Phylogeny and Divergence of the 100 Most Common *Salmonella* Serovars Available in the NCBI Pathogen Detection Database

Figure Legends for Supplementary Figures 2 – 95

* For maximum likelihood phylogenetic trees of *Salmonella* Enteritidis, Cerro, Dublin, Infantis, Kentucky, Montevideo, Reading, and Saintpaul, refer to by our group Chen et al., 2022; Chen et al., 2024.

Supplementary Figure 2.   *S.* **Adelaide**

Maximum likelihood phylogenetic tree for *S.* Adelaide. *S.* Adelaide is a polyphyletic serovar that contains six phylogenetic lineages (Adelaide A, B, C, D, E, and F) along with three stand-alone singletons (Adelaide S1, S2, and S3). Adelaide A is the largest lineage with 1,249 genomes representing 46 SNP clusters, and 73 singletons. Adelaide B contains 79 genomes representing only 1 SNP cluster. Adelaide C contains 42 genomes representing 6 SNP clusters, and 8 singletons. Adelaide D contains 26 genomes representing 5 SNP clusters, and 10 singletons. Adelaide E contains 7 genomes representing 1 SNP cluster, and 1 singleton. Adelaide F contains 5 genomes representing only 5 singletons. Adelaide C is a paraphyletic lineage since other non-Adelaide serovar clusters within this lineage (i.e. *S.* Ealing clusters within Adelaide C). Adelaide A, B, D, E and F are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Adelaide lineage with a bootstrap value higher than 0.7.

Supplementary Figure 3.   *S.* **Agama**

Maximum likelihood phylogenetic tree for *S.* Agama. *S.* Agama is a polyphyletic serovar that contains one phylogenetic lineage (Agama) along with one stand-alone singleton (shown as Agama S1). Agama lineage has 433 genomes representing 42 SNP clusters, and 92 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Agama lineage with a bootstrap value higher than 0.7.

Supplementary Figure 4.   *S.* **Agbeni**

Maximum likelihood phylogenetic tree for *S.* Agbeni. *S.* Agbeni is a paraphyletic serovar as other non-Agbeni serovars cluster within this serovar (i.e. *S.* Limete and *S.* Ituri cluster within serovar Agbeni). In total, *S.* Agbeni has 1,851 genomes representing 34 SNP clusters, and 43 singletons.

The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Agbeni lineage with a bootstrap value higher than 0.7.

Supplementary Figure 5.　　*S*. **Agona**

Maximum likelihood phylogenetic tree for *S*. Agona. *S*. Agona is a polyphyletic serovar that contains one phylogenetic lineage (Agona) along with one stand-alone singleton (shown as Agona S1). Agona lineage has 7,809 genomes representing 219 SNP clusters, and 275 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Agona lineage with a bootstrap value higher than 0.7.

Supplementary Figure 6.　　*S*. **Alachua**

Maximum likelihood phylogenetic tree for *S*. Alachua**.** *S*. Alachua is a polyphyletic serovar that contains two phylogenetic lineages (Alachua A, and B). Alachua A is the largest lineage with 611 genomes representing 46 SNP clusters, and 75 singletons. Alachua B contains 9 genomes representing 3 SNP clusters, and 2 singletons. Both Alachua A and B are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 9. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Alachua lineage with a bootstrap value higher than 0.7.

Supplementary Figure 7.　　*S*. **Albany**

Maximum likelihood phylogenetic tree for *S*. Albany. *S*. Albany is a polyphyletic serovar that contains two phylogenetic lineages (Albany A, and B). Albany A is the largest lineage with 720 genomes representing 33 SNP clusters, and 59 singletons. Albany B contains 6 genomes representing 1 SNP cluster, and 1 singleton. Albany A is a paraphyletic lineage since other non-Albany serovar clusters within this lineage (i.e. *S*. Duesseldorf clusters within Albany A; the non-Albany serovar Duesseldorf was shown with an asterisk as it could not be clearly shown in the tree separately). Albany B is a monophyletic lineage. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange

stars represent the most recent common ancestor of each Albany lineage with a bootstrap value higher than 0.7.

Supplementary Figure 8.   *S.* **Altona**

Maximum likelihood phylogenetic tree for *S.* Altona. *S.* Altona is a polyphyletic serovar that contains three phylogenetic lineages (Altona A, B, and C). Altona A is the largest lineage with 526 genomes representing 22 SNP clusters, and 38 singletons. Altona B contains 5 genomes representing 1 SNP cluster, and 1 singleton. Altona C contains 2 genomes representing only 1 SNP cluster. Altona A is a paraphyletic lineage since other non-Altona serovars cluster within this lineage. For example, *S.* Kentucky clusters within Altona A. Altona B and C are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Altona lineage with a bootstrap value higher than 0.7.

Supplementary Figure 9.   *S.* **Anatum**

Maximum likelihood phylogenetic tree for *S.* Anatum. *S.* Anatum is a monophyletic serovar with 8,221 genomes representing 538 SNP clusters, and 823 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Anatum lineage with a bootstrap value higher than 0.7.

Supplementary Figure 10.   *S.* **Baildon**

Maximum likelihood phylogenetic tree for *S.* Baildon. *S.* Baildon is a paraphyletic serovar as other non-Baildon serovar clusters within this serovar (i.e. *S.* Worb clusters within serovar *S.* Baildon). In total, *S.* Baildon has 804 genomes representing 4 SNP clusters, and 17 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 8. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Baildon lineage with a bootstrap value higher than 0.7.

Supplementary Figure 11.   *S.* **Bareilly**

Maximum likelihood phylogenetic tree for *S.* Bareilly. *S.* Bareilly is a polyphyletic serovar that contains four phylogenetic lineages (Bareilly A, B, C, and D) along with one stand-alone

singleton (Bareilly S1). Bareilly A is the largest lineage with 2,224 genomes representing 297 SNP clusters, and 1,221 singletons. Bareilly B contains 1,735 genomes representing 141 SNP clusters, and 322 singletons. Bareilly C contains 652 genomes representing 53 SNP clusters, and 138 singletons. Bareilly D contains 2 genomes representing only 2 singletons. Bareilly C is a paraphyletic lineage since other non-Bareilly serovar clusters within this lineage (i.e. *S.* Richmond clusters within Bareilly C). Bareilly A, B, and D are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 10. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Bareilly lineage with a bootstrap value higher than 0.7.

Supplementary Figure 12. *S.* Berta

Maximum likelihood phylogenetic tree for *S.* Berta. *S.* Berta is a monophyletic serovar with 2,691 genomes representing 109 SNP clusters, and 231 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Berta lineage with a bootstrap value higher than 0.7.

Supplementary Figure 13. *S.* Blockley

Maximum likelihood phylogenetic tree for *S.* Blockley. *S.* Blockley is a polyphyletic serovar that contains three phylogenetic lineages (Blockley A, B, and C). Blockley A is the largest lineage with 957 genomes representing 25 SNP clusters, and 39 singletons. Blockley B contains 5 genomes representing 2 SNP clusters, and 1 singleton. Blockley C contains 3 genomes representing only 3 singletons. Blockley A is a paraphyletic lineage since other non-Blockley serovar clusters within this lineage (i.e. *S.* Haardt clusters within Blockley A; the non-Blockley serovar Haardt was shown with an asterisk as it could not be clearly shown in the tree separately). Blockley B, and C are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Blockley lineage with a bootstrap value higher than 0.7.

