The model world

Agent-based models were developed initially in Netlogo 4.1, and then subsequently in Netlogo 5.0. To initialize the model, a series of turtles with the identity of either *cxcr4-cell* or *cxcr7-cell* are spawned. Links are established between neighboring turtles (not including diagonal neighbors). Patches along a horizontal stripe on patch wide at the center of the model world begin releasing Cxcl12a at a constant rate (defined by the Cxcl12a-production slider), which diffuses via the Netlogo *diffuse* primitive. The rate and extent of diffusion can be controlled by the Cxcl12a-diffusion-rate and Cxcl12a-diffusion-distance sliders. Diffusion in the model works by removing a fraction (defined by Cxcl12a-diffusion-rate) from the current patch and distributing it equally among all six neighboring patches. This process is repeated *n* number of times (defined by Cxcl12a-diffusion-distance) to produce the final, diffused, pattern.

At each time step, patches provide basal degradation of Cxcl12a, by removing a set percentage of the Cxcl12a from the patch(s) beneath them. This operation is equivalent to the first-order reaction of the form:

$$d[A]/dt = k[A]$$

Where [A] is the Cxcl12a concentration at the patch, and the rate constant *k* is controlled by the Cxcl12a-degredation slider. In the case of degradation by *cxcr4b*- and *cxcr7b-cells*, a similar equation is used, with k controlled by slider determining the rate of degradation by Cxcr4b and Cxcr7b. While degradation by *cxcr7b-cells*, is relatively high, in our model leading *cxcr4-cells* also degrade local Cxcl12a, albeit at a lower rate than *cxcr7-cells*. This degradation by *cxcr4-cells* was essential for leading fragment stretching after severing from trailing cells. To simplify in this case, we assume that the receptors are not limiting for internalization, and do not include a separate term for receptor expression. To model the greater ability of the Cxcr7b protein to internalize and degrade local Cxcl12a, *cxcr7-turtles* also degrade Cxcl12a in all patches which are direct neighbors, and the net degradation rate of these turtles is the sum of the degradation rates assigned to Cxcr4 and Cxcr7.

Agent behavior in response to Cxcl12a

As we assume that all cells in the PLLp contain some level of Cxcr4b protein, all turtles are competent to respond to Cxcl12a. At each time step, turtles choose a heading randomly within a 120-degree cone around their previous heading and sample the amount of Cxcl12a on the patch ahead of them. Each turtle then determines whether or not it is mechanically restricted from moving by checking whether or not a turtle is present in a 90-degree cone around their current heading. If so, the turtle randomly selects another heading within a 120-degree cone and does nothing further.

If no turtle is present, the agent then calculates whether or not to move in the current heading. In threshold mode, the turtle checks whether the saturating function Cxcl12a / (1 + Cxcl12a) for the patch directly ahead is above the defined threshold. If so, the turtle moves forward a set number of patches (defined by the move variable). If not, the turtle does nothing. In gradient mode, the turtle checks whether the gradient between the current patch and the patch ahead is above a threshold (again, provided by the function Cxcl12a-gradient / (1 + Cxcl12a-gradient). If the gradient is above the gradient threshold, then the turtle moves forward. If not, the turtle does nothing.

After agents have moved, the model recalculates the agent positions based on spring properties of the links that join the agents using the Netlogo *layout-spring* primitive and parameters that can be defined by the user (*spring-constant*, *spring-length* and *repulsion-constant*).

Turtle behavior after cutting

pLLP cutting and rejoining is performed by calculating the links that join turtles at the position defined by the cut-position slider. Links at this position are removed, but the identity of these links (in terms of the turtles they join) is saved. This results in two separate populations of linked cells are subsequently treated independently in the *layout-spring* operation but otherwise operate the same as turtles described above. At each time point a check is performed to see whether turtles from one group are within a minimum range of turtles from the other group (typically within one patch). If this check is passed, the links that were cut are re-established and the agents are reconnected into a single group. Note that to simplify “re-connection”, only one turtle needs to be in range of its previous partner turtle for complete reconnection of all severed links.

