1 **SUPPLMENTARY MATERIAL FOR**

2

3 **COONEY ET AL. – MULTI-MODAL SIGNAL EVOLUTION IN BIRDS: RE-EXAMINING A**

4 **STANDARD PROXY FOR SEXUAL SELECTION**

5

6 APPENDIX 1

7

8 Supplementary methods

9

10 Supplementary figures (S1-S10) and tables (S1-S12)

11

12   **APPENDIX 1**

13

14   **SUPPLMENTARY METHODS**

15

16   **Compiling species pair datasets**

17   Following Seddon et al. (2013) and Cooney et al. (2017), we assembled a dataset of passerine

18   species pairs for which we could collect detailed data on song traits. We compiled a list of species

19   pairs from published phylogenetic trees of passerine families or genera generated using genetic

20   data. We only included trees in which (i) > 70% of taxa had been sampled, and (ii) node support

21   was high, with either posterior probability > 95% or ML bootstrap support > 70%. When several

22   phylogenies were presented in a paper, we only selected species pairs resolved in all trees. When

23   nodal support varied with the method of phylogenetic reconstruction, ML bootstrap values took

24   precedence. We assumed that consensus trees and trees based on concatenated molecular

25   datasets provided the most reliable source of phylogenetic information and thus, whenever possible,

26   we assessed nodal support based on the values given in these trees.

27

28   **Principal component analysis of song measurements**

29   Raw song traits were correlated across species (Table S1). Such correlations can lead to

30   overinflated divergence estimates if each trait axis is treated as independent. Therefore, to avoid

31   this issue and to reduce the dimensionality of our dataset, following previous studies (Tobias et al.

32   2014a; Tobias et al. 2014b) we conducted a principal components (PC) analysis on the covariance

33   matrix of individual (log-transformed) song measurements. The first three PCs from this analysis

34   accounted for over 83% of the variance in the original acoustic dataset, with each PC capturing a

35   distinct component of overall signal structure (Table S1). Specifically, PC1 (41%) primarily loaded

36   with variables related to song pitch, PC2 (24%) with variables related to song length, and PC3

37   (18%) with song pace. We chose not to retain PC4 (14%) in our analysis because of its

38   comparatively small eigenvalue (1.006) (Kaiser 1960) and because the loadings indicated that it

39   was primarily related to variation in minimum song frequency (loading = 0.66), which is more difficult

40   to quantify from song spectra and therefore potentially subject to greater levels of error. By focusing

41   exclusively on variation in the first three PCs, which are interpretable in terms of song pitch (PC1),

42   length (PC2) and pace (PC3), respectively, our analyses are directly comparable with previous

43   studies (e.g. Tobias et al. 2014b) using the same combination of traits (PCs) to define a three-

44   dimensional acoustic space (Fig. S2).

45

46   **Alternative dataset: accounting for intraspecific variation**

47   Intraspecific trait variation can generate overinflated estimates of interspecific disparity, especially

48   when sample sizes are low relative to levels of intraspecific variation and/or measurement error

49 (Silvestro et al. 2015). To test whether our results were sensitive to these issues, we repeated our

50 main analyses using an alternative version of our dataset in which within-species song disparity

51 estimates were corrected for observed levels of intraspecific variation using an approach based on

52 ANOVA (Weir and Wheatcroft 2011; Weir et al. 2012).

53

54 **Sexual dichromatism**

55 Although it would be preferable to estimate dichromatism using more objective measurements of

56 bird plumage colouration, such as those generated by a spectrophotometer, these types of

57 measurements are currently unavailable for most species. However, the high correlation between

58 spectrophotometric and human estimates of dichromatism indicate that human vision can provide a

59 reliable estimate of avian colouration in general (Bergeron and Fuller 2018) and sexual

60 dichromatism in particular (Armenta et al. 2008; Seddon et al. 2010). To test this assumption in our

61 dataset, we used spectrophotometric measurements of plumage colouration from museum

62 specimens described in (Cooney et al. 2017) to calculate objective estimates of dichromatism for

63 species and pairs common to both datasets, following methods outlined previously (Seddon et al.

64 2013; Cooney et al. 2017). This resulted in dichromatism estimates for 264 species (132 pairs),

65 which we compared to our scores based on handbook illustrations using Spearman's rank

66 correlation. We found that estimates of dichromatism based on spec measurements and human

67 vision were highly positively correlated (Fig. S9) across both species (Spearman's r = 0.76, P <

68 0.001) and species pairs (Spearman's r = 0.79, P < 0.001). Thus, we conclude that scores of

69 dichromatism based on published illustrations are valid for our dataset, in line with previous studies

70 (e.g. Dale et al. 2015).

71

72 **Additional predictors of song divergence**

73 To explore the role of other factors known to influence song divergence in birds, we collected data

74 for a suite of additional explanatory variables. Details are given below.

75   *Pair age.* We generated estimates of pair age (i.e. time from the present to the most recent

76 common ancestor) by calculating the mean height of the node connecting the pair in the (pruned)

77 Jetz et al. (2012) phylogenies (see above).

78   *Body mass.* Estimates of body mass were extracted from Wilman et al. (2014) and we used

79 the mean of species (ln-transformed) values to generate pair-level averages.

80   *Generation length.* Data on species' generation length, forest dependency and migratory

81 status were compiled from BirdLife International (http://www.datazone.birdlife.org; accessed 18-10-

82 2017), and we used the mean of species' generation length values to provide pair-level averages.

83   *Forest dependency.* In the BirdLife dataset species are assigned to one of four categories,

84 depending on whether they "do not normally occur in forests", or exhibit "low", "medium" or "high"

85 levels of forest dependency. To convert this into a quantitative variable capturing broad differences

86 in habitat usage, we converted this classification system into a 4-point scoring scheme, giving each

87 species a score of 0, 1, 2 or 3 based on whether they were recorded as having no, low, medium or

88 high forest dependency, respectively. To capture the average level of forest dependency within a

89 pair, we took the mean score for each pair.

90 *Migratory status.* Similarly, in the BirdLife dataset species are categorised as "not a migrant",

91 "nomadic", "altitudinal migrant" or "full migrant", so again we converted this classification system into

92 a 2-point scoring scheme, giving each species a score of 0 (not a migrant) or 1 (nomadic, altitudinal

93 migrant or full migrant) and then took the mean score for each pair.

94 *Latitude.* All variables relating to species' geographical distributions are based on (breeding)

95 range maps provided by BirdLife International and NatureServe (2016, version 9;

96 http://www.datazone.birdlife.org). To estimate the latitudinal midpoint of each pair, we first

97 calculated each species' range centroids using the R package *PBSmapping* (Schnute 2015) and

98 then took the mean of species (absolute) latitudinal values (Weir and Schluter 2007; Weir and

99 Wheatcroft 2011; Weir et al. 2012).

100 *Island-dwelling.* To characterise species as island-dwelling, we used a high-resolution

101 database of global geography (GSHHG version 2.3.6; http://www.soest.hawaii.edu/pwessel/gshhg/)

102 to identify all landmasses >1 km^2 in size surrounded by ocean and smaller than Greenland

103 (following Weigelt et al. 2013). We then overlaid species range maps on top of this dataset and

104 calculated the proportion of species' ranges occurring on islands. We consider species with >80%

105 of their range occurring on islands to be primarily island dwelling and turned this into a pair-level

106 variable by counting whether neither (0), one (1) or both (2) of the species in a pair were

107 characterised as island dwelling.

108 *Within-pair range overlap.* To calculate range overlap between species within a pair, we took

109 the standard approach of calculating the area of overlap between species, divided by the area of the

110 smaller species' range (Pigot and Tobias 2013; Tobias et al. 2014a; Cooney et al. 2017).

