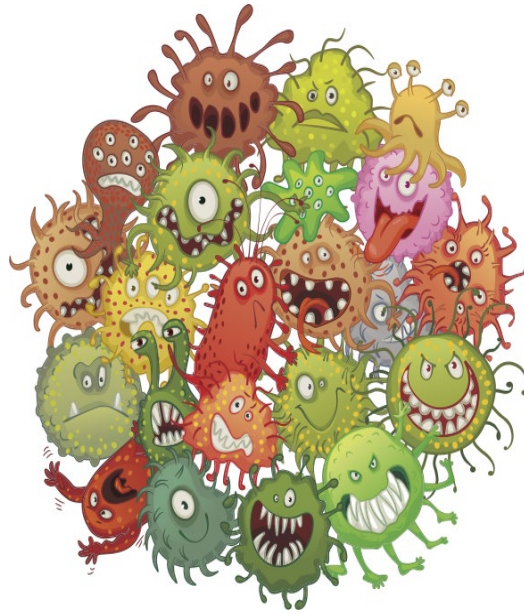


Flowcytometry applications

Gene expression/
Fluorescent
proteins

Immune
Phenotyping



Phosphorylation

Activity / metabolism dyes:

- Cell proliferation: CFSE
- Cell Cycle: PI
- Apoptosis: Annexin
- Mitoprobes
- ROS-assay (oxidative stress)
- Ca-flux: FuraRed
- Caspase-activity: FLICA

Cytokine expression

Cell isolation (sorting)

Flowcytometry applications

Cell viability
(PI, 7-AAD,
Amine dyes)



Proliferation

(CFSE, CytoTRACK dyes,
BrdU, EdU, Ki-67)



Apoptose

(AnxV,
Caspase FLICA kits)



Autophagy

(Cathepsins, autophagy probe
Beclin-1, Lamp-1/2)



Cell Cycle

(PI)

Flowcytometry applications

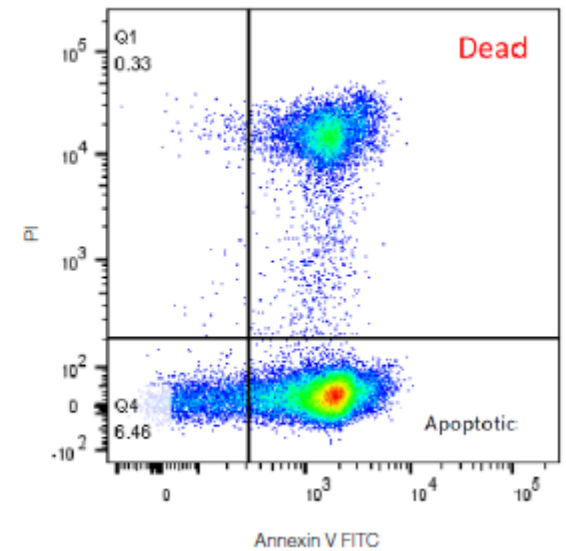
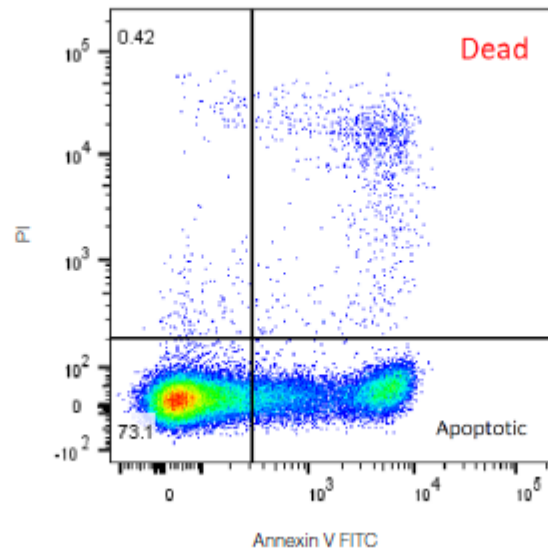
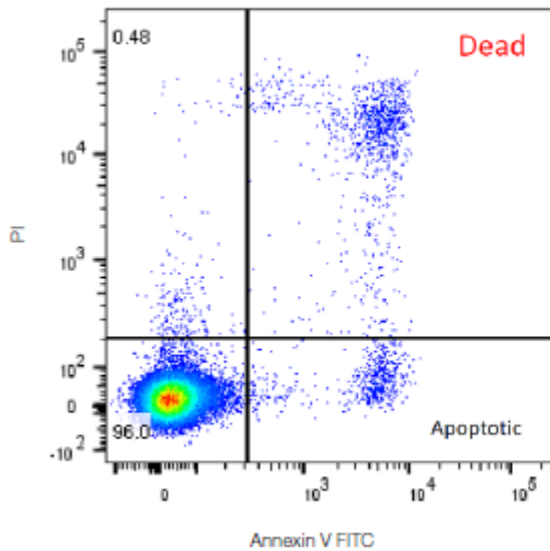
Apoptosis



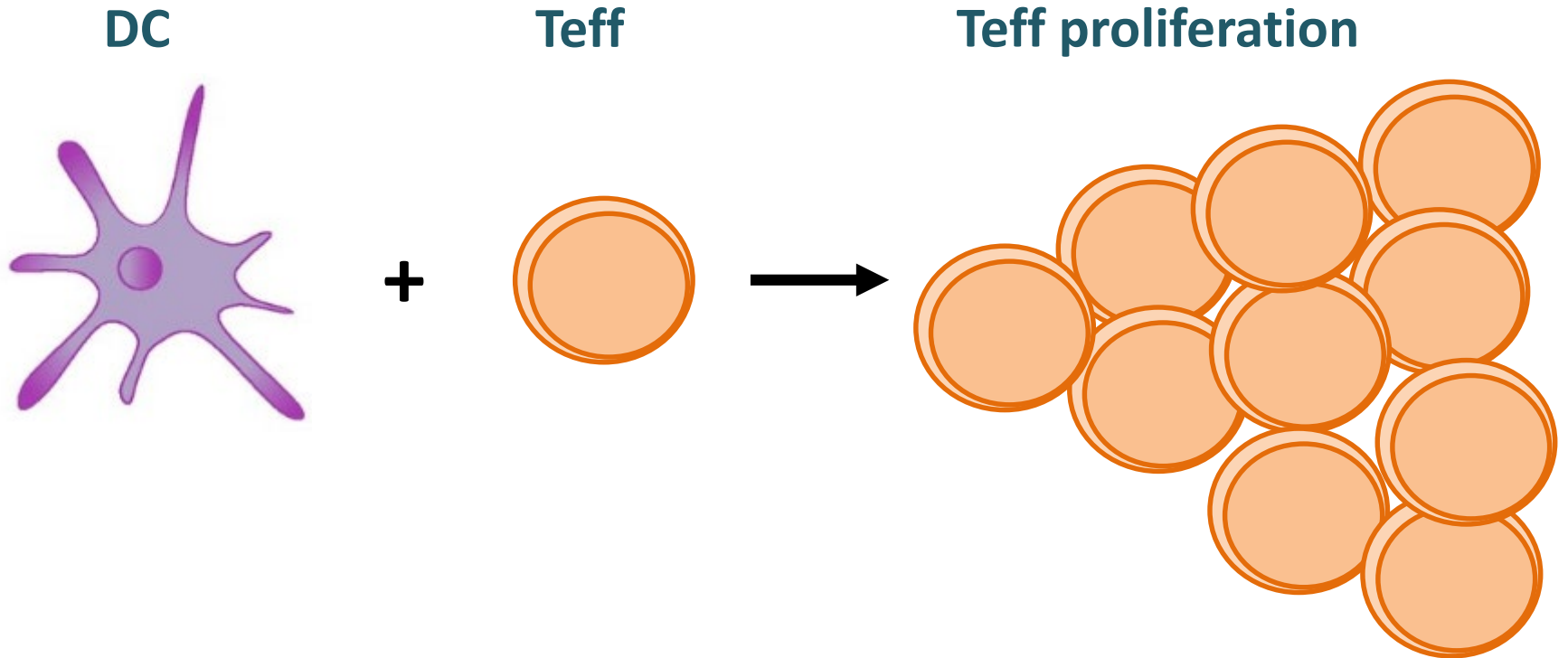
No staurosporine

1 hr staurosporine

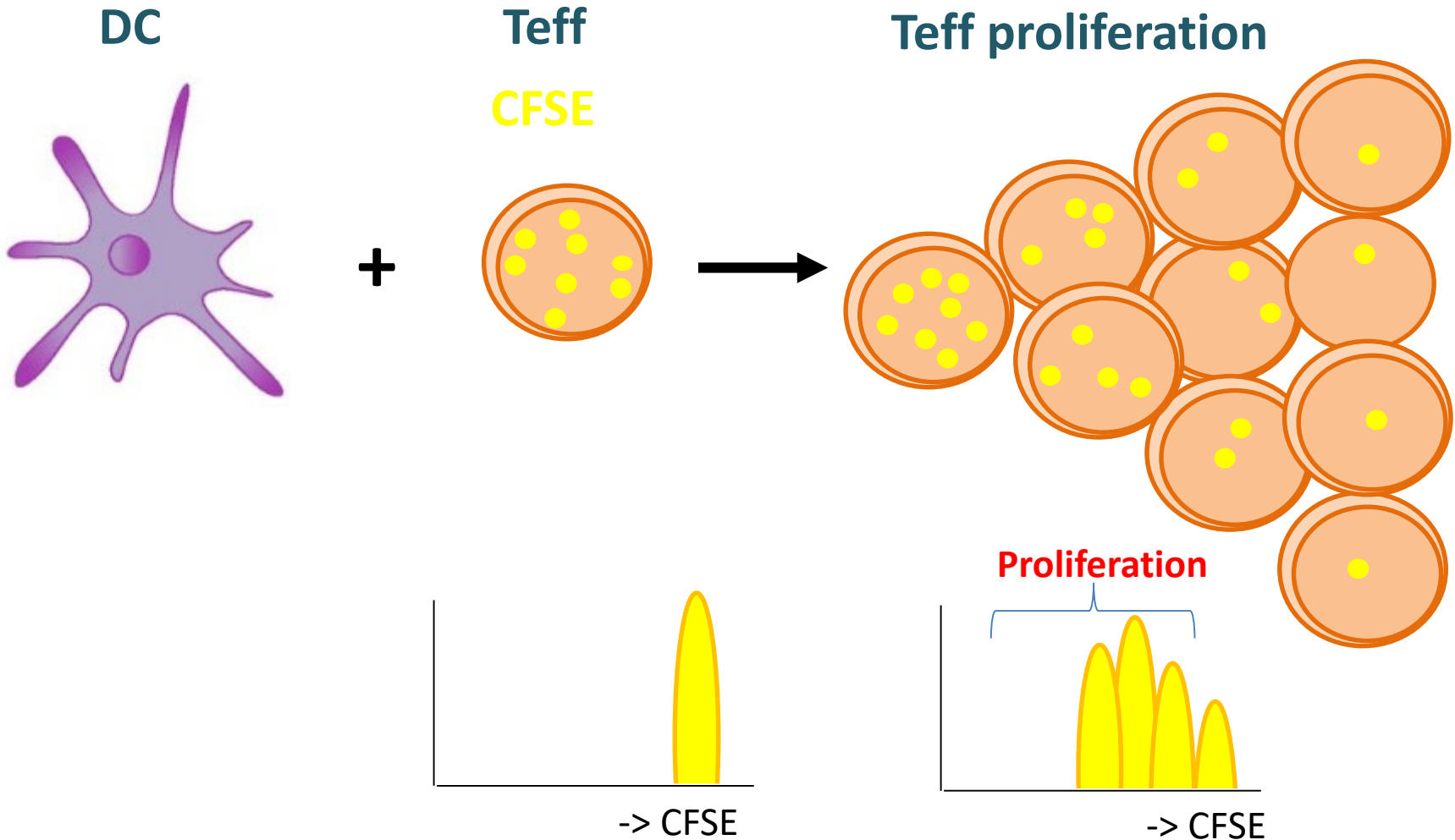
6 hr staurosporine



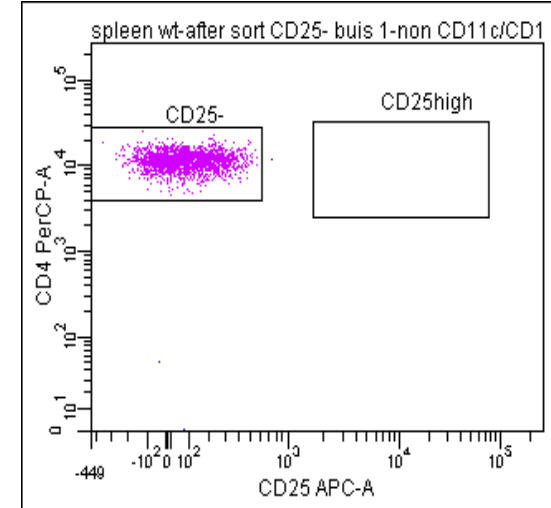
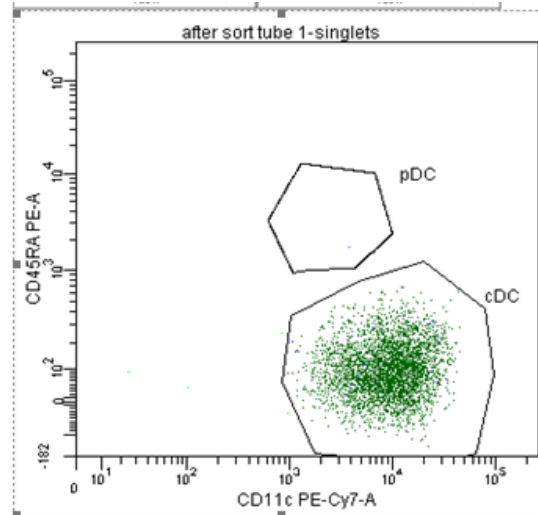
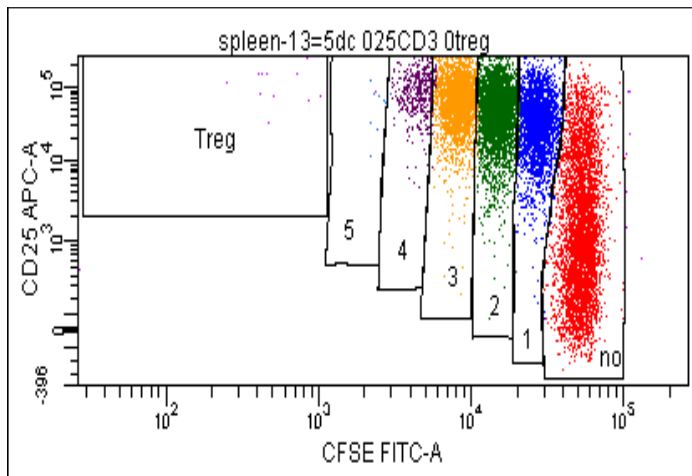
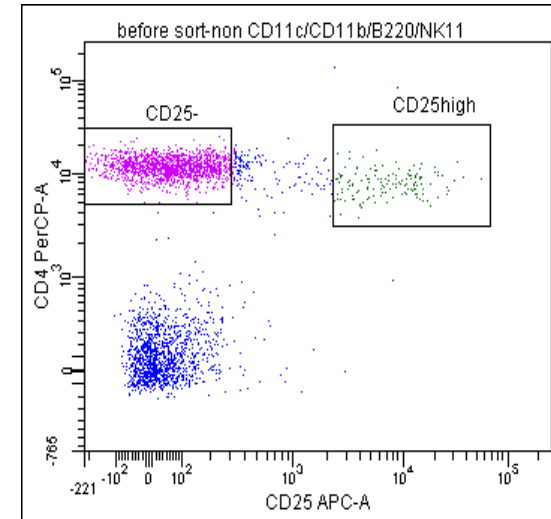
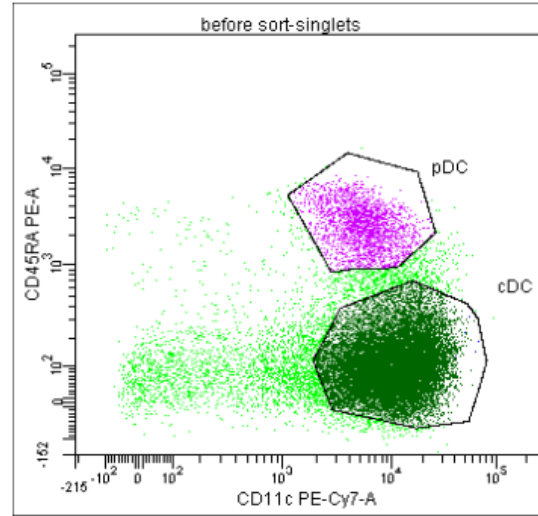
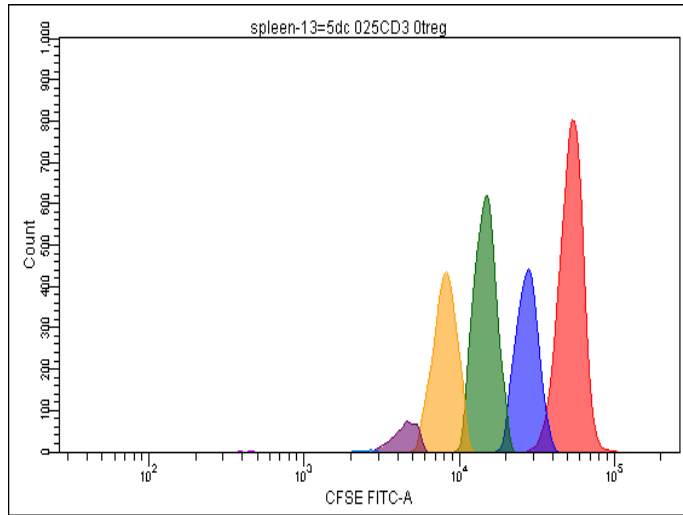
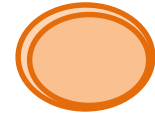
Teff-proliferation and Treg suppression



