

Supplemental File: PCR Sequences and BLAST Analyses from Individual Patient Cultures.

UNH, University of New Haven; AB, Australian Biologics; UCI, University of California Irvine.

SEQUENCES FROM UNIVERSITY OF NEW HAVEN

Sequences for Case #1 UNH

Whole callus

pyrG

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NNNNNNNNNNNNANNNNNNNNNNNNNNNNNNGGGAGTGGTAATATTTCTTTTATTCATTTAA  
CATATGTGCCAAGTCCAGCTGGAATTAATGAGCAAAAATCTAAACCTACTCAACAAAGTGT  
TAAAACCTTAAATAAAGCAGGTATTTTCCCCGATTTAATTATTGCTAGAAGTTCACAAGTAT  
TGACAGACCAAATCAGAAAAAAGTGGCAATGTTTTGCAATGTTGAGAGCACTTCTATTAT  
TGACAATGTTGATGTTTCTACTATTTATGAAATTCCTATATCTTTTTATAAGCAGGGTGTACA  
TGAGATTTTAAGCTCTAAGTTAAATATTAAGGTTGATCCAAAAATAGAAGAGCTTTCAAAG  
CTTGTAGGAGTTATAAAATCTAATTTTTTTGTGCCTAAAAAAATTATTAATATTGCTATTTGT  
GGTAAATATGCTGAACTTGATGATTCTTATGCATCAATTAGAGAGTCTTTGGTTCATGTTGC  
AGCCCATTTGGATTTGCTTATTAAGCACTTTAATTGATTCTAATGATTTAAATGAGAGCT  
GTTTAAAGAGTTTGACGGCATTATTGTTTCTGGCGGCTTTGGAGGCAAAGGATATGAAGG  
TAAAATTATGGCTATTAATATGCTCGTGAGAATAATATCCCTTTCTTGGAATTTGNCCTTG  
NNN
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Length 680 bp, BLAST 100% identity with Bbss, e value 0

Whole callus

Fla

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NNNNNNNNNNNNNNNNNNNNNANNACTNNNNNNNNNCGAAATTAATAGAATTGCTGATC  
AAGCTCAATATAACCAAATGCACATGTTATCAAACAAATCTGCTTCTCAAATGTAAGAAC  
AGCTGAAGAGCTTGGAATGCAGCCTGCAAAAATTAACACACCAGCATCACTTTCAGGGTCT  
CAAGCGTCTTGACTTTAAGAGTTCATGTTGGAGCAAACCAAGATGAAGCTATTGCTGTAA  
ATATTTATGCAGCTAATGTTGCAAATCTTTTCTCTGGTGAGGGAGCTCAAACCTGCTCAGGCT  
GCACCGTTCAAGAGGGTGTTCACAGGAAGGAGCTCAACAGCCAGCACCTGCTACAGCA  
CCTTCA
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Length 367 bp, BLAST 100% identity with Bbss, e value 2e-172

Blood culture

Fla

Forward

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NNNNNNNNNNNNANNNNNANCAACNNACAGACGAAATTAATAGAATTGCTGATCAAGC  
TCAATATAACCAAATGCACATGTTATCAAACAAATCTGCTTCTCAAATGTAAGAACAGCT  
GAAGAGCTTGGAATGCAGCCTGCAAAAATTAACACACCAGCATCACTTTCAGGGTCTCAA  
GCGTCTTGACTTTAAGAGTTCATGTTGGAGCAAACCAAGATGAAGCTATTGCTGTAAATA
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TTTATGCAGCTAATGTTGCAAATCTTTTCTCTGGTGAGGGAGCTCAAACCTGCTCAGGCTGCA
CCGGTTCAAGAGGGTGTTCACAGGAAGGAGCTCAACAGCCAGCACCTGCTACAGCACCT
TCA

