

Table S5: gene annotation of the contigs that showed a high similarity to sequences from representatives of the genus *Francisella*.

Contigs	Blastx	Max score	Score	Query Cover	e-value	Identity	Blastn	Score	Query Cover	e-value	Identity
<p>>contig50994 length=360 numreads=13 CCAAGTGGTAACGAGCTTtAGGAAGAGTGTGTGACGCTCTGGTAACCAATTG ATGGT AAAGGTGAAGTTGCAACAGATCTTACATCTCTATTGAAAAATGACACTGGTG TGATT TGGAGAAAAATCAGTTGATCAAGCTTTACAAACAGGTATTAAGTCAATCGATTCA ATGGTT CCAATTGGCTGGACAGCGTGaaCTTATtATTGGTGATAGACAGATGgTAAAC AGCA ATCGCTGTAGACACAATCATTAAACAAAAAGATTCTGGTGAATGTTTTATG TTGCT ATAGGTCAAAAGCTTCAACAATTGCAACATTGTAAAGACAGTTAGAAGAGCAT GATGCT >contig45579 length=399 numreads=28 CTGTAGTTACAGGCCATAAAGAACCTGTACGCCCAATTGATAAGTGCATCAG CACTTG CTGTTATAAAACCTTTATTCTCGTTACTATCCCACTCTAAAGCTCTTTTTCCA AGC ATATATTAgCCTAAAAACAGCACCACCAAAAAATAATATCCTCGAAAAACGCA TGATT AGATATAGCTGGCACTGTGACCAAGCTCTAAGGTTTATGCCCGAGGGAATAAT AAATGC CAGCTCCAAGTCAAAATatcAAAAATAACTGCTATTAATAAATCGTACATCA AGCTT CTCTCTTGATCACCAAAATGcAGGgAaGCCACACTCAAAAGTCTCTCTTTTGTCT TACT GGGATTGTTAGCCCACTATTACAGATAAACTTTACC >contig109648 length=200 numreads=30 CTGTCTCGAATTTCTCTGAGTTAGAACTCAAATAGTCAAGGGTGGTATTTCA AGGTC GACTCCAACAATCTAGCGACTGCTTCTCATAGTCTCCCACTATCTACACATAA ATAT TCAAAGTCCAGTCAAAGCTGTAGTAAAGTTACGGGgTCTTTCCGTCTAACCG CGGGT ACACAGCATCTTCACTGCGA >contig118995 length=188 numreads=8 GTCAATCATTACCATAAGATACCTGTTATAGCTGTAGACATGCGATAT AAAT TTTAGGCTGCTAGTTGTTAGTCAATTTATCTCTTTGTTTTACTGTTACAACAAC TTG AAGGACGCCAATTACAACAATATTAATCAAGGTGGAACCTCACAGGCAAAACC TTGATT TAAATATGG</p>	<p>ATP synthase F0F1 subunit alpha [Francisella tularensis subsp. tularensis SCHU S4]</p>	229	229	100%	6,00E-70	95%	Francisella cantonensis strain 08HL01032 ATP synthase F1 alpha subunit (AtpA) gene, partial cds	292	94%	1,00E-75	82%
<p>>contig118995 length=188 numreads=8 GTCAATCATTACCATAAGATACCTGTTATAGCTGTAGACATGCGATAT AAAT TTTAGGCTGCTAGTTGTTAGTCAATTTATCTCTTTGTTTTACTGTTACAACAAC TTG AAGGACGCCAATTACAACAATATTAATCAAGGTGGAACCTCACAGGCAAAACC TTGATT TAAATATGG</p>	<p>NADH dehydrogenase I subunit A [Francisella tularensis subsp. tularensis SCHU S4]</p>	172	172	68%	7,00E-52	93%	Francisella cf. novicida 3523, complete genome 401	401	98%	2,00E-108	85%
<p>>contig84610 length=241 numreads=8 AaaGCCATTTTATGAGAAGAAGAAATAAAAAAGTTTTTATGAAAAAAGAGCAA TGTTG AGATCAATGTAGTACCATACATTGATGTAATGCTTATTACTAGTTATATTATG ATTA CCACGCCAATTTAAACACAGGGTGTAAAGTTGATTTGCCGAAAGCAACATCAG AAAAA TCCCATCAAATGATAGTAAACCAATAGTTGTACAGTCAATAAAGATGGTCAATA TTTTA T</p>	<p>antirestriction protein [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012281159.1 antirestriction protein [Francisella philomiragia] >gb ABZ88118.1 putative antirestriction protein [Francisella philomiragia subsp. philomiragia ATCC 25017] TolR protein [Francisella novicida U112] >ref YP_005825267.1 hypothetical protein [Francisella cf. novicida Fx1] >ref WP_003035506.1 biopolymer transporter TolR [Francisella novicida] >gb ABK89259.1 group A colicin translocation; tolR protein [Francisella novicida U112] >gb EDN37182.1 hypothetical protein FTDG_01591 [Francisella novicida GA99-3548] >gb AEB27307.1 Tol biopolymer transport system, TolR protein [Francisella cf. novicida Fx1]</p>	62.0	62.0	33%	4,00E-10	93%	Francisella cf. novicida 3523, complete genome	261	74%	2,00E-66	92%
<p>>contig90166 length=230 numreads=11 AAGTACAGTTGCATAAGCCTTTTAAACATTGCAGCATTCAACAATCAGCTTGA ATTGT AGCAATTTCTTACTTGGCCAAATATCTGCAAGCATCATCATTGCCCTCAG CATC AACACCTATAGCATCTTACTGACTGCAAAATCAACTGTCCGACTAATGCATAA GCAAC CACATGAATAGGAGATGCAAGATAGTTAGCTTTTACATGAGGGTTAATAC</p>	<p>aconitate hydratase [Francisella noatunensis subsp. orientalis LADL-07- 285A] >gb AHB98943.1 aconitate hydratase [Francisella noatunensis subsp. orientalis LADL-07-285A]</p>	138	138	67%	2,00E-35	86%	Francisella cf. novicida 3523, complete genome	198	68%	2,00E-47	82%
<p>>contig109648 length=200 numreads=30 CTGTCTCGAATTTCTCTGAGTTAGAACTCAAATAGTCAAGGGTGGTATTTCA AGGTC GACTCCAACAATCTAGCGACTGCTTCTCATAGTCTCCCACTATCTACACATAA ATAT TCAAAGTCCAGTCAAAGCTGTAGTAAAGTTACGGGgTCTTTCCGTCTAACCG CGGGT ACACAGCATCTTCACTGCGA >contig118995 length=188 numreads=8 GTCAATCATTACCATAAGATACCTGTTATAGCTGTAGACATGCGATAT AAAT TTTAGGCTGCTAGTTGTTAGTCAATTTATCTCTTTGTTTTACTGTTACAACAAC TTG AAGGACGCCAATTACAACAATATTAATCAAGGTGGAACCTCACAGGCAAAACC TTGATT TAAATATGG</p>	<p>Francisella cf. novicida 3523, ribosomal rRNA</p>	917		88%	9,00E-80	94%		917	88%	9,00E-80	94%

<p>>contig157498 length=151 numreads=9 GCATTAAACTCTAATATATCAAAGATATACCTCTAAACAACTACACCTCTAAAC TTTT ACTAAACATCTCAAAGACATTCTGTAGGATTGAAGCTTTGATTTCTCAAGA GCATT TTTCATCATAGCTGTCTATCAGATCATAG</p>	<p>aminopeptidase [Francisella novicida] >gb EDN35376.1 aminopeptidase N [Francisella novicida GA99-3549]</p>	70.5	70.5	55%	3,00E-12	97%	Francisella cf. novicida 3523, complete genome	158	54%	2,00E-35	94%
<p>>contig69126 length=281 numreads=13 CTGCCGCTGAAGCAAATGAAGAAATGATGAAAAGTATCTTGAAGCGAAGAG CTTACAG AAGATGAAATTCATGAAGGCTGCGTCAGCGTGATCAATAaCGAAATCGTTC TTGCTT TCTGTGTTCTGCGTTTAAAGATAAAGGTTTCAGCGCTGACTTGTGTTAT CCGTT ATTTACCTGCTCAAACCAAGTCTCTGCAATTAAGTGAAGAACTGAAGATGGTGA GCCAG cTCAAGAAAGTCATCTGATGATGAGCCGTTCTCAGCTTTA >contig135655 length=171 numreads=6 TAGAGTACCAGCATATTCGCCTTTTTCAGTAGCGGAGCATACATTGGCGCTTTA TTATG CTTAAACCGTAAATACCAAAGCTTCAACAGAGTTCTGAAAGTAATTTTAAAT ATCGA AGGTTTAGAAGGATTTGATATTATCAAAAGACTATCGGAATTGTTGTTT</p>	<p>elongation factor G [Francisella tularensis subsp. holarctica FTNF002-00] >ref YP_007008412.1 elongation factor G [Francisella tularensis subsp. holarctica F92] >ref WP_010030786.1 elongation factor G [Francisella tularensis] >sp A7N954.1 EFG_FRATF RecName: Full=Elongation factor G; Short=EF-G >gb ABU60727.1 translation elongation factor G [Francisella tularensis subsp. holarctica FTNF002-00] >gb AFX69949.1 elongation factor G [Francisella tularensis subsp. holarctica F92]</p>	143	143	63%	2,00E-37	88%	Francisella cf. novicida 3523, complete genome	209	66%	1,00E-50	83%
<p>>contig106755 length=203 numreads=8 GCTTTAGTTAAAGAAAGCTTTAAATGCATCAGCATCATCAGAAGCCATTTTTGAA CTGG TTCATAAGGTCTGTGATTGCTCATAGCTTTTTCAAGTACAGCTGAGCTGAGC TTTA TCAGTGTTCAGCTTTATCTGCGTAGCAGCATCTTTTGCATcC-TTTTGCATCG TCA TTAGCAACATCATCTTCTCTTC</p>	<p>D-lactate dehydrogenase [Francisella cf. novicida 3523] >ref WP_014549102.1 D- lactate dehydrogenase [Francisella novicida] >gb AEE27132.1 D-lactate dehydrogenase [Francisella cf. novicida 3523]</p>	109	109	65%	7,00E-27	96%	Francisella cf. novicida 3523, complete genome	222	73%	1,00E-54	90%
<p>>contig182118 length=129 numreads=6 TCGAGACCTTAATCTCCTGTACCTTGAGCACCACTAAACTTAGACATATCGTTGA TCTT ACTCTTCTATTTACCACCAGCTTTTTGATAGCTCTTTTCGCACCTTTTGTGCAAG CTA TACCCTGAA >contig66300 length=290 numreads=13 ATAAGTTGAGCAGCTAGTCTATCACCCATAGTGTTCCTTACGCTTACGCGCAGC ATCT ATGATCCATCTCATACCCAAGTTTGCAGCAGCTCAGGCTAACCTCTACAGGTA CTTGA TAAGTAGCACCAACACGACGAGATTAACTCAACATGCGGACTTATGCTTT CTAAA GCAGTTTCAAAAACCTCAACTCATTTAATGAAGCATCTTTAGCTTTAATTCTATC AAAC GCACCATAAACAATTTTTCAGCTACTGATTTTTACCATCTAGCATAAT >contig95182 length=221 numreads=10 TAAATACAGCTACTAAAGAAAGCTTACTAAGTCAAGTGTAGCAGATGACAGCCCTA ACGGTT TAATACTAGAAATgATGAGTTGATGGACTTTATACAGTCAGTTATTAGAGCTGA AAAAA TAGAAGACCATAAACTATAGTAGAGGCTTACAATAATGGAAGTTTCAAAGCA AAACAA TATCTAGGGGTaCTCAATATATAGATAATGTAACAATATCT</p>	<p>outer hypothetical protein [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012280140.1 membrane protein [Francisella philomiragia] >gb AB286928.1 conserved outer membrane protein of unknown function [Francisella philomiragia subsp. philomiragia ATCC 25017]</p>	100	100	66%	6,00E-24	81%	Francisella cf. novicida 3523, complete genome	163	65%	8,00E-37	82%
<p>>contig66300 length=290 numreads=13 ATAAGTTGAGCAGCTAGTCTATCACCCATAGTGTTCCTTACGCTTACGCGCAGC ATCT ATGATCCATCTCATACCCAAGTTTGCAGCAGCTCAGGCTAACCTCTACAGGTA CTTGA TAAGTAGCACCAACACGACGAGATTAACTCAACATGCGGACTTATGCTTT CTAAA GCAGTTTCAAAAACCTCAACTCATTTAATGAAGCATCTTTAGCTTTAATTCTATC AAAC GCACCATAAACAATTTTTCAGCTACTGATTTTTACCATCTAGCATAAT >contig95182 length=221 numreads=10 TAAATACAGCTACTAAAGAAAGCTTACTAAGTCAAGTGTAGCAGATGACAGCCCTA ACGGTT TAATACTAGAAATgATGAGTTGATGGACTTTATACAGTCAGTTATTAGAGCTGA AAAAA TAGAAGACCATAAACTATAGTAGAGGCTTACAATAATGGAAGTTTCAAAGCA AAACAA TATCTAGGGGTaCTCAATATATAGATAATGTAACAATATCT</p>	<p>50S ribosomal protein L15 [Francisella tularensis subsp. mediasiatica FSC147] >ref WP_012429815.1 50S ribosomal protein L15 [Francisella tularensis] >sp B25DW6.1 RL15_FRATM RecName: Full=50S ribosomal protein L15 >gb ACD31330.1 50S ribosomal protein L15 [Francisella tularensis subsp. mediasiatica FSC147]</p>	40.0	40.0	33%	0.011	90%	Francisella cf. novicida 3523, complete genome	115	52%	1,00E-22	89%
<p>>contig95182 length=221 numreads=10 TAAATACAGCTACTAAAGAAAGCTTACTAAGTCAAGTGTAGCAGATGACAGCCCTA ACGGTT TAATACTAGAAATgATGAGTTGATGGACTTTATACAGTCAGTTATTAGAGCTGA AAAAA TAGAAGACCATAAACTATAGTAGAGGCTTACAATAATGGAAGTTTCAAAGCA AAACAA TATCTAGGGGTaCTCAATATATAGATAATGTAACAATATCT</p>	<p>30S ribosomal protein S7 [Francisella sp. TX077308] >ref WP_013922016.1 30S ribosomal protein S7 [Francisella sp. TX077308] >gb AEI35157.1 SSU ribosomal protein S7p (S5e) [Francisella sp. TX077308]</p>	183	183	84%	1,00E-56	92%	Francisella cf. novicida 3523, complete genome	316	82%	7,00E-83	87%
<p>>contig95182 length=221 numreads=10 TAAATACAGCTACTAAAGAAAGCTTACTAAGTCAAGTGTAGCAGATGACAGCCCTA ACGGTT TAATACTAGAAATgATGAGTTGATGGACTTTATACAGTCAGTTATTAGAGCTGA AAAAA TAGAAGACCATAAACTATAGTAGAGGCTTACAATAATGGAAGTTTCAAAGCA AAACAA TATCTAGGGGTaCTCAATATATAGATAATGTAACAATATCT</p>	<p>hypothetical protein Fphi_0982 [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012280381.1 hypothetical protein [Francisella philomiragia] >gb AB287206.1 conserved hypothetical protein [Francisella philomiragia subsp. philomiragia ATCC 25017]</p>	147	147	79%	1,00E-39	96%	Francisella cf. novicida 3523, complete genome	311	79%	2,00E-81	92%

>contig13758 length=1492 numreads=222 TCTAAATAAGAAAAATGATACTGTAACGACTCAGCTAAAAACAaGCCATA CGTCTC ATGGAAGACGAGGGTCAGGACGGATACTTCATTCGCGTTGGCGTTGAGGGGGG AGGATGT TCTGGATTGATGTACAAATGGACTTCGATAACGAGCATAAAGAAACAGACAAA TCGTTT GAAGACAACGGAATTGAAGTTGTTGTAGACAAAAAAGCTTTTATACCTCGTT GGAACG ACTCTAGATTTTTCTGGAGGACTGAATGGCAAAGGCTTCATATTTGTAACCCGA ATGCG GATAGAACCTCGGGATGTTGGTAATCATTTTCAATATAATCGGAATATGTCAAA TTATA CGAAACGAAATTAGCAAAGACCTTGAAGACCAAGAAATGAATTTGGTTTTA CAACAG ATATTGAATCTGACAAGATTCCTAAAGGACTTAGTGAAGAAGTAATCGATTTAT TTCTG CTAAAAAAGAAAGAGCCGAATGGCTGCTTGATTTAGGCTGGAATCTTATCGTA AGTGGC AAGACATGATCGAACCAAGATGGCGCACGTTTATTACGAAACAGACTTTC AAGATA TAAGCTATTATTCTCTCAAAGCAGACTAAAAAATACGAGAGTTGGGATGATG TTGATC CTGAGATGAAGGAGACCATGAAAAAGTTGGGAATCTCGATGGAAGAGCAAAA CGCCTTA CTGGAACGAACGTCGAGTTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG >contig57016 length=328 numreads=14 TTTAACTCTGTCAGCTAAATCTCCATACCAACaCATCTGCCAGCTCTTTAGC TGC TTCTGCTGCAGGACCTTAGCAAATACTGCAACTCTTACAGATTACCAAGTCCAT TaG AAGTACAGACGACCTCACTACTCTGATCAGATTACGTTGATCTACACCCAAA GCAAC TGAACATCTACCCGCcCAACAACCTTAACGAGAAGTAAGCTTTTAAAGATACCA AATGC TTCTAGCAGAACTCTTTTTCAGCTCAACTTAGCAGCGATATTTTTCATTCT TTT AGATAATTAGACATTATTCACTCCCT >contig105103 length=206 numreads=8 ATTTAGAGGCAAGAGTTTAGCTAAAACCTCTGATCGTAGAGTGGGCTTCT GTGGTG ATGGTGAATGGATGAACAGAGTCAATGGTCTATCAACAAGAGCTGGTCGAG AAGGTT TAGATAACCTTATATTGTAGTGAAGTGAATTTACAAGACTAGATGGTCTTGT AAACG GTAATGGTAATTTGTTGAAGAATTA >contig93901 length=223 numreads=7 ATCTCTTGCAAGATTTTAACTTACCAGTGTCGTTGATCTATTTCGCGACCAG TTTT TTCTGCAATACCTttACAGTAGAACCCACGACCAACAACATCTTAACTTAGC TGG TTTGTAGTtATAACATGAATTTGAGGAGCAACATTAGAAACAGTTCTTTATGTT CTTT AATTACTTATTATAATACCAAGTATATGTAATCTACCACTA >contig163622 length=146 numreads=6 GTTTCTGTATGCTTGGGCTTTTTAAAAGTTAAAATACCTGAAAAAATATATA CATA CCCATATCTATAGCTTTGTTCCATATCGTAATCTCAGTAAAGCAATGCAGTAT TCCG CCACATTTTTCTACATTTTCAGATTT >contig93979 length=223 numreads=11 TAAGATTCAAAAATCCTATCGACGGTATGTAAGCTGGGATGATGCCGTAAGG GTAGAA TTACAATGCAAAAACAGGCTGATGATGATGATGATGATGATGATGATGATGATG GCCCAA CATATACTTTGTTAGTTGTTGATGATGATGATGATGATGATGATGATGATGATG CGTG GTGATGATCATGTAATAACTCTCAAGCAAAATAATATTA	Iron-regulated ABC transporter membrane component SufB [Fluviicola taffensis DSM 16823] >ref WP_013686844.1 cysteine desulfurase activator complex subunit SufB [Fluviicola taffensis] >gb AEA44074.1 Iron-regulated ABC transporter membrane component SufB [Fluviicola taffensis DSM 16823]	686	686	68%	0.0	86%	Francisella cf. novicida 3523, complete genome	283	34%	4,00E-72	76%
50S ribosomal protein L1 [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012280432.1 50S ribosomal protein L1 [Francisella philomiragia] >sp B0TX07.1 RL1_FRAP2 RecName: Full=50S ribosomal protein L1 >gb ABZ87265.1 50S ribosomal protein L1 [Francisella philomiragia subsp. philomiragia ATCC 25017]	138	138	82%	1,00E-37	84%	Francisella cf. novicida 3523, complete genome	270	85%	6,00E-69	82%	
pyruvate dehydrogenase [Francisella philomiragia] >gb EET20950.1 pyruvate dehydrogenase subunit E1 [Francisella philomiragia subsp. philomiragia ATCC 25015]	147	147	72%	7,00E-39	100%	Francisella cf. novicida 3523, complete genome	248	71%	2,00E-62	89%	
polynucleotide phosphorylase [Francisella tularensis subsp. tularensis SCHU 54]	137	137	75%	2,00E-35	88%	Francisella cf. novicida 3523, complete genome	195	68%	3,00E-46	84%	
deoxyribonuclease YcfH [Francisella sp. TX077308] >ref WP_013922675.1 TatD family hydrolase [Francisella sp. TX077308] >gb AEI35837.1 Putative deoxyribonuclease YcfH [Francisella sp. TX077308]	101	101	98%	9,00E-25	96%	Francisella cf. novicida 3523, complete genome	176	100%	4,00E-41	88%	
glutamyl-tRNA synthetase [Francisella sp. TX077308] >ref WP_013922001.1 glutaminyl-tRNA synthetase [Francisella sp. TX077308] >gb AEI35141.1 Glutamyl-tRNA synthetase [Francisella sp. TX077308]	145	145	87%	1,00E-39	92%	Francisella cf. novicida 3523, complete genome	171	84%	3,00E-39	83%	

