

1 Utilising citizen science data to rapidly assess potential wild
2 bridging hosts and reservoirs of infection: avian influenza
3 outbreaks in Great Britain

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20 **Keywords**

21 HPAIV, spill over, viral incursion, disease vector, ebird

22 **Abstract**

23 High pathogenicity avian influenza virus (HPAIV) is a rapidly evolving orthomyxovirus causing
24 significant economic and environmental harm. Wild birds are a key reservoir of infection and an
25 important source of viral incursions into poultry populations. However, we lack thorough
26 understanding of which wild species drive incursions and whether this changes over time. We
27 explored associations between abundances of 152 avian species and cases of HPAI in poultry
28 premises across Great Britain between October-2021 and January-2023. Spatial generalised additive
29 models were used, with species abundance distributions sourced from eBird modelled predictions.
30 Associations were investigated at the species-specific level and across aggregations of species.
31 During autumn/winter, associations were generally strongest with waterbirds such as ducks and
32 geese; however, we also found significant associations in other groups such as non-native
33 gamebirds, and rapid change in species-specific associations over time. Our results demonstrate the
34 value of citizen science in rapid exploration of wild reservoirs of infection as facilitators of disease
35 incursion into domestic hosts, especially in regions where surveillance programmes in wild birds are
36 absent. This can be a critical step towards improving species-specific biosecurity measures and
37 targeted surveillance; particularly for HPAIV, which has undergone sudden shifts in host-range and
38 continues to rapidly evolve.

39 **1. Introduction**

40 The emergence and rapid evolution of transboundary animal pathogens poses significant economic
41 and zoonotic risks (Clemons et al 2021). Many transboundary animal diseases are caused by multi-
42 host pathogens with assemblages of reservoirs of infection and bridging species that may change
43 over time and/or vary greatly in breadth (Portier et al. 2019). Which host species are most affected
44 can vary seasonally alongside changes in species ecology or shift rapidly as a result of pathogen
45 evolution or diffusion into new areas (Bonneaud & Longdon 2020). Therefore, continuous
46 monitoring of possible reservoirs of infection and bridging species is essential for designing effective

47 control measures and developing predictive disease transmission models (Viana et al. 2014).
48 However, widespread surveillance in wildlife is often too challenging and expensive to implement,
49 especially for hosts with broad species distributions.

50

51 Avian influenza virus (AIV) has among the widest geographic and host range of all transboundary
52 animal diseases (Lupiana & Reddy 2009). In 2020, the emergence of high pathogenicity AIV (HPAIV)
53 subtype H5Nx clade 2.3.4.4b led to an epizootic of HPAIV that profoundly impacted both the poultry
54 industry and wild bird populations, causing significant economic and environmental harm (Lewis et
55 al. 2021, EFSA et al. 2023A). During annual HPAI epizootics in Great Britain since 2020, farm contact
56 tracing and genetic analysis of viruses from infected poultry has strongly implicated wild birds as the
57 likely primary source of repeated independent incursions of HPAIV infection (Byrne et al. 2023), even
58 if the exact pathway of virus movement from wild birds to poultry cannot be proven.

59

60 Our understanding of which wild bird species are responsible for such incursions and whether this
61 varies between epizootics due to virus evolution and heightened premise biosecurity remains
62 relatively coarse (Hill et al. 2019, Blagodatski et al. 2021). The main wild host reservoir of infection
63 for AIV is generally considered to be ducks and other waterfowl (Order Anseriformes, family
64 *Anatidae*), with infection in these species resulting in disease outcomes ranging from subclinical to
65 severe (Keawcharoen et al. 2008). In contrast, HPAIV H5Nx infection of poultry invariably results in
66 severe disease with high morbidity and mortality rates (Ramey et al. 2022). Interestingly, recent
67 outbreaks of H5Nx clade 2.3.4.4b have been characterised by high levels of mortality across a
68 broader range of wild birds, including anatids, than seen previously. Infection has also shifted, likely
69 through emergence of novel H5N1 genotypes, to cause extensive outbreaks. High susceptibility and
70 increased virus shedding in a range of wild bird species has increased the levels of infection pressure
71 through elevated levels of environmental contamination. This in turn has resulted in previously
72 rarely affected groups of birds such as seabirds becoming exposed and infected (Banyard et al. 2022,

73 Falchieri et al. 2022, Pohlmann et al. 2023). Although the host range for HPAI H5Nx are known to be
74 broad based on challenge studies and wild-bird surveillance (Lee et al. 2017, Empress-i 2023),
75 virulence and transmissibility appear to be highly variable across taxa. Mass mortality events
76 attributed to H5 clade 2.3.4.4b have been recorded in several groups such as wildfowl, shorebirds,
77 seabirds, and raptors (Abolnik et al. 2023, Adlhoch & Baldinelli 2023, Lane et al. 2023, Pohlmann et
78 al. 2023), whereas in other groups, such as passerines, such reports are lacking. However, passerines
79 have demonstrated moderate to high seroprevalence against older clades of HPAI H5Nx, likely
80 indicative of past infection (Kou et al. 2005, Kaplan & Webby 2013), and detecting increased
81 mortality in these less conspicuous species is likely to be more difficult. Importantly, commonly
82 tested species that contribute to the long-distance spread of HPAIV internationally (particularly
83 wildfowl (Order Anseriformes) and gulls (Family *Laridae*); Kim et al. 2009, Hill et al. 2022) may not
84 necessarily be sufficient to explain incursions onto premises. Instead, there may be additional
85 species acting as local amplifiers of viruses, which could be critical in facilitating viral incursion into
86 premises.

87
88 Understanding species-specific patterns of spillover from wild to domestic birds is difficult due to
89 obstacles in effective monitoring of HPAIV in potential wild bird hosts, and the changes in species
90 assemblages and abundance across the annual cycle. Despite significant advances in testing protocols
91 (James et al. 2022, Slomka et al. 2023), surveillance of HPAI outbreaks in wild birds can be severely
92 limited by financial constraints, detection and sampling of carcasses, and requirements for high
93 biosecurity testing facilities (Hill et al. 2018). Testing may therefore be heavily skewed towards species
94 with overt clinical symptoms or for which carcasses are more easily detectable. For example, while all
95 suspected kept bird premise cases of HPAI in Great Britain are tested, only a relatively small subset of
96 reported wild bird carcasses suspected of being HPAI cases can be tested (DEFRA 2023C). Therefore,
97 methods to refine targeted surveillance of HPAIV are essential to maximise disease control efforts.

98

99 One way to potentially achieve better targeted surveillance is by assessing associations between the
100 abundance of potential reservoirs of infection or bridging species and confirmed HPAIV infection in
101 premises housing domestic poultry or other captive birds (henceforth referred to collectively as
102 “captive avian premises”), on the assumption that there will often be a higher incidence of cases
103 where one or more reservoirs of infection or bridging species are at higher abundance. While this
104 approach does not rely upon *a priori* knowledge of a single host species, as several species can be
105 assessed concurrently, it does rely on an accurate understanding of spatiotemporal patterns of
106 possible host species abundance across the region of interest. Modelling spatiotemporal patterns of
107 wild host abundance at national scales is complex, because it requires a large amount of
108 observational data and computationally intensive analyses (Fink et al. 2013). However, citizen
109 science initiatives alongside advances in computational power and novel analytical approaches that
110 account for biases in semi-structured data collection procedures can enable rapid advances in our
111 understanding of species abundance and distributions. The citizen science initiative eBird launched
112 by the Cornell Lab of Ornithology (CLO) and the National Audubon Society in 2002 has amassed over
113 1 billion bird observations globally and currently produces estimates of the full annual cycle
114 distributions, abundances, and environmental associations for over 2000 species (Fink et al. 2022).
115 With these advances, it is now possible to rapidly assess the associations between the spatial
116 distribution of wild bird populations and HPAI in poultry at larger scales than previously possible.
117
118 As many different wild bird species may be involved in HPAIV transmission, with varying levels of
119 interaction with each other and captive avian premises, assessing species-level drivers of virus
120 incursions into captive flocks can be challenging. Using eBird-modelled species abundance estimates
121 that are publicly available for a broad selection of wild avian species, we investigate spatial
122 associations between species-specific wild-bird abundance and patterns of HPAI cases in captive
123 avian premises across Great Britain. This will enable us to identify potentially under-prioritised key
124 species, or species groups, that may be facilitating the incursion of HPAI into captive avian premises.

125 The use of citizen science recording schemes such as eBird benefits from being non-reliant on any
126 field- or laboratory-led surveillance in potential wild viral hosts, and as such can be rapidly deployed
127 against pathogens with wild reservoirs of infection in areas with limited wild host testing capacity.
128 Continued monitoring of associations between wild hosts and detected outbreaks in 'captive avian'
129 premises could also prove useful as an early-warning sign of a possible virus host range expansion
130 into a new wild species that is not currently subject to surveillance.

131 **2. Methods**

132 We used publicly available model-predicted relative abundance distributions (RADs) of wild birds to
133 explore how wild bird abundance is associated with HPAI cases in premises across Great Britain
134 between 19th October 2021 and 20th January 2023. RADs are built upon data from eBird, a global
135 community science bird monitoring program administered by The Cornell Lab of Ornithology
136 (Strimas-Mackey et al. 2022; Fink et al. 2023).

137

138 **A. Data processing**

139 RADs were retrieved from eBird Status and Trends using R package ebirdst (Strimas-Mackey et al.
140 2022). These RADs provided estimates for the full annual cycle at weekly intervals, modelled on the
141 year 2021, across a regular grid which we use at a resolution of 26.7km². Predicted RADs are derived
142 from an ensemble modelling strategy based on the Adaptive Spatio-Temporal Exploratory Model
143 (AdaSTEM; Fink et al. 2013). For full RAD methodology see Fink et al. (2020). RADs that include Great
144 Britain are currently available for 256 species, each with seasonal quality ratings assessed between 0
145 (lowest quality) and 3 (highest quality). We consider only those species with seasonal quality rating
146 scores of 2 or 3 during the modelled period (to exclude predictions with low confidence), and a sum
147 of relative weighted abundance scores within the relevant time period of >1 (to exclude uncommon
148 and rare species). This produced a final pool of 152 species. Seasonal quality rating scores are

149 assigned based upon expert human review, whereby a rating of 0 implies the modelled predictions

150 failed review and ratings of 1–3 correspond to increasing levels of extrapolation and/or omission.

151

152 During our study period, there were 312 HPAI cases across commercial ($n = 216$), backyard ($n = 70$),

153 mixed ($n = 12$), and miscellaneous (e.g., rescue centres, zoos, etc.; $n = 14$) premises in Great Britain

154 (referred to here collectively as premises; Fig 1). Case data on infected premises housing captive

155 birds was obtained from the Animal and Plant Health Agency (APHA), who lead diagnostic

156 surveillance for AIV in Great Britain (Byrne et al. 2023). Through visual inspection of epidemic curves,

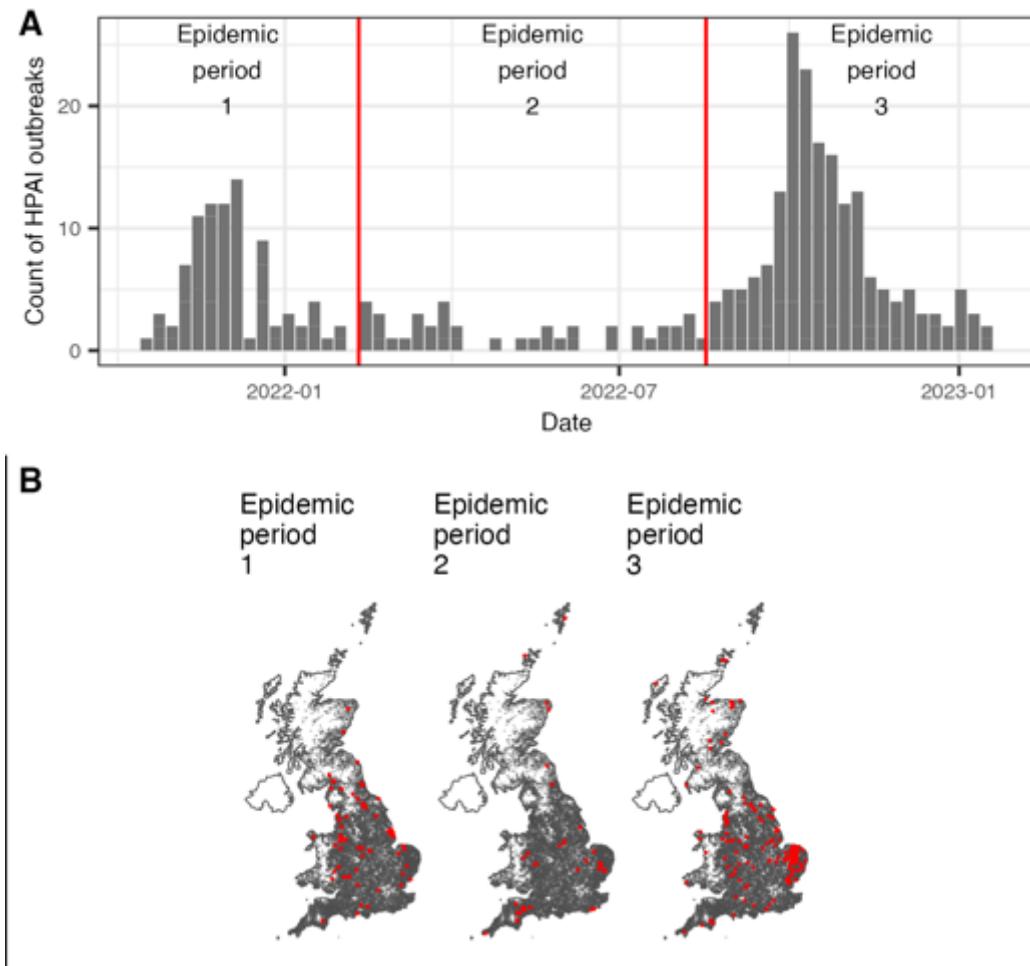
157 cases were split into three distinct EP's. EP 1 covered 19th October 2021 – 9th February 2022

158 coinciding with a large peak in cases, EP 2 covered 10th February 2022 – 16th August 2022 during

159 which cases occurred infrequently, and EP 3 covered a large peak in cases between 17th August 2022

160 – 20th January 2023 (Fig 1A).

161



162

163 **Fig 1.** HPAI cases in captive avian premises in Great Britain between 19th October 2021–20th January
164 2023. **A)** Epidemic curve split into three distinct epidemic periods (EP1 = 19th October 2021 – 9th
165 February 2022; EP2 = 10th February 2022 – 16th August 2022; EP3 = 17th August 2022 – 20th January
166 2023). Number of cases per period were 86, 40, and 186, respectively. **B)** Map of cases (red points)
167 against a map of premises (black points) as listed in the Great British Poultry Register (jittered here to
168 maintain anonymity).

