Supporting Information

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Category	**Class**	**Number of studies**	**Definition**
Reference		211	Publication identifier
Pathogen(s)			Pathogens for which the study reported data; must be *Campylobacter* spp., *E. coli*, and/or *Salmonella* spp. Other pathogens not included in meta-analysis
Campylobacter	0 – study did not report data on *Campylobacter* spp. 1 – study reported data on *Campylobacter* spp.	61	If study reported data on *Campylobacter* spp.
E. coli	0 – study did not report data on *E. coli* 1 – study reported data on *E. coli*	80	If study reported data on *E. coli*; generic or pathogenic
Salmonella	0 – study did not report data on *Salmonella* spp. 1 – study reported data on *Salmonella* spp.	134	If study reported data on *Salmonella* spp.
REJECTED?			Indicates if paper did not meet criteria 7–9; any papers not meeting criteria 1–6 for inclusion were excluded from the meta-data in Supplementary Data 1. (1) paper reported if one or more of the 431 North American breeding birds was/were tested for *Campylobacter* spp., *Escherichia coli*, and/or *Salmonella* spp.; (2) study presented primary data that were not duplicated from other studies included in the meta-analysis; (3) study identified bird species that provided sample (e.g. *Larus* spp. was not sufficient but *Larus argentatus* was); (4) study reported natural infections, i.e. no experimental infection data; (5) paper was in English, Spanish, or French or had all data extractable from English language abstract; and (6) birds had not been in captivity for more than 24 h at the start of the study (no farm, long-term rehabilitation centre, or laboratory animals). Data were further considered unsuitable for generating pathogen prevalence estimates but suitable for reporting presence/absence of bacteria if they: (7) reported only generic *E. coli*; (8) did not report number of individuals tested or positive (including only reporting number of isolates); or (9) only reported data on birds collected after death (excluding hunted birds which we assumed to be a random sample of wild bird populations) or were brought to a rehabilitation centre.

Source			Where paper was found; *Web of Science* search or within another publication
Substance tested			Written description of substances tested; N/A, not available
Blood	0 – substance not tested 1 – substance tested	15	Blood was tested for one or more bacteria included in the meta-analysis
Body surface	0 – substance not tested 1 – substance tested	3	The body surface (feathers, feet, etc.) was tested for one or more bacteria included in the meta-analysis
Intestines	0 – substance not tested 1 – substance tested	38	Whole intestines or extruded intestinal contents were tested for one or more bacteria included in the meta-analysis
Choana	0 – substance not tested 1 – substance tested	2	The choana was tested for one or more bacteria included in the meta-analysis
Cloacal swab	0 – substance not tested 1 – substance tested	81	Swab was inserted into cloaca and tested for one or more bacteria included in the meta-analysis
Faeces	0 – substance not tested 1 – substance tested	83	Faeces were tested for one or more bacteria included in the meta-analysis; excludes faecal matter recovered by squeezing a dissected intestine
Egg	0 – substance not tested 1 – substance tested	1	Egg surfaces or insides were tested for one or more bacteria included in the meta-analysis
Tissues	0 – substance not tested 1 – substance tested	44	Tissues (liver, pancreas, spleen, heart, etc.) were tested for one or more bacteria included in the meta-analysis
Pharynx	0 – substance not tested 1 – substance tested	8	Pharynx, larynx, or other throat area was tested for one or more bacteria included in the meta-analysis
Other	0 – substance not tested 1 – substance tested	5	Substance other than those listed above (e.g. bile, crop, lymph nodes, and nests) was tested for one or more bacteria included in the meta-analysis
N/A	0 – substance tested included 1 – substance tested not included	3	Not enough information to determine what substance was tested
Condition			Written description of bird condition upon testing; N/A, not available
Environmental	0 – birds not tested in condition	35	Faeces on ground upon collection; to be included in meta-analysis, researchers had to identify defecating species

	1 – birds tested in condition		
Hunted	0 – birds not tested in condition 1 – birds tested in condition	32	Hunters or researchers shot birds which were subsequently tested for bacteria
Live	0 – birds not tested in condition 1 – birds tested in condition	130	Live, healthy birds, captured using trapping or mist-netting
Necropsy	0 – birds not tested in condition 1 – birds tested in condition	33	Birds found dead and submitted for necropsy
Sick	0 – birds not tested in condition 1 – birds tested in condition	10	Bird showing signs of illness upon capture; birds admitted to rehabilitation centre for less than 24 h
N/A	0 – bird condition tested was listed 1 – bird condition tested was not listed	4	Not enough information to determine condition of bird upon testing
Test method			Written description of how individual birds were determined as positive or negative for individual bacteria included in meta-analysis
Agglutination	0 – study did not use method on 1+ bacteria 1 – study used method on 1+ bacteria	40	Bacterial identification confirmed using agglutination
Culture	0 – study did not use method on 1+ bacteria 1 – study used method on 1+ bacteria	190	Bacteria cultured
PCR	0 – study did not use method on 1+ bacteria 1 – study used method on 1+ bacteria	67	Bacterial identification confirmed using polymerase chain reaction (PCR) or bacterial presence/absence determined using PCR in rare cases
PFGE	0 – study did not use method on 1+ bacteria 1 – study used method on 1+ bacteria	22	Pulsed field gel electrophoresis (PGFE) used to compare isolates

Biochemical confirmation	0 – study did not use method on 1+ bacteria 1 – study used method on 1+ bacteria	111	Biochemical confirmation used to determine bacterial identification following culture
Sequencing	0 – study did not use method on 1+ bacteria 1 – study used method on 1+ bacteria	11	Some form of sequencing used to confirm bacterial identification or compare isolates; Multi-locus sequence typing (MLST), High Throughput Multi Locus Sequence Typing (HiMLST), Sanger sequencing, etc.
16S	0 – study did not use method on 1+ bacteria 1 – study used method on 1+ bacteria	10	16S gene used for bacterial identification
Serotyping	0 – study did not use method on 1+ bacteria 1 – study used method on 1+ bacteria	64	Bacterium sent for serotyping to confirm serovar
Necropsy	0 – study did not use method on 1+ bacteria 1 – study used method on 1+ bacteria	25	Morbid birds visually examined and dissected for signs of disease
ELISA	0 – study did not use method on 1+ bacteria 1 – study used method on 1+ b4acteria	7	Enzyme-linked immunosorbent assay (ELISA) used to test for antibodies to bacteria
Other	0 – study did not use method on 1+ bacteria 1 – study used method on 1+ bacteria	8	Other method used: Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), Vero cell cytotoxity assay, random amplified polymorphic DNA
N/A	0 – study listed method used 1 – study did not list method used	4	Not enough information to determine how study determined bacterial presence/absence
Setting			Written description of habitat type in which study was conducted; N/A, not available
Agriculture	0 – study did not test individuals from habitat type 1 – study tested individuals from habitat type	21	Non-livestock agriculture such as row cropping and orchards

Captivity	0 – study did not test individuals from habitat type 1 – study tested individuals from habitat type	2	Birds at rehabilitation centre tested upon admission
Livestock	0 – study did not test individuals from habitat type 1 – study tested individuals from habitat type	32	Livestock farm such as a concentrated animal feeding operation (CAFO) or chicken house
Natural	0 – study did not test individuals from habitat type 1 – study tested individuals from habitat type	36	Native habitat such as forest, wetland, grassland, etc.; does not include urban parks or beaches with surrounding native habitat
Urban	0 – study did not test individuals from habitat type 1 – study tested individuals from habitat type	77	Urban, suburban, or residential areas; includes urban parks
Open water	0 – study did not test individuals from habitat type 1 – study tested individuals from habitat type	39	Open or fast-moving water bodies such as large lakes, oceans, estuaries, bays, beaches, and rivers
Closed water	0 – study did not test individuals from habitat type 1 – study tested individuals from habitat type	17	Closed water bodies such as urban ponds and small lakes
Refuse	0 – study did not test individuals from habitat type 1 – study tested individuals from habitat type	14	Landfill site with human garbage
Sewage	0 – study did not test individuals from habitat type 1 – study tested individuals from habitat type	4	Waste water from humans or livestock
Zoo	0 – study did not test individuals from habitat type 1 – study tested individuals from habitat type	4	Wild birds tested within zoo grounds

N/A	0 – study listed habitat type 1 – study did not list habitat type	64	Study did not list habitat in which birds were tested or recovered from
Continent		Africa – 2 Asia – 12 Europe – 78 Europe and North America – 1 North America – 95 South America – 18 Zealandia – 5	Continent in which study took place
Country		Algeria – 1 Argentina – 1 Belgium – 2 Brazil – 8 Canada – 13 Canada, England, United States – 1 Chile – 6 Costa Rica – 1 Croatia – 2 Czech Republic – 5 Denmark – 3 Ecuador – 1 Egypt – 1 England – 15 Germany – 5 India – 2 Iran – 2 Ireland – 2 Italy – 8 Japan – 7 Lithuania – 1 Mexico – 2 New Zealand – 5 Norway – 4 Peru – 1 Poland – 7 Saudi Arabia – 1 Scotland – 2 Slovenia – 2 Spain – 9 Sweden – 6 The Netherlands	Country in which study took place

		and Poland – 1 Trinidad – 1 Turkey – 2 United States – 79 Wales – 2	
Lat			Approximate or exact latitude of study site
Long			Approximate or exact longitude of study site
Exact?	Yes – coordinates listed are exact study site location No – coordinates estimated due to lack of information	33 178	If study location is exact or estimated
Notes			Any notes on data acquisition or study
Salm_pos			Number of individuals from the 431 species examined that tested positive for *Salmonella* spp. that met criteria for inclusion 1–9
Salm_tested			Number of individuals from the 431 species examined that were tested for *Salmonella* spp. that met criteria for inclusion 1–9
Salm_prev	Proportion 0–1 N/A – no individuals tested		Overall study prevalence for individuals tested that met criteria for inclusion 1–9; Salm_pos/Salm_tested
Path_ecoli_pos			Number of individuals from the 431 species examined that tested positive for *E. coli* that met criteria for inclusion 1–9
Path_ecoli _tested			Number of individuals from the 431 species examined that were tested for *E. coli* that met criteria for inclusion 1–9
Path_ecoli _prev	Proportion 0–1 N/A – no individuals tested		Overall study prevalence for individuals tested that met criteria for inclusion 1–9; Path_ecoli_pos/Path_ecoli_tested
Campy_pos			Number of individuals from the 431 species examined that tested positive for *Campylobacter* spp. that met criteria for inclusion 1–9
Campy_tested			Number of individuals from the 431 species examined that were tested for *Campylobacter* spp. that met criteria for inclusion 1–9
Campy_prev	Proportion 0–1 N/A – no individuals tested		Overall study prevalence for individuals tested that met criteria for inclusion 1–9; Campy_pos/Campy_tested
Habitat (Exposure)	0 – study reported	22	Study tested individuals from multiple, listed habitat types and reported estimates by habitat location

	estimates in results 1 – study did not report estimates in results		
Landscape (Exposure)	0 – study reported estimates in results 1 – study did not report estimates in results	5	Study explicitly examined effects of landscape context on pathogen presence/absence or prevalence
Diet guild (Exposure)	0 – study reported estimates in results 1 – study did not report estimates in results	8	Study reported estimates of pathogen presence/absence or prevalence summarized by diet guild or gut content
Foraging traits (Exposure)	0 – study reported estimates in results 1 – study did not report estimates in results	4	Study reported estimates of pathogen presence/absence or prevalence for multiple foraging traits (not diet guild; foraging strata)
Movement ability (Exposure)	0 – study reported estimates in results 1 – study did not report estimates in results	6	Study reported pathogen presence/absence or prevalence for species divided into groups with differing movement or dispersal capacity; monitored daily movement capacity
Migratory pattern (Exposure)	0 – study reported estimates in results 1 – study did not report estimates in results	5	Study reported pathogen presence/absence or prevalence for birds divided into migratory strategy groups; migratory, partial migratory, long distance migratory, short distance migratory, resident
Taxa (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	2	Paper conducts statistical analysis comparing pathogen presence/absence or prevalence by bird taxonomic order or family
Sex (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	15	Study summarized pathogen presence/absence or prevalence by sex; reported positive and negative individuals by sex

Age (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	29	Study reported pathogen presence/absence or prevalence by individual's age; hatch year, after-hatch year, juvenile, adult, nestling; reported positive and negative individuals by age
Condition (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	15	Study reported pathogen presence/absence or prevalence in relation to individual's condition or conducted statistical analyses on a condition gradient including body size, mass, etc.; mentioning general appearance and condition not sufficient
Microbiome (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	0	Study reported impacts of microbiome diversity or composition on pathogen presence/absence or prevalence
Coinfection (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	23	Study reported coinfection data for one or more pathogens in one or more wild bird species included in meta-analysis; could include coinfection of meta-analysis pathogen with non-meta-analysis pathogen
Immunity (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	0	Study estimated impacts of innate or acquired immunity on pathogen presence/absence or prevalence
Infectious dose (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	0	Study quantified infectious dose required for shedding or disease in wild birds
Shedding amount (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	13	Study quantified the number of microorganisms included in meta-analysis that were shed in faeces
Shedding duration (Reservoir competence)	0 – study reported estimates in results	5	Study examined duration of pathogen shedding or reported carrier state at various capture times

	1 – study did not report estimates in results		
Species/serovar (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	143	Study identified bacteria to *Campylobacter* species or *Salmonella* serovar; did not stop at genus
Strain (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	80	Study identified bacterial strain; would include *E. coli* O157:H7 but not *E. coli* with *stx*1; would include *S.* Typhimurium ST40 but not *S.* Typhimurium which would be under species/serovar
Ability of strain to colonize (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	1	Study inoculated wild birds with one or more strains and examined differential ability to colonize or cause disease
Virulence (Reservoir competence)	0 – study reported estimates in results 1 – study did not report estimates in results	8	Study tested virulence of bacteria to wild birds or livestock through inoculation, mark–recapture, population changes, or other survival metric
Faecal output (Contact)	0 – study reported estimates in results 1 – study did not report estimates in results	4	Study quantified faecal output per unit time of wild birds or used published estimates in analyses
Direct contact (Contact)	0 – study reported estimates in results 1 – study did not report estimates in results	9	Study quantified direct contact rates of wild birds with livestock, humans, produce, etc. by indexing abundance or contact frequency in sensitive areas
Indirect contact (Contact)	0 – study reported estimates in results 1 – study did not report estimates in results	6	Study quantified faecal contamination in water, ability to mechanically vector, or contact of non-avian mechanical vectors with faeces
Seasonality (Contact)	0 – study reported	45	Study examined seasonal variation in pathogen prevalence, shedding intensity, etc.

	estimates in results 1 – study did not report estimates in results		
Survival in faeces (Bacterial survival and transmission)	0 – study reported estimates in results 1 – study did not report estimates in results	1	Study examined survival of pathogen in faeces; inoculated or naturally occurring bacteria
Other survival (Bacterial survival and transmission)	0 – study reported estimates in results 1 – study did not report estimates in results	0	Study examined survival of pathogen in water, compost, soil, etc.
Crossover (Bacterial survival and transmission)	0 – study reported estimates in results 1 – study did not report estimates in results	49	Study attempted to demonstrate crossover of pathogens between wild birds and people, livestock, zoo animals, and/or domestic pets by presenting pathogen data from wild birds and people, livestock, zoo animals, and/or domestic pets (beyond citing literature)
Shared strains (Bacterial survival and transmission)	0 – study reported estimates in results 1 – study did not report estimates in results	25	Study quantifies wild bird bacterial strain similarity to bacterial strains found in humans, livestock, domestic pets, etc. using genetic approach to examine crossover robustly
Antibiotic resistance (Bacterial survival and transmission)	0 – study did not test for antibiotic resistance 1 – study tested for antibiotic resistance	60	Study tested for antibiotic resistance in one or more bacteria recovered from one or more individual birds in study
Outbreak (Bacterial survival and transmission)	0 – study reported estimates in results 1 – study did not report estimates in results	1	Study robustly isolated wild bird faeces as cause of human foodborne illness outbreak

Table S2. List of variables used in Supplementary Data S2.

Category	**Class**	**Definition**
AOU		American Ornithologists' Union four-letter code for species (https://www.birdpop.org/docs/misc/Alpha_codes_tax.pdf)
Common_name		Species common name following American Ornithologist's Union
Scientific		Scientific name following Birds of North America Online (last searched November 2018)
Order		Scientific order following Birds of North America Online (last searched November 2018)
Family		Scientific family following Birds of North America Online (last searched November 2018)
Diet	Carnivore – reptiles, amphibians, birds, mammals Frugivore – fruits, drupes Granivore – seeds, maize, nuts, grains, spores Herbivore – grass, ground vegetation, weeds, vegetables, fungi, aquatic vegetation, etc. Invertebrate – aquatic invertebrates, ground insects, insect larvae, flying insects, etc. Nectarivore – nectar, pollen, plant exudates, gums Omnivore – ≤ 50% in all four binned categories in Wilman *et al*. (2014) Piscivore – fish Scavenger – garbage, carcasses, carrion	Classified as guild if diet category represents ≥ 60% of content Diet guild as classified by Wilman *et al*. (2014), Birds of North America Online, de Graff *et al*. (1985), and Smith *et al*. (2019) http://www.esapubs.org/archive/ecol/E095/178/metadata.php http://birdsna.org
Forg_strat	Aerial – foraging in air; doesn't include sallying from perch Canopy – foraging in tree canopy Ground – on ground Midhigh – mid-high levels in trees or bushes (2 m to just below canopy)	Foraging strata; classified as highest percentage of foraging time in strata estimated in Wilman *et al*. (2014), Birds of North America Online, and de Graff *et al*. (1985) http://www.esapubs.org/archive/ecol/E095/178/metadata.php http://birdsna.org

	Understorey – below 2 m in understorey Wataroundsurf – foraging on or just (<12.5 cm) below water surface Watbelowsurf – foraging below water surface	
Campy_pos		Number of individuals testing positive for any *Campylobacter* spp. across all studies in meta-analysis that met inclusion criteria 1–9
Canadensis		Number of individuals testing positive for *Campylobacter canadensis* across all studies in meta-analysis that met inclusion criteria 1–9
Coli		Number of individuals testing positive for *Campylobacter coli* across all studies in meta-analysis that met inclusion criteria 1–9
Jejuni		Number of individuals testing positive for *Campylobacter jejuni* across all studies in meta-analysis that met inclusion criteria 1–9
Lari		Number of individuals testing positive for *Campylobacter lari* across all studies in meta-analysis that met inclusion criteria 1–9
Campy_tested		Number of individuals tested for any *Campylobacter* spp. across all studies in meta-analysis that met inclusion criteria 1–9
Campy_prev	Proportion 0–1 N/A – no individuals tested	Campy_pos/Campy_tested; *Campylobacter* spp. prevalence across all studies in meta-analysis that met inclusion criteria 1–9
Campy_prev_rma.mv	Proportion 0-1 N/A – not calculated	Estimated *Campylobacter* spp. prevalence using random effects models in the rma.mv function in the metafor package in R (Viechtbauer, 2010; R Core Team, 2018) including study as a random effect. Only calculated when data came from two or more studies and we estimated that sufficient observations were available based on the Thrusfield (2007) formula
Campy_prev_se_rma.mv	Proportion 0–1 N/A – not calculated	Standard error of estimated *Campylobacter* spp. prevalence using random effects models in the rma.mv function in the metafor package in R
Campy_studies		Number of studies that tested for any *Campylobacter* spp. across all studies in meta-analysis that met inclusion criteria 1–9
Campy_total_pos		Number of individuals testing positive for any *Campylobacter* spp. across all studies in meta-analysis that met inclusion criteria 1–6
Campy_total_tested		Number of individuals tested for any *Campylobacter* spp. across all studies in meta-analysis that met inclusion criteria 1–6
Campy_yes	Yes – one or more individuals of bird species tested positive for *Campylobacter* spp. No – no *Campylobacter* spp. found in bird species	If one or more individuals tested positive for *Campylobacter* spp. across all studies in meta-analysis that met inclusion criteria 1–9

