

SUPPORTING INFECTIOUS DISEASE RESEARCH

Salmonella enterica subsp. enterica, Strain Ty2 (Serovar Typhi), Gateway[®] Clone Set, Recombinant in *Escherichia coli*, Plate 13

Catalog No. NR-19534

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Contributor:

Pathogen Functional Genomics Resource Center at the J. Craig Venter Institute

Manufacturer:

BEI Resources

Product Description:

Clone plates are replicated using a BioMek® FX robot. 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 only confirms the clone plate orientation and viability of randomly picked clones. BEI Resources does not confirm or validate individual clone identities provided by the contributor.

The Salmonella enterica subsp. enterica (S. enterica subsp. enterica), strain Ty2 (serovar Typhi), Gateway[®] clone set consists of approximately 3380 sequence validated clones from S. enterica subsp. enterica, strain Ty2, cloned in Escherichia coli (E. coli) DH10B-T1 cells. Each open reading frame was constructed in vector pDONR™221 (Invitrogen™) with an ATG 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 orientation and viability were confirmed for NR-19534.

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-19534 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:

- Scrape top of frozen well with a pipette tip and streak onto agar plate.
- 2. Incubate the plates at 37°C for 24 hours.

Citation:

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: Salmonella enterica subsp. enterica, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in Escherichia coli, Plate 13, NR-19534."

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.

Disclaimers:

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Fax: 703-365-2898



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References:

 Deng, W., et al. "Comparative Genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18." <u>J.</u> <u>Bacteriol.</u> 185 (2003): 2330-2337. PubMed: 12644504.

ATCC[®] is a trademark of the American Type Culture Collection.

Table 1: Salmonella enterica subsp. enterica, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in Escherichia coli, Plate 13 (ZSTDM)¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
88005	A01	t2772	oxygen-related invasion protein	613	NP_806473.1	-
87917	A02	t2977	hypothetical protein t2977	613	NP_806669.2	2
87997	A03	t3429	phage baseplate assembly protein	613	NP_807092.1	1.954323
88189	A04	t3939	holo-(acyl carrier protein) synthase 2	613	NP_807550.1	2
87889	A05	t0751	deoxycytidine triphosphate deaminase	616	NP_804595.1	1.647727
88193	A06	t1058	lipoprotein	616	NP_804875.1	2
87969	A07	t2288	TetR family transcriptional regulator	616	NP_806029.1	2
88209	A08	t3103	esterase	616	NP_806786.1	2
88205	A09	t3877	3-methyl-adenine DNA glycosylase	616	NP_807495.1	1.423701
87874	A10	t0518	hypothetical protein t0518	589	NP_804375.1	2
87922	A11	t0544	NADH dehydrogenase subunit J	589	NP_804401.1	2
87866	A12	t0762	colanic acid biosynthesis acetyltransferase WcaF	589	NP_804605.1	2
87906	B01	t0820	propanediol utilization protein PduT	589	NP_804660.1	2
87994	B02	t1783	hypothetical protein t1783	589	NP_805557.1	2
88150	B03	t1886	bacteriophage protein	589	NP_805654.1	2
88114	B04	t2320	type-1 fimbrial protein subunit A	589	NP_806054.1	2
87986	B05	t0220	ribosome recycling factor	592	NP_804101.1	2
88106	B06	t0616	thiol:disulfide interchange protein	592	NP_804472.1	1.425676
88046	B07	t1119	outer membrane invasion protein	592	NP_804932.1	2
88038	B08	t1571	thiol peroxidase	592	NP_805353.1	2
87862	B09	t2635	hypothetical protein t2635	592	NP_806346.1	2
88066	B10	t3942	hypothetical protein t3942	592	NP_807553.1	2
87910	B11	t4458	hypothetical protein t4458	592	NP_808045.1	2
87982	B12	t4631	fimbrial subunit	592	NP_808201.1	2
88010	C01	t1423	spermidine N1-acetyltransferase	595	NP_805217.1	2
88134	C02	t1773	RNase III inhibitor	595	NP_805547.1	2
88142	C03	t2296	hypothetical protein t2296	595	NP_806037.1	2
88058	C04	t0152	N-acetyl-anhydromuranmyl-L-alanine amidase	598	NP_804035.1	1.879599
87902	C05	t1855	lipoprotein	598	NP_805624.1	2
87926	C06	t3008	hypothetical protein t3008	598	NP_806700.1	2
88078	C07	t4012	ADP-ribose diphosphatase NudE	598	NP_807622.2	2
88222	C08	t4036	para-aminobenzoate synthase component II	598	NP_807645.1	2

