

Rapid DNA sequencing technology based on the Sanger method for bacterial identification

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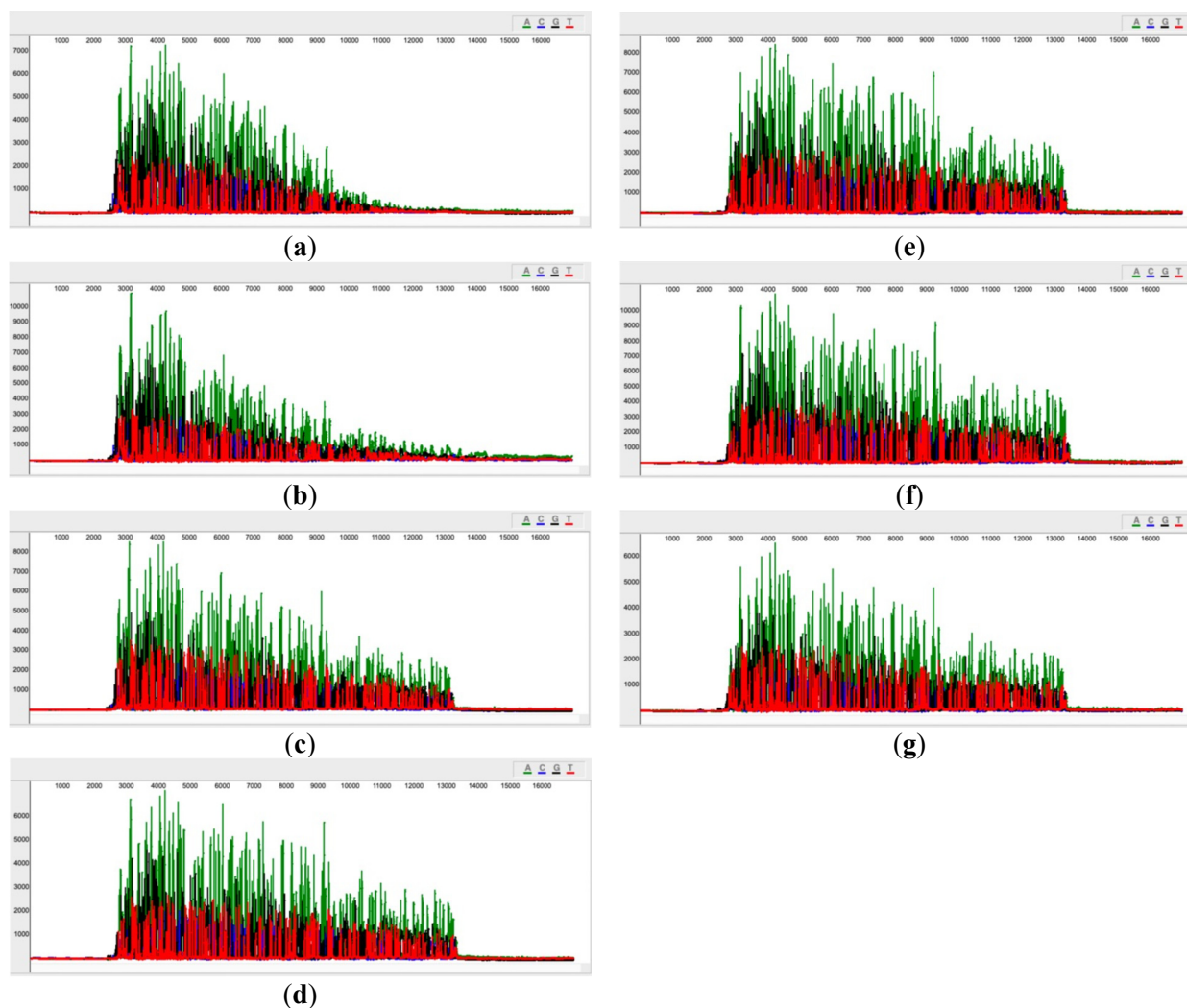


Figure S1. Raw data from a capillary DNA sequencer for different cycle sequencing reaction durations. (a) 20 s. (b) 30 s. (c) 40 s. (d) 50 s. (e) 60 s. (f) 90 s. (g) 120 s. Blue shaded portions indicate the fluorescence intensity of the end portion of the amplification product.

