

Supplementary data 1. Cloned bacterial sequences obtained at the ABC using primers designed to target *Y. pestis*

All sequences are presented *without* primers. Sample name interpretation is as follows:

For example – tg9_V2_pla_8

where

tg9=Authors' sample extraction name

V2=Original sample name

pla=PCR primer pair abbreviation (see below)

8=Authors' sequencing reaction reference

PCR primer pair abbreviations

pla=Primer set E: YPpla728H (YP12D)/YPpla876L (YP11R)

rpb=Primer set A: Yrprob1/Yrprob2

16s=Primer set D: Yp16s586H/Yp16s786L

>tg9_V8_pla_8: Best hit gi|16418274|gb|AC022463.5| *Homo sapiens* BAC clone RP11-562N

ACTTGGGAATTACTCCTNTAGAGGGCGCAAAAACCCAGAAAACCTTTTGCAAACCTACTAAAAACGTTTCAGAGTCC
AAAGTAAGAGCCATGGGGCACTNTCATCCTGATGANTGGGTTAGTGTACAAAGCAGTTACCTATGTGGGCAGGT
GTGATATGAAAAGGCTGCGGAAAGCAGCATATAACACTCAAAGAATTCCTAGGTGNGTTTTTCAGGTGATAGAGC
CAGCGTaGGGGGCATGCAGGTGTTTTCTA

>tg9_V8_pla_8: no significant match with BLASTN

ATCCGGTCTCAACTGCGGTATG

>tg9_V8_pla_8: Best hit gi|16418274|gb|AC022463.5| *Homo sapiens* BAC clone RP11-562N2 from 4

ACTTGGGAATTACTCCTCTAGAGGGCGCAAAAACCCAGAAAACCTTTTGCAAACCTACTAAAAACGTTTCAGAGTCC
AAAGTAAGAGCCATGGGGCACTCTCATCCTGATGACTGGGTTAGTGTACAAAGCAGTTACCTAGGTGGGCAGGT
GTGATATGAAAAGGCTGCGGAAAGCAGCATATAACACTCAGAGAATTCCTAGGTGAGTTTTTCAGGTGATAGAGC
CAGCGTAGGGGCATGCAGGTGTTTT

>tg9_V8_pla_8: Best hit gi|16418274|gb|AC022463.5| *Homo sapiens* BAC clone RP11-562N

ACTTGGGAATTACTCCTCTAGAGGGCGCAAAAACCCAGAAAACCTTTTGCAAACCTACTAAAAACGTTTCAGAGTCC
AAAGTAAGAGCCATGGGGCACTCTCATCCTGATGACTGGGTTAGTGTACAAAGCAGTTACCTATGTGGGCAGGT
GTGATATGAAAAGGCTGCGGAAAGCAGCATATAACACTCAAAGAATTCCTAGGTGAGTTTTTCAGGTGATAGAGC
CAGCGTAGGGGCATGCAGGTGTTTT

>tg13_V1_pla_8: no significant match with BLASTN

AGAGCCTTCAATCCTGCAGCTCAAGAGATACTGCTCCGGCGTGCTGCCGAGCTACATGGTGCCGGACCGGTTCA
GATTCTTGCCGTCCCTTCCCAAGACGTGACCCGACAAGACCGACTATCAGAAGCTGAAAGAGCTCGGATGATGG
ATCTGAGCCTTTCAACCGAGGACGCGGAGCTCCGCGAGAAGATCGTGCGGTTTGCACAGAAGGAGTTGTCGTCC
GGTGTGATCGCGCGGATCGGTCTCACGAATTCTCCCGCGACCTTTGGGACAAGTGCGGCCGCATGGGCCTGAC
CGGGCTTcCTGTCCCCGAGGC

>tg13_V1_pla_8: no significant match with BLASTN

TCCGGACGTCACGGAAGCGGCCGTTATCAGCCGCTCCGATTCCGACGGCAGGTGAGCGTGACGCATTTCTTG
CCTGGAGCGCGAAAGAAGAGCCTTCAATCCTGCAGCTCAAGAGATACTGCTCCGGCGTGCTGCCGAGCTACATG
GTGCCGGACCGGTTTCAGATTCTTGCCGTCCCTTCCCAAGACGTGACCCGACAAGACCGACTATCAGAAGCTGAA
AGAGCTCGGATGATGGATCTGAGCCTTTCAACCGAGGACGCGGAGCTCCGCGAGAAGATCGTGCGGTTTGCACA
GAAGGAGCTGTGTCGGTGTGATCGCGCGGATCGGTCTCACGAATTCTCCCGCGACCTTTGGGACAAGTGCG
GCCGCATGGGCCTGACCGGGCTTCCTGTCCCCGAGGC

