

***Francisella tularensis* subsp. *tularensis*,
Strain SCHU S4, Gateway® Clone Set,
Recombinant in *Escherichia coli*, Plate 9**

Catalog No. NR-19466

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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-19466 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 9, NR-19466."

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 9 (ZFTKS)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
7126	A01	NT06FT0073	superoxide dismutase	613	CAG44701.1	4.228384992
7127	A02	NT06FT0658	CRISPR-associated protein Cas4	613	CAG45219.1	3.128874388
7129	A03	NT06FT0683	DUF152	613	CAG45241.1	3.233278956
7131	A04	NT06FT0802	uracil phosphoribosyltransferase	613	CAG45349.1	3.827079935
7133	A05	NT06FT1210	Protein of unknown function (DUF1526) superfamily	613	N/A	3.778140294
7135	A06	NT06FT1506	methyltransferase, putative	613	CAG45956.1	3.838499184
7137	A07	NT06FT1729	hypothetical protein	613	CAG46139.1	3.825448613
7139	A08	NT06FT1792	non-canonical purine NTP pyrophosphatase, rdgB/HAM1 family	613	CAG46193.1	3.789559543
7142	A09	NT06FT2084	glutamine amido/phosphoribosyl anthranilate transferase	613	N/A	3.530179445
7143	A10	NT06FT0114	hypothetical protein	616	CAG44736.1	3.423701299
7145	A11	NT06FT0142	hypothetical protein	616	CAG44761.1	3.819805195
7149	A12	NT06FT0654	conserved hypothetical protein	616	N/A	1.99025974
7155	B02	NT06FT0175	acid phosphatase, class B, putative	619	CAG44789.1	2
7157	B03	NT06FT1116	Uncharacterized ACR, COG1678	619	CAG45618.1	1.996768982
7159	B04	NT06FT1497	hypothetical protein	619	CAG45947.1	2
7161	B05	NT06FT0740	hypothetical protein	622	CAG45293.1	1.990353698
7169	B08	NT06FT0237	flavodoxin	625	CAG44845.1	2
7171	B09	NT06FT0570	-	625	N/A	2
7176	B11	NT06FT0891	DoxX subfamily, putative	625	CAG45420.1	2
7178	B12	NT06FT1031	HD domain protein	625	CAG45544.1	2
7179	C01	NT06FT1089	Modulator of drug activity B	625	CAG45594.1	2
7183	C03	NT06FT1203	hypothetical protein	625	CAG45697.1	2
7190	C06	NT06FT1868	hypothetical protein	625	CAG46258.1	2
7191	C07	NT06FT1922	Na ⁺ /H ⁺ antiporter NhaP	625	N/A	2
7194	C08	NT06FT0579	hypothetical protein	628	CAG45153.1	1.993630573
7195	C09	NT06FT0710	ribosome biogenesis GTP-binding protein YsxC	628	CAG45269.1	2
7197	C10	NT06FT0976	hypothetical protein	628	CAG45494.1	2
7201	C12	NT06FT2035	cytochrome b561, putative	628	CAG46391.1	2
7204	D01	NT06FT0354	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	631	CAG44953.1	3.250396197

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
7208	D02	NT06FT1316	type IV pilus biogenesis protein PilO, putative	631	CAG45791.1	1.996830428
7209	D03	NT06FT1933	phosphoheptose isomerase	631	CAG46314.1	2
7218	D04	NT06FT1738	CDP-alcohol phosphatidyltransferase family	634	CAG46148.1	1.993690852
7220	D05	NT06FT0314	Cytochrome c oxidase subunit III	637	CAG44916.1	2
7227	D09	NT06FT1474	conserved hypothetical protein TIGR00257	637	CAG45925.1	2
7230	D10	NT06FT0043	NADH dehydrogenase I, J subunit	640	CAG44673.1	2
7238	E01	NT06FT0933	MutT/nudix family protein, putative	640	CAG45456.1	1.990625
7239	E02	NT06FT0938	-	640	N/A	2
7241	E03	NT06FT1109	hypothetical protein	640	CAG45611.1	2
7246	E04	NT06FT1924	riboflavin synthase, alpha subunit	640	CAG46305.1	1.9921875
7252	E05	NT06FT1769	lipoprotein, putative	643	CAG46173.1	4.236391913
7255	E06	NT06FT0621	oxidoreductase, short-chain dehydrogenase/reductase family, putative	646	CAG45191.1	2
7267	E11	NT06FT1555	-	649	N/A	2
7275	F02	NT06FT0221	hypothetical protein	652	CAG44833.1	1.996932515
7287	F06	NT06FT1943	methyltransferase GidB	652	CAG46320.1	2
7290	F07	NT06FT0382	ribosomal protein S4	655	CAG44982.1	2
7294	F09	NT06FT1164	lipoate-protein ligase B	655	CAG45664.1	-
7296	F10	NT06FT1632	oxidoreductase, 2OG-Fe(II) oxygenase family family	655	CAG46055.1	2
7297	F11	NT06FT1816	-	655	N/A	2
7306	G01	NT06FT0953	peptidoglycan-associated lipoprotein Pal	658	CAG45475.1	1.990881459
7308	G02	NT06FT0963	conserved hypothetical protein	658	CAG45483.1	1.996960486
7309	G03	NT06FT1183	SPV125 CD47-like protein, putative	658	CAG45679.1	2
7314	G05	NT06FT1541	conserved hypothetical protein	658	CAG45984.1	-
7321	G07	NT06FT0180	PAP2 family protein, putative	661	CAG44794.1	2
7324	G08	NT06FT0483	orotate phosphoribosyltransferase	661	CAG45070.1	-
7325	G09	NT06FT1159	Protein of unknown function (DUF1239) superfamily	661	CAG45659.1	2
7332	G10	NT06FT1899	contains ESTs AU064040(E3520),C99291(E10609), C19561(E10609),AU094166	661	CAG46284.1	2
7335	G12	NT06FT0136	-	664	N/A	2
7337	H01	NT06FT0728	iron-sulfur cluster-binding protein	664	CAG45282.1	2
7341	H02	NT06FT0899	conserved hypothetical protein	664	CAG45428.1	4.237951807
7344	H03	NT06FT0994	MGC83915 protein, putative	664	CAG45510.1	2.802710843
7345	H04	NT06FT1149	acyl-CoA thioesterase I, putative	664	CAG45649.1	2.703313253
7348	H05	NT06FT1547	IgIC	664	CAG45990.1	3.512048193
7349	H06	NT06FT1977	IgIC	664	CAG46345.1	4.24246988
7351	H07	NT06FT0748	transporter, putative	667	CAG45301.1	4.247376312
7353	H08	NT06FT1730	hypothetical protein	667	CAG46140.1	3.433283358
7355	H09	NT06FT1895	orotidine 5-phosphate decarboxylase	667	CAG46281.1	2.701649175
7357	H10	NT06FT0298	outer membrane lipoprotein LoIB	670	CAG44903.1	3.619402985
7359	H11	NT06FT0359	ribosomal protein L3	670	CAG44958.1	3.43880597
7363	H12	NT06FT0598	ubiquinone biosynthesis protein	670	CAG45170.1	4.229850746