

Expanded View Figures

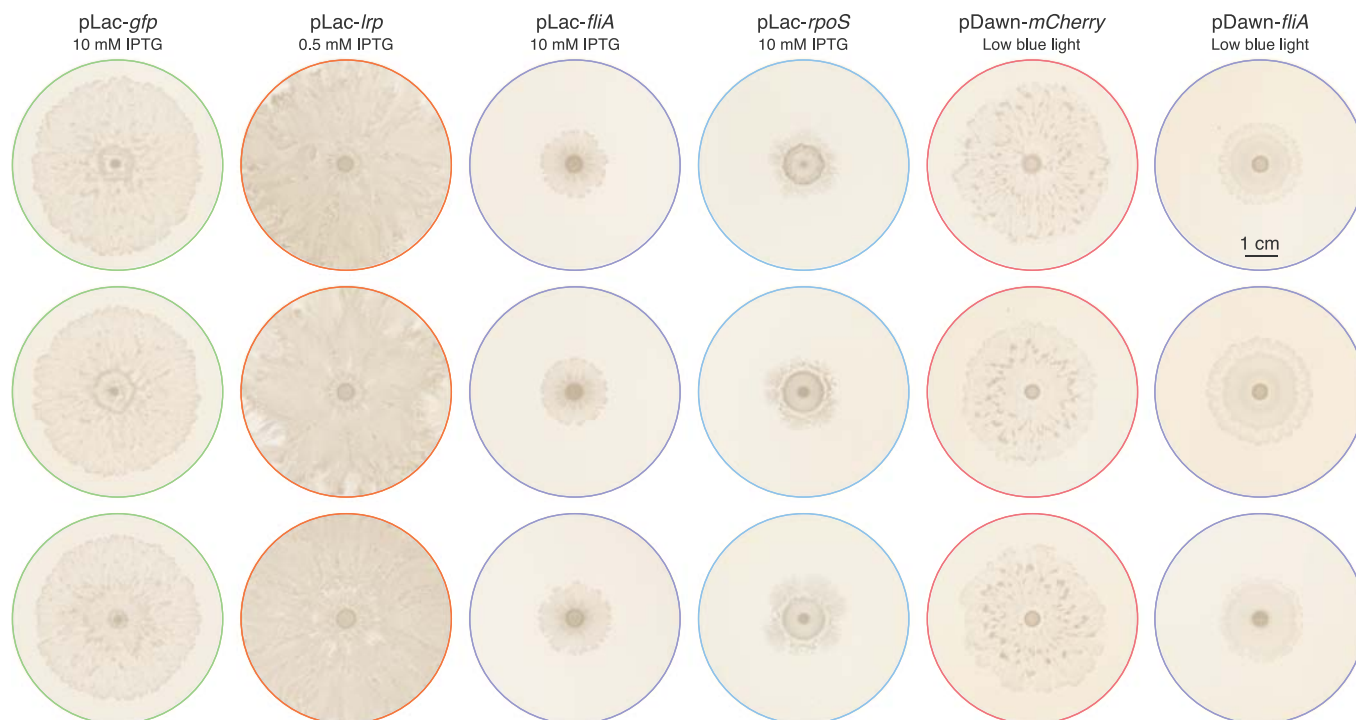


Figure EV1. Engineered swarm colonies exhibit reproducible morphologies across biological replicates and experimental days.

Representative replicate images of 24-h swarm colonies formed by engineered MG1655hm strains on swarming medium with select induction conditions (IPTG or blue light, as indicated). For each strain, a single induction condition was chosen from screening assays to illustrate characteristic morphologies. Across rows, three independent biological replicates are shown ($n = 3$), demonstrating reproducibility across experiments.

