Bacterial population dynamics during colonization of solid tumors

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Abstract

Bacterial colonization of cancer tumors is widespread. While the clinical significance of intratumor bacteria is widely investigated, the dynamics of tumor colonization remain underexplored. We monitored bacterial population dynamics in murine tumors after introducing genetically barcoded *Escherichia coli* cells by intravenous or intratumor injections. Barcode sequencing from resected tumors after intravenous injection suggested that narrow bottlenecks dominate infection and are followed by rapid, yet highly nonuniform growth. Within a day, bacteria reached a steady state and subsequently sustained load and clone diversity. Results from intratumor injections, circumventing the infection bottleneck, revealed that sizes of bacterial progenies followed a scale-free distribution matching Zipf's law. Theory suggested that our observations are compatible with a growth model constrained by a local niche load, competition for a global resource, and noise. Our work provides the first dynamical model of tumor colonization and suggests that descriptive statistics may allow distinguishing genuine tumor microbiomes from contamination.

Introduction

The human microbiota that resides within different organs, such as the skin, mouth and gut, is a key player that affects cancer progression and that can influence treatment success [1–3]. Research over the past decade suggested that solid tumors can frequently harbor their own microbiome [4–6]. Recent surveys revealed that two-thirds of breast and pancreatic tumors harbor intratumor bacteria and that even tumors developing in sterile body sites, such as the brain and bones, frequently harbor a microbiome [7]. Bacterial widespread presence in tumors is attributed to opportunistic colonization of the immunosuppressive microenvironment that exists after solid tumors have already formed [4,8]. Notably, very recent publications argued against some studies in the field such as those detecting bacterial DNA signature in patient blood samples [9–12] and claims of fungal microbiome involvement in pancreatic cancer [13,14]. Interest in intratumor bacteria in recent years has also surged with multiple efforts to intentionally administer to patients genetically engineered bacteria for detection and treatment of solid tumors [15,16].

While the significance of tumor microbiome promoted research in this field, it has left fundamental questions on the biological processes underlying this phenomenon underexplored. A key gap in knowledge concerns the process of tumor infection and colonization. Studies of human patients typically aim to uncover evidence of bacterial presence

in cancer tumors by inspecting tumors and healthy tissues that were removed during surgery. Common methodologies are quantitative PCR for detection of microbial DNA or microscopy imaging of tumor sections with stains or antibodies that are unique for microbial components such as the bacterial lipopolysaccharides (e.g., [17,18]). While these end-point measurements can provide extreme sensitivity for detecting microbial presence, they provide little information about the temporal dynamics of infection and colonization.

The suggested models on tumor colonization rely on the observed overlap between species composition in specific "natural" microbiome sites and the species identified in tumors in specific body sites [19,20] and suggest translocation events of bacteria between organs [21] or into the blood stream [22]. Yet little has been empirically determined in human patients beyond this association. It therefore remains unclear how bacteria initially colonize the tumor niche and how a multi-species microbiome emerges [23]. It remains unknown if multi-species colonization arises through simultaneous infections by multiple species or whether colonization follows a sequential seeding process reminiscent of gut colonization during development. Lastly, little is known about population turnover of intratumor bacteria, including the growth and death rate of colonizing bacteria and whether population bottlenecks exist in different stages of infection and colonization.

Key insights about the composition and dynamics of bacterial communities in different environments, such as the mammalian digestive tract, soil ecosystems, and aquatic environments have come from mathematical modeling. Models originally developed for macroecological communities have been adapted to describe the diversity, stability, structure, and dynamics of microbial systems [24–27]. However, many models focus on describing general phenomena rather than explaining specific empirical data. Modeling efforts that do interface with data often focus on explaining composition statistics or population dynamics, but not both in the same system. Holistic mathematical descriptions that explain both the dynamics and statistics of empirical data are lacking, particularly for collective colonization processes such as tumor infection.

Here we use an established mouse model of intratumor bacteria to explore the bacterial population dynamics in controlled experiments (Figure 1A). We introduced genetically barcoded *E. coli* cells by intravenous or intratumor injections and monitored how the bacterial load and clone diversity changed on different days post injection. We then used mathematical modeling to explore alternative modes of niche infection and bacterial growth (Figure 1B). Our modeling revealed that the experimental observations are compatible with a growth model that is constrained by a local niche load, competition for a global resource, and noise. Taken together our controlled experiments and theory provide the first dynamical model of tumor colonization and suggest that descriptive statistics may allow distinguishing genuine tumor microbiomes from contamination.

Results

Cloning the *E. coli* barcoded strain collection

We prepared a library of barcode-tagged clones using the *E. coli* Nissle 1917 strain (EcN). This commensal isolate, currently prescribed as a probiotic, is widely used for studying intratumor bacteria in mouse models [18,28–32]. We prepared the strain collection by PCR amplifying a kanamycin resistance cassette with a forward primer that included an upstream region of twenty random nucleotides and integrating the amplicon into the *lacZ* gene locus (Figure 1C). We pooled together roughly 50,000 individual colonies and grew them overnight before characterizing the barcode diversity. We extracted DNA from the culture and sequenced the barcode region in four technical replicates. We identified and enumerated the individual barcodes with the bartender software package [33] and found 39,091 unique barcodes that met our thresholds (methods). Figure 1D shows the frequency of barcodes in our library ordered by their rank and normalized to a million reads (RPM). We observed that barcodes followed a narrow frequency distribution with 99% of barcodes represented within a six-fold frequency range. This clone collection was used for the mouse experiments in our work (Figure 1E).

Even in a constant environment, clone proportions within the barcoded collection are expected to gradually change over time, despite all clones being equally fit, due to natural variability in growth and death rates in a finite population of cells. To evaluate the magnitude of this expected variability, which we term *intrinsic noise*, we inoculated the barcoded strain library into four different media types and allowed it to grow until reaching late-log phase (supplementary figure 1A). Supplementary figure 1B shows a comparison between the barcode frequencies before and after the experiment. Importantly, while we observed the expected variation in clone frequency after this simple growth experiment, we also noted that the overall distribution of clone frequencies was not altered by growth, demonstrated by the histograms in supplementary figure 1B. Mathematical analysis reveals that a Monod model (described later) with intrinsic noise captures behavior in all four growth conditions and can therefore be used as a null model for barcode variation in our barcoded strain collection.

Tumor colonization after intravenous injection

We studied bacterial tumor colonization in a syngeneic murine model previously used by others to study intratumor bacteria [18,28,29]. Figure 2A outlines our experimental approach. First, tumors were seeded by subcutaneous injection of a mouse CT-26 cancer cell line into the left and right flanks of each immunocompetent mouse (BALB/c). Tumors were allowed to form over ten days before systemic bacterial infection. To allow controlled tumor infection and colonization, the barcoded clone library was introduced by tail vein injection, and the mice were continuously monitored throughout the remainder of the experiment. Groups of five mice were euthanized after one, three, or seven days post bacterial injection. Tumors were then removed, weighed, and homogenized. Lastly, the homogenized tissue was used to determine the bacterial load, by plating on selective agar plates, and to determine clone diversity by extracting DNA and deep sequencing of the barcode region.

A summary of the bacterial load and clone diversity is shown in Figure 2B. Overall we observed that rapid changes in bacterial load and clonal frequency took place within a day of injection and seemed to stabilize for the remainder of the experiment. As the pink graph shows, we detected roughly only a hundred unique barcodes in each of the tumors resected throughout

133 the experiment (average barcode number was 52, 132, and 84, on days 1, 3 and 7,
134 respectively). When comparing the clone identity in same-mouse tumor pairs, we observed that
135 the number of overlapping barcodes was higher than that expected by random in 8 out of 13
136 mice (Fisher exact test, p-val<0.05/30). This overlap likely arises from relatively rare migration
137 of bacteria between tumors previously reported in this mouse model [34]. However, overlapping
138 barcodes frequencies in all mice but one were not correlated across tumor pairs (Spearman
139 correlation, p-val<0.05/30). Thus, tumor pairs seem to have operated as separate and
140 independent niches (supplementary table 1). We observed that the average bacteria load per
141 tumor reached ~$5*10^8$ cells within a day of injection and further increased to ~$4.7*10^9$ cells by
142 the third day, and then slightly decreased to $2.6*10^9$ cells. Taken together, our data suggested
143 that a very narrow bottleneck limits bacterial colonization of the tumor niche, yet that once
144 infection occurs, bacteria rapidly grow and almost saturate the tumor niche within a day.
145
146 We tested if colonization statistics were correlated in same-mouse tumor pairs across twelve
147 mice from the entire experiment. Figure 2C shows the relationship between the number of
148 detected barcodes. A Spearman test suggested this correlation is not statistically significant (p-
149 val = 0.22). Figure 2D shows the relationship between the number of detected barcodes and
150 the tumor carrying capacity (bacteria per gram of tumor), which were not found to be
151 correlated (Spearman test, p-val = 0.90). Lastly, Figure 2E shows the relationship between the
152 carrying capacity across tumor pairs, which were observed to be correlated (Spearman test,
153 pval = 5.38e-04). Taken together, these statistics suggest the following: bacteria infected each
154 of the tumors independently and the number of bacteria seeding the infection is independent
155 from the total bacterial load observed after colonization. However, the significant correlation in
156 tumor bacterial carrying capacity suggested this characteristic is likely determined at the host
157 level.
158
159 Finally, we evaluated the uniformity of bacterial load within each tumor by inspecting the size
160 of each successful colonizing clone. Figure 2F shows results from a representative single mouse
161 (euthanized a single day after infection). As the figure shows, we observed that clone sizes were
162 highly nonuniform with 54% of all bacteria in the right tumor originating from a single clone.
163 The second most common clone contributed 14% of the bacteria load. Similar trends were
164 observed across all tumors isolated after intravenous injections (supplementary table 2). We
165 used Shannon entropy to quantify clone diversity across all days and compare it to the entropy
166 of the injected clone library. Figure 2G shows the entropy calculated across all twenty-seven
167 tumors collected after intravenous injections. As the figure shows, all the tumors were
168 characterized by a considerably lower entropy relative to the injected library. This lower
169 entropy reflects both the overall low number of barcodes as well as their non-uniform clone
170 sizes.
171
172 In summary, measurements of bacterial load and clone diversity in tumors infected after
173 intravenous injection revealed that roughly only a hundred individual bacteria successfully
174 colonized the tumor niche, yet that they rapidly grew to reach almost load saturation within a
175 single day. The relative size of each detected clone revealed that infecting bacteria experience
176 varying degrees of colonization success, with leading clones taking up over half of the total

bacterial load. If we assume that the leading clone originated from a single cell, we can roughly estimate the bacterial growth rate within the tumor niche. If the most successful clone reaches a population size of $2.5*10^8$ within a day of injection, it divided roughly 28 times during that period (corresponding to a generation time of ~50 minutes).

