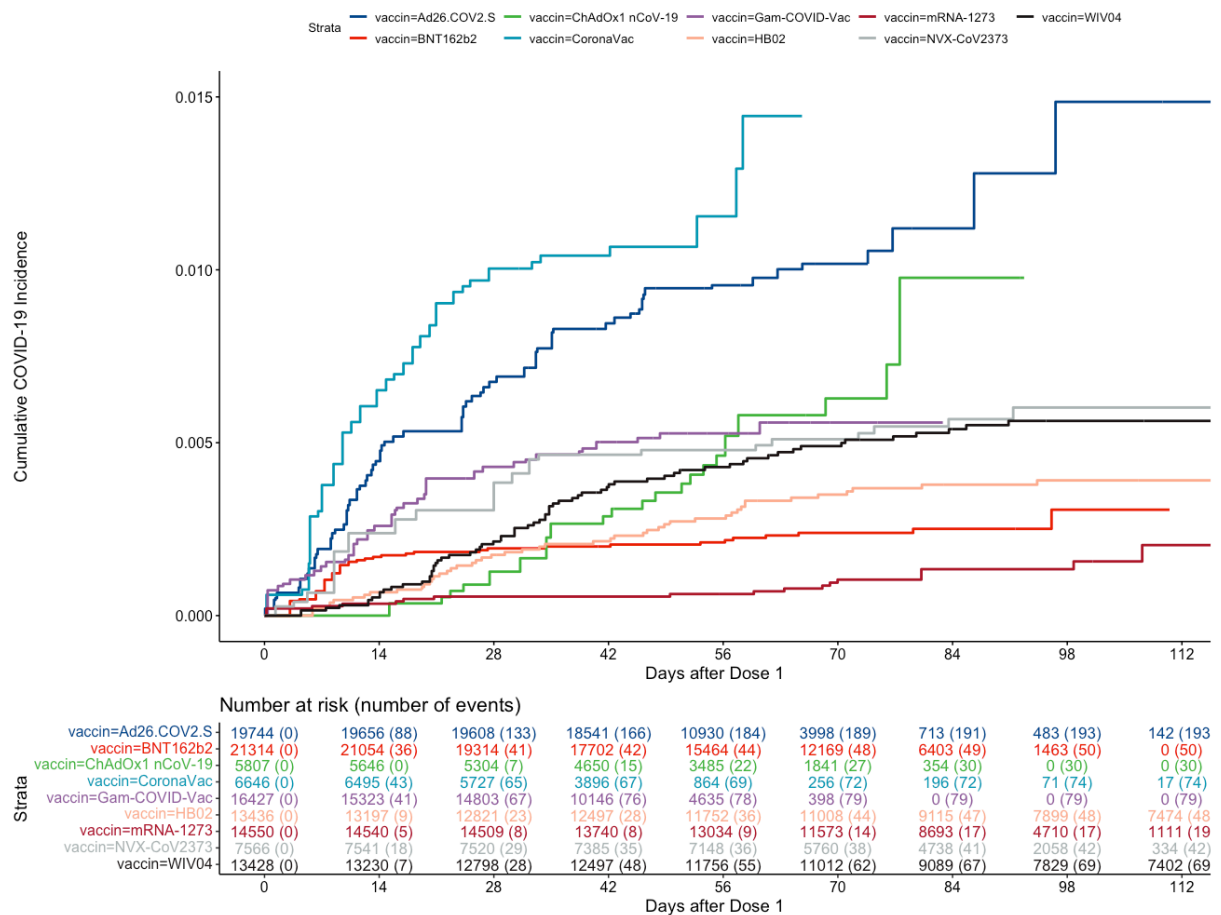


## Appendix

**Figure S1: Efficacy of vaccines against COVID-19 after the first dose from reconstructed individual patient data**



**BNT162b2** (lipid nanoparticle-formulated, nucleoside-modified RNA encoding the SARS-CoV-2 full-length spike): 30 µg; **ChAdOx1 nCoV-19** (AZS1222): recombinant-deficient chimpanzee adenoviral vector containing the SARS-CoV-2 structural glycoprotein antigen (spike protein; nCoV-19): 2.2–6.5×10<sup>10</sup> viral particle (VP); **mRNA-1273** lipid nanoparticle (LNP)-encapsulated modified RNA encoding the perfusion stabilized full-length spike protein of the SARS-CoV-2 virus): 100 µg; **WIV04** (5 µg) and **HB02** (4 µg): inactivated SARS-CoV-2 strains created from Vero cells with aluminum hydroxide adjuvant; **Gam-COVID-Vac**: Heterologous prime-boost which combined two vector vaccine based on rAd type 26 (rAd26) and rAd type 5 (rAd5) carrying the gene for SARS-CoV-2 full-length glycoprotein S; **Ad26.COV2.S**: replication-incompetent adenovirus type 26 (Ad26) vectored vaccine encoding a stabilized variant of the SARS-CoV-2 S protein (5×10<sup>10</sup> VP); **NVX-CoV2373**: recombinant nanoparticle encoding the full-length spike glycoprotein of the prototype strain plus Matrix-M adjuvant (5 µg of NVX-CoV2373 plus 50 µg of Matrix-M adjuvant); **CoronaVac**: inactivated whole-virion SARS-CoV-2 vaccine (3 µg of SARS-CoV-2 virion plus 0.45 mg/ml of aluminum hydroxide).

**Figure S4: Summary of risk bias assessment for COVID-19 vaccines comparisons**

Study	Risk of bias domains					Overall
	D1	D2	D3	D4	D5	
Polack, 2020						
Baden, 2020						
Voysey, 2020						
Logunov, 2020						
Al Kaabi, 2021						
Sadoff, 2021						
Heath, 2021						
Tanriover, 2021						

Domains:  
D1: Bias due to randomisation.  
