Bacterial community assembly from cow teat skin to ripened cheeses is influenced by grazing systems

Frétin Marie[1,2], Martin Bruno[2], Rifa Etienne[1], Verdier-Metz Isabelle[1], Pomiès Dominique[2], Ferlay Anne[2], Montel Marie-Christine[1], Delbès Céline[1*]

Table S1. Overall bacterial composition in teat skin and dairy product samples

	Teat skin (*n=12*)	Raw milk (*n=12*)	Cheese core (*n=12*)	Cheese rind (*n=12*)
Total OTU	300	112	43	75
Total number of genera	98	52	14	23
Total OTUs > 1%	18	17	1	5

n: number of samples by habitat

Table S2. Taxonomic distribution of isolates obtained from raw milk

Phylum	Genus and/or species[1]	July		September	
		EXT[2]	SEMI[3]	EXT[2]	SEMI[3]
Actinobacteria	*Bifidobacterium crudilactis*	2	1	1	
(32.4%)	*Gordonia sputi*				1
	Rhodococcus coprophilus				1
	Salana sp.	1			
	Brachybacterium paraconglomeratum	1		1	1
	Dermacoccus nishinomiyaensis		1	1	1
	Curtobacterium flaccumfaciens				1
	Leifsonia aquatica			1	
	Microbacterium aurum		1		
	Microbacterium flavum	1		1	
	Microbacterium lacticum		2		2
	Microbacterium oxydans	5	2	2	1
	Microbacterium sp.				1
	Pseudoclavibacter helvolus			2	
	Kocuria carniphila	1	1		
	Kocuria palustris			2	1
	Kocuria rhizophila	1			
	Kocuria salsicia	9	8	5	3
	Propioniciclava sp.	3	5	4	4
	Total for phylum	24	21	20	17
Bacteroidetes	*Chryseobacterium bovis*	1			1
(5.5%)	*Chryseobacterium meningosepticum*	1			
	Chryseobacterium oncorhynchi	1			
	Chryseobacterium shigense	1	4		
	Chryseobacterium sp.		1	2	2
	Total for phylum	4	5	2	3
Deinococcus-Thermus	*Deinococcus* sp.			2	
(1.2%)	*Deinococcus xinjiangensis*	1			
	Total for phylum	1	0	2	0
Firmicutes	*Bacillus cereus*	2			
(33.2%)	*Bacillus pumilus*			1	
	Bacillus sp.		2		
	Macrococcus caseolyticus	2	2		
	Staphylococcus aureus	2	1	1	1
	Staphylococcus chromogenes	3	2	1	2
	Staphylococcus devriesei	1	3	3	
	Staphylococcus haemolyticus	4	2	5	2
	Staphylococcus saprophyticus		1	1	
	Staphylococcus sp.	1	1		
	Aerococcus viridans				1
	Enterococcus faecium				2
	Enterococcus gilvus			1	
	Lactobacillus casei		5	5	9
	Lactobacillus helveticus	1	2	3	1
	Lactobacillus parabuchneri		1	1	
	Lactobacillus paracasei		1		
	Leuconostoc citreum	1			
	Lactococcus lactis	2	1		

	Streptococcus uberis				1
	Total for phylum	19	24	22	19
Proteobacteria (27.7%)	*Brevundimonas aurantiaca*	2			
	Brevundimonas intermedia	3			
	Brevundimonas nasdae		1		
	Brevundimonas sp.	4	4	1	3
	Brevundimonas vesicularis	2	2		1
	Ochrobactrum rhizosphaerae	1	1		1
	Devosia sp.		1		
	Rhizobium radiobacter			1	
	Rhizobium sp.		1		
	Shinella zoogloeoides	2			
	Paracoccus yeei	1			
	Sphingomonas melonis	2			
	Sphingomonas sp.				1
	Variovorax paradoxus	1			
	Escherichia coli	1			
	Pseudomonas sp.				1
	Stenotrophomonas maltophilia	16	4	1	
	Stenotrophomonas rhizophila		3		
	Stenotrophomonas sp.		2	3	3
	Total for phylum	35	19	6	10
Total identified		83	69	52	49

Values reported correspond to the number of clones identified from triplicate milk sample

[1] The underlined genera were not detected by 16S rRNA gene metabarcoding in raw milks

