Figure S1 The distribution of core genes in *Salmonella*, *S.*Typhimurium complex and *S.*Typhimurium based on *S.*Typhimurium genome strain LT2. Zone 1: *Salmonella* core genes; Zone 2: Unique *S.*Typhimurium complex core genes(excluded the *Salmonella* core genes); Zone 3: Unique *S.*Typhimurium core genes(excluded the *S.* Typhimurium complex core genes).

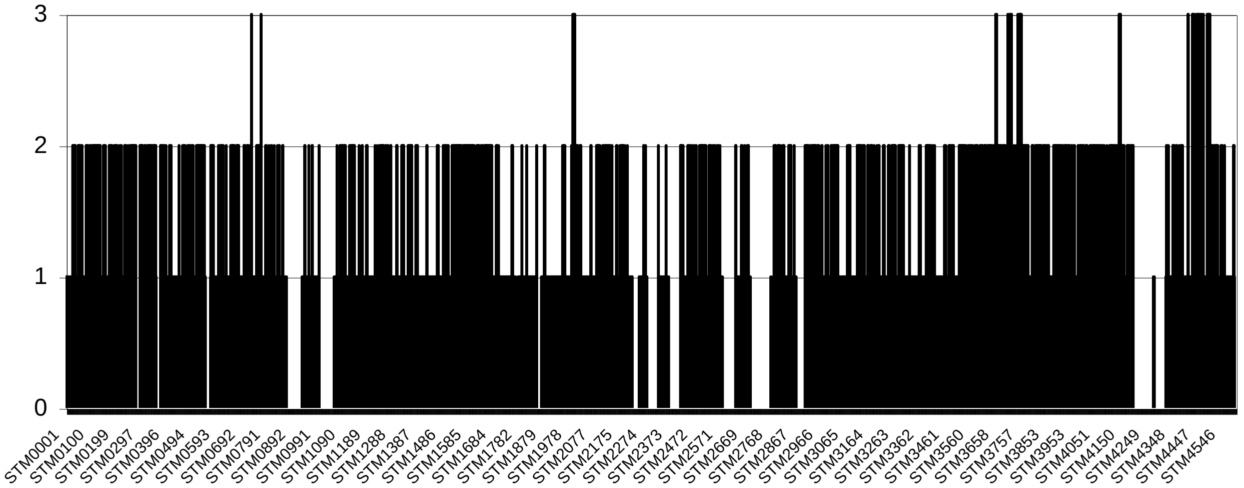


Figure S2 Divergence of core coding genes and their 5’ core intergenic regions in D23580 (N=1576)