111 *Confamilial sympatry.* To quantify the extent of interactions with related species, we used the

112 taxonomy of Jetz et al. (2012) and the range maps to tally up the number of same-family

113 (confamilial) species that are sympatric with the focal species (Morinay et al. 2013), where sympatry

114 is defined as >20% range overlap between species—a threshold commonly used to define

115 'substantial' sympatry (Tobias et al. 2014a). We then divided this number by the total number of

116 species in the family and took the mean of these values to generate a pair-level average.

117 *Climatic disparity.* To quantify divergence in species' climatic niches, we extracted range-

118 wide climatic information for each species from WorldClim (http://www.worldclim.org/) using a global

119 resolution of 10 arc minutes (~100 km^2). Following Lawson and Weir (2014), we focused on 48

120 climatic variables, 36 related to temperature (maximum, minimum and mean for each month of the

121 year) and 12 to precipitation (mean for each month of the year). We then conducted a PC analysis

122 on these (sorted) values across all species (Lawson and Weir 2014), retaining the first four PC axes

123   that together accounted for 96% of the variation. Euclidean distances between the species' midpoint

124   (median) values in each of the four axes were used as an overall measure of climatic divergence

125   within a pair.

126   *Body mass disparity.* To calculate within-pair disparity in body mass, we took the absolute

127   difference between (ln-transformed) body mass values for species within a pair.

128   *Beak disparity.* Variables relating to species' beak traits are based on a dataset of biometric

129   measurements collected from museum specimens. For each species, we measured linear

130   measurements of beak morphology (length, width and depth, measures at the nares) for multiple

131   individuals per species (mean = 6.5) per sex. To quantify divergence in beak morphology, we

132   followed the methods outlined in Pigot and Tobias (2013) and calculated beak divergence as the

133   Euclidean distance between species mean (ln-transformed) values for all three axes.

134   *Song learning.* Finally, we identified whether species pairs belonged to the oscine (Passeri)

135   or suboscine (Tyranni) passerine suborders, which do and do not exhibit song learning,

136   respectively.

137

138   **Collinearity among predictor variables**

139   Collinearity among predictor variables is a potential problem in multiple regression modelling

140   (Graham 2003). However, methods based on the type of information theoretic-based model

141   averaging approach we employ here are generally robust to collinearity (Graham 2003; Freckleton

142   2011). Nonetheless, we checked for collinearity among predictors by calculating pairwise Pearson

143   correlation coefficients (r^2) and variance inflation factors (VIF) for all variables. Only one pair of

144   predictors (latitude and migration) showed evidence of (strong) collinearity ($r^2 = 0.75$; Table S12),

145   and calculating VIFs for our full dataset revealed no evidence of severe (VIF > 10) or even

146   moderate (VIF > 4) multicollinearity (range = 1.16 – 3.14; mean = 1.61), indicating that

147   multicollinearity is unlikely to affect our results.