Campy_resistant	Yes – one or more individuals of bird species had *Campylobacter* spp. that was antibiotic resistant No – no *Campylobacter* spp. with antibiotic resistance found in bird species tested for antibiotic resistance N/A – no *Campylobacter* spp. tested for antibiotic resistance in bird species	If antibiotic resistance was found in *Campylobacter* spp. from bird species
Path_ecoli_pos		Number of individuals testing positive for pathogenic *E. coli* across all studies in meta-analysis that met inclusion criteria 1–9
Generic_ecoli_pos		Number of individuals testing positive for generic *E. coli* across all studies in meta-analysis that met inclusion criteria 1–6 and 8–9
Path_ecoli_tested		Number of individuals tested for pathogenic *E. coli* across all studies in meta-analysis that met inclusion criteria 1–9
Generic_ecoli_tested		Number of individuals tested for generic *E. coli* across all studies in meta-analysis that met inclusion criteria 1–6 and 8–9
Path_ecoli_prev	Proportion 0–1 N/A – no individuals tested	Path_ecoli_pos/Path_ecoli_tested; pathogenic *E.coli* prevalence across all studies in meta-analysis that met inclusion criteria 1–9
Path_ecoli_prev_rma.mv	Proportion 0–1 N/A – not calculated	Estimated *Campylobacter* spp. prevalence using random effects models in the rma.mv function in the metafor package in R (Viechtbauer, 2010; R Core Team, 2018) including study as a random effect. Only calculated when data came from two or more studies and we estimated that sufficient observations were available based on the Thrusfield (2007) formula
Path_ecoli_prev_se_rma.mv	Proportion 0–1 N/A – not calculated	Standard error of estimated *Campylobacter* spp. prevalence using random effects models in the rma.mv function in the metafor package in R
Generic_ecoli_prev	Proportion 0–1 N/A – no individuals tested	Generic_ecoli_pos/Generic_ecoli_tested; pathogenic *E.coli* prevalence across all studies in meta-analysis that met inclusion criteria 1–6 and 8–9
Path_ecoli_studies		Number of studies that tested for pathogenic *E. coli* across all studies in meta-analysis that met inclusion criteria 1–9
Generic_ecoli_studies		Number of studies that tested for generic *E. coli* across all studies in meta-analysis that met inclusion criteria 1–6 and 8–9
Path_ecoli_tot_pos		Number of individuals testing positive for pathogenic *E. coli* across all studies in meta-analysis that met inclusion criteria 1–9
Path_ecoli_tot_tested		Number of individuals tested for pathogenic *E. coli* across all studies in meta-analysis that met inclusion criteria 1–9

Path_ecoli_yes	Yes – one or more individuals of bird species tested positive for pathogenic *E. coli* spp. No – no pathogenic *E. coli* found in bird species	If one or more individual tested positive for pathogenic *E. coli* across all studies in meta-analysis that met inclusion criteria 1–6 and 8–9
Generic_ecoli_resistant	Yes – one or more individuals of bird species had *E. coli* that was antibiotic resistant No – no *E. coli* with antibiotic resistance found in bird species tested for antibiotic resistance N/A – no *E. coli* tested for antibiotic resistance in bird species	If antibiotic resistance was found in *E. coli* from bird species
Ecoli_test_any		Number of individuals tested for *E. coli* across all studies in meta-analysis
Salm_pos		Number of individuals testing positive for any *Salmonella* spp. across all studies in meta-analysis that met inclusion criteria 1–9
Salm_tested		Number of individuals tested for any *Salmonella* spp. across all studies in meta-analysis that met inclusion criteria 1–9
Salm_prev	Proportion 0–1 N/A – no individuals tested	Salm_pos/Salm_tested; *Salmonella* spp. prevalence across all studies in meta-analysis that met inclusion criteria 1–9
Salm_prev_rma.mv	Proportion 0–1 N/A – not calculated	Estimated *Salmonella* spp. prevalence using random effects models in the rma.mv function in the metafor package in R (Viechtbauer, 2010; R Core Team, 2018) including study as a random effect. Only calculated when data came from two or more studies and we estimated that sufficient observations were available based on the Thrusfield (2007) formula
Salm_prev_se_rma.mv	Proportion 0–1 N/A – not calculated	Standard error of estimated *Salmonella* spp. prevalence using random effects models in the rma.mv function in the metafor package in Program R
Salm_studies		Number of studies that tested for any *Salmonella* spp. across all studies in meta-analysis that met inclusion criteria 1–9
Salm_total_pos		Number of individuals testing positive for any *Salmonella* spp. across all studies in meta-analysis that met inclusion criteria 1–6
Salm_total_tested		Number of individuals tested for any *Salmonella* spp. across all studies in meta-analysis that met inclusion criteria 1–6
Salm_yes	Yes – one or more individuals of bird species tested positive for *Salmonella* spp.	If one or more individuals tested positive for *Salmonella* spp. across all studies in meta-analysis that met inclusion criteria 1–9

	No – no *Salmonella* spp. found in bird species	
Salm_resistant	Yes – one or more individuals of bird species had *Salmonella* spp. that was antibiotic resistant No – no *Salmonella* spp. with antibiotic resistance found in bird species tested for antibiotic resistance N/A – no *Salmonella* spp. tested for antibiotic resistance in bird species	If antibiotic resistance was found in *Salmonella* spp. from bird species
Abony to 11:d-		Number of individuals testing positive for *Salmonella* serovar named in column across all studies in meta-analysis that met inclusion criteria 1–9

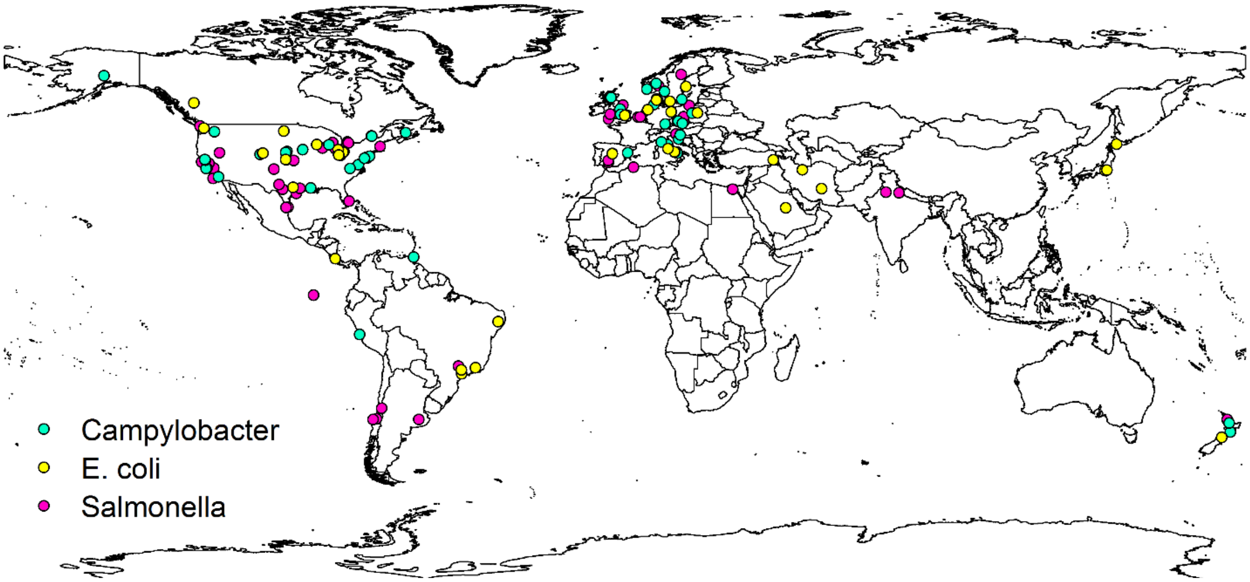

Fig. S1. Map showing locations of studies (*N* = 211) used in meta-analysis.

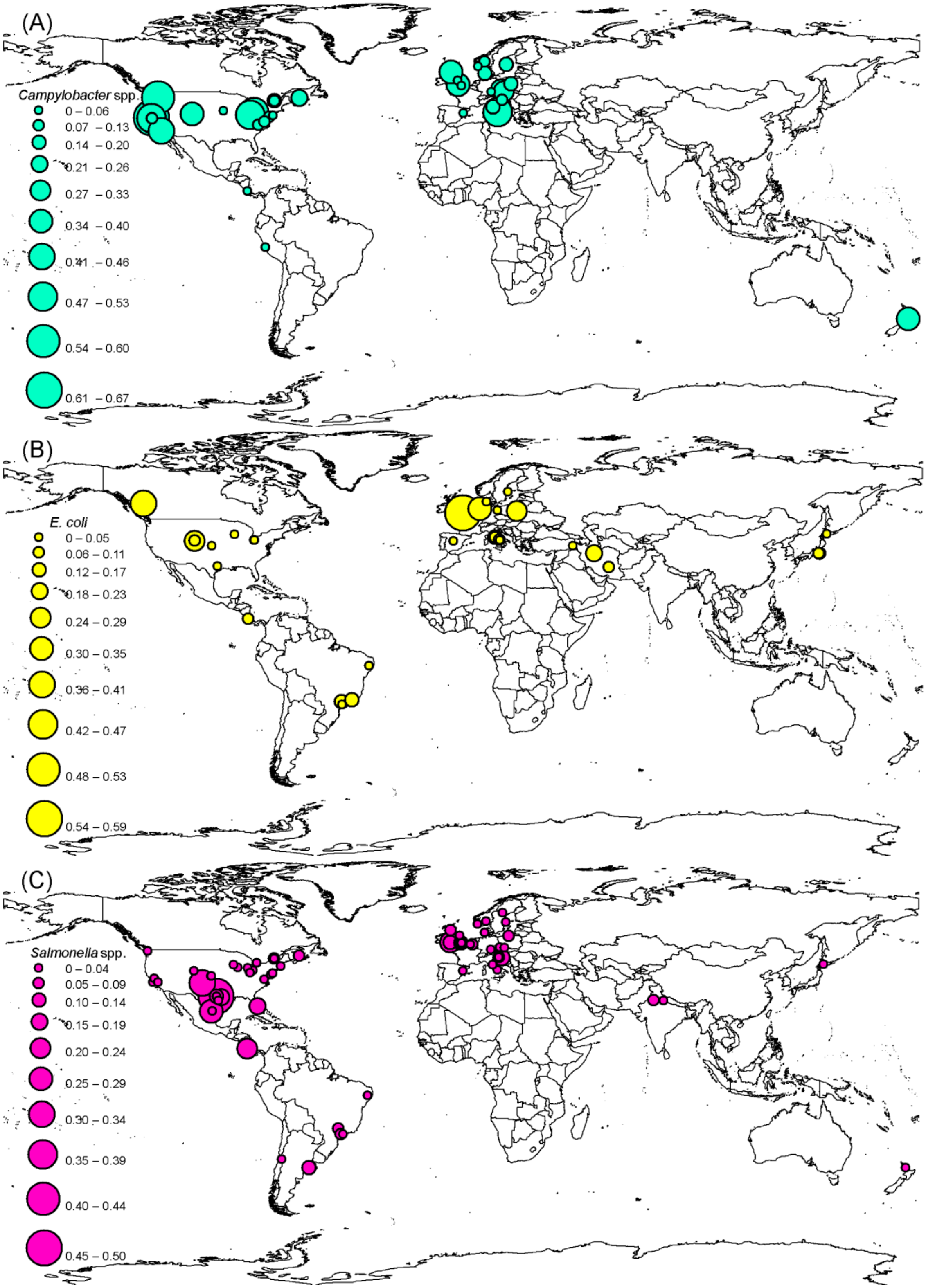

Fig. S2. Map showing number of samples positive/number of samples tested for (A) *Campylobacter* spp., (B) pathogenic *E. coli*, and (C) *Salmonella* spp. by study location.

Table S3. List of variables used in Supplementary Data S3. One tab is included for data on each of *Campylobacter* spp., pathogenic *E. coli*, generic *E. coli*, and *Salmonella* spp. (4 tabs in total).

Category	**Class**	**Definition**
Study		Publication identifier
Species		American Ornithologists' Union four-letter code for species https://www.birdpop.org/docs/misc/Alpha_codes_tax.pdf
Positive		Number of individual samples that tested positive for bacteria for that species in that study
Negative		Number of individual samples that tested negative for bacteria for that species in that study
Tested		Total number of individual samples tested for bacteria for that species in that study
Order		Scientific order following Birds of North America Online (last searched November 2018)
Family		Scientific family following Birds of North America Online (last searched November 2018)
Diet	Carnivore – reptiles, amphibians, birds, mammals Frugivore – fruits, drupes Granivore – seeds, maize, nuts, grains, spores Herbivore – grass, ground vegetation, weeds, vegetables, fungi, aquatic vegetation, etc. Invertebrate – aquatic invertebrates, ground insects, insect larvae, flying insects, etc. Nectarivore – nectar, pollen, plant exudates, gums Omnivore - ≤ 50% in all four binned categories in Wilman *et al*. (2014) Piscivore – fish Scavenger – garbage, carcasses, carrion	Classified as guild if diet category represents ≥ 60% of content Diet guild as classified by Wilman *et al*. (2014), Birds of North America Online, de Graff *et al*. (1985), and Smith *et al*. (2019) http://www.esapubs.org/archive/ecol/E095/178/metadata.php http://birdsna.org
Forg_strat	Aerial – foraging in air; doesn't include sallying from perch Canopy – foraging in tree canopy	Foraging strata; classified as highest percentage of foraging time in strata estimated in Wilman *et al*. (2014), Birds of North America Online, and de Graff *et al*. (1985) http://www.esapubs.org/archive/ecol/E095/178/metadata.php

	Ground – on ground Midhigh – mid-high levels in trees or bushes (2 m to just below canopy) Understorey – below 2 m in understorey Wataroundsurf – foraging on or just (<12.7 cm) below water surface Watbelowsurf – foraging below water surface	http://birdsna.org

Table S4. Studies reporting data on pathogen prevalence by sex (male, female). Studies that tested for significant differences between the sexes are highlighted in bold. N/A, not available.

Study	**Bacteria**	**Female positive**	**Female tested**	**Female prevalence**	**Male positive**	**M tested**	**M prevalence**	**Higher?**	**Significant?**	**Species**	**Notes**
Colles *et al.* (2009)	*C. jejuni*	N/A	N/A	N/A	N/A	N/A	N/A	**Same**	**No**	EUST	
Hald *et al.* (2016)	*Campylobacter* spp.	N/A	N/A	N/A	N/A	N/A	N/A	**Same**	**No**	ROPI, HOSP, ETSP, EUST, European birds	
Sulzner *et al.* (2014)	*Campylobacter* spp.	N/A	N/A	N/A	N/A	N/A	N/A	**Same**	**No**	TUVU	Author doesn't report numbers tested but reports statistical results
Brittingham *et al.* (1988)	Generic *E. coli*	N/A	63	N/A	N/A	83	N/A	**Same**	**No**	BCCH	Does not clarify which sex was positive
Gaulker *et al.* (2009)	Generic *E. coli*	N/A	N/A	N/A	N/A	N/A	N/A	**Same**	**No**	EUST	
Sulzner *et al.* (2014)	Generic *E. coli*	N/A	N/A	N/A	N/A	N/A	N/A	**Same**	**No**	TUVU	Author doesn't report numbers tested but reports statistical results
Gibbs *et al.* (2007)	Pathogenic *E. coli*	1	7	14.3%	1	14	7.1%	Female	Not tested	YHBL	
Monaghan *et al.* (1985)	*Salmonella* spp.	45	316	14.2%	42	385	10.9%	**Female**	**Yes**	HERG	Only higher in non-breeding season
Sinai *et al.* (2017)	*Salmonella* spp.	0	1	0.0%	0	30	0.0%	Same	Not tested	GRSG	
Sulzner *et al.* (2014)	*Salmonella enterica*	N/A	N/A	N/A	N/A	N/A	N/A	**Same**	**No**	TUVU	Author doesn't report numbers

											tested but reports statistical results
Espinosa-Arguelles *et al.* (2010)	*Salmonella* Gallinarum-Pullorum	27	78	34.6%	26	123	21.1%	**Female**	**Marginally significant**	MODO, WWDO	
Brittingham *et al.* (1988)	*Salmonella* spp.	0	63	0.0%	0	83	0.0%	**Same**	**No**	BCCH	
Gonzalez-Acuna *et al.* (2007)	*Salmonella* spp.	0	47	0.0%	4	49	8.2%	**Male**	**No**	ROPI	
Grigar *et al.* (2017)	*Salmonella* spp.	2	132	1.5%	0	243	0.0%	Female	Not tested	BWTE, REDH	
Hughes *et al.* (2008)	*Salmonella* spp.	19	19	100.0%	10	10	100.0%	Same	Not tested	HOSP, EUST, EUCD, European birds	Necropsies
Lawson *et al.* (2010)	*Salmonella* spp.	12	12	100.0%	12	12	100.0%	**Same**	**No**	HOSP	Necropsies
Toro *et al.* (1999)	*Salmonella* spp.	N/A	53	N/A	N/A	47	N/A	Same	Not tested	ROPI	"The results…are presented as a group because there were no important differences among them depending on…sex" (p. 620)
Daoust *et al.* (2000)	*Salmonella* Typhimurium	12	12	100.0%	19	19	100.0%	Same	Not tested	PISI, PUFI, EVGR, AMGO, CORE	Necropsies

Table S5. Studies reporting data on pathogen prevalence by age (juvenile, nestling, adult). Studies that tested for significant differences between age groups are highlighted in bold. N/A, not available.

