

# Identification of *Bacillus Anthracis*, *Brucella Spp.*, and *Coxiella Burnetii* DNA Signatures From Bushmeat

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## Research Article

**Keywords:** wildlife species (bushmeat), Meat , dietary protein, zoonotic pathogens

**Posted Date:** January 5th, 2021

**DOI:** <https://doi.org/10.21203/rs.3.rs-137945/v1>

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**Version of Record:** A version of this preprint was published at Scientific Reports on July 21st, 2021. See the published version at <https://doi.org/10.1038/s41598-021-94112-9>.

# Abstract

Meat from wildlife species (bushmeat) represents a major source of dietary protein in low- and middle-income countries where humans and wildlife live in close proximity. Despite the occurrence of zoonotic pathogens in wildlife, their prevalence in bushmeat remains unknown. To assess the risk of exposure to major pathogens in bushmeat, a total of 3,784 samples were collected from three major regions in Tanzania during both rainy and dry seasons, both fresh and processed and screened by real-time PCR for the presence of DNA signatures of *Bacillus anthracis*, *Brucella spp* and *Coxiella burnetii* (*Coxiella*). The analysis identified DNA signatures of *B. anthracis* (0.48%), *Brucella* (0.9%), and *Coxiella* (0.66%) in a total of 77 samples. Highest prevalence rates of *B. anthracis*, *Brucella*, and *Coxiella* were observed in wildebeest, dik-dik, and impala, respectively. Fresh samples, those collected during the rainy season, and samples from Selous or the Serengeti had a greater relative risk of being positive. Microbiome characterization identified *Firmicutes* and *Proteobacteria* as the most abundant phyla. The results highlight and define potential risks of exposure to endemic wildlife diseases from bushmeat and the need for future investigations to address the public health and emerging infectious disease risks associated with bushmeat harvesting, trade, and consumption.

## Introduction

“Bushmeat”, the meat and organs derived from harvested wildlife species, is a common source of animal protein throughout the tropics of the Americas, Asia, Australia, and Africa. In Tanzania, although bushmeat hunting is unlawful without permits, illegal wildlife poaching is a common practice year-round [1]. Bushmeat is not only a source of food and income for the poachers, their families, and communities, but is also used in many cultural, social, and religious practices [2]. A recent survey in the regions surrounding the Greater Serengeti ecosystem revealed that between 2 to 5 meals per week in a household contained bushmeat [3]. While the majority of bushmeat is consumed locally, a considerable amount is also smuggled illegally into the United States and Western Europe. Reports suggest that up to 5 tons of bushmeat is smuggled via a single airport in Western Europe each week [4]. Bushmeat smuggling from Africa and elsewhere could act as a conduit for pathogen spread as suggested by the recent discovery of retroviruses and herpesviruses in bushmeat illegally imported to the US [5]. This is of particular relevance in light of the current global pandemic of SARS-CoV-2, and the increasing risk of newly emerging infectious diseases of zoonotic origin [6]. It is widely recognized that 60% of emerging infectious diseases are zoonotic in origin, and of these 70% originate in wildlife [7]. In this study we shall examine the prevalence of endemic *Brucella spp.* (*Brucella*), and *Coxiella burnetii* (*Coxiella*) in bushmeat samples collected within Tanzania.

*Bacillus anthracis* is a spore-forming, Gram-positive bacterium and the causative agent of anthrax, a zoonotic disease that mostly affects grazing livestock and wild ungulates and poses a threat to human health. Studies have estimated that 20,000 to 100,000 human cases of anthrax occur worldwide annually, the disease is endemic in poor rural areas, especially where there are extensive interactions between human, livestock and wildlife [8, 9]. Outbreaks are regularly reported with an early event in 1962, causing

mortality in 1200 impalas in Tanzania [10]. More recently, an outbreak in 2016-17 in Northern Tanzania recorded positive cases in 131 wildlife and 39 livestock carcasses that were also used for consumption [8, 10]. The recurrence of outbreaks in Tanzania are mainly the result of interactions between humans, wildlife, and livestock at specific “hotspots” of interaction where both domestic and wildlife animals are potential sources of infections to humans [11]. People become infected when handling and consuming infected livestock and also bushmeat. Periods of drought facilitate anthrax outbreaks since they lead to aggregations of animals close to water sources, heavy overgrazing that exposes soil and the infective stages and in some instances, atypical migration patterns [12].

*Brucella*, a genus of Gram-negative bacteria, is the causative agent of a number of zoonotic infections including brucellosis. Infection passes to humans through direct contact with infected animals, by the consumption of unpasteurized dairy products (often raw milk), or via occupational contact with infected animals as well as by the inhalation of airborne agents [13]. In sub-Saharan Africa, including Tanzania, studies have indicated the presence of *Brucella* in wildlife that then passes via livestock to humans and is considered an endemic problem causing devastating economic losses and challenges for public health [14–17]. A recent study in Kenya on *Brucella* suggested that transmission to humans increased as a consequence of close contact between livestock and wildlife [18]. Another study from Tanzania identified geographical “hotspots” with high anti-*Brucella* antibodies in humans, cattle, goats, and buffalos [14]. Other studies have emphasized that transmission of *Brucella* to humans was caused by the preparation and consumption of bushmeat [19–21].

*Coxiella burnetii*, a Gram-negative bacterial CDC select agent that causes Q fever is also transmitted to livestock, wildlife, and humans via byproducts and the direct contact with infected animals. There are few studies on the prevalence of Q fever in Tanzania. One study on humans, livestock and wildlife found that the incidence of Q fever in cattle and wildlife was associated with arthropod vectors [22]. Another cross sectional sero-epidemiological study conducted in South Africa concluded higher risk of zoonotic transmission and economic loss was associated with the livestock-wildlife interface [23] and this has been supported by a number of studies across Africa [21, 24, 25].

Metagenomics has transformed microbiology by leading the way for a cultivation-independent determination of microbial profiles in samples, especially in samples similar to bushmeat that are subjected to a supply chain before consumption. Recent microbiome analyses have provided preliminary evidence for the presence of select agents in bushmeat samples [21], and suggest that characterization of the microbiomes of bushmeat samples with evidence of DNA signatures for the three select agents may help better assess the overall microbial burden and potential public health risks associated with bushmeat harvest, handling, and consumption.

