

1 **SUPPLEMENTARY FIGURES AND TABLES**

2 **Effect of water, sanitation, and hygiene interventions on detection of**  
3 **enteropathogens and host-specific fecal markers in the environment: an individual-**  
4 **participant data meta-analysis**

5 Andrew Mertens PhD, Benjamin F. Arnold PhD, Jade Benjamin-Chung PhD, Prof Alexandria B. Boehm PhD, Joe  
6 Brown PhD, Drew Capone PhD, Prof Thomas Clasen PhD, Erica Fuhrmeister PhD, Jessica A. Grembi PhD, David  
7 Holcomb PhD, Jackie Knee PhD, Laura H Kwong PhD, Audrie Lin PhD, Prof Stephen P. Luby MD, Rasul Nala MPH,  
8 Prof Kara Nelson PhD, Sammy M. Njenga PhD, Clair Null PhD, Amy J. Pickering PhD, Mahbubur Rahman MBBS,  
9 Heather E. Reese PhD, Lauren Steinbaum PhD, Prof Jill Stewart PhD, Ruwan Thilakaratne MPH, Oliver Cumming  
10 PhD, Prof John M. Colford Jr. MD, Ayse Ercumen PhD

11 **TABLE OF CONTENTS**

12

13       Supplementary FIGURES AND TABLES..... 1

14       Figure S1..... 2

15       Figure S2..... 2

16       Figure S3..... 2

17       Figure S4..... 2

18       Figure S5..... 2

19       Figure S6..... 2

20       Figure S7 ..... 2

21       Figure S8..... 2

22       Figure S9..... 2

23       Figure S10... ..... 2

24       Table S1. Systematic review search terms .....13

25       Table S2. Pubmed search string.....13

26       Table S3. PRISMA Checklist.....15

27       Table S4. Risk of bias based on modified Newcastle-Ottawa scale .....21

28       Table S5. Prevalence of pathogens by sample type tested in each study .....24

29       Table S6. Prevalence of microbial source tracking markers by sample type tested in each study .....26

30       Table S7. Unadjusted and adjusted results by study, sample type, and aggregated variables for pathogen

31       targets.....28

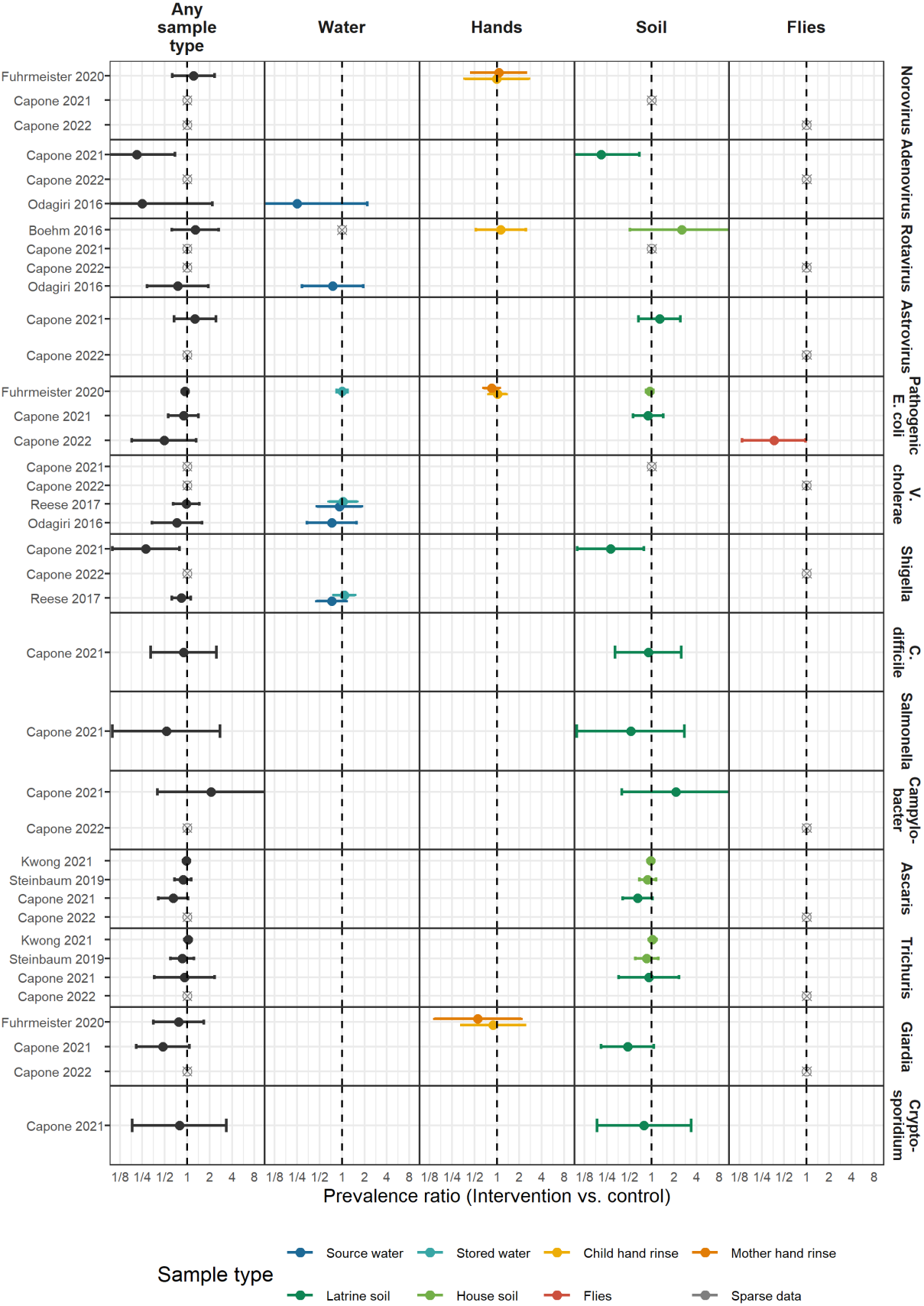
32       Table S8. Unadjusted and adjusted results by study, sample type, and aggregated variables for MST

33       targets.....32

34       Table S9. Baseline covariates by study .....36

35

36

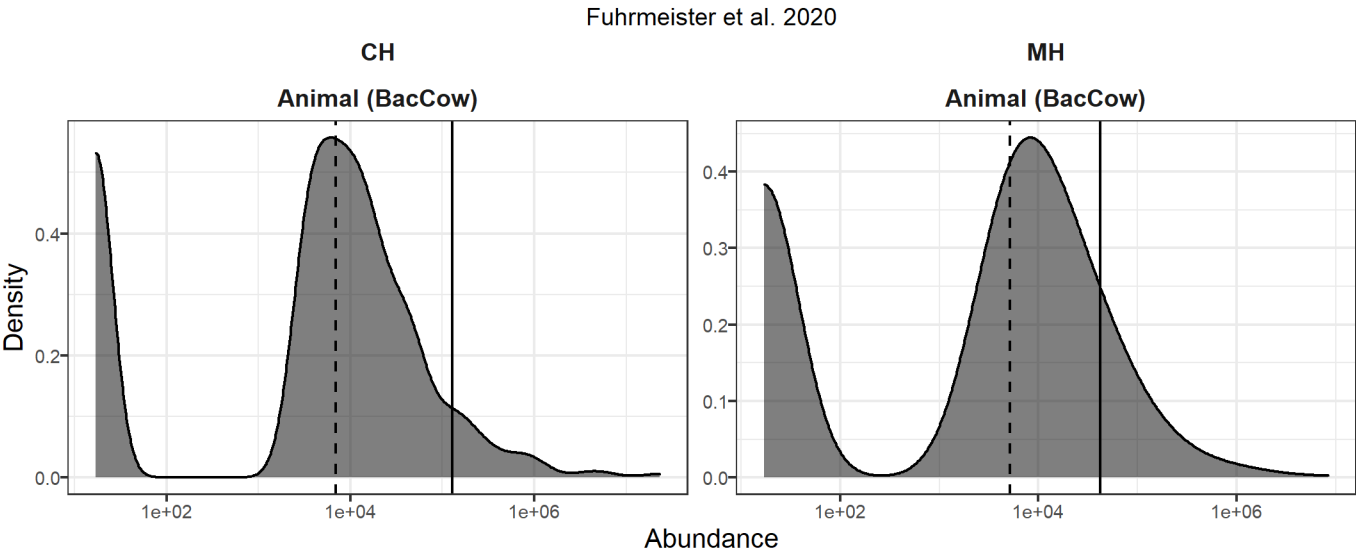
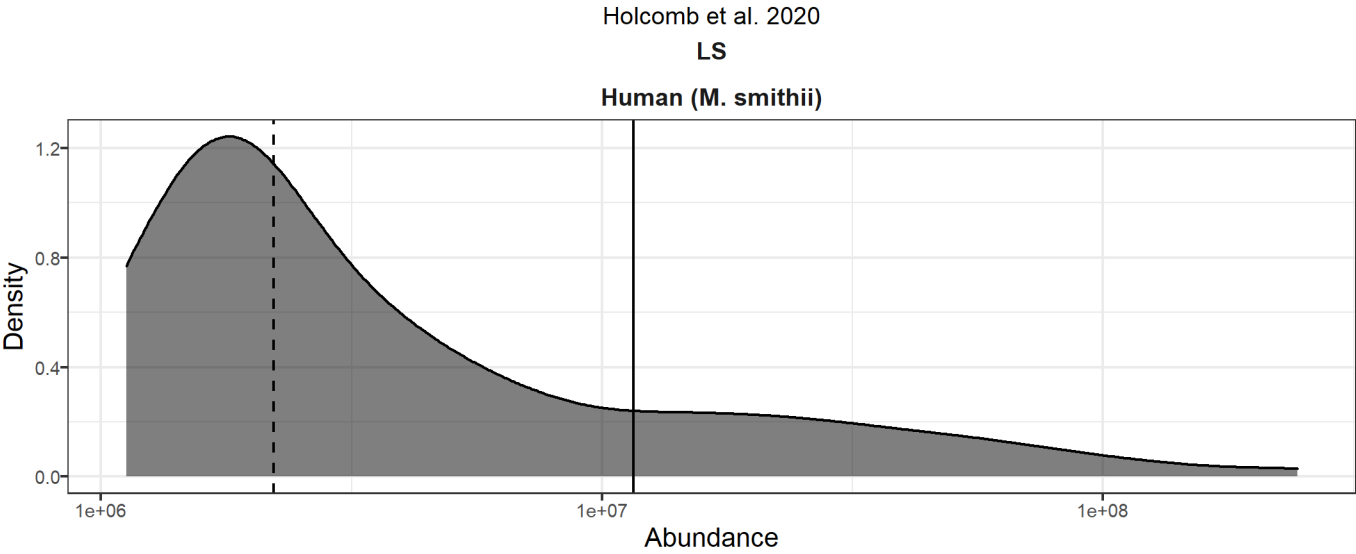
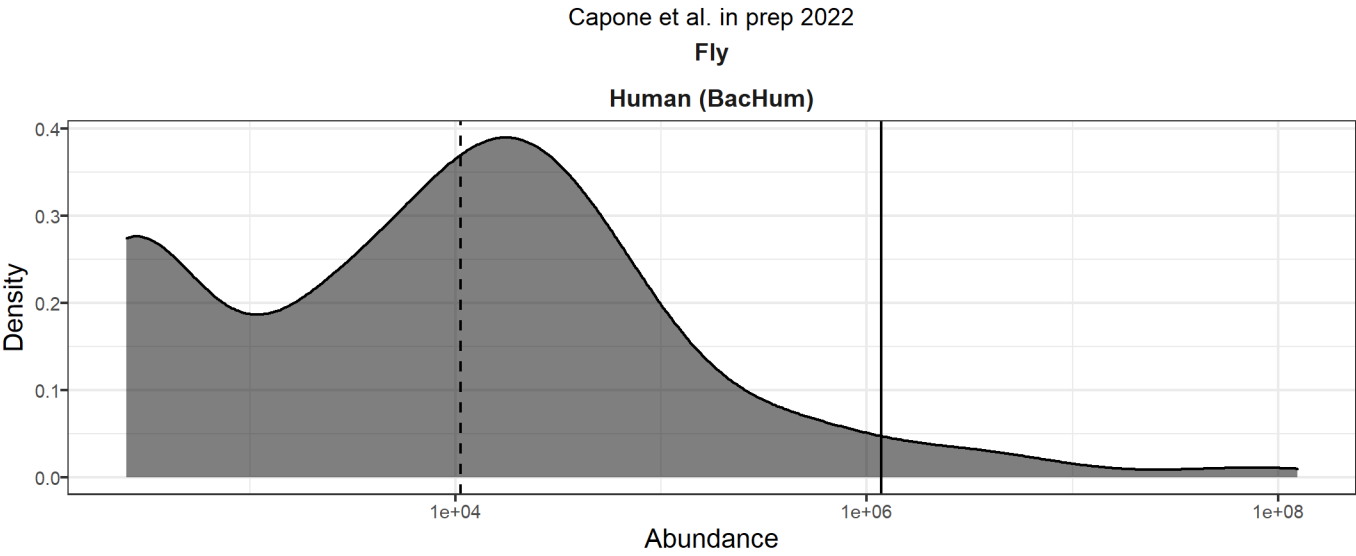


