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Technical Advisory Group on COVID-19 Vaccine Composition (TAG-CO-VAC)

COVID-19 vaccine antigen composition, May 2026

World Health Organization

Dr. Bart Haagmans, TAG-CO-VAC Chair
FDA VRBPAC meeting
28 May 2026

TAG-CO-VAC Members

Chair

Dr Bart Haagmans

Associate professor at the Department of Viroscience of Erasmus MC, Rotterdam, the Netherlands

Learn more ›

Vice-Chair

Professor Cheryl Cohen

Professor in epidemiology at the University of the Witwatersrand and Head of the Centre for Respiratory Disease and Meningitis at the National Institute for Communicable Diseases

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Scientific Director for Vaccines at the Norwegian Institute of Public Health, Norway

Prof Narendra Kumar Arora ›
Executive Director of The INCLEN Trust International, India

Prof Laith Abu-Raddad ›
Prof of Infectious Disease Epidemiology at Weill Cornell Medicine–Qatar, Cornell University, USA

Associate Professor Deborah Cromer ›
Lead of the Infection, Epidemiology and Policy Analytics Group at the Kirby Institute, University of New South Wales

Dr Irene Owusu Donkor ›
Fellow in the Epidemiology Department of the Noguchi Memorial Institute for Medical Research (NMIMR)

Professor Kanta Subbarao ›
Director of the WHO Collaborating Centre for Reference and Research on Influenza and Professor, Department of Microbiology and Immunology

Dr Hideki Hasegawa ›
Director of the WHO Collaborating Centre for Reference and Research on Influenza, Japan

Dr Janine Kimpel ›
Group leader and deputy Director at the Institute of Virology at the Medical University of Innsbruck, Austria

Prof Bette Liu ›
Professor at the Population Health Group at the National Centre for Immunisation Research and Surveillance (NCIRS) in Australia

Professor Elizabeth Miller ›
Professor in Infectious Disease Epidemiology at the London School of Hygiene and a visiting professor at the Sackler School of Public Health at Tel Aviv University

Dr Sergio Nishioka ›
Technical Adviser for Capacity Building and Clinical Evaluation of COVID-19 vaccines

Dr Stanley Perlman ›
Professor of Microbiology and Immunology, and of Pediatrics at the University of Iowa

Prof Derek Smith ›
Director of the Center for Pathogen Evolution, and Professor of Infectious Disease Informatics at the University of Cambridge in the United Kingdom

Dr Pragya Yadav ›
Director-in-Charge of the National Institute of One Health, Nagpur, and a Scientist 'F' at the Indian Council of Medical Research-National Institute of Virology (ICMR-NIV), Pune, India

TAG-CO-VAC Secretariat:
tagcovac@who.int

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More information:
https://www.who.int/groups/technical-advisory-group-on-covid-19-vaccine-composition-(tag-co-vac)/about

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Technical Advisory Group on COVID-19 Vaccine Composition

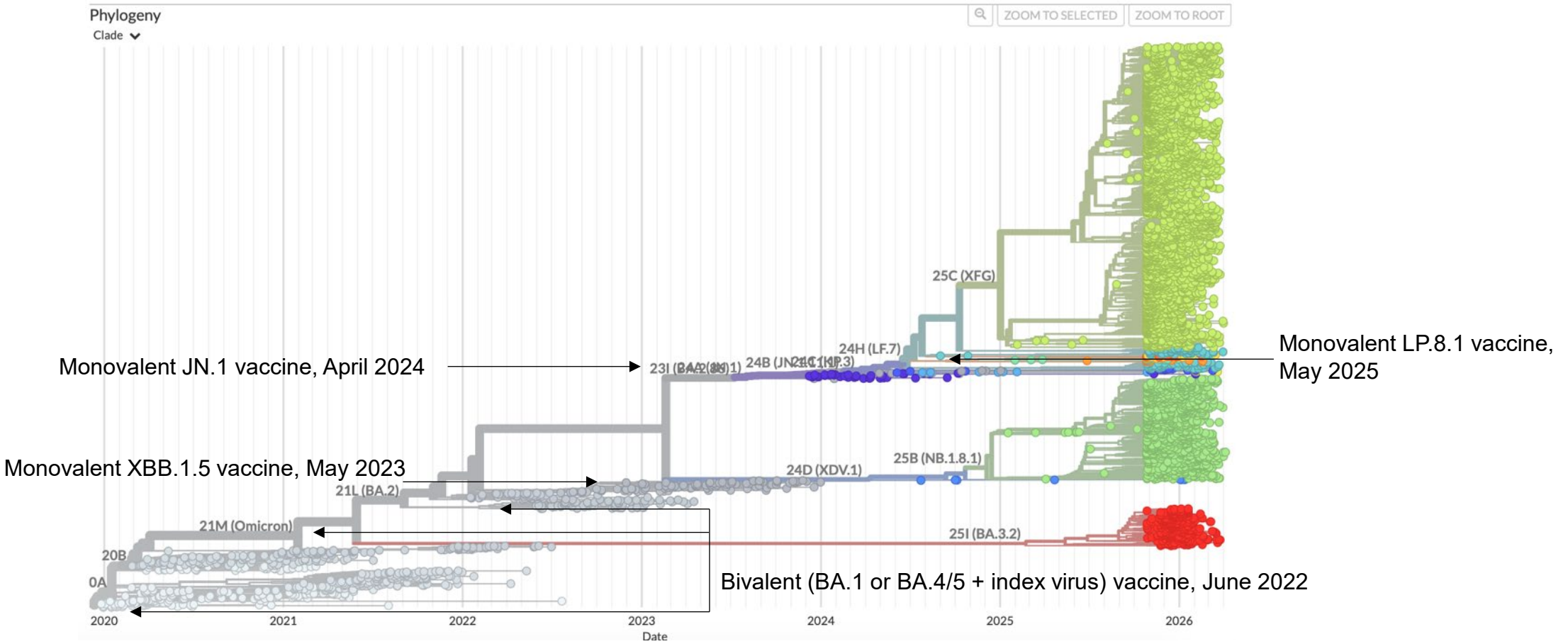
Functions of the TAG-CO-VAC:

- Make recommendations to WHO on the **methods to assess the impact of SARS-CoV-2 variants** on COVID-19 vaccines;
- Provide **interpretation of available evidence on the effect of SARS-CoV-2 variants on COVID-19 vaccines**, including but not limited to vaccine effectiveness;
- **Recommend to WHO, for each COVID-19 vaccine platform, adaptations (if any) needed** so that vaccines continue to safely provide protection against SARS-CoV-2 variants.

Meeting frequency:

- The TAG-CO-VAC continues to convene closed, decision-making meetings approximately every six months. After each meeting, recommendations to either maintain current vaccine composition or to consider updates are issued.
- The most recent decision-making meeting was held on 7-8 May 2026.

SARS-CoV-2 evolution and COVID-19 vaccine antigen composition



Phylogeny of SARS-CoV-2 variants in humans **in the last six months** illustrated using Nextstrain.

The year is shown on the x axis and various clades labeled as Nextclade (Pango lineage) at the branches. Clades that included vaccine antigens are indicated with the date of previous TAG-CO-VAC recommendations for vaccine antigen composition.

