Supporting Information for:

Effect of sanitation improvements on pathogens and microbial source tracking markers in the rural Bangladeshi household environment

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Methods
PCR Quality Control
Laboratory blanks consisted of each lab technician processing sterile distilled water for *E. coli* enumeration and archiving once per week. For extraction blanks, empty tubes were processed alongside samples and went through the same procedure. We processed 1 extraction blank for every 2 QIAcube runs for pathogenic *E. coli* genes. All extraction blanks were negative for pathogenic *E. coli* genes. 2 of 72 lab blanks were positive for *eaeA*, 1 of 72 lab blanks was positive for *stx1* and *stx2,* and 2 of 72 lab blanks were positive for *lt1*. All samples corresponding to the date of the positive blanks were removed from analysis. This resulted in removing 6 child hand, 9 mother hand, 11 stored water, and 12 soil samples for *eaeA* analyses. 3 child hand, 5 mother hand, 5 stored water, and 6 soil samples were removed for *stx1/stx2* analyses. For *lt1* analyses, 4 child hand, 6 mother hand, 9 stored water, and 8 soil samples were removed. All PCR no template controls were negative.

qPCR Quality Control
For laboratory blanks, each lab technician filtered 5 mL of sterile distilled water with 0.5 mL MgCl$_2$ followed by RNAlater once per day. Extraction blanks consisted of an empty tube (no filter or soil) processed with each set of samples. 6 of 119 extraction blanks were positive for HumM2, 2 of 51 extraction blanks were positive for norovirus GII, 2 of 51 extraction blanks were positive for *G. lamblia*, 5 of 119 extraction blanks were positive for BacCow. 14 of 168 lab blanks were positive for HumM2, 4 of 168 lab blanks were positive for norovirus, 28 of 168 lab blanks were positive for *G. lamblia*, 1 of 168 lab blanks was positive for BacCow. For binary markers (HumM2, norovirus GII, *G. lamblia*), samples corresponding to positive blanks were removed from the analysis according to date and lab technician. This resulted in removing 30 child and 33 mother hand samples for norovirus GII, and 51 child and 115 mother hands for *Giardia* gene analyses. For HumM2, 29 child hand, 74 mother hand, 76 stored water, and 92 soil samples were removed. For BacCow, all positive blanks amplified below the limit of quantification (BLOQ). Samples corresponding to positive blanks that amplified BLOQ were treated as below the limit of detection (LOD). All qPCR no template controls were negative.

Limits of Detection for non-Quantitative Assays
Most samples did not amplify within the quantifiable range for norovirus GII, *G. lamblia* and HumM2. Samples were considered positive if there was amplification in at least 1 of 3 replicates. Limits of detection (LOD) for norovirus GII and *Giardia* on hands were estimated to be 62.5 and 1020 target copies per 2 hands, respectively. For HumM2, the LOD was 173 target copies per 2 hands, 21-103 target copies per 100 mL of stored water, and 254-478 target copies per gram dry soil. The LOD was determined based on the lowest gene copy that amplified in at least 1 of 3 replicates in each sample type. The range of LODs for stored water and soil correspond to variation in volumes filtered (100mL - 500mL) and soil moisture content (0 - 88%).

Sensitivity Analysis and Limits of Detection and Quantification for BacCow (Quantitative)
To determine which quantities to assign to samples BLOD and BLOQ in stored water and soil samples, which were impacted by differences in processing volume and moisture content, we conducted a sensitivity analysis with four scenarios: 1.) Samples BLOD were assigned half the LOD

accounting for the volume of water filtered and the moisture content for each sample. Samples BLOQ were assigned the midpoint between the LOD and LOQ. 2.) Samples BLOD were assigned the lowest detectable value. Samples BLOQ were assigned the lowest quantifiable value. Lowest detectable values and quantifiable values correspond to the maximum volume of water filtered (500 mL) and minimum soil moisture content (0%). 3.) Sample BLOD were assigned the LOD accounting for the volume of water filtered and the moisture content for each sample. Samples BLOQ were assigned the LOQ accounting for the volume of water filtered and the soil moisture content. 4.) Samples BLOD were assigned half the lowest detectable value. Samples BLOQ were assigned the midpoint between the lowest detectable value and lowest quantifiable value.

The overall results for difference in concentration of BacCow between arms were similar in all scenarios (**Table S3**). Thus, we conducted the primary analysis with Scenario 1 because it was more plausible that the concentration of samples below the limit of detection (BLOD) and below the limit of quantification (BLOQ) were lower than the limit of detection (LOD) and limit of quantification (LOQ). It was also more reasonable to assume that the LOD and LOQ of samples with less than 500 mL filtered and moisture content >0% had higher detection limits than samples where 500 mL was filtered and the moisture content was 0%. The resulting LOD of BacCow was 285 gene copies (gc)/2 hands, 8.1- 40.5 gc/100mL stored water (depending on the volume of water filtered) and 130- 244 gc/g dry soil weight (depending on the soil moisture content). The LOQ of BacCow was 2500 gene copies (gc)/2 hands, 100- 500 gc/100mL stored water and 2000- 3760 gc/dry gram. The limit of quantification (LOQ) was defined as 10 gc/2µL and corresponds to the lowest point on the pooled standard curve. The limit of detection (LOD) was based on the lowest gene copy that amplified in at least 1 of 3 replicates in each sample type.

Tables

Table S1: Genes, primers, product size and run conditions for three multiplex reactions used to detect pathogenic *E. coli*.

	Path *E. coli* Type	Gene	Primer Name	Sequence	Product Size	Annealing Time (sec)	Annealing Temperature
Multiplex 1	EAEC	*aggR*	aggRKs1-F	GTATACACAAAAGAAGGAAGC	254		
			aggRks2-R	ACAGAATCGTCAGCATCAGC		90	60˚C
	EPEC/EHEC	*eaeA*	eaeA-F	TCAATGCAGTTCCGTTATCAGTT	482		
			eaeA-R	GTAAAGTCCGTTACCCCAACCTG			
Multiplex 2	STEC	*stx1*	stx1-F	AAATCGCCATTCGTTGACTACTTCT	370		
			stx1-R	TGCCATTCTGGCAACTCGCGATGCA			
	STEC	*stx2*	stx2-F	CAGTCGTCACTCACTGGTTTCATCA	283	90	58˚C
			stx2-R	GGATATTCTCCCCACTCTGACACC			
	EIEC	*ipaH*	ipaIll-F	GTTCCTTGACCGCCTTTCCGATACCGTC	619		
			ipaIV-R	GCCGGTCAGCCACCCTCTGAGAGTAC			
Multiplex 3	ETEC	*lt1*	lt1-F	TCTCTATGTGCATACGGAGC	322		
			lt1-R	CCATACTGATTGCCGCAAT		180	51˚C
	ETEC	*st1b*	st1b-F	ATTTTTCTTTCTGTATTGTCTT	192		
			st1b-R	CACCCGGTACAAGCAGGATT			

Table S2: Primer sequences, probe sequences, reaction volume, bovine serum albumin (BSA) concentration, master mix and qPCR standard for all qPCR assays used in this study.

