Diagnostic accuracy of rapid point-of-care tests for diagnosis of current SARS-CoV-2 infections in children: A systematic review and meta-analysis

N. Fujita-Rohwerder, L. Beckmann, Y. Zens, A. Verma

Appendix 1: Supplementary tables and figures

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All tables and figures were created by the authors.

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Table S1: *Eligibility criteria for primary studies.*

(Sub-)Population	Children (i.e. pediatric study participants <18 years of age) • with symptoms suggestive of COVID-19, or • without symptoms, but at an increased risk of infection (e.g. due to recent exposure to SARS-CoV-2 → contact tracing), or • participating in mass testing (e.g. in schools) regardless of symptoms.
Index test	Any rapid point-of-care test that is designed to detect an active SARS-CoV-2 infection and that meets the following criteria: • performed in a non-laboratory setting at or near the point of care (including non-healthcare settings such as schools or community testing sites) • minimal or no training required for end user • sample condition: fresh • time to result ≤ 60 minutes • commercially available
Reference standard	Any validated laboratory-based reverse transcription-polymerase chain reaction (RT-PCR) assay alone or in combination with clinical findings or clinical follow-up.
Main outcome	Diagnostic test accuracy (DTA)
Target condition	Current SARS-CoV-2 infection
Study design	Diagnostic cross-sectional or cohort studies with prospective sampling.
Unit of analysis	Individual study participants
Sample size	At least 10 (pediatric)[a] study participants each identified as positive or negative by the reference standard
Reported results	Sufficient data that allows constructing a complete 2x2 contingency table for (pediatric)[a] study participants per index test
Publication type	Full-text journal articles (including preprints) and reports (including clinical study reports)
Language	English or German

a: upon availability of pediatric study data

Table S2: *Data extraction items.*

General study characteristics	• First author • Publication date • Publication status • Study design • Type of enrolment • Indication for testing • Inclusion and exclusion criteria • Definition of symptoms suggestive for infection with SARS-CoV-2 • Setting • Location • Country • Total number of study participants • Number of pediatric study participants • Recruitment period • Funding sources • Potential conflicts of interest • Study registry entry
Characteristics of pediatric study population	• Age • Proportion of males • Exposure history • Proportion of symptomatic individuals at the time of testing (if applicable) • Duration of symptoms prior to testing (if applicable)
Index test	• Name • Manufacturer • Regulatory status • Assay target • Test method • Readout • Target analyte • Specimen type used in study • Conduct of test according to manufacturer's instructions for use (as judged and reported by authors)
Reference standard	• Name • Manufacturer • Viral target(s) • (Pre-specified) positivity threshold(s) • Specimen type used in study
Flow and timing	• Specimen for index test collected by • Specimen for reference standard collected by • Time interval between specimen collection for index test and reference standard • Time interval between specimen collection and use of index test

	• Time interval between specimen collection and use of reference standard • Index test performed by • Result of index test interpreted by • Reference standard • Result of reference standard interpreted by • Blinding • Time to result index test • Time to result reference standard • Inconclusive or invalid result(s) of index test • Inconclusive or invalid result(s) of reference standard • Missing data
Reported outcomes for pediatric study population	• True positives (TP) • False negatives (FN) • True negatives (TN) • False positives (FP) (if available: separate outcome data depending on symptom status, symptom onset or positivity threshold of reference standard)

Table S3: *Study pool of the systematic review.*

Study identifier	Data sources	Registry entry
Akingba	Preprint [1], unpublished data provided by author	N/A
Bianco	Journal article [2], unpublished data provided by author	N/A
Drevinek	Preprint [3], unpublished data provided by author	N/A
Gonzalez-Donapetry	Journal article [4]	N/A
Homza	Journal article [5], unpublished data provided by author	N/A
Kiyasu	Preprint [6], unpublished data provided by author	N/A
L'Huillier	Preprint [7]	N/A
Möckel	Journal article [8]	yes[a]
Pilarowski	Journal article [9]	N/A
Pollock a	Journal article [10]	N/A
Pollock b	Preprint [11]	N/A
Prince-Guerra	Journal article [12]	N/A
Sood	Journal article [13]	N/A
Shah	Journal article [14], supplementary file provided by authors (published in [15] after finalization of the study pool)	N/A
Takeuchi	Journal article [16], unpublished data provided by author	N/A
Torres	Journal article [17], unpublished data provided by author	N/A
Villaverde	Journal article [18]	N/A

N/A: not available

a: Study registry identifier: DRKS00019207

Table S4: *Potentially relevant studies identified through searching clinical study registries.*

Study registry identifier	Country	Enrollment	Ages eligible for study	Name of index test	Recruitment status[a] (study completion date)
NCT04513990	USA	1,500	not specified (children included)	unspecified point-of-care test	Recruiting (estimated: Apr 2021)
NCT04557046	USA	400	any	LumiraDx SARS-CoV-2 Ag Test	Recruiting (estimated: Dec 2021)
NCT04583189	France	500	≤18 years	Biosynex Covid-19 Ag BSS Rapid test	Completed (Nov 2020)
NCT04720235	USA	304	14-75 years	Lucira COVID-19 All-In-One Test Kit	Completed (Mar 2021)
NCT04750629	USA	100	≥ 1 year	CoviDx™ Rapid Antigen Test	Not yet recruiting (estimated: Mar 2021)
NCT04808921	USA	151	any	Xiamen Wiz Biotech SARS-CoV-2 Antigen Rapid Test	Completed (Apr 2021)
NCT04859023	France	10,000	≥10 years	unspecified SARS-CoV-2 antigen test	Completed (Feb 2021)
NCT04878068	not reported	300	≥ 12 years	Therma COVID-19 Rapid Antigen Test	Not yet recruiting (estimated: June 2021)

a: Status as of May 24, 2021

Table S5: *Conduct, flow and timing, and interpretation of index test and reference standard.*