Thus, to better assess the prevalence of select agents and risks associated with the handling and consumption of bushmeat, we screened a total of 3,784 fresh and processed bushmeat samples representing 42 animal species from the Serengeti, Ruaha, and Selous regions in Tanzania collected during rainy and dry seasons over a 2-year period for the presence of DNA signatures of *B. anthracis*,

*Brucella spp.*, and *Coxiella*. Taken together, the results highlight the presence of select agent signatures and help define potential risks of exposure to endemic wildlife diseases from bushmeat in the country.

## Methods

### Study Area

The sampling was carried out at three study savannah dominant sites in Tanzania: the Serengeti National Park (Serengeti), the Ruaha National Park (Ruaha), and the Selous Game Reserve (Selous). The ~25,000 km<sup>2</sup> Serengeti ecosystem is located in northern Tanzania, bordering southern parts of Kenya [26]. The ecosystem in Tanzania consists of several protected areas including the Serengeti National Park (14,760 km<sup>2</sup>, between 1° and 3°30'S and 34° and 36°E) and adjacent Ngorongoro Conservation Area, Game Reserves and Game Controlled Areas. The climate of the Serengeti has a bimodal rainfall pattern with two rainy and two dry seasons. Typically, the short rains are in November-December, and the long rains in March-May [27, 28]. The Ruaha ecosystem (7°30'S 35°00'E), located in the southern region of Tanzania and at 20,226 km<sup>2</sup> (7,809 sq mi), is comprised of Ruaha National Park and surrounding Game Reserves and Wildlife Management Areas. Similar to the Serengeti, it has a biannual rainfall pattern with a short rainy season (November-February) a long rainy season (March-April), and a dry season (June-October) [29]. For the purpose of this study, dry season includes the months of June to October while rainy season spans from the months of March to May. The Selous Game Reserve (9°0'S 37°24'E) 50,000 km<sup>2</sup> (partitioned to form Nyerere National Park, a largest Park in the country) is another protected area in Southern Tanzania. It is contiguous with the Mikumi National Park and Udzungwa Mountains National Park and contains one third of the abundant wildlife of Tanzania. The climate is dry sub-humid influenced by the prevailing southeasterly winds which bring rainfall to the reserve.

### Bushmeat Sample Collection

Sample collection occurred over a two-year period between July 2016 to July 2018, from both dry and rainy seasons. Samples were identified as either “fresh” or “processed”. Fresh samples were those that appeared to be recently harvested while the processed samples included those that were either heavily salted, sun or air-dried, semi-boiled, or a combination of methods that resulted in dehydrated meat samples [30]. The samples were collected by teams of veterinarians, anti-poaching units, and local enumerator networks from villages surrounding the protected areas, where bushmeat is sold [31]. All samples were collected through incidental sampling after obtaining requisite permits from national authorities and in consultation with village leaders. No wildlife species were harmed or directly surveyed as part of this investigation.

Bushmeat samples (~ 250-500g) were collected in double zip lock freezer bags containing sterile non-toxic Silica Gel desiccant moisture absorbers/dehumidifiers. The samples were stored in -20°C vehicle freezers prior to transferring to -20°C solar freezers in the field. The samples were then transported to the

Nelson Mandela African Institution of Science and Technology (NM-AIST) in Arusha via vehicle freezers, where they were stored at -80°C until processing. Cold chain maintenance was ensured through temperature trackers included with the samples throughout the entire process. Sample identification sheets were completed for all collected samples and the metadata, including information regarding sample condition, wildlife species, the collection site (using GPS coordinates), and seasonality.

## Nucleic Acid Extraction

To avoid potential issues associated with surface contamination, three replicates of ~ 120 mg each, were obtained from the muscle tissue using sterile, disposable Rapid Core punch (World Precision Instruments, Sarasota, FL) and sterile disposable safety scalpels (VWR, Bridgeport, NJ). The samples were placed in the MagMAX™ Lysis/Binding Solution Concentrate buffer (Thermo Fisher Scientific, Waltham, Massachusetts). The homogenization protocol was optimized and the settings with the best DNA yield for both fresh and processed samples can be found in the Appendix 1.

Nucleic acid extractions were performed using MagMAX™ 96 DNA Multi-Sample Kit (Thermo Fisher Scientific, Grand Island, NY) and KingFisher Flex automated DNA purification system (Thermo Fisher Scientific, Grand Island, NY) per manufacturer's instructions with minor modifications. If the yield and purity of extractions were not adequate for a specific sample, such as the DNA concentration was less than 4 ng/μl and/or if the quality of the amplicons analyzed by the Bioanalyzer did not pass the quality control, DNA was extracted manually using DNeasy PowerSoil Kit (Qiagen, Hilden, Germany) per manufacturer's instructions. Extracted DNA was quantified using Qubit™ 3.0 Fluorometer (Thermo Fisher Scientific, Grand Island, NY). To ensure purified DNA was of high-quality, DNA was also visualized through agarose gel electrophoresis.

## Real Time PCR

Real-time PCR for the detection of *B. anthracis*, *Brucella* and *Coxiella* were carried in 20 μl reactions with both positive and negative controls internal controls (Appendix 1; Supplemental Table 1) [32]. Samples were considered positive for *B. anthracis* when both plasmids, pXO1 and pXO2, were detected through RT-PCR. All positive samples were verified through repeating the nucleic acid extraction from the original sample and RT-PCRs were performed in technical triplicates.

## Microbiome Sequencing

The purified DNA was transported to the Biosciences eastern and central Africa-International Livestock Research Institute (BeCA-ILRI) Hub in Nairobi, Kenya for the microbiome sequencing. The V3-V4 hypervariable region of the 16S rRNA gene sequenced on the Illumina MiSeq System generating 2x300 bp

paired-end reads (see methods in Appendix 1). Sequence datasets are deposited in NCBI's Sequence Read Archive (SRA) repository (Bioproject [PRJNA477349](#)).

