Supplementary Figures

The simulation results in this supplement illustrate that the Nodal community effect model is not sensitive to any of its curve fitted kinetic parameters.

Each figure is accompanied by an explanatory caption.

Supplementary Figures

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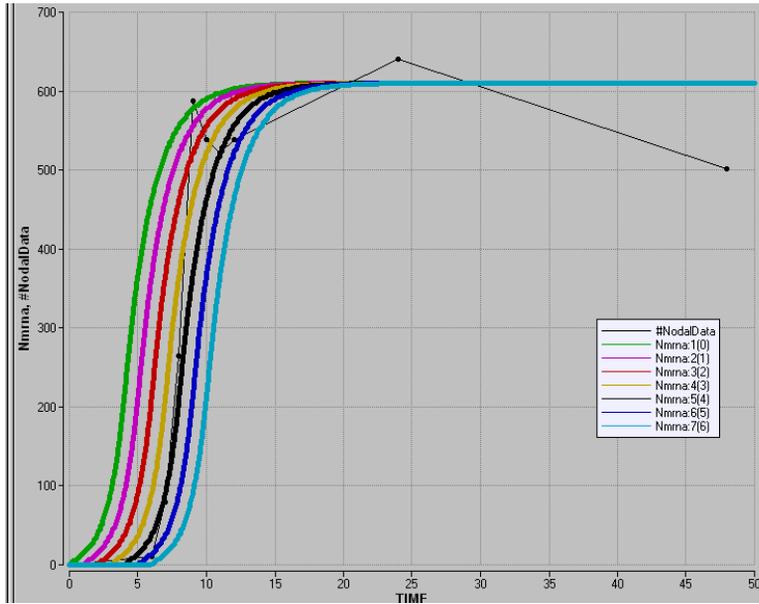Each figure is accompanied by an explanatory caption.

Fig. S1. Effect of varying the onset time of the ubiquitous activating input to *nodal* (between 0 and 6 hours hpf). Experimental data are shown as black disks. Variations in the time at which the initial activators becomes available have little effect on the *nodal mRNA* time-course. In particular, the state value of Nodal mRNA is not affected by the onset time.
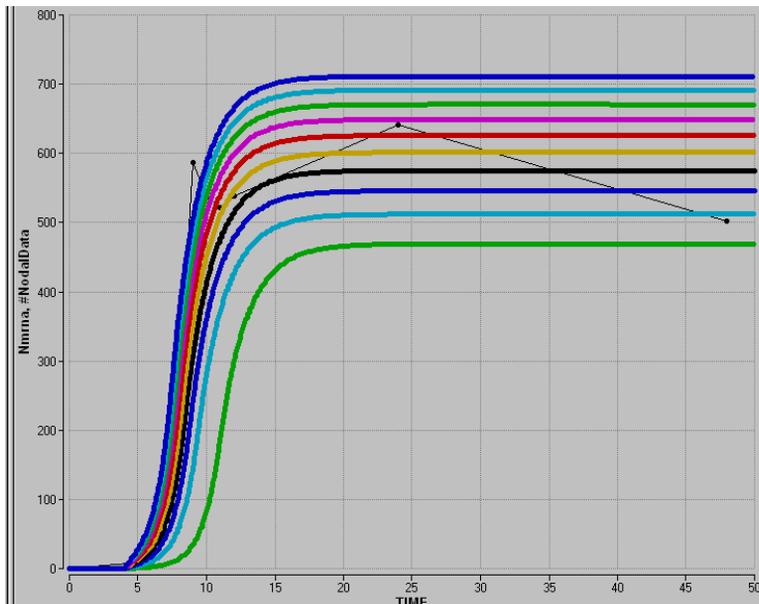

Fig. S2. Varying the magnitude of the initial activating input s to *nodal* within +/- 50% of nominal value has little effect on the time-course profile of *nodal mRNA*. Measured *nodal mRNA* levels are indicated as black disks.
