

## Supplemental material

Tonnessen-Murray et al., <https://doi.org/10.1083/jcb.201904051>

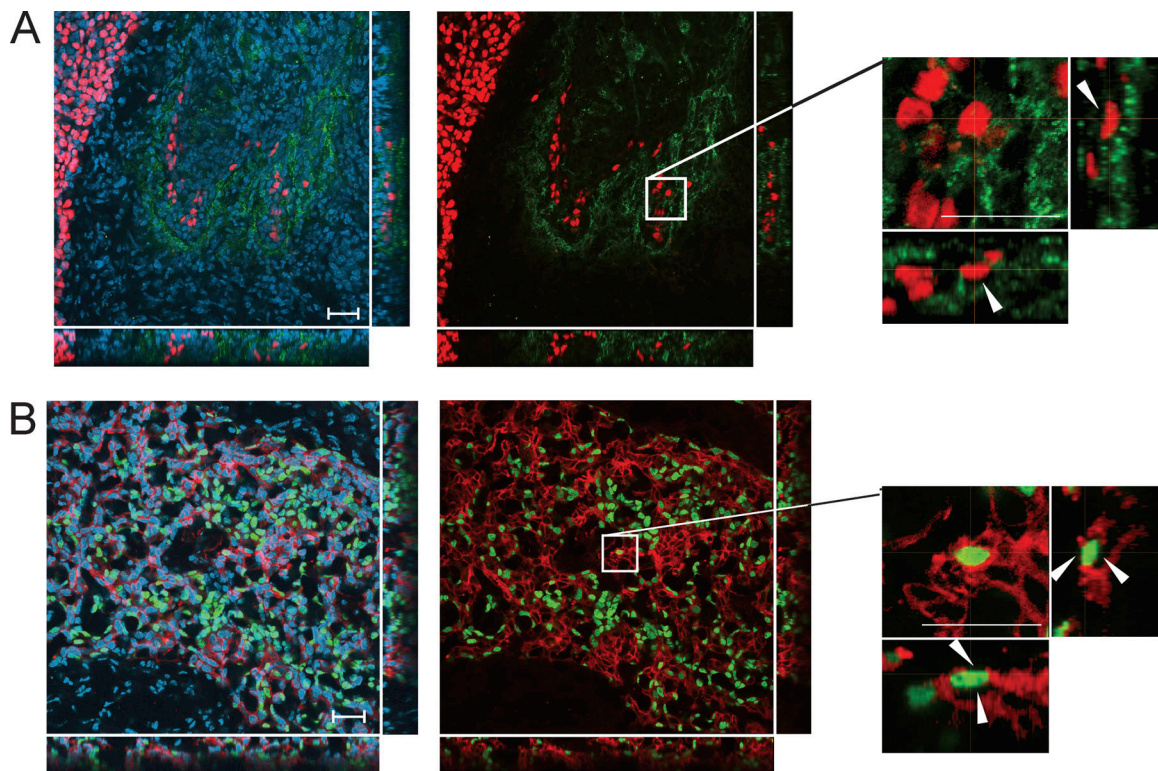


Figure S1. **Examples of images in treated MMTV-*Wnt1* tumors that are not considered to be cell-in-cell structures.** Additional images from experiments presented in Fig. 1 (A and B). **(A)** Tumor cells expressing either H2B mCherry or cytoplasmic GFP were mixed, transplanted, treated, and imaged. Z-stack projections display 20 images taken in 2- $\mu$ m steps, with a total z-range of 37.82  $\mu$ m. **(B)** Tumor cells expressing either H2B GFP or farnesylated mCherry were mixed, transplanted, treated, and imaged. Z-stack projections display 24 images taken in 2- $\mu$ m steps, with a total z-range of 45.88  $\mu$ m. Arrowheads indicate incomplete or inconclusive engulfment. Scale bars represent 50  $\mu$ m; 25  $\mu$ m in zoomed images.

