Francisella tularensis subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 5

Catalog No. NR-19462

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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 *att*B substrate (*att*B-PCR product or a linearized *att*B expression clone) with an *att*P substrate (pDONR™221) to create an *att*L-containing entry clone. The entry clone contains recombinational cloning sites, *att*L1 and *att*L2 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-19462 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 5, NR-19462."

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:

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 5 (ZFTKO)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
6305	A01	NT06FT0107	IS630-Spn1, transposase Orf1, putative	415	N/A	2
6309	A02	NT06FT0190	IS630-Spn1, transposase Orf1, putative	415	N/A	2
6312	A03	NT06FT0241	IS630-Spn1, transposase Orf1, putative	415	N/A	3.219277
6313	A04	NT06FT0254	IS630-Spn1, transposase Orf1, putative	415	N/A	3.190361
6316	A05	NT06FT0274	IS630-Spn1, transposase Orf1, putative	415	N/A	3.2
6318	A06	NT06FT0282	IS630-Spn1, transposase Orf1, putative	415	N/A	2
6319	A07	NT06FT0291	hypothetical protein	415	CAG44896.1	2.383133
6321	A08	NT06FT0301	IS630-Spn1, transposase Orf1, putative	415	N/A	2
6323	A09	NT06FT0385	IS630-Spn1, transposase Orf1, putative	415	N/A	3.20241
6326	A10	NT06FT0390	IS630-Spn1, transposase Orf1, putative	415	N/A	3.180723
6327	A11	NT06FT0393	IS630-Spn1, transposase Orf1, putative	415	N/A	2.607229
6329	A12	NT06FT0400	IS630-Spn1, transposase Orf1, putative	415	N/A	2.609639
6331	B01	NT06FT0416	IS630-Spn1, transposase Orf1, putative	415	N/A	2.604819
6334	B02	NT06FT0487	IS630-Spn1, transposase Orf1, putative	415	N/A	3.214458
6335	B03	NT06FT0568	IS630-Spn1, transposase Orf1, putative	415	N/A	2.607229
6337	B04	NT06FT0624	IS630-Spn1, transposase Orf1, putative	415	N/A	2.585542
6340	B05	NT06FT0655	-	415	N/A	2
6341	B06	NT06FT0776	IS630-Spn1, transposase Orf1, putative	415	N/A	2.614458
6343	B07	NT06FT0810	IS630-Spn1, transposase Orf1, putative	415	N/A	2.575904

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Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
6345	B08	NT06FT0864	IS630-Spn1, transposase Orf1, putative	415	N/A	2.578313
6347	B09	NT06FT0882	IS630-Spn1, transposase Orf1, putative	415	N/A	2.616867
6349	B10	NT06FT0921	glycine cleavage system H protein	415	CAG45445.1	2
6351	B11	NT06FT0931	IS630-Spn1, transposase Orf1, putative	415	N/A	3.156627
6353	B12	NT06FT1040	IS630-Spn1, transposase Orf1, putative	415	N/A	3.115663
6355	C01	NT06FT1205	IS630-Spn1, transposase Orf1, putative	415	N/A	3.178313
6357	C02	NT06FT1218	IS630-Spn1, transposase Orf1, putative	415	N/A	3.149398
6359	C03	NT06FT1297	IS630-Spn1, transposase Orf1, putative	415	N/A	2.607229
6362	C04	NT06FT1380	IS630-Spn1, transposase Orf1, putative	415	N/A	3.204819
6363	C05	NT06FT1402	IS630-Spn1, transposase Orf1, putative	415	N/A	2.604819
6366	C06	NT06FT1436	IS630-Spn1, transposase Orf1, putative	415	N/A	3.180723
6367	C07	NT06FT1441	IS630-Spn1, transposase Orf1, putative	415	N/A	2
6369	C08	NT06FT1492	IS630-Spn1, transposase Orf1, putative	415	N/A	2.561446
6371	C09	NT06FT1523	endoribonuclease L-PSP, putative	415	CAG45971.1	2.60241
6373	C10	NT06FT1557	IS630-Spn1, transposase Orf1, putative	415	N/A	3.2
6375	C11	NT06FT1584	IS630-Spn1, transposase Orf1, putative	415	N/A	2.607229
6378	C12	NT06FT1637	IS630-Spn1, transposase Orf1, putative	415	CAG46060.1	3.180723
6380	D01	NT06FT1665	IS630-Spn1, transposase Orf1, putative	415	N/A	3.20241
6381	D02	NT06FT1699	IS630-Spn1, transposase Orf1, putative	415	N/A	3.183133
6383	D03	NT06FT1777	IS630-Spn1, transposase Orf1, putative	415	N/A	2.604819
6385	D04	NT06FT1820	IS630-Spn1, transposase Orf1, putative	415	N/A	3.180723
6387	D05	NT06FT1836	IS630-Spn1, transposase Orf1, putative	415	N/A	2.604819
6389	D06	NT06FT1854	IS630-Spn1, transposase Orf1, putative	415	N/A	2
6391	D07	NT06FT1862	IS630-Spn1, transposase Orf1, putative	415	N/A	2.59759
6393	D08	NT06FT1889	IS630-Spn1, transposase Orf1, putative	415	N/A	2
6395	D09	NT06FT1920	IS630-Spn1, transposase Orf1, putative	415	N/A	2.607229
6397	D10	NT06FT1949	IS630-Spn1, transposase Orf1, putative	415	N/A	2.583133