Target	Sequence (5', 3') (concentration in rxn)	Reaction Volume (μL)	BSA (mg/ml)	Master Mix	Standard
HumM2[1]	F-CGTCAGGTTTGTTTCGGTATTG (1.2 μM) R-TCATCACGTAACTTATTTATATGCATTAGC (1.2 μM) P-FAM /TATCGAAAATCTCACGGATTAACTCTTGTGTACGC/TAMRA (0.1μM)	25	0.2	TaqMan Environmental	Plasmid
BacCow[2]	F-CCAACYTTCCCGWTACTC (0.4 μM) R-GGACCGTGTCTCAGTTCCAGTG (0.4 μM) P-FAM/TAGGGGTTCTGAGAGGAAGGTCCCCC/TAMRA (0.08 μM)	25	0.05	TaqMan Environmental	Plasmid
Norovirus GII[3]	F-ATGTTCAGRTGGATGAGRTTCTCWGA (0.4 μM) R-TCGACGCCATCTTCATTCACA (0.4 μM) P-FAM/AGCACGTGGGAGGGGATCG/BHQ (0.2 μM)	20	0.4	TaqMan Fast Virus 1, Step	Plasmid
Giardia lamblia (β, Giardin P241)[4]	F-CATCCGCGAGGAGGTCAA (0.3 μM) R-GCAGCCATGGTGTCGATCT (0.3 μM) P-FAM/AAGTCCGCCGACAACATGTACCTAACGA/BHQ (0.2 μM)	25	0.2	TaqMan Universal PCR	Plasmid
Cryptosporidium spp. (JVA) [5]	F-ATGACGGGTAACGGGGAAT (0.6 μM) R-CCAATTACAAAACCAAAAAGTCC (0.6 μM) P-FAM/CGCGCCTGCTGCCTTCCTTAGATG/BHQ (0.12 μM)	25	0.2	TaqMan Universal PCR	Plasmid
Pph6[6]	F-GGTTCTGGGCCGATGATG (0.9 μM) R-CAGGCCCTAGCGTGGAAAC (0.9 μM) P-FAM/CACTGAAAAGGCTGTTCA/MGBNFQ (0.25 μM)	25	0.2	TaqMan Universal PCR	Plasmid
MS2[7]	F-CGGCTGCTCGCGGATA (0.9 μM) R-ACTTCGCTTCTCGAGCGATAC (0.9 μM) P-FAM/CCGTACCTCGGGTTTCCGTCTTGCT/TAMARA (0.25 μM)	20	0.2	TaqMan Fast Virus 1, Step	Genomic RNA

Table S3: Mean $\log_{10}$ concentrations of BacCow in soil (gc/g dry weight) and stored water (gc/100 mL) samples for each sensitivity analysis scenario.

	Mean $\log_{10}$ Concentration (95% CI)		$\Delta\log_{10}$ Concentration (95% CI)	p-value
	Control	Sanitation		
Scenario 1[a]				
Stored Water	1.27 (1.20, 1.34)	1.24 (1.17, 1.32)	-0.02 (-0.13, 0.09)	0.78
Soil	3.34 (3.20, 3.47)	3.35 (3.19, 3.51)	0.04 (-0.16, 0.23)	0.72
Scenario 2[b]				
Stored Water	1.70 (1.64, 1.77)	1.67 (1.61, 1.74)	-0.03 (-0.12, 0.07)	0.58
Soil	3.66 (3.56, 3.77)	3.67 (3.54, 3.79)	0.02 (-0.13, 0.17)	0.78
Scenario 3[c]				
Stored Water	1.74 (1.67, 1.80)	1.71 (1.64, 1.78)	-0.02 (-0.12, 0.07)	0.64
Soil	3.71 (3.61, 3.81)	3.71 (3.59, 3.83)	0.02 (-0.13, 0.17)	0.81
Scenario 4[d]				
Stored Water	1.24 (1.17, 1.31)	1.21 (1.14, 1.29)	-0.02 (-0.13, 0.09)	0.71
Soil	3.29 (3.15, 3.43)	3.31 (3.15, 3.47)	0.04 (-0.16, 0.24)	0.71

[a]: Non-detects were assigned half the LOD accounting for the volume of water filtered and the moisture content for each sample. Samples BLOQ were assigned the midpoint between the LOD and LOQ.
[b]: Non-detects were assigned the lowest detectable value. Samples BLOQ were assigned the lowest quantifiable value. Lowest detectable values and quantifiable values correspond to the maximum volume of water filtered (500 mL) and minimum soil moisture content (0%).
[c]: Non-detects were assigned the LOD accounting for the volume of water filtered and the moisture content for each sample. Samples BLOQ were assigned the LOQ accounting for the volume of water filtered and the soil moisture content.
[d]: Non-detects were assigned half the lowest detectable value. Samples BLOQ were assigned the midpoint between the lowest detectable value and lowest quantifiable value.

Table S4: Number of samples below the limit of detection and limit of quantification for BacCow. Distribution of samples above the lower limit of quantification and lower limits of quantification and detection by sample type.

	Child Hands	Mother Hands	Stored Water	Soil
n<LLOD[a]	9	25	242	97
n <LLOQ[b]	79	218	414	281
n >LLOQ	278	483	72	360
Mean (std) of samples > LLOQ[c]	4.19 (0.64)	4.14 (0.56)	2.52 (0.44)	4.36 (0.80)
LLOD	285	285	8.1-40.5[d]	130-244[e]
LLOQ	2500	2500	100-500[d]	2000-3760[e]

[a]: Lower limit of detection
[b]: Lower limit of quantification
[c]: Units are gc/2 hands, gc/100 mL, and gc/g dry weight
[d]: Corresponds to volumes of 100 and 500 mL filtered
[e]: Corresponds to soil moisture contents ranging from 0 to 88%

Table S5: Prevalence and 95% confidence interval (95% CI) of pathogenic *E. coli* virulence genes, microbial source tracking markers, norovirus GII gene, and *Giardia* gene on child hands, mother hands, stored water and soil in the sanitation and control arms.

	N	Control Prevalence (95% CI)	N	Sanitation Prevalence (95% CI)
Child Hands				
Any ECVG	183	32.2 (25.7, 38.7)	181	32.6 (25.8, 39.4)
eaeA (EPEC/EHEC)	184	13.0 (7.6, 18.5)	183	9.8 (5.8, 13.9)
aggR (EAEC)	187	12.3 (7.8, 16.8)	186	11.3 (6.9, 15.7)
stx1/stx2 (STEC)	186	13.4 (8.6, 18.3)	184	16.8 (11.2, 22.5)
ipaH (EIEC)	187	NA	186	0.5 (0.0, 1.6)
st1b/lt1 (ETEC)	185	9.7 (5.6, 13.9)	184	7.6 (3.4, 11.8)
Norovirus	167	4.2 (1.2, 7.2)	169	4.1 (1.3, 7.0)
Giardia	157	5.1 (1.7, 8.5)	154	4.5 (1.3, 7.8)
BacCow	183	99.5 (98.4, 100.0)	182	95.6 (92.4, 98.9)
HumM2	167	26.3 (19.7, 33.0)	170	17.6 (12.0, 23.3)
Mother Hands				
Any ECVG	367	23.7 (19.7, 27.7)	353	20.4 (16.5, 24.3)
eaeA (EPEC/EHEC)	370	8.1 (5.7, 10.5)	359	7.2 (4.5, 9.9)
aggR (EAEC)	376	9.3 (6.3, 12.3)	362	6.1 (3.6, 8.5)
stx1/stx2 (STEC)	374	9.1 (5.9, 12.3)	359	7.5 (4.7, 10.4)
ipaH (EIEC)	376	1.1 (0.0, 2.1)	362	0.6 (0.0, 1.3)
st1b/lt1 (ETEC)	374	4.0 (2.2, 5.8)	358	3.9 (2.0, 5.8)
Norovirus	344	2.9 (1.0, 4.8)	342	3.2 (1.4, 5.0)
Giardia	302	3.0 (0.9, 5.0)	301	1.7 (0.0, 3.6)
BacCow	368	97.6 (96.0, 99.1)	358	95.8 (93.9, 97.7)
HumM2	325	18.5 (13.8, 23.1)	328	17.7 (13.3, 22.1)
Stored Water				
Any ECVG	381	37.5 (33.0, 42.1)	343	36.4 (31.3, 41.6)
eaeA (EPEC/EHEC)	380	15.3 (12.0, 18.6)	351	14.5 (11.0, 18.1)
aggR (EAEC)	386	10.4 (7.4, 13.4)	356	11.8 (9.0, 14.6)
stx1/stx2 (STEC)	385	16.6 (12.6, 20.6)	352	16.5 (12.6, 20.4)
ipaH (EIEC)	386	1.8 (0.5, 3.1)	356	0.6 (0.0, 1.3)
st1b/lt1 (ETEC)	383	10.4 (7.6, 13.3)	350	6.6 (3.6, 9.5)
BacCow	363	70.0 (65.1, 74.8)	342	67.0 (61.6, 72.4)
HumM2	337	3.6 (1.5, 5.6)	315	1.6 (0.2, 2.9)
Soil				
Any ECVG	382	61.5 (56.4, 66.6)	358	58.9 (53.9, 64.0)
eaeA (EPEC/EHEC)	383	38.6 (33.2, 44.1)	360	36.7 (31.7, 41.6)
aggR (EAEC)	390	17.4 (13.5, 21.4)	365	14.2 (11.0, 17.5)
stx1/stx2 (STEC)	388	26.0 (21.6, 30.4)	361	23.5 (19.2, 27.9)
ipaH (EIEC)	390	1.5 (0.4, 2.7)	365	0.8 (0.0, 1.7)
st1b/lt1 (ETEC)	387	17.3 (13.3, 21.3)	360	13.1 (9.6, 16.5)
BacCow	331	91.2 (88.4, 94.1)	315	90.2 (86.1, 94.2)
HumM2	332	18.4 (14.3, 22.5)	314	22.0 (17.3, 26.6)