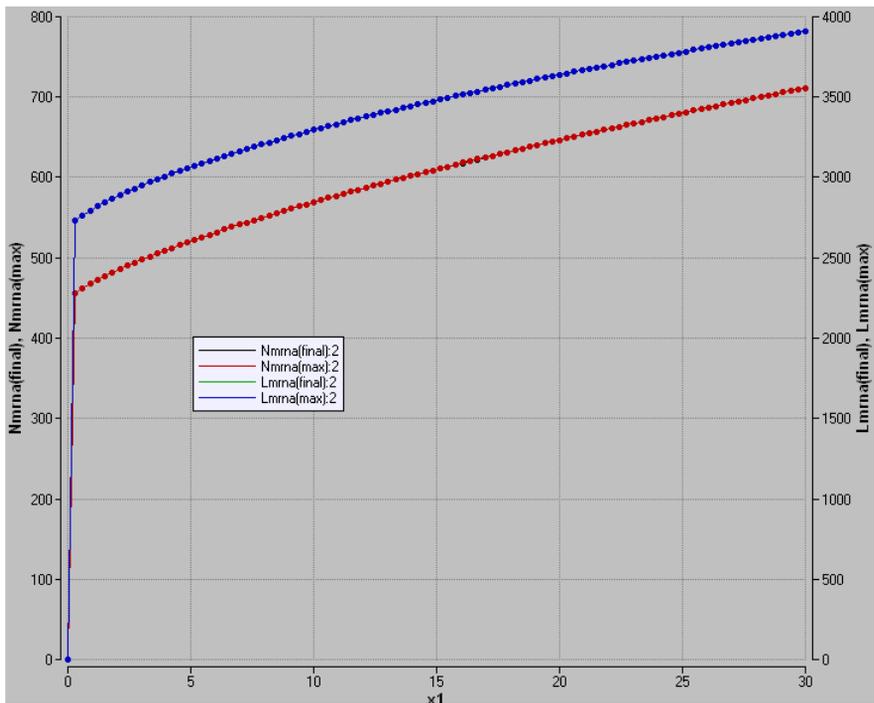
Fig. S3. Steady state levels of Nodal (red, left axis) and Lefty (blue, right axis) mRNA molecules as functions of the magnitude of the initial *nodal* activators. As shown, the magnitude of this activation has little effect on steady states of *nodal* and *lefty mRNA*. The nominal magnitude of the activator used in all simulations is 15, in the middle of the x axis.
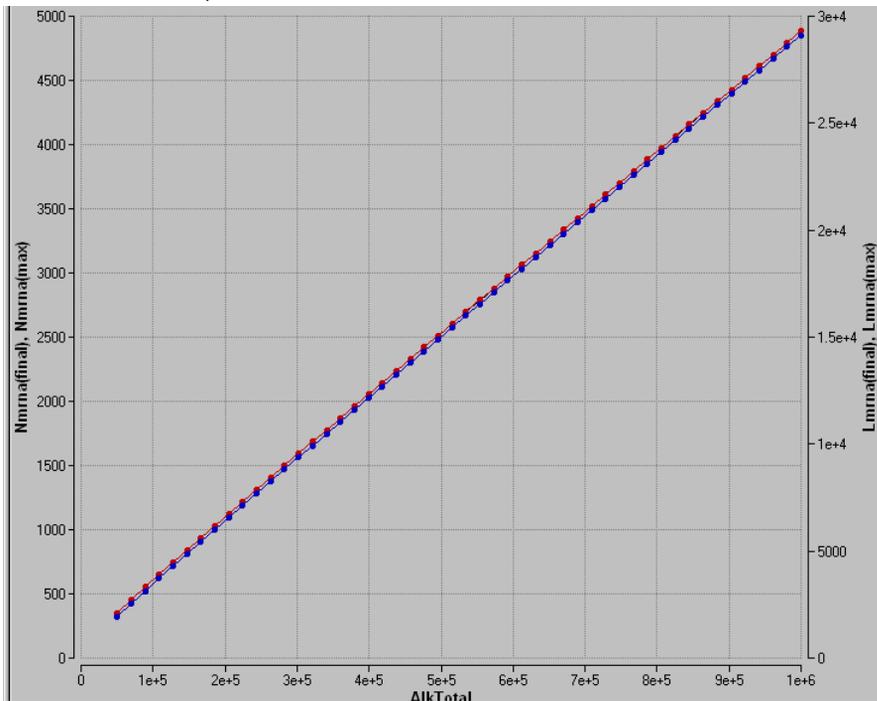

Fig. S4. The effect of varying the assumed number of Alk4 receptors per cell on steady state levels of *nodal and lefty mRNA*. Since both are modeled as linear functions of Nodal:Alk4 complex abundance, they are also linear functions of total number of Alk4 molecules, as shown.
