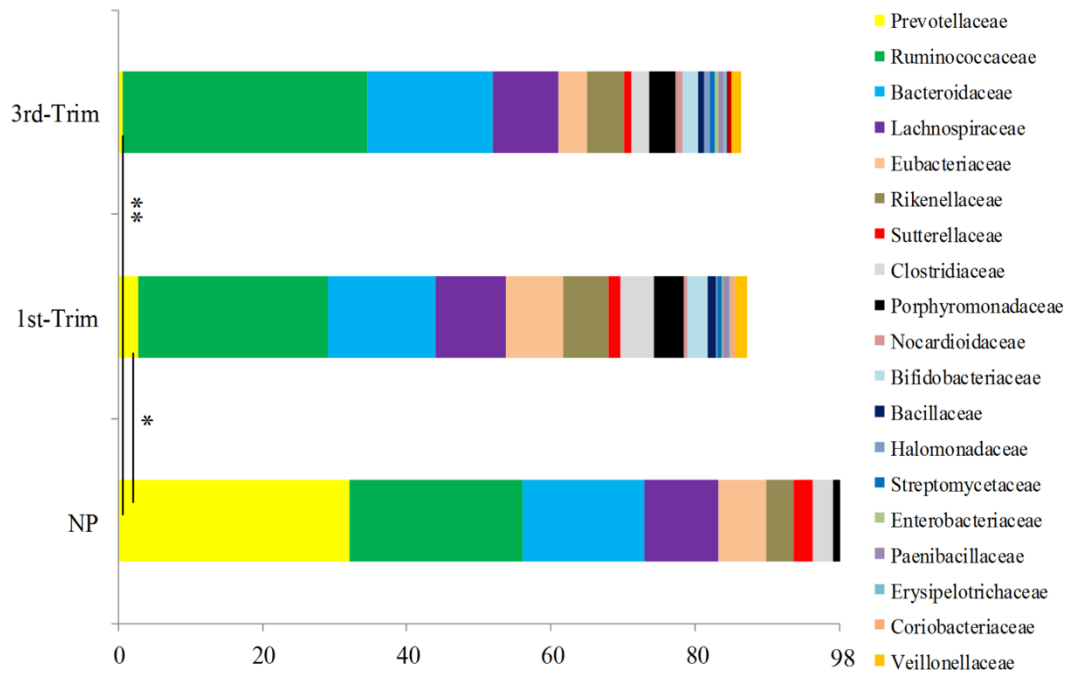# Supplementary materials

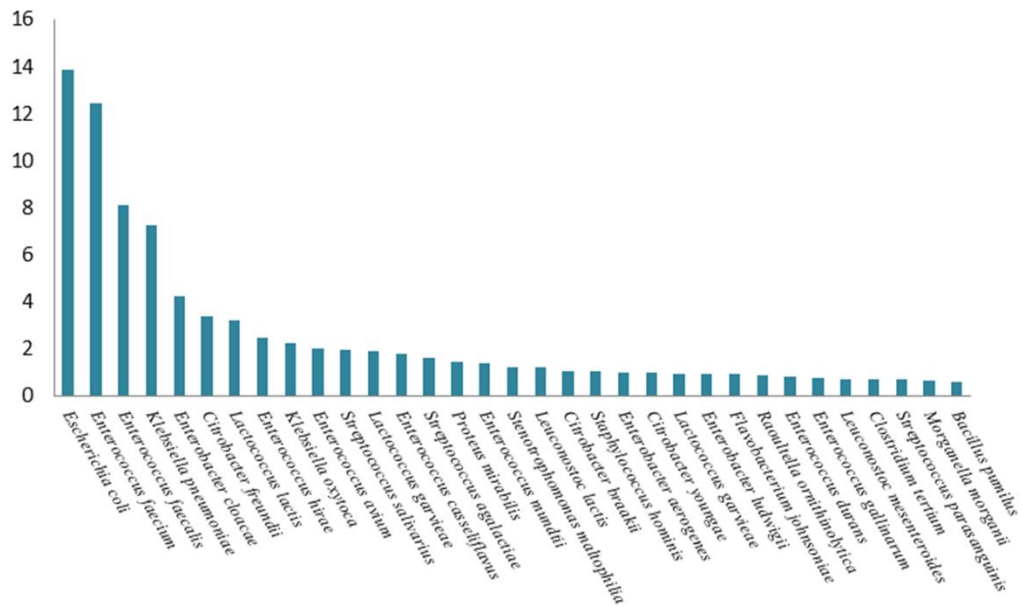**Figure S1** Average relative abundance of detected major families in 16S amplicon sequencing data. The *x*-axis indicates the average relative abundance as percentages, and the *y*-axis represents the group name. Kruskal–Wallis was performed for determining significant changes. *Significant at p <0.05. ** Highly significant at p ≤0.01. NP, non-pregnant group; 1st-Trim, first trimester; 3rd-Trim, third trimester.
