

## ***Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 9**

### **Catalog No. NR-19530**

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

### **For research use only. Not for human use.**

#### **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-19530.

#### **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-19530 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 9, NR-19530."

#### **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](http://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.

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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 9 (ZSTDI)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
86178	A01	t3638	D-ribose pyranase	454	NP_807275.1	1.889868
86270	A02	t4240	hypothetical protein t4240	454	NP_807841.1	2
86334	A03	t2886	fucose operon fucU protein	457	NP_806582.1	2
86066	A04	t3105	hypothetical protein t3105	457	NP_806788.1	1.859956
85990	A05	t0409	acetyltransferase	460	NP_804278.1	2
85982	A06	t2585	hypothetical protein t2585	460	NP_806303.1	2
86262	A07	t4093	zinc-responsive transcriptional regulator	460	NP_807700.1	2
86326	A08	t1874	bacteriophage protein	463	NP_805642.1	1.855292
85994	A09	t3478	50S ribosomal protein L11	463	NP_807134.1	2
86106	A10	t3535	hypothetical protein t3535	463	NP_807182.1	1.987041
86082	A11	t3710	heat shock chaperone lbpB	463	NP_807345.1	2
85986	A12	t0330	nucleoside diphosphate kinase	466	NP_804204.1	1.967811
86010	B01	t1382	hypothetical protein t1382	466	NP_805178.1	1.688841
85998	B02	t2682	hypothetical protein t2682	466	NP_806392.1	2
86062	B03	t3427	phage tail protein	466	NP_807090.1	1.72103
86302	B04	t1271	pathogenicity island protein	469	NP_805074.1	2
86114	B05	t1441	DNA-binding transcriptional repressor MarR	469	NP_805234.2	2
86250	B06	t1555	hypothetical protein t1555	469	NP_805338.1	1.936034
86002	B07	t4084	50S ribosomal protein L15	469	NP_807691.1	2
86274	B08	t1328	hypothetical protein t1328	475	NP_805129.1	2
86110	B09	t1882	bacteriophage protein	475	NP_805650.1	2
86330	B10	t3435	hypothetical protein t3435	475	NP_807098.1	2
86094	B11	t3876	hypothetical protein t3876	475	NP_807494.1	2
86226	B12	t0520	sugar phosphotransferase subunit IIA	478	NP_804377.1	2
86078	C01	t0904	flagellar biosynthesis chaperone	478	NP_804733.1	2
86342	C02	t1170	methionine sulfoxide reductase B	478	NP_804978.1	2
86266	C03	t2564	hypothetical protein t2564	478	NP_806283.1	2
86158	C04	t2802	cell adherence/invasion protein	478	NP_806503.1	2
86070	C05	t2893	hypothetical protein t2893	478	NP_806589.1	1.516736
86026	C06	t3644	flavodoxin	478	NP_807281.1	2
86346	C07	t4195	hypothetical protein t4195	478	NP_807799.1	2
86150	C08	t1160	hypothetical protein t1160	481	NP_804971.1	1.839917
86042	C09	t3428	phage tail protein	481	NP_807091.1	-
86594	C10	t4492	hypothetical protein t4492	481	NP_808079.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
86493	C11	t4601	ribosomal-protein-alanine N-acetyltransferase	481	NP_808173.1	2
86433	C12	t0733	hypothetical protein t0733	484	NP_804577.1	2
86393	D01	t0755	tyrosine phosphatase	484	NP_804599.1	2
86589	D02	t1501	hypothetical protein t1501	484	NP_805287.1	2
86581	D03	t1546	hypothetical protein t1546	484	NP_805330.1	2.584711
86353	D04	t1851	hypothetical protein t1851	487	NP_805620.1	1.665298
86501	D05	t1881	bacteriophage protein	487	NP_805649.1	2.997947
86637	D07	t2360	hypothetical protein t2360	487	NP_806092.1	2.014374