## Bioinformatics for Microbiota Composition

To guarantee a high quality data set, microbiome analyses were performed using an open source platform, Empowering the Development of Genomics Expertise (EDGE) [33]. The EDGE Bioinformatics platform (v2.3.0) implementation is based on QIIME v1.9.1 and includes demultiplexing and quality filtering, operational taxonomic unit (OTU) clustering, taxonomic assignment, phylogenetic reconstruction, diversity analyses, and visualizations of each of these analyses. [33]. QIIME started the pre-processing step with 43,095,486 paired-end reads (in FASTQ format) by removing reads with a PHRED quality score lower than Q20. Data were further filtered to remove reads with more than one ambiguous base. If less than 50% of a read contained consecutive high-quality bases, the read was discarded. The forward and reverse reads were merged before analysis. A 94% nucleotide identity sequence clustering threshold (approximately genus level) was used to generate OTUs. The representative sequence for each OTU was then queried against the Greengenes database [34] for taxonomic classification assignment. The depth filter was set to 1000 reads – any barcoded sample that had less than 1000 assembled reads did not undergo taxonomic classification or further alpha- and beta-diversity analyses. Next, the integrated phylotype command generated the consensus taxonomy using phylotype-based approach, where taxonomy-linked sequences were assigned to OTUs based on similarity.

## Statistical Analysis

All the statistical analyses were performed using the software R (v1.2.1335, RStudio, Inc), if not otherwise stated. The proportion of positive samples by season (dry, rainy), sampling region (Serengeti, Ruaha, Selous) and meat condition (fresh, processed) was estimated using *prop.test* with continuity correction function in the 'stats' package [36]. The relative risk of a sample being positive for one or more of the select pathogens was calculated using the risk-ratio function of the 'epitools' package [35]. To investigate the additive effects of all three categories on the outcome of a sample being positive for any of the pathogens, a multivariate analysis was performed using logistic Generalized Linear Model (GLM with logit link) with region, season and meat condition included as categorical variables [36]. To examine the potential for sample size biases in the microbiota sequencing, a rarefaction analysis was conducted where the fraction of taxa was captured for each sample [37]. Results show that we were able to consistently identify all the detectable OTUs present in every sample with a minimum reading depth of 14,050 sequences per sample. This suggests that the variation of the microbiota among samples is not likely caused by low sequence coverage and that further sequencing would not detect additional genera (Supplemental Figure 1). The microbiome alpha diversity (species richness) was calculated using the Shannon Diversity Index in the package 'Vegan' [38]. Statistical analysis for the microbial diversity

between the groups was performed using Welch's t-test [36]. Hierarchical clustering of the samples based on relative abundance of phyla was performed using the package 'pvclust', with 1000 bootstrapped replications of the clusters [39]. To examine the beta diversity of the samples, Principal Coordinate Analysis (PCoA) was performed using the Bray-Curtis Matrix at the phylum level using the package 'Vegan' [38]. Groups were clustered graphing ellipses estimating the 95% confidence interval (CI) around the average value, for each variable.

## Results

### Bushmeat Samples

A total of 3,784 samples were collected in and around the three geographical study locations: Ruaha ( $n=1,688$ ; 33 villages), Selous ( $n=1,187$ ; 27 villages), and Serengeti ( $n=909$ ; 54 villages) as shown in Figure 1A. The samples represent wildlife from both high and low densities and include the predominant herbivores, such as wildebeest (*Connochaetes taurinus*), zebra (*Equus burchellii quagga*), buffalo (*Syncerus caffer*), impala (*Aepyceros melampus*), dik-dik (*Madoqua spp.*), and other less common species, including eland (*Tragelaphus oryx*), topi (*Damaliscus lunatus*), and the African savannah hare (*Lepus microtis*) (Table 1).

### Signatures of Select Agents in Bushmeat Samples

Of the 3,784 collected bushmeat samples, 77 (1.99%, CI 95%: 1.6-2.5) samples were identified as positive for at least one of the three tested pathogens, *B. anthracis*, *Brucella*, *Coxiella*. There was an overall prevalence of 0.48% ( $n = 18$ , CI: 0.3-0.8%) of *B. anthracis* in the collected bushmeat samples, 0.9% ( $n = 34$ , CI: 0.6-1.3%) prevalence of *Brucella*, and 0.7% ( $n = 25$ , CI: 0.4 -0.99%) prevalence of *Coxiella*. The proportion of the positive samples from each location indicates that the highest prevalence of *B. anthracis* was found in the Serengeti, the highest percentage of *Brucella* (% , CI) in Ruaha, and the highest percentage of *Coxiella* (% , CI) in Selous (Figure 1B). Overall, from each location, there was a 2.3% (CI: 1.5% - 3.6%) prevalence of the three select agents in the Serengeti, 1.4% (CI: 0.9% - 2.1%) prevalence in Ruaha, and 2.7% (CI: 1.9% - 3.8%) prevalence in Selous (Table 1). Of those that were positive, 0.50% (0.3 - 0.8%) were positive for *B. anthracis*, 0.90% (0.6 - 1.3%) were positive for *Brucella*, and 0.66% (0.4 - 0.99%) were positive for *Coxiella* (Figure 2). All Confidence Intervals (CI) were calculated at 95% threshold.

The samples positive for *B. anthracis* were primarily wildebeest ( $n = 10$ ) and the samples positive for *Brucella* were mostly from dik-dik ( $n = 17$ ) (Figure 2). The samples positive for *Coxiella* had a larger range of species, with impala and dik-dik being the most prevalent (Figure 2). Remarkably, all of the wildebeest samples that were positive for *B. anthracis* were fresh samples from the Serengeti collected during the rainy season (Figure 2). Also, all of the dik-dik samples positive for *Brucella* were fresh samples from Ruaha collected during the dry season (Figure 2). Only one of the *Coxiella*-positive samples was from the Serengeti and this was a fresh sample from an eland collected during rainy season (Figure 2).

# Relative Risk and Multivariate Analyses

The relative risk (RR) associated with a sample being positive for one or more of the select pathogens was determined (Figure 3). The relative risk for pathogens collected during rainy season was 1.4 (CI: 1.1 - 1.7) and significantly higher compared to the RR of 0.64 (CI: 0.5 - 0.8) for samples collected during dry season; in other words, there was a 71% higher risk of samples collected during rainy season to be positive. The relative risk of getting a pathogen from fresh samples was 1.96 (CI: 1.1 - 3.6) and significantly higher than the relative risk of 0.87 (CI: 0.08 - 0.95) for processed samples, indicating a 109% higher risk for a fresh sample being found to be positive than those that were processed. The RR of samples from Ruaha was 0.8 (CI: 0.7 - 0.9) and it was significantly lower than samples collected from the other locations, in particular, Selous (RR = 1.2; CI: 0.97 - 1.4) (Figure 3).