>contig171911 length=139 numreads=6 TGTGCTAAAGCGTAAATAGTAATATTACAGCTGGTATGGACATGACTATTGG TGAATT TGAAGAAGTTGGTGAAGTTATTATGATCATTTATTCTGATGATGCTATTGTTATT GCCGG TACTGTGATTGATATGGAT	cell division protein FtsZ [Francisella novicida] >gb EDX18862.1 tubulin/FtsZ family protein [Francisella tularensis subsp. novicida FTE]	84.7	84.7	64%	1,00E-18	93%	Francisella cf. novicida 3523, complete genome	158	62%	3,00E-35	88%
>contig182107 length=129 numreads=6 AAAAAGATGTGATGGAGTTTTGCTTATAAACCATCCGCTTGTTGCCAATATG TGATC AAGGTGGTGGAGTGAGCTGCAAGATATAGCGATGGTTTACGGTAAACGCACA TCTGACT ATAAAGAGT	NADH dehydrogenase subunit G [Francisella noatunensis subsp. orientalis str. Toba 04] >ref YP_008893902.1 NADH dehydrogenase subunit G [Francisella noatunensis subsp. orientalis LADL-07- 285A] >ref WP_014714597.1 NADH dehydrogenase subunit G [Francisella noatunensis] >gb AFJ43052.1 NADH dehydrogenase subunit G [Francisella noatunensis subsp. orientalis str. Toba 04] >gb AHB98989.1 NADH dehydrogenase subunit G [Francisella noatunensis subsp. orientalis LADL-07-285A]	93.6	93.6	86%	1,00E-20	91%	Francisella cf. novicida 3523, complete genome	154	81%	2,00E-34	89%
>contig162313 length=147 numreads=9 AGAACTATGCTTCCACTTCTATGTCAGCAGATCATAGAGTAATTGGAGCGT TAGCT GCTAAGTTCTGACTAGATATAATCAGATTCTTCTGATTACGCCGAAATATAAT GTAA ATTCAATATTAGCGGAGTTTAAAAA	dihydroliipoamide acetyltransferase component of pyruvate dehydrogenase complex [Francisella sp. TX077308] >ref WP_013922551.1 dihydroliipoamide acetyltransferase [Francisella sp. TX077308] >gb AEI35711.1 Dihydroliipoamide acetyltransferase component of pyruvate dehydrogenase complex [Francisella sp. TX077308]	79.0	79.0	59%	5,00E-16	97%	Francisella cf. novicida 3523, complete genome	154	61%	3,00E-34	89%
>contig126626 length=180 numreads=9 AAGCGGATGTTTATTAGAAGCAGGACTTTACTTGTATGAAAATCTGTTGAGTTA CTTG ATGATAATGCTATTGATATGATCAAACTAGATGCCAAATGCTGTAATACTCGT CGTG GACTATGTGCTACTTGTATGGCTGCTGCTGGCTGCTGAGAGAAAAGATAAAG TTGGTG >contig84111 length=241 numreads=12 IATCAGAAACTTTAGCACCAACAGATCTGAAAATGACTCTGTATTGTTTC AAAA GCTGTAGATATGCAAAAGCTTTATGATGCAACACTTGATACAGCATTGTAAaTTC CTAAT GACAGTATTCTTCTTATGACATCAGAGACTGATAAGGTAGAAAGTCACTAAA AAGTTT GCAGATGCGAAGGtTAATAGGTGATAAGTCCGACTTATTGGTAGTATAGCAA cAaGT G	DNA-directed RNA polymerase subunit beta' [Francisella sp. TX077308] >ref WP_013922414.1 DNA-directed RNA polymerase subunit beta' [Francisella sp. TX077308] >gb AEI35571.1 DNA-directed RNA polymerase beta' subunit [Francisella sp. TX077308]	84.0	84.0	85%	1,00E-16	85%	Francisella cf. novicida 3523, complete genome	147	75%	6,00E-32	83%
>contig177855 length=132 numreads=6 AttttTAATGATATTTAATACATTTCCGCCATTAATGGTTCAAATAGAGCTTATCA GA AGTATCATAATCAGTTGAAACTGTCTCAGGATTACAGTTAATCATAATAGTTTCA ATACT CTCTCAGCTAA	universal stress protein [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012280178.1 universal stress protein [Francisella philomiragia] >gb AB286969.1 universal stress protein [Francisella philomiragia subsp. philomiragia ATCC 25017]	127	127	78%	1,00E-33	74%	Francisella cf. novicida 3523, complete genome	147	67%	8,00E-32	79%
>contig173680 length=137 numreads=6 TATTTTGCCAGAGTCCAAACCATTTGCTTGATGATGTTGAGCATTACTTTTTAGT AGTG CTGTAGTCTAGCTAAACGCTCTTTTTAACTCCATAGGAGTATCATCTGGTAA TCTG CAGCTGGAGTACCAGGG	hypothetical protein [Francisella cf. novicida Fx1] >ref WP_014549144.1 carbamoyl phosphate synthase large subunit [Francisella novicida] >gb AEB26974.1 Carbamoyl-phosphate synthase large chain [Francisella cf. novicida Fx1] hypothetical protein [Francisella cf. novicida Fx1] >ref WP_014549887.1 (dimethylallyl)adenosine tRNA methylthiotransferase [Francisella novicida] >gb AE87490.1 tRNA-(6)A37 methylthiotransferase [Francisella cf. novicida Fx1]	89.0	128	62%	1,00E-18	95%	Francisella cf. novicida 3523, complete genome	139	59%	9,00E-30	87%
>contig152911 length=155 numreads=7 TTAATTCATATGCTATCAGATTCAGCAGGTGATTTAGTGAGCTAAACATAGACT aTCCA TTTCCATTTTATAGTACAGGATTACAGTTTGTATTATTTTAAATGGAAATAT TGTT GGTACGCTATCTAAAAATAAAGGTAATCTATC >contig168055 length=142 numreads=6 TAATAAGAATACATGAAAaGAAGTTTATAGTAAAGGTTACTTATTATGGTAAC AACGG TTTTAATGTAATAATCTGTGTAGCATTATTTTCGAGTCCAAATGGTTTTAT GATG CAGCAAATGTTGTGCAACACC	ZIP family zinc transporter [Francisella sp. TX077308] >ref WP_013923135.1 zinc transporter [Francisella sp. TX077308] >gb AEI36302.1 Zinc transporter, ZIP family [Francisella sp. TX077308]	99.0	99.0	86%	9,00E-24	92%	Francisella cf. novicida 3523, complete genome	122	88%	7,00E-25	81%
	inorganic phosphate transporter (PiT) family protein, partial [Francisella tularensis]	38.5	38.5	26%	0.094	100%	Francisella cf. novicida 3523, complete genome	97.1	31%	5,00E-17	95%

>contig129188 length=177 numreads=8 TACTAATATAGTAGCTTATTCaGGAACCTCATGATAATAACACGCTGAAAGGCTGG TATGA TGATTTAAGTAAGTgCAACGAAAACCTTCAAGAggATTTTCAAAGCTAATGAT AAAAA TATCATCTCAAAAATATAAAATACATGTGTTTCATGTAATGCTGATATGTAATAG T	4-alpha-glucanotransferase [Francisella novicida] >gb [EDN37315.1] hypothetical protein FTDG_00097 [Francisella novicida GA99-3548]	95.1	95.1	88%	3,00E-21	73%	Francisella cf. novicida 3523, complete genome	80.5	58%	5,00E-12	79%
>contig92365 length=226 numreads=8 CAGATTCAATTGAAACAGTGTCTGCCACTGGTATGATGGTTAGTTTCAAT ACCTG GTTGGTAAAAAATGCTGGCTGTATGATGGCTTTAGGACGATTAATAGAC CTGGAT TTGTTATATATGGTGTACAATTCAAGCTGGCATAATGCGTGGTAAACCAATAG ATATCG TTACTGCTTTCCAAAGTTATGGAGCATGCTTATCTGGTAGTATCAC	dihydroxy-acid dehydratase [Francisella noatunensis subsp. orientalis str. Toba 04] >ref [WP_014715277.1] dihydroxy-acid dehydratase [Francisella noatunensis] >gb [AFJ43747.1] dihydroxy-acid dehydratase [Francisella noatunensis subsp. orientalis str. Toba 04]	158	158	64%	5,00E-44	97%	Francisella cf. novicida Fx1, complete genome	235	65%	2,00E-58	85%
>contig114906 length=193 numreads=10 TCACATACTAGGTGACAGCCATATAATACTAAAAATACTGCTAGAGATAGTTTT ATAAC TGCTTTAGTACTGGTGGTGAAGGTTATCATAATTACCCATGCTTTGCTGGT GACTA TAGAAAATGGTATTAGATGGTTGATTTGATCCTCTAAATGGCTTATCGCAGGT TTAGC TAAAATAGGCTGG	fatty acid desaturase [Francisella sp. TX077308] >ref [WP_013922417.1] fatty acid desaturase [Francisella sp. TX077308] >gb [AEI35574.1] Fatty acid desaturase; Delta-9 fatty acid desaturase [Francisella sp. TX077308]	126	126	79%	7,00E-33	88%	Francisella cf. novicida Fx1, complete genome	191	79%	3,00E-45	85%
>contig56997 length=328 numreads=15 TGTAACGCATCTATTGATGGTGACGATATTGTTTATCATAACTATTTGACATAA GTAT AGCAGTTGGTACAGACCGAGGCTTAGTTGTTCTGTTGAAAGATGTTGATGA TATGAG TTTGGCAGATTAGAAAATGCTGTAGTTGATAAGGCTATTAAAGCCAGGGATGG TAAACT AACTCTTGAAGATATGCAAGGTGTACATTACTACTAATGGTGGTACTTAT GGTTC TATGCTTTCTACTCCAATCAATCACCACAAAGTGCTATATTAGGCATGCATA ATAT CGTTGAAAGACCAATGGTTGTAATGGT	dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex [Francisella sp. TX077308] >ref [WP_013922347.1] dihydrolipoamide succinyltransferase [Francisella sp. TX077308] >gb [AEI35504.1] Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex [Francisella sp. TX077308]	201	201	75%	2,00E-59	88%	Francisella cf. novicida Fx1, complete genome	191	70%	5,00E-45	78%
>contig11296 length=197 numreads=8 AAGTGTITTTGTTGATCTTTTGAACCTAGTTAAGCTATAAATCTACTAAGTTA TTAT TCITAGATTTTTAGTATTACCTTAcTCAACTTCTTGAATCAACTCTGCAAT AG TACCAGGTTTCTAGCAACGATACAGTTACCTGAATCTCTAGCAACAATCTTCC ATAC CAGTACCAACCATGGC	DNA-directed RNA polymerase subunit beta [Francisella sp. TX077308] >ref [WP_013922413.1] DNA-directed RNA polymerase subunit beta [Francisella sp. TX077308] >gb [AEI35570.1] DNA-directed RNA polymerase beta subunit [Francisella sp. TX077308]	94.7	94.7	70%	3,00E-20	85%	Francisella cf. novicida Fx1, complete genome	147	67%	7,00E-32	81%
>contig164872 length=145 numreads=6 CAACGATACCAATACCATAAACTCTTCAATGACTCTCGTTAGCTAATCTTTCC ACTA ACTCTAGAGATATTTGTAACCTTTCAGTTCTTCAGCATCAATATTCATACCAACA TTAT ATTGTTTTGCTAACTGAGTCAATTT	proline dehydrogenase [Francisella sp. TX077308] >ref [WP_013923002.1] pyrroline-5-carboxylate dehydrogenase [Francisella sp. TX077308] >gb [AEI36168.1] Proline dehydrogenase (Proline oxidase) / Delta-1-pyrroline-5-carboxylate dehydrogenase [Francisella sp. TX077308]	87.0	87.0	62%	1,00E-17	90%	Francisella cf. novicida Fx1, complete genome	124	58%	3,00E-25	83%
>contig168285 length=140 numreads=7 TCtCTTACAAGTACCAGTTCCACCCTCATCTGAGTTACAAAACACATACTTTTGA CCAG GCATACTACGGGGCATAAAGCTCCATTCAAACCTGTTGGGAAACCCAGCACCCAC CACGAC CTCTAAGACCAGACTTTTT	NADH dehydrogenase [Fangia hongkongensis]	95.9	95.9	84%	4,00E-22	93%	Francisella cf. novicida Fx1, complete genome	126	82%	5,00E-26	84%
>contig100890 length=212 numreads=12 GCTATAGTAACTTTGATAGCCTCGACCATTTGCTAAAGAATAAACCTTATAcCtT GTCT TTCTGTGGTAACTATCCGTAACGATTAAACATATAAAAGCTAGCAGCATGAT GTCC ACCTAAAATTTGCTAGCTGTGTAGCATCTTGCTACATCGTGTATCTCAATAACCA CACG GTTTGCACCTGCTTGAAGCACTGATGCTTCAG	Protein-export membrane protein SecD [Francisella sp. TX077308] >ref [WP_013923354.1] preprotein translocase subunit SecD [Francisella sp. TX077308] >gb [AEI36523.1] Protein-export membrane protein SecD [Francisella sp. TX077308]	139	139	86%	1,00E-36	94%	Francisella cf. novicida Fx1, complete genome	228	87%	2,00E-56	86%
>contig135083 length=171 numreads=6 GAAGGTGCACCGTTATTTGATGATGAAAACCAACAGATTACAATGCTTTCAAGC AATCAA GTAGCTCTTAATTTTGGATAACAATGGTAACTGAAAATATCCACAGA ACCTT AATGGTGAATAGATGGTCAACAGCTGTTACAGCCCTAAATGGTCGTGA	Phosphoribosylformylglycinamide synthase, synthetase subunit / Phosphoribosylformylglycinamide synthase, glutamine amidotransferase subunit [Francisella cf. novicida 3523]	87.4	87.4	77%	6,00E-18	68%	Francisella cf. novicida Fx1, complete genome	82.4	29%	2,00E-12	89%

<p>>contig58976 length=318 numreads=11 GGACTAATCGTAGCACCCCAAGACTGGTAAAAAATCATGATGCAAAATATC GCAACT TCAATTGCAAAAAACCATCTGAATgtAACCTAATCATGCTTTAATTGATGAAAG ACCA GAGGAAGTAACAGAAaTGCAACGCTCTGCGTGGTGAAGTTGTAGCAAGTAC ATTTGAT GAACCAGCTGCTCGCATGTACAGCTAGCAGAGATTGAATGAAAAAGCTAAA AGATTA GTTGAGCATAAAACAAGATGTAGTAATCTTACTTGACTCAATCAAGACTTGCTC GTGCA TACAACACAGTATCTCT >contig90038 length=230 numreads=11 AGCCTACATTACTGTCTATCAAAACGACCGGCTTAAAAAGTCATTATCTAGC ACAT CTGGTCTATTAGTAGCAGCAATTACAATTACACCTTATTATCTGCAAAACCATCC ATTT CTACAAGTAGTTGGTTAAGAGTTTGCTCAGCTCATCTATTACCACCCACCTACCT GAGC CACGATGACGACCAACTGCATCTATCTCATCAATAATACCAAGCATGGA ATAC >contig151752 length=156 numreads=7 CAGTGTCTAAATCAGATGCTGTTATTTTAACTTATTCTGTATGTCAAAAA ATAC ATGACAGTAATGGCATAGTACTTTTGCTATTtCTATAGATAACATTGATTGCAA GGCT TAAGCAAGTCTCTCTATTAGTACAAAATTCATTT >contig52685 length=350 numreads=17 AGAGCTCGTAAAGTTAGATTGTGCGGATAATTGGAAAAACACTACTACTC ATGGAT GCGTGATTACAAGATTGGTGGTGTCAAGACAGCTTTGGTGGGTCATAGAAT ACCTGC TTGGTTTGATAATGATGGTAATGTATTTGGTGGCGAgTCAGAAACAATCCGT ACAAA GCATAAICTAGCTGAGAGCATAGAGCTTAATCAAGACAATGATGATTGATACA TGTT CTCATCTGATTGGCCATTTAGTACTAGTTGGCTGAGCAAACCTCTGAGC TAGC TAAACTACTCTCAACAGCTGCTGTAACAGTTTTGATATTCTCT</p>	<p>transcription termination factor Rho [Francisella tularensis subsp. holarctica F92] >ref WP_015083803.1 transcription termination factor Rho [Francisella tularensis] >gb AFX70309.1 transcription termination factor Rho [Francisella tularensis subsp. holarctica F92]</p>	218	218	87%	1,00E-68	100%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	359	85%	1,00E-95	87%
<p>>contig90038 length=230 numreads=11 AGCCTACATTACTGTCTATCAAAACGACCGGCTTAAAAAGTCATTATCTAGC ACAT CTGGTCTATTAGTAGCAGCAATTACAATTACACCTTATTATCTGCAAAACCATCC ATTT CTACAAGTAGTTGGTTAAGAGTTTGCTCAGCTCATCTATTACCACCCACCTACCT GAGC CACGATGACGACCAACTGCATCTATCTCATCAATAATACCAAGCATGGA ATAC >contig151752 length=156 numreads=7 CAGTGTCTAAATCAGATGCTGTTATTTTAACTTATTCTGTATGTCAAAAA ATAC ATGACAGTAATGGCATAGTACTTTTGCTATTtCTATAGATAACATTGATTGCAA GGCT TAAGCAAGTCTCTCTATTAGTACAAAATTCATTT >contig52685 length=350 numreads=17 AGAGCTCGTAAAGTTAGATTGTGCGGATAATTGGAAAAACACTACTACTC ATGGAT GCGTGATTACAAGATTGGTGGTGTCAAGACAGCTTTGGTGGGTCATAGAAT ACCTGC TTGGTTTGATAATGATGGTAATGTATTTGGTGGCGAgTCAGAAACAATCCGT ACAAA GCATAAICTAGCTGAGAGCATAGAGCTTAATCAAGACAATGATGATTGATACA TGTT CTCATCTGATTGGCCATTTAGTACTAGTTGGCTGAGCAAACCTCTGAGC TAGC TAAACTACTCTCAACAGCTGCTGTAACAGTTTTGATATTCTCT</p>	<p>ATP-dependent metalloprotease [Francisella philomiragia] >gb EET21773.1 ATP-dependent metalloprotease [Francisella philomiragia subsp. philomiragia ATCC 25015]</p>	125	125	75%	3,00E-31	97%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	254	72%	5,00E-64	88%
<p>>contig132923 length=173 numreads=6GTGCAAATGAAGCTGTTCTAAAATGCTTGCTGAAATAGAGAGTG TTGAAAATATTGATA AATTTATAGCAaaAGCAAAAGATAAGAATGATCCATTTAGACTAATGGGCTTTG GTCATA GAGTTTACAAAAACACTGACCCAAGAGCTACAGCTATGAAAGAAAATTGCGAA >contig78870 length=254 numreads=10 ATCGTTGCTAAAATAATATCAGGATTTGAGTATGAGTAAGATAATAGATGTAG AAACAA GCATAAATAAACACCTTTAAAAGAACCTTTACAACAGCGGTAAGAAGTACTA ACCATA TAGACTCTAGCTTAAAGATAACTACTGATGATGgTTTAGTTGGTTTTGGAGTT GCTC caGCTACTACGGCGATTACTGGTGATACCCTtGAGGGATGAAGTATATTGCTGA AGAAC TTTTACACCTGTT >contig66992 length=288 numreads=12 CTCTTAGAGCTAAAAGTTTAGGATGTCTGTATAGAGCATTTGAATCAAGATTGAT TTTAC CATCAACACATACGATCTCACCATTTCTCTACAGCAAGGGTTAATCTCAaAT AGTG CAAAGTCACATTCACAAAATGCTTTGTAaGCACCTATCATAGCTTTGTGAAGTC GTTGA TTgTtGCTTCTAAGCCTAGTTGAAAAGCAACATCACGAGCTTGAATGGTTG AAGGC CTACTAATGGATCTACTCTACTTTAAGAAATTTTTCTGGAGTTAT</p>	<p>DNA polymerase III subunit beta [Francisella tularensis] >gb EET20098.1 DNA polymerase III [Francisella tularensis subsp. tularensis MA00-2987]</p>	94.4	94.4	82%	9,00E-22	92%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	132	78%	1,00E-27	83%
<p>>contig132923 length=173 numreads=6GTGCAAATGAAGCTGTTCTAAAATGCTTGCTGAAATAGAGAGTG TTGAAAATATTGATA AATTTATAGCAaaAGCAAAAGATAAGAATGATCCATTTAGACTAATGGGCTTTG GTCATA GAGTTTACAAAAACACTGACCCAAGAGCTACAGCTATGAAAGAAAATTGCGAA >contig78870 length=254 numreads=10 ATCGTTGCTAAAATAATATCAGGATTTGAGTATGAGTAAGATAATAGATGTAG AAACAA GCATAAATAAACACCTTTAAAAGAACCTTTACAACAGCGGTAAGAAGTACTA ACCATA TAGACTCTAGCTTAAAGATAACTACTGATGATGgTTTAGTTGGTTTTGGAGTT GCTC caGCTACTACGGCGATTACTGGTGATACCCTtGAGGGATGAAGTATATTGCTGA AGAAC TTTTACACCTGTT >contig66992 length=288 numreads=12 CTCTTAGAGCTAAAAGTTTAGGATGTCTGTATAGAGCATTTGAATCAAGATTGAT TTTAC CATCAACACATACGATCTCACCATTTCTCTACAGCAAGGGTTAATCTCAaAT AGTG CAAAGTCACATTCACAAAATGCTTTGTAaGCACCTATCATAGCTTTGTGAAGTC GTTGA TTgTtGCTTCTAAGCCTAGTTGAAAAGCAACATCACGAGCTTGAATGGTTG AAGGC CTACTAATGGATCTACTCTACTTTAAGAAATTTTTCTGGAGTTAT</p>	<p>valyl-tRNA synthetase [Francisella tularensis subsp. tularensis WY96-3418]</p>	215	215	89%	1,00E-62	81%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	241	84%	5,00E-60	80%
<p>>contig132923 length=173 numreads=6GTGCAAATGAAGCTGTTCTAAAATGCTTGCTGAAATAGAGAGTG TTGAAAATATTGATA AATTTATAGCAaaAGCAAAAGATAAGAATGATCCATTTAGACTAATGGGCTTTG GTCATA GAGTTTACAAAAACACTGACCCAAGAGCTACAGCTATGAAAGAAAATTGCGAA >contig78870 length=254 numreads=10 ATCGTTGCTAAAATAATATCAGGATTTGAGTATGAGTAAGATAATAGATGTAG AAACAA GCATAAATAAACACCTTTAAAAGAACCTTTACAACAGCGGTAAGAAGTACTA ACCATA TAGACTCTAGCTTAAAGATAACTACTGATGATGgTTTAGTTGGTTTTGGAGTT GCTC caGCTACTACGGCGATTACTGGTGATACCCTtGAGGGATGAAGTATATTGCTGA AGAAC TTTTACACCTGTT >contig66992 length=288 numreads=12 CTCTTAGAGCTAAAAGTTTAGGATGTCTGTATAGAGCATTTGAATCAAGATTGAT TTTAC CATCAACACATACGATCTCACCATTTCTCTACAGCAAGGGTTAATCTCAaAT AGTG CAAAGTCACATTCACAAAATGCTTTGTAaGCACCTATCATAGCTTTGTGAAGTC GTTGA TTgTtGCTTCTAAGCCTAGTTGAAAAGCAACATCACGAGCTTGAATGGTTG AAGGC CTACTAATGGATCTACTCTACTTTAAGAAATTTTTCTGGAGTTAT</p>	<p>GlhA [Francisella sp. TX119]</p>	112	112	87%	3,00E-29	88%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	176	87%	6,00E-41	85%
<p>>contig132923 length=173 numreads=6GTGCAAATGAAGCTGTTCTAAAATGCTTGCTGAAATAGAGAGTG TTGAAAATATTGATA AATTTATAGCAaaAGCAAAAGATAAGAATGATCCATTTAGACTAATGGGCTTTG GTCATA GAGTTTACAAAAACACTGACCCAAGAGCTACAGCTATGAAAGAAAATTGCGAA >contig78870 length=254 numreads=10 ATCGTTGCTAAAATAATATCAGGATTTGAGTATGAGTAAGATAATAGATGTAG AAACAA GCATAAATAAACACCTTTAAAAGAACCTTTACAACAGCGGTAAGAAGTACTA ACCATA TAGACTCTAGCTTAAAGATAACTACTGATGATGgTTTAGTTGGTTTTGGAGTT GCTC caGCTACTACGGCGATTACTGGTGATACCCTtGAGGGATGAAGTATATTGCTGA AGAAC TTTTACACCTGTT >contig66992 length=288 numreads=12 CTCTTAGAGCTAAAAGTTTAGGATGTCTGTATAGAGCATTTGAATCAAGATTGAT TTTAC CATCAACACATACGATCTCACCATTTCTCTACAGCAAGGGTTAATCTCAaAT AGTG CAAAGTCACATTCACAAAATGCTTTGTAaGCACCTATCATAGCTTTGTGAAGTC GTTGA TTgTtGCTTCTAAGCCTAGTTGAAAAGCAACATCACGAGCTTGAATGGTTG AAGGC CTACTAATGGATCTACTCTACTTTAAGAAATTTTTCTGGAGTTAT</p>	<p>Muconate cycloisomerase [Francisella cf. novicida 3523] >ref WP_014547998.1 mandelate racemase [Francisella novicida] >gb AEB28546.1 Muconate cycloisomerase [Francisella cf. novicida 3523]</p>	119	119	79%	3,00E-30	76%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	134	82%	6,00E-28	77%
<p>>contig132923 length=173 numreads=6GTGCAAATGAAGCTGTTCTAAAATGCTTGCTGAAATAGAGAGTG TTGAAAATATTGATA AATTTATAGCAaaAGCAAAAGATAAGAATGATCCATTTAGACTAATGGGCTTTG GTCATA GAGTTTACAAAAACACTGACCCAAGAGCTACAGCTATGAAAGAAAATTGCGAA >contig78870 length=254 numreads=10 ATCGTTGCTAAAATAATATCAGGATTTGAGTATGAGTAAGATAATAGATGTAG AAACAA GCATAAATAAACACCTTTAAAAGAACCTTTACAACAGCGGTAAGAAGTACTA ACCATA TAGACTCTAGCTTAAAGATAACTACTGATGATGgTTTAGTTGGTTTTGGAGTT GCTC caGCTACTACGGCGATTACTGGTGATACCCTtGAGGGATGAAGTATATTGCTGA AGAAC TTTTACACCTGTT >contig66992 length=288 numreads=12 CTCTTAGAGCTAAAAGTTTAGGATGTCTGTATAGAGCATTTGAATCAAGATTGAT TTTAC CATCAACACATACGATCTCACCATTTCTCTACAGCAAGGGTTAATCTCAaAT AGTG CAAAGTCACATTCACAAAATGCTTTGTAaGCACCTATCATAGCTTTGTGAAGTC GTTGA TTgTtGCTTCTAAGCCTAGTTGAAAAGCAACATCACGAGCTTGAATGGTTG AAGGC CTACTAATGGATCTACTCTACTTTAAGAAATTTTTCTGGAGTTAT</p>	<p>succinyl-CoA synthetase subunit beta [Francisella philomiragia subsp. philomiragia ATCC 25017]</p>	193	193	84%	1,00E-57	96%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	307	84%	4,00E-80	86%

