Refined quantification of infection bottlenecks and pathogen dissemination with STAMPR

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Abstract

Pathogen population dynamics during infection are critical determinants of infection susceptibility and define patterns of dissemination. However, deciphering pathogen population dynamics, particularly founding population sizes in host organs and patterns of dissemination between organs, is difficult due to the fact that measuring bacterial burden alone is insufficient to observe these patterns. Introduction of allelic diversity into otherwise identical bacteria using DNA barcodes enables sequencing-based measurements of these parameters, in a method known as STAMP (Sequence Tag-Based analysis of Microbial Population dynamics). However, bacteria often undergo unequal expansion within host organs, resulting in marked differences in the frequencies of barcodes in input and output libraries. Here, we show that these differences confound STAMP-based analyses of founding population sizes and dissemination patterns. We present STAMPR, a successor to STAMP that accounts for such population expansions. Using data from systemic infection of barcoded Extraintestinal Pathogenic *E. coli* we show that this new framework along with the metrics it yields enhances the fidelity of measurements of bottlenecks and dissemination patterns. STAMPR was also validated on an independent, barcoded *Pseudomonas aeruginosa* dataset, uncovering new patterns of dissemination within the data. This framework (available at https://github.com/hullahalli/stampr_rtisan), when coupled with barcoded datasets, enables a more complete assessment of within-host bacterial population dynamics.

Importance

Barcoded bacteria are often employed to monitor pathogen population dynamics during infection. The accuracy of these measurements is diminished by unequal bacterial expansion rates. Here, we develop computational tools to circumvent this limitation and establish additional metrics that collectively enhance the fidelity of measuring within-host pathogen founding population sizes and dissemination patterns. These new tools will benefit future studies of the dynamics of pathogens and symbionts within their respective hosts, and may have additional barcode-based applications beyond host-microbe interactions.

Introduction

During infection, microbial pathogens encounter a variety of barriers that impede colonization and help prevent subsequent disease. These obstacles include innate and adaptive effectors of the immune system, the microbiota, and anatomical and chemical barriers, such as stomach acidity, and physical niche availability (1). Collectively, these restrictions, which generally act to protect the host and reduce the size of the pathogen population post-inoculation, are often referred to as a bottleneck. When bacteria in the inoculum contain multiple alleles, the allelic composition of the bacterial population found at sites of colonization will differ from that in the inoculum after passing through the bottleneck, a phenomenon more broadly referred to as genetic drift (2). In infection biology, bottlenecks are key determinants of whether a host becomes colonized by a pathogen, govern paths of dissemination within individual hosts, and influence transmission between hosts (3–9). However, the set of host mechanisms that govern bottlenecks remain incompletely understood. Genome-scale genetic screens in bacteria can be used to investigate host defense axes, but are themselves confounded by bottleneck effects that cause mutant strains in a population to be eliminated by the host by chance alone, rather than through selection (10–16).

Infection bottlenecks are difficult to quantify if the experimental inoculum is composed of bacteria of uniform genotype. Several methods that introduce allelic diversity have been used to circumvent this issue and measure bottlenecks (7, 17). One approach involves the introduction of artificial and fitness-neutral short random sequence tags (barcodes) into otherwise identical cells. The comparison of barcode abundances before and after infection through high throughput DNA sequencing then enables bottleneck quantification. Combining barcoding with deep sequencing is widely generalizable and can be applied in several different contexts, such as experimental evolution and cancer progression (18). Different analytical approaches and metrics for comparisons of barcode frequencies have been created (19–21), including Sequence Tag-based Analysis of Microbial Populations (STAMP), for analysis of infection bottlenecks (22). In STAMP, deep sequencing is used to determine the distribution of barcode frequencies in an inoculum (the input) and in various organs (output). The changes in barcode distributions (i.e., allele frequencies) between input and output are used to quantify the magnitude of genetic drift, which approximates the magnitude of the bottleneck

(23). Bottlenecks are measured as the size of the founding population (FP), the number of unique cells from the inoculum that give rise to the population in a given sample. A small value of FP is indicative of a “tight” bottleneck, whereas a large FP indicates a “wide” bottleneck. FP is estimated by an application of an equation from Krimbas and Tsakas, originally used to quantify genetic drift in insect populations (23). In STAMP, the estimate of FP is known as N_b. We distinguish FP and N_b to emphasize that FP is impossible to measure precisely, as it would require every cell in the inoculum to possess a different tag and infinite sequencing depth. N_b calculation circumvents these limitations by quantifying the differences in barcode frequencies between a reference inoculum and output organ samples. STAMP has been used in several infection models across multiple anatomical sites to estimate FP and unveil host determinants of infection bottlenecks (22, 24–27). Recent work has also enabled the use of STAMP to measure bacterial replication and death rates (28).

Two key assumptions that underlie the calculation of N_b are that 1) all sampled bacteria in the population have experienced a singular, identical bottleneck and that 2) all cells grow at similar rates after passing through the bottleneck (22, 28). These assumptions oversimplify conditions within the host, as bacteria within an organ are likely exposed to different environments depending on their sub-organ localization. For example, variation in the immune state of diverse host cells can impose different pressures on bacteria (29). Furthermore, organ reseeding events can result in multiple populations of bacteria within an organ that have undergone distinct bottlenecks. Phenotypic heterogeneity in the pathogen population can also influence post-bottleneck expansion rates (30, 31). These additional sources of variation in barcode frequencies result in a consistent underestimation of FP by N_b, because calculation of N_b relies on comparing the similarity of barcode frequencies between an output organ sample and a diverse input. The N_b value of an output sample will be larger if the barcode frequency distribution in the organ sample more closely resembles the inoculum. As genetic drift or uneven growth rates cause the barcode frequency distribution in the output sample to vary, N_b decreases. However, N_b alone cannot distinguish between genetic drift or uneven growth, and since both are prevalent in biological data, additional metrics are warranted and would markedly improve data interpretation. For example, two organs may possess very similar FPs but one organ may be permissive to increased replication of a sub-population. These organs would have different N_b and would therefore be interpreted to differ in FP.

We found that in biological data, uneven growth often manifests as the expansion of very few clones, which are evident as disproportionately abundant barcodes, and lead to consistent underestimates of the true FP by N_b. In infection contexts, uneven pathogen growth may arise from multiple causes, including local host permissiveness or phenotypic heterogeneity in the pathogen. Here, we present STAMPR, a computational approach that overcomes this limitation of STAMP. STAMPR is a successor to STAMP that relies on an iterative barcode removal algorithm to account for the contribution of clonal expansion to bottlenecks and dissemination patterns. Using data from systemic infection of barcoded Extraintestinal Pathogenic *E. coli* (ExPEC) (32), we show that STAMPR enhances the fidelity of measurements of bottlenecks and population dynamics by accounting for every barcode. We use these tools to reanalyze an independently generated and published dataset that explored *Pseudomonas aeruginosa* systemic spread (24). Our tools readily detected and quantified previously unappreciated instances of clonal expansion and dissemination in these data. STAMPR (freely available at https://github.com/hullahalli/stampr_rtisan) therefore enables a deeper and more complete understanding of within-host bacterial population dynamics.

Results and discussion

Highly abundant barcodes confound measurement of founding population sizes

Our motivation for questioning the fidelity of N_b as a proxy of FP came from observations where N_b values were often much smaller than the number of detected barcodes in sequencing data. This discrepancy became particularly clear in analyses of STAMP-based experiments to study within-host ExPEC dissemination, the biological findings of which are described further in a companion manuscript (32). In the ExPEC systemic infection model, the pathogen is inoculated intravenously, and samples are taken from different organs to monitor dissemination and expansion. In multiple organs, we found clonally expanded bacterial populations, intermixed with less abundant, more diverse bacterial populations. By introducing additional variance to output barcode frequencies, these highly abundant “outliers” confounded N_b, as samples with hundreds of detectable tags yielded much lower N_b values (occasionally >10 fold). The discrepancy between N_b (as a true measure of

FP) and the number of barcodes is not biologically plausible; if 100 barcodes are detected, the founding population must be composed of at least 100 unique bacteria. While it is possible for an individual cell to possess two barcodes, it is highly unlikely. During library preparation, individual colonies are Sanger sequenced, confirming that the presence of multiple tags per cell is below detection. Furthermore, within-run sequencing controls (samples with known numbers of barcodes) serve to rule out the significant influence of cross-contamination or sequencing errors.

We sought to develop a computational approach that can recognize and account for disproportionately abundant barcodes. This approach would not only need to account for highly abundant tags, but be sufficiently unbiased to enable determination of FP when it is difficult to identify "outliers" by visual inspection of barcode frequency graphs. In an ideal system, every bacterium from the inoculum would be tagged with a single *unique* barcode, in which case counting the number of barcodes would yield a more accurate measure of FP than N_b. However, creation of highly diverse libraries has been technically challenging, particularly for non-model organisms. An alternative approach to improve the accuracy of FP estimates leverages the power of computational resampling, which, unlike N_b, is not affected by unequal growth rates. Simulations can be performed on the input at a variety of sampling depths to determine the sample depth S_s that yields the same number of barcodes detected in the output sample. For example, if 100 barcodes are detected from an output sample derived from an input library of 1000 barcodes, then S_s represents the number of reads that were sampled from the input such that 100 barcodes are detected; this value will always be slightly larger than 100. Therefore S_s, unlike N_b, is not skewed when there is increased variation in barcode frequencies between an output organ and the input.

To demonstrate our methodology, we first artificially recreated a sample in which N_b underestimates FP by using a series of barcode frequency distributions from known bottleneck sizes collected from in vitro generated bottlenecks where FP sizes are known. Combining the barcode frequencies observed in a ~10^3 CFU FP and a ~10^1 CFU FP (Figure 1A) yielded distributions as shown in Figure 1B. This mimics a sample where 10 cells have expanded faster than the other ~1000, after both populations have passed through the same, singular bottleneck. The true FP for this artificial population is close to 10^3. However, the calculated N_b is 150, ~7 fold

lower than the true FP. Experimental data from the ExPEC model revealed similar patterns, where calculated N_b values were lower than the number of detected barcodes, therefore smaller than the true FPs (Figure 2).

