Table S2. 16S rRNA gene copy numbers ($\log_{10}$ mL^{-1} of effluent) of specific bacterial groups measured by qPCR in effluent samples from CR and TR1-4.

		***Bifidobacterium* spp.**	***Bacteroides-Prevotella* group**	***Enterobacteriaceae***	***Lactobacillus/ Pediococcus/ Leuconostoc* spp.**	***Clostridium* Cluster IV**
Stabilization 1	**CR**	5.4 ± 0.7	10.5 ± 0.1	9.4 ± 0.2	8.4 ± 0.4	9.4 ± 0.3
	TR1	5.1 ± 0.2	10.3 ± 0.1	9.5 ± 0.3	8.0 ± 0.2	9.4 ± 0.2
	TR2	4.9 ± 0.3	10.4 ± 0.1	9.4 ± 0.3	7.8 ± 0.4	9.5 ± 0.2
	TR3	5.6 ± 0.4	10.3 ± 0.2	9.5 ± 0.4	8.1 ± 0.2	9.4 ± 0.3
	TR4	4.8 ± 0.4	10.2 ± 0.3	9.5 ± 0.2	8.1 ± 0.3	9.3 ± 0.1
Stabilization 2	**CR**	5.9 ± 0.3	10.4 ± 0.1	9.6 ± 0.03	8.0 ± 0.2	10.0 ± 0.1
	TR1	6.0 ± 0.7	10.5 ± 0.2	9.8 ± 0.1	7.9 ± 0.5	9.9 ± 0.1
	TR2	6.0 ± 0.6	10.5 ± 0.1	9.8 ± 0.04	8.4 ± 0.6	10.0 ± 0.2
	TR3	5.8 ± 0.8	10.4 ± 0.1	9.6 ± 0.1	7.6 ± 0.7	9.8 ± 0.1
	TR4	6.0 ± 0.6	10.4 ± 0.2	9.8 ± 0.1	7.8 ± 0.6	9.9 ± 0.2
Stabilization 3	**CR**	6.1 ± 0.1	10.3 ± 0.1	9.7 ± 0.1	8.3 ± 0.1	10.1 ± 0.1
	TR1	5.8 ± 0.4	10.5 ± 0.1	9.5 ± 0.04	8.7 ± 0.3	9.9 ± 0.3
	TR2	6.0 ± 0.4	10.5 ± 0.2	9.9 ± 0.1	8.8 ± 0.5	9.9 ± 0.2
	TR3	5.8 ± 0.2	10.4 ± 0.1	9.7 ± 0.1	8.3 ± 0.6	9.8 ± 0.2
	TR4	5.9 ± 0.3	10.3 ± 0.1	9.8 ± 0.1	8.7 ± 0.6	9.8 ± 0.1
Stabilization 4	**CR**	6.6 ± 0.1	9.9 ± 0.1	9.9 ± 0.03	7.7 ± 0.3	10.0 ± 0.1
	TR1	7.3 ± 0.1	10.0 ± 0.2	9.8 ± 0.1	8.4 ± 0.2	10.1 ± 0.1
	TR2	6.4 ± 0.1	9.9 ± 0.1	9.9 ± 0.3	7.8 ± 0.1	10.1 ± 0.1
	TR3	6.5 ± 0.04	10.0 ± 0.1	10.1 ± 0.2	8.2 ± 0.3	10.2 ± 0.2
	TR4	6.3 ± 0.1	10.0 ± 0.1	9.9 ± 0.2	8.0 ± 0.4	10.2 ± 0.1
Stabilization 5	**CR**	6.7 ± 0.2	10.0 ± 0.2	9.9 ± 0.02	8.4 ± 0.2	9.8 ± 0.3
	TR1	7.7 ± 0.6	10.1 ± 0.1	9.8 ± 0.1	8.7 ± 0.4	9.6 ± 0.1
	TR2	6.3 ± 0.7	10.0 ± 0.1	9.9 ± 0.2	8.6 ± 0.5	9.7 ± 0.3
	TR3	6.5 ± 0.6	10.0 ± 0.1	9.9 ± 0.1	8.8 ± 0.5	9.7 ± 0.2
	TR4	6.6 ± 0.6	10.1 ± 0.1	10.0 ± 0.1	8.7 ± 0.5	9.9 ± 0.3

Data are $\log_{10}$ transformed and mean values for the last three days of each stabilization period. No significant differences were observed for all time points tested using the Mann-Whitney U test ($P<0.05$)