1   **MacPherson et al. Supplementary Materials**

2   **Deriving a general expression for local adaptation -** Local adaptation is most effectively defined as the

3   difference between the expected fitness of individuals tested in their local environment and the

4   expected fitness of individuals in all possible environments [1]. To express this mathematically, let $\overline{W}_{\alpha,\beta}$

5   be the expected fitness of individuals from population α in environment β. Local adaptation, δ, is then

6   given by the difference:

7      $$\delta = E_\alpha[\overline{W}_{\alpha,\alpha}] - E_{\alpha,\beta}[\overline{W}_{\alpha,\beta}] \qquad \text{(S1)}$$

8   where the notation $E_j[*]$ expresses the expectation of $[*]$ taken over index j. Equation (S1) can be

9   written more insightfully if we assume individual fitness depends on the extent to which an individual's

10   vector of trait values, z, matches the optimal values favored by conditions in environment α, θ_α.

11   Specifically, we assume the fitness of individual i from population α in environment β is given by:

12     $$W_{\alpha,\beta}(z_i) = e^{-\gamma \sum_{t=1}^{n}(z_{i,t} - \theta_{t,\beta})^2} \qquad \text{(S2)}$$

13   Where γ measures the strength of stabilizing selection, and the sum is over the n traits influencing

14   fitness.   If we assume that stabilizing selection is relatively weak (i.e. $\gamma \approx 0$) then (S2) can be

15   approximated by the first two terms of its taylor expansion with respect to γ.

16     $$W_{\alpha,\beta}(z_i) \approx 1 - \gamma \sum_{t=1}^{n}(z_{i,t} - \theta_{t,\beta})^2 + \mathcal{O}(\gamma^2) \qquad \text{(S3)}$$

17   Equation (S3) can now be used to calculate the average finesses in equation (S1). The first of

18   these average finesses $\overline{W}_{\alpha,\alpha}$ is given by:

19     $$\overline{W}_{\alpha,\alpha} = E_i[W_{\alpha,\alpha}(z_i)] \approx 1 - \gamma \sum_{t=1}^{n}\left[(\bar{z}_{t,\alpha} - \theta_{t,\alpha})^2 + Var_i[z_{i,t}]\right] + \mathcal{O}(\gamma^2) \qquad \text{(S4a)}$$

20   and similarly the second expectation $\overline{W}_{\alpha,\beta}$ is given by:

21     $\bar{W}_{\alpha,\beta} = E_i\big[W_{\alpha,\beta}(z_i)\big] \approx 1 - \gamma \sum_{t=1}^{n}\Big[\big(\bar{z}_{t,\alpha} - \theta_{t,\beta}\big)^2 + Var_i\big[z_{i,t}\big]\Big] + \mathcal{O}(\gamma^2)$ (S4b)

22   Where $\bar{z}_{t,\alpha}$ is the average value of trait t in population α. The notation $Var_j[*]$ is the variance of $[*]$ with

23   respect to index j. Taking the expectation of (S4a) and (S4b) over α and β gives the two terms in (S1).

24   Let $\hat{z}_t$ be the global average value of trait t and $\hat{\theta}_t$ the global average phenotypic optima of trait t. Then:

25     $E_\alpha\big[\bar{W}_{\alpha,\alpha}\big] \approx 1 - \gamma \sum_{t=1}^{n}\Big(\hat{z}_t^{\,2} + Var_\alpha\big[\bar{z}_{t,\alpha}\big] + E_\alpha\big[Var_i\big[z_{i,t}\big]\big] - 2Cov_\alpha\big(\bar{z}_{t,\alpha},\theta_{t,\alpha}\big) + \hat{\theta}_t^{\,2} + Var_\alpha\big[\theta_{t,\alpha}\big]\Big) +$

26     $\mathcal{O}(\gamma^2)$ (S5a)

27   describes the average fitness of populations in their local environments and:

28     $E_{\alpha,\beta}\big[\bar{W}_{\alpha,\beta}\big] \approx 1 - \gamma \sum_{t=1}^{n}\Big(\hat{z}_t^{\,2} + Var_\alpha\big[\bar{z}_{t,\alpha}\big] + E_\alpha\big[Var_i\big[z_{i,t}\big]\big] - \hat{\theta}_t^{\,2} + Var_\beta\big[\theta_{t,\beta}\big]\Big) + \mathcal{O}(\gamma^2)$ (S5b)

29   describes the average fitness of populations across all possible environments. In (S5), $Cov_j[*]$ is the

30   covariance of $[*]$ over index j. Taking the difference between (S5a) and (S5b) shows that local

31   adaptation is given by:

32     $\delta \approx 2\gamma \sum_{t=1}^{n}\Big(Cov_\alpha\big(\bar{z}_{t,\alpha},\theta_{t,\alpha}\big)\Big) + \mathcal{O}(\gamma^2)$ (S6)

33   which is equation (2) of the main text.