>tg15_V6_pla_8: no significant match with BLASTN

CAACGCATTGTCTTTCATCCCCAACTGCTCCCACGAATGAACCCGACGGGAAAGACCCTGAGCCACTGGCTGG
TCACATCATTATCAACGTGCAAGCGCAGTGGCCTTCGACGGACGCACAAGCCTTTCGCGGATCGTTTCTTCAC
CATGCTGCAACGGA

>tg15_V6_pla_8: no significant match with BLASTN

CAACGCATTGTCTTTCATCCCCAACTGCTCCCACGAATGAACCCGACGGGAAAGACCCTGAGCCACTGGCTGG
TCACATCATTATCAACGTGCAAGCGCAGTGGCCTTCGACGGACGCACAAGCCTTTCGCGGATCGTTTCTTCAC
CATGCTGCAACGGA

>tg15_V6_pla_8: no significant match with BLASTN

CAACGCATTGTCTTTCATCCCCAACTGCTCCCACGAATGAACCCGACGGGAAAGACCCTGAGCCACTGGCTGG
TCACATCATTATCAACGTGCAAGCGCAGTGGCCTTCGACGGACGCACAAGCCTTTCGCGGATCGTTTCTTCAC
CATGCTGCAACGGA

>tg15_V6_pla_8: no significant match with BLASTN

CAACGCATTGTCTTTCATCCCCAACTGCTCCCACGAATGAACCCGACGGGAAAGACCCTGAGCCACTGGCTGG
TCACATCATTATCAACGTGCAAGCGCAGTGGCCTTCGACGGACGCACAAGCCTTTCGCGGATCGTTTCTTCAC
CATGCTGCAACGGA

>tg15_V6_pla_8: no significant match with BLASTN

CAACGCATTGTCTTTCcTCCCCAACTGCTCCCACGAATGAACCCGACGGGAAAGACCCTGAGCCACTGGCTGGT
CACATCATTATCAACGTGCAAGCGCAGTGGCCTTCGACGGACGCACAAGCCTTTCGCGGATCGTTTCTTCACC
ATGCTGCAACGGA

>tg15_V6_pla_8: no significant match with BLASTN

CAACGCATTGTCTTTCATCCCCAACTGCTCCCACGAATGAACCCGACGGGAAAGACCCTGAGCCACTGGCTGG
TCACATCATTATCAACGTCGAAGCGCAGTGGCCTTCGACGGACGCACAAGCCTTCCGCCGATCGTTTCTTCAC
CATGCTGCAACGGA

>tg19_V4_pla_8: no significant match with BLASTN

NAANGCATTGTCTTTCATCCCCAACTGCTCCCACGAATGAACCCNACGGGAAAGACCCTGAGCCACTGGCTGG
TCACATCATTATCAACGTCGAAGCGCAGTGGCCTTCGACGGACGCACAAGCCTTCCGCCGATCGTTTCTTCAC
CATGCTGCAACGGA

>tg19_V4_pla_8: no significant match with BLASTN

CAACGCATTGTCTTTCATCCCCAACTGCTCCCACGAATGAACCCGACGGGAAAGACCCTGAGCCACTGGCTGG
TCACATCATTATCAACGTCGAAGCGCAGTGGCCTTCGACGGACGCACAAGCCTTCCGCCGATCGTTTCTTCAC
CATGCTGCAACGGA

>tg19_V4_pla_8: no significant match with BLASTN

CAACGCATTGTCTTTCATCCCCAACTGCTCCCACGAATGAACCCGACGGGAAAGACCCTGAGCCACTGGCTGG
TCACATCATTATCAACGTCGAAGCGCAGTGGCCTTCGACGGACGCACAAGCCTTCCGCCGATCGTTTCTTCAC
CATGCTGCAACGGA

>tg19_V4_pla_8 no significant match with BLASTN

CAACGCATTGTCTTTCATCCCCAACTGCTCCCACGAACGAACCCGACGGGAAAGACCCTGAGCCACTGGCTGG
TCACATCATTATCAACGTCGAAGCGCAGTGGCCTTCGACGGACGCACAAGCCTTCCGCCGATCGTTTCTTCAC
CATGCTGCAACGGA

>tg20_V4_pla_8: BLASTN match gi|5524160|gb|AF125322.1|AF125322 *Escherichia coli* O7-specific lipopolysaccharide biosynthesis gene Score 5e-05

ACTTTTACCCGTTTATGATAAGCCGATGATTTATTATCCTTTGTCTACCCTAATGCTGGCTGGGCTAAATGATATT
CTCATCATCACGACTCCTCGCGAGTTACCGATGTTTAATTATTATTAGGAGATGGCTCTCATTGGGGGATCTCTC
TGCGTTACGCGGCACAACAAAATCCGAATGGTATTGCTGAGGCTTTTATTATTGGTGAAGAATTCATCGGTAATG
ATAGTGTCTGTCTCATCCTTGGAGATAAATTTTATATGGCGATAATTTATCCGTTAAATTACAACAGGCAGCGC
AATTAATAAATGGCGCCACTATTTTGGATATTATGTCTCCGATCCAGAACGCTATGGTGTAATTCTTTTTGATA
AAAAAGGTGATGCACTCGATGTAATCGAAAAACCTCCTACGCCGATTTCTCA

