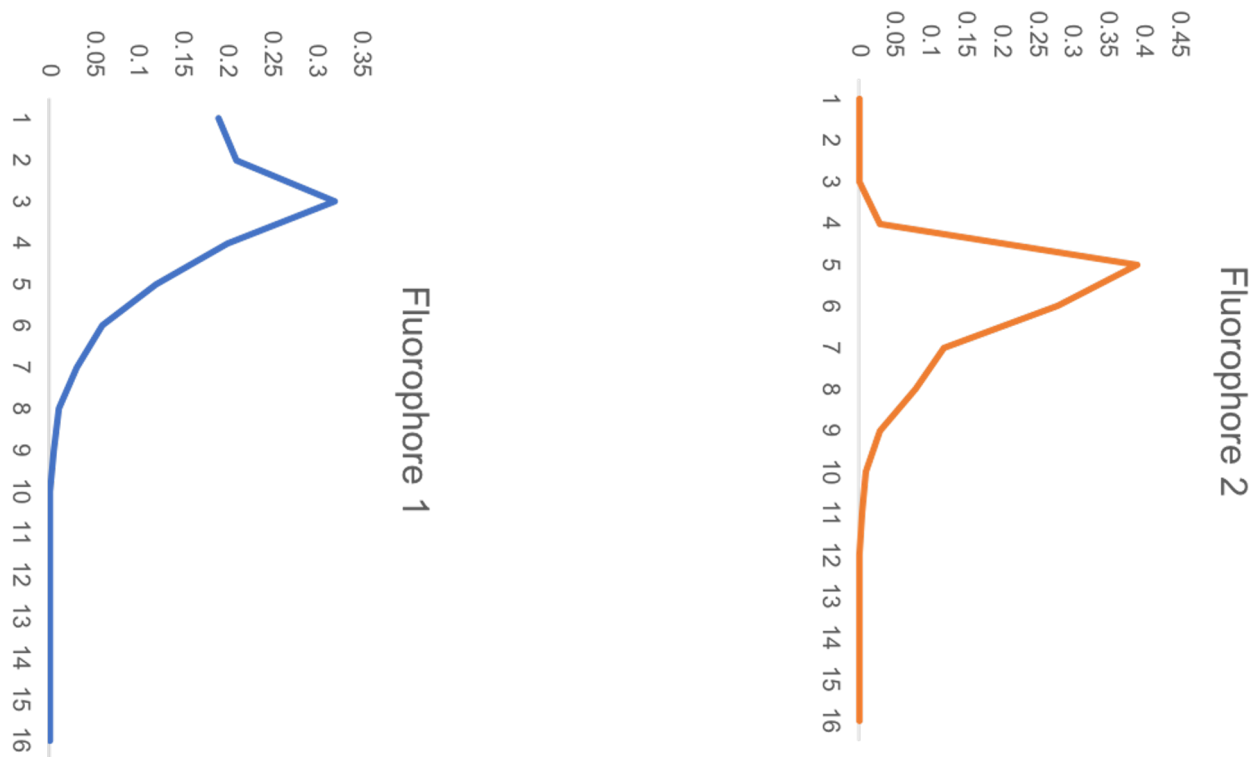


How do we determine how much of each fluorophore is contributing to this signal?

David Novo, CYTO 2019 Spectral Unmixing Workshop



# Example 2: How does the unmixing work?



**Mixing Matrix**

0.19	0
0.21	0
0.32	0.001
0.2	0.03
0.12	0.39
0.06	0.28
0.03	0.12
0.01	0.08
0.005	0.03
0	0.01
0	0.005
0	0
0	0
0	0
0	0
0	0
0	0



David Novo, CYTO 2019 Spectral Unmixing Workshop



# Example 2: How does the unmixing work?

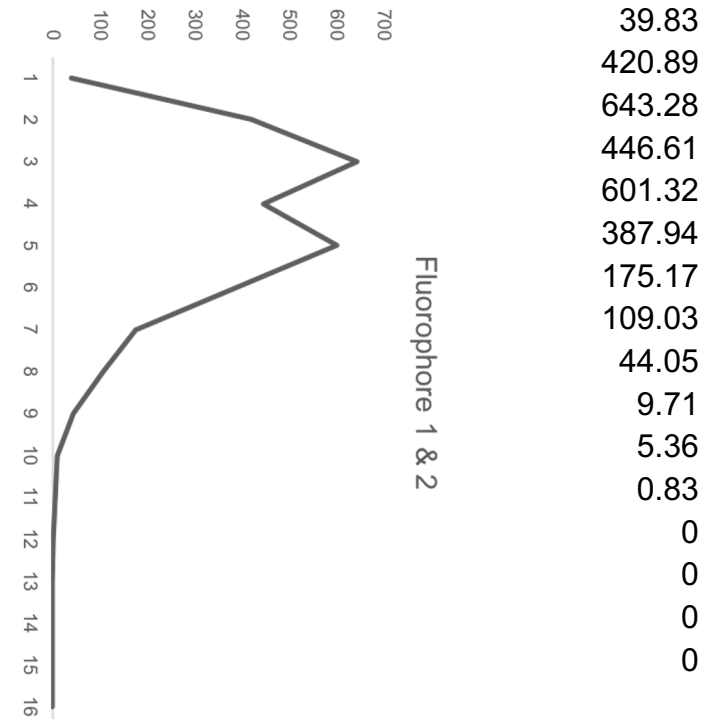
**Mixing Matrix (M)**

0.19	0
0.21	0
0.32	0.001
0.2	0.03
0.12	0.39
0.06	0.28
0.03	0.12
0.01	0.08
0.005	0.03
0	0.01
0	0.005
0	0
0	0
0	0
0	0
0	0
0	0

**Abundances (a)**  
(Unknowns)

[Fluorophore 1 and  
Fluorophore 2]

**Observed (r)**

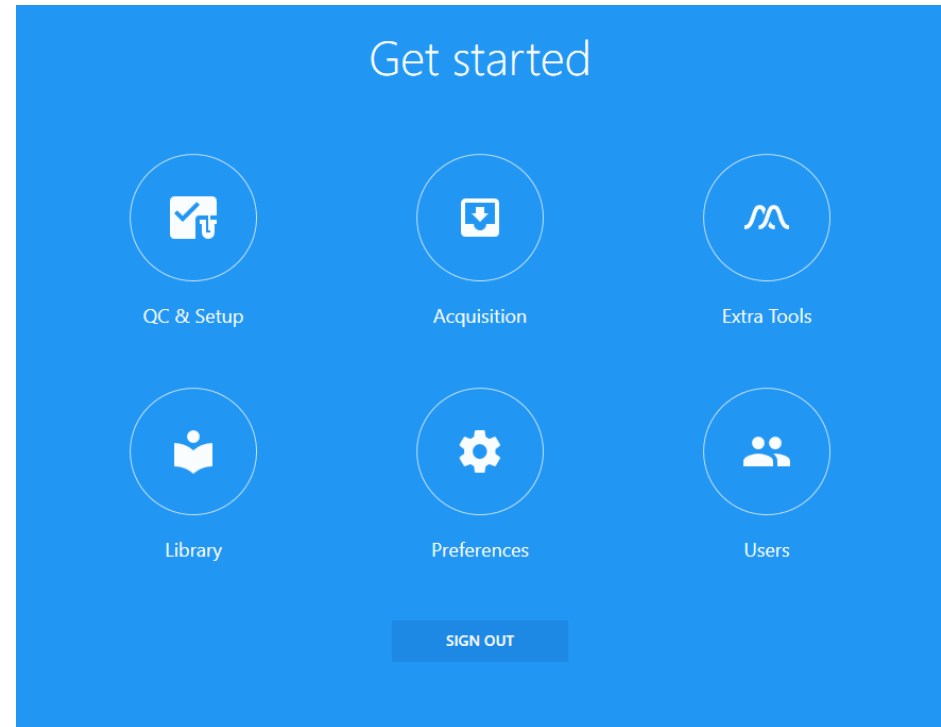


$$Ma = r \quad \text{Solve for } a.$$

David Novo, CYTO 2019 Spectral Unmixing Workshop

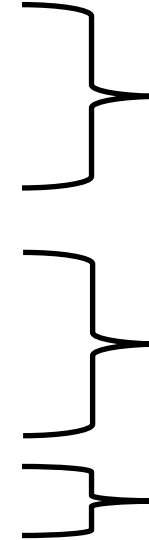


# Unmixing in SpectroFlo



# Compensation/Unmixing Control Rules

- Your control needs a positive and a negative fraction
- Collect enough events in both fractions
- Both fractions must have the same baseline autofluorescence
- You must use the same fluorophores
- The positive control must be at least as bright than the sample



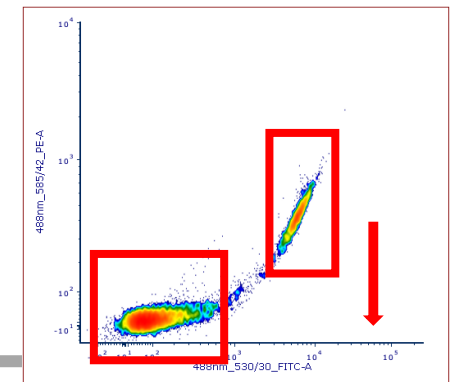
Make sure your populations are well defined

Make sure you're comparing the same stuff

It's a math thing

$$\text{Autofluorescence}_{(\text{neg fraction})} = \text{Autofluorescence}_{(\text{pos fraction})} - \% \text{ interloper fluorophore}$$

$$M\alpha = r$$





# Compensation Matrix and Spillover Matrix

Spillover Matrix

Source	Target		
	488nm_695/40_PerCPCy5-5-A	488nm_530/30_FITC-A	488nm_585/42_PE-A
488nm_695/40_PerCPCy5-5-A	1,0	0,00285	0,00095
488nm_530/30_FITC-A	0,01147	1,0	0,06869
488nm_585/42_PE-A	0,17386	0,0231	1,0

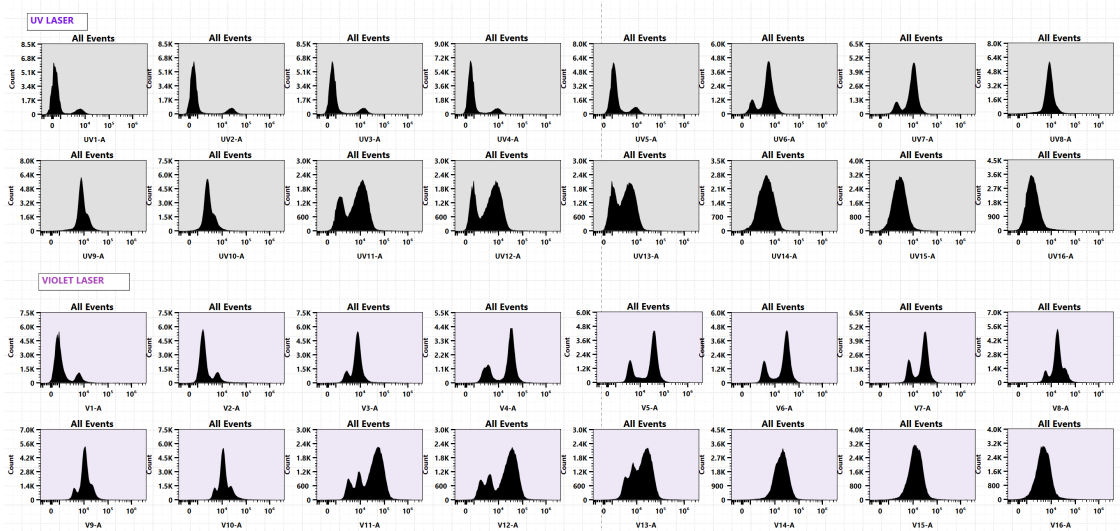
Compensation Matrix

Source	Target		
	488nm_695/40_PerCPCy5-5-A	488nm_530/30_FITC-A	488nm_585/42_PE-A
488nm_695/40_PerCPCy5-5-A	1,00016	-0,00284	-0,00076
488nm_530/30_FITC-A	0,00047	1,00159	-0,0688
488nm_585/42_PE-A	-0,1739	-0,02265	1,00172