Supplementary Figure 14. *S.* Bovismorbificans

Maximum likelihood phylogenetic tree for *S.* Bovismorbificans. *S.* Bovismorbificans is a polyphyletic serovar that contains three phylogenetic lineages (Bovismorbificans A, B, and C)

along with one stand-alone singleton (shown as Bovismorbificans S1). Bovismorbificans A is the largest lineage with 1,440 genomes representing 123 SNP clusters, and 208 singletons. Bovismorbificans B contains 727 genomes representing 44 SNP clusters, and 96 singletons. Bovismorbificans C contains 8 genomes representing only 1 SNP cluster. All three lineages are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Bovismorbificans lineage with a bootstrap value higher than 0.7.

Supplementary Figure 15.   *S.* **Braenderup**

Maximum likelihood phylogenetic tree for *S.* Braenderup. *S.* Braenderup is a monophyletic serovar with 9,943 genomes representing 332 SNP clusters, and 664 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Braenderup lineage with a bootstrap value higher than 0.7.

Supplementary Figure 16.   *S.* **Brandenburg**

Maximum likelihood phylogenetic tree for *S.* Brandenburg. *S.* Brandenburg is a polyphyletic serovar that contains two phylogenetic lineages (Brandenburg A, and B) along with two stand-alone singletons (shown as Brandenburg S1, and S2). Brandenburg A is the largest lineage with 1,689 genomes representing 73 SNP clusters, and 91 singletons. Brandenburg B contains 26 genomes representing 4 SNP clusters, and 8 singletons. Both Brandenburg A, and B are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Brandenburg lineage with a bootstrap value higher than 0.7.

Supplementary Figure 17.   *S.* **Bredeney**

Maximum likelihood phylogenetic tree for *S.* Bredeney. *S.* Bredeney is a paraphyletic serovar as other non-Bredeney serovar clusters within this serovar (i.e. *S.* Give clusters within serovar *S.* Bredeney). In total, *S.* Bredeney has 782 genomes representing 91 SNP clusters, and 166 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 8. The

Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Bredeney lineage with a bootstrap value higher than 0.7.

Supplementary Figure 18.   *S.* **Carrau**

Maximum likelihood phylogenetic tree for *S.* Carrau. *S.* Carrau is a paraphyletic serovar that contains one phylogenetic lineage (Carrau) with 572 genomes representing 62 SNP clusters and 141 singletons. *S.* Madelia clusters within Carrau (the non-Carrau serovar Medelia was shown with an asterisk as it could not be clearly shown in the tree separately). The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Carrau lineage with a bootstrap value higher than 0.7.

Supplementary Figure 19.   *S.* **Chester**

Maximum likelihood phylogenetic tree for *S.* Chester. *S.* Chester is a polyphyletic serovar that contains two phylogenetic lineages (Chester A, and B). Chester A is the largest lineage with 1,308 genomes representing 107 SNP clusters, and 220 singletons. Chester B contains 6 genomes representing only 2 SNP clusters. Chester A is a paraphyletic lineage since other non-Chester serovar clusters within this lineage (i.e. *S.* Eastborne clusters within Chester A). Chester B is a monophyletic lineage. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Chester lineage with a bootstrap value higher than 0.7.

Supplementary Figure 20.   *S.* **Choleraesuis**

Maximum likelihood phylogenetic tree for *S.* Choleraesuis. *S.* Choleraesuis is a polyphyletic serovar that contains four phylogenetic lineages (Choleraesuis A, B, C, and D). Choleraesuis A is the largest lineage with 795 genomes representing 64 SNP clusters, and 97 singletons. Choleraesuis B contains 15 genomes representing 2 SNP clusters, and 9 singletons. Choleraesuis C contains 11 genomes representing 2 SNP clusters, and 1 singleton. Choleraesuis D contains 2 genomes representing only 2 singletons. Choleraesuis A is a paraphyletic lineage since other non-Choleraesuis serovar clusters within this lineage (i.e. *S.* Paratyphi C clusters within Choleraesuis A). Choleraesuis B, C, and D are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000

resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Choleraesuis lineage with a bootstrap value higher than 0.7.

Supplementary Figure 21.   *S.* Coeln

Maximum likelihood phylogenetic tree for *S.* Coeln. *S.* Coeln is a polyphyletic serovar that contains two phylogenetic lineages (Coeln A, and B) along with one stand-alone singleton (Coeln S1). Coeln A is the largest lineage with 335 genomes representing 26 SNP clusters, and 39 singletons. Coeln B contains 17 genomes representing only 17 singletons. Coeln B is a paraphyletic lineage since other non-Coeln serovar clusters within this lineage (i.e. *S.* Typhimurium clusters within Coeln B). Coeln A is a monophyletic lineage. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 9. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Coeln lineage with a bootstrap value higher than 0.7.

Supplementary Figure 22.   *S.* Concord

Maximum likelihood phylogenetic tree for *S.* Concord. *S.* Concord is a polyphyletic serovar that contains three phylogenetic lineages (Concord A, B, and C) along with one stand-alone singleton (Concord S1). Concord A is the largest lineage with 323 genomes representing 21 SNP clusters, and 51 singletons. Concord B contains 25 genomes representing 3 SNP clusters, and 11 singletons. Concord C contains 13 genomes representing 1 SNP cluster, and 1 singleton. All three lineages are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Concord lineage with a bootstrap value higher than 0.7.

Supplementary Figure 23.   *S.* Corvallis

Maximum likelihood phylogenetic tree for *S.* Corvallis. *S.* Corvallis is a polyphyletic serovar that contains six phylogenetic lineages (Corvallis A, B, C, D, E, and F). Corvallis A is the largest lineage with 918 genomes representing 34 SNP clusters, and 53 singletons. Corvallis B contains 10 genomes representing 2 SNP clusters, and 5 singletons. Corvallis C contains 8 genomes representing 1 SNP cluster, and 2 singletons. Corvallis D contains 7 genomes representing 1 SNP cluster, and 5 singletons. Corvallis E contains 6 genomes representing 2 SNP clusters, and 1 singleton. Corvallis F contains 4 genomes representing only 4 singletons. All six Corvallis lineages are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by

100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Corvallis lineage with a bootstrap value higher than 0.7.

Supplementary Figure 24. *S.* **Cotham**

Maximum likelihood phylogenetic tree for *S.* Cotham. *S.* Cotham is a monophyletic serovar with 378 genomes representing 12 SNP clusters, and 17 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Cotham lineage with a bootstrap value higher than 0.7.

Supplementary Figure 25. *S.* **Cubana**

Maximum likelihood phylogenetic tree for *S.* Cubana. *S.* Cubana is a polyphyletic serovar that contains six phylogenetic lineages (Cubana A, B, C, D, E, and F) along with 3 stand-alone singletons (Cubana S1, S2, and S3). Cubana A is the largest lineage with 460 genomes representing 51 SNP clusters, and 68 singletons. Cubana B contains 53 genomes representing 4 SNP clusters, and 2 singletons. Cubana C contains 32 genomes representing 5 SNP clusters and 5 singletons. Cubana D contains 4 genomes representing 1 SNP cluster and 1 singleton. Cubana E contains 3 genomes representing 1 SNP cluster and 1 singleton. Cubana F contains 3 genomes representing only 3 singletons. Cubana A, C and F are paraphyletic lineages since other non-Cubana serovars clusters within these lineages. For example, *S.* Meleagridis, *S.* Lille and *S.* Rissen cluster within Cubana A. Cubana B, D and E are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 10. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Cubana lineage with a bootstrap value higher than 0.7.

