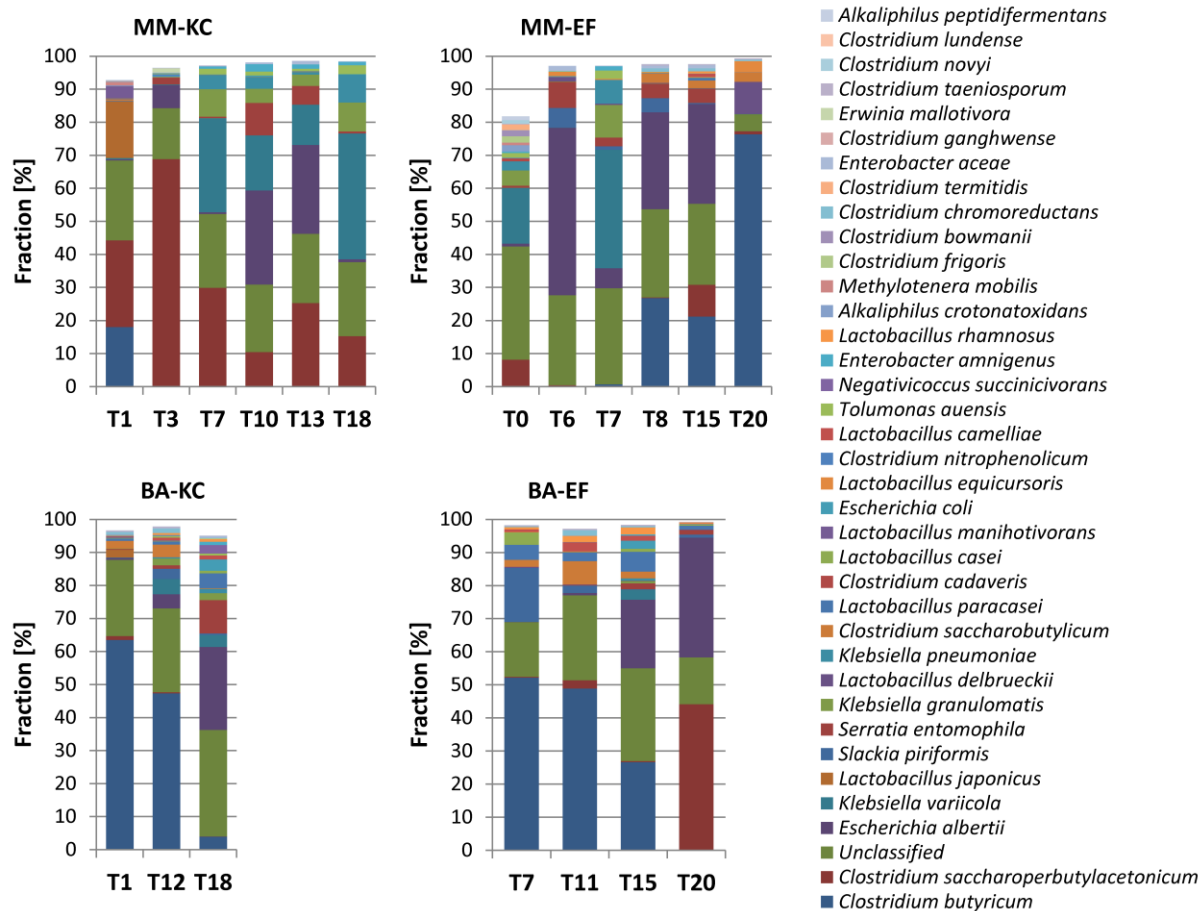


1 SUPPLEMENTARY MATERIAL

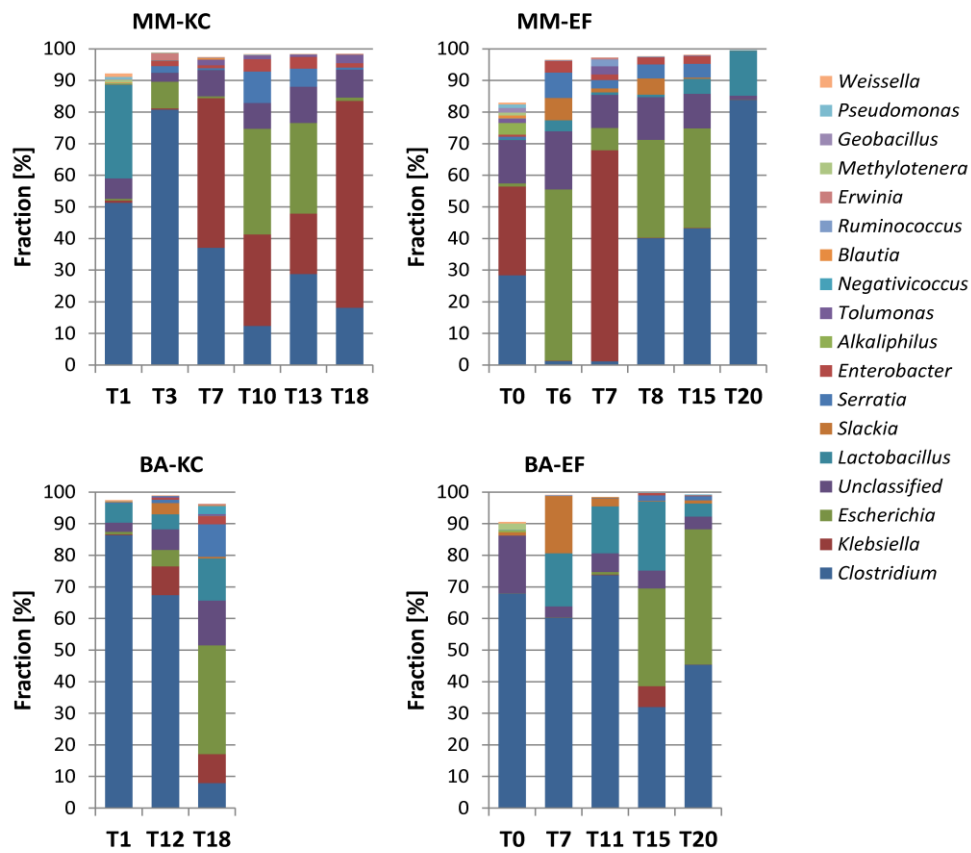