34   **Trait Evolution-**The first section of this appendix showed that local adaptation at any particular point in

35   time can be approximated using equation (S6). Equation (S6) suggests that local adaptation should

36   increase with the number of traits under selection simply because the total strength of selection

37   accumulates as traits are added. However, this simple logic holds true only if increasing the number of

38   traits, n, does not systematically reduce the values of $Cov_\alpha\big(\bar{z}_{t,\alpha},\theta_{t,\alpha}\big)$ that ultimately evolve within the

39   metapopualtion. We next explore how the number of traits under selection, n, influences the evolution

40   of this important covariance by developing expressions for the change in the vector of population mean

41   phenotypes that occurs within each population. As long as selection is weak, the additive genetic

42 variance/covariance matrix is fixed over time, and phenotypes are multivariate normally distributed, we

43 can predict the change in the vector of population mean phenotypes which occurs in response to

44 selection within population α using the multivariate breeder's equation:

45 $\quad \Delta \bar{z}_{t,\alpha} = G \frac{1}{\overline{W}_{\alpha,\alpha}} \frac{\partial \overline{W}_{\alpha,\alpha}}{\partial \bar{z}_{t,\alpha}}$ (S7)

46 where G is the additive genetic variance/covariance matrix and $\overline{W}_{\alpha,\alpha}$ is the population mean fitness

47 within population α.

48 $\quad$ Substituting (S4a) into (S7) yields the following expression for the mean value of trait t within

49 popualtion α after a single bout of selection and mating:

50 $\quad \bar{z}_{t,\alpha}' \approx \bar{z}_{t,\alpha} - 2\gamma \sum_{k=1}^{n} \left(\left(\bar{z}_{k,\alpha} - \theta_{k,\alpha} \right) \right) + \epsilon_t + \mathcal{O}(\gamma^2)$ (S8)

51 where ϵ_t is a random deviation in the mean phenotype caused by genetic drift and is drawn from a

52 multivariate normal distribution with mean zero and covariance matrix $\frac{G}{N}$. To incorporate the impact of

53 gene flow we assume individuals move among populations at rate of m according to an island model.

54 Assuming m is of the same small order as γ, the phenotypic mean of trait t, within population α, after a

55 single round of gene flow is:

56 $\quad \bar{z}_{t,\alpha}'' \approx \bar{z}_{t,\alpha}' + m(\hat{z}_t - \bar{z}_{t,\alpha}) + \mathcal{O}(\gamma^2)$ (S9)

57 $\quad$ Although (S9) can, in principle, be used to predict the crucial quantity $Cov_\alpha(\bar{z}_{t,\alpha}, \theta_{t,\alpha})$ upon

58 which local adaptation depends, this rapidly becomes intractable as the number of populations

59 increases. Previous studies have sidestepped this increasing complexity by addressing phenotypic

60 differences between populations [2, 3] rather than local adaptation as it is commonly measured in

61 empirical studies. Because our goal is to predict values of local adaptation a measured using reciprocal

62   transplant studies we must confront this challenge directly. In the next section, we will develop a

63   moment based approach which allows us to overcome this practical hurdle.

64   **Evaluating Local Adaptation at equilibrium-** The key to developing analytical predictions for the

65   evolution of local adaptation within large metapopulations is to recognize that population mean trait

66   values can be descried more conveniently as a multivariate frequency distribution. With this realization,

67   it becomes clear that evolution can be tracked by following the statistical moments describing this

68   distribution rather than by following the population mean values within each population [4, 5]. Because

69   equation (S6) shows that one of these statistical moments, $Cov_\alpha(\bar{z}_{t,\alpha}, \theta_{t,\alpha})$, is the key to quantifying

70   local adaptation, we begin by predicting how this particular statistical moment evolves. Using nothing

71   more than the standard definition of a covariance, it is possible to write down an expression for the

72   value of $Cov_\alpha(\bar{z}_{t,\alpha}, \theta_{t,\alpha})$ in the next generation:

73    $$Cov_\alpha(\bar{z}_{t,\alpha}, \theta_{t,\alpha})'' = E_\alpha\left[\left(\bar{z}_{t,\alpha}'' - \hat{z}_t''\right)\left(\theta_{t,\alpha} - \hat{\theta}_t\right)\right] \quad\quad\quad\quad (S10)$$

74   The only two quantities that are time dependent in (S10a) are $\bar{z}_{t,\alpha}''$ and $\hat{z}_t''$. The expression for the

75   former was derived above in (S9) and the later can the found by taking the expectation of (S9) over α.

