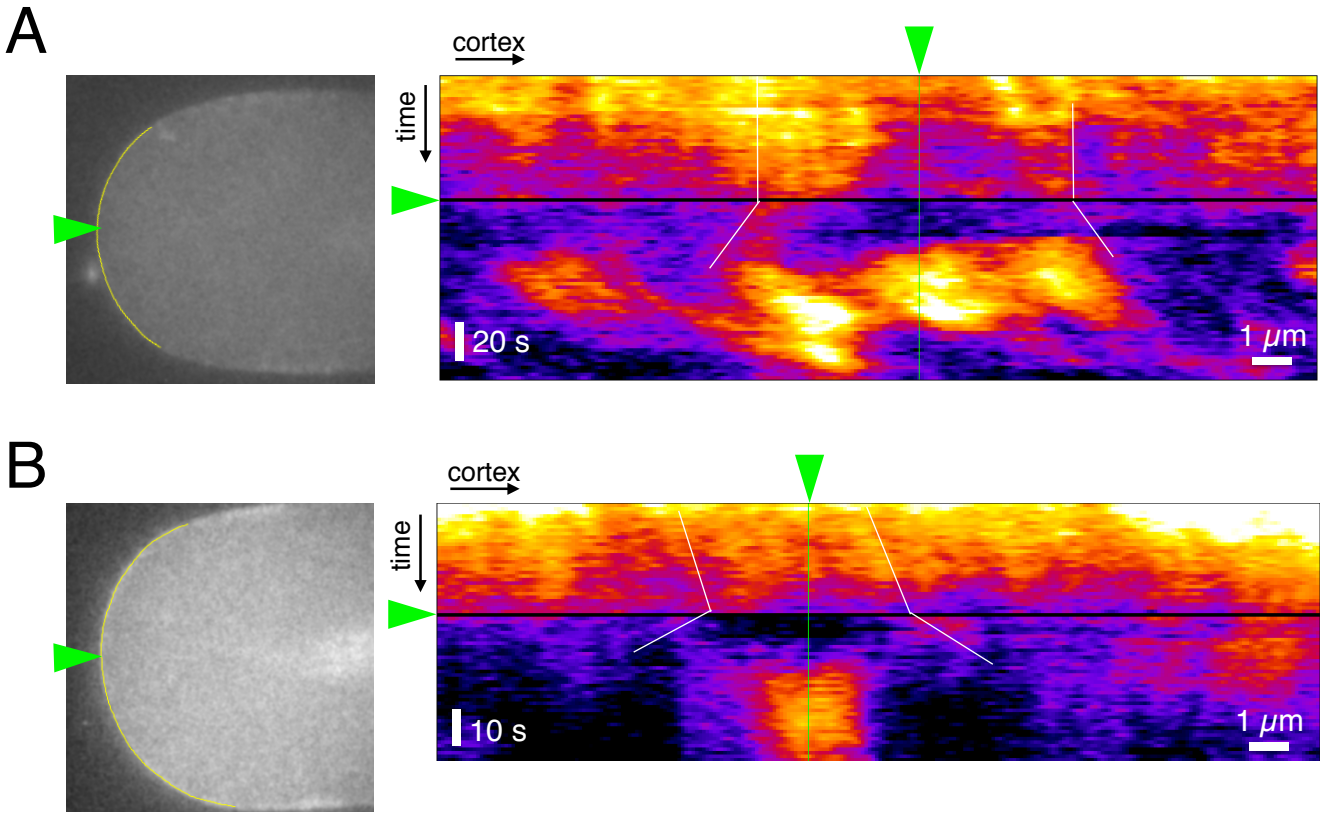
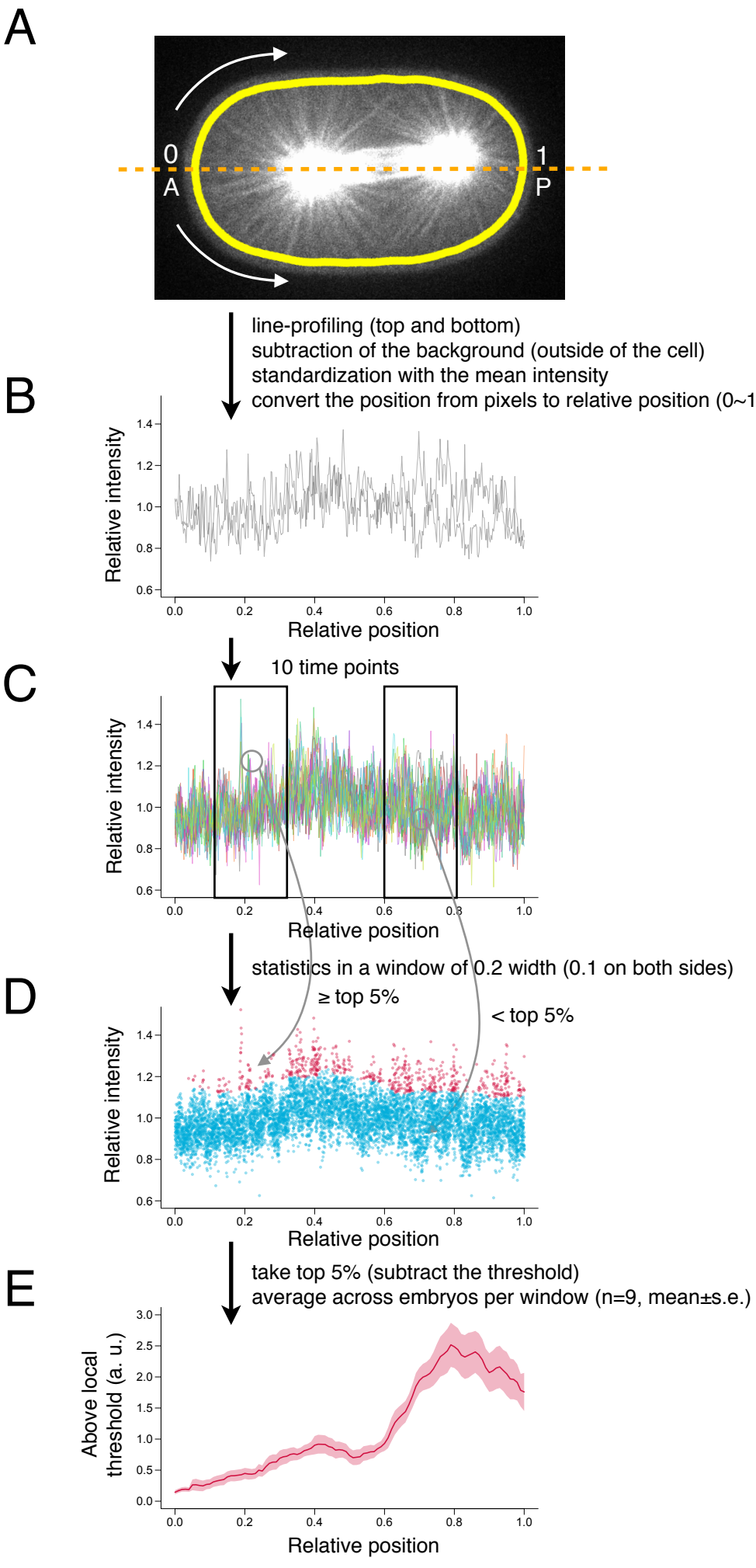


