

SUPPORTING INFECTIOUS DISEASE RESEARCH

# Francisella tularensis subsp. tularensis, Strain SCHU S4, Gateway<sup>®</sup> Clone Set, Recombinant in Escherichia coli, Plate 1

## Catalog No. NR-19458

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#### Contributor:

Pathogen Functional Genomics Resource Center at the J. Craig Venter Institute

#### Manufacturer:

**BEI Resources** 

### **Product Description:**

The Francisella tularensis (F. tularensis) subsp. tularensis, strain SCHU S4, Gateway® clone set consists of 19 plates which contain 1693 sequence validated clones from F. tularensis subsp. tularensis, strain SCHU S4 cloned in Escherichia coli (E. coli) DH10B-T1 cells. Each open reading frame was constructed in vector pDONR™221 (Invitrogen™) with a native start codon and no stop codon. The sequence was validated by full length sequencing of each clone with greater than 1X coverage and a mutation rate of less than 0.2%. Detailed information about each clone is shown in Table 1.

Information related to the use of Gateway<sup>®</sup> Clones can be obtained from Invitrogen<sup>™</sup>. Recombination was facilitated through an attB substrate (attB-PCR product or a linearized attB expression clone) with an attP substrate (pDONR™221) to create an attL-containing entry clone. The entry clone contains recombinational cloning sites, attL1 and attL2 to facilitate gene transfer into a destination vector, M13 forward and reverse priming sites for sequencing and a kanamycin resistance gene for selection. Please refer to the Invitrogen™ Gateway<sup>®</sup> Technology Manual for additional details.

### **Material Provided:**

Each inoculated well of the 96-well plate contains approximately 60  $\mu L$  of  $\emph{E. coli}$  culture (strain DH10B-T1) in Luria Bertani (LB) Broth containing 50  $\mu g/mL$  kanamycin supplemented with 15% glycerol.

Note: Production in the 96-well format has increased risk of cross-contamination between adjacent wells. Individual clones should be purified (e.g. single colony isolation and purification using good microbiological practices) and sequence-verified prior to use. BEI Resources cannot confirm or validate any clone not identified on the plate information table.

## Packaging/Storage:

NR-19458 was packaged aseptically in a 96-well plate. The

product is provided frozen and should be stored at -80°C or colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze-thaw cycles should be avoided.

#### **Growth Conditions:**

Media:

LB Broth or Agar containing 50 µg/mL kanamycin.

Incubation

Temperature: *E. coli*, strain DH10B-T1 clones should be grown at 37°C.

Atmosphere: Aerobic

**Propagation**:

- Scrape top of frozen well with a pipette tip and streak onto agar plate.
- 2. Incubate the plates at 37°C for 18 to 24 hours.

#### Citation:

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: Francisella tularensis subsp. tularensis, Strain SCHU S4, Gateway® Clone Set, Recombinant in Escherichia coli, Plate 1, NR-19458."

## **Biosafety Level: 1**

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. Biosafety in Microbiological and Biomedical Laboratories. 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see www.cdc.gov/biosafety/publications/bmbl5/index.htm.

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#### References:

- Larsson, P., et. al. "The Complete Genome Sequence of Francisella tularensis, the Causative Agent of Tularemia." Nat. Genet. 37 (2005): 153-159. PubMed: 15640799.
- Pandya, G. A., et. al. "Whole Genome Single Nucleotide Polymorphism Based Phylogeny of *Francisella tularensis* and its Application to the Development of a Strain Typing Assay." <u>BMC Microbiology</u> 9 (2009): 213. PubMed: 19811647.

ATCC<sup>®</sup> is a trademark of the American Type Culture Collection.

