Supplementary Information

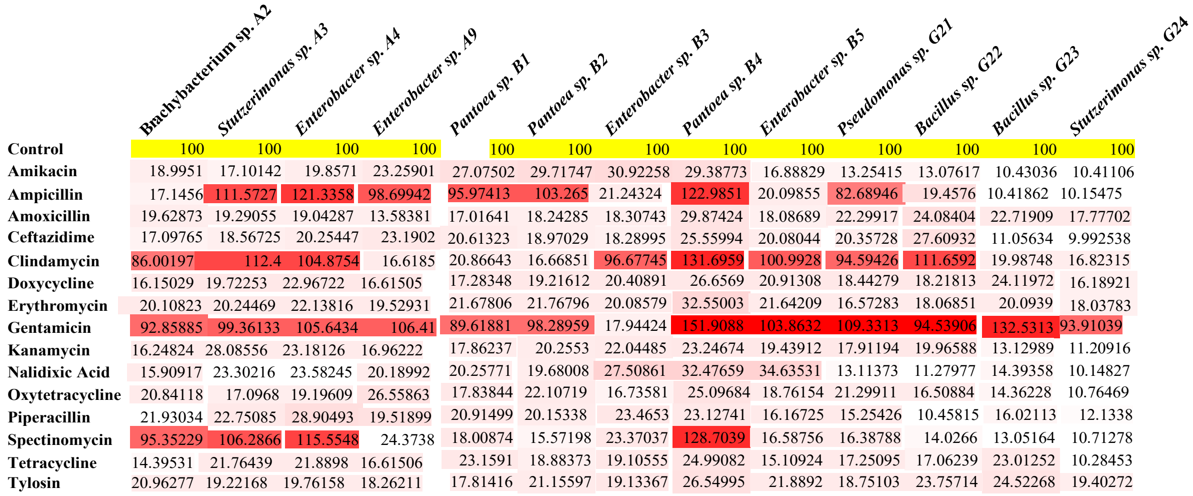
Antibiotic	Gene	Primer (5’-3’)	Reference
Amikacin	*AphA6*	CATTTGCGGGGTTTTTAATG	(Aris *et al.*, 2019)
		TTAGATAATGCTTGGAATCA	
Ampicillin	*Ampc*	CTACGGTCTGGCTGCTA	(Olesen *et al.*, 2004)
		TGGAGCAAGAGGCGGTA	
Amoxicillin	*Pbp1A*	AGTTTGGGTAACTACGGATA	(Diab *et al.*, 2018)
		AATCTTACCGGTGCTCGTGT	
Clindamycin	*Erm (c)*	AATCGTCAATTCCTGCATGT	(Strommenger *et al.*, 2003)
		TAATCGTGGAATACGGGTTTG	
Ceftazidime	*Pen A*	CGGGCAATACCTTTATGGTGGAAC	(Dormanesh *et al.*, 2015)
		ACAACGGCGGCGGGGATATAAC	
Doxycycline	*tetA*	GCTACATCCTGCTTGCCTTC	(Dormanesh *et al.*, 2015)
		CATAGATCGCCGTGAAGAGG	
Erythromycin	*Erm (A)*	AAGCGGTAAACCCCTCTGA	(Diab *et al.*, 2018)
		TTCGCAAATCCCTTCTCAAC	
Gentamicin	*aacA-aphD*	TAATCCAAGAGCAATAAGGGC	(Dormanesh *et al.*, 2015)
		GCCACACTATCATAACCA CTA	
Kanamycin	*Kan R*	GAGCCATATTCAACGGGAGA	(Diab *et al.*, 2018)
		ATTCCGACTCGTCCAACATC	
Nalidixic acid	*Gyr A*	TGTCCGAGATGGCCTGAAGC	(Suman *et al.*, 2016)
		CGTTGATGACTTCCGTCAG	
Oxytetracycline	*Tetk*	GTAGCGACAATAGGTAATAGT	(Olesen *et al.*, 2004)
		GTAGTGACAATAAACCTCCTA	
Piperacillin	*tem*	GCGGAACCCCTATTTG	(Olesen *et al.*, 2004)
		ACCAATGCTTAATCAGTGAG	

Spectinomycin	*Aad A14*	TCACTTGTTTGGTTCCGCAGT	(Kehrenberg *et al.*, 2005)
		TCTTTCGGATAAGCTGCCAGA	
Tetracycline	*Tet A*	GTAATTCTGAGCACTGTCGC	(Diab *et al.*, 2018)
		CTGCCTGGACAACATTGCTT	
Tylosin	*Erm BCT*	GAAATTGGAACAGGTAAAGG	(Jost *et al.*, 2004)
		TTTACTTTTGGTTTAGGATG	

Supplementary Table 1. Primers used for detection of antibiotic resistance gene in bacterial isolate.

Bacteria	**Name**	**% Identity**	**Phylogenetic tree**
A2	*Brachybacterium* sp. A2	98.93	Supplementary Figure 2
A3	*Stutzerimonas* sp. A3	98.07	Supplementary Figure 3
A4	*Enterobacter* sp. A4	98.54	Supplementary Figure 4
A9	*Enterobacter* sp. A9	98.61	Supplementary Figure 5
B1	*Pantoea* sp. B1	96.67	Supplementary Figure 6
B2	*Pantoea* sp. B2	98.65	Supplementary Figure 7
B3	*Enterobacter* sp. B3	99.05	Supplementary Figure 8
B4	*Pantoea* sp. B4	85.53	Supplementary Figure 9
B5	*Enterobacter* sp. B5	97.4	Supplementary Figure 10
G21	*Pseudomonas* sp. G21	98.88	Supplementary Figure 11
G22	*Bacillus* sp. G22	98.54	Supplementary Figure 12
G23	*Bacillus* sp. G23	97.2	Supplementary Figure 13
G24	*Stutzerimonas* sp. G24	98	Supplementary Figure 14

Supplementary Table 2. Bacteria identified after sequence alignment using BLASTn tool available at NCBI. https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome

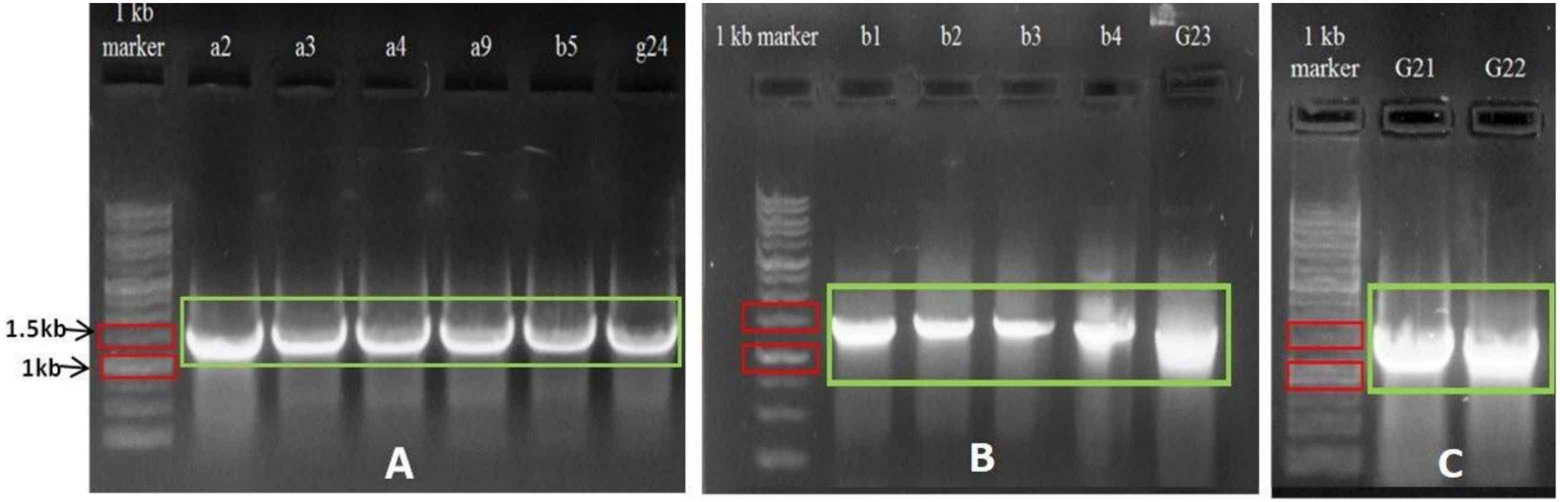


	Brachybacterium sp. A2	*Stutzerimonas sp.* A3	*Enterobacter sp.* A4	*Enterobacter sp.* A9	*Pantoea sp.* B1	*Pantoea sp.* B2	*Enterobacter sp.* B3	*Pantoea sp.* B4	*Enterobacter sp.* B5	*Pseudomonas sp.* G21	*Bacillus sp.* G22	*Bacillus sp.* G23	*Stutzerimonas sp.* G24
Control	100	100	100	100	100	100	100	100	100	100	100	100	100
Amikacin	18.9951	17.10142	19.8571	23.25901	27.07502	29.71747	30.92258	29.38773	16.88829	13.25415	13.07617	10.43036	10.41106
Ampicillin	17.1456	111.5727	121.3358	98.69942	95.97413	103.265	21.24324	122.9851	20.09855	82.68946	19.4576	10.41862	10.15475
Amoxicillin	19.62873	19.29055	19.04287	13.58381	17.01641	18.24285	18.30743	29.87424	18.08689	22.29917	24.08404	22.71909	17.77702
Ceftazidime	17.09765	18.56725	20.25447	23.1902	20.61323	18.97029	18.28995	25.55994	20.08044	20.35728	27.60932	11.05634	9.992538
Clindamycin	86.00197	112.4	104.8754	16.6185	20.86643	16.66851	96.67745	131.6959	100.9928	94.59426	111.6592	19.98748	16.82315
Doxycycline	16.15029	19.72253	22.96722	16.61505	17.28348	19.21612	20.40891	26.6569	20.91308	18.44279	18.21813	24.11972	16.18921
Erythromycin	20.10823	20.24469	22.13816	19.52931	21.67806	21.76796	20.08579	32.55003	21.64209	16.57283	18.06851	20.0939	18.03783
Gentamicin	92.85885	99.36133	105.6434	106.41	89.61881	98.28959	17.94424	151.9088	103.8632	109.3313	94.53906	132.5313	93.91039
Kanamycin	16.24824	28.08556	23.18126	16.96222	17.86237	20.2553	22.04485	23.24674	19.43912	17.91194	19.96588	13.12989	11.20916
Nalidixic Acid	15.90917	23.30216	23.58245	20.18992	20.25771	19.68008	27.50861	32.47659	34.63531	13.11373	11.27977	14.39358	10.14827
Oxytetracycline	20.84118	17.0968	19.19609	26.55863	17.83844	22.10719	16.73581	25.09684	18.76154	21.29911	16.50884	14.36228	10.76469
Piperacillin	21.93034	22.75085	28.90493	19.51899	20.91499	20.15338	23.4653	23.12741	16.16725	15.25426	10.45815	16.02113	12.1338
Spectinomycin	95.35229	106.2866	115.5548	24.3738	18.00874	15.57198	23.37037	128.7039	16.58756	16.38788	14.0266	13.05164	10.71278
Tetracycline	14.39531	21.76439	21.8898	16.61506	23.1591	18.88373	19.10555	24.99082	15.10924	17.25095	17.06239	23.01252	10.28453
Tylosin	20.96277	19.22168	19.76158	18.26211	17.81416	21.15597	19.13367	26.54995	21.8892	18.75103	23.75714	24.52268	19.40272

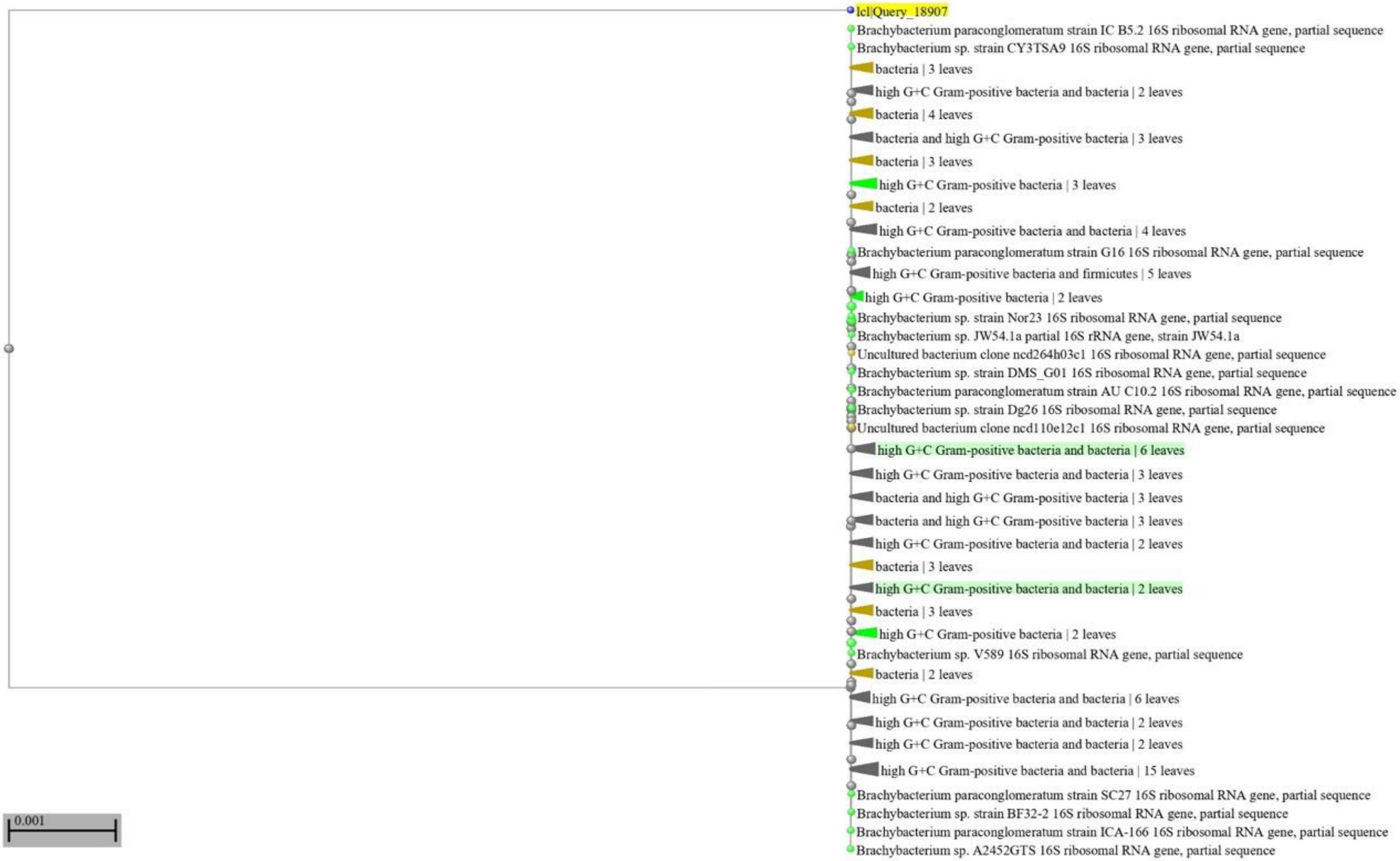
Supplementary Table 3. Percent inhibition of isolated bacteria against 15 antibiotics. Bacteria were cultured with 15 different antibiotics individually on micro titer plate. Bacteria without any antibiotic was treated as control. Plates were kept in incubator at 37 ºC with constant shaking at 200 rpm for 24 hrs. Absorbance was recorded using BioTek UV-Vis spectrophotometer and percent inhibition was calculatedwith respect to control. Bacteria resistant to antibiotic are represented in red.

