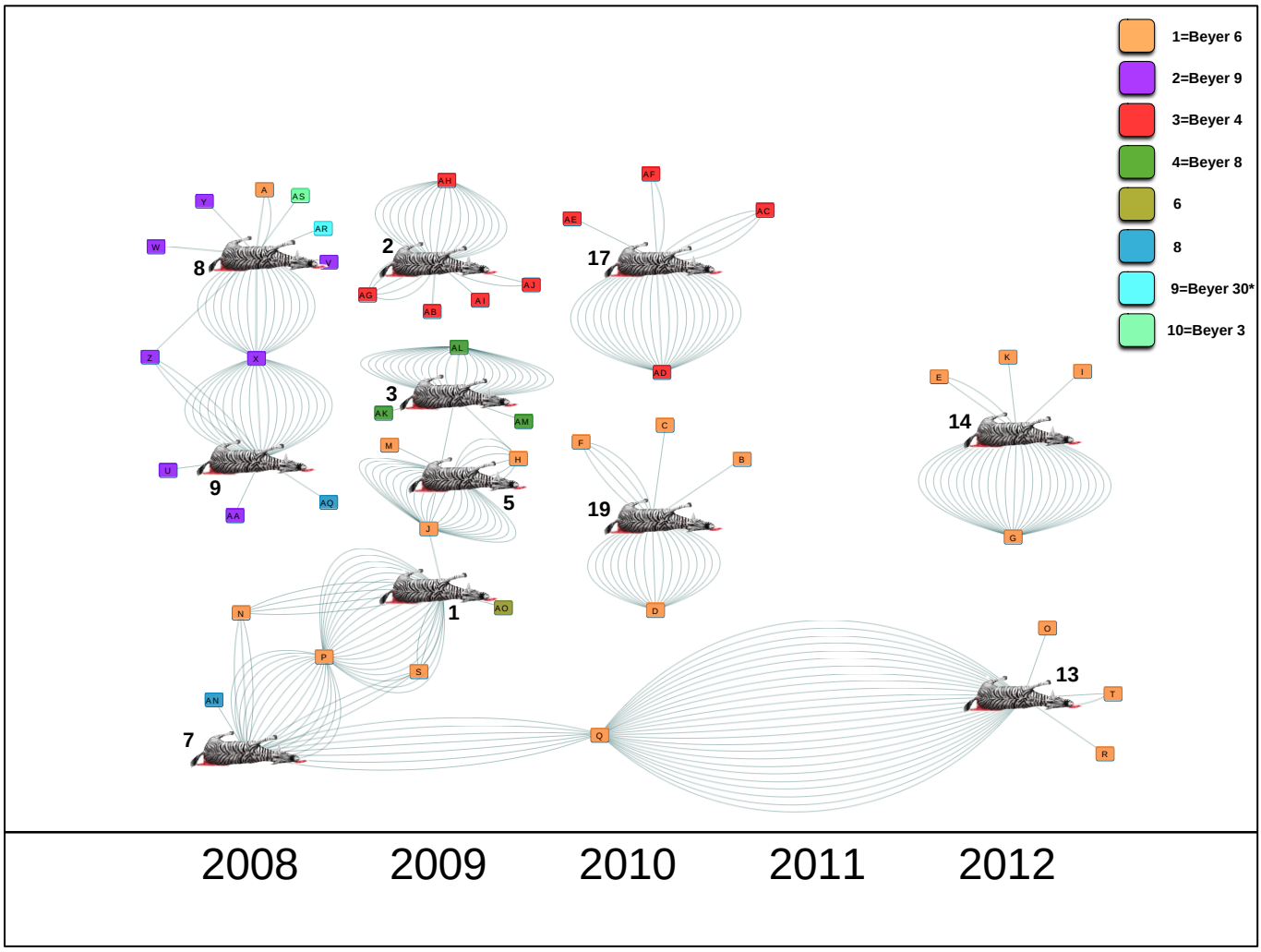
Supplementary Information:

SI Results



SI Figure 1. Diversity of *B. anthracis* populations within and among terminal infections from 11 zebra carcasses in ENP. The network consists of individual carcasses (numbered) and unique SNR genotypes (rectangles); colors represent shared MLVA types. Each line connecting carcass to genotype is an individual isolate (*N*=30 isolates/carcass). Carcasses are oriented by year of death. MLVA genotypes found in these zebra are compared to Beyer et al. (1).

