promoting access to White Rose research papers



## Universities of Leeds, Sheffield and York http://eprints.whiterose.ac.uk/

These are supporting texts and figures for an author produced version of a paper published in **Developmental Biology**.

White Rose Research Online URL for this paper: <u>http://eprints.whiterose.ac.uk/10964</u>

#### Published paper

Irons, D.J., Wojcinski, A., Glise, B., Monk, N.A.M. (2010) *Robustness of positional specification by the Hedgehog morphogen gradient*, Developmental Biology, 342 (2), pp. 180-193 http://dx.doi.org/10.1016/j.ydbio.2010.03.022

White Rose Research Online eprints @whiterose.ac.uk

## Supporting Text

This supporting text is split into the following three sections

- 1. Description of simplified models.
- 2. Justification of parameter constraints.
- 3. Supplementary results and proofs (Results S1–S13).

The first section describes the derivation of a set of simplified models (A–C), which are used to generate analytic expressions concerning robustness (Equations (9)–(17), main text). The second section describes and justifies a number of constraints (C1–C10) that were used in estimating parameter from existing experimental data. The final section provides mathematical proofs that complement the results in the first two sections and in the main text.

#### 1 Description of simplified models

In order to analyse specific aspects of the full model, and to facilitate parameter estimation, we introduce three simplified models that focus on different aspects of gradient formation. Model A is a simple free diffusion model for Hedgehog movement, neglecting any effects of HSPGs. Model B simplifies the anterior compartment equations, so that the anterior gradient can be approximated as an exponential. To focus on feedbacks and regulation within the signalling pathway, Model C is a simplified model of the Hedgehog gradient in the anterior compartment. As can be seen in the figure below (Fig. ST1), Models B and C provide reasonable approximations to the full model.

Using these models, we can obtain approximations for the steady-state Hedgehog gradient in the full model, and for a number of quantities of relevance for our investigation of robustness, including  $\alpha_0$  (Eqns. (9) and (10)),  $x_P$  (Eqn. (11)),  $\alpha_A$  (Eqn. (13)),  $x_A$  (Eqn. (14)), g (Eqn. (15)) and  $\beta$  (Eqns. (16) and (17)).



Figure ST1: Steady state HH gradients in Models B and C (dashed line) compared to that in the full model (red line).  $\gamma(A) = 0.75k_{on}$  and  $\delta k_{on} = 0.6k_{on}$ , respectively. The remaining parameters are listed in Table 1 of main text.

#### Model A: Simplified free diffusion model

To address the role of regulated diffusion in the full model, we introduce a free diffusion model for Hedgehog gradient formation (for comparison with regulated diffusion models). As in the full model we represent the disc as a one dimensional cross section  $-L_A \leq x \leq L_P$ , with distinct equations for the posterior and anterior compartments:

$$\frac{\partial [HH_b]}{\partial t} = \begin{cases} \rho_h + D_b(P) \frac{\partial^2 [HH_b]}{\partial x^2} - \gamma(P) [HH_b], & 0 \le x \le L_P \text{ (posterior)}, \\\\ D_b(A) \frac{\partial^2 [HH_b]}{\partial x^2} - \gamma(A) [HH_b], & -L_A \le x < 0 \text{ (anterior)}. \end{cases}$$

In this model, we assume that Hedgehog is produced only in the posterior compartment, but that it can diffuse and is degraded in both compartments. There are no effects of HSPGs on Hedgehog movement or stability. However, for generality, we allow diffusion and degradation rates ( $D_b$  and  $\gamma$  respectively) to vary between the posterior and anterior compartments.

The steady state solutions (setting  $\frac{\partial [HH_b]}{\partial t} = 0$ ) are given by

$$[HH_b] = \begin{cases} \frac{\rho_h}{\gamma(P)} + a \cosh\left(\frac{x}{\lambda_P}\right) + b \sinh\left(\frac{x}{\lambda_P}\right), & 0 \le x \le L_P \text{ (posterior)}, \\ c \exp\left(\frac{x}{\lambda_A}\right) + d \exp\left(\frac{-x}{\lambda_A}\right), & -L_A \le x < 0 \text{ (anterior)}, \end{cases}$$

for arbitrary constants a, b, c and d, where  $\lambda_i = \sqrt{\frac{D_b(i)}{\gamma(i)}}$ . Assuming zero flux boundary conditions at  $x = -L_A$  and  $x = L_P$ , we obtain

(i) 
$$b = -a \tanh\left(\frac{L_P}{\lambda_P}\right)$$
,  
(ii)  $d = c \exp\left(\frac{-2L_A}{\lambda_A}\right)$ .

Assuming  $L_A \gg \lambda_A$ , then (ii) implies that  $d \ll c$ , and so we can approximate d = 0 and treat the anterior compartment gradient as a pure exponential decay.

By matching  $[HH_b]$  at x = 0, we obtain

(iii) 
$$a = c - \frac{\rho_h}{\gamma_b(P)}$$

Although unequal diffusion rates  $(D_b(P) \neq D_b(A))$  can lead to discontinuity at the AP boundary, the magnitudes of the posterior gradient  $(g_P)$  and anterior gradient  $(g_A)$  at the AP boundary are still related by  $D_b(P)g_P = D_b(A)g_A$  (Result S1 in Section 3 of this Supporting Text). This then leads to

(iv) 
$$b = c \frac{D_b(A)}{D_b(P)} \frac{\lambda_P}{\lambda_A}$$

Solving in terms of  $c = \alpha_0$  ([ $HH_b$ ] at x = 0), then gives

$$\alpha_0 = \frac{\rho_h}{\gamma(P)} \left( \frac{\tanh\left(\frac{L_P}{\lambda_P}\right)}{\frac{D_b(A)}{D_b(P)}\frac{\lambda_P}{\lambda_A} + \tanh\left(\frac{L_P}{\lambda_P}\right)} \right).$$
(Giving Eqn 9)

Solutions for a, b and d then follow. Moreover, as proved in Result S2 (in Section 3 of this Supporting Text), the ratio between Hedgehog levels at the posterior margin  $(x = L_P)$  and the AP border (x = 0) is given by

$$\beta = 1 + \frac{D_b(A)}{D_b(P)} \frac{\lambda_P}{\lambda_A} \left( \frac{1}{\tanh \frac{L_P}{\lambda_P}} \left( 1 - \frac{1}{\cosh \frac{L_P}{\lambda_P}} \right) \right).$$
(Giving Eqn 16)

#### Model B: Simplified regulated transport model

To approximate the steady-state HH gradient for the full model, and to analyse further the role of regulated transport, we focus on  $[HH_b]$  and split the posterior compartment into two distinct regions. We assume that HSPGs become saturated with HH in the posterior-most region of the disc (i.e. for  $x_P < x \leq L_P$ ). In this region,  $[HH_b] = \mu$ , where  $\mu$  is the carrying capacity of HSPGs. In the remainder of the disc, Hedgehog gradient formation is described by the following equations:

$$\frac{\partial [HH_b]}{\partial t} = \begin{cases} \rho_h + D_b(P) \frac{\partial^2 [HH_b]}{\partial x^2}, & 0 \le x \le x_P \text{ (posterior)}, \\\\ D_b(A) \frac{\partial^2 [HH_b]}{\partial x^2} - \gamma(A) [HH_b], & -L_A \le x < 0 \text{ (anterior)}. \end{cases}$$

The regulation of HH transport and stability are incorporated via the parameters  $\mu$ ,  $D_b$  and  $\gamma_b$ in the full model. HSPGs can modulate HH transport through the parameter  $D_b$ . For simplicity, we assume that this rate is constant within each compartment but may differ between posterior and anterior compartments  $(D_b(P) \text{ vs } D_b(A))$ . Stabilisation of HH by HSPGs is incorporated in the parameter  $\gamma_b$  (by assuming that  $\gamma_b$  is small).

We derive an approximate equation for HH for  $x \in [0, x_P]$  as follows. In the full model (Eqns. (1) and (2), main text), assume that  $D_f$ ,  $k_{in}$  and  $\gamma_b$  are relatively small. Setting  $[HH_f]$  to steady state  $(\frac{\partial [HH_f]}{\partial t} = 0)$  then gives

$$\frac{\partial [HH_b]}{\partial t} \approx \frac{\rho_h k_{out} (\mu - [HH_b])}{\gamma_f + k_{out} (\mu - [HH_b])} + D_b(P) \frac{\partial^2 [HH_b]}{\partial x^2}.$$

By assuming that  $k_{out}$  is sufficiently large, we arrive at the approximate equation for  $[HH_b]$  for  $x \in [0, x_P]$ . As for model A, we approximate the dynamics of HH in the anterior compartment as a simple diffusion-degradation system, giving an approximately exponential gradient.