[2] EXT = extensive grazing system; [3]SEMI = semi-intensive grazing system

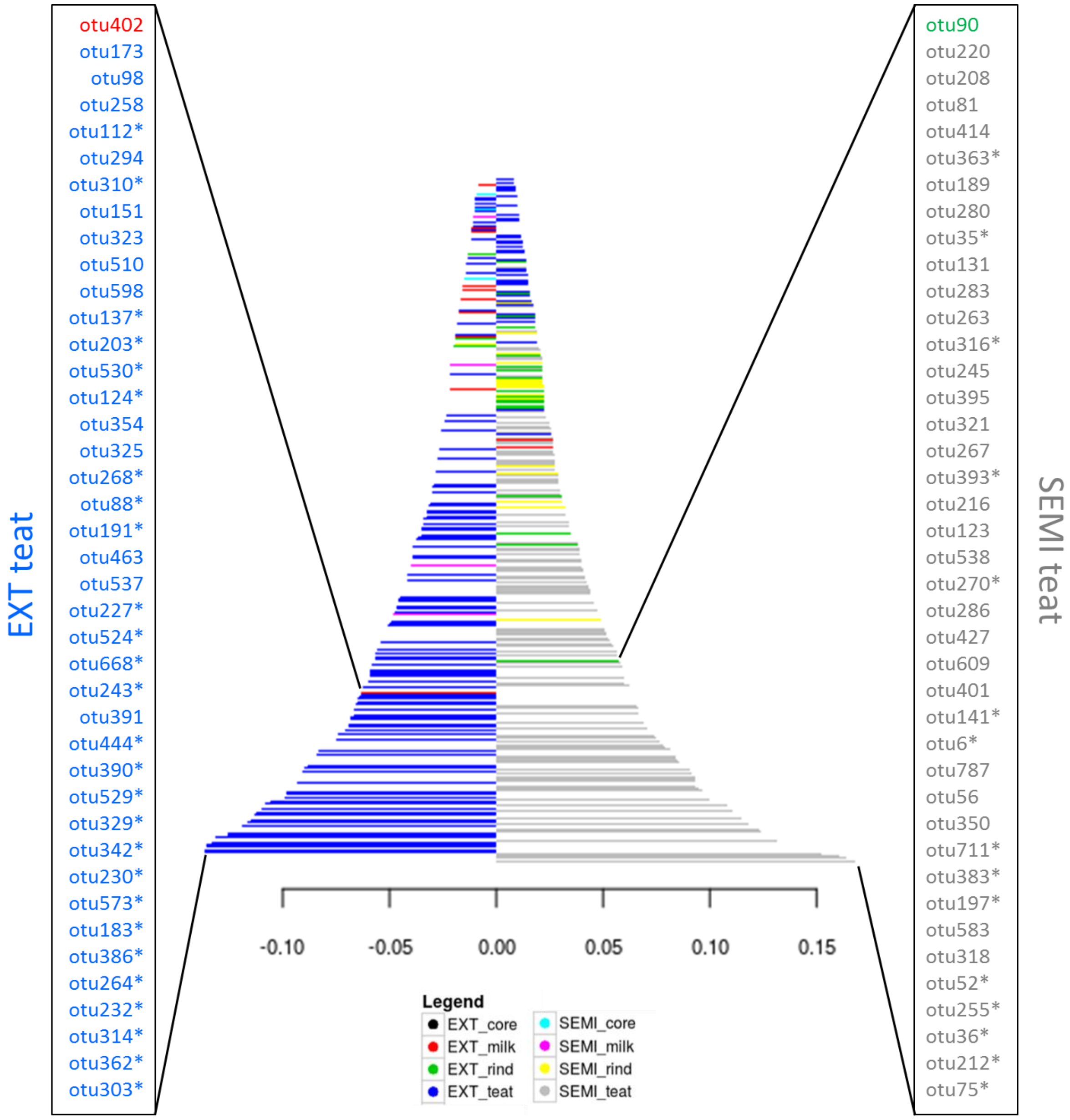

Figure S1. Contribution to PC3 of 365 variables of the PLS-DA performed on all the samples (teat skin swab, milk, cheese core and rind) of July. The 82 OTUs that contribute the most to PC3 were reported. The symbol * indicates the OTUs with a differential abundance using LEfSe (Table S2 and S3).

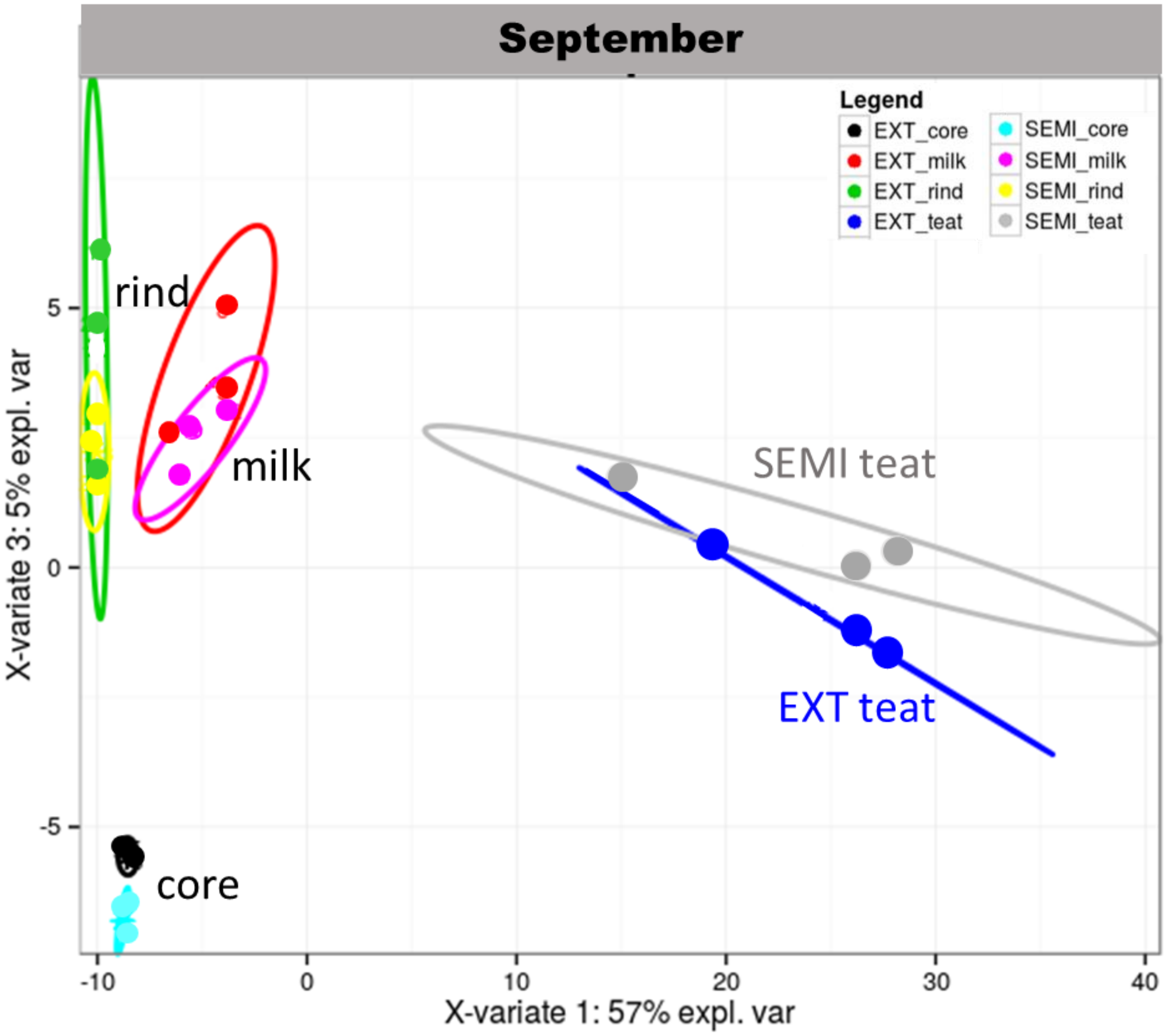

Figure S2. PLS-DA performed on the relative abundance of 365 OTUs found on all the samples of September from two grazing systems. Plot of sample distribution is projected on principal components 1 and 3.

Table S3. Differentially abundant taxa on teat skin in July between EXT (*n*=3) and SEMI (*n*=3) systems as determined by the LDA method[1].