Escherichia coli strain LD26-1 chromosome, complete genome

Sequence ID: [CP047665.1](#) Length: **4774827** Number of Matches: **7**

Range 1: 2685604 to 2686163 GenBank Graphics ▼ Next Match ▲ Previous Match					
Score	Expect	Identities	Gaps	Strand	
905 bits(490)	0.0	542/564(96%)	15/564(2%)	Plus/Minus	
Query 1	AGC-TGCTGCTTTTCGCTGACGAGTGGCGGAGGGTGAGTAATGCTCGGAAACTGC-TGA	58			
Sbjct 2686163	AGCTTGCTG-TTTTCGCTGACGAGTGGCGGAGGGTGAGTAATGCTCGGAAACTGCCCTGA	2686105			
Query 59	TGGGAGGGGGAATACTACTGAAACG-TAGCTAATACCGCATAACGTCGCA-GACCAAAG	116			
Sbjct 2686104	T-GGAGGGGGAATACTACTGGAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAG	2686046			
Query 117	AGGGGACCTTCGGGCTGCTTG-CATCGGATGTGCCAGATGGGAT-AGTAGTAGGTG	174			
Sbjct 2686045	AGGGGACCTTCGGGCTT-CTTGCCATCGGATGTGCCAGATGGGATAGCTAGTAGGTG	2685987			
Query 175	GGGGTAACGGCTCACTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAAGCACAC	234			
Sbjct 2685986	GGGGTAACGGCTCACTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAAGCACAC	2685927			
Query 235	TGGAATCGAGACACGGTCCAGACTCTACGGGAGGACGAGTGGGGAATATTGCACAATG	294			
Sbjct 2685926	TGGAATCGAGACACGGTCCAGACTCTACGGGAGGACGAGTGGGGAATATTGCACAATG	2685867			
Query 295	GGCGCAAGCTCGATGACGCTATGCCCGCTGTATGAAGAAGGCTTCGGGTTGTAAAGTAC	354			
Sbjct 2685866	GGCGCAAGCTCGATGACGCTATGCCCGCTGTATGAAGAAGGCTTCGGGTTGTAAAGTAC	2685807			
Query 355	TTTCAGCGGGGAGGAAGGAGTAAGATTAAATACCTTTGCTCATTTGACGTACCGCAGAGA	414			
Sbjct 2685806	TTTCAGCGGGGAGGAAGGAGTAAGATTAAATACCTTTGCTCATTTGACGTACCGCAGAGA	2685748			
Query 415	AGAAGCAAGCTGATGACGCTATGCCCGCTGTATGAAGAAGGCTTCGGGTTGTAAAGTAC	473			
Sbjct 2685747	AGAAGCAAGCTGATGACGCTATGCCCGCTGTATGAAGAAGGCTTCGGGTTGTAAAGTAC	2685688			
Query 474	CGGAAT-ACTGGGCTAAAGGG-ACCGCGCGGTTTGT-AAGTCAGATGGGAAATCC-G	529			
Sbjct 2685687	CGGAATTACTGGGCTAAAGGCGCACGAGCGGTTTGTAAAGTCAGATGTGAATCCCGG	2685628			
Query 530	GGCTCAACTCTGGGAACGTCATTGG 553				
Sbjct 2685627	GGCTCAACTCTGGGAACGTCATCTG 2685604				

(a)