SI Table 1. Summary of MLVA/SNR haplotypes frequencies, number of samples and segregating sites in each zebra. Haplotypes correspond to vrrB2, cg3, Bam5, Bam1, Bam44, Bam15, vrrC1, Bam3, vrrB1, Bam53, Bam28, vrrC2, Bam31, Bam13, vrrA, Bam25, Bam34, bam24, Bam21, pX01, pX02, Bam51, Bam23, Bam22, Bam30, HM.9, HM.6, HM.93, HM.2 in the same order. The last column (111) corresponds to the laboratory experiment performed.

Haplotype	**1**	**2**	**3**	**5**	**7**	**8**	**9**	**13**	**14**	**17**	**19**	**111**
00000000000000000000000000000000	17	15	22	28	19	11	14	17	21	20	11	36
00000000000000000000000000000001	8	5	1	1	5	1	3	3	8	5	5	7
00000000000000000000000000000010	0	0	0	0	0	0	0	0	0	1	4	0
00000000000000000000000000000011	0	0	1	0	0	0	0	0	0	0	1	0
00000000000000000000000000000100	0	1	0	0	0	0	1	1	0	0	0	0
00000000000000000000000000000101	0	1	0	0	0	0	0	0	0	0	0	0
00000000000000000000000000001000	0	0	0	0	1	0	0	2	0	0	0	0
00000000000000000000000000001001	1	0	0	0	0	0	0	0	0	0	0	0
00000000000000000000000000001010	0	0	0	0	0	0	0	0	0	1	0	0
00000000000000000000000000010000	0	0	1	0	0	0	0	0	0	0	0	0
00000000000000000000100000000	0	0	2	0	0	0	0	0	0	0	0	0
00000000000000000000100000001	0	0	1	0	0	0	0	0	0	0	0	0
00000000000000000010000000000	1	0	0	0	0	0	0	0	0	0	0	0
00000000000000000100000000000	0	1	0	0	0	0	0	0	0	0	0	0
00000000000000000100000000001	0	2	0	0	0	0	0	0	0	0	0	0
00000000000001000000000000000	2	1	0	0	0	0	0	0	0	0	0	0
00000000000001000000100000001	0	0	0	0	0	0	0	0	0	0	0	2
00000000001000000000000000000	0	0	0	0	0	0	0	0	0	0	0	1
00000010000000000000000000000	0	0	0	0	0	0	0	1	0	0	0	0
00000010000000000000000001000	0	0	0	0	0	0	0	0	0	0	1	0
Number of samples	29	26	28	29	25	12	18	24	29	27	22	46
Number of Segregating Sites	4	4	3	2	4	3	2	4	2	2	1	2

SI Table 2. A) The following is an example of the type of data analyzed and transformations performed for the analyses. This dataset corresponds to one of the observed zebra (zebra 2) sampled for *B. anthracis*. In this table columns represent the MLVA and SNR region sampled and the numbers in each cell represent the allele type for that particular region.