Table S6: Unadjusted and adjusted prevalence ratios (PR) and 95% confidence intervals (95% CI) comparing the prevalence of pathogenic *E. coli* virulence genes, norovirus GII gene, *Giardia* gene and microbial source tracking markers on child hands, mother hands, stored water and soil in the sanitation and control arms.

	Unadjusted			Adjusted		
	PR (95% CI)	p-value	Corrected p-value[a]	PR (95% CI)	p-value	Corrected p-value[a]
Child Hands						
Any ECVG	1.06 (0.75, 1.49)	0.75	1.00	1.00 (0.76, 1.33)	0.99	1.00
eaeA (EPEC/EHEC)	0.82 (0.41, 1.61)	0.56	1.00	0.73 (0.40, 1.33)	0.30	1.00
aggR (EAEC)	0.91 (0.50, 1.67)	0.76	1.00	0.90 (0.54, 1.51)	0.69	1.00
stx1/stx2 (STEC)	1.30 (0.73, 2.29)	0.37	1.00	1.16 (0.72, 1.85)	0.54	1.00
ipaH (EIEC)	NA			NA		
st1b/lt1 (ETEC)	0.77 (0.33, 1.78)	0.54	1.00	0.80 (0.41, 1.56)	0.52	1.00
Norovirus	1.00 (0.33, 3.03)	0.99	1.00	1.02 (0.39, 2.64)	0.97	1.00
Giardia	1.00 (0.27, 3.71)	1.00	1.00	1.00 (0.32, 3.10)	1.00	1.00
BacCow	0.96 (0.93, 1.00)	0.05*	0.21	0.95 (0.92, 0.97)	<0.001*	<0.001*
HumM2	0.67 (0.41, 1.11)	0.12	0.48	0.66 (0.44, 0.99)	0.05*	0.19
Mother Hands						
Any ECVG	0.89 (0.68, 1.15)	0.38	1.00	0.87 (0.68, 1.11)	0.26	1.00
eaeA (EPEC/EHEC)	0.91 (0.51, 1.62)	0.75	1.00	0.90 (0.51, 1.58)	0.72	1.00
aggR (EAEC)	0.66 (0.38, 1.14)	0.14	0.55	0.67 (0.40, 1.13)	0.13	0.53
stx1/stx2 (STEC)	0.84 (0.48, 1.46)	0.54	1.00	0.82 (0.51, 1.32)	0.42	1.00
ipaH (EIEC)	0.62 (0.10, 3.72)	0.60	1.00	0.52 (0.09, 2.88)	0.45	1.00
st1b/lt1 (ETEC)	0.98 (0.47, 2.05)	0.96	1.00	0.97 (0.51, 1.85)	0.93	1.00
Norovirus	1.16 (0.42, 3.18)	0.78	1.00	1.07 (0.46, 2.47)	0.88	1.00
Giardia	0.60 (0.15, 2.42)	0.47	1.00	0.54 (0.19, 1.50)	0.24	0.95
BacCow	0.98 (0.96, 1.01)	0.28	1.00	0.98 (0.96, 1.01)	0.24	0.94
HumM2	1.01 (0.66, 1.53)	0.97	1.00	0.95 (0.67, 1.36)	0.79	1.00
Stored Water						
Any ECVG	0.96 (0.79, 1.17)	0.67	1.00	0.95 (0.79, 1.15)	0.60	1.00
eaeA (EPEC/EHEC)	0.95 (0.67, 1.36)	0.79	1.00	0.93 (0.67, 1.30)	0.67	1.00
aggR (EAEC)	1.16 (0.79, 1.70)	0.45	1.00	1.12 (0.78, 1.60)	0.54	1.00
stx1/stx2 (STEC)	0.97 (0.70, 1.34)	0.84	1.00	0.98 (0.72, 1.33)	0.91	1.00
ipaH (EIEC)	0.29 (0.05, 1.58)	0.15	0.61	0.32 (0.07, 1.43)	0.13	0.54
st1b/lt1 (ETEC)	0.66 (0.41, 1.08)	0.10	0.41	0.64 (0.39, 1.03)	0.07	0.27
BacCow	0.95 (0.85, 1.07)	0.42	1.00	0.98 (0.88, 1.08)	0.64	1.00
HumM2	0.46 (0.15, 1.39)	0.17	0.67	0.45 (0.18, 1.11)	0.08	0.33
Soil						
Any ECVG	0.96 (0.86, 1.08)	0.52	1.00	0.96 (0.86, 1.06)	0.42	1.00
eaeA (EPEC/EHEC)	0.96 (0.80, 1.16)	0.68	1.00	0.97 (0.82, 1.15)	0.71	1.00
aggR (EAEC)	0.87 (0.62, 1.22)	0.42	1.00	0.82 (0.59, 1.14)	0.23	0.93
stx1/stx2 (STEC)	0.89 (0.68, 1.15)	0.37	1.00	0.89 (0.69, 1.14)	0.35	1.00
ipaH (EIEC)	0.55 (0.14, 2.19)	0.40	1.00	0.43 (0.09, 2.17)	0.31	1.00
st1b/lt1 (ETEC)	0.76 (0.53, 1.07)	0.12	0.48	0.74 (0.54, 1.03)	0.07	0.29
BacCow	0.99 (0.93, 1.04)	0.60	1.00	1.00 (0.95, 1.05)	0.99	1.00
HumM2	1.21 (0.88, 1.65)	0.24	0.97	1.16 (0.86, 1.56)	0.34	1.00

[a]: p-values were corrected for multiple comparisons using the Bonferroni method

*significant at p-value < 0.05

Table S7: Unadjusted and adjusted difference and 95% confidence interval in the $\log_{10}$ concentration of BacCow on hands, in stored water, and soil.

	Unadjusted			Adjusted		
	$\Delta\log_{10}$ Concentration (95% CI)	p-value	Corrected p-value[a]	$\Delta\log_{10}$ Concentration (95% CI)	p-value	Corrected p-value[a]
Child Hands	-0.19 (- 0.42, 0.03)	0.09	0.36	-0.10 (-0.47, 0.28)	0.62	1.00
Mother Hands	-0.16 (-0.30, -0.03)	0.02*	0.07	-0.37 (-0.66, -0.08)	0.01*	0.05
Stored Water	-0.02 (-0.13, 0.09)	0.78	1.00	0.01 (-0.11, 0.13)	0.91	1.00
Soil	0.04 (-0.16, 0.23)	0.72	1.00	0.07 (-0.27, 0.40)	0.71	1.00

Note: Units of concentration are gene copies of BacCow per 2 hands, 100 mL, and dry gram

[a]: p-values were corrected for multiple comparisons using the Bonferroni method

*significant at p-value < 0.05

Table S8: Prevalence ratios (PR) and 95% confidence intervals (95% CI) comparing the prevalence of pathogenic *E. coli* virulence genes, norovirus GII gene, *Giardia* gene and microbial source tracking markers on child hands, mother hands, stored water and soil in the sanitation and control arms in the wet and dry season.

