

Table S1. Statistical analysis of eight candidate housekeeping genes.

| Statistics | Gene name | | | | | | | |
|----------------|-----------|------------|------------|-------------|-------------|-------------|-------------|------------|
| | 16S rRNA | <i>pta</i> | <i>rho</i> | <i>gyrB</i> | <i>recA</i> | <i>rplD</i> | <i>rpoB</i> | <i>tpo</i> |
| GM [Cq] | 22.77 | 26.58 | 30.22 | 26.33 | 31.43 | 30.95 | 29.96 | 27.19 |
| Min [Cq] | 21.81 | 25.03 | 25.48 | 24.58 | 26.30 | 27.18 | 24.76 | 24.90 |
| Max [Cq] | 23.60 | 28.00 | 33.76 | 27.41 | 36.70 | 34.09 | 34.56 | 30.18 |
| SD [\pm Cq] | 0.44 | 0.90 | 2.96 | 1.04 | 3.17 | 2.05 | 2.66 | 1.92 |
| CV [% Cq] | 1.95 | 3.38 | 9.73 | 3.95 | 10.01 | 6.59 | 8.83 | 7.03 |
| CC [r] | 0.930 | 0.877 | 0.811 | -0.034 | 0.595 | -0.068 | -0.133 | 0.669 |
| <i>p</i> value | 0.001 | 0.001 | 0.001 | 0.915 | 0.041 | 0.830 | 0.683 | 0.017 |

Cq – cycle of quantification; GM – geometric mean; Min – minimal value; Max – maximal value; SD – standard deviation; CV – coefficient of variance; CC [r] – correlation coefficient between each candidate and the BestKeeper index. BestKeeper performs repeated pairwise correlation and regression analyses for a given gene with all other genes.

Table S2. Cycle of quantification (Cq) obtained in this study.

| Samples | Media | Cq \pm SEM | | | | | | |
|---------------------------------|-------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|
| | | 16S rRNA | <i>sea</i> | <i>sec</i> | <i>sel</i> | <i>agrA</i> | <i>hld</i> | <i>rot</i> |
| Unexposed to the RMFs (control) | A | 18.15 \pm 0.24 | 29.17 \pm 0.17 | 27.38 \pm 0.30 | 22.83 \pm 0.31 | 22.75 \pm 0.23 | 23.75 \pm 0.29 | 25.89 \pm 0.13 |
| | B | 19.59 \pm 0.13 | 30.85 \pm 0.25 | 29.01 \pm 0.59 | 24.09 \pm 0.65 | 23.90 \pm 0.53 | 25.02 \pm 1.0 | 26.95 \pm 0.18 |
| | C | 18.23 \pm 0.39 | 28.44 \pm 0.44 | 27.80 \pm 0.35 | 22.67 \pm 0.15 | 21.67 \pm 0.24 | 23.01 \pm 0.37 | 25.62 \pm 0.65 |
| Exposed to the RMF I (5 Hz) | A | 19.25 \pm 0.08 | 30.22 \pm 0.69 | 29.22 \pm 0.39 | 24.70 \pm 0.26 | 23.76 \pm 0.66 | 24.42 \pm 0.18 | 27.38 \pm 0.36 |
| | B | 19.67 \pm 0.22 | 30.17 \pm 0.13 | 28.91 \pm 0.51 | 20.61 \pm 0.84 | 23.68 \pm 0.21 | 25.10 \pm 0.23 | 26.63 \pm 0.57 |
| | C | 19.41 \pm 1.04 | 31.27 \pm 0.19 | 29.27 \pm 0.19 | 23.14 \pm 0.92 | 23.74 \pm 0.18 | 24.90 \pm 0.11 | 26.90 \pm 0.11 |
| Exposed to the RMF II (50 Hz) | A | 16.97 \pm 0.03 | 24.90 \pm 0.68 | 28.31 \pm 0.36 | 21.82 \pm 0.22 | 20.42 \pm 0.38 | 21.85 \pm 0.06 | 23.90 \pm 0.56 |
| | B | 18.45 \pm 0.49 | 26.68 \pm 0.10 | 27.80 \pm 0.97 | 23.51 \pm 0.24 | 21.70 \pm 0.15 | 23.81 \pm 0.26 | 25.28 \pm 0.23 |
| | C | 19.61 \pm 0.39 | 30.68 \pm 0.41 | 30.15 \pm 0.65 | 24.80 \pm 0.56 | 23.73 \pm 0.35 | 24.15 \pm 0.35 | 27.08 \pm 0.16 |

SEM – standard error of measurement; RMF – rotating magnetic field; A – Mueller-Hinton agar (MHA) non-supplemented with *trans*-anethole; B – MHA supplemented with 1% (*v/v*) Tween 80; C – MHA supplemented with 1% (*v/v*) Tween 80 and subinhibitory concentration (MIC₅₀) of *trans*-anethole.

Table S3. Correlation analysis between staphylococcal enterotoxin (SE) genes expression and SEs production.

| Samples | SE | Media | Spearman coefficient [r] | <i>p</i> value |
|---------------------------------|--------------------|-------|--------------------------|----------------|
| Unexposed to the RMFs (control) | | A+B+C | 0.7622 | 0.0040 |
| Exposed to the RMF I (5 Hz) | <i>sea</i> vs. SEA | A+B+C | 0.7566 | 0.0044 |
| Exposed to the RMF II (50 Hz) | | A+B+C | 0.5359 | 0.0725 |
| Unexposed to the RMFs (control) | | A+B+C | 0.8392 | 0.0006 |
| Exposed to the RMF I (5 Hz) | <i>sec</i> vs. SEC | A+B+C | -0.2487 | 0.4357 |
| Exposed to the RMF II (50 Hz) | | A+B+C | 0.0541 | 0.8674 |
| Unexposed to the RMFs (control) | | A+B+C | 0.5315 | 0.0754 |
| Exposed to the RMF I (5 Hz) | <i>sel</i> vs. SEL | A+B+C | -0.4685 | 0.1245 |
| Exposed to the RMF II (50 Hz) | | A+B+C | -0.3986 | 0.1993 |

RMF – rotating magnetic field; A – Mueller-Hinton agar (MHA) non-supplemented with *trans*-anethole; B – MHA supplemented with 1% (*v/v*) Tween 80; C – MHA supplemented with 1% (*v/v*) Tween 80 and MIC₅₀ of *trans*-anethole.