Multivariate analysis was undertaken to investigate the combined effects of all three categories on the outcome of a sample being positive for any of the pathogens. Results showed that samples collected during the rainy seasons increase the log odds of being positive by 0.70, compared to the dry season. On the contrary, processed samples decrease the log odds of being positive by 1.1, compared to processed samples. Among the regions analysis indicated that compared to Ruaha, samples collected from Selous increase the log odds of being positive by 0.70, and samples collected from Serengeti increase the log odds of being positive by 0.70 (Table 2).

## The Microbiome Associated with Select Pathogen-Positive Bushmeat Samples

Microbiome characterization of the 77 positive samples showed that the two most abundant phyla across all samples were *Firmicutes* and *Proteobacteria* (Figure 4) (Supplemental Table 2). Rarefaction analyses showed consistent identification of the detectable OTUs present in each sample with a minimum reading depth of 14,050 sequences per sample [37]. This suggests that the variation of the microbiota among samples is not likely caused by low sequence coverage (Supplemental Figure 1). The alpha and beta diversity for the different variables associated with each sample was assessed. The first two principal coordinates of the Principal Coordinate Analysis (PCoA) accounted for 95% of the total variation. The first principal coordinate was driven by the effect of the relative abundance of *Proteobacteria* (coefficient = 0.86) and *Firmicutes* (-0.90) and the second principal coordinate by the relative abundance of *Bacteroidetes* (0.99) (Supplemental Figure 2).

In addition, lower alpha diversity and significant differences in beta diversity were observed in *B. anthracis*-positive samples, and samples collected from the Serengeti, which were primarily wildebeest. The results showed that *B. anthracis*-positive samples had significantly lower alpha diversity than either of the *Brucella*- or *Coxiella*-positive samples (p-value < 0.001; Supplemental Figure 3) and tended to cluster separately in the Principal Coordinate Analysis (PCoA) (Supplemental Figure 2). There was a

similar pattern for wildebeest samples, which showed lower overall diversity and clustering separately from dik-dik or other species ( $p$ -value < 0.001; Supplemental Figures 2 and 3).

Hierarchical clustering based on the relative abundance of phyla grouped the samples into five distinct clusters (Figure 4A). The associated Approximately Unbiased (AU) and Bootstrap Probability (BP) are represented at the base node of each cluster (AU > 95 are statistically significant). Cluster I ( $n=6$ ) contained six samples, of which five were *Brucella*-positive with the majority of the samples being freshly collected (Figure 4). Cluster II ( $n=18$ ) included 12 *B. anthracis*-positive samples collected from Serengeti, of which eight were from fresh wildebeest samples collected during the rainy season. Cluster III ( $n=24$ ) included 16 *Coxiella*-positive samples, of which 15 were fresh, with thirteen of these collected from the Selous ecosystem. Samples in cluster IV ( $n=24$ ) included 17 *Brucella*-positive samples collected from Ruaha and Selous, four *Coxiella*-positive samples collected from Selous, and three *B. anthracis*-positive samples collected from the Serengeti ecosystem. The final cluster, cluster V ( $n=5$ ) was the most diverse and included three *Brucella*-positive and two *Coxiella*-positive samples (Figure 4).

The relative abundance was also analyzed at the family level (Supplemental Figure 4). At this level, the top three most abundant taxa in these samples include, *Streptococcaceae* (26%), *Enterobacteriaceae* (22%), and *Moraxellaceae* (14%). The alpha diversity revealed differences according to pathogen, host species, and region (Supplemental Figure 5) and the beta diversity clustered the wildebeest samples separately from the other species (Supplemental Figure 6).

Interestingly, when the data were investigated at the genus-level, hierarchical clustering tended to group the samples by pathogen. The *B. anthracis*-positive samples were high in *Bacillus*, which was not found in the *Brucella*- or *Coxiella*-positive samples (Figure 5). On the other hand, the *Brucella*- and *Coxiella*-positive samples showed a higher abundance of species represented by the *Lactococcus* and *Macroccoccus* genera (Figure 5). These differences were further confirmed through examining the alpha and beta diversity associated with the samples. Within each variable, samples that had lower alpha diversity were *B. anthracis*-positive, wildebeest samples, and those collected from Serengeti (Supplemental Figure 7), which were also shown to be the most significant in the PCoA analysis (Supplemental Figure 8).

## Discussion

A goal of this study was to assess the potential for risk of human exposure to three select agents, *Bacillus anthracis*, *Brucella spp.*, and *Coxiella burnetii* associated with bushmeat handling and consumption in Tanzania. Our initial focus was on three major locations in Tanzania: Ruaha and Selous in the south and the Serengeti in the north. Sites were selected to represent the distinct environments (habitat and climate) with diverse wildlife composition and density, and proximity to major urban centers (including Arusha, Dodoma and Dar es Salaam) where the bushmeat is often sold.

While the presence of DNA signatures does not imply the presence of a viable organism, given that bushmeat consumption is as high as 5 meals per week in some households, and with an overall

pathogen prevalence of 2% (1.6–2.6%), this risk of exposure remains a concern and worthy of further investigation. This is especially problematic considering that the risks associated with endemic infections such as *Brucella* and *Coxiella* often go unrecognized and remain under-reported despite the considerable risks of causing disease [40].

Relative risk associated with positive DNA signatures was assessed for variables including season, sample condition, animal species, and regions (ecosystems) and revealed notable associations. There was a higher risk of a sample being positive if it was collected during a rainy season, or if the sample was fresh, in contrast there was a lower risk if the sample was collected from Ruaha, than Serengeti or Selous (Fig. 3). Studies have shown that climate-related factors, such as prolonged rain, can contribute to disease outbreaks [41]. Changes in weather conditions force the movement and interactions of animals where rainy seasons and/or droughts affect animals spatial grazing patterns [42, 43]. Also, exposure to anthrax may be higher for migratory ungulates like wildebeest that are found in different parts of the regions throughout the year [3]. This may be one reason why there is a higher likelihood of positive samples being collected during the rainy season. Also, during the rainy season there may be a higher consumption of fresh samples, which is consistent with the higher risk of positives in fresh samples, probably associated with methods of processing being unavailable or unsuitable during this season, or simply a higher availability of fresh meat. High salt, UV exposure, and boiling of processed samples may reduce pathogen loads associated with the fresh meat samples [44, 45]; however, UV light does not necessarily decrease the microbial content of meat [46, 47]. Results also indicate that there is a lower risk of a sample being positive if it was collected from Ruaha. There are some substantial differences among the three ecosystems, both biotic and abiotic, and we have no evidence of a dominant factor affecting the samples, and suggest that multiple components might be contributing to the relative risks associated with each ecosystem [48, 49].

