

Salmonella enterica subsp. enterica, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in Escherichia coli, Plate 19

Catalog No. NR-19540

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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-19540.

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-19540 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 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 19, NR-19540."

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

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Table 1: *Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 19 (ZSTDs)¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
90517	A01	t0294	transcriptional regulator	799	NP_804170.1	2
90661	A02	t2820	DeoR family transcriptional regulator	799	NP_806517.1	2
90829	A03	t4504	hypothetical protein t4504	799	NP_808091.1	2
90577	A04	t2629	tRNA (guanine-N-(1)-methyltransferase	802	NP_806340.1	2
90505	A05	t2749	formate hydrogenlyase subunit 7	802	NP_806450.1	2
90809	A06	t3537	triosephosphate isomerase	802	NP_807184.1	2
90801	A07	t3906	diguanylate phosphodiesterase	802	NP_807520.1	2
90729	A08	t0177	ABC transporter ATP-binding protein	805	NP_804060.1	1.990062
90486	A09	t0761	glycosyl transferase	781	NP_804604.1	2
90534	A10	t1165	hypothetical protein t1165	781	NP_804975.1	2
90846	A11	t1239	cysteine desulfurase	781	NP_805045.1	2
90734	A12	t2261	disulfide isomerase/thiol-disulfide oxidase	781	NP_806003.1	2
90582	B01	t3534	ferredoxin-NADP reductase	781	NP_807181.1	2
90614	B02	t1223	vitamin B12-transporter ATPase	784	NP_805029.1	2
90654	B03	t1277	pathogenicity island lipoprotein	784	NP_805080.1	2
90670	B04	t2044	molybdopterin biosynthesis protein MoeB	784	NP_805807.1	2
90650	B05	t3749	PTS system protein	784	NP_807378.1	2
90642	B06	t1564	fumarate/nitrate reduction transcriptional regulator	787	NP_805346.2	2
90742	B07	t2115	phosphoglyceromutase	787	NP_805872.1	1.669632
90702	B08	t2194	UMP phosphatase	787	NP_805944.1	2
90606	B09	t4225	nonspecific acid phosphatase	787	NP_807827.1	2
90850	B10	t1742	flagellar basal body rod protein FlgF	790	NP_805517.1	2
90726	B11	t1873	bacteriophage protein	790	NP_805641.1	2
90746	B12	t2091	biotin biosynthesis protein BioC	790	NP_805848.1	1.337975
90526	C01	t2270	2,3-dihydroxybenzoate-2,3-dehydrogenase	790	NP_806012.1	1.663291
90498	C02	t2604	hydroxyacylglutathione hydrolase	790	NP_806320.1	2
90558	C03	t2768	AraC family transcriptional regulator	790	NP_806469.1	2
90766	C04	t3327	ubiquinone/menaquinone biosynthesis methyltransferase	790	NP_806995.1	2
90818	C05	t4432	transcriptional repressor UlaR	790	NP_808019.1	2
90754	C06	t0555	acyl-CoA thioester hydrolase	793	NP_804412.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
90554	C07	t1207	hypothetical protein t1207	793	NP_805014.1	2
90490	C08	t4261	hypothetical protein t4261	793	NP_807859.1	2
90786	C09	t0036	hypothetical protein t0036	796	NP_803920.1	2
90638	C10	t1630	short chain dehydrogenase	796	NP_805408.1	2
90634	C11	t1955	lipoprotein	796	NP_805720.1	2
90598	C12	t2927	2-deoxy-D-gluconate 3-dehydrogenase	796	NP_806621.1	2
90826	D01	t1623	phosphatidylglycerophosphatase B	799	NP_805401.1	2
90706	D02	t0109	DedA family integral membrane protein	802	NP_803992.1	2
90626	D03	t2542	hypothetical protein t2542	802	NP_806266.1	1.905237
90622	D04	t3134	hypothetical protein t3134	802	NP_806816.1	2
90722	D05	t0076	electron transfer flavoprotein FixA	805	NP_803960.1	2
91165	D06	t2179	hypothetical protein t2179	805	NP_805929.1	1.930435
90957	D07	t2606	methyltransferase	805	NP_806322.1	2
91009	D08	t3471	thiazole synthase	805	NP_807127.1	1.654658
91169	D09	t0005	hypothetical protein t0005	808	NP_803890.1	2
