

24 offspring sired by extra-pair males, and increased up to intermediate proportions of extra-
25 pair banded offspring but decreased with higher proportions (table S1; *Results* fig. 3A).

26 $\text{Diff}_{\text{life_monandry-gen}}$ was likewise predicted by whether or not a female produced any banded
27 extra-pair offspring, with means of 0.63 ± 0.23 (median 0.7, range 0–1.00) and 0.11 ± 0.22
28 (median 0, range 0–0.71) for females that did and did not produce any extra-pair offspring
29 respectively (table S1). $\text{Diff}_{\text{life_monandry-gen}}$ increased up to intermediate proportions of extra-
30 pair banded offspring but decreased with higher proportions (table S1; *Results* fig. 3B).

31 Similar to sibships among banded offspring, $\text{Diff}_{\text{social-gen}}$ for recruited offspring varied
32 with whether or not a female produced any extra-pair recruited offspring, with a raw mean
33 difference of 0.33 ± 0.30 (median 0.26, range 0.00–1.00) for females that produced at least
34 one extra-pair recruited offspring compared to zero for females that did not (table S1).

35 $\text{Diff}_{\text{social-gen}}$ increased up to intermediate proportions of extra-pair recruits and again
36 decreased with higher proportions (table S1; *Results* fig. 3C). $\text{Diff}_{\text{life_monandry-gen}}$ was likewise
37 predicted by whether or not a female produced any extra-pair recruited offspring, with
38 means of 0.65 ± 0.30 (median 0.7, range 0–1.00) and 0.29 ± 0.40 (median 0, range 0–1.00) for
39 females that did and did not produce any extra-pair recruited offspring, respectively (table
40 S1). $\text{Diff}_{\text{life_monandry-gen}}$ also increased up to intermediate proportions of extra-pair recruited
41 offspring, but decreased with higher proportions (table S1; *Results* fig. 3D).

42 **Table S1:** Generalized linear models estimating whether changes in sibship structure of
43 females' banded (A–D) and recruited (E–H) offspring given the genetic versus social
44 pedigrees ($\text{Diff}_{\text{social-gen}}$), and given the genetic pedigree versus strict lifelong monandry
45 ($\text{Diff}_{\text{life_monandry-gen}}$), varied in relation to whether or not females produced any extra-pair
46 offspring over their lifetime (Any EPO; Models A,C,E,G), or with the proportion of a female's
47 lifetime offspring that were extra-pair offspring (Prop EPO; Models B, D,F,H). All models
48 utilized a binomial error structure weighted by total number of sibships (N_{sibs}). Linear and
49 quadratic effects of Prop EPO were modelled. Estimated effects of extra-pair reproduction
50 (on latent scales) are presented ± 1 standard error (SE), df is the residual degrees of
51 freedom, R^2 is the coefficient of determination.

52 **Table S1**

Response variable	df	R²	Predictor	Estimate (±SE)	Z	p
Banded offspring						
A) Diff _{social-gen}	96	0.04	Intercept	-0.96 (0.10)		
			Any EPO	0.38 (0.10)	3.6	0.0002
B) Diff _{social-gen}	95	0.14	Intercept	-2.20 (0.04)		
			Prop EPO	4.90 (0.41)	11.93	<0.0001
			(Prop EPO) ²	-3.23 (0.57)	-5.65	<0.0001
C) Diff _{life_monandry-gen}	96	0.29	Intercept	-1.73 (0.12)		
			Any EPO	2.64 (0.12)	21.2	<0.0001
D) Diff _{life_monandry-gen}	95	0.25	Intercept	0.59 (0.03)		
			Prop EPO	4.04 (0.32)	12.64	<0.0001
			(Prop EPO) ²	-6.73 (0.39)	17.5	<0.0001
Recruited offspring						
E) Diff _{social-gen}	35	0.25	Intercept	-1.66 (0.30)		
			Any EPO	1.07 (0.32)	3.4	0.0008
F) Diff _{social-gen}	34	0.37	Intercept	-1.37 (0.17)		
			Prop EPO	4.88 (1.21)	4.04	<0.0001
			(Prop EPO) ²	-2.49 (1.09)	-2.47	0.01
G) Diff _{life_monandry-gen}	35	0.34	Intercept	-0.81 (0.24)		
			Any EPO	1.56 (0.26)	6.0	<0.0001
H) Diff _{life_monandry-gen}	34	0.50	Intercept	0.29 (0.14)		
			Prop EPO	2.77 (1.14)	2.43	0.02
			(Prop EPO) ²	-4.56 (0.83)	5.47	<0.0001

54 **Supporting Information S2. Sibship structure among banded offspring of females that**
55 **produced recruits**

