

Product Information Sheet for NR-42843

SUPPORTING INFECTIOUS DISEASE RESEARCH

Salmonella enterica subsp. enterica, Strain 14028s (Serovar Typhimurium) Single-Gene Deletion Mutant Library, Plate SGD_065/066_Kan

Catalog No. NR-42843

For research use only. Not for human use.

Contributor:

Michael McClelland, Professor, Scientific Director, Vaccine Research Institute of San Diego, San Diego, California, USA

Manufacturer:

BEI Resources

Product Description:

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 does not confirm or validate individual mutants provided by the contributor.

The Salmonella enterica (S. enterica) subsp. enterica, strain 14028s (serovar Typhimurium) targeted single-gene deletion (SGD) mutant library contains a total of 3,773 individual genes deleted simultaneously across two collections of mutants differentiated by kanamycin or chloramphenicol resistance. The kanamycin-resistant mutant collection contains 3,517 mutants distributed among 11 96-well plates, in which a single gene is replaced by a cassette conferring the kanamycin resistance gene, and includes 9 double mutants that contain both kanamycin and chloramphenicol cassettes. Deletions were confirmed by the depositor. 1.2

Genes were targeted for deletion by primers designed to preserve the first and last 30 bases of each deleted gene.² Gene replacement followed a modified Lambda-Red technique, with an added T7 RNA polymerase promoter positioned in plasmid <u>pCLF3</u> to generate a gene-specific transcript from the *Salmonella* genome directly downstream of each mutant.²⁻⁴ Detailed information about each mutant is shown in Table 1.

Note: The strain designation on the plate, strain CDC 6516-60, is incorrect. The correct strain designation is strain 14028s. *S. enterica* subsp. *enterica*, strain 14028s was originally known as strain 14028. A variant of the original strain with a rough colony morphology was designated 14028r and the original smooth strain was renamed 14028s. Strain 14028 is a descendent of strain CDC 6516-60, which was isolated from pools of hearts and livers of 4-week-old chickens.⁵ The complete genome of *S. enterica* subsp. *enterica*, strain 14028s (GenBank: CP001363.1) and plasmid (GenBank: CP001362.1) sequences are available.

Material Provided:

Each inoculated well of the 96-well plate contains approximately 50 μ L of culture in Luria Bertani (LB) broth containing 60 μ g/mL kanamycin supplemented with 10% glycerol.

Packaging/Storage:

NR-42843 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 60 µg/mL kanamycin

Incubation:

Temperature: 37°C Atmosphere: Aerobic

Propagation:

- 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 14028s (Serovar Typhimurium) Single-Gene Deletion Mutant Library, Plate SGD_065/066_Kan, NR-42843."

Biosafety Level: 2

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.

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References:

1. McClelland, M., Personal Communication.

- Porwollik, S., et al. "Defined Single-Gene and Multi-Gene Deletion Mutant Collections in Salmonella enterica sv Typhimurium." <u>PLoS One</u> 9 (2014): e99820. PubMed: 25007190.
- Santiviago, C. A., et al. "Analysis of Pools of Targeted Salmonella Deletion Mutants Identifies Novel Genes Affecting Fitness during Competitive Infection in Mice." <u>PLoS Pathog.</u> 5 (2009): e1000477. PubMed: 19578432.
- Datsenko, K. A. and B. L. Wanner. "One-step Inactivation of Chromosomal Genes in *Escherichia coli* K-13 Using PCR Products." <u>Proc. Natl. Acad. Sci. USA</u> 97 (2000): 6640-6645. PubMed: 10829079.
- Jarvik, T., et al. "Short-Term Signatures of Evolutionary Change in the Salmonella enterica Serovar Typhimurium 14028 Genome." J. Bacteriol. 192 (2010): 560-567. PubMed: 19897643.