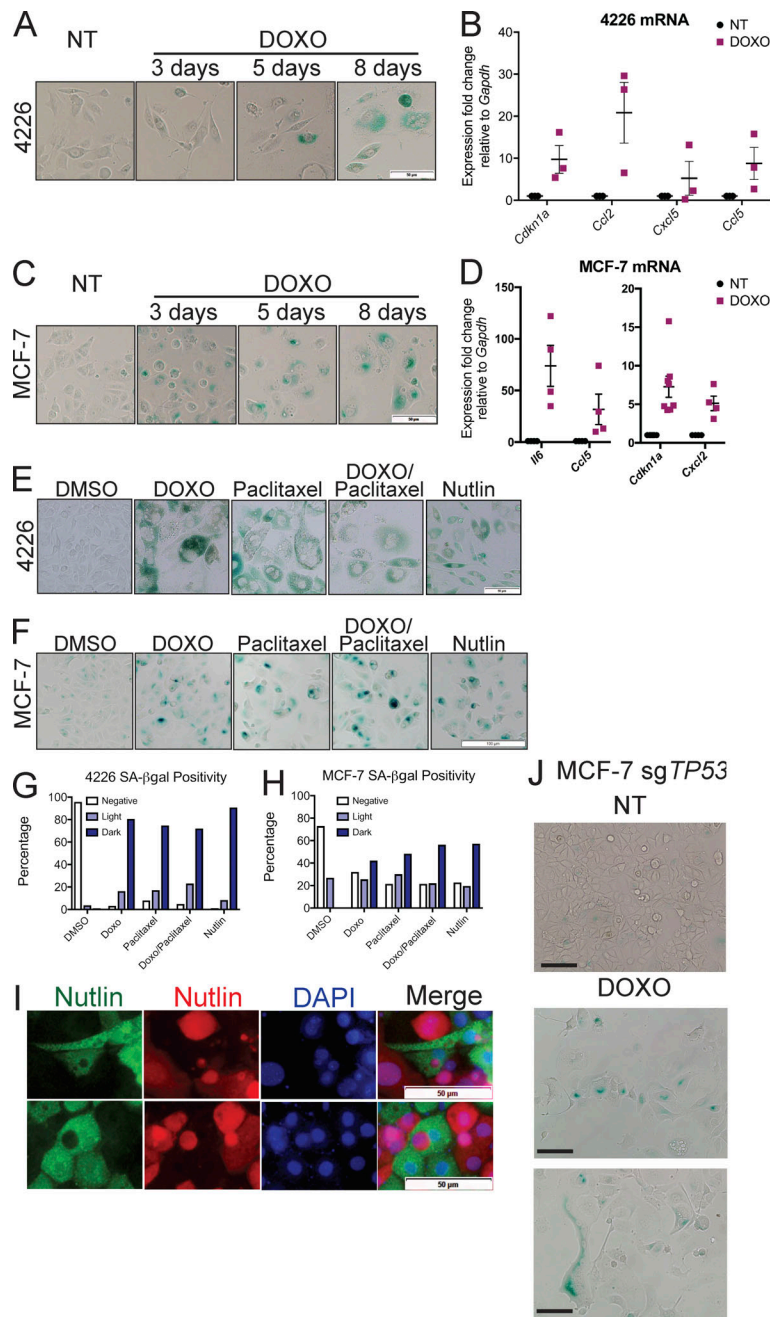


Figure S2. **Senescent phenotypes are expressed by chemotherapy-treated breast cancer cell lines.** (A) Staining for SA-βGal activity was performed on senescent doxorubicin (DOXO)-treated 4226 cells in four separate experiments. In each experiment, at least five random fields of view were taken. (B) RNA was isolated from 4226 cells from three independent experiments. Quantitative RT-PCR was performed in duplicate. Levels of expression relative to *Gapdh* were determined using the method of Pfaffl (2001). Although the trend shows an increase in expression of each gene, the error bars were too large to be deemed significant by *t* test. (C) Staining for SA-βGal activity was performed on senescent doxorubicin-treated MCF-7 cells in three separate experiments. In each experiment, at least five random fields of view were taken. (D) RNA was isolated from MCF-7 cells from four independent experiments. Quantitative RT-PCR was performed in duplicate. Relative levels of expression relative to *Gapdh* were determined. Although the trend shows an increase in expression of *Ccl5*, the error bars were too large to be deemed significant by *t* test. *Cdkn1a*, *Cxcl2*, and *Il6* had *P* values of <0.001, <0.01, and <0.05, respectively. (E) 4226 cells were plated and then treated with drugs as indicated: 0.75 μM DOXO, 10 nM Paclitaxel, or both drugs combined, and changed 24 h later. Nutlin was applied every other day to a final concentration of 15 μM. 8 d later, SA-βGal assay was performed. Three separate experiments were performed; at least five