>tg20_V4_pla_8: Best BLASTN hit gi|3907597|gb|AF094575.1|AF094575 *Streptococcus pneumoniae* 2e-10. "glucose-1-phosphate thimidylyl transferase Cps19aL"

ACTTTTACCCGTTTATGATAAGCCGATGATTTATTATCCTTTGTCTACCCTAATGCTGGCTGGGCTAAATGATATT
CTCATCATCACGACTCCTCGCGAGTTACCGATGTTTAATTATTATTAGGAGATGGCTCTCATTGGGGGATCTCTC
TGCGTTACGCGGCACAACAAAATCCGAATGGTATTGCTGAGGCTTTTATTATTGGTGAAGAATTCATCGGTAATG
ATAGTGTCTGTCTCATCCTTGGAGATAAATTTTATATGGCGATAATTTATCCGTTAAATTACAACAAGCAGCGC
AATTAATAAATAGCGCCACTATTTTGGATATTATGTCTCCGATCCAGAACGCTATGGTGTAATTCTTTTTGATA
AAAAAGGTGATGCACTCAATGTAATCGAAAAACCTCCTACGCCGATTTCTCA

>tg22_V3_pla_8: Best BLASTN hit gi|23504816|emb|AJ509828.1|SSU509828 *Streptococcus suis* 5e-19 rmlA"glucose-1-phosphate thymidyltransferase"

```
ACTTTTACCCGTTTATGATAAACCAATGATTTATTATCCTTTGTCTACCCTAATGCTGGCTGGATTAATGATATT
CTCATCATCACGACTCCTCGCGAGTTACCGATGTTTAATTATTATTAGGAGATGGCTCTCATTGGGGGATCTCTC
TTTCGATATGCTGCCCAACAAAATCCGAATGGTATTGCCGAGGCTTTTATTATTGGCGAAGAATTTATCGGTAATG
AAAGTGTCTGCCTCATCCTTGGAGATAAATTTTTATATGGCGATAATTTATCCGTTAAATTACAACAAGCAGCGC
AATTAATAAATGGCGCCACTATTTTTGGATATTATGTCTCCGATCCAGAACGCTATGGTGTAATTCTTTTTGATA
AAAAAGGTGATGCACTGGATGTAATCGAAAAACCCCTACGCCGATTTCTCA
```

>tg38_BK_rpb_17: Best BLASTN hit gi|17429991|emb|AL646073.1| *Ralstonia solanacearum* GMI1000 chromosome, complete sequence; segment 17/19 Length=204050 Score=67.9 bits (34), Expect=1e-09 Identities=49/54 (90 %)

```
CACCACGGAGCCGCAGGAAGCGCTGCTGCTGGGCGGCCACACCGTCGTCATGCA
```

>tg38_BK_rpb_17: Best BLASTN Hit gi|17431588|emb|AL646083.1| *Ralstonia solanacearum* GMI1000 megaplasmid, complete sequence; segment 8/11 Length=2080 Score=83.8 bits (42), Expect=2e-14 Identities=48/50 (96 %)

```
GGCGCTGTGGACGGACGACCTGTTCAGCGCTGCACCCTGTTCCGCCCCGA
```

>tg38_BK_rpb_17: Best BLASTN Hit gi|17431588|emb|AL646083.1| *Ralstonia solanacearum* GMI1000 megaplasmid, complete sequence; segment 8/11 Length=2080 Score=83.8 bits (42), Expect=2e-14 Identities=48/50 (96 %)

```
GGCGCTGTGGACGGACGACCTGTTCAGCGCTGCACCCTGTTCCGCCCCGA
```

>tg75_DB_rpb_17 `; Best hit gi|4001755|gb|AF008578.1|AF008578 *Yersinia pestis* RNA polymerase beta-subunit (rpoB) gene, partial cds Length=512 Score=50.1 bits (25), Expect=7e-04 Identities=28/29 (96 %) Strand=Plus/Minus. This sequence match is in fact a primer dimer of the PCR primer Yprpob1 as indicated by arrows below.

```
CGTGGAGTGCAGAGAACAACGTCCTCGGCCGCTCGGGAACGAAGACGAGATCGCACAAGCAGTGTCTATCTC
TTCACCAACACGTACACGACGATAAGGTGTTA
```

```
Yprpob1      Yprpob1
      ----><-----
Cloned sequence: 77  caccaacacgtacacgacgataaggtggt 105
                   |||||  |||||
Y. pestis rpoB: 295  caccatcacgtacacgacgataaggtggt 267
```

