Francisella tularensis subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 6

Catalog No. NR-19463

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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-19463 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 6, NR-19463."

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 6 (ZFTKP)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
6505	A01	NT06FT1625	lipoprotein, putative	448	CAG46049.1	2
6507	A02	NT06FT2036	probable dioxygenase Rieske iron-sulfur component, putative	448	N/A	3.171875
6510	A03	NT06FT2078	transcriptional regulator, AraC family, putative	448	CAG46429.1	3.176339286
6512	A04	NT06FT0003	putative transposase	451	CAG44637.1	3.186252772
6514	A05	NT06FT0011	Modification methylase HaeIII (Cytosine-specificmethyltransferase HaeIII) (M.HaeIII)	451	N/A	3.177383592
6517	A08	NT06FT0145	putative transposase	451	CAG44764.1	3.197339246
6520	A09	NT06FT0251	unnamed protein product	451	N/A	3.150776053
6522	A10	NT06FT0253	putative transposase	451	CAG44859.1	3.186252772
6523	A11	NT06FT0281	putative transposase	451	CAG44886.1	2.197339246
6525	A12	NT06FT0389	putative transposase	451	CAG44988.1	2.592017738
6527	B01	NT06FT0392	putative transposase	451	CAG44990.1	3.250554324
6531	B02	NT06FT0567	putative transposase	451	CAG45146.1	2.592017738
6533	B03	NT06FT0775	putative transposase	451	CAG45325.1	2.567627494
6536	B04	NT06FT0809	putative transposase	451	CAG45355.1	2.596452328
6537	B05	NT06FT1178	thioesterase family protein, putative	451	CAG45674.1	2
6539	B06	NT06FT1204	putative transposase	451	CAG45698.1	2.567627494
6541	B07	NT06FT1273	hypothetical protein	451	CAG45755.1	2.596452328
6543	B08	NT06FT1296	putative transposase	451	CAG45775.1	3.250554324
6545	B09	NT06FT1323	hypothetical protein	451	CAG45796.1	3.257206208
6547	B10	NT06FT1379	putative transposase	451	CAG45843.1	3.250554324
6549	B11	NT06FT1440	putative transposase	451	CAG45898.1	2.592017738
6553	B12	NT06FT1613	Fe-S metabolism associated domain subfamily	451	CAG46042.1	2.576496674
6555	C01	NT06FT1698	putative transposase	451	CAG46114.1	2.587583149
6557	C02	NT06FT1819	putative transposase	451	CAG46217.1	2.567627494
6562	C03	NT06FT1911	major acid phosphatase	451	N/A	3.155210643
6565	C04	NT06FT1986	putative transposase	451	CAG46351.1	3.246119734
6568	C05	NT06FT2015	putative transposase	451	CAG46375.1	3.184035477
6570	C06	NT06FT2030	putative transposase	451	CAG46389.1	2.594235033

