

Table S5.1. Details of the Salmonella virulence genes for which probes and labeling pri

<b>Gene</b>	<b>Gene Function</b>	<b>Accession No.</b>	<b>Position</b>
<i>agfA</i>		FQ312003.1	1187770 to 1188225
<i>bcfC</i>		FQ312003.1	25803 to 28424
<i>bcfG</i>		FQ312003.1	30505 to 31209
<i>fimA</i>		FQ312003.1	603618 to 604160
<i>fimI</i>		FQ312003.1	604236 to 604769
<i>lpfD</i>		FQ312003.1	3844343 to 3845412
<i>pefA</i>		AB041905.1	2871 to 3395
<i>pefB</i>		JN885080.1	17312 to 17614
<i>pefD</i>		AB041905.1	6029 to 6712
<i>pefI</i>		JN885080.1	23605 to 23814
<i>safC</i>		FQ312003.1	343044 to 345554
<i>sefA</i>		CP000026.1	4472704 to 4473201
<i>sefR</i>		CP000026.1	4476999 to 4477443
<i>srgA</i>	Adhesion	JN885080.1	24399 to 25049
<i>srgB</i>		JN885080.1	25236 to 26081
<i>srgC</i>		JN885080.1	26994 to 27740
<i>staA</i>		AE014613.1	216818 to 217402
<i>stbD</i>		FQ312003.1	379183 to 380508
<i>stcC</i>		FQ312003.1	2241571 to 2244060
<i>stdB</i>		FQ312003.1	3209943 to 3212432
<i>stdC</i>		FQ312003.1	3209159 to 3209902
<i>steB</i>		FQ312003.1	1676474 to 1676875
<i>stfE</i>		FQ312003.1	234790 to 235257
<i>stgA</i>		AL627280.1	52596 to 53171
<i>stiC</i>		AE006468.1	205079 to 207625
<i>stjB</i>		AE006468.1	4826467 to 4828875
<i>stm4595</i>		AE006468.1	4852849 to 4853400
<i>tcfA</i>		AE014613.1	2628639 to 2629349
<i>avrA</i>		FQ312003.1	3032477 to 3033382
<i>hilA</i>		AE006468.1	3019856 to 3021517
<i>hilD</i>		AE006468.1	3017836 to 3018765
<i>iacP</i>		AE006468.1	3024412 to 3024660
<i>invA</i>		FQ312003.1	3060976 to 3061755
<i>invB</i>		AE006468.1	3037969 to 3038376
<i>invE</i>		AE006468.1	3040482 to 3041600
<i>invH</i>		AE006468.1	3044389 to 3044832
<i>invI</i>		AE006468.1	3036256 to 3036699
<i>orgA</i>		AE006468.1	3014425 to 3015024
<i>prgH</i>		AE006468.1	3016342 to 3017520
<i>prgJ</i>		FQ312003.1	3038327 to 3038632
<i>sipA</i>	SPI-1	FQ312003.1	3047255 to 3049312

<i>sipD</i>		AE006468.1	3026755 to 3027786
<i>sirA</i>		FQ312003.1	1995815 to 1996471
<i>sitA</i>		FQ312003.1	3028947 to 3029864
<i>slrP</i>		FQ312003.1	866199 to 868496
<i>sopA</i>		AE006468.1	2141570 to 2143918
<i>sopD</i>		AF234268.1	1 to 642
<i>sopD2</i>		FQ312003.1	1010628 to 1011587
<i>sopE2</i>		FQ312003.1	1909580 to 1910302
<i>spaO</i>		AE006468.1	3034335 to 3035246
<i>spaR</i>		AE006468.1	3032590 to 3033381
<i>sprB</i>		AE006468.1	3010967 to 3011722
<i>sptP</i>		FQ312003.1	3044647 to 3046278
<i>pipB2</i>		AE006468.1	2926802 to 2927854
<i>orf242</i>		FQ312003.1	1432112 to 1432840
<i>orf408</i>		FQ312003.1	1421658 to 1422884
<i>sifA</i>		AE006468.1	1309844 to 1310854
<i>sifB</i>		AE006468.1	1692181 to 1693131
<i>ssaJ</i>	SPI-2	AE006468.1	1490277 to 1491026
<i>ssaQ</i>		AE006468.1	1497708 to 1498676
<i>sseB</i>		AE006468.1	1483934 to 1484524
<i>sseC</i>		AE006468.1	1484997 to 1486451
<i>sseF</i>		AE006468.1	1487975 to 1488757
<i>ssrB</i>		AE006468.1	1476167 to 1476805
<i>ttrC</i>		FQ312003.1	1426262 to 1427284
<i>marT</i>		FQ312003.1	3979512 to 3980300
<i>mgtC</i>		FQ312003.1	3985802 to 3986497
<i>misL</i>	SPI-3	FQ312003.1	3976075 to 3978942
<i>rhuM</i>		FQ312003.1	3973047 to 3974084
<i>sugR</i>		FQ312003.1	3971323 to 3972860
<i>siiD</i>		FQ312003.1	4502472 to 4503749
<i>siiE</i>	SPI-4	FQ312003.1	4503766 to 4520445
<i>siiF</i>		FQ312003.1	4520485 to 4522551
<i>pipD</i>	SPI-5	FQ312003.1	1136960 to 1138429
<i>sopB</i>		FQ312003.1	1134553 to 1136238
<i>pagN</i>	SPI-6	FQ312003.1	349371 to 350090
<i>pilR</i>		JN983049.1	94063 to 95160
<i>pilV</i>	SPI-7	JN983049.1	91117 to 92232
<i>vexA</i>		AL627283.1	43425 to 44492
<i>vexE</i>		AL627283.1	38583 to 40553
<i>cdtB</i>	Toxin	AE014613.1	1194935 to 1195744
<i>spvC</i>	Virulence plasmid	HE663166.1	26580 to 27305
<i>SpvR</i>		HE663166.1	30821 to 31714
<i>ratB</i>	CS54 island	FQ312003.1	2632119 to 2639425
<i>shdA</i>		FQ312003.1	2625306 to 2631425
<i>STMMW_34781</i>	Enterotoxin	FN424405.1	3666282 to 3667520

