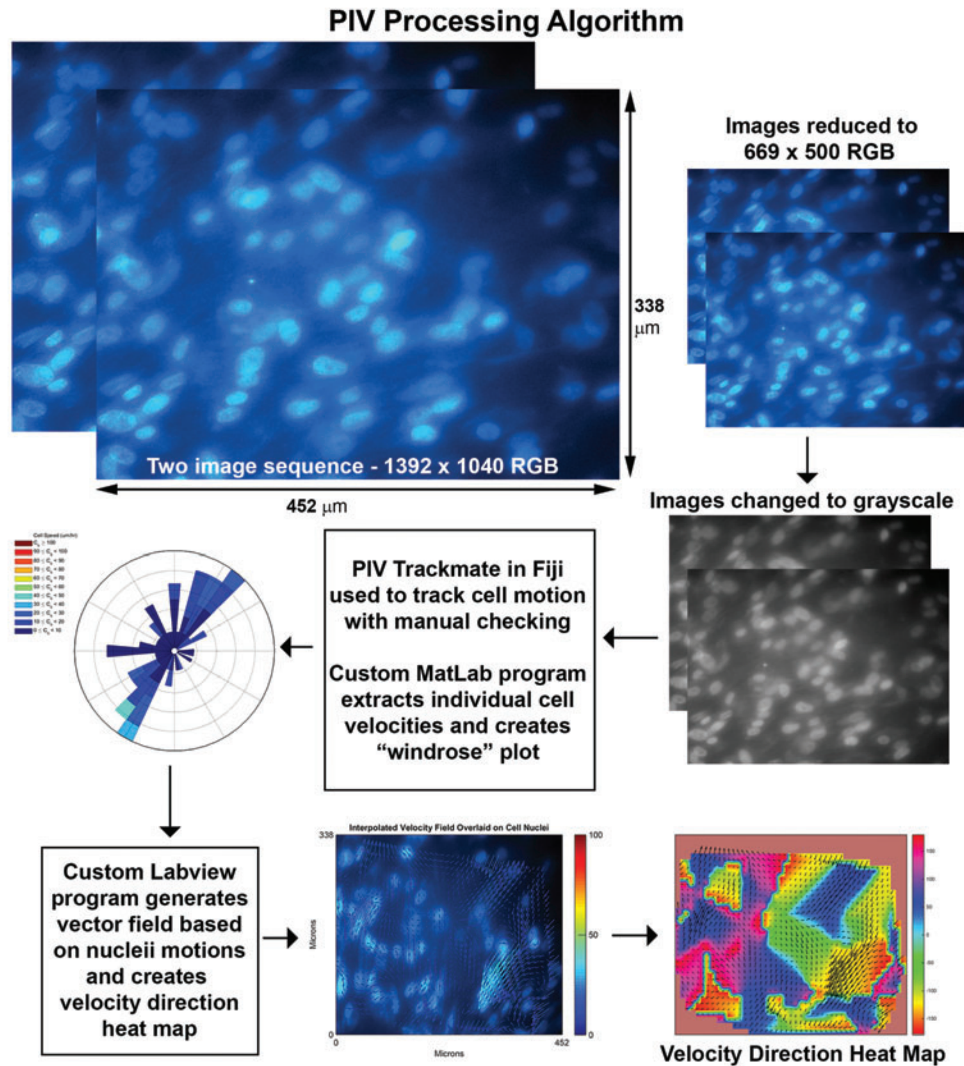

SUPPLEMENTARY FIG. S2. PIV processing algorithm. Nuclei, fluorescently labeled with a live Hoechst stain, were imaged at $20\times$ every hour during the experimental period to produce a series of RGB images (each 1392×1040 pixels). The example image sequence shown is from a single coverslip position separated in time by 1 h. The images were reduced to 669×500 pixels and converted to gray scale. The grayscale series was imported into Fiji and the Trackmate plug-in was used to find the displacement vectors for each trackable cell. Trackmate manual track correction was used to repair errors in tracking and each track was visually examined. The displacement vectors, converted into velocity vectors, were imported into a custom Matlab program to produce the windrose plots. Windrose plots show the velocity direction, magnitude, and frequency of cellular motion in a particular direction. The scale correlates color with velocity magnitude. The number of cells moving in a particular direction correlates with the radial length of a wedge. Each wedge is a 5° bin. In the same program, the individual velocity vectors were interpolated to produce vector fields, which were then overlaid on the processed image of the stained cell nuclei (velocity magnitude reflected in vector length and color and the scale bar correlates vector color with velocity in µm/h). Interpolated cell motion direction heat map with overlaid interpolated velocity field (velocity magnitude reflected in vector length). Scale bar correlates direction of cell motion with color. PIV, particle imaging velocimetry.