ACTA (Anybody Can Titrate Antibody) Report v3.6.11

2026-11-12

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A. MiFlowCyt metadata

1 Experiment Overview

MiFlowCyt 1.0. Structured to MiFlowCyt but not self-contained: purpose, experiment variables, organization, conclusions, specimen source and collection, and instrument QC are recorded in the ELN and referenced here. Not a compliant submission document on its own.

Category	Value
Purpose	See ELN EXPOQ_Test1 (ELN)
Keywords	(not supplied)
Experiment variables	Stain volume (uL) per antibody; see Reagents. See ELN EXPOQ_Test1 (ELN)
Organization	See ELN EXPOQ_Test1 (ELN)
Primary contact	JD
Acquisition date	2026-07-30
Conclusions	See ELN EXPOQ_Test1 (ELN)
Quality control	6 automated check(s) per antibody group; see the QC section.

2 Flow Sample/Specimen Details

Category	Value
Test material	HD Human T cells
Cells per well (e6)	1
Well volume (uL)	100
Source	See ELN EXPOQ_Test1 (ELN)
Collection	See ELN EXPOQ_Test1 (ELN)
SOP	(not supplied)
Fixed	TRUE
Permeabilised	TRUE
Protocol	See ELN EXPOQ_Test1 (ELN)

2.4 Fluorescence Reagent Description

Strep_PE

Channel	Markername
SSC-H	—
SSC-A	—
FSC-H	—
FSC-A	—
SSC-B-H	—
SSC-B-A	—
BUV496-A	CD4
BUV805-A	CD3
Alexa Fluor 488-A	Antigen
Alexa Fluor 532-A	CD8
eFluor 780-A	Viability
PE-A	Strep

Table 1: Costain panel 'Iteration1' from 'Master_Panel_Inventory.xlsx': 4 of 4 reagents matched.

Antigen	Fluorochrome	Matched to	Verdict	Catalogue	Vendor	Clone	Type
CD3	BUV805	CD3	matched	612893	BD	SK7	Base
CD4	BUV496	CD4	matched	612936	BD	SK3	Base
CD8	Alexa Fluor 532	CD8	matched	58-0088-42	Thermo	RPA-T8	Base
Live Dead eFluor 780 (LD) (Viability)	efluor780	Viability	matched	65-0865-14	TS	NA	Base

3 Instrument Details

Category	Value
Manufacturer and model	Aurora
Detectors with a recorded gain	6
Instrument QC	See ELN EXPOQ_Test1 (ELN)

Detector voltages ($PnV)

detector	marker	voltage
SSC-H	NA	126
SSC-A	NA	126
FSC-H	NA	574
FSC-A	NA	574
SSC-B-H	NA	132
SSC-B-A	NA	132

4 Data Analysis Details

Everything below is MiFlowCyt part 4 – what was done to the events between acquisition and the numbers in this report, in the order it happened: events read, compensation, transformation, gating, and the software that did it.

4.1 List-mode data files: downsampling

Info!Downsample_to: *(blank)*

No downsampling performed.

Events read: 660,970 across 12 file(s) (smallest 970, largest 60,000).

4.2 Compensation Description

Info!compensation: *(blank)*

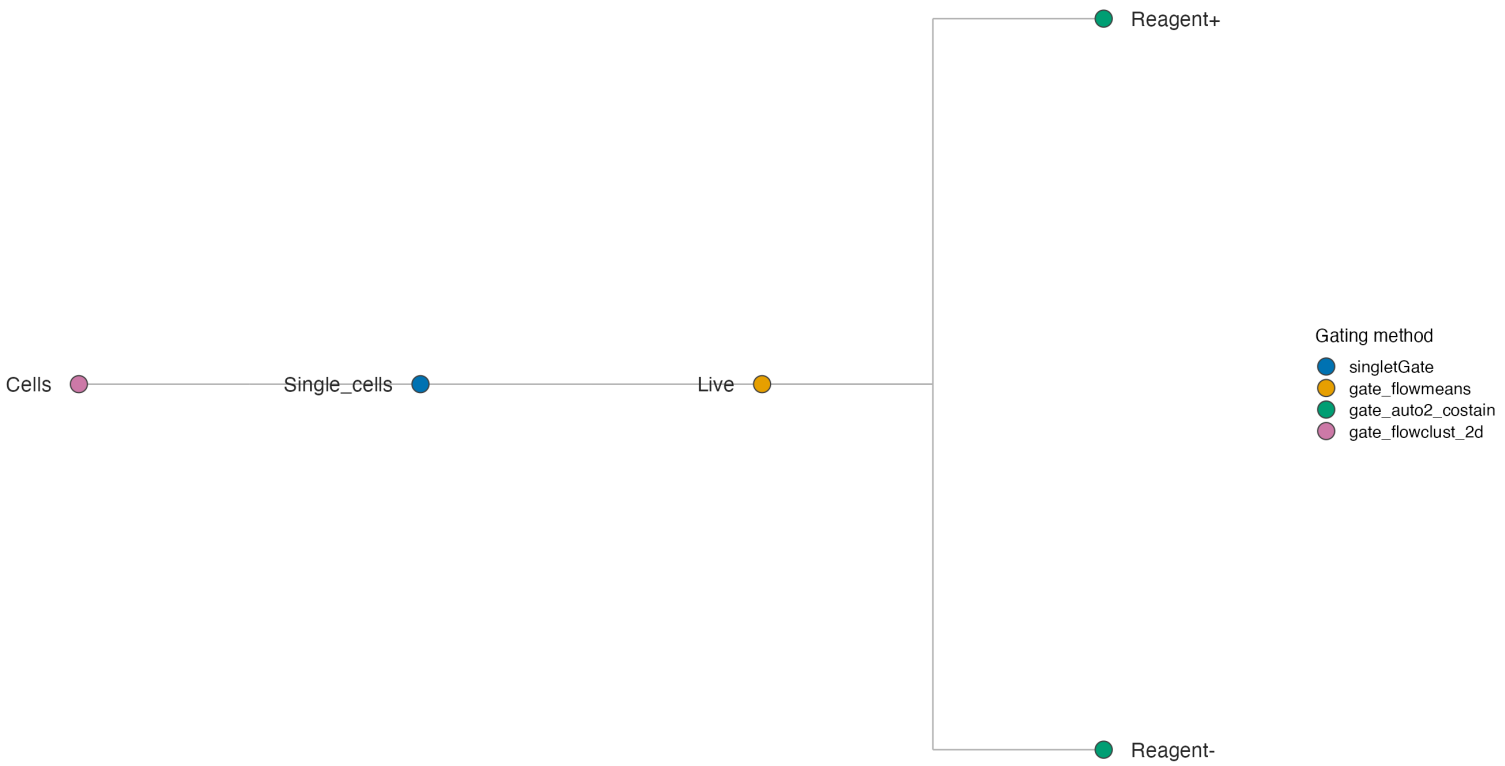
Identity matrix was applied – the data were not compensated.