We developed an algorithm that provides a more complete estimate of FP (Figure 1B-D, computational workflow described in the Methods and Text S1). Our algorithm was developed on computational samples (such as in Figure 1A) and our ExPEC STAMP experiments, ultimately yielding an unbiased method to determine more accurate estimates of FP. In brief, the algorithm iteratively removes barcodes from the output sample (from greatest to least abundant) and calculates N_b after each iteration. The best estimation of FP for the artificial sample described above is equal to the N_b after the first ~10 most abundant barcodes are removed, which is ~10^3. Subsequent removal of barcodes does little to change N_b (i.e., the y values plateau), and we refer to 10^3 as a more "resilient" estimate of FP. We refer to plots of N_b versus iteration as "Resiliency plots" (Figure 1C) and this algorithm as the "Resiliency algorithm" below. The Resiliency plot can be used to define "breaks" that delineate discrete subpopulations within the sample (shown as red lines in Figure 1CD separating high abundance barcodes, low abundance barcodes, and noise). Then, these subpopulations are weighted by the fractional abundance of barcodes within breaks, enabling determination of a noise threshold. After removing noise, a second Resiliency plot is generated. Using this graph, the algorithm then determines the maximum value for N_b. The maximum value among 1) S_s 2) the first N_b estimate, or 3) the new maximum Nb from the second Resiliency plot, is set equal to the output and referred to as N_r. S_s is used in this manner since it is completely independent of relative barcode abundances and takes into account only their presence or absence. For example, populations that have undergone significant uneven growth post-bottleneck will have low N_b values, so S_s would yield the greatest estimate of FP. Furthermore, this logic ensures that N_r will always be equal to or greater than N_b. By accounting for the presence of every barcode, this approach more completely estimates FP regardless of the presence of disproportionately abundant barcodes in biological data (e.g. Figure 2, Figure S1). The sensitivity of N_b to highly abundant tags can further be exploited by measuring the ratio of N_r/N_b, which in effect quantifies unequal barcode distributions, usually providing information about clonal expansion.

Identifying, quantifying, and visualizing shared barcodes between samples

Barcoded libraries also permit analysis of inter-organ dissemination by analyzing the similarity of tag frequencies between organs. Previous STAMP analyses identified the Cavalli-Sforza chord distance (33) between samples to quantify the genetic distance (GD), although other methods to assess allelic similarity between populations can be employed (20–22, 25, 26). GD is high when two samples are dissimilar, and low when they are more similar. We leveraged iterative barcode removal to obtain a more granular understanding of the similarity between samples. Our motivation arose from the fact that genetic relatedness between samples can be due to varying numbers of tags and detecting the number of shared tags would improve understanding of dissemination patterns. Highly similar samples can result from the sharing of many barcodes or very few highly abundant ones, and we reasoned that our iterative barcode removal strategy could distinguish between the two scenarios. In biological data, the expansion of different clones that overlay similar populations yields high GD values (Fig S2A); conversely, the sharing of dominant clones between two samples yields low GD values, even if the underlying populations are dissimilar (Fig S2B).

Similar to the approach taken with the Resiliency algorithm, we iteratively removed the most abundant barcodes in both samples and created a score between 0 and 1 quantifying the number of barcodes that contribute to genetic similarity between the samples (RD, “resilient” genetic distance) (Figure 3, Figure S1). Low RD values indicate that relatively few barcodes are shared between samples. Samples with both low RD and low GD share only a few tags but are nevertheless highly similar; in this case, very few barcodes are shared, but they represent significant fractions of the total CFU in both samples (Fig. S2B). Samples with both high RD and GD share many tags, but the bulk of the population (in terms of CFU) are dissimilar; this can occur when different sets of bacteria expand in two samples, but both expansion events overlay relatively similar populations containing many barcodes (Fig. S2A). Samples with high RD and low GD are very similar and share many barcodes; this is typically seen in samples with high FP because they closely resemble the inoculum and therefore each other (e.g., early after infection) (Fig S2C). Samples with low RD and high GD are completely dissimilar, suggesting they are unlikely to be related to each other physically or temporally. In our ExPEC data, application of this approach enabled us to distinguish between samples that were similar due to

the dissemination of clones (low RD, low GD) versus when they were similar because they all closely resembled the inoculum (high RD, low GD, and high FP).

Note in this framework, “low” and “high” RD values are relative to the number of barcodes in the library. We created an additional metric where RD values are log-normalized (plus one) to the total number of detectable barcodes in the sample (an output from the Resiliency algorithm). FRD essentially normalizes RD across all samples, and therefore permits comparisons between samples. We refer to this metric as a fractional RD (FRD), which represents the relative abundance of *shared* barcodes in a given sample. Similar to how high N_r/N_b ratios signify the presence of expanded clones that overlay a diverse population, low FRD values signify the presence of abundant *shared* clones that overlay diverse dissimilar populations. The directionality of FRD calculations provides further information about similarity between populations. For example, consider a situation where organ A and organ B are similar samples (low GD) that resemble the data in Figure S2B. If RD = 11 (i.e., 11 barcodes are shared between A and B), $FRD_{A\text{-}B} = \log(11 + 1)/\log(B_B + 1)$, where B_B is the number of barcodes in sample B, while $FRD_{B\text{-}A} = \log(11 + 1)/\log(B_A + 1)$, where B_A is the number of barcodes in sample A. High $FRD_{A\text{-}B}$ signifies that the barcodes that were shared between the two populations represent a large fraction of all the barcodes in sample B. Correspondingly, a low $FRD_{B\text{-}A}$, means that the barcodes that are shared between A and B only represent a small fraction of the barcodes detected in sample A. The difference between $FRD_{A\text{-}B}$ and $FRD_{B\text{-}A}$ implies the existence of a larger, more diverse and dissimilar underlying population in sample A but not sample B. In this example, we can conclude that 1) samples A and B are similar (low GD), 2) the similarity is driven by only a few barcodes (low RD), and 3) these few barcodes represent a large population of sample B but overlay a more diverse resident population in sample A (high $FRD_{A\text{-}B}$, low $FRD_{B\text{-}A}$). Note that FRD is strictly a metric that uses the number of barcodes, not their abundance. Barcode abundance is taken into account in GD calculations, and therefore a combined approach using all of these metrics (GD, RD, FRD) is superior to using any one metric individually.

<u>Reanalysis of *Pseudomonas aeruginosa* bacteremia</u>

We built our tools using an systemic model of ExPEC infection (32). We then tested our tools and associated metrics by re-analyzing data published in a recent study examining the trafficking of a barcoded library of *P. aeruginosa* following its intravenous inoculation into mice (24). This study revealed that gallbladder seeding by *P. aeruginosa* allows the pathogen to disseminate to the intestines and ultimately to be shed in the feces (24). Our re-analysis buttresses these conclusions and also uncovered unappreciated patterns of *P. aeruginosa* expansion and dissemination that were hidden in the datasets. In most of the samples N_r was greater than N_b and in many cases the N_r / N_b ratio was >10, particularly in the liver and lungs (Figure 4A), indicating that there were significant clonal expansions at these sites. Here, clonal expansion refers to markedly uneven tag distribution in the sequencing data. Importantly, the N_r / N_b ratio reveals the presence of clonal expansion, but not the biological source. For example, highly abundant barcodes could result from confined expansion within an organ or arise from transit from a different organ. These reanalyses also revealed profound heterogeneity in N_r values within and between organs 24hr post infection, despite very similar N_b values (Figure 2C of (24)). The large variance in N_r values, for example in the liver and lung (Fig 4A-C) reveals considerable differences in the sizes of the bottlenecks in different animals that were not captured by N_b. Note that this library was created by mixing two pools, resulting in two distinct distributions. The barcode frequency distribution plots shown in Fig4B-G underscore that N_b is extremely sensitive to highly abundant tags and therefore does not adequately quantify the marked differences of pathogen population structure within and between organs. N_b is more similar to N_r when barcode frequencies are relatively even (compare Figure 4D and 4E). Therefore, using N_r in addition to N_b enables a more complete understanding of the entire population structure in the host, including acounting for less abundant barcodes. These underlying populations are important to capture, as they may occupy distinct niches, contribute to persistent infections, or disseminate to other organs in the host.

The potency of our approach is well-illustrated by re-analysis of the data from single animals infected with *P. aeruginosa*. For example, in Mouse 1 (Figure 5), there is a 2.5 log difference between N_b and N_r in the lung, indicating a large clonal expansion. The lung sample was somewhat similar to the liver (GD = 0.66, RD = 739) and spleen (GD = 0.56, RD = 523), but completely dissimilar to gastrointestinal organs (cecum, colon, feces and small intestine) and the gallbaldder (GD > 0.8, RD = 0) (Figure 5), revealing that a set of dominant clones circulated systemically, but not enterically. However, the fact that these GD values are modest and not closer

to 0 suggests that some dominant clones in each sample were not shared. Additionally, the relatively high RD values indicates that removal of a few dominant barcodes does not abolish genetic similarity. Therefore, the populations in these systemic samples consist of underlying subpopulations that are both similar and diverse. For example, the lung and liver do not share many highly abundant barcodes, but both samples have similar underlying populations (Figure 5C, blue brackets). Comparisons of N_r/N_b ratios in these organs also reveals that dominant clones are present in the lung, liver, and spleen (460, 165, and 24 respectively) (Fig 4C). These observations are consistent with a model where the liver, spleen, and lung each received a large portion of the inoculum and had distinct clonal expansion events, some of which spread systemically. Elsewhere in the animal, there was marked sharing of barcodes between the gallbladder and the intestines (GD < 0.2) and these transferred barcodes comprised nearly all of the barcodes in the intestinal organs ($FRD_{gallbladder\text{-}intestine}$ > 0.9). Consistent with N_r values, the small number of barcodes transferred between the gallbladder and liver (GD = .74, RD = 28) comprised a large fraction of the gallbladder population ($FRD_{liver\text{-}gallbladder}$ = 0.8) but only a small fraction of the liver barcodes ($FRD_{gallbladder\text{-}Liver}$= 0.42). These FRD differences reveal that large subpopulations of liver resident bacteria are distinct from those in the gallbladder. Inspection of the barcode frequency distributions confirm that the majority of expanded clones in the liver are not derived from the gallbladder (Fig 5D), consistent with their expansion in the liver in an independent manner rather than from transit to/from the gallbladder. These analyses illustrate how our tools enable high resolution mapping of population dynamics in a single animal.