			Wet			Dry		Interaction	Corrected
			Prevalence			Prevalence			
		N	(95% CI)	PR (95% CI)	N	(95% CI)	PR (95% CI)	p-value	p-value[a]
Child Hands									
Any ECVG	Control	96	36.5 (26.5, 46.4)		87	27.6 (17.3, 37.9)			
	Sanitation	92	37 (26.3, 47.7)	1.08 (0.67, 1.75)	89	28.1 (17.8, 38.4)	1.06 (0.59, 1.92)	0.96	1.00
eaeA (EPEC/EHEC)	Control	95	14.7 (7.8, 21.7)		89	11.2 (4.3, 18.2)			
	Sanitation	92	12.0 (5.4, 18.5)	0.94 (0.37, 2.37)	91	7.7 (2.2, 13.1)	0.69 (0.26, 1.88)	0.66	1.00
aggR (EAEC)	Control	98	13.3 (6.6, 20)		89	11.2 (4.2, 18.3)			
	Sanitation	95	7.4 (2.0, 12.7)	0.52 (0.18, 1.50)	91	15.4 (8.0, 22.8)	1.46 (0.65, 3.28)	0.15	0.58
stx1/stx2 (STEC)	Control	98	17.3 (9.6, 25.1)		88	9.1 (3.3, 14.9)			
	Sanitation	95	22.1 (13.2, 31.0)	1.43 (0.70, 2.95)	89	11.2 (4.8, 17.7)	1.19 (0.45, 3.17)	0.76	1.00
ipaH (EIEC)	Control	98	NA		89	NA			
	Sanitation	95	1.1 (-1.0, 3.1)	NA	91	NA	NA		
st1b/lt1 (ETEC)	Control	97	9.3 (2.9, 15.6)		88	10.2 (4.3, 16.2)			
	Sanitation	94	5.3 (-0.1, 10.7)	0.55 (0.13, 2.33)	90	10.0 (3.1, 16.9)	0.98 (0.34, 2.82)	0.53	1.00
Norovirus	Control	97	2.1 (-0.8, 4.9)		70	7.1 (1.2, 13.1)			
	Sanitation	93	4.3 (0.2, 8.4)	2.49 (0.61, 10.24)	76	3.9 (-0.4, 8.3)	0.49 (0.08, 2.88)	0.16	0.63
Giardia	Control	79	2.5 (-0.9, 5.9)		78	7.7 (1.7, 13.7)			
	Sanitation	75	2.7 (-1.0, 6.4)	1.14 (0.13, 9.90)	79	6.3 (0.9, 11.8)	0.92 (0.21, 3.95)	0.87	1.00
BacCow	Control	98	100 (100, 100)		85	98.8 (96.5, 101.1)			
	Sanitation	95	92.6 (86.6, 98.6)	0.92 (0.86, 1.00)	87	98.9 (96.6, 101.1)	1.00 (0.97, 1.04)	0.09	0.34
HumM2	Control	89	29.2 (20.9, 37.5)		78	23.1 (13.6, 32.6)			
	Sanitation	86	14.0 (6.0, 21.9)	0.54 (0.25, 1.17)	84	21.4 (12.7, 30.2)	0.86 (0.41, 1.78)	0.40	1.00
Mother Hands									
Any ECVG	Control	188	26.1 (19.8, 32.4)		179	21.2 (14.6, 27.9)			
	Sanitation	181	19.3 (13.5, 25.2)	0.76 (0.51, 1.11)	172	21.5 (15.6, 27.4)	1.06 (0.71, 1.58)	0.25	0.98
eaeA (EPEC/EHEC)	Control	189	9.5 (5.6, 13.4)		181	6.6 (3.2, 10.1)			
	Sanitation	183	5.5 (1.9, 9.0)	0.57 (0.24, 1.38)	176	9.1 (5.2, 13.0)	1.45 (0.67, 3.17)	0.12	0.47
aggR (EAEC)	Control	195	10.8 (5.8, 15.8)		181	7.7 (3.7, 11.8)			
	Sanitation	186	6.5 (2.7, 10.2)	0.59 (0.27, 1.28)	176	5.7 (2.4, 9.0)	0.77 (0.34, 1.74)	0.64	1.00
stx1/stx2 (STEC)	Control	195	8.7 (4.3, 13.2)		179	9.5 (4.4, 14.6)			
	Sanitation	186	7.0 (3.2, 10.8)	0.72 (0.33, 1.56)	173	8.1 (3.7, 12.5)	0.99 (0.47, 2.08)	0.56	1.00
ipaH (EIEC)	Control	195	1.5 (-0.2, 3.3)		181	0.6 (-0.5, 1.6)			
	Sanitation	186	1.1 (-0.4, 2.6)	1.46 (0.13, 16.88)	176	NA	NA		

		N			N				
st1b/lt1 (ETEC)	Control	193	3.1 (0.7, 5.5)		181	5.0 (1.9, 8.0)			
	Sanitation	184	5.4 (2.3, 8.6)	1.81 (0.59, 5.59)	174	2.3 (0.1, 4.5)	0.45 (0.14, 1.42)	0.10	0.41
Norovirus	Control	191	2.6 (0.4, 4.9)		153	3.3 (-0.1, 6.6)			
	Sanitation	178	2.2 (0.1, 4.4)	0.94 (0.22, 4.05)	164	4.3 (1.3, 7.3)	1.30 (0.32, 5.30)	0.75	1.00
Giardia	Control	155	3.2 (0.5, 6.0)		147	2.7 (0.1, 5.3)			
	Sanitation	144	2.1 (-0.2, 4.4)	0.59 (0.13, 2.57)	157	1.3 (-0.5, 3.0)	0.59 (0.10, 3.66)	1.00	1.00
BacCow	Control	196	98.5 (96.8, 100.2)		172	96.5 (93.8, 99.2)			
	Sanitation	185	94.6 (91.5, 97.7)	0.96 (0.92, 1.00)	173	97.1 (94.6, 99.6)	1.01 (0.97, 1.06)	0.08	0.34
HumM2	Control	175	18.3 (12.6, 24.0)		150	18.7 (11.8, 25.6)			
	Sanitation	164	15.9 (9.8, 21.9)	0.92 (0.51, 1.66)	164	19.5 (13.7, 25.3)	1.09 (0.62, 1.91)	0.68	1.00
Stored Water									
Any ECVG	Control	176	40.9 (33.8, 48)		205	34.6 (28.2, 41.0)			
	Sanitation	162	39.5 (32.4, 46.6)	0.95 (0.72, 1.24)	181	33.7 (26.6, 40.8)	0.97 (0.72, 1.29)	0.92	1.00
eaeA (EPEC/EHEC)	Control	175	19.4 (13.8, 25.1)		205	11.7 (7.5, 15.9)			
	Sanitation	163	19 (12.8, 25.2)	0.96 (0.61, 1.52)	188	10.6 (6.2, 15.0)	0.92 (0.51, 1.67)	0.91	1.00
aggR (EAEC)	Control	181	10.5 (6.4, 14.6)		205	10.2 (5.9, 14.5)			
	Sanitation	168	13.7 (9.0, 18.4)	1.29 (0.75, 2.20)	188	10.1 (6.1, 14.1)	1.03 (0.56, 1.89)	0.60	1.00
stx1/stx2 (STEC)	Control	181	18.2 (12.6, 23.8)		204	15.2 (9.7, 20.7)			
	Sanitation	168	18.5 (12, 24.9)	1.01 (0.64, 1.58)	184	14.7 (9.9, 19.5)	0.93 (0.57, 1.49)	0.80	1.00
ipaH (EIEC)	Control	181	1.1 (-0.4, 2.6)		205	2.4 (0.3, 4.5)			
	Sanitation	168	0.6 (-0.6, 1.8)	0.50 (0.04, 6.93)	188	0.5 (-0.5, 1.6)	0.24 (0.02, 2.44)	0.69	1.00
st1b/lt1 (ETEC)	Control	179	10.6 (6.3, 14.9)		204	10.3 (6.4, 14.2)			
	Sanitation	165	4.2 (1.2, 7.2)	0.42 (0.19, 0.95)	185	8.6 (3.6, 13.6)	0.90 (0.45, 1.77)	0.18	0.74
BacCow	Control	182	64.8 (58.1, 71.6)		181	75.1 (68.9, 81.4)			
	Sanitation	168	63.1 (55.7, 70.5)	0.96 (0.82, 1.12)	174	70.7 (63.6, 77.8)	0.95 (0.82, 1.09)	0.89	1.00
HumM2	Control	159	2.5 (0.1, 4.9)		178	4.5 (1.5, 7.4)			
	Sanitation	143	2.1 (-0.2, 4.4)	0.80 (0.15, 4.13)	172	1.2 (-0.4, 2.8)	0.28 (0.05, 1.67)	0.41	1.00
Soil									
Any ECVG	Control	201	67.7 (61.0, 74.3)		181	54.7 (47.0, 62.4)			
	Sanitation	185	62.7 (55.4, 70.0)	0.94 (0.80, 1.10)	173	54.9 (46.4, 63.4)	1.00 (0.82, 1.21)	0.66	1.00
eaeA (EPEC/EHEC)	Control	201	42.3 (35.2, 49.4)		182	34.6 (26.7, 42.5)			
	Sanitation	182	40.7 (33.9, 47.5)	0.99 (0.76, 1.28)	178	32.6 (25.2, 40.0)	0.95 (0.72, 1.25)	0.83	1.00
aggR (EAEC)	Control	208	18.8 (13.8, 23.7)		182	15.9 (10.0, 21.9)			
	Sanitation	187	16.0 (10.7, 21.3)	0.92 (0.59, 1.44)	178	12.4 (7.5, 17.2)	0.82 (0.45, 1.48)	0.76	1.00
stx1/stx2 (STEC)	Control	208	26.9 (21.1, 32.8)		180	25.0 (18.7, 31.3)			
	Sanitation	187	27.3 (20.7, 33.9)	0.99 (0.71, 1.38)	174	19.5 (13.3, 25.8)	0.77 (0.49, 1.19)	0.38	1.00
ipaH (EIEC)	Control	208	1.9 (0.1, 3.8)		182	1.1 (-0.4, 2.6)			
	Sanitation	187	1.1 (-0.4, 2.5)	0.48 (0.07, 3.19)	178	0.6 (-0.5, 1.7)	0.59 (0.05, 6.42)	0.91	1.00
st1b/lt1 (ETEC)	Control	205	18.5 (13.4, 23.7)		182	15.9 (10.3, 21.6)			
	Sanitation	185	13.0 (7.8, 18.1)	0.73 (0.41, 1.29)	175	13.1 (8.2, 18.1)	0.79 (0.53, 1.18)	0.81	1.00