>contig77912 length=256 numreads=10 ATGATGCATGCTCAAGTGGTGGCAGCTGCAAAACCTTTAGAAGCTCATCATA ATGCC TTAGATATGCCGTTGACTTGGTGTATAGCTCCAGAGCTTTATCTAAAAAGATTAG TTGTT GGTGGTTTTGAGCGTGTTCAGAAATAAACCCGTAATTCCTGAATGAAGGTGAT CTCA AGACATAATCTGAAATTTACTATGTCTAGAGTTTTACATGGCGTATGCTGATTATA ATGAT CTTATGGATCTAACAG >contig153082 length=155 numreads=8 AAAAAGAGCAAGgTATAGATCTTCATAATGATAAGCTAGCTCTACAAAGAGTAA GAGAAG CAGCTGAAAAAGCTAAAGTAGAATGCTCTCTGCTCAGCAAAACAGATGTAACCT TACCTT ATGTAACAGCTGATGCTACAGGACCTAACATTTA >contig155456 length=153 numreads=8 GCTAGATCTCATGCTAACTATGCTTTTACTTAGGTGCTACAAATGACAATGCTGG AAGAG CTAAAACCGCTGAAACCAATGATGCTTGCTATTAAAGATTTCAATGGGTGCTT CAACT GGTAATATGCTAGTCAATAACAAAGAACTCTT	lysyl-tRNA synthetase [Francisella cf. novicida 3523] >ref WP_014547489.1 lysyl-tRNA synthetase [Francisella novicida] >gb AE828010.1 Lysyl-tRNA synthetase (class II) [Francisella cf. novicida 3523]	182	182	90%	2,00E-52	99%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	302	90%	2,00E-78	88%
>contig153082 length=155 numreads=8 AAAAAGAGCAAGgTATAGATCTTCATAATGATAAGCTAGCTCTACAAAGAGTAA GAGAAG CAGCTGAAAAAGCTAAAGTAGAATGCTCTCTGCTCAGCAAAACAGATGTAACCT TACCTT ATGTAACAGCTGATGCTACAGGACCTAACATTTA >contig155456 length=153 numreads=8 GCTAGATCTCATGCTAACTATGCTTTTACTTAGGTGCTACAAATGACAATGCTGG AAGAG CTAAAACCGCTGAAACCAATGATGCTTGCTATTAAAGATTTCAATGGGTGCTT CAACT GGTAATATGCTAGTCAATAACAAAGAACTCTT	chaperone protein DnaK [Francisella guangzhouensis]	106	106	79%	5,00E-25	96%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	209	79%	6,00E-51	91%
>contig155456 length=153 numreads=8 GCTAGATCTCATGCTAACTATGCTTTTACTTAGGTGCTACAAATGACAATGCTGG AAGAG CTAAAACCGCTGAAACCAATGATGCTTGCTATTAAAGATTTCAATGGGTGCTT CAACT GGTAATATGCTAGTCAATAACAAAGAACTCTT	dihydroorotase [Francisella sp. TX077308] >ref WP_013921817.1 dihydroorotase [Francisella sp. TX077308] >gb AEI34954.1 Dihydroorotase [Francisella sp. TX077308]	106	106	81%	9,00E-26	98%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	182	71%	1,00E-42	91%
Contigs	Blastx	Max score	Score	Query Cover	e-value	Identity	Blastn	Score	Query Cover	e-value	Identity
>contig98282 length=216 numreads=9 CCCATAGCGGATAGTTCTAACTACACCATCACCGATTTGTTGGTCACTCTAGTAC AAGA GATGCCCTCTCTACTTTAATGCTTCATATATCTTTGGTATTATCGCGTGA CTCC ACATCGATAACAGGACCAATTACTTGAATAATTTTACCAGTACTATTATCTCTC CTAA ACTGCTGCTGCACCTGAACAAATTCAGCAAGCTCT >contig100997 length=212 numreads=8 ACTGATAGTTTACTGGGCTAGTTCTACTTGTAGCTTACCTCATGAGTTTTAGCC CTTA ATGAAAAATTTCAAGAAATAAGCTAGTTCTATCaTGATTTTACACTCAAGAAAT TTTT CAATAATTTCTCTCTTGAGATGGCTTAATGGgTGGTTAAAAACAACACTACATCAGC ATCCA ACTCATCGCGTTGTTTTTATCATTCCATT	FOF1 ATP synthase subunit beta [Francisella philomiragia subsp. philomiragia ATCC 25017]	102	102	63%	5,00E-24	91%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	261	82%	2,00E-66	88%
>contig100997 length=212 numreads=8 ACTGATAGTTTACTGGGCTAGTTCTACTTGTAGCTTACCTCATGAGTTTTAGCC CTTA ATGAAAAATTTCAAGAAATAAGCTAGTTCTATCaTGATTTTACACTCAAGAAAT TTTT CAATAATTTCTCTCTTGAGATGGCTTAATGGgTGGTTAAAAACAACACTACATCAGC ATCCA ACTCATCGCGTTGTTTTTATCATTCCATT	GTP-binding protein HflX [Francisella sp. TX077308] >ref WP_013923337.1 protease [Francisella sp. TX077308] >gb AEI36505.1 GTP-binding protein HflX [Francisella sp. TX077308]	142	142	82%	2,00E-38	97%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	231	83%	2,00E-57	86%
>contig155433 length=153 numreads=6 TTGAGCTTGAGACTAGCCATTTGTTTACAACAAATCTCATGTTTCAACGG TTAT AAAACCTATTGATAACATTACACGAATCTGCTTATCATTTGACTTTAAAAGTGT GAAA ATGCAGTTTGTGGTCTGCTCATATTATCAGCAT >contig65820 length=291 numreads=14 CGATTTACTCTCTGATAACTCGGTATCATGGTTTATACTTTGCGTGAATGAG AAAT ACTATCGATAATCTTGTAGTACAAAAAGATATTATCGAAGATAGAGTAAAGGGT ACAAGT GCATACCTATCAAGCTTCTACCTACACTCTTGATGCAAAACACTgAGTTTATGCG TGAA GATTGCTACAAAATCgTACAGCAAGTAGCATTTGAGCTTAAAGCTGGCGAATCAT TCTCA CAAAAGCTACAAGCTATTATGAAGTctGAGCATGATGATCGACTAAGCGTT	aminopeptidase N [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012280259.1 aminopeptidase [Francisella philomiragia] >gb AB287056.1 aminopeptidase N [Francisella philomiragia subsp. philomiragia ATCC 25017]	102	102	80%	1,00E-23	94%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	204	81%	3,00E-49	91%
>contig155433 length=153 numreads=6 TTGAGCTTGAGACTAGCCATTTGTTTACAACAAATCTCATGTTTCAACGG TTAT AAAACCTATTGATAACATTACACGAATCTGCTTATCATTTGACTTTAAAAGTGT GAAA ATGCAGTTTGTGGTCTGCTCATATTATCAGCAT >contig65820 length=291 numreads=14 CGATTTACTCTCTGATAACTCGGTATCATGGTTTATACTTTGCGTGAATGAG AAAT ACTATCGATAATCTTGTAGTACAAAAAGATATTATCGAAGATAGAGTAAAGGGT ACAAGT GCATACCTATCAAGCTTCTACCTACACTCTTGATGCAAAACACTgAGTTTATGCG TGAA GATTGCTACAAAATCgTACAGCAAGTAGCATTTGAGCTTAAAGCTGGCGAATCAT TCTCA CAAAAGCTACAAGCTATTATGAAGTctGAGCATGATGATCGACTAAGCGTT	adenylosuccinate lyase [Francisella novicida] >gb EDN36974.1 adenylosuccinate lyase [Francisella novicida GA99-3549]	174	174	92%	4,00E-50	81%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	198	72%	2,00E-47	82%
>contig119776 length=186 numreads=6 CAATCCCTGTGCTTCAATATCATCTTAAAAGTACAAAGCTTTCTTTATATTCT CAA GAATACAGTAGCATATTACACGCAATATCTCCAGTCAAAAACACATTTGG GAATC TATTTTTAGCTTGAACATAAATCTCTATAAACTCATCaGTTTACCTGAGAGA CTC TTGGTA	malate dehydrogenase [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012279885.1 malate dehydrogenase [Francisella philomiragia] >gb AB286612.1 Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP(+)) [Francisella philomiragia subsp. philomiragia ATCC 25017]	126	126	88%	2,00E-32	89%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	196	88%	5,00E-47	86%

>contig104939 length=206 numreads=10 AaGCGATTGAAGTATAAAATCATTCCAGGGTTAGTTGCTGGAATTGTTGAACGA GGAATA TTTATTTTCATCAAATCATTATAAGTTGTGACCAAAAAACACTACCAATAGCATC ATTA AAAGAGTGTATATCATTTGgAACTTTCTTTAAAGTATTTTTTAACTCAATTTCA CAT TGATCACAATAACACATACACTTGT >contig109684 length=199 numreads=8 TGTTGCTTAATLAgGTTATTTCTAAAAGATATGCTCATAATCACTTGGTGAAT AGTT ATCTCTATTTCTCAACTGTGATGCCATTAGTAAAGTTTTATTATCTTTCGCACCT TTT GAGAAATAGCTATTTACCCGGTTTTGAGATTTTTGCTTACCAACATAGATTAT CTCA CCATTAGCATCAATCATT	beta-galactosidase [Francisella cf. novicida 3523] >ref WP_014547803.1 beta-galactosidase [Francisella novicida] >gb AEI28345.1 Beta-galactosidase [Francisella cf. novicida 3523]	133	133	90%	1,00E-34	86%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	183	88%	5,00E-43	83%
>contig182245 length=129 numreads=6 CTCTTTGAAAAGTCCAGCAACCATAGTTTCCATCGTAGACATAATGATTCTTCAT CAAT AAATGAAGCCTCGATCTATTTGTGTAATCTGGCTGTCTATGCTCTCTAAAT CTTC ATCACGGAA	Aspartyl-tRNA(Asn) synthetase [Francisella sp. TX077308] >ref WP_013921913.1 aspartyl-tRNA synthetase [Francisella sp. TX077308] >gb AEI35052.1 Aspartyl-tRNA synthetase / Aspartyl-tRNA(Asn) synthetase unambiguous [Francisella sp. TX077308]	82.8	82.8	81%	5,00E-17	91%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	159	75%	5,00E-36	91%
>contig154187 length=154 numreads=8 CTGTAAACTATAGCTGGAGCGTGGGACGTTTGTACTACTGCTCAAGAgTA agAA GCCATTGTGATGCTCTAGTACAGATATAAGGCCTTCAACTAATGGTAAG CCAGC AGGTGCTTTAAAGTAACTACCTTCTTTCTTCC >contig148550 length=159 numreads=6 AAATCCAAATGCCAAACTACTTGGTGTGGCTCATCTTTTCTGTATAATAAT CTTA CATATTTTTTCAAAGAACATTTAATGAGAGTACTATGAAAAATTGCAAAATTT GAAG TAGGTAaTGGTAAACCATTTTTTTAATGtCTGGACCAT >contig85088 length=240 numreads=8 AAATTTGATGAGTtHCTTTCGCAAAAAGGGTATAGCTATTAATAATCAATCTC TCAA GATTTATCAGTGATGAGACAGtCACTATACCAGGGCTTTGAATGCTTTTAAAGC AAAT GTAACCTGCCAAACCAAGGAGGTTAGATGTTTGAAGGAGGCTGTTTTAAA CTTGAG AATGGTACTAGAAAACAGTTTATAGAAATGCAAGGCTAGCATTTGGTGAGCTA AATAGC >contig90173 length=230 numreads=9 TTCACATAATTTTTATTTAATCATGTACACAGACTGTAGCTTCTCTCAACTTGC TCA TCTATAAACCATTTGAAAAAGCTTTAGTTGCATGCTCTTCTCATCTAAAGCAAT ATCC ATTAGGTGATAAAGTTTTgATGTTATATCTTCTCAgTCTTAATGTTCTCGAAA ACT TCAAGTAGCGAGTTAAATGATTTTGAAGGAGCAGCAGTTGCTTGAACCTC >contig185798 length=125 numreads=6 TAGCTTTCAAATAAGCTCAATTGCAAGCTTCAATTTGATGGAAGGCTGGGGCATA ACCA CCTCATCAACCAACAGCAACACTATAACCATCTGTTAACTAACACTTTTTTAAGT GTAT GGAAT	dihydroorotase [Francisella sp. TX077308] >ref WP_013921817.1 dihydroorotase [Francisella sp. TX077308] >gb AEI34954.1 Dihydroorotase [Francisella sp. TX077308]	103	103	89%	7,00E-25	98%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	156	87%	7,00E-35	85%
>contig149725 length=158 numreads=7 TAGCTAATGATAAAGGTGACTTGGGCGTAATGCTACTAGCAACAGCTG ATTTGA TGAAATATCAGGTTTAAATAGTCTGTTTATGTGAGCTGATGAATAAAAA TGTTA CTATGATGAATGGTACGAACTTGAACGATTTGCTAA	2-dehydro-3-deoxyphosphoconate aldolase [Francisella tularensis subsp. tularensis SCHU 54]	45.4	45.4	28%	6,00E-04	100%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	150	100%	3,00E-33	85%
	phenylalanyl-tRNA synthetase subunit beta [Francisella cf. novicida 3523] >ref WP_014548208.1 phenylalanyl-tRNA synthetase subunit beta [Francisella novicida] >gb AEE26207.1 Phenylalanyl-tRNA synthetase beta chain [Francisella cf. novicida 3523]	124	124	72%	7,00E-31	82%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	150	64%	6,00E-33	82%
	ferritin [Francisella sp. TX077308] >ref WP_013923318.1 ferritin [Francisella sp. TX077308] >gb AEI36486.1 Ferritin [Francisella sp. TX077308]	129	129	95%	7,00E-36	78%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	147	89%	6,00E-32	79%
	phosphopyruvate hydratase [Francisella novicida U112] >ref WP_003035924.1 enolase [Francisella novicida]	68.2	68.2	90%	4,00E-12	95%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	137	89%	2,00E-29	87%
	GTP cyclohydrolase II [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012280147.1 3,4-dihydroxy-2-butanone 4-phosphate synthase [Francisella philomiragia] >gb ABZ86936.1 GTP cyclohydrolase II [Francisella philomiragia subsp. philomiragia ATCC 25017]	99.4	99.4	83%	2,00E-23	89%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	137	68%	3,00E-29	86%

<p>>contig72436 length=271 numreads=8 CACACTTACATATTTCAACTACAAAGTTtCAACTAACTGTTGCCATGTTCTGTAT GAG TAGTTTCAGGATGGAAGCTGCACACCATAAAAAGTTTATGTTTTATGAGATACAG CTGCAA TTGGAGACTTTATAGATGAAGCAATATCTCAAAATGTTCCCGGTATCTGTAAC TTTAT CGCTATGGCTCATCAAACAAGTTGTTTCAGAACCTAGCTTTGCAAAATACTTATT TCAT CTGTGCTATATTTATAGCTTTACCAA >contig117242 length=190 numreads=12 TTTCTTAAAATCATAAGTTTTCTCATCATCACAGAAGACCAACGAGCTTGAA CCAC ATTACACCTTCGTACGAGCATTTTACATTGTACTACTAGCTAAGCGTTGTGCTA CTAC ATCAAACCTGAAGTACACCTACCGACCAAGCAGATCATTGAAATCATTGGT TTAAA CACTTGCCTA >contig81714 length=247 numreads=11 TCCCATTTCAAACACATTAGCTCTACCTCTTCTCTTAGGATCATTTCATAACTC TTA AGAGCATTTGAAATACTTCAAACCTAATACCTAATTTAAATGATAAAGCTATAG CAACT AATGCATTTTCAATATATGCTAGCAAACCTTTAACAGTAGAGTGATGCATCAA CCAAT TTTAAAAGAGATTTTTTAAACACCCTTTCAATCCATATAAACTCTCCATCTCAACA ACA CTCGCAT >contig83316 length=244 numreads=11 TAGAGCTATCTCTCAAAAACTTAGCTGGAAGATAAATCATATCATATAAGT TATTG CTTTTGATTTCTCACACTCTTTTAAAAGCTTCAAAACCTTATCCAGTAATTTTT TAT CTTACTATTTATAGCAAGATTTTTTATTTGAAAGCTTAGGTGAGATTTAAA AGAG AGATATATCTTTAAAAGTTCAACTCTTTCAGTATCAATATCTTTGATTATCTTCA GCT CTTT >contig84437 length=241 numreads=8CCATTAATGAAGTACTTATAAAGGAACCAACGGAATAATGATT TCGCTATATTAAT GACACCTTCGTGATGCTGTAAGAGAAATAATGCTCCAGGAAATGGTTTATT AATGGT TCAACTCATAATAGTAATTAATGGGTAAGTTGTTGAAGTTTATATGGCTCAG TTAC ACACTAACCGCTAACGCAATGAATCAGTAACTATGTTGATGCTCATGATAACT ATACT C</p>	<p>GMP synthase [Francisella novicida] >gb EDN36210.1 GMP synthetase [Francisella novicida GA99-3549]</p>	125	125	92%	8,00E-32	76%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	134	61%	6,00E-28	80%
<p>peptide chain release factor 3 [Francisella philomiragia] >gb EET20777.1 peptide chain release factor [Francisella philomiragia subsp. philomiragia ATCC 25015]</p>	130	130	87%	6,00E-34	95%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	130	88%	6,00E-27	79%	
<p>Mur ligase [Francisella novicida] >gb EDN37892.1 conserved hypothetical protein [Francisella novicida GA99-3548]</p>	129	129	93%	2,00E-33	72%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	126	66%	9,00E-26	80%	
<p>ATP-dependent DNA helicase UvrD/PcrA/Rep family, Francisella type [Francisella cf. novicida 3523] >ref WP_014548398.1 DNA helicase [Francisella novicida] >gb AE26402.1 ATP-dependent DNA helicase UvrD/PcrA/Rep family, Francisella type [Francisella cf. novicida 3523]</p>	100	100	84%	1,00E-22	77%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	108	76%	4,00E-20	76%	
<p>pullulanase [Francisella philomiragia] >gb EET21947.1 pullulanase [Francisella philomiragia subsp. philomiragia ATCC 25015]</p>	125	125	92%	3,00E-31	69%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	91.6	87%	3,00E-15	74%	
<p>glucose-6-phosphate isomerase [Glaciecola psychrophila 170] >ref WP_007636341.1 glucose-6-phosphate isomerase [Glaciecola psychrophila] >dbj GAC36712.1 glucose-6-phosphate isomerase [Glaciecola psychrophila 170] >gb AGH42824.1 glucose-6-phosphate isomerase [Glaciecola psychrophila 170]</p>	127	127	80%	7,00E-33	80%	Francisella noatunensis subsp. orientalis LADL-07-285A, complete genome	60.2	19%	8,00E-06	89%	
<p>GroEL, partial [Francisella sp. LA112445]</p>	83.6	83.6	62%	8,00E-18	95%	Francisella philomiragia strain CCUG 19701 GroEL (groEL) gene, partial cds	220	73%	3,00E-54	93%	
<p>replication initiator [Francisella tularensis subsp. holarctica] >emb CAJ98758.1 replication initiator [Francisella tularensis subsp. holarctica]</p>	119	119	74%	8,00E-32	84%	Francisella philomiragia subsp. noatunensis strain 2005/50/F292-6C DnaA (dnaA) gene, partial cds	196	61%	7,00E-47	88%	

<p>>contig154340 length=154 numreads=8 CCACATCTCCATCGGAGACATCATCAACAGCTCACTTTAAAACCGACTACTGCTCC CCAAC GCATATACATACGCTCAGCAGCTTTACGCCAATCTTGTCTTCTACCTCCAGAA CCTG ACTGTATTCTAGAAAACGATTATTGCACTCCAT >contig27632 length=704 numreads=67 AGATAATATATGGTAGGGGAGCGTCTGTAAAGCCGATGAAGGTGTGTGGAA GCATGCT GGAGGTATCAGAAGTGCAGATGCTGACATGAGTAACGTAATAAAGTGAAGT CTTATTG GCCGAATACCCAAGGATTCTACGCAATGTTAATCAACGTAGGGTAAGCCGGCA CCTAAG GCGTAGCTGAAGAGTGAAGTCGATGGAAAACAGGTTAATATCTGTGCTGCTT ATATGA ATGATGGAGGACGGAGAAAGGCTAGGTAGGCCCGGCAATGGTTGCCGGGT GAAAAGTAA GTAGGTAGATATGCTAGGTAATCCGGTGTATTGTTGATGCTGAGATACGAGACG AAGTCA AACTGTTTACGAAGCTATTGATGCCATGCTCCAGAAAATCTTCAAGTATAT TGTA TAGGTAACCGTACTGTAACCGACACTGGTGGTAGGTAGAGAATACTAAGGCT ATGAGA CAACTCTGGTGAAGGAAGTACGCAAAATAACCCGTAACCTTGGAAAGAGGTGT GCCCAT GTTATGTGAAGGACTGCTCTGGAGCAGAGTGGTTGCAATTATCAGGTGG CTGCGA CTGTTTATCAAAAACACGCACTCTGCGAAATCGTAAGATGAAGTATAGGGTGT GACGCC TGCCCGGTGCTGGAAGGTTAATTGAAGTGGTTAGCGCAAGCGAA >contig52227 length=353 numreads=13CTTCATTACAAAAGTTTGCAATTTCCATTTTCAATTTGAAAA AGgAATAGAAACCA CTTCCTTCTGTGCAAGAACCGTTTCTCACTTTGTAACATATCCGCTATAGGA TCTT GCATACATAACTTAAATCTTATTACCAACTAGCTTTTTCAACAGGAACA TCAC CTGCCATTGCATCTCTAAGTTTATTACGGCATAAGCCAACTTTCTGTATACA GCGT GTGGTCTACCTGTAACCTTACATCTTCTTGCACACGAGTCTGAAGAGTTTACT GGTA GTTTTGACAGCTTGATATTAGCTTCCATCTTCTTCTCAGTAGAATTACA >contig117077 length=190 numreads=9 GCCAGGATATACATCCATATCTAAGCCATCTATAAGTAATTTCTCAAACTGACT TAAC AAGATCTTAACTTTGATGACATTGTTACCAAGTCTTCCACAGTGGGATATAT AAGTC TTGAGTTTCATTCGTTTTGGAACTCTTGAGAGCTTAACCTCAAACTTAGCTA ATCT TGATTTAGAT >contig123706 length=183 numreads=6 TAAGATCTTCATCAAACTCAATAAGAGCTCTAGTTACACCAAGCGCAATTGCACC AGCTT GACCAAGTAGTACCCACCTTTAACTGTTACTTAAAGTCAAAGTTTTCAGCATT TCAG TAAGAACTAGAGGTTGCTTAAACATCATGCAATCAGTTTACGACATAAATACTG CTCTA ATG >contig142976 length=164 numreads=6 AGTGTAACAACAAGCAAGGTTTGAATTTGCTGCGCATAAAaTcATTCTTAag ACAA GATCCAGATATAATCATGTTGGTGAAGTACAGGgATATCGAAACTGGATCTATT GGTATT AAAGCATCTCAAAACAGGTCACTTAGTTATGTCACGCTACATAC</p>	<p>peptide chain release factor 2 [Francisella tularensis subsp. tularensis NE061598] >ref WP_014551162.1 peptide chain release factor 2 [Francisella tularensis] >gb ADA77879.1 peptide chain release factor 2 [Francisella tularensis subsp. tularensis NE061598]</p>	87.4	87.4	62%	2,00E-19	98%	Francisella philomiragia subsp. noatunensis strain 2005/50/F292-6C PrfB (prfB) gene, partial cds	171	79%	3,00E-39	87%
<p>30S ribosomal protein S14 [Francisella philomiragia subsp. philomiragia ATCC 25017]</p>	143	143	52%	4,00E-41	97%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	473	90%	4,00E-130	91%	
<p>hypothetical protein [Francisella cf. novicida Fx1] >ref WP_014550345.1 heme ABC transporter ATP-binding protein [Francisella novicida] >gb AEE88185.1 ABC transporter, ATP-binding family protein [Francisella cf. novicida Fx1]</p>	125	125	84%	2,00E-32	95%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	239	83%	9,00E-60	90%	
<p>30S ribosomal protein S9 [Francisella philomiragia] >gb EET21162.1 30S ribosomal protein S9 [Francisella philomiragia subsp. philomiragia ATCC 25015]</p>	84.3	84.3	85%	7,00E-19	93%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	209	86%	7,00E-51	87%	
<p>type II secretion system protein/type IV-A pilus assembly ATPase PilB, partial [Francisella tularensis]</p>	110	110	79%	2,00E-27	98%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	172	79%	9,00E-40	86%	