4.3 Data Transformation Details

Argument	Strep_PE
maxValue (from $PnR)	4194304
channelRange	9000
pos	4.5
neg	0
widthBasis	-10

4.4 Gating Details

Gating scheme



4.4.2 Gate Statistics

Count, percent of parent, median fluorescence intensity and robust SD were collected for 33 population/well combinations and written to the **Pop_stats** sheet of the titration export beside this report.

In `gating_template`, mark `stats_export` as TRUE to make sure that population's stats are exported.

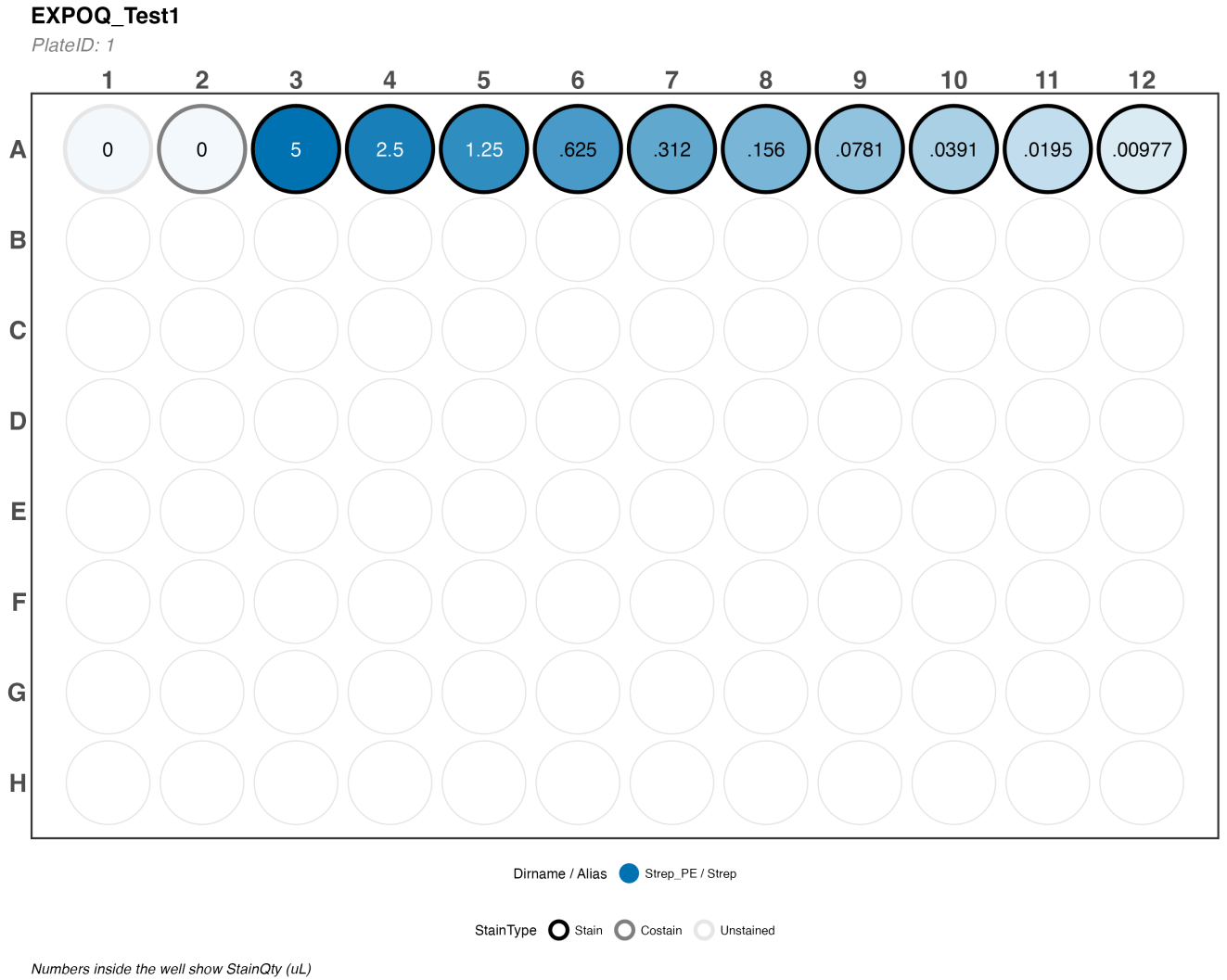
4.5 Analysis software

Category	Value
ACTA version	3.6.11
R version	R version 4.5.1 (2025-06-13)

This pipeline can be driven from R without the app: see **Automating ACTA** in `README.md` in the script folder.

