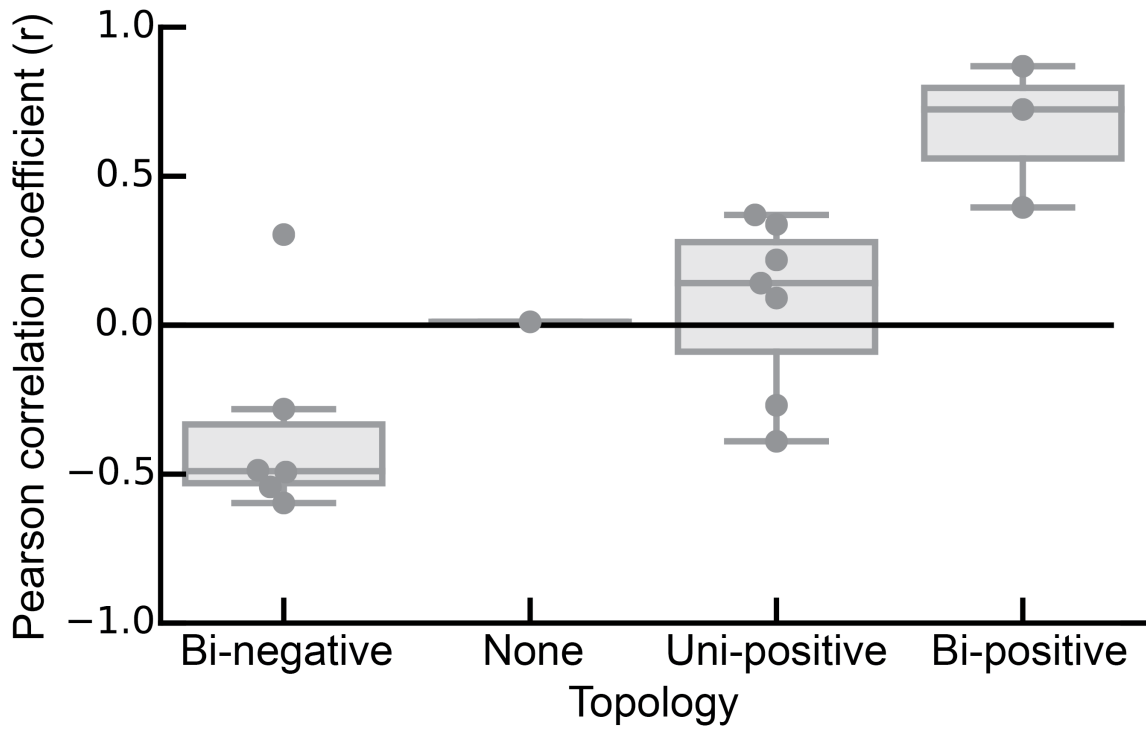**Figure S1. Computational algorithm for droplet identification and cell counting, Related to Figure 1. (a)** Quantification of strain abundance by automated cell counting or average fluorescence intensity (relative fluorescence units, RFU). A representative droplet containing CFP and RFP labeled cells (left) contained seven times fewer CFP cells (blue), yet exhibited higher average CFP fluorescence intensity than a different representative droplet (right). Phase-contrast (PC) and fluorescence microscopy (FL) are shown. **(b)** Representative microscopy images showing the droplet segmentation pipeline. First, the raw phase-contrast microscopy image is loaded (1) and droplet positions and size (2, blue circles) are identified via the Hough transformation (OpenCV). The identified droplet locations and raw fluorescence microscopy images (3) are used to segment the droplets (4, white circles). **(c)** Representative fluorescence microscopy images showing cell counting pipeline. Each segmented droplet image (1) is split into separate images for each fluorescent channel (2). Cells are counted by identifying connected regions of intensity using a blob detection algorithm in OpenCV (3). **(d)** Representative fluorescence microscopy image showing the final combined droplets for an experiment binned according to the presence and absence of each fluorescently labeled strain.
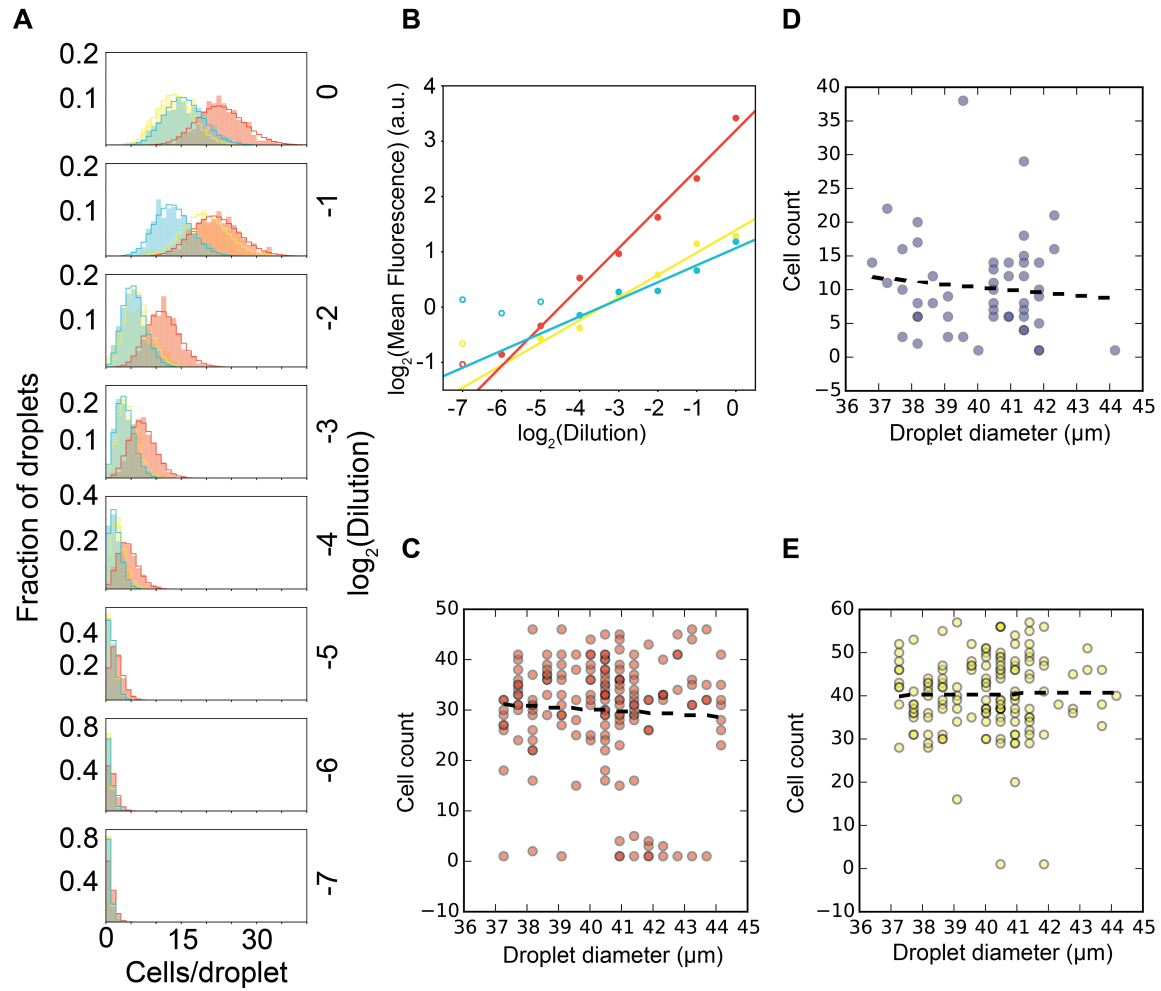
Figure S2. Characterization of cell counting method in microfluidic droplets, Related to Figure 1. (a) Histograms of the number of cells in each droplet for a mixed culture of CFP-labeled *E. coli* (blue), RFP-labeled *E. coli* (red) and YFP-labeled *S. typhimurium* (yellow) as described in **Figure 1b-c**. Each subplot represents a different dilution. Solid lines represent the expected Poisson distributions with the mean (λ) equal to the mean number of counts for the corresponding distribution. **(b)** Scatter plot of the dilution factor of the mixed culture vs. the $\log_2$ transform of the mean fluorescence from the data described in **Figure S2a** and **Figure 1b,c**. Each data point represents the mean of 400-600 droplets and lines denote linear regression fits to the data excluding the low dilutions that diverge from the linear trend indicated by empty circles. **(c)** Scatter plot of droplet diameter vs. EC WT cell count (slope=-0.35, r = -0.06, n=177). Data corresponds to a three-member consortium (EC WT, EC Met- and ST Lac*, **Table S1**, E6) grown in glucose minimal media supplemented with methionine. **(d)** Scatter plot of droplet diameter vs. EC Met- cell count (slope=-0.43, r = -0.10, n=50). **(e)** Scatter plot of droplet size vs. ST Lac* cell count (slope=0.12, r = -0.02, n=148).

Figure S3. Correlation analysis of cell counts for each pair of strains across a set of experiments, Related to Figures 2 and 3. (a) Scatter plot of BS Trp- and EC Met- cell counts for experiment E1 (**Table S1**). The black line represents the regression line and the gray regions represent the bootstrapped 95% confidence interval for the regression line. Axes and nodes are colored by the fluorescent reporter of each strain and the network schematic represents the inferred interaction topology. **(b)** Scatter plot of sender and receiver *E. coli* strains in experiment E2 (**Table S1**). **(c)** Scatter plot of all pairs of strains in the three-member experiment E3-E6 (**Table S1**) grown in lactose minimal media (left column), lactose minimal media supplemented with methionine (second column from the left), glucose minimal media (third column from the left) or glucose minimal media supplemented with methionine (right column). **(d)** Scatter plot of all pairs of strains in the engineered higher-order interaction experiment E7 (**Table S1**).