148

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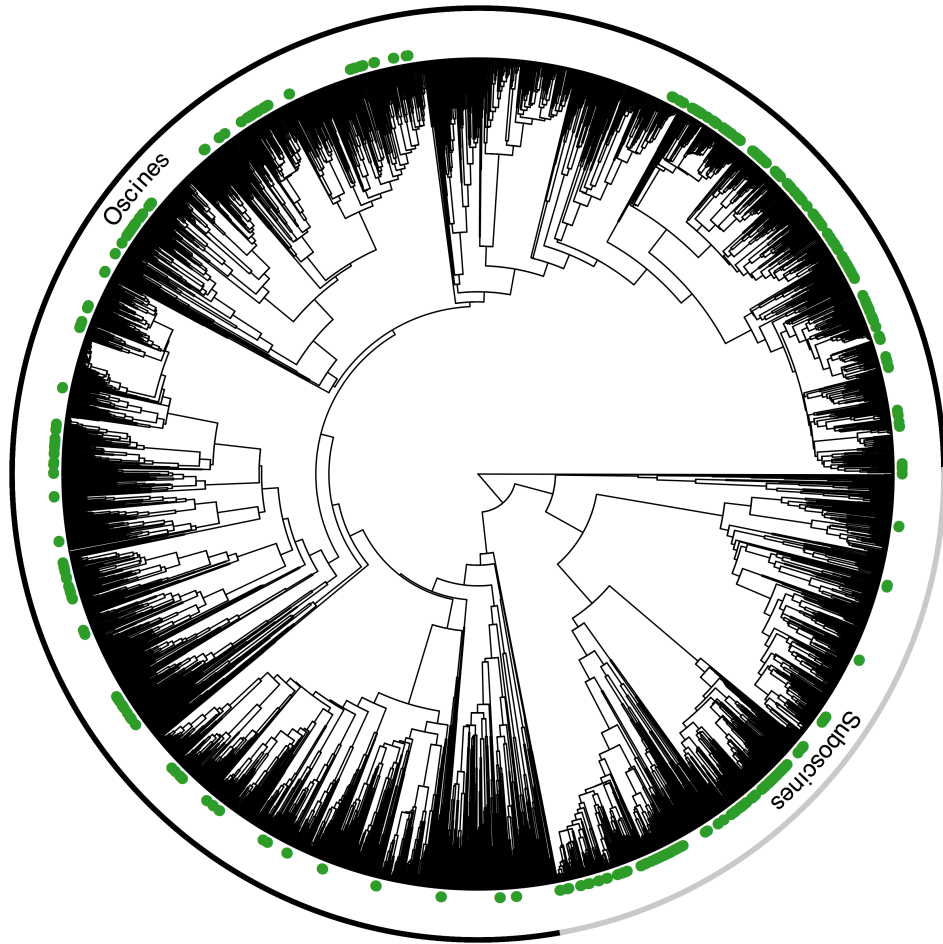
Figure S1. A representative phylogeny of passerines from Jetz et al. (2012) showing the location of species sampled in this study (green points).
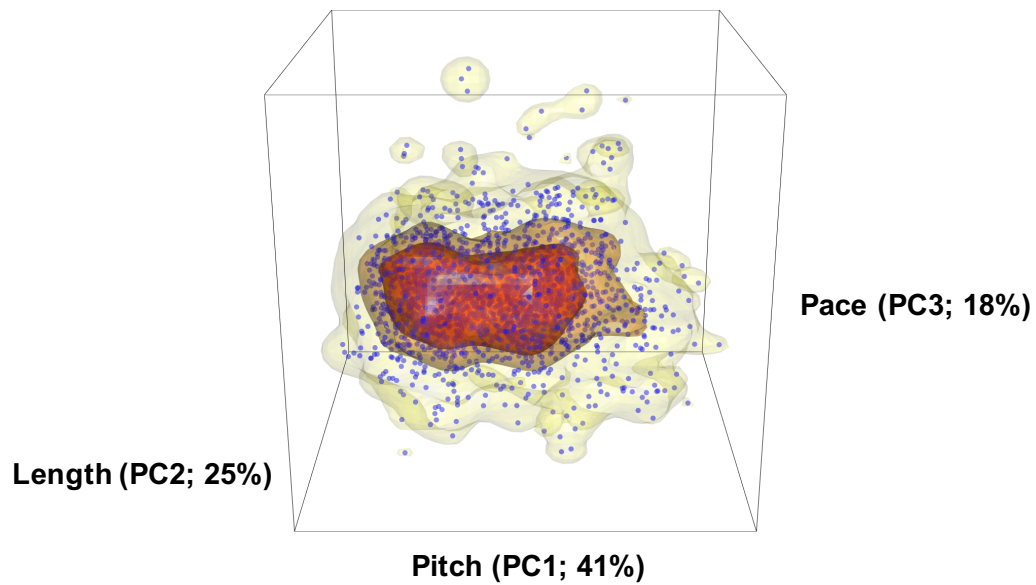
Figure S2. Plot showing the distribution of individual song recordings (n = 2476) in acoustic 'trait space', a defined by the first three principal component (PC) axes of variation, corresponding to variation among song in pitch (PC1), length (PC2) and pace (PC3). Coloured areas represent kernel density estimates of 50% (red), 75% (orange) and 100% (yellow) of the data (for illustrative purposes only).
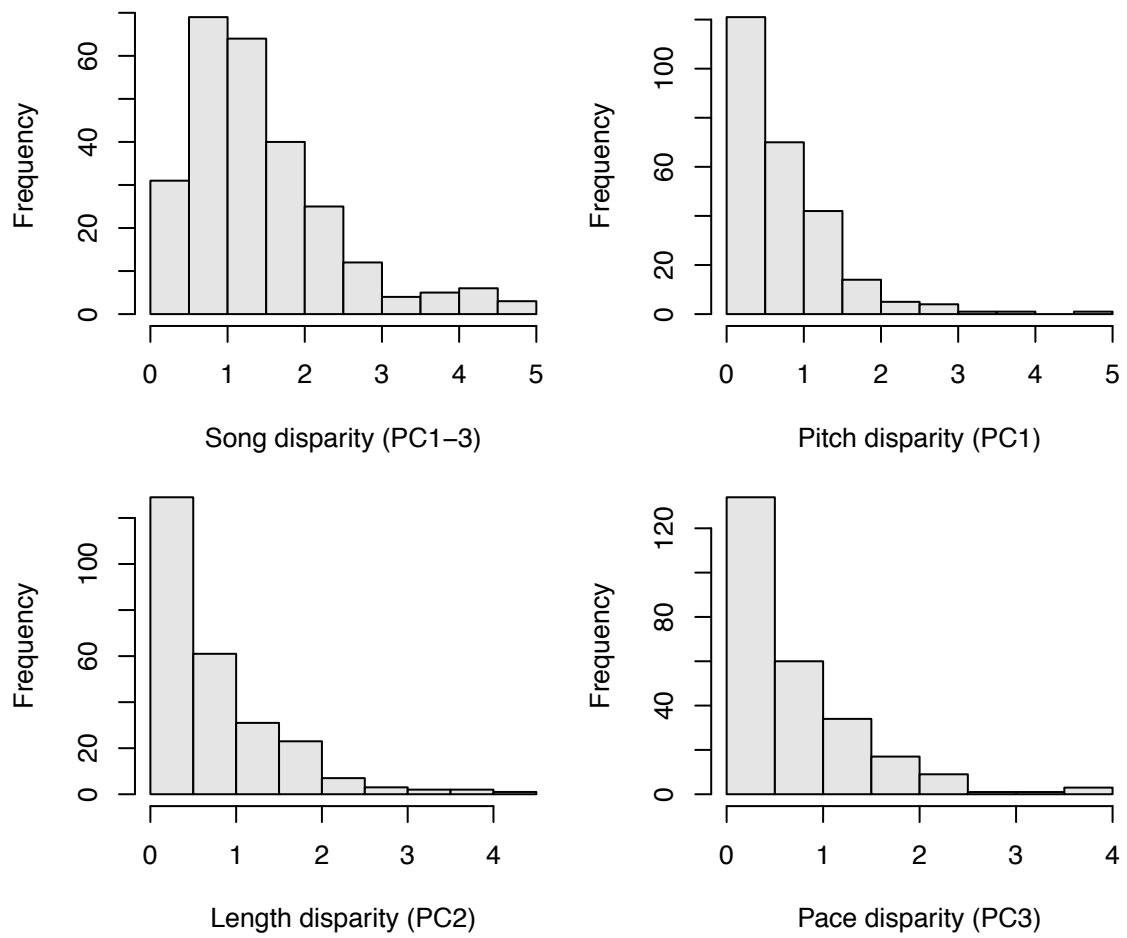
Figure S3. Histograms showing the distribution of within-pair song disparity estimates for species pairs (n = 259).
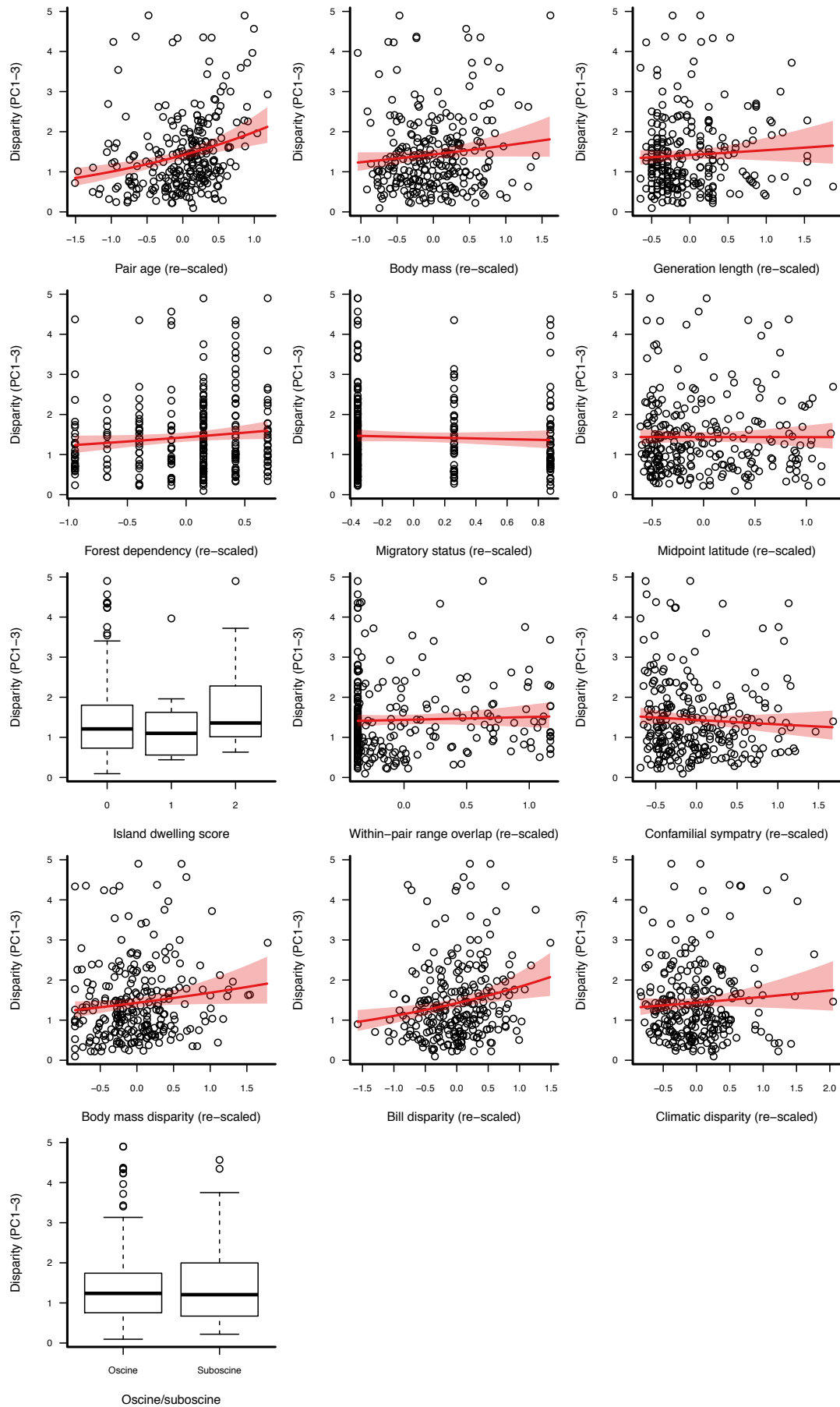
Figure S4. Plots showing the relationship between overall within-pair song disparity (PC1-3) and each of the additional predictors included in our analysis. For all continuous predictors, regressions lines (with prediction intervals, shaded) indicate the best-fitting relationship between the two variables.