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NextStrain https://nextstrain.org/ncov 4 May 2026

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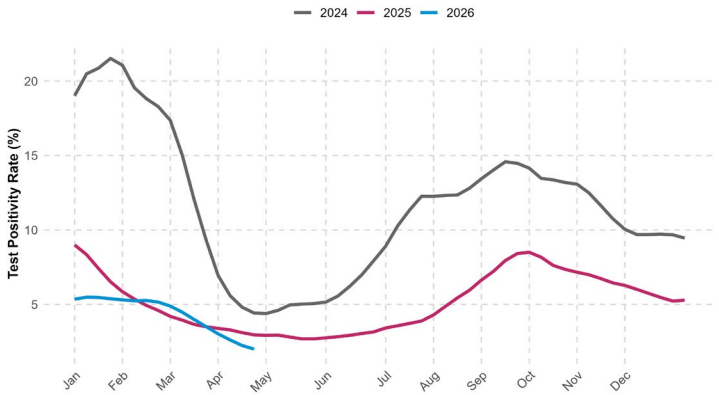
TAG-CO-VAC Evidence review: May 2026

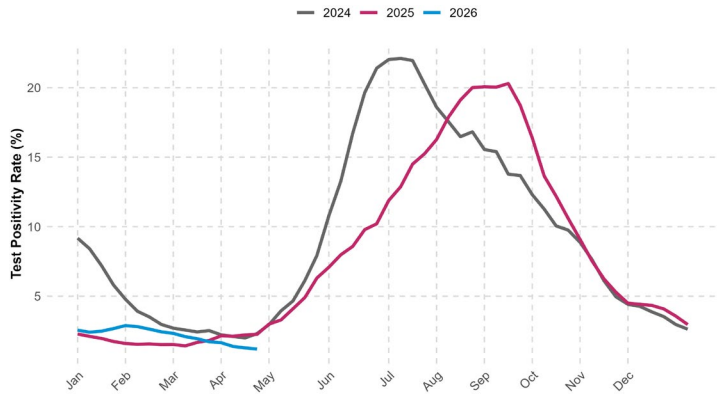
1. SARS-CoV-2 **genetic evolution**, with additional support from the WHO Technical Advisory Group on Virus Evolution (TAG-VE);
2. **Antigenic characterization** of previous and emerging SARS-CoV-2 variants using virus neutralization tests with animal antisera and further analysis of antigenic relationships using antigenic cartography;
3. **Immunogenicity data on the breadth of neutralizing antibody responses** elicited by currently approved vaccine antigens against circulating SARS-CoV-2 variants using animal and human sera, with additional support from WHO Coronavirus Network (CoViNet);
4. Preliminary clinical immunogenicity data on **immune responses following infection** with circulating SARS-CoV-2 variants;
5. Available COVID-19 **vaccine effectiveness (VE) estimates** of currently approved vaccines; and
6. Preliminary non-clinical and clinical immunogenicity data on the **performance of approved or candidate vaccines with updated antigens** shared by vaccine manufacturers with TAG-CO-VAC (data not shown).

Regional SARS-CoV-2 test positivity, 2024-2026

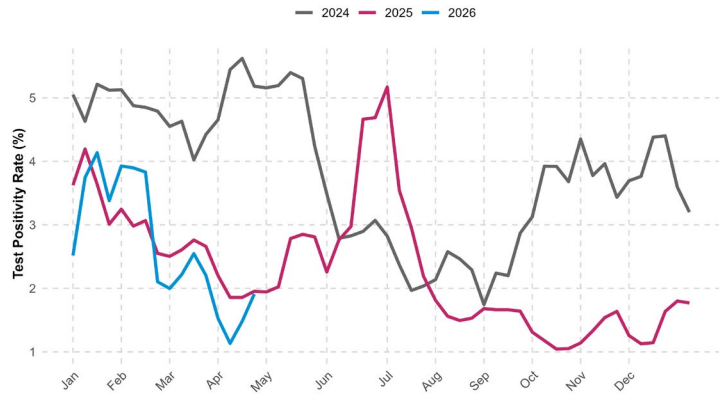
Americas



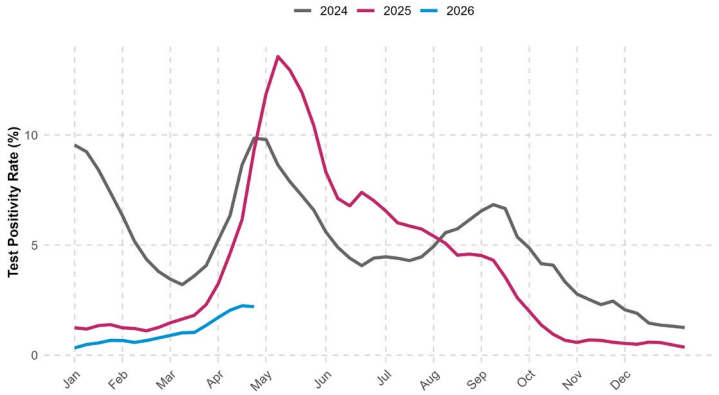
Europe



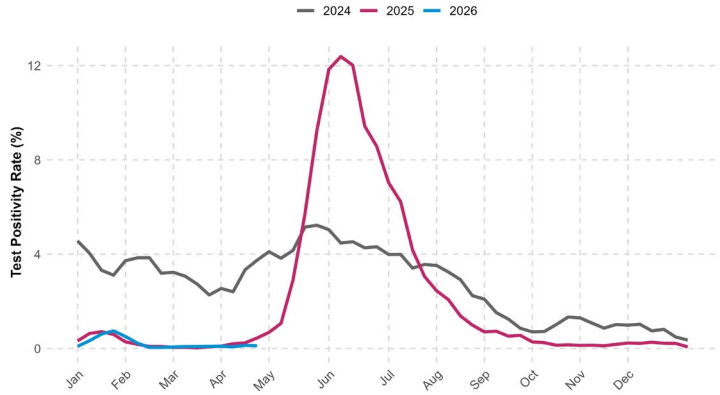
Africa



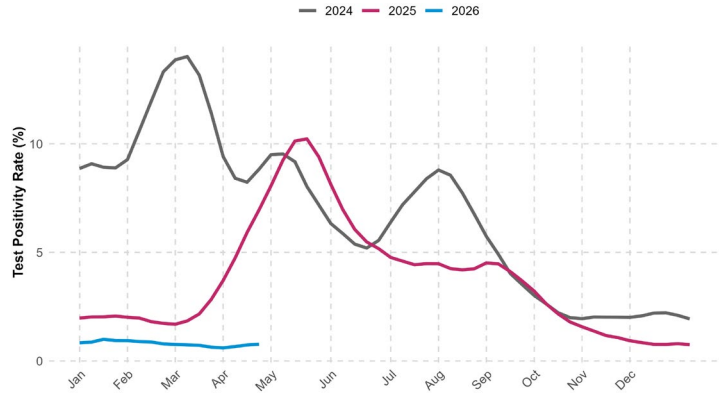
Eastern Mediterranean



South-East Asia



Western Pacific



World Health Organization

Source: World Health Organization

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SARS-CoV-2 variant circulation

Monthly proportions of SARS-CoV-2 sequences from 30 June 2025 – 12 April 2026.

Figure produced by WHO based on SARS-CoV-2 sequence and metadata from GISAID as of 3 May 2026. SARS-CoV-2 variants shown are VUMs, with the exception of JN.1 which is a VOI and includes all sublineages that are not part of one of the other labelled VUMs.

