

Figure S1. Experimental design.

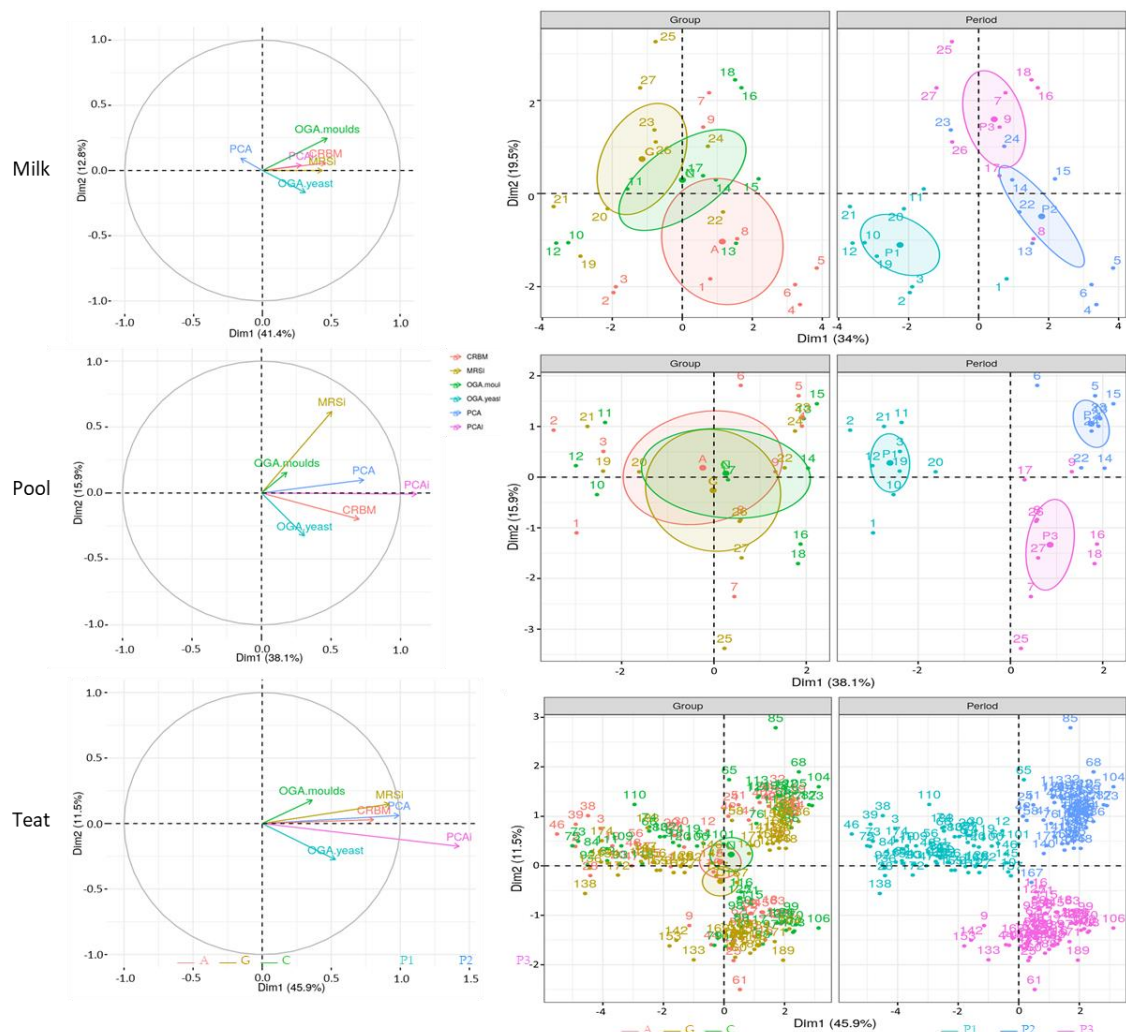


Figure S2: Multi-Factor Analysis of the microbial numeration from cultural media according to post-milking group and period.