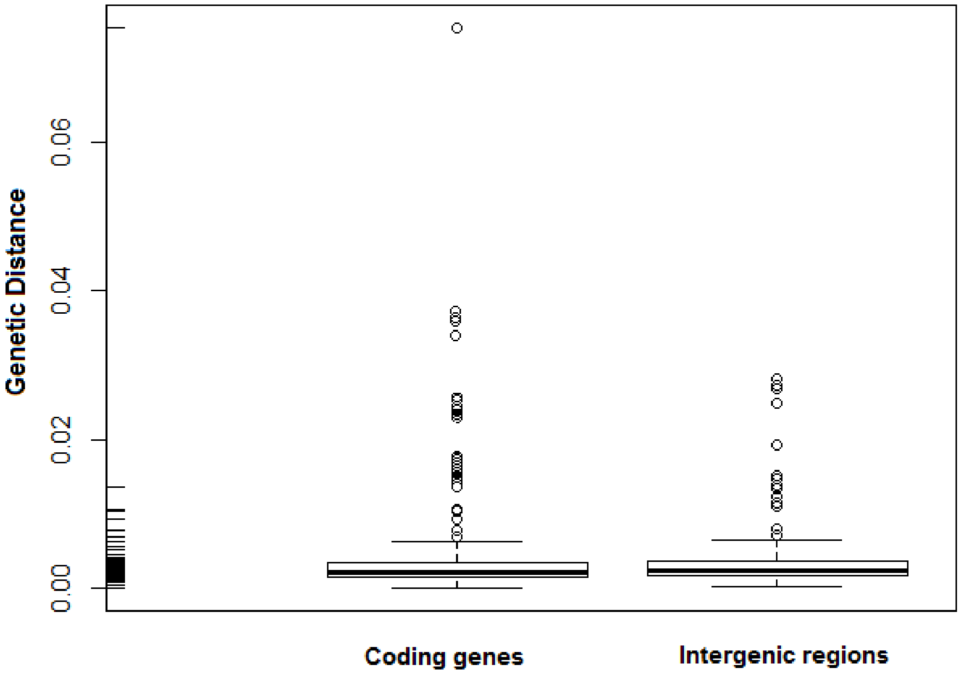
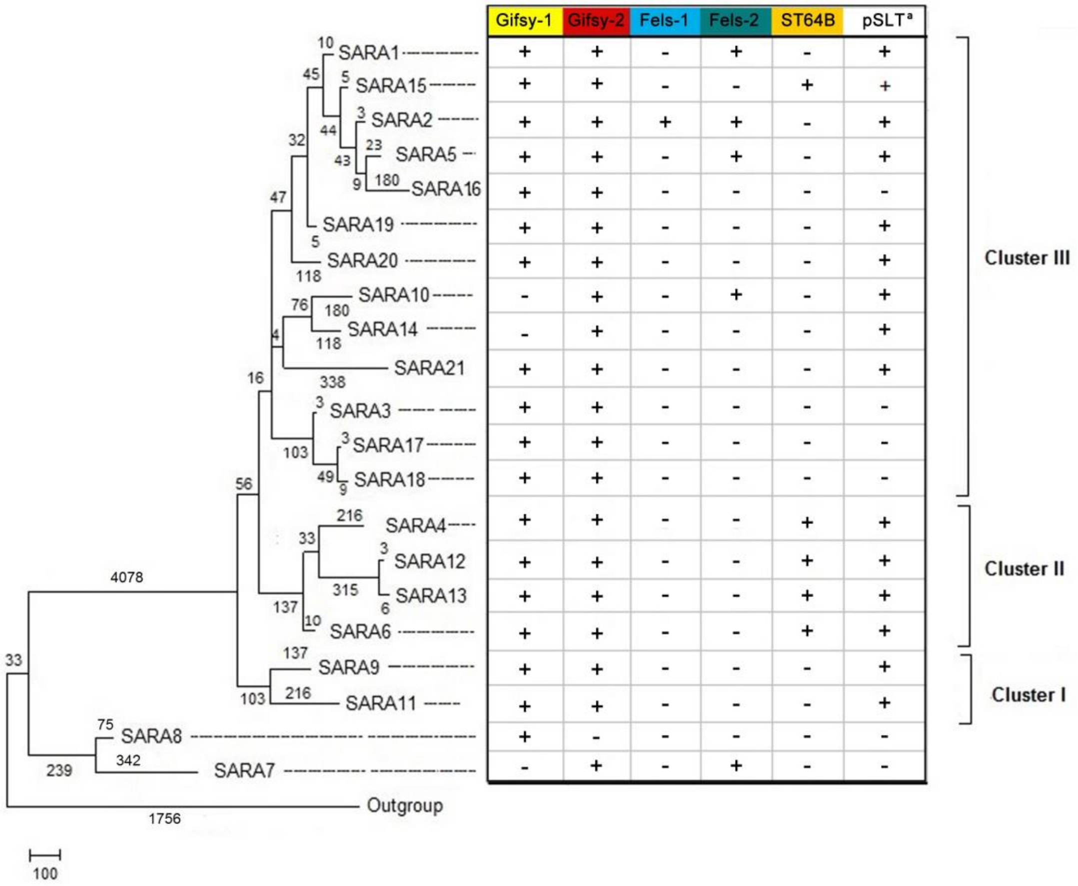


Figure S3 Phylogenetic relationships of *S*. Typhimurium isolates based on *S*. Typhimurium core genome(STCG + core IGRs). The Minimum Evolution method was used to infer evolutionary relationships of the isolates. The numbers in bracket represent outbreak number. The trees were inferred from 1000 replicates. The bootstrap values (1000 replicates; >50%) are shown next to the branches. The unit of scale bar indicates the evolutionary distance in substitutions per nucleotide.