Assuming  $L_A$  and  $\gamma(A)$  are sufficiently large to ensure that an exponential approximation for the anterior gradient is appropriate, we obtain the following steady state solutions for  $[HH_b]$ :

$$[HH_b] = \begin{cases} \mu, & x_P < x \le L_P \text{ (posterior)}, \\ -\frac{\rho_h}{2D_b(P)}x^2 + bx + c, & 0 \le x \le x_P \text{ (posterior)}, \\ d \exp\left(\frac{x}{\lambda_A}\right), & -L_A \le x < 0 \text{ (anterior)}, \end{cases}$$

for arbitrary constants b, c and d and  $\lambda_A = \sqrt{\frac{D_b(A)}{\gamma(A)}}$ . Imposing continuity of the gradient and flux within the posterior compartment (and assuming  $x_P < L_P$ ) gives

(i) 
$$\frac{\rho_h}{2D_b(P)}x_P^2 - bx_P + (\mu - c) = 0,$$
  
(ii)  $b = \frac{\rho_h}{D_b(P)}x_P.$ 

Moreover, ensuring  $[HH_b]$  is equal at x = 0, in both the anterior and posterior equations, we obtain

(iii) 
$$c = d$$
.

Although unequal diffusion rates  $(D_b(P) \neq D_b(A))$  can lead to discontinuity at the AP boundary (x = 0), the magnitude of the posterior gradient  $(g_P)$  and anterior gradient  $(g_A)$  at the AP boundary are related by  $D_b(P)g_P = D_b(A)g_A$  (analogous to model A; Result S1). This then leads to

(iv) 
$$d = b\lambda_A \frac{D_b(P)}{D_b(A)}.$$

Substituting from conditions (ii)–(iv) into (i), and solving the quadratic, yields the following expression for  $c = \alpha_0$  ([ $HH_b$ ] at x = 0):

$$\alpha_0 = \frac{\rho_h \lambda_A^2 D_b(P)}{D_b(A)^2} \left( -1 + \sqrt{1 + \frac{2\mu D_b(A)^2}{\rho_h \lambda_A^2 D_b(P)}} \right).$$
 (Giving Eqn 10:  $x_P < L_P$ )

The corresponding expression for  $x_P$  can then be calculated as

$$x_P = \lambda_A \frac{D_b(P)}{D_b(A)} \left( -1 + \sqrt{1 + \frac{2\mu D_b(A)^2}{\rho_h \lambda_A^2 D_b(P)}} \right).$$
(Giving Eqn 11)

Moreover, as proved in Result S3 (in Section 3 of this Supporting Text), the ratio between HH levels at the posterior margin ( $\mu$ ) and the AP boundary ( $\alpha_0$ ) is given by

$$\beta = \frac{\mu}{\alpha_0} = \frac{1}{2} + \sqrt{\frac{1}{4} + \frac{\mu D_b(A)^2}{2\rho_h \lambda_A^2 D_b(P)}}.$$
 (Giving Eqn 17)

If  $x_P \ge L_P$ , then HSPGs do not become saturated with HH within the disc and model B is equivalent to model A with  $\gamma(P) = 0$ . As proved in Results S4 an S5 (in Section 3 of this Supporting Text), letting  $\gamma(P) \to 0$  in model A results gives

$$\alpha_0 = \frac{\rho_h \lambda_A L_P}{D_b(A)}, \qquad \beta = 1 + \frac{L_P D_b(A)}{2\lambda_A D_b(P)}.$$
 (Giving Eqn 10:  $x_P > L_P$ )

#### Model C: Simplified anterior model

Since the Hedgehog signalling pathway is operative only in anterior compartment cells, we also introduce an approximate model that focuses on the Hedgehog gradient in anterior cells. Here, we consider the anterior compartment to be a one dimensional cross section  $x \in [0, L_A]$  (for convenience, we take x to be positive here, as opposed to negative in the full model, when describing anterior distances).

We fix the level of  $[HH_b]$  at the AP boundary to  $\alpha_0$  and then split the anterior compartment into two distinct regions by assuming that when HH levels are above a certain threshold  $([HH_b] > \alpha_A; x < x_A)$ , Patched is up-regulated at the highest rate  $\rho_{p1} + \rho_{p2}$  (i.e.  $f_p([S]) = 1$ ). The model equations for the two regions of the anterior compartment are then

$$\frac{\partial [HH_b]}{\partial t} = \begin{cases} D_b \frac{\partial^2 [HH_b]}{\partial x^2} - (\rho_{p1} + \rho_{p2}), & 0 \le x < x_A, \\ \\ D_b \frac{\partial^2 [HH_b]}{\partial x^2} - k_{on} \delta [HH_b], & x_A \le x \le L_A. \end{cases}$$

To obtain the above approximation for  $x \in [0, x_A)$  from the full model, we set [PH] to steady state  $\left(\frac{\partial [PH]}{\partial t} = 0 \text{ in Eqn. (6)}\right)$  to give

$$k_{on}[HH_b][PTC] - k_{off}[PH] = \gamma_{ph}[PH]$$

Then, assuming that  $[HH_f]$ ,  $k_{in}$  and  $\gamma_b$  are relatively small, Eqn. (4) becomes

$$\frac{\partial [HH_b]}{\partial t} = D_b \frac{\partial^2 [HH_b]}{\partial x^2} - \gamma_{ph} [PH]$$

Then, using Result S8(c) (in Section 3 of this Supporting Text) and letting  $f_p([S]) = 1$ , this approximates to

$$\frac{\partial [HH_b]}{\partial t} = D_b \frac{\partial^2 [HH_b]}{\partial x^2} - (\rho_{p1} + \rho_{p2}) \left( \frac{\frac{\gamma_{ph} k_{on} [HH_b]}{k_{off} + \gamma_{ph}}}{\gamma_p + \frac{\gamma_{ph} k_{on} [HH_b]}{k_{off} + \gamma_{ph}}} \right).$$

Assuming  $\gamma_p < k_{on}[HH_b]$  (which is necessary for a realistic gradient) and that  $k_{off}$  is relatively small yields the above approximation for  $x \in [0, x_A)$ .

As with models A and B, we approximate HH dynamics in the remainder of the anterior compartment  $(x \ge x_A)$  as a simple diffusion-degradation system, giving an approximately exponential gradient. Since the dominant process for removal of HH is binding to PTC at rate  $k_{on}$ , we represent degradation by the single term  $k_{on}[HH_b][PTC]$  from the full model, approximating [PTC] levels by a constant  $\delta$ . As can be seen in Results S9 and S10 (in Section 3 of this Supporting Text),  $\delta \equiv [PTC]$  levels in this region can be bound as follows (assuming  $k_{off}$  is relatively small)

$$\frac{z_A(\gamma_{ph} + r\rho_{p1})}{\gamma_{ph} + r\gamma_p z_A} \le \delta \le \frac{z_A(\gamma_{ph} + r(\rho_{p1} + \rho_{p2}))}{\gamma_{ph} + r\gamma_p z_A + k_{off}},$$
(Eqn 18)

where  $z_A$  is value of  $[Z] = \frac{[PTC]}{1 + r[PH]}$  corresponding to the Patched production threshold (note that this value of  $z_A$  also corresponds to a unique value  $(s_A)$  of [S]).

Using this model, we can determine the position of the boundary of the region of Patched up-regulation  $(x_A)$ , and the level of  $[HH_b]$  at that position  $(\alpha_A)$ . Considering just the high Patched-producing region, Result S8(a) (with  $f_p([S]) = 1$ ) gives the following approximation for  $\alpha_A$ :

$$\alpha_A = \frac{(\rho_{p1} + \rho_{p2} - \gamma_p z_A)(\gamma_{ph} + k_{off})}{(\gamma_{ph} + r(\rho_{p1} + \rho_{p2}))k_{on} z_A}.$$
 (Giving Eqn 13)

We can then use this result to solve the steady-state equations and obtain an expression for  $x_A$ .

Assuming  $L_A$  and  $k_{on}\delta$  are sufficiently large that an exponential approximation to the anterior tail gradient is appropriate, the steady state solutions are

$$[HH_b] = \begin{cases} \frac{\rho_{p1} + \rho_{p2}}{2D_b} x^2 + bx + c, & 0 \le x < x_A, \\\\ \alpha_A \exp \frac{(x_A - x)}{\lambda_A}, & x_A \le x \le L_A, \end{cases}$$

for arbitrary constants b and c and where  $\lambda_A = \sqrt{\frac{D_b}{k_{on}\delta}}$ .