169

170 To account for changes in each species' relative abundance and HPAI case intensity across an EP, we
171 weighted the weekly RADs by multiplying each cell value by the proportion of HPAI cases that
172 occurred nationally within that week of the EP. We then sum these weekly weighted values to
173 produce a single weighted relative species abundance for each grid-cell for the relevant period (S1
174 Fig). Weighted RADs therefore represented how the species abundance varied across the UK during
175 the period, with higher weighting given to weeks with more premise cases.

176

177 In order to control for greater case likelihood being expected in areas with higher farm and poultry
178 density, we used information on location and stock numbers of premises obtained from the Great
179 Britain Poultry Register (GBPR). As reporting to the GBPR is non-compulsory for flocks of fewer than
180 50 birds, we only used data from those farms with 50 or more birds (19,680 farms). Farm locations
181 and reported stock counts were rasterised across a regular grid at a resolution of 26.7km² to match
182 wild bird RAD data, giving a count of farms and sum of stock numbers at the grid-cell level (S1 Fig).

183

184 As an alternative to wild bird RAD data, we also explored associations of premise cases with PCR-
185 confirmed wild bird HPAI cases within each period. Spatial data on individual HPAI cases in wild birds
186 was sourced from the Empres-i open-access database (Martin et al. 2007). Case locations were
187 rasterised across a regular grid at a resolution of 26.7km² to match wild bird RAD data to give a
188 count of cases at the grid-cell level within each period (S2 Fig).

189

190 **B. Primary data analysis**

191 We fit spatial generalised additive models (GAMs; package *mgcv*; Wood 2011) with a binomial error
192 family and a logit link function to test the effect of relative species abundance on premise cases at a
193 26.7km² grid-cell level. Our dependent variable (proportion of all infected premises over the
194 epidemic period which were located in each grid cell) was included as a two-column count matrix of
195 infected premises and uninfected premises in order to perform weighted regression using the total
196 number of premises within the grid-cell as weights. Explanatory variables of weighted species
197 abundance and average stock number per premise were included as linear terms, which were scaled
198 prior to model fitting. To account for spatial autocorrelation between neighbouring grid-cells, we
199 also include a two-dimensional splined variable of latitude and longitude, fit with an isotropic
200 smooth on the sphere. The default basis dimension (k) value of -1 was used, and Generalised Cross-
201 Validation was used to estimate smoothness parameters. A separate model was fit for each species
202 and epidemic period where sufficient species abundance was present (defined as species with a sum

203 of weighted relative abundance across all grid cells within that period greater than 1). Models that
204 did not converge were removed from the model pool.

205

206 In addition to this, we also fit models where the count of wild bird HPAI cases at the grid-cell level
207 was used instead of weighted relative species abundance. This resulted in a total of 389 independent
208 models. To account for multiple testing, p-values for species-specific models were adjusted using
209 two methods. We first used the false discovery rate method which accounts for the expected
210 proportion of false discoveries amongst the rejected hypotheses (Benjamini & Hochberg 1995), and
211 second the more conservative Holm-Bonferroni method (Holm 1979).

212

213 **C. Post-hoc analysis**

214 We fit linear models (LMs) in order to assess group-level effects across our species-specific relative
215 abundance associations. The linear slope coefficient of relative abundance from each of the species-
216 specific independent models was used as the dependent variable, and the model was weighted by
217 the reciprocal of the squared standard error of this slope coefficient. Categorical explanatory
218 variables included the Epidemic Period (1, 2, or 3), species grouping (see below), and the two-way
219 interaction between these terms. Several models of the same structure were run with varying
220 coarseness of the species grouping variable. Our coarsest grouping categorised species into three
221 ecological sets of species – *Landbirds*, *Seabirds*, and *Waterbirds*, following classifications described in
222 Geen et al. (2019). We then assessed group-level patterns based upon commonly used colloquial
223 species groups. These groupings were chosen to reflect similarity in species behaviour, habitat-use,
224 and phylogeny, which may all influence a species likelihood of interacting with premises and being a
225 HPAIV carrier. Some groupings were however poorly represented as not all species present in Great
226 Britain are modelled by eBird or because model outputs were poorly supported (i.e., low seasonal
227 quality rating scores). We measured grouping coverage by comparing against the BOU British list
228 (excluding vagrants; BOU 2023; S5 Table).

229 To assess correlation between species-specific slope coefficients for the effect of species abundance
230 across EP's, Pearson's product moment correlation was used. We assessed group-level estimates of
231 change in species-specific slope coefficients for the effect of species abundance between EP's 1 and
232 3 using a general linear model, change in slope coefficient from EP1 to EP3 explained by a single
233 explanatory variable of species grouping. A separate model was run for each level of coarseness in
234 species groupings.

235

236 All statistical analyses were performed with R 4.3.0 (R Core Team 2023).

237

238 **3. Results**

239 To assess which wild bird species are associated with HPAIV incursions into captive-avian premises,
240 we modelled spatial associations between the abundance of 152 wild bird species and cases of
241 HPAIV in premises during three distinct epidemic periods (EP's) between October 2021 and January
242 2023 (Fig 1). We use "case" to refer to any captive-avian premise in which 1 or more captive birds
243 are confirmed to have HPAIV by PCR and/or genetic sequencing; and "premises" to refer collectively
244 to commercial, backyard, and miscellaneous (e.g., rescue centres, zoos, etc.) premises where captive
245 birds are kept. Most cases were, however, reported from commercial premises ($n = 216$, 69.2%). EP's
246 1 and 3 (19th October 2021 – 9th February 2022 and 17th August 2022 – 20th January 2023,
247 respectively) covered large peaks in cases ($n = 86$ and $n = 186$, respectively) with a broad spread of
248 cases throughout much of Great Britain. Conversely, EP 2 (10th February 2022 – 16th August 2022)
249 had lower case incidence ($n = 40$) and less ubiquitous spatial occurrence of cases, with regions such
250 as northern and central-southern England having no cases despite relatively high farm density (Fig
251 1B, S1 Fig).

252

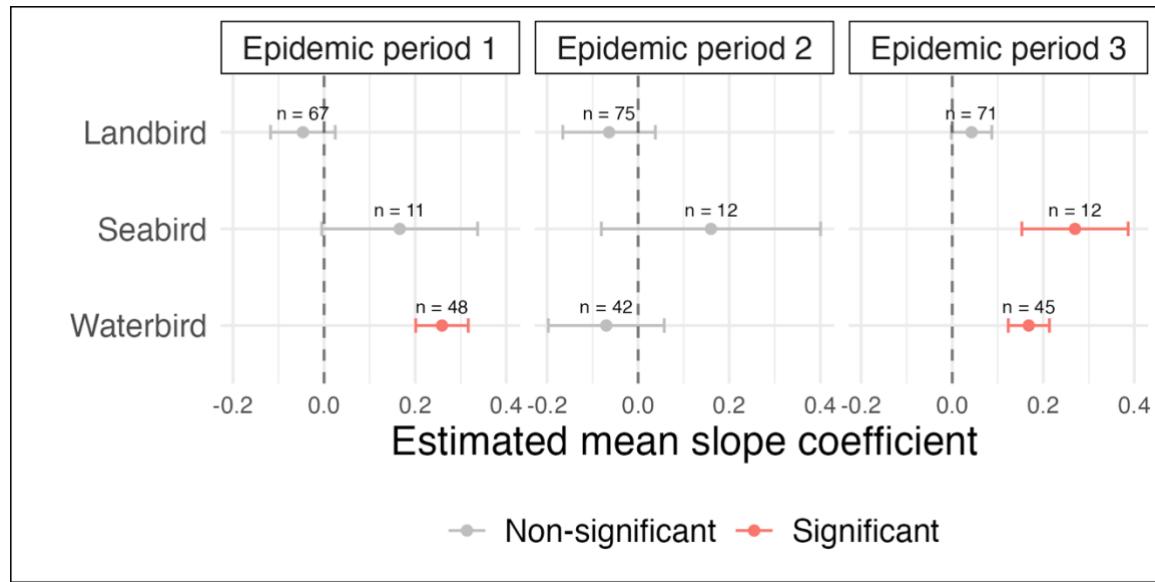
253 We assessed associations aggregated across groups of ecologically and phenotypically similar species
254 (to minimise type-1 errors; S1 Table), and at the individual species level (for full species-specific

255 model coefficients see S1 Data). Groupings of different species were chosen to reflect similarity in
256 species behaviour, habitat-use, and phylogeny which may influence either a species likelihood of
257 interacting with a premise and/or being a HPAIV reservoir of infection or bridging species. Species-
258 specific abundance associations with HPAIV cases were obtained from models in which the effects of
259 total poultry stock within the area were controlled for. Linear slope estimates for the effect of total
260 poultry stock varied between models but were always positive (average slope estimates (95% CI):
261 EP1 = 15.1 (14.6–15.5), EP2 = 23.1 (22.5–23.7), EP3 = 2.9 (2.8–3.1)), indicating areas with higher total
262 poultry numbers had a greater proportion of infected premises during an epidemic period.

263

264 *A. Species groupings*

265 Our most coarse grouping considered 3 species groups: *landbirds*, *seabirds*, and *waterbirds* as
266 described in Geen et al. (2019). *Waterbirds* showed consistent group-level significant positive
267 associations with HPAI cases across EPs 1 and 3 (Fig 2; S2 Table). This indicates that areas with high
268 *waterbird* abundance were likely to have a higher proportion of premises experiencing HPAI cases
269 during these epidemic periods than areas with lower abundance for this group. *Seabirds*, in contrast,
270 had positive associations in all EPs but only showed a significant positive association within EP 3,
271 indicating an increased importance for this group during this later period (Fig 2, S2 Table). *Landbirds*
272 showed no significant positive association in any EP (Fig 2, S2 Table), and this was driven in part by a
273 lack of consistency in the direction of associations between species or species groups within this
274 wider grouping. We subsequently considered subgroups of species within our *landbird*, *seabird*, and
275 *waterbird* groupings based upon taxonomy.



276

277 **Fig 2.** Estimated first-order group-level means for linear model coefficients describing effects of
278 weighted relative species abundance on probability of HPAI cases in premises. Estimated means
279 derived from a GLM assessing group effects across epidemic periods (EP1 = 19th October 2021 – 9th
280 February 2022; EP2 = 10th February 2022 – 16th August 2022; EP3 = 17th August 2022 – 20th January
281 2023). Values above points indicate the number of species within each grouping. Error bars indicate
282 the 95% confidence interval.

283

284 B. Landbirds

285 Despite no significant association for *landbirds* as a wider group in any EP, significant associations
286 were found in some subgroupings (Fig 3, S3 Fig, S3 Table, S4 Table). HPAI cases in premises during EP
287 1 had a significant positive association with *birds of prey* (families *Strigiformes*, *Accipitridae*, and
288 *Falconidae*), although this was limited to *diurnal raptors* (families *Accipitridae* and *Falconidae*), which
289 also had a significant positive association during EP 3. The subgroup *Passerines* (order Passeriformes)
290 showed a significant negative association, however there was inconsistency amongst subgroups.
291 Subgroupings such as *tit* (family *Paridae*), *flycatchers & chats* (family *Muscicapidae*), and *thrushes*
292 (family *Turdidae*) showed significant negative associations, whereas *sparrows* (family *Passeridae*)
293 had a significant positive association with HPAI cases in premises. This later significant positive
294 association is of note, as some sparrows such as House Sparrow *Passer domesticus* may be regular
295 visitors to poultry farms (Sánchez-Cano et al. 2024), may nest or roost in eaves of barns and other

296 farm buildings, and therefore may have elevated potential to act as direct sources of infection.

297 Furthermore, this significant positive association with *sparrows* is also observed during EP3.

298

299 During EP3, *gamebirds* (family *Phasianidae*) gained a significant positive association with HPAI cases

300 in premises (Fig 3, S3 Table). This effect was strongest amongst *non-native gamebirds*, which are

301 bred and released in large numbers during the late-summer and early-autumn period that is

302 included within EP 3 (Madden 2021, S3 Fig, S4 Table). In *native gamebirds*, the significant positive

303 association was primarily driven by Grey Partridge *Perdix perdix*, which are also bred and released in

304 some areas as part of species recovery projects, albeit in far smaller numbers (Ewald et al. 2022; S4

305 Fig). As was the case in EP 1, *passerine* subgroupings displayed inconsistency; *flycatchers & chats* had

306 a significant negative association with cases, whereas other groups such as *buntings* (family

307 *Emberizidae*) and *larks, pipits, & wagtails* (families *Alaudidae* and *Motacillidae*) had a significant

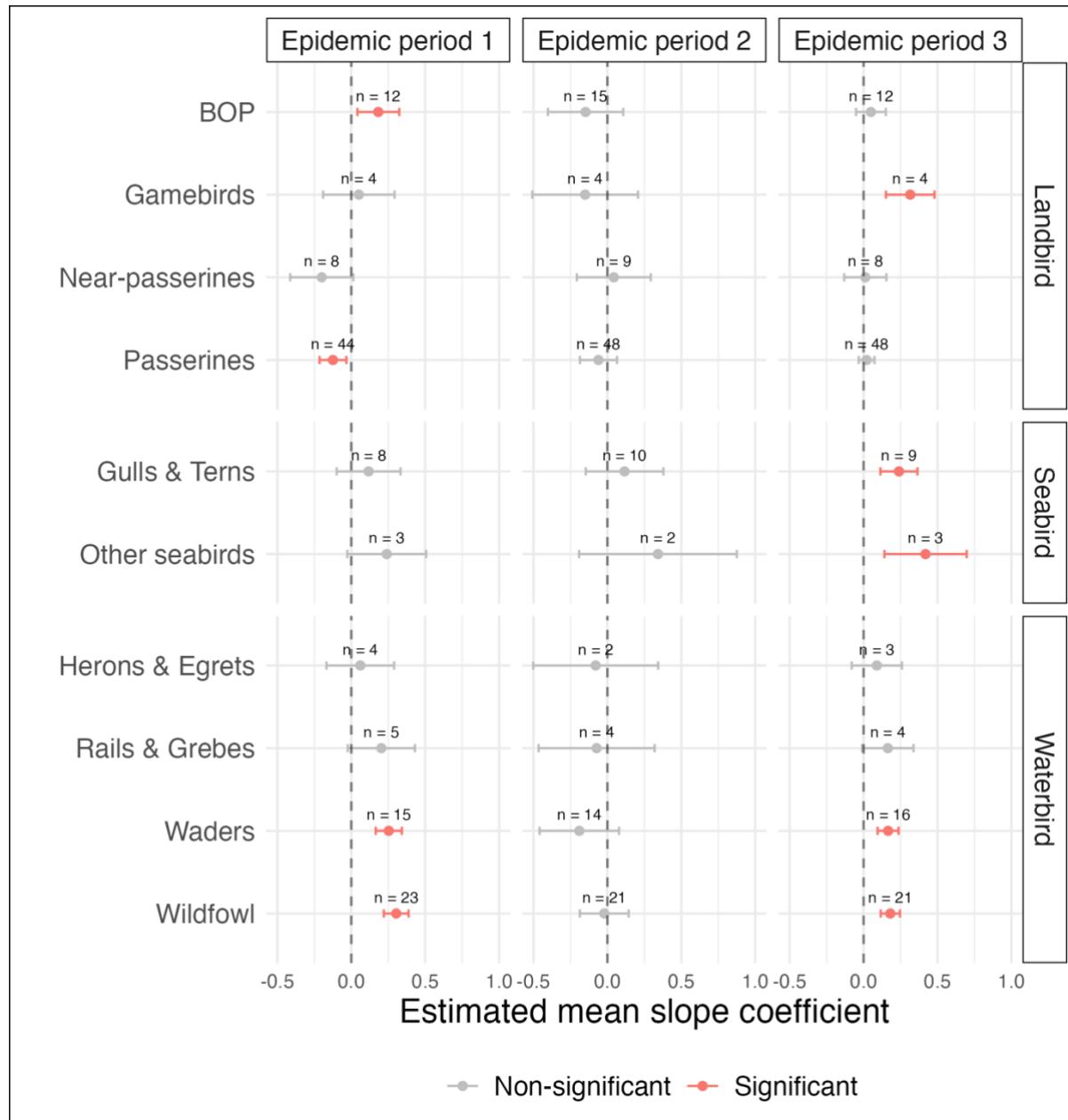
308 positive association (S3 Fig, S4 Table).