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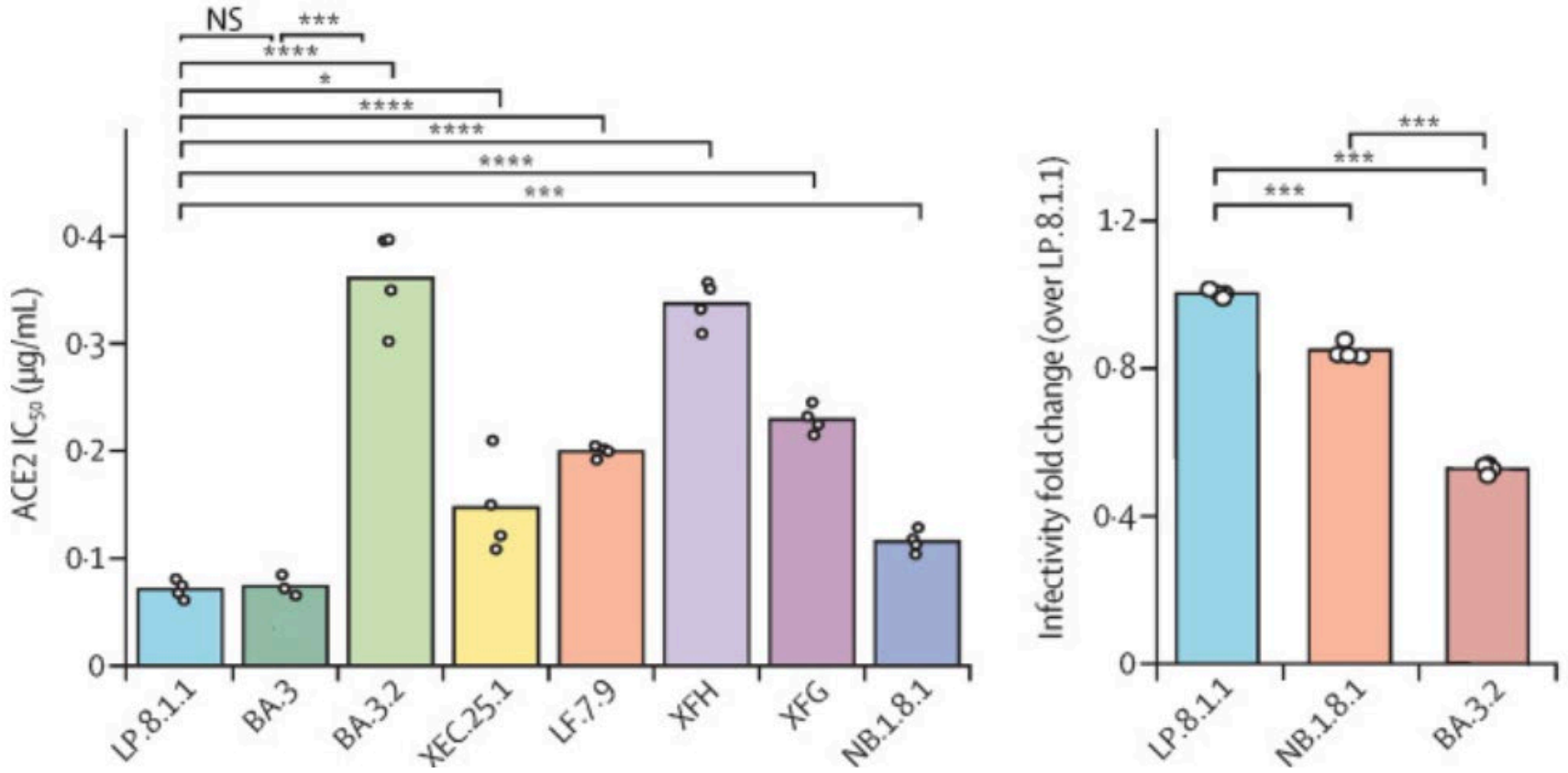
BA.3.2



Left: IC50 values for the neutralisation of LP.8.1.1, BA.3, BA.3.2, XEC.25.1, LF.7.9, XFH, XFG, and NB.1.8.1 pseudoviruses by soluble human ACE2. IC50 (µg/mL) was log-transformed before two-tailed t test analysis. Right: Relative infectivity of NB.1.8.1 and BA.3.2 compared with LP.8.1.1 in Vero cells.3 Infectivity was assessed by use of vesicular stomatitis virus pseudoviruses.

World Health Organization

Guo C, et al. Lancet Infect Dis. 2025;25(7):e374-e377.

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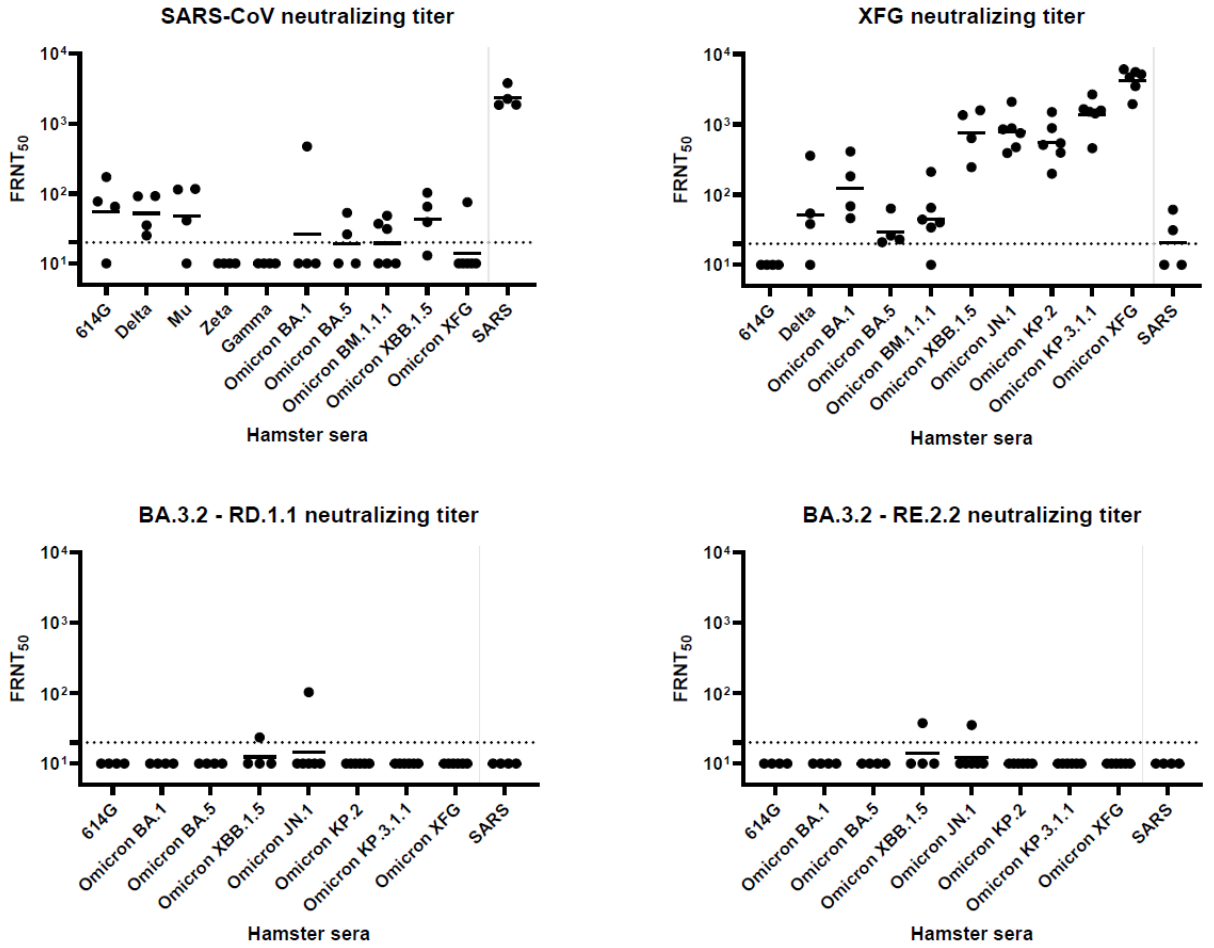
Non-clinical data (hamsters)

