

Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 20*Catalog No. NR-19541**

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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* 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-19541.

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-19541 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 20, NR-19541."

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 20 (ZSTD1)¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
83764	A01	t3680	50S ribosomal protein L34	175	NP_807316.1	1.982857
82815	A02	t2088	hypothetical protein t2088	208	NP_805845.1	2.331731
82957	A03	t3486	hypothetical protein t3486	208	NP_807138.1	4.158654
83970	A04	t1150	hypothetical protein t1150	217	NP_804961.1	2.847926
82918	A05	t3894	hypothetical protein t3894	226	NP_807509.1	2.707965
83906	A06	t0894	hypothetical protein t0894	232	NP_804723.1	1.642241
82840	A07	t3351	lipoprotein	238	NP_807019.1	2.634454
84192	A08	t1357	bacteriophage tail fiber protein	250	NP_805153.1	3.068
84188	A09	t3129	30S ribosomal protein S21	250	NP_806812.1	3.272
84160	A10	t4331	hypothetical protein t4331	262	NP_807925.1	2.629771
84132	A11	t3407	hypothetical protein t3407	268	NP_807070.1	3.302239
82967	A12	t4595	hypothetical protein t4595	271	NP_808170.1	2.280443
84300	B01	t4483	bifunctional antitoxin/transcriptional repressor RelB	277	NP_808070.1	2
83271	B02	t1927	bacteriophage protein	280	NP_805694.1	1.217857
84304	B03	t2631	30S ribosomal protein S16	283	NP_806342.1	3.162544
84404	B04	t1628	hypothetical protein t1628	286	NP_805406.1	3.213287
84330	B05	t2782	hypothetical protein t2782	295	NP_806483.1	2.552542
83535	B06	t2498	hypothetical protein t2498	310	NP_806226.1	1.609677
83661	B07	t0703	hypothetical protein t0703	316	NP_804551.1	2.724684
83594	B08	t0836	propanediol utilization protein PduA	319	NP_804675.1	3.084639
84650	B09	t4366	hypothetical protein t4366	361	NP_807959.1	2.144044
85077	B10	t0561	hypothetical protein t0561	370	NP_804418.1	1.754054
85151	B11	t1344	hypothetical protein t1344	370	NP_805143.1	1.586486
85081	B12	t1380	hypothetical protein t1380	385	NP_805176.1	3.036364
85415	C01	t2737	DNA-binding transcriptional activator GutM	394	NP_806438.1	2.134518
85283	C02	t3154	hypothetical protein t3154	400	NP_806835.1	1.125
85551	C03	t1281	pathogenicity island protein	403	NP_805084.1	2.163772
85491	C04	t3948	hypothetical protein t3948	406	NP_807559.1	-
85337	C05	t0560	hypothetical protein t0560	412	NP_804417.1	1.17233
85345	C06	t3480	preprotein translocase subunit SecE	418	NP_807136.1	2.126794
85477	C07	t3957	hypothetical protein t3957	418	NP_807567.1	1.990431
85653	C08	t0443	hypothetical protein t0443	427	NP_804308.1	2.82904
85934	C09	t0973	hypothetical protein t0973	430	NP_804796.1	2.881395

