

Supplementary Figures

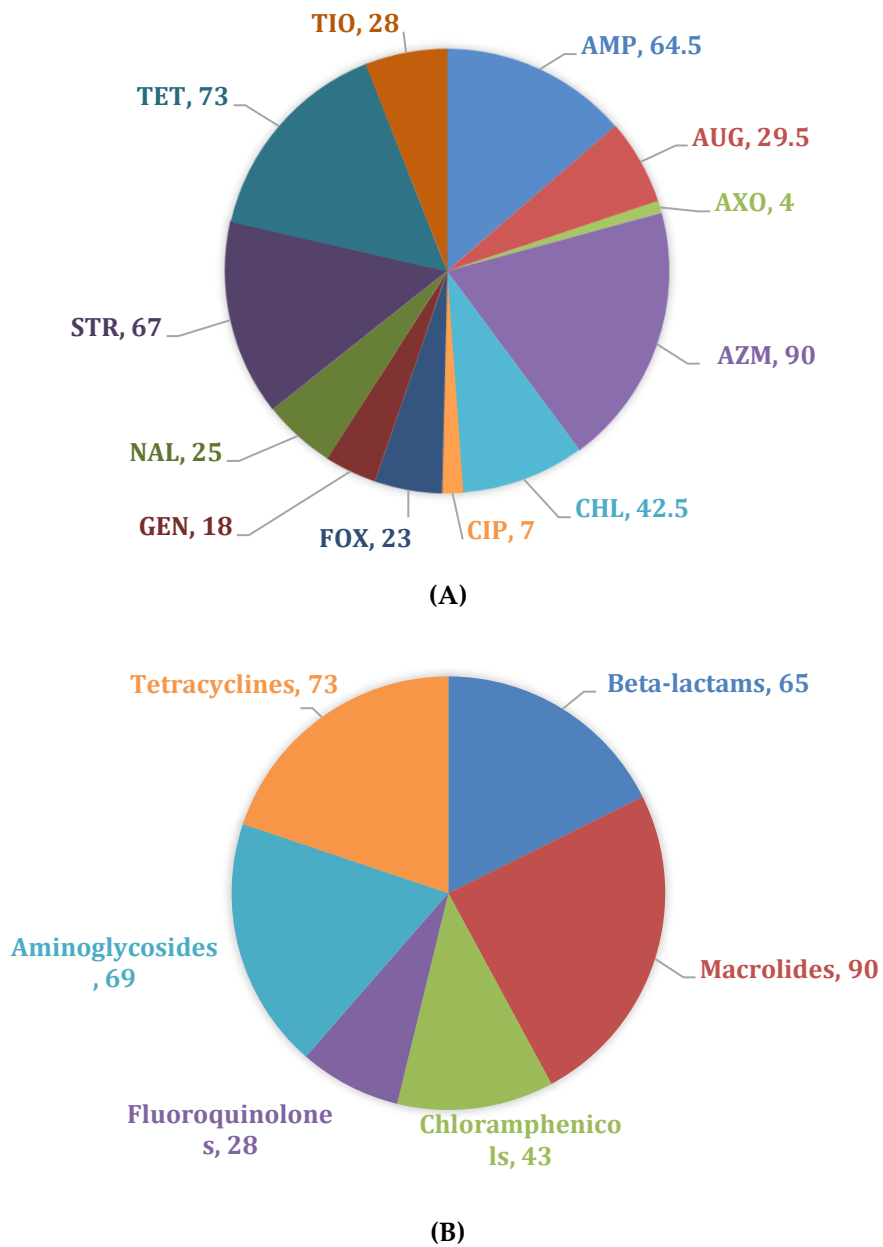
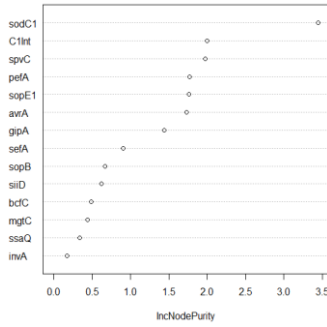
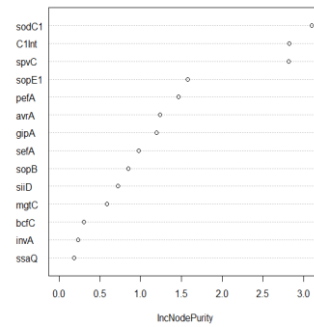


Figure S1. Antibiotic resistance distribution across all *Salmonella* isolates (n=211). A) Displays individual resistance status across all *Salmonella* isolates. B) Displays resistance status by class across all *Salmonella* isolates. **Key:** amoxicillin/clavulanic acid (AUG), ampicillin (AMP), azithromycin (AZM), cefoxitin (FOX), ceftiofur (TIO), ceftriaxone (AXO), chloramphenicol (CHL), ciprofloxacin (CIP), gentamicin (GEN), nalidixic acid (NAL), streptomycin (STR), and tetracycline (TET).