Table 1: Francisella tularensis subsp. tularensis, Strain SCHU S4, Gateway® Clone Set, Plate 1 (ZFTKK)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
5426	A01	NT06FT0656	hypothetical protein	130	N/A	2
5432	A02	NT06FT1981	-	130	N/A	-
5436	A03	NT06FT0308	hypothetical protein	133	CAG44910.1	2
5442	A04	NT06FT1025	hypothetical protein	133	N/A	-
5444	A05	NT06FT1288	hypothetical protein	133	N/A	2
5446	A06	NT06FT1620	hypothetical protein	133	N/A	2
5448	A07	NT06FT1743	lipoprotein, putative	133	N/A	2
5450	A08	NT06FT0017	hypothetical protein	136	N/A	-
5452	A09	NT06FT0834	hypothetical protein	136	N/A	2
5453	A10	NT06FT1682	hypothetical protein	136	N/A	-
5457	A11	NT06FT0422	lipoprotein, putative	139	CAG45015.1	-
5460	A12	NT06FT0440	hypothetical protein	142	N/A	-
5462	B01	NT06FT0715	2-isopropylmalate synthase	145	CAG45272.1	-
5464	B02	NT06FT0835	hypothetical protein	145	N/A	-
5465	B03	NT06FT1166	hypothetical protein	145	N/A	1.848276
5467	B04	NT06FT0555	hypothetical protein	148	N/A	-
5470	B05	NT06FT0677	hypothetical protein	148	N/A	-
5472	B06	NT06FT0721	-	148	N/A	2.614865
5474	B07	NT06FT1605	hypothetical protein	148	N/A	-
5475	B08	NTL06FT0346	50S ribosomal protein L36	148	N/A	-
5478	B09	NT06FT0550	proton/peptide symporter family protein, putative	151	N/A	-
5480	B10	NT06FT1176	hypothetical protein	151	N/A	-
5481	B11	NT06FT1658	hypothetical protein	151	CAG46076.1	-
5484	B12	NT06FT1664	Second ORF in transposon ISC1395	151	N/A	=
5486	C01	NT06FT0548	hypothetical protein	154	N/A	=
5487	C02	NT06FT0675	hypothetical protein	154	CAG45234.1	-
5489	C03	NT06FT0843	hypothetical protein	154	N/A	-
5492	C04	NT06FT1220	hypothetical protein	154	N/A	2.649351
5494	C05	NT06FT1221	hypothetical protein	154	N/A	
5496	C06	NT06FT1615	hypothetical protein	154	N/A	-
5498	C07	NT06FT1294	general stress protein gsiB	157	N/A	-
5501	C08	NT06FT0113	hypothetical protein	163	N/A	-
5503	C09	NT06FT0830	hypothetical protein	163	CAG45370.1	-
5505	C10	NT06FT1619	hypothetical protein	163	N/A	-