Study identifier	Timing of specimen collection for index test and reference standard	Index test					Reference standard			Missing data	Invalid or inconclusive tests
		Specimen collected by	Time to conduct of test after specimen collection	Test performed by / interpreted by	Blinded to reference standard	IFU-conform conduct[a]	Specimen collected by	Time to conduct of test	Blinded to index test		
Akingba	only one swab for both tests (swab used for Ag-test was subsequently used for RT-PCR	n.r.	n.r. (result reported to participants onsite)	n.r. / n.r.	n.r., result determined prior to conduct of RT-PCR	n.r.	n.r.	n.r. (swab previously used for Ag-test)	n.r.	n.r., no participant flow diagram provided	19/677 PCR inconclusive, pediatric subgroup: 2/41 PCR inconclusive
Bianco	"in parallel"	n.r.	n.r.	trained staff / n.r.	n.r.	yes	trained staff	within a few hours	n.r.	n.r., no participant flow diagram provided	n.r.
Drevinek	n.r., but same participant encounter	n.r.	immediately	n.r. / n.r.	n.r.	yes	n.r.	n.r.	n.r.	none, no participant flow diagram provided	0
Gonzalez-Donapetry	paired sample collection	n.r.	n.r.	n.r. / n.r.	n.r.	yes	n.r.	n.r.	n.r.	none, no participant flow diagram provided	0
Homza	paired sample collection	HCW	immediately	n.r. / n.r.	n.r.	yes	HCW	n.r.	n.r.	none, no participant flow diagram provided	0
Kiyasu	"simulta-neously"	n.r.	n.r.	n.r. / n.r.	n.r.	yes	n.r.	n.r.	n.r.	5/1939[b] no symptom data, no participant flow diagram provided	0
L'Huillier	n.r., but same participant encounter	HCW	immediately	n.r. / two members of the study team independently	n.r., result determined prior to RT-PCR	yes	HCW	n.r.	n.r.	58/883 refused Ag-test, 2/825 Ag-test result not reported	1/825 Ag-test result invalid

Study identifier	Timing of specimen collection for index test and reference standard	Index test					Reference standard			Missing data	Invalid or inconclusive tests
		Specimen collected by	Time to conduct of test after specimen collection	Test performed by / interpreted by	Blinded to reference standard	IFU-conform conduct[a]	Specimen collected by	Time to conduct of test	Blinded to index test		
				(consensus required)							
Möckel	n.r., but same participant encounter	HCW	immediately	HCW / two HCW (consensus required)	n.r., result determined prior to RT-PCR	yes	HCW	n.r. (time to result (h): median: 8.2 range:3.8-39)	yes	none	0
Pilarowski	paired sample collection	certified lab assistants	n.r. (1 hour from onsite registration to return of positive test result)	n.r. / certified technician readers	n.r., result determined prior to RT-PCR	n.r. (only specimen collection according to IFU reported)	certified lab assistants	n.r.	n.r.	none, no participant flow diagram provided	0
Pollock a	paired sample collection	trained staff	within 1 hour	laboratorian / two laboratorians independently (1st read = official result)	n.r., result determined prior to RT-PCR	yes	trained staff	n.r.	n.r.	94/2482 samples tested at <53°F, 54/2482 missing data	26/2482 inconclusive RT-PCR
Pollock b	paired sample collection	trained staff	99.7% within 1 hour	laboratorian / two laboratorians independently (1st read = official result)	n.r., result determined prior to RT-PCR	yes	trained staff	n.r.	n.r.	48/1603 invalid or missing RT-PCR result, 57/1603 missing clinical data	invalid missing RT-PCR results, see missing data
Prince-Guerra	paired sample collection	HCW	immediately	n.r. / n.r.	n.r.	yes	HCW	within 24-48 hours	n.r.	n.r., no participant flow diagram provided	n.r.
Shah	same participant encounter	participants (self-collected,	n.r. (participants provided documentation of	trained staff / n.r.	n.r., result determined	yes	participants (self-collected,	n.r. (specimen with inconclu-	n.r.	7/2127 missing RT-PCR result, no participant flow diagram provided	4/2127 indeterminate Ag test result,

Study identifier	Timing of specimen collection for index test and reference standard	Index test					Reference standard			Missing data	Invalid or inconclusive tests
		Specimen collected by	Time to conduct of test after specimen collection	Test performed by / interpreted by	Blinded to reference standard	IFU-conform conduct[a]	Specimen collected by	Time to conduct of test	Blinded to index test		
		super-vised)	the initial test result about 30 minutes after initial sample collection)		prior to RT-PCR		super-vised)	sive results were retested)			6/2127 inconclusive RT-PCR result
Sood	n.r., but same participant encounter	trained staff	n.r.	n.r. / two study staff (no consensus required)	n.r.	yes	participant s (self-collected, super-vised)	n.r.	n.r.	4/783 (pediatric subgroup) reason not reported, no participant flow diagram provided	5/779 (pediatric subgroup) inconclusive result of index test
Takeuchi	"simulta-neously"	n.r.	immediately	n.r. / examiner	n.r.	yes	n.r.	in-house RT-PCR: same day as sample collection, reference RT-PCR: up to 1 week	n.r.	22/1208 not the first participant encounter, 4/1208 missing symptom data, no participant flow diagram provided	0
Torres	paired sample collection	HCW	immediately	n.r. / n.r.	n.r.	n.r.	HCW	within 24 hours of specimen collection	n.r.	none, no participant flow diagram provided	0
Villaverde	"concur-rently"	HCW	n.r.	n.r. / HCW	n.r.	yes	HCW	within 24 hours of specimen collection	n.r.	none, no participant flow diagram provided	0

Abbreviations

HCW: health care worker; IFU: instructions for use; n.r.: not reported; RT-PCR: reverse transcription-polymerase chain reaction