<i>sodCIII</i>	Fels-1	AF254764.1	152 to 676
<i>gogB</i>	Gifsy-1	FQ312003.1	2726744 to 2728186
<i>grvA</i>	Gifsy-2	AF266469.1	323 to 676
<i>sodC1</i>		FQ312003.1	1086605 to 1087138
<i>sspH1</i>	Gifsy-3	CP001363.1	1332051 to 1334153
<i>sspH2</i>		FQ312003.1	2338601 to 2340967
<i>hldD_DT104</i>		AY462995.1	1 to 252
<i>eac1</i>		CP003416.1	1112914 to 1113549
<i>gene8</i>	her prophage encod	AY052766.1	28022 to 28933
<i>sieB</i>		CP000026.1	2519096 to 2519683
<i>sopE1</i>		FQ312003.1	2863004 to 2863726
<i>STM14_1441</i>		CP001363.1	1299077 to 1299676
<i>bigA</i>	Putative virulence	FQ312003.1	3650653 to 3656547
<i>phoP</i>	Regulation	FQ312003.1	1275542 to 1276216
<i>phoQ</i>		DQ787014.1	1 to 748
<i>rck</i>	Serum resistance	CP003387.1	4891 to 5448
<i>entF</i>		FQ312003.1	644950 to 648834
<i>envR</i>		FQ312003.1	3581448 to 3582110
<i>fhuA</i>		FQ312003.1	223735 to 225924
<i>iroB</i>		FQ312003.1	2938953 to 2940068
<i>leuO</i>		FQ312003.1	134572 to 135516
<i>msgA</i>	Islet	FQ312003.1	1286319 to 1286558
<i>oxyR</i>		FQ312003.1	4364518 to 4365435
<i>slyA</i>		FQ312003.1	1476732 to 1477172
<i>srfJ</i>		FQ312003.1	4689596 to 4690939
<i>sseK2</i>		FQ312003.1	2229212 to 2230258
<i>SU5_0826</i>		CP003416.1	948998 to 951595
<i>pagK</i>		FQ312003.1	1920747 to 1920947

imers were designed in this study.

<b>Function</b>	<b>Serotype</b>
Major curlin subunit precursor	S. Typhimurium
Fimbrial usher protein	S. Typhimurium
Fimbrial chaperone	S. Typhimurium
Type-1 fimbrial protein, a chain precursor	S. Typhimurium
Major pilin protein	S. Typhimurium
Hypothetical fimbrial protein	S. Typhimurium
Plasmid-encoded major fimbrial subunit	S. Typhimurium
Kappa-fimbriae regulatory protein	S. Enteritidis
Kappa-fimbriae chaperone protein	S. Enteritidis
Putative regulatory protein	S. Enteritidis
<i>Salmonella</i> atypical fimbria outer membrane usher	S. Typhimurium
Fimbrial structural protein	S. Paratyphi
Fimbrial regulator	S. Paratyphi
Thiol:disulfide interchange protein dsbA precursor	S. Enteritidis
Outer membrane protein	S. Enteritidis
Porin thermoregulatory protein envY	S. Enteritidis
Putative fimbrial protein	S. Typhi
Hypothetical fimbrial protein	S. Typhimurium
Hypothetical outer membrane usher protein	S. Typhimurium
Probable outer membrane fimbrial usher protein	S. Typhimurium
Probable fimbrial chaperone protein	S. Typhimurium
Type III secretion system effector protein	S. Typhimurium
Minor fimbrial subunit stfe (putative minor fimbrial subunit)	S. Typhimurium
Probable fimbrial subunit protein	S. Typhi
Fimbrial usher	S. Typhimurium
Fimbrial usher protein	S. Typhimurium
Putative fimbrial chaperone protein	S. Typhimurium
Fimbrial protein	S. Typhi
Type III secretion system effector protein-regulator of <i>Salmonella</i>	S. Typhimurium
Invasion genes transcription activator	S. Typhimurium
Regulatory helix-turn-helix proteins, araC family	S. Typhimurium
Acyl carrier protein	S. Typhimurium
Secretory apparatus of type III secretion system	S. Typhimurium
Secretory proteins; surface presentation of antigens protein SP	S. Typhimurium
Invasion protein	S. Typhimurium
Needle complex outer membrane lipoprotein precursor	S. Typhimurium
Surface presentation of antigens	S. Typhimurium
Needle complex assembly protein	S. Typhimurium
Cell invasion protein	S. Typhimurium
Type III secretion system apparatus	S. Typhimurium
Pathogenicity island 1 Type III secretion system effector protein	S. Typhimurium

Cell invasion protein	S. Typhimurium
Invasion response-regulator	S. Typhimurium
Iron transport protein, periplasmic-binding protein	S. Typhimurium
Type III secretion system effector protein, leucine rich repeat-A	S. Typhimurium
Secreted effector protein	S. Typhimurium
Type III secretion system effector protein-involved in bacterial i	S. Typhimurium
Type III secretion system effector protein	S. Typhimurium
Type III secretion system effector protein, protein-causes meml	S. Typhimurium
Surface presentation of antigens protein SpaO	S. Typhimurium
Surface presentation of antigens protein SpaR	S. Typhimurium
Transcriptional regulator	S. Typhimurium
Type III secretion system effector protein, Inhibits Cdc42 and R;	S. Typhimurium
Secreted effector protein	S. Typhimurium
Hypothetical transcriptional regulator	S. Typhimurium
Hypothetical ribokinase/regulatory protein	S. Typhimurium
Lysosomal glycoprotein (Igp)-containing structures, replication	S. Typhimurium
Secreted effector protein	S. Typhimurium
Needle complex inner membrane lipoprotein	S. Typhimurium
Type III secretion system protein	S. Typhimurium
Translocation machinery component	S. Typhimurium
Translocation machinery component	S. Typhimurium
Secreted effector protein	S. Typhimurium
Transcriptional activator	S. Typhimurium
Tetrathionate reductase subunit C	S. Typhimurium
Hypothetical transcriptional regulator	S. Typhimurium
Mg(2+) transport ATPase protein C	S. Typhimurium
Hypothetical autotransported protein	S. Typhimurium
Hypothetical DNA-binding protein	S. Typhimurium
Hypothetical ATP binding protein	S. Typhimurium
Hypothetical type-I secretion protein	S. Typhimurium
Large repetitive protein	S. Typhimurium
Hypothetical type-1 secretion protein	S. Typhimurium
Hypothetical secreted peptidase	S. Typhimurium
Type III secretion system effector protein	S. Typhimurium
Possible outer membrane adhesin	S. Typhimurium
Pilus integral membrane protein	S. Heidelberg
Type IV prepilin	S. Heidelberg
Vi polysaccharide export protein	S. Typhi
Vi polysaccharide export protein	S. Typhi
Putative toxin-like protein	S. Typhi
<i>Salmonella</i> plasmid virulence protein	S. Enteritidis
<i>Salmonella</i> plasmid virulence lysR family regulator	S. Enteritidis
Hypothetical outer membrane protein	S. Typhimurium
Host colonisation factor	S. Typhimurium
Type II secretion system protein	S. Typhimurium