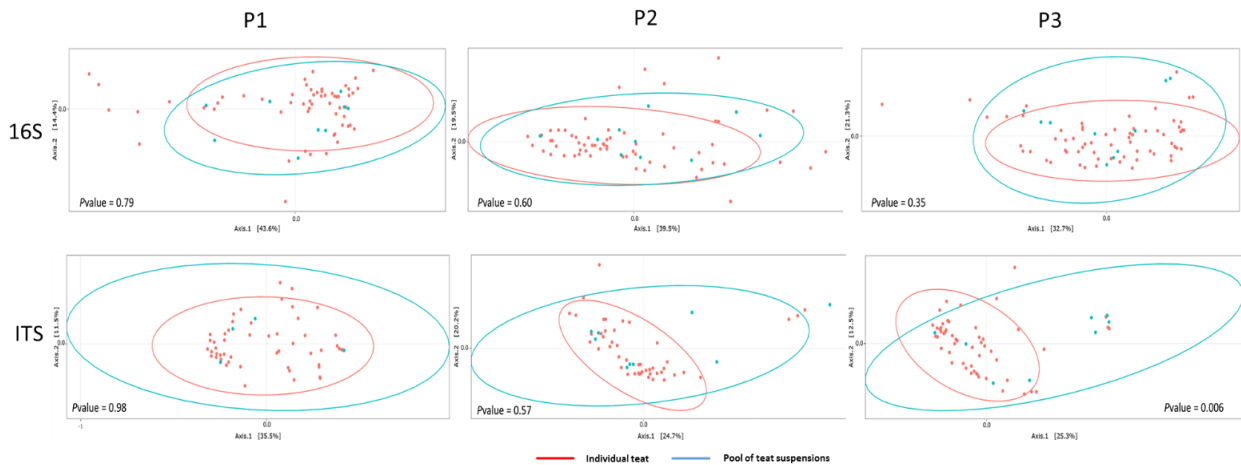
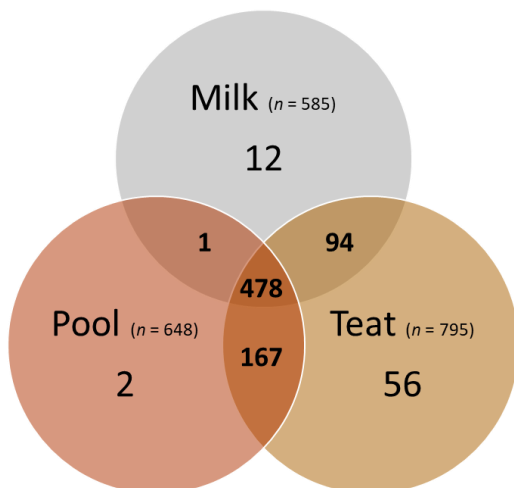


Figure S3: Bacterial (16S) and fungal (ITS) betadiversity of individual and pooled teat suspensions according to the period of treatment (P1, P2 and P3) and all treatments together.

(a) Bacterial ASVs



(b) Fungal ASVs

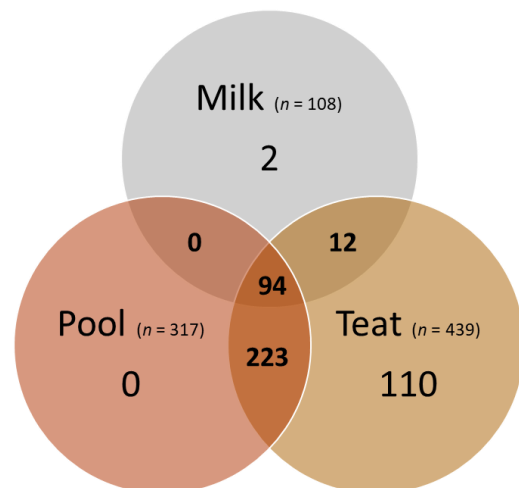


Figure S4: Number of the bacterial (a) and fungal (b) ASVs shared between milk, pooled and individual teat suspensions.

Table S1: Cow group characteristics.

	A		G		C	
	Mean	SD	Mean	SD	Mean	SD
Primiparous cow	1		1		1	
Multiparous cows	6		6		6	
Parity (for multiparous)	3.17	1.47	3	0.89	3.17	1.16
Overall parity	2.85	1.57	2.72	1.12	2.85	1.34
Cows in early lactation	5		5		5	
Cows in late lactation	2		2		2	
Overall lactation stage (d)	110.6	96.6	108.0	71.2	93.6	81.7
Lactation stage for early lactating cows (d)	56.4	32.6	68.2	8.5	47.5	32.5
Lactation stage for late lactating cows (d)	246	19.8	208	48.8	206	7.8
Milk yield (kg.d ⁻¹)	28.5	5.86	27.4	6.47	28.9	4.80

Table S2: *P*value of the bacterial (16S) and fungal (ITS) betadiversity of the pooled teat suspensions according to the treatment and the period

	A	G	C	P1	P2	P3
16S	0.07	0.55	0.038	0.37	0.75	0.17
ITS	0.06	0.73	0.19	0.50	0.55	0.62

Table S3: *P*value of the bacterial (16S) and fungal (ITS) dispersion of individual teat suspensions evaluated through TukeyHSD test

	16S			ITS		
	A	G	C	A	G	C
P2-P1	0.952	0.997	0.855	0.071	2.2×10^{-5}	0.013
P3-P1	0.397	0.039	0.999	0.237	5.40×10^{-4}	0.213
P3-P2	0.561	0.023	0.874	0.696	8.00×10^{-1}	0.356