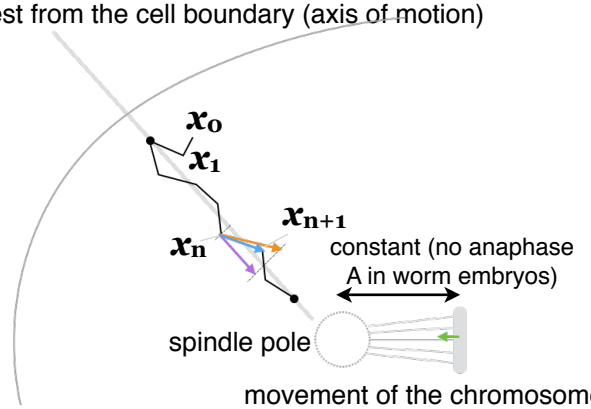
Chapa y Lazo, et al. Fig. S1



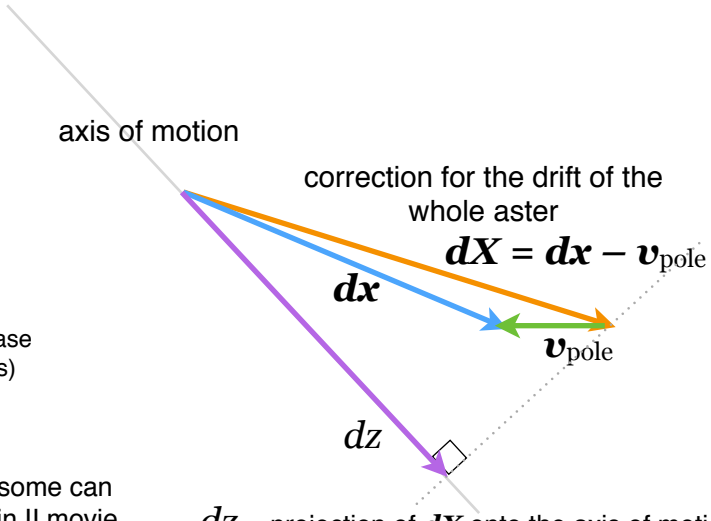
Chapa y Lazo, et al. Fig. S2

A

a straight line linking the points closest to and furthest from the cell boundary (axis of motion)