Figure S4. Pearson correlation coefficient clusters by pairwise network topology, Related to Figures 2 and 3.
Box and whiskers plot of the Pearson Correlation coefficients of cell counts for each pair of strains across all experiments binned by the inferred network topology using MINI-Drop. The center line indicates the median, the bottom and top edges of the box indicate the 25th and 75th percentiles, respectively. The whiskers extend to the most extreme data points not considered outliers and outliers are plotted individually using the diamond symbol.
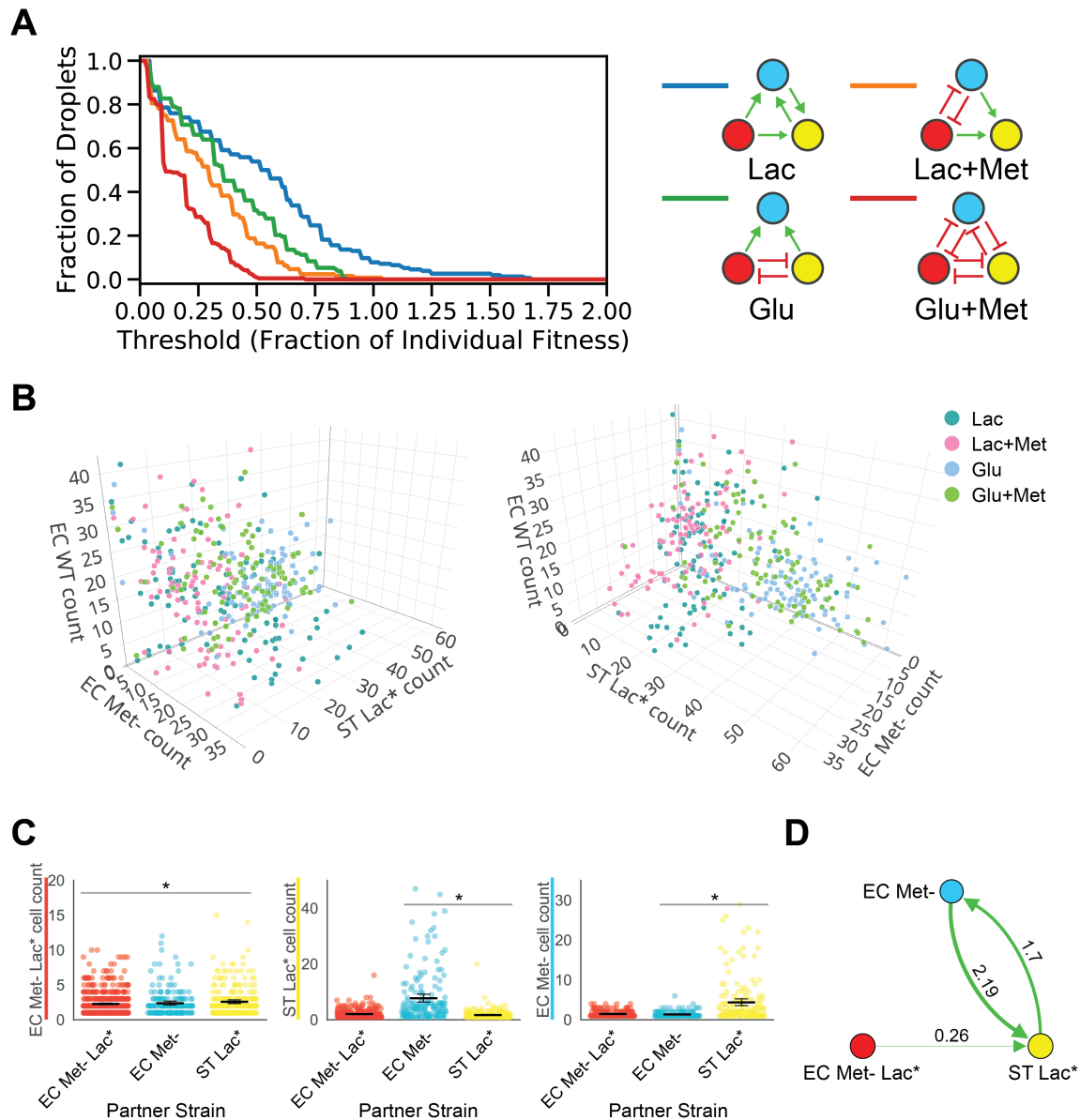
Figure S5. Quantification of strain coexistence and microbial interactions in a three-member consortium, Related to Figure 3. (a) Fraction of three-member droplets that exhibit strain coexistence in a three-member consortium (EC Met-, EC WT, ST Lac*, **Table S1**, E3-6) following 18 hr incubation at 37°C. For a droplet to be counted as a co-existence droplet, all three strains must have a number of cells greater than the threshold fraction multiplied by their respective mean cell count in single strain droplets. Lines of different colors represent the community grown in different media conditions. **(b)** Three-dimensional scatter plot of cell counts in a three-member consortium (**Table S1**, E3-6) from two perspectives. Only droplets that contained all three strains are shown. **(c)** Categorical scatter plot showing cell count distributions of EC Met- Lac* (top), ST Lac* (middle) and EC Met- (bottom) in lactose minimal media (**Table S1**, E7) The black horizontal line represents the mean and the error bars denote the bootstrapped 95% confidence intervals for the mean. The gray horizontal bars indicate a statistically significant difference (p < 0.05, **Table S2**). **(d)** Schematic of the inferred interaction network. The edge width is proportional to the $\log_2$ ratio of the average cell count in the presence of a partner compared to the cell count in the absence of the partner. Node size is proportional to the average cell count of each strain grown in isolation.
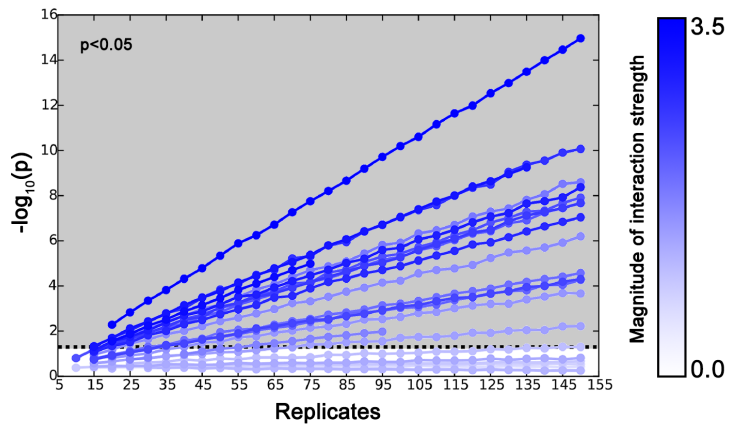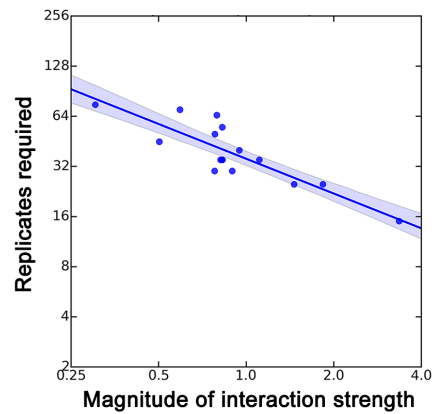
Figure S6. Number of droplets (replicates) required to infer microbial interactions of varying strengths using MINI-Drop, Related to Figures 2 and 3. (a) Scatter plot of the number of droplets (replicates) vs. the statistical significance of the interaction ($-\log_{10}(p)$) based on the Mann-Whitney U test in experiments E1-7 (**Table S1**). Each data point represents an average p-value computed by sub-sampling the data 500 times across a range of depths. The dashed line represents a p-value equal to 0.05 (statistical significance threshold). The gray box represents the parameter regime for statistical significance ($p < 0.05$). The shade of blue represents the magnitude of the inferred interaction using MINI-Drop. **(b)** The number of droplet replicates required for the p-value to be equal to or less than 0.05.
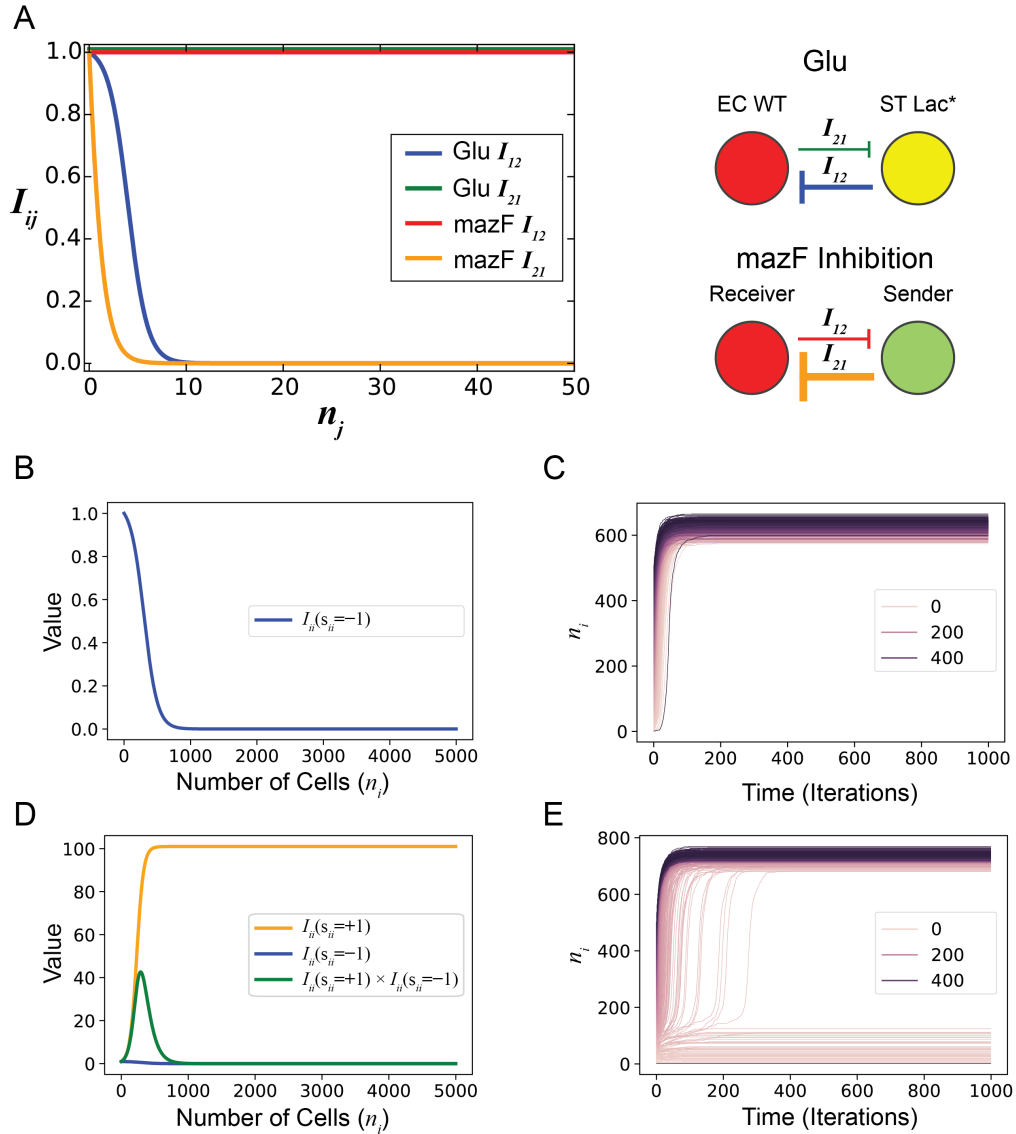
Figure S7. Model analysis of interaction strengths in bidirectional negative interaction networks and modified stochastic model that displays an Allee effect, Related to Figure 5. **(a)** Inferred interaction network topologies of pairwise consortia in experiments E2 and E5 (**Table S1**) were modeled using the discrete-time Markov growth model. The inter-strain interactions in the model are represented as I_{ij} (see STAR Methods). The toxin mediated negative interaction (orange, right) exhibited a higher sensitivity to partner cell number in the model compared to the outgoing negative