Putative Cu/Zn superoxide dismutase precursor	<i>S. phage Fels-1</i>
Type III secretion system effector protein	<i>S. Typhimurium</i>
Gifsy related virulence gene	<i>S. Typhimurium</i>
Bacteriophage encoded superoxide dismutase	<i>S. Typhimurium</i>
Hypothetical protein	<i>S. Typhimurium</i>
Type III secretion system effector protein-E3 ubiquitin ligase	<i>S. Typhimurium</i>
HldD-like protein	<i>S. Typhimurium</i>
Phage EaC protein	<i>S. Heidelberg</i>
Scaffold protein, similar to bacteriophage P22 gp8	<i>S. Typhimurium</i>
Superinfection exclusion protein [Enterobacteria phage P22]	<i>S. Paratyphi</i>
Type III secretion system effector protein, invasion-associated s	<i>S. Typhimurium</i>
Protein of unknown function	<i>S. Typhimurium</i>
Hypothetical surface-exposed virulence protein	<i>S. Typhimurium</i>
Transcriptional regulatory protein PhoP, regulator of virulence	<i>S. Typhimurium</i>
Sensor protein PhoQ, regulator of virulence determinants	<i>S. Typhimurium</i>
Resistance to complement killing	<i>S. Typhimurium</i>
Enterobactin synthetase component F	<i>S. Typhimurium</i>
TetR-family transcriptional regulator	<i>S. Typhimurium</i>
Ferrichrome-iron receptor	<i>S. Typhimurium</i>
Hypothetical glycosyltransferase	<i>S. Typhimurium</i>
Probable activator protein in leuABCD operon	<i>S. Typhimurium</i>
Hypothetical virulence protein	<i>S. Typhimurium</i>
Hydrogen peroxide-inducible regulon activator	<i>S. Typhimurium</i>
Transcriptional regulator slyA	<i>S. Typhimurium</i>
A virulence factor, a glycoside hydrolase family enzyme	<i>S. Typhimurium</i>
Type III secretion system effector protein	<i>S. Typhimurium</i>
Outer membrane usher protein HtrE	<i>S. Heidelberg</i>
Bacteriophage encoded pagK	<i>S. Typhimurium</i>







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Jarvik et al. <i>J. Bacteriol.</i> 192 (2), 560-567 (2010)	Phage
Kröger et al. <i>Proc. Natl. Acad. Sci. USA</i> 109 (20), E1277-E1286 (2012)	Chromosome
Kröger et al. <i>Proc. Natl. Acad. Sci. USA</i> 109 (20), E1277-E1286 (2012)	Chromosome
unpublished	Chromosome
Patterson et al. <i>PLoS ONE</i> 7 (8) E43592 (2012)	Plasmid
Kröger et al. <i>Proc. Natl. Acad. Sci. USA</i> 109 (20), E1277-E1286 (2012)	Chromosome
Kröger et al. <i>Proc. Natl. Acad. Sci. USA</i> 109 (20), E1277-E1286 (2012)	Chromosome
Kröger et al. <i>Proc. Natl. Acad. Sci. USA</i> 109 (20), E1277-E1286 (2012)	Chromosome
Kröger et al. <i>Proc. Natl. Acad. Sci. USA</i> 109 (20), E1277-E1286 (2012)	Chromosome
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Kröger et al. <i>Proc. Natl. Acad. Sci. USA</i> 109 (20), E1277-E1286 (2012)	Chromosome
Kröger et al. <i>Proc. Natl. Acad. Sci. USA</i> 109 (20), E1277-E1286 (2012)	Chromosome
Kröger et al. <i>Proc. Natl. Acad. Sci. USA</i> 109 (20), E1277-E1286 (2012)	Chromosome
Le Bars et al. <i>J. Bacteriol.</i> 194 (13), 3537-3538 (2012)	Chromosome
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## Microarrays

Microarray primer name	Microarray primer sequence (5'-3')	Microarray probe name
lb_csgA_651	GGCGTCGTTCCACAATG	hp_csgA_611
lb_bcfC_651	ACCAGAGACATTGCCTTCC	hp_bcfC_611
lb_bcfG_651	TAAAATTGCTCTATCGCCCTG	hp_bcfG_611
lb_fimA_651	TCCTCTGCGGACAATAGC	hp_fimA_611
lb_fimI_651	GTGTGGTTTACGCTGGTTTA	hp_fimI_611
lb_lpfD_651	CGCTCTATATTCTCCATCCG	hp_lpfD_611
lb_fedA-pefA_651	ACACGCTGCCAATGAAGT	hp_fedA-pefA_611
lb_pefB_651	AGGAACATTTCTGGTTACTCATC	hp_pefB_611
lb_pefD_651	GTGGATAGACAACACCACC	hp_pefD_611
lb_pefI_651	GATTATGGCGTCTGCTCTG	hp_pefI_611
lb_safC_651	CGGAAGATTACCCTCAGTTG	hp_safC_611
lb_sefA_651	CAGCTGGCTTTGTTGGTAA	hp_sefA_611
lb_sefR_651	GTCTCACGTAGTTTTCTGATATTG	hp_sefR_611
lb_srgA_651	TTCCGTGTATGTCCGTGG	hp_srgA_611
lb_srgB_651	GTGCTCACCTGTGTTTC	hp_srgB_611
lb_srgC_651	TATTGTCCTGACGAAAGTGC	hp_srgC_611
lb_staA_651	GACTACCGGTCATGTAACCA	hp_staA_611
lb_stbD_651	GGTAATATCGGTTTGCCAAC	hp_stbD_611
lb_stcC_651	CAAGCGCATGCGGATAC	hp_stcC_611
lb_stdB_651	AGGCCACGGAGTTCAATG	hp_stdB_611
lb_stdC_651	GAATAACGATGACAAAACCACG	hp_stdC_611
lb_steB_651	GTTATGTAGGTAATCGGCTTCT	hp_steB_611
lb_stfE_651	TACCTGAAGTTACAGATTCAGG	hp_stfE_611
lb_stgA_651	GAAGTGGTTGACAGCACC	hp_stgA_611
lb_stiC_651	CGGGCGAATTTGAAATCAAC	hp_stiC_611
lb_stjB_651	GGTAGCGATAGCCGAAACTA	hp_stjB_611
lb_stm4595_651	CACGGATAACCACCATTGATT	hp_stm4191_611
lb_tcfA_651	AGGGCGAATATGCTCGTTT	hp_tcfA_611
lb_avrA_651	GCCTGATTGTTATTTTGCTATGG	hp_avrA_611
lb_hilA_651	AGTCAATATTCCGCCAAAAGA	hp_hilA_611
lb_hilD_651	TTCTCCTGTACGAAGGATACAA	hp_hilD_611
lb_iacP_651	TCTTGAGTCCAGGGTGTAG	hp_iacP_611
lb_invA_651	GTATCTGCTGAAGTTGAGGAT	hp_invA_611
lb_invB_651	GAGGAATAGATAGCCATTCAACA	hp_invB_611
lb_invE_651	TATTTCCCTGACCCAGTGA	hp_invE_611
lb_invH_651	GATGAAGAGCAACTCATGACC	hp_invH_611
lb_invl_651	ACTCCAGATTATACAAATTCAGGAA	hp_invl_611
lb_orgA_651	CGGCAAATGAGTTAATACTGG	hp_orgA_611
lb_prgH_651	AATTGCTTATCCTGATTCGCC	hp_prgH_611
lb_prgJ_651	TGGCTATTTGCAAGAGATG	hp_prgJ_611
lb_sipA_651	GAACATAACTTTGGCTGTACG	hp_sipA_611