images were taken per condition each time. Representative images shown. (F) MCF-7 cells were plated and then treated with drugs as indicated: 0.25 μM DOXO, 5 nM Paclitaxel, or both drugs combined, and changed 24 h later. Nutlin was applied every other day to a final concentration of 2.5 μM. 8 d later, SA-βGal assay was performed. Two experiments were performed at least five images were taken per condition; representative images shown. (G and H) Quantifications of SA-βGal positivity from representative experiments pictured in E and F. (I) 4226 cells expressing GFP or mCherry were mixed and then treated with 15 μM nutlin for 8 d. Representative images shown from experiments discussed in Fig. 2 C. Scale bars represent 50 μm (A, C, E, and I) and 100 μm (F). (J) MCF-7 sgTP53 cells were treated with doxorubicin as in F, and 7 d later the treated cells and NT cells were stained for SA-βGal as in F. Representative images were captured; scale bars represent 50 μm.

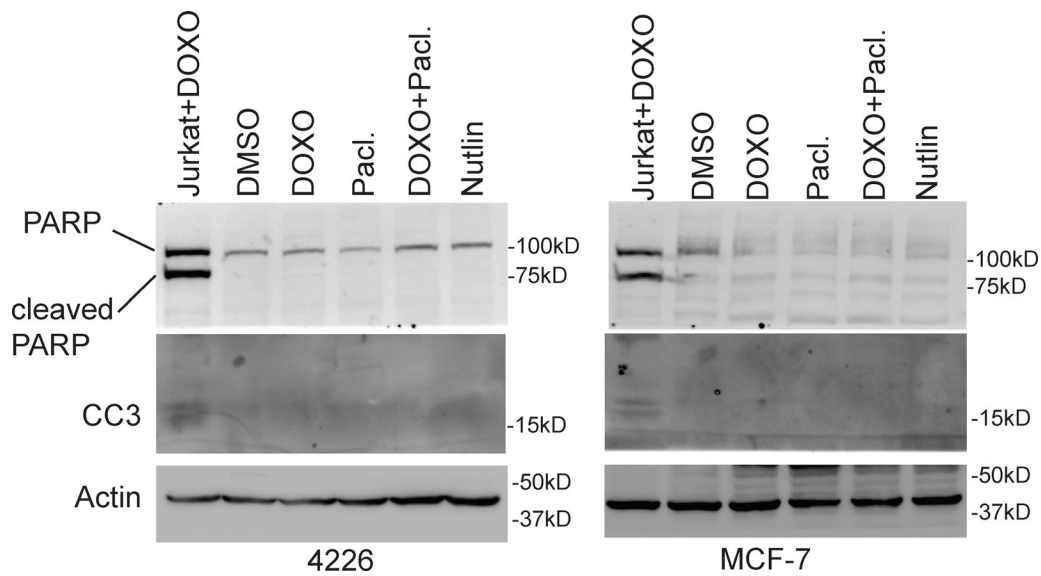


Figure S3. **Expression of apoptotic markers in treated breast cancer cell lines.** Indicated cell lines were treated with DMSO control, doxorubicin (DOXO), paclitaxel (Pacl.), doxorubicin plus paclitaxel, or nutlin as in Fig. 2 (C and D), and then were harvested after 7 d. Immunoblots were performed with antibodies to PARP (detecting the full-length and cleaved isoforms) and cleaved caspase 3, followed by actin. Lysates from Jurkat cells treated for 24 h with 250 nM doxorubicin are included as positive controls. Molecular weight markers are indicated at the right of each gel.