interaction from ST Lac* to EC WT (blue, right). **(b)** The self-inhibition curve (blue) as a function of self-cell count (n_i) for a stochastic logistic growth model. **(c)** Simulated cell counts as a function of time for a stochastic logistic growth model from a range of initial populations sizes represented by the line color (1-500 cells, $n_{i,t=0}$). **(d)** The positive self-interaction curve (yellow), self-inhibition curve (blue), and overall growth modifier (green) as a function of self-cell count (n_i) for a modified stochastic growth model designed to display positive density-dependent growth referred to as the Allee effect. **(e)** The simulated cell counts as a function of time for a modified stochastic model that exhibits an Allee effect ($n_{i,t=0}$). The color of the lines represents the initial population size.
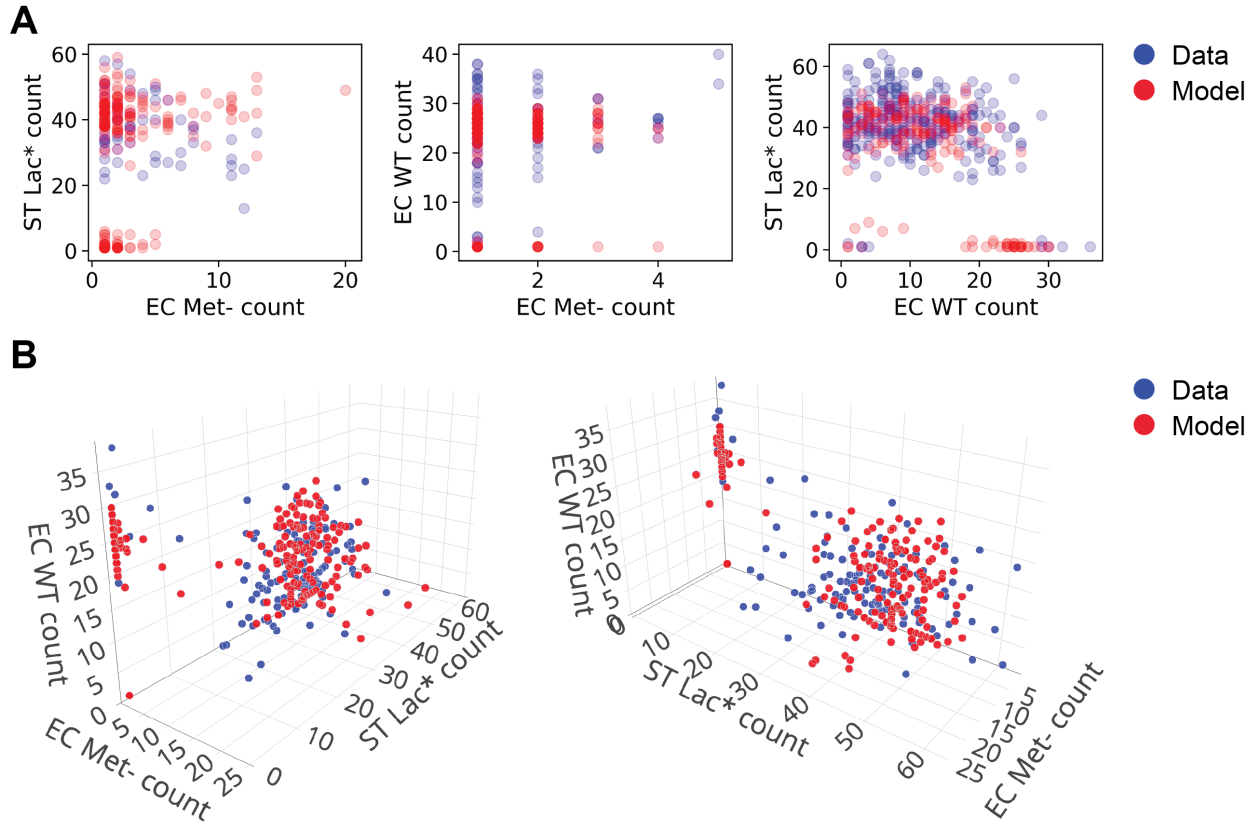
Figure S8. Parameterized model can recapitulate cell count distributions in two and three-member droplets, Related to Figures 3 and 5. (a) Scatter plots of cell counts in two-member droplets in a parameterized model (red) and experimental data (blue). The community was grown in a media containing glucose (**Table S1**, E5). **(b)** Three-dimensional scatter plots of cell counts in three-member droplets in a parameterized model (red) and experimental data (blue) using the same parameter set as in (a) (**Table S4**).
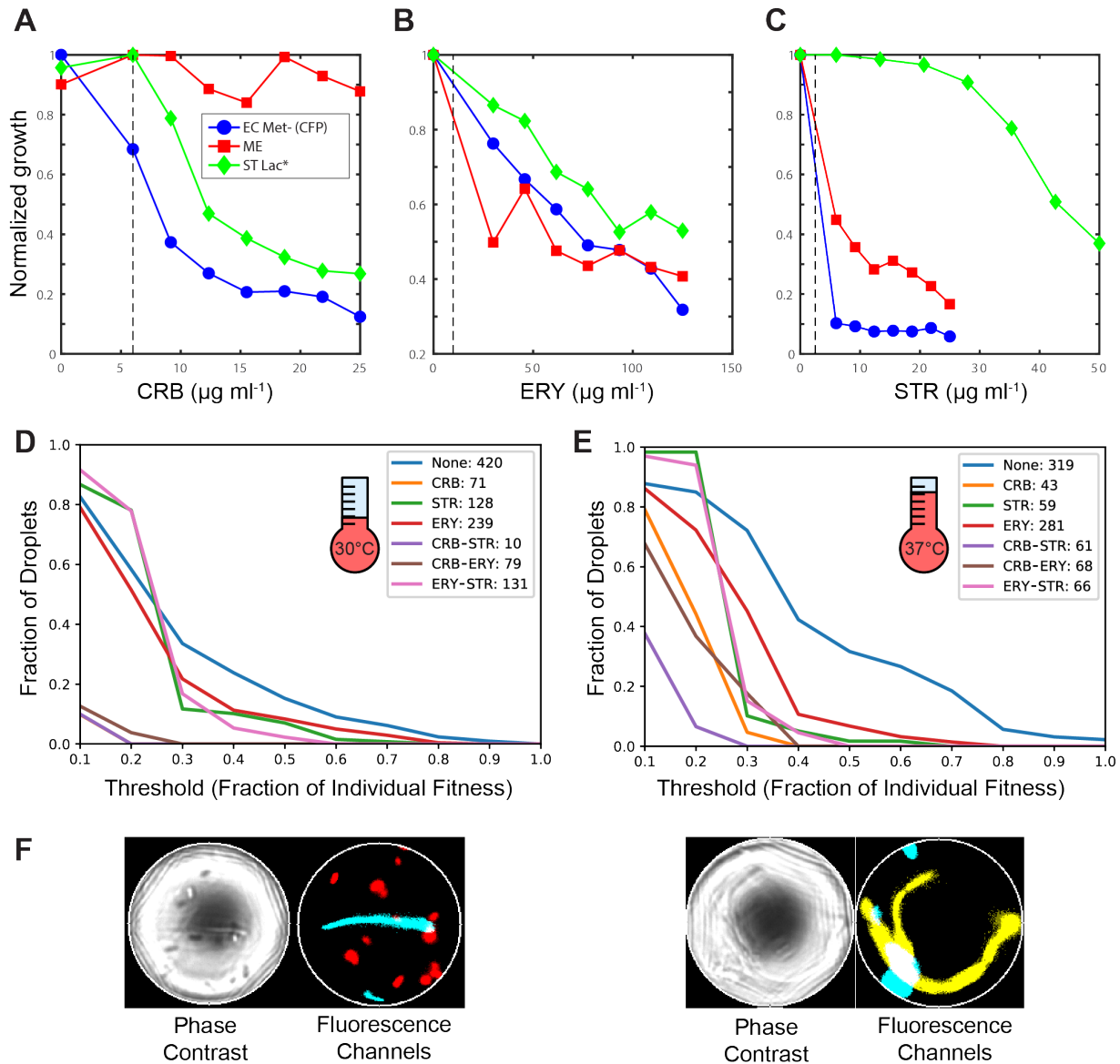
Figure S9. Antibiotic susceptibilities and coexistence of EC Met- (CFP), ME, and ST Lac*, Related to Figure 6. Normalized growth of each species over a range of **(a)** carbenicillin (CRB)**, (b)** erythromycin (ERY**)**, and **(c)** streptomycin (STR) concentrations (µg mL^{-1}) in microtiter plates. Normalized growth was computed as the integral of the growth response based on OD600 values of each condition over 24 hours divided by the maximum growth of each strain across all concentrations of a given antibiotic. The dashed line denotes the concentration of antibiotic that was used in the droplet experiments (**Table S1**, E8-21). Fraction of three-species droplets (**Table S1**, E8-21) where all three species co-exist a function of a threshold at 30°C **(d)** or 37°C **(e)**. For a droplet to be counted as a co-existence droplet, all three strains must have a number of cells greater than the threshold fraction multiplied by their mean cell count in single strain droplets in the absence of antibiotics (**Tables S6 and S7**). Numbers in the legend indicate the number of three-species droplets observed in each condition. Note that in (d) the CRB curve (orange) is obscured by the CRB-STR curve (purple). **(f)** Representative images of CRB droplets with elongated EC Met- (cyan, left) or ST Lac* (yellow, right) cells.
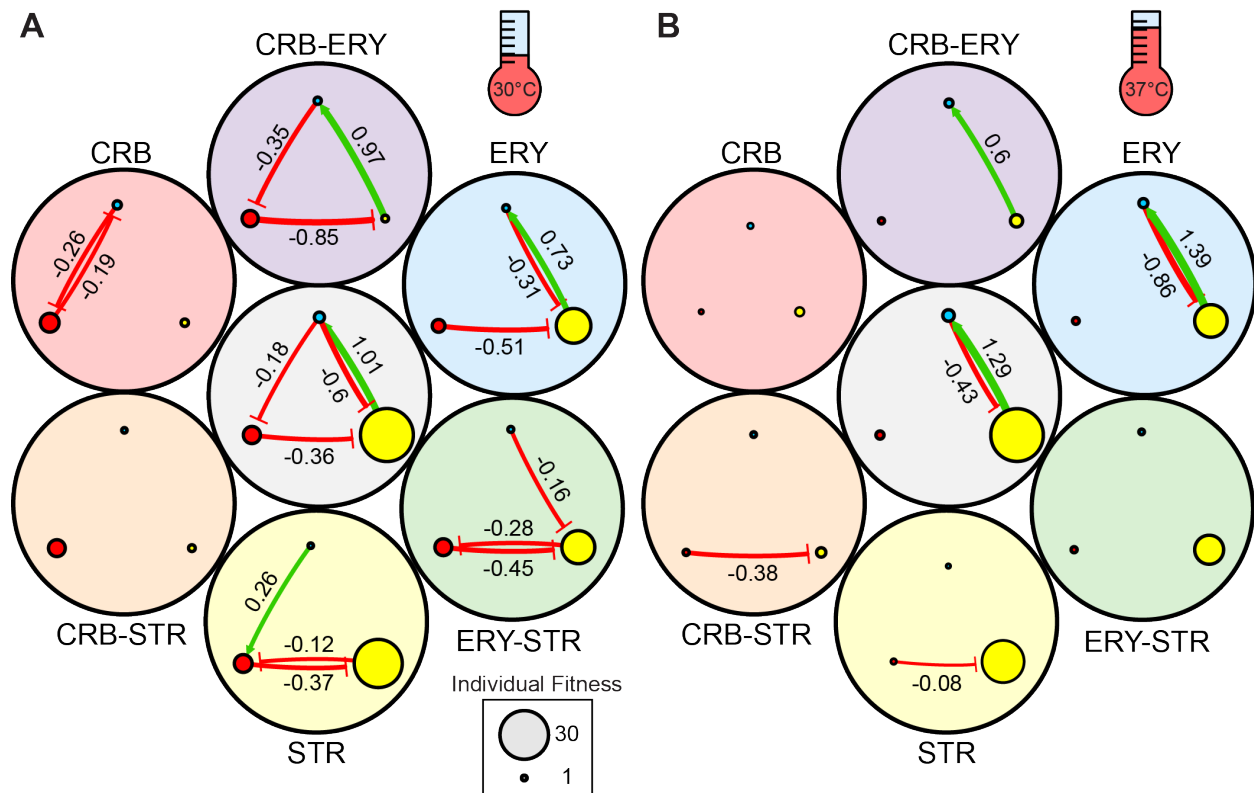
Figure S10. Pairwise microbial interaction networks in each antibiotic condition at different temperatures, Related to Figure 6. Inferred interaction networks in the presence of the specified combination of streptomycin (STR), carbenicillin (CRB), and erythromycin (ERY) at 30°C **(a)** or 37°C **(b)**. The gray circle in center indicates the no antibiotic case. The edge width is proportional to the log$_2$ ratio of the average cell count in the presence of a partner to the average cell count in the absence of the partner. Node size is proportional to the average cell count of each strain grown in isolation. Red nodes represent ME, yellow nodes represent ST Lac*, and blue nodes represent EC Met-. Only those interactions with $p<0.05$ according to a two-sided Mann-Whitney U test are shown (**Table S11**).