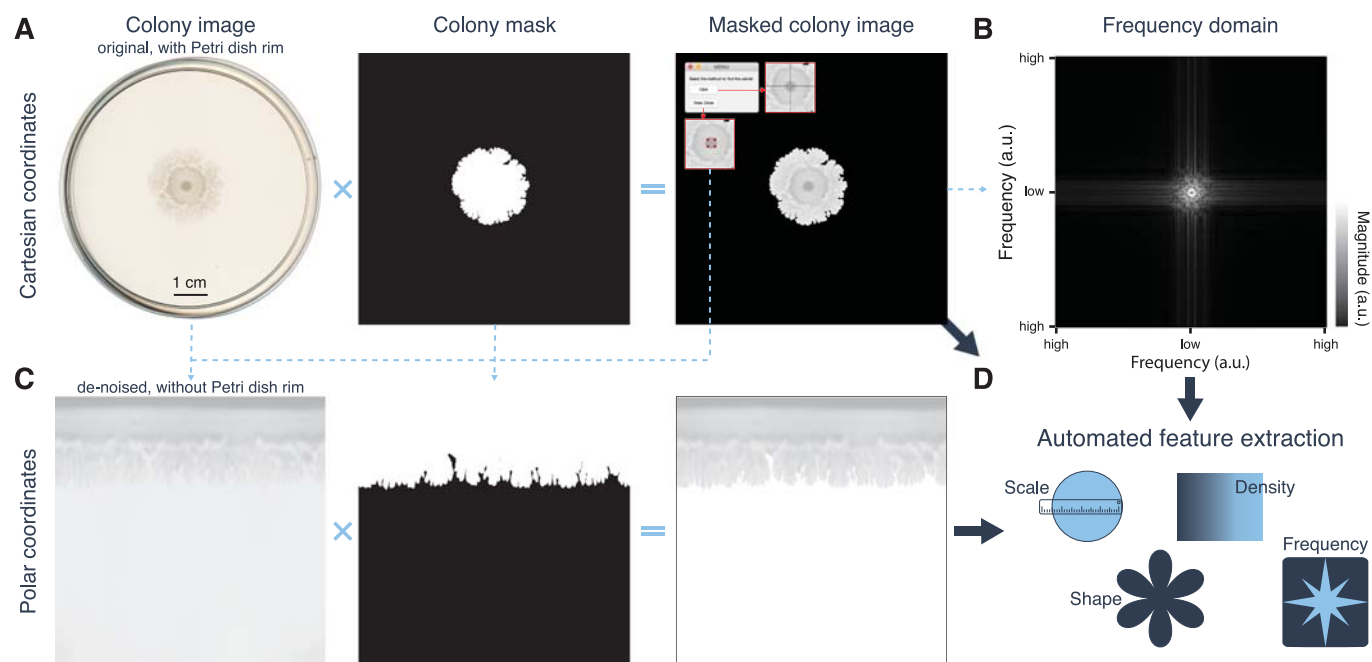


Figure EV2. Semi-automated computational pipeline for swarm pattern quantification.

(A) Swarm colonies in 100-mm Petri dishes were scanned at 400 dpi using a commercially available flatbed document scanner. Colony images were segmented with image-processing functions and minor manual refinement in Adobe Photoshop as needed. Masked colonies were transformed from the spatial to (B) frequency domain (via Fourier transform), and from Cartesian to (C) polar coordinates, with user input to locate the inoculum center. (D) From these three colony representations (Cartesian, Fourier, and polar), features of scale, density, shape, and frequency were extracted for downstream analysis. (Example shown: MG1655hm pLac-*rpoS* at 2.5 mM IPTG, 24 h).