Findings indicated that most of the differences in the microbiome are driven by the relative abundance of Firmicutes and Proteobacteria, as demonstrated by the PCoA (Supplemental Fig. 2). This is expected, since *B. anthracis* belongs to the Firmicutes phylum and *Brucella* and *Coxiella* both belong to Proteobacteria. The microbiome analysis revealed significant lower alpha diversity and PCoA clustering associated with the *B. anthracis*-positive samples, wildebeest samples, and samples collected from the Serengeti (Supplemental Fig. 2, 3, 5, 6, 7, and 8). These results are also supported by the hierarchical clustering at both the phylum- and the genus-levels, where the *B. anthracis*-positive samples tended to cluster together (Fig. 4 - Cluster II and Fig. 5). This is expected since the highest abundance of *B. anthracis*-positive samples were in the Serengeti, where most of the wildebeest samples were collected (Fig. 1). These results are consistent with previous studies that documented many Anthrax outbreaks in Northern Tanzania, and particularly in the Serengeti [21, 50–52].

Samples that were collected in the same condition were generally available to be sold to the public, hence they represent microbial communities that are endogenous to the samples, as well as the microbiota that is acquired during harvesting, processing, and transporting. While the analysis suggests that fresh samples, samples collected during rainy season, and samples collected from the Serengeti and Selous

had a higher likelihood of being positive for one of the three pathogens, positive samples carrying DNA signatures of the tested select agents were also collected during dry season, from other animal species, and ecosystems. Interestingly, the results also revealed that a subset ( $n = 39$ ) of purported “bushmeat” samples from Selous that were instead speciated as being of cattle in origin had a combined prevalence of 28.7% of the three select agents, highlighting a potential public health risk associated with the endemic diseases in livestock production. This suggests that *B. anthracis*, *Brucella*, and *Coxiella* circulate throughout the year in all the ecosystems and confirms their endemicity and the recurrent risk for the nearby communities, including the larger markets where the meat is regularly sold.

While this study represents the first comprehensive assessments of the prevalence of DNA signatures of select agents in bushmeat in Tanzania, there are several unanswered questions that remain. For instance, it remains unclear how these DNA signatures represent / correlate with presence of viable pathogens and, with this, the risk of transmission to humans. It is also unclear whether there are any differences in the health risks associated with exposure during harvest, butchering, handling or consuming of bushmeat. Future studies investigating the role of other select agents (bacterial and viral) in the ecosystems, and the role of endemic and emerging strains in the microbial community, caused by sedentary and migrating animal species in the region are also warranted since the extent of an outbreak varies from year to year and place to place. In conclusion, the current investigations provide important insights and a rational basis for the formulation of future studies to assess and address the public health and emerging infectious disease risks associated with bushmeat harvesting, trade, and consumption in Tanzania and elsewhere.

## Declarations

## Acknowledgments

The authors would like to thank the following agencies for permission to conduct research in the Serengeti ecosystem in Tanzania: Tanzania Commission for Science and Technology, Tanzania Wildlife Research Institute (permit number TWRI/RS-331/VOL.II/2013/58 and TWRI/RS-331/VOL.II/2013/88), Tanzania National Parks (permit number TNP/HQ/C.10/1), Ngorongoro Conservation Area Authority (permit number NCAA/D/240/Vol.XXVIII/54), and Tanzania Wildlife Authority (permit number CB.517/519/01/14). Collection of samples would not have been possible without the cooperation of enumerators, rangers and management authorities.

The authors would also like to thank Karen Davenport, Blake Hovde, and Mark Flynn from Los Alamos National Laboratory for their technical support with The Empowering the Development of Genomics Expertise- “EDGE” analysis. The authors would also like to thank other *Bushmeat Biosecurity Research Consortium* members for their continued hard work and dedication throughout the project.

## Author Contributions Statement

V.K. and J.J.B. developed the study concept and design. E.E., A.M., and A.B.E. collected the samples and the metadata associated with each sample. R.K., M.A.S., B.L., S.L., and L.M. performed sample processing. T.T., C.K.T., and F.S. performed sequencing. R.K. and M.A.S. performed the bioinformatic and statistical analysis. R.K. and M.A.S. analyzed data and drafted the manuscript. I.M.C and P.J.H. advised on the data analysis. B.L., E.E., A.M., T.T., I.M.C., S.C.F., A.B.E., D.R., S.S., S.L., L.M., C.K.T., F.S., P.G., F.M., P.J.H., J.J.B., and V.K. critically revised the content. All authors have read and approved the manuscript.

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## **Additional Information**

### **Availability of Data and Materials**

The datasets generated and analyzed during the current study are available in the NCBI Sequence Read Archive (SRA) repository, <https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP151593>.

### **Competing Interests**

The authors declare that they have no competing interests.

### **Funding**

This research was supported by grant from the U.S. Department of Defense, Defense Threat Reduction Agency, Biological Threat Reduction Program, Project # HDTRA1-16-1-0005 (to V.K. and J.J.B. ).

# Funding Statement

This research was supported by grant from the U.S. Department of Defense, Defense Threat Reduction Agency, Biological Threat Reduction Program, Project # HDTRA1-16-1-0005 (V.K and J.J.B.).