Supplementary Figure 26. *S.* **Derby**

Maximum likelihood phylogenetic tree for *S.* Derby. *S.* Derby is a polyphyletic serovar that contains seven phylogenetic lineages (Derby A, B, C, D, E, F and G) along with two stand-alone singletons (Derby S1, and S2). Derby A is the largest lineage with 3,566 genomes representing 261 SNP clusters, and 413 singletons. Derby B contains 519 genomes representing 27 SNP clusters, and 66 singletons. Derby C contains 279 genomes representing 6 SNP clusters, and 86 singletons. Derby D contains 14 genomes representing 3 SNP clusters, and 8 singletons. Derby E contains 5 genomes representing only 5 singletons. Derby F contains 2 genomes representing only 2 singletons. Derby G contains 2 genomes representing only 1 SNP cluster. Derby B and D

are paraphyletic lineages since other non-Derby serovars cluster within these lineages. For example, *S.* Hato clusters within Derby B. Derby A, C, E, F, and G are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 9. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Derby lineage with a bootstrap value higher than 0.7.

Supplementary Figure 27.　　*S.* Eastbourne

Maximum likelihood phylogenetic tree for *S.* Eastbourne. *S.* Eastbourne is a polyphyletic serovar that contains three phylogenetic lineages (Eastborne A, B, and C). Eastbourne A is the largest lineage with 340 genomes representing 45 SNP clusters, and 76 singletons. Eastbourne B contains 30 genomes representing 5 SNP clusters, and 8 singletons. Eastbourne C contains 3 genomes representing only 3 singletons. Eastbourne B is a paraphyletic lineage since other non-Eastbourne serovar clusters within this lineage. For example, *S.* Javiana clusters within Eastbourne B. Eastbourne A, and C are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 10. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Eastbourne lineage with a bootstrap value higher than 0.7.

Supplementary Figure 28.　　*S.* Enteritidis *

Maximum likelihood phylogenetic tree for *S.* Enteritidis. *S.* Enteritidis is a polyphyletic serovar that contains eight phylogenetic lineages (Enteritidis A, B, C, D, E, F, G, and H) along with two stand-alone singletons (Enteritidis S1, and S2). Enteritidis A is the largest lineage with 65,761 genomes representing 838 SNP clusters, and 1,217 singletons. Enteritidis B contains 178 genomes representing 17 SNP clusters, and 41 singletons. Enteritidis C contains 81 genomes representing 19 SNP clusters, and 26 singletons. Enteritidis D contains 60 genomes representing 11 SNP clusters, and 33 singletons. Enteritidis E contains 46 genomes representing 6 SNP clusters, and 26 singletons. Enteritidis F contains 41 genomes representing 5 SNP clusters, and 30 singletons. Enteritidis G contains 38 genomes representing 8 SNP clusters, and 7 singletons. Enteritidis H contains 3 genomes representing only 1 SNP cluster. Enteritidis A is a paraphyletic lineage since other non-Enteritidis serovars cluster within these lineages. For example, *S.* Gallinarum clusters within Enteritidis A. Enteritidis B, C, D, E, F, G, and H are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence.

The orange stars represent the most recent common ancestor of each Enteritidis lineage with a bootstrap value higher than 0.7.

* To infer the phylogenetic grouping (i.e., mono-, para-, or polyphyly) of *S.* Enteritidis, maximum likelihood phylogenetic reconstructed by previous studies from our group (Chen et al., 2022; Chen et al., 2024) was used to infer the phylogenetic grouping of *S.* Enteritidis. These studies used 285 reference serovars. As the maximum likelihood phylogenetic tree of *S.* Enteritidis to infer the antigenic formula diversification reconstructed in this study used 301 reference serovars, there are slight differences in inference about phylogenetic grouping. Accordingly, here we report that lineage Enteritidis E is monophyletic and there are two singletons according to our inference of phylogenetic grouping based on the phylogenetic tree retrieved from previous studies by our group, while Enteritidis S2 clusters within the lineage Enteritidis E making it a paraphyletic lineage in phylogenetic tree for diversification events built in this study with a broadscale of reference serovars (see Supplementary Figure 96).

Supplementary Figure 29.   *S.* **Gaminara**

Maximum likelihood phylogenetic tree for *S.* Gaminara. *S.* Gaminara is a paraphyletic serovar that contains one phylogenetic lineage (Gaminara) with 985 genomes representing 93 SNP clusters and 466 singletons. *S.* Welikade clusters within Gaminara. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Gaminara lineage with a bootstrap value higher than 0.7.

Supplementary Figure 30.   *S.* **Give**

Maximum likelihood phylogenetic tree for *S.* Give. *S.* Give is a polyphyletic serovar that contains two phylogenetic lineages (Give A, and B). Give A is the largest lineage with 1,533 genomes representing 155 SNP clusters, and 533 singletons. Give B contains 563 genomes representing 90 SNP clusters, and 186 singletons. Both Give A, and B are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Give lineage with a bootstrap value higher than 0.7.

Supplementary Figure 31.   *S.* **Goldcoast**

Maximum likelihood phylogenetic tree for *S.* Goldcoast. *S.* Goldcoast is a paraphyletic serovar that contains one phylogenetic lineage (Goldcoast) with 625 genomes representing 21 SNP clusters and 21 singletons. *S.* Benue clusters within Goldcoast. The average pairwise number of

nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 9. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Goldcoast lineage with a bootstrap value higher than 0.7.

Supplementary Figure 32.   *S.* **Hadar**

Maximum likelihood phylogenetic tree for *S.* Hadar. *S.* Hadar is a polyphyletic serovar that contains two phylogenetic lineages (Concord A, and B) along with two stand-alone singletons (Hadar S1, and S2). Hadar A is the largest lineage with 4,893 genomes representing 53 SNP clusters, and 79 singletons. Hadar B contains 14 genomes representing 2 SNP clusters, and 8 singletons. Hadar A is a paraphyletic lineage since other non-Hadar serovar clusters within this lineage (i.e. *S.* Bonariensis clusters within Hadar A). Hadar B is a monophyletic lineage. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 8. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Hadar lineage with a bootstrap value higher than 0.7.

Supplementary Figure 33.   *S.* **Haifa**

Maximum likelihood phylogenetic tree for *S.* Haifa. *S.* Haifa is a monophyletic serovar with 353 genomes representing 33 SNP clusters, and 30 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Haifa lineage with a bootstrap value higher than 0.7.

Supplementary Figure 34.   *S.* **Hartford**

Maximum likelihood phylogenetic tree for *S.* Hartford. *S.* Hartford is a polyphyletic serovar that contains two phylogenetic lineages (Hartford A, and B) along with one stand-alone singleton (Hartford S1). Hartford A is the largest lineage with 1,901 genomes representing 246 SNP clusters, and 661 singletons. Hartford B contains 7 genomes representing 1 SNP cluster, and 2 singletons. Both Hartford A and B are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Hartford lineage with a bootstrap value higher than 0.7.

Supplementary Figure 35.   *S.* Havana

Maximum likelihood phylogenetic tree for *S.* Havana. *S.* Havana is a polyphyletic serovar that contains seven phylogenetic lineages (Havana A, B, C, D, E, F and G). Havana A is the largest lineage with 402 genomes representing 32 SNP clusters, and 50 singletons. Havana B contains 227 genomes representing 34 SNP clusters, and 51 singletons. Havana C contains 111 genomes representing 16 SNP clusters, and 30 singletons. Havana D contains 62 genomes representing 5 SNP clusters, and 3 singletons. Havana E contains 13 genomes representing only 4 SNP clusters. Havana F contains 12 genomes representing 3 SNP clusters, and 4 singletons. Havana G contains 2 genomes representing only 2 singletons. Havana D and G are paraphyletic lineages since other non-Havana serovars cluster within these lineages. For example, *S.* Cubana clusters within Havana D. Havana A, B, C, E, and F are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 9. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Havana lineage with a bootstrap value higher than 0.7.

