SUPPLEMENTAL MATERIALS

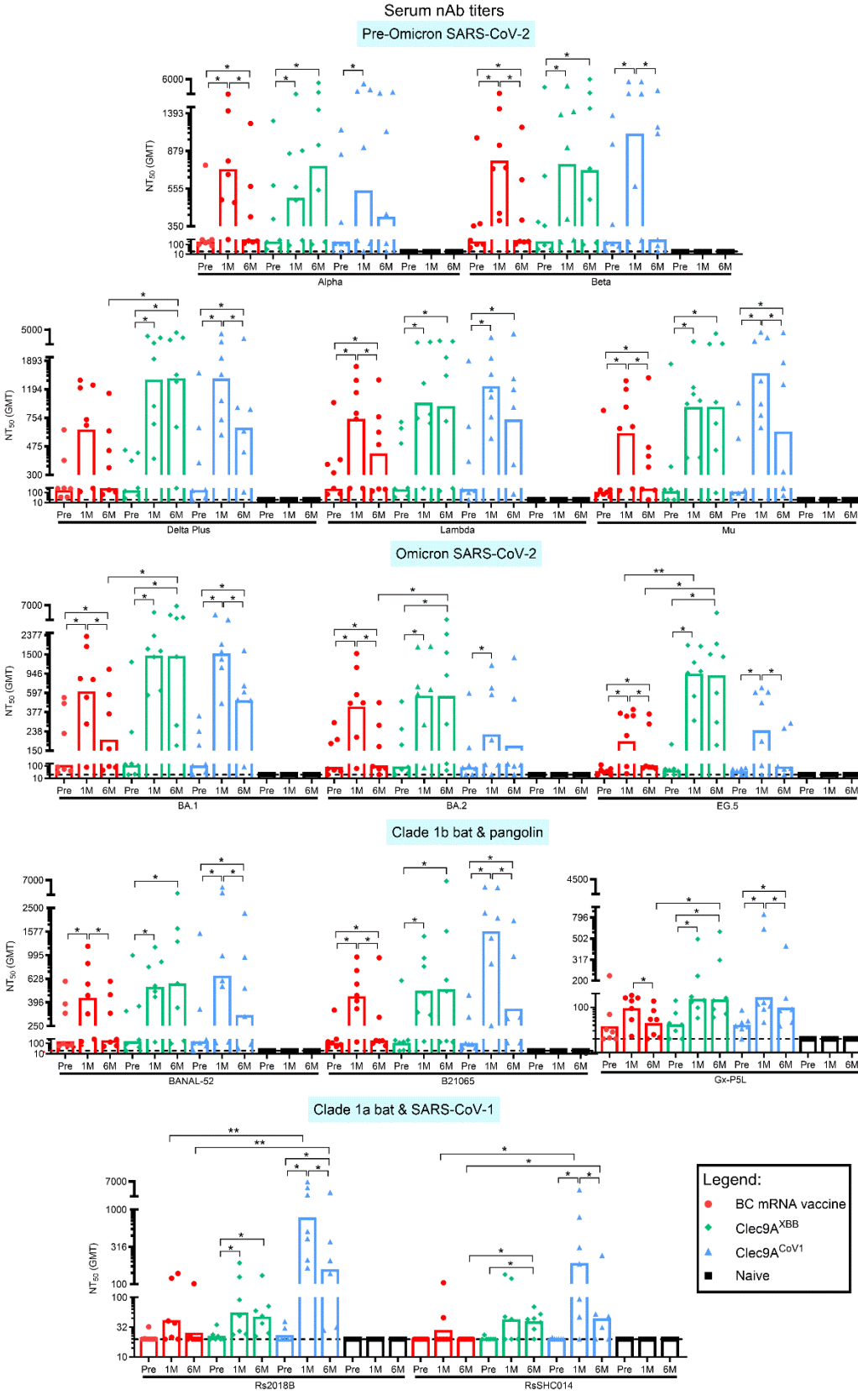

Figure S1. Serum neutralizing antibody titers upon systemic booster with Clec9A^{XBB}, Clec9A^{CoV1} or bivalent Comirnaty (BC) mRNA vaccine. Five to six-week-old BALB/c mice were immunized twice three weeks apart (0.05 µg per dose; i.m) with Pfizer-BioNTech original Comirnaty mRNA vaccine. Three months after the last immunization dose, mice were boosted either with Pfizer-BioNTech BA.4/5 bivalent Comirnaty (BC) mRNA vaccine (0.05 µg; i.m), Clec9A^{XBB} (10 µg adjuvanted with 50 µg poly I:C; s.c) or Clec9A^{CoV1} (10 µg adjuvanted with 50 µg poly I:C; s.c). A control group of non-immunized mice (naïve) was also included for baseline. The serum nAb titers against 13 sarbecoviruses representative of clades 1b and 1a at pre-boost, one- and six months post-boost were determined by multiplex sVNT. Data are from one representative experiment performed twice with similar results, n = 6-7 per group/experiment. Symbols represent individual animals and data shown are geometric means. Statistical analysis: Non-parametric two-tailed Kruskal Walis test with Dunn's multiple-comparison test and Friedman test with Dunn's multiple-comparison test. *$p < 0.05$, **$p < 0.01$.

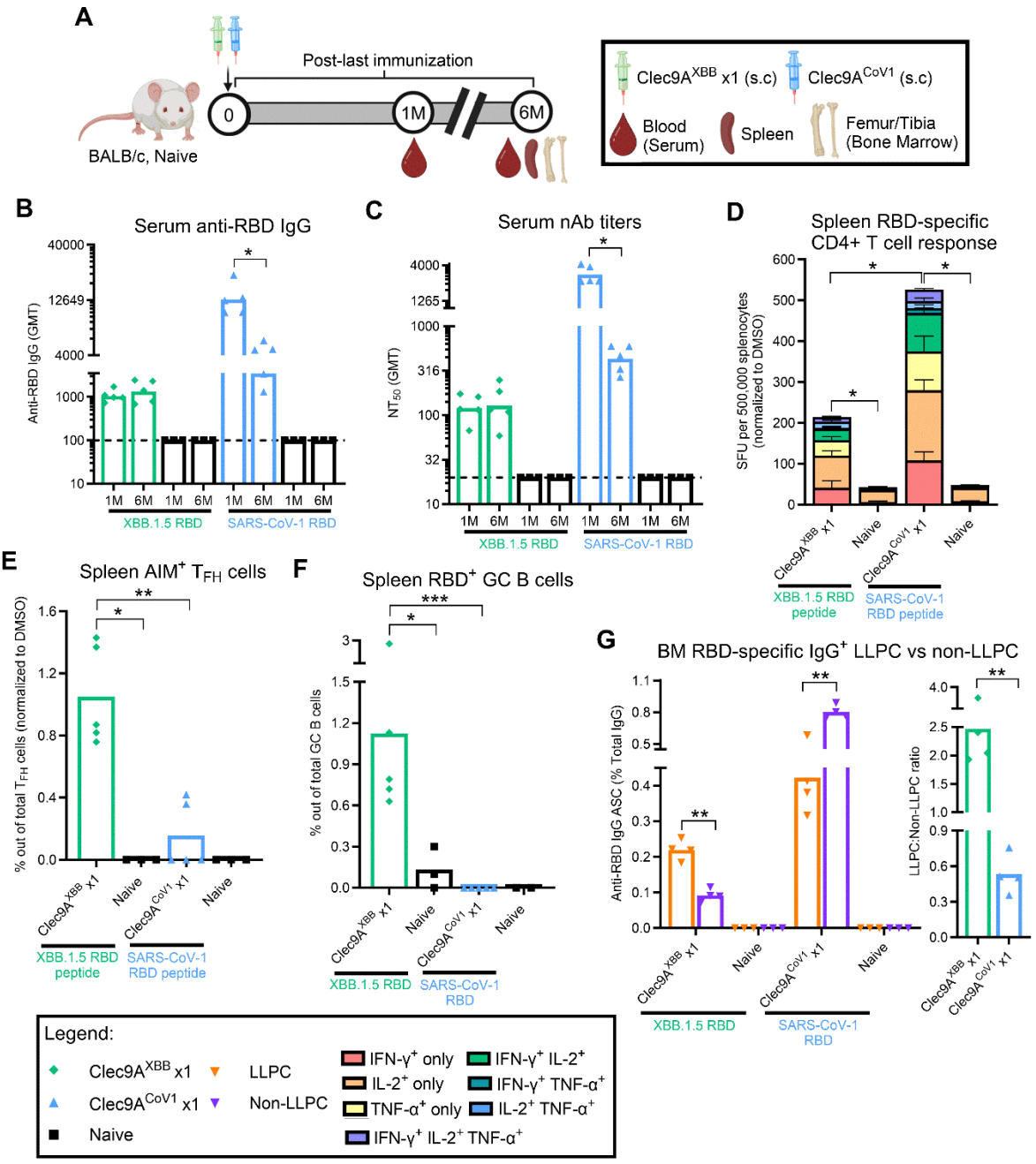

Figure S2. Durability of immune responses upon single shot immunization with Clec9A^{XBB} or Clec9A^{CoV1} in naïve mice. A) Five to six-week-old BALB/c mice were immunized with a single dose (2 µg adjuvanted with 50 µg poly I:C; s.c) of Clec9A^{XBB} or Clec9A^{CoV1}. **(B, C)** Blood was collected one- and six months after immunization. **(B)** Serum anti-RBD IgG titers against XBB.1.5 and SARS-CoV-1 RBD 1 at one- and six months post-immunization were determined by ELISA. **(C)** Serum nAb titers against

XBB.1.5 and SARS-CoV-1 at one- and six months post-immunization were determined by sVNT. **(D-G)** Mice were euthanized at six months post-immunization, and spleen and BM from femur/tibia were harvested. **(D)** Frequency of IFN-γ, IL-2 and/or TNF-α secreting $CD4^+$-enriched splenocytes at six months post-immunization was determined by FluoroSPOT upon re-stimulation with XBB.1.5 and SARS-CoV-1 RBD peptides. **(E, F)** Percentage of **(E)** AIM^+ T_{FH} and **(F)** RBD^+ GC B cells in spleen at six months post-immunization was determined by flow cytometry. **(G)** Frequency of BM RBD-specific IgG^+ LLPC and non-LLPC (normalized to total IgG) at six months post-immunization was determined by B cell ELISPOT. **(B-G)** Data are from one representative experiment performed twice with similar results, n = 4-5 per group/experiment. **(B, C, E-G)** Symbols represent individual animals and data shown are **(B, C)** geometric means and **(D-G)** means ± **(D)** SD. Statistical analysis: Non-parametric two-tailed **(B, C)** Wilcoxon matched-pairs signed rank test and **(D-G)** Mann-Whitney test. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$.