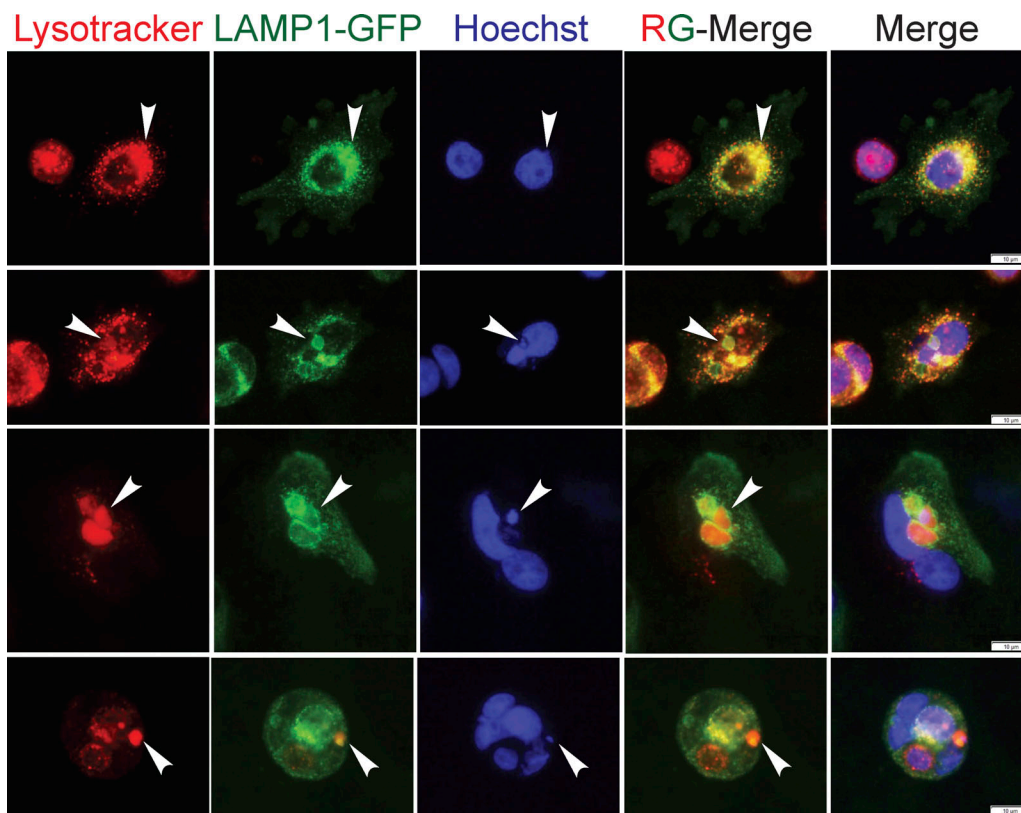


Figure S4. **LysoTracker and LAMP-1 GFP colocalize to engulfed cells within senescent cells.** LAMP1-GFP-expressing MCF-7 cells were treated with 0.25 μM doxorubicin for 24 h and then mixed with NT parental MCF-7 cells. 7 d later, cultures were fixed and stained with LysoTracker, and images were captured of senescent cells with engulfed clear cells (white arrowheads). LAMP1 MCF-7 cells were stained with LysoTracker in one experiment; representative images of engulfed cells are shown. Scale bars represent 10 μm.