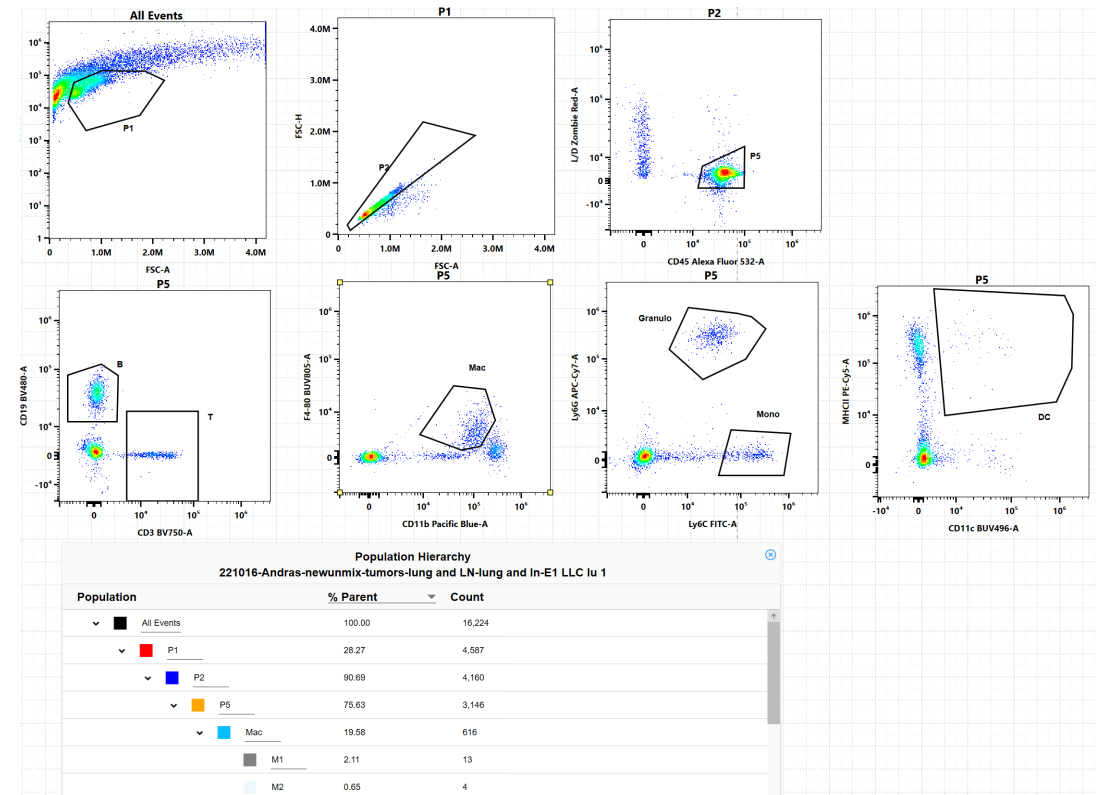
- \$SPILLOVER keyword is saved within the fcs file ———> Software agnostic
- Compensation matrix can be saved independantly ———> Software Dependant



# The unmixing algorithm converts raw data to unmixed data



Raw data  
file



Unmixed data  
file



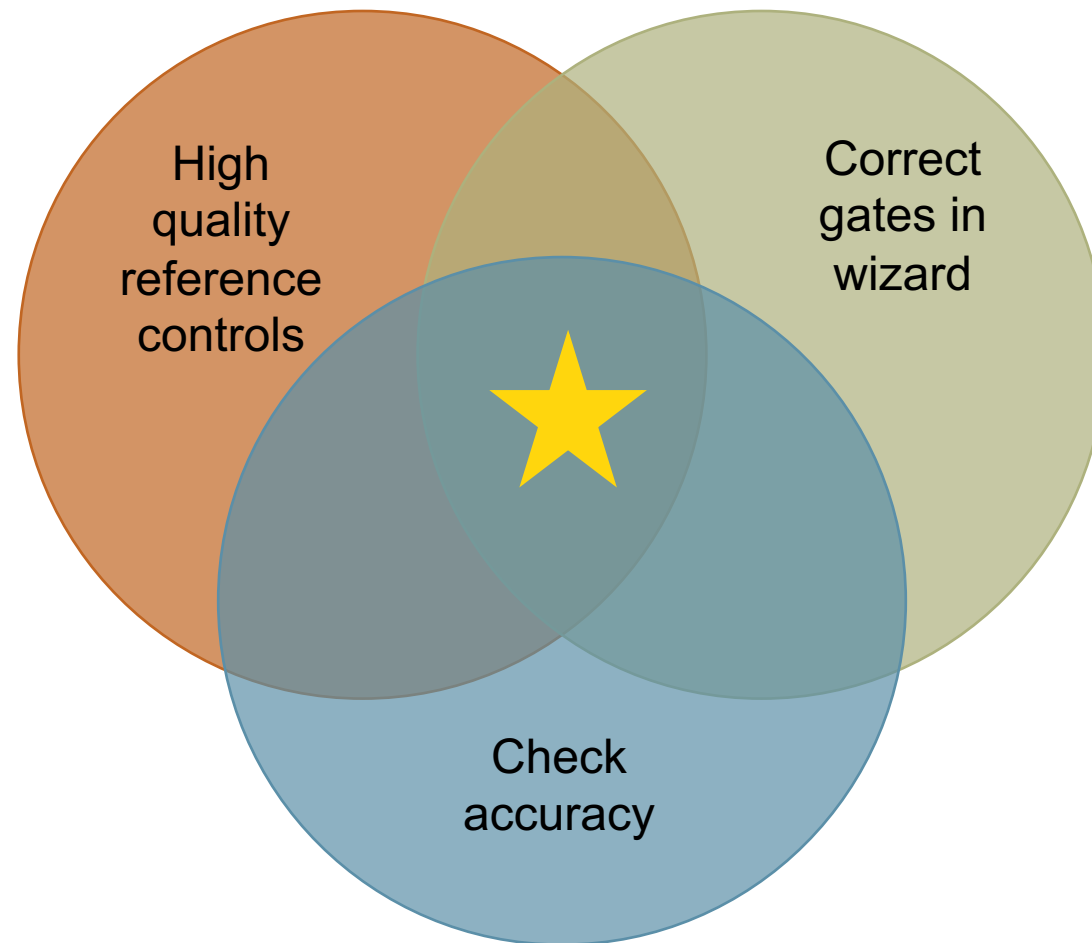
# Troubleshooting Spectral Correction and Panel design