Enforcing continuity of the gradient and flux when moving between regions and setting  $[HH_b] = \alpha_0$  at the AP boundary (x = 0) gives the following conditions:

(i) 
$$c = \alpha_0$$
,  
(ii)  $\frac{\rho_{p1} + \rho_{p2}}{2D_b} x_A^2 + bx_A + c = \alpha_A$ ,

(iii) 
$$b = -\frac{\alpha_A}{\lambda_A} - \frac{\rho_{p1} + \rho_{p2}}{D_b} x_A$$

Substituting (i) and (iii) into (ii), and solving the quadratic, gives

$$x_A = \frac{D_b}{\rho_{p1} + \rho_{p2}} \left( \sqrt{\frac{2(\rho_{p1} + \rho_{p2})}{D_b}} (\alpha_0 - \alpha_A) + \left(\frac{\alpha_A}{\lambda_A}\right)^2 - \frac{\alpha_A}{\lambda_A} \right).$$
 (Giving Eqn 14)

This expression can then be used to give an expression for b. Using this model, we can calculate the magnitude g of the Hedgehog gradient at the AP boundary (x = 0). We consider two cases, depending on whether or not the level of HH at the AP boundary is above the level required for maximal Patched up-regulation. If  $\alpha_0 > \alpha_A$ , the gradient at the AP boundary (x = 0) is equal to b. Therefore, the magnitude of the gradient is

$$g = \frac{\alpha_A}{\lambda_A} + \frac{\rho_{p1} + \rho_{p2}}{D_b} x_A = \sqrt{\frac{2(\rho_{p1} + \rho_{p2})}{D_b}} (\alpha_0 - \alpha_A) + \frac{\delta k_{on} \alpha_A^2}{D_b}.$$
 (Giving Eqn 15)

If  $\alpha_0 \leq \alpha_A$ , we ignore the first region  $(x \in [0, x_A))$  and assume  $x_A = 0$  and let  $\alpha_A = \alpha_0$  in the equation for the second region  $(x \in [x_A, L_A])$  to give an exponential gradient. Then, the gradient at the AP boundary is

$$g = \frac{\alpha_0}{\lambda_A} = \alpha_0 \sqrt{\frac{\delta k_{on}}{D_b}}.$$
 (Giving Eqn 15)

#### 2 Justification of parameter constraints

Table 1 lists a number of parameter constraints and assumptions for the non-dimensionalised model, based on a number of published experimental results and model approximations (described above). Here, we justify each of the constraints C1–C10.

#### C1,C2: Reversible binding

The binding of HH to HSPGs and PTC is reversible, but the forward reaction is assumed to be dominant—i.e.  $k_{in} \ll k_{out}$  (C1) and  $k_{off} \ll k_{on}$  (C2). This is in line with the approach taken by previous models (e.g. Eldar et al. (2003), Hufnagel et al. (2006)).

#### C3,C4,C5: Degradation rates

Since HSPGs stabilise HH (Lin (2004), Bornemann et al. (2004)), we also assume that the degradation rate for the HH-HSPG complex is lower than those associated with other forms of PTC or HH. i.e.  $\gamma_b \ll \gamma_f, \gamma_p$  and  $\gamma_{ph}$  (C3).

Experimental evidence has shown that the degradation rate of HH-PTC is faster than that of unbound PTC (Incardona et al. (2002)). Therefore, in the model  $\gamma_{ph} > \gamma_p$ , and in simulations we assume that  $\gamma_{ph} = 6\gamma_p$  (C4).

Dally and Dally-like protect HH from degradation (Lin (2004), Bornemann et al. (2004)). Therefore, in the model, we assume that free HH is (relatively) unstable. In simulations we assume that  $\gamma_f = 6\gamma_p \gg \gamma_b$  (C5).

#### C6: Free HH Diffusion

Dally and Dally-like are necessary for transporting HH across the disc tissue (Han et al. (2004)). Therefore, in the model, we assume that free HH diffuses slowly. i.e.  $D_f \ll D_b$ .

#### C7: PTC antagonism by HH-PTC

Experimental evidence has shown that both PTC and HH-PTC (PH) levels play important roles in Hedgehog signalling and in regulating the level of expression of target genes col and dpp (Casali and Struhl (2004)). In particular

- (a) 220% HH-PTC and 80% PTC leads to target gene expression,
- (b) 50% HH-PTC and 80% PTC does not lead to target gene expression,
- (c) 220% HH-PTC and 140% PTC does not lead to target gene expression,

where the levels are a percentage of PTC levels at the margin  $(\frac{\rho_{p1}}{\gamma_p}$  in our model). In our model, signalling activity is regulated by  $[Z] = \frac{[PTC]}{1 + r[PH]}$ , which can be rearranged to give  $r = \frac{[PTC] - [Z]}{[PH][Z]}$ . For different threshold values  $Z_T$  (scaled between 0 and 1 after non-dimensionalisation), the above data can then be substituted in to estimate reasonable values for r.

$Z_T$	$r_{\min}$	$r_{\max}$
0.1	3.18	5.91
0.2	1.36	2.72
0.3	0.76	1.67
0.4	0.45	1.14
0.5	0.27	0.82
0.6	0.15	0.61

From Glise et al. (2002), *col* and *dpp* are expressed in stripes of width 7 and 12 cells from the AP boundary, respectively (in 3rd instar wing discs), and so we need r to be consistent with a range of values for  $Z_T$ . A value of r = 0.8 is chosen to be consistent with Z-thresholds between 0.3 and 0.5 (moderate levels of signalling), where lower values of [Z] correspond to high signalling.

#### C8: Patched up-regulation near the AP-boundary

Patched is up-regulated at the AP boundary, with total protein levels ([PTC] + [PH]) approximately seven times higher than at the the anterior margin, where there is virtually no signalling (Casali and Struhl (2004)). Using Result S8 (in Section 3 of this Supporting Text),  $[PTC] + [PH] \rightarrow \frac{\rho_{p1} + \rho_{p2}}{\gamma_{ph}}$  as  $[HH_b] \rightarrow \infty$  and  $f_p([S]) \rightarrow 1$ . However, [PTC] + [PH] levels can be higher in other sections of the high Patched producing region (see e.g. Fig. 4A of main text). Therefore, to ensure  $[PTC] + [PH] > 6\frac{\rho_{p1}}{\gamma_p}$  in the high Patched producing region, we let  $\rho_{p2} = 6\frac{\gamma_{ph}\rho_{p1}}{\gamma_p}$ . Simulations show that this approximation is reasonable for this model (red line in Fig. 4A of main text).

#### C9: Diffusion and binding rates

Patched up-regulation is evident in a band approximately five cells wide on the anterior side of the AP boundary (in 3rd instar wing discs, Glise et al. (2002)). In Model C, this corresponds to a Patched up-regulation boundary  $x_A \approx 5$  cell widths. From Eqn 13 and 14

$$x_A = \frac{D_b}{\rho_{p1} + \rho_{p2}} \left( \sqrt{\frac{2(\rho_{p1} + \rho_{p2})}{D_b}} (\alpha_0 - \alpha_A) + \left(\frac{\alpha_A}{\lambda_A}\right)^2 - \frac{\alpha_A}{\lambda_A} \right),$$

where  $\lambda_A = \sqrt{\frac{D_b}{\delta k_{on}}}$ ,  $\alpha_A = \frac{(\rho_{p1} + \rho_{p2} - \gamma_p z_A)(\gamma_{ph} + k_{off})}{(\gamma_{ph} + r(\rho_{p1} + \rho_{p2}))k_{on}z_A}$  and  $\delta$  is an approximation of [PTC] and constrained by Eqn 18 (see Model C). Re-arranging the above (as shown in Result S13 in Section 3 of this *Supporting Text*) then gives

$$D_b = \left(\frac{x_A(\rho_{p1} + \rho_{p2})}{-\alpha_A\sqrt{\delta k_{on}} + \sqrt{2(\rho_{p1} + \rho_{p2})(\alpha_0 - \alpha_A) + \alpha_A^2\delta k_{on}}}\right)^2.$$

From available data, we cannot yet constrain either  $\alpha_0$  (the level of  $[HH_b]$  at the AP boundary) or  $z_A$  (the [Z] threshold for Patched production). If we assume  $\alpha_0 = 10$  and  $z_A = 0.3$ , then the non-dimensionalised model and constraints **C1–C8** can be used to give  $D_b$  in terms of  $k_{on}$ . Fig. ST2 (below) shows  $D_b$  as a function of  $k_{on}$  (when  $\delta = 0.6$ ), together with the maximum signalling range for those values of  $D_b$  and  $k_{on}$ . For large  $k_{on}$ , the maximum range is less than the range of dpp (12–15 cells). Meanwhile, for small  $k_{on}$ ,  $D_b$  and  $\alpha_A$  become very large, implying a very shallow Hh gradient close to the source (which is not evident from experimental data such as Su et al. (2007)). For the purposes of this paper we select non-dimensionalised  $k_{on} =$ 8 and  $D_b = 60$  in the moderate region. From Supporting Figure S16, we see that  $\delta = 0.6$  is an appropriate value to use.



Figure ST2: Dashed line: Diffusion rate  $D_b$  in terms of  $k_{on}$  in Constraint C9 (for Model C). Dotted line: Signalling range when the model has those values  $D_b$  and  $k_{on}$ . This is defined as the position (number of cells from AP boundary) at which [S] = 0.1.