Tumor colonization after intratumor injection

We studied bacterial tumor colonization in a model that allows significantly widening tumor infection bottlenecks by modifying the route of inoculation. In this model, we infected mice with an identical number of bacteria from the barcoded collection by direct injection into the tumors (Figure 3A). A summary of the bacterial load and clone diversity is shown in Figure 3B. As the pink graph shows, we detected thousands of unique barcodes in each of the tumors resected throughout the experiment (the average number of detected barcodes were 7238, 3460, and 3566, on days 1, 3, and 7, respectively). We did not detect a significant correlation in the frequency of overlapping barcodes identified in same-mouse tumor pairs (Spearman test, p-val<0.05/30). Thus, similarly to intravenous injection, tumor pairs in the intratumor injection model seem to have operated as separate and independent niches (supplementary table 1). Calculation of bacterial load showed a trend similar to that observed after intravenous injection. We observed that the average bacteria load per tumor reached ~$1.4*10^9$ cells within a day of injection and further increased to $4.7*10^9$ cells by the third day and then slightly decreased to $1.9*10^9$ cells. A clear difference seen in the two infection models was in the number of detected barcodes. After intratumor injection, we detected almost two orders of magnitude more barcodes than we detected after intravenous injection.

We tested if colonization statistics were correlated in same-mouse tumor pairs across fifteen mice from the entire experiment. Figure 3C shows the relationship between the number of detected barcodes. A Spearman test suggested this correlation is not statistically significant (p-val = 0.7). Figure 3D shows the relationship between the number of detected barcodes and the tumor carrying capacity (bacteria per gram of tumor), which were not found to be correlated (Spearman test, p-val = 0.54). Taken together, these statistics suggested that the identity of clones that successfully colonized the tumors was independent across same mouse tumor pairs and that the number of successful colonizing clones was independent from the total bacterial load. These trends are similar to those observed in the intravenous injection model.

Finally, we evaluated the uniformity of bacterial load within each tumor by inspecting the size of each successful colonizing clone. Figure 3E shows results from a representative single mouse (euthanized after a single day). As the figure shows, we observed that clone sizes were highly nonuniform with 6.3% of all bacteria in the left tumor originating from a single clone. The second most common clone contributed 2.2% of the bacteria load. Similar trends were observed across all tumors isolated after intratumor injections (supplementary table 2). Calculation of Shannon entropy to quantify clone diversity across all days showed considerable entropy decrease relative to the injected clone library (Figure 3F). To better evaluate the variability in clone representation we decided to inspect the relative proportion of successfully colonizing clones in each tumor. Figure 3G shows the proportion of each clone within each tumor relative to its rank presented on a logarithmic scale. Surprisingly, this analysis uncovered

a linear relationship, with a slope of -1, between the logarithm of the clone rank and the logarithm of its proportion across the entire rank range. Moreover, this quantitative relationship held across all tumors and all days of the experiment. This relationship revealed that clone sizes followed a characteristic power-law distribution termed Zipf's law [35].

In summary, measurement of tumors infected by direct intratumor injections revealed shared trends across all days and mice: overall a high number of unique barcodes, attributed to significantly widening the infection bottleneck, and highly nonuniform representation across colonizing clones. The lack of uniformity allows ruling out the infection route as the cause for high variability in clone proportions, e.g., due to variable time of arrival to the niche. This observation suggests growth dynamics within the tumor likely underlie the high variability in clone proportions. Lastly, an inspection of the distribution in clone proportion uncovered they follow a specific power law distribution matching Zipf's law. This surprising trend was evident across tumor samples collected throughout the experiment.

Theoretical framework for tumor colonization

To quantitatively understand the growth dynamics and the emergence of Zipf's law, we developed a theory of bacterial colonization and growth in the tumor. We started with a simple model that accounts for nutrient-limited growth and environmental noise. Motivated by the experimental observations, we improved our model by adding local growth limitation and an infection bottleneck. Lastly, we tested if the model can quantitatively match the experimental observations.

Stochastic consumer-resource model of tumor colonization

We began with a consumer-resource model [24–27] that encompasses competition for nutrients and environmental stochasticity:

$$\frac{dN_i}{dt} = \frac{gs}{s+k} N_i + \sigma \eta_i N_i, \tag{1}$$

$$\frac{ds}{dt} = -\gamma \sum_{i=1}^{B} \frac{gs}{s+k} N_i + D(s_0 - s), \tag{2}$$

In Equations (Eq.) (1) and (2), N_i represents the abundance of barcode i, and s is the concentration of a shared resource within the tumor microenvironment. For simplicity we assumed that growth is limited by a single resource. The growth rate of each clone in Eq. (1) depends on s via a Monod function [36], where g is the maximum growth rate and k is the half-saturation constant. In turn, growth depletes the resource in Eq. (2), where γ is the inverse yield coefficient and B is the number of surviving barcodes. The resource is replenished (e.g., via passive diffusion into the tumor microenvironment) at a rate D from the rest of the surrounding healthy tissue with background concentration s_0. Since all barcodes are genetically identical, we assumed that they share the same resource preferences and have the same fitness. Thus, model parameters are the same for all barcodes. Nevertheless, the individual growth rates of each barcode differ because of the noise term, described next.

The environmental stochasticity is modeled in Eq. (1) as multiplicative noise with strength σ, where η_i is a barcode-specific white Gaussian noise term with zero mean and unit standard deviation. The noise term signifies environmental effects that are not explicitly modeled, such as fluctuations in access to resources, effects from the mouse's immune system, and other biotic and abiotic factors. Such multiplicative noise is typical in microbial ecology models [37], as opposed to demographic noise which has a different functional form and is due to the intrinsic dynamics of the system [38], or additive noise which accounts for fluctuations in the immigration rates of species [39].

Numerical simulation of Eqs. (1) and (2) is shown in Figure 4A, as a frequency-vs-rank plot (like Figure 3G) at various times. Our simulations showed that the statistics do not converge to Zipf's law, and most barcodes eventually become extinct, i.e., the maximum rank continues to decrease over time. The reason for these dynamics is that several barcodes, selected at random due to the noise, come to dominate the system, leaving an insufficient amount of resource for the rest. We conclude that the model in Eqs. (1) and (2) cannot capture the experimental phenomena.

Incorporating local growth limitation

To prevent fast-growing clones from dominating the system, we modified the Monod function to make the half-maximal constant proportional to the clone abundance (k becomes kN_i):

$$\frac{dN_i}{dt} = \frac{gs}{s + kN_i} N_i + \sigma \eta_i N_i, \tag{3}$$

$$\frac{ds}{dt} = -\gamma \sum_{i=1}^{B} \frac{gs}{s + kN_i} N_i + D(s_0 - s), \tag{4}$$

This modification is widely used and was first deduced from empirical observations of bacterial growth shortly after Monod's work, by Contois [40]. Conceptually, this modification means that a larger population will grow at a smaller rate, e.g., due to crowding or any other effect that limit cells' access to nutrients within a larger population. Within our model, this modification assumes that a clone's growth is limited by its own abundance and not that of other clones. This assumption only makes sense if each clone exists in its own niche, e.g., if clones are spatially segregated. We give experimental evidence for this assumption in the next section when we model the infection bottleneck.

Numerical simulation of Eqs. (3) and (4) is shown in Figure 4B (purple; see Methods for theoretical analysis, blue). We see that this model exhibits Zipf's law, consistent with the experimental data (Figure 3G). This result demonstrates that the small modification to the Monod function in Eqs. (3) and (4) has significant implications to population stability and extinction prevention in the presence of stochasticity, which we expand upon further in the Discussion. Further incorporating the infection bottleneck into the model (see next section)

does not change the presence of Zipf's law, even as it decreases the number of surviving barcodes (Figure 4C).

Next, we asked whether the model can capture the experimentally observed dynamics of the total CFU count and the number of surviving barcodes (Figs. 2B and 3B). Figure 4D-E shows the dynamics of our model for example parameter values. We see that, in general, the total CFU count increases then saturates while the number of surviving barcodes decreases then saturates, consistent with the experiments.

More specifically, we investigated the effects of the model parameters on the dynamics. We see in Figure 4D that the final total CFU count, but not the final barcode number, is primarily determined by the ratio s_0/γ. This makes sense because the background nutrient concentration s_0, converted to cells via the yield coefficient γ, ultimately determines the total number of cells that can be sustained. We see in Figure 4E that the probability that cells go extinct (as well as the amount of fluctuations) is primarily determined by the noise strength σ. This makes sense because the noise term, when negative, represents an effective cell death in our model. Specifically, when it overpowers the growth term ($\sigma \gg \sqrt{g}$; in Figure 4E $g = 2\ hr^{-1}$), total extinction is very likely. Finally, we see in Figure 4F that the final number of surviving barcodes (and to some degree the final total CFU count) is primarily determined by the bottleneck size. This makes sense because, as we describe next, shrinking the bottleneck reduces the probability that any cell survives the inoculation process, and barcodes with no surviving cells post-inoculation are not present at later times. Because this is a continuum model, we choose an arbitrary threshold for barcode extinction (set to $N_i < 1$ in Figure 4). We later relax this condition in Figure 5, as barcode extinction only occurs immediately after injection when the number of cells per barcode is small. Consequently, the inferred bottleneck values from the experiments account for all initial extinction sources.