B. Titration results

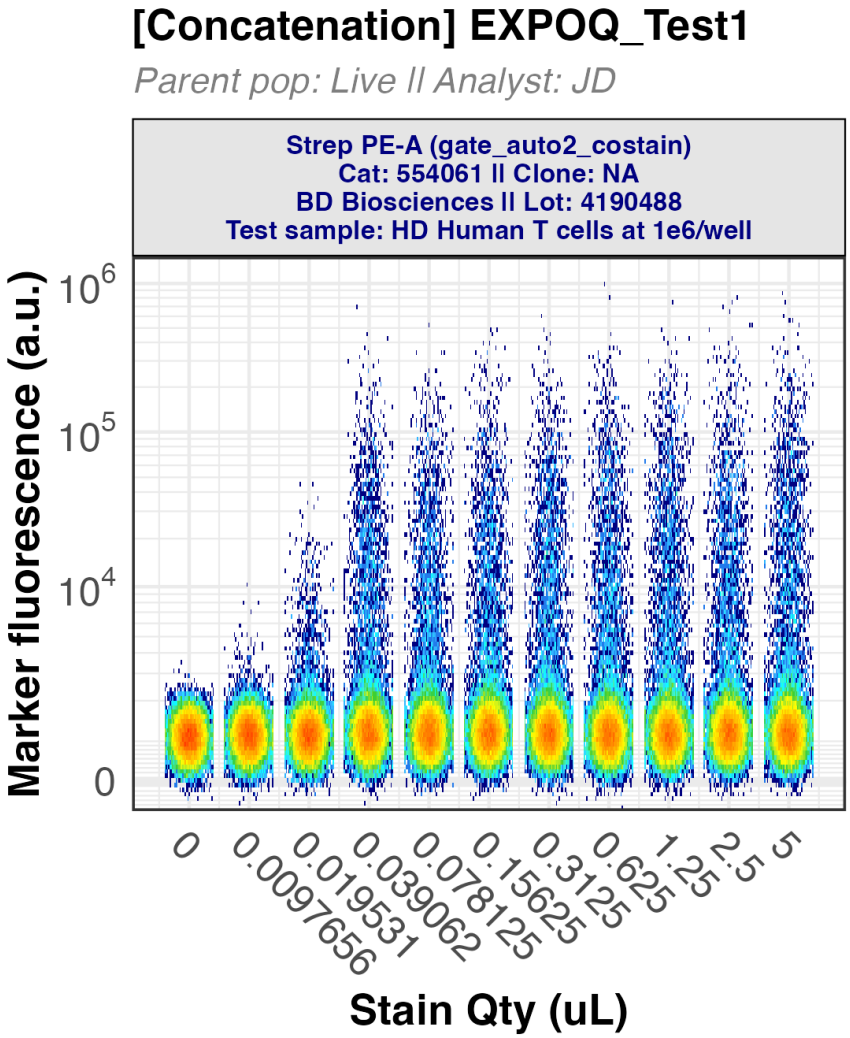
1 Plate map



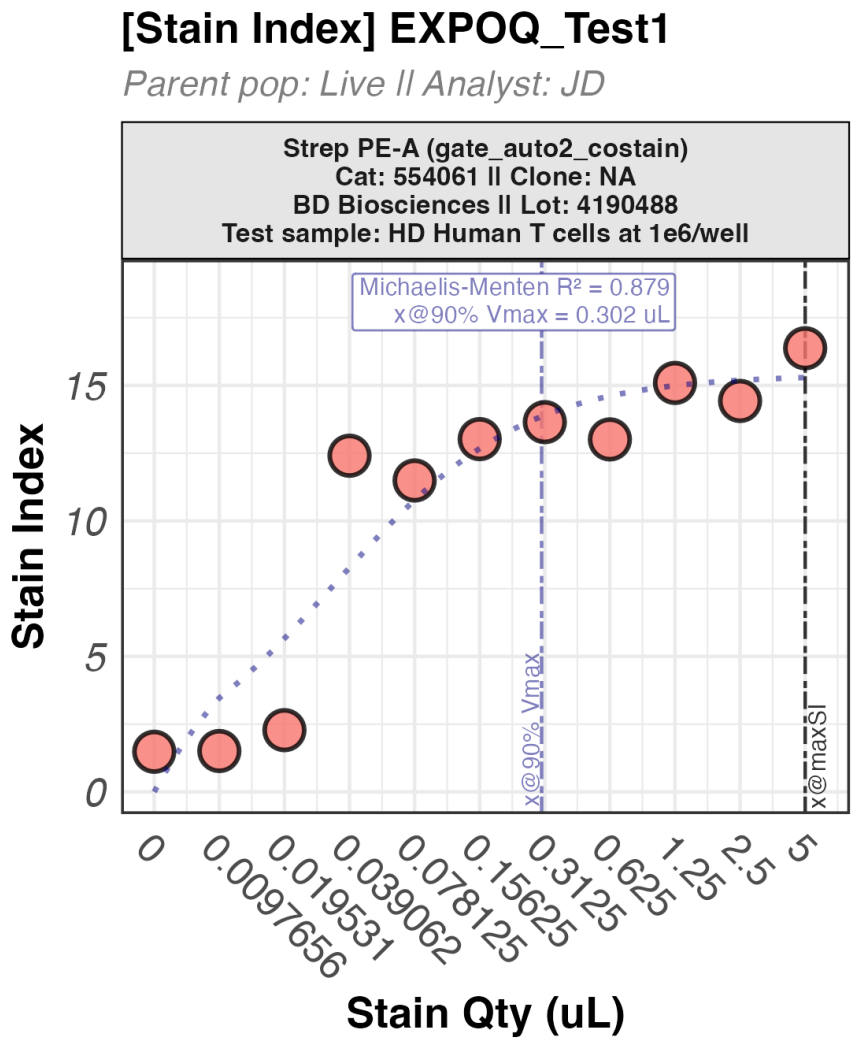
2 QC

Check	Strep_PE
Median FSC-A of Cells is at least 50% of the median of all events	**PASS**
More than 50% Live cells	**PASS**
More than 80% single cells	**PASS**
Costain SI is the lowest in the group	**PASS**
Co-stain is less than 5% positive	**PASS**
Every population has at least 100 events in every well (except costain)	**PASS**
Overall	**PASS**

3 Resolution of populations

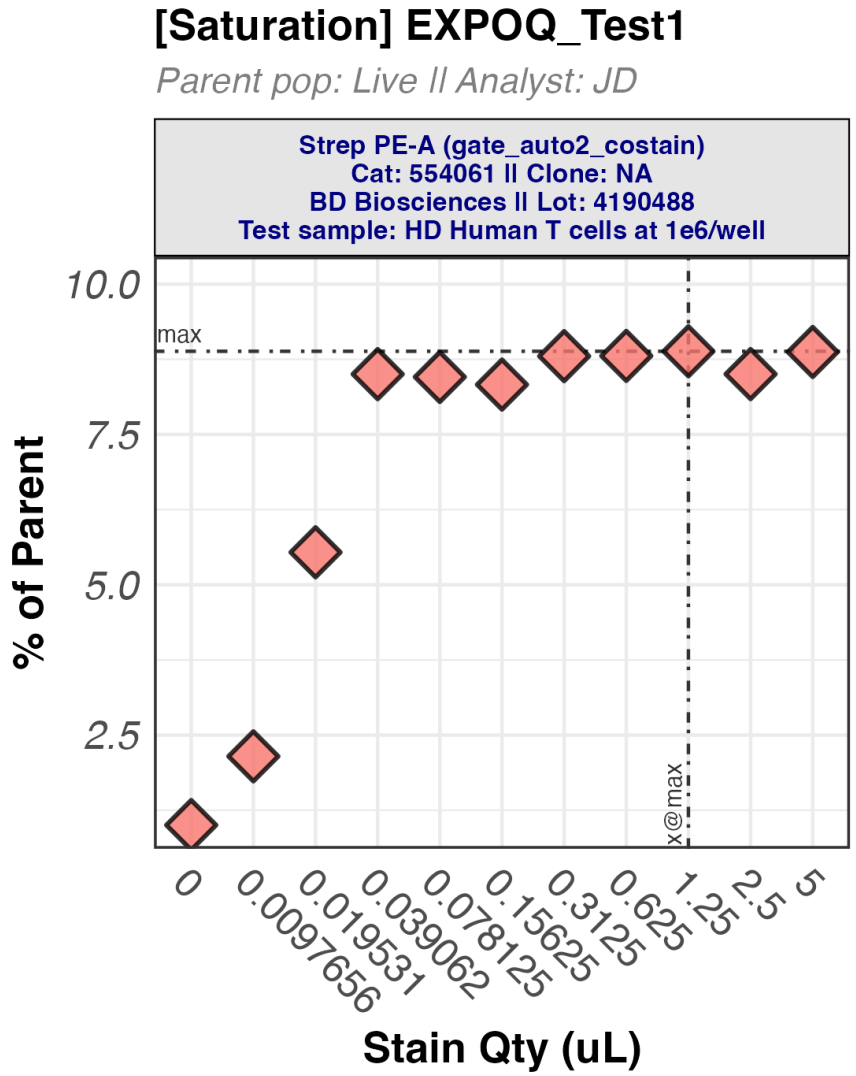


Concatenated events, up to 20,000 per FCS.



