

**Supporting Information for:**

**Interactive effects of multiscale diversification practices on farmland bird stress**

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Appendix S1: Descriptive statistics (mean and range) of local diversification practices and farm features, percent seminatural area, and bird community metrics for strawberry farm sites.

Variable	Value
<i>Local farm characteristics</i>	
Percent cover seminatural area on farms	11% (2-31%)
No. vegetative strata	1.21 (0.75-2)
Weediness within crop fields	1.33 (1-3)
Crop diversity	0.46 (0-0.84)
Local diversification index	-0.01 (-0.91-1.96)
Fencing and wire density (m/100 m <sup>2</sup> )	0.53 (0-1.35)
Farm size (ha)	19.59 (1.3-100.34)
Crop diversity (500 m)	0.61 (0.08-0.84)
Strawberry production (500 m)	11% (1-30%)
<i>Seminatural area (1 km)<sup>a</sup></i>	
250 Gaussian decay rate	32% (0-68%)
750 Gaussian decay rate	34% (0-72%)
1250 Gaussian decay rate	34% (0-73%)
No Gaussian decay	36% (0-76%)
<i>Bird community metrics</i>	
Abundance <sup>b</sup>	40.90 (12.50-88.40)
Mean occupancy probability <sup>c</sup>	0.17 (0.07-0.33)
Diversity <sup>1</sup>	1.95 (1.18-2.95)
Species richness <sup>2</sup>	14.98 (5.68-30.76)

<sup>a</sup> The Gaussian decay function weighs seminatural area closer to sampling points more than areas further away. Lower Gaussian decay rate values result in greater emphasis on seminatural areas closer to sampling points compared to higher Gaussian decay rate values.

<sup>b</sup>Raw estimates per point across three visits

<sup>c</sup>Estimates per farm derived from multispecies occupancy models

## Appendix S2: Supplemental methods

### *Local farm diversification index*

We quantified local (on-farm) diversification by building a composite index from measurements of crop diversity, non-crop vegetation cover, and vegetation complexity within each 50m radius point count and then averaging across all point counts on each farm. Specifically, we visually estimated the percent seminatural cover (*e.g.*, trees, shrubs, grasses, weeds, and floral strips), the percent cover of weeds within crop fields (1=0–5%; 2=5–50%; 3>50%), crop diversity (Simpson's index), and the number of vegetative strata (herbaceous vegetation or row crops, understory shrubs, and trees).

We let  $W_{ijk}$  denote the vegetation measurement  $i$  for point count  $j$  on farm  $k$  and averaged vegetation measurements across all  $n_k$  point count locations on the same farm. Specifically, we let  $X_{ik}$  denote the mean farm-level vegetation measurement  $i$  on farm  $k$ :

$$X_{ik} = \frac{1}{n_k} \sum_{j=1}^{n_k} W_{ijk}$$

We let  $\mu_i$  and  $\sigma_i$  denote the mean and standard deviation of farm-level vegetation measurements across all 24 farms.

$$\mu_i = \frac{1}{24} \sum_{k=1}^{24} X_{ik}$$
$$\sigma_i = \sqrt{\frac{1}{24} \sum_{k=1}^{24} (X_{ik} - \mu_i)^2}$$

We created a local diversification index,  $Z_k$ , for each farm  $k$  by first standardizing and then averaging the 4 mean farm-level vegetation measurements ( $X_{ik}$ ) on each farm. Specifically,

$$Z_k = \frac{1}{4} \sum_{i=1}^4 (X_{ik} - \mu_i) / \sigma_i$$

### *Surrounding landscape context*

We then calculated the proportion of seminatural area within concentric rings (every 50m from 50 to 1,000m) surrounding each farm. Next, we applied a Gaussian decay function (below) to weigh seminatural areas closer to sampling points more than areas further away:

$$W = \exp(-I^2 / (2 * d^2))$$

where  $W$  is the weight assigned to each buffer ring,  $I$  is the inner edge distance of the ring, and  $d$  is the decay rate parameter (in this case, 250, 750, or 1250; Karp et al. 2016). The resulting

values were used to create a weighted average of seminatural area values across all concentric rings. We also calculated the proportion of seminatural area within 1 km without Gaussian weighting.

#### *Bird point count surveys*

We surveyed birds on each focal farm with 10-minute, 50-m fixed-radius point count surveys, repeated three times over consecutive days from May-June of 2018-2019. Point count locations were separated by at least 100m (range 100m-1103m, mean=275m). A maximum of 6 point-count locations were placed on a single farm (Ralph et al. 1993), and we included as many point count locations as we could fit on each farm (up to 6). Thus, the number of point counts per farm varied by farm size (point counts: range 1-6, mean=4.7; point counts per 10 hectares: range 0.6-12.8, mean=5.5). All point count survey locations were centered in crop fields and primarily included row crop fields where the probability of detecting individuals is high. Half of the count locations on each farm were centered in strawberry crops; the other half were located within other dominant crop types (e.g., lettuce, squash, broccoli) to reflect the diversity of other crops and management practices used on each farm. All surveys were conducted by the same skilled observer (K. Garcia), primarily between sunrise and 10:30am and always in the absence of rain or heavy fog. We excluded individuals detected as fly overs, unless they were aerial insectivores foraging directly above the crops (e.g., swallows, swifts). All other individuals seen or heard within the survey radius were identified to species and recorded.

#### *Observer bias correction*

Each observer completed a set of five blood smear training slides and processed each slide three times. Observers counted 100 white blood cells on each slide and identified cell types as heterophil, lymphocyte, eosinophil, basophil, or monocyte. Observers cycled through all training slides before recounting the same slide. First, we calculated the mean number of heterophils and lymphocytes that each observer counted for each slide across their three counts. We designated the average number of heterophils and lymphocytes that all observers counted as the true value for each training slide. Then, we calculated a scaling factor to correct for observer bias; specifically, the difference between each observer's mean count and the average count of heterophils and lymphocytes. Finally, we applied the scaling factors to heterophil and lymphocyte counts for all blood smears, and then calculated corrected heterophil:lymphocyte ratios (H:L) (Appendix S3) for subsequent analyses.