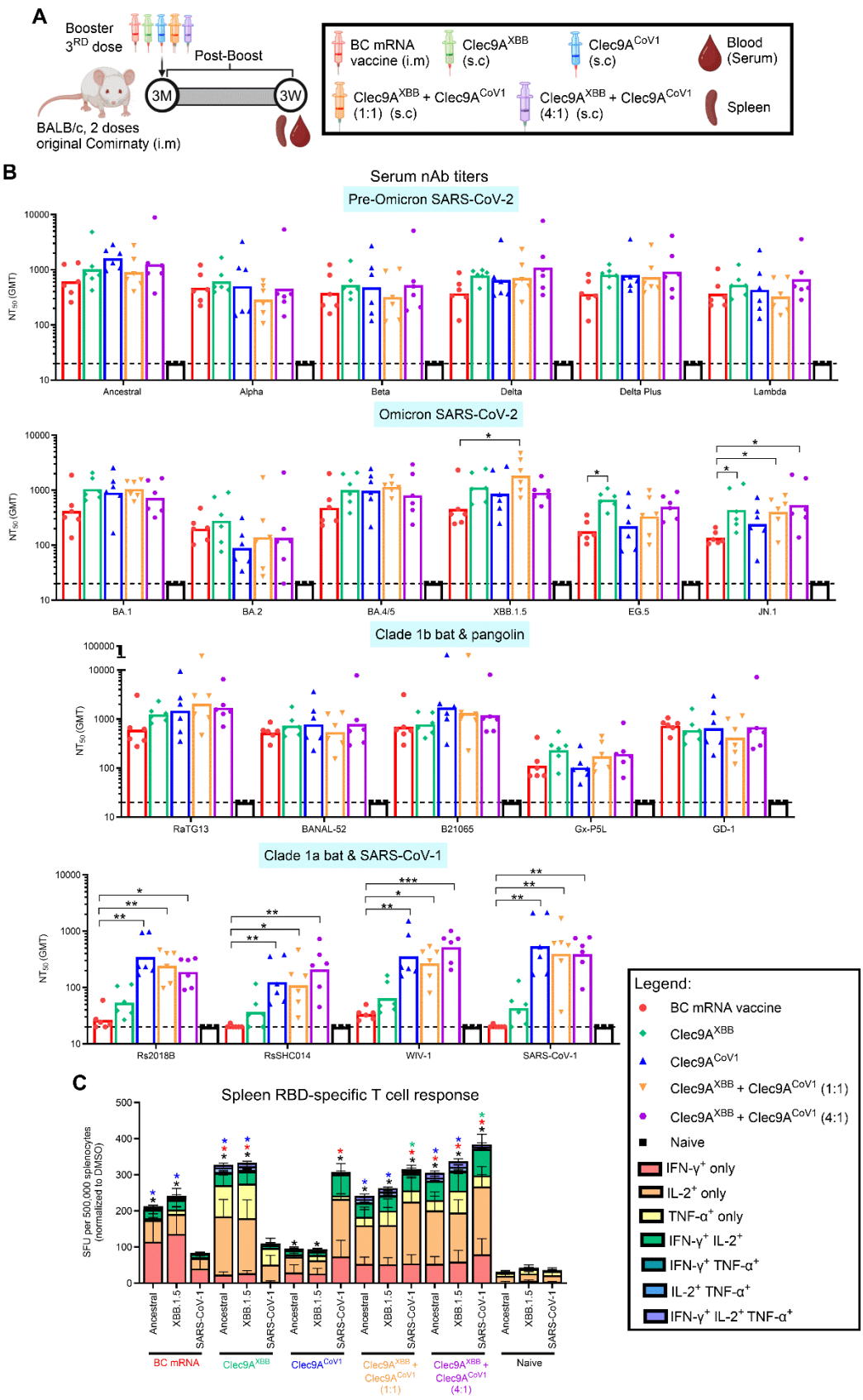
A
Booster 3RD dose
Post-Boost
3M
3W
BALB/c, 2 doses original Comirnaty (i.m)
BC mRNA vaccine (i.m)
Clec9AXBB (s.c)
Clec9ACoV1 (s.c)
Blood (Serum)
Clec9AXBB + Clec9ACoV1 (1:1) (s.c)
Clec9AXBB + Clec9ACoV1 (4:1) (s.c)
Spleen
B
Serum nAb titers
Pre-Omicron SARS-CoV-2
NT50 (GMT)
Ancestral
Alpha
Beta
Delta
Delta Plus
Lambda
Omicron SARS-CoV-2
BA.1
BA.2
BA.4/5
XBB.1.5
EG.5
JN.1
Clade 1b bat & pangolin
RaTG13
BANAL-52
B21065
Gx-P5L
GD-1
Clade 1a bat & SARS-CoV-1
Rs2018B
RsSHC014
WIV-1
SARS-CoV-1
Legend:
BC mRNA vaccine
Clec9AXBB
Clec9ACoV1
Clec9AXBB + Clec9ACoV1 (1:1)
Clec9AXBB + Clec9ACoV1 (4:1)
Naive
IFN-γ+ only
IL-2+ only
TNF-α+ only
IFN-γ+ IL-2+
IFN-γ+ TNF-α+
IL-2+ TNF-α+
IFN-γ+ IL-2+ TNF-α+
C
Spleen RBD-specific T cell response
SFU per 500,000 splenocytes (normalized to DMSO)
Ancestral
XBB.1.5
SARS-CoV-1
BC mRNA
Clec9AXBB
Clec9ACoV1
Clec9AXBB + Clec9ACoV1 (1:1)
Clec9AXBB + Clec9ACoV1 (4:1)
Naive

Figure S3. Dose optimization of [Clec9A^{XBB} + Clec9A^{CoV1}] booster. (A) Five to six-week-old BALB/c mice were immunized twice three weeks apart (0.05 µg per dose; i.m) with original Comirnaty mRNA vaccine. Three months after the second immunizing dose, mice were boosted with either BC mRNA vaccine (0.05 µg; i.m), Clec9A^{XBB} (10 µg), Clec9A^{CoV1} (10 µg), [Clec9A^{XBB} + Clec9A^{CoV1}] (5 µg + 5 µg) or [Clec9A^{XBB} + Clec9A^{CoV1}] (8 µg + 2 µg). All Clec9A-based formulations were adjuvanted with 50 µg poly I:C and administered s.c. At three weeks post-boost, blood was collected, and mice were euthanized to harvest spleen. **(B)** Serum nAb titers against 21 sarbecoviruses from clades 1a and 1b at three weeks post-boost was determined by multiplex sVNT. **(C)** Frequency of IFN-γ, IL-2 and/or TNF-α secreting splenocytes at three weeks post-boost was determined by FluoroSPOT upon re-stimulation with ancestral SARS-CoV-2, XBB.1.5 and SARS-CoV-1 RBD peptides. **(B, C)** Data are from one representative experiment performed twice with similar results, n = 5-6 per group/experiment. **(B)** Symbols represent individual animals and data shown are **(B)** geometric means and **(C)** means ± SD. Statistical analysis: Non-parametric two-tailed Kruskal Walis test with Dunn's multiple-comparison test. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$. **(C)** Asterisk colors represent statistical significance between corresponding groups.