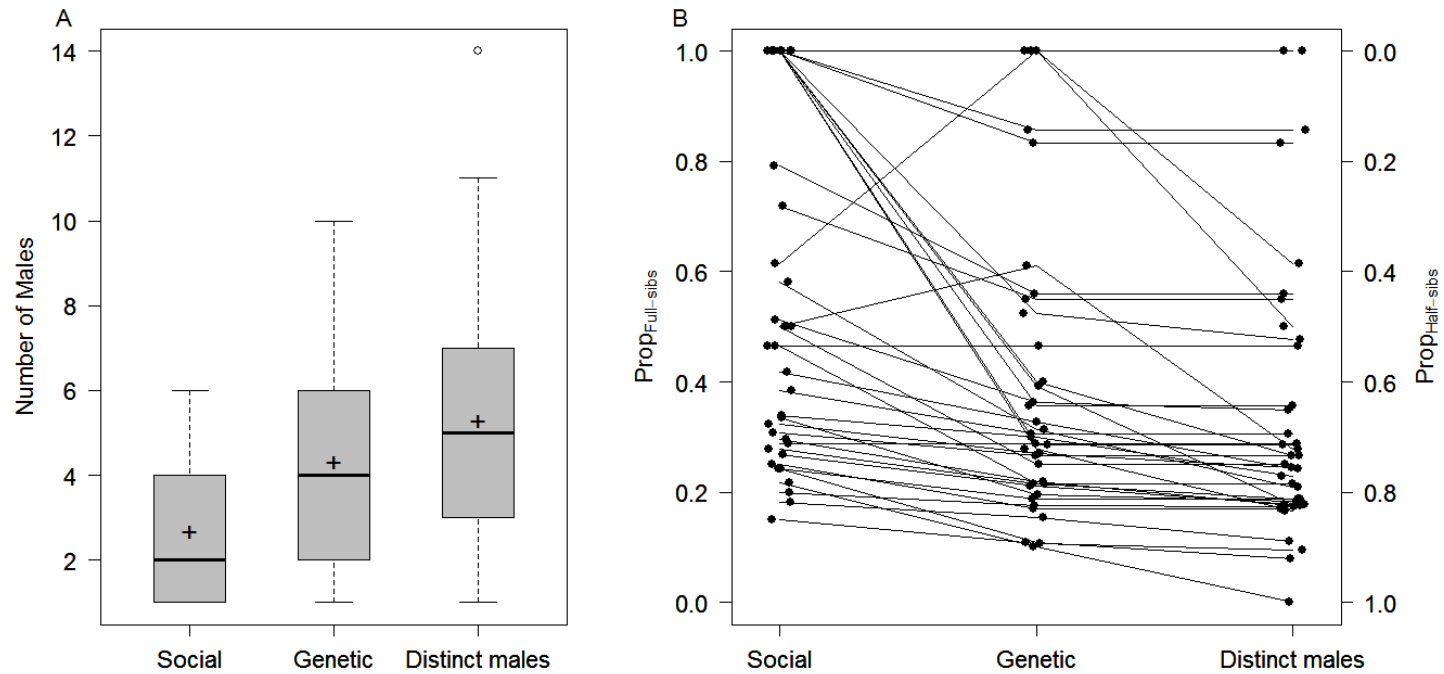
56

57 We quantified whether differences between females' banded and recruited offspring for
58 both the number of male sires and proportion of full-sibships ($\text{Prop}_{\text{Full-sibs}}$) across pedigrees
59 (*Results*, table 1; fig. 2) were consistent across the exact same females over different
60 offspring life-stages, rather than an artefact of the reduced sample size of females for
61 analyses of recruits. To do so, we conducted further analysis of sibship structures among
62 banded offspring of the 37 females that had at least two recruited offspring (see main
63 manuscript *Methods, Sibship structure*).

64 Results from the subset of 37 females were quantitatively similar to those from the
65 full dataset of 98 females, in that the number of different males that sired each female's
66 banded offspring was greater given the genetic pedigree than given the social pedigree, but
67 did not differ significantly between the genetic pedigree and the 'distinct males' pedigree
68 (*Results*, table 1). Mean $\text{Prop}_{\text{Full-sibs}}$ among females' banded offspring was greater given the
69 social versus genetic pedigrees, which was in turn greater than given the 'distinct males'
70 pedigree (*Results*, table 1). $\text{Prop}_{\text{Full-sibs}}$ among the banded offspring of most (81%; 30/37)
71 females was lower given the genetic versus social pedigrees, for 14% (5/37) of females there
72 was no change in lifetime sibships among banded offspring between the pedigrees, and
73 0.5% (2/37) of females had greater $\text{Prop}_{\text{Full-sibs}}$ among banded offspring given the genetic
74 pedigree than given the social pedigree. Most females (57%; 21/37) had even lower $\text{Prop}_{\text{Full-}}$
75 sibs given the 'distinct males' pedigree than given the genetic pedigree, whereas 43% (16/37)

76 of females had no change between the two pedigrees, and no females had greater $\text{Prop}_{\text{Full-sibs}}$
77 sibs given the 'distinct males' pedigree (fig. S1).

78 Thus, results reported in the main manuscript (*Results*, table 1) regarding the lack of
79 change in mean $\text{Prop}_{\text{Full-sibs}}$ given the 'distinct males' pedigree compared to the genetic
80 pedigree, as well as the lack of difference in mean number of male sires among all three
81 pedigrees for recruited offspring are likely not an artefact of the relatively small sample size
82 for recruit sibship structures. Rather, these differences in sibship structures among banded
83 and recruited offspring may be due to differential survival among within-pair (i.e., sired by
84 social male) offspring versus their extra-pair brood-mates, as found previously in song
85 sparrows (Sardell et al. 2011). These results suggest that the ultimate consequences of
86 polyandry for the potential for different degrees of inbreeding and consequent fitness
87 among descendants of polyandrous females in natural populations, with natural levels of
88 offspring mortality, could be smaller than expected from laboratory populations (e.g.,
89 Power and Holman 2014).



90

91 **Figure S1:** The (A) numbers of different males that sired offspring, and (B) sibship structures of females' banded offspring given the social
 92 pedigree ('Social'), genetic pedigree ('Genetic'), and given the 'distinct males' pedigree ('Distinct males') using a restricted dataset of 37
 93 females that produced >1 recruited offspring. In (A), box lines represent the median, upper and lower quartiles, whiskers demarcate 1.5× the
 94 interquartile range, and '+' shows the mean. In (B) the left and right axes respectively show the proportions of sibships among each female's
 95 offspring that are full-sibships ($\text{Prop}_{\text{Full-sibs}}$) and half-sibships ($\text{Prop}_{\text{Half-sibs}}$), where points denote individual females (jittered for clarity), and lines
 96 join observations for individual females given the three pedigrees.

97 Unlike our main analyses involving all females which produced >1 banded offspring,
98 $\text{Diff}_{\text{social-gen}}$ did not vary with whether or not a female produced any banded extra-pair
99 offspring, with a raw mean of 0.21 ± 0.22 (median 0.13, range 0.00–0.72) for females that
100 produced at least one extra-pair offspring compared to zero for females that did not (table
101 S2). However, similar to our main analyses, $\text{Diff}_{\text{social-gen}}$ varied with the proportion of a
102 female's total banded offspring that were sired by extra-pair males, showing that $\text{Diff}_{\text{social-gen}}$
103 increased significantly with intermediate proportions of extra pair offspring (linear slope,
104 table S2), but tended to decrease with higher proportions, though this later relationship was
105 not significant (quadratic slope, table S2). $\text{Diff}_{\text{life_monandry-gen}}$ likewise varied with whether or
106 not a female produced any banded extra-pair offspring, with means of 0.63 ± 0.25 (median
107 0.7, range 0–0.90) and 0.31 ± 0.37 (median 0.3, range 0–0.71) for females that did and did
108 not produce any extra-pair offspring respectively. $\text{Diff}_{\text{life_monandry-gen}}$ also varied with the
109 proportion of a female's total banded offspring that were sired by extra-pair males, where
110 $\text{Diff}_{\text{life_monandry-gen}}$ increased with up to intermediate proportions of extra-pair offspring
111 (linear slope, table S2) but once again decreased with higher proportions (quadratic slope,
112 table S2).

113 **Table S2:** Generalized linear models estimating whether changes in sibship structure of
114 females' banded offspring given the genetic versus social pedigrees ($\text{Diff}_{\text{social-gen}}$), and given
115 the genetic pedigree versus strict lifelong monandry ($\text{Diff}_{\text{lifelong-monandry-gen}}$) varied in relation to
116 whether or not females produced any extra-pair offspring over their lifetime (Any EPO;
117 Models A,C,E,G), or in relation to linear or quadratic effects of the proportion of a female's
118 lifetime offspring that were extra-pair offspring (Prop EPO; Models B, D,F,H). Models A–D
119 are from the full female dataset (reproduced from table S1 for comparison), and models E–
120 H utilise a restricted dataset considering the banded offspring of females that produced at
121 least two recruited offspring. All models utilized a binomial error structure weighted by total
122 number of sibships (N_{sibs}), and $\text{Diff}_{\text{social-gen}}$ was range scaled 0–1. Estimated effects of extra-
123 pair reproduction (on latent scales) are presented ± 1 standard error (SE), df is the residual
124 degrees of freedom, R^2 is the coefficient of determination.