86565	D08	t2770	hypothetical protein t2770	487	NP_806471.1	2.991786
86497	D09	t4502	arginine deiminase	487	NP_808088.1	2.628337
86429	D10	t1777	curlin minor subunit	490	NP_805551.1	1.746939
86557	D11	t2546	transcriptional regulator	490	NP_806270.1	1.606122
86425	D12	t3787	deoxyuridine 5'-triphosphate nucleotidohydrolase	490	NP_807409.1	2.563265
86517	E01	t4159	lipoprotein	490	NP_807763.1	3
86369	E02	t0700	lipoprotein	493	NP_804548.1	2.31643
86401	E03	t1045	hypothetical protein t1045	493	NP_804862.1	2.900609
86405	E04	t1370	bacteriophage protein	493	NP_805166.1	2.985801
86421	E05	t1844	methylglyoxal synthase	493	NP_805613.1	3
86633	E07	t3447	transposase	493	NP_807108.1	3
86641	E08	t3643	DNA-binding transcriptional regulator AsnC	493	NP_807280.1	1.701826
86445	E09	t3732	hypothetical protein t3732	493	NP_807365.1	1.604462
86681	E10	t4592	hypothetical protein t4592	493	NP_808167.1	3
86601	E11	t0551	hypothetical protein t0551	496	NP_804408.1	3
86529	E12	t1685	MutT-family protein	496	NP_805461.1	3
86541	F01	t1933	transcriptional regulator	496	NP_805699.1	3
86437	F02	t2575	hypothetical protein t2575	496	NP_806294.1	3
86569	F03	t2755	formate hydrogenlyase regulatory protein HycA	496	NP_806456.1	3
86697	F04	t4363	hypothetical protein t4363	496	NP_807956.1	3
86533	F05	t4408	ATPase	496	NP_807997.1	3
86609	F06	t4563	hypothetical protein t4563	496	NP_808141.1	2.705645
86653	F07	t1224	lipoprotein	499	NP_805030.1	3
86689	F08	t1365	hypothetical protein t1365	499	NP_805161.1	3
86525	F09	t3759	hypothetical protein t3759	499	NP_807387.1	2.759519
86537	F10	t4194	aminoalkylphosphonic acid N-acetyltransferase	499	NP_807798.1	3
86549	F11	t4317	capsid completion protein	499	NP_807912.1	3
86685	F12	t4436	PTS system L-ascorbate-specific transporter subunit IIA	499	NP_808023.1	2.713427
86509	G01	t0698	hypothetical protein t0698	502	NP_804546.1	2.302789
86361	G02	t0813	DNA gyrase inhibitor	502	NP_804653.1	1.7251
86449	G03	t0902	flagellar basal body protein FlilL	502	NP_804731.1	2.370518
86673	G04	t2226	rRNA large subunit methyltransferase	502	NP_805969.1	3
86389	G05	t2602	ribonuclease H	502	NP_806318.1	3
86705	G06	t3866	acetyltransferase	502	NP_807484.1	1.878486
86714	G07	t3591	hypothetical protein t3591	481	NP_807234.1	2
86606	G08	t0031	hypothetical protein t0031	484	NP_803915.1	2
86478	G09	t0410	hypothetical protein t0410	484	NP_804279.1	2
86598	G10	t0608	citrate reductase cytochrome c-type subunit	484	NP_804464.1	2
86486	G11	t2448	transcriptional regulator NrdR	484	NP_806178.1	2
86662	G12	t2696	hypothetical protein t2696	484	NP_806404.1	2
86666	H01	t2872	flavodoxin	484	NP_806568.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
86442	H02	t4235	hypothetical protein t4235	484	NP_807837.1	2
86678	H03	t4445	50S ribosomal protein L9	484	NP_808032.1	2
86546	H04	t0818	propanediol utilization protein PduV	487	NP_804658.1	2
86418	H05	t0977	dATP pyrophosphohydrolase	487	NP_804800.1	1.977413
86694	H06	t1396	hypothetical protein t1396	487	NP_805191.1	2
86522	H07	t4360	hypothetical protein t4360	487	NP_807953.1	2
86646	H08	t0228	(3R)-hydroxymyristoyl-ACP dehydratase	490	NP_804109.1	2
86506	H09	t0255	hypothetical protein t0255	490	NP_804132.1	2
86454	H10	t0528	hypothetical protein t0528	490	NP_804385.1	2
86414	H11	t1776	cryptic curling major subunit	490	NP_805550.1	2
86350	H12	t2477	hypothetical protein t2477	490	NP_806205.1	2

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