Study	**Bacteria**	**Juvenile positive**	**Juvenile tested**	**Juvenile prevalence**	**Adult positive**	**Adult tested**	**Adult prevalence**	**Higher**	**Significant**	**Species**	**Notes**
Keller & Shriver (2014)	*Campylobacter jejuni*	8	92	8.7%	8	35	22.9%	Adult	Not tested	Larus spp.	
Lillehaug *et al.* (2005)	*Campylobacter jejuni*	3	102	2.9%	4	103	3.9%	Adult	Not tested	ROPI, MALL	
Colles *et al.* (2009)	*Campylobacter jejuni*	N/A	N/A	N/A	N/A	N/A	N/A	**Juvenile**	**Yes**	EUST	
Gabriele-Rivet *et al.* (2015)	*Campylobacter jejuni*	1	6	16.7%	14	167	8.4%	**Juvenile**	**No**	ROPI	
Keller & Shriver (2014)	*Campylobacter jejuni*	6	36	16.7%	2	206	1.0%	Juvenile	Not tested	CANG	
Taff *et al.* (2016)	*Campylobacter jejuni*	73	102	71.6%	106	235	45.1%	**Nestling**	**Yes**	AMCR	Nestlings
Waldenstrom *et al.* (2002)	*Campylobacter* spp.	11	20	55.0%	276	364	75.8%	**Adult**	**Yes**	European shorebirds	
Lombardo *et al.* (1996)	*Campylobacter* spp.	5	13	38.5%	8	8	100.0%	**Adult**	**Yes**	TRES	
Weis *et al.* (2014)	*Campylobacter* spp.	59	91	64.8%	27	40	67.5%	Adult	Not tested	AMCR	Nestlings *versus* adults/subadults
Waldenstrom *et al.* (2002)	*Campylobacter* spp.	50	676	7.4%	7	115	6.1%	**Juvenile**	**No**	European Passerines, EUST	
Levesque *et al.* (2000)	*Campylobacter* spp.	N/A	N/A	N/A	N/A	N/A	N/A	**Juvenile**	**Marginally significant**	RBGU	Testing bacterial concentration in colony

											forming units (CFU)/g rather than prevalence
Sulzner *et al.* (2014)	*Campylobacter* spp.	N/A	N/A	N/A	N/A	N/A	N/A	**Same**	**No**	TUVU	Author doesn't report numbers tested but reports statistical results
Hald *et al.* (2016)	*Campylobacter* spp.	N/A	N/A	N/A	N/A	N/A	N/A	**Same**	**No**	ROPI, HOSP, ETSP, EUST, European birds	
Gibbs *et al.* (2007)	*E. coli*	1	15	6.7%	1	6	16.7%	Adult	Not tested	YHBL	
Morabito *et al.* (2001)	*E. coli* (STEC)	30	156	19.2%	40	487	8.2%	**Juvenile**	**Yes**	ROPI	
Sulzner *et al.* (2014)	Generic *E. coli*	N/A	N/A	N/A	N/A	N/A	N/A	**Same**	**No**	TUVU	Author doesn't report numbers tested but reports statistical results
Gaulker *et al.* (2009)	Generic *E. coli*	N/A	N/A	N/A	N/A	N/A	N/A	**Same**	**No**	EUST	
Espinosa-Arguelles *et al.* (2010)	*Salmonella* Gallinarum-Pullorum	8	26	30.8%	45	175	25.7%	**Juvenile**	**Marginally significant**	MODO, WWDO	
Gonzalez-Acuna *et al.* (2007)	*Salmonella* spp.	1	40	2.5%	3	56	5.4%	**Adult**	**No**	ROPI	
Kapperud & Rosef (1983)	*Salmonella* spp.	2	125	1.6%	2	54	3.7%	**Adult**	**No**	Larus spp.	
Monaghan *et al.* (1985)	*Salmonella* spp.	24	125	19.2%	63	552	11.4%	**Juvenile**	**No**	HERG	
Butterfield *et al.* (1983)	*Salmonella* spp.	3	118	2.5%	9	656	1.4%	**Juvenile**	**No**	HERG	November–February
Sulzner *et al.* (2014)	*Salmonella enterica*	N/A	N/A	N/A	N/A	N/A	N/A	**Same**	**No**	TUVU	Author doesn't report numbers tested but reports statistical results
Wood & Trust (1972)	*Salmonella* spp.	0	103	0.0%	0	51	0.0%	**Same**	**No**	GWGU	

Levesque *et al.* (2000)	*Salmonella* spp.	N/A	N/A	N/A	N/A	N/A	N/A	**Same**	**No**	RBGU	Testing bacterial concentration in CFU/g rather than prevalence
Grigar *et al.* (2017)	*Salmonella* spp.	0	43	0.0%	2	332	0.6%	Adult	Not tested	BWTE, REDH	
Phalen *et al.* (2010)	*Salmonella* spp.	82	135	60.7%	0	10	0.0%	Juvenile	Not tested	CAEG	
Sinai *et al.* (2017)	*Salmonella* spp.	0	7	0.0%	0	22	0.0%	Same	Not tested	GRSC	
Toro *et al.* (1999)	*Salmonella* spp.	N/A	N/A	N/A	N/A	N/A	N/A	Same	Not tested	ROPI	“The results…are presented as a group because there were no important differences among them depending on…age” (p. 620)
Hughes *et al.* (2008)	*Salmonella* spp.	12	12	100.0%	11	11	100.0%	Same	Not tested	HOSP, EUST, EUCD, HERG, European birds	Necropsies
Lillehaug *et al.* (2005)	*Salmonella* spp.	0	102	0.0%	0	103	0.0%	Same	Not tested	ROPI, MALL	
Daoust *et al.* (2000)	*Salmonella* Typhimurium	12	12	100.0%	31	31	100.0%	Same	Not tested	PISI, PUFI, EVGR, AMGO, CORE	Necropsies
Fukui *et al.* (2014)	*Salmonella* Typhimurium	13	13	100.0%	8	8	100.0%	Same	Not tested	ETSP	Necropsies
Butterfield *et al.* (1983)	*Salmonella* spp.	25	258	9.7%	18	902	2.0%	**Juvenile**	**Yes**	HERG	July–October
Hernandez *et al.* (2016)	*Salmonella* spp.	8	22	36.4%	4	33	12.1%	**Nestling**	**Yes**	WHIB	Nestling>subadult>adult

Table S6. Summary of studies reporting coinfection data. Bird species are identified according to AOU four-letter codes (see Supplementary Data S2).

Study	Bacteria	Positive	Tested	Prevalence	Birds	Notes
Borilova *et al.* (2007)	*C. coli*/*C. jejuni*	3	200	1.5%	RNPH	
Callaway *et al.* (2014)	*Salmonella*/*E. coli* O157:H7	3	376	0.8%	BHCO, COGR	
Doumandji *et al.* (2010)	*Salmonella*/generic *E. coli*	1	34	2.9%	CAEG	
Fichtel (1978)	*Salmonella*/*Sacrosporidiosis* (fungus)	2	6	33.3%	NOCA, WTSP, DEJU	
Gaukler *et al.* (2009)	*Salmonella*/generic *E. coli*	3	434	0.7%	EUST	
Gibbs *et al.* (2007)	*E. coli*/*Serratia* spp.	1	21	4.8%	YHBL	
Gibbs *et al.* (2007)	*E. coli*/*Enterobacter* spp.	1	21	4.8%	YHBL	
Glunder *et al.* (1992)	*C. jejuni*/*Salmonella* Typhimurium	2	37	5.4%	HERG	
Kalisinka *et al.* (2008)	*E. coli*/trematodes (*Strigea falconis, Conodiplostomum spathula*)/cestodes (*Cladotaenia cylindracea*)/nematodes (*Serratospiculum tendo*)/*Aspergillus nidulans*/*Cladophialophora boppi*/*Micrococcus luteus*/*Proteus mirabilis*	1	1	100.0%	PEFA	
Kapperud & Rosef (1983)	*C. jejuni*/nalidixic acid-resistant thermophilic *Campylobacters*	3	138	2.2%	Larus spp.	
Levre *et al.* (1989)	*Campylobacter* spp./*Salmonella* spp.	1	217	0.5%	GRAP, RNPH, EUST, European birds	
Levre *et al.* (1989)	*Campylobacter* spp./*Salmonella* spp./*Yersinia* spp.	1	217	0.5%	GRAP, RNPH, EUST, European birds	
Levre *et al.* (1989)	*Campylobacter* spp./*Yersinia* spp.	9	217	4.1%	GRAP, RNPH, EUST, European birds	
Moriarty *et al.* (2011)	*Campylobacter* spp./*E. coli*	N/A	320	N/A	CANG	Spearman rank correlation analysis $r_s = 0.116$ between bacterial species
Nebola *et al.* (2007)	*C. coli*/*C. jejuni*	3	55	5.5%	RNPH	

Oteo *et al.* (2018)	Generic *E. coli*/*Klebsiella pneumoniae*	2	95	2.1%	Gulls, egrets, vultures, owls, ducks, European birds	
Pao *et al.* (2014)	*C. jejuni*/*Salmonella* spp.	0	446	0.0%	EUST, BHCO, MODO, CHSP, HOSP, ROPI, and others	
Pennycott *et al.* (2006)	*Salmonella* Typhimurium/*Ichthyocotylurus platycephalus* (trematode)	1	495	0.2%	HOSP, ETSP, ROPI, HERG, European birds	Necropsies
Pennycott *et al.* (2006)	*Salmonella* Typhimurium/*Pasteurella* spp.	1	495	0.2%	HOSP, ETSP, ROPI, HERG, European birds	Necropsies
Pennycott *et al.* (2006)	*Salmonella* Typhimurium/Avian tuberculosis (*Mycobacterium avium*)	1	495	0.2%	HOSP, ETSP, ROPI, HERG, European birds	Necropsies
Radwan & Lampky (1972)	*Salmonella* Typhimurium/generic *E. coli*	1	5	20.0%	HERG, RTHU, ATSP, HOSP, OVEN	Can infer for these five because one tested of each
Robino *et al.* (2010)	*C. coli*/*C. jejuni*	5	116	4.3%	Hooded crows, MALL, HOSP, ROPI	
Sovada *et al.* (2008)	BoNT Type C/*Salmonella*	3	28	10.7%	AWPE	
Sovada *et al.* (2008)	WNV/*Salmonella*	8	40	20.0%	AWPE	
Vasconcelos *et al.* (2017)	*E. coli*/*Pseudomonas aeruginosa*	1	1	100.0%	ROPI	
Vaughan-Higgins *et al.* (2013)	Nematodes (*Cyanthostoma*, *Porracaecum*), metazoan parasite eggs, *E. coli*	1	1	100.0%	NOHA	
Waldenstrom *et al.* (2002)	*C. coli*/*C. jejuni*	10	1794	0.6%	N/A	
Yogasundram *et al.* (1989)	*C. jejuni*/endoparasites	11	445	2.5%	Ducks, Galliformes, owls, doves, etc.	Some turned in for necropsy and some hunted
Yogasundram *et al.* (1989)	*C. jejuni*/fungal infection	7	445	1.6%	Ducks, Galliformes, owls, doves, etc.	Some turned in for necropsy and some hunted
Yogasundram *et al.* (1989)	*C. jejuni*/protozoan infection	3	445	0.7%	Ducks, Galliformes, owls, doves, etc.	Some turned in for necropsy and some hunted
Yogasundram *et al.* (1989)	*C. jejuni*/viral infection	4	445	0.9%	Ducks, Galliformes, owls, doves, etc.	Some turned in for necropsy and some hunted
Yogasundram *et al.* (1989)	*C. jejuni*/other bacterial infection	7	445	1.6%	Ducks, Galliformes, owls, doves, etc.	Some turned in for necropsy and some hunted

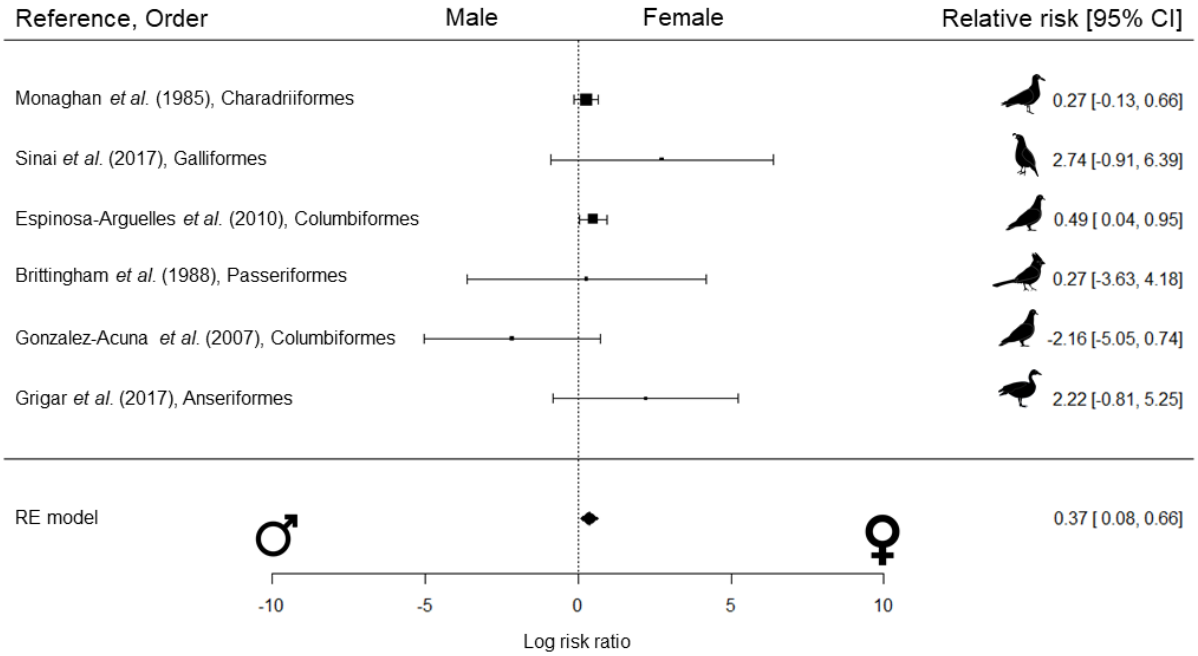

Fig. S3. Forest plot showing the results of six studies examining the difference in *Salmonella* spp. prevalence in female *versus* male birds. The figure shows the relative risk of detecting *Salmonella* spp. in female (right of 0) *versus* male (left of 0) birds with corresponding 95% confidence intervals in the individual studies using a random effects model in the metaphor package in R.

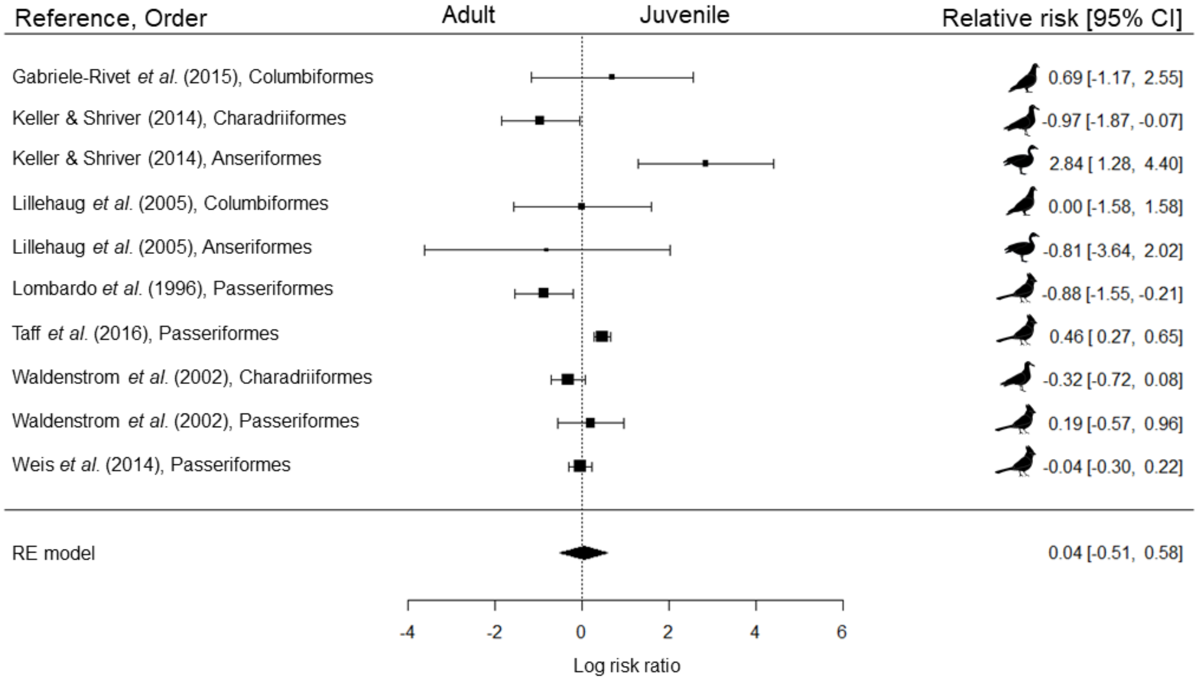

Fig. S4. Forest plot showing the results of 10 estimates from seven studies examining the difference in *Campylobacter* spp. prevalence in juvenile versus adult birds from four orders. The figure shows the relative risk of detecting *Campylobacter* spp. in adult (left of 0) *versus* juvenile (right of 0) birds with corresponding 95% confidence intervals in the individual studies using a random effects model in the metaphor package in R.

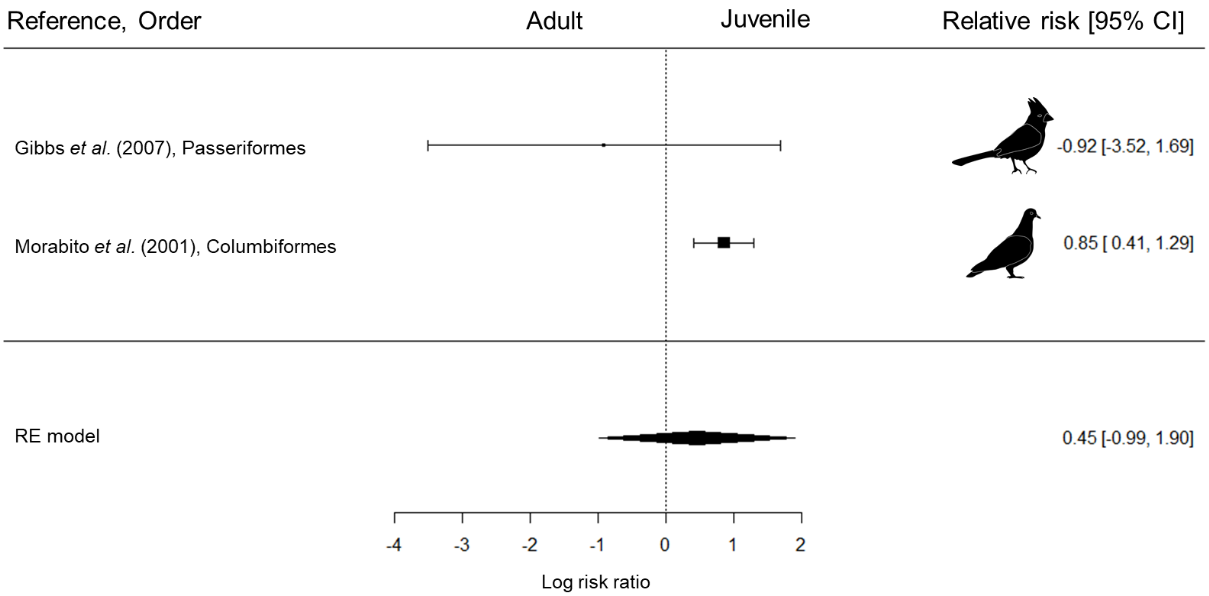

Fig. S5. Forest plot showing the results of two estimates from two studies examining the difference in pathogenic *E. coli* prevalence in juvenile *versus* adult birds. The figure shows the relative risk of detecting pathogenic *E. coli* in adult (left of 0) *versus* juvenile (right of 0) birds with corresponding 95% confidence intervals in the individual studies using a random effects model in the metaphor package in R.

