Salmonella enterica subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 24

Catalog No. NR-19545

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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-19545.

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-19545 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 24, NR-19545."

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.

Support Provided by NIAID

Table 1: *Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 24 (ZSTDX)[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
92669	A01	t1477	hemolysin E	952	NP_805266.1	3.551471
92533	A02	t2359	hypothetical protein t2359	952	NP_806091.1	1.862395
92409	A03	t2763	iron transporter periplasmic-binding protein	952	NP_806464.1	1.430672
92497	A04	t2839	hypothetical protein t2839	952	NP_806536.1	3.747899
92581	A05	t2890	DNA-binding transcriptional activator GcvA	952	NP_806586.1	2.156513
92577	A06	t3500	DNA-binding transcriptional regulator OxyR	952	NP_807148.1	1.816176
92607	A07	t4138	maltose regulon periplasmic protein	952	NP_807742.1	2.147059
92429	A08	t0134	D-alanine—D-alanine ligase	955	NP_804017.1	1.884817
92657	A09	t0457	lipid A biosynthesis palmitoleoyl acyltransferase	955	NP_804320.1	3.394764
92702	A10	t0888	hypothetical protein t0888	955	NP_804718.1	1.874346
92722	A11	t1614	hypothetical protein t1614	955	NP_805392.1	2.303665
92565	A12	t1657	oligopeptide transporter permease	955	NP_805434.1	2.405236
92613	B01	t1808	curved DNA-binding protein CbpA	955	NP_805581.1	1.658639
92977	B02	t2039	ABC transporter permease	955	NP_805802.1	1.824084
93101	B03	t2050	hypothetical protein t2050	955	NP_805813.1	1.375916
93086	B04	t2998	agmatinase	955	NP_806690.1	1.991623
92902	B05	t3725	carbohydrate kinase	955	NP_807358.1	1.981152
92786	B06	t4280	hypothetical protein t4280	955	NP_807878.1	1.974869
92777	B07	t2381	hypothetical protein t2381	958	NP_806111.1	1.784969
93134	B08	t2752	formate hydrogenlyase subunit 4	958	NP_806453.1	1.927975
93041	B09	t3717	DNA-binding transcriptional regulator DsdC	958	NP_807351.1	1.461378
92801	B10	t0178	ABC transporter integral membrane protein	961	NP_804061.1	2.146722
93010	B11	t1446	glutaminase	961	NP_805239.1	1.973985
92985	B12	t2208	glutamate and aspartate transporter subunit	961	NP_805952.1	1.219563
92846	C01	t2305	bactoprenol glucosyltransferase	961	NP_806043.1	1.978148
92766	C02	t3959	branched-subunit amino acid transporter permease LivH	961	NP_807569.1	1.961498
93069	C03	t3998	hypothetical protein t3998	961	NP_807608.1	2.336108
93018	C04	t4446	hypothetical protein t4446	961	NP_808033.1	1.806452