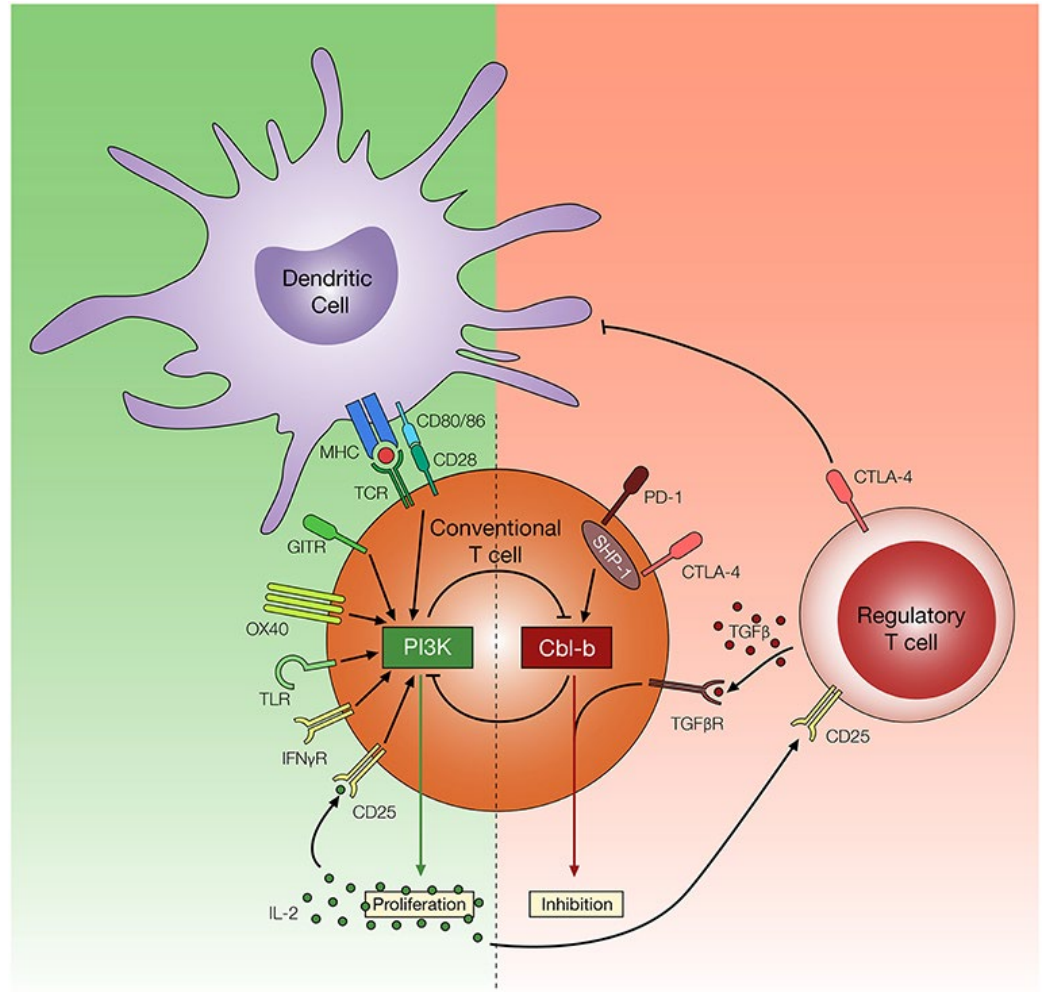
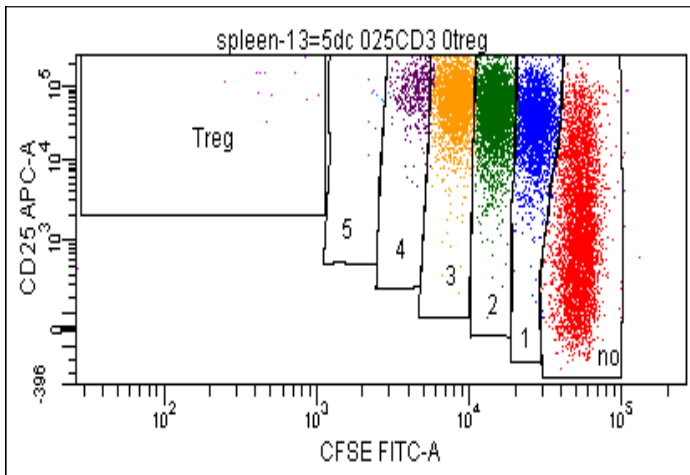
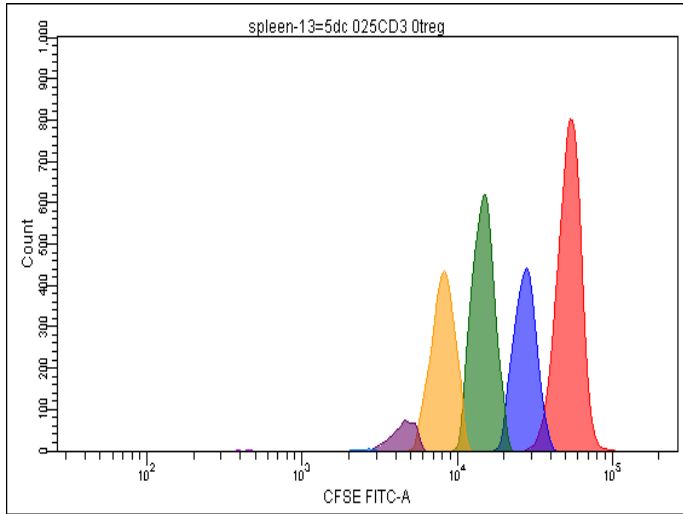
Teff-proliferation and Treg suppression



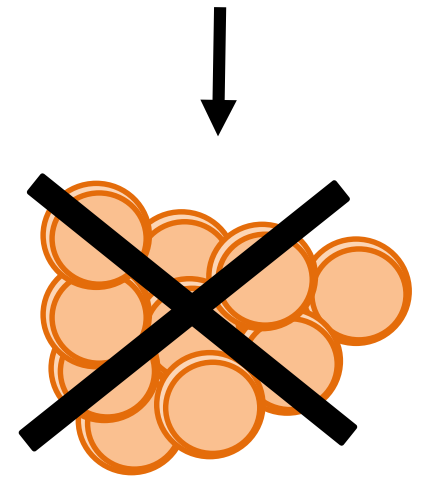
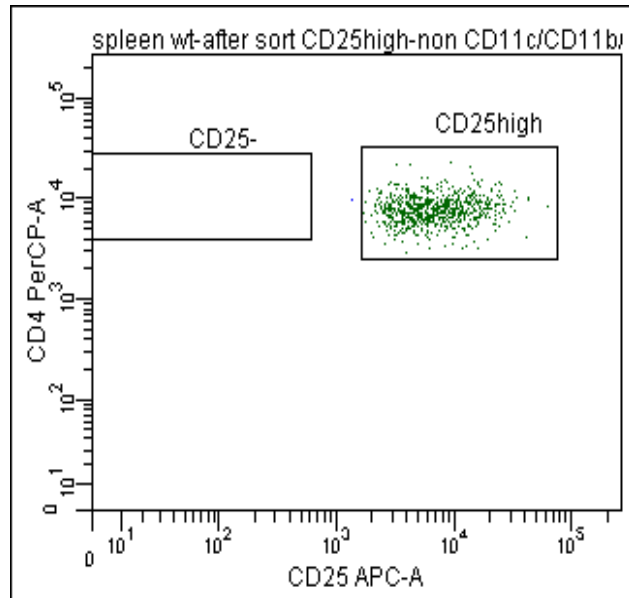
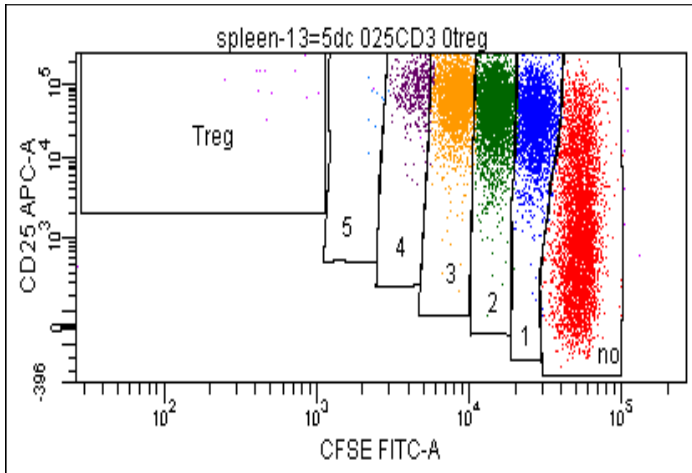
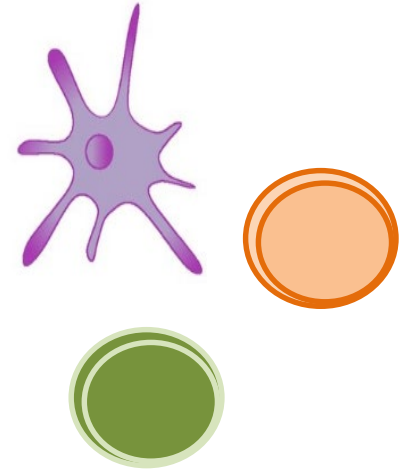
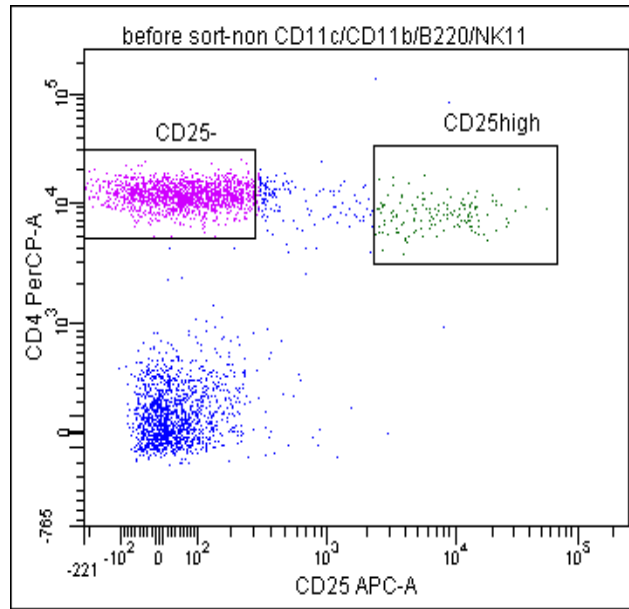
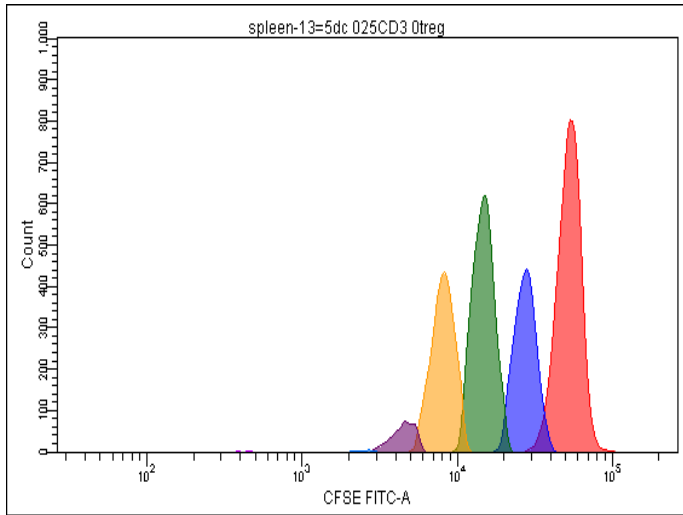
Teff-proliferation and Treg suppression



Teff-proliferation and Treg suppression



Teff-proliferation and Treg suppression

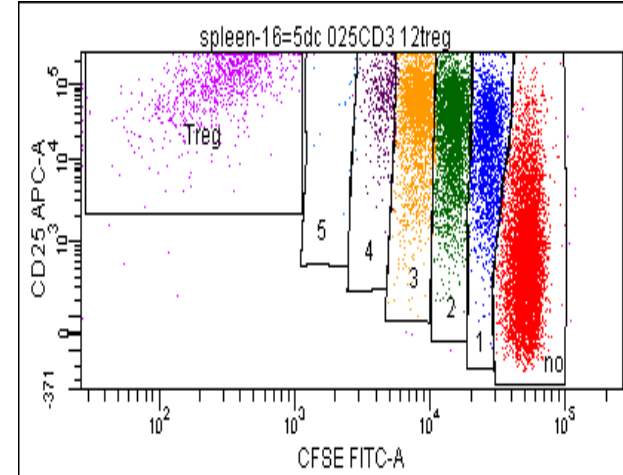
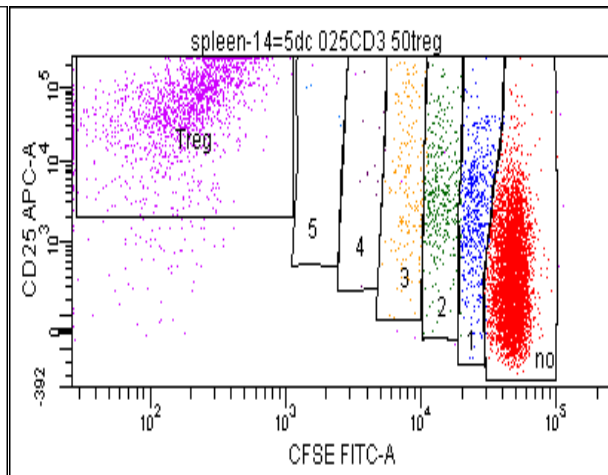
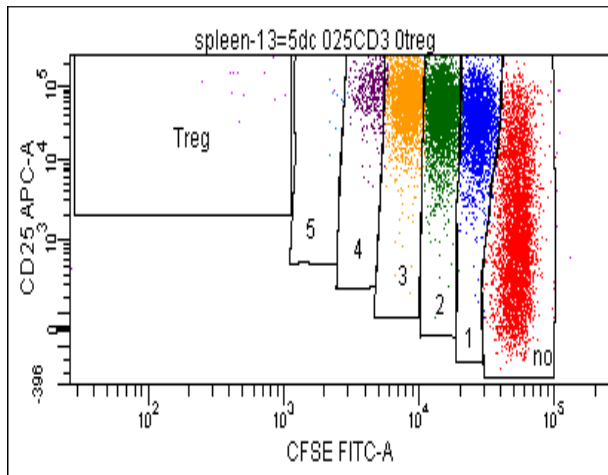
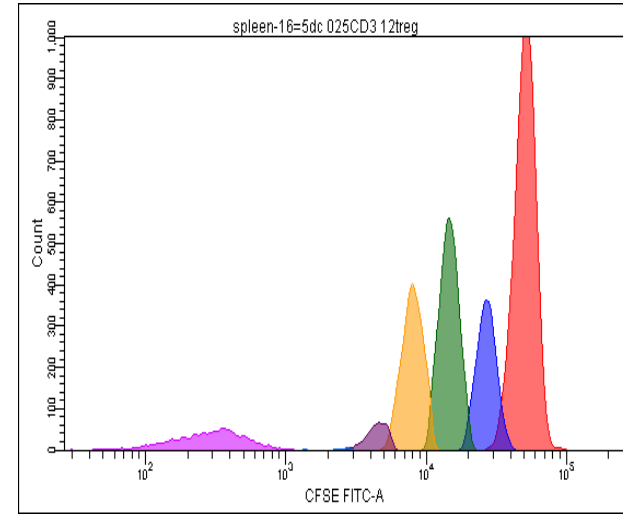
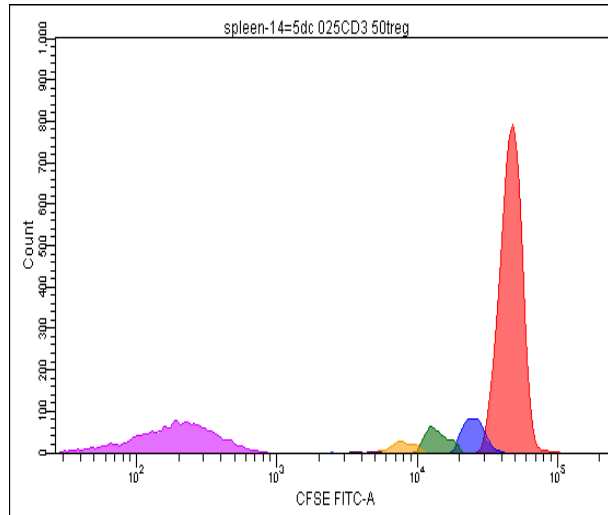
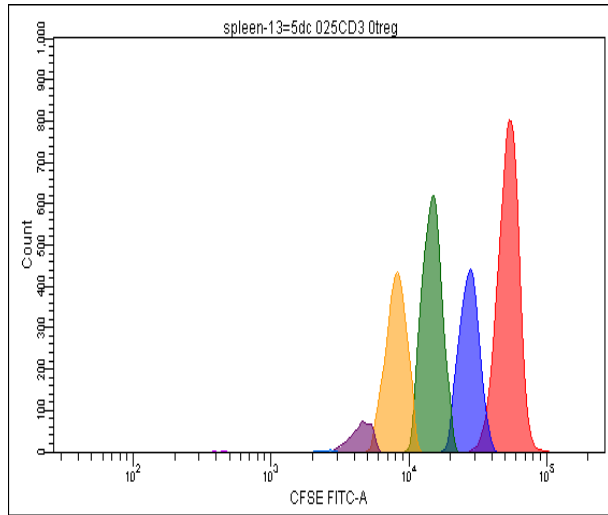


