

Table S2. Table of agreement between the 16S rRNA sequencing and the MALDI TOF tests for the identification of different NAS species.

16S rRNA	<i>S. epidermidis</i>	<i>S. chromogenes</i>	<i>S. haemolyticus</i>	<i>S. hominis</i>	<i>S. hyicus</i>	<i>S. sciuri</i>	<i>S. simulans</i>	<i>S. xylois</i>	<i>S. warneri</i>
MALDI-TOF									
<i>S. epidermidis</i>	16	1							
<i>S. chromogenes</i>	1	99	1						
<i>S. haemolyticus</i>			16						
<i>S. hominis</i>				0					1
<i>S. hyicus</i>					1				
<i>S. sciuri</i>						1			
<i>S. simulans</i>							5		
<i>S. xylois</i>								3	
<i>S.warneri</i>									0
Total	17	100	17	0	1	1	5	3	1
Observed agreement	0.94	0.99	0.94	0	1	1	1	1	0

Table S3. Inter-herd relation and species variation of non-aureus staphylococci species isolated from milk samples of 17 dairy herds with different farming systems and herd size.

Herd identification	Non-aureus staphylococcus (NAS) species									Number of NAS isolated	% <i>S. chromogenes</i> per herd	Number of lactating cows / herd	Pasture / Total mixed ration systems
	<i>S. chromogenes</i>	<i>S. epidermidis</i>	<i>S. haemolyticus</i>	<i>S. hominis</i>	<i>S. hyicus</i>	<i>S. sciuri</i>	<i>S. simulans</i>	<i>S. xylosus</i>					
A	15	0	1	0	0	0	4	0	20	75.0	1493	TMR	
B	2	0	0	0	0	0	0	1	3	66.7	843	Pas	
C	9	0	2	0	0	0	0	0	11	81.8	165	TMR	
D	3	0	1	0	0	0	0	0	4	75.0	412	Pas	
E	20	1	1	0	0	0	0	0	22	90.9	566	Pas	
F	27	4	4	0	0	1	0	2	38	71.1	1432	Pas	
G	5	5	1	0	0	0	0	0	11	45.5	706	TMR	
H	10	4	3	0	0	0	0	0	17	58.8	612	Pas	
I	2	0	0	0	0	0	0	0	2	100.0	1030	Pas	
J	13	0	0	0	0	0	0	1	14	92.9	1320	Pas	
K	13	0	0	0	0	0	0	1	14	92.9	594	Pas	
L	2	0	0	0	0	0	0	0	2	100.0	401	Pas	
M	2	2	0	0	0	0	0	0	4	50.0	765	Pas	
N	4	0	0	0	0	0	0	0	4	100.0	550	Pas	
O	5	1	0	0	0	0	0	0	6	83.3	469	Pas	
P	19	2	0	0	1	0	1	0	23	82.6	1020	Pas	
Q	10	1	6	1	0	0	1	0	19	52.6	630	TMR	