91013	D10	t2739	DNA-binding transcriptional repressor SrlR	808	NP_806440.1	2
91145	D11	t2858	periplasmic fimbrial chaperone	808	NP_806554.1	2
91073	D12	t3111	zinc transporter ZupT	808	NP_806794.1	2
91109	E01	t3182	galactitol utilization operon repressor	808	NP_806860.1	2
91137	E02	t3669	phosphate transporter ATP-binding protein	808	NP_807305.1	2
90961	E03	t4214	dimethyl sulfoxide reductase subunit C	808	NP_807816.1	2
91105	E04	t4556	DNA-binding transcriptional repressor UxuR	808	NP_808134.1	1.991337
91065	E05	t4606	hypothetical protein t4606	808	NP_808178.1	1.949257
91029	E06	t1944	metallothionein SmtA	811	NP_805709.1	1.990136
91037	E07	t2342	hydroxypyruvate isomerase	811	NP_806075.1	2
91093	E08	t0970	copper homeostasis protein CutC	814	NP_804793.1	2
91185	E09	t2357	hypothetical protein t2357	814	NP_806089.1	1.945946
90981	E10	t4014	hypothetical protein t4014	814	NP_807624.1	2
91177	E11	t0510	histidine-binding periplasmic protein	817	NP_804367.1	2
91225	E12	t0571	transcriptional regulator	817	NP_804428.1	2
90953	F01	t1272	pathogenicity island effector protein	817	NP_805075.1	2
91205	F02	t0071	carnitiny-CoA dehydratase	820	NP_803955.1	2
90985	F03	t0321	enhanced serine sensitivity protein SseB	820	NP_804196.1	2
91001	F04	t2335	hypothetical protein t2335	820	NP_806069.1	2
90997	F05	t0229	UDP-N-acetylglucosamine acyltransferase	823	NP_804110.1	1.737546
91025	F06	t1613	enoyl-ACP reductase	823	NP_805391.1	2
90881	F07	t2126	tol-pal system protein YbgF	823	NP_805880.1	2
90925	F08	t1036	transcriptional regulator KdgR	826	NP_804853.1	1.945521
91077	F09	t1705	hypothetical protein t1705, partial	826	NP_805481.1	2
91113	F10	t2437	2-aminoethylphosphonate transporter membrane protein	826	NP_806167.1	1.996368
91233	F11	t3257	transcriptional regulator NanR	826	NP_806932.1	2
91217	F12	t0183	3-methyl-2-oxobutanoate hydroxymethyltransferase	829	NP_804066.1	2
91181	G01	t0216	methionine aminopeptidase	829	NP_804097.1	2
90901	G02	t0896	flagellar biosynthesis protein FliR	829	NP_804725.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
91041	G03	t0200	iron-hydroxamate transporter ATP-binding protein	832	NP_804082.1	1.995192
91157	G04	t1718	metallodependent hydrolase	832	NP_805493.1	2
91102	G05	t1508	D-alanyl-D-alanine dipeptidase	805	NP_805294.1	2
91210	G06	t2355	short chain dehydrogenase	805	NP_806087.1	2
91230	G07	t3169	alpha-dehydro-beta-deoxy-D-glucarate aldolase	805	NP_806848.1	2
91018	G08	t3997	carboxylesterase BioH	805	NP_807607.1	2
90886	G09	t0780	glucose-1-phosphate citdyltransferase	808	NP_804622.1	2
90914	G10	t0845	precorrin-4 C11-methyltransferase	808	NP_804683.1	1.971535
91190	G11	t2106	molybdate transporter periplasmic protein	808	NP_805863.1	2
91162	G12	t2657	reverse transcriptase	808	NP_806368.1	2
91214	H01	t3465	NADH pyrophosphatase	808	NP_807121.1	2
91130	H02	t3502	acetylglutamate kinase	808	NP_807150.1	2
90878	H03	t0796	imidazole glycerol phosphate synthase subunit HisF	811	NP_804638.1	2
90950	H04	t4477	hypothetical protein t4477	811	NP_808064.1	2
90870	H05	t1289	type III secretion protein	814	NP_805092.1	2
90934	H06	t1697	spermidine/putrescine ABC transporter membrane protein	814	NP_805473.1	2
90894	H07	t2607	hypothetical protein t2607	814	NP_806323.1	1.719902
90930	H08	t2746	hypothetical protein t2746	814	NP_806447.1	2
91174	H09	t3322	twin-arginine protein translocation system subunit TatC	814	NP_806990.1	2
91118	H10	t4233	hypothetical protein t4233	814	NP_807835.1	2
91222	H11	t0509	lysine-arginine-ornithine-binding periplasmic protein	817	NP_804366.1	2
90890	H12	t1741	flagellar basal body rod protein FlgG	817	NP_805516.1	2

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