Mycobacterium tuberculosis Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 38

Catalog No. NR-19674

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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 *att*B substrate (*att*B-PCR product or a linearized *att*B expression clone) with an *att*P substrate (pDONR™221) to create an *att*L-containing entry clone. The entry clone contains recombinational cloning sites, *att*L1 and *att*L2 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-19674.

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-19674 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 38, NR-19674."

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. 6th ed. Washington, DC: U.S. Government Printing Office, 2020; see www.cdc.gov/biosafety/publications/bmbl5/index.htm.

Disclaimers:

You are authorized to use this product for research use only. It is not intended for human use.

Use of this product is subject to the terms and conditions of the BEI Resources Material Transfer Agreement (MTA). The MTA is available on our Web site at www.beiresources.org.

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Use Restrictions:

This material is distributed for internal research, non-

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.

Support Provided by NIAID

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Table 1: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 38 (ZMTMB)[1]

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
11008	A02	1774	Rv3409c	cholesterol oxidase precursor	NP_217926.1	7.218714769
11064	A03	1774	Rv3132c	two component sensor histidine kinase DEVS	NP_217648.1	7.399098083
11068	A04	1777	Rv1349	drugs-transport transmembrane ATP-binding protein ABC transporter	NP_215865.1	6.949915588
10976	A05	1780	Rv2941	acyl-CoA synthetase	NP_217457.1	7.542696629
11062	A06	1780	Rv2483c	bifunctionnal putative L-3-phosphoserine phosphatase/1-acyl-SN-glycerol-3-phosphate acyltransferase	NP_216999.1	7.308426966
10967	A07	1780	Rv1562c	maltooligosyltrehalose trehalohydrolase TreZ	YP_177819.1	6.698876404
10911	A08	1780	Rv2608	PPE family protein	YP_177893.1	7.162921348
10952	A09	1786	Rv1273c	drugs-transport transmembrane ATP-binding protein ABC transporter	NP_215789.1	7.422732363
10991	A10	1786	Rv0118c	putative oxalyl-CoA decarboxylase	NP_214632.1	6.694848824
10908	A11	1789	Rv1552	fumarate reductase flavoprotein subunit	NP_216068.1	8.358300727
11056	A12	1789	Rv1521	acyl-CoA synthetase	NP_216037.1	8.397428731
10906	B02	1792	Rv1529	acyl-CoA synthetase	NP_216045.1	8.267857143
11088	B03	1792	Rv0754	PE-PGRS family protein	YP_177752.1	5.471540179
11026	B04	1795	Rv3302c	glycerol-3-phosphate dehydrogenase	NP_217819.1	8.084122563
11034	B05	1795	Rv0404	acyl-CoA synthetase	NP_214918.1	8.143175487
11018	B06	1798	Rv1699	CTP synthetase	NP_216215.1	7.9243604
11006	B07	1801	Rv1696	DNA repair protein recN (recombination protein N)	NP_216212.1	6.681288173
11081	B08	1801	Rv2787	hypothetical protein Rv2787	NP_217303.1	8.162687396
10963	B09	1801	Rv1069c	hypothetical protein Rv1069c	NP_215585.1	6.541365908
10948	B10	1804	Rv0151c	PE family protein	YP_177695.1	8.087028825
11050	B11	1807	Rv1431	hypothetical protein Rv1431	NP_215947.1	8.157719978
11070	B12	1810	Rv3318	succinate dehydrogenase flavoprotein subunit	NP_217835.1	8.203867403
11238	C01	1813	Rv1459c	integral membrane protein	NP_215975.1	8.200772201
11248	C02	1813	Rv3871	hypothetical protein Rv3871	NP_218388.1	8.171538886
11226	C03	1816	Rv2214c	short chain dehydrogenase	NP_216730.1	7.883810573
11277	C04	1816	Rv2264c	hypothetical protein Rv2264c	NP_216780.1	7.281387665
11096	C05	1819	Rv0917	glycine betaine transport integral membrane protein BetP	NP_215432.1	7.73062122
11160	C06	1819	Rv3797	acyl-CoA dehydrogenase FADE35	NP_218314.1	8.213853766
11170	C07	1831	Rv1779c	integral membrane protein	NP_216295.1	8.206990715
11194	C08	1837	Rv1508c	hypothetical protein Rv1508A	YP_177649.1	8.20413718
11240	C09	1840	Rv2187	long-chain-fatty-acid-CoA ligase fadD15 (fatty-acid-CoA synthetase) (fatty-acid-CoA synthase)	NP_216703.1	7.916304348
11104	C10	1849	Rv2864c	penicillin-binding lipoprotein	NP_217380.1	8.132504056
11168	C11	1849	Rv3077	hydrolase	YP_177923.1	7.979989183
11206	C12	1858	Rv0211	phosphoenolpyruvate carboxykinase	NP_214725.1	7.953175457
11126	D01	1867	Rv1467c	acyl-CoA dehydrogenase FADE15	NP_215983.1	7.893947509
11230	D02	1870	Rv1798	hypothetical protein Rv1798	NP_216314.1	7.826203209