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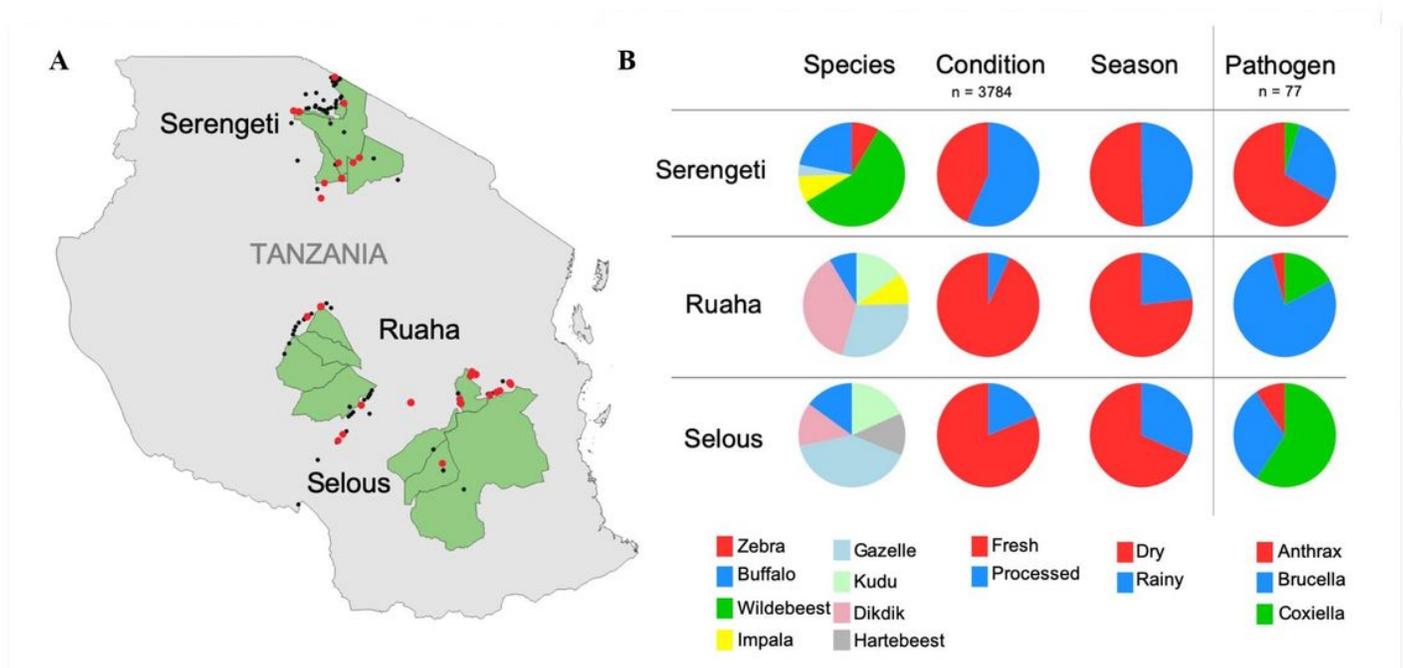
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## Tables

Due to technical limitations, tables are only available as a download in the Supplemental Files section.

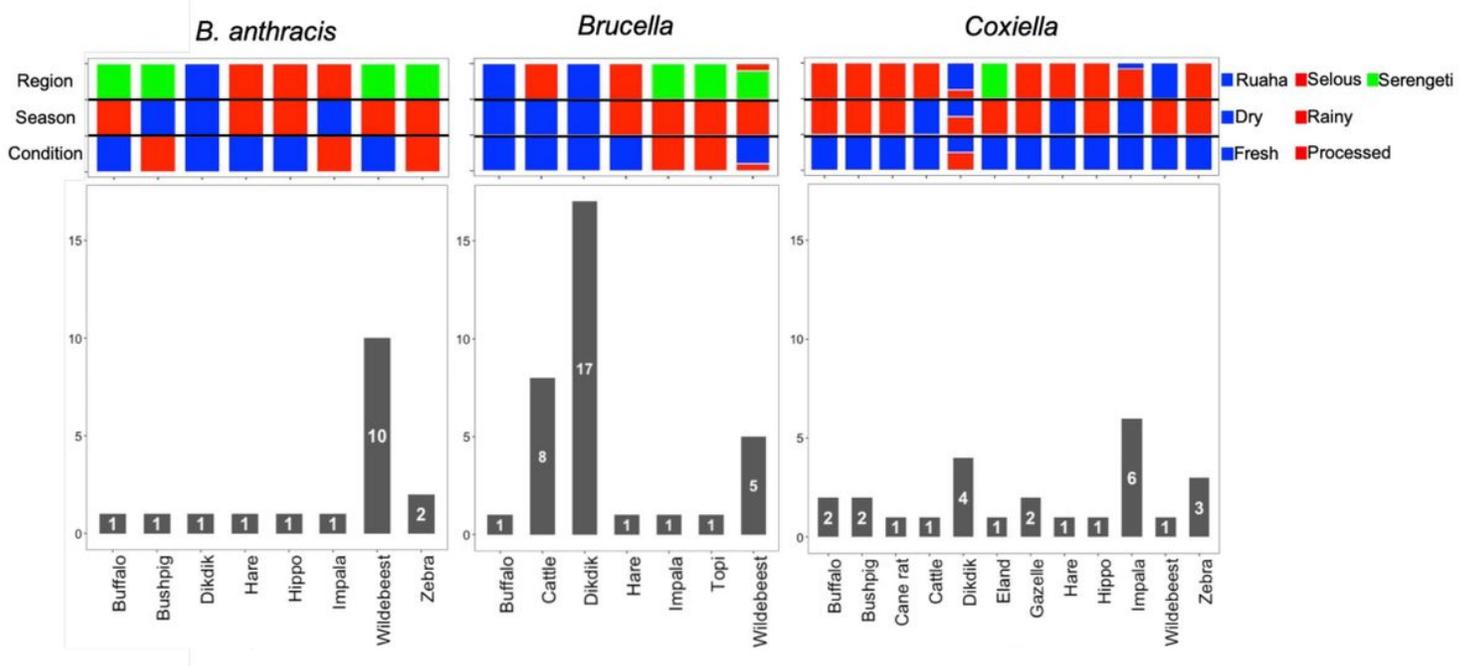
## Figures



**Figure 1**

Map and distribution of bushmeat samples collected from the three ecosystems in Tanzania. A) Map of the sample collection sites. In the map, the three regions are shown in green. The points show the distribution of samples collected (black circles) and samples positive for one of the three pathogens (red

