Supplementary Materials: The microbiota of Edam cheeses determined by cultivation and high-throughput sequencing of the 16S rRNA amplicon

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Table S1. Percentages of the most abundant taxonomic groups in Edam cheese samples after 52 days of ripening.

Taxon		Cheese sample	
		Autumn	Spring
Actinobacteria		**16.77* ± 8.47**	**11.66 ± 1.57**
	Actinomyces	0.03 ± 0.01	0.10 ± 0.12
	Alloscardovia	0.00 ± 0.00	0.08 ± 0.13
	Bifidobacterium	0.94 ± 0.05	0.40 ± 0.53
	Cellulomonas	2.68 ± 0.11	1.11 ± 1.51
	Corynebacterium	0.05 ± 0.01	0.04 ± 0.04
	Leucobacter	0.33 ± 0.11	0.18 ± 0.18
	Mycobacterium	0.04 ± 0.00	0.02 ± 0.03
	Propionibacterium	12.37 ± 8.17	9.41 ± 1.02
	Rothia	0.16 ± 0.00	0.22 ± 0.27
Bacteroidetes		**0.52 ± 0.04**	**0.84 ± 0.93**
	Bacteroides	0.30 ± 0.06	0.15 ± 0.06
	Chryseobacterium	0.13 ± 0.14	0.07 ± 0.04
	Prevotella	0.00 ± 0.00	0.56 ± 0.80
Firmicutes		**49.1 ±15.56**	**61.52 ± 23.09**
	Alkaliphilus	0.71 ±0.91	0.42 ± 0.25
	Bacillus	0.66 ±0.05	1.47 ± 0.51
	Caloramator	0.11 ±0.08	0.10 ± 0.04
	Clostridium	1.03 ±0.30	2.00 ± 2.48
	Dialister	0.13 ±0.06	0.05 ± 0.04
	Enterococcus	0.12 ±0.01	0.06 ± 0.04
	Erysipelothrix	0.00 ±0	0.11 ± 0.16
	Eubacterium	0.36 ±0.12	0.02 ± 0.02
	Gemella	0.00 ±0	0.09 ± 0.13
	Laceyella	0.44 ±0.60	0.15 ± 0.02
	Lactobacillus	0.69 ±0.44	2.21 ± 2.83
	Lactococcus	43.78 ±14.5	53.35 ± 14.64
	Leuconostoc	0.12 ±0.13	0.04 ± 0.06
	Lysinibacillus	0.05 ±0.04	0.01 ± 0.01
	Ruminococcus	0.11 ±0.15	0.00 ± 0.00
	Streptococcus	0.25 ±0.34	0.05 ± 0.06
	Veillonella	0.08 ±0.04	1.22 ± 1.70
Proteobacteria		**8.69 ±3.27**	**3.26 ± 1.34**
	Acetobacter	1.01 ±0.20	0.39 ± 0.26
	Acinetobacter	0.05 ±0.06	1.56 ± 2.17
	Klebsiella	0.00 ± 0.06	0.04 ± 0.00

γ-Proteobacteria (unclassified)	7.11 ± 3.0	1.11 ± 0.41
Archaea	0.50 ± 0.03	0.16 ± 0.01
Other bacteria	0.51 ± 0.57	0.42 ± 0.28
Unclassified	23.9 ± 26.72	22.12 ± 24.52

* The calculated percentage accounts for the number of unclassified sequences.