>tg75_DB_rpb_17: >gi|17429991|emb|AL646073.1| *Ralstonia solanacearum* GMI1000 chromosome, complete sequence; segment 17/19 Score=75.7 bits (39), Expect=4e-12 Identities=49/54 (90 %)

```
CACCACGGAGCCGCAGGAAGCGCTGCTGCTGGGCGGCCACACCGTCGTCATGCA
```

>tg38_BK_16s_52: Best BLASTN Hit *Klebsiella oxytoca* 16S rRNA gene, Expect=4e-80. Numerous other *Enterobacter*, *Pantoea* and *Klebsiella* species show same match

```
TTGGAGGTTGTTCCCTTGAGGAGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCA
AGGTTAAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAAATTCGATGCAACGCGA
AGAACTTA
```

>tg62_CV_16s_52: Best BLASTN hit >gi|29372948|gb|AY226278.1| Uncultured gamma proteobacterium clone DBBB-107 16S rRNA gene. 131/152 identity. Expect=1e-61. Same match with *Pseudomonas alcaligenes*, *Pseudomonas* sp., *Achromatium*, *Halomonas*.

TAGCCGTTGGAGACCCTCGTGGTTTTTAGTGGCGAAGCTAACGCGATAAGTCGACCGCCTGGgAAGTACGGCCG
CAAGTTGAAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACgc
GAAGAACCTTA

>tg62_CV_16s_52: Best BLASTN hit gi|9856929|emb|AJ252639.1|ASO252639 Agricultural soil bacterium clone SC-I-50, 16S rRNA gene. Expect=7e-82 100 % Identity (no other 100 % matches)

TAGTTGTCGGAGGGTAACTCCTTCGGTAACGCAGCTAACCGTGAAGTCGACCGCCTGGGGAGTACGGTCGCAA
GATTAATAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGA
AAAACCTTA

>tg62_CV_16s_52: Best BLASTN hit *Pseudomonas alcaligenes* isolate LB19 16S rRNA gene Score=236 bits (119),
Expect=9e-60 Identities=130/134 (97 %)

TAgCCGGTGGAGAcCCTCGTGGTTTTTAGTGGCGAAGCTANCGCGATAAGTCGACCGCCTGGGAAGTACGGCCGC
AAGGTTGAAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCG
AAGAACCTTA

>tg62_CV_16s_52: Best BLASTN Hit gi|1403312|emb|X93493.1|HP16SRRN1 *H.pantelleriense* 16S rRNA gene Length=1477
Score=246 bits (128), Expect=6e-63 Identities=149/159 (93 %), Gaps=2/159 (1 %)

TAGCTGTTGGAGACCCTCGTGGTTTTTAGTGGCGAAGCTAACGCGATAAGTCGACCGCCTGGGAAGTACGGCCG
CAAGGTTGAAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGC
GAAGAACCTTA

>tg62_CV_16s_52; Best BLASTN hit gi|18644645|gb|AF371936.1| Uncultured bacterium clone p-5145-2Wb3 16S rRNA gene
Score=296 bits (154), Expect=5e-78 Identities=156/157 (99 %). Same match shared by *Y. pestis*, *Y. pseudotuberculosis* and *Y. enterocolitica* and numerous other *Enterobacteriaceae*

TTGGAGGGTGTGCCCTTGAGGCGTGGCTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCA
AGGTTAAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGA
AGAACCTTA

>tg66_BN_16s_52; Best BLASTN hit gi|20145609|emb|AJ441082.1|RBA441082 *Rheinheimera baltica* partial 16S rRNA gene,
strain OSBAC5 Score=291 bits (151), Expect=3e-76 Identities=155/157 (98 %)

TAGCTGTTTCGTGGTCTGTACTGTGAGTAGCGCAGCTAACGCACTAAGTAGACCGCCTGGGGAGTACGGTCGCA
AGATTAATAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAACATGTGGTTTAATTCGACGCAACGCG
AAGAACCTTA

>tg66_BN_16s_52: Best BLASTN hit gi|20145609|emb|AJ441082.1|RBA441082 *Rheinheimera baltica* partial 16S rRNA gene,
strain OSBAC5 Score=291 bits (151), Expect=3e-76 Identities=155/157 (98 %)

TAGCTGTTTCGTGGTCTTGTACTGTGAGTAGCGCAGCTAACGCACTAAGTAGACCGCCTGGGGAGTACGGTCGCA
AGATTA AAAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGA
AGAACCTTA

>tg73_DB_16s_52: Best BLASTN Hit gi|19171189|emb|AJ414655.1|MSP414655 *Methylobacter* sp. SV96 16S rRNA, strain
SV96 Score=304 bits (158), Expect=3e-80 Identities=158/158 (100 %)