Supplementary Figure 36.   *S.* Heidelberg

Maximum likelihood phylogenetic tree for *S.* Heidelberg. *S.* Heidelberg is a monophyletic serovar with 8,203 genomes representing 159 SNP clusters, and 332 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Heidelberg lineage with a bootstrap value higher than 0.7.

Supplementary Figure 37.   *S.* Hvittingfoss

Maximum likelihood phylogenetic tree for *S.* Hvittingfoss. *S.* Hvittingfoss is a polyphyletic serovar that contains four phylogenetic lineages (Hvittingfoss A, B, C, and D) along with one stand-alone singleton (Hvittingfoss S1). Hvittingfoss A is the largest lineage with 644 genomes representing 30 SNP clusters, and 99 singletons. Hvittingfoss B contains 342 genomes representing 54 SNP clusters, and 172 singletons. Hvittingfoss C contains 6 genomes representing only 6 singletons. Hvittingfoss D contains 5 genomes representing only 5 singletons. All the four Hvittingfoss lineages are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Hvittingfoss lineage with a bootstrap value higher than 0.7.

Supplementary Figure 38. *S.* **I 4,[5],12:b:-**

Maximum likelihood phylogenetic tree for *S.* I 4,[5],12:b:-. *S.* I 4,[5],12:b:- is a polyphyletic serovar that contains three phylogenetic lineages (I 4,[5],12:b:- A, B, and C) along with one stand-alone singleton (I 4,[5],12:b:- S1). *S.* I 4,[5],12:b:- A is the largest lineage with 3,405 genomes representing 470 SNP clusters, and 1,291 singletons. *S.* I 4,[5],12:b:- B contains 48 genomes representing 2 SNP clusters, and 1 singleton. *S.* I 4,[5],12:b:- C contains 10 genomes representing only 1 SNP cluster. *S.* I 4,[5],12:b:- A is a paraphyletic lineage since other non- *S.* I 4,[5],12:b:- serovars cluster within this lineage (i.e. *S.* Paratyphi B and *S.* Schleissheim cluster within *S.* I 4,[5],12:b:- A). *S.* I 4,[5],12:b:- B and C are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each *S.* I 4,[5],12:b:- lineage with a bootstrap value higher than 0.7.

Supplementary Figure 39. *S.* **I 4,[5],12:i:-**

Maximum likelihood phylogenetic tree for *S.* I 4,[5],12:i:- (often referred to as monophasic Typhimurium). *S.* I 4,[5],12:i:- is a polyphyletic serovar that contains four phylogenetic lineages (I 4,[5],12:i:- A, B, C, and D) and one stand-alone singleton (I 4,[5],12:i:- S1). I 4,[5],12:i:-A is the largest lineage with 27,728 genomes which represent 268 SNP clusters, and 503 singletons. I 4,[5],12:i:- B contains 485 genomes which represent 3 SNP clusters, and 12 singletons. I 4,[5],12:i:- C contains 12 genomes which represent 2 SNP clusters, and 7 singletons. I 4,[5],12:i:- D includes 10 genomes, which are all singletons. There is one stand-alone singleton that does not cluster with any I 4,[5],12:i:- lineages and was labeled as I 4,[5],12:i:- S1. I 4,[5],12:i:- A, and C are paraphyletic since other non-I 4,[5],12:i:- serovars cluster within these lineages. For example, *S.* Agama clusters within I 4,[5],12:i:- C. Finally, I 4,[5],12:i:- B and D are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each I 4,[5],12:i:- lineage with a bootstrap value higher than 0.7. *S.* Heidelberg and *S.* Kentucky (which paraphyletically cluster within Typhimurium B and C, respectively) were also highlighted in this figure to identify whether the I 4,[5],12:i:- lineages all diverged from *S.* Typhimurium.

Supplementary Figure 40. *S.* **I 9:l,z_{28}:-**

Maximum likelihood phylogenetic tree for *S.* I 9:l,z_{28}:-. *S.* I 9:l,z_{28}:-is a monophyletic serovar with 371 genomes representing 19 SNP clusters, and 10 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one

genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of I 9:l,z_{28}:-lineage with a bootstrap value higher than 0.7.

Supplementary Figure 41.   *S.* **IIIa 41:z_4,z_{23}:-**

Maximum likelihood phylogenetic tree for *S.* IIIa 41:z_4,z_{23}:-. *S.* IIIa 41:z_4,z_{23}:- is a polyphyletic serovar that contains four phylogenetic lineages (IIIa 41:z_4,z_{23}:- A, B, C, and D) along with one stand-alone singleton (IIIa 41:z_4,z_{23}:- S1). IIIa 41:z_4,z_{23}:- A is the largest lineage with 242 genomes representing 7 SNP clusters, and 4 singletons. IIIa 41:z_4,z_{23}:- B contains 44 genomes representing 8 SNP clusters, and 23 singletons. IIIa 41:z_4,z_{23}:- C contains 39 genomes representing 4 SNP clusters and 22 singletons. IIIa 41:z_4,z_{23}:- D contains 2 genomes representing only 2 singletons. IIIa 41:z_4,z_{23}:- A and C are paraphyletic lineages since other non-IIIa 41:z_4,z_{23}:- serovar clusters within these lineages. For example, *S.* IIIa 44:z_4,z_{23}:- clusters within IIIa 41:z_4,z_{23}:- A. IIIa 41:z_4,z_{23}:- B, and D are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *bongori* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each IIIa 41:z_4,z_{23}:- lineage with a bootstrap value higher than 0.7.

Supplementary Figure 42.   *S.* **IIIb 61:k:1,5,(7)**

Maximum likelihood phylogenetic tree for *S.* IIIb 61:k:1,5,(7). *S.* IIIb 61:k:1,5,(7) is a polyphyletic serovar that contains two phylogenetic lineages (IIIb 61:k:1,5,(7) A, and B) along with one stand-alone singleton (IIIb 61:k:1,5,(7) S1). IIIb 61:k:1,5,(7) A is the largest lineage with 474 genomes representing 30 SNP clusters, and 74 singletons. IIIb 61:k:1,5,(7) B contains 2 genomes representing only 1 SNP cluster. All the IIIb 61:k:1,5,(7) lineages are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *arizonae* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each IIIb 61:k:1,5,(7) lineage with a bootstrap value higher than 0.7.

Supplementary Figure 43.   *S.* **Indiana**

Maximum likelihood phylogenetic tree for *S.* Indiana. *S.* Indiana is a polyphyletic serovar that contains one phylogenetic lineage (Indiana) along with one stand-alone singleton (shown as Indiana S1). Indiana lineage has 1,751 genomes representing 57 SNP clusters, and 71 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The

Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Indiana lineage with a bootstrap value higher than 0.7.

Supplementary Figure 44.   *S.* **Inverness**

Maximum likelihood phylogenetic tree for *S.* Inverness. *S.* Inverness is a monophyletic serovar with 577 genomes representing 78 SNP clusters, and 190 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Inverness lineage with a bootstrap value higher than 0.7.

Supplementary Figure 45.   *S.* **IV 48:g,z$_{51}$:-**

Maximum likelihood phylogenetic tree for *S.* IV 48:g,z$_{51}$:-. *S.* IV 48:g,z$_{51}$:- is a polyphyletic serovar that contains four phylogenetic lineages (IV 48:g,z$_{51}$:- A, B, C, and D) along with one stand-alone singleton (IV 48:g,z$_{51}$:- S1). IV 48:g,z$_{51}$:- A is the largest lineage with 524 genomes representing 21 SNP clusters, and 25 singletons. IV 48:g,z$_{51}$:- B contains 100 genomes representing 11 SNP clusters and 16 singletons. IV 48:g,z$_{51}$:- C contains 43 genomes representing 4 SNP clusters, and 14 singletons. IV 48:g,z$_{51}$:- D contains 4 genomes representing only 4 singletons. All the IV 48:g,z$_{51}$:- lineages are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *diarizonae* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each IV 48:g,z$_{51}$:- lineage with a bootstrap value higher than 0.7.