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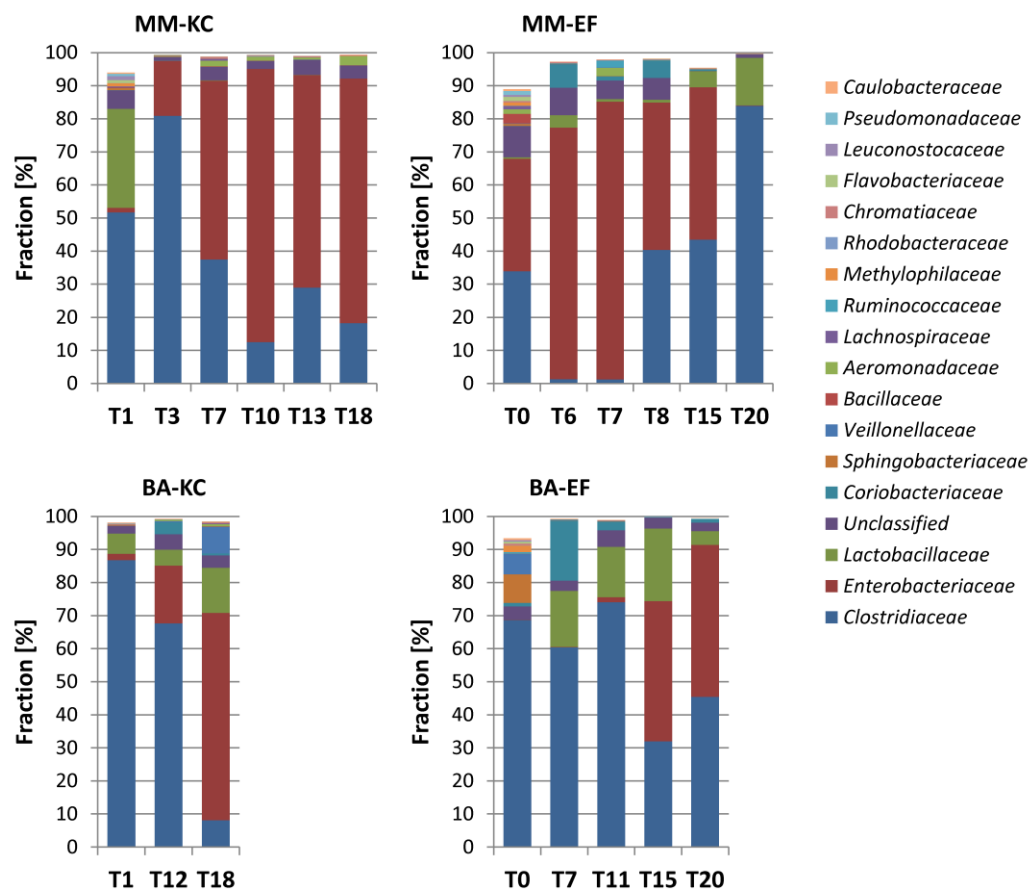
3