Notation on Fig. 2A	Taxa	N°OTU	Average abundance		Standard deviation		LDA score	pval
			EXT	SEMI	EXT	SEMI		
Taxa more abundant in EXT								
	Actinobacteria							
f	Actinobacteria|Corynebacteriales|Corynebacteriaceae|Corynebacterium|Corynebacterium spp.	OTU12	3.95	0.96	2.23	0.26	4.166	0.0495
g	Actinobacteria|Corynebacteriales|Corynebacteriaceae|Corynebacterium	**OTU137**	0.27	0.02	0.18	0.02	3.119	0.0495
h	Actinobacteria|Corynebacteriales|Corynebacteriaceae|Corynebacterium	**OTU183**	0.19	-	0.24	-	3.096	0.0369
i	Actinobacteria|Corynebacteriales|Corynebacteriaceae|Corynebacterium	**OTU444**	0.09	<0.01	0.06	0.00	2.713	0.0463
	Coriobacteriia	class	1.72	0.60	0.66	0.17	4.242	0.0495
	Coriobacteriia|Coriobacteriales	order	1.72	0.60	0.66	0.17	4.198	0.0495
r	Coriobacteriia|Coriobacteriales|Coriobacteriaceae	family	1.72	0.60	0.66	0.17	3.763	0.0495
k	Coriobacteriia|Coriobacteriales|Coriobacteriaceae|Atopobium	genus	1.53	0.46	0.70	0.15	3.742	0.0495
l	Coriobacteriia|Coriobacteriales|Coriobacteriaceae|Atopobium	**OTU112**	0.67	0.05	0.36	0.03	3.512	0.0495
m	Coriobacteriia|Coriobacteriales|Coriobacteriaceae|Atopobium	**OTU124**	0.36	0.05	0.19	0.07	3.207	0.0495
n	Coriobacteriia|Coriobacteriales|Coriobacteriaceae|Atopobium	OTU130	0.35	0.11	0.23	0.04	3.096	0.0495
q	Coriobacteriia|Coriobacteriales|Coriobacteriaceae|Gordonibacter	**OTU329**	0.07	0.01	0.03	0.01	2.945	0.0495
	Firmicutes							
u	Bacilli|Bacillales|Planococcaceae|Solibacillus	OTU205	0.10	0.06	0.01	0.04	2.760	0.0495
x	Bacilli|Lactobacillales|Aerococcaceae|Aerococcus	genus	2.39	0.41	2.54	0.19	3.982	0.0495
y	Clostridia|Clostridiales|Christensenellaceae	OTU146	0.50	0.07	0.22	0.06	3.366	0.0495
z	Clostridia|Clostridiales|Christensenellaceae	OTU193	0.10	0.02	0.03	0.01	2.797	0.0495
a0	Clostridia|Clostridiales|Christensenellaceae	**OTU227**	0.09	0.01	0.05	0.00	2.655	0.0495
a1	Clostridia|Clostridiales|Christensenellaceae	OTU258	0.21	0.03	0.13	0.03	2.959	0.0495
a2	Clostridia|Clostridiales|Christensenellaceae	**OTU268**	0.08	0.01	0.05	0.01	2.688	0.0495
a3	Clostridia|Clostridiales|Christensenellaceae	OTU285	0.28	0.03	0.23	0.02	3.119	0.0495
a4	Clostridia|Clostridiales|Christensenellaceae	**OTU303**	0.09	-	0.01	-	2.962	0.0369
a5	Clostridia|Clostridiales|Christensenellaceae	**OTU390**	0.15	<0.01	0.17	0.01	2.879	0.0463
a6	Clostridia|Clostridiales|Christensenellaceae	OTU398	0.06	0.02	0.02	0.00	2.936	0.0495

a7	Clostridia|Clostridiales|Christensenellaceae	OTU402	0.09	0.02	0.05	0.01	2.670	0.0495
a8	Clostridia|Clostridiales|Christensenellaceae	**OTU530**	0.06	0.01	0.05	0.00	2.525	0.0495
b3	Clostridia|Clostridiales|FamilyXIII	family	0.30	0.07	0.16	0.04	3.108	0.0495
b2	Clostridia|Clostridiales|Family XIII|Mogibacterium	OTU135	0.30	0.07	0.16	0.04	3.096	0.0495
c1	Clostridia|Clostridiales|Lachnospiraceae	family	4.63	1.47	2.51	0.68	4.213	0.0495
d1	Clostridia|Clostridiales|Lachnospiraceae	**OTU88**	0.56	0.04	0.22	0.05	3.428	0.0495
c2	Clostridia|Clostridiales|Lachnospiraceae	OTU156	0.15	0.02	0.12	0.01	2.859	0.0495
c3	Clostridia|Clostridiales|Lachnospiraceae	OTU181	0.13	0.04	0.04	0.02	2.743	0.0495
c4	Clostridia|Clostridiales|Lachnospiraceae	**OTU203**	0.27	0.03	0.16	0.01	3.106	0.0495
c5	Clostridia|Clostridiales|Lachnospiraceae	**OTU232**	0.04	-	0.01	-	2.951	0.0369
c6	Clostridia|Clostridiales|Lachnospiraceae	**OTU243**	0.10	0.01	0.05	0.01	2.730	0.0495
c8	Clostridia|Clostridiales|Lachnospiraceae	OTU313	0.08	0.01	0.02	0.01	2.725	0.0495
c9	Clostridia|Clostridiales|Lachnospiraceae	**OTU362**	0.08	<0.01	0.00	0.00	2.945	0.0463
d0	Clostridia|Clostridiales|Lachnospiraceae	**OTU529**	0.05	<0.01	0.02	0.01	2.858	0.0495
b4	Clostridia|Clostridiales|Lachnospiraceae|Acetitomaculum		1.25	0.11	0.65	0.04	3.796	0.0495
b7	Clostridia|Clostridiales|Lachnospiraceae|Acetitomaculum	OTU37	0.97	0.08	0.56	0.04	3.637	0.0495
b5	Clostridia|Clostridiales|Lachnospiraceae|Acetitomaculum	**OTU264**	0.09	<0.01	0.04	0.00	2.725	0.0463
b6	Clostridia|Clostridiales|Lachnospiraceae|Acetitomaculum	**OTU314**	0.07	<0.01	0.01	0.00	2.863	0.0463
b8	Clostridia|Clostridiales|Lachnospiraceae|Acetitomaculum	**OTU573**	0.05	-	0.03	-	2.529	0.0369
c0	Clostridia|Clostridiales|Lachnospiraceae|Coprococcus	**OTU191**	0.19	0.02	0.08	0.02	2.984	0.0495
d5	Clostridia|Clostridiales|Ruminococcaceae	**OTU230**	0.09	<0.01	0.01	0.01	2.991	0.0463
d6	Clostridia|Clostridiales|Ruminococcaceae	**OTU310**	0.13	0.02	0.11	0.01	2.784	0.0495
d7	Clostridia|Clostridiales|Ruminococcaceae	**OTU342**	0.09	<0.01	0.04	0.01	2.727	0.0463
d9	Clostridia|Clostridiales|Ruminococcaceae	**OTU668**	0.07	<0.01	0.08	0.01	2.594	0.0463
d3	Clostridia|Clostridiales|Ruminococcaceae|Ruminiclostridium	**OTU524**	0.09	0.01	0.09	0.01	2.748	0.0463
d4	Clostridia|Clostridiales|Ruminococcaceae|Saccharofermentans	OTU356	0.16	0.04	0.04	0.00	2.871	0.0495
e0	Erysipelotrichia|Erysipelotrichales|Erysipelotrichaceae|Solobacterium	**OTU386**	0.05	<0.01	0.03	0.00	2.709	0.0463
Taxa more abundant in SEMI								
	Actinobacteria							
	Actinobacteria|Bifidobacteriales	order	0.48	10.5	0.59	5.69	4.694	0.0495
e	Actinobacteria|Bifidobacteriales|Bifidobacteriaceae	family	0.48	10.5	0.59	5.69	4.675	0.0495