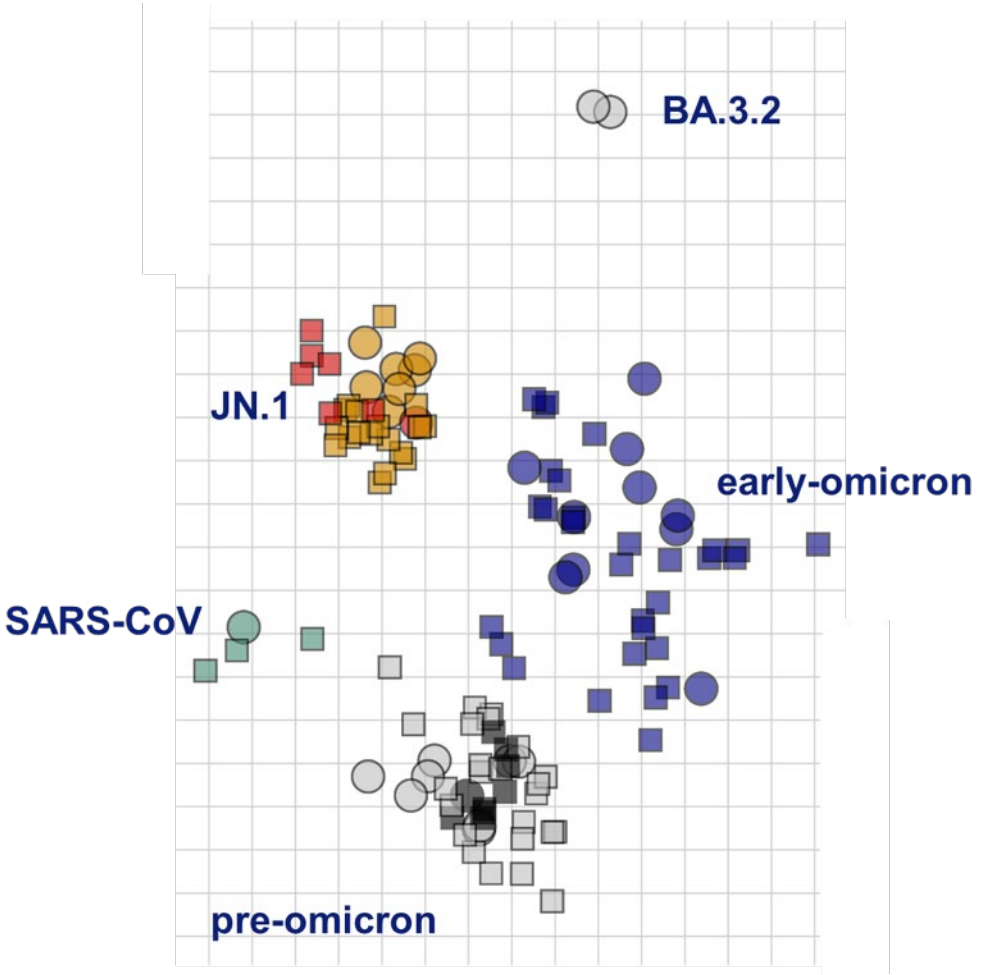


Neutralizing antibody titers (FRNT50) of sera from naïve hamsters infected with either SARS-CoV-1 (top left), XFG (top right) or BA.3.2 (bottom) against 614G, Delta, Mu, Zeta, Gamma, BA.1, BA.5, BM.1.1, XBB.1.5, XFG and SARS-CoV-1.

Horizontal lines represent GMT.

Antigenic characterization of SARS-CoV-2 variants (1)

Non-clinical data (hamsters)



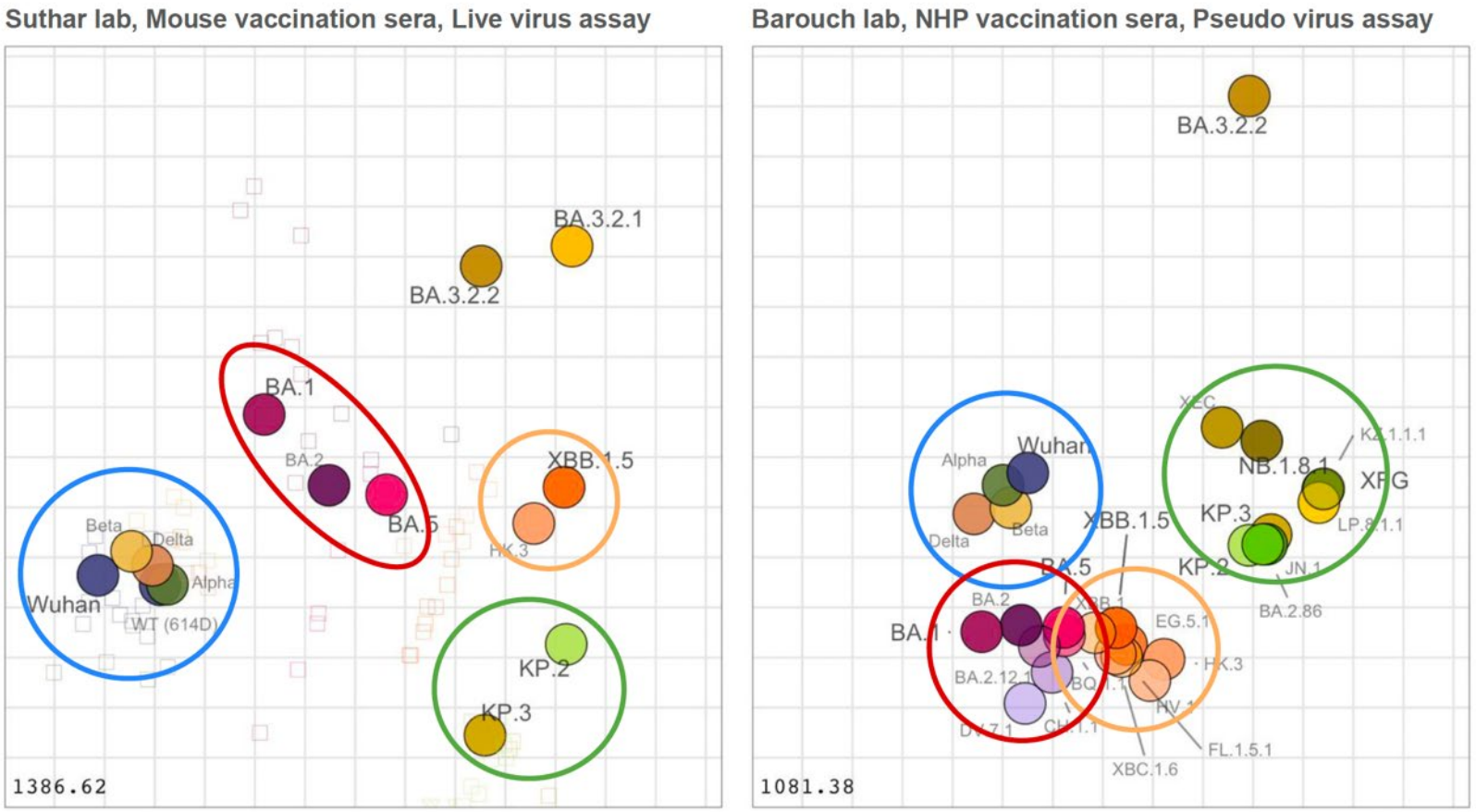
Antigenic cartography of hamster sera following primary infection.