For more details on manipulating the model, see the “Info” tab in the model itself.

Click here to Download PLLp model

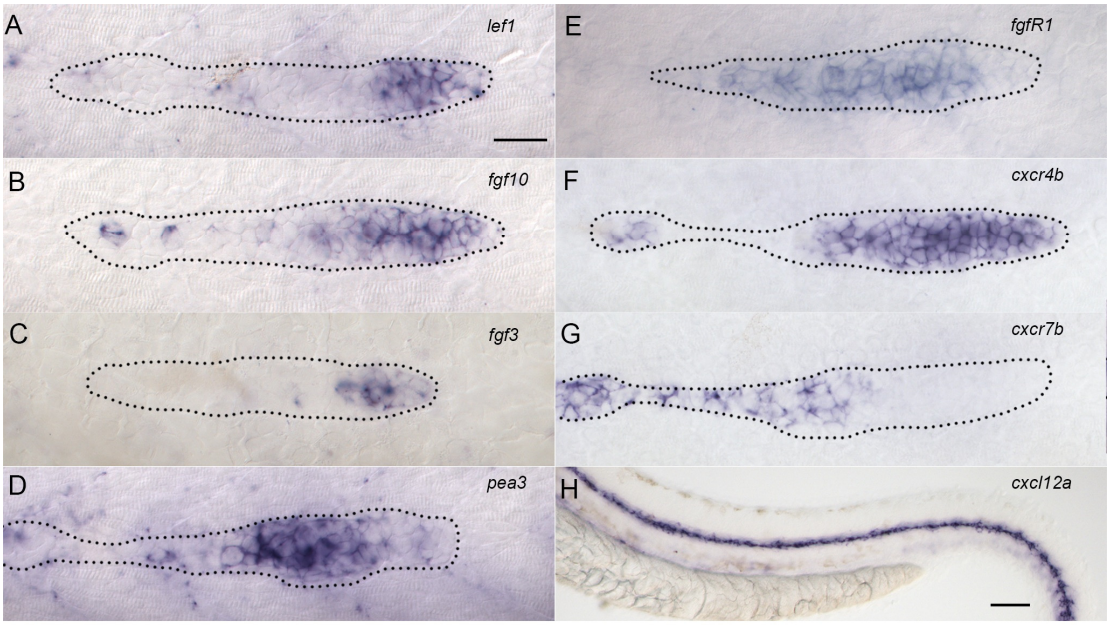


Figure S1
Expression patterns for a selected set of lateral line genes at 32hpf. Scale bar in A-G 10 µm, in H 50 µm.

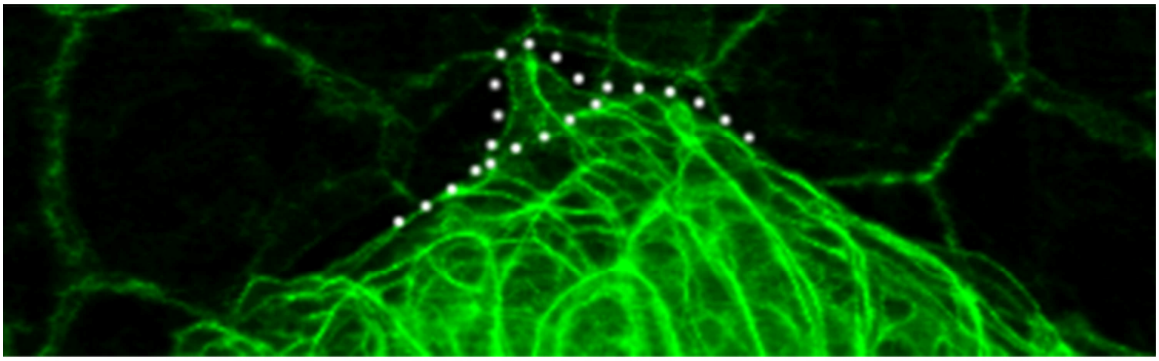


Figure S2: Example of a lateral protrusion from a PLLp after induction of *cxcl12a* expression quantified in figure 2D