Table S1. Strains and Media Conditions for Each Experiment, Related to Figures 2-4 and 6

Number	Strains	Condition	Figure
E1	BS Trp- EC Met- (RFP)	M9 Glucose	2a-d
E2	EC Sender EC Receiver	LB	2e-h
E3	EC Met- (CFP) ST Lac* EC WT	M9 Lactose	3a,e,i 4d,e
E4	EC Met- (CFP) ST Lac* EC WT	M9 Lactose + Met	3b,f,j
E5	EC Met- (CFP) ST Lac* EC WT	M9 Glucose	3c,g,k
E6	EC Met- (CFP) ST Lac* EC WT	M9 Glucose + Met	3d,h,l
E7	EC Met- (CFP) ST Lac* EC Met- Lac* (RFP)	M9 Lactose	4b,c
E8	EC Met- (CFP) ST Lac* ME	Modified Hypho Media, 30°C	6b
E9	EC Met- (CFP) ST Lac* ME	Modified Hypho Media + STR, 30°C	6b
E10	EC Met- (CFP) ST Lac* ME	Modified Hypho Media + CRB, 30°C	6b
E11	EC Met- (CFP) ST Lac* ME	Modified Hypho Media + ERY, 30°C	6b
E12	EC Met- (CFP) ST Lac* ME	Modified Hypho Media + STR + CRB, 30°C	6b
E13	EC Met- (CFP) ST Lac* ME	Modified Hypho Media + STR + ERY, 30°C	6b
E14	EC Met- (CFP) ST Lac* ME	Modified Hypho Media + CRB + ERY, 30°C	6b
E15	EC Met- (CFP) ST Lac* ME	Modified Hypho Media, 37°C	6c
E16	EC Met- (CFP) ST Lac* ME	Modified Hypho Media + STR, 37°C	6c
E17	EC Met- (CFP) ST Lac* ME	Modified Hypho Media + CRB, 37°C	6c
E18	EC Met- (CFP) ST Lac* ME	Modified Hypho Media + ERY, 37°C	6c
E19	EC Met- (CFP) ST Lac* ME	Modified Hypho Media + STR + CRB, 37°C	6c
E20	EC Met- (CFP) ST Lac* ME	Modified Hypho Media + STR + ERY, 37°C	6c
E21	EC Met- (CFP) ST Lac* ME	Modified Hypho Media + CRB + ERY, 37°C	6c

Table S2. Interaction Magnitudes and Statistics for Experiments 1-7, Related to Figures 2 and 3

Experiment	Strain (Sink Node)	Grown With (Source Node)	p-value	<0.05	Mean Count Alone	Mean Count With Partner	Fold Change	Fold Change LCI	Fold Change UCI	Interaction Strength	Interaction Strength LCI	Interaction Strength UCI	Number of Droplets
Glucose	EC Met-	EC WT	0.010489677	TRUE	1.15	1.73	1.51	1.19	1.87	0.59	0.25	0.9	95
Glucose	EC Met-	ST Lac*	6.84E-06	TRUE	1.15	4.1	3.57	2.65	4.68	1.84	1.41	2.23	78
Glucose	EC WT	EC Met-	0.798942338	FALSE	22.48	24.13	1.07	0.95	1.2	0.1	-0.07	0.27	265
Glucose	EC WT	ST Lac*	1.01E-23	TRUE	22.48	10.42	0.46	0.41	0.52	-1.11	-1.27	-0.95	447
Glucose	ST Lac*	EC Met-	0.019029857	TRUE	39.37	37.09	0.94	0.87	1.02	-0.09	-0.2	0.02	227
Glucose	ST Lac*	EC WT	0.088821192	FALSE	39.37	40.99	1.04	0.99	1.1	0.06	-0.01	0.13	426
Glucose +Methionine	EC Met-	EC WT	2.58E-05	TRUE	10.34	6.02	0.58	0.44	0.77	-0.78	-1.17	-0.38	151
Glucose +Methionine	EC Met-	ST Lac*	2.96E-10	TRUE	10.34	3.75	0.36	0.28	0.48	-1.46	-1.86	-1.06	139
Glucose +Methionine	EC WT	EC Met-	2.12E-11	TRUE	29.98	21.16	0.71	0.62	0.79	-0.5	-0.68	-0.34	278
Glucose +Methionine	EC WT	ST Lac*	3.94E-37	TRUE	29.98	16.11	0.54	0.5	0.58	-0.9	-1.01	-0.78	574
Glucose +Methionine	ST Lac*	EC Met-	0.000676812	TRUE	40.37	35.51	0.88	0.81	0.95	-0.19	-0.3	-0.08	237
Glucose +Methionine	ST Lac*	EC WT	2.01E-12	TRUE	40.37	32.73	0.81	0.77	0.85	-0.3	-0.38	-0.23	545
Lactose	EC Met-	EC WT	3.82E-05	TRUE	1.61	2.85	1.77	1.44	2.19	0.83	0.52	1.13	155
Lactose	EC Met-	ST Lac*	1.29E-20	TRUE	1.61	16.48	10.25	8.5	12.32	3.36	3.09	3.62	202
Lactose	EC WT	EC Met-	0.089775303	FALSE	23.33	21.37	0.92	0.79	1.06	-0.13	-0.34	0.08	236
Lactose	EC WT	ST Lac*	0.171934431	FALSE	23.33	22.63	0.97	0.87	1.1	-0.04	-0.21	0.13	339
Lactose	ST Lac*	EC Met-	3.93E-18	TRUE	11.55	19.82	1.72	1.47	2.01	0.78	0.56	1.01	317
Lactose	ST Lac*	EC WT	8.04E-19	TRUE	11.55	20.51	1.78	1.53	2.07	0.83	0.61	1.05	373
Lactose +Methionine	EC Met-	EC WT	4.89E-07	TRUE	20.38	11.76	0.58	0.48	0.69	-0.79	-1.06	-0.54	239
Lactose +Methionine	EC Met-	ST Lac*	0.810598122	FALSE	20.38	20.17	0.99	0.86	1.15	-0.01	-0.22	0.2	246
Lactose +Methionine	EC WT	EC Met-	8.47E-14	TRUE	26.09	14.81	0.57	0.48	0.66	-0.82	-1.05	-0.61	267
Lactose +Methionine	EC WT	ST Lac*	0.332001813	FALSE	26.09	25.48	0.98	0.89	1.08	-0.03	-0.17	0.11	307
Lactose +Methionine	ST Lac*	EC Met-	1.13E-13	TRUE	8.6	16.58	1.93	1.61	2.3	0.95	0.69	1.2	290
Lactose +Methionine	ST Lac*	EC WT	6.55E-17	TRUE	8.6	15.25	1.77	1.5	2.1	0.83	0.58	1.07	323
Higher Order Interaction	EC Met-	EC Met-Lac*	0.086973747	FALSE	1.34	1.47	1.09	0.98	1.22	0.13	-0.03	0.29	350
Higher Order Interaction	EC Met-	ST Lac*	1.37E-14	TRUE	1.34	4.38	3.26	2.61	4.03	1.7	1.38	2.01	317
Higher Order Interaction	EC Met-Lac*	EC Met-	0.882671829	FALSE	2.28	2.37	1.04	0.92	1.18	0.06	-0.13	0.24	765
Higher Order Interaction	EC Met-Lac*	ST Lac*	0.122587282	FALSE	2.28	2.58	1.13	1.01	1.27	0.18	0.02	0.35	839
Higher Order Interaction	ST Lac*	EC Met-	2.70E-29	TRUE	1.69	7.71	4.56	3.63	5.67	2.19	1.86	2.5	378
Higher Order Interaction	ST Lac*	EC Met-Lac*	0.004930119	TRUE	1.69	2.03	1.2	1.01	1.41	0.26	0.02	0.49	485
Mutualism	BS Trp-	EC Met-	1.49E-06	TRUE	1.61	6.78	4.2	3.06	5.69	2.07	1.61	2.51	187
Mutualism	EC Met-	BS Trp-	3.81E-26	TRUE	2.38	7.81	3.27	2.8	3.78	1.71	1.49	1.92	372
mazF Inhibition	Sender	Reciever	0.000223434	TRUE	54.24	43.59	0.8	0.71	0.9	-0.32	-0.49	-0.16	1512
mazF Inhibition	Reciever	Sender	3.75E-14	TRUE	3.25	1.24	0.38	0.33	0.44	-1.4	-1.61	-1.18	421