Teff-proliferation and Treg suppression

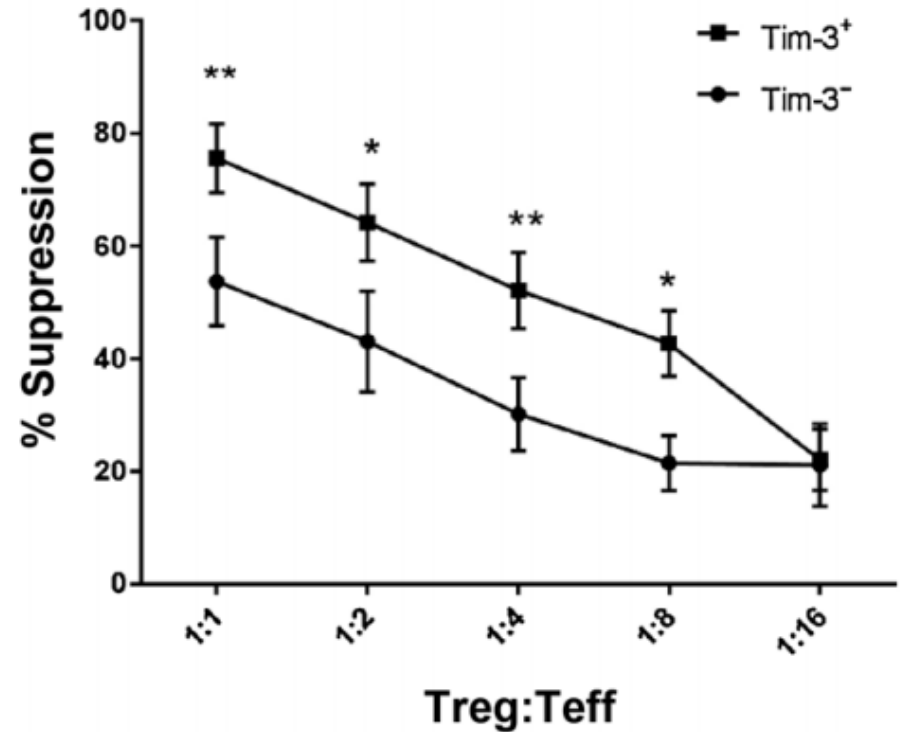
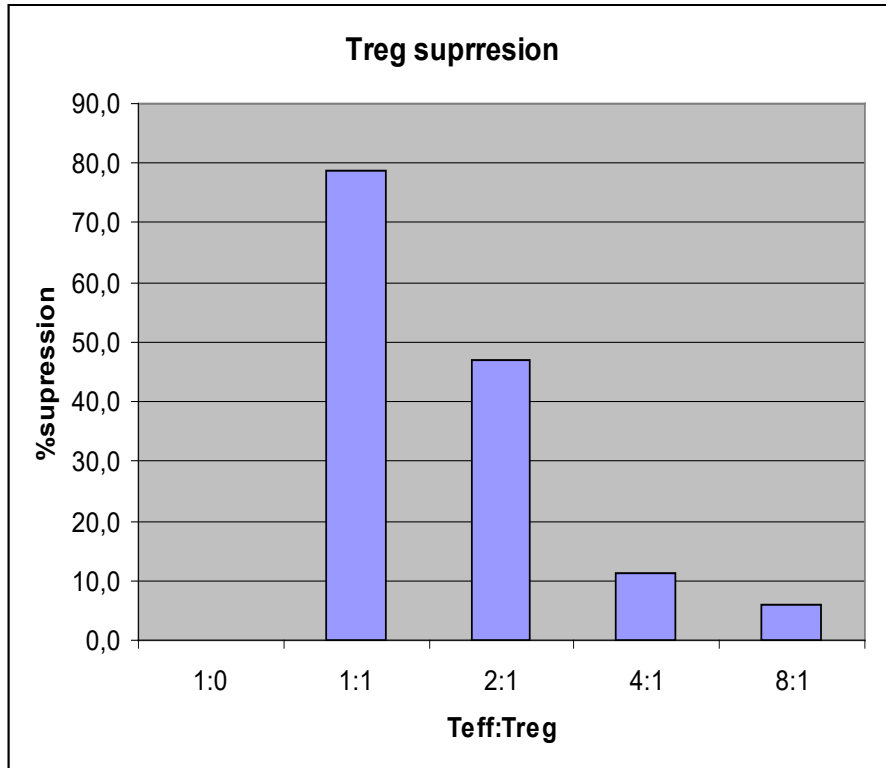
Teff only

Teff:Treg = 1:1

Teff:Treg = 4:1



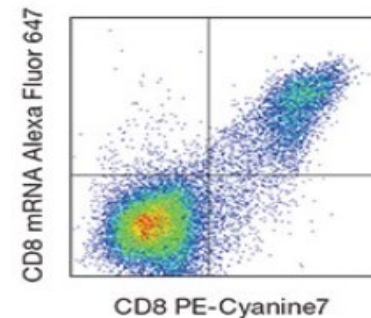
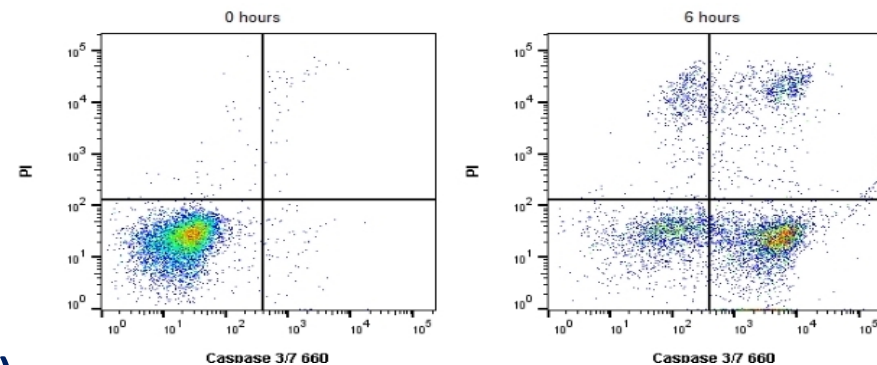
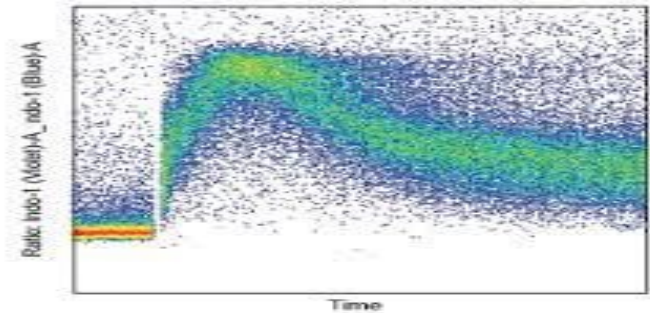
Teff-proliferation and Treg supression



Flowcytometry applications

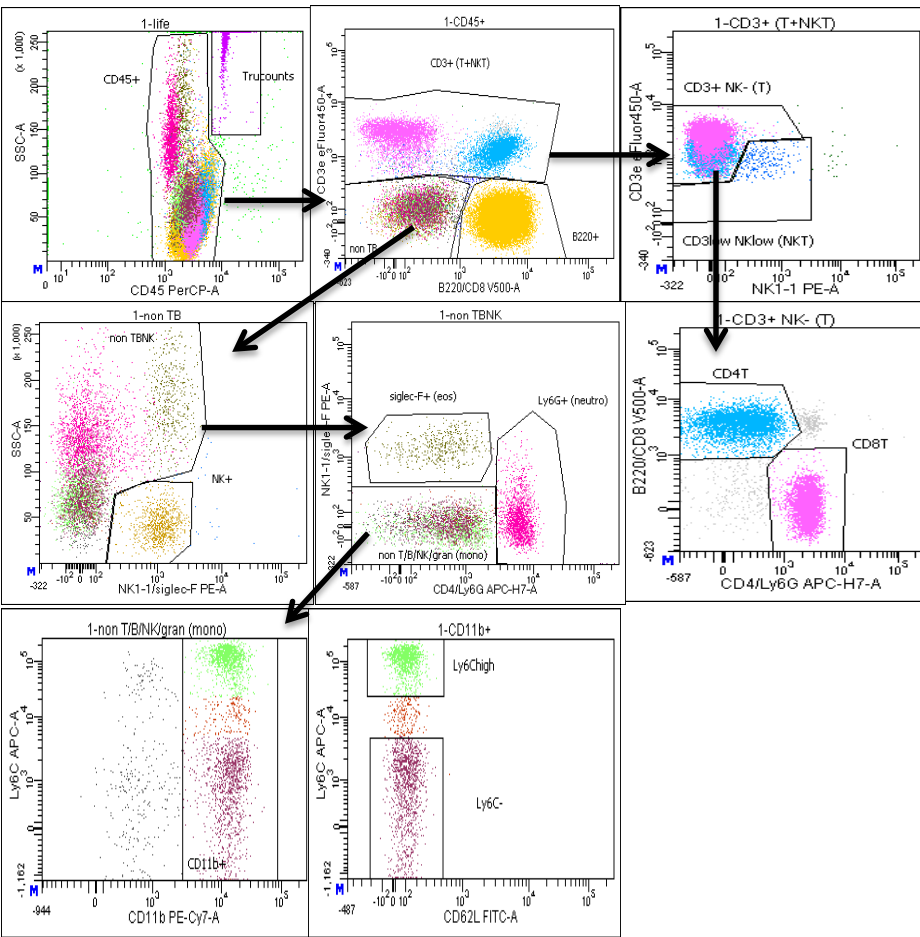
Activity / metabolic dyes

- Ca-flux: FuraRed / Indo-1
- Mitoprobes (Mitochondrial activity)
- Caspase-activity: FLICA
- ROS-assay (oxidative stress)
- mRNA detection