D2: Bias due to deviations from intended intervention.  
D3: Bias due to missing data.  
D4: Bias due to outcome measurement.  
D5: Bias due to selection of reported result.

Judgement  
 High  
 Some concerns  
 Low

**Table S3: League table of pairwise comparisons in network meta-analysis for COVID-19 Vaccine efficacy after the first dose**

mRNA-1273	.	.	.	.	.	.	.	.	.	0.07 (0.04- 0.11)
<b>0.39 (0.22- 0.67)</b>	<b>BNT162b2</b>	.	.	.	.	.	.	.	.	0.18 (0.13- 0.24)
<b>0.25 (0.15- 0.44)</b>	0.66 (0.43- 1.00)	<b>Gam-COVID-Vac</b>	.	.	.	.	.	.	.	0.28 (0.21- 0.37)
<b>0.24 (0.13- 0.42)</b>	<b>0.61 (0.39- 0.97)</b>	0.93 (0.59- 1.47)	<b>NVX-CoV2373</b>	.	.	.	.	.	.	0.30 (0.21- 0.42)
<b>0.24 (0.13- 0.44)</b>	0.61 (0.37- 1.02)	0.93 (0.56- 1.55)	1.00 (0.59- 1.71)	<b>ChAdOx1 nCoV-19</b>	.	.	.	.	.	0.30 (0.20- 0.44)
<b>0.21 (0.12- 0.37)</b>	<b>0.54 (0.34- 0.84)</b>	0.82 (0.53- 1.28)	0.88 (0.55- 1.42)	0.88 (0.52- 1.48)	<b>HB02</b>	.	0.69 (0.48- 1.00)	.	.	0.34 (0.24- 0.47)
<b>0.16 (0.10- 0.26)</b>	<b>0.41 (0.29- 0.57)</b>	<b>0.62 (0.44- 0.88)</b>	<b>0.67 (0.45- 0.98)</b>	0.66 (0.43- 1.03)	0.76 (0.52- 1.10)	<b>Ad26.COVS2.S</b>	.	.	.	0.45 (0.38- 0.53)
<b>0.14 (0.08- 0.25)</b>	<b>0.37 (0.25- 0.57)</b>	<b>0.57 (0.38- 0.86)</b>	<b>0.61 (0.39- 0.96)</b>	0.61 (0.37- 1.01)	0.69 (0.48- 1.00)	0.92 (0.66- 1.28)	<b>WIV04</b>	.	.	0.49 (0.36- 0.65)
<b>0.13 (0.07- 0.23)</b>	<b>0.33 (0.21- 0.52)</b>	<b>0.51 (0.33- 0.79)</b>	<b>0.54 (0.34- 0.87)</b>	<b>0.54 (0.32- 0.91)</b>	<b>0.62 (0.39- 0.98)</b>	0.82 (0.57- 1.18)	0.89 (0.58- 1.37)	<b>CoronaVac</b>	.	0.54 (0.40- 0.75)
<b>0.07 (0.04- 0.11)</b>	<b>0.18 (0.13- 0.24)</b>	<b>0.28 (0.21- 0.37)</b>	<b>0.30 (0.21- 0.42)</b>	<b>0.30 (0.20- 0.44)</b>	<b>0.34 (0.24- 0.47)</b>	<b>0.45 (0.38- 0.53)</b>	<b>0.49 (0.36- 0.65)</b>	<b>0.54 (0.40- 0.75)</b>	<b>Control</b>	.