#### C10: HH levels at the AP boundary

Quantitative experimental data on the Hedgehog gradient show that the level of HH at the AP boundary is lower than that at the margin, but not by a large factor (Tabata and Takei (2004), Eugster et al. (2007)). Denoting the ratio between  $[HH_b]$  at the posterior margin and the AP boundary by  $\beta$ , Eqn. (17) provides an approximation

$$\beta = \frac{1}{2} + \sqrt{\frac{1}{4} + \frac{\mu D_b(A)\gamma(A)}{2\rho_h D_b(P)}},$$

where  $\gamma(A)$  is a generic degradation rate for HH in the anterior compartment. As with Model C, we can estimate this to be  $\gamma(A) = \delta_B k_{on}$ , although we note that  $\delta_B$  may differ from  $\delta$  in Model C.

If we further assume that  $D_b$  is uniform across the whole disc  $(D_b(P) = D_b(A))$ , we get

$$\rho_h = \frac{\mu \delta_B k_{on}}{2\beta \left(\beta - 1\right)}.$$

For the purposes of the parameter estimation, we assume  $\alpha_0 = 10$  and this ratio to be approximately  $\beta = 2$  (giving  $\mu = \alpha_0 \beta = 20$ ). Moreover, we have  $k_{on} = 8$  (from **C9**) and assume  $\delta_B = 0.75$  from numerical simulations. This then gives  $\rho_h = 30$ . From Supporting Figure S16, we can see that  $\delta = 0.75$  is a suitable value to use.

#### **3** Supplementary results and proofs

For the purposes of completeness, we provide proofs for a number of results stated in the text. These results relate to the three model approximations (A, B and C) introduced in the main text and we deal with each of these models in turn

#### Model A results

**Result S1.** In Model A, suppose  $g_A$  and  $g_P$  are the steady state anterior and posterior gradients at the AP border. i.e.  $g_i = \frac{d[HH]_b}{dx}$  as  $x \to 0$  and  $t \to \infty$ , for the anterior and posterior equations.

Then,

 $\frac{g_P}{g_A} = \frac{D_b(A)}{D_b(P)}$ 

#### **Proof:**

If  $D_b(P) \neq D_b(A)$ , then we have a discontinuity in the gradient at the AP boundary. In this case the (transitional) diffusion term can be written as

$$D_b \frac{\partial^2 [HH_b]}{\partial x^2} = \lim_{\Delta \to 0} \frac{D_b(P)([HH_b](\Delta) - [HH_b](0)) - D_b(A)([HH_b](0) - [HH_b](-\Delta))}{\Delta^2}$$

Then, at steady state  $(\frac{\partial [HH_b]}{\partial t} = 0)$ ,

$$\begin{split} \rho + \gamma [HH_b] &= \lim_{\Delta \to 0} \frac{D_b(P)([HH_b](\Delta) - [HH_b](0)) - D_b(A)([HH_b](0) - [HH_b](-\Delta))}{\Delta^2}, \\ \lim_{\Delta \to 0} \Delta (\rho + \gamma [HH_b]) &= \lim_{\Delta \to 0} \frac{D_b(P)([HH_b](\Delta) - [HH_b](0))}{\Delta} - \frac{D_b(A)([HH_b](0) - [HH_b](-\Delta))}{\Delta}, \\ 0 &= D_b(P)g_P - D_b(A)g_A, \\ \frac{g_P}{g_A} &= \frac{D_b(A)}{D_b(P)}. \end{split}$$

**Result S2.** In Model A, the ratio between Hedgehog levels at the Posterior margin  $(x = L_P)$ and AP border (x = 0) is

$$\beta = 1 + \frac{D_b(A)}{D_b(P)} \frac{\lambda_P}{\lambda_A} \left( \frac{1}{\tanh \frac{L_P}{\lambda_P}} \left( 1 - \frac{1}{\cosh \frac{L_P}{\lambda_P}} \right) \right).$$
(Eqn 16)

#### **Proof:**

From Model A, we can calculate the the level of HH at the Posterior margin  $(x = L_P)$  as

$$[HH_b](x = L_P) = \frac{\rho_h}{\gamma(P)} + \left(\alpha_0 - \frac{\rho_h}{\gamma(P)}\right) \cosh\frac{L_P}{\lambda_P} + \left(\alpha_0 \frac{D_b(A)}{D_b(P)} \frac{\lambda_P}{\lambda_A}\right) \sinh\frac{L_P}{\lambda_P}$$
$$= \frac{\rho_h}{\gamma(P)} \left(1 - \cosh\frac{L_P}{\lambda_P}\right) + \alpha_0 \left(\cosh\frac{L_P}{\lambda_P} + \frac{D_b(A)}{D_b(P)} \frac{\lambda_P}{\lambda_A} \sinh\frac{L_P}{\lambda_P}\right).$$

Therefore

$$\beta = \frac{[HH_b](x = L_P)}{\alpha_0} = \frac{\rho_h}{\gamma(P)} \frac{1}{\alpha_0} \left(1 - \cosh\frac{L_P}{\lambda_P}\right) + \cosh\frac{L_P}{\lambda_P} + \frac{D_b(A)}{D_b(P)} \frac{\lambda_P}{\lambda_A} \sinh\frac{L_P}{\lambda_P},$$

and after substituting  $\alpha_0$  (from Eqn. (9) in main text) back in, we get

$$\beta = 1 + \frac{D_b(A)}{D_b(P)} \frac{\lambda_P}{\lambda_A} \frac{1}{\tanh \frac{L_P}{\lambda_P}} \left( 1 - \cosh \frac{L_P}{\lambda_P} + \sinh \frac{L_P}{\lambda_P} \tanh \frac{L_P}{\lambda_P} \right)$$
$$= 1 + \frac{D_b(A)}{D_b(P)} \frac{\lambda_P}{\lambda_A} \frac{1}{\tanh \frac{L_P}{\lambda_P}} \left( 1 - \frac{\cosh^2 \frac{L_P}{\lambda_P} - \sinh^2 \frac{L_P}{\lambda_P}}{\cosh \frac{L_P}{\lambda_P}} \right)$$
$$= 1 + \frac{D_b(A)}{D_b(P)} \frac{\lambda_P}{\lambda_A} \left( \frac{1}{\tanh \frac{L_P}{\lambda_P}} \left( 1 - \frac{1}{\cosh \frac{L_P}{\lambda_P}} \right) \right).$$

г		
L		
L		
L		
L		

#### Model B results

**Result S3.** When  $x_P < L_P$ , in Model B, the ratio between HH levels at the Posterior margin  $(x = L_P)$  and AP border (x = 0) is

$$\beta = \frac{1}{2} + \sqrt{\frac{1}{4} + \frac{\mu D_b(A)^2}{2\rho_h \lambda_A^2 D_b(P)}}.$$
 (Eqn 17)

#### **Proof:**

First, we note that  $\beta = \frac{\mu}{\alpha_0}$ . Substituting  $\mu = \beta \alpha_0$  into Eqn. (10) of main text (case:  $x_P < L_P$ ) and re-arranging, gives

$$\alpha_0 + \frac{\rho_h \lambda_A^2 D_b(P)}{D_b(A)^2} = \frac{\rho_h \lambda_A^2 D_b(P)}{D_b(A)^2} \sqrt{1 + \frac{2\alpha_0 \beta D_b(A)^2}{\rho_h \lambda_A^2 D_b(P)}}.$$

Squaring both sides then gives

$$\alpha_0^2 + \frac{2\alpha_0\rho_h\lambda_A^2D_b(P)}{D_b(A)^2} = \frac{2\alpha_0\beta\rho_h\lambda_A^2D_b(P)}{D_b(A)^2},$$

and re-arranging gives

$$\beta = 1 + \frac{\alpha_0 D_b(A)^2}{2\rho_h \lambda_A^2 D_b(P)}.$$

Substituting Eqn. (10) back into the above then gives

$$\beta = 1 + \frac{1}{2} \left( -1 + \sqrt{1 + \frac{2\mu D_b(A)^2}{\rho_h \lambda_A^2 D_b(P)}} \right)$$
$$= \frac{1}{2} + \sqrt{\frac{1}{4} + \frac{\mu D_b(A)^2}{2\rho_h \lambda_A^2 D_b(P)}}.$$

**Result S4.** When  $x_P > L_P$ , in Model B, the HH concentration at the AP boundary (x = 0) is

$$\alpha_0 = \frac{\rho_h \lambda_A L_P}{D_b(A)}.$$
 (Eqn 10:  $x_P > L_P$ )

