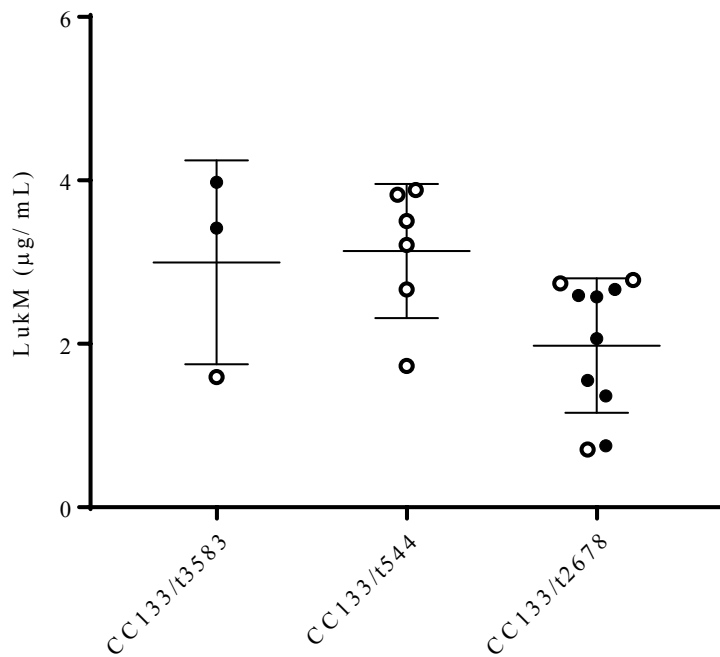


Supplemental Table S1. Goat herd and sheep flock distribution of 85 *S. aureus* isolates obtained from cases of ovine and caprine mastitis in the Netherlands

CC ¹	<i>spa</i> -type	Goat herds										Sheep flocks						Total			
		A	B	C	D	E	F	I	J	A	C	D	G	I	J	M	O				
133	t2678		1	4	1								3	6	3	5	1	2	3		29
	t3583	7	6											2							15
	t544	6			2	2	1	1	3												15
	t16713												3		1						4
	t16712												2								2
	t16710												1								1
	t12382												1								1
	t3495			1																	1
	t4560				1																1
	t17048			1																	1
	t17047	1																			1
	NA ²												1					1			2
398	t011	5	1																		6
425	t15002															2					2
	t16711															2					2
45	t015												1								1
	t715																		1		1
Total		19	8	6	3	3	1	1	3				5	6	6	11	5	3	4	1	85

¹Clonal complex.

²Isolates not typeable using any of the *spa* primer sets used in our study.



Supplemental Figure S1. LukM levels *in vitro* after eight hours of culture of *lukM-lukF'*-positive *S. aureus* mastitis isolates obtained from sheep (black) and goats (white) in subset of single isolate of the same *spa*-type per farm. When multiple isolates of the same *spa*-type were present within a single farm, the average lukM production of these isolates was used. Isolates belong to genotypes CC133/t3583 ($n = 3$), CC133/t544 ($n = 6$) and CC133/t2678 ($n = 10$), tested by ELISA. Statistical significance was analyzed by Kruskal-Wallis test followed by Dunn's test.