BacCow	Control	187	89.8 (85.7, 94.0)		144	93.1 (88.9, 97.2)			
	Sanitation	167	88.0 (82.5, 93.6)	0.97 (0.90, 1.05)	148	92.6 (88.1, 97.0)	1.00 (0.92, 1.08)	0.67	1.00
HumM2	Control	192	15.6 (10.5, 20.8)		140	22.1 (15.0, 29.3)			
	Sanitation	170	12.4 (7.2, 17.5)	0.81 (0.46, 1.42)	144	33.3 (25.5, 41.2)	1.52 (0.98, 2.36)	0.10	0.39

[a]: p-values were corrected for multiple comparisons using the Bonferroni method

Table S9: Prevalence ratios (PR) and 95% confidence intervals (95% CI) comparing the prevalence of pathogenic *E. coli* virulence genes, norovirus GII gene, *Giardia* gene and microbial source tracking markers on child hands, mother hands, stored water and soil in the sanitation and control arms in households with < 20 and ≥ 20 animals.

			<20 animals			≥20 animals		Interaction p-value	Corrected p-value[a]
		N	Prevalence (95%CI)	PR (95% CI)	N	Prevalence (95%CI)	PR (95% CI)		
Child Hands									
Any ECVG	Control	93	29.0 (19.8, 38.3)		90	35.6 (25.1, 46.0)			
	Sanitation	93	36.6 (27.3, 45.9)	1.54 (0.83, 2.88)	88	28.4 (18.2, 38.6)	0.71 (0.41, 1.25)	0.12	0.49
eaeA (EPEC/EHEC)	Control	95	11.6 (4.4, 18.8)		89	14.6 (7.3, 22.0)			
	Sanitation	94	10.6 (4.8, 16.5)	1.33 (0.47, 3.80)	89	9.0 (3.2, 14.7)	0.49 (0.15, 1.64)	0.28	1.00
aggR (EAEC)	Control	97	10.3 (4.4, 16.2)		90	14.4 (7.1, 21.7)			
	Sanitation	97	10.3 (4.5, 16.1)	1.22 (0.40, 3.76)	89	12.4 (5.8, 18.9)	0.67 (0.27, 1.70)	0.48	1.00
stx1/stx2 (STEC)	Control	96	13.5 (6.9, 20.2)		90	13.3 (6.2, 20.5)			
	Sanitation	95	17.9 (9.5, 26.3)	1.17 (0.46, 2.98)	89	15.7 (7.8, 23.6)	1.50 (0.62, 3.64)	0.74	1.00
ipaH (EIEC)	Control	97	NA		90	NA			
	Sanitation	97	NA	NA	89	1.1 (-1.1, 3.3)	NA		
st1b/lt1 (ETEC)	Control	95	6.3 (1.7, 11.0)		90	13.3 (5.9, 20.8)			
	Sanitation	96	10.4 (3.8, 17.1)	2.41 (0.65, 8.94)	88	4.5 (0.3, 8.8)	0.22 (0.04, 1.06)	0.04*	0.16
Norovirus	Control	85	2.4 (-0.9, 5.6)		82	6.1 (1.0, 11.2)			
	Sanitation	88	3.4 (-0.4, 7.2)	2.48 (0.22, 27.4)	81	4.9 (0.3, 9.6)	0.47 (0.08, 2.87)	0.33	1.00
Giardia	Control	83	7.2 (1.6, 12.8)		74	2.7 (-1.0, 6.4)			
	Sanitation	80	1.3 (-1.2, 3.7)	0.33 (0.03, 4.31)	74	8.1 (2.1, 14.1)	4.20 (0.32, 54.64)	0.17	0.69
BacCow	Control	94	98.9 (96.9, 101)		89	100 (100, 100)			
	Sanitation	95	94.7 (89.5, 99.9)	0.96 (0.90, 1.02)	87	96.6 (92.8, 100.3)	0.97 (0.91, 1.03)	0.80	1.00
HumM2	Control	87	21.8 (13.1, 30.6)		80	31.3 (21.1, 41.4)			
	Sanitation	87	10.3 (4.1, 16.6)	0.32 (0.12, 0.82)	83	25.3 (15.7, 34.9)	1.21 (0.62, 2.35)	0.03*	0.13
Mother Hands									
Any ECVG	Control	200	23.5 (18.2, 28.8)		167	24.0 (18.1, 29.8)			
	Sanitation	181	16.0 (10.6, 21.4)	0.71 (0.47, 1.06)	172	25.0 (19.1, 30.9)	1.06 (0.70, 1.61)	0.21	0.83
eaeA (EPEC/EHEC)	Control	203	9.9 (6.1, 13.6)		167	6.0 (2.6, 9.4)			
	Sanitation	184	4.3 (1.5, 7.2)	0.45 (0.19, 1.05)	175	10.3 (5.7, 14.9)	1.70 (0.71, 4.08)	0.03*	0.14
aggR (EAEC)	Control	206	9.7 (5.5, 13.9)		170	8.8 (4.5, 13.1)			
	Sanitation	187	2.7 (0.3, 5.0)	0.27 (0.09, 0.83)	175	9.7 (5.4, 14.1)	1.15 (0.54, 2.48)	0.05	0.21
stx1/stx2 (STEC)	Control	204	9.8 (5.7, 13.9)		170	8.2 (3.7, 12.8)			
	Sanitation	185	7.0 (3.3, 10.7)	0.79 (0.42, 1.52)	174	8.0 (4, 12.1)	0.92 (0.39, 2.18)	0.78	1.00
ipaH (EIEC)	Control	206	1.9 (0.1, 3.8)		170	NA			
	Sanitation	187	0.5 (-0.5, 1.6)	0.31 (0.03, 3.04)	175	0.6 (-0.6, 1.7)	NA		
st1b/lt1 (ETEC)	Control	205	2.9 (0.7, 5.1)		169	5.3 (2.1, 8.5)			

