

## ***Salmonella enterica* subsp. *enterica*, Strain Ty2 (Seroovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 10**

### **Catalog No. NR-19531**

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-19531.

#### **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-19531 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 (Seroovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 10, NR-19531."

#### **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:**

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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 10 (ZSTDJ)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
86474	A01	t2654	hypothetical protein t2654	490	NP_806365.1	2
86374	A02	t3087	hypothetical protein t3087	490	NP_806771.1	2
86578	A03	t3459	zinc resistance protein	490	NP_807115.1	2
86554	A04	t0123	cell division protein MraZ	493	NP_804006.1	2
86622	A05	t2986	insertion sequence element IS200 transposase	493	NP_806678.1	2
86358	A06	t3343	hypothetical protein t3343	493	NP_807011.1	2
86710	A07	t4172	soxR protein	493	NP_807776.1	2
86626	A08	t4494	aspartate carbamoyltransferase	496	NP_808081.1	2
86722	A09	t4554	hypothetical protein t4554	496	NP_808132.1	2
86410	A10	t4585	hypothetical protein t4585	496	NP_808160.1	2
86366	A11	t3178	PTS-system galactitol-specific transporter subunit IIA	499	NP_806856.1	2
86650	A12	t3850	hypothetical protein t3850	499	NP_807470.1	2
86466	B01	t1313	outer membrane lipoprotein SlyB	502	NP_805114.1	2
86658	B02	t3341	hypothetical protein t3341	502	NP_807009.1	2
87041	B03	t4253	hypothetical protein t4253	502	NP_807851.1	2
86769	B04	t0887	patch repair protein	505	NP_804717.1	2.831683
86985	B05	t2389	hypothetical protein t2389	505	NP_806119.1	2.992079
86841	B06	t2576	hypothetical protein t2576	505	NP_806295.1	3
86969	B07	t2747	hydrogenase 3 maturation protease	505	NP_806448.1	1.831683
86829	B08	t2860	fimbrial subunit	505	NP_806556.1	2
87085	B09	t2908	hypothetical protein t2908	505	NP_806602.1	1.932673
86989	B10	t4058	30S ribosomal protein S7	505	NP_807665.1	1.79802
86869	B11	t4314	lysozyme	505	NP_807909.1	2.809901
86757	B12	t1914	methyltransferase	508	NP_805681.1	2.816929
86961	C01	t2015	hypothetical protein t2015	508	NP_805778.1	2.80315
86745	C02	t2214	hypothetical protein t2214	508	NP_805957.1	2.78937
86833	C03	t3424	lysozyme	508	NP_807087.1	3
86821	C04	t3824	tRNA/rRNA methyltransferase YibK	508	NP_807445.1	3
86957	C05	t3848	2,3-diketo-L-gluconate TRAP transporter small permease YiaM	508	NP_807468.1	3
86965	C06	t3853	electron-transport protein	508	NP_807473.1	3
86849	C07	t4003	transcription elongation factor GreB	508	NP_807613.1	3