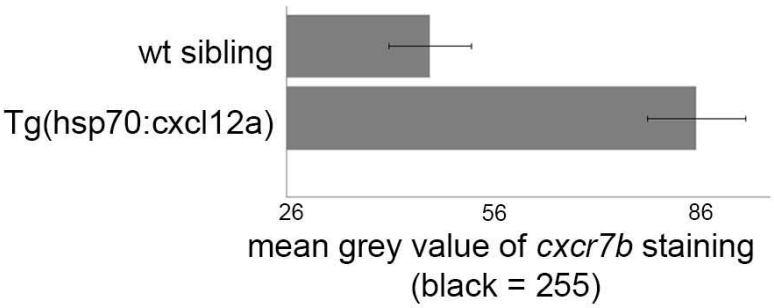


Figure S3: Quantification of mean grey value (+/- st. dev.) for *cxcr7b* staining in *Tg(hsp70:cxcl12a)* and wt sibling embryos 4 hours after heat shock for 30 minutes at 37.5C. Graph is scaled to the average grey value of the *cxcr7b*-free domain of the pLLP (= 26).
$p < 0.001$, Student's two-tailed t-test.

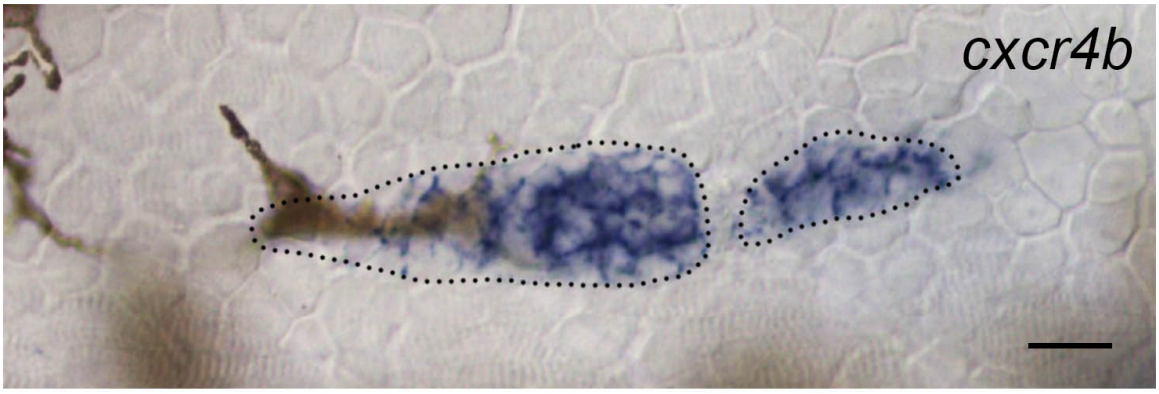


Figure S4
Expression of *cxcr4b* in the PLLp after ablation to sever leading cells. Note that *cxcr4b* is unpolarized in leading cells, while expression remains polarized in trailing cells, as in the unablated PLLp. Scale bar 10 μM.

Table S1. Embryos examined for each ablation condition. Summary of number of embryos examined for each experimental condition described in the text.