76   This leads to the following expression for $\hat{z}_t''$.

77    $$\hat{z}_t'' = \hat{z}_t - 2\gamma \sum_{k=1}^{n} \mathbf{G}_{tk}\left(\hat{z}_t - \hat{\theta}_t\right) \quad\quad\quad\quad (S11)$$

78   Substituting (S9) and (S11) into (S10) gives the following expression for the change in $Cov_\alpha(\bar{z}_{t,\alpha}, \theta_{t,\alpha})$

79   over a single generation:

80    $$\Delta Cov_\alpha(\bar{z}_{t,\alpha}, \theta_{t,\alpha}) = -2\gamma \sum_{k=1}^{n} G_{t,k}\left(Cov_\alpha(\bar{z}_{k,\alpha}, \theta_{t,\alpha}) - Cov_\alpha(\theta_{k,\alpha}, \theta_{t,\alpha})\right) - m\, Cov_\alpha(\bar{z}_{t,\alpha}, \theta_{t,\alpha}) \text{ (S12a)}$$

81   Inspection of this expression reveals the remarkable fact that, at least in the case of weak selection and

82   gene flow, the evolution of local adaptation is completely described by $Cov_\alpha(\bar{z}_{t,\alpha}, \theta_{t,\alpha})$ and

83      $Cov_\alpha(\bar{z}_{k,\alpha}, \theta_{t,\alpha})$. Note that $Cov_\alpha(\theta_{k,\alpha}, \theta_{t,\alpha})$ cannot evolve and thus does not depend on time. Hence,

84   to form a complete description of the evolution of local adaptation requires only (S12a) and the

85   following expression for the change in $Cov_\alpha(\bar{z}_{k,\alpha}, \theta_{t,\alpha})$:

86      $\Delta Cov_\alpha(\bar{z}_{t,\alpha}, \theta_{j,\alpha}) = -2\gamma \sum_{k=1}^{n} G_{t,k} \left(Cov_\alpha(\bar{z}_{k,\alpha}, \theta_{j,\alpha}) - Cov_\alpha(\theta_{k,\alpha}, \theta_{j,\alpha}) \right) - m\, Cov_\alpha(\bar{z}_{t,\alpha}, \theta_{j,\alpha})$ (S12b)

87   Because equations (S12) depend on no other moments they define a closed system and can thus be

88   used for studying the evolution of local adaptation. The fact that ϵ_t is absent from (S12) demonstrates

89   that drift does not influence the evolution of local adaptation, as has been shown previously for a similar

90   model [4]. Predicting local adaptation at evolutionary equilibrium requires evaluating (S6) at the point

91   where the system of equations in (S12) are simultaneously zero. Unfortunately, finding and simplifying

92   this equilibrium expression becomes cumbersome for large numbers of traits without further

93   manipulation.

94   To simplify the equilibrium expression for local adaptation, we define a matrix, $\mathbf{\Theta}$, as the

95   variance-covariance matrix of optimal trait values across the metapopulation. For any number

96   of traits, n, the expression for local adaptation is complicated by products between elements of

97   the environmental variance-covariance matrix, $\mathbf{\Theta}$, and the genetic variance covariance matrix,

98      $\boldsymbol{G}$. Many of these terms can, however, be eliminated by defining new uncorrelated traits, given

99   by the principal components of $\boldsymbol{G}$. Before performing this coordinate rotation, however, it is

100   important that each of the original traits be measured in equivalent units to prevent distortion.

101   Although in some cases traits will already meet this criteria, in general, some form of

102   standardization, such as conversion to units of standard deviations, will be necessary.

103   Without risk of distortion we can now perform the coordinate rotation into the principal

104   component space of G, which is represented by the spanning set A defined by the eigenvalues

105   of G:

106      $A = \{e_1, e_2, \dots, e_n\}$ (S13)

107   where e_i is the ith eigenvector of G. If we let G' be the representation of G in the principal

108   component basis:

109      $G' = A^{-1}.G.A$ (S14a)

110   And similarly for the matrix Θ:

111      $\Theta' = A^{-1}.\Theta.A$ (S14b)

112   It is important to note that the matrix A used in equation (S14) is defined by the eigenvectors of

113   the G matrix not those of the Θ matrix.

114   The only other variable in our equilibrium solution for local adaptation which involves

115   units of trait value, and hence must be transformed, is the strength of selection, γ. Here, our

116   assumption that selection is equivalent on every trait is convenient because it assures that the

117   fitness surface is circular. Since the above basis transformation represents a coordinate rotation

118   without scaling or translation, the strength of selection on the principal components will be

119   equivalent to that on the original traits. With this coordinate rotation the equilibrium

120   expression for local adaptation simplifies to:

121      $\hat{\delta} = 4\gamma^2 \sum_{t=1}^{n} \frac{G'_{t,t}\Theta'_{t,t}}{m+2\gamma G'_{t,t}}$ (S15)

122   which is equation (4) of the main text.