125 **Table S2**

Response variable	df	R²	Predictor	Estimate (±SE)	Z	p
Banded offspring – Full dataset						
A) Diff _{social-gen}	96	0.04	Intercept	-0.96 (0.10)		
			Any EPO	0.38 (0.10)	3.6	0.0002
B) Diff _{social-gen}	95	0.14	Intercept	-2.20 (0.04)		
			Prop EPO	4.90 (0.41)	11.93	<0.0001
			(Prop EPO) ²	-3.23 (0.57)	-5.65	<0.0001
C) Diff _{life_monandry-gen}	96	0.29	Intercept	-1.73 (0.12)		
			Any EPO	2.64 (0.12)	21.2	<0.0001
D) Diff _{life_monandry-gen}	95	0.25	Intercept	0.59 (0.03)		
			Prop EPO	4.04 (0.32)	12.64	<0.0001
			(Prop EPO) ²	-6.73 (0.39)	17.5	<0.0001
Banded offspring – Restricted dataset						
E) Diff _{social-gen}	35	0.01	Intercept	-0.63 (0.23)		
			Any EPO	0.37 (0.23)	1.6	0.11
F) Diff _{social-gen}	34	0.12	Intercept	-2.04 (0.04)		
			Prop EPO	2.61 (0.29)	8.97	<0.0001
			(Prop EPO) ²	0.16 (0.37)	0.45	0.66
G) Diff _{life_monandry-gen}	35	0.01	Intercept	0.30 (0.22)		
			Any EPO	0.63 (0.23)	2.8	0.005
H) Diff _{life_monandry-gen}	34	0.14	Intercept	0.96 (0.03)		
			Prop EPO	1.63 (0.27)	6.03	<0.0001
			(Prop EPO) ²	-2.06 (0.28)	7.43	<0.0001

127 **Supporting Information S3. Sibship structure among males' banded and recruited offspring**

128

129 Analyses of sibship structure among lifetime banded and recruited offspring of male song
130 sparrows given the social and genetic pedigrees were implemented as for females
131 (described in *Methods*). However the 'distinct males' pedigree is arbitrary for males, and so
132 was not analyzed.

133 A total of 99 males produced at least two banded offspring (i.e., at least one
134 offspring sibship) given both the social and genetic pedigrees (males with >1 offspring under
135 one pedigree but ≤ 1 under the other were excluded from analyses). These males socially
136 reared a mean of 10.9 ± 8.4 offspring (median 8, range 2–44) and sired a mean of 11.3 ± 9.5
137 genetic offspring (median 8, range 2–52). Both the number of females with which males
138 produced banded offspring and $\text{Prop}_{\text{Full-sibs}}$ among banded offspring were greater given the
139 genetic versus social pedigrees (table S3; fig. S2A,B). Similar to females, most males (62%,
140 62/99) had fewer full-sibships among lifetime banded offspring given the genetic versus
141 social pedigree, whereas 30% (30/99) males had no change in $\text{Prop}_{\text{Full-sibs}}$ between the
142 pedigrees, and 7% (7/99) of males had greater $\text{Prop}_{\text{Full-sibs}}$ given the genetic pedigree.

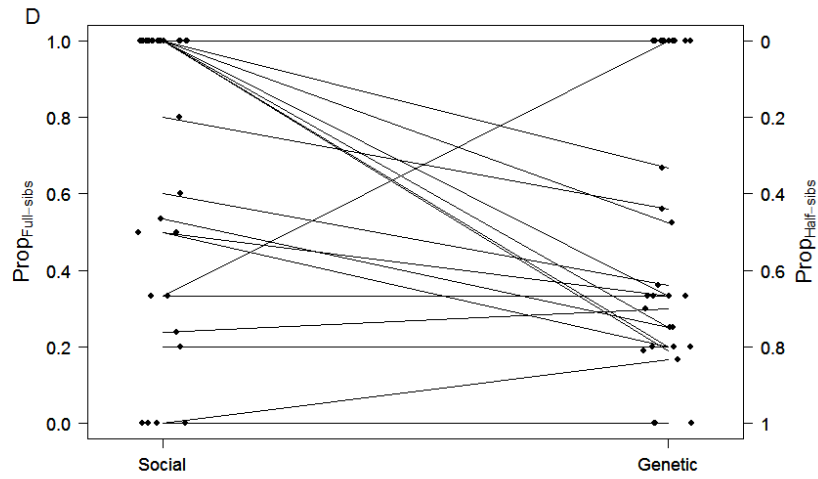
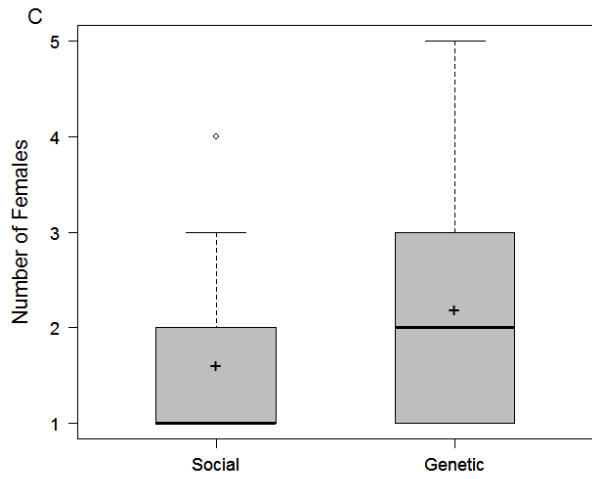
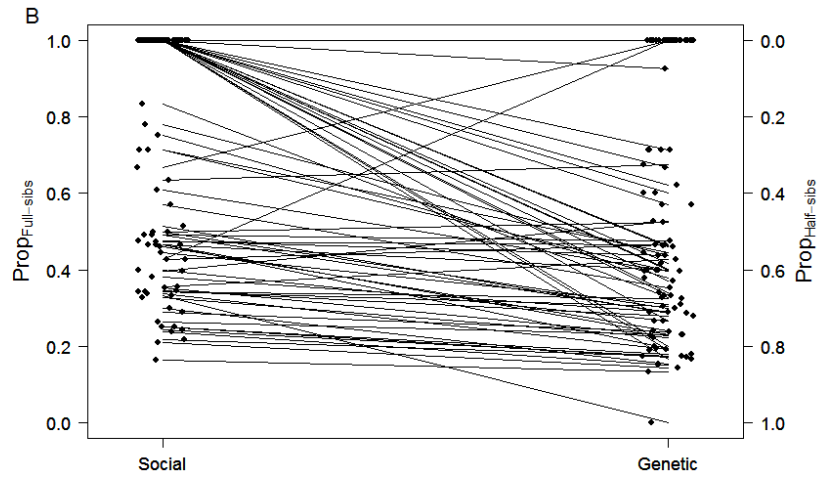
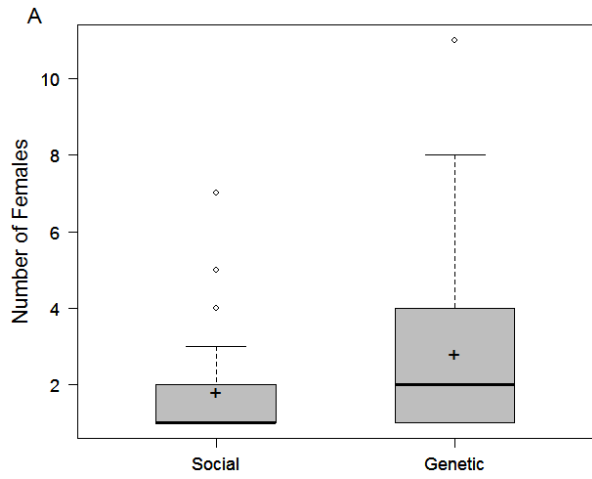
143 A total of 31 male song sparrows produced at least two recruited offspring under
144 both the social and genetic pedigrees, with means of 4.4 ± 2.9 social offspring (median 3,
145 range 2–16) produced and 4.7 ± 3.3 genetic offspring sired (median 3, range 2–17) over their
146 lifetimes. While $\text{Prop}_{\text{Full-sibs}}$ among males' recruits was greater given the genetic than given
147 the social pedigree, the number of females with which males produced recruited offspring
148 did not significantly differ between the two pedigrees (table S3; fig. S2C,D). Once again
149 similar to females, 39% (12/31) of males had fewer full-sibships among their lifetime