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Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
6571	C07	NT06FT0688	15.7 kDa putative exported protein	454	CAG45246.1	2.579295154
6575	C08	NT06FT0940	DNA processing protein DprA, putative	454	N/A	2
6577	C09	NT06FT1780	conserved hypothetical protein	454	CAG46182.1	2.5969163
6579	C10	NT06FT2014	predicted NAD-dependent formate dehydrogenase	454	N/A	2
6582	C11	NT06FT0033	Ferric uptake regulation protein (Ferric uptake regulator)	457	CAG44663.1	3.153172867
6583	C12	NT06FT0411	nucleoside diphosphate kinase	457	CAG45006.1	2.582056893
6585	D01	NT06FT0873	glycerate kinase	457	N/A	2
6587	D02	NT06FT0969	hypothetical conserved protein	457	CAG45487.1	2.577680525
6589	D03	NT06FT1432	lipoprotein, putative	457	CAG45893.1	2.582056893
6593	D04	NT06FT2001	ABC transporter, ATP-binding protein, putative	457	N/A	2.58643326
6595	D05	NT06FT2022	rhodanese-like domain protein, putative	457	CAG46381.1	2.58643326
6599	D06	NT06FT0197	Acetyltransferase	460	CAG44810.1	3.152173913
6602	D07	NT06FT0556	hypothetical protein	460	CAG45135.1	3.189130435
6603	D08	NT06FT1075	conserved hypothetical protein	460	N/A	2.584782609
6605	D09	NT06FT1192	hypothetical protein	460	CAG45688.1	2.57826087
6607	D10	NT06FT1344	-	460	N/A	2
6609	D11	NT06FT1627	transcription antitermination factor NusB	460	CAG46051.1	2
6611	D12	NT06FT1449	ribosomal protein L13	463	CAG45906.1	2
6614	E01	NT06FT2076	stress response protein	463	CAG46427.1	3.17062635
6615	E02	NT06FT0056	ribosome-binding factor A	466	CAG44684.1	3.182403433
6617	E03	NT06FT0157	preprotein translocase SecE subunit, putative	466	CAG44771.1	2
6619	E04	NT06FT0378	ribosomal protein L15	466	N/A	2.58583691
6622	E05	NT06FT0726	conserved hypothetical protein	466	CAG45280.1	3.135193133
6623	E06	NT06FT1130	transporter, ZIP family, putative	466	N/A	3.180257511
6625	E07	NT06FT1133	transcriptional regulator, putative	466	CAG45634.1	2.605150215
6627	E08	NT06FT1182	hypothetical protein	466	CAG45678.1	2.592274678
6629	E09	NT06FT1332	Cold-shock DNA-binding domain protein	466	CAG45805.1	3.152360515
6632	E10	NT06FT1350	Oligoketide cyclase/lipid transport protein	466	CAG45818.1	3.17167382
6633	E11	NT06FT0159	ribosomal protein L11	469	CAG44773.1	2.857142857
6635	E12	NT06FT0320	lipoprotein, putative	469	CAG44922.1	2.590618337
6637	F01	NT06FT0589	DNA polymerase IV	469	N/A	2
6639	F02	NT06FT0681	putative YbgI protein	469	N/A	2
6641	F03	NT06FT1953	membrane protein, putative	469	CAG46327.1	2
6644	F04	NT06FT0070	ATP synthase F1, epsilon subunit	472	CAG44698.1	3.173728814
6645	F05	NT06FT0330	DNA polymerase III holoenzyme chi subunit XF0136 , putative	472	CAG44931.1	2.578389831
6647	F06	NT06FT0384	ribosomal protein L17	472	CAG44984.1	2
6649	F07	NT06FT0519	3-dehydroquinate dehydratase, type II	472	CAG45104.1	2
6651	F08	NT06FT0713	-	472	N/A	2.572033898
6654	F09	NT06FT1753	arsenate reductase, putative	472	CAG46160.1	3.163135593

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Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
6655	F10	NT06FT1898	periplasmic monofunctional chorismate mutase, putative	472	CAG46283.1	2.591101695
6659	F11	NT06FT1355	major facilitator family transporter	475	N/A	3.181052632
6661	F12	NT06FT1654	bacterioferritin	475	CAG46074.1	2
6663	G01	NT06FT0857	Acetyl-coenzyme A synthetase (Acetate--CoA ligase) (Acyl-activating enzyme)	478	N/A	2
6665	G02	NT06FT1722	protein-export protein SecB	478	CAG46133.1	2.589958159
6669	G03	NT06FT1926	6,7-dimethyl-8-ribityllumazine synthase	478	CAG46307.1	2.583682008
6671	G04	NT06FT0353	deoxyuridine 5`-triphosphate nucleotidohydrolase	481	CAG44952.1	3.145530146
6673	G05	NT06FT0750	conserved membrane protein, putative	481	CAG45303.1	2.567567568
6676	G06	NT06FT0820	hypothetical protein	481	CAG45364.1	3.172557173
6677	G07	NT06FT0949	tolR protein	481	CAG45471.1	2
6680	G08	NT06FT0967	-	481	N/A	3.16008316
6681	G09	NT06FT1244	hypothetical protein	481	CAG45730.1	2
6683	G10	NTL06FT0090	conserved hypothetical membrane protein	481	N/A	2
6686	G11	NT06FT0402	hypothetical protein	484	CAG44997.1	3.194214876
6687	G12	NT06FT0614	-	484	N/A	2
6689	H01	NT06FT0867	hypothetical protein	484	CAG45400.1	2.601239669
6691	H02	NT06FT1020	17 kDa major membrane protein precursor (TUL4)	484	CAG45534.1	2.584710744
6693	H03	NT06FT1117	conserved hypothetical protein TIGR00250	484	CAG45619.1	2
6695	H04	NT06FT1258	-	484	N/A	2
6697	H05	NT06FT1631	Hypothetical UPF0260 protein	484	CAG46054.1	2
6699	H06	NT06FT2023	protein-export protein SecB	484	CAG46382.1	2
6701	H07	NT06FT0053	unnamed protein product	487	CAG44681.1	2.59137577
6703	H08	NT06FT0090	conserved hypothetical protein	487	CAG44716.1	2
6705	H09	NT06FT1719	hypothetical protein	487	CAG46130.1	2
6707	H10	NT06FT2025	regulatory protein RecX	487	CAG46384.1	2
6711	H11	NT06FT0096	conserved hypothetical protein	490	N/A	3.130612245
6713	H12	NT06FT1197	ribosomal protein L9	490	CAG45693.1	2

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