123   **Individual Based Simulations —** Although our analytical solution (S15) is quite general, it does

124   rely on some important assumptions. The most important of these are weak selection and a

125   fixed additive genetic variance/covariance matrix. In order to relax these assumptions, and

126   evaluate the robustness of our analytical approximation, we developed and analyzed individual

127   based simulations.   These individual based simulations assumed a life cycle consisting of

128   selection, gene flow, and mating/reproduction. In the paragraphs below, we describe the

129   details behind each step of this life cycle.

130   *Stabilizing selection:*

131   To simulate selection, we begin by calculating the fitness of individuals using equation

132   (S2) rather than the approximation given by equation (S3). An individual's fitness represents its

133   probability of surviving to produce offspring. Specifically, selective mortality was simulated by

134   drawing a random number between 0 and 1 for each individual; individuals died and were

135   removed from the population if this number was greater than their fitness but survived and

136   remained within the population otherwise.

137   *Gene Flow:*

138   Individuals surviving selection were allowed to move between populations. As in the

139   analytical model, simulations assumed movement among any pair of populations was equally

140   likely and occurred at rate m. Gene flow was implemented by drawing a random number

141   between 0 and 1 for each individual; if this number was less than m, the individual moved to

142   another population whose identity was determined by drawing a random integer between 1

143   and the number of populations.   For large values of m, movement among populations could

144 significantly alter local population sizes, and, in extreme cases, result in stochastic extinction of

145 some populations, particularly when coupled with strong selection. In those rare cases where

146 this occurred, the simulation was aborted and rerun.

147 *Mating and Reproduction:*

148   The system of mating was particularly important in these simulations since it is in this

149 step that the shape of the G matrix was incorporated. To produce the next generation,

150 parental pairs were drawn at random from within each population with replacement. Each

151 parental pair produced a single offspring whose phenotype was drawn from a multivariate

152 normal distribution with a vector of means equal to the average phenotype of the parents, and

153 a variance covariance matrix given by the desired G matrix. This process continued until an

154 offspring population of a size equal to the size of the parental population before selection was

155 produced. The parental population was then eliminated.

156 *Analysis:*

157   Simulations were run for metapopulations containing 200 demes, each of which

158 contained 400 individuals. The trait optima for each environment were drawn randomly at the

159 beginning of the simulation from a multivariate normal distribution specified by a given

160 variance-covariance matrix centered about 0. Simulations were run to equilibrium with

161 equilibrium identified by plotting the average trait value as a function of time and inspecting

162 the final slope of this curve.

163   To analyze the accuracy of the analytical prediction, the level of local adaptation at

164 equilibrium was measured in two different ways. First we calculated local adaptation using the

165   exact definition given by equation (S1). Second, we calculated local adaptation using the

166   analytical approximation given by equation (S15).To calculate local adaptation using the exact

167   definition (S1), a reciprocal transplant experiment was simulated where the fitness of all

168   individuals were measured within all possible environments. In order to test our analytical

169   approximation, we then calculated local adaptation using the approximate expression (S15).

170   The use of (S15) required us to calculate the realized Θ matrix and realized P matrix, which was

171   used as a proxy for G. This use of P results in an additional complication of this measurement

172   of local adaptation because, in contrast to our analytical model, the simulations do not

173   explicitly assume that that there is equal variance in each trait. Hence trait value

174   standardization is necessary; this standardization was performed on the Θ matrix and P matrix

175   by dividing the $(t, k)^{th}$ component of each matrix by the phenotypic standard deviation of the

176   t^{th} trait and the phenotypic standard deviation of the kth trait. Let $\widetilde{\Theta}$ and $\widetilde{G}$ be the

177   standardized version of the Θ and P matrices.

178    $$\widetilde{\Theta} = \begin{bmatrix} \dfrac{\Theta_{11}}{G_{11}} & \cdots & \dfrac{\Theta_{1n}}{\sqrt{G_{nn}}\sqrt{G_{11}}} \\ \vdots & \vdots & \vdots \\ \dfrac{\Theta_{1j}}{\sqrt{G_{11}}\sqrt{G_{nn}}} & \cdots & \dfrac{\Theta_{nn}}{G_{nn}} \end{bmatrix} \tag{S16}$$

179

180    $$\widetilde{G} = \begin{bmatrix} 1 & \cdots & \dfrac{P_{1n}}{\sqrt{G_{nn}}\sqrt{G_{11}}} \\ \vdots & 1 & \vdots \\ \dfrac{P_{1j}}{\sqrt{G_{11}}\sqrt{G_{nn}}} & \cdots & 1 \end{bmatrix} \tag{S17}$$

181

182   It is then possible to use the same technique described in equations (S12) through (S14) to

183   generate principal component representations of these two matrices. In order to use the

184   analytical prediction described by equation (S15) it is also necessary to standardize the strength

185   of selection. For a single trait one could simply multiply γ by the genetic variance. However,

186   when multiple traits are involved this procedure is complicated by the fact that multiple genetic

187   variances exist.   Fortunately, at equilibrium the genetic variances across traits are fairly

188   uniform so standardizing by the average genetic (phenotypic) variance seemed reasonable.