d	Actinobacteria|Bifidobacteriales|Bifidobacteriaceae|Bifidobacterium	genus	0.48	10.5	0.59	5.69	4.674	0.0495
c	Actinobacteria|Bifidobacteriales|Bifidobacteriaceae|Bifidobacterium|B.pseudolongum	**OTU6**	0.46	9.90	0.58	5.46	4.640	0.0495
a	Actinobacteria|Bifidobacteriales|Bifidobacteriaceae|Bifidobacterium|B.choerinum	**OTU36**	<0.01	0.34	0.00	0.30	3.238	0.0495
b	Actinobacteria|Bifidobacteriales|Bifidobacteriaceae|Bifidobacterium|B.merycicum	**OTU52**	0.02	0.27	0.01	0.07	3.118	0.0495
j	Actinobacteria|Propionibacteriales|Nocardioidaceae	**OTU363**	0.02	0.06	0.00	0.07	3.107	0.0495
p	Coriobacteriia|Coriobacteriales|Coriobacteriaceae|Atopobium	**OTU75**	-	0.15	-	0.02	3.033	0.0369
o	Coriobacteriia|Coriobacteriales|Coriobacteriaceae|Atopobium	**OTU212**	-	0.04	-	0.02	3.026	0.0369
	Firmicutes							
s	Bacilli|Bacillales|Bacillaceae|Bacillus	**OTU141**	0.06	0.49	0.03	0.33	3.362	0.0495
t	Bacilli|Bacillales|Paenibacillaceae|Paenibacillus|Paenibacillus spp.	OTU359	0.05	0.08	0.02	0.00	2.676	0.0495
w	Bacilli|Bacillales|Planococcaceae|Sporosarcina	**OTU393**	0.02	0.06	0.01	0.01	2.891	0.0495
v	Bacilli|Bacillales|Planococcaceae|Sporosarcina|S. globispora	**OTU316**	0.03	0.07	0.01	0.01	2.666	0.0495
a9	Clostridia|Clostridiales|Clostridiaceae|Clostridium	genus	0.62	2.35	0.26	0.91	3.989	0.0495
b0	Clostridia|Clostridiales|Clostridiaceae|Clostridium|Clostridium spp.	**OTU35**	0.34	1.89	0.12	0.83	3.881	0.0495
b1	Clostridia|Clostridiales|Clostridiaceae|Clostridium	OTU85	0.19	0.40	0.12	0.08	3.032	0.0495
c7	Clostridia|Clostridiales|Lachnospiraceae	**OTU255**	-	0.23	-	0.22	3.134	0.0369
b9	Clostridia|Clostridiales|Lachnospiraceae|Cellulosilyticum	**OTU270**	0.03	0.11	0.02	0.06	2.758	0.0495
d2	Clostridia|Clostridiales|Ruminococcaceae	**OTU197**	0.01	0.27	0.01	0.23	3.168	0.0463
d8	Clostridia|Clostridiales|Ruminococcaceae	**OTU383**	0.02	0.12	0.02	0.09	2.831	0.0495
e1	Erysipelotrichia|Erysipelotrichales|Erysipelotrichaceae|Turicibacter	**OTU711**	0.01	0.08	0.00	0.03	2.871	0.0495

[1] Average abundances (expressed as percentages) as well as standard deviation are presented for each taxon. EXT = extensive grazing system; SEMI = semi-intensive grazing system

The bold OTUs correspond to the OTUs that contribute the most to the third principal component (PC3) of PLS-DA on Figure S1.

Table S4. Differentially abundant taxa on teat skin in September between EXT (*n*=3) and SEMI (*n*=3) systems as determined by the LDA method[1].

Notation on Fig. 2B	Taxa	N°OTU	Average abundance		Standard deviation		LDA score	pval
			EXT	SEMI	EXT	SEMI		
Taxa more abundant in EXT								
	Actinobacteria							
	Actinobacteria|Corynebacteriales	order	34.5	17.1	9.23	5.22	4.961	0.0495
h	Actinobacteria|Corynebacteriales|Corynebacteriaceae	family	31.9	15.5	7.49	4.75	5.172	0.0495
f	Actinobacteria|Corynebacteriales|Corynebacteriaceae|Corynebacterium	genus	31.9	15.5	7.49	4.75	4.976	0.0495
g	Actinobacteria|Corynebacteriales|Corynebacteriaceae|Corynebacterium	OTU260	0.36	0.03	0.30	0.01	3.309	0.0495
q	Coriobacteriia|Coriobacteriales|Coriobacteriaceae|Gordonibacter	OTU329	0.06	0.01	0.05	0.01	3.331	0.0495
	Firmicutes							
u	Clostridia|Clostridiales|Christensenellaceae	OTU370	0.05	0.01	0.03	0.01	3.402	0.0495
a0	Clostridia|Clostridiales|Lachnospiraceae	OTU362	0.08	0.01	0.06	0.01	3.185	0.0495
a1	Clostridia|Clostridiales|Peptostreptococcaceae|Terrisporobacter	OTU357	0.07	<0.01	0.04	0.00	3.409	0.0463
	Proteobacteria							
a6	Alphaproteobacteria|Rhizobiales|Phyllobacteriaceae|Aminobacter	OTU169	0.21	0.05	0.15	0.02	3.282	0.0495
Taxa more abundant in SEMI								
	Actinobacteria							
	Actinobacteria|Bifidobacteriales	order	1.55	21.6	0.57	24.89	4.990	0.0495
e	Actinobacteria|Bifidobacteriales|Bifidobacteriaceae	family	1.55	21.6	0.57	24.89	4.983	0.0495
d	Actinobacteria|Bifidobacteriales|Bifidobacteriaceae|Bifidobacterium	genus	1.55	21.6	0.57	24.89	5.021	0.0495
c	Actinobacteria|Bifidobacteriales|Bifidobacteriaceae|Bifidobacterium|B.pseudolongum	OTU6	1.36	17.5	0.62	20.96	4.904	0.0495
a	Actinobacteria|Bifidobacteriales|Bifidobacteriaceae|Bifidobacterium|B.choerinum	OTU36	0.07	2.69	0.06	3.28	4.102	0.0495
b	Actinobacteria|Bifidobacteriales|Bifidobacteriaceae|Bifidobacterium|B.merycicum	OTU52	0.12	1.35	0.13	0.74	3.779	0.0495
j	Actinobacteria|Corynebacteriales|Nocardiaceae	family	0.21	0.31	0.05	0.03	3.073	0.0495
i	Actinobacteria|Corynebacteriales|Nocardiaceae|Rhodococcus	genus	0.18	0.30	0.03	0.03	3.385	0.0495
k	Actinobacteria|Micrococcales|Dermatophilaceae	OTU281	0.03	0.05	0.02	0.01	3.380	0.0495

