

TABLE S3 Multi locus Sequence Typing of the genes in *S. enterica* Typhimurium ms202.

Gene¹	Alignment Length² = DB Allele Length
<i>aroc-3</i>	501
<i>dnan-3</i>	501
<i>hemd-7</i>	432
<i>hisd-4</i>	501
<i>pure-3</i>	399
<i>suca-3</i>	501
<i>thra-7</i>	501

¹ Individual gene is added separately to the identified Sequence Type unless all alleles in the input genome match perfectly to a database allele. % Identify = 100, and Gaps = 0 for sequence of all genes.

² Length (in bp) of the alignment between the MLST allele in the database (DB) and the corresponding sequence in the input genome.