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Analyte	Arm	N			N			p	p-adj
	Sanitation	185	3.8 (1.1, 6.5)	1.34 (0.40, 4.49)	173	4.0 (1.3, 6.8)	0.75 (0.25, 2.23)	0.52	1.00
Norovirus	Control	182	2.7 (0.0, 5.5)		162	3.1 (0.5, 5.6)			
	Sanitation	177	1.7 (-0.2, 3.6)	0.64 (0.11, 3.78)	165	4.8 (1.7, 8.0)	1.66 (0.48, 5.67)	0.40	1.00
Giardia	Control	166	3.0 (-0.1, 6.1)		136	2.9 (0.1, 5.8)			
	Sanitation	155	1.9 (-0.8, 4.7)	0.94 (0.17, 5.07)	146	1.4 (-1.3, 4)	0.37 (0.03, 5.16)	0.56	1.00
BacCow	Control	199	95.5 (92.7, 98.2)		169	100 (100, 100)			
	Sanitation	186	94.1 (90.9, 97.3)	0.99 (0.94, 1.04)	172	97.7 (95.4, 99.9)	0.98 (0.95, 1.01)	0.70	1.00
HumM2	Control	174	17.8 (11.4, 24.2)		151	19.2 (12.9, 25.5)			
	Sanitation	169	13.6 (8.2, 19.1)	0.74 (0.37, 1.48)	159	22.0 (15.2, 28.8)	1.32 (0.77, 2.25)	0.22	0.87
Stored Water									
Any ECVG	Control	215	36.3 (30.2, 42.3)		166	39.2 (32.1, 46.2)			
	Sanitation	183	35.0 (28.5, 41.4)	0.94 (0.70, 1.27)	160	38.1 (30.9, 45.4)	0.98 (0.72, 1.32)	0.88	1.00
eaeA (EPEC/EHEC)	Control	215	14.4 (9.8, 19)		165	16.4 (10.5, 22.2)			
	Sanitation	188	12.2 (8.1, 16.4)	0.89 (0.50, 1.60)	163	17.2 (10.9, 23.4)	0.99 (0.56, 1.72)	0.83	1.00
aggR (EAEC)	Control	218	9.6 (6.0, 13.3)		168	11.3 (6.4, 16.3)			
	Sanitation	192	12.0 (7.9, 16.1)	1.33 (0.74, 2.41)	164	11.6 (7.0, 16.2)	0.99 (0.48, 2.06)	0.59	1.00
stx1/stx2 (STEC)	Control	217	15.2 (10.1, 20.3)		168	18.5 (12.4, 24.5)			
	Sanitation	189	13.8 (9.0, 18.5)	0.86 (0.52, 1.44)	163	19.6 (13.8, 25.5)	1.07 (0.65, 1.78)	0.58	1.00
ipaH (EIEC)	Control	218	1.4 (-0.2, 2.9)		168	2.4 (0.0, 4.7)			
	Sanitation	192	NA	NA	164	1.2 (-0.4, 2.9)	0.30 (0.06, 1.38)		
st1b/lt1 (ETEC)	Control	216	9.3 (5.6, 12.9)		167	12.0 (7.3, 16.6)			
	Sanitation	189	5.8 (2.2, 9.5)	0.68 (0.30, 1.54)	161	7.5 (3.8, 11.1)	0.65 (0.36, 1.17)	0.92	1.00
BacCow	Control	205	65.9 (58.6, 73.1)		158	75.3 (68.6, 82.0)			
	Sanitation	187	59.9 (52.6, 67.2)	0.89 (0.74, 1.07)	155	75.5 (67.4, 83.5)	1.02 (0.88, 1.18)	0.30	1.00
HumM2	Control	190	3.2 (0.8, 5.6)		147	4.1 (0.5, 7.6)			
	Sanitation	174	2.3 (0.1, 4.5)	0.72 (0.14, 3.81)	141	0.7 (-0.7, 2.1)	0.19 (0.02, 2.05)	0.42	1.00
Soil									
Any ECVG	Control	205	55.6 (49.0, 62.2)		177	68.4 (61.1, 75.6)			
	Sanitation	185	57.8 (50.9, 64.8)	1.01 (0.84, 1.20)	173	60.1 (52.9, 67.4)	0.92 (0.77, 1.10)	0.52	1.00
eaeA (EPEC/EHEC)	Control	207	36.7 (30.3, 43.2)		176	40.9 (32.2, 49.6)			
	Sanitation	185	31.9 (24.9, 38.8)	0.84 (0.63, 1.13)	175	41.7 (34.3, 49.1)	1.08 (0.79, 1.48)	0.30	1.00
aggR (EAEC)	Control	211	17.1 (11.9, 22.2)		179	17.9 (12.0, 23.7)			
	Sanitation	189	14.3 (9.4, 19.2)	0.70 (0.43, 1.14)	176	14.2 (9.2, 19.2)	1.17 (0.64, 2.14)	0.25	1.00
stx1/stx2 (STEC)	Control	209	22.0 (16.6, 27.4)		179	30.7 (24.4, 37.0)			
	Sanitation	187	22.5 (16.9, 28.0)	1.00 (0.66, 1.50)	174	24.7 (18.3, 31.1)	0.79 (0.58, 1.09)	0.37	1.00
ipaH (EIEC)	Control	211	1.4 (-0.2, 3.0)		179	1.7 (-0.2, 3.5)			
	Sanitation	189	1.1 (-0.4, 2.5)	0.84 (0.10, 6.83)	176	0.6 (-0.5, 1.7)	0.32 (0.03, 3.36)	0.57	1.00
st1b/lt1 (ETEC)	Control	209	15.8 (10.7, 20.8)		178	19.1 (13.0, 25.2)			
	Sanitation	187	16.0 (10.6, 21.5)	1.15 (0.71, 1.86)	173	9.8 (5.0, 14.6)	0.46 (0.23, 0.92)	0.05	0.21
BacCow	Control	176	88.1 (83.8, 92.4)		155	94.8 (91.5, 98.2)			

	Sanitation	165	89.1 (82.7, 95.5)	1.01 (0.93, 1.10)	150	91.3 (86.6, 96.1)	0.96 (0.88, 1.04)	0.39	1.00
HumM2	Control	175	16.0 (10.6, 21.4)		157	21.0 (14.9, 27.1)			
	Sanitation	165	22.4 (16.6, 28.3)	1.37 (0.81, 2.32)	149	21.5 (14.6, 28.4)	1.06 (0.69, 1.65)	0.49	1.00

[a]: p-values were corrected for multiple comparisons using the Bonferroni method

*significant at p-value < 0.05

Table S10: Prevalence ratios (PR) and 95% confidence intervals (95% CI) comparing the prevalence of pathogenic *E. coli* virulence genes, norovirus GII gene, *Giardia* gene and microbial source tracking markers on child hands, mother hands, stored water and soil in the sanitation and control arms in households with < 10 and ≥ 10 individuals.