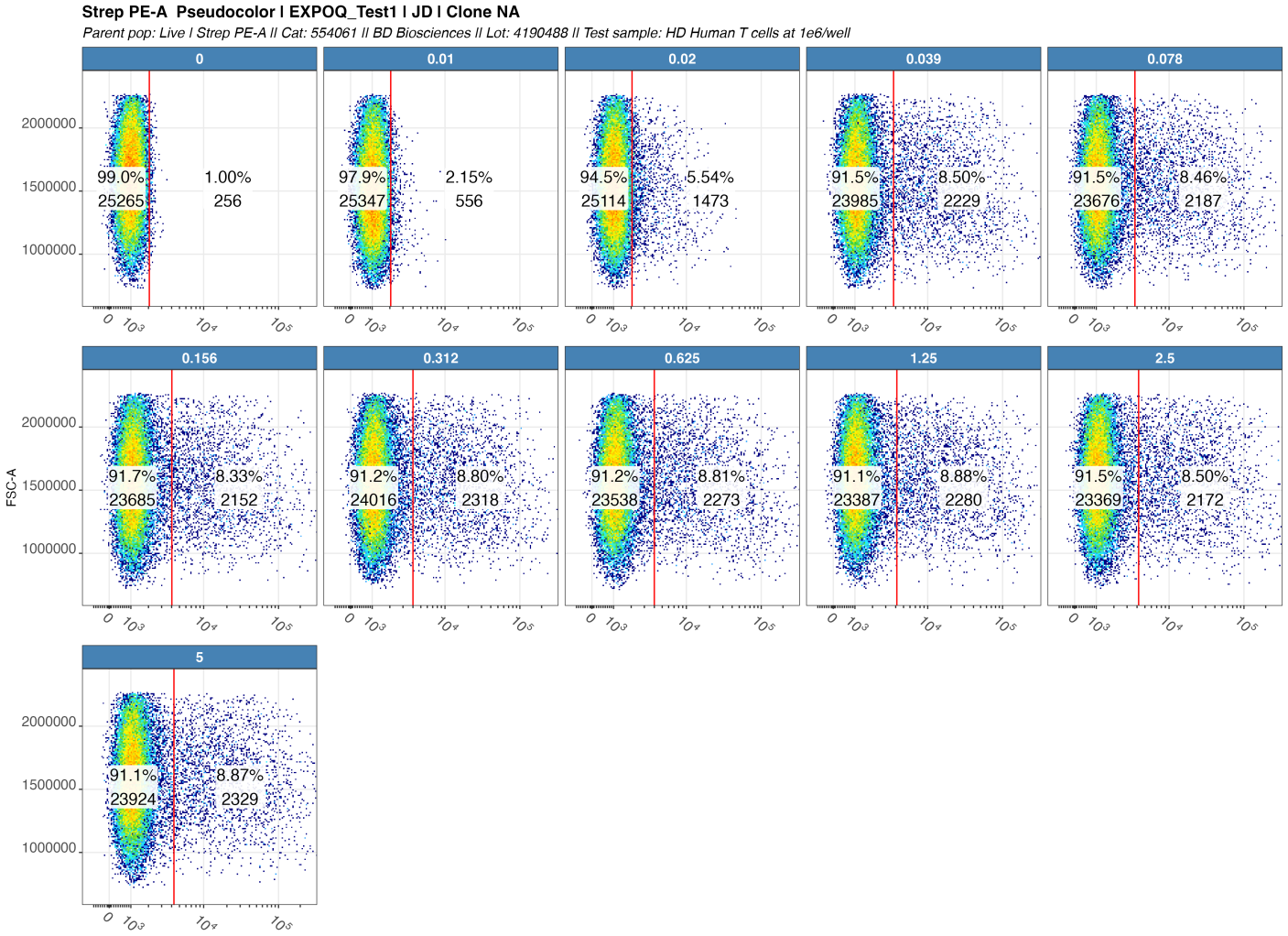
MFI calculated on untransformed (linear) values. || Compensation: —