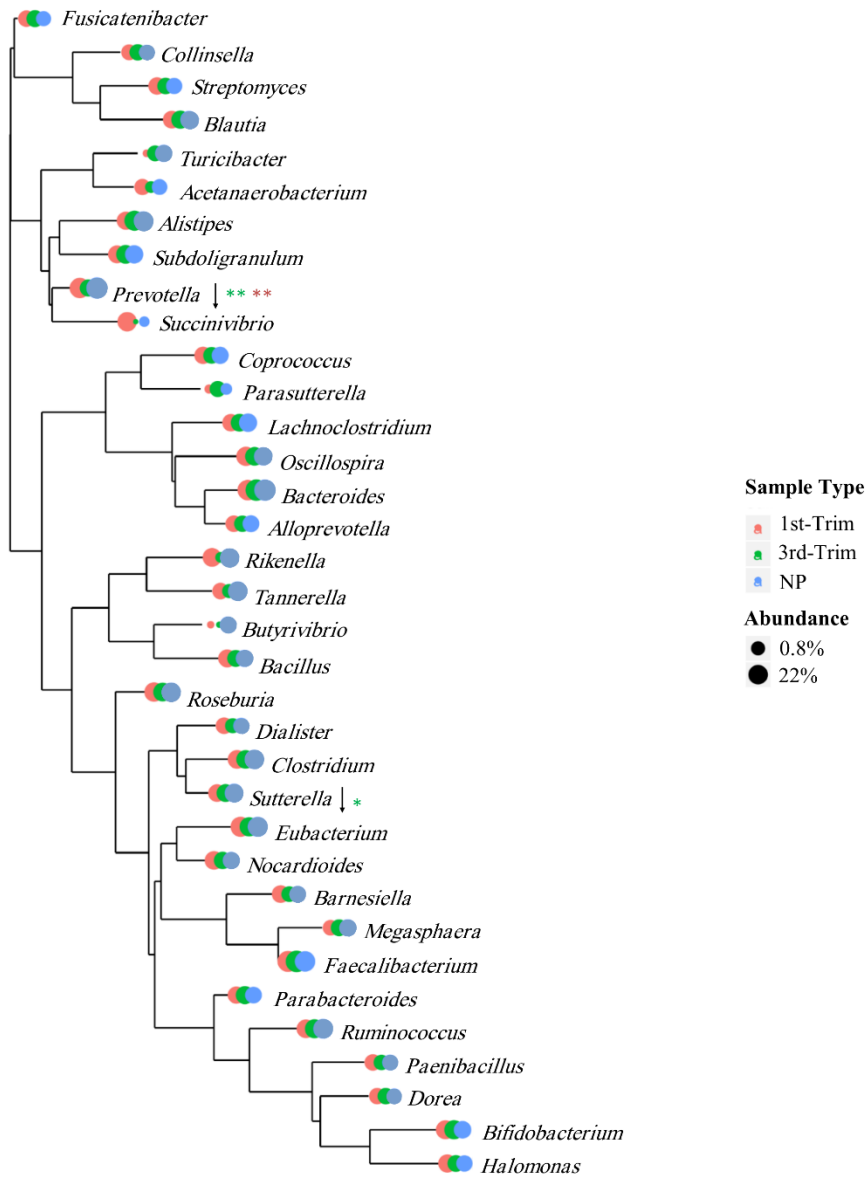
Figure S2 Annotated phylogenetic tree representation of dominant genera. Dots are showing genera relative abundance. The cutoff point for genera abundance was set 0.5%. *Indicates significant at *p* <0.05. The arrow direction is indicating decrease (↓) or increase (↑) in OTUs abundance. Kruskal–Wallis was performed for determining significant changes. *Significant at *p* <0.05. ** Highly significant at *p* ≤0.01. Abbreviations are as described for Figure S1.