309

310 There was no significant association for *near-passerines* (families *Columbidae*, *Picidae*, *Psittaculidae*,

311 and *Alcedinidae*) during any EP, nor were there any significant associations amongst any of the

312 *landbird* subgroupings during EP2 (Fig 3, S3 Fig, S3 Table, S4 Table).



313

314 **Fig 3.** Estimated second-order group-level means for linear model coefficients describing effects of
 315 weighted relative species abundance on probability of HPAI cases in premises. Estimated means
 316 derived from a GLM assessing group effects across epidemic periods (EP1 = 19th October 2021 – 9th
 317 February 2022; EP2 = 10th February 2022 – 16th August 2022; EP3 = 17th August 2022 – 20th January
 318 2023).

319

320 C. Waterbirds

321 Wildfowl (order Anseriformes) showed significant positive associations across EP 1 and EP 3 (Fig 3;
 322 S3 Table). All subgroupings had positive associations, although not all are significant (S3 Fig; S4

323 Table). *Dabbling ducks* (subfamily *Anatinae*) were significant in both periods, whereas *diving ducks*
324 (subfamily *Athyinae* and tribe *Mergini*) were only significant in EP 3 (S3 Fig; S4 Table). Other
325 subgroupings were non-significant; however, there were significant positive species-specific
326 associations in highly abundant, and therefore potentially important, species such as Greylag Goose
327 *Anser anser* and Mute Swan *Cygnus olor* (S4 Fig). *Waders* (suborders *Charadrii* and *Scolopaci*) also
328 showed significant positive associations in both EP 1 and 3 (Fig 3; S3 Table), driven by subgroups
329 *plovers* and *sandpipers* (families *Charadriidae* and *Scolopacidae*) in both periods (S3 Fig; S4 Table).
330 Across the other subgroups within *waterbirds*, namely *herons & egrets* (family *Ardeidae*) and *rails &*

331 *grebes* (families *Rallidae* and *Podicipedidae*), there were no significant associations during any of the
332 EPs (Fig 3; S3 Fig).

333

334 *D. Seabirds*

335 Despite having a positive association across all EPs, *seabirds* were only found to have a significant
336 association in EP 3. This broad grouping generally had a poorer species coverage in the available
337 modelled eBird abundance datasets compared to *waterbirds* and *landbirds* (S5 Table). Many of the
338 more substantial sub-groupings, such as Auks (family *Alcidae*), could not be assessed. Here, *seabirds*
339 are predominantly represented by the *gulls & terns* (family *Laridae*) subgrouping, which had a
340 significant positive association with premise cases in EP 3 (Fig 3; S3 Table). This significant
341 association also remained when this subgrouping was split into *gulls* (subfamily *Larinae*) and *terns*
342 (subfamily *Sterninae*) separately (S3 Fig; S4 Table).

343

344 The *other seabirds* grouping was also significantly positive in EP 3 (Fig 3; S3 Table). This grouping only
345 represents a limited range of seabird species (mainly divers), and the only significant subgrouping
346 was *divers* (family *Gaviidae*) in EP 3 (S3 Fig; S4 Table). Seabird groups such as Auks and species such
347 as the Northern Gannet *Morus bassanus* or Great Skua *Stercorarius skua*, which have been linked to

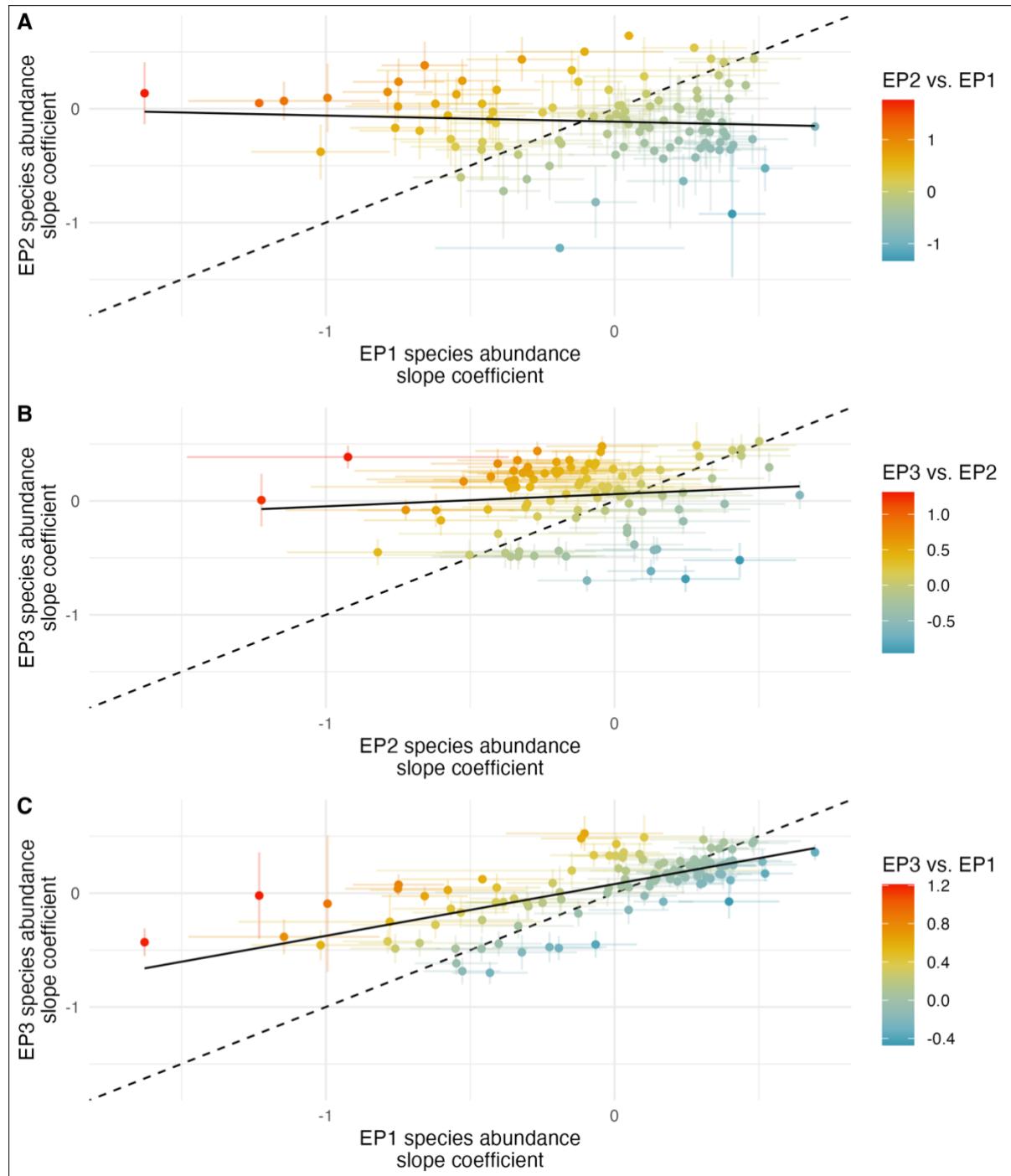
348 mass HPAI outbreaks in wild birds in Great Britain (Banyard et al. 2022, Lane et al. 2023), were not
349 represented in the modelled eBird dataset.

350

351 *E. Species-specific associations*

352 Generally, for species assessed in multiple EP's, species-specific associations were poorly correlated
353 between subsequent periods (EP1–EP2: $\text{cor} = -0.075$ (95% CI: -0.264–0.119), $df = 102$, $p = 0.447$;
354 EP2–EP3: $\text{cor} = 0.113$ (95% CI: -0.085–0.303), $df = 98$, $p = 0.263$; Fig 4A & B), indicating a potential
355 change in viral dynamics and potential host species during the summer period of low HPAIV
356 incidence compared to the winter periods of high incidence. Conversely, species-specific
357 associations were significantly correlated between EPs 1 and 3, which are both characterised by
358 large epidemic peaks (EP1–EP3: $\text{cor} = 0.691$ (95% CI: 0.581–0.776), $df = 112$, $p < 0.001$; Fig 4C).

359

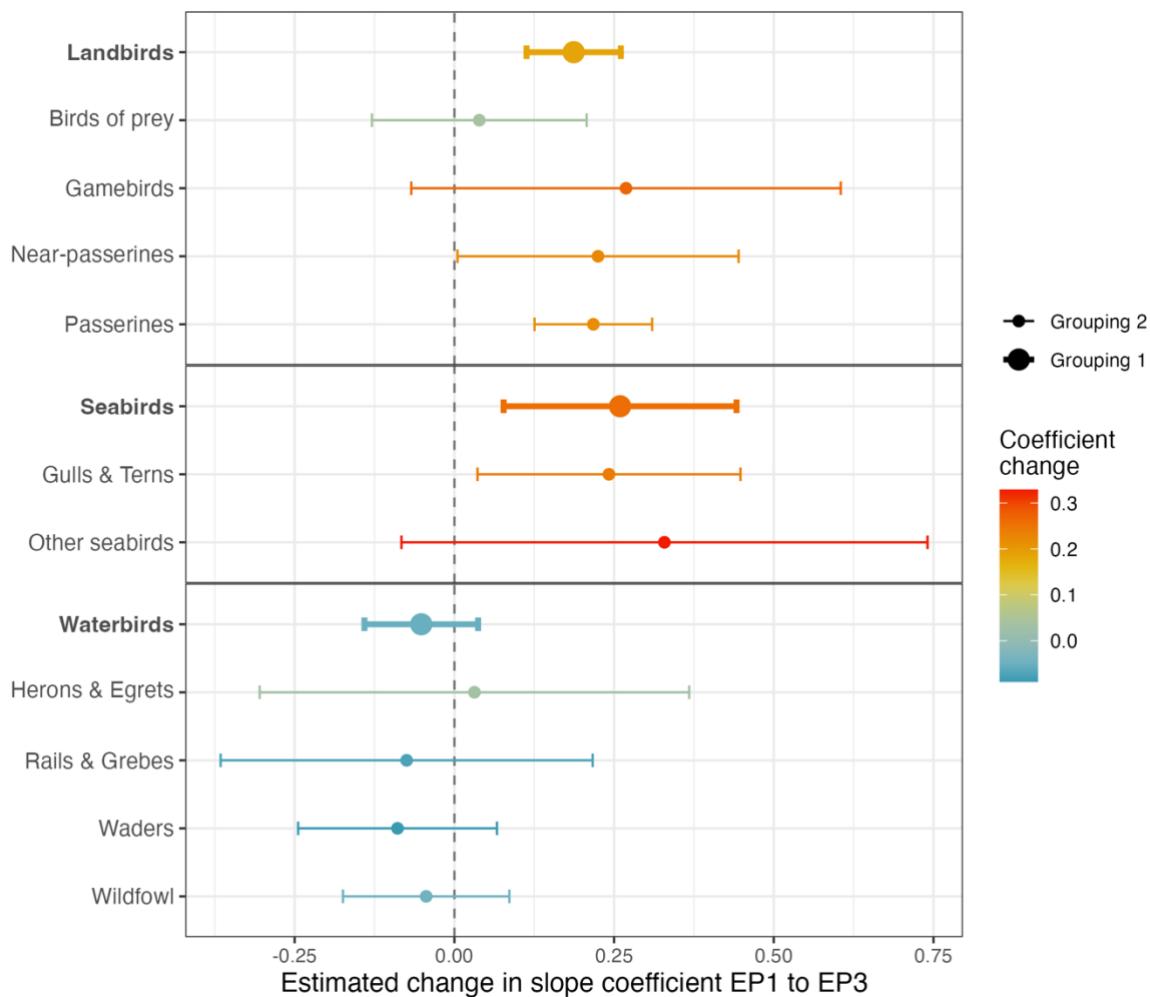


360

361 **Fig 4.** Change in species-specific slope coefficient for the effect of species abundance on case
362 probability in premises across Great Britain. **A)** Epidemic period (EP) 2 compared to EP1. **B)** EP3
363 compared to EP2. **C)** EP3 compared to EP1. Dashed black line has a slope of 1 and indicates the
364 relationship if there was no change between EPs. Solid black line is the actual line of best fit through
365 points based upon a linear model. Error bars around points indicate standard error.

366

367 Despite significant positive correlation between species abundance slope coefficients in EP 1 and 3,
368 there were also distinct outliers where coefficients shifted between EPs. These outliers are of
369 potential interest, as they may represent changes in typical viral host range. Both *landbirds* and
370 *seabirds* had significant increases in effect sizes in EP3, as did subgroups *gulls & terns* and *passerines*.
371 All other *landbird* and *seabird* subgroupings had non-significant increases. *Waterbirds*, and its
372 subgroupings, all showed small non-significant decreases (Fig 5, S6 Table).



373
374 **Fig 5.** Estimated means for change between epidemic periods in the linear model coefficients
375 describing effects of weighted relative species abundance on probability of HPAI cases in premises.
376 Estimated means derived from a GLM assessing group effects (separate model for grouping 1 and
377 grouping 2). Change is calculated as slope coefficient in epidemic period 3 minus slope coefficient in
378 epidemic period 1. Bold text and thicker error bars indicate models under the coarsest species
379 grouping (Grouping 1).