#### Proof

In this case, Model B is equivalent to Model A, with  $\gamma(P) = 0$ . From model A and Eqn. (9)

$$\alpha_0 = \frac{\rho_h}{\gamma(P)} \left( \frac{\frac{\lambda_A}{\lambda_P} \tanh \frac{L_P}{\lambda_P}}{\frac{D_b(A)}{D_b(P)} + \frac{\lambda_A}{\lambda_P} \tanh \frac{L_P}{\lambda_P}} \right), \quad \text{where } \lambda_i = \sqrt{\frac{D_b(i)}{\gamma(i)}}.$$
  
Letting  $x = \frac{L_P}{\lambda_P}$  and noting that  $\frac{1}{\lambda_P \gamma(P)} = \frac{L_P}{x D_b(P)}$ , the above can then be rewritten as

$$\alpha_0 = \frac{\rho_h}{D_b(P)} \left( \frac{\frac{\lambda_A L_P}{x} \tanh x}{\frac{D_b(A)}{D_b(P)} + \frac{\lambda_A x}{L_P} \tanh x} \right)$$

Then we get the result since

$$\begin{split} & x \to 0 \text{ as } \gamma(P) \to 0, \\ & \frac{1}{x} \tanh x \to 1 \text{ as } x \to 0, \\ & x \tanh x \to 0 \text{ as } x \to 0. \end{split}$$

**Result S5.** When  $x_P > L_P$ , in Model B, the ratio between HH levels at the Posterior margin  $(x = L_P)$  and AP border (x = 0) is

$$\beta = 1 + \frac{L_P D_b(A)}{2\lambda_A D_b(P)}.$$

#### Proof

In this case, Model B is equivalent to Model A, with  $\gamma(P) = 0$ . From model A and Result S2

$$\beta = 1 + \frac{D_b(A)}{D_b(P)} \frac{1}{\frac{\lambda_A}{\lambda_P} \tanh \frac{L_P}{\lambda_P}} \left( 1 - \frac{1}{\cosh \frac{L_P}{\lambda_P}} \right), \quad \text{where } \lambda_i = \sqrt{\frac{D_b(i)}{\gamma(i)}}.$$

Letting  $x = \frac{L_P}{\lambda_P}$ , the above can be rewritten as

$$\beta = 1 + \frac{D_b(A)}{D_b(P)} \frac{L_P}{\lambda_A} \left( \frac{\cosh x - 1}{x \sinh x} \right)$$

Then we get the result since

 $x \to 0 \text{ as } \gamma(P) \to 0,$  $\cosh x - 1 \approx \frac{x^2}{2} \text{ for small } x,$  $x \sinh x \approx x^2 \text{ for small } x.$ 

**Result S6.** In Model B, consider the the value of  $[HH_b]$  at the AP boundary ( $\alpha_0$ , Eqn 10 in main text) and the position of the target gene expression boundary ( $x_T$ , Eqn 12 in main text).

The sensitivity coefficients (in response to  $\rho_h$ ) are

Case: 
$$x_P > L_P$$

$$\frac{\partial \alpha_0}{\partial \rho_h} = \frac{\alpha_0}{\rho_h}$$
 and  $\frac{\partial x_T}{\rho_h} = \frac{\lambda_A}{\rho_h}$ .

Case:  $x_P < L_P$ 

$$\frac{\partial \alpha_0}{\partial \rho_h} = \frac{\alpha_0}{\rho_h} - \frac{\mu D_b(P) \lambda_A^2}{\alpha_0 D_b(A)^2 + \rho_h \lambda_A^2 D_b(P)} \qquad and \qquad \frac{\partial x_T}{\rho_h} = \frac{\lambda_A}{\rho_h} - \frac{\mu D_b(P) \lambda_A^3}{\alpha_0 (\alpha_0 D_b(A)^2 + \rho_h \lambda_A^2 D_b(P))}.$$

#### Proof

From Eqn. (12) (in the main text), the target gene expression boundary (corresponding to a HH concentration  $[HH_b]_T$ ) can be approximated as

$$x_T = \lambda_A \ln\left(\frac{\alpha_0}{[HH_b]_T}\right),$$

and so

(a) 
$$\frac{\partial x_T}{\partial \rho_h} = \frac{\lambda_A}{\alpha_0} \frac{\partial \alpha_0}{\partial \rho_h}.$$

In the case  $x_P > L_P$ ,  $\alpha_0 = \frac{\rho_h \lambda_A L_P}{D_b(A)}$  (from Eqn. (10) in the main text), and so

$$\frac{\partial \alpha_0}{\partial \rho_h} = \frac{\lambda_A L_P}{D_b(A)} = \frac{\alpha_0}{\rho_h},$$

as required. The result for  $\frac{\partial x_T}{\rho_h}$  then follows from (a).

In the case  $x_P < L_P$ ,

$$\alpha_0 = \frac{\rho_h \lambda_A^2 D_b(P)}{D_b(A)^2} \left( -1 + \sqrt{1 + \frac{2\mu D_b(A)^2}{\rho_h \lambda_A^2 D_b(P)}} \right)$$

(from Eqn. (10) in the main text), and so

$$\frac{\partial \alpha_0}{\partial \rho_h} = \frac{\lambda_A^2 D_b(P)}{D_b(A)^2} \left( -1 + \sqrt{1 + \frac{2\mu D_b(A)^2}{\rho_h \lambda_A^2 D_b(P)}} \right) - \frac{\mu}{\rho_h} \frac{1}{\sqrt{1 + \frac{2\mu D_b(A)^2}{\rho_h \lambda_A^2 D_b(P)}}}$$

$$=\frac{\alpha_0}{\rho_h}-\frac{\mu\rho_h D_b(P)\lambda_A^2}{\rho_h(\alpha_0 D_b(A)^2+\rho_h\lambda_A^2 D_b(P))},$$

as required. The result for  $\frac{\partial x_T}{\rho_h}$  then follows from (a).

**Result S7.** Consider model B and the case  $x_P < L_P$ . Let  $\rho'_h = c\rho_h$  and consider the resulting change in  $\alpha_0$  (to  $\alpha'_0$ ). Then

- if  $c \ge 1$ , then  $\alpha_0 \le \alpha'_0 \le \sqrt{c}\alpha_0$  and  $x_T \le x'_T \le x_T + \lambda_A \ln \sqrt{c}$ ,
- if  $c \leq 1$ , then  $\alpha_0 \geq \alpha'_0 \geq \sqrt{c}\alpha_0$  and  $x_T \geq x'_T \geq x_T + \lambda_A \ln \sqrt{c}$ .

#### Proof

From Eqn. (10) in main text (case:  $x_P < L_P$ )

$$\begin{aligned} \alpha_{0} &= \frac{\rho_{h} \lambda_{A}^{2} D_{b}(P)}{D_{b}(A)^{2}} \left( -1 + \sqrt{1 + \frac{2\mu D_{b}(A)^{2}}{\rho_{h} \lambda_{A}^{2} D_{b}(P)}} \right), \\ \alpha_{0}' &= \sqrt{c} \frac{\rho_{h} \lambda_{A}^{2} D_{b}(P)}{D_{b}(A)^{2}} \left( -\sqrt{c} + \sqrt{c + \frac{2\mu D_{b}(A)^{2}}{\rho_{h} \lambda_{A}^{2} D_{b}(P)}} \right), \end{aligned}$$

and so

(1) 
$$\frac{\alpha_0'}{\alpha_0} = \sqrt{c} \frac{-\sqrt{c} + \sqrt{c + \frac{2\mu D_b(A)^2}{\rho_h \lambda_A^2 D_b(P)}}}{-1 + \sqrt{1 + \frac{2\mu D_b(A)^2}{\rho_h \lambda_A^2 D_b(P)}}}$$

Now consider  $y = -\sqrt{c} + \sqrt{c+a}$  where a is a positive constant. Then

$$\frac{dy}{dc} = \frac{\sqrt{c} - \sqrt{c+a}}{2\sqrt{c(c+a)}} \le 0.$$

Therefore, using (1),

if c ≥ 1 then α<sub>0</sub><sup>'</sup>/α<sub>0</sub> ≤ √c,
if c ≤ 1 then α<sub>0</sub><sup>'</sup>/α<sub>0</sub> ≥ √c.

This combined with Eqns. (10) and (12), and the fact that  $\frac{\partial \alpha_0}{\partial \rho_h} > 0$  and  $\frac{\partial x_T}{\partial \rho_h} > 0$  gives the result.