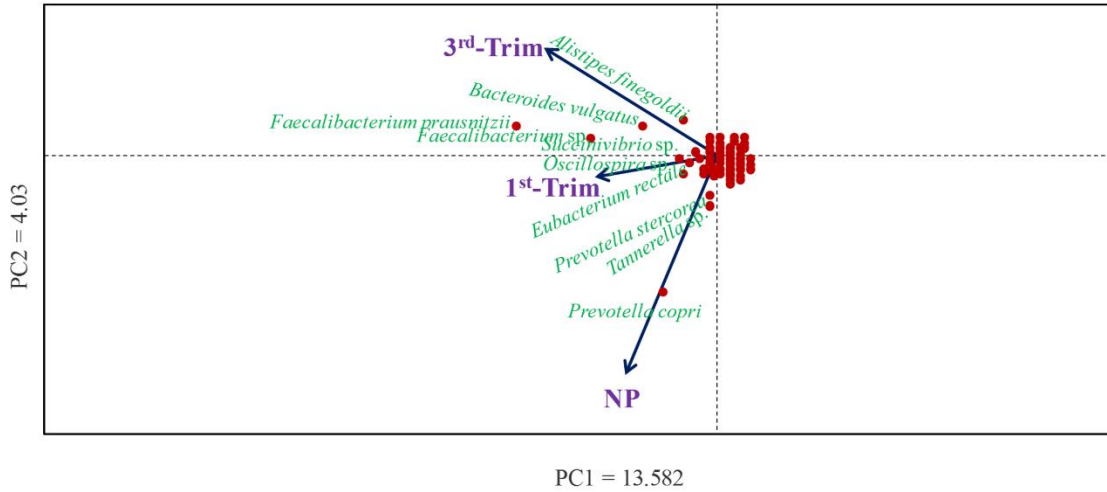
**Figure S3** The multivariate principal coordinate analysis of the studied groups using type-1 scaling. The vectors are representing groups and their direction is showing variability. Dots are showing relative position of each species. Abbreviations are as described for Figure S1.

Figure S4 Average percentage abundance of dominant bacterial species (abundance ≥0.6%)
identified through culturomics.
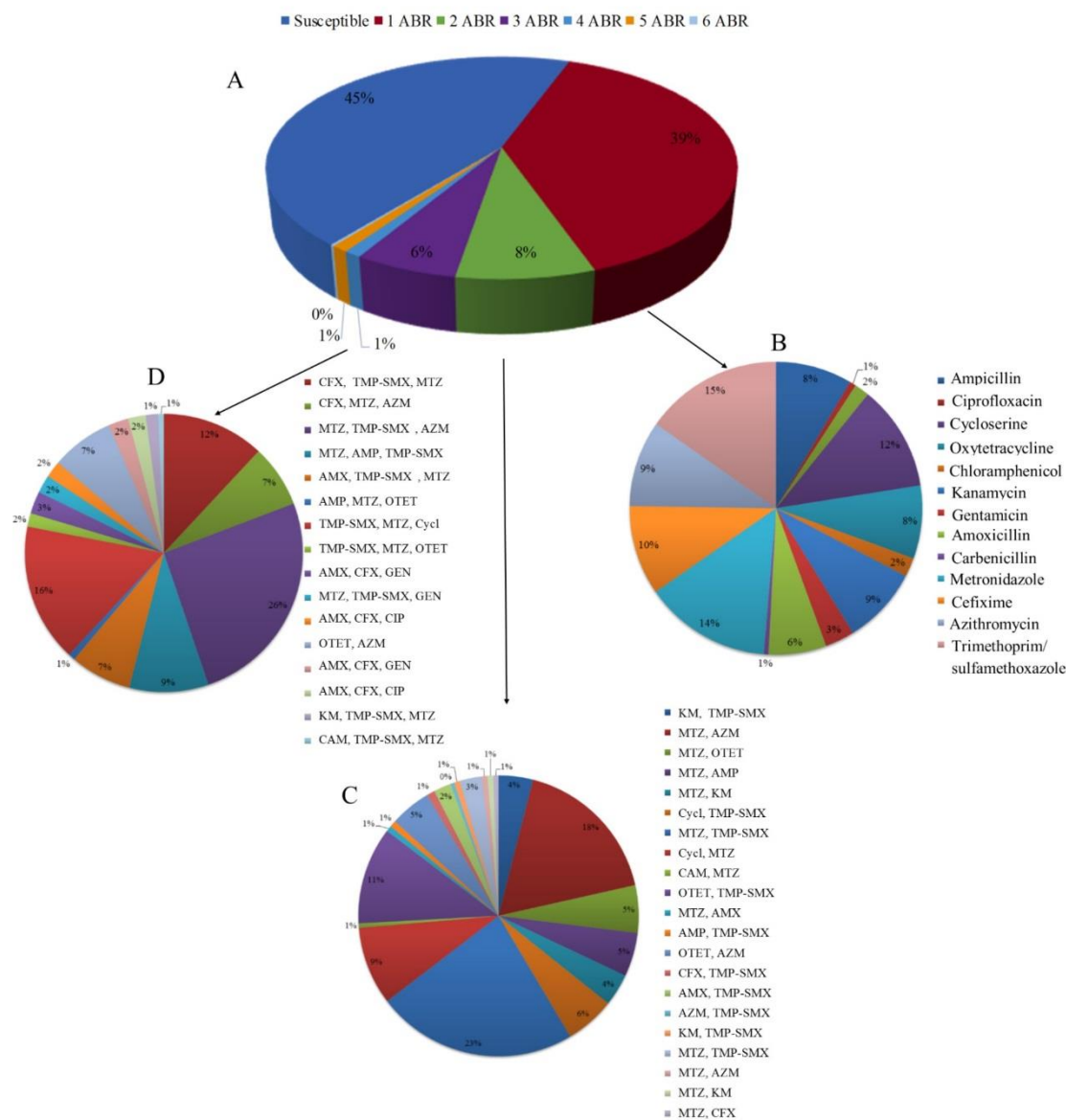
Figure S5 Percentage presentation of total resistant isolates. (A) Relative percentage abundance of total isolates resistant to single and multiple antibiotics. (B) Relative percentage abundance of isolates resistant to single antibiotic. (C) Relative percentage abundance of isolates resistant to two antibiotics. (D) Relative percentage abundance of isolates resistant to three antibiotics. Abbreviations: TMP-SMX, trimethoprim/sulfamethoxazole, MTZ, metronidazole; AZM, azithromycin; OTET, oxytetracycline; AMP, ampicillin; KM, kanamycin; Cyclo, cycloserine; CAM, chloramphenicol; AMX, amoxicillin; CFX, cefixime; GEN, gentamicin; CIP, ciprofloxacin.
