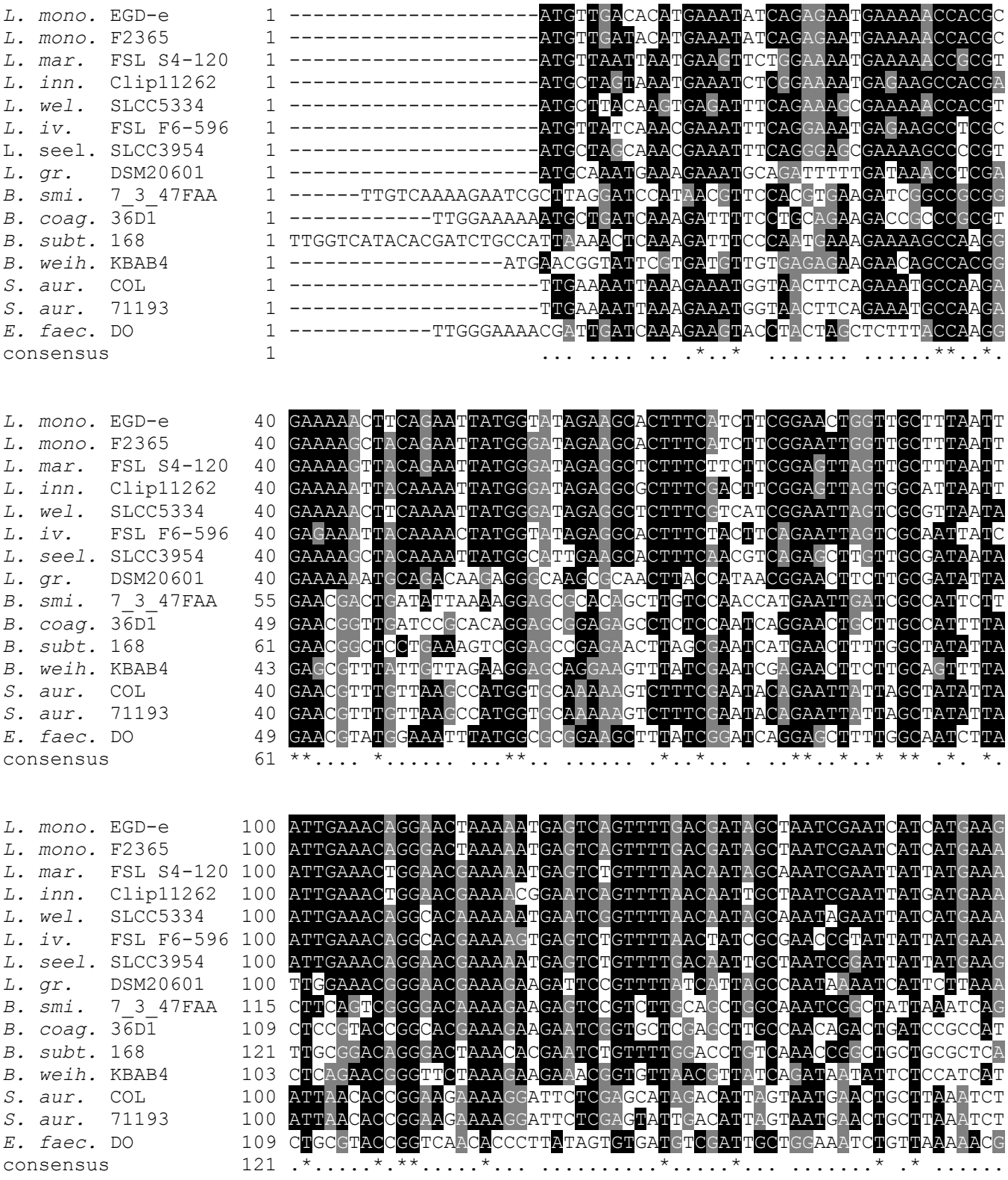
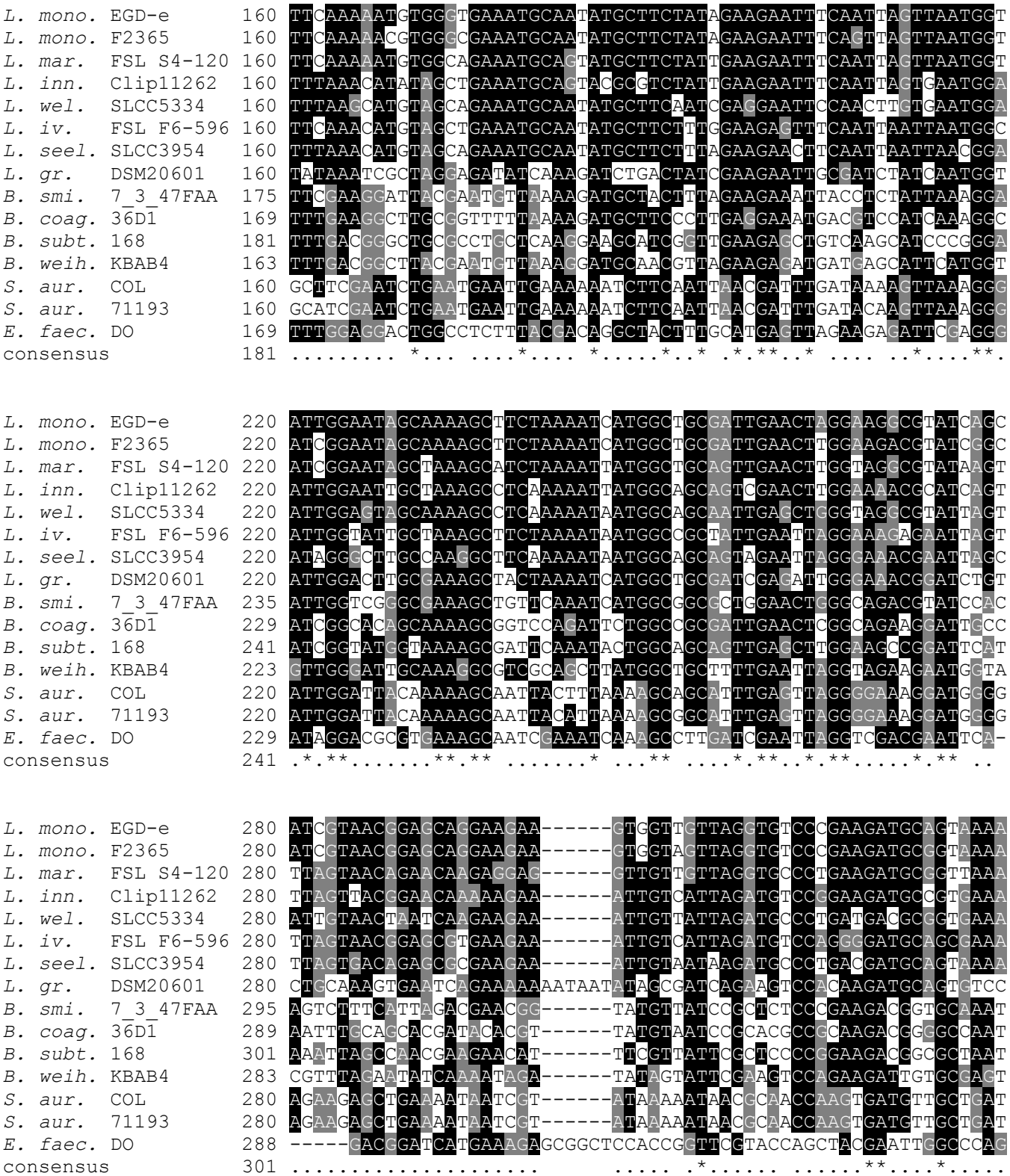
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