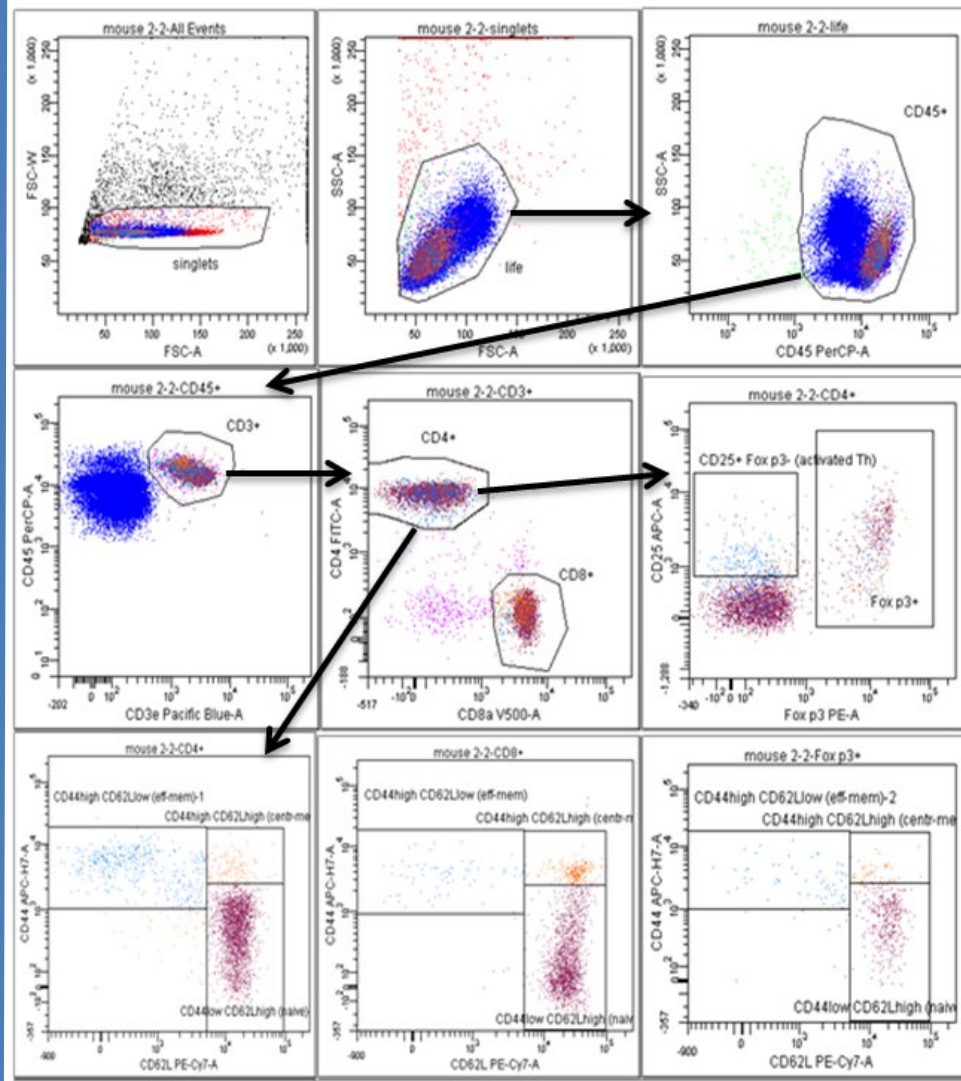


Immune phenotyping

Blood leucocytes

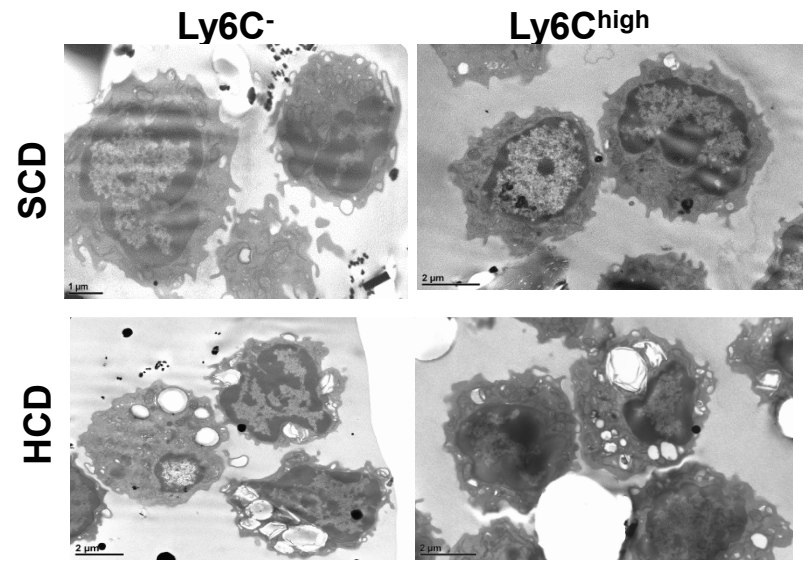
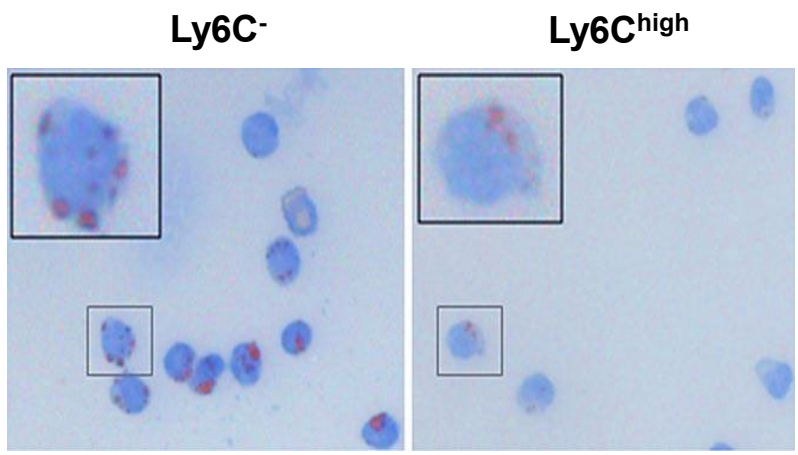
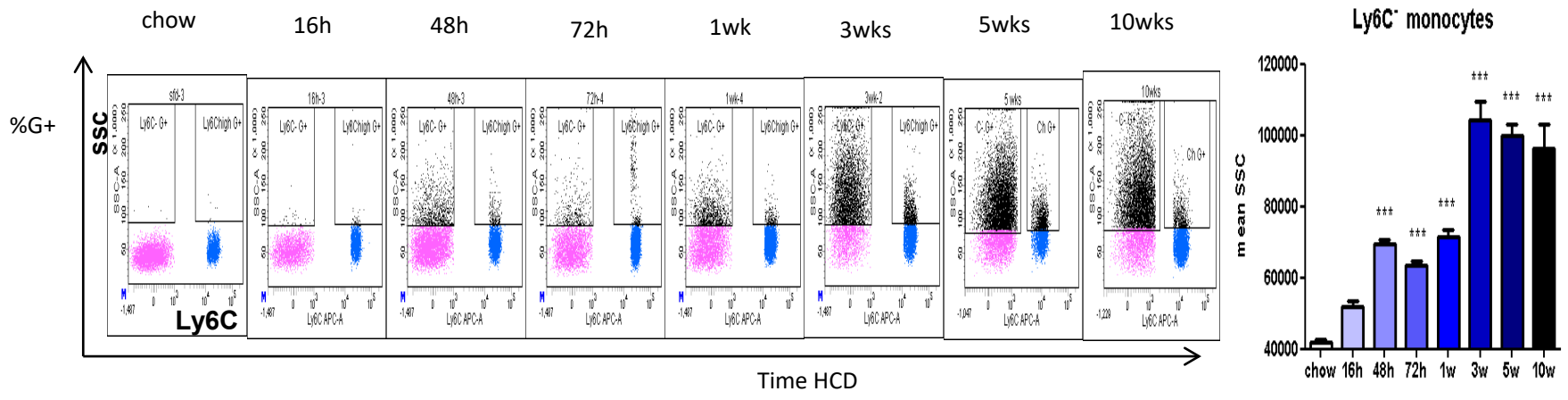


T-cells

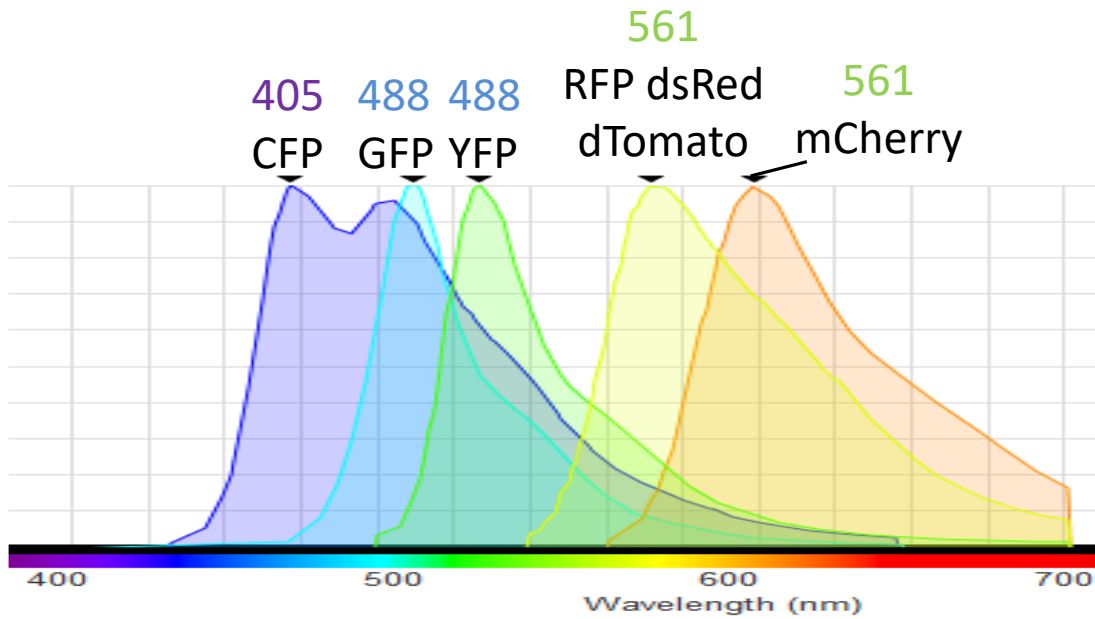


Immune phenotyping

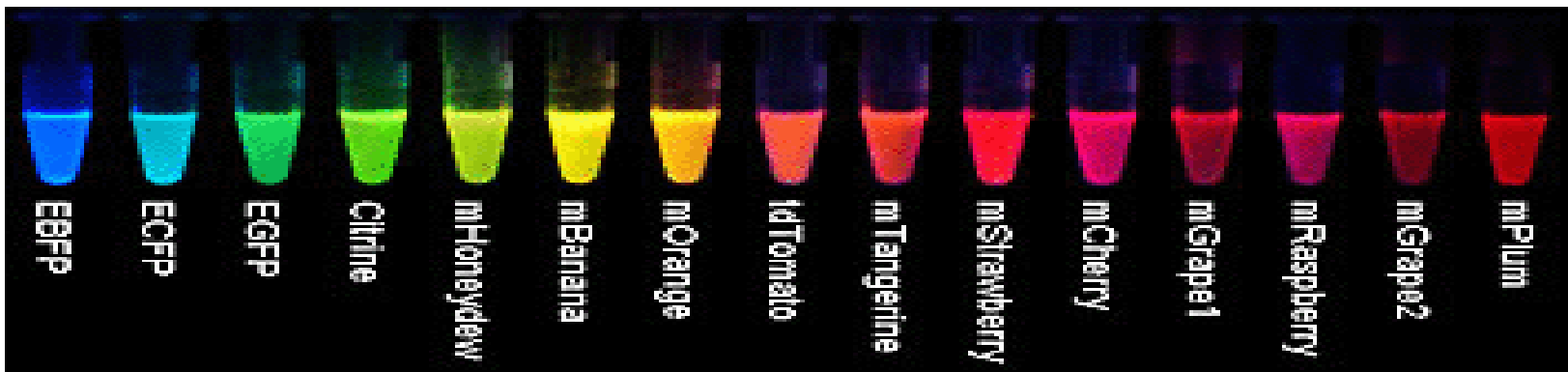
Monocytes: SSC is also a parameter



Fluorescent proteins



Extra filters-sets for
CFP, GFP and YFP



Fluorescent proteins

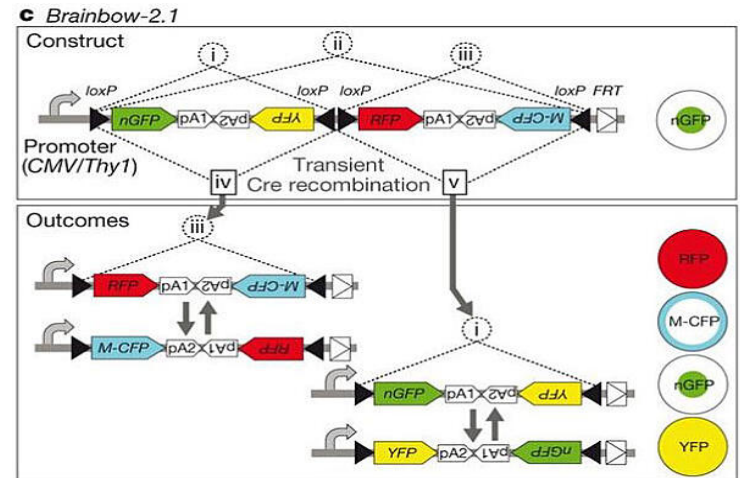
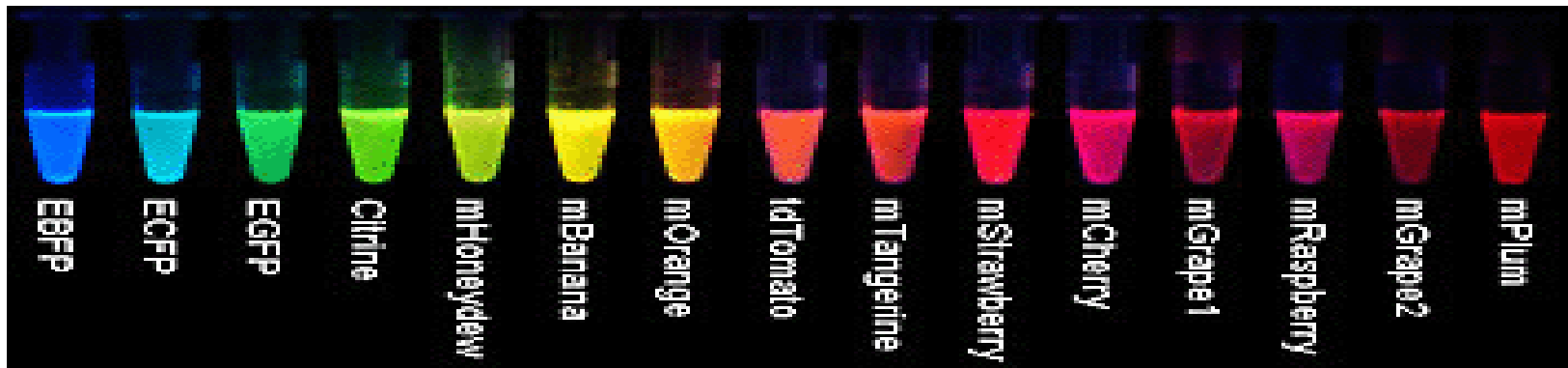


Figure 3: The Brainbow 2.1 construct contains two pairs of XFP, for a total of four possible colors. Cre-mediated recombination leads to the deletion of one pair of XFP, and expression of one of the two remaining XFP. Image from Livet et al., 2007 with permission.

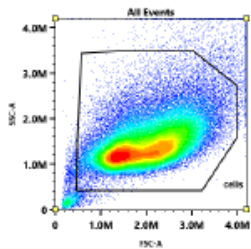
Extra filters-sets for
CFP, GFP and YFP



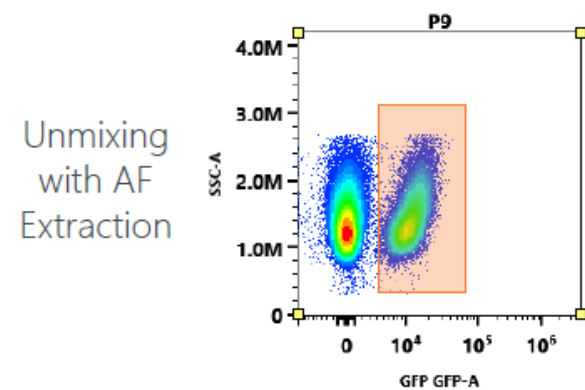
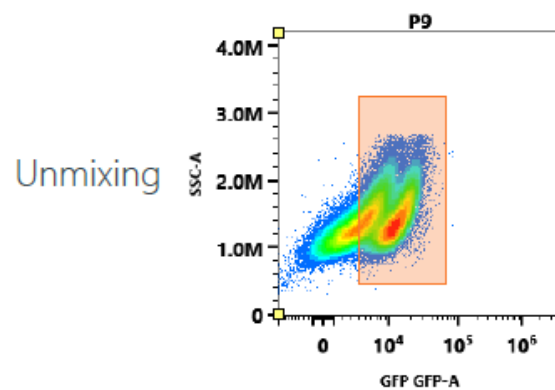
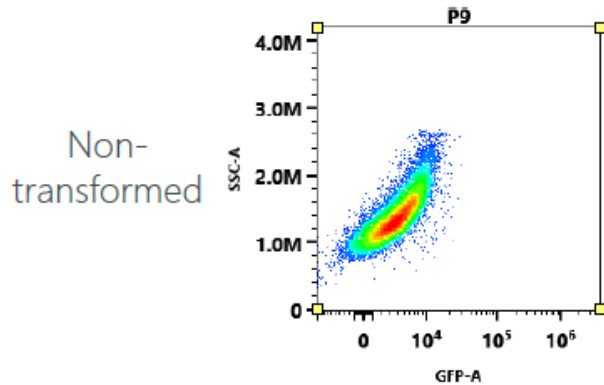
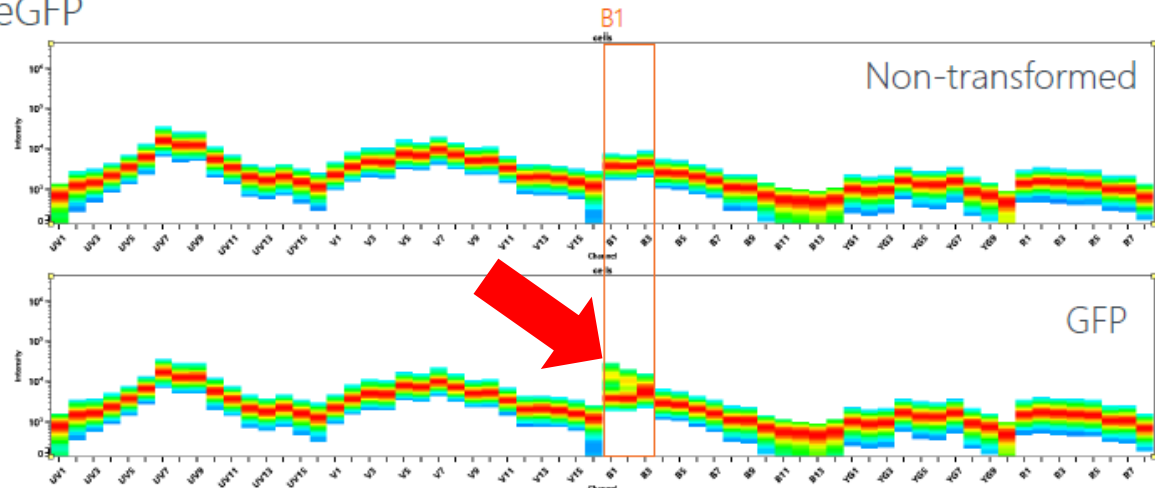
Autofluorescence extraction