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
92882	C05	t0003	homoserine kinase	964	NP_803888.1	1.848548
92945	C06	t0859	hypothetical protein t0859	964	NP_804694.1	1.573651
92893	C07	t0955	flagellar motor protein MotB	964	NP_804779.1	3.059129
93093	C08	t1338	DNA replication terminus site-binding protein	964	NP_805137.1	1.53112
92914	C09	t1582	oxidoreductase	964	NP_805364.1	1.95332
92929	C10	t1726	ACP S-malonyltransferase	964	NP_805501.1	1.381743
92917	C11	t2675	virulence protein	964	NP_806386.1	1.795643
92906	C12	t2777	AraC family transcriptional regulator	964	NP_806478.1	2
92926	D01	t3246	hypothetical protein t3246	964	NP_806922.1	1.865145
92773	D02	t3282	DNA-binding transcriptional regulator	964	NP_806957.1	1.447095
93130	D03	t3395	branched subunit amino acid aminotransferase	964	NP_807059.1	1.862033
92793	D04	t3528	1,4-dihydroxy-2-naphthoate octaprenyltransferase	964	NP_807175.1	2.001037
92822	D05	t3589	lipase	964	NP_807232.1	1.821577
92898	D06	t3634	ribokinase	964	NP_807271.1	1.669087
92829	D07	t3905	2,3-dehydro-3-deoxyglucokinase	964	NP_807519.1	3.211618
93053	D08	t4110	homoserine O-succinyltransferase	964	NP_807714.1	3.712656
92909	D09	t0479	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	967	NP_804337.1	3.487073
92957	D10	t1297	DNA-binding transcriptional regulator	967	NP_805098.1	3.916236
92862	D11	t2163	hypothetical protein t2163	967	NP_805914.1	1.978283
92833	D12	t3280	p-hydroxybenzoic acid efflux subunit AaeA	967	NP_806955.1	1.557394
93014	E01	t3849	hypothetical protein t3849	967	NP_807469.1	1.902792
93030	E02	t4204	DNA-binding transcriptional regulator MelR	967	NP_807808.1	1.827301
92975	E03	t4500	carbamate kinase	967	NP_808087.1	2.141675
92889	E04	t1558	C32 tRNA thiolase	970	NP_805341.1	1.408247
92790	E05	t2212	ribonucleoside hydrolase 1	970	NP_805956.1	1.979381
93110	E06	t2924	LysR family transcriptional regulator	970	NP_806618.1	1.907216
92965	E07	t4495	aspartate carbamoyltransferase	970	NP_808082.1	1.540206
92798	E08	t0047	bifunctional riboflavin kinase/FMN adenylyltransferase	973	NP_803931.1	1.986639
93077	E09	t0534	NADH dehydrogenase operon transcriptional regulator	973	NP_804391.1	1.903392
92809	E10	t1785	2-hydroxyacid dehydrogenase	973	NP_805559.1	1.759507
92995	E11	t2120	zinc transporter ZitB	973	NP_805877.1	1.436793
92841	E12	t3165	DNA-binding transcriptional activator TdcA	973	NP_806844.1	3.380267
92949	F01	t3274	malate dehydrogenase	973	NP_806949.1	1.619733
93125	F02	t0077	electron transfer flavoprotein FixB	976	NP_803961.1	1.322746
92937	F03	t0143	LysR family transcriptional regulator	976	NP_804026.1	1.877049
93117	F04	t0471	hypothetical protein t0471	976	NP_804329.1	1.900615
92857	F05	t1889	bacteriophage protein	976	NP_805657.1	1.909836
92962	F06	t2042	L-asparaginase	976	NP_805805.1	1.936475
92849	F07	t3359	porphobilinogen deaminase	976	NP_807027.1	1.857582
92877	F08	t3752	hypothetical protein t3752	976	NP_807382.1	1.765369
92769	F09	t0119	leucine transcriptional activator	979	NP_804002.1	1.684372
93006	F10	t0986	high-affinity zinc transporter periplasmic protein	979	NP_804809.2	1.855975
92874	F11	t1398	hypothetical protein t1398	979	NP_805193.1	1.884576

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93025	F12	t2554	LysR family transcriptional regulator	979	NP_806276.1	1.861083
93122	G01	t3202	tRNA pseudouridine synthase B	979	NP_806880.1	1.947906
92817	G02	t0014	regulatory protein	982	NP_803899.1	1.744399
93081	G03	t0691	permease transmembrane protein	982	NP_804539.1	2.284114
92825	G04	t1096	ribose-phosphate pyrophosphokinase	982	NP_804910.1	3.427699
92982	G05	t1448	hypothetical protein t1448	982	NP_805241.1	1.92668
92990	G06	t1565	universal stress protein UspE	982	NP_805347.1	1.903259
92969	G07	t3171	carbohydrate kinase	982	NP_806850.1	1.583503
92781	G08	t4097	methionyl-tRNA formyltransferase	982	NP_807704.1	1.433809
92867	G09	t4490	trehalose repressor	982	NP_808077.1	2.143585
93046	G10	t0051	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	985	NP_803935.1	1.770558
92871	G11	t0154	glycosyl hydrolase	985	NP_804037.1	2.132995
93089	G12	t0386	transaldolase A	985	NP_804255.1	3.198985
93049	H01	t1511	secreted effector protein	985	NP_805297.1	2.93401
93106	H02	t1738	flagellar rod assembly protein/muramidase FlgJ	985	NP_805513.1	1.906599
93002	H03	t1993	virK protein	985	NP_805756.1	1.82132
92998	H04	t2815	hypothetical protein t2815	985	NP_806514.1	1.903553
93097	H05	t3487	pantothenate kinase	985	NP_807139.1	1.719797
93401	H06	t4411	tRNA delta(2)-isopentenylpyrophosphate transferase	985	NP_808000.1	1.730964
93306	H07	t0007	transaldolase B	988	NP_803892.1	1.847166
93182	H08	t0166	2-keto-3-deoxygluconate permease	988	NP_804049.1	1.878543
93515	H09	t0524	transketolase C-terminal section, partial	988	NP_804381.1	1.879555
93382	H10	t0576	deubiquitinase	988	NP_804433.1	1.938259
93158	H11	t1727	3-oxoacyl-ACP synthase	988	NP_805502.1	1.824899
93325	H12	t2017	putrescine ABC transporter membrane protein	988	NP_805780.1	1.697368

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

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