In contrast to measuring multiple parameters in a single animal, comparing single metrics across animals enables detection of both consistent and heterogeneous facets of population dynamics. For example, we consistently observed significantly higher $FRD_{liver\text{-}gallbladder}$ than $FRD_{gallbladder\text{-}Liver}$, indicating that the bacteria that are shared between the liver and gallbladder consistently represented a larger fraction of the population in the gallbladder than the liver (Figure 6A). This contrasts to comparisons between the gallbladder and the feces, which have FRD values in both directions consistently near 1, suggesting that the fecal population is nearly entirely derived from the gallbladder (Figure 6B). The underlying anatomy in this infection model likely explains these differences. As proposed by Batcha et al (24), the liver first captures bacteria from blood and a small number of these cells then seed the gallbladder, where they subsequently replicate in bile. This model can

explain why the liver often possesses its own resident population distinct from the gallbladder, and FRD enables robust quantification of this phenomenon. This pattern was observed in most animals, but Mouse 9 was a clear exception (Figure 6C). In this animal, the gallbladder population was one of the most diverse (high N_r) observed. Furthermore, the gallbladder population in Mouse 9 was nearly identical to all other organs (low GD). For example, the gallbladder appears to account entirely for the population in the liver ($FRD_{Gallbladder\text{-}Liver}$ =1, contrasting with Mouse 1 in Figure 5) and the GI organs. The gallbladder population includes a set of non-transferred barcodes that are absent from the liver and gastrointestinal organs ($FRD_{colon\text{-}gallbladder}$ = $FRD_{cecum\text{-}gallbladder}$ = $FRD_{SI\text{-}gallbladder}$ = 0.6 , while $FRD_{gallbladder\text{-}colon} \approx FRD_{gallbladder\text{-}cecum} \approx FRD_{gallbladder\text{-}SI} \approx 1$) (Figure 6BC). Thus, in Mouse 9, the gallbladder seeded the intestines with only a fraction of its population.

By plotting the GD and FRD of each organ against all organs in the animal in a heatmap, we are able to rapidly detect consistency and variability in spreading events. For example, examination of the heatmaps in Figure 5 and Figure S3 reveal two groups of animals that vary in the levels of systemic spread of gallbladder bacteria. In Mice 1, 4, 5, 6, 7, and 10, the gallbladder appeared to be dissimilar to the lungs and the spleen. In contrast, in mice 2, 3, 8, and 9, the gallbladder population was highly similar to that in the lungs and spleen. The variable magnitudes of the stochastic systemic spread of gallbladder bacteria, very likely via blood, potentially explains these distinct dissemination patterns. Therefore, the fate of bacteria that have seeded and replicated in bile can profoundly alter pathogen populations in distal organs. More broadly, the STAMPR framework developed here can rapidly uncover stochastic and more subtle patterns of dissemination.

Summary and perspectives

Coupling barcoded bacteria with high throughput DNA sequencing enables powerful investigations of bacterial population dynamics. In infection biology, comparisons of barcode abundances in an experimental inoculum with those found in various host organs (the output) at different times post-inoculation enables inferences about the sizes of bottlenecks and patterns of pathogen dissemination. However, bacteria often undergo unequal expansion within an organ, resulting in marked differences in the frequencies of barcodes in the output library compared to the input. Here, we show that these differences confound calculations underlying

quantification of founding population sizes and dissemination patterns. We created a new framework, called STAMPR, that provides a more complete assessment of within-host population dynamics

Our approach accounts for unequal growth and abundant tags to provide a more holistic assessment of infection population dynamics. Two metrics (N_r and N_b) define the number of organisms from the inoculum that give rise to the population in an organ. N_b is highly sensitive to disproportionately abundant tags, while N_r is agnostic to these highly abundant barcodes. The N_r/N_b ratio indicates the magnitude of unequal growth, which is most apparent in samples where very few clones have expanded dramatically. Comparisons of barcode frequencies between samples further enables assessment of bacterial dissemination, quantified by GD. We further refine GD to determine the precise number of barcodes that are transferred between samples, in a metric called RD. Combining RD with founding population sizes results in a directional metric (FRD) that quantifies the relative abundance of shared bacteria within two samples. Taken together, we refine and establish eight metrics for a pair of samples (N_b and N_r for samples A and B, and GD, RD, $FRD_{A\text{-}B}$, and $FRD_{B\text{-}A}$) from which the entire underlying barcode frequency distributions can be summarized (Figure S1). Furthermore, when used across many organs, these metrics enable high-resolution analysis of population dynamics in a single animal.

Reanalysis of previous infection data also highlights the utility of our method to uncover new dissemination dynamics. Importantly, though our approach removes clonal expansions for more accurate calculation of the FP, it inadvertently identifies them. Our analyses of these heterogenous expansion events in organs and across animals reveals that this previously unrecognized phenomenon is highly prevalent in infection contexts. Approaches to visualize and quantify such events will set the stage for future studies to characterize how host responses, spatial relationships, and interventions may govern these uneven replication dynamics. We anticipate that applications of our new tools in future studies will deepen our understanding of within (and between) host bacterial population dynamics. Finally, our strategy to account for unequal tag abundance will also have utility in studies beyond infection dynamics that rely on barcode frequency analysis, including lineage tracing, cancer progression, and experimental evolution (18).

Methods

Processing of STAMP reads

Reads were first demultiplexed on Illumina BaseSpace via i7, and then further demultiplexed on CLC Genomics Workbench using the first 6 nucleotides. Trimming was performed using the default parameters and only reads between 18 and 22 nt were kept. Trimmed reads were mapped to the list of 1329 barcodes (obtained from (32)) using the default parameters in CLC, and the mapping file was exported directly from CLC as a csv file containing barcodes and read counts.

Calculation of Nb and Nr

Previous studies have "calibrated" N_b values to a known standard curve, and the calibrated values were referred to as N_b'. However, this calibration is only meaningful when the biological data generally satisfies the assumptions of equal growth rates and uniform bottleneck that is used to generate the standard curve and was therefore omitted from this manuscript. Comparison of Figure 5 (uncalibrated) and Figure S2C from (24) (calibrated) shows the negligible impact of calibration on these data. To calculate N_b and N_r, metadata is first retrieved from a csv file containing the barcode frequencies of the references and samples and from a table of CFU for each sample. Replicates for reference vectors (i.e., values sequenced from the inoculum) are averaged. A bottleneck for the reference vector is then iteratively simulated by resampling the reference vector from a multivariate hypergeometric distribution. Each iteration is resampled to different depths, ranging from 1 read to 10 times the total number of barcodes in the sample in increments of 10. Therefore, a library with 1000 barcodes is iteratively resampled 1000 times from 1 read to 10,000 reads. This is typically sufficient to generate a plateau in the graph. At each iteration, the number of nonzero barcodes is calculated and plotted against the resampling size. This plot is referred to as the "reference resample plot". The x-axis value of this plot is referred to as S_s and represents a bottleneck size that yields a desired number of barcodes. This plot is

used later to identify the size of the computation-derived bottleneck (S_s) that gives rise to the observed number of barcodes in the sample.

A user specified noise filtering step is included to assist the Resiliency algorithm in locating noise. In practice, this is estimated from control samples within a sequencing run for which the precise number of barcodes is known. Reads that map to other barcodes are therefore a result of noise, likely due to index hopping. Measuring the relative abundance of these reads enables a preliminary user-controlled noise filtering prior to the more unbiased steps in the algorithm, described below. For the ExPEC study, noise was set to 0.5% (indicated by controls), while it was set to 1% for reanalysis of *P. aeruginosa* data (a conservative estimate). The desired number of reads is simulated on the reference vector with a multivariate hypergeometric distribution and subtracted from the output vector.

Next, we determine the number of required iterations for barcode removal, which is set to a minimum value among the CFU of the sample (plus one) or the number of barcodes with more than 1 read. This ultimately helps speed computation of N_r for low CFU samples. The reference and output vectors are then matched and ordered by the output vector, and the first N_b is calculated from the Krimbas and Tsakas equation. Next, the last row that contains the most abundant output barcode is removed, along with the corresponding input barcode. Note that at early iterations, this is essentially the same as setting the output barcode equal to the input barcode. After this removal, the second N_b is calculated; this process is then iterated for the previously determined number of iterations to generate the first Resiliency plot.

A local minimum can arise in the resiliency plot when barcodes resulting from bacteria present in the sample ("real" barcodes) have been removed. This is due to the relatively similar sequence noise is relatively similar across all samples, which are multiplexed in >50 samples per MiSeq lane. As the real barcodes have been removed, the "noise" resembles the inoculum and begins to raise the N_b value. For example, if there are 100 "real" evenly distributed barcodes in the sample and 100 "noise" barcodes, removal of the 90 most abundant barcodes will yield a population that resembles one where there is no noise, but 10 highly abundant clones overlaying a more diverse population. This results in a low N_b value. When the 100 more abundant barcodes

are removed, there are no longer any highly abundant barcodes, so N_b temporarily increases. Biological data, however, is rarely this clear, and therefore a goal of the algorithm is to identify all local minima, as they represent potential locations in which the barcode distribution could be approaching noise.

