

Supplementary Table 1A.**Full genomic information of all genomes included the study.**

Isolate no.	Read length (bp)
1	95
5	35-251
6	35-251
7	95
8	35-251
9	95
12	95
13	95
14	95
15	95
31	31-100
34	35-100
35	45-100
36	35-251
42	29-100
46	49-100
49	35-251
53	55-100
54	35-251
70	55-100
71	43-100
1012	35-251
12	35-251
1341	35-251
225	35-251
269	35-251
279	35-251
361	35-251
674	35-251
739	35-251
748	35-251
911	35-251

Public genomes

Isolate ID	Country
CT18	Vietnam
AG3	Vietnam
E02-2759	India
ISP-04-06979	Central Africa
E03-9804	Nepal
ISP-03-07467	Morocco

Total Reads (no)	Average read depth	Insert size	GC content (%)
10465710	117.2	-	51
502445	32.5	158	51
1211293	11.4	169	51
5720046	78.8	-	51
1161340	14.6	177	51
11664325	122.5	-	51
6091141	81.6	-	51
5118271	71.5	-	51
7236224	90.5	-	51
6006275	82.2	-	51
3046914	115.4	374	51
3351745	129.0	402	51
2580654	97.5	403	51
1349664	12.8	189	51
2582796	99.1	433	51
1484940	56.6	427	51
972455	11.5	187	51
1762789	67.2	452	51
1263152	10.9	158	51
1492338	56.7	497	51
1884095	72.0	456	51
1233724	62.5	162	51
993271	56.7	155	51
1392883	63.9	159	51
1152319	61.9	166	51
1088375	60.7	153	51
1022280	60.8	181	51
881620	53.0	198	51
1327234	87.6	264	51
1241995	75.6	214	51
1394046	84.3	192	51
1376523	66.5	147	51

Year	Haplotype	Genbank ID	Source
1993	H1	AL513382	NCBI
2004	H58	CAAY00000000	NCBI
2002	H58	-	Sanger
2004	H58	-	Sanger
2003	H58	-	Sanger
2003	H58	-	Sanger

Sequencing platform	N50 (bp)	Total contigs	Total length of sequence (bp)
Illumina (BGI)	25180	374	4744214
Illumina MiSeq	59520	177	4729455
Illumina MiSeq	143433	88	4780503
Illumina (BGI)	24726	377	4744419
Illumina MiSeq	153429	85	4685827
Illumina (BGI)	25179	385	4745648
Illumina (BGI)	24206	390	4745025
Illumina (BGI)	23938	389	4746965
Illumina (BGI)	23676	404	4783218
Illumina (BGI)	24765	391	4742136
Illumina HiSeq	206184	78	4750645
Illumina HiSeq	204269	75	4750804
Illumina HiSeq	186675	84	4792846
Illumina MiSeq	144286	88	4732620
Illumina HiSeq	204269	74	4751179
Illumina HiSeq	221745	78	4751180
Illumina MiSeq	143479	80	4737442
Illumina HiSeq	206193	74	4752104
Illumina MiSeq	154782	84	4741519
Illumina HiSeq	206120	68	4755515
Illumina HiSeq	204269	78	4750221
Illumina MiSeq	28409	480	4699244
Illumina MiSeq	2694182	58	4713610
Illumina MiSeq	28980	363	4742770
Illumina MiSeq	35231	309	4718813
Illumina MiSeq	4612297	73	4746801
Illumina MiSeq	32411	317	4710498
Illumina MiSeq	30284	359	4703371
Illumina MiSeq	42197	224	4716255
Illumina MiSeq	4671909	46	4785946
Illumina MiSeq	42747	264	4715900
Illumina MiSeq	3821004	351	4681861

Total contigs	Total length of sequence (bp)	Download link
1	4809037	-
7336	4751206	-
1	4809037	ftp://ftp.sanger.ac.uk/pub/pathogens/Salmonella/typhi/so
1	4809037	ftp://ftp.sanger.ac.uk/pub/pathogens/Salmonella/typhi/so
1	4809037	ftp://ftp.sanger.ac.uk/pub/pathogens/Salmonella/typhi/so
1	4809037	ftp://ftp.sanger.ac.uk/pub/pathogens/Salmonella/typhi/so

Accession
ERS540069
ERS540030
ERS540031
ERS540070
ERS540033
ERS540071
ERS540072
ERS540073
ERS540074
ERS540075
ERS540039
ERS540040
ERS540041
ERS540042
ERS540043
ERS540044
ERS540045
ERS540046
ERS540047
ERS540048
ERS540049
ERS540050
ERS540051
ERS540052
ERS540053
ERS540054
ERS540055
ERS540056
ERS540057
ERS540058
ERS540059
ERS540060

lexa/E02-2759_solexa_genome.fastq
lexa/ISP-04-06979_solexa_genome.fastq
lexa/E03-9804_solexa_genome.fastq
lexa/ISP-03-07467_solexa_genome.fastq