**ChUG**  
**Cytometry**

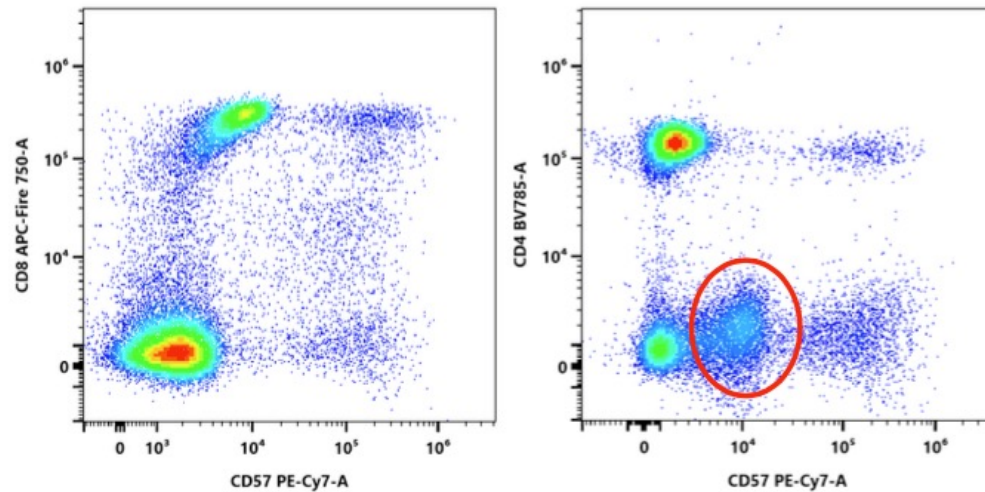


# How to get accurate correction

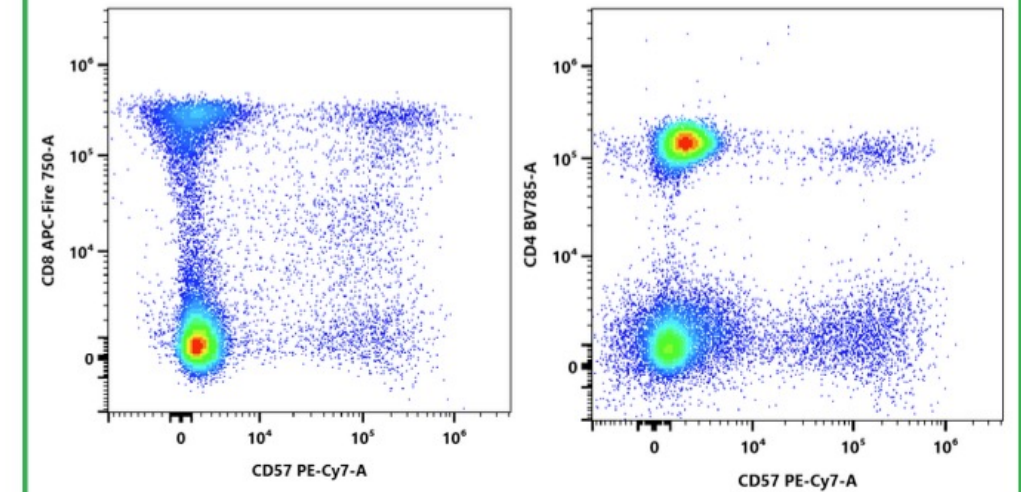


# Check the correction every time!

Data WITH Unmixing Error

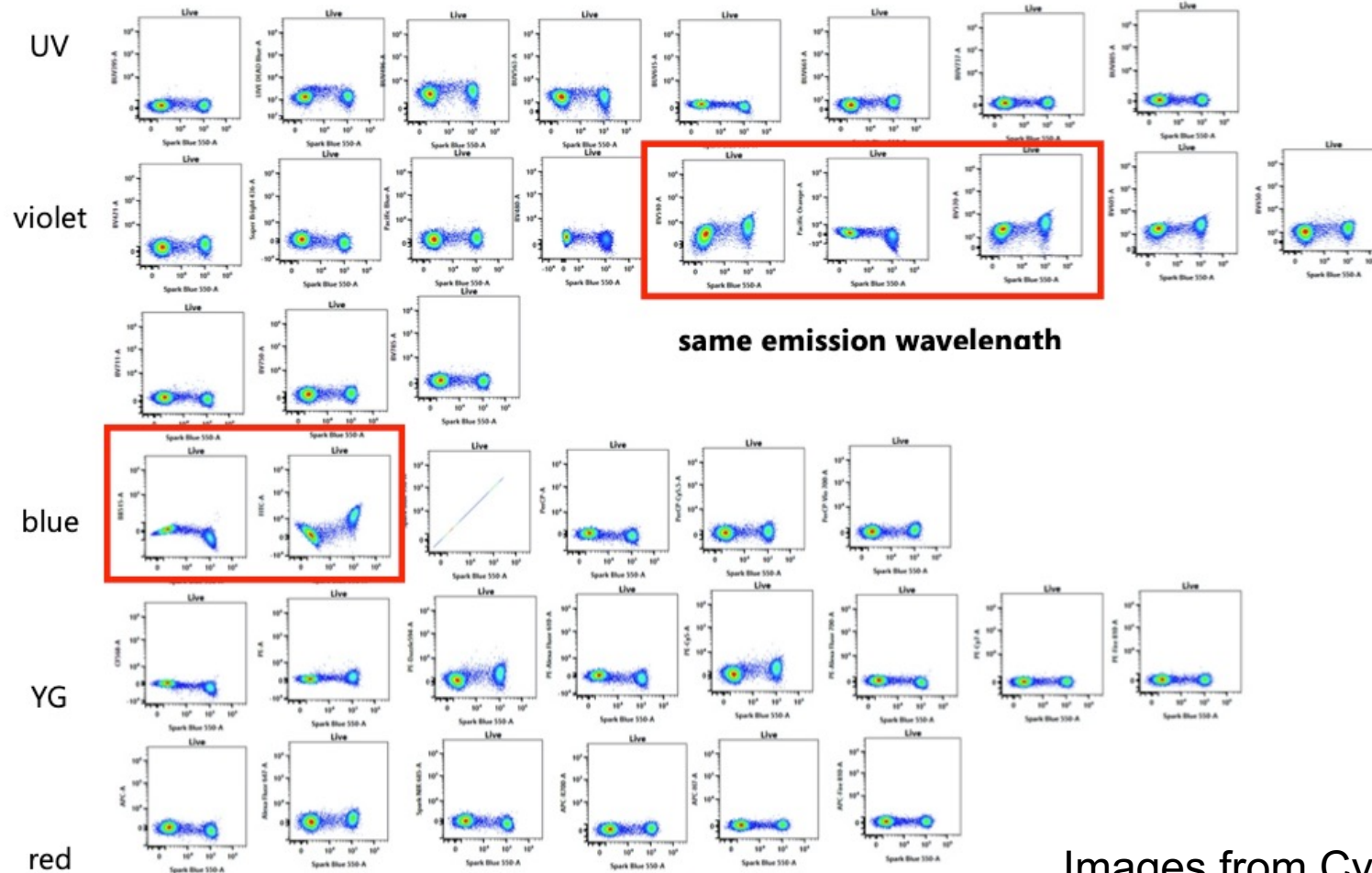


Correct Unmixing





# Always check correction with single stain data

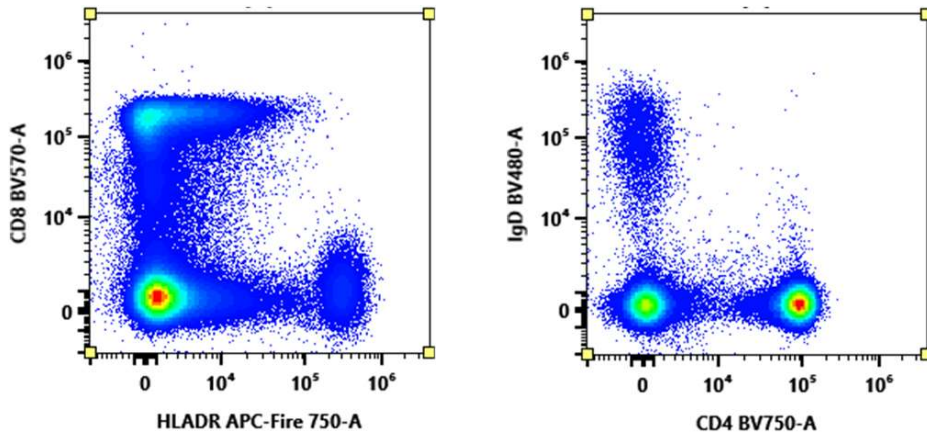


Images from Cytex

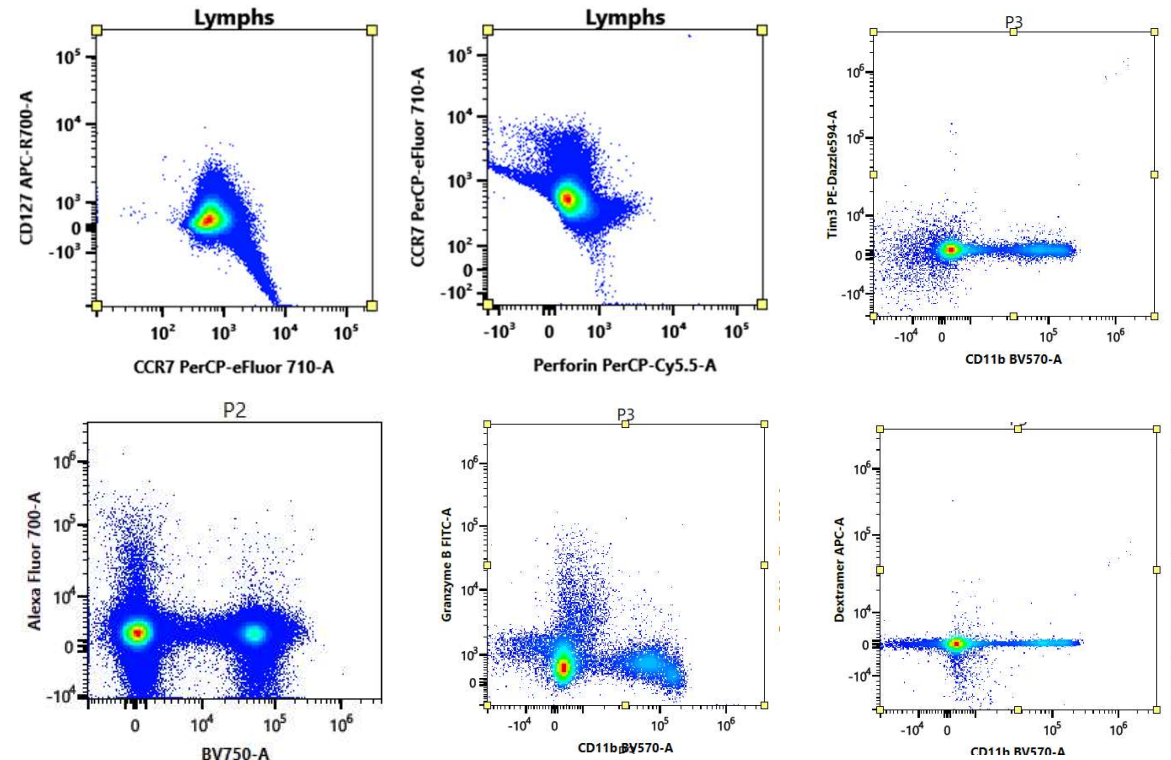


# Unmixing errors can be seen in fully stained samples by looking at negative populations

Examples of correct unmixing:



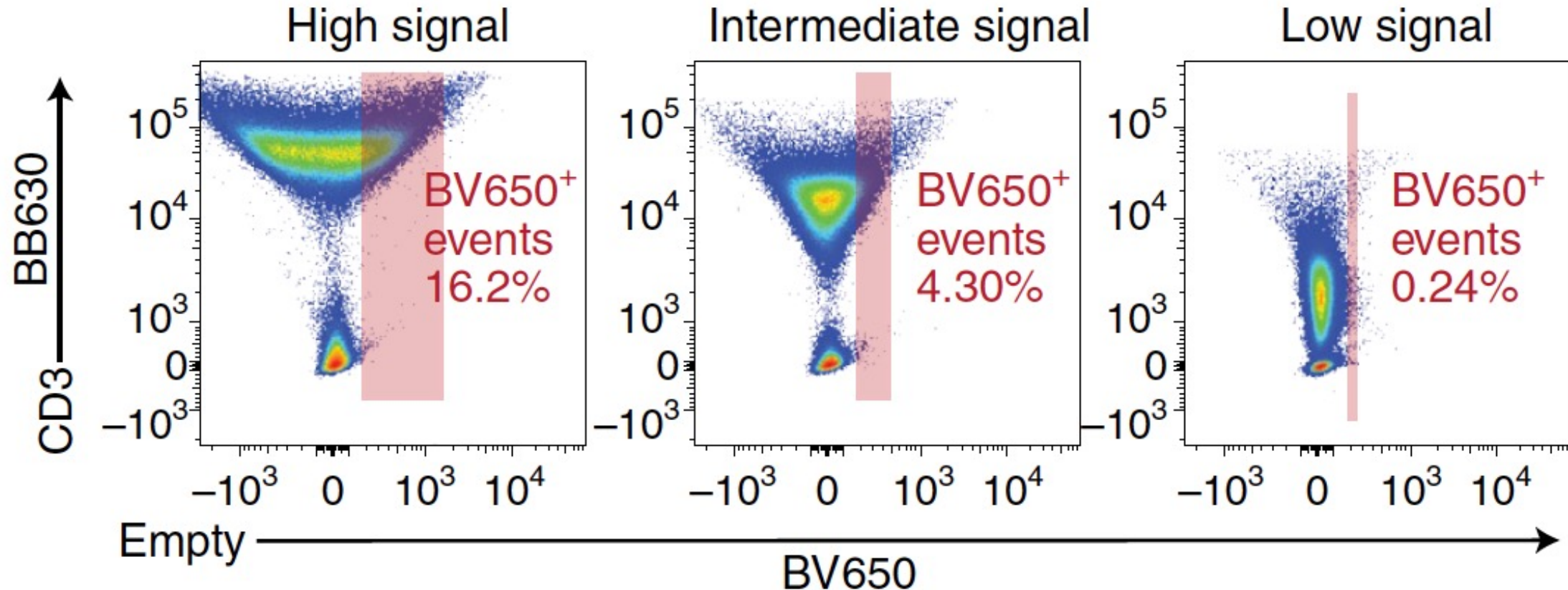
Examples of unmixing errors:



Images from Cytex



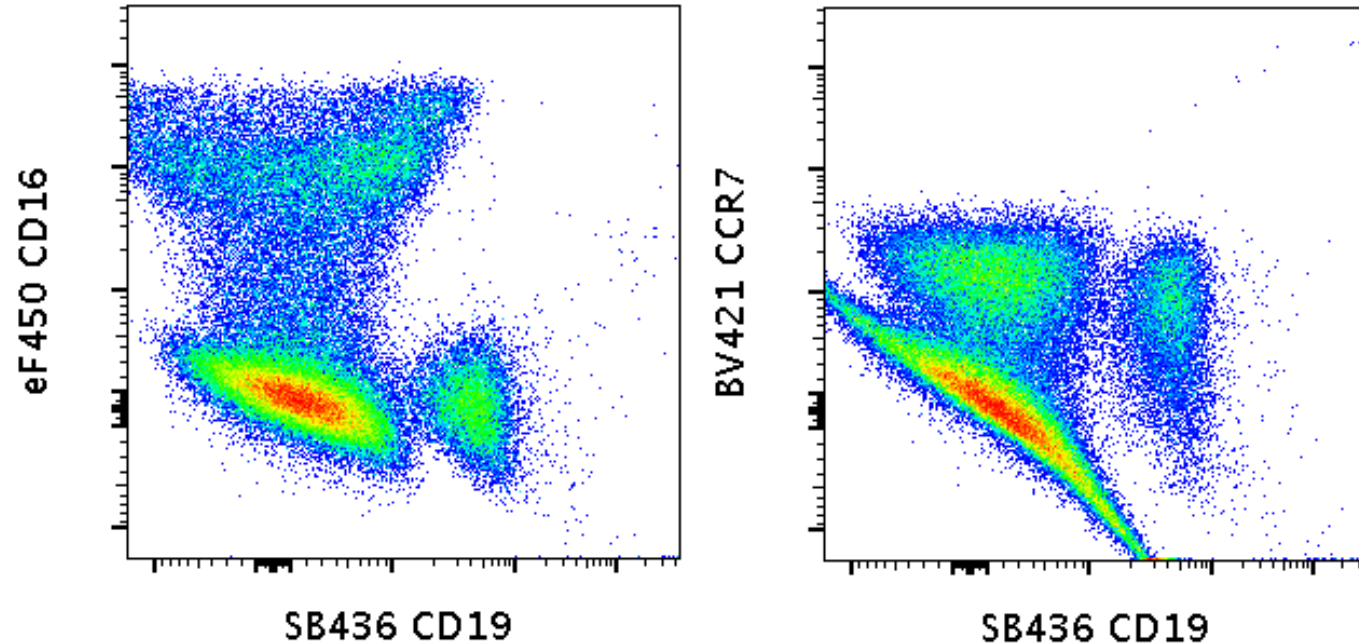
# How should your data look like?



Liechti T et al. Nat. Immunol. 2021



# Spectral flow weirdness



- Are these plots pretty? No.
- Am I going to make this a critically important figure in my paper? No.
- Can I gate on CD19<sup>+</sup> cells? Yes!