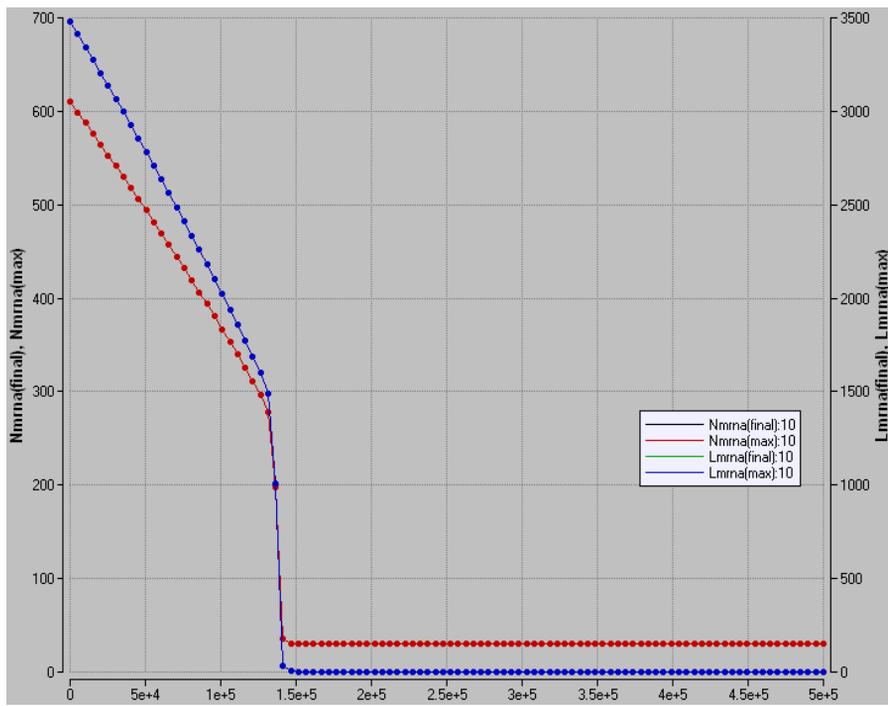
Fig. S5. The effect of varying the Lefty diffusion rate. Shown are the levels of *nodal* (red, left axis) and *lefty* (blue, right axis) mRNA molecules as functions of the amount of Lefty protein diffusing in from neighboring cells. For up to ~ 1.5×10^5 molecules of Lefty diffusing into a cell from the outside, the positive feedback loop via Nodal dominates. Such cells become part of the community effect zone. When more than ~ 1.5×10^5 molecules of Lefty protein diffuse in to a cell, they shut down *nodal* (and therefore *lefty*) transcription to basal levels.