**Figure S1** Forest plots of intervention effects on the prevalence of specific pathogens

41

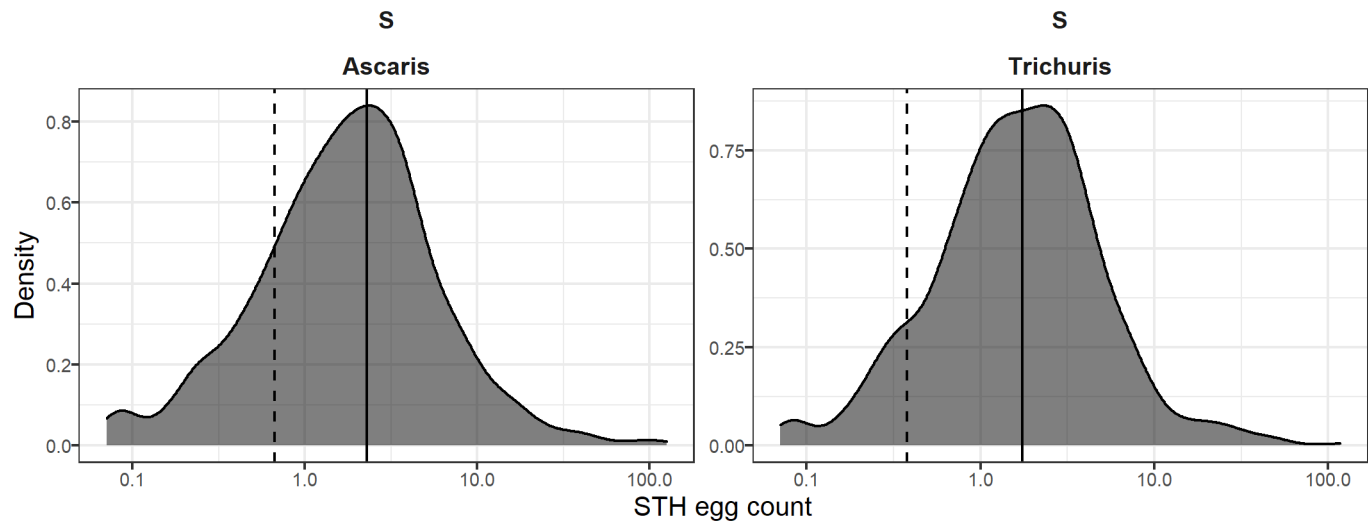


**Figure S2.** Forest plots of intervention effects on the prevalence of specific MST markers.



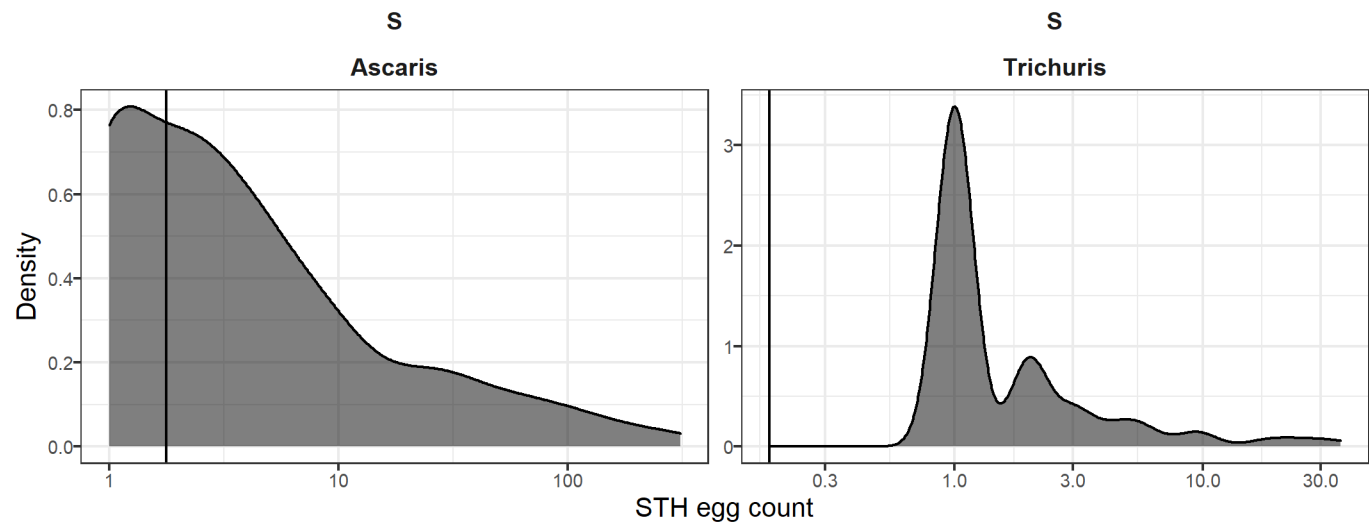
46

Kwong et al. 2021



47

Steinbaum et al. 2019



48

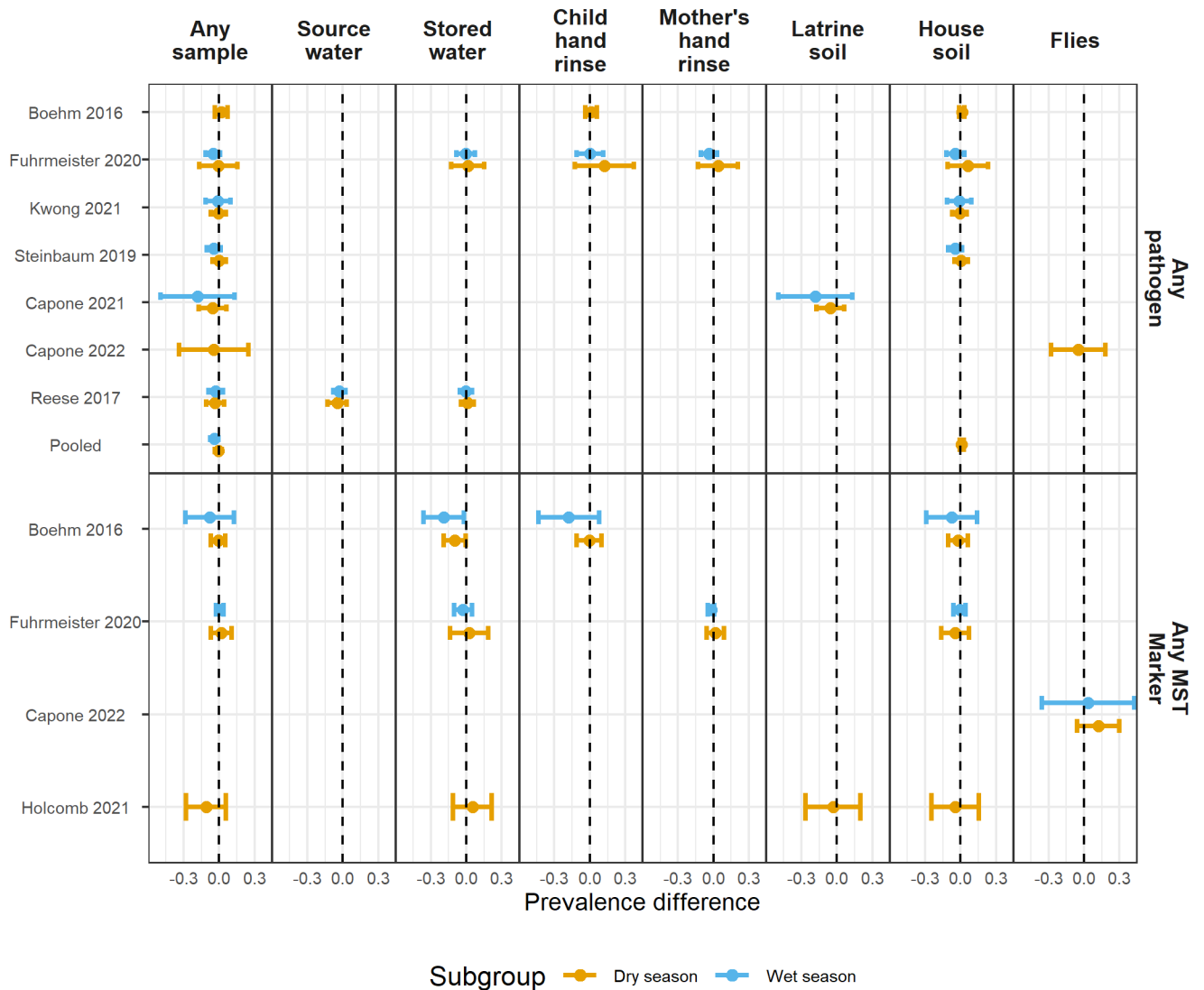
49

50

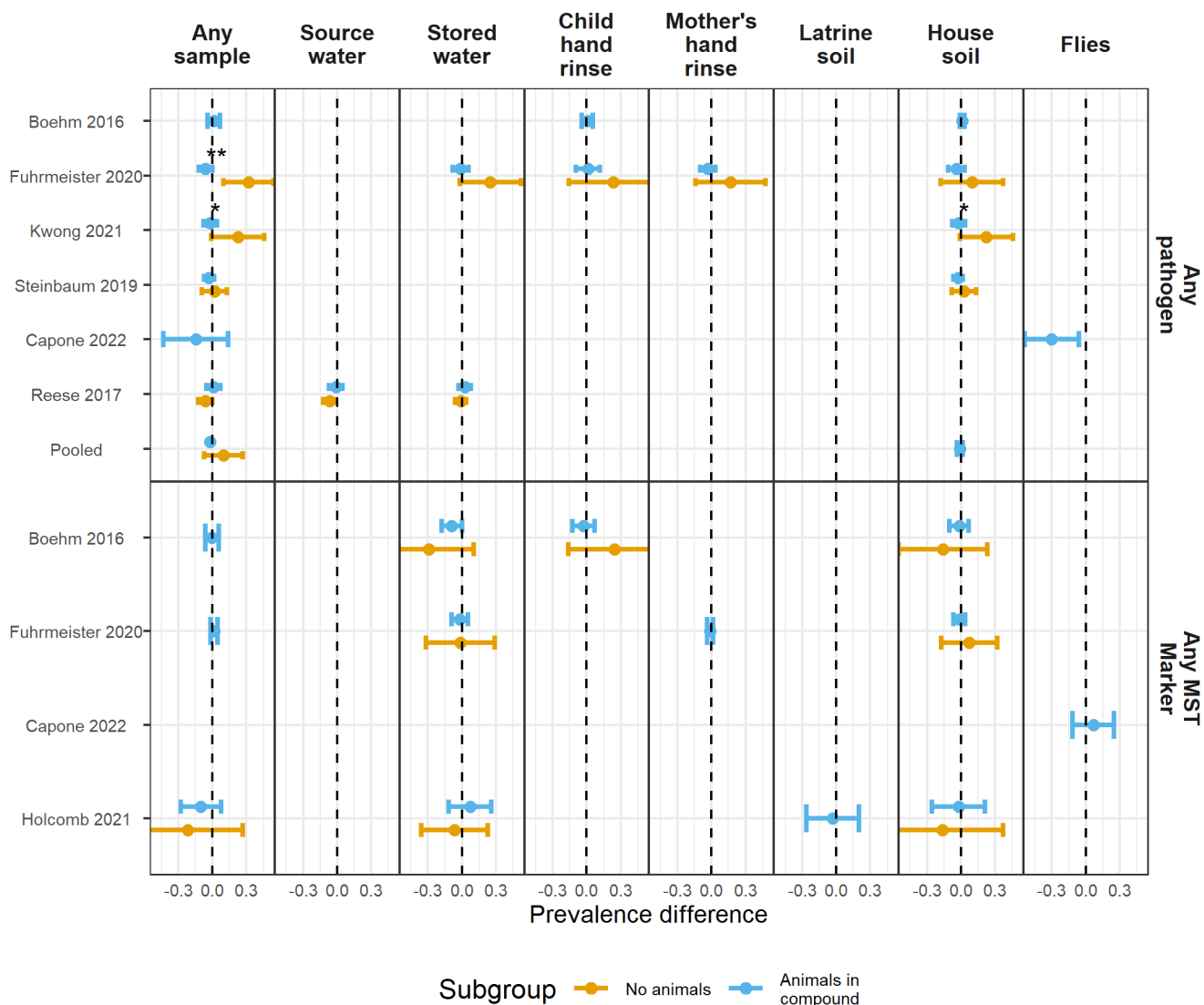
51

52

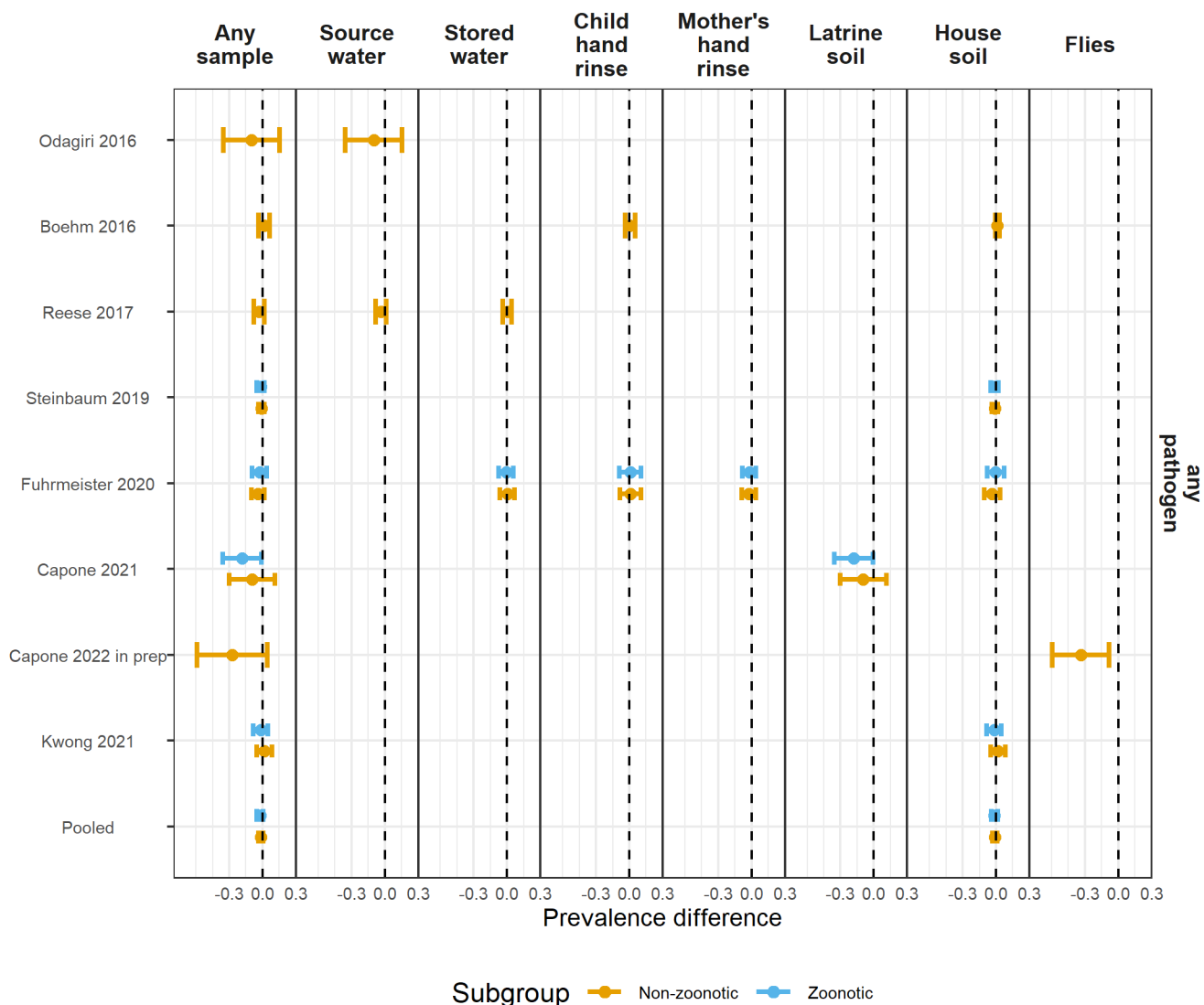
**Figure S3.** Distributions of abundance outcomes. The X-axes are displayed on the log-10 scale. Black vertical lines mark the means, and dashed lines mark the medians. Values below the limit of detection were imputed with with half the limit of detection and values below the limit of quantification were imputed with the midpoint between the limits of detections and quantification, leading to some bimodal distributions.



**Figure S4.** Forest plots of any enteropathogen prevalence differences or any MST prevalence differences between intervention and control arms, stratified by whether the sample was collected during the wet versus dry season (defined by the 6 months of highest average rainfall). Significant effect modification, as determined by the p-values on the regression model interaction term, is marked above points with asterisks (P < 0.05 = \*, P < 0.01 = \*\*, P < 0.001 = \*\*\*). Grey crossed points denote data that were too sparse to estimate a prevalence ratio (i.e., <10 positive observations).

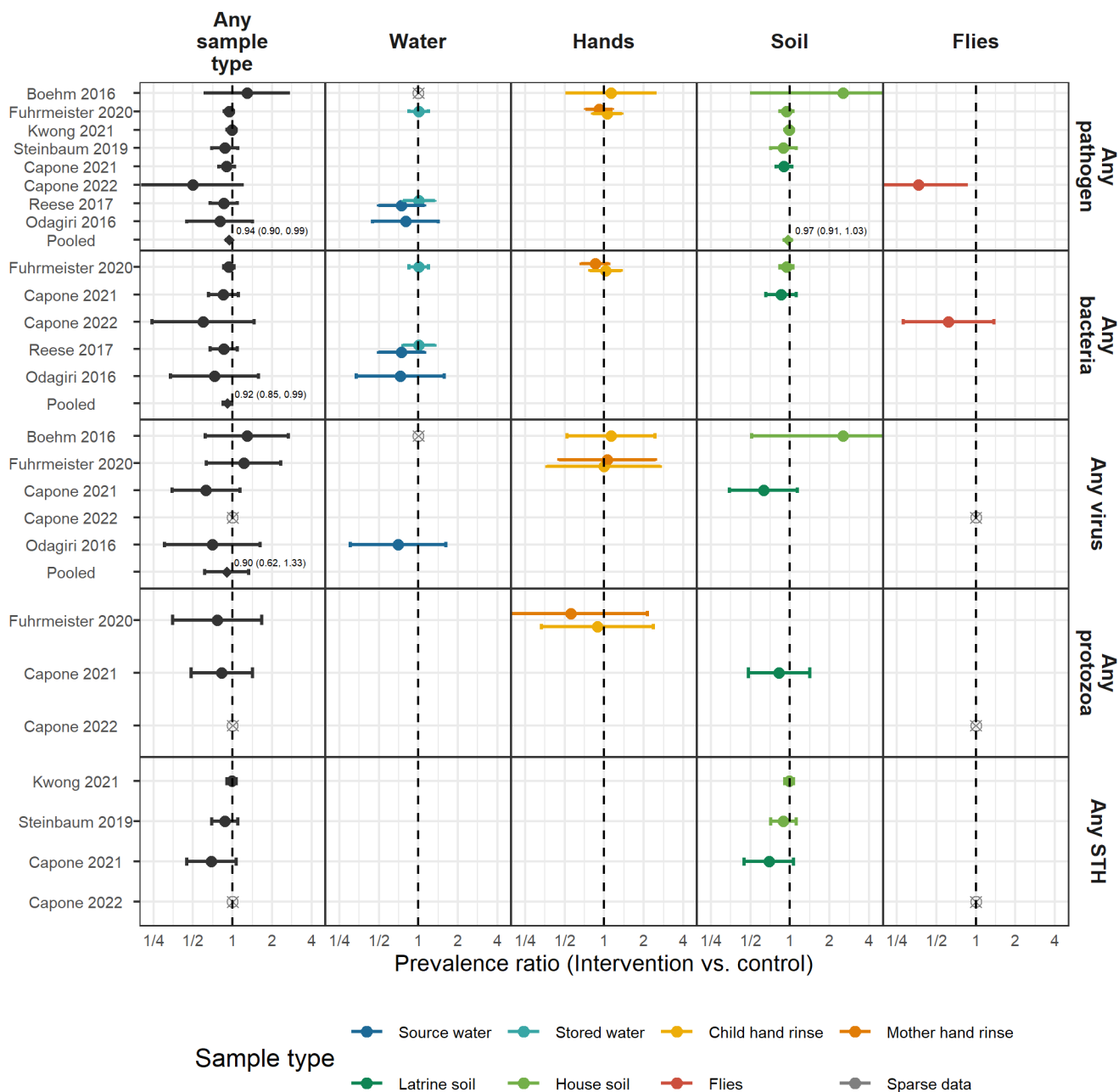