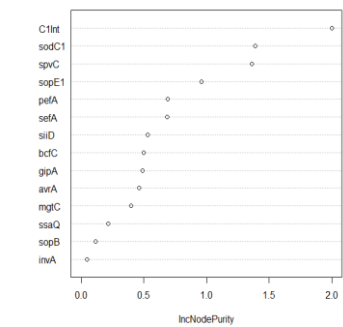
Supplementary Information



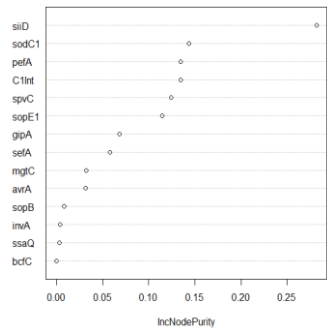
(A) Tetracyclines



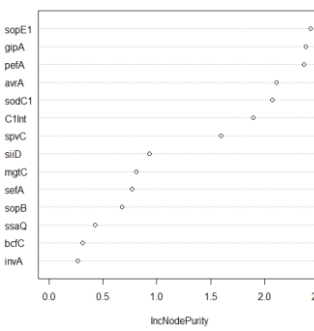
(B) Ampicillin



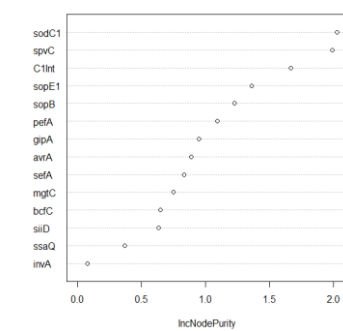
(C) Amoxicillin/Clavulanic Acid



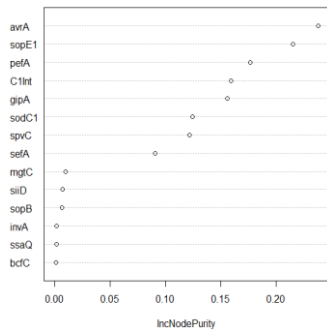
(D) Ceftriaxone



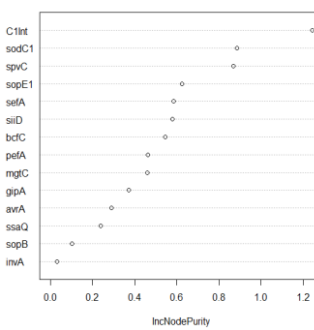
(E) Azithromycin



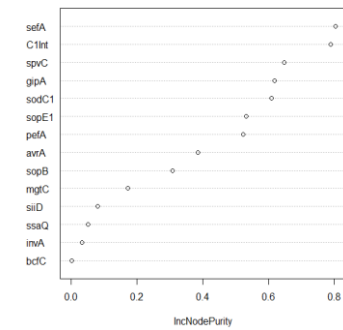
(F) Chloramphenicol



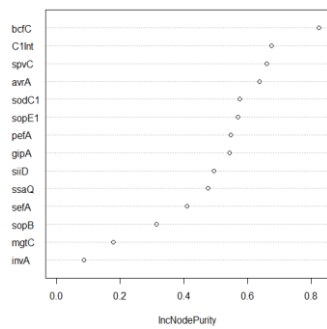
(G) Ciprofloxacin



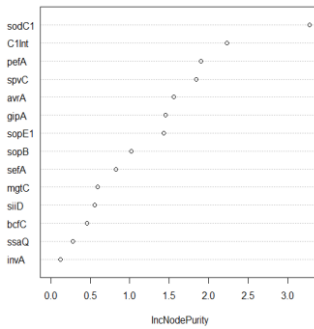
(H) Cefoxitin



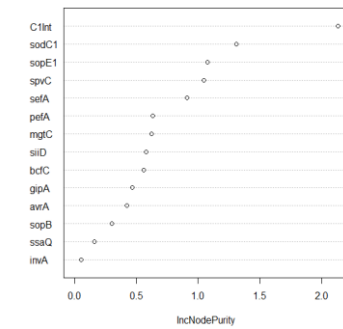
(I) Gentamicin



(J) Nalidixic Acid



(K) Streptomycin



(L) Ceftiofur

Figure S2. Random Forest analysis of association of virulence genes with resistance status by individual drug in *Salmonella* isolates (n=210). Along the Y axis indicates the importance score of each virulence gene. Virulence genes which are at top of the graph are the most important genes in determining resistance status (multidrug resistance, resistance to specific class of antibiotics, etc.). **A-L)** Displays a prediction of important genes for all isolates that have phenotypical resistance to a specific drug.

Supplementary Information

Supplementary Table S1. Virulence genes and the primers used for PCR-based virulotyping.