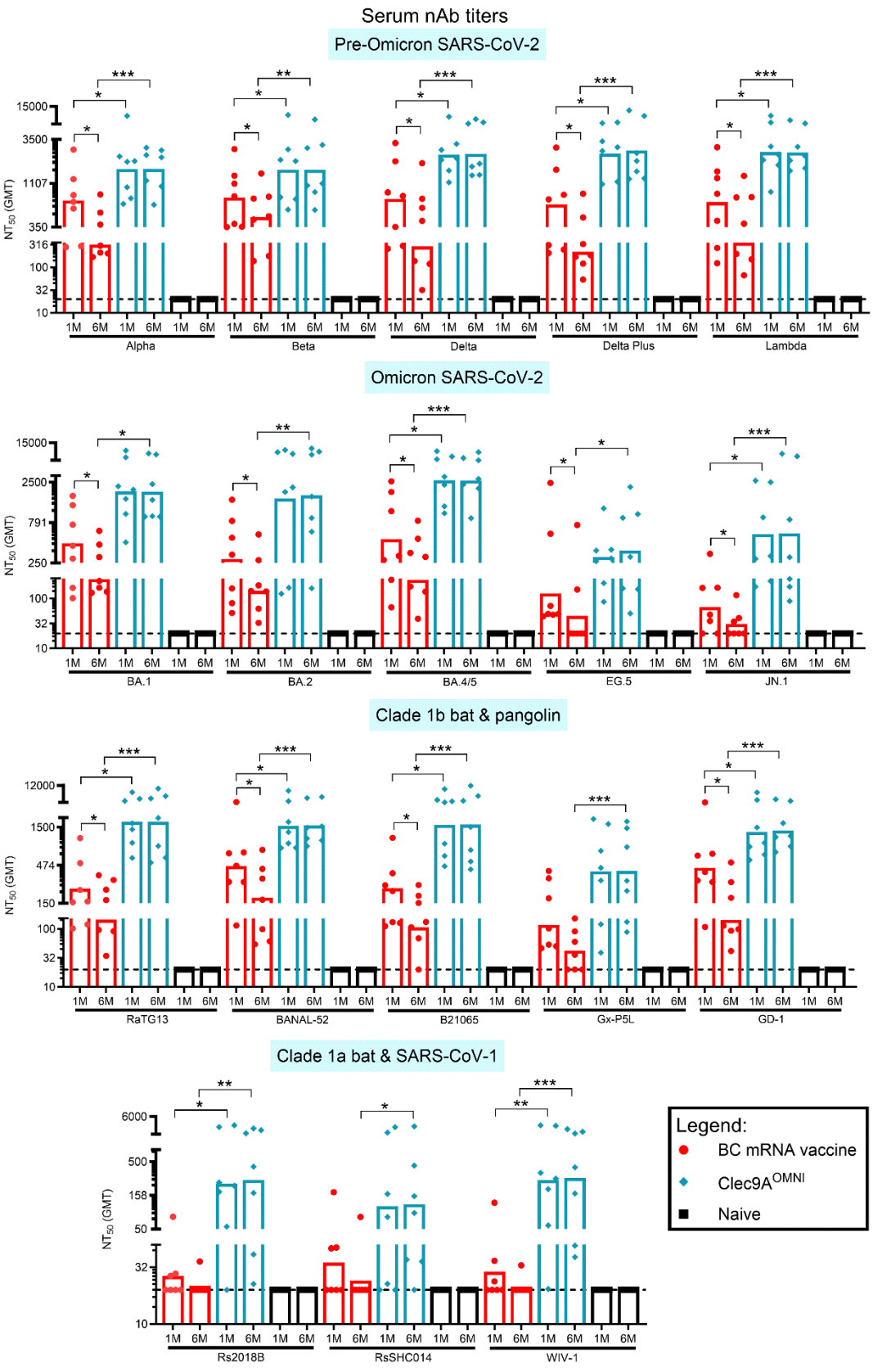
Serum nAb titers
Pre-Omicron SARS-CoV-2
NT50 (GMT)
15000
3500
1107
350
316
100
32
10
1M 6M 1M 6M 1M 6M 1M 6M 1M 6M 1M 6M 1M 6M 1M 6M 1M 6M 1M 6M 1M 6M 1M 6M 1M 6M 1M 6M
Alpha
Beta
Delta
Delta Plus
Lambda
Omicron SARS-CoV-2
15000
2500
791
250
100
32
10
BA.1
BA.2
BA.4/5
EG.5
JN.1
Clade 1b bat & pangolin
12000
1500
474
150
100
32
10
RaTG13
BANAL-52
B21065
Gx-P5L
GD-1
Clade 1a bat & SARS-CoV-1
6000
500
158
50
32
10
Rs2018B
RsSHC014
WIV-1
Legend:
BC mRNA vaccine
Clec9A^OMNI
Naive

Figure S4. Serum neutralizing antibody responses upon systemic booster with Clec9A^{OMNI} versus BC mRNA vaccine. Five to six-week-old BALB/c mice were immunized twice three weeks apart (0.05 µg per dose; i.m) with original Comirnaty mRNA vaccine. Three months after the second immunization dose, mice were boosted with either BC mRNA vaccine (0.05 µg; i.m), or Clec9A^{OMNI} (8 µg Clec9A^{XBB} + 2 µg Clec9A^{CoV1} adjuvanted with 50 µg poly I:C; s.c). Serum nAb titers against 18 sarbecoviruses from clades 1a and 1b at one- and six months post-boost were determined by multiplex sVNT. Data are from one representative experiment performed twice with similar results, n = 5-6 per group/experiment. Symbols represent individual animals and data shown are geometric means. Statistical analysis: Non-parametric two-tailed Mann-Whitney test, and Friedman test with Dunn's multiple-comparison test. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$.

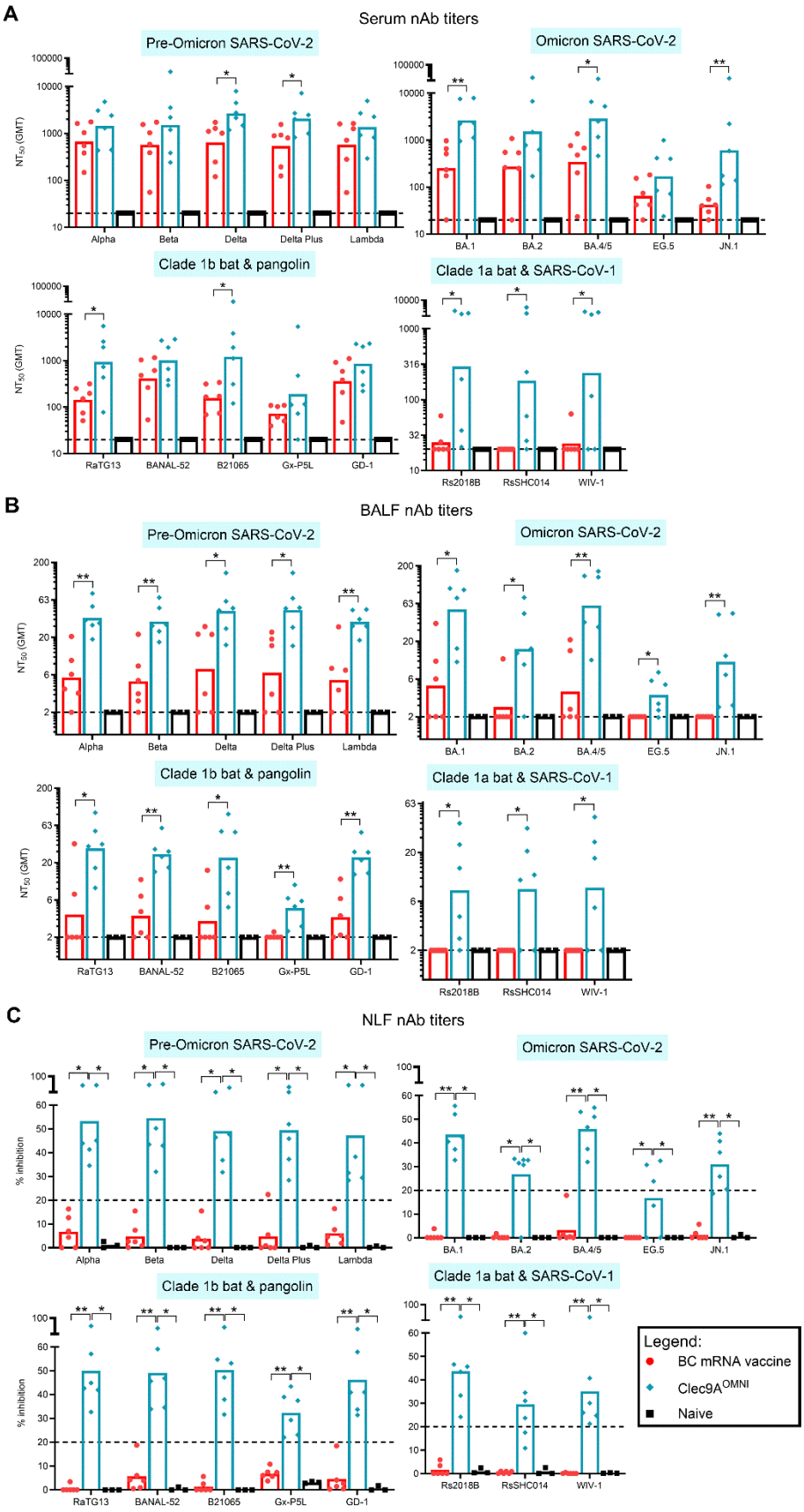
A
Serum nAb titers
Pre-Omicron SARS-CoV-2
Omicron SARS-CoV-2
Clade 1b bat & pangolin
Clade 1a bat & SARS-CoV-1
NT50 (GMT)
Alpha
Beta
Delta
Delta Plus
Lambda
BA.1
BA.2
BA.4/5
EG.5
JN.1
RaTG13
BANAL-52
B21065
Gx-P5L
GD-1
Rs2018B
RsSHC014
WIV-1
B
BALF nAb titers
C
NLF nAb titers
% inhibition
Legend:
BC mRNA vaccine
Clec9A^OMNI
Naive

Figure S5. Neutralizing antibody responses upon nasal booster with Clec9A^{OMNI} versus systemic booster with BC mRNA vaccine. Five to six-week-old BALB/c mice were immunized twice three weeks apart with original Comirnaty mRNA vaccine (0.05 µg per dose; i.m). Three months after the second immunization dose, mice were boosted with either BC mRNA vaccine (0.05 µg; i.m), or Clec9A^{OMNI} (4 µg Clec9A^{XBB} + 1 µg Clec9A^{CoV1} adjuvanted with 50 µg poly I:C; i.n). **(A)** Serum, **(B)** BALF and **(C)** NLF nAb titers against 18 sarbecoviruses from clades 1a and 1b at one month post-boost were determined by multiplex sVNT. **(A-C)** Data are from one representative experiment performed twice with similar results, n = 5-6 per group/experiment. Symbols represent individual animals and data shown are **(A, B)** geometric means and **(C)** means. Statistical analysis: Non-parametric two-tailed **(A, B)** Mann-Whitney test and **(C)** Kruskal Walis test with Dunn's multiple-comparison test. *$p < 0.05$, **$p < 0.01$.