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Table 1: S. enterica subsp. enterica, Strain 14028s (Serovar Typhimurium) Single-Gene Deletion Mutant Library, Plate SGD 065/066 Kan^{1,2}

Well Position	Gene Type	Gene Start	Gene End	Target Gene (Locus Tag)	Deleted Region Start	Deleted Region End	Gene Strand	Description
A02	CDS		4612745	STM14_5237	4611228	4612714	-	Hypothetical protein
A03	CDS	4589814	4590185	STM14_5209	4589850	4590154	-	Putative outer membrane lipoprotein
A04	CDS	4591372	4592400	STM14_5213	4591402	4592369	+	Putative aminomutase
A05	CDS	4600129	4601631	STM14_5226	4600159	4601600	-	Putative amino-acid transport protein
A06	CDS	4602064	4605390	STM14_5228	4602094	4605335	+	Hypothetical protein
A07	CDS	4610060	4611199	STM14_5236	4610090	4611183	+	Putative FeS protein
A08	CDS	4626423	4627154	STM14_5251	4626453	4627123	-	23S rRNA (guanosine-2'-O-)-methyltransferase
A09	CDS	4634111	4634431	STM14_5260	4634141	4634400	+	Putative inner membrane protein
A10	CDS	4635776	4636531	STM14_5263	4635806	4636500	+	Transcriptional repressor UlaR
A11	CDS	4636636	4637700	STM14_5264	4636666	4637669	+	Putative L-ascorbate 6-phosphate lactonase
A12	CDS	4694012	4694563	STM14_5328	4694042	4694532	+	Hypothetical protein
B01	CDS	4725750	4726166	STM14_5365	4725780	4726135	-	Hypothetical protein
B02	CDS	4715866	4716252	STM14_5351	4715896	4716221	+	Putative translation initiation inhibitor
B04	CDS	4727819	4728322	STM14_5369	4727849	4728291	+	Putative acetyltransferase
B06	CDS	4783517	4784788	STM14_5424	4783547	4784757	+	Putative inner membrane protein
B07	CDS	4784875	4786116	STM14_5425	4784905	4786085	+	Putative transport protein
B08	CDS		4800303	STM14_5444	4800130	4800272	+	Putative cytoplasmic protein
B09	CDS	4800398	4802548	STM14_5445	4800428	4802517	+	Putative carbon starvation protein
B10	CDS	4825952	4826629	STM14_5477	4825979	4826598	-	Nucleotidase
B11	CDS	4849992	4851659	STM14_5502	4850022	4851607	+	Putative ABC transporter ATP-binding protein
B12	CDS	4829743	4830816	STM14_5482	4829773	4830785	-	Putative phosphoesterase
C01	CDS	527508	527978	STM14_0555	527538	527947	+	Putative inner membrane protein
C03	CDS	922656	923576	STM14_0993	922686	923545	-	Putative ABC transporter periplasmic binding protein
C08	CDS	1282422	1283087	STM14_1415	1282452	1283056	+	Putative ribosomal large subunit pseudouridine synthase
C09	CDS	1756108	1756542	STM14_1997	1756138	1756511	-	Putative universal stress protein
C12	CDS	1591284	1591625	STM14_1815	1591314	1591594	+	Hypothetical protein
D01	CDS	1576425	1577120	STM14_1800	1576455	1577089	-	Putative dithiobiotin synthetase
D02	CDS	1574052	1574951	STM14_1798	1574082	1574920	-	Putative transcriptional regulator
D03	CDS	1572679	1573932	STM14_1797	1572709	1573901	+	Putative transport protein
D04	CDS	1467394	1467810	STM14_1668	1467424	1467779	-	Cysteine desufuration protein SufE
D05	CDS	1413133	1413669	STM14_1607	1413163	1413638	-	Putative regulatory protein