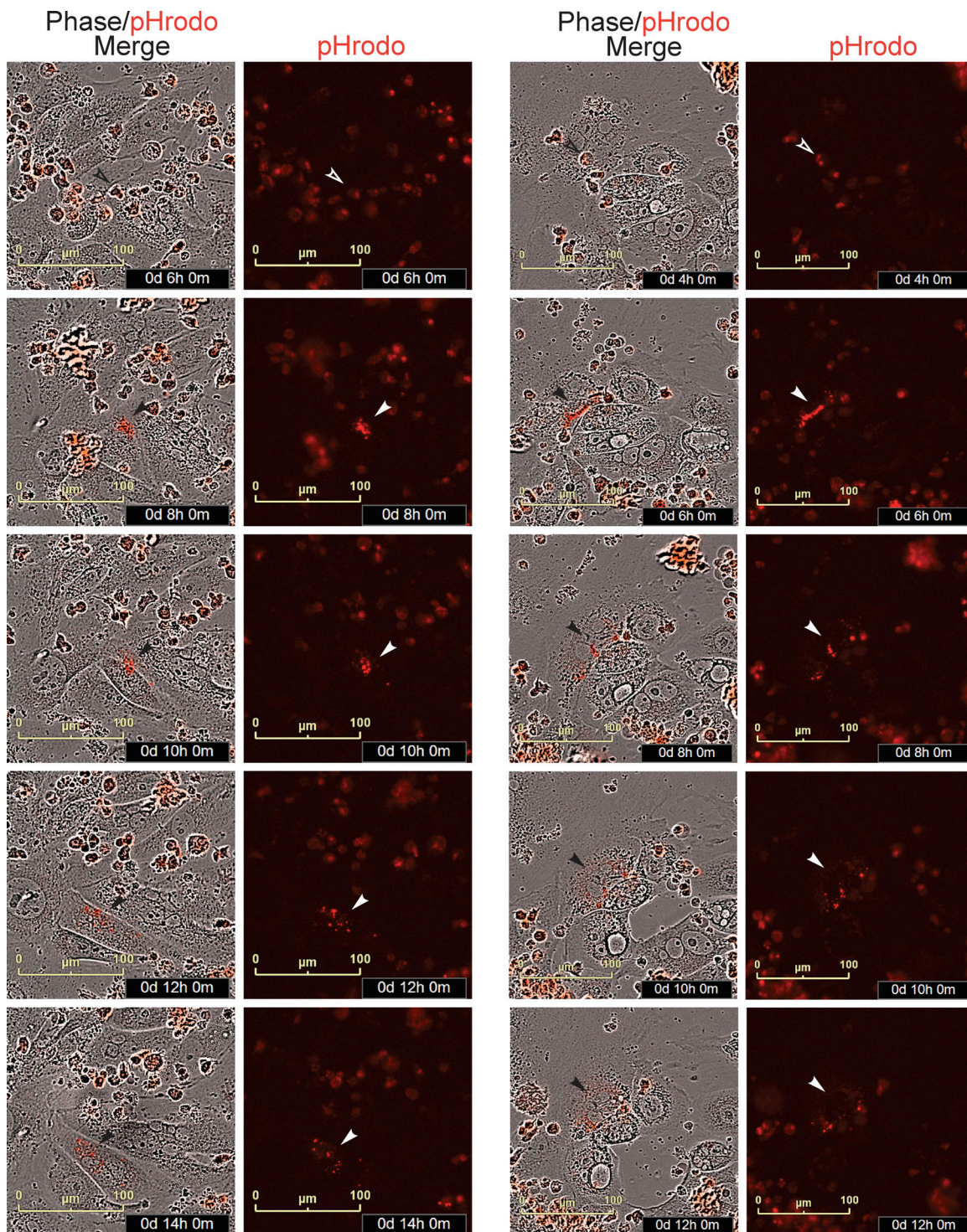
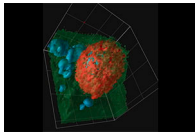
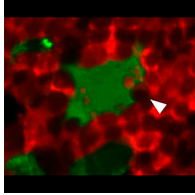


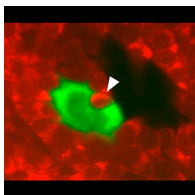
Figure S5. **Doxorubicin-induced senescent breast cancer cells engulf apoptotic Jurkat cells.** pHrodo-labeled Jurkat cells that were treated with doxorubicin for 24 h to induce apoptosis were placed onto cultures of senescent 4226 cells. Two additional representative phase and red fluorescence images of senescent 4226 cells engulfing pHrodo-labeled Jurkat cells and processing to the lysosome were captured over a time course on IncuCyte. Scale bar represents 100  $\mu\text{m}$ ; time of capture after addition of pHrodo Jurkats is shown. Open arrowheads indicate pHrodo Jurkats before engulfment; closed arrowheads indicated pHrodo fluorescence activation at low pH, consistent with processing to the lysosome.