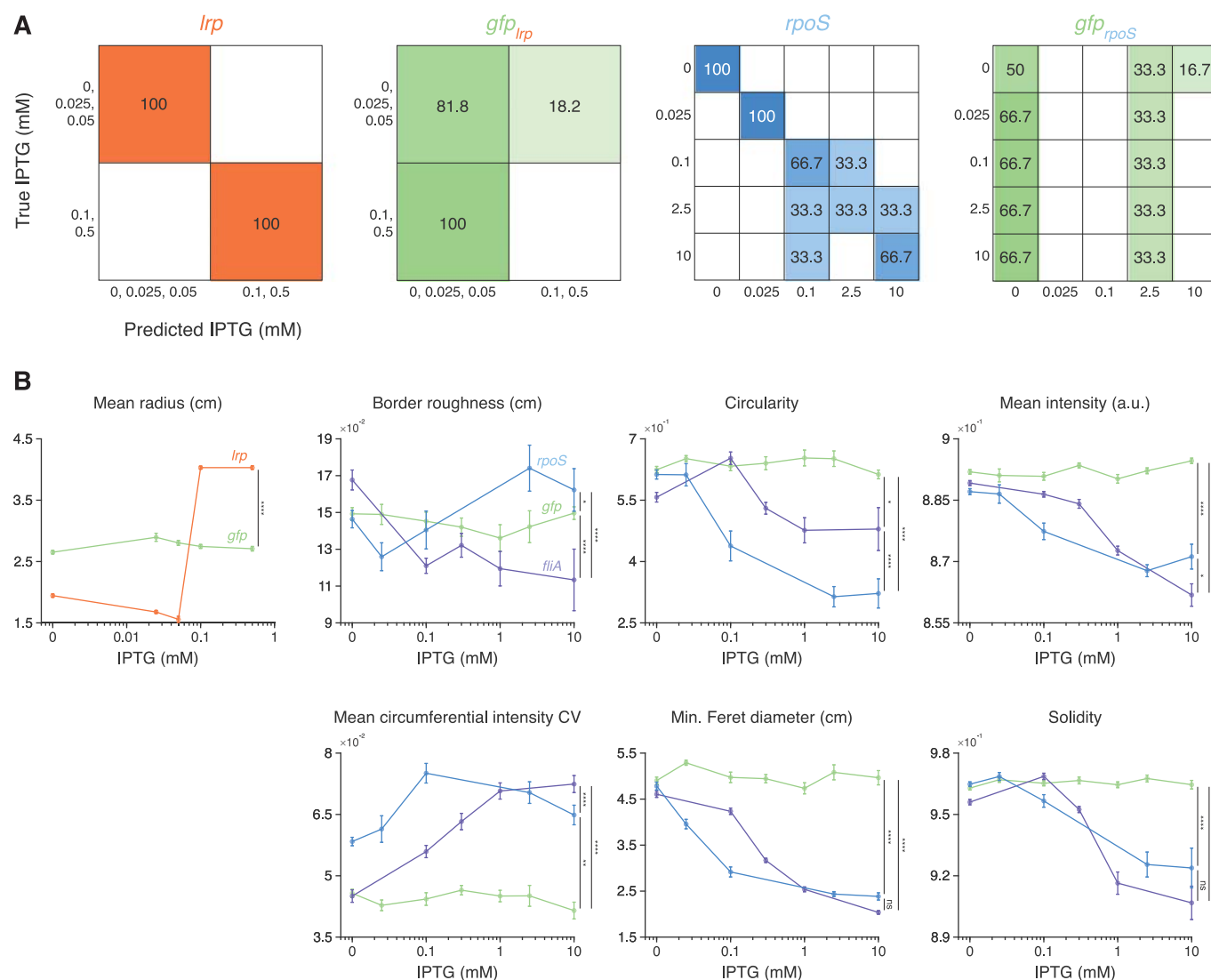


Figure EV3. Regression models decode IPTG from swarm pattern features.

(A) Test confusion matrices of regression models decoding IPTG concentration from 24-h colony features of pLac-*lrp*, pLac-*rpoS*, and their corresponding pLac-*gfp* control strains. Confusion matrices share the same axes; inner values indicate the percentage of test predictions within each true IPTG class. Confusion matrices for the pLac-*fliA* model and its corresponding pLac-*gfp* control model are shown in Fig. 4A. (B) Select IPTG-dependent trends of morphological and intensity-based features identified through strain-specific model fitting. The pLac-*lrp* model used mean radius; the pLac-*fliA* model used border roughness, circularity, and mean intensity; and the pLac-*rpoS* model used mean circumferential intensity CV, minimum Feret diameter, and solidity. Points represent the mean of independent biological replicates (swarm colonies): $n = 9$ –18 for the pLac-*lrp/gfp* strain set, and $n = 9$ –35 for the pLac-*fliA/rpoS/gfp* strain sets, collected across ≥ 3 independent experiments per condition performed on different days. Error bars represent SEM. Asterisks denote significant differences between the overall IPTG-response curves, determined using linear mixed-effects models with ANOVA for the pLac-*lrp/gfp* strain set and with post hoc comparisons for the pLac-*fliA/rpoS/gfp* strain sets (both based on the Strain $\times$ IPTG interaction; $P \leq 0.01$; see Methods, “Statistical analysis of colony features”). Exact P values are reported in Appendix Table S3.