380

381 Due to the potential for type 1 errors (i.e., false positives) with multiple testing across many
382 independent models, single-species relationships may risk overinterpretation of model results, as
383 some significant positive spatial associations may arise by chance alone. Without correcting for
384 multiple testing, significant positive associations were found in 41 (32.3%), 8 (6.2%), and 59 (45.7%)
385 species across the three EPs, respectively (S4 Fig). To account for this, p-values (and therefore
386 significance) can be adjusted. After applying the false discovery rate method (FDR) to account for the
387 expected proportion of false discoveries amongst the rejected hypotheses (Benjamini & Hochberg
388 1995), significant positive associations were found in 37 (29.1%), 1 (0.8%), and 54 (41.9%) species
389 across the three EPs, respectively (S4 Fig). However, the alternative and more conservative Holm-
390 Bonferoni (Holm 1979) adjustment method left only 22 (17.3%), 1 (0.8%), and 27 (20.9%) species
391 significant across the three periods, respectively (S4 Fig).

392

393 Significant negative associations were also found in 25 (19.7%), 5 (3.9%), and 21 (16.3%) species
394 across the three EPs, respectively (S5 Fig; FDR: 23 (18.1%), 0 (0%), 20 (15.5%); Holm-Bonferoni: 10
395 (7.9%), 0 (0%), 16 (12.4%)). Negative associations were, however, generally of lower magnitude and
396 were also relatively uncommon in EP1 and EP3, where we had greater statistical power due to larger
397 numbers of HPAI cases.

398

399 *F. Associations with wild-bird HPAI cases*

400 Our methods do not require data on HPAIV detections in wild birds. To explore whether premise
401 infections can be predicted by use of wild bird abundance data alone as effectively as or more
402 effectively as when using data on confirmed cases in wild birds, we tested whether PCR-diagnosed
403 AIV-positive wild bird cases were associated with infected premises. The number of HPAI confirmed
404 cases in wild birds fell across the EPs, with 425, 163, and 96 cases reported, respectively (Empres-I
405 database; S6 Fig); however, this was likely a substantial under-representation of actual wild bird
406 HPAI-mortality rates across these periods. Wild bird cases were positively associated with infected

407 premises across all EPs, but the association was only significant within EPs 1 and 2 (EP 1 (winter
408 2021/22): Estimate = $0.050 \pm 0.019\text{SE}$, $p = 0.009$; EP 2 (spring/summer 2022): Estimate = $0.641 \pm$
409 0.112SE , $p < 0.001$; EP 3 (autumn/winter 2022/23): Estimate = $0.051 \pm 0.123\text{SE}$, $p = 0.679$; S4 Fig).

410

411 *G. Model performance*

412 The species-specific models fitted to EPs 1 and 3 generally performed better than models fitted to EP
413 2, with a broadly similar median deviance explained across the species assessed in these periods
414 (EP1 = $0.341 \pm 0.002\text{SE}$, $n = 127$; EP2 = $0.242 \pm 0.002\text{SE}$, $n = 130$; EP3 = $0.373 \pm 0.002\text{SE}$, $n = 129$; S7
415 Fig). The poorer model performance in EP 2 is likely driven by the comparatively low number of
416 cases of infected premises ($n = 40$; S6 Fig), combined with the occurrence of a weaker spatial
417 clustering of cases. Furthermore, this poor model performance is also likely to be a major
418 contributing factor to the greater dissimilarity between species-specific associations during EP2
419 across closely related species.

420 4. Discussion

421 Gaining an understanding of which wild species may be key reservoirs of infection or bridging
422 species can be extremely challenging, particularly in dynamic, multi-host systems. Our study
423 demonstrates how publicly available citizen science outputs of wild species abundance can be a
424 powerful tool for exploring associations between wild host abundance and disease cases in
425 domesticated species, without relying upon targeted surveillance across potential wild host
426 populations. Specifically, we assessed which avian abundance distributions from eBird best
427 explained cases of HPAI in premises across Great Britain. Across three distinct epidemic periods
428 between October 2021 and January 2023, 103 species had a significant association in at least one
429 period, and several groups of ecologically similar species were also found to be significant. There
430 was broad consistency between epidemic wave periods (EPs 1 and 3), with groups such as *wildfowl*
431 having consistent significant group-level positive associations with infected premises, alongside
432 some inter-epidemic changes at both the group and species-specific level. In contrast, during the
433 summer period where infected premises were uncommon, our models performed comparatively
434 poorly, failed to find consistent effects across similar species, and wild bird abundance distributions
435 had a less clear association with HPAI occurrence in premises.

436

437 Significant positive associations were comparatively much more frequent than negative associations,
438 and consistency between effect sizes of associations across similar species that share morphological
439 and behavioural traits (i.e., group-level effects explored here) helps support a potential causative
440 relationship in these cases. Importantly, despite our method not relying on wild bird HPAIV
441 surveillance or any prior assumptions for susceptibility, many of the associations we have
442 demonstrated are commensurate with our existing understanding of which avian species play a
443 greater role in the dissemination of HPAIVs. Although more than 220 wild bird species have tested
444 positive for HPAIV globally since 2020 (Empres-i, 2023), the primary wild bird species typically
445 associated with maintenance and spread belong to the orders Anseriformes (i.e., wildfowl – ducks,

446 geese, swans) and Charadriiformes (i.e., waders, gulls, terns), with other less commonly implicated
447 orders usually also associated with aquatic habitats such as Gaviiformes (Divers) and Gruiformes
448 (i.e., Rails & Grebes) (Poulson and Brown 2020). However, large-scale, systematic studies of HPAIV
449 are largely lacking in other Orders, despite the limited studies that have been undertaken finding
450 widespread prevalence (albeit often at low levels) (Wille et al. 2023). In this study, *waterbirds* were
451 consistently found as significant predictors in both epidemic waves (EPs 1 and 3) with little change in
452 effect sizes.

453
454 We also found that the group *seabirds* showed significant increases in effect sizes during EP3. This
455 matches a widely noted step-change in host-range during the summer of 2022 across Europe, where
456 major HPAI outbreaks were recorded in many seabird species at a scale previously not seen
457 (Caliendo 2023, EFSA 2023B, Pearce-Higgins et al. 2023). Our results for *seabirds* are however largely
458 driven by *gulls & terns* that have more extensive terrestrial distributions than many other seabird
459 species and can often be found terrestrially in the UK year-round. Many other species of *seabirds*
460 across the wider group may therefore be unlikely to have such correlation with outbreaks in captive
461 avian premises. One subgroup we were able to assess and did find significant associations with was
462 *divers*, which was unexpected due to their relatively sparse and coastal distribution in much of the
463 UK and life history that would mean direct contact with captive avian premises being unlikely.
464 However, divers have been shown to have seroprevalence for AIV in other regions, albeit at low
465 levels (Ucher-Koch et al. 2019). They may therefore play a small role in some regions across the
466 coarse spatial scale we assess, with other bridging species driving incursions. Subgroups such as *gulls*
467 are likely to interact with other seabirds, such as Northern Gannets or divers, through the breeding
468 season and may therefore play a key role as a bridge species between HPAI outbreaks in isolated
469 seabird colonies and terrestrial bird populations.

470

471 Many of the most conspicuous mass-mortality events within seabirds occurred within species that
472 we could not assess here due to their omission from the eBird modelled species abundance and
473 distribution dataset. This included species such as Northern Gannet and Great Skua where significant
474 proportions of breeding populations were lost (Banyard et al. 2022, Lane et al. 2023). However,
475 these species tend to be present in the UK only in the breeding season and are highly restricted to
476 small islands and coastal edge when not at sea. They are therefore unlikely to have abundance
477 distributions that correlate with HPAIV outbreaks in premises.

478
479 We also found significant group-level associations of HPAI cases with abundance of some passerine
480 groupings, such as *sparrows* during EPs 1 and 3. While there is little existing evidence of passerines
481 having a major role as a maintenance reservoir host or bridge species for facilitating premise
482 incursions, this finding may reflect the importance of passerines as an under-studied host species.
483 Furthermore, while passerines tend to show low test positivity rates for HPAI infection (Wade et al.
484 2023, EFSA 2022) and may therefore have limited capacity as biological sources of virus (i.e., virus
485 replicates inside the wild host), they may also play a role as mechanical transporters via fomite (e.g.,
486 virus carried externally on feet or feathers). External swabbing of small passerines in the United
487 States during previous outbreaks found no support for mechanical transport potential via fomites
488 (Houston et al. 2017). However, small sample sizes together with large populations typical of small
489 passerines lead to low confidence in prevalence. If passerines are acting as sources of transmission
490 (mechanical or biological), many species are small and can be difficult to exclude from poultry
491 premises or adjacent habitats via biosecurity measures unless bird exclusion measures are of high
492 standard and well-maintained, and therefore may pose a significant ongoing risk of incursion.
493 Traditional surveillance programs may also be likely to miss mechanical transmission of virus in these
494 species, as testing is often targeted towards detection of active or past infection.

495

496 Of particular note was the association of HPAI infected premises with free-living *non-native*
497 *gamebirds* during EP 3. Although exact numbers are undefined, tens of millions of non-native
498 gamebirds are reared and released in the United Kingdom each year to bolster feral breeding
499 populations (breeding pop. est. ~4.4 million; Blackburn and Gaston 2018) for the purpose of
500 gamebird shooting (Madden 2021). Both Common Pheasant *Phasianus colchicus* and Red-legged
501 Partridge *Alectoris rufa*, the two non-native gamebirds released in highest numbers annually, had
502 species-specific positive associations during EP 3. EBird-modelled population abundances for non-
503 native gamebirds are not a direct measure of gamebird release locations. However, it is expected
504 that there would be a high degree of correlation between the two as released birds typically only
505 disperse a short distance from release sites and have low survival rates following release. For
506 instance, typically 90–95% of released pheasants and partridges remain within ~1 km of release sites
507 and only ~15% of releases survive to the end of the shooting season (Madden et al. 2018). Significant
508 numbers of Mallard *Anas platyrhynchos* are also released for shooting within this period (estimated
509 ~2.6 million per year compared to ~31.5 and ~9.1 million Common Pheasant and Red-legged
510 Partridge, respectively; Madden 2021). However, while Mallard also had a significant positive
511 association during EP 3, it was not possible to consider truly wild and released birds separately.

512
513 The role of reared and released birds in HPAI is controversial; in 2022 the Royal Society for the
514 Protection of Birds (RSPB) called for a moratorium on gamebird releases as a precautionary measure
515 to reduce the spread of HPAI in wild birds, an approach dismissed by the British Association for
516 Shooting and Conservation (BASC) citing a lack of supporting evidence (Gray and Loeb 2022). Despite
517 cases of HPAI within gamebird hatcheries and rearing premises (Fujiwara et al. 2022; DEFRA 2023A),
518 there remains a lack of conclusive evidence for the role of released gamebirds in the spread of virus
519 to poultry or wild birds. The likelihood of incursions into the gamebird sector was considered low
520 based on egg and chick movements (Fujiwara et al. 2022) but higher during “catching-up” (when
521 surviving released gamebirds may be re-caught after cessation of the shooting period; DEFRA

522 2023B). However, the risk of HPAI spread from free-roaming gamebirds to wild birds post-release
523 was deemed high and has potential to contribute to viral maintenance in other wild bird
524 populations, ultimately leading to increased infection pressure (DEFRA 2022). Furthermore,
525 experimental *in vivo* inoculation with clade 2.3.4.4b H5N6 has shown that Common Pheasant is
526 capable of both acquiring HPAIV and subsequently transmitting to poultry (Liang et al. 2022). Similar
527 outcomes were seen following experimental infection of pheasants with clade 2.3.4.4b H5N1 and
528 H5N8 viruses, with pheasants being more susceptible to infection than red legged partridges
529 (Seekings et al., 2023). The significant positive associations with *non-native gamebirds* that we
530 identify here strongly suggest that increasing surveillance of this group is necessary to more robustly
531 assess whether non-native gamebirds are a key source of HPAI spillover onto captive avian premises,
532 particularly following release.

533

534 Spatial associations between wild bird abundance and HPAI cases in premises provide tentative
535 evidence of which species may be driving viral incursions (either directly onto premises or indirectly
536 by acting as local amplifiers), with a higher species abundance increasing the likelihood of cases in
537 that area. However, purely associative relationships such as these cannot be used as unequivocal
538 evidence of causation. Associations may arise from chance alone, or due to co-linear effects rather
539 than a causal link. Indeed, this is likely to be the driver for the few negative associations found in this
540 study, as there is no clear causative hypothesis for higher abundance of a wild bird species driving
541 lower HPAI incidence in premises. It is perhaps more likely for many species with negative
542 associations that their abundance is either negatively correlated with species that are drivers of HPAI
543 incursions or they arose by random chance.

544

545 Despite these limitations, our approach benefits from the ability for rapid deployment without the
546 requirement for extensive prior surveillance of disease in all potential host species, which is often
547 financially and logistically prohibitive. Even in developed countries such as Great Britain, logistical

548 constraints such as the reporting, triage, collection, and transport of carcasses, as well as legal
549 restrictions on sample handling, can limit testing capacity. Notably, we saw a marked decline in
550 positive HPAI tests in wild birds across our three EPs despite an increase in premise cases (S6 Fig).
551 Indeed, insufficient positive wild bird cases may be the cause for the lack of predictive power
552 observed in EP 3, where wild bird HPAI cases did not significantly predict premise cases.

553

554 Our research shows that the use of publicly available wild bird abundance and distribution data can
555 complement surveillance in wild birds to help identify species that should be prioritised for testing in
556 close to real time. This could help to target limited surveillance resources and to monitor potential
557 changes in infected wild species even in the absence of high mortality. Rapid deployment may also
558 aid in risk mitigation for incursions onto premises, by enabling improved biosecurity measures to be
559 put in place with minimal delay that are better tailored towards higher-risk species. The use of eBird
560 data is particularly valuable because predictions are made at the global scale, at relatively high
561 resolution, and are free to access for over 2000 species (Strimas-Mackey et al. 2022). However,
562 continued efforts may be needed to improve capacity building in regions where the requisite citizen
563 science data may be lacking, and species abundance distributions cannot be accurately modelled.

564

565 Despite our analyses largely relying on publicly available data, we controlled for avian livestock and
566 farm density using poultry distribution datasets that are not publicly available in Great Britain.
567 Controlling for avian livestock density may be somewhat achievable globally with The Gridded
568 Livestock of the World 3 (Gilbert et al. 2018; $\sim 10\text{km}^2$ resolution), but farm density data may only be
569 available for some countries. In our analyses, we used The Great British Poultry Register (GBPR), as it
570 enabled poultry stock and farm density to be calculated at much finer spatial resolutions, yet it is not
571 publicly available due to data protection constraints and is only compulsory for sites with >50 birds.
572 We also lack sufficient data on how biosecurity (in terms of preventing wild bird incursion) may vary
573 across premises, either by type or size, and whether there are significant spatial patterns in this

574 across Great Britain. Improved understanding of these potential biases would enable more accurate
575 spatial associations between wild bird abundance and HPAI case risk in premises.

