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|------------------------------------|--|
| Title | Tn6188 - a novel transposon in <i>Listeria monocytogenes</i> responsible for tolerance to benzalkonium chloride |
| Author(s) | Mueller, Anneliese; Rychli, Kathrin; Muhterem-Uyar, Meryem; Zaiser, Andreas; Stessl, Beatrix; Guinane, Caitriona M.; Cotter, Paul D.; Wagner, Martin; Schmitz-Esser, Stephan |
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Figure S2

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L. mono. EGD-e           1  -----ATGTTGACACATGAAATATCAGAGAATGAAAAACCACGC
L. mono. F2365          1  -----ATGTTGATACATGAAATATCAGAGAATGAAAAACCACGC
L. mar. FSL S4-120     1  -----ATGTTAATTAATGAAGTTCTGGAAAATGAAAAACCGCCT
L. inn. Clip11262     1  -----ATGCTAGTAAATGAAATCTCGGAAAATGAGAAGCCACGA
L. wel. SLCC5334       1  -----ATGCTTACAAGTGAGATTTTCAGAAAAGCGAAAAACCACGT
L. iv. FSL F6-596     1  -----ATGTTATCAAACGAAATTTTCAGGAAATGAGAAGCCTCGC
L. seel. SLCC3954     1  -----ATGCTAGCAAACGAAATTTTCAGGGAGCGAAAAGCCCCGT
L. gr. DSM20601       1  -----ATGCAAATGAAAGAAATGCAGATTTTTTGATAAACCTCGA
B. smi. 7_3_47FAA     1  -----TTGTCAAAGAATCGCTTAGGATCCATAACCTTCACGTGAAGATCGGCCGCGG
B. coag. 36D1         1  -----TTGGAAAAATGCTGATCAAAGATTTTCTGCAGAAAGACCGCCCGCT
B. subt. 168          1  TTGGTCATACACGATCTGCCATTAATACTCAAAGATTTCCCAATGAAAGAAAAGCCAAAG
B. weih. KBAB4        1  -----ATGAACGGTATTCGTGATGTTGTGAGAGAAGAACGCCACGG
S. aur. COL           1  -----TTGAAAATTAAGAAATGGTAACTTCAGAAATGCCAAGA
S. aur. 71193         1  -----TTGAAAATTAAGAAATGGTAACTTCAGAAATGCCAAGA
E. faec. DO           1  -----TTGGAAAACGATTGATCAAAGAAGTACCTACTAGCTCTTTACCAAG
consensus              1  . . . . . * . . . * . . . . . * . . . . . * . . . . .

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L. mono. EGD-e           40  GAAAAACTTCAGAATTATGGGTATAGAAGCACTTTCATCTTCGGAACCTGGTTGCTTTAATT
L. mono. F2365          40  GAAAAGCTACAGAATTATGGGATAGAAGCACTTTCATCTTCGGAATTGGTTGCTTTAATT
L. mar. FSL S4-120     40  GAAAAGTTACAGAATTATGGGATAGAGGCTCTTTCCTTCTTCGGAGTTAGTTGCTTTAATT
L. inn. Clip11262     40  GAAAAATTACAAAATTATGGGATAGAGGCGCTTTCGACTTCGGAGTTAGTTGGCATTAAATT
L. wel. SLCC5334       40  GAAAAACTTCAAAATTATGGGATAGAGGCTCTTTCGTCATCGGAATTAGTCGCGTTAATA
L. iv. FSL F6-596     40  GAGAAATTACAAAATATGGTATAGAGGCACTTTCATCTTCAGAATTAGTCGCAATTATC
L. seel. SLCC3954     40  GAAAAGCTACAAAATTATGGCATTGAAGCACTTTCACGTCAGAGCTTGTTCGATAATA
L. gr. DSM20601       40  GAAAAATGCAGACAAGAGGGCAAGCCCAACTTACCATAACGGAACTTCTTGCATATTA
B. smi. 7_3_47FAA     55  GAACGACTGATATTAAGAGGAGCGCACAGCTTGTCCAACCATGAATTGATCGCCATTCTT
B. coag. 36D1         49  GAACGGTTGATCCGCACAGGAGCGGAGAGCTCTCCAATCAGGAATTTGCTGCCATTTTA
B. subt. 168          61  GAACGGCTCCTGAAGTCGGAGCCGAGAACTTAGCGAATCATGACTTTTGGCTATATTA
B. weih. KBAB4        43  GAGCGTTTATTGTTAGAAAGGAGCAGGAAGTTTATCGAATCGAGAACTTCTTGCAGTTTTA
S. aur. COL           40  GAACGTTTGTAAAGCCATGGTGCAAAAGTCTTTCGAATACAGAATTATTAGCTATATTA
S. aur. 71193         40  GAACGTTTGTAAAGCCATGGTGCAAAAGTCTTTCGAATACAGAATTATTAGCTATATTA
E. faec. DO           49  GAACGTATGAAAATTTATGGCGCGGAAGCTTTTATCGGATCAGGAGCTTTTGGCAATCTTA
consensus              61  ** . . . . * . . . . . ** . . . . . * . . . * . . . . . * . . . . . ** * . . *