189   This however will introduce small levels of error in our analytical prediction especially when

190   dimensionality is large. However, considering the concurrence between many of the

191   simulations and analytical predictions with high trait dimensionalities this does not seem to

192   present much of a problem.

193   Simulations were run for strengths of selection ranging from 0.001 to 0.05 and three

194   different correlation regimes; high (+0.9,-0.1), moderate (+0.5,-0.05), and low (+0.1,-0.01). We

195   then compared the value of local adaptation calculated using the exact definition (S1) and the

196   analytical approximation (S15) for between one and eight traits for each parameter

197   combination (Figures S1-S6).

198   **Estimating dimensionality from reciprocal transplant data** — To estimate dimensionality from

199   published datasets, we adapted the method of Hohenlohe & Arnold [6]. In brief, the method

200   requires a matrix of measurements of fitness from reciprocal transplant experiments, where

201   the matrix is formed by pairwise trials of individuals from source populations tested at different

202   sites (In the original analysis [6], the data were measures of mating success from pairwise

203   mating trials of males and females sampled from the same or different populations. Here are

204   analogously using the same approach on measures of fitness, estimated from testing individuals

205   from different populations against either their home or a different environment). The method

206   then fits points representing the mean phenotype of each source population and the selective

207   optimum of each site in a d-dimensional space, such that the distances between phenotypic

208   means and optima best match the observed fitness data across all cells of the matrix, as

209   follows. The first step is to specify a model of fitness as a function of the distance between the

210   local optimum and the mean phenotype of the source population, and here we analyzed two

211   types of fitness data, requiring two different models. Viability data, in the form of k survivors

212   out of n individuals for each population-site pair, were analyzed with a binomial model, exactly

213   as described by Hohenlohe & Arnold [6]. Briefly, for any pairwise source population and site,

214   the probability of survival in the binomial model is given by the height of a multivariate

215   Gaussian fitness surface, measured at the source population phenotypic mean. The selective

216   optimum of the site is at the peak of the Gaussian surface, which also has no covariance and

217   equal variance across site optima (i.e. uniform stabilizing selection and no correlational

218   selection).

219   For fitness measurements on a continuous scale (either fecundity or a composite fitness

220   measure), we used a modification of the multivariate Gaussian fitness surface model described

221   above and in Hohenlohe & Arnold [6]. Because scaling and rotation of the space are arbitrary,

222   we scale the space by phenotypic (co)variance within each population. The variance of each

223   site's fitness surface along each axis was assumed to be $\omega = 10$. Choosing higher or lower values

224   of ω had a negligible effect on fitting the points or on estimates of dimensionality; essentially

225   this parameter re-scaled the space, but not the points' relative positions or the likelihood of any

226 particular arrangement. Fitness at each optimum was taken to be the maximum fitness

227 measured in any cell of the matrix. Given the positions of any site optimum and source

228 population mean phenotype in the space, the expected fitness of an individual from that

229 population tested at that site is calculated from the Gaussian fitness surface. Variance around

230 this expectation was set equal to the square of the mean fitness across all site-population

231 comparisons. These parameter assumptions were based on maximizing the fit of the model to

232 simulated datasets where dimensionality is known. Software to conduct this analysis is

233 available online at (http://webpages.uidaho.edu/hohenlohe/software.html).

234   The method then fits points in the d-dimensional space by maximum likelihood, based

235 on the binomial or Gaussian model of fitness described above [6]. The log likelihood for any

236 particular arrangement of points in d-dimensional space is calculated by summing log

237 likelihoods of the data given the distance between the two points for each source

238 population/site pair, allowing us to find the maximum likelihood arrangement of points for any

239 value of d by heuristic hill-climbing algorithms (see Hohenlohe & Arnold [6]). The likelihood for

240 each value of d is used to find the best value of d given the data using information criteria. We

241 calculated corrected AIC (AICc), BIC, and HQC [7]. BIC consistently supported lower

242 dimensionality than the other two measures; here we report results from AICc. We also

243 calculated the effective dimensionality n_D when points representing population mean

244 phenotypes and selective optima are fit in a high-dimensional space (here we used the total

245 number of source populations or sites as the maximum value of d, beyond which additional

246 axes do not add to the likelihood). The n_D statistic is calculated as the sum of eigenvalues of the

247 covariance matrix of points, divided by the leading eigenvalue [8].