lb_sipD_651	GATATCATTTCATTATCGCAGGC	hp_sipD_611
lb_sirA_651	GCCTGTGTAATGCGGAGA	hp_sirA_611
lb_sitA_651	GCGATATTAACGAGCGCA	hp_sitA_611
lb_slrP_651	CCAGAAGAGATCAAAAGCAAG	hp_slrP_611
lb_sopA_651	CCGGAGAGAACGTTTCCA	hp_sopA_611
lb_sopD_651	ACCCGCTTGTCGAATGG	hp_sopD_611
lb_sopD2_651	CCATCTCAACAAGACCGCT	hp_sopD2_611
lb_sopE2_651	TCGTCCCCCTCATTGCT	hp_sopE2_611
lb_spaO_651	CAATTGCCCCGTCAAAC TG	hp_spaO_611
lb_spaR_651	TTGATACCTCGAAATGGCT	hp_spaR_611
lb_sprB_651	ACGAACTATCCTGCGCTAT	hp_sprB_611
lb_sptP_651	AAAGCAATGCAAGCCCAG	hp_sptP_611
lb_pipB2_651	CGTGTCGAATTTAATCTTCCTG	hp_pipB2_611
lb_orf242_651	CAGCGACGCTATGGTTTATT	hp_orf242_611
lb_orf408_651	TTTTAAACCGTGACGCGC	hp_orf408_611
lb_sifA_651	GATTGAAAAGACAACGCGC	hp_sifA_611
lb_sifB_651	AATTTATGTGACTGGAAGGAACA	hp_sifB_611
lb_ssaJ_651	GAATTGAAGGAATGCTGAGTC	hp_ssaJ_611
lb_ssaQ_651	GGCGACATCAGACTCGG	hp_ssaQ_611
lb_sseB_651	CTCAGGAGCTTAACGCTGT	hp_sseB_611
lb_sseC_651	AAATTAGTCTTCAGGAGGCAA	hp_sseC_611
lb_sseF_651	GCTTGCTGTGCGTATCATA	hp_sseF_611
lb_ssrB_651	AGCAATGAATATTCTGGTTTACAC	hp_ssrB_611
lb_ttrC_651	CCCTGTCAGCCAAATATTACG	hp_ttrC_611
lb_marT1_651	GCTGATAATCACGGTTCCG	hp_marT1_611
lb_mgtC_651	CATGCTGATTATCGTAAAACGC	hp_mgtC_611
lb_misL_651	GCCTCTATGGTATTTCCCTC	hp_misL_611
lb_rhuM_651	ACAGCACATTAAGCGATCT	hp_rhuM_611
lb_sugR1_651	CGCTGAACATGAAAATGTC	hp_sugR1_611
lb_siiD_651	ACCCAAATACCGTGACCAA	hp_siiD_611
lb_siiE_651	GATGGAAACTGGAGTTATGAATTT	hp_siiE_611
lb_siiF_651	CTGATAAAGTATTTTGACCGGG	hp_siiF_611
lb_pipD_651	GTAGGCAATCAGGCTTCG	hp_pipD_611
lb_sopB_651	ATGGCAAACCAAATGGAGTT	hp_sopB_611
lb_pagN_651	GATCTATATCACCGGGAAAGC	hp_pagN_611
lb_pilR_651	CCCTACAGGGTGCAATTTT	hp_pilR_611
lb_pilV_651	CAGCGGGTTTACTGAGACA	hp_pilV_611
lb_vexA_651	TTAATCAGGACGATCCTCGT	hp_vexA_611
lb_vexE_651	TCAGCATCCCGAAAAAGTG	hp_vexE_611
lb_cdtB-var1_651	CCTGGAATCTTCAGGGCT	hp_cdtB-var1_611
lb_spvC_651	ACCGATATGGAGAAGGTGCG	hp_spvC_611
lb_spvR_651	CTGTACCTCCTTGATTACCC	hp_spvR_611
lb_ratB_651	ACCGCTACGTAAAGTCGAT	hp_ratB_611
lb_shdA_651	CCGACTATCTGACCGTAA	hp_shdA_611
lb_STMMW_34781_651	CAGACGGTGGTCAATAGC	hp_STMMW_34781_611