Each square indicates a plasma sample, and each circle indicates a SARS-CoV-2 variant.

Unpublished data shared with permission by Bart Haagmans, Erasmus MC

Antigenic characterization of SARS-CoV-2 variants (2)

Non-clinical data (mice, non-human primates)



Antigenic cartography of mice (left) or non-human primate (right) sera following following primary infection or vaccination.

Each square indicates a plasma sample, and each circle indicates a SARS-CoV-2 variant. Larger circles represent antigenically similar variants.

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Unpublished data shared with permission by Derek Smith, University of Cambridge

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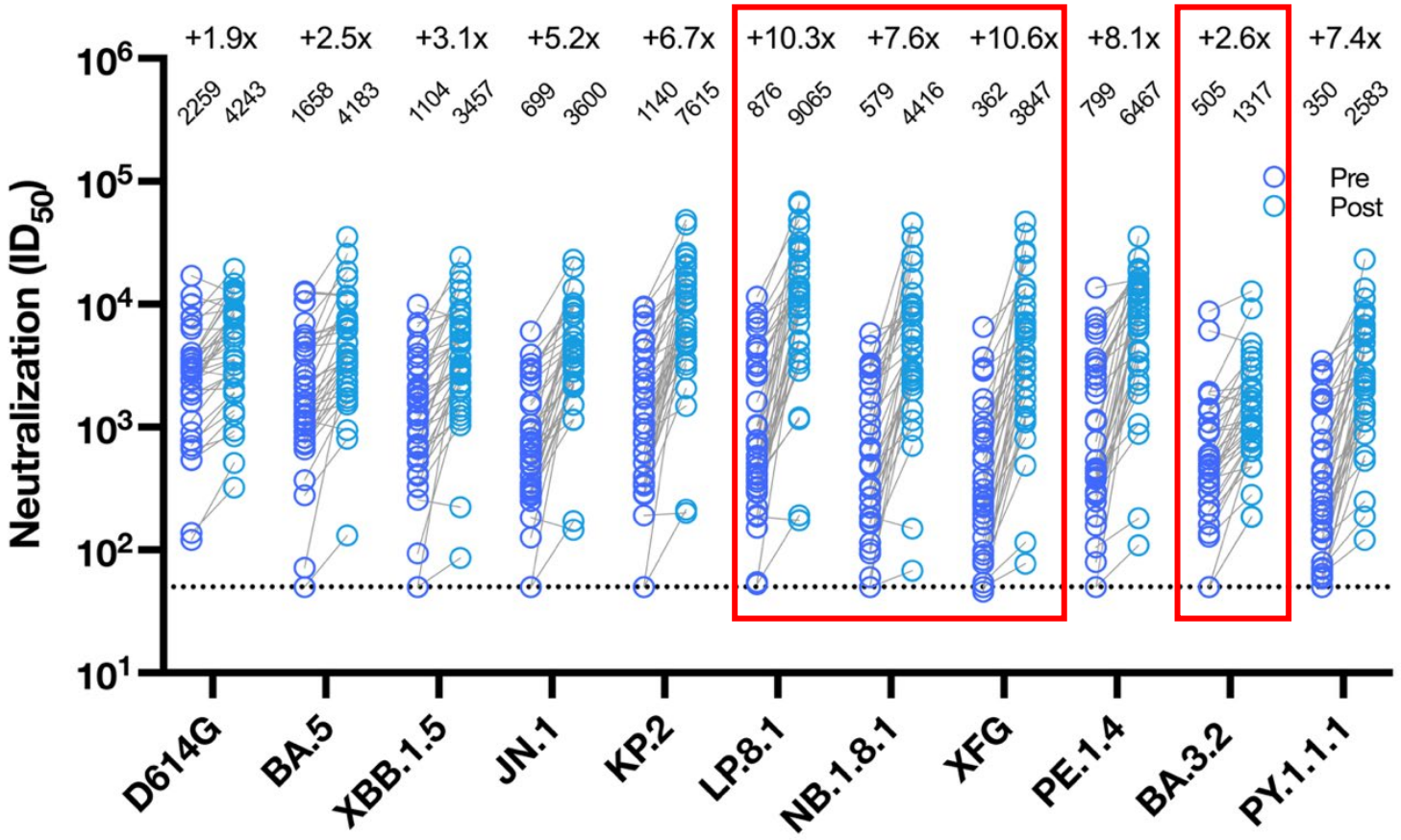
Breadth of neutralizing antibody responses (1)

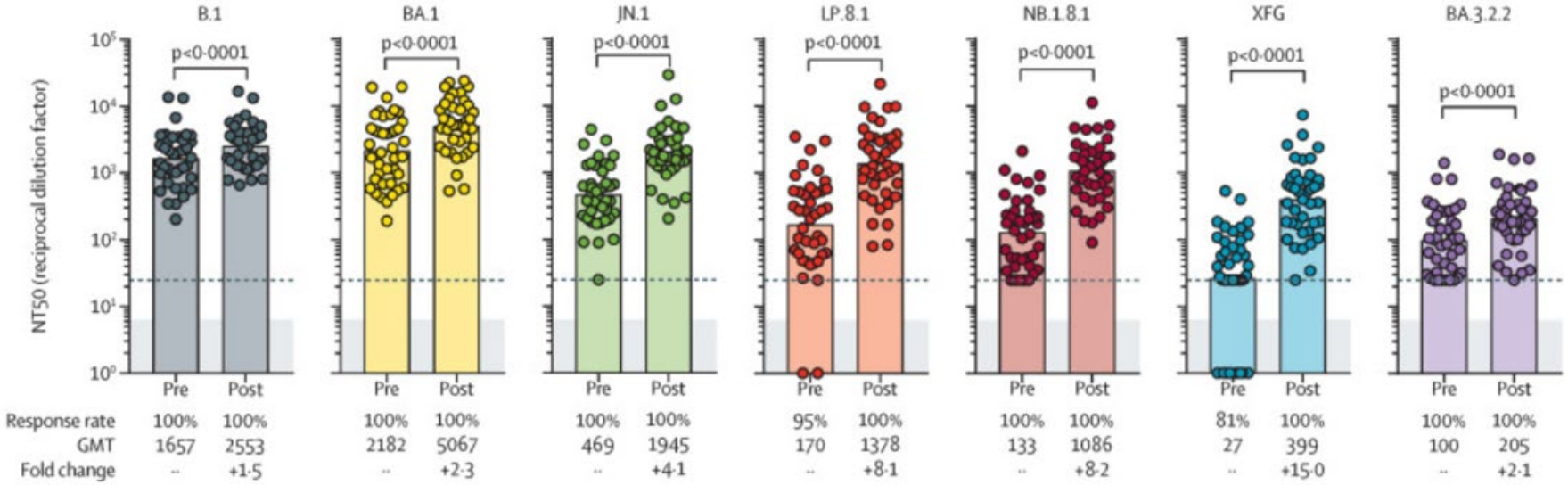


Neutralizing antibody titers against D614G, BA.5, XBB.1.5, JN.1, KP.2, LP.8.1, NB.1.8.1, XFG, PE.1.4, BA.3.2 and PY.1.1.1 of sera pre- and post-LP.8.1 vaccination.

Information on GMT and fold change is indicated above the graph.