Footnotes

a: as judged and reported by the authors; b: unit of analysis = samples, but unit of analysis for paediatric subgroup = individual study participants

Table S6: *QUADAS-2 risk of bias and applicability concerns summary – review authors' judgment about each domain for 18 test evaluations reported in 17 included studies.*

Study identifier	Risk of bias				Applicability concerns		
	Patient selection	Index test	Reference standard	Flow and timing	Patient selection	Index test	Reference standard
Akingba	unclear	unclear	unclear	low	low	unclear	low
Bianco	unclear	unclear	unclear	unclear	low	unclear	low
Drevinek (IT1)	unclear	unclear	unclear	low	low	unclear	low
Drevinek (IT2)	unclear	low	unclear	low	low	unclear	low
Gonzalez-D.	unclear	unclear	unclear	low	high	unclear	low
Homza	low	unclear	unclear	low	low	unclear	low
Kiyasu	unclear	unclear	unclear	low	low	unclear	low
L'Huillier	low	low	unclear	high	low	low	low
Möckel	low	low	low	low	low	unclear	low
Pilarowski	unclear	unclear	unclear	low	low	unclear	low
Pollock a	unclear	unclear	unclear	high	low	unclear	low
Pollock b	unclear	unclear	unclear	high	low	low	low
Prince-G.	unclear	unclear	unclear	unclear	low	low	low
Shah	unclear	unclear	unclear	low	low	unclear	low
Sood	unclear	high	unclear	unclear	low	high	low
Takeuchi	unclear	unclear	unclear	low	low	unclear	low
Torres	low	unclear	unclear	low	low	unclear	low
Villaverde	high	unclear	unclear	low	high	unclear	low

IT1: Index test 1; IT 2: Index test 2

Table S7: *Calculated RT-PCR positivity rate, sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) with 95% confidence interval (CI) for each included study based on the 2x2 contingency tables extracted for the entire paediatric study populations irrespective of symptom status.*

Study identifier	TP	FP	TN	FN	RT-PCR positivity rate	Sensitivity (95% CI)	Specificity (95% CI)	PPV (95% CI)	NPV (95% CI)
Akingba	9	0	28	2	28.2	81.8 (52.3-94.9)	100 (87.9-100)	95.0 (65.6-99.5)	91.9 (77.2-97.5)
Bianco	12	8	141	4	9.7	75.0 (50.5-89.8)	94.6 (89.8-97.3)	60.0 (38.7-78.1)	97.2 (93.1-98.9)
Drevinek (IT1)	8	0	19	4	38.7	66.7 (39.1-86.2)	100 (83.2-100)	94.4 (62.9-99.4)	81.2 (61.8-92.1)
Drevinek (IT2)	8	0	19	4	38.7	66.7 (39.1-86.2)	100 (83.2-100)	94.4 (62.9-99.4)	81.2 (61.8-92.1)
Gonzales-Donapetry	14	0	422	4	4.1	77.8 (54.8-91.0)	100 (99.1-100)	96.7 (74.7-99.7)	98.9 (97.4-99.6)
Homza	8	1	11	4	50.0	66.7 (39.1-86.2)	91.7 (64.6-98.5)	88.9 (56.5-98.0)	73.3 (48.0-89.1)
Kiyasu	7	0	80	3	11.1	70.0 (39.7-89.2)	100 (95.4-100)	93.8 (59.8-99.3)	95.8 (89.2-98.5)
L'Huillier	78	1	702	41	14.5	65.5 (56.6-73.5)	99.9 (99.2-100)	98.7 (93.2-99.8)	94.5 (92.6-95.9)
Möckel	18	1	176	7	12.4	72.0 (52.4-85.7)	99.4 (96.9-99.9)	94.7 (75.4-99.1)	96.2 (92.3-98.1)
Pilarowski	30	0	174	5	16.7	85.7 (70.6-93.7)	100 (97.8-100)	98.4 (86.3-99.8)	96.9 (93.3-98.6)
Pollock a	94	7	786	41	14.5	69.6 (61.4-76.8)	99.1 (98.2-99.6)	93.1 (86.4-96.6)	95.0 (93.3-96.3)
Pollock b	26	7	200	20	18.2	56.5 (42.2-69.8)	96.6 (93.2-98.4)	78.8 (62.3-89.3)	90.9 (86.4-94.0)
Prince-Guerra	9	1	213	13	9.3	40.9 (23.3-61.3)	99.5 (97.4-99.9)	90.0 (59.6-98.2)	94.2 (90.4-96.6)
Shah	25	0	182	10	16.1	71.4 (54.9-83.7)	100 (97.9-100)	98.1 (84.0-99.8)	94.6 (90.4-97.0)
Sood	127	9	539	99	29.2	56.2 (49.7-62.5)	98.4 (96.9-99.1)	93.4 (87.9-96.5)	84.5 (81.5-87.1)
Takeuchi	9	0	153	2	6.7	81.8 (52.3-94.9)	100 (97.6-100)	95.0 (65.6-99.5)	98.4 (95.0-99.5)
Torres	5	0	58	10	20.5	33.3 (15.2-58.3)	100 (93.8-100)	91.7 (51.7-99.1)	84.8 (74.5-91.4)
Villaverde	35	3	1540	42	4.8	45.5 (34.8-56.5)	99.8 (99.4-99.9)	92.1 (79.2-97.3)	97.3 (96.4-98.0)

TP: true positive, FP: false positive, TN: true negative, FN: false negative
RT-PCR: reverse transcription-polymerase chain reaction
IT1: Index test 1; IT2: Index test 2

Table S8: *Calculated RT-PCR positivity rate, sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) with 95% confidence interval (CI) for each included study based on the 2x2 contingency tables extracted for symptomatic paediatric study populations.*

