

Supplemental Material for “**Augmentation of granular anaerobic sludge with algalytic bacteria enhances methane production from microalgal biomass**”

Anna Doloman <sup>1</sup>, Yehor Pererva <sup>1</sup>, Michael H. Cortez <sup>2</sup>, Ronald C. Sims <sup>1</sup>, Charles D. Miller <sup>1,\*</sup>

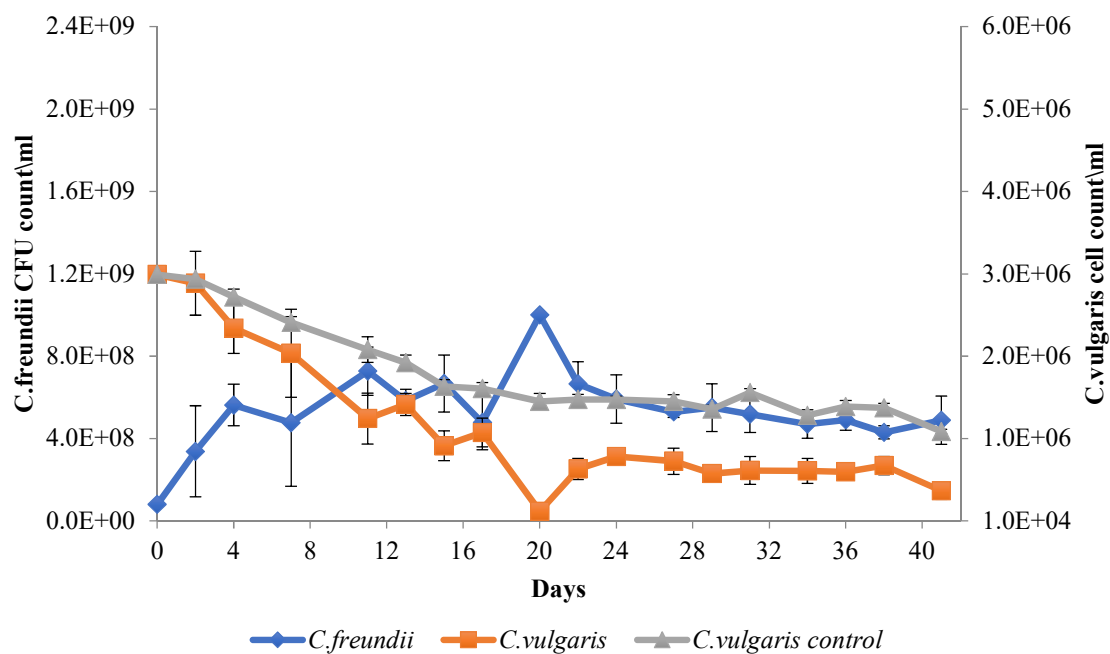
<sup>1</sup> Department of Biological Engineering, Utah State University, Old Main Hill 4105, Logan, UT, USA, 84322-4105; anna.doloman@gmail.com (A.D); ye.pererva@gmail.com (Ye.P.); ron.sims@usu.edu (R.C.S); charles.miller@usu.edu (C.D.M)

<sup>2</sup> Department of Mathematics and Statistics, Utah State University, Old Main Hill 3900, Logan, UT, USA, 84322-3900; michael.cortez@usu.edu (M.H.C)

\* Correspondence: charles.miller@usu.edu; Tel.: +1(435)881-2101 (C.D.M)

Figure S1. Changes in the bacterial and microalgal cell counts over time, during incubation at 35±2 °C in the dark. (a) Bacterium *Citrobacter freundii* sp. isolate 13 with microalgae *Chlorella vulgaris*; (b) bacterium *Escherichia coli* K12 with microalgae *Chlorella vulgaris*.

a.



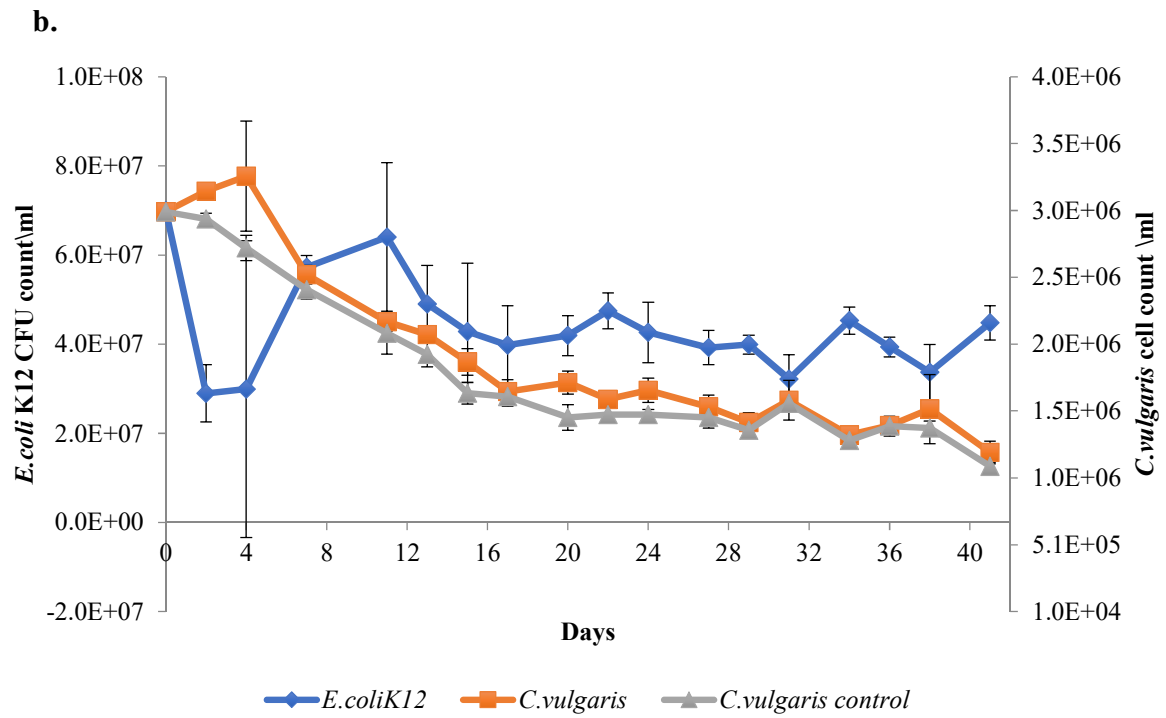


Figure S2. Gel electrophoresis of PCR-amplified *cfa* gene fragment of *Citrobacter* spp. in all the tested anaerobic digestion samples. Labels: (ng) negative control, (1) *C. freundii*13 genomic DNA, (2) Granules control, (3) Granules+Bacteria, (4) Algae+Granules, (5) Algae+Granules+Bacteria