Supplementary Figure 46.   *S.* **IV 50:z$_4$,z$_{23}$:-**

Maximum likelihood phylogenetic tree for *S.* IV 50:z$_4$,z$_{23}$:-. *S.* IV 50:z$_4$,z$_{23}$:- is a polyphyletic serovar that contains four phylogenetic lineages (IV 50:z$_4$,z$_{23}$:- A, B, C, and D) along with one stand-alone singleton (IV 50:z$_4$,z$_{23}$:- S1). IV 50:z$_4$,z$_{23}$:- A is the largest lineage with 1,114 genomes representing 16 SNP clusters, and 37 singletons. IV 50:z$_4$,z$_{23}$:- B contains 5 genomes representing only 5 singletons. IV 50:z$_4$,z$_{23}$:- C contains 4 genomes representing only 4 singletons. IV 50:z$_4$,z$_{23}$:- D contains 3 genomes representing only 3 singletons. All the IV 50:z$_4$,z$_{23}$:- lineages are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *diarizonae* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each IV 50:z$_4$,z$_{23}$:- lineage with a bootstrap value higher than 0.7.

Supplementary Figure 47.   *S.* **Javiana**

Maximum likelihood phylogenetic tree for *S.* Javiana. *S.* Javiana is a monophyletic serovar with 16,637 genomes representing 634 SNP clusters, and 1,051 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Javiana lineage with a bootstrap value higher than 0.7.

Supplementary Figure 48.   *S.* **Johannesburg**

Maximum likelihood phylogenetic tree for *S.* Johannesburg. *S.* Johannesburg is a paraphyletic serovar that contains one phylogenetic lineage (Johannesburg) with 1,730 genomes representing 38 SNP clusters and 70 singletons. *S.* Urbana clusters within Johannesburg. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Johannesburg lineage with a bootstrap value higher than 0.7.

Supplementary Figure 49.   *S.* **Kedougou**

Maximum likelihood phylogenetic tree for *S.* Kedougou. *S.* Kedougou is a polyphyletic serovar that contains one phylogenetic lineage (Kedougou) along with one stand-alone singleton (shown as Kedougou S1). Kedougou lineage has 421 genomes representing 18 SNP clusters, and 25 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Kedougou lineage with a bootstrap value higher than 0.7.

Supplementary Figure 50.   *S.* **Kiambu**

Maximum likelihood phylogenetic tree for *S.* Kiambu. *S.* Kiambu is a polyphyletic serovar that contains one phylogenetic lineage (Kiambu) along with two stand-alone singletons (shown as Kiambu S1 and S2). Kiambu lineage has 767 genomes representing 32 SNP clusters, and 74 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 9. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence.

The orange stars represent the most recent common ancestor of Kiambu lineage with a bootstrap value higher than 0.7.

Supplementary Figure 51.   *S.* **Kottbus**

Maximum likelihood phylogenetic tree for *S.* Kottbus. *S.* Kottbus is a polyphyletic serovar that contains four phylogenetic lineages (Kottbus A, B, C, and D) along with two stand-alone singletons (Kottbus S1 and S2). Kottbus A is the largest lineage with 339 genomes representing 30 SNP clusters, and 46 singletons. Kottbus B contains 131 genomes representing 4 SNP clusters, and 4 singletons. Kottbus C contains 87 genomes representing 15 SNP clusters, and 47 singletons. Kottbus D contains 9 genomes representing 1 SNP cluster, and 4 singletons. All the four Kottbus lineages are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Kottbus lineage with a bootstrap value higher than 0.7.

Supplementary Figure 52.   *S.* **Litchfield**

Maximum likelihood phylogenetic tree for *S.* Litchfield. *S.* Litchfield is a polyphyletic serovar that contains two phylogenetic lineages (Litchfield A, and B). Litchfield A is the largest lineage with 2,032 genomes representing 135 SNP clusters, and 288 singletons. Litchfield B contains 10 genomes representing 1 SNP cluster, and 1 singleton. Both Litchfield A and B are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Litchfield lineage with a bootstrap value higher than 0.7.

Supplementary Figure 53.   *S.* **Liverpool**

Maximum likelihood phylogenetic tree for *S.* Liverpool. *S.* Liverpool is a polyphyletic serovar that contains one phylogenetic lineage (Liverpool) along with one stand-alone singleton (shown as Liverpool S1). Liverpool lineage has 617 genomes representing 13 SNP clusters, and 15 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 8. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Liverpool lineage with a bootstrap value higher than 0.7.

Supplementary Figure 54.   *S.* **Livingstone**

Maximum likelihood phylogenetic tree for *S.* Livingstone. *S.* Livingstone is a polyphyletic serovar that contains four phylogenetic lineages (Livingstone A, B, C, and D) along with one stand-alone singleton (Livingstone S1). Livingstone A is the largest lineage with 339 genomes representing 38 SNP clusters, and 45 singletons. Livingstone B contains 335 genomes representing 37 SNP clusters, and 50 singletons. Livingstone C contains 9 genomes representing 1 SNP cluster, and 5 singletons. Livingstone D contains 3 genomes representing only 3 singletons. Livingstone B and D are paraphyletic lineages since other non-Livingstone serovars cluster within this lineage. For example, *S.* Ohio clusters within Livingstone B. Livingstone A, and C are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 6. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Livingstone lineage with a bootstrap value higher than 0.7.

Supplementary Figure 55.   *S.* Lomalinda

Maximum likelihood phylogenetic tree for *S.* Lomalinda. *S.* Lomalinda is a polyphyletic serovar that contains two phylogenetic lineages (Lomalinda A, and B). Lomalinda A is the largest lineage with 388 genomes representing 11 SNP clusters, and 6 singletons. Lomalinda B contains 2 genomes representing only 2 singletons. Both Lomalinda A and B are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 10. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Lomalinda lineage with a bootstrap value higher than 0.7.

Supplementary Figure 56.   *S.* London

Maximum likelihood phylogenetic tree for *S.* London. *S.* London is a polyphyletic serovar that contains two phylogenetic lineages (London A, and B). London A is the largest lineage with 1,560 genomes representing 63 SNP clusters, and 57 singletons. London B contains 24 genomes representing 3 SNP clusters, and 13 singletons. Both London A and B are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each London lineage with a bootstrap value higher than 0.7.

Supplementary Figure 57.   *S.* Lubbock

Maximum likelihood phylogenetic tree for *S.* Lubbock. *S.* Lubbock is a monophyletic serovar with 440 genomes representing 19 SNP clusters, and 29 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Lubbock lineage with a bootstrap value higher than 0.7.

Supplementary Figure 58.   *S.* Manhattan

Maximum likelihood phylogenetic tree for *S.* Manhattan. *S.* Manhattan is a polyphyletic serovar that contains two phylogenetic lineages (Manhattan A, and B) along with four stand-alone singletons (Manhattan S1, S2, S3, and S4). Manhattan A is the largest lineage with 1,494 genomes representing 121 SNP clusters, and 277 singletons. Manhattan B contains 2 genomes representing only 2 singletons. Both Manhattan A and B are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Manhattan lineage with a bootstrap value higher than 0.7.