248   We gathered data from all studies analyzed by Hereford [9] that met the following

249   criteria: at least 3 source populations and sites, a full reciprocal transplant matrix (i.e. all

250   pairwise fitness measures were available), and sample sizes available. In these 35 datasets

251   (Table S2), fitness measures took the form of either viability (n=18), which we analyzed with a

252   binomial model [6], fecundity, or a composite fitness measure (n=17), which we analyzed with

253   the continuous Gaussian fitness model described above. We calculated local adaptation for

254   each dataset as in Equation (1) of the main text. We tested the correlation between local

255   adaptation and dimensionality (either the AICc estimate of d, or n_D; see Figure S7) across all

256   datasets and within each model type (binomial and Gaussian). We repeated the analysis after

257   log-transforming the fecundity fitness measures, and both correlations (local adaptation with d

258   and n_D) remained significant (Figures S10, S11). We also corrected for non-independence of

259   datasets from the same published study or the same reciprocal transplant experiment by using

260   these as random effects factors in a linear mixed model, using the R package lme(). For each, a

261   likelihood ratio test was used to compare models with and without dimensionality as a factor.

262   The dimensionality method does not take into account which population came from

263   which site; that is, it does not treat "home" or "away" differently in any way. To verify that the

264   dimensionality estimate is not biased by local adaptation, we randomly permuted all 17

265   continuous-fitness data matrices. This produces a set of matrices for which local adaptation has

266   mean zero. We applied the dimensionality analysis to these datasets and found no correlation

267   between local adaptation and dimensionality. We also found no correlation between local

268   adaptation and dimensionality across many permutations of single empirical matrices as well as

269   randomly generated datasets.

13

270   Finally, we tested the dimensionality estimation method against data produced from the

271 simulation approach described above. We simulated datasets in a full factorial design across

272 the following parameter values: m = 0.01, 0.001; γ = 0.001, 0.1; number of traits from 2 to 8;

273 and alignment or misalignment between G and Theta as shown in Figure 1, plus the case of no

274 covariance in both matrices. Each simulation included 6 populations tested in six sites in a

275 complete reciprocal transplant experiment, with fitness measured for 100 randomly sampled

276 individuals in each pair. We estimated dimensionality as described above under the continuous

277 fitness model. Effective dimensionality (n_D) was significantly correlated with local adaptation

278 across all parameter values (r^2 = 0.0355; p = 0.0257). It did not appear to be affected by

279 alignment (mean nD = 1.981) versus misalignment (mean nD = 1.979) or by other factors.

280

281   **Table S1:** Summary of notation

282

Expression	Equivalent Expression	Description
δ		Local adaptation
α, β		Population/ environment indices
t, k		Trait indices
i		Individual index
$E_j[*]$		Expectation of $[*]$ over index j
$E_{i,j}[*]$	$E_i\big[E_j[*]\big]$	Expectation of $[*]$ over index j then index i
$Var_j[*]$		Variance in $[*]$ over index j
$Cov_j[*]$		Covariance in $[*]$ over index j
$z_{i,t}$		The value of individual $i's$ trait t
$\bar{z}_{t,\alpha}$	$E_i\big[z_{i,t}\big]$	Average value of trait t in population α
$\hat{z}_t$	$E_\alpha\big[\bar{z}_{t,\alpha}\big] = E_{\alpha,i}\big[z_{i,t}\big]$	Global average value of trait t
$\theta_{t,\alpha}$		Phenotypic optima of trait t in environment α
$\hat{\theta}_t$	$E_\alpha\big[\theta_{t,\alpha}\big]$	Global average phenotypic optima for trait t
$W_{\alpha,\beta}(z_i)$		Absolute fitness of individual i from popualtion α in environment β
$\bar{W}_{\alpha,\beta}$	$E_i\big[W_{\alpha,\beta}(z_i)\big]$	Average fitness of population α in environment β
$\boldsymbol{G}$		Genetic Variance/Covariance matrix
$\boldsymbol{\Theta}$		Variance/Covariance matrix of phenotypic optima across the metapopulation
$\boldsymbol{G'}$		Diagonalized (principal component) $\boldsymbol{G}$
$\boldsymbol{\Theta'}$		$\boldsymbol{\Theta}$ rotated into the principal component space of $\boldsymbol{G}$

283

284

Table S2: Published reciprocal transplant datasets used in estimates of dimensionality.