# What to do about unmixing errors

	Unmixing Errors?	
Single Stained Controls	YES	NO
Full Stained Sample	YES	YES





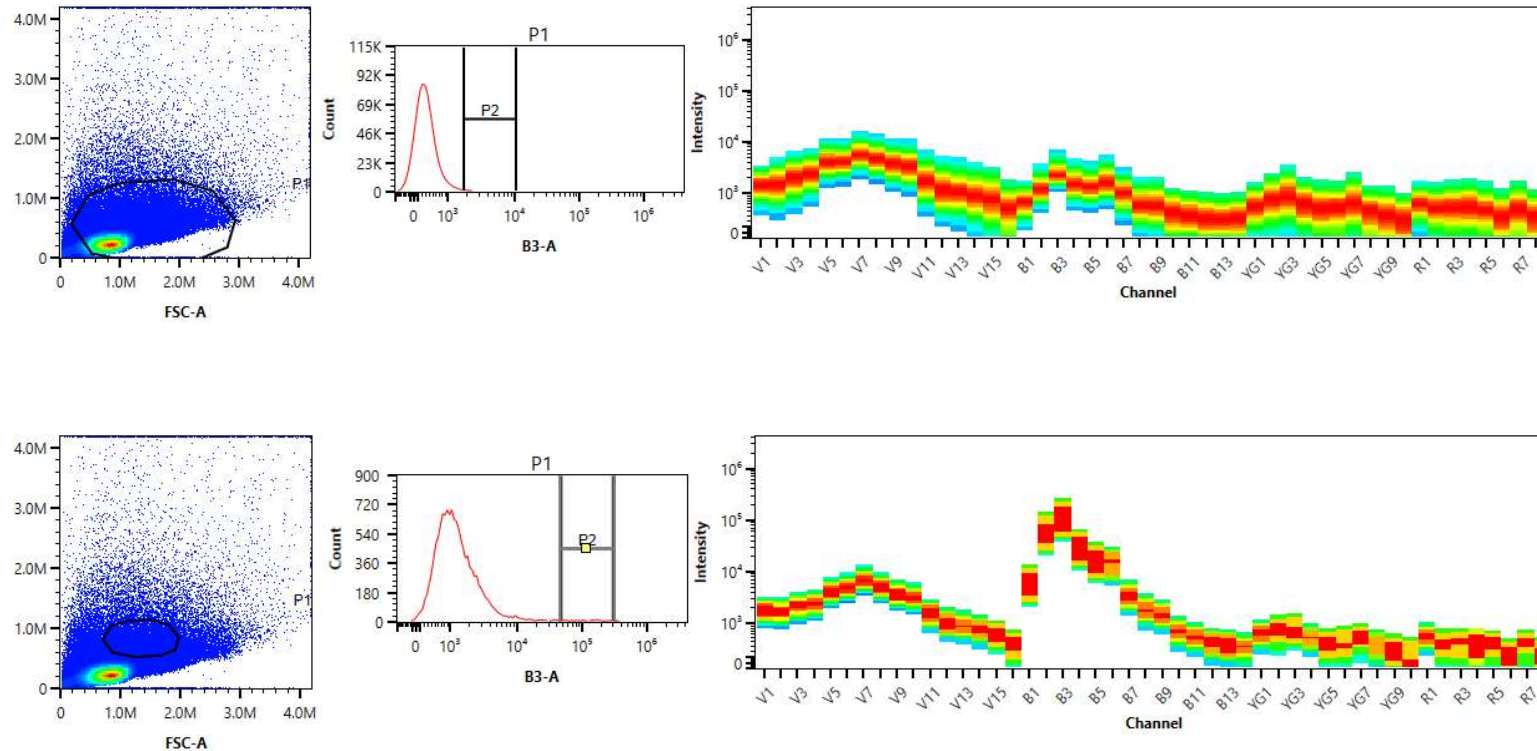
# Revisit your gating in the wizard

- Gate only the cells of interest in FSCxSSC
  - Cells expressing your marker
  - Exclude irrelevant populations
- Tippytop



# Reference Controls Troubleshooting Examples (5)

Where are the YFP positive cells ?



Slides from Cytek



<https://www.chugcytometry.com>



@chugcytometry

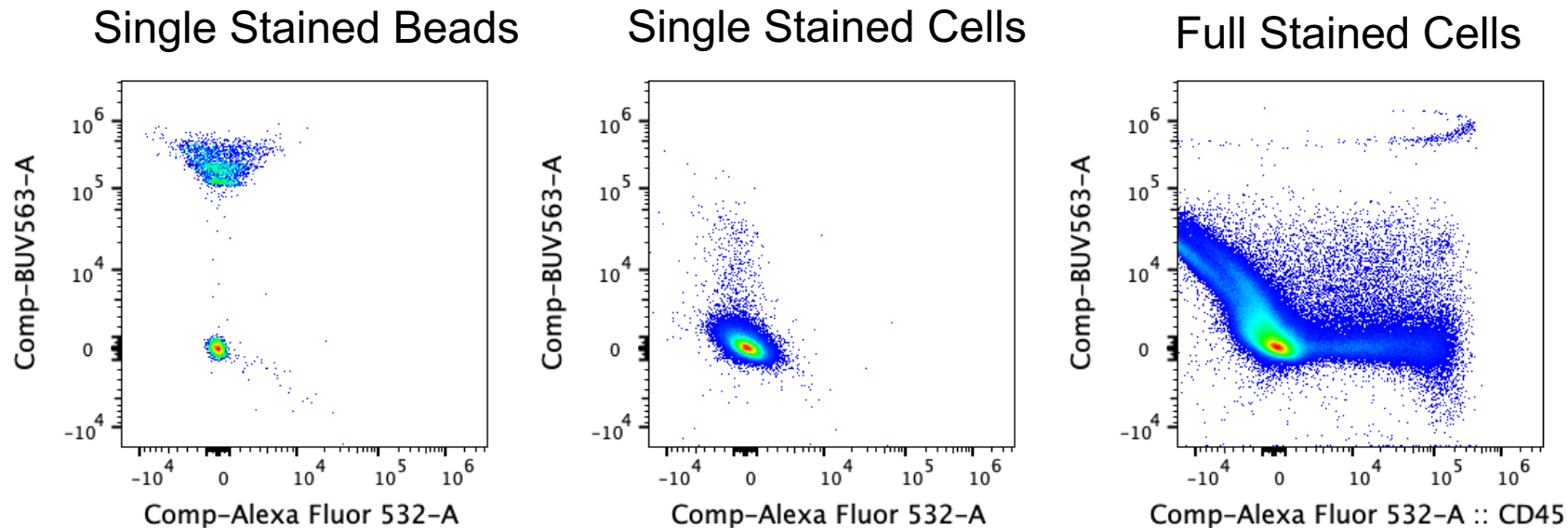


ChUG Cytometry

Troubleshooting

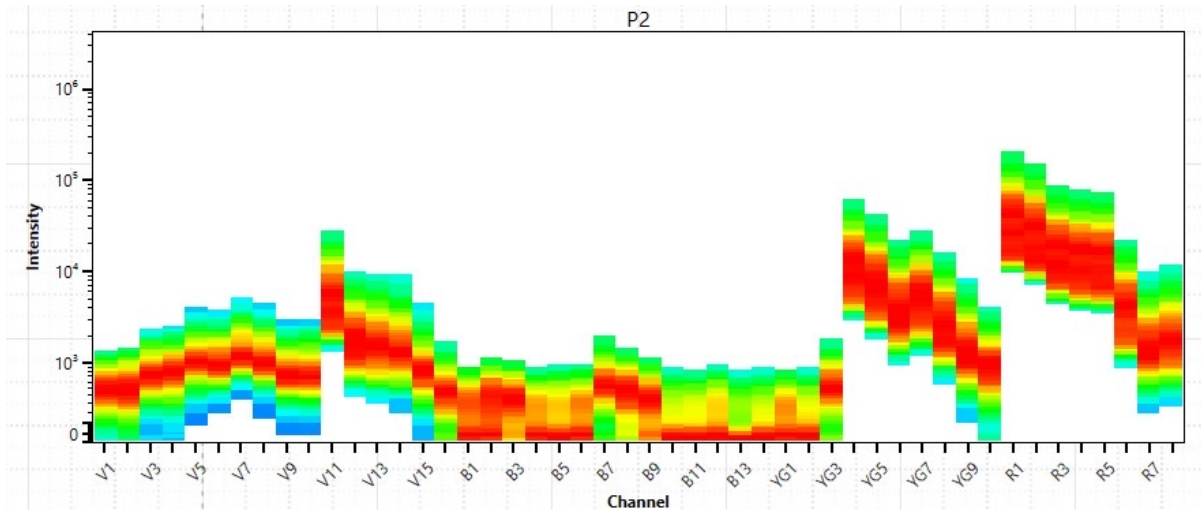
# Revisit your controls

- If single stained controls are correctly unmixed but full stained is not, look deeper at your controls

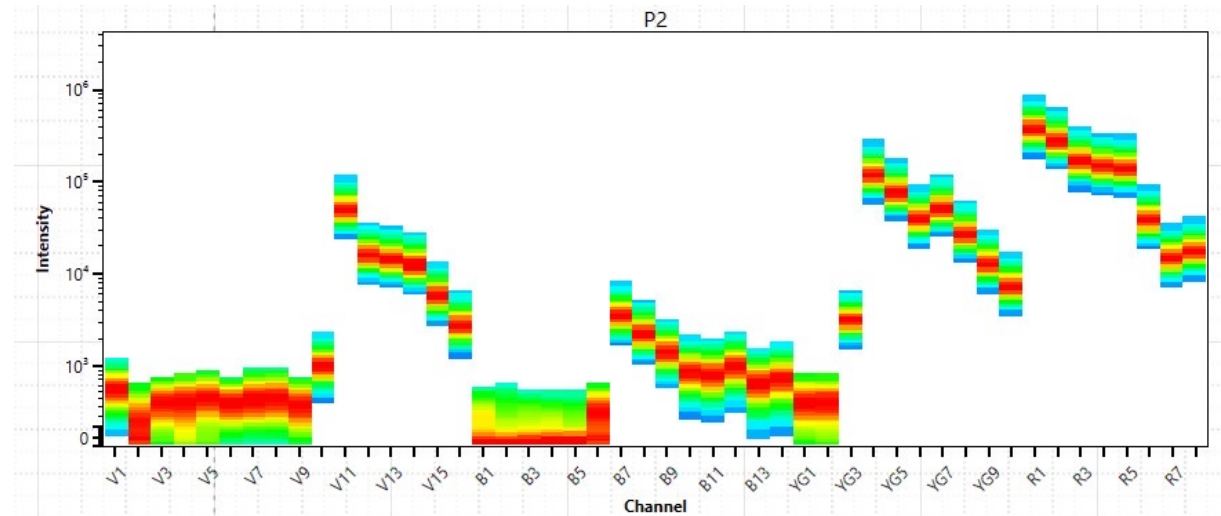


# Should you use compensation beads or cells?

CD62L APC on cells



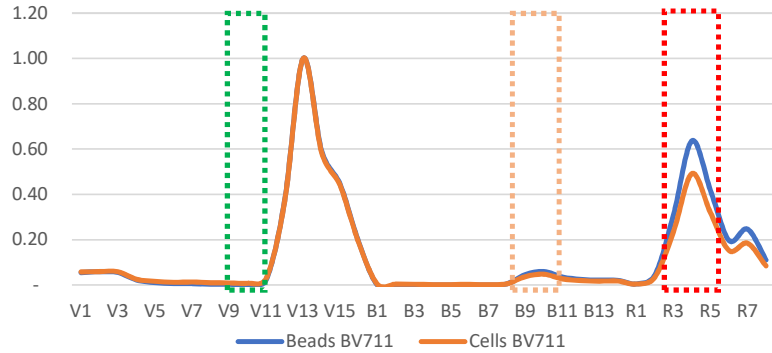
CD62L APC on beads



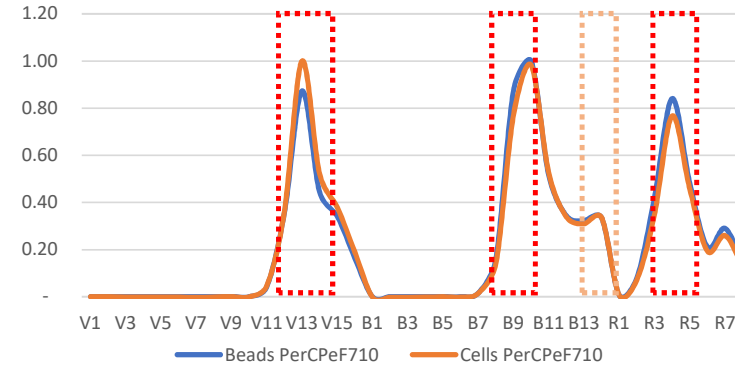
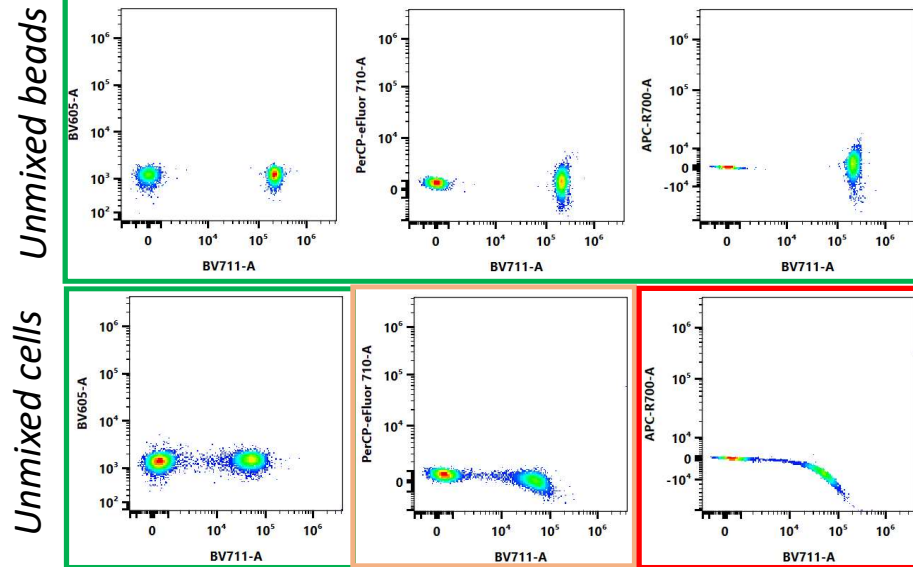
Compensation beads can give a cleaner signature than cells for some markers.  
BUT beads are not cells, and sometimes beads do not provide accurate unmixing.



