ACTA (Anybody Can Titrate Antibody) Report v3.6.11

2026-11-12

Contents

A. MiFlowCyt metadata **2**

1 Experiment Overview **2**

2 Flow Sample/Specimen Details **3**

2.4 Fluorescence Reagent Description 4

3 Instrument Details **6**

4 Data Analysis Details **8**

4.1 List-mode data files: downsampling 8

4.2 Compensation Description 9

4.3 Data Transformation Details 9

4.4 Gating Details 10

4.4.2 Gate Statistics 11

4.5 Analysis software 11

B. Titration results **12**

1 Plate map **13**

2 QC **14**

3 Resolution of populations **15**

4 Saturation of positive population proportion **17**

5 Layouts for each antibody **18**

5.1 CD19 19

5.2 CD7 24

5.3 CD56 29

6 Info **34**

7 Session Information **36**

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_Test2 (ELN)
Keywords	(not supplied)
Experiment variables	Stain volume (uL) per antibody; see Reagents. See ELN EXPOQ_Test2 (ELN)
Organization	See ELN EXPOQ_Test2 (ELN)
Primary contact	JD
Acquisition date	2026-04-01
Conclusions	See ELN EXPOQ_Test2 (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 PBMC
Cells per well (e6)	1
Well volume (uL)	100
Source	See ELN EXPOQ_Test2 (ELN)
Collection	See ELN EXPOQ_Test2 (ELN)
SOP	(not supplied)
Fixed	TRUE
Permeabilised	FALSE
Protocol	See ELN EXPOQ_Test2 (ELN)

2.4 Fluorescence Reagent Description

CD19

Channel	Markername
T0	TLSW
T1	TMSW
INFO	Event Info
FS00-H	FSC 488/10-H
FS00-A	FSC 488/10-A
FS01-H	FSC 405/10 (spd)-H
FS01-A	FSC 405/10 (spd)-A
SS02-H	SSC 488/10-H
SS02-A	SSC 488/10-A
FL05-H	RB780-H
FL05-A	RB780-A
FL06-H	RB705-H
FL06-A	RB705-A
FL11-H	BUV 395-H
FL11-A	BUV 395-A
FL15-H	BV 711-H
FL15-A	BV 711-A
FL16-H	BV 786-H
FL16-A	BV 786-A
FL17-H	Pacific Blue-H
FL17-A	Pacific Blue-A
FL18-H	BV 421-H
FL18-A	BV 421-A
FL19-H	BV 605-H
FL19-A	BV 605-A
FL21-H	RY655-H
FL21-A	RY655-A
FL27-H	eFluor 780 Fixable Viability-H
FL27-A	eFluor 780 Fixable Viability-A
FL29-H	APC (Allophycocyanin)-H
FL29-A	APC (Allophycocyanin)-A

CD7

Channel	Markername
T0	TLSW
T1	TMSW
INFO	Event Info
FS00-H	FSC 488/10-H
FS00-A	FSC 488/10-A
FS01-H	FSC 405/10 (spd)-H
FS01-A	FSC 405/10 (spd)-A
SS02-H	SSC 488/10-H
SS02-A	SSC 488/10-A
FL05-H	RB780-H
FL05-A	RB780-A
FL06-H	RB705-H
FL06-A	RB705-A
FL11-H	BUV 395-H
FL11-A	BUV 395-A
FL15-H	BV 711-H
FL15-A	BV 711-A
FL16-H	BV 786-H
FL16-A	BV 786-A
FL17-H	Pacific Blue-H
FL17-A	Pacific Blue-A
FL18-H	BV 421-H
FL18-A	BV 421-A
FL19-H	BV 605-H
FL19-A	BV 605-A
FL21-H	RY655-H
FL21-A	RY655-A
FL27-H	eFluor 780 Fixable Viability-H
FL27-A	eFluor 780 Fixable Viability-A
FL29-H	APC (Allophycocyanin)-H
FL29-A	APC (Allophycocyanin)-A

CD56

Channel	Markername
T0	TLSW
T1	TMSW
INFO	Event Info
FS00-H	FSC 488/10-H
FS00-A	FSC 488/10-A
FS01-H	FSC 405/10 (spd)-H
FS01-A	FSC 405/10 (spd)-A
SS02-H	SSC 488/10-H
SS02-A	SSC 488/10-A
FL05-H	RB780-H
FL05-A	RB780-A
FL06-H	RB705-H
FL06-A	RB705-A
FL11-H	BUV 395-H
FL11-A	BUV 395-A
FL15-H	BV 711-H
FL15-A	BV 711-A
FL16-H	BV 786-H
FL16-A	BV 786-A
FL17-H	Pacific Blue-H
FL17-A	Pacific Blue-A
FL18-H	BV 421-H
FL18-A	BV 421-A
FL19-H	BV 605-H
FL19-A	BV 605-A
FL21-H	RY655-H
FL21-A	RY655-A
FL27-H	eFluor 780 Fixable Viability-H
FL27-A	eFluor 780 Fixable Viability-A
FL29-H	APC (Allophycocyanin)-H
FL29-A	APC (Allophycocyanin)-A

Table 1: Costain panel 'Iteration1' from 'Master_Panel_Inventory.xlsx': 0 of 1 reagents matched.

Antigen	Fluorochrome	Matched to	Verdict	Catalogue	Vendor	Clone	Type
Live Dead eFluor 780 (LD) (Viability)	efluor780	—	no match	—	—	—	Base

3 Instrument Details

Category	Value
Manufacturer and model	Bio-Rad ZE5
Detectors with a recorded gain	28
Instrument QC	See ELN EXPOQ_Test2 (ELN)

Detector voltages ($PnV)

detector	marker	voltage
FS00-H	FSC 488/10-H	352
FS00-A	FSC 488/10-A	352
FS01-H	FSC 405/10 (spd)-H	326
FS01-A	FSC 405/10 (spd)-A	326
SS02-H	SSC 488/10-H	558
SS02-A	SSC 488/10-A	558
FL05-H	RB780-H	746
FL05-A	RB780-A	746
FL06-H	RB705-H	547
FL06-A	RB705-A	547
FL11-H	BUV 395-H	487
FL11-A	BUV 395-A	487
FL15-H	BV 711-H	593
FL15-A	BV 711-A	593
FL16-H	BV 786-H	705
FL16-A	BV 786-A	705
FL17-H	Pacific Blue-H	465
FL17-A	Pacific Blue-A	465
FL18-H	BV 421-H	481
FL18-A	BV 421-A	481
FL19-H	BV 605-H	616
FL19-A	BV 605-A	616
FL21-H	RY655-H	700
FL21-A	RY655-A	700
FL27-H	eFluor 780 Fixable Viability-H	629
FL27-A	eFluor 780 Fixable Viability-A	629
FL29-H	APC (Allophycocyanin)-H	651

(continued)

detector	marker	voltage
FL29-A	APC (Allophycocyanin)-A	651

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: `12,000`

Downsampled to 12,000 events per FCS file.

Events read: 252,000 across 21 file(s) (smallest 12,000, largest 12,000).

4.2 Compensation Description

Info!compensation: `csv`

Read from OQ_Test2_CompMatrix.csv and applied to every sample.

Matrix file: `OQ_Test2_CompMatrix.csv`

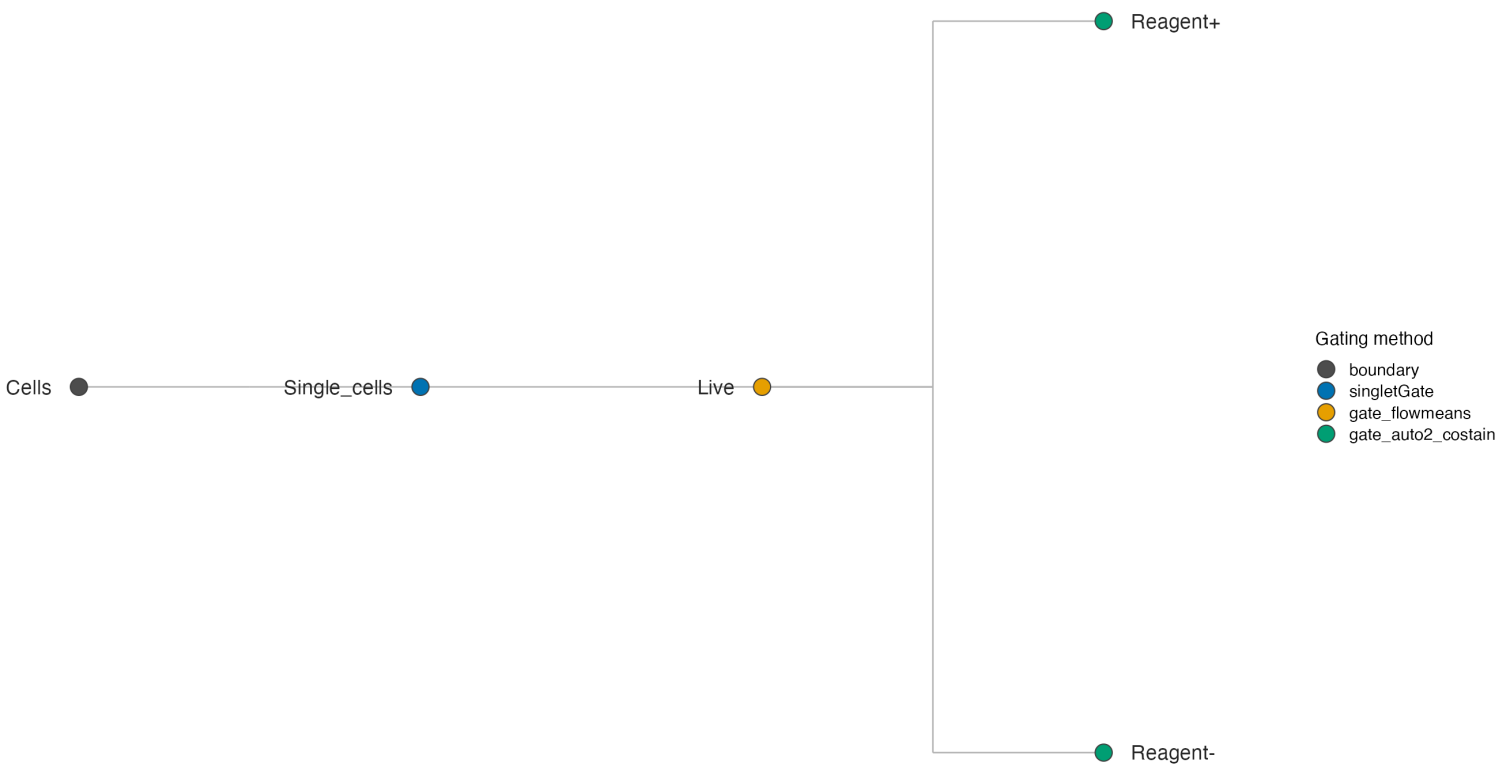
	FL18-A	FL05-A	FL19-A	FL27-A
FL18-A	1.00	0.01	0.00	0.00
FL05-A	0.01	1.00	0.00	0.00
FL19-A	0.00	0.00	1.00	0.01
FL27-A	0.00	0.00	0.01	1.00

4.3 Data Transformation Details

Argument	CD19	CD7	CD56
maxValue (from $PnR)	262144	262144	262144
channelRange	9000	9000	9000
pos	4.5	4.5	4.5
neg	0	0	0
widthBasis	-10	-10	-10

4.4 Gating Details

Gating scheme



4.4.2 Gate Statistics

No gating statistics were collected: no population in the gating_template was flagged for export.

