



Supplementary Figure S1. Gel electrophoresis of genomic DNA extraction of 7 isolates obtained from ice cream (1, 2, 3, 4, 5, 9 and 10) in 1% agarose gel in 1x TBE buffer at 100 V (a), PCR amplification pattern of 7 isolates obtained from ice cream amplified by primer pairs 16s27f and 16s1492R as well as molecular marker 100 bp (b). Agarose gel (1%) of purified PCR product from 7 isolates obtained from ice cream indicated (C).

	10	20	30	40	50
gi 5373665	CAGTCGAACG	GTAACAGGAA	GCAGCTTGCT	TCTTTGCTGA	CGAGTGGCGG
1	CAGTCGA-CG	GTAACAGGAA	GCAGCTTGCT	GCTTTGCTGA	CGAGTGGCGG
2	CAGTCGA-CG	GTAACAGGAA	A-AGCTTGCT	GCTTCGCTGA	CGAGTGGCGG
3	CAGTCGA-CG	GTAACAGGAA	A-AGCTTGCT	GCTTCGCTGA	CGAGTGGCGG
4	CAGTCGA-CG	GTAACAGGAA	C-AGCTTGCT	GCTTCGCTGA	CGAGTGGCGG
5	CAGTCGA-CG	GTAACAGGAA	GCAGCTTGCT	GCTTTGCTGA	CGAGTGGCGG
9	CAGTCGA-CG	GTAACAGGAA	ACAGCTTGCT	GCTTCGCTGA	CGAGTGGCGG
10	CAGTCGA-CG	GTAACAGGAA	AAAGCTTGCT	GCTTCGCTGA	CGAGTGGCGG

	60	70	80	90	100
gi 5373665	ACGGGTGAGT	AATGTCTGGG	AAACTGCCTG	ATGGAGGGGG	ATAACTACTG
1	ACGGGTGAGT	AATGTCTGGG	AAACTGCCTG	ATGGAGGGGG	ATAACTACTG
2	ACGGGTGAGT	AATGTCTGGG	AAACTGCCTG	ATGGAGGGGG	ATAACTACTG
3	ACGGGTGAGT	AATGTCTGGG	AAACTGCCTG	ATGGAGGGGG	ATAACTACTG
4	ACGGGTGAGT	AATGTCTGGG	AAACTGCCTG	ATGGAGGGGG	ATAACTACTG
5	ACGGGTGAGT	AATGTCTGGG	AAACTGCCTG	ATGGAGGGGG	ATAACTACTG
9	ACGGGTGAGT	AATGTCTGGG	AAACTGCCTG	ATGGAGGGGG	ATAACTACTG
10	ACGGGTGAGT	AATGTCTGGG	AAACTGCCTG	ATGGAGGGGG	ATAACTACTG

	110	120	130	140	150
gi 5373665	GAAACGGTAG	CTAATACCGC	ATAACGTCGC	AAGACCAAAG	AGGGGGACCT
1	GAAACGGTAG	CTAATACCGC	ATAACGTCGC	AAGACCAAAG	AGGGGGACCT
2	GAAACGGTAG	CTAATACCGC	ATAACGTCGC	AAGACCAAAG	AGGGGGACCT
3	GAAACGGTAG	CTAATACCGC	ATAACGTCGC	AAGACCAAAG	AGGGGGACCT
4	GAAACGGTAG	CTAATACCGC	ATAACGTCGC	AAGACCAAAG	AGGGGGACCT
5	GAAACGGTAG	CTAATACCGC	ATAACGTCGC	AAGACCAAAG	AGGGGGACCT
9	GAAACGGTAG	CTAATACCGC	ATAACGTCGC	AAGACCAAAG	AGGGGGACCT
10	GAAACGGTAG	CTAATACCGC	ATAACGTCGC	AAGACCAAAG	AGGGGGACCT

	160	170	180	190	200
gi 5373665	TCGGGCCTCT	TGCCATCGGA	TGTGCCCAGA	TGGGATTAGC	TTGTTGGTGG
1	TCGGGCCTCT	TGCCATCGGA	TGTGCCCAGA	TGGGATTAGC	TTGTTGGTGG
2	TCGGGCCTCT	TGCCATCGGA	TGTGCCCAGA	TGGGATTAGC	TTGTTGGTGG
3	TCGGGCCTCT	TGCCATCGGA	TGTGCCCAGA	TGGGATTAGC	TTGTTGGTGG
4	TCGGGCCTCT	TGCCATCGGA	TGTGCCCAGA	TGGGATTAGC	TTGTTGGTGG
5	TCGGGCCTCT	TGCCATCGGA	TGTGCCCAGA	TGGGATTAGC	TTGTTGGTGG
9	TCGGGCCTCT	TGCCATCGGA	TGTGCCCAGA	TGGGATTAGC	TTGTTGGTGG
10	TCGGGCCTCT	TGCCATCGGA	TGTGCCCAGA	TGGGATTAGC	TTGTTGGTGG