Supplementary Table 1B**SNP positions of the 33 WGST isolates.**

pos	ref	alt	ref_codon	alt_codon	aa_change
12478	C	T	CAC	CAT	His
17187	G	A	GTG	GTA	Val
22623	T	C	TTG	CTG	Leu
32762	G	A	CTG	CTA	Leu
35122	T	C	-	-	-
40159	G	A	GGG	GAG	Gly11Glu
61892	T	C	TAC	CAC	Tyr520His
63831	C	T	ACG	ATG	Thr339Met
76422	A	G	AGC	GGC	Ser243Gly
80983	T	C	TAC	CAC	Tyr150His
89102	A	G	AAA	AGA	Lys201Arg
93158	A	G	TAG	TGG	*388Trp
115909	C	T	-	-	-
117735	T	C	-	-	-
124045	C	T	ATC	ATT	Ile
136763	T	C	TGC	CGC	Cys261Arg
158891	G	T	GCG	GCT	Ala
160293	T	C	TTG	CTG	Leu
163958	G	A	CTG	CTA	Leu
175120	C	T	CCT	CTT	Pro415Leu
202039	C	T	CTG	TTG	Leu
204478	C	T	CCG	CTG	Pro37Leu
214999	A	G	ACC	GCC	Thr286Ala
219989	C	T	GCA	GTA	Ala265Val
260848	T	C	TTG	CTG	Leu
313260	G	A	GCG	GCA	Ala
316812	C	G	ACT	AGT	Thr147Ser
354895	G	A	GTG	ATG	Val563Met
362463	A	T	CAC	CTC	His642Leu
381217	A	G	AAT	AGT	Asn748Ser
381514	G	A	CGG	CAG	Arg649Gln
387082	G	A	CGA	CAA	Arg33Gln
387595	C	T	ACC	ATC	Thr204Ile
397389	A	G	AAC	GAC	Asn171Asp
399478	T	C	CTT	CTC	Leu
401918	T	C	ACT	ACC	Thr
408989	G	A	CTG	CTA	Leu
413125	T	C	CTG	CCG	Leu452Pro
426870	A	G	AGG	GGG	Arg205Gly
429115	T	C	-	-	-
435831	C	T	GCG	GTG	Ala122Val
445543	A	G	GCA	GCG	Ala
448607	G	A	GGG	GGA	Gly

448862	A	G	CTA	CTG	Leu
461438	C	T	CGT	TGT	Arg4Cys
461883	A	T	-	-	-
479552	G	A	GCT	ACT	Ala117Thr
484623	A	G	GAA	GAG	Glu
490361	A	G	-	-	-
510606	T	C	CCT	CCC	Pro
529155	A	G	AAA	GAA	Lys590Glu
542934	T	C	ACT	ACC	Thr
549399	G	A	CTG	CTA	Leu
552803	A	G	ATG	GTG	Met290Val
574463	T	C	GGT	GGC	Gly
593977	G	A	GTG	GTA	Val
596844	T	C	TAG	CAG	*47Gln
601409	A	G	AAA	AAG	Lys
610111	G	A	GAG	GAA	Glu
612535	C	T	CTG	TTG	Leu
615940	C	T	GGC	GGT	Gly
621496	G	A	GAA	AAA	Glu102Lys
650335	C	T	GCC	GCT	Ala
651393	T	C	ACT	ACC	Thr
651929	A	C	ACC	CCC	Thr23Pro
656747	G	A	GAG	GAA	Glu
661114	T	C	GGT	GGC	Gly
667579	T	C	TAC	CAC	Tyr199His
670885	C	G	CAC	GAC	His53Asp
679680	G	T	TGT	TTT	Cys304Phe
690176	T	G	GTC	GGC	Val85Gly
693560	G	A	ATG	ATA	Met100Ile
704744	C	T	GTC	GTT	Val
736002	C	A	CCC	ACC	Pro87Thr
738393	G	A	GTG	ATG	Val326Met
743950	G	T	TGT	TTT	Cys543Phe
751854	C	T	TGC	TGT	Cys
754490	T	C	CTC	CCC	Leu48Pro
775503	A	G	CTA	CTG	Leu
788874	G	A	CAG	CAA	Gln
789347	G	A	-	-	-
817881	A	G	AAA	AAG	Lys
845672	T	G	GCT	GCG	Ala
869699	T	C	TTG	CTG	Leu
874298	G	A	GAG	GAA	Glu
879431	T	A	-	-	-
880083	A	G	ACC	GCC	Thr201Ala
902056	C	T	ACC	ACT	Thr
909985	A	G	ATA	ATG	Ile340Met