TAGCCGTTGGTCCTATTTACAGGATTAGTGCGCAGCTAACGCATTAAGTCGACCGCCTGGGGAGTACGGCCGC
AAGGTTAAA ACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCG
AAGAACCTTA

>tg73_DB_16s_52: Best BLASTN Hit gi|19171189|emb|AJ414655.1|MSP414655 *Methylobacter* sp. SV96 16S rRNA, strain
SV96 Score=287 bits (149), Expect=4e-75 Identities=155/158 (98 %)

TAGCCGTTGGTCCTATTTACAGGATTAGTGCGCAGCTAACGCATTAAGTCGACCGCCCGGGGAGTACGGCCGC
AAGGTTAAA ACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATTCGATGCAATGCG
AAGAACCTTA

>tg75_XA_16s_52: Best BLASTN Hit gi|1403312|emb|X93493.1|HP16SRRN1 *H. pantelleriense* 16S rRNA gene Score=241
bits (125), Expect=3e-61 Identities=148/159 (93 %), Gaps=3/159 (1 %)

TAgCCGGTGGAGACCTCGTGGTTTTTAGTGCGAAGCTANCGCGATAAGTCGACCGCCTGGGAAGTACGGCCGC
AAGGTTGAA ACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCG
AAGAACCTTA

>tg75_XA_16s_52: Best bacterial BLASTN hit gi|14317935|gb|AF257292.1|AF257292 Uncultured marine gamma
proteobacterium DHB-2 16S rRNA gene, partial sequence Length=1577 Score=69.9 bits (36), Expect=2e-10 Identities=36/36
(100 %)

AGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTGGCTGTAAACGATGTCGA

>tg75_XA_16s_52: Best bacterial BLASTN hit: numerous proteobacterial 16S rRNA including *Y. pestis*, *Y. pseudotuberculosis*
and *Y. enterocolitica* show 100 % identity Score=302 bits (157), Expect=1e-79 Identities=157/157 (100 %)

TTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCA
AGGTTAAA ACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGA
AGAACCTTA

>tg10_V14_rpb_53: No significant BLASTN hits

CTTCGCCGTGGCCATCTACCGCCGCAAGATCTCCTGACAGTTTTTCTAGGCGGTGTCGGATCGGGTGAGGGCGG
TTCGTAGCAGGGG

>tg10_V14_rpb_53: Best BLASTN hit gi|1403312|emb|X93493.1|HP16SRRN1 *H. pantelleriense* 16S rRNA gene Score=241
bits (125), Expect=3e-61 Identities=148/159 (93 %), Gaps=3/159 (1 %)

GCgCGATGTCGTCTGGGTCGTCCCCGGTGTTCGTCTCGTACGTGCCGTTGCCGTCGAGGTCCC ACTCGTAGCGGA
TGATCGTCCCGTCGGGATCGGCCGACGCCGTGGCGTTGAAGGCCACCGACGAGCCGCTGGTCACCGGGTTCGGC
GTGGCGG

>tg10_V14_rpb_53: No significant BLASTN match

CGCCACCATCGATGTCGCCGCTGATCGATATGTCTACGATCCTGAACATCCGACGCCCGACGACAGGAGGCAG
CATCGTATCGTACGTGTACACGCCAGGCAGTGTGGATGTGAGCGCGATTACGCGACGATCCGATGTGTTGA

>tg10_V14_rpb_53: Best BLASTN hit >gi|26106080|dbj|AB088420.1| *Pseudomonas resinovorans* plasmid pCAR1, complete
sequence Length=199035 Score=40.1 bits (20), Expect=1.4 Identities=23/24 (95 %)

TCGTCTCCAGCAGGCGTACATCGCGCGTGGCTGCGACGGTTCGACGCNACGCTCaCCGGGCCCGCAGTTCGCCGTCC
TCACCGCGGTGGAGACCTATCCCGGCACCGACCAGGTACNCTGGCCATGTCGGTTCGACCTGGACCGCTCGACCA
TGGCCGATATCGTCCGCAGGCTGGAGGAACGCGGCCTGATCACGCGCTGTCCCGACGTACACGA