**Figure S5.** Forest plots of any enteropathogen prevalence differences or any MST prevalence differences between intervention and control arms, stratified by whether any animals were present in the compound. Significant effect modification, as determined by the p-values on the regression model interaction term, is marked above points with asterisks ( $P < 0.05 = *$ ,  $P < 0.01 = **$ ,  $P < 0.001 = ***$ ). Grey crossed points denote data that were too sparse to estimate a prevalence ratio (i.e.,  $<10$  positive observations).

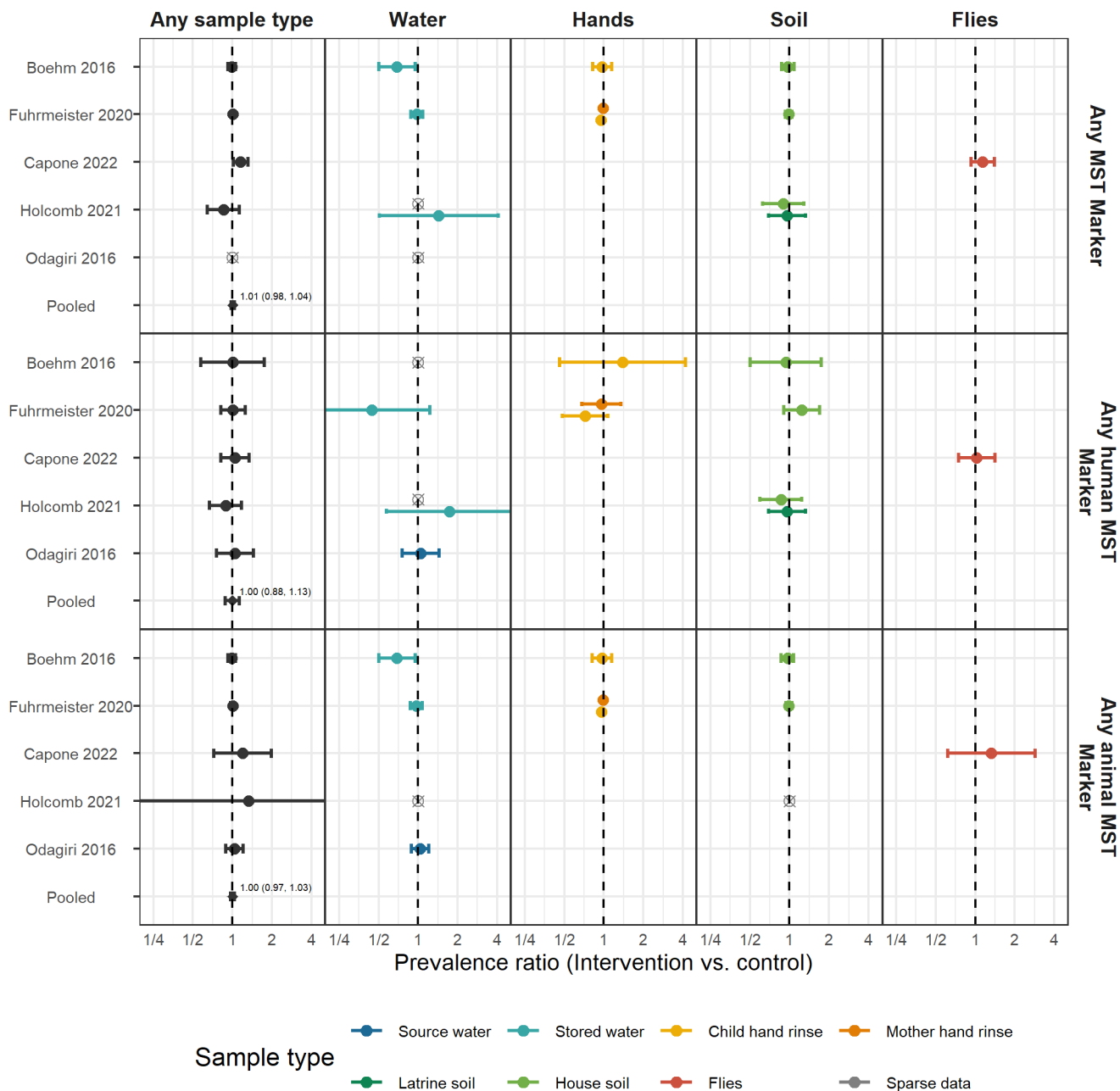


**Figure S6.** Forest plots of any enteropathogen prevalence differences or any MST prevalence differences between intervention and control arms, stratified by whether the pathogen is zoonotically transmitted. Grey crossed points denote data that were too sparse to estimate a prevalence ratio (i.e., <10 positive observations). Significant effect modification, as determined by the p-values on the regression model interaction term, is marked above points with asterisks ( $P < 0.05 = *$ ,  $P < 0.01 = **$ ,  $P < 0.001 = ***$ ). Grey crossed points denote data that were too sparse to estimate a prevalence ratio (i.e., <10 positive observations).