576

577 **5. Conclusions**

578 Publicly available wild bird abundance and distribution predictions developed using citizen science
579 bird-counting initiatives, such as those offered by eBird, can be a powerful tool in helping to identify
580 potential drivers of wild-bird mediated HPAIV incursions into premises. Higher abundance in avian
581 groups such as wildfowl (ducks, geese, etc.) was found to be consistently associated with a higher
582 incidence of HPAI cases in premises between epidemic waves. Some avian species groups became
583 more important in the most recent epidemic wave, perhaps linked to a change in viral host range, or
584 species-specific drivers such as *non-native gamebirds* only being associated with HPAI in premises
585 during epidemic waves coinciding with mass-release. These associations may help guide future
586 targeted mass-surveillance and aid understanding of the changing host-range of HPAIV as it
587 continues to adapt and spread in wild bird populations.

588

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591 The authors declare that there are no conflicts of interest.

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612

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778 Supplementary Material

779 Utilising citizen science data to rapidly assess potential wild bridging hosts and
780 reservoirs of infection: avian influenza outbreaks in Great Britain.

781
782 **S1 Table.** Species groupings

Common name	Scientific name	Grouping 1	Grouping 2	Grouping 3
Barn Owl	<i>Tyto alba</i>	Landbird	Birds of prey	Owls
Little Owl	<i>Athene noctua</i>	Landbird	Birds of prey	Owls
Long-eared Owl	<i>Asio otus</i>	Landbird	Birds of prey	Owls
Tawny Owl	<i>Strix aluco</i>	Landbird	Birds of prey	Owls
Common Buzzard	<i>Buteo buteo</i>	Landbird	Birds of prey	Diurnal raptors
Eurasian Kestrel	<i>Falco tinnunculus</i>	Landbird	Birds of prey	Diurnal raptors

Eurasian Marsh-Harrier	<i>Circus aeruginosus</i>	Landbird	Birds of prey	Diurnal raptors
Eurasian Sparrowhawk	<i>Accipiter nisus</i>	Landbird	Birds of prey	Diurnal raptors
Golden Eagle	<i>Aquila chrysaetos</i>	Landbird	Birds of prey	Diurnal raptors
Hen Harrier	<i>Circus cyaneus</i>	Landbird	Birds of prey	Diurnal raptors
Merlin	<i>Falco columbarius</i>	Landbird	Birds of prey	Diurnal raptors
Northern Goshawk	<i>Accipiter gentilis</i>	Landbird	Birds of prey	Diurnal raptors
Osprey	<i>Pandion haliaetus</i>	Landbird	Birds of prey	Diurnal raptors
Peregrine Falcon	<i>Falco peregrinus</i>	Landbird	Birds of prey	Diurnal raptors
Red Kite	<i>Milvus milvus</i>	Landbird	Birds of prey	Diurnal raptors
Gray Partridge	<i>Perdix perdix</i>	Landbird	Gamebirds	Native gamebirds
Rock Ptarmigan	<i>Lagopus muta</i>	Landbird	Gamebirds	Native gamebirds
Red-legged Partridge	<i>Alectoris rufa</i>	Landbird	Gamebirds	Non-native gamebirds
Ring-necked/Green Pheasant	<i>Phasianus colchicus</i>	Landbird	Gamebirds	Non-native gamebirds
Eurasian Green Woodpecker	<i>Picus viridis</i>	Landbird	Near-passerines	Other near-passerines
Great Spotted Woodpecker	<i>Dendrocopos major</i>	Landbird	Near-passerines	Other near-passerines
Rose-ringed Parakeet	<i>Psittacula krameri</i>	Landbird	Near-passerines	Other near-passerines
Common Wood-Pigeon	<i>Columba palumbus</i>	Landbird	Near-passerines	Pigeons & Doves
Eurasian Collared-Dove	<i>Streptopelia decaocto</i>	Landbird	Near-passerines	Pigeons & Doves
European Turtle-Dove	<i>Streptopelia turtur</i>	Landbird	Near-passerines	Pigeons & Doves
Rock Pigeon	<i>Columba livia</i>	Landbird	Near-passerines	Pigeons & Doves
Stock Dove	<i>Columba oenas</i>	Landbird	Near-passerines	Pigeons & Doves
Snow Bunting	<i>Plectrophenax nivalis</i>	Landbird	Passerines	Buntings
Yellowhammer	<i>Emberiza citrinella</i>	Landbird	Passerines	Buntings
Carriion Crow	<i>Corvus corone</i>	Landbird	Passerines	Corvids
Eurasian Jay	<i>Garrulus glandarius</i>	Landbird	Passerines	Corvids
Eurasian Magpie	<i>Pica pica</i>	Landbird	Passerines	Corvids
Hooded Crow	<i>Corvus cornix</i>	Landbird	Passerines	Corvids
Red-billed Chough	<i>Pyrrhocorax pyrrhocorax</i>	Landbird	Passerines	Corvids
Rook	<i>Corvus frugilegus</i>	Landbird	Passerines	Corvids
Common Chaffinch	<i>Fringilla coelebs</i>	Landbird	Passerines	Finches
Common Redpoll	<i>Acanthis flammea</i>	Landbird	Passerines	Finches
Eurasian Bullfinch	<i>Pyrrhula pyrrhula</i>	Landbird	Passerines	Finches
Eurasian Linnet	<i>Linaria cannabina</i>	Landbird	Passerines	Finches
Eurasian Siskin	<i>Spinus spinus</i>	Landbird	Passerines	Finches
European Goldfinch	<i>Carduelis carduelis</i>	Landbird	Passerines	Finches

European Greenfinch	<i>Chloris chloris</i>	Landbird	Passerines	Finches
Hawfinch	<i>Coccothraustes coccothraustes</i>	Landbird	Passerines	Finches
Lesser Redpoll	<i>Acanthis cabaret</i>	Landbird	Passerines	Finches
Red Crossbill	<i>Loxia curvirostra</i>	Landbird	Passerines	Finches
Black Redstart	<i>Phoenicurus ochruros</i>	Landbird	Passerines	Flycatchers & Chats
European Robin	<i>Erithacus rubecula</i>	Landbird	Passerines	Flycatchers & Chats
European Stonechat	<i>Saxicola rubicola</i>	Landbird	Passerines	Flycatchers & Chats
Spotted Flycatcher	<i>Muscicapa striata</i>	Landbird	Passerines	Flycatchers & Chats
Bank Swallow	<i>Riparia riparia</i>	Landbird	Passerines	Hirundines
Barn Swallow	<i>Hirundo rustica</i>	Landbird	Passerines	Hirundines
Common House-Martin	<i>Delichon urbicum</i>	Landbird	Passerines	Hirundines
Eurasian Skylark	<i>Alauda arvensis</i>	Landbird	Passerines	Larks, Pipits & Wagtails
Gray Wagtail	<i>Motacilla cinerea</i>	Landbird	Passerines	Larks, Pipits & Wagtails
Meadow Pipit	<i>Anthus pratensis</i>	Landbird	Passerines	Larks, Pipits & Wagtails
Rock Pipit	<i>Anthus petrosus</i>	Landbird	Passerines	Larks, Pipits & Wagtails
Western Yellow Wagtail	<i>Motacilla flava</i>	Landbird	Passerines	Larks, Pipits & Wagtails
Wood Lark	<i>Lullula arborea</i>	Landbird	Passerines	Larks, Pipits & Wagtails
Common Firecrest	<i>Regulus ignicapilla</i>	Landbird	Passerines	Other passerines
Dunnock	<i>Prunella modularis</i>	Landbird	Passerines	Other passerines
Eurasian Nuthatch	<i>Sitta europaea</i>	Landbird	Passerines	Other passerines
Eurasian Wren	<i>Troglodytes troglodytes</i>	Landbird	Passerines	Other passerines
European Starling	<i>Sturnus vulgaris</i>	Landbird	Passerines	Other passerines
White-throated Dipper	<i>Cinclus cinclus</i>	Landbird	Passerines	Other passerines
Eurasian Tree Sparrow	<i>Passer montanus</i>	Landbird	Passerines	Sparrows
House Sparrow	<i>Passer domesticus</i>	Landbird	Passerines	Sparrows
Eurasian Blackbird	<i>Turdus merula</i>	Landbird	Passerines	Thrushes
Fieldfare	<i>Turdus pilaris</i>	Landbird	Passerines	Thrushes
Mistle Thrush	<i>Turdus viscivorus</i>	Landbird	Passerines	Thrushes
Redwing	<i>Turdus iliacus</i>	Landbird	Passerines	Thrushes
Song Thrush	<i>Turdus philomelos</i>	Landbird	Passerines	Thrushes
Coal Tit	<i>Periparus ater</i>	Landbird	Passerines	Tits
Eurasian Blue Tit	<i>Cyanistes caeruleus</i>	Landbird	Passerines	Tits
Great Tit	<i>Parus major</i>	Landbird	Passerines	Tits
Marsh Tit	<i>Poecile palustris</i>	Landbird	Passerines	Tits
Cetti's Warbler	<i>Cettia cetti</i>	Landbird	Passerines	Warblers

Common Chiffchaff	<i>Phylloscopus collybita</i>	Landbird	Passerines	Warblers
Common Reed Warbler	<i>Acrocephalus scirpaceus</i>	Landbird	Passerines	Warblers
Eurasian Blackcap	<i>Sylvia atricapilla</i>	Landbird	Passerines	Warblers
Greater Whitethroat	<i>Currucà communis</i>	Landbird	Passerines	Warblers
Lesser Whitethroat	<i>Currucà curruca</i>	Landbird	Passerines	Warblers
Willow Warbler	<i>Phylloscopus trochilus</i>	Landbird	Passerines	Warblers
Black-headed Gull	<i>Chroicocephalus ridibundus</i>	Seabird	Gulls & Terns	Gulls
Glaucous Gull	<i>Larus hyperboreus</i>	Seabird	Gulls & Terns	Gulls
Great Black-backed Gull	<i>Larus marinus</i>	Seabird	Gulls & Terns	Gulls
Herring Gull	<i>Larus argentatus</i>	Seabird	Gulls & Terns	Gulls
Lesser Black-backed Gull	<i>Larus fuscus</i>	Seabird	Gulls & Terns	Gulls
Little Gull	<i>Hydrocoloeus minutus</i>	Seabird	Gulls & Terns	Gulls
Mediterranean Gull	<i>Ichthyaetus melanocephalus</i>	Seabird	Gulls & Terns	Gulls
Yellow-legged Gull	<i>Larus michahellis</i>	Seabird	Gulls & Terns	Gulls
Common Tern	<i>Sterna hirundo</i>	Seabird	Gulls & Terns	Terns
Little Tern	<i>Sternula albifrons</i>	Seabird	Gulls & Terns	Terns
Sandwich Tern	<i>Thalasseus sandvicensis</i>	Seabird	Gulls & Terns	Terns
Arctic Loon	<i>Gavia arctica</i>	Seabird	Other seabirds	Divers
Common Loon	<i>Gavia immer</i>	Seabird	Other seabirds	Divers
Red-throated Loon	<i>Gavia stellata</i>	Seabird	Other seabirds	Divers
Great Cormorant	<i>Phalacrocorax carbo</i>	Seabird	Other seabirds	Sulids & Cormorants
Cattle Egret	<i>Bubulcus ibis</i>	Waterbird	Herons & Egrets	Herons & Egrets
Eurasian Spoonbill	<i>Platalea leucorodia</i>	Waterbird	Herons & Egrets	Herons & Egrets
Gray Heron	<i>Ardea cinerea</i>	Waterbird	Herons & Egrets	Herons & Egrets
Great Egret	<i>Ardea alba</i>	Waterbird	Herons & Egrets	Herons & Egrets
Common Kingfisher	<i>Alcedo atthis</i>	Waterbird	Near-passerines	Other near-passerines
Eurasian Coot	<i>Fulica atra</i>	Waterbird	Rails & Grebes	Rails & Grebes
Eurasian Moorhen	<i>Gallinula chloropus</i>	Waterbird	Rails & Grebes	Rails & Grebes
Great Crested Grebe	<i>Podiceps cristatus</i>	Waterbird	Rails & Grebes	Rails & Grebes
Horned Grebe	<i>Podiceps auritus</i>	Waterbird	Rails & Grebes	Rails & Grebes
Water Rail	<i>Rallus aquaticus</i>	Waterbird	Rails & Grebes	Rails & Grebes
Eurasian Oystercatcher	<i>Haematopus ostralegus</i>	Waterbird	Waders	Other waders
Black-bellied Plover	<i>Pluvialis squatarola</i>	Waterbird	Waders	Plovers
Common Ringed Plover	<i>Charadrius hiaticula</i>	Waterbird	Waders	Plovers
European Golden-Plover	<i>Pluvialis apricaria</i>	Waterbird	Waders	Plovers

Little Ringed Plover	<i>Charadrius dubius</i>	Waterbird	Waders	Plovers
Northern Lapwing	<i>Vanellus vanellus</i>	Waterbird	Waders	Plovers
Bar-tailed Godwit	<i>Limosa lapponica</i>	Waterbird	Waders	Sandpipers
Black-tailed Godwit	<i>Limosa limosa</i>	Waterbird	Waders	Sandpipers
Common Greenshank	<i>Tringa nebularia</i>	Waterbird	Waders	Sandpipers
Common Redshank	<i>Tringa totanus</i>	Waterbird	Waders	Sandpipers
Common Sandpiper	<i>Actitis hypoleucos</i>	Waterbird	Waders	Sandpipers
Dunlin	<i>Calidris alpina</i>	Waterbird	Waders	Sandpipers
Eurasian Curlew	<i>Numenius arquata</i>	Waterbird	Waders	Sandpipers
Eurasian Woodcock	<i>Scolopax rusticola</i>	Waterbird	Waders	Sandpipers
Green Sandpiper	<i>Tringa ochropus</i>	Waterbird	Waders	Sandpipers
Purple Sandpiper	<i>Calidris maritima</i>	Waterbird	Waders	Sandpipers
Red Knot	<i>Calidris canutus</i>	Waterbird	Waders	Sandpipers
Ruddy Turnstone	<i>Arenaria interpres</i>	Waterbird	Waders	Sandpipers
Ruff	<i>Calidris pugnax</i>	Waterbird	Waders	Sandpipers
Sanderling	<i>Calidris alba</i>	Waterbird	Waders	Sandpipers
Whimbrel	<i>Numenius phaeopus</i>	Waterbird	Waders	Sandpipers
Common Shelduck	<i>Tadorna tadorna</i>	Waterbird	Wildfowl	Dabbling duck
Eurasian Wigeon	<i>Mareca penelope</i>	Waterbird	Wildfowl	Dabbling duck
Gadwall	<i>Mareca strepera</i>	Waterbird	Wildfowl	Dabbling duck
Green-winged Teal	<i>Anas crecca</i>	Waterbird	Wildfowl	Dabbling duck
Mallard	<i>Anas platyrhynchos</i>	Waterbird	Wildfowl	Dabbling duck
Northern Pintail	<i>Anas acuta</i>	Waterbird	Wildfowl	Dabbling duck
Northern Shoveler	<i>Spatula clypeata</i>	Waterbird	Wildfowl	Dabbling duck
Common Eider	<i>Somateria mollissima</i>	Waterbird	Wildfowl	Diving duck
Common Goldeneye	<i>Bucephala clangula</i>	Waterbird	Wildfowl	Diving duck
Greater Scaup	<i>Aythya marila</i>	Waterbird	Wildfowl	Diving duck
Long-tailed Duck	<i>Clangula hyemalis</i>	Waterbird	Wildfowl	Diving duck
Tufted Duck	<i>Aythya fuligula</i>	Waterbird	Wildfowl	Diving duck
Velvet Scoter	<i>Melanitta fusca</i>	Waterbird	Wildfowl	Diving duck
Barnacle Goose	<i>Branta leucopsis</i>	Waterbird	Wildfowl	Geese
Brant	<i>Branta bernicla</i>	Waterbird	Wildfowl	Geese
Canada Goose	<i>Branta canadensis</i>	Waterbird	Wildfowl	Geese
Egyptian Goose	<i>Alopochen aegyptiaca</i>	Waterbird	Wildfowl	Geese
Graylag Goose	<i>Anser anser</i>	Waterbird	Wildfowl	Geese

Greater White-fronted Goose	<i>Anser albifrons</i>	Waterbird	Wildfowl	Geese
Pink-footed Goose	<i>Anser brachyrhynchus</i>	Waterbird	Wildfowl	Geese
Common Merganser	<i>Mergus merganser</i>	Waterbird	Wildfowl	Sawbills
Red-breasted Merganser	<i>Mergus serrator</i>	Waterbird	Wildfowl	Sawbills
Mute Swan	<i>Cygnus olor</i>	Waterbird	Wildfowl	Swans
Tundra Swan	<i>Cygnus columbianus</i>	Waterbird	Wildfowl	Swans

783

784 **S2 Table.** Linear model estimated mean slope coefficients across species groupings and epidemic
785 periods. SE = standard error, df = degrees of freedom.