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L. mono. EGD-e           100  ATTGAAACAGGAACATAAAAATGAGTCAGTTTTGACGATAGCTAATCGAATCATCATGAAG
L. mono. F2365          100  ATTGAAACAGGGACTATAAAAATGAGTCAGTTTTGACGATAGCTAATCGAATCATCATGAAA
L. mar. FSL S4-120     100  ATTGAAACTGGAACGAAAAATGAGTCTGTTTTAACAATAGCAAATCGAATTATTATGAAA
L. inn. Clip11262     100  ATTGAAACTGGAACGAAAAATGAGTCTGTTTTAACAATAGCAAATCGAATTATTATGAAA
L. wel. SLCC5334       100  ATTGAAACAGGCACAAAAAATGAATCGGTTTTAACAATAGCAAATAGAATTATCATGAAA
L. iv. FSL F6-596     100  ATTGAAACAGGCACGAAAAGTGAATCGGTTTTAACAATAGCAAATCGAATTATTATGAAA
L. seel. SLCC3954     100  ATTGAAACAGGAACGAAAAATGAGTCTGTTTTGACAATAGCAAATCGAATTATTATGAAG
L. gr. DSM20601       100  TTGGAAACGGGAACGAAAGAAGATTCGGTTTTATCATTAGCCAATAAAAATCATTCTTAAA
B. smi. 7_3_47FAA     115  CTCAGTTCGGGACAAAAGAAGAGTCCGTCTGCAGCTGGCAAATCGGCTATTAATCAG
B. coag. 36D1         109  CTCCTTACCCTGACGAAAGAAGAAATCGTGTGCTCGAGCTTGCCAACAGACTGATCCGCCAT
B. subt. 168          121  TTGCGGACAGGGACTAAACACGAATCTGTTTTGGACCTGTCAAACCGGCTGCTGCGCTCA
B. weih. KBAB4        103  CTCAGAACGGGTTCTAAAGAAGAAACGGTGTAAACGTTATCAGATAAATTCTCCATCAT
S. aur. COL           100  ATTAACACCGGAAGAAAAGGATTCTCGAGCATAGACATTAGTAATGAACTGCTTAAATCT
S. aur. 71193         100  ATTAACACCGGAAGAAAAGGATTCTCGAGTATTACATTAGTAATGAACTGCTTAAATCT
E. faec. DO           109  CTGCGTACCCTGCAACACCCTTATAGTGTGATGTGATGCTGGAAATCTGTTAAAAACG
consensus              121  . * . . . . * . . . . . * . . . . . * . . . . . * . . . . . * . . . . .