	210	220	230	240	250
gi 5373665	GGTAACGGCT	CACCTAGGCG	ACGATCCCTA	GCTGGTCTGA	GAGGATGACC
1	GGTAACGGCT	CACCTAGGCG	ACGATCCCTA	GCTGGTCTGA	GAGGATGACC
2	GGTAACGGCT	CACCTAGGCG	ACGATCCCTA	GCTGGTCTGA	GAGGATGACC
3	GGTAACGGCT	CACCTAGGCG	ACGATCCCTA	GCTGGTCTGA	GAGGATGACC
4	GGTAACGGCT	CACCTAGGCG	ACGATCCCTA	GCTGGTCTGA	GAGGATGACC
5	GGTAACGGCT	CACCTAGGCG	ACGATCCCTA	GCTGGTCTGA	GAGGATGACC

9 GGTAACGGCT CACCTAGGCG ACGATCCCTA GCTGGTCTGA GAGGATGACC
10 GGTAACGGCT CACCTAGGCG ACGATCCCTA GCTGGTCTGA GAGGATGACC

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260 270 280 290 300
gi|5373665 AGCCCACTG GAACTGAGAC ACGGTCCAGA CTCCTACGGG AGGCAGCAGT
1 AGCCCACTG GAACTGAGAC ACGGTCCAGA CTCCTACGGG AGGCAGCAGT
2 AGCCCACTG GAACTGAGAC ACGGTCCAGA CTCCTACGGG AGGCAGCAGT
3 AGCCCACTG GAACTGAGAC ACGGTCCAGA CTCCTACGGG AGGCAGCAGT
4 AGCCCACTG GAACTGAGAC ACGGTCCAGA CTCCTACGGG AGGCAGCAGT
5 AGCCCACTG GAACTGAGAC ACGGTCCAGA CTCCTACGGG AGGCAGCAGT
9 AGCCCACTG GAACTGAGAC ACGGTCCAGA CTCCTACGGG AGGCAGCAGT
10 AGCCCACTG GAACTGAGAC ACGGTCCAGA CTCCTACGGG AGGCAGCAGT

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310 320 330 340 350
gi|5373665 GGGGAATATT GCACAATGGG CGCAAGCCTG ATGCAGCCAT GCCGCGTGTA
1 GGGGAATATT GCACAATGGG CGCAAGCCTG ATGCAGCCAT GCCGCGTGTA
2 GGGGAATATT GCACAATGGG CGCAAGCCTG ATGCAGCCAT GCCGCGTGTA
3 GGGGAATATT GCACAATGGG CGCAAGCCTG ATGCAGCCAT GCCGCGTGTA
4 GGGGAATATT GCACAATGGG CGCAAGCCTG ATGCAGCCAT GCCGCGTGTA
5 GGGGAATATT GCACAATGGG CGCAAGCCTG ATGCAGCCAT GCCGCGTGTA
9 GGGGAATATT GCACAATGGG CGCAAGCCTG ATGCAGCCAT GCCGCGTGTA
10 GGGGAATATT GCACAATGGG CGCAAGCCTG ATGCAGCCAT GCCGCGTGTA

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360 370 380 390 400
gi|5373665 TGAAGAAGGC CTTCGGGTTG TAAAGTACTT TCAGCGGGGA GGAAGGGAGT
1 TGAAGAAGGC CTTCGGGTTG TAAAGTACTT TCAGCGGGGA GGAAGGGAGT
2 TGAAGAAGGC CTTCGGGTTG TAAAGTACTT TCAGCGGGGA GGAAGGGAGT
3 TGAAGAAGGC CTTCGGGTTG TAAAGTACTT TCAGCGGGGA GGAAGGGAGT
4 TGAAGAAGGC CTTCGGGTTG TAAAGTACTT TCAGCGGGGA GGAAGGGAGT
5 TGAAGAAGGC CTTCGGGTTG TAAAGTACTT TCAGCGGGGA GGAAGGGAGT
9 TGAAGAAGGC CTTCGGGTTG TAAAGTACTT TCAGCGGGGA GGAAGGGAGT
10 TGAAGAAGGC CTTCGGGTTG TAAAGTACTT TCAGCGGGGA GGAAGGGAGT