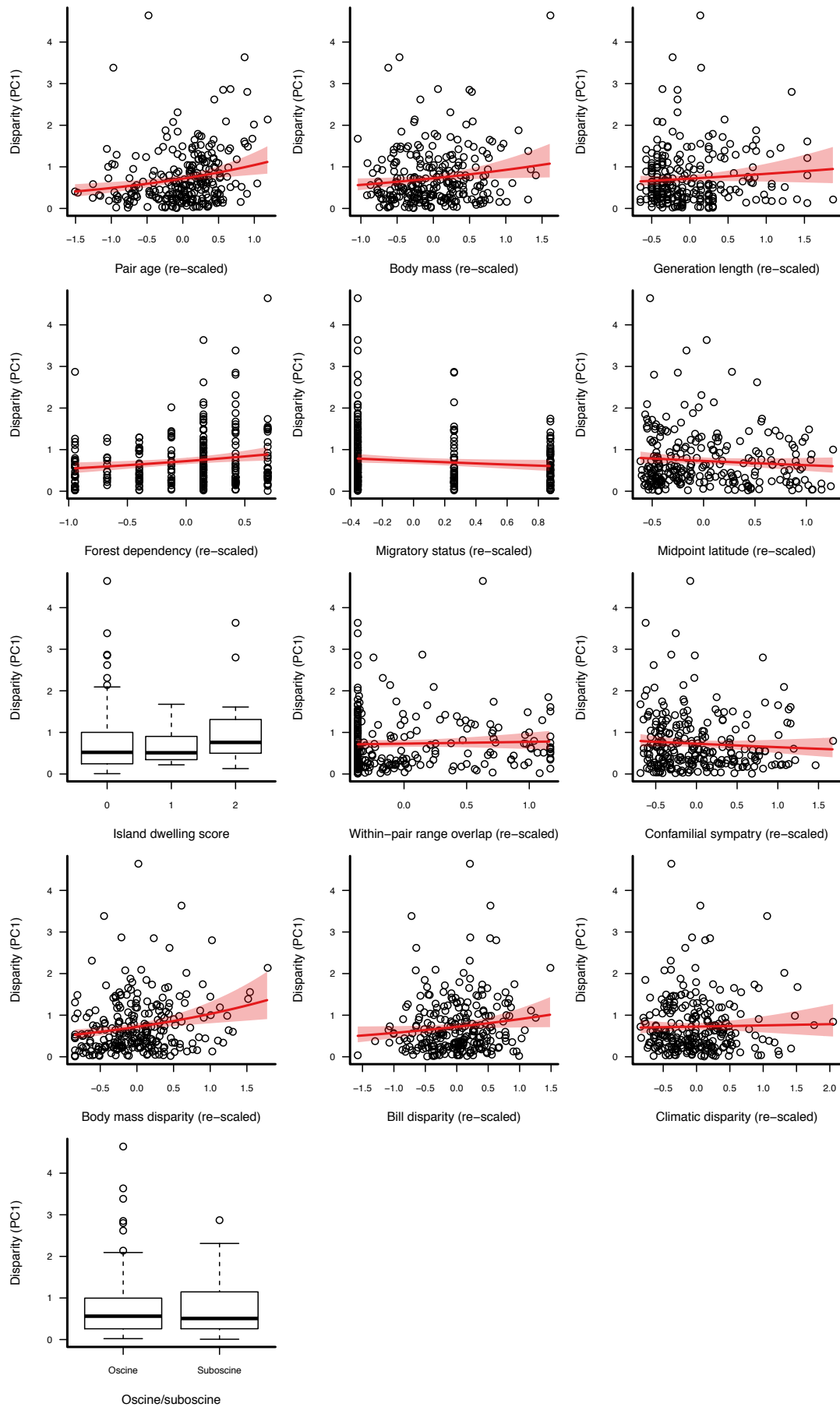
Figure S5. Plots showing the relationship between within-pair disparity in pitch (PC1) and each of the additional predictors included in our analysis. For all continuous predictors, regressions lines (with prediction intervals, shaded) indicate the best-fitting relationship between the two variables.
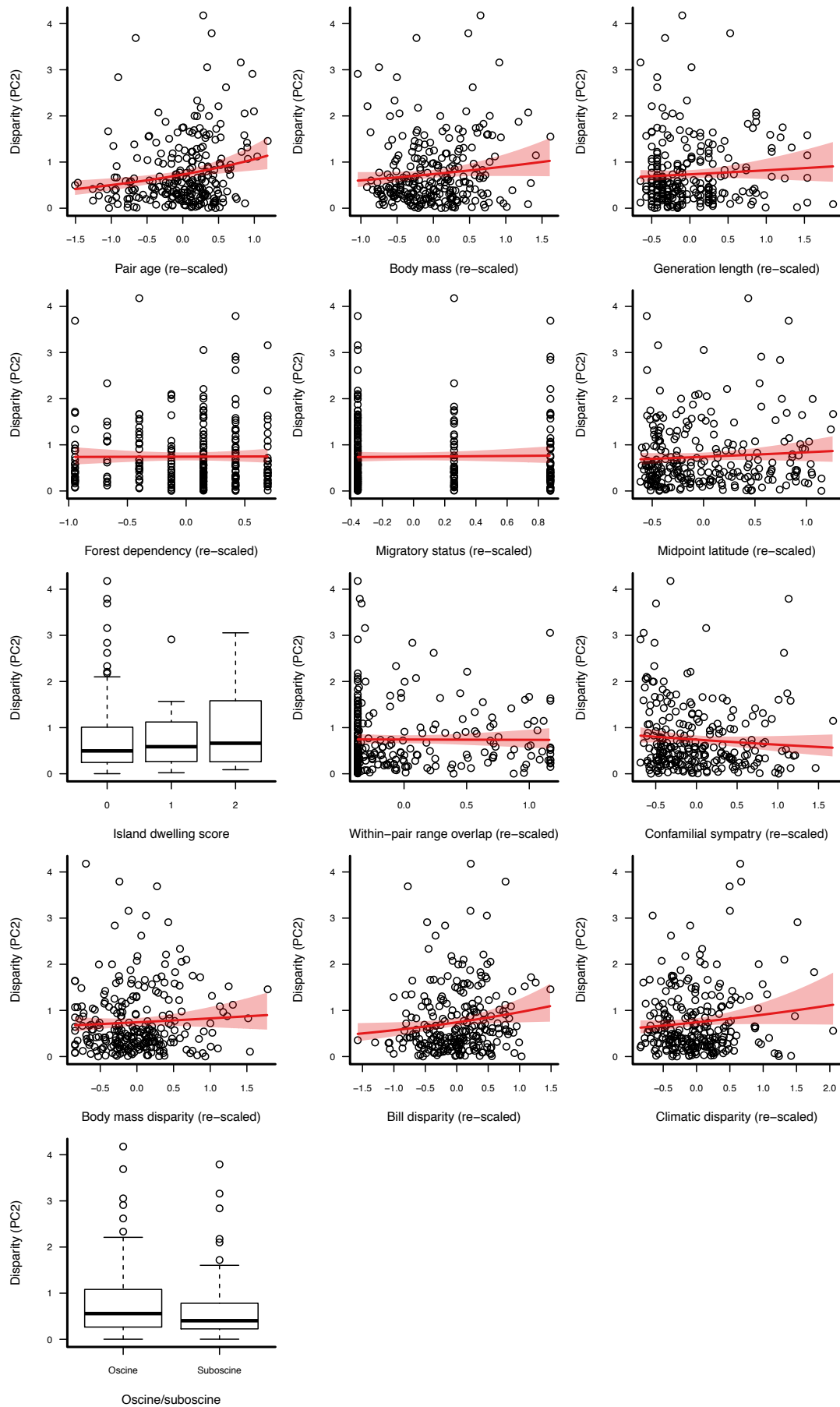
Figure S6. Plots showing the relationship between within-pair disparity in length (PC2) and each of the additional predictors included in our analysis. For all continuous predictors, regressions lines (with prediction intervals, shaded) indicate the best-fitting relationship between the two variables.
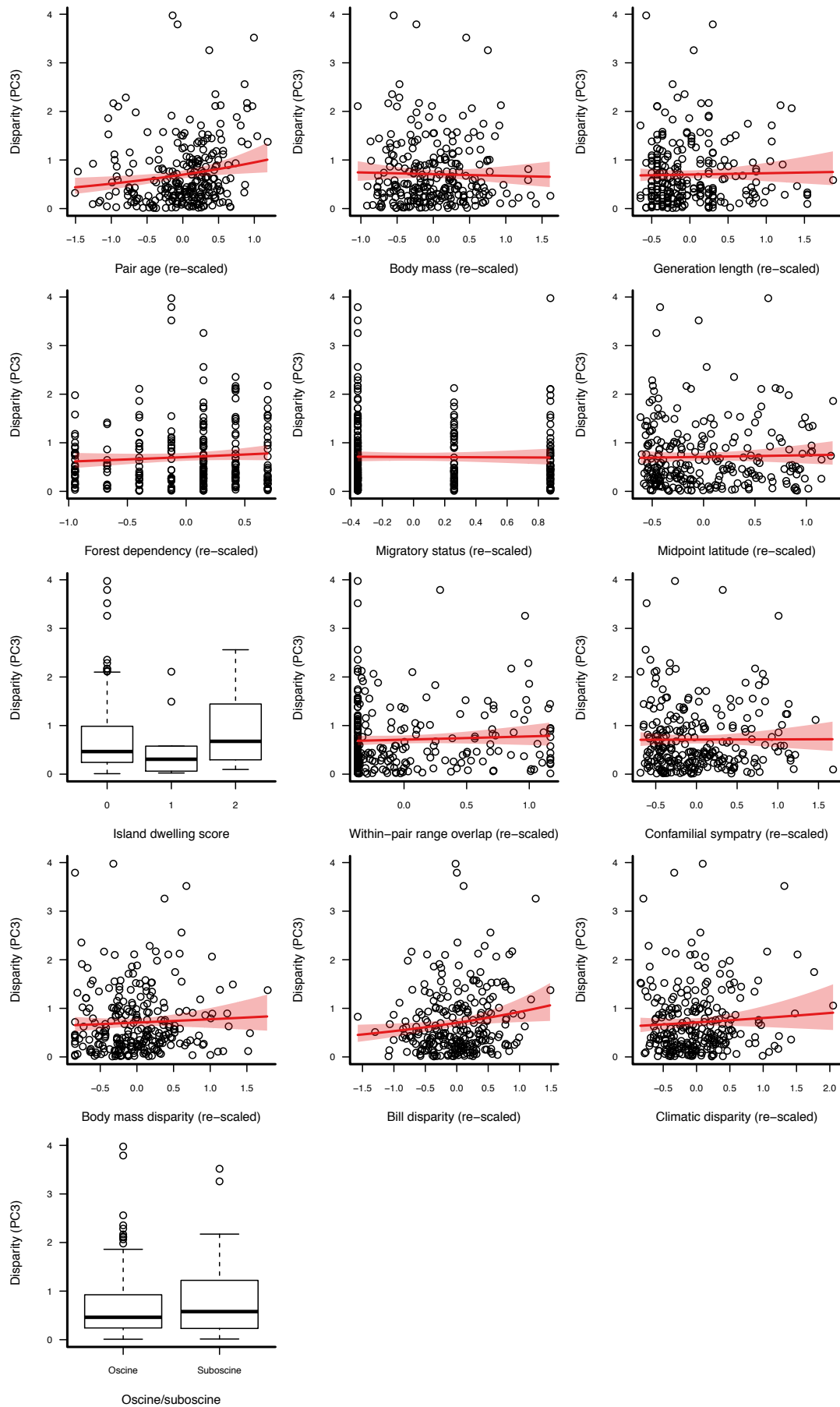
Figure S7. Plots showing the relationship between within-pair disparity in pace (PC3) and each of the additional predictors included in our analysis. For all continuous predictors, regressions lines (with prediction intervals, shaded) indicate the best-fitting relationship between the two variables.
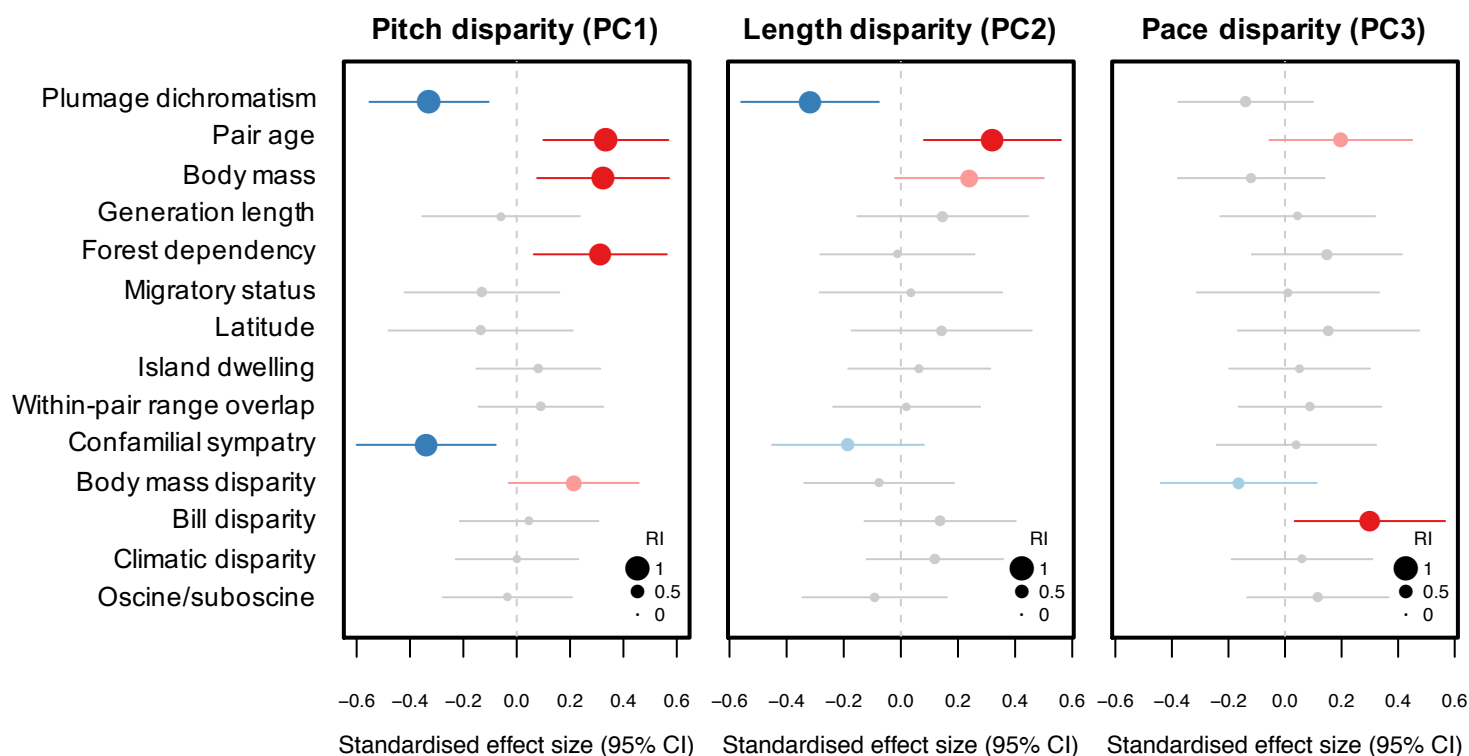