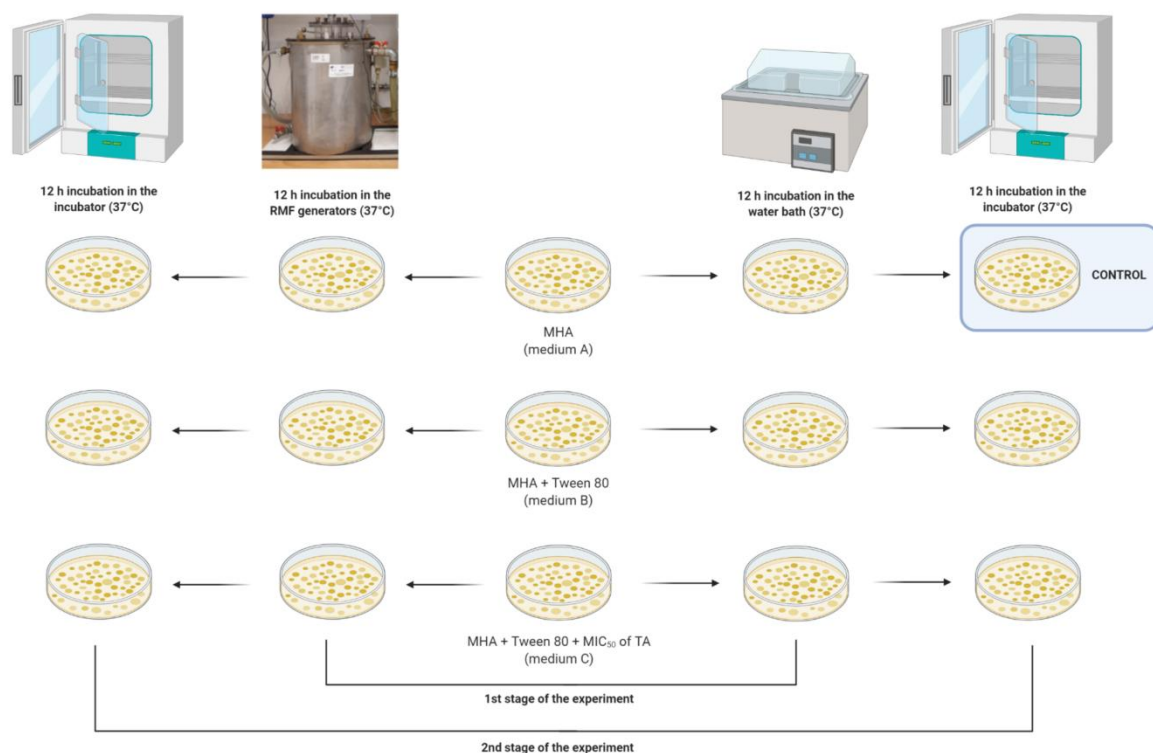


Figure S1. Schematic diagram of the experiment. Created with BioRender.com.

Table S4. Primer sequences for real-time quantitative PCR analysis.

| Gene | Sequence | Amplicon length (bp) | References |
|-------------|--|----------------------|------------|
| <i>sea</i> | F: 5'-CAG CAT ACT ATA TTG TTT AAA GGC-3' R: 5'-CCT CTG AAC CTT CCC ATC-3' | 400 | [1] |
| <i>sec</i> | F: 5'-CTC AAG AAC TAG ACA TAA AAG CTA GG-3' R: 5'-TCA AAA TCG GAT TAA CAT TAT CC-3' | 271 | [1] |
| <i>sel</i> | F: 5'-TAA CGG CGA TGT AGG TCC AGG-3' R: 5'-CAT CTA TTT CTT GTG CGG TAA C-3' | 383 | [1] |
| <i>agrA</i> | F: 5'-CCT CGC AAC TGA TAA TCC TTA TG-3' R: 5'-ACG AAT TTC ACT GCC TAA TTT GA-3' | 127 | [2] |
| <i>hld</i> | F: 5'-TAA GGA AGG AGT GAT TTC AAT GG-3' R: 5'-GTG AAT TTG TTC ACT GTG TCG AT-3' | 90 | [2] |
| <i>rot</i> | F: 5'-TGC AGT ATT TCA ACC ACA CAC-3' R: 5'-GTA TCG TTA ATG CGC CAG T-3' | 140 | [2] |

References

1. Park, J.Y.; Fox, L.K.; Seo, K.S.; McGuire, M.A.; Park, Y.H.; Rurangirwa, F.R.; Sischo, W.M.; Bohach, G.A. Detection of classical and newly described staphylococcal superantigen genes in coagulase-negative staphylococci isolated from bovine intramammary infections. *Vet. Microbiol.* **2011**, *147*, 149–154, doi:10.1016/j.vetmic.2010.06.021.
2. Schubert, J.; Podkowik, M.; Bystroń, J.; Bania, J. Production of staphylococcal enterotoxins D and R in milk and meat juice by *Staphylococcus aureus* strains. *Foodborne Pathog. Dis.* **2017**, *14*, 223–230, doi:10.1089/fpd.2016.2210.