lb_sodCIII_651	TCTCGGTCCGTATAATCCTG	hp_sodCIII_611
lb_gogB_651	CAGATATTGAGAAGGAGGAGC	hp_gogB_611
lb_grvA_651	GCCTTTTCATCCCCTCAA	hp_grvA_611
lb_sodC1_651	ATGAACGATGCCCTGTCC	hp_sodC1_611
lb_sspH1_651	GAGGCATCTCCGGAAGAAA	hp_sspH1_611
lb_sspH2_651	TGCCGGAAAAGTCTCATTCA	hp_sspH2_611
lb_hldD_DT104_651	AGACTCTATAAGCGCCTCTTT	hp_hldD_DT104_611
lb_SU5_0961_651	TGGATGCAATCATGCATAACG	hp_SU1_0961_611
lb_g8_651	AAGACTTAACCCTGTCCGG	hp_g8_611
lb_sieB_651	AATGAACTTATTGCACAGGACG	hp_sieB_611
lb_sopE1_651	AGACCCGTGAAGCTATACTATC	hp_sopE1_611
lb_STM14_1441_651	GTCCTGTGGAAGTGGATTC	hp_STM14_1441_611
lb_bigA_651	GCTTCTATTTCTATAACGAAGAGG	hp_bigA_611
lb_phoP_651	TGGCAGGATAAAGTCGAGG	hp_phoP_611
lb_phoQ_651	GAGATGACCCACTCGGTA	hp_phoQ_611
lb_rcK_651	TATGAGGGAAGTAAAGTTGGC	hp_rcK_611
lb_entF_651	CCTTAATAATACGGCGGTAACG	hp_entF_611
lb_envR_651	CCATCTACTGGCACTTTGAGA	hp_envR_611
lb_fhuA_651	GTTCAACCGAAAGAAGAAACCA	hp_fhuA_611
lb_iroB_651	GACTGCTATAACCTGTGCT	hp_iroB_611
lb_leuO_651	ATGCAAGAGCAGAATATTACGC	hp_leuO_611
lb_msgA_651	GGCGAACGCATTAACAGT	hp_msgA_611
lb_oxyR_651	CCTATTTGCTGCCGCTTAT	hp_oxyR_611
lb_slyA_651	CTCTGGAATTGACGCAGAC	hp_slyA_611
lb_srfJ_651	TCAGCAATTCCTTGTTGAGC	hp_srfJ_611
lb_sseK2_651	GGGTTGAGGCATTATTTTGAC	hp_sseK2_611
lb_htrE_651	CGGTAGCGAATACAACAATC	hp_htrE_611
lb_pagK_651	CCTTCCCTGAAGATTGGTTAAA	hp_pagK_611
		hp_pagK_612
		hp_pagK_613
		hp_pagK_614

**Microarray probe sequence (5'-3')**

GCATTCGCAGCAATCGTAGTTTCTGGC  
ATGTATCGCGTTGACGTTTACCTGAACA  
GCGAACCGTGACAAATGGCGTTTC  
GGCTTTCTCTGGTCAGGCAGATAACAC  
TTCAGAAAATATGACGCCGGGACGAA  
GATGCAATATGGACATCCGGTGGCAAAG  
GCATTATTGCTCCATTATTGCACTGGGTG  
GAGGGGCGCTGATACCTGCAAAAG  
AACCAGGCGGATGAGACCTTTGGC  
GCTTGAGAAAGTGAATGCCGGAAAGGG  
ACGGTCAGTCAGCTTTCACGCTACG  
TGCTTTAATTGCATGTGGCAGTGCC  
CGAGCAGCTATACACATCTCTGTGCATT  
TGTTTAAGGAATATGGCGTGAGGGGGA  
CACTGCTGACCGCCATTCTCCTGAT  
CAGGGAAAGGCATTTTCATTTGTTGCG  
CTTACGTTTCGTGCCGATGCTTCTAAAGA  
TACACGGCGCAAAACTGGATCGG  
GTTCAATAGCGGTTTCAATCTGTTGGGC  
TGCCATTCTGATTACCCTGACATTTCCG  
GACCGGACCCGTATTATCATGGATGC  
CCACAGCATAAGCTTGC GGCCA  
GCCTGAGCTGTAACGGCAGAGTGAG  
GCATCTGATGGCACCGTTCACTTCT  
GCAGGTTATCGTGCGGCAAAACGG  
CTATAACCTGTACGCCAGTCGCAGC  
TACGATCAGGCGTGACGGTTCAGGT  
TCTCTGTGTCGCTATGTTTGCATGTGG  
TTGAGGACCAAAGCAGCTCTTGAACG  
ATTTCACTCAACATGGACGGCTCCCT  
CCTGCCAGAAGAGAGGTATTTGAACATCTG  
GACCTTTGCGGATATATGCCGTGTTGTT  
CCAATGGCGGCGAATTACGAGCAG  
CACTGGAAGTAAGTGGTTGCGATCCTTCA  
TACATGGCGGCGCGTTAGAAAGATT  
AGGAACATCCACAATACATGCGTTCGAA  
AAGCAGTCTATTGTTGCCGGCAGATAA  
GATAGCGCCGAAATGATTGTCAGACC  
TCGGTGCAATTAATACGCCAATACAGGT  
ATTGAGGACCCTAATCTGGTGACGGA  
TGCAGGAGGTGATGCCCTATATTGCC

## Validation PCR

**PCR left primer (5'-3')**

TAAAAGTGGCAGCATTTCG  
CAGCGTAACTAAACCCGTAT  
AGCGTCCTGGTTAATTGATA  
GATCAAACGGTGACGCTGG  
ATGATAAGGAAAGGCGCGG  
TTCCTCTGGCCTTTGTTACG  
ACCTGTGACCTGACCACTTC  
TGATGCTGAACAGAAAAGATG  
ATGAGGAAGGGAGAAAAGAAC  
CCGGA CT CAGTATCTACCAG  
CACCCGTGATGTGGTGTTT  
GTAAATCAGCATCTGCAGTAGC  
AACGATATTTATGAAATTGCCTG  
GGATGGTCAAGTACCATGTC  
AGATATTTATGTAACCAGAAAGCA  
GGAGGACTCTGTGTTCCG  
AAGGTATACATTGCGTTCGT  
GCCATTTGTGAATACATCT  
GGTAGCACGTGATTTCAACTG  
TGACAACAGACATGGTGGC  
CAGAACAGTGTTTCCCTGTC  
GTGCAAGTCAGTCATCATCA  
TAAGACGGTCAACATGACGC  
TGCTGGTAGGTAATGCAATG  
GTTTTCGCAACTACAGTAACTGG  
AGACTGGAGTTGACGTTGAT  
TGTGAAGCGTTCTGAATAGA  
TGGATCATCTCCAGTTCAG  
AGGTTCTTACCACACAGAC  
GCCTTACGACGTATTCTGTGCG  
GCAGGTAGTTAACGTGACG  
CTACACCCTGGACTCAAGAC  
GCAACGTCAATGAATATTTCCG  
GCTCCCCCAGTAGTAATTG  
GCCTGGTTTTAACGATAATG  
TTCCTCCGTGAGCAAACC  
TTGATAGTTCCCTTCTTTGC  
GCGAAATCGTCAAATGAATAGG  
TTATCCCGCTGGACCATG  
ATGTCGATTGCAACTATTGTCC  
GAAGACGCTACTGATGAAGG