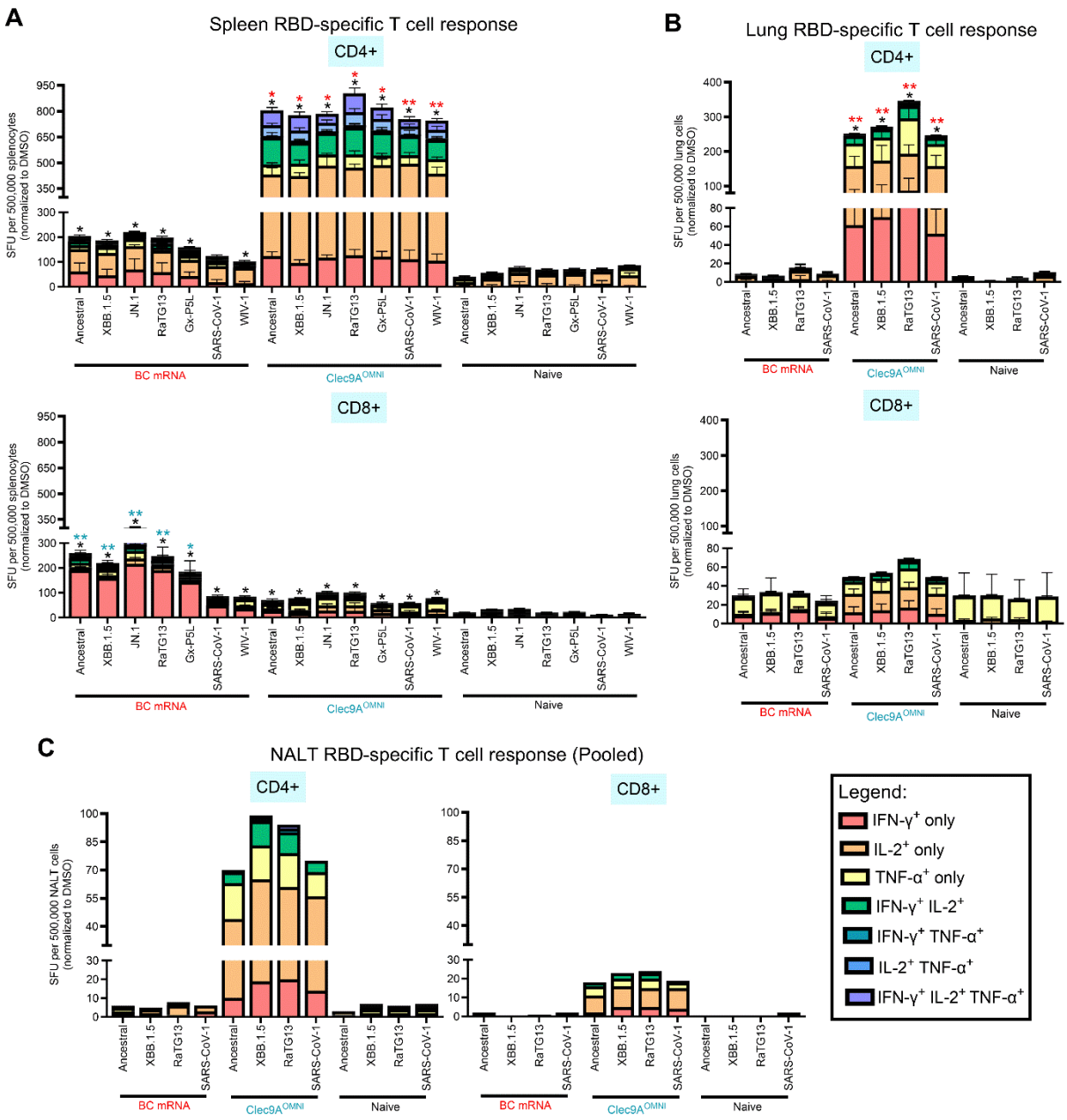

Figure S6. CD4$^+$ and CD8$^+$ T cell responses upon nasal booster with Clec9A^{OMNI} versus systemic booster with BC mRNA vaccine. Five to six-week-old BALB/c mice were immunized twice three weeks apart with original Comirnaty mRNA vaccine (0.05 μg per dose; i.m). Three months after the second immunization dose, mice were boosted with either BC mRNA vaccine (0.05 μg; i.m), or Clec9A^{OMNI} (4 μg Clec9A^{XBB} + 1 μg Clec9A^{CoV1} adjuvanted with 50 μg poly I:C; i.n). **(A-C)** At two weeks post-boost, mice were euthanized and the frequencies of IFN-γ, IL-2 and/or TNF-α secreting CD4$^+$ and CD8$^+$ subsets from

(A) spleen, **(B)** lungs, and **(C)** NALT were determined by FluoroSPOT upon restimulation with ancestral SARS-CoV-2, XBB.1.5, JN.1, RaTG13, Gx-P5L, SARS-CoV-1 and WIV-1 RBD peptides. **(A-C)** Data are from one representative experiment performed twice with similar results, n = 5 per group/experiment. Data shown are means ± **(A, B)** SD. Statistical analysis: **(A, B)** Non-parametric two-tailed Kruskal Walis test with Dunn's multiple-comparison test. *p < 0.05, **p < 0.01. Asterisk colors represent statistical significance between corresponding groups.

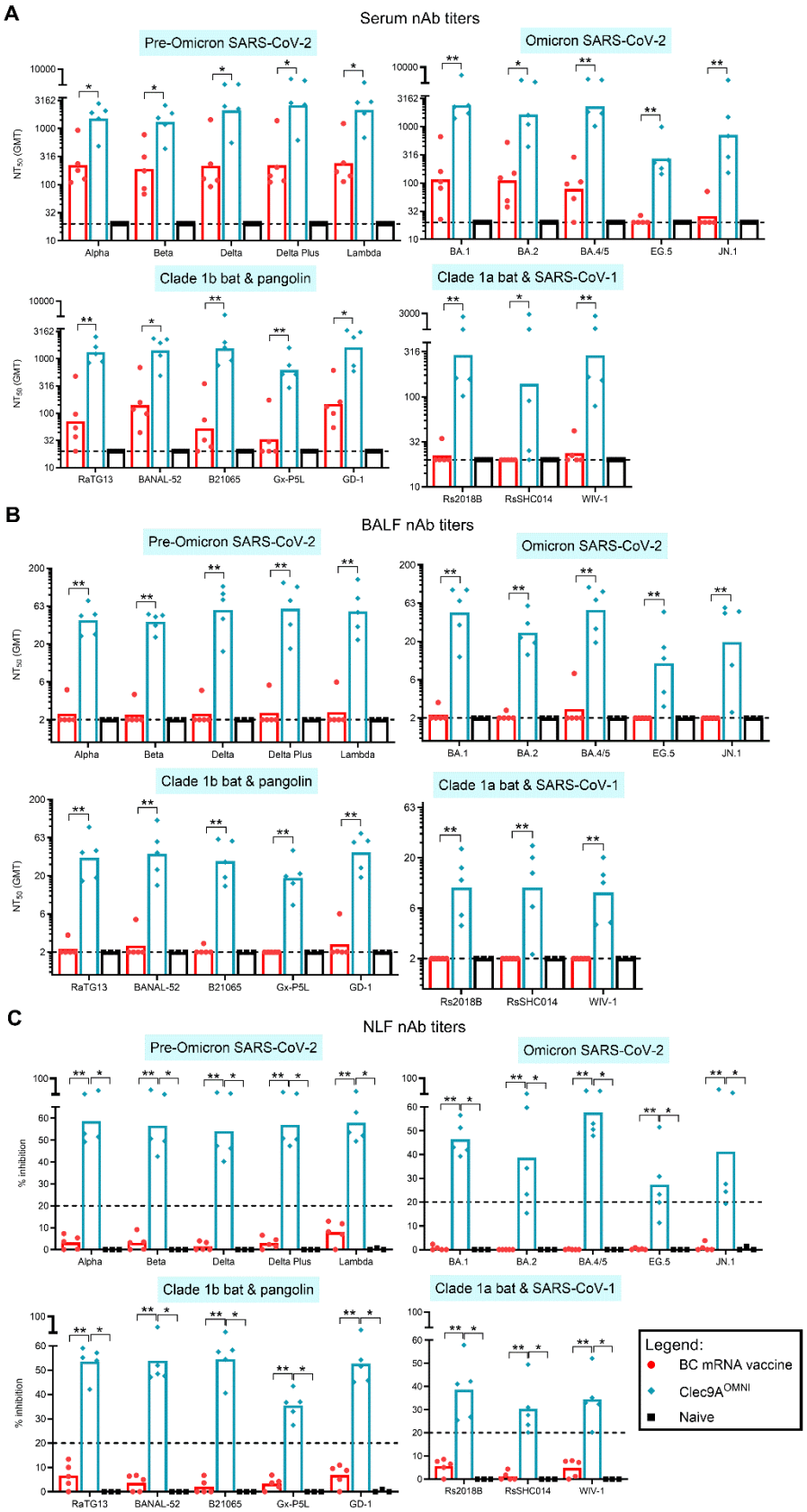
A
Serum nAb titers
Pre-Omicron SARS-CoV-2
Omicron SARS-CoV-2
Clade 1b bat & pangolin
Clade 1a bat & SARS-CoV-1
NT50 (GMT)
Alpha
Beta
Delta
Delta Plus
Lambda
BA.1
BA.2
BA.4/5
EG.5
JN.1
RaTG13
BANAL-52
B21065
Gx-P5L
GD-1
Rs2018B
RsSHC014
WIV-1
B
BALF nAb titers
C
NLF nAb titers
% inhibition
Legend:
BC mRNA vaccine
Clec9A^OMNI
Naive