911156	T	C	TTT	TTC	Phe
936286	C	T	GGC	GGT	Gly
955573	C	T	TAC	TAT	Tyr
1055966	C	T	-	-	-
1090397	A	G	-	-	-
1092870	C	T	CAC	TAC	His411Tyr
1095905	T	C	GTC	GCC	Val87Ala
1098125	C	T	-	-	-
1113205	C	T	CTC	TTC	Leu19Phe
1136685	C	T	CAT	TAT	His108Tyr
1171121	A	G	ACT	GCT	Thr347Ala
1181520	G	A	CTG	CTA	Leu
1193220	T	C	GGT	GGC	Gly
1217400	T	C	GGT	GGC	Gly
1223740	A	G	CAC	CGC	His280Arg
1241351	C	A	ATC	ATA	Ile
1241623	G	A	GGG	AGG	Gly113Arg
1245025	G	T	ATG	ATT	Met314Ile
1254424	T	C	ACT	ACC	Thr
1264214	G	A	-	-	-
1269646	G	A	GAT	AAT	Asp189Asn
1270888	G	A	CGA	CAA	Arg252Gln
1286044	A	G	GAC	GGC	Asp372Gly
1289728	T	C	TTC	CTC	Phe234Leu
1302907	G	A	GTC	ATC	Val67Ile
1307379	C	T	GCT	GTT	Ala597Val
1339645	A	G	-	-	-
1348205	T	C	ATG	ACG	Met293Thr
1350330	G	T	AGC	ATC	Ser10Ile
1360939	C	T	CAG	TAG	Gln30*
1363837	T	C	-	-	-
1369705	G	A	GCG	ACG	Ala613Thr
1399284	T	C	GTG	GCG	Val164Ala
1408039	C	T	CAG	TAG	Gln185*
1431936	C	T	CTG	TTG	Leu
1437437	A	G	CCA	CCG	Pro
1444653	G	A	GGT	GAT	Gly67Asp
1448782	C	T	-	-	-
1471515	A	C	GAA	GAC	Glu101Asp
1488469	T	C	TAC	CAC	Tyr162His
1503591	T	G	-	-	-
1505774	C	A	TGC	TGA	Cys182*
1510047	G	A	-	-	-
1520015	T	C	-	-	-
1522643	A	T	AAC	TAC	Asn28Tyr
1524915	C	T	CCA	CTA	Pro345Leu

1526887	A	G	ACA	ACG	Thr
1548268	A	G	TGA	TGG	*140Trp
1554449	A	G	GAG	GGG	Glu56Gly
1557613	G	A	CTG	CTA	Leu
1564004	G	A	CTG	CTA	Leu
1564778	G	A	GCA	ACA	Ala17Thr
1588391	C	T	-	-	-
1595011	A	G	ACG	GCG	Thr548Ala
1601413	C	T	GCG	GTG	Ala166Val
1603790	G	A	CTG	CTA	Leu
1615350	G	A	CAG	CAA	Gln
1618891	A	C	ATG	CTG	Met284Leu
1628069	T	C	TGT	TGC	Cys
1628960	C	T	ACC	ACT	Thr
1629304	C	T	GCG	GTG	Ala25Val
1649036	T	C	TTT	CTT	Phe656Leu
1656288	C	T	CTG	TTG	Leu
1666219	A	G	AAA	GAA	Lys370Glu
1673231	T	C	TAC	CAC	Tyr176His
1685355	A	C	ATC	CTC	Ile35Leu
1693292	C	T	-	-	-
1699046	C	T	TGC	TGT	Cys
1721603	C	T	-	-	-
1755898	C	T	AGC	AGT	Ser
1758607	C	A	CCC	ACC	Pro48Thr
1772249	C	T	CGC	CGT	Arg
1777278	A	G	AGT	GGT	Ser130Gly
1784272	G	A	-	-	-
1784324	G	A	GGC	AGC	Gly17Ser
1786966	T	G	CGT	CGG	Arg
1810914	G	A	GCT	ACT	Ala99Thr
1824170	C	T	GCC	GCT	Ala
1832572	C	T	ACC	ACT	Thr
1838206	A	G	GTA	GTG	Val
1838566	G	A	ACG	ACA	Thr
1840765	C	T	CTG	TTG	Leu
1841558	C	T	GCC	GCT	Ala
1858280	A	G	GCA	GCG	Ala
1858850	C	T	CTT	TTT	Leu11Phe
1867762	A	G	ACG	GCG	Thr101Ala
1868657	C	T	GCC	GTC	Ala399Val
1873870	G	A	GGG	AGG	Gly69Arg
1875747	G	A	AAG	AAA	Lys
1877172	T	C	-	-	-
1943833	C	T	CTC	TTC	Leu414Phe
1978044	T	G	CTC	CGC	Leu219Arg