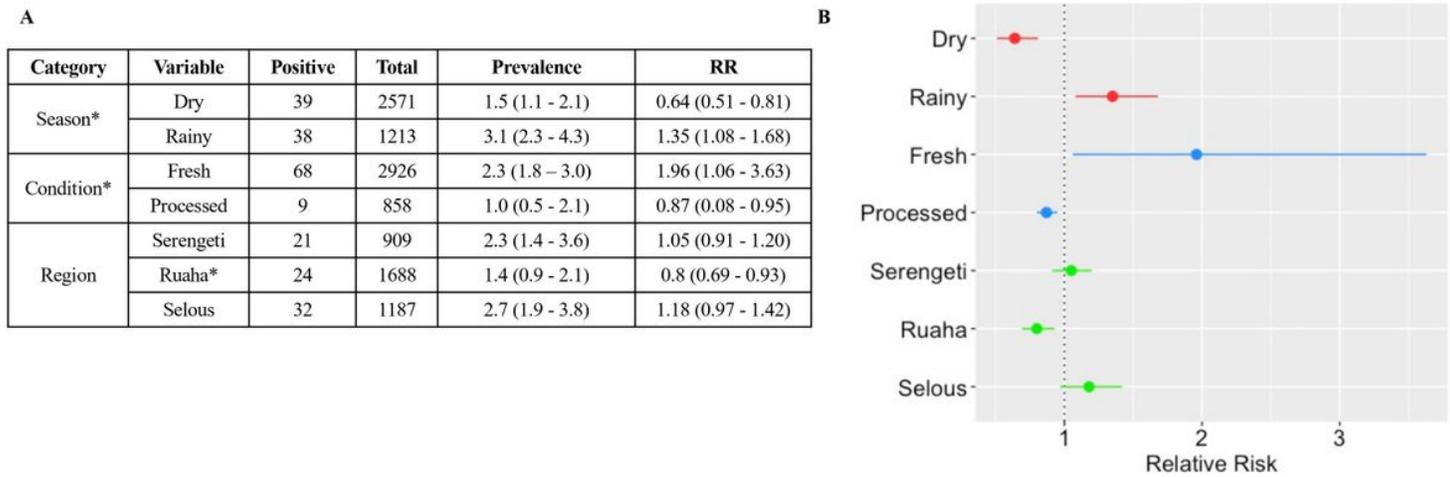
circles). B) Distribution of the collected bushmeat samples. The pie charts show the stratification of the collected bushmeat samples. For the species category (n = 3784), the top 5 species most abundant species collected from the particular region are shown: Serengeti – Wildebeest (green), Buffalo (blue), Zebra (red), Impala (yellow), Gazelle (light blue); Ruaha – Dik-dik (pink), Gazelle (light blue), Kudu (light green), Impala (yellow), Buffalo (blue); Selous – Gazelle (light blue), Buffalo (blue), Dik-dik (pink), Kudu (light green), Hartebeest (gray). For the condition category (n = 3784), the red represents fresh samples and blue represents processed samples. For the season category (n = 3784), dry and rainy seasons are represented by the red and blue colors, respectively. The pathogen column (n = 77) shows the proportion of each pathogen from each region with B. anthracis shown in red, Brucella in blue, and Coxiella in green. The samples were collected from both dry and rainy seasons, Ruaha (dry; I = 1297; rainy = 391), Selous (dry = 813; rainy = 374), Serengeti (dry = 461; rainy = 448), and from two sample conditions, Ruaha (fresh = 1571; processed = 117), Selous (fresh = 962; processed = 223), Serengeti (fresh = 393; processed = 516). Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.



**Figure 2**

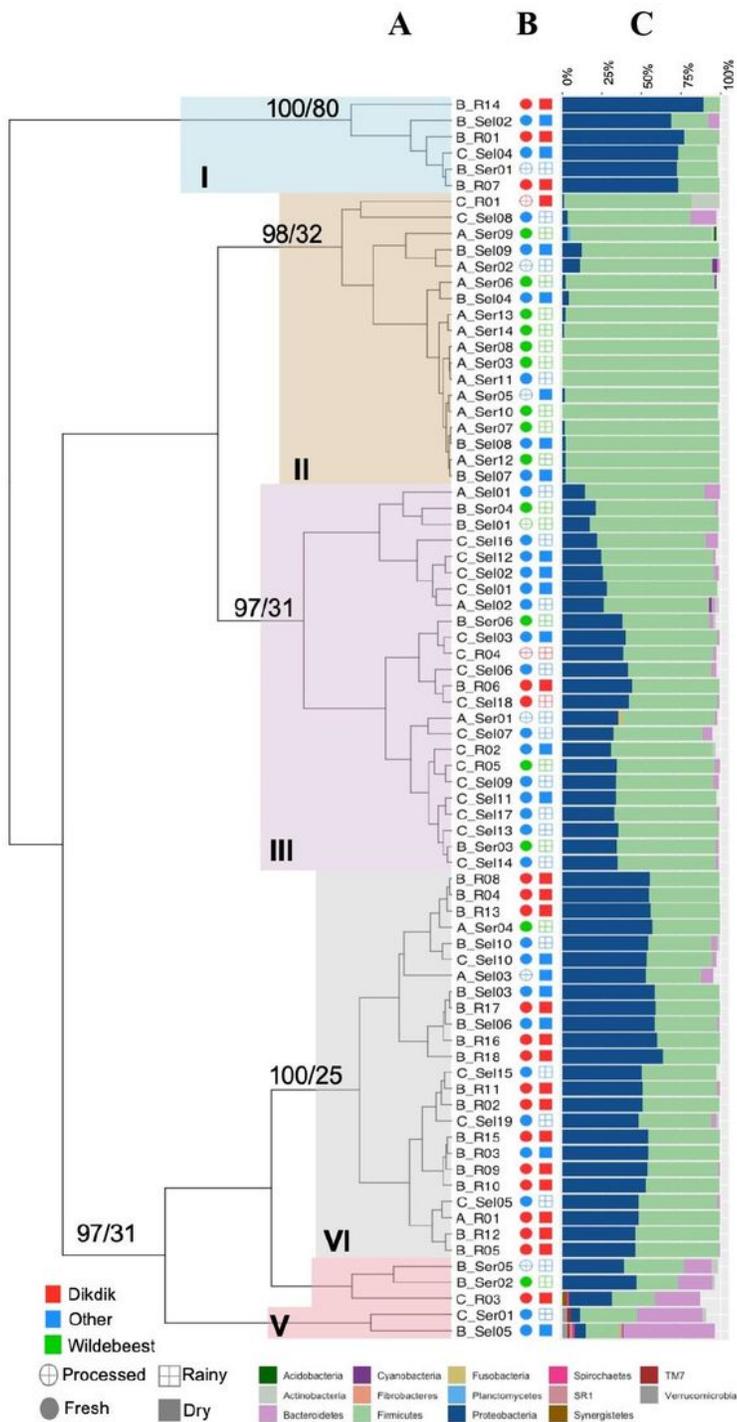
Counts of Bushmeat Samples Positive for Select Agents. The count of positives for each species are included in the bar charts (with the total count in the bar with white font), separated by B. anthracis-positive in the left panel, Brucella-positive in the middle panel, and Coxiella-positive in the right panel. The coloring above the bar graphs show the proportion of samples within the species that are in each category (Region, Season, and Condition). The blue color represents samples collected from Ruaha, collected during dry season, and fresh samples. The red color represents samples collected from Selous, collected during Rainy season, and processed samples. The green color represents samples collected

from the Serengeti. For instance, in the *B. anthracis* panel, one positive fresh (Blue) buffalo sample was collected during rainy season (Red), from Serengeti region (Green).