Figure S7. Long-term neutralizing antibody responses upon nasal booster with Clec9A^{OMNI} versus systemic booster with BC mRNA vaccine. Five to six-week-old BALB/c mice were immunized twice three weeks apart with original Comirnaty mRNA vaccine (0.05 µg per dose; i.m). Three months after the second immunization dose, mice were boosted with either BC mRNA vaccine (0.05 µg; i.m), or Clec9A^{OMNI} (4 µg Clec9A^{XBB} + 1 µg Clec9A^{CoV1} adjuvanted with 50 µg poly I:C; i.n). **(A)** Serum, **(B)** BALF and **(C)** NLF nAb titers against 18 sarbecoviruses from clades 1a and 1b at six months post-boost were determined by multiplex sVNT. **(A-C)** Data are from one representative experiment performed twice with similar results, n = 5-6 per group/experiment. Symbols represent individual animals and data shown are **(A, B)** geometric means and **(C)** means. Statistical analysis: Non-parametric two-tailed **(A, B)** Mann-Whitney test and **(C)** Kruskal Walis test with Dunn's multiple-comparison test. *$p < 0.05$, **$p < 0.01$.

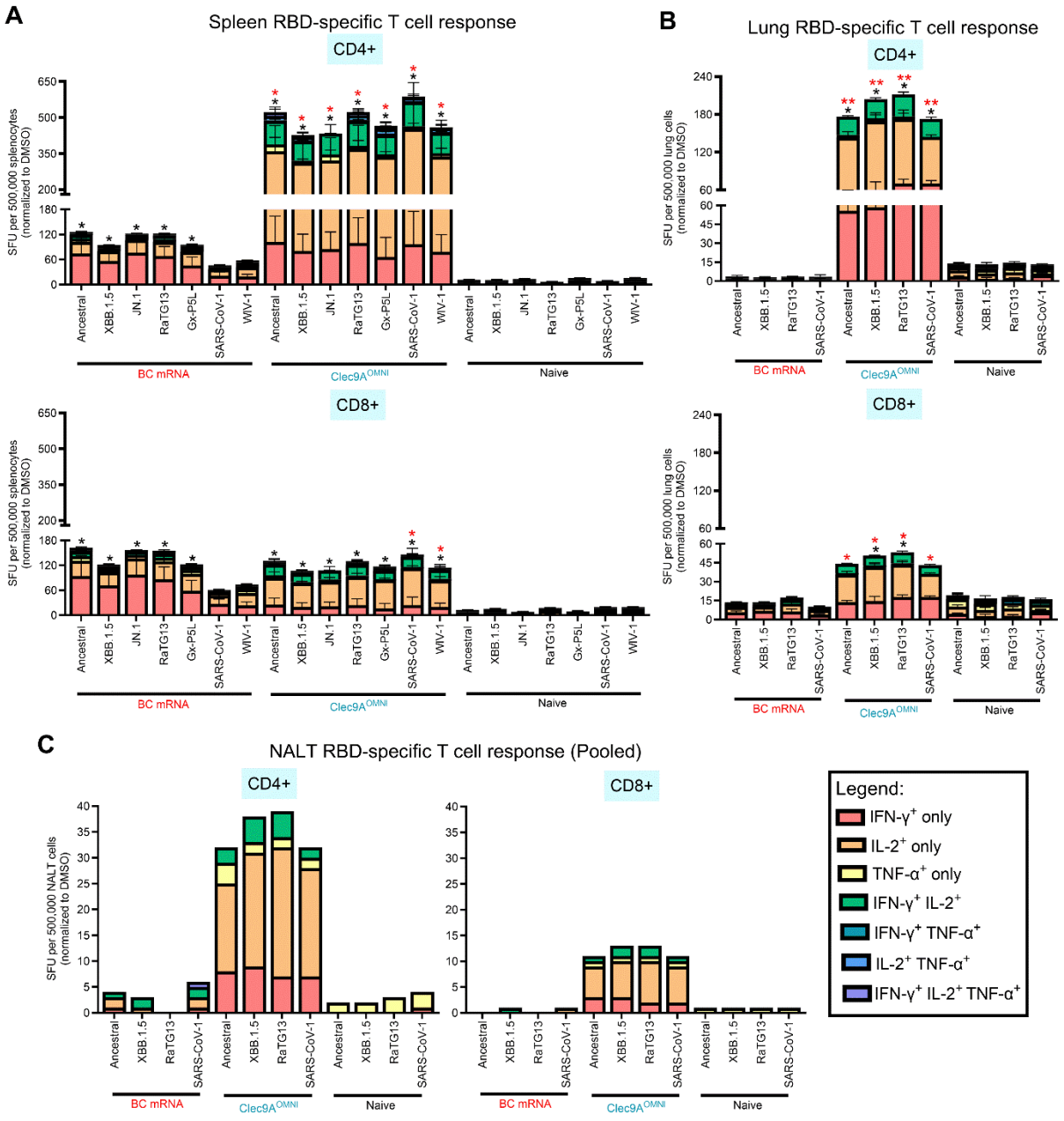

Figure S8. Long-term CD4$^+$ and CD8$^+$ T cell responses upon nasal booster with Clec9A^{OMNI} versus systemic booster with BC mRNA vaccine. Five to six-week-old BALB/c mice were immunized twice three weeks apart with original Comirnaty mRNA vaccine (0.05 μg per dose; i.m). Three months after the second immunization dose, mice were boosted with either BC mRNA vaccine (0.05 μg; i.m), or Clec9A^{OMNI} (4 μg Clec9A^{XBB} + 1 μg Clec9A^{CoV1} adjuvanted with 50 μg poly I:C; i.n). **(A-C)** Frequencies of IFN-γ, IL-2 and/or TNF-α secreting CD4$^+$ and CD8$^+$ subsets in **(A)** spleen, **(B)** lungs, and **(C)** NALT were determined

at four months post-boost by FluoroSPOT upon restimulation with ancestral SARS-CoV-2, XBB.1.5, JN.1, RaTG13, Gx-P5L, SARS-CoV-1 and WIV-1 RBD peptides. **(A-C)** Data are from one representative experiment performed twice with similar results, n = 5 per group/experiment. Data shown are means ± **(A, B)** SD. Statistical analysis: **(A, B)** Non-parametric two-tailed Kruskal Walis test with Dunn's multiple-comparison test. *p < 0.05, **p < 0.01. Asterisk colors represent statistical significance between corresponding groups.

A

```
XBB.1.5 RBD      1    KSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFHEVFNATTFASVYAWNRKRISNCVA  60
                      KSF ++KGIYQTSNFRV P+  +VRFPNITNLCPF EVFNAT F SVYAW RK+ISNCVA
SARS-CoV-1 RBD   1    KSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAWERKKISNCVA  60

XBB.1.5 RBD      61   DYSVIYNFAPFFAFKCYGVSPTKLNDLCFTNVYADSFVIRGNEVSQIAPGQTGNIADYNY  120
                      DYSV+YN   F  FKCYGVS TKLNDLCF+NVYADSFV++G++V QIAPGQTG IADYNY
SARS-CoV-1 RBD   61   DYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNY  120

XBB.1.5 RBD      121  KLPDDFTGCVIAWNSNKLDSKPSGNYNYLYRLFRKSKLKPFERDISTEIYQAGNKPCNGV  180
                      KLPDDF GCV+AWN+  +D+  +GNYNY YR  R  KL+PFERDIS   +    KPC
SARS-CoV-1 RBD   121  KLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCTPP  180

XBB.1.5 RBD      181  AGPNCYSPLQSYGFRPTYGVGHQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  240
                      A  NCY PL  YGF  T G+G+QPYRVVVLSFELL+APATVCGPK ST+L+KN+CVNFNF
SARS-CoV-1 RBD   181  A-LNCYWPLNDYGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNF  239

XBB.1.5 RBD      241  NGLTGTG  247
                      NGLTGTG
SARS-CoV-1 RBD   240  NGLTGTG  246
```