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|-----------------|------------|-----|--|
| <i>L. mono.</i> | EGD-e | 160 | TTC AAAAATGTGGGTGAAATGCAATATGCTTCTATAGAAGAATTCAATTAGTTAATGGT |
| <i>L. mono.</i> | F2365 | 160 | TTC AAAAACGTGGCCGAAATGCAATATGCTTCTATAGAAGAATTCAAGTTAGTTAATGGT |
| <i>L. mar.</i> | FSL S4-120 | 160 | TTC AAAAATGTGGCAGAAATGCAGTATGCTTCTATTGAAGAATTCAATTAGTTAATGGT |
| <i>L. inn.</i> | Clip11262 | 160 | TTTAAACATATAGCTGAAATGCAGTACGGCTCTATTGAAGAATTCAATTAGTTAATGGT |
| <i>L. wel.</i> | SLCC5334 | 160 | TTTAAACATGTAGCAGAAATGCAATATGCTTCAATCGAAGAAATCCAACCTTGTGAATGGA |
| <i>L. iv.</i> | FSL F6-596 | 160 | TTCAAACATGTAGCTGAAATGCAATATGCTTCTTTTGAAGAGTTCAATTAAATTAATGGC |
| <i>L. seel.</i> | SLCC3954 | 160 | TTTAAACATGTAGCAGAAATGCAATATGCTTCTTTAGAAGAACTTCAATTAATTAACGGA |
| <i>L. gr.</i> | DSM20601 | 160 | TATAAATCGCTAGGAGATATCAAAGATCTGACTATCGAAGAATTGCGATCTATCAATGGT |
| <i>B. smi.</i> | 7_3_47FAA | 175 | TTTGAAGGATTACGAATGTTAAAAGATGCTACTTTAGAAGAAATTACCTCTATTAAAGGA |
| <i>B. coag.</i> | 36D1 | 169 | TTTGAAGGCTTGGCGTTTTTAAAAGATGCTTCCCTTGAGGAAATGACGTCATCAAAGGC |
| <i>B. subt.</i> | 168 | 181 | TTTGACGGGCTGCGCCTGCTCAAGGAAGCATCGGTTGAAGAGCTGTCAAGCATCCCGGGA |
| <i>B. weih.</i> | KBAB4 | 163 | TTTGACGGCTTACGAATGTTAAAGGATGCAACGTTAGAAGAGATGATGAGCATTTCATGGT |
| <i>S. aur.</i> | COL | 160 | GCTTCGAATCTGAATGAATTGAAAAAATCTTCAATTAACGATTTGATAAAAAGTTAAAGGG |
| <i>S. aur.</i> | 71193 | 160 | GCATCGAATCTGAATGAATTGAAAAAATCTTCAATTAACGATTTGATACAGTTAAAGGG |
| <i>E. faec.</i> | DO | 169 | TTTGGAGGACTGGCCTCTTTACGACAGGCTACTTTGCATGAGTTAGAAGAGATTTCGAGG |
| consensus | | 181 |*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....* |

| | | | |
|-----------------|------------|-----|--|
| <i>L. mono.</i> | EGD-e | 220 | ATTGGAATAGCAAAAGCTTCTAAAATCATGGCTGCGATTGAACTAGGAAGGCGTATCAGC |
| <i>L. mono.</i> | F2365 | 220 | ATCGGAATAGCAAAAGCTTCTAAAATCATGGCTGCGATTGAACTTGGAAAGACGTATCGGC |
| <i>L. mar.</i> | FSL S4-120 | 220 | ATCGGAATAGCTAAAGCATCTAAAATATGGCTGCAGTTGAACTTGGTAGGCGTATAAGT |
| <i>L. inn.</i> | Clip11262 | 220 | ATTGGAATTGCTAAAGCCTCAAAAATATGGCAGCAGTCAACTTGGAAAACGCATCAGT |
| <i>L. wel.</i> | SLCC5334 | 220 | ATTGGACTAGCAAAGCCTCAAAAATAATGGCAGCAATTGAGCTGGGTAGGCGTATTAGT |
| <i>L. iv.</i> | FSL F6-596 | 220 | ATTGGTATTGCTAAAGCTTCTAAAATAATGGCCGCTATTGAATTAGGAAAGAGAATTAGT |
| <i>L. seel.</i> | SLCC3954 | 220 | ATAGGCTTGGCAAAGCCTTCAAAAATAATGGCAGCAGTAGAATTAGGAAACGAATTAGC |
| <i>L. gr.</i> | DSM20601 | 220 | ATTGGACTTGGCAAAGCTACTAAAATCATGGCTGCGATCGAGATTGGGAAACGGATCTGT |
| <i>B. smi.</i> | 7_3_47FAA | 235 | ATTGGTTCGGGCGAAAGCTGTTCAAAATCATGGCGGCGCTGGAACTGGGCAGACGTATCCAC |
| <i>B. coag.</i> | 36D1 | 229 | ATCGGCACAGCAAAAGCGGTCCAGATTCTGGCCGCGATTGAACTCGGCAGAAGGATTGCC |
| <i>B. subt.</i> | 168 | 241 | ATCGGTATGGTAAAAGCGATTCAAATACTGGCAGCAGTTGAGCTTGGAAAGCCGGATTTCAT |
| <i>B. weih.</i> | KBAB4 | 223 | GTGGGATTGCAAAGCGCTCGCAGCTTATGGCTGCTTTTGAATTAGGTAGAAGAATGGTA |
| <i>S. aur.</i> | COL | 220 | ATTGGATTACAAAAGCAATTAATTTAAAAGCAGCATTGAGTTAGGGGAAAGGATGGGG |
| <i>S. aur.</i> | 71193 | 220 | ATTGGATTACAAAAGCAATTAATTTAAAAGCGGCATTGAGTTAGGGGAAAGGATGGGG |
| <i>E. faec.</i> | DO | 229 | ATAGGACGCGTGAAGCAATCGAAATCAAAGCCTTGATCGAATTAGGTGACGAATTCA- |
| consensus | | 241 | .*.**.....**.*.....*.....*.....*.....*.....*.....*.....*.....*.....* |