Mycoplasma pneumoniae strain 16-734 chromosome, complete genome

Sequence ID: [CP039761.1](#) Length: **818445** Number of Matches: **1**

Range 1: 118272 to 118814 GenBank Graphics ▼ Next Match ▲ Previous Match					
Score	Expect	Identities	Gaps	Strand	
761 bits(412)	0.0	513/555(92%)	34/555(6%)	Plus/Plus	
Query 1	ATACATTTTCGGGAGCGAAACGGGTGGAGTAACACGTTATCCCAATCTACCTTATAATGGG	60			
Sbjct 118272	ATAC-TTTAGAG-GCG-AACGGGT-GAGTAACACG-TAT-CCAATCTACCTTATAATGGG	118325			
Query 61	GGGATAACTAG-TGAAAGACTAGCTAATACCGCATAAGAACTTTGGTTGCGATGAATCAT	119			
Sbjct 118326	GG-ATAACTAGTTGAAAGACTAGCTAATACCGCATAAGAACTTTGGTTGCGATGAATCA-	118383			
Query 120	AAGTTGAAAGGACCTCGAAGGGTTTCGTTATTTGATGAGGGTGCGCCATATCAGCTAGTTG	179			
Sbjct 118384	AAGTTGAAAGGACCTCGAAGGGTTTCGTTATTTGATGAGGGTGCGCCATATCAGCTAGTTG	118443			
Query 180	GTGGGGGTAACTGGGCTACCAAGGCAATGACGTGTAGCTATGCTGAGAAGTAGAATAGCCA	239			
Sbjct 118444	GT-GGGGTAACTGGGCTACCAAGGCAATGACGTGTAGCTATGCTGAGAAGTAGAATAGCCA	118502			
Query 240	CAATGGGACTGAGACACGG-CCATACTCTACGGGAGGCGAGCT-GGGAAATTTTCACA	297			
Sbjct 118503	CAATGGGACTGAGACACGGCCATACTCTACGGGAGGCGAGCTAGGGAAATTTTCACA	118562			
Query 298	ATGAGCGAAAGCTTGATGGAGCAATGCCGCTGAACGATGATTGCTTTAAAGATGG-AAA	356			
Sbjct 118563	ATGAGCGAAAGCTTGATGGAGCAATGCCGCTGAACGATGAAAGTCTTTAAAGATGTAAA	118622			
Query 357	GT-C-TTTATTTGGGAAGAATGATGCTTTAGCAGGTAATGGCTAGGTTTGAAGTGTCCC	414			
Sbjct 118623	GTCTCTTTATTTGGGAAGAATGA-CTTAGCA-GGAATGGCTAGAGTTGACTGTACC	118679			
Query 415	ATTTTGAATAA-TGACGCACTAATATGGGCGAGCACTGCGGTAA-CATAG-TCG-AAG	469			
Sbjct 118680	ATTTTGAATAAGTGACGACTAATATGTGCGAGCACTGCGGTAAATACATAGGTCGCAAG	118739			
Query 470	C-T-ATCCGGA-TTATTTGGGCGTAAAGCA-GC-CAG-CGG-TTGAAT-GTCTGG-GTTAA	520			
Sbjct 118740	CGTTATCCGGATTATTTGGGCGTAAAGCAAGCGAGCGGATGAAAGATCTGGTGTAA	118799			
Query 521	---GAGCTGCTTAAAC 533				
Sbjct 118800	AGGCAGCTGCTTAAAC 118814				

(c)

Escherichia coli strain 2014C-3307 chromosome, complete genome

Sequence ID: [CP027368.1](#) Length: **4965987** Number of Matches: **7**

Range 1: 2606877 to 2607626 GenBank Graphics ▼ Next Match ▲ Previous Match					
Score	Expect	Identities	Gaps	Strand	
1349 bits(730)	0.0	740/750(99%)	0/750(0%)	Plus/Minus	
Query 3	AGGCCTAACMCATGCAAGTCAAYGTTAAACAGGAARMAGCTTGCTKYTTYGCTGACGAGT	62			
Sbjct 2607626	AGGCCTAACACATGCAAGTCAACGGTAAACAGGAACAGCTTGCTGTTTCCTGACGAGT	2607567			
Query 63	GGCGGACGGGTGAGTAATGCTCGGAAACTGCCCTGATGGAGGGGGATAACTACTGGAAC	122			
Sbjct 2607566	GGCGGACGGGTGAGTAATGCTCGGAAACTGCCCTGATGGAGGGGGATAACTACTGGAAC	2607507			
Query 123	GGTAGCTAATACCGCATAACGTCGAAGACAAAGAGGGGGACCTTCGGGCTCTTGCCA	182			
Sbjct 2607586	GGTAGCTAATACCGCATAACGTCGAAGACAAAGAGGGGGACCTTCGGGCTCTTGCCA	2607447			
Query 183	TCGGATGTGCCAGATGGGATTAGCTWGTWGTGGGTAAACGGCTCACWAGGCGACGAT	242			
Sbjct 2607446	TCGGATGTGCCAGATGGGATTAGCTTGTGGTGGGTAAACGGCTCACCAAGGCGACGAT	2607387			
Query 243	CCCTAGCTGGTCTGAGAGGATGACCAAGCACTGGAACGAGACACGGTCAGACTCCT	302			
Sbjct 2607386	CCCTAGCTGGTCTGAGAGGATGACCAAGCACTGGAACGAGACACGGTCAGACTCCT	2607327			
Query 303	ACGGGAGGACGAGTGGGGAATATTGCAACATGGGCGCAAGCTGATGACAGCATGCCGC	362			
Sbjct 2607326	ACGGGAGGACGAGTGGGGAATATTGCAACATGGGCGCAAGCTGATGACAGCATGCCGC	2607267			
Query 363	GTGTATGAAGAAGGCTTCGGGTTGTAAAGTACTTTACGCGGGGAGGAAGGAGTAAAGT	422			
Sbjct 2607266	GTGTATGAAGAAGGCTTCGGGTTGTAAAGTACTTTACGCGGGGAGGAAGGAGTAAAGT	2607207			
Query 423	TAATACCTTTGCTCAATTGACGTTACC CGCAGAGAAGCAACGGCTAACTCGTGCCAGCA	482			
Sbjct 2607206	TAATACCTTTGCTCAATTGACGTTACC CGCAGAGAAGCAACGGCTAACTCGTGCCAGCA	2607147			
Query 483	GCCGCGGTAAATCGGAGGGTGCAAGCGTAAATCGGAATTACGTGGCGTAAAGCGACGCA	542			
Sbjct 2607146	GCCGCGGTAAATCGGAGGGTGCAAGCGTAAATCGGAATTACGTGGCGTAAAGCGACGCA	2607087			
Query 543	GGCGGTTTGTAAAGTCAGATGTGAATCCCGGGCTCAACCTGGGAACGCACTGTGATAC	602			
Sbjct 2607086	GGCGGTTTGTAAAGTCAGATGTGAATCCCGGGCTCAACCTGGGAACGCACTGTGATAC	2607027			
Query 603	TGGCAAGCTTGAGTCTCTGAGAGGGGGTAGAATTCGGAATCTAGCGGTGAAGTGCAGTAG	662			
Sbjct 2607026	TGGCAAGCTTGAGTCTCTGAGAGGGGGTAGAATTCGGAATCTAGCGGTGAAGTGCAGTAG	2606967			
Query 663	AGATCTGGAGGAATACCGGTGGCGAAGCGGCCCCCTGGACGAAGACTGACGCTCAGGTG	722			
Sbjct 2606966	AGATCTGGAGGAATACCGGTGGCGAAGCGGCCCCCTGGACGAAGACTGACGCTCAGGTG	2606907			
Query 723	CGAAAGCGTGGGAGCAACAGGATTAGATA 752				
Sbjct 2606906	CGAAAGCGTGGGAGCAACAGGATTAGATA 2606877				