>contig116307 length=191 numreads=8 AAATCTGTACACCAAGAGGCTTTCCGAGTCCCATATAGAGCATHCCATAGTT TCCC AATGTCATCTGTACACCTTTGTTATTACCATTTCAGTGATATCAATCCAGCA CCAT GCTCTTtgCAAAGAGCTCAAATGCACACTCACAAAAGCCTGCCATAGGAGCTAG CACTA CATTATTTCT >contig46381 length=392 numreads=19 ATTTAGCTATAAGTTTTGTCAACAAGTTGGTGATGAAGGTAAGGTTATTTAAG TggTA TTAACTCATCAAGTCTAGAAGTTGGTAAAGAAAACTACTAATAGAGGTTGGT TGCTA ATATCGAaTATGTACAAGCAAAATCGGAAAGCTTGCCTTTCTGACAACTATTT TGATT GCATAACAATCTCTTTGGCTTAAGAAATGTTACAGATAAGGCAAAAGCACTAG CTTCGA TATGTAGAGTATTAACCAGGTGGTAGGTTACTAGTCTAGAGTTCTTAAGC CTATAG TACCAATGCTTTCTAAAATACAGATGAATCACTATTTAAAGCTTACCATTATG GGTA AAATCATCACTCAAGTCTGAAAGTTACAAA >contig84512 length=241 numreads=10 ATACACCAAACTCAGTGATAGATCTGATTTTACCATGAACCTTATCACCAACTTG AAAT TATCTTCAAAGAAATCCCAAGGTTAGCTTACATTGCTTAATCACTAGAGAAAT TCTGT GTTTCTGAGCATCAACTCAAGTACGATACTCAACTCTTGCCAAATGATACA GCTT TGTGAGGGTTAACTCTTGTAGTCCAATCCATTCAGATGTGTAACAAGACC TTCTA T >contig112895 length=195 numreads=10 GCTATAGCTAATGTCATGTTGCTAGCTgCAGCATTAACTAcGAAaCAATCCATAAAG ATCT AAATGTTCTTTCTTATTTTGGCATCTCTGTAAGCATATTGACCTGCTTAAATAC CGC TTGTTTAGCTACTATATACTCTGAAAGCAGCACCATAAACCCTTTGCTGTTT TAA GACTTCTTATGTCT >contig128384 length=178 numreads=6 ATAGCGGATTGCTAGGAAATAAGTTGTTTAGATATTGATGATAGAAAAGCC TATCT ATTCTTTGGGGTATGCTAATAGGGGATAGTGAACAGGGAAAACCCCTAGATC AATGAA CCTATGAAACCAATTAAGAAATAGATAAACAGCTTTTATGATGATTATTTAAAG ACT >contig170526 length=140 numreads=6 ATTGAAAACTCTAGAAATTGGAGTTGATAGAGTAGTTGTLGGTAGTTTAGCTG TTAAG GATACAGCATTAAACGAAGAAAGTTTTTgAgAaATATGGCGCTGAAAAGATGTT TAGCT TTAGATGTTTTATCAAAGA >contig146987 length=160 numreads=7 TTAACTATACAGCTTTAAGTGATGAAGATCACAAGTTGCTGAACATTTGGTG TATGG ggTGAAGAAATTTATgGgTAAAGTATATGATGGTATCCATAGAATAGCTTTT TaTA GACAAAGAAGGTAAGATTGATCATGCTTTAATAAGTTTA >contig73718 length=267 numreads=12 TTAGCGAAACGATTTTGTGTTAGTTATCACTGATTCCTATAGTACAGACTAC CATA ATCTAGCTTTHCAACACCCATAAACTCAGCAATAGTTGGCCTATATCTGCAAAATG TATC TCTTGGGCAACAAATCTGATCAATATTTTACCACCAATAAGAACGGTACG CAATC ACGTGTGGTGCAGTACCAGGTGCAGTTGGATCACAACCATGGTCTGCTGCTAA AATCAC GATAGTATCTCATCTAAATATTTATC	tRNA-dihydrouridine synthase [Francisella tularensis subsp. mediasiatica FSC147] >ref WP_012429621.1 hypothetical protein [Francisella tularensis] >gb ACD31045.1 tRNA-dihydrouridine synthase [Francisella tularensis subsp. mediasiatica FSC147]	124	124	84%	2,00E-32	87%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	159	85%	7,00E-36	82%
Ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Francisella sp. TX077308] >ref WP_013922247.1 ubiquinone/menaquinone biosynthesis methyltransferase [Francisella sp. TX077308] >gb AEI35399.1 Ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Francisella sp. TX077308]	256	256	90%	4,00E-83	93%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	326	90%	1,00E-85	82%	
30S ribosomal protein S1 [Francisella sp. TX077308] >ref WP_013921941.1 30S ribosomal protein S1 [Francisella sp. TX077308] >gb AEI35080.1 SSU ribosomal protein S1p [Francisella sp. TX077308]	150	298	92%	4,00E-41	89%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	279	91%	6,00E-72	88%	
50S ribosomal protein L20 [Francisella noatunensis subsp. orientalis str. Toba 04]	126	126	83%	3,00E-35	98%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	261	82%	2,00E-66	91%	
hypothetical protein [Francisella novicida] >gb EDN38529.1 predicted protein [Francisella novicida GA99-3548]	119	119	88%	2,00E-30	93%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	257	89%	2,00E-65	93%	
phosphoribosylformimino-5- aminoimidazole carboxamide ribotide isomerase [Francisella sp. TX077308]	85.9	85.9	76%	6,00E-19	98%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	191	76%	2,00E-45	91%	
thioredoxin-dependent thiol peroxidase [Francisella philomiragia] >gb EET20615.1 bacterioferritin comigratory protein [Francisella philomiragia subsp. philomiragia ATCC 25015]	106	106	86%	4,00E-27	93%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	211	84%	2,00E-51	91%	
phosphopentomutase [Francisella philomiragia] >gb EET20772.1 phosphopentomutase [Francisella philomiragia subsp. philomiragia ATCC 25015]	130	130	100%	2,00E-34	86%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	165	72%	2,00E-37	81%	

>contig191739 length=118 numreads=6 CTCTTGCTCTACCTGACCTTCTGCTCCAAGGTTTTGCACCCACCACGACACT TCTG ATCTAGTTTTTTCGCTTTAGTTCCTGACGACACCTgCCATATAGGCACTACA AC	50S ribosomal protein L4 [Francisella noatunensis subsp. orientalis str. Toba 04]	80.9	80.9	75%	2,00E-17	100%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	169	75%	8,00E-39	92%
>contig97494 length=217 numreads=8 CCGACAAATAGCTTCGTTAAAATGACCTTAAATTCGTTAAAAGATGGAACCAT AGCAG AGGATACGAAAATAACAGACACTTTTGTATTCAAATGGGTCAAGGATGCTT TACCG ATAAAGTTGAAAATGAACTTATAGTTCGAAATGGTGACAGTAAACGAGTGG TGTTAA TGCCAGATGAAGCTTTTGGTGAAAAACATCCTTCTAG	peptidyl-prolyl cis-trans isomerase [Francisella philomiragia] >gb EET20256.1 peptidyl-prolyl cis-trans isomerase [Francisella philomiragia subsp. philomiragia ATCC 25015]	139	139	87%	1,00E-39	88%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	193	83%	8,00E-46	84%
>contig87198 length=236 numreads=8 AAAAGAATTTGTATAGCAGGAATGAATGTTATACCGGCCAGATTTTAAAGAAA CTGATA AATAATCTCAAAATTTTGAGCTAGTTGGAAGCTAGGTCTATCAATAAATAA AAGAT CAATATAGATATTTTGGTAGCTAAATAGTGAATTTCCAGATGGATTTTTT ATTA TTAGCTACACCTGCAGATATTTCTATAGAAATCGTAGATAAGATCAATCAAAGA A	N-acetyl-gamma-glutamyl-phosphate reductase [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012280023.1 N-acetyl-gamma- glutamyl-phosphate reductase [Francisella philomiragia] >gb ABZ86774.1 N-acetyl- gamma-glutamyl-phosphate reductase [Francisella philomiragia subsp. philomiragia ATCC 25017]	115	115	79%	8,00E-29	68%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	161	70%	3,00E-36	81%
>contig136666 length=169 numreads=7 TTTGATTATAGTATCATCTATAGCTCCAGCATATAGTTGTACCAGCAACCACT CAA CATCATCATGTATCACAACACGGCCAAAGCTGGAAATTTTGTCCAACCATC ATCAT CTCtGgCATTACCAAAACCcTACAACCAACTTACTGAGTTTTGATGAAT	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Francisella sp. TX077308] >ref WP_013922561.1 UDP-3-O-(3- hydroxymyristoyl) glucosamine N- acyltransferase [Francisella sp. TX077308] >gb AEI35721.1 UDP-3-O-(3- hydroxymyristoyl) glucosamine N- acyltransferase [Francisella sp. TX077308]	110	110	80%	2,00E-27	91%	Francisella philomiragia subsp. philomiragia	132	79%	1,00E-27	81%
>contig122027 length=185 numreads=9 CTATGGTATTAGAAAATATTGATATGAAGAAATCTAAGTACATCCCTGCTAG CTTGT TTACCAAGTCAAGCTACTTTTTCCTTCTAGCAATATCTCAGCTTTTCAATCAc ACT TTGTATCTTGCTGTTTATATGCTTTTGTAGCTGATTGCTGATGCTTTGATGGC AAGG TTGCT	CDP-alcohol phosphatidyltransferase [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012279958.1 CDP-alcohol phosphatidyltransferase [Francisella philomiragia] >gb ABZ86691.1 CDP- alcohol phosphatidyltransferase [Francisella philomiragia subsp. philomiragia ATCC 25017]	75.5	75.5	79%	9,00E-15	90%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	128	75%	2,00E-26	80%
>contig157653 length=150 numreads=6 CTTTACCTGGTGCAAGGTAAATACCACTAccttGTAGTAAAGTAATAGCTTCATTA GTCA CAGGCAATGTAGATGCTTCAACAACATATTAACACCGTTGCTTAATGTCTCT GCTT CTTTTTCAAAATTCATTTTGTGGTGCAG	NADP-specific glutamate dehydrogenase [Francisella sp. TX077308] >ref WP_013922474.1 glutamate dehydrogenase [Francisella sp. TX077308] >gb AEI35633.1 NADP-specific glutamate dehydrogenase [Francisella sp. TX077308]	79.0	79.0	81%	1,00E-15	82%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	82.4	29%	1,00E-12	94%
>contig95932 length=220 numreads=7 CATCTTTTTCTTAAACAAGTATCTCTTAAATGTAGTCCAGGAGTTTCAGGTATC ATCT TGCCAATCATATCACCAGCAATCAACTTCCGCCATCACACGCACACTACCTCG TACTA CACCCCTAGCTGCCATAGTACCGTAAGTATACTGTCCAACACTTGTCTACC GTACT TCTGCTCTACATTTGATAACTCTATCACGACCCTCTAT	DNA-directed DNA polymerase [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012279847.1 DNA polymerase III subunit alpha [Francisella philomiragia] >gb ABZ86566.1 DNA- directed DNA polymerase [Francisella philomiragia subsp. philomiragia ATCC 25017]	132	132	77%	2,00E-33	93%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	211	73%	2,00E-51	87%
>contig146290 length=159 numreads=6 GCTAAACTATTAATCTTATGAGTAATGCAATGATCTACTTATAATGACCGAAA CTCA GATCTTGGAGATCCAGATTTTGTAAAATGGATATTAaGgTCTTGTCTAAAA AGTAT GCAAAACAAGTAGCAGAAAAATAACGACAGATAAACAT	gamma-glutamyltransferase [Francisella novicida] >gb EDX19567.1 gamma- glutamyltransferase [Francisella tularensis subsp. novicida FTE]	104	104	79%	2,00E-24	89%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	156	77%	9,00E-35	84%
>contig140924 length=166 numreads=7 AAAGAAGTTGATGGCGTAATGCACGAACCACTTgAGCAAGCTATTATTGATGT GATGAC ACTTCCAAAGTGTGTGATGGAGAGAATGGTCTCGCTCAAGGTGAGCTTAAA AATATG GAACCTGATGGTAAAGCTGTGTAACCTGAGTTTATAATTCAT	GTP-binding protein TypA [Fangia hongkongensis and Francisella philomiragia subsp. philomiragia ATCC 25017]	97.4	97.4	85%	7,00E-22	82%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	141	86%	2,00E-30	82%

>contig43527 length=417 numreads=24 TATTACAATAaTGGTGAGAAAAAGACATTGAGTCATTAACCTGTGTATATG ATGGC TAATTCTGGTGCaaGGgTTCTTATAACCAATGCGTCAGTTAGCAGGTATGCGT GGATT GATGGCTAAACAGATGGTACGATGACGAGACTGCTATTACTGCAAACCTTAG AgAAGG CTGTGCACTACTCAACTACTTACATCTACGCATGGTCTGCTAAAGGCTTGCCG ATAC AGCTCTTAAGACTGCTAACGCAGGTTACTTAACGCGTAGACTAGTAGATGATG TCAAGA TTTAGTTATCATCGAAGAAGATTGGTACAGAAAGACGGACTTATGTTCTCAGCT ATTGT TGAAGACGGTGAAGTTAAAGTACCTAGCTGAAAGAGCGTTAGGTAGAACCTT AGC	DNA-directed RNA polymerase subunit beta' [Francisella cf. novicida 3523] >ref WP_014548914.1 DNA-directed RNA polymerase subunit beta' [Francisella novicida] >gb AEE26935.1 DNA-directed RNA polymerase beta' subunit [Francisella cf. novicida 3523]	275	275	91%	8,00E-83	96%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	446	90%	1,00E-121	86%
Contigs	Blastx	Max score	Score	Query Cover	e-value	Identity	Blastn	Score	Query Cover	e-value	Identity
>contig79157 length=253 numreads=13 CTTCAGGATCATGAGTAAAACATTTGTGCGACCTAGTTCTCAAAGCAATTTT ACAG AGGCCAAATTAACCCACAACAATCTTATTGCTCATATAAATCCCTTTTGAGC TTGG AATCTCACCTATACCCTTTAGCAACCTGCTTTAAGAACTTCACTAAACCTT TAAA GCAAAGCTTCTATCTTATGATGCGTATTTCCAGCACTTGTATGATGATGTTG CCTT TAGACCTTCAGCA	imidazole glycerol-phosphate dehydratase/histidinol phosphatase [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012279625.1 imidazoleglycerol-phosphate dehydratase [Francisella philomiragia] >gb AB286286.1 Histidinol-phosphatase [Francisella philomiragia subsp. philomiragia ATCC 25017]	96.7	96.7	49%	8,00E-22	92%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	274	81%	4,00E-70	86%
>contig180890 length=130 numreads=6 TGTCAGCATAGATGAAATTAATCTACTATGATGATAATCCACATCTTTCTCTAT AAGC TTCTATTTCTGCTGACGCGAAGATCTTAATTTCTGTAACGAGCTCTGTAAG GAGG ATTAACCTTC >contig61537 length=308 numreads=11 TTCAGCTAAAGATTTTGAAGCATGCACACAAGCATAATCAAACCTTATACCTTGA CCAAAT AGGATTTGGCCCTCCGCAAGTATTACTTTTTGTTATCAGTAATATCAGATT CACA ATCTCTTATGATCTCTTATGAGAAAATGCTCATAAAGTGGATACATATAGAA GATGA AGAATCAAACCTCAGCTGCACAAGATCAaCCTTCTATATGTTGGATAAATCTCTT TACC ATAACGATAGTTACGTACATATTTTTCTGTTCTACCAACTAGCTTTGCAATTTCTG CATC AGAAAAAC >contig117499 length=190 numreads=7 CCACTCTATCTGTCATCAAGATTAATCTGATACCTTTTTCTTGAAGACTTCAAGCT GAG GGTTGTTAAAGCTGCTTATAGCTATCTGCTGTGATGATGATAGATAGTATCCTG CTCT CTTTCATACGAGAGATATAGTCTGCTAAAGAACTGTTGCTTAGCATCAGTACT CTCTG TAGTTGTA >contig70644 length=276 numreads=13 CAGTATGATCTCCTGGATGTTAGTGTATCTGTTATGATGACACCTAATCCTGAC GCTT GAATTATAGAGTTTTTACCCCAATTAATATATTACAAACGATACTAGCATTCCAA GCAC CACAGCAGCAGTAATGACCAAGTACATAGTATGCACTTACAGCTGGGAATA AGAATT TTTTCCATTTGTGAAACCTTTTAGCTGCATATTAAGCTGCGCCGAAGCTTTAGCTCA TCTG GAATTGCTGAAGCACGGCAATCACATTGAATAATA	hypothetical protein Fphi_1895 [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012281160.1 hypothetical protein [Francisella philomiragia] >gb AB288119.1 conserved hypothetical protein [Francisella philomiragia subsp. philomiragia ATCC 25017]	89.0	89.0	77%	5,00E-19	98%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	226	78%	5,00E-56	98%
>contig61537 length=308 numreads=11 TTCAGCTAAAGATTTTGAAGCATGCACACAAGCATAATCAAACCTTATACCTTGA CCAAAT AGGATTTGGCCCTCCGCAAGTATTACTTTTTGTTATCAGTAATATCAGATT CACA ATCTCTTATGATCTCTTATGAGAAAATGCTCATAAAGTGGATACATATAGAA GATGA AGAATCAAACCTCAGCTGCACAAGATCAaCCTTCTATATGTTGGATAAATCTCTT TACC ATAACGATAGTTACGTACATATTTTTCTGTTCTACCAACTAGCTTTGCAATTTCTG CATC AGAAAAAC >contig117499 length=190 numreads=7 CCACTCTATCTGTCATCAAGATTAATCTGATACCTTTTTCTTGAAGACTTCAAGCT GAG GGTTGTTAAAGCTGCTTATAGCTATCTGCTGTGATGATGATAGATAGTATCCTG CTCT CTTTCATACGAGAGATATAGTCTGCTAAAGAACTGTTGCTTAGCATCAGTACT CTCTG TAGTTGTA >contig70644 length=276 numreads=13 CAGTATGATCTCCTGGATGTTAGTGTATCTGTTATGATGACACCTAATCCTGAC GCTT GAATTATAGAGTTTTTACCCCAATTAATATATTACAAACGATACTAGCATTCCAA GCAC CACAGCAGCAGTAATGACCAAGTACATAGTATGCACTTACAGCTGGGAATA AGAATT TTTTCCATTTGTGAAACCTTTTAGCTGCATATTAAGCTGCGCCGAAGCTTTAGCTCA TCTG GAATTGCTGAAGCACGGCAATCACATTGAATAATA	carbamoyl phosphate synthase large subunit [Francisella philomiragia] >gb EET20567.1 carbamoyl-phosphate synthase large chain [Francisella philomiragia subsp. philomiragia ATCC 25015]	191	231	84%	7,00E-54	82%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	198	82%	3,00E-47	79%
>contig117499 length=190 numreads=7 CCACTCTATCTGTCATCAAGATTAATCTGATACCTTTTTCTTGAAGACTTCAAGCT GAG GGTTGTTAAAGCTGCTTATAGCTATCTGCTGTGATGATGATAGATAGTATCCTG CTCT CTTTCATACGAGAGATATAGTCTGCTAAAGAACTGTTGCTTAGCATCAGTACT CTCTG TAGTTGTA >contig70644 length=276 numreads=13 CAGTATGATCTCCTGGATGTTAGTGTATCTGTTATGATGACACCTAATCCTGAC GCTT GAATTATAGAGTTTTTACCCCAATTAATATATTACAAACGATACTAGCATTCCAA GCAC CACAGCAGCAGTAATGACCAAGTACATAGTATGCACTTACAGCTGGGAATA AGAATT TTTTCCATTTGTGAAACCTTTTAGCTGCATATTAAGCTGCGCCGAAGCTTTAGCTCA TCTG GAATTGCTGAAGCACGGCAATCACATTGAATAATA	heat shock protein 90 [Francisella noatunensis subsp. orientalis str. Toba 04]	118	118	82%	4,00E-29	89%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	195	78%	2,00E-46	86%
>contig132469 length=174 numreads=6 AAAGCTCTAGCAATGTTAATAGAGTGTGAGACTCTGGAAGcAaCTGGTGAGTT GATGG ATGAGATCAATGTAATGAACATGATTACCAAGTGGTTGGGGTACAGGTTCC CTGCAT ATTTCCAGGCATCTACAACCTTCCCTGAGCAAAACCACTACTCAAATAGAGTAT	ABC transporter permease [Francisella sp. TX077308] >ref WP_013921923.1 ABC transporter permease [Francisella sp. TX077308] >gb AEI35062.1 ABC transporter, permease protein [Francisella sp. TX077308]	166	166	91%	4,00E-46	87%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	180	66%	8,00E-42	83%
>contig132469 length=174 numreads=6 AAAGCTCTAGCAATGTTAATAGAGTGTGAGACTCTGGAAGcAaCTGGTGAGTT GATGG ATGAGATCAATGTAATGAACATGATTACCAAGTGGTTGGGGTACAGGTTCC CTGCAT ATTTCCAGGCATCTACAACCTTCCCTGAGCAAAACCACTACTCAAATAGAGTAT	glycosyl hydrolase family chitinase [Francisella philomiragia subsp. philomiragia ATCC 25017]	97.8	97.8	75%	7,00E-22	90%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	152	81%	1,00E-33	84%

