



Predicting vaccine protection from SARS-CoV-2 variants.

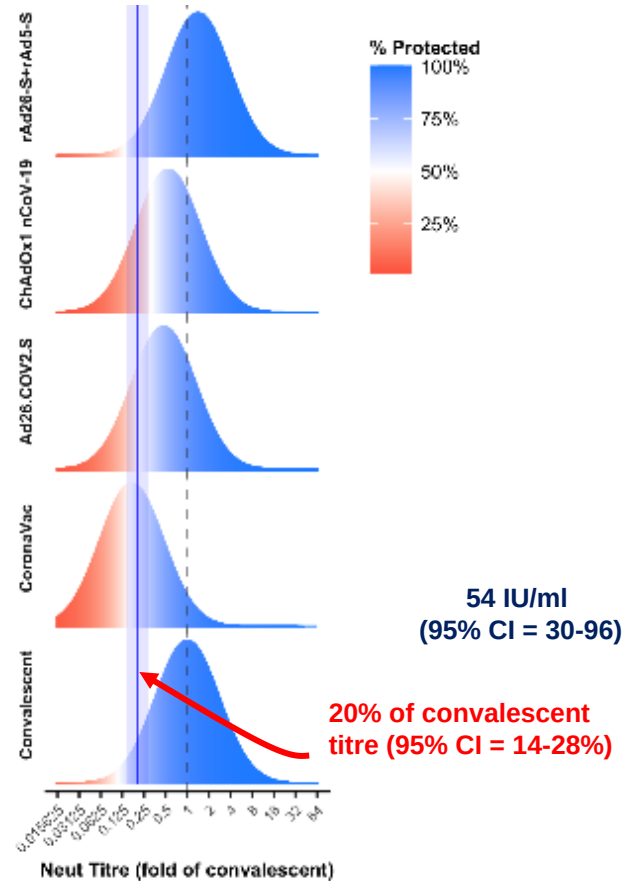
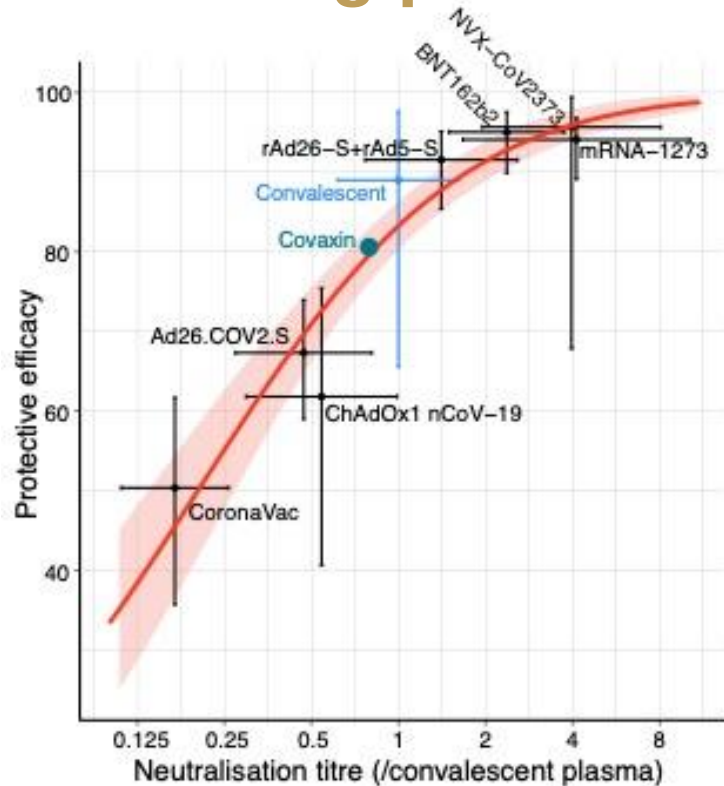
Miles Davenport | WHO COVID-19 Vaccines, 3 September 2021

Declaration of potential conflicts:

Professor Davenport receives funding from:

- National Health and Medical Research Council (Australia)
- Medical Research Futures Fund (Australia)
- Australian Research Council
- University of New South Wales (Australia)
- National Institutes of Health (USA)
- eLife journal

Predicting protection;



Predicting protection against SARS-CoV-2 VOC?

