

Supporting information for:

Comparative assessments of BTX natural attenuation by quantitative PCR of a catabolic gene, signature metabolites, and compound-specific isotope analysis

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SI includes three figures

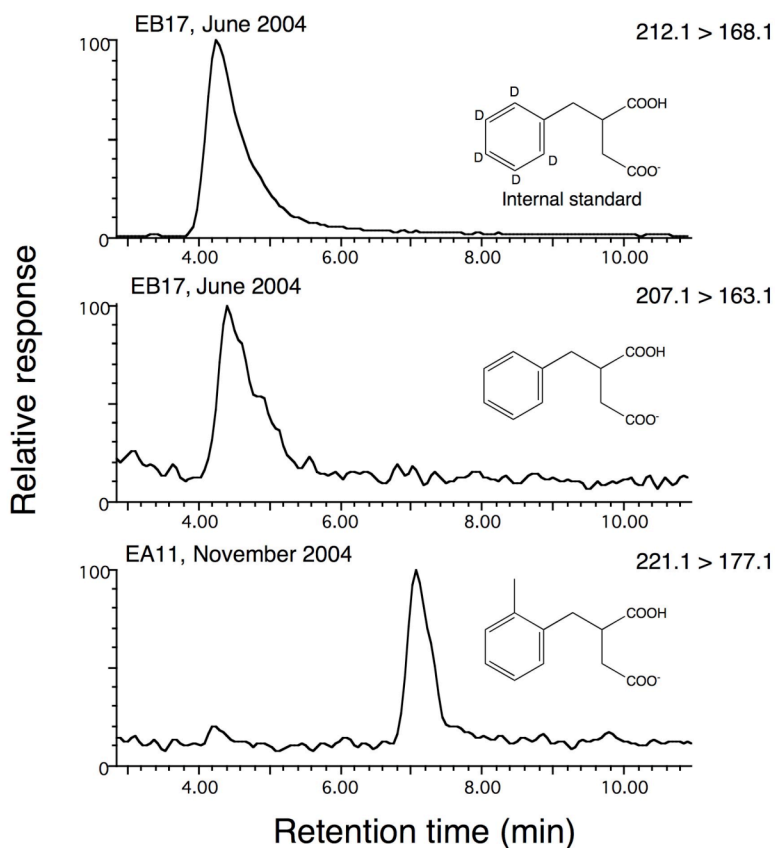


Figure S1. Mass chromatograms for LC/MS/MS (selected reaction monitoring) analysis of the internal standard BS-*d*₅ (m/z 212 \rightarrow 168 transition) (top), BS (m/z 207 \rightarrow 163 transition) (middle), and 2MeBS (m/z 221 \rightarrow 177 transition) (bottom). As shown, BS and the deuterium-labeled internal standard have the same retention time.