Table S3. Higher-Order Interaction Calculations for Experiments 1-7, Related to Figure 4

Experiment	Grown With	Strain	Sign	Int Strength	p-value	HOI Detected
Glu	EC Met-	EC WT	0	0.102114968	0.798942338	0
Glu	ST Lac*	EC WT	-	-1.109524627	1.01E-23	0
Glu	3m	EC WT	-	-1.148448126	2.38E-17	0
Glu	EC WT	EC Met-	+	0.591915261	0.010489677	0
Glu	ST Lac*	EC Met-	+	1.835202907	6.84E-06	0
Glu	3m	EC Met-	+	1.798366139	1.30E-05	0
Glu	EC Met-	ST Lac*	-	-0.086099068	0.019029857	0
Glu	EC WT	ST Lac*	0	0.058231313	0.088821192	0
Glu	3m	ST Lac*	-	-0.117580117	0.004504493	0
Glu+Met	EC Met-	EC WT	-	-0.5026437	2.12E-11	0
Glu+Met	ST Lac*	EC WT	-	-0.895618839	3.94E-37	0
Glu+Met	3m	EC WT	-	-1.193141705	2.83E-36	0
Glu+Met	EC WT	EC Met-	-	-0.78044825	2.58E-05	0
Glu+Met	ST Lac*	EC Met-	-	-1.462193419	2.96E-10	0
Glu+Met	3m	EC Met-	-	-1.438228555	1.40E-12	0
Glu+Met	EC Met-	ST Lac*	-	-0.18529422	0.000676812	0
Glu+Met	EC WT	ST Lac*	-	-0.302928912	2.01E-12	0
Glu+Met	3m	ST Lac*	-	-0.476371913	8.67E-17	0
Lac	EC Met-	EC WT	0	-0.126502372	0.089775303	0
Lac	ST Lac*	EC WT	0	-0.043722704	0.171934431	0
Lac	3m	EC WT	-	-0.665029763	2.87E-10	1
Lac	EC WT	EC Met-	+	0.827527832	3.82E-05	0
Lac	ST Lac*	EC Met-	+	3.35824958	1.29E-20	0
Lac	3m	EC Met-	+	2.855790575	2.25E-18	0
Lac	EC Met-	ST Lac*	+	0.778602072	3.93E-18	0
Lac	EC WT	ST Lac*	+	0.828481936	8.04E-19	0
Lac	3m	ST Lac*	+	0.645157283	4.63E-12	0
Lac+Met	EC Met-	EC WT	-	-0.816832143	8.47E-14	0
Lac+Met	ST Lac*	EC WT	0	-0.033922516	0.332001813	0
Lac+Met	3m	EC WT	-	-0.738184601	3.03E-15	0
Lac+Met	EC WT	EC Met-	-	-0.793309929	4.89E-07	0
Lac+Met	ST Lac*	EC Met-	0	-0.014625345	0.810598122	0
Lac+Met	3m	EC Met-	-	-0.768469587	2.01E-07	0
Lac+Met	EC Met-	ST Lac*	+	0.947643409	1.13E-13	0
Lac+Met	EC WT	ST Lac*	+	0.826752374	6.55E-17	0
Lac+Met	3m	ST Lac*	+	0.554962381	4.19E-09	0
hoi	EC Met-	EC Met- Lac*	0	0.057889933	0.882671829	0
hoi	ST Lac*	EC Met- Lac*	0	0.180899803	0.122587282	0
hoi	3m	EC Met- Lac*	+	0.502234034	0.001246654	1
hoi	EC Met- Lac*	EC Met-	0	0.130811642	0.086973747	0
hoi	ST Lac*	EC Met-	+	1.704864099	1.37E-14	0
hoi	3m	EC Met-	+	0.974726786	2.54E-07	0
hoi	EC Met-	ST Lac*	+	2.187905903	2.70E-29	0
hoi	EC Met- Lac*	ST Lac*	+	0.264819775	0.004930119	0
hoi	3m	ST Lac*	+	1.384703855	8.20E-15	0

Table S4. Stochastic Model Parameters, Related to STAR Methods and Figure 5

Parameters for Figure 5C

strain_1	EC WT
strain_2	ST Lac*
r_div_1	0.542
r_death_1	0.05
r_div_2	0.215
r_death_2	0.05
s_11	-1
s_22	-1
s_12	-1
s_21	-1
k_11	0.2
a_11	0.449328964
k_22	0.06
a_22	2.718281828
k_12	1
a_12	0.018315639
k_21	0.05
a_21	2.06E-09

Parameters for Figure 5D

strain_1	EC Met-
strain_2	ST Lac*
r_div_1	0.057
r_death_1	0.01
r_div_2	0.029
r_death_2	0.006
s_11	-1
s_22	-1
s_12	-1
s_21	1
k_11	0.05
a_11	9.487735836
k_22	0.05
a_22	9.487735836
k_12	0
a_12	0
k_21	1
a_21	1

Parameters for Figure S8

strain_1	EC Met-
strain_2	ST Lac*
strain_3	EC WT
r_div_1	0.0004
r_death_1	0.05
r_div_2	0.21515
r_death_2	0.05
r_div_3	0.54205
r_death_3	0.05
s_11	-1
s_22	-1
s_33	-1
s_12	0
s_13	0
s_21	1
s_23	-1
s_31	1
s_32	-1
k_11	0.05
a_11	5.754602676
k_22	0.06
a_22	6
k_33	0.2
a_33	4.49E-01
k_21	2
a_21	0.0098
k_23	1
a_23	0.0183
k_31	1
a_31	2.1
k_32	0.05
a_32	0

Parameters for Figure 5E

strain_1	EC Met-
strain_2	ST Lac*
r_div_1	0.004
r_death_1	0.015
r_div_2	0.011
r_death_2	0.015
s_11	-1
s_22	-1
s_12	1
s_21	1
k_11	0.05
a_11	5.754602676
k_22	0.05
a_22	5.754602676
k_12	1
a_12	0.049787068
k_21	1
a_21	0.135335283

Parameters for Fig. 5F

strain_1	Sender
strain_2	Receiver
r_div_1	0.06
r_death_1	0.015
r_div_2	0.015
r_death_2	0.01
s_11	-1
s_22	-1
s_12	-1
s_21	-1
k_11	0.02
a_11	9.025013499
k_22	0.05
a_22	9.487735836
k_12	0.05
a_12	3.06E-07
k_21	1
a_21	2.718281828

Parameters for Figure S7B,C

r_div_1	0.005
r_death_1	0.05
s_11_-	-1
k_11_-	0.01
a_11_-	0.05

Parameters for Figure S7D,E

r_div_1	0.005
r_death_1	0.05
s_11_-	-1
s_11_+	1
k_11_-	0.01
a_11_-	0.05
k_11_+	0.02
k_11_+	0.01

Table S5. Modified Hypho Media Composition, Related to STAR Methods

Chemical	Concentration
$ZnCl_2$	1.2 µM
$MnCl_2$ $4H_2O$	1 µM
$FeCl_2$	18 µM
$(NH_4)_6Mo_7O_{24}$ $4H_2O$	2 µM
$CuSO_4$	1 µM
$CoCl_2$ $6H_2O$	2 µM
Na_2WO_4 $2H_2O$	0.33 µM
K_2HPO_4	14.5 mM
NaH_2PO_4 2H2O	16.3 mM
Na_2SO_4	3.78 mM
$MgSO_4$	814 µM
$C_{12}H_{22}O_{11}$ (Lactose)	2.78 mM
CH_5N (Methylamine)	231 µM
$C_5H_{11}NO_2S$ (Methionine)	20 µM
$C_2H_3NaO_2$ (Sodium acetate)	750 µM
NH_4Cl (Ammonium chloride)	7.56 mM
$C_6H_{12}O_6$ (Glucose)	5.55 mM
$(CH_2)_2(CO_2H)_2$ (Succinate)	3.7 mM

Table S6. Types of Interactions in the Antibiotic Interaction Networks, Related to Figure 6

Interaction Type	Description	Abbreviation	Numerator	Denominator	Comparing Different Populations of Droplets?	Network Arrow Sign Modifier
1	Impact of partner on grower	species-species	Cell Count in Two-Species, No Antibiotic Droplets	Cell Count in One-Species, No Antibiotic Droplets	No	1
2	Impact of antibiotic on grower	antibiotic-species	Cell Count in One-Species, One-Antibiotic Droplets	Cell Count in One-Species, No Antibiotic Droplets	Yes	1
3	Impact of partner strain on antibiotic's effect on grower	species-antibiotic-species	Cell Count in Two-Species, One-Antibiotic Droplets	Cell Count in One-Species, One-Antibiotic Droplets	No	-1
4	Impact of secondary (less effective) antibiotic on primary (more effective) antibiotic's effect on grower	antibiotic-antibiotic-species	Cell Count in One-Species, Two-Antibiotic Droplets	Cell Count in One-Species, One-Antibiotic Droplets	Yes	-1

Table S7. Interactions from Antibiotics Experiments 8-14 (30°C), Related to Figure 6

