

Francisella tularensis subsp. tularensis, Strain SCHU S4, Gateway® Clone Set, Recombinant in Escherichia coli, Plate 2

Catalog No. NR-19459

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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-19459 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 2, NR-19459."

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/bmbl5/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 2 (ZFTKL)

| Clone | Well Position | Locus ID | Description (Gene name) | ORF Length | Accession Number | Average Depth of Coverage |
|-------|---------------|-------------|--|------------|------------------|---------------------------|
| 5679 | A01 | NT06FT0430 | ribosomal protein S21 | 232 | CAG45023.1 | 1.810345 |
| 5682 | A02 | NT06FT0591 | ABC transporter domain protein | 232 | N/A | 2.668103 |
| 5684 | A03 | NT06FT0849 | hypothetical protein | 232 | CAG45385.1 | 2 |
| 5685 | A04 | NT06FT0928 | ribosomal protein L35 | 232 | CAG45452.1 | - |
| 5688 | A05 | NT06FT1174 | ribosomal protein S21 | 232 | CAG45671.1 | 2.706897 |
| 5690 | A06 | NT06FT1295 | hypothetical protein | 232 | CAG45773.1 | 1.655172 |
| 5691 | A07 | NT06FT1839 | hypothetical protein | 232 | N/A | 3.452586 |
| 5694 | A08 | NTL06FT0987 | hypothetical protein | 232 | N/A | 2.349138 |
| 5695 | A09 | NT06FT0367 | ribosomal protein L29 | 235 | CAG44966.1 | - |
| 5697 | A10 | NT06FT0851 | ribosomal protein S21 | 235 | CAG45386.1 | 2 |
| 5699 | A11 | NT06FT1356 | putative aldehyde dehydrogenase MIS1 | 235 | N/A | 2 |
| 5701 | A12 | NT06FT1518 | hypothetical protein | 235 | CAG45966.1 | 2 |
| 5704 | B01 | NT06FT0431 | Cold shock-like protein cspE | 238 | CAG45024.1 | 2.340336 |
| 5705 | B02 | NT06FT0848 | cold shock DNA binding protein | 238 | CAG45384.1 | 2.697479 |
| 5707 | B03 | NT06FT1103 | Amidino transferase superfamily, putative | 238 | N/A | 3.277311 |
| 5709 | B04 | NT06FT1142 | transcription regulator, Cro/Ci family - related protein | 238 | CAG45643.1 | 1.848739 |
| 5716 | B06 | NT06FT1882 | hypothetical protein | 238 | N/A | 2.47479 |
| 5720 | B07 | NT06FT2019 | ferredoxin, 2Fe-2S | 238 | N/A | 3.331933 |
| 5722 | B08 | NT06FT0585 | hypothetical protein | 241 | CAG45159.1 | 2.360996 |
| 5724 | B09 | NT06FT1302 | cation transport regulator ChaB STY1282 -related protein | 241 | CAG45778.1 | - |
| 5725 | B10 | NTL06FT0760 | hypothetical lipoprotein | 241 | N/A | 1.854772 |
| 5728 | B11 | NTL06FT1052 | hypothetical protein | 241 | N/A | - |
| 5729 | B12 | NT06FT0222 | putative transport protein | 244 | N/A | 2 |
| 5731 | C01 | NT06FT1222 | hypothetical protein | 244 | N/A | 3.364754 |
| 5733 | C02 | NT06FT1336 | hypothetical protein | 244 | CAG45807.1 | 2.663934 |
| 5735 | C03 | NT06FT2000 | - | 244 | N/A | 2 |
| 5737 | C04 | NT06FT2064 | hypothetical protein | 247 | CAG46418.1 | 2 |
| 5740 | C05 | NTL06FT0234 | conserved hypothetical protein | 247 | N/A | 3.319838 |
| 5741 | C06 | NT06FT0607 | hypothetical protein | 250 | CAG45178.1 | 2 |
| 5743 | C07 | NT06FT1554 | conserved hypothetical protein | 250 | N/A | 2 |
| 5746 | C08 | NT06FT1559 | trehalase | 250 | N/A | 1.668 |

