

***Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 16**

Catalog No. NR-19537

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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-19537.

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-19537 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 16, NR-19537."

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 16 (ZSTDP)¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
89150	A01	t0402	ethanolamine utilization protein EutL	694	NP_804271.1	2
89262	A02	t0530	phosphatase	694	NP_804387.2	2
89030	A03	t0997	hypothetical protein t0997	694	NP_804820.1	2
89018	A04	t1747	flagellar basal body P-ring biosynthesis protein FlgA	694	NP_805522.1	2
89338	A05	t2967	hypothetical protein t2967	694	NP_806659.1	1.659942
89122	A06	t3578	hypothetical protein t3578	694	NP_807221.1	2
89234	A07	t0176	carbonic anhydrase	697	NP_804059.1	2
89138	A08	t3146	hypothetical protein t3146	697	NP_806827.1	2
89298	A09	t3521	hypothetical protein t3521	697	NP_807168.1	2
89062	A10	t0647	hypothetical protein t0647	700	NP_804499.1	2
88990	A11	t0940	hypothetical protein t0940	700	NP_804765.1	2
89278	A12	t1498	DNA-binding transcriptional regulator	700	NP_805284.1	-
89290	B01	t3789	bifunctional phosphopantothienoylcysteine decarboxylase	700	NP_807410.2	2
89078	B02	t3943	hypothetical protein t3943	700	NP_807554.1	2
89326	B03	t0924	ABC transporter membrane protein	703	NP_804752.1	2
89302	B04	t1202	2-deoxyglucose-6-phosphatase	703	NP_805009.1	2
89469	B05	t3952	cell division protein FtsE	703	NP_807563.1	1.662873
89489	B06	t2426	hypothetical protein t2426	706	NP_806156.1	2
89613	B07	t0833	diol dehydratase medium subunit	709	NP_804672.1	1.777151
89377	B08	t1689	DNA-binding transcriptional regulator PhoP	709	NP_805465.1	2
89705	B09	t2210	glutamate/aspartate transport system permease GltK	709	NP_805954.1	2
89357	B10	t1670	respiratory nitrate reductase 1 subunit gamma	712	NP_805446.1	-
89537	B11	t1941	chromosome partition protein MukE	712	NP_805707.2	2
89481	B12	t2358	ABC transporter ATP-binding protein YbbL	712	NP_806090.1	2
89473	C01	t3114	disulfide oxidoreductase	712	NP_806797.1	2
89649	C02	t4023	ribulose-phosphate 3-epimerase	712	NP_807633.1	2
89697	C03	t0260	hypothetical protein t0260	715	NP_804137.1	1.997203
89409	C04	t0277	GTP-binding protein Era	715	NP_804153.1	2
89477	C05	t1823	transcriptional regulator YedW	715	NP_805595.2	1.998601

