

Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 26*Catalog No. NR-19547**

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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* (*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-19547.

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-19547 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 containing 50 µg/mL kanamycin

LB 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 26, NR-19547."

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/bmb15/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 26 (ZSTDZ)¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
93907	A02	t3909	hypothetical protein t3909	1063	NP_807523.1	3.202258
93934	A04	t2647	hypothetical protein t2647	1066	NP_806358.1	1.658537
94205	A05	t3812	glycosyl transferase	1069	NP_807434.1	1.894294
94106	A06	t3971	phosphotriesterase	1069	NP_807581.1	1.815716
94018	A07	t0262	methyltransferase	1072	NP_804139.1	1.713619
93957	A08	t1499	NADP-dependent oxidoreductase	1072	NP_805285.1	1.458955
94141	A09	t3416	capsid portal protein	1072	NP_807079.1	4.093284
94137	A10	t3693	TMAO reductase system periplasmic protein TorT	1075	NP_807329.1	1.59814
94055	A11	t0147	guanosine 5'-monophosphate oxidoreductase	1078	NP_804030.1	2.877551
93926	A12	t1629	periplasmic permease	1081	NP_805407.1	1.655874
94135	B01	t3808	ADP-heptose:LPS heptosyltransferase II	1081	NP_807430.1	3.408881
94113	B02	t0653	hypothetical protein t0653	1084	NP_804505.1	4.098708
93942	B03	t2333	ureidoglycolate dehydrogenase	1084	NP_806067.1	1.661439
94209	B04	t2829	tRNA pseudouridine synthase D	1084	NP_806526.1	1.673432
93966	B05	t3940	hypothetical protein t3940	1084	NP_807551.1	1.632841
94006	B06	t0404	transcriptional regulator EutR	1087	NP_804273.1	1.678013
94245	B08	t0715	fructose-bisphosphate aldolase	1087	NP_804562.1	1.656854
94070	B09	t1764	hypothetical protein t1764	1087	NP_805538.1	1.735051
94342	B10	t2530	outer membrane phosphoprotein E	1087	NP_806254.1	1.683533
94314	B11	t2674	hypothetical protein t2674	1087	NP_806385.1	1.607176
94557	B12	t3023	adenine DNA glycosylase	1087	NP_806715.1	4.297148
94551	C01	t3063	ABC transporter periplasmic-binding protein	1087	NP_806749.1	4.051518
94474	C02	t3400	bacteriophage integrase	1087	NP_807063.1	1.544618
94574	C03	t0846	cobalamin biosynthesis protein CbiG	1090	NP_804684.1	1.566055
94322	C04	t2401	lyase	1090	NP_806131.1	1.683486
94618	C05	t2537	DNA polymerase IV	1090	NP_806261.1	1.588991
94270	C06	t2104	molybdate transporter ATP-binding protein	1093	NP_805861.1	1.700823
94302	C07	t0599	ADA regulatory protein	1096	NP_804455.1	1.568431
94389	C08	t0787	glycosyl transferase	1096	NP_804629.1	3.665146
94345	C11	t1589	hypothetical protein t1589	1096	NP_805371.1	2.773723
94379	D01	t2459	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	1099	NP_806189.1	3.828935