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410 420 430 440 450
gi|5373665 AAAGTTAATA CCTTTGCTCA TTGACGTTAC CCGCAGAAGA AGCACCGGCT
1 AAAGTTAATA CCTTTGCTCA TTGACGTTAC CCGCAGAAGA AGCACCGGCT
2 AAAGTTAATA CCTTTGCTCA TTGACGTTAC CCGCAGAAGA AGCACCGGCT
3 AAAGTTAATA CCTTTGCTCA TTGACGTTAC CCGCAGAAGA AGCACCGGCT
4 AAAGTTAATA CCTTTGCTCA TTGACGTTAC CCGCAGAAGA AGCACCGGCT
5 AAAGTTAATA CCTTTGCTCA TTGACGTTAC CCGCAGAAGA AGCACCGGCT
9 AAAGTTAATA CCTTTGCTCA TTGACGTTAC CCGCAGAAGA AGCACCGGCT
10 AAAGTTAATA CCTTTGCTCA TTGACGTTAC CCGCAGAAGA AGCACCGGCT

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460 470 480 490 500
gi|5373665 AACTCCGTGC CAGCAGCCGC GGTAATACGG AGGGTGCAAG CGTTAATCGG
1 AACTCCGTGC CAGCAGCCGC GGTAATACGG AGGGTGCAAG CGTTAATCGG
2 AACTCCGTGC CAGCAGCCGC GGTAATACGG AGGGTGCAAG CGTTAATCGG

3	AAC TCC GTG C	CAG CAG CCG C	GGT AAT ACG G	AGG GTG CAA G	CGT TAA TCG G
4	AAC TCC GTG C	CAG CAG CCG C	GGT AAT ACG G	AGG GTG CAA G	CGT TAA TCG G
5	AAC TCC GTG C	CAG CAG CCG C	GGT AAT ACG G	AGG GTG CAA G	CGT TAA TCG G
9	AAC TCC GTG C	CAG CAG CCG C	GGT AAT ACG G	AGG GTG CAA G	CGT TAA TCG G
10	AAC TCC GTG C	CAG CAG CCG C	GGT AAT ACG G	AGG GTG CAA G	CGT TAA TCG G

	
	510520530540550	
gi 5373665	AATTACTGGG CGTAAAGCGC ACGCAGGCGG TTTGTTAAGT CAGATGTGAA	
1	AATTACTGGG CGTAAAGCGC ACGCAGGCGG TTTGTTAAGT CAGATGTGAA	
2	AATTACTGGG CGTAAAGCGC ACGCAGGCGG TTTGTTAAGT CAGATGTGAA	
3	AATTACTGGG CGTAAAGCGC ACGCAGGCGG TTTGTTAAGT CAGATGTGAA	
4	AATTACTGGG CGTAAAGCGC ACGCAGGCGG TTTGTTAAGT CAGATGTGAA	
5	AATTACTGGG CGTAAAGCGC ACGCAGGCGG TTTGTTAAGT CAGATGTGAA	
9	AATTACTGGG CGTAAAGCGC ACGCAGGCGG TTTGTTAAGT CAGATGTGAA	
10	AATTACTGGG CGTAAAGCGC ACGCAGGCGG TTTGTTAAGT CAGATGTGAA	

	560	570	580	590	600
gi 5373665	ATCCCCGGGC	TCAACCTGGG	AAGTGCATCT	GATACTGGCA	AGCTTGAGTC
1	ATCCCCGGGC	TCAACCTGGG	AAGTGCATCT	GATACTGGCA	AGCTTGAGTC
2	ATCCCCGGGC	TCAACCTGGG	AAGTGCATCT	GATACTGGCA	AGCTTGAGTC
3	ATCCCCGGGC	TCAACCTGGG	AAGTGCATCT	GATACTGGCA	AGCTTGAGTC
4	ATCCCCGGGC	TCAACCTGGG	AAGTGCATCT	GATACTGGCA	AGCTTGAGTC
5	ATCCCCGGGC	TCAACCTGGG	AAGTGCATCT	GATACTGGCA	AGCTTGAGTC
9	ATCCCCGGGC	TCAACCTGGG	AAGTGCATCT	GATACTGGCA	AGCTTGAGTC
10	ATCCCCGGGC	TCAACCTGGG	AAGTGCATCT	GATACTGGCA	AGCTTGAGTC