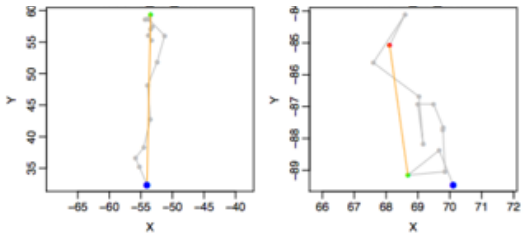
movement of the chromosome can be measured in the myosin II movie



dz = projection of dX onto the axis of motion
= the component of the motion towards the centrosome

B

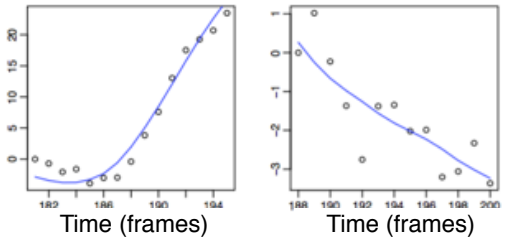
(x, y) coordinates of a trajectory x_i



- the point furthest from the cortex
- the start point
- the end point

C

centrosome-directed component of the movement z

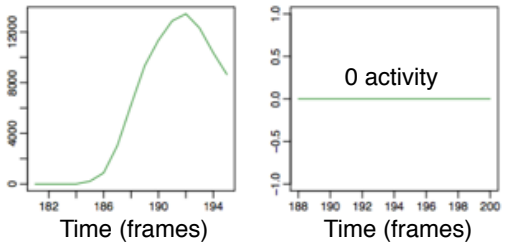


$$z = \sum_{i=0}^{N} dz_i$$

z' : z smoothened

D

centrosome-directed transporting activity



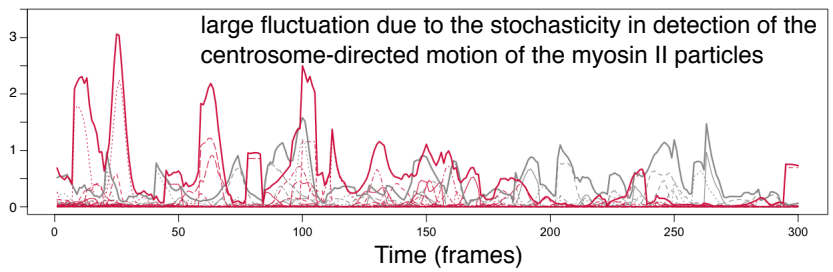
I : intensity (~size) of particle

$$\text{activity} = \begin{cases} 0 & (\text{if } dz' < 0) \\ I \cdot dz'^2 & (\text{if } dz' \geq 0) \end{cases}$$

E

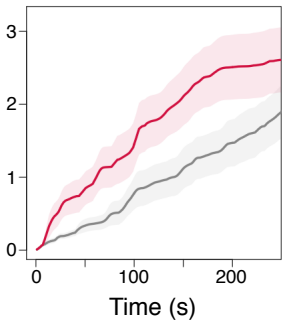
transporting activity of all the detected particles (a. u.)

multiple embryos

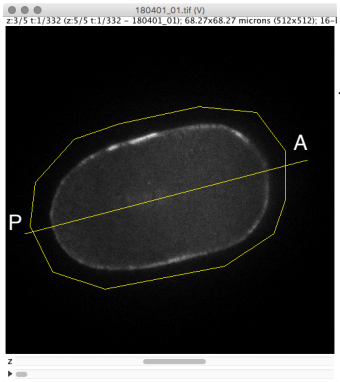


F

cumulative sum of the transporting activity (a.u.)