Taxon	# populations	Fitness measure	Year	Local adaptation	Reference
Phlox drummondii	8	Viability	1980	0.1583	Schmidt & Levin 1985
Phlox drummondii	8	Fecundity	1980	0.1697	Schmidt & Levin 1985
Phlox drummondii	8	Composite	1980	0.3415	Schmidt & Levin 1985
Phlox drummondii	7	Viability	1979	0.1231	Schmidt & Levin 1985
Phlox drummondii	7	Fecundity	1979	0.3269	Schmidt & Levin 1985
Phlox drummondii	7	Composite	1979	0.4458	Schmidt & Levin 1985
Anondonta piscinalis	6	Viabiliaty	1990	0.0906	Jokela & Mutikainen 1995
Anondonta piscinalis	6	Viability	1990	0.0673	Jokela & Mutikainen 1995
Dactylis glomerata	6	Composite	1997	0.3671	Joshi et al 2001
Trifolium pratense	6	Composite	1997	0.2178	Joshi et al 2001
Plantago lanceolata	5	Viability	1975	-0.0815	Antonovics & Primack 1982
Plantago lanceolata	5	Composite	1997	0.0134	Joshi et al 2001

Plantago laneolata	4	Viability	1974	0	Antonovics & Primack 1982
Ranunculus adoneus	4	Viability	2000	0.0069	Baak & Stanton 2005
Ranunculus adoneus	4	Viability	2002	-0.0278	Baak & Stanton 2005
Agrostis stolonifera	4	Viability	1986	0.0455	Kik et al 1990
Aphidius ervi	4	Fecundity	1997	0.0385	Hufbauer 2002
Littorina saxatilis	3	Viability	1983	-0.016	Janson 1983
Littorina saxatilis	3	Viability	1995	0.1885	Rolan-Alvarez et al 1997
Littorina saxatilis	3	Viability	1995	0.0772	Rolan-Alvarez et al 1997
Plantago lanceolata	3	Viability	1983	0.0422	Van Tienderen & Van Der Torn 1991
Plantago lanceolata	3	Viability	1984	0.0284	Van Tienderen & Van Der Torn 1991
Artemisia tridentata	3	Viability	1995	0.0278	Wang et al 1997
Hordeum jubatum	3	Viability	1991	0.0833	Wang & Redmann 1996
Hordeum jubatum	3	Viability	1992	0.1111	Wang & Redmann 1996
Chamaecrista fasciculata	3	Fecundity	2005	0.4725	Etterson 2004
Lupinus guadelupensis	3	Fecundity	1995	-0.1369	Helenurm 1998

Hordeum spontaneum	3	Fecundity	1997	0.1239	Volis et al 2002
Hordeum spontaneum	3	Fecundity	1998	0.0721	Volis et al 2002
Artemisia tridentata	3	Fecundity	1995	0.2472	Wang et al 1997
Hordeum jubatum	3	Fecundity	1991	0.2847	Wang & Redmann 1996
Pennisetum setaceum	3	Fecundity	1990	0.0238	Williams et al 1995
Pennisetum setaceum	3	Fecundity	1991	0.0351	Williams et al 1995
Chamaecrista fasciculata	3	Composite	1996	0.2185	Galloway & Fenster 2000
Artemisia tridentata	3	Composite	2002	0.22	Miglia et al 2005

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297   **Figure S1:** The effect of dimensionality on the extent of local adaptation produced in individual based

298   simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200

299   deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium.   The

300   strength of selection varied stochastically about $\gamma = 0.001$. Traits and optimal values were drawn from

301   multivariate normal distribution with unit variances and the following correlations: Row A: ($\rho_G =$

302    $0.9, \rho_\Theta = 0.9$), Row B: ($\rho_G = -0.1, \rho_\Theta = -0.1$), Row C: ($\rho_G = 0.9, \rho_\Theta = -0.1$), and Row D: ($\rho_G =$

303    $-0.1, \rho_\Theta = 0.9$).

304   **Figure S2:** The effect of dimensionality on the extent of local adaptation produced in individual based

305   simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200

306   deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium.   The

307   strength of selection varied stochastically about $\gamma = 0.001$. Traits and optimal values were drawn from

308   multivariate normal distribution with unit variances and the following correlations: Row A: ($\rho_G =$

309    $0.5, \rho_\Theta = 0.5$), Row B: ($\rho_G = -0.05, \rho_\Theta = -0.05$), Row C: ($\rho_G = 0.5, \rho_\Theta = -0.05$), and Row D:

310   ($\rho_G = -0.05, \rho_\Theta = 0.5$).

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312   **Figure S3:** The effect of dimensionality on the extent of local adaptation produced in individual based

313   simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200

314   deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium.   The

315   strength of selection varied stochastically about $\gamma = 0.001$. Traits and optimal values were drawn from

316   multivariate normal distribution with unit variances and the following correlations: Row A: ($\rho_G =$

317    $0.1, \rho_\Theta = 0.1$), Row B: ($\rho_G = -0.01, \rho_\Theta = -0.01$), Row C: ($\rho_G = 0.1, \rho_\Theta = -0.01$), and Row D:

318   ($\rho_G = -0.01, \rho_\Theta = 0.1$).