2002943	C	T	CTT	TTT	Leu63Phe
2013993	A	G	CAA	CAG	Gln
2019207	A	G	ATC	GTC	Ile23Val
2020244	A	G	ACC	GCC	Thr34Ala
2024187	G	A	GGC	AGC	Gly225Ser
2036369	G	A	GAT	AAT	Asp12Asn
2051128	T	C	CTG	CCG	Leu469Pro
2053289	G	C	CGT	CCT	Arg223Pro
2069797	T	C	TTG	CTG	Leu
2073793	T	C	CCT	CCC	Pro
2090176	C	T	CCG	TCG	Pro231Ser
2111111	G	A	ACG	ACA	Thr
2129439	A	G	AAA	AAG	Lys
2145434	G	A	GTG	ATG	Val305Met
2157050	C	T	GTC	GTT	Val
2160804	C	T	-	-	-
2169657	C	T	CAT	TAT	His222Tyr
2178761	T	C	GGT	GGC	Gly
2190276	C	T	-	-	-
2191673	C	T	-	-	-
2202853	C	T	CGT	TGT	Arg334Cys
2207564	A	G	-	-	-
2207806	A	T	-	-	-
2212276	G	A	CAG	CAA	Gln
2221187	A	G	ATG	GTG	Met181Val
2221582	T	C	ATG	ACG	Met49Thr
2225193	T	C	GTG	GCG	Val154Ala
2233752	A	G	AAG	GAG	Lys199Glu
2238594	T	C	TCG	CCG	Ser205Pro
2239954	C	T	CCG	CTG	Pro339Leu
2269835	A	G	GCA	GCG	Ala
2273669	T	C	GTC	GCC	Val15Ala
2288504	C	T	-	-	-
2291051	A	G	CTA	CTG	Leu
2296505	G	A	AGC	AAC	Ser400Asn
2316433	T	C	ATG	ACG	Met55Thr
2326896	T	A	GTC	GAC	Val880Asp
2332398	G	A	GAT	AAT	Asp538Asn
2333751	G	A	GAC	AAC	Asp87Asn
2333762	C	A	TCC	TAC	Ser83Tyr
2341469	C	T	ACC	ACT	Thr
2341863	A	G	ATC	GTC	Ile136Val
2343508	G	A	GGG	GAG	Gly185Glu
2348633	G	A	GGC	AGC	Gly260Ser
2348902	C	T	ACC	ACT	Thr
2353129	A	G	ACA	GCA	Thr262Ala

2355869	C	T	CCG	CTG	Pro383Leu
2373091	A	T	AAT	TAT	Asn44Tyr
2382070	G	A	GCG	GCA	Ala
2388057	C	T	ACT	ATT	Thr530Ile
2401233	C	T	CGC	TGC	Arg116Cys
2413152	C	G	CAC	GAC	His250Asp
2413211	C	A	CGC	CGA	Arg
2438053	A	G	GGA	GGG	Gly
2472090	G	A	GGG	GGA	Gly
2482601	G	A	GGA	GAA	Gly17Glu
2492505	A	C	-	-	-
2492526	T	C	-	-	-
2495154	T	C	GCT	GCC	Ala
2497610	G	T	AGG	ATG	Arg232Met
2501090	A	G	ACC	GCC	Thr179Ala
2502356	G	A	CCG	CCA	Pro
2506744	C	A	CAC	AAC	His346Asn
2508939	A	T	AAC	TAC	Asn101Tyr
2509943	T	C	TTA	CTA	Leu
2524800	G	A	GAG	GAA	Glu
2529964	T	C	ATT	ATC	Ile
2538236	C	T	CAC	CAT	His
2538933	A	G	GAC	GGC	Asp42Gly
2543029	C	T	GCG	GTG	Ala98Val
2546877	G	A	GAC	AAC	Asp99Asn
2563769	G	A	GGT	GAT	Gly190Asp
2582347	C	G	CAG	GAG	Gln723Glu
2634864	A	G	AAA	AAG	Lys
2647676	C	A	-	-	-
2662406	A	G	-	-	-
2669640	G	A	GGG	GAG	Gly207Glu
2675634	C	T	CGC	TGC	Arg199Cys
2680154	T	G	TCT	GCT	Ser168Ala
2689095	A	G	CAC	CGC	His186Arg
2737371	T	C	ATC	ACC	Ile172Thr
2743543	G	C	GTG	CTG	Val17Leu
2748900	T	C	AAT	AAC	Asn
2750755	G	A	GCG	ACG	Ala2421Thr
2751236	A	C	CAG	CCG	Gln2581Pro
2760034	G	T	TGT	TTT	Cys158Phe
2796634	C	T	CGA	TGA	Arg244*
2797242	T	C	CCT	CCC	Pro
2797490	C	T	CGC	CGT	Arg
2806924	G	A	CGC	CAC	Arg507His
2819619	G	T	GGT	GTT	Gly21Val
2846417	T	C	TGC	CGC	Cys120Arg