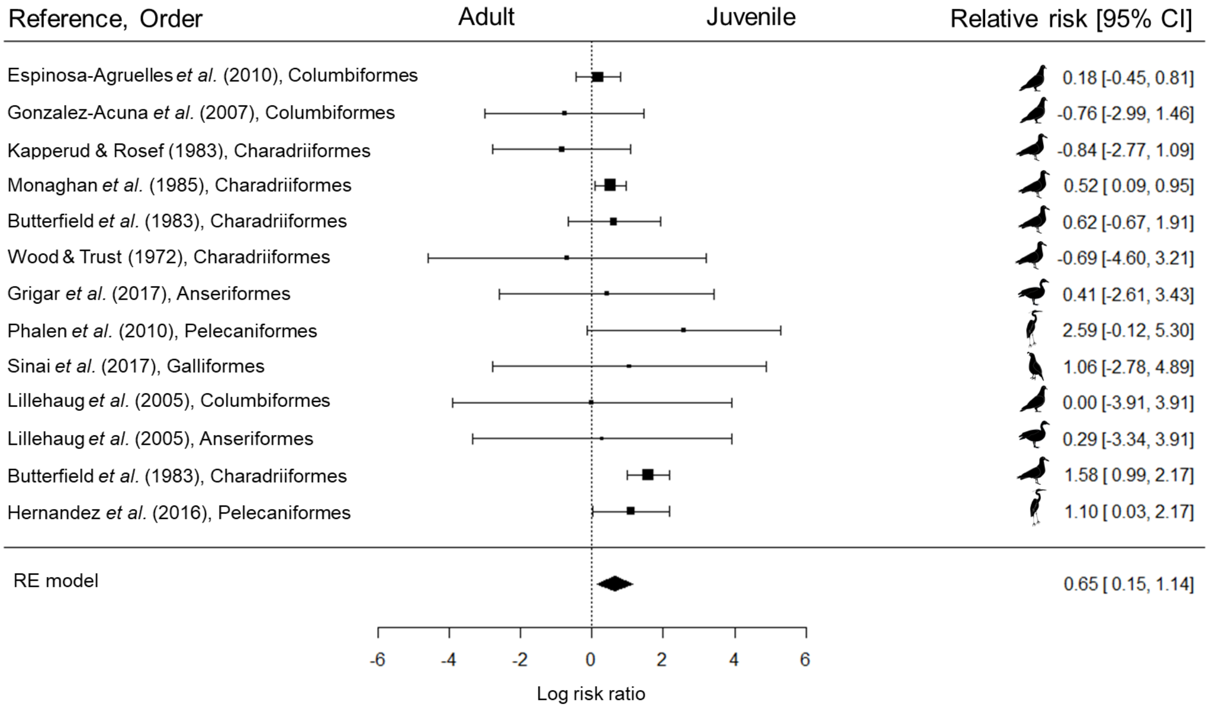

Fig. S6. Forest plot showing the results of 13 estimates from 12 studies examining the difference in *Salmonella* spp. prevalence in juvenile *versus* adult birds. The figure shows the relative risk of detecting *Salmonella* spp. in adult (left of 0) *versus* juvenile (right of 0) birds with corresponding 95% confidence intervals in the individual studies using a random effects model in the metaphor package in R.

Table S7. Studies reporting data on pathogen prevalence *versus* condition metrics. Bird species are identified according to AOU four-letter codes (see Supplementary Data S2). Studies that found significant relationships are highlighted in bold. N/A, not available.

Study	**Bacteria**	**Condition metric**	**Significant**	**Direction**	**Species**	**Notes**
Taff & Townsend (2017)	*C. jejuni*	Condition index	**Yes**	**Negative**	AMCR	Adult crows in winter
Colles *et al.* (2009)	*C. jejuni*	Mass	**Yes**	**Negative**	EUST	
Taff & Townsend (2017)	*C. jejuni*	Mass	**Yes**	**Negative**	AMCR	Adult crows in winter
Colles *et al.* (2009)	*C. jejuni*	Wing cord	**Yes**	**Negative**	EUST	
Gabriele-Rivet *et al.* (2015)	*C. jejuni*	Body score	**Yes**	**Positive**	ROPI	Score 1 (very thin) to 5 (very fat)
Gabriele-Rivet *et al.* (2015)	*C. jejuni*	Condition index	No		ROPI	Weight in g/average metatarsus length
Taff & Townsend (2017)	*C. jejuni*	Condition index	No		AMCR	Nestlings
Gabriele-Rivet *et al.* (2015)	*C. jejuni*	Metatarsus length	No		ROPI	
Taff & Townsend (2017)	*C. jejuni*	Skeletal size	No		AMCR	Adult crows in winter
Mills *et al.* (1999)	*Campylobacter* spp.	Left tarsus length	**Yes**	**Positive**	TRES	Nestlings
Waldenstrom *et al.* (2002)	*Campylobacter* spp.	Mass	**Yes**	**Positive**	European birds (66 species), EUST	Tested whether larger body size led to higher prevalence across species
Hald *et al.* (2016)	*Campylobacter* spp.	Fat score	No		ROPI, HOSP, ETSP, EUST,	

					European birds	
Mills *et al.* (1999)	*Campylobacter* spp.	Left wing length	No		TRES	Nestlings
Mills *et al.* (1999)	*Campylobacter* spp.	Mass	No		TRES	Nestlings
Vazquez *et al.* (2010)	*Campylobacter* spp.	Mass	No		ROPI	
Vazquez *et al.* (2010)	*Campylobacter* spp.	Packed cell volume	No		ROPI	
Mills *et al.* (1999)	*Campylobacter* spp.	Tarsus asymmetry	No		TRES	Nestlings
Vazquez *et al.* (2010)	*Campylobacter* spp.	Tarsus length	No		ROPI	
Mills *et al.* (1999)	*Campylobacter* spp.	Wing asymmetry	No		TRES	Nestlings
Vazquez *et al.* (2010)	*Campylobacter* spp.	Wing cord	No		ROPI	
Mills *et al.* (1999)	*Campylobacter* spp.	Wing parasites	No		TRES	Nestlings
Mills *et al.* (1999)	Desoxycholate citrate lactose sugar agar (DCLS) media for *E. coli, Salmonella, Vibrio, Shigella*	Tarsus asymmetry	**Yes**	**Negative**	TRES	Nestlings
Mills *et al.* (1999)	DCLS media for *E. coli, Salmonella, Vibrio, Shigella*	Left tarsus length	**Yes**	**Positive**	TRES	Nestlings
Mills *et al.* (1999)	DCLS media for *E. coli, Salmonella, Vibrio, Shigella*	Left wing length	No		TRES	Nestlings
Mills *et al.* (1999)	DCLS media for *E. coli, Salmonella, Vibrio, Shigella*	Mass	No		TRES	Nestlings
Mills *et al.* (1999)	DCLS media for *E. coli, Salmonella, Vibrio, Shigella*	Wing asymmetry	No		TRES	Nestlings
Mills *et al.* (1999)	DCLS media for *E. coli, Salmonella, Vibrio, Shigella*	Wing parasites	No		TRES	Nestlings
Morabito *et al.* (2001)	*E. coli* (STEC)	Mass	**Yes**	**Negative**	ROPI	Juvenile/subadult

Morabito *et al.* (2001)	*E. coli* (STEC)	Mass	No		ROPI	Adult
Kalisinka *et al.* (2008)	Generic *E. coli*	Condition index	Not tested	Negative	PEFA	One bird tested
Gaukler *et al.* (2009)	Generic *E. coli*	Mass	No		EUST	
Monaghan *et al.* (1985)	*Salmonella* spp.	Scaled mass	No		HERG	
Espinosa-Arguelles *et al.* (2010)	*Salmonella* Gallinarum-Pullorum	Mass	**Yes**	**Negative**	MODO, WWDO	
Lawson *et al.* (2010)	*Salmonella* spp.	Mass	Not tested	Negative	HOSP	Salmonellosis cases *versus* trauma cases
Fichtel (1978)	*Salmonella* Typhimurium	Mass	Not tested	Negative	NOCA, American tree sparrow	Compared weight at death to earlier banding records for Salmonellosis cases
Fukui *et al.* (2014)	*Salmonella* Typhimurium	Mass	**Yes**	**Negative**	ETSP	Compared Salmonellosis case birds to healthy birds

Table S8. Bacterial concentration shed in wild bird faeces and duration of shedding for naturally occurring faeces (surveys) and inoculation experiments. Bird species are identified according to AOU four-letter codes (see Supplementary Data S2). CE = cell equivalents, CFU = colony forming units, MPN = most probable number

Study	**Species**	**Species/strain**	**Average**	**Minimum**	**Maximum**	**Inoculum Concentration**	**Mean duration (d)**	**Max duration (d)**	**Sample size**	**Study duration (d)**	**Type**	**Notes**
Atterby *et al*. (2018)	MALL	*C. jejuni* mallard ST	10^4 — 10^6 CFU/ml	10^3 CFU/ml	10^8 CFU/ml	5 × 10^4 CFU/ml of water	18	18	10	18	Experiment	Data from Experiment 1 only. All birds shed for full 18 days of study.
Atterby *et al.* (2018)	MALL	*C. jejuni* thrush ST	10^3 — 10^4 CFU/ml	10^2 CFU/ml	10^7 CFU/ml	5 × 10^4 CFU/ml of water		16	10	18	Experiment	Data from Experiment 1 only. Mean value of 10^3 — 10^4 CFU/ml occurred in first few days of experiment. Discrepancy in maximum shedding duration reported in main text abstract, results, and supporting table.
Atterby *et al.* (2018)	MALL	*C. jejuni* chicken ST	10^4 CFU/ml	10^2 CFU/ml	10^6 CFU/ml	5 × 10^4 CFU/ml of water		18	10	18	Experiment	Data from Experiment 1 only. 2/6 birds still shed bacteria at day 18. 10^4 CFU/ml described as “peak mean level” [p. 3]
Glunder *et al.* (1992)	HERG	*C. jejuni*						35	27	329	Survey	Taken into lab
Levesque *et al.* (2000)	HERG	*Campylobacter* spp.	2.44 × 10^5 CFU/g	2 × 10^3 CFU/g	1.2 × 10^7 CFU/g						Survey	Average for adults; min and max adult and juvenile

Lu *et al.* (2011)	CAGU	*Campylobacter* spp.	6.7 × 10^6 CE/g	340 CE/g	1 × 10^8 CE/g						Survey	
Lu *et al.* (2013)	SACR	*Campylobacter* spp.	5 × 10^3 CE/g								Survey	
Moriarty *et al.* (2011)	CANG	*Campylobacter* spp.	4.84 × 10^3 CFU/g								Survey	
Murphy *et al.* (2005)	MALL	*Campylobacter* spp.	6 × 10^3 CFU/g								Survey	
Seguino *et al.* (2018)	RNPH	*Campylobacter* spp.	2.7 × 10^4 CFU/g		1 × 10^8 CFU/g						Survey	
Waldenstrom *et al.* (2010)	European Robin	*C. jejuni* thrush ST				10^5 CFU	6.8	10	8	25	Experiment	
Waldenstrom *et al.* (2010)	European Robin	*C. jejuni* human ST				10^5 CFU		3	16	25	Experiment	Includes 8 thrush initially inoculated with *C. jejuni* human ST then reinoculated on day 14 (reported in main text of this manuscript) and control group of 8 birds inoculated on day 19 (not reported in main text of this manuscript)
Kauffman & LeJeune (2011)	EUST	*E. coli* O157:H7 strain 977	10^3 CFU/g	10^1 CFU/g	10^6 CFU/g	1 × $10^{0.6}$ to 5 × 10^6 CFU		14		14	Experiment	Infectious dose varied by strain; higher doses led to longer duration and higher intensity of shedding. Mean value reported is for higher doses.
Doumandji *et al.* (2010)	CAEG	Generic *E. coli*	6.6 log CFU/ml	4.0 log CFU/ml	9.3 log CFU/ml						Survey	

Fogarty *et al.* (2003)	*Larus* spp.	Generic *E. coli*	1.4×10^7 to 4.9×10^8 CFU/g	$<10^5$ CFU/g	1.9×10^9 CFU/g						Survey	
Lu *et al.* (2013)	SACR	Generic *E. coli*	6.9×10^7 CE/g								Survey	
Middleton & Ambrose (2005)	CANG	Generic *E. coli*	3.6×10^5 CFU/g	0	1×10^7 CFU/g						Survey	
Moriarty *et al.* (2011)	CANG	Generic *E. coli*	3.61×10^4 CFU/g								Survey	
Murphy *et al.* (2005)	MALL	Generic *E. coli*	1.36×10^5 CFU/g								Survey	
Nelson *et al.* (2008)	HERG	Generic *E. coli*	1.0×10^6 CFU/g	1.9×10^2 CFU/g	2.5×10^9 CFU/g						Survey	
Vogel *et al.* (2013)	SACR	Generic *E. coli*	2.8×10^4 MPN/g						30		Survey	
Girdwood *et al.* (1985)	HERG	*Salmonella* spp.	22 MPN/g		170 MPN/g		3	4	84	21	Survey	Taken into laboratory
Glunder *et al.* (1992)	HERG	*S.* typhimurium						56	27	56	Survey	Taken into laboratory; one came in with *S. typhimurium* and spread to four others; treated at day 56
Levesque *et al.* (2000)	HERG	*Salmonella* spp.	1.9×10^6 CFU/g	2.3×10^2 CFU/g	2.4×10^9 CFU/g						Survey	Average for adults; min. and max.for adults and juveniles
Albuquerque *et al.* (2013)	ROPI	*S.* Enteritidis		1.5×10^4 CFU/g	2×10^5 CFU/g	9.5×10^7 CFU/ml		14	24	35	Experiment	Low dose inoculum
Albuquerque *et al.* (2013)	ROPI	*S.* Enteritidis		1×10^7 CFU/g	2×10^9 CFU/g	9.5×10^9 CFU/ml		7	24	35	Experiment	High dose inoculum

Connolly *et al.* (2006)	HOSP	*S.* Typhimurium DT160	0 CFU/g		0 CFU/g	10^{1} CFU		0	6	10	Experiment	100% survival
Connolly *et al.* (2006)	HOSP	*S.* Typhimurium DT160				10^{2} CFU		5	6	10	Experiment	100% survival
Connolly *et al.* (2006)	HOSP	*S.* Typhimurium DT160				10^{3} CFU		10	6	10	Experiment	100% survival
Connolly *et al.* (2006)	HOSP	*S.* Typhimurium DT160				10^{5} CFU			6	10	Experiment	2/6 birds died on day 8 and day 10
Connolly *et al.* (2006)	HOSP	*S.* Typhimurium DT160				2×10^{8} CFU		8	6	10	Experiment	6/6 birds died on days 3, 4, 5, 6, and 8
Doumandji *et al.* (2010)	CAEG	*Salmonella* spp.	5.78 log CFU/ml								Survey	

Table S9. Seasonal variation in bacterial prevalence and shedding. Bird species are identified according to AOU four-letter codes (see Supplementary Data S2). Studies that tested for significant differences between seasons are highlighted in bold.

Study	**Species/strain**	**Highest prevalence**	**Lowest prevalence**	**Significant**	**Highest concentration**	**Lowest concentration**	**Significant**	**Bird**	**Notes**
Pao *et al*. (2014)	*Campylobacter* spp.	**Same**	**Same**	**No**				Passerines, doves	
Colles *et al*. (2009)	*Campylobacter coli*	Same	Same	Not tested				EUST	Always low
Yogasundram *et al*. (1989)	*Campylobacter jejuni*	Autumn		Not tested				Ducks, Galliformes, owls, doves, etc.	Some turned in for necropsy and some hunted
Colles *et al*. (2009)	*Campylobacter lari*	Spring		Not tested				EUST	
Sippy *et al*. (2012)	*Campylobacter* spp.	Autumn	Spring	Not tested				HOSP, RBGR, WTSP	
Wahlstrom *et al*. (2003)	*Campylobacter* spp.	Spring	Summer	Not tested				Gulls	
Waldenstrom *et al*. (2002)	*Campylobacter* spp.	Autumn	Spring	Not tested				European birds, EUST	Tested spring and autumn migration
Taff *et al*. (2016)	*Campylobacter jejuni*	**Winter**	**Summer**	**Yes**				AMCR	
Colles *et al*. (2009)	*Campylobacter jejuni*	**Summer**	**Winter**	**Yes**				EUST	
Gargiulo *et al*. (2014)	*Campylobacter jejuni*	**Summer**	**Winter**	**Yes**				ROPI	
Mohan *et al*. (2013)	*Campylobacter* spp.	**Winter/ Spring**	**Summer**	**Yes**				EUST, MALL	
Vazquez *et al*. (2010)	*Campylobacter* spp.	**Spring**	**Autumn**	**Yes**				ROPI	
Hald *et al*. (2016)	*Campylobacter* spp.	**Summer**	**Winter**	**Yes**				ROPI, HOSP, ETSP, EUST, European birds	