Theory of infection bottleneck

We modeled the bottleneck as a survival probability, q, for individual cells. Upon injection, each cell either establishes in the tumor and remains viable (survives) with probability q, or it does not (dies) with probability $1 - q$. This formulation allows us to describe both the intravenous and intratumor experiments with a single parameter, and we expect direct injection into the tumor to correspond to a value of q that is significantly higher than that for intravenous injection.

We infer the value of q directly from the experimental data by predicting the probability of observing a particular barcode in the tumor as a function of its frequency in the inoculum (see Methods). The comparison of this prediction with the data is shown in Figs. 5A and B. To test this prediction over the whole range of possible inoculum frequencies from 0 to 1, we aggregated multiple barcodes at random to achieve higher frequencies in the inoculum and higher probability of observation in the tumor (Figs. 5A and B). We see that the agreement between theory and experiment is excellent over the full range of frequencies. Moreover, the q values are 2.6×10^{-3} and 5.0×10^{-5} for the intratumor and intravenous injections,

respectively, quantitatively confirming our expectation that direct injection into the tumor significantly widens the bottleneck, in this case by about two orders of magnitude.

The value $q = 2.6 \times 10^{-3}$ allows us to estimate the founding size of barcodes in the intratumor experiments. An inoculum of 5 million cells across roughly 40,000 barcodes (Figure 3B) corresponds to an average of about 100 cells per barcode. A survival probability of $q = 2.6 \times 10^{-3}$ per cell means that the chance of a 100-member barcode having 0, 1, or 2 cells post-inoculation is 77%, 20%, or 2.6%, respectively (see Methods). This means that most barcodes go extinct immediately (77%), and the vast majority of the surviving barcodes are founded from a single cell. Because bacterial progeny founded by a single cell are likely to stay proximal within the solid tumor, single-cell founding is consistent with barcodes remaining spatially segregated as they grow. This spatial segregation justifies the heterogeneous resource access among barcodes assumed in the dynamical model above.

Direct comparison of dynamics and statistics with experiment

Combining the bottleneck model with Eqs. (3) and (4), we compared our predictions for the dynamics and statistics directly with the experimental data (see Methods for simulation details). Figures 5C and D show comparisons of the dynamics with the data for the intratumor and intravenous cases, respectively (note in the simulations the immediate drop of both the total CFUs and the barcode number due to the bottleneck, followed by the recovery of the CFUs). Here we have used the q values inferred above, set $\sigma = \sqrt{g}$, and used plausible values for the maximal growth rate $g = 2\ \mathrm{hr}^{-1}$ and molecular diffusion timescale $D = 1\ \mathrm{s}^{-1}$. The final parameter values are set by recognizing that the maximum total CFU number in our model is roughly $N \sim B s_0/k$, so knowing N/B from experiments allows us to set s_0/k. Specifically, we set $s_0/\gamma = 5 \times 10^4$ and use $k/\gamma = 1$ and 0.01 for the intratumor and intravenous cases, respectively. We see in Figures 5C and D that the dynamics of the model agree very well with the experimental data.

Finally, we used the model to calculate the expected barcode frequencies in the intratumor and intravenous cases. Figure 5E show the barcode frequences plotted as a function of barcode rank according to our model and as observed in experiments (similarly to Figure 3G). The top panels show the plots we generated by the models (using only the q value determined from each of the mouse tumors; see Methods). The bottom panels show the corresponding plots from resected tumors. This comparison shows that simulations for both the intratumor and intravenous cases agree very well with the experimental statistics. Moreover, we observed that while the statistics of the intratumor case follow Zipf's law, the statistics of intravenous case do not, matching the experimental observations.

Discussion

Studies of intratumor bacteria are primarily driven by research of the tumor-microbiome found in many types of cancers [4–6] and by research of genetically modified bacteria that are introduced to the tumor microenvironment [15,16]. Yet, despite wide interest in intra-tumor bacteria, basic questions about this phenomenon remain underexplored. Specifically, the population dynamics governing tumor infection and colonization remain largely uncharted. We

addressed some of these questions using a murine tumor model allowing intravenous and intratumor infections of non-pathogenic bacteria. Our controlled experiments revealed that bottlenecks dominate infection and are followed by rapid, yet highly nonuniform growth (Figures 2B, 2F, 3B and 3E). Surprisingly, we revealed that intratumor injections repeatedly gave rise to bacterial progenies that are characterized by a scale-free distribution that match Zipf's law (Figure 4E). Our theoretical work then proceeded to explore growth models that can explain the experimental observations.

Our work reveals how the fundamental criteria required for Zipf's law [41] can emerge in microbial population dynamics, as illustrated in Figure 6A. First, Zipf's law requires the lack of a dynamic attractor (equivalently, a potential minimum), because an attractor would introduce a characteristic scale, yet Zipf's law is scale-free. In our model, no strong attractor exists because the environment is assumed to be very noisy: fluctuations outweigh any deterministic contribution to cell death, which would otherwise balance cell growth to create a characteristic scale for each barcode's population size. Second, Zipf's law requires biased fluctuations, such that lower values of a quantity (here, clone size) are more probable than higher values. In our model, biased fluctuations are provided by multiplicative noise; in fact, the specific choice of multiplicative noise is responsible for the scaling of frequency with inverse rank as opposed to some other power (see Methods). It is important to note that the multiplicative noise that scales linearly with the population size, and that we found is required for Zipf's law, is incompatible with neutral theories of ecology [42] . In neutral theories, the primary driver is intrinsic stochasticity [42,43] , which has a sublinear scaling with population size[38]. Therefore, neutral theories of ecology cannot explain the scaling of Zipf's law that we observe here. Last, Zipf's law requires a mechanism to prevent extinction. In our model, this mechanism is provided by local growth limitation (the dependence of growth rate on clone size in Eqs. (3) and (4)), which prevents the largest clones from consuming all the resources and driving all smaller clones to extinction. Together, as illustrated in Figure 6A, these criteria result in a probability distribution whose tail follows a power law with power -2, (equivalent to a rank-frequency plot with power -1). Figure 6B shows the bacterial population dynamics expected under our infection and colonization model. As the simulation demonstrates, our model predicts that dominant clones will fluctuate over time. Moreover, we expect that at each point in time, most bacteria will belong to only a handful of transient dominant clones.

Zipf's law is also known to arise from mechanisms other than the three criteria above. Mutations can give rise to subpopulations whose sizes can be distributed according to Zipf's law, as in the classic Luria-Delbruck process [44] or within spatially expanding populations [45]. The clonal dynamics of the adaptive immune system can also be described by geometric Brownian motion, a limit of which is Zipf's law [45]. These systems are distinct from ours in that new populations arise at various points in time or space due to mutations or immigration from a repertoire, whereas in our system no new barcodes emerge. More broadly, Zipf's law has been argued to arise in many systems as a sign of criticality [46,47] or due to the presence of unobserved variables [48]. It is an interesting open question whether these broader explanations for Zipf's law are applicable to microbial populations dynamics.

The work presented here relies on a well-established yet simple animal model of infected tumors [18,28–32]. However, the combined experimental and theoretical framework we developed can serve as the basis for two important future research directions. The first direction is continued exploration of principles underlying tumor colonization. This line of work will use highly-controlled experiments to systematically map and disentangle how discrete parameters of tumor and bacterial biology impact the tumor-microbiome. These experiments can include more complex animal models, such as orthotopic implantations or genetically engineered mouse models, which better reflect the native tumor environment, and even patient-derived xenografts that more closely mimic human tumor heterogeneity. These host models can reveal if bacterial population dynamics are altered by the tumor conditions. Additional experiments can be designed to explore key parameters of the colonizers and can include multiple infection waves, multi-species colonization, and different selection pressures, such as those imposed by antibiotics.

The second direction to which our work contributes is the ongoing discussion in the field about the origin of bacteria in tumor samples. While recent publications argued against a few studies in the field [9–14], a broader concern is whether evidence of intra-tumor bacteria arises from PCR amplification of bacterial contaminants, as was previously determined for placenta and brain tissues. Our work suggests that descriptive statistics of bacterial populations can provide strong evidence for a genuine tumor-microbiome. Specifically, if frequencies of same-species clones across a tumor follow Zipf's law, they very likely arose from the unique growth dynamics characteristic to the tumor microenvironment. While our approach relied on genetic barcodes, alternative terminal assays can also be performed on resected tumor tissues. Specifically, if human tumors are initially seeded by a low number of bacteria, as we observed in our mouse models, and clones arise from spatially separated single cells, spatial bacterial signal should follow similar statistics. Therefore, species-specific bacterial staining of tumors sections [49] may allow distinguishing genuine tumor microbiomes from contamination.

