Analysis of bacteria stress responses to contaminants derived from shale energy extraction

Inês C. Santos[a,b*], Alex Chaumette [a], Jonathan Smuts[c], Zacariah L. Hildenbrand[b,d], Kevin A. Schug[a,b]

[a] Department of Chemistry and Biochemistry, The University of Texas at Arlington, Arlington, TX, USA

[b] Affiliate of the Collaborative Laboratories for Environmental Analysis and Remediation, The University of Texas at Arlington, Arlington TX 76019

[c] VUV Analytics, Inc., Cedar Park, TX, USA

[d] Inform Environmental, LLC, Dallas TX 75206

[*] Corresponding author at: 700 Planetarium Pl.; Box 19065; Arlington, TX 76019-0065, USA. Tel.: +1 817 272 0618; e-mail address: ines.santos@uta.edu.

Electronic Supplementary Information (ESI)

Fig. S1 Relative composition of FAMEs in each microorganism grown in the presence of 4% benzene, ethanol, propanol, toluene, and salt: A) *E. coli*; B) *K. oxytoca*; C) *A. hydrophila*; D) *P. aeruginosa;* E) *P. putida*; F) *P. stutzeri*; G) *B. cereus;* and H) *B. subtilis*.

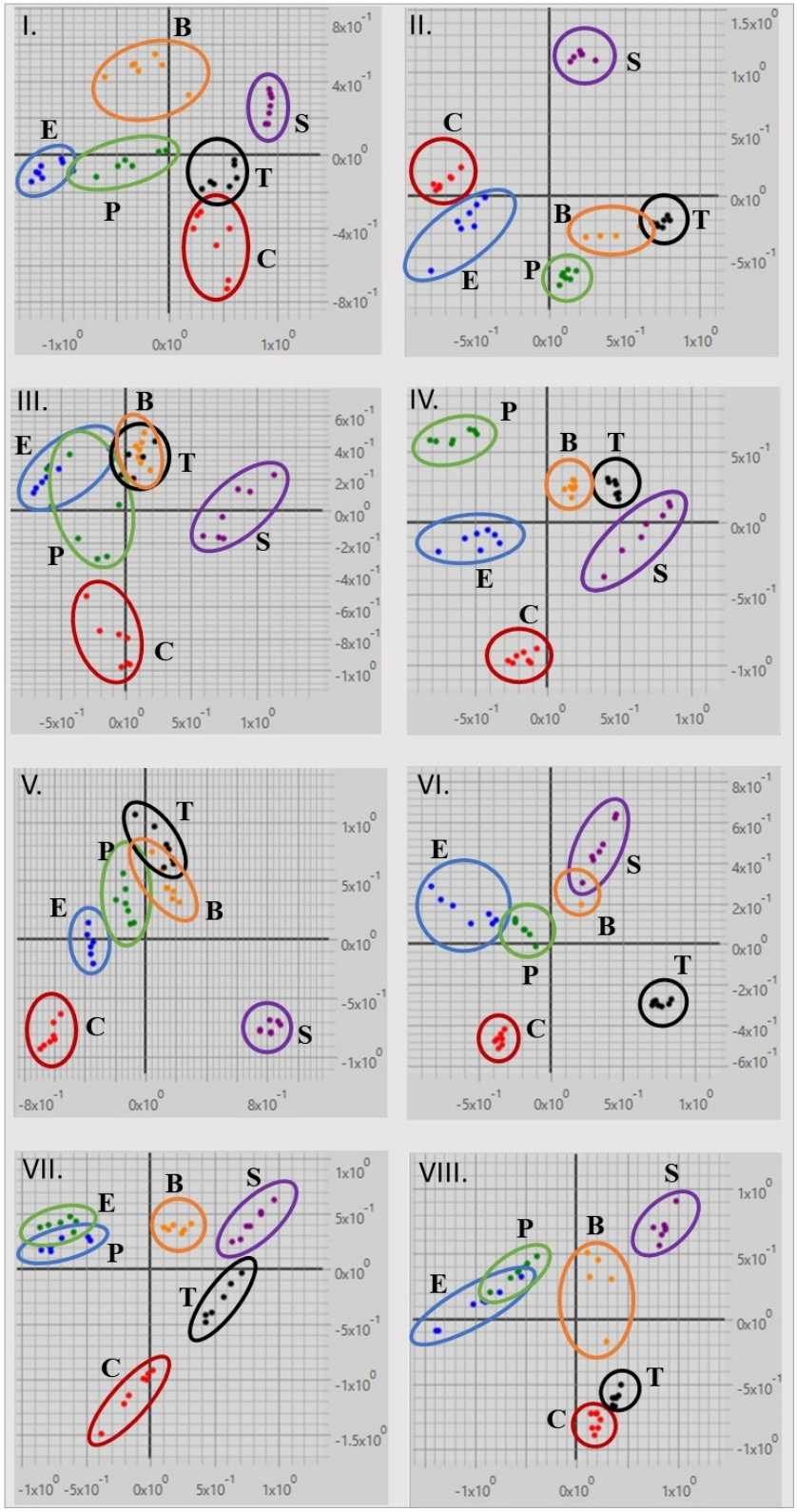

Fig. S2 PLS-DA analysis of the protein profiles of I. *E. coli*; II. *K. oxytoca*; III. *B. cereus*; IV. *B. subtilis*; V. *A. hydrophila*; VI. *P. aeruginosa*; VII. *P. stutzeri*; VIII. *P. putida*, grown under different environments:

E (blue), 4% ethanol; P (green), 4% propanol; B (orange), 4% benzene; T (black), 4% toluene; S (purple), 4% salt; C (red), control.