150 recruited offspring given the genetic pedigree than given the social pedigree, while 52%
151 (16/31) had no change, and 10% (3/31) had greater $\text{Prop}_{\text{Full-sibs}}$ given the genetic pedigree.

152 **Table S3:** Summary statistics (left panel) and generalized linear mixed models (right panel)
153 estimating differences in the number of females with which a male sired (A) banded and (C)
154 recruited offspring, and the proportion of full-sibships ($\text{Prop}_{\text{Full-sibs}}$) among males' (B) banded
155 and (D) recruited offspring given the social and genetic pedigrees. Analyses include 99 and
156 31 males for analyses of banded and recruited offspring, respectively, and assumed (A and
157 C) Poisson or (B and D) binomial error structures. Raw means are presented ± 1 standard
158 deviation (SD). Estimated effects of pedigree are presented ± 1 standard error (SE), df is the
159 residual degrees of freedom (where the social pedigree represents the intercept), R^2 is the
160 conditional coefficient of determination, and Z and p values are presented for the effects of
161 the genetic pedigree compared to the social pedigree.

162 **Table S3**

Response variable	Pedigree	Mean (\pmSD)	Median (Range)	df	R²	Estimate (\pmSE)	Z	p
Banded offspring								
A) Number of females	Social	1.8 (1.2)	1 (1–7)	195	0.34	0.51 (0.09)	4.6	<0.001
	Genetic	2.8 (1.9)	2 (2–11)			0.44 (0.10)		
B) Prop _{Full-sibs}	Social	0.75 (0.30)	1.00 (0.17–1.00)	195	0.55	1.63 (0.25)	24.4	<0.001
	Genetic	0.58 (0.33)	0.5 (0.00–1.00)			-0.91 (0.04)		
Recruited offspring								
C) Number of females	Social	1.6 (0.8)	1 (1–4)	59	0.05	0.48 (0.14)	1.7	0.10
	Genetic	2.2 (1.2)	2 (1–5)			0.31 (0.18)		
D) Prop _{Full-sibs}	Social	0.71 (0.38)	1.00 (0.00–1.00)	59	0.61	1.48 (0.50)	6.2	<0.001
	Genetic	0.56 (0.39)	0.36 (0.00–1.00)			-1.17 (0.18)		



163

164 **Figure S2**

165 **Figure S2:** The numbers of different females with which male song sparrows produced (A)
166 banded and (C) recruited offspring, and the sibship structures of males' (B) banded and (D)
167 recruited offspring given the social pedigree ('Social') and genetic pedigree ('Genetic'). In (A)
168 and (C), box lines represent the median, upper and lower quartiles, whiskers demarcate
169 $1.5\times$ the interquartile range, and '+' shows the mean. In (B) and (D), the left and right axes
170 respectively show the proportions of sibships among each male's offspring that are full-
171 sibships ($\text{Prop}_{\text{Full-sibs}}$) and half-sibships ($\text{Prop}_{\text{Half-sibs}}$), where points denote individual males
172 (jittered for clarity), and lines join observations for individual males given the two pedigrees.

173 **Supporting Information S4. Population-wide effects of polyandry on the distribution of**
174 **relatedness**

175

176 To quantify the degree to which the observed individual-level differences in relationship
177 frequencies extended across the population, we calculated the absolute and proportional
178 changes in the total number of possible matings at each relationship level given the genetic
179 versus social pedigrees. To do so, we pooled the number of possible matings among all
180 females for a relationship level given the genetic pedigree and subtracted the number of
181 possible matings at the same relationship level given the social pedigree.

182 Individual-level differences in the distribution of relatives that were available as
183 possible mates given the genetic versus social pedigrees (*Results*, table 2) translated into
184 substantial population-level differences; overall, extra-pair reproduction meant that females
185 had more possible matings with half-brothers than with full-brothers, and with 4th degree
186 relatives than with analogous 2nd and 3rd degree relatives (table S4).

187

188

189 **Table S4:** Total population-wide numbers of possible matings at 15 specified relationships,
190 and with more distant relatives and unrelated individuals, given the social and genetic
191 pedigrees. 'Difference' and 'proportional difference' show the decrease (negative values) or
192 increase (positive values) in the absolute number and proportion of possible matings at
193 each relationship level given the genetic versus social pedigrees. The absolute and
194 proportional net total differences for each degree of relationship are also shown.

195 **Table S4**

Relationship		Social pedigree	Genetic pedigree	Difference	Proportional difference
1 st degree	Father	105	97	-8	-8%
	Full-brother	171	103	-68	-40%
	Son	102	102	0	+0%
	Net total			-76	-20%
2 nd degree	Grandfather	46	40	-6	-13%
	Uncle	89	44	-45	-51%
	Half-brother	109	290	+181	+166%
	Double first cousin	8	0	-8	-100%
	Nephew	159	74	-85	-54%
	Grandson	42	44	+2	+5%
	Net total			+39	+9%
3 rd degree	Great-grandfather	19	17	-2	-11%
	Single first cousin	266	87	-179	-67%
	Great-grandson	12	14	+2	+17%
	Net total			-179	-60%
4 th degree	Half-uncle	123	228	+105	+85%
	Half-single first cousin	280	615	+335	+120%
	Half-nephew	226	322	+96	+43%
	Net total			+536	+85%
More distant		5463	5143	-320	-6%
Unrelated		808	808	0	0%

197 **Supporting Information S5. Distribution of relatedness excluding all 1st degree relatives**

198

199 We repeated tests on the distribution of relatedness among possible mates given the social
200 and genetic pedigrees to evaluate how our general conclusions apply to systems where
201 individuals actively avoid close inbreeding with 1st degree relatives through social pairing or
202 extra-pair reproduction. From our full ‘relatedness’ dataset (main manuscript), we removed
203 all possible matings between females and their 1st degree relatives from both the social
204 (father = 105, son = 102, full-sib = 171) and genetic (father = 23 additional, son = no
205 additional, full-sib = 1 additional) pedigrees, resulting in a reduced sample size of 7626
206 possible matings across eight years. We again quantified the effects of extra-pair
207 reproduction on the distributions of relatedness with possible mates for individual females
208 in this subset in two ways, similar to the main manuscript.