Study identifier	TP	FP	TN	FN	RT-PCR positivity rate	Sensitivity (95% CI)	Specificity (95% CI)	PPV (95% CI)	NPV (95% CI)
Akingba	9	0	28	2	28.2	81.8 (52.3-94.9)	100 (87.9-100)	95.0 (65.6-99.5)	91.9 (77.2-97.5)
Bianco	5	0	9	2	43.8	71.4 (35.9-91.8)	100 (70.1-100)	91.7 (51.7-99.1)	79.2 (50.9-93.3)
Drevinek (IT1)	6	0	3	1	70.0	85.7 (48.7-97.4)	100 (43.9-100)	92.9 (56.1-99.2)	70.0 (29.9-92.7)
Drevinek (IT2)	6	0	3	1	70.0	85.7 (48.7-97.4)	100 (43.9-100)	92.9 (56.1-99.2)	70.0 (29.9-92.7)
Gonzales-Donapetry	14	0	422	4	4.1	77.8 (54.8-91.0)	100 (99.1-100)	96.7 (74.7-99.7)	98.9 (97.4-99.6)
L'Huillier	65	1	443	24	16.7	73.0 (63.0-81.2)	99.8 (98.7-100)	98.5 (91.9-99.7)	94.9 (92.5-96.5)
Möckel	18	1	176	7	12.4	72.0 (52.4-85.7)	99.4 (96.9-99.9)	94.7 (75.4-99.1)	96.2 (92.3-98.1)
Pilarowski	12	0	23	1	36.1	92.3 (66.7-98.6)	100 (85.7-100)	96.2 (71.7-99.6)	94.0 (77.7-98.6)
Pollock a	22	0	65	4	28.6	84.6 (66.5-93.8)	100 (94.4-100)	97.8 (82.2-99.8)	93.6 (85.3-97.3)
Pollock b	7	3	20	2	28.1	77.8 (45.3-93.7)	87 (67.9-95.5)	70.0 (39.7-89.2)	90.9 (72.2-97.5)
Shah	20	0	89	7	23.3	74.1 (55.3-86.8)	100 (95.9-100)	97.6 (80.8-99.8)	92.3 (85.2-96.1)
Sood	56	4	91	31	47.8	64.4 (53.9-73.6)	95.8 (89.7-98.4)	93.3 (84.1-97.4)	74.6 (66.2-81.5)
Takeuchi	1	0	89	0	1.1	100 (20.7-100)	100 (95.9-100)	75.0 (19.8-97.3)	99.4 (94.9-99.9)
Villaverde	35	3	1540	42	4.8	45.5 (34.8-56.5)	99.8 (99.4-99.9)	92.1 (79.2-97.3)	97.3 (96.4-98.0)

TP: true positive, FP: false positive, TN: true negative, FN: false negative
RT-PCR: reverse transcription-polymerase chain reaction
IT1: Index test 1; IT 2: Index test 2

Table S9: *Calculated RT-PCR positivity rate, sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) with 95% confidence interval (CI) for each included study based on the 2x2 contingency tables extracted for asymptomatic paediatric study populations.*

Study identifier	TP	FP	TN	FN	RT-PCR positivity rate	Sensitivity (95% CI)	Specificity (95% CI)	PPV (95% CI)	NPV (95% CI)
Bianco	7	8	132	2	6.0	77.8 (45.3-93.7)	94.3 (89.1-97.1)	46.7 (24.8-69.9)	98.5 (94.7-99.6)
Drevinek (IT1)	2	0	16	3	23.8	40.0 (11.8-76.9)	100 (80.6-100)	83.3 (31.0-98.2)	82.5 (61.1-93.4)
Drevinek (IT2)	2	0	16	3	23.8	40.0 (11.8-76.9)	100 (80.6-100)	83.3 (31.0-98.2)	82.5 (61.1-93.4)
Kiyasu	7	0	76	3	11.6	70.0 (39.7-89.2)	100 (95.2-100)	93.8 (59.8-99.3)	95.6 (88.7-98.4)
L'Huillier	13	0	259	17	10.4	43.3 (27.4-60.8)	100 (98.5-100)	96.4 (73.2-99.6)	93.7 (90.2-96.0)
Pollock a	70	7	715	37	12.9	65.4 (56.0-73.8)	99.0 (98.0-99.5)	90.9 (82.4-95.5)	95.1 (93.3-96.4)
Pollock b	19	4	180	18	16.7	51.4 (35.9-66.6)	97.8 (94.5-99.2)	82.6 (62.9-93.0)	90.9 (86.1-94.2)
Shah	4	0	90	3	7.2	57.1 (25.0-84.2)	100 (95.9-100)	90.0 (46.3-99.0)	96.3 (90.3-98.6)
Sood	71	5	448	68	23.5	51.1 (42.9-59.2)	98.9 (97.4-99.5)	93.4 (85.5-97.2)	86.8 (83.6-89.5)
Takeuchi	8	0	64	2	13.5	80.0 (49.0-94.3)	100 (94.3-100)	94.4 (62.9-99.4)	96.3 (88.7-98.8)
Torres	5	0	58	10	20.5	33.3 (15.2-58.3)	100 (93.8-100)	91.7 (51.7-99.1)	84.8 (74.5-91.4)

TP: true positive, FP: false positive, TN: true negative, FN: false negative
RT-PCR: reverse transcription-polymerase chain reaction
IT1: Index test 1; IT 2: Index test 2

Table S10: *Calculated RT-PCR positivity rate, sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) with 95% confidence interval (CI) for each included study based on the 2x2 contingency tables extracted for mixed paediatric study populations.*