- Understand changes in neutralisation titre
- Validate model on efficacy data

The problem of assays: (*Ancestral*)

No progress to standardized assay

Technical Name	Dosage	Dose 2 (Day)	Measured on Day	Assay*
mRNA-1273	100 µg	29	42	Live WT virus PRNT ₈₀ ¹
NVX-CoV2373	5 µg + 50 µg Matrix-M1 adjuvant	21	35	Live WT MN IC ₅₀ ²
BNT162b2	30 µg	21	28	Live fluorescent WT virus PRNT IC ₅₀ ³
rAd26-S+rAd5-S	10 ¹¹ viral particles	21	42	Live WT virus MN IC ₅₀ ⁴
ChAdOx1 nCoV-19	5x10 ¹⁰ viral particles (SD)	28	42	Live WT virus MN IC ₅₀ ⁵
Ad26.COV2.S	5x10 ¹⁰ viral particles	N/A	29	Live WT virus PRNT IC ₅₀ ⁶
CoronaVac	3 µg	14	28	Live WT virus MN IC ₅₀ ⁷
BBV152	6 µg with Algel-IMDG	28	42	Live WT virus PRNT ₅₀ ⁸
Convalescent Plasma	N/A	N/A	N/A	Live WT virus MN IC ₅₀ ⁹

Assay variation:

Khoury et al, Nature Reviews Immunology (2020)

Khoury, D., et al, Nature Medicine 2021

Variants

Titre to ancestral



Titre to variant

Cromer et al, MedRxiv

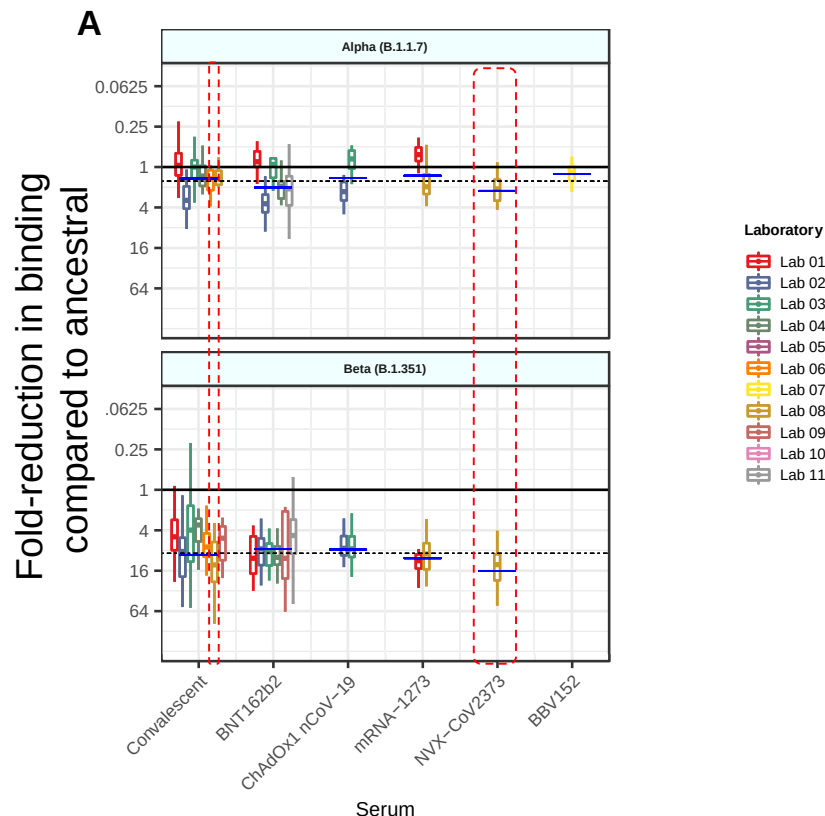
<https://www.medrxiv.org/content/10.1101/2021.08.11.21261876v1>

Variants

Titre to ancestral



Titre to variant



Cromer et al, MedRxiv

<https://www.medrxiv.org/content/10.1101/2021.08.11.21261876v1>

Variants

Titre to ancestral



Titre to variant

Fold-reduction in binding
compared to ancestral



Cromer et al, MedRxiv

<https://www.medrxiv.org/content/10.1101/2021.08.11.21261876v1>

DROP in titre:

(regression model)