4 Saturation of positive population proportion



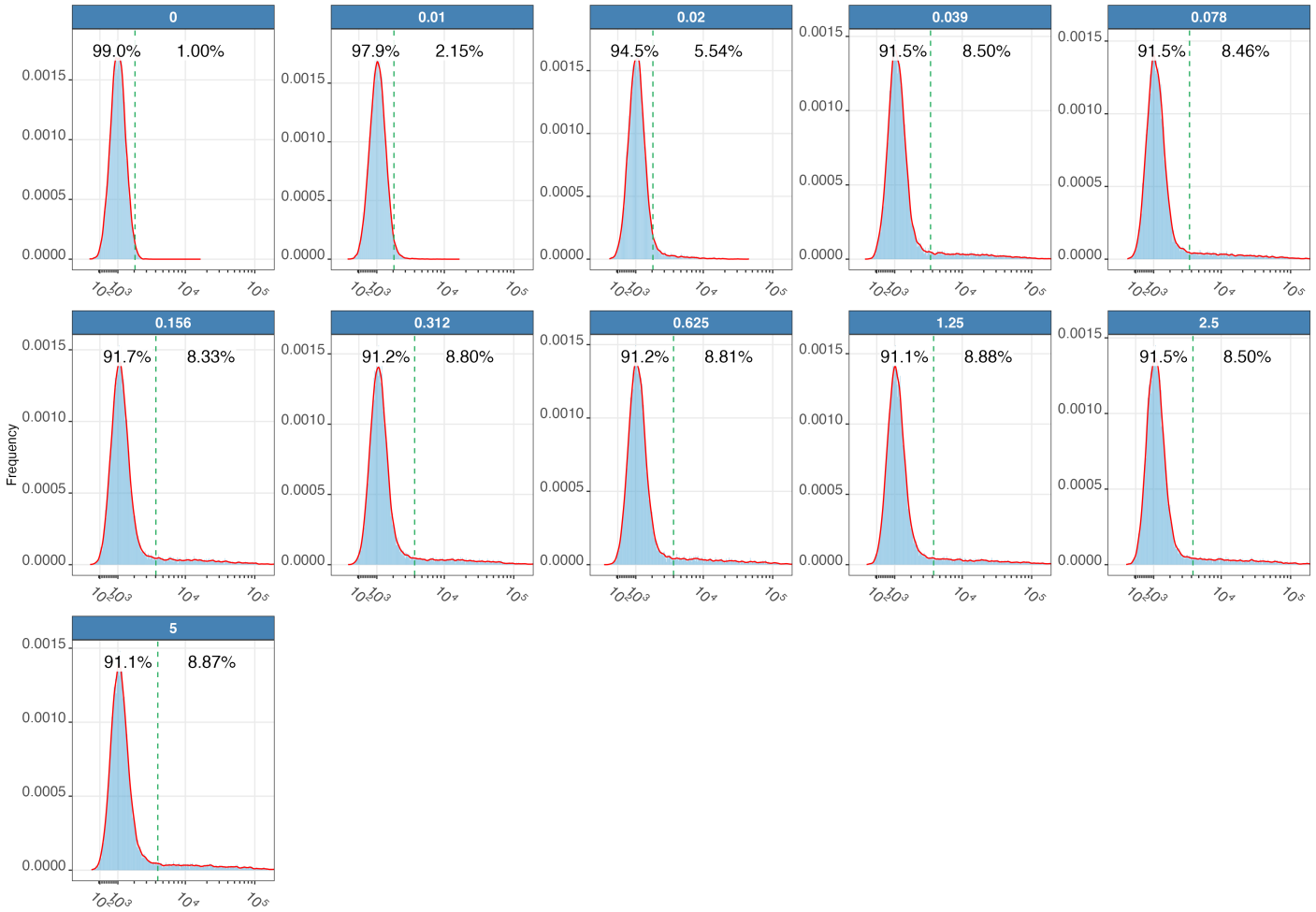
5 Layouts for each antibody

5.1 Strep_PE

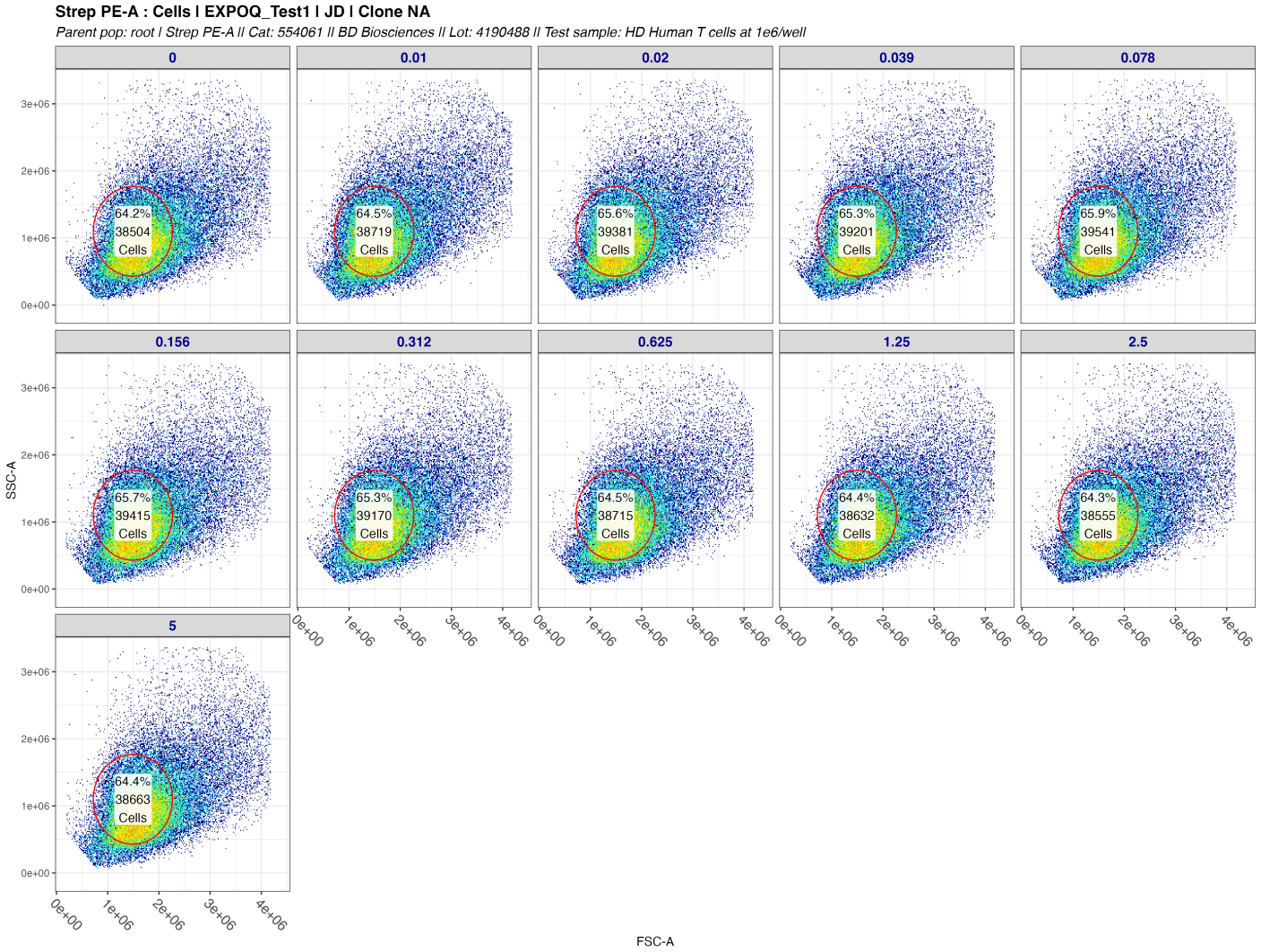

Strep PE-A Pseudocolor | EXPOQ_Test1 | JD | Clone NA
Parent pop: Live | Strep PE-A || Cat: 554061 || BD Biosciences || Lot: 4190488 || Test sample: HD Human T cells at 1e6/well
0
99.0%
25265
1.00%
256
0.01
97.9%
25347
2.15%
556
0.02
94.5%
25114
5.54%
1473
0.039
91.5%
23985
8.50%
2229
0.078
91.5%
23676
8.46%
2187
0.156
91.7%
23685
8.33%
2152
0.312
91.2%
24016
8.80%
2318
0.625
91.2%
23538
8.81%
2273
1.25
91.1%
23387
8.88%
2280
2.5
91.5%
23369
8.50%
2172
5
91.1%
23924
8.87%
2329
FSC-A
PE-A
Gating method: gate_auto2_costain || args: cluster='neg', quantile=0.99, K=2 || collapse: FALSE || groupBy: Dirname || pp: pp_auto2_costain || pp args: costain_quantile=0.99, sat_threshold=0.90, dip_pval=0.05
Compensation: —

Strep PE-A Histogram | EXPOQ_Test1 | JD | Clone NA

Parent pop: Live || Strep PE-A || Cat: 554061 || BD Biosciences || Lot: 4190488 || Test sample: HD Human T cells at 1e6/well