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Clone         Well Position         Locus ID         Description (Gene name)         ORF Length Number         Accession Number           5510         C11         NT06FT0846         hypothetical protein         166         N/A           5513         D01         NT06FT1482         hypothetical protein         166         CAG45933.1           5515         D02         NT06FT1871         hypothetical protein         166         N/A           5517         D03         NTL06FT0870         hypothetical protein         166         N/A           5520         D04         NT06FT0263         ribosomal protein L34         169         CAG44869.1           5525         D05         NT06FT1215         hypothetical protein         169         N/A           5527         D06         NT06FT1700         IS1016 family transposase, degenerate         169         N/A           5529         D07         NT06FT0290         Iipoprotein, putative         172         CAG44895.1           5531         D08         NT06FT0961         conserved hypothetical protein         172         CAG45481.1           5533         D09         NT06FT1188         hypothetical protein         172         N/A           5535         D10         NT06FT0458 <th>Average Depth of Coverage  1.86747  1.674419</th>	Average Depth of Coverage  1.86747  1.674419
5513         D01         NT06FT1482         hypothetical protein         166         CAG45933.1           5515         D02         NT06FT1871         hypothetical protein         166         N/A           5517         D03         NTL06FT0870         hypothetical protein         166         N/A           5520         D04         NT06FT0263         ribosomal protein L34         169         CAG44869.1           5525         D05         NT06FT1215         hypothetical protein         169         N/A           5527         D06         NT06FT1700         IS1016 family transposase, degenerate         169         N/A           5529         D07         NT06FT0290         Ilipoprotein, putative         172         CAG44895.1           5531         D08         NT06FT0961         conserved hypothetical protein         172         CAG45481.1           5533         D09         NT06FT1188         hypothetical protein         172         N/A           5535         D10         NT06FT0458         Glucose-1-phosphate adenylyltransferase         175         N/A	Coverage  1.86747
5513         D01         NT06FT1482         hypothetical protein         166         CAG45933.1           5515         D02         NT06FT1871         hypothetical protein         166         N/A           5517         D03         NTL06FT0870         hypothetical protein         166         N/A           5520         D04         NT06FT0263         ribosomal protein L34         169         CAG44869.1           5525         D05         NT06FT1215         hypothetical protein         169         N/A           5527         D06         NT06FT1700         IS1016 family transposase, degenerate         169         N/A           5529         D07         NT06FT0290         lipoprotein, putative         172         CAG44895.1           5531         D08         NT06FT0961         conserved hypothetical protein         172         CAG45481.1           5533         D09         NT06FT1188         hypothetical protein         172         N/A           5535         D10         NT06FT0458         Glucose-1-phosphate adenylyltransferase         175         N/A	- - - 2
5515         D02         NT06FT1871         hypothetical protein         166         N/A           5517         D03         NTL06FT0870         hypothetical protein         166         N/A           5520         D04         NT06FT0263         ribosomal protein L34         169         CAG44869.1           5525         D05         NT06FT1215         hypothetical protein         169         N/A           5527         D06         NT06FT1700         IS1016 family transposase, degenerate         169         N/A           5529         D07         NT06FT0290         lipoprotein, putative         172         CAG44895.1           5531         D08         NT06FT0961         conserved hypothetical protein         172         CAG45481.1           5533         D09         NT06FT1188         hypothetical protein         172         N/A           5535         D10         NT06FT1684         -         172         N/A           5538         D11         NT06FT0458         Glucose-1-phosphate adenylyltransferase         175         N/A	- - - 2
5517         D03         NTL06FT0870         hypothetical protein         166         N/A           5520         D04         NT06FT0263         ribosomal protein L34         169         CAG44869.1           5525         D05         NT06FT1215         hypothetical protein         169         N/A           5527         D06         NT06FT1700         IS1016 family transposase, degenerate         169         N/A           5529         D07         NT06FT0290         lipoprotein, putative         172         CAG44895.1           5531         D08         NT06FT0961         conserved hypothetical protein         172         CAG45481.1           5533         D09         NT06FT1188         hypothetical protein         172         N/A           5535         D10         NT06FT1684         -         172         N/A           5538         D11         NT06FT0458         Glucose-1-phosphate adenylyltransferase         175         N/A	- - - 2
5520         D04         NT06FT0263         ribosomal protein L34         169         CAG44869.1           5525         D05         NT06FT1215         hypothetical protein         169         N/A           5527         D06         NT06FT1700         IS1016 family transposase, degenerate         169         N/A           5529         D07         NT06FT0290         lipoprotein, putative         172         CAG44895.1           5531         D08         NT06FT0961         conserved hypothetical protein         172         CAG45481.1           5533         D09         NT06FT1188         hypothetical protein         172         N/A           5535         D10         NT06FT1684         -         172         N/A           5538         D11         NT06FT0458         Glucose-1-phosphate adenylyltransferase         175         N/A	- 2 -
5525         D05         NT06FT1215         hypothetical protein         169         N/A           5527         D06         NT06FT1700         IS1016 family transposase, degenerate         169         N/A           5529         D07         NT06FT0290         lipoprotein, putative         172         CAG44895.1           5531         D08         NT06FT0961         conserved hypothetical protein         172         CAG45481.1           5533         D09         NT06FT1188         hypothetical protein         172         N/A           5535         D10         NT06FT1684         -         172         N/A           5538         D11         NT06FT0458         Glucose-1-phosphate adenylyltransferase         175         N/A	- 2 -
5527         D06         NT06FT1700         IS1016 family transposase, degenerate         169         N/A           5529         D07         NT06FT0290         lipoprotein, putative         172         CAG44895.1           5531         D08         NT06FT0961         conserved hypothetical protein         172         CAG45481.1           5533         D09         NT06FT1188         hypothetical protein         172         N/A           5535         D10         NT06FT1684         -         172         N/A           5538         D11         NT06FT0458         Glucose-1-phosphate adenylyltransferase         175         N/A	- 2 -
5527         D06         NT06FT1700         degenerate         169         N/A           5529         D07         NT06FT0290         lipoprotein, putative         172         CAG44895.1           5531         D08         NT06FT0961         conserved hypothetical protein         172         CAG45481.1           5533         D09         NT06FT1188         hypothetical protein         172         N/A           5535         D10         NT06FT1684         -         172         N/A           5538         D11         NT06FT0458         Glucose-1-phosphate adenylyltransferase         175         N/A	-
5529         D07         NT06FT0290         lipoprotein, putative         172         CAG44895.1           5531         D08         NT06FT0961         conserved hypothetical protein         172         CAG45481.1           5533         D09         NT06FT1188         hypothetical protein         172         N/A           5535         D10         NT06FT1684         -         172         N/A           5538         D11         NT06FT0458         Glucose-1-phosphate adenylyltransferase         175         N/A	-
5531         D08         NT06FT0961         conserved hypothetical protein         172         CAG45481.1           5533         D09         NT06FT1188         hypothetical protein         172         N/A           5535         D10         NT06FT1684         -         172         N/A           5538         D11         NT06FT0458         Glucose-1-phosphate adenylyltransferase         175         N/A	-
5533         D09         NT06FT1188         hypothetical protein         172         N/A           5535         D10         NT06FT1684         -         172         N/A           5538         D11         NT06FT0458         Glucose-1-phosphate adenylyltransferase         175         N/A	1.674419
5535         D10         NT06FT1684         -         172         N/A           5538         D11         NT06FT0458         Glucose-1-phosphate adenylyltransferase         175         N/A	1.074419
5538 D11 NT06FT0458 Glucose-1-phosphate adenylyltransferase 175 N/A	
adenylyltransferase 175 N/A	<del>-</del>
	-
5539 D12 NT06FT0471 ABL080Wp 175 N/A	1.577143
5541 E01 NT06FT1005 hypothetical protein 175 N/A	1.36
5544 F02 NT06FT1335 type I restriction-modification system	-
specificity subunit 175 N/A 5545 E03 NT06FT1837 hypothetical protein 175 N/A	1.874286
	2.876404
5551 E05 NT06FT1114 hypothetical protein 178 CAG45616.1	2.679775
5555 E06 NT06FT0626 hypothetical protein 181 N/A	1.762431
5557         E07         NT06FT1653         hypothetical protein         181         N/A	1.878453
5559 E08 NT06FT2081 conserved hypothetical protein 181 N/A	-
5561         E09         NT06FT0850         hypothetical protein         184         N/A	3.391304
5563         E10         NT06FT1107         hypothetical protein         184         N/A	1.880435
5566 E11 NT06FT1936 conserved hypothetical protein 184 N/A	2.695652
5573 E12 NT06FT0112 - 190 N/A	2
5575 F01 NT06FT1434 - 190 N/A	1.984211
5577         F02         NT06FT1831         hypothetical protein         190         CAG46228.1	2
5579         F03         NT06FT1843         ribosomal protein L33         190         CAG46237.1	2
5581 F04 NT06FT0097 hypothetical protein 193 N/A	2
5584 F05 NT06FT0137 oligopeptide ABC transporter, permease protein VC1093 193 N/A	2
5585 F06 NT06FT1988 cytosine specific DNA methyltransferase 193 N/A	2.875648
5587 F07 NT06FT1629 hypothetical protein 196 N/A	2.69898
5595 F08 NT06FT1140 hypothetical protein 199 CAG45641.1	1.673367
5601   F09   NT06FT1941   hypothetical protein   199   N/A	2
5604 F10 NTL06FT1051 hypothetical protein 199 N/A	2
5607 F11 NT06FT0668 Rubredoxin 205 CAG45228.1	1.843902
5609   F12   NT06FT0234   hypothetical protein   208   N/A	2.701923
5611 G01 NT06FT0292 conserved hypothetical protein 208 CAG44897.1	-
5614 G02 NT06FT1144 hypothetical protein 208 N/A	-
5615 G03 NT06FT1859 drug resistance transporter, Bcr/CflA family, putative 208 N/A	1.980769
5619 G04 NT06FT0580 type I restriction-modification system 211 N/A	2
5621 G05 NT06FT0643 hypothetical protein 211 N/A	2
5623 G06 NT06FT1714 transposase 211 N/A	1.824645
5626 G07 NT06FT0466 hypothetical protein 214 CAG45056.1	2.672897
5627 G08 NT06FT0678 hypothetical protein 214 CAG45236.1	2