Full spectrum flowcytometry: Aurora

iPS cells transformed to express eGFP

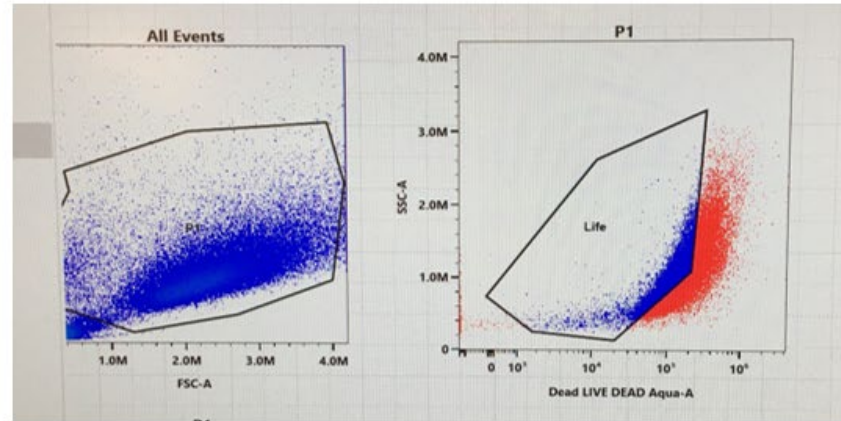


The cells have homogenous signal which indicates we are dealing with 1 AF signature



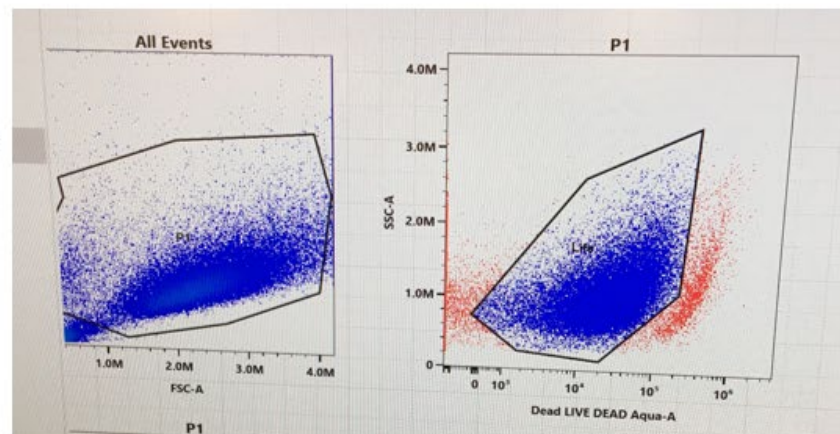
Autofluorescence extraction

Full spectrum flowcytometry: Aurora



Life-dead
resolution not
possible

Autofluorescence
extraction

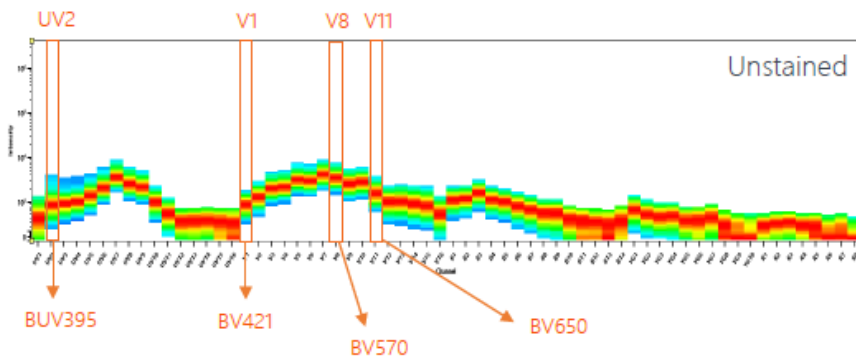
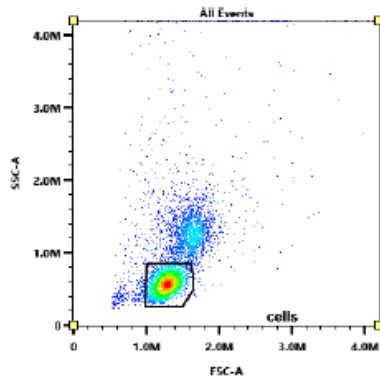


Life-dead
resolution clear!

Autofluorescence extraction

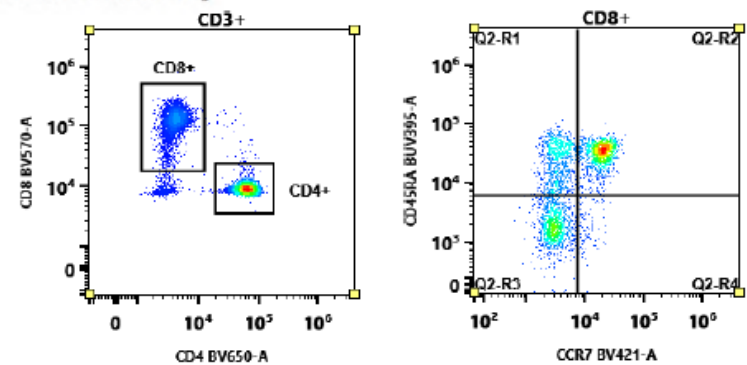
Full spectrum flowcytometry: Aurora

Human PBMCs – 18C Panel



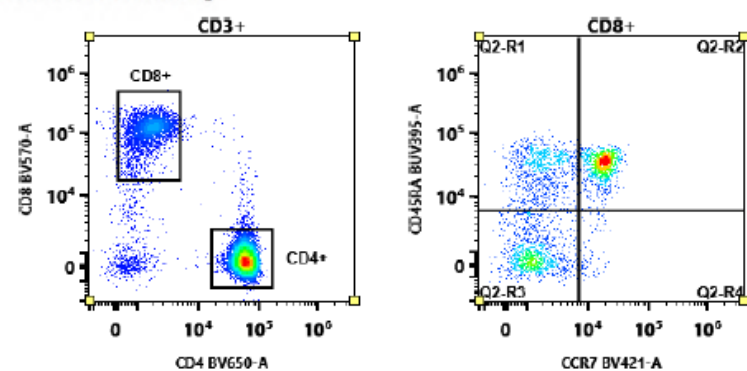
Unmixing

Auto Fluorescence as a Fluorescent Tag

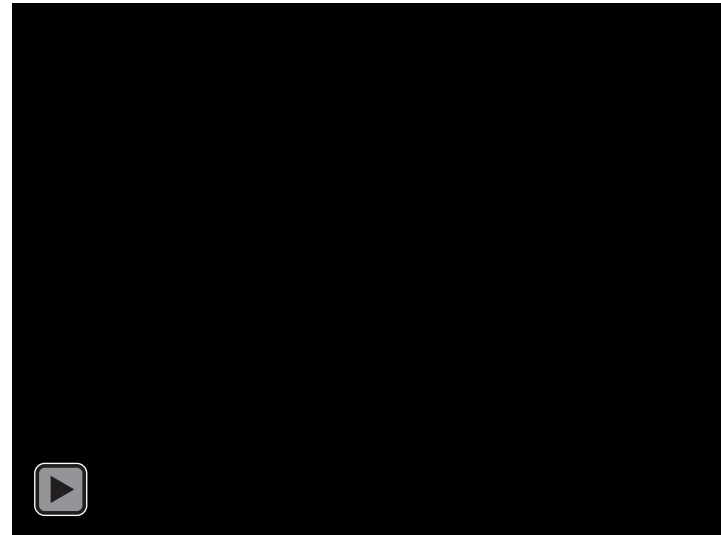
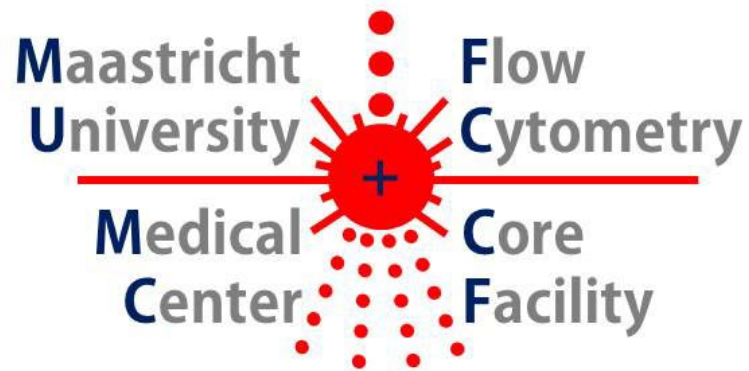


Unmixing with AF Extraction

Auto Fluorescence as a Fluorescent Tag

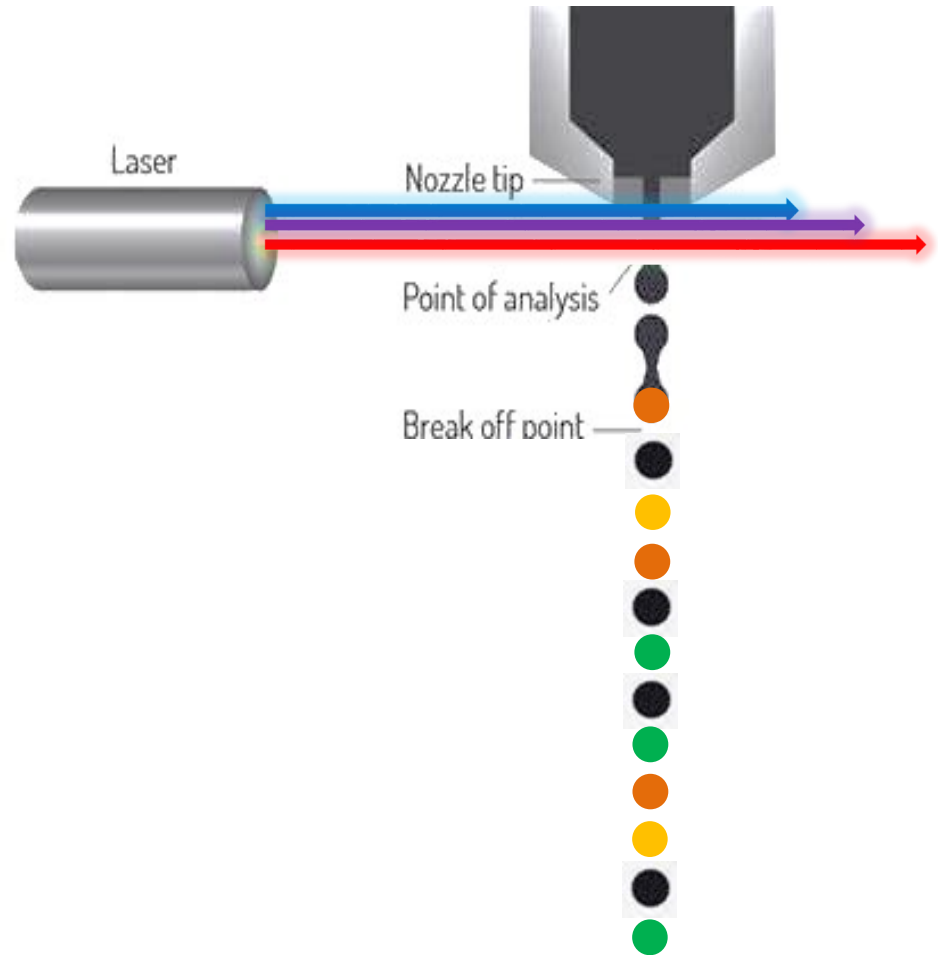
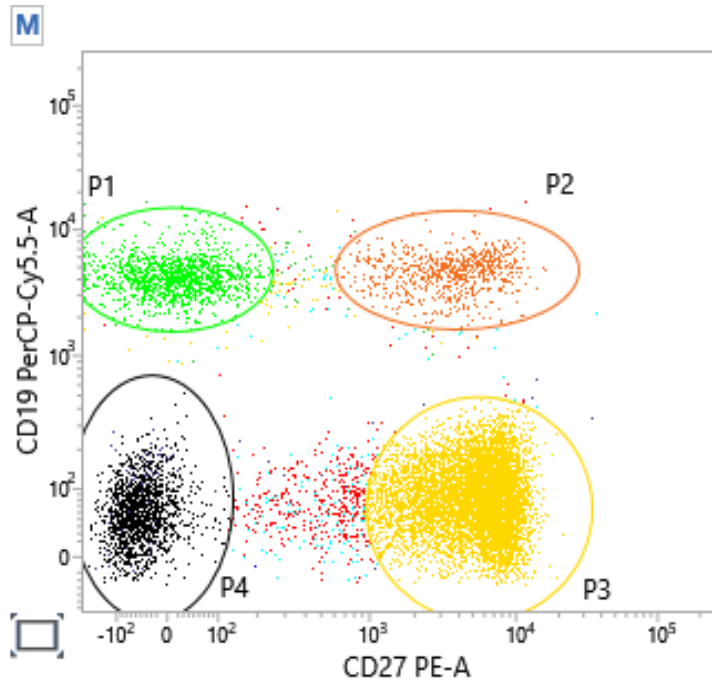


CELL SORTING

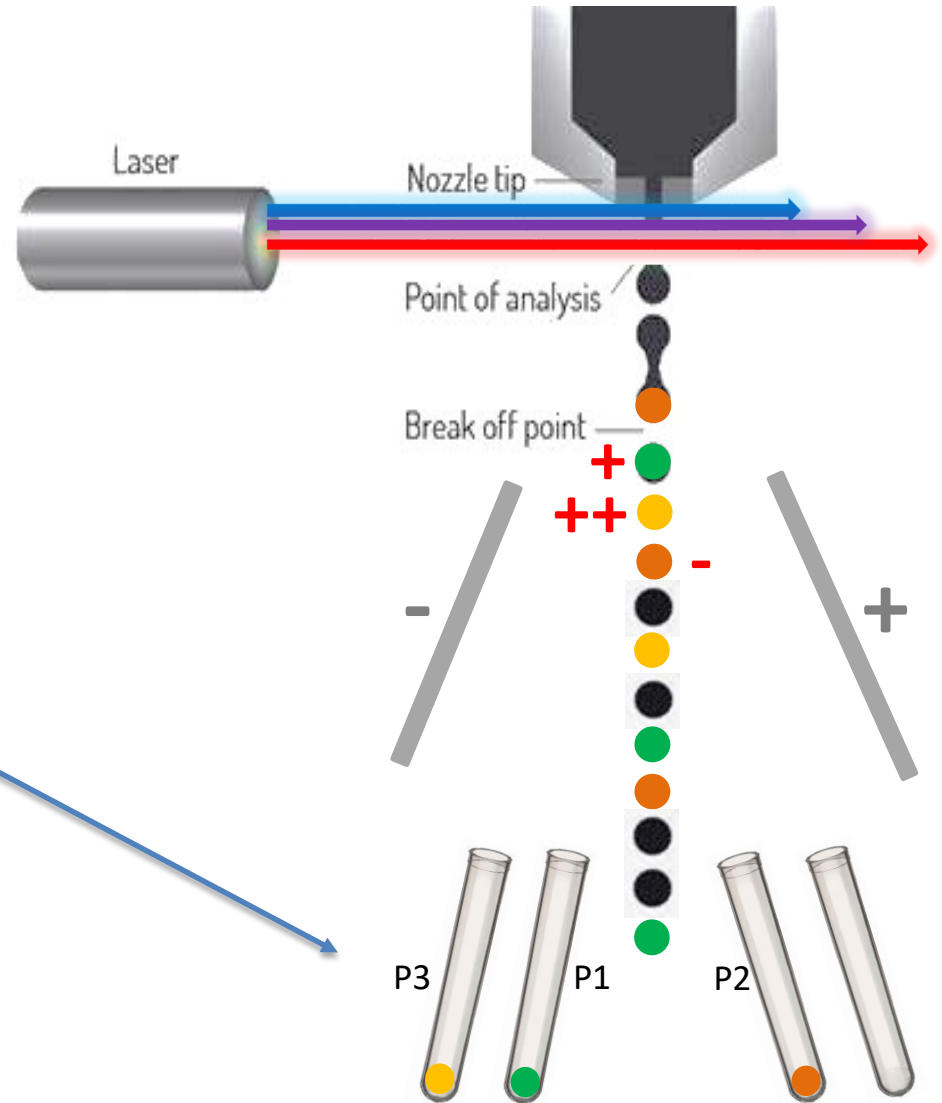
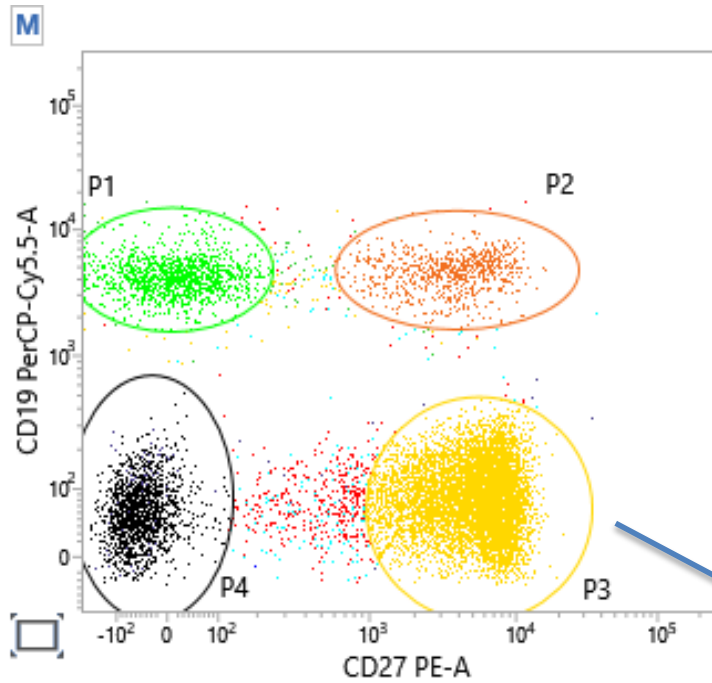