>tg10_V14_rpb_53: No significant BLASTN matches

CTTCGCCCCGTGGGCCATCTACCGCCGCAAGAATCTCCTGACAGTTTTTCTAGCGGTGTCGGATCGGGTGAGGGC
GGTTCGTA_gCAGGGG

>tg10_V14_rpb_53: No significant BLASTN matches

CGCGTGCCCGCCCTGAATGTCGACCATGG

>tg20_V4_rpb_53: No significant BLASTN matches

CACCGACAACGGCTGGCTACAGGATCCGAAAAGTTACCACAATGCGCCGAAATCGAAGCTCTCGCAGTACGAC
GCAGGGCATCGGACGCCGATCATGCTGAGCTGGCCTGGGAGGATCGAGCCGAAGAAGGTCGACGCGCCCATCT
CCAGCATCGACCTGGCGCCGACGCTCCTGCGTGTGCTCGGCATCGATCCGCCTGTGCAAAATGACTGGCGTTCGACT
TGCTCGATCCCGCCGACGTCGCCGCGGGAAGCGGGTTTTTCGGCGAAACGTTTTTCGCATGACGCCGTTCGACGTC
GATCGGCCTGCGGCCTGCCTGGAGTACCGCTGGTGCCTGCGTCGAGTGGCCGTGGCGATTGATCGTGCCGAACACGGA
CGTTGTTCCCCAGGGGAAACTCGAGCTGTTCAACTTGGCAGACGATCCCTGGGAGGAAAAGAATCTGGCGGAAG
TGCATCTGAAATGGTCGACCGCTTGGCTCGGCGCCTTGGATGGTTGGTGAATCCGGCGGCGGATCAGTAGCTG
CTAAATGCGCTCAAATCGCAACAGCTCATTAAATTAATTGATGCGGGCGAGTTGCGGTTGCCTTGCAGCCAAAG
GGTAACAAGGTAATGACGAGTAGTAGTCTATAGGGCCCCCATATTGGCCTTGGCTCGTACGGGAATTACCGTCA
TAAACAAGCCGGCGTACTGGCATTGCGATGACAGTGTGATCTCGTCAGGTGAGTGTAATGATTGTAGAACCCC
GAGGTATCGTTGCGGCCTTCTTTCTGTGGACGCTTGGATTCAATAGCTTGCATGCGGCGAATGCGGCCACCATT
GCTATTATGCGGAGGTCAAATCACGCCAAACAGCGCAGATCCATGAAAATTGGTAGTGAATGGTTTGATTTT
GAGCTATCTCTTCGCGTTGACAGCAATGCACTTGATCTGAATTCGAACG

>tg20_V4_rpb_53: No significant BLASTN matches

GAGGCGAGCGTCAGGATGATGAGCGAGAAGCGCATCGAGCCGAGGTAGA

>tg20_V4_rpb_53; Best BLASTN hit gi|28854265|gb|AE016870.1| *Pseudomonas syringae* pv. tomato str. DC3000 section 15 of
21 of the complete genome Score=196 bits (102), Expect=1e-47 Identities=155/180 (86 %), Gaps=6/180 (3 %)

TGAGGTTCGATGGTGTAGATGAAGCACAGTTCGGAGGACTTTTTGCGCGCGTTCGTAGCTGCGCTTGAACAAGGTG
AAATCGAGCAGGTCATCGCTGGCGATGCCAGGCGCTGCACGATGGCAACGCGCAGGTCTTCTTCGGGATGGTC
GATTGGCAGCTTGAATTCAGTATTGTAACATGGCGAGGATCCGGGTTTCGCGGGGCGCACAACTGCGCCAGGG
CGT

>tg20_V4_rpb_53: No significant BLASTN matches

TGAAGCTGATTCCAACAAACGATGATTCGTGCGTCTGACTTTTCAGCTGGTCATCCCAAATTGGCAAAGATCGCGCC
AAAGCCCATCTCGGACAGCATCATTGCAATACGAGAATTCAGCCGGATGCTTTTTTTGAGCAGATTCGGCATCGC
AATTCAGTCTTCAAGCGTGACCGAATCATATCGCAAGACATAGGGATCGACCACGG

>tg21_V5_rpb_53: Best hit gi|18092639|gb|AF458081.1| *Citrobacter freundii* isolate CF-12 class I integron IntI1 (intI1)gene,
partial cds; and streptomycin 3'adenyltransferase (ant(3')-1b) gene Score=69.9 bits (36), Expect=9e-10 Identities=36/36 (100
%)

ATTGACCTGGAATCCGACCCGACGGGTTGCTGAGCCGGCGAGCTCCGGCAGGACCNNTACCAGGAGTCCCAAG
GGTCGGACTGCTGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTAACACCTTATCGTAGTGTACG

>tg21_V5_rpb_53: Best hit gi|24431433|gb|AF544953.1| Uncultured alpha proteobacterium clone 5-7-8 16S rRNA gene
Score=52.6 bits (27), Expect=3e-05 Identities=30/31 (96 %), Gaps=1/31 (3 %)