4 **S1.** Metagenomic classification of the MMC at the species level. Results of batch transfers, during the enrichment of
5 activated sludge. MM-KC = Minimum Medium with Kinetic Control (21h); MM-EF = Minimum Medium with End of
6 Fermentation (72h); BA-KC = Basal Medium with Kinetic Control (21h); BA-EF = Basal Medium with End of
7 Fermentation (72h). T0-T20 = Transfer numbers. Species appearing at frequencies below 1% in all samples were
8 omitted.

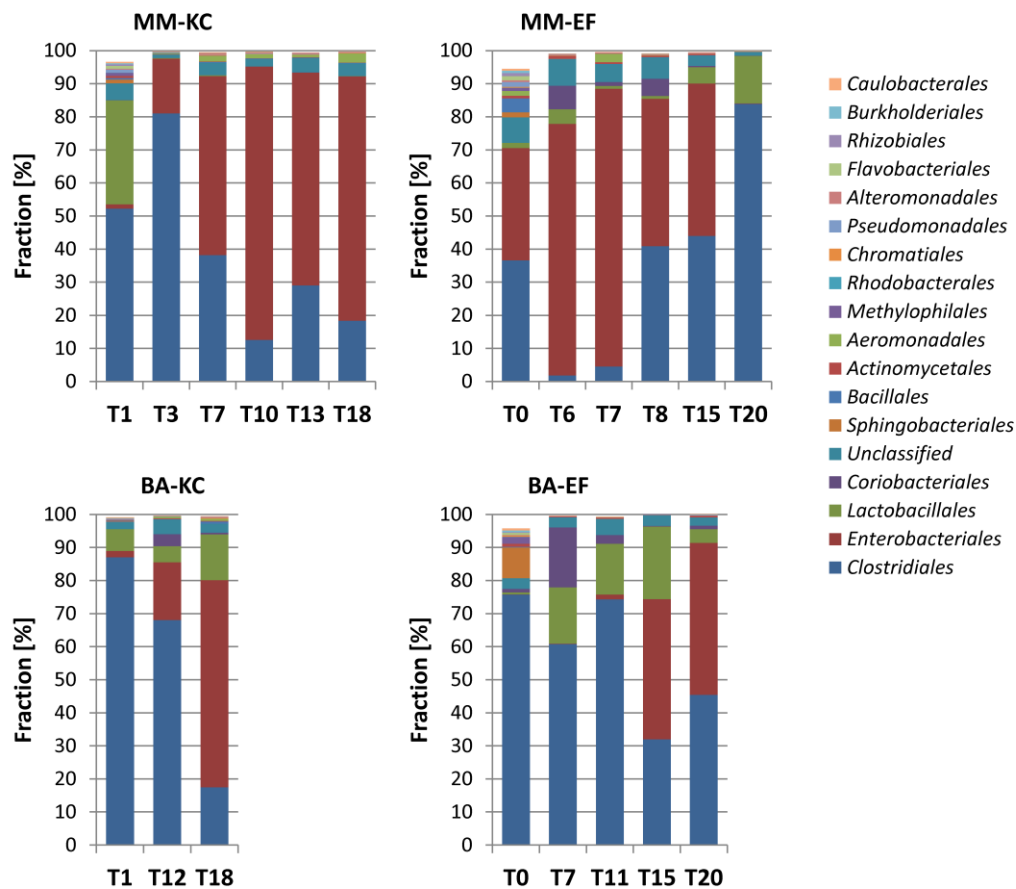
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S2. Metagenomic classification of the MMC at the genus level. Results of batch transfers, during the enrichment of activated sludge. MM-KC = Minimum Medium with Kinetic Control (21h); MM-EF = Minimum Medium with End of Fermentation (72h); BA-KC = Basal Medium with Kinetic Control (21h); BA-EF = Basal Medium with End of Fermentation (72h). T0-T20 = Transfer numbers. Species appearing at frequencies below 1% in all samples were omitted.



