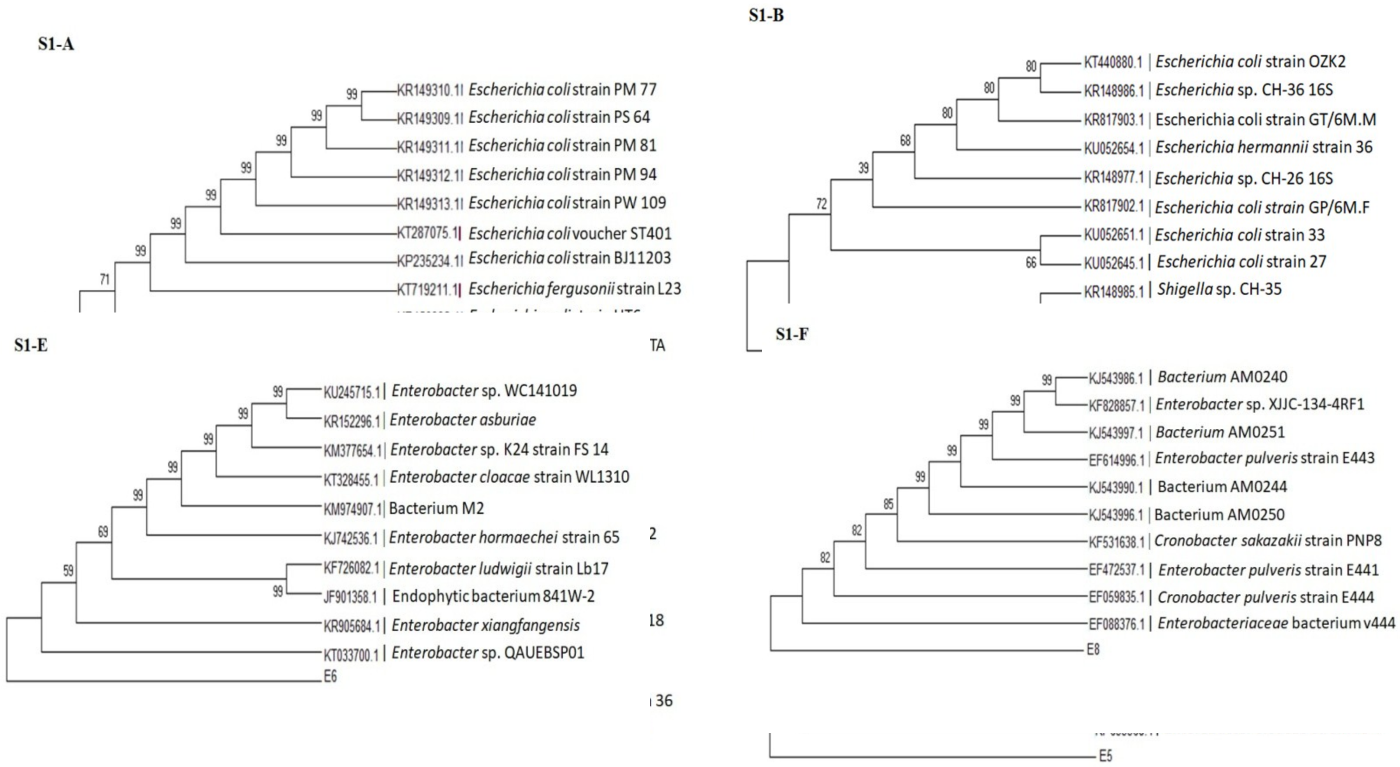
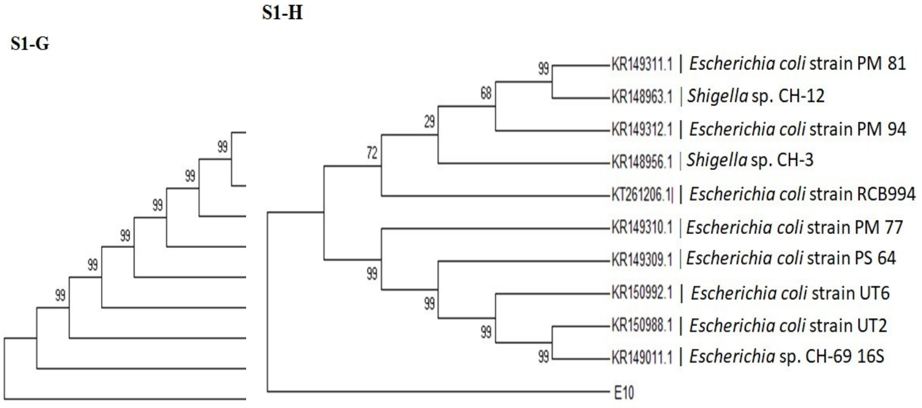
ESI S1.