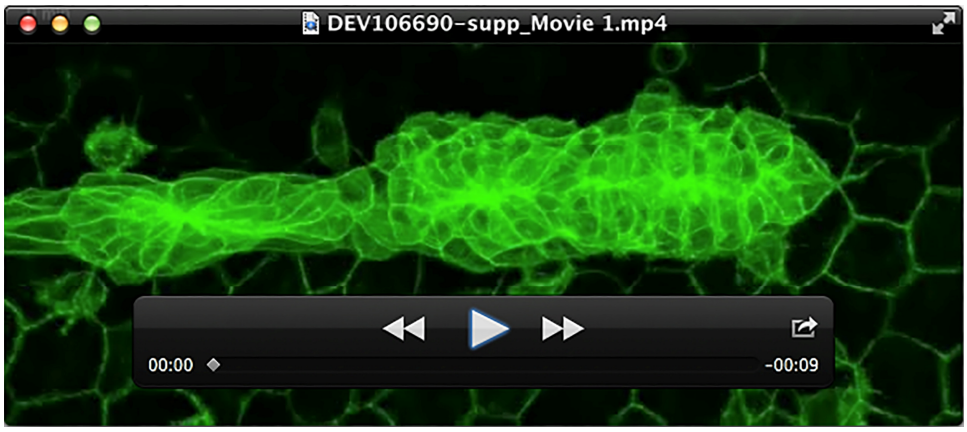
Condition	n (embryos)
Basic Ablations	
Leading edge severed	4
Isolated with front and back	4
Isolated	13
Isolated with back	5
Isolated with front	5
Treated embryos	
with SU5402	9
With SU5402 washout	7
With Chalcone-4-Hydrate	13
Tg(hsp70l:dnfgfr1)	6
Tg(hsp70l:dnfgfr1) sibling control	3
Bilateral Bead Transplants	
Trailing FGF bead	6
Leading FGF bead	6
Total	82

Table S2: table of pairwise statistical significance of middle fragment centroid movement in various experimental conditions (see Fig. 4N). Students 2-tailed t-test. NS $p > 0.05$

						with SU5402	hs:dnFGFR1	hs:dnFGFR1 sibling
		X	NS	$p < 0.01$	$p < 0.001$	$p < 0.01$	$p < 0.01$	NS
			X	$p < 0.01$	$p < 0.001$	$p < 0.05$	$p < 0.01$	NS
				X	NS	NS	$p < 0.01$	$p < 0.05$
					X	$p < 0.05$	$p < 0.01$	$p < 0.001$
	with SU5402					X	NS	$p < 0.05$
	dnFGFR1						X	NS
	dnFGFR1 sibling							X

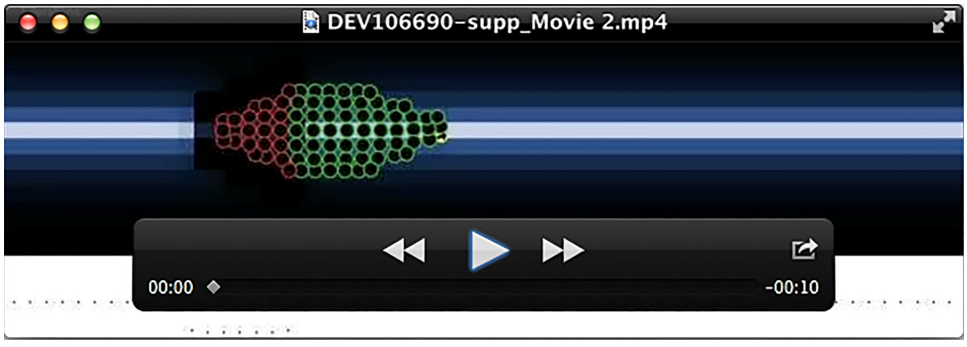
Movie S1

Time-lapse movie of PLLp in *Tg(hsp:cxcl12a)* embryos after 1 hour heatshock at 37.5°C.



