



**Figure S1.** Phylogenetic tree based on 16S rRNA sequences of *E. faecalis*, *E. faecium*, *E. hirae* and *E. avium* isolates recovered from backyard chickens.



**Table S2.** Primers and PCR condition for detection of virulence and antimicrobial resistance genes and Rep-families

Genes	Oligonucleotide sequences (5'-3')	Length (bp)	Annealing temperature	References
<i>vanA</i>	GCGCGGTCCACTTGTAGATA	314	54	[114]
	TGAGCAACCCCCAAACAGTA			
<i>vanB</i>	AGACATTCCGGTCGAGGAAC	220	54	[114]
	GCTGTCAATTAGTGCGGGAA			
<i>Cat</i>	GGATATGAAATTTATCCCTC	486	50	[11]
	CAATCATCTACCCTATGAAT			
<i>ermA</i>	GCGGTAAACCCCTCTGAG	434	51	[115]
	GCCTGTCGGAATTGG			
<i>ermB</i>	CATT TAACGACGAAACTGGC	425	51	[116]
	GGAACATCTGTGGTATGGCG			
<i>tetM</i>	GTGGACAAAGGTACAACGAG	406	57	[117]
	CGGTAAAGTTCGTCACACAC			
<i>tetA</i>	GCT ACA TCC TGC TTG CCTTC	210	58	[117]
	CAT AGA TCG CCG TGA AGAGG			
<i>tetB</i>	TTG GTTA GGG GCA AGT TTTG	659	58	[117]
	GTA ATG GGC CAA TAA CACCG			
<i>tetL</i>	ATAAATTGTTTCGGGTCGGTAAT	1,077	55	[118]
	AACCAGCCAACTAATGACAATGAT			
<i>optrA</i>	AGGTGGTCAGCGAACTAA	1395	55	[119]
	ATCAACTGTTCCATTCA			
<i>pbp5</i>	AACAAAATGACAAACGGG	779	54	[120]
	TATCCTTG GTTATCAGGG			
<i>gelE</i>	TATGACAATGCTTTTTGGGAT	312	56	[125]
	AGATGCACCCGAAATAATATA			
<i>cylA</i>	ACTCGGGGATTGATAGGC	688	56	[125]
	GCTGCTAAAGCTGCGCTT			
<i>Agg</i>	CCAGTAATCAGTCCAGAAACAACC	406	54	[124]
	TAGCTTTTTTCATTCTTGTGTTTGTT			
rep1(pIP501)	TCGCTCAATCACTACCAAGC	624	56	[37]
	CTTGAACGAGTAAAGCCCTT			
rep2 (pRE25)	GAGAACCATCAAGGCGAAAT	630	56	
	ACCAGAATAAGCACTACGTACAATCT			
rep3 (pAW63)	CCTAATGTATATAATTTTGGTACATAT	304	52	
	ACATTTTCCTCAAAGAACAT			
rep4 (pMBB1)	ACTATGTCGTTGAGTCTAATGACT	304	52	
	AGCAAGATAGAATATTTACTTTTAAGTTT			
rep5 (pSAS)	ATGTGTAATAAATTAAGAGCA	637	52	
	ATTGTCTTGATTTATCTATCTTG			
rep6 (pS86)	ACGAATGAAAGATAAAGGAGTAG	551	56	
	TAAATTCTAGTTTGGCAATCTTAT			
rep7 (pUSA02)	CCAAAATAYTTYGTTTCTGG	227	56	
	CCAATCATGTAATGTTACAACC			
rep8 (pAM373)	TAGATACGACAAAAGAAGAATTACA	394	56	
	CCAATCATGTAATGTTACAACC			
rep9 (pCF10)	GCTCGATCARTTTTCAGAAG	210	56	
	CGCAAACATTTGTCWATTTCTT			
rep10 (pIM13)	TATAAAGGCTCTCAGAGGCT	382	56	
	CCAAATTCGAGTAAGAGGTA			
rep11(pEF1071)	TCTAGAATGCGTAAAAAGG	500	52	
	CCTTTGAAGATWGCRTWAG			
rep12 (pBMB67)	GAGCCTATAACAGAGTACACA	470	52	
	CAAATATAGGCTTTGTAGTTC			
rep13 (pC194)	ATGATGCAATATATTAAGCA	402	52	
	TACCAGAATAYTTAGCCATTTT			
rep14( pRI)	GAAAGYTTRGATAGYTTTGC	164	52	
	RTTTTGRCTTTCTTSYTTCA			
rep15(pUSA03)	CAGTAGAAGAAAATTATAAAGAAC	327	52	
	GTTATGGCTGGTTTTAATAAA			
rep16 (pSAS)	CAGGAAAACACTTCGTTTAT	592	52	
	CTTCTATATCACTATCATTGTCATT			
rep17 (pRUM)	TACTAACTGTTGGTAATTCGTTAAAT	604	52	
	ATCAAGGACTCAACCGTAATT			
rep 18 (pEF418)	ACACCAGTCGAAATGAATTT	462	56	
	AGGAATATCAAGTAATTCATGAAAGT			
rep19 (pUB101)	GWGATCGCTTARAYTTATCTAT	543	52	
	YMTTGTTSTGGMAATTCTT			