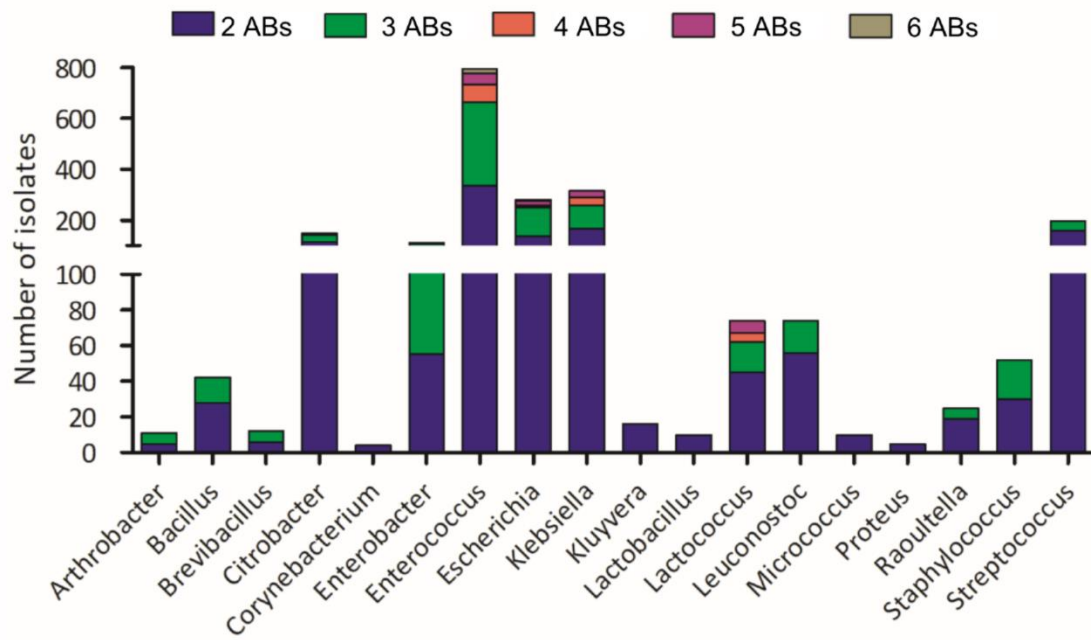
Figure S6 Relative abundance of multiple- antibiotics resistant genera. Number of isolates are showing on Y-axis.
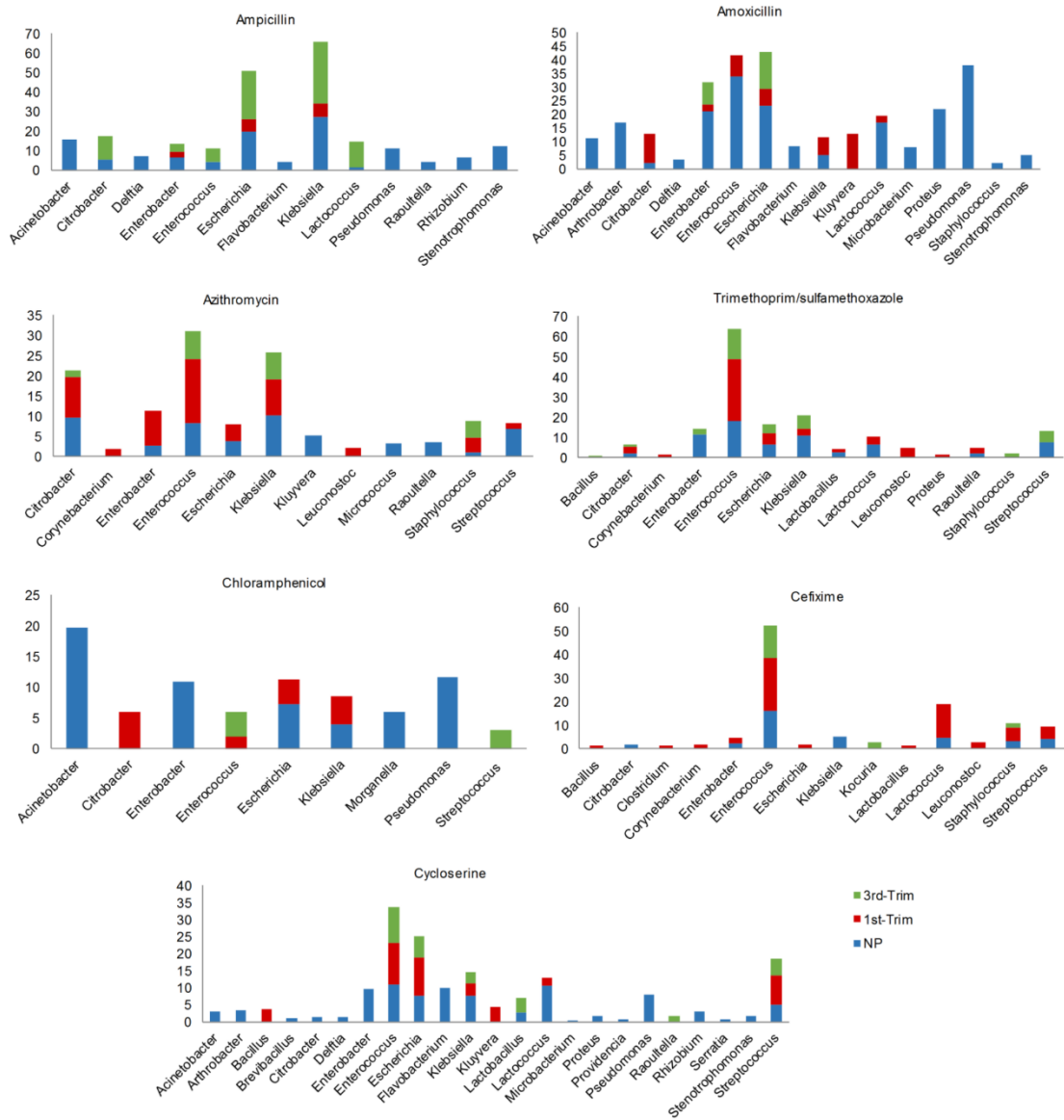
Figure S7 Comparison of the bacterial genera between non-pregnant and pregnant groups that showed resistant toward ampicillin, amoxicillin, azithromycin, trimethoprim/sulfamethoxazole, chloramphenicol, cefixime, and cycloserine. Average abundance of genera is showing on Y-axis.