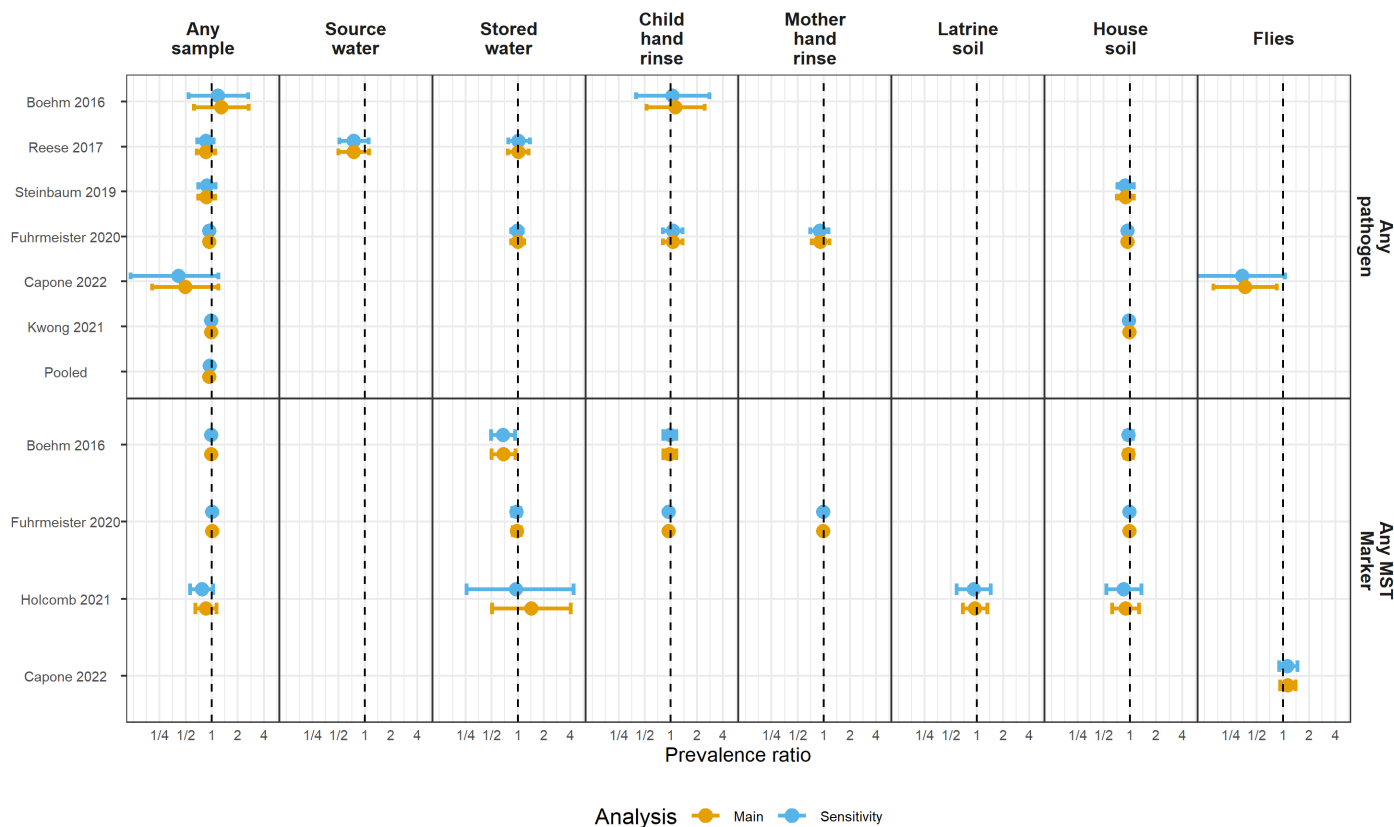




**Figure S7.** Forest plots of unadjusted intervention effects on the prevalence of any enteropathogen or type of enteropathogen (any bacteria, any virus, any protozoa and any STH) in different types of environmental samples. Point estimates and confidence intervals are printed next to pooled estimates. Grey crossed points denote data that were too sparse to estimate a prevalence ratio (i.e., <10 positive observations).



**Figure S8.** Forest plots of unadjusted intervention effects on the prevalence of any MST marker or type of MST marker (human or animal MST markers) in different types of environmental samples. Point estimates and confidence intervals are printed next to pooled estimates. Grey crossed points denote data that were too sparse to estimate a prevalence ratio (i.e., <10 positive observations).



**Figure S9.** Forest plots of results from the primary analysis (orange) compared to a sensitivity analysis to the covariate prescreening method (blue) for the outcomes of any pathogen detection (top row) and any MST marker detection (bottom row) for different studies and sample types (columns). The sensitivity analysis used LASSO penalized regressions to select covariates across 200 bootstrap iterations with replacement, with 95% confidence intervals estimated with using the quantile method.



## Table S1. Systematic review search terms

Search terms were combined with “OR” within columns and with “AND” across columns. We developed a search strategy from a two-step process. First, known key studies prior to the systematic review (WASH Benefits, Mapsan, Gram Vikas, Odisah [Table 1]) were examined for keywords and Medical Subject Heading (MeSH) terms relating to each of the following categories of terms comprising our search string: WASH interventions; microbial source tracking and environmental contamination; enteric infection; diarrhea; and child growth and development. Next, we performed an initial search using these terms and extracted other relevant terms and synonyms from relevant articles in the search results, resulting in the final list presented in this table.

Study design	WASH	Environmental markers	Child health
matched, trial, RCT, experiment, intervention, randomized, randomised, quasi-randomized, quasi-randomised, quasi-experimental, pseudo-randomized, pseudo-randomised, non-randomized controlled trials	Water, Sanitation, Hygiene, Handwashing, WSH, Sanitation, Water Supply, Sanitary Drainage, Toilet Facilities, Drinking Water, Hand Hygiene, Water Purification, Waste Water, disinfection	molecular source tracking, microbial source tracking, microbial transmission, diarrheal pathogen, diarrheal pathogens, diarrhoeal pathogen, diarrhoeal pathogens, fecal-oral, faecal-oral, entericpathogen, entericpathogens, ruminant, avian, Feces, Faeces, Fecal, Faecal, Fecally, Faecally	Entericinfection, Soil-transmitted helminth, Protozoan, Seroconversion, Fecal microbiology, Faecal microbiology, Fecal biomarker, Faecal biomarker, Intestinal Diseases, Parasitic, Seroconversion, Enteritis, Helminthiasis, Helminthiases, Intestinal infection, Viral infection, Bacterial infection, Parasite infection, Parasitic infection, Helminth infection, Fecal sampling, Faecal sampling, Stool sampling, Stool collection, Diarrhea, Dysentery, Child growth faltering, Growth faltering, Child development, Length-for-age, Height-for-age, Weight-for-age, Head circumference, Waist circumference, Stunting, Stunted, Wasting, Wasted, Linear growth, Anthropometric measurement, Malnutrition, Undernourished, Undernutrition, Underweight, Growth Disorders, Childnutrition disorder, Wasting syndrome, Thinness, Growth velocity

## Table S2. Pubmed search string

[MH] are mesh headers and [TW] are text words. Search strings for other databases are available in the Open Science Framework analysis preregistration materials (<https://osf.io/8sgzn/>).

((matched [tw]) OR (trial [tw]) OR (RCT [tw]) OR (experiment [tw]) OR (intervention [tw]) OR (randomized [tw]) OR (randomised [tw]) OR (quasi-randomized [tw]) OR (quasi-randomised [tw]) OR (quasi-experimental [tw]) OR (pseudo-randomized [tw]) OR (pseudo-randomised [tw]) OR (“non-randomized controlled trials as topic” [mh])) AND ((Water [tw]) OR (Sanitation [tw]) OR (Hygiene [tw]) OR (Handwashing [tw]) OR (WSH [tw]) OR (“Sanitation” [mh]) OR (“Water Supply” [mh]) OR (“Drainage, Sanitary” [mh]) OR (Sanitary Drainage [tw]) OR (“Toilet Facilities” [mh]) OR (“Drinking Water” [mh]) OR (“Hand Hygiene” [mh]) OR (“Water Purification” [mh]) OR (“Waste Water” [mh]) OR (disinfect\* [tw])) AND ((molecular source tracking [tw]) OR (microbial source tracking [tw]) OR (microbial transmission [tw]) OR (diarrheal pathogen [tw]) OR (diarrheal pathogens [tw]) OR (diarrhoeal pathogen [tw]) OR (diarrhoeal pathogens [tw]) OR (fecal-oral [tw]) OR (faecal-oral [tw]) OR (enteric pathogen [tw]) OR (enteric pathogens [tw]) OR (ruminant\* [tw]) OR (avian\* [tw]) OR (“Feces” [mh]) OR (Feces [tw]) OR (Faeces [tw]) OR (Fecal [tw]) OR (Faecal [tw]) OR (Fecally [tw]) OR (Faecally [tw])) AND (((Enteric infection\* [tw]) OR (Soil-transmitted helminth\* [tw]) OR (Protozoan\* [tw]) OR (Seroconversion [tw]) OR (Fecal microbio\* [tw]) OR (Faecal microbio\* [tw]) OR (Fecal biomarker\* [tw]) OR (Faecal biomarker\* [tw]) OR (“Intestinal Diseases,

Parasitic/epidemiology" [mh]) OR ("Seroconversion" [mh]) OR (Seroconversion [tw]) OR ("Enteritis/epidemiology" [mh]) OR ("Helminthiasis/complications" [mh]) OR (Helminthiasis [tw]) OR (Helminthiasis) OR ("Helminthiasis/epidemiology" [mh]) OR ("Helminthiasis/prevention and control" [mh]) OR (Intestinal infection\* [tw]) OR (Viral infection\* [tw]) OR (Bacterial infection\* [tw]) OR (Parasite infection\* [tw]) OR (Parasitic infection\* [tw]) OR (Helminth infection\* [tw]) OR (Fecal sampling [tw]) OR (Faecal sampling [tw]) OR (Bacterial infection\* [tw]) OR (Parasite infection\* [tw]) OR (Parasitic infection\* [tw]) OR (Helminth infection\* [tw]) OR (Fecal sampling [tw]) OR (Faecal sampling [tw]) OR (Stool sampling [tw]) OR (Stool collection [tw])) OR ((Diarrh\* [tw]) OR (Dysentery [tw]) OR ("Diarrhea/epidemiology" [mh]) OR ("Diarrhea/etiology" [mh]) OR ("Diarrhea/prevention and control" [mh]) OR ("Diarrhea, Infantile" [mh]) OR ("Dysentery" [mh])) OR (Child growth faltering [tw]) OR (Growth faltering [tw]) OR (Child development [tw]) OR (Length-for-age [tw]) OR (Height-for-age [tw]) OR (Weight-for-age [tw]) OR (Head circumference [tw]) OR (Waist circumference [tw]) OR (Stunt\* [tw]) OR (Wasting [tw]) OR (Wasted [tw]) OR (Linear growth [tw]) OR (Anthropometric measurement\* [tw]) OR (Maln\* [tw]) OR (Undernourish\* [tw]) OR (Undernutrition [tw]) OR (Underweight [tw]) OR ("Growth Disorders" [mh]) OR (Growth Disorders [tw]) OR ("Child nutrition disorders" [mh]) OR (Child nutrition disorder\* [tw]) OR ("Malnutrition" [mh]) OR ("Wasting Syndrome" [mh]) OR (Wasting syndrome [tw]) OR ("Thinness" [mh]) OR (Thinness [tw]) OR (Growth velocity [tw]))

103 **Table S3. PRISMA Checklist**

Topic	o.	Item	Location where item is reported
<b>TITLE</b>			
<b>Title</b>		Identify the report as a systematic review.	Page 1
<b>ABSTRACT</b>			
<b>Abstract</b>		See the PRISMA for Abstracts checklist below	
<b>INTRODUCTION</b>			
<b>N</b>	<b>Rationale</b>	Describe the rationale for the review in the context of existing knowledge.	Introduction paragraph 2
	<b>Objectives</b>	Provide an explicit statement of the objective(s) or question(s) the review addresses.	Introduction paragraph 3
<b>METHODS</b>			
<b>Eligibility criteria</b>	<b>Eligibility criteria</b>	Specify the inclusion and exclusion criteria for the review and how studies were grouped for the syntheses.	Line 161-164
	<b>Information sources</b>	Specify all databases, registers, websites, organisations, reference lists and other sources searched or consulted to identify studies. Specify the date when each source was last searched or consulted.	Line 159-160, Fig. S1
	<b>Search strategy</b>	Present the full search strategies for all databases, registers and websites, including any filters and limits used.	Tables S1-S2
	<b>Selection process</b>	Specify the methods used to decide whether a study met the inclusion criteria of the review, including how many reviewers screened each record and each report retrieved, whether they worked independently, and if applicable, details of automation tools used in the process.	Line 169-173