l	Actinobacteria|Micrococcales|Microbacteriaceae|Agreia	OTU335	0.01	0.04	0.00	0.02	3.424	0.0495
	Actinobacteria|Micromonosporales	Order	0.01	0.03	0.01	0.00	3.781	0.0495
n	Actinobacteria|Micromonosporales|Micromonosporaceae	family	0.01	0.03	0.01	0.00	3.683	0.0495
m	Actinobacteria|Micromonosporales|Micromonosporaceae|Micromonospora	OTU379	0.01	0.03	0.01	0.00	3.810	0.0495
p	Coriobacteriia|Coriobacteriales|Coriobacteriaceae|Atopobium	OTU75	0.05	1.15	0.06	0.78	3.758	0.0495
o	Coriobacteriia|Coriobacteriales|Coriobacteriaceae|Atopobium	OTU212	<0.01	0.28	0.00	0.36	3.445	0.0463
	Firmicutes							
r	Bacilli|Bacillales|Planococcaceae	OTU302	0.01	0.13	0.02	0.08	3.017	0.0495
t	Bacilli|Lactobacillales|Streptococcaceae|Lactococcus	genus	0.18	0.23	0.02	0.04	3.000	0.0495
s	Bacilli|Lactobacillales|Streptococcaceae|Lactococcus|Lc. lactis	OTU1	0.18	0.21	0.01	0.02	3.566	0.0495
x	Clostridia|Clostridiales|Clostridiaceae|Clostridium	genus	0.49	1.18	0.23	0.55	3.581	0.0495
y	Clostridia|Clostridiales|Clostridiaceae|Clostridium spp.	OTU35	0.26	0.72	0.01	0.05	3.369	0.0495
w	Clostridia|Clostridiales|Clostridiaceae|Clostridium|C. hylemonae	OTU271	0.01	0.07	-	0.09	3.284	0.0495
v	Clostridia|Clostridiales|Clostridiaceae|Clostridium|C. chartababidum	OTU321	-	0.11	0.23	0.55	2.996	0.0369
z	Clostridia|Clostridiales|Lachnospiraceae|Coprococcus	OTU248	-	0.02	-	0.03	3.260	0.0369
a2	Clostridia|Clostridiales|Ruminococcaceae	OTU197	-	0.04	-	0.03	3.217	0.0463
a3	Clostridia|Clostridiales|Ruminococcaceae|Ruminococcus	OTU216	0.01	0.28	0.01	0.20	3.188	0.0495
a4	Clostridia|Clostridiales|Ruminococcaceae|Ruminococcus	OTU322	0.01	0.08	0.00	0.05	3.666	0.0495
a5	Clostridia|Clostridiales|Ruminococcaceae|Ruminococcus	OTU334	0.02	0.11	0.01	0.11	3.131	0.0495

[1] Average abundances (expressed as percentages) as well as standard deviation are presented for each taxon. EXT = extensive grazing system; SEMI = semi-intensive grazing system

Table S5. Differentially abundant taxa in raw milk **(A)** in July and **(B)** in September between EXT (*n*=3) and SEMI (*n*=3) systems as determined by the LDA method[1].

A

Taxa	Average abundance		Standard deviation		LDA score	pval
	EXT	SEMI	EXT	SEMI		
Taxa more abundant in EXT						
Firmicutes						
Clostridia|Clostridiales|Lachnospiraceae	0.33	0.06	0.19	0.06	3.546	0.0495
Proteobacteria						
Gammaproteobacteria	3.48	0.14	2.98	0.08	4.308	0.0495
Gammaproteobacteria|Pseudomonadales	3.09	0.01	2.47	0.02	4.234	0.0463

B

Taxa	Average abundance		Standard deviation		LDA score	pval
	EXT	SEMI	EXT	SEMI		
Taxa more abundant in EXT						
Actinobacteria						
Actinobacteria|Corynebacteriales|Nocardiaceae|Rhodococcus|Rhodococcus spp._otu100	3.26	0.82	1.07	1.32	4.209	0.0495
Actinobacteria|Micrococcales|Micrococcaceae|Kocuria|Kocuria spp._otu72	0.09	-	0.12	-	4.131	0.0339
Taxa more abundant in SEMI						
Firmicutes	19.9	48.5	6.37	18.6	5.177	0.0495
Clostridia|Clostridiales|Lachnospiraceae	0.05	0.46	0.05	0.33	3.841	0.0463
Clostridia|Clostridiales|Lachnospiraceae_otu203	-	0.29	-	0.28	3.888	0.0369

[1] Average abundances (expressed as percentages) as well as standard deviation are presented for each taxon. EXT = extensive grazing system; SEMI = semi-intensive grazing system

Table S6. Differentially abundant taxa in cheese core **(A)** in July and **(B)** in September between EXT (*n*=3) and SEMI (*n*=3) systems as determined by the LDA method[1].

A

Taxa	Average abundance		Standard deviation		LDA score	pval
	EXT	SEMI	EXT	SEMI		
Taxa more abundant in EXT						
Firmicutes						
Bacilli|Lactobacillales|Lactobacillaceae	1.52	0.66	0.83	0.32	4.028	0.0495
Bacilli|Lactobacillales|Lactobacillaceae|Lactobacillus| Lb. helveticus_otu27	0.62	0.09	0.42	0.07	3.436	0.0495
Bacilli|Lactobacillales|Lactobacillaceae|Lactobacillus| Lb. parabuchneri_otu57	0.11	0.04	0.02	0.03	2.977	0.0495
Bacilli|Lactobacillales|Lactobacillaceae|Lactobacillus| Lactobacillus spp._otu180	0.04	0.01	0.02	0.00	2.845	0.0495
Bacilli|Lactobacillales|Lactobacillaceae|Lactobacillus| Lb. helveticus_otu229	0.06	0.01	0.05	0.01	2.524	0.0495
Taxa more abundant in SEMI						
Fusobacteria						
Fusobacteriia|Fusobacteriales|Fusobacteriaceae| Fusobacterium_ otu223	0.03	0.16	0.03	0.09	2.999	0.0495