**Table S4: League table of pairwise comparisons in network meta-analysis for COVID-19 Vaccine efficacy from randomization to 21 days after dose 1**

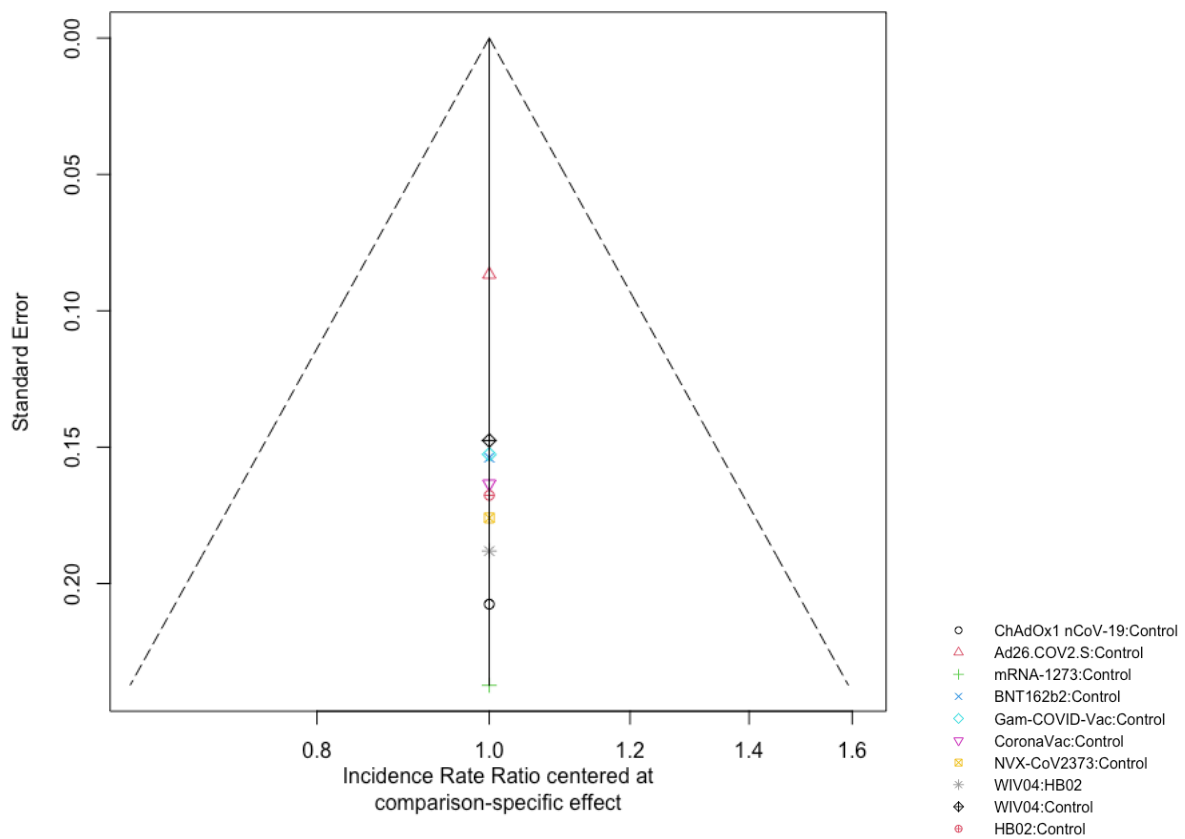
<b>Gam-COVID-Vac</b>	.	.	.	.	.	0.38 (0.27-0.53)	.	.	.	.
0.84 (0.18- 3.93)	<b>ChAdOx1 nCoV-19</b>	.	.	.	.	0.45 (0.10-2.03)	.	.	.	.
0.65 (0.39- 1.09)	0.77 (0.16- 3.63)	<b>BNT162b2</b>	.	.	.	0.59 (0.40-0.87)	.	.	.	.
0.59 (0.29- 1.22)	0.70 (0.14- 3.58)	0.91 (0.43- 1.92)	<b>HB02</b>	0.82 (0.43-1.59)	.	0.64 (0.34-1.22)	.	.	.	.
<b>0.49 (0.25- 0.95)</b>	0.58 (0.12- 2.89)	0.75 (0.37- 1.51)	0.82 (0.43- 1.59)	<b>WIV04</b>	.	0.78 (0.44-1.40)	.	.	.	.
<b>0.40 (0.24- 0.68)</b>	0.48 (0.10- 2.26)	0.62 (0.35- 1.09)	0.68 (0.32- 1.45)	0.83 (0.41- 1.68)	<b>CoronaVac</b>	0.95 (0.63-1.42)	.	.	.	.
<b>0.38 (0.27- 0.53)</b>	0.45 (0.10- 2.03)	<b>0.59 (0.40- 0.87)</b>	0.64 (0.34- 1.22)	0.78 (0.44- 1.40)	0.95 (0.63- 1.42)	<b>Control</b>	0.96 (0.62-1.49)	0.89 (0.42-1.92)	0.75 (0.66-0.85)	.
<b>0.37 (0.21- 0.64)</b>	0.43 (0.09- 2.08)	0.56 (0.31- 1.01)	0.62 (0.29- 1.34)	0.75 (0.36- 1.56)	0.91 (0.50- 1.66)	0.96 (0.62- 1.49)	<b>NVX-CoV2373</b>	.	.	.
<b>0.34 (0.15- 0.79)</b>	0.40 (0.08- 2.18)	0.53 (0.22- 1.24)	0.58 (0.21- 1.56)	0.70 (0.27- 1.83)	0.85 (0.36- 2.01)	0.89 (0.42- 1.92)	0.93 (0.39- 2.24)	<b>mRNA-1273</b>	.	.
<b>0.29 (0.20- 0.41)</b>	0.34 (0.07- 1.52)	<b>0.44 (0.29- 0.66)</b>	<b>0.48 (0.25- 0.92)</b>	0.58 (0.32- 1.06)	0.71 (0.46- 1.08)	<b>0.75 (0.66- 0.85)</b>	0.78 (0.49- 1.23)	0.83 (0.39- 1.81)	<b>Ad26.COVS2.S</b>	.

