

***Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 11****Catalog No. NR-19468**

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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-19468 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 11, NR-19468."

**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](http://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 11 (ZFTKU)**

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
7585	A01	NT06FT1934	lipoprotein, putative	739	N/A	4.223275
7587	A02	NT06FT0638	conserved hypothetical protein	742	CAG45204.1	3.78841
7589	A03	NT06FT0948	tolQ protein	742	CAG45470.1	4.203504
7592	A04	NT06FT0973	ribonuclease PH	742	CAG45491.1	3.105121
7595	A05	NT06FT1085	3-oxoacyl-acyl carrier protein reductase	742	CAG45591.1	4.216981
7597	A06	NT06FT1608	hypothetical protein	742	CAG46037.1	4.203504
7599	A07	NT06FT0695	outer membrane protein precursor	745	CAG45253.1	4.194631
7601	A08	NT06FT1168	putative glycosidase	745	N/A	3.797315
7603	A09	NT06FT0149	membrane protein, putative	748	CAG44767.1	4.219251
7606	A10	NT06FT0435	conserved hypothetical protein	748	CAG45028.1	3.505348
7608	A11	NT06FT0885	decarboxylase family protein	748	CAG45414.1	3.502674
7609	A12	NT06FT1383	COG1738:Uncharacterized ACR, putative	748	CAG45846.1	3.796791
7611	B01	NT06FT1442	putative pirin-like protein	748	CAG45899.1	3.411765
7615	B02	NT06FT0482	UDP-2,3-diacetylglucosamine hydrolase	751	CAG45069.1	3.105193
7618	B03	NT06FT1736	amino acid permease	751	N/A	4.043941
7619	B04	NT06FT1958	predicted NAD-dependent formate dehydrogenase	751	CAG46331.1	4.214381
7622	B05	NT06FT0347	ribosomal protein S2	754	CAG44946.1	4.19496
7623	B06	NT06FT0532	hypothetical protein	754	CAG45117.1	4.225464
7625	B07	NT06FT1010	lipid A 1-phosphatase	754	CAG45524.1	3.809019
7630	B08	NT06FT2039	endonuclease/Exonuclease/phosphatase family superfamily	754	CAG46394.1	4.200265
7631	B09	NT06FT0442	conserved hypothetical protein	757	CAG45034.1	3.787318
7633	B10	NT06FT0544	copper homeostasis protein VC0730	757	CAG45127.1	3.808454
7637	B11	NT06FT0866	purine nucleoside phosphorylase	757	CAG45399.1	3.800528
7639	B12	NT06FT1139	hypothetical protein	757	CAG45640.1	4.186262
7642	C01	NT06FT1370	oxidoreductase, short chain dehydrogenase/reductase family	757	CAG45834.1	4.221929
7644	C02	NT06FT1147	BacC	760	CAG45647.1	3.815789
7645	C03	NT06FT1269	membrane protein, putative	760	CAG45751.1	4.201316
7647	C04	NT06FT1293	deoxyribodipyrimidine photolyase	760	N/A	4.223684
7649	C05	NT06FT1421	ABC transporter, periplasmic substrate-binding protein, putative	760	CAG45882.1	4.194737

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
7651	C06	NT06FT1670	formyltransferase	760	CAG46087.1	3.817105
7654	C07	NT06FT1709	hypothetical protein	760	CAG46122.1	3.184211
7655	C08	NT06FT1727	conserved hypothetical protein	760	CAG46137.1	4.194737
7659	C09	NT06FT0232	iron, putative	763	CAG44841.1	4.204456
7662	C10	NT06FT0279	branched-chain amino acid aminotransferase	763	CAG44884.1	3.201835
7663	C11	NT06FT0547	asparaginase	763	N/A	3.817824
7665	C12	NT06FT1424	conserved hypothetical protein TIGR00046	763	CAG45885.1	3.397117
7669	D01	NT06FT0403	oxidoreductase, FAD-binding, putative	766	CAG44998.1	3.815927
7671	D02	NT06FT0618	conserved hypothetical protein	766	CAG45188.1	4.220627
7674	D03	NT06FT1157	ABC transporter, ATP-binding protein	766	CAG45657.1	4.041775
7675	D04	NT06FT0125	deoxyribose-phosphate aldolase	769	CAG44747.1	3.807542
7677	D05	NT06FT0195	ABC transporter, permease protein, putative	772	N/A	3.088083
7681	D07	NT06FT1870	hypothetical protein	772	CAG46260.1	3.801813
7683	D08	NT06FT2029	succinate-semialdehyde dehydrogenase	775	N/A	4.19871
7685	D09	NT06FT2040	1-acyl-sn-glycerol-3-phosphate acyltransferase, putative	775	CAG46395.1	3.821935
7687	D10	NT06FT0108	ISSod6, transposase	778	CAG44732.1	3.79563
7689	D11	NT06FT0223	ISSod6, transposase	778	CAG44835.1	4.215938
7691	D12	NT06FT0342	ISSod6, transposase	778	CAG44942.1	4.209512
7693	E01	NT06FT0421	ISSod6, transposase	778	CAG45014.1	3.811054
7695	E02	NT06FT0630	ISSod6, transposase	778	CAG45198.1	3.811054
7699	E03	NT06FT0819	ISSod6, transposase	778	CAG45363.1	3.113111
7701	E04	NT06FT0983	ISSod6, transposase	778	N/A	3.808483
7704	E05	NT06FT1262	ISSod6, transposase	778	CAG45744.1	2.692802
7705	E06	NT06FT1282	CinA-like protein	778	N/A	3.796915
7708	E07	NT06FT1304	aldose 1-epimerase, putative	778	N/A	4.212082
7710	E08	NT06FT1525	ISSod6, transposase	778	CAG45973.1	4.199229
7712	E09	NT06FT1571	3-oxoacyl-(acyl-carrier-protein) reductase	778	CAG46008.1	4.195373
7713	E10	NT06FT1648	ISSod6, transposase	778	CAG46069.1	4.209512
7715	E11	NT06FT1681	ISSod6, transposase	778	CAG46098.1	3.424165
7717	E12	NT06FT1749	ISSod6, transposase	778	CAG46156.1	4.200514
7719	F01	NT06FT1782	oxidoreductase, short-chain dehydrogenase/reductase family, putative	778	CAG46184.1	3.802057
7721	F02	NT06FT1825	conserved hypothetical protein	778	CAG46222.1	4.176093
7723	F03	NT06FT0734	conserved hypothetical protein TIGR01033	781	CAG45288.1	3.085787
7725	F04	NT06FT0862	hydrolase, TatD family	781	CAG45396.1	3.81178
7728	F05	NT06FT1235	glycine cleavage T-protein (aminomethyl transferase) superfamily	781	CAG45721.1	4.193342
7729	F06	NT06FT1894	dihydroorotate dehydrogenase (dihydroorotate oxidase)(DHODehase) (DHODase) (DHOD), putative	781	CAG46280.1	3.099872