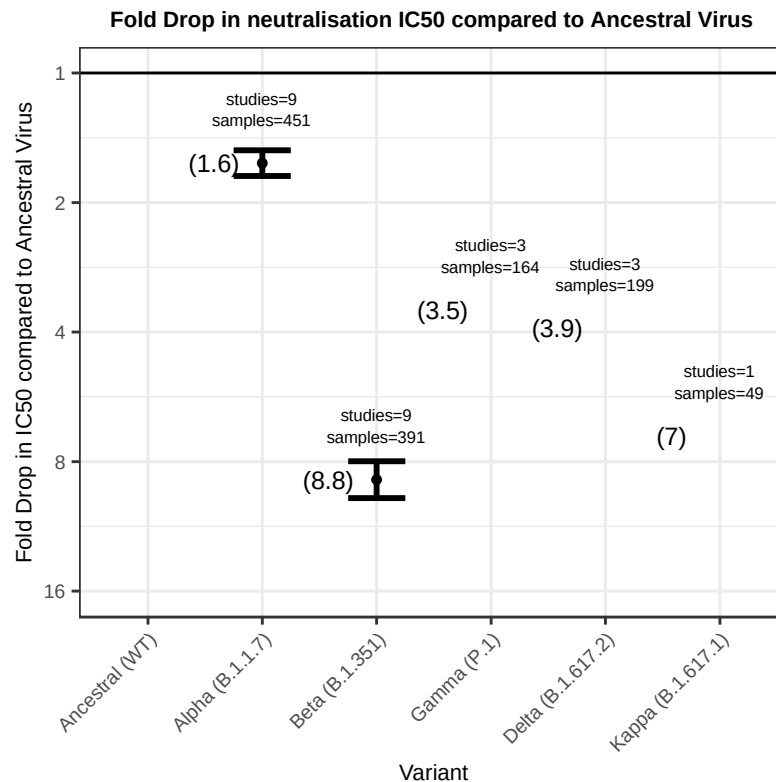
- Variant
- Lab
- ~~Vaccine~~ (compared to convalescent)

***You should not rely on the
results of any (single)
neutralisation assay***

DROP in titre:

(regression model)

- Variant
- Lab
- ~~Vaccine~~ (compared to convalescent)



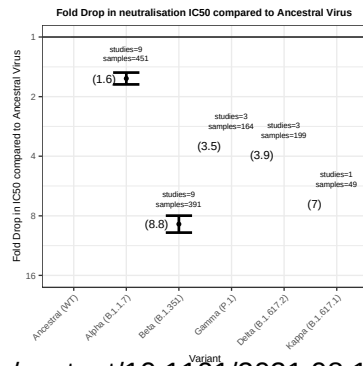
Cromer et al, MedRxiv

<https://www.medrxiv.org/content/10.1101/2021.08.11.21261876v1>

DROP in titre:

(regression model)

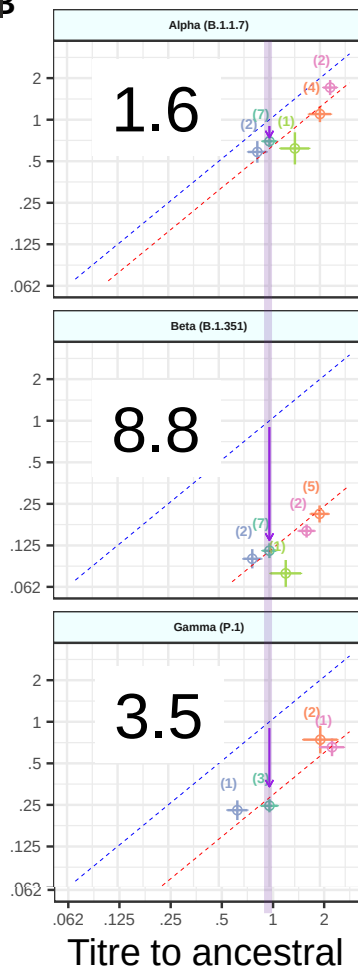
- Variant
- Lab
- ~~Serum~~ (convalescent / vaccine X)