ESI S1. The phylogenetic trees of *E. coli* (isolate E1) (**S1-A**); *Escherichia hermannii* (isolate E3) (**S1-B**); *E. coli* (isolate E4) (**S1-C**); *Enterobacter cloacae* (isolate E5) (**S1-D**); *Enterobacter ludwigii* (isolate E6) (**S1-E**); *Enterobacter pulveris* (isolate E8) (**S1-F**) *Pseudomonas mosselii* (isolate E9) (**S1-G**) and *E. coli* (isolate E10) (**S1-H**). The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei, 1987). The confidence probability (multiplied by 100) of the interior branch length is greater than 0, as estimated using the bootstrap test (500 replicates is shown next to the branches (Dopazo et. al., 1994; Rzhetsky and Nei, 1992). Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 651 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 (Tamura et al., 2007).

ESI S2:

S2-A

>E1 Consensus data

GGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGCCCAGATGGGATTAGC
TAGTAGGTGGGGTAACGGCTCACCTACGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGAC
TCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTAATGCAGCCATGCCGCGTGTATGAAGAAAGCCTTCGGGTTGTA
AAGTACTTTCAGCGGGGAGGAAGGGAGTAAAGTTAATACCTTTGCTCATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCACC
AGCCGCGGTAATACGGAGGGTGCAAGCATTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTTTGTTAAGTCAGATGTGAAATCCC
CGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAGCTTGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGA
GATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACGAAACTGACGCTCACGTGCAAAGCGTGGGAGCAAACAGGATTAATACCCG
GTAGTCCACGCCGTAACGATGTCCATTGAGGTTGTGGCTTGAGGCTGGCTTCCGAGCTACGCGTTAGTCGCCGCCTGGGAGTACGCCGCAAG
TTA

S2-B

>E3 Consensus data

AATGCGTGTCGCACGGTAACAGGAAGCAGCTTGCTGCTTCACTGACCAGTAGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAG
GGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGCCC
AGATGGGATTAGCTTGTTGGTGGGGTAACGGCTCACCCAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAG
ACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTAATGCAGCCATGCCGCGTGTATGAAGAAGG
CCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGGAGTAAAGTAACCTTTGCTCATTGACGTTACCCGCAGAAGAAGCACCCCTAACTC
TTGCCAGCAGCCGCGGTAATACGAGGGTGCAAGCGTTAATCGGAATTACGGGCGTAAAGCGCACGCGGCGGTTTTTAAGTCAGATGGAAAT
CCCCGGGCTCAACCTGGAACGCATCTGATACGGCAAGCTTGAGTCTCGTGAGGGGGGTGATTCCAGGTGTAGCGGTAATGCGTAGAGATCT
GGAGGAATACCGGTGGCGAAGGCGGTTCCCTGGACCAGAGCTGACGATTGGGTGCGAAAGGCTGGCGAGCAAACAGGATTTGATACCGTG
GTAGTACACGCCGTGAACGTATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTTGCTTCCGGAGGCAACGCGTTAAGTGGACCGCCTGGGGA
GTACGGCCGCAAGGTTAAAACTTAACTGAATTGACGGGGGCCCCCTAAGCCGTGGAGCATTTGGTTTAATTCGATGCAACTTGAAGTACCTTA
CCTGGTCTTGACATCCACGGAAGTTTTCAGAGATGTGTAATGTGTCTTCGGGAACTGTATACAGAGTTGGTGACATGCTCTCCGTACAGCCTA
CGTTTAACGC