**Figure 3**

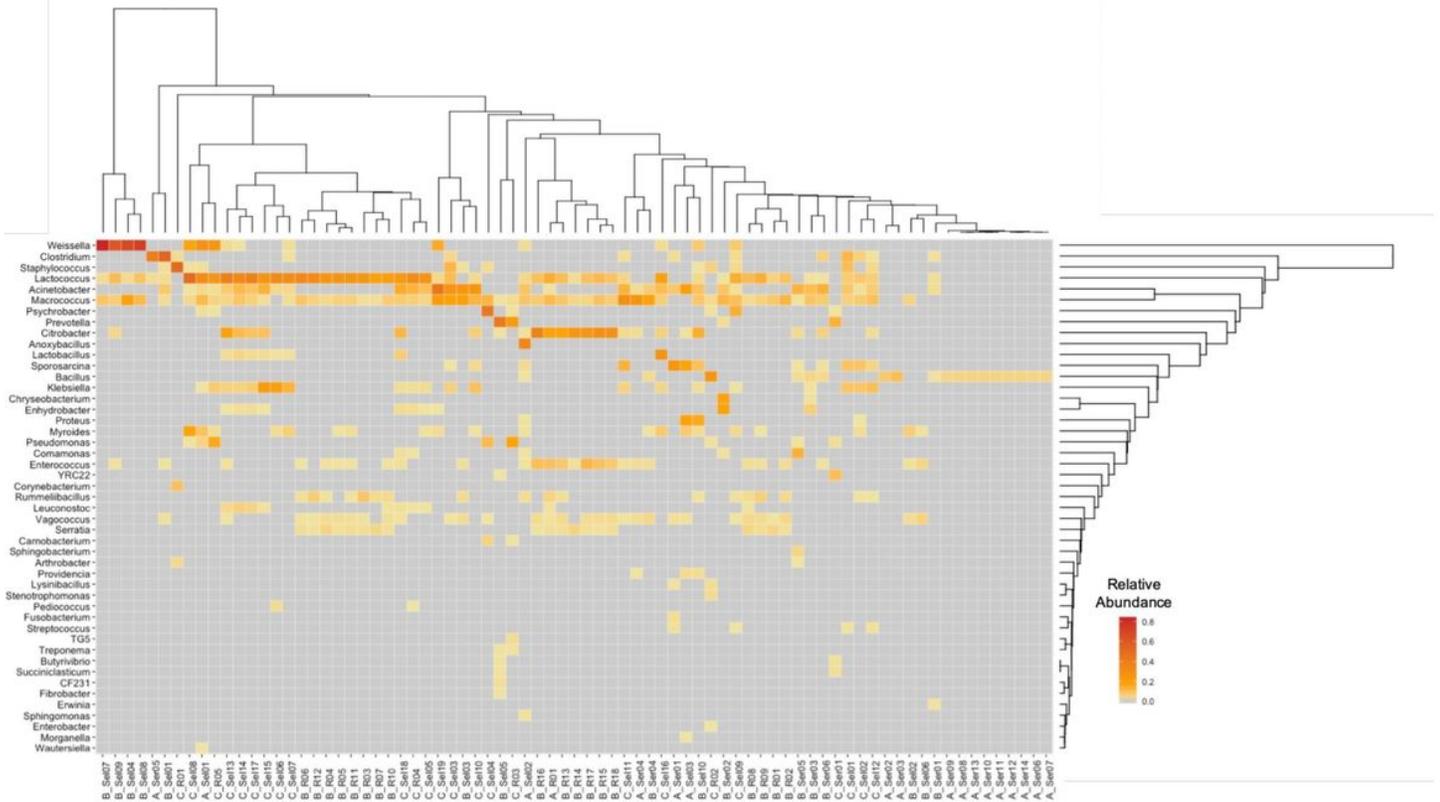
Relative risk (RR) of the positive bushmeat samples associated with different variables. A) Counts (positive and total samples), prevalence and RR associated with each variable. The 95% confidence intervals are reported in parenthesis. B) Graph of the RR for each variable. The relative risk (pointS) and 95% confidence interval (lines) for each variable are reported for the seasonal data (red), sample condition (blue) and regions (green). Results indicate that there is a 71% higher risk of a sample collected from rainy season being positive than samples collected during dry season. There is a 109% higher risk of a fresh sample being positive than processed sample. There is also a 64% lower risk of a sample collected from Ruaha being positive that the other regions (the RR of samples collected from both Selous and Serengeti is 1.44). Significant differences in RR analysis are reported (\*= $p < 0.05$ ).



**Figure 4**

Hierarchical clustering of the samples positive for one of the three pathogens based on the relative abundance of phyla in each sample. A) Hierarchical clustering of samples. The samples grouped into 5 clusters: I – blue, II – tan, III – purple, IV – gray, V – red. The samples are labeled with the first letter representing the pathogen (A – B. anthracis, B – Brucella, C – Coxiella) and the ending representing the ecosystem (R – Ruaha, Sel – Selous, Ser – Serengeti). The AU/BP values for the clustering are shown at

the base of each node. B) Sample metadata. These columns show the other metadata associated with each sample. The open circles represent processed samples, and the closed are fresh samples. The open squares are from rainy season and the closed squares are from dry season. The shapes are colored according to species of wildlife from which the bushmeat originated: dik-dik – red, wildebeest – green, all other species – blue. C) Bar graph of the relative abundance of phyla. The relative abundance of phyla > 1% is shown in the stacked bar graph. The colors corresponding to each respective phylum is in the legend at the bottom.



**Figure 5**

Heatmap of the genus-level relative abundance in the samples positive for one of the three pathogens. The heatmap shows the relative abundance for any genus present at > 1%. The color ranges from pale yellow (low abundance) to dark orange (high abundance). Hierarchical clustering was performed for both the samples and the genera. The samples are labeled with the first letter representing the pathogen (A – B. anthracis, B – Brucella, C – Coxiella) and the ending representing the regions (R – Ruaha, Sel – Selous, Ser – Serengeti).

## Supplementary Files

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