Length 364 bp, BLAST 99% identity with Bbss, e value 2e-176

Reverse

NNNNNNNNNNNNNNNNNNNNNANNACTNNNNNNNNNCGAAATTAATAGAATTGCTGATC
AAGCTCAATATAACCAAATGCACATGTTATCAAACAAATCTGCTTCTCAAATGTAAGAAC
AGCTGAAGAGCTTGGAATGCAGCCTGCAAAAATTAACACACCAGCATCACTTTCAGGGTCT
CAAGCGTCTTGGACTTTAAGAGTTCATGTTGGAGCAAACCAAGATGAAGCTATTGCTGTAA
ATATTTATGCAGCTAATGTTGCAAATCTTTTCTCTGGTGAGGGAGCTCAAACCTGCTCAGGCT
GCACCGTTCAAGAGGGTGTTCACAGGAAGGAGCTCAACAGCCAGCACCTGCTACAGCA
CCTTCA

Length 367 bp, BLAST100% identity with Bbss, e value 2e-172

Sequences for Case #2 UNH

Vaginal culture

pyrG

Forward

ATAGCCATAATTTTACCTTCNTATCCTTTGCCTCCAAAGCCGCCAGGAACAATAATGCCGTC
AAACTCTTTTAAACAGCTCTCATTTAAATCATTAGAATCAATTAAGTGTCTTTAATAAGCA
AATCCAAATGGGCTGCAACATGAACCAAAGACTCTCTAATTGATGCATAAGAATCATCAA
GTTTCAGCATATTTACCACAAATAGCAATATTAATAATTTTTTTAGGCACAAAAAATTAGAT
TTTATAACTCCTACAAGCTTTGAAAGCTCTTCTATTTTTGGATCAACCTTAATATTTAACTTA
GAGCTTAAAATCTCATGTACACCCTGCTTATAAAAAGATATAGGAATTCATAAATAGTAG
AAACATCAACATTGTCAATAATAGAAGTGCTCTCAACATTGCAAAACATTGCCACTTTTTTT
CTGATTTGGTCTGTCAATACTTGTGAACTTCTAGCAATAATTAATTCGGGGAAAATACCTGC
TTTATTTAAGTTTTAACACTTTGTTGAGTAGGTTTAGATTTTTGCTCATTAAATCCAGCTGGA
CTTGGCACATATGTTAAATGAATAAAAGAAATATTACCACTCCCAATCTCCTGTCTTATTTG
TCTTACTGTCTCAATAAATAAAATATTTTTCCATAT 99% B31 sequence, it has one nucleotide
difference

Length 656 bp, BLAST 99% identity with Bbss, e value 0

Reverse

GATGGGAGTGGTAATATTTCTTTTATTCATTTAACATATGTGCCAAGTCCAGCTGGAATTA
ATGAGCAAAAATCTAAACCTACTCAACAAAGTGTTAAAACCTTAAATAAAGCAGGTATTTT
CCCCGATTTAATTATTGCTAGAAGTTCACAAGTATTGACAGACCAAATCNGAAAAAAGTG
GCAATGTTTTGCAATGTTGAGAGCACTTCTATTATTGACAATGTTGATGTTTCTACTATTTAT
GAAATTCCTATATCTTTTTATAAGCAGGGTGTACATGAGATTTTAAAGCTCTAAGTTAAATAT
TAAGGTTGATCCAAAAATAGAAGAGCTTTCAAAGCTTGTAGGAGTTATAAAATCTAATTTTT
TTGTGCCTAAAAAATTATTAATATTGCTATTTGTGGTAAATATGCTGAACTTGATGATTCTT
ATGCATCAATTAGAGAGTCTTTGGTTCATGTTGCAGCCCATTTGGATTTGCTTATTAAGC
ACTTAAATTGATTCTAATGATTTAAATGAGAGCTGTTTAAAAGAGTTTGACGGCATTATTGTT
CCTGGCGGCTTTGGAGGCAAAGGATATGAAGGTTAAATATGGCTATTAATATGCTCGTG
AGAATAATATTCCCTTTCTTGAATTTGTCTTGGTATAA

Length 659 bp, BLAST 99% identity with Bbss, e value 0

Sequences for Case #3 UNH

Blood culture

16S rRNA

Forward

NNNNNNNNNNNNNNNNNNNNNNNNNNNGNNTGTAGCATAATTTCAGTGGCGAACGGGTGAG
TAACGCGTGGATGATCTACCTATGAGATGGGGATAACTATTAGAAATAGTAGCTAATACCG
AATAAGGTCAGTTAATTTGTTAATTGATGAAAGGAAGCCTTTAAAGCTTCGCTTGTAGATGA
GTCTGCGTCTTATTAGCTAGTTGGTAGGGTAAATGCCTACCAAGGCAATGATAAGTAACCG
GCCTGAGAGGGTGAACGGTCACACTGGAAGTACGATAACGGTCCAGACTCCTACGGGAGGC
AGCAGCTAAGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCGACACTGCGTGAATGAA
GAAGGTCGAAAGATTGTAATAATTCTTTTATAAATGAGGAATAAGCTTTGTAGGA