Cromer et al, MedRxiv

<https://www.medrxiv.org/content/10.1101/2021.08.11.21261876v1>

Titre to variant

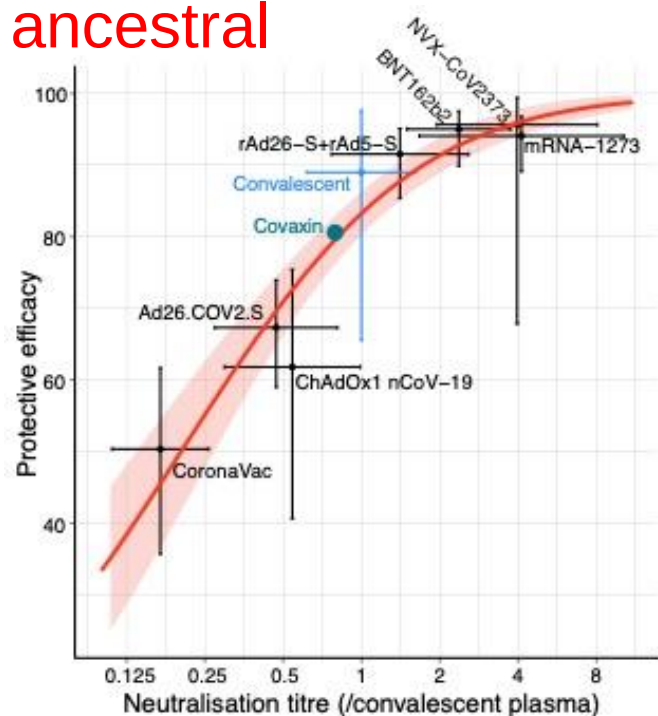


Serum

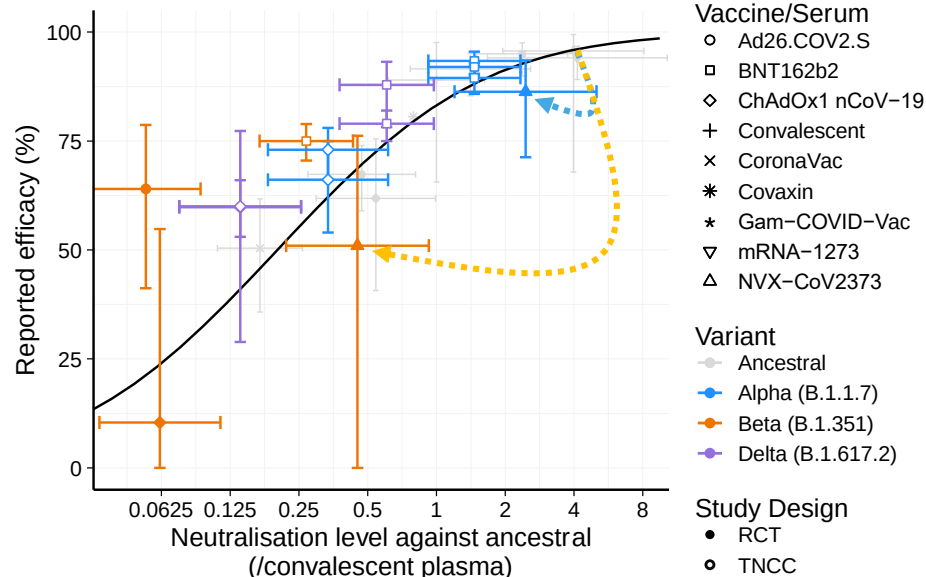
- Convalescent
- BNT162b2
- ChAdOx1 nCoV-19
- mRNA-1273
- NVX-CoV2373

Scaling existing model

ancestral



1) Move 'dots'