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Methods

Bacteria and growth conditions

E. coli Nissle 1917 strain (Ardeypharm, GmBH, Germany) was used for cloning the barcoded strain collection. For all *in vivo* experiments, bacteria were inoculated into Lysogeny Broth (LB) containing 50 µg/mL kanamycin and grown overnight at 37°C, 200 rpm orbital shaking. In the *in vitro* experiment in was performed in four different media types that were supplemented with 50 µg/mL kanamycin. We used LB for nutrient-rich experiments and M9 for nutrient-poor

476 experiments (M9 minimal media with 0.2% amicase). Nutrient poor media was supplemented
477 with one of these carbon sources: 0.4% glucose, 0.4% glycerol or 0.4% acetate.
478
479 **Cloning the barcoded library**
480 Kanamycin resistance cassette with 20 random nucleotide barcodes, targeting *lacZ* locus of *E.*
481 *coli* Nissle 1917 genome, was amplified using the following forward and reverse primers:
482 5'GTTGTGTGAAATTATGAGCGGATAACAATTTCACACAGGATACAGCTATTCCGGGGATCCGTCGACC3'
483 and 5'ACGGGCAGACATAGCCTGCCCGGTTATTATTATTTTTGACACCAGACCAANNNNNNNNNNNNN
484 NNNNNNNTGTAGGCTGGAGCTGCTTCG 3'. We used the genomic DNA of a knockout strain from
485 KEIO collection as a template amplifying the kanamycin resistance cassette [50]. The PCR product
486 was purified from an agarose gel. Competent cells with induction of beta, gam, and exo genes
487 from pSIM6 plasmid [51] were prepared from a single transformant as described previously [52]. We
488 transformed 2.5 ug of the PCR product to aliquots of competent cell and plated them on
489 selective media agar plates. We collected roughly 50,000 single colonies from multiple plates
490 after overnight incubation at 37°C. The colonies were scraped from the agar plates and
491 homogenized in PBS before freezing the collection by adding 40% glycerol (1:1 v/v) and storing
492 it at -80°C. To cure the pSIM6 plasmid, the pooled library was inoculated and grown for three
493 days in liquid LB containing kanamycin, passaging daily (1:2000 dilution). The final library was
494 stored as glycerol stock (20% glycerol v/v) at -80°C.
495
496 **Barcoded library injection**
497 We thawed 100 µL of the barcoded library glycerol stock and resuspended it in 20 mL of LB
498 supplemented with kanamycin and grew the culture overnight. On the next morning we diluted
499 the culture 1:100 into 30 mL of LB supplemented with kanamycin and grew the culture until
500 reaching OD_{600} of 0.5. We pelleted and washed the bacteria with PBS three times. Washed
501 bacteria were incubated at room temperature for an hour, and the OD_{600} was measured.
502 Considering OD_{600} of 1 culture contains 4.71×10^8 CFU/mL. For i.v. injections, we prepared 5×10^7
503 CFU/mL. For i.t. condition, we prepared 2.5×10^8 CFU/mL. Four technical replicates of timepoint
504 zero samples were frozen as glycerol stock, and gDNA was isolated directly from these stocks.
505
506 **Mouse experiments**
507 30 five-week-old female, BALB/cJ mice (Jackson Laboratory, Bar Harbor, Maine) were allowed
508 to acclimate in the animal facility for seven days. To form subcutaneous tumors, all mice were
509 injected with 1×10^6 CT-26 cells on both flanks subcutaneously and tumor growth was
510 monitored every 2-4 days. When tumors reached a volume of 300-500 mm^3, mice were injected
511 with barcoded bacteria in two groups (15/14 mice each group). Mice in the *i.t.* group were
512 injected with 5×10^6 CFU per tumor and mice in the *i.v.* group were injected with 10^7 CFU per
513 mouse by tail vein injection. Mice were then euthanized according to experimental endpoints
514 on days 1, 3 or 7 after bacterial injection and tumors were flash-frozen and kept at -80°C for

515 later analysis. Exceptions to tumor development: One mouse in the *i.v.* group (day 1) did not
516 develop tumor on the left flank and had a single tumor. One mouse, to be assigned to *i.v.* (day
517 7), did not develop any tumors and was excluded from the study.
518
519 **Determining bacterial CFU in tumors**
520 Tumors removed from euthanized mice we were finely cut with a sterile scalpel and 200 mg of
521 processed tumor was added to lyzing matrix I tubes (Cat# 6918100, MP Biomedicals) filled with
522 300 µL PBS. Tumor samples were homogenized twice at a speed of 6m/s for 40 seconds using
523 MP Biomedicals Fastprep-24 instrument. 20 µL of the homogenate was used to make serial
524 dilutions of 1:1000, 1:10000 and 1:100000 in 200 µL of PBS. 100µL of these serial dilutions were
525 plated on selective LB plates containing kanamycin. Plates were incubated overnight and next
526 day colonies were counted. We determined the CFU by counting colonies on dilution plates
527 that had 100-500 colonies. The weights of homogenized samples and the total tumor weights
528 were used to calculate the CFU per gr of tumor, and the total CFU per tumor. For some tumor
529 samples we repeated the CFU counting once again after freezing the homogenized tumor. In
530 these cases, we used the average CFU numbers from frozen and fresh tumors for downstream
531 analysis.
532
533 **Sequencing Library Preparation**
534 We purified DNA from the homogenized frozen tumor samples using Zymo Quick-DNA
535 Midiprep plus kit (Cat# 4075) and determined the DNA concentration using Qubit High
536 Sensitivity DNA reagent (Thermo-fisher, Cat#Q32854). Since the total gDNA contains high
537 amount of mouse DNA relative to the bacterial DNA, we used 10 µg of DNA as a template for
538 each PCR. A region of ~400 bp around the barcoded region was amplified using 2x KAPA HiFi
539 HotStart Ready Mix (Kapa Biosystems, Cat#KK2602) and the following forward and reverse
540 primers: 5' TCGTCGGCAGCGTCAGATGTGTATAAGA GACAG(1-3N)cctgcccggttattattattttg 3' and
541 '5 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGgattcatcgactgtggcc 3'. We set 4-7 PCR
542 reactions were per tumor sample depending on the amount of DNA extracted from the tumor
543 tissue. We pooled together 10 µL of each of these technical replicate PCR and run the mixture
544 on a 3% agarose gel. We then purified amplicon from the gel and determined the DNA
545 concentration using Qubit high-sensitivity DNA reagent. A second 13 cycle PCR was performed
546 using Illumina Nextera XT indexes and 2x KAPA HiFi HotStart ReadyMix for multiplexing. The
547 products were run on 3% agarose gel and purified again. Libraries were normalized to the same
548 concentration, denatured, and diluted according to Illumina NextSeq System Denature and
549 Dilute Libraries Guide. Sequencing was performed using Nextseq 500/550 High Output Reagent
550 Kit, 75-cycles on Illumina NextSeq 500 device. We sequenced each tumor sample as two
551 technical replicates to validate that our library preparation procedure did not introduce any
552 bottlenecks in barcode amplification before deep amplicon sequencing.

553
554 **Targeted Barcode Sequencing Analysis**
555 We used Bartender[33] to extract and cluster the barcodes from raw fastq files. We first ran
556 bartender extractor (bartender_extractor_com) with the following parameters: Average base
557 quality score cutoff of 30 and allowing no mismatch on upstream and downstream anchor
558 sequences: "-q ? -p ACCAA[20]TGTAG -m 0". Next, we ran Bartender Clustering
559 (bartender_single_com) with the following parameters "-d 2 -z 10 -l 5 -t 1 -s 1". A matlab script
560 was used to further organize the barcode clusters. First, we generated a master list of barcodes
561 that was based on the four technical T0 samples. This master barcode list defined identify and
562 the total number of barcodes present in the collection. The list of T0 barcodes was used to filter
563 out any new barcodes that were observed only in mouse tumors (the vast majority of excluded
564 barcodes originate from errors in DNA replication, PCR, and next next-generation sequencing).
565 For a barcode to appear in the master barcode list, it had to be present in two out of four T0
566 replicates with a normalized frequency above 10 RPM (39,091 barcodes in total). Since each
567 tumor sample was processed and sequenced as two technical replicates, an average RPM value
568 was calculated.
569
570 ***In vitro* growth experiments**
571 We thawed 15 µL of the barcoded library glycerol stock and added it to 6mL each of four media
572 types used. We grew cultures overnight at 37°C in a 200 rpm shaker. Next day, OD_{600} of the
573 cultures was measured and each culture was diluted to OD_{600} of 0.5 before further diluting
574 them 1:200 into 80 mL of their respective media type. Each culture condition was plated into
575 three 96-well plates for growth (each 96-well plate was considered a technical replicate at this
576 point). Cultures were incubated on a benchtop incubator at 37°C at 750 rpm shaking. We
577 simultaneously monitored the growth of identical cultures grown in a single 96-well plate with a
578 plate absorbance reader growing in similar conditions (Biotek/Eon). We collected samples from
579 all technical replicates of a specific growth conditions when absorbance reached ~0.4 in the
580 plate reader. Cultures each of the 96-well plate were pooled together and centrifuged at 4°C to
581 pellet the cells. Genomic DNA was isolated from the cell pellets using Zymo Bacterial/Fungal
582 DNA extraction kit. Extracted gDNAs were normalized to 40 ng/µL and total of 500 ng input was
583 used for the NGS library preparation. Similar library preparation and sequencing approach as
584 previously described for mouse tumor samples was followed, however since these were pure
585 bacteria cultures only single reaction per sample was set-up. Sequencing data was analyzed
586 using the same parameters as the mouse experiments.
587
588 **Theoretical derivation of Zipf's law from the stochastic model**
589 To find the statistics from the stochastic model in Eqs. (3) and (4), we first utilize the fact that
590 the statistics are measured after growth has significantly slowed down. At this point, $kN_i \gg s$,
591 and Eqs. (3) and (4) simplify to
592
$$\frac{dN_i}{dt} = \frac{gs}{k} + \sigma\eta_i N_i, \tag{5}$$

$$\frac{ds}{dt} = -\gamma B \frac{gs}{k} + D(s_0 - s), \tag{6}$$

where $\sum_{i=1}^{B} 1 = B$. Eq. (6) is solved at steady state and substituted into Eq. (5) to give

$$\frac{dN}{dt} = \frac{gDs_0}{Dk+Bg\gamma} + \sigma\eta N. \tag{7}$$

The index (i) is dropped since the dynamics of all barcodes is equivalent. Now, we are left with a simple one-dimensional Langevin equation with a constant force term and a noise term. Eq. (7) is simply solved using a Fokker-Planck equation, $\partial p(n,t)/\,\partial t = -\partial/\partial n[\mu(n,t)p(n,t)] + \partial^2/\,\partial n^2[\sigma(n,t)p(n,t)]$, where $\mu(n,t) = g/k\big(Dks_0/(Dk+Bg\gamma)\big)$, and $\sigma(n,t) = \sigma^2 n^2/2$. Therefore, the dynamics of $p(n,t)$ is given by

$$\frac{p(n,t)}{\partial t} = -\frac{gDs_0}{Dk+Bg\gamma}\frac{\partial p(n,t)}{\partial n} + \frac{\sigma^2}{2}\frac{\partial^2}{\partial n^2}[n^2 p(n,t)] \tag{8}$$