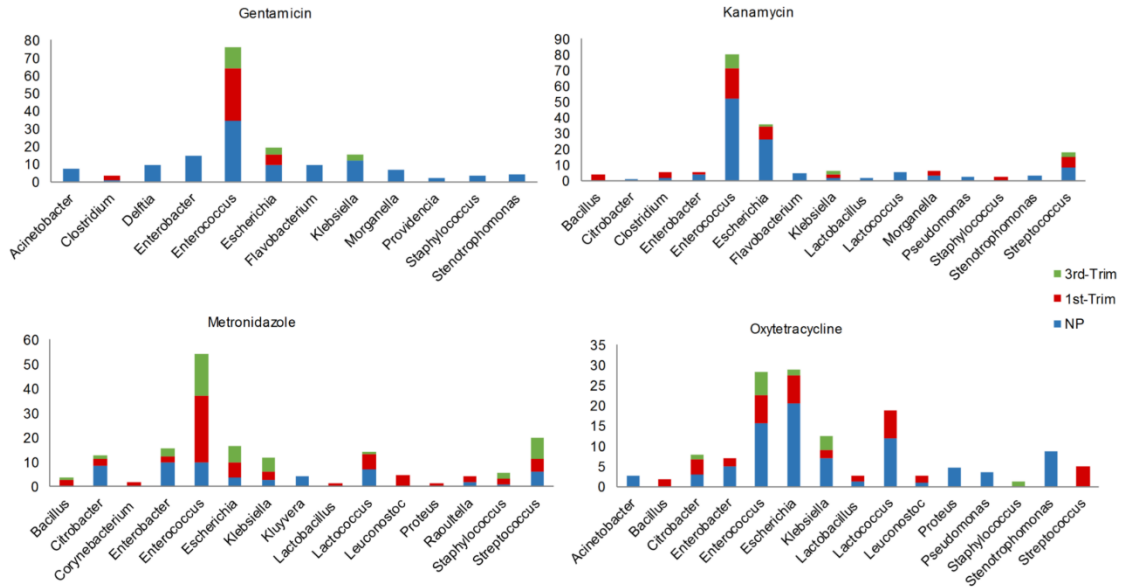
Figure S8 Comparison of the bacterial genera between non-pregnant and pregnant individuals that showed resistant toward gentamicin, kanamycin, metronidazole, and oxytetracycline. Average abundance of genera is showing on y-axis.