Levesque *et al.* (2000)	*Campylobacter* spp.				**Same**		**No**	RBGU	
Morabito *et al.* (2001)	Shiga toxin-producing *E. coli* (STEC)	**Summer**	**Winter**	**No**				ROPI	
Hsu *et al.* (2016)	*E. coli*	Winter		Not tested				CANG	
Medhanie *et al.* (2014)	*E. coli* O157:H7	Autumn/Winter		Not tested				EUST	
Medhanie *et al.* (2014)	*E. coli* O157:H7	Autumn		Not tested				EUST	
Kullas *et al.* (2002)	*E. coli*	**Summer**	**Winter**	**Yes**				CANG	
Gargiulo *et al.* (2014)	*E. coli* O157	**Summer**	**Winter**	**Yes**				ROPI	
Pedersen *et al.* (2006)	Pathogenic *E. coli*	**Summer/ Autumn**	**Winter**	**Yes**				ROPI	
Hughes *et al.* (2009)	STEC (*eae*) (Shiga toxin-producing *E. coli* attachment gene)	**Autumn**	**Winter**	**Yes**				Owls, ducks, geese, doves, passerines, falcons, shorebirds	
Hughes *et al.* (2009)	STEC (*stx1*) (Shiga toxin-producing gene for *E. coli*)	**Summer**	**Winter**	**Yes**				Owls, ducks, geese, doves, passerines, falcons, shorebirds	
Hughes *et al.* (2009)	STEC (*stx2*) (Shiga toxin-producing gene for *E. coli*)	**Autumn**	**Spring**	**Yes**				Owls, ducks, geese, doves, passerines, falcons, shorebirds	
Middleton & Ambrose (2005)	Generic *E. coli*	Autumn	Winter	Not tested	Winter	Autumn	Not tested	CANG	
Gaukler *et al.* (2009)	Generic *E. coli*	**Summer**	**Winter**	**Yes**				EUST	
Torres-Mejia *et al.* (2018)	*Salmonella* Braenderup	**Same**	**Same**	**No**				ROPI	Dry *versus* wet season
Monaghan *et al.* (1985)	*Salmonella* spp.	**Same**	**Same**	**No**				HERG	Male

Pedersen *et al.* (2006)	*Salmonella* spp.	**Same**	**Same**	**No**				ROPI	
Butterfield *et al.* (1983)	*Salmonella* spp.	**Same**	**Same**	**No**				HERG	Adults
Hernandez *et al.* (2016)	*Salmonella* spp.	**Same**		**No**				WHIB	
Galbraith *et al.* (2017)	*Salmonella* Typhimurium	**Same**		**No**				HOSP	
Skov *et al.* (2008)	*Salmonella* Typhimurium	**Same**	**Same**	**No**				BARS, HOSP, EUST, European birds	
Coulson *et al.* (1983)	*Salmonella* Montevideo	Same		Not tested				HERG	
Millan *et al.* (2004)	*Salmonella* spp.	Winter/Spring		Not tested				Raptors	Necropsies
Williams *et al.* (1977)	*Salmonella* spp.	Autumn		Not tested				Gull	
Gaukler *et al.* (2009)	*Salmonella* spp.	Same		Not tested				EUST	
Girdwood *et al.* (1985)	*Salmonella* spp.	Autumn	Winter	Not tested				HERG	
Gorski *et al.* (2011)	*Salmonella* spp.	Summer		Not tested				AMCR, WCSP, SPTO	
Hughes *et al.* (2008)	*Salmonella* spp.	Winter	Summer	Not tested				EUST, HOSP, EUCD, HERG, European birds	Necropsies
Lawson *et al.* (2010)	*Salmonella* spp.	Winter		Not tested				HOSP, European birds	Necropsies
Lopez-Martin *et al.* (2011)	*Salmonella* spp.	Winter	Summer	Not tested				FRGU, Kelp Gull	
Pennycott *et al.* (2006)	*Salmonella* Typhimurium	Winter		Not tested				HOSP, ETSP, ROPI, gulls, raptors, European passerines	Necropsies
Refsum *et al.* (2002)	*Salmonella* Typhimurium	Winter/Spring		Not tested				Small passerines	Necropsies
Refsum *et al.* (2002)	*Salmonella* Typhimurium	Same	Same	Not tested				Gulls, ducks, doves, corvids, geese, murres, raptors	Necropsies
Wobeser & Finlayson (1969)	*Salmonella* Typhimurium	Winter		Not tested				HOSP	Necropsies

Daoust *et al.* (2000)	*Salmonella* Typhimurium	Winter/Spring		Not tested				PISI, PUFI, EVGR, AMGO, CORE	Necropsies
Faddoul *et al.* (1966)	*Salmonella* Typhimurium	Winter		Not tested				BHCO, HOSP, HERG, WTSP	Necropsies
Fukui *et al.* (2014)	*Salmonella* Typhimurium	Winter		Not tested				ETSP	Necropsies
Grigar *et al.* (2016)	*Salmonella* Typhimurium	Summer	Spring	Not tested				GTGR	
Hernandez *et al.* (2012)	*Salmonella* Typhimurium	Winter		Not tested				PISI, NOCA	Necropsies
Hurvell *et al.* (1975)	*Salmonella* Typhimurium	Winter	Autumn	Not tested				HOSP, ETSP, European birds	Necropsies
Monaghan *et al.* (1985)	*Salmonella* spp.	**Winter**	**Summer**	**Yes**				HERG	Female
Rodriguez *et al.* (2012)	*Salmonella* spp.	**Autumn**	**Spring**	**Yes**				FRGU	
Butterfield *et al.* (1983)	*Salmonella* spp.	**Summer**	**Winter**	**Yes**				HERG	Juveniles
Gonzalez-Acuna *et al.* (2007)	*Salmonella* spp.	**Summer**		**Yes**				ROPI	
Gargiulo *et al.* (2014)	*Salmonella* Typhimurium	**Summer**	**Winter**	**Yes**				ROPI	
Levesque *et al.* (2000)	*Salmonella* spp.				**Same**		**No**	RBGU	

Table S10. Studies seeking to demonstrate crossover of bacteria between wild birds and humans and/or livestock, including molecular technique used (comparison method), extent of coverage/comparison group, the number of isolates or strains from wild birds that matched human/livestock isolates/strain types, number of birds tested or number of bird isolates, and wild bird species tested. Bird species are identified according to AOU four-letter codes (see Supplementary Data S2). *Bln*I = restriction enzyme for PFGE, *fla*A = flagellin-encoding A gene, HiMLST = high-throughput multilocus sequence typing, *Kpn*I = restriction enzyme for PFGE, MLST = Multilocus sequence typing, MLVA = Multiple loci variable-number tandem repeat analysis, N/A = not available, NCBI BLAST = National Center for Biotechnology Information Basic Local Alignment Search Tool, *Not*I = restriction enzyme for PFGE, PFGE = pulsed-field gel electrophoresis, *por*A = major outer-membrane protein gene, PubMLST = Public databases for molecular typing, RFLP = restriction fragment length polymorphism, rRNA = ribosomal ribonucleic acid, *Sfi*I = restriction enzyme for PFGE, *Sma*I = restriction enzyme for PFGE, *Spe*I = restriction enzyme for PFGE, ST = sequence type, STEC = Shiga toxin-producing *E. coli*, SVR = short variable region, VTEC = Verocytotoxin-producing E. coli, *Xba*I = restriction enzyme for PFGE

Study	**Bacteria**	**Comparison method**	**Comparison group**	**Human/ livestock**	**Tested**	**Species**	**Notes**
Mohan *et al*. (2013)	*Campylobacter jejuni*	MLST; *fla*A SVR and *por*A gene sequence typing	PubMLST	14	43	EUST, MALL	Sequence types
Palmgren *et al.* (2004)	*Campylobacter jejuni*	PFGE (*Sma*I and *Kpn*I)	Malmö, Sweden region database of *C. jejuni* profiles with gull, chicken, and human isolates; 172 profiles from wild bird and human isolates from Kalmar County, Sweden	2	2	PEFA	
Pao *et al.* (2014)	*Campylobacter jejuni*	PFGE (*Sma*I)	Small ruminants from farms on which birds were caught	0	19	BHCO, CHSP, EUST, HOSP, MODO, ROPI	
Sanad *et al.* (2013)	*Campylobacter jejuni*	PFGE (*Sma*I); Antimicrobial resistance typing; MLST (7 housekeeping genes)	Dairy cattle from farms on which starlings were caught; *Campylobacter* MLST database for ST	20	57	EUST	Comparing EUST to cattle on feedlot
Weis *et al.* (2014)	*Campylobacter jejuni*	16S rRNA and Sanger sequencing	NCBI BLAST reference sequences	5	65	AMCR	
Lawton *et al.* (2018)	*Campylobacter jejuni* subsp. *jejuni*	Whole-genome sequencing and MLST	Chickens; *Campylobacter* MLST database for ST	3	19	AMCR, MALL	

Colles *et al.* (2009)	*Campylobacter* spp.	MLST and *fla*A SVR sequence typing	PubMLST	N/A	277	EUST	Unclear how many matches there were
Colles *et al.* (2011)	*Campylobacter* spp.	MLST and *fla*A SVR sequence typing	PubMLST	1	109	MALL	
Gardner *et al.* (2011)	*Campylobacter* spp.	PFGE (*Sma*I and *Kpn*I)	Clinical isolates, PulseNet, farm environmental samples	3	14	SACR	
Nebola *et al.* (2007)	*Campylobacter* spp.	PFGE (*Sma*I) and *fla*-RFLP	Farmed and wild pheasants	2	51	RNPH	Comparing farmed to wild RNPH
Seguino *et al.* (2018)	*Campylobacter* spp.	HiMLST	PubMLST	16	80	RNPH	
Sippy *et al.* (2012)	*Campylobacter* spp.	PFGE (*Sma*I or *Kpn*I) and MLST on 7 target gene loci (*asp*A, *gln*A, *glt*A, *gly*A, *pgm*, *tkt* and *unc*A)	PubMLST, sheep abortion isolates, small wild mammals	2	9	HOSP, RBGR, WTSP	Comparing to sheep
Torres-Mejia *et al.* (2018)	*Salmonella* Braenderup	PFGE	N/A but mentions it matching human clinical isolate from Costa Rica	0	34	ROPI	
Hernandez *et al.* (2012)	*Salmonella enterica*	PFGE and MLVA	PulseNet, archived wild bird outbreak strains	28	72	NOCA, AMGO, PUFI, PISI, BHCO, CORE	Necropsy study
Haesendonck *et al.* (2016)	*Salmonella* Enteritidis	PFGE (*Xba*I, *Not*I, *Sfi*I)	BioNumerics *S.* Enteritidis database at the Institute for Agricultural and Fisheries Research including human, poultry, wildlife, and food isolates from Belgium 1999–2010	10	10	ROPI	
Luque *et al.* (2009)	*Salmonella* Indiana	PFGE (*Xba*I)	Sheep from farm with outbreak	6	6	ROPI, turtledove	
Gorski *et al.* (2011)	*Salmonella* spp.	PFGE (*Xba*I and *Bln*I)	PulseNet, mammalian wildlife, environmental samples	0	7	AMCR, SPTO, WCSP	

Hernandez *et al.* (2016)	*Salmonella* spp.	PFGE	PulseNet; archived wild bird, domesticated bird, environmental, and human isolates	15	72	WHIB	
Pao *et al.* (2014)	*Salmonella* spp.	PFGE (*Xba*I)	Small ruminants from farms on which birds were caught	0	1	EUST	
Hughes *et al.* (2008)	*Salmonella* Typhimurium	PFGE (*Xba*I and *Spe*I)	N/A	0	32	HOSP, EUST, EUCD, European birds	Necropsy study
Skov *et al.* (2008)	*Salmonella* Typhimurium	PFGE (*Xba*I and *Bln*I)	Cattle, pigs, pets, rodents, and insects from farms on which birds were caught	82	82	HOSP, BARS, EUST, European birds	At outbreak livestock farms
Morabito *et al.* (2001)	Shiga toxin-producing *E. coli* (STEC)	PFGE (*Xba*I)	Human O45 STEC strain	0	18	ROPI	
Nielsen *et al.* (2004)	Verocytotoxin-producing *E. coli* (VTEC)	PFGE (*Xba*I)	Cattle, pigs, and rats from farms on which birds were caught	1	3	EUST	

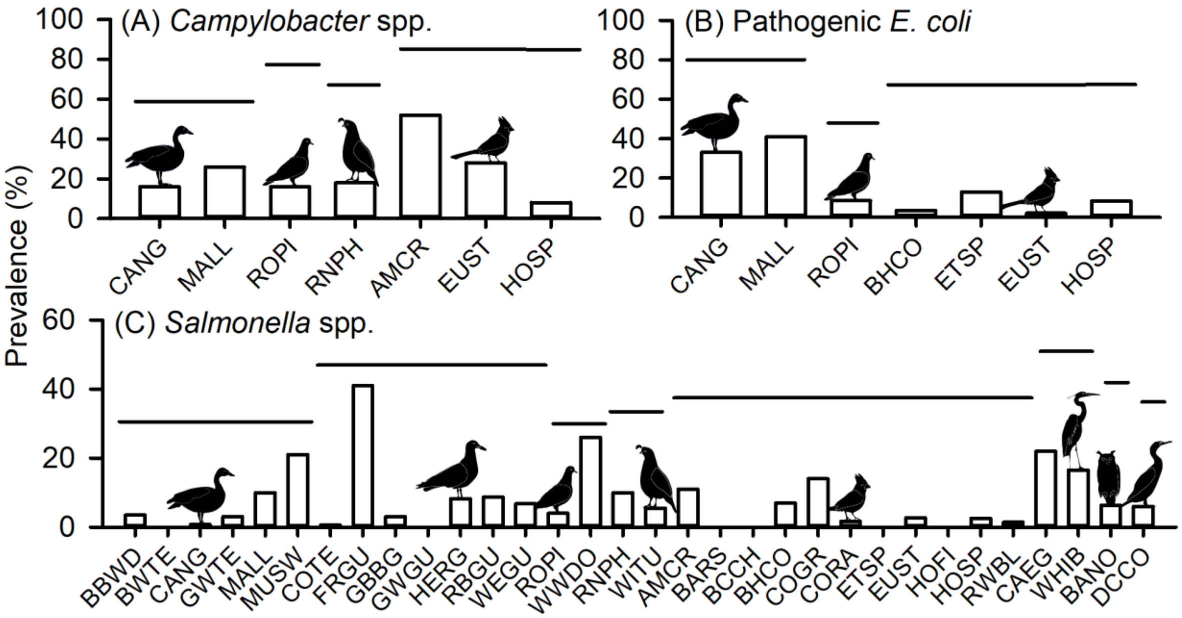

Fig. S7. Estimated prevalence of (A) *Campylobacter* spp., (B) pathogenic *E. coli*, and (C) *Salmonella* spp. for all species with enough observations to estimate prevalence with 5% precision. Bars span taxonomic groups with illustrated representations of order. Four-letter codes follow the American Ornithological Society and can be found in Supplementary Data S2.

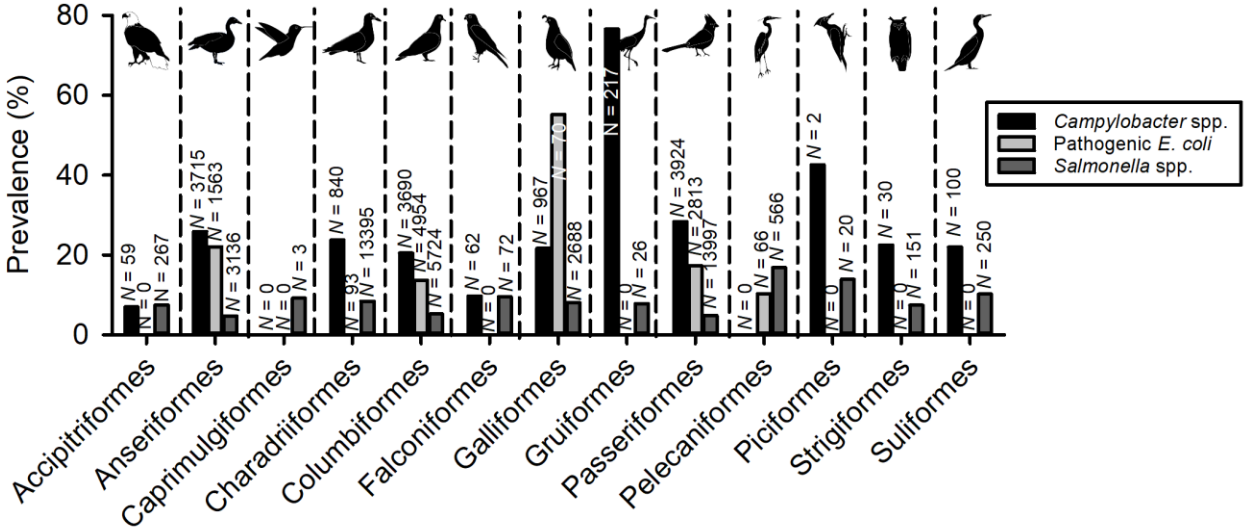

Fig. S8. Estimated prevalence of *Campylobacter* spp., pathogenic *E. coli*, and *Salmonella* spp. by taxonomic order. Number above bar shows number of individuals tested for each pathogen by order.

Table S11. Prevalence of *Campylobacter* spp. by taxonomic order. Total number of individuals reported positive and tested for *Campylobacter* spp. across the literature and prevalence (total positive across the literature/total number tested; *Campylobacter* prevalence) by taxonomic order. Estimated prevalence by taxonomic order using mixed–effects models and corresponding standard errors and 95% confidence intervals are also presented. N/A, not available.

Order	**Positive *Campylobacter* spp.**	**Tested *Campylobacter* spp.**	***Campylobacter* spp. prevalence**	**Estimated prevalence**	**Estimated standard error**	**Estimated 95% confidence interval**
Accipitriformes	3	59	5.1%	7.0%	14.0%	(–20.4, 34.4%)
Anseriformes	997	3715	26.8%	25.9%	4.7%	(16.6%, 35.1%)
Caprimulgiformes	0	0	N/A	N/A	N/A	N/A
Charadriiformes	171	840	20.4%	23.8%	5.6%	(12.7%, 34.8%)
Ciconiiformes	0	0	N/A	N/A	N/A	N/A
Columbiformes	1034	3690	28.0%	20.5%	7.0%	(6.8%, 34.2%)
Coraciiformes	0	0	N/A	N/A	N/A	N/A
Cuculiformes	0	0	N/A	N/A	N/A	N/A
Falconiformes	6	62	9.7%	9.7%	24.1%	(–37.5, 56.9%)
Galliformes	221	967	22.9%	21.7%	7.2%	(7.6%, 35.7%)
Gaviiformes	0	0	N/A	N/A	N/A	N/A
Gruiformes	134	217	61.8%	76.6%	10.6%	(55.9%, 97.3%)
Passeriformes	1270	3924	32.4%	28.4%	4.2%	(20.2%, 36.6%)
Pelecaniformes	0	0	N/A	N/A	N/A	N/A
Piciformes	0	2	0.0%	42.6%	22.9%	(–2.3%, 87.5%)
Podicipediformes	0	0	N/A	N/A	N/A	N/A
Strigiformes	1	30	3.3%	22.5%	9.9%	(3.1%, 41.8%)
Suliformes	22	100	22.0%	22.0%	24.1%	(–25.3%, 69.3%)

Table S12. Tukey HSD pairwise comparisons of *Campylobacter* spp. prevalence in avian taxonomic orders. Values in bold indicate the comparison was significant at *P* = 0.05; SE = standard error.