#### *Occupancy modeling*

We constructed multi-species occupancy models to estimate species richness and each species' occurrence probability at each farm, correcting for potential detection biases. We let  $\Psi[i, j, k]$  denote the probability that species  $i$  is present at farm  $j$  in year  $k$ . We assume that  $Z[i, j, k]$ , the true, but unknown occupancy state, is drawn from a Bernoulli distribution with probability  $\Psi[i, j, k]$ ,

$$Z[i, j, k] \sim \text{Bernoulli}(\Psi[i, j, k])$$

We parameterize occupancy probability by including an intercept,  $\Psi_0$ , which denotes the mean occupancy in year 2018, an effect of year,  $\Psi_{year}$ , which allows for potential differences between

the two sampling years, and species and farm-specific random effects ( $\Psi_{sp[i]}$  and  $\Psi_{farm[j]}$ ). Specifically:

$$\text{logit}(\Psi[i, j, k]) = \Psi_0 + \Psi_{sp[i]} + \Psi_{farm[j]} + \Psi_{year} * k$$

Note:  $k$  takes values 0 or 1 for year 2018 and 2019, respectively.

We let  $p[i, j, k, t]$  denote the probability that species  $i$  is detected in the  $t^{\text{th}}$  visit to farm  $j$  in year  $k$ , given that that species is present. We assume that our actual detection records (letting  $X[i, j, k, t]$  denote the detection/non-detection of species  $i$  during the  $t^{\text{th}}$  visit to farm  $j$  in year  $k$ ) are drawn from a Bernoulli distribution such that

$$X[i, j, k, t] \sim \text{Bernoulli}(p[i, j, k, t] * Z[i, j, k])$$

We include a number of fixed and random effects in order to account for potential factors that might impact detection probability. Specifically, we include random effects of species and farm, and fixed effects of temperature, time of day, noise level, number of people present within the point count radius during the survey, and day of the year (Julian date). Specifically,

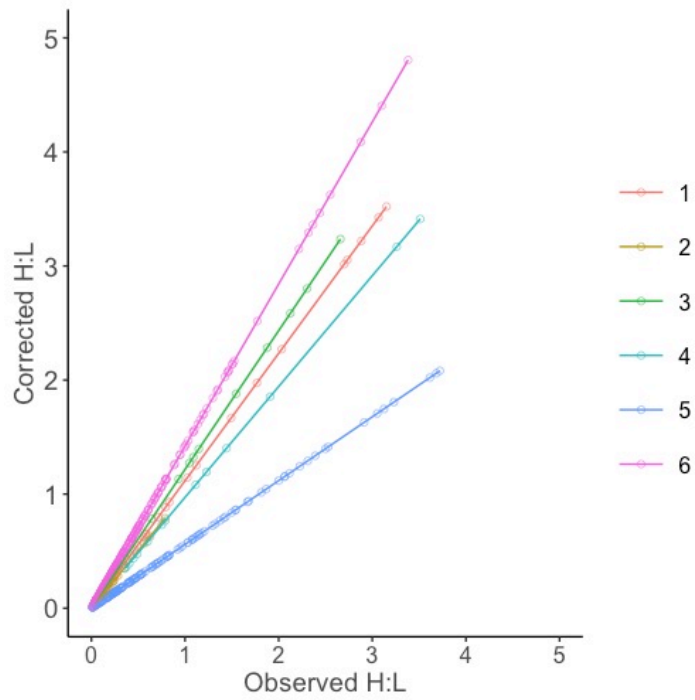
$$\begin{aligned} \text{logit}(p[i, j, k, t]) &= p_0 + p_{sp[i]} + p_{farm[j]} + p_{temp} * temp[j, k, t] + p_{timeday} \\ &* timeday[j, k, t] + p_{noise} * noise[j, k, t] + p_{ppl} * ppl[j, k, t] + p_{day} \\ &* day[j, k, t] \end{aligned}$$

We calculate species richness at each site with posterior chains for  $Z[i, j, k]$  and, thus, they include species that were present at a site, but unobserved. We limit our analysis only to species we observed at least once somewhere.

We used uninformative priors throughout. We ran models in JAGS version 4.3.0 (Plummer 2017) and R (version 4.0.0). Models were run for 10,000 iterations, thinning every 10 iterations and with a burn-in of 1,000 iterations.

#### *Agriculture affiliation score*

To quantify agricultural affiliation, we used eBird data and filtered data according to best practices (Strimas-Mackey et al. 2020). We used the MODIS MCD12Q1 v006 land cover product (500-m resolution) to calculate the proportion of agricultural land cover within a 700m radius of each eBird checklist location (Friedl & Sulla-Menashe 2015). We used generalized additive models to quantify species' responses to agricultural land cover while accounting for nuisance variables and spatial autocorrelation (Wood 2006). We modelled the effect of each land cover type on occupancy to determine each species' most preferred natural habitat type. Then, we calculated the agricultural affiliation score as the relative log-fold increase (or decrease) of occurrence probability in agriculture versus the natural habitat where the species was most abundant. Specifically, this score was calculated as the slope of a species' response to agriculture minus the slope of their response to their preferred natural land cover. For more details, refer to Smith et al. (*accepted at Ecological Applications*).



Appendix S3: Relationship between mean observed and corrected heterophil:lymphocyte ratios (H:L) for observers who processed avian blood smears.

Appendix S4: Number of samples by species (number of farms captures were from) used in analyses for each avian physiological stress indicator.

Species code	Common name	Scientific name	H:L	Hematocrit	Body condition	Feather growth
AMGO	American Goldfinch	<i>Spinus tristis</i>	0	18 (6)	23 (8)	0
AMRO	American Robin	<i>Turdus migratorius</i>	0	25 (9)	36 (12)	0
BARS	Barn Swallow	<i>Hirundo rustica</i>	0	16 (6)	15 (7)	0
BEWR	Bewick's Wren	<i>Thryomanes bewickii</i>	0	0	10 (6)	0
BHCO	Brown-headed Cowbird	<i>Molothrus ater</i>	0	0	11 (6)	0
BHGR	Black-headed Grosbeak	<i>Pheucticus melanocephalus</i>	0	21 (4)	26 (5)	0
BLPH	Black Phoebe	<i>Sayornis nigricans</i>	0	25 (9)	28 (11)	0
BRBL	Brewer's Blackbird	<i>Euphagus cyanocephalus</i>	0	23 (5)	32 (6)	0
BUSH	Bushtit	<i>Psaltriparus minimus</i>	0	0	12 (5)	0
CALT	California Towhee	<i>Melospiza crissalis</i>	0	37 (14)	48 (18)	0
CAQU	California Quail	<i>Callipepla californica</i>	0	18 (6)	0	0
CBCH	Chestnut-backed Chickadee	<i>Poecile rufescens</i>	0	0	10 (6)	0
EUST	European Starling	<i>Sturnus vulgaris</i>	0	14 (5)	20 (7)	0
HOFI	House Finch	<i>Haemorhous mexicanus</i>	132 (15)	133 (13)	202 (18)	62 (8)
HOSP	House Sparrow	<i>Passer domesticus</i>	0	29 (3)	39 (5)	0
LEGO	Lesser Goldfinch	<i>Spinus psaltria</i>	0	24 (7)	33 (10)	0
NOMO	Northern Mockingbird	<i>Mimus polyglottos</i>	0	14 (5)	22 (6)	0
OATI	Oak Titmouse	<i>Baeolophus inornatus</i>	0	11 (7)	17 (10)	0
DEJU	Dark-eyed Junco	<i>Junco hyemalis</i>	129 (10)	140 (9)	152 (11)	74 (7)
PSFL	Pacific-slope Flycatcher	<i>Empidonax difficilis</i>	0	39 (10)	45 (14)	0
PUFI	Purple Finch	<i>Haemorhous purpureus</i>	0	0	11 (6)	0
RWBL	Red-winged Blackbird	<i>Agelaius phoeniceus</i>	0	0	11 (4)	0
SOSP	Song Sparrow	<i>Melospiza melodia</i>	175 (14)	180 (12)	230 (17)	86 (13)
SPTO	Spotted Towhee	<i>Pipilo maculatus</i>	0	40 (11)	49 (16)	0
WIWA	Wilson's Warbler	<i>Cardellina pusilla</i>	0	0	11 (3)	0

