

CORRECTION

# Correction: Genomic Comparison of Non-Typhoidal Salmonella enterica Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky Isolates from Broiler Chickens

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There are errors in the published article. The isolate # 3172 ABBSB1189-1 (genome 14) was named as Enteritidis by mistake. The correct isolate should be Typhimurium.

Serotyping was incorrect for the isolate # 3193 ABBSB1050-2 (genome 13). It was incorrectly labeled as Enteritidis. The correct label should be Thompson.

These errors affect Figs [1C](#) and [2–7](#), [S3](#) and [S4](#) Figs, and [S1](#) and [S2](#) Tables. Please view correct versions of the files [here](#).

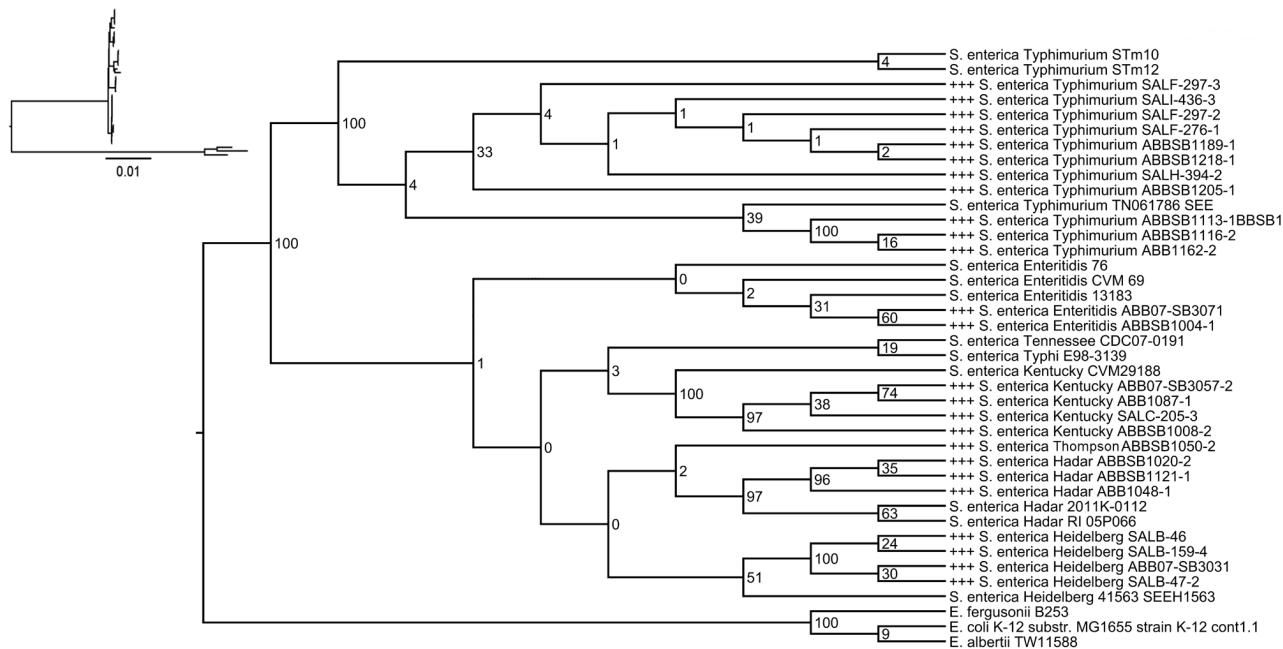


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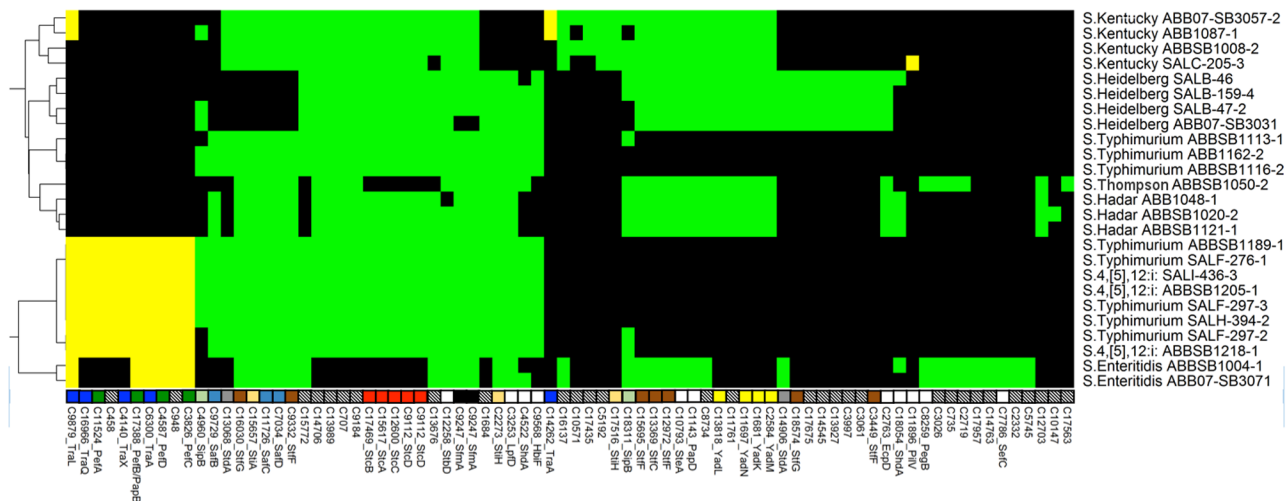
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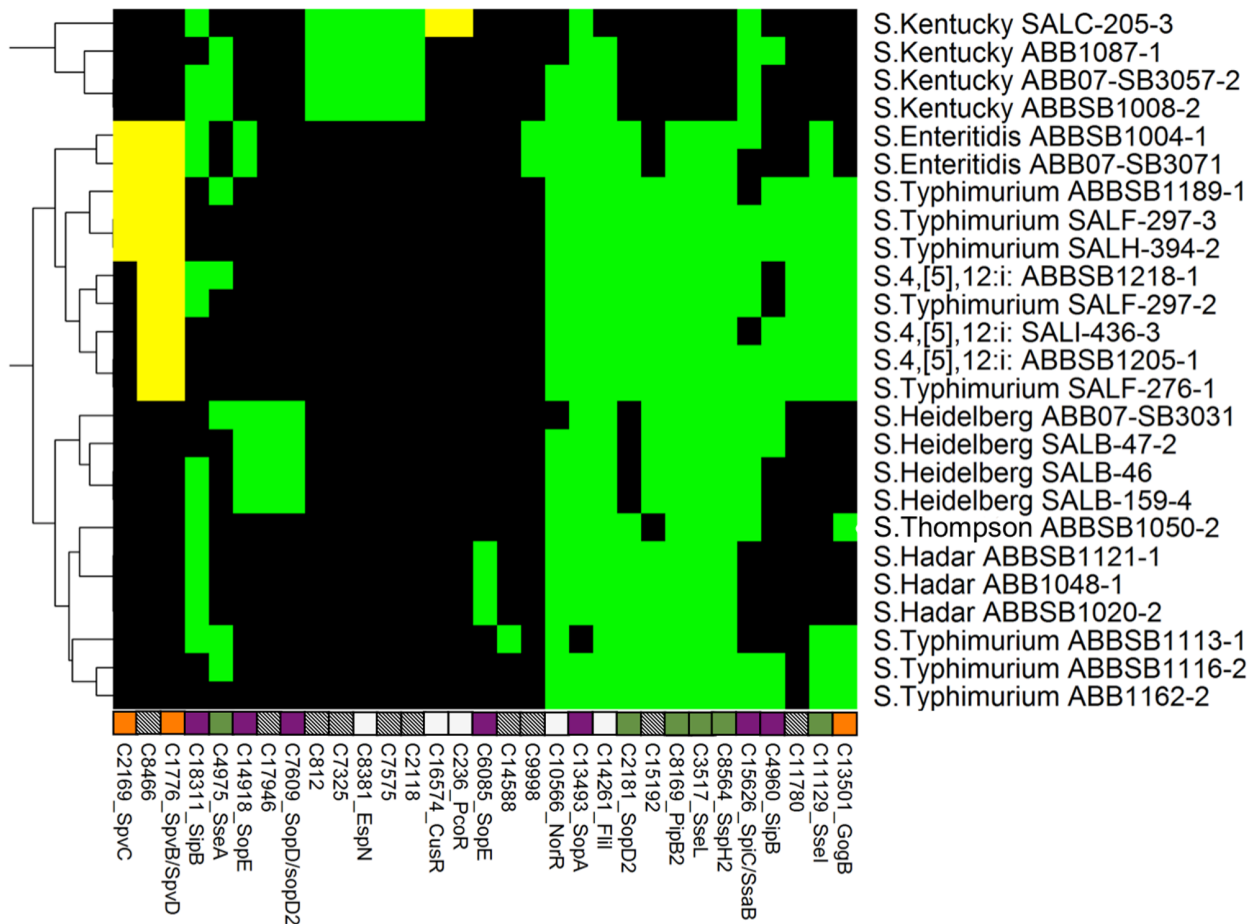
**Fig 1. Projected phylogeny of isolate genomes extracted from the full tree of *Escherichia* and *Salmonella* isolates (see S2 Fig).** Numbers at internal nodes correspond to bootstrap values supporting the indicated clades in the full tree. “+++” indicates newly sequenced isolates. Inset: pruned tree shown with branch lengths corresponding to substitutions per site.