| Clone | Well Position | Locus ID | Description (Gene name) | ORF Length | Accession Number | Average Depth of Coverage |
|-------|---------------|------------|--|------------|------------------|---------------------------|
| 5747 | C09 | NT06FT1775 | conserved hypothetical protein | 250 | N/A | 3.376 |
| 5749 | C10 | NT06FT1984 | conserved hypothetical protein | 250 | N/A | 1.976 |
| 5751 | C11 | NT06FT2006 | outer membrane protein | 250 | N/A | 2.788 |
| 5753 | C12 | NT06FT0304 | hypothetical protein | 253 | CAG44907.1 | - |
| 5755 | D01 | NT06FT0307 | extracellular solute-binding lipoprotein | 253 | N/A | 3.237154 |
| 5758 | D02 | NT06FT0394 | predicted flavoprotein | 253 | N/A | - |
| 5760 | D03 | NT06FT0535 | lipoprotein, putative | 253 | N/A | 2 |
| 5762 | D04 | NT06FT0787 | DNA-directed RNA polymerase, omega subunit | 253 | CAG45336.1 | 2 |
| 5763 | D05 | NT06FT1095 | translation initiation factor IF-1 | 253 | CAG45599.1 | 1.857708 |
| 5765 | D06 | NT06FT1198 | ribosomal protein S18 | 253 | CAG45694.1 | 2.778656 |
| 5767 | D07 | NT06FT1989 | - | 253 | N/A | 2 |
| 5769 | D08 | NT06FT1272 | IS1016 family transposase, degenerate | 256 | N/A | 2 |
| 5771 | D09 | NT06FT1410 | hypothetical protein | 256 | N/A | 1.863281 |
| 5773 | D10 | NT06FT0947 | lipoprotein, putative | 259 | CAG45469.1 | 2.671815 |
| 5777 | D11 | NT06FT1607 | hypothetical protein | 259 | CAG46036.1 | 3.305019 |
| 5779 | D12 | NT06FT0012 | FnuDI restriction endonuclease | 262 | N/A | 2.770992 |
| 5781 | E01 | NT06FT0165 | conserved hypothetical protein | 262 | CAG44779.1 | 1.866412 |
| 5784 | E02 | NT06FT1223 | COG1396:Predicted transcriptional regulators, putative | 262 | CAG45708.1 | 2 |
| 5785 | E03 | NT06FT1617 | reverse transcriptase homologue ND5 i4 grp II protein | 262 | N/A | 2 |
| 5787 | E04 | NT06FT0475 | beta-galactosidase | 265 | N/A | 2 |
| 5789 | E05 | NT06FT0549 | hypothetical protein | 265 | N/A | 2 |
| 5791 | E06 | NT06FT0837 | hypothetical protein | 265 | CAG45374.1 | 3.392453 |
| 5793 | E07 | NT06FT1856 | hypothetical protein | 265 | N/A | 2 |
| 5795 | E08 | NT06FT0224 | putative transport protein | 268 | N/A | 2 |
| 5799 | E10 | NT06FT0604 | - | 271 | N/A | 3.346863 |
| 5802 | E11 | NT06FT1201 | hypothetical protein | 271 | N/A | 3.284133 |
| 5804 | E12 | NT06FT1640 | hypothetical protein | 271 | N/A | 2.675277 |
| 5806 | F01 | NT06FT1824 | hypothetical protein | 271 | N/A | 3.317343 |
| 5808 | F02 | NT06FT1842 | ribosomal protein L28-related protein | 271 | CAG46236.1 | 3.328413 |
| 5809 | F03 | NT06FT1852 | BolA-like protein | 271 | CAG46246.1 | 2.649446 |
| 5811 | F04 | NT06FT1917 | Anr-N, putative | 271 | CAG46300.1 | 2.638376 |
| 5813 | F05 | NT06FT0957 | predicted CsgA, Rossman fold oxidoreductase | 274 | N/A | 3.306569 |
| 5817 | F06 | NT06FT1744 | hypothetical protein | 274 | N/A | 3.273723 |
| 5819 | F07 | NT06FT1346 | hypothetical protein | 277 | N/A | 3.144404 |
| 5821 | F08 | NT06FT1907 | hypothetical protein | 277 | CAG46291.1 | 3.3213 |
| 5823 | F09 | NT06FT2013 | potassium-transporting ATPase, A subunit | 277 | N/A | 2.592058 |
| 5826 | F10 | NT06FT0651 | ferredoxin | 280 | CAG45215.1 | 3.260714 |
| 5827 | F11 | NT06FT0952 | lipoprotein, putative | 280 | CAG45474.1 | 2 |
| 5829 | F12 | NT06FT1286 | conserved hypothetical protein | 280 | N/A | 2.65 |
| 5831 | G01 | NT06FT1299 | hypothetical protein | 280 | CAG45776.1 | 3.289286 |
| 5833 | G02 | NT06FT1359 | transglutaminase domain protein | 280 | N/A | 3.292857 |
| 5835 | G03 | NT06FT1458 | hypothetical protein | 280 | CAG45915.1 | 2.646429 |
| 5837 | G04 | NT06FT1649 | conserved hypothetical protein | 280 | N/A | 3.267857 |