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Doc CDS	Well	Gene	Gene	Gene	Target Gene	Deleted	Deleted	Gene	Description
D07	Position	Type	Start	End	(Locus Tag)	Region Start	Region End	Strand	Description
D08	D06	CDS	1412316	1412984	STM14_1606	1412346	1412953	+	2-deoxyglucose-6-phosphatase
D09	D07	CDS	1929920	1931830	STM14_2203	1929950	1931799	+	
D10	D08							+	Putative inner membrane protein
D11		CDS	2318191	2318778		2318221	2318747	+	Putative transport protein
D12					STM14_2677			-	Hypothetical protein
E02 CDS 3203592 3203864 STM14 3651 3203622 3203833 Putative cytoplasmic protein								+	
E03								-	Hypothetical protein
E04	E02	CDS	3203592	3203864	STM14_3651	3203622	3203833	+	
COS	E03	CDS	2412315	2413958	STM14_2793	2412345	2413927	+	binding component
E05	E04	CDS	2418861	2421530	STM14_2800	2418891	2421499	-	
E07 CDS 3135354 3136318 STM14 3573 3135398 313608 - Tr. Cyanor-7-deazaguanine reductase E08 CDS 31399467 3200645 STM14 3464 3199497 3200614 + Acetyl-CoA acetyltransferase E10 CDS 3199467 3200645 STM14 3468 3199497 3200614 + Acetyl-CoA acetyltransferase E10 CDS 3227153 3227781 STM14 3462 3227781 + Putative Innowlysin E11 CDS 3293586 3294282 - Putative Innowlysin - Hypothetical protein F02 CDS 3343525 33335019 STM14 3818 3334526 3342182 - Hypothetical protein F03 CDS 33423851 STM14 3812 3343520 - Putative iranscriptional regulator F04 CDS 3343484 S3443551 STM14 3834 334552 - Putative iranscriptional regulator F06 CDS 33435857 S344583 S36414 336414 3364718 <td>E05</td> <td>CDS</td> <td>2988803</td> <td>2989228</td> <td>STM14 3404</td> <td>2988833</td> <td>2989197</td> <td>+</td> <td></td>	E05	CDS	2988803	2989228	STM14 3404	2988833	2989197	+	
EOB									
E09	E08	CDS	3137691	3138539	STM14_3577		3138508	-	
E10		CDS						+	
E11	E10	CDS	3227153	3227812	STM14_3682	3227183	3227781	+	
F12	E11	CDS	3293586	3294293		3293616	3294262	-	Putative inner membrane protein
F02 CDS 3334525 3335019 STM14 3818 3341282 Hypothetical protein F03 CDS 3341296 3342121 STM14 3829 3342182 + Putative transcriptional regulator F04 CDS 3343881 3343551 STM14 3831 3342182 + Putative alcohol dehydrogenase F05 CDS 3346173 3344484 STM14 3832 3343687 3344453 - 2.5-diketo-D-gluconate reductase A F06 CDS 3364314 3364715 STM14 3855 3364684 + Esterase YqiA F07 CDS 3365987 3365989 STM14 3855 3366987 + ADP-ribose pyrophosphatase NudF F10 CDS 3415757 STM14 3912 3415389 3415757 STM14 3914 3415389 3416682 - Hypothetical protein F11 CDS 3445584 3446447 STM14 3944 3445614 3446612 446416 + Putative inner membrane protein F12 CDS	E12	CDS						-	
F03	F02	CDS	3334525	3335019	STM14_3818	3334555	3334988	+	
FO4	F03							+	
F06	F04						3343520	-	
F06	F05	CDS	3343657	3344484	STM14_3832	3343687	3344453	-	2,5-diketo-D-gluconate reductase A
F07	F06	CDS				3364164	3364684	+	
F08					STM14_3857		3365958	+	Hypothetical protein
F10	F08	CDS				3366016	3366587	+	ADP-ribose pyrophosphatase NudF
F11 CDS 3416198 3416683 STM14_3914 3416228 3416652 - Hypothetical protein F12 CDS 3445584 3446447 STM14_3945 3445614 3446416 + Putative methyltransferase G01 CDS 3448511 3448906 STM14_3947 3448957 - Hypothetical protein G02 CDS 3448918 STM14_3948 34489487 - Dnak initiator-associating protein DiaA G03 CDS 3449528 3450103 STM14_3949 3449558 3450072 - Hypothetical protein G04 CDS 3450170 3450838 STM14_3995 3450200 3450774 + Putative nucleoside-diphosphate-sugar epimerase G05 CDS 3490147 STM14_3995 3490366 + Putative transport protein G06 CDS 3491496 3492047 STM14_3999 3491526 3492016 + Putative transport protein G07 CDS 3491496 3492834 STM14_4000 3492882 3492803 + Putative transport protein G08	F10	CDS					3415726	-	
F12	F11	CDS						-	