Supplementary Figure 59.   *S.* Mbandaka

Maximum likelihood phylogenetic tree for *S.* Mbandaka. *S.* Mbandaka is a polyphyletic serovar that contains one phylogenetic lineage (Mbandaka) along with one stand-alone singleton (shown as Mbandaka S1). Mbandaka lineage has 4,685 genomes representing 233 SNP clusters, and 330 singletons. Mbandaka is a paraphyletic lineage since other non-Mbandaka serovar clusters within this lineage (i.e. *S.* Lubbock clusters within Mbandaka). The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Mbandaka lineage with a bootstrap value higher than 0.7.

Supplementary Figure 60.   *S.* Meleagridis

Maximum likelihood phylogenetic tree for *S.* Meleagridis. *S.* Meleagridis is a polyphyletic serovar that contains one phylogenetic lineage (Meleagridis) along with one stand-alone singleton (shown as Meleagridis S1). Meleagridis lineage has 872 genomes representing 48 SNP clusters, and 52 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by

8. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Meleagridis lineage with a bootstrap value higher than 0.7.

Supplementary Figure 61.   *S.* **Miami**

Maximum likelihood phylogenetic tree for *S.* Miami. *S.* Miami is a polyphyletic serovar that contains seven phylogenetic lineages (Miami A, B, C, D, E, F and G). Miami A is the largest lineage with 947 genomes representing 114 SNP clusters, and 366 singletons. Miami B contains 108 genomes representing 12 SNP clusters, and 55 singletons. Miami C contains 29 genomes representing 4 SNP clusters, and 21 singletons. Miami D contains 15 genomes representing 3 SNP clusters, and 6 singletons. Miami E contains 6 genomes representing only 6 singletons. Miami F contains 6 genomes representing 1 SNP cluster, and 2 singletons. Miami G contains 5 genomes representing 1 SNP cluster, and 3 singletons. Miami C, D, and F are paraphyletic lineages since other non-Miami serovars cluster within these lineages. For example, *S.* Javiana clusters within Miami C. Miami A, B, E, and G are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Miami lineage with a bootstrap value higher than 0.7.

Supplementary Figure 62.   *S.* **Mikawasima**

Maximum likelihood phylogenetic tree for *S.* Mikawasima. *S.* Mikawasima is a polyphyletic serovar that contains three phylogenetic lineages (Mikawasima A, B, and C). Mikawasima A is the largest lineage with 663 genomes representing 45 SNP clusters, and 73 singletons. Mikawasima B contains 13 genomes representing 3 SNP clusters, and 4 singletons. Mikawasima C contains 3 genomes representing 1 SNP cluster, and 1 singleton. All three Mikawasima lineages are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 9. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Mikawasima lineage with a bootstrap value higher than 0.7.

Supplementary Figure 63.   *S.* **Minnesota**

Maximum likelihood phylogenetic tree for *S.* Minnesota. *S.* Minnesota is a monophyletic serovar with 792 genomes representing 75 SNP clusters, and 157 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 7. The Shimodaira-Hasegawa test with 1,000

resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Minnesota lineage with a bootstrap value higher than 0.7.

Supplementary Figure 64. *S.* **Mississippi**

Maximum likelihood phylogenetic tree for *S.* Mississippi. *S.* Mississippi is a polyphyletic serovar that contains three phylogenetic lineages (Mississippi A, B, and C). Mississippi A is the largest lineage with 4,597 genomes representing 582 SNP clusters, and 1,442 singletons. Mississippi B contains 435 genomes representing 28 SNP clusters, and 23 singletons. Mississippi C contains 33 genomes representing only 3 SNP clusters. All three Mississippi lineages are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Mississippi lineage with a bootstrap value higher than 0.7.

Supplementary Figure 65. *S.* **Montevideo**

Maximum likelihood phylogenetic tree for *S.* Montevideo. *S.* Montevideo is a polyphyletic serovar that contains three phylogenetic lineages (Montevideo A, B, and C). Montevideo A is the largest lineage with 7,608 genomes representing 487 SNP clusters, and 1,072 singletons. Montevideo B contains 8 genomes representing 1 SNP cluster, and 3 singletons. Montevideo C contains 2 genomes representing only 1 SNP cluster. Montevideo A is a paraphyletic lineage since other non-Montevideo serovar clusters within this lineage (i.e. *S.* Oranienburg clusters within Montevideo A). Montevideo B, and C are monophyletic lineages The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Montevideo lineage with a bootstrap value higher than 0.7.

Supplementary Figure 66. *S.* **Muenchen**

Maximum likelihood phylogenetic tree for *S.* Muenchen. *S.* Muenchen is a polyphyletic serovar that contains four phylogenetic lineages (Muenchen A, B, C, and D). Muenchen A is the largest lineage with 9,453 genomes representing 710 SNP clusters, and 2,948 singletons. Muenchen B contains 16 genomes representing 2 SNP clusters, and 12 singletons. Muenchen C contains 12 genomes representing 1 SNP cluster, and 7 singletons. Muenchen D contains 5 genomes representing only 1 SNP cluster. Muenchen A is a paraphyletic lineage since other non-Muenchen serovar clusters within these lineages (i.e. *S.* Manhattan clusters within Muenchen A). Muenchen B, C, and D are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-

Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Muenchen lineage with a bootstrap value higher than 0.7.

Supplementary Figure 67. *S.* **Muenster**

Maximum likelihood phylogenetic tree for *S.* Muenster. *S.* Muenster is a polyphyletic serovar that contains two phylogenetic lineages (Muenster A, and B) along with two stand-alone singletons (Muenster S1, and S2). Muenster A is the largest lineage with 1,947 genomes representing 103 SNP clusters, and 158 singletons. Muenster B contains 8 genomes representing 3 SNP clusters, and 2 singletons. Both Muenster A and B are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Muenster lineage with a bootstrap value higher than 0.7.

Supplementary Figure 68. *S.* **Napoli**

Maximum likelihood phylogenetic tree for *S.* Napoli. *S.* Napoli is a monophyletic serovar with 425 genomes representing 63 SNP clusters, and 207 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Napoli lineage with a bootstrap value higher than 0.7.

Supplementary Figure 69. *S.* **Newport**

Maximum likelihood phylogenetic tree for *S.* Newport. *S.* Newport is a polyphyletic serovar that contains four phylogenetic lineages (Newport A, B, C, and D). Newport A is the largest lineage with 23,633 genomes representing 694 SNP clusters, and 1,271 singletons. Newport B contains 14,230 genomes representing 732 SNP clusters, and 1,900 singletons. Newport C contains 509 genomes representing 44 SNP clusters, and 70 singletons. Newport D contains 5 genomes representing 1 SNP cluster, and 3 singletons. All four Newport lineages are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Newport lineage with a bootstrap value higher than 0.7.

Supplementary Figure 70. *S.* **Norwich**

Maximum likelihood phylogenetic tree for *S.* Norwich. *S.* Norwich is a monophyletic serovar with 1,412 genomes representing 38 SNP clusters, and 213 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Norwich lineage with a bootstrap value higher than 0.7.

Supplementary Figure 71.   *S.* Ohio

Maximum likelihood phylogenetic tree for *S.* Ohio. *S.* Ohio is a monophyletic serovar with 1,174 genomes representing 117 SNP clusters, and 111 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Ohio lineage with a bootstrap value higher than 0.7.