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
7734	F07	NT06FT1101	FeS assembly ATPase SufC	784	CAG45605.1	3.468112
7738	F08	NT06FT1431	NAD <sup>+</sup> synthetase	784	CAG45892.1	4.179847
7739	F09	NT06FT1612	hypothetical protein	784	CAG46041.1	3.784439
7741	F10	NT06FT1633	membrane protein, putative	784	CAG46056.1	3.482143
7743	F11	NT06FT1687	quinolinate synthetase complex, A subunit	784	CAG46102.1	3.086735
7745	F12	NT06FT1860	drug resistance transporter, Bcr/CflA family, putative	784	N/A	3.082908
7749	G01	NT06FT1283	glycerophosphoryl diester phosphodiesterase, putative	787	CAG45765.1	3.792884
7751	G02	NT06FT1478	ubiquinone/menaquinone biosynthesis methyltransferase UbiE	787	CAG45929.1	2.698856
7753	G03	NT06FT1696	3-deoxy-D-manno-octulosonate cytidyltransferase	787	CAG46111.1	4.188056
7755	G04	NT06FT2041	1-acyl-sn-glycerol-3-phosphate acyltransferase, putative	787	CAG46396.1	2.698856
7757	G05	NT06FT0249	urea amidolyase-related protein	790	CAG44855.1	4.18481
7761	G06	NT06FT1001	-	790	N/A	4.220253
7763	G07	NT06FT0171	tRNA (guanine-N1)-methyltransferase	793	CAG44785.1	3.094578
7765	G08	NT06FT0964	membrane protein, putative	793	CAG45484.1	3.094578
7767	G09	NT06FT1609	hydroxyacylglutathione hydrolase	793	CAG46038.1	3.083228
7769	G10	NT06FT0085	triosephosphate isomerase	796	CAG44713.1	3.805276
7775	G11	NT06FT1543	conserved hypothetical protein	796	CAG45986.1	4.182161
7777	G12	NT06FT1973	conserved hypothetical protein	796	CAG46341.1	3.174623
7779	H01	NT06FT0148	glycerol uptake facilitator protein	799	CAG44766.1	3.801001
7781	H02	NT06FT0546	conserved hypothetical protein	799	CAG45129.1	4.175219
7783	H03	NT06FT0793	nicotinamide mononucleotide transporter PnuC, putative	799	CAG45340.1	4.191489
7785	H04	NT06FT1578	membrane protein, putative	799	N/A	3.397997
7787	H05	NT06FT1795	phosphatidyltransferase homolog	799	CAG46196.1	4.185232
7789	H06	NT06FT1848	ABC transporter, permease protein	799	CAG46242.1	3.789737
7791	H07	NT06FT0319	pyridoxal kinase	802	CAG44921.1	4.169576
7793	H08	NT06FT0561	BcfH, putative	802	CAG45140.1	3.765586
7795	H09	NT06FT0791	glucokinase (EC 2.7.1.2), putative	802	N/A	3.461347
7797	H10	NT06FT1360	-	802	N/A	3.802993
7799	H11	NT06FT1651	hydrolase, TatD family	802	CAG46072.1	4.170823
7801	H12	NT06FT1888	-	802	N/A	4.169576