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
86825	C08	t4015	hypothetical protein t4015	508	NP_807625.1	3
86897	C09	t4100	hypothetical protein t4100	508	NP_807707.1	3
87097	C10	t4626	hypothetical protein t4626	508	NP_808197.1	3
86805	C11	t1021	hypothetical protein t1021	511	NP_804840.1	3
86797	C12	t4062	bacterioferritin	511	NP_807669.1	2.714286
86725	D01	t4248	hypothetical protein t4248	511	NP_807847.1	3
86777	D02	t4379	FxsA protein	511	NP_807970.1	2.951076
86753	D03	t0273	SoxR reducing system protein RseC	514	NP_804149.1	2.805447
86945	D04	t2779	cell invasion protein	517	NP_806480.1	2.624758
86881	D05	t2083	molybdenum cofactor biosynthesis protein MoaC	520	NP_805841.1	2.936538
86973	D06	t2176	5-nitroimidazole antibiotic resistance	520	NP_805926.1	2.926923
87053	D07	t2584	hypothetical protein t2584	520	NP_806302.1	2.501923
86793	D08	t2661	bacteriophage tail protein	520	NP_806372.1	3
86929	D09	t3052	hypothetical protein t3052	520	NP_806738.1	2.711538
86774	D10	t3152	hypothetical protein t3152	520	NP_806833.1	2
86917	D11	t3529	ribonuclease activity regulator protein RraA	520	NP_807176.1	2.813462
86910	D12	t4296	phage tail protein	520	NP_807893.1	2
86853	E01	t4614	hypothetical protein t4614	520	NP_808186.1	1.469231
86901	E02	t1466	regulatory protein	523	NP_805256.1	2.604207
87017	E03	t3320	transcriptional activator RfaH	523	NP_806988.1	2.342256
86817	E04	t3466	anti-RNA polymerase sigma 70 factor	523	NP_807122.1	2.871893
86785	E05	t3975	acetyl-transferase YhhY	523	NP_807585.1	3
86885	E06	t4497	transcriptional regulator	523	NP_808084.1	2.370937
87037	E07	t4506	hypothetical protein t4506	523	NP_808093.1	2.764818
87009	E08	t3239	PTS system transporter subunit IIA-like nitrogen regulatory protein PtsN	526	NP_806915.1	1.846008
87033	E09	t3287	rod shape-determining protein MreD	526	NP_806962.1	3
86857	E10	t3920	hypothetical protein t3920	526	NP_807533.1	2.762357
87061	E11	t4224	acetyltransferase	526	NP_807826.1	2.562738
86729	E12	t0121	acetolactate synthase 3 regulatory subunit	529	NP_804004.1	3
86893	F01	t0403	ethanolamine utilization protein EutK	529	NP_804272.1	2.567108
87089	F02	t0602	ecotin	529	NP_804458.1	3
86861	F03	t1975	leucine-responsive transcriptional regulator	529	NP_805739.1	2.94707
86977	F04	t2325	peptidyl-prolyl cis-trans isomerase B	529	NP_806059.1	1.941399
86814	F05	t1128	heat shock protein	505	NP_804940.1	2
87058	F06	t2557	fimbrial structural subunit	505	NP_806278.1	2
87014	F07	t3275	arginine repressor ArgR	505	NP_806950.1	-
86750	F08	t3294	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	505	NP_806969.1	2
86738	F09	t3650	ATP synthase F0F1 subunit B	505	NP_807287.1	1.992079
86934	F10	t4244	pilus assembly protein	505	NP_807843.1	2
87002	F11	t1267	type III secretion system chaperone protein	508	NP_805070.1	2
86942	F12	t2052	manganese transport regulator MntR	508	NP_805815.1	2
87082	G01	t2205	metalloprotease	508	NP_805949.1	2
86866	G02	t2095	kinase inhibitor protein	511	NP_805852.1	1.902153
87066	G03	t3216	transcription elongation factor GreA	511	NP_806892.1	2
87006	G04	t0090	dihydrofolate reductase	514	NP_803974.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
86734	G05	t0191	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase	514	NP_804074.1	2
86906	G06	t0390	ethanolamine utilization protein EutP	514	NP_804259.1	2
86982	G07	t0614	cytochrome c-type biogenesis protein CcmE	514	NP_804470.1	2
87070	G08	t0732	hypothetical protein t0732	514	NP_804576.1	2
87094	G09	t2830	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	514	NP_806527.1	2
86874	G10	t3793	formamidopyrimidine-DNA glycosylase	514	NP_807414.1	1.784047
86878	G11	t0828	propanediol utilization protein PduK	517	NP_804667.1	2
86766	G12	t2257	hypothetical protein t2257	517	NP_805999.1	2
86790	H01	t2931	hypothetical protein t2931	517	NP_806625.1	2
86802	H02	t4511	DNA polymerase III subunit chi	517	NP_808098.1	2
87046	H03	t0226	periplasmic chaperone	520	NP_804107.1	2
86810	H04	t0477	phosphohistidine phosphatase	520	NP_804335.1	2
87022	H05	t1187	periplasmic protein	520	NP_804994.1	1.928846
86914	H06	t3747	PTS system protein	520	NP_807377.1	2
86922	H07	t3868	acetyltransferase	520	NP_807486.1	2
87050	H08	t0758	colanic acid biosynthesis acetyltransferase WcaB	523	NP_804602.1	1.548757
87026	H09	t3066	hydrogenase 2-specific chaperone	523	NP_806752.1	2
86838	H10	t0604	ferredoxin-type protein	526	NP_804459.1	2
86762	H11	t0826	hypothetical protein t0826	526	NP_804665.1	2
86954	H12	t2428	nucleotide-binding protein	526	NP_806158.2	2

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