Table S1 Composition of media used for culturomic analysis

Ingredients	Concentration
Acid hydrolysate of casein	0.24 g/L
Yeast extract	0.24 g/L
Dextrose	0.87 g/L
Soluble starch	0.24 g/L
Dipotassium phosphate	1.42 g/L
Magnesium sulfate heptahydrate	0.024 g/L
Sodium pyruvate	0.14 g/L
Calf brain	30.76 g/L
Beef heart	38.4 g/L
Proteose peptone	2.16 g/L
Sodium chloride	1.58 g/L
Disodium phosphate	0.43 g/L
Pancreatic digest of casein	1.7 g/L
Papaic digest of soyabean meal	0.3 g/L
Ascorbic acid	1g/L
Blood	5%
Agar	13 g/L

Table S2 List of primer sequence used for the amplification of antimicrobial resistant gene from the genomic DNA of the studied stool samples

Primer Name	Sequence/gene	Size (bp)	Annealing Temp. (°C)	Reference
*eme*A-F	GTGACAGCCTTTGTGGCAGAT	687	57	1
*eme*A--R	TAGTCCGTTGATGGTTCCTTG			
*aac*6-*aph*2-F	CCAAGAGCAATAAGGGCATA	220	55	
*aac*6-*aph*2-R	CACTATCATAACCACTACCG			
*aph*3-II-F	GCCGATGTGGATTGCGAAAA	292	55	
*aph*3-II-R	GCTTGATCCCCAGTAAGTCA			
*ant*6-I-F	ACTGGCTTAATCAATTTGGG	597	55	
*ant*6-I-R	GCCTTTCCGCCACCTCACC			
*gyr*A *faecium*-F	CGGGATGAACGAATTGGGTGTGA	240	58	2
*gyr*A *faecium*-R	AATTTTACTCATACGTGCTTCGG			
*gyr*A *faecalis*-F	CGGGATGAACGAATTGGGTGTGA	241	55	
*gyr*A *faecalis*-R	AATTTTACTCATACGTGCTTCGG			
*par*C *faecium*-F	TTCCCGTGCATTTCGATCAGTACTTC	151	58	3
*par*C *faecium*-R	CGTATGACAAAGGATTCGGTAAATC			
*par*C *faecalis*-F	AATGAATAAAGACGGCAATA	191	48.7	
*par*C *faecalis*-R	CGCCATCCATACTTCCGTTG			
*van*A-F	GGGAAAACGACAATTGC	1030	48.7	4
*van*A-R	GTACAATGCGGCCGTTA			
*van*B-F	ATGGGAAGCCGATAGTC	433	54	
*van*B-R	GATTTCGTTCCTCGACC			
*van*R-F	AGCGATAAAATACTTATTGTGGA	645	62	
*van*R-R	CGGATTATCAATGGTGTCGTT			
*van*S-F	AACGACTATTCCAAACTAGAAC	1094	60	
*van*S-R	GCTGGAAGCTCTACCCTAAA			
*van*H-F	ATCGGCATTACTGTTTATGGAT	943	60	
*van*H-R	TCCTTTCAAAATCCAAACAGTTT			
*van*Y-F	ACTTAGGTTATGACTACGTTAAT	866	55	
*van*Y-R	CCTCCTTGAATTAGTATGTGTT			
*van*C2/C3-F	5'-CGGGGAAGATGGCAGTAT-3'	484	54	1
*van*C2/C3-R	5'-CGCAGGGACGGTGATTTT-3'			
orf-1A-F	AGGGCGACATATGGTGTAACA	844	58	4
orf-1A-R	GGGCGACGGTACAACATCTT			
orf-1B-F	TGGTGGCTCCTTTTCCCAGTTC	1007	60	
orf-1B-R	CGTCCTGCCGACTATGATTATTT			
orf-1C-F	ACCGTTTTTGCAGTAAGTCTAAAT	1066	60	
orf-1C-R	AAACGGGATTTAGAAATAGTTAAT			
orf-1D-F	CCATTTCTGTATTTTCAATTTATTA	925	58	

orf-1D-R	CATAGTTATCACCCTTTCACATA			
orf-1E-F	TTGCGGAAAATCGGTTATATTC	540	56	