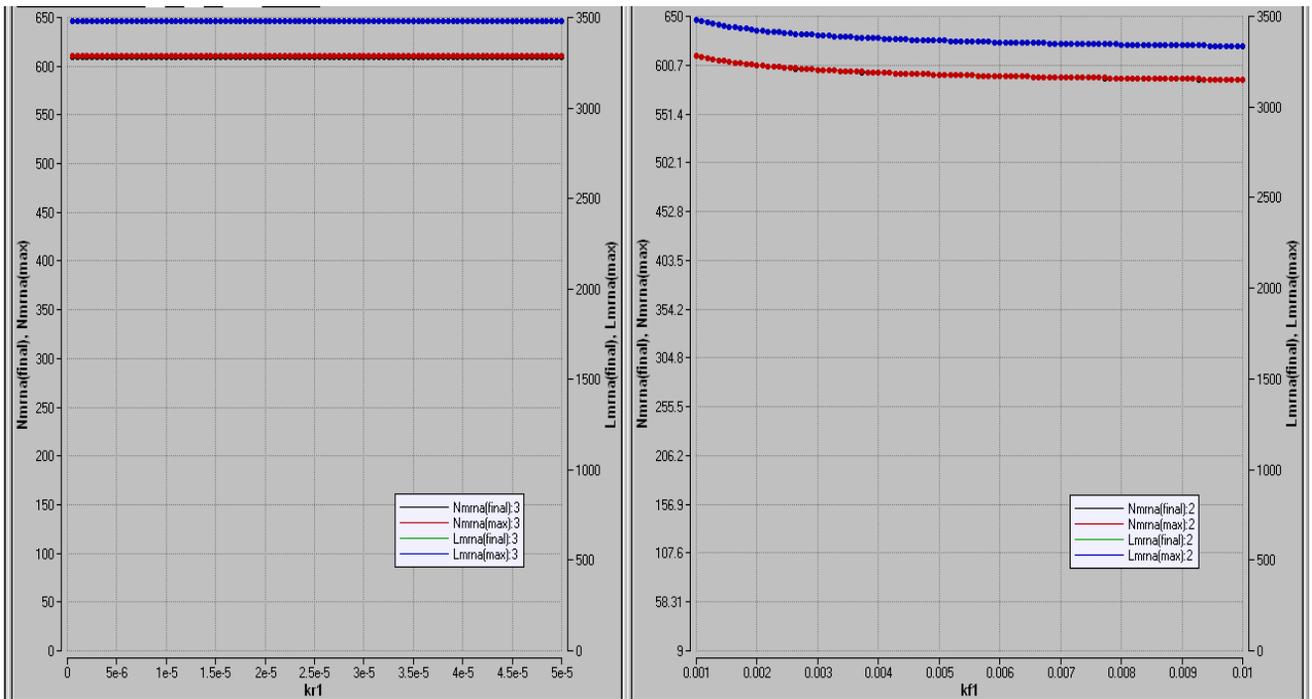

Fig. S6(a). The model is not sensitive to the assumed kinetic rates of Nodal, Lefty and Alk4 protein interactions. (a). Changing the forward (kf1, right panel) and reverse (kr1, left panel) rates of Lefty-Alk4 binding within 1 order of magnitude has little effect on *nodal mRNA* (red, left axis) and *lefty mRNA* (blue, right axis) steady state levels.
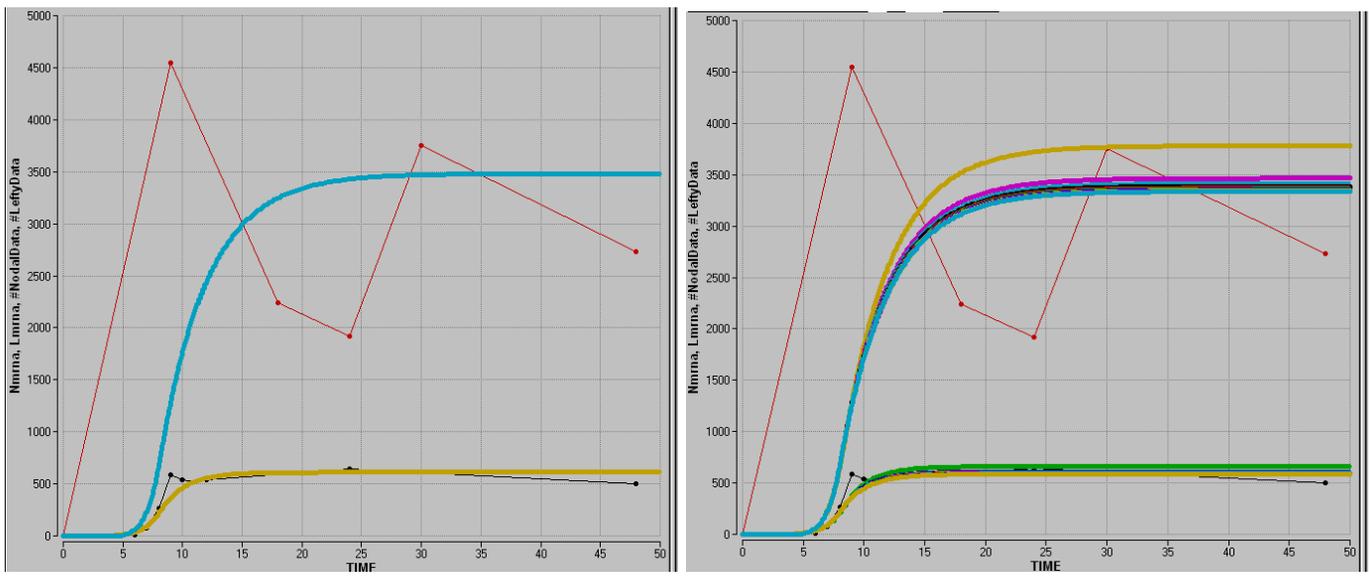
Fig. S6(b). Same as previous simulation, but here 10 sample time course profiles over the