Length 415 bp, BLAST 99% identity with Bbss, e value 0

Reverse

NNNNNNNNNNNNNNNNNNNNNNNNNTCTTCNNNCCNCNGNNGNGCGCTCCGTCAGGCTTTC
GCCATTGCGGAAGATTCTTAGCTGCTGCCCTCCCGTAGGAGTCTGGACCGTATCTCAGTTCC
AGTGTGACCGTTCACCCTCTCAGGCCGGTTACTTATCATTGCCTTGGTAGGCATTTACCCTAC
CAACTAGCTAATAAGACGCAGACTCATCTACAAGCGAAGCTTTAAAGGCTTCCTTTCATCA
ATTAACAAATTAAGTACCTTATTTCGGTATTAGCTACTATTTCTAATAGTTATCCCCATCTCA
TAGGTAGATCATCCACGCGTACTCACCCGTTCCGCACTGAATGTATTGCTACATCCCGTTT
GACTTGCATGCTTAAGACGCACACTGCCAGCGTTAGTTCTAAGCCAGGA

Length 415 bp, BLAST 100% identity with Bbss, e value 0

Seminal culture

16S rRNA

GTAGCATAATTTCAGTGGCGAACGGGTGAGTAACGCGTGGATGATCTACCTATGAGATGGG
GATAACTATTAGAAATAGTAGCTAATACCGAATAAGGTCAGTTAATTTGTTAATTGATGAA
AGGAAGCCTTTAAAGCTTCGCTTGTAGATGAGTCTGCGTCTTATTAGCTAGTTGGTAGGGTA
AATGCCTACCAAGGCAATGATAAGTAACCGGCCTGAGAGGGTGAACGGTCACACTGGAAC
TGAGATACGGTCCAGACTCCTACGGGAGGCAGCAGCTAAGAATCTTCCGCAATGGGCGAA
AGCCTGACGGAGCGACACTGCGTGAATGAAGAAGGTCGAAAGATTGTAATAATTCTTTTATA
AATGAGGAATAAGCTTTGTAGGA

Length 388 bp, BLAST 99% identity with Bbss, e value 0

Sequences for Case #7 UNH

Vaginal culture

16S rRNA

NNNNNGNNNNNNNGCNNNCTTCNGTGGCGACGGGTGAGTAACGCGTGGATGATCTACCTA
TGAGATGGGGATAACTATTAGAAATAGTAGCTAATACCGAATAAGGTCAGTTAATTTGTTA
ATTGATGAAAGGAAGCCTTTAAAGCTTCGCTTGTAGATGAGTCTGCGTCTTATTAGCTAGTT
GGTAGGGTAAATGCCTACCAAGGCAATGATAAGTAACCGGCCTGAGAGGGTGAACGGTCA
CACTGGAAGTACGATAACGGTCCAGACTCCTACGGGAGGCAGCAGCTAAGAATCTTCCGCA
ATGGGCGAAAGCCTGACGGAGCGACACTGCGTGAATGAAGAAGGTCGAAAGATTGTAATA
ATTCTTTTATAAATGAGGAATAGCCTTTTGTAGGA

Length 396 bp, BLAST 99% identity with Bbss, e value 0

Sequences for Case #8 UNH

Seminal culture

16S rRNA

AGCTTTGTAGGACCTGGCTTAGAACTAACGCTGGCAGTGCGTCTTAAGCATGAGGAATAAG
CTTTGTAGGACCTGGCTTAGAACTAACGCTGGCAGTGCGTCTTAAGCATGAGGAATAAGCT
TTGTAGGACCTGGCTTAGAACTAACGCTGGCAGTGCGTCTTAAGCATGAGGAATAAGCTTT
GTAGGACCTGGCTTAGAACTAACGCTGGCAGTGCGTCT

