

***Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 17**

Catalog No. NR-19538

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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-19538.

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-19538 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 17, NR-19538."

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 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 17 (ZSTDQ)¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
89414	A01	t0632	16S rRNA pseudouridylate synthase A	730	NP_804484.1	2
89957	A02	t0885	hypothetical protein t0885	730	NP_804715.1	1.99589
89893	A03	t1057	hypothetical protein t1057	730	NP_804874.1	1.90137
90097	A04	t3842	L-ribulose-5-phosphate 4-epimerase	730	NP_807463.1	2
89869	A05	t0999	exodeoxyribonuclease X	733	NP_804822.1	2
90009	A06	t1740	flagellar basal body L-ring protein	733	NP_805515.1	1.995907
89941	A07	t1744	flagellar basal body rod modification protein	733	NP_805519.1	2
89741	A08	t3656	hypothetical protein t3656	733	NP_807293.1	2
89865	A09	t3660	fimbrial chaperone protein	733	NP_807297.1	2
89913	A10	t0243	copper homeostasis and adhesion lipoprotein	736	NP_804123.1	2
90013	A11	t0678	FAA-hydrolase-family protein	736	NP_804527.1	1.991848
89953	A12	t0835	propanediol utilization protein PduB	736	NP_804674.1	-
90061	B01	t3156	hypothetical protein t3156	736	NP_806837.1	2
89757	B02	t3318	FMN reductase	736	NP_806986.1	2
89745	B03	t0028	fimbrial chaperone	739	NP_803912.1	2
89773	B04	t1476	hypothetical protein t1476	739	NP_805265.1	2
90105	B05	t2284	enterobactin synthase multienzyme complex phosphopantetheinyltransferase	739	NP_806025.1	2
89797	B06	t3477	50S ribosomal protein L1	739	NP_807133.1	2
89765	B07	t3631	hypothetical protein t3631	739	NP_807269.1	2
90017	B08	t3878	hypothetical protein t3878	739	NP_807496.1	2
89989	B09	t0110	thiamine transporter ATP-binding subunit	742	NP_803993.1	2
89949	B10	t0512	histidine transport system permease	742	NP_804369.1	2
89753	B11	t1611	hypothetical protein t1611	742	NP_805389.1	2
89973	B12	t3005	endonuclease I	742	NP_806697.1	1.985175
89785	C01	t3349	hypothetical protein t3349	742	NP_807017.1	2
89917	C02	t1422	hypothetical protein t1422	745	NP_805216.1	2
89737	C03	t2153	polysaccharide export ABC transporter ATP-binding protein	745	NP_805905.1	1.997315
89861	C04	t2294	hypothetical protein t2294, partial	745	NP_806035.1	2
89981	C05	t2550	fimbrial protein	745	NP_806274.1	2
89749	C06	t3872	hypothetical protein t3872	745	NP_807490.1	2
89805	C07	t0010	hypothetical protein t0010	748	NP_803895.1	1.994652
89845	C08	t0850	cobalt-precorrin 2 C(20)-methyltransferase	748	NP_804686.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
89901	C09	t1225	hypothetical protein t1225	748	NP_805031.1	2
90089	C10	t2915	hypothetical protein t2915	748	NP_806609.1	2
89829	C11	t3062	molybdate ABC transporter periplasmic molybdate-binding protein	748	NP_806748.1	1.629679
90057	C12	t3962	leucine/isoleucine/valine transporter ATP-binding protein	748	NP_807572.1	2
89817	D01	t2007	arginine transporter permease ArtQ	751	NP_805770.1	2
89969	D02	t3347	flavin mononucleotide phosphatase	751	NP_807015.1	2
89781	D03	t4549	hypothetical protein t4549	751	NP_808127.2	2
90025	D04	t2121	pnuC protein	754	NP_805878.1	2
90065	D05	t2141	succinate dehydrogenase iron-sulfur subunit	754	NP_805895.1	2
89793	D06	t2433	2-aminoethylphosphonate uptake and metabolism operon regulator	754	NP_806163.1	2
89777	D07	t2951	hypothetical protein t2951	754	NP_806644.1	2
89733	D08	t3054	hydrolase	754	NP_806740.1	2
89790	D09	t0729	hypothetical protein t0729	730	NP_804573.1	2
