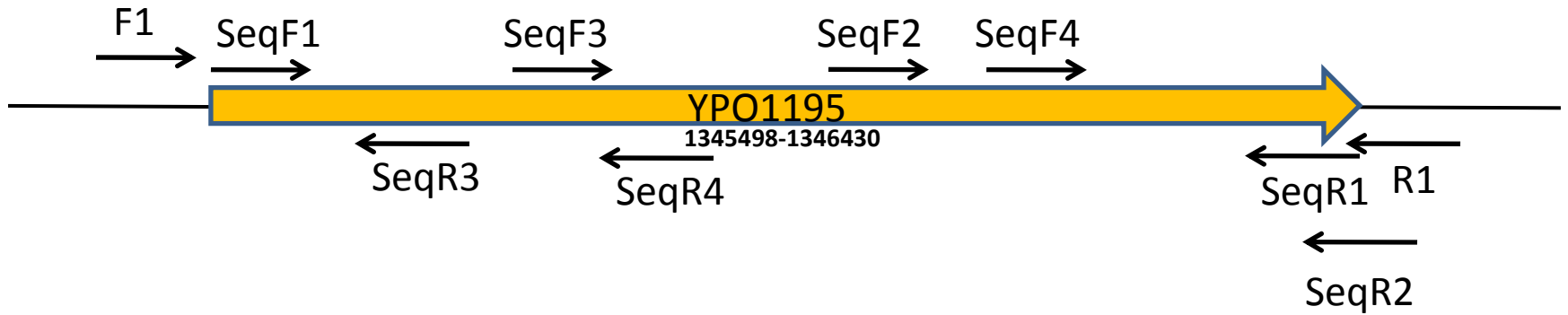
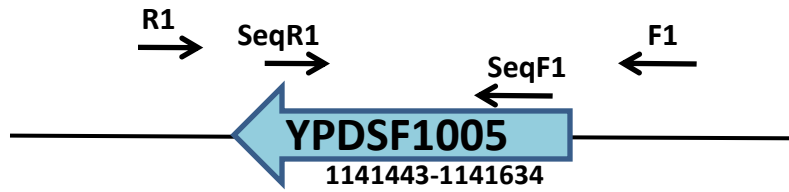


Sequence Validation:

50 ng of CO92 genomic DNA was used as template for amplification of target PCR products. Phusion High Fidelity DNA Polymerase (New England BioLabs, Inc.) with the Phusion HF Reaction Buffer using gene specific primers in Table 1 at a final concentration of 500 nM were used for targeted amplification. The sample was amplified for 30 cycles of 98C for 30 seconds, 55C for 30 seconds and 72C for 60 seconds. The amplified products were purified over a QIAQuick column per manufacturer's recommendation (Qiagen). Purified products were sequenced on the Applied BioSystems 3730/XL instrument using manufacturer's standard operating procedures. Amplified and purified PCR products for YPDSF1005 and YPO1195 were sequenced on an Applied BioSystems 3730/XL per manufacturer's recommendation. Gene YPDSF1005 was sequenced in 4 independent lanes using primers YPDSF1005F1, YPDSF1005R1, YPDSF1005RSEQ2 and YPDSF1005FSEQ2. Gene YPO1195 was amplified using primers YPO1195F1 and YPO1195R1. The amplified material was sequenced by all primers in Table 1 to increase sequence resolution and coverage over the amplicon.

TABLE 1. PCR AND SEQUENCING PRIMERS			
PRIMER NAME	SEQUENCE (5'-3')	GENE TARGET	COORDINATES (5'-3')
YPDSF1005F1	AGCAGATAAGGGCTACATAGG	YPDSF1005	1142260
YPDSF1005R1	CGATTGACCGAACTTGGCTAT	YPDSF1005	1141287
YPDSF1005FSEQ2	GCTATCAGAAACAACGATT	YPDSF1005	1141671
YPDSF1005RSEQ2	TTCCTTGAGCATATCGTTCC	YPDSF1005	1141834
 			