Topic	o.	Item	Location where item is reported
<b>Data collection process</b>		Specify the methods used to collect data from reports, including how many reviewers collected data from each report, whether they worked independently, any processes for obtaining or confirming data from study investigators, and if applicable, details of automation tools used in the process.	Line 169-173
<b>Data items</b>	0a	List and define all outcomes for which data were sought. Specify whether all results that were compatible with each outcome domain in each study were sought (e.g. for all measures, time points, analyses), and if not, the methods used to decide which results to collect.	Line 177-179
	0b	List and define all other variables for which data were sought (e.g. participant and intervention characteristics, funding sources). Describe any assumptions made about any missing or unclear information.	Line 177-179
<b>Study risk of bias assessment</b>	1	Specify the methods used to assess risk of bias in the included studies, including details of the tool(s) used, how many reviewers assessed each study and whether they worked independently, and if applicable, details of automation tools used in the process.	Line 173-174
<b>Effect measures</b>	2	Specify for each outcome the effect measure(s) (e.g. risk ratio, mean difference) used in the synthesis or presentation of results.	Line 193-253
<b>Synthesis methods</b>	3a	Describe the processes used to decide which studies were eligible for each synthesis (e.g. tabulating the study intervention characteristics and comparing against the planned groups for each synthesis (item 5)).	Line 193-253
	3b	Describe any methods required to prepare the data for presentation or synthesis, such as handling of missing summary statistics, or data conversions.	Line 193-253
	3c	Describe any methods used to tabulate or visually display results of individual studies and syntheses.	Figure captions
	3d	Describe any methods used to synthesize results and provide a rationale for the choice(s). If meta-analysis was performed, describe the model(s), method(s) to identify the presence and extent of statistical heterogeneity, and software package(s) used.	Line 161-193



Topic	o.	Item	Location where item is reported
<b>Reporting bias assessment</b>	3e	Describe any methods used to explore possible causes of heterogeneity among study results (e.g. subgroup analysis, meta-regression).	Line 224-253
	3f	Describe any sensitivity analyses conducted to assess robustness of the synthesized results.	Line 203-253
	4	Describe any methods used to assess risk of bias due to missing results in a synthesis (arising from reporting biases).	Not applicable
	5	Describe any methods used to assess certainty (or confidence) in the body of evidence for an outcome.	Not applicable
<b>RESULTS</b>			
<b>Study selection</b>	6a	Describe the results of the search and selection process, from the number of records identified in the search to the number of studies included in the review, ideally using a flow diagram.	Figure S1
	6b	Cite studies that might appear to meet the inclusion criteria, but which were excluded, and explain why they were excluded.	Line 262-265
<b>Study characteristics</b>	7	Cite each included study and present its characteristics.	Line 219-230, Table 1
<b>Risk of bias in studies</b>	8	Present assessments of risk of bias for each included study.	Table S4
<b>Results of individual studies</b>	9	For all outcomes, present, for each study: (a) summary statistics for each group (where appropriate) and (b) an effect estimate and its precision (e.g. confidence/credible interval), ideally using structured tables or plots.	Figures 1,2 S2-S3, S5-S8, Tables 2, S6-S9
<b>Results of syntheses</b>	0a	For each synthesis, briefly summarise the characteristics and risk of bias among contributing studies.	Not applicable
	0b	Present results of all statistical syntheses conducted. If meta-analysis was done, present for each the summary estimate and its precision (e.g. confidence/credible interval) and measures of statistical heterogeneity. If comparing groups, describe the direction of the effect.	Figures1 ,2 S2-S3, S5-S8, Tables 2, S6-S9

Topic	o.	Item	Location where item is reported
<b>Reporting biases</b>	0c	Present results of all investigations of possible causes of heterogeneity among study results.	Line 370-382
	0d	Present results of all sensitivity analyses conducted to assess the robustness of the synthesized results.	Line 370-382
	1	Present assessments of risk of bias due to missing results (arising from reporting biases) for each synthesis assessed.	Not applicable
	2	Present assessments of certainty (or confidence) in the body of evidence for each outcome assessed.	Figures 1, 2 S2-S3, S5-S8, Tables 2, S6-S9
<b>DISCUSSION</b>			
<b>Discussion</b>	3a	Provide a general interpretation of the results in the context of other evidence.	Line 385-419
	3b	Discuss any limitations of the evidence included in the review.	Line 444-465
	3c	Discuss any limitations of the review processes used.	Line 444-465
	3d	Discuss implications of the results for practice, policy, and future research.	Line 466-498
<b>OTHER INFORMATION</b>			
<b>Registration and protocol</b>	4a	Provide registration information for the review, including register name and registration number, or state that the review was not registered.	<a href="https://osf.io/8sgzn/">https://osf.io/8sgzn/</a>
	4b	Indicate where the review protocol can be accessed, or state that a protocol was not prepared.	<a href="https://osf.io/8sgzn/">https://osf.io/8sgzn/</a>
	4c	Describe and explain any amendments to information provided at registration or in the protocol.	Not applicable

Topic	o.	Item	Location where item is reported
<b>Support</b>	5	Describe sources of financial or non-financial support for the review, and the role of the funders or sponsors in the review.	Line 73
<b>Competing interests</b>	6	Declare any competing interests of review authors.	Line 512
<b>Availability of data, code and other materials</b>	7	Report which of the following are publicly available and where they can be found: template data collection forms; data extracted from included studies; data used for all analyses; analytic code; any other materials used in the review.	Lines 513-516

104

Topic	o.	Item	Re ported?
<b>TITLE</b>			
<b>Title</b>		Identify the report as a systematic review.	Yes
<b>UND</b>			
<b>BACKGRO</b>			
<b>Objective</b>		Provide an explicit statement of the main objective(s) or question(s) the review addresses.	Yes
<b>S</b>			
<b>METHOD</b>			
<b>S</b>			
<b>Eligibility criteria</b>		Specify the inclusion and exclusion criteria for the review.	Yes
<b>Information sources</b>		Specify the information sources (e.g. databases, registers) used to identify studies and the date when each was last searched.	No

Topic	No.	Item	Reported?
<b>Risk of bias</b>		Specify the methods used to assess risk of bias in the included studies.	Yes
<b>Synthesis of results</b>		Specify the methods used to present and synthesize results.	Yes
<b>RESULTS</b>			
<b>Included studies</b>		Give the total number of included studies and participants and summarise relevant characteristics of studies.	Yes
<b>Synthesis of results</b>		Present results for main outcomes, preferably indicating the number of included studies and participants for each. If meta-analysis was done, report the summary estimate and confidence/credible interval. If comparing groups, indicate the direction of the effect (i.e. which group is favoured).	Yes
<b>DISCUSSION</b>			
<b>Limitations of evidence</b>		Provide a brief summary of the limitations of the evidence included in the review (e.g. study risk of bias, inconsistency and imprecision).	Yes
<b>Interpretation</b>	0	Provide a general interpretation of the results and important implications.	Yes
<b>OTHER</b>			
<b>Funding</b>	1	Specify the primary source of funding for the review.	Yes
<b>Registration</b>	2	Provide the register name and registration number.	Yes

**Table S4.** Risk of bias based on modified Newcastle-Ottawa scale

Study	Refer ence	Select ion bias	Respo nse bias	Follo w-up bias	Misclassi fication bias	Outco me assessment	Outco me measurement	Bias in analysis	Total
		Is there evidence of selection bias, which refers to systematic differences between baseline characteristics of the groups that are compared? <sup>a</sup>	Is there evidence of response bias? <sup>b</sup>	Is there evidence of bias due to missing follow-up data? <sup>c</sup>	Is there risk of households not receiving the intervention being misclassified as having received it, or vice versa? <sup>d</sup>	Is there evidence of bias arising from how the outcome was assessed? <sup>e</sup>	Is there evidence of ascertainment bias? <sup>f</sup>	Is there evidence that analysis was not appropriately adjusted for clustering and/or confounding, if appropriate? <sup>g</sup>	Total number of stars (x/9 possible stars).
Clase n T, et al. Effectiveness of a rural sanitation programme on diarrhoea, soil- transmitted helminth infection, and child malnutrition in Odisha, India: a cluster- randomised trial. Lancet Glob Health. 2014.		*	* no, laboratory assessed and blinded	possib le (86% of possible weeks are reported weeks)	*	**	*	** adjusted for clustering	8
Luby, S.P. et al.. Effects of water quality, sanitation, handwashing, and nutritional interventions on diarrhoea and child growth in rural Bangladesh: a cluster randomised controlled trial. The Lancet Global Health		*	* no, laboratory assessed and blinded	* 94% complete FU	*	**	*	**	9

**Table S4.** Risk of bias based on modified Newcastle-Ottawa scale

Study	Refer ence	ion bias	Select ion bias	Respo nse bias	Follow-up bias	Follo w-up bias	Misclassi fication bias	Outco me assessment	Outco me measurement	Outco me measurement	Bias in analysis	Total
2018												
Null, C. et al., Effects of water quality, sanitation, handwashing, and nutritional interventions on diarrhoea and child growth in rural Kenya: a cluster-randomised controlled trial. The Lancet Global Health 2018			*	* no, laboratory assessed and blinded	* <1% loss to FU		* household-level interventions	**	*		**	9
Reese, H. et al. Assessing longer-term effectiveness of a combined household-level piped water and sanitation intervention on child diarrhoea, acute respiratory infection, soil-transmitted helminth infection and nutritional status: a matched cohort study in rural Odisha, India. International journal of epidemiology 2019			selecti on bias is possible, as the study is not randomized and there are some baseline differences between intervention and control group	* no, laboratory assessed and blinded	substa ntial loss to FU		* household-level interventions	**	*		**	7

**Table S4.** Risk of bias based on modified Newcastle-Ottawa scale

Study	Refer	Select	Respo	Follo	Misclassi	Outco	Outco	Bias	Total
ence	ion bias	nse bias	w-up bias	w-up bias	fication bias	me assessment	me measurement	in analysis	
J. et al. Effects of an urban sanitation intervention on childhood enteric infection and diarrhea in Maputo, Mozambique: A controlled before-and-after trial. eLife 2011		selecti on bias is possible, as the study is not randomized, but intervention and control groups were mostly balanced at baseline. Control households were more likely to have covered floors and higher quality walls and intervention groups had more people per household.	* no, laboratory assessed and blinded	substa ntial loss to FU	* household-level interventions	**	*	**	7

<sup>a</sup> RCTs receive 1 star, unless evidence of selection bias (e.g. randomisation procedures not followed). Meaningful differences between groups at baseline in RCTs receive 0 stars. Rates of declining to participate >10% receive 0 stars. Non- or quasi-randomised studies receive 0 stars.

<sup>b</sup> If intervention recipient was not blinded to intervention status, 0 stars.

<sup>c</sup> <10% receives 1 star, greater than or equal to 10% receives 0 stars.

<sup>d</sup> Interventions delivered at the household/individual level receive 1 star. Interventions delivered at the community level that missed a substantial, i.e. greater than or equal to 10%, proportion of the target population receive 0 stars, including when there is insufficient information to verify whether this is the case. Interventions with substantial risk of contamination (control households receiving intervention) receive 0 stars.

<sup>e</sup> Parent / person recall (=0 stars). Fieldworker assessed (=1 star). Physician/microbiologically assessed (=2 stars)

<sup>f</sup> If outcome measurement staff were not blinded to intervention status, 0 stars.

<sup>g</sup> Scoring is based on losing stars (max. 2). Individual RCTs with baseline balance on covariates are unlikely to require adjustment (=2 stars). Cluster-RCTs and non-randomised trials may require adjustment for clustering (-1 star if not done). RCTs or cRCTs may require adjustment for covariates, with justification (-1 star if not done). Non-randomised studies require adjustment for covariates (-1 star if not done), but also adequate justification for covariate selection (-1 star if not included), and there can be too few or too many covariates.