209 First, we calculated each female’s mean k_{SOC} and k_{GEN} with all possible mates that
210 were 2nd degree relatives given the social pedigree and tested for differences between them
211 using a Wilcoxon rank sum test. We repeated this process for all possible mates that were
212 3rd and 4th degree relatives given the social pedigree, as well as for more distantly related
213 and unrelated possible mates, to evaluate whether differences in k given the genetic rather
214 than social pedigree were greater among females and their close or more distant social
215 relatives when excluding all 1st degree social relatives. There was again substantial variation
216 in mean kinship (k) with possible mates that were 2nd degree social relatives (fig. S3A),
217 similar to our main analyses (*Results*, fig. 5B). The majority of females (85% [83/98]) had
218 lower mean k given the genetic pedigree for 2nd degree social relationships (fig. S3A), and
219 individual mean k_{GEN} was significantly lower than mean k_{SOC} (table S5). There was again less

220 variation in k given both the social and genetic pedigrees for possible mates classified as 3rd
221 and 4th degree social relatives, but 87% (68/78) and 77% (75/97) of females had lower mean
222 k given the genetic pedigree for both degrees of relationship given the social pedigree (fig.
223 S3B,C), and mean k_{GEN} was significantly lower than mean k_{SOC} for both 3rd and 4th degree
224 relationships given the social pedigree (table S5). The majority of females (68% [75/110])
225 likewise had lower mean k given the genetic pedigree for more distant relatives (fig. S3D),
226 but mean k_{SOC} and mean k_{GEN} did not differ substantially for this degree of relatedness given
227 the social pedigree (table S5). Once again similar to our main analyses (*Results*, table 3; fig.
228 5f), there was no difference in mean k for unrelated individuals between the two pedigrees
229 (table S5; fig. S3E).

230 Second, to quantify continuous differences in k among individual females and their
231 possible mates given the social and genetic pedigrees, we again calculated the difference in
232 k for each possible mating in this data subset as: $k_{DIFF} = k_{GEN} - k_{SOC}$, calculated mean k_{DIFF} for
233 each individual female, and evaluated the proportion of females that experienced an
234 increase, decrease, or no change in mean relatedness with all possible mates given the
235 genetic pedigree versus the social pedigree. Mean k_{DIFF} among all possible matings for
236 individual females in this subset was -0.006 ± 0.01 (median -0.006 , range -0.033 – 0.018),
237 indicating that, on average, females were less related to all possible mates given the genetic
238 pedigree than given the social pedigree (fig. S4), similar to our main analyses.

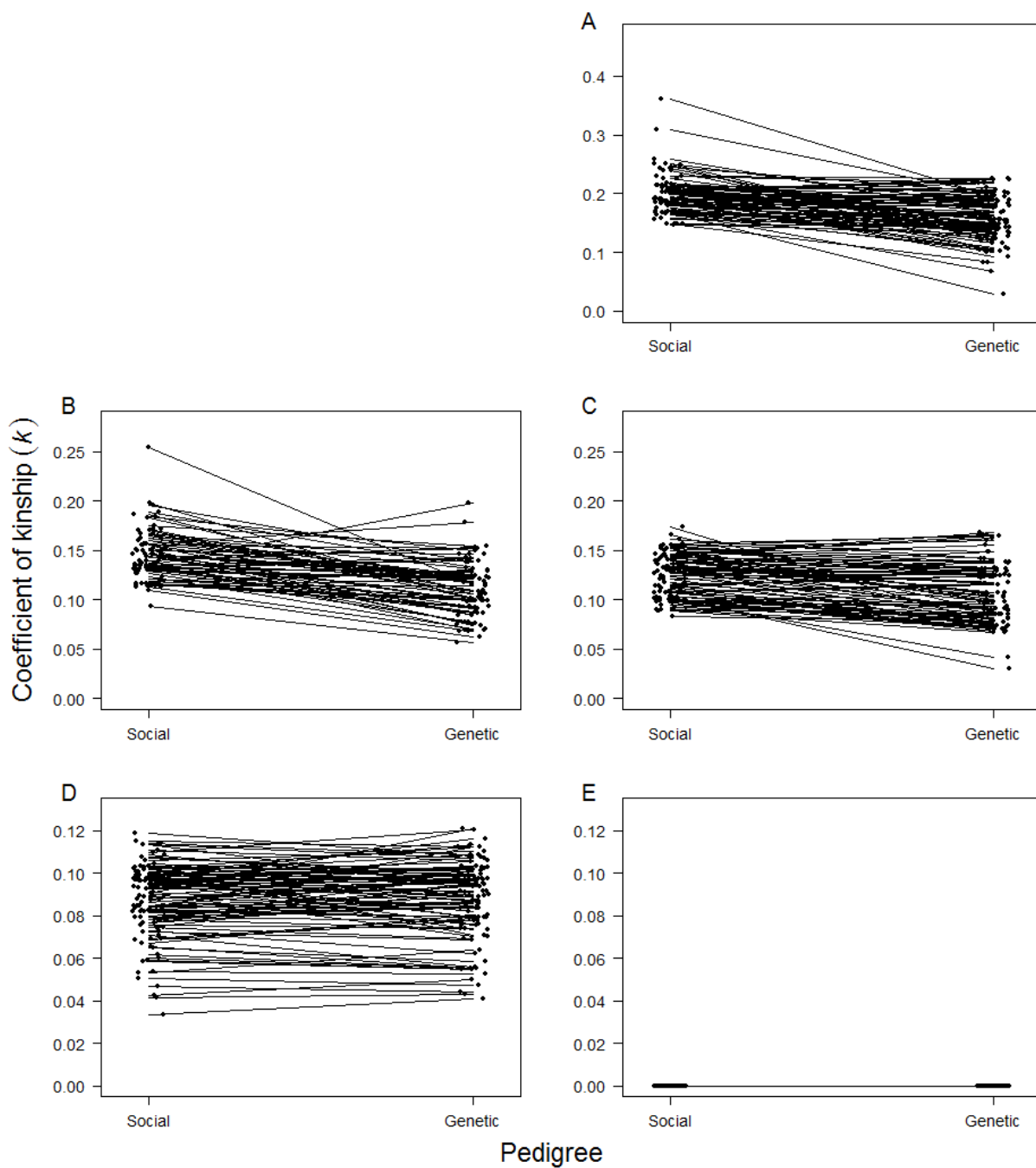
239 Proportionally, 68% (77/114) of females had lower mean k_{DIFF} given the genetic pedigree,
240 while 29% (33/114) of females had higher mean k_{DIFF} , and 4% (4/114) of females had no
241 change in mean k_{DIFF} given the genetic versus social pedigrees (corresponding to immigrants
242 breeding in only one season).

243 **Table S5:** Mean \pm SD (and range) of pairwise kinship given the social (k_{SOC}) and genetic (k_{GEN})
 244 pedigrees between individual female song sparrows and all possible mates, excluding 1st
 245 degree relatives, that were classified as 2nd, 3rd, and 4th degree relatives given the social
 246 pedigree, as well as more distantly related and unrelated possible mates. n and ♀
 247 respectively represent the numbers of possible matings and individual females in each
 248 category. Mean difference denotes the mean decrease (negative values) or increase
 249 (positive values) in mean kinship for individual females given the genetic pedigree. Z and p
 250 denote Z value of the Wilcoxon rank sum test statistic and associated p value. Degrees of
 251 social relationships where mean k decreased significantly given the genetic pedigree rather
 252 than the social pedigree are highlighted in bold.