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Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
11251	D03	1882	Rv1286	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	NP_215802.1	7.876195537
11258	D04	1885	Rv0193c	hypothetical protein Rv0193c	NP_214707.1	7.736870027
11136	D05	1894	Rv3003c	acetolactate synthase 1 catalytic subunit	YP_177917.1	7.623020063
11192	D06	1897	Rv2950c	acyl-CoA synthetase	NP_217466.2	8.024775962
11262	D07	1900	Rv0312	hypothetical protein Rv0312	NP_214826.1	7.921052632
11215	D08	1909	Rv1354c	hypothetical protein Rv1354c	NP_215870.1	7.697223677
11236	D09	1912	Rv3436c	glucosamine--fructose-6-phosphate aminotransferase	NP_217953.1	7.891736402
11219	D10	1918	Rv2917	hypothetical protein Rv2917	NP_217433.1	7.577163712
11110	D11	1918	Rv3762c	hydrolase	NP_218279.1	7.717935349
11188	D12	1918	Rv0014c	transmembrane serine/threonine-protein kinase B PKNB (protein kinase B) (STPK B)	NP_214528.1	7.475495308
11244	E01	1918	Rv2930	acyl-CoA synthetase	NP_217446.2	7.927528676
11178	E02	1924	Rv1165	GTP-binding translation elongation factor TypA	NP_215681.1	7.865904366
11204	E03	1939	Rv3156	NADH dehydrogenase subunit L	NP_217672.1	7.401753481
11200	E04	1945	Rv1166	lipoprotein LpqW	NP_215682.1	7.630848329
11264	E05	1951	Rv0669c	hydrolase	NP_215183.1	7.833931317
11129	E06	1957	Rv2343c	DNA primase	NP_216859.1	6.201328564
11098	E07	1960	Rv0342	isoniazid inductible gene protein INIA	NP_214856.1	7.606632653
11282	E08	1966	Rv2402	hypothetical protein Rv2402	NP_216918.1	7.805696846
11124	E09	1969	Rv2394	gamma-glutamyltranspeptidase precursor GgtB	NP_216910.1	7.845606907
11210	E10	1975	Rv2191	hypothetical protein Rv2191	NP_216707.1	7.946329114
11100	E11	1990	Rv3391	short chain dehydrogenase	NP_217908.1	7.214572864
11167	E12	1990	Rv0873	acyl-CoA dehydrogenase FADE10	NP_215388.1	6.363819095
11222	F01	1996	Rv2201	asparagine synthetase AsnB	NP_216717.1	6.596693387
11150	F02	1996	Rv2332	malate dehydrogenase	NP_216848.2	7.644789579
11122	F03	1999	Rv2455c	oxidoreductase alpha subunit	NP_216971.1	7.260630315
11268	F04	1999	Rv1364c	hypothetical protein Rv1364c	YP_177802.1	7.632316158
11209	F05	1999	Rv2404c	GTP-binding protein LepA	NP_216920.1	6.815907954
11116	F06	2002	Rv2501c	acetyl-/propionyl-coenzyme A carboxylase subunit alpha	NP_217017.1	7.664835165
11162	F07	2005	Rv1800	PPE family protein	YP_177839.1	7.607481297
11120	F08	2005	Rv1402	primosome assembly protein PriA	NP_215918.1	6.463341646
11242	F09	2011	Rv1469	cation transporter P-type ATPase D	NP_215985.1	6.860268523
11165	F10	2011	Rv2690c	hypothetical protein Rv2690c	NP_217206.1	7.05619095
11386	F11	2029	Rv0198c	zinc metalloprotease	NP_214712.1	7.521931986
11288	F12	2032	Rv1329c	ATP-dependent helicase DING	NP_215845.1	7.405019685
11294	G01	2038	Rv3876	hypothetical protein Rv3876	NP_218393.1	5.626104024
11446	G02	2041	Rv0973c	acetyl-/propionyl-coenzyme A carboxylase subunit alpha	NP_215488.1	7.955414013
11473	G03	2062	Rv1175c	NADPH dependent 2,4-dienoyl-CoA reductase	NP_215691.1	6.511154219
11451	G04	2095	Rv0111	transmembrane acyltransferase	NP_214625.1	6.988066826
11296	G05	2119	Rv3051c	ribonucleotide-diphosphate reductase subunit alpha	NP_217567.1	6.812175555
11300	G06	2125	Rv2874	integral membrane C-type cytochrome biogenesis protein DipZ	NP_217390.1	8.029647059
11343	G07	2137	Rv2721c	hypothetical protein Rv2721c	NP_217237.1	7.196069256
11415	G08	2140	Rv3198c	glutaredoxin protein	YP_177941.1	6.45
11390	G10	2155	Rv2948c	acyl-CoA synthetase	NP_217464.1	7.618097448
11332	G11	2167	Rv1030	potassium-transporting ATPase subunit B	NP_215546.1	8.101522843
11312	G12	2182	Rv0005	DNA gyrase subunit B	NP_214519.1	7.068744271
11376	H01	2185	Rv1355c	hypothetical protein Rv1355c	NP_215871.1	7.774828375
11330	H02	2194	Rv3270	metal cation-transporting P-type ATPase C CtpC	NP_217787.1	7.783500456
11362	H03	2200	Rv0860	fatty oxidation protein FadB	NP_215375.1	7.216363636
11306	H05	2203	Rv3061c	acyl-CoA dehydrogenase FADE22	NP_217577.1	7.856559237
11403	H06	2230	Rv2435c	cyclase	NP_216951.1	7.399103139
11421	H07	2233	Rv0271c	acyl-CoA dehydrogenase FADE6	NP_214785.1	5.800268697
11302	H08	2233	Rv1326c	glycogen branching enzyme	NP_215842.1	7.938199731
11470	H09	2251	Rv2973c	ATP-dependent DNA helicase RecG	NP_217489.1	7.128387383
11086	H10	2260	Rv1908c	catalase-peroxidase-peroxynitritase T KATG	NP_216424.1	7.721238938
11285	H11	2275	Rv0066c	isocitrate dehydrogenase	NP_214580.1	7.195164835
11408	H12	2290	Rv1493	methylmalonyl-CoA mutase	NP_216009.1	7.523580786

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

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