full parameter range are shown, indicating that the time course profiles are not affected by one order of magnitude changes in kinetic parameter values.
For comparison, *nodal* and *lefty mRNA* data are shown in black and red respectively.
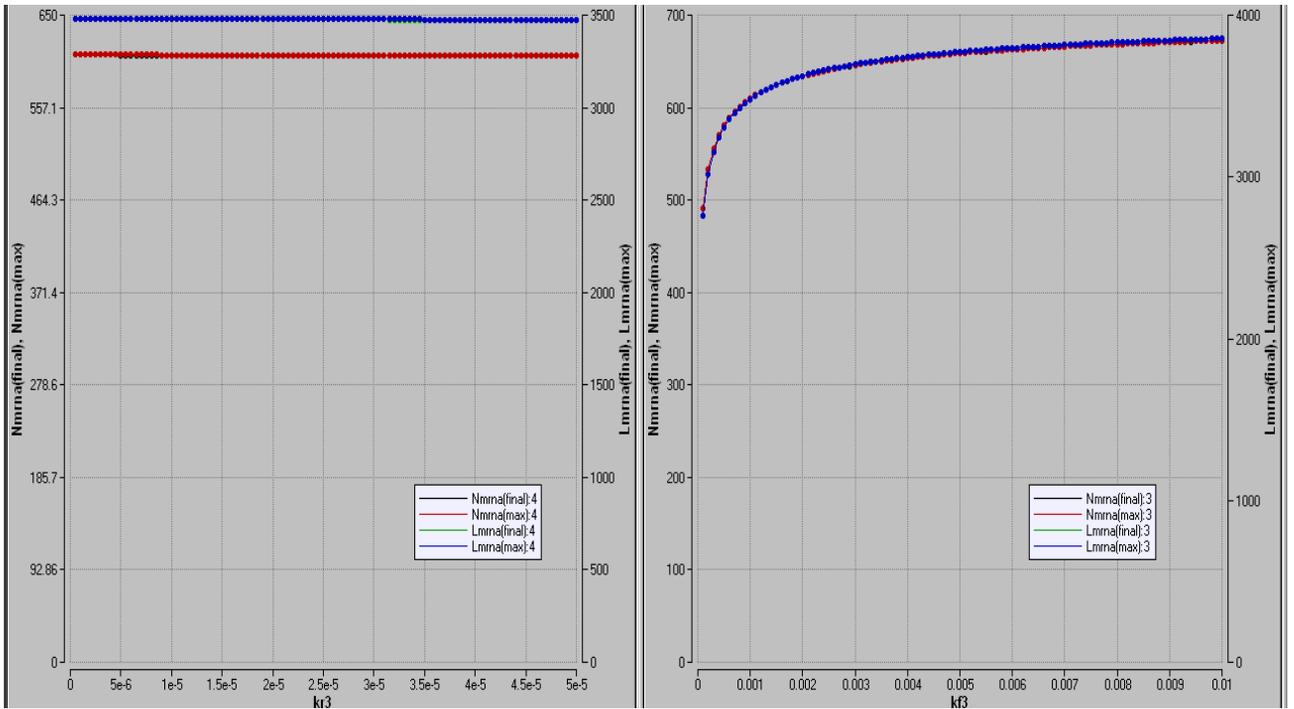

Fig. S6(c). Changing the forward (kf3, right panel) and reverse (kr3, left panel) rates of Nodal-Alk4 binding within 1 order of magnitude has little effect on *nodal mRNA* (red, left axis) and *lefty mRNA* (blue, right axis) steady state levels.