S2-C

>E4 Consensus data
AACGGTAACAGGAAGAGCTTGCTGCTTTACTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTAC
TGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGCCCAGATGGGATTAG
CTTGTTGGTGGGGTAACGGCTCACCAAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGA
CTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTAATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGT
AAAGTACTTTCAGCGGGGAGGAAGGGAGTAAAGTTAATACCTTTGCTCATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAG
CAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCCGGCGGTTTGTTAAGTCAGATTGAAATCCC
CGGGCTCAACCTGGAACTGCAATGATACGGCAAGCTTGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGAT
CTGGAGGAATACCGGTGGCGAAGGCGGTCCCCTGGACGCAGACTGACGATCAGGTGCGAAAGGCTGGGGAGCAAACAGGATTTGATACCC
TGGTAGTCCACGCCGTGAATGATGTCGACTTGGAGGTTGTGCCCTTGGGGCGTTGCTTCCGGAGGCAACGCGTTAAGTGGACCGCCTGGGG
AGTACGGCCGCAAGGTTAAAACTCAACAGAATTGACGGGGGCCCCCTCAAGCCGTGGAGCATTTGGTTTAATTCGATGCAACTTGAAGTACC
TTACCTGGTCTTGACATCCACGGAATTTTCAGAGATGTATTGTTTTTCGGGAATTGTGATACAGTGGTGCATTGCTCTCTCAGCT

S2-D

>E5 Consensus data
CTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCAGATGTGCCCAGATGGGAT
TAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACAAGGTCC
AGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTAATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGT
TGTAAAGTACTTTCAGCGGGGAGGAAGGTGTTGTGGTTAATAACCACAGCAATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGC
CAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAGCGCACGCAGGCGGTCTGTCAGTCGGATGTGAATCC
CCGGGCTCACCTGGGAACTGCATTCGAAACTGGCAGCTGGAGTCTTGTAGAGGGGGTAGATTCCGGTGTACGGTGAATGCGTAGAATCTGG

AGGAAACCCGTGGCAAGGCGCCCCTGGACAAGACGGCGCTAAGTGCCAAACGTGGGAACAAAAAGATTAAAACCCGGTATCCCGCCGGAACGAATCCATTTGAGGTTTGCCCTTAGGGTGGGTTTCGAGCTAAACGTTTAAAT

S2-E

>E6 Consensus data
TTACACATGCAGTCGAACGGTAACAGGAAGCAGCTTGCATGCTTTGCTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTAATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCGATAAGGTTAATAACCTCGTCGATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAGCGTTNATCGGAATTACTGGGCGTAAAGCGCACGCNGGCGGTCTGTCAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGAC

S2-F

>E8 Consensus data
AAAAGTTGGAGAGTCGAGCGGCCGCGGGAAGTAGCTTGCTCCTTGCCGGCGAGCAGCGGACGGGTGACTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCAGGCAATCACCGCACCCAAGTGGGGGACCTTCGGGCCTCATGCCATCAGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTAATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGTGAGGAGGAAGGCGTGATGTTTAATACGCATCGCGATTGACGTTACTCACAGAAGAAGCACCGGCTAACTCCTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCAGATGTGAAATCCCCGGGCTCAACCCGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGTCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCCCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGATGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAAC

S2-G

>E9 Consensus data
CCAAAAACTTGCAGTCGAGCGGATGACGGGAGCTTGCTCCTTGATTCAGCGGCGGNACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGAAAGGAACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTGCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTAGGTGAGGTAATGGCTCACCTAGGCGACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCAAATCCAGCCATGCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAGTAAGCTAATACCTTGCTGTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTCGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGGCGAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGTGAGTATAATCACAGCTAGGTGTGAAAGCGTGGGGCGCACACAAGACTAGCAACCCTGGTGGTCCACGCGAGAAAGGATGTCAACTAGCCGCGGAATCCTTGAGATTTTAGTGGCGCAGGCAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGAAGGGGGCCCGCACAAGCCGTGGAGCTTGTGGTTTAATTTAAGCAACGCGAAGAACCTTACCAGGCCTTGACCACCTGGGAACTTTCCAGAGATGTATTGGTGCCTTCGGGAACTCTGACACAGATGGTGACACGCTCTCA

