

***Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 13**

Catalog No. NR-19470

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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-19470 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 13, NR-19470."

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 13 (ZFTKW)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
8027	A01	NT06FT0847	radical SAM domain protein	895	CAG45383.1	4.072626
8029	A02	NT06FT1124	ParA family protein	895	CAG45627.1	4.053631
8033	A03	NT06FT1668	glycosyltransferase	895	CAG46085.1	4.040223
8035	A04	NT06FT0565	pyridoxine biosynthesis protein	898	CAG45144.1	3.982183
8038	A05	NT06FT0686	beta-lactamase	898	CAG45244.1	4.168151
8040	A06	NT06FT0856	UTP-glucose-1-phosphate uridylyltransferase	898	CAG45390.1	3.782851
8041	A07	NT06FT0907	asparaginase family protein, putative	898	CAG45436.1	3.662584
8043	A08	NT06FT1686	nicotinate-nucleotide pyrophosphorylase	898	CAG46101.1	4.08686
8045	A09	NT06FT1787	signal peptidase I	898	CAG46189.1	4.073497
8047	A10	NT06FT0383	DNA-directed RNA polymerase, alpha subunit	901	CAG44983.1	4.067703
8050	A11	NT06FT1063	adenosine deaminase	901	CAG45572.1	4.162042
8052	A12	NT06FT0333	hypothetical protein	904	CAG44934.1	4.170354
8053	B01	NT06FT0348	translation elongation factor Ts	904	CAG44947.1	3.68031
8056	B02	NT06FT0477	spermidine synthase	904	CAG45064.1	4.153761
8057	B03	NT06FT0619	oxidative stress regulatory protein OxyR	904	CAG45189.1	4.00885
8060	B04	NT06FT1265	protein-export membrane protein SecF	904	CAG45747.1	4.167035
8066	B07	NT06FT0215	CAAX protease family protein, putative	907	CAG44827.1	2
8070	B08	NT06FT0399	hypothetical protein	907	CAG44995.1	4.157663
8071	B09	NT06FT0557	succinyl-CoA synthetase, alpha chain NMB0960	907	CAG45136.1	4.050717
8073	B10	NT06FT0667	conserved hypothetical protein	907	CAG45227.1	4.025358
8077	B11	NT06FT0981	-	907	N/A	4.034179
8080	B12	NT06FT1329	GTPase of unknown function subfamily	907	CAG45802.1	4.157663
8081	C01	NT06FT1270	transcription regulator LysR family VC0896, putative	910	CAG45752.1	3.617582
8083	C02	NT06FT1486	hypothetical protein	910	CAG45936.1	3.959341
8087	C03	NT06FT0201	1-acyl-sn-glycerol-3-phosphate acyltransferase	913	CAG44813.1	3.443593
8091	C04	NT06FT1263	alternative sigma factor RpoH	913	CAG45745.1	4.019715

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
8095	C05	NT06FT1726	integrase/recombinase XerC	913	CAG46136.1	3.997809
8097	C06	NT06FT1916	3-hydroxyisobutyrate dehydrogenase, putative	913	CAG46299.1	3.626506
8099	C07	NT06FT0101	Predicted nucleoside-diphosphate sugar epimerase	916	CAG44726.1	4.00655
8101	C08	NT06FT1030	GDSL-like Lipase/Acylhydrolase, putative	916	CAG45543.1	3.996725
8103	C09	NT06FT1794	geranyltranstransferase	916	N/A	3.989083
8106	C10	NT06FT0176	licB protein , putative	919	CAG44790.1	4.154516
8109	C11	NT06FT1667	glucose-1-phosphate thymidyltransferase	919	CAG46084.1	3.990207
8112	C12	NT06FT1716	glucokinase regulator-related protein	919	CAG46127.1	4.170838
8113	D01	NT06FT1734	membrane protein, putative	919	CAG46144.1	4.001088
8115	D02	NT06FT1747	diaminopimelate decarboxylase	919	N/A	3.998912
8118	D03	NT06FT0531	ribosome-associated GTPase YjeQ	922	CAG45116.1	3.78308
8120	D04	NT06FT1751	Chain length determinant protein domain protein	922	CAG46158.1	4.158351
8122	D05	NT06FT0206	D-alanine--D-alanine ligase B	925	CAG44818.1	4.163243
8123	D06	NT06FT1408	glycosyl transferase, family 8, putative	925	CAG45870.1	3.947027
8125	D07	NT06FT1460	putative transcriptional regulator	925	CAG45918.1	3.974054
8127	D08	NT06FT0345	conserved hypothetical protein	928	CAG44944.1	3.552802
8129	D09	NT06FT0925	chitin binding protein, putative	928	CAG45449.1	3.519397
8132	D10	NT06FT1136	transporter, drug/metabolite exporter family	928	CAG45637.1	4.177802
8133	D11	NT06FT1254	-	928	N/A	3.974138
8135	D12	NT06FT1324	GTP-binding protein Era	928	CAG45797.1	3.595905
8138	E01	NT06FT0068	ATP synthase F1, gamma subunit	931	CAG44696.1	4.149302
8139	E02	NT06FT0979	transcriptional regulator, LysR family	931	CAG45497.1	3.970999
8141	E03	NT06FT1443	transcriptional regulator, LysR family, putative	931	CAG45900.1	3.585392
8144	E04	NT06FT1939	transcriptional regulator, putative	931	CAG46317.1	4.16971
8145	E05	NT06FT0260	cold shock-induced palmitoleoyl transferase	934	CAG44865.1	3.950749
8147	E06	NT06FT1371	transcription regulator LysR family VCA1058	934	CAG45835.1	3.948608
8149	E07	NT06FT1516	fructokinase (EC 2.7.1.4)	934	CAG45964.1	3.963597
8152	E08	NT06FT0287	porphobilinogen deaminase	937	CAG44892.1	4.176094
8153	E09	NT06FT0312	ubiquinol oxidase, subunit II	937	CAG44914.1	3.529349
8155	E10	NT06FT0410	acetyl-CoA carboxylase, carboxyl transferase, beta subunit	937	CAG45005.1	3.49413
8157	E11	NT06FT0772	lipote-protein ligase A	937	CAG45323.1	3.557097
8159	E12	NT06FT1624	hypothetical protein	937	CAG46048.1	3.570971
8161	F01	NT06FT1657	ATPase, AAA family protein	937	CAG46075.1	3.972252
8163	F02	NT06FT0703	tRNA delta(2)-isopentenylpyrophosphate transferase	940	CAG45262.1	4.011702
8165	F03	NT06FT1094	predicted permease	940	CAG45598.1	3.579787
8168	F04	NT06FT1194	probable fimbrial biogenesis and twitching motility protein VC1612 , putative	940	CAG45690.1	4.174468
8169	F05	NT06FT1211	conserved hypothetical protein	940	CAG45702.1	3.95
8171	F06	NT06FT1372	membrane protein, putative	940	CAG45836.1	3.961702