Interaction Type (Table S6)	Source	Sink	Numerator	Denominator	Numerator Mean	Denominator Mean	n (Numerator)	n (Denominator)	Ratio	p	p<0.05	Included in Fig. 6b
1	RFP	YFP	Number of YFP with RFP	Number of YFP alone	23.7	30.4	120	47	0.78	2.7E-04	TRUE	FALSE
1	RFP	CFP	Number of CFP with RFP	Number of CFP alone	3.7	4.0	265	124	0.93	2.0E-01	FALSE	FALSE
1	YFP	RFP	Number of RFP with YFP	Number of RFP alone	7.5	8.3	120	112	0.91	1.4E-01	FALSE	FALSE
1	YFP	CFP	Number of CFP with YFP	Number of CFP alone	8.0	4.0	172	124	2.01	9.6E-15	TRUE	TRUE
1	CFP	RFP	Number of RFP with CFP	Number of RFP alone	7.3	8.3	265	112	0.88	3.0E-02	TRUE	FALSE
1	CFP	YFP	Number of YFP with CFP	Number of YFP alone	20.1	30.4	172	47	0.66	4.1E-08	TRUE	TRUE
2	CRB	RFP	Number of RFP with CRB	Number of RFP with no antibiotic	9.3	8.3	256	112	1.12	6.4E-02	FALSE	FALSE
2	STR	RFP	Number of RFP with STR	Number of RFP with no antibiotic	8.7	8.3	188	112	1.04	5.1E-01	FALSE	FALSE
2	ERY	RFP	Number of RFP with ERY	Number of RFP with no antibiotic	5.6	8.3	145	112	0.68	4.7E-08	TRUE	TRUE
2	CRB	YFP	Number of YFP with CRB	Number of YFP with no antibiotic	2.3	30.4	33	47	0.07	4.7E-14	TRUE	TRUE
2	STR	YFP	Number of YFP with STR	Number of YFP with no antibiotic	27.4	30.4	114	47	0.90	1.1E-01	FALSE	FALSE
2	ERY	YFP	Number of YFP with ERY	Number of YFP with no antibiotic	19.1	30.4	91	47	0.63	2.4E-09	TRUE	TRUE
2	CRB	CFP	Number of CFP with CRB	Number of CFP with no antibiotic	2.8	4.0	174	124	0.71	1.3E-04	TRUE	FALSE
2	STR	CFP	Number of CFP with STR	Number of CFP with no antibiotic	1.1	4.0	23	124	0.27	3.3E-09	TRUE	TRUE
2	ERY	CFP	Number of CFP with ERY	Number of CFP with no antibiotic	1.9	4.0	66	124	0.48	3.3E-09	TRUE	TRUE
3	YFP	CRB to RFP	Number of RFP with CRB and YFP	Number of RFP with CRB alone	8.1	9.3	21	256	0.88	6.0E-01	FALSE	FALSE
3	YFP	STR to RFP	Number of RFP with STR and YFP	Number of RFP with STR alone	8.0	8.7	238	188	0.92	4.8E-02	TRUE	FALSE
3	YFP	ERY to RFP	Number of RFP with ERY and YFP	Number of RFP with ERY alone	5.8	5.6	151	145	1.03	8.5E-01	FALSE	FALSE
3	CFP	CRB to RFP	Number of RFP with CRB and CFP	Number of RFP with CRB alone	7.7	9.3	301	256	0.83	6.5E-04	TRUE	FALSE
3	CFP	STR to RFP	Number of RFP with STR and CFP	Number of RFP with STR alone	10.4	8.7	73	188	1.20	3.4E-03	TRUE	FALSE
3	CFP	ERY to RFP	Number of RFP with ERY and CFP	Number of RFP with ERY alone	5.3	5.6	92	145	0.94	5.4E-01	FALSE	FALSE
3	RFP	CRB to YFP	Number of YFP with CRB and RFP	Number of YFP with CRB alone	2.2	2.3	21	33	0.98	9.9E-01	FALSE	FALSE
3	RFP	STR to YFP	Number of YFP with STR and RFP	Number of YFP with STR alone	21.2	27.4	238	114	0.77	3.7E-10	TRUE	FALSE
3	RFP	ERY to YFP	Number of YFP with ERY and RFP	Number of YFP with ERY alone	13.5	19.1	151	91	0.70	4.1E-06	TRUE	TRUE
3	CFP	CRB to YFP	Number of YFP with CRB and CFP	Number of YFP with CRB alone	2.2	2.3	42	33	0.96	6.8E-01	FALSE	FALSE
3	CFP	STR to YFP	Number of YFP with STR and CFP	Number of YFP with STR alone	25.1	27.4	42	114	0.92	8.3E-02	FALSE	FALSE
3	CFP	ERY to YFP	Number of YFP with ERY and CFP	Number of YFP with ERY alone	15.5	19.1	150	91	0.81	2.3E-03	TRUE	FALSE
3	RFP	CRB to CFP	Number of CFP with CRB and RFP	Number of CFP with CRB alone	2.5	2.8	301	174	0.88	9.1E-03	TRUE	FALSE
3	RFP	STR to CFP	Number of CFP with STR and RFP	Number of CFP with STR alone	1.3	1.1	73	23	1.17	2.8E-01	FALSE	FALSE
3	RFP	ERY to CFP	Number of CFP with ERY and RFP	Number of CFP with ERY alone	1.9	1.9	92	66	1.01	7.9E-01	FALSE	FALSE
3	YFP	CRB to CFP	Number of CFP with CRB and YFP	Number of CFP with CRB alone	3.4	2.8	42	174	1.22	6.0E-02	FALSE	FALSE

3	YFP	STR to CFP	Number of CFP with STR and YFP	Number of CFP with STR alone	1.1	1.1	42	23	1.01	9.2E-01	FALSE	FALSE
3	YFP	ERY to CFP	Number of CFP with ERY and YFP	Number of CFP with ERY alone	3.2	1.9	150	66	1.66	6.7E-05	TRUE	TRUE
4	STR	CRB to RFP	Number of RFP with CRB and STR	Number of RFP with CRB only	8.1	9.3	478	256	0.87	4.0E-03	TRUE	FALSE
4	CRB	ERY to RFP	Number of RFP with ERY and CRB	Number of RFP with ERY only	7.7	5.6	241	145	1.36	7.7E-07	TRUE	FALSE
4	STR	ERY to RFP	Number of RFP with ERY and STR	Number of RFP with ERY only	8.1	5.6	212	145	1.44	2.8E-11	TRUE	TRUE
4	STR	CRB to YFP	Number of YFP with CRB and STR	Number of YFP with CRB only	1.9	2.3	52	33	0.83	4.1E-01	FALSE	FALSE
4	ERY	CRB to YFP	Number of YFP with CRB and ERY	Number of YFP with CRB only	1.9	2.3	10	33	0.84	5.0E-01	FALSE	FALSE
4	STR	ERY to YFP	Number of YFP with ERY and STR	Number of YFP with ERY only	18.1	19.1	135	91	0.94	2.1E-01	FALSE	FALSE
4	CRB	STR to CFP	Number of CFP with STR and CRB	Number of CFP with STR only	1.1	1.1	36	23	1.02	1.0E+00	FALSE	FALSE
4	CRB	ERY to CFP	Number of CFP with ERY and CRB	Number of CFP with ERY only	2.2	1.9	179	66	1.15	8.2E-02	FALSE	FALSE
4	ERY	STR to CFP	Number of CFP with STR and ERY	Number of CFP with STR only	1.4	1.1	43	23	1.28	1.4E-01	FALSE	FALSE

Table S8. Interactions from Antibiotics Experiments 15-21 (37°C), Related to Figure 6

Interaction Type (Table S6)	Source	Sink	Numerator	Denominator	Numerator Mean	Denominator Mean	n (Numerator)	n (Denominator)	Ratio	p	p<0.05	Included in **Fig. 6c**
1	RFP	YFP	Number of YFP with RFP	Number of YFP alone	30.0	29.7	57	38	1.01	7.4E-01	FALSE	FALSE
1	RFP	CFP	Number of CFP with RFP	Number of CFP alone	4.3	4.7	159	99	0.92	3.1E-01	FALSE	FALSE
1	YFP	RFP	Number of RFP with YFP	Number of RFP alone	2.3	2.6	57	49	0.88	7.6E-01	FALSE	FALSE
1	YFP	CFP	Number of CFP with YFP	Number of CFP alone	11.4	4.7	179	99	2.45	6.2E-15	TRUE	TRUE
1	CFP	RFP	Number of RFP with CFP	Number of RFP alone	2.4	2.6	159	49	0.94	9.5E-01	FALSE	FALSE
1	CFP	YFP	Number of YFP with CFP	Number of YFP alone	22.1	29.7	179	38	0.74	1.5E-04	TRUE	FALSE
2	CRB	RFP	Number of RFP with CRB	Number of RFP with no antibiotic	1.7	2.6	220	49	0.67	8.1E-04	TRUE	TRUE
2	STR	RFP	Number of RFP with STR	Number of RFP with no antibiotic	1.9	2.6	251	49	0.74	1.3E-02	TRUE	FALSE
2	ERY	RFP	Number of RFP with ERY	Number of RFP with no antibiotic	1.9	2.6	70	49	0.73	3.1E-02	TRUE	FALSE
2	CRB	YFP	Number of YFP with CRB	Number of YFP with no antibiotic	5.2	29.7	110	38	0.18	2.7E-11	TRUE	TRUE
2	STR	YFP	Number of YFP with STR	Number of YFP with no antibiotic	29.8	29.7	150	38	1.01	2.0E-01	FALSE	FALSE
2	ERY	YFP	Number of YFP with ERY	Number of YFP with no antibiotic	17.8	29.7	76	38	0.60	5.3E-07	TRUE	TRUE
2	CRB	CFP	Number of CFP with CRB	Number of CFP with no antibiotic	2.6	4.7	127	99	0.56	5.5E-10	TRUE	TRUE
2	STR	CFP	Number of CFP with STR	Number of CFP with no antibiotic	1.1	4.7	22	99	0.23	3.5E-10	TRUE	TRUE
2	ERY	CFP	Number of CFP with ERY	Number of CFP with no antibiotic	3.3	4.7	127	99	0.70	1.1E-05	TRUE	TRUE
3	YFP	CRB to RFP	Number of RFP with CRB and YFP	Number of RFP with CRB alone	2.0	1.7	95	220	1.16	9.9E-02	FALSE	FALSE
3	YFP	STR to RFP	Number of RFP with STR and YFP	Number of RFP with STR alone	2.0	1.9	234	251	1.03	8.7E-01	FALSE	FALSE
3	YFP	ERY to RFP	Number of RFP with ERY and YFP	Number of RFP with ERY alone	1.8	1.9	81	70	0.93	6.2E-01	FALSE	FALSE
3	CFP	CRB to RFP	Number of RFP with CRB and CFP	Number of RFP with CRB alone	1.8	1.7	138	220	1.06	9.4E-02	FALSE	FALSE
3	CFP	STR to RFP	Number of RFP with STR and CFP	Number of RFP with STR alone	2.0	1.9	43	251	1.07	5.5E-01	FALSE	FALSE
3	CFP	ERY to RFP	Number of RFP with ERY and CFP	Number of RFP with ERY alone	1.9	1.9	125	70	0.98	8.2E-01	FALSE	FALSE
3	RFP	CRB to YFP	Number of YFP with CRB and RFP	Number of YFP with CRB alone	5.0	5.2	95	110	0.96	5.3E-01	FALSE	FALSE
3	RFP	STR to YFP	Number of YFP with STR and RFP	Number of YFP with STR alone	28.2	29.8	234	150	0.95	4.6E-02	TRUE	FALSE
3	RFP	ERY to YFP	Number of YFP with ERY and RFP	Number of YFP with ERY alone	18.1	17.8	81	76	1.02	6.3E-01	FALSE	FALSE