To accomplish this, the algorithm starts at multiple “initiation sites” across the resiliency plot. The number of initiation sites is set equal to 1/15 the number of elements in the Resiliency plot, which can be calibrated as needed but is practical for STAMP data with ~10^2-10^3 barcodes. Each initiation site is an x coordinate on the Resiliency plot. For each of these sites, the algorithm performs the following computation. A sample is drawn from a normal distribution with a mean equal to the position of the initiation site and standard deviation equation to 1/10 the number of elements in the Resiliency plot. Decreasing the standard deviation decreases the “search space” and therefore increases the number of local minima that can potentially be found. If the standard deviation is too large, only the global minimum will be found. This sample is a “guess” for where to potentially move on the Resiliency plot. Since this “guess” is another x-coordinate on the Resiliency plot, the corresponding y-coordinate is determined. If this new y-coordinate is less than the y-coordinate of the initiation site, the mean of the next normal distribution is set to equal the guess. This process is repeated 1000 times, where “guesses” are repeatedly drawn from a normal distribution and accepted only if they result in a lower y-coordinate on the Resiliency plot. In this manner, the initiation site settles to some value on the Resiliency plot. The x-coordinates where this process settles after 1000 iterations and across all initiation sites are known as “breaks”. The location of the greatest log change in the Resiliency plot is also determined and added to the breaks; a similar parameter was used to separate true and false barcodes in a previous approach (19). Collectively each break represents some notable transition in the barcode frequencies of the output sample relative to the input.

An “indices table” is then constructed around the breaks. For each break, fractional abundance for those barcodes in between is calculated (referred to as “weights”). For example, if two breaks are located at position 5 and 200 in the Resiliency plot, then we calculate the fractional abundance of the first 5 barcodes and barcodes 6-200. Additionally, we identify the maximum N_b up to each break. In this example, this would mean

identifying the maximum N_b in the first 5 values of the Resiliency plot and the maximum N_b in the first 200 values. The indices table combines the maximum N_b, weight, and breaks.

Next, noise is defined from the indices table as the greatest log change in weight; the breakpoint immediately prior to the greatest log change represents the iteration in the Resiliency plot after which all real barcodes have been removed. Since the resiliency plot is derived from an ordered list of barcode frequencies, this iteration can be traced back to barcodes above and below a specific number of reads. A verification step is performed to ensure that all non-noise barcodes represent a set minimum of the total number of reads (97% in this study). After noise is determined, all barcodes determined to be noise are set to 0 and a new Resiliency plot is generated from this noise-less set of data.

The final FP estimation from the Resiliency algorithm, referred to as N_r, is equal to the maximum value among 1) the maximum N_b in this new second Resiliency plot, 2) the original N_b estimate (i.e., the output of the first iteration), or 3) the value of S_s, which corresponds to the number of non-noise derived barcodes derived from the reference resample plot, using the NLSstClosestX function in R. This ensures that N_r will always be greater than or equal to N_b and that N_r will never be less than the observed number of counted barcodes. In this manner, this algorithm can choose the strategy which determines the FP that most adequately captures all barcodes. Very complex libraries, such as one with ~1,000,000 barcodes, would almost always derive N_r values from the reference resample plot, while smaller libraries will more often use Resiliency plots to find the maximum N_b. Similarly, if there is a substantial amount of variation in barcode frequency due to sources other than the bottleneck (such as phenotypic heterogeneity) such that N_b is very low, N_r will be equal to S_s. An important implication of the use of S_s by the Resiliency algorithm is that the resolution limit of S_s increases when there are more barcodes. For example, if the data is highly variable but all barcodes are present, S_s will be greater for a library of 1000 barcodes than for a library of 200 barcodes. Additionally, since N_r relies on simulations, the precise value differs slightly each time the algorithm is run. One notable class of edge cases are samples with 1 CFU that can yield N_r values of ~2; these cases can easily be corrected post hoc and do not affect data interpretation.

Calculation of GD and RD

Genetic distance (GD) is calculated by the Cavalli-Sforza chord distance as described (22, 33). We analogize our approach for calculating N_r to genetic distance and created a metric we refer to as RD. RD measures the number of barcodes that "contribute" to relatedness between samples. Low values of RD imply that few barcodes are shared, whereas high values of RD imply that many barcodes are shared.

RD is calculated in single script as follows. Barcode frequency vectors are obtained after running the Resiliency algorithm after removal of noise. Both organs are paired and ordered by the geometric mean abundance of each barcode. GD is calculated iteratively, and barcodes are removed as done in the Resiliency algorithm. RD is equal to the number of barcodes that yield GD values below 0.8 on the graph of GD vs iteration. Figure S2 shows how this graph behaves for a variety of given inputs, and how the RD value is derived from them. 0.8 approximates the GD of two unrelated samples (24). FRD is then manually determined by dividing the log of each value (plus one) in each column of the output table (all pairwise comparisons) by the log of the maximum value in each column (plus one). The maximum value of each column is the RD value of the sample compared with itself, which defines the column.

Data and code availability

All scripts used in this manuscript are available at https://github.com/hullahalli/stampr_rtisan. Barcode frequency counts for ExPEC STAMP experiments were experimentally derived from our companion manuscript (32) and are available at the above link to reproduce plots in Figures 2, 3, and S2. Barcode counts for *P. aeruginosa* STAMP experiments are provided at (24).

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Figure Legends

Figure 1. Overview of the Resiliency algorithm

A) Two barcode frequency distributions from known CFU dilutions (and thus known FPs) are shown, with calculated N_b values. The raw read counts of each barcode in these samples are summed to give rise to the plot in B. This results in a computational sample that mimics a scenario where ~10 cells have expanded at a much faster rate than the other ~1000, despite both populations having passed through the bottleneck. From the data plotted in B the resiliency algorithm is run to generate a Resiliency plot, which is displayed in C, by iteratively removing the most abundant barcodes and calculating N_b after each iteration. Breaks in the graph (red lines in C) are algorithmically identified and visually superimposed to the plot in B, resulting in the diagram shown in D. Breaks signify potentially discrete populations, and the weight of each population is determined as a fraction of total reads. An initial noise assumption is set by the user, and in this example was set to 1% of all reads. The largest log change in the weights determines a computationally defined threshold for noise. From this, a new Resiliency plot is generated without noise, and the greatest value among the original N_b value, the new maximum N_b from the second Resiliency plot, or S_s is used to determine N_r. In this example, S_s was the largest of these values, and is therefore the resulting value of N_r.

Figure 2. Variations in N_r and N_b

Barcode frequency distributions for six samples from ExPEC systemic infection (32) are shown. The y-axes are displayed on a log scale to facilitate identification of noise. For each sample, a red line indicates the first break identified by the Resiliency algorithm and delineates discrete sub-populations. The blue line indicates the

threshold for noise. In each sub-population, the fraction of total barcodes represented is displayed. N_b and N_r values are indicated.

Figure 3. Workflow for RD calculation

A, B) Barcode frequency distributions in two samples. The top ten most abundant barcodes in the top sample (A) are highlighted in red and identified in the bottom sample (B). The RD algorithm iteratively removes the most abundant barcodes and calculates GD after each iteration to generate the plot in C. These samples are moderately related to each other, since they share the same dominant barcode, but their underlying populations are dissimilar. RD is defined as the number of points on the plot in B that are below 0.8.

Figure 4. Reanalysis of *P. aeruginosa* systemic infection population dynamics

A) N_b values are displayed across organs from Figure 2C (24) along with N_r values determined here. B-G) Barcode frequency distributions from individual samples B-G (as shown in A) are displayed to visualize the underlying distributions that give rise to N_b and N_r values. These distributions are prior to noise correction by the Resiliency algorithm. These plots represent a wide range of barcode frequency distributions, despite the fact that N_b is similar in all of them. N_r, by accounting for all barcodes, more robustly captures and quantifies the differences between these samples.

Figure 5. Reanalysis of *P. aeruginosa* population dynamics in a single animal

A) GD and B) FRD values were calculated for all organs in Mouse 1 from Figure 2C of (24). A) Since GD is the same for a pair of samples in either direction, GD heatmaps are symmetric along the diagonal. B) The asymmetry of color along the diagonal in the FRD heatmap arises from the fact that only one of the axes (the column names) serves as the reference, while the row names are simply the other sample in the pair used to calculate RD. The liver and cecum are modestly similar samples as measured by genetic distance; however, $FRD_{liver\text{-}cecum}$ is greater than $FRD_{cecum\text{-}liver}$ (asterisks). This indicates that the shared barcodes between the liver and cecum represent smaller fractions of the total liver barcodes than the total cecum barcodes. Therefore, the liver, but not the cecum, has a larger resident non-shared population. C) Barcode frequency distributions after noise removal are shown for the lung. The top 10 barcodes are highlighted in red and identified in the spleen

and liver samples, demonstrating that these samples share some, but not all, dominant tags. This is reflected in GD values in A. N_r and N_b values are displayed for reference. Blue brackets indicate the diverse underlying population. D) Same as C but the gallbladder (GB) serves as the reference for the top 10 barcodes and these barcodes are identified in the colon, cecum, and liver.

Figure 6. Gallbladder transmission dynamics

A) FRD values are displayed for liver/gallbladder and feces/gallbladder pairs. There is no significant difference between $FRD_{gallbladder\text{-}feces}$ and $FRD_{feces\text{-}gallbladder}$. In contrast, $FRD_{gallbladder\text{-}liver}$ is significantly less than $FRD_{liver\text{-}gallbladder}$ (two-tailed paired t-test), indicating that shared tags typically represent a smaller fraction of tags in the liver than the gallbladder. The difference in FRD values indicate that the liver has a resident population that is not shared with the gallbladder. Asterisks represent an animal (Mouse 9) that was a notable exception to this trend. The barcode frequency distribution (after noise removal by the Resiliency algorithm) of the gallbladder of this animal is presented in B). The top 100 most abundant barcodes in the gallbladder are highlighted in red, and these barcodes are highlighted in other organs in C). In this animal, the gallbladder appeared to be more diverse and only shared a fraction of its population with other organs.