253

Relationship given social pedigree	k_{SOC}	k_{GEN}	Mean difference	Z (p)
2 nd degree ($n = 452$, ♀ = 98)	0.197 \pm 0.033 (0.147–0.361)	0.155 \pm 0.038 (0.03–0.226)	-0.042\pm0.042 (-0.165–0.022)	7.3 (<0.001)
3 rd degree ($n = 296$, ♀ = 78)	0.145 \pm 0.026 (0.094–0.255)	0.112 \pm 0.028 (0.057–0.198)	-0.033\pm0.031 (-0.14–0.063)	6.8 (<0.001)
4 th degree ($n = 624$, ♀ = 97)	0.125 \pm 0.022 (0.084–0.174)	0.106 \pm 0.03 (0.031–0.168)	-0.019\pm0.023 (-0.099–0.023)	4.9 (<0.001)
More distant ($n = 5446$, ♀ = 110)	0.087 \pm 0.017 (0.034–0.119)	0.088 \pm 0.018 (0.041–0.121)	-0.0002 \pm 0.011 (-0.032–0.03)	0.04 (0.97)
Unrelated ($n = 808$, ♀ = 114)	0.000 \pm 0.000 --	0.000 \pm 0.000 --	0.00 \pm 0.00 --	0.0 (1.00)

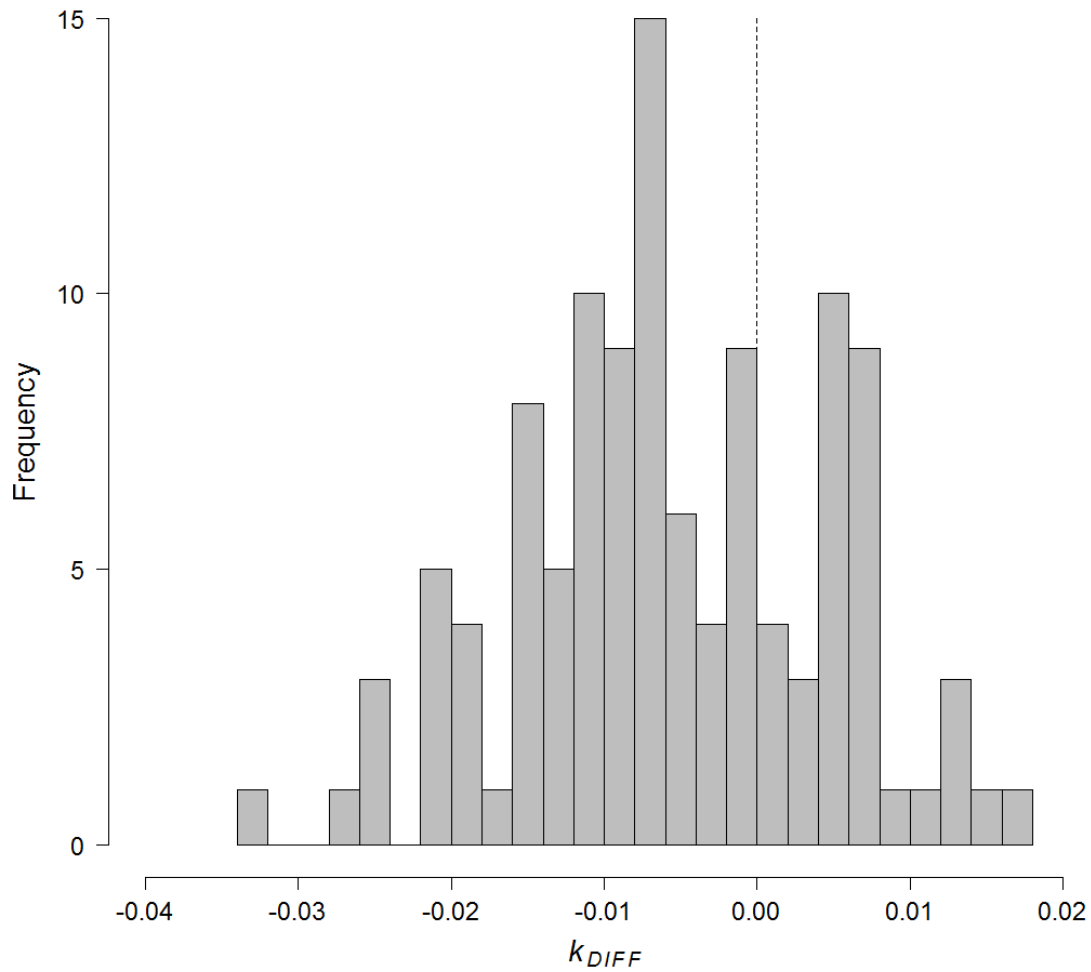
254



255

256 **Figure S3**

257 **Figure S3:** Mean coefficient of kinship (k) given the social and genetic pedigrees for
258 individual female song sparrows and all possible mates, excluding 1st degree relatives,
259 classified as (A) 2nd degree, (B) 3rd degree, and (C) 4th degree relatives given the social
260 pedigree, as well as (D) more distantly related, and (E) unrelated possible mates. Points
261 denote individual females and are jittered for clarity, and lines join observations for
262 individual females given the two pedigrees. Sample sizes for each category of relatedness
263 are presented in table S5.

