

Electronic Supplementary Material - Kayser *et al.*

Materials and Methods

Experimental setup

Initial experiments showing the effects of collective pushing in dense cellular populations in this work serve to demonstrate the phenomenon on a qualitative basis. For a more comprehensive study examining the effect in greater detail see ref. [35] in the main text. Experiments in this work, based on the non-motile yeast *Saccharomyces cerevisiae* (see Fig.3 in main text), were conducted with the strains yMM9 ("wild-type") and yJHK111 ("mutant") [26,40], both a kind gift of Andrew Murray. yJHK111 constitutively expresses the yellow fluorescent protein ymCitrine. yMM9 was derived from the yJHK111 ancestor yJHK102 by integrating the red fluorescent protein ymCherry instead of ymCitrine and modifying the CYH2 gene to confer resistance to the drug cycloheximide, a translation inhibitor [40]. The full genotypes (W303, MATa) are:

- **yJHK111:** BUD4-S288C his3 Δ ::prACT1-ymCitrine-tADH1-HIS3MX6
- **yMM9:** BUD4-S288C his3 Δ ::prACT1-ymCherry-tADH1-HIS3MX6 CYH2::cyh2-Q37E

Populations of yMM9 were inoculated by running a droplet (10 μ L) of concentrated culture ($OD_{600} > 10$) across a vertically inclined agar plate (YPD, 1% (w/v) agar), resulting in a linear front. A section of this front was removed by rolling a sterile glass bead across it, lifting cells from the substrate. The resulting gap was filled by applying a very small volume ($\approx 0.5 \mu$ L) of concentrated yJHK111 culture to create a "mutant sector". Difference in initial width of the mutant clone (see Fig. 3c in main text) are due to the inherent variability of the replacement process. The ensuing progression of these "sectors" was then tracked via fluorescence microscopy on an Axio Zoom.V16 upright fluorescence microscope (Carl Zeiss, Germany). Experiments were conducted on plates containing 90 nM cycloheximide, corresponding to a growth rate disadvantage $\Delta s = -0.06$ of yJHK111 relative to yMM9 [26].

Non-mechanical model

We contrast our findings with a previously published non-mechanical model assuming constant front velocities [40]. In this model, displacement of the front at a given location is solely determined by the present cell-type (wild-type or mutant) and its associated growth speed. For a linear front this model predicts a constant rate of decay of sector width, set by the ratio of front velocities $s = v_{mut}/v_{wt} - 1$ such that sector boundaries approach each other at a constant s -dependent angle $\theta = 2 \tan^{-1} \sqrt{s(2+s)}$. The expected length y_{model} of the sector can hence be expressed as a function of the initial width w_{ini} via the relation $y_{model}(s, w_{ini}) = w_{ini}/(2\sqrt{s(2+s)})$. This is the basis for the analytical prediction indicated by the dashed gray line in Fig. 3c in the main text. In addition, we extrapolated the initial straight trajectories of both boundaries, using the point of their crossing as an alternative non-mechanical prediction of sector length.

Data evaluation

Sector lengths in Fig. 3 correspond to six individual sectors grown on two independent plates. Data file notation: p=plate, R=region/sector (failed inoculations where excluded). The initial width of the sector was recorded at the start of the time-lapse after 24h of pre-growth. The point of observed expulsion of the mutant clone from the front was determined by visually identifying the position of the most forward fluorescent signal. Initial straight sector trajectories were extrapolated manually for each individual sectors as a non-mechanical null expectation. Initial straight sector trajectories were extrapolated manually for each individual sector to obtain a null expectation for the sector length, as expected from the non-mechanical model (see previous section).