Figure S1. Schematic of STAMP measurements

A) Each barcode is represented as a colored marble. In the inoculum, each color is evenly represented. A specific number of marbles are removed from the inoculum and replicate in a separate bucket, in different scenarios depicted in schematics in B-E. B-E) Representations of various output barcode frequencies are shown, each of which is present in biological data from (32). N_r and N_b are indicated adjacent to each sample. GD, RD, and FRD between pairs of selected samples are shown. B is representative of a population that results from a large resampling (wide bottleneck) of the inoculum (A), where each color has replicated relatively evenly after sampling. C and D represent populations that resulted from a large resampling of the inoculum but where one color replicated at a much faster rate (red in C and black in D). E represents a population resulting from a very small resampling (tight bottleneck) of the inoculum, where the black marble has replicated much faster than the red marble.

Figure S2. Examples of GD and RD

Three examples of GD and RD are shown. In each panel, barcode frequency distributions for two samples from (32) are displayed. The ten most abundant barcodes on the left graph in A-C are highlighted in red and identified on the middle graph in each panel. The right plot shows the transformation resulting from the RD algorithm. A) In this example, separate clonal expansion events have occurred in two organs, but the underlying non-expanded populations are still apparent. These samples are overall dissimilar, since GD is high. However, after removal of the clonally expanded barcodes, these samples become highly similar and remain so for the remainder of the iterations. B) An example where two samples are highly similar but share only few dominant barcodes is shown. After iterative removal of the most abundant barcodes, GD rapidly increases. C) These two samples are both highly diverse and similar to the inoculum, so they are very similar and share many tags.

Figure S3. GD and FRD heatmap representations of data derived from Figure 2C of (24)

GD (left) and RD (right) are displayed as heatmaps across all organs for each mouse. The column names represent the reference in RD heatmaps. Heatmaps for mouse 1 are shown in Figure 5. SI and GB are abbreviations for the small intestine and gallbladder, respectively.

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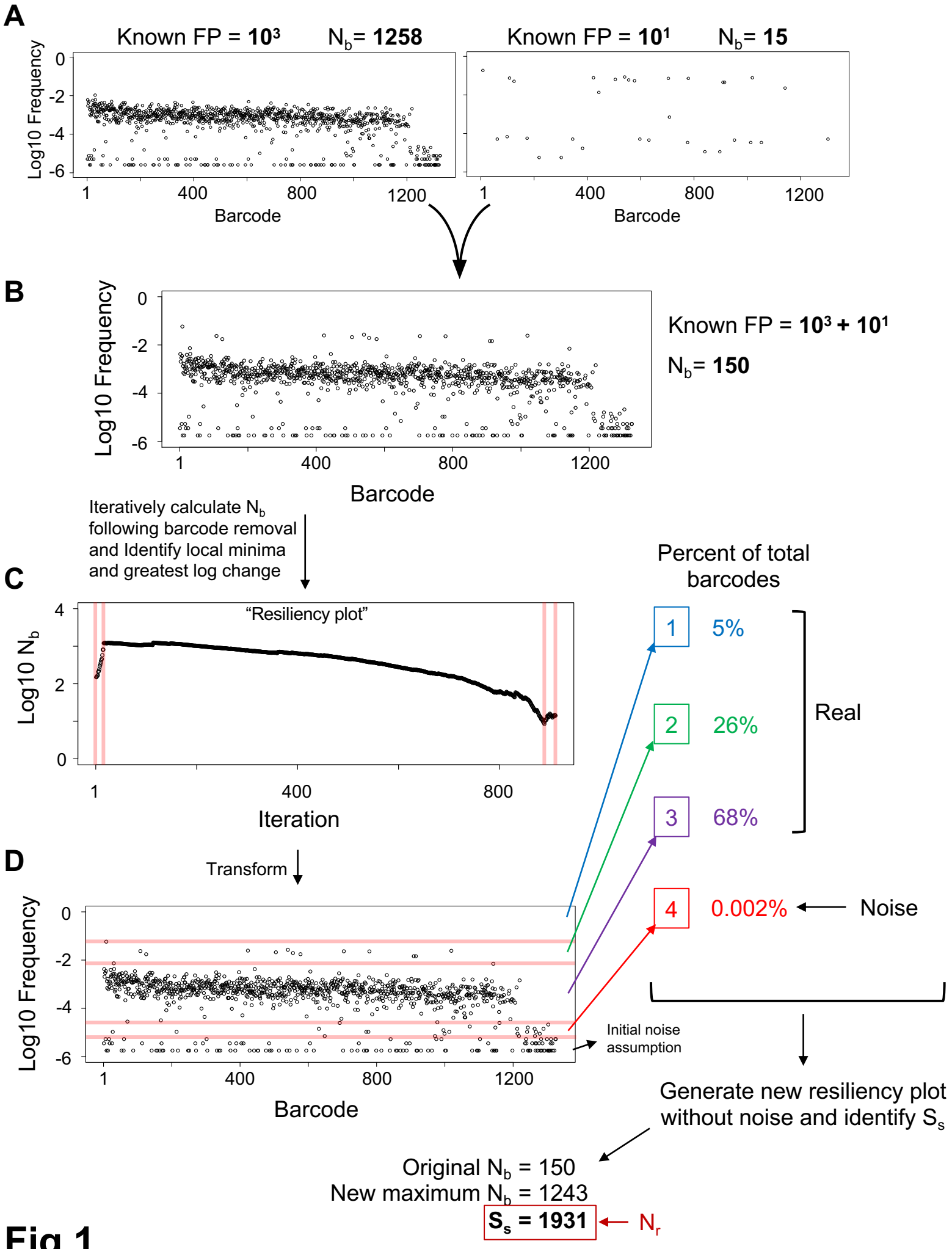
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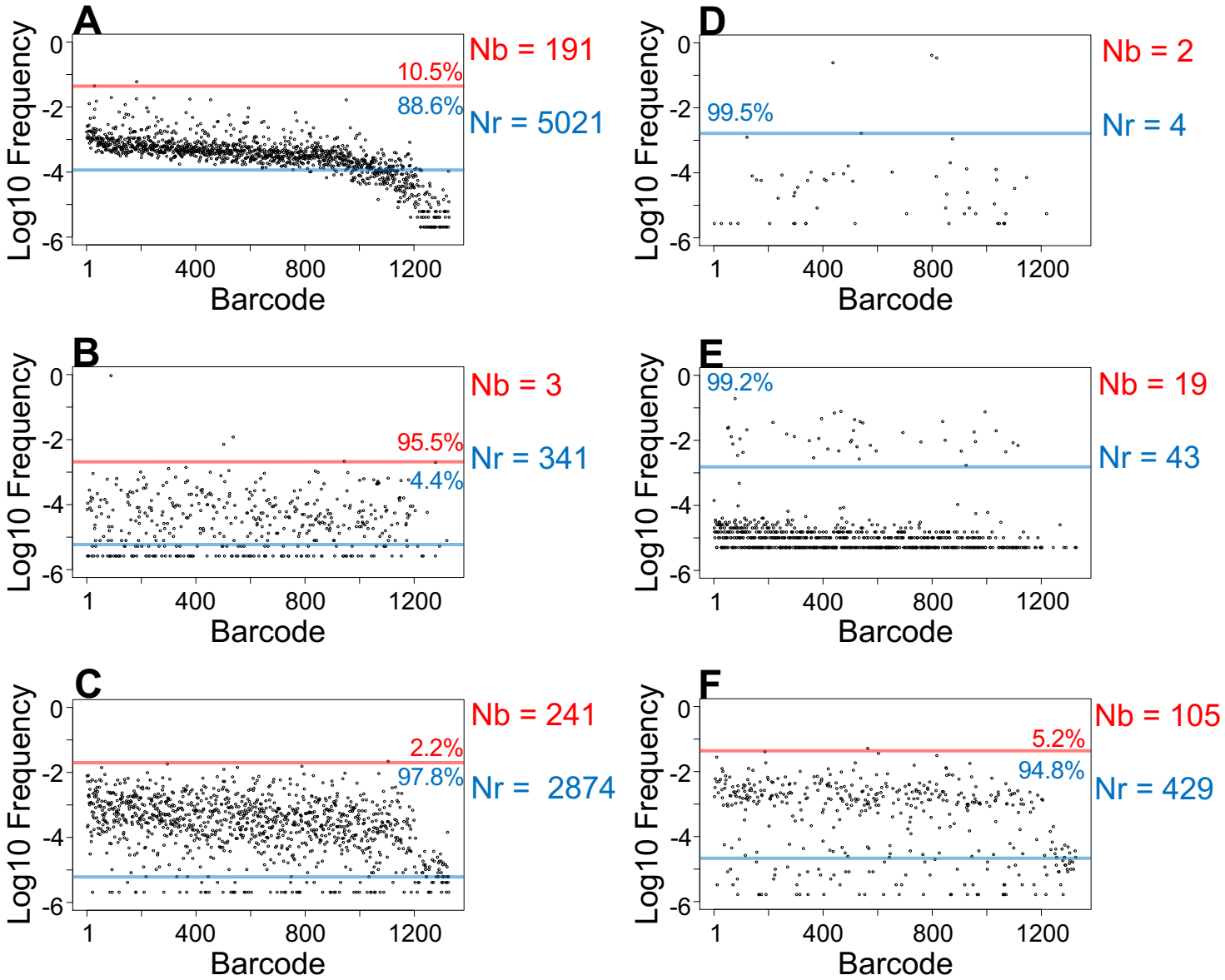
N_b = 1258
Known FP = 10¹
N_b = 15
Log10 Frequency
Barcode
B
Known FP = 10³ + 10¹
N_b = 150
Iteratively calculate N_b following barcode removal and Identify local minima and greatest log change
C
"Resiliency plot"
Log10 N_b
Iteration
Percent of total barcodes
1 5%
2 26%
3 68%
Real
4 0.002%
Noise
D
Transform
Initial noise assumption
Generate new resiliency plot without noise and identify S_s
Original N_b = 150
New maximum N_b = 1243
S_s = 1931
N_r