89878	D10	t1410	dithiobiotin synthetase	730	NP_805205.1	2
89898	D11	t2406	hypothetical protein t2406	730	NP_806136.1	2
90030	D12	t2914	DNA mismatch repair protein	730	NP_806608.1	2
89762	E01	t3754	hypothetical protein t3754	730	NP_807384.1	2
89934	E02	t3977	hypothetical protein t3977	730	NP_807587.1	2
89826	E03	t4323	hypothetical protein t4323	730	NP_807918.1	2
90070	E04	t4346	VI polysaccharide export ATP-binding protein	730	NP_807939.1	2
89822	E05	t0208	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	733	NP_804090.1	1.663029
89946	E06	t3560	DNA-binding transcriptional regulator CpxR	733	NP_807205.1	2
89810	E07	t1702	lipoprotein transporter ATP-binding subunit	736	NP_805478.1	2
89814	E08	t4071	30S ribosomal protein S3	736	NP_807678.1	2
90050	E09	t4572	hypothetical protein t4572	736	NP_808149.1	2
89922	E10	t0021	hypothetical protein t0021	739	NP_803906.1	2
89858	E11	t0195	sugar fermentation stimulation protein A	739	NP_804078.1	2
89994	E12	t2840	hypothetical protein t2840	739	NP_806537.1	2
90038	F01	t3012	hypothetical protein t3012	739	NP_806704.1	1.932341
89802	F02	t0738	hypothetical protein t0738	742	NP_804582.1	2
89938	F03	t1063	septum formation inhibitor	742	NP_804880.1	2
89966	F04	t2079	hypothetical protein t2079	742	NP_805838.1	2
90054	F05	t3028	hypothetical protein t3028	742	NP_806719.1	2
89838	F06	t1671	respiratory nitrate reductase 1 subunit delta	745	NP_805447.1	2
90034	F07	t2831	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	745	NP_806528.1	2
89886	F08	t0372	phosphoribosylaminoimidazole-succinocarboxamide synthase	748	NP_804241.1	2
89962	F09	t0735	hypothetical protein t0735	748	NP_804579.1	2
89882	F10	t1579	oxidoreductase	748	NP_805361.1	2
90094	F11	t2483	hypothetical protein t2483	748	NP_806211.1	2
89986	F12	t2961	thiol:disulfide interchange protein DsbC	748	NP_806653.1	2
89834	G01	t4155	acid phosphatase/phosphotransferase	748	NP_807759.1	2
90042	G02	t4637	two-component response regulator	751	NP_808206.1	2
89854	G03	t0420	glutamine amidotransferase	754	NP_804289.1	2
89926	G04	t0642	hypothetical protein t0642	754	NP_804494.1	2
90102	G05	t0671	hypothetical protein t0671	754	NP_804520.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
90022	G06	t0920	flagellar biosynthesis sigma factor	754	NP_804748.1	1.961538
89842	G07	t2544	outer membrane adhesin	754	NP_806268.1	2
89910	G08	t3020	hypothetical protein t3020	754	NP_806712.1	2
90046	G09	t3022	tRNA (guanine-N-(7)-)-methyltransferase	754	NP_806714.1	2
89930	G10	t3915	GntR family transcriptional regulator	754	NP_807529.1	1.79443
90429	G11	t4004	osmolarity response regulator	754	NP_807614.1	2
90209	G12	t4210	DNA-binding transcriptional activator DcuR	754	NP_807814.1	2
90181	H01	t0741	DNA-binding transcriptional regulator BaeR	757	NP_804585.1	1.940555
90413	H02	t2326	UDP-2,3-diacetylglucosamine hydrolase	757	NP_806060.1	1.564069
90141	H03	t4303	invasion-associated secreted protein	757	NP_807899.1	1.926024
90245	H04	t2098	histidine utilization repressor	760	NP_805855.1	1.836842
90397	H05	t2841	hypothetical protein t2841	760	NP_806538.1	1.982895
90137	H06	t3670	transcriptional regulator PhoU	760	NP_807306.1	1.932895
90177	H07	t0278	DNA repair protein RecO	763	NP_804154.1	2
90345	H08	t1258	transcriptional regulator	763	NP_805061.1	2
90445	H09	t1584	murein peptide amidase A	763	NP_805366.1	2
90269	H10	t2005	arginine transporter ATP-binding subunit	763	NP_805768.1	2
90393	H11	t0279	pyridoxine 5'-phosphate synthase	766	NP_804155.1	2
90293	H12	t0695	transcriptional regulator	766	NP_804543.1	2

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