		<10 individuals			≥ 10 individuals			Interaction p-value	Corrected p-value[a]
		N	Prevalence (95% CI)	PR (95% CI)	N	Prevalence (95% CI)	PR (95% CI)		
Child Hands									
CH Any ECVG	Control	91	34.1 (24.6, 43.6)		92	30.4 (20.7, 40.1)			
	Sanitation	90	37.8 (29.1, 46.5)	1.36 (0.82, 2.27)	91	27.5 (17.7, 37.2)	0.80 (0.47, 1.35)	0.18	0.71
eaeA (EPEC/EHEC)	Control	91	12.1 (4.4, 19.8)		93	14.0 (6.0, 21.9)			
	Sanitation	90	11.1 (4.7, 17.5)	1.83 (0.53, 6.35)	93	8.6 (3.3, 14.0)	0.40 (0.16, 1.01)	0.07	0.30
aggR (EAEC)	Control	93	10.8 (4.5, 17.0)		94	13.8 (7.0, 20.7)			
	Sanitation	91	13.2 (6.8, 19.6)	0.85 (0.31, 2.32)	95	9.5 (3.1, 15.8)	0.94 (0.32, 2.78)	0.90	1.00
stx1/*stx2* (STEC)	Control	92	20.7 (12.4, 28.9)		94	6.4 (1.6, 11.2)			
	Sanitation	91	18.7 (10.4, 27.0)	1.02 (0.53, 1.97)	93	15.1 (7.6, 22.5)	2.20 (0.70, 6.90)	0.25	1.00
ipaH (EIEC)	Control	93	NA		94	NA			
	Sanitation	91	1.1 (-1.0, 3.2)	NA	95	NA	NA		
st1b/*lt1* (ETEC)	Control	93	4.3 (0.3, 8.3)		92	15.2 (8.2, 22.3)			
	Sanitation	90	12.2 (5.2, 19.2)	5.08 (1.08, 23.82)	94	3.2 (-0.3, 6.7)	0.11 (0.02, 0.77)	0.01*	0.04*
Norovirus	Control	80	2.5 (-0.9, 5.9)		87	5.7 (1.0, 10.5)			
	Sanitation	82	2.4 (-0.9, 5.8)	1.21 (0.13, 11.30)	87	5.7 (0.9, 10.6)	0.81 (0.23, 2.84)	0.76	1.00
Giardia	Control	84	4.8 (0.2, 9.3)		73	5.5 (0.2, 10.8)			
	Sanitation	81	2.5 (-0.9, 5.8)	0.23 (0.01, 4.60)	73	6.8 (1.2, 12.5)	3.33 (0.37, 30.28)	0.23	0.91
BacCow	Control	90	98.9 (96.7, 101)		93	100 (100, 100)			
	Sanitation	87	93.1 (87.7, 98.5)	0.93 (0.85, 1.01)	95	97.9 (95.0, 100.7)	1 .00 (0.97, 1.03)	0.13	0.53
HumM2	Control	85	21.2 (12.8, 29.5)		82	31.7 (20.9, 42.5)			
	Sanitation	85	18.8 (10.1, 27.5)	0.85 (0.39, 1.87)	85	16.5 (8.6, 24.4)	0.54 (0.23, 1.28)	0.49	1.00
Mother Hands									
MH Any ECVG	Control	182	19.2 (13.3, 25.2)		185	28.1 (21.8, 34.4)			
	Sanitation	174	18.4 (13.0, 23.8)	0.96 (0.62, 1.50)	179	22.3 (16.0, 28.7)	0.83 (0.55, 1.26)	0.69	1.00
eaeA (EPEC/EHEC)	Control	185	8.6 (4.9, 12.4)		185	7.6 (4.0, 11.1)			
	Sanitation	175	7.4 (3.5, 11.4)	0.89 (0.40, 2.00)	184	7.1 (3.4, 10.8)	0.93 (0.44, 1.97)	0.94	1.00
aggR (EAEC)	Control	186	8.1 (3.7, 12.4)		190	10.5 (6.2, 14.8)			
	Sanitation	175	4.6 (1.7, 7.5)	0.62 (0.24, 1.61)	187	7.5 (3.5, 11.5)	0.64 (0.32, 1.29)	0.96	1.00
stx1/*stx2* (STEC)	Control	184	7.1 (3.3, 10.9)		190	11.1 (6.0, 16.1)			
	Sanitation	175	4.6 (1.3, 7.8)	0.55 (0.24, 1.25)	184	10.3 (5.6, 15.1)	1.08 (0.50, 2.33)	0.24	0.95
ipaH (EIEC)	Control	186	0.5 (-0.5, 1.6)		190	1.6 (-0.1, 3.3)			
	Sanitation	175	0.6 (-0.6, 1.7)	0.74 (0.02, 27.62)	187	0.5 (-0.5, 1.6)	0.45 (0.04, 5.46)	0.83	1.00
st1b/*lt1* (ETEC)	Control	185	2.7 (0.4, 5.0)		189	5.3 (2.3, 8.3)			
	Sanitation	173	4.0 (1.2, 6.9)	1.42 (0.42, 4.81)	185	3.8 (1.2, 6.4)	0.76 (0.27, 2.19)	0.47	1.00
Norovirus	Control	165	3.6 (0.4, 6.8)		179	2.2 (0.1, 4.4)			

