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corresponding author(s):	Dr Merryn voysey
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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

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For	all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
n/a	Confirmed
	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
	The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.
	A description of all covariates tested
\boxtimes	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
\boxtimes	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
	Estimates of effect sizes (e.g. Cohen's d, Pearson's r), indicating how they were calculated
	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.
So	ftware and code
Poli	cy information about <u>availability of computer code</u>
Da	ata collection RedCap 10.6.13 has been used for data collection (© 2021 Vanderbilt University)

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data analysis was done using R version 3.6.1 or later. The GAM was coded using the mgcv package in R. Three knots were used for each GAM,

Data

Data analysis

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

and the smoothing parameter was estimated by generalized cross validation.

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Anonymised participant data will be made available when the trials are complete, upon requests directed to the corresponding author. Proposals will be reviewed and approved by the sponsor, investigator, and collaborators on the basis of scientific merit. After approval of a proposal, data can be shared through a secure online platform after signing a data access agreement. All data will be made available for a minimum of 5 years from the end of the trial.

Field-specific reporting					
Please select the o	e below that is the best fit for your research. If you are not sure, read the appropriate sections before maki	ng your selection.			
Life sciences	Behavioural & social sciences Ecological, evolutionary & environmental sciences				
For a reference copy of t	e document with all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>				
Life scier	ces study design				
All studies must dis	ose on these points even when the disclosure is negative.				
Sample size	All available data in the trial have been used in this post-hoc analysis on correlates of protection. The sample size for the the primary outcomes which are not reported here.	data in the trial have been used in this post-hoc analysis on correlates of protection. The sample size for the trial was based on outcomes which are not reported here.			
Data exclusions		were excluded if they were baseline seropositive or unknown to the SARS-CoV-2 N protein at first vaccination, or had their PB28 a 14 to 42 day window after the second dose, or were followed up to <= 7 days after PB28 with no prior evidence of infection, or ed schedules in error (details shown in Figure S1). Exclusions were prespecifed in the statistical analysis plan.			
Replication	Replication of findings would be impossible as this is a clinical trial of a vaccine against a rapidly mutating pandemic virus	findings would be impossible as this is a clinical trial of a vaccine against a rapidly mutating pandemic virus in humans			
Randomization	Participants were randomized with full allocation concealment to receive either ChAdOx nCoV-19 vaccine or MenACWY	vaccine.			
Blinding	This is a single-blinded trial where participants were blinded.				
We require informations	for specific materials, systems and methods In from authors about some types of materials, experimental systems and methods used in many studies. Here, indicated is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before the erimental systems Methods Involved in the study Methods Methods N/a Involved in the study Methods Methods				
Antibodies	ChIP-seq				
Eukaryotic					
	gy and archaeology MRI-based neuroimaging				
Animals and other organisms Animals and participants Human research participants					
Clinical data					
Dual use research of concern					
Human rese	rch participants				
Policy information	pout studies involving human research participants				
Population chara	eristics UK adults aged 18 years old or above; both male and female; generally healthy				
Recruitment	Recruitment was done at 19 sites in the UK with a focus on healthcare workers. No selection biases are affect results.	Recruitment was done at 19 sites in the UK with a focus on healthcare workers. No selection biases are known of that would affect results.			
Ethics oversight	Ethics oversight This study was approved in the UK by the Medicines and Healthcare products Regulatory Agency (MHRA), reference 21584/0428/001 0001, and the South-Central Berkshire Research Ethics Committee, reference 20/SC/0179. All necessary patient/participant informed consent has been obtained and the appropriate institutional forms have been archived.				

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Clinical data

Policy information about <u>clinical studies</u>

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration NCT04400838

Study protocol The study protocol has been appended in previous publications and is accessible through https://doi.org/10.1016/ S0140-6736(20)32661-1

Data collection

19 clinical study sites in the England, Scotland and Wales. Participants were enrolled since May 2020 and the study is still ongoing.

Outcomes

Primary symptomatic COVID-19 defined as NAAT+ with at least one of the five COVID symptoms (fever≥ 37.8oC; cough; shortness of breath; anosmia orageusia), and asymptomatic SARS-CoV-2 infections defined as a NAAT+ swab with no symptom reported (see more details in Methods and Statistical Plan in supplementary). Outcomes were predefined in the statistical analysis plan.