**Table S5. Prevalence of pathogens by sample type tested in each study**

Study	Sample	Target	(n/N)	Percent positive	PR (95% CI)	
Odagiri 2016	Source water	V. cholerae		31.7% (19/60)	1.57)	0.73 (0.34,
-	-	Adenovirus		8.3% (5/60)	2.19)	0.25 (0.03,
-	-	Rotavirus		23.3% (14/60)	1.93)	0.75 (0.29,
Boehm 2016	Stored water	Rotavirus		0.6% (3/493)		-
-	Child hand rinse	Rotavirus		6.1% (30/493)		-
-	House soil	Rotavirus		1.4% (7/496)	12.42)	2.52 (0.51,
Reese 2017	Source water	Shigella		10.7% (161/1499)	1.15)	0.73 (0.46,
-	-	V. cholerae		13% (36/276)	1.85)	0.93 (0.46,
-	Stored water	Shigella		10.1% (190/1874)	1.51)	1.08 (0.77,
-	-	V. cholerae		23.7% (100/422)		1.03 (0.66, 1.6)
Steinbaum 2019	House soil	Ascaris		13% (273/2107)	1.13)	0.88 (0.68,
-	-	Trichuris		6.9% (146/2107)		0.86 (0.6, 1.23)
Fuhrmeister 2020	Stored water	Pathogenic E. coli		38.6% (286/741)		1 (0.84, 1.19)
-	Child hand rinse	Pathogenic E. coli		34% (127/373)		-
-	-	Giardia		4.8% (15/311)		-
-	-	Norovirus		4.2% (14/337)		-
-	rinse	Mother's hand		24% (177/737)		-
-	-	Giardia		2.3% (14/602)		-
-	-	Norovirus		3.1% (21/684)		-
-	House soil	Pathogenic E. coli		61.3% (453/739)	1.06)	0.94 (0.84,
Capone 2021	Latrine soil	C. difficile		14.8% (13/88)		0.9 (0.32, 2.48)
-	-	Campylobacter		6.8% (6/88)	11.05)	2.09 (0.4,
-	-	Pathogenic E. coli		56.8% (50/88)	1.42)	0.89 (0.56,
-	-	Salmonella		6.8% (6/88)		0.52 (0.1, 2.76)
-	-	Shigella		21.6% (19/88)		0.28 (0.1, 0.78)
-	-	V. cholerae		0% (0/88)		-



**Table S5. Prevalence of pathogens by sample type tested in each study**

Study	Sample	Target	(n/N)	Percent positive	PR (95% CI)
-	-	Yersinia		4.5% (4/88)	-
-	-	Ascaris		60.2% (53/88)	1.02)
-	-	Trichuris		17% (15/88)	2.33)
-	-	Cryptosporidium		8% (7/88)	3.36)
-	-	Entamoeba histolytica		1.1% (1/88)	-
-	-	Giardia		31.8% (28/88)	1.07)
-	-	Adenovirus		20.5% (18/88)	0.68)
-	-	Astrovirus		29.5% (26/88)	2.43)
-	-	Norovirus		2.3% (2/88)	-
-	-	Rotavirus		4.5% (4/88)	-
-	-	Sapovirus		0% (0/88)	-
prep	Capone 2022 in	Flies			
-	-	Campylobacter		1.2% (1/86)	-
-	-	Pathogenic E. coli		30.2% (26/86)	-
-	-	Shigella		2.3% (2/86)	-
-	-	V. cholerae		2.3% (2/86)	-
-	-	Ascaris		0% (0/86)	-
-	-	Trichuris		3.5% (3/86)	-
-	-	Giardia		4.7% (4/86)	-
-	-	Adenovirus		4.7% (4/86)	-
-	-	Astrovirus		0% (0/86)	-
-	-	Norovirus		2.3% (2/86)	-
-	-	Pan enterovirus		0% (0/86)	-
-	-	Rotavirus		1.2% (1/86)	-
-	-	Sapovirus		0% (0/86)	-
Kwong 2021	House soil	Ascaris		62.1% (886/1426)	1.08)
-	-	Trichuris		56% (798/1426)	1.15)

**Table S6. Prevalence of microbial source tracking markers by sample type tested in each study**

Study	Sample	Target	Percent positive (n/N)		PR (95% CI)
Odagiri 2016	Source water	Animal (BacCow)	91.7% (55/60)	1.21)	1.04 (0.89,
-	-	Human (BacHum)	71.7% (43/60)	1.45)	1.05 (0.76,
Boehm 2016	Stored water	Avian (GFD)	9.3% (46/493)	1.36)	0.71 (0.37,
-	-	Ruminant (BacR)	21.9% (108/493)	0.9)	0.62 (0.43,
-	-	Human (HumM2)	0% (0/493)	-	-
-	Child hand rinse	Avian (GFD)	16.2% (80/493)	-	-
-	-	Ruminant (BacR)	54.2% (267/493)	-	-
-	-	Human (HumM2)	2.4% (12/493)	-	-
-	House soil	Avian (GFD)	33.3% (165/496)	1.27)	0.98 (0.76,
-	-	Ruminant (BacR)	66.7% (331/496)	1.12)	0.98 (0.85,
-	-	Human (HumM2)	8.9% (44/496)	1.75)	0.94 (0.5,
Fuhrmeister 2020	Stored water	Animal (BacCow)	68.5% (482/704)	1.08)	0.97 (0.87,
-	-	Human (HumM2)	2.6% (17/651)	1.23)	0.44 (0.16,
-	Child hand rinse	Animal (BacCow)	97.5% (356/365)	-	-
-	-	Human (HumM2)	21.9% (74/338)	-	-
-	rinse	Mother's hand	Animal (BacCow)	96.7% (702/726)	-
-		Human (HumM2)	18.1% (118/651)	-	-
-	House soil	Animal (BacCow)	90.6% (572/631)	1.04)	0.99 (0.94,
-	-	Human (HumM2)	20.1% (127/631)	1.7)	1.24 (0.91,
Holcomb 2021	Source water	Avian (GFD)	0% (0/41)	-	-
-	-	Human (HF183)	2.4% (1/41)	-	-
-	-	Human (M. smithii)	0% (0/41)	-	-
-	Stored water	Avian (GFD)	1.1% (1/94)	-	-
-	-	Human (HF183)	14.9% (14/94)	5.18)	1.72 (0.57,
-	-	Human (M. smithii)	0% (0/94)	-	-
-	Latrine soil	Avian (GFD)	3.3% (2/60)	-	-

**Table S6. Prevalence of microbial source tracking markers by sample type tested in each study**

Study	Sample	Target	Percent positive (n/N)		PR (95% CI)
-	-	Human (HF183)	50% (30/60)	1.52)	0.88 (0.51,
-	-	Human (M. smithii)	45% (27/60)	1.55)	0.74 (0.36,
-	House soil	Avian (GFD)	3.6% (3/83)		-
-	-	Human (HF183)	42.2% (35/83)	1.34)	0.81 (0.49,
-	-	Human (M. smithii)	24.1% (20/83)	2.73)	1.3 (0.62,
prep	Capone 2022 in	Animal (BacCow)	12.8% (11/86)		-
	-	Dog (BacCan)	30.2% (26/86)		-
	-	Human (BacHum)	72.1% (62/86)		-

**Table S7.**  
Unadjusted and adjusted results by study, sample type, and aggregated variables for pathogen targets (any pathogen, any bacteria, any viruses, any protozoa, any STH).

Study	Pathogen target	Sample type	Positive, Intervention	Negative, Intervention	Positive, Control	Negative, Control	Total observations	Unadjusted Prevalence Ratio	adjusted p-value	Unadjusted Prevalence Ratio	Adjusted Prevalence Ratio
Cabin	any pathogen	Air sample	7	13	20	17	57	PR=0.65 (95% CI: 0.33, 1.28)	1	0.2	PR=0.65 (95% CI: 0.21, 1.19)
Cabin	any pathogen	Air sample	37	6	43	2	88	PR=0.9 (95% CI: 0.78, 1.03)	3	0.1	PR=0.9 (95% CI: 0.78, 1.03)
Furniture	any pathogen	Air sample	314	136	348	123	921	PR=0.94 (95% CI: 0.87, 1.02)	7	0.1	PR=0.94 (95% CI: 0.87, 1.02)
Steiner 19	any pathogen	Air sample	206	979	173	707	2,065	PR=0.88 (95% CI: 0.7, 1.11)	9	0.2	PR=0.88 (95% CI: 0.7, 1.11)
Recess	any pathogen	Air sample	185	792	238	825	2,040	PR=0.85 (95% CI: 0.66, 1.08)	8	0.1	PR=0.85 (95% CI: 0.68, 1.09)
Boys	any pathogen	Air sample	19	229	15	234	497	PR=1.27 (95% CI: 0.6, 2.68)	3	0.5	PR=1.27 (95% CI: 0.62, 2.66)
Odors	any pathogen	Air sample	12	18	15	15	60	PR=0.8 (95% CI: 0.45, 1.42)	5	0.4	PR=0.8 (95% CI: 0.45, 1.42)
Recess	any pathogen	Air source water	68	588	122	747	1,525	PR=0.74 (95% CI: 0.49, 1.12)	5	0.1	PR=0.74 (95% CI: 0.5, 1.08)
Odors	any pathogen	Air source water	12	18	15	15	60	PR=0.8 (95% CI: 0.45, 1.42)	5	0.4	PR=0.8 (95% CI: 0.45, 1.42)
Furniture	any pathogen	Air stored water	138	218	148	237	741	PR=1.01 (95% CI: 0.85, 1.2)	3	0.9	PR=1.01 (95% CI: 0.84, 1.19)
Recess	any pathogen	Air stored water	134	786	147	860	1,927	PR=1 (95% CI: 0.75, 1.32)	9	0.9	PR=1 (95% CI: 0.77, 1.34)
Boys	any pathogen	Air stored water	2	243	1	245	491	Not estimated			Not estimated
Kwame	any pathogen	Air ouse soil	363	125	687	221	1,396	PR=0.98 (95% CI: 0.91, 1.06)	7	0.6	PR=0.98 (95% CI: 0.91, 1.06)
Furniture	any pathogen	Air ouse soil	217	144	236	142	739	PR=0.96 (95% CI: 0.86, 1.08)	3	0.5	PR=0.96 (95% CI: 0.84, 1.06)
Steiner 19	any pathogen	Air ouse soil	209	1,000	173	725	2,107	PR=0.9 (95% CI: 0.72, 1.13)	5	0.3	PR=0.9 (95% CI: 0.71, 1.11)
Boys	any pathogen	Air ouse soil	5	242	2	247	496	PR=2.52 (95% CI: 0.51, 12.42)	6	0.2	PR=2.52 (95% CI: 0.51, 12.42)

**Table S7.**  
Unadjusted and adjusted results by study, sample type, and aggregated variables for pathogen targets (any pathogen, any bacteria, any viruses, any protozoa, any STH).

Study	Pathogen Target	Sample Type	Positive, Intervention	Negative, Intervention	Positive, Control	Negative, Control	Total observations	Unadjusted Prevalence Ratio	adjusted p-value	Unadjusted Prevalence Ratio	Adjusted Prevalence Ratio
Campylobacter	any pathogen	Agric. soil	37	6	43	2	88	PR=0.9 (95% CI: 0.78, 1.03)	3	0.1	PR=0.9 (95% CI: 0.78, 1.03)
Campylobacter	any pathogen	Agric. soil	8	23	25	30	86	PR=0.57 (95% CI: 0.28, 1.15)	2	0.1	PR=0.57 (95% CI: 0.16, 0.85)
Enterobacteriaceae	any pathogen	Agric. soil	75	113	72	116	376	PR=1.04 (95% CI: 0.8, 1.35)	6	0.7	PR=1.04 (95% CI: 0.81, 1.37)
Enterobacteriaceae	any pathogen	Agric. soil	96	266	110	267	739	PR=0.91 (95% CI: 0.72, 1.15)	3	0.4	PR=0.91 (95% CI: 0.72, 1.16)
Salmonella	any pathogen	Agric. soil	16	231	14	232	493	PR=1.14 (95% CI: 0.52, 2.48)	5	0.7	PR=1.14 (95% CI: 0.52, 2.44)
Campylobacter	any bacteria	Agric. sample	7	13	17	20	57	PR=0.76 (95% CI: 0.38, 1.54)	5	0.4	PR=0.76 (95% CI: 0.24, 1.46)
Campylobacter	any bacteria	Agric. sample	28	15	35	10	88	PR=0.84 (95% CI: 0.64, 1.1)		0.2	PR=0.84 (95% CI: 0.65, 1.11)
Enterobacteriaceae	any bacteria	Agric. sample	306	144	40	131	921	PR=0.94 (95% CI: 0.86, 1.03)	8	0.1	PR=0.94 (95% CI: 0.86, 1.02)
Enterobacteriaceae	any bacteria	Agric. sample	185	792	238	825	2,040	PR=0.85 (95% CI: 0.66, 1.08)	8	0.1	PR=0.85 (95% CI: 0.68, 1.09)
Shigella	any bacteria	Agric. sample	8	22	11	19	60	PR=0.73 (95% CI: 0.34, 1.57)	2	0.4	
Enterobacteriaceae	any bacteria	Drinking water	68	588	122	747	1,525	PR=0.74 (95% CI: 0.49, 1.12)	5	0.1	PR=0.74 (95% CI: 0.5, 1.08)
Shigella	any bacteria	Drinking water	8	22	11	19	60	PR=0.73 (95% CI: 0.34, 1.57)	2	0.4	
Enterobacteriaceae	any bacteria	Treated water	138	218	148	237	741	PR=1.01 (95% CI: 0.85, 1.2)	3	0.9	PR=1.01 (95% CI: 0.84, 1.19)
Enterobacteriaceae	any bacteria	Treated water	134	786	147	860	1,927	PR=1 (95% CI: 0.75, 1.32)	9	0.9	PR=1 (95% CI: 0.77, 1.34)
Enterobacteriaceae	any bacteria	Household soil	217	144	236	142	739	PR=0.96 (95% CI: 0.86, 1.08)	3	0.5	PR=0.96 (95% CI: 0.84, 1.06)
Campylobacter	any bacteria	Agric. soil	28	15	35	10	88	PR=0.84 (95% CI: 0.64, 1.1)		0.2	PR=0.84 (95% CI: 0.65, 1.11)

**Table S7.**  
Unadjusted and adjusted results by study, sample type, and aggregated variables for pathogen targets  
(any pathogen, any bacteria, any viruses, any protozoa, any STH).