	Arm	N	% (95% CI)	Ratio (95% CI)	N	% (95% CI)	Ratio (95% CI)	p	adj p
	Sanitation	168	2.4 (0.2, 4.6)	0.69 (0.13, 3.76)	174	4 (1.2, 6.8)	1.84 (0.42, 7.96)	0.43	1.00
Giardia	Control	161	3.1 (-0.1, 6.3)		141	2.8 (0.2, 5.5)			
	Sanitation	159	1.9 (-0.8, 4.6)	0.63 (0.05, 8.18)	142	1.4 (-1.3, 4.2)	0.54 (0.05, 5.98)	0.94	1.00
BacCow	Control	181	97.8 (95.7, 99.8)		187	97.3 (95.0, 99.6)			
	Sanitation	173	94.2 (91.0, 97.5)	0.96 (0.92, 1.01)	185	97.3 (95.0, 99.6)	1.00 (0.96, 1.04)	0.20	0.80
HumM2	Control	160	17.5 (11.0, 24.0)		165	19.4 (13.0, 25.7)			
	Sanitation	168	16.7 (10.5, 22.8)	1.04 (0.54, 1.99)	160	18.8 (12.7, 24.8)	0.97 (0.55, 1.72)	0.89	1.00
Stored Water									
SW Any ECVG	Control	195	35.9 (29.5, 42.3)		186	39.2 (32.2, 46.3)			
	Sanitation	169	37.9 (30.6, 45.2)	1.07 (0.76, 1.51)	174	35.1 (27.8, 42.3)	0.86 (0.66, 1.13)	0.36	1.00
eaeA (EPEC/EHEC)	Control	195	15.9 (10.5, 21.3)		185	14.6 (9.6, 19.6)			
	Sanitation	171	15.2 (10.3, 20.2)	0.99 (0.56, 1.78)	180	13.9 (8.8, 19.0)	0.92 (0.52, 1.64)	0.87	1.00
aggR (EAEC)	Control	196	7.7 (4.0, 11.3)		190	13.2 (8.1, 18.2)			
	Sanitation	173	13.9 (9.1, 18.6)	2.05 (1.08, 3.88)	183	9.8 (5.7, 14.0)	0.70 (0.37, 1.30)	0.03*	0.12
stx1/*stx2* (STEC)	Control	195	14.9 (9.8, 20.0)		190	18.4 (12.8, 24.1)			
	Sanitation	172	16.3 (10.9, 21.6)	1.24 (0.73, 2.09)	180	16.7 (10.7, 22.6)	0.78 (0.48, 1.28)	0.26	1.00
ipaH (EIEC)	Control	196	1.5 (-0.2, 3.2)		190	2.1 (0.1, 4.1)			
	Sanitation	173	0.6 (-0.6, 1.7)	0.33 (0.02, 4.49)	183	0.5 (-0.5, 1.6)	0.26 (0.03, 2.10)	0.89	1.00
st1b/*lt1* (ETEC)	Control	196	10.2 (6.3, 14.1)		187	10.7 (6.6, 14.8)			
	Sanitation	171	7.0 (2.5, 11.6)	0.64 (0.28, 1.45)	179	6.1 (2.4, 9.9)	0.66 (0.34, 1.26)	0.96	1.00
BacCow	Control	185	64.3 (57.3, 71.3)		178	75.8 (69.7, 82.0)			
	Sanitation	171	63.2 (55.6, 70.7)	1.00 (0.84, 1.20)	171	70.8 (63.3, 78.2)	0.91 (0.77, 1.07)	0.42	1.00
HumM2	Control	170	1.8 (-0.2, 3.7)		167	5.4 (1.8, 9.0)			
	Sanitation	157	1.9 (-0.2, 4.1)	1.48 (0.21, 10.54)	158	1.3 (-0.4, 3.0)	0.19 (0.03, 1.29)	0.19	0.77
Soil									
Soil Any ECVG	Control	187	56.1 (48.6, 63.7)		195	66.7 (60.2, 73.2)			
	Sanitation	172	63.4 (55.6, 71.1)	1.08 (0.88, 1.31)	186	54.8 (47.9, 61.8)	0.86 (0.72, 1.04)	0.15	0.58
eaeA (EPEC/EHEC)	Control	189	33.9 (27.5, 40.3)		194	43.3 (35.0, 51.6)			
	Sanitation	173	37.6 (30.7, 44.4)	1.08 (0.82, 1.43)	187	35.8 (28.8, 42.9)	0.87 (0.65, 1.16)	0.32	1.00
aggR (EAEC)	Control	191	13.6 (8.2, 19.0)		199	21.1 (15.6, 26.6)			
	Sanitation	174	14.4 (9.6, 19.1)	1.10 (0.64, 1.87)	191	14.1 (9.2, 19.0)	0.73 (0.44, 1.19)	0.29	1.00
stx1/*stx2* (STEC)	Control	189	25.4 (18.9, 31.9)		199	26.6 (20.4, 32.9)			
	Sanitation	174	24.7 (17.9, 31.5)	0.90 (0.57, 1.42)	187	22.5 (16.7, 28.2)	0.87 (0.60, 1.26)	0.90	1.00
ipaH (EIEC)	Control	191	1.0 (-0.4, 2.5)		199	2.0 (0.1, 3.9)			
	Sanitation	174	1.1 (-0.4, 2.7)	0.71 (0.06, 8.88)	191	0.5 (-0.5, 1.5)	0.41 (0.04, 4.17)	0.76	1.00
st1b/*lt1* (ETEC)	Control	190	15.3 (9.9, 20.6)		197	19.3 (13.9, 24.7)			
	Sanitation	172	14.0 (8.7, 19.3)	0.72 (0.42, 1.22)	188	12.2 (7.5, 16.9)	0.78 (0.42, 1.45)	0.87	1.00
BacCow	Control	156	89.1 (84.3, 93.9)		175	93.1 (89.8, 96.5)			
	Sanitation	154	87.0 (81.7, 92.4)	0.97 (0.89, 1.06)	161	93.2 (88.1, 98.2)	1.00 (0.94, 1.08)	0.53	1.00
HumM2	Control	155	15.5 (9.6, 21.4)		177	20.9 (14.6, 27.2)			
	Sanitation	151	23.2 (16.5, 29.9)	1.69 (1.00, 2.85)	163	20.9 (14.6, 27.1)	0.90 (0.59, 1.38)	0.08	0.33

[a]:p-values were corrected for multiple comparisons using the Bonferroni method

*significant at p-value < 0.05

Table S11: Unadjusted mean and unadjusted difference in the $\log_{10}$concentration of BacCow on hands, in stored water, and soil by season, number of individuals in the household, and number of animals in the household.

		N	Mean $\log_{10}$ Concentration (95% CI)	$\Delta\log_{10}$ Concentration (95% CI)	N	Mean $\log_{10}$ Concentration (95% CI)	$\Delta\log_{10}$ Concentration (95% CI)	Interaction p-value	Corrected p-value[a]
Season			Wet			Dry			
Child Hands	Control	98	3.9 (3.8, 4.1)		85	3.9 (3.7, 4.1)			
	Sanitation	95	3.7 (3.5, 3.9)	-0.26 (-0.55, 0.02)	88	3.8 (3.7, 4.0)	-0.13 (-0.46, 0.21)	0.53	1.00
Mother Hands	Control	196	3.8 (3.7, 3.9)		172	3.7 (3.6, 3.8)			
	Sanitation	185	3.5 (3.4, 3.7)	-0.25 (-0.43, 0.07)	173	3.6 (3.5, 3.7)	-0.07 (-0.24, 0.11)	0.13	0.54
Stored Water	Control	182	1.2 (1.1, 1.3)		195	1.3 (1.2, 1.4)			
	Sanitation	169	1.2 (1.1, 1.3)	-0.05 (-0.20, 0.09)	182	1.3 (1.2, 1.4)	0.02 (-0.14, 0.17)	0.50	1.00
Soil	Control	209	3.3 (3.1, 3.5)		170	3.4 (3.2, 3.6)			
	Sanitation	187	3.2 (3.0, 3.4)	-0.07 (-0.33, 0.18)	172	3.5 (3.3, 3.7)	0.15 (-0.14, 0.43)	0.25	0.99
Number of Individuals			<10 individuals			≥ 10 individuals			
Child Hands	Control	90	3.8 (3.6, 4.0)		93	4.1 (3.9, 4.2)			
	Sanitation	88	3.6 (3.4, 3.8)	-0.27 (- 0.6, 0.06)	95	3.9 (3.8, 4.1)	-0.13 (-0.46, 0.21)	0.56	1.00
Mother Hands	Control	181	3.7 (3.6, 3.8)		187	3.8 (3.7, 3.9)			
	Sanitation	173	3.4 (3.3, 3.6)	-0.25 (-0.44, - 0.07)	185	3.7 (3.6, 3.9)	-0.08 (-0.27, 0.11)	0.19	0.76
Stored Water	Control	192	1.2 (1.1, 1.3)		185	1.4 (1.3, 1.5)			
	Sanitation	173	1.2 (1.1, 1.3)	0.04 (-0.10, 0.17)	178	1.3 (1.2, 1.4)	-0.07 (-0.25, 0.10)	0.33	1.00
Soil	Control	184	3.3 (3.1, 3.5)		195	3.4 (3.2, 3.6)			
	Sanitation	172	3.3 (3.1, 3.5)	-0.02 (-0.30, 0.26)	187	3.4 (3.2, 3.6)	0.08 (-0.23, 0.40)	0.65	1.00
Number of Animals			<20 animals			≥ 20 animals			
Child Hands	Control	94	3.7 (3.6, 3.9)		89	4.1 (4.0, 4.3)			
	Sanitation	95	3.7 (3.5, 3.9)	-0.14 (-0.45, 0.17)	88	3.9 (3.7, 4.0)	-0.26 (-0.61, 0.10)	0.64	1.00
Mother Hands	Control	199	3.6 (3.5, 3.7)		169	3.9 (3.8, 4.0)			
	Sanitation	186	3.4 (3.2, 3.5)	-0.24 (-0.44, -0.05)	172	3.8 (3.7, 4.0)	-0.10 (-0.27, 0.08)	0.28	1.00
Stored Water	Control	214	1.2 (1.1, 1.3)		163	1.3 (1.2, 1.4)			
	Sanitation	191	1.1 (1.1, 1.2)	-0.07 (-0.20, 0.06)	160	1.4 (1.3, 1.5)	0.04 (-0.13, 0.21)	0.31	1.00
Soil	Control	204	3.2 (3.0, 3.3)		175	3.5 (3.3, 3.7)			
	Sanitation	187	3.3 (3.1, 3.5)	0.14 (-0.08, 0.37)	172	3.4 (3.1, 3.6)	-0.10 (-0.45, 0.25)	0.28	1.00

Note: Units of concentration are gene copies of BacCow per 2 hands, 100 mL, and dry gram

[a]: p-values were corrected for multiple comparisons using the Bonferroni method

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