>contig100652 length=212 numreads=10 TTTTAGCTATATCTGCCATAGTTATGCTAAAACCTGCTTTTCTCTATCTATGT CAA TATCAACAACCTGGTGTCAAACTTAAGTCACTTTGCGCAAAAAACAACATACC ACTGC TCATCATTTTATCTATCAGCTATTTGTTGGTTTGTATAGCTTCATAGTCATTAA CAC TTTGAATAACAAGAGACATTGGTGACACGCA >contig67462 length=286 numreads=14 CTTTGTAATTACAGAAGACTTTACTCATTAAACAACAAACCAAGTGTACTA GCAGC AGGGTAACTCTGGCATTAGTCGTATAGTCGGCAAGCAACTCATGCAGGACA TATAGT CGCTGCTAATTTGATCATATCATGTTGAGTAGTGGTGGCTTTTATTCTTAA TGGT CGCGATGGCATACATCAATCTTATGGAAGATCgTAATGATTTGAAAACTCAA AGCAT ACTAGTCCGAGCAGGGTTAGTATCTGGAGTTTTTGGCTTACA >contig125719 length=181 numreads=8 CGATAACTTGTATAGGGGAAGTCTCTTCAACCCATCAACCATATAGCAC ACCTT GAGAAAGACCATGAGCAGTAtcAACTACAACACATCAACCTCTCTGCAAG AGCTG TAACTCTTCTTAGTATTTGACAGCAGTACCAACAGCAGCAGCTCTCAAGCG ACCAA G	multidrug transporter AcrB [Francisella philomiragia] >gb EET20764.1 RND efflux transporter [Francisella philomiragia subsp. philomiragia ATCC 25015]	134	134	86%	4,00E-34	88%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	147	76%	7,00E-32	81%
>contig148374 length=157 numreads=7 AGCGTATGGTGTGACATAAAGATAACCTGGTATTTGGCATGATAAACAATACC AAAGC AATATTTGgATTATCTACAGCATTGGTGAGCTAGATATGTGACAAAGATTGC ATTAT GTATATCCATACCCCTCATGTTGATAAAAATTGTACCAC	sodium:proton antiporter [Francisella philomiragia] >gb EET20661.1 Na ⁺ :H ⁺ antiporter [Francisella philomiragia subsp. philomiragia ATCC 25015]	156	156	88%	5,00E-43	79%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	145	88%	3,00E-31	76%
>contig167076 length=143 numreads=7 TTTGGCCTTTTACCAGTCTGATGAGCTGTTGGCAAACTATTGAACAA TTTAT TCCTGCTTTAAAAAATGAAGTACGCAATATGCTTGGTTCATTTGCTGCTCGTG AAGG TATTTCATAAAGACTTACGCC >contig140594 length=165 numreads=8 TTCAGTGGCTATCATAAGGcAGTTTTGAAgGTGGTCAAATGCCTTTGCAAAGA AGATT ACCAAAATTTGGTTTACTTCCCACTAAAAGATTTCAGCTGAAGTTAGGCTA CATGA ATTAATAATGTAGATGCTGATGTTGAACAATGATGTGCTTAA >contig174035 length=137 numreads=6 ATGAATTAATAAATACTAAAGAAAGATTATGAGCTAGAAAATATAGagCTgTATAT GGTG GTCACAAGATATTGAACAAGCTACTAAAATTTGGTTAGCAATTGCTTGGTCA AAATT ATGCTAAAGATTTACAA >contig166790 length=143 numreads=6 AGTTGTTGATAAAGTCAAGGTTAAAGTGAACAATGAGGTCCTTGGTAA TCCTGC AGCAGAGGTTGTAGCTATGAGAAGAAAGCGCATGTGATGTAATTGTGCTAG GTTCTCA TGCAACTCATGGTATAAATTTAC >contig124775 length=180 numreads=6 TAATCAAAGGAGAGATATAAGTGAAGTATAAATCAGGGTTTAAAGGTTTGG GTTACG AGTTAAGGATATATGTTTTTATGTTGCTCTAaGATATTAAGTACTGCTTATA AAAC TTAGGTTCAAATCTACACCGTATTTTACATTCACCATCTACTGATAAaaCTT TGC	inosine-5'-monophosphate dehydrogenase [Francisella cf. novicida 3523]	113	113	84%	6,00E-28	90%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	141	71%	3,00E-30	84%
>contig174035 length=137 numreads=6 ATGAATTAATAAATACTAAAGAAAGATTATGAGCTAGAAAATATAGagCTgTATAT GGTG GTCACAAGATATTGAACAAGCTACTAAAATTTGGTTAGCAATTGCTTGGTCA AAATT ATGCTAAAGATTTACAA >contig166790 length=143 numreads=6 AGTTGTTGATAAAGTCAAGGTTAAAGTGAACAATGAGGTCCTTGGTAA TCCTGC AGCAGAGGTTGTAGCTATGAGAAGAAAGCGCATGTGATGTAATTGTGCTAG GTTCTCA TGCAACTCATGGTATAAATTTAC >contig124775 length=180 numreads=6 TAATCAAAGGAGAGATATAAGTGAAGTATAAATCAGGGTTTAAAGGTTTGG GTTACG AGTTAAGGATATATGTTTTTATGTTGCTCTAaGATATTAAGTACTGCTTATA AAAC TTAGGTTCAAATCTACACCGTATTTTACATTCACCATCTACTGATAAaaCTT TGC	ribosomal protein S12p Asp88 methylthiotransferase [Francisella sp. TX077308] >ref WP_013922163.1 ribosomal protein S12 methylthiotransferase [Francisella sp. TX077308] >gb AEI35313.1 Ribosomal protein S12p Asp88 methylthiotransferase [Francisella sp. TX077308]	90.9	90.9	61%	6,00E-20	93%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	130	73%	5,00E-27	82%
>contig167076 length=143 numreads=7 TTTGGCCTTTTACCAGTCTGATGAGCTGTTGGCAAACTATTGAACAA TTTAT TCCTGCTTTAAAAAATGAAGTACGCAATATGCTTGGTTCATTTGCTGCTCGTG AAGG TATTTCATAAAGACTTACGCC >contig140594 length=165 numreads=8 TTCAGTGGCTATCATAAGGcAGTTTTGAAgGTGGTCAAATGCCTTTGCAAAGA AGATT ACCAAAATTTGGTTTACTTCCCACTAAAAGATTTCAGCTGAAGTTAGGCTA CATGA ATTAATAATGTAGATGCTGATGTTGAACAATGATGTGCTTAA >contig174035 length=137 numreads=6 ATGAATTAATAAATACTAAAGAAAGATTATGAGCTAGAAAATATAGagCTgTATAT GGTG GTCACAAGATATTGAACAAGCTACTAAAATTTGGTTAGCAATTGCTTGGTCA AAATT ATGCTAAAGATTTACAA >contig166790 length=143 numreads=6 AGTTGTTGATAAAGTCAAGGTTAAAGTGAACAATGAGGTCCTTGGTAA TCCTGC AGCAGAGGTTGTAGCTATGAGAAGAAAGCGCATGTGATGTAATTGTGCTAG GTTCTCA TGCAACTCATGGTATAAATTTAC >contig124775 length=180 numreads=6 TAATCAAAGGAGAGATATAAGTGAAGTATAAATCAGGGTTTAAAGGTTTGG GTTACG AGTTAAGGATATATGTTTTTATGTTGCTCTAaGATATTAAGTACTGCTTATA AAAC TTAGGTTCAAATCTACACCGTATTTTACATTCACCATCTACTGATAAaaCTT TGC	ribonucleotide reductase of class la (aerobic) subunit beta [Francisella sp. TX077308] >ref WP_013923022.1 ribonucleoside diphosphate reductase subunit beta [Francisella sp. TX077308] >gb AEI36188.1 Ribonucleotide reductase of class la (aerobic), beta subunit [Francisella sp. TX077308]	99.8	99.8	77%	2,00E-23	98%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	126	72%	6,00E-26	84%
>contig166790 length=143 numreads=6 AGTTGTTGATAAAGTCAAGGTTAAAGTGAACAATGAGGTCCTTGGTAA TCCTGC AGCAGAGGTTGTAGCTATGAGAAGAAAGCGCATGTGATGTAATTGTGCTAG GTTCTCA TGCAACTCATGGTATAAATTTAC >contig124775 length=180 numreads=6 TAATCAAAGGAGAGATATAAGTGAAGTATAAATCAGGGTTTAAAGGTTTGG GTTACG AGTTAAGGATATATGTTTTTATGTTGCTCTAaGATATTAAGTACTGCTTATA AAAC TTAGGTTCAAATCTACACCGTATTTTACATTCACCATCTACTGATAAaaCTT TGC	50S ribosomal protein L15 [Francisella novicida U112]	99.4	99.4	87%	1,00E-24	81%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	124	68%	2,00E-25	84%
>contig174035 length=137 numreads=6 ATGAATTAATAAATACTAAAGAAAGATTATGAGCTAGAAAATATAGagCTgTATAT GGTG GTCACAAGATATTGAACAAGCTACTAAAATTTGGTTAGCAATTGCTTGGTCA AAATT ATGCTAAAGATTTACAA >contig166790 length=143 numreads=6 AGTTGTTGATAAAGTCAAGGTTAAAGTGAACAATGAGGTCCTTGGTAA TCCTGC AGCAGAGGTTGTAGCTATGAGAAGAAAGCGCATGTGATGTAATTGTGCTAG GTTCTCA TGCAACTCATGGTATAAATTTAC >contig124775 length=180 numreads=6 TAATCAAAGGAGAGATATAAGTGAAGTATAAATCAGGGTTTAAAGGTTTGG GTTACG AGTTAAGGATATATGTTTTTATGTTGCTCTAaGATATTAAGTACTGCTTATA AAAC TTAGGTTCAAATCTACACCGTATTTTACATTCACCATCTACTGATAAaaCTT TGC	hypothetical protein [Francisella cf. novicida Fx1] >ref WP_014549578.1 cytochrome C oxidase subunit II [Francisella novicida] >gb AEB27615.1 Cytosol aminopeptidase PepA [Francisella cf. novicida Fx1]	72.8	72.8	83%	2,00E-13	76%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	89.8	45%	7,00E-15	88%
>contig166790 length=143 numreads=6 AGTTGTTGATAAAGTCAAGGTTAAAGTGAACAATGAGGTCCTTGGTAA TCCTGC AGCAGAGGTTGTAGCTATGAGAAGAAAGCGCATGTGATGTAATTGTGCTAG GTTCTCA TGCAACTCATGGTATAAATTTAC >contig124775 length=180 numreads=6 TAATCAAAGGAGAGATATAAGTGAAGTATAAATCAGGGTTTAAAGGTTTGG GTTACG AGTTAAGGATATATGTTTTTATGTTGCTCTAaGATATTAAGTACTGCTTATA AAAC TTAGGTTCAAATCTACACCGTATTTTACATTCACCATCTACTGATAAaaCTT TGC	universal stress protein [Francisella tularensis subsp. holarctica PHIT-F049]	51.6	51.6	59%	3,00E-06	92%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	86.1	66%	1,00E-13	79%
>contig166790 length=143 numreads=6 AGTTGTTGATAAAGTCAAGGTTAAAGTGAACAATGAGGTCCTTGGTAA TCCTGC AGCAGAGGTTGTAGCTATGAGAAGAAAGCGCATGTGATGTAATTGTGCTAG GTTCTCA TGCAACTCATGGTATAAATTTAC >contig124775 length=180 numreads=6 TAATCAAAGGAGAGATATAAGTGAAGTATAAATCAGGGTTTAAAGGTTTGG GTTACG AGTTAAGGATATATGTTTTTATGTTGCTCTAaGATATTAAGTACTGCTTATA AAAC TTAGGTTCAAATCTACACCGTATTTTACATTCACCATCTACTGATAAaaCTT TGC	putrescine/spermidine ABC transporter substrate-binding protein [Francisella philomiragia] >gb EET21885.1 putrescine- binding periplasmic protein [Francisella philomiragia subsp. philomiragia ATCC 25015]	49.3	49.3	32%	5,00E-05	80%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	75.0	30%	3,00E-10	86%

<p>>contig172525 length=138 numreads=11 TTACTCTATAGTTACTAACTATAGCCTATATGGTCTCTCAAATCAATTCTAACCT TTT TATAAAAAATCAGTATTATCGTATCTGCTAAAAGCTTATTTCAAAGTCTATT CTGA GCAATATCCCGATCGTAT >contig188530 length=121 numreads=7 AAAGGAAATACGAAAAATAGAAATAAACTTTAACTGTTGTTCTCAAGTATTAA ACTTA GTGTTGTAGATAATATATTTTAGTGTAAATAAATaCGGGTCTGTAGCTCAGCTG GTTAG A >contig69877 length=279 numreads=32 TGTGGATCGGAGTGAAGGCTAATCAAGCAGGAGATAGCTGGTTCTCCCGGA AAACTAT TTAGGTAGTGCCTCGGTATAACTGATTGGGGTAAAGCACTGTTTCGACTAGGG GGGTTT TACGACCTTACCGACTCGATGCAAACTCAGAATACGATCAAGTCAATCACGGG AGACAC ACTGCGGGTCTAAGGTCGTAGTGAGAGGGAAACAGCCAGACCCCAACT AAGGTCC CAAAGTCATaGcTAAGTGGGAACGAaGTGGGAAGGCC</p>	<p>cell division protein FtsW [Francisella novicida] >gb EDX19776.1 cell division protein FtsW [Francisella tularensis subsp. novicida FTE]</p>	55.8	55.8	54%	1,00E-07	83%	Francisella philomiragia subsp. philomiragia ATCC 25017, complete genome	71.3	35%	2,00E-09	89%
<p>>contig65400 length=293 numreads=26 GCTATCTCCGGCTTGATTAGCCTTCACTCCGATCCaCACTCATCCcGTAATTT GCA ACATtAGTGGGTTCCGGTCTCCAGTTAGTATTACCTAACCTCAACCTGGTCATGG ATAG ATCGCGCCGGTTCCGGTCTACTCCTAGCAACTATACgCCCTATTAAGACTCGCTT TCGC TACGGATCCCTTATTCAAGTATCCTTGCTACTAAAAGTAACTCgCTGACCCATTAT ACAA AAGGTACGCACTCACATAACTAAATTTGCTCCTACTGCTTGTATGCAAGTGG >contig42998 length=422 numreads=20 AAAAGTTGGCAAGACcATTAGATAAACATCTAACTTTAGAAcAAGAAAAAGA TTTTCC AAATATCCCACTTATTGAATTAAGTAAATTTGCTGTaGcCCCTGAGAAAGATTTG ACAC TACAGTTTATCTTTCAAAGATACTCATGATAcATATCATCAGCTACTAGCACTT CTGG CTGGGGTTGGCGATATCCTGGTAGCCTGGAGATAGCCCTATAAATCGGAGCTGg CTCGTA TGCAGACTCTGTTATGGTGCCTGTGCTTACTACTACTGGTGGAGATGGCTaTtC GCTG TGGTACCCTCGCTCTGTGgTtHtATATATGAAAATGGGAATGCTGTAAGAAAG GCTGT ACTTGAAGCTGCTAAAGATTTACGCCATCTAAAAACTGGTTACTTATGATGAGCTA ACTAT TC >contig90118 length=229 numreads=9 CATCACACCcCAATAGTCTCAATACCTACAGATAGAGGAGTTACATCAAGAAGC AATAC ATCTTTAAcATCTCCTGTAATACACCACTTGAATAGCTGCACCAACTGCCACAG CTTC ATCAGGGTtHACATCTTtACCGGGCTCTTACCAAAAGAACTCTTTACTTTTCTTG TAC TAGAGGCATACGAGTTTGTCCACCTACTAAAAGCACTTCTGTAATATCA >contig55868 length=334 numreads=22 TCCTtAAGATTAGATATCCAGGTCTTAGACCTGTAAAGGAACGTTGGAGACTAC GACGT TGATAGGCTGGGTGTGAAGTACAGCAATGTATGAAGCTTACCACTACTAATGA TCCGAG AGACTTAAGTCTATTCTATGCTGAATTGTTAAATATCTTTATGATATGCAATTA AAC GTAAATACAAAACAAaCATTAGAGATTAAGTTTGGCGATGATAGCTGT AGGTAC CACCTGATCCcATTCCGAACCTCAGAAGTGAACCTATAACACGCgATGATAGTTT AGCAT TCGCTAAGTGAAGTAGGTAGTGCCTTTTATT</p>	<p>N(4)-(beta-N-acetylglucosaminy)-L- asparaginase [Francisella sp. TX077308] >ref WP_013923506.1 asparaginase [Francisella sp. TX077308] >gb AEI36677.1 N(4)-(Beta-N-acetylglucosaminy)-L- asparaginase precursor [Francisella sp. TX077308]</p>	274	274	92%	1,00E-89	93%	Francisella sp. TX077308, complete genome	1410	98%	4,00E-129	96%
<p>>contig90118 length=229 numreads=9 CATCACACCcCAATAGTCTCAATACCTACAGATAGAGGAGTTACATCAAGAAGC AATAC ATCTTTAAcATCTCCTGTAATACACCACTTGAATAGCTGCACCAACTGCCACAG CTTC ATCAGGGTtHACATCTTtACCGGGCTCTTACCAAAAGAACTCTTTACTTTTCTTG TAC TAGAGGCATACGAGTTTGTCCACCTACTAAAAGCACTTCTGTAATATCA >contig55868 length=334 numreads=22 TCCTtAAGATTAGATATCCAGGTCTTAGACCTGTAAAGGAACGTTGGAGACTAC GACGT TGATAGGCTGGGTGTGAAGTACAGCAATGTATGAAGCTTACCACTACTAATGA TCCGAG AGACTTAAGTCTATTCTATGCTGAATTGTTAAATATCTTTATGATATGCAATTA AAC GTAAATACAAAACAAaCATTAGAGATTAAGTTTGGCGATGATAGCTGT AGGTAC CACCTGATCCcATTCCGAACCTCAGAAGTGAACCTATAACACGCgATGATAGTTT AGCAT TCGCTAAGTGAAGTAGGTAGTGCCTTTTATT</p>	<p>molecular chaperone DnaK [Francisella sp. TX077308] >ref WP_013922807.1 molecular chaperone DnaK [Francisella sp. TX077308] >gb AEI35971.1 Chaperone protein DnaK [Francisella sp. TX077308]</p>	117	117	90%	8,00E-29	99%	Francisella sp. TX077308, complete genome	315	91%	2,00E-82	91%
<p>>contig90118 length=229 numreads=9 CATCACACCcCAATAGTCTCAATACCTACAGATAGAGGAGTTACATCAAGAAGC AATAC ATCTTTAAcATCTCCTGTAATACACCACTTGAATAGCTGCACCAACTGCCACAG CTTC ATCAGGGTtHACATCTTtACCGGGCTCTTACCAAAAGAACTCTTTACTTTTCTTG TAC TAGAGGCATACGAGTTTGTCCACCTACTAAAAGCACTTCTGTAATATCA >contig55868 length=334 numreads=22 TCCTtAAGATTAGATATCCAGGTCTTAGACCTGTAAAGGAACGTTGGAGACTAC GACGT TGATAGGCTGGGTGTGAAGTACAGCAATGTATGAAGCTTACCACTACTAATGA TCCGAG AGACTTAAGTCTATTCTATGCTGAATTGTTAAATATCTTTATGATATGCAATTA AAC GTAAATACAAAACAAaCATTAGAGATTAAGTTTGGCGATGATAGCTGT AGGTAC CACCTGATCCcATTCCGAACCTCAGAAGTGAACCTATAACACGCgATGATAGTTT AGCAT TCGCTAAGTGAAGTAGGTAGTGCCTTTTATT</p>	<p>Francisella sp. TX0773083-dehydroquinato synthase and 23S ribosomal RNA gene (by blastn)</p>	43.1	43.1	27%	0.001	57%	Francisella sp. TX077308, complete genome	996	88%	2,00E-78	84%

>contig95299 length=221 numreads=8 CCTGCTAAGATAACAAGGAATACCTTTTCTTATCTCATAGCAGCATCAA ATACA TACTGTTGTGAACCACTAAAATGATACTAGTATACCCGCTTACACCGTCAA GAAGT AAGTTACGGATACGAATATTTGCAAATGTACCAGCATCATCTTCATGGTTAC CACGA CGAGAACCGTAAAGGTTAAAGCTTTTTCTACACCGTG >contig171333 length=139 numreads=24 ATTCAGACAAGGTTTCTCGTCCCGCCCTACTTGTTCGTATgtCTAGTCCACTAA GAT TATTTGCTATACGGGACTATCACCTCTATCGTCAAGCTTCCCACTGTTCTACT ATAA TTCTAGCTATATCATACCA >contig159845 length=149 numreads=6 AAATATCTAAGAGTGAAGCAAAAATTACTCAAGCTAAAAAGAGATGATTGAAG CAAACT TAAGATTGGTTGTTCTGAAGCTAAAAATATACAAACAGAGTTTACACTTCT AGATA TTATCCAAGAGGGTAATATTGGTCTAATG >contig161267 length=148 numreads=7 TTAAATTAGATAATAATGGAAGTCCCGCTATTGAGAAGATTACTTAAAT GGGTG TTGGTGATGCTGCAAAAGACAAAAGTTAgtACTTTGTGTAATGATTGAC TGCAA TtGCTGGTCAAAAGCCAGTTGTTACTAA	Aconitate hydratase [Francisella sp. TX077308] >ref WP_013922367.1 aconitate hydratase [Francisella sp. TX077308] >gb AEI35524.1 Aconitate hydratase [Francisella sp. TX077308]	155	155	91%	9,00E-42	97%	Francisella sp. TX077308, complete genome	287	86%	4,00E-74	91%
>contig195973 length=111 numreads=6 CATGGGTAATAGCACTACTGACTCTTGTACTCTGTAAGAATTTCTCAACCAT GCTA CAGATTACAGCTAAAGTGGTTAGTAGGCTCATCTAGTAGTATATCAG >contig85008 length=240 numreads=11 GGAAAGCTTCTTTGTCATACCATATCAGTGAAGTAAACGATAAAGCACTT GATAA TTCCATGATACACCACCAAGTAAACACCTCTTTACCAAAAGATATCAGAGCGATA TTCCA TTTCCATAGTTTGGGAATACAAATGTGCGCCACAAGCTATAGCCAGCCTA GAGCTT GTTCAAGTTGTTTACCGTAAATATCTTGATAAACCACTACTACTATTGATACCA GCAC >contig64191 length=298 numreads=15 TACGAAGATCTGTATCGATATTTACTTTACGCACACCGTACTTAATAGCTTACG ATTT CACTTACAGGTACGCCGTAAGTTTCAACCATAGAAcCACCGTAATTATTGATAACT TCTA ACCAAGCTTGAAGTACAGATGAAGAACCATGCAATACaAGGTGAGTGTAGGGA TTCTAG CGTGAATCTCTTTACTCTGCTTATAGATAAAACATCACCTGTAGGTGGCTTAGT GAACT TATAAGCACCGTGAGAAGTACCTATAGCAATTGCTAAAGCATCAACCTTAGTTTT CTT >contig86933 length=236 numreads=14 TCATCATACCAGGAATAATAGTCAATACCTTCAGGTTTGAGTTAGTATCTA CAacA GACACTACTTAATACCTAATTTTTGAGCTTCTGAATAGcGATGTGCTCTTTATTA CTA TCAATAACAACGATTGCATCAGGAATACCCACCTTCTTAATACCAACGA CTTTT TCAAGCTTCTCGATGTTCTCATGTTTTGTAGCATTCTTTTTAGTTAAAGATTC	RNA polymerase sigma-70 factor [Francisella noatunensis subsp. orientalis str. Toba 04]	100	100	77%	4,00E-23	98%	Francisella cf. novicida 3523, complete genome	182	74%	1,00E-42	89%
	50S ribosomal protein L5 [Francisella sp. TX077308] >ref WP_013922028.1 50S ribosomal protein L5 [Francisella sp. TX077308] >gb AEI35172.1 LSU ribosomal protein L5p [L11e] [Francisella sp. TX077308]	90.9	90.9	85%	3,00E-21	94%	Francisella sp. TX077308, complete genome	198	84%	1,00E-47	92%
	ABC transporter ATP-binding family protein [Francisella sp. TX077308] >ref WP_013923710.1 heme ABC transporter ATP-binding protein [Francisella sp. TX077308] >gb AEI36885.1 ABC transporter, ATP-binding family protein [Francisella sp. TX077308]	76.3	113	75%	8,00E-15	100%	Francisella sp. TX077308, complete genome	163	78%	3,00E-37	93%
	Ketol-acid reductoisomerase [Francisella sp. TX077308] >ref WP_013923608.1 ketol- acid reductoisomerase [Francisella sp. TX077308] >gb AEI36780.1 Ketol-acid reductoisomerase [Francisella sp. TX077308]	164	164	90%	3,00E-46	96%	Francisella sp. TX077308, complete genome	364	90%	2,00E-97	94%
	fructose-1,6-bisphosphate aldolase [Francisella philomiragia subsp. philomiragia ATCC 25017]	197	197	86%	1,00E-59	95%	Francisella sp. TX077308, complete genome	348	87%	2,00E-92	88%
	RecName: Full=30S ribosomal protein S2Francisella philomiragia subsp. philomiragia ATCC 25017	153	153	87%	3,00E-44	95%	Francisella sp. TX077308, complete genome	292	84%	9,00E-76	90%