Mellis IA, et al. bioRxiv 2026 doi:10.64898/2026.01.03.697434

Breadth of neutralizing antibody responses (2)

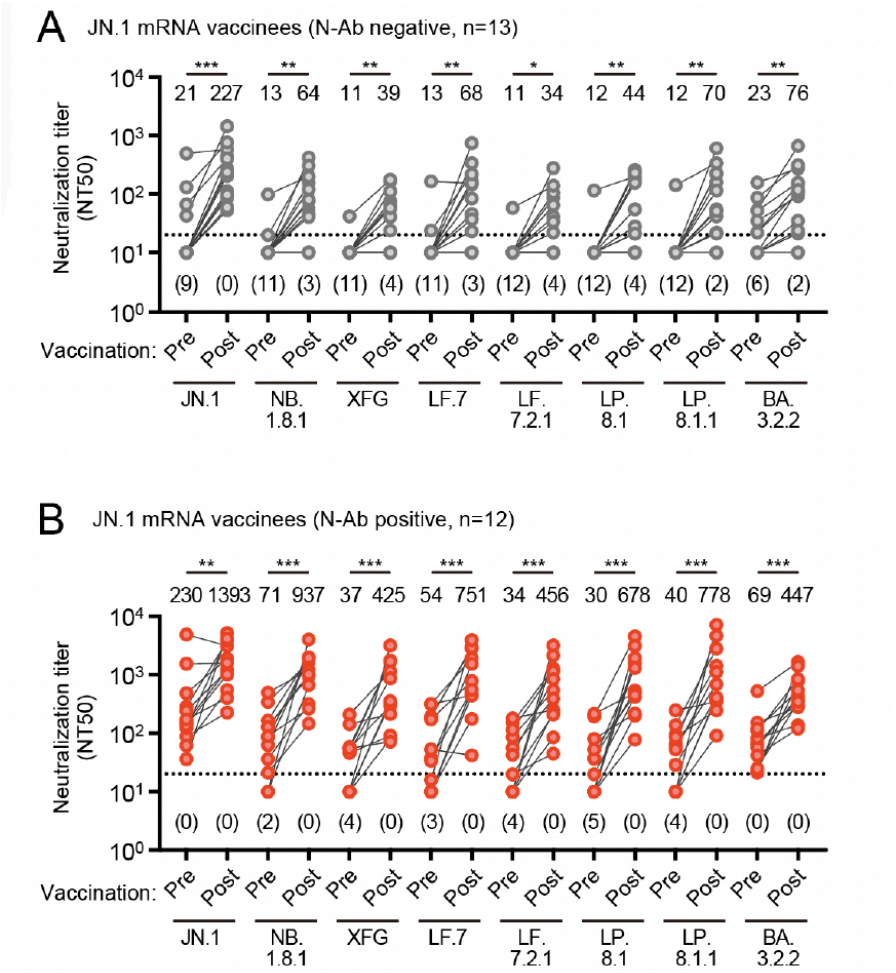


Neutralization titers measured using a pseudovirus assay against B.1, BA.1, JN.1, LP.8.1, NB.1.8.1, XFG or BA.3.2.2 pre- and post-monovalent LP.8.1 vaccination (n=41).

Information on response rates, GMT (also indicated by coloured bars) and fold changes is indicated below the graphs.

Happle C, et al. Lancet Infect Dis. 2026;26(1):e3-e5.

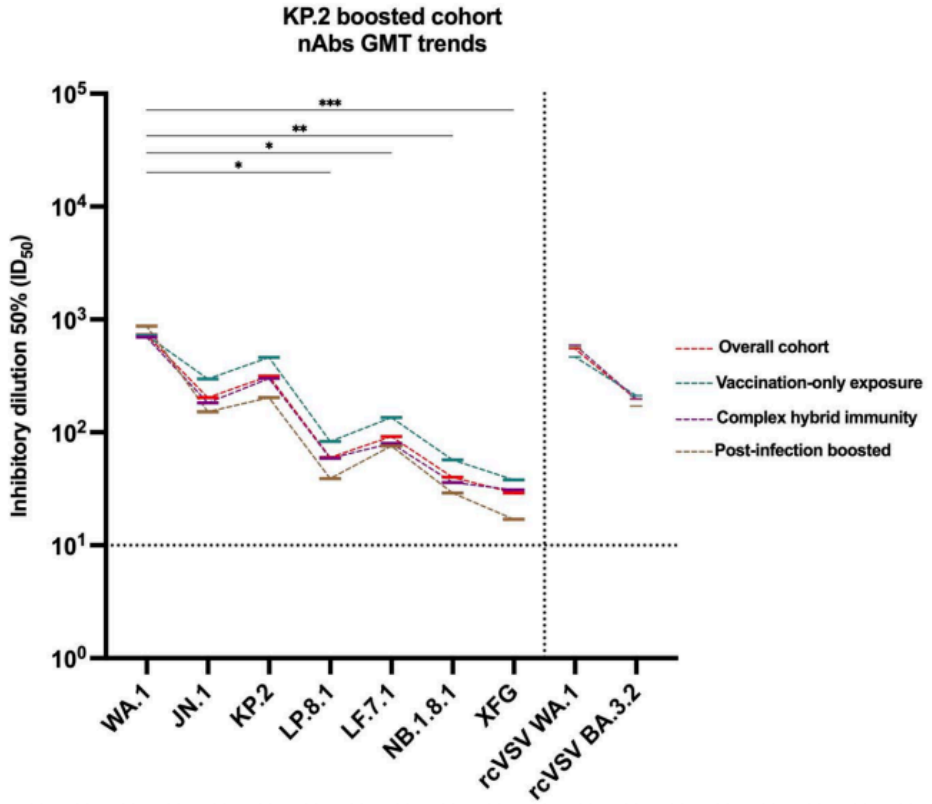
Breadth of neutralizing antibody responses (3)



Neutralization titers against JN.1, NB.1.8.1, XFG, LF.7, LF.7.2.1, LP.8.1, LP.8.1.1 and BA.3.2.2 pre- and post-monovalent JN.1 mRNA vaccination.

Information on GMT indicated above the graphs. The number of sera below the limit of detection is shown under each graph in brackets.

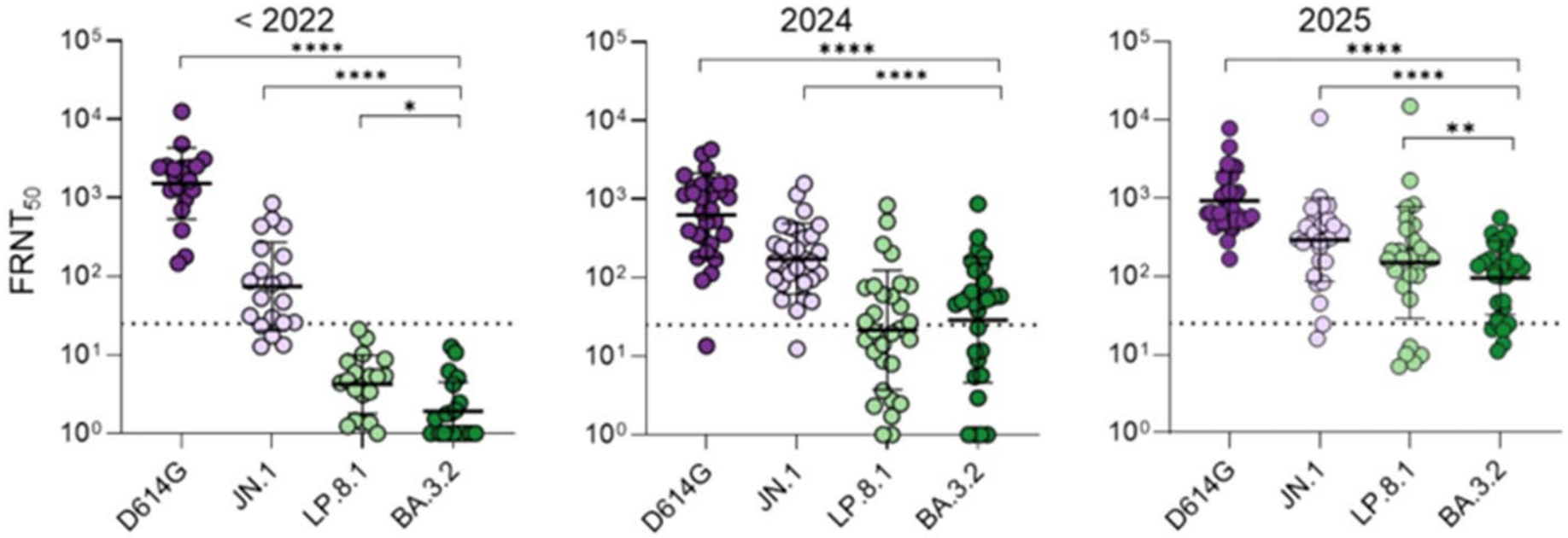
Breadth of neutralizing antibody responses (4)



