Salmonella enterica subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 14

Catalog No. NR-19535

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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 *att*B substrate (*att*B-PCR product or a linearized *att*B expression clone) with an *att*P substrate (pDONR™221) to create an *att*L-containing entry clone. The entry clone contains recombinational cloning sites, *att*L1 and *att*L2 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-19535.

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-19535 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 14, NR-19535."

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:

You are authorized to use this product for research use only. It is not intended for human use.

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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.

Support Provided by NIAID

Table 1: *Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 14 (ZSTDN)[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
88229	A01	t4066	50S ribosomal protein L4	640	NP_807673.1	2
88245	A02	t1093	peptidyl-tRNA hydrolase	643	NP_804907.1	2
88569	A03	t2031	undecaprenyl pyrophosphate phosphatase	643	NP_805794.1	2
88417	A04	t2754	formate hydrogenlyase subunit 2	643	NP_806455.1	2
88249	A05	t0795	Bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase	646	NP_804637.1	2
88325	A06	t1416	twin-arginine leader-binding protein DmsD	649	NP_805211.1	2
88341	A07	t1899	bacteriophage protein	649	NP_805667.1	2
88305	A08	t1973	outer-membrane lipoprotein carrier protein	649	NP_805737.1	2
88377	A09	t2353	multifunctional acyl-COA thioesterase I and protease I and lysophospholipase L1	649	NP_806086.1	2
88369	A10	t2419	cytochrome o ubiquinol oxidase subunit III	649	NP_806149.1	2
88577	A11	t2535	peptide chain release factor-like protein	649	NP_806259.1	-
88294	A12	t1731	Maf-like protein	619	NP_805506.1	2
88482	B01	t1753	ribosomal-protein-S5-alanine N-acetyltransferase	619	NP_805528.1	2
88538	B02	t3626	molybdopterin-guanine dinucleotide biosynthesis protein MobA	619	NP_807267.1	2
88542	B03	t4330	exonuclease	619	NP_807924.1	2
88242	B04	t0686	hypothetical protein t0686	622	NP_804535.1	2
88442	B05	t1201	hypothetical protein t1201	622	NP_805008.2	-
88522	B06	t1269	pathogenicity island effector protein	622	NP_805072.1	2
88282	B07	t0008	molybdenum cofactor biosynthesis protein MogA	625	NP_803893.1	2
88514	B08	t0798	imidazole glycerol phosphate synthase subunit HisH	625	NP_804640.1	2
88582	B09	t1137	ABC transport ATP-binding subunit	625	NP_804949.1	1.9984
88434	B10	t2220	LPS-assembly lipoprotein RlpB	625	NP_805963.1	2
88238	B11	t2429	DJ-1 family protein	625	NP_806160.1	1.5136
88290	B12	t3186	chromosome replication initiator DnaA	625	NP_806864.1	1.9968
88318	C01	t3832	mannitol repressor protein	625	NP_807453.1	2
88594	C02	t4050	FKBP-type peptidylprolyl isomerase	625	NP_807657.1	2
88446	C03	t3015	deoxyribonucleotide triphosphate pyrophosphatase	628	NP_806707.1	2
88382	C04	t3286	Maf-like protein	628	NP_806961.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
88358	C05	t0185	fimbrial protein	631	NP_804068.1	2
88330	C06	t2311	fimbriae w protein	631	NP_806045.1	2
88506	C07	t3766	hypothetical protein t3766	631	NP_807390.1	2
88274	C08	t0532	hypothetical protein t0532	634	NP_804389.1	2
88366	C09	t0980	hypothetical protein t0980	634	NP_804803.1	2
88486	C10	t1305	TetR family transcriptional regulator	634	NP_805106.1	1.454259
88566	C11	t3293	sulfite oxidase subunit YedZ	634	NP_806968.1	2
88410	C12	t1906	bacteriophage protein	637	NP_805674.1	2
88562	D01	t3911	LuxR family transcriptional regulator	637	NP_807525.1	2
88262	D02	t1545	azoreductase	640	NP_805329.1	2
88490	D03	t2374	recombination protein RecR	640	NP_806105.1	2
88458	D04	t1455	hydrogenase 1 maturation protease	643	NP_805247.1	2
88470	D05	t4143	LexA repressor	643	NP_807747.1	2
88258	D06	t4552	hypothetical protein t4552	643	NP_808130.1	-
88602	D07	t0982	Holliday junction DNA helicase RuvA	646	NP_804805.1	1.998452
88350	D08	t1078	membrane-bound lytic murein transglycosylase E	646	NP_804895.1	2
88426	D09	t1905	hypothetical protein t1905	646	NP_805673.1	2
88526	D10	t3127	glycerol-3-phosphate acyltransferase PlsY	646	NP_806810.1	2
88310	D11	t0186	fimbrial protein	649	NP_804069.1	2
88338	D12	t1014	hypothetical protein t1014	649	NP_804834.1	2
88953	E01	t3123	signal transduction protein	649	NP_806806.1	2
88889	E02	t3313	hypothetical protein t3313	649	NP_806981.1	2
88925	E03	t0721	hypothetical protein t0721	652	NP_804567.1	2
88865	E04	t1418	dimethyl sulfoxide reductase subunit	652	NP_805213.1	2
88877	E05	t1661	thymidine kinase	652	NP_805438.1	2
88829	E06	t1969	anaerobic dimethyl sulfoxide reductase subunit B	652	NP_805733.1	2
88609	E07	t2263	hypothetical protein t2263	652	NP_806006.1	2
88721	E08	t3780	hypothetical protein t3780	652	NP_807402.1	1.996933
88853	E09	t2027	TetR family transcriptional regulator	655	NP_805790.1	2
88929	E10	t3337	homoserine/homoserine lactone efflux protein	655	NP_807005.1	1.993893
88801	E11	t3564	superoxide dismutase	655	NP_807209.1	2
88657	E12	t4089	30S ribosomal protein S4	655	NP_807696.1	2
88633	F01	t1805	secreted copper-sensitivity suppressor C	658	NP_805578.1	2
88637	F03	t3623	periplasmic protein disulfide isomerase I	658	NP_807264.1	2
88769	F04	t3778	guanylate kinase	658	NP_807401.1	2
88693	F05	t1778	DNA-binding transcriptional regulator CsgD	661	NP_805552.1	2
88649	F06	t0327	anaerobic reductase subunit	664	NP_804201.1	2
88849	F07	t3273	GntR family transcriptional regulator	664	NP_806948.1	2
88677	F08	t4065	50S ribosomal protein L3	664	NP_807672.1	2
88957	F09	t1526	epimerase	667	NP_805312.1	2
88897	F10	t2314	transcriptional regulator FimZ	667	NP_806048.1	2
88749	F11	t2941	hypothetical protein t2941	667	NP_806634.2	2
88813	F12	t3242	hypothetical protein t3242	667	NP_806918.1	2
88673	G01	t3620	ribosome biogenesis GTP-binding protein YsxC	667	NP_807261.1	2
88817	G02	t3697	chaperone protein TorD	667	NP_807332.1	2
88613	G03	t4162	hypothetical protein t4162	667	NP_807766.1	1.998501
88797	G04	t0288	hypothetical protein t0288	670	NP_804164.1	2
88905	G05	t1707	TetR family regulatory protein	670	NP_805483.1	2
88949	G06	t2984	arginine exporter protein	670	NP_806676.1	1.998507