2875160	C	T	CAA	TAA	Gln185*
2908219	T	C	TAT	CAT	Tyr81His
2915648	G	T	CGC	CTC	Arg141Leu
2915666	A	C	GAC	GCC	Asp135Ala
2932803	G	A	CGC	CAC	Arg23His
2948465	A	G	-	-	-
2952080	G	A	GCG	ACG	Ala797Thr
2963499	G	T	GGC	GTC	Gly481Val
2972433	C	T	-	-	-
2975982	T	C	-	-	-
3004181	A	G	GAA	GGA	Glu337Gly
3006737	C	A	CGC	CGA	Arg
3031998	C	T	ACC	ACT	Thr
3126273	G	A	GCG	GCA	Ala
3127706	G	T	-	-	-
3132774	A	G	TTA	TTG	Leu
3134993	T	A	ATT	ATA	Ile
3144053	T	G	GTG	GGG	Val203Gly
3152879	G	A	ATG	ATA	Met286Ile
3161974	C	T	GGC	GGT	Gly
3179172	G	A	CGC	CAC	Arg159His
3182059	A	G	-	-	-
3185766	G	A	GGA	GAA	Gly203Glu
3228109	C	T	CGC	TGC	Arg261Cys
3234470	G	A	GAG	GAA	Glu
3237694	C	T	CAG	TAG	Gln12*
3239301	A	G	CGA	CGG	Arg
3245844	T	C	-	-	-
3250850	G	A	-	-	-
3252042	A	G	TTA	TTG	Leu
3253322	A	G	CTA	CTG	Leu
3299998	A	C	ATC	CTC	Ile167Leu
3354611	T	C	CGT	CGC	Arg
3360344	A	G	CAT	CGT	His97Arg
3372628	C	T	ACG	ATG	Thr339Met
3380051	G	A	GGA	GAA	Gly35Glu
3382573	A	G	GAA	GGA	Glu38Gly
3382712	G	A	GAG	GAA	Glu
3385249	G	A	TGT	TAT	Cys106Tyr
3390057	T	G	TGT	TGG	Cys1094Trp
3398551	C	T	GCT	GTT	Ala620Val
3426250	A	G	ACA	ACG	Thr
3426843	G	A	GTG	GTA	Val
3434756	G	A	GGT	AGT	Gly384Ser
3441649	T	C	TTT	TTC	Phe
3445498	A	G	AGC	GGC	Ser201Gly

3466292	T	C	GTG	GCG	Val40Ala
3475293	G	A	CCG	CCA	Pro
3476189	C	T	ACC	ACT	Thr
3479997	G	C	-	-	-
3483324	A	G	CAA	CAG	Gln
3484294	G	A	GTA	ATA	Val213Ile
3508980	G	A	TGC	TAC	Cys255Tyr
3524058	G	A	GGC	GAC	Gly166Asp
3550968	T	C	TAG	CAG	*138Gln
3559850	A	G	AGC	GGC	Ser458Gly
3563369	C	T	CTG	TTG	Leu
3564730	G	A	GTG	ATG	Val127Met
3582556	T	C	TTT	TCT	Phe917Ser
3585890	C	T	GTC	GTT	Val
3612820	T	G	TGC	GGC	Cys349Gly
3623826	T	C	GTC	GCC	Val143Ala
3659647	G	A	GGG	GAG	Gly251Glu
3689465	A	G	CAA	CAG	Gln
3693688	C	T	-	-	-
3759228	A	T	ATA	ATT	Ile
3768874	C	T	CGC	CGT	Arg
3824631	T	G	GAT	GAG	Asp60Glu
3841111	T	C	GTG	GCG	Val524Ala
3841969	G	A	GGG	AGG	Gly60Arg
3843665	G	A	GGC	GAC	Gly204Asp
3847076	A	G	GTA	GTG	Val
3857080	T	C	CTG	CCG	Leu199Pro
3863384	T	G	-	-	-
3879688	C	T	GCC	GCT	Ala
3880961	A	G	ATA	ATG	Ile240Met
3908621	A	G	GAC	GGC	Asp176Gly
3918596	C	T	CTC	TTC	Leu98Phe
3951813	C	T	-	-	-
3953229	C	T	CTG	TTG	Leu
3980159	T	C	-	-	-
4002581	T	C	TAT	CAT	Tyr27His
4020211	C	T	ACG	ATG	Thr44Met
4025665	C	T	CCG	CTG	Pro123Leu
4050187	C	T	TCA	TTA	Ser164Leu
4077356	A	G	GGA	GGG	Gly
4079882	C	T	CTG	TTG	Leu
4081497	G	A	GCG	GCA	Ala
4084601	T	C	AGT	AGC	Ser
4105638	A	G	ACT	GCT	Thr5Ala
4124891	A	C	AAA	CAA	Lys474Gln
4129460	G	A	-	-	-