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

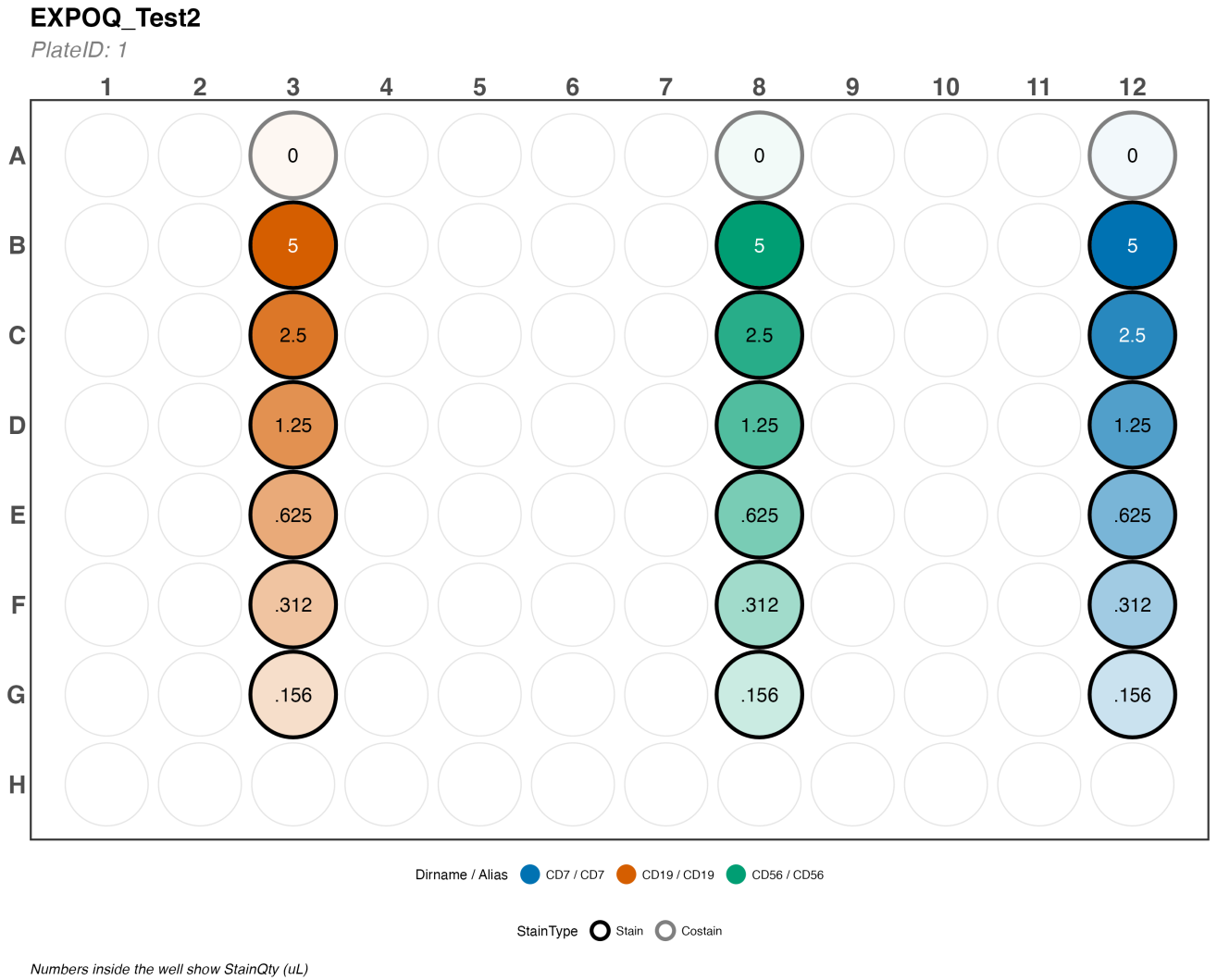
4.5 Analysis software

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

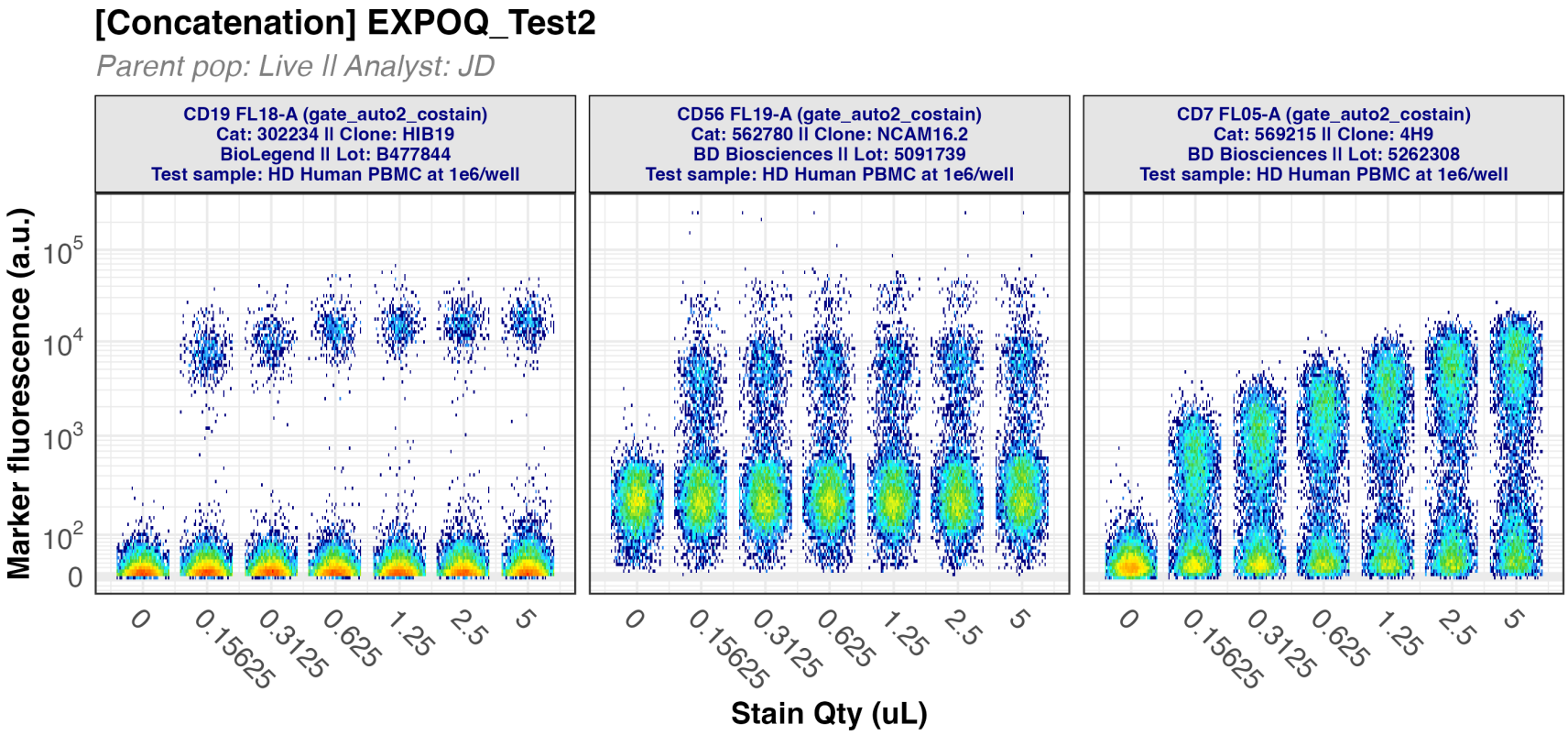
1 Plate map



2 QC

Check	CD19	CD7	CD56
Median FS00-A of Cells is at least 50% of the median of all events	**PASS**	**PASS**	**PASS**
More than 50% Live cells	**PASS**	**PASS**	**PASS**
More than 80% single cells	**PASS**	**PASS**	**PASS**
Costain SI is the lowest in the group	**PASS**	**PASS**	**PASS**
Co-stain is less than 5% positive	**PASS**	**PASS**	**PASS**
Every population has at least 100 events in every well (except costain)	**PASS**	**PASS**	**PASS**
Overall	**PASS**	**PASS**	**PASS**

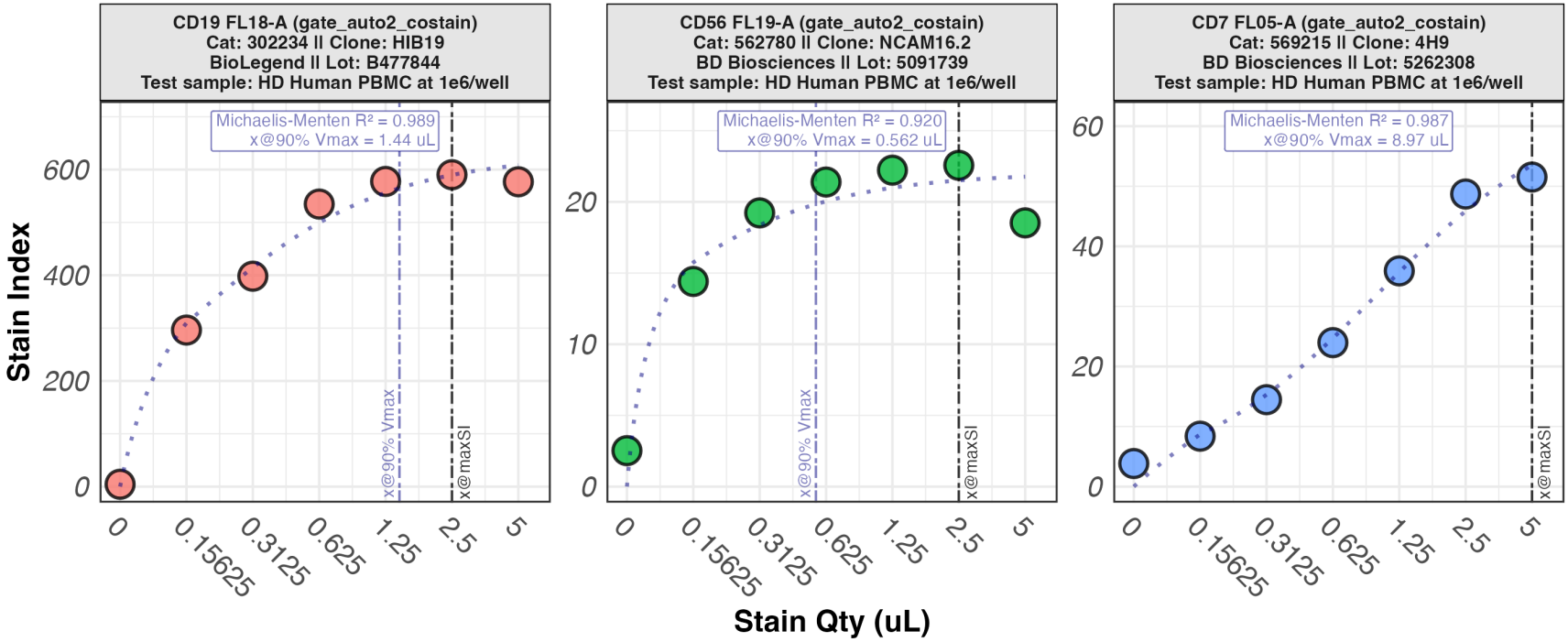
3 Resolution of populations



Concatenated events, up to 20,000 per FCS.