Solving Eq. (8) at equilibrium gives

$$\mathrm{p(n)} = \frac{n_*}{n^2} e^{-n_*/n}, \tag{9}$$

where $n_* = 2gDs_0/(Dk+Bg\gamma)\sigma^2$. Then, we integrate Eq. (9) to find the cumulant to the cumulative distribution

$$c(n) = \int_n^\infty p(x)dx,$$

$$c(n) = 1 - e^{-n_*/n}. \tag{10}$$

The cumulant, $c(n)$, is inversely proportional to the rank, r. This can be seen by considering the effect of different abundances, n, on $c(n)$ and r. As n increases, $c(n)$ decreases and a barcode with $N_i = n$ is assigned a smaller r. The proportionality relation is $c(n) = \mathrm{r/B}$. The frequency-abundance relation is straightforwardly given by $f = n/N$, where $N = \sum_{i=1}^{B} N_i$. Consequently, the stochastic model gives the rank-frequency relation

$$f = \frac{-n_*}{N\, ln(1 - r/B)}. \tag{11}$$

For high abundances, Eq. (11), to leading order, becomes $f \sim \mathrm{r}^{-1}$ (Zipf's law). Equation (11) predicts that Zipf's law is lost at lower abundances (large r) and for populations with fewer surviving barcodes (small B). This is consistent with intravenous injection not satisfying Zipf's law, where the number of surviving barcodes is much smaller than intratumor injection.

Bottleneck model

A bottleneck is modeled as a survival probability, q, for individual cells. $q = 0$ represents the full extinction of all barcodes before reaching the tumor, while $q = 1$ means that all cells successfully reach the tumor. In other words, each cell is a Bernoulli trial with probability of success, q. Thus, the probability of x cells successfully reaching the tumor for a barcode of N_i cells and inoculum frequency f_i is given by the binomial distribution $g(x) = \binom{N_i}{x} q^x (1 - q)^{N_i - x}$, substituting $N_i = Nf_i$, the distribution becomes

$$g(x) = \binom{Nf_i}{x} q^x (1-q)^{Nf_i - x}. \tag{12}$$

Note that with $Nf_i = 100$ and $q = 2.6 \times 10^{-3}$, we obtain $g(0) = 77\%$, $g(1) = 20\%$, and $g(2) = 2.6\%$, as stated in the main text. The probability of observing a barcode in the tumor is the probability that any number of cells of this barcode survive. Hence, $g_{obs}(f) = 1 - g(0) =$

$1-(1-q)^{Nf_i}$. We calculate the predicted mean of surviving barcodes from theory as a function of q and f_i

$$\bar{B} = \sum_{i}^{B} 1-(1-q)^{Nf_i}, \tag{13}$$

where f_i is the inoculum frequency of barcode i, and f_i and $\bar{B}$ are both known from data. q is straightforwardly found numerically for intratumor and intravenous injections by plotting both sides of Eq. (13) and finding the q value at the intersection of both curves. The inferred q value is likely an underestimation because it encompasses additional effects from the dynamics beyond the initial bottleneck, such as barcode death due to stochasticity in the tumor environment.

Simulation

To determine the appropriate bottleneck size, q, for capturing the correct range of surviving barcodes, *B*, in the experiment, we simulated the dynamics using several q values that give different *B* values by day 1. Then, we fitted the q and the resulting B values to a power law of the form $B = aq^b$. Using the fitted function, we invert the relation to infer the appropriate q values from the experimental *B* values. The same inference procedure was applied to intratumor and intravenous injections, separately.

After determining the appropriate q values for intratumor and intravenous injections as explained in the paper, these values are used to simulate intratumor and intravenous injections. First, barcode sizes are initialized using the inoculum dataset used in the experiments to ensure similar initial conditions between theory and experiment. Then, the bottleneck is applied to the inoculum data using Eq. (12). Right after injection, the population goes through a significant decrease in population size as well as in the number of surviving barcodes. This gives the initial population that successfully reaches the tumor. Afterwards, we use Eqs. (3) and (4) to simulate the dynamics. We discretize Eqs. (3) and (4) using Euler's method. We repeat the same procedure for different days for intratumor and intravenous, such that we have a simulation curve corresponding to each experimental curve with the same final B and a unique q for this specific day and injection method. This provides a direct comparison between theory and experimental curves across days and conditions (Figure 5E).

In all simulations, the noise term, η, is modeled as a delta-correlated noise with a mean of 0 and a standard deviation of 1. Except for q and k, all parameters are kept the same for intratumor and intravenous simulations. k is set to 1 and 0.01 for intratumor and intravenous simulations, respectively, to reflect the ecological niche of each barcode. k is smaller for intravenous which allows for a larger ecological niche per barcode, resulting from having fewer surviving barcodes compared to intratumor. Other parameters are set to $g = 2\ hr^{-1}$, $D = 1\ s^{-1} = 3600\ hr^{-1}$, $\sigma = \sqrt{g}$, and $s_0/\gamma = 50000$ which is set to match the final total population CFU.

Ethics statement

All of the mouse experiments in this manuscript have been approved by University of Massachusetts Chan Medical School, Institutional Animal Care and Use Committee (IACUC) with the protocol number PROTO202100199.

Data and code availability:

Barcode Sequencing data have been deposited in NCBI SRA under bioproject IDs PRJNA1136987 and PRJNA1136830. All of the custom scripts developed for the bioinformatics analysis in this paper have been deposited to github (Private Repository, Request Access).

Supplement

Figure S1: Variation in barcode frequency after in-vitro growth follows the Monod model with intrinsic noise.

Table S1: Statistics about common barcodes found between right and left tumor of individual mice

Table S2: Barcode data including list of barcode sequences and frequency (RPM) found in inoculum and mouse tumors, Metadata including the mice in the experiment, experimental conditions, tumor weight at termination points, number of barcodes found in each tumor, CFU/gr tumor and CFU in total tumor

In-vitro limit

In the in-vitro experiment, the population was not subject to an initial bottleneck. Therefore, local niches do not form, and different barcode populations remain well-mixed. In this case, the growth function becomes the Monod growth function. Another important distinction between tumor and in-vitro growth dynamics is the source of noise in each. In the tumor, external noise is the dominant form, whereas in the in-vitro experiment, intrinsic noise—due to the randomness in the division time of individual cells—dominates. The final in-vitro model is given by

$$\frac{dN_i}{dt} = \frac{gs}{s+k} N_i + \eta_i \sqrt{\frac{gs}{s+k} N_i}, \tag{14}$$

$$\frac{ds}{dt} = -\gamma \sum_{i=1}^{B} \frac{gs}{s+k} N_i + D(s_0 - s). \tag{15}$$

Comparison between simulations of Eqs. (14) and (15) and in-vitro experimental results is illustrated in Figure S1.

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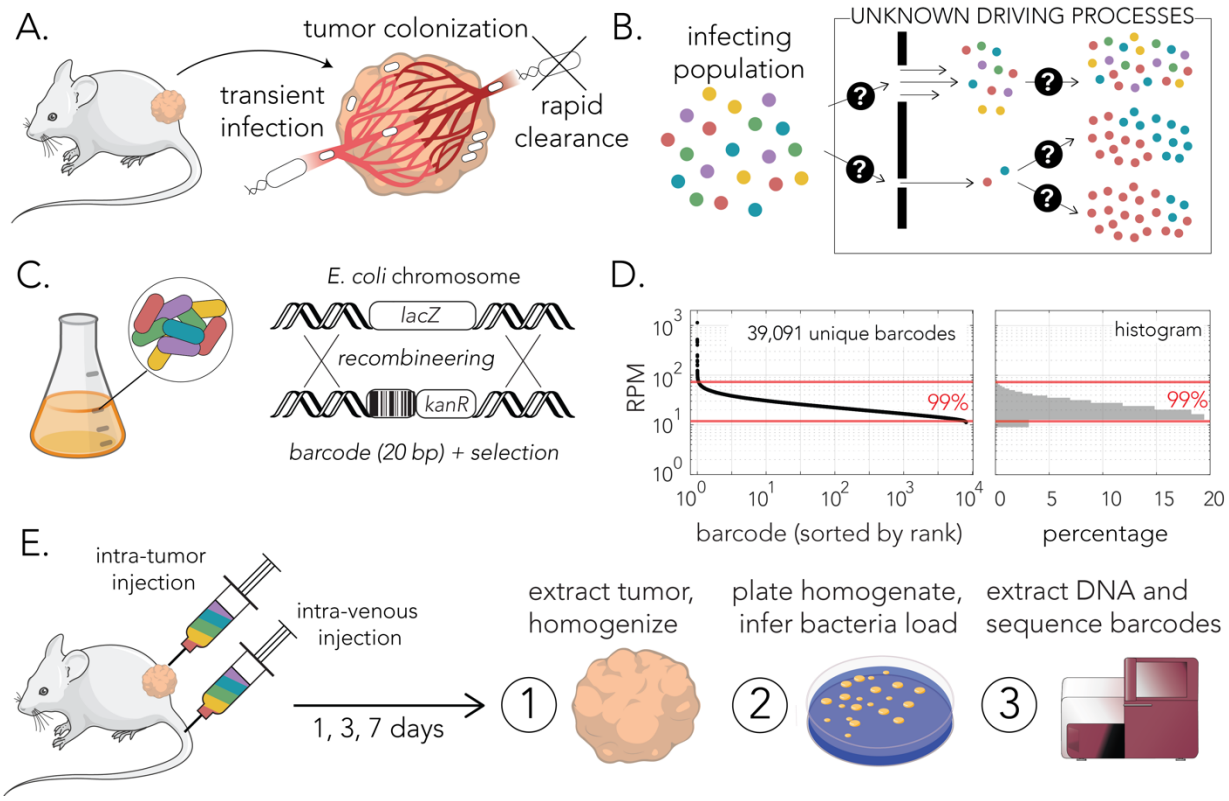