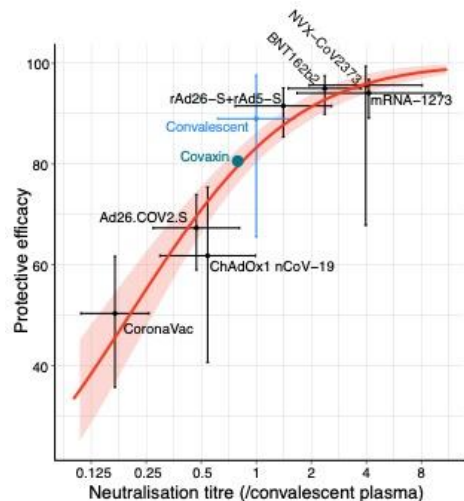


Scaling existing model

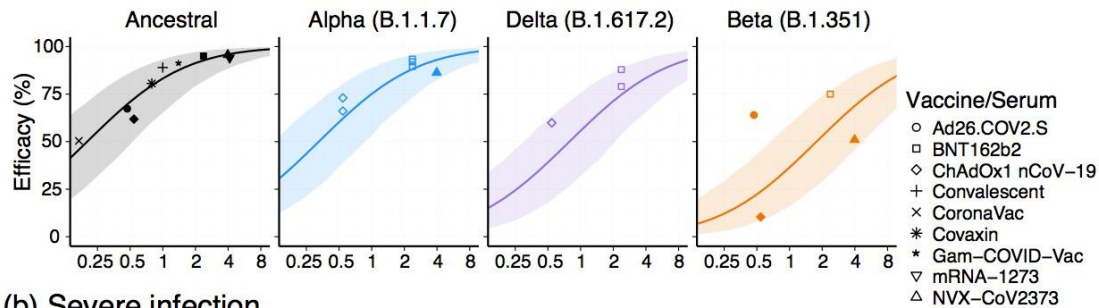
ancestral

2) Move 'curves'

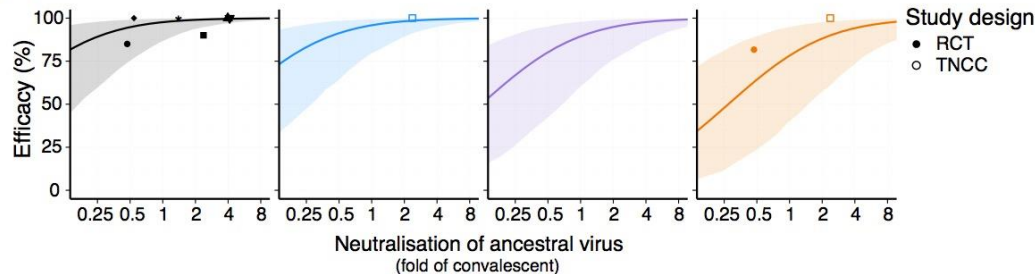
13/14 VOC efficacy
22/23 Ancestral + VOC



(a) Symptomatic SARS-CoV-2 infection



(b) Severe infection



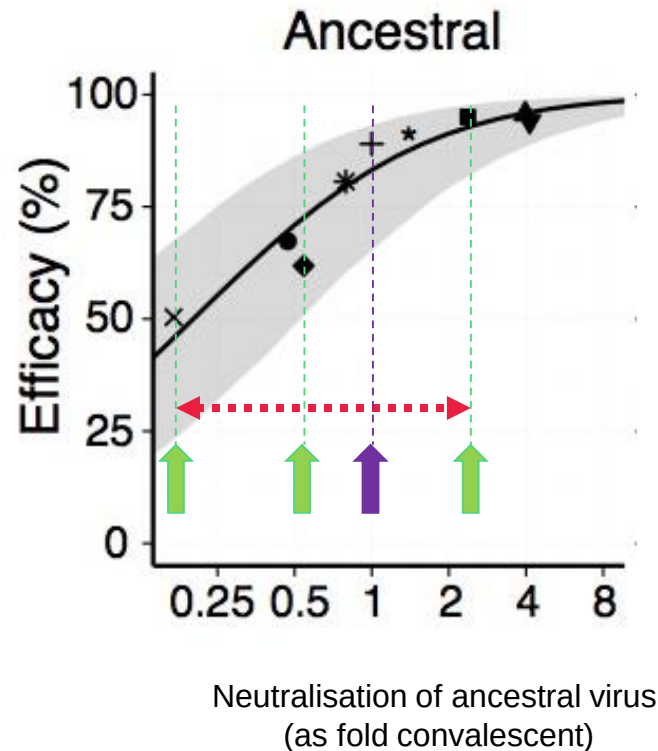
Predicting efficacy

New vaccine:

- Estimate neutralisation against ancestral virus

Benchmark in SAME ASSAY:

- Intl Standards
- Coronavac
- ChAdOx1 nCoV19
- Convalescent (1-2 months)
- BNT162b2