Figure S8. Model averaged coefficient estimates from multipredictor GLMs predicting variation in within-pair disparity in song pitch (PC1), length (PC2) and pace (PC3) among passerine species pairs (n = 246). Within each dataset, points indicate the standardised effect sizes for each of the (scaled) predictor variables and lines indicate 95% confidence intervals (CI). Sizes of points represent the relative importance (RI) of each of the predictor variables, where a value of RI = 0 indicates low importance and a value of RI = 1 indicates high importance. Predictors included in the AIC$_c$ top model for each dataset are coloured (blue = negative effect; red = positive effect), with significant ($P < 0.05$) model-averaged coefficients shown in darker colours.
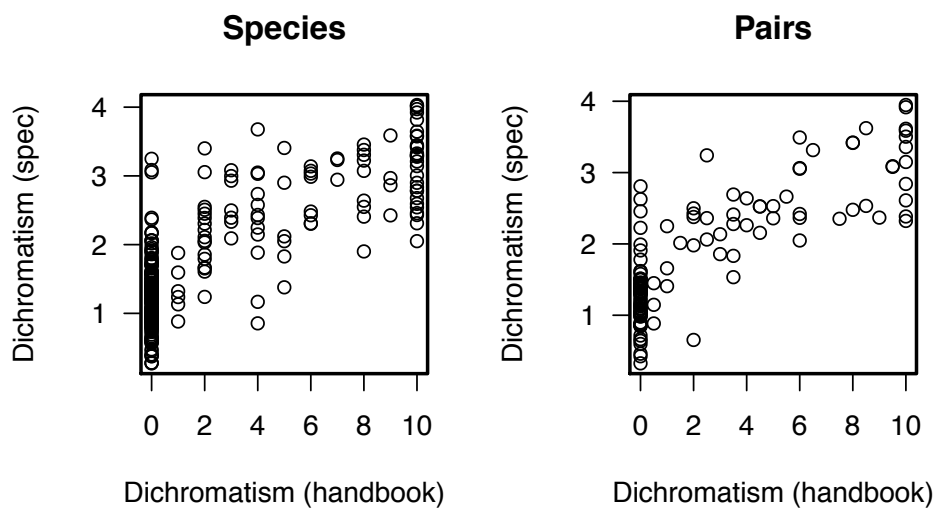
Figure S9. Scatterplots showing the relationship between dichromatism estimates based on spectrophotometric measurements of colouration from museum specimens and handbook illustrations for species (n = 264) and species pairs (n = 132) of birds.
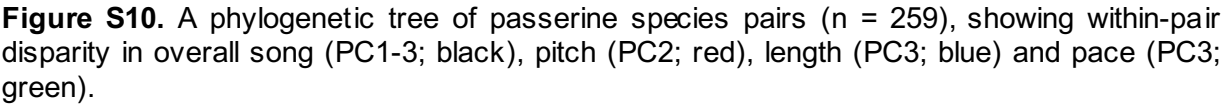
Figure S10. A phylogenetic tree of passerine species pairs (n = 259), showing within-pair disparity in overall song (PC1-3; black), pitch (PC2; red), length (PC3; blue) and pace (PC3; green).