YPO1195F1	TAGCCCGTAGAACCACCAACG	YPO1195	1345419
YPO1195R1	CCATGAAACGAATAGCACCA	YPO1195	1346505
YPO1195FSEQ1	ATGGCACTGTTCTAACTC	YPO1195	1345498
YPO1195RSEQ1	TTAGTTTTTAATAAATCCGTTATC	YPO1195	1346430
YPO1195FSEQ2	GCTCCAATCATCCGTGAAGT	YPO1195	1346245
YPO1195RSEQ2	AAGCTTATAGTGCCACACTGGTC	YPO1195	1346475
YPO1195FSEQ3	ATTGGTATGGCTCTCTCC	YPO1195	1345860
YPO1195RSEQ3	CAATCTCACCGGCAGTAATCG	YPO1195	1345738
YPO1195FSEQ4	TGAAAGCTCACCCGAACATC	YPO1195	1346270
YPO1195RSEQ4	CATTGATCCACTAACCTAAATC	YPO1195	1345975

Primer Maps



YPDSF_1005

Query: Sanger sequence of sample

Subject: Y. pestis Pestoides F genome sequence

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Query 1      ATGAACAAATATATAGCGAACGAGAAAATGCCATTACTTATCCCCGCGGCTGGCTTTGAT 60
          |||
Sbjct 1142086 ATGAACAAATATATAGCGAACGAGAAAATGCCATTACTTATCCCCGCGGCTGGCTTTGAT 1142027

Query 61     GCCAAACTAAGCATGACAGAGAAAAACATAGAGCATACTGAAGCCTTTATGGCATCAGGC 120
          |||
Sbjct 1142026 GCCAAACTAAGCATGACAGAGAAAAACATAGAGCATACTGAAGCCTTTATGGCATCAGGC 1141967

Query 121    GTGAAAGAATTCTCTTTGCCTGGATTTGTAACCTCCTCACGGGTATCGTCTACTGTTTCT 180
          |||
Sbjct 1141966 GTGAAAGAATTCTCTTTGCCTGGATTTGTAACCTCCTCACGGGTATCGTCTACTGTTTCT 1141907

Query 181    GTAAACGGGGAGCATTACCGCCTTGTTACAGACGCAGCTATAACGGAAACAGTATATGCG 240
          |||
Sbjct 1141906 GTAAACGGGGAGCATTACCGCCTTGTTACAGACGCAGCTATAACGGAAACAGTATATGCG 1141847

Query 241    GTGAAACTGGCTTTCCTTGAGCATATCGTTCCTACACGTAAAACATGTACTCAGATTTTA 300
          |||
Sbjct 1141846 GTGAAACTGGCTTTCCTTGAGCATATCGTTCCTACACGTAAAACATGTACTCAGATTTTA 1141787

Query 301    GTCTGGCGTACTGTTCAACCACAGCATGATAGTGCAGTCCATGGTTTGCCTCAGGAGTTT 360
          |||
Sbjct 1141786 GTCTGGCGTACTGTTCAACCACAGCATGATAGTGCAGTCCATGGTTTGCCTCAGGAGTTT 1141727

Query 361    TTTCCGCACTTCTGACTCAGTACTCACTCAGTACTCAATCGTTGTTTCTGATAGCGAAC 420
          |||
Sbjct 1141726 TTTCCGCACTTCTGACTCAGTACTCACTCAGTACTCAATCGTTGTTTCTGATAGCGAAC 1141667

Query 421    AGACTAATGAAGGTCGTCGTTTCTGGGAGCGAATGATTGCATGGGCTATTCAGGCTGAAG 480
          |||
Sbjct 1141666 AGACTAATGAAGGTCGTCGTTTCTGGGAGCGAATGATTGCATGGGCTATTCAGGCTGAAG 1141607

Query 481    GGCATTATGTATATGTGTGCGAATGGCTCAGAGGAAGATCGCCCACTGACTTTTATGACTA 540
          |||
Sbjct 1141606 GGCATTATGTATATGTGTGCGAATGGCTCAGAGGAAGATCGCCCACTGACTTTTATGACTA 1141547

Query 541    ACTGGGATGATTTTTATGGGACATGGGCTGATTTTTGTTGGGGTGATGACAGAGATTGCC 600
          |||
Sbjct 1141546 ACTGGGATGATTTTTATGGGACATGGGCTGATTTTTGTTGGGGTGATGACAGAGATTGCC 1141487

Query 601    ATTGCCATAGACTATTCGTGATCAGTACAGAACAATTGCACTAA 644
          |||
Sbjct 1141486 ATTGCCATAGACTATTCGTGATCAGTACAGAACAATTGCACTAA 1141443
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YPO1195

Query: Sanger sequence of sample

Subject: Y. pestis CO92 genome sequence

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Query 1          GTGGCTGCTATCATGCTGTCTGCATCGAGTGGTATATCGCACGGCAGATAACGTCCGT 60
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|
Sbjct 1345534    GTGGCTGCTATCATGCTGTCTGCATCGAGTGGTATATCGCACGGCAGATAACGTCCGT 1345593