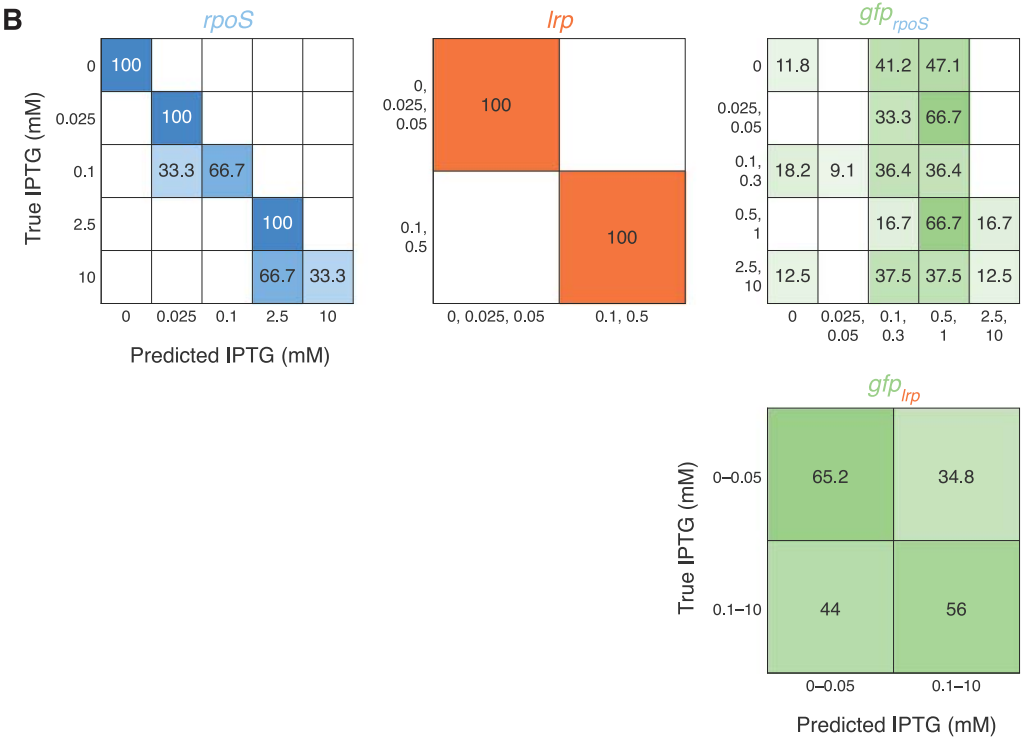