(b)

Streptococcus pneumoniae strain 4559 genome assembly, chromosome: 1

Sequence ID: [LR595848.1](#) Length: **2150981** Number of Matches: **4**

Range 1: 15238 to 15604 GenBank Graphics ▼ Next Match ▲ Previous Match					
Score	Expect	Identities	Gaps	Strand	
460 bits(249)	4e-125	335/372(90%)	23/372(6%)	Plus/Plus	
Query 5	TCTGGGTAGAGTTGCGAACGGGTGAGTA-CGCGTATGTAAACCTGCCCTGGGAGCGGGGGG	63			
Sbjct 15238	TCTGGAT-GAGTTGCGAACGGGTGAGTAACCGTAGGT-AACCTGCCCTGGTGAAGCGGGG-	15294			
Query 64	ATAACTATTGGGAAACGAT-GCTAATACCGCATAAGAGTAGATGTTGATGACACTTTGC	122			
Sbjct 15295	ATAACTATT-GGAACGATAGCTAATACCGCATAAGAGTAGATGTTGATGACA-TTTGC	15352			
Query 123	TTAAAA-GTGCACTTGCACTACTACAGATGGACCTGCGTTGATTAGCTAGTTGTGGGG	181			
Sbjct 15353	TTAAAAAGTGCACTTGCACTACTACAGATGGACCTGCGTTGATTAGCTAGTTGTGGGG	15412			
Query 182	GTAAC-GCTACCAAGGCGACGAT-CATAGCGACCTGAGAGGGTGATCGG-CACACTGG	238			
Sbjct 15413	GTAACGGCTCACCAGGCGACGATACATAGCGACCTGAGAGGGTGATCGGCGACACTGG	15472			
Query 239	GACTGAGACACGGCC-AGACT-CTACGGGAGGCGAGTGGGGAATCTTCG-CA-TGGAC	294			
Sbjct 15473	GACTGAGACACGGCCAGACTCTACGGGAGGCGAGTAGGGAATCTTCGGCAATGGAC	15532			
Query 295	GGA-GTCTGTCC--GCATCGCCGCTGGGTGA-GATG-TTTCGGGTCTAATG-TCTGT	347			
Sbjct 15533	GGAACTGTGACGAGCAACGCCGCTGAGTGAAGAAGTTTTCGATCGTAAAGCTCTGT	15592			
Query 348	TGGAGG-GAAGA 358				
Sbjct 15593	TGAAGAGAAGA 15604				

(d)

Figure S2. Alignment results of an NCBI BLAST search. (a) *E. coli* by microchip electrophoresis. (b) *E. coli* by capillary DNA sequencer. (c) *M. pneumoniae* by microchip electrophoresis. (d) *S. pneumoniae* by microchip electrophoresis.