

***Francisella tularensis* subsp. *tularensis*,
Strain SCHU S4, Gateway® Clone Set,
Recombinant in *Escherichia coli*, Plate 7**

Catalog No. NR-19464

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For research use only. Not for human use.

Contributor:

Pathogen Functional Genomics Resource Center at the J. Craig Venter Institute

Manufacturer:

BEI Resources

Product Description:

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 does not confirm or validate individual mutants provided by the contributor.

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.

Plate viability was confirmed for NR-19464.

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.

Packaging/Storage:

NR-19464 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 1 day.

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 7, NR-19464.”

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.

Disclaimers:

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- 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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References:

- Larsson, P., et. al. "The Complete Genome Sequence of *Francisella tularensis*, the Causative Agent of Tularemia." *Nat. Genet.* 37 (2005): 153-159. PubMed: 15640799.

Table 1: *Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Plate 7 (ZFTKQ)¹

Clone ID	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
6715	A01	NT06FT1239	conserved hypothetical protein	490	CAG45725.1	-
6719	A02	NT06FT0264	hypothetical protein	493	CAG44870.1	2.578093
6721	A03	NT06FT0588	DNA polymerase IV	493	N/A	2.553753
6723	A04	NT06FT0663	RNase H	493	CAG45223.1	2
6725	A05	NT06FT1642	tRNA (guanine-N(7)-)-methyltransferase	493	N/A	2.572008
6727	A06	NT06FT0015	-	496	N/A	2.586694
6729	A07	NT06FT0205	cytidine/deoxycytidylate deaminase family protein	496	CAG44817.1	2
6733	A08	NT06FT1386	hypothetical protein	496	CAG45849.1	2
6736	A09	NT06FT1650	-	496	N/A	3.147177
6737	A10	NT06FT0236	outer membrane lipoprotein Pcp	499	CAG44844.1	2.57515
6739	A11	NT06FT0737	membrane protein, putative	499	N/A	3.222445
6741	A12	NT06FT0915	CapC protein	499	CAG45439.1	3.158317
6744	B01	NT06FT0943	peptidyl-prolyl cis-trans isomerase, FKBP-type, putative	499	CAG45465.1	2
6745	B02	NTL06FT0622	hypothetical membrane protein	499	N/A	2.150301
6747	B03	NT06FT0179	pyrophosphatase, MutT/nudix family	502	CAG44793.1	2.577689
6749	B04	NT06FT0511	RNA methyltransferase, TrmH family, group 2	502	CAG45096.1	2.579681
6751	B05	NT06FT0927	translation initiation factor IF-3	502	CAG45451.1	2
6753	B06	NT06FT1023	17 kDa lipoprotein	502	CAG45537.1	2.575697
6756	B07	NT06FT1033	lipoprotein, putative	502	CAG45546.1	3.153386
6757	B08	NT06FT1630	hypothetical protein	502	CAG46053.1	2
6759	B09	NT06FT0020	hypothetical protein	505	CAG44649.1	2
6762	B10	NT06FT0065	ATP synthase F0, B subunit	505	CAG44693.1	3.162376
6763	B11	NT06FT0268	hypothetical protein	505	CAG44874.1	3.170297
6765	B12	NT06FT0396	hypothetical protein	505	CAG44992.1	2.580198
6767	C01	NT06FT0822	glutathione peroxidase	505	CAG45366.1	3.156436
6769	C02	NT06FT0356	ribosomal protein S7	508	CAG44955.1	2.596457
6771	C03	NT06FT0520	acetyl-CoA carboxylase, biotin carboxyl carrier protein	508	CAG45105.1	3.141732
6773	C04	NT06FT0611	peptidase	508	CAG45182.1	3.163386
6776	C05	NT06FT0649	mrp protein homolog	508	CAG45213.1	2.572835
6777	C06	NT06FT1300	oxidoreductase, short-chain dehydrogenase/reductase family	508	N/A	2.584646
6779	C07	NT06FT1351	SsrA-binding protein	508	CAG45819.1	2
6781	C08	NT06FT2037	iron-sulfur cluster-binding protein, rieske family, putative	508	N/A	3.137795
6784	C09	NT06FT2066	-	508	N/A	3.159449
6785	C10	NT06FT0035	NADH-quinone oxidoreductase, B subunit	511	CAG44665.1	3.129159
6787	C11	NT06FT0306	cyclohexadienyl dehydratase, putative	511	N/A	3.158513
6790	C12	NT06FT0323	conserved hypothetical protein	511	CAG44925.1	3.146771
6792	D01	NT06FT1076	putative exported protein	511	N/A	3.154599
6793	D02	NT06FT1127	-	511	N/A	2.585127
6795	D03	NT06FT1256	benzodiazepine receptor TspO	511	CAG45739.1	3.156556
6797	D04	NT06FT2021	outer membrane protein OmpH, putative	511	CAG46380.1	2.579256
6799	D05	NT06FT2026	SSB	511	CAG46385.1	2
6801	D06	NT06FT0229	dienelactone hydrolase family protein	514	N/A	2
6805	D07	NT06FT1021	lipoprotein, putative	514	CAG45535.1	2

