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Supplementary Data

Estimation of concentration ratio of indicator to pathogen-related gene in environmental water based on left-censored data

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Table S1

Table S1. Latitude and longitude locations of sampling sites

Sampling site number	North latitude	East longitude
Site 1	43.039395	141.357157
Site 2	43.040242	141.355548
Site 3	43.065643	141.469038
Site 4	43.090704	141.469316
Site 5	43.067352	141.416509
Site 6	43.082947	141.482416

Table S2.

Table S1. Primers and probes used in this study

Target	Primer	Sequence (5'-3')	Reference
Total Bac	qBac560F	TTTATTGGGTTTAAAGGGAGCGTA	Okabe et al. 2007
	qBac725R	CAATCGGAGTTCTTCGTGATATCTA	
Human Bac	qHS601F	GTTGTGAAAGTTTGCGGCTCA	Okabe et al. 2007
	qBac725R	-	
	qHS624MGB	(FAM)-CGTAAAATTGCAGTTGA-(MGB)	
Chicken Bac	qC160F-HU	AAGGGAGATTAATACCCGATGATG	Kobayashi et al. 2013b
	qBac265R-HU	CCGTTACCCCGCCTACTAC	
<i>E. coli</i> MG1655 Δ lac::kan	Kan-res-F	ATCGCCTTCTTGACGAGTTC	Kobayashi et al. 2013a
	DS-Kan-R	TTTGCACCAGTACGTTTTCC	
Enteropathogenic <i>E. coli</i> (<i>eaeA</i>)	eaeA_877F	GGCGAATACTGGCGAGACTA	Ishii et al. 2013
	eaeA_976R	GGCGCTCATCATAGTCTTTCTT	
	#28	-	Universal ProbeLibrary-probe (Roche)
<i>Campylobacter jejuni</i> (<i>ciaB</i>)	ciaB_718F	GCGTTTTGTGAAAAAGATGAAGATAG	Ishii et al. 2013
	ciaB_797R	GGTGATTTTACTTTCATCCAAGC	
	#137	-	Universal ProbeLibrary-probe (Roche)

Table S3

Table S2. Chi-square test for normality and expected values of geometric mean and standard deviation

	Total coliforms	general <i>E. coli</i>	Total Bac ^a	Human Bac ^b	<i>eaeA</i> ^c	<i>ciaB</i> ^d
Total sample number	144	144	144	144	144	144
Positive sample number	144	143	144	143	39	28
p-value	3.16 x 10 ⁻³	0.22	0.03	0.01	0.18	3.76 x 10 ⁻⁴
Geometric mean (logarithmic geometric SD) calculated from raw data (MPN or copies/mL)	0.87 (-0.01)	- ^e	3.45 (0.03)	- ^e	- ^e	- ^e
Geometric mean (logarithmic geometric SD) estimated from normality probability plot (MPN or copies/mL)	1.87 (0.01)	0.85 (0.01)	3.45 (0.03)	3.00 (0.05)	-1.73 (0.07)	0.19 (-0.22)

a, genetic marker for *total Bacteroides* (Kobayashi et al., 2013a); b, genetic marker for human-specific *Bacteroides* (Kobayashi et al., 2013a); c, a virulence gene of enteropathogenic *E. coli*; d, a virulence gene of *Campylobacter jejuni*; e, geometric mean and standard deviation are not appropriate as expected values of population mean and standard deviation because of left-censored data.

Table S4

Table S3. Pearson's product-moment correlation coefficient between quantities of indicators and *eaeA*, a virulence gene of pathogenic *Escherichia coli*

	general <i>E. coli</i>	Total Bac	Human Bac
Pearson's product-moment correlation coefficient	0.24	0.72	0.62
p value	0.17	2.31×10^{-7}	2.74×10^{-5}