Erwin Wijnands

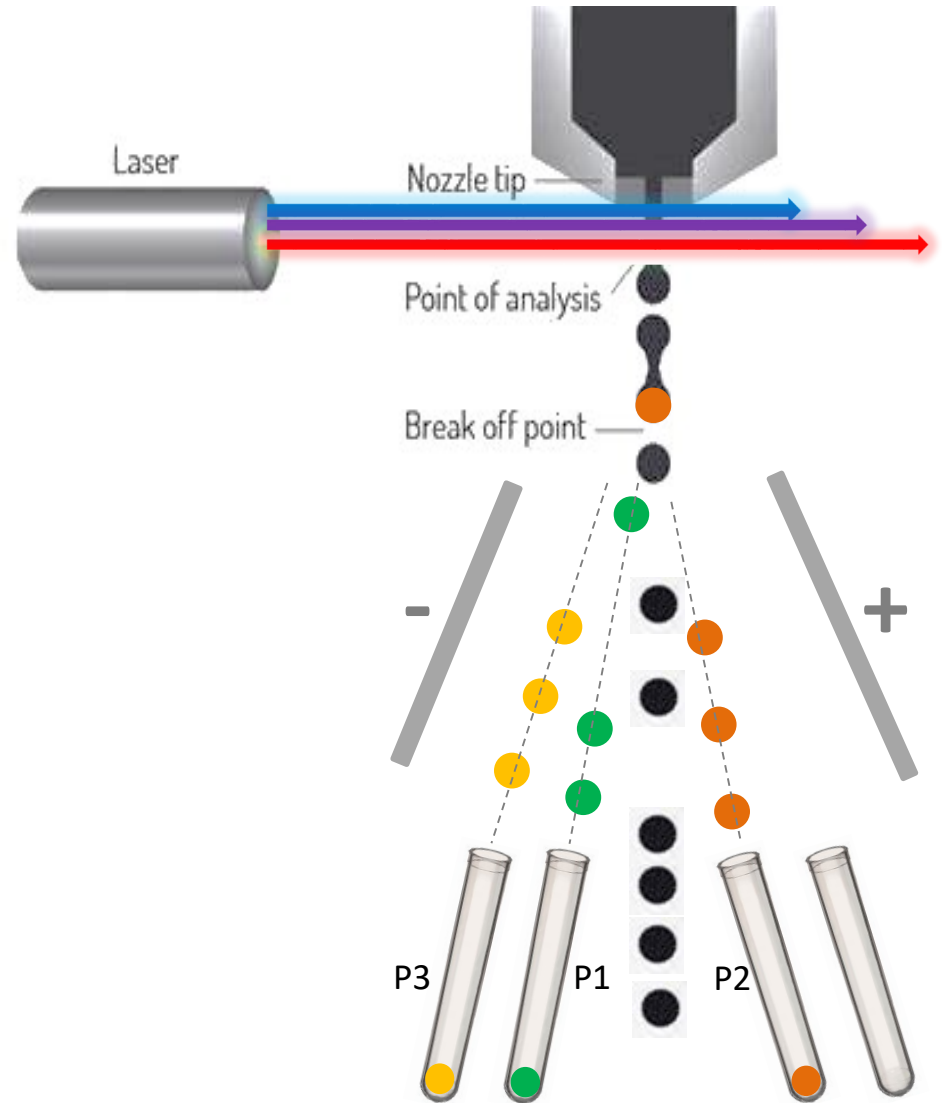
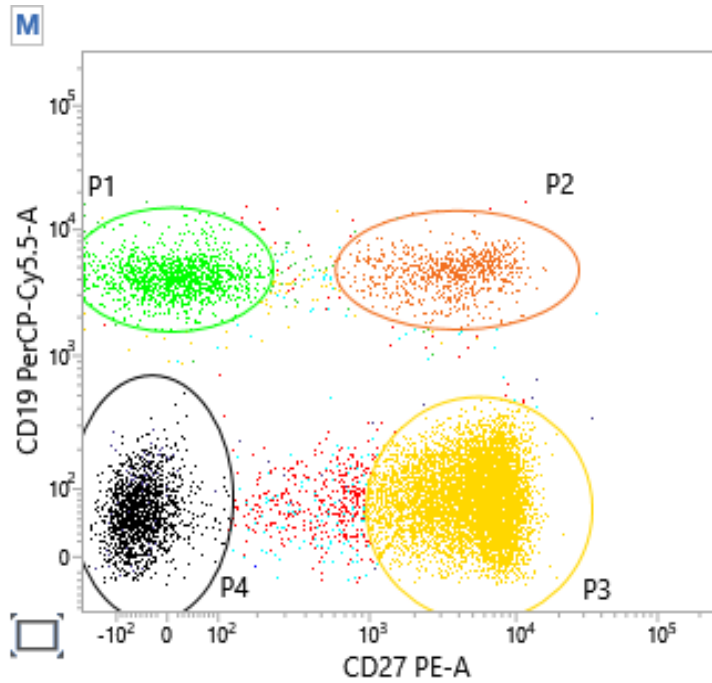
Principle of cell sorting



Principle of cell sorting



Principle of cell sorting

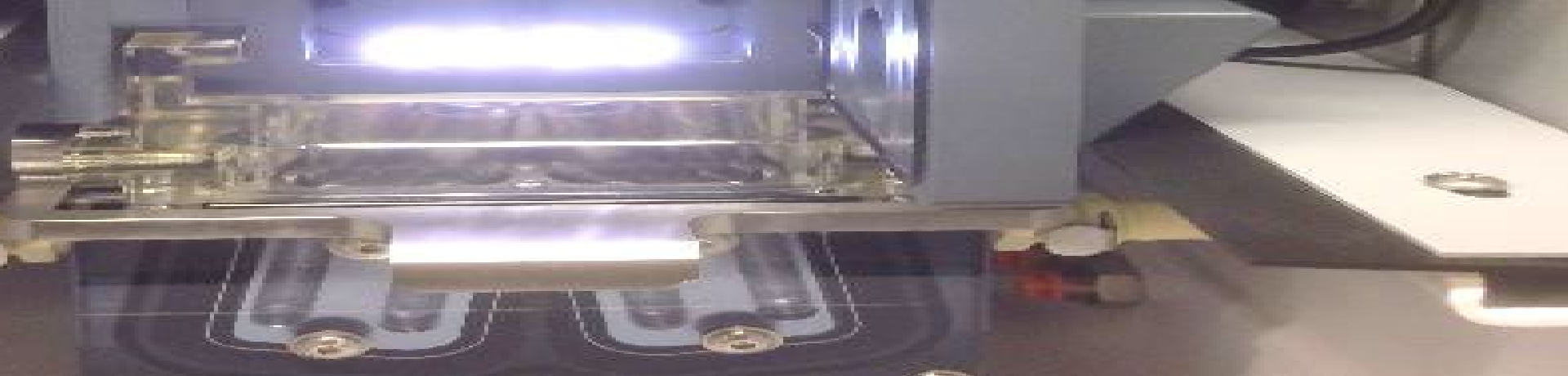




BD Fusion cell sorter

fccf.cdl@mumc.nl



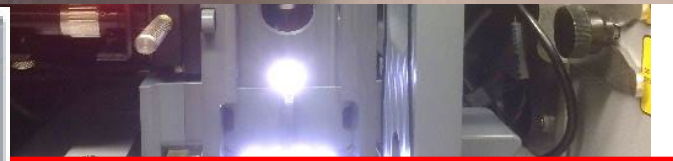


after sort: Sort Layout_001

Device: 4 Tube Precision: 4-Way Purity Target Events: Continuous Save Sort Reports: Ask User Save Conflicts: Index Sorting:

| | Far Left | Left | Right | Far Right |
|--------------|------------|-----------|----------------|-----------|
| | MDM : 2844 | KC : 8980 | granulo : 1556 | |
| Sort Rate: | 4 evt/s | 32 evt/s | 8 evt/s | NA |
| Confl. Cnt: | 460 evt | 1414 evt | 274 evt | NA |
| Confl. Rate: | 0 evt/s | 8 evt/s | 0 evt/s | NA |
| Efficiency: | 88% | 93% | 87% | NA |

Sort Pause View Counters



100 micron

Voltage Test Sort Optical Filter Attenuation Waste Drawer Drop Delay: 27.62 Auto Delay

Four Tube

87 34 29 82

Voltage Center: Plate Voltage: 2,500

2nd Drop: 18 3rd Drop: 8 4th Drop: 0 Phase: 0

Sort Pause View Counters

2020-7-non dump

2020-7-CD11b+

100 micron

Stream Sweet Spot

#Events

| |
|---------|
| 100,000 |
| 26,644 |
| 25,409 |
| 23,234 |
| 5,591 |
| 369 |
| 5,072 |
| 3,764 |
| 2,528 |
| 1,872 |
| 590 |
| 348 |
| 682 |

100 micron

Voltage Test Sort Optical Filter Attenuation Waste Drawer Drop Delay: 27.62 Auto Delay

Four Tube

87 34 29 82

Voltage Center: Plate Voltage: 2,500

2nd Drop: 18 3rd Drop: 8 4th Drop: 0 Phase: 0

Acquisition Dashboard

Current Activity

Active Tube/Well: 2020-7 Threshold Rate: 2820 evt/s Stopping Gate Events: 839178 evt Elapsed Time: 00:07:42

Basic Controls

Unload Stop Acquiring Stop Recording Restart

Acquisition Setup

Stopping Gate: All Events Events to Record: 1000000 evt Stopping Time (sec): 0

Storage Gate: All Events Events to Display: 100000 evt Flow Rate: 2.2

Acquisition Status

Processed Events: 839178 evt Electronic Abort Rate: 12 evt/s

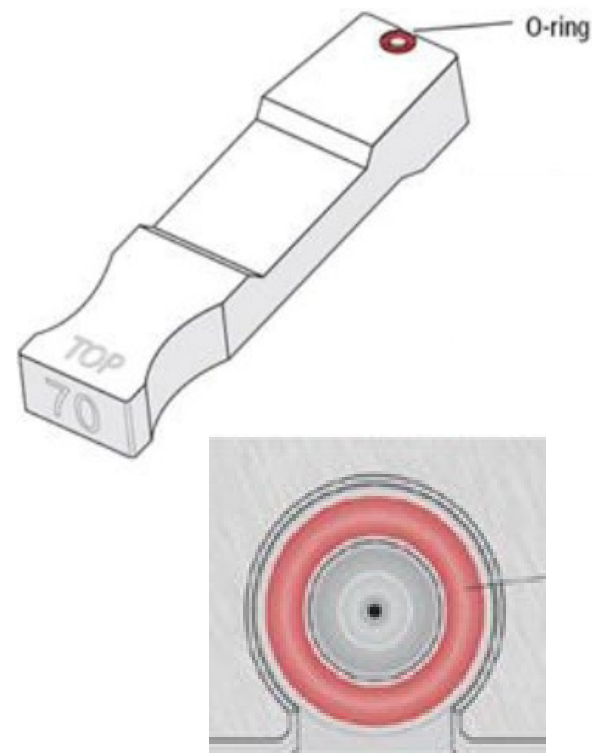
Threshold Count: 551539 evt Electronic Abort Count: 1834 evt

Ampl: 3.5 Freq: 30.4 Drop 1: 205 213 Gap: 13 13

Options of the BD Fusion cell sorter

Nozzle sizes

| Cell types | Nozzle size |
|---|-------------|
| Lymphocytes | 70 |
| Activated lymphocytes, small cell-lines | 85 |
| Monocytes, large adherent cells, iPSC's, solid tissue preparations | 100 |
| Cardiomyocytes, fibroblasts, very large cells | 130 |



Options of the BD Fusion cell sorter

Nozzle sizes



70uM



70uM



100uM

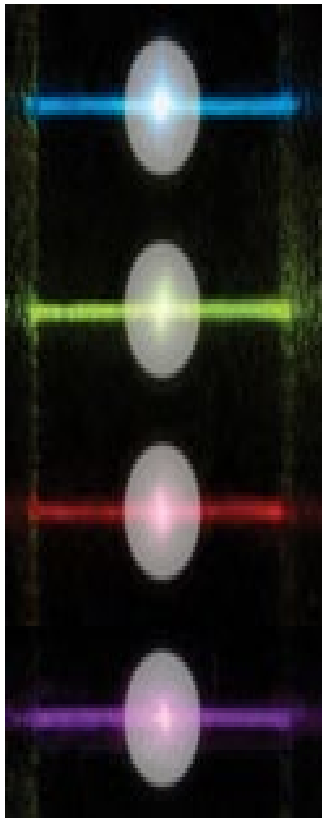
Options of the BD Fusion cell sorter

Nozzle sizes

| Nozzle size | Max event/rate | Max # Cells/hour |
|-------------|----------------|------------------|
| 70 | 20K/s | 40*10e6 |
| 85 | 10K/s | 20*10e6 |
| 100 | 8K/s | 15*10e6 |
| 130 | 2K/s | 7*10e6 |

Options of the BD Fusion cell sorter

Lasers and detectors

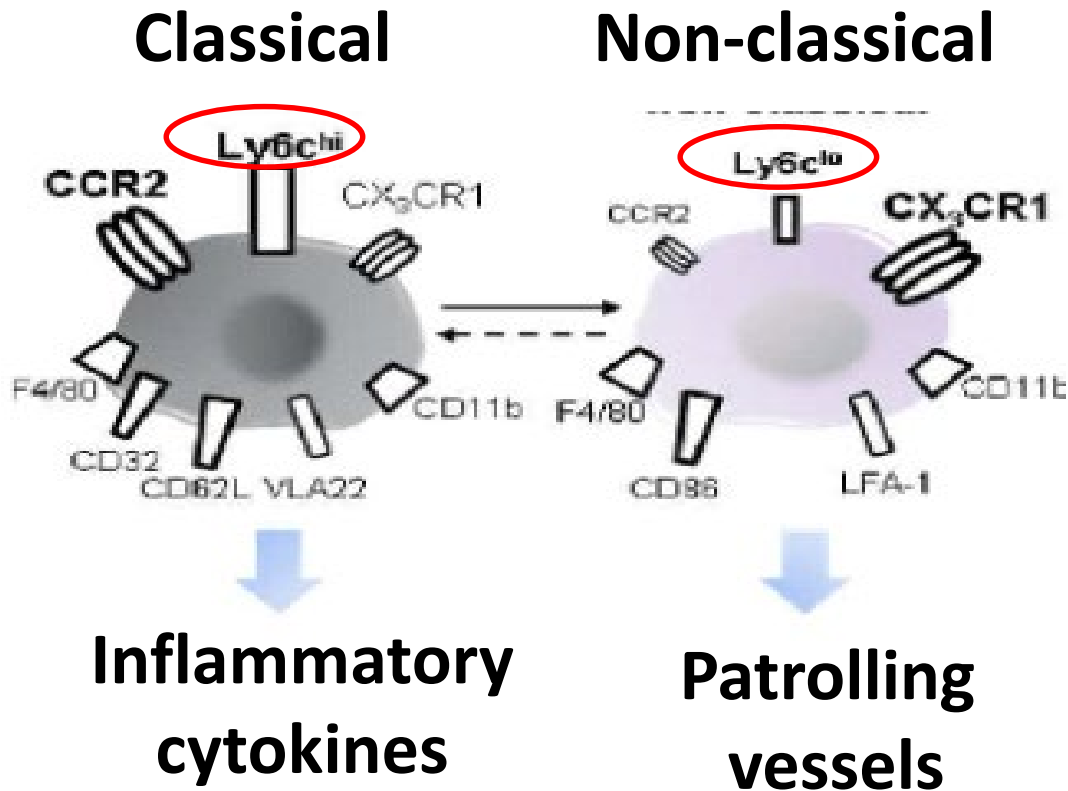


| Laser | LP | BP | Examples |
|-------|-----|--------|-------------------------|
| 488 | 655 | 695/40 | PerCp-Cy5.5, PerCp, YFP |
| | 502 | 530/30 | FITC, CFSE, GFP |
| | - | 488/10 | SSC |
| 561 | 735 | 780/60 | PE-Cy7 |
| | 685 | 710/50 | PE-Cy5.5 |
| | 630 | 670/14 | PE-Cy5 |
| | 600 | 610/20 | PE-Cy594, PI, mCherry |
| | - | 582/15 | PE, DsRed |
| 640 | 755 | 780/60 | APC-Cy7, APC-H7 |
| | - | 670/30 | APC, Alexa647 |
| | 690 | 730/45 | Alexa700 |
| 405 | 750 | 780/60 | BV786 |
| | 690 | 710/50 | BV711 |
| | 630 | 660/20 | BV650 |
| | 595 | 610/20 | BV605 |
| | 505 | 525/50 | BV480, BV510, V500, CFP |
| | - | 450/40 | BV421, V450, PB, DAPI |