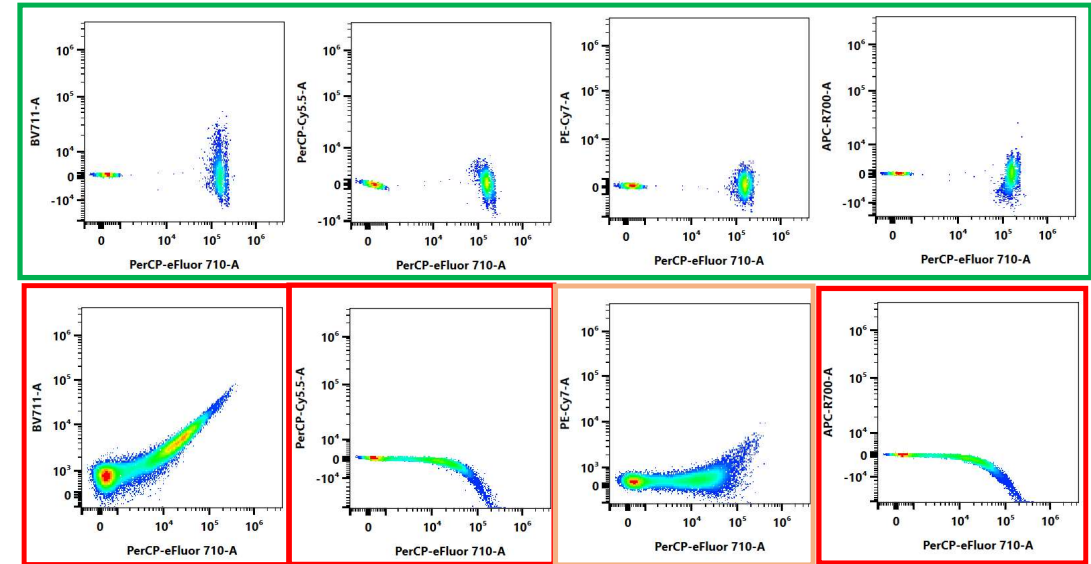
# Spectrum Mismatch = Unmixing Inaccuracy



*Use BV711 beads as control*



*Use PerCP-eFluor 710 beads as control*



Slides from Cytex





**Recommended Assay Procedure:**

BD™ CompBeads can be used as surrogates to assess fluorescence spillover (Compensation). When fluorochrome conjugated antibodies are bound to BD CompBeads, they have spectral properties very similar to cells. However, for some fluorochromes there can be small differences in spectral emissions compared to cells, resulting in spillover values that differ when compared to biological controls. It is strongly recommended that when using a reagent for the first time, users compare the spillover on cells and BD CompBead to ensure that BD CompBeads are appropriate for your specific cellular application.

When compensating dyes in this spectral range (such as Horizon™ V500 and AmCyan), the most accurate compensation can be obtained using single stained cellular controls. Due to spectral differences between cells and beads in this channel, using BD CompBeads can result in spillover errors for V500 and AmCyan reagents. Therefore, the use of BD CompBeads or BD CompBeads Plus to determine spillover values for these reagents is not recommended. Different V500 reagents (e.g. CD4 vs. CD45) can have slightly different fluorescence spillover therefore, it may also be necessary to use clone specific compensation controls when using these reagents.

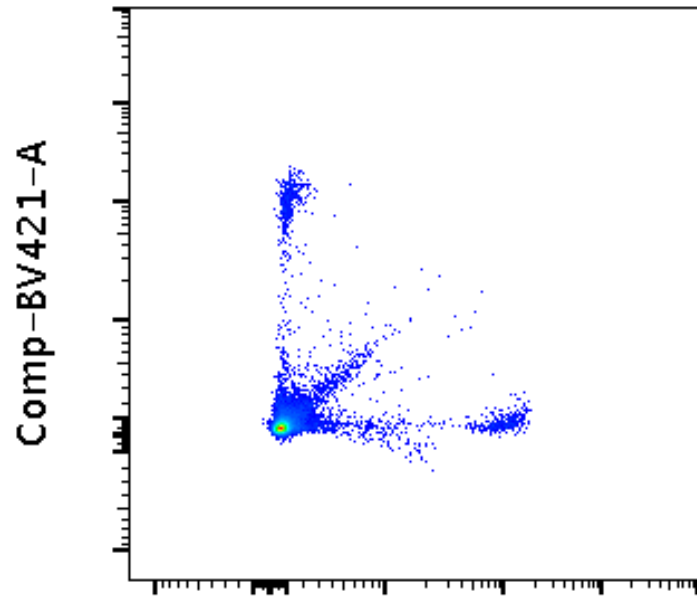
Due to spectral differences between labeled cells and beads, using BD™ CompBeads can result in incorrect spillover values when used with BD Horizon BUV661 reagents. Therefore, the use of BD CompBeads or BD CompBeads Plus to determine spillover values for these reagents is not recommended. Different BUV661 reagents (eg, CD4 vs. CD45) can have slightly different fluorescence spillover therefore, it may also be necessary to use clone-specific compensation controls when using these reagents.

Slides from Cytex



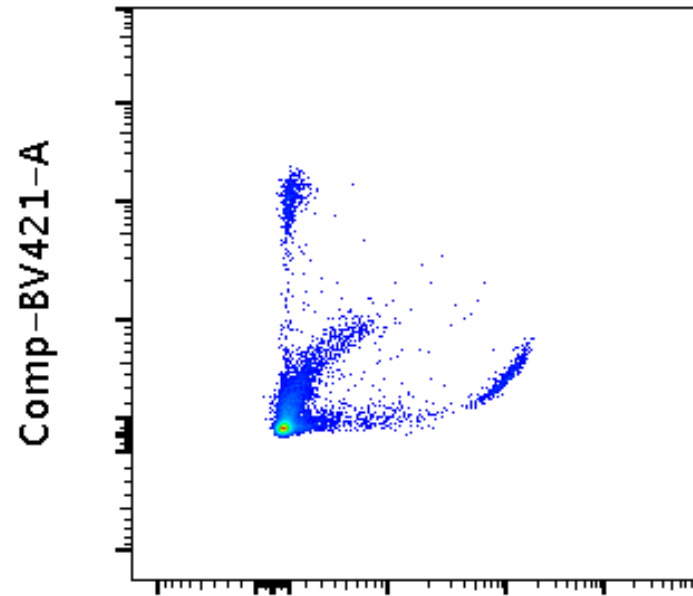


# Unmixing a “fully stained” sample with different reference controls (mixed multiple CD4 single stains)



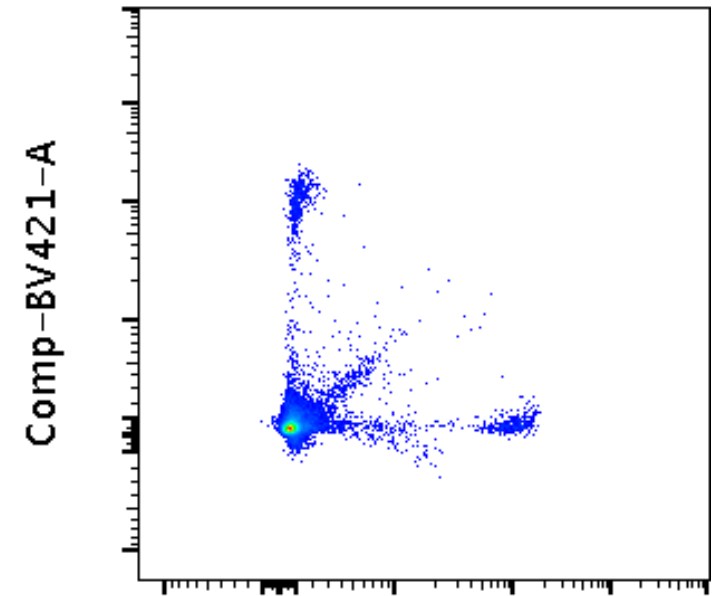
Comp-BV605-A

Cells



Comp-BV605-A

AbC Total



Comp-BV605-A

UltraComp

“Full stain” cells  
were unmixed  
with:



<https://www.chugcytometry.com>



@chugcytometry



ChUG Cytometry

# \*New Product\* Improved Comp Beads (Summer 2020)

- UltraComp eBeads™ Plus Compensation Beads
  - ThermoFisher 01-3333-41, 01-3333-42
  - “Unlike the first generation beads, UltraComp eBeads Plus compensate in a manner similar to cells when used with Brilliant Violet 785/786-, Brilliant Violet 711-, Super Bright 780- and Super Bright 702-conjugated antibodies.”



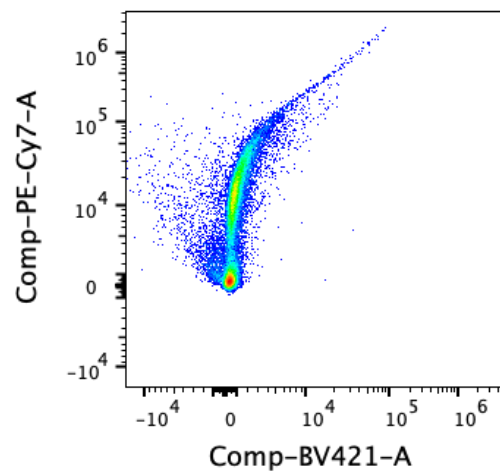
# Slingshot!

