

***Francisella tularensis* subsp. *tularensis*,
Strain SCHU S4, Gateway® Clone Set,
Recombinant in *Escherichia coli*, Plate 8**

Catalog No. NR-19465

This reagent is the tangible property of the U.S. Government.

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-19465.

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-19465 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 8, NR-19465."

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/bmbli5/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 8 (ZFTKR)¹

Clone ID	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
6919	A01	NT06FT0995	peptide methionine sulfoxide reductase	547	CAG45511.1	2.736746
6922	A02	NT06FT1639	acetyltransferase, GNAT family, putative	550	CAG46061.1	2.723636
6923	A03	NT06FT0161	ribosomal protein L10	553	CAG44775.1	3.462929
6926	A04	NT06FT0219	lipoprotein Blc	553	CAG44831.1	3.508137
6927	A05	NT06FT0429	hypothetical protein	553	CAG45022.1	2.735986
6929	A06	NT06FT1361	Glutamine amidotransferases class-II domain protein	553	CAG45826.1	3.437613
6931	A07	NT06FT1636	rhodanese family protein , putative	553	CAG46059.1	3.433996
6933	A08	NT06FT1927	peptide deformylase	553	CAG46308.1	2.730561
6935	A09	NT06FT1161	inorganic pyrophosphatase	556	CAG45661.1	2.726619
6937	A10	NT06FT1539	conserved hypothetical protein	556	CAG45982.1	3.508993
6940	A11	NT06FT1969	conserved hypothetical protein	556	CAG46337.1	2.726619
6941	A12	NT06FT2067	LysE family protein, putative	556	CAG46420.1	3.444245
6943	B01	NT06FT0066	ATP synthase F1, delta subunit	559	CAG44694.1	3.457961
6945	B02	NT06FT0181	ampD protein	559	CAG44795.1	2.733453
6947	B03	NT06FT0620	AhpC/TSA family protein	559	CAG45190.1	2.73703
6949	B04	NT06FT1042	conserved hypothetical protein	559	N/A	3.454383
6953	B05	NT06FT2058	membrane protein, putative	559	N/A	2.708408
6956	B06	NT06FT0083	adenine phosphoribosyltransferase	562	CAG44711.1	3.117438
6957	B07	NT06FT0088	putative transcriptional regulator	562	CAG44721.1	2.717082
6959	B08	NT06FT1216	conserved hypothetical protein	562	CAG45705.1	3.448399
6962	B09	NT06FT0269	HAD superfamily (subfamily IIIA) phosphatase, TIGR01668, putative	565	CAG44875.1	2.720354
6963	B10	NT06FT1313	shikimate kinase	565	CAG45788.1	3.851327
6965	B11	NT06FT1347	lipoprotein, putative	565	N/A	3.440708
6968	B12	NT06FT1476	Intracellular septation protein A	565	CAG45927.1	3.138053
6969	C01	NT06FT1813	conserved hypothetical protein	565	CAG46213.1	3.433628
6971	C02	NT06FT0158	transcription termination/antitermination factor NusG	568	CAG44772.1	2
6973	C03	NT06FT0228	hypoxanthine phosphoribosyltransferase	568	CAG44838.1	2.714789
6975	C04	NT06FT0609	hypothetical protein	568	CAG45180.1	3.126761
6977	C05	NT06FT1123	deoxycytidine triphosphate deaminase	568	CAG45626.1	2.723592
6981	C06	NT06FT0256	Oligoribonuclease	571	CAG44861.1	2.735552
6983	C07	NT06FT0374	ribosomal protein L6	571	CAG44973.1	3.443082
6985	C08	NT06FT0642	-	571	N/A	2.772329
6987	C09	NT06FT0735	crossover junction endodeoxyribonuclease RuvC	571	CAG45289.1	2.714536
6989	C10	NT06FT0989	hypothetical protein	571	CAG45505.1	3.436077
6991	C11	NT06FT1141	conserved hypothetical protein	571	CAG45642.1	2.725044
6995	D01	NT06FT1616	conserved membrane protein	571	CAG46043.1	3.436077
6997	D02	NT06FT1770	hypothetical protein	571	CAG46175.1	3.448336
6999	D03	NT06FT0297	carbonic anhydrase, family 3	574	CAG44902.1	3.45993
7001	D04	NT06FT0371	ribosomal protein L5	574	CAG44970.1	3.447735
7003	D05	NT06FT0825	hypothetical protein	574	N/A	3.452962
7005	D06	NT06FT0203	Unknown function	577	N/A	2.727903
7007	D07	NT06FT0214	conserved hypothetical protein TIGR00645	577	CAG44826.1	3.443674
7009	D08	NT06FT0346	dihydrofolate reductase	577	CAG44945.1	3.435009
7014	D10	NT06FT1789	conserved hypothetical protein	577	N/A	3.005199