S3. Metagenomic classification of the MMC at the family level. Results of batch transfers, during the enrichment of activated sludge. MM-KC = Minimum Medium with Kinetic Control (21h); MM-EF = Minimum Medium with End of Fermentation (72h); BA-KC = Basal Medium with Kinetic Control (21h); BA-EF = Basal Medium with End of Fermentation (72h). T0-T20 = Transfer numbers. Families appearing at frequencies below 1% in all samples were omitted.

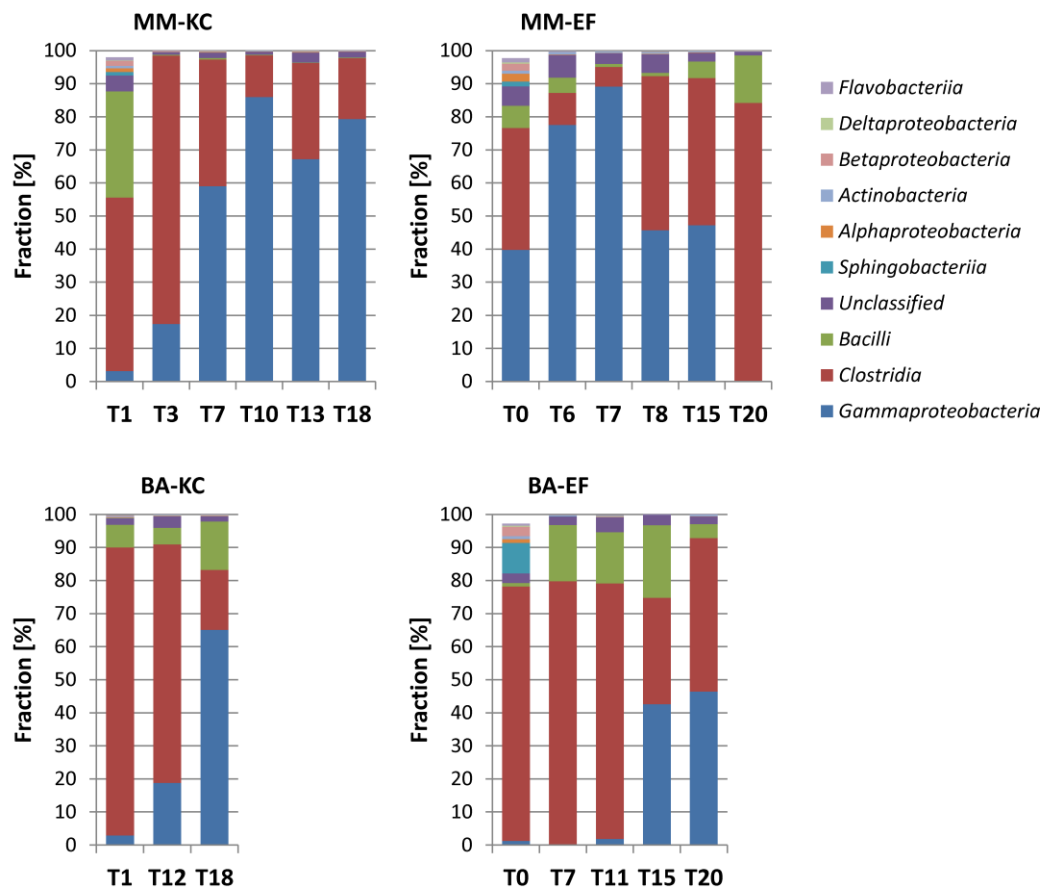


29

30 **S4.** Metagenomic classification of the MMC at the order level. Results of batch transfers, during the enrichment of
 31 activated sludge. MM-KC = Minimum Medium with Kinetic Control (21h); MM-EF = Minimum Medium with End of