Study identifier	TP	FP	TN	FN	RT-PCR positivity rate	Sensitivity (95% CI)	Specificity (95% CI)	PPV (95% CI)	NPV (95% CI)
Homza	8	1	11	4	50.0	66.7 (39.1-86.2)	91.7 (64.6-98.5)	88.9 (56.5-98.0)	73.3 (48.0-89.1)
Pilarowski	18	0	137	4	13.8	81.8 (61.5-92.7)	100 (97.3-100)	97.4 (79.1-99.7)	96.8 (92.5-98.7)
Prince-Guerra	9	1	213	13	9.3	40.9 (23.3-61.3)	99.5 (97.4-99.9)	90.0 (59.6-98.2)	94.2 (90.4-96.6)

TP: true positive, FP: false positive, TN: true negative, FN: false negative
RT-PCR: reverse transcription-polymerase chain reaction

Table S11: *Calculated RT-PCR positivity rate, sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) with 95% confidence interval (CI) for each included study based on the 2x2 contingency tables extracted for entire paediatric study populations irrespective of symptom status when the RT-PCR cycle threshold cut-off value is set to 30.*

Study identifier	TP	FP	TN	FN	RT-PCR positivity rate	Sensitivity (95% CI)	Specificity (95% CI)	PPV (95% CI)	NPV (95% CI)
Akingba	9	0	30	0	23.1	100 (70.1-100)	100 (88.6-100)	95.0 (65.6-99.5)	98.4 (86.3-99.8)
Pilarowski	24	6	179	0	11.5	100 (86.2-100)	96.8 (93.1-98.5)	79.0 (61.9-89.7)	99.7 (97.4-100)
Pollock a	84	17	818	9	10.0	90.3 (82.6-94.8)	98.0 (96.8-98.7)	83.2 (74.7-89.2)	98.9 (97.9-99.4)
Pollock b	24	9	215	5	11.5	82.8 (65.5-92.4)	96.0 (92.5-97.9)	72.7 (55.8-84.9)	97.7 (94.8-99.0)
Sood	42	91	625	11	6.9	79.2 (66.5-88.0)	87.3 (84.7-89.5)	31.6 (24.3-39.9)	98.3 (96.9-99.0)
Torres	5	0	60	8	17.8	38.5 (17.7-64.5)	100 (94.0-100)	91.7 (51.7-99.1)	87.7 (77.9-93.5)

TP: true positive, FP: false positive, TN: true negative, FN: false negative
RT-PCR: reverse transcription-polymerase chain reaction

Table S12: *Calculated RT-PCR positivity rate, sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) with 95% confidence interval (CI) for each included study based on the 2x2 contingency tables extracted for entire paediatric study populations irrespective of symptom status when the RT-PCR cycle threshold cut-off value is set to 25.*

Study identifier	TP	FP	TN	FN	RT-PCR positivity rate	Sensitivity (95% CI)	Specificity (95% CI)	PPV (95% CI)	NPV (95% CI)
Akingba	4	5	30	0	10.3	100 (51.0-100)	85.7 (70.6-93.7)	45.0 (20.1-72.6)	98.4 (86.3-99.8)
Pollock a	61	40	826	1	6.7	98.4 (91.4-99.7)	95.4 (93.8-96.6)	60.4 (50.6-69.4)	99.9 (99.3-100)
Pollock b	20	13	220	0	7.9	100 (83.9-100)	94.4 (90.7-96.7)	60.3 (43.6-74.9)	99.8 (97.9-100)
Sood	15	118	635	1	2.1	93.8 (71.7-98.9)	84.3 (81.6-86.8)	11.3 (7.0-17.8)	99.8 (99.1-100)
Torres	4	1	65	3	9.6	57.1 (25.0-84.2)	98.5 (91.9-99.7)	80.0 (37.5-96.4)	95.6 (87.8-98.5)

TP: true positive, FP: false positive, TN: true negative, FN: false negative
RT-PCR: reverse transcription-polymerase chain reaction

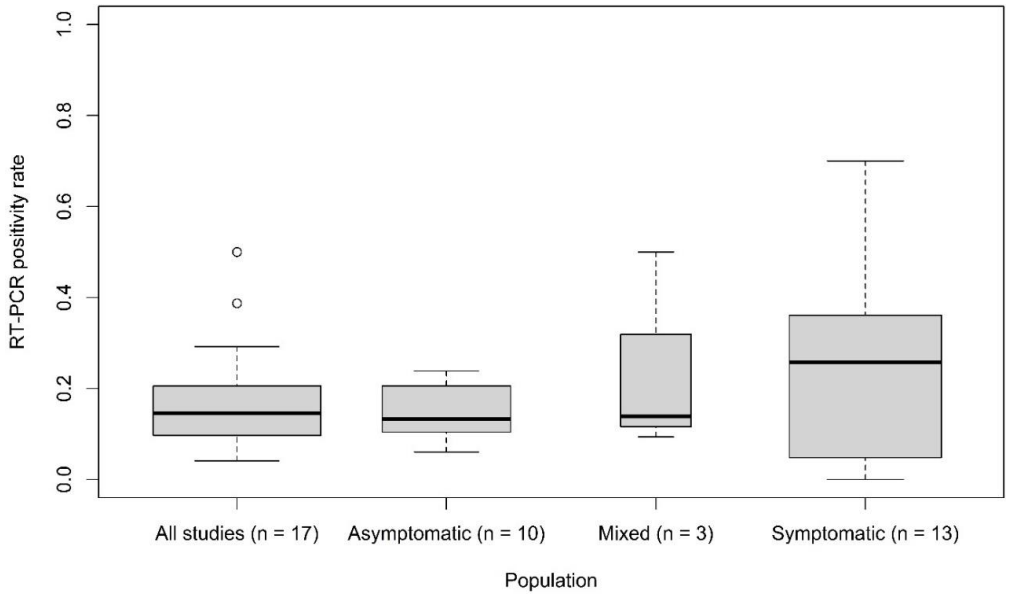

Figure S1: *Box and whisker plots of the RT-PCR positivity rates in entire paediatric study populations irrespective of symptoms and in asymptomatic, mixed, and symptomatic paediatric study populations. The box is drawn from the first to the third quartile, defined via hinges. The bold horizontal line in the box denotes the median. The whiskers extend out of the box by 1.5 times the difference between the hinges. Outliers are plotted as small circle. The width of the box corresponds to the number of considered studies.*