Epidemic period	Grouping	Estimated mean	SE	df	t ratio	p value
Epidemic period 1	Landbird	-0.046	0.036	374	-1.286	0.199
Epidemic period 2	Landbird	-0.064	0.052	374	-1.235	0.218
Epidemic period 3	Landbird	0.043	0.023	374	1.886	0.060
Epidemic period 1	Seabird	0.166	0.087	374	1.907	0.057
Epidemic period 2	Seabird	0.160	0.122	374	1.307	0.192
Epidemic period 3	Seabird	0.270	0.059	374	4.541	<0.001
Epidemic period 1	Waterbird	0.259	0.029	374	8.833	<0.001
Epidemic period 2	Waterbird	-0.070	0.065	374	-1.080	0.281
Epidemic period 3	Waterbird	0.168	0.023	374	7.330	<0.001

786

787 **S3 Table.** Linear model estimated mean slope coefficients across species groupings and epidemic
788 periods. SE = standard error, df = degrees of freedom.

Epidemic period	Grouping	Estimated mean	SE	df	t ratio	p value
Epidemic period 1	Birds of prey	0.183	0.072	353	2.545	0.011
Epidemic period 2	Birds of prey	-0.148	0.13	353	-1.141	0.255
Epidemic period 3	Birds of prey	0.050	0.051	353	0.972	0.332
Epidemic period 1	Gamebirds	0.051	0.123	353	0.417	0.677
Epidemic period 2	Gamebirds	-0.151	0.182	353	-0.829	0.408
Epidemic period 3	Gamebirds	0.315	0.084	353	3.772	<0.001
Epidemic period 1	Gulls & Terns	0.117	0.11	353	1.071	0.285
Epidemic period 2	Gulls & Terns	0.116	0.134	353	0.868	0.386
Epidemic period 3	Gulls & Terns	0.239	0.064	353	3.752	<0.001
Epidemic period 1	Herons & Egrets	0.061	0.116	353	0.526	0.599
Epidemic period 2	Herons & Egrets	-0.079	0.215	353	-0.369	0.712

Epidemic period 3	Herons & Egrets	0.090	0.086	353	1.037	0.300
Epidemic period 1	Near-passerines	-0.200	0.109	353	-1.84	0.067
Epidemic period 2	Near-passerines	0.043	0.127	353	0.341	0.734
Epidemic period 3	Near-passerines	0.011	0.073	353	0.158	0.875
Epidemic period 1	Other seabirds	0.240	0.135	353	1.773	0.077
Epidemic period 2	Other seabirds	0.342	0.271	353	1.260	0.209
Epidemic period 3	Other seabirds	0.419	0.141	353	2.963	0.003
Epidemic period 1	Passerines	-0.124	0.046	353	-2.69	0.007
Epidemic period 2	Passerines	-0.061	0.064	353	-0.95	0.343
Epidemic period 3	Passerines	0.020	0.027	353	0.757	0.449
Epidemic period 1	Rails & Grebes	0.203	0.115	353	1.764	0.079
Epidemic period 2	Rails & Grebes	-0.073	0.199	353	-0.366	0.714
Epidemic period 3	Rails & Grebes	0.164	0.088	353	1.854	0.065
Epidemic period 1	Waders	0.254	0.045	353	5.654	<0.001
Epidemic period 2	Waders	-0.190	0.137	353	-1.390	0.165
Epidemic period 3	Waders	0.166	0.036	353	4.584	<0.001
Epidemic period 1	Wildfowl	0.304	0.043	353	7.144	<0.001
Epidemic period 2	Wildfowl	-0.021	0.084	353	-0.254	0.800
Epidemic period 3	Wildfowl	0.181	0.033	353	5.489	<0.001

789

790 **S4 Table.** Linear model estimated mean slope coefficients across species groupings and epidemic
791 periods. SE = standard error, df = degrees of freedom.

Epidemic period	Grouping	Estimated mean	SE	df	t ratio	p value
Epidemic period 1	Buntings	0.219	0.125	293	1.754	0.080
Epidemic period 2	Buntings	-0.088	0.356	293	-0.248	0.804
Epidemic period 3	Buntings	0.329	0.154	293	2.141	0.033
Epidemic period 1	Corvids	-0.249	0.143	293	-1.737	0.083
Epidemic period 2	Corvids	0.139	0.158	293	0.877	0.381
Epidemic period 3	Corvids	0.062	0.085	293	0.732	0.465
Epidemic period 1	Dabbling duck	0.360	0.059	293	6.098	<0.001
Epidemic period 2	Dabbling duck	-0.268	0.147	293	-1.828	0.069
Epidemic period 3	Dabbling duck	0.216	0.043	293	4.969	<0.001
Epidemic period 1	Divers	0.301	0.187	293	1.608	0.109
Epidemic period 2	Divers	0.342	0.256	293	1.333	0.184

Epidemic period 3	Divers	0.419	0.134	293	3.135	0.002
Epidemic period 1	Diving duck	0.226	0.125	293	1.801	0.073
Epidemic period 2	Diving duck	0.175	0.132	293	1.330	0.185
Epidemic period 3	Diving duck	0.210	0.082	293	2.567	0.011
Epidemic period 1	Finches	-0.135	0.091	293	-1.479	0.140
Epidemic period 2	Finches	-0.204	0.167	293	-1.223	0.222
Epidemic period 3	Finches	-0.004	0.064	293	-0.057	0.954
Epidemic period 1	Flycatchers & Chats	-0.468	0.230	293	-2.032	0.043
Epidemic period 2	Flycatchers & Chats	0.198	0.198	293	1.000	0.318
Epidemic period 3	Flycatchers & Chats	-0.606	0.142	293	-4.264	<0.001
Epidemic period 1	Geese	0.286	0.075	293	3.797	<0.001
Epidemic period 2	Geese	-0.172	0.220	293	-0.779	0.436
Epidemic period 3	Geese	0.105	0.074	293	1.416	0.158
Epidemic period 1	Gulls	0.145	0.111	293	1.307	0.192
Epidemic period 2	Gulls	0.137	0.133	293	1.035	0.302
Epidemic period 3	Gulls	0.226	0.069	293	3.285	0.001
Epidemic period 1	Herons & Egrets	0.061	0.110	293	0.556	0.579
Epidemic period 2	Herons & Egrets	-0.079	0.203	293	-0.391	0.696
Epidemic period 3	Herons & Egrets	0.090	0.082	293	1.097	0.273
Epidemic period 1	Hirundines	-1.018	0.461	293	-2.207	0.028
Epidemic period 2	Hirundines	-0.340	0.238	293	-1.432	0.153
Epidemic period 3	Hirundines	-0.072	0.137	293	-0.529	0.597
Epidemic period 1	Larks, Pipits, & Wagtails	-0.150	0.134	293	-1.116	0.265
Epidemic period 2	Larks, Pipits, & Wagtails	-0.080	0.211	293	-0.379	0.705
Epidemic period 3	Larks, Pipits, & Wagtails	0.117	0.047	293	2.462	0.014
Epidemic period 1	Native gamebirds	0.098	0.206	293	0.477	0.634
Epidemic period 2	Native gamebirds	-0.151	0.276	293	-0.548	0.584
Epidemic period 3	Native gamebirds	0.291	0.140	293	2.072	0.039
Epidemic period 1	Non-native gamebirds	0.029	0.141	293	0.209	0.835
Epidemic period 2	Non-native gamebirds	-0.150	0.219	293	-0.684	0.494
Epidemic period 3	Non-native gamebirds	0.327	0.096	293	3.417	0.001
Epidemic period 1	Other near-passerines	-0.394	0.156	293	-2.518	0.012
Epidemic period 2	Other near-passerines	0.128	0.216	293	0.593	0.554
Epidemic period 3	Other near-passerines	-0.040	0.098	293	-0.404	0.686
Epidemic period 1	Other passerines	-0.135	0.116	293	-1.169	0.244

Epidemic period 2	Other passerines	0.020	0.157	293	0.130	0.896
Epidemic period 3	Other passerines	-0.020	0.087	293	-0.233	0.816
Epidemic period 1	Other waders	0.245	0.146	293	1.684	0.093
Epidemic period 2	Other waders	NA	NA	NA	NA	NA
Epidemic period 3	Other waders	0.137	0.126	293	1.087	0.278
Epidemic period 1	Owls	-0.057	0.146	293	-0.394	0.694
Epidemic period 2	Owls	-0.152	0.191	293	-0.796	0.427
Epidemic period 3	Owls	-0.130	0.086	293	-1.518	0.130
Epidemic period 1	Pigeons & Doves	-0.053	0.136	293	-0.389	0.697
Epidemic period 2	Pigeons & Doves	0.005	0.145	293	0.037	0.971
Epidemic period 3	Pigeons & Doves	0.061	0.096	293	0.631	0.529
Epidemic period 1	Plovers	0.278	0.078	293	3.568	<0.001
Epidemic period 2	Plovers	-0.199	0.215	293	-0.927	0.355
Epidemic period 3	Plovers	0.192	0.062	293	3.085	0.002
Epidemic period 1	Rails & Grebes	0.203	0.109	293	1.866	0.063
Epidemic period 2	Rails & Grebes	-0.073	0.189	293	-0.388	0.699
Epidemic period 3	Rails & Grebes	0.164	0.084	293	1.961	0.051
Epidemic period 1	Diurnal raptors	0.250	0.077	293	3.252	0.001
Epidemic period 2	Diurnal raptors	-0.145	0.160	293	-0.908	0.365
Epidemic period 3	Diurnal raptors	0.134	0.059	293	2.282	0.023
Epidemic period 1	Sandpipers	0.243	0.054	293	4.510	<0.001
Epidemic period 2	Sandpipers	-0.185	0.162	293	-1.143	0.254
Epidemic period 3	Sandpipers	0.156	0.043	293	3.618	<0.001
Epidemic period 1	Sawbills	0.201	0.182	293	1.104	0.270
Epidemic period 2	Sawbills	0.233	0.262	293	0.888	0.375
Epidemic period 3	Sawbills	0.149	0.160	293	0.928	0.354
Epidemic period 1	Sparrows	0.331	0.152	293	2.173	0.031
Epidemic period 2	Sparrows	-0.082	0.306	293	-0.268	0.789
Epidemic period 3	Sparrows	0.236	0.118	293	2.001	0.046
Epidemic period 1	Sulids & Cormorants	0.186	0.175	293	1.063	0.288
Epidemic period 2	Sulids & Cormorants	NA	NA	NA	NA	NA
Epidemic period 3	Sulids & Cormorants	NA	NA	NA	NA	NA
Epidemic period 1	Swans	0.225	0.128	293	1.754	0.080
Epidemic period 2	Swans	-0.044	0.226	293	-0.197	0.844
Epidemic period 3	Swans	0.120	0.088	293	1.372	0.171

Epidemic period 1	Terns	-0.072	0.290	293	-0.247	0.805
Epidemic period 2	Terns	-0.091	0.413	293	-0.220	0.826
Epidemic period 3	Terns	0.285	0.126	293	2.266	0.024
Epidemic period 1	Thrushes	-0.414	0.182	293	-2.271	0.024
Epidemic period 2	Thrushes	-0.297	0.213	293	-1.392	0.165
Epidemic period 3	Thrushes	-0.213	0.192	293	-1.106	0.270
Epidemic period 1	Tits	-0.502	0.159	293	-3.160	0.002
Epidemic period 2	Tits	-0.071	0.188	293	-0.380	0.705
Epidemic period 3	Tits	-0.141	0.081	293	-1.735	0.084
Epidemic period 1	Warblers	-0.035	0.188	293	-0.185	0.853
Epidemic period 2	Warblers	-0.115	0.202	293	-0.568	0.570
Epidemic period 3	Warblers	0.026	0.074	293	0.344	0.731

792

793 **S5 Table.** Counts of species within each of our grouping variables and the number of those in which
794 we were able to model associations with HPAI cases in premises. Total counts are based upon the
795 BOU British List excluding vagrants.