<p>>contig40455 length=449 numreads=28</p> <p>ATGCAAGAAGTCTCCATCTGTAAGAGCTTCTTTCTCGCTCCATCATCTTAG AAAC TGGAAATACCTGTAGCTTTTGAACCTACATCTGCAATCTCAATTTCTGTAACCTGACG TTCT AACTAGCTTATTTTCACTTAAATCAGAAGCTGTCTCTCTATCTGCTTAATCTGAG CTTC AAGCTCTGGAATTTACCGTATTGACAGTTCTGACATCTTTAATGACGCTGCTC TTTG ATACTTTTCAAGCTCAAACTAGCTTTCTCAAGTTTTTCTTCAGCTGCTGTGATACC TTG CATTTTTAGCTTCTCTGCTTTCAAATCTCCCTAAGCCCTGTACTCAGAATCCAG ACC TTTTATTTCAATCTCAAgTATCTCAAACGCTTCTCGTAGCATCATCTTTTCTTTT TT AAAGTTGCTCGCGCTGCATTTTTAGCTGGA >contig55745 length=334 numreads=11 CCTATAACACCTTTTCAaCTACTGTGTAATAGCATCACAGTGATCTGCACATA TAAC CAGTCACGGATATTTGAACCATCTCCATATACAGGAATAAGTTTTGATTAATAC AACTT TTGATAACTACAGGTATTAGCTTCTGCTGATGCTGATGACCATAGTTGTTG AACAG TTAGATATAGTTACAGGTAGCTTAAAGTATGTAATAGGCTTCTATATAGGT CAGAA CCTGCTTTACTAGCTGAGTATGGTGAATTTGGTTCATAAGCCTTATCTCTGTAAA TGCT GGATCATCTTTATCAAGAGTACCAAACTCAT >contig97732 length=217 numreads=7 ATTGATTAGTTTTAATTGTTGGTTTGGAGGCACGGTTAAGCCATTTTGTAT CTGC ATGACGATTACCGAGCATTTGAAATCAGCAGTCAGTACTAATgCACTACAACCA GCATG CTTGCATCTGCTATGAGATTTGCCATAAATTTCTATCTTTCATATACAGCTG GAA CCAAAATGGCTGGTTGTGTGTTTGGCACTCTCA >contig93736 length=222 numreads=9 CAGCTTactAaaGtttAGAGAATATCTTCTTACACATCCGCTTATTCCATTT AT TACAGAGAGTATTATCAGCAGTAAAAGCTCATCTGATaTGCTCAAACTTCA ATTAT GGATGTTAGCTACCTGAACTACTCAAGATTAGAAGCTCCAGAGGCTGAGAA AGCTAT CAGATGGTTACAGAACATCGTAACAACCTCTAGAAATATGCG</p> <p>>contig13396 length=173 numreads=7 TTATCGAGAGAAATACGACTATACCTACTAAGAAATCACAAGTATTCTACAGC TGAAG ATAATCAGCCTGAGTTACAATACATGTAATGCAAGGTGAGCGTAAATGGCGT CAGCAA ATAAATCTTTAGGTAGATTTGACTAGCTGATATCCACAGCACCTCGTGGT >contig111355 length=197 numreads=8 TTAATAGTAGCTAAGCCTGCTGCACAAGTACTGGGTGCCATATATGATGCTC CAAGC ACGAATGCTGATCTTGGAAATTTAGCCATGATTTATCAGATAACATACAGCAAC CTAGA GGTAAATATGATGATGTAATACCTTTTCCATCTTACGATATCAGGCACGATAT CATAA TTCATAAAACCAACCA >contig141672 length=165 numreads=8 TTCGTTTTGATTTTGGTGATGGTGAATGAGCTGTA AACATTCTTACGCTTT TAGC AGGTACGATAGTAAATAGCATGCTTATAAACCAATTTGGTTTACAGTATTTCTG AGTAC GATACAAAATTGATCAAAAGCTTCTACTTGACCTGTAGTTAAT</p> <p>>contig129053 length=176 numreads=7 CTGCTTTGGGATATCATATATGTA AACCATCACCAACTGAAATGCTAATAT CATAA GCTGCTTTTCTACTCATCATCTGCAACAGGAATCAAAATAGGCATAGTAGC TAAAG CTTGACCTGACCCACAGGTATAAAGAAGTTTTAAACGCTTTgggCTAGTGTCAATT</p>	<p>protein disaggregation chaperone [Francisella novicida] >gb EDN38479.1 hypothetical protein FTDG_01296 [Francisella novicida GA99-3548]</p> <p>dTDP-glucose 4,6-dehydratase [Francisella sp. TX077308] >ref WP_013922615.1 dTDP- glucose 4,6-dehydratase [Francisella sp. TX077308] >gb AEI35776.1 dTDP-glucose 4,6-dehydratase [Francisella sp. TX077308]</p> <p>L-lactate dehydrogenase, partial [Francisella tularensis]</p> <p>valyl-tRNA synthetase [Francisella sp. TX077308] >ref WP_013921990.1 valyl- tRNA synthetase [Francisella sp. TX077308] >gb AEI35130.1 Valyl-tRNA synthetase [Francisella sp. TX077308]</p> <p>molecular chaperone DnaK [Francisella tularensis subsp. mediasiatica FSC147]</p> <p>adenosylmethionine-8-amino-7- oxononanoate aminotransferase [Francisella sp. TX077308]</p> <p>RNA-binding protein Hfq [Francisella sp. TX077308] >ref WP_013923338.1 RNA- binding protein Hfq [Francisella sp. TX077308] >gb AEI36506.1 RNA-binding protein Hfq [Francisella sp. TX077308]</p> <p>Arginine/ornithine antiporter ArcD [Francisella sp. TX077308] >ref WP_013922004.1 C4-dicarboxylate ABC transporter [Francisella sp. TX077308] >gb AEI35144.1 Arginine/ornithine antiporter ArcD [Francisella sp. TX077308]</p>	<p>214</p> <p>217</p> <p>151</p> <p>132</p> <p>122</p> <p>140</p> <p>114</p> <p>119</p>	<p>214</p> <p>217</p> <p>151</p> <p>132</p> <p>122</p> <p>140</p> <p>114</p> <p>119</p>	<p>93%</p> <p>93%</p> <p>87%</p> <p>89%</p> <p>87%</p> <p>82%</p> <p>89%</p> <p>85%</p>	<p>7,00E-62</p> <p>2,00E-67</p> <p>1,00E-42</p> <p>7,00E-34</p> <p>1,00E-30</p> <p>7,00E-38</p> <p>5,00E-31</p> <p>4,00E-30</p>	<p>91%</p> <p>94%</p> <p>97%</p> <p>88%</p> <p>97%</p> <p>97%</p> <p>96%</p> <p>100%</p>	<p>Francisella sp. TX077308, complete genome</p> <p>Francisella sp. TX077308, complete genome</p> <p>Francisella sp. TX077308, complete genome</p> <p>Francisella sp. TX077308, complete genome</p> <p>Francisella sp. TX077308, complete genome</p> <p>Francisella sp. TX077308, complete genome</p> <p>Francisella sp. TX077308, complete genome</p> <p>Francisella sp. TX077308 complete genome</p>	<p>287</p> <p>276</p> <p>248</p> <p>237</p> <p>226</p> <p>226</p> <p>213</p> <p>207</p>	<p>92%</p> <p>93%</p> <p>85%</p> <p>88%</p> <p>86%</p> <p>83%</p> <p>86%</p> <p>92%</p>	<p>8,00E-74</p> <p>1,00E-70</p> <p>2,00E-62</p> <p>4,00E-59</p> <p>6,00E-56</p> <p>8,00E-56</p> <p>4,00E-52</p> <p>2,00E-50</p>	<p>78%</p> <p>82%</p> <p>88%</p> <p>86%</p> <p>90%</p> <p>87%</p> <p>91%</p> <p>88%</p>
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>contig102038 length=210 numreads=11 CTGTAATTTGCTAGACGAAGTTGAgAAAGCTCAGCAGATGATTTAACATACT TCTAC AAGTATTAGATGATGGTCTGCTTACAGATGGACAGGACGTACAGTGGATTTA AAAAACA CTGTAATGTTATGACTTCAAACCTGGTTCGCAATAAGATTCAAGAAATGCAGGG TGATG ACTATGAACTGTAAAATCTGCTGTGATGG >contig119829 length=186 numreads=8 TTAAATTCATTATCAACTACATAAGGATTTCCGACAGTAAATCTAAACAGAGC AGCA TTACCTTCAACATGCATGATTATCAGGAATAGACATTCACCAACTTACCCAT ACCT TTCAITTTGCCGAAACGTTGGAAGTTAAGAAGCATGGCAAAATGATGCAATAAT GCAACA CCTTCA >contig139909 length=167 numreads=7 ACCAACAACATTCCCTAAAGCATGATAGTGGTTCTAAaCctGCTTCTTGATCCA ACT ATCGATAACAGGAATAATTTGCTGTCTTTGCTCAAAAACAGGcGAGTAACTC CCCT TTCTGATGAGCTAAAAGTCGAGCTGATCAAAGTACTTTTTAACT >contig164444 length=145 numreads=7 ATTATTAGTCAATAATCATTATGATCATTAGATTCAAAGTTATAAAaGATTTCC AAAT AAAGGAAGATACAAAGTAATAGTACCTCTGGGCTTAGTAGCTTTTTATCAAAA GAGGG TTTAGTAATGTAAGTAAATGAACT >contig182212 length=129 numreads=7 TTATTCAAGTCAACAGAAGATTAGTTGGTGTGGTGGAGAATAAATGTATCTC CTAAT GCTGTTAATGTGATCTCTGATCATGATGGATAGCAGTAAATCACTGCTCCAC ATAGT CACCTAAGA >contig92296 length=226 numreads=10 CAAAAGCTGGAGATTAGATTATTTTTATTGCTGGAGAAAAGATAGCAGAAG TAACAG AAACATTCAGCGGAATAACAGGTAAAGCAATCTCCACCATATTGGAGTTGTA TTATT CTGGTTCAACATGACTTACTGATTTACCTGATGCTCAGCATCAAAATGCAAA TTTCA TAAATGATTGTCAGCAGTATAATCCAATGGGATCATTTCAGCT >contig103984 length=207 numreads=10 TTTAATCGTTCTTCAAAGTCACCTCTAAaTTTTTGCACTGCTAGcaGTGCCCCATA TCT AAGGATAGTACTTTTTCCCTTtCCcTtCAGGAACTTCACTTTGATTATCCTTT GA GCTAAGCCCTTACTATAGCTGTTTACCTACCCCTGGCTCACCATTAGTACAG GATTA TTCTTAGTACGCTGTAATACTGT >contig90764 length=229 numreads=9 TAACAACACTTACGCCAGCCCTAGCTTTACCAAATTTGATTTTTCAcCtTCAACA AGTA TCACAACCTGAACCACTATACTACCCACTATAGCGATACCTGAGTATTCTAAA AGCAA CTAAAATCAGTGGTCAAATATACCAATGGTTCATAGATGGTAAAGGTGCCA TACCTA CGGTAGGAACCCCCATAAAGAATGCGGCTAAGCTAGAGCAGTTGTTCT	protein disaggregation chaperone [Francisella novicida] >gb EDN38479.1 hypothetical protein FTDG_01296 [Francisella novicida GA99-3548] bifunctional gluaredoxin/ribonucleoside- diphosphate reductase subunit beta [Francisella tularensis subsp. holarctica LVS] N-carbamoyl-L-amino acid hydrolase [Francisella sp. TX077308] outer membrane protein romA [Francisella sp. TX077308] N-carbamoyl-L-amino acid hydrolase [Francisella sp. TX077308] Alpha-glucosidase [Francisella cf. novicida 3523] >ref WP_014548203.1 alpha- glucosidase [Francisella novicida] >gb AEE26202.1 Alpha-glucosidase [Francisella cf. novicida 3523] protein disaggregation chaperone [Francisella philomiragia] >gb EET20631.1 chaperone clpB [Francisella philomiragia subsp. philomiragia ATCC 25015] major facilitator transporter [Francisella philomiragia] >gb EET20522.1 metabolite:H+ symporter [Francisella philomiragia subsp. philomiragia ATCC 25015]	140 140 130 114 92.4 88.6 141 137 133	140 130 114 92.4 88.6 141 137 133	87% 72% 84% 85% 82% 90% 86% 88%	2,00E-36 3,00E-34 7,00E-29 3,00E-21 2,00E-19 4,00E-37 1,00E-35 3,00E-35	96% 97% 95% 92% 98% 88% 97% 88%	Francisella sp. TX077308, complete genome Francisella sp. TX077308, complete genome Francisella sp. TX077308, complete genome Francisella sp. TX077308, complete genome Francisella sp. TX077308, complete genome Francisella sp. TX077308, complete genome Francisella sp. TX077308, complete genom	207 206 196 193 187 185 178 172	87% 72% 85% 86% 75% 91% 87% 83%	3,00E-50 1,00E-49 5,00E-47 5,00E-46 2,00E-44 1,00E-43 2,00E-41 1,00E-39	85% 87% 88% 90% 95% 81% 82% 81%
Contigs	Blastx	Max score	Score	Query Cover	e-value	Identity	Blastn	Score	Query Cover	e-value	Identity
>contig152012 length=156 numreads=7 GGTATTTCTGTGGTGTATAATGGCGAGCCAGTACTAGATCTTGACTATGATG AAGAC TCAAATGCTGAGACAGATATGAATGATGAATGAATCTGAAGGTGGTATGATT GAGATT CAAGGTACAGCAGAAGTAAAGCTTTTCAGAAGAA >contig198083 length=107 numreads=6 CTGTAAGTGGTGAATGTTCCGTAAGCTTCTGATCGTGGAGAAGCTGGIGA TAACG TTGGGTaCTAGTTCGTGGTCTTAAGAGAGATGATGTTGAGCGTGGT	ribonuclease PH [Francisella philomiragia] >gb EET20213.1 ribonuclease PH [Francisella philomiragia subsp. philomiragia ATCC 25015] translation elongation factor Tu [Francisella sp. TX077308]	102 71.2	102 71.2	88% 80%	6,00E-25 2,00E-13	94% 94%	Francisella sp. TX077308, complete genome Francisella sp. TX077308, complete genome	167 150	85% 78%	3,00E-38 2,00E-33	87% 92%