G01	F12	CDS	3445584	3446447		3445614	3446416	+	Putative methyltransferase
G02 CDS 3448928 3449518 STM14_3948 3448958 3449487 - DnaA initiator-associating protein DiaA G03 CDS 3449528 3450103 STM14_3949 3449558 3450072 - Hypothetical protein G04 CDS 3450170 3450838 STM14_3995 3450200 3450774 + Putative nucleoside-diphosphate-sugar epimerase G05 CDS 3490104 3490397 STM14_3995 3490134 3490366 + Putative transport protein G06 CDS 3490842 3491477 STM14_3998 3490162 3492016 + Putative transport protein G07 CDS 3491496 3492047 STM14_3999 3491526 3492016 + Putative transport protein G08 CDS 3492052 3492834 STM14_4000 3492872 3493623 + Putative ABC transporter ATP-binding protein YrbF G10 CDS 3493867 3494844 STM14_4001 3493887 3494813 - Putative calcium/sodium:proton antiporter G11 CDS 3586340 3586864 <td>G01</td> <td>CDS</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>-</td> <td></td>	G01	CDS						-	
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G04 CDS 3450170 3450838 STM14_3950 3450200 3450774 + Putative nucleoside-diphosphate-sugar epimerase G05 CDS 3490104 3490397 STM14_3995 3490134 3490366 + Putative transcriptional regulator G06 CDS 3490842 3491477 STM14_3998 3490872 3491446 + Putative transport protein G07 CDS 3491496 3492047 STM14_3999 3491526 3492016 + Putative transport protein G08 CDS 3492052 3492834 STM14_4000 3492802 3492803 + Putative transport protein G09 CDS 3492842 3493654 STM14_4001 3492872 3493623 + Putative transport protein G10 CDS 3493867 3494844 STM14_4001 3492872 3493623 + Putative ABC transporter ATP-binding protein YrbF G11 CDS 3493867 3494844 STM14_4003 3494888 3495813 - D-arabinose 5-phos	G03	CDS					3450072	-	
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G10 CDS 3493867 3494844 STM14_4002 3493897 3494813 - Putative calcium/sodium:proton antiporter G11 CDS 3494858 3495844 STM14_4003 3494888 3495813 - D-arabinose 5-phosphate isomerase G12 CDS 3586340 3586894 STM14_4102 3586370 3586863 - Putative ferripyochelin-binding protein H02 CDS 3588524 3589066 STM14_4106 3588554 3589035 + Putative DNA topoisomerase H03 CDS 3663196 3663759 STM14_4206 3663226 3663761 + ADP-ribose diphosphatase NudE H05 CDS 3666979 3666947 STM14_4209 3666309 3666916 - Putative hydrolase H06 CDS 3666958 3667359 STM14_4210 3666988 3667328 - Ribosome-associated heat shock protein Hsp15 H08 CDS 4649199 4649861 STM14_5283 4649229 4649830 + Cell morphogenesis/cel	G09	CDS	3492842	3493654	STM14_4001	3492872	3493623	+	Putative ABC transporter ATP-binding protein YrbF
G11 CDS 3494858 3495844 STM14_4003 3494888 3495813 - D-arabinose 5-phosphate isomerase G12 CDS 3586340 3586894 STM14_4102 3586370 3586863 - Putative ferripyochelin-binding protein H02 CDS 3588524 3589066 STM14_4106 3588554 3589035 + Putative DNA topoisomerase H03 CDS 3663196 3663759 STM14_4206 3663226 3663761 + ADP-ribose diphosphatase NudE H05 CDS 3666279 3666947 STM14_4209 3666309 3666916 - Putative hydrolase H06 CDS 3666958 3667359 STM14_4210 3666988 3667328 - Ribosome-associated heat shock protein Hsp15 H08 CDS 4649199 4649861 STM14_5283 4649229 4649830 + Cell morphogenesis/cell wall metabolism regulator H09 CDS 4649964 4650929 STM14_5284 4649994 4650898 + Putative reduc						3493897		-	Putative calcium/sodium:proton antiporter
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H02 CDS 3588524 3589066 STM14_4106 3588554 3589035 + Putative DNA topoisomerase H03 CDS 3663196 3663759 STM14_4206 3663226 3663761 + ADP-ribose diphosphatase NudE H05 CDS 3666279 3666947 STM14_4209 3666309 3666916 - Putative hydrolase H06 CDS 3666958 3667359 STM14_4210 3666988 3667328 - Ribosome-associated heat shock protein Hsp15 H08 CDS 4649199 4649861 STM14_5283 4649229 4649830 + Cell morphogenesis/cell wall metabolism regulator H09 CDS 4649964 4650929 STM14_5284 4649994 4650898 + Putative cationic amino acid transporter H10 CDS 4651010 4651858 STM14_5285 4651040 4651827 + Putative reductase H11 CDS 4651946 4652332 STM14_5286 4651976 4652301 - Putative transcriptional regulator	G12	CDS			STM14_4102		3586863	-	
