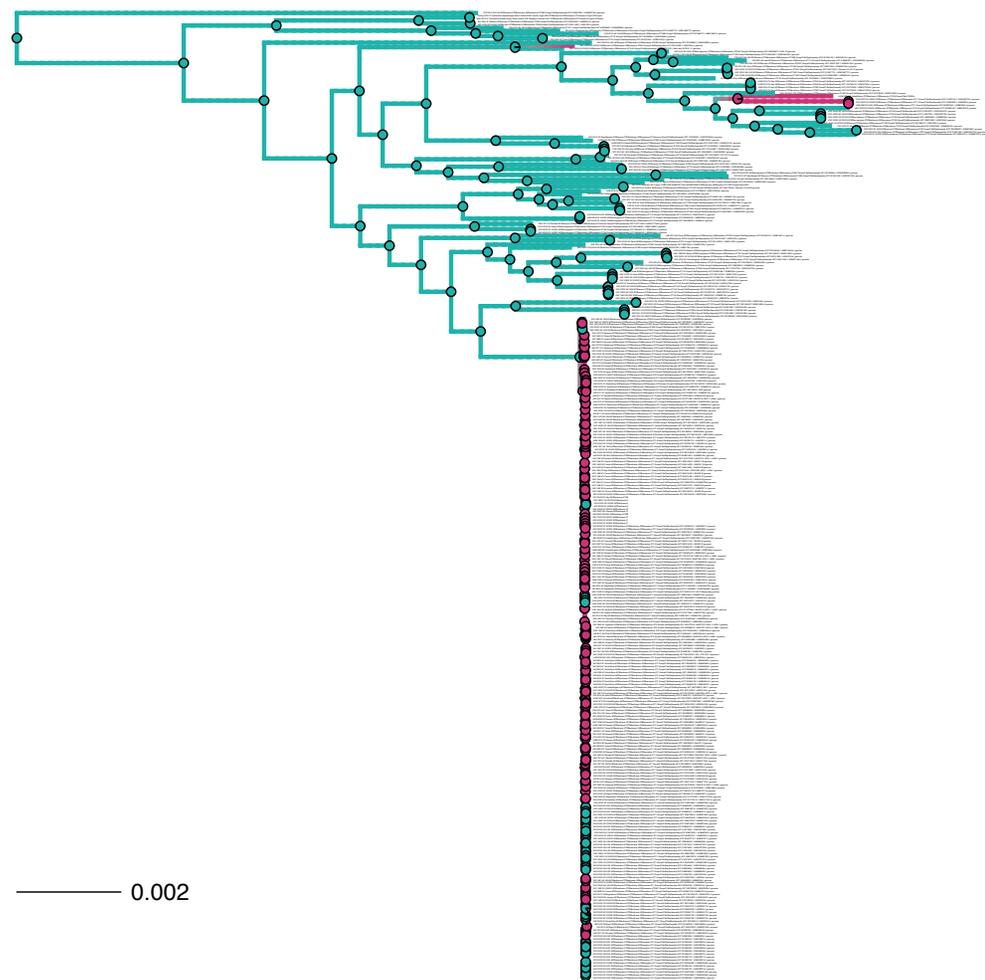
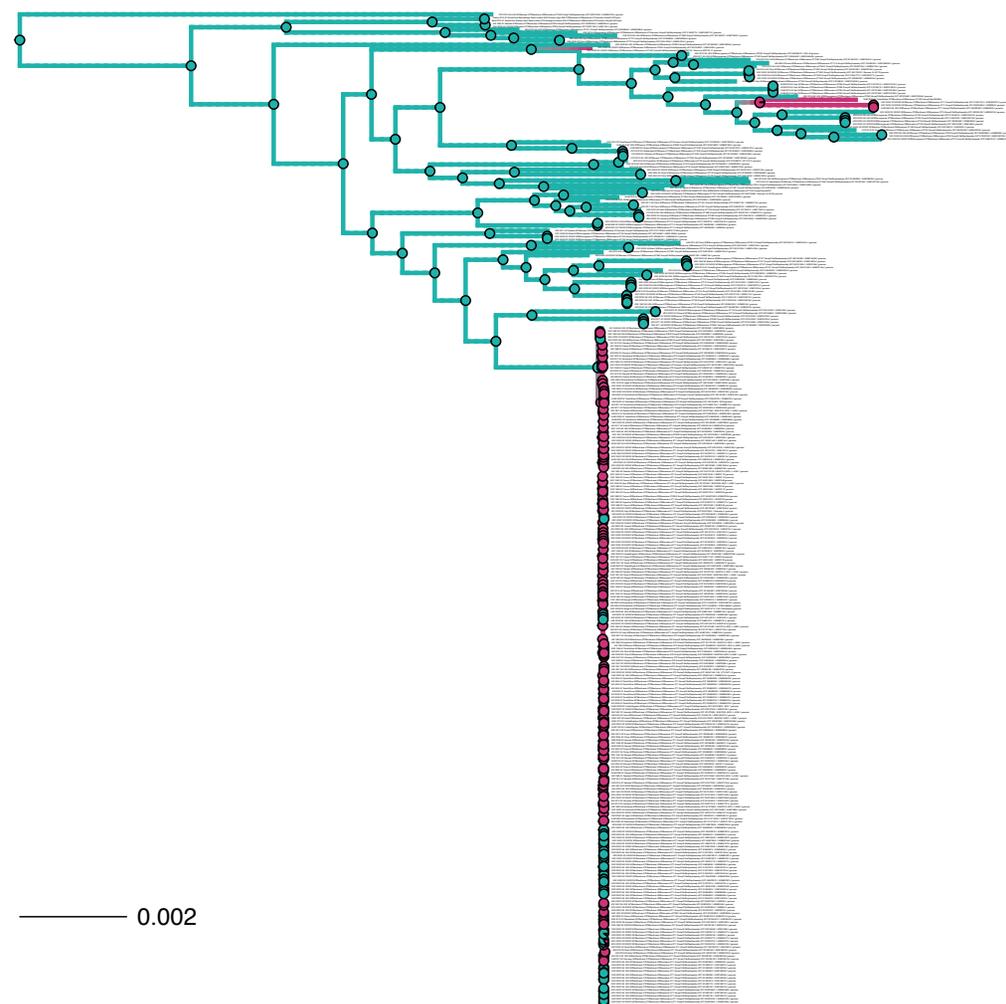


A.



0 PP(state=Non-Anthrax) 1
length=0.008

B.



0 PP(state=Non-Anthrax) 1
length=0.008

Supplementary Figure S4. Maximum likelihood phylogeny constructed using core SNPs detected among 326 genomes assigned to the Genome Taxonomy Database (GTDB) *B. anthracis* species, plus GTDB *B. paranthracis* outgroup genome *B. cereus s.l.* strain AH187 (NCBI RefSeq Assembly Accession GCF_000021225.1; omitted for readability). Tree edge and node colors correspond to the posterior probability (PP) of anthrax toxin gene absence (i.e., “Non-Anthrax”), obtained using an empirical Bayes approach, in which a continuous-time reversible Markov model was fitted, followed by 100 simulations of stochastic character histories using the fitted model and tree tip states. Root node prior probabilities for “Anthrax” and “Non-Anthrax” states were (A) equal (i.e., 0.5 each) or (B) estimated using the `make.simmap` function in the `phytools` package in R. Trees are rooted using the outgroup genome, and branch lengths are reported in substitutions per site.