Appendix S5: Top model set for heterophil:lymphocyte ratios (H:L) of farmland birds (values represent coefficient estimates, models with a minimum weight of 0.05 are shown).

Intercept	Julian day	Sex	Age and breeding status	Species	Local diversification index	Strawberry production (500 m)	Seminatural area (1 km)	Local diversification index: Seminatural area (1 km)	df	$\Delta AIC_c$	weight
-0.81		+		+	-0.10		0.18	0.27	10	0.00	0.46
-0.80		+		+	-0.09	0.02	0.18	0.26	11	2.06	0.16
-0.69		+		+					7	2.43	0.14
-0.67		+		+	0.05				8	4.24	0.06
-0.66		+		+	0.05		0.05		8	4.24	0.06
-0.69		+		+	0.03				8	4.38	0.05



Appendix S6: Top model set for hematocrit of farmland birds (values represent coefficient estimates, models with a minimum weight of 0.05 are shown).

Intercept	Julian day	Relative capture time	Sex	Age and breeding status	Local diversification index	Strawberry production (500 m)	Seminatural area (1 km)	Local diversification index: Seminatural area (1 km)	df	$\Delta AIC_c$	weight
2.21	-0.06		+		0.02				8	0.00	0.23
2.21	-0.05		+						7	0.21	0.20
2.21	-0.05		+		0.03	0.02			9	0.72	0.16
2.21	-0.06		+		0.02		-0.01		9	1.68	0.10
2.21	-0.05		+			0.01			8	2.01	0.08
2.21	-0.06		+				0.00		8	2.25	0.07
2.21	-0.05		+		0.03	0.02	-0.01		10	2.49	0.07

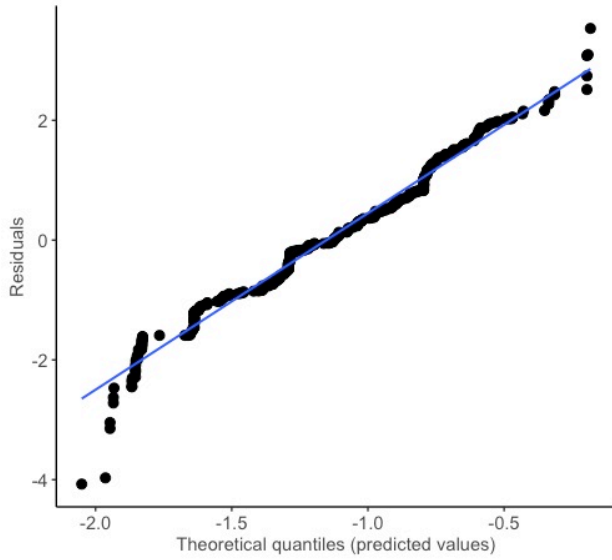
Appendix S7: Top model set for body condition of farmland birds (values represent coefficient estimates, models with a minimum weight of 0.05 are shown).

Intercept	Julian day	Relative capture time	Sex	Age and breeding status	Local diversification index	Strawberry production (500 m)	Seminatural area (1 km)	Local diversification index: Seminatural area (1 km)	df	$\Delta AIC_c$	weight
1.00			+	+	1.94E-03		0.00	0.00	11	0.00	0.59
1.00			+	+	2.14E-03	4.00E-04	0.00	0.00	12	1.90	0.23
1.00			+	+					8	4.61	0.06

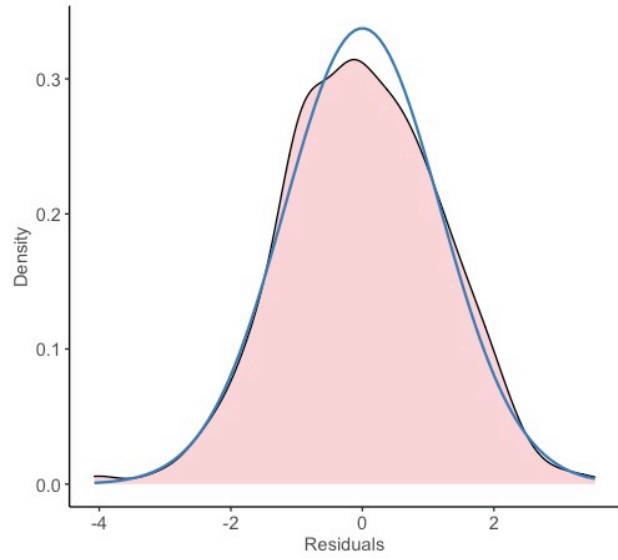
Appendix S8: Top model set for feather growth of farmland birds (values represent coefficient estimates, models with a minimum weight of 0.05 are shown).