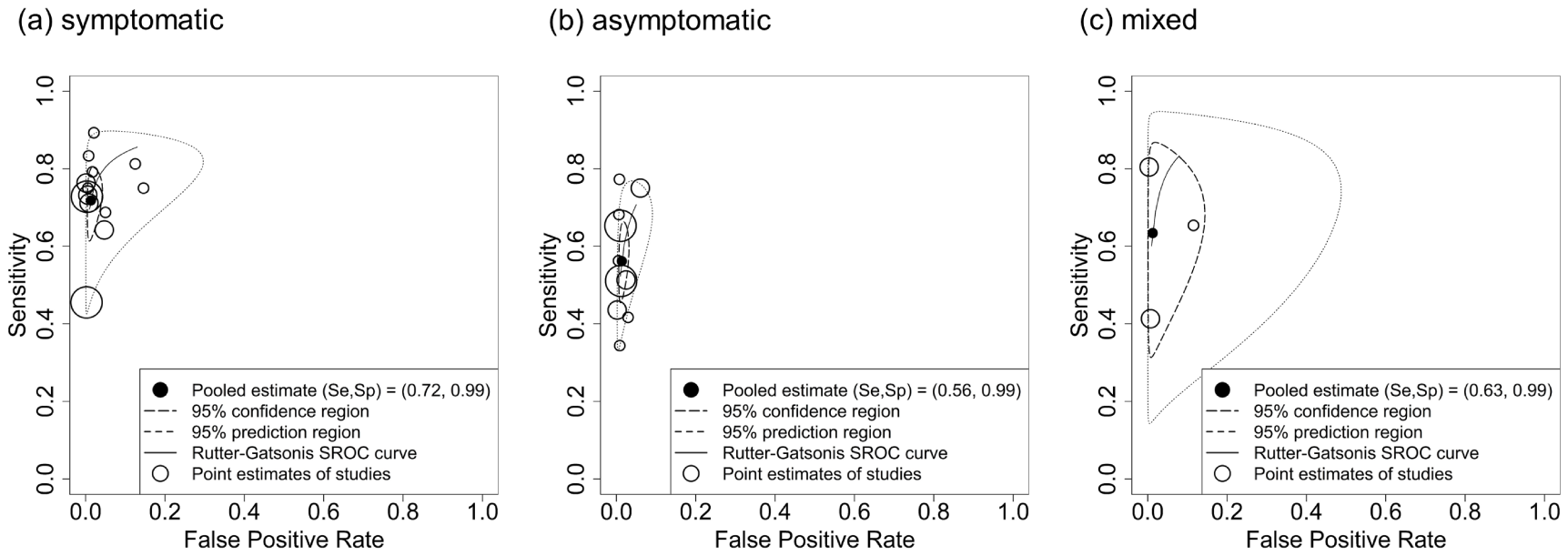

Figure S2: *Summary receiver operating characteristic (SROC) plot of sensitivity and specificity of antigen tests for diagnosis of current SARS-CoV-2 infections in (a) symptomatic, (b) asymptomatic, and (c) mixed symptomatic and asymptomatic paediatric study populations. Each circle represents the point estimate of an individual study, whereas the size of the circle correlates with the number of paediatric study participants (small circle: <100 participants, medium circle: between 100 and 500 participants, large circle: >500 participants). The pooled estimate (black dot) of the pair of sensitivity (Se) and specificity (Sp) is surrounded by its 95% confidence region (closed curve with short dashes) and prediction region (closed curve with long dashes). The estimation of the SROC curve is based on the bivariate approach by Rutter and Gatsonis* [19].