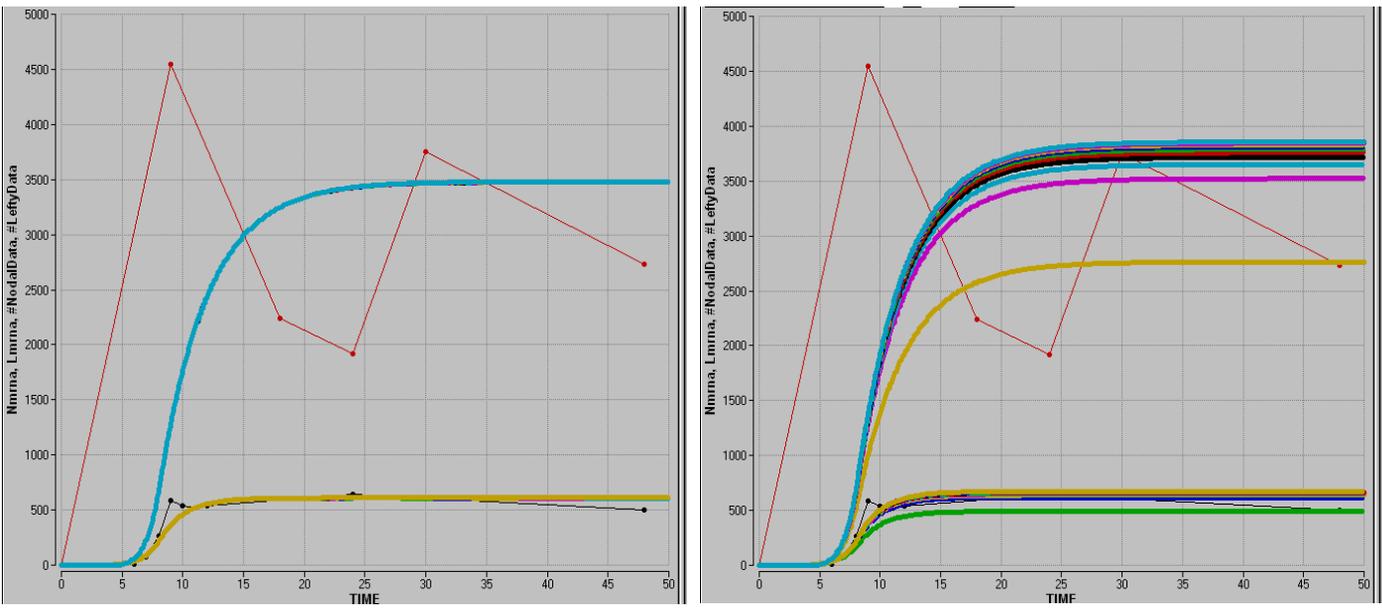
Fig. S6(d). Same as previous simulation, but here 10 sample time course profiles over the full parameter range are shown, indicating that the time course profiles are not affected by one order of magnitude changes in kinetic parameter values. For comparison, *nodal* and *lefty mRNA* data are shown in black and red respectively.