Study	Pathogen target	Sample type	Positive, Intervention	Negative, Intervention	Positive, Control	Negative, Control	Total observations	Unadjusted Prevalence Ratio	adjusted p-value	Unadjusted Prevalence Ratio	Adjusted Prevalence Ratio
Cabin	any bacteria	A	8	23	21	34	86	PR=0.68 (95% CI: 0.32, 1.41)		0.3	PR=0.68 (95% CI: 0.28, 1.38)
Fu	any bacteria	A	64	122	63	124	373	PR=1.02 (95% CI: 0.78, 1.35)	8	0.8	PR=1.02 (95% CI: 0.78, 1.35)
Fu	any bacteria	A	81	281	96	279	737	PR=0.87 (95% CI: 0.68, 1.13)		0.3	PR=0.87 (95% CI: 0.67, 1.09)
Cabin	any virus	A ny sample	0	20	4	33	57	Not estimated			Not estimated
Cabin	any virus	A ny sample	16	27	22	23	88	PR=0.76 (95% CI: 0.46, 1.25)	8	0.2	PR=0.76 (95% CI: 0.35, 1.14)
Fu	any virus	A ny sample	17	330	14	338	699	PR=1.23 (95% CI: 0.63, 2.4)	4	0.5	PR=1.23 (95% CI: 0.63, 2.34)
Bo	any virus	A ny sample	19	229	15	234	497	PR=1.27 (95% CI: 0.6, 2.68)	3	0.5	PR=1.27 (95% CI: 0.62, 2.66)
Od	any virus	A ny sample	7	23	10	20	60	PR=0.7 (95% CI: 0.3, 1.62)		0.4	
Od	any virus	A ource water	7	23	10	20	60	PR=0.7 (95% CI: 0.3, 1.62)		0.4	
Bo	any virus	A tored water	2	243	1	245	491	Not estimated			Not estimated
Bo	any virus	A ouse soil	5	242	2	247	496	PR=2.52 (95% CI: 0.51, 12.42)	6	0.2	PR=2.52 (95% CI: 0.51, 12.42)
Cabin	any virus	A atrine soil	16	27	22	23	88	PR=0.76 (95% CI: 0.46, 1.25)	8	0.2	PR=0.76 (95% CI: 0.35, 1.14)
Cabin	any virus	A	0	31	5	50	86	PR=0 (95% CI: 0, 0)		0	PR=0 (95% CI: 0, 0)
Fu	any virus	A	7	162	7	161	337	PR=0.99 (95% CI: 0.37, 2.69)	9	0.9	PR=0.99 (95% CI: 0.37, 2.69)
Fu	any virus	A	11	331	10	332	684	PR=1.1 (95% CI: 0.47, 2.57)	3	0.8	PR=1.1 (95% CI: 0.45, 2.46)
Bo	any virus	A	16	231	14	232	493	PR=1.14 (95% CI: 0.52, 2.48)	5	0.7	PR=1.14 (95% CI: 0.52, 2.44)

Table S7.

Unadjusted and adjusted results by study, sample type, and aggregated variables for pathogen targets (any pathogen, any bacteria, any viruses, any protozoa, any STH).

Study	Pathogen Target	Sample Type	Positive, Intervention	Negative, Intervention	Positive, Control	Negative, Control	Total observations	Unadjusted Prevalence Ratio	Unadjusted p-value	Unadjusted Prevalence Ratio	Adjusted Prevalence Ratio
Cabin	any protozoa	Any sample	0	20	3	34	57	Not estimated			Not estimated
Cabin	any protozoa	Any sample	15	28	19	26	88	PR=0.83 (95% CI: 0.48, 1.42)	9	0.4	PR=0.83 (95% CI: 0.48, 1.42)
Fu	any protozoa	Any sample	12	293	16	291	612	PR=0.75 (95% CI: 0.35, 1.65)	8	0.4	PR=0.75 (95% CI: 0.35, 1.67)
Cabin	any protozoa	Atrine soil	15	28	19	26	88	PR=0.83 (95% CI: 0.48, 1.42)	9	0.4	PR=0.83 (95% CI: 0.48, 1.42)
Cabin	any protozoa	Any sample	0	31	4	51	86	Not estimated			Not estimated
Fu	any protozoa	Any sample	7	147	8	149	311	PR=0.89 (95% CI: 0.33, 2.38)	2	0.8	PR=0.89 (95% CI: 0.33, 2.38)
Fu	any protozoa	Any sample	5	296	9	292	602	PR=0.56 (95% CI: 0.14, 2.13)	9	0.3	PR=0.56 (95% CI: 0.14, 2.13)
Cabin	any STH	Any sample	0	20	3	34	57	Not estimated			Not estimated
Cabin	any STH	Any sample	20	23	34	11	88	PR=0.62 (95% CI: 0.43, 0.89)	1	0.0	PR=0.62 (95% CI: 0.45, 1.07)
Ste 19	any STH	Any sample	206	979	173	707	2,065	PR=0.88 (95% CI: 0.7, 1.11)	9	0.2	PR=0.88 (95% CI: 0.7, 1.11)
Kw	any STH	House soil	363	125	687	221	1,396	PR=0.98 (95% CI: 0.91, 1.06)	7	0.6	PR=0.98 (95% CI: 0.91, 1.06)
Ste 19	any STH	House soil	209	1,000	173	725	2,107	PR=0.9 (95% CI: 0.72, 1.13)	5	0.3	PR=0.9 (95% CI: 0.71, 1.11)
Cabin	any STH	Atrine soil	20	23	34	11	88	PR=0.62 (95% CI: 0.43, 0.89)	1	0.0	PR=0.62 (95% CI: 0.45, 1.07)
Cabin	any STH	Any sample	0	31	3	52	86	Not estimated			Not estimated

**Table S8.**  
Unadjusted and adjusted results by study, sample type, and aggregated variables for MST targets (any MST, any general MST, any human MST, any animal MST).

Study	Target	Sample	Positive, Intervention	Negative, Intervention	Positive, Control	Negative, Control	Observations	Total	Unadjusted Prevalence Ratio	Adjusted p-value	Unadjusted Prevalence	Adjusted Prevalence
Cabin	MST Marker	Any sample	20	0	32	5	57	PR=1.16 (95% CI: 1.02, 1.32)	3	0.0	6 (95% CI: 1.13)	PR=1.16 (95% CI: 1.02, 1.32)
Holmes	MST Marker	Any sample	41	28	44	17	130	PR=0.82 (95% CI: 0.62, 1.09)	8	0.1	6 (95% CI: 0.113)	PR=0.82 (95% CI: 0.62, 1.09)
Fu	MST Marker	Any sample	421	26	438	29	914	PR=1 (95% CI: 0.97, 1.04)		0.8	1 (95% CI: 0.104)	PR=1 (95% CI: 0.97, 1.04)
Bo	MST Marker	Any sample	220	28	222	27	497	PR=0.99 (95% CI: 0.93, 1.06)	8	0.8	9 (95% CI: 0.106)	PR=0.99 (95% CI: 0.93, 1.06)
DO	MST Marker	Any sample	30	0	28	2	60	Not estimated				Not estimated
Holmes	MST Marker	Any source water	1	21	0	19	41	Not estimated				Not estimated
DO	MST Marker	Any source water	30	0	28	2	60	Not estimated				Not estimated
Holmes	MST Marker	Any stored water	9	39	6	40	94	PR=1.44 (95% CI: 0.51, 4.08)		0.5	4 (95% CI: 0.408)	PR=1.44 (95% CI: 0.51, 4.08)
Fu	MST Marker	Any stored water	230	119	256	119	724	PR=0.97 (95% CI: 0.87, 1.07)	2	0.5	7 (95% CI: 0.108)	PR=0.97 (95% CI: 0.87, 1.07)
Bo	MST Marker	Any stored water	57	188	82	164	491	PR=0.7 (95% CI: 0.51, 0.96)	3	0.0	9 (95% CI: 0.095)	PR=0.7 (95% CI: 0.51, 0.96)
Holmes	MST Marker	Any house soil	21	18	26	18	83	PR=0.91 (95% CI: 0.6, 1.38)	6	0.6	9 (95% CI: 0.128)	PR=0.91 (95% CI: 0.6, 1.38)
Fu	MST Marker	Any house soil	283	38	297	36	654	PR=0.99 (95% CI: 0.93, 1.05)		0.7	9 (95% CI: 0.105)	PR=0.99 (95% CI: 0.93, 1.05)
Bo	MST Marker	Any house soil	180	67	187	62	496	PR=0.97 (95% CI: 0.87, 1.08)	9	0.5	7 (95% CI: 0.108)	PR=0.97 (95% CI: 0.87, 1.08)
Holmes	MST Marker	Any atrine soil	21	9	22	8	60	PR=0.95 (95% CI: 0.69, 1.32)	8	0.7	5 (95% CI: 0.132)	PR=0.95 (95% CI: 0.69, 1.32)
Cabin	MST Marker	Any	27	4	42	13	86	PR=1.14 (95% CI: 0.93, 1.39)		0.2	4 (95% CI: 0.139)	PR=1.14 (95% CI: 0.93, 1.39)
Fu	MST Marker	Any	174	11	182	1	368	PR=0.95 (95% CI: 0.91, 0.98)	1	0.0	5 (95% CI: 0.098)	PR=0.95 (95% CI: 0.91, 0.98)



**Table S8.**  
Unadjusted and adjusted results by study, sample type, and aggregated variables for MST targets  
(any MST, any general MST, any human MST, any animal MST).

Study	Target	Sample	Positive, Intervention	Negative, Intervention	Positive, Control	Negative, Control	Total observations	Unadjusted Prevalence Ratio	Unadjusted p-value	Unadjusted Prevalence	Adjusted Prevalence
Fu	MST Marker	Any	346	14	359	9	728	PR=0.99 (95% CI: 0.96, 1.01)	6	0.2	9 (95% CI: 0.1, 1.01)
Bo	MST Marker	Any	145	102	148	98	493	PR=0.98 (95% CI: 0.82, 1.16)	8	0.7	7 (95% CI: 0.1, 1.15)
Ca in	human MST Marker	Any sample	17	3	30	7	57	PR=1.05 (95% CI: 0.82, 1.34)	1	0.7	5 (95% CI: 0.1, 1.34)
Ho 1	human MST Marker	Any sample	41	28	43	18	130	PR=0.84 (95% CI: 0.63, 1.12)	4	0.2	9 (95% CI: 0.1, 1.18)
Fu	human MST Marker	Any sample	124	313	133	30	900	PR=0.99 (95% CI: 0.8, 1.22)	1	0.9	1 (95% CI: 0.1, 1.25)
Bo	human MST Marker	Any sample	26	222	26	23	497	PR=1 (95% CI: 0.57, 1.75)	9	0.9	9 (95% CI: 0.5, 1.76)
DO	human MST Marker	Any sample	22	8	21	9	60	PR=1.05 (95% CI: 0.76, 1.45)	8	0.7	
Ho 1	human MST Marker	Any source water	1	21	0	19	41	Not estimated			Not estimated
DO	human MST Marker	Any source water	22	8	21	9	60	PR=1.05 (95% CI: 0.76, 1.45)	8	0.7	
Ho 1	human MST Marker	Any stored water	9	39	5	41	94	PR=1.72 (95% CI: 0.57, 5.18)	3	0.3	2 (95% CI: 0.1, 5.18)
Fu	human MST Marker	Any stored water	5	310	12	324	651	PR=0.44 (95% CI: 0.16, 1.23)	2	0.1	4 (95% CI: 0.1, 1.23)
Bo	human MST Marker	Any stored water	0	245	0	246	491	Not estimated			Not estimated
Ho 1	human MST Marker	Any house soil	20	19	26	18	83	PR=0.87 (95% CI: 0.57, 1.32)		0.5	6 (95% CI: 0.1, 1.24)
Fu	human MST Marker	Any house soil	68	243	59	261	631	PR=1.19 (95% CI: 0.87, 1.61)	8	0.2	4 (95% CI: 0.1, 1.7)
Bo	human MST Marker	Any house soil	21	226	23	226	496	PR=0.92 (95% CI: 0.5, 1.71)	9	0.7	4 (95% CI: 0.1, 1.75)
Ho 1	human MST Marker	Any atrine soil	21	9	22	8	60	PR=0.95 (95% CI: 0.69, 1.32)	8	0.7	5 (95% CI: 0.1, 1.32)

**Table S8.**  
Unadjusted and adjusted results by study, sample type, and aggregated variables for MST targets (any MST, any general MST, any human MST, any animal MST).