Comparison	**Estimate**	**SE**	***Z***	***P***
Gruiformes – Passeriformes	**–0.48**	**0.11**	**–4.51**	**<0.0001**
Accipitriformes – Gruiformes	**0.70**	**0.17**	**4.03**	**<0.0001**
Galliformes – Gruiformes	**0.55**	**0.12**	**4.51**	**<0.0001**
Columbiformes – Gruiformes	**0.56**	**0.12**	**4.65**	**<0.0001**
Charadriiformes – Gruiformes	**0.53**	**0.11**	**4.69**	**<0.0001**
Anseriformes – Gruiformes	**0.51**	**0.11**	**4.73**	**<0.0001**
Gruiformes – Strigiformes	**–0.54**	**0.14**	**–3.88**	**0.0001**
Falconiformes – Gruiformes	**0.67**	**0.26**	**2.55**	**0.011**
Gruiformes – Suliformes	**–0.55**	**0.26**	**–2.07**	**0.038**
Accipitriformes – Passeriformes	0.21	0.14	1.51	0.13
Accipitriformes – Anseriformes	0.19	0.14	1.31	0.19
Columbiformes – Passeriformes	0.079	0.068	1.16	0.25
Accipitriformes – Charadriiformes	0.17	0.15	1.14	0.26
Accipitriformes – Galliformes	0.15	0.15	0.95	0.34
Galliformes – Passeriformes	0.067	0.071	0.95	0.34
Accipitriformes – Strigiformes	0.15	0.17	0.93	0.35
Accipitriformes – Columbiformes	0.13	0.15	0.89	0.38
Charadriiformes – Passeriformes	0.046	0.058	0.81	0.42
Falconiformes – Passeriformes	0.19	0.24	0.77	0.44
Anseriformes – Columbiformes	–0.054	0.074	–0.73	0.47
Anseriformes – Falconiformes	–0.16	0.25	–0.66	0.51
Passeriformes – Strigiformes	–0.059	0.10	–0.61	0.54
Charadriiformes – Falconiformes	–0.14	0.25	–0.57	0.57
Anseriformes – Galliformes	–0.042	0.075	–0.56	0.58
Accipitriformes – Suliformes	0.15	0.28	0.54	0.59
Anseriformes – Passeriformes	0.025	0.047	0.53	0.59
Falconiformes – Strigiformes	0.13	0.26	0.49	0.62
Falconiformes – Galliformes	0.12	0.25	0.48	0.63
Columbiformes – Falconiformes	–0.11	0.25	–0.43	0.67
Charadriiformes – Columbiformes	–0.033	0.080	–0.41	0.68
Falconiformes – Suliformes	0.12	0.34	0.36	0.72
Anseriformes – Charadriiformes	–0.021	0.061	–0.35	0.73
Anseriformes – Strigiformes	–0.034	0.10	–0.34	0.74
Passeriformes – Suliformes	–0.064	0.24	–0.26	0.79
Charadriiformes – Galliformes	–0.021	0.083	–0.25	0.80
Columbiformes – Strigiformes	0.020	0.11	0.17	0.86
Anseriformes – Suliformes	–0.039	0.25	–0.16	0.88
Columbiformes – Galliformes	0.012	0.091	0.13	0.90

Charadriiformes – Strigiformes	–0.013	0.11	–0.12	0.90
Accipitriformes – Falconiformes	0.026	0.28	0.09	0.92
Charadriiformes – Suliformes	–0.018	0.25	–0.07	0.94
Galliformes – Strigiformes	0.008	0.12	0.07	0.94
Columbiformes – Suliformes	0.015	0.25	0.06	0.95
Strigiformes – Suliformes	–0.005	0.26	–0.02	0.99
Galliformes – Suliformes	0.003	0.25	0.01	0.99

Table S13. Prevalence of pathogenic (path) *E. coli* by taxonomic order. Total number of individuals reported positive and tested for pathogenic *E. coli* across the literature and prevalence (total positive across the literature/total number tested; Path *E. coli* prevalence) by taxonomic order. Estimated prevalence by taxonomic order using mixed-effects models and corresponding standard errors and 95% confidence intervals are also presented. N/A, not available.

Order	**Positive path *E. coli***	**Tested path *E. coli***	**Path *E. coli* prevalence**	**Estimated prevalence**	**Estimated standard error**	**Estimated 95% confidence interval**
Accipitriformes	0	0	N/A	N/A	N/A	N/A
Anseriformes	553	1563	35.4%	22.1%	10.3%	(2.0%, 42.2%)
Caprimulgiformes	0	0	N/A	N/A	N/A	N/A
Charadriiformes	0	93	0.0%	–1.7%	20.9%	(–42.6%, 39.2%)
Ciconiiformes	0	0	N/A	N/A	N/A	N/A
Columbiformes	402	4954	8.1%	13.6	3.5	(6.7%, 20.5%)
Coraciiformes	0	0	N/A	N/A	N/A	N/A
Cuculiformes	0	0	N/A	N/A	N/A	N/A
Falconiformes	0	0	N/A	N/A	N/A	N/A
Galliformes	40	70	57.1%	55.2%	16.6%	(22.6%, 87.8%)
Gaviiformes	0	0	N/A	N/A	N/A	N/A
Gruiformes	0	0	N/A	N/A	N/A	N/A
Passeriformes	179	2439	7.3%	17.3%	8.3%	(1.1%, 33.6%)
Pelecaniformes	1	66	1.5%	10.3%	13.4%	(–15.5%, 36.0%)
Piciformes	0	0	N/A	N/A	N/A	N/A
Podicipediformes	0	0	N/A	N/A	N/A	N/A
Strigiformes	0	0	N/A	N/A	N/A	N/A
Suliformes	0	0	N/A	N/A	N/A	N/A

Table S14. Tukey HSD pairwise comparisons of pathogenic *E. coli* prevalence in avian taxonomic orders. Values in bold indicate the comparison was significant at *P* = 0.05; SE = standard error.

Comparison	**Estimate**	**SE**	***Z***	***P***
Charadriiformes – Galliformes	**0.57**	**0.26**	**2.23**	**0.026**
Galliformes – Pelecaniformes	**–0.45**	**0.21**	**–2.17**	**0.030**
Galliformes – Passeriformes	**–0.38**	**0.18**	**–2.12**	**0.034**
Anseriformes – Galliformes	**0.33**	**0.18**	**1.80**	**0.072**
Columbiformes – Galliformes	0.41	0.26	1.56	0.12
Anseriformes – Charadriiformes	–0.24	0.22	–1.07	0.28
Charadriiformes – Passeriformes	0.19	0.22	0.87	0.38
Anseriformes – Pelecaniformes	–0.12	0.16	–0.74	0.46
Charadriiformes – Columbiformes	0.16	0.29	0.56	0.58
Passeriformes – Pelecaniformes	–0.071	0.14	–0.50	0.61
Charadriiformes – Pelecaniformes	0.12	0.24	0.49	0.62
Anseriformes – Passeriformes	–0.048	0.12	–0.39	0.70
Anseriformes – Columbiformes	–0.077	0.23	–0.34	0.73
Columbiformes – Pelecaniformes	–0.042	0.24	–0.18	0.86
Columbiformes – Passeriformes	0.029	0.22	0.13	0.89

Table S15. Prevalence of *Salmonella* spp. by taxonomic order. Total number of individuals reported positive and tested for *Salmonella* spp. across the literature and prevalence (total positive across the literature/total number tested; *Salmonella* prevalence) by taxonomic order. Estimated prevalence by taxonomic order using mixed-effects models and corresponding standard errors and 95% confidence intervals are also presented. N/A, not available.

Order	**Positive *Salmonella* spp.**	**Tested *Salmonella* spp.**	***Salmonella* spp. prevalence**	**Estimated prevalence**	**Estimated standard error**	**Estimated 95% confidence interval**
Accipitriformes	22	267	8.2%	7.5%	3.5%	(0.7%, 14.3%)
Anseriformes	71	3136	2.3%	4.7%	1.2%	(2.3%, 7.0%)
Caprimulgiformes	0	3	0.0%	9.2%	17.9%	(–25.9%, 44.2%)
Charadriiformes	1063	13395	7.9%	8.4%	1.5%	(5.5%, 11.2%)
Ciconiiformes	0	0	N/A	N/A	N/A	N/A
Columbiformes	211	5724	3.7%	5.2%	1.3%	(2.7%, 7.7%)
Coraciiformes	0	0	N/A	N/A	N/A	N/A
Cuculiformes	0	0	N/A	N/A	N/A	N/A
Falconiformes	2	72	2.8%	9.5%	6.2%	(–2.7%, 21.8%)

Galliformes	52	2688	1.9%	8.0%	2.6%	(2.8%, 13.1%)
Gaviiformes	0	0	N/A	N/A	N/A	N/A
Gruiformes	1	26	3.8%	7.8%	6.6%	(–5.0%, 20.7%)
Passeriformes	377	13997	2.7%	4.8%	1.0%	(2.9%, 6.8%)
Pelecaniformes	136	566	24.0%	16.8%	3.7%	(9.6%, 24.0%)
Piciformes	3	20	15.0%	13.9%	6.4%	(1.2%, 26.5%)
Podicipediformes	0	0	N/A	N/A	N/A	N/A
Strigiformes	11	151	7.3%	7.4%	3.1%	(1.5%, 13.4%)
Suliformes	15	250	6.0%	10.2%	3.2%	(4.0%, 16.4%)

Table S16. Tukey HSD pairwise comparisons of *Salmonella* spp. prevalence in avian taxonomic orders. Values in bold indicate the comparison was significant at *P* = 0.05; SE = standard error.

Comparisons	**Estimate**	**SE**	***Z***	***P***
Passeriformes – Pelecaniformes	**0.12**	**0.037**	**3.25**	**0.0011**
Anseriformes – Pelecaniformes	**0.12**	**0.038**	**3.23**	**0.0012**
Columbiformes – Pelecaniformes	**0.12**	**0.038**	**3.08**	**0.0020**
Charadriiformes – Passeriformes	**–0.035**	**0.013**	**–2.70**	**0.007**
Anseriformes – Charadriiformes	**0.037**	**0.015**	**2.45**	**0.014**
Charadriiformes – Pelecaniformes	**0.084**	**0.039**	**2.19**	**0.029**
Charadriiformes – Columbiformes	**–0.032**	**0.016**	**–2.02**	**0.043**
Pelecaniformes – Strigiformes	**–0.094**	**0.047**	**–1.99**	**0.047**
Galliformes – Pelecaniformes	**0.088**	**0.045**	**1.97**	**0.049**
Accipitriformes – Pelecaniformes	0.093	0.050	1.86	0.064
Anseriformes – Suliformes	0.056	0.032	1.72	0.085
Passeriformes – Suliformes	0.054	0.031	1.72	0.086
Columbiformes – Suliformes	0.050	0.032	1.54	0.12
Anseriformes – Piciformes	0.092	0.064	1.43	0.15
Passeriformes – Piciformes	0.091	0.064	1.42	0.16
Pelecaniformes – Suliformes	–0.066	0.048	–1.38	0.17
Columbiformes – Piciformes	0.087	0.064	1.35	0.18
Anseriformes – Galliformes	0.033	0.028	1.19	0.24
Galliformes – Passeriformes	–0.031	0.027	–1.16	0.25
Falconiformes – Pelecaniformes	0.072	0.072	1.00	0.32
Columbiformes – Galliformes	0.028	0.028	0.98	0.33
Anseriformes – Strigiformes	0.028	0.030	0.94	0.35
Piciformes – Strigiformes	–0.064	0.071	–0.91	0.36
Accipitriformes – Piciformes	0.064	0.073	0.88	0.38
Passeriformes – Strigiformes	0.026	0.030	0.86	0.39
Galliformes – Piciformes	0.059	0.069	0.85	0.39
Charadriiformes – Piciformes	0.055	0.065	0.85	0.40
Accipitriformes – Anseriformes	–0.028	0.036	–0.78	0.44

Anseriformes – Falconiformes	0.049	0.063	0.77	0.44
Falconiformes – Passeriformes	–0.047	0.063	–0.75	0.45
Accipitriformes – Passeriformes	–0.026	0.036	–0.74	0.46
Columbiformes – Strigiformes	0.023	0.031	0.72	0.47
Columbiformes – Falconiformes	0.044	0.064	0.69	0.49
Strigiformes – Suliformes	0.028	0.043	0.64	0.52
Charadriiformes – Suliformes	0.018	0.029	0.64	0.52
Accipitriformes – Columbiformes	–0.023	0.037	–0.62	0.54
Accipitriformes – Suliformes	0.027	0.047	0.59	0.56
Galliformes – Suliformes	0.022	0.041	0.55	0.58
Piciformes – Suliformes	–0.037	0.071	–0.52	0.60
Anseriformes – Gruiformes	0.032	0.066	0.49	0.63
Falconiformes – Piciformes	0.043	0.090	0.48	0.63
Gruiformes – Passeriformes	–0.030	0.066	–0.46	0.65
Anseriformes – Columbiformes	0.005	0.013	0.43	0.67
Columbiformes – Gruiformes	0.026	0.066	0.40	0.69
Pelecaniformes – Piciformes	–0.029	0.074	–0.40	0.69
Columbiformes – Passeriformes	–0.004	0.010	–0.38	0.71
Accipitriformes – Falconiformes	0.021	0.063	0.33	0.74
Falconiformes – Strigiformes	–0.021	0.068	–0.31	0.76
Charadriiformes – Strigiformes	–0.009	0.032	–0.29	0.78
Accipitriformes – Charadriiformes	0.009	0.037	0.24	0.81
Falconiformes – Galliformes	–0.016	0.068	–0.23	0.81
Falconiformes – Gruiformes	–0.017	0.090	–0.19	0.85
Anseriformes – Passeriformes	0.002	0.009	0.19	0.85
Charadriiformes – Falconiformes	0.012	0.064	0.18	0.85
Charadriiformes – Galliformes	–0.004	0.029	–0.14	0.89
Galliformes – Strigiformes	–0.005	0.040	–0.13	0.90
Accipitriformes – Galliformes	0.005	0.044	0.11	0.91
Falconiformes – Suliformes	0.007	0.070	0.094	0.93
Charadriiformes – Gruiformes	–0.005	0.067	–0.080	0.94
Accipitriformes – Gruiformes	0.004	0.074	0.050	0.96
Galliformes – Gruiformes	–0.001	0.071	–0.018	0.99
Accipitriformes – Strigiformes	–0.0002	0.042	–0.005	1.00

Table S17. Chi-square test for bias in testing within bird orders for *Campylobacter* spp., *E. coli*, and *Salmonella* spp. for a vulnerable farming population. Comparison uses percentage of species within an order. Exp. = expected, path = pathogenic, gen = generic; *Campylobacter* spp. (χ^2_{13} =73,612, $P < 0.0001$), pathogenic *E. coli* (χ^2_{13} =90,389, $P < 0.0001$), generic *E. coli* (χ^2_{13} =69,170, $P < 0.0001$), and *Salmonella* spp. (χ^2_{13} =215,468, $P < 0.0001$).

Order	**Species**	**% Farm bird species**	**Tested *Campylobacter* spp.**	**Exp. *Campylobacter* spp.**	**Tested path *E. coli***	**Exp. path *E. coli***	**Tested gen *E. coli***	**Exp. gen *E. coli***	**Tested *Salmonella* spp.**	**Exp. *Salmonella* spp.**
Accipitriformes	11	8.15%	59	1109	0	779	111	251	267	3283
Anseriformes	3	2.22%	3715	302	1563	212	1949	69	3136	895
Caprimulgiformes	5	3.70%	0	504	0	354	0	114	3	1492
Charadriiformes	3	2.22%	843	302	93	212	730	69	13395	895
Columbiformes	4	2.96%	3690	403	4954	283	1055	91	5724	1194
Cuculiformes	1	0.74%	0	101	0	71	0	23	0	298
Falconiformes	3	2.22%	62	302	0	212	1	69	72	895
Galliformes	3	2.22%	967	302	70	212	180	69	2688	895
Gruiformes	1	0.74%	217	101	0	71	30	23	26	298
Passeriformes	91	67.41%	3924	9171	2439	6443	2872	2080	13997	27162
Pelecaniformes	1	0.74%	0	101	66	71	72	23	566	298
Piciformes	7	5.19%	2	705	0	496	0	160	20	2089
Podicipediformes	1	0.74%	0	101	0	71	0	23	0	298
Strigiformes	1	0.74%	30	101	0	71	2	23	151	298

Table S18. Chi-square test for bias in testing within bird orders for *Campylobacter* spp., *E. coli*, and *Salmonella* spp. for a vulnerable farming population. Comparison uses percentage of total sightings. Exp. = expected, path = pathogenic, gen = generic; *Campylobacter* spp. (χ^2_{13} =172,355, $P < 0.0001$), pathogenic *E. coli* (χ^2_{13} =58,180, $P < 0.0001$), generic *E. coli* (χ^2_{13} =210,390, $P < 0.0001$), and *Salmonella* spp. (χ^2_{13} =318,036, $P < 0.0001$).

Order	**Species**	**% Sightings**	**Tested *Campylobacter* spp.**	**Exp. *Campylobacter* spp.**	**Tested path *E. coli***	**Exp. path *E. coli***	**Tested gen *E. coli***	**Exp. gen *E. coli***	**Tested *Salmonella* spp.**	**Exp. *Salmonella* spp.**
Accipitriformes	11	0.78%	59	107	0	75	111	24	267	316
Anseriformes	3	0.62%	3715	84	1563	59	1949	19	3136	249
Caprimulgiformes	5	1.34%	0	183	0	128	0	41	3	541
Charadriiformes	3	1.67%	843	227	93	159	730	51	13395	672
Columbiformes	4	10.79%	3690	1468	4954	1032	1055	333	5724	4348
Cuculiformes	1	0.01%	0	1	0	1	0	0	0	3
Falconiformes	3	0.20%	62	27	0	19	1	6	72	79
Galliformes	3	1.12%	967	152	70	107	180	34	2688	450
Gruiformes	1	0.29%	217	40	0	28	30	9	26	119
Passeriformes	91	81.72%	3924	11119	2439	7812	2872	2522	13997	32929
Pelecaniformes	1	0.05%	0	6	66	4	72	1	566	18
Piciformes	7	1.40%	2	190	0	133	0	43	20	562
Podicipediformes	1	0.01%	0	1	0	1	0	0	0	3
Strigiformes	1	0.02%	30	2	0	1	2	0	151	6

Table S19. Number and percentage of farm bird species and number of combined sightings of species and percentage of total sightings for species with enough data to calculate prevalence for three, two, or one pathogen, those with some data and those with no data. Data on farm bird species from Smith *et al*. (2019).