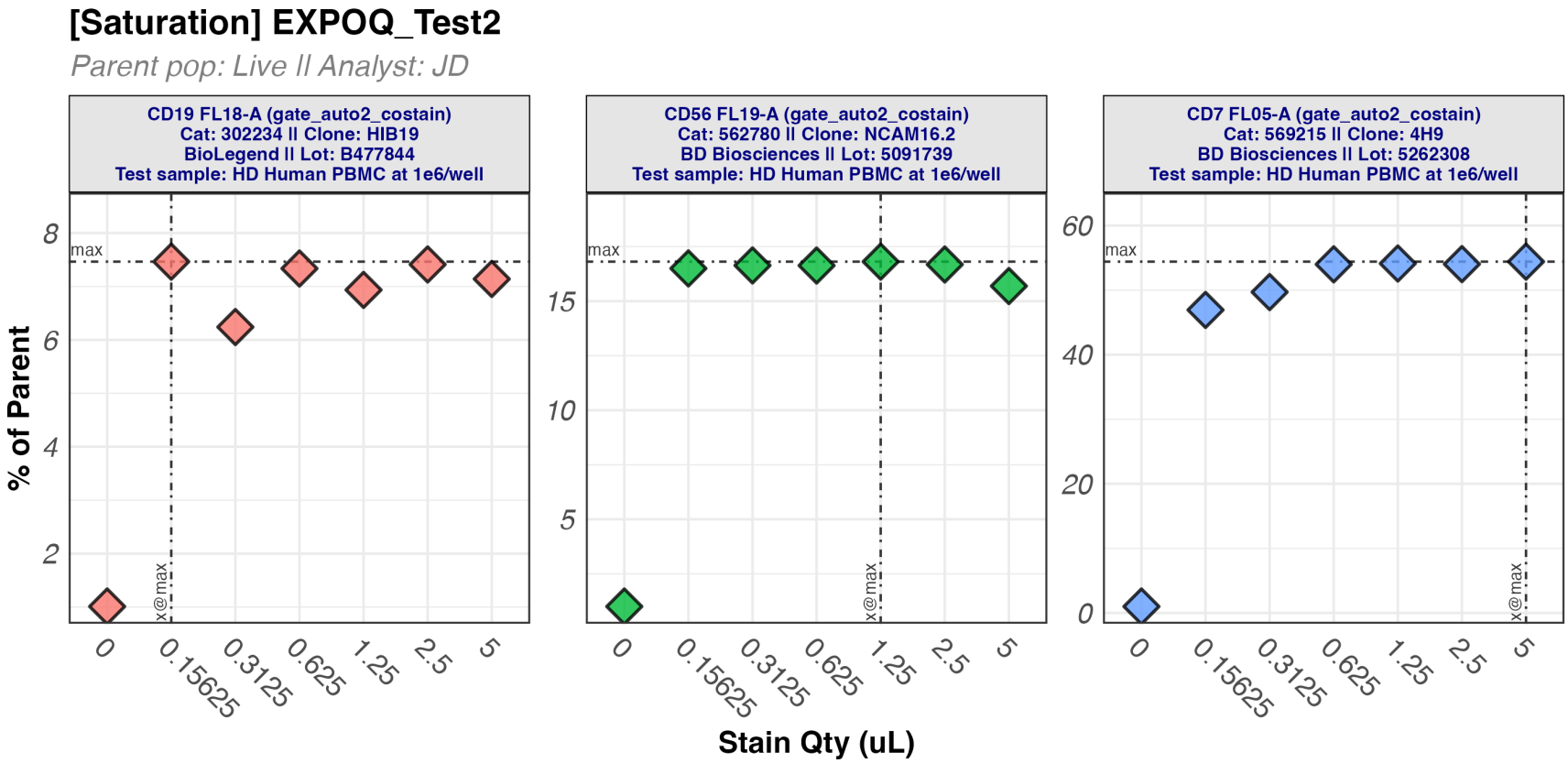
[Stain Index] EXPOQ_Test2

Parent pop: Live || Analyst: JD



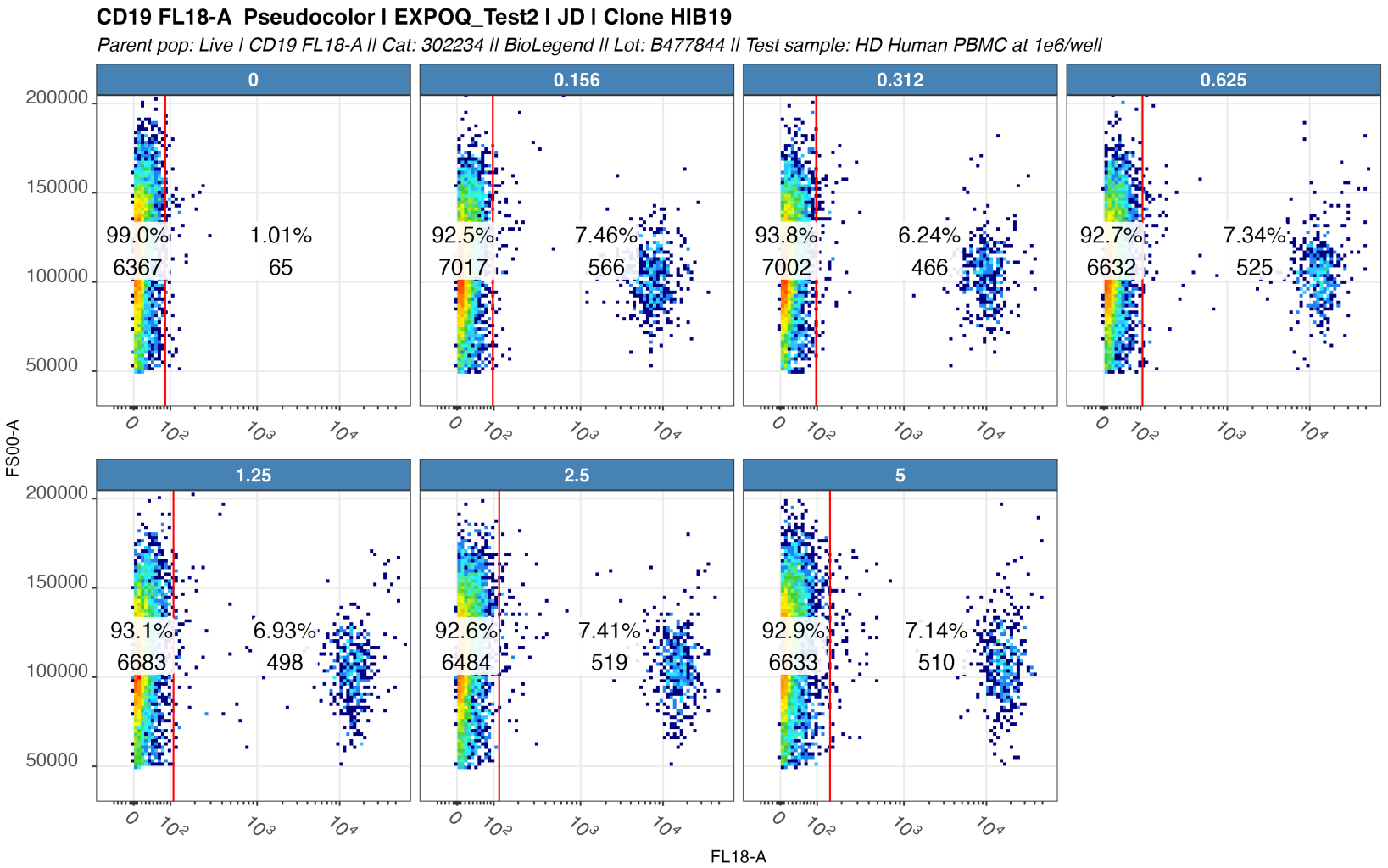
MFI calculated on untransformed (linear) values. || Compensation: csv