Figure 1 Monitoring bacterial population dynamics in a syngeneic mouse tumor model. **(A)** Infection and colonization of subcutaneous murine tumors in immunocompetent mice is achieved by transient systemic infection. Bacteria reaching the tumor niche can proliferate and persist due to limited access of the immune system. **(B)** Alternative modes of bacterial infection and growth in the tumor niche can be evident by clone diversity in resected tumors. **(C)** The design of the barcoded *E. coli* clone collection. A kanamycin resistance cassette with an upstream barcode region was integrated into the *lacZ* gene locus. **(D)** Distribution of barcode frequencies used for mouse experiments. **(E)** Outline of experimental approach. The clone collection was introduced by intravenous or intratumor injection (each mouse had two subcutaneous tumors). Mice were euthanized and tumors were resected after 1, 3 or 7 days after infection. Tumor homogenates were used calculate bacterial load and to extract DNA deep sequencing of barcode region.

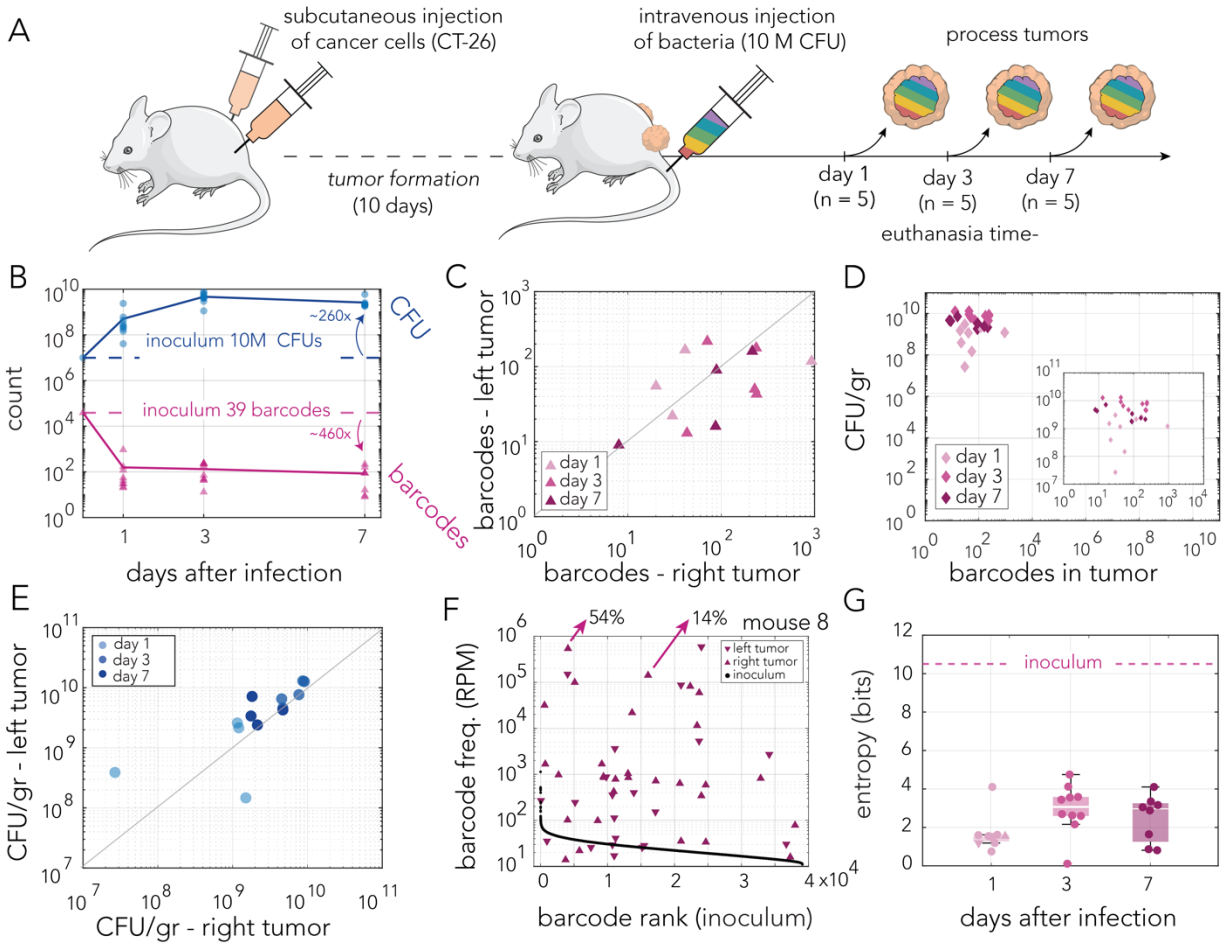

Figure 2 Tumor colonization after intravenous injection. (A) Outline of experimental approach. Subcutaneous tumors were formed on the right and left flanks. After tumor formation, mice were infected intravenously by injection of ten million CFUs. Groups of five mice were euthanized on days 1,3 and 7 post infection. Resected tumors were processed to determine bacteria load and clone diversity. **(B)** Bacterial load and number of detected barcodes are shown in blue and pink color, respectively. The bacteria number of clones in the inoculum are show for comparison (dashed lines). **(C)** Scatter plot showing the number of barcodes detected in tumor pairs resected from individual mice (p=0.22, Spearman's Rank Correlation). **(D)** Scatter plot showing the number of detected unique barcodes from the tumors and the carrying capacity (CFU/gr tumor). Inset shows the same data with a narrower axis range (p=0.90, Spearman's Rank correlation). **(E)** Scatter plot showing the carrying capacity (CFU/gr tumor) in tumor pairs resected from individual mice (p=5.38e-04, Spearman's Rank Correlation). **(F)** Frequency of detected unique barcodes from both tumor of a representative mouse from euthanized at day 1. Barcode frequency distribution of the inoculum is plotted for comparison (black dots). The two highest frequency barcodes found in the right tumor are shown with arrows to highlight that top barcodes make up the majority of the bacteria population. **(G)** Shannon entropy index of each tumor based on the number of unique barcodes detected. Data points from individual tumors are shown as circles (triangles match tumors from panel F). The Shannon entropy Index of the inoculum is shown for comparison (dashed line).