4165815	G	A	TGC	TAC	Cys214Tyr
4179017	T	C	GAT	GAC	Asp
4185249	T	G	ACT	ACG	Thr
4192610	C	T	AAC	AAT	Asn
4192687	C	T	GCG	GTG	Ala32Val
4192891	A	G	AAG	AGG	Lys100Arg
4196909	C	T	GCC	GTC	Ala56Val
4197624	G	A	CTG	CTA	Leu
4214165	C	T	-	-	-
4215341	A	G	CTA	CTG	Leu
4253640	G	A	GCT	ACT	Ala315Thr
4265892	C	T	CAC	TAC	His386Tyr
4273783	C	A	CGT	AGT	Arg1019Ser
4296944	T	C	TAT	CAT	Tyr315His
4306542	T	C	CAT	CAC	His
4319612	C	T	ATC	ATT	Ile
4321191	T	C	-	-	-
4321540	A	G	AAG	AGG	Lys44Arg
4330627	G	T	TCG	TCT	Ser
4380684	A	G	GGA	GGG	Gly
4448855	A	T	AAC	ATC	Asn282Ile
4454925	G	A	GGT	AGT	Gly33Ser
4460147	G	A	AGT	AAT	Ser252Asn
4470928	C	T	TCG	TTG	Ser84Leu
4499497	C	T	CAC	TAC	His54Tyr
4504639	A	G	TAC	TGC	Tyr21Cys
4517865	T	C	TGT	CGT	Cys137Arg
4519519	G	A	AGC	AAC	Ser673Asn
4520947	T	A	GTG	GAG	Val197Glu
4531906	G	A	-	-	-
4581043	T	G	GAT	GAG	Asp40Glu
4581633	A	T	ATA	ATT	Ile
4584882	A	G	GAA	GAG	Glu
4620427	A	G	AGA	GGA	Arg96Gly
4621521	G	A	-	-	-
4638263	C	T	GAC	GAT	Asp
4653151	T	G	TCC	GCC	Ser383Ala
4653522	A	T	GAC	GTC	Asp259Val
4653622	T	G	TGC	GGC	Cys226Gly
4665891	C	T	GCG	GTG	Ala245Val
4666765	C	T	-	-	-
4701741	G	T	GTA	TTA	Val77Leu
4732669	C	T	-	-	-
4742018	C	A	ACC	AAC	Thr457Asn
4759129	C	T	AGC	AGT	Ser
4761354	C	T	CTG	TTG	Leu

4775254	C	A	CCG	CAG	Pro237Gln
4791187	T	C	GTG	GCG	Val120Ala
4804749	T	C	CTG	CCG	Leu86Pro
4805736	T	C	TTA	CTA	Leu

Synonymous SNPs = 141

Non-synonymous SNPs = 222

* = SNPs in stop codon

"-" = SNPs in intergenic region

dN/dS = 0.940

Supplementary Table 1C

Biallelic polymorphisms positions (BiP) assigning haplotypes.

Marker	Gene
BiP1	STY0006*
BiP2	STY0006*
BiP89	STY0135
BiP3	STY0135*
BiP4	STY0175*
BiP5	STY0214*
BiP90	STY0321
BiP6	STY0321*
BiP7	STY0336*
BiP68	STY0539
BiP69	STY0539
BiP8	STY0573*
BiP91	STY0831
BiP9	STY0831*
BiP10	STY0961*
BiP84a	STY0961*
BiP84b	STY0961*
BiP84c	STY0961*
BiP11	STY0962*
BiP85a	STY0962*
BiP85b	STY0962*
BiP85c	STY0962*
BiP85d	STY0962*
BiP85e	STY0962*
BiP92	STY0981
BiP86a	STY0981*
BiP86b	STY0981*
BiP87a	STY0984*
BiP87b	STY0984*
BiP12	STY1097*
BiP13	STY1121*
BiP80	STY1286
BiP14	STY1286*
BiP15	STY1327*
BiP70	STY1440
BiP88a	STY1503*
BiP88b	STY1503*
BiP88c	STY1503*
BiP88d	STY1503*
BiP88e	STY1503*
BiP88f	STY1503*
BiP16	STY1556*
BiP17	STY1693*

BiP18	STY1720*
BiP19	STY1808*
BiP81	STY1914
BiP82	STY1914
BiP93	STY1919
BiP20	STY1919*
BiP21	STY1919*
BiP22	STY1947*
BiP23	STY1948*
BiP71	STY1995
BiP24	STY2093*
BiP25	STY2211*
BiP26	STY2211*
BiP27	STY2281*
BiP28	STY2281*
BiP72	STY2311
BiP73	STY2311
BiP94	STY2389
BiP95	STY2389
BiP96	STY2389
BiP97	STY2389
BiP98	STY2389
BiP99	STY2389
BiP100	STY2389
BiP101	STY2389
BiP105	STY2389
BiP106	STY2389
BiP29	STY2389*
BiP30	STY2389*
BiP31	STY2389*
BiP74	STY2418
BiP102	STY2441
BiP112a	STY2441
BiP112b	STY2441
BiP32	STY2441*
BiP33	STY2513*
BiP107	STY2575
BiP34	STY2575*
BiP35	STY2621*
BiP103	STY2629
BiP36	STY2629*
BiP37	STY2629*
BiP38	STY2629*
BiP39	STY2629*
BiP40	STY2711*
BiP41	STY2785*

BiP42	STY2834*
BiP67	STY2877*
BiP43	STY2948*
BiP44	STY2971*
BiP45	STY3033*
BiP108	STY3082
BiP46	STY3082*
BiP47	STY3082*
BiP48	STY3196*
BiP75	STY3338
BiP76	STY3397
BiP49	STY3444*
BiP50	STY3499*
BiP51	STY3499*
BiP52	STY3499*
BiP53	STY3507*
BiP77	STY3570
BiP78	STY3570
BiP54	STY3614*
BiP55	STY3614*
BiP56	STY3622*
BiP57	STY3876*
BiP58	STY3876*
BiP59	STY3940*
BiP109	STY4339
BiP60	STY4417*
BiP104	STY4499
BiP61	STY4499*
BiP79	STY4537
BiP62	STY4545*
BiP63	STY4562*
BiP64	STY4562*
BiP65	STY4793*
BiP66	STY4851*