4 Saturation of positive population proportion



5 Layouts for each antibody

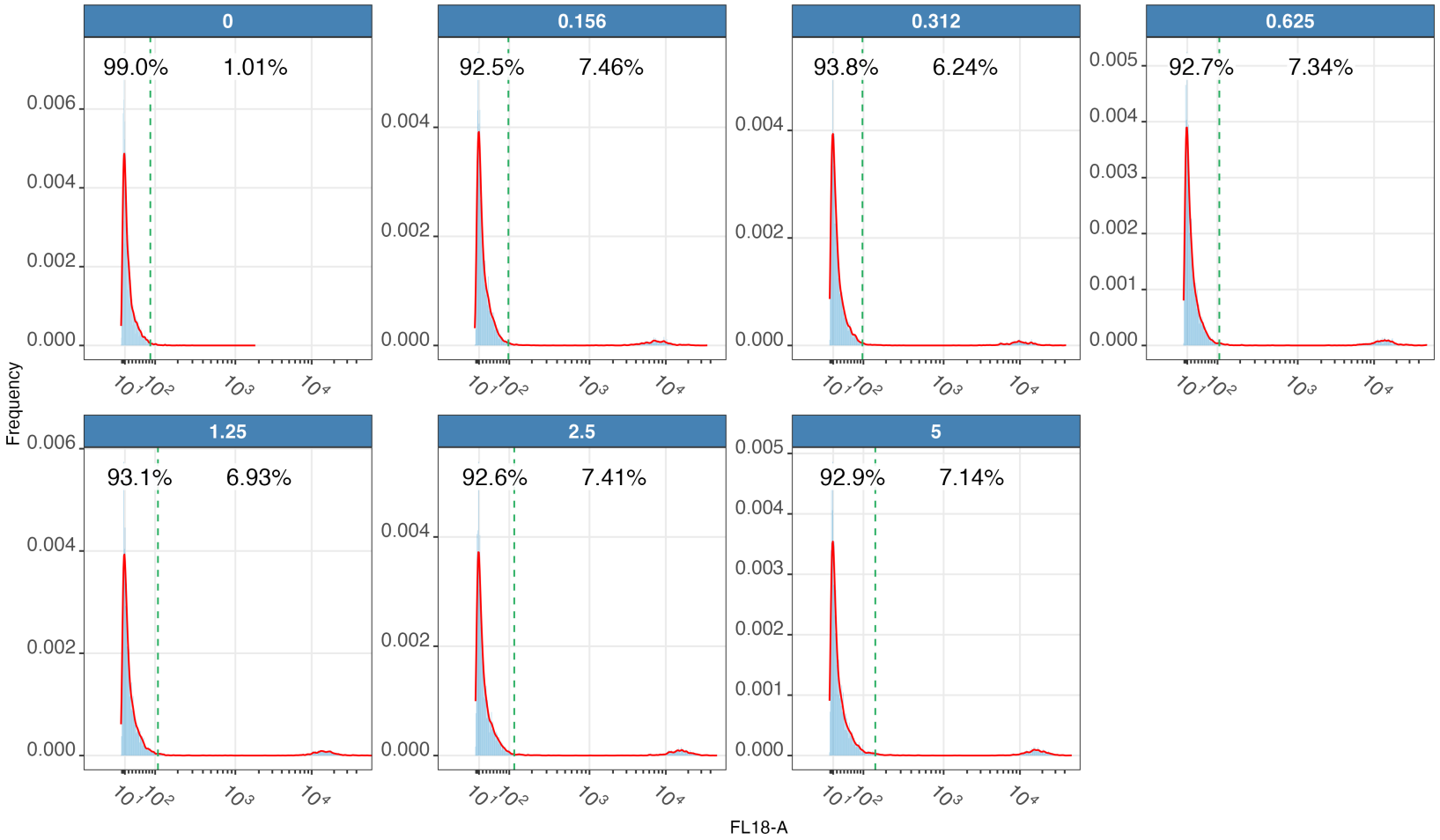
5.1 CD19



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: csv

CD19 FL18-A Histogram | EXPOQ_Test2 | JD | Clone HIB19

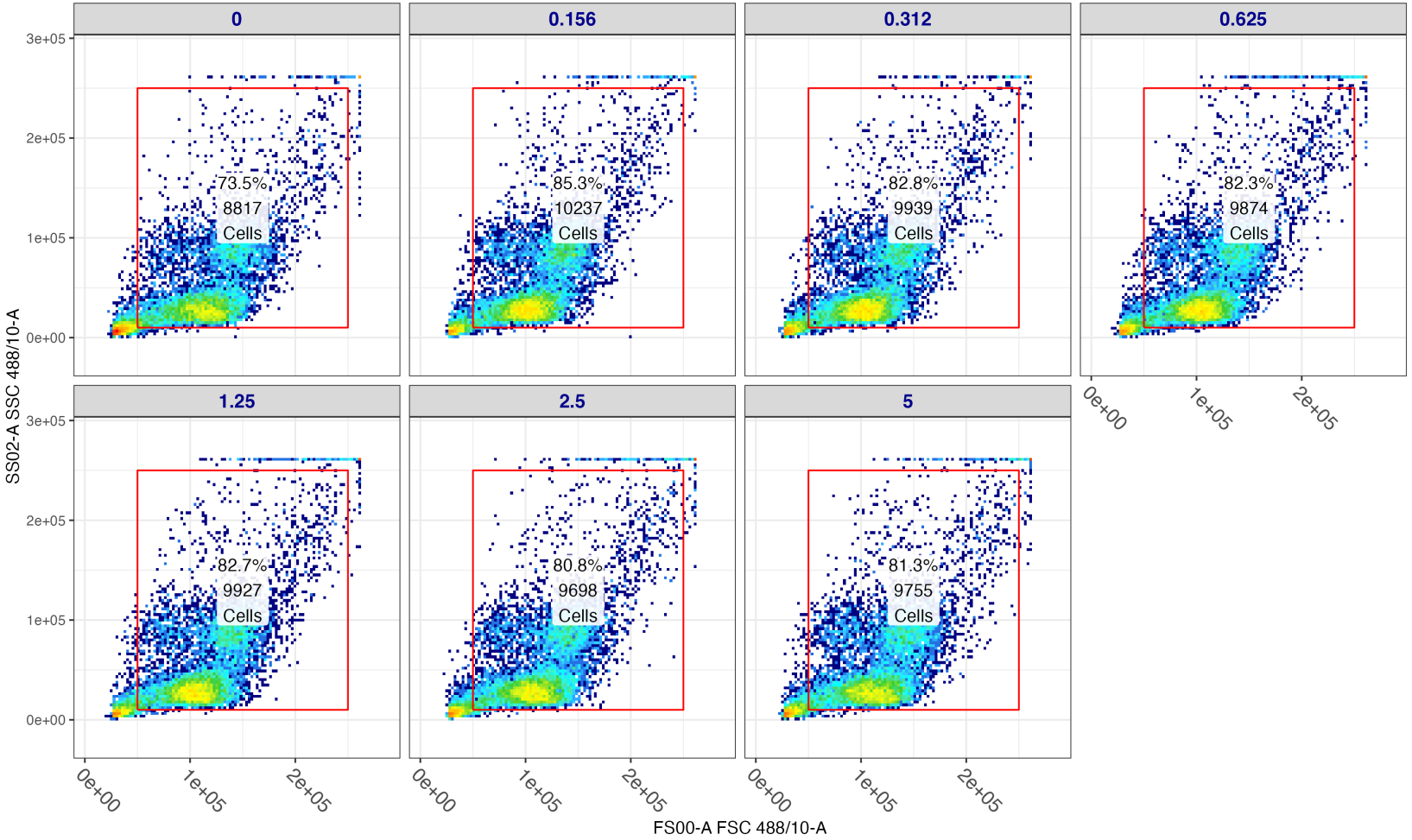
Parent pop: Live || CD19 FL18-A || Cat: 302234 || BioLegend || Lot: B477844 || Test sample: HD Human PBMC at 1e6/well



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: csv

CD19 FL18-A : Cells | EXPOQ_Test2 | JD | Clone HIB19

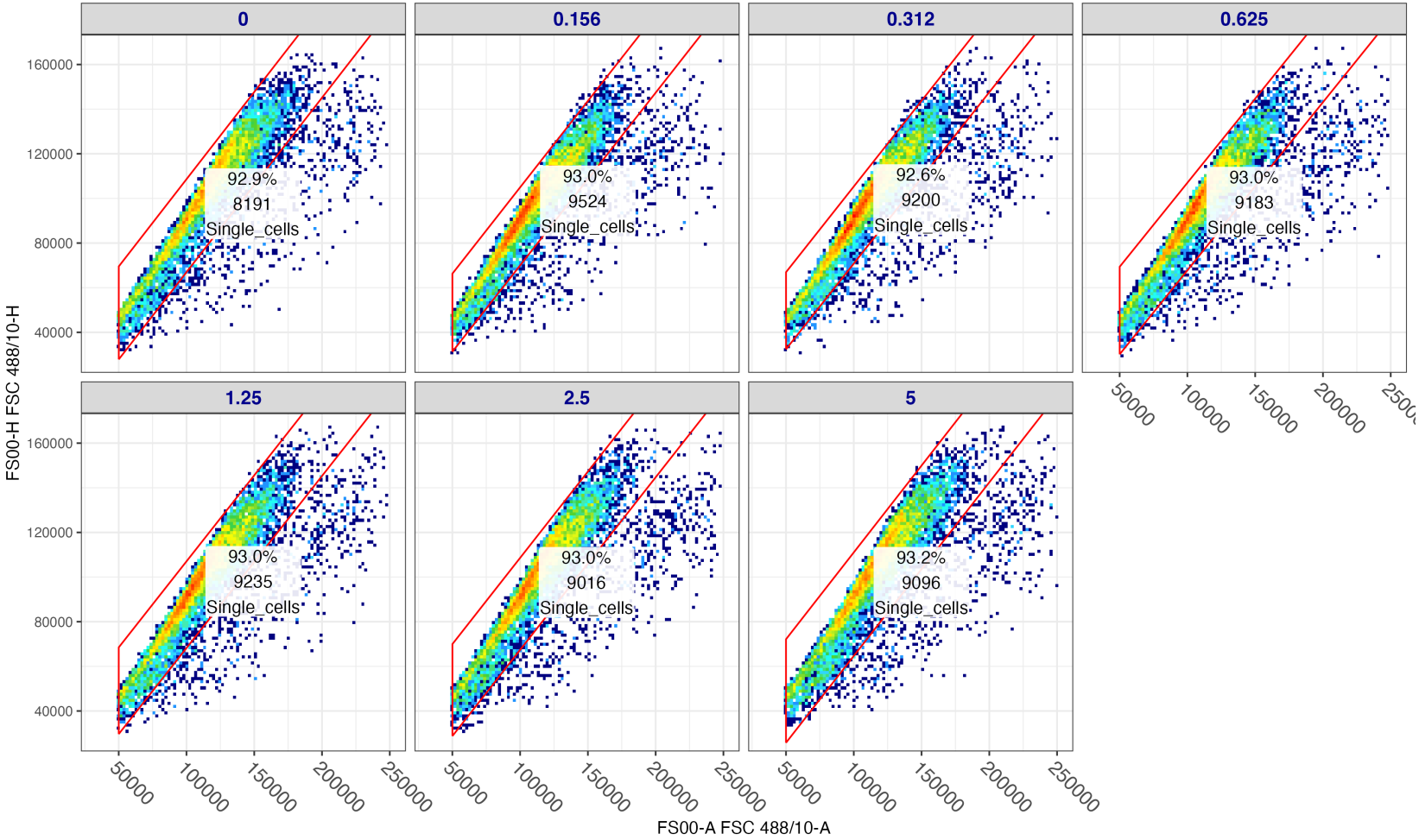
Parent pop: root | CD19 FL18-A || Cat: 302234 || BioLegend || Lot: B477844 || Test sample: HD Human PBMC at 1e6/well



Gating method: boundary || args: min=c(50000,10000), max=c(250000,250000) || collapse: TRUE || groupBy: Dirname || pp: — || pp args: — Compensation: csv