Comparative GMT trends for the overall cohort of individuals following monovalent KP.2 vaccination (Overall cohort, n=56, red) and subgroups with Vaccination-only exposure (self-reported with no strong evidence of any past infection, n=16, teal), Post-infection boosted (monovalent KP.2 vaccination shortly after SARS-CoV-2 infection, n=11, brown) and Complex hybrid immunity (individuals with ≥2 prior infections and ≥3 prior COVID-19 vaccine doses, n=29, purple).

Abbad A, et al. mBio. 2026;17(1):e0290125

Breadth of neutralizing antibody responses (5)

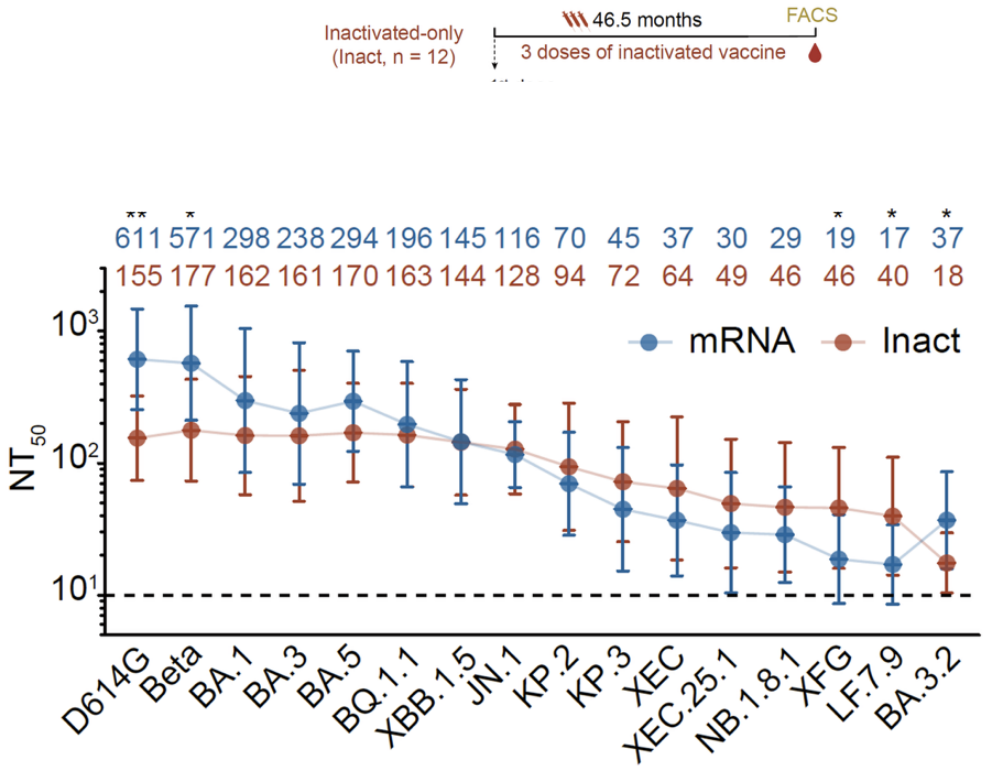


Neutralization titers against D614G, JN.1, LP.8.1 and BA.3.2 by pre-2022 plasma from infected unvaccinated South Africans (left), by February 2024 collected plasma from South Africans with no Covid-19 symptoms (middle) and by March 2025 collected plasma from South Africans with no Covid-19 symptoms (right).

Information on GMT is indicated above each graph and by horizontal lines.

Jule Z, et al. Virus Evol. 2025 doi:10.1093/ve/veag011

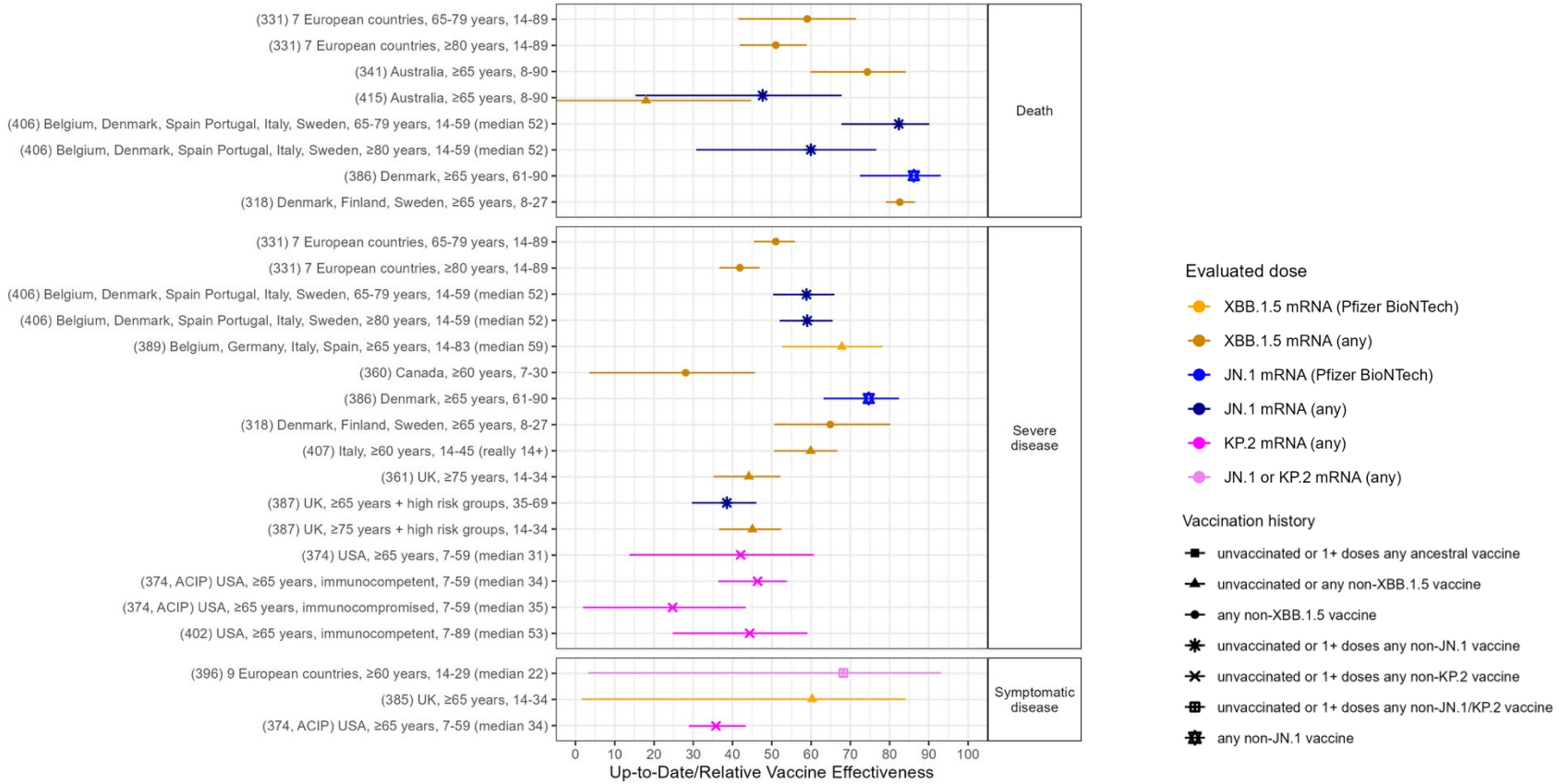
Breadth of neutralizing antibody responses (6)



