

In this supplementary information, we do three things: derive the fitness function Equation (10) used in the main paper; calculate the ESS for the fitness function in Equation (10); more generally, demonstrate the method in solving for an ESS and ‘closing a model’ (writing relatedness in terms of model parameters).

### 0.1 Deriving the Fitness Function in the Text

Here, we derive the fitness function in Equation (10). If an individual survives (with probability  $k$ ), its fitness is 1; otherwise, with probability  $(1 - k)$ , its fitness is equal to its offsprings’ fitnesses. A proportion  $d$  compete globally, and therefore have fitness relative to the global average, which we assume to be 1 (the population is neither growing nor shrinking). A proportion  $1 - d$  remain locally, and their fitness is relative to the average fitness in the social group. After diffusion, the number of individuals on a patch is equal to the number of individuals produced on a patch that stay (with probability  $1 - d$ ) plus the number of individuals arriving from elsewhere ( $dN$ ) ([? ]). So, the total number of offspring on a patch after diffusion is:

$$(1 - d) [N + N (bZ (1 - Z) - cZ)] + dN = N[1 + (1 - d) (bZ (1 - Z) - cZ)]. \quad (1)$$

From this, we can write the fitness function in the text, Equation (10):

$$w(x, y, Z) = (1 - k) (d) (x (1 - c + by) + (1 - x) (1 + by)) + (1 - d) \frac{x (1 - c + by) + (1 - x) (1 + by)}{1 + (1 - d) (bZ (1 - Z) - cZ)} + k. \quad (2)$$

## 0.2 Calculating the ESS

To calculate the ESS for Equation (10), we use the Taylor–Frank approach. However, the solution is not analytically tractable. Instead, if we assume  $b$  and  $c$  to be small, we can write a first-order approximation of Equation (10) as

$$w(x, y) = (1 - k) [1 - cx + (1 - x)by - (bZ(1 - Z) - cZ)(1 - d)^2] + k. \quad (3)$$

We previously showed that relaxing the assumption of small  $b$  and  $c$  does not qualitatively alter the results ([? ]). From this, we can use the Taylor–Frank (1996) approach to solve for the ESS ([? ]). We take the derivative of fitness with respect to phenotype, solving for  $x = y = x^*$ , and candidate ESSs occur where:

$$\begin{aligned} \frac{dw}{dg} &= \frac{\partial w}{\partial x} + R \frac{\partial w}{\partial y} \\ &= -c - bx - (1 - d)^2 \left( -\left(\frac{c}{n}\right) - \frac{b(x + (-1 + n)x)}{n^2} + \frac{b\left(1 - \frac{x + (-1 + n)x}{n}\right)}{n} \right) + \\ &\quad r * \left( b(1 - x) - (1 - d)^2 \left( -\frac{c(-1 + n)}{n} - \frac{b(-1 + n)(x + (-1 + n)x)}{n^2} + \right. \right. \\ &\quad \left. \left. \frac{b(-1 + n)\left(1 - \frac{x + (-1 + n)x}{n}\right)}{n} \right) \right) \\ &= 0. \end{aligned} \quad (4)$$

Solving for  $x^*$ , we get:

$$x^* = \frac{cN - bNR + b(1-d)^2 - c(1-d)^2 - bR(1-d)^2 + cR(1-d)^2 + bNR(1-d)^2 - cNR(1-d)^2}{b(-N - NR + 2(1-d)^2 - 2R(1-d)^2 + 2NR(1-d)^2)}, \quad (5)$$

which is the ESS value of cooperation.

### 0.3 Writing Relatedness in Terms of Model Parameters

Equation (S5) gives the ESS in terms of  $R$  and other model parameters, but we expect  $R$  to depend on  $d$ ,  $k$ , and  $N$ . Here, we calculate  $R$  in terms of those parameters, though more generally any parameters may impact  $R$ , and the following approach readily extends to such cases. We start by determining the relatedness, at equilibrium, of a focal RNA molecule to a random molecule in its social group, including itself. This is known as whole-group relatedness (denoted by  $\mathbb{R}$ ), because it includes the focal individual, in contrast to others-only relatedness ( $R$ ), which does not include the focal individual ([? ]). Our model requires others-only relatedness, because  $y$  is the average of the individuals on the patch, excluding the focal individual.  $\mathbb{R}$  is the relatedness between two individuals drawn randomly from a local group with replacement. We can write this as the probability that those two individuals are the same individual ( $1/N$ ), and thus have relatedness 1, plus the probability that those two individuals are not the same ( $(N-1)/N$ ), and thus have the relatedness of two random individuals drawn without replacement, or others-only relatedness,  $R$ :

$$\mathbb{R} = \frac{1}{N} + \frac{N-1}{N}R \quad (6)$$

Equation (S6) is a general equation for relatedness, for any infinite population of individuals subdivided into  $N$  social groups. Now we take two individuals (without replacement) on the same patch with relatedness  $R$ , and determine the

relatedness of their representatives in the previous generation. With chance  $k^2$ , they are both survivors from the previous generation, in which case their relatedness is the same ( $R$ ). With chance  $2k(1 - k)$ , one is a survivor and the other is a new offspring, which is native with probability  $(1 - d)$ , in which case their relatedness is  $\mathbb{R}$ . Otherwise, with chance  $(1 - k)^2$ , they are both new offspring, are both native with probability  $(1 - d)^2$ , and thus have relatedness  $\mathbb{R}$ . Others-only relatedness between two individuals in the current generation is equal to

$$R_t = k^2 R_{t-1} + 2k(1 - k)(1 - d)\mathbb{R}_{t-1} + (1 - k)^2(1 - d)^2 \mathbb{R}_{t-1} \quad (7)$$

Here,  $R_t$  is relatedness in the current generation, or time step, and  $R_{t-1}$  and  $\mathbb{R}_{t-1}$  are others-only and whole-group relatednesses, respectively, in the previous one. Note that Equation (S7) was derived assuming that the only population processes affecting relatedness were survival and diffusion, but a similar recursion could be written taking into account any parameters that affect relatedness. Setting  $R_t = R_{t-1}$ , we find the equilibrium others-only relatedness. Plugging into equation (A5), we find the equilibrium value of whole-group relatedness,  $\mathbb{R}^*$ , to be:

$$\mathbb{R}^* = \frac{1 + k}{N + kN + 2k(1 - d) - 2kN(1 - d) + (1 - d)^2 - k(1 - d)^2 - N(1 - d)^2 + kN(1 - d)^2} \quad (8)$$

This equation for relatedness was identified by Taylor and Irwin 2000 ([? ]). However, our model in Equation (10) in the text is modelling an others only-trait, and thus requires others-only relatedness,  $R$ .  $\mathbb{R}N$  gives us the number of relatives on our patch. Subtracting the focal individual, and dividing by the total number of remaining individuals ( $N - 1$ ), gives us  $R^*$ :

$$R^* = \frac{\frac{N(1+k)}{(1+k)N - (N-1)(2k + (1-d) - k(1-d))(1-d)} - 1}{N-1} \quad (9)$$

Plugging into Equation (S5) gives us Equation (11) in the text.