doi:10.1371/journal.pone.0148706.g001



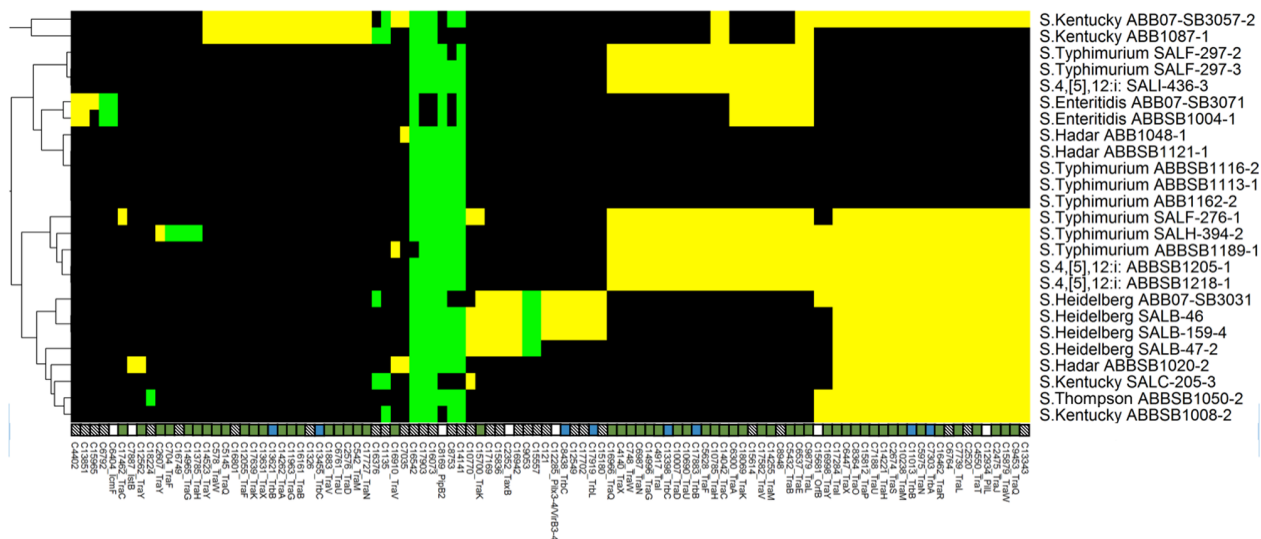
**Fig 2. Heatmap showing the distribution of 78 adhesion-associated proteins across the 25 newly sequenced *Salmonella* genomes.** Another 54 ubiquitous proteins are not shown. Column labels indicate unique cluster IDs (see S1 File), and gene names where appropriate. Black cells = absence of a gene from a given strain, green cells = probable chromosomal, yellow = probable plasmid. The tree on the left-hand side of the figure shows a hierarchical complete-linkage clustering of the profiles based on Euclidean distance. Multiple genes affiliated with the same operon are identified by coloured square boxes above the cluster legends. Empty boxes represent a single, independent cluster and boxes with patterns represent clusters without annotated gene names.