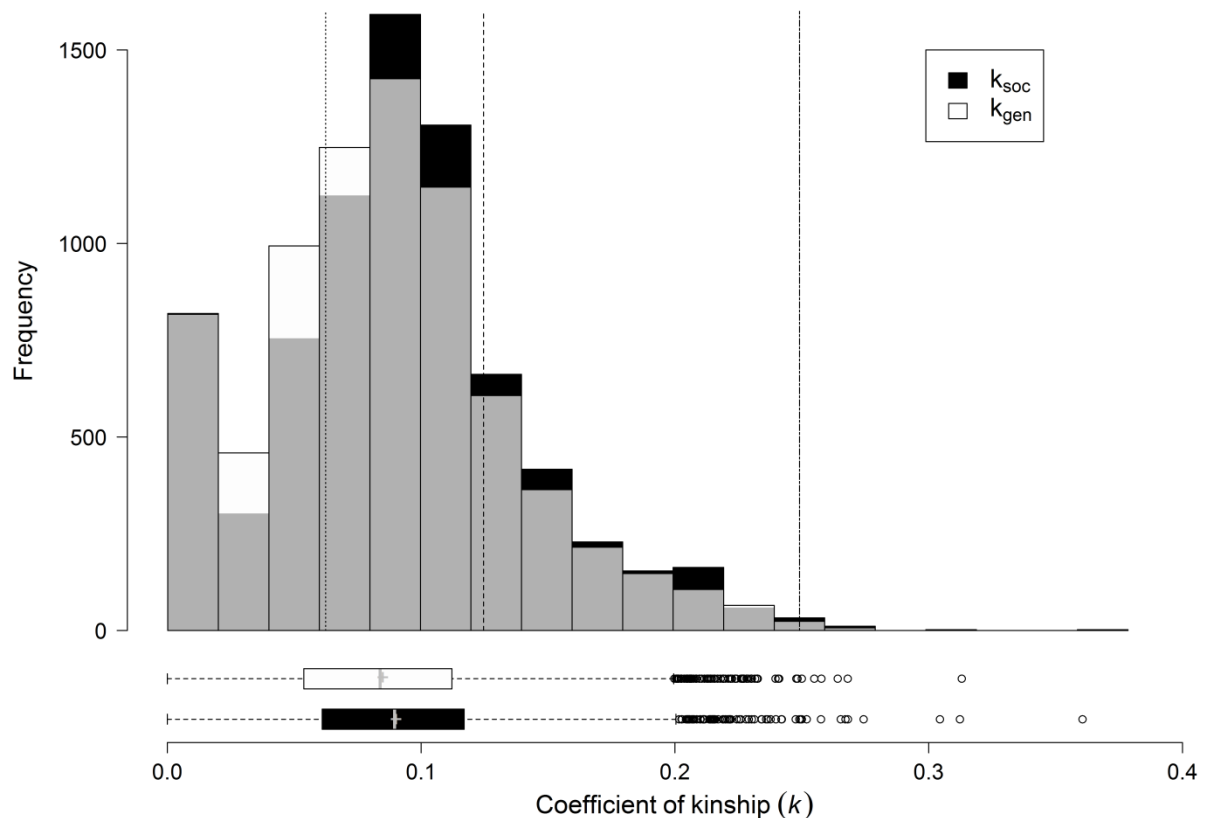


264

265 **Figure S4:** Distribution of the mean difference in coefficient of kinship (k_{DIFF}) given the
 266 genetic and social pedigrees ($k_{GEN} - k_{SOC}$) among all possible matings for individual female
 267 song sparrows, excluding those between 1st degree relatives. Dashed line demarcates $k_{DIFF} =$
 268 0, negative values indicate a lower mean k given the genetic pedigree.

269 Across all pooled possible matings for all females in this subset, results were again
270 very similar to those from the full dataset (*Results*, fig. 6), such that the distributions of k_{GEN}
271 and k_{SOC} were significantly different (two-sample Anderson-Darling test, $AD = 30.31$, $T =$
272 38.50 , $p < 0.001$), again based on resampling of each for 10,000 permutations (fig. S5).
273 Specifically the distribution of k_{GEN} included fewer possible matings at higher k (fig. S5, black
274 bars), but more possible matings at lower but non-zero k (fig. S5, white bars), and again no
275 difference in the number of possible matings among unrelated individuals (i.e., $k = 0$, fig.
276 S5). Note that despite the removal of all first order relatives, kinship among some possible
277 mates exceeded that between 1st degree relatives in an outbred population (i.e., $k = 0.25$,
278 fig. S5).

279 Thus, results from analyses on this subset of possible matings were highly congruent
280 with those presented throughout the main text (*Results*), indicating that our results and
281 interpretations are likely applicable to systems where individuals avoid mating with 1st
282 degree relatives (e.g., Stow and Sunnucks 2004; Gerlach and Lysiak 2006; Archie et al. 2007;
283 Brouwer et al. 2011).



284

285 **Figure S5:** Overall distributions of pairwise coefficients of kinship across all possible song
 286 sparrow matings excluding those between 1st degree relatives (female-father, female-son,
 287 full-siblings), calculated from the social pedigree (black bars) and from the genetic pedigree
 288 (white bars), where grey bars denote overlap between the two distributions. Dotted,
 289 dashed, and dot-dashed lines are included for visualization and depict kinship values
 290 equivalent to first cousin (0.0625), half-sib (0.125), and full-sib (0.25) matings, respectively.
 291 Box plots further visualize the distribution in values of k given each pedigree, where box
 292 lines represent the median, upper and lower quartiles, whiskers demarcate 1.5× the
 293 interquartile range and '+' represents the mean. Mean k_{SOC} was 0.090 ± 0.05 (range 0.00–
 294 0.36) and mean k_{GEN} was 0.085 ± 0.05 (range 0.00–0.31), again corresponding to a significant
 295 (Wilcoxon signed rank test: $Z = 17.30$, $p < 0.001$) but relatively small decrease in mean k
 296 given the genetic versus social pedigrees for this restricted dataset.

297 ***Supporting Information S6. Distribution of relatedness within cohorts***

298

299 A potential limitation of our approach of comparing social and genetic pedigrees is that
300 analyses of relationships and relatedness implicitly assume that all pairings (and hence
301 assumed matings) that resulted in offspring in the social pedigree are the same as the
302 matings that would have occurred if all ancestral social parents had been the true genetic
303 parents of the offspring that they reared. This in turn requires that mating decisions are not
304 affected by pedigree structure, which might imply an absence of active inbreeding
305 preference or avoidance, and that recruitment and subsequent mating among females'
306 descendants does not depend on paternity. Indeed, there is little evidence of active
307 inbreeding avoidance (or preference) through social pairing or extra-pair reproduction in
308 song sparrows (Reid et al. 2015), and no genetic correlation between female extra-pair
309 reproductive rate and the subsequent survival (to recruitment) of her offspring (Reid 2012),
310 but pre-reproductive mortality may differ somewhat between females' within-pair versus
311 extra-pair offspring offspring (Sardell et al. 2011). To examine the potential implications of
312 this assumption, we additionally quantified differences in k at the level of individual cohorts,
313 where the social and genetic pedigrees differed only in the sires of individuals in that cohort,
314 and not in previous years, to quantify the effects of extra-pair reproduction on the potential
315 for inbreeding within that cohort. In doing so, we lose effects of polyandry on different
316 degrees of relationships and relatedness in the population that are generated across
317 multiple generations, but gain additional insight on the effects of polyandry within a single
318 generation.

319 To quantify differences in k at the level of individual cohorts, we modified the social
320 pedigree such that, beginning in ~1993, paternity was assigned to true genetic sires (i.e., a
321 female's socially-paired or extra-pair male) up to year $t-1$ (where t represents the year of
322 hatching for the focal cohort) and to a female's socially-paired males in year t . We then
323 calculated pairwise k from this modified social pedigree (k_{SOC_cohort}) for all possible matings
324 of offspring produced in year t which survived to independence from parental care (~24
325 days after hatching). We quantified differences in relatedness for independent offspring in
326 year t rather than adults in year $t+1$ to ensure adequate sample sizes for each cohort (mean
327 = 2577.5 ± 1476.8 possible cross-sex matings per cohort, range 1665–6048).