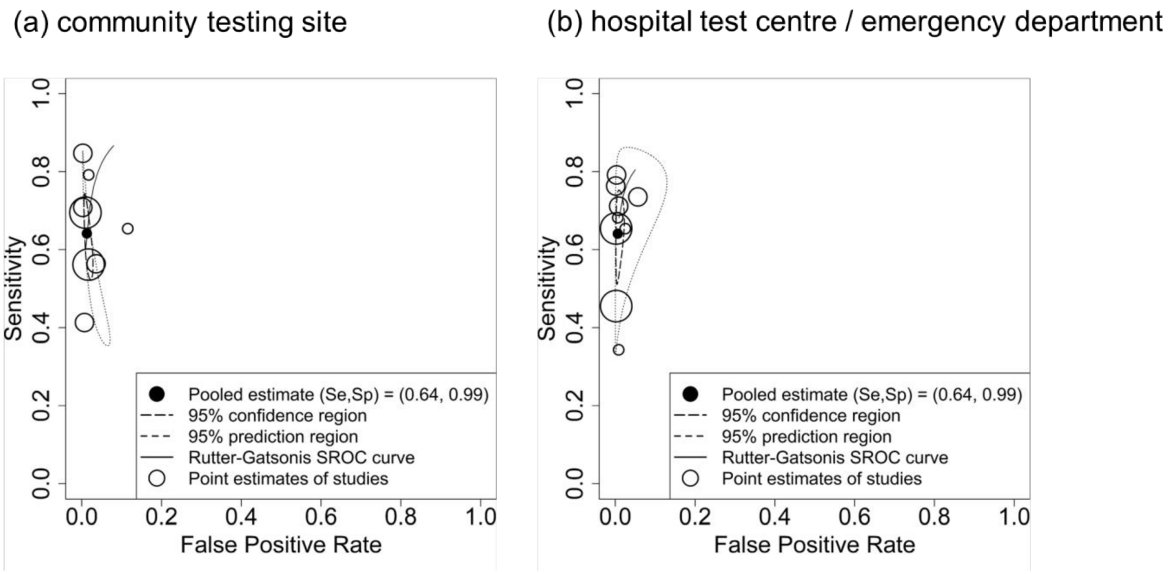

Figure S3: *Summary receiver operating characteristic (SROC) plot of sensitivity and specificity of antigen tests for diagnosis of current SARS-CoV-2 infections with respect to the setting.* (a) community testing site, (b) hospital test centre / emergency department. *Each circle represents the point estimate of an individual study, whereas the size of the circle correlates with the number of paediatric study participants (small circle: <100 participants, medium circle: between 100 and 500 participants, large circle: >500 participants). The pooled estimate (black dot) of the pair of sensitivity (Se) and specificity (Sp) is surrounded by its 95% confidence region (closed curve with short dashes) and prediction region (closed curve with long dashes). The estimation of the SROC curve is based on the bivariate approach by Rutter and Gatsonis* [19].

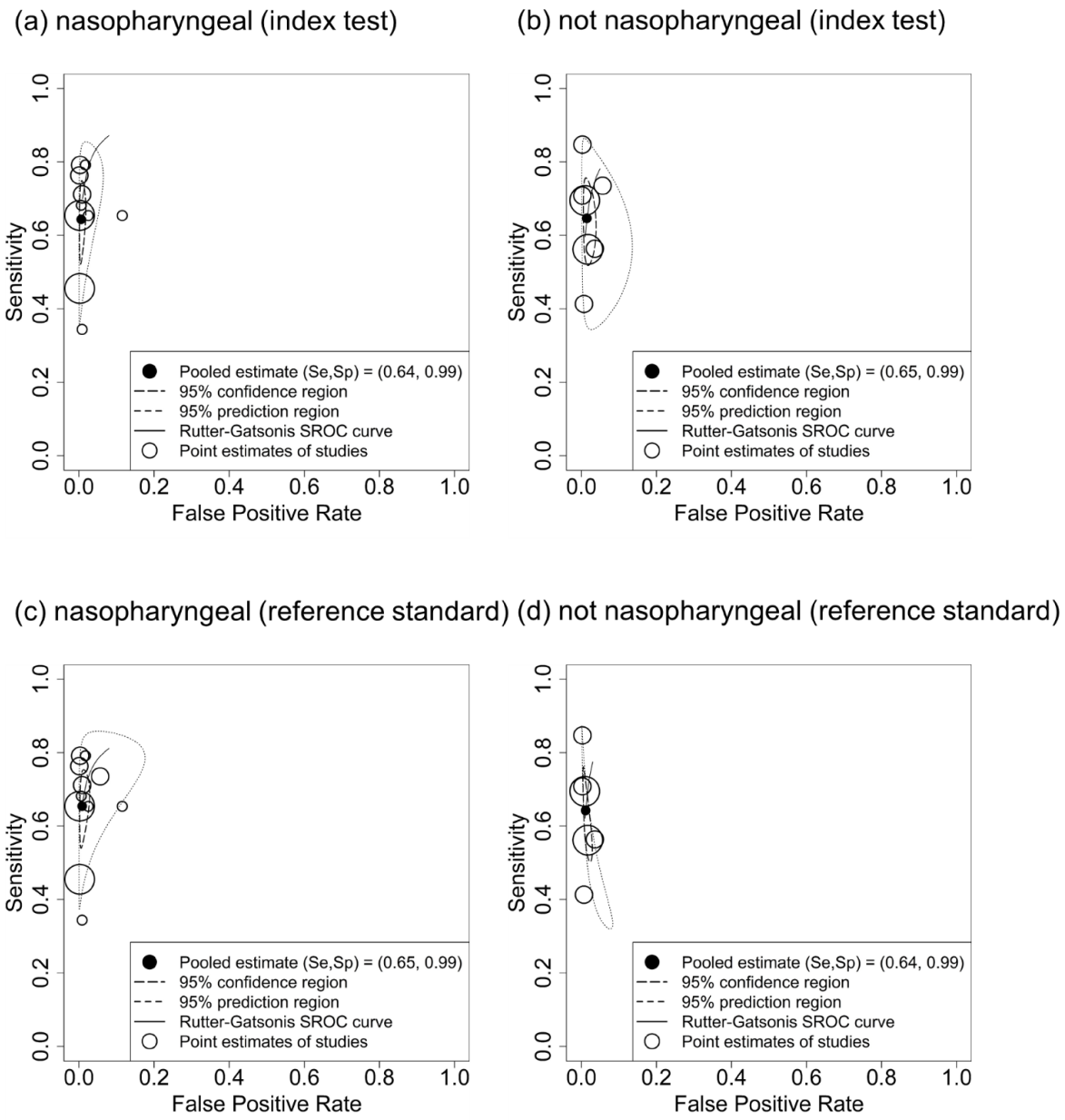

Figure S4: *Summary receiver operating characteristic (SROC) plot of sensitivity and specificity of antigen tests for diagnosis of current SARS-CoV-2 infections with respect to the sample type of index test (Ag test) and reference standard (RT-PCR). (a) nasopharyngeal (index test), (b) not nasopharyngeal (index test), (c) nasopharyngeal (reference standard), (d) not nasopharyngeal (reference standard). Each circle represents the point estimate of an individual study, whereas the size of the circle correlates with the number of paediatric study participants (small circle: <100 participants, medium circle: between 100 and 500 participants, large circle: >500 participants). The pooled estimate (black dot) of the pair of sensitivity (Se) and specificity (Sp) is surrounded by its 95% confidence region (closed curve with short dashes) and prediction region (closed curve with long dashes). The estimation of the SROC curve is based on the bivariate approach by Rutter and Gatsonis* [19].