doi:10.1371/journal.pone.0148706.g002



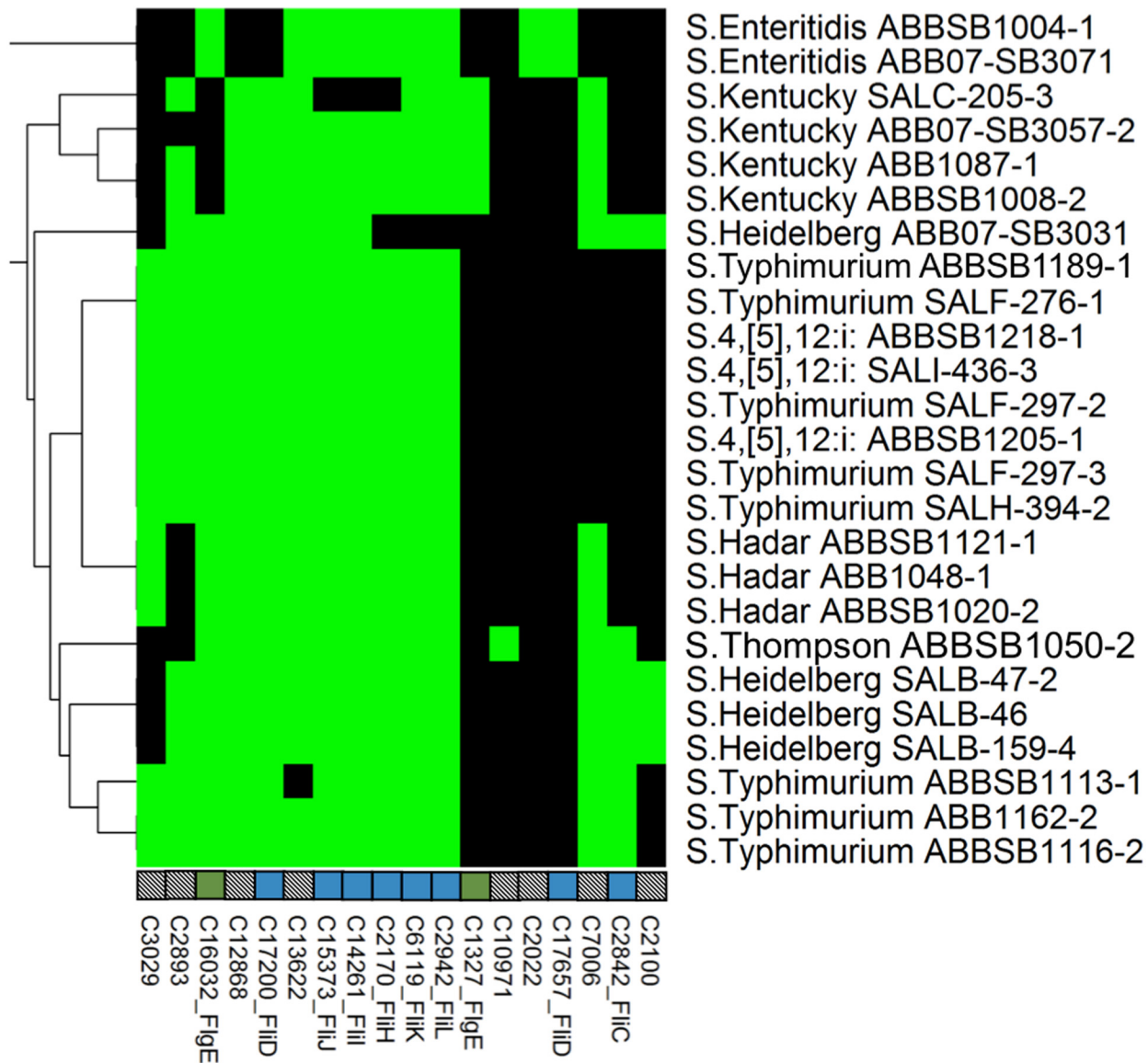
**Fig 3. Heatmap showing the distribution of 31 type 3 secretion system proteins.** Another 111 ubiquitous proteins are not shown. Labels, colors and clustering are consistent with Fig 2.