CD19 FL18-A : Single_cells | EXPOQ_Test2 | JD | Clone HIB19

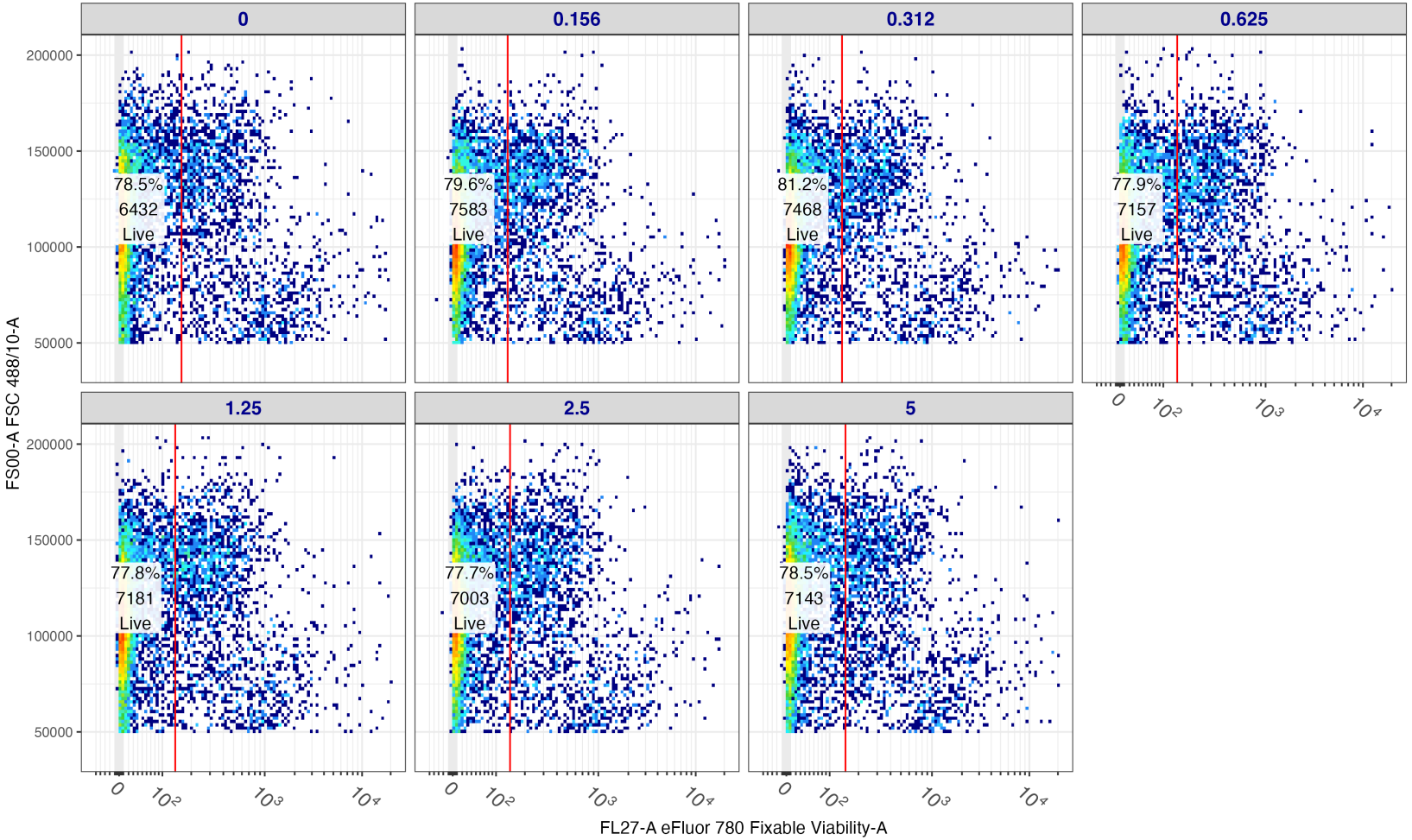
Parent pop: Cells | CD19 FL18-A || Cat: 302234 || BioLegend || Lot: B477844 || Test sample: HD Human PBMC at 1e6/well



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

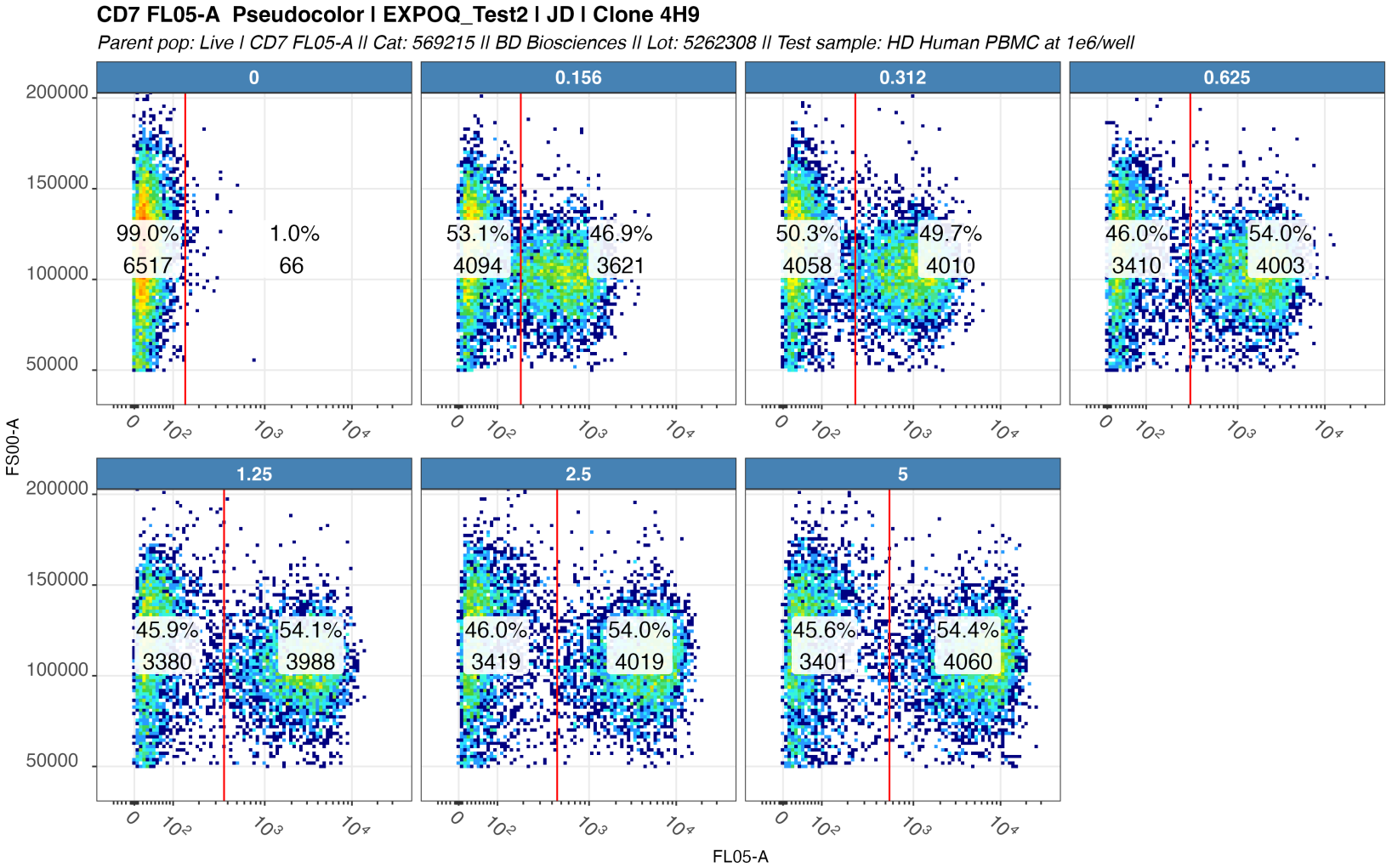
CD19 FL18-A : Live | EXPOQ_Test2 | JD | Clone HIB19

Parent pop: Single_cells | CD19 FL18-A || Cat: 302234 || BioLegend || Lot: B477844 || Test sample: HD Human PBMC at 1e6/well