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320 **Figure S4:** The effect of dimensionality on the extent of local adaptation produced in individual based

321 simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200

322 deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The

323 strength of selection varied stochastically about $\gamma = 0.005$. Traits and optimal values were drawn from

324 multivariate normal distribution with unit variances and the following correlations: Row A: ($\rho_G =$

325 $0.9, \rho_\Theta = 0.9$), Row B: ($\rho_G = -0.1, \rho_\Theta = -0.1$), Row C: ($\rho_G = 0.9, \rho_\Theta = -0.1$), and Row D: ($\rho_G =$

326 $-0.1, \rho_\Theta = 0.9$).

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328 **Figure S5:** The effect of dimensionality on the extent of local adaptation produced in individual based

329 simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200

330 deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The

331 strength of selection varied stochastically about $\gamma = 0.005$. Traits and optimal values were drawn from

332 multivariate normal distribution with unit variances and the following correlations: Row A: ($\rho_G =$

333 $0.5, \rho_\Theta = 0.5$), Row B: ($\rho_G = -0.05, \rho_\Theta = -0.05$), Row C: ($\rho_G = 0.5, \rho_\Theta = -0.05$), and Row D:

334 ($\rho_G = -0.05, \rho_\Theta = 0.5$).

335 **Figure S6:** The effect of dimensionality on the extent of local adaptation produced in individual based

336 simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200

337 deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The

338 strength of selection varied stochastically about $\gamma = 0.005$. Traits and optimal values were drawn from

339 multivariate normal distribution with unit variances and the following correlations: Row A: ($\rho_G =$

340 $0.1, \rho_\Theta = 0.1$), Row B: ($\rho_G = -0.01, \rho_\Theta = -0.01$), Row C: ($\rho_G = 0.1, \rho_\Theta = -0.01$), and Row D:

341 ($\rho_G = -0.01, \rho_\Theta = 0.1$).

342　**Figure S7:** The effect of dimensionality on the extent of local adaptation produced in individual based

343　simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200

344　deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The

345　strength of selection varied stochastically about $\gamma = 0.05$. Traits and optimal values were drawn from

346　multivariate normal distribution with unit variances and the following correlations: Row A: ($\rho_G =$

347　$0.9, \rho_\Theta = 0.9$), Row B: ($\rho_G = -0.1, \rho_\Theta = -0.1$), Row C: ($\rho_G = 0.9, \rho_\Theta = -0.1$), and Row D: ($\rho_G =$

348　$-0.1, \rho_\Theta = 0.9$).

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350　**Figure S8:** The effect of dimensionality on the extent of local adaptation produced in individual based

351　simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200

352　deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The

353　strength of selection varied stochastically about $\gamma = 0.05$. Traits and optimal values were drawn from

354　multivariate normal distribution with unit variances and the following correlations: Row A: ($\rho_G =$

355　$0.5, \rho_\Theta = 0.5$), Row B: ($\rho_G = -0.05, \rho_\Theta = -0.05$), Row C: ($\rho_G = 0.5, \rho_\Theta = -0.05$), and Row D:

356　($\rho_G = -0.05, \rho_\Theta = 0.5$).

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358　**Figure S9:** The effect of dimensionality on the extent of local adaptation produced in individual based

359　simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200

360　deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The

361　strength of selection varied stochastically about $\gamma = 0.05$. Traits and optimal values were drawn from

362　multivariate normal distribution with unit variances and the following correlations: Row A: ($\rho_G =$

363　$0.1, \rho_\Theta = 0.1$), Row B: ($\rho_G = -0.01, \rho_\Theta = -0.01$), Row C: ($\rho_G = 0.1, \rho_\Theta = -0.01$), and Row D:

364　($\rho_G = -0.01, \rho_\Theta = 0.1$).

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Figure S10. Correlation (r = 0.3995; p = 0.0174) between dimensionality, as estimated by effective

dimensionality nD, and local adaptation across 35 published datasets using fitness estimated as viability

(black), fecundity (red), or a composite fitness measure (blue). Symbols indicate different published

studies.

Figure S11. Correlation (r = 0.3716; p = 0.0280) between dimensionality, as estimated by corrected AIC,

and local adaptation across 35 published datasets using fitness estimated as viability (black), log-

transformed fecundity (red), or a composite fitness measure (blue). Symbols indicate different published

studies.

Figure S12. Correlation (r = 0.4072; p = 0.0152) between dimensionality, as estimated by effective

dimensionality nD, and local adaptation across 35 published datasets using fitness estimated as viability

(black), log-transformed fecundity (red), or a composite fitness measure (blue). Symbols indicate

different published studies.

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