**Table S5: League table of pairwise comparisons in network meta-analysis for COVID-19 Vaccine efficacy starting 7 days after dose 2**

<b>mRNA-1273</b>	.	.	.	.	.	.	.	.	.	.	0.05 ( 0.03- 0.09)
0.95 ( 0.37- 2.42)	<b>BNT162b2</b>	.	.	.	.	.	.	.	.	.	0.05 ( 0.03- 0.11)
0.61 ( 0.23- 1.62)	0.64 ( 0.22- 1.82)	<b>NVX-CoV2373</b>	.	.	.	.	.	.	.	.	0.08 ( 0.04- 0.18)
<b>0.32 ( 0.12- 0.91)</b>	0.34 ( 0.11- 1.02)	0.53 ( 0.17- 1.66)	<b>CoronaVac</b>	.	.	.	.	.	.	.	0.15 ( 0.07- 0.35)
<b>0.25 ( 0.08- 0.77)</b>	<b>0.27 ( 0.08- 0.86)</b>	0.42 ( 0.12- 1.40)	0.78 ( 0.22- 2.73)	<b>Gam-COVID-Vac</b>	.	.	.	.	.	.	0.19 ( 0.08- 0.49)
<b>0.24 ( 0.11- 0.52)</b>	<b>0.25 ( 0.11- 0.59)</b>	<b>0.40 ( 0.16- 0.98)</b>	0.74 ( 0.29- 1.93)	0.95 ( 0.33- 2.69)	<b>HB02</b>	.	.	.	0.75 ( 0.43- 1.32)	.	0.21 ( 0.13- 0.33)
<b>0.22 ( 0.10- 0.50)</b>	<b>0.23 ( 0.09- 0.57)</b>	<b>0.36 ( 0.14- 0.93)</b>	0.68 ( 0.25- 1.84)	0.87 ( 0.30- 2.55)	0.92 ( 0.45- 1.88)	<b>ChAdOx1 nCoV-19</b>	.	.	.	.	0.22 ( 0.13- 0.38)
<b>0.18 ( 0.09- 0.38)</b>	<b>0.19 ( 0.08- 0.43)</b>	<b>0.30 ( 0.12- 0.71)</b>	0.56 ( 0.22- 1.41)	0.71 ( 0.26- 1.97)	0.75 ( 0.43- 1.32)	0.82 ( 0.41- 1.62)	<b>WIV04</b>	.	.	.	0.27 ( 0.18- 0.42)
<b>0.16 ( 0.08- 0.32)</b>	<b>0.16 ( 0.07- 0.36)</b>	<b>0.26 ( 0.11- 0.60)</b>	0.48 ( 0.20- 1.19)	0.62 ( 0.23- 1.67)	0.65 ( 0.36- 1.17)	0.71 ( 0.37- 1.35)	0.87 ( 0.50- 1.50)	<b>Ad26.COV2.S</b>	.	.	0.32 ( 0.22- 0.45)
<b>0.05 ( 0.03- 0.09)</b>	<b>0.05 ( 0.03- 0.11)</b>	<b>0.08 ( 0.04- 0.18)</b>	<b>0.15 ( 0.07- 0.35)</b>	<b>0.19 ( 0.08- 0.49)</b>	<b>0.21 ( 0.13- 0.33)</b>	<b>0.22 ( 0.13- 0.38)</b>	<b>0.27 ( 0.18- 0.42)</b>	<b>0.32 ( 0.22- 0.45)</b>	<b>Control</b>	.	

