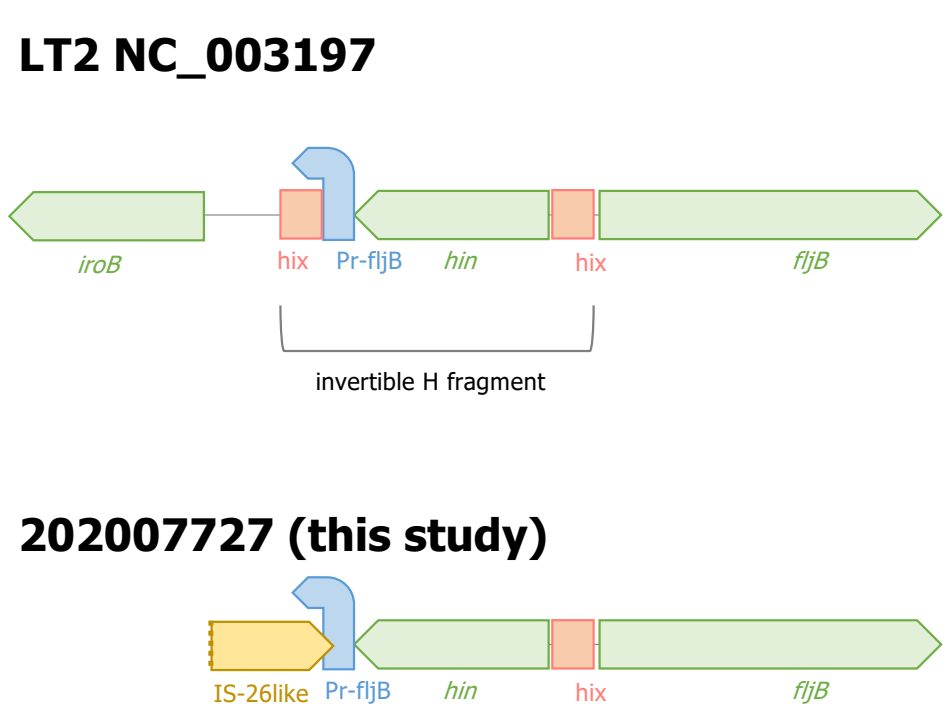
Supplementary Table S1. Primers and probe sequences used in this study.

Primer or probe	Sequence 5' -> 3'	Target gene	Target taxa	Reference
invA_176_F	CAACGTTTCCTGCGGTACTGT			
invA_291_R	CCCGAACGTGGCGATAATT	*inv*A gene	*S. enterica*	[30]
Probe: SCS-Salmo2	CTCTTTCGTCTGGCATTATCGATCAGTACCA			
PF-179	CCGTATACGGCTCGCACG			
PF-181	ACTCAGTTGGTTTGCGCACG	CRISPR2	*S.* Bovismorbificans	This study
Probe: Taq-91	AATACCGGGCAGGAAATGAATGAGACGC			
STM2-F	AGATATTCCGTAGCAATTGAGTTG			
STM2-R	AATAGCTAAAAATGACTGGGACTC	*pglX* gene	*S.* Typhimurium or its monophasic variant 4,[5],12:i:-	[31]
STM2-P	TGTGTTCAAGCAATGGTGAACAAACATAATCCC			
fliA-IS200F	CATTACACCTTCAGCGGTAT			
fliA-IS200R	CTGGTAAGAGAGCCTTATAGG	*fli*A gene	*S.* Typhimurium or its monophasic variant 4,[5],12:i:-	[32]
Probe: fliA-IS200-probe2	CGGCATGATTATCCGTTTCTACAGAGG			