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6399	D11	NT06FT1957	IS630-Spn1, transposase Orf1, putative	415	N/A	2.583133
6402	D12	NT06FT1987	IS630-Spn1, transposase Orf1, putative	415	N/A	2.604819
6404	E01	NT06FT2016	IS630-Spn1, transposase Orf1, putative	415	N/A	3.180723
6405	E02	NT06FT2031	IS630-Spn1, transposase Orf1, putative	415	N/A	2.60241
6407	E03	NT06FT2059	IS630-Spn1, transposase Orf1, putative	415	N/A	2.609639
6411	E04	NT06FT0118	hypothetical protein	418	CAG44740.1	3.162679
6413	E05	NT06FT0239	nicotinamide mononucleotide transporter PnuC, putative	418	N/A	2
6416	E06	NT06FT0450	glycine cleavage system H protein	418	CAG45041.1	3.210526
6417	E07	NT06FT1310	conserved hypothetical protein	418	CAG45785.1	2.61244
6419	E08	NT06FT1382	lactoylglutathione lyase	418	CAG45845.1	2.578947
6421	E09	NT06FT0603	antioxidant, AhpC/Tsa family,	421	N/A	2.581948
6425	E10	NT06FT1600	normocyte binding protein 2b	421	CAG46033.1	2.598575
6427	E11	NT06FT0381	ribosomal protein S11	424	CAG44981.1	2.596698
6430	E12	NT06FT1250	-	424	N/A	2.584906
6431	F01	NT06FT1450	ribosomal protein S9	424	CAG45907.1	2.57783
6433	F02	NT06FT0288	crcB protein	427	CAG44893.1	2.58548
6435	F03	NT06FT0632	putative proton dependent peptide transporter	427	N/A	2
6437	F04	NT06FT1375	lipoprotein, putative	427	CAG45839.1	2.522248
6439	F05	NT06FT1381	hypothetical protein	427	CAG45844.1	2.578454
6441	F06	NT06FT1818	IS1016 family transposase, degenerate	427	N/A	3.222482
6443	F07	NT06FT2057	lipoprotein, putative	427	CAG46411.1	2.393443
6445	F08	NT06FT1695	hit1 protein	430	CAG46110.1	2.6
6448	F09	NT06FT1715	hypothetical protein	430	CAG46126.1	3.172093
6449	F10	NT06FT0018	hypothetical protein	433	CAG44647.1	3.161663
6452	F11	NT06FT0034	NADH dehydrogenase I, A subunit	433	CAG44664.1	3.159353
6454	F12	NT06FT0373	ribosomal protein S8	433	CAG44972.1	3.184758
6456	G01	NT06FT0637	hypothetical protein	433	CAG45203.1	3.184758
6458	G02	NT06FT1046	hypothetical protein	433	CAG45557.1	3.191686
6459	G03	NT06FT1832	hypothetical protein	433	CAG46229.1	2.579677
6462	G04	NT06FT2055	hypothetical protein	433	CAG46409.1	3.191686
6464	G05	NT06FT0262	ribonuclease P protein component	436	CAG44868.1	3.15367
6465	G06	NT06FT1173	GatB/Yqey family protein	436	CAG45670.1	2.603211
6467	G07	NT06FT1510	cytidine deaminase	436	CAG45960.1	2.56422
6469	G08	NT06FT1552	-	436	N/A	2.575688
6471	G09	NT06FT1982	-	436	N/A	2
6473	G10	NT06FT0002	amino acid MFS transporter	439	N/A	2.587699
6476	G11	NT06FT0026	hypothetical protein	442	CAG44655.1	2.606335
6477	G12	NT06FT0258	hypothetical protein	442	CAG44863.1	3.165158
6480	H01	NT06FT0718	acetolactate synthase large subunit	442	N/A	3.187783
6481	H02	NT06FT0752	putative transport protein	442	N/A	3.151584
6484	H03	NT06FT1009	type IV pilin	442	CAG45523.1	3.192308
6486	H04	NT06FT1072	putative to nasA protein	442	N/A	3.201357
6488	H05	NT06FT1248	iojap domain protein	442	CAG45733.1	3.190045
6489	H06	NT06FT1452	stringent starvation protein B	442	CAG45909.1	2.58371

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6491	H07	NT06FT1901	lipoprotein, putative	442	CAG46286.1	2.576923
6494	H08	NT06FT0376	ribosomal protein S5	445	CAG44975.1	3.170787
6495	H09	NT06FT0408	Uncharacterised P-loop hydrolase UPF0079	445	CAG45003.1	2.586517
6497	H10	NT06FT1099	iron-sulfur cluster assembly transcription factor IscR, putative	445	CAG45603.1	3.177528
6501	H11	NT06FT0366	ribosomal protein L16	448	CAG44965.1	2.582589
6503	H12	NT06FT0813	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase, putative	448	N/A	3.158482

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