	
	610620630640650	
gi 5373665	TCGTAGAGGG GGGTAGAATT CCAGGTGTAG CGGTGAAATG CGTAGAGATC	
1	TCGTAGAGGG GGGTAGAATT CCAGGTGTAG CGGTGAAATG CGTAGAGATC	
2	TCGTAGAGGG GGGTAGAATT CCAGGTGTAG CGGTGAAATG CGTAGAGATC	
3	TCGTAGAGGG GGGTAGAATT CCAGGTGTAG CGGTGAAATG CGTAGAGATC	
4	TCGTAGAGGG GGGTAGAATT CCAGGTGTAG CGGTGAAATG CGTAGAGATC	
5	TCGTAGAGGG GGGTAGAATT CCAGGTGTAG CGGTGAAATG CGTAGAGATC	
9	TCGTAGAGGG GGGTAGAATT CCAGGTGTAG CGGTGAAATG CGTAGAGATC	
10	TCGTAGAGGG GGGTAGAATT CCAGGTGTAG CGGTGAAATG CGTAGAGATC	

	660	670	680	690	700
gi 5373665	TGGAGGAATA	CCGGTGGCGA	AGGCGGCCCC	CTGGACGAAG	ACTGACGCTC
1	TGGAGGAATA	CCGGTGGCGA	AGGCGGCCCC	CTGGACGAAG	ACTGACGCTC
2	TGGAGGAATA	CCGGTGGCGA	AGGCGGCCCC	CTGGACGAAG	ACTGACGCTC
3	TGGAGGAATA	CCGGTGGCGA	AGGCGGCCCC	CTGGACGAAG	ACTGACGCTC
4	TGGAGGAATA	CCGGTGGCGA	AGGCGGCCCC	CTGGACGAAG	ACTGACGCTC
5	TGGAGGAATA	CCGGTGGCGA	AGGCGGCCCC	CTGGACGAAG	ACTGACGCTC
9	TGGAGGAATA	CCGGTGGCGA	AGGCGGCCCC	CTGGACGAAG	ACTGACGCTC
10	TGGAGGAATA	CCGGTGGCGA	AGGCGGCCCC	CTGGACGAAG	ACTGACGCTC

gi|5373665 AGGTGCGAAA GCGTGGGGAG CAAACAGGAT TAGATACCCT GGTAGTCCAC
1 AGGTGCGAAA GCGTGGGGAG CAAACAGGAT TAGATACCCT GGTAGTCCAC
2 AGGTGCGAAA GCGTGGGGAG CAAACAGGAT TAGATACCCT GGTAGTCCAC
3 AGGTGCGAAA GCGTGGGGAG CAAACAGGAT TAGATACCCT GGTAGTCCAC
4 AGGTGCGAAA GCGTGGGGAG CAAACAGGAT TAGATACCCT GGTAGTCCAC
5 AGGTGCGAAA GCGTGGGGAG CAAACAGGAT TAGATACCCT GGTAGTCCAC
9 AGGTGCGAAA GCGTGGGGAG CAAACAGGAT TAGATACCCT GGTAGTCCAC
10 AGGTGCGAAA GCGTGGGGAG CAAACAGGAT TAGATACCCT GGTAGTCCAC

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760 770 780 790 800

gi|5373665 GCCGTAAACG ATGTCGACTT GGAGGTTGTG CCCTTGAGGC GTGGCTTCCG
1 GCCGTAAACG ATGTCGACTT GGAGGTTGTG CCCTTGAGGC GTGGCTTCCG
2 GCCGTAAACG ATGTCGACTT GGAGGTTGTG CCCTTGAGGC GTGGCTTCCG
3 GCCGTAAACG ATGTCGACTT GGAGGTTGTG CCCTTGAGGC GTGGCTTCCG
4 GCCGTAAACG ATGTCGACTT GGAGGTTGTG CCCTTGAGGC GTGGCTTCCG
5 GCCGTAAACG ATGTCGACTT GGAGGTTGTG CCCTTGAGGC GTGGCTTCCG
9 GCCGTAAACG ATGTCGACTT GGAGGTTGTG CCCTTGAGGC GTGGCTTCCG
10 GCCGTAAACG ATGTCGACTT GGAGGTTGTG CCCTTGAGGC GTGGCTTCCG