TAACGCCGCCATGTGCTGGAATTCGCCCTTAACACCTTATCGTCGTGTACG

>tg21_V5_rpb_53: No significant hits

ACAGCATCGTGCAGGACCACCCGACTGCGCGGACGGCGAGCCGTTTCGCGGTGG

>tg21_V5_rpb_53: No significant hits

TCCCCGGGTCCCGAGACCTGGAGCGACAAACCGGCTGTCCGCAGACATCCAGAGCGTCTTCGTTCATGCCGGAGC
AGCGAGGCCGGGAATCGGCTCAGCACTGG

>tg21_V5_rpb_53: No significant hits

GCTGACGTGTCGGCGCTGGTTCTTCTCAAGTAACCTAAATGGCGGAAGCGGGTGGGAATCGAACCCA
CCGCTGCGGGGGTTANCCCGCAGCCGGACGGCTT

>tg21_V5_rpb_53: no significant hits

GCTGCTGATCTTCGGCGTGTTCGGCTATGTGCTGG

>tg21_V5_rpb_53: Best BLASTN hit gi|17431113|emb|AL646080.1| *Ralstonia solanacearum* GMI1000 megaplasmid

Score=50.7 bits (26), Expect=0.003 Identities=45/54 (83 %), Gaps=2/54 (3 %)

TGGCGATGCTGTCTTCGATCTTGCGCGTCCCTCCGTTTCCAACCTGAACGGCGGTCATGCCACTCAGCTGCGCTGT
AACGGTGACTACCGGCAGCTCGATATCGGGCATGTCTTGGATCGGCAGCCGATAGAACCCGTACGCCCCCGCGA
GGACCGCGAGCACAAAGATAACGACAACCTGGAATCGGTCGGCGGATCGACCAGGTTGCAAGATTCATGGCGAC
GCCTGGAACGCCACGCTGGCCTCGCCGGCGAGACGCGCACGAGATCGCCGTCGTGCAGAAAGCCGCCGCCGCT
GACGACGATGGCCTGCTCGACCGACAAGCCACTCAGCACTTCGACATCGGGCGCCATTGCGTCGGNCGCTCTTCA
CGGAAGTCTGCACTACCTTGTTCGGCACCGATAGCGAAGACATACTGACGCCGTCACGCATCACGACGCTG
CTCATGGGTACGGTGAGCGCCTGCNAAGCACCGCTGACGATCGTACCGTTGAGATACATGCCGATACGGGCGAG
TGCTGCGCGTCTNTGCGCAACTTCACGTACACGAACGATA+run out of seq

>tg25_V11_rpb_53: Best BLASTN hit gi|14022051|dbj|AP002997.2| *Mesorhizobium loti* DNA, complete genome, section 4

Score=79.5 bits (41), Expect=1e-12 Identities=74/90 (82 %), Gaps=6/90 (6 %)

GCCGGTAAAGCTCACNCANGCATTCCGCAATTTTCGATTTCTCTCGCCTTGGGAAGGCATGACGCTGCCGGGCG
ATGAAAAAGCGGGCGATCCGAAgCCATGAGCGCGGGTCAAATCCGTGACGCGACGCTGTGCTCCTCGTCAAGG
ACGTGG

>tg25_V11_rpb_53: Best BLASTN Hit gi|13423427|gb|AE005870.1| *Caulobacter crescentus* CB15 section 196 of 359 of the complete genome Score=54.5 bits (28), Expect=6e-05 Identities=32/34 (94 %)

CCTCATCCAGTTTGAACGGCTTGATGATGGCTTCAATGAGTTTCATCGTGATGTCTCCTATGAATAGGCCCGCTC
ATTATGTTGGGTCAGATCCAACCCCGTGGCTTCTTCGTCTTGTGACACGCGCAAGCCGATCGAACCGTCTACAAG
TTTGAGGATCACATAGGTCCCGACGAATGAGAACACGATCGTGAAAAAGACCGCGACAGCT

>tg25_V11_rpb_53: Best BLASTN Hit gi|34101612|gb|AE016911.1| *Chromobacterium violaceum* ATCC 12472 Score=44.9 bits (23), Expect=0.030 Identities=28/30 (93 %), Gaps=1/30 (3 %)

GCTGCCGCGCCTTGCTCGCCGAACCGCCGTCGGCGCCGTCGGCCTGAGCCTGGCCGCTGCGGCAAGGGCAAG
AAGACCGACTCCAAGACCGTCACTGTCTCATCCACGACTCCTTCTACGTCTCGGACGACCTCA

>tg25_V11_rpb_53: No significant hits

CGCTCGGCGACATCCCCGTGGGCCTTGCGTCAACCGCTGGTTCTCCCTGTCGTTTGACAAGCCGGAATT

>tg25_V11_rpb_53: Best BLASTN hit gi|33575721|emb|BX640444.1| *Bordetella bronchiseptica* strain RB50, complete genome; segment 8/16 Score=96.8 bits (50), Expect=1e-17 Identities=130/167 (77 %), Gaps=12/167 (7 %)

CGAGGACCGCGTCGTCGATCTTAAGCGTCCGGCCACGTCGTGAACGCCGCGCCTCGCCTCGGGTGAGACGT
TGCGTGGCAGACATTCGTCAACGCCGCGGGAGCGTGGTCCGCGCAGCTTTGCGCGATGGCCGGGATGCCGCTG
CCCGTCGTCCCGCTACGCAGGTTTCGAGCATTACTTCACCGCAGGCAACCCGATCGAGCGCCTGCCTTATGTCAAG
GATCTCGACCGGCTCGCGTCCGCTC