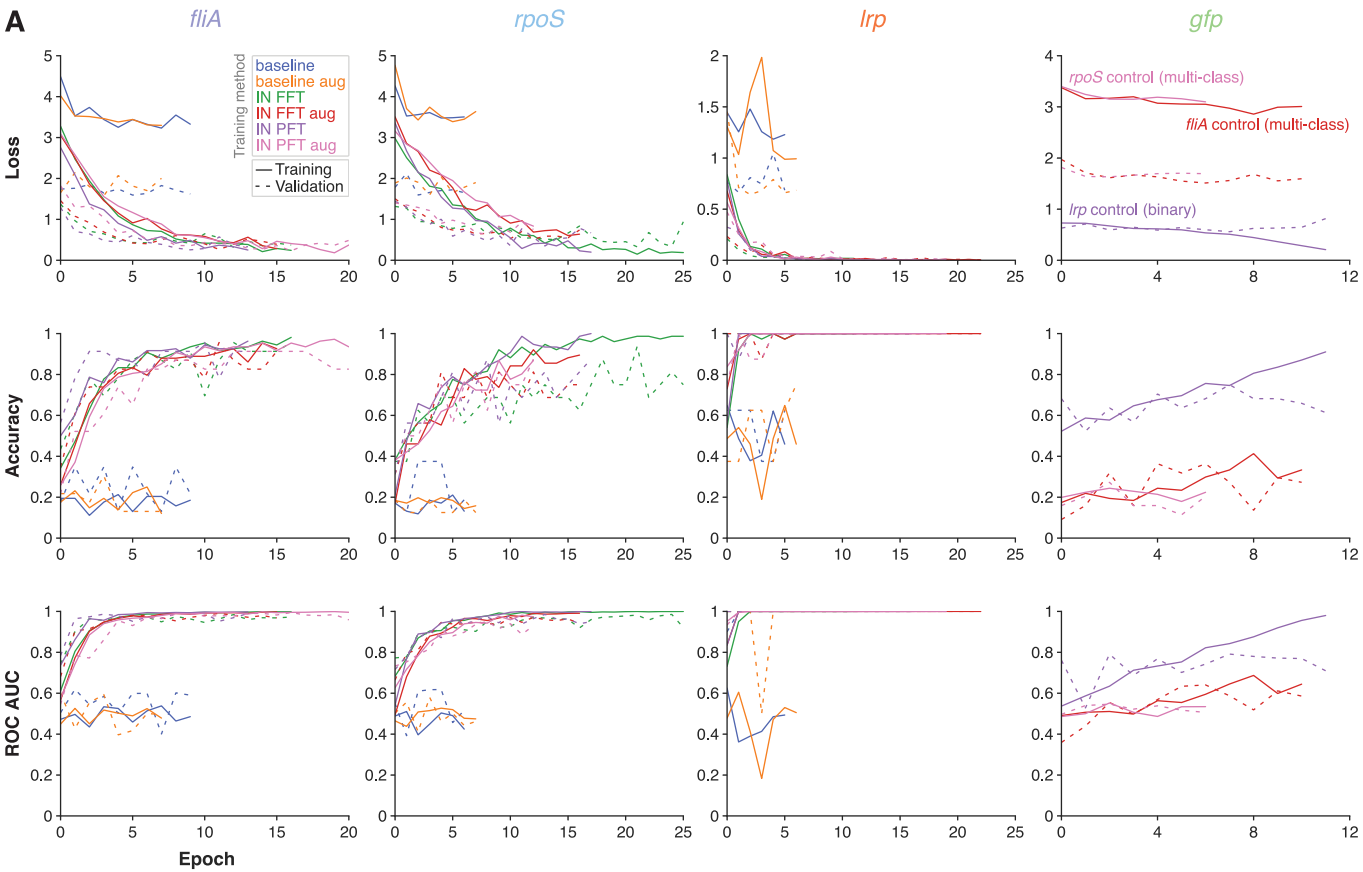