Chapa y Lazo, et al. Fig. S3

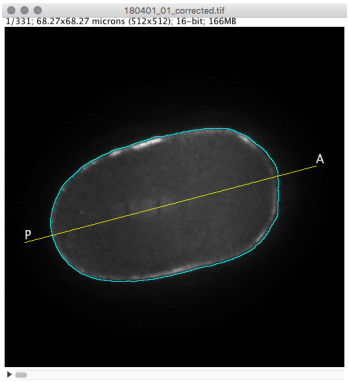


original 4D image of NMY-2::GFP
16 bit, 512 (x) × 512 (y) × 5 (z) × 300 (t)

a polygonal ROI surrounding an embryo
and the A-P axis are manually specified

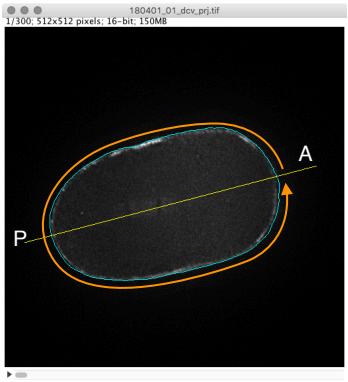
corrected for photobleaching
average z-projection

deconvolution
average z-projection
correction for photobleaching



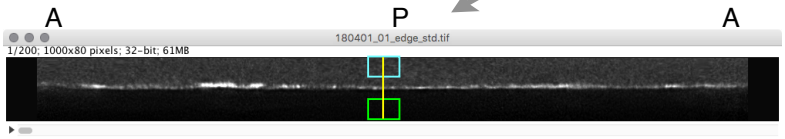
16 bit, 512 (x) × 512 (y) × 1 (z) × 300 (t)

segmentation frame by frame
coordinates of the cell periphery



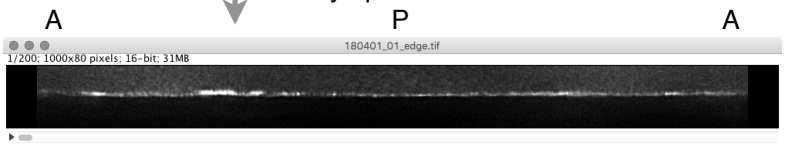
16 bit, 512 (x) × 512 (y) × 1 (z) × 300 (t)

straighten along the cell periphery frame by frame

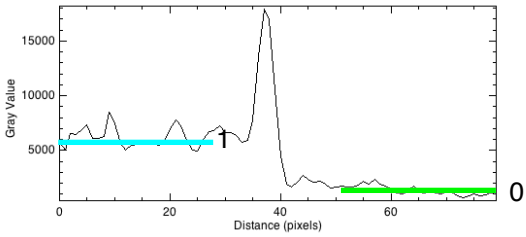


16 bit, 1000 (x) × 80 (y) × 1 (z) × 200 (t)

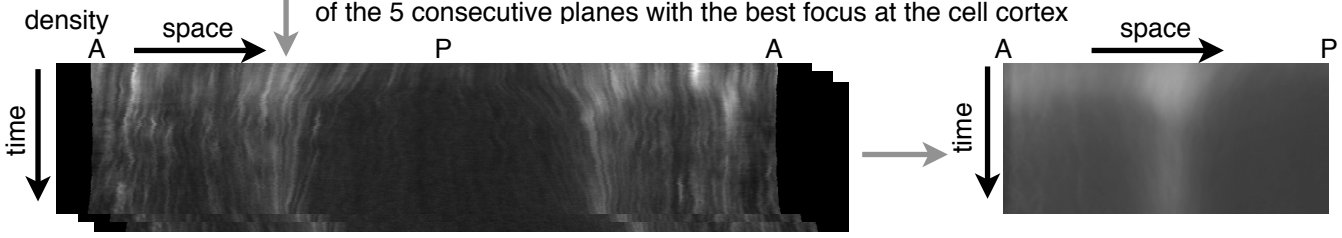
normalization with local background
and cytoplasmic levels



32 bit, 1000 (x) × 80 (y) × 1 (z) × 200 (t)



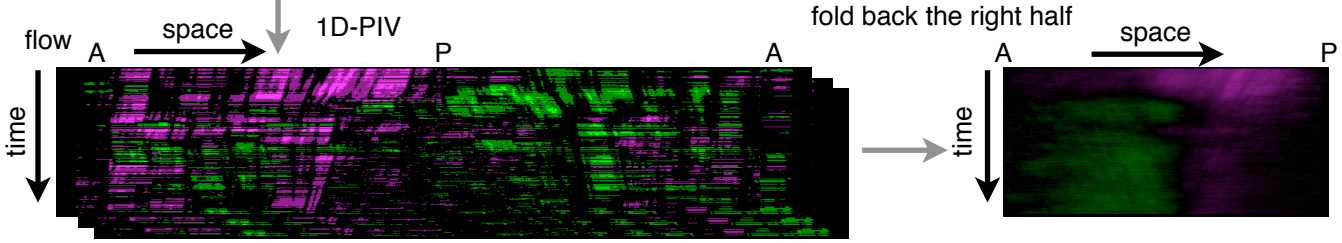
reslice with horizontal lines with 1 pixel intervals & average projection
of the 5 consecutive planes with the best focus at the cell cortex