>contig163781 length=146 numreads=6 AATTAATACTCTGACGTAAACGCTAGCTTATGTAAACCCCTAAAGAGGAAACAAA TATTT GGTTTGATGCTTATGATTCCAAAGGTGCCAAAGATGTTGATAGTGCCTATGA GCTTA TGAACATATCATAGATCCTTATGTA >contig145874 length=161 numreads=6 ATAGTTAATCCTCAAAAACCAATAAACAACAAAGTATAGATGGAAAAATAAACAA TTCCA ACCAAGTTGCCATTAAGACAACCTGAGAACCAAGATTGCTaccTGCAAGTA AAGCC CCACCAATATTATGAGACATATCCACAAACCTAAGAAGAA >contig81334 length=248 numreads=8 GAGAAAAAGGGAACGCATAATACCTAaTGAAAAAATCTTTCTCAAGGATAT ATAAGA GTACGCATAAATGGCGAGTTTTATAACCTTGATGAGAGCACCCAGAATTAGAT CGCTAT AAGAAACATAATAGATAGTAGTGTGCATCGCTTAAACCTAAAAAGATAAT GACCCAG CGTATAGCTGAATCTATAGAAACGGCTTATAGACTGGGTAATGTTATTAAAG TTGCA AATATGAA	putrescine ABC transporter putrescine-binding protein PotF [Francisella sp. TX077308]	92.0	92.0	75%	1,00E-20	91%	Francisella sp. TX077308, complete genome	150	75%	4,00E-33	86%
>contig130219 length=176 numreads=7 CTCTTTGCTTTGTGCAAAATTTATAAACCTAACTTTCTCATGCTCAAAATCAAATTC ATC ATCAGTAAACCAACTCTTTTTTAGTTAGTTCAGCAGGTAAGAGTGAAGAGTAGA TCTCT TGCTAATCCATAGCTCGTAAGCCAACATCTTTTTGCTTATTATAAACCATAT >contig126294 length=180 numreads=10 CTATGATAAGTGCaaTGGCAGTTTTAAATGGCTTTGTTGGTATAAAATcATTCATA AGCT TTGGCCACTATATTTGATGAGTTACTGTGATGCActCAGTGGTGTAGCTAGTAT TATG GGACTGCAATGACATTAGTCAACCTATTGCTACTGTTATAGGATTACTTTAGTT GATG	excinuclease ABC subunit A [Francisella cf. novicida 3523] >ref WP_014547926.1 excinuclease ABC subunit A [Francisella novicida] >gb AEB28472.1 excinuclease ABC subunit A [Francisella cf. novicida 3523]	90.9	90.9	78%	8,00E-20	78%	Francisella sp. TX077308, complete genome	143	75%	7,00E-31	83%
>contig165644 length=144 numreads=6 AAAAGTACCTCACGCCCTTTGGGTAGTAAAGCCTCATCTATCTGCAATAAAA TTATA GATATTCGAAGGAGTAAATAGCATCGCTCGTCAAACTCAAAAACAAAC TATCAA CACAAATGCAACAAAGCAACTAC >contig55685 length=334 numreads=15 AAACCTGAGCCTCGTATTGCTTGAAGTAAAGAGTTTCAGCTTGGTCATCTGGT GATGT CCTAACGATAAATAGGAGCAGGGTAGTTAGCCATTTGTTCAAAAAAGCT ATTCGT TGCTGCTTCCCAAGCTTCAAACTTTCTCCTTAGTACTTTTCAAGTTTATGT GTA ATAAATGCGATATTGTTATCATCAAAATATTGTTACAATACTGTTGCCAATATT AGCA TCAGAGTGAATAGCATGGTTTATATATAGTATgATGGAAATTTAATTTCTTT GAAA ATATCAACTAATACGCTAGAGTCAATGCCACCAC >contig149397 length=158 numreads=10 CAAAGATTCTTCTTAAATCACCGTCAGTAAATATACCTAGTAGCTCATTGTTTCA GTAA TAAGAGTATTACCTATACCTTACTACTAATTTGCGATTTGCTTACGAATAGTG TCTG TTGGTTTATAGTGGGATTTCATTTCTCTACGCATA >contig74482 length=266 numreads=14 cccccttgcctCCTaCTATGTCGAGTAGGTAACCAGACTGCTCGTTGGGTTCC C CCCATTCGAAATCTCCGGATCATAGGTCATTTACCACCTAACGAgAAGCTTATCGC AGAT TAACACGTCCTTCTCGCTCTGAATGCCAAGGCACTCCGCCACTTGCACTTATTTT CTTA AGTCTATCTTACTAAATGTTAAATATCTCTATCTCATGCAAAATAATATTG GTGG AGCCTAGCGGGATGAAACCGCTGACC	Cyanophycin synthase [Francisella cf. novicida 3523] >ref WP_014548065.1 cyanophycin synthetase [Francisella novicida] >gb AEB28614.1 Cyanophycin synthase [Francisella cf. novicida 3523]	73.9	73.9	85%	2,00E-13	86%	Francisella sp. TX077308, complete genome	119	84%	1,00E-23	79%
>contig165644 length=144 numreads=6 AAAAGTACCTCACGCCCTTTGGGTAGTAAAGCCTCATCTATCTGCAATAAAA TTATA GATATTCGAAGGAGTAAATAGCATCGCTCGTCAAACTCAAAAACAAAC TATCAA CACAAATGCAACAAAGCAACTAC >contig55685 length=334 numreads=15 AAACCTGAGCCTCGTATTGCTTGAAGTAAAGAGTTTCAGCTTGGTCATCTGGT GATGT CCTAACGATAAATAGGAGCAGGGTAGTTAGCCATTTGTTCAAAAAAGCT ATTCGT TGCTGCTTCCCAAGCTTCAAACTTTCTCCTTAGTACTTTTCAAGTTTATGT GTA ATAAATGCGATATTGTTATCATCAAAATATTGTTACAATACTGTTGCCAATATT AGCA TCAGAGTGAATAGCATGGTTTATATATAGTATgATGGAAATTTAATTTCTTT GAAA ATATCAACTAATACGCTAGAGTCAATGCCACCAC >contig149397 length=158 numreads=10 CAAAGATTCTTCTTAAATCACCGTCAGTAAATATACCTAGTAGCTCATTGTTTCA GTAA TAAGAGTATTACCTATACCTTACTACTAATTTGCGATTTGCTTACGAATAGTG TCTG TTGGTTTATAGTGGGATTTCATTTCTCTACGCATA >contig74482 length=266 numreads=14 cccccttgcctCCTaCTATGTCGAGTAGGTAACCAGACTGCTCGTTGGGTTCC C CCCATTCGAAATCTCCGGATCATAGGTCATTTACCACCTAACGAgAAGCTTATCGC AGAT TAACACGTCCTTCTCGCTCTGAATGCCAAGGCACTCCGCCACTTGCACTTATTTT CTTA AGTCTATCTTACTAAATGTTAAATATCTCTATCTCATGCAAAATAATATTG GTGG AGCCTAGCGGGATGAAACCGCTGACC	Arabinose-proton symporter [Francisella cf. novicida 3523] >ref WP_014548791.1 MFS transporter [Francisella novicida] >gb AEE26810.1 Arabinose-proton symporter [Francisella cf. novicida 3523]	94.4	94.4	85%	3,00E-21	76%	Francisella sp. TX077308, complete genome	108	74%	2,00E-20	79%
>contig165644 length=144 numreads=6 AAAAGTACCTCACGCCCTTTGGGTAGTAAAGCCTCATCTATCTGCAATAAAA TTATA GATATTCGAAGGAGTAAATAGCATCGCTCGTCAAACTCAAAAACAAAC TATCAA CACAAATGCAACAAAGCAACTAC >contig55685 length=334 numreads=15 AAACCTGAGCCTCGTATTGCTTGAAGTAAAGAGTTTCAGCTTGGTCATCTGGT GATGT CCTAACGATAAATAGGAGCAGGGTAGTTAGCCATTTGTTCAAAAAAGCT ATTCGT TGCTGCTTCCCAAGCTTCAAACTTTCTCCTTAGTACTTTTCAAGTTTATGT GTA ATAAATGCGATATTGTTATCATCAAAATATTGTTACAATACTGTTGCCAATATT AGCA TCAGAGTGAATAGCATGGTTTATATATAGTATgATGGAAATTTAATTTCTTT GAAA ATATCAACTAATACGCTAGAGTCAATGCCACCAC >contig149397 length=158 numreads=10 CAAAGATTCTTCTTAAATCACCGTCAGTAAATATACCTAGTAGCTCATTGTTTCA GTAA TAAGAGTATTACCTATACCTTACTACTAATTTGCGATTTGCTTACGAATAGTG TCTG TTGGTTTATAGTGGGATTTCATTTCTCTACGCATA >contig74482 length=266 numreads=14 cccccttgcctCCTaCTATGTCGAGTAGGTAACCAGACTGCTCGTTGGGTTCC C CCCATTCGAAATCTCCGGATCATAGGTCATTTACCACCTAACGAgAAGCTTATCGC AGAT TAACACGTCCTTCTCGCTCTGAATGCCAAGGCACTCCGCCACTTGCACTTATTTT CTTA AGTCTATCTTACTAAATGTTAAATATCTCTATCTCATGCAAAATAATATTG GTGG AGCCTAGCGGGATGAAACCGCTGACC	Rhamnogalacturonide transporter RhiT [Francisella cf. novicida 3523] >ref WP_014548204.1 Rhamnogalacturonide transporter RhiT [Francisella novicida] >gb AEE26203.1 Rhamnogalacturonide transporter RhiT [Francisella cf. novicida 3523]	70.1	70.1	52%	2,00E-12	97%	Francisella sp. TX077308, complete genome	106	62%	7,00E-20	84%
>contig165644 length=144 numreads=6 AAAAGTACCTCACGCCCTTTGGGTAGTAAAGCCTCATCTATCTGCAATAAAA TTATA GATATTCGAAGGAGTAAATAGCATCGCTCGTCAAACTCAAAAACAAAC TATCAA CACAAATGCAACAAAGCAACTAC >contig55685 length=334 numreads=15 AAACCTGAGCCTCGTATTGCTTGAAGTAAAGAGTTTCAGCTTGGTCATCTGGT GATGT CCTAACGATAAATAGGAGCAGGGTAGTTAGCCATTTGTTCAAAAAAGCT ATTCGT TGCTGCTTCCCAAGCTTCAAACTTTCTCCTTAGTACTTTTCAAGTTTATGT GTA ATAAATGCGATATTGTTATCATCAAAATATTGTTACAATACTGTTGCCAATATT AGCA TCAGAGTGAATAGCATGGTTTATATATAGTATgATGGAAATTTAATTTCTTT GAAA ATATCAACTAATACGCTAGAGTCAATGCCACCAC >contig149397 length=158 numreads=10 CAAAGATTCTTCTTAAATCACCGTCAGTAAATATACCTAGTAGCTCATTGTTTCA GTAA TAAGAGTATTACCTATACCTTACTACTAATTTGCGATTTGCTTACGAATAGTG TCTG TTGGTTTATAGTGGGATTTCATTTCTCTACGCATA >contig74482 length=266 numreads=14 cccccttgcctCCTaCTATGTCGAGTAGGTAACCAGACTGCTCGTTGGGTTCC C CCCATTCGAAATCTCCGGATCATAGGTCATTTACCACCTAACGAgAAGCTTATCGC AGAT TAACACGTCCTTCTCGCTCTGAATGCCAAGGCACTCCGCCACTTGCACTTATTTT CTTA AGTCTATCTTACTAAATGTTAAATATCTCTATCTCATGCAAAATAATATTG GTGG AGCCTAGCGGGATGAAACCGCTGACC	tRNA(Ile)-lysine synthetase [Francisella cf. novicida 3523] >ref WP_014548610.1 tRNA(Ile)-lysine synthetase [Francisella novicida] >gb AEE26621.1 tRNA(Ile)-lysine synthetase [Francisella cf. novicida 3523]	134	134	91%	5,00E-35	68%	Francisella sp. TX077308, complete genome	93.5	41%	1,00E-15	78%
>contig165644 length=144 numreads=6 AAAAGTACCTCACGCCCTTTGGGTAGTAAAGCCTCATCTATCTGCAATAAAA TTATA GATATTCGAAGGAGTAAATAGCATCGCTCGTCAAACTCAAAAACAAAC TATCAA CACAAATGCAACAAAGCAACTAC >contig55685 length=334 numreads=15 AAACCTGAGCCTCGTATTGCTTGAAGTAAAGAGTTTCAGCTTGGTCATCTGGT GATGT CCTAACGATAAATAGGAGCAGGGTAGTTAGCCATTTGTTCAAAAAAGCT ATTCGT TGCTGCTTCCCAAGCTTCAAACTTTCTCCTTAGTACTTTTCAAGTTTATGT GTA ATAAATGCGATATTGTTATCATCAAAATATTGTTACAATACTGTTGCCAATATT AGCA TCAGAGTGAATAGCATGGTTTATATATAGTATgATGGAAATTTAATTTCTTT GAAA ATATCAACTAATACGCTAGAGTCAATGCCACCAC >contig149397 length=158 numreads=10 CAAAGATTCTTCTTAAATCACCGTCAGTAAATATACCTAGTAGCTCATTGTTTCA GTAA TAAGAGTATTACCTATACCTTACTACTAATTTGCGATTTGCTTACGAATAGTG TCTG TTGGTTTATAGTGGGATTTCATTTCTCTACGCATA >contig74482 length=266 numreads=14 cccccttgcctCCTaCTATGTCGAGTAGGTAACCAGACTGCTCGTTGGGTTCC C CCCATTCGAAATCTCCGGATCATAGGTCATTTACCACCTAACGAgAAGCTTATCGC AGAT TAACACGTCCTTCTCGCTCTGAATGCCAAGGCACTCCGCCACTTGCACTTATTTT CTTA AGTCTATCTTACTAAATGTTAAATATCTCTATCTCATGCAAAATAATATTG GTGG AGCCTAGCGGGATGAAACCGCTGACC	arabinose phosphate isomerase [Francisella tularensis subsp. tularensis SCHU S4]	87.8	87.8	81%	2,00E-19	77%	Francisella sp. TX077308, complete genome	62.1	20%	2,00E-06	95%
>contig165644 length=144 numreads=6 AAAAGTACCTCACGCCCTTTGGGTAGTAAAGCCTCATCTATCTGCAATAAAA TTATA GATATTCGAAGGAGTAAATAGCATCGCTCGTCAAACTCAAAAACAAAC TATCAA CACAAATGCAACAAAGCAACTAC >contig55685 length=334 numreads=15 AAACCTGAGCCTCGTATTGCTTGAAGTAAAGAGTTTCAGCTTGGTCATCTGGT GATGT CCTAACGATAAATAGGAGCAGGGTAGTTAGCCATTTGTTCAAAAAAGCT ATTCGT TGCTGCTTCCCAAGCTTCAAACTTTCTCCTTAGTACTTTTCAAGTTTATGT GTA ATAAATGCGATATTGTTATCATCAAAATATTGTTACAATACTGTTGCCAATATT AGCA TCAGAGTGAATAGCATGGTTTATATATAGTATgATGGAAATTTAATTTCTTT GAAA ATATCAACTAATACGCTAGAGTCAATGCCACCAC >contig149397 length=158 numreads=10 CAAAGATTCTTCTTAAATCACCGTCAGTAAATATACCTAGTAGCTCATTGTTTCA GTAA TAAGAGTATTACCTATACCTTACTACTAATTTGCGATTTGCTTACGAATAGTG TCTG TTGGTTTATAGTGGGATTTCATTTCTCTACGCATA >contig74482 length=266 numreads=14 cccccttgcctCCTaCTATGTCGAGTAGGTAACCAGACTGCTCGTTGGGTTCC C CCCATTCGAAATCTCCGGATCATAGGTCATTTACCACCTAACGAgAAGCTTATCGC AGAT TAACACGTCCTTCTCGCTCTGAATGCCAAGGCACTCCGCCACTTGCACTTATTTT CTTA AGTCTATCTTACTAAATGTTAAATATCTCTATCTCATGCAAAATAATATTG GTGG AGCCTAGCGGGATGAAACCGCTGACC	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome ribosomal rRNA						Francisella tularensis subsp. holarctica PHIT-FT049, complete genome ribosomal rRNA	1111	90%	4,00E-99	92%

>contig75395 length=263 numreads=9 GTCTCAGTCAACATCTAGAGGTAGAATTACTGCTCGTCAAATCGAAGCAGGAA GAAGAG CTATTAACCGTCATGTTAAGCGTGGTGAAGGTTGGATCAGAATTTTCCAGA CAAGC CTATTACTAAGAAACCTCTTGAaGTTCTGTATGGTAAAGTAAaGGTTCGGTTGA GTATT GGGTGCTCAAATCAACCAGTCTGTACTATATGAATAACTGGTGTAAAG AAGAGC TAGCACGTGAAGCTTCCAGAGA >contig46885 length=388 numreads=16 TTCTACTATAGACAATTACATAGCAATCTAAAATGATAAAAATAAATAAGATT CACT AAACTTTAACTAAAATGATCAAAGTACTCATTAAACGCAAATGGTATCCGTGC AGCTA CTCGTaaGGGTTTTGGGATTTGGTTCAAACTCAAGATATCGACTTTTTATGTATC CAAG AAACAAAGGCTCAATTTCACTCACTGAGGAGATAGTCAGTACTTCCCGAAG GTTATC ATTATGACTTTAAAGATGCTGTTAAAAAGGCTATAGTGGTACTGCTATTATGC AAAGA AAAAAACCCTAAAAGTTATCAAAGAGCTTGGGTTGACTGGGCTGATAATGAAG GTCGTT ATATTCAATTTGATTATGAGAAtttAG >contig100814 length=212 numreads=10 TATAACTTTTCTATAAGGTGCTTCTAAGAAACCATAAATCATTACACGACATAAC TTGC CAATGAGTTAATTAGACCAATATTGGACCTCTGGAGTTCAATCGGACATAAT CTACC ATAGTGAGTAGCATGATACACGCACTTCAAAGCCTGCTCTATCTAGATAAAC CACC TGGGCTTAAAGCTGAGATTCTACGCTTATGCG >contig89845 length=230 numreads=9 ATCTCTCTACCAATGCAAACCAATTGGCTCCATACCCATAGACTCTAAAGATA CCGT ACCTGCTAGCACAAATCAATCAGACCATGAAACAGCATACCGTATTTTTTTTA ATTGG CCATAAAAGTTGACGGGCTTTATCAAGGTTTAcATTATCTGGCCAGCTGTTAAAT GGAGA GAACCTTTGTTGGCCACGGTTAGCTCTCCACGACCATCAGATACTCTAT >contig137266 length=169 numreads=6 TACAAAACCTGCTGATTACCTAATGGTAAATCAGTACCAGAAAGTTTTGTATCA GGCAA CCATAAAATATAGCAAAATGGAGCGTAAACAAAAGTTAATAAGAACTATGA GCGTCG TAAAGATTTAATGAAGTGCCTATGCCTACCCAGAAGATAAGCAATTA >contig116524 length=190 numreads=6 AATGTAAATaacTAGAGCAGGTTAGAGCTGTGATGGAAGCTGTGATAAAGTAA acTCA CCAGTTATCTCAAGGTTCTGACAGTGCAAGAAAGTACGAGGTGCTCCTTCA TCAGA CATCTTGATTAGTCTGCTATTGAAGAGTATCCACATCTGCTGTATATGCACCA AGAT CATGGTACAT >contig83550 length=243 numreads=10 ATCAATGATAAAGGTTACAATCTCTCAAATAATAGTAAATTAAGTGTATGTC ACTG AATGCTGACAAATTTCTCTAGCAGATGGTAAACATTAAGAAGAGTCAAGTTTTG ATCTA TCTCAACAAGATTTTCATCATATTATTTCAAAAATTGATTTTCAATGGCAAATGA TGAT ACAAGATATTCTCTTAACGGAATGTTTTGGGAAGTGAATGTAATCTTTAAGAG CGGTA TCT >contig153145 length=155 numreads=8 TTTCTGAGTGAACATCAATAAGCTTATGATCAAAGGCTTTTAATCTTATCTG ATTC TTTGATTTTTATAGCAATTTTATTTTATCTTAAATATGATGACGAGATTGG ATG ATATCTTCAGCGATATTGTTGGAACCTCAGCATAAaCcGGCGCGATGCAATCG TACTCATGACCGAATGGAATCAGTACC	50S ribosomal protein L16 [Halomonas] >gb EGP19020.1 50S ribosomal protein L16 [Halomonas sp. TD01] >gb EHA14395.1 50S ribosomal protein L16 [Halomonas sp. HAL1] >gb EHJ94064.1 50S ribosomal protein L16 [Halomonas boliviensis LC1] >gb EHK60828.1 50S ribosomal protein L16 [Halomonas sp. GFAJ- 1] >emb CDG52359.1 50S ribosomal protein L16 [Halomonas sp. A3H3] hypothetical protein [Francisella cf. novicida Fx1] >ref WP_014549715.1 hypothetical protein [Francisella novicida] >gb AEB27795.1 Exodeoxyribonuclease III [Francisella cf. novicida Fx1] DNA-directed RNA polymerase subunit beta [Francisella tularensis subsp. holarctica F92] >ref WP_015083882.1 DNA- directed RNA polymerase subunit beta [Francisella tularensis] >gb AFX71360.1 DNA-directed RNA polymerase subunit beta [Francisella tularensis subsp. holarctica F92] catalase/peroxidase HPI, partial [Francisella tularensis] hypothetical protein [Francisella cf. novicida Fx1] fructose-1,6-bisphosphate aldolase [Francisella noatunensis subsp. orientalis str. Toba 04] DNA polymerase III subunit beta [Francisella tularensis] >gb EET20098.1 DNA polymerase III [Francisella tularensis subsp. tularensis MA00-2987] 30S ribosomal protein S10 [Francisella tularensis subsp. holarctica LVS]	159	159	85%	1,00E-47	88%	Francisella tularensis subsp. holarctica F92, complete genome	313	85%	8,00E-82	89%
		196	196	76%	6,00E-60	88%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	292	72%	1,00E-75	85%
		156	156	80%	5,00E-42	99%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	278	79%	2,00E-71	91%
		154	154	91%	7,00E-45	96%	Francisella tularensis subsp. holarctica F92, complete genome	248	91%	2,00E-62	86%
		107	107	83%	6,00E-27	84%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	215	82%	1,00E-52	90%
		133	133	80%	1,00E-35	98%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	191	80%	3,00E-45	85%
		145	145	89%	5,00E-40	83%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	183	87%	6,00E-43	80%
		55.1	55.1	32%	6,00E-08	96%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	187	65%	4,00E-44	89%

>contig67256 length=287 numreads=13 CAGATGGAAaGGCATTGTATTCTGCATTTTTCTCTTTATAGATAACtCAA TAA ACTCATCACCTAAAACACTTCAGCACCTAATGCTTCAAGCCCTCAAGATGTAT ATCAA AAGGTCTTTTTCTACTAAAACCTACAGCCTCTGGAAACCAATTTTACAGACTT TTTT GCTTTAGCATCGCTCTAGAAGCATTAGTGAACAACGAGTTTTGTGTTGATT ACCAC ATAACTCTAACGTATCCTTTGTAATTTACTTGTATCTATAGCTACA >contig116293 length=191 numreads=6 AATCTCTGTTAGAGATTTCTACCTAAATAGGTATTTTCATCAACTGTGACTCAG AATA CTGTACCAAAATCACCAAGATACCTGATATttCAGCTCTAAACAGTTAGAAGATC TAAC AGTAAGCTCTAAATCATCAATTGGTTTTAGTAACATTGGTCAATATTAGAATCC GCCAA AGGATCCCCG >contig81323 length=247 numreads=9 TATAGATGCAGAAGCTAGTGATATAACTATCGAGATACAAGAGGGCGGTAAGT CATTAT TCGTATAAGAGATAATGGTAAAGGATTTCAAAGATGATTTAGCACTAGCACT AGCAC TCATGCTaCAAGTAAGGTTTTAATCTTGATGAGCTAgAATCTGATAGTATG GGTTT TCGTGGCAGGCTTAGCAAGTATTGGTTCTGTTGCAAAGTTAAGATAATCTCA AAACA cATAAGT >contig170585 length=140 numreads=7 AAGATACGAATCTATAGCAAATGCTGATTTAAaCGAAGGTGATGCTGATTATGC AATCAA AGTTGATTTGATAAAGATGCAAAAACATAACTGTTAGCGATAATGtTaTCGGT ATGAC TGAAGAAGGTTATCGAAA >contig140423 length=166 numreads=6 TAAGTTTAAGTTCATTAAACATTGAACAAAATAGCGCCATATTTGATTAAAC AGATG ATCTtttHGATATAAATCACCAGAATCTGGTTATCTCAGTATAGAAAGACCA ATAA GCCAGTACAAGAAACATCCCCTATATCCTTCAAAGATATCCTTT >contig185854 length=125 numreads=6 CGACAACACCCATAAAATGTAAGTGGTATAAATTTTTCCAACCTAAACGCAT AATTT GGTCATATCTGTATCTGGGTAAGTAGCTCTTATCCATAAAAACATAAACATAAA TATAC CTGTT >contig152091 length=156 numreads=7 TTtCAAATTTGGTTTTATATAGTTACCATCTTTGCAATAGCAGATGCTCTCG CAAC TAGTTGCATATCAGTAGCATTACACATAACAAAAGATAATGTAGCAAGTTGG AAATC ACCCCACTTATCTTAAACAGGCACAAATCCTTCTCG >contig85599 length=239 numreads=12 TATTCCACCCTCTtttAGGAAGCTCTGTAATCTGTTGATATGCTCCAATATGTT GAT TAGATATTACAAAATCTCTAACAGCACCTTCGCCACCATTTTTGACATCTTA CATC AGCATAATCTTAAACAATATCCATAGAATCGCTGGAGCTGCAGATATCCCAACT TTATT CATAAGAGTTATATCAGGCAATCATACCCATATAAGCAATTTGTGAATCGTTG AGAC >contig110799 length=198 numreads=7 TTCTTTTTCAAGATGATTCGTAACACTACAAATTGCTCACCTGAAGGTGACTTT CTGC ATACAAAGATAATGcTCTGTGATAGAGGGTCAACGGCTCAAAGGTTTTATAG CAACC TGAAAACAATGTTATAACTTCATCAAGAAGAAGTTGATATCTTAATGAAGGTT GAGAC TCACAATCACCTACAGC	UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Francisella tularensis] >gb EBA52105.1 UDP-N- acetylglucosamine 1- carboxyvinyltransferase [Francisella tularensis subsp. holarctica 257]	166	166	86%	2,00E-48	81%	Francisella tularensis subsp. holarctica F92, complete genome	182	68%	2,00E-42	81%
DNA-directed RNA polymerase subunit alpha [Francisella noatunensis]	122	122	82%	9,00E-32	94%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	176	71%	8,00E-41	86%	
DNA mismatch repair protein [Francisella tularensis subsp. tularensis SCHU 54]	135	135	82%	4,00E-35	84%	Francisella tularensis subsp. holarctica F92, complete genome	182	71%	2,00E-42	82%	
chaperone protein HtpG [Francisella sp. TX077308] >ref WP_013922041.1 heat shock protein 90 [Francisella sp. TX077308] >gb AEI35188.1 Chaperone protein HtpG [Francisella sp. TX077308]	83.6	83.6	77%	4,00E-17	87%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	167	69%	3,00E-38	91%	
hypothetical protein [Francisella philomiragia] >gb EET1254.1 conserved hypothetical protein [Francisella philomiragia subsp. philomiragia ATCC 25015]	110	110	87%	2,00E-27	93%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	163	88%	5,00E-37	84%	
NADH dehydrogenase I subunit H [Francisella tularensis subsp. mediasiatica FSC147]	85.9	85.9	71%	8,00E-19	95%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	150	68%	3,00E-33	90%	
Cell division protein FtsI/penicillin-binding protein [Francisella noatunensis subsp. orientalis str. Toba 04] >ref WP_014715143.1 cell division protein [Francisella noatunensis] >gb AFJ43612.1 Cell division protein FtsI/penicillin-binding protein [Francisella noatunensis subsp. orientalis str. Toba 04]	104	104	75%	1,00E-24	92%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	139	61%	9,00E-30	87%	
3-deoxy-D-manno-octulosonate 8- phosphate phosphatase [Francisella cf. novicida 3523]	115	115	85%	4,00E-30	65%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	143	60%	1,00E-30	82%	
phosphoribosylformylglycinamide synthase [Francisella tularensis subsp. holarctica]	119	119	78%	8,00E-29	85%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	130	59%	6,00E-27	83%	