- Synthetic cells
- ViaComp
- SpectraComp

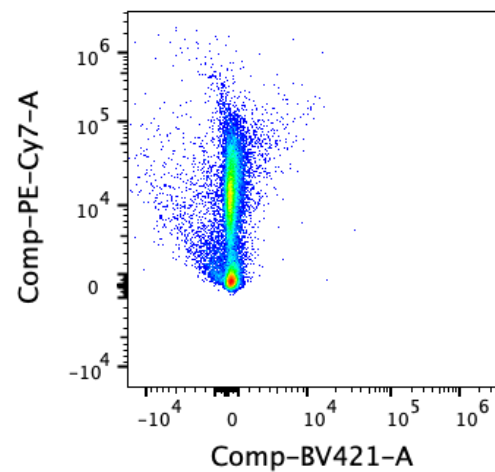


# Apply Manual Compensation on top of unmixed data?

Single Stained Cells

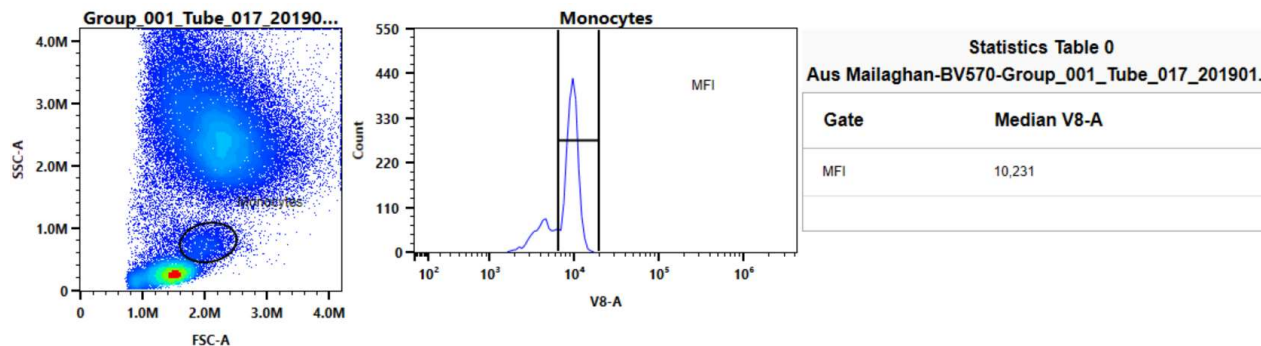


Single Stained Cells

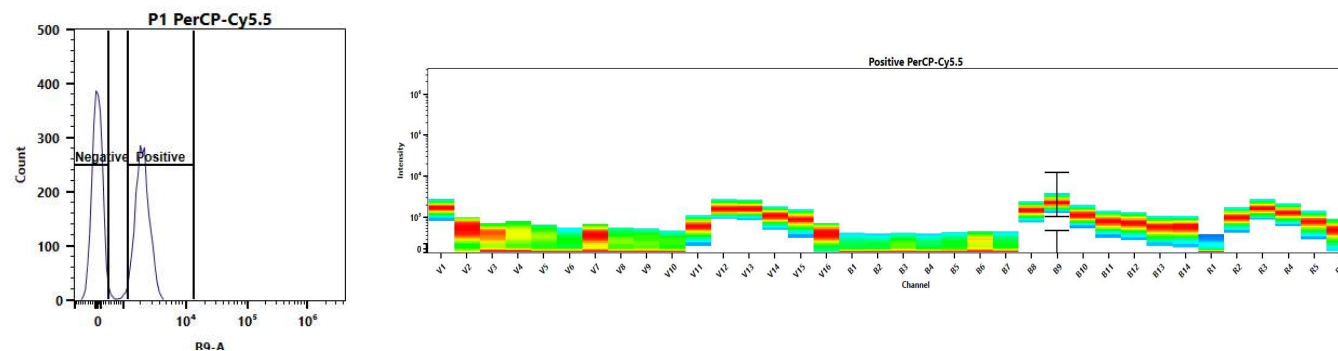


# Reference Controls Troubleshooting Examples (1)

## Case 1



## Case 2



These controls are too dim, not meeting Rule 1 of what a good control should be

Slides from Cytex



<https://www.chugcytometry.com>



@chugcytometry



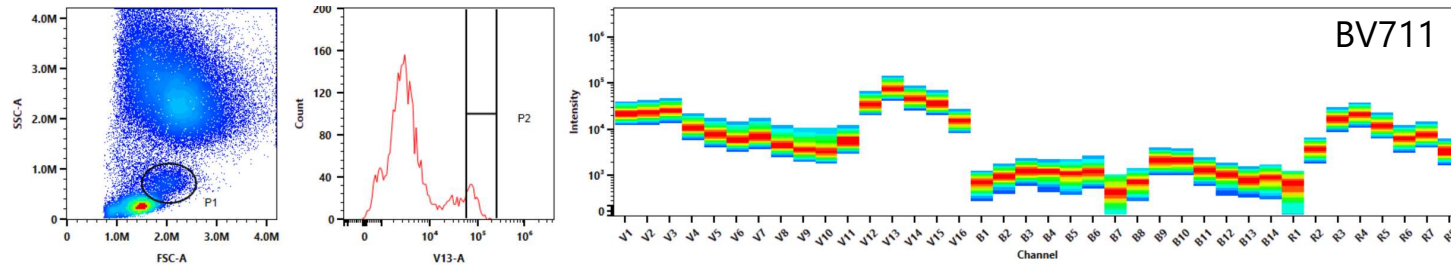
ChUG Cytometry



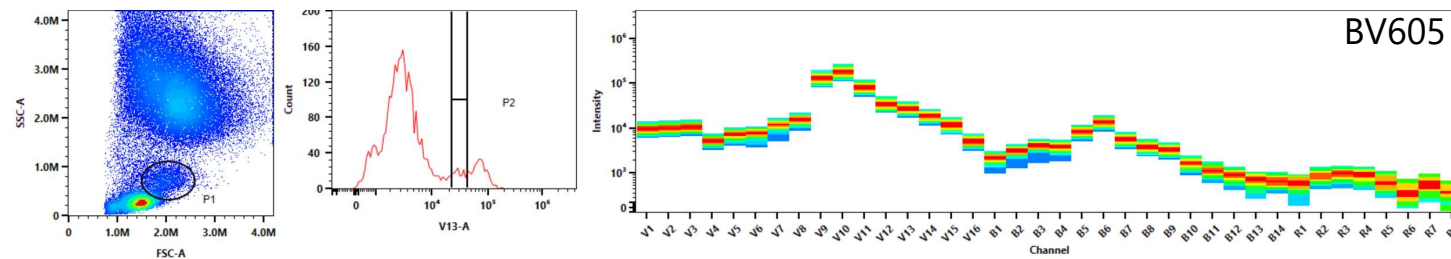
Troubleshooting

# Reference Controls Troubleshooting Examples (3)

Gated on Brightest Positive Peak



Gated on Dimmer Positive Peak



Carry over?

Slides from Cytex



<https://www.chugcytometry.com>



@chugcytometry



ChUG Cytometry



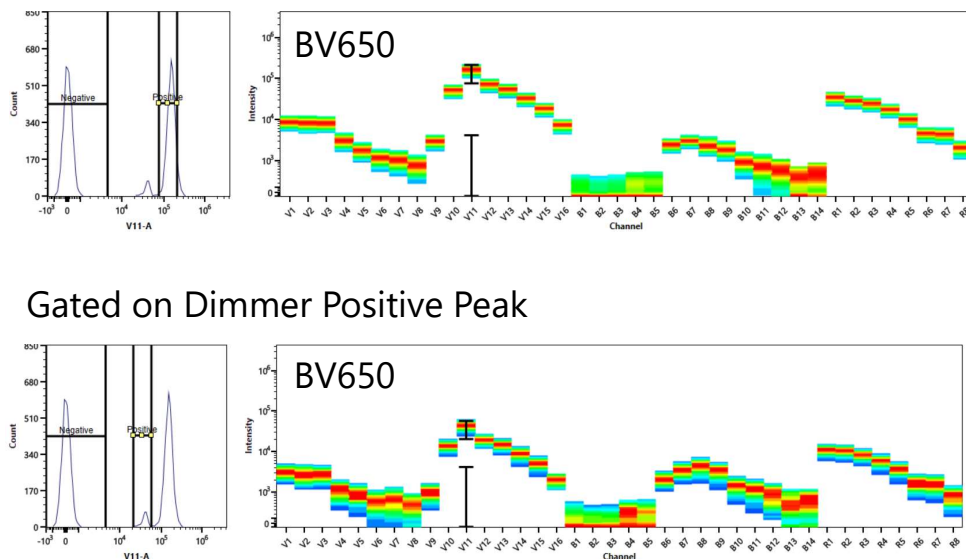
21

Troubleshooting

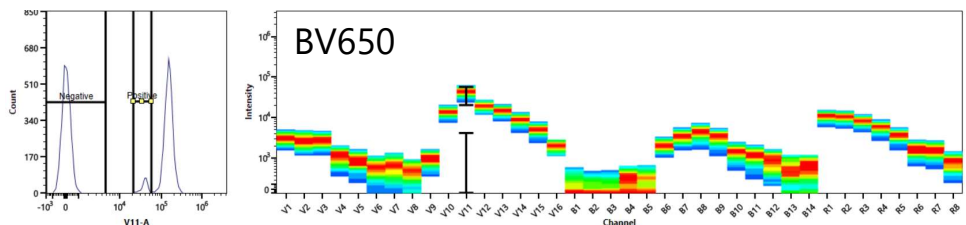


# Reference Controls Troubleshooting Examples (4)

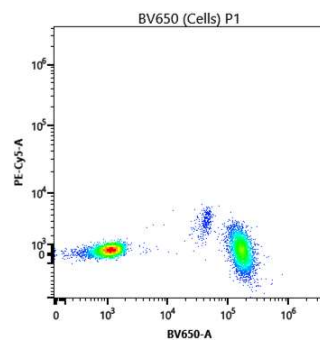
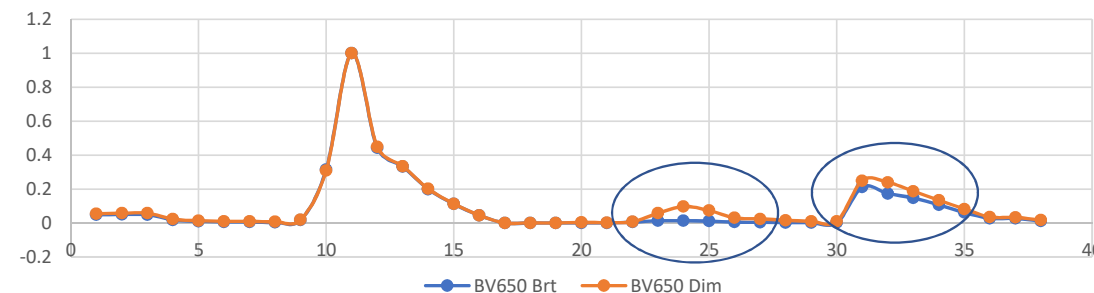
Gated on Brightest Positive Peak



Gated on Dimmer Positive Peak



BV650 Bright and BV650 Dim



The intermediate population appears uncompensated when looking at BV650 vs PE-Cy5

# Testing your pannel



Unlikely to work form the get-go



Don't try your full pannel on your first try!!



# FMO to the rescue – bad panel experiment

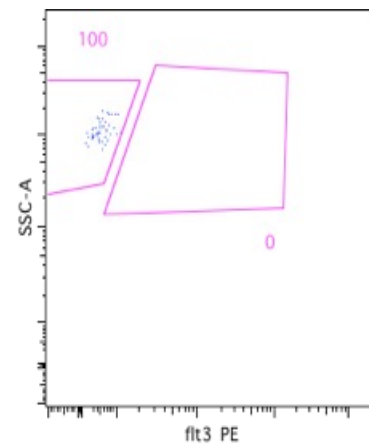
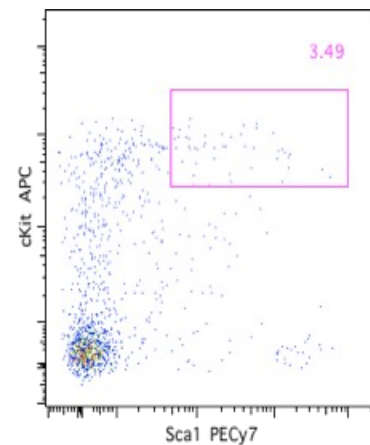
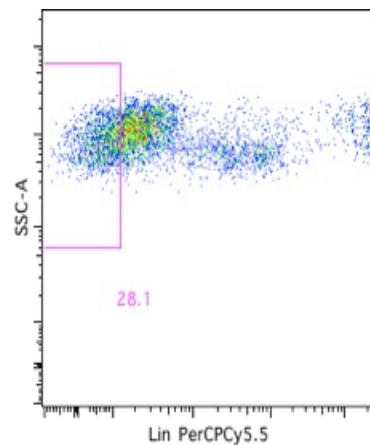
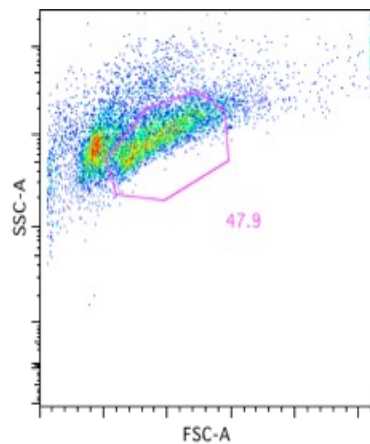
- Untitrated everything
- Heavy in the far red

Fluorophore	Marker
BV510	KLRG1
FITC	CD3
PE	CD25
PerCP-Cy5.5	CD4
PE-Dazzle594	CD24
PE-Cy5	ICOS
PE-Cy7	CD62L
APC	Thy1.2
AF700	TCRb
APC-eFluor780	CD8
Zombie NIR	Live/dead

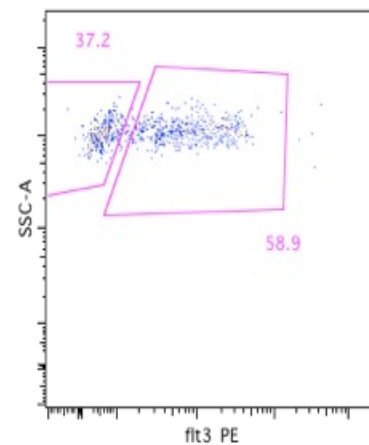
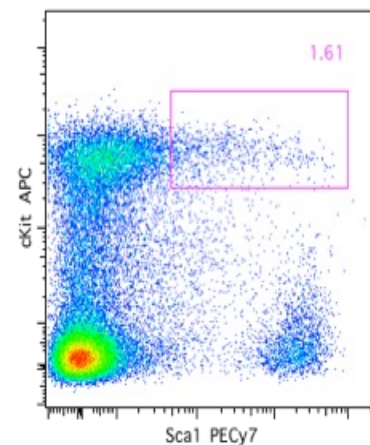
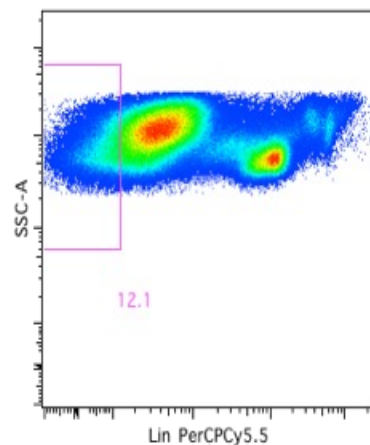
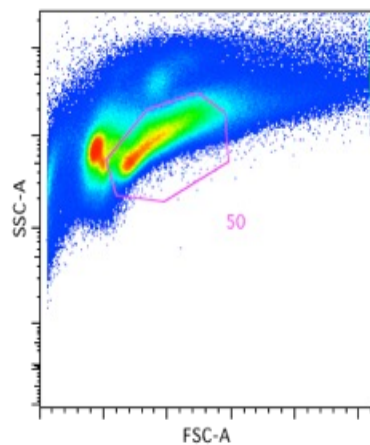