>tg25_V11_rpb_53: No significant hit

CATGCTCCAACCCTGTTGCGACATAAGGCGCTGCCCGGCTCCTGGAGTGCTGATAGGCGAGACACCACTTGCA
GTATAGGCATAGCGAGCATAGCTATGAGCGGCTGCCCGACGGGTGTGTGCCCATTGCTTCCATTGCTCTGATGC
TGCATGATGCGCCCCTGGAGTTCTGCTGGTTGGAATAGATCGGCATTGACGCTCTCAACGCGTGCAGTCAACGA
CTGATCGGTGAGGAAGAGGACCGGGATCTGGTAGCGCTCCGCCATAT

>tg25_V11_rpb_53: No significant hits

GGTCAACAACAACGGCTCTCTCAACCAGGAGATCCCGCTGG

>tg25_V11_rpb_53: Best BLASTN Hit gi|17131110|dbj|AP003588.1| *Nostoc* sp. PCC 7120 DNA, complete genome, section 8/19 Length=334520 Score=41.1 bits (21), Expect=0.004 Identities=21/21 (100 %)

CGAGCTGCCGAAGGTCAACACCGCGG

>tg26_2654_Yprp1/2_53: No significant hits

GGTCAACAACAACGGCTCTCTCAACCAGGAGATCCCGCTGG

>tg26_2654_Yprp1/2_53: No significant hits

GGAGTATACGGGCACCGCCCTTACCGCCATCC

>tg26_2654_Yprp1/2_53: No significant hits

GCTGCTGATCTTCGGCGTGCTCGGCTATGCGCTGG

>tg26_2654_Yprp1/2_53. Best BLASTN Hit: gi|16648601|gb|AY055309.1| *Homo sapiens* isolate siria34 mitochondrial D-loop, partial sequence. Length=360 Score=187 bits (97), Expect=3e-45 Identities=99/100 (99 %)

TACCAACAAATCTACCTACCCTAACAGTACATAGTACATAAAGCCATTTACCGTATATAGCACATTACAGTCAA
ATCCCTTCTCGTCCCCATGGATGAC

>tg27_2654_Yprp1/2_53. Best BLASTN Hit >gi|34529081|dbj|AK123515.1| *Homo sapiens* cDNA FLJ41521 fis, clone BRTHA2012980, moderately similar to INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1) Length=1797 Score=41.1 bits (21), Expect=0.059 Identities=26/28 (92 %), Gaps=2/28 (7 %)

GGTCAACAACAACGGCTCTCTCAACCAGGAGATCCCGCTGG

>tg27_2654_Yprp1/2_53. No significant hits

GGAGTATACGGGCACCGCCCTTACCGCCATCC

>tg27_2654_Yprp1/2_53. No significant hits

GCTGCTGATCTTCGGCGTGCTCGGCTATGCGCTGG

>tg27_2654_Yprp1/2_53. est BLASTN hit >gi|16648601|gb|AY055309.1| *Homo sapiens* isolate siria34 mitochondrial D-loop, partial sequence Length=360 Score=187 bits (97), Expect=3e-45 Identities=99/100 (99 %)

GTCATCCATGGGGACGAGAAGGGATTTGACTGTAATGTGCTATATACGGTAAATGGCTTTATGTACTATGTACTG
TTAAGGGTAGGTAGATTTGTTGGTA

Supplementary data 2. Specific PCR conditions used in study

SBH PCR

Pla A, Primer set H: 94 °C 5 min, 35 cycles of (94 °C 1 min, 59 °C 1 min, 72 °C 1 min), 72 °C 1 min.

Pla B, Primer set I: 95 °C 1.5 min, 40 cycles of (95 °C 20 s, 53 °C 20 s, 72 °C 30 s).

Pla C, Primer set J: 94 °C 5 min, 40 cycles of (94 °C 30 s, 52 °C 30 s, 72 °C 90 s), 72 °C 1 min.

Beta globin PCO3/4, Primer set K: 94 °C 5 min, 35 cycles of (94 °C 1 min, 56 °C 1 min, 72 °C 1 min), 72 °C 5 min.

BlaTEM, Primer set L: 95 °C 3 min, 35 cycles of (95 °C 1 min, 55 °C 1 min, 72 °C 1 min) 72 °C 4 min.

ABC PCR

All primer sets used at the ABC incorporated specific annealing temperatures indicated in Table 2 into the following conditions: These conditions were used at SBH for PCRs performed both at ABC and SBH.

94 °C 1.5 min, 40 cycles of (94 °C 45 s, annealing 45 s, 68 °C 1.5 min) 68 °C 10 min.