Neutralization titers against D614G, Beta, BA.1, BA.3, BA.5, BQ.1.1, XBB.1.5, JN.1, KP.2, KP.3, XEC, XEC.25.1, NB.1.8.1, XFG, LF.7.9 and BA.3.2 by sera from individuals vaccinated with 3 doses of inactivated COVID-19 vaccine, 46.5 months since the first vaccine dose (n=12, red) and by sera from individuals vaccinated with at least 1 dose of mRNA COVID-19 vaccine, 46.0 months since the first vaccine dose (n=8 blue).

These individuals have resided in the same region since 2021 and have experienced multiple Omicron infections. Information on GMT is indicated above the graphs for each cohort. Dashed lines indicate the limit of detection (NT50 = 10). Two-tailed Wilcoxon rank-sum tests were used. *P < 0.05, **P < 0.01, ***P < 0.001, ****P < 0.0001.

Recent vaccine effectiveness estimates



Estimates and 95%CI of relative or up-to-date vaccine effectiveness (rVE) in adults over 65 years within three months of a dose of monovalent XBB.1.5, JN.1 or KP.2 mRNA vaccines during periods of circulation of JN.1 or later variants.

The top panel shows rVE estimates against death, the middle panel shows rVE estimates against hospitalization and severe disease, and the bottom panel shows rVE estimates against symptomatic disease. The colour of the rVE estimates indicate the dose evaluated and the symbol represents the vaccination history of the comparator group. Analysis conducted by WHO using data from www.viewhub.org with published studies up to 8 January 2026.

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Summary of available evidence (1)

- SARS-CoV-2 continues to circulate globally, causing severe disease, post COVID-19 condition, and death. In 2026, all WHO regions are reporting lower SARS-CoV-2 test positivity rates than during the corresponding period in previous years.

- Globally, the current predominant variant among SARS-CoV-2 sequences remains Variant Under Monitoring (VUM) XFG, however the weekly proportion is now declining. The proportion of VUM BA.3.2 is increasing, with heterogeneous dynamics across countries where genomic surveillance continues.

- BA.3.2 appears to have lower fitness than JN.1-descendant variants, which may explain why BA.3.2 has not displaced JN.1-descendant variants in regions where it has been detected.

Summary of available evidence (2)

- Neutralization data using antisera from naïve animals infected or vaccinated with JN.1, LP.8.1, NB.1.8.1 or XFG, indicated that recent JN.1-descendant variants are antigenically closely related. In contrast, these antisera showed limited neutralizing activity against BA.3.2. Antisera from naïve animals infected with BA.3.2 showed very limited cross-reactivity with recent JN.1-descendant variants.

- Sera from cohorts that are representative of recent population immunity and pre-LP.8.1 vaccination sera demonstrated cross-reactivity with recent JN.1-descendant variants and with BA.3.2.

- Pre- and post-vaccination sera from individuals immunized with LP.8.1 demonstrated significant increases in neutralizing activity against JN.1 and its descendant variants, including NB.1.8.1 and XFG. Post-vaccination neutralizing antibody titers and the fold change against BA.3.2 were lower than against the homologous LP.8.1 antigen and other JN.1- descendant variants.

- Pre- and post-vaccination sera from individuals immunized with JN.1 or KP.2 demonstrated significant increases in neutralizing activity against JN.1 and its descendant variants. However, post-vaccination neutralizing antibody titers against NB.1.8.1 and XFG were lower than those against the homologous JN.1 or KP.2 antigens, with even larger reductions typically observed for BA.3.2.

Overview of data from vaccine manufacturers

- Immunization of naïve mice with monovalent LP.8.1, XFG or NB.1.8.1 induced high neutralizing antibody titers against the homologous antigen, as well as other JN.1-descendant variants. Low or non-detectable neutralizing antibody titers were consistently observed against BA.3.2. In contrast, immunization of naïve mice with monovalent BA.3.2 induced immune responses largely restricted to the homologous antigen. Overall immunogenicity was lower than after LP.8.1, XFG or NB.1.8.1 immunization.

- Immunization of mice previously immunized with SARS-CoV-2 variants and then immunized with LP.8.1, XFG or NB.1.8.1 induced high neutralizing antibody titers against JN.1-descendant variants. Lower neutralizing antibody titers against BA.3.2 were observed.

- In humans, vaccination with LP.8.1 induced strong increases in neutralizing antibody titers against JN.1, LP.8.1, NB.1.8.1 and XFG. As in mice, post- vaccination neutralizing antibody titers against BA.3.2 were lower than those against the homologous LP.8.1 antigen. A single clinical immunogenicity study using a BA.3.2 vaccine candidate showed increased neutralizing antibody titers against the homologous antigen, and a back boost against JN.1-descendant variants, but overall lower immunogenicity than the LP.8.1 vaccine.

Limitations of available evidence

- There are persistent and increasing gaps and delays in epidemiological and genetic/genomic surveillance of SARS-CoV-2 globally.

- Currently, two antigenically distinct lineages (JN.1-descendant and BA.3.2-descendant variants) are circulating and the comparative evolutionary potential of these lineages remains uncertain.

- Data on the immune responses following JN.1-descendant variant infection or monovalent LP.8.1 vaccination are largely restricted to neutralizing antibodies. Data and interpretation of other aspects of the immune response, including cellular immunity, are limited.

- Recent estimates of rVE are limited in terms of the number of studies, geographic diversity, vaccine platforms evaluated, populations assessed, duration of follow-up, and contemporary comparisons of vaccines with different antigen composition. There are currently only a limited number of available rVE estimates using monovalent LP.8.1 mRNA vaccines; there are no rVE estimates in populations in which BA.3.2 was the predominant variant.

Recommendation for COVID-19 vaccine composition, May 2026

- **Monovalent LP.8.1** is the recommended COVID-19 vaccine antigen.
- Other antigens (e.g. XFG, NB.1.8.1) or other approaches that demonstrate broad and robust neutralizing antibody responses or efficacy against currently circulating SARS-CoV-2 variants could also be considered.
- As per the WHO Strategic Advisory Group of Experts on Immunization (SAGE) recommendations, Member States should consider routine COVID-19 vaccination of groups at highest risk of severe COVID-19 disease and vaccination should not be delayed in anticipation of access to vaccines with an updated antigen composition.

LP.8.1 (Nextstrain: 25A; GenBank: PV074550.1; GISAID: EPI_ISL_19467828)