doi:10.1371/journal.pone.0148706.g003



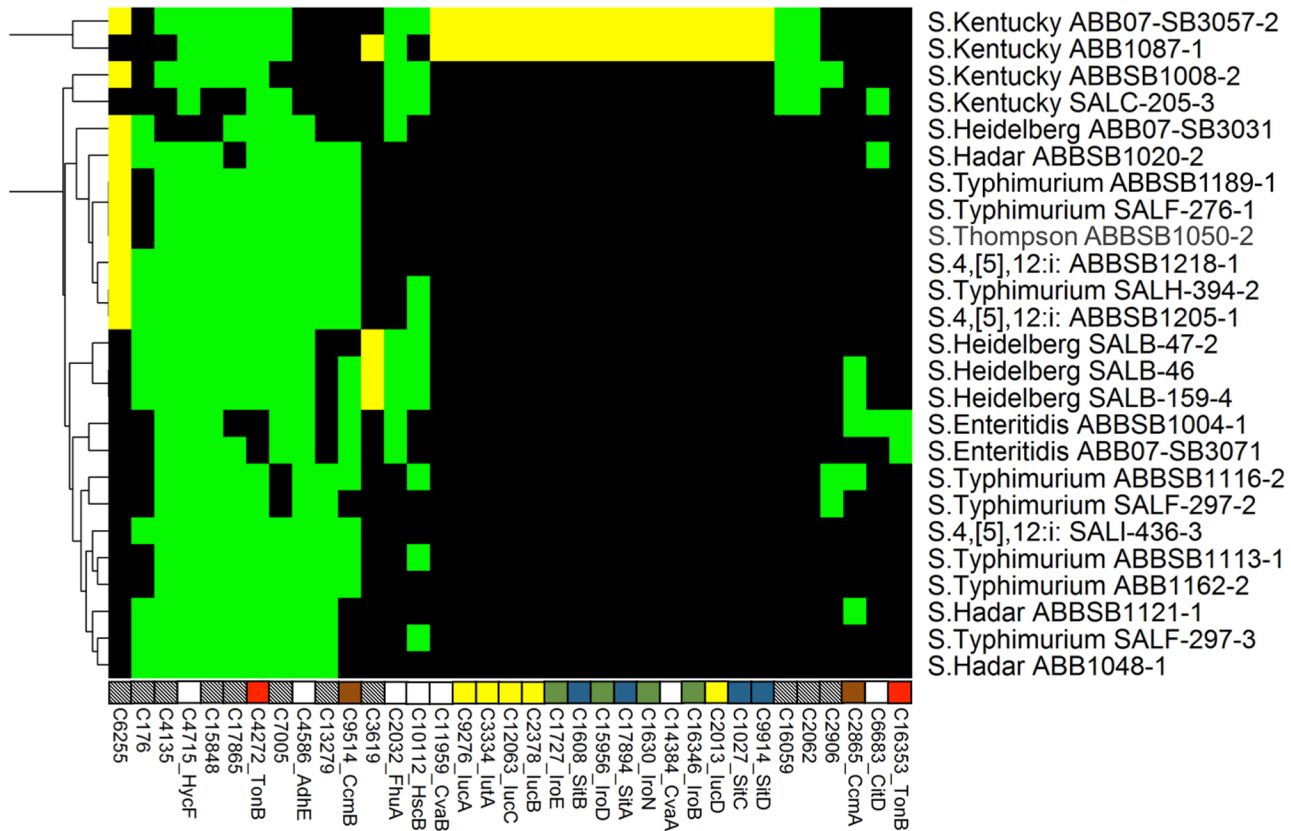
**Fig 4. Heatmap showing the distribution of 102 T4SS proteins.** Another 17 ubiquitous proteins are not shown. Labels, colors and clustering are consistent with Fig 2.