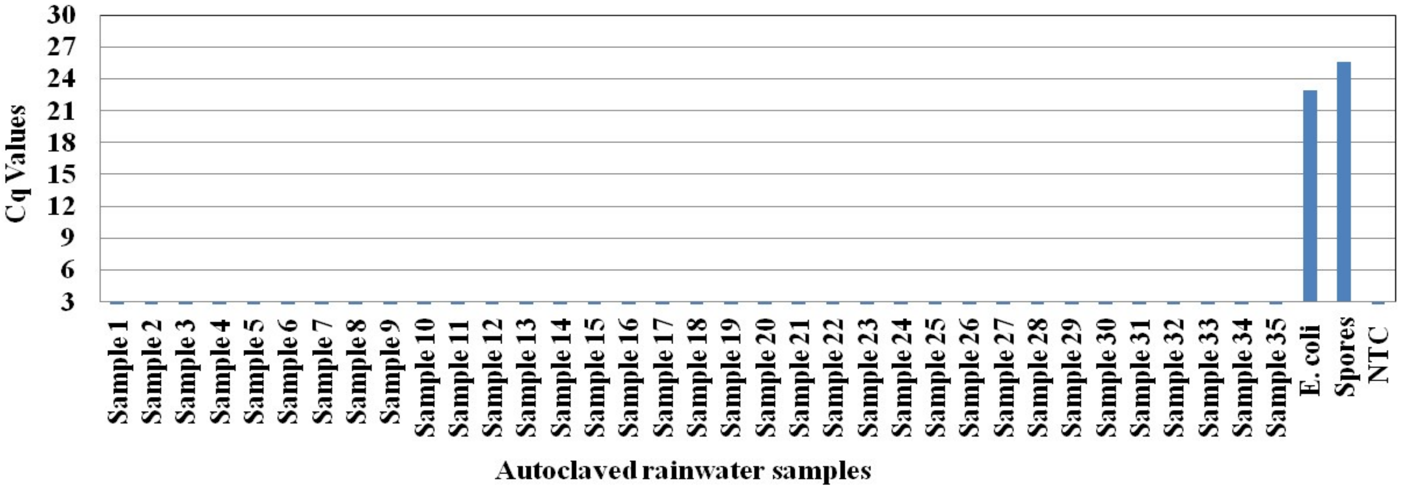
S2-H

>E10 Consensus data

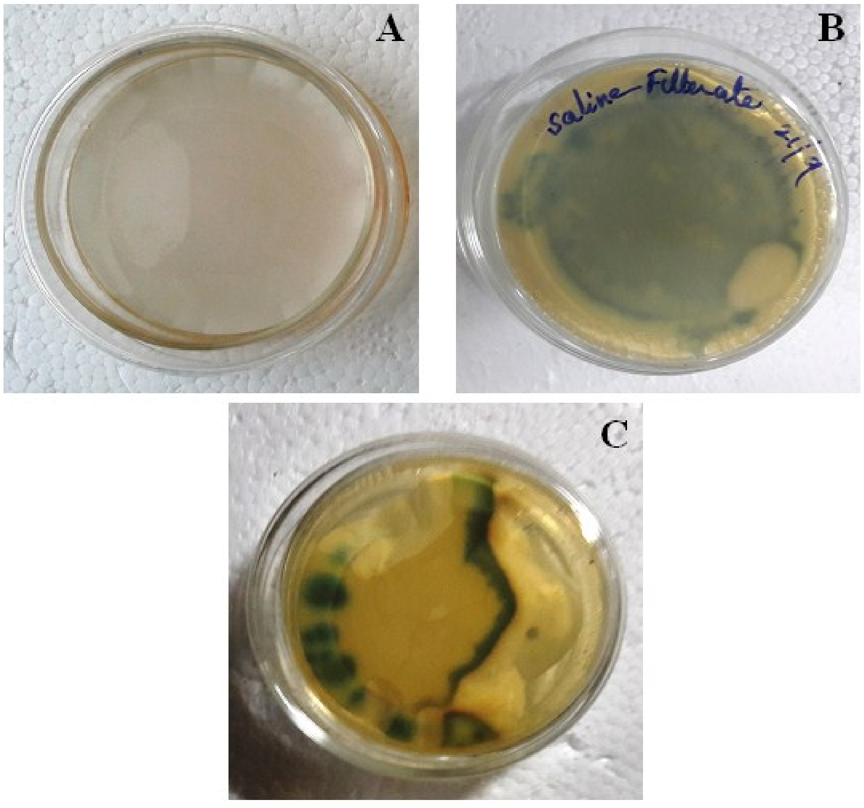
GGTAACAGGAAGAAGCTANGCTGCTTTACTGACGAGTGNCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTAC
TGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGCCCAGATGGGATTAG
CTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGA
CTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTAATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGT
AAAGTACTTTCAGCGGGGAGGAAGGGAGTAAAGTTAATACCTTTGCTCATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAG
CAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCTGGCGGTTTTTAAGTCAGATGTAAATCCCC
GGGCTCAACCTGGGAACTGCATCTGATACTGGCAAGCTTGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAG
ATCTGGAGGAATACCGGTGGCGAAGGCGGTTCCCTGGATCAGACTGACGATTAGGTGCGAAAGGCGTGGCGAGCAAACAGGATTTGATACC
CTGGTAGTACACGCCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTTGCTTCCGGAGCTAACGCGTTAAGTGGACCGCCTGGGG
AGTACGGCCGCAAGGTTAAAACTCAAAAGAACTGATGGGGGCCCCCTAAGGCGTGGAGCATGTGGTTTAATTCGATGCAACTTGAAGAACCT