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
89501	C06	t1869	bacteriophage protein	715	NP_805637.1	2
89601	C07	t1924	exonuclease	715	NP_805691.1	2
89653	C08	t2241	two-component response regulator DpiA	715	NP_805983.1	2
89565	C09	t4602	nucleotidase	715	NP_808174.2	1.993007
89389	C10	t0705	fimbrial chaperone protein	718	NP_804553.1	2
89493	C11	t3568	hypothetical protein t3568	718	NP_807212.1	2
89725	C12	t3829	lipoprotein	718	NP_807450.1	2
89641	D01	t4424	hypothetical protein t4424	718	NP_808011.2	2
89573	D02	t4633	fimbrial chaperone protein	718	NP_808202.1	1.994429
89513	D03	t0054	transcriptional regulator CitB	721	NP_803938.1	2
89373	D04	t1032	solute/DNA competence effector	721	NP_804850.1	2
89721	D05	t1569	hypothetical protein t1569	721	NP_805351.1	2
89445	D06	t2090	dithiobiotin synthetase	721	NP_805847.1	2
89381	D07	t2354	ABC transporter ATP-binding protein YbbA	721	NP_806085.1	2
89557	D08	t3010	global regulatory protein	721	NP_806702.1	2
89661	D09	t0391	ethanolamine utilization protein EutQ	724	NP_804260.1	2
89421	D10	t0394	ethanolamine utilization protein EutN	724	NP_804263.1	2
89369	D11	t1273	pathogenicity island effector protein	724	NP_805076.1	2
89385	D12	t2467	transcriptional regulator PhoB	724	NP_806197.1	2
89689	E01	t3563	hypothetical protein t3563	724	NP_807208.2	2
89625	E02	t3775	tRNA guanosine-2'-O-methyltransferase	724	NP_807398.1	2
89429	E03	t4178	hypothetical protein t4178	724	NP_807782.1	2
89673	E04	t2131	colicin uptake protein TolQ	727	NP_805885.1	2
89581	E05	t2318	fimbrial chaperone protein	727	NP_806052.1	1.804677
89521	E06	t3092	hypothetical protein t3092	727	NP_806776.1	2
89425	E07	t0589	hypothetical protein t0589	730	NP_804446.1	2
89729	E08	t0606	quinol dehydrogenase periplasmic protein	730	NP_804462.1	1.993151
89506	E09	t4173	glutathione S transferase	703	NP_807777.1	-
89518	E10	t4199	DNA-binding transcriptional regulator BasR	703	NP_807803.1	2
89686	E11	t2771	oxygen-regulated invasion protein	706	NP_806472.1	2
89658	E12	t2852	hypothetical protein t2852	706	NP_806549.1	2
89526	F01	t3113	disulfide isomerase	706	NP_806796.1	2
89598	F02	t3463	endonuclease V	706	NP_807119.1	1.604816
89638	F03	t4635	transcriptional regulator protein	706	NP_808204.1	-
89618	F04	t0981	hypothetical protein t0981	709	NP_804804.1	2
89418	F05	t1279	pathogenicity island protein	709	NP_805082.1	1.994358
89590	F06	t2069	DNA-binding transcriptional regulator	709	NP_805829.1	2
89434	F07	t2679	transcriptional regulator	709	NP_806389.1	2
89550	F08	t2792	surface presentation of antigens protein SpaP	709	NP_806493.1	2
89670	F09	t2992	hypothetical protein t2992	709	NP_806684.1	1.980254
89454	F10	t0853	cobalt transport protein CbiQ	712	NP_804688.1	2
89398	F11	t1983	hypothetical protein t1983	712	NP_805747.1	2
89406	F12	t2172	DNA-binding transcriptional activator KdpE	712	NP_805924.1	2
89498	G01	t2568	hypothetical protein t2568	712	NP_806287.1	2
89438	G02	t2689	DNA-binding transcriptional regulator CisR	712	NP_806398.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
89578	G03	t1539	amino acid ABC transporter	715	NP_805323.1	2
89562	G04	t1791	N-acetylmannosamine-6-phosphate 2-epimerase	715	NP_805564.1	1.955245
89486	G05	t1831	hypothetical protein t1831	715	NP_805603.1	2
89714	G06	t3757	hypothetical protein t3757	715	NP_807386.1	2
89646	G07	t1954	cytidylate kinase	718	NP_805719.1	2
89366	G08	t2993	ABC transporter ATP-binding protein	718	NP_806685.1	2
89530	G09	t3046	LysR family transcriptional regulator	718	NP_806732.1	2
89466	G10	t3996	gluconate periplasmic binding protein	718	NP_807606.1	2
89594	G11	t0023	fimbrial chaperone	721	NP_803908.1	2
89710	G12	t0511	histidine transport system permease	721	NP_804368.1	2
89394	H01	t4215	hypothetical protein t4215	721	NP_807817.1	2
89678	H02	t4439	L-ribulose-5-phosphate 4-epimerase	721	NP_808026.1	2
89586	H03	t4639	RNA methyltransferase	721	NP_808208.1	2
89542	H04	t0349	hypothetical protein t0349	724	NP_804220.1	1.948895
89442	H05	t2105	molybdate ABC transporter permease	724	NP_805862.1	1.562155
89510	H06	t4117	peptidase E	724	NP_807721.1	2
89622	H07	t4191	hypothetical protein t4191	724	NP_807795.1	2
89666	H08	t4627	DNA-binding response regulator CreB	724	NP_808198.1	2
89402	H09	t1322	electron transport complex RsxE subunit	727	NP_805123.1	2
89702	H10	t3460	hypothetical protein t3460	727	NP_807116.1	2
89630	H11	t3605	porin	727	NP_807247.1	2
89606	H12	t0105	L-ribulose-5-phosphate 4-epimerase	730	NP_803988.1	2

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