

***Mycobacterium tuberculosis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 15**

**Catalog No. NR-19651**

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

**For research use only. Not for use in humans.**

**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 *Mycobacterium tuberculosis* (*M. tuberculosis*) Gateway® clone set consists of 42 plates which contain 3724 sequence validated clones [3294 *M. tuberculosis*, strain H37Rv clones supplemented with 430 unique open reading frames (ORF) from *M. tuberculosis*, strain CDC1551] cloned in *Escherichia coli* (*E. coli*) DH10B-T1 cells. Each ORF was recombined in vector pDONR™221 with an ATG start codon and no stop codon. The sequence was validated by full-length sequencing of each entry 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 orientation and viability were confirmed for NR-19651.

**Material Provided:**

Each inoculated well of the 96-well plate contains approximately 60 µL of culture in Luria Bertani (LB) broth containing 50 µg/mL kanamycin supplemented with 15% glycerol.

**Packaging/Storage:**

NR-19651 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: 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: *Mycobacterium tuberculosis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 15, NR-19651.”

**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 \(BMBL\)](#), 6th ed. Washington, DC: U.S. Government Printing Office, 2020.

**Disclaimers:**

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**References:**

1. Cole, S. T., et al. "Deciphering the Biology of *Mycobacterium tuberculosis* from the Complete Genome Sequence." *Nature* 393 (1998): 537-544. PubMed: 9634230.

2. Camus, J. C., et al. "Re-Annotation of the Genome Sequence of *Mycobacterium tuberculosis* H37Rv." *Microbiology* 148 (2002): 2967-2973. PubMed: 12368430.

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**Table 1: *Mycobacterium tuberculosis* Gateway® Clones, Plate 15 (ZMTLE)<sup>1</sup>**

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
40645	A01	427	Rv1871c	hypothetical protein Rv1871c	NP_216387.1	2
40637	A02	427	Rv0870c	hypothetical protein Rv0870c	NP_215385.1	2
40656	A03	427	Rv3541c	hypothetical protein Rv3541c	NP_218058.1	1.5971897
40642	A04	427	Rv1643	50S ribosomal protein L20	NP_216159.1	2
40639	A05	427	Rv1034c	transposase	NP_215550.1	2.20140515
40651	A06	427	Rv2661c	hypothetical protein Rv2661c	NP_217177.1	2
40654	A07	427	Rv3354	hypothetical protein Rv3354	NP_217871.1	2
40646	A08	427	Rv2186c	hypothetical protein Rv2186c	NP_216702.1	2
40647	A09	427	Rv2556c	hypothetical protein Rv2556c	NP_217072.1	2.56206089
40630	A10	427	Rv0076c	hypothetical protein Rv0076c	NP_214590.1	2.57142857
40644	A11	427	Rv1720c	hypothetical protein Rv1720c	NP_216236.1	2.60421546
40648	A12	427	Rv2562	hypothetical protein Rv2562	NP_217078.1	2
40634	B01	427	Rv0786c	hypothetical protein Rv0786c	NP_215300.1	3.05854801
40652	B02	427	Rv2705c	hypothetical protein Rv2705c	NP_217221.1	2
40664	B04	430	Rv1671	hypothetical protein Rv1671	NP_216187.1	2.57209302
40658	B05	430	Rv0396	hypothetical protein Rv0396	NP_214910.1	3.24418605
40666	B06	430	Rv2523c	4'-phosphopantetheinyl transferase	NP_217039.1	2
40659	B07	430	Rv0595c	hypothetical protein Rv0595c	NP_215109.1	2
40662	B08	430	Rv0847	lipoprotein LpqS	NP_215362.1	2.9
40665	B09	430	Rv2359	ferric uptake regulation protein FURB	NP_216875.1	2
40660	B10	430	Rv0652	50S ribosomal protein L7/L12	NP_215166.1	3.44651163
40661	B11	430	Rv0827c	transcriptional regulatory protein	NP_215342.1	2
40674	B12	430	Rv3750c	excisionase	NP_218267.1	2.92325581
40673	C01	430	Rv3384c	hypothetical protein Rv3384c	NP_217901.1	3.05116279
40689	C03	433	Rv2759c	hypothetical protein Rv2759c	NP_217275.1	2
40682	C04	433	Rv1066	hypothetical protein Rv1066	NP_215582.1	2
40676	C05	433	Rv0034	hypothetical protein Rv0034	NP_214548.1	3.18013857
40683	C06	433	Rv1224	sec-independent translocase	NP_215740.1	2
40690	C07	433	Rv3110	pterin-4- $\alpha$ -carbinolamine dehydratase MoaB1	YP_177926.1	2.4665127
40691	C08	433	Rv3742c	oxidoreductase	NP_218259.1	2
40686	C10	433	Rv1838c	hypothetical protein Rv1838c	NP_216354.1	2
40680	C11	433	Rv0624	hypothetical protein Rv0624	NP_215138.1	2.59122402
40687	C12	433	Rv2183c	hypothetical protein Rv2183c	NP_216699.1	-
40688	D01	433	Rv2549c	hypothetical protein Rv2549c	NP_217065.1	2
40697	D02	436	Rv2451	hypothetical protein Rv2451	NP_216967.1	2
40695	D03	436	Rv1616	hypothetical protein Rv1616	NP_216132.1	2
40696	D04	436	Rv2010	hypothetical protein Rv2010	NP_216526.1	2
40692	D05	436	Rv0718	30S ribosomal protein S8	NP_215232.1	2
40698	D06	436	Rv3069	camphor resistance protein CrcB	NP_217585.1	2
40700	D07	436	Rv3135	PPE family protein	YP_177934.1	2.5733945
40728	D08	439	Rv3716c	hypothetical protein Rv3716c	NP_218233.1	2.65831435
40711	D09	439	Rv1414	hypothetical protein Rv1414	NP_215930.1	2