Figure S4 Maximum Parsimony tree based on STCG+ core IGRs of 21 *S*. Typhimurium and the presence and absence of five prophages and pSLT in 21 *S*. Typhimurium genomes compared to the reference LT2 strain. The number on the internal and terminal branches corresponds to the number of core SNPs supporting each corresponding branch. SARA23 (*S*. Saintpaul) was used as the outgroup. The tree length between the clade of SARA7 and SARA8 and the clade of remaining strains have been shortened for readability. a: pSLT: plasmid of *Salmonella* Typhimurium. The presence and absence of prophages and pSLT are depicted as "+" and "-".



	Gifsy-1	Gifsy-2	Fels-1	Fels-2	ST64B	pSLT^a
SARA1	+	+	-	+	-	+
SARA15	+	+	-	-	+	+
SARA2	+	+	+	+	-	+
SARA5	+	+	-	+	-	+
SARA16	+	+	-	-	-	-
SARA19	+	+	-	-	-	+
SARA20	+	+	-	-	-	+
SARA10	-	+	-	+	-	+
SARA14	-	+	-	-	-	+
SARA21	+	+	-	-	-	+
SARA3	+	+	-	-	-	-
SARA17	+	+	-	-	-	-
SARA18	+	+	-	-	-	-
SARA4	+	+	-	-	+	+
SARA12	+	+	-	-	+	+
SARA13	+	+	-	-	+	+
SARA6	+	+	-	-	+	+
SARA9	+	+	-	-	-	+
SARA11	+	+	-	-	-	+
SARA8	+	-	-	-	-	-
SARA7	-	+	-	+	-	-

Figure S5 Homology variation among plasmid pSARA10-2, pSARA9-2, pCFSAN002069_01 and pSH1148_107. BRIG diagram showing the pSARA9-2 as a reference; coloured rings indicate the coverage of pSARA10-2 sequences among contigs from other two reference plasmids.

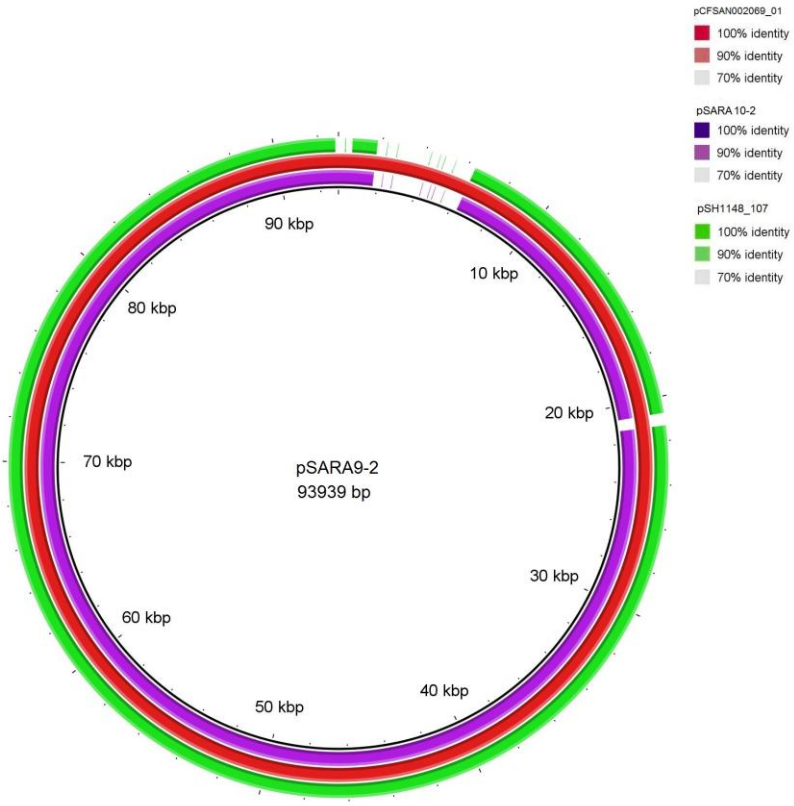


Figure S6 Heatmap of virulotyping determinants data for 21 SARA strains. Red and yellow indicates the absence and presence of genes, respectively. The heatmap was generated by using R package.