B

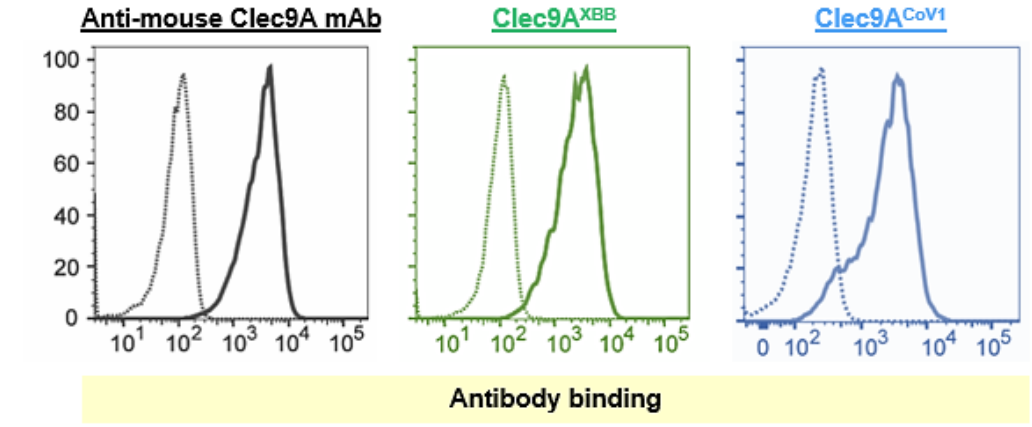

Figure S9. Antigenic sequence and validation of Clec9A-RBD constructs. (A) BLAST amino acid sequence alignment for RBD antigens (XBB.1.5 and SARS-CoV-1) used for expression of Clec9A-RBD constructs (Clec9A^{XBB} and Clec9A^{CoV1}). **(B)** Binding of Clec9A-RBD constructs to mouse Clec9A was verified by flow cytometry. CHO-K1 (dotted lines) or CHO-Clec9A cells (solid lines) were incubated with control anti-mouse Clec9A mAb (black, left panel), purified Clec9A^{XBB} construct (green, middle panel) or

Clec9A^{CoV1} construct (blue, right panel). Binding was detected with PE-conjugated anti-rat Ig and dead cells were excluded by forward/side scatter and live/dead staining.

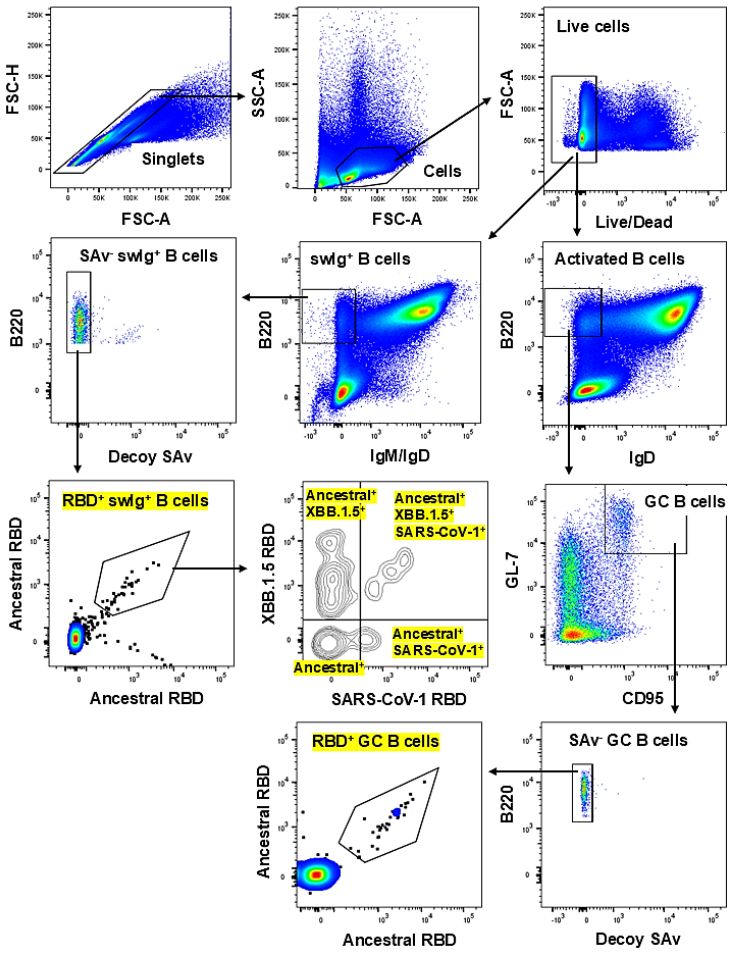

Figure S10. Gating strategy to identify antigen-specific swIg$^+$ and GC B cell subsets. Single cells were first identified via FSC-H/FSC-A and SSC-A/FSC-A. Dead cells were excluded with eFluor780 Fixable Viability Dye, and swIg$^+$ (B220$^+$ IgD$^-$ IgM$^-$) and activated (B220$^+$ IgD$^-$) B cells were identified from live cell population (Live/Dead$^-$). For the former, swIg$^+$ B cells that bind non-specifically to SAv were excluded using decoy SAv probe, and RBD-specific swIg$^+$ B cells were identified from the SAv$^-$ swIg$^+$ B cell population via a double discrimination gate where cells must be double positive for both ancestral RBD-BV421 and -PE to be considered as antigen-specific. Cross-reactivity to XBB.1.5 and SARS-CoV-1 RBD were further determined from the gated total RBD$^+$ swIg$^+$ B cell population. For the latter, GC B cells (GL-7$^+$ CD95$^+$) were identified from the activated B cell population, and those binding non-specifically to SAv were excluded using decoy SAv probe. RBD-specific GC B cells were subsequently identified from the SAV$^-$ GC B cell population via double discrimination gating.

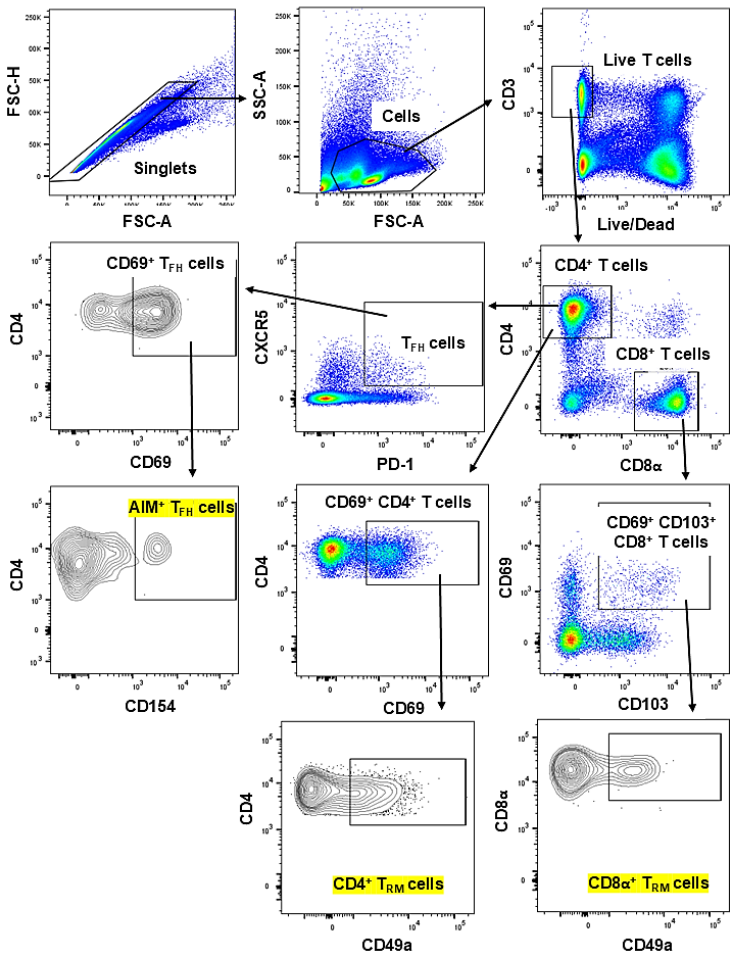

Figure S11. Gating strategy to identify AIM$^+$ T$_{FH}$ and T$_{RM}$ cells. Single cells were first identified via FSC-H/FSC-A and SSC-A/FSC-A. Dead cells were excluded with eFluor780 Fixable Viability Dye, and CD4$^+$ and CD8$^+$ T cells were identified from the total live T cell (Live/Dead$^-$ CD3$^+$) population. AIM$^+$ T$_{FH}$ cells were examined by first identifying total T$_{FH}$ cells (CXCR5$^+$ PD-1$^+$) from the CD4$^+$ T cell population, followed by gating on those that are double positive for both CD69 and CD154 AIM. T$_{RM}$ cells in lung and NALT tissues were identified from total CD4$^+$ and CD8$^+$ T cells by gating into CD69$^+$ and CD69$^+$ CD103$^+$ populations respectively, followed by further gating into cells that were also CD49a$^+$ (CD4$^+$: CD69$^+$ CD49a$^+$, CD8$^+$: CD69$^+$ CD103$^+$ CD49a$^+$).