Clone ID	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
7015	D11	NT06FT0105	conserved hypothetical protein	580	CAG44730.1	3.432759
7017	D12	NT06FT0600	Dinucleotide-utilizing enzyme involved in molybdopterin and thiamine biosynthesis family 1	580	N/A	2.694828
7019	E01	NT06FT1809	hypothetical protein	580	CAG46209.1	2.727586
7021	E02	NT06FT1884	hypothetical protein	580	CAG46272.1	2.713793
7026	E03	NT06FT1160	phosphatase, YrbI family	583	CAG45660.1	2.734134
7027	E04	NT06FT1390	5-formyltetrahydrofolate cyclo-ligase family protein	583	CAG45853.1	2.725557
7032	E05	NT06FT1887	HsdR	583	N/A	3.552316
7033	E06	NT06FT0770	protease HslVU, subunit HslV	586	CAG45321.1	3.435154
7035	E07	NT06FT1772	PUTATIVE SENSOR HISTIDINE KINASE TRANSMEMBRANE PROTEIN, putative	586	N/A	2.721843
7037	E08	NT06FT1904	conserved hypothetical protein	586	CAG46289.1	3.44198
7039	E09	NT06FT0506	stringent starvation protein A, putative	589	CAG45091.1	2.716469
7042	E10	NT06FT1044	probable fatty acid hydroxylase, putative	589	CAG45555.1	3.531409
7043	E11	NT06FT1053	acetoacetate decarboxylase	589	N/A	2
7045	E12	NT06FT1070	anthranilate synthase component II	589	CAG45579.1	3.432937
7047	F01	NT06FT1549	IgIA	589	CAG45992.1	3.443124
7049	F02	NT06FT1759	sugar-proton symporter, putative	589	N/A	2.719864
7051	F03	NT06FT1979	IgIA	589	CAG46347.1	3.448217
7054	F04	NT06FT2010	potassium-transporting ATPase, C subunit	589	CAG46370.1	3.134126
7055	F05	NT06FT0350	ribosome recycling factor	592	CAG44949.1	3.432432
7057	F06	NT06FT0569	L-lactate dehydrogenase	592	N/A	3.442568
7060	F07	NT06FT0576	-	592	N/A	2.731419
7061	F08	NT06FT0753	-	592	N/A	3.429054
7063	F09	NT06FT0996	Superoxide dismutase [Cu-Zn] precursor	592	CAG45512.1	3.423986
7065	F10	NT06FT0225	-	595	N/A	3.482353
7067	F11	NT06FT0804	-	595	N/A	2.707563
7071	F12	NT06FT0696	thymidine kinase	598	CAG45254.1	3.43311
7077	G01	NT06FT1454	ribonuclease HII	598	CAG45911.1	3.826087
7079	G02	NT06FT1185	hypothetical protein	601	CAG45681.1	2.71381
7082	G03	NT06FT0193	membrane protein, putative	604	CAG44807.1	3.238411
7084	G04	NT06FT0257	translation elongation factor P	604	CAG44862.1	4.246689
7085	G05	NT06FT0599	lipoprotein, putative	604	CAG45171.1	2.720199
7087	G06	NT06FT1057	biotin-(acetyl-CoA carboxylase) ligase, putative	604	N/A	3.124172
7090	G07	NT06FT1463	conserved membrane protein	604	CAG45921.1	2.730132
7091	G08	NT06FT1553	-	604	N/A	3.433775
7093	G09	NT06FT1983	-	604	N/A	3.427152
7096	G10	NT06FT1999	ABC transporter, ATP-binding protein, putative	604	N/A	3.438742
7097	G11	NT06FT0575	alcohol dehydrogenase, iron-containing	607	N/A	3.443163
7099	G12	NT06FT0789	hypothetical protein	607	CAG45337.1	3.113674
7102	H01	NT06FT1121	PUTATIVE LIPOPROTEIN B PRECURSOR TRANSMEMBRANE, putative	607	CAG45624.1	3.140033
7103	H02	NT06FT1268	isochorismatase family protein	607	CAG45750.1	3.240527
7106	H03	NT06FT1595	membrane protein, putative	607	CAG46029.1	2.415157
7107	H04	NT06FT1688	Guanylate kinase (GMP kinase)	607	CAG46103.1	3.449753
7110	H05	NT06FT1742	E. coli Ada protein (O6-methylguanine-DNA methyltransferase) homolog lin0068	607	CAG46151.1	4.24547
7112	H06	NT06FT2017	-	607	N/A	4.235585
7113	H07	NT06FT0761	peptidyl-tRNA hydrolase	610	CAG45313.1	3.822951
7115	H08	NT06FT0954	MiaB-like tRNA modifying enzyme YliG, TIGR01125	610	N/A	3.422951
7117	H09	NT06FT0978	lemA protein, putative	610	CAG45496.1	4.209836
7119	H10	NT06FT1014	phosphoribosylglycinamide formyltransferase	610	CAG45528.1	2.114754
7121	H11	NT06FT1545	conserved hypothetical protein	610	CAG45988.1	3.847541
7123	H12	NT06FT1975	conserved hypothetical protein	610	CAG46343.1	2.714754

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