

***Francisella tularensis* subsp. *tularensis*,
Strain SCHU S4, Gateway® Clone Set,
Recombinant in *Escherichia coli*, Plate 4**

Catalog No. NR-19461

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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-19461 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 4, NR-19461."

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.

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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 4 (ZFTKN)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
6093	A01	NT06FT1150	hypothetical protein	370	CAG45650.1	3.227027
6095	A02	NT06FT1199	ribosomal protein S6	370	CAG45695.1	3.224324
6097	A03	NT06FT1289	lipoprotein, putative	370	CAG45769.1	3.213514
6099	A04	NT06FT1576	TsgA protein homolog, putative	370	N/A	2.586486
6101	A05	NT06FT1590	aspartate 1-decarboxylase	370	CAG46024.1	3.210811
6103	A06	NT06FT0919	conserved hypothetical protein TIGR00103	373	CAG45443.1	3.211796
6105	A07	NT06FT1481	HIT family protein	373	CAG45932.1	2.581769
6111	A08	NT06FT1189	-	376	N/A	3.18883
6113	A09	NT06FT1206	hypothetical protein	376	CAG45699.1	3.210106
6117	A10	NT06FT0805	hypothetical protein	379	CAG45351.1	2.221636
6119	A11	NT06FT0871	DNA-3-methyladenine glycosylase I	379	N/A	3.229551
6121	A12	NT06FT1841	12 kDa putative exported protein	379	CAG46235.1	3.237467
6123	B01	NT06FT2048	nicotinamide mononucleotide transporter PnuC, putative	379	N/A	3.195251
6125	B02	NTL06FT0024	hypothetical protein	379	N/A	3.197889
6127	B03	NT06FT0172	ribosomal protein L19	382	CAG44786.1	3.191099
6130	B04	NT06FT0244	cytochrome b561, putative	382	N/A	2.732984
6131	B05	NT06FT0780	putative cell division protein FtsL	382	CAG45329.1	3.240838
6133	B06	NT06FT0821	hypothetical protein	382	CAG45365.1	3.227749
6136	B07	NT06FT1737	conserved hypothetical protein	382	CAG46147.1	3.204188
6137	B08	NT06FT1849	ABC transporter, periplasmic substrate-binding protein	382	N/A	3.091623
6140	B09	NT06FT0712	threonine synthase	385	N/A	3.023377
6141	B10	NT06FT0714	2-isopropylmalate synthase, putative	385	CAG45271.1	2.6
6143	B11	NT06FT0784	iron-sulfur cluster assembly accessory protein	385	CAG45333.1	3.238961
6146	B12	NT06FT0878	drug resistance transporter, Bcr/CflA family, putative	385	N/A	2.21039
6147	C01	NT06FT1483	ComF family protein, putative	385	N/A	3.225974
6150	C02	NT06FT1861	acetyltransferase, GNAT family, putative	385	N/A	3.2
6151	C03	NT06FT0078	succinate dehydrogenase, hydrophobic membrane anchor protein, putative	388	CAG44706.1	3.201031
6153	C04	NT06FT0086	preprotein translocase, SecG subunit	388	CAG44714.1	3.188144