>contig134387 length=172 numreads=8 AAAATACTGTAACACAGTAAAGTTGATAATTCAAATGCCATGCATCACCTGC AGTTA GAAAGCTTGAAGAATCTTGAATGAAACCAAGCAAGTAAAGCGCACTGGTC GCAAG GTAGAGTTCAAAAAGATTGTATAACTATATAAAAATGCTGTAACACA	dihydropolipoamide acetyltransferase component of pyruvate dehydrogenase complex [Francisella sp. TX077308] >ref WP_013922551.1 dihydropolipoamide acetyltransferase [Francisella sp. TX077308] >gb AEI35711.1 Dihydropolipoamide acetyltransferase component of pyruvate dehydrogenase complex [Francisella sp. TX077308] cell division protein FtsW [Francisella sp. TX077308] >ref WP_013923546.1 cell division protein FtsW [Francisella sp. TX077308] >sp F8GAB4.1 FTSW_FRAST RecName: Full=Lipid II flippase FtsW; AltName: Full=Cell division protein FtsW >gb AEI36717.1 Cell division protein FtsW [Francisella sp. TX077308]	100	100	75%	1,00E-23	88%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	126	73%	7,00E-26	80%
>contig146319 length=160 numreads=9 CCTATTCACCTCTGGTTGTATAGCTATACTTTGCTGATGCAACAGATTTGGT TCT ACAGTgTTATATCAATATGTGCTCTGGCATGCTTTTTGTTGGTGAATAAAGT TCAA TGGTATGGTTTACTTATTGTTGCTATGATAccAATGGCTG >contig108310 length=201 numreads=8 GCAAAAGTATAAAAGTATCGCTTTGCATATTGACTGTTCAACTAGGAAGCAAAA TATCGA TCAAAAATATATTGATGCTTTAAATAGTGTGCAAAAGAAAGTTGAACTCTGAA ATGAT ATATTGTTGGTTTTGCTGGTGAATAAGGCTTTAGTGTACCGGAGTAAATGCT AGTAG TTTATCGGGATTGCAGTCTCA >contig59621 length=316 numreads=10 AATTATGAATATTGTATGGGTACTTACGCTGCTGATTTTATGATCTTAAAA TAAT ATACTATCCACCTTAGCTAAAATAGCAGGGCGTTTAAAGCAAGCTGGTAAATTT TAATC AAAACCTCACATCAAAACCATAGTACTAACTATGTTTTCTTAATGATAGCCA TCTA CTACTATCACATAaGCACACCAAAAATACTAAATTTTAGTGGAGTtATTAGATG ATTT ATTAcTTTGTCAAAGCAAGTAAATAATCAAGCTAGTACTGCAAAATATAAA CCCT TTAGGCTACTTTATAA	4Fe-4S ferredoxin [Francisella tularensis] >gb EBA52400.1 4Fe-4S ferredoxin, FAD dependent [Francisella tularensis subsp. holarctica 257]	92.0	92.0	85%	1,00E-20	85%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	122	64%	8,00E-25	85%
>contig134628 length=172 numreads=6 GACTTATGGTCTTTTGGAAAGTTTTGAATAGCTTAGCTGATGGCCCTGGCGATT CCATa gAAAGAGCAAGaAcAAGAGGACCGACTAAAGCGTcATCAAGCACTCAAAGTCA GTTCTC TtAaTTGCTAAACGTGCTAAGTTGTTGGTCAACAACCTTAAATAAACTCCAG >contig96801 length=218 numreads=12 AAAGGCGCAAAATTTTGAATATACTCTTTTTCAACCTTTGTTATTTGCCATTTT TCC AGTcaGTAACCTCTCAGAAAGATCAATTTTCATCTTCTACAGTGAAGCTTTTTCA TGCT TAACCGTTAGTCAACAGCCCATGGATACAAAAAGGTTTATAAGTTTTGAAG CAGTAG TTAATGATGAGCCTTAACCTGATTAATAACCTCACCA	50S ribosomal protein L10 [Francisella tularensis subsp. mediasiatica FSC147] >ref WP_012429128.1 50S ribosomal protein L10 [Francisella tularensis] >sp B25FD4.1 RL10_FRATM RecName: Full=50S ribosomal protein L10 >gb ACD30287.1 50S ribosomal protein L10 [Francisella tularensis subsp. mediasiatica FSC147]	103	103	82%	1,00E-25	84%	Francisella tularensis subsp. mediasiatica FSC147, complete genome	224	81%	2,00E-55	91%
>contig87468 length=235 numreads=10 TGCGTTTATTTTACTGGCACATATATTTTGAATAATAATCTGGCACAGCA ACCT TGTTATAACCGATAGTTTATATACTTTTGTCTTTTATATATATGACCGTGTATACA CAT AAATACTATCATACATATTTGCCAGATTCTCTCATCTGTTCTAATCTTTCCCAAC CTT GCCTATTTAAGCCCGCTTTTGTGGCAGCATATTTGATGATAAAAATGATTATC >contig106923 length=201 numreads=8 ATGCTCAGCATTAGCTATAGCTGAATTAAGAACTCCTTAATTAGCACAGCAGCT TTTTT GTACTGAAGTCAAAGATTGATAGCTTCTACAGGTAGTCTCTGATTTGAT CAGC AACTAACCTACACTTTTGGAGTGAGATcTtgCAAAttttAAATTTAGCTTGTACTCC AT AAATACCTCAACTATTCTTC	bifunctional gluaredoxin/ribonucleoside- diphosphate reductase subunit [Francisella noatunensis subsp. orientalis str. Toba 04]	142	142	75%	2,00E-38	96%	Francisella tularensis subsp. mediasiatica FSC147, complete genome	222	76%	1,00E-54	85%
>contig87468 length=235 numreads=10 TGCGTTTATTTTACTGGCACATATATTTTGAATAATAATCTGGCACAGCA ACCT TGTTATAACCGATAGTTTATATACTTTTGTCTTTTATATATATGACCGTGTATACA CAT AAATACTATCATACATATTTGCCAGATTCTCTCATCTGTTCTAATCTTTCCCAAC CTT GCCTATTTAAGCCCGCTTTTGTGGCAGCATATTTGATGATAAAAATGATTATC >contig106923 length=201 numreads=8 ATGCTCAGCATTAGCTATAGCTGAATTAAGAACTCCTTAATTAGCACAGCAGCT TTTTT GTACTGAAGTCAAAGATTGATAGCTTCTACAGGTAGTCTCTGATTTGAT CAGC AACTAACCTACACTTTTGGAGTGAGATcTtgCAAAttttAAATTTAGCTTGTACTCC AT AAATACCTCAACTATTCTTC	DNA/RNA endonuclease G [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012279592.1 DNA/RNA endonuclease G [Francisella philomiragia] >gb ABZ86251.1 DNA/RNA endonuclease G [Francisella philomiragia subsp. philomiragia ATCC 25017]	158	158	85%	7,00E-45	94%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	226	84%	9,00E-56	84%
>contig106923 length=201 numreads=8 ATGCTCAGCATTAGCTATAGCTGAATTAAGAACTCCTTAATTAGCACAGCAGCT TTTTT GTACTGAAGTCAAAGATTGATAGCTTCTACAGGTAGTCTCTGATTTGAT CAGC AACTAACCTACACTTTTGGAGTGAGATcTtgCAAAttttAAATTTAGCTTGTACTCC AT AAATACCTCAACTATTCTTC	50S ribosomal protein L22 [Francisella philomiragia] >gb EET20366.1 50S ribosomal protein L22 [Francisella philomiragia subsp. philomiragia ATCC 25015]	116	116	82%	2,00E-31	93%	Francisella tularensis subsp. mediasiatica FSC147, complete genome	207	88%	3,00E-50	86%

<p>>contig97529 length=217 numreads=10 TAGTCAATTTAGGAAACAAAACGGTTTTATTATCTATAAACCCATAAAAGATAT ATTGG TCAAATTCGAAAGATACGATTATAACAGCATAGACCTTATTCTGTAACAGAT GGTGA AGCTGTACTGGgaTAGGAGATCAAGGTATAGTGGGAATGAATATCAGTATCGG TAAGAT TATGGTATATGTTGCTGCAAGTGGATTGACCCAGCT >contig62529 length=303 numreads=14 TGCTTTGTATGAGCATAAAATTTGTTCAAGGTGTTATCTGGGAAGTCTATTCT TCGA TCAGTGGGGCGTCAAGTTAGGCAAAGCTTAGCGACGCGAGTTGCTCTGTATGT GCAGTC CAGCTGCCAGTCACTCAATACGACAGTTCACCAATGGCCTACTCAACATTTT AAGGC TATTAATAAACCTGTTTATTATTACTGTAGCTTGTGTCAGCGTACCCCGCAA GCGTT GTGGGTATTTGCCGCAAAATTTATCATCATGAATGAATAAATGCGGCTGT AATCT TCA >contig95667 length=220 numreads=11 ATATATCTTAGCTCAATTAGACGAGCCTATAGATGAGAAAAAGAAAGCTTATA ATTCTG CAAAGATAAaTTTTGATCaGTTATTTCTATCTACTACTCGAGCGACTAATC GAGC AGGtgAGAAAATTAAGCTGATATCAAGCTGAGTTTGACACTGAAACTCAAA AAGAA ACCAAATCAAGAAAAGTIGACAGAGCTACAAGAGAAGTTA</p>	<p>malate dehydrogenase [Francisella tularensis subsp. mediasiatica FSC147] >ref WP_012429279.1 malate dehydrogenase [Francisella tularensis] >gb ACD30522.1 NAD-dependent malic enzyme [Francisella tularensis subsp. mediasiatica FSC147]</p>	135	135	84%	2,00E-35	89%	Francisella tularensis subsp. mediasiatica FSC147, complete genome	185	82%	1,00E-43	83%
<p>>contig137414 length=169 numreads=9 GTATGGAAGTGTCCATCTTTAGTGAGCTCACTCTGCTAATTTTTACCAGC TTTT TGGTCAAGCAAGGCTTATCCCACTCACTACTCCATAACACCTTGATAACATCC AACCA GCACCTCAAAACAGCCTGTAATCTTCAACAATATTACCATTACCGT</p>	<p>hypothetical protein EMIHURAF_446110 [Emiliania huxleyi CCMP1516] >gb EOD11446.1 cytosolic glucose-6-phosphate isomerase, partial CCMP1516]</p>	97.1	97.1	57%	3,00E-21	68%	Francisella tularensis subsp. mediasiatica FSC147, complete genome	75.0	25%	4,00E-10	82%
<p>>contig141718 length=165 numreads=9 AGTATTACAAGCATACACCCATTGGGTACCAATGTTTTACTGTACTTTTCT AAA GTTAGTAGTGCATCTACTAGCTACTACCGCTACTATAGGAGTACTGTTTGTAT GATC AACTGATGGACTAGCTCCAATAATATCAGCTCCACCAGCAACAGC</p>	<p>transposase [Francisella tularensis subsp. tularensis NE061598]</p>	129	129	85%	4,00E-36	89%	Francisella tularensis subsp. novicida U112, complete genome	307	86%	3,00E-80	92%
<p>>contig95191 length=221 numreads=10 CCATTCTCTCTATAGATATTGCTCTAAAACACTCTTAACCCACTCCATCTAGTA GAG CCATCATGACTATAAGGtATTTCCAACATGAAAGAATTTGTTAAATGGAACT TGAG CGATATATAAAATAGTCATATGGTTCATCTCCACAAATCAATTTTGCAAAATATC TAAA AAATAGTTTCTGGATTTCTAATGCTGATCTATAAATTT >contig80341 length=250 numreads=11 GAAAACAGGCGAGACTGATTCTTAAAAGCTAAGATAACAATTTTACTGACAGGT GGaGCT GGTCTGATATAGTCAAGCACAAATGCTATATcAaTACAGGtgATGGTATGG GTCTA CCCTTAaGAGTGCATCCCATTTGAGGATATGGAATTTTGGCAGTTCCATCAA CAGGT ATTGCTGGAGCTGGTACTTGTACTGAAGGGTCCCGTGGGAGGTGGTATC TTGCGT AATAAAGATG >contig109098 length=200 numreads=7 GCAGATGTATCAAAAATTTACAGCCAGGTAGTATTCTHATACAGTTGATTTGC TGCT ACGATATATCTTTTCTTCTCACTCTTTAGTATTAATCTAAAGAAACG CGG GATATCTTAAGAAATCTGGTCTTATTTCTGGTGAgaCTGGCGAGCAAA CTGCC AAATATATTGATGAGTAAT</p>	<p>Pyruvate dehydrogenase E1 component [Francisella cf. novicida 3523] >ref WP_014548839.1 pyruvate dehydrogenase [Francisella novicida] >gb AEE26858.1 Pyruvate dehydrogenase E1 component [Francisella cf. novicida 3523]</p>	107	107	83%	4,00E-25	89%	Francisella tularensis subsp. novicida U112, complete genome	159	83%	7,00E-36	84%
<p>>contig109098 length=200 numreads=7 GCAGATGTATCAAAAATTTACAGCCAGGTAGTATTCTHATACAGTTGATTTGC TGCT ACGATATATCTTTTCTTCTCACTCTTTAGTATTAATCTAAAGAAACG CGG GATATCTTAAGAAATCTGGTCTTATTTCTGGTGAgaCTGGCGAGCAAA CTGCC AAATATATTGATGAGTAAT</p>	<p>Protein-export membrane protein SecD [Francisella sp. TX077308] >ref WP_013923354.1 preprotein translocase subunit SecD [Francisella sp. TX077308] >gb AEI36523.1 Protein-export membrane protein SecD [Francisella sp. TX077308]</p>	100	100	85%	5,00E-23	85%	Francisella tularensis subsp. novicida U112, complete genome	147	87%	5,00E-32	83%
<p>>contig80341 length=250 numreads=11 GAAAACAGGCGAGACTGATTCTTAAAAGCTAAGATAACAATTTTACTGACAGGT GGaGCT GGTCTGATATAGTCAAGCACAAATGCTATATcAaTACAGGtgATGGTATGG GTCTA CCCTTAaGAGTGCATCCCATTTGAGGATATGGAATTTTGGCAGTTCCATCAA CAGGT ATTGCTGGAGCTGGTACTTGTACTGAAGGGTCCCGTGGGAGGTGGTATC TTGCGT AATAAAGATG >contig109098 length=200 numreads=7 GCAGATGTATCAAAAATTTACAGCCAGGTAGTATTCTHATACAGTTGATTTGC TGCT ACGATATATCTTTTCTTCTCACTCTTTAGTATTAATCTAAAGAAACG CGG GATATCTTAAGAAATCTGGTCTTATTTCTGGTGAgaCTGGCGAGCAAA CTGCC AAATATATTGATGAGTAAT</p>	<p>hypothetical protein FTN_1490 [Francisella novicida U112] >ref WP_003040476.1 hypothetical protein [Francisella novicida] >gb ABK90357.1 protein of unknown function [Francisella novicida U112] >gb EDX20130.1 hypothetical protein FTE_0876 [Francisella tularensis subsp. novicida FTE]</p>	141	141	89%	2,00E-39	88%	Francisella tularensis subsp. novicida U112, complete genome	289	89%	1,00E-74	90%
<p>>contig80341 length=250 numreads=11 GAAAACAGGCGAGACTGATTCTTAAAAGCTAAGATAACAATTTTACTGACAGGT GGaGCT GGTCTGATATAGTCAAGCACAAATGCTATATcAaTACAGGtgATGGTATGG GTCTA CCCTTAaGAGTGCATCCCATTTGAGGATATGGAATTTTGGCAGTTCCATCAA CAGGT ATTGCTGGAGCTGGTACTTGTACTGAAGGGTCCCGTGGGAGGTGGTATC TTGCGT AATAAAGATG >contig109098 length=200 numreads=7 GCAGATGTATCAAAAATTTACAGCCAGGTAGTATTCTHATACAGTTGATTTGC TGCT ACGATATATCTTTTCTTCTCACTCTTTAGTATTAATCTAAAGAAACG CGG GATATCTTAAGAAATCTGGTCTTATTTCTGGTGAgaCTGGCGAGCAAA CTGCC AAATATATTGATGAGTAAT</p>	<p>succinate dehydrogenase flavoprotein subunit [Francisella sp. TX077308] >ref WP_013922344.1 succinate dehydrogenase flavoprotein subunit [Francisella sp. TX077308] >gb AEI35501.1 Succinate dehydrogenase flavoprotein subunit [Francisella sp. TX077308]</p>	171	171	87%	3,00E-48	98%	Francisella tularensis subsp. novicida U112, complete genome	257	87%	3,00E-65	85%
<p>>contig109098 length=200 numreads=7 GCAGATGTATCAAAAATTTACAGCCAGGTAGTATTCTHATACAGTTGATTTGC TGCT ACGATATATCTTTTCTTCTCACTCTTTAGTATTAATCTAAAGAAACG CGG GATATCTTAAGAAATCTGGTCTTATTTCTGGTGAgaCTGGCGAGCAAA CTGCC AAATATATTGATGAGTAAT</p>	<p>preprotein translocase subunit SecY [Francisella cf. novicida 3523] >ref WP_014547570.1 preprotein translocase subunit SecY [Francisella novicida] >gb AEB28102.1 Preprotein translocase secY subunit [Francisella cf. novicida 3523]</p>	137	137	84%	9,00E-37	97%	Francisella tularensis subsp. novicida U112, complete genome	193	84%	8,00E-46	84%

<p>>contig87058 length=236 numreads=10 CAACTTCATTAAACAGTCTTTCTTTAGCTAAAGGTATACGATTGCAAGCCTAAAA ATAT GTGTGTCAACAGCATAACAGGTTTACCAAAAGCAGTATTTAAAACTACATTTGC TGTTT TACGACCAACACCGCTAGAGATATTAGACTATCAAAATCATCAGGAACAGTACT ATCAA ACITTTCTATCAAGTCTTTGCTAGTTTGGATTACATTTTGGCTTTTGTCTTATAT >contig87142 length=236 numreads=10 TTGAGCCTTTTAAAGAGCAACTGCAAGCACTCTTTAGTGTATTACAaTAGTAT CACT TTGCGTAAAAATCCATTTCTTGCTTCATAACCACTTTTGCACCTGTGCGA GGGC TAAGTTTTGTAGCGTTTTCAAGTCTTTCCATGAGCTTGGCATTAGATGCTC GTTG AGCCATTTCTTAGAGCCACCCCAACCGGATAATCCAACACCTGCTTACT A</p>	<p>Endonuclease III [Francisella cf. novicida 3523] >ref WP_014548454.1 endonuclease III [Francisella novicida] >gb AE26459.1 Endonuclease III [Francisella cf. novicida 3523]</p>	146	146	91%	7,00E-42	91%	Francisella tularensis subsp. novicida U112, complete genome	187	92%	4,00E-44	81%
<p>>contig152880 length=155 numreads=6 GGATTGATTTCTATATCAATATCATCACTCTCTGGTAAATAAACGCCGATG CAAAAT GAAGTGTGCTTTTACTGTTGAATCAAAAGGCGACTTTCTTACAAGTCTGTGAA TACCT GTCTCGGTGCGTAAACCAACCATTAAGCATATTCACC >contig94026 length=223 numreads=10 ATAGAGCAAGTCAAAATATCTAGTATATTGAGTATTTCTTTGACCAGATTC ACCCCT CTTTCTTAACTCAATAAATTCGGATAAACTGCTGACAGCATTGAAATATAATT GAGG CAGAAATATATGGCATCACACCAAGGCAAAATATACTCATTGAGTAAGAGCAC CACCCAG AGAACATATTAACATGCTCATCAAAACCCACTGTGCTGATGA >contig39042 length=466 numreads=20 GTGTTAGAGCATTATAAATGCTATCGGTTGTATTGCGACTTTTATAGTCTTGCTG ACAA TTATTGAGAGTAAATTTTTGAAGTGTGGATTGTTATTATAGCTATATCTATA ATCA TGTACTGCTGTATAAGGTAATAAAACACTATCTCATAAGAGAAACAAATTTGAC TATTA GTGTGTGATGAAGCAATAGTTAGTGGTAAATAGAGGACTAAGCCAAAG ATTGTTT TTTTAGTTTCTGATTCATAAAGGAACAATAGAAGCACTACAGTTGGCAAGAAA TTTTAT CTGATGATATACTCCAGTATATGTATCTGCAGATGAGAAAAAGATAGCTAAGA TCAAAG gACAATGGAAGGGCTAGCTTTTCAGGAAAGCTACTTATTTGAGACCAGTTTA TAATT CCTTCATCACTCTATTGTAATAATCTGCATAAAATGATTGCG >contig82784 length=244 numreads=11 TTGCAGAACACTCTATATGCCAACCTGGCGACCCATGGTGAATCCC AAGCAG GTTACCTCTTTAGCACTTTTCAAAGAAACAAAGTCCATAGGATTTTCTTAATA TCAG ATATTTCTACTCTGACCTTGTGTAGAGCTTCTATATTGTTACTAAGTTTAC CAT AGCCATCAAACCTTACTACAGGATAAAAAACATCACCATTTGGTacttGATGCA AAAC CTTT >contig101992 length=210 numreads=7 ATCACATGAAAATACCACTTTCAAGCTTCTCTGTAATTACATTATATAAGACC TAGG TCAACTATATTACAGGATTTCCAGGATCATAAACAGTCTTCTACTGATCCATAC TGCA TCCATATAATGAGTACACAGCTTAAATATTACTCTTCTACTGGGTATTTAAC TACC TGCTTACTATCGCATCAGCATCTTACCA</p>	<p>3-hydroxyacyl-CoA dehydrogenase [Francisella novicida] >gb ED290840.1 fusion of 3-hydroxyacyl-CoA dehydrogenase and enoyl-CoA hydratase [Francisella novicida FTG]</p> <p>peptide chain release factor 2 [Francisella sp. TX077308] >ref WP_013921950.1 peptide chain release factor 2 [Francisella sp. TX077308] >gb AEI35089.1 Peptide chain release factor 2 [Francisella sp. TX077308]</p> <p>preprotein translocase subunit SecY [Francisella novicida] >gb EDN35612.1 preprotein translocase [Francisella novicida GA99-3549]</p> <p>amino acid transporter [Francisella tularensis subsp. holarctica F92] >ref WP_015083892.1 amino acid transporter [Francisella tularensis] >gb AFX71477.1 amino acid transporter [Francisella tularensis subsp. holarctica F92]</p> <p>cysteinyl-tRNA synthetase [Francisella noatunensis subsp. orientalis str. Toba 04]</p> <p>conserved hypothetical protein [Francisella novicida] >gb EDN36094.1 conserved hypothetical protein [Francisella novicida GA99-3549]</p>	135	135	87%	9,00E-35	82%	Francisella tularensis subsp. novicida U112, complete genome	150	86%	5,00E-33	79%
		94.0	94.0	84%	1,00E-21	98%	Francisella tularensis subsp. novicida U112, complete genome	137	77%	3,00E-29	84%
		145	145	85%	1,00E-39	99%	Francisella tularensis subsp. tularensis WY96-3418, complete genome	257	85%	3,00E-65	88%
		233	233	92%	7,00E-71	74%	Francisella tularensis subsp. tularensis WY96-3418, complete genome	207	91%	6,00E-50	75%
		161	161	83%	3,00E-45	86%	Francisella cf. novicida 3523, complete genome	251	99%	2E-63	83%
		135	135	94%	4,00E-38	84%	Francisella tularensis TIGB03, complete genome	178	87%	2,00E-41	82%

<p>>contig71088 length=275 numreads=10 AATGCTTGCACAGCACCTATATCACACCAATAGAGCTAAAGTTTGC AAAAGAAA CCAAAG AAAAGTATATAACGGCTTTGGTATGCTCAGAAATTTCTGTAGAATGCTTTGCTA AATCT TGCAATTGCAACAAATTCATTTGTAACAATCTTTGTACCCATTATCTGGCTTGAAAG CATC ACCTCATTACCATGAATATTTAAAACCCATGCCAAAGGATAaaaTACATACCCCTAT AATT TGGGTAAACGTAATGCCGATGACATGTGAAAAAAT</p>	<p>Nucleoside permease nupC [Francisella cf. novicida 3523] >ref WP_014548943.1 nucleoside permease [Francisella novicida] >gb AEE26966.1 Nucleoside permease nupC [Francisella cf. novicida 3523]</p>	159	159	91%	1,00E-44	80%	Francisella tularensis subsp. holarctica PHIT-FT049, complete genome	165	86%	2,00E-37	78%
<p>>contig195357 length=112 numreads=7 ATATTTATttttAGATTACCTCCTGGTACGGGTGATATACAACAAATTTCAA AAA ATATGCCTGTTACAGGAGCTGTAATTGTAACACTACaCcACAAGATTTATCCTT</p>	<p>sodium:proton antiporter [Francisella philomiragia] >gb EET21499.1 conserved hypothetical protein [Francisella philomiragia subsp. philomiragia ATCC 25015]</p>	75.5	75.5	81%	3,00E-15	97%	Francisella tularensis TIGB03, complete genome	130	79%	3,00E-27	88%
<p>>contig132323 length=174 numreads=8 GCTTCATTATGTATTGTTGGTCTTTTCATGTTTTTCGGTGCATAAGCTTGATATAT GCC TCTGTGCATGCAACCGCTTTGcAAaTAATACTTACAAAACTAATTgTTtAGATGTT AGT TTAGTAGCCATAGATTAATAATAGAAACAAATTTAATACTAGTAATTATATCAGC</p>	<p>phage terminase small subunit [Francisella philomiragia subsp. philomiragia ATCC 25017] >ref WP_012280385.1 terminase [Francisella philomiragia] >gb AB287210.1 phage terminase, small subunit [Francisella philomiragia subsp. philomiragia ATCC 25017]</p>	91.7	91.7	56%	2,00E-21	95%	Francisella cf. novicida 3523, complete genome	222	73%	1,00E-54	90%