| | | | |
|-----------------|------------|-----|--|
| <i>L. mono.</i> | EGD-e | 280 | ATCGTAACGGAGCAGGAAGAA-----GTGGTTGTTAGGTGTCCCGAAGATGCAGTAAAA |
| <i>L. mono.</i> | F2365 | 280 | ATCGTAACGGAGCAGGAAGAA-----GTGGTAGTTAGGTGTCCCGAAGATGCGGTAAAA |
| <i>L. mar.</i> | FSL S4-120 | 280 | TTAGTAACAGAACAAAGAGGAG-----GTTGTTGTTAGGTGCCCTGAAGATGCCGTTAAA |
| <i>L. inn.</i> | Clip11262 | 280 | TTAGTTACGGAACAAAAGAA-----ATTGTCATTAGATGTCCGGAAGATGCCCGTGAAA |
| <i>L. wel.</i> | SLCC5334 | 280 | ATTGTAACATAACAAGAA-----ATTGTTATTAGATGCCCTGATGACGCGGTGAAA |
| <i>L. iv.</i> | FSL F6-596 | 280 | TTAGTAACGGAGCGTGAAGAA-----ATTGTCATTAGATGTCCAGGGGATGCAGCGAAA |
| <i>L. seel.</i> | SLCC3954 | 280 | TTAGTGACAGAGCGCGAAGAA-----ATTGTAATAAGATGCCCTGACGATGCAGTAAAA |
| <i>L. gr.</i> | DSM20601 | 280 | CTGCAAAGTGAATCGAAAAAATAATATAGCGATCGAAGTCCACAAGATGCAGTGTCC |
| <i>B. smi.</i> | 7_3_47FAA | 295 | AGTCTTTCATTAGACGAACGG-----TATGTTATCCGCTCTCCCGAAGACGGTGCAAAAT |
| <i>B. coag.</i> | 36D1 | 289 | AATTTGCAGCACGATACACGT-----TATGTAATCCGCACGCCGCAAGACGGGGCCAAT |
| <i>B. subt.</i> | 168 | 301 | AAATTAGCCACGAAGAACAT-----TTCGTTATTTCGCTCCCGGAAGACGGCGCTAAT |
| <i>B. weih.</i> | KBAB4 | 283 | CGTTTAGAATATCAAATAGA-----TATAGTATTTCGAAGTCCAGAAGATTGTGCGAGT |
| <i>S. aur.</i> | COL | 280 | AGAAGAGCTGAAAATAATCGT-----ATAAAAATAACGCAACCAAGTGATGTTGCTGAT |
| <i>S. aur.</i> | 71193 | 280 | AGAAGAGCTGAAAATAATCGT-----ATAAAAATAACGCAACCAAGTGATGTTGCTGAT |
| <i>E. faec.</i> | DO | 288 | -----GACGGATCATGAAAGAGCGGCTCCACCGTTTCGTACCAGCTACGAATTGGCCAG |
| consensus | | 301 |*.....*.....*.....*.....*.....*.....*.....*.....*.....* |