Ancestral Nucleotide	Derived Nucleotide	CT18 position
C	T	6317
C	T	6261
C	A	138729
C	T	138680
C	T	180029
G	T	224642
G	A	332683
G	A	332645
C	T	343912
T	C	546949
G	A	547274
T	C	580916
C	T	830308
C	T	830630
G	A	955273
C	T	954935
T	C	954997
C	T	955144
G	A	958002
C	T	957702
T	C	957875
G	A	957954
T	C	958056
T	A	958089
G	A	976842
C	T	976730
C	T	977027
A	G	979505
G	A	979526
C	T	1076027
T	C	1089517
G	A	1240750
G	A	1240637
C	T	1285129
C	T	1391782
C	T	1459270
A	G	1459275
A	G	1459277
C	T	1459363
A	G	1459445
A	G	1459472
C	T	1509712
C	T	1619556

T	C	1641434
C	T	1726442
G	A	1808734
G	A	1809013
G	A	1813023
A	G	1812993
G	A	1812968
G	A	1836117
C	T	1838206
G	A	1878360
C	T	1943523
G	A	2048732
T	G	2048739
C	T	2108140
G	A	2108322
G	A	2141684
G	A	2141535
C	T	2221033
A	G	2221015
C	A	2220992
C	A	2220857
G	T	2220836
A	G	2221084
C	T	2221025
C	T	2221022
G	A	2221061
G	A	2221217
C	T	2221079
G	A	2220955
A	G	2221024
C	T	2249287
G	A	2271858
C	T	2272180
C	T	2272181
C	G	2271853
C	T	2348902
T	C	2412815
A	G	2413077
C	T	2456099
G	A	2463900
A	G	2464185
C	A	2463810
G	A	2463831
G	A	2464093
G	A	2544044
G	A	2643935

G	A	2697121
T	G	2757499
G	A	2825733
G	A	2847564
G	A	2902990
G	A	2947124
G	T	2946833
G	A	2947118
C	T	3062270
G	A	3181174
G	A	3245128
C	T	3287913
C	T	3339407
C	T	3339598
G	A	3339665
G	A	3346870
C	T	3415355
T	C	3415394
T	C	3469152
C	T	3469195
C	T	3476189
G	A	3731468
C	T	3731453
G	A	3806041
C	T	4218089
C	T	4286222
C	T	4391261
C	T	4391077
C	T	4422904
G	A	4429843
G	A	4443365
A	T	4443328
T	G	4651341
A	G	4714977

Supplementary Table 1D

Genomic deletions detected in this study.

ID

D1

D2

D3

D4

D5

D6

D7

D8

D9

D10

D11

D12

D13

D14

D15

D16

D17

D18

D19

D20

D21

D22

D23

D24

D25

D26

D27

D28

D29

D30

D31

D32

D33

D34

D35

Gene id	CT18 positions	Size (bp)
STY0096	95086 - 95881	194
STY0308	320531 - 324393	3861
STY0525	531966 - 532482	515
STY0765	764172 - 765946	1773
STY0833	831540 - 833805	2264
STY0947	937728 - 937935	206
STY1648	1575901 - 1576261	359
STY1748	1667459 - 1668460	1000
STY2091	1942582 - 1943224	641
STY2157, STY2158	2003593 - 2004607	1014
STY2163	2008364 - 2008916	551
STY2166	2009890 - 2011095	1204
STY2169, STY2170	2014368 - 2015144	776
STY2181, STY2182, STY2183, STY2184, STY2185, STY2186	2024907 - 2028945	4038
STY2192, STY2193	2032030 - 2033383	1353

STY2194	2033361 - 2035065	1703
STY2195, STY2196	2035229 - 2036403	1174
STY2199, STY2200, STY2201, STY2202	2037487 - 2040529	3042
STY2210	2047166 - 2047340	173
STY2226	2059701 - 2060438	736
STY2418	2248211 - 2249446	1234
STY2668	2505709 - 2507438	1728
STY2758	2599532 - 2605213	5680
STY2775	2627135 - 2629513	2377
STY3169	3041128 - 3041989	860
STY3325	3170215 - 3171859	1643
STY3426	3267539 - 3268870	1330
STY3570	3413541 - 3416656	3114
STY3621	3474982 - 3475924	941
STY3828	3689433 - 3690260	826
STY4166	4025298 - 4026623	1324
STY4184	4046091 - 4049524	3432
STY4318	4194856 - 4200465	5608

STY4716

4578042 - 4579899 1856

STY4782

4641054 - 4641831 776

Number of genes

1

1

1

1

1

1

1

1

1

2

1

1

2

6

2

1

2

4

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

Strain(s) harbouring the deletion

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

6, 8, 31, 34, 35, 42, 46, 53, 54, 70, 71, 225, 269, 279, 674, 739, 748, 911, 1341