GGTACCGTCTACCACAGAACATCGCG  
TGTTGAGCTGACTCACCTGGCAATC  
CCCGGCGCTGAAATCCATGAGTATCA  
TCGCTTATCTTTGTCATCCACCTGAAACC  
TGACACTGCATGGGACAACCTTTACCTG  
CGGTTTATGAGATGATGCGTCCCGCA  
CGGCATGGAGAAGATACATGCCTTTACAC  
GTATTTACTCCAGGTGGGGCAGGGG  
ACTGCAGAACTCTGCCTGGCTTG  
GAGGGGCAACGCTAAGTAGTAGTATCGAT  
ATCGATCGCTGTGTGCTGCAATATTTG  
TCACGGAACAATAGAATGCTGGAAGACG  
GAGGTGCTCCGTTGCCAGAAAACATCAT  
TTGCCAGACTATGCGGTATCAATGCC  
GTATGCTTCAGCGTTGCTATGGCGGA  
AACCTACCTGGCAGCGAAAATTCAGTC  
AGAGACGCTTATCGCCATGGCAGA  
GGTATCACCCAGGAAGAACAGCAGAA  
CGGCATGGGCGTTCCGATTATTG  
GCCAACCGGAATACCGATCTTATGAGTC  
GAATTCTACTTTTGGCGATGGCAACGC  
GCGGCGCTCGTGATTGCTATTGG  
CTGGCATCAATGGCCTGGATATCATTCC  
GCACGGCAATCCGTCAGTGGATT  
GGATTACGTACCGTTGGCGAAAATGAAG  
CCGCTCAGGAACAGGGCTATAAAGAAAT  
CATCGCCATAGCGGTATCAGCAGC  
GGCAACCATCGCCAACCTTTATCAGAT  
GAAGATGTACGTCTGGTTTTCCGCC  
ACCAAAAGTAAGGACTATGCTGGCCG  
AACTGGTTGCCAGCGTTGATGTCGA  
ACGTTGATCATGGTGACGCATCGTC  
CGTTACGCTGCTGGGTATGGGTAAAG  
GGCAACCGTTCTGGGTAAACAAGACC  
CCTGGTCCGCTACTGCATCAGCAA  
CGGCTGAGGCGTTTTATTGTCAGAAA  
GCCGTTATCACGACAACCATGCTGA  
GCTTTCGGGATGCACTATTCCAGGG  
CCCTACTCAAACAAGAGGATTGGGAGGG  
GCCTGCGCTAATATCAGTGACTACAAAGT  
TCAGAGGACAGTCCGGTAGATAAGTGGA  
CACGCACTGCACATCAAAGGCGTA  
GGTAAAACTACCAGGACAGCACCGCC  
GCGACTTTACCAGCCTGACGATGAA  
GGGACATTATCGCTACATCTGACGGATG

ATTATTCCGCTTCTCCTCATCC  
CACTGGCTTGTTAACGTCTC  
CCACGTTTACCGTTATTGCC  
GCAAGGCATCAAAGTATTAGC  
TCCTCCAAGATTCAGACAC  
GATGAGTCCTGATAAAGAAGAAGC  
ACGGCTACAACATCTGGC  
AATGCGAGTAAAGATCCGG  
ACGTTAAGTTCAGCATTGGT  
ATTAGCCATTTCCGAGGTAT  
CTTTGAACCCGCATGAGC  
GAGGTGCATACCAACAGC  
GGGACTTCTGCTGCTATGC  
CGGCCACAGTCATAAATCA  
TGAAGTATCTTTGCCACT  
TTCGCATCATGGATCAAACG  
CGGTTACAACCTCTCGCTATC  
AATCAAATGCTGGCATTACT  
GAGCGACAACAGATTTATCC  
GGATGAGGTGATTGCTAAAG  
AGTAACCGCCTTAACACATC  
AGCGGCAAGTAATATAGTCG  
TTGATGATTGGTCGTGTCAG  
GTTAAATTGCGCGTTGAACT  
TCTATTGCCTGAGCGAAGTC  
CGCGTTTTACGATAATCAGC  
CAACTCCCCAAAATTACTION  
CTTTGAGCAAGAGACGCTAT  
AGCACATTACGATTCTGGTT  
CACTACTCATGGTGGTGTGA  
CGTTACCGATAAACCAACAT  
GATGTTTTATTACCGGAAC  
GTGATTCCCGTTTTTGTAC  
TCTTTTGCAGGTAAGCCATC  
TAAGTGGTCATTCGGACCTG  
AAAACCAAGAGCACCCTCC  
ACTGACCAGGAACGTAATGC  
CATAAGGCACCTGAACGGTA  
CAGCAACAGTCGCATATTGT  
CAACATCAATAGCCGAGTGG  
CTGAAATAACCCCATTTTCG  
GGACTGTTTCAGTTCCTGCT  
AGGCGAAGTGAGCGTTATC  
TCCCGTTACGGTCAGATAG  
TTGGTGCGCTTATCTACCAT