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
85925	C10	t1779	curli assembly protein CsgE	430	NP_805553.1	2.097674
85687	C11	t0913	hypothetical protein t0913	448	NP_804742.1	1.589286
86617	C12	t3206	hypothetical protein t3206	487	NP_806884.2	3.64271
86399	D01	t0234	insertion sequence element IS200 transposase	493	NP_804115.1	1.576065
86573	D02	t2400	transcriptional regulator	493	NP_806130.1	2.46856
86563	D03	t2510	hypothetical protein t2510	502	NP_806237.1	1.569721
86457	D04	t3818	preprotein translocase subunit SecB	502	NP_807440.1	3.217131
86469	D05	t4063	type III leader peptidase	502	NP_807670.1	1.904382
86949	D06	t0764	O-antigen biosynthesis protein	514	NP_804608.1	2.09144
86889	D07	t2365	hypothetical protein t2365	514	NP_806097.1	2.819066
86997	D08	t0501	colicin V production protein	523	NP_804358.1	2.063098
87409	D09	t2788	hypothetical protein t2788	532	NP_806489.1	1.150376
87187	D10	t1528	aminoglycoside 6'-N-acyltransferase	553	NP_805314.1	1.412297
87469	D11	t1915	hypothetical protein t1915	559	NP_805682.1	4.255814
87167	D12	t2127	peptidoglycan-associated outer membrane lipoprotein	559	NP_805881.1	2.13059
87271	E01	t0088	glutathione-regulated potassium-efflux system ancillary protein KefF	565	NP_803972.1	1.40354
87687	E02	t0704	fimbrial subunit protein	565	NP_804552.1	1.424779
87633	E03	t1381	hypothetical protein t1381	565	NP_805177.1	3.063717
87543	E04	t0241	hypothetical protein t0241	580	NP_804121.1	1.503448
88051	E05	t2907	hypothetical protein t2907	598	NP_806601.1	1.780936
87883	E06	t3437	DNA-invertase	601	NP_807099.1	1.960067
87870	E07	t3234	hypothetical protein t3234	610	NP_806910.1	3.796721
88155	E08	t4373	transcriptional regulator	610	NP_807964.1	2.847541
88534	E09	t0953	transcriptional activator FlhC	619	NP_804777.1	3.812601
88555	E10	t0070	carnitine operon protein CaiE	631	NP_803954.1	2.095087
88345	E11	t3608	hypothetical protein t3608	643	NP_807250.1	1.81493
88451	E12	t3835	glutathione S-transferase	643	NP_807456.1	2.522551
88793	F01	t3269	L(+)-tartrate dehydratase beta subunit	652	NP_806944.1	2.211656
88617	F02	t3118	hypothetical protein t3118	655	NP_806801.1	2.262595
88763	F03	t0206	hypothetical protein t0206	658	NP_804088.1	2.363222
88787	F04	t2034	glutathione S-transferase	661	NP_805797.1	2.839637
88775	F05	t4039	cAMP-regulatory protein	667	NP_807647.1	2.211394
88827	F06	t1321	endonuclease III	670	NP_805122.1	2.677612
88683	F07	t0750	uridine kinase	676	NP_804594.1	2.421598
88963	F08	t1720	thymidylate kinase	676	NP_805495.1	1.884615
89215	F09	t3135	hypothetical protein t3135	679	NP_806817.1	2.02651
89318	F10	t2981	ribose-5-phosphate isomerase A	694	NP_806673.1	3.445245
89333	F11	t3671	6-phosphogluconate phosphatase	700	NP_807307.1	3.635714
89351	F12	t3799	hypothetical protein t3799	703	NP_807421.1	2.755334
89535	G01	t3108	hypothetical protein t3108	706	NP_806791.1	2.103399
89361	G02	t4185	cytochrome c-type biogenesis protein	706	NP_807789.1	3.189802
89693	G03	t0500	hypothetical protein t0500	709	NP_804357.1	3.42031
89553	G04	t1789	hypothetical protein t1789	727	NP_805562.1	2.177442
89681	G05	t2453	DeoR family transcriptional regulator	727	NP_806183.1	3.303989
90001	G06	t1865	hypothetical protein t1865	736	NP_805634.1	3.197011
90007	G07	t1979	leucyl/phenylalanyl-tRNA—protein transferase	739	NP_805743.1	3.035183
90078	G08	t0246	hypothetical protein t0246	742	NP_804126.1	3.955526
89997	G09	t1072	fatty acid metabolism regulator	754	NP_804889.1	3.187003

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
90327	G10	t0219	uridylylate kinase	760	NP_804100.1	2.680263
90359	G11	t0588	3-demethylubiquinone-9 3-methyltransferase	763	NP_804445.1	3.157274
90315	G12	t3612	hypothetical protein t3612	769	NP_807253.1	2.628088
90479	H01	t2517	transmembrane regulator	778	NP_806243.1	2.988432
90279	H02	t3751	hypothetical protein t3751	778	NP_807381.1	2.70437
90565	H03	t2580	hypothetical protein t2580	784	NP_806298.1	3.701531
90610	H04	t4431	esterase	784	NP_808018.1	3.145408
90561	H05	t2032	DNA-binding transcriptional repressor DeoR	793	NP_805795.1	3.385876
90674	H06	t2525	fimbrial chaperone protein	793	NP_806250.1	3.176545
90541	H07	t0169	transcriptional regulator	802	NP_804052.1	2.718204
90549	H08	t2254	molybdopterin-containing oxidoreductase membrane anchor subunit	802	NP_805996.1	3.816708
90842	H09	t1451	ATP/GTP-binding protein	805	NP_805243.1	3.72795
91022	H10	t2873	tRNA pseudouridine synthase C	817	NP_806569.1	1.98164
91054	H11	t3321	DNase TatD	817	NP_806989.1	2
90946	H12	t4367	hypothetical protein t4367	817	NP_807960.1	1.992656

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