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
6155	C05	NT06FT0375	ribosomal protein L18	388	CAG44974.1	3.203608
6158	C06	NT06FT0727	endonuclease III	388	CAG45281.1	3.17268
6159	C07	NT06FT0934	ArsC family protein, putative	388	CAG45457.1	2.608247
6161	C08	NT06FT1017	conserved hypothetical protein TIGR00252	388	CAG45531.1	2.600515
6163	C09	NT06FT1067	Probable dihydroneopterin aldolase (DHNA), putative	388	CAG45576.1	3.203608
6166	C10	NT06FT1261	histidine-rich glycoprotein 1, putative	388	CAG45743.1	2.92268
6168	C11	NT06FT2050	hypothetical protein	388	CAG46404.1	2.719072
6169	C12	NT06FT0380	ribosomal protein S13p/S18e	391	CAG44980.1	3.209719
6171	D01	NT06FT0648	iron-sulfur cluster assembly accessory protein	391	CAG45212.1	3.202046
6173	D02	NT06FT0929	ribosomal protein L20	391	CAG45453.1	3.176471
6175	D03	NT06FT1267	preprotein translocase, YajC subunit	391	CAG45749.1	3.189258
6178	D04	NT06FT1732	conserved hypothetical protein	391	CAG46142.1	2.598465
6179	D05	NT06FT1932	outer membrane lipoprotein, putative, putative	391	CAG46313.1	3.163683
6181	D06	NT06FT2005	outer membrane protein	391	N/A	2
6183	D07	NTL06FT0745	hypothetical protein	391	N/A	2.616368
6185	D08	NT06FT0970	conserved hypothetical protein	394	CAG45488.1	2
6190	D09	NT06FT0945	chorismate mutase	397	CAG45467.1	2.599496
6192	D10	NT06FT0999	Mannose-6-phosphate isomerase	397	N/A	2.211587
6195	D11	NT06FT2072	conserved hypothetical protein	397	CAG46424.1	2.609572
6199	D12	NT06FT0986	predicted Transcriptional regulator	400	CAG45501.1	2.57
6201	E01	NT06FT1301	-	400	N/A	3.2175
6203	E02	NT06FT1484	probable amidophosphoribosyltransferase, ComFC B.suntillis ortholog , putative	400	N/A	2.62
6208	E03	NT06FT0414	Short-chain fatty acids transporter	403	N/A	2.419355
6210	E04	NT06FT0833	heat shock protein 15	403	CAG45372.1	3.022333
6211	E05	NT06FT2080	conserved hypothetical protein	403	CAG46431.1	2
6215	E06	NT06FT1019	13 kDa major membrane protein	406	CAG45533.1	3.179803
6217	E07	NT06FT1217	TriL protein	406	CAG45706.1	2.596059
6220	E08	NT06FT1893	D-tyrosyl-tRNA(Tyr) deacylase	406	CAG46279.1	2.576355
6221	E09	NTL06FT0254	hypothetical protein	406	N/A	3.110837
6223	E10	NT06FT0355	ribosomal protein S12	409	CAG44954.1	2
6225	E11	NT06FT0583	HI1162	409	CAG45157.1	3.242054
6227	E12	NT06FT0881	hypothetical protein	409	CAG45411.1	2.623472
6229	F01	NT06FT1006	granule lattice protein 1 precursor, putative	409	CAG45520.1	3.178484
6231	F02	NTL06FT1541	hypothetical protein	409	N/A	2.599022
6233	F03	NT06FT0092	membrane protein, putative	412	CAG44718.1	3.196602
6235	F04	NT06FT0162	ribosomal protein L7/L12	412	CAG44776.1	2.67233
6238	F05	NT06FT0191	putative transposase	412	CAG44804.1	2.59466
6239	F06	NT06FT0242	putative transposase	412	CAG44849.1	2.980583
6241	F07	NT06FT0275	putative transposase	412	CAG44880.1	2.592233
6244	F08	NT06FT0302	putative transposase	412	CAG44906.1	3.208738
6245	F09	NT06FT0338	MutT/nudix family protein	412	CAG44938.1	2
6248	F10	NT06FT0386	putative transposase	412	CAG44985.1	3.208738
6249	F11	NT06FT0401	putative transposase	412	CAG44996.1	3.201456
6251	F12	NT06FT0417	putative transposase	412	CAG45010.1	2

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6254	G01	NT06FT0587	conserved hypothetical protein	412	CAG45161.1	2.589806
6255	G02	NT06FT0625	putative transposase	412	CAG45194.1	2.580097
6257	G03	NT06FT0736	membrane protein, putative	412	N/A	2.61165
6259	G04	NT06FT0865	putative transposase	412	CAG45398.1	2.584951
6261	G05	NT06FT0876	Uncharacterized conserved protein	412	CAG45407.1	2.601942
6263	G06	NT06FT0883	putative transposase	412	CAG45412.1	2.61165
6265	G07	NT06FT0932	putative transposase	412	CAG45455.1	3.157767
6267	G08	NT06FT1041	putative transposase	412	CAG45553.1	2.531553
6269	G09	NT06FT1219	putative transposase	412	CAG45707.1	2.606796
6271	G10	NT06FT1249	iron-sulfur cluster-binding protein	412	N/A	2.599515
6273	G11	NT06FT1403	putative transposase	412	CAG45865.1	2
6275	G12	NT06FT1437	putative transposase	412	CAG45895.1	2.589806
6277	H01	NT06FT1536	-	412	N/A	2.59466
6279	H02	NT06FT1585	putative transposase	412	CAG46019.1	2
6281	H03	NT06FT1638	putative transposase	412	CAG46061.1	3.201456
6283	H04	NT06FT1778	putative transposase	412	CAG46181.1	2.194175
6286	H05	NT06FT1855	putative transposase	412	CAG46248.1	3.160194
6289	H06	NT06FT1890	putative transposase	412	N/A	2.589806
6293	H07	NT06FT1950	putative transposase	412	CAG46325.1	2.592233
6296	H08	NT06FT1966	-	412	N/A	3.201456
6297	H09	NT06FT2060	putative transposase	412	CAG46413.1	2.589806
6299	H10	NT06FT0004	IS630-Spn1, transposase Orf1, putative	415	N/A	2.583133
6301	H11	NT06FT0009	IS630-Spn1, transposase Orf1, putative	415	N/A	1.913253
6303	H12	NT06FT0077	succinate dehydrogenase, cytochrome b556 subunit, putative	415	CAG44705.1	2