TACGTGGTATTGACATCCACGGAAGTTATCAGAGATGTGTAATGTGTATTCGGGAACTCTGATACAGATTGGTGACATGTCTCTACAGCTACG
GTTGTTACTCAGACC

ESI S2: Partial 16S ribosomal RNA gene sequencing results of environmental isolates. *E. coli* (isolate E1) (**S2-A**); *Escherichia hermannii* (isolate E3) (**S2-B**); *E. coli* (isolate E4) (**S2-C**); *Enterobacter cloacae* (isolate E5) (**S2-D**); *Enterobacter ludwigii* (isolate E6) (**S2-E**); *Enterobacter pulveris* (isolate E8) (**S2-F**) *Pseudomonas mosselii* (isolate E9) (**S2-G**) and *E. coli* (isolate E10) (**S2-H**).

ESI S3.



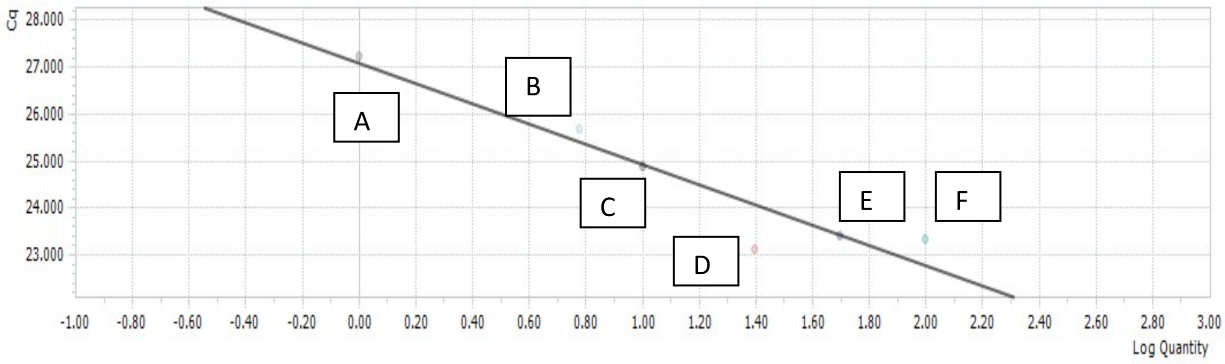
ESI S3. CoDEX-qPCR of autoclaved harvested roof-top rainwater samples. A total of 35 rainwater samples (5 [number of replicates] ×7 [total number of spiking experiments]) were tested negative for *xanQ* gene detection before spiking experiments for determination of recovery and efficiency CoDEX-qPCR. *E. coli* MTCC 3221 and *B. atrophaeus* spores were maintained as positive and process controls respectively. NTC denotes no template control.