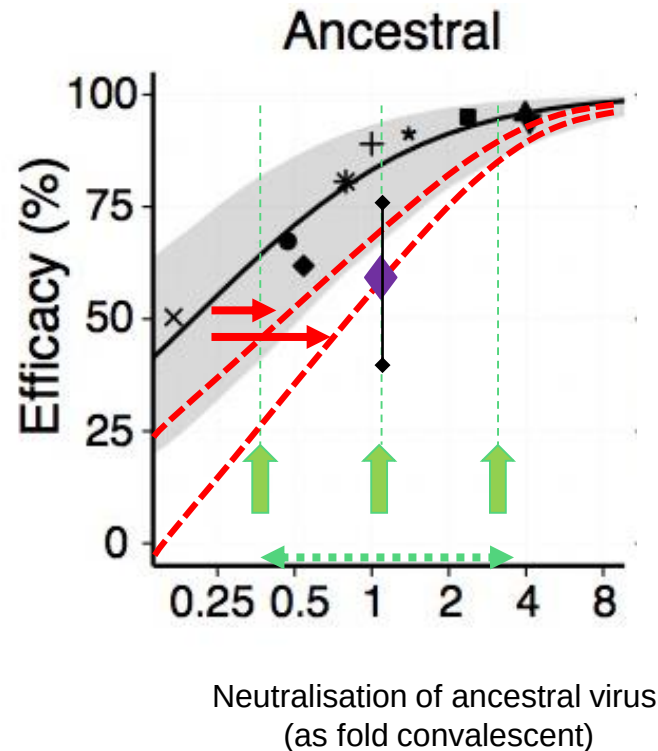
Predicting efficacy

New vaccine:

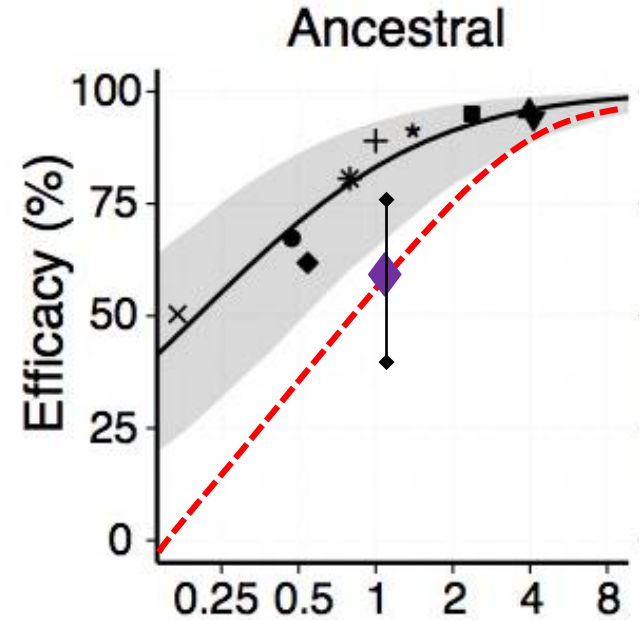
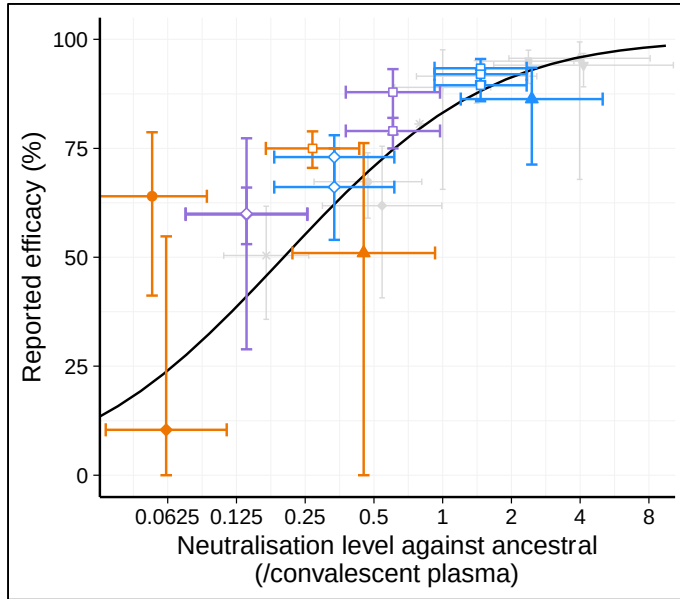
- Estimate neutralisation against ancestral virus

New variant:

- Estimate fold-drop (from ancestral)
(across several assays)



Predicting efficacy



Neutralisation of ancestral virus
(as fold convalescent)

Details of primary sources of all studies analysed:

Cromer, D. *et al*,

*SARS-CoV-2 variants: levels of neutralisation
required for protective immunity*. MedRxiv

<https://www.medrxiv.org/content/10.1101/2021.08.11.21261876v1>

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