1, 5, 6, 7, 8, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 361, 674, 739, 748, 911, 1012, 1341

1, 6, 7, 8, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 6, 7, 8, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 6, 8, 12 (01-10-2012), 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 674, 748, 911, 1012

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 1012, 1341

1, 5, 6, 7, 8, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 42, 46, 49, 53, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 5, 6, 7, 8, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 361, 674, 739, 748, 911, 1012, 1341

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 54, 70, 71, 225, 269, 279, 361, 674, 748, 1341

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 748, 1012, 1341

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 1012

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 5, 6, 7, 8, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 361, 674, 748, 1012, 1341

1, 5, 6, 7, 8, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 6, 7, 8, 9, 12 (11-05-2010), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 279, 361, 674, 739, 748, 1012, 1341

1, 5, 6, 7, 9, 12 (11-05-2010), 13, 14, 15, 31, 34, 35, 42, 46, 49, 53, 70, 71

1, 5, 6, 7, 8, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 361, 674, 739, 748, 1012

1, 7, 9, 12 (11-05-2010), 13, 14, 15, 31, 42, 46

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 5, 6, 7, 8, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

5, 6, 8, 12 (01-10-2012), 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

5, 6, 8, 12 (01-10-2012), 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

5, 6, 8, 12 (01-10-2012), 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 911, 1012, 1341

1, 5, 6, 7, 8, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 361, 674, 739, 748, 911

1, 6, 7, 8, 9, 12 (11-05-2010), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 269, 279, 361, 674, 739, 748, 1012, 1341

1, 5, 6, 7, 8, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 225, 674, 739, 748, 1012, 1341

1, 5, 7, 9, 12 (11-05-2010), 13, 14, 15, 31, 34, 35, 42, 46, 49, 53, 54, 70, 71, 269, 1012

1, 5, 6, 7, 9, 12 (11-05-2010), 12 (01-10-2012), 13, 14, 15, 31, 34, 35, 36, 42, 46, 49, 53, 54, 70, 71, 269, 279, 674

Supplementary Table 1E**Annotated genes of the translocated region illustrated in figure 3**

Gene	PfamA profile
DUF484	PF04340
yifL	PF01678
dapF	PF13627
DUF3021	PF11457
cyaY	PF01491
insA	PF03811_PF12759
IS1	PF03400
merR	PF00376_PF09278
merT	PF02411
merP	PF00403
merC	PF03203
merA	PF00070_PF00403_PF02852_PF07992
merD	PF13411
merE	PF05052
tnpM	PF00563
IS3	PF00665_PF13518
Δ repA	
repC	PF06504
sul2	PF00809
strA	PF01636
strB	PF04655
tnpB	PF14319
blaTEM-1	PF13354
tnpR	PF00239_PF02796
sul1	PF00809
qacE	PF00893
drfA7	PF00186
Δ aadA1	
int	PF00589_PF13495
tnpM	PF00563_PF11809
tnpR	PF00239_PF02796
tnpA	PF01526_PF13700
GNAT	PF00583
catA1	PF00302
insA	PF03811_PF12759
IS1	PF03400
cyaA	PF01295_PF12633
hemC	PF01379_PF03900
hemD	PF02602
hemX	PF04375
hemY	PF07219_PF07719

Function

Protein of unknown function DUF484
Diaminopimelate epimerase
Prokaryotic lipoprotein-attachment site
Protein of unknown function DUF3021
Frataxin-like domain
InsA N-terminal domain
IS1 transposase
MerR family regulatory protein
MerT mercuric transport protein
Heavy-metal-associated domain
MerC mercury resistance protein
Pyridine nucleotide-disulphide oxidoreductase
Mercuric resistance transcriptional repressor protein MerD
MerE protein
Transposition modulator TnpM
Integrase core domain
Replication protein A (RepA)
Replication protein C (RepC)
Pterin binding enzyme
Phosphotransferase enzyme family
Aminoglycoside/hydroxyurea antibiotic resistance kinase
Transposase zinc-binding domain
Beta-lactamase enzyme family
Resolvase
Pterin binding enzyme
Small Multidrug Resistance protein
Dihydrofolate reductase
aadA1 streptomycin and spectinomycin resistance
Phage integrase family
Transposition modulator TnpM
Resolvase
Tn3 transposase
Acetyltransferase (GNAT) family
Chloramphenicol acetyltransferase
InsA N-terminal domain
IS1 transposase
Adenylate cyclase class-I
Porphobilinogen deaminase
Uroporphyrinogen-III synthase HemD
HemX protein
HemY protein

Supplementary Table 1F
SOAPdenovo assembly details

Strain	Number of scaffolds	Estimated genome size N50	
Salmonella enterica serovar Typhi str. 31	106	4753057	607315
Salmonella enterica serovar Typhi str. 34	84	4776348	712521
Salmonella enterica serovar Typhi str. 54	471	4800417	72347
Salmonella enterica serovar Typhi str. 71	86	4763979	711616

scaffold no containing the region

10

6

11

9