Vaccines are ordered in the rank of their chance of being the best vaccine. Vaccine estimates are provided as incidence risk ratio (IRR) with 95% confidence interval. Comparisons between vaccines should be red left to right, and their IRR is in the cell in common between the column-defining vaccine and the row-defining vaccine. IRRs < 1 favor the column-defining vaccine for the network estimates. Significant pairwise comparisons are highlighted (Bolted *P values* were < 0.05). **BNT162b2** (lipid nanoparticle-formulated, nucleoside-modified RNA encoding the SARS-CoV-2 full-length spike): 30 µg; **ChAdOx1 nCoV-19** (AZS1222): recombinant-deficient chimpanzee adenoviral vector containing the SARS-CoV-2 structural glycoprotein antigen (spike protein; nCoV-19): 2.2–6.5×10<sup>10</sup> viral particle (VP); **mRNA-1273** lipid nanoparticle (LNP)-encapsulated modified RNA encoding the perfusion stabilized full-length spike protein of the SARS-CoV-2 virus): 100 µg; **WIV04** (5 µg) and **HB02** (4 µg): inactivated SARS-CoV-2 strains created from Vero cells with aluminum hydroxide adjuvant; **Gam-COVID-Vac**: Heterologous prime-boost which combined two vector vaccine based on rAd type 26 (rAd26) and rAd type 5 (rAd5) carrying the gene for SARS-CoV-2 full-length glycoprotein S; **Ad26.COV2.S**: replication-incompetent adenovirus type 26 (Ad26) vectored vaccine encoding a stabilized variant of the SARS-CoV-2 S protein (5×10<sup>10</sup> VP); **NVX-CoV2373**: recombinant nanoparticle encoding the full-length spike glycoprotein of the prototype strain plus Matrix-M adjuvant (5 µg of NVX-CoV2373 plus 50 µg of Matrix-M adjuvant); **CoronaVac**: inactivated whole-virion SARS-CoV-2 vaccine (3 µg of SARS-CoV-2 virion plus 0.45 mg/ml of aluminum hydroxide).

**Figure S3: Comparison-adjusted funnel plot assessment for COVID-19 vaccines trials**



Y-axis corresponds to the standard deviation of vaccine effect and X-axis the comparison-adjusted vaccine effect which was the difference between the estimated of vaccine effect (IRR) versus control and the pooled estimate from direct evidences (effect of the vaccines from direct comparisons). The outer dashed lines indicate the triangular region within which 95% of trials are expected to lie due to the absence of evidence of the presence of publication bias. The solid vertical line corresponds to no vaccine effect. Trial with more precision (lower standard deviation) of vaccine effect estimation are towards the top and those with less precision higher of vaccine effect towards the bottom. IRR: incidence rate ratio.