

***Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 12**

Catalog No. NR-19533

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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-19533.

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-19533 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 12, NR-19533."

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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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 (Seroovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 12 (ZSTD1)

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
87561	A01	t0350	hypothetical protein t0350	574	NP_804221.1	2
87689	A02	t3869	hypothetical protein t3869	574	NP_807487.1	2
87845	A03	t4077	50S ribosomal protein L5	574	NP_807684.1	2
87709	A04	t4353	VI polysaccharide biosynthesis protein	574	NP_807946.1	2
87545	A05	t4587	primosomal protein DnaI	574	NP_808162.1	2
87797	A06	t0022	fimbrial subunit	577	NP_803907.1	2
87777	A07	t1109	hypothetical protein t1109	577	NP_804923.1	1.292894
87841	A08	t1214	translation initiation factor IF-3	577	NP_805020.1	2
87493	A09	t1710	hypothetical protein t1710	577	NP_805486.1	2
87653	A10	t2588	hypothetical protein t2588	577	NP_806305.1	2
87597	A11	t2750	formate hydrogenlyase complex iron-sulfur subunit	577	NP_806451.1	2
87481	A12	t3356	hypothetical protein t3356	577	NP_807024.1	2
87609	B01	t4101	hypothetical protein t4101	577	NP_807708.1	2
87849	B02	t4279	hypothetical protein t4279	577	NP_807877.1	2
87809	B03	t0026	fimbrial subunit	580	NP_803910.1	2
87649	B04	t1147	chorismate mutase	580	NP_804958.1	2
87785	B05	t1861	cell division protein ZapC	580	NP_805630.1	2
87525	B06	t2425	hypothetical protein t2425, partial	580	NP_806155.1	2
87501	B07	t2476	shikimate kinase II	580	NP_806204.1	2
87701	B08	t2875	SecY interacting protein Syd	580	NP_806571.1	2
87749	B09	t2957	isopentenyl-diphosphate delta-isomerase	580	NP_806649.1	2
87769	B10	t3311	protoporphyrinogen oxidase	580	NP_806979.1	2
87641	B11	t3479	transcription antitermination protein NusG	580	NP_807135.1	2
87813	B12	t4402	oligoribonuclease	580	NP_807993.1	2
87513	C01	t4634	fimbrial protein	580	NP_808203.1	2
87721	C02	t0931	phosphatidylglycerophosphate synthetase	583	NP_804759.1	2
87601	C03	t1938	hypothetical protein t1938	583	NP_805704.1	2
87833	C04	t2516	hypothetical protein t2516	583	NP_806242.1	2
87621	C05	t2630	16S rRNA-processing protein RimM	583	NP_806341.1	2
87761	C06	t2979	ligase	583	NP_806671.1	2
87765	C07	t3323	sec-independent translocase	583	NP_806991.1	2
87581	C08	t0289	tRNA-specific adenosine deaminase	586	NP_804165.1	1.994881
87781	C09	t0778	dTDP-4-dehydrorhamnose 3,5-epimerase	586	NP_804620.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
87801	C10	t0921	flagella biosynthesis protein FliZ	586	NP_804749.1	2
87637	C11	t1175	hypothetical protein t1175	586	NP_804983.1	2
87617	C12	t1222	glutathione peroxidase	586	NP_805028.1	2
87673	D01	t2377	adenine phosphoribosyltransferase	586	NP_806108.1	2
87613	D02	t3228	hypothetical protein t3228	586	NP_806904.1	2
87477	D03	t4047	glutathione-regulated potassium-efflux system ancillary protein KefG	586	NP_807654.1	2
87818	D04	t0699	lipoprotein	565	NP_804547.1	2
87718	D05	t1131	cytochrome	565	NP_804943.1	2
87790	D06	t1387	bacteriophage host-nuclease inhibitor protein	565	NP_805182.1	2
87738	D07	t2181	flavodoxin FldA	565	NP_805931.1	2
87518	D08	t2710	transcriptional repressor MprA	565	NP_806416.1	2