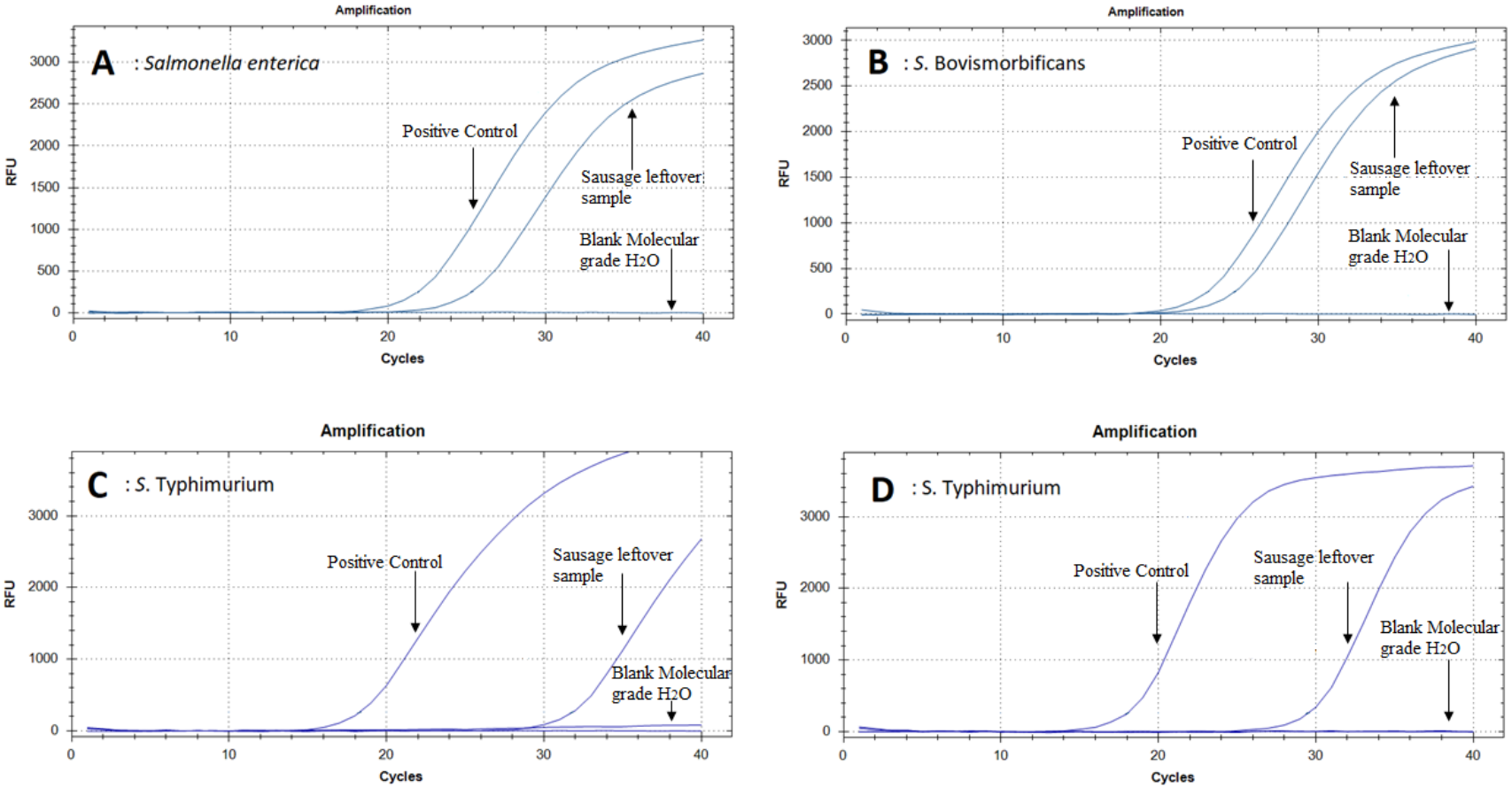
The primers and hydrolysis probes targeting *S.* Bovismorbificans were designed by hand on chromosome of *S.* Bovismorbificans strain 02-7038 CRISPR2 repeat region (JF725071.1) and validated using 900 bacterial strains and 10 *Salmonella* surrogate plasmids. Strains used for validation were divided into *S. enterica* subsp. *enterica* strains (n=798) corresponding to 64 different serovars, and *S. enterica* subsp. other than *enterica* (n=38) and strains other than *Salmonella* (n=64). The exclusivity and inclusivity of the three PCR assays was 100% (data not shown).

Supplementary Figure S1. Outbreak genetic configuration of invertible Fragment H scheme.



The classical structure of the invertible fragment H in *S.* Typhimurium contains *hin* DNA-invertase and the promoter of fljB, flanked by two *hix* sequences. In the isolates belonging to the ST34 HC5_198125 second outbreak cluster in this study, an insertion sequence of the IS-26 family was inserted upstream to the promoter of *fljB* in the invertible H fragment, preventing fragment H (including *hin* and the *fljB* promoter) from inverting its genetic configuration. This blocked permanently the expression of *fljB*. This is why these isolates were considered as monophasic, in spite of the presence of both *fliC*:i and *fljB*:1,2 flagellin genes in their genomes.

Supplementary Figure S2. Data output from qPCR analysis of the DNA extracts from the pre-enrichment broths (batch I).



Non-routine in-house quantitative real-time PCR assays (CFX apparatus, BioRad)) targeting S. Bovismorbificans and S. Typhimurium/S. 1,4,[5],12:i:- performed in the leftover food sample from Batch I ('Sausage leftover sample') A: curve of the qPCR targeting *S. enterica,* showing Ct values of ca. 20 cycles for the food sample. B: curve of the qPCR results targeting *S.* Bovismorbificans, showing Ct values of ca. 20 cycles for the food sample. C: curve of the qPCR targeting *S.* Typhimurium/monophasic variant*,* showing Ct values of ca. 30 cycles for the food sample. D: curve of the qPCR targeting *S. enterica,* showing Ct values of ca. 20 cycles for the food sample. Primers and probes are detailed in Supplementary Table S1.