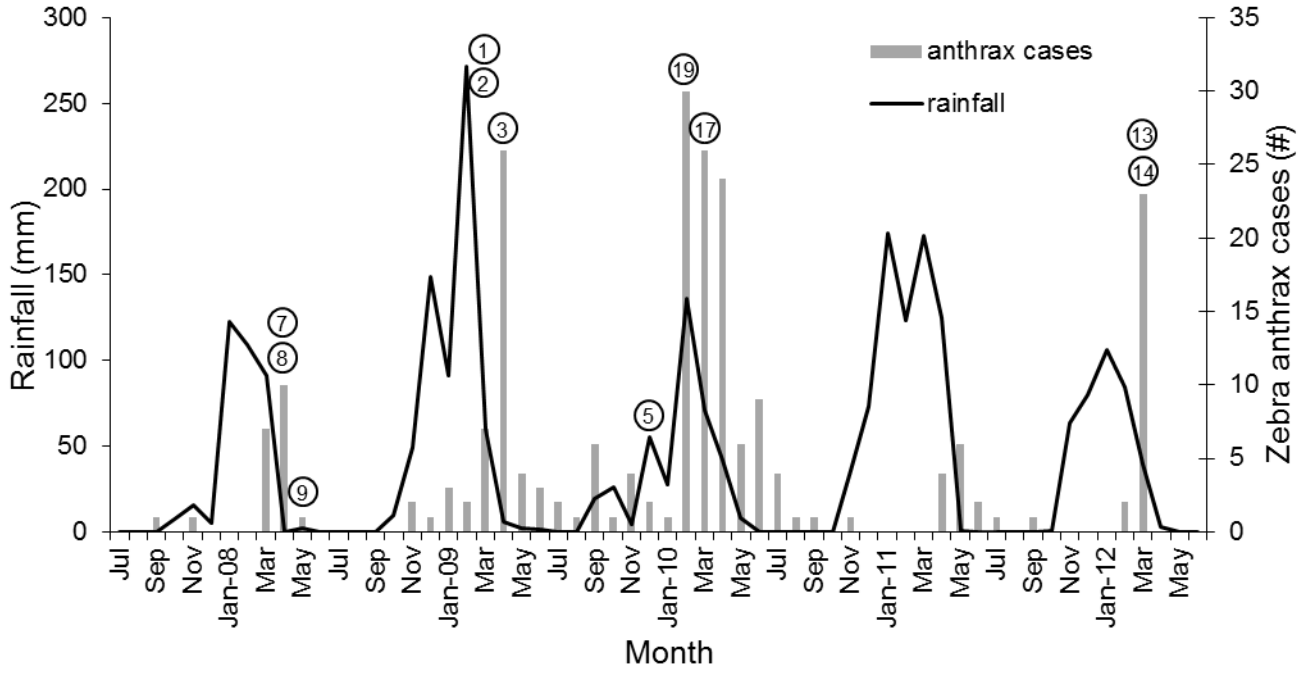
vrrB2	cg3	Bam5	Bam1	Bam44	Bam15	vrrC1	Bam3	vrrB1	Bam53	Bam28	vrrC2	Bam31	Bam13	vrrA	Bam25	Bam34	bam24	Bam21	pX01	pX02	Bam51	Bam23	Bam22	Bam30	HM.9	HM.6	HM.93	HM.2
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	587	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	587	663	130	137	499	635	718	728	74	91	118	120
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	587	663	130	137	499	635	718	728	74	91	118	122
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	90	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	696	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	120
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	120
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	120
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	121
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	122
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	91	118	120
155	154	225	317	409	600	606	607	224	232	499	524	696	588	308	394	379	597	663	130	137	499	635	718	728	74	92	118	116

B) Following we found the most common allele in each region and coded it as 0 and the rest as 1 to give the following table of MLVA-SNR haplotypes for each sample in each zebra.

vrrB2	cg3	Bam5	Bam1	Bam44	Bam15	vrrC1	Bam3	vrrB1	Bam53	Bam28	vrrC2	Bam31	Bam13	vrrA	Bam25	Bam34	bam24	Bam21	pX01	pX02	Bam51	Bam23	Bam22	Bam30	HM.9	HM.6	HM.93	HM.2
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1