328 Because 'relationships' within each cohort are restricted to full- and half-sibs, single
329 and half-single first cousins, and double first cousins (because all offspring are hatched in
330 the same year) unlike our main analyses which incorporate overlapping generations, we
331 binned values of pairwise k into six categories to evaluate whether differences in the
332 number of possible matings given the genetic rather than modified social pedigree were
333 greater among females and their closely (i.e., higher values of k) or more distantly related
334 (i.e., lower values of k) possible mates. Categories of k were: (1) $k \geq 0.25$; (2) $0.125 \leq k <$
335 0.25 ; (3) $0.0625 \leq k < 0.125$; (4) $0.0313 \leq k < 0.0625$; (5) $0.00 < k < 0.0313$; and (6) $k = 0$,
336 where $k = 0.25, 0.125, 0.0625, 0.0313$, and 0 represent matings among outbred full-sibs,
337 half-sibs, single first cousins, half-single first cousins, and unrelated individuals, respectively.
338 There were fewer possible matings among close relatives (i.e., $k \geq 0.25$) and more possible
339 matings among distant relatives (i.e., $0.00 < k < 0.03125$) given the genetic pedigree
340 versus the modified social pedigree within cohorts (table S6). However, there was little
341 change in the mean number of possible matings among pairs with intermediate levels of

342 kinship ($0.03125 \leq k < 0.25$), and no change in the number of possible matings among
343 unrelated pairs (table S6). We further evaluated the proportion of females that experienced
344 an increase, decrease, or no change in the number of matings in each kinship category.
345 Proportionally, ~38% of females had fewer possible matings at $k \geq 0.25$ given the genetic
346 pedigree versus the modified social pedigree across cohorts, but 57% of females
347 experienced no change in the number of possible matings in this kinship category given the
348 genetic pedigree (table S7). Higher proportions (~47% and 40%, respectively) of females
349 experienced decreases in the number of matings at kinship levels greater than 0.0625 but
350 less than 0.125 given the genetic pedigree, but more females experienced increases in the
351 number of matings given the genetic pedigree at $0.125 \leq k < 0.25$ and $0.00 < k < 0.03125$
352 (table S7). Thus, differences in (k_{SOC_cohort}) and (k_{GEN}) within cohorts appear to be driven by
353 fewer possible matings at $k \leq 0.25$ and more possible matings at $0.00 < k < 0.03125$, leading
354 to greater differences in k at these levels of kinship, whereas increases/decreases in the
355 number of matings at intermediate levels cancel each other out, leading to smaller
356 differences in mean k (table S6).

357 **Table S6:** Mean \pm SD (and range) of the number of possible matings independent (from
 358 parental care) female song sparrows experienced with all independent males in their cohort
 359 in six categories of pairwise kinship (k) given a modified social pedigree (k_{SOC_cohort}) among
 360 their parents, and given the genetic pedigree (k_{GEN}). Mean difference denotes the mean
 361 decrease (negative values) or increase (positive values) in the number of matings at each
 362 kinship level given the genetic pedigree. Analyses include 391 individual females across
 363 eight cohorts. Z and p denote Z value of the Wilcoxon rank sum test statistic and associated
 364 p value. Kinship categories where frequencies decreased or increased significantly given the
 365 genetic pedigree rather than the social pedigree are highlighted in bold.

366

Relatedness category	k_{SOC_cohort}	k_{GEN}	Mean difference	Z (p)
$k \geq 0.25$	2.00 \pm 1.59 (0-7)	1.43 \pm 1.44 (0-6)	-0.57 \pm1.21 (-6-3)	5.3 (<0.001)
$0.125 \leq k < 0.25$	8.66 \pm 7.30 (0-33)	9.38 \pm 7.62 (0-37)	+0.72 \pm 4.51 (-22-26)	1.4 (0.16)
$0.0625 \leq k < 0.125$	31.10 \pm 14.16 (1-79)	30.10 \pm 13.60 (1-77)	-1.00 \pm 6.76 (-57-24)	0.8 (0.41)
$0.03125 \leq k < 0.0625$	9.86 \pm 9.61 (0-55)	10.35 \pm 10.28 (0-65)	+0.49 \pm 6.28 (-23-55)	0.1 (0.94)
$0.00 < k < 0.03125$	1.11 \pm 2.47 (0-21)	1.47 \pm 3.00 (0-23)	+0.36 \pm1.79 (-6-18)	2.6 (0.01)
$k = 0$	0.00 \pm 0.00 --	0.00 \pm 0.00 --	0.00 \pm 0.00 --	0.0 (1.00)

367

368 **Table S7:** Absolute and proportional (%) number of independent (from parental care)
 369 female song sparrows that experienced a decrease, increase, or no change in the number of
 370 possible matings with independent males in their cohort across six categories of pairwise
 371 kinship (k) given the genetic pedigree (k_{GEN}) versus given the modified social pedigree
 372 (k_{SOC_cohort}) among their parents. Analyses include 391 individual females across eight
 373 cohorts.

374

Relatedness category	Decrease given genetic pedigree	Increase given genetic pedigree	No change
$k \leq 0.25$	147 (37.6%)	21 (5.4%)	223 (57.0%)
$0.125 \leq k < 0.25$	109 (27.9%)	191 (48.8%)	91 (23.3%)
$0.0625 \leq k < 0.125$	182 (46.6%)	158 (40.4%)	51 (13.0%)
$0.0313 \leq k < 0.0625$	155 (39.6%)	147 (37.6%)	89 (22.8%)
$0.00 < k < 0.03125$	22 (5.6%)	81 (20.7%)	288 (73.7%)
$k = 0$	0 (0%)	0 (0%)	391 (100%)

375

376

Literature cited

377 Archie, E. A., J. A. Hollister-Smith, J. H. Poole, P. C. Lee, C. J. Moss, J. E. Maldonado, R. C.
378 Fleischer, et al. 2007. Behavioural inbreeding avoidance in wild African elephants. *Molecular*
379 *Ecology* 16:4138–4148.

380 Brouwer, L., M. Van De Pol, E. Atema, and A. Cockburn. 2011. Strategic promiscuity helps
381 avoid inbreeding at multiple levels in a cooperative breeder where both sexes are
382 philopatric. *Molecular Ecology* 20:4796–4807.

383 Gerlach, G., and N. Lysiak. 2006. Kin recognition and inbreeding avoidance in zebrafish,
384 *Danio rerio*, is based on phenotype matching. *Animal Behaviour* 71:1371–1377.

385 Power, D. J., and L. Holman. 2014. Polyandrous females found fitter populations. *Journal of*
386 *Evolutionary Biology* 27:1948–1955.

387 Reid. 2012. Predicting evolutionary responses to selection on polyandry in the wild: additive
388 genetic covariances with female extra-pair reproduction. *Proceedings of the Royal Society of*
389 *London B* 279:4652–4660.

390 Reid, J. M., P. Arcese, L. F. Keller, R. R. Germain, A. B. Duthie, S. Losdat, M. E. Wolak, et al.
391 2015. Quantifying inbreeding avoidance through extra-pair reproduction. *Evolution* 69:59–
392 74.

393 Sardell, R. J., P. Arcese, L. F. Keller, and J. M. Reid. 2011. Sex-specific differential survival of
394 extra-pair and within-pair offspring in song sparrows, *Melospiza melodia*. *Proceedings of the*
395 *Royal Society of London B* 278:3251–3259.

396 Stow, A. J., and P. Sunnucks. 2004. Inbreeding avoidance in Cunningham's skinks (*Egernia*
397 *cunninghami*) in natural and fragmented habitat. *Molecular Ecology* 13:443–447.

398