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

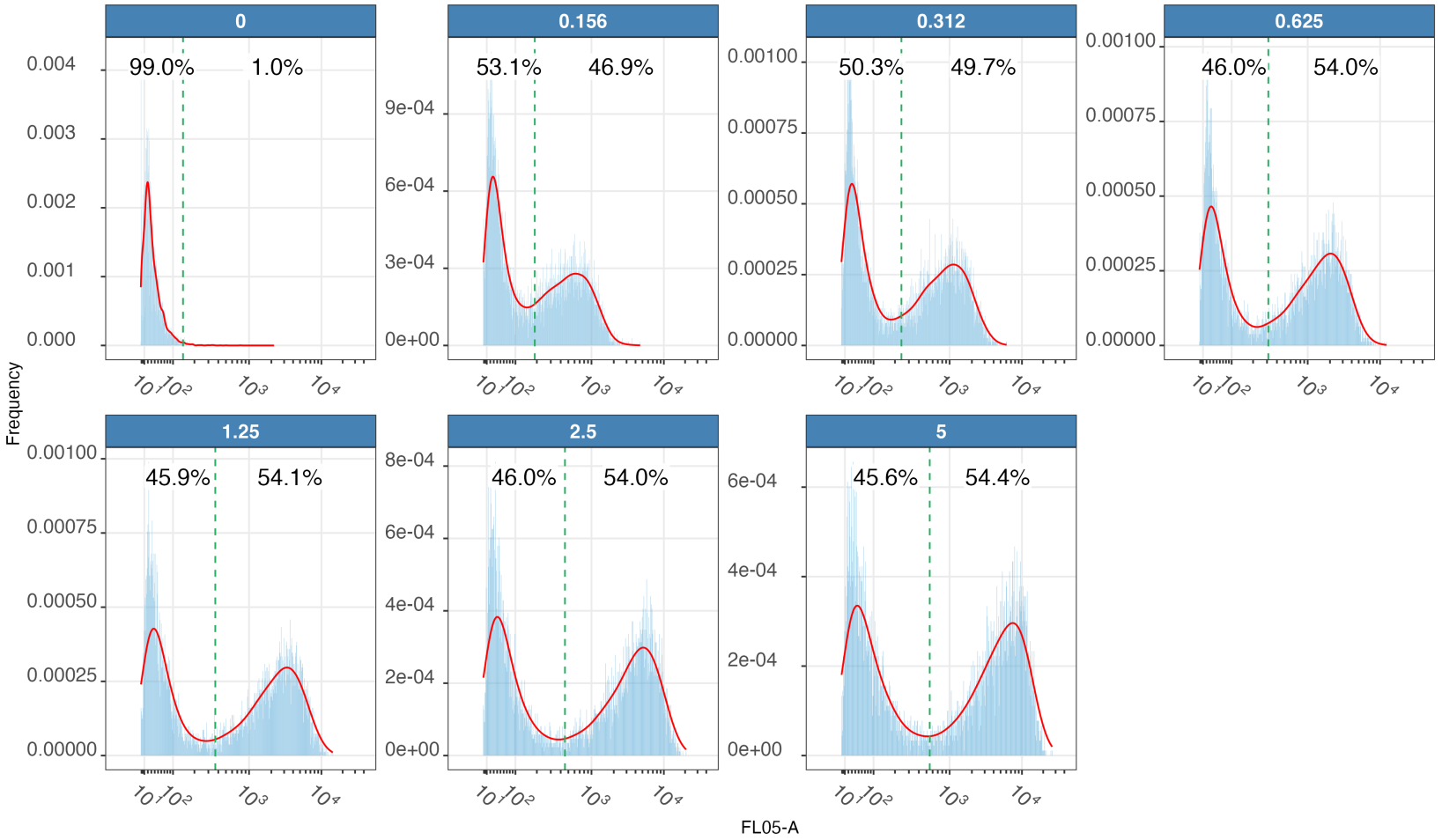
5.2 CD7



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: csv

CD7 FL05-A Histogram | EXPOQ_Test2 | JD | Clone 4H9

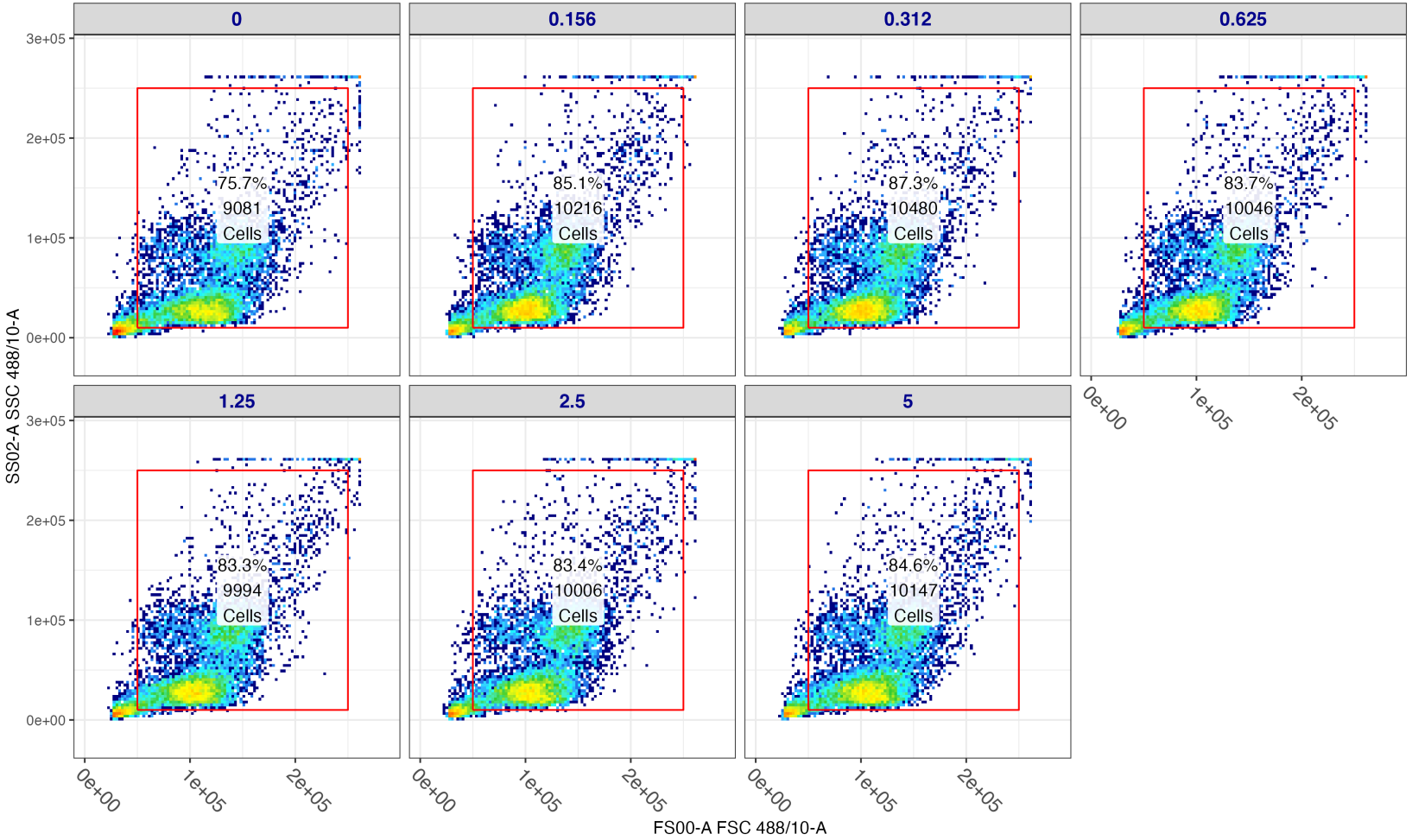
Parent pop: Live || CD7 FL05-A || Cat: 569215 || BD Biosciences || Lot: 5262308 || Test sample: HD Human PBMC at 1e6/well



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: csv

CD7 FL05-A : Cells | EXPOQ_Test2 | JD | Clone 4H9

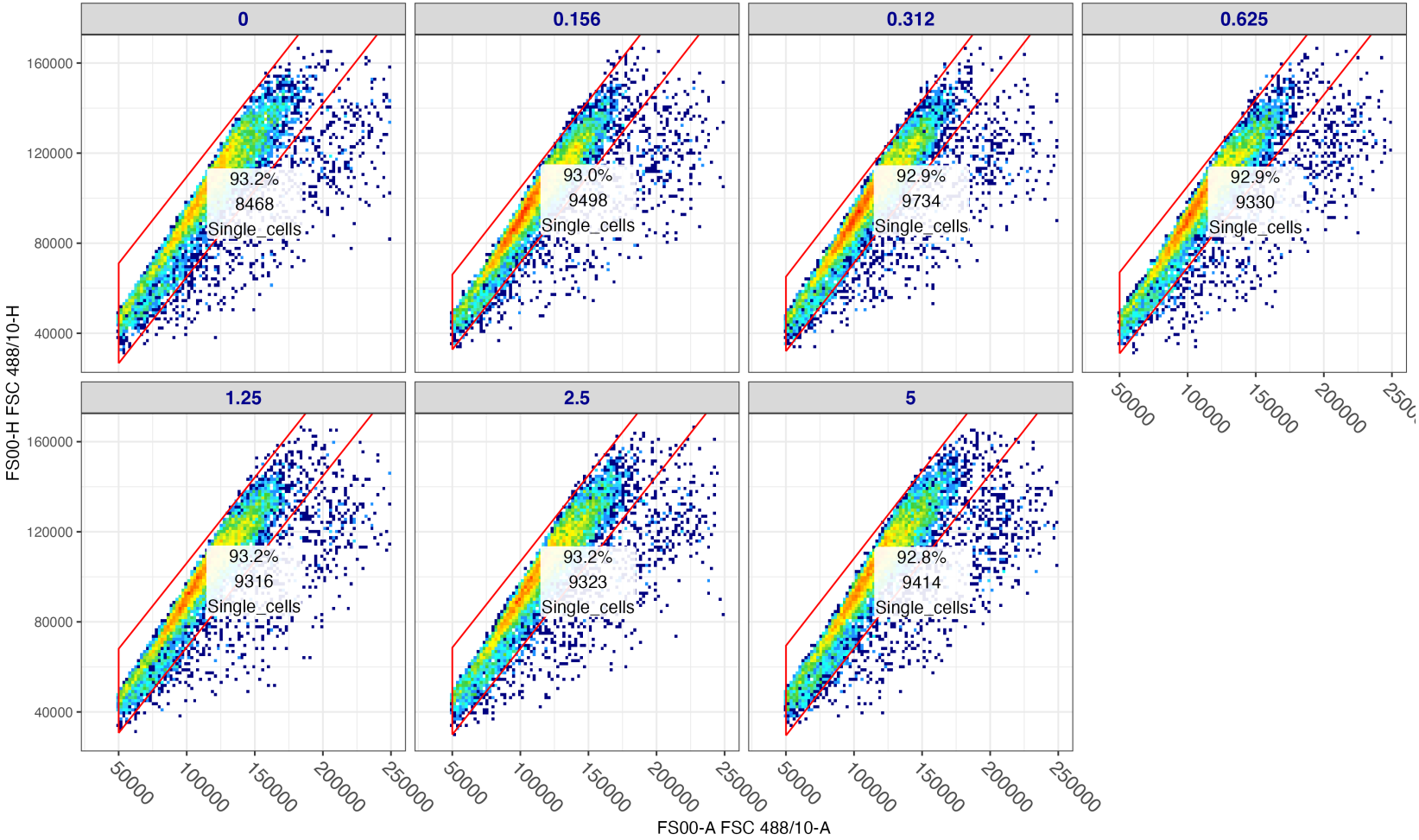
Parent pop: root | CD7 FL05-A || Cat: 569215 || BD Biosciences || Lot: 5262308 || Test sample: HD Human PBMC at 1e6/well



Gating method: boundary || args: min=c(50000,10000), max=c(250000,250000) || collapse: TRUE || groupBy: Dirname || pp: — || pp args: — Compensation: csv

CD7 FL05-A : Single_cells | EXPOQ_Test2 | JD | Clone 4H9

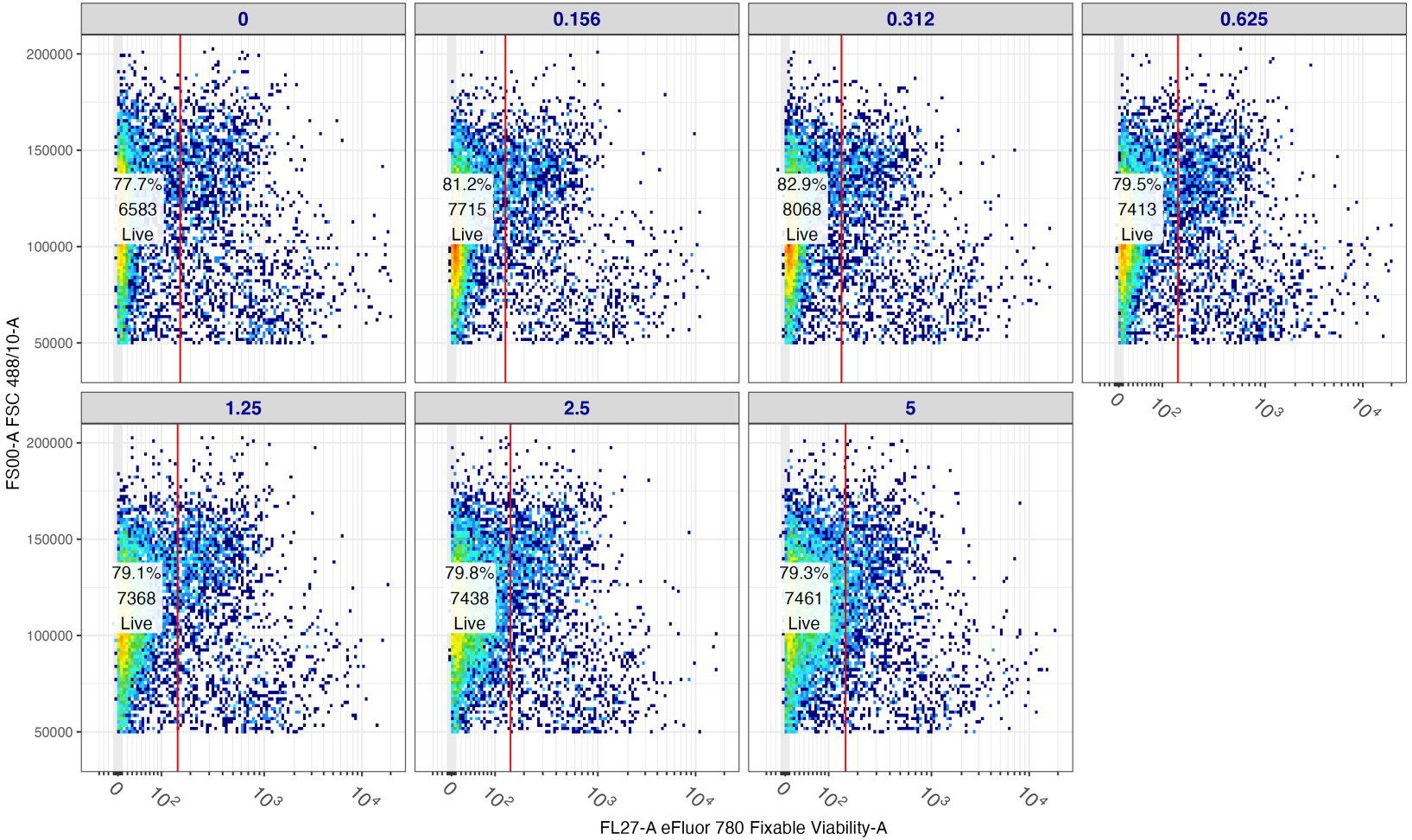
Parent pop: Cells | CD7 FL05-A || Cat: 569215 || BD Biosciences || Lot: 5262308 || Test sample: HD Human PBMC at 1e6/well