H03 CDS 3663196 3663759 STM14_4206 3663226 3663761 + ADP-ribose diphosphatase NudE H05 CDS 3666279 3666947 STM14_4209 3666309 3666916 - Putative hydrolase H06 CDS 3666958 3667359 STM14_4210 3666988 3667328 - Ribosome-associated heat shock protein Hsp15 H08 CDS 4649199 4649861 STM14_5283 4649229 4649830 + Cell morphogenesis/cell wall metabolism regulator H09 CDS 4649964 4650929 STM14_5284 4649994 4650898 + Putative cationic amino acid transporter H10 CDS 4651010 4651858 STM14_5285 4651040 4651827 + Putative reductase H11 CDS 4651946 4652332 STM14_5286 4651976 4652301 - Putative transcriptional regulator	H02	CDS				3588554	3589035	+	
H05 CDS 3666279 3666947 STM14_4209 3666309 3666916 - Putative hydrolase H06 CDS 3666958 3667359 STM14_4210 3666988 3667328 - Ribosome-associated heat shock protein Hsp15 H08 CDS 4649199 4649861 STM14_5283 4649229 4649830 + Cell morphogenesis/cell wall metabolism regulator H09 CDS 4649964 4650929 STM14_5284 4649994 4650898 + Putative cationic amino acid transporter H10 CDS 4651010 4651858 STM14_5285 4651040 4651827 + Putative reductase H11 CDS 4651946 4652332 STM14_5286 4651976 4652301 - Putative transcriptional regulator	H03	CDS	3663196	3663759		3663226	3663761	+	ADP-ribose diphosphatase NudE
H06 CDS 3666958 3667359 STM14_4210 3666988 3667328 - Ribosome-associated heat shock protein Hsp15 H08 CDS 4649199 4649861 STM14_5283 4649229 4649830 + Cell morphogenesis/cell wall metabolism regulator H09 CDS 4649964 4650929 STM14_5284 4649994 4650898 + Putative cationic amino acid transporter H10 CDS 4651010 4651858 STM14_5285 4651040 4651827 + Putative reductase H11 CDS 4651946 4652332 STM14_5286 4651976 4652301 - Putative transcriptional regulator							3666916	-	Putative hydrolase
H08 CDS 4649199 4649861 STM14_5283 4649229 4649830 + Cell morphogenesis/cell wall metabolism regulator H09 CDS 4649964 4650929 STM14_5284 4649994 4650898 + Putative cationic amino acid transporter H10 CDS 4651010 4651858 STM14_5285 4651040 4651827 + Putative reductase H11 CDS 4651946 4652332 STM14_5286 4651976 4652301 - Putative transcriptional regulator	H06							-	Ribosome-associated heat shock protein Hsp15
H09 CDS 4649964 4650929 STM14_5284 4649994 4650898 + Putative cationic amino acid transporter H10 CDS 4651010 4651858 STM14_5285 4651040 4651827 + Putative reductase H11 CDS 4651946 4652332 STM14_5286 4651976 4652301 - Putative transcriptional regulator	H08	CDS	4649199	4649861	STM14_5283	4649229	4649830	+	
H10 CDS 4651010 4651858 STM14_5285 4651040 4651827 + Putative reductase H11 CDS 4651946 4652332 STM14_5286 4651976 4652301 - Putative transcriptional regulator					STM14_5284	4649994	4650898	+	
H11 CDS 4651946 4652332 STM14_5286 4651976 4652301 - Putative transcriptional regulator									
	H11	CDS	4651946	4652332		4651976	4652301	-	Putative transcriptional regulator
								+	

¹All information in this table was provided by the depositor at the time of deposition.

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²Construction of each listed mutant has been confirmed either by PCR or by an array indicating a functional T7 promoter in the correct location and orientation. Mutants that did not produce such a signal on the array, or did not yield the expected mutant product during PCR, are not listed.