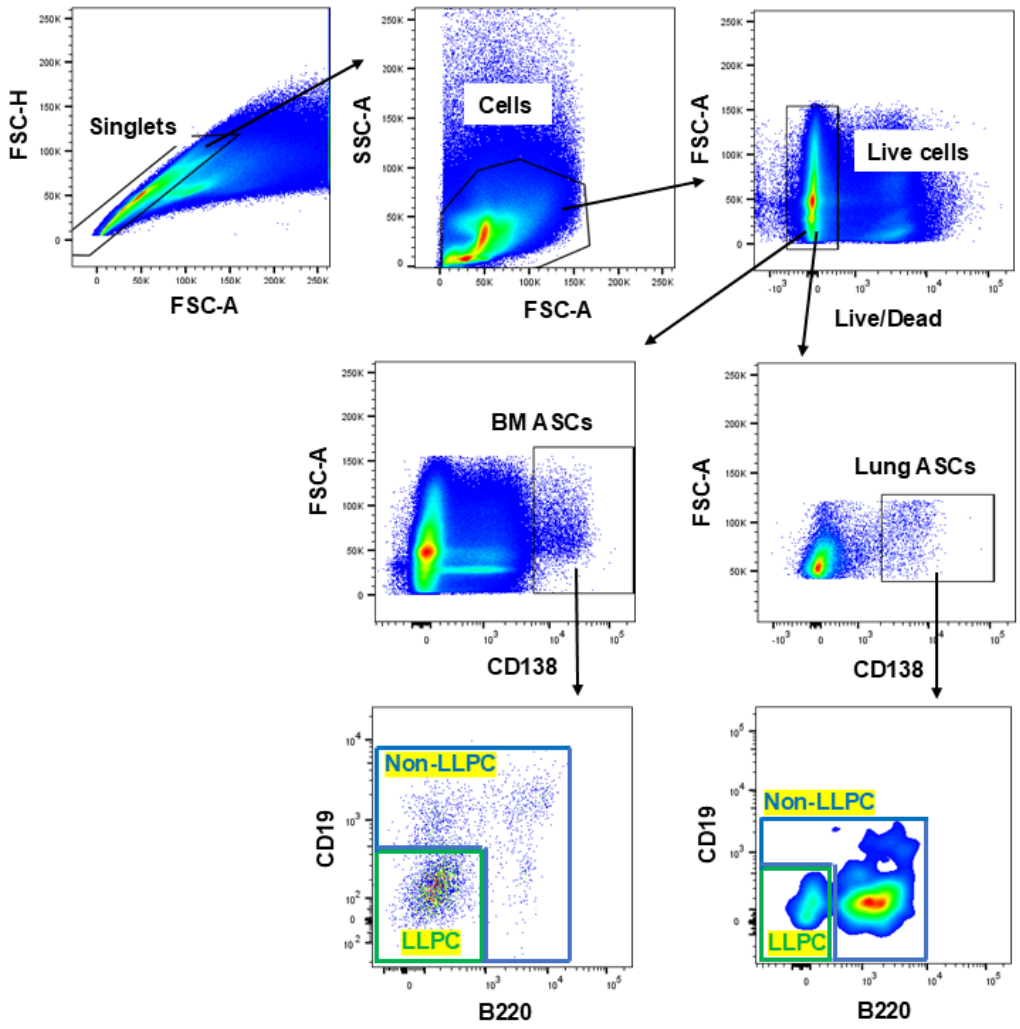

Figure S12. Gating strategy for sorting BM and lung LLPC and non-LLPC ASC subsets. Single cells were first identified via FSC-H/FSC-A and SSC-A/FSC-A. Dead cells were excluded with eFluor780 Fixable Viability Dye, and BM and lung ASC populations were identified as live cells that highly express CD138 (Live/Dead^{-} CD138^{hi}). Boolean gating was subsequently applied to identify LLPC and non-LLPC ASC subsets based on their expression of B220 and CD19; LLPC = CD138^{hi} B220^{lo} CD19^{lo} (green), non-LLPC = inverse of LLPC gating (blue).

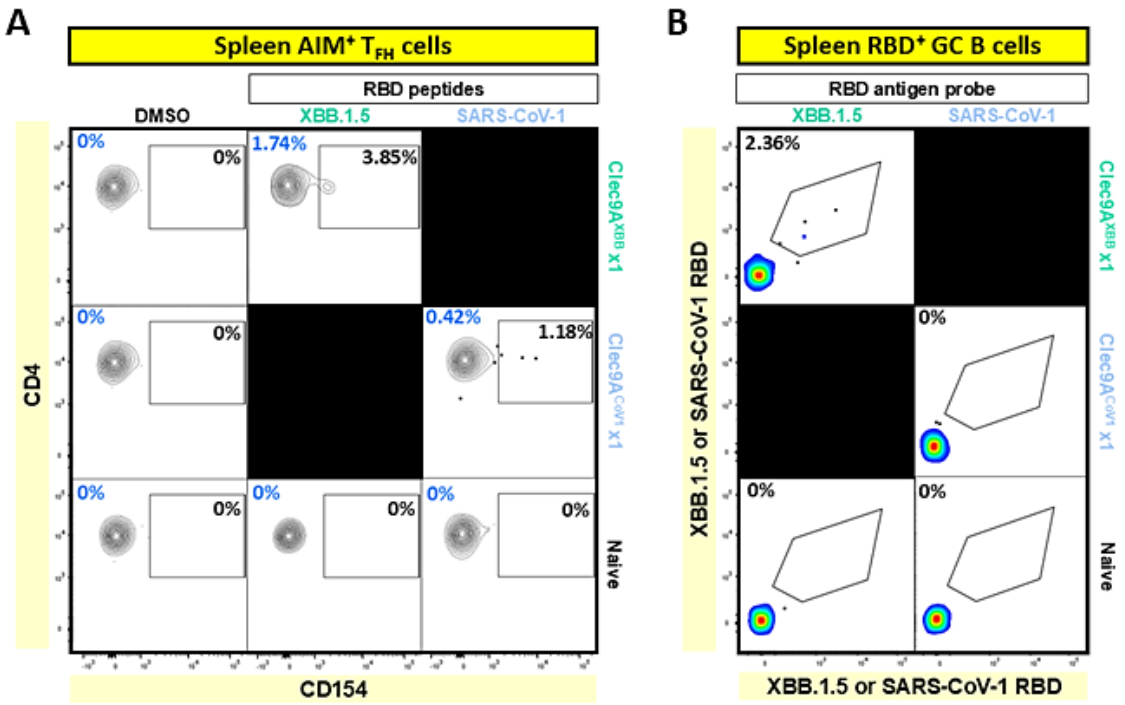

Figure S13. Representative flow cytometric analysis results of AIM$^+$ T$_{FH}$ and RBD$^+$ GC B cells following single dose Clec9A^{XBB} or Clec9A^{CoV1} immunization. **(A)** Representative plots of spleen AIM$^+$ T$_{FH}$ cells at six months post-boost. Values indicated in black and blue represent percentage AIM$^+$ T$_{FH}$ cells out of CD69$^+$ T$_{FH}$ cells and total T$_{FH}$ cells respectively. **(B)** Representative plots of RBD-specific spleen GC B cells at six months post-boost.

