

Subspecies	subsp. <i>enterica</i> clade ^a	Serovar	Assembly	<i>pltA</i> length (% identity with <i>S. Javiana pltA</i>) ^b	<i>pltB</i> length (% identity with <i>S. Javiana pltB</i>) ^c
<i>arizonae</i>	-	IIIa 41:Z ₄ ,Z ₂₃ :-	GCA_000018625	732 nt. (81%)	456 nt. (67%)
<i>diarizonae</i>	-	IIIb 50:r:z	GCF_002107575	732 nt. (82%)	453 nt. (68%)
<i>enterica</i>	A2	Inverness	GCA_000487155	732 nt. (81%)	426 nt. (65%)
<i>enterica</i>	B	Tanger	GCA_007009285	738 nt. (79%)	423 nt. (67%)
<i>enterica</i>	D	Brazzaville	GCA_007644865	735 nt. (79%)	414 nt. (66%)
<i>enterica</i>	D	Kalina	GCA_007414785	735 nt. (79%)	414 nt. (66%)
<i>enterica</i>	D	Westminster	GCA_009249885	735 nt. (79%)	414 nt. (66%)
<i>enterica</i>	Section Typhi	Mississippi	GCA_008588385	732 nt. (82%)	414 nt. (67%)

^aclade assigned based on phylogenetic assessment from core SNP analysis.

^bcomparison of *pltA* in given genome with *pltA* from *S. Javiana* CFSAN001992, which has a nucleotide length of 729 nt.; Inverness GCA_000487155 encodes two different TT islets that share 100% identity with each other, therefore the results presented here are representative of both loci.

^ccomparison of *pltB* in given genome with *pltB* from *S. Javiana* CFSAN001992, which has a nucleotide length of 414 nt.; Inverness GCA_000487155 encodes two different TT islets that share 100% identity with each other, therefore the results presented here are representative of both loci.