3	CFP	CRB to YFP	Number of YFP with CRB and CFP	Number of YFP with CRB alone	5.4	5.2	47	110	1.05	5.7E-01	FALSE	FALSE
3	CFP	STR to YFP	Number of YFP with STR and CFP	Number of YFP with STR alone	28.5	29.8	41	150	0.96	4.9E-01	FALSE	FALSE
3	CFP	ERY to YFP	Number of YFP with ERY and CFP	Number of YFP with ERY alone	9.8	17.8	220	76	0.55	4.8E-13	TRUE	TRUE
3	RFP	CRB to CFP	Number of CFP with CRB and RFP	Number of CFP with CRB alone	2.8	2.6	138	127	1.08	3.8E-01	FALSE	FALSE
3	RFP	STR to CFP	Number of CFP with STR and RFP	Number of CFP with STR alone	1.1	1.1	43	22	1.04	7.5E-01	FALSE	FALSE
3	RFP	ERY to CFP	Number of CFP with ERY and RFP	Number of CFP with ERY alone	3.5	3.3	125	127	1.07	4.3E-01	FALSE	FALSE
3	YFP	CRB to CFP	Number of CFP with CRB and YFP	Number of CFP with CRB alone	2.6	2.6	47	127	1.01	9.5E-01	FALSE	FALSE
3	YFP	STR to CFP	Number of CFP with STR and YFP	Number of CFP with STR alone	1.3	1.1	41	22	1.18	1.4E-01	FALSE	FALSE
3	YFP	ERY to CFP	Number of CFP with ERY and YFP	Number of CFP with ERY alone	8.5	3.3	220	127	2.61	1.6E-20	TRUE	TRUE
4	STR	CRB to RFP	Number of RFP with CRB and STR	Number of RFP with CRB only	1.5	1.7	204	220	0.87	3.7E-02	TRUE	FALSE
4	ERY	CRB to RFP	Number of RFP with CRB and ERY	Number of RFP with CRB only	1.5	1.7	216	220	0.87	5.0E-02	FALSE	FALSE
4	STR	ERY to RFP	Number of RFP with ERY and STR	Number of RFP with ERY only	1.5	1.9	130	70	0.77	1.5E-02	TRUE	FALSE
4	STR	CRB to YFP	Number of YFP with CRB and STR	Number of YFP with CRB only	3.5	5.2	181	110	0.68	6.7E-08	TRUE	TRUE
4	ERY	CRB to YFP	Number of YFP with CRB and ERY	Number of YFP with CRB only	5.3	5.2	68	110	1.02	8.9E-01	FALSE	FALSE
4	STR	ERY to YFP	Number of YFP with ERY and STR	Number of YFP with ERY only	15.6	17.8	230	76	0.88	1.5E-01	FALSE	FALSE
4	CRB	STR to CFP	Number of CFP with STR and CRB	Number of CFP with STR only	1.2	1.1	107	22	1.10	3.1E-01	FALSE	FALSE
4	ERY	CRB to CFP	Number of CFP with CRB and ERY	Number of CFP with CRB only	2.7	2.6	144	127	1.04	7.5E-01	FALSE	FALSE
4	ERY	STR to CFP	Number of CFP with STR and ERY	Number of CFP with STR only	1.2	1.1	17	22	1.08	7.7E-01	FALSE	FALSE

Table S9. Strains Used in this Work, Related to STAR Methods

Species	Strain	Fluorescent Reporter	Abbreviation	Reference
B. subtilis	B. subtilis 168, trpC2, cat	None	-	(Burkholder and Giles, 1947)
B. subtilis	*B. subtilis* 168, trpC2, cat, amyE::Pveg-gfp-spec	GFP	BS Trp-	This work
E. coli	*E. coli* BW27783	None	-	(Khlebnikov et al., 2001)
E. coli	*E. coli* MG1655z1	None	-	(Cox et al., 2007)
E. coli	*E. coli* BW25113 pheA::Kan	None	-	(Baba et al., 2006)
E. coli	*E. coli* BW25113, metA::Kan	None	-	(Baba et al., 2006)
E. coli	*E. coli* K12 BW25113, ΔmetB, att::pLC280 [kan P_L'-cfp oriR6K]	CFP	EC Met- (CFP)	(Adamowicz et al., 2018)
E. coli	*E. coli* BW25113, pheA::Kan, pOSV006	RFP	EC Met- Lac* and EC Met- (RFP)	This work
E. coli	*E. coli* BW25113, metA::Kan, pOSV006	RFP	EC WT	This work
E. coli	*E. coli* BW27783, pOSV022	GFP	Sender	This work
E. coli	*E. coli* MG1655z1, pOSV151	RFP	Receiver	This work
M. extorquens AM1	*M. extorquens* AM1, ΔhprA::kan	RFP	ME	(Adamowicz et al., 2018)
S. typhimurium	*S. typhimurium* LT2, metA(P35L), metJ(16:IS10), att::pLC246 [kan P_L'-yfp oriR6K]	YFP	ST Lac*	(Adamowicz et al., 2018; Douglas et al., 2016)

Table S10. Plasmids Used to Generate Strains in Table S9, Related to STAR Methods

Plasmid	Description	Reference
pOSV006	mCherry expression vector	This work
pOSV022	Quorum sensing production vector (sender)	This work
pOSV151	Quorum sensing regulated toxin vector (receiver)	This work
pVP038	amyE::Pveg-gfp-spec transformation vector	(Radzinski, N. P., Wang, M., and Burton, B. M., Unpublished.)

Table S11. Interaction Magnitudes and Statistics for Experiments 8-21, Related to Figures 6 and S10