Study	Target	Sample	Positive, Intervention	Negative, Intervention	Positive, Control	Negative, Control	Total observations	Unadjusted Prevalence Ratio	Unadjusted p-value	Unadjusted Prevalence	Adjusted Prevalence
Carrin	Any human MST Marker		24	7	38	17	86	PR=1.12 (95% CI: 0.83, 1.51)	6	0.4	2 (95% CI: 0.141)
Fu	Any human MST Marker		30	142	44	122	338	PR=0.66 (95% CI: 0.44, 0.99)	4	0.0	2 (95% CI: 0.107)
Fu	Any human MST Marker		58	268	60	265	651	PR=0.96 (95% CI: 0.68, 1.37)	4	0.8	6 (95% CI: 0.135)
Bo	Any human MST Marker		7	240	5	241	493	PR=1.39 (95% CI: 0.46, 4.2)	6	0.5	9 (95% CI: 0.42)
Carrin	Any animal MST Marker	ny sample	12	8	17	20	57	PR=1.31 (95% CI: 0.78, 2.17)		0.3	(95% CI: 0.71.99)
Hol	Any animal MST Marker	ny sample	3	66	2	59	130	PR=1.33 (95% CI: 0.18, 9.59)	8	0.7	3 (95% CI: 0.959)
Fu	Any animal MST Marker	ny sample	419	26	437	28	910	PR=1 (95% CI: 0.97, 1.04)	1	0.9	(95% CI: 0.91.04)
Bo	Any animal MST Marker	ny sample	219	29	221	28	497	PR=0.99 (95% CI: 0.93, 1.06)	8	0.8	9 (95% CI: 0.106)
Do	Any animal MST Marker	ny sample	28	2	27	3	60	PR=1.04 (95% CI: 0.89, 1.21)	5	0.6	
Hol	Any animal MST Marker	ource water	0	22	0	19	41	Not estimated			Not estimated
Do	Any animal MST Marker	ource water	28	2	27	3	60	PR=1.04 (95% CI: 0.89, 1.21)	5	0.6	
Hol	Any animal MST Marker	tored water	0	48	1	45	94	Not estimated			Not estimated
Fu	Any animal MST Marker	tored water	229	113	253	109	704	PR=0.96 (95% CI: 0.86, 1.07)	3	0.4	7 (95% CI: 0.108)
Bo	Any animal MST Marker	tored water	57	188	82	164	491	PR=0.7 (95% CI: 0.51, 0.96)	3	0.0	9 (95% CI: 0.095)
Hol	Any animal MST Marker	ouse soil	2	37	1	43	83	Not estimated			Not estimated
Fu	Any animal MST Marker	ouse soil	281	30	291	29	631	PR=0.99 (95% CI: 0.94, 1.05)	2	0.8	9 (95% CI: 0.104)

**Table S8.**  
 Unadjusted and adjusted results by study, sample type, and aggregated variables for MST targets  
 (any MST, any general MST, any human MST, any animal MST).

Study	Target	Sample	Positive, Intervention	Negative, Intervention	Positive, Control	Negative, Control	Total observations	Unadjusted Prevalence Ratio	Unadjusted p-value	Adjusted Prevalence Ratio
Bo	Any animal MST Marker	house soil	178	69	186	63	496	PR=0.96 (95% CI: 0.86, 1.08)	3	0.56 (95% CI: 0.1.08)
Ho1	Any animal MST Marker	atrine soil	2	28	0	30	60	Not estimated		Not estimated
Ca in	Any animal MST Marker		12	19	18	37	86	PR=1.18 (95% CI: 0.7, 2)	3	0.53 (95% CI: 0.2.86)
Fu	Any animal MST Marker		174	8	182	1	365	PR=0.96 (95% CI: 0.93, 1)	3	0.06 (95% CI: 0.1)
Fu	Any animal MST Marker		344	15	358	9	726	PR=0.98 (95% CI: 0.96, 1.01)	7	0.18 (95% CI: 0.1.01)
Bo	Any animal MST Marker		144	103	147	99	493	PR=0.98 (95% CI: 0.82, 1.16)	8	0.77 (95% CI: 0.1.15)

Table S9.

Baseline covariates by study. Note that Odigari et al. 2016 is not included as data shared from this study were from village water sources and did not have associated covariates from individual households; therefore all estimates

		m 2016	Boeh	eese 2017	F	einbaum 2019	St	Fuhr	olcomb 2021	H	apone 2021	C	Capo	ne 2022 in prep.	ng 2021	Kwo	
Number of rooms in the household																	
Household wealth	Low	(25.2%)	125	8 (11.6%)	2	1 (40.9%)	86	(25.6%)	153	5 (27.6%)	4	2 (25.0%)	2	(24.6%)	14	(25.4%)	355
	Medium-low	(24.9%)	124	1 (21.1%)	5	9 (20.8%)	43	(24.3%)	145	6 (28.2%)	4	3 (26.1%)	2	(31.6%)	18	(24.6%)	343
	Medium-high	(25.2%)	125	9 (16.1%)	3	2 (19.1%)	40	(24.6%)	147	5 (21.5%)	3	2 (25.0%)	2	(21.1%)	12	(25.1%)	351
	High	(24.7%)	123	5 (26.9%)	6	3 (19.1%)	40	(25.5%)	152	7 (22.7%)	3	1 (23.9%)	2	(22.8%)	13	(24.9%)	347
	Missing	(0%)	0	9 (24.4%)	5	(0.1%)	2	(0%)	0	(0%)	0	(0%)	0		0 (0%)	(0%)	0
Number of people in the household																	
<5	(54.5%)	271	7 (7.0%)	1	2 (29.0%)	61	(56.1%)	335	8 (23.3%)	3	(0%)	0		0 (0%)	(56.1%)	783	
5-8	(40.0%)	199	71 (70.7%)	1	49 (54.5%)	11	(37.5%)	224	4 (27.0%)	4	(8.0%)	7	(5.3%)	3	(37.8%)	528	
5-8	(40.0%)	199	71 (70.7%)	1	49 (54.5%)	11	(37.5%)	224	4 (27.0%)	4	(8.0%)	7	(5.3%)	3	(37.8%)	528	
>8	(5.4%)	27	4 (22.3%)	5	5 (11.6%)	24	(6.4%)	38	1 (49.7%)	8	1 (92.0%)	8	(94.7%)	54	(6.1%)	85	
Missing	(0%)	0	(0%)	0	1 (4.8%)	10	(0%)	0	(0%)	0	(0%)	0		0 (0%)	(0%)	0	
Number of rooms in the household																	
1-2	(0%)	0	(0%)	0	(0%)	0	(0%)	0	8 (60.1%)	9	1 (69.3%)	6	(71.9%)	41	(0%)	0	
>3	(0%)	0	(0%)	0	(0%)	0	(0%)	0	5 (39.9%)	6	7 (30.7%)	2	(28.1%)	16	(0%)	0	
Missing	(100%)	497	42 (100%)	2	07 (100%)	21	(100%)	597	(0%)	0	(0%)	0		0 (0%)	(100%)	1396	
Improved roof																	
0	(1.6%)	8	(0%)	0	3 (32.9%)	69	(1.3%)	8	(0%)	0	(0%)	0		0 (0%)	(1.6%)	23	

Table S9.

Baseline covariates by study. Note that Odigari et al. 2016 is not included as data shared from this study were from village water sources and did not have associated covariates from individual households; therefore all estimates

	Odigari et al. 2016	Boehmer et al. 2017	Fischer et al. 2019	Stein et al. 2019	Fuhrman et al. 2020	Polcomb et al. 2021	Hopkins et al. 2021	Capone et al. 2022 in prep.	Kwo et al. 2022
Father in agriculture									
0	14 (98.4%)	489	0	14 (67.1%)	589	0	0	0	1373
Missing	0	42 (100%)	2	0	0	63 (100%)	8 (100%)	57	0
Land owned									
0	9 (66.8%)	332	26 (52.1%)	1	0	419	0	0	952
1	165 (33.2%)	9	36.8%	8	0	178	0	0	444
Missing	0	7 (11.2%)	2	21 (100%)	0	63 (100%)	8 (100%)	57	0
Acres of land owned									
0	0	7 (40.1%)	9	0	0	0	0	0	0
1	0	17 (48.3%)	1	0	0	0	0	0	0
Missing	497 (100%)	8 (11.6%)	2	21 (100%)	597	63 (100%)	8 (100%)	57	1396
Maternal education									
No education	85 (17.1%)	0	0	0	86	6	0	0	207
Primary	0	3 (34.3%)	8	10	0	3	0	0	0
Secondary	180 (36.2%)	0	3	51	183	1	0	0	449
More than secondary	232 (46.7%)	0	7	49	328	4	0	0	740
Missing	0	1 (4.5%)	1	0	0	0	0	0	0

Table S9.

Baseline covariates by study. Note that Odigari et al. 2016 is not included as data shared from this study were from village water sources and did not have associated covariates from individual households; therefore all estimates

		Odigari et al. 2016	Boehmer et al. 2017	Feyzioglu et al. 2019	Stein et al. 2020	Fuhrman et al. 2020	Polcomb et al. 2021	Hopkins et al. 2021	Campbell et al. 2022 in prep.	Capone et al. 2021	Kwo et al. 2021						
Age	Missing	(0%)	0	8 (19.8%)	4 (0.1%)	2	(0%)	0	4 (39.3%)	6	8 (100%)	57	(0%)	0			
	Maternal																
	Mean (SD)	(5.18)	23.7	Missing	15.4 (6.32)	26	(5.08)	23.7	Missing	15.4 (6.32)	26	Missing	(5.03)	24.0			
Max	Median [Min, Max]	[15.0, 42.0]	23.0	Missing	15.5 [14.9, 47.9]	25	[15.0, 41.0]	23.0	Missing	15.5 [14.9, 47.9]	25	Missing	[15.0, 43.0]	24.0			
	Missing	(0%)	0	42 (100%)	2 (0.5%)	11	(0%)	0	63 (100%)	1	8 (100%)	57	(0.1%)	2			
	Improved wall																
	0	(15.7%)	78	(0%)	0	19 (95.8%)	20	(33.0%)	197	4	6 (18.2%)	1	(17.5%)	10	(26.4%)	369	
	1	(84.3%)	419	(0%)	0	(4.2%)	88	(67.0%)	400	22 (74.8%)	1	2 (81.8%)	7	(82.5%)	47	(73.6%)	1027
	Missing	(0%)	0	42 (100%)	2 (0%)	0	(0%)	0	(0%)	0	(0%)	0	(0%)	0	(0%)	0	
	Improved floor																
	0	(92.8%)	461	(0%)	0	99 (94.9%)	19	(87.8%)	524	(2.5%)	4	(1.1%)	1	(1.8%)	1	(89.8%)	1253
	1	(7.2%)	36	(0%)	0	8 (5.1%)	10	(12.2%)	73	59 (97.5%)	1	7 (98.9%)	8	(98.2%)	56	(10.2%)	143
	Missing	(0%)	0	42 (100%)	2 (0%)	0	(0%)	0	(0%)	0	(0%)	0	(0%)	0	(0%)	0	
	Electricity																
	0	(47.1%)	234	4 (14.0%)	3	58 (92.9%)	19	(41.2%)	246	(1.8%)	3	(4.5%)	4	(3.5%)	2	(41.8%)	584
	1	(52.9%)	263	202 (83.5%)	2	7 (7.0%)	14	(58.8%)	351	60 (98.2%)	1	4 (95.5%)	8	(96.5%)	55	(58.2%)	812
	Missing	(0%)	0	(2.5%)	6	(0.1%)	2	(0%)	0	(0%)	0	(0%)	0	(0%)	0	(0%)	0
Animal ownership																	
	Mean (SD)	(0.206)	0.956	.423 (0.495)	0	0.899 (0.302)	0	(0.208)	0.955	.896 (0.307)	0	.966 (0.183)	0	(0.132)	0.982	(0.177)	0.968

Table S9.

Baseline covariates by study. Note that Odigari et al. 2016 is not included as data shared from this study were from village water sources and did not have associated covariates from individual households; therefore all estimates

		m 2016	Boeh	eese 2017	F einbaum 2019	St	Fuhr meister 2020	olcomb 2021	H	apone 2021	C	Capo ne 2022 in prep.	ng 2021	Kwo
Max]	Median [Min,	[0, 1.00]	1.00	[0, 1.00]	0 00 [0, 1.00]	1. [0, 1.00]	1.00	.00 [0, 1.00]	1	.00 [0, 1.00]	1	1.00	[0, 1.00]	1.00
	Missing	(0.2%)	1	9 (12.0%)	2 (0%)	0	(0.2%)	1	(0%)	0	0	0 (0%)	(0.1%)	1