	Pitch (PC1)	Length (PC2)	Pace (PC3)
Maximum frequency	**−0.57**	0.06	0.11
Minimum frequency	−0.27	−0.26	0.41
Peak	**−0.54**	−0.08	0.22
Bandwidth	**−0.48**	0.16	−0.07
Duration	0.12	**0.64**	0.45
Note number	−0.09	**0.70**	−0.16
Pace	−0.25	0.07	**−0.73**
Eigenvalue	2.85	1.72	1.25
Cumulative variance explained (%)	41	65	83

Table S1. Variable loadings and variance explained by the first three principal components (PCs) of an analysis of measurements of individual song recordings (n = 2476) for the species included in our analyses (n = 518). Standardised loadings of the main contributors to each component are highlighted in bold.

	Full dataset			Alternative dataset		
Variable	λ (95% CI)	$P\,(\lambda = 0)$	$P\,(\lambda = 1)$	λ (95% CI)	$P\,(\lambda = 0)$	$P\,(\lambda = 1)$
Total disparity (PC1-3)	0.00 (NA, 0.39)	1.000	<0.001	0.00 (NA, 0.29)	1.000	<0.001
Pitch disparity (PC1)	0.00 (NA, 0.09)	1.000	<0.001	0.00 (NA, 0.08)	1.000	<0.001
Length disparity (PC2)	0.00 (NA, 0.50)	1.000	<0.001	0.00 (NA, 0.14)	1.000	<0.001
Pace disparity (PC3)	0.00 (NA, 0.18)	1.000	<0.001	0.01 (NA, 0.30)	0.719	<0.001

Table S2. Maximum likelihood estimates (and 95% confidence intervals; CI) of phylogenetic signal (Pagel's lambda; λ) for each measure of within-pair song disparity across passerine species pairs (n = 259).

Response variable	Term	Full dataset			Alternative dataset		
		Estimate (SE)	P	R^2	Estimate (SE)	P	R^2
Total disparity (PC1-3)	Dichromatism	−0.25 (0.08)	0.002	0.04	−0.16 (0.06)	0.001	0.03
Pitch disparity (PC1)	Dichromatism	−0.27 (0.11)	0.015	0.03	−0.13 (0.05)	0.015	0.04
Length disparity (PC2)	Dichromatism	−0.33 (0.12)	0.005	0.04	−0.14 (0.06)	0.019	0.03
Pace disparity (PC3)	Dichromatism	−0.21 (0.12)	0.074	0.02	−0.08 (0.05)	0.137	0.01
Total disparity (PC1-3)	Dichromatism	−0.26 (0.08)	0.001	0.06	−0.17 (0.06)	0.005	0.06
	Forest dependency	0.17 (0.08)	0.039		0.15 (0.06)	0.013	
	Interaction	−0.08 (0.15)	0.585		−0.05 (0.11)	0.627	
Pitch disparity (PC1)	Dichromatism	−0.25 (0.10)	0.009	0.07	−0.14 (0.05)	0.009	0.07
	Forest dependency	0.30 (0.10)	0.006		0.13 (0.05)	0.011	
	Interaction	−0.10 (0.21)	0.633		−0.02 (0.10)	0.803	
Length disparity (PC2)	Dichromatism	−0.33 (0.12)	0.005	0.04	−0.14 (0.06)	0.019	0.04
	Forest dependency	0.02 (0.12)	0.875		0.06 (0.06)	0.311	
	Interaction	−0.10 (0.22)	0.641		−0.06 (0.11)	0.623	
Pace disparity (PC3)	Dichromatism	−0.22 (0.12)	0.065	0.02	−0.09 (0.05)	0.116	0.02
	Forest dependency	0.16 (0.12)	0.181		0.06 (0.05)	0.261	
	Interaction	−0.06 (0.22)	0.796		0.02 (0.10)	0.820	

Table S3. Standardised coefficient estimates from GLMs predicting variation in within-pair disparity in song traits among passerine species pairs (n = 259). SE, standard error. R^2, pseudo-R^2.

	N pairs	Estimate (SE)	P	R^2
		Full dataset		
Plumage dichromatism	259	–0.25 (0.08)	0.002	0.04
Pair age	259	0.34 (0.08)	<0.001	0.09
Body mass	259	0.15 (0.08)	0.081	0.02
Generation length	251	0.08 (0.08)	0.334	<0.01
Forest dependency	259	0.15 (0.08)	0.063	0.02
Migratory status	259	–0.06 (0.08)	0.467	<0.01
Latitude	257	0.00 (0.08)	0.987	<0.01
Island dwelling	259	0.12 (0.08)	0.150	0.01
Within-pair range overlap	257	0.05 (0.08)	0.565	<0.01
Confamilial sympatry	257	–0.08 (0.08)	0.330	0.01
Body mass disparity	259	0.16 (0.08)	0.053	0.02
Bill disparity	257	0.25 (0.08)	0.003	0.04
Climatic disparity	254	0.10 (0.08)	0.252	0.01
Oscine/suboscine	259	0.01 (0.08)	0.919	<0.01

Table S4. Standardised coefficient estimates from single predictor GLMs predicting variation in within-pair song disparity (PC1-3) among passerine species pairs (n = 259). SE, standard error. R^2, pseudo-R^2.