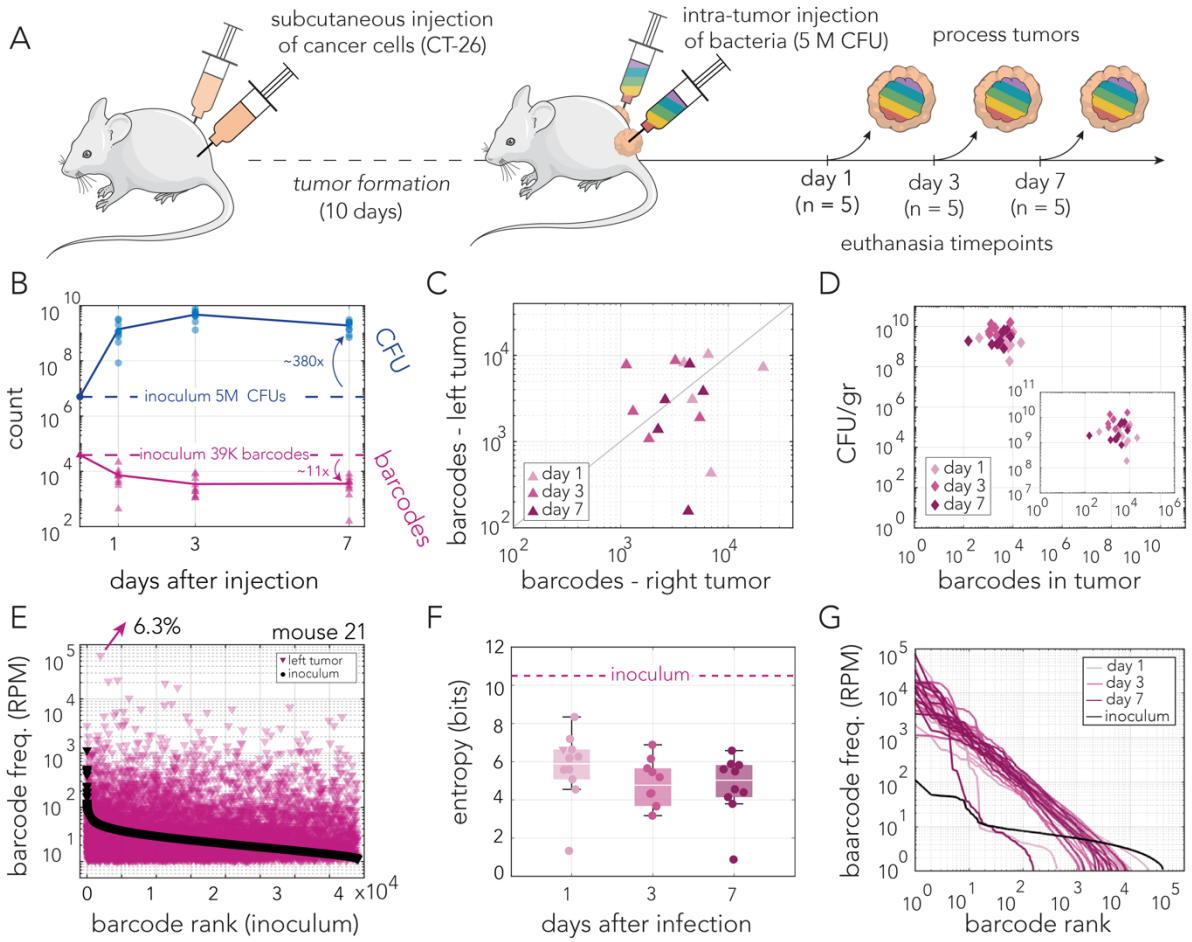

Figure 3 Tumor colonization after intratumor injection. (A) Outline of experimental approach. Subcutaneous tumors were formed on the right and left flanks. After tumor formation, mice were infected by intratumor injection of five million CFUs. Groups of five mice were euthanized on days 1,3 and 7 post infection. Resected tumors were processed to determine bacteria load and clone diversity. **(B)** Bacterial load and number of detected barcodes are shown in blue and pink color, respectively. The bacteria number of clones in the inoculum are show for comparison (dashed lines). **(C)** Scatter plot showing the number of barcodes detected in tumor pairs resected from individual mice (p=0.70, Spearman's Rank Correlation). **(D)** Scatter plot showing the number of detected unique barcodes from the tumors and the carrying capacity (CFU/gr tumor). Inset shows the same data with a narrower axis range (p=0.54, Spearman's Rank correlation). **(E)** Frequency of detected unique barcodes from a single tumor of a representative mouse from euthanized at day 1. A total of 10,258 unique barcodes were detected in this tumor. Barcode frequency distribution of the inoculum is plotted for comparison (black dots). The highest frequency barcode is shown with the arrow. **(F)** Shannon entropy index of each tumor based on the number of unique barcodes detected. Data points from individual tumors are shown as circles (the triangle matches the tumor from panel E). Shannon entropy Index of the inoculum is shown for comparison (dashed line). **(G)** Ranked frequency distribution of the detected unique barcodes from each tumor in the experiment (shades of pink for days 1,3 and 7) and the inoculum. Barcodes detected in each tumor or inoculum were ranked individually in descending order.

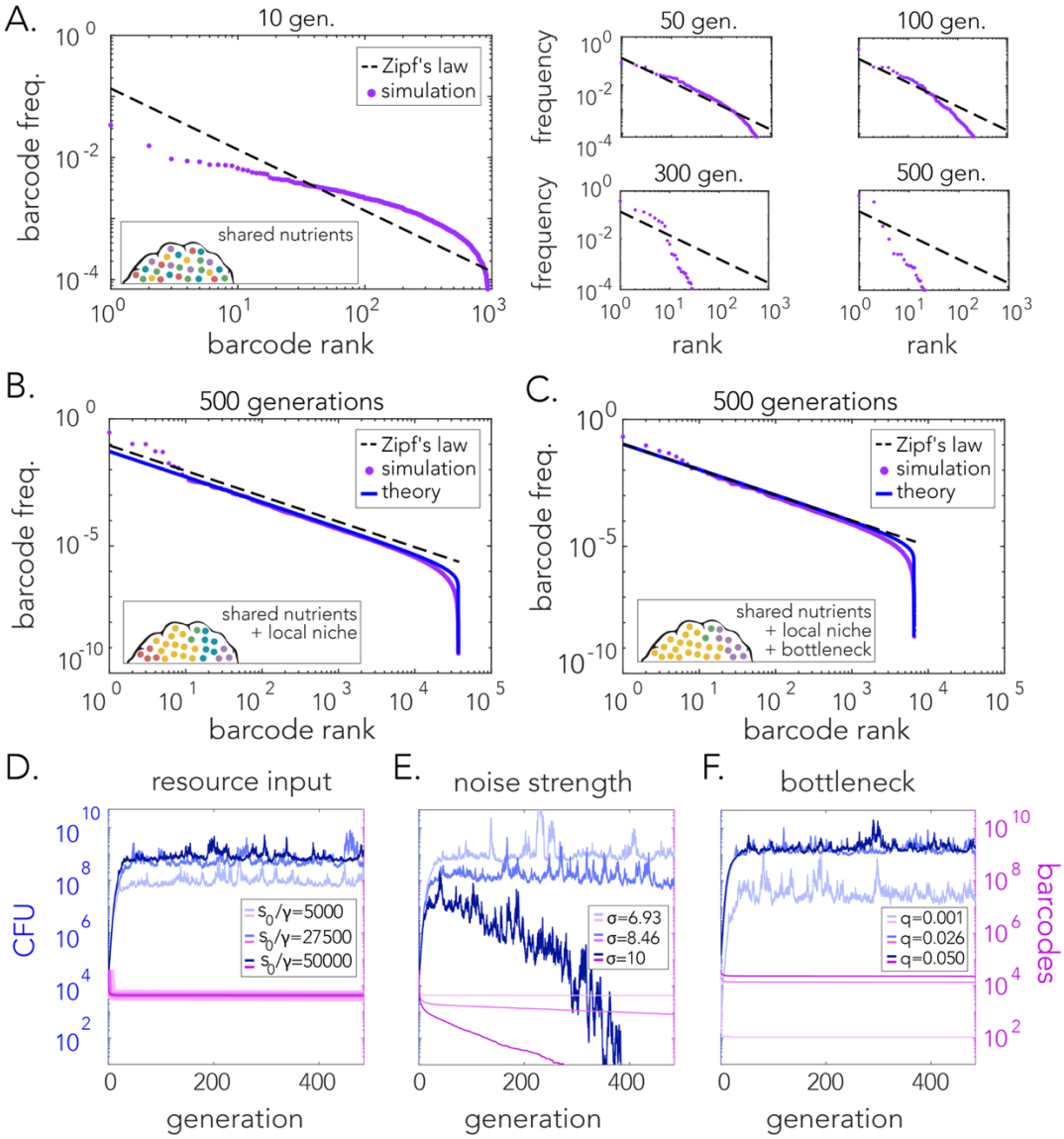

Figure 4 (A) Simulations of the Monod model [Eqs. (**Error! Reference source not found.**) and (**Error! Reference source not found.**)] across different generations demonstrate deviation of the statistics from Zipf's law and the eventual extinction of the population after many generations. (B) Simulation of the Contois model [Eqs. (**Error! Reference source not found.**) and (**Error! Reference source not found.**)] demonstrate that the statistics satisfy Zipf's law even after 500 generations. (C) Same simulation as in B after the inclusion of an initial bottleneck leading to the extinction of some barcodes. (D-F) Illustrations of the effects different model parameters have on the dynamics of the total population CFU and the number of surviving barcodes. The ratio of introduced resources to the inverse yield coefficient, s_0/γ, affects the final CFU without affecting the number of barcodes. Increasing s_0/γ results in an increase in the final CFU. Noise strength, σ, affects the CFU and barcode numbers. A large σ can push the population to extinction. Survival probability (bottleneck size), q, affects the number of surviving barcodes and consequently the final total CFU. See Methods for parameter values.