Length 221 bp, BLAST 100% identity with Bbss, e value 7e-10

Sequences for Case #12 UNH

Whole callus

uvrA

Forward

CNNNNNNNNNNNNNNNANNGNNTATCAGGTAGTCTATCTGGTGGCGAGGCTCAGCGTA
TTAGGCTTGCTACTCAAATAGGATCAGCACTTTCGGGTGTTATTTATGTTCTTGATGAGCCA
AGTATTGGTCTTCATCAAAGAGATAATGAAAAATTAATCTCTACTCTTGTTAATCTTAAAAA
TCTTGTAATACTGTAATTGTTGTTGAACATGATGAGCAAACCTTTCGCTACTGCGGACTATA
TTATTGATATGGGTCTGCTGCTGGAATTCTTGAGGGGAAATAGTTGCAAAGGGAGCCTT
GATTGATATTTTAAATAGCAAAAATAGTTTAACTGGTCAATATCTTAGCGGCAAGTTTAAAA
TAGATGTTCCAAGCTCTAGAAGAAAGGCAGATAAGGGAGAAATTTTGCTTTTGGGCTCTAA
TAAAAATAATCTTAAAAATATAGACTTAAGTATCCCTTTGGGAGTTTTTACCGTAATAACAG
GTGTTTCTGGTAGCGGAAAAAGTACTTTACTTAAACGAGGTGTTATATCCAGCTCTTGATAGT
AGATTAAAGCTTAATGAAAAGTATTGTGATGGCTTAAAGATATTGTTGGGTATGAAAAAA
TCGATAAAATTATTCAAATAAATCAAAAACCCCAATAGGA

Length 653 bp, BLAST 99% identity with Bbss, e value 0

Reverse

NNNNNNNANTNNNNNCNACNNNNNNATATCTTTAAAGCCATCACAATACTTTTCATTAAG
CTTTAATCTACTATCAAGAGCTGGATATAACACCTCGTTAAGTAAAGTACTTTTTCCGCTAC
CAGAAACACCTGTTATTACGGTAAAACTCCCAAAGGGATACTTAAGTCTATATTTTAAAG
ATTATTTTATTAGAGCCCAAAGCAAATTTCTCCCTTATCTGCCTTCTTCTAGAGCTTGG
AACATCTATTTTAAACTTGCCGCTAAGATATTGACCAGTTAAACTATTTTTGCTATTTAAAAT
ATCAATCAAGGCTCCCTTTGCAACTATTTCCCTCCAAGAATTCCAGCACCAGGACCCATAT
CAATAATATAGTCGCAGTACGCAAAGTTTGCTCATCATGTTCAACAACAATTACAGTATT
ACCAAGATTTTAAAGATTAACAAGAGTAGAGATTAATTTTTCATTATCTCTTTGATGAAGAC
CAATACTTGGCTCATCAAGAACATAAATAACACCCGAAAGTGCTGATCCTATTTGAGTAGC
AAGCCTAATACGCTGAGCCTCGCCACCAGATAGACTACCTGATATTCTATTTAAATATAAA
TAAGAAAGGCCAACATCAATTAANANTTTTNNNGCN

Length 651 bp, BLAST 99% identity with Bbss, e value 0

SEQUENCES FROM AUSTRALIAN BIOLOGICS

Sequences for Case #2 AB

Vaginal culture

rpoC

GGAGATGTTGTAAGCAGGAGATATGCTTTGTGATGGTAGAATTAATCCTCATGATGTGC
TTGAAATTTTAGGTGGGA

Length 79 bp, BLAST 100% identity with Bbss, e value 4e-032

Sequences for Case #3 AB

Blood culture

rpoC

TAAAGGGTACTCTCTAGCCTTTTACCTTTTTGATTAGACTCCACCTAAAATTTCAAGCAGG
GGATTCTACATCTACTAAGCCTTTTACCTTTTTGAATTGAA

Length 103bp, BLAST 96% identity with Bbss, e value 0.11

Seminal culture, 1 month on abx

rpoC

ATTTCTGCAGTGACATCCATGCTATCTCCTGCTTTTACAACATCTCCATCTCTAACCCAAAAG
ATGTTTTCCAGCTGGAATATAATGCTTATGTTCAACCCCATACTCATCTAAAATATTAATAA
GCCTTTTACCTTTTTGAATTGA