Supplementary Figure 72.   *S.* Oranienburg

Maximum likelihood phylogenetic tree for *S.* Oranienburg. *S.* Oranienburg is a polyphyletic serovar that contains ten phylogenetic lineages (Oranienburg A, B, C, D, E, F, G, H, I, and J) along with two stand-alone singletons (Oranienburg S1, and S2). Oranienburg A is the largest lineage with 7,436 genomes representing 733 SNP clusters, and 1,236 singletons. Oranienburg B contains 857 genomes representing 75 SNP clusters, and 165 singletons. Oranienburg C contains 231 genomes representing 33 SNP clusters, and 82 singletons. Oranienburg D contains 132 genomes representing 24 SNP clusters, and 28 singletons. Oranienburg E contains 35 genomes representing 8 SNP clusters, and 15 singletons. Oranienburg F contains 12 genomes representing 2 SNP clusters, and 8 singletons. Oranienburg G contains 11 genomes representing 1 SNP cluster, and 8 singletons. Oranienburg H contains 11 genomes representing 2 SNP clusters, and 1 singleton. Oranienburg I contains 10 genomes representing only 3 SNP clusters. Oranienburg J contains 3 genomes representing only 1 SNP cluster. Oranienburg D, E, and F are a paraphyletic lineage since other non-Oranienburg serovars cluster within these lineages. For example, *S.* Montevideo clusters within Oranienburg D. Oranienburg A, B, C, G, H, I and J are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Oranienburg lineage with a bootstrap value higher than 0.7.

Supplementary Figure 73.   *S.* Orion

Maximum likelihood phylogenetic tree for *S.* Orion. *S.* Orion is a polyphyletic serovar that contains two phylogenetic lineages (Orion A, and B) along with one stand-alone singleton (Orion S1). Orion A is the largest lineage with 386 genomes representing 39 SNP clusters, and 68 singletons. Orion B contains 8 genomes representing 1 SNP cluster, and 1 singleton. Both Orion A and B are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 9. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Orion lineage with a bootstrap value higher than 0.7.

Supplementary Figure 74.   ***S.* Oslo**

Maximum likelihood phylogenetic tree for *S.* Oslo. *S.* Oslo is a polyphyletic serovar that contains two phylogenetic lineages (Oslo A, and B) along with one stand-alone singleton (Oslo S1). Oslo A is the largest lineage with 559 genomes representing 74 SNP clusters, and 127 singletons. Oslo B contains 85 genomes representing 9 SNP clusters, and 16 singletons. Both Oslo A and B are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 9. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Oslo lineage with a bootstrap value higher than 0.7.

Supplementary Figure 75.   ***S.* Ouakam**

Maximum likelihood phylogenetic tree for *S.* Ouakam. *S.* Ouakam is a polyphyletic serovar that contains three phylogenetic lineages (Ouakam A, B, and C). Ouakam A is the largest lineage with 332 genomes representing 12 SNP clusters, and 17 singletons. Ouakam B contains 13 genomes representing 4 SNP clusters, and 2 singletons. Ouakam C contains 12 genomes representing 3 SNP clusters and 2 singletons. Ouakam B is a paraphyletic lineage since other non-Ouakam serovar clusters within this lineage (i.e. *S.* Fresno clusters within Ouakam B). Ouakam A, and C are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Ouakam lineage with a bootstrap value higher than 0.7.

Supplementary Figure 76.   ***S.* Panama**

Maximum likelihood phylogenetic tree for *S.* Panama. *S.* Panama is a monophyletic serovar with 3,062 genomes representing 330 SNP clusters, and 826 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one

genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Panama lineage with a bootstrap value higher than 0.7.

Supplementary Figure 77.   *S.* Paratyphi A

Maximum likelihood phylogenetic tree for *S.* Paratyphi A. *S.* Paratyphi A is a polyphyletic serovar that contains three phylogenetic lineages (Paratyphi A A, B, and C). Paratyphi A A is the largest lineage with 3,898 genomes representing 61 SNP clusters, and 65 singletons. Paratyphi A B contains 16 genomes representing only 1 SNP cluster. Paratyphi A C contains 2 genomes representing only 1 SNP cluster. All three Paratyphi A lineages are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Paratyphi A lineage with a bootstrap value higher than 0.7.

Supplementary Figure 78.   *S.* Paratyphi B

Maximum likelihood phylogenetic tree for *S.* Paratyphi B. *S.* Paratyphi B is a polyphyletic serovar that contains four phylogenetic lineages (Ouakam A, B, C, and D). Paratyphi B A is the largest lineage with 4,306 genomes representing 335 SNP clusters, and 563 singletons. Paratyphi B B contains 406 genomes representing 4 SNP clusters, and 16 singletons. Paratyphi B C contains 38 genomes representing 9 SNP clusters and 17 singletons. Paratyphi B D contains 23 genomes representing 5 SNP clusters and 10 singletons. Paratyphi B D is a paraphyletic lineage since other non-Paratyphi B serovar clusters within this lineage (i.e. *S.* Schleissheim clusters within Paratyphi B D). Paratyphi B A, B, and C are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 10. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Paratyphi B lineage with a bootstrap value higher than 0.7.

Supplementary Figure 79.   *S.* Pomona

Maximum likelihood phylogenetic tree for *S.* Pomona**.** *S.* Pomona is a polyphyletic serovar that contains two phylogenetic lineages (Pomona A, and B). Pomona A is the largest lineage with 572 genomes representing 46 SNP clusters, and 96 singletons. Pomona B contains 2 genomes representing 1 SNP cluster, and 1 singleton. Pomona A is a paraphyletic lineage since other non-Pomona serovar clusters within this lineage (i.e. *S.* Yarrabah clusters within Pomona A). Pomona B is a monophyletic lineage. The average pairwise number of nucleotide substitutions per site

was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 10. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Pomona lineage with a bootstrap value higher than 0.7.

Supplementary Figure 80.   *S.* Poona

Maximum likelihood phylogenetic tree for *S.* Poona. *S.* Poona is a paraphyletic serovar as other non-Poona serovar clusters within this serovar (i.e. *S.* Bristol clusters within serovar Poona). In total, *S.* Poona has 3,908 genomes representing 382 SNP clusters, and 800 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Poona lineage with a bootstrap value higher than 0.7.

Supplementary Figure 81.   *S.* Rissen

Maximum likelihood phylogenetic tree for *S.* Rissen. *S.* Rissen is a polyphyletic serovar that contains three phylogenetic lineages (Rissen A, B, and C) along with one stand-alone singleton (Rissen S1). Rissen A is the largest lineage with 1,226 genomes representing 74 SNP clusters, and 128 singletons. Rissen B contains 67 genomes representing 5 SNP clusters, and 11 singletons. Rissen C contains 3 genomes representing only 1 SNP cluster. Rissen B is a paraphyletic lineage since other non-Rissen serovars cluster within this lineage (i.e. *S.* Cubana and *S.* Tamberma cluster within Rissen B). Rissen A and C are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Rissen lineage with a bootstrap value higher than 0.7.

Supplementary Figure 82.   *S.* Rubislaw

Maximum likelihood phylogenetic tree for *S.* Rubislaw. *S.* Rubislaw is a polyphyletic serovar that contains two phylogenetic lineages (Rubislaw A, and B). Rubislaw A is the largest lineage with 2,787 genomes representing 243 SNP clusters, and 615 singletons. Rubislaw B contains 31 genomes representing 6 SNP clusters, and 9 singletons. Rubislaw A is a paraphyletic lineage since other non-Rubislaw serovar clusters within this lineage (i.e. *S.* Abaetetuba clusters within Rubislaw A). Rubislaw B is a monophyletic lineage. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome

belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Rubislaw lineage with a bootstrap value higher than 0.7.

Supplementary Figure 83. *S.* **Sandiego**

Maximum likelihood phylogenetic tree for *S.* Sandiego. *S.* Sandiego is a polyphyletic serovar that contains two phylogenetic lineages (Sandiego A, and B). Sandiego A is the largest lineage with 3,085 genomes representing 281 SNP clusters, and 856 singletons. Sandiego B contains 2 genomes representing only 2 singletons. Sandiego A is a paraphyletic lineage since other non-Sandiego serovar clusters within this lineage (i.e. *S.* Goettingen clusters within Sandiego A). Sandiego B is a monophyletic lineage. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Sandiego lineage with a bootstrap value higher than 0.7.