ESI S4:

ESI S4: Treatment of PES membrane filters with PBS and methanol. **A**: The PES membrane filter was washed using PBS and placed on the MI agar and incubated for 24 hour at 37 ^{O}C (the rainwater sample was spiked with 10^3 CFU *E. coli* cells); **B:** PBS filtrate (containing concentrated *E. coli* cells) obtained after washing the PES membrane was filtered again on another PES membrane and placed on the MI agar followed by 24 hours incubation at 37 ^{O}C; **C:** PES membrane was treated with methanol for 8-10 seconds and placed on the MI agar for 24 hour at 37 ^{O}C.

ESI S5:

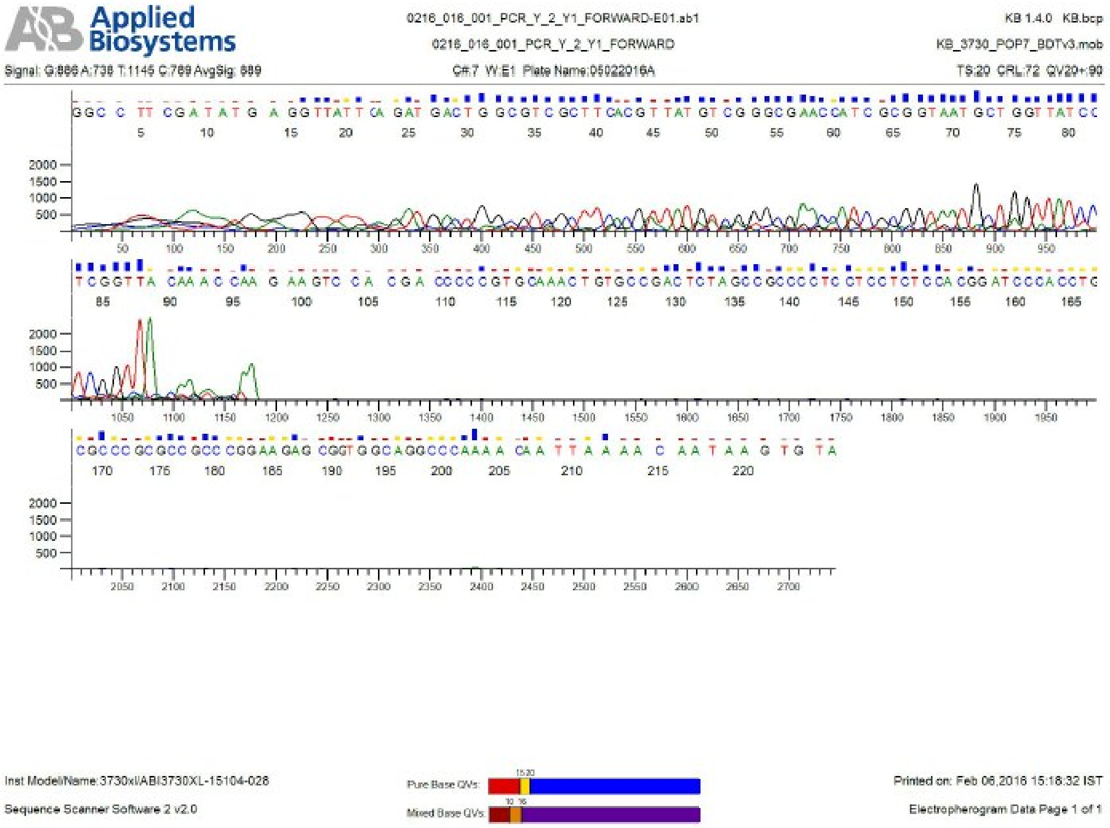


ESI S3. The CoDEX-qPCR quantification of *E. coli* MTCC 3221. A series of bacterial suspensions consisting of 100, 50, 25, 14, 6 and 1 CFU/mL of *E. coli* MTCC 3221. A: 1 cell; B: 6 cells; C: 14 cells; D: 25 cells; E: 50 cells; F: 100 cells.