#### Model C results

**Result S8.** Letting the anterior equations (Eqns (3)-(8) in the main text) reach steady state, we get

(a) 
$$[HH_b] = \frac{(\rho_{p1} + \rho_{p2}f_p([S]) - \gamma_p[Z])}{(\gamma_{ph} + r(\rho_{p1} + \rho_{p2}f_p([S])))k^{\star}[Z]},$$
  
(b)  $[PTC] = \frac{\rho_{p1} + \rho_{p2}f_p([S])}{\gamma_p + \gamma_{ph}k^{\star}[HH_b]},$ 

(c) 
$$[PH] = \frac{(p_{p1} + p_{p2}J_p([J]))\kappa [HH_b]}{\gamma_p + \gamma_{ph}k^*[HH_b]},$$

where

$$k^{\star} = \frac{k_{on}}{k_{off} + \gamma_{ph}}$$
 and  $[Z] = \frac{[PTC]}{1 + r[PH]}$ 

#### Proof

First, we prove parts (b) and (c). Setting  $\frac{\partial [PH]}{\partial t}$  to 0 (in Eqn. (6)) gives

(1) 
$$[PH] = k^{\star}[HH_b][PTC],$$
  
(2)  $k_{on}[HH_b][PTC] - k_{off}[PH] = \gamma_{ph}[PH] = \gamma_{ph}k^{\star}[HH_b][PTC],$ 

where 
$$k^{\star} = \frac{k_{on}}{k_{off} + \gamma_{ph}}.$$

Setting  $\frac{\partial [PTC]}{\partial t}$  to 0 (in Eqn. (5)), and using the above (2), then gives

**(b)** 
$$[PTC] = \frac{\rho_{p1} + \rho_{p2} f_p([S])}{\gamma_p + \gamma_{ph} k^* [HH_b]}.$$

Substituting back into (1), then gives

(c) 
$$[PH] = \frac{k^{\star}[HH_b](\rho_{p1} + \rho_{p2}f_p([S]))}{\gamma_p + \gamma_{ph}k^{\star}[HH_b]}.$$

Since  $[Z] = \frac{[PTC]}{1 + r[PH]}$ , (b) and (c) then give

(3) 
$$[Z] = \frac{\rho_{p1} + \rho_{p2} f_p([S])}{\gamma_p + k^{\star} [HH_b] (\gamma_{ph} + r(\rho_{p1} + \rho_{p2} f_p([S])))}.$$

Rearranging then gives part (a).

**Result S9.** Suppose Patched is up-regulated according to a step function  $f_p$ , where  $f_p = 0$  (or 1) if  $[Z] > z_A$  ( $[Z] < z_A$ ). Then, at steady state, [PTC] is bounded above and below by

$$[PTC]_{max} = \frac{z_A(\gamma_{ph} + r(\rho_{p1} + \rho_{p2}))}{\gamma_{ph} + r\gamma_p z_A}$$
$$[PTC]_{min} = \frac{z_A(\gamma_{ph} + r\rho_{p1})}{\gamma_{ph} + r\gamma_p z_A} \qquad (away from the AP border).$$

#### **Proof:**

First, let  $k^{\star} = \frac{k_{on}}{\gamma_{ph} + k_{off}}$ . Then, from the steady state equations, we get

(1) 
$$[PH] = k^{\star} [PTC] [HH_b]$$

(see proof of Result S8). Then, since  $[Z] = \frac{[PTC]}{1 + r[PH]}$ , we can use (1) to get

(2) 
$$[PTC] = \frac{[Z]}{1 - rk^{\star}[HH_b][Z]}$$

Moreover, substituting in Result S8(a), we get

(3) 
$$[PTC] = \frac{[Z](\gamma_{ph} + r(\rho_{p1} + \rho_{p2}f_p))}{\gamma_{ph} + r\gamma_p[Z]}.$$

Now, since we have a step function  $f_p$ , we have the following three scenarios

(a)  $[Z] < z_A$  and  $[PTC] = \frac{\rho_{p1} + \rho_{p2}}{\gamma_p + \gamma_{ph}k^*[HH_b]}$  (from Result S8(b) with  $f_p = 1$ ) (b)  $[Z] = z_A$  and  $[PTC] = \frac{z_A}{1 - rk^*[HH_b]z_A}$  (from (2)) (c)  $[Z] > z_A$  and  $[PTC] = \frac{\rho_{p1}}{\gamma_p + \gamma_{ph}k^*[HH_b]}$  (from Result S8(b) with  $f_p = 0$ ).

Therefore, we have

(a) 
$$\frac{\partial [PTC]}{\partial [HH_b]} < 0,$$
  
(b)  $\frac{\partial [PTC]}{\partial [HH_b]} > 0,$   
(c)  $\frac{\partial [PTC]}{\partial [HH_b]} < 0.$ 

Therefore, away from the AP border (where PTC may be completely saturated by HH) the maximum and minimum for Patched occurs as  $[Z] \rightarrow z_A$  in the cases (a) and (c) respectively. Therefore, we get  $[PTC]_{max}$  ( $[PTC]_{min}$ ) by letting  $[Z] = z_A$  and  $f_p = 1(0)$  in (3) above.

**Result S10.** Suppose  $k_{off}$  is relatively small, so that we can choose  $\delta$  satisfying

$$\delta \leq \frac{z_A(\gamma_{ph} + r(\rho_{p1} + \rho_{p2}))}{\gamma_{ph} + r\gamma_p z_A + k_{off}} , \qquad \delta \leq [PTC]_{max},$$
  
$$\delta \geq [PTC]_{min},$$

where  $[PTC]_{min}$  and  $[PTC]_{max}$  are as defined in Result S9. Then we get

$$\left(\left(\rho_{p1} + \rho_{p2}\right) - \alpha_A \delta k_{on}\right) \ge 0,$$

where 
$$\alpha_A = \frac{(\rho_{p1} + \rho_{p2} - \gamma_p z_A)(\gamma_{ph} + k_{off})}{(\gamma_{ph} + r(\rho_{p1} + \rho_{p2}))k_{on}z_A}$$
 (as defined in Eqn. (13) in the main text).

#### **Proof:**

From Eqn. (13) (main text)

$$\alpha_{A} = \frac{(\rho_{p1} + \rho_{p2} - \gamma_{p}z_{A})(\gamma_{ph} + k_{off})}{(\gamma_{ph} + r(\rho_{p1} + \rho_{p2}))k_{on}z_{A}}$$

is defined as the level of  $[HH_b]$  when  $[Z] = z_A$  in the high Patched production region. Therefore,

$$\begin{aligned} \alpha_{A}\delta k_{on} &\leq k_{on} \frac{(\rho_{p1} + \rho_{p2} - \gamma_{p}z_{A})(\gamma_{ph} + k_{off})}{(\gamma_{ph} + r(\rho_{p1} + \rho_{p2}))k_{on}z_{A}} \frac{z_{A}(\gamma_{ph} + r(\rho_{p1} + \rho_{p2}))}{\gamma_{ph} + r\gamma_{p}z_{A} + k_{off}} \\ &\leq \frac{((\rho_{p1} + \rho_{p2}) - \gamma_{p}z_{A})(\gamma_{ph} + k_{off})}{\gamma_{ph} + r\gamma_{p}z_{A} + k_{off}} \\ &\leq (\rho_{p1} + \rho_{p2}) - \gamma_{p}z_{A} \\ &\leq (\rho_{p1} + \rho_{p2}). \end{aligned}$$

(a) 
$$\frac{\partial x_A}{\partial r} > 0$$
,  
(b)  $\frac{\partial x_A}{\partial t} > 0$ .

(b) 
$$\frac{\partial k_{on}}{\partial k_{on}} >$$

#### Proof

First, we show  $\frac{\partial x_A}{\partial \alpha_A} < 0$ . Then since  $\frac{\partial \alpha_A}{\partial r} < 0$  and  $\frac{\partial \alpha_A}{\partial k_{on}} < 0$  (from Eqn 13), we get the result. Differentiating  $x_A$  (Eqn 14) with respect to  $\alpha_A$  and noting that  $\lambda_A = \sqrt{\frac{D_b}{\delta k_{on}}}$ , we get

$$\begin{aligned} \frac{\partial x_A}{\partial \alpha_A} &= \frac{D_b}{2(\rho_{p1} + \rho_{p2})\sqrt{\left(\frac{\alpha_A}{\lambda_A}\right)^2 + \frac{2(\rho_{p1} + \rho_{p2})}{D_b}(\alpha_0 - \alpha_A)}} \left(-\frac{2(\rho_{p1} + \rho_{p2})}{D_b} + \frac{2\alpha_A}{\lambda_A^2}\right) - \frac{D_b}{(\rho_{p1} + \rho_{p2})\lambda_A} \\ &< \frac{D_b}{(\rho_{p1} + \rho_{p2})\sqrt{\left(\frac{\alpha_A}{\lambda_A}\right)^2 + \frac{2(\rho_{p1} + \rho_{p2})}{D_b}(\alpha_0 - \alpha_A)}} \left(-\frac{(\rho_{p1} + \rho_{p2}) + \alpha_A \delta k_{on}}{D_b}\right). \end{aligned}$$

Then, since  $((\rho_{p1} + \rho_{p2}) - \alpha_A \delta k_{on}) \ge 0$  from Result S10, we get  $\frac{\partial x_A}{\partial \alpha_A} < 0$ .