GGCACCTTGACCCTCAGCACACAAAT  
GTAACGAGGGCGACATCAAACCTTGAGT  
CGAAGCGTTCTGCGATAAGTGCATCC  
CAGCAATGGCAGAGAATACCCTGACTG  
AGTATGCAGGCTATTGCTGGTGCAGC  
CGCTGTCGGTCTATCGTAACCAGCT  
ATGACCATTGTTCTGTTTCATCGCATAGGT  
GAAACACAAAGGAAGGCCGCGCATA  
ATGGAACCAACCACCGAAATTCAGGC  
ATGAGTGCTACATGAGATTTGCCGGG  
GCGAGTAAAGACCCCGCATACGC  
TATGGACGAAACCGAGTTTCAACAGGTC  
CGGAAGATGGCAAATCGCTGGTCAG  
TTCCTGCGGTTCTGGTGTTAACCG  
CCGCGCAGGAAAACTCAAAGAAGTACG  
GTTTAATCCGGTGGAAAATGTGGTTCATCG  
TGCTGGCGGAAGAACAAACGCAATTA  
TGAATGATATCGCTGATGCCGCTGATGT  
AGCGGCATGTCTGTCTATGCACAG  
GCGTATTCTGTTTGTCTGTCACCAC  
CGCATGGTTGATTTGAACCTATTGACCG  
TTCCCGATGCGCAAGTAAAAGTTAAGC  
CCCGCTGCATATTGGTTTAATCCCAAC  
GCATTTGGCGTGCTCTGATTGACC  
GAAAGGCAGACTCATCTCTCCGATCC  
ATGGCGATCCCTATAATGACTGGCTCA  
TCCCGAGGTAGCCTTAACTGGAACAAAG  
AAAAGTGGTGTAAATCTTTGGCCTGCTGA  
CAAAAGTGGTGTAAATCTTTGGCCTACTGGC  
CAAAAGTGGTGTACTCTTTGGCCTGCTG  
CCTCAAAAGTGGTGTAAATCTTTGGCCTGC

ACATTTGCCTCACTTCCAG  
GTAACGAGGGCGACATCAAAC  
TTGATGTTGACCTTCATGC  
ATATGGGCCAAGATGTTTCC  
AATATCCGCAATACACAACC  
AGCTTGAGGTTGCCTCTGTT  
CACAGCGAACAAAAATACAA  
AATCCCGTAGTGGTTGGTTA  
ATGGAACCAACCACCGAA  
TGTTTCGTCCTGTGCAATAAG  
GCAAAAAGTATTCTCGCAGT  
TTTAAACTCCTTCAGCTTGG  
ACGGTACTGAAACCCTGAAC  
GTAAGGTTGTAGAGGATAATGC  
CGGCTTCCATGAAATTGAAACC  
CGCCAACTTTACTTCCCTCA  
GGATCTTCTGGCATAACAG  
GGCCTGTTCCGATATCATAAC  
AAATCGCAGTTGTAGTAGCC  
GCGTATTCTGTTTGTCTGCTC  
TTTAGATATGGGCAAACCAC  
CGTTATATCGTCACAGACAGC  
GCAAATACGTAAGCTGGAAG  
ATCGCCACTAGGTTCTGAT  
GAAAGGCAGACTCATCTCTTCC  
CTGGTAAACCTGGTTGTCAT  
TGCGGTCATCGTTATACATC  
TCAATAACCTCTACACATTTTAAACC

<b>PCR right primer (5'-3')</b>	<b>PCR fragment si:</b>	<b>Positive control strain</b>	<b>Validation</b>
TATCGGAGTTTTAGCGTTC	327	Typhimurium LT2	Validated
TACCCCATATTTTAAGCA	313	Typhimurium LT2	Validated
ATAGGGTGTAGGATTGCGTA	370	Typhimurium LT2	Validated
TAAAGGTGGCGTCGGCATT	382	Typhimurium LT2	Validated
TCTTCCGCAGGCGTAACG	302	Typhimurium LT2	Validated
ATACACTGGGTTTCTTTGTAC	309	Typhimurium LT2	Validated
GCCACAGATTTGAAGTCACC	398	Typhimurium LT2	Validated
TATGAATAATAACAACCATCTGC	301	Typhimurium LT2	Validated
GTAAATCAGCTTCACCTTCG	308	Typhimurium LT2	Validated
CAGAGCAGACGCCATAAT	210	Typhimurium LT2	Validated
GTTGCAGTTGTACCCAGG	386	Typhimurium LT2	Validated
GCGTTTCTTGAGAGCTGGC	404	Enteritidis PT4 S97	Validated
GAAATATGATACGCTTGACATTC	336	Enteritidis PT4 S97	Validated
CATAACGGCTCCTGAAGTCT	372	Enteritidis PT4 S97	Validated
AGGTATTCGATGGCCTCA	302	Enteritidis PT4 S97	Unvalidated
GCACTGATATGCCACTTTCT	388	Enteritidis PT4 S97	Validated
CTCCGTTCTCTATCATCCTG	337	Typhi CT18	Unvalidated
TAGTTCCGAACGCTATTGT	352	Typhimurium LT2	Validated
GCTCCAGATACAATGTGTTGC	418	Typhimurium LT2	Validated
AGCTGAGGTACGTCTGTCC	483	Typhimurium LT2	Validated
GAAGCCGTGTGATTTACTC	313	Typhimurium LT2	Validated
AGGTTAGCAGATGTTTCAGG	309	Typhimurium LT2	Validated
CCTGTTAACGTTACGCCATTAT	384	Typhimurium LT2	Validated
GTAAATACGGATCGCTACGC	353	Typhi CT18	Unvalidated
TCGGCAGCGAAGAGTAGG	423	Typhimurium LT2	Validated
CTGCCATAGCCTACAAGAAG	387	Typhimurium LT2	Validated
CAGAACACGATTACGTTCAA	317	Typhimurium LT2	Validated
ATACTCTTCCCGGGGTGT	377	Typhi CT18	Validated
CCCGATTCTCGTAAATATG	329	Typhimurium LT2	Validated
GGCGTAATTGATCCATGAGC	304	Typhimurium LT2	Validated
CACTGTCTACTGGGTGACG	423	Typhimurium LT2	Validated
TATTGCCGTTGATGTTGATA	202	Typhimurium LT2	Validated
CATCGACAGACGTAAGGAGG	477	Typhimurium LT2	Validated
ATCGCTGAATTAGTTCGTTT	265	Typhimurium LT2	Validated
CTGGAGGATGAGGCTTTAC	297	Typhimurium LT2	Validated
TAAATTCGGTCATGAGTTGCTC	293	Typhimurium LT2	Validated
TCGCTGACCAGAATTAAGT	357	Typhimurium LT2	Validated
AGGCCAGTAGCAAAATTGAC	542	Typhimurium LT2	Validated
TTGCGCAGCGACATAGAG	416	Typhimurium LT2	Validated
CATGAGCGTAATAGCGTTTC	305	Typhimurium LT2	Validated
CAGGGGTATCAACGTTTGC	421	Typhimurium LT2	Validated