Fig. S1

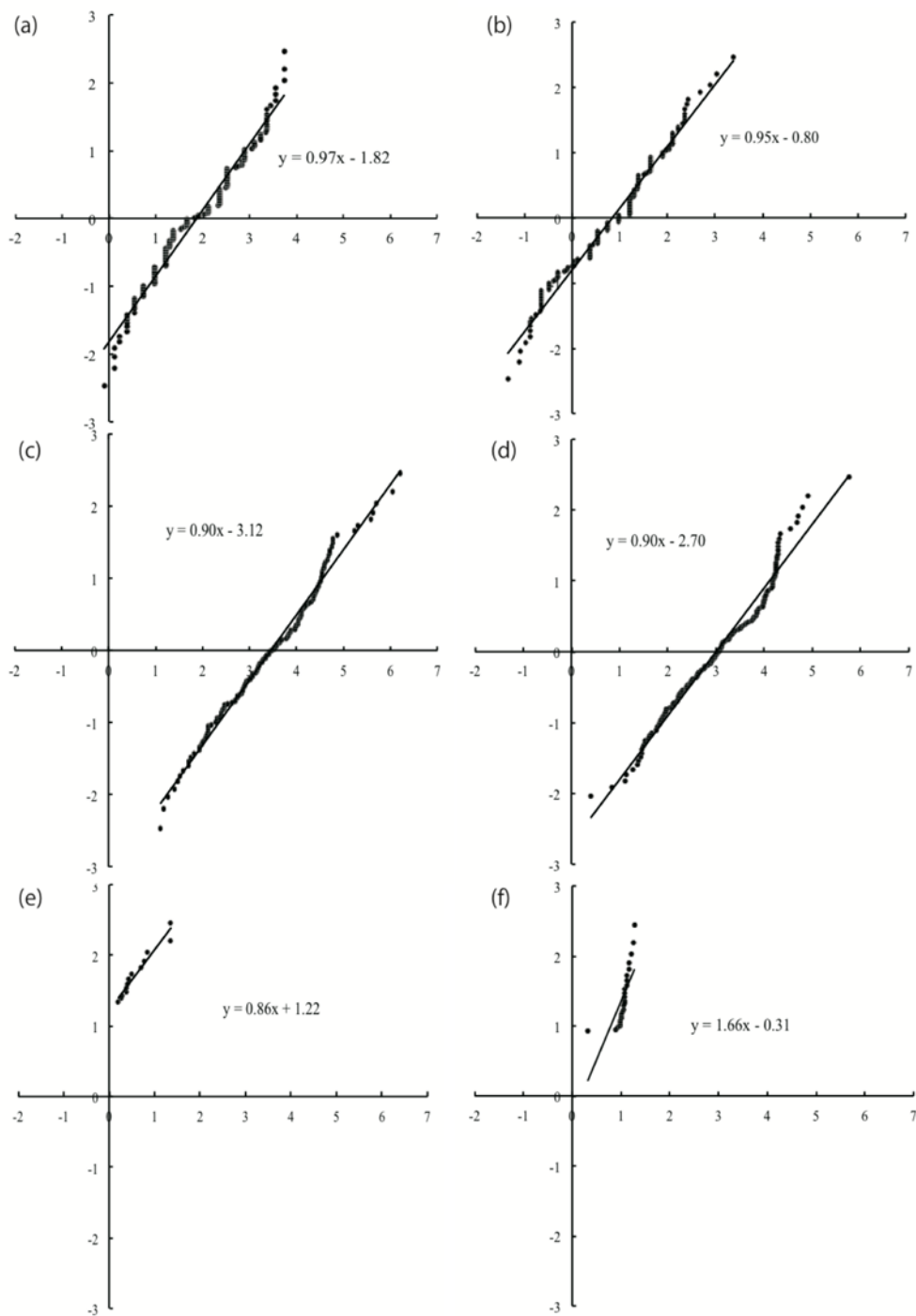


Figure S1. Normal probability plot of observed data. X-axis is logarithmic value of observed data (Log(copies/mL)), and Y-axis is normal probability. a) Total coliforms, b) general *Escherichia coli*, c) Total Bac, d) Human Bac, e) *eaeA* (a virulence gene of enteropathogenic *E. coli*), and f) *ciaB* (a virulence gene of *Campylobacter jejuni*).

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