doi:10.1371/journal.pone.0148706.g004



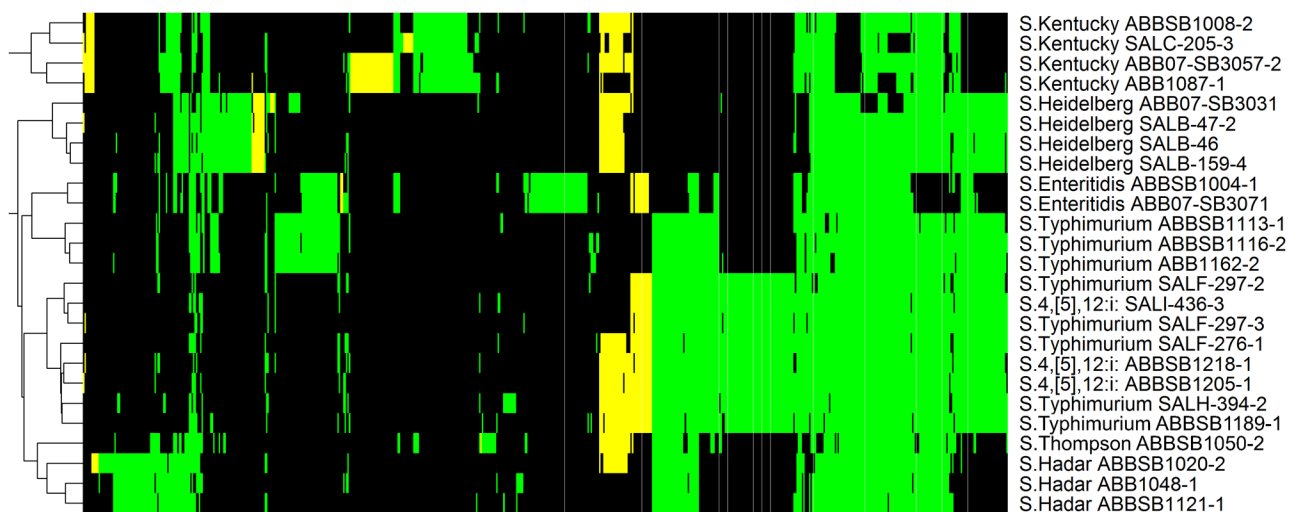
**Fig 5. Heatmap showing the distribution of 18 flagellar proteins.** Another 40 ubiquitous proteins are not shown. Labels, colors and clustering are consistent with Fig 2 (no flagellar proteins were predicted to be plasmid associated).

doi:10.1371/journal.pone.0148706.g005



**Fig 6. Heatmap showing the distribution of 35 iron resistance proteins.** Another 87 ubiquitous proteins are not shown. Labels, colors and clustering are consistent with Fig 2.

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**Fig 7. Heatmap of 647 proteins matching to the MVirDB database.** Another 784 ubiquitous proteins are not shown. Colors are consistent with Fig 2; column labels are shown in S4 Fig.

doi:10.1371/journal.pone.0148706.g007

## Supporting Information

**S3 Fig. Phylogenetic tree of all sequenced *Escherichia* and *Salmonella* isolates using the concatenated ribosomal genes with RAxML version 7.2.5-mpi.** The *Escherichia coli* clade is collapsed into a single branch. Numbers at internal nodes correspond to bootstrap support values. \*\*\* indicates the 25 newly sequenced *Salmonella* genomes of this study.

(TIFF)

**S4 Fig. Heatmap of all matches to MVirDB as shown in Fig 7, with cluster and gene names added.** Another 111 ubiquitous proteins are not shown. Labels and colors are consistent with Fig 2.

(TIFF)

**S1 Table. Assembly statistics for genomes sequenced in this study.**

(XLSX)

**S2 Table. Summary of inferred protein clusters, with unique ID, patterns of presence and absence across genomes from *Escherichia* and *Salmonella* isolates, aggregated names of homologous matches from these two genera, and statistics on the minimum, mean and maximum cluster length.**

(XLSX)

## Reference

1. Dhanani AS, Block G, Dewar K, Forgetta V, Topp E, Beiko RG, et al. (2015) Genomic Comparison of Non-Typhoidal *Salmonella enterica* Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky Isolates from Broiler Chickens. PLoS ONE 10(6): e0128773. PMID: [26083489](https://pubmed.ncbi.nlm.nih.gov/26083489/)