Name	**Calculated generation time (in Hrs)**		
	pH 4.5	**pH 7.0**	**pH 9.0**
Brachybacterium sp. A2	6.4	4.3	3.5
Stutzerimonas sp. A3	5.0	4.3	3.5
Enterobacter sp. A4	4.5	4.2	3.4
Enterobacter sp. A9	5.1	4.1	3.6
Pantoea sp. B1	6.3	4.2	4.2
Pantoea sp. B2	5.2	4.2	3.4
Enterobacter sp. B3	5.2	5.3	4.7
Pantoea sp. B4	5.9	5.4	4.7
Enterobacter sp. B5	4.6	5.1	4.6
Pseudomonas sp. G21	5.1	4.1	3.6
Bacillus sp. G22	7.1	4.0	3.9
Bacillus sp. G23	5.9	4.1	3.4
Stutzerimonas sp. G24	6.0	3.9	3.2

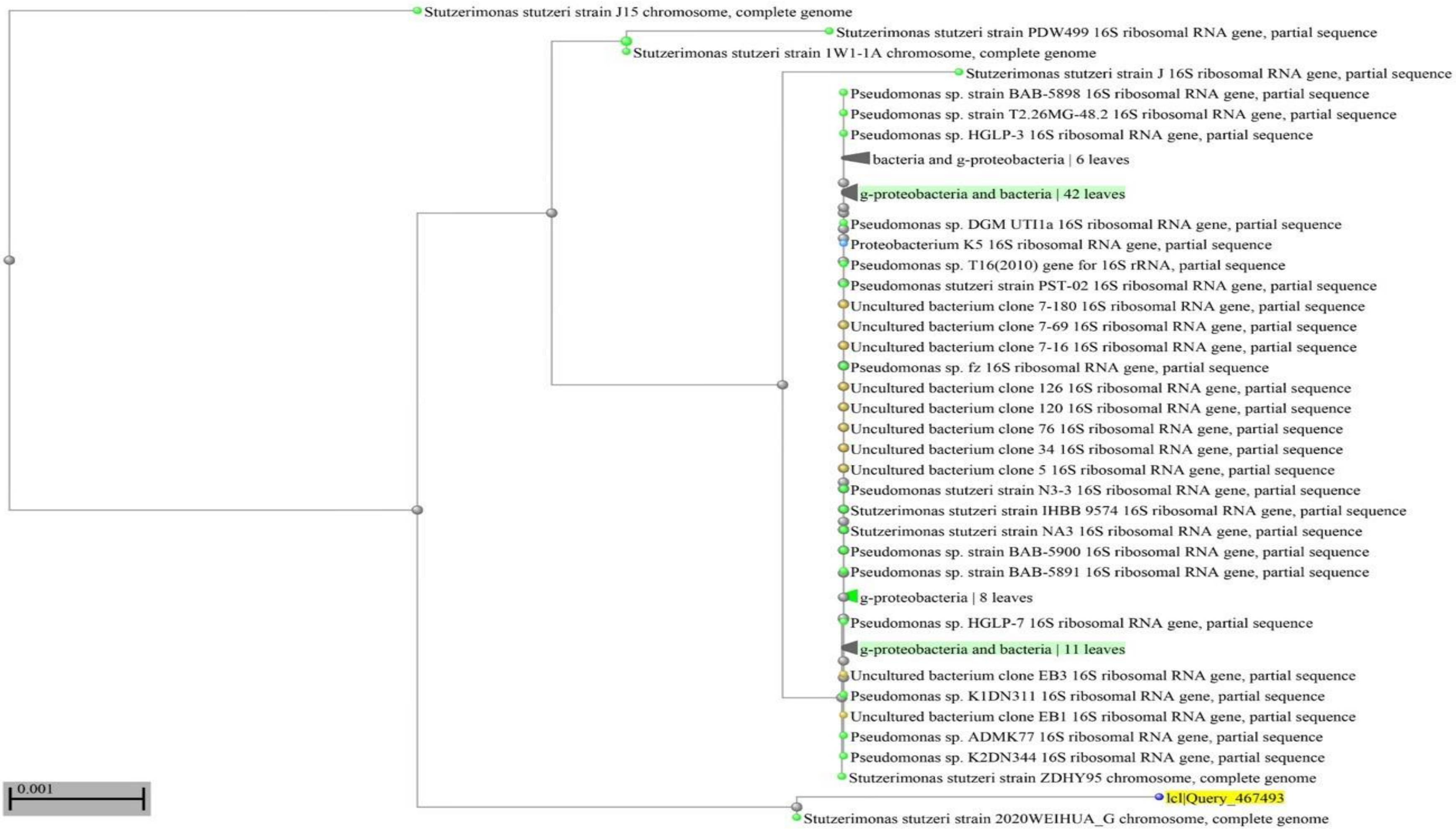
Supplementary Table 4: Calculated generation time of different bacterial isolates grown at different pH 4.5, 7 and 9.0