Query 61         GTAGGCTCTAAAATTGATACCGAAGGCTCCTTGCTGGGCAATATTATTGTGCAGGTTTTG 120
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|
|
Sbjct 1345594    GTAGGCTCTAAAATTGATACCGAAGGCTCCTTGCTGGGCAATATTATTGTGCAGGTTTTG 1345653

Query 121        GAGGCTAACGGGATTAAAACCACCAATAAATCCCACTGGGAGCAACCAAAGTCGTACGT 180
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|
|
Sbjct 1345654    GAGGCTAACGGGATTAAAACCACCAATAAATCCCACTGGGAGCAACCAAAGTCGTACGT 1345713

Query 181        GGGGCGATTACTGCCGGTGAGATTGATATTTATCCTGAATATACGGGGAATGGGGCTTTC 240
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Sbjct 1345714    GGGGCGATTACTGCCGGTGAGATTGATATTTATCCTGAATATACGGGGAATGGGGCTTTC 1345773

Query 241        TTCTTTTCTGATGAACAAGATCCTGCCTGGAAGAGCGCCAAAGCGGGCTATGAGAAAAGTA 300
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|
|
Sbjct 1345774    TTCTTTTCTGATGAACAAGATCCTGCCTGGAAGAGCGCCAAAGCGGGCTATGAGAAAAGTA 1345833

Query 301        AAAGCACTGGATTACGaaaaaaaaTAAATTGGTATGGCTCTCTCCCGCGCCAGCGAACAAT 360
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|
|
Sbjct 1345834    AAAGCACTGGATTACGAAAAAAAAATAAATTGGTATGGCTCTCTCCCGCGCCAGCGAACAAT 1345893

Query 361        ACCTGGACCATTGCTGTACGAAAAGACTTAGCCACGGCCAATAATTTGCGAACGCTGGAT 420
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|
|
Sbjct 1345894    ACCTGGACCATTGCTGTACGAAAAGACTTAGCCACGGCCAATAATTTGCGAACGCTGGAT 1345953

Query 421        GATTTAGGTTAGTGGATCAATGGCGGAGGTGAGTTTAAATTAGCCGCCTCAGCCGAGTTT 480
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|
|
Sbjct 1345954    GATTTAGGTTAGTGGATCAATGGCGGAGGTGAGTTTAAATTAGCCGCCTCAGCCGAGTTT 1346013

Query 481        ATCGAGCGGCCTGATGCGTTACCCGCTTTCCAACAGGCGTATGGTTTTACGCTGAATCAA 540
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|
|
Sbjct 1346014    ATCGAGCGGCCTGATGCGTTACCCGCTTTCCAACAGGCGTATGGTTTTACGCTGAATCAA 1346073

Query 541        GATCAACTACTGTCCCTGGCTGGGGGAGATACCGCTGTGACGATTAAGCGGCAGCAGA- 599
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|
|
Sbjct 1346074    GATCAACTACTGTCCCTGGCTGGGGGAGATACCGCTGTGACGATTAAGCGGCAGCAGAA 1346133

Query 600        CAGATCTCAGGAGTGAATGCCGCCATGGCTTATGGTACCGATGGTCCTGTAGCGGCAC TG 659
|
|
|
Sbjct 1346134    CAGATCTCAGGAGTGAATGCCGCCATGGCTTATGGTACCGATGGTCCTGTAGCGGCAC TG 1346193

Query 660        GGTTTACAGACTCTGGAAGATACTAAAGGCGTGCAGCCGATTTATGCGCCAGCTCCAATC 719
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|
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Sbjct 1346194    GGTTTACAGACTCTGGAAGATACTAAAGGCGTGCAGCCGATTTATGCGCCAGCTCCAATC 1346253

Query 720        ATCCGTGAAGTTACTCTGAAAGCTCACCCGAACATCCCGGCTTTGCTTAATCCGGTATTC 779
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Sbjct 1346254    ATCCGTGAAGTTACTCTGAAAGCTCACCCGAACATCCCGGCTTTGCTTAATCCGGTATTC 1346313

Query 780        GCCACACTGGATGGCCCAACGTTACAAAAGCTGAATGCACGTATTGCGGTGGA 832
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Sbjct 1346314    GCCACACTGGATGGCCCAACGTTACAAAAGCTGAATGCACGTATTGCGGTGGA 1346366
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