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
94393	D02	t2842	hypothetical protein t2842	1099	NP_806539.1	1.43949
94457	D04	t4325	hypothetical protein t4325	1099	NP_807920.1	3.77616
94381	D05	t4433	L-ascorbate 6-phosphate lactonase	1099	NP_808020.1	1.431301
94519	D06	t0799	imidazole glycerol-phosphate dehydratase/histidinol phosphatase	1102	NP_804641.1	2.478221
94515	D07	t3662	fimbrial protein	1102	NP_807298.1	3.175136
94309	D08	t0582	glycerophosphodiester phosphodiesterase	1105	NP_804439.1	4.374661
94318	D09	t4519	protein kinase	1111	NP_808104.1	1.774977
94305	D10	t2547	fimbrial protein	1114	NP_806271.1	3.426391
94601	D11	t2987	fructose-bisphosphate aldolase	1114	NP_806679.1	1.420108
94386	D12	t4153	alanine racemase	1114	NP_807757.1	1.710952
94631	E01	t4198	sensor protein BasS/PmrB	1114	NP_807802.1	3.13465
94495	E02	t0480	chorismate synthase	1120	NP_804338.1	4.167857
94354	E03	t0775	dTDP-glucose 4,6 dehydratase	1120	NP_804617.1	1.550893
94563	E04	t3718	hypothetical protein t3718	1120	NP_807352.1	4.034821
94365	E05	t0116	3-isopropylmalate dehydrogenase	1126	NP_803999.1	1.66341
94439	E06	t0417	sulfate/thiosulfate transporter subunit	1129	NP_804286.1	2.686448
94613	E07	t2484	D-alanyl-alanine synthetase A	1129	NP_806212.1	1.495128
94905	E08	t2660	bacteriophage late gene regulator	1135	NP_806371.1	1.597357
94669	E09	t3496	tRNA (uracil-5-)-methyltransferase	1135	NP_807144.1	1.601762
94825	E10	t3580	lipoprotein	1135	NP_807223.1	1.604405
94890	E11	t3682	DNA polymerase III subunit beta	1135	NP_807318.1	3.728634
94806	E12	t4295	regulator of late gene expression	1135	NP_807892.1	1.514537
94785	F01	t4513	hypothetical protein t4513	1135	NP_808100.1	3.822907
94842	F02	t1458	uptake hydrogenase small subunit	1138	NP_805249.1	4.149385
94857	F03	t1739	flagellar basal body P-ring biosynthesis protein FlgA	1138	NP_805514.1	3.136204
94650	F04	t2432	2-aminoethylphosphonate—pyruvate transaminase	1138	NP_806162.1	1.637083
94929	F05	t2529	gamma-glutamyl kinase	1138	NP_806253.1	3.026362
94701	F06	t3249	hypothetical protein t3249	1138	NP_806925.1	1.52109
94833	F07	t3509	glycerol dehydrogenase	1138	NP_807157.1	3.826889
94809	F08	t1686	tRNA-specific 2-thiouridylase MnmA	1141	NP_805462.1	1.550394
94814	F09	t0702	ATPase	1144	NP_804550.1	1.502622
94718	F10	t1860	hypothetical protein t1860	1144	NP_805629.1	4.066434
94970	F11	t2435	2-aminoethylphosphonate ABC transporter ATP-binding protein	1144	NP_806165.1	1.620629
94733	F12	t3750	transferase	1144	NP_807380.1	4.158217
94966	G01	t3900	endo-1,4-D-glucanase	1144	NP_807515.1	1.708042
94954	G02	t4136	maltose ABC transporter ATP-binding protein	1144	NP_807740.1	1.488636
94686	G03	t0822	propanol dehydrogenase	1147	NP_804662.1	1.625109
94874	G04	t2019	putrescine ABC transporter periplasmic-binding protein	1147	NP_805782.1	1.608544
94837	G05	t2051	hypothetical protein t2051	1147	NP_805814.1	1.639058
94674	G06	t2479	diguanylate cyclase AdrA	1147	NP_806207.1	1.539669
94753	G07	t1369	hypothetical protein t1369	1150	NP_805165.1	1.446957
94689	G08	t0333	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	1153	NP_804207.1	1.608846
94886	G09	t1232	hypothetical protein t1232	1153	NP_805038.1	1.677363
94782	G10	t1521	hypothetical protein t1521	1153	NP_805307.1	1.714657

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
95001	G11	t1760	N-methyltryptophan oxidase	1153	NP_805535.1	1.576756
94663	G12	t1992	macrolide transporter subunit MacA	1153	NP_805755.1	3.417173
94757	H01	t2285	carboxylate-amine ligase	1153	NP_806026.1	3.552472
94773	H02	t2799	cell invasion protein	1153	NP_806500.1	3.824805
94713	H03	t2862	hypothetical protein t2862	1153	NP_806558.1	1.507372
94937	H04	t3071	hydrogenase 2 small subunit	1153	NP_806757.1	1.588899
94681	H05	t4480	hypothetical protein t4480	1153	NP_808067.1	1.500434
94829	H06	t0763	GDP-mannose 4,6-dehydratase	1156	NP_804606.1	2.852076
94870	H07	t1314	anhydro-N-acetylmuramic acid kinase	1156	NP_805115.1	1.408304
94949	H08	t1691	hypothetical protein t1691	1156	NP_805467.1	1.593426
94881	H09	t2035	oxidoreductase	1156	NP_805798.1	1.596886
94729	H10	t2759	hydrogenase isoenzyme formation protein HypD	1156	NP_806460.1	1.618512
94645	H11	t2826	lipoprotein NlpD	1156	NP_806523.1	1.653979
94821	H12	t2948	hypothetical protein t2948	1156	NP_806641.1	1.641003

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