Intercept	Species	Local diversification index	Strawberry production (500 m)	Seminatural area (1 km)	Local diversification index: Seminatural area (1 km)	df	$\Delta AIC_c$	weight
1.98	+		-0.04			6	0.00	0.35
1.96	+		-0.05	-0.02		7	1.74	0.15
1.99	+					5	1.95	0.13
1.99	+	0.01	-0.04			7	2.08	0.12
2.00	+	0.02				6	2.98	0.08
1.96	+	0.02	-0.05	-0.03		8	3.55	0.06
2.00	+			0.01		6	3.88	0.05

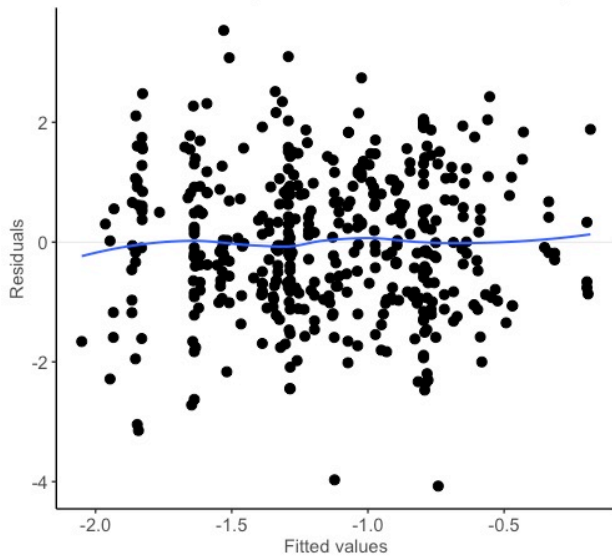
**A** Non-normality of residuals and outliers  
Dots should be plotted along the line



**B** Non-normality of residuals  
Distribution should look like normal curve

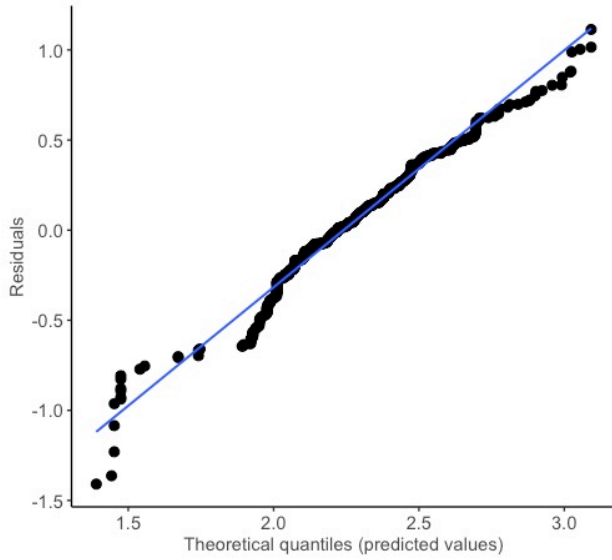


**C** Homoscedasticity (constant variance of residuals)  
Amount and distance of points scattered above/below line is equal or randomly spread

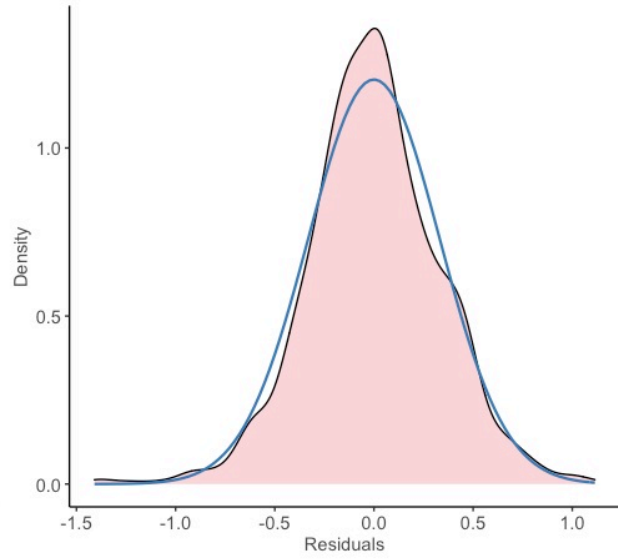


Appendix S9: Diagnostic plots of the normality (A,B) and heterogeneity (C) of residuals for the top-selected heterophil:lymphocyte ratio (H:L) model for farmland birds.

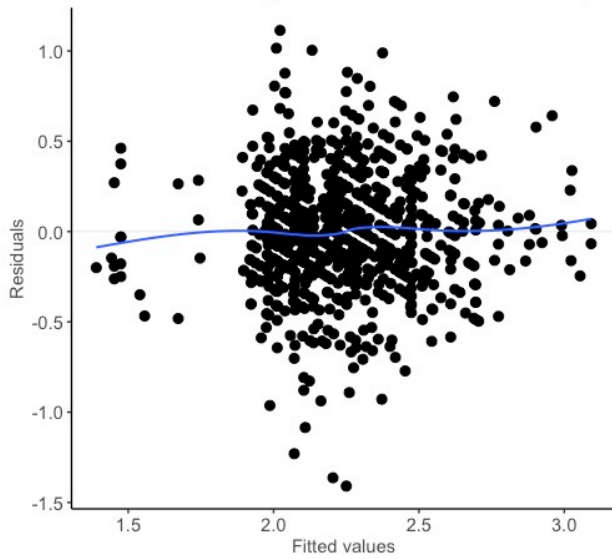
**A** Non-normality of residuals and outliers  
Dots should be plotted along the line



