

**Supplementary Table S1:** 16S rRNA gene concentrations ( $\log_{10}$  copy numbers  $\text{mL}^{-1}$  fermentation effluent) of specific bacterial groups and species determined by qPCR in effluent samples during 'Normal Fe' conditions in the control reactor (CR) and 'High Fe', low Fe '200  $\mu\text{M}$  dip' and very low Fe '300  $\mu\text{M}$  dip' conditions in test reactors (TR1 and TR2).

	total 16S	<i>Bacteroides</i> spp.	Firmicutes	<i>Roseburial</i> <i>E. rectale</i>	<i>Clostridium</i> Cluster IV	<i>F.</i> <i>prausnitzii</i>	<i>E. hallii</i>	<i>Bifidobacte</i> <i>rium</i> spp.	<i>Enterobac</i> <i>teriaceae</i>	lactobacilli
<b>Stabilization</b>										
CR	11.0 ± 0.04	10.7 ± 0.1	10.6 ± 0.02	10.1 ± 0.1	8.1 ± 0.1	n.d.	6.4 ± 0.2	7.7 ± 0.3	8.1 ± 0.2	6.0 ± 0.1
TR1	10.6 ± 0.6	10.5 ± 0.7	10.2 ± 0.6	10.1 ± 0.1	7.7 ± 0.7	n.d.	6.3 ± 0.1	7.5 ± 0.4	7.7 ± 0.4	6.1 ± 0.1
TR2	10.9 ± 0.03	10.7 ± 0.1	10.6 ± 0.1	10.1 ± 0.1	8.0 ± 0.1	n.d.	6.5 ± 0.2	7.7 ± 0.3	7.3 ± 0.1	6.2 ± 0.1
<b>Period 1</b>										
CR	11.0 ± 0.1	10.6 ± 0.1	10.7 ± 0.1	10.2 ± 0.1	10.1 ± 0.2	6.3 ± 0.2	7.6 ± 0.3	7.1 ± 0.1	9.4 ± 0.5	6.4 ± 0.1
TR1 - 300 $\mu\text{M}^{\text{a}}$	10.7 ± 0.1*	9.1 ± 0.2*	10.2 ± 0.1*	8.9 ± 0.1*	8.0 ± 0.2*	4.1 ± 0.4 <sup>b</sup>	6.5 ± 0.1*	10.1 ± 0.04*	9.7 ± 0.8	5.2 ± 0.3*
TR2 - High Fe	10.9 ± 0.1	10.7 ± 0.2	10.4 ± 0.1*	9.8 ± 0.1*	9.5 ± 0.4	5.8 ± 0.5	7.8 ± 0.1	7.0 ± 0.2	8.8 ± 0.4	6.3 ± 0.2
<b>Period 2</b>										
CR	11.1 ± 0.02	10.6 ± 0.1	10.8 ± 0.1	10.3 ± 0.1	10.0 ± 0.04	6.4 ± 0.2	7.8 ± 0.1	7.0 ± 0.2	9.9 ± 0.7	6.3 ± 0.4
TR1 - 200 $\mu\text{M}^{\text{a}}$	11.1 ± 0.1	9.5 ± 0.1*	10.9 ± 0.7	10.4 ± 0.1	9.6 ± 0.3*	5.8 ± 0.2*	8.8 ± 0.1*	9.3 ± 0.1*	9.9 ± 0.4	6.1 ± 0.2
TR2 - 300 $\mu\text{M}^{\text{a}}$	10.9 ± 0.1*	9.7 ± 0.2*	10.6 ± 0.1*	10.2 ± 0.2	8.5 ± 0.5*	6.6 ± 0.1	8.2 ± 0.1*	9.8 ± 0.1*	9.8 ± 0.7	5.8 ± 0.2*
<b>Period 3 - beads</b>										
CR	10.8 ± 0.2	10.6 ± 0.1	10.8 ± 0.2	10.2 ± 0.1	9.2 ± 0.1	7.0 ± 0.1	7.0 ± 0.2	6.5 ± 0.2	9.9 ± 0.3	5.9 ± 0.1
TR1 - 200 $\mu\text{M}^{\text{a}}$	10.9 ± 0.1	10.1 ± 0.2*	10.8 ± 0.1	10.3 ± 0.03	9.2 ± 0.1	6.0 ± 0.2*	8.1 ± 0.2*	9.2 ± 0.1*	9.0 ± 0.2*	5.7 ± 0.2
TR2 - 300 $\mu\text{M}^{\text{a}}$	11.0 ± 0.1	8.5 ± 0.5*	10.6 ± 0.1	9.6 ± 0.1*	5.5 ± 0.2*	4.4 ± 0.1*	7.6 ± 0.2*	10.2 ± 0.1*	10.3 ± 0.3	4.9 ± 0.3*

Data are means ± SD of the last 3 days of each fermentation period. Means with an asterisk (\*) are significantly different from control reactor (CR) within the same bacterial group,  $P < 0.05$ .

n.d., not detected

<sup>a</sup> 2,2'-dipyridyl concentrations in the feed medium of the reactors.

<sup>b</sup> one of three values below detection limit.