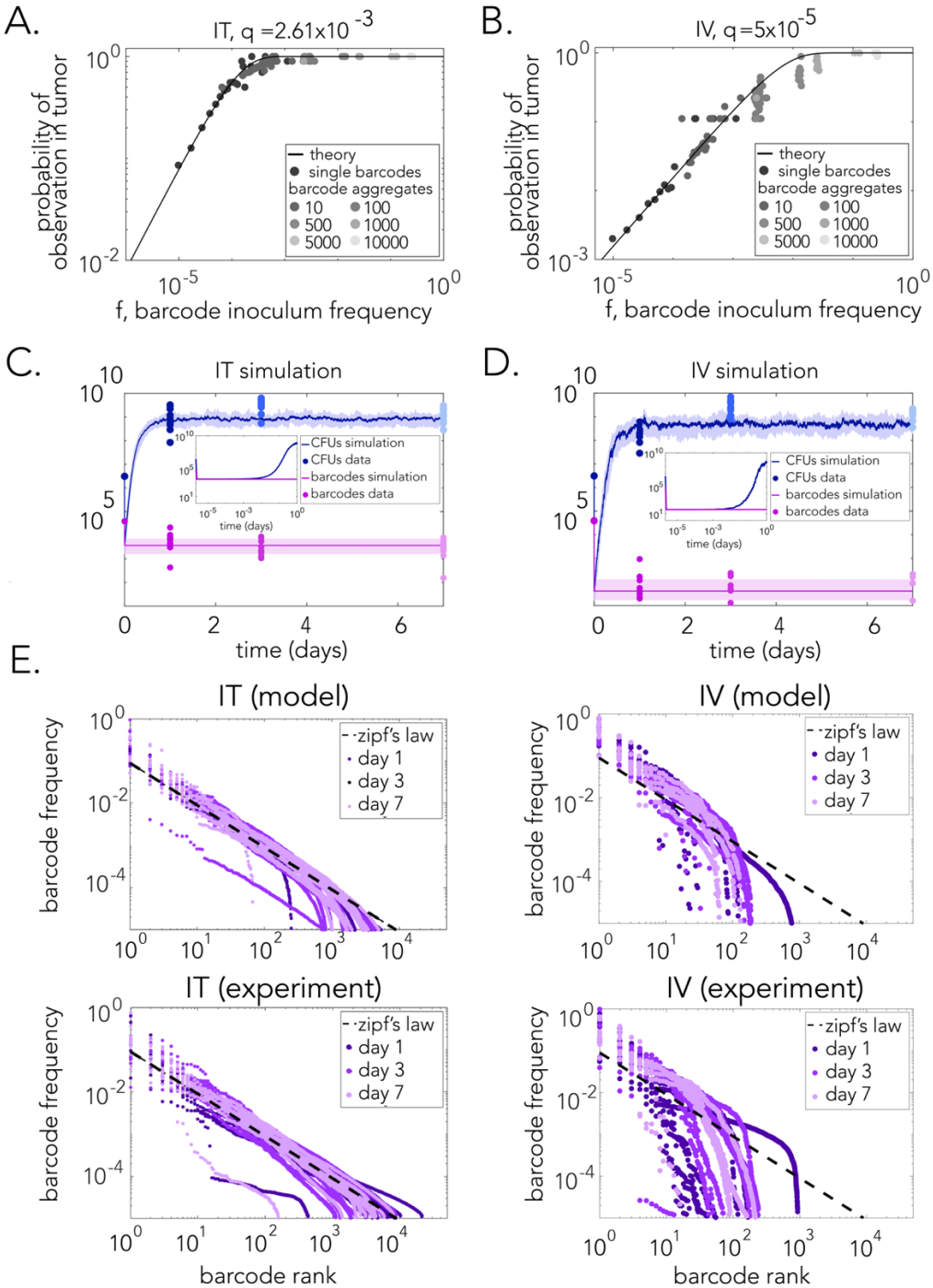

Figure 5 Mathematical model captures dynamics of bacteria load and barcode frequencies. **(A-B)** Bottleneck theory predicting the probability of observing a barcode in the tumor given its inoculum frequency. q represents the inferred survival probability from data for the IV and IT injections. Barcode data was aggregated to populate higher frequencies and confirm they obey the theory **(C-D)** IT and IV simulations of total CFU and barcode number dynamics. Experimental data is overlaid with circles. Solid dark lines indicate the median value of different stochastic trajectories. Shaded areas represent the range between the first and third quartiles. Insets: Immediate post-injection dynamics showing the initial bottleneck effect **(E)** Comparison between IT and IV statistics at different days for both simulations and experiments. IT data satisfies Zipf's law, while IV data does not. See Methods for parameter values.

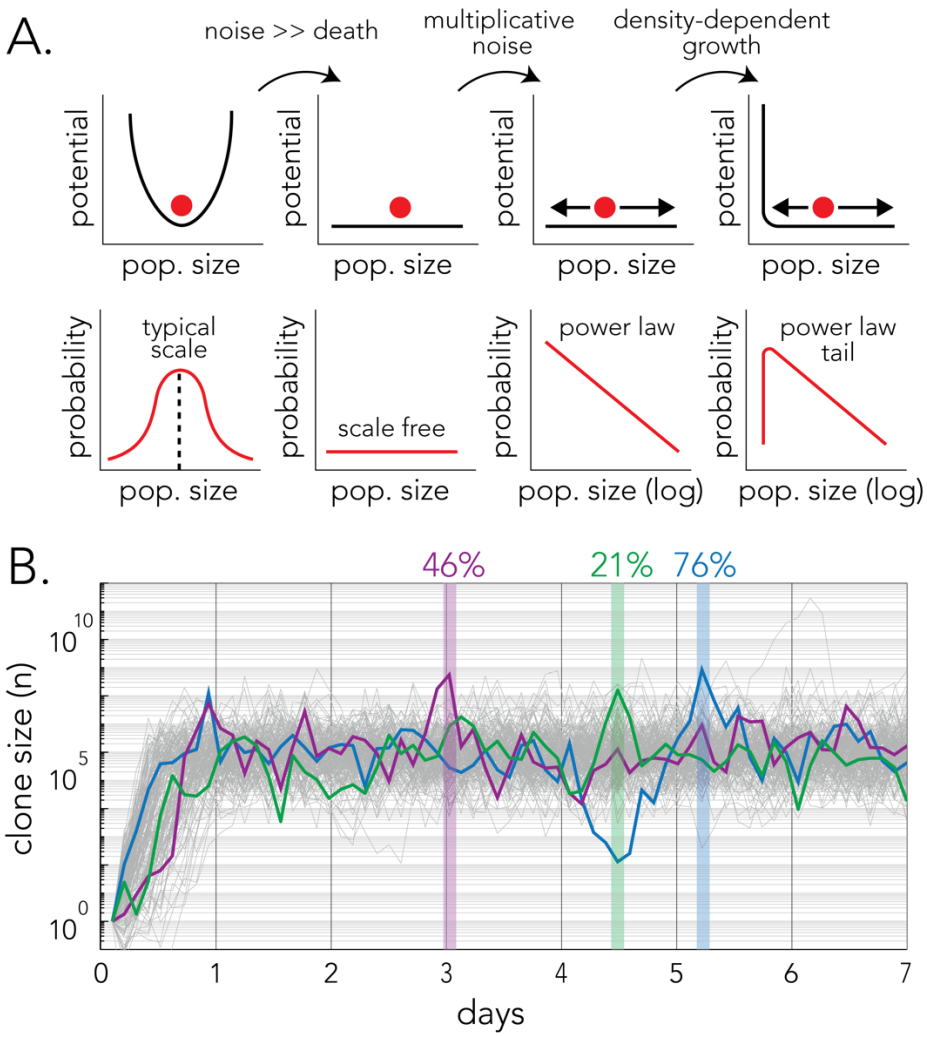

Figure 6 The criteria required for Zipf's law emergence and the underlying microbial population dynamics. **(A)** Zipf's law requires the lack of a dynamic attractor, biased fluctuations, and extinction prevention. In our model, these criteria are provided by noisy cell death, multiplicative noise, and local growth limitation, respectively. Together, these criteria result in a probability distribution whose tail follows a power law with power -2, equivalent to a rank-frequency plot with power -1 (Zipf's law). **(B)** The population dynamics expected during tumor colonization after intravenous infection. The graphs show the simulated dynamics in 178 successfully colonizing a tumor after intravenous infection. The dynamics of three random clones is highlighted in color and their respective maximum sizes are shown with vertical lines. The numbers on top mark the proportion of cells from the corresponding same color clone out of all bacteria in the tumor.

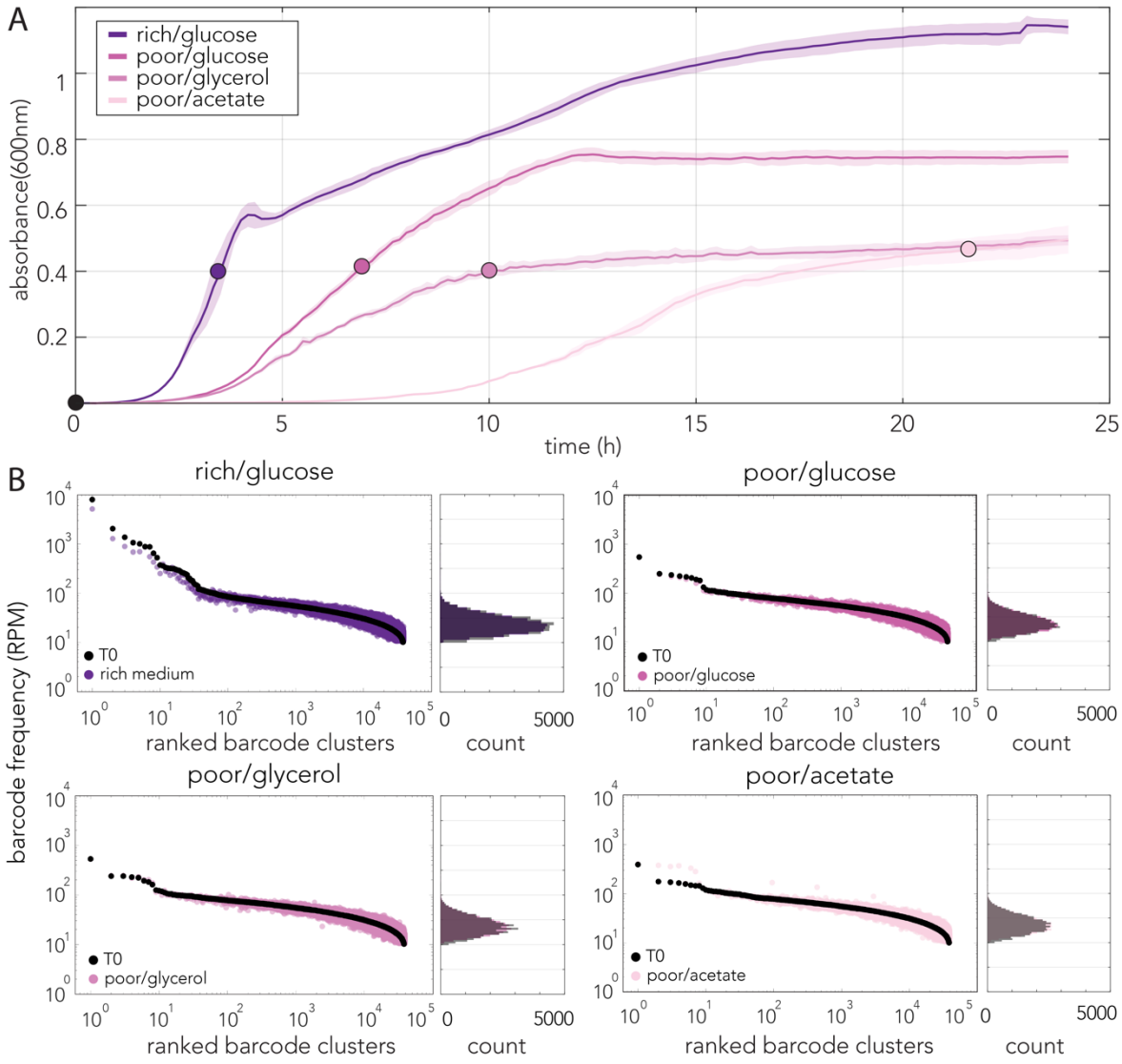

Figure S1 Variation in barcode frequency after in-vitro growth follows the Monod model with intrinsic noise. **(A)** Growth of barcoded strain collection and isolation points for barcode extraction. **(B)** Variation in barcode frequency before and after growth. The frequency of barcodes in the inoculum is shown and compared to experiment and model simulation results without reranking to show growth noise. Intrinsic noise does not change the relative frequency of barcodes; reranking results in the same rank-frequency distribution as the inoculum.