

Additional file 2

Alignment of the 16S rRNA gene sequence from the type strain of *Bacteroides dorei* (DSM 17855) and

that obtained by Sanger sequencing from the patient's specimen. Total genomic DNA was purified from the

patient's infected aortic wall and subjected to PCR amplification using the 500F (5'-

GGATTAGATACCCTGGTA-3') and 1500R (5'-TACCTTGTTACGACTT-3') universal primers. Sanger

sequencing of the amplicon was performed, and the sequence obtained for the single-peak electropherogram

read was compared with that of the type strain of *B. dorei* (DSM 17855). The 500F and 1500R primers are

shown as red arrows, and the aligned sequence is provided below the *B. dorei* 16S rRNA gene sequence. The

full-length sequence from the V5 to V9 segments completely coincides with the corresponding sequence of *B.*

dorei.

1 ATTTTACAA TGAAGAGTTT GATCCTGGCT CAGGATGAAC GCTAGCTACA GGCTTAACAC 60
61 ATGCAAGTCG AGGGGCAGCA TGGTCTTAGC TTGCTAAGGC TGATGGCGAC CGGCGCACGG 120
121 GTGAGTAACA CGTATCCAAC CTGCCGTCTA CTCTTGGCCA GCCTTCTGAA AGGAAGATTA 180
181 ATCCAGGATG GGATCATGAG TTCACATGTC CGCATGATTA AAGGTATTTT CCGGTAGACG 240
241 ATGGGGATGC GTTCCATTAG ATAGTAGGCG GGGTAAACGGC CCACCTAGTC AACGATGGAT 300
301 AGGGGTCTG AGAGGAAGGT CCCCACATT GGAAGTGAAG CACGGTCCAA ACTCCTACGG 360
361 GAGGCAGCAG TGAGGAATAT TGGTCAATGG GCGATGGCCT GAACCAGCCA AGTAGCGTGA 420
421 AGGATGACTG CCCTATGGGT TGTAAGTCTC TTTTATAAAG GAATAAAGTC GGGTATGCAT 480
481 ACCCGTTTGC ATGTACTTTA TGAATAAGGA TCGGCTAACT CCGTGCCAGC AGCCGCGGTA 540
541 ATACGGAGGA TCCGAGCGTT ATCCGGATTT ATTGGGTTTA AAGGGAGCGT AGATGGATGT 600
601 TTAAGTCAGT TGTGAAAGTT TGC GGCTCAA CCGTAAAATT GCAGTTGATA CTGGATGTCT 660
661 TGAGTGCAGT TGAGGCAGGC GGAATTCGTG GTGTAGCGGT GAAATGCTTA GATATCACGA 720
721 AGAACTCCGA TTGCGAAGGC AGCCTGCTAA GCTGCAACTG ACATTGAGGC TCGAAAGTGT 780
781 GGGTATCAAA CA **800F primer**
GGATTAGA TACCCTGGTA GTCCACACGG TAAACGATGA ATACTCGCTG 840
CTGGTA GTCCACACGG TAAACGATGA ATACTCGCTG
841 TTTGCGATAT ACGGCAAGCG GCCAAGCGAA AGCGTTAAGT ATTCCACCTG GGGAGTACGC 900
TTTGCGATAT ACGGCAAGCG GCCAAGCGAA AGCGTTAAGT ATTCCACCTG GGGAGTACGC
901 CGGCAACGGT GAAACTCAAA GGAATTGACG GGGGCCCGCA CAAGCGGAGG AACATGTGGT 960
CGGCAACGGT GAAACTCAAA GGAATTGACG GGGGCCCGCA CAAGCGGAGG AACATGTGGT
961 TTAATTCGAT GATACGCGAG GAACCTTACC CGGGCTTAAA TTGCACTCGA ATGATCCGGA 1020
TTAATTCGAT GATACGCGAG GAACCTTACC CGGGCTTAAA TTGCACTCGA ATGATCCGGA
1021 AACGGTTCAG CTAGCAATAG CGAGTGTGAA GGTGCTGCAT GGTGTGTCGTC AGCTCGTGCC 1080
AACGGTTCAG CTAGCAATAG CGAGTGTGAA GGTGCTGCAT GGTGTGTCGTC AGCTCGTGCC
1081 GTGAGGTGTC GGCTTAAAGT CCATAACGAG CGCAACCCTT GTTGTGAGTT ACTAACAGGT 1140
GTGAGGTGTC GGCTTAAAGT CCATAACGAG CGCAACCCTT GTTGTGAGTT ACTAACAGGT
1141 GATGCTGAGG ACTCTGACAA GACTGCCATC GTAAGATGTG AGGAAGGTGG GGATGACGTC 1200
GATGCTGAGG ACTCTGACAA GACTGCCATC GTAAGATGTG AGGAAGGTGG GGATGACGTC
1201 AAATCAGCAC GGCCCTTACG TCCGGGGCTA CACACGTGTT ACAATGGGGG GTACAGAGGG 1260
AAATCAGCAC GGCCCTTACG TCCGGGGCTA CACACGTGTT ACAATGGGGG GTACAGAGGG
1261 CCGCTACCAC GCGAGTGGAT GCCAATCCCT AAAACCCCTC TCAGTTCGGA CTGGAGTCTG 1320
CCGCTACCAC GCGAGTGGAT GCCAATCCCT AAAACCCCTC TCAGTTCGGA CTGGAGTCTG
1321 CAACCCGACT CCACGAAGCT GGATTCGCTA GTAATCGCGC ATCAGCCACG GCGCGGTGAA 1380
CAACCCGACT CCACGAAGCT GGATTCGCTA GTAATCGCGC ATCAGCCACG GCGCGGTGAA
1381 TACGTTCCCG GGCCTTGATC ACACCGCCCG TCAAGCCATG GGAGCCGGGG GTACCTGAAG 1440
TACGTTCCCG GGCCTTGATC ACACCGCCCG TCAAGCCATG GGAGCCGGGG GTACCTGAAG
1441 TGCCTAACCG CGAGGATCGC CCTAGGGTAA AACTGGTGAC TGGGGCTAAG **1500R primer**
TGCCTAACCG CGAGGATCGC CCTAGGGTAA AACTGGTGAC TGGGGCTAAG TC 1500
1501 **GTA**GCCGTAC CGGAAGGTGC GGCTGGAACA CCTCCTTTCT 1540