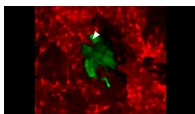
Video 1. **3D reconstruction of a GFP-expressing doxorubicin-treated senescent 4226 cell engulfing an mCherry NT 4226 cell.** Related to [Fig. 2 A](#).



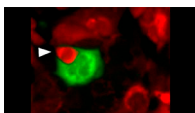
Video 2. **First example of a doxorubicin-treated senescent GFP-expressing 4226 cell engulfing an NT mCherry-expressing 4226 cell.** 49 frames, 1 frame/h. Scale bar represents 50  $\mu\text{m}$ . White arrowhead marks cell to be engulfed and degraded.



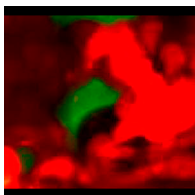
Video 3. **Second example of a doxorubicin-treated senescent GFP-expressing 4226 cell engulfing an NT mCherry-expressing 4226 cell.** 38 frames, 1 frame/h. Scale bar represents 50  $\mu\text{m}$ . White arrowhead marks cell to be engulfed and degraded.



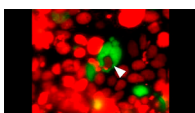
Video 4. **Third example of a doxorubicin-treated senescent GFP-expressing 4226 cell engulfing an NT mCherry-expressing 4226 cell.** 61 frames, 1 frame/h. Scale bar represents 50  $\mu\text{m}$ . White arrowhead marks cell to be engulfed and degraded.



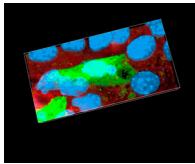
Video 5. **Fourth example of a doxorubicin-treated senescent GFP-expressing 4226 cell engulfing NT mCherry-expressing 4226 cells.** 48 frames, 1 frame/h. Scale bar represents 50  $\mu\text{m}$ . White arrowhead marks cell to be engulfed and degraded.



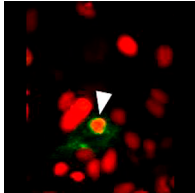
Video 6. **Doxorubicin-treated senescent GFP-expressing MCF-7 cell engulfing NT mCherry-expressing MCF-7 cells.** 31 frames, 1 frame/h. Scale bar represents 50  $\mu\text{m}$ . White arrowhead marks cell to be engulfed and degraded.



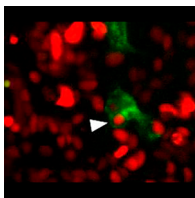
Video 7. **Doxorubicin-treated senescent H2B-GFP-expressing MCF-7 cell plated with NT H2B-mCherry MCF-7.** 93 frames, 1 frame/h. Scale bars represent 50  $\mu\text{m}$ . White arrowhead marks cell to be engulfed and degraded.



Video 8. **3D reconstruction of images taken of nutlin-treated senescent 4226 cells using NIS-Elements software.** Both GFP-expressing and mCherry-expressing cells are senescent. Scale bar represents 20  $\mu\text{m}$ . White arrowhead marks engulfed cell.



Video 9. **First example of a doxorubicin-treated senescent MCF-7 LAMP-1-GFP cell engulfing NT H2B-mCherry MCF-7 cells.** Representative of 16 total videos captured. 71 frames, 1 frame/h. Scale bar represents 50  $\mu\text{m}$ . White arrowhead marks cell to be engulfed and degraded.



Video 10. **Second example of a doxorubicin-treated senescent MCF-7 LAMP-1-GFP cell engulfing NT H2B-mCherry MCF-7 cells.** 71 frames, 1 frame/h. Scale bar represents 50  $\mu\text{m}$ . White arrowhead marks cell to be engulfed and degraded.

## Reference

Pfaffl, M.W. 2001. A new mathematical model for relative quantification in real-time RT-PCR. *Nucleic Acids Res.* 29:e45. <https://doi.org/10.1093/nar/29.9.e45>

Provided online are two tables. Table S1 (PDF) is a guide to supplemental videos. Table S2 (Excel) shows the statistical analysis of gene expression data in Fig. 7.