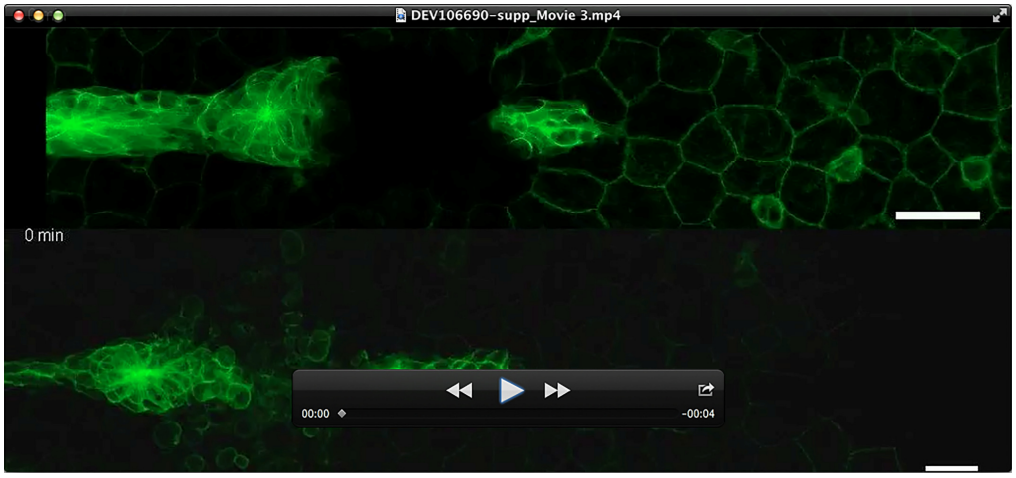
Movie S2

Migration of model PLLp (red and green circles) along a stripe of Cxcl12a (blue). Graph indicates Cxcl12a level at the midline. Yellow turtles show active movement, and arrow within turtles indicates direction of movement.



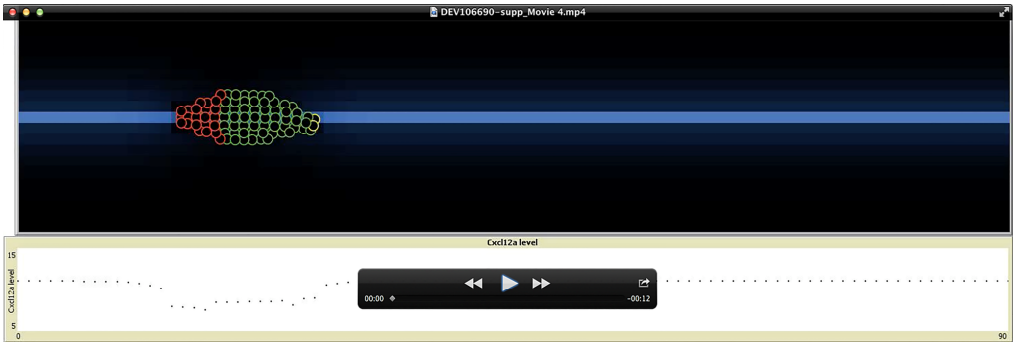
Movie S3

Two examples of laser ablation separating a leading fragment from the rest of the PLLp in a *Tg(cldnb:lynEGFP)* embryo. Movie starts at approximately 32hpf. Scale bar = 20µm.



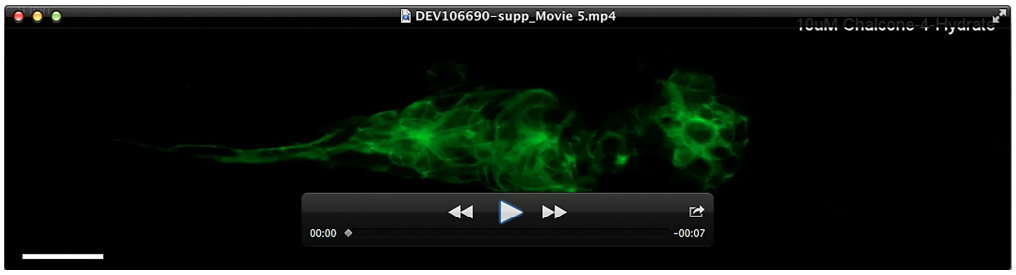
Movie S4

Model output when ~20 cells are severed from the tip of the PLLp. Graph indicates Cxcl12a level at midline.



