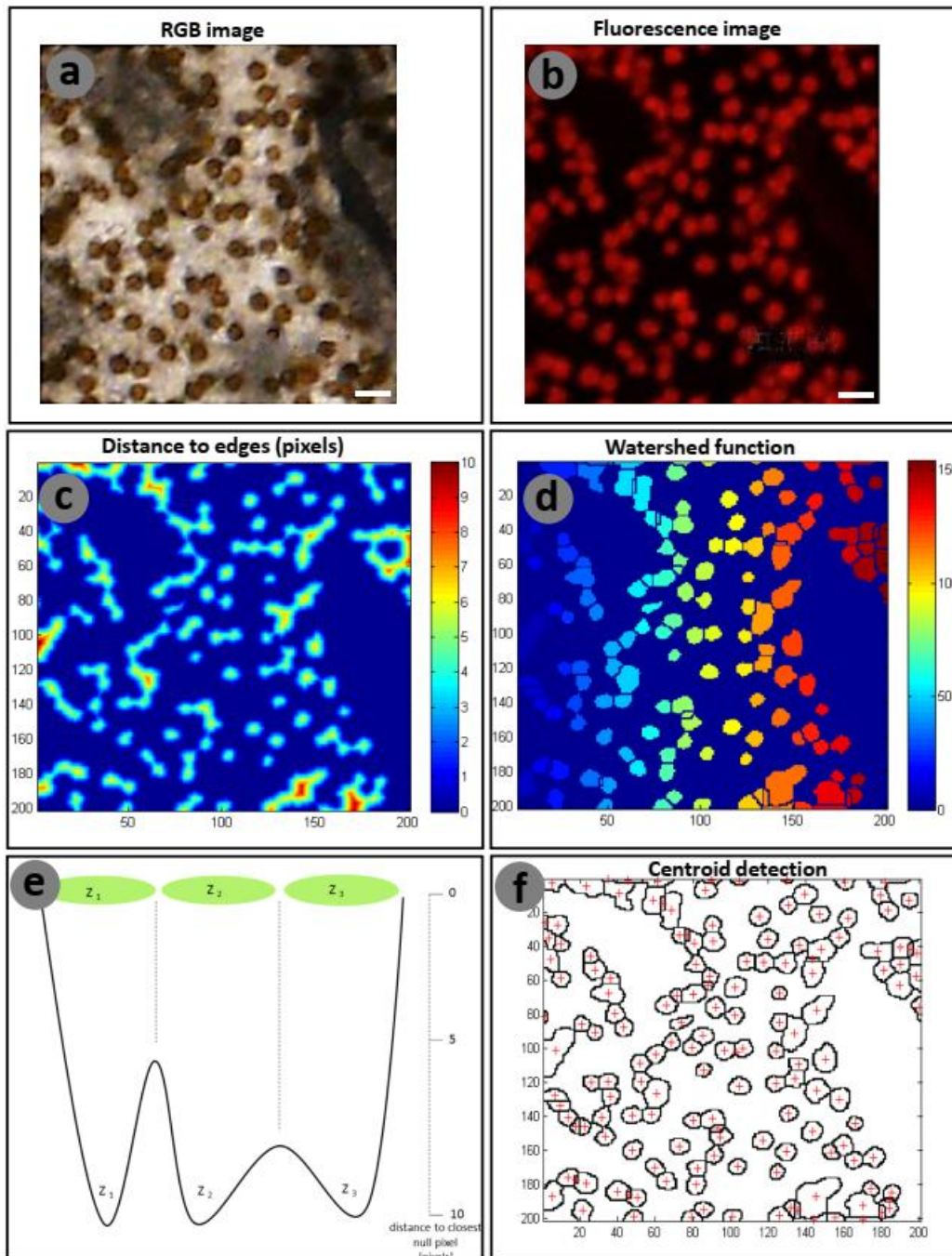
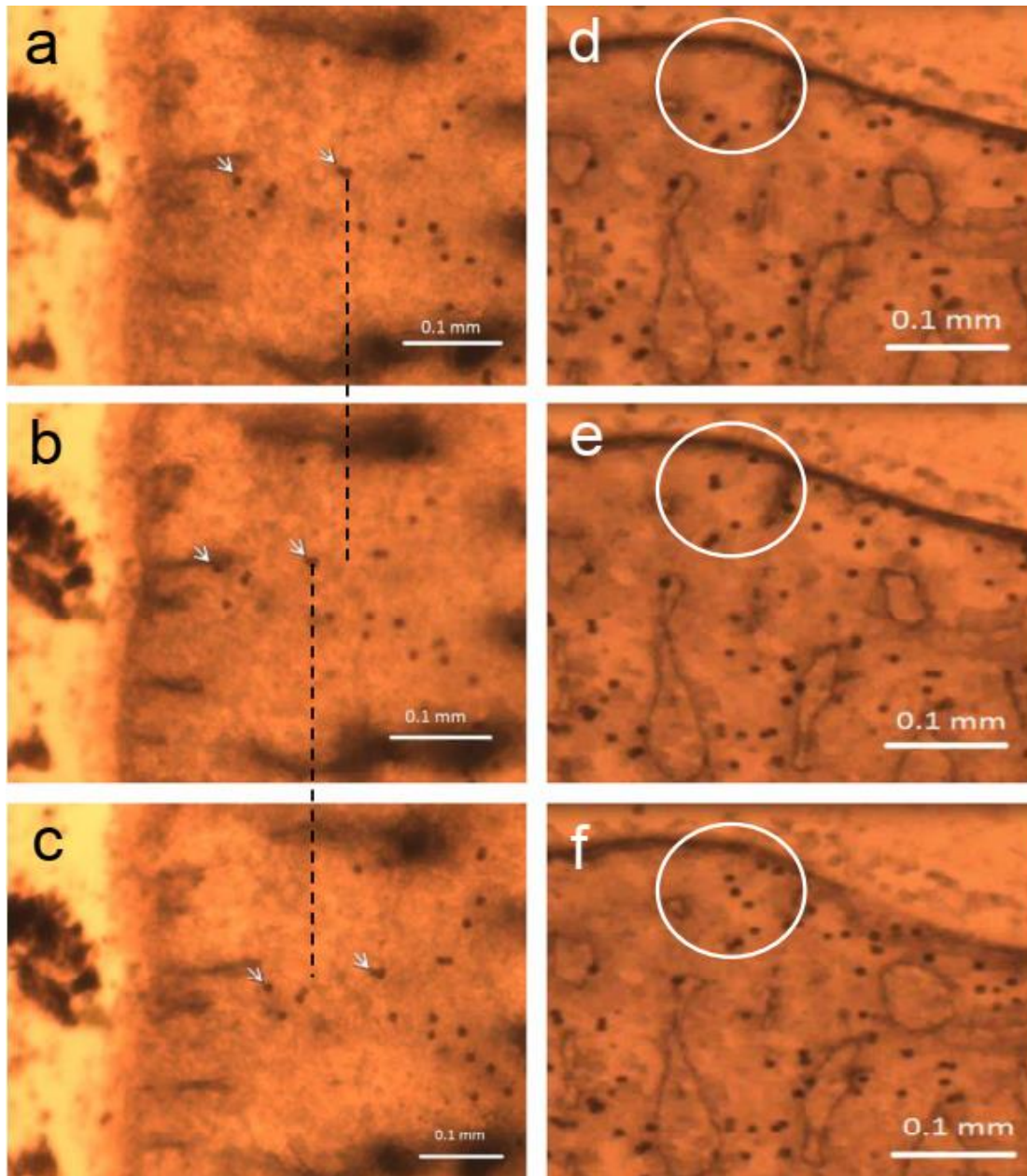