Group	Total species in Britain	Modelled species	Proportion	Grouping
Accipitriformes	12	8	0.667	Order
Anseriformes	33	24	0.727	Order
Apodiformes	1	0	0	Order
Caprimulgiformes	1	0	0	Order
Charadriiformes	59	32	0.542	Order
Ciconiiformes	1	0	0	Order
Columbiformes	5	5	1	Order
Coraciiformes	1	1	1	Order
Cuculiformes	1	0	0	Order
Falconiformes	4	3	0.750	Order
Galliformes	8	4	0.500	Order
Gaviiformes	3	3	1	Order
Gruiformes	6	3	0.500	Order
Passeriformes	87	55	0.632	Order
Pelecaniformes	6	4	0.667	Order
Piciformes	3	2	0.667	Order
Podicipediformes	5	2	0.400	Order

Procellariiformes	6	0	0	Order
Psittaciformes	1	1	1	Order
Strigiformes	6	4	0.667	Order
Suliformes	3	1	0.333	Order
<i>Accipitridae</i>	11	7	0.636	Family
<i>Acrocephalidae</i>	2	1	0.500	Family
<i>Aegithalidae</i>	1	0	0	Family
<i>Alaudidae</i>	3	2	0.667	Family
<i>Alcedinidae</i>	1	1	1	Family
<i>Alcidae</i>	5	0	0	Family
<i>Anatidae</i>	33	24	0.727	Family
<i>Apodidae</i>	1	0	0	Family
<i>Ardeidae</i>	5	3	0.600	Family
<i>Bombycillidae</i>	1	0	0	Family
<i>Burhinidae</i>	1	0	0	Family
<i>Calcariidae</i>	2	1	0.500	Family
<i>Caprimulgidae</i>	1	0	0	Family
<i>Certhiidae</i>	1	0	0	Family
<i>Cettiidae</i>	1	1	1	Family
<i>Charadriidae</i>	6	5	0.833	Family
<i>Ciconiidae</i>	1	0	0	Family
<i>Cinclidae</i>	1	1	1	Family
<i>Columbidae</i>	5	5	1	Family
<i>Corvidae</i>	8	6	0.750	Family
<i>Cuculidae</i>	1	0	0	Family
<i>Emberizidae</i>	4	1	0.250	Family
<i>Falconidae</i>	4	3	0.750	Family
<i>Fringillidae</i>	14	10	0.714	Family
<i>Gaviidae</i>	3	3	1	Family
<i>Gruidae</i>	1	0	0	Family
<i>Haematopodidae</i>	1	1	1	Family
<i>Hirundinidae</i>	3	3	1	Family
<i>Hydrobatidae</i>	2	0	0	Family
<i>Laridae</i>	17	11	0.647	Family
<i>Locustellidae</i>	1	0	0	Family

<i>Motacillidae</i>	7	4	0.571	Family
<i>Muscicapidae</i>	9	4	0.444	Family
<i>Pandionidae</i>	1	1	1	Family
<i>Panuridae</i>	1	0	0	Family
<i>Paridae</i>	6	4	0.667	Family
<i>Passeridae</i>	2	2	1	Family
<i>Phalacrocoracidae</i>	2	1	0.500	Family
<i>Phasianidae</i>	8	4	0.500	Family
<i>Phylloscopus</i>	3	2	0.667	Family
<i>Picidae</i>	3	2	0.667	Family
<i>Podicipedidae</i>	5	2	0.400	Family
<i>Procellariidae</i>	4	0	0	Family
<i>Prunellidae</i>	1	1	1	Family
<i>Psittaculidae</i>	1	1	1	Family
<i>Rallidae</i>	5	3	0.600	Family
<i>Recurvirostridae</i>	1	0	0	Family
<i>Regulidae</i>	2	1	0.500	Family
<i>Scolopacidae</i>	24	15	0.625	Family
<i>Sittidae</i>	1	1	1	Family
<i>Stercorariidae</i>	4	0	0	Family
<i>Strigidae</i>	5	3	0.600	Family
<i>Sturnidae</i>	1	1	1	Family
<i>Sulidae</i>	1	0	0	Family
<i>Sylviidae</i>	5	3	0.600	Family
<i>Threskiornithidae</i>	1	1	1	Family
<i>Troglodytidae</i>	1	1	1	Family
<i>Turdidae</i>	6	5	0.833	Family
<i>Tytonidae</i>	1	1	1	Family
Landbird	129	82	0.636	Grouping 1
Seabird	38	15	0.395	Grouping 1
Waterbird	85	55	0.647	Grouping 1
BOP	22	15	0.682	Grouping 2
Gamebirds	8	4	0.500	Grouping 2
Gulls & Terns	17	11	0.647	Grouping 2
Herons & Egrets	8	4	0.500	Grouping 2

Near-passerines	13	9	0.692	Grouping 2
Other seabirds	21	4	0.19	Grouping 2
Passerines	87	55	0.632	Grouping 2
Rails & Grebes	10	5	0.500	Grouping 2
Waders	33	21	0.636	Grouping 2
Wildfowl	33	24	0.727	Grouping 2
Auks	5	0	0	Grouping 3
Buntings	6	2	0.333	Grouping 3
Corvids	8	6	0.750	Grouping 3
Dabbling duck	9	7	0.778	Grouping 3
Divers	3	3	1	Grouping 3
Diving duck	9	6	0.667	Grouping 3
Finches	14	10	0.714	Grouping 3
Flycatchers & Chats	9	4	0.444	Grouping 3
Geese	9	7	0.778	Grouping 3
Gulls	11	8	0.727	Grouping 3
Herons & Egrets	8	4	0.500	Grouping 3
Hirundines	3	3	1	Grouping 3
Larks, Pipits, & Wagtails	10	6	0.600	Grouping 3
Native gamebirds	6	2	0.333	Grouping 3
Non-native gamebirds	2	2	1	Grouping 3
Other near-passerines	8	4	0.500	Grouping 3
Other passerines	10	6	0.600	Grouping 3
Other waders	3	1	0.333	Grouping 3
Owls	6	4	0.667	Grouping 3
Pigeons & Doves	5	5	1	Grouping 3
Plovers	6	5	0.833	Grouping 3
Rails & Grebes	10	5	0.500	Grouping 3
Diurnal raptors	16	11	0.688	Grouping 3
Sandpipers	24	15	0.625	Grouping 3
Sawbills	3	2	0.667	Grouping 3
Skuas	4	0	0	Grouping 3
Sparrows	2	2	1	Grouping 3
Sulids & cormorants	3	1	0.333	Grouping 3
Swans	3	2	0.667	Grouping 3

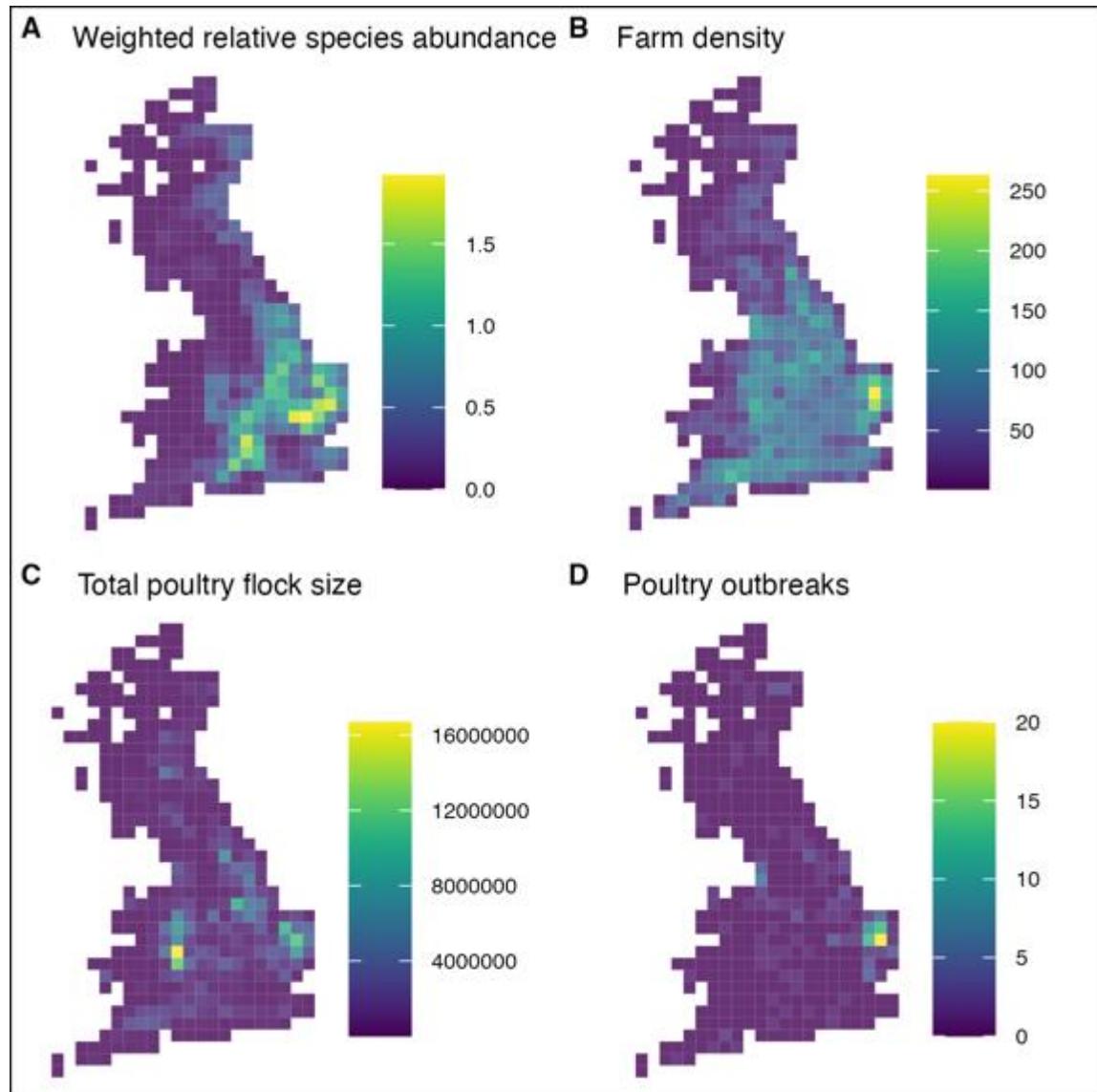
Terns	6	3	0.500	Grouping 3
Thrushes	6	5	0.833	Grouping 3
Tits	7	4	0.571	Grouping 3
Tubenoses	6	0	0	Grouping 3
Warblers	12	7	0.583	Grouping 3

796

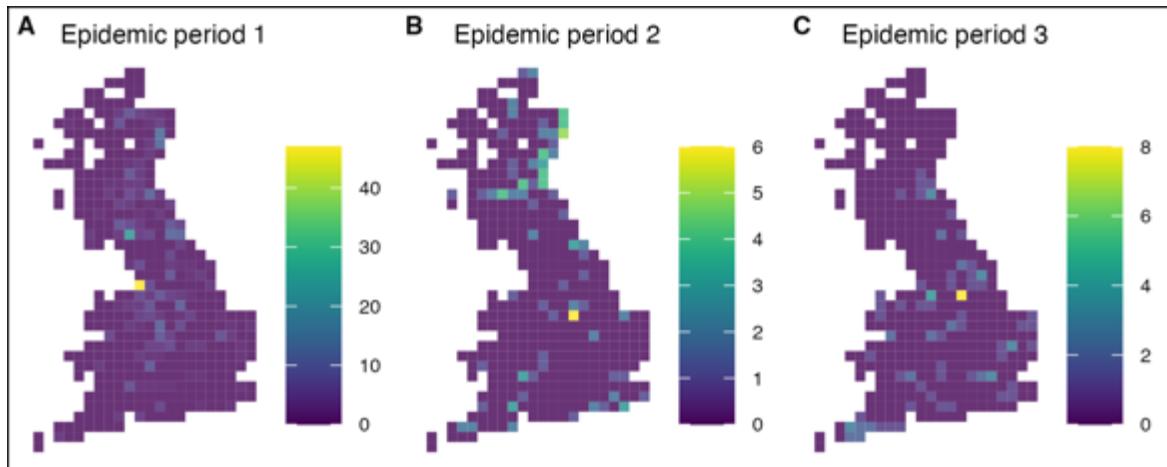
797 S6 Table. Linear model estimated mean change in species abundance slope coefficients between
798 epidemic period 3 and epidemic period 1, across species groupings. SE = standard error, df = degrees
799 of freedom.

Grouping	Estimated mean	SE	df	t ratio	p value	Model
Landbird	0.187	0.038	110	4.959	<0.001	Grouping 1
Seabird	0.259	0.093	110	2.788	0.006	Grouping 1
Waterbird	-0.052	0.045	110	-1.142	0.256	Grouping 1
BOP	0.039	0.086	103	0.455	0.650	Grouping 2
Gamebirds	0.269	0.172	103	1.566	0.120	Grouping 2
Gulls & Terns	0.242	0.105	103	2.304	0.023	Grouping 2
Herons & Egrets	0.031	0.172	103	0.183	0.855	Grouping 2
Near-passerines	0.225	0.112	103	2.003	0.048	Grouping 2
Other seabirds	0.329	0.210	103	1.565	0.121	Grouping 2
Passerines	0.218	0.047	103	4.631	<0.001	Grouping 2
Rails & Grebes	-0.075	0.149	103	-0.503	0.616	Grouping 2
Waders	-0.089	0.079	103	-1.121	0.265	Grouping 2
Wildfowl	-0.044	0.066	103	-0.665	0.508	Grouping 2

800



801
802 **S1 Fig.** Example spatial data used within our modelling process. Maps are for Yellowhammer
803 *Emberiza citrinella* within epidemic period 3 (17th August 2022 – 20th January 2023). Each spatial unit
804 is 26.7km². **A**) Weighted sum of relative species abundance derived from eBird Status and Trends
805 species relative abundance modelling weighted by the weekly proportion of HPAI outbreaks in
806 premises within that period. **B**) Count of premises with >50 captive birds within each spatial unit as
807 listed in the Great British Poultry Register. **C**) Total poultry flock size with each spatial unit as listed in
808 the Great British Poultry Register. **D**) Count of HPAI cases in premises within the period.
809