Category	**# Species**	**% Species**	**# Sightings**	**% Sightings**
3 pathogens	5	3.7%	3306	25.0%
2 pathogens	3	2.2%	441	3.3%
1 pathogens	7	5.2%	2031	15.3%
Some observations	65	48.5%	6413	48.5%
No observations	54	40.3%	1043	7.9%

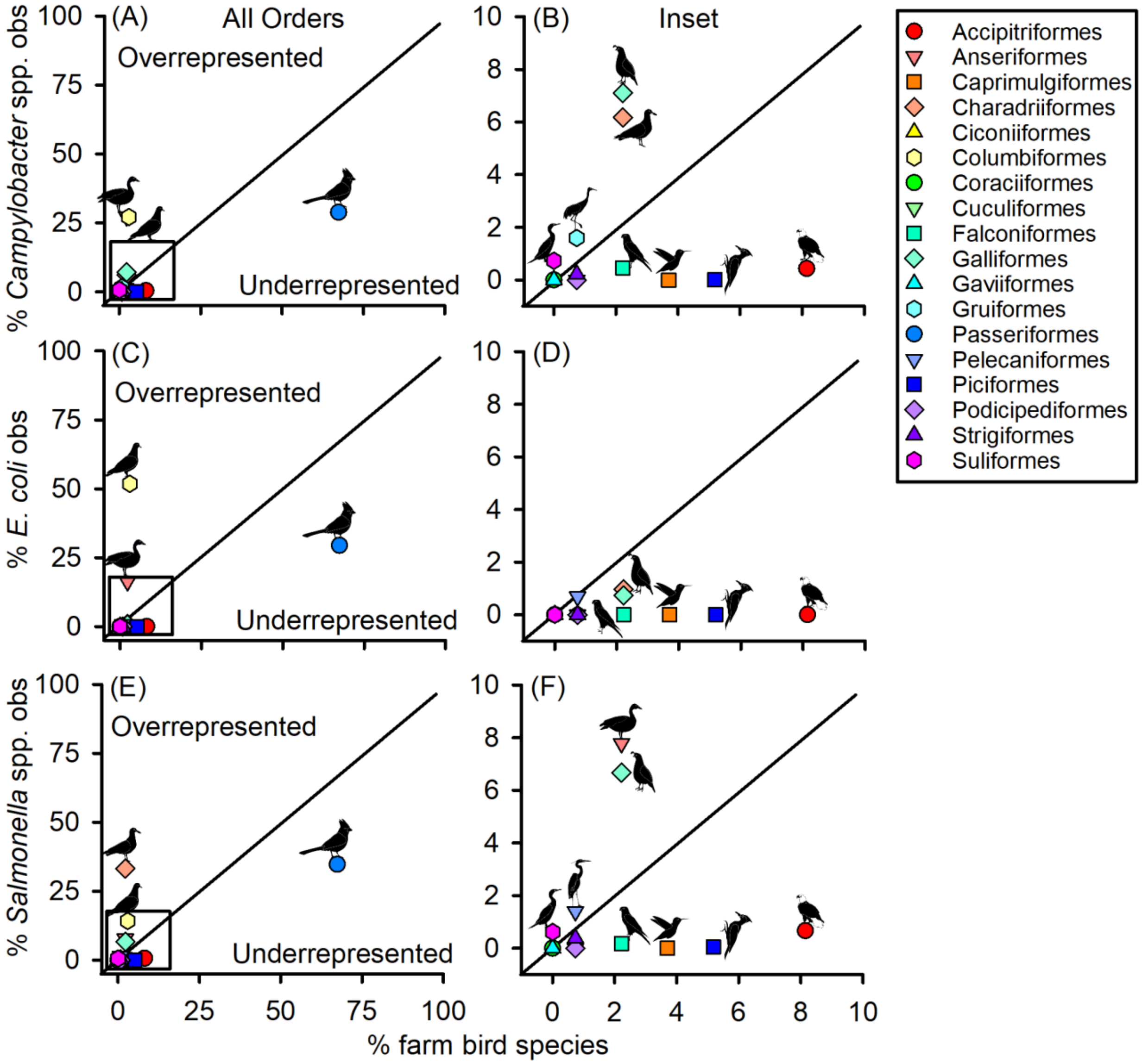

Fig. S9. Scatterplot showing the percentage of pathogen observations (obs) belonging to each taxonomic order *versus* % of farm bird species observed by Smith *et al.* (2019). A, C and E show all orders; B, D and F show orders that comprise less than 10% of pathogen observations and less than 10% of farm bird observations (boxed regions in A, C and E, respectively).

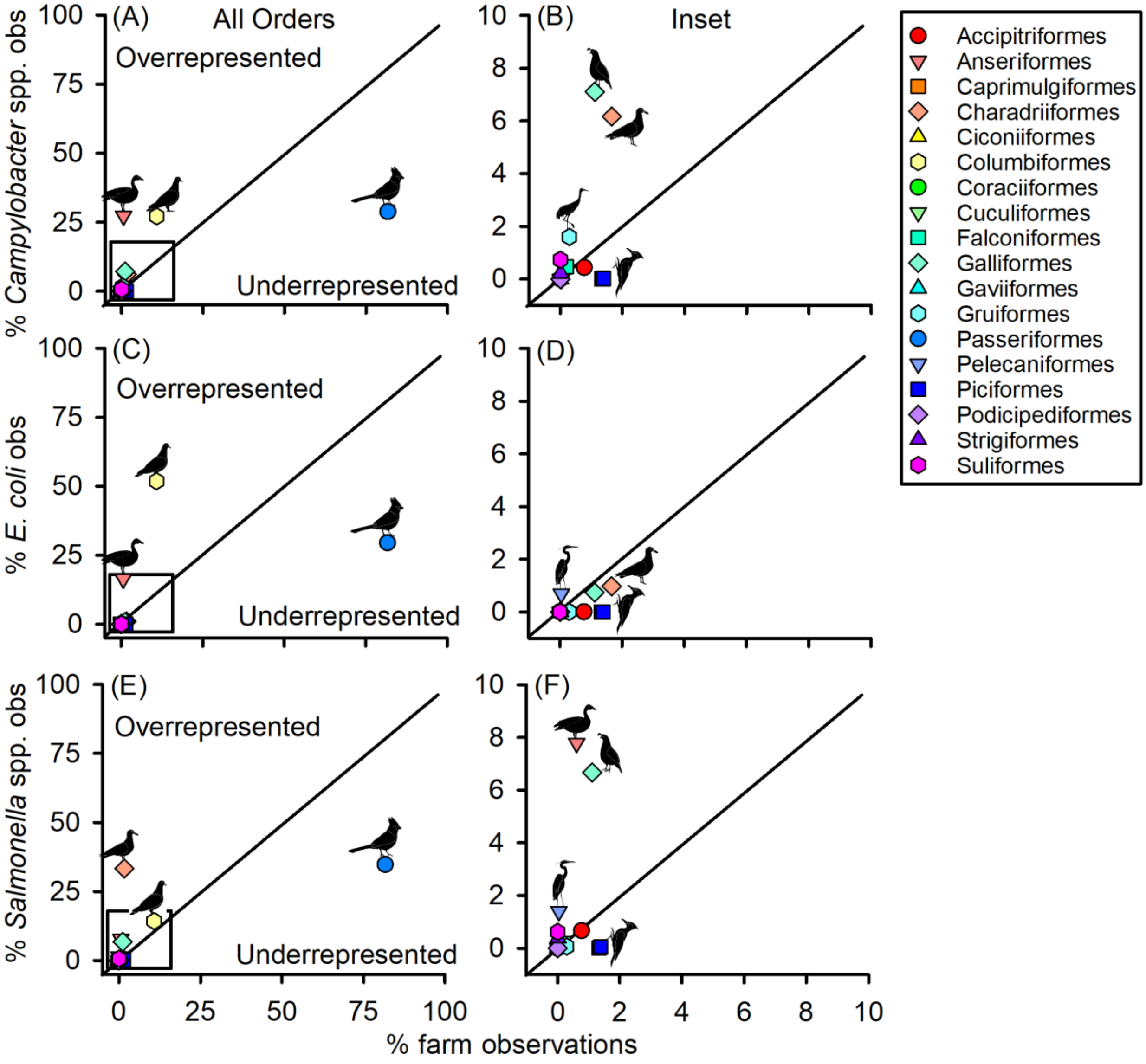

Fig. S10. Scatterplot showing the percentage of pathogen observations (obs) belonging to each taxonomic order *versus* % of total observations on farms within each taxa by Smith *et al.* (2019). A, C and E show all orders; B, D and F show orders that comprise less than 10% of pathogen observations and less than 10% of farm bird observations (boxed regions in A, C and E, respectively).

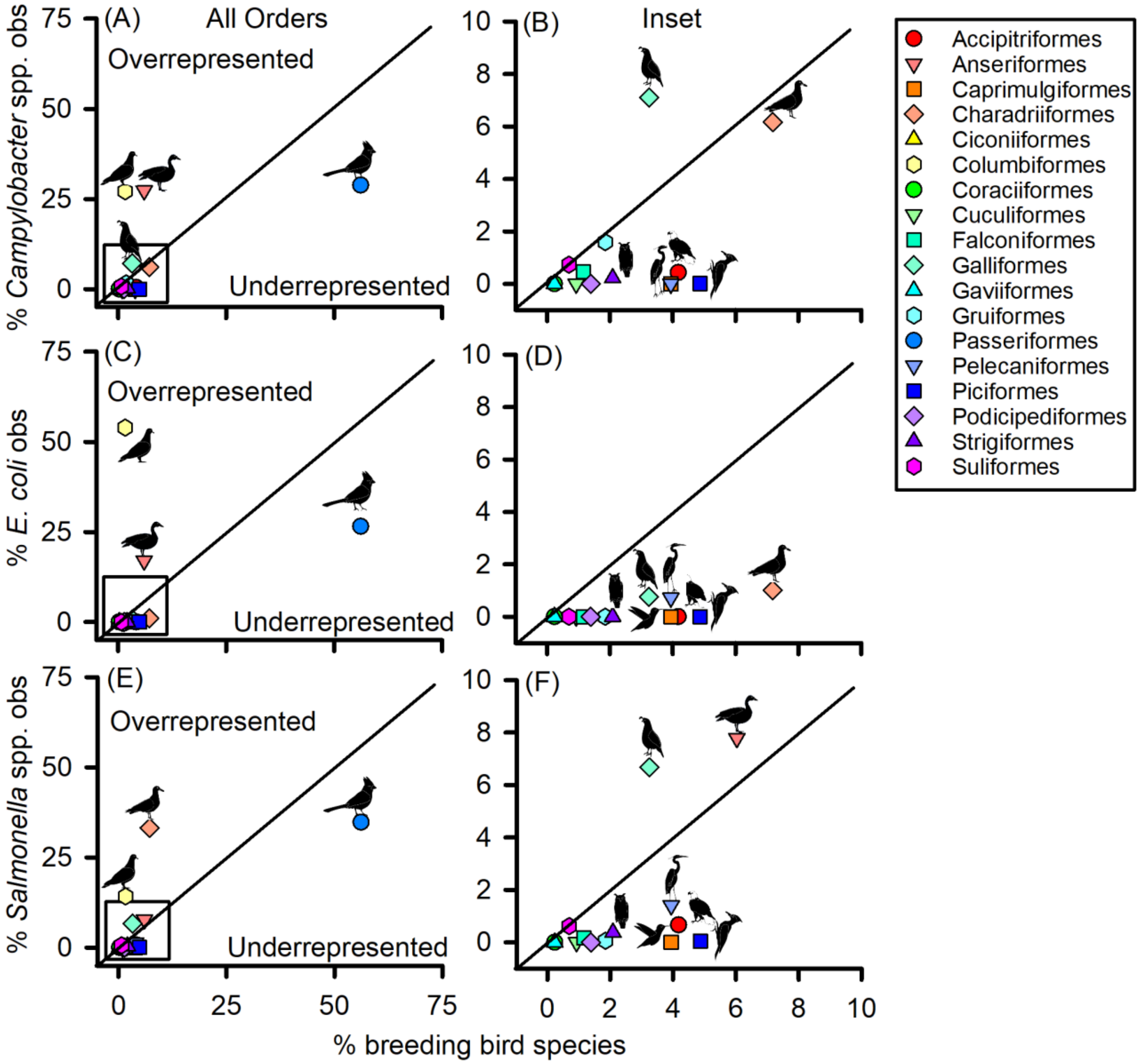

Fig. S11. Scatterplot showing the percentage of pathogen observations (obs) belonging to each taxonomic order *versus* % of North American breeding birds each taxon comprises. A, C and E show all orders; B, D and F show orders that comprise less than 10% of pathogen observations and less than 10% of North American breeding bird species (boxed regions in A, C and E, respectively).

Table S20. Chi-square test for bias in testing within bird order for *Campylobacter* spp., *E. coli*, and *Salmonella* spp. in North American breeding birds by percentage of species within each order. NA = North American, Exp. = expected, path = pathogenic, gen = generic.

Order	**Species**	**% NA species**	**Tested *Campylobacter* spp.**	**Exp. *Campylobacter* spp.**	**Tested path *E. coli***	**Exp. path *E. coli***	**Tested gen *E. coli***	**Exp. gen *E. coli***	**Tested *Salmonella* spp.**	**Exp. *Salmonella* spp.**
Accipitriformes	18	4.18%	59	569	0	340	111	129	267	1684
Anseriformes	26	6.03%	3715	821	1563	577	1949	186	3136	2431
Caprimulgiformes	17	3.94%	0	537	0	377	0	122	3	1589
Charadriiformes	31	7.19%	840	978	93	687	730	222	13395	2897
Ciconiiformes	1	0.23%	0	32	0	22	0	7	0	93
Columbiformes	7	1.62%	3690	221	4954	155	1055	50	5724	654
Coraciiformes	1	0.23%	0	32	0	22	0	7	0	93
Cuculiformes	4	0.93%	0	126	0	89	0	29	0	374
Falconiformes	5	1.16%	62	158	0	111	1	36	72	467
Galliformes	14	3.25%	967	442	70	311	180	100	2688	1309
Gaviiformes	1	0.23%	0	32	0	22	0	7	0	93
Gruiformes	8	1.86%	217	253	0	177	30	57	26	748
Passeriformes	242	56.15%	3924	7640	2439	5367	2872	1733	13997	22625
Pelecaniformes	17	3.94%	0	537	66	377	72	122	566	1589
Piciformes	21	4.87%	2	663	0	466	0	150	20	1963
Podicipediformes	6	1.39%	0	189	0	133	0	43	0	561
Strigiformes	9	2.09%	30	284	0	200	2	64	151	841
Suliformes	3	0.70%	100	95	0	67	0	21	250	280

Table S21. Chi-square test for bias in testing within bird order for *Campylobacter* spp., *E. coli*, and *Salmonella* spp. in North American breeding birds by relative abundance reported in eBird. Exp. = expected, path = pathogenic, gen = generic.

Order	**Species**	**% eBird reports**	**Tested *Campylobacter* spp.**	**Exp. *Campylobacter* spp.**	**Tested path *E. coli***	**Exp. path *E. coli***	**Tested gen *E. coli***	**Exp. gen *E. coli***	**Tested *Salmonella* spp.**	**Exp. *Salmonella* spp.**
Accipitriformes	18	5.16%	59	702	0	493	111	159	267	2080
Anseriformes	26	8.76%	3715	1192	1563	838	1949	270	3136	3531
Caprimulgiformes	17	1.50%	0	204	0	143	0	46	3	604
Charadriiformes	31	5.62%	840	764	93	537	730	173	13395	2263
Ciconiiformes	1	0.06%	0	8	0	6	0	2	0	25
Columbiformes	7	4.11%	3690	559	4954	393	1055	127	5724	1656
Coraciiformes	1	0.58%	0	79	0	55	0	18	0	234
Cuculiformes	4	0.21%	0	28	0	20	0	6	0	83
Falconiformes	5	0.77%	62	105	0	74	1	24	72	312
Galliformes	14	0.63%	967	86	70	60	180	19	2688	253
Gaviiformes	1	0.24%	0	33	0	23	0	7	0	96
Gruiformes	8	1.06%	217	144	0	101	30	33	26	426
Passeriformes	242	59.19%	3924	8054	2439	5658	2872	1827	13997	23851
Pelecaniformes	17	4.10%	0	558	66	392	72	127	566	1652
Piciformes	21	5.80%	2	789	0	554	0	179	20	2336
Podicipediformes	6	0.88%	0	119	0	84	0	27	0	353
Strigiformes	9	0.33%	30	45	0	32	2	10	151	135
Suliformes	3	1.01%	100	137	0	96	0	31	250	405

Table S22. Number and percentage of North American breeding bird species and number of combined eBird sightings of species and percentage of total sightings with enough data to calculate prevalence for three, two, or one pathogen, those with some data and those with no data.

Category	**# Species**	**% Species**	**# Sightings**	**% Sightings**
3 pathogens	5	1.2%	26,477,111	7.6%
2 pathogens	4	0.9%	10,962,473	3.1%
1 pathogens	23	5.3%	41,837,705	12.0%
Some observations	119	27.6%	178,879,007	51.4%
No observations	280	65.0%	90,065,928	25.9%

Table S23. Comparison of estimated prevalence by substance tested for house sparrow. Table includes prevalence estimated by summing across literature [positive (+)/number tested (*N*) (percentage); positive/tested] and estimated through a mixed-effects model in the rma.mv function in the metafor package in R (estimated prevalence). The column on the left in each case indicates the substance listed first in the comparison column, and the column on the right indicates the substance listed second in the comparison column. The right side of the table includes Tukey HSD pairwise comparisons.

Comparison	**Positive/tested**		**Estimated prevalence**		**Tukey HSD comparison**			
	+/*N* (%)	+/*N* (%)	% ± SE	% ± SE	Estimate	SE	*Z*	*P*
Cloaca – Faeces	25/3847 (0.9%)	0/557 (0%)	0.7% ± 0.2%	0.2% ± 0.2%	–0.005	0.002	–2.1	0.035
Cloaca – Necropsy	25/3847 (0.9%)	57/1046 (5.4%)	0.7% ± 0.2%	4.0% ± 0.6%	0.033	0.006	5.33	< 0.0001
Faeces – Necropsy	0/557 (0%)	57/1046 (5.4%)	0.2% ± 0.2%	4.0% ± 0.6%	0.038	0.006	6.06	< 0.0001

Table S24. Comparison of estimated prevalence by substance tested for European starling. Table includes prevalence estimated by summing across literature [positive (+)/number tested (*N*) (percentage); positive/tested] and estimated through a mixed-effects model in the rma.mv function in the metafor package in R (estimated prevalence). The column on the left in each case indicates the substance listed first in the comparison column, and the column on the right indicates the substance listed second in the comparison column. The right side of the table includes Tukey HSD pairwise comparisons.

Comparison	**Positive/tested**		**Estimated prevalence**		**Tukey HSD comparison**			
	+/*N* (%)	+/*N* (%)	% ± SE	% ± SE	Estimate	SE	*Z*	*P*
Cloaca – Faeces	63/1013 (6.2%)	6/858 (0.7%)	3.3% ± 2.5%	1.0% ± 2.3%	–0.023	0.034	–0.66	0.51
Cloaca – Necropsy	63/1013 (6.2%)	35/378 (9.3%)	3.3% ± 2.5%	4.9% ± 2.3%	0.016	0.034	0.48	0.63
Faeces – Necropsy	6/858 (0.7%)	35/378 (9.3%)	1.0% ± 2.3%	4.9% ± 2.3%	0.039	0.033	1.19	0.23

Table S25. Comparison of estimated prevalence by substance tested for rock pigeon. Table includes prevalence estimated by summing across literature [positive (+)/number tested (*N*) (percentage); positive/tested] and estimated through a mixed-effects model in the rma.mv function in the metafor package in R (estimated prevalence). The column on the left in each case indicates the substance listed first in the comparison column, and the column on the right indicates the substance listed second in the comparison column. The right side of the table includes Tukey HSD pairwise comparisons.