B

Taxa	Average abundance		Standard deviation		LDA score	pval
	EXT	SEMI	EXT	SEMI		
Taxa more abundant in EXT						
Proteobacteria						
Gammaproteobacteria|Enterobacteriales	0.13	-	0.18	-	2.914	0.0369
Gammaproteobacteria|Enterobacteriales|Enterobacteriaceae	0.13	-	0.18	-	2.905	0.0369
Gammaproteobacteria|Pseudomonadales| Pseudomonadaceae|Pseudomonas|Ps. putida_otu326	0.02	-	0.02	-	2.185	0.0369
Taxa more abundant in SEMI						
Firmicutes						
Bacilli|Lactobacillales|Lactobacillaceae|Lactobacillus| Lb. curvatus_otu315	-	0.02	-	0.01	2.407	0.0339
Bacilli|Lactobacillales|Streptococcaceae|Streptococcus	0.03	0.11	0.02	0.03	2.627	0.0495
Bacilli|Lactobacillales|Streptococcaceae|Lactococcus| Lc. lactis_otu46	0.09	0.36	0.07	0.08	3.153	0.0495
Bacilli|Lactobacillales|Streptococcaceae|Lactococcus_otu139	0.02	0.07	0.01	0.03	2.440	0.0495
Bacilli|Lactobacillales|Streptococcaceae|Lactococcus_otu175	0.02	0.06	0.01	0.03	2.307	0.0495
Bacilli|Lactobacillales|Streptococcaceae|Lactococcus| Lc. chungangensis/raffinolactis_otu48	0.07	0.30	0.06	0.09	3.048	0.0495
Bacilli|Lactobacillales|Streptococcaceae|Lactococcus_otu89	0.06	0.23	0.05	0.03	2.922	0.0495

[1] Average abundances (expressed as percentages) as well as standard deviation are presented for each taxon. EXT = extensive grazing system; SEMI = semi-intensive grazing system

Table S7. Differentially abundant taxa in cheese rind **(A)** in July and **(B)** in September between EXT (*n*=3) and SEMI (*n*=3) systems as determined by the LDA method[1].

A

Taxa	Average abundance		Standard deviation		LDA score	pval
	EXT	SEMI	EXT	SEMI		
Taxa more abundant in EXT						
Firmicutes						
Bacilli|Lactobacillales|Lactobacillaceae|Lactobacillus| Lb. helveticus_otu27	0.72	0.16	0.49	0.02	3.499	0.0495
Bacilli|Lactobacillales.|Lactobacillaceae|Lactobacillus| Lb. helveticus_otu229	0.05	0.01	0.04	0.01	2.536	0.0495
Taxa more abundant in SEMI						
Bacteroidetes						
Flavobacteriia|Flavobacteriales|Flavobacteriaceae| Chryseobacterium spp._otu372	-	0.02	-	0.01	2.649	0.0495
Firmicutes						
Bacilli|Lactobacillales|Streptococcaceae|Lactococcus| Lc. lactis_otu214	-	0.01	-	0.01	2.770	0.0495
Bacilli|Lactobacillales|Streptococcaceae|Lactococcus| Lc. chungangensis/raffinolactis_otu48	0.06	0.18	0.01	0.04	2.878	0.0495

B

Taxa	Average abundance		Standard deviation		LDA score	pval
	EXT	SEMI	EXT	SEMI		
Taxa more abundant in EXT						
Proteobacteria						
Gammaproteobacteria|Enterobacteriales| Enterobacteriaceae|Escherichia|E. coli_otu90	0.15	0.004	0.25	0.002	2.958	0.0495
Taxa more abundant in SEMI						
Actinobacteria						
Actinobacteria|Micrococcales|Brevibacteriaceae| Brevibacterium_otu94	0.26	0.41	0.06	0.06	2.969	0.0495
Firmicutes						
Bacilli|Lactobacillales|Streptococcaceae|Lactococcus| Lc. lactis_otu46	0.07	0.23	0.05	0.09	2.924	0.0495
Bacilli|Lactobacillales|Streptococcaceae|Lactococcus| Lc. chungangensis/raffinolactis_otu48	0.06	0.31	0.05	0.14	3.135	0.0495
Bacilli|Lactobacillales|Streptococcaceae|Lactococcus_ otu89	0.04	0.21	0.03	0.08	3.006	0.0495

[1] Average abundances (expressed as percentages) as well as standard deviation are presented for each taxon. EXT = extensive grazing system; SEMI = semi-intensive grazing system

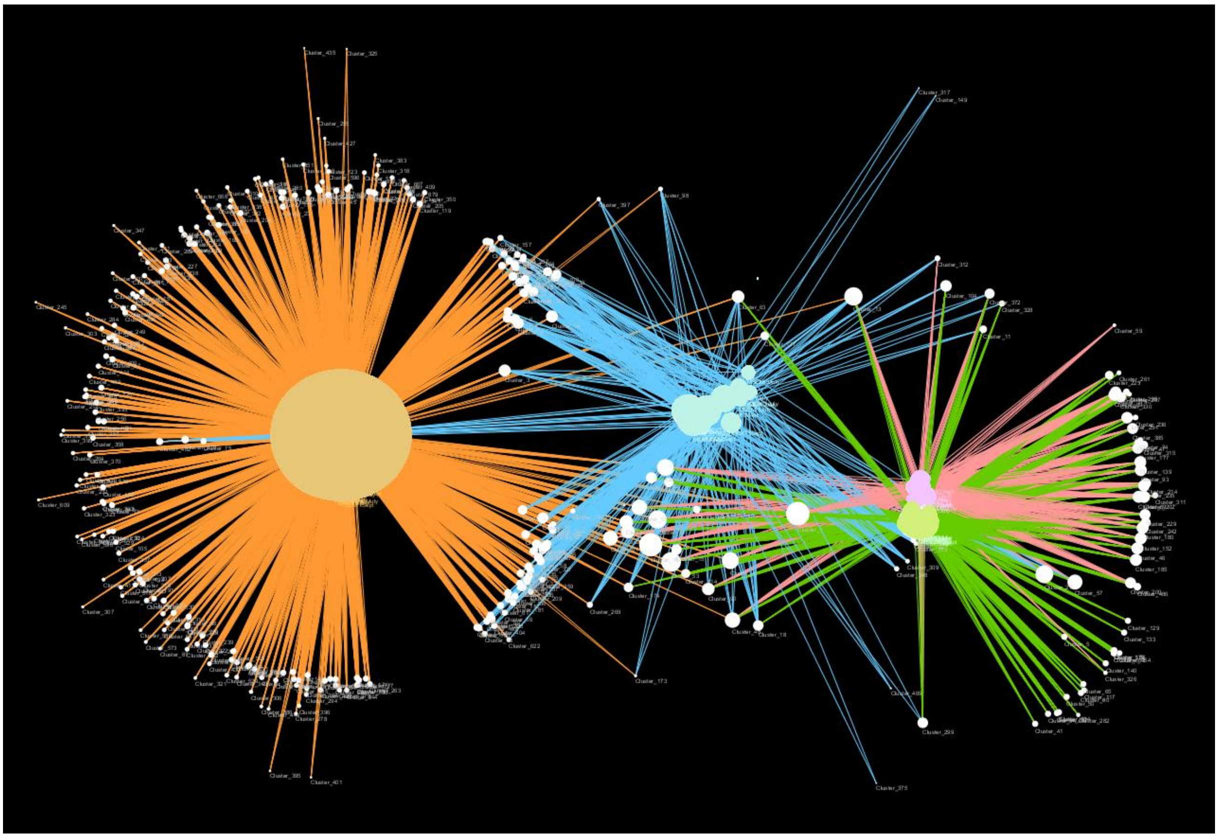

Figure S3. Network analysis from teat skin to ripened cheeses. The teat skin samples were coloured in orange, raw milk samples in blue, cheese core samples in pink, and cheese rind samples in green. The white nodes correspond to OTUs. The node size is proportional to the number of the edges (lines connecting the nodes). The OTUs detected in at least two samples of the same habitat were conserved.