AACCAGCTCCCATTTTGG	517	Typhimurium LT2	Validated
GCTATTCGTTCCGGTGTATTC	317	Typhimurium LT2	Validated
GTTAATTGGCCAGAGATAAAGC	548	Typhimurium LT2	Validated
TTCACGATTTGCTGCCTC	468	Typhimurium LT2	Validated
CACTGAGGCATCATCAATCA	330	Typhimurium LT2	Validated
CTTCTCCAGATCGCATAAGC	515	Typhimurium LT2	Validated
GAGTTGTAGGCTCAAAGTTACC	428	Typhimurium LT2	Unvalidated
AACTGAAATTGTTGTGGCG	383	Typhimurium LT2	Unvalidated
GCTTTGTAATCGGTAGCAGT	343	Typhimurium LT2	Validated
TTTTACGCGTTGACTTTGA	378	Typhimurium LT2	Validated
GTTCAATTGCCGGATGTCC	393	Typhimurium LT2	Validated
GCTTGCCGTCGCATAAG	438	Typhimurium LT2	Validated
CGCTTAAGTCTGCGTCAC	472	Typhimurium LT2	Validated
GTCGTATTCTATCGGCGAAT	321	Typhimurium LT2	Validated
TCCGATCTACGCTATTTCCA	373	Typhimurium LT2	Validated
TTTTCGCTGCCAGGTAGG	336	Typhimurium LT2	Validated
TGAGAGGAACTTTCTTCCAG	347	Typhimurium LT2	Validated
CCCTCATCATAAGTCGGTAG	314	Typhimurium LT2	Validated
GGTATCTGCTCAAGTTCGAC	308	Typhimurium LT2	Validated
AGTACGTTTTCTGCGCTATC	344	Typhimurium LT2	Validated
TGGATCTGCTCCTGATACTC	378	Typhimurium LT2	Validated
GTTTGTAAATGGCTCCTTTTG	357	Typhimurium LT2	Validated
TAATGCCTGTTGTGCATACG	319	Typhimurium LT2	Validated
TATTGTGGGGACAAATCTGG	311	Typhimurium LT2	Unvalidated
TATCGAGGCCAGATCTCAAC	301	Typhimurium LT2	Validated
CAGATTGTCTCTGGGATTGG	422	Typhimurium LT2	Validated
TGAATAACCGTGACAGTGTG	304	Typhimurium LT2	Validated
TCAAAATAGTCGGGTACAGC	366	Typhimurium LT2	Validated
GATAAAGCATTAGGGGAAGC	387	Typhimurium LT2	Validated
TCATCAAGGGAGATAACAGG	374	Typhimurium LT2	Validated
CTATCATCCAGCTCAATCGT	330	Typhimurium LT2	Validated
TTTCCACCTTTCATTACCAG	380	Typhimurium LT2	Validated
TATCTTGCATTCGCCGTTAC	386	Typhimurium LT2	Validated
CAACGGAATGCAGATTCTCT	369	Typhimurium LT2	Validated
CATCATTCCCCTTGTGGTAG	348	Typhimurium LT2	Validated
GAGGCGTTTCATTGTCAGAA	487	Heidelberg Nikki	Unvalidated
CAAACAAAAGGATGGCAAAC	383	Heidelberg Nikki	Validated
CTTTCGGGATGCACTATTCC	313	Typhi CT18	Unvalidated
ATATCGCCAACCACCCTACT	364	Typhi CT18	Validated
GACCATGATCATCTGCAGCT	320	Typhi CT18	Validated
AGTGTGCTCAGGGATATGGT	262	Typhimurium LT2	Validated
ACCCTGCATTCAAGTTTTGAT	239	Typhimurium LT2	Validated
GCGACAATACGGAAAACAAC	338	Typhimurium LT2	Validated
GCACCGGTCTGGTAGACAAT	390	Typhimurium LT2	Validated
AGACTTTAGCCGAGCAGGAG	346	Typhimurium LT2	Validated

GGATGATCTTCATGGTTGTC	312	Typhimurium LT2	Validated
AAGGTAATGCGGGGAAAGTA	360	Typhimurium LT2	Validated
TAAAGAGCGGAGATCTGGTA	338	Typhimurium LT2	Validated
TATTGTGCTGGTAGCTGGT	308	Typhimurium LT2	Validated
CTGTACCCCTGACAATTCAC	362	Typhimurium	Unvalidated
GTCGCTGTCGGTCTATCGTA	464	Typhimurium LT2	Validated
CTTTATGCTGTTATGCACGA	239	Typhimurium DT104	Validated
AGGCCAGAGCAAATATTACG	400	Heidelberg 3835/11	Validated
GCACGGCTGTTGTCATAGTC	368	Heidelberg 3835/11	Validated
ATTCCGTTTATCACGCTGTT	346	Heidelberg 3835/11	Validated
AACGTCATTTTTGGTTGTTCC	390	Heidelberg 3835/11	Validated
AACAGAATCCAGTTCCACAG	383	Enteritidis PT4 S97	Validated
GTAAGCGTAGCGTCCTCTTC	382	Typhimurium LT2	Validated
GCTATTACGGCGCATTAACG	354	Typhimurium LT2	Validated
TCTCCGGATTGAGCATTTCG	377	Typhimurium LT2	Validated
TGGGGTGAACCTGAAATACC	377	Typhimurium LT2	Validated
GCATTTACGGTAGGTAAAG	386	Typhimurium LT2	Validated
GGCAACATTTGATTGAAACC	347	Typhimurium LT2	Validated
GATAGTTGTTCTGGCTCAGG	372	Typhimurium LT2	Validated
TGCATCACTACCGGAATGTC	381	Typhimurium LT2	Validated
CACGCAAAGATTGAATACAC	322	Typhimurium LT2	Validated
CAAAACGCGTACATCAACTT	233	Typhimurium LT2	Validated
GAGTTGCGCTAACAACTGAT	307	Typhimurium LT2	Validated
GAATGACCTCTCCATCTCA	317	Typhimurium LT2	Validated
GGTATTAATGCGCTTCATCG	372	Typhimurium LT2	Validated
CAAAATGCGTCATAATCTTG	313	Typhimurium LT2	Validated
GGTATGTTGACCCCTCACTG	336	Heidelberg Nikki	Validated
ATGAAACACGTCAAGAGC	201	Typhimurium LT2	Validated



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