Clone ID	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
6807	D08	NT06FT1177	conserved hypothetical protein	514	CAG45673.1	2.579767
6809	D09	NT06FT1279	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	514	CAG45761.1	1.992218
6811	D10	NT06FT1741	related to mercuric reductase	514	CAG46150.1	2.593385
6813	D11	NT06FT1912	-	514	CAG46296.1	3.163424
6815	D12	NT06FT0329	hypothetical protein	517	CAG44930.1	3.141199
6817	E01	NT06FT0566	amidotransferase BH0023	517	CAG45145.1	2
6819	E02	NT06FT1496	Transcription elongation factor greA (Transcript cleavage factorgreA)	517	CAG45946.1	2
6824	E03	NT06FT1773	amine oxidase, flavin-containing	517	N/A	3.16441
6825	E04	NT06FT1776	cyclopropane-fatty-acyl-phospholipid synthase	517	N/A	3.17795
6827	E05	NT06FT0543	major facilitator family transporter, putative	520	N/A	2
6829	E06	NT06FT0709	low molecular weight protein-tyrosine-phosphatase	520	CAG45268.1	2
6832	E07	NT06FT1034	signal peptidase II	520	CAG45547.1	3.161538
6833	E08	NT06FT0038	NADH dehydrogenase I, E subunit	523	CAG44668.1	2
6835	E09	NT06FT0042	NADH dehydrogenase I, I subunit	523	CAG44672.1	3.166348
6837	E10	NT06FT0476	S-adenosylmethionine decarboxylase	523	CAG45063.1	3.130019
6839	E11	NT06FT0650	pantetheine-phosphate adenyllyltransferase	523	CAG45214.1	3.156788
6841	E12	NT06FT0691	predicted metal-dependent hydrolase	523	CAG45249.1	3.151052
6843	F01	NT06FT1115	mutator protein (7,8-dihydro-8-oxoguanine-triphosphatase)	523	CAG45617.1	2
6845	F02	NT06FT1191	ribosomal-protein-alanine acetyltransferase, putative	523	CAG45687.1	2.558317
6847	F03	NT06FT1236	pyrazinamidase	523	CAG45722.1	2.565966
6850	F04	NT06FT1238	isochorismatase family protein	523	CAG45724.1	2.499044
6852	F05	NT06FT1264	conserved hypothetical protein	523	CAG45746.1	3.147228
6853	F06	NT06FT1758	thioesterase family protein domain protein	523	CAG46165.1	3.152964
6855	F07	NT06FT0014	lacX protein, truncation, putative	526	N/A	2
6859	F08	NT06FT1015	phosphoribosylaminoimidazole carboxylase, catalytic subunit	526	CAG45529.1	2
6861	F09	NT06FT1439	-	526	N/A	2.581749
6863	F10	NT06FT1582	unnamed protein product; Similar to hypothetical acetyltransferase YjaB of Escherichia coli, putative	526	CAG46017.1	2.595057
6865	F11	NT06FT1803	beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ	526	CAG46203.1	2.564639
6867	F12	NT06FT0854	hypothetical protein	529	CAG45388.1	3.155009
6870	G01	NT06FT1537	Rhs element Vgr protein subfamily, putative	529	CAG45980.1	3.122873
6871	G02	NT06FT1967	Rhs element Vgr protein subfamily, putative	529	CAG46335.1	2
6875	G03	NT06FT0731	ferritin	532	CAG45285.1	2.575188
6877	G04	NT06FT0276	hypothetical protein	535	CAG44881.1	2.571963
6879	G05	NT06FT0472	homoserine kinase	535	N/A	2
6881	G06	NT06FT1064	conserved hypothetical protein	535	CAG45573.1	3.149533
6883	G07	NT06FT0189	unnamed protein product	538	N/A	3.855019
6885	G08	NT06FT0545	conserved hypothetical protein	538	CAG45128.1	3.871747
6887	G09	NT06FT0747	putative amidase	538	CAG45300.1	2.717472
6890	G10	NT06FT1022	LPXTG-motif cell wall anchor domain protein, putative	538	CAG45536.1	3.150558
6891	G11	NT06FT1084	Shy8	538	CAG45590.1	2
6894	G12	NT06FT1566	Uncharacterized ACR, COG1399	538	CAG46003.1	4.269517
6895	H01	NT06FT1805	Cell envelope, putative	538	CAG46205.1	3.135688
6899	H03	NT06FT1214	antirestriction protein, putative	541	CAG45704.1	3.560074
6901	H04	NT06FT1781	conserved hypothetical protein	541	CAG46183.1	3.436229
6903	H05	NT06FT0170	16S rRNA processing protein RimM	544	CAG44784.1	3.400735
6905	H06	NT06FT0467	hypothetical protein	544	CAG45057.1	2.426471
6908	H07	NT06FT0824	-	544	N/A	2.726103
6909	H08	NT06FT1246	related to ATP-dependent DNA helicase II, putative	544	N/A	3.137868
6911	H09	NT06FT1519	Protein, putative	544	CAG45967.1	3.273897
6913	H10	NT06FT1618	Tn10-like transposase, putative	544	N/A	2.707721
6915	H11	NT06FT1764	-	544	N/A	3.891544
6917	H12	NT06FT0597	hypothetical protein	547	CAG45169.1	2

¹All information in this table was provided by J. Craig Venter Institute at the time of deposition.