Table S8. Average relative abundance (%) of 133 OTUs present in at least two habitats. The 9 OTUs detected in all habitats were framed.

🟩 0.1% 🟨 0.5% 🟧 1% 🟧 5% 🟥 10% 🟪 50% 🟥

Taxa	N°otu	Teat skin (n=12)	Milk (n=12)	Core (n=12)	Rind (n=12)
Actinobacteria					
Brevibacterium linens	OTU4	0.01	0.06	0.02	12.8
Bifidobacterium pseudolongum	OTU6	7.31	0.38		
Corynebacterium marinum	OTU8	5.87	1.58		
Brevibacterium linens	OTU11		0.05		1.87
Corynebacterium spp.	OTU12	3.62	0.83		
Brachybacterium paraconglomeratum/sacelli	OTU15	0.01	0.04		1.22
Corynebacterium	OTU17	1.70	1.01		
Bifidobacterium crudilactis/psychraerophilum	OTU18		10.7		0.01
Dietzia maris	OTU19	1.34	0.85		
Corynebacterium callunae	OTU20	1.37	0.86		
Corynebacterium camporealensis	OTU21	1.36	0.11		
Corynebacterium spp.	OTU22	1.28	0.24		
Corynebacterium glutamicum	OTU25	1.12	0.16		
Corynebacteriumhumireducens	OTU32	0.84	0.38		
Rhodococcus spp.	OTU33	0.04	6.10		
Bifidobacterium choerinum	OTU36	0.78	0.06		
Brevibacterium	OTU42	0.07			0.51
Brachybacterium sacelli	OTU44	0.03			0.30
Bifidobacterium merycicum	OTU52	0.44	0.3		
Yaniella halotolerans	OTU54	0.01			0.24
Nocardioides	OTU55	0.51	0.03		
Corynebacterium	OTU56	0.61	0.03		
Pseudoclavibacter helvolus	OTU58	0.35	0.31		
Arthrobacter spp.	OTU66	0.36	0.14		
Kocuria spp.	OTU72	0.33	0.03		
Atopobium	OTU75	0.34	0.02		
Corynebacterium lactis	OTU76	0.63	0.02		
Micrococcus luteus/terreus	OTU78	0.39	0.12		
Micrococcus	OTU79	0.29	0.01		
Tetrasphaera	OTU91	0.29	0.02		
Dietzia lutea	OTU99	0.25	0.02		
Rhodococcus spp.	OTU100	0.02	2.25		
Atopobium	OTU112	0.38	0.02		
Nocardioides solisilvae	OTU120	0.27	0.02		
Atopobium	OTU124	0.27	0.02		
Dietzia cercidiphylli	OTU127	0.01	0.01		0.09
Atopobium	OTU130	0.27	0.01		
Corynebacterium	OTU137	0.17	0.02		
Janibacter spp.	OTU153	0.22	0.07		0.02
Nocardioides daphniae	OTU157	0.13	0.07		
Kocuria rhizophila/salsicia	OTU174	0.01	0.64		0.01
Micrococcus spp.	OTU234	0.09	0.04		

Corynebacterium bovis	OTU269	0.02	0.3		
Corynebacterium variabile	OTU328		0.04		0.02
Agreia	OTU335	0.05	0.07		
Rhodococcus spp.	OTU397	0.01	0.21		
Leucobacter spp.	OTU404	0.10	0.16		
Bacteroidetes					
Chryseobacterium spp.	OTU372		0.25	0.01	0.01
Firmicutes					
Lactococcus lactis	OTU1	0.23	11.6	97.4	69.7
Romboutsia	OTU3	14.6	1.85		
Intestinibacter	OTU7	6.42	0.87		
Turicibacter	OTU9	5.59	1.53		
Peptoclostridium	OTU10	5.58	0.30		
Lactobacillus casei/paracasei	OTU13	0.01	6.61	0.42	0.60
Staphylococcus haemolyticus/petrasii	OTU16	2.37	0.80	0.10	0.25
Bacillus spp.	OTU24	0.02	6.71		
Aerococcus urinaeequi/viridans	OTU26	1.21	0.04		
Lactobacillus helveticus	OTU27		3.45	0.23	0.27
Bacillus	OTU29	1.03	0.09		
Jeotgalicoccus spp.	OTU34	1.39	0.04		0.08
Clostridium spp.	OTU35	0.80	0.04		
Acetitomaculum	OTU37	0.73	0.05		
Lactococcus lactis	OTU39			0.42	0.21
Lactococcus lactis	OTU46			0.16	0.11
Lactococcus chungangensis/raffinolactis	OTU48	0.01	0.06	0.12	0.15
Macrococcus caseolyticus	OTU51	0.29	0.25	0.06	0.10
Streptococcus porcinus/uberis	OTU53	0.04	4.04	0.03	0.06
Lactobacillus parabuchneri	OTU57		0.16	0.06	0.27
Proteiniclasticum	OTU60	0.52	0.07		
Aerococcaceae	OTU62	0.72	0.01		
Enterococcus spp.	OTU63	0.02	0.48		0.11
Staphylococcus chromogenes	OTU67	0.36	0.40	0.01	
Streptococcus dysgalactiae	OTU81	0.12	0.26	0.02	0.03
Clostridium	OTU85	0.27	0.04		
Lachnospiraceae	OTU88	0.24	0.03		
Lactococcus	OTU89			0.10	0.09
Lactococcus lactis	OTU93			0.11	0.04
Turicibacter sanguinis	OTU95	0.23	0.01		
Facklamia	OTU96	0.29	0.02		
Staphylococcus equorum	OTU114	0.02	0.01		0.11
Ruminococcaceae	OTU122	0.44	0.21		
Marvinbryantia	OTU132	0.30			
Mogibacterium	OTU135	0.22	0.09		
Lactococcus	OTU139			0.04	0.03
Christensenellaceae	OTU146	0.29	0.01		
Lactococcus	OTU152			0.07	0.05
Lachnospiraceae	OTU156	0.10	0.04		
Christensenellaceae	OTU164	0.11	0.04		
Lactococcus	OTU175			0.04	0.04
Lactobacillus brevis	OTU177			0.02	0.03