L. mono. EGD-e 334 CTTGTAATGCCAGAGCTTGCTTTTCTGTTTCAAGAACATTTCCATTGCGCTATTTTTTAAAT
L. mono. F2365 334 CTTGTAATGCCAGAGCTTGCTTTTCTTTTCAAGAACATTTCCATTGCTATTTTTTAAAT
L. mar. FSL S4-120 334 TTGGTAATGCCTGAGTTAGCGTTTCTTTTCAAGAACATTTCCACTGCCTCTTTTTTAAAC
L. inn. Clip11262 334 CTAGTAATGCCTGAGTTAGCTTTCTTTTCAAGAACATTTCCACTGTATTTTTTAAAC
L. wel. SLCC5334 334 TTAGTAATGCCTGAATAGCTTTTTTTGTTTCAAGAACATTTTCACTGTATTTTTCTAAAT
L. iv. FSL F6-596 334 TTAGTTATGCCGGAATAGCTTTTCTTTTCAAGAACATTTTCACTGCATTTTTTAAAT
L. seel. SLCC3954 334 TTAGTTATGCCAGAAATAGCAATTTCTATTTCAAGAACATTTTCACTGCATTTTTCTAAAT
L. gr. DSM20601 340 ATTGTTTGGCCAGAGCTTGCTTTTCTTTTCAAGAACATTTTCCATTGCGTGCCTTTTGAAT
B. smi. 7_3_47FAA 349 TATGTCATGCAAGAAATGCGGTTTTTTAACACAAGAACATTTTCGTGTGCCTCTTCCCTAAC
B. coag. 36D1 343 TATGTCATGAATGATATGCGCTTTTTTATCCCAAGGAGCATTTTTGTCTGCCTGTATTTAAAT
B. subt. 168 355 CTTGTCATGGAGGATATGCGCTTTTTTAAACCAGGAGCATTTTTGTCTGTTTATACTTAAAT
B. weih. KBAB4 337 TATATGATGGAAGAGATGCGTTTTTTGCAACAGGAGCATTTTTGTGTTTATATTTGAAT
S. aur. COL 334 TATATGATTTCCAACAATGAAAGATTTAACAACAAGAACATTTTGTGATTTTATTGTTAAAT
S. aur. 71193 334 TATATGATTTCCAACAATGAAAGATTTAACAACAAGAACATTTTGTGATTTTATTGTTAAAT
E. faec. DO 343 CAATGATTTCTGGAATGAAAGATCACAACAAGAACATTTGGTTGTATTTATTGGGAC
consensus 361*.....*.....**..**..*****.....*.....*..*..

L. mono. EGD-e 394 ACCAAAAATCAAGTAATATATCGGCAAACGATTTTTGTTGGTGGTCTGAATGCTTCCATC
L. mono. F2365 394 ACCAAAAATCAAGTAATATATCGGCAAACGATTTTTGTTGGTGGTCTGAATGCTTCCATC
L. mar. FSL S4-120 394 ACAAGAATCAAGTGATTTATCGACAACAATCTTTGTTGGTGGACTGAATGCGTCAATC
L. inn. Clip11262 394 ACCAAGAATCAAGTGATTTATAGGCAAACAATCTTTGTCGGTGGTTGAATGCTTCCATT
L. wel. SLCC5334 394 ACTAAGAATCAAGTCATTTATAGCAAAACTATTTTTGTTGGAGGATTAATGCATCGATT
L. iv. FSL F6-596 394 ACTAAAAATCAAGTCATTTACAGACAACGATTTTTGTTGGGGACTAAATGCATCTATT
L. seel. SLCC3954 394 ACAAAAAATCAAGTAATCTATAGACAACAATTTTTCGTTGGTGGATTAATGCATCCATC
L. gr. DSM20601 400 ACACGAAATCAGATTGTTTCATCGTCAGACTATCTTTATCGGCAGTTTGAATGCTTCTATT
B. smi. 7_3_47FAA 409 ACCAAAAATCAAGTTCTCCACAACAACCATTTTTTATCGGTAGTTTGAATGCTTCGATT
B. coag. 36D1 403 ATTAAAAATCAAGTGATCCACCGGCAGACGATTTTCATCGGAAGCTTAAATGCCTCGATC
B. subt. 168 415 ACAAAAAATCAAGTCATCCATAAACGCACCGTATTTTATCGGAAGCCTGAATTCATCTATT
B. weih. KBAB4 397 ACGAAAAATCAAGTTATACATAGGCAAACATTTTTTATTGGAAGTTAAATACGTCGATT
S. aur. COL 394 TCAAAAAATGTAGTGATTAAGAAACCTGTGTTTTTAAAGGTACATTAAATAGTTCGATT
S. aur. 71193 394 TCAAAAAATGTAGTGATTAAGAAACCTGTGTTTTTAAAGGTACATTAAATAGTTCGATT
E. faec. DO 403 ACGAAGAATCAAGTGATCTTAAAAAACAAGTGTTCATCGGTCGCTGAATCAGTCAGTC
consensus 421**.....*..*.....*..**....**....*..*****..*..*..