		Full dataset								
		Pitch disparity (PC1)			Length disparity (PC2)			Pace disparity (PC3)		
	N pairs	Estimate (SE)	P	R^2	Estimate (SE)	P	R^2	Estimate (SE)	P	R^2
Plumage dichromatism	259	–0.27 (011)	0.015	0.03	–0.33 (0.12)	0.001	0.04	–0.21 (0.12)	0.074	0.02
Pair age	259	0.38 (0.12)	0.001	0.07	0.37 (0.12)	0.002	0.06	0.31 (0.12)	0.010	0.04
Body mass	259	0.25 (0.11)	0.028	0.03	0.20 (0.12)	0.088	0.02	–0.05 (0.12)	0.677	<0.01
Generation length	251	0.15 (0.12)	0.203	0.01	0.11 (0.12)	0.353	0.01	0.04 (0.12)	0.741	<0.01
Forest dependency	259	0.29 (0.11)	0.008	0.04	0.01 (0.12)	0.941	<0.01	0.14 (0.12)	0.229	0.01
Migratory status	259	–0.21 (0.11)	0.060	0.02	0.03 (0.12)	0.783	<0.01	–0.02 (0.12)	0.868	<0.01
Latitude	257	–0.15 (0.11)	0.180	0.01	0.12 (0.12)	0.299	0.01	0.05 (0.12)	0.701	<0.01
Island dwelling	259	0.19 (0.11)	0.096	0.02	0.14 (0.12)	0.234	0.01	0.08 (0.12)	0.518	<0.01
Within-pair range overlap	257	0.06 (0.11)	0.621	<0.01	–0.01 (0.12)	0.937	<0.01	0.09 (0.12)	0.448	<0.01
Confamilial sympatry	257	–0.12 (0.11)	0.281	0.01	–0.16 (0.12)	0.182	0.01	0.01 (0.12)	0.954	<0.01
Body mass disparity	259	0.36 (0.11)	0.002	0.06	0.11 (0.12)	0.371	<0.01	0.09 (0.12)	0.441	<0.01
Bill disparity	257	0.23 (0.11)	0.047	0.02	0.26 (0.12)	0.030	0.03	0.28 (0.12)	0.018	0.03
Climatic disparity	254	0.04 (0.12)	0.738	<0.01	0.20 (0.12)	0.086	0.02	0.12 (0.12)	0.315	0.01
Oscine/suboscine	259	–0.01 (0.11)	0.919	<0.01	–0.14 (0.12)	0.234	0.01	0.15 (0.12)	0.215	0.01

Table S5. Standardised coefficient estimates from single predictor GLMs predicting variation in within-pair disparity in three independent axes of song variation among passerine species pairs (n = 259). SE, standard error. R^2, pseudo-R^2.

	Full dataset				
	Model averaged			AIC$_c$ top model	
	Estimate (SE)	*P*	RI	Estimate (SE)	*P*
Plumage dichromatism	-0.25 (0.09)	0.004	0.98*	-0.25 (0.08)	0.003
Pair age	0.28 (0.09)	0.002	0.99*	0.26 (0.09)	0.002
Body mass	0.17 (0.09)	0.070	0.74*	0.16 (0.09)	0.057
Generation length	0.04 (0.11)	0.731	0.29	-	-
Forest dependency	0.15 (0.09)	0.106	0.61*	0.17 (0.09)	0.064
Migratory status	-0.01 (0.11)	0.959	0.26	-	-
Latitude	0.02 (0.13)	0.868	0.28	-	-
Island dwelling	0.05 (0.09)	0.576	0.29	-	-
Within-pair range overlap	0.06 (0.09)	0.492	0.31	-	-
Confamilial sympatry	-0.16 (0.10)	0.093	0.65*	-0.18 (0.09)	0.045
Body mass disparity	-0.02 (0.10)	0.854	0.27	-	-
Bill disparity	0.15 (0.09)	0.104	0.62*	0.14 (0.09)	0.098
Climatic disparity	0.03 (0.09)	0.737	0.27	-	-
Oscine/suboscine	0.00 (0.09)	0.968	0.26	-	-

Table S6. Standardised coefficient estimates from model averaged and AIC$_c$ top model multipredictor GLMs predicting variation in within-pair song disparity (PC1-3) among passerine species pairs (n = 246). SE, standard error; RI, relative importance. Pseudo-R^2 for AIC$_c$ top model = 0.17.

	Full dataset								
	Pitch disparity (PC1)			Length disparity (PC2)			Pace disparity (PC3)		
	Estimate (SE)	*P*	RI	Estimate (SE)	*P*	RI	Estimate (SE)	*P*	RI
Plumage dichromatism	-0.33 (0.11)	0.004	0.97*	-0.32 (0.12)	0.010	0.91*	-0.14 (0.12)	0.252	0.39
Pair age	0.33 (0.12)	0.005	0.96*	0.32 (0.12)	0.009	0.92*	0.20 (0.13)	0.126	0.56*
Body mass	0.32 (0.13)	0.010	0.93*	0.24 (0.13)	0.071	0.69*	-0.12 (0.13)	0.366	0.34
Generation length	-0.06 (0.15)	0.698	0.28	0.15 (0.15)	0.337	0.38	0.04 (0.14)	0.748	0.27
Forest dependency	0.31 (0.13)	0.014	0.89*	-0.01 (0.14)	0.930	0.27	0.15 (0.13)	0.275	0.39
Migratory status	-0.13 (0.15)	0.378	0.35	0.04 (0.16)	0.829	0.28	0.01 (0.16)	0.951	0.28
Latitude	-0.13 (0.18)	0.444	0.34	0.14 (0.16)	0.375	0.36	0.15 (0.16)	0.348	0.37
Island dwelling	0.08 (0.12)	0.492	0.31	0.06 (0.13)	0.611	0.29	0.05 (0.13)	0.685	0.28
Within-pair range overlap	0.09 (0.12)	0.446	0.32	0.02 (0.13)	0.877	0.26	0.09 (0.13)	0.494	0.31
Confamilial sympatry	-0.34 (0.13)	0.011	0.92*	-0.19 (0.13)	0.172	0.49*	0.04 (0.14)	0.779	0.27
Body mass disparity	0.21 (0.12)	0.085	0.61*	-0.08 (0.13)	0.569	0.29	-0.16 (0.14)	0.245	0.42*
Bill disparity	0.05 (0.13)	0.725	0.28	0.14 (0.13)	0.309	0.38	0.30 (0.14)	0.027	0.82*
Climatic disparity	0.00 (0.12)	0.992	0.26	0.12 (0.12)	0.329	0.35	0.06 (0.13)	0.638	0.28
Oscine/suboscine	-0.03 (0.12)	0.778	0.26	-0.09 (0.13)	0.477	0.31	0.12 (0.13)	0.363	0.34

Table S7. Standardised coefficient estimates from model averaged multipredictor GLMs predicting variation in within-pair disparity in three independent axes of song variation among passerine species pairs (n = 246). SE, standard error; RI, relative importance. * Denotes predictor variables included in the AIC_c top model.

	Full dataset					
	Pitch disparity (PC1)		Length disparity (PC2)		Pace disparity (PC3)	
	Estimate (SE)	*P*	Estimate (SE)	*P*	Estimate (SE)	*P*
Plumage dichromatism	-0.34 (0.11)	0.002	-0.30 (0.12)	0.010	-	-
Pair age	0.31 (0.12)	0.007	0.34 (0.12)	0.004	0.21 (0.12)	0.095
Body mass	0.33 (0.11)	0.002	0.27 (0.12)	0.027	-	-
Generation length	-	-	-	-	-	-
Forest dependency	0.34 (0.12)	0.005	-	-	-	-
Migratory status	-	-	-	-	-	-
Latitude	-	-	-	-	-	-
Island dwelling	-	-	-	-	-	-
Within-pair range overlap	-	-	-	-	-	-
Confamilial sympatry	-0.31 (0.12)	0.010	-0.21 (0.12)	0.075	-	-
Body mass disparity	0.21 (0.12)	0.070	-	-	-0.20 (0.13)	0.131
Bill disparity	-	-	-	-	0.30 (0.13)	0.024
Climatic disparity	-	-	-	-	-	-
Oscine/suboscine	-	-	-	-	-	-

Table S8. Standardised coefficient estimates from AIC_c top models predicting variation in within-pair disparity in song traits among passerine species pairs (n = 246). SE, standard error. Pseudo-R^2 for each model: PC1 = 0.22; PC2 = 0.12; PC3 = 0.06.

