

Supplementary Figure Legends

Figure S1. Minimum spanning tree of STs using the Achtman 7-gene MLST scheme for 985 *Salmonella* Reading isolates. Three isolates (swine-, chicken-, and human-source) are not included because their STs could not be determined. Tree is colored based on isolate collection year. B-C)

Figure S2. Minimum spanning tree of STs using the EnteroBase core genome sequence typing (cgMLST) scheme allowing for up to A) two allelic differences and B) five allelic differences. Seven isolates (three turkey-source and four human-source) are not included because their cgMLST profiles could not be determined. Tree is colored based on isolate host source.

Figure S3. A-B) Box and whisker plots displaying the distribution of genome sizes in kilobases between A) Clades 1-3 of the all-host phylogenetic tree ($n = 988$) and B) the historical, contemporary, and emergent subclades of the turkey-source phylogenetic tree ($n = 565$). The upper and lower edges of the boxes correspond to the first and third quartiles, respectively, and the upper and lower whiskers extend to the largest and smallest values no further than $1.5 \times$ inter-quartile range. Data beyond these whiskers are considered outliers.

Figure S4. Clustering of turkey-source *S. Reading* isolates ($n = 565$) based on A) a phylogenetic tree based on variant sites in the core genome alignment (1072 core SNPs) and B) a complete linkage cluster dendrogram based on Euclidean distances of presence/absence of pan-genome genes. The inner green rings around both trees denote the collection year range of each isolate. The outer rings denote the core SNP-based phylogenetic tree clade designations from Figure 3.

Figure S5. The presence of the Col440II-like replicon in *Salmonella enterica* by serotype over time.

Figure S6. Presence-absence heatmap displaying the distribution of accessory genes across turkey-source isolates. Genes were identified by clustering coding sequences based on 95% sequence identity.

Figure S7. A-C) Genetic maps of bacteriophage regions of the *Salmonella* Reading genome based on representative genome assembly, SRR2407706. Maps consist primarily of genes identified in the pan-genome-wide association analysis (Figure 7), including A) phage region A, B) phage region B, and C) phage region C. Arrows indicate predicted genes and the direction of transcription and are colored to indicate predicted functional category based on PHASTER annotations.

Figure S8. A time-scaled phylogeny of turkey sequences ($n = 398$ after removal of duplicated sequences). Tips are annotated according to the main clades and the main nodes ages (HPD_{95%}) are indicated.

Figure S9. Phylogenetic tree of *Salmonella* Reading isolates from turkey ($n = 565$) and humans ($n = 250$) based on 1242 core SNPs in nonrecombinant genome regions. Only human-source isolates classified as part of the 2017-19 *S. Reading* outbreaks in the U.S. and Canada were included. The inner colored ring around the tree denotes the core SNP-based phylogenetic tree

clade designations (based on Figure 3). Colored stars indicate country of origin for each human-source isolate (USA- blue, Canada- red). The outer four rings denote the presence of genetic elements *sopE*, *uidA*, full *cirA*, frameshifted *cirA*, and truncated *cirA*. The tree is rooted with a turkey-source isolate collected in 2002 (SRR1195634).

Figure S10. Schematic depicting quality filtering steps within the bioinformatic processing pipeline. Thirty-three isolates were removed during filtering for a final sample size of 988 high-quality *Salmonella* Reading isolate genomes.