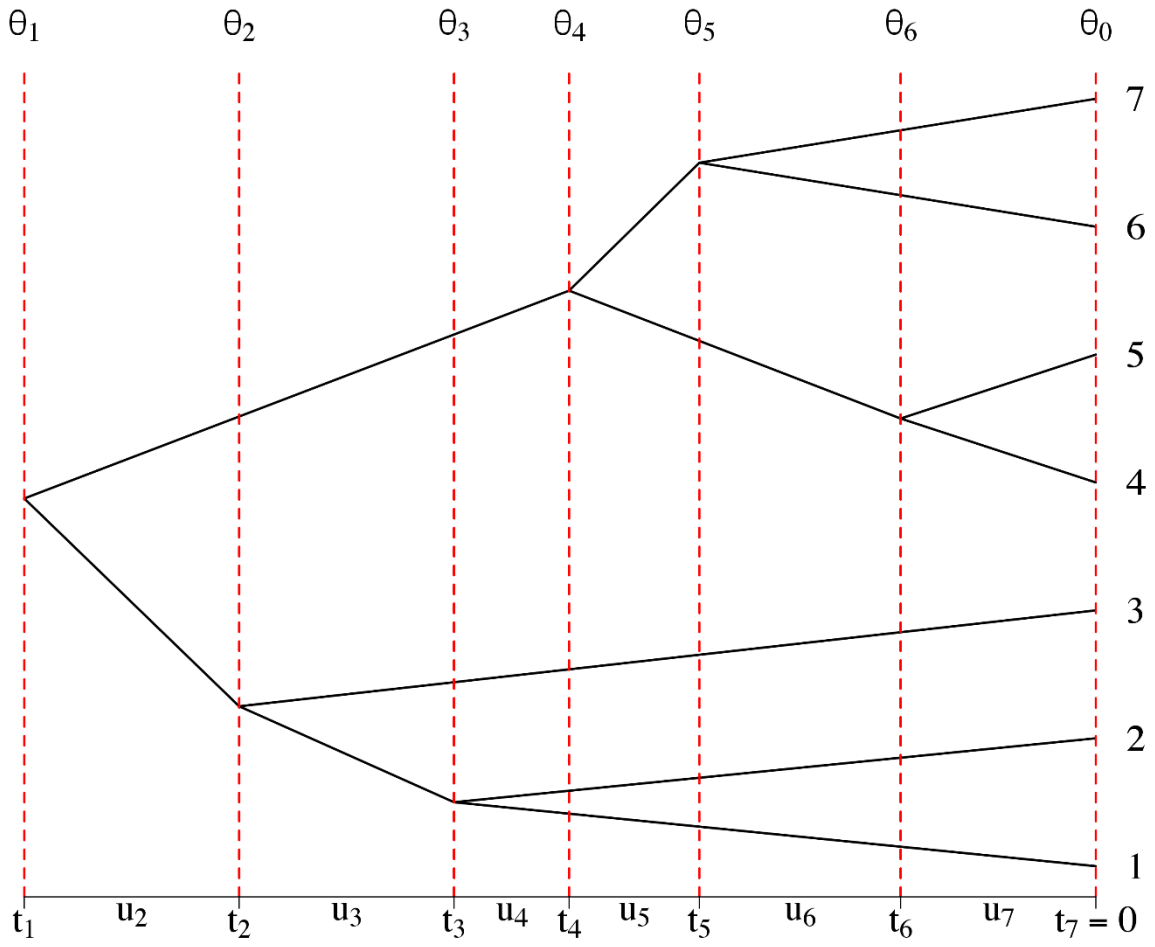
C) We obtained the frequencies of each haplotype and the number of segregating sites. In this case, there were seven haplotypes present in the sample and four segregating sites represented in the table below. In this case, we are only showing the codes of the haplotypes for the segregating sites. We define a segregating site as a MLVA-SNR region that has more than one allele in the set of samples from a single zebra.

Bam13	bam24	HM.6	HM.2	Frequency
0	0	0	0	15
0	0	0	1	5
0	0	1	0	1
0	0	1	1	1
0	1	0	0	1
0	1	0	1	2
1	0	0	0	1



SI Figure 2. Monthly accumulated rainfall and number of confirmed anthrax cases recorded for plains zebra (*Equus quagga*) in central Etosha from July 2007-June 2012. The carcasses sampled in this study are denoted above their month of death in circles with identifying numbers.

SI Figure 3. Random Coalescent tree of seven individuals used to explain the notation used to derive the models used in the data analyses. In the figure, **t** represent Coalescent times, **u** represent inter-Coalescent times and **θ** represents the average number of mutations per generation.



Reference:

1. Beyer W, *et al.* (2012) Distribution and Molecular Evolution of *Bacillus anthracis* Genotypes in Namibia. *PLoS Negl Trop Dis* 6(3):e1534.