	Alternative dataset				
	Model averaged			AIC$_c$ top model	
	Estimate (SE)	*P*	RI	Estimate (SE)	*P*
Plumage dichromatism	-0.16 (0.06)	0.010	0.94	-0.16 (0.06)	0.001
Pair age	0.21 (0.06)	0.001	0.99	0.20 (0.06)	0.001
Body mass	0.10 (0.07)	0.137	0.58	0.09 (0.06)	0.158
Generation length	0.03 (0.08)	0.722	0.29	-	-
Forest dependency	0.17 (0.07)	0.017	0.91	0.17 (0.06)	0.009
Migratory status	0.04 (0.08)	0.611	0.30	-	-
Latitude	0.06 (0.09)	0.497	0.34	-	-
Island dwelling	0.01 (0.07)	0.849	0.26	-	-
Within-pair range overlap	0.06 (0.07)	0.388	0.35	-	-
Confamilial sympatry	-0.15 (0.07)	0.040	0.80	-0.16 (0.07)	0.017
Body mass disparity	0.01 (0.07)	0.872	0.27	-	-
Bill disparity	0.10 (0.07)	0.124	0.58	0.09 (0.06)	0.134
Climatic disparity	0.03 (0.07)	0.647	0.28	-	-
Oscine/suboscine	0.07 (0.07)	0.298	0.40	-	-

Table S9. Standardised coefficient estimates from model averaged and AIC$_c$ top model multipredictor GLMs predicting variation in within-pair song disparity (PC1-3) using an alternative dataset of passerine species pairs (n = 246). SE, standard error; RI, relative importance. Pseudo-R^2 for AIC$_c$ top model = 0.16.

| | Alternative dataset | | | | | | | | |
| | Pitch disparity (PC1) | | | Length disparity (PC2) | | | Pace disparity (PC3) | | |
	Estimate (SE)	P	RI	Estimate (SE)	P	RI	Estimate (SE)	P	RI
Plumage dichromatism	-0.15 (0.05)	0.004	0.99*	-0.14 (0.06)	0.022	0.92*	-0.06 (0.06)	0.288	0.41
Pair age	0.16 (0.05)	0.004	0.99*	0.14 (0.06)	0.018	0.93*	0.10 (0.06)	0.085	0.71*
Body mass	0.15 (0.06)	0.009	0.97*	0.13 (0.07)	0.056	0.82*	-0.06 (0.06)	0.309	0.40
Generation length	-0.01 (0.07)	0.889	0.26	0.05 (0.08)	0.497	0.34	0.01 (0.07)	0.888	0.27
Forest dependency	0.16 (0.06)	0.005	0.98*	0.08 (0.07)	0.237	0.47*	0.07 (0.06)	0.264	0.44
Migratory status	0.00 (0.07)	0.970	0.26	0.04 (0.08)	0.599	0.32	0.01 (0.08)	0.928	0.29
Latitude	-0.01 (0.07)	0.885	0.26	0.09 (0.08)	0.262	0.47*	0.09 (0.07)	0.210	0.51*
Island dwelling	0.04 (0.05)	0.502	0.31	-0.01 (0.06)	0.819	0.26	0.03 (0.06)	0.579	0.30
Within-pair range overlap	0.02 (0.05)	0.702	0.27	0.03 (0.07)	0.615	0.30	0.03 (0.06)	0.597	0.29
Confamilial sympatry	-0.17 (0.06)	0.003	0.99*	-0.08 (0.07)	0.227	0.49	-0.01 (0.07)	0.911	0.27
Body mass disparity	0.10 (0.06)	0.078	0.69*	-0.04 (0.07)	0.595	0.30	-0.06 (0.06)	0.311	0.41
Bill disparity	0.01 (0.06)	0.810	0.27	0.07 (0.07)	0.319	0.41	0.14 (0.06)	0.026	0.90*
Climatic disparity	0.00 (0.05)	0.981	0.25	0.07 (0.06)	0.291	0.42	0.02 (0.06)	0.756	0.27
Oscine/suboscine	0.02 (0.06)	0.763	0.26	0.01 (0.06)	0.869	0.26	0.09 (0.06)	0.124	0.61*

Table S10. Standardised coefficient estimates from model averaged multipredictor GLMs predicting variation in within-pair disparity in song traits using an alternative dataset of passerine species pairs (n = 246). SE, standard error; RI, relative importance. * Denotes predictor variables included in the AIC_c top model.

| | Alternative dataset | | | | | |
| | Pitch disparity (PC1) | | Length disparity (PC2) | | Pace disparity (PC3) | |
	Estimate (SE)	P	Estimate (SE)	P	Estimate (SE)	P
Plumage dichromatism	-0.15 (0.05)	0.003	-0.14 (0.06)	0.018	-	-
Pair age	0.15 (0.05)	0.004	0.14 (0.06)	0.018	0.09 (0.06)	0.116
Body mass	0.14 (0.05)	0.007	0.14 (0.06)	0.021	-	-
Generation length	-	-	-	-	-	-
Forest dependency	0.16 (0.05)	0.003	0.09 (0.07)	0.175	-	-
Migratory status	-	-	-	-	-	-
Latitude	-	-	-0.13 (0.07)	0.055	0.08 (0.06)	0.145
Island dwelling	-	-	-	-	-	-
Within-pair range overlap	-	-	-	-	-	-
Confamilial sympatry	-0.17 (0.05)	0.002	-	-	-	-
Body mass disparity	0.10 (0.05)	0.066	-	-	-	-
Bill disparity	-	-	-	-	0.12 (0.06)	0.036
Climatic disparity	-	-	-	-	-	-
Oscine/suboscine	-	-	-	-	0.09 (0.06)	0.098

Table S11. Standardised coefficient estimates from AIC_c top models predicting variation in within-pair disparity in song traits using an alternative dataset of passerine species pairs (n = 246). SE, standard error. Pseudo-R^2 for each model: PC1 = 0.23; PC2 = 0.12; PC3 = 0.08.

	Pair age	Body mass	Generation length	Forest dependency	Migratory status	Latitude	Island dwelling	Plumage dichromatism	Within-pair range overlap	Confamilial sympatry	Body mass disparity	Bill disparity	Climate disparity
Body mass	0.03												
Generation length	0.06	0.52											
Forest dependency	0.13	0.07	0.27										
Migratory status	-0.02	-0.34	-0.31	-0.31									
Latitude	0.01	-0.29	-0.27	-0.46	0.75								
Island dwelling	0.07	0.18	0.36	0.14	-0.16	-0.18							
Plumage dichromatism	0.02	0.15	0.30	0.08	0.03	-0.05	0.06						
Within-pair range overlap	0.14	-0.01	-0.05	-0.06	0.11	0.13	0.12	-0.02					
Confamilial sympatry	0.07	0.22	0.26	0.37	-0.40	-0.55	0.11	0.09	0.10				
Body mass disparity	0.25	0.18	0.09	-0.10	-0.10	-0.05	0.13	0.02	0.04	-0.01			
Bill disparity	0.26	0.18	0.10	-0.07	-0.03	-0.02	0.13	-0.05	0.13	0.04	0.47		
Climate disparity	0.00	0.02	0.02	-0.05	0.08	0.02	-0.07	0.02	-0.41	-0.10	0.06	0.06	
Oscine/suboscine	0.03	0.04	0.10	0.25	-0.29	-0.31	-0.18	0.11	-0.04	0.33	0.01	-0.03	-0.07

Table S12. Pearson correlation coefficients (r^2) for all pairwise combinations of (standardised) predictor variables considered in our analysis