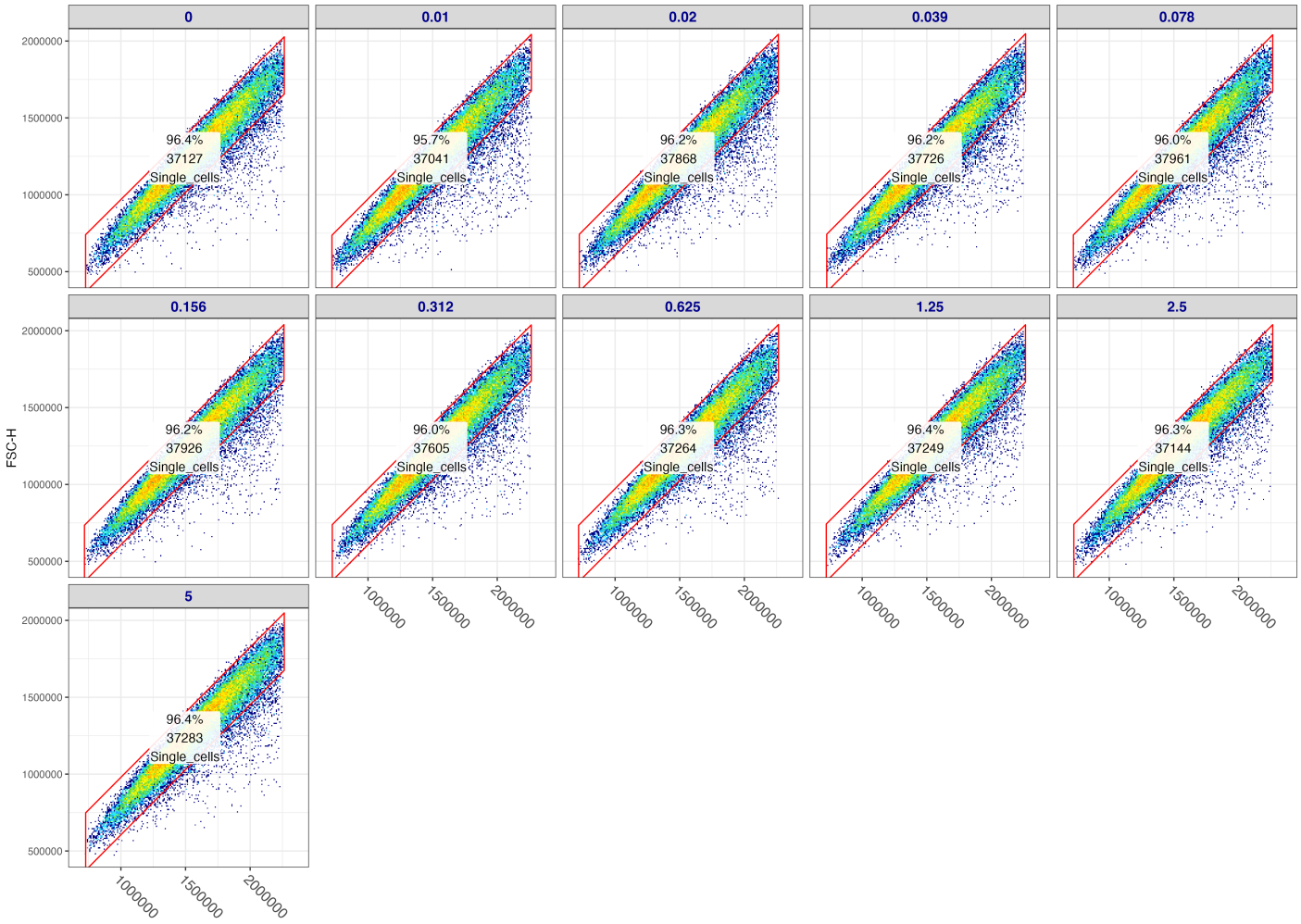


Gating method: gate_auto2_costain || args: cluster='neg', quantile=0.99, K=2 || collapse: FALSE || groupBy: Dirname || pp: pp_auto2_costain || pp args: costain_quantile=0.99, sat_threshold=0.90, dip_pval=0.05
Compensation: —


Strep PE-A : Cells | EXPOQ_Test1 | JD | Clone NA
Parent pop: root | Strep PE-A || Cat: 554061 || BD Biosciences || Lot: 4190488 || Test sample: HD Human T cells at 1e6/well
0
64.2%
38504
Cells
0.01
64.5%
38719
Cells
0.02
65.6%
39381
Cells
0.039
65.3%
39201
Cells
0.078
65.9%
39541
Cells
0.156
65.7%
39415
Cells
0.312
65.3%
39170
Cells
0.625
64.5%
38715
Cells
1.25
64.4%
38632
Cells
2.5
64.3%
38555
Cells
5
64.4%
38663
Cells
SSC-A
FSC-A
0e+00
1e+06
2e+06
3e+06
4e+06
Gating method: gate_flowclust_2d || args: K=5, quantile=0.9, min=NULL, max=NULL || collapse: TRUE || groupBy: Dirname || pp: — || pp args: —
Compensation: —

Strep PE-A : Single_cells | EXPOQ_Test1 | JD | Clone NA

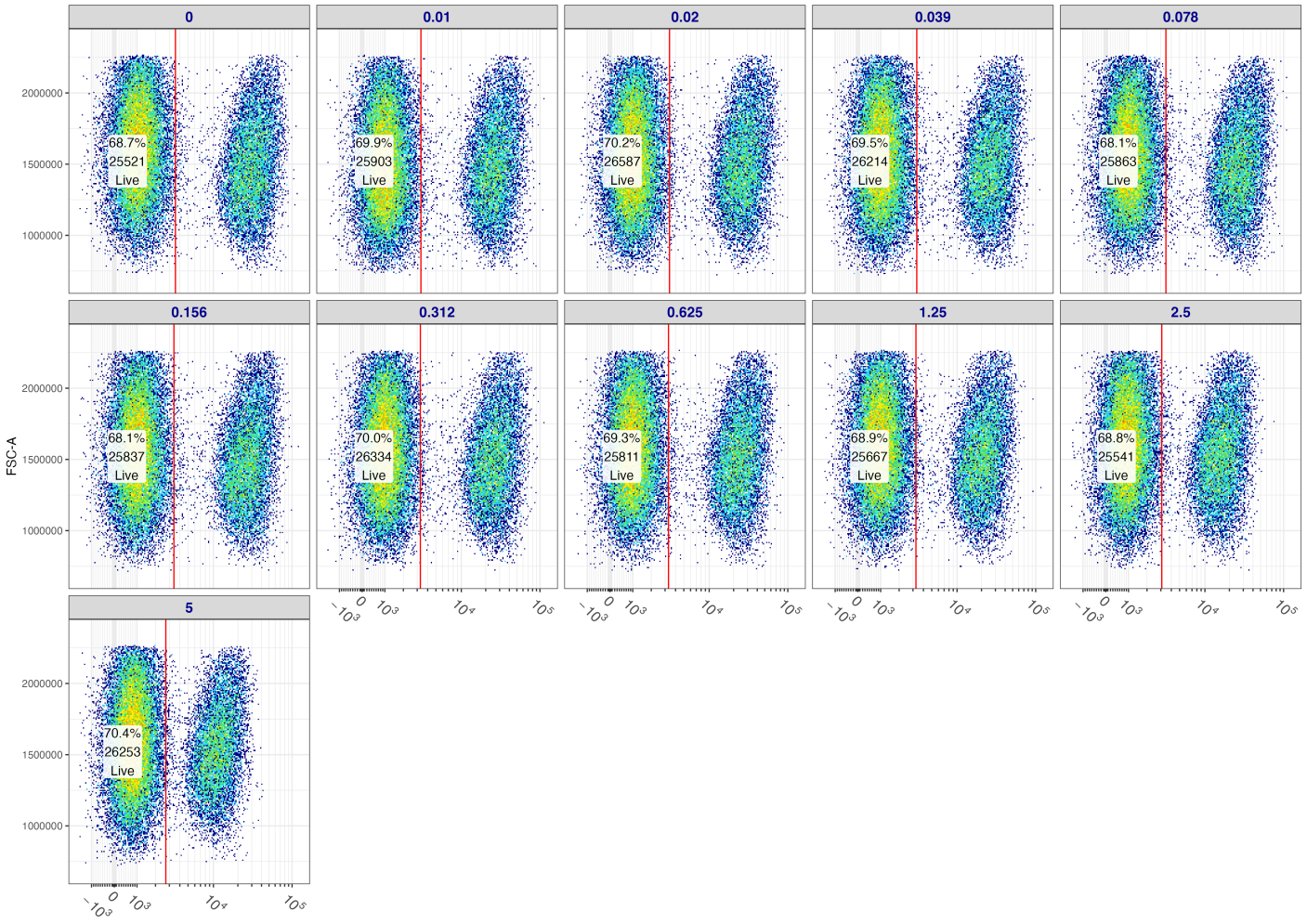
Parent pop: Cells | Strep PE-A || Cat: 554061 || BD Biosciences || Lot: 4190488 || Test sample: HD Human T cells at 1e6/well