# Deciding on gates: FMO Controls

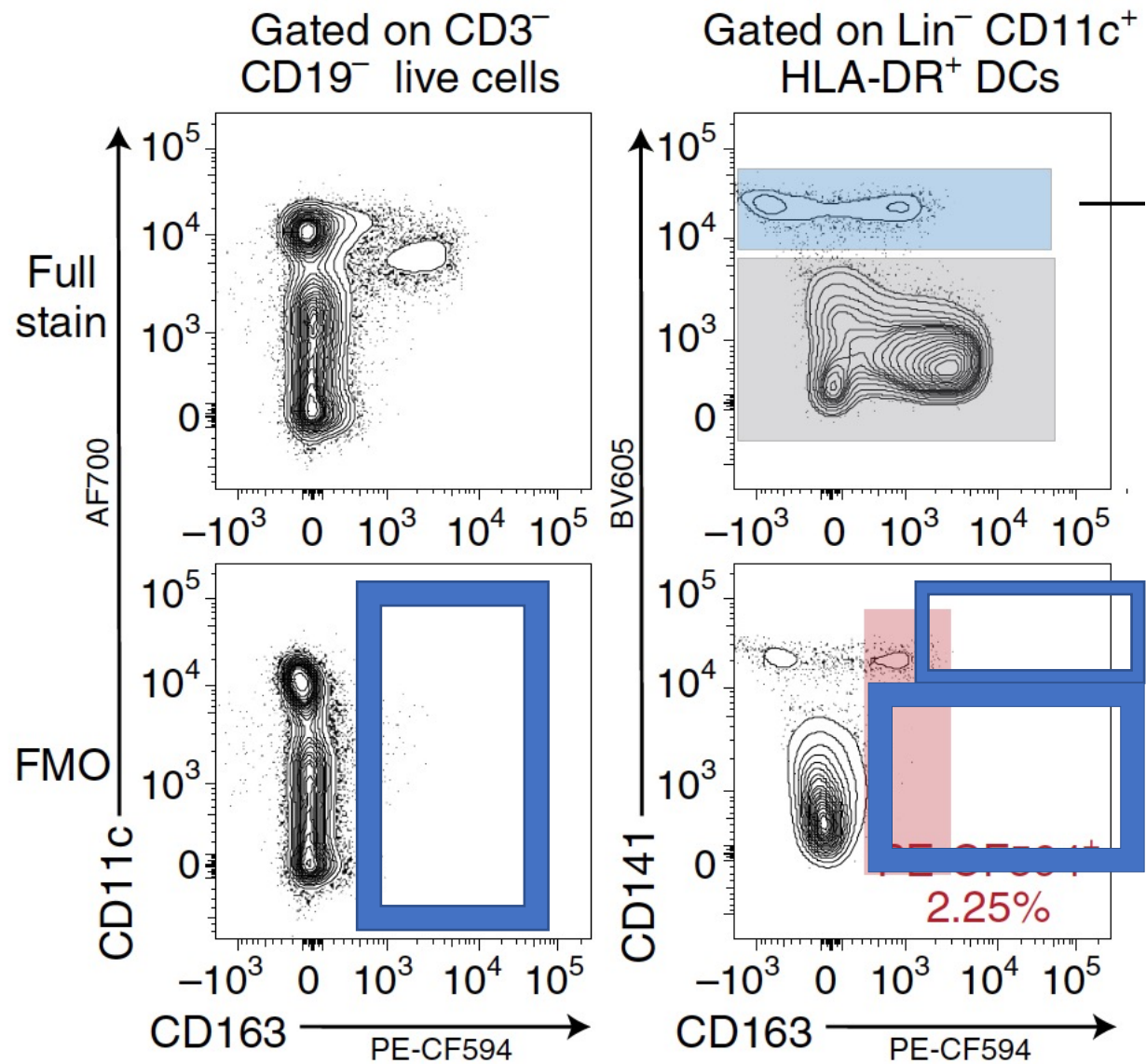
FMO PE



Sample



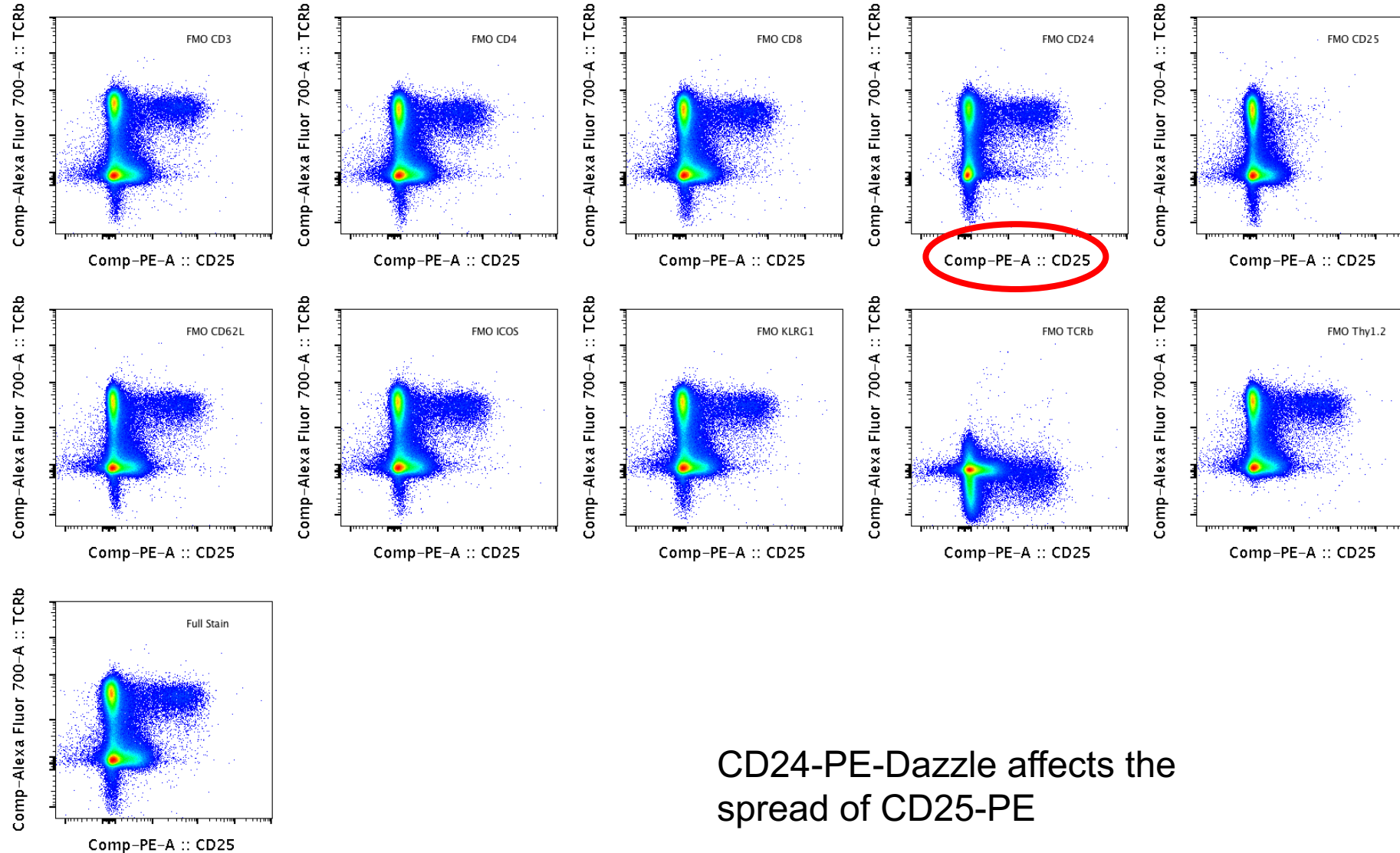
# FMOs and brightness



Liechti T et al. Nat. Immunol. 2021



# Using FMOs to determine issues with the panel

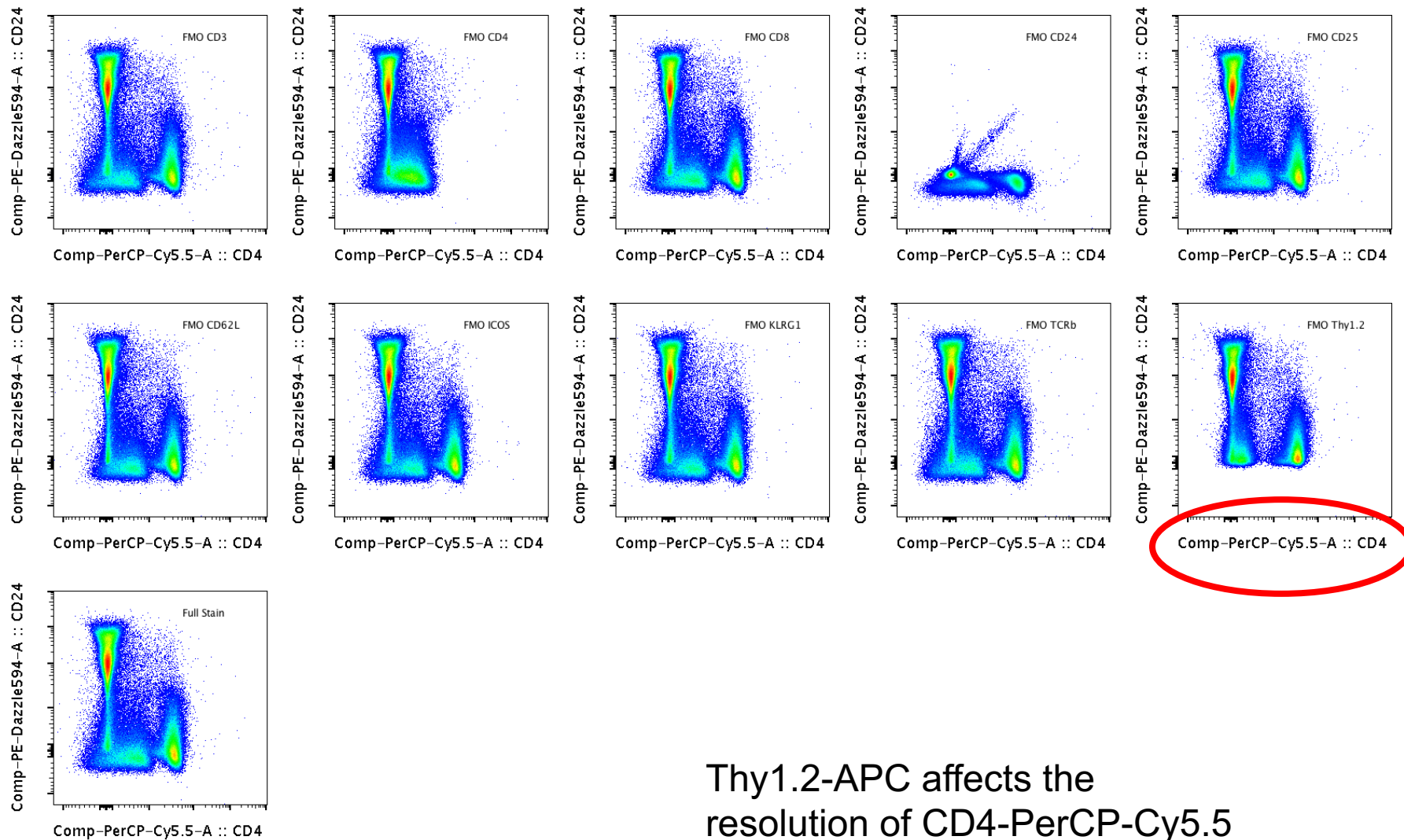


CD24-PE-Dazzle affects the spread of CD25-PE





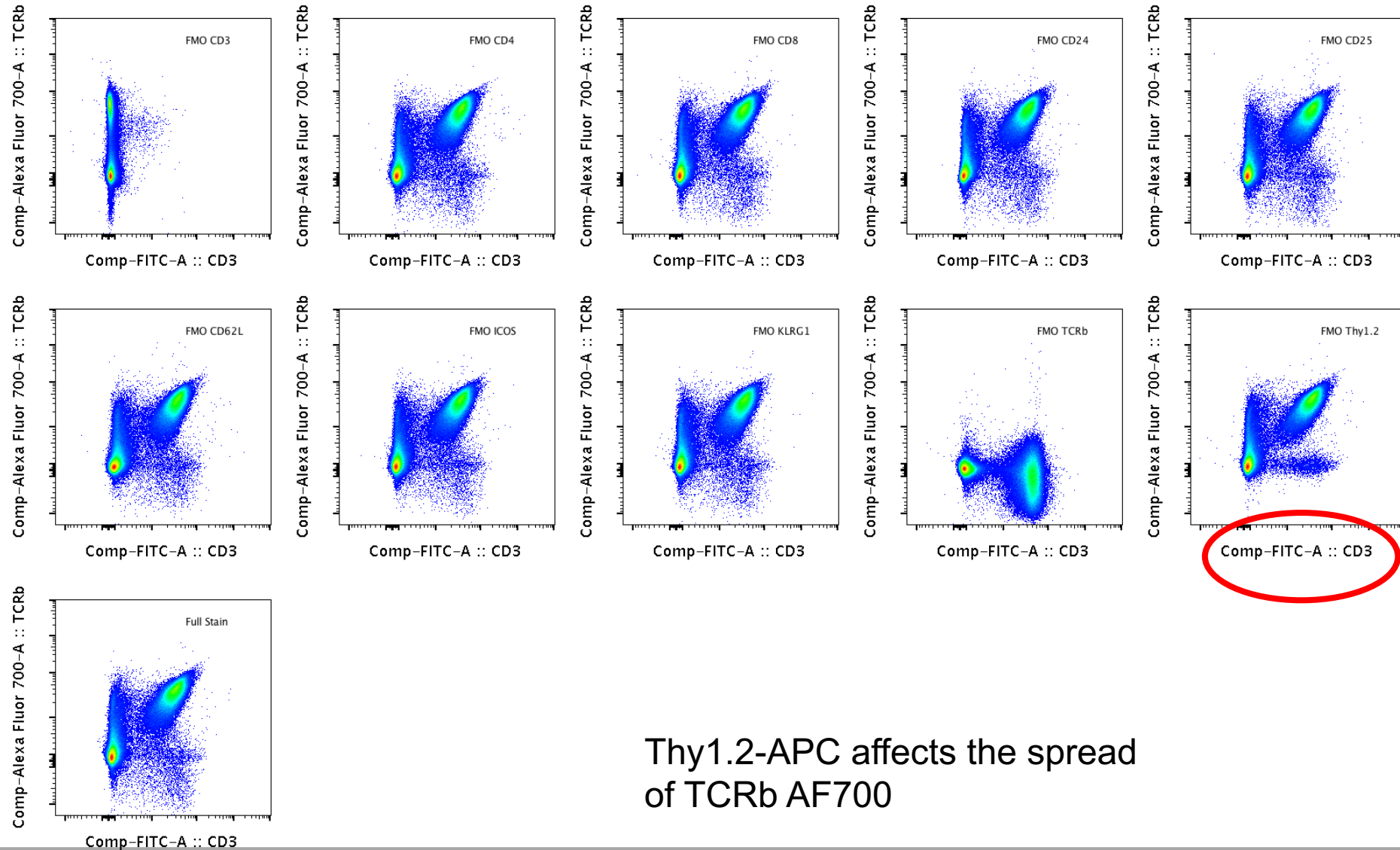
# Using FMOs to determine issues with the panel



Thy1.2-APC affects the  
resolution of CD4-PerCP-Cy5.5



# Using FMOs to determine issues with the panel

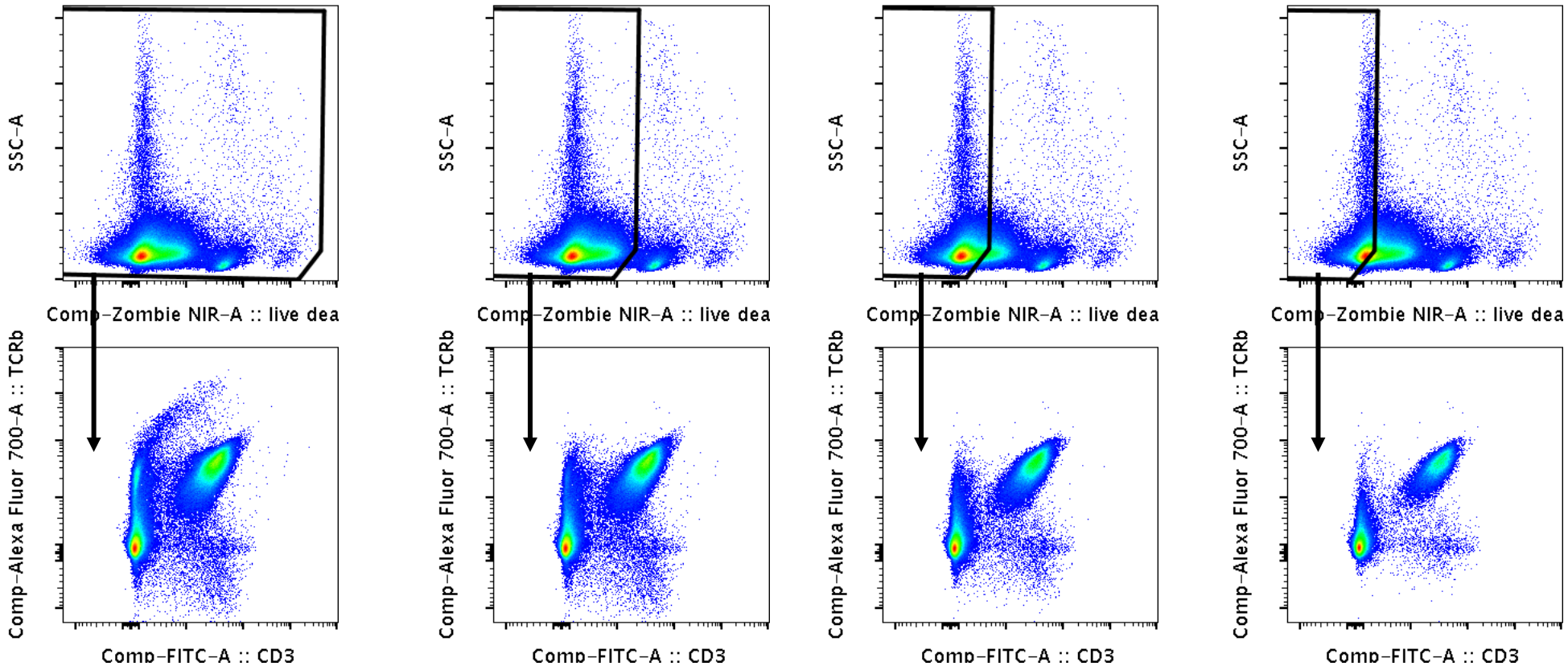