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8173	F07	NT06FT0462	glycyl-tRNA synthetase, alpha subunit	943	CAG45052.1	3.54825
8175	F08	NT06FT1785	tRNA pseudouridine synthase B	943	CAG46187.1	3.934252
8177	F09	NT06FT0049	Mg chelatase, subunit D/I family protein	946	N/A	3.878436
8179	F10	NT06FT0322	Protein of unknown function family	946	CAG44924.1	3.493658
8181	F11	NT06FT0508	DNA metabolism, putative	946	CAG45093.1	3.948203
8183	F12	NT06FT0950	ToIA protein superfamily	946	CAG45472.1	3.948203
8185	G01	NT06FT0502	glycosyl transferase, group 2 family protein	949	CAG45087.1	3.95785
8187	G02	NT06FT1028	chromosome segregation protein	949	CAG45541.1	3.978925
8189	G03	NT06FT1765	Uncharacterized protein conserved in bacteria	949	CAG46169.1	3.58588
8192	G04	NT06FT0233	cation ABC transporter, periplasmic cation-binding protein, putative	952	CAG44842.1	3.627101
8193	G05	NT06FT0628	putrescine ABC transporter, permease protein	952	CAG45196.1	3.953782
8195	G06	NT06FT0779	S-adenosyl-methyltransferase MraW	952	CAG45328.1	3.037815
8197	G07	NT06FT0859	Hypothetical transport protein yyaM, putative	952	CAG45392.1	3.922269
8199	G08	NT06FT1875	fructose-1,6-bisphosphatase, class II	952	CAG46264.1	3.903361
8202	G09	NT06FT0962	sodium/bile acid symporter family protein, putative	955	CAG45482.1	4.165445
8204	G10	NT06FT1036	riboflavin biosynthesis protein RibF	955	CAG45549.1	4.175916
8205	G11	NT06FT1065	lipase/esterase, putative	955	CAG45574.1	3.907853
8207	G12	NT06FT1074	Hypothetical UPF0012 protein yhcX, putative	955	N/A	3.915183
8209	H01	NT06FT1570	malonyl CoA-acyl carrier protein transacylase	955	CAG46007.1	3.935079
8211	H02	NT06FT1865	hypothetical protein	955	CAG46255.1	3.965445
8213	H03	NT06FT1915	aspartate carbamoyltransferase	955	CAG46298.1	3.564398
8219	H04	NT06FT1462	cysteine synthase/cystathionine beta-synthase family protein, putative	958	CAG45920.1	3.925887
8222	H05	NT06FT1647	YagD	958	CAG46068.1	4.10334
8223	H06	NT06FT2020	peptidase, U7 family protein	958	CAG46379.1	3.509395
8225	H07	NT06FT0541	transcriptional regulator, LysR family, putative	961	CAG45125.1	4.165453
8227	H08	NT06FT0708	HflC protein	961	CAG45267.1	3.476587
8230	H09	NT06FT0887	Ars, putative	961	CAG45416.1	4.164412
8233	H10	NT06FT1202	coproporphyrinogen III oxidase, aerobic	961	CAG45696.1	3.520291
8236	H11	NT06FT1232	rhodanese-like domain protein	961	CAG45718.1	4.155047
8237	H12	NT06FT1362	Bacterial domain of unknown function (DUF403) superfamily	961	CAG45827.1	3.527575