**Figure EV4. Deep-learning models decode IPTG from swarm colony images.**

(A) Training and validation learning curves (loss, accuracy, ROC-AUC) for SwinTransformer models trained on pLac-*fliA*, pLac-*rpoS*, pLac-*lrp*, and pLac-*gfp* image datasets. Model configurations included ImageNet pretraining (IN), full or partial fine-tuning (FFT, PFT), and random data augmentation (aug). Baseline models lacked ImageNet pretraining and fine-tuning. (B) Test confusion matrices of the optimal models for pLac-*rpoS* and pLac-*lrp*, defined as those achieving the lowest validation loss, and their corresponding pLac-*gfp* control models. The pLac-*gfp* models were trained and evaluated for multiclass IPTG classification (top; corresponding to the pLac-*rpoS* model configurations) and binary IPTG classification (bottom; corresponding to the pLac-*lrp* model configurations). Confusion matrices for the pLac-*fliA* model and its corresponding pLac-*gfp* control model are shown in Fig. 4C. Axes are shared across confusion matrices.

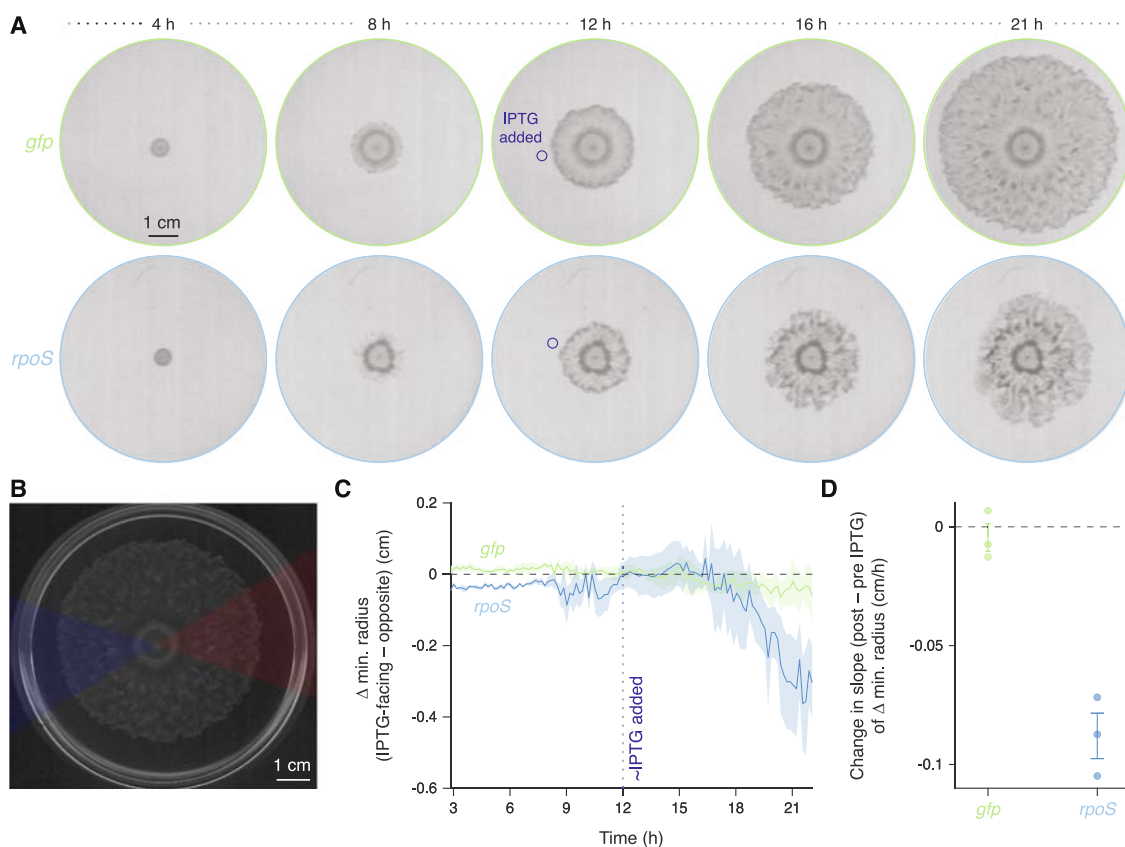


Figure EV5. Localized IPTG perturbation induces asymmetric swarm expansion.

(A) Four-hour snapshot images from representative time-lapse swarming assays. Shown are the control strain (*pLac-gfp*) and an analog strain (*pLac-rpoS*) on swarming medium. At ~12 h, 2 μL of 1 M IPTG was spotted just outside the expanding colony front. (B) Representative uncropped endpoint image of a *pLac-gfp* swarm colony (~22 h) with overlaid analysis masks. The blue wedge denotes the IPTG-facing region, and the red wedge denotes the opposite, untreated control region. (C) Time course of the difference in minimum colony radius between the IPTG-facing and opposite regions, with the timing of localized IPTG addition indicated. (D) Change in the slope of the minimum-radius difference post-IPTG relative to pre-IPTG. Two-sample, two-tailed Welch's *t*-test: $P = 3.5 \times 10^{-3}$; Wilcoxon rank-sum test: $P = 0.1$. In plots (C, D), lines represent the mean of $n = 3$ biological replicates; shaded regions and error bars represent SEM; points indicate individual biological replicates.