Thy1.2-APC affects the spread  
of TCRb AF700



# Zombie NIR seems to affect AF700

Decreasing live/dead gate



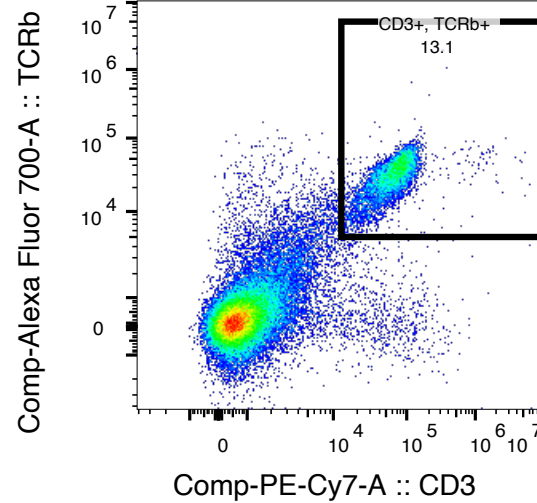
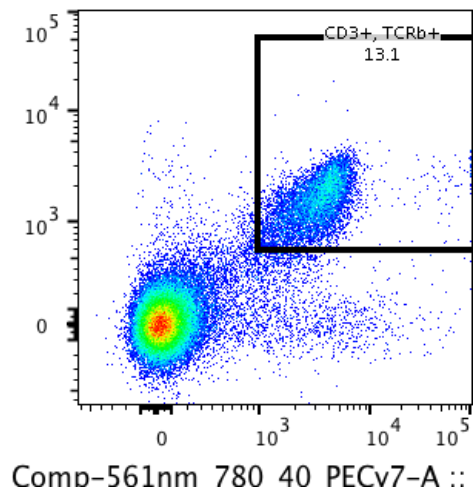
TCRb<sup>+</sup>CD3<sup>+</sup>  
cells should  
not exist!!



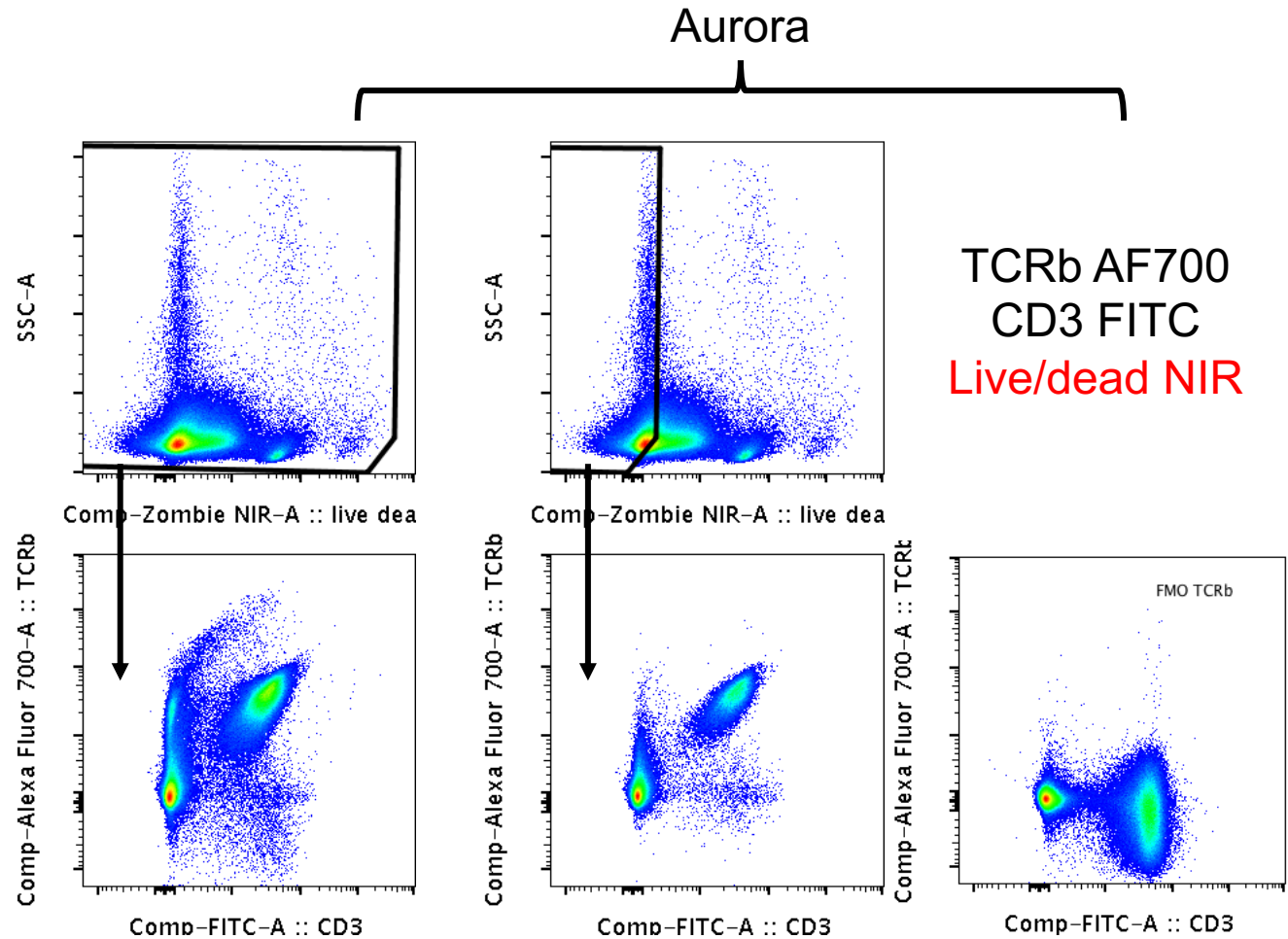
# Mystery TCRb+CD3- population disappears with switch to Zombie Aqua, but TCRb FMO is not as helpful

Fortessa 4-15

Aurora



TCRb AF700  
CD3 PE-Cy7  
Live/dead Aqua



This FMO is not helpful, but other FMOs work as expected