Length 146bp, BLAST 100% identity with Bbss, e value 9e-57

Seminal culture, 4 months on abx

rpoC

TTAAGAGGCAGCAGCACGTGTATGAGTGTGAATACATAAGTGTTATATTCCAGCTGGAAAA
CATCTTTTGGTTAGAGACGGAGATGTTGTAAAAGCAGGAGATATGCTTTGTGATGGTAGAA
TTAATCCTCATGATGTGCTTCAAATTTTAGGTGGGA

Length 158bp, BLAST 98% identity with Bbss, e value 3e-52

Sequences for Case #4 AB

Vaginal culture

rpoC

TGCTTTTACAACATCTCCGTCTCTAACCCAAAAGATGTTTTCCAGCTGGAATATAATGCTTAT
GTTCAACCCCATACTCATCTAAAATATTAATAAGCCTTTTACCTTTTTGAATTGAA

Length 118bp, BLAST 99% identity with Bbss, e value 1e-51

Sequences for Case #5 AB

Vaginal culture

rpoC

TCCAGCTGGAAAACATCTTTTGGTTAGAGATGGAGATGTTGTAAAAGCAGGAGATATGCTT
TGTGATGGTAGAATTAATCCTATGATGTGCTTCAAATTTTAGGTGGGA

Length 109 bp, BLAST 99% identity with Bbss, e value 6e-47

Sequences for Case #11 AB

Vaginal culture

rpoC

TATGGTAATGATCATGTGTATGAGGTAGGACGGTGGCGATGATTGTCCTTTTAGGTGGCAAG
GTGGGATGCTTGATGTTTTTGGTGGAAAAGCAGGAGATATGCTTTGTGATGGTAGAATTAAT
CCTCATGATGTGCTTGAAATTTAGGTGGGAA

Length 156 Bp, BLAST 100% identity with Bbss, e value 1e-25

SEQUENCES FROM UNIVERSITY OF CALIFORNIA, IRVINE

Sequences for Case #2 UCI

16S-23S Intergenic spacer

Vaginal culture

ATGCGTTTTGCTTCACATCACTGTTTCGCTTCGCTTTGTACAGGCCATTGTAGCACGTGTGTA
GCCCAGGACATAAGGGCCATGATGATTTGACGTCATCCTCACCTTCCTCCGACTTATCACCG
GCAGTCTTATCTGAGTCCCCACCATTACATGCTGGTAACAGATAACAAGGGTTGCGCTCGTT
GCGGGACTTAACCCAACACCTCACAGCACGAGCTGACGACAACCATGCAGCACCTGTATA
TAGACCCCAAACGGGGAATAATTATCTCTAACTATATCCTATATATGTCAAGCCCTGGTAA
GGTTCCTCGCGTATCATCGAATTAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAAT
TCCTTTGAGTTTCACTCTTGCGAGCATACTCCCCAGGCGGCACACTTAACACGTTAGCTTCG
GTACTAACTTTTAGTTAACACCAAGTGTGCATCGTTTACAGC

Length 474bp, BLAST 100% identity with Bbss, e value 0

Sequences for Case #10 UCI

16S-23S Intergenic spacer

Seminal culture

ATGCGTTTTGCTTCACATCACTGTTTCGCTTCGCTTTGTACAGGCCATTGTAGCACGTGTGTA
GCCCAGGACATAAGGGCCATGATGATTTGACGTCATCCTCACCTTCCTCCGACTTATCACCG
GCAGTCTTATCTGAGTCCCCACCATTACATGCTGGTAACAGATAACAAGGGTTGCGCTCGTT
GCGGGACTTAACCCAACACCTCACAGCACGAGCTGACGACAACCATGCAGCACCTGTATA
TAGACCCCAAACGGGGGATAATTATCTCTAACTATATCCTATATATGTCAAGCCCTGGTAA
GGTTCCTCGCGTATCATCGAATTAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAAT
TCCTTTGAGTTTCACTCTTGCGGGCATACTCCCCAGGCGGCACACTTAACACGTTAGCCTCG
GTACTAACTTTTAGTTAACACCAAGTGTGCATCGTTTACAGC

Length 474bp, BLAST 99% identity with Bbss, e value 0