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
88122	C09	t0009	hypothetical protein t0009	601	NP_803894.1	2
87978	C10	t0187	fimbrial protein	601	NP_804070.1	2
87858	C11	t0251	D,D-heptose 1,7-bisphosphate phosphatase	601	NP_804131.1	2
88218	C12	t2160	DNA recombinase	601	NP_805911.1	2
88138	D01	t2717	fructose-1-phosphatase	601	NP_806423.1	2
88054	D02	t3233	3-deoxy-D-manno-octulosonate 8- phosphate phosphatase	601	NP_806909.1	2
87942	D03	t3577	hypothetical protein t3577	601	NP_807220.1	2
88002	D04	t3673	hypothetical protein t3673	601	NP_807309.2	2
88170	D05	t4386	elongation factor P	601	NP_807977.1	2
88158	D06	t0508	3-octaprenyl-4-hydroxybenzoate carboxy- lyase	604	NP_804365.1	1.456954
88070	D07	t2394	lipoprotein	604	NP_806124.1	2
88030	D08	t3402	repressor protein	604	NP_807065.1	2
87950	D09	t0369	glycine cleavage system transcriptional repressor	607	NP_804238.2	2
88174	D10	t0644	elongation factor P	607	NP_804496.1	2
88110	D11	t1346	DNA-invertase	607	NP_805145.1	2
88042	D12	t2239	palmitoyl transferase	607	NP_805981.1	2
88178	E01	t4033	peptidyl-prolyl cis-trans isomerase A	607	NP_807642.1	2
88034	E02	t0382	hypothetical protein t0382	610	NP_804251.1	-
88226	E03	t0411	hypothetical protein t0411	610	NP_804280.1	2
87930	E04	t1530	hypothetical protein t1530	610	NP_805316.1	2
87898	E05	t3659	fimbrial subunit protein	610	NP_807296.1	2
88086	E06	t0810	thiosulfate reductase electron transport protein	613	NP_804651.1	1.71615
88118	E07	t1052	hypothetical protein t1052	613	NP_804869.1	2
87946	E08	t4309	phage baseplate assembly protein	613	NP_807905.1	2
87954	E09	t1299	superoxide dismutase	616	NP_805100.1	2
87886	E10	t1327	Na(+)-translocating NADH-quinone reductase subunit E	616	NP_805128.1	2
88198	E11	t2460	ACP phosphodiesterase	616	NP_806190.1	2
88186	E12	t2940	fimbrial protein	616	NP_806633.1	2
88321	F01	t4230	hypothetical protein t4230	616	NP_807832.1	2
88509	F02	t0190	fimbrial protein	619	NP_804073.1	1.720517
88585	F03	t1031	free methionine-(R)-sulfoxide reductase	619	NP_804849.1	2
88501	F04	t4283	hypothetical protein t4283	619	NP_807881.1	2
88493	F05	t0265	neutral amino-acid efflux protein	622	NP_804142.1	2
88233	F06	t2171	potassium-transporting ATPase subunit C	622	NP_805922.1	2
88597	F07	t4389	transcriptional regulator	622	NP_807980.1	2
88465	F08	t1266	pathogenicity island effector protein	625	NP_805069.1	2
88269	F09	t1578	transcriptional regulator	625	NP_805360.1	2
88393	F10	t1624	GTP cyclohydrolase II	625	NP_805402.1	2
88413	F11	t1631	cob(l)yrinic acid a,c-diamide adenosyltransferase	625	NP_805409.1	2
88589	F12	t2636	heat shock protein GrpE	625	NP_806347.1	2
88285	G01	t3462	hypothetical protein t3462	625	NP_807118.1	2
88497	G02	t1143	regulatory protein	628	NP_804954.1	2
88397	G03	t2822	decarboxylase	628	NP_806519.1	2
88405	G04	t3434	hypothetical protein t3434	628	NP_807097.1	2
88385	G05	t0231	ribonuclease HII	631	NP_804112.1	2
88517	G06	t1087	hydrogenase I maturation protease	631	NP_804902.1	2

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88401	G07	t1517	tellurite resistance protein TehB	631	NP_805303.1	2
88353	G08	t1801	TrpR binding protein WrbA	631	NP_805574.1	2
88265	G09	t3536	hypothetical protein t3536	631	NP_807183.1	2
88389	G10	t3786	nucleoid occlusion protein	631	NP_807408.1	2
88557	G11	t3950	16S rRNA m(2)G966-methyltransferase	631	NP_807561.1	2
88461	G12	t3595	phosphatase	634	NP_807238.1	2
88313	H01	t0609	cytochrome c-type protein NapC	637	NP_804465.1	2
88429	H02	t0731	hypothetical protein t0731	637	NP_804575.1	2
88333	H03	t1568	DNA-binding protein	637	NP_805350.1	2
88473	H04	t2461	peroxidase	637	NP_806191.1	2
88573	H05	t2843	hypothetical protein t2843	637	NP_806540.1	2
88297	H06	t0114	Isopropylmalate isomerase small subunit	640	NP_803997.1	2
88545	H07	t0567	Ais protein	640	NP_804424.1	2
88529	H08	t1319	glutathionine S-transferase	640	NP_805120.1	2
88437	H09	t1848	hypothetical protein t1848	640	NP_805617.1	2
88477	H10	t3272	transcriptional regulator	640	NP_806947.1	2
88453	H11	t3326	hypothetical protein t3326	640	NP_806994.1	2
88549	H12	t3432	phage tail protein	640	NP_807095.1	2

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

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