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

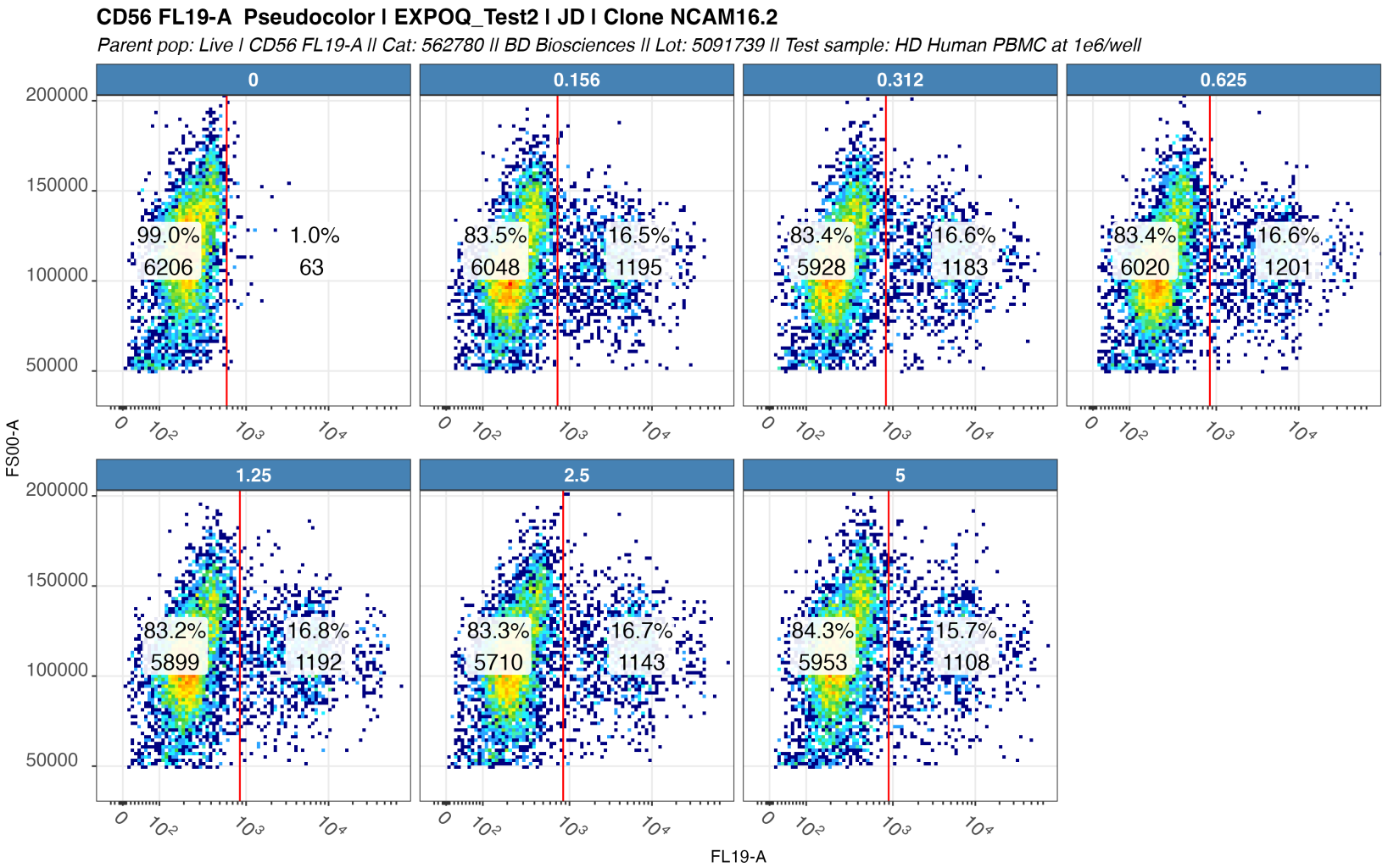
CD7 FL05-A : Live | EXPOQ_Test2 | JD | Clone 4H9

Parent pop: Single_cells | CD7 FL05-A || Cat: 569215 || BD Biosciences || Lot: 5262308 || Test sample: HD Human PBMC at 1e6/well



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

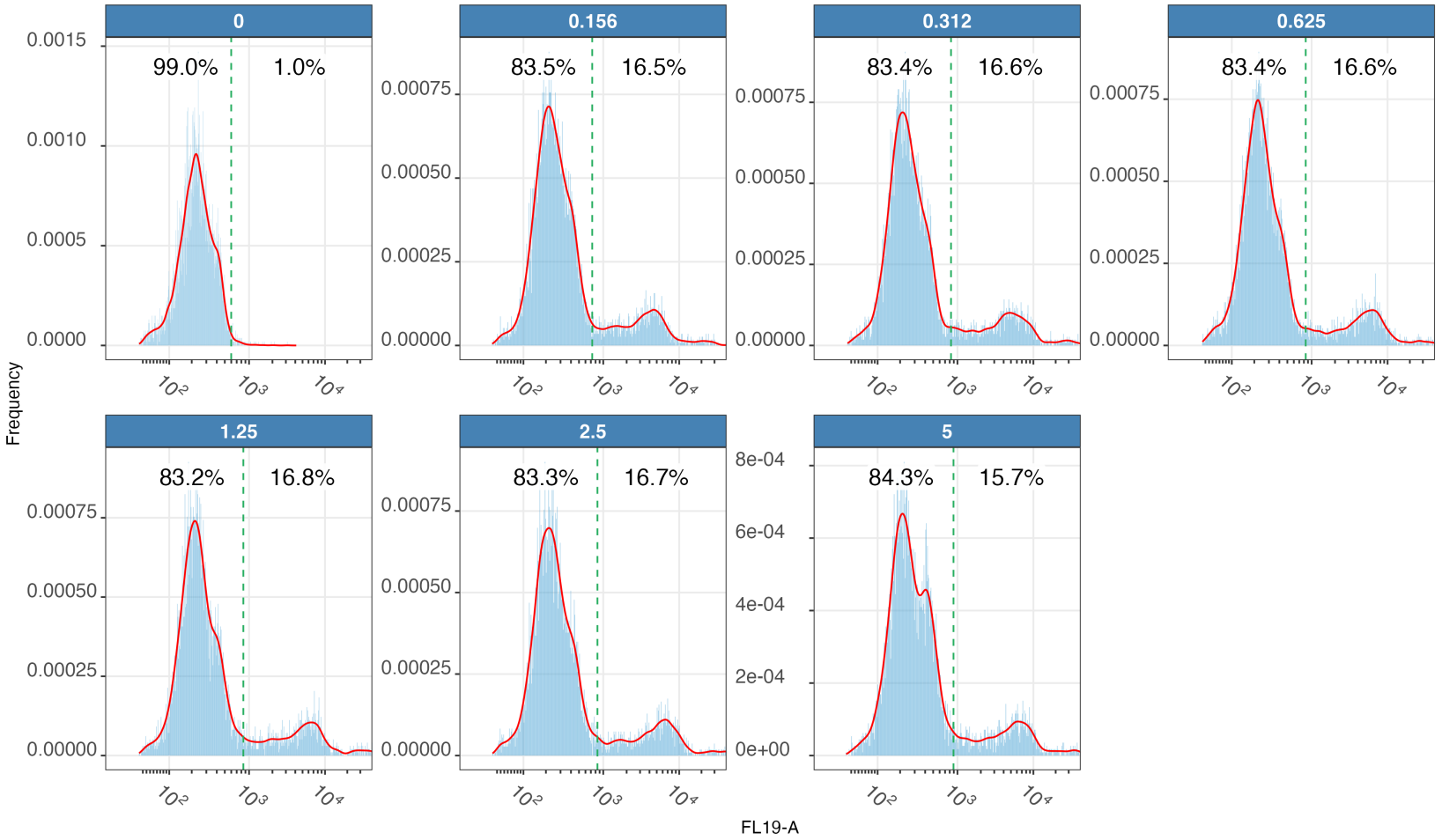
5.3 CD56



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: csv

CD56 FL19-A Histogram | EXPOQ_Test2 | JD | Clone NCAM16.2

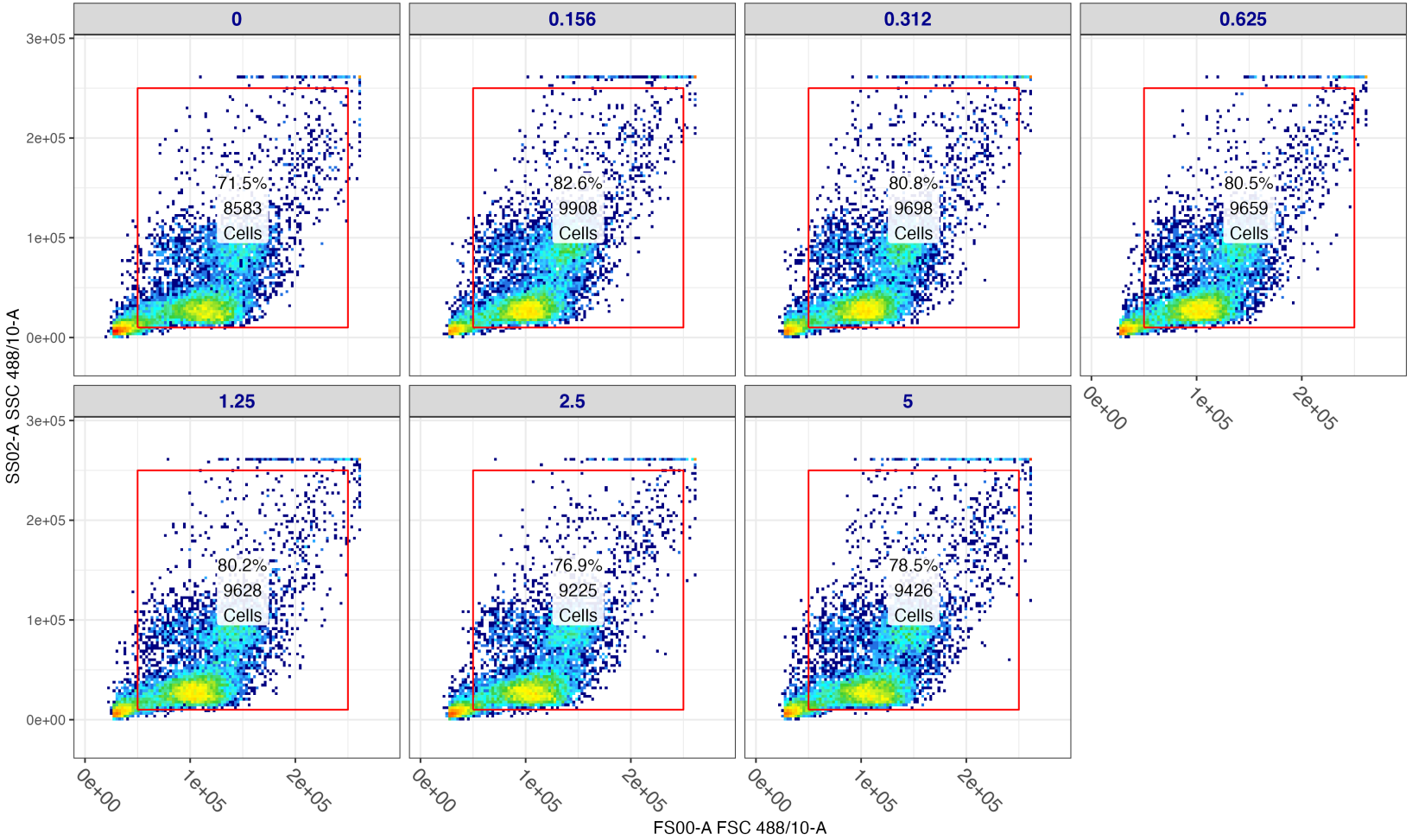
Parent pop: Live || CD56 FL19-A || Cat: 562780 || BD Biosciences || Lot: 5091739 || Test sample: HD Human PBMC at 1e6/well