Genes	Location	Function	Primer sequence (5'-3')	Amplicon size (bp)	Reference
<i>avrA</i>	SPI-1, Centisome 63	Inhibits the key proinflammatory, antiapoptotic NF-kappa B pathway	CCTGTATTGTTGAGCGTCTGG AGAAGAGCTTCGTTGAATGTCC	422	[1]
<i>ssaQ</i>	SPI-2, Centisome 31-30, 5	Secretion system apparatus protein, component of second T3SS	GAATAGCGAATGAAGAGCGTCC CATCGTGTATCCTCTGTCAGC	455	[1]
<i>mgtC</i>	SPI-3, Centisome 82	Intramacrophage survival protein	TGACTATCAATGCTCCAGTGAAT ATTTACTGGCCGCTATGCTGTTG	677	[1]
<i>siiD</i>	SPI-4, Centisome 92	HLYD family secretion protein	GAATAGAAGACAAAGCGATCATC GCTTTGTCCACGCCTTTCATC	655	[1]
<i>sopB</i>	SPI-5, Centisome 20	Translocated effector protein via T3SS	TCAGAAGRCGTCTAACCCTC TACCGTCCTCATGCACACTC	517	[1]
<i>gipA</i>	Gifsy-1 bacteriophage	Peyer's patch-specific virulence factor	ACGACTGAGCAGGCTGAG TTGGAAATGGTGACGGTAGAC	518	[1]
<i>sodC1</i>	Gifsy-2 bacteriophage	Periplasmic Cu, Zn-superoxide dismutases	CCAGTGAGCAGGTTTATCG GGTGCGCTCATCAGTTGTTT	424	[1]
<i>sopE1</i>	Cryptic bacteriophage	Translocated T3SS effector protein	CGGGCAGTGTTGACAAATAAAG TGTTGGAATTGCTGTGGAGTC	422	[1]
<i>spvC</i>	Virulence pSLT plasmid	Spv region promotes rapid growth and survival within host	ACTCCTTGCACAACCAATGCGGA TGTCTTCTGCATTTGCGCCACC	467	[1]
<i>bcfC</i>	Chromosome, Fimbrial gene cluster	Bovine colonization factor, fimbrial usher	ACCAGAGACATTGCCTTCC TTCTGATCGCCGCTATTTCG	467	[1]
<i>invA</i>	SPI-1	Triggers internalization required for invasion of deep tissue cells	TTGTTACGGCTATTTTGACCA CTGACTGCTACCTTGCTGATG	521	[2,3]
<i>sefA</i>	Chromosome-encoded fimbrial operon	Encodes major subunit fimbrial protein of <i>S. Enterica</i> serotype	GCAGCGTTACTATTGCAGC TGTGACAGGGACATTTAGCG	330	[2,4]
<i>pefA</i>	Plasmid-encoded major fimbrial subunit	Fimbrial virulence gene of <i>S. Typhimurium</i>	TTCCATTATTGCACTGGGTG GGCATCTTTCGCTGTGGCTT	497	[2,5]
Class 1 Integrons	<i>Salmonella</i> genomic island 1	Associated with a variety of resistance gene cassettes	CGAACGAGTGGCGGAGGGTG TACCCGAGAGCTTGGCACCCA	312	[6,7]

Supplementary Information

Reference:

1. Huehn, S.; La Ragione, R.M.; Anjum, M.; Saunders, M.; Woodward, M.J.; Bunge, C.; Helmuth, R.; Hauser, E.; Guerra, B.; Beutlich, J., Virulotyping and antimicrobial resistance typing of *Salmonella enterica* serovars relevant to human health in Europe. *Foodborne Pathogens and Disease* **2010**, *7*, 523-535.
2. Cortez, A.; Carvalho, A.; Ikuno, A.; Bürger, K.; Vidal-Martins, A., Identification of *Salmonella* spp. isolates from chicken abattoirs by multiplex-PCR. *Research in veterinary science* **2006**, *81*, 340-344.
3. van der Velden, A.W.; Lindgren, S.W.; Worley, M.J.; Heffron, F., *Salmonella* pathogenicity island 1-independent induction of apoptosis in infected macrophages by *Salmonella enterica* serotype typhimurium. *Infect Immun* **2000**, *68*, 5702-5709.
4. Doran, J.L.; Collinson, S.K.; Clouthier, S.C.; Cebula, T.A.; Koch, W.H.; Burian, J.; Banser, P.A.; Todd, E.C.; Kay, W.W., Diagnostic potential of *sefA* DNA probes to *Salmonella enteritidis* and certain other O-serogroup D1 *Salmonella* serovars. *Mol Cell Probes* **1996**, *10*, 233-246.
5. Figueiredo, R.; Card, R.; Nunes, C.; AbuOun, M.; Bagnall, M.C.; Nunez, J.; Mendonca, N.; Anjum, M.F.; da Silva, G.J., Virulence Characterization of *Salmonella enterica* by a New Microarray: Detection and Evaluation of the Cytolethal Distending Toxin Gene Activity in the Unusual Host *S. Typhimurium*. *PLoS One* **2015**, *10*, e0135010.
6. Mulvey, M.R.; Boyd, D.A.; Olson, A.B.; Doublet, B.; Cloeckert, A., The genetics of *Salmonella* genomic island 1. *Microbes Infect* **2006**, *8*, 1915-1922.
7. Gillings, M.R.; Gaze, W.H.; Pruden, A.; Smalla, K.; Tiedje, J.M.; Zhu, Y.G., Using the class 1 integron-integrase gene as a proxy for anthropogenic pollution. *ISME J* **2015**, *9*, 1269-1279.