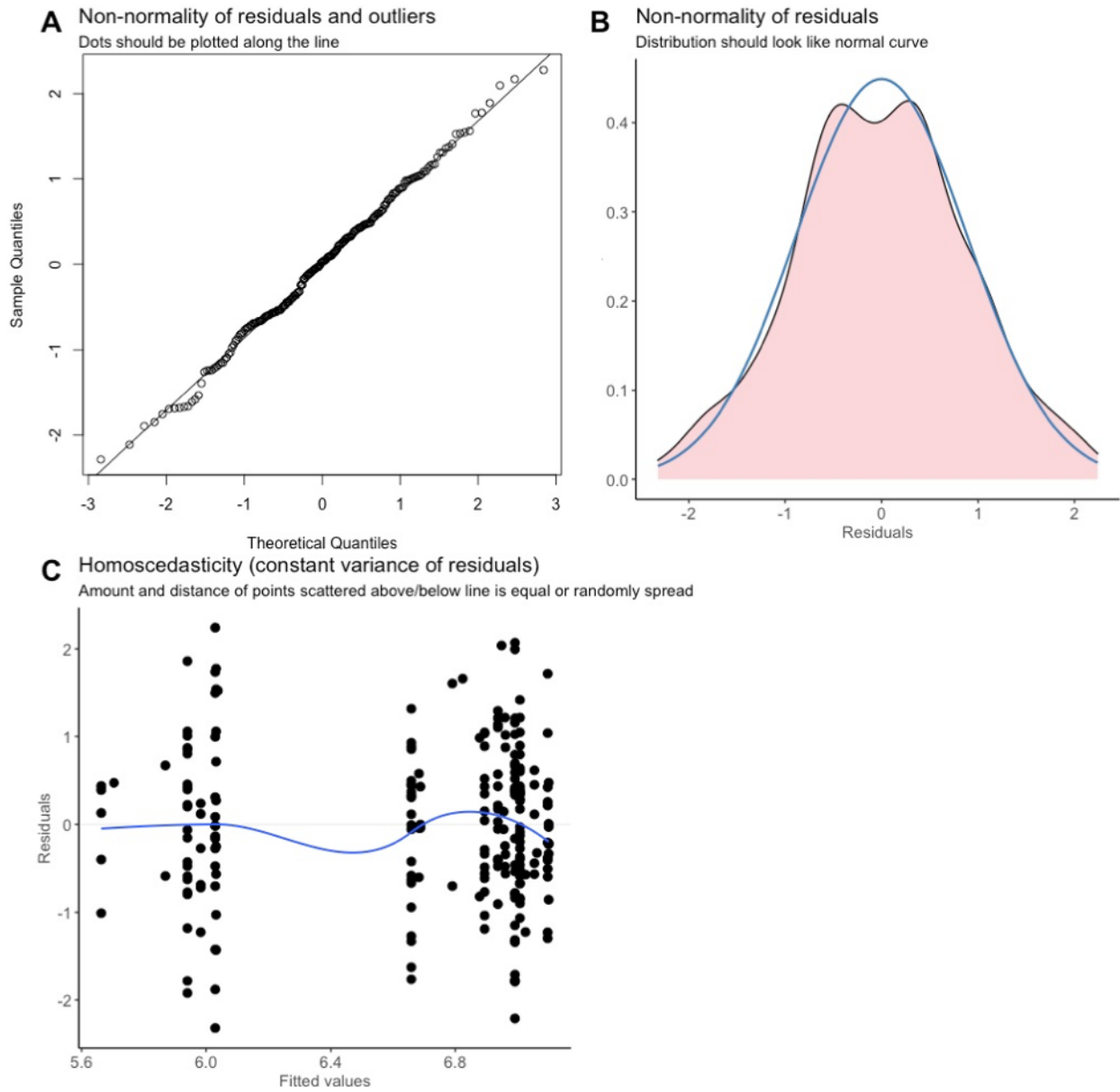
**B** Non-normality of residuals  
Distribution should look like normal curve



**C** Homoscedasticity (constant variance of residuals)  
Amount and distance of points scattered above/below line is equal or randomly spread



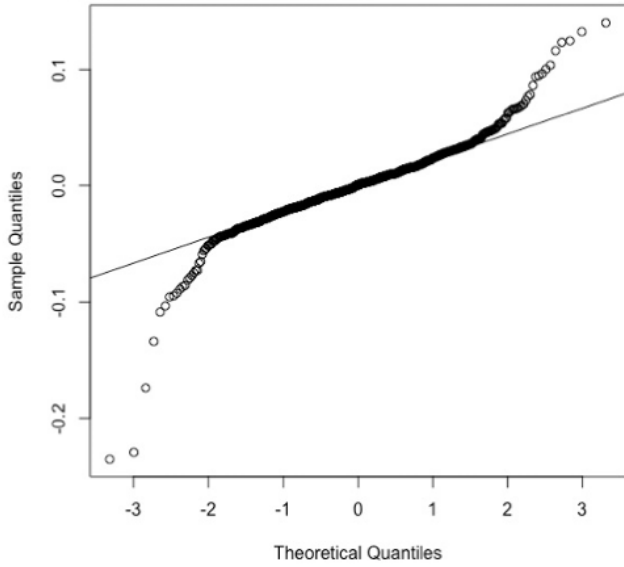
Appendix S10: Diagnostic plots of the normality (A,B) and heterogeneity (C) of residuals for the top-selected hematocrit model for farmland birds.



Appendix S11: Diagnostic plots of the normality (A,B) and heterogeneity (C) of residuals for the top-selected feather growth model for farmland birds.

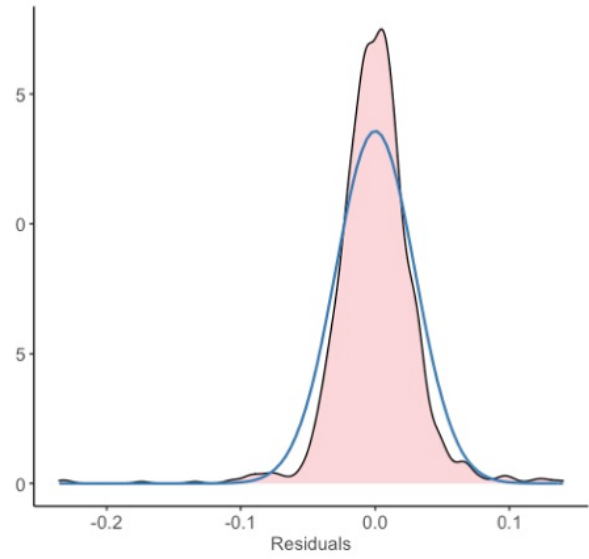
**A** Non-normality of residuals and outliers

Dots should be plotted along the line



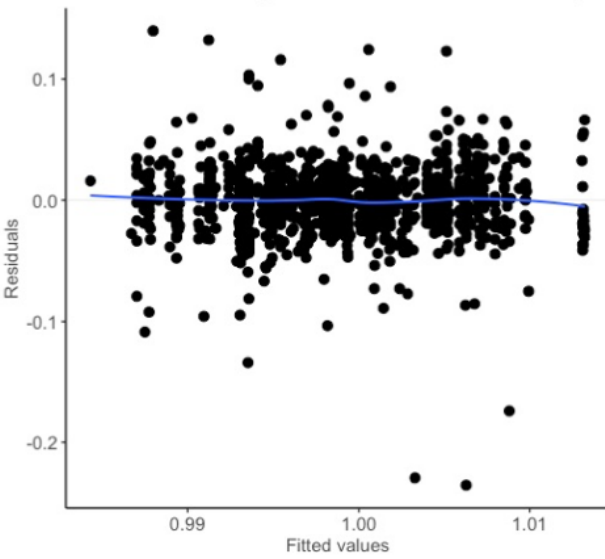
**B** Non-normality of residuals

Distribution should look like normal curve



**C** Homoscedasticity (constant variance of residuals)

Amount and distance of points scattered above/below line is equal or randomly spread



Appendix S12: Diagnostic plots of the normality (A,B) and heterogeneity (C) of residuals for the top-selected body condition model for farmland birds.