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|-------|---------------|-------------|--|------------|------------------|---------------------------|
| 5839 | G05 | NTL06FT0826 | hypothetical lipoprotein | 280 | N/A | 3.217857 |
| 5841 | G06 | NT06FT0169 | ribosomal protein S16 | 283 | CAG44783.1 | 3.275618 |
| 5843 | G07 | NT06FT0404 | ribosomal protein L31 | 283 | CAG44999.1 | 3.300353 |
| 5845 | G08 | NT06FT0492 | - | 283 | N/A | 2.272085 |
| 5847 | G09 | NT06FT0924 | unknown function U3, putative | 283 | CAG45448.1 | 3.279152 |
| 5849 | G10 | NT06FT1334 | type I restriction enzyme EcoEI specificity protein | 283 | N/A | 2.650177 |
| 5855 | G12 | NT06FT0368 | ribosomal protein S17 | 286 | CAG44967.1 | 3.258741 |
| 5858 | H01 | NT06FT0975 | hypothetical protein | 286 | CAG45493.1 | 2.237762 |
| 5859 | H02 | NT06FT1290 | hypothetical protein | 286 | CAG45770.1 | 3.167832 |
| 5861 | H03 | NT06FT0826 | similar to chloromuconate cycloisomerase ykfB of B. subtilis | 289 | N/A | 3.290657 |
| 5864 | H04 | NT06FT0875 | ribosomal protein L27 | 289 | CAG45406.1 | 3.311419 |
| 5865 | H05 | NT06FT1230 | hypothetical protein | 292 | CAG45716.1 | 3.30137 |
| 5867 | H06 | NT06FT1558 | major facilitator family transporter | 292 | N/A | 3.270548 |
| 5872 | H07 | NT06FT0553 | hypothetical protein | 295 | CAG45133.1 | 2.576271 |
| 5873 | H08 | NT06FT0594 | Glutaredoxin | 295 | CAG45166.1 | 2.657627 |
| 5875 | H09 | NT06FT0803 | FORMYLTETRAHYDROFOLATE DEFORMYLASE | 295 | N/A | 2.213559 |
| 5877 | H10 | NT06FT1227 | hypothetical protein | 295 | CAG45712.1 | 2.613559 |
| 5879 | H11 | NT06FT1253 | drug resistance transporter, Bcr/CflA family protein, putative | 295 | N/A | 3.298305 |
| 5881 | H12 | NT06FT2034 | - | 295 | N/A | 3.284746 |