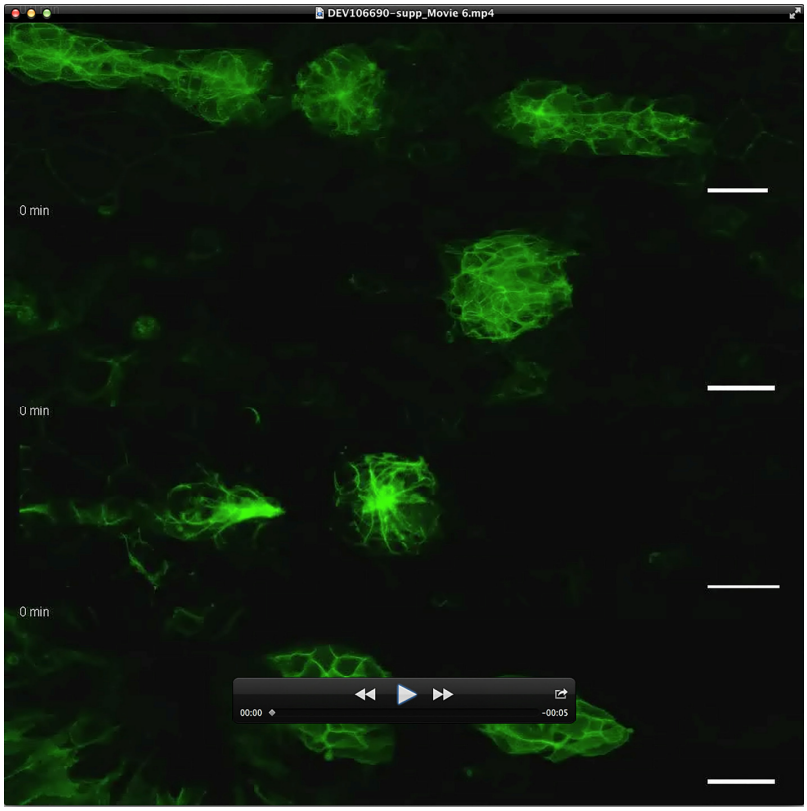
Movie S5

Laser ablation separating a leading fragment from the rest of the PLLp in a *Tg(cldnb:lynEGFP)* embryo treated with 10 µM Chalcone-4-Hydrate. Scale bar 10µm.



Movie S6

Laser ablation to isolate PLLp fragments in *Tg(cldnb:lynEGFP)* embryos. Top panel: Laser ablation of cells surrounding a protoneuromast in a *Tg(cldnb:lynEGFP)* embryo. Second panel: ablation of leading and trailing cells leaving an isolated neuromast. Third panel: ablation mechanically isolating a protoneuromast and ablation of leading cells. Lower panel: ablation mechanically isolating a protoneuromast and ablation of trailing cells. Movies start at approximately 32hpf. Scale bar = 20 µm.



Movie S7

Top panel: laser ablation mechanically isolating a protoneuromast and ablation of trailing cells in the presence of 80 µM SU5402 in a *Tg(cldnb:lynEGFP)* embryo. Bottom Panel: laser ablation mechanically isolating a protoneuromast and ablation of trailing cells in the presence of 80µM SU5402 followed by washout of SU5402 with fresh embryo media in a *Tg(cldnb:lynEGFP)* embryo. Movies start at approximately 34hpf. Scale bar = 20 µm.

Movie S8

Behavior of an isolated PLLp fragment with beads soaked in recombinant human FGF3 placed either caudally (top panel) or rostrally (bottom panel). BSA soaked beads are transplanted on the opposite side to the FGF3 soaked beads. Scale bar = 20 µm.