Appendix S13: Coefficient estimates for top models (from Appendices S5-S8) that were modified to include an interaction between species identity and diversification as a fixed effect (heterophil:lymphocyte ratio [H:L], feather growth) or a random slope effect (hematocrit, body condition).<sup>a</sup>

Intercept	Date	Relative capture time	Sex	Species	Age and breeding status	Local diversification index	Strawberry production (500 m)	Seminatural area (1 km)	Local diversification index: Seminatural area (1 km)	Interaction between Species and diversification	df
<b>H:L Ratio</b>											
-8.10E-01	-		+	+	-	-1.36E-01	-	1.88E-01	2.60E-01	Local diversification index*Species	12
-8.07E-01	-		+	+	-	-9.85E-02	-	2.01E-01	2.74E-01	Seminatural area*Species	12
<b>Hematocrit</b>											
2.23E+00	+	-	+		-	2.19E-02	-	-	-	Local diversification index   Species	11
<b>Body condition</b>											
1.00E+00	-	-	+		+	2.01E-03	-	-2.78E-03	-3.78E-03	Seminatural area   Species	14
1.00E+00	-	-	+		+	1.60E-03	-	-2.60E-03	-4.09E-03	Local diversification index   Species	14
<b>Feather growth</b>											
1.98E+00	-			+		-	-5.23E-02	-	-	Strawberry production*Species	8

<sup>a</sup>Farm was included as a random intercept in all models; hematocrit and body condition models also included a species random intercept. Minus signs that do not precede numerals indicate the predictor was included as a fixed effect in full models but not included in top model sets.



Appendix S14: Results of likelihood ratio tests (LRTs) comparing top models (Appendices S5-S8; indicated in this table as ‘no interaction’) and top models that were modified to include an interaction between species and diversification practices (Appendix S13) as a fixed effect (heterophil:lymphocyte ratio [H:L], feather growth) or random slope effect (hematocrit, body condition).

Response	Interaction between Species and diversification practices	AIC	LRT $\chi^2$	df	<i>p</i>
H:L	no interaction	1402.2			
	Local diversification index*Species	1406.0	0.24	2	0.89
	Seminatural area*Species	1406.1	0.12	2	0.94
Hematocrit	no interaction	598.48			
	Local diversification index  Species	604.27	0.21	3	0.98
Body condition	no interaction	-4587.4			
	Local diversification index   Species	-4581.7	0.25	3	0.97
	Seminatural area  Species	-4581.6	0.11	3	0.99
Feather growth	no interaction	100.53			
	Strawberry production*Species	103.94	0.58	2	0.75

Appendix S15: Coefficient estimates for models testing the relationship between physiological stress indicators and farmland bird abundance and occupancy probability.<sup>a</sup>

H:L <sup>b</sup>	Total abundance <sup>c</sup> (SE)	Mean occupancy (all species) <sup>d</sup> (SE)	Mean occupancy (species included in model) <sup>d</sup> (SE)
Intercept	-0.68 (0.17)***	-0.66 (0.17)***	-0.64 (0.18)***
Male	-0.30 (0.17)†	-0.30 (0.17)†	-0.31 (0.17)†
Unknown sex	-0.60 (0.16)***	-0.59 (0.16)***	-0.59 (0.16)***
Dark-eyed junco	-0.54 (0.17)**	-0.57 (0.18)**	-0.59 (0.18)***
Song sparrow	0.10 (0.15)	0.07 (0.16)	0.05 (0.16)
Biodiversity <sup>c</sup>	0.03 (0.08)	0.05 (0.08)	0.07 (0.08)
Hematocrit			
Intercept	2.22 (0.07)***	2.22 (0.07)***	2.22 (0.07)***
Male	0.18 (0.03)***	0.18 (0.03)***	0.18 (0.03)***
Unknown sex	0.03 (0.03)	0.03 (0.03)	0.03 (0.03)
Julian day	-0.06 (0.01)***	-0.06 (0.01)***	-0.06 (0.01)***
Biodiversity <sup>c</sup>	0.03 (0.01)*	0.02 (0.02)	0.02 (0.02)
Body condition			
Intercept	1.00 (3.25E-03)***	1.00 (3.25E-03)***	1.00 (3.25E-03)***
Male	-7.72E-03 (2.33E-03)***	-7.71E-03 (2.33E-03)***	-7.71E-03 (2.33E-03)***
Unknown sex	-2.71E-03 (3.99E-03)	-2.69E-03 (3.99E-03)	-2.67E-03 (3.99E-03)
Reproductive adult <sup>f</sup>	4.26E-03 (3.12E-03)	4.28E-03 (3.13E-03)	4.29E-03 (3.13E-03)
Non-reproductive juvenile <sup>f</sup>	-4.66E-03 (3.49E-03)	-4.68E-03 (3.48E-03)	-4.68E-03 (3.48E-03)
Biodiversity <sup>c</sup>	-2.57E-04 (1.14E-03)	-2.60E-04 (1.11E-03)	-3.35E-04 (1.12E-03)
Feather growth			
Intercept	1.98 (0.04)***	1.98 (0.04)***	1.98 (0.04)***
Dark-eyed junco	0.30 (0.05)***	0.31 (0.06)***	0.31 (0.06)***
Song sparrow	0.34 (0.05)***	0.35 (0.06)***	0.34 (0.06)***
Biodiversity <sup>c</sup>	-0.01 (0.02)	-4.36E-03 (0.02)	-1.39E-03 (0.02)

<sup>a</sup> Significance: †, 0.05 < p < 0.10; \*, p < 0.05; \*\*, p < 0.01; \*\*\*, p < 0.001. Categorical predictors are relative to female birds (sex), house finches (species), and nonreproductive adults (age and breeding characteristics).

<sup>b</sup> Heterophil:lymphocyte ratio

<sup>c</sup> Estimates derived from raw point count data

<sup>d</sup> Estimates derived from occupancy models

<sup>e</sup>Biodiversity is a placeholder for the biodiversity predictor listed at the top of each column.