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: csv

CD56 FL19-A : Cells | EXPOQ_Test2 | JD | Clone NCAM16.2

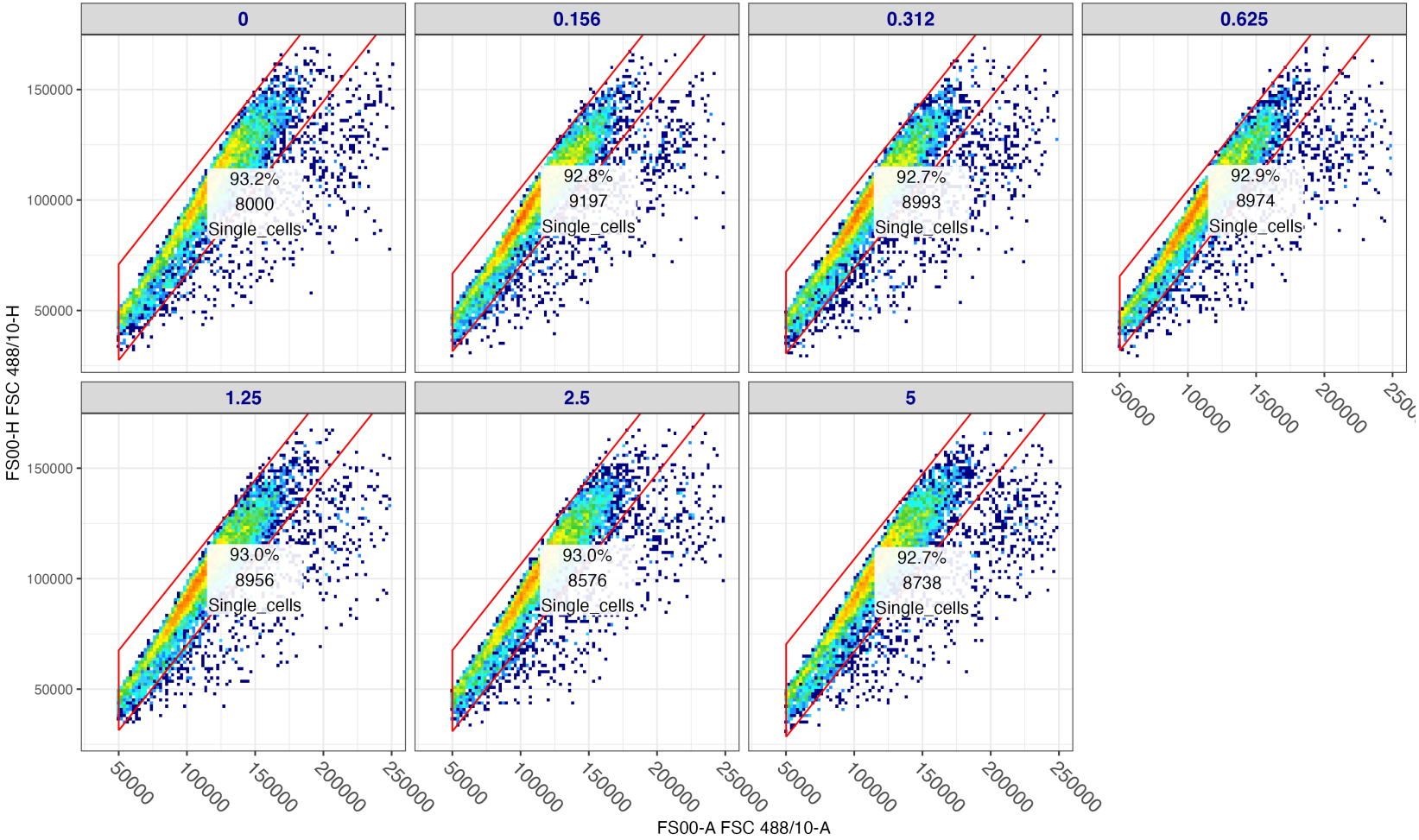
Parent pop: root | CD56 FL19-A || Cat: 562780 || BD Biosciences || Lot: 5091739 || Test sample: HD Human PBMC at 1e6/well



Gating method: boundary || args: min=c(50000,10000), max=c(250000,250000) || collapse: TRUE || groupBy: Dirname || pp: — || pp args: — Compensation: csv

CD56 FL19-A : Single_cells | EXPOQ_Test2 | JD | Clone NCAM16.2

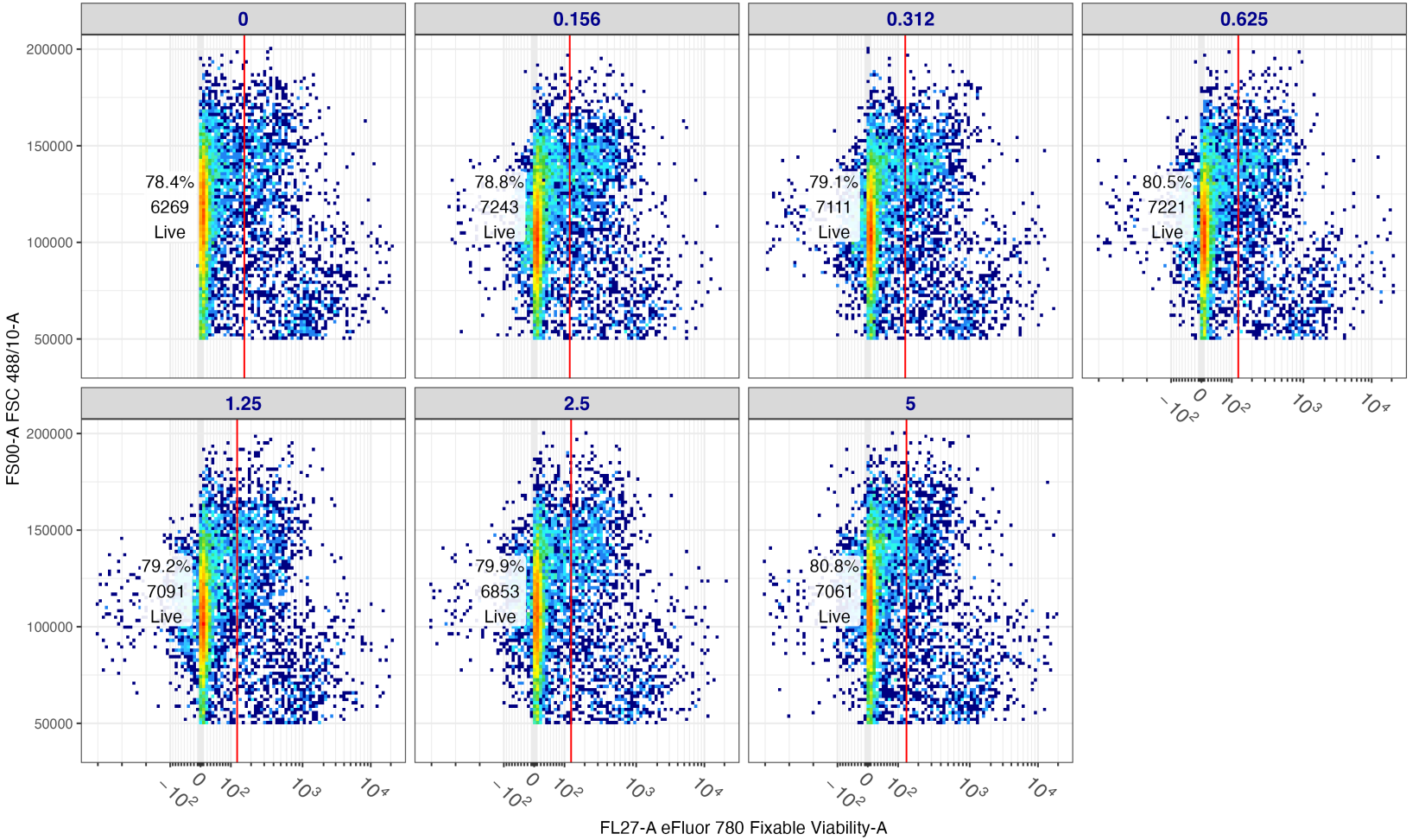
Parent pop: Cells | CD56 FL19-A || Cat: 562780 || BD Biosciences || Lot: 5091739 || Test sample: HD Human PBMC at 1e6/well



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

CD56 FL19-A : Live | EXPOQ_Test2 | JD | Clone NCAM16.2

Parent pop: Single_cells / CD56 FL19-A // Cat: 562780 // BD Biosciences // Lot: 5091739 // Test sample: HD Human PBMC at 1e6/well



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

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	csv	Info sheet
miflowcyt_export (L)	TRUE	Info sheet
dashboard_dir	(not set)	not set
titration_export_dir	(not set)	not set
dashboard_tabbed_by	ScriptVersion	Info sheet
MM_R2_threshold	0.9	Info sheet
Downsample_to (N)	12000	Info sheet
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	Everest	Info sheet
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	Bio-Rad	Info sheet
Equipment_Model	ZE5	Info sheet
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_Test2	Info sheet

7 Session Information

Script version: ACTA v3.6.11

Render timestamp: 2026-11-12 20:24:25 PST

Operator: JD

Layout workbook: OQ_Test2_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)
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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)
```

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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)
```

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 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.

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