**Fluorescent Activated
Cell sorting
Applications**

Monocyte subsets in high fat diet

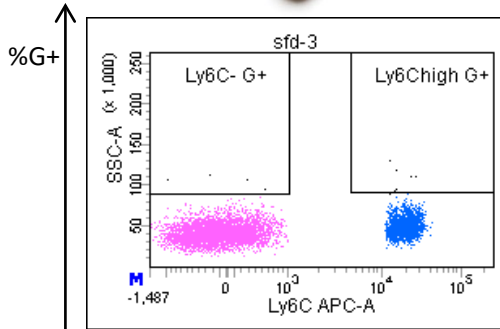
Isolation of monocyte subsets by FACS-sorting:



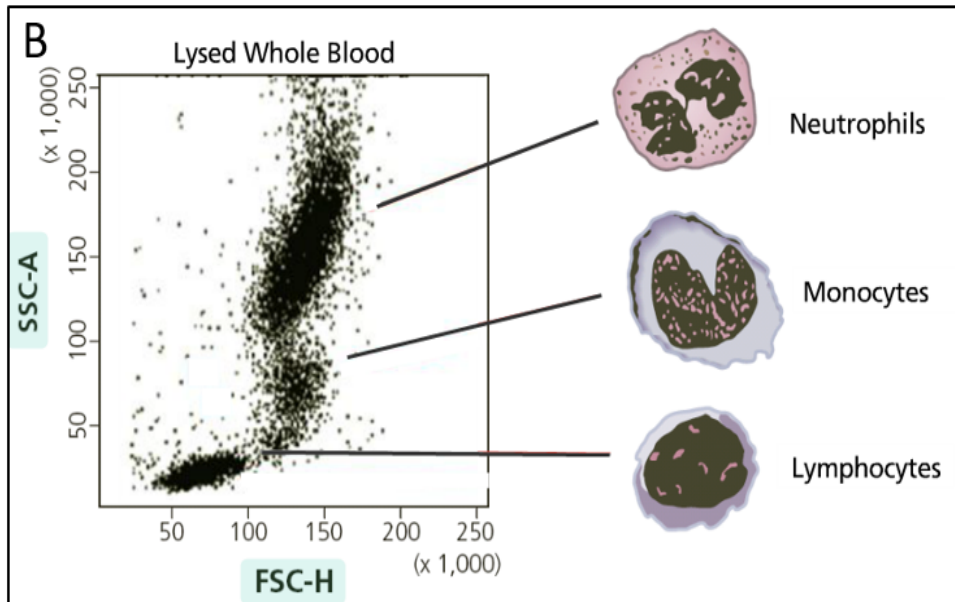
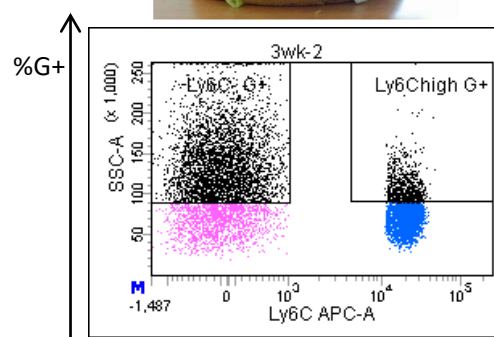
Monocyte-subsets in high fat diet

Isolation of monocyte subsets by FACS-sorting:

chow

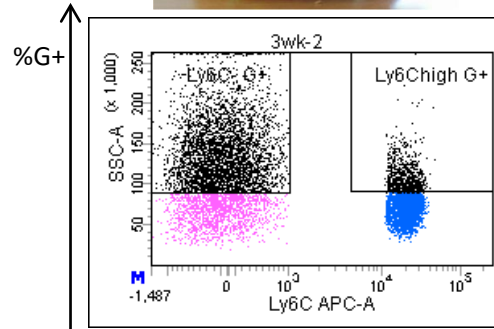
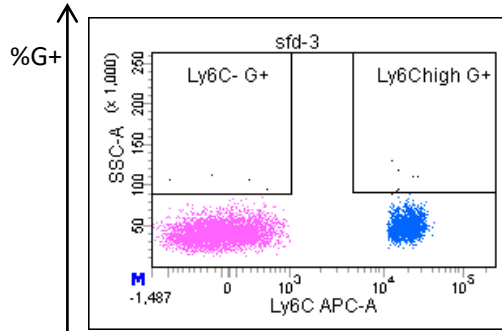


3wks HFD

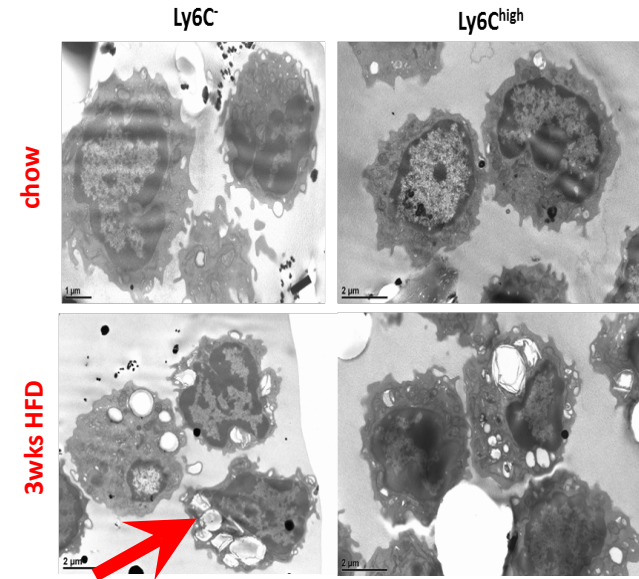


Monocyte-subsets in high fat diet

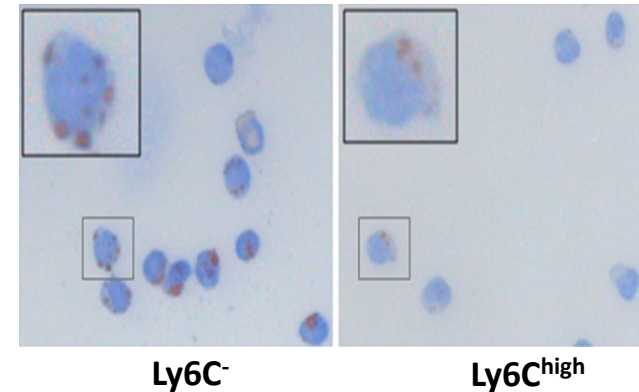
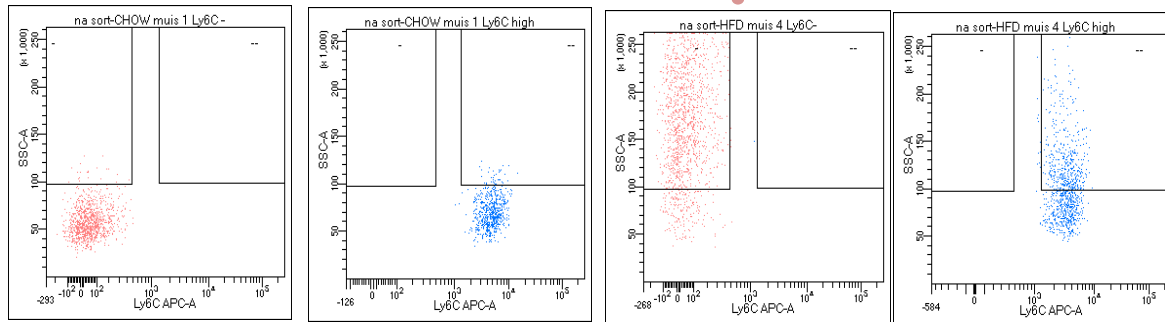
Isolation of monocyte subsets by FACS-sorting:



EM:

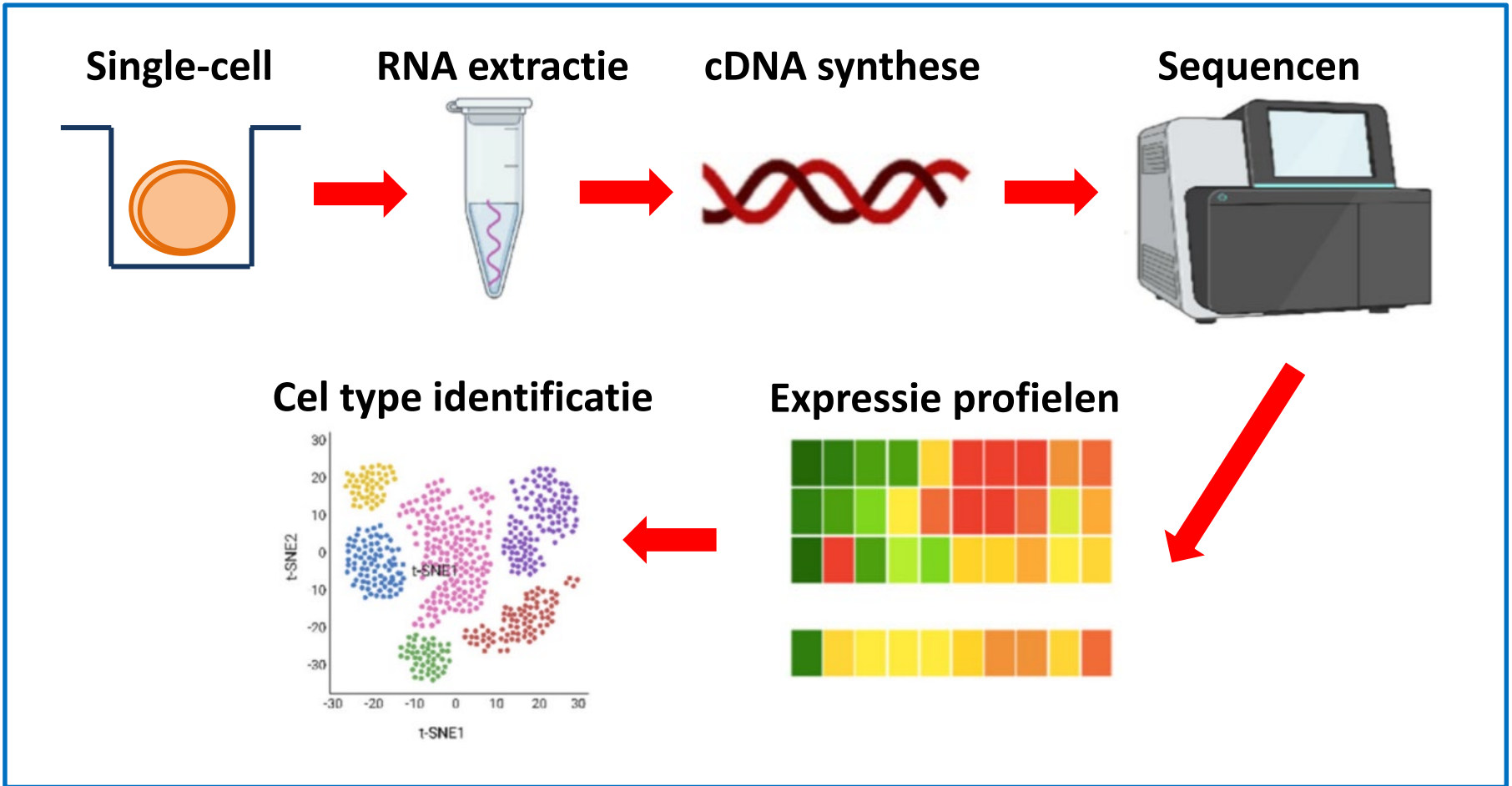


OilRedO fat stain:



Single Cell Sorting

Single cell RNAseq (uencen)



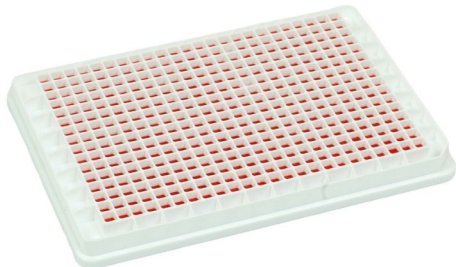
Single Cell Sorting

Single cell RNAseq (uencen)



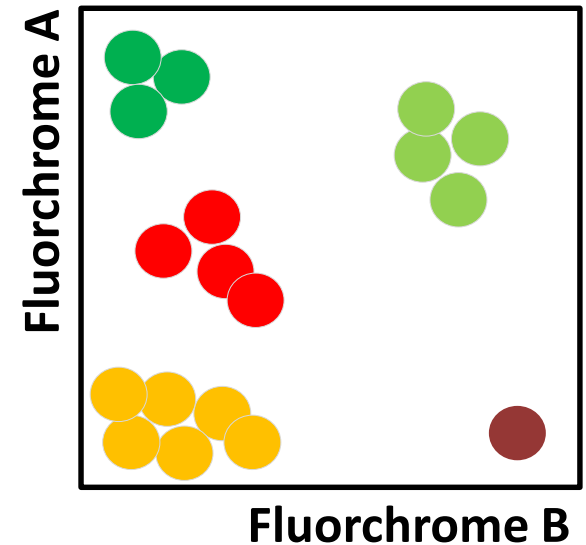
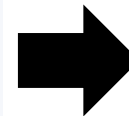
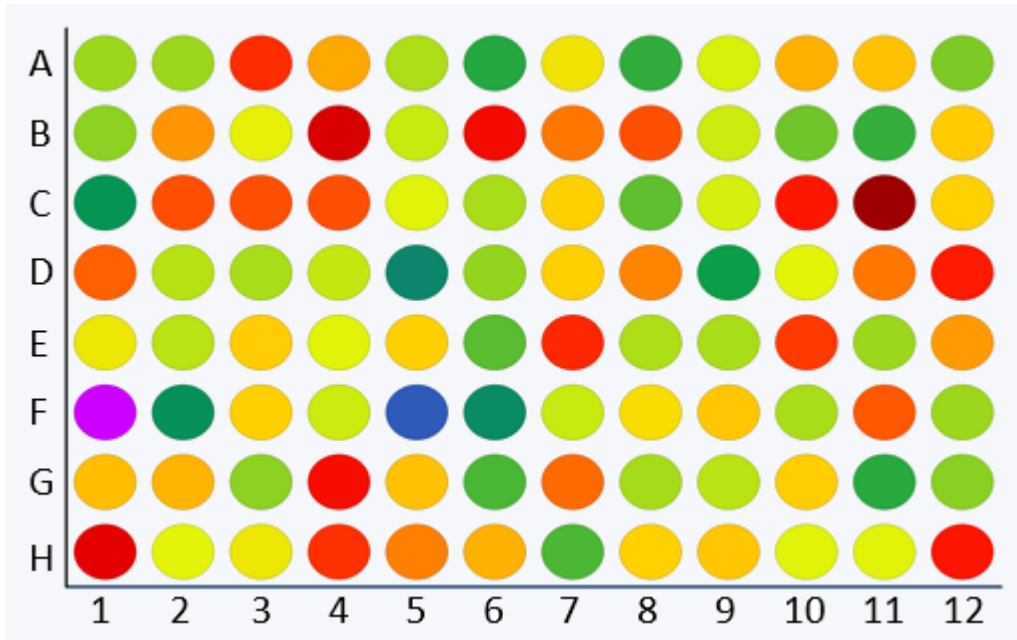
Global Sheet1: Sort Layout_002

| Device: | Precision: | Target Events: | Save Sort Reports: | Save Conflicts | Index Sorting | |
|------------------|---|---|---|---|---|---|
| 96 Well - Falcon | Single Cell | 1 | Ask User | <input type="checkbox"/> | <input checked="" type="checkbox"/> | |
| | 1 | 2 | 3 | 4 | 5 | 6 |
| A | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 |
| B | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 |
| C | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 |
| D | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 |
| E | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 |
| F | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 |
| G | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 |
| H | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 | <input checked="" type="checkbox"/> GFP : 1 |