<sup>f</sup>Age and breeding characteristics

Appendix S16: Coefficient estimates for models testing the relationship between physiological stress indicators and bird species richness, diversity, relative abundance, and relative occupancy.<sup>a</sup>

H:L <sup>b</sup>	Species richness <sup>c</sup> (SE)	Species diversity <sup>d</sup> (SE)	Species relative abundance <sup>d</sup> (SE)	Species relative occupancy <sup>c</sup> (SE)
Intercept	-0.67 (0.17)***	-0.71 (0.18)***	-0.60 (0.17)***	-0.64 (0.17)***
Male	-0.30 (0.17) †	-0.30 (0.17) †	-0.29 (0.17)†	-0.31 (0.17)†
Unknown sex	-0.59 (0.16)***	-0.59 (0.16)***	-0.64 (0.16)***	-0.59 (0.16)***
Dark-eyed junco	-0.57 (0.18)**	-0.52 (0.19)**	-0.65 (0.17)***	-0.59 (0.18)***
Song sparrow	0.08 (0.16)	0.12 (0.16)	0.06 (0.15)	0.05 (0.16)
Biodiversity <sup>c</sup>	0.04 (0.08)	-0.03 (0.09)	-0.20 (0.07)**	0.08 (0.08)
Hematocrit				
Intercept	2.22 (0.07)***	2.21 (0.07)***	2.21 (0.07)***	2.22 (0.07)***
Male	0.18 (0.03)***	0.18 (0.03)***	0.19 (0.03)***	0.18 (0.03)***
Unknown sex	0.03 (0.03)	0.03 (0.03)	0.04 (0.03)	0.03 (0.03)
Julian day	-0.06 (0.01)***	-0.05 (0.01)***	-0.06 (0.01)***	-0.06 (0.01)***
Biodiversity <sup>c</sup>	0.02 (0.02)	0.01 (0.02)	-3.14E-03 (0.01)	0.02 (0.02)
Body condition				
Intercept	1.00 (3.25E-03)***	1.00 (3.26E-03)***	1.00 (3.28E-03)***	1.00 (3.26E-03)***
Male	-7.71E-03 (2.33E-03)***	-7.74E-03 (2.34E-03)***	-7.72E-03 (2.33E-03)***	-7.70E-03 (2.33E-03)***
Unknown sex	-2.70E-03 (3.99E-03)	-2.79E-03 (4.00E-03)	-2.77E-03 (3.99E-03)	-2.67E-03 (3.99E-03)
Reproductive adult <sup>f</sup>	4.27E-03 (3.13E-03)	4.19E-03 (3.13E-03)	4.25E-03 (3.12E-03)	4.30E-03 (3.13E-03)
Non-reproductive juvenile <sup>f</sup>	-4.69E-03 (3.49E-03)	-4.68E-03 (3.49E-03)	-4.62E-03 (3.49E-03)	-4.68E-03 (3.48E-03)
Biodiversity <sup>c</sup>	-1.78E-04 (1.10E-03)	2.29E-04 (1.13E-03)	-3.08E-04 (7.52E-04)	-3.01E-04 (1.11E-03)
Feather growth				
Intercept	1.98 (0.04)***	1.97 (0.05)***	1.98 (0.04)***	1.98 (0.04)***
Dark-eyed junco	0.31 (0.06)***	0.32 (0.07)***	0.31 (0.05)***	0.31 (0.06)***
Song sparrow	0.35 (0.06)***	0.36 (0.06)***	0.34 (0.05)***	0.34 (0.06)***
Biodiversity <sup>c</sup>	-4.43E-03 (0.02)	-0.01 (0.03)	-0.01 (0.02)	-1.05E-03 (0.02)

<sup>a</sup> Significance: †, 0.05 < p < 0.10; \*, p < 0.05; \*\*, p < 0.01; \*\*\*, p < 0.001. Categorical predictors are relative to female birds (sex), house finches (species), and nonreproductive adults (age and breeding characteristics).

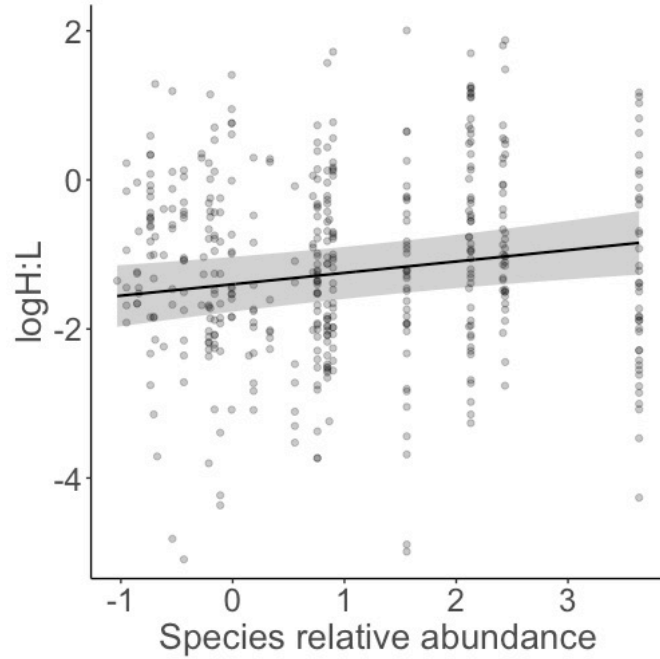
<sup>b</sup> Heterophil:lymphocyte ratio

<sup>c</sup> Estimates derived from occupancy models

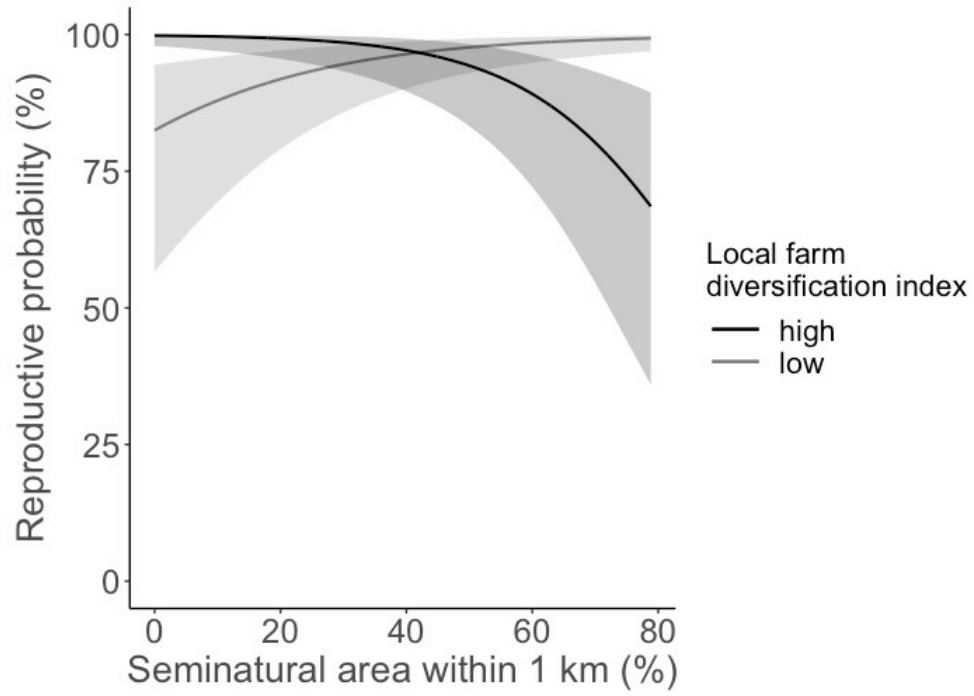
<sup>d</sup> Estimates derived from raw point count data

<sup>e</sup>Biodiversity is a placeholder for the biodiversity predictor listed at the top of each column.