 32 Fermentation (72h); BA-KC = Basal Medium with Kinetic Control (21h); BA-EF = Basal Medium with End of
 33 Fermentation (72h). T0-T20 = Transfer numbers. Orders appearing at frequencies below 1% in all samples were
 34 omitted.

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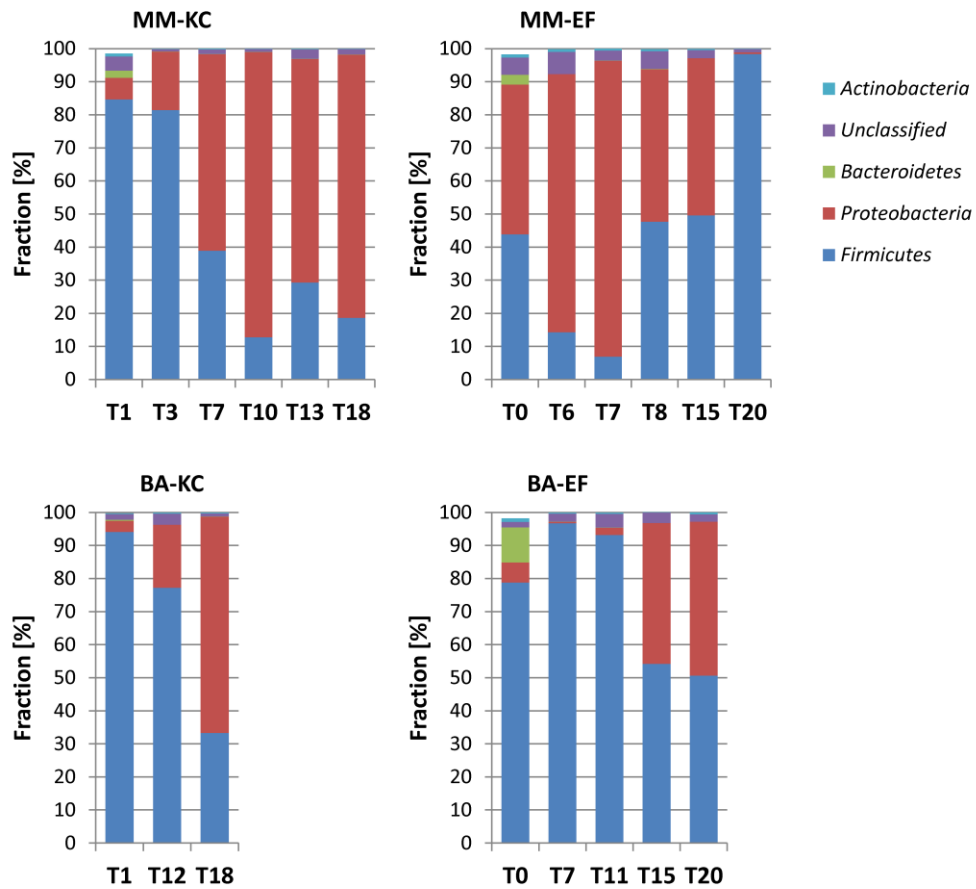
37

38 **S5.** Metagenomic classification of the MMC at the class level. Results of batch transfers, during the enrichment of
 39 activated sludge. MM-KC = Minimum Medium with Kinetic Control (21h); MM-EF = Minimum Medium with End of
 40 Fermentation (72h); BA-KC = Basal Medium with Kinetic Control (21h); BA-EF = Basal Medium with End of
 41 Fermentation (72h). T0-T20 = Transfer numbers. Classes appearing at frequencies below 1% in all samples were
 42 omitted.

