

***Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 3**

**Catalog No. NR-19460**

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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® Clones can be obtained from [Invitrogen™](#). 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® Technology Manual](#) for additional details.

**Material Provided:**

Each inoculated well of the 96-well plate contains approximately 60 µL of *E. coli* culture (strain DH10B-T1) in Luria Bertani (LB) Broth containing 50 µg/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-19460 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:

1. 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 3, NR-19460."

**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/bmb15/index.htm](http://www.cdc.gov/biosafety/publications/bmb15/index.htm).

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**References:**

1. Larsson, P., et. al. "The Complete Genome Sequence of *Francisella tularensis*, the Causative Agent of Tularemia." *Nat. Genet.* 37 (2005): 153-159. PubMed: 15640799.
2. 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." *BMC Microbiology* 9 (2009): 213. PubMed: 19811647.

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**Table 1: *Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Plate 3 (ZFTKM)**

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
5883	A01	NT06FT0111	ISPg3, transposase	298	N/A	3.251678
5886	A02	NT06FT0504	Protein yggX	298	CAG45089.1	3.241611
5887	A03	NT06FT1763	ornithine cyclodeaminase, putative	298	N/A	3.255034
5889	A04	NT06FT0134	oligopeptide ABC transporter, permease protein	301	N/A	2.641196
5891	A05	NT06FT0782	ribosomal protein S15	301	CAG45331.1	3.275748
5893	A06	NT06FT1093	conserved hypothetical protein	301	N/A	3.239203
5895	A07	NT06FT1303	aldose 1-epimerase, putative	301	N/A	3.295681
5897	A08	NT06FT1391	bolA family protein	301	CAG45854.1	3.259136
5899	A09	NT06FT1641	conserved hypothetical protein	301	N/A	2.259136
5901	A10	NT06FT1739	mercuric reductase	301	N/A	3.282392
5904	A11	NT06FT0884	G-protein coupled receptor, putative	304	CAG45413.1	3.269737
5905	A12	NT06FT0958	conserved hypothetical protein	304	CAG45478.1	3.259868
5909	B01	NT06FT0098	-	307	N/A	3.270358
5911	B02	NT06FT0617	Uncharacterized BCR, COG1937 family	307	CAG45187.1	3.296417
5913	B03	NT06FT0701	DNA-binding protein hu-beta	307	CAG45260.1	3.260586
5916	B04	NT06FT1846	cell division topological specificity factor MinE	307	CAG46240.1	2.596091
5917	B05	NT06FT1931	ribosomal protein S20	307	CAG46312.1	3.254072
5919	B06	NT06FT0759	lipoprotein, putative	310	CAG45311.1	2.654839
5921	B07	NT06FT1000	glutathione-dependent formaldehyde dehydrogenase	310	N/A	3.254839
5923	B08	NT06FT1746	diaminopimelate decarboxylase	310	N/A	2.287097
5926	B09	NT06FT0363	ribosomal protein S19	313	CAG44962.1	2
5927	B10	NT06FT0509	conserved hypothetical protein TIGR00253	313	CAG45094.1	3.268371
5929	B11	NT06FT1077	conserved hypothetical protein	313	N/A	2.236422
5931	B12	NT06FT1292	DNA photolyase, putative	313	N/A	3.246006
5934	C01	NT06FT1690	peptidyl-prolyl trans isomerase	313	CAG46105.1	2.600639
5936	C02	NT06FT1867	hypothetical protein	313	CAG46257.1	2.610224
5937	C03	NT06FT0023	glutamyl-tRNA(Gln) amidotransferase, C subunit	316	CAG44652.1	2.231013
5939	C04	NT06FT0303	hypothetical protein	316	N/A	3.268987
5942	C05	NT06FT1298	predicted protein	316	N/A	3.278481