<sup>f</sup>Age and breeding characteristics



Appendix S17: Birds had higher heterophil:lymphocyte ratios (H:L), suggesting higher stress, on farms with higher conspecific relative abundances ( $p=0.002$ ) (intercept, song sparrows [*Melospiza melodia*] of unknown sex; points, samples from individual birds; lines, coefficient estimates; shaded regions, SEs of coefficient estimates).



Appendix S18: Relationship between reproductive status of adult birds and surrounding seminatural area.

Appendix S19: Top model set for post hoc analyses of reproductive characteristics in adult farmland birds (values represent coefficient estimates, models with a minimum weight of 0.05 are shown).

Intercept	Date	Sex	Local diversification index	Strawberry production (500 m)	Seminatural area (1 km)	Local diversification index: Seminatural area (1 km)	df	$\Delta AIC_c$	weight
1.86	-0.3	+	3.32E-03	0.02	4.50E-03	-0.06	11	0.00	0.48
1.86	-0.4	+	6.11E-04		4.51E-03	-0.05	10	0.01	0.48



Appendix S20: Coefficient estimates for conditional model averaging for adult reproductive status<sup>a</sup>.

	Adult reproductive status (SE)
Intercept	1.86 (0.04)***
Julian day	-0.03 (0.01)**
Male	-0.12 (0.02)***
Unknown sex	-0.90 (0.04)***
Local diversification index	-01.38E-03 (0.01)
Strawberry production (500 m)	-0.02 (0.01)
Seminatural area (1 km) <sup>b</sup>	4.51E-03 (0.01)
Local diversification index: Seminatural area (1 km) <sup>b</sup>	-0.57 (0.01)***

<sup>a</sup> Significance: †,  $0.05 < p < 0.10$ ; \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$ . Categorical predictors are relative to female birds.

<sup>b</sup> Seminatural area without decay

Appendix S21: Top model set for post hoc analyses of the effect of agricultural affiliation on hematocrit (values represent coefficient estimates, models with a minimum weight of 0.05 are shown).

Intercept	Sex	Agriculture affiliation	Local diversification index	Strawberry production (500 m)	Seminatural area (1 km)	Local diversification index: Seminatural area (1 km)	Local diversification index: Agriculture affiliation	Seminatural area (1 km): Agriculture affiliation	df	$\Delta AIC_c$	weight
-0.89	+	0.28	-0.08		0.19	0.24			9	0.00	0.23
-0.82	+	0.28							6	1.79	0.10
-0.89	+	0.29	-0.06	0.04	0.20	0.23			10	1.83	0.09
-0.88	+	0.27	-0.08		0.18	0.25		0.03	10	1.93	0.09
-0.88	+	0.29	-0.07		0.19	0.24	-0.02		10	2.00	0.09

Appendix S22: Top model set for post hoc analyses of the effect of agricultural affiliation on body condition (values represent coefficient estimates, models with a minimum weight of 0.05 are shown).

Intercept	Sex	Age and breeding status	Agriculture affiliation	Local diversification index	Strawberry production (500 m)	Seminatural area (1 km)	Local diversification index: Seminatural area (1 km)	Local diversification index: Agriculture affiliation	Seminatural area (1 km): Agriculture affiliation	df	$\Delta AIC_c$	weight
1.00	+	+	-5.66E-04	1.94E-03		-2.61E-03	-3.53E-03			11	0.00	0.27
1.00	+	+	-3.93E-04	2.30E-03		-2.56E-03	-3.70E-03		-1.21E-03	12	0.89	0.17
1.00	+	+	-5.37E-04	2.12E-03	3.46E-04	-2.64E-03	-3.65E-03			12	1.92	0.10
1.00	+	+	-5.57E-04	1.95E-03		-2.59E-03	-3.55E-03	-8.41E-05		12	2.04	0.10
1.00	+	+	-3.44E-04	2.56E-03	4.71E-04	-2.59E-03	-3.87E-03		-1.27E-03	13	2.72	0.07
1.00	+	+	-4.15E-04	2.30E-03		-2.65E-03	-3.61E-03	4.22E-04	-1.38E-03	13	2.81	0.07

Appendix S23: Coefficient estimates for conditional model averaging for physiological stress indicators of farmland birds.<sup>a</sup>

Predictor <sup>b</sup>	Hematocrit	Body condition
Intercept	2.23 (0.02)***	1.00 (3.47E-03)***
Julian day	-0.02 (0.02)	-9.45 (2.35E-03)***
Relative capture time		-5.33 (4.345E-03)
Male	0.13 (0.04)***	2.60E-03 (3.22E-03)
Unknown sex	-0.08 (0.04)*	-5.94E-03 (3.86E-03)
Reproductive adult (age and breeding status)	-	-
Nonreproductive juvenile (age and breeding status)	-	-
Agriculture affiliation	0.06 (0.02)**	7.55E-03 (1.13E-03)
Local diversification index	-0.02 (0.02)	1.63E-03 (1.305E-03)
Strawberry production (500 m)	0.01 (0.02)	5.30E-04 (1.055E-03)
Seminatural area (1 km) <sup>c</sup>	-0.04 (0.02)	1.34E-03 (1.24E-03)
Local diversification index: Seminatural area (1 km) <sup>c</sup>	-	-3.57E-03 (1.34E-03)**
Local diversification index: Agriculture affiliation	-	1.19E-03 (1.23E-03)
Seminatural area (1 km) <sup>c</sup> : Agriculture affiliation	0.03 (0.02)	-2.19E-03 (1.21E-03) †

<sup>a</sup> Significance: †, 0.05 < p < 0.10; \*, p < 0.05; \*\*, p < 0.01; \*\*\*, p < 0.001. Minus signs that do not precede numerals indicate the predictor was included as a fixed effect in full models but not included in top model sets.

<sup>b</sup> Categorical predictors are relative to female birds (sex), house finches (species), and nonreproductive adults (age and breeding characteristics)

<sup>c</sup> Seminatural area without decay was used for body condition models, a Gaussian decay rate of 1250 was used for feather growth models, and a Gaussian decay rate of 750 was used for H:L and hematocrit models. The Gaussian decay function weighs seminatural area closer to sampling points more than areas further away. Lower Gaussian decay rate parameters result in greater emphasis on seminatural areas closer to sampling points compared to higher Gaussian decay rate parameters.

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