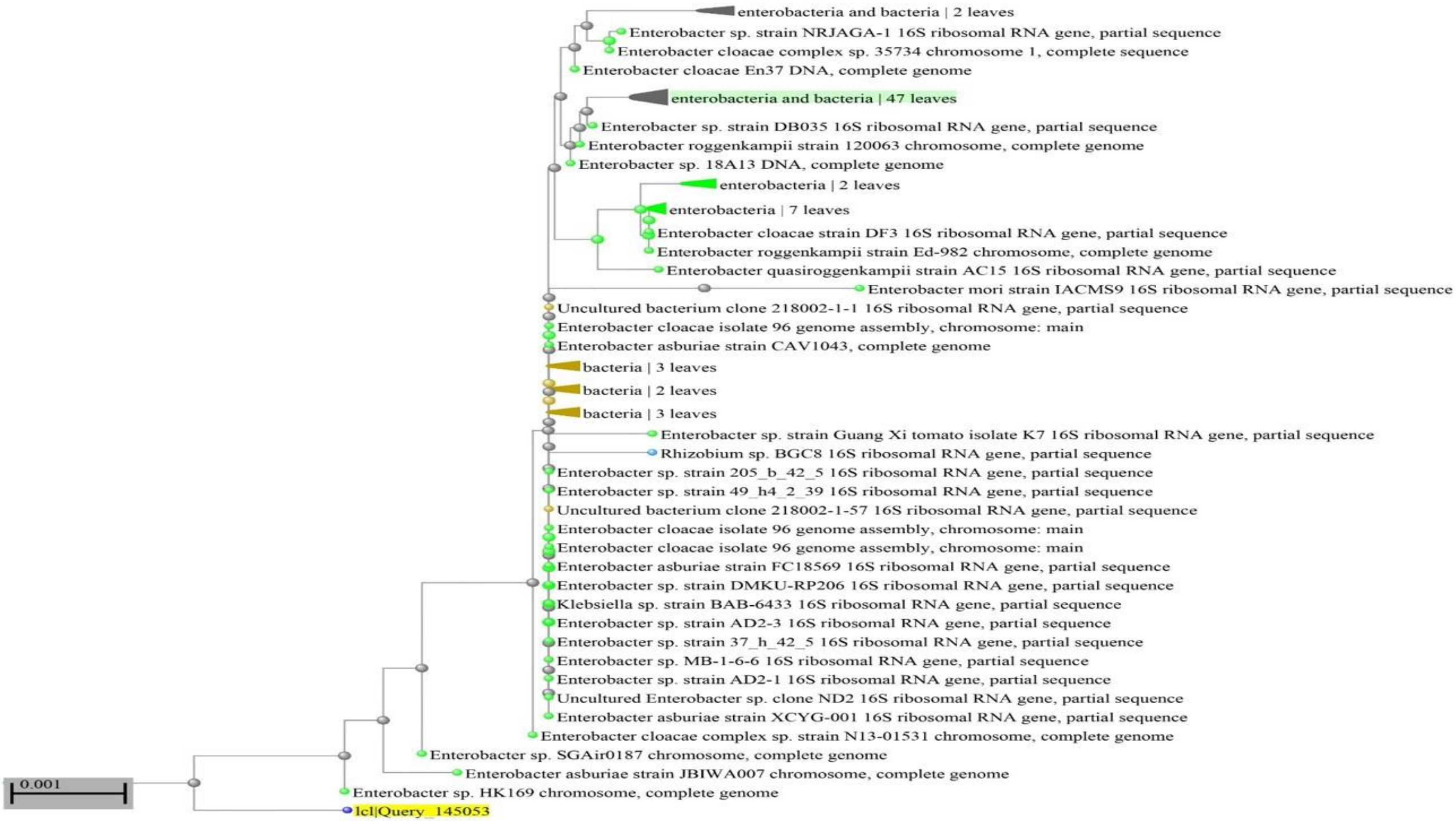
Supplementary Figure 1. An ethidium bromide stained agarose gel showing DNA fragments produced by PCR amplification of the 16S ribosomal RNA gene. Left lane of A, B, C contains 1kb DNA ladder; 1.0 kband 1.5 kb fragments are labeled by red box. The 1500 bp fragment produced by PCR is marked by green box. Amplified 16s rRNA segment of different bacteria is indicated above each lane.



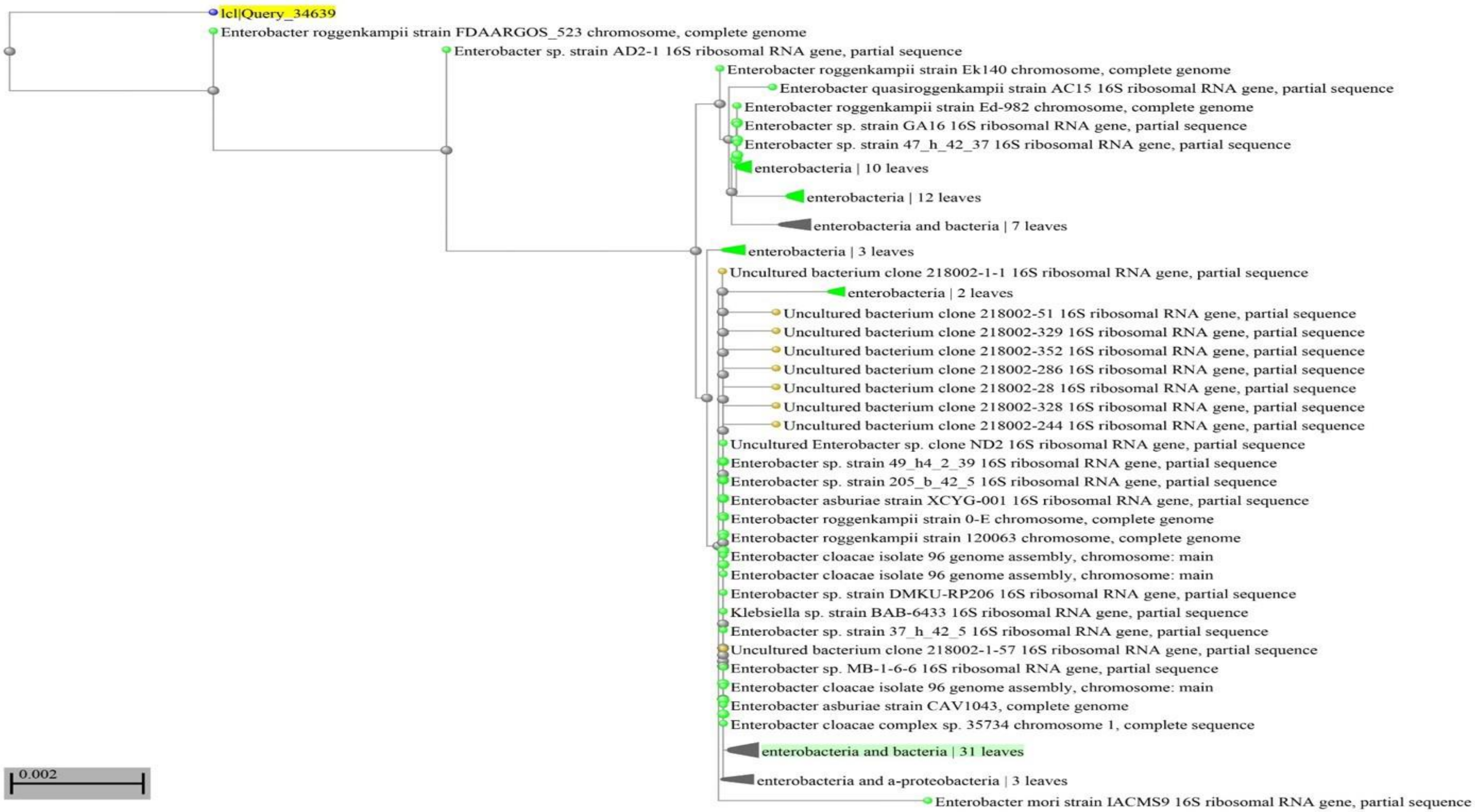
Supplementary Figure 2. Phylogenetic tree of bacterial isolate A2 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI



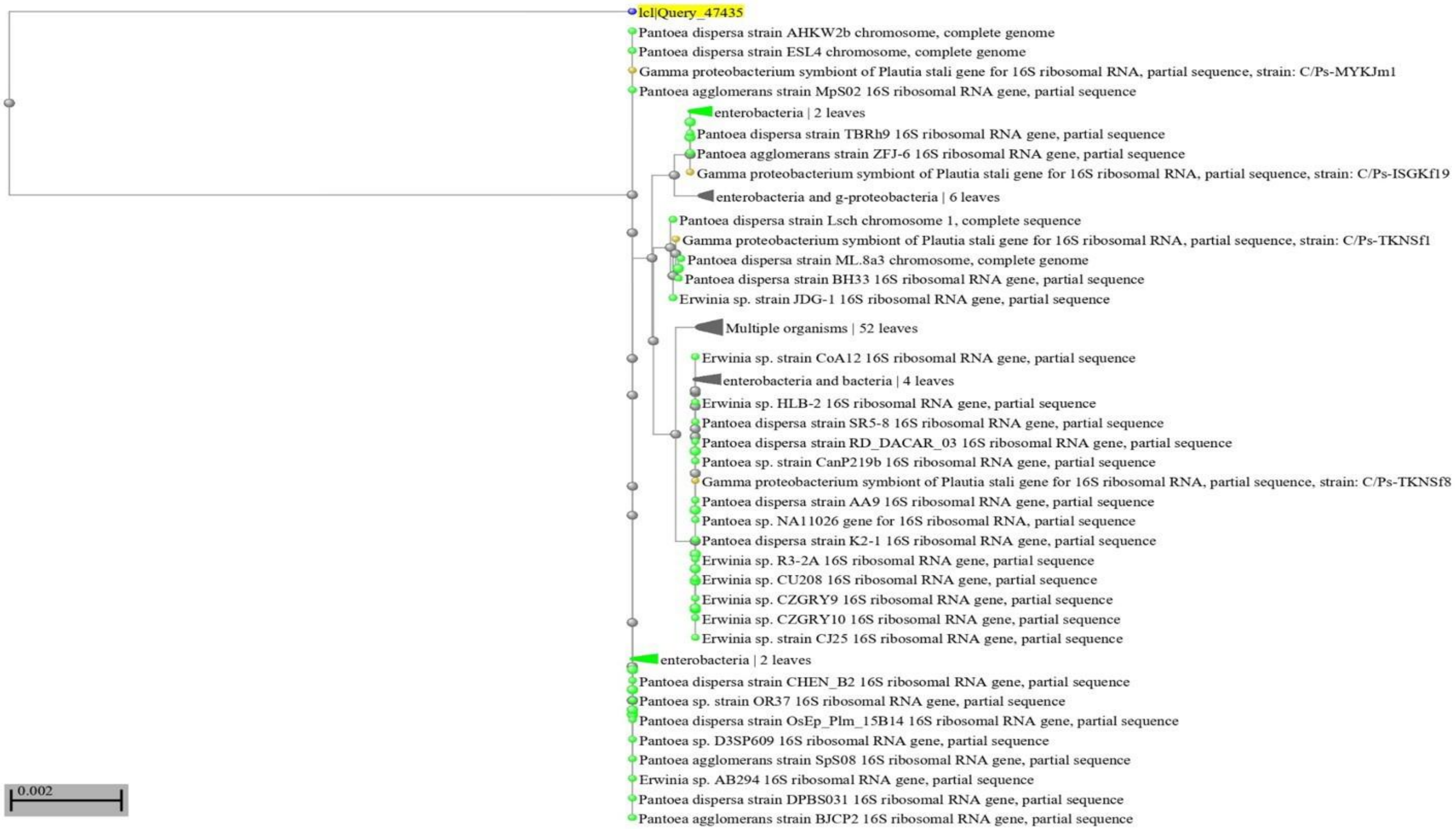
Supplementary Figure 3. Phylogenetic tree of bacterial isolate A3 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI



Supplementary Figure 4. Phylogenetic tree of bacterial isolate A4 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI

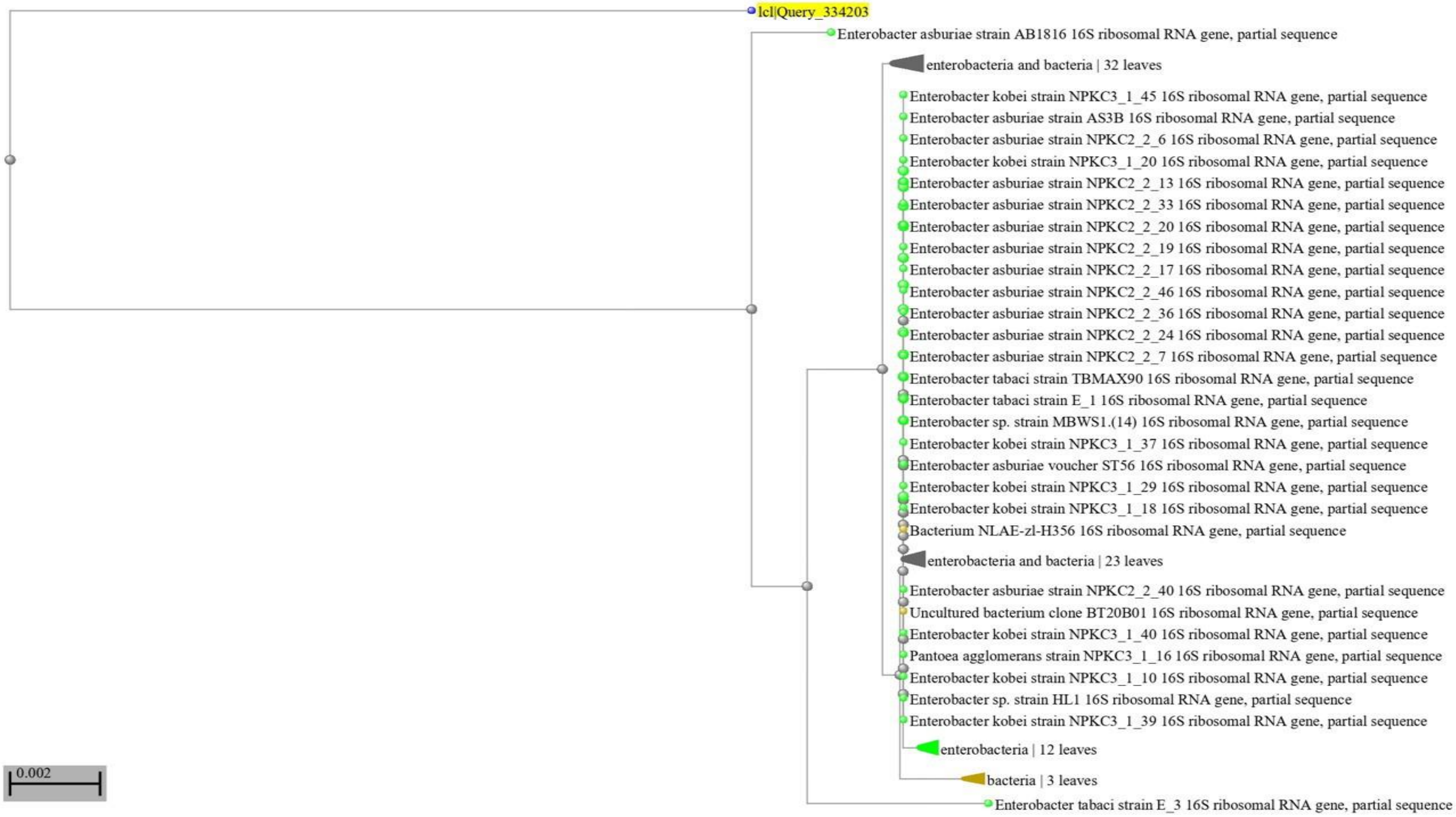


Supplementary Figure 5. Phylogenetic tree of bacterial isolate A9 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI

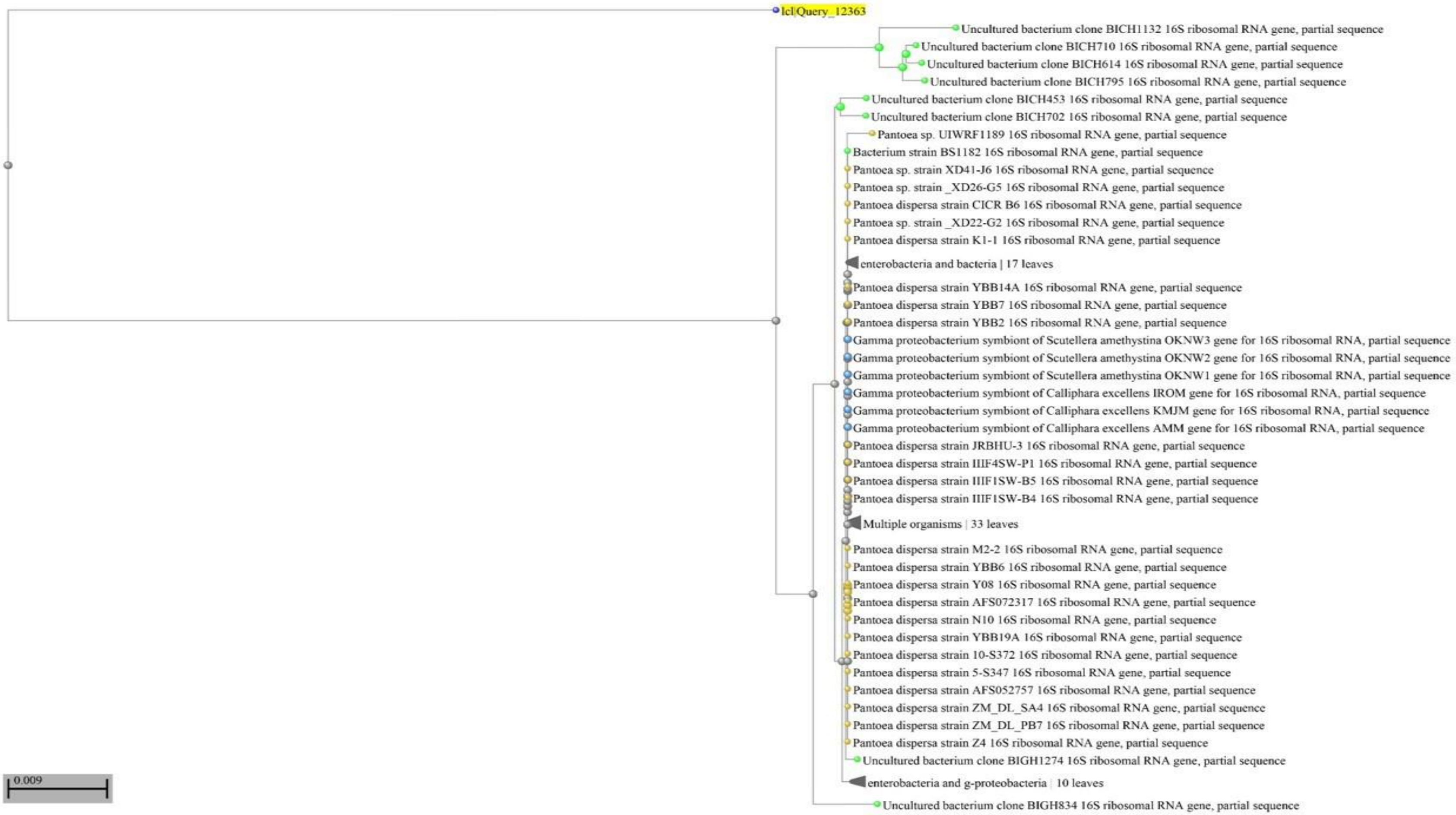


Supplementary Figure 6. Phylogenetic tree of bacterial isolate B1 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI

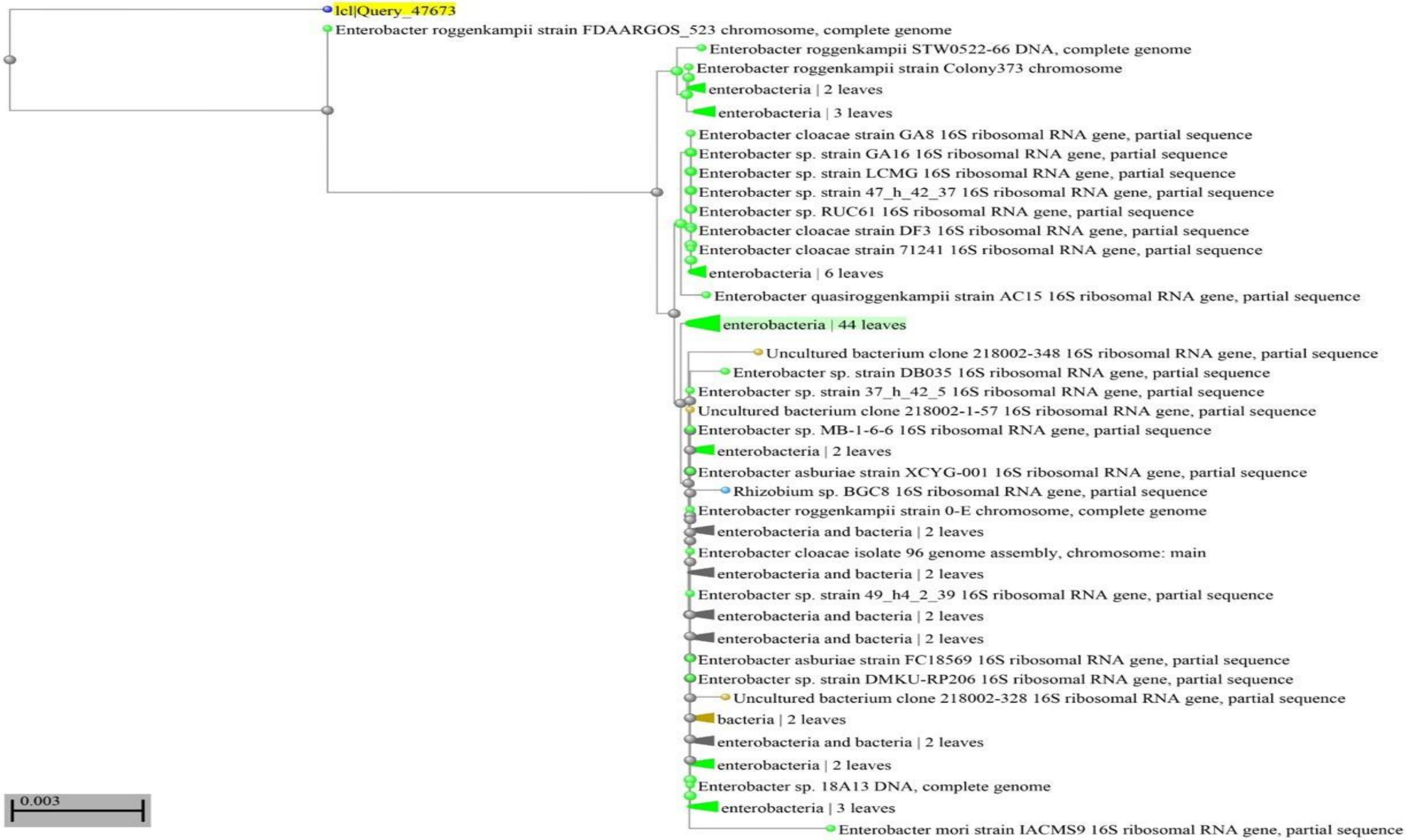
Supplementary Figure 7. Phylogenetic tree of bacterial isolate B2 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI



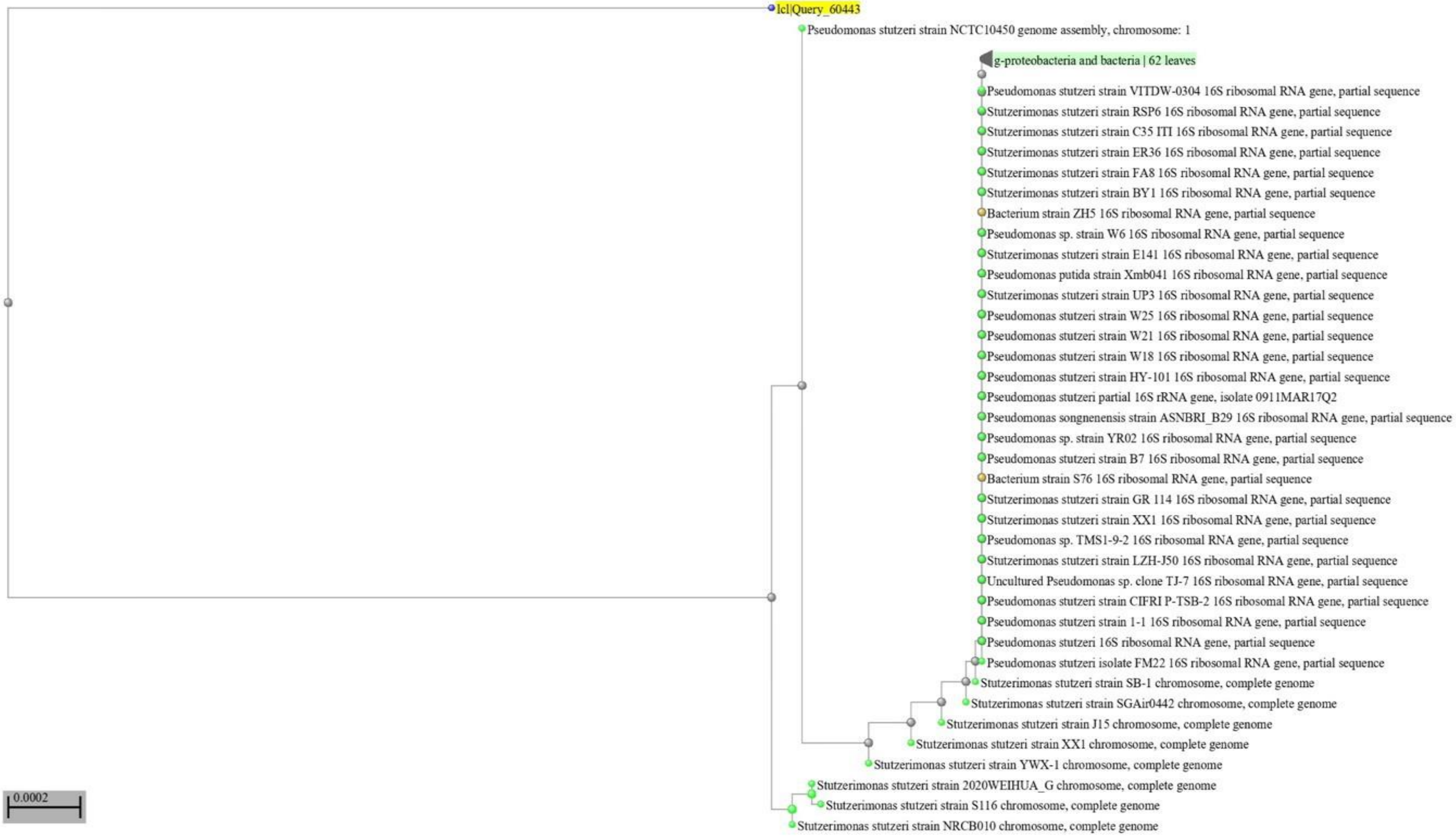
Supplementary Figure 8. Phylogenetic tree of bacterial isolate B3 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI



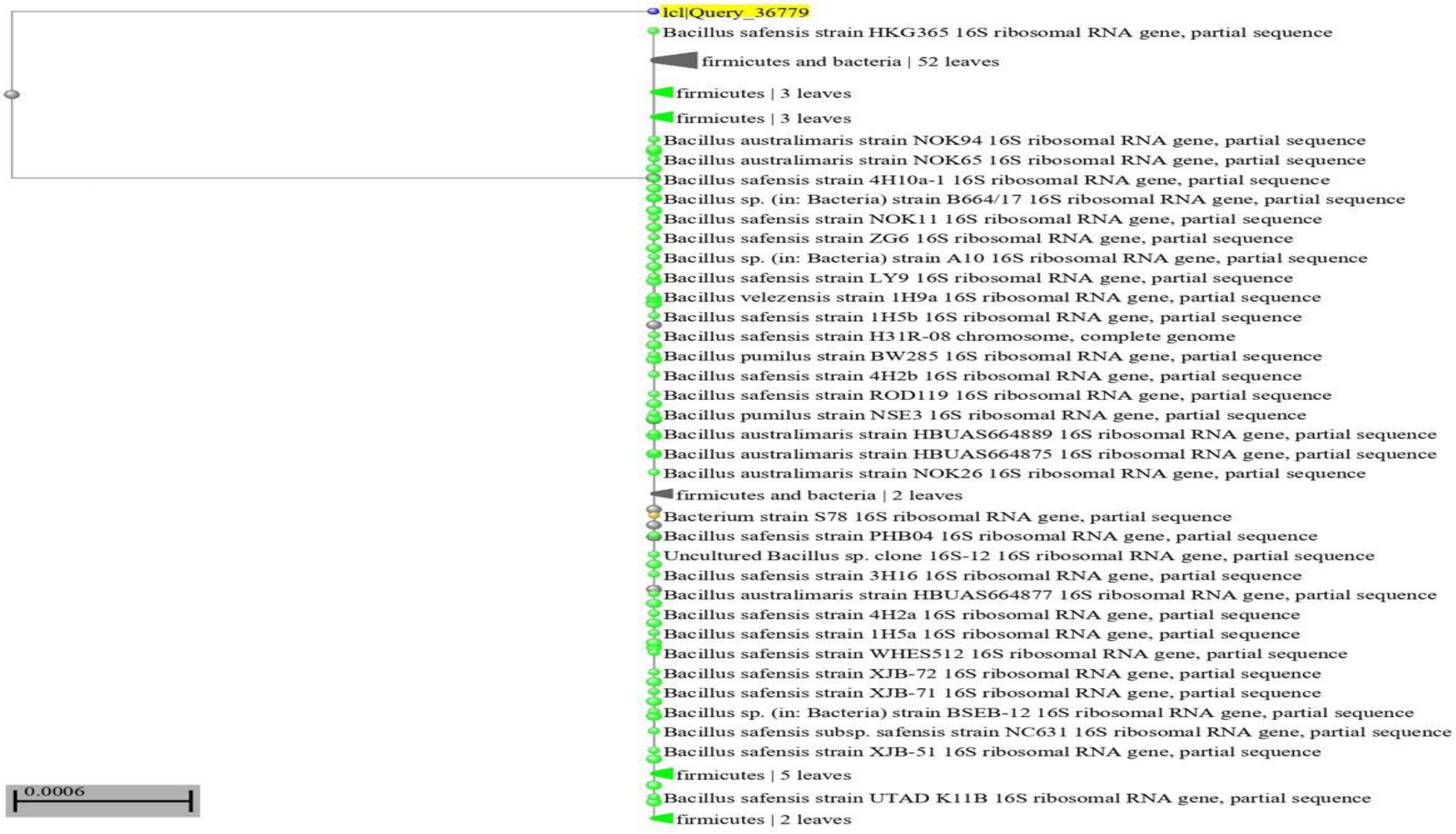
Supplementary Figure 9. Phylogenetic tree of bacterial isolate B4 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI



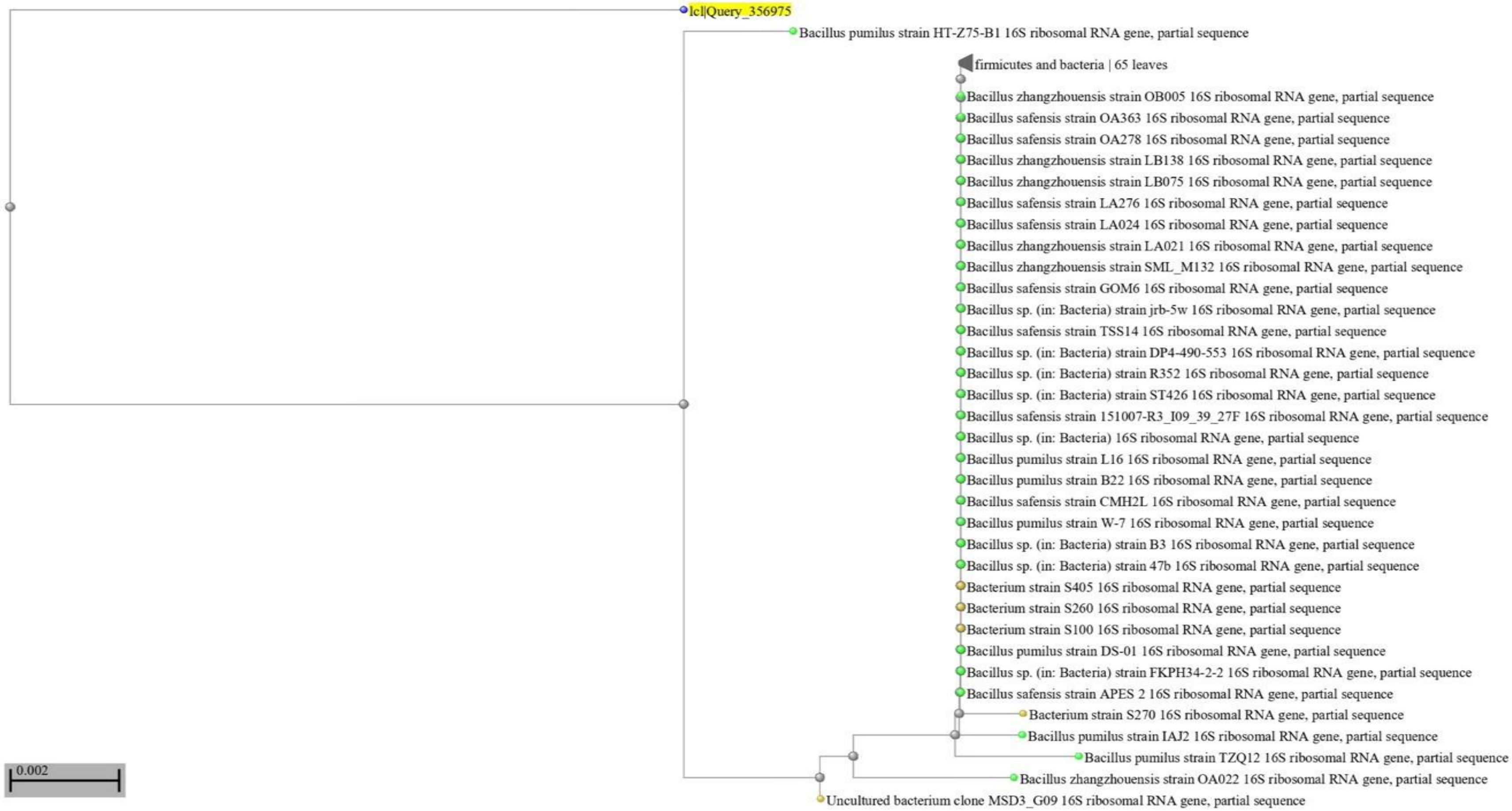
Supplementary Figure 10. Phylogenetic tree of bacterial isolate B5 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI



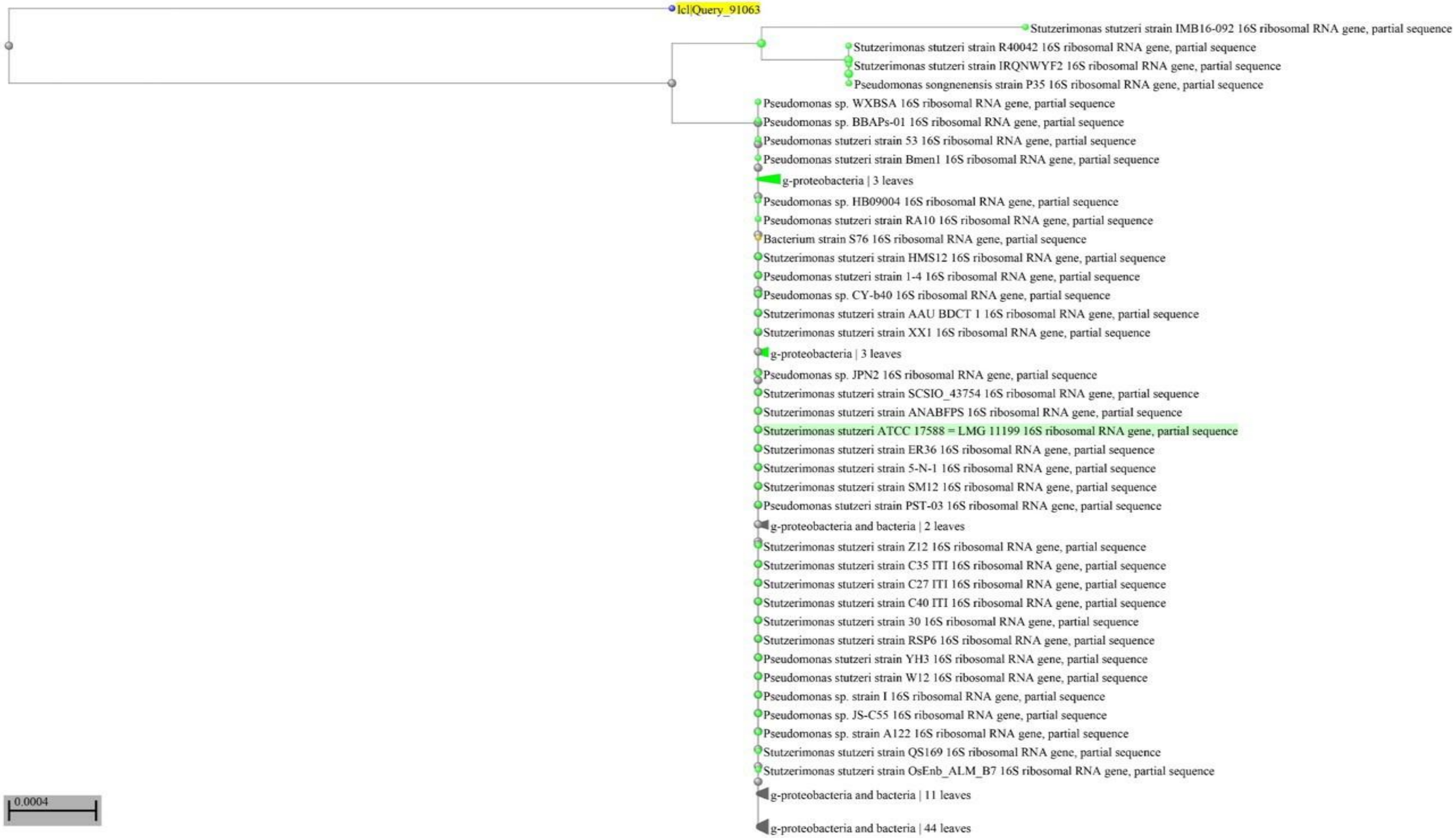
Supplementary Figure 11. Phylogenetic tree of bacterial isolate G21 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI



Supplementary Figure 12. Phylogenetic tree of bacterial isolate G22 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI



Supplementary Figure 13. Phylogenetic tree of bacterial isolate G23 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI



Supplementary Figure 14. Phylogenetic tree of bacterial isolate G24 generated after sequence alignment of its sequenced 16s rRNA fragment against nucleotide database of NCBI