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
5943	C06	NT06FT1822	hypothetical protein	316	CAG46219.1	2.642405
5945	C07	NT06FT1935	-	316	N/A	3.246835
5948	C08	NT06FT2068	chromosome initiation inhibitor IciA, putative	316	N/A	2.617089
5949	C09	NT06FT1163	Hypothetical UPF0250 protein	319	CAG45663.1	2
5951	C10	NT06FT1572	acyl carrier protein	319	CAG46009.1	1.605016
5953	C11	NT06FT1309	TPR repeat region family	322	CAG45784.1	3.251553
5955	C12	NT06FT1954	chaperonin, 10 kDa	322	CAG46328.1	3.217391
5959	D01	NT06FT2086	trp operon repressor	322	CAG46436.1	3.28882
5963	D02	NT06FT0756	Ribosomal L25p family	325	CAG45308.1	3.227692
5965	D03	NT06FT0796	septum formation initiator family protein, putative	325	CAG45343.1	3.230769
5969	D04	NT06FT0860	hypothetical protein	328	CAG45394.1	3.262195
5971	D05	NT06FT1108	conserved hypothetical protein	328	CAG45610.1	3.231707
5973	D06	NT06FT1247	ABC transporter homolog lmo1746 , putative	328	CAG45732.1	2.259146
5975	D07	NT06FT1851	hypothetical protein	328	CAG46245.1	3.228659
5977	D08	NT06FT0243	hypothetical protein	331	N/A	1.634441
5979	D09	NT06FT0741	conserved hypothetical protein	331	CAG45294.1	3.220544
5981	D10	NT06FT0922	hypothetical protein	331	CAG45446.1	2.63142
5983	D11	NT06FT1131	transporter, ZIP family, putative	331	N/A	3.23565
5986	D12	NT06FT1190	-	331	N/A	3.23565
5987	E01	NT06FT1457	ribosomal subunit interface protein	331	CAG45914.1	2.628399
5989	E02	NT06FT1799	conserved hypothetical protein	331	CAG46199.1	3.247734
5991	E03	NT06FT2074	-	331	N/A	3.265861
5993	E04	NT06FT0361	ribosomal protein L23	334	CAG44960.1	3.218563
5998	E05	NT06FT0064	ATP synthase F0, C subunit	340	CAG44692.1	2.6
5999	E06	NT06FT0372	ribosomal protein S14p/S29e	340	CAG44971.1	3.25
6001	E07	NT06FT1349	TGS domain protein	340	CAG45817.1	3.191176
6003	E08	NT06FT1814	Predicted endonuclease	340	CAG46214.1	2.632353
6005	E09	NTL06FT1784	hypothetical protein	343	N/A	3.259475
6007	E10	NT06FT0984	cadmium-translocating P-type ATPase	346	N/A	3.236994
6009	E11	NTL06FT1733	hypothetical protein	346	N/A	2.598266
6011	E12	NT06FT0505	DsrC like protein superfamily	349	CAG45090.1	3.255014
6014	F01	NT06FT0560	hypothetical protein	349	CAG45139.1	3.240688
6015	F02	NT06FT0874	ribosomal protein L21	349	CAG45405.1	3.191977
6019	F03	NT06FT1712	conserved hypothetical UU527 , putative	349	CAG46124.1	2.845272
6021	F04	NT06FT1906	hypothetical protein	349	N/A	1.587393
6023	F05	NT06FT0044	NADH dehydrogenase I, K subunit	352	CAG44674.1	3.227273
6026	F06	NT06FT0358	ribosomal protein S10	352	CAG44957.1	3.221591
6029	F07	NT06FT0719	acetohydroxyacid synthase small subunit, putative	352	CAG45275.1	3.198864
6031	F08	NT06FT1321	-	352	N/A	3.178977
6033	F09	NT06FT1081	conserved protein	355	CAG45587.1	3.219718
6036	F10	NT06FT1866	hypothetical protein	355	CAG46256.1	2.228169
6037	F11	NTL06FT0272	hypothetical membrane protein	355	N/A	1.219718
6039	F12	NT06FT0974	unnamed protein product, putative	358	CAG45492.1	3.231844
6041	G01	NT06FT1343	putative S-adenosyl methionine dependent methyltransferase like protein	358	N/A	3.24581

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6043	G02	NT06FT1660	thioredoxin	358	CAG46078.1	3.22905
6046	G03	NT06FT2042	Ferredoxin	358	CAG46397.1	2.592179
6047	G04	NT06FT0109	transposase	361	N/A	3.238227
6051	G05	NT06FT1106	thioredoxin	361	CAG45609.1	3.207756
6053	G06	NT06FT1628	11.6 kDa putative exported protein	361	CAG46052.1	3.210526
6055	G07	NT06FT2073	-	361	N/A	3.238227
6057	G08	NT06FT0072	glutaredoxin-related protein	364	CAG44700.1	3.225275
6059	G09	NT06FT0432	conserved protein	364	CAG45025.1	3.208791
6061	G10	NT06FT0704	Hfq	364	CAG45263.1	3.244505
6064	G11	NT06FT0888	conserved hypothetical protein	364	CAG45417.1	3.087912
6066	G12	NT06FT1104	Amidinotransferase superfamily, putative	364	N/A	3.21978
6068	H01	NT06FT1395	hypothetical protein	364	CAG45858.1	2.228022
6069	H02	NT06FT0289	hypothetical protein	367	CAG44894.1	2
6071	H03	NT06FT0315	ubiquinol oxidase, subunit IV	367	CAG44917.1	3.209809
6074	H04	NT06FT0606	alkylphosphonate utilization operon protein PhnA	367	CAG45177.1	3.212534
6075	H05	NT06FT0631	hypothetical protein	367	CAG45199.1	3.226158
6078	H06	NT06FT0679	-	367	N/A	2.495913
6080	H07	NT06FT0742	conserved hypothetical protein	367	CAG45295.1	3.234332
6084	H08	NT06FT0334	hypothetical protein	370	CAG44935.1	3.172973
6085	H09	NT06FT0364	ribosomal protein L22	370	CAG44963.1	3.213514
6087	H10	NT06FT0423	hypothetical protein	370	CAG45016.1	3.216216
6089	H11	NT06FT0613	conserved hypothetical protein	370	N/A	2.218919
6091	H12	NT06FT0935	lipoprotein, putative	370	CAG45458.1	3.191892