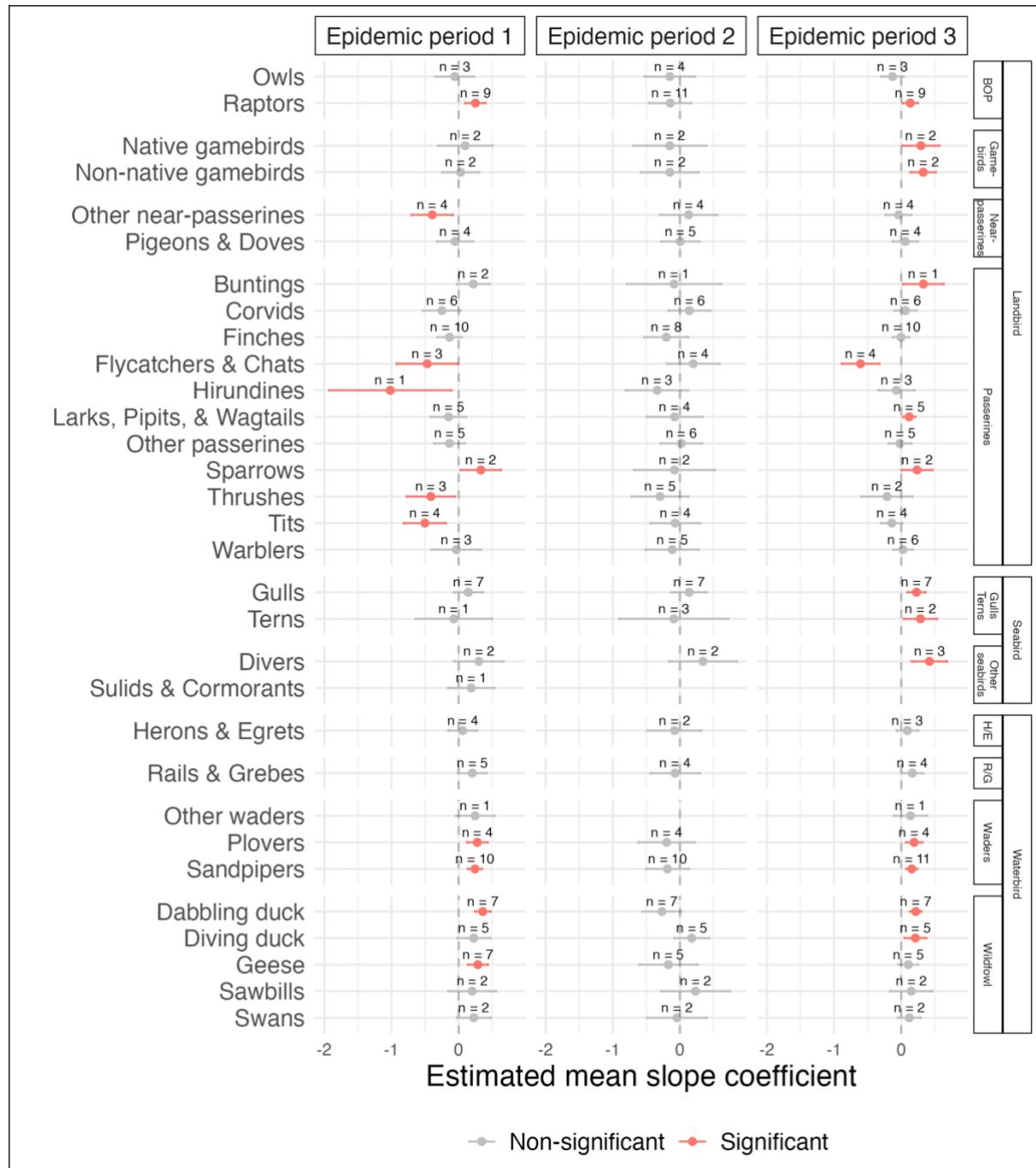


810

811 **S2 Fig.** Rasterized counts of positive wild bird HPAI cases from the Empres-i database within the three

812 distinct epidemic periods (EP1 = 19th October 2021 – 9th February 2022; EP2 = 10th February 2022 –

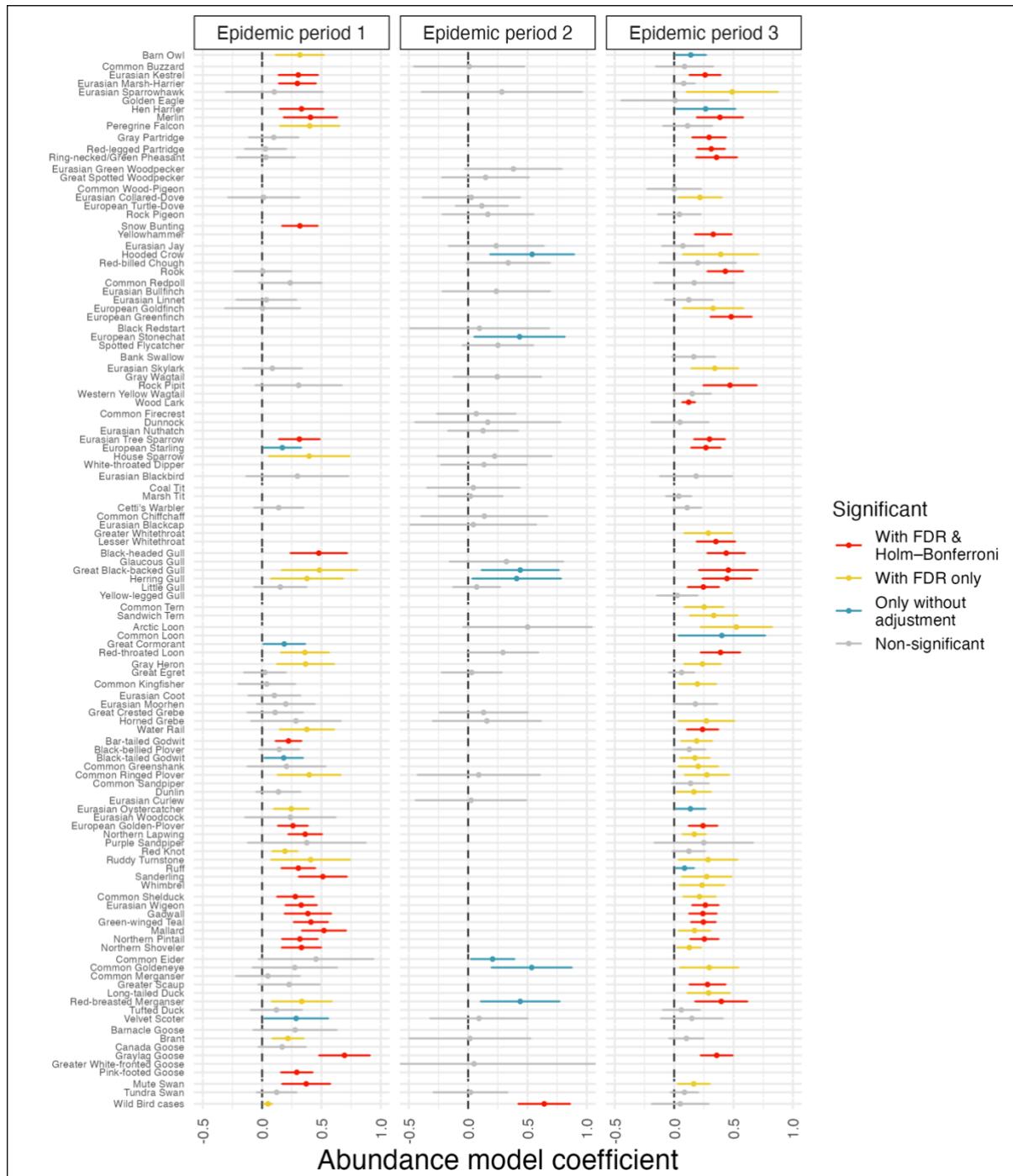
813 16th August 2022; EP3 = 17th August 2022 – 20th January 2023).



814

815 **S3 Fig.** Estimated third-order group-level means for linear model coefficients describing effects of
 816 weighted relative species abundance on probability of HPAI cases in premises. Estimated means
 817 derived from a GLM assessing group effects across epidemic periods (EP1 = 19th October 2021 – 9th
 818 February 2022; EP2 = 10th February 2022 – 16th August 2022; EP3 = 17th August 2022 – 20th January
 819 2023). 'H/G' = Herons & Egrets, 'R/G' = Rails & Grebes.

820



821

822 **S4 Fig.** Linear model coefficients for effects of weighted relative species abundance on probability of
 823 HPAI cases in premises. 'Wild Bird cases' refers to a count of HPAI positive cases in wild birds within
 824 the relevant epidemic period rather than weighted relative species abundance. Only positive model
 825 coefficients are shown. Error bars indicate the 95% confidence interval. Model coefficients were
 826 derived from independent spatial GAM models run for each species and epidemic period (EP1 = 19th
 827 October 2021 – 9th February 2022; EP2 = 10th February 2022 – 16th August 2022; EP3 = 17th August
 828 2022 – 20th January 2023).

829

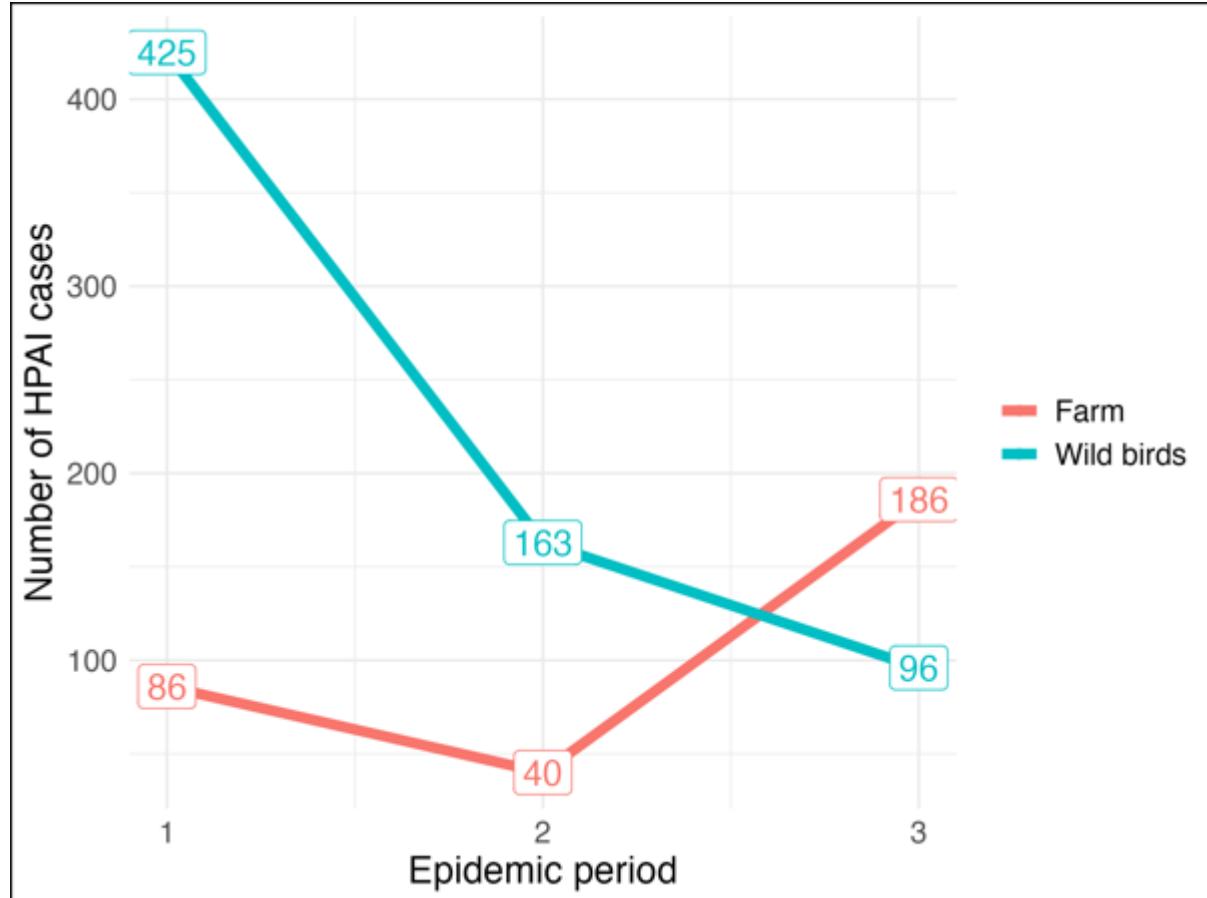


830

831 **S5 Fig.** Linear model coefficients for effects of weighted relative species abundance on probability of
 832 HPAI cases in premises. 'Wild Bird cases' refers to a count of HPAI positive cases in wild birds within
 833 the relevant period rather than weighted relative species abundance. Only negative model
 834 coefficients are shown. Error bars indicate the 95% confidence interval. Model coefficients were
 835 derived from independent spatial GAM models run for each species and epidemic period (EP1 = 19th

836 *October 2021 – 9th February 2022; EP2 = 10th February 2022 – 16th August 2022; EP3 = 17th August*
837 *2022 – 20th January 2023).*

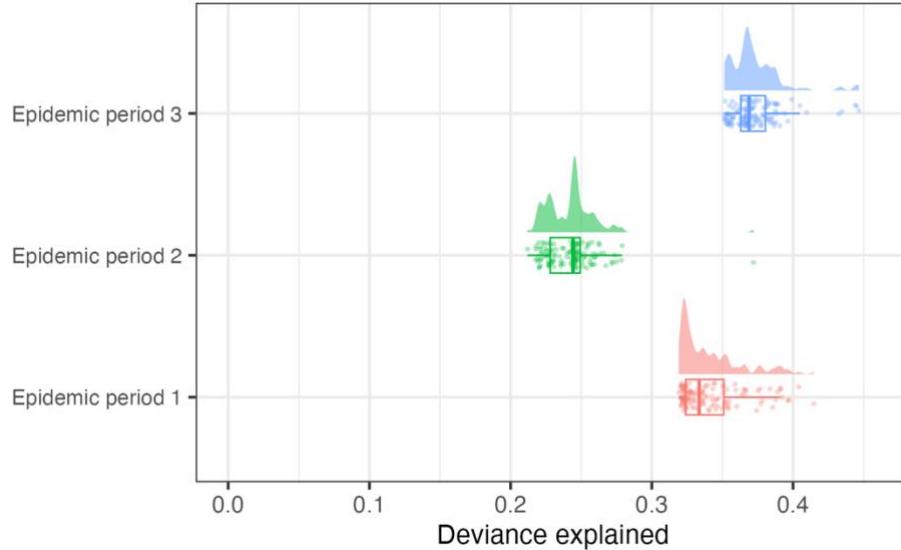
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839

840 *S6 Fig. Count of reported cases of highly pathogenic avian influenza (HPAI) across three epidemic*
841 *periods (EP1 = 19th October 2021 – 9th February 2022; EP2 = 10th February 2022 – 16th August 2022;*
842 *EP3 = 17th August 2022 – 20th January 2023) on premises (red) and in wild birds (blue). Where*
843 *multiple individual birds are infected at the same location at the same time this represents a single*
844 *case.*

845



846

847 **S7 Fig.** Adjusted R-squared values for each of the 389 independent spatial-GAM models assessing
848 associations between weighted relative species abundance and HPAI cases in premises for each
849 species and epidemic period (EP1 = 19th October 2021 – 9th February 2022; EP2 = 10th February 2022
850 – 16th August 2022; EP3 = 17th August 2022 – 20th January 2023).

851

852 *S1 Data. Linear model coefficients for the intercept, and effects of weighted relative species*
853 *abundance and total poultry stock numbers on probability of HPAI cases in premises. 'Wild Bird*
854 *cases' refers to a count of HPAI positive cases in wild birds within the relevant period rather than*
855 *weighted relative species abundance. Model coefficients were derived from independent spatial GAM*
856 *models run for each species and epidemic period (EP1 = 19th October 2021 – 9th February 2022; EP2 =*
857 *10th February 2022 – 16th August 2022; EP3 = 17th August 2022 – 20th January 2023). Species codes*
858 *are those used by eBird.*