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
88705	G07	t3188	hypothetical protein t3188	670	NP_806866.1	2
88833	G08	t3227	hypothetical protein t3227	670	NP_806903.1	2
88653	G09	t3468	thiamine-phosphate pyrophosphorylase	670	NP_807124.1	2
88741	G10	t3585	formate dehydrogenase-O subunit gamma	670	NP_807228.1	2
88757	G11	t4247	prepilin	670	NP_807846.1	1.664179
88881	G12	t0249	DL-methionine transporter permease	673	NP_804129.1	2
88685	H01	t0304	hypothetical protein t0304	673	NP_804180.1	2
88689	H02	t0357	phosphoribosylglycinamide formyltransferase	673	NP_804227.1	2
88901	H03	t1799	transcriptional regulator	673	NP_805572.1	1.469539
88917	H04	t2817	aldolase	673	NP_806516.1	2
88737	H05	t4129	lipoprotein	673	NP_807733.1	2
88605	H06	t4426	hypothetical protein t4426	673	NP_808013.1	2
88821	H07	t0993	keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase	676	NP_804816.1	2
88666	H08	t4278	hypothetical protein t4278	649	NP_807876.1	2
88642	H09	t0610	cytochrome c biogenesis protein CcmA	652	NP_804466.1	1.849693
88710	H10	t1349	bacteriophage tail fiber assembly protein	652	NP_805146.1	2
88790	H11	t2545	hypothetical protein t2545	652	NP_806269.1	2
88922	H12	t3761	hypothetical protein t3761	652	NP_807388.1	2

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

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