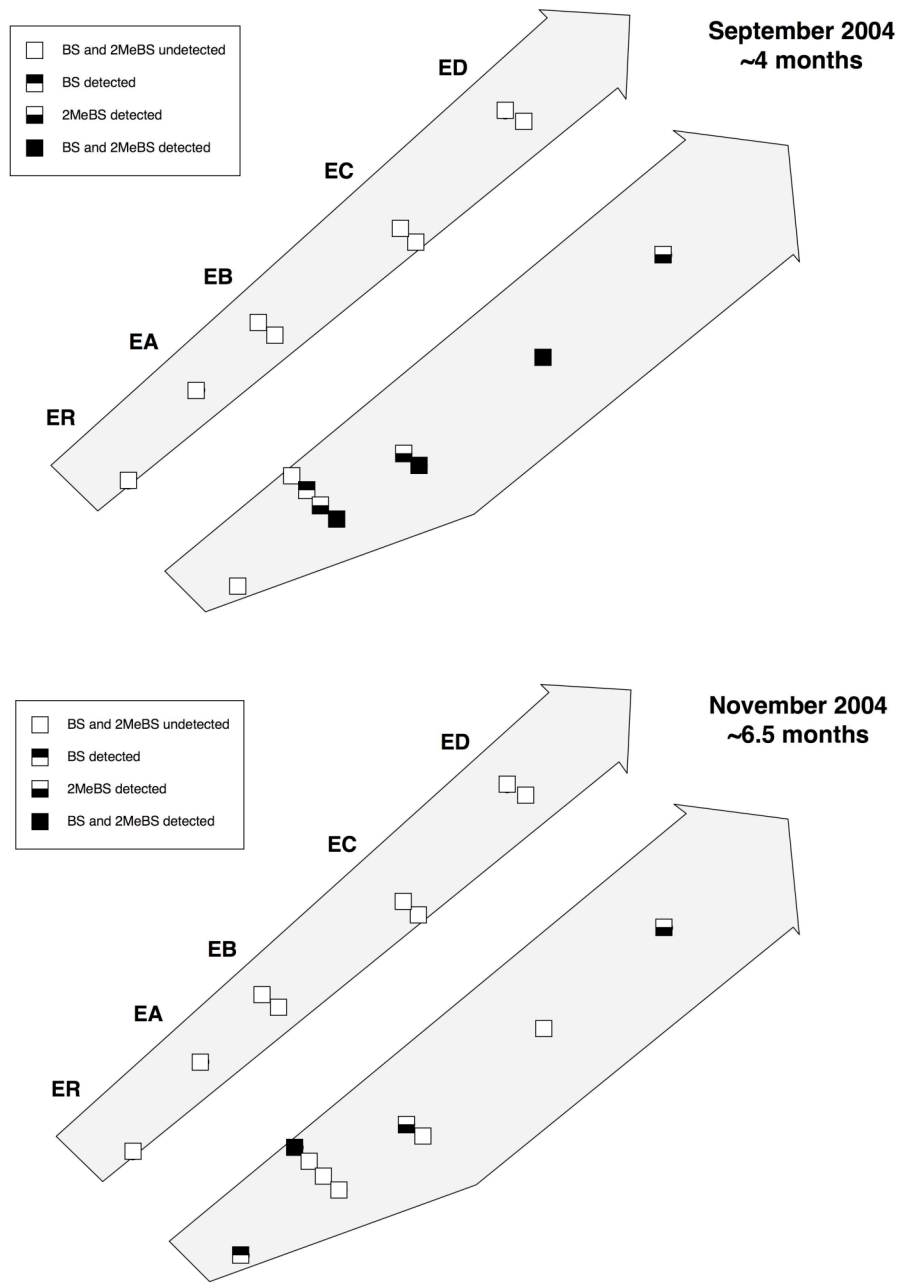


Figure S2. Signature metabolite [benzylsuccinate, or BS, and (2-methylbenzyl)succinate, or 2MeBS] detections at two sampling times: ~4 months after the controlled release began (upper), and ~6.5 months after the controlled release began (lower).

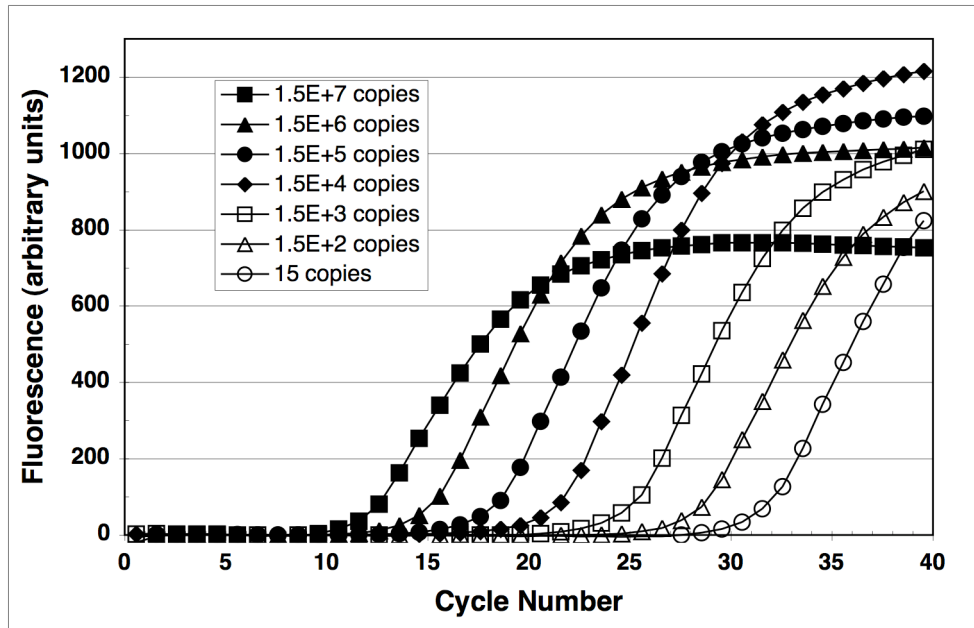
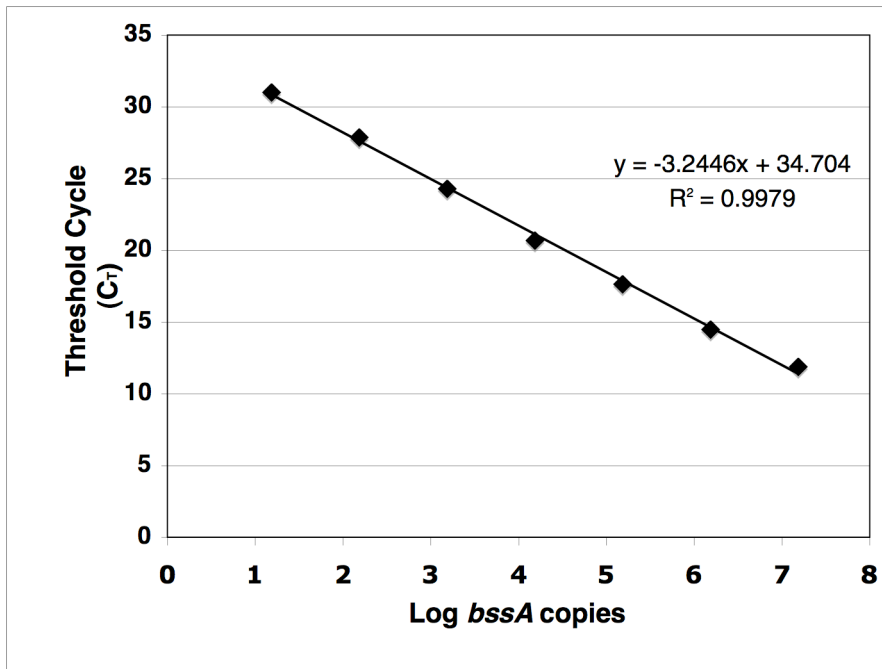
A**B**

Figure S3. Example of a calibration curve for *bssA* (using genomic DNA from strain PRTOL1, a SRB). (A) Fluorescence vs. PCR cycle number for seven *bssA* standard concentrations. A line denotes the threshold level; the threshold cycle (C_T) is defined as the PCR cycle at which fluorescence exceeds the threshold level. (B) Threshold cycle vs. log *bssA* copies for the data presented in panel A.