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810 820 830 840 850

gi|5373665 GAGCTAACGC GTTAAGTCGA CCGCCTGGGG AGTACGGCCG CAAGGTTAAA
1 GAGCTAACGC GTTAAGTCGA CCGCCTGGGG AGTACGGCCG CAAGGTTAAA
2 GAGCTAACGC GTTAAGTCGA CCGCCTGGGG AGTACGGCCG CAAGGTTAAA
3 GAGCTAACGC GTTAAGTCGA CCGCCTGGGG AGTACGGCCG CAAGGTTAAA
4 GAGCTAACGC GTTAAGTCGA CCGCCTGGGG AGTACGGCCG CAAGGTTAAA
5 GAGCTAACGC GTTAAGTCGA CCGCCTGGGG AGTACGGCCG CAAGGTTAAA
9 GAGCTAACGC GTTAAGTCGA CCGCCTGGGG AGTACGGCCG CAAGGTTAAA
10 GAGCTAACGC GTTAAGTCGA CCGCCTGGGG AGTACGGCCG CAAGGTTAAA

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860 870 880 890 900

gi|5373665 ACTCAAATGA ATTGACGGGG GCCCGCACAA GCGGTGGAGC ATGTGGTTTA
1 ACTCAAATGA ATTGACGGGG GCCCGCACAA GCGGTGGAGC ATGTGGTTTA
2 ACTCAAATGA ATTGACGGGG GCCCGCACAA GCGGTGGAGC ATGTGGTTTA
3 ACTCAAATGA ATTGACGGGG GCCCGCACAA GCGGTGGAGC ATGTGGTTTA
4 ACTCAAATGA ATTGACGGGG GCCCGCACAA GCGGTGGAGC ATGTGGTTTA
5 ACTCAAATGA ATTGACGGGG GCCCGCACAA GCGGTGGAGC ATGTGGTTTA
9 ACTCAAATGA ATTGACGGGG GCCCGCACAA GCGGTGGAGC ATGTGGTTTA
10 ACTCAAATGA ATTGACGGGG GCCCGCACAA GCGGTGGAGC ATGTGGTTTA

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910 920 930 940 950

gi|5373665 ATTCGATGCA ACGCGAAGAA CCTTACCTGG TCTTGACATC CACGGAAGTT
1 ATTCGATGCA ACGCGAAGAA CCTTACCTGG TCTTGACATC CACGGAAGTT
2 ATTCGATGCA ACGCGAAGAA CCTTACCTGG TCTTGACATC CACGGAAGTT
3 ATTCGATGCA ACGCGAAGAA CCTTACCTGG TCTTGACATC CACGGAAGTT
4 ATTCGATGCA ACGCGAAGAA CCTTACCTGG TCTTGACATC CACGGAAGTT
5 ATTCGATGCA ACGCGAAGAA CCTTACCTGG TCTTGACATC CACGGAAGTT
9 ATTCGATGCA ACGCGAAGAA CCTTACCTGG TCTTGACATC CACGGAAGTT
10 ATTCGATGCA ACGCGAAGAA CCTTACCTGG TCTTGACATC CACGGAAGTT

	960	970	980	990	1000
gi 5373665	TTCAGAGATG	AGAATGTGCC	TTCGGGAACC	GTGAGACAGG	TGCTGCATGG
1	TTCAGAGATG	AGAATGTGCC	TTCGGGAACC	GTGAGACAGG	TGCTGCATGG
2	TTCAGAGATG	AGAATGTGCC	TTCGGGAACC	GTGAGACAGG	TGCTGCATGG
3	TTCAGAGATG	AGAATGTGCC	TTCGGGAACC	GTGAGACAGG	TGCTGCATGG
4	TTCAGAGATG	AGAATGTGCC	TTCGGGAACC	GTGAGACAGG	TGCTGCATGG
5	TTCAGAGATG	AGAATGTGCC	TTCGGGAACC	GTGAGACAGG	TGCTGCATGG
9	TTCAGAGATG	AAAATGTGCC	TTCGGGAACC	GTGAGACAGG	TGCTGCATGG
10	TTCAGAGATG	AAAATGTGCC	TTCGGGAACC	GTGAGACAGG	TGCTGCATGG

Supplementary Figure S2. Alignment: 16S Aligned Seqs. of *E. coli* strains obtained from ice cream (1,2,3,4,5,9, 10) in comparison with *E.coli* (gi|537366568|gb| KF574803.1| *Escherichia coli* strain CRTY15 16S ribosomal RNA gene, partial sequence)from NCBI.fas