Comparison	**Positive/tested**		**Estimated prevalence**		**Tukey HSD comparison**			
	+/*N* (%)	+/*N* (%)	% ± SE	% ± SE	Estimate	SE	*Z*	*P*
Blood – Cloaca	1/240 (0.4%)	96/3904 (2.5%)	0.4% ± 4.8%	3.7% ± 1.3%	0.033	0.49	0.66	0.51
Blood – Faeces	1/240 (0.4%)	20/832 (2.4%)	0.4% ± 4.8%	1.9% ± 2.4%	0.014	0.054	0.27	0.79
Blood – Necropsy	1/240 (0.4%)	16/265 (6.0%)	0.4% ± 4.8%	6.6% ± 3.6%	0.062	0.055	1.13	0.26
Cloaca – Faeces	96/3904 (2.5%)	96/3904 (2.5%)	3.7% ± 1.3%	1.9% ± 2.4%	–0.018	0.028	–0.67	0.50
Cloaca – Necropsy	96/3904 (2.5%)	16/265 (6.0%)	3.7% ± 1.3%	6.6% ± 3.6%	0.029	0.029	0.98	0.33
Faeces – Necropsy	20/832 (2.4%)	16/265 (6.0%)	1.9% ± 2.4%	6.6% ± 3.6%	0.047	0.036	1.32	0.19

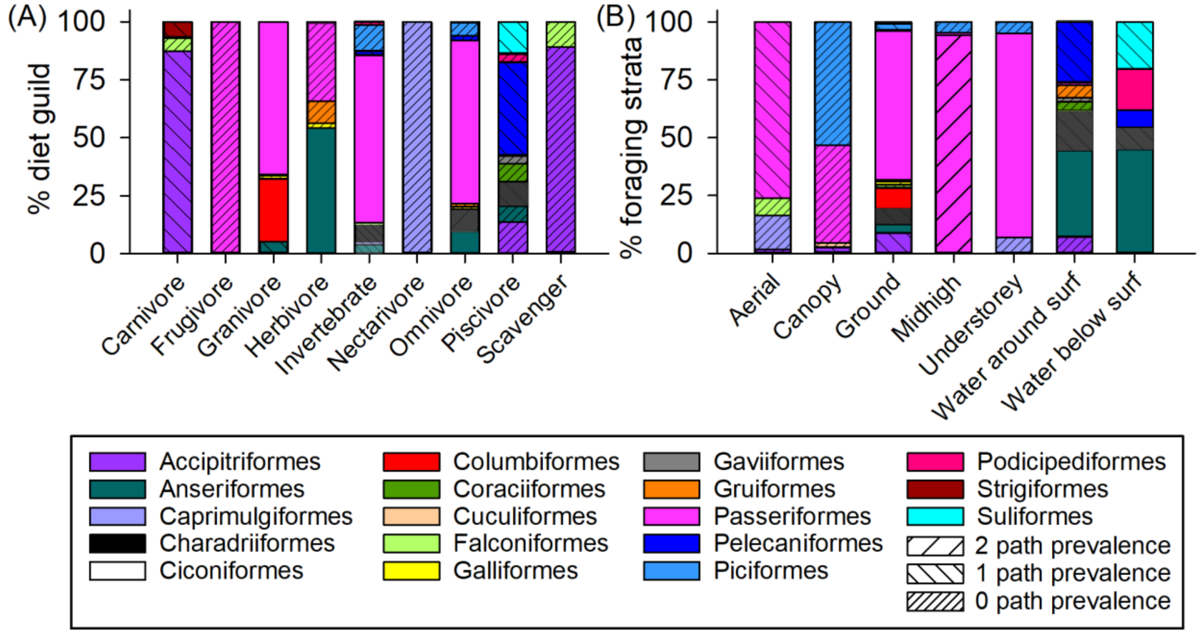

Fig. S12. Percentage of total (A) diet guild and (B) foraging strata comprised by each taxonomic order denoted by colour. Pattern indicates if enough data were available to determine prevalence with 5% precision for 0 (smallest grain stripe) to three pathogens (no pattern).

Table S26. Prevalence of *Campylobacter* spp. by diet guild in wild birds. Total number of individuals reported positive and tested for *Campylobacter* spp. across the literature and prevalence (total positive across the literature/total number tested) by diet guild. Estimated prevalence by diet guild using mixed-effects models and corresponding standard errors and 95% confidence intervals are also presented.

Diet guild	***Campylobacter* spp. positive**	***Campylobacter* spp. tested**	***Campylobacter* spp. prevalence**	**Estimated prevalence**	**Estimated standard error**	**Estimated 95% confidence interval**
Scavenger	0	3	0.0%	–1.6%	21.6%	(–43.9%, 40.6%)
Carnivore	10	148	6.8%	18.6%	9.6%	(–0.2%, 37.3%)
Piscivore	25	315	7.9%	19.3%	11.7%	(–3.6%, 42.2%)
Herbivore	313	1519	20.6%	23.4%	6.3%	(11.0%, 35.8%)
Invertebrate	54	258	20.9%	35.1%	7.0%	(21.5%, 48.8%)
Granivore	1228	4791	25.6%	22.2%	5.4%	(11.5%, 32.9%)
Omnivore	2229	6572	33.9%	30.9%	4.3%	(22.6%, 39.2%)
Frugivore	0	0	N/A	N/A	N/A	N/A
Nectarivore	0	0	N/A	N/A	N/A	N/A

Table S27. Tukey HSD pairwise comparisons examining *Campylobacter* spp. prevalence by diet guild. SE = standard error.

Comparison	**Estimate**	**SE**	***Z***	***P***
Granivore – Invertebrate	0.13	0.077	1.67	0.095
Granivore – Omnivore	0.087	0.056	1.56	0.12
Carnivore – Invertebrate	0.17	0.11	1.47	0.14
Herbivore – Invertebrate	0.12	0.085	1.39	0.16
Carnivore – Omnivore	0.12	0.10	1.25	0.21
Invertebrate – Piscivore	–0.16	0.13	–1.21	0.23
Herbivore – Omnivore	0.075	0.064	1.17	0.24
Omnivore – Piscivore	–0.12	0.12	–0.98	0.33
Invertebrate – Omnivore	–0.042	0.071	–0.59	0.55
Carnivore – Herbivore	0.048	0.11	0.44	0.66
Carnivore – Granivore	0.036	0.10	0.35	0.73
Herbivore – Piscivore	–0.041	0.13	–0.32	0.75
Granivore – Piscivore	–0.029	0.12	–0.24	0.81
Granivore – Herbivore	0.012	0.072	0.16	0.87
Carnivore – Piscivore	0.007	0.15	0.048	0.96

Table S28. Prevalence of *Campylobacter* spp. by foraging strata in wild birds. Total number of individuals reported positive and tested for *Campylobacter* spp. across the literature and prevalence (total positive across the literature/total number tested) by foraging strata. Estimated prevalence by foraging strata using mixed-effects models and corresponding standard errors and 95% confidence intervals are also presented.

Foraging strata	***Campylobacter* spp. positive**	***Campylobacter* spp. Tested**	***Campylobacter* spp. prevalence**	**Estimated prevalence**	**Estimated standard error**	**Estimated 95% confidence interval**
Canopy	0	2	0.0%	42.3%	23.7%	(–4.2%, 88.6%)
Midhigh	1	23	4.3%	29.5%	11.1%	(7.8%, 51.1%)
Water below surf	37	338	10.9%	32.9%	9.6%	(14.1%, 51.6%)
Aerial	33	245	13.5%	15.8%	10.8%	(–5.3%, 36.9%)
Understorey	43	311	13.8%	29.1%	8.8%	(11.8%, 46.3%)
Ground	2989	10136	29.5%	28.2%	4.1%	(20.2%, 36.3%)
Water around surf	756	2551	29.6%	24.2%	5.4%	(14.1%, 51.6%)

Table S29. Tukey HSD pairwise comparisons examining *Campylobacter* spp. prevalence by foraging strata. SE = standard error.

Comparison	**Estimate**	**SE**	***Z***	***P***
Aerial – Water below surf	0.17	0.14	1.21	0.22
Aerial – Ground	0.12	0.11	1.13	0.26
Aerial – Understorey	0.13	0.13	0.99	0.32
Aerial – Midhigh	0.14	0.15	0.91	0.36
Water Around Surf – Water below surf	0.087	0.10	0.85	0.40
Ground – Water around surf	–0.041	0.054	–0.75	0.45
Aerial – Water around surf	0.084	0.12	0.73	0.47
Understorey – Water around surf	–0.049	0.095	–0.51	0.61
Ground – Water below surf	0.046	0.10	0.48	0.63
Midhigh – Water around surf	–0.053	0.12	–0.45	0.65
Understorey – Water below surf	0.038	0.12	0.31	0.76
Ground – Midhigh	0.012	0.11	0.11	0.91
Ground – Understorey	0.008	0.087	0.094	0.93
Midhigh – Understorey	–0.004	0.13	–0.030	0.98

Table S30. Prevalence of pathogenic *E. coli* by diet guild in wild birds. Total number of individuals reported positive and tested for pathogenic *E. coli* across the literature and prevalence (total positive across the literature/total number tested) by diet guild. Estimated prevalence by diet guild using mixed-effects models and corresponding standard errors and 95% confidence intervals are also presented.

Diet	***E. coli* positive**	***E. coli* tested**	***E. coli* prevalence**	**Estimated prevalence**	**Estimated standard error**	**Estimated 95% confidence interval**
Invertebrate	6	248	2.4%	9.8%	14.0%	(–17.6%, 37.2%)
Piscivore	1	41	2.4%	10.3%	23.5%	(–35.8%, 56.4%)
Granivore	540	6121	8.8%	13.7%	11.1%	(–8.1%, 35.4%)
Omnivore	157	1638	9.6%	27.3%	9.1%	(9.4%, 45.2%)
Herbivore	471	1137	41.4%	27.1%	15.8%	(–3.9%, 58.0%)
Carnivore	0	0	N/A	N/A	N/A	N/A
Frugivore	0	0	N/A	N/A	N/A	N/A
Nectarivore	0	0	N/A	N/A	N/A	N/A
Scavenger	0	0	N/A	N/A	N/A	N/A

Table S31. Tukey HSD pairwise comparisons examining pathogenic *E. coli* prevalence by diet guild. SE = standard error.

Comparison	**Estimate**	**SE**	***Z***	***P***
Invertebrate – Omnivore	0.18	0.16	1.10	0.27
Granivore – Omnivore	0.14	0.13	1.02	0.31
Herbivore – Invertebrate	–0.17	0.21	–0.83	0.41
Granivore – Herbivore	0.13	0.19	0.72	0.47
Herbivore – Piscivore	–0.17	0.28	–0.60	0.55
Granivore – Invertebrate	–0.039	0.17	–0.23	0.82
Granivore – Piscivore	–0.034	0.25	–0.13	0.89
Invertebrate – Piscivore	0.005	0.27	0.019	0.98
Herbivore – Omnivore	0.002	0.17	0.014	0.99

Table S32. Prevalence of pathogenic *E. coli* by foraging strata in wild birds. Total number of individuals reported positive and tested for pathogenic *E. coli* across the literature and prevalence (total positive across the literature/total number tested) by foraging strata. Estimated prevalence by foraging strata using mixed-effects models and corresponding standard errors and 95% confidence intervals are also presented.

Foraging strata	***E. coli* positive**	***E. coli* tested**	***E. coli* prevalence**	**Estimated prevalence**	**Estimated standard error**	**Estimated 95% confidence interval**
Midhigh	0	0	N/A	N/A	N/A	N/A
Aerial	4	84	4.8%	12.8%	23.1%	(–32.5%, 58.1%)
Ground	1004	8175	12.3%	22.6%	8.4%	(6.2%, 39.1%)
Understorey	52	297	17.5%	13.3%	23.1%	(–32.1%, 58.6%)
Water around surf	115	629	18.3%	18.1%	9.6%	(–0.7%, 36.8%)
Canopy	0	0	N/A	N/A	N/A	N/A
Water below surf	0	0	N/A	N/A	N/A	N/A

Table S33. Tukey HSD pairwise comparisons examining pathogenic *E. coli* prevalence by foraging strata. SE = standard error.

Comparison	**Estimate**	**SE**	***Z***	***P***
Aerial – Ground	0.10	0.24	0.41	0.68
Ground – Water around surf	–0.046	0.12	–0.40	0.69
Ground – Understorey	–0.094	0.24	–0.39	0.70
Aerial – Water around surf	0.052	0.24	0.21	0.83
Understorey – Water around surf	0.048	0.24	0.20	0.84
Aerial – Understorey	0.004	0.32	0.013	0.99

Table S34. Prevalence of *Salmonella* spp. by diet guild in wild birds. Total number of individuals reported positive and tested for *Salmonella* spp. across the literature and prevalence (total positive across the literature/total number tested) by diet guild. Estimated prevalence by diet guild using mixed-effects models and corresponding standard errors and 95% confidence intervals are also presented

Diet	***Salmonella* spp. positive**	***Salmonella* spp. tested**	***Salmonella* spp. prevalence**	**Estimated prevalence**	**Estimated standard error**	**Estimated 95% confidence interval**
Frugivore	0	4	0.0%	17.2%	14.7%	(–11.5%, 46.0%)
Nectarivore	0	2	0.0%	6.7%	21.8%	(–36.0%, 49.3%)
Herbivore	49	2642	1.9%	4.9%	1.3%	(2.4%, 7.3%)
Granivore	418	13252	3.2%	5.4%	1.0%	(3.4%, 7.4%)
Invertebrate	83	2416	3.4%	6.1%	1.2%	(3.9%, 8.4%)
Omnivore	1293	20577	6.3%	6.9%	1.0%	(4.9%, 9.0%)
Carnivore	34	472	7.2%	7.6%	2.4%	(2.3%, 12.4%)
Scavenger	1	11	9.1%	7.3%	8.3%	(–9.0%, 23.5%)
Piscivore	86	919	9.4%	9.6%	2.3%	(5.0%, 14.1%)

Table S35. Tukey HSD pairwise comparisons examining *Salmonella* spp. prevalence by diet guild. Bold values indicate the comparison was significant at *P* = 0.05; SE = standard error.

Comparison	**Estimate**	**SE**	***Z***	***P***
Granivore – Omnivore	**0.016**	**0.007**	**2.33**	**0.020**
Herbivore – Omnivore	**0.021**	**0.011**	**1.99**	**0.047**
Herbivore – Piscivore	0.047	0.024	1.93	0.054
Granivore – Piscivore	0.042	0.023	1.80	0.071
Invertebrate – Piscivore	0.034	0.024	1.43	0.15
Omnivore – Piscivore	0.026	0.023	1.16	0.25
Herbivore – Invertebrate	0.013	0.011	1.13	0.26
Carnivore – Herbivore	–0.028	0.025	–1.12	0.26
Granivore – Invertebrate	0.008	0.008	0.96	0.34
Invertebrate – Omnivore	0.008	0.009	0.91	0.36
Carnivore – Granivore	–0.022	0.025	–0.90	0.37
Carnivore – Piscivore	0.019	0.033	0.60	0.55
Carnivore – Invertebrate	–0.015	0.026	–0.58	0.56
Granivore – Herbivore	–0.005	0.010	–0.53	0.59
Herbivore – Scavenger	0.024	0.083	0.29	0.77
Carnivore – Omnivore	–0.007	0.025	–0.27	0.79
Piscivore – Scavenger	–0.023	0.085	–0.27	0.79

Granivore – Scavenger	0.019	0.083	0.22	0.82
Invertebrate – Scavenger	0.011	0.083	0.13	0.89
Carnivore – Scavenger	–0.004	0.082	–0.04	0.96
Omnivore – Scavenger	0.003	0.083	0.04	0.97

Table S36. Prevalence of *Salmonella* spp. by foraging strata in wild birds. Total number of individuals reported positive and tested for *Salmonella* spp. across the literature and prevalence (total positive across the literature/total number tested) by foraging strata. Estimated prevalence by foraging strata using mixed-effects models and corresponding standard errors and 95% confidence intervals are also presented

Foraging strata	***Salmonella* positive**	***Salmonella* tested**	***Salmonella* prevalence**	**Estimated prevalence**	**Estimated standard error**	**Estimated 95% confidence interval**
Aerial	4	1706	0.2%	5.4%	1.4%	(2.5%, 8.2%)
Understorey	2	610	0.3%	5.4%,	1.4%	(2.7%, 8.1%)
Midhigh	4	443	0.9%	6.3%	1.6%	(3.1%, 9.4%)
Canopy	2	119	1.7%	5.1%	3.5%	(–1.8%, 12.1%)
Ground	828	22373	3.7%	6.1%	1.0%	(4.2%, 8.0%)
Water below surf	17	434	3.9%	8.1%	2.9%	(2.4%, 13.9%)
Water around surf	1107	14610	7.6%	8.0%	1.2%	(5.6%, 10.4%)

Table S37. Tukey HSD pairwise comparisons examining *Salmonella* spp. prevalence by foraging strata. SE = standard error.

Comparison	**Estimate**	**SE**	**Z-value**	**P-value**
Ground – Water around surf	0.018	0.010	1.92	0.055
Understorey – Water around surf	0.025	0.014	1.85	0.064
Aerial – Water around surf	0.026	0.014	1.82	0.068
Midhigh – Water around surf	0.017	0.016	1.05	0.29
Aerial – Water below surf	0.028	0.030	0.92	0.36
Understorey – Water below surf	0.027	0.030	0.91	0.37
Canopy – Water around surf	0.028	0.036	0.80	0.43
Ground – Water below surf	0.020	0.028	0.72	0.47
Canopy – Water below surf	0.030	0.044	0.68	0.50
Aerial – Ground	0.008	0.012	0.66	0.51
Ground – Understorey	–0.007	0.011	–0.64	0.52
Midhigh – Understorey	–0.008	0.016	–0.52	0.60
Aerial – Midhigh	0.009	0.017	0.52	0.60
Canopy – Midhigh	0.011	0.037	0.31	0.76

Canopy – Ground	0.010	0.035	0.29	0.77
Ground – Midhigh	0.001	0.014	0.10	0.92
Canopy – Understorey	0.003	0.036	0.08	0.93
Water around surf – Water below surf	0.002	0.030	0.06	0.95
Aerial – Canopy	–0.002	0.036	–0.06	0.95
Aerial – Understorey	0.001	0.015	0.05	0.96