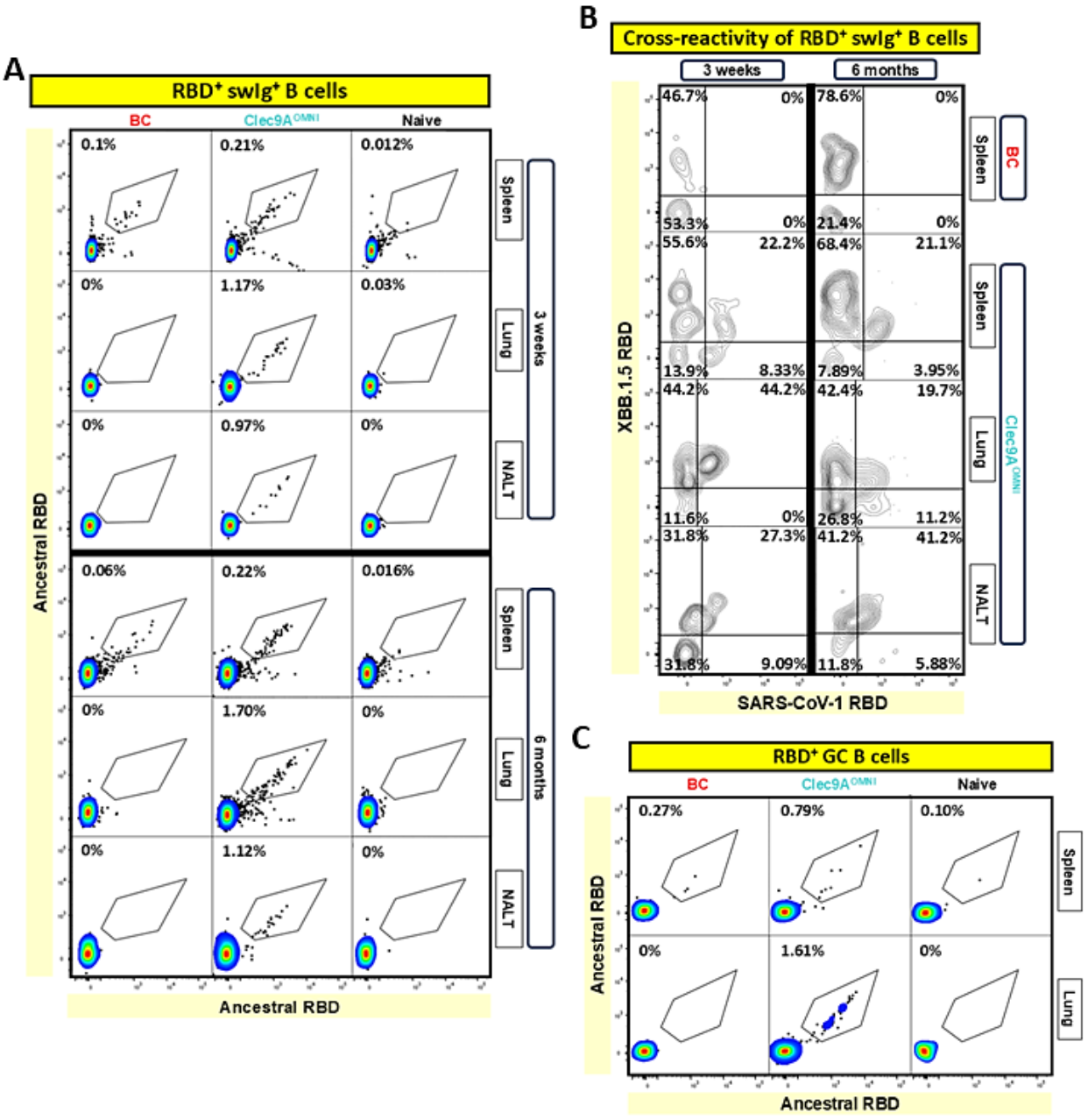

Figure S14. Representative flow cytometric analysis results of antigen-specific B cell subsets following BC mRNA vaccine and Clec9A^{OMNI} booster immunization. **(A, B)** Representative plots of ancestral SARS-CoV-2 RBD-specific spleen, lung and NALT **(A)** swIg^{+} B cells and their **(B)** cross-reactivity to XBB.1.5 and SARS-CoV-1 RBD, at three weeks and six months post-boost. **(C)** Representative plots of RBD-specific spleen and lung GC B cells at six months post-boost.

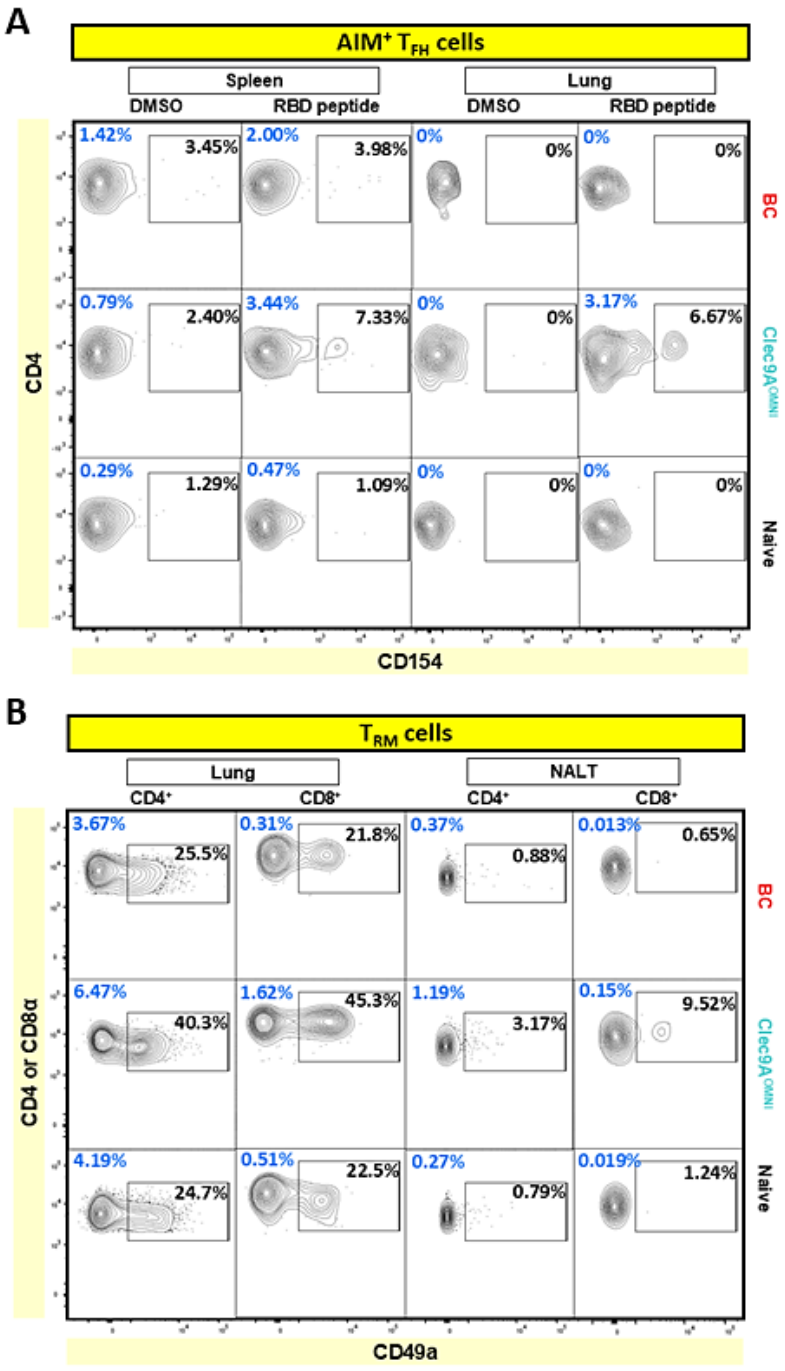

Figure S15. Representative flow cytometric analysis results of AIM$^+$ T_{FH} and T_{RM} cells following BC mRNA vaccine and Clec9A^{OMNI} booster immunization. **(A)** Representative plots of spleen and lung AIM$^+$ T_{FH} cells at six months post-boost. Values indicated in black and blue represent percentage AIM$^+$ T_{FH} cells out of CD69$^+$ T_{FH} cells and total T_{FH} cells respectively. **(B)** Representative plots of lung and NALT

$CD4^+$ and $CD8^+$ T_{RM} cells at one-month post-boost. Values indicated in black and blue represent percentage T_{RM} cells out of $CD69^+$ $CD4^+$ or $CD69^+$ $CD103^+$ $CD8^+$ T cells, and total $CD4^+$ or $CD8^+$ T cells respectively.

Table S1. Sarbecovirus RBD antigens used in the Multiplex sVNT.

Clade	Sarbecovirus	Variant/Strain	Source
1B	Pre-Omicron SARS-CoV-2	Ancestral	Custom made by Genscript
		Alpha	
		Beta	
		Delta	ACROBiosystems, SPD-C82Ed
		Delta Plus	Produced in-house in HEK293T cells as described previously (2)
		Lambda	
		Mu	
	Omicron SARS-CoV-2	BA.1	ACROBiosystems, SPD-C522K
		BA.2	ACROBiosystems, SPD-C82Eq
		BA.4/5	ACROBiosystems, SPD-C82Ew
		XBB.1.5	Produced in-house in HEK293T cells as described previously (2)
		EG.5	
		JN.1	
	Bat	RaTG13	Custom made by Genscript
		BANAL-52	Produced in-house in HEK293T cells as described previously (2)
		B21065	
	Pangolin	Gx-P5L	Custom made by Genscript
		GD-1	Produced in-house in HEK293T cells as described previously (2)
1A	Bat	Rs2018B	Produced in-house in HEK293T cells as described previously (2)
		RsSHC014	
		WIV-1	
	SARS-CoV-1	SARS-CoV-1	Custom made by Genscript

Table S2. Antibodies used for flow cytometry staining of antigen-specific B cell subsets, AIM^+ T_{FH} cells, T_{RM} cells, and sorting of LLPC and non-LLPC ASC subsets.

Marker	Fluorophore	Manufacturer & catalogue #	Dilution/Concentration
RBD^+ $swIg^+$ B cells			
B220	Alexa Fluor 488	BD Biosciences, 557669	1:200
IgM	BUV395	BD Biosciences, 564025	
IgD		BD Biosciences, 564274	
Decoy (SAv)	BV605	BD Biosciences, 563260	1 µg/mL
Ancestral RBD	BV421	[redacted]	
	PE		
XBB.1.5 RBD	BV711		
SARS-CoV-1 RBD	APC		
RBD^+ GC B cells			
B220	BUV395	BD Biosciences, 563793	1:200
IgD	BV711	BD Biosciences, 564275	
GL-7	Alexa Fluor 647	BD Biosciences, 561529	
CD95	BV605	Biolegend, 152612	
Decoy (SAv)	BB515	BD Biosciences, 564453	1 µg/mL
Ancestral RBD	BV421	[redacted]	
	PE		
AIM^+ T_{FH} cells			
CD3	FITC	BD Biosciences, 555274	1:200
CD4	BUV395	BD Biosciences, 563790	
CXCR5	APC	BD Biosciences, 560615	
PD-1	BV605	BD Biosciences, 563059	
CD69	BV421	BD Biosciences, 562920	
CD154	PE	BD Biosciences, 553658	1:100, added in culture
T_{RM} cells			
CD3	FITC	BD Biosciences, 555274	1:200
CD4	BUV395	BD Biosciences, 563790	
CD8α	BV711	BD Biosciences, 563046	
CD69	BV421	BD Biosciences, 562920	
CD103	APC	BD Biosciences, 562772	
CD49a	PE	BD Biosciences, 562115	
LLPC and non-LLPC ASC subset sorting			
CD138	BV605	BD Biosciences, 563147	1:200
B220	Alexa Fluor 488	BD Biosciences, 557669	
CD19	BUV395	BD Biosciences, 563557	