**Result S12.** Suppose  $\delta$  is bounded by the conditions in Result S10. Then, the gradient at the AP border increases (or remains unchanged) in any of the following circumstances:

- 1.  $\alpha_A$  decreases due to a single parameter change (excluding  $p_{p1}$  or  $p_{p2}$ ),
- 2.  $D_b$  decreases,
- 3.  $\alpha_0$  increases.

#### Proof

From Eqn. (15) (main text), this absolute gradient can be approximated by

Case A.  $\alpha_0 \geq \alpha_A$ 

$$g_{A} = \sqrt{\frac{2(\rho_{p1} + \rho_{p2})}{D_{b}}(\alpha_{0} - \alpha_{A}) + \frac{\delta k_{on}\alpha_{A}^{2}}{D_{b}}}$$

Case B.  $\alpha_0 < \alpha_A$ 

$$g_B = \alpha_0 \sqrt{\frac{\delta k_{on}}{D_b}},$$

where  $\alpha_A = \frac{(\rho_{p1} + \rho_{p2} - \gamma_p z_A)(\gamma_{ph} + k_{off})}{(\gamma_{ph} + r(\rho_{p1} + \rho_{p2}))k_{on}z_A}$  is the HH concentration threshold, above which Patched is highly up-regulated.

In both cases A and B, it is clear that  $\frac{\partial g}{\partial D_b} \leq 0$  and  $\frac{\partial g}{\partial \alpha_0} \geq 0$ . Then, since  $g_A = g_B$ , when  $\alpha_A = \alpha_0$ , 2 and 3 must be true.

Therefore, we just need to prove the first case. We assume that  $\rho_{p1} + \rho_{p2}$  and  $\delta$  remain unchanged, and consider the following two cases.

**1a:**  $k_{on}$  increases (leading to a decrease in  $\alpha_A$ ),

**1b:**  $\alpha_A$  decreases independently of  $k_{on}$ ,  $\rho_{p1} + \rho_{p2}$ .

In case 1a,

$$\frac{dg_A}{dk_{on}} = \frac{1}{2D_b\sqrt{\frac{2(\rho_{p1}+\rho_{p2})}{D_b}(\alpha_0-\alpha_A) + \frac{\delta k_{on}\alpha_A^2}{D_b}}} \left(\delta\alpha_A^2 - 2\frac{d\alpha_A}{dk_{on}}\left((\rho_{p1}+\rho_{p2}) - \alpha_A\delta k_{on}\right)\right).$$

Then since,  $\frac{d\alpha_A}{dk_{on}} \leq 0$  and  $((\rho_{p1} + \rho_{p2}) - \alpha_A \delta k_{on}) \geq 0$  (from Result S10), we get  $\frac{dg_A}{dk_{on}} \geq 0$ . Moreover,  $\frac{dg_B}{dk_{on}} = \alpha_0 \frac{\sqrt{\delta}}{2\sqrt{D_b k_{on}}} \geq 0$  and so we get the desired result. In case 1b,

$$\frac{dg_A}{d\alpha_A} = \frac{1}{2D_b \sqrt{\frac{2(\rho_{p1} + \rho_{p2})}{D_b}(\alpha_0 - \alpha_A) + \frac{\delta k_{on} \alpha_A^2}{D_b}}} \left(-2\left((\rho_{p1} + \rho_{p2}) - \alpha_A \delta k_{on}\right)\right).$$

Then since  $((\rho_{p1} + \rho_{p2}) - \alpha_A \delta k_{on}) \ge 0$  (from Result S10), we get  $\frac{dg_A}{d\alpha_A} \le 0$ . Moreover,  $\frac{dg_B}{\alpha_A} = 0$  in this case and so we get the desired result.

Result S13. In Model C,

$$D_b = \left(\frac{x_A(\rho_{p1} + \rho_{p2})}{-\alpha_A\sqrt{\delta k_{on}} + \sqrt{2(\rho_{p1} + \rho_{p2})(\alpha_0 - \alpha_A) + \alpha_A^2\delta k_{on}}}\right)^2.$$

#### Proof

From Eqn. (14) (main text)

$$x_A = \frac{D_b}{\rho_{p1} + \rho_{p2}} \left( -\frac{\alpha_A}{\lambda_A} + \sqrt{\frac{2(\rho_{p1} + \rho_{p2})}{D_b}(\alpha_0 - \alpha_A) + \left(\frac{\alpha_A}{\lambda_A}\right)^2} \right),$$

where

• 
$$\lambda_A = \sqrt{\frac{D_b}{\delta k_{on}}},$$
  
•  $\alpha_A = \frac{(\rho_{p1} + \rho_{p2} - \gamma_p z_A)(\gamma_{ph} + k_{off})}{(\gamma_{ph} + r(\rho_{p1} + \rho_{p2}))k_{on} z_A}$ 

Therefore

$$x_A(\rho_{p1} + \rho_{p2}) = D_b \left( -\frac{\alpha_A \sqrt{\delta k_{on}}}{\sqrt{D_b}} + \sqrt{\frac{2(\rho_{p1} + \rho_{p2})}{D_b}}(\alpha_0 - \alpha_A) + \frac{\alpha_A^2 \delta k_{on}}{D_b} \right)$$
$$= \sqrt{D_b} \left( -\alpha_A \sqrt{\delta k_{on}} + \sqrt{2(\rho_{p1} + \rho_{p2})(\alpha_0 - \alpha_A) + \alpha_A^2 \delta k_{on}} \right).$$

Squaring both sides and rearranging then gives the result.

## References

- Bornemann, D., Duncan, J., Staatz, W., Selleck, S., Warrior, R., 2004. Abrogation of heparan sulfate synthesis in *drosophila* disrupts the wingless, hedgehog and decapentaplegic signaling pathways. Development 131, 1927–1938.
- Casali, A., Struhl, G., 2004. Reading the hedgehog morphogen gradient by measuring the ratio of bound to unbound patched protein. Nature 431, 76–80.
- Eldar, A., Rosin, D., Shilo, B., Barkai, N., 2003. Self-enhanced ligand degradation underlies robustness of morphogen gradients. Dev. Cell 5, 635–646.
- Eugster, C., Pánaková, D., Mahmoud, A., Eaton, S., 2007. Lipoprotein-heparan sulfate interactions in the hh pathway. Dev. Cell 13, 57–71.
- Glise, B., Jones, D., Ingham, P., 2002. Notch and wingless modulate the response of cells to hedgehog signalling in the drosophila wing. Dev. Biol. 248, 93–106.
- Han, C., Belenkaya, T., Wang, B., Lin, X., 2004. Drosophila glypicans control the cell-to-cell movement of hedgehog by a dynamin-independent process. Development 131, 601–611.
- Hufnagel, L., Kreuger, J., Cohen, S. M., Shraiman, B. I., 2006. On the role of glypicans in the process of morphogen gradient formation. Dev. Biol. 300, 512–522.
- Incardona, J., Gruenberg, J., Roelink, H., 2002. Sonic hedgehog induces the segregation of Patched and Smoothened in endosomes. Curr. Biol. 12, 983–995.
- Lin, X., 2004. Functions of heparan sulfate proteoglycans in cell signaling during development. Development 131, 6009–6021.
- Su, V., Jones, K., Brodsky, M., The, I., 2007. Quantitative analysis of hedgehog gradient formation using an inducible expression system. BMC Dev. Biol. 7, 43.
- Tabata, T., Takei, Y., 2004. Morphogens, their identification and regulation. Development 131, 703–712.

# Supplementary figures

#### Parameter sets

This section presents a number of addition figures to supplement those in the main text. In the figures below (S1-2;S5-13) we consider 4 different parameter sets. Default parameters are taken from Table 1 (of main text) but differ as follows

Green:  $r = 0, \rho_{p2} = 0$ 

Blue:  $r = 0, \rho_{p2} = 36$ 

**Red:**  $r = 0.8, \rho_{p2} = 36$ 

**Black Dashed:** r = 0,  $\rho_{p2} = 36$  and  $k_{on}$  increases up to 5-fold in response to high Hh signalling (see *Materials and Methods* in main text)

#### **FigS1:** Anterior concentration profiles

These figures show HH, Total PTC ([PTC] + [PH]), S and Target gene levels across the anterior compartment, when we fix HH levels at the AP boundary ( $\alpha_0$ ). We have matched the four models in four different ways (A-D)

- (A) Models are matched so that HH levels match at the AP boundary.
- (**B**,**C**) Models are matched so that HH levels match at both the AP boundary and 12 cells from the boundary. This is done by changing  $\rho_{p1}$  in the green model and (B)  $k_{on}$  in the blue model; (C)  $k_{on}$  in the red and black dashed model.
- (D) Models are matched so that the magnitude of the HH gradient is equal at the AP boundary. This is done by changing  $\rho_{p1}$  in the green model and  $k_{on}$  in the blue model.