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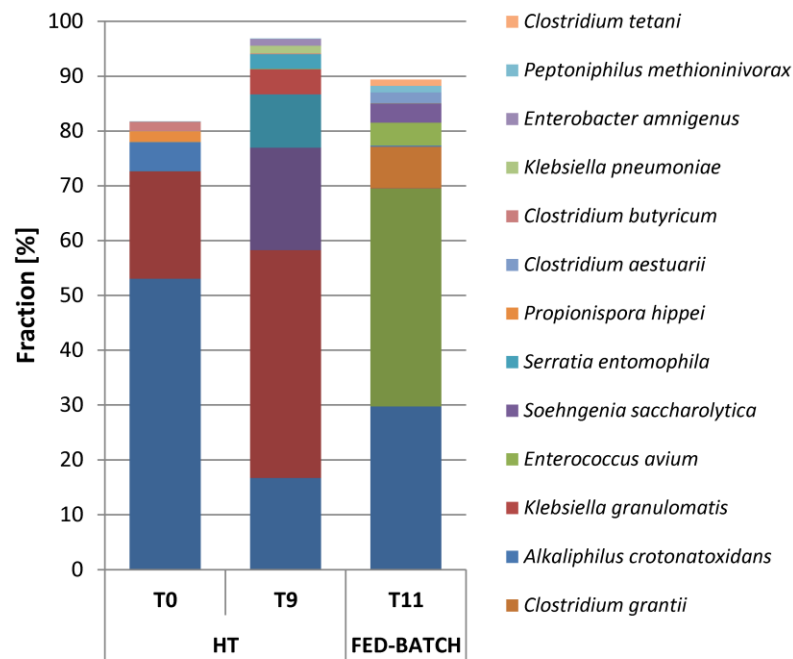


46

47 **S6.** Metagenomic classification of the MMC at the phylum level. Results of batch transfers, during the enrichment of
 48 activated sludge. MM-KC = Minimum Medium with Kinetic Control (21h); MM-EF = Minimum Medium with End of
 49 Fermentation (72h); BA-KC = Basal Medium with Kinetic Control (21h); BA-EF = Basal Medium with End of
 50 Fermentation (72h). T0-T20 = Transfer numbers. Phyla appearing at frequencies below 1% in all samples were
 51 omitted.

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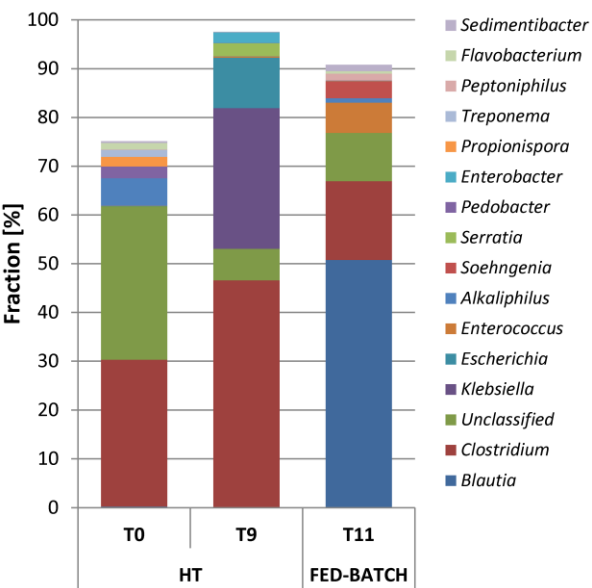


54

55 **S7.** Metagenomic classification of the MMC, at the species level, for the anaerobic sludge enriched on hexane-
56 pretreated crude glycerol in batch tests (HT) and with the untreated crude glycerol in fed-batch. T0-T11= Transfer
57 numbers. Species appearing at frequencies below 1% in all samples were omitted.