L. mono. EGD-e 454 GTTCACCTAGAGAAGTTTTTAGATTGCGCTCAGAAAATCAGCAGCGTCAATTATGTGC
L. mono. F2365 454 GTTCATCCTAGAGAAGTTTTTAGATTAGCGCTCAGAAAATCAGCAGCATCAATCATGTGC
L. mar. FSL S4-120 454 GTTCATCCAAGAGAAGTTTTAGATTAGCGCTAAGAAAATCAGCTGCATCTATTATGTGT
L. inn. Clip11262 454 GTTCATCCTAGAGAAGTTTTTAGACTGGCATTAGAAAATCAGCTGCTTCTATAATGTGT
L. wel. SLCC5334 454 GTTCATCCGAGAGAGTATTTTAGATTAGCACTTAGAAAAGTCTGCTGCTTCTATCATGTGC
L. iv. FSL F6-596 454 GTTCATCCTAGAGAAGTTTTTAGGTTAGCATTAGAAAAGTCTGCTGCTTCTATCATGTGC
L. seel. SLCC3954 454 GTTCATCCGAGAGAAGTTTTTAGATTAGCTTTAAGAAAATCAGCTGCGTCTCTTATGTGT
L. gr. DSM20601 460 GTTCATCCGCGAGAAGTTTTATGGATTAGCTGTACGGAAAATCTGCCGCCAAATCATGTGT
B. smi. 7_3_47FAA 469 GTTCATCCTAGGGAAGTGTTTAAGAAGCGCTTCGCCGCTCCGCTGCCTCCATTATTTGC
B. coag. 36D1 463 GTCCATCCCGCGAAGTGTTCAAAGAAGCGCTCAGGCGTTTCAGCTGCTTCCATTATTTGT
B. subt. 168 475 GTCCACCCCGGAGAGGTGTTTAAAGAAGCGTTTTAAACGATCTGCCGCTTCTTTATCTGT
B. weih. KBAB4 457 GTGCACCCAGGGAAGTTTTTAAAGAAGCGTTCCGTCGGGCAGCAGCCTCTATTATATGT
S. aur. COL 454 GTACATCCACGTGAAATTTTTAGTATTGCGGTGAGAGAAAATGCCAATGCAATCATCGCA
S. aur. 71193 454 GTACATCCACGTGAAATTTTTAGTATTGCGGTGAGAGAAAATGCCAATGCAATCATCGCA
E. faec. DO 463 GCTCATCCTAGAGAAATTTTCCATTTATGCTGTACGTTATTGTGCAGCAAGGATCGTTTTTA
consensus 481 *..**..**..*..**..*..*.....**..*.....*.....*..*..*..*..*..*..*..

Figure S2: Nucleic acid based alignment of *radC* sequences from various *Firmicutes*.

The alignment was done with MAFFT (Kato H, Toh H (2008), Brief Bioinform 9: 286-298), shading of conserved residues was performed with Boxshade. The insertion site of Tn6188 and other Tn554-like transposons is highlighted in red. The consensus is displayed at the bottom of each alignment block, asterisks indicate identical positions, dots indicate similar positions.

Abbreviations and accession numbers: *L. mono.* EGD-e (*L. monocytogenes* EGD-e, NC_003210), *L. mono.* F2365 (*L. monocytogenes* F2365, NC_002973), *L. mar.* FSL S4-120 (*L. marthii* FSL S4-120, ADXF01000663), *L. inn.* Clip11262 (*L. innocua* Clip11262, NC_003212), *L. wel.* SLCC5334 (*L. welshimeri* SLCC5334, NC_00855), *L. iv.* FSL F6-596 (*L. ivanovii* FSL F6-596, ADXI01000816), *L. seel.* SLCC3954 (*L. seeligeri* SLCC3954, NC_013891), *L. gr.* DSM20601 (*L. grayi* DSM 20601, ACCR02000005), *B. smi.* 7_3_47FAA (*Bacillus smithii* 7_3_47FAA, EHL73379), *B. coag.* 36D1 (*Bacillus coagulans* 36D1, NC_016023), *B. subt.* 168 (*Bacillus subtilis* 168, NC_000964), *B. weih.* KBAB4 (*Bacillus weihenstephanensis* KBAB4, NC_010184), *S. aur.* COL_S. (*Staphylococcus aureus* COL, NC_002951), *S. aur.* 71193 (*Staphylococcus aureus* 71193, AFH69892), *E. faec.* DO (*Enterococcus faecium* DO, AFK59806).