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
40712	D10	439	Rv1744c	hypothetical protein Rv1744c	NP_216260.1	2
40718	D12	439	Rv2600	integral membrane protein	NP_217116.1	3.14578588
40713	E01	439	Rv1947	hypothetical protein Rv1947	NP_216463.1	2
40716	E03	439	Rv2527	hypothetical protein Rv2527	NP_217043.1	2
40726	E04	439	Rv3607c	dihydroneopterin aldolase FolB	YP_177996.1	2.58997722
40721	E05	439	Rv3078	hydroxylaminobenzene mutase HAB	NP_217594.1	2
40706	E06	439	Rv0609	hypothetical protein Rv0609	NP_215123.1	2.59453303
40717	E07	439	Rv2532c	hypothetical protein Rv2532c	NP_217048.1	-
40722	E08	439	Rv3143	response regulator	NP_217659.1	2
40732	E09	442	Rv1826	glycine cleavage system protein H	NP_216342.1	2
40737	E10	442	Rv2774c	hypothetical protein Rv2774c	NP_217290.1	2
40735	E11	442	Rv2169c	transmembrane protein	NP_216685.1	2
40740	E12	442	Rv3852	histone-like protein HNS	NP_218369.1	2
40730	F01	442	Rv0856	hypothetical protein Rv0856	NP_215371.1	2
40734	F02	442	Rv2061c	hypothetical protein Rv2061c	NP_216577.1	2
40733	F03	442	Rv1903	hypothetical protein Rv1903	NP_216419.1	3.57239819
40736	F04	442	Rv2596	hypothetical protein Rv2596	NP_217112.1	2
40729	F05	442	Rv0395	hypothetical protein Rv0395	NP_214909.1	2
40731	F06	442	Rv1561	hypothetical protein Rv1561	NP_216077.1	2
40750	F07	445	Rv1976c	hypothetical protein Rv1976c	NP_216492.1	2
40753	F08	445	Rv2358	ArsR family transcriptional regulator	NP_216874.1	3.51235955
40745	F09	445	Rv1042c	IS like-2 transposase	NP_215558.1	2.15955056
40743	F10	445	Rv0871	cold shock-like protein B CspB	NP_215386.1	2
40749	F11	445	Rv1962c	hypothetical protein Rv1962c	NP_216478.1	2.18651685
40746	F12	445	Rv1149	transposase	NP_215665.1	2
40748	G01	445	Rv1914c	hypothetical protein Rv1914c	NP_216430.1	2
40747	G02	445	Rv1891	hypothetical protein Rv1891	NP_216407.1	2
40752	G03	445	Rv2233	hypothetical protein Rv2232	NP_216748.2	3.16629213
40741	G04	445	Rv0582	hypothetical protein Rv0582	NP_215096.1	2.57303371
40742	G05	445	Rv0627	hypothetical protein Rv0628c	NP_215142.1	2
40766	G06	448	Rv1444c	hypothetical protein Rv1444c	NP_215960.1	2
40773	G07	448	Rv2445c	nucleoside diphosphate kinase	NP_216961.1	2
40775	G08	448	Rv3067	hypothetical protein Rv3067	NP_217583.1	2
40774	G09	448	Rv2674	hypothetical protein Rv2674	NP_217190.1	2
40767	G10	448	Rv1542c	hemoglobin glbN	NP_216058.1	2
40772	G11	448	Rv2432c	hypothetical protein Rv2432c	NP_216948.1	2
40769	G12	448	Rv1573	phiRV1 phage protein	NP_216089.1	3.20089286
40763	H01	448	Rv0420c	transmembrane protein	NP_214934.1	2
40778	H02	448	Rv3412	hypothetical protein Rv3412	NP_217929.1	2
40757	H03	448	Rv0141c	hypothetical protein Rv0141c	NP_214655.1	2.59151786
40756	H04	448	Rv0095c	hypothetical protein Rv0095c	NP_214609.1	2
40781	H05	451	Rv0549c	hypothetical protein Rv0549c	NP_215063.1	2.57871397
40787	H06	451	Rv2137c	hypothetical protein Rv2137c	NP_216653.1	2
40782	H07	451	Rv0598c	hypothetical protein Rv0598c	NP_215112.1	2
40791	H08	451	Rv2923c	hypothetical protein Rv2923c	NP_217439.1	3.23281596
40786	H09	451	Rv2074	hypothetical protein Rv2074	NP_216590.1	3.09534368
40792	H10	451	Rv3288c	hypothetical protein Rv3288c	NP_217805.1	2
40796	H11	451	Rv3840	transcriptional regulatory protein	NP_218357.1	3.10864745
40805	H12	454	Rv2757c	hypothetical protein Rv2757c	NP_217273.1	3.22907489

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