Fig 1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88.6%
Nr = 5021
B
Nb = 3
95.5%
4.4%
Nr = 341
C
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2.2%
97.8%
Nr = 2874
D
Nb = 2
99.5%
Nr = 4
E
99.2%
Nb = 19
Nr = 43
F
Nb = 105
5.2%
94.8%
Nr = 429
Log10 Frequency
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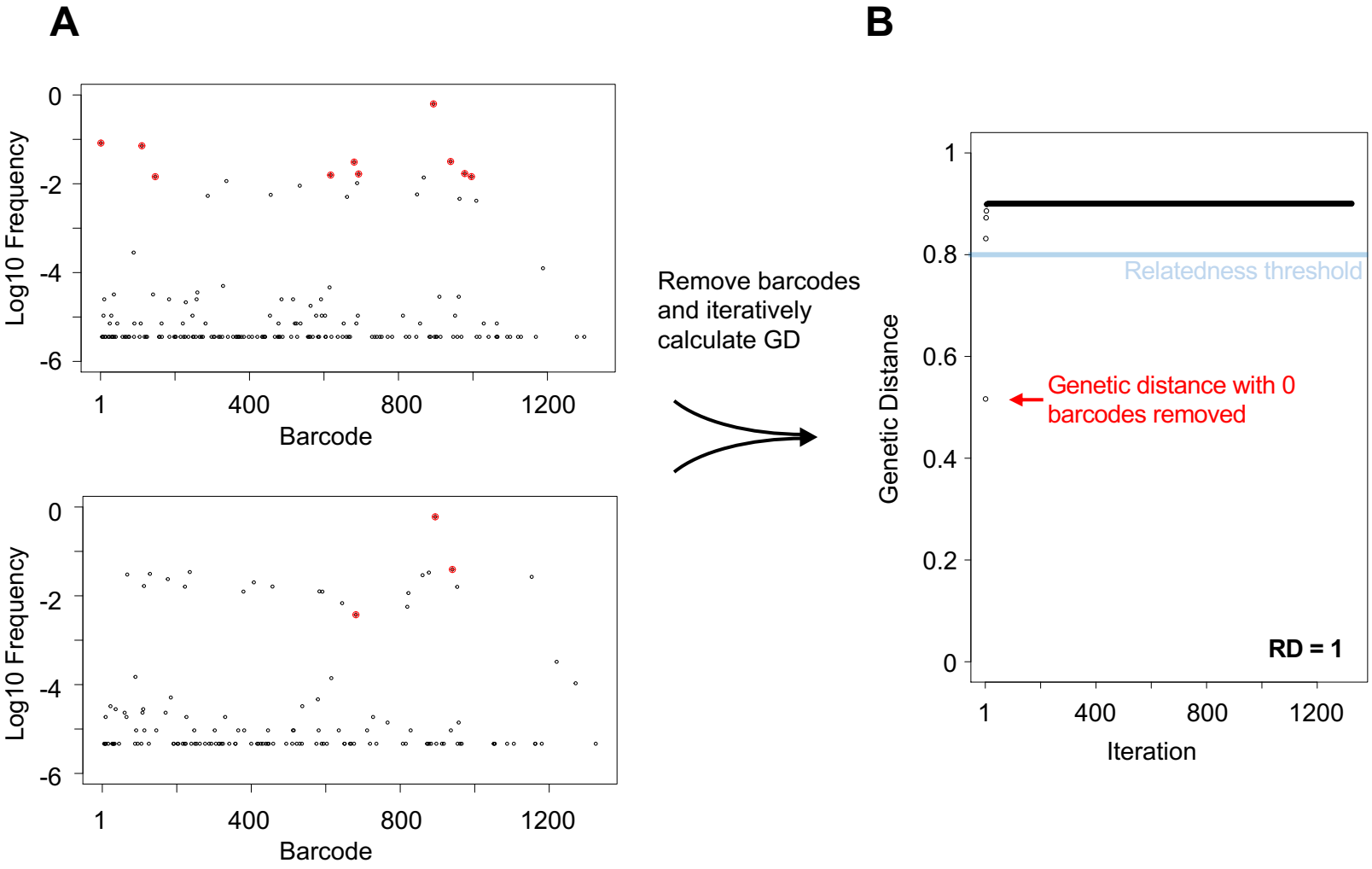
-4
-6
1
400
800
1200
Barcode

Fig 2


A
B
Log10 Frequency
0
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-4
-6
1
400
800
1200
Barcode
Log10 Frequency
0
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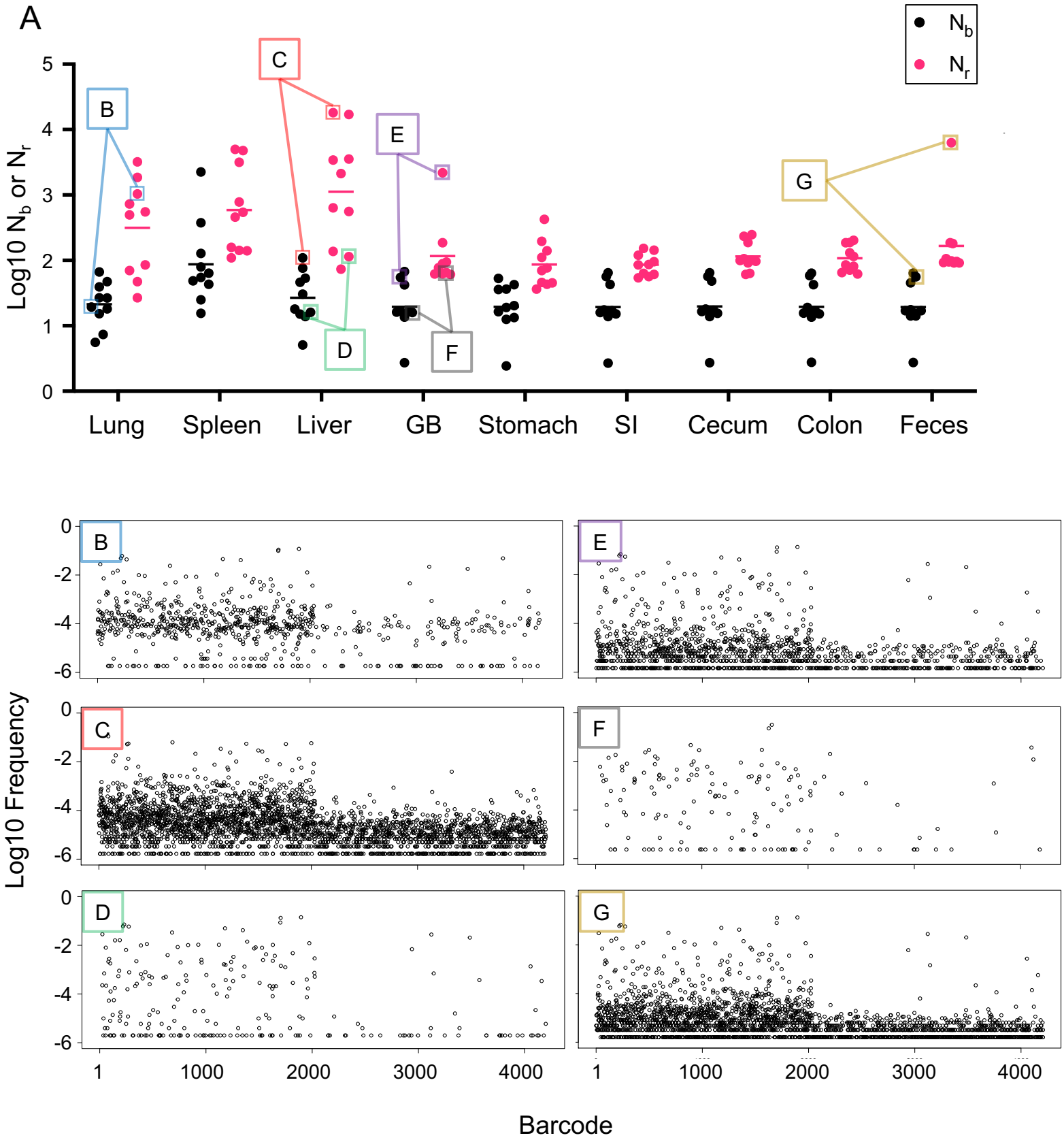
-4
-6
1
400
800
1200
Barcode
Remove barcodes
and iteratively
calculate GD
Genetic Distance
1
0.8
0.6
0.4
0.2
0
Relatedness threshold
Genetic distance with 0
barcodes removed
RD = 1
1
400
800
1200
Iteration