Supplementary



**Figure S1.** Steps for the endosymbiotic dinoflagellates automatic counting methodology; a–f were performed on the same image. The algorithm first transformed the image from the standard Red Green Blue (RGB) colors (a) with endosymbiotic dinoflagellates (white arrow;  $\times 40$ ) and fluorescent image and (b) with zooxanthellae (white arrow,  $\times 40$ ) to a grayscale image, hence assigning a single value to each pixel of the image. The image was then processed into a binary image through a filter, setting a value of “zero” for all the pixels with values below a specific threshold (empirically set to 0.075 in order to count every symbiotic cell, even those located near the calcicoblastic layer) and a value of “one” for all the other pixels. The binary image was then inverted, assigning a value of zero to each endosymbiotic dinoflagellate pixel. Then, the Euclidean distance to the nearest non-zero pixel was calculated for each null pixel of the image, making it the pixel’s value (c) distances to nearest edge/black pixel [pixels], from the small distance in blue to the large distance in red. In the next step,

every pixel in the image was multiplied by  $-1$ , setting the non-zooxanthellae pixel values to  $-\text{Inf}$ . The watershed function was then applied to the image, attributing a different number, greater or equal to one, to all pixels included in the same “watershed”, and a value of zero to pixels not included in a single watershed (d) zooxanthellae, depicted as green circles (each local maximum of distance (Y axis) is associated with a new cell (z)). These pixels represent the edge of the watersheds, where every single watershed represents one symbiotic cell. The image was then reprocessed as a binary matrix, with a value of one for every pixel greater than or equal to 1, and a value of zero to all other pixels (e, watershed function rational). The total number of zooxanthellae in the image was finally counted, and their centroids and areas were derived from the algorithm (f, each centroid is marked with a red cross). Scale bars  $\sim 20 \mu\text{m}$ .



**Figure S2.** Tissue and algal movements. Expansion–retraction tissue movements in *P. damicornis*' spreading tissue after (a) 0 min, (b) 5 min, and (c) 10 min (white arrows = zooxanthellae). Endosymbiotic dinoflagellates relocation (within a white circle) inside the *S. pistillata* spreading tissue, after (d) 0 min (6 algal cells), (e) 5 min (8 algal cells), and (f) 10 min (10 algal cells).