Gating method: singletGate || args: prediction_level=0.99, wider_gate=FALSE || collapse: FALSE || groupBy: Dirname || pp: — || pp args: —
Compensation: —

Strep PE-A : Live | EXPOQ_Test1 | JD | Clone NA

Parent pop: Single_cells | Strep PE-A || Cat: 554061 || BD Biosciences || Lot: 4190488 || Test sample: HD Human T cells at 1e6/well



Gating method: gate_flowmeans || args: K=2, cluster='neg', quantile=0.99 || collapse: FALSE || groupBy: Dirname || pp: — || pp args: —
Compensation: —

6 Info

Table 3: Info sheet: script-level settings of this run

Variable	Value	Source
General		
Template_Version	3.6.8	Info sheet
working_directory	(not set)	not set
compensation	(not set)	not set
miflowcyt_export (L)	TRUE	Info sheet
dashboard_dir	(not set)	not set
titration_export_dir	(not set)	not set
dashboard_tabbed_by	ACTA_version	Info sheet
MM_R2_threshold	0.9	Info sheet
Downsample_to (N)	(not set)	not set
flowjo_transformation_arg	channelRange=9000, pos=4.5, neg=0, widthBasis=-10	Info sheet
keywords	(not set)	not set
TiterPubs		
titerpubs_export	TRUE	Info sheet
scrub_confidential	TRUE	Info sheet
Organization/Affiliation	(not set)	not set
Submitter_Name	(not set)	not set
Submitter_ORCID	(not set)	not set
Submitter_Email	<redacted-email>	Info sheet
Quality_Control_Measures	(not set)	not set
Collection_Software	(not set)	not set
Target_Species	Human	Info sheet
Cell_Type_Fallback	(not set)	not set
Sample_Details	(not set)	not set
Tissue_Fallback	(not set)	not set
References	https://doi.org/10.5281/zenodo.24181307	Info sheet
Protocol		
Incubation_Time	30	Info sheet
Incubation_Temperature_C	4	Info sheet
Equipment		
Equipment_Make	(not set)	not set
Equipment_Model	(not set)	not set
Provenance		
master_panel_inventory_path	Master_Panel_Inventory.xlsx	run folder
Protocol		
Preparation_Protocol	(not set)	not set
Protocol_reference	https://www.biolegend.com/en-us/protocols/intracellular-flow-cytometry-staining-protocol	Info sheet