87554	D09	t2913	dinucleoside polyphosphate hydrolase	565	NP_806607.1	2
87550	D10	t3041	hypothetical protein t3041	565	NP_806727.1	1.846018
87754	D11	t3526	ATP-dependent protease peptidase subunit	565	NP_807173.1	2
87662	D12	t3714	hypothetical protein t3714	565	NP_807348.1	2
87746	E01	t4161	single-stranded DNA-binding protein	565	NP_807765.1	2
87806	E02	t4468	inorganic pyrophosphatase	565	NP_808055.1	2
87826	E03	t4559	hypothetical protein t4559	565	NP_808137.1	2
87734	E04	t0016	hypothetical protein t0016	568	NP_803901.1	2
87698	E05	t2319	hypothetical protein t2319	568	NP_806053.1	2
87726	E06	t3980	gluconate kinase 1	568	NP_807589.1	1.994718
87658	E07	t4080	50S ribosomal protein L6	568	NP_807687.1	2
87594	E08	t0175	hypoxanthine-guanine phosphoribosyltransferase	571	NP_804058.1	2
87794	E09	t1203	hypothetical protein t1203	571	NP_805010.1	2
87774	E10	t2521	fimbrial protein	571	NP_806247.1	2
87586	E11	t2583	lipoprotein	571	NP_806301.1	2
87530	E12	t4237	single-stranded DNA-binding protein	571	NP_807839.1	2
87670	F01	t1520	ribosomal-protein-L7/L12-serine acetyltransferase	574	NP_805306.1	2
87490	F02	t1647	intracellular septation protein A	574	NP_805425.1	2
87506	F03	t1708	hypothetical protein t1708	574	NP_805484.1	2
87558	F04	t1898	hypothetical protein t1898	574	NP_805666.1	2
87706	F05	t2449	hypothetical protein t2449	574	NP_806179.1	2
87830	F06	t4015	hypothetical protein t4015	574	NP_807626.1	2
87758	F07	t4119	hypothetical protein t4119	574	NP_807723.1	2
87822	F08	t0543	NADH dehydrogenase subunit I	577	NP_804400.1	2
87522	F09	t2178	replication initiation regulator SeqA	577	NP_805928.1	2
87606	F10	t0856	adenosylcobinamide kinase	580	NP_804691.1	2
87570	F11	t1374	hypothetical protein t1374	580	NP_805170.1	2
87714	F12	t2745	electron transport protein HydN	580	NP_806446.1	1.987931
87630	G01	t1884	bacteriophage protein	583	NP_805652.1	2
87486	G02	t2323	hypothetical protein t2323	583	NP_806057.1	2
87534	G03	t3373	TDP-fucosamine acetyltransferase	583	NP_807037.1	2
87682	G04	t0064	citx protein	586	NP_803948.1	2
87742	G05	t0478	hypothetical protein t0478	586	NP_804336.1	2
87730	G06	t2388	maltose O-acetyltransferase	586	NP_806118.1	2
87694	G07	t4257	hypothetical protein t4257	586	NP_807855.1	2
88017	G08	t4105	transferase	589	NP_807712.1	1.828523
88093	G09	t2255	molybdopterin-containing oxidoreductase iron-sulfur unit	592	NP_805997.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
87989	G10	t1562	hypothetical protein t1562	598	NP_805344.1	2
88129	G11	t2260	alkyl hydroperoxide reductase	598	NP_806002.1	2
87877	G12	t3013	hypothetical protein t3013	601	NP_806705.1	2
87853	H01	t4184	cytochrome c nitrite reductase pentaheme subunit	601	NP_807788.1	2
88013	H02	t4259	hypothetical protein t4259	604	NP_807857.1	2
87893	H03	t0641	outer membrane lipoprotein	607	NP_804493.1	2
88101	H04	t2648	hypothetical protein t2648	607	NP_806359.1	2
88073	H05	t4102	ribosome maturation factor	607	NP_807709.1	2
87973	H06	t0270	RNA polymerase sigma factor RpoE	610	NP_804146.1	2
88181	H07	t2549	fimbrial subunit	610	NP_806273.1	2
88165	H08	t3995	DNA uptake protein	610	NP_807605.1	2
87965	H09	t0844	Cobalt-precorrin-6Y C(15)-methyltransferase	613	NP_804682.1	2
88021	H10	t1486	regulatory protein	613	NP_805273.1	2
87937	H11	t2415	hypothetical protein t2415	613	NP_806145.1	2
87913	H12	t2540	phosphoheptose isomerase	613	NP_806264.1	2

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