Fig 3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N_b
N_r
Log10 N_b or N_r
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1
2
3
4
5
B
C
D
E
F
G
Lung
Spleen
Liver
GB
Stomach
SI
Cecum
Colon
Feces
Log10 Frequency
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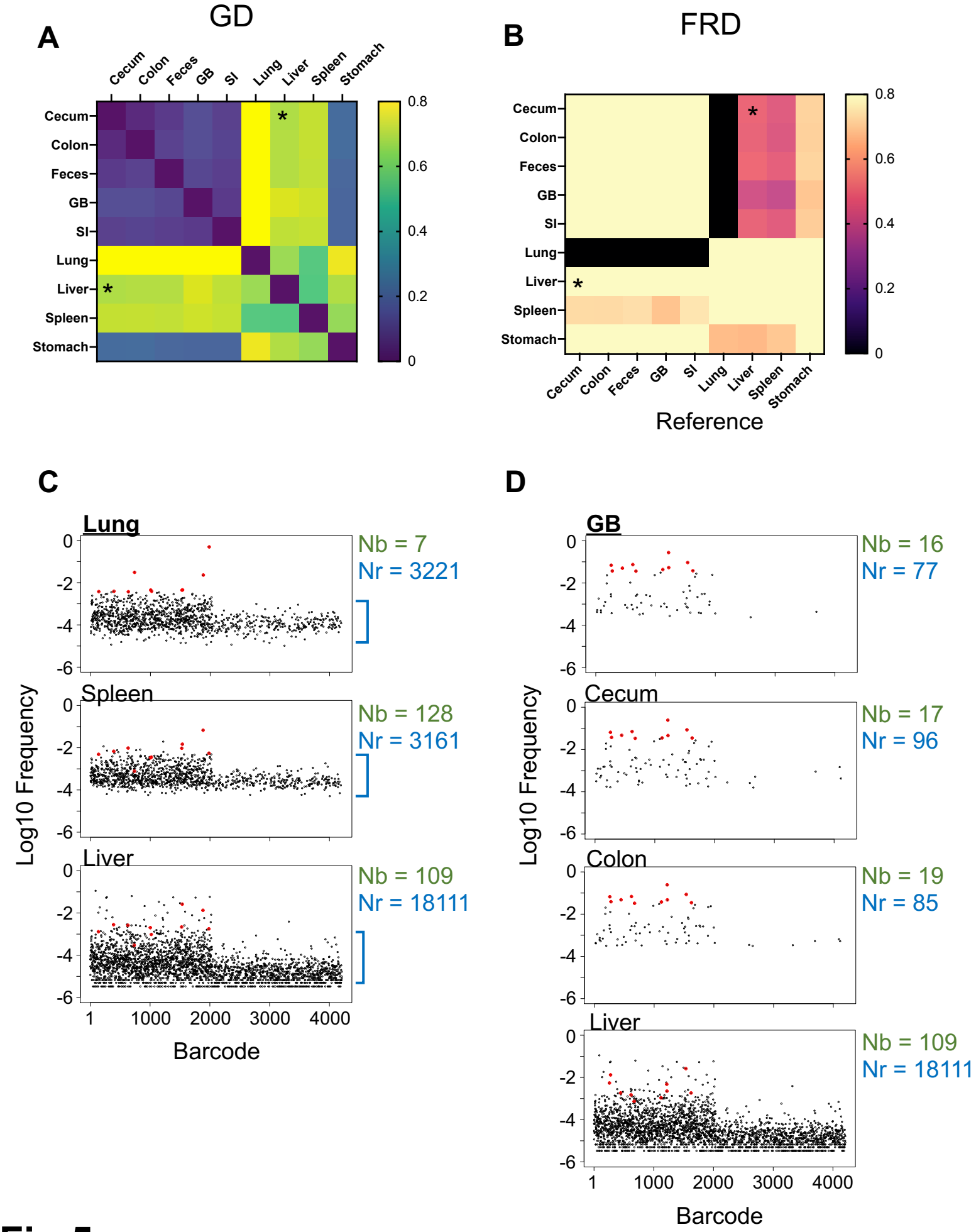
-4
-6
1
1000
2000
3000
4000
Barcode

Fig 4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GD
Cecum
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Feces
GB
SI
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Liver
Spleen
Stomach
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0.6
0.4
0.2
0
B
FRD
Reference
C
Lung
Nb = 7
Nr = 3221
Spleen
Nb = 128
Nr = 3161
Liver
Nb = 109
Nr = 18111
Log10 Frequency
Barcode
D
GB
Nb = 16
Nr = 77
Cecum
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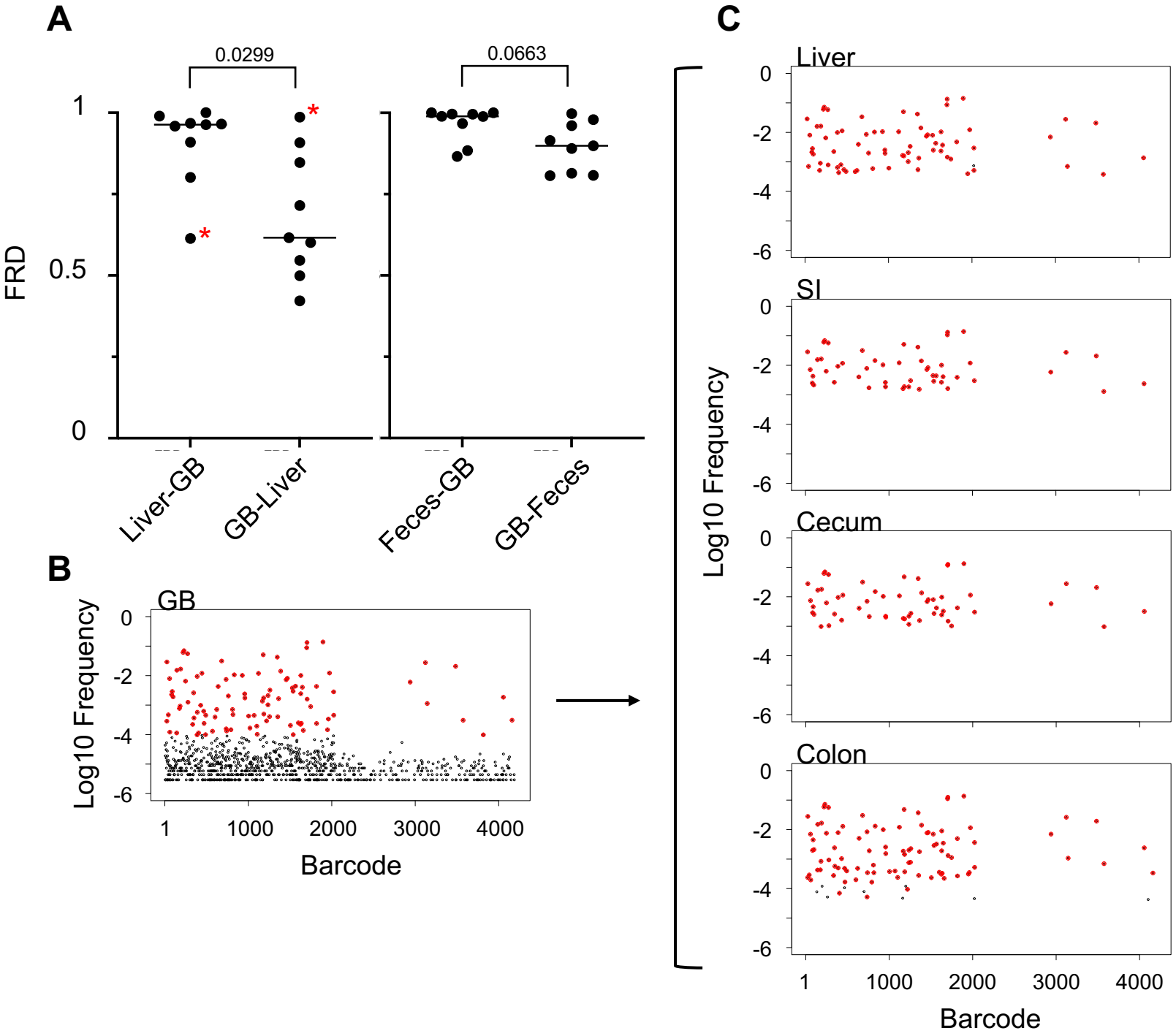
Log10 Frequency
Barcode

Fig 5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FRD
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0.5
0
Liver-GB
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Feces-GB
GB-Feces
B
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Log10 Frequency
0
-2
-4
-6
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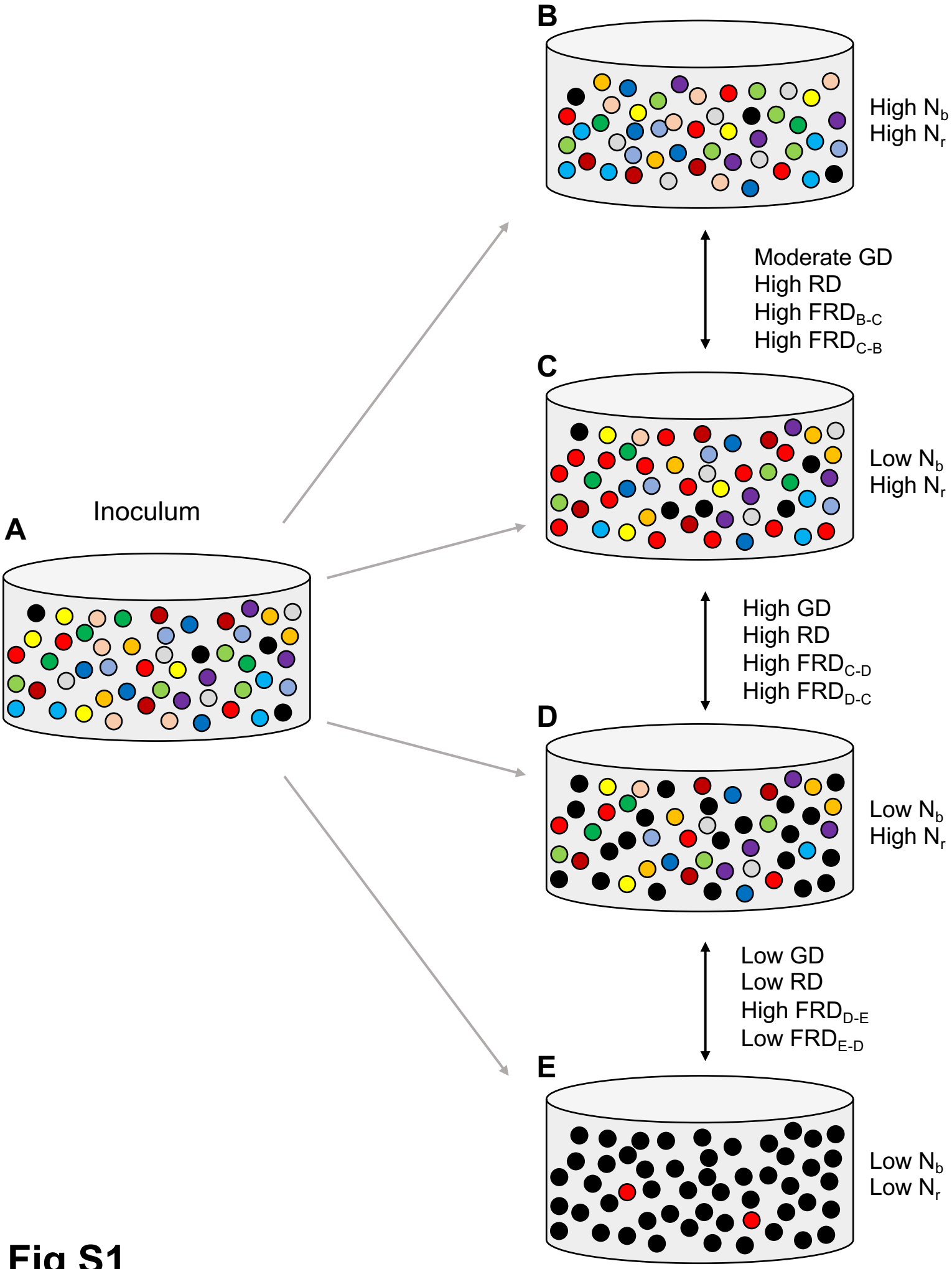
2000
3000
4000
Barcode
C
Liver
SI
Cecum
Colon
Log10 Frequency
Barcode