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Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
5629	G09	NT06FT0831	hypothetical protein	214	N/A	2.691589
5633	G10	NT06FT0956	predicted CsgA,Rossman fold oxidoreductase	214	N/A	1.682243
5635	G11	NTL06FT1480	hypothetical protein	214	N/A	-
5641	G12	NT06FT1052	beta-hydroxybutyrate dehydrogenase	217	N/A	2.700461
5645	H01	NT06FT0074	hypothetical protein	220	CAG44702.1	2
5649	H02	NT06FT0230	small basic protein sbpA	223	N/A	2
5651	H03	NT06FT0479	hypothetical protein	223	CAG45066.1	2
5655	H04	NT06FT1118	unnamed protein product; similar to CA0541 IPF14574 Candida albicans IPF14574 unknown function, start by similarity	223	CAG45621.1	1.825112
5657	H05	NT06FT1143	hypothetical protein	223	CAG45644.1	2.64574
5665	H06	NT06FT2007	DNA-binding response regulator KdpE	226	N/A	2
5670	H08	NT06FT0255	hypothetical protein	229	CAG44860.1	2.310044
5671	H09	NT06FT0657	conserved hypothetical protein	229	N/A	2
5674	H10	NT06FT0870	DNA-3-methyladenine glycosylase I	229	N/A	2.358079
5675	H11	NT06FT0980	conserved hypothetical protein	229	N/A	2
5677	H12	NTL06FT1284	hypothetical protein	229	N/A	2.676856

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