Temperature	Antibiotics	Time	Strain (Sink Node)	Grown With (Source Node)	p-value	<0.05	Mean Count Alone	Mean Count With Partner	Fold Change	Fold Change LCI	Fold Change UCI	Interaction Strength	Interaction Strength LCI	Interaction Strength UCI	Number of Droplets
30C	CRB	36hr	EC Met-	ME	0.009050247	TRUE	2.81	2.47	0.88	0.78	0.99	-0.19	-0.36	-0.02	475
30C	CRB	36hr	EC Met-	ST Lac*	0.059942167	FALSE	2.81	3.43	1.22	1	1.47	0.29	0	0.56	216
30C	CRB	36hr	ME	EC Met-	0.000649828	TRUE	9.25	7.72	0.83	0.76	0.92	-0.26	-0.39	-0.13	557
30C	CRB	36hr	ME	ST Lac*	0.604954812	FALSE	9.25	8.14	0.88	0.6	1.15	-0.18	-0.73	0.2	277
30C	CRB	36hr	ST Lac*	EC Met-	0.683073499	FALSE	2.27	2.19	0.96	0.53	1.71	-0.05	-0.91	0.78	75
30C	CRB	36hr	ST Lac*	ME	0.99207931	FALSE	2.27	2.24	0.98	0.48	1.94	-0.02	-1.04	0.96	54
30C	CRBxERY	36hr	EC Met-	ME	0.478250977	FALSE	2.2	2.35	1.07	0.96	1.19	0.1	-0.06	0.25	517
30C	CRBxERY	36hr	EC Met-	ST Lac*	5.51E-06	TRUE	2.2	4.31	1.96	1.51	2.51	0.97	0.59	1.33	208
30C	CRBxERY	36hr	ME	EC Met-	4.52E-07	TRUE	7.68	6.04	0.79	0.72	0.86	-0.35	-0.47	-0.22	579
30C	CRBxERY	36hr	ME	ST Lac*	0.897016135	FALSE	7.68	7.61	0.99	0.75	1.24	-0.01	-0.41	0.31	259
30C	CRBxERY	36hr	ST Lac*	EC Met-	0.931901508	FALSE	1.9	2.1	1.11	0.75	1.64	0.15	-0.41	0.72	39
30C	CRBxERY	36hr	ST Lac*	ME	0.00171774	TRUE	1.9	1.06	0.56	0.42	0.79	-0.85	-1.26	-0.33	28
30C	CRBxSTR	36hr	EC Met-	ME	0.102836497	FALSE	1.11	1.02	0.91	0.8	1.02	-0.13	-0.32	0.02	99
30C	CRBxSTR	36hr	EC Met-	ST Lac*	0.493776269	FALSE	1.11	1	0.9	0.8	1	-0.15	-0.32	0	42
30C	CRBxSTR	36hr	ME	EC Met-	0.152563475	FALSE	8.08	9.21	1.14	0.98	1.31	0.19	-0.02	0.39	541
30C	CRBxSTR	36hr	ME	ST Lac*	0.156116394	FALSE	8.08	9.18	1.14	0.97	1.31	0.18	-0.04	0.39	540
30C	CRBxSTR	36hr	ST Lac*	EC Met-	0.096977868	FALSE	1.88	2.83	1.5	0.72	2.58	0.59	-0.48	1.37	58
30C	CRBxSTR	36hr	ST Lac*	ME	0.950352974	FALSE	1.88	1.63	0.86	0.63	1.2	-0.21	-0.67	0.26	114
30C	ERY	36hr	EC Met-	ME	0.786536325	FALSE	1.91	1.92	1.01	0.83	1.22	0.01	-0.27	0.29	158
30C	ERY	36hr	EC Met-	ST Lac*	6.69E-05	TRUE	1.91	3.16	1.66	1.39	1.98	0.73	0.48	0.99	216
30C	ERY	36hr	ME	EC Met-	0.538353407	FALSE	5.64	5.33	0.94	0.81	1.1	-0.08	-0.31	0.14	237
30C	ERY	36hr	ME	ST Lac*	0.849079234	FALSE	5.64	5.79	1.03	0.89	1.18	0.04	-0.16	0.24	296
30C	ERY	36hr	ST Lac*	EC Met-	0.002282559	TRUE	19.14	15.45	0.81	0.7	0.93	-0.31	-0.51	-0.11	241
30C	ERY	36hr	ST Lac*	ME	4.09E-06	TRUE	19.14	13.48	0.7	0.61	0.81	-0.51	-0.71	-0.31	242
30C	ERYxSTR	36hr	EC Met-	ME	0.804396337	FALSE	1.4	1.28	0.92	0.72	1.16	-0.12	-0.47	0.22	131
30C	ERYxSTR	36hr	EC Met-	ST Lac*	0.463863896	FALSE	1.4	1.51	1.08	0.82	1.43	0.11	-0.29	0.52	108
30C	ERYxSTR	36hr	ME	EC Met-	0.952501961	FALSE	8.14	8.1	1	0.89	1.1	-0.01	-0.16	0.14	300
30C	ERYxSTR	36hr	ME	ST Lac*	8.75E-08	TRUE	8.14	6.7	0.82	0.76	0.9	-0.28	-0.4	-0.16	486
30C	ERYxSTR	36hr	ST Lac*	EC Met-	0.043210584	TRUE	18.09	16.14	0.89	0.79	1	-0.16	-0.33	0	200
30C	ERYxSTR	36hr	ST Lac*	ME	2.96E-12	TRUE	18.09	13.25	0.73	0.67	0.79	-0.45	-0.57	-0.33	409
30C	NONE	36hr	EC Met-	ME	0.200875517	FALSE	3.97	3.69	0.93	0.81	1.08	-0.1	-0.31	0.11	389
30C	NONE	36hr	EC Met-	ST Lac*	9.60E-15	TRUE	3.97	7.97	2.01	1.74	2.33	1.01	0.8	1.22	296
30C	NONE	36hr	ME	EC Met-	0.030184249	TRUE	8.29	7.3	0.88	0.8	0.98	-0.18	-0.33	-0.03	377
30C	NONE	36hr	ME	ST Lac*	0.136328763	FALSE	8.29	7.52	0.91	0.8	1.03	-0.14	-0.32	0.04	232
30C	NONE	36hr	ST Lac*	EC Met-	4.12E-08	TRUE	30.45	20.13	0.66	0.59	0.74	-0.6	-0.76	-0.44	219
30C	NONE	36hr	ST Lac*	ME	0.000266852	TRUE	30.45	23.73	0.78	0.7	0.87	-0.36	-0.52	-0.21	167
30C	STR	36hr	EC Met-	ME	0.282065416	FALSE	1.09	1.27	1.17	0.98	1.39	0.23	-0.02	0.47	96
30C	STR	36hr	EC Met-	ST Lac*	0.923708788	FALSE	1.09	1.1	1.01	0.88	1.14	0.01	-0.18	0.19	65
30C	STR	36hr	ME	EC Met-	0.003395288	TRUE	8.65	10.4	1.2	1.05	1.36	0.26	0.07	0.45	261
30C	STR	36hr	ME	ST Lac*	0.048202448	TRUE	8.65	7.96	0.92	0.83	1.02	-0.12	-0.27	0.03	426
30C	STR	36hr	ST Lac*	EC Met-	0.083226748	FALSE	27.38	25.12	0.92	0.8	1.04	-0.12	-0.32	0.05	156
30C	STR	36hr	ST Lac*	ME	3.71E-10	TRUE	27.38	21.19	0.77	0.71	0.84	-0.37	-0.49	-0.24	352
37C	CRB	18hr	EC Met-	ME	0.378819723	FALSE	2.6	2.8	1.08	0.91	1.27	0.11	-0.14	0.35	265
37C	CRB	18hr	EC Met-	ST Lac*	0.945587449	FALSE	2.6	2.62	1.01	0.8	1.26	0.01	-0.32	0.33	174
37C	CRB	18hr	ME	EC Met-	0.094372932	FALSE	1.74	1.85	1.06	0.94	1.2	0.09	-0.09	0.27	358
37C	CRB	18hr	ME	ST Lac*	0.09883517	FALSE	1.74	2.02	1.16	0.99	1.36	0.22	-0.02	0.45	315
37C	CRB	18hr	ST Lac*	EC Met-	0.572060235	FALSE	5.21	5.45	1.05	0.86	1.26	0.06	-0.22	0.33	157
37C	CRB	18hr	ST Lac*	ME	0.527350351	FALSE	5.21	4.98	0.96	0.81	1.12	-0.07	-0.3	0.16	205
37C	ERY	18hr	EC Met-	ME	0.427710743	FALSE	3.27	3.49	1.07	0.87	1.31	0.09	-0.2	0.38	252

37C	ERY	18hr	EC Met-	ST Lac*	1.63E-20	TRUE	3.27	8.54	2.61	2.23	3.09	1.39	1.16	1.63	347
37C	ERY	18hr	ME	EC Met-	0.818175148	FALSE	1.9	1.86	0.98	0.82	1.17	-0.03	-0.29	0.23	195
37C	ERY	18hr	ME	ST Lac*	0.620316363	FALSE	1.9	1.77	0.93	0.76	1.14	-0.11	-0.4	0.18	151
37C	ERY	18hr	ST Lac*	EC Met-	4.80E-13	TRUE	17.8	9.83	0.55	0.48	0.64	-0.86	-1.05	-0.66	296
37C	ERY	18hr	ST Lac*	ME	0.632419672	FALSE	17.8	18.09	1.02	0.9	1.16	0.02	-0.16	0.22	157
37C	ERYxCRB	18hr	EC Met-	ME	0.641068381	FALSE	2.7	2.87	1.06	0.9	1.26	0.09	-0.16	0.33	281
37C	ERYxCRB	18hr	EC Met-	ST Lac*	0.003466896	TRUE	2.7	4.1	1.52	1.21	1.88	0.6	0.27	0.91	203
37C	ERYxCRB	18hr	ME	EC Met-	0.972932977	FALSE	1.51	1.59	1.05	0.93	1.19	0.07	-0.1	0.25	353
37C	ERYxCRB	18hr	ME	ST Lac*	0.585487891	FALSE	1.51	1.64	1.08	0.94	1.24	0.11	-0.08	0.31	318
37C	ERYxCRB	18hr	ST Lac*	EC Met-	0.185841771	FALSE	5.34	4.29	0.8	0.64	1.01	-0.32	-0.64	0.02	127
37C	ERYxCRB	18hr	ST Lac*	ME	0.910746634	FALSE	5.34	5.26	0.99	0.81	1.22	-0.02	-0.3	0.29	170
37C	ERYxSTR	18hr	EC Met-	ME	0.627371052	FALSE	1.18	1.07	0.91	0.71	1.13	-0.14	-0.5	0.18	32
37C	ERYxSTR	18hr	EC Met-	ST Lac*	0.741988596	FALSE	1.18	1.09	0.93	0.74	1.13	-0.1	-0.43	0.18	70
37C	ERYxSTR	18hr	ME	EC Met-	0.299075248	FALSE	1.47	1.67	1.13	0.86	1.44	0.18	-0.21	0.53	145
37C	ERYxSTR	18hr	ME	ST Lac*	0.183957134	FALSE	1.47	1.67	1.14	1.01	1.27	0.19	0.02	0.35	421
37C	ERYxSTR	18hr	ST Lac*	EC Met-	0.913148686	FALSE	15.61	15.58	1	0.86	1.14	0	-0.22	0.19	283
37C	ERYxSTR	18hr	ST Lac*	ME	0.678671532	FALSE	15.61	15.29	0.98	0.89	1.07	-0.03	-0.16	0.1	521
37C	NONE	18hr	EC Met-	ME	0.308918711	FALSE	4.68	4.31	0.92	0.8	1.06	-0.12	-0.32	0.09	258
37C	NONE	18hr	EC Met-	ST Lac*	6.16E-15	TRUE	4.68	11.44	2.45	2.12	2.83	1.29	1.08	1.5	278
37C	NONE	18hr	ME	EC Met-	0.949676376	FALSE	2.59	2.44	0.94	0.77	1.17	-0.09	-0.38	0.23	208
37C	NONE	18hr	ME	ST Lac*	0.760149583	FALSE	2.59	2.28	0.88	0.7	1.11	-0.18	-0.51	0.15	106
37C	NONE	18hr	ST Lac*	EC Met-	0.000154565	TRUE	29.66	22.08	0.74	0.63	0.89	-0.43	-0.66	-0.16	217
37C	NONE	18hr	ST Lac*	ME	0.740792136	FALSE	29.66	30.02	1.01	0.84	1.23	0.02	-0.24	0.3	95
37C	STR2	18hr	EC Met-	ME	0.747104099	FALSE	1.09	1.14	1.04	0.9	1.21	0.06	-0.16	0.27	65
37C	STR2	18hr	EC Met-	ST Lac*	0.136312455	FALSE	1.09	1.29	1.18	0.99	1.4	0.24	-0.01	0.49	63
37C	STR2	18hr	ME	EC Met-	0.548856184	FALSE	1.91	2.05	1.07	0.87	1.31	0.1	-0.21	0.39	294
37C	STR2	18hr	ME	ST Lac*	0.869785752	FALSE	1.91	1.97	1.03	0.92	1.15	0.04	-0.12	0.21	485
37C	STR2	18hr	ST Lac*	EC Met-	0.494558739	FALSE	29.82	28.51	0.96	0.85	1.06	-0.06	-0.24	0.08	191
37C	STR2	18hr	ST Lac*	ME	0.045619766	TRUE	29.82	28.23	0.95	0.89	1.01	-0.08	-0.17	0.01	384
37C	STRxCRB	18hr	EC Met-	ME	0.442430656	FALSE	1.2	1.24	1.04	0.93	1.16	0.05	-0.11	0.22	173
37C	STRxCRB	18hr	EC Met-	ST Lac*	0.663219573	FALSE	1.2	1.28	1.07	0.93	1.23	0.1	-0.11	0.3	168
37C	STRxCRB	18hr	ME	EC Met-	0.656653487	FALSE	1.51	1.53	1.01	0.88	1.16	0.01	-0.19	0.22	270
37C	STRxCRB	18hr	ME	ST Lac*	0.190977433	FALSE	1.51	1.69	1.12	0.99	1.27	0.16	-0.02	0.34	338
37C	STRxCRB	18hr	ST Lac*	EC Met-	0.414125805	FALSE	3.55	2.98	0.84	0.67	1.05	-0.25	-0.59	0.06	242
37C	STRxCRB	18hr	ST Lac*	ME	0.026109391	TRUE	3.55	2.73	0.77	0.63	0.93	-0.38	-0.67	-0.11	315