TABLE S1.

Complete list of *E. coli* K-12 mutants tested in this study and their impact on HS-SPME/GC-MS propanol signal.

Mutants with no or strongly impaired[1] 1-propanol HS-SPME/GC-MS signal
adhE, tdcB, crp, cyaA, fnr, tdcC, ***tdcE***
Mutants with partial[2] 1-propanol HS-SPME/GC-MS signal
rng, nadB
Mutants with wild-type[3] 1-propanol HS-SPME/GC-MS signal
eutG, fucO, yqhD, yiaY, glpQ, ackA, atoA, atoD, ilvI, ilvB, tynA, ilvA, leuA, mhpE, gldA, gcl, yfdU, poxB, tdh, ydjG, pta, tdcD, pflB, thrB, rcsB, pspF, phoP, slyA, evgA, lexA, rpoS, hns, arcA, soxR, cpxR, oxyR, aspC, luxS, relA, recA, fruR, ltaE, kbL, fis

In bold: mutants with severe biofilm formation defect preventing meaningful comparison with wild-type 1-propanol production in biofilm conditions.

[1] <30% of WT HS-SPME/GC-MS signal

[2] 30-80% of WT HS-SPME/GC-MS signal

[3] ≥85% of WT HS-SPME/GC-MS signal