Supplementary Figure 84. *S.* **Schwarzengrund**

Maximum likelihood phylogenetic tree for *S.* Schwarzengrund. *S.* Schwarzengrund is a polyphyletic serovar that contains four phylogenetic lineages (Schwarzengrund A, B, C, and D) along with one stand-alone singleton (Schwarzengrund S1). Schwarzengrund A is the largest lineage with 4,335 genomes representing 115 SNP clusters, and 148 singletons. Schwarzengrund B contains 28 genomes representing 2 SNP clusters, and 2 singletons. Schwarzengrund C contains 4 genomes representing only 4 singletons. Schwarzengrund D contains 3 genomes representing 1 SNP cluster, and 1 singleton. Schwarzengrund C is a paraphyletic lineage since other non-Schwarzengrund serovars cluster within this lineage (i.e. *S.* Stockholm and *S.* Plymouth cluster within Schwarzengrund C). Schwarzengrund A, B, and D are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 9. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Schwarzengrund lineage with a bootstrap value higher than 0.7.

Supplementary Figure 85. *S.* **Senftenberg**

Maximum likelihood phylogenetic tree for *S.* Senftenberg. *S.* Senftenberg is a polyphyletic serovar that contains two phylogenetic lineages (Senftenberg A, and B) along with two stand-alone singletons (Senftenberg S1, and S2). Senftenberg A is the largest lineage with 3,705 genomes representing 211 SNP clusters, and 270 singletons. Senftenberg B contains 369

genomes representing 57 SNP clusters, and 84 singletons. Senftenberg A is a paraphyletic lineage since other non-Senftenberg serovar clusters within this lineage (i.e. *S.* Yoruba clusters within Senftenberg A). Senftenberg B is a monophyletic lineage. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 8. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Senftenberg lineage with a bootstrap value higher than 0.7.

Supplementary Figure 86.　　*S.* Stanley

Maximum likelihood phylogenetic tree for *S.* Stanley. *S.* Stanley is a polyphyletic serovar that contains two phylogenetic lineages (Stanley A, and B) along with two stand-alone singletons (Stanley S1, and S2). Stanley A is the largest lineage with 2,978 genomes representing 347 SNP clusters, and 647 singletons. Stanley B contains 2 genomes representing only 1 SNP cluster. Both Stanley A, and B are monophyletic lineages. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Stanley lineage with a bootstrap value higher than 0.7.

Supplementary Figure 87.　　*S.* Tennessee

Maximum likelihood phylogenetic tree for *S.* Tennessee. *S.* Tennessee is a polyphyletic serovar that contains two phylogenetic lineages (Tennessee A, and B). Tennessee A is the largest lineage with 893 genomes representing 118 SNP clusters, and 196 singletons. Tennessee B contains 16 genomes representing 2 SNP clusters, and 1 singleton. Tennessee A is a paraphyletic lineage since other non-Tennessee serovar clusters within this lineage (i.e. *S.* Tamberma clusters within Tennessee A). Tennessee B is a monophyletic lineage. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Tennessee lineage with a bootstrap value higher than 0.7.

Supplementary Figure 88.　　*S.* Thompson

Maximum likelihood phylogenetic tree for *S.* Thompson. *S.* Thompson is a polyphyletic serovar that contains four phylogenetic lineages (Thompson A, B, C, and D) along with one stand-alone singleton (Thompson S1). Thompson A is the largest lineage with 7,504 genomes representing 159 SNP clusters, and 268 singletons. Thompson B contains 568 genomes representing 50 SNP clusters, and 141 singletons. Thompson C contains 22 genomes representing 3 SNP clusters, and

5 singletons. Thompson D contains 3 genomes representing 1 SNP cluster, and 2 singletons. All four Thompson lineages are monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Thompson lineage with a bootstrap value higher than 0.7.

Supplementary Figure 89.   *S.* Typhi

Maximum likelihood phylogenetic tree for *S.* Typhi. *S.* Typhi is a monophyletic serovar with 13,735 genomes representing 410 SNP clusters, and 670 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 10. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Typhi lineage with a bootstrap value higher than 0.7.

Supplementary Figure 90.   *S.* Typhimurium

Maximum likelihood phylogenetic tree for *S.* Typhimurium. *S.* Typhimurium is a polyphyletic serovar that contains four phylogenetic lineages (Typhimurium A, B, C, and D). Typhimurium A is the largest lineage with 62,911 genomes which represent 2,979 SNP clusters, and 4,952 singletons. Typhimurium B contains 56 genomes which represent 12 SNP clusters, and 24 singletons. Typhimurium C contains 3 genomes, which are all singletons. Typhimurium D includes 2 genomes, which are all singletons. Typhimurium A, B, and C are paraphyletic since other non-Typhimurium serovars cluster within these lineages. For example, *S.* Heidelberg clusters within Typhimurium B. Finally, Typhimurium D is monophyletic. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Typhimurium lineage with a bootstrap value higher than 0.7.

Supplementary Figure 91.   *S.* Uganda

Maximum likelihood phylogenetic tree for *S.* Uganda. *S.* Uganda is a monophyletic serovar with 2,540 genomes representing 38 SNP clusters, and 62 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 100. The Shimodaira-Hasegawa test with 1,000

resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Uganda lineage with a bootstrap value higher than 0.7.

Supplementary Figure 92.   *S.* Urbana

Maximum likelihood phylogenetic tree for *S.* Urbana. *S.* Urbana is a paraphyletic serovar as other non-Urbana serovar clusters within this serovar (i.e. *S.* Johannesburg clusters within serovar Urbana). In total, *S.* Urbana has 613 genomes representing 59 SNP clusters, and 150 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 8. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Urbana lineage with a bootstrap value higher than 0.7.

Supplementary Figure 93.   *S.* Virchow

Maximum likelihood phylogenetic tree for *S.* Virchow. *S.* Virchow is a polyphyletic serovar that contains two phylogenetic lineages (Virchow A, and B). Virchow A is the largest lineage with 1,992 genomes representing 161 SNP clusters, and 291 singletons. Virchow B contains 422 genomes representing 42 SNP clusters, and 125 singletons. Virchow A is a paraphyletic lineage since other non-Virchow serovar clusters within this lineage (i.e. *S.* Colindale clusters within Virchow A). Virchow B is a monophyletic lineage. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 10. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of each Virchow lineage with a bootstrap value higher than 0.7.

Supplementary Figure 94.   *S.* Weltevreden

Maximum likelihood phylogenetic tree for *S.* Weltevreden. *S.* Weltevreden is a monophyletic serovar with 2,765 genomes representing 149 SNP clusters, and 360 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Weltevreden lineage with a bootstrap value higher than 0.7.

Supplementary Figure 95.   *S.* Worthington

Maximum likelihood phylogenetic tree for *S.* Worthington. *S.* Worthington is a polyphyletic serovar that contains one phylogenetic lineage (Worthington) along with one stand-alone singleton (shown as Worthington S1). Worthington lineage has 803 genomes representing 42

SNP clusters, and 49 singletons. The average pairwise number of nucleotide substitutions per site was used to report branch lengths. For rooting the tree, one genome belonging to *Salmonella enterica* subsp. *indica* was used as the outgroup and the branch length of the outgroup was shortened by 9. The Shimodaira-Hasegawa test with 1,000 resamples was used to assess the clustering confidence. The orange stars represent the most recent common ancestor of Worthington lineage with a bootstrap value higher than 0.7.