Single Cell Sorting

Index sorting

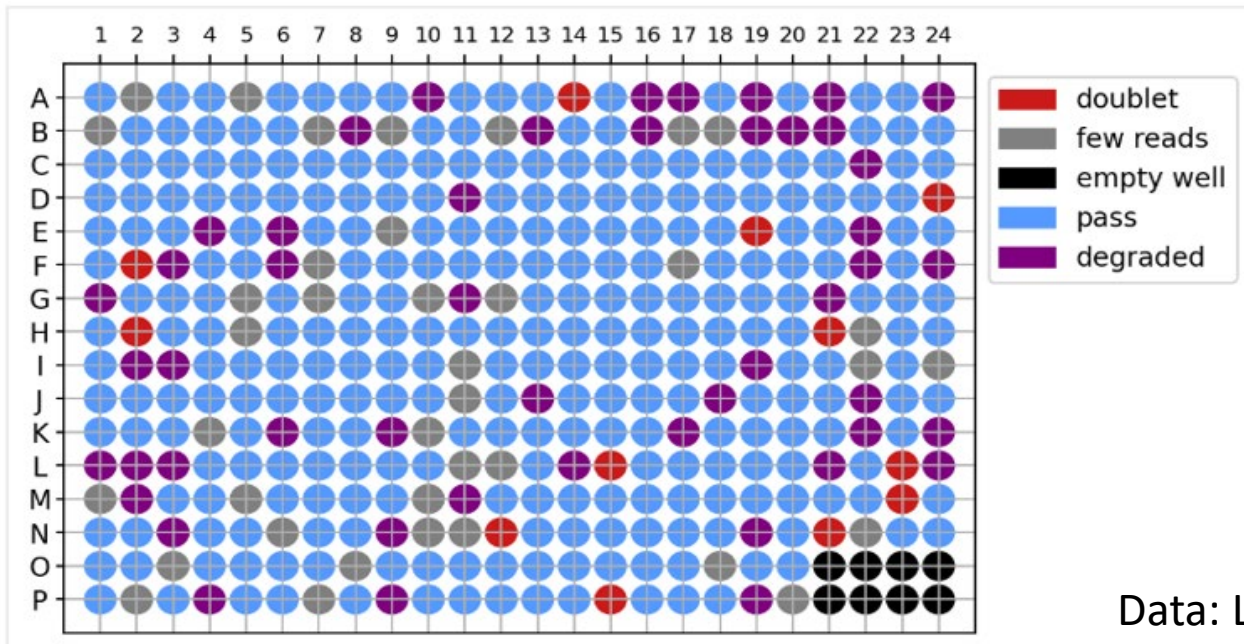


Met terugwerkende kracht toekennen van populaties aan het moleculiare profiel van oppervlakte marker expressie

Single Cell Sorting

Single cell RNAseq (uencen)

| Sample Name | Enzyme | Condition | Library type | Sample | Mapped reads % |
|-------------------------|--------|-----------|--------------|---------|----------------|
| SCC-scKaryo-MMC-VOO-007 | NlaIII | Organoid | sc | PGO-007 | 89.8% |
| SCC-scKaryo-MMC-VOO-008 | NlaIII | Organoid | sc | PGO-027 | 87.2% |
| SCC-scKaryo-MMC-VOO-009 | NlaIII | Organoid | sc | PGO-027 | 86.4% |
| SCC-scKaryo-MMC-VOO-010 | NlaIII | Organoid | sc | PGO-030 | 87.1% |



Data: Linde Hoosemans
MAASTRO-lab

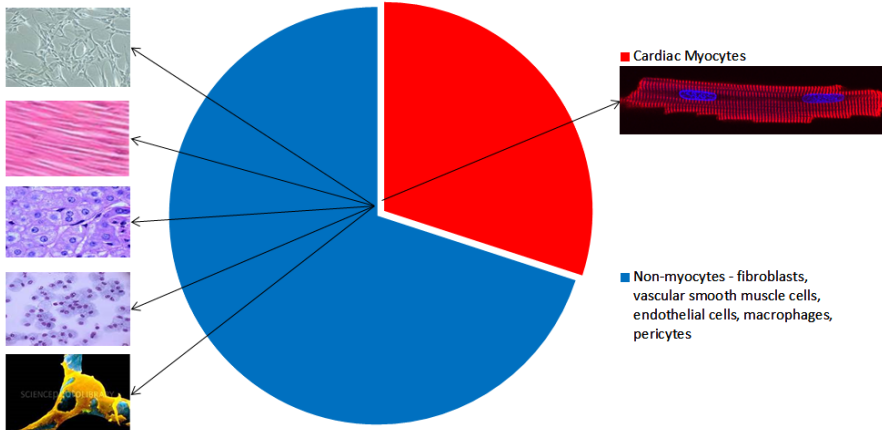
Nuclear sorting

Cell-type specific transcriptomics and epigenomics



Cardiomyocytes:

- Too big
- Changes in genome during long isolation



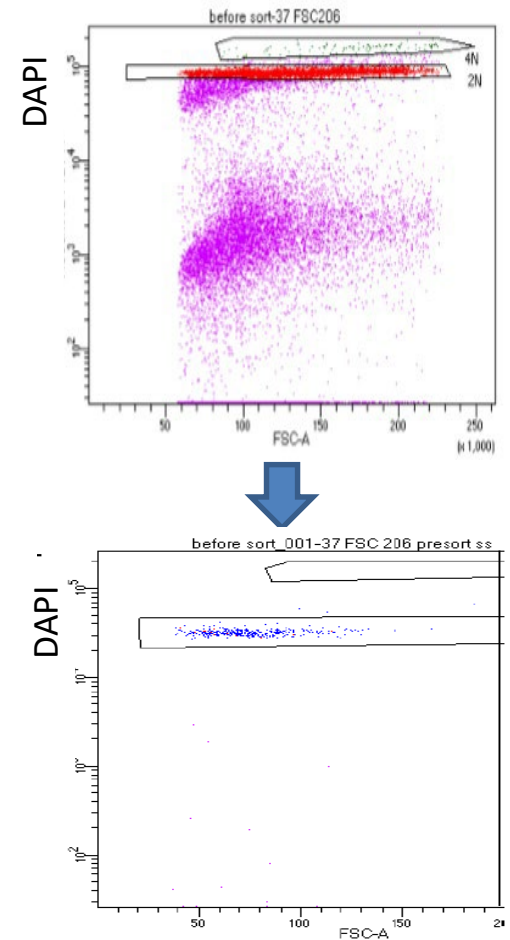
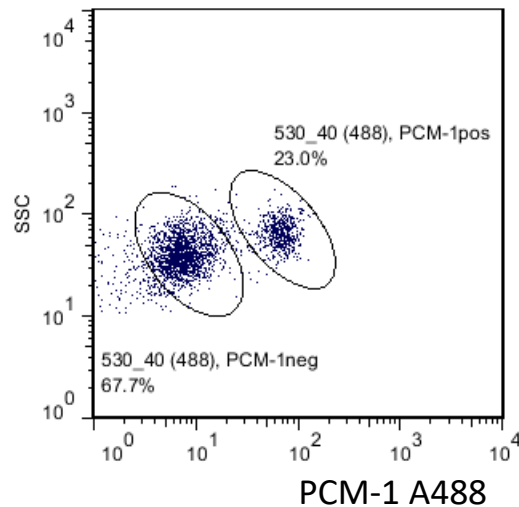
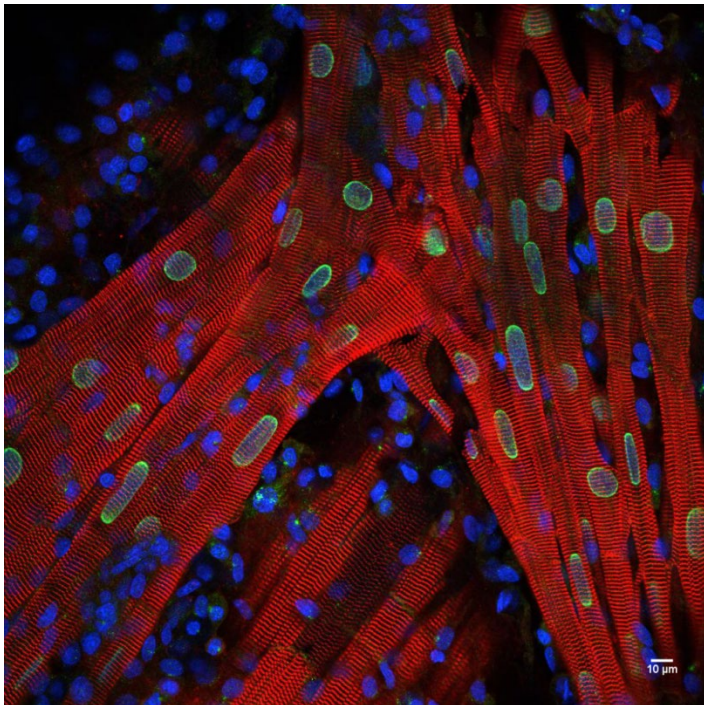
Data: Emma Robinson
JCI, Vol 127, Nr1, Jan 2017

Nuclear sorting

Cell-type specific transcriptomics and epigenomics

PCM-1 is cardiomyocyte specific nuclear marker

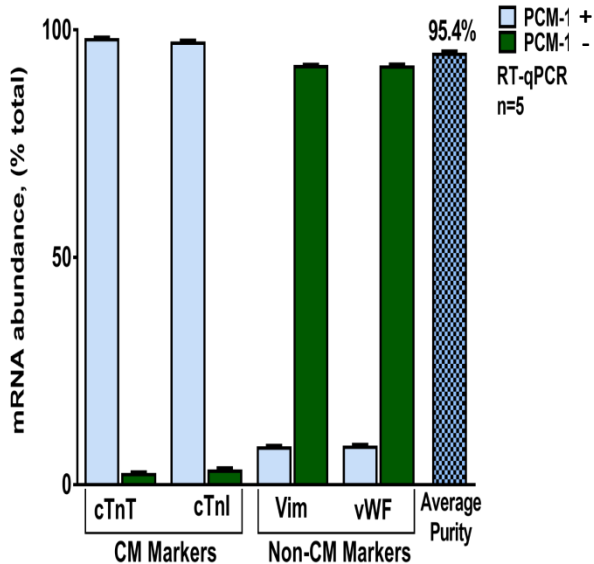
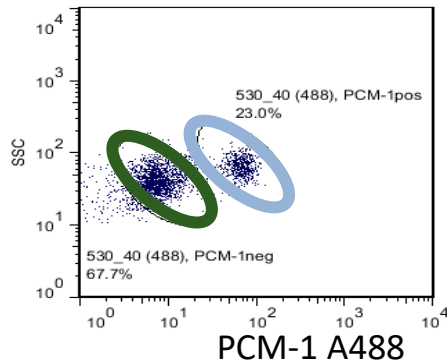
PCM-1, alpha actinin, DAPI



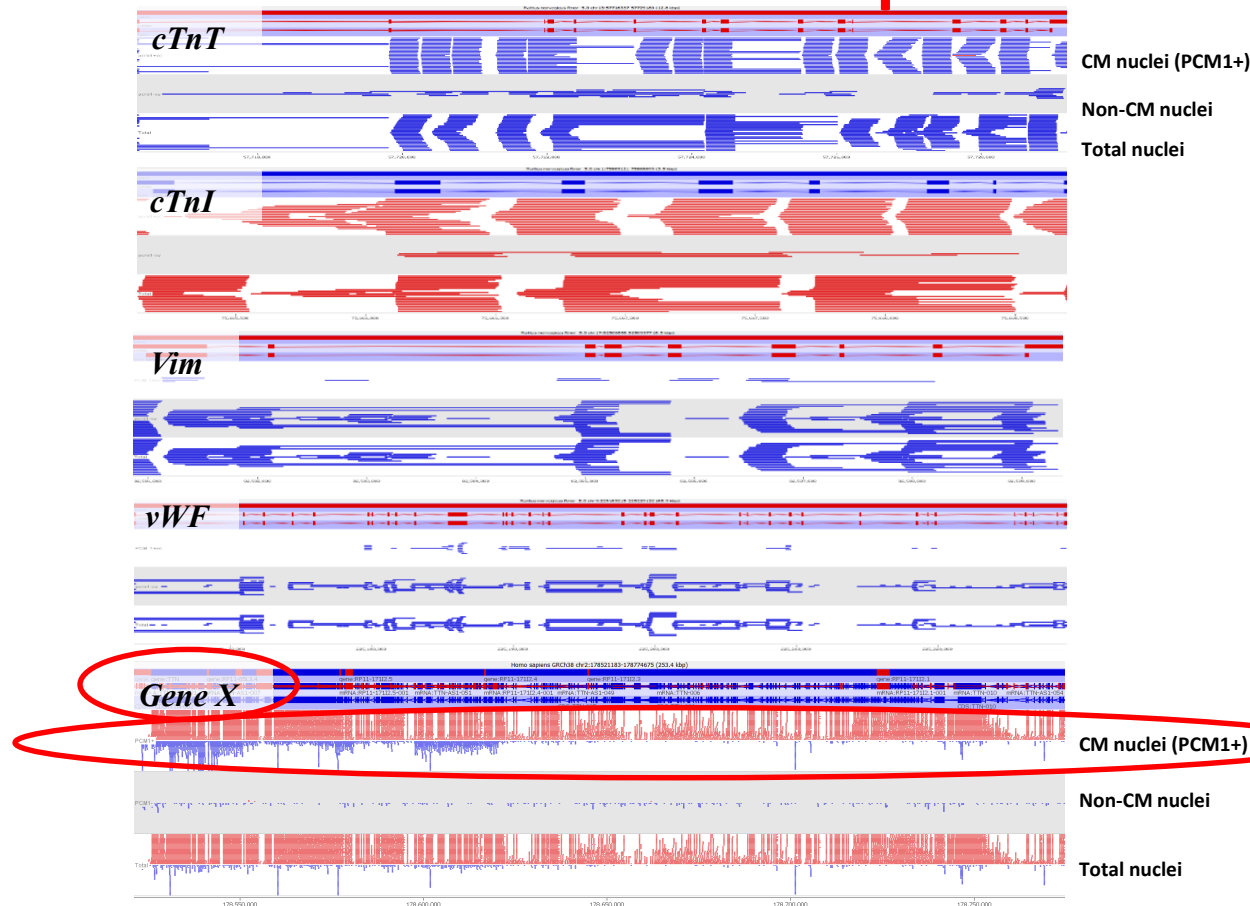
Data: Emma Robinson
JCI, vol 127, Nr1, Jan 2017

Nuclear sorting

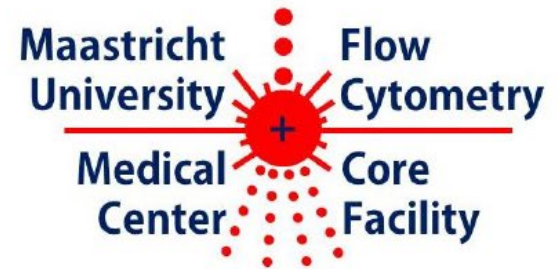
Cell-type specific transcriptomics and epigenomics



RNAseq:



Guidelines for Cell Sorting



Sample preparation is a key to a successful sort. These guidelines state how to prepare and collect your cells in the best way.

Questions?



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