The four different parameter sets (green, blue, red and blacked dashed) are described at the start of this supporting file.



Figure S1: Anterior concentration profiles for the four models and four cases (A-D) described above.

**FigS2:** Posterior-Anterior concentration profiles



Figure S2: HH levels across a 1D cross section of disc for the full anterior-posterior model (posterior right, anterior left).(A) Models are matched so that Hedgehog production is equal  $(\rho_h = 15)$ . (B) Hedgehog production is altered in each model to ensure HH levels are equal at the AP boundary ( $\alpha_0 = 10$ ).  $\rho_h = 30$  (red, black dashed), 15 (blue) and 1.5 (green). Otherwise, the four different parameter sets (green, blue, red and blacked dashed) are as described at the start of this supporting file.

# FigS3 and FigS4: Shift in target gene boundaries for different parameter sets



Figure S3: Shift in target gene boundary in response to changes in Hedgehog production (red). Black dashed lines correspond to theoretical predictions for free diffusion scenario, whilst dotted line corresponds to outer bound in regulated transport case ( $\sqrt{c}$  case in Fig 5A of main text). Diamond corresponds to threshold ( $x_P = L_P$ ) separating the two behaviours. In all cases parameters are taken from Table 1 but differ in the following way (A)  $k_{out} = 10$ ,  $\gamma_f = 6$  and  $D_f$ = 0.6. (B)  $k_{out} = 2.5$  and  $\gamma_f = 24$  and  $D_f = 0.6$ . (C)  $k_{out} = 10$ ,  $\gamma_f = 6$  and  $D_f = 60$ .



Figure S4: Shift in (A,B) HH levels at AP boundary and (C,D) target gene boundary in response to changes in Hedgehog production, for different modes of HH-HSPG interactions (achieved by varying  $\mu$ ,  $\gamma_b$  and  $D_b(P)$  in the model). In all figures red and black lines differ because of the saturation parameter  $\mu$ : red  $\mu = 20$  vs black  $\mu = 2000$ . (A,C) Effect of changing the HH-HSPG degradation rate  $\gamma_b$ : solid line  $\gamma_b = 0.01$  vs dotted line  $\gamma_b = 1$ . (B,D) Effect of changing the HH-HSPG diffusion rate of  $D_b(P)$ : solid line  $D_b(P) = 60$  vs dotted line  $D_b(P) = 120$ . All other parameters are from Table 1 of main text.



FigS5: Robustness to changes in HH levels at the AP boundary

Figure S5: Shift in target gene boundary in response to changes in HH levels at the AP boundary  $(\alpha_0)$ , for the different parameter sets (green, blue, red and blacked dashed) described at the start of this supporting file. Top (High): The base levels of  $\alpha_0$  are taken from FigS1 (A-D) (scaled to 1 on x axis). Bottom (Low): Same but with a base levels of  $\alpha_0$  halved. In all cases, the HH concentration at 12 cells (when  $\alpha_0$  is at its base value) is used to define the target gene boundary.





Figure S6: Shift in target gene boundary, in response to changes in Hedgehog production  $\rho_h$ , for the different parameter sets (green, blue, red and blacked dashed) described at the start of this supporting file. Top: Production rate is the same in each model (as in *Supporting Figure* S2A). Bottom: Base production rate (scaled to 1) varies in each model to ensure they match at the AP boundary (as in *Supporting Figure* S2B). These base production rates are as follows. High: red and black dashed = 30, blue = 15, green = 1.5. Med: red and black dashed = 15, blue = 7, green = 1.15. Low: red and black dashed = 7.5, blue = 3, green = 0.86. In all cases, the HH concentration at 12 cells (when  $\rho_h$  is at its base value) is used to define the target gene boundary.

#### FigS7 and FigS8: Robustness to changes in parameters

Shift in target gene boundary in response to parameter changes. Here, we use the full anteriorposterior model, along with the parameter sets (green, blue, red and blacked dashed) described at the start of this supporting file. In addition, the black dotted line corresponds to the case where r = 0.4 and  $k_{on}$  is increased 3.6-fold in response to signalling (mix of red and black dashed case). Target gene boundaries correspond to the HH concentration at 12 cells, when the parameter in question is at its default value (in Table 1) and  $\rho_h$  is its base value (from *Supporting Figure* S2B). Parameters are varied in the anterior and posterior compartments independently (Fig S7 and Fig S8 respectively)



Figure S7: Shift in target gene boundary, in response to anterior parameter changes. Top:  $D_b(A)$ ,  $D_f$ ,  $\gamma_p$ . 2nd row:  $\gamma_{ph}$ ,  $\gamma_b$ ,  $\gamma_f$ . 3rd row:  $k_{on}$ ,  $k_{out}$ ,  $\rho_{p1}$ . 4th row:  $\rho_{p2}$ ,  $c_p$ ,  $n_p$ . 5th row:  $c_s$ ,  $n_s$ . In all cases, the HH concentration at 12 cells (when parameter is at its base level) is used to define the target gene boundary.

### **Posterior parameters**



Figure S8: Shift in target gene boundary, in response to posterior parameter changes. Top:  $D_b(P)$ ,  $D_f$ ,  $\mu$ . 2nd row:  $\gamma_b$ ,  $\gamma_f$ ,  $k_{out}$ . In all cases, the HH concentration at 12 cells (when parameter is at its base level) is used to define the target gene boundary.





Figure S9: S and target gene response for changing HH levels. In each figure we use parameters and thresholds from A-C of *Supporting Figure* S1.

## FigS10-S11: Supplementary figures for the case $n_p = 4$

In the main simulations, Patched is up-regulated according to a non-linear hill function  $f = \frac{[S]^n}{[S]^n + c^n}$  where c is signalling threshold, for the response, and n is sharpness of that response. In the main text and above figures, we used a relatively high n = 8 since it gave a better fit with experimental data and allowed Patched production to reach a maximum (given that c is relatively large also). Here, we have repeated some of the simulations for the more conservative case n = 4.





Figure S11: Repeat of Fig6A,B for the case  $n_p = 4$ 

## FigS12-S13: Supplementary figures for linear functions

In the main simulations, PTC and S are up-regulated according non-linear hill functions. However, for comparison we have also repeated some of the simulations for the case where these functions are linear. i.e.  $f = \frac{[S]}{2c}$  and  $g = 1 - \frac{[Z]}{2c}$  where c is the threshold corresponding to 50% response and [S] and [Z] are scaled between 0 and 1.



Figure S13: Repeat of Fig6A,B for the case of linear functions

## FigS14-S15: Supplementary figures for alternative positive feedback

In the main model and simulations, the model considers two cases where a negative and positive feedback combine to regulate Hedgehog signalling (red and black dashed lines in Fig 4 and 6). Here, we repeat those simulations, but for an alternative positive feedback (new black dashed line in the Fig. S14 and S15).

Data suggests that an additional positive feedback loop exists between SMO and FU within the signalling pathway, which is functional in response to high levels of signalling. We therefore incorporate this feedback into the model to demonstrate that it has a qualitatively similar function to those already discussed in the main text. In order to incorporate this in the model, we altered the signalling input [Z] to

$$[Z] = \frac{g_z([S])[PTC]}{1 + r[PH]}$$

where  $g_z([S])$  is a decreasing (Hill) function analogous to those used in the main model. Although we don't explicitly add FU and SMO to the model, incorporating the extra interaction in this way ensures that it functions in line with the available experimental data (Claret et al. (2007), Liu et al. (2007))

- (a) The positive feedback is dependent on signalling. i.e. The positive feedback can't sustain a cellular response, following transient Hedgehog exposure
- (b) The positive feedback (FU, in particular) disables the ability of Patched to inhibit signalling.

Other ways of incorporating positive feedback still result in qualitatively similar results (results not shown).



Figure S14: Repeat of Fig4 for the case when the positive feedback loop between SMO and FU is included in the model, alongside the negative feedback up-regulating Patched (Black dashed). Green, Blue, Red are as before.



Figure S15: Repeat of Fig6A,B for the case when the positive feedback loop between SMO and FU is included in the model, alongside the negative feedback up-regulating Patched (Black dashed). Green, Blue, Red are as before.



FigS16: Model Approximations compared to full model

Figure S16: Model B and C approximations (dashed line) to the full model (red line), with  $\gamma(A) = 0.75k_{on}$  and  $\delta k_{on} = 0.6k_{on}$  respectively. The remaining parameters are those in Table 1 of main text.

# Bibliography

- Claret, S., Sanial, M., Plessis, A., 2007. Evidence of a novel feedback loop in the hedgehog pathway involving smoothened and fused. Curr. Biol. 17, 1326–1333.
- Liu, Y., Cao, X., Jiang, J., Jia, J., 2007. Fused-costal2 protein complex regulates hedgehoginduced smo phosphorylation and cell-surface accumulation. Genes & Dev 21, 1949–1963.