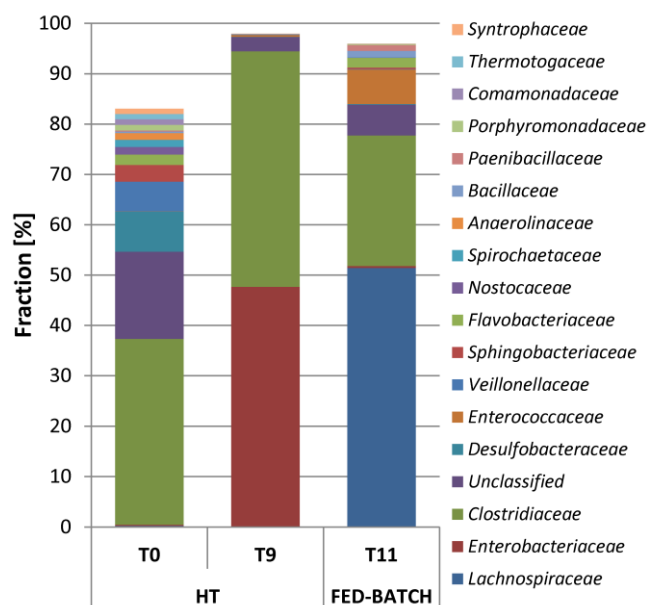
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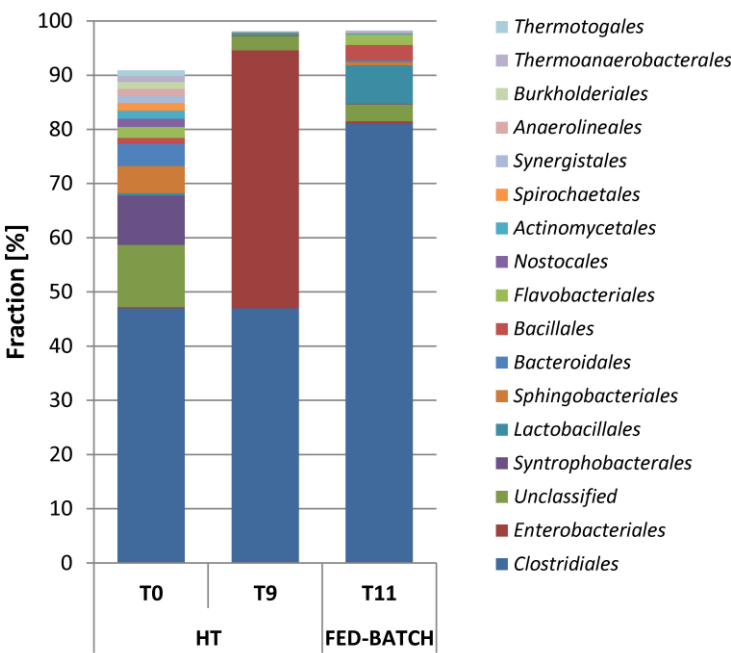
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S8. Metagenomic classification of the MMC, at the genus level, for the anaerobic sludge enriched on hexane-pretreated crude glycerol in batch tests (HT) and with the untreated crude glycerol in fed-batch. T0-T11= Transfer numbers. Species appearing at frequencies below 1% in all samples were omitted.



S9. Metagenomic classification of the MMC, at the family level, for the anaerobic sludge enriched on hexane-pretreated crude glycerol in batch tests (HT) and with the untreated crude glycerol in fed-batch. T0-T11= Transfer numbers. Families appearing at frequencies below 1% in all samples were omitted.