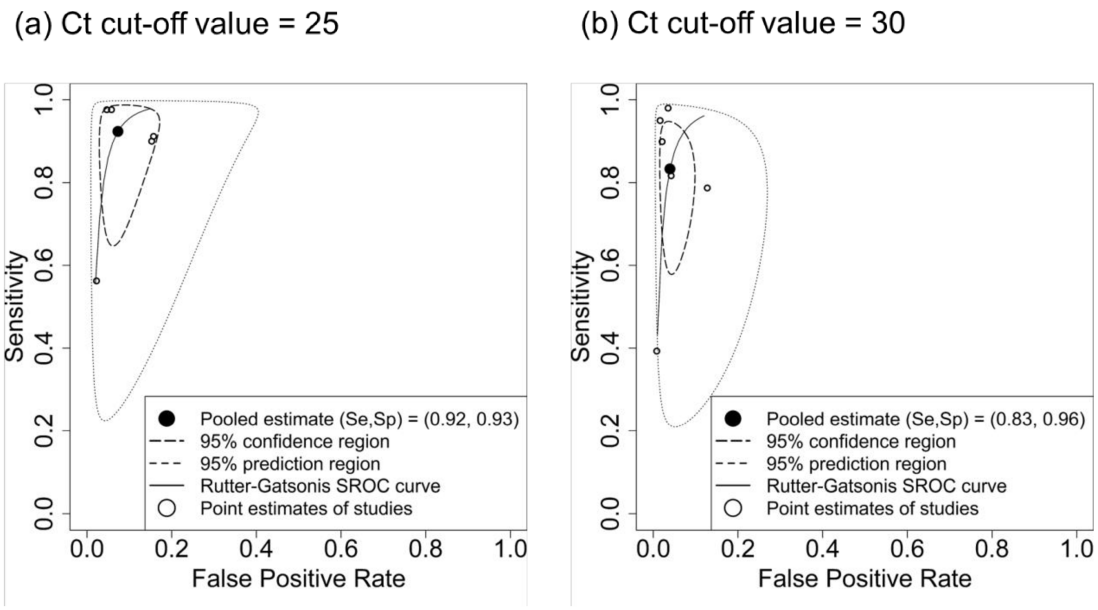

Figure S5: *Summary receiver operating characteristic (SROC) plot of sensitivity and specificity of antigen tests for diagnosis of current SARS-CoV-2 infections with respect to the chosen RT-PCR positivity threshold.* (a) Ct cut-off value = 25, (b) Ct cut-off value = 30. *Each circle represents the point estimate of an individual study, whereas the size of the circle correlates with the number of paediatric study participants (small circle: <100 participants, medium circle: between 100 and 500 participants, large circle: >500 participants). The pooled estimate (black dot) of the pair of sensitivity (Se) and specificity (Sp) is surrounded by its 95% confidence region (closed curve with short dashes) and prediction region (closed curve with long dashes). The estimation of the SROC curve is based on the bivariate approach by Rutter and Gatsonis* [19].

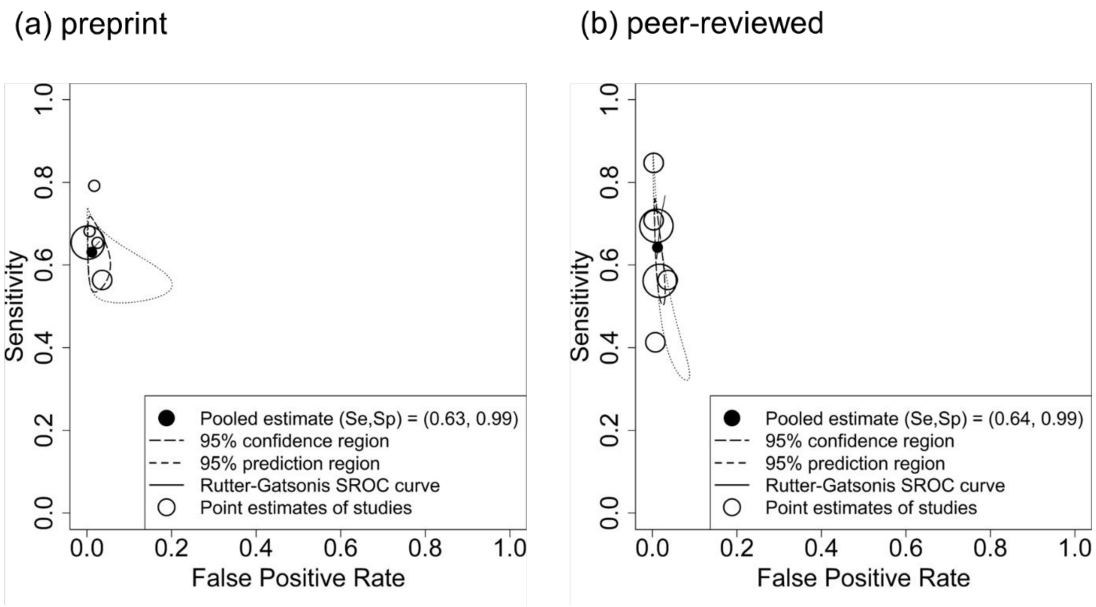

Figure S6: *Summary receiver operating characteristic (SROC) plot of sensitivity and specificity of antigen tests for diagnosis of current SARS-CoV-2 infections with respect to the publication status.* (a) preprint, (b) peer-reviewed. *Each circle represents the point estimate of an individual study, whereas the size of the circle correlates with the number of paediatric study participants (small circle: <100 participants, medium circle: between 100 and 500 participants, large circle: >500 participants). The pooled estimate (black dot) of the pair of sensitivity (Se) and specificity (Sp) is surrounded by its 95% confidence region (closed curve with short dashes) and prediction region (closed curve with long dashes). The estimation of the SROC curve is based on the bivariate approach by Rutter and Gatsonis* [19].

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