Fig 6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Inoculum
B
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High N_r
Moderate GD
High RD
High FRD_{B-C}
High FRD_{C-B}
C
Low N_b
High N_r
High GD
High RD
High FRD_{C-D}
High FRD_{D-C}
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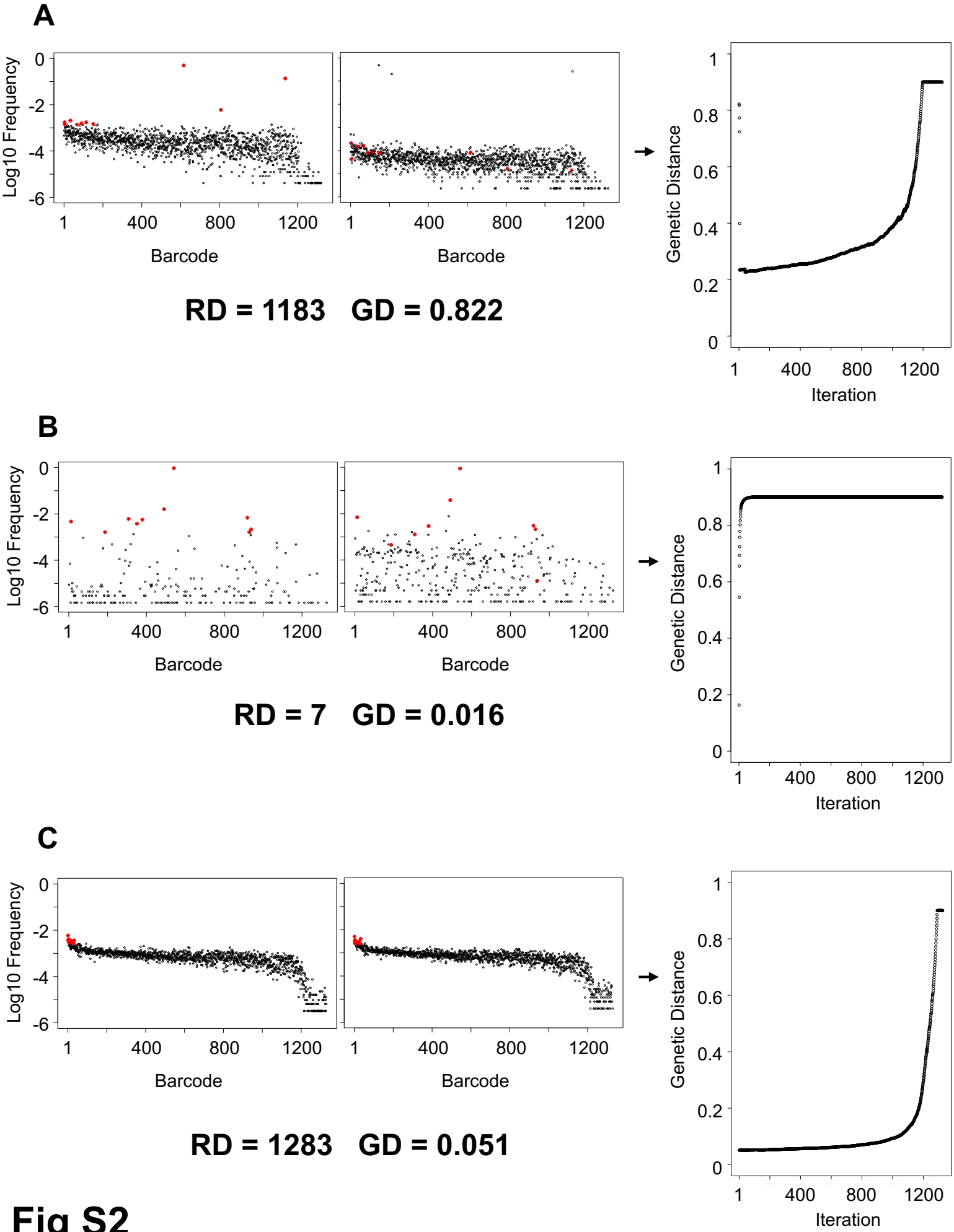
Low FRD_{E-D}
E
Low N_b
Low N_r

Fig S1


A
Log10 Frequency
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-2
-4
-6
1
400
800
1200
Barcode
Barcode
RD = 1183 GD = 0.822
Genetic Distance
1
0.8
0.6
0.4
0.2
0
Iteration
B
RD = 7 GD = 0.016
C
RD = 1283 GD = 0.051

Fig S2

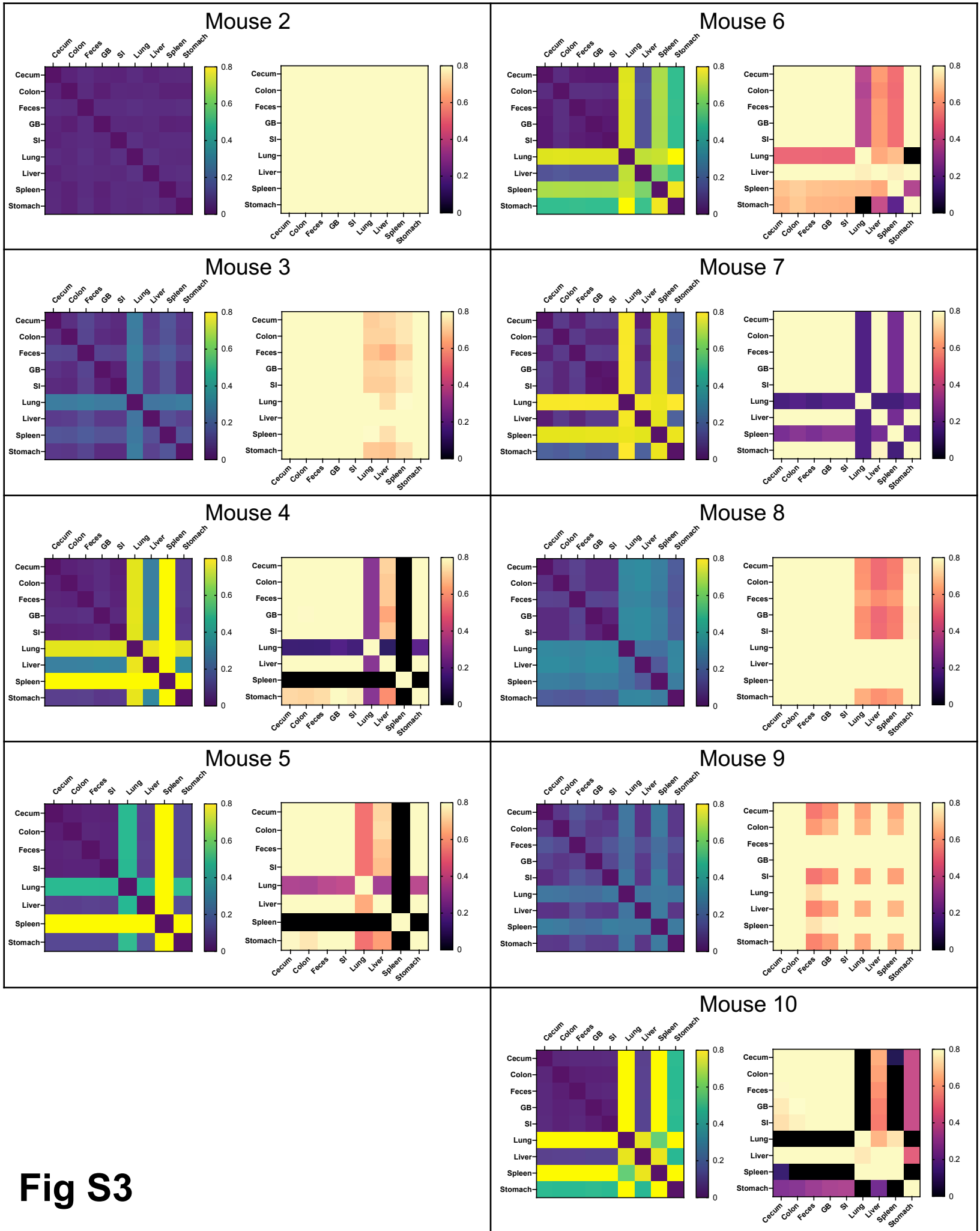
Mouse 2
Mouse 6
Mouse 3
Mouse 7
Mouse 4
Mouse 8
Mouse 5
Mouse 9
Mouse 10
Cecum
Colon
Feces
GB
SI
Lung
Liver
Spleen
Stomach
0
0.2
0.4
0.6
0.8

Fig S3