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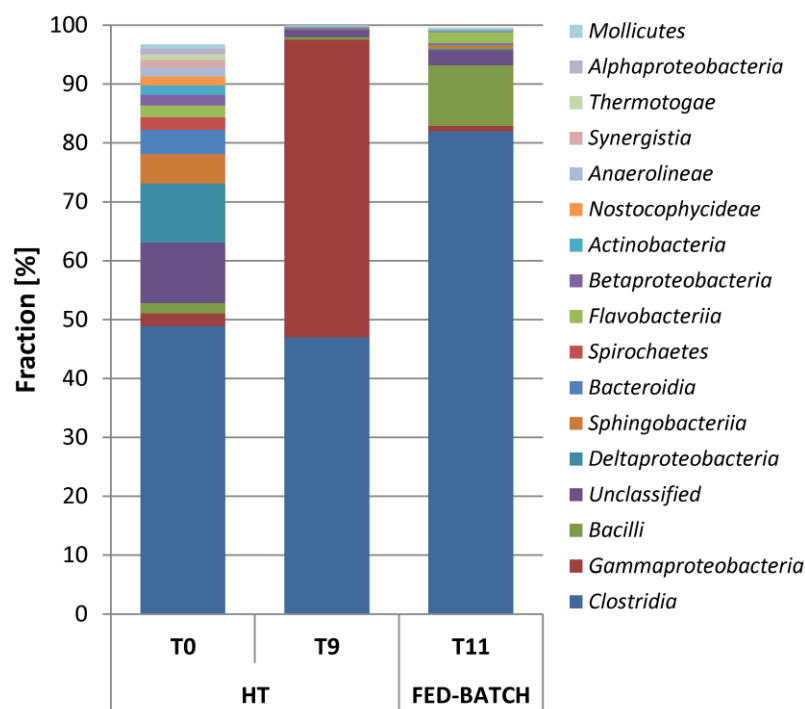


78

79 **S10.** Metagenomic classification of the MMC, at the order level, for the anaerobic sludge enriched on hexane-
80 pretreated crude glycerol in batch tests (HT) and with the untreated crude glycerol in fed-batch. T0-T11= Transfer
81 numbers. Orders appearing at frequencies below 1% in all samples were omitted.

82

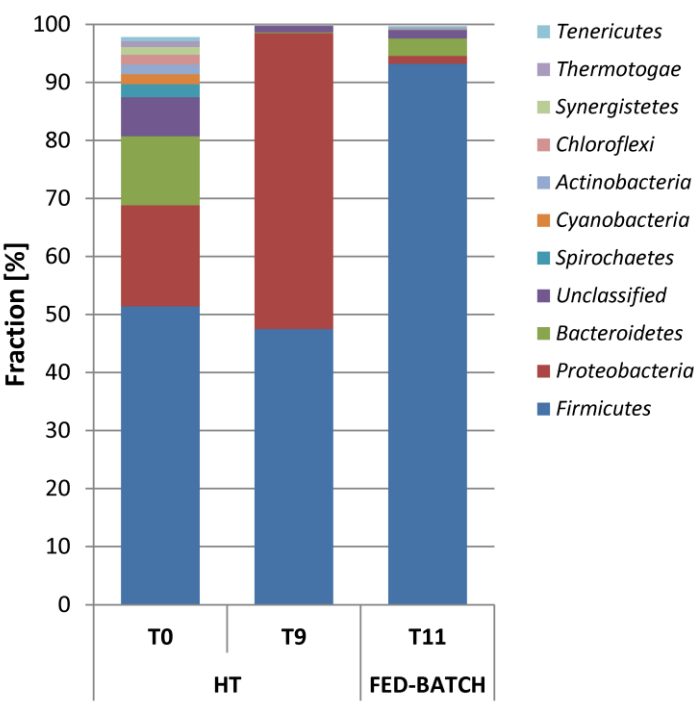
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84

85 **S11.** Metagenomic classification of the MMC, at the class level, for the anaerobic sludge enriched on hexane-pretreated
86 crude glycerol in batch tests (HT) and with the untreated crude glycerol in fed-batch. T0-T11= Transfer numbers.
87 Classes appearing at frequencies below 1% in all samples were omitted.

88



91 **S12.** Metagenomic classification of the MMC, at the phylum level, for the anaerobic sludge enriched on hexane-
92 pretreated crude glycerol in batch tests (HT) and with the untreated crude glycerol in fed-batch. T0-T11= Transfer
93 numbers. Phyla appearing at frequencies below 1% in all samples were omitted.