Lactobacillus spp.	OTU180			0.02	0.03
Lachnospiraceae	OTU181	0.15	0.01		
Lactococcus	OTU185			0.07	0.06
Ruminococcaceae	OTU186	0.18	0.01		
Ruminococcaceae	OTU197	0.08	0.13		
Lactococcus lactis	OTU200			0.03	0.02
Lactobacillus spp.	OTU202			0.03	0.03
Lachnospiraceae	OTU203	0.20	0.07		
Ruminococcaceae	OTU206	0.15	0.02		
Streptococcus pluranimalium	OTU209	0.06	0.32		
Lactococcus lactis	OTU214			0.02	0.01
Lactobacillus helveticus	OTU229			0.02	0.02
Lactobacillus spp.	OTU235			0.02	0.02
Lactococcus	OTU242			0.01	0.01
Lactobacillus parabuchneri	OTU251			0.01	0.04
Christensenellaceae	OTU258	0.12	0.10		
Planomicrobium	OTU295			0.02	0.01
Macrococcus caseolyticus	OTU311			0.02	0.02
Lactobacillus curvatus	OTU315			0.01	0.01
Lachnospiraceae	OTU327	0.06	0.02		
Streptococcus	OTU330			0.02	0.01
Ruminococcaceae	OTU339	0.06	0.06		
Paenibacillus spp.	OTU359	0.04	0.03		
Lactococcus lactis	OTU385			0.02	0.01
Christensenellaceae	OTU402	0.07			
Fastidiosipila	OTU417	0.03		0.01	0.01
Fusobacteria					
Fusobacterium	OTU223			0.05	0.01
Proteobacteria					
Sphingomonas spp.	OTU14	0.24	19.6		
Paracocccus chinensis	OTU61	0.67	0.16		
Escherichia coli	OTU90	0.01	0.01	0.05	0.07
Cupriavidus gilardii	OTU98	0.01	1.43		
Sphingomonas spp.	OTU101	0.20	0.41		
Brevundimonas spp.	OTU103	0.02	1.11		
Pseudomonas spp.	OTU104		0.73	0.01	0.04
Paracocccus spp.	OTU107	0.36	0.01		
Sphingomonadaceae changbaiensis	OTU173	0.01	0.58		
Bradyrhizobium spp.	OTU267	0.04	0.11		
Rhizobium	OTU288	0.08	0.04		
Acinetobacter guillouiae	OTU299		0.06	0.01	0.01
Acinetobacter	OTU312		0.31	0.02	
Pseudomonas putida	OTU326			0.01	0.02
Enterobacteriaceae	OTU486			0.01	0.02
Bosea	OTU622	0.02	0.04		

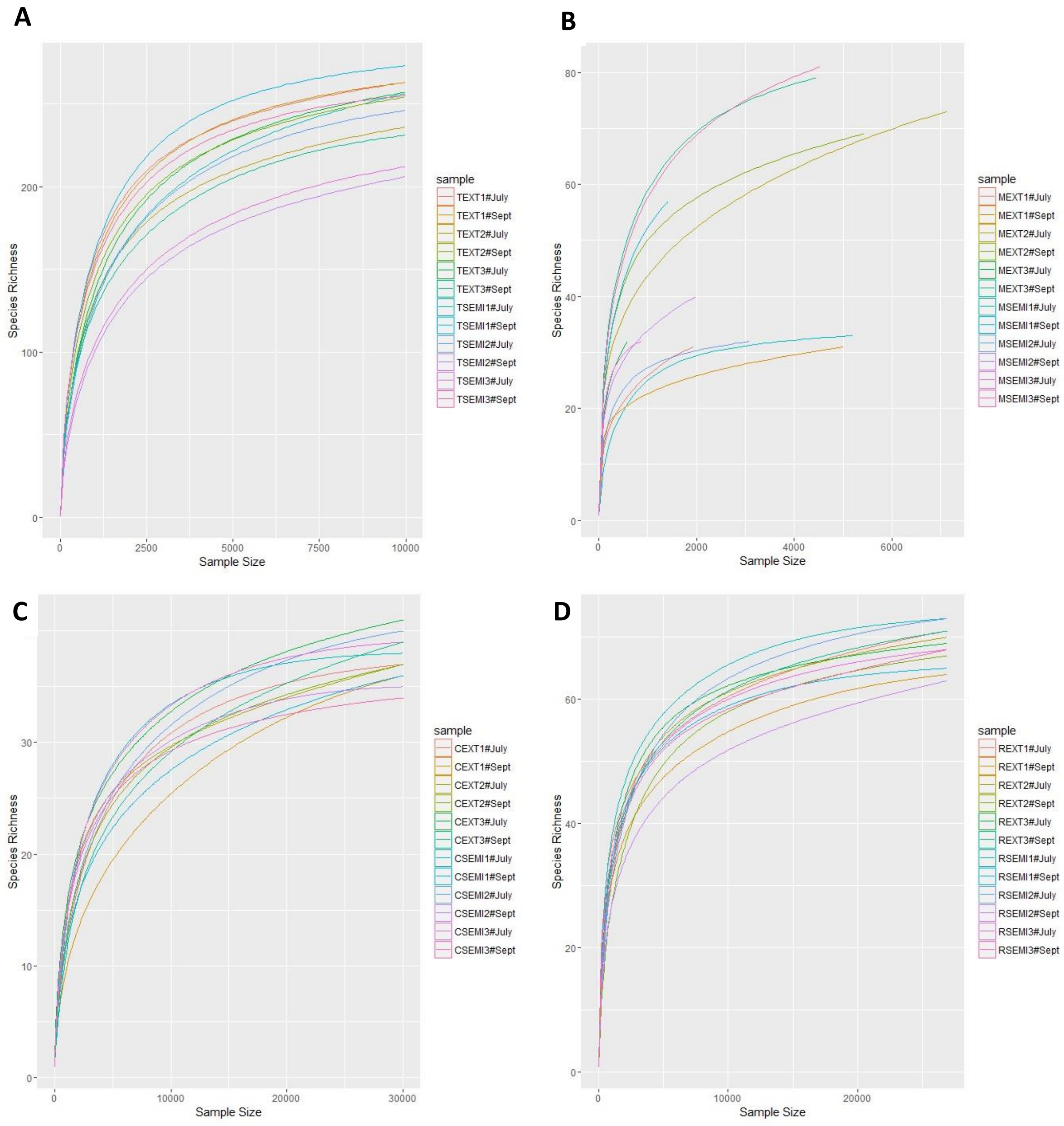

Figure S4. Rarefaction curves from the V3-V4 region of the 16S rRNA from teat skin (A), raw milk (B), cheese core (C), and cheese rind (D) samples.