32 bit, 1000 (x) × 200 (y=t), multiple embryos

average across embryos
fold back the right half

1D-PIV

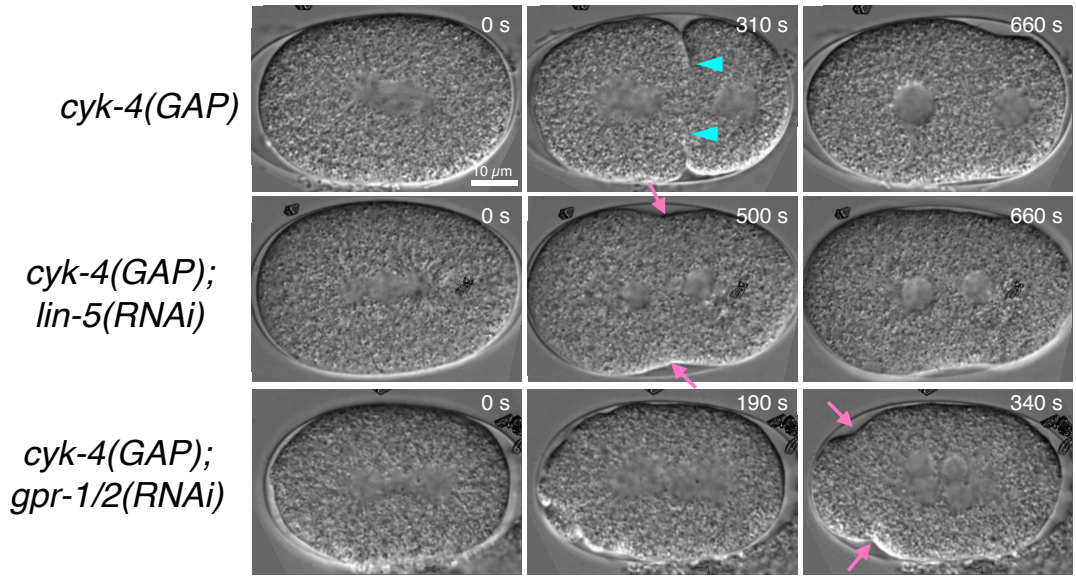


32 bit, 1000 (x) × 200 (y=t), multiple embryos

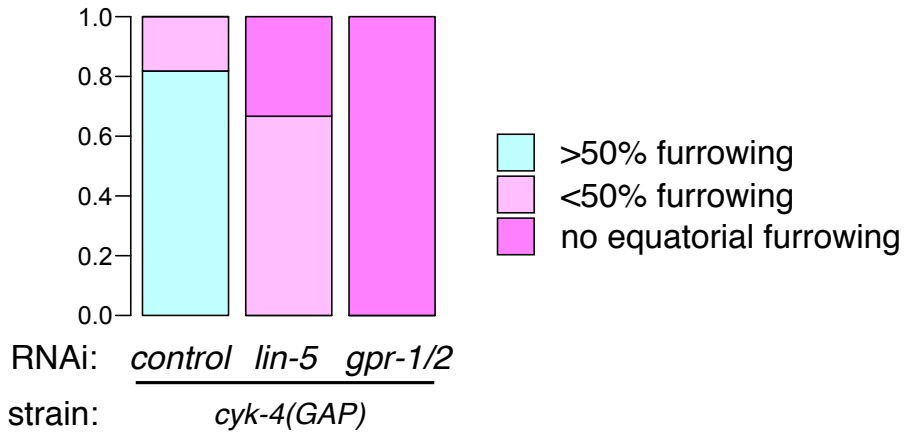
P to A A to P

Chapa y Lazo, et al. Fig. S4

A


cyk-4(GAP)
cyk-4(GAP); lin-5(RNAi)
cyk-4(GAP); gpr-1/2(RNAi)
0 s
310 s
660 s
10 µm
0 s
500 s
660 s
0 s
190 s
340 s

B


1.0
0.8
0.6
0.4
0.2
0.0
RNAi: control lin-5 gpr-1/2
strain: cyk-4(GAP)
>50% furrowing
<50% furrowing
no equatorial furrowing