Table 3: Info sheet: script-level settings of this run *(continued)*

Variable	Value	Source
TiterPubs		
scrub_eln_placeholder	EXPOQ_Test1	Info sheet

7 Session Information

Script version: ACTA v3.6.11

Render timestamp: 2026-11-12 20:21:45 PST

Operator: JD

Layout workbook: OQ_Test1_Ab_Titration_Instructions.xlsx

```
- Session info -------------------------------------------------------------
 setting  value
 version  R version 4.5.1 (2025-06-13)
 os       macOS Tahoe 26.7.2
 system   aarch64, darwin20
 ui       X11
 language (EN)
 collate  C.UTF-8
 ctype    C.UTF-8
 tz       America/Los_Angeles
 date     2026-11-12
 pandoc   3.9.0.2 @ /opt/homebrew/bin/ (via rmarkdown)
 quarto   NA

- Packages -----------------------------------------------------------------
 package       * version   date (UTC) lib source
 ACTA          * 3.6.11    2026-11-13 [1] Bioconductor
 askpass         1.2.1     2024-10-04 [2] CRAN (R 4.5.0)
 BH            * 1.90.0-1  2025-12-14 [2] CRAN (R 4.5.2)
 Biobase         2.70.0    2025-10-29 [2] Bioconductor 3.22 (R 4.5.1)
 BiocGenerics    0.56.0    2025-10-29 [2] Bioconductor 3.22 (R 4.5.1)
 BiocManager   * 1.30.27   2025-11-14 [2] CRAN (R 4.5.2)
 bslib           0.11.0    2026-05-16 [2] CRAN (R 4.5.2)
 cachem          1.1.0     2024-05-16 [2] CRAN (R 4.5.0)
 cellranger      1.1.0     2016-07-27 [2] CRAN (R 4.5.0)
 cli             3.6.6     2026-04-09 [2] CRAN (R 4.5.2)
 cytolib         2.22.0    2025-10-29 [2] Bioconductor 3.22 (R 4.5.1)
 data.table      1.18.4    2026-05-06 [2] CRAN (R 4.5.2)
 DEoptimR        1.2-0     2026-06-07 [2] CRAN (R 4.5.2)
 digest          0.6.39    2025-11-19 [2] CRAN (R 4.5.2)
```

```
diptest       * 0.77-2    2025-08-20 [2] CRAN (R 4.5.0)
dplyr         * 1.2.1     2026-04-03 [2] CRAN (R 4.5.2)
evaluate        1.0.5     2025-08-27 [2] CRAN (R 4.5.0)
farver          2.1.2     2024-05-13 [2] CRAN (R 4.5.0)
fastmap         1.2.0     2024-05-15 [2] CRAN (R 4.5.0)
feature         1.2.16    2026-05-11 [2] CRAN (R 4.5.2)
flowClust       3.48.0    2025-10-29 [2] Bioconductor 3.22 (R 4.5.1)
flowCore      * 2.22.1    2026-01-01 [2] https://bioc-release.r-universe.dev (R 4.5.2)
flowMeans     * 1.70.0    2025-10-29 [2] Bioconductor 3.22 (R 4.5.1)
flowWorkspace * 4.22.1    2026-01-01 [2] https://bioc-release.r-universe.dev (R 4.5.2)
generics        0.1.4     2025-05-09 [2] CRAN (R 4.5.0)
ggcyto        * 1.39.1    2026-02-25 [2] Github (RGLab/ggcyto@e5ed286)
ggplate       * 0.4.0     2026-09-01 [2] CRAN (R 4.5.2)
ggplot2       * 4.0.3     2026-04-22 [2] CRAN (R 4.5.2)
glue            1.8.1     2026-04-17 [2] CRAN (R 4.5.2)
graph           1.88.1    2025-12-08 [2] Bioconductor 3.22 (R 4.5.2)
gridExtra       2.3       2017-09-09 [2] CRAN (R 4.5.0)
gtable          0.3.6     2024-10-25 [2] CRAN (R 4.5.0)
hexbin          1.28.5    2024-11-13 [2] CRAN (R 4.5.0)
htmltools       0.5.9     2025-12-04 [2] CRAN (R 4.5.2)
jquerylib       0.1.4     2021-04-26 [2] CRAN (R 4.5.0)
jsonlite        2.0.0     2025-03-27 [2] CRAN (R 4.5.0)
kableExtra    * 1.4.0     2024-01-24 [2] CRAN (R 4.5.0)
KernSmooth      2.23-26   2025-01-01 [2] CRAN (R 4.5.1)
knitr         * 1.51      2025-12-20 [2] CRAN (R 4.5.2)
ks              1.15.2    2026-05-09 [2] CRAN (R 4.5.2)
labeling        0.4.3     2023-08-29 [2] CRAN (R 4.5.0)
lattice         0.22-9    2026-02-09 [2] CRAN (R 4.5.2)
lifecycle       1.0.5     2026-01-08 [2] CRAN (R 4.5.2)
lubridate     * 1.9.5     2026-02-04 [2] CRAN (R 4.5.2)
magrittr        2.0.5     2026-04-04 [2] CRAN (R 4.5.2)
Matrix          1.7-5     2026-03-21 [2] CRAN (R 4.5.2)
matrixStats     1.5.0     2025-01-07 [2] CRAN (R 4.5.0)
mclust        * 6.1.2     2025-10-31 [2] CRAN (R 4.5.0)
mvtnorm         1.4-1     2026-06-06 [2] CRAN (R 4.5.2)
ncdfFlow      * 2.56.0    2025-10-29 [2] Bioconductor 3.22 (R 4.5.1)
openCyto      * 2.22.0    2025-10-29 [2] Bioconductor 3.22 (R 4.5.1)
openxlsx      * 4.2.8.1   2025-10-31 [2] CRAN (R 4.5.0)
otel            0.2.0     2025-08-29 [2] CRAN (R 4.5.0)
```

```
pcaPP           2.0-5     2024-08-19 [2] CRAN (R 4.5.0)
pdftools        3.9.0     2026-05-14 [2] CRAN (R 4.5.2)
pillar          1.11.1    2025-09-17 [2] CRAN (R 4.5.0)
pkgconfig       2.0.3     2019-09-22 [2] CRAN (R 4.5.0)
plyr            1.8.9     2023-10-02 [2] CRAN (R 4.5.0)
pracma          2.4.6     2025-10-22 [2] CRAN (R 4.5.0)
purrr           1.2.2     2026-04-10 [2] CRAN (R 4.5.2)
qpdf            1.4.1     2025-07-02 [2] CRAN (R 4.5.0)
R6              2.6.1     2025-02-15 [2] CRAN (R 4.5.0)
ragg          * 1.5.2     2026-03-23 [2] CRAN (R 4.5.2)
RBGL            1.86.0    2025-10-29 [2] Bioconductor 3.22 (R 4.5.1)
RColorBrewer    1.1-3     2022-04-03 [2] CRAN (R 4.5.0)
Rcpp            1.1.1-1.1 2026-04-24 [2] CRAN (R 4.5.2)
readxl        * 1.5.0     2026-05-16 [2] CRAN (R 4.5.2)
Rgraphviz       2.54.0    2025-10-29 [2] Bioconductor 3.22 (R 4.5.1)
rlang           1.2.0     2026-04-06 [2] CRAN (R 4.5.2)
rmarkdown       2.31      2026-03-26 [2] CRAN (R 4.5.2)
robustbase      0.99-7    2026-02-05 [2] CRAN (R 4.5.2)
RProtoBufLib    2.22.0    2025-10-29 [2] Bioconductor 3.22 (R 4.5.1)
rrcov           1.7-7     2025-04-21 [2] CRAN (R 4.5.0)
rstudioapi    * 0.19.0    2026-06-11 [2] CRAN (R 4.5.2)
S4Vectors       0.48.1    2026-04-04 [2] https://bioc-release.r-universe.dev (R 4.5.3)
S7              0.2.2     2026-04-22 [2] CRAN (R 4.5.2)
sass            0.4.10    2025-04-11 [2] CRAN (R 4.5.0)
scales          1.4.0     2025-04-24 [2] CRAN (R 4.5.0)
sessioninfo   * 1.2.4     2026-06-04 [2] CRAN (R 4.5.2)
stringi         1.8.7     2025-03-27 [2] CRAN (R 4.5.0)
stringr       * 1.6.0     2025-11-04 [2] CRAN (R 4.5.0)
svglite         2.2.2     2025-10-21 [2] CRAN (R 4.5.0)
systemfonts     1.3.2     2026-03-05 [2] CRAN (R 4.5.2)
textshaping     1.0.5     2026-03-06 [2] CRAN (R 4.5.2)
this.path     * 2.8.0     2026-04-10 [2] CRAN (R 4.5.2)
tibble          3.3.1     2026-01-11 [2] CRAN (R 4.5.2)
tidyr         * 1.3.2     2025-12-19 [2] CRAN (R 4.5.2)
tidyselect      1.2.1     2024-03-11 [2] CRAN (R 4.5.0)
timechange      0.4.0     2026-01-29 [2] CRAN (R 4.5.2)
vctrs           0.7.3     2026-04-11 [2] CRAN (R 4.5.2)
viridisLite     0.4.3     2026-02-04 [2] CRAN (R 4.5.2)
withr           3.0.2     2024-10-28 [2] CRAN (R 4.5.0)
```

```
 xfun            0.58      2026-06-01 [2] CRAN (R 4.5.2)
 XML             3.99-0.23 2026-03-20 [2] CRAN (R 4.5.2)
 xml2            1.5.2     2026-01-17 [2] CRAN (R 4.5.2)
 yaml            2.3.12    2025-12-10 [2] CRAN (R 4.5.2)
 zip             3.0.0     2026-06-10 [2] CRAN (R 4.5.2)

 [1] ~/ACTA_release/lib3611
 [2] /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/library
 * -- Packages attached to the search path.

------------------------------------------------------------------------------
```