orf-1E-R	AGCCCTAGATACATTAGTAATT			
*bla*SHV-F	CTTTATCGG CCCTCACTCAA	327	48.5	
*bla*SHV-R	AGGTGCTCATCATGGGAAAG			
*bla*TEM-F	KACAATAACCCTGRTAAATGC	940	48.5	5
*bla*TEM-R	AGTATATATGAGTAAACTTGG			
*bla*CTXM-F	ATGTGCAGYACCAGTAARGTKATGGC	593	48.5	
*bla*CTXM-R	TGGGTRAARTARGTSACCAGAAYCAGCGG			
*bla*OXA-51-F	TAATGCTTTGATCGGCCTTG	353	52	
*bla*OXA-51-R	TGGATTGCACTTCATCTTGG			
*bla*OXA-23-F	GATCGGATTGGAGAACCAGA	501	52	
*bla*OXA-23-R	ATTTCTGACCGCATTTCCAT			
*bla*OXA-24-F	GGTTAGTTGGCCCCCTTAAA	240	52	
*bla*OXA-24-R	AGTTGAGCGAAAAGGGGATT			
*bla*OXA-58-F	AAGTATTGGGGCTTGTGCTG	590	52	
*bla*OXA-58-R	CCCCTCTGCGCTCTACATAC			
*bla*OXA-143-F	TGGCACTTTCAGCAGTTCCT	149	52	
*bla*OXA-143-R	TAATCTTGAGGGGGCCAACC			
IS*Aba*/*bla*OXA-23-F	AGAGCATTACCATATAGATT	327	41	
IS*Aba*/*bla*OXA-23-R	CACAATTTCTGATAAAGATA			6
IS*Aba*/*bla*OXA-51-F	AAGCATGATGAGCGCAAAG	227	52	
IS*Aba*/*bla*OXA-51-R	GGTGAGCAGGCTGAAATAAAA			
ISAba 4/*bla*OXA-23-F	CACAATTTCTGATAAAGATA	327	41	
ISAba 4/*bla*OXA-23-R	TTTATTAAATTATGCTGAAC			
*bla*ACT-F	ATTCGTATGCTGGATCTCGCCACC	396	50	
*bla*ACT-R	CATGACCCAGTTCGCCATATCCTG			
*bla*FOX-F	CACCACGAGAATAACC	1184	50	
*bla*FOX-R	GCCTTGAACTCGACCG			
*bla*IMI-F	ATGTCATTAGGTGATATGGC	879	50	7
*bla*IMI-R	GCATAATCATTTGCCGTACC			
*bla*CMY-G1-**F**	GCTGACAGCCTCTTTCTCCAC	1082	56	
*bla*CMY-G1-R	CCTCGACACGGRCAGGGTTA			
*bla*CMY-G2-F	GGTCTGGCCCATGCAGGTGA	963	56	

*bla*CMY-G2-R	GGTCGAGCCGGTCTTGTTGA			
tet (A)-F	F: GCT ACA TCC TGC TTG CCT TC	210	55	1
tet (A)-R	R: CAT AGA TCG CCG TGA AGA GG			
*erm*B-F	F: GAT ACC GTT TAC GAA ATT GG	364	58	
*erm*B-R	R: GAA TCG AGA CTT GAG TGT GC			
*Str*A-F	TTGATGTGGTGTCCCGCAATGC	383	57	8
*Str*A-R	CCAATCGCAGATAGAAGGCAA			
*Str*B-F	CCGCGATAGCTAGATCGCGTT	470	59	9
*Str*B-R	CGACTACCAGGCGACCGAAAT			
*cml*A-F	CCGCCACGGTGTTGTTATC	698	55	10
*cml*A-R	CACCTTGCCTGCCCATCATTAG			
*cat*A1-F	AGTTGCTCAATGTACVTATAACC	547	55	
*cat*A1-R	TTGTAATTCATTAAGCATTCTGCC			
*bla*DHA-F	AACTTTCACAGGTGTGCTGGGT	405	60	7
*bla*DHA-R	CCGTACGCATACTGGCTTTGC			
*bla*GES-F	ATGCGCTTCATTCACGCAC	591	56	
*bla*GES-R	CTATTTGTCCGTGCTCAGG			
*bla*ADC-F	CCGCGACAGCAGGTGGATA	420	60	11
*bla*ADC-R	TCGGCTGATTTTCTTGGTT			
IS*Aba*/*bla*ADC-F	CATTGGCATTAAACTGAGGAGAAA	451	55	
IS*Aba*/*bla*ADC-R	TTGGAAATGGGGAAAACGAA			
IS*Adc*/*bla*ADC-F	GTTGCACTTGGTCGAATGAAAA	751	60	
IS*Adc*/*bla*ADC-R	ACGTCGCGAGTTGAAGTAAGTT			

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