ESI S6A.

>*xanQ* Forward (starting from 25th to 97th ntd.)

ATGACTGGCGTCGCTTCACGTTATGTCGGGCGAACCATCGCGGTAATGCTGGTTATCCTCGGTTACAAACCAA

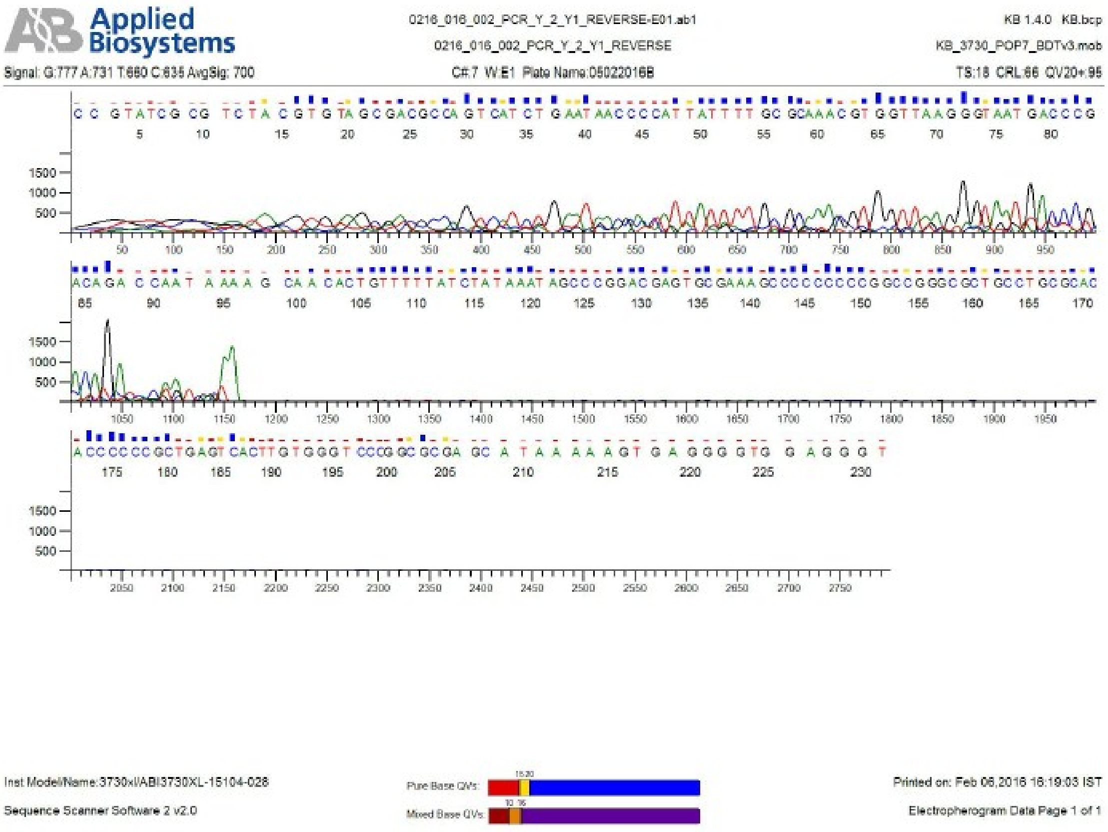


ESI S6A. Sequencing result of *xanQ* amplicon (forward)**.**

ESI S6B.

>*xanQ* Reverse (starting from 14th ntd to 97th ntd)

ACGTGTAGCGACGCCAGTCATCTGAATAACCCCATTATTTTGCGCAAACGTGGTTAAGGGTAATGACCCGACAGACCAATAAA
A



ESI S6-B. Sequencing result of *xanQ* amplicon (reverse)**.**

ESI Table 1: Detection and quantification of *E. coli* from environmental samples by MI agar and CoDEX-qPCR assay.

Region/year	**Sample Number**	**No. of CFU of *E. coli* on MI agar**	**Cq values (CoDEX-qPCR)**	**Detection of *Bacillus atrophaeus* spores**
Shantinagar/ 2016	1	Negative	26.34	Positive
	2	18	23.74	Positive
	3	Negative	Negative	Positive
	4	1	26.85	Positive
	5	2	22.26	Positive
	6	9	22.41	Positive
	7	5	24.75	Positive
	8	21	23.58	Positive
Sancoale /2016	9	19	25.16	Positive
	10	4	23.40	Positive
	11	3	26.43	Positive
	12	6	26.09	Positive
	13	11	25.59	Positive
	14	16	24.08	Positive
	15	2	25.53	Positive
	16	Negative	Negative	Positive
Vasco Da Gama /2016	17	4	23.18	Positive
	18	Negative	Negative	Positive
	19	Negative	Negative	Positive
	20	Negative	Negative	Positive
	21	8	22.44	Positive
	22	4	22.96	Positive
	23	3	25.60	Positive
	24	5	24.17	Positive
	25	Negative	Negative	Positive
	26	Negative	Negative	Positive
Panjim/2016	27	Negative	Negative	Positive
	28	Negative	Negative	Positive
	29	Negative	Negative	Positive
	30	11	22.22	Positive
	31	Negative	23.49	Positive
	32	Negative	Negative	Positive
	33	Negative	Negative	Positive
	34	Negative	Negative	Positive

	35	Negative	21.65	Positive
	36	Negative	21.74	Positive
	37	Negative	26.36	Positive
	38	Negative	Negative	Positive
	39	Negative	Negative	Positive
	40	Negative	Negative	Positive
	41	Negative	Negative	Positive
Shantinagar /2017	42	Negative	Negative	Positive
	43	Negative	22.26	Positive
	44	Negative	22.41	Positive
	45	Negative	24.75	Positive
	46	Negative	23.58	Positive
	47	2	25.16	Positive
	48	5	23.40	Positive
	49	8	26.43	Positive
	50	1	26.09	Positive
	51	Negative	25.59	Positive
	52	Negative	24.08	Positive
Vasco Da Gama /2017	53	Negative	Negative	Positive
	54	Negative	Negative	Positive
	55	Negative	23.18	Positive
	56	Negative	Negative	Positive
Sancoale/2017	57	Negative	Negative	Positive
	58	Negative	Negative	Positive
	59	Negative	22.44	Positive
	60	Negative	22.96	Positive
	61	Negative	25.60	Positive
	62	Negative	24.17	Positive
	63	Negative	21.62	Positive
	64	Negative	Negative	Positive
	65	Negative	Negative	Positive
	66	Negative	Negative	Positive
	67	Negative	Negative	Positive
	68	2	26.78	Positive
	69	6	26.63	Positive
	70	Negative	25.36	Positive
	71	Negative	Negative	Positive
	72	20	26.34	Positive

	73	29	23.74	Positive
	74	Negative	Negative	Positive
Panjim /2017	75	26	26.85	Positive
	76	2	22.26	Positive
	77	9	22.41	Positive
	78	5	24.75	Positive
	79	6	23.58	Positive
	80	3	25.59	Positive
	81	16	24.08	Positive
	82	2	25.53	Positive
	83	21	22.44	Positive
	84	19	25.16	Positive
	85	4	23.40	Positive
	86	1	26.43	Positive
	87	8	22.96	Positive
	88	4	25.60	Positive
	89	2	26.09	Positive
	90	5	24.17	Positive
	91	Negative	Negative	Positive
	92	9	26.43	Positive
	93	5	26.09	Positive
	94	2	25.59	Positive
	95	5	22.41	Positive
	96	8	24.75	Positive
	97	14	23.40	Positive
	98	1	25.16	Positive
	99	3	22.26	Positive
Margoa/2017	100	4	23.58	Positive
	101	1	24.08	Positive
	102	Negative	Negative	Positive
	103	5	25.60	Positive
	104	2	24.17	Positive
	105	14	22.44	Positive
	106	17	23.58	Positive
	107	3	25.16	Positive
	108	12	22.96	Positive
	109	7	21.62	Positive

110	Negative	Negative	Positive
No template control	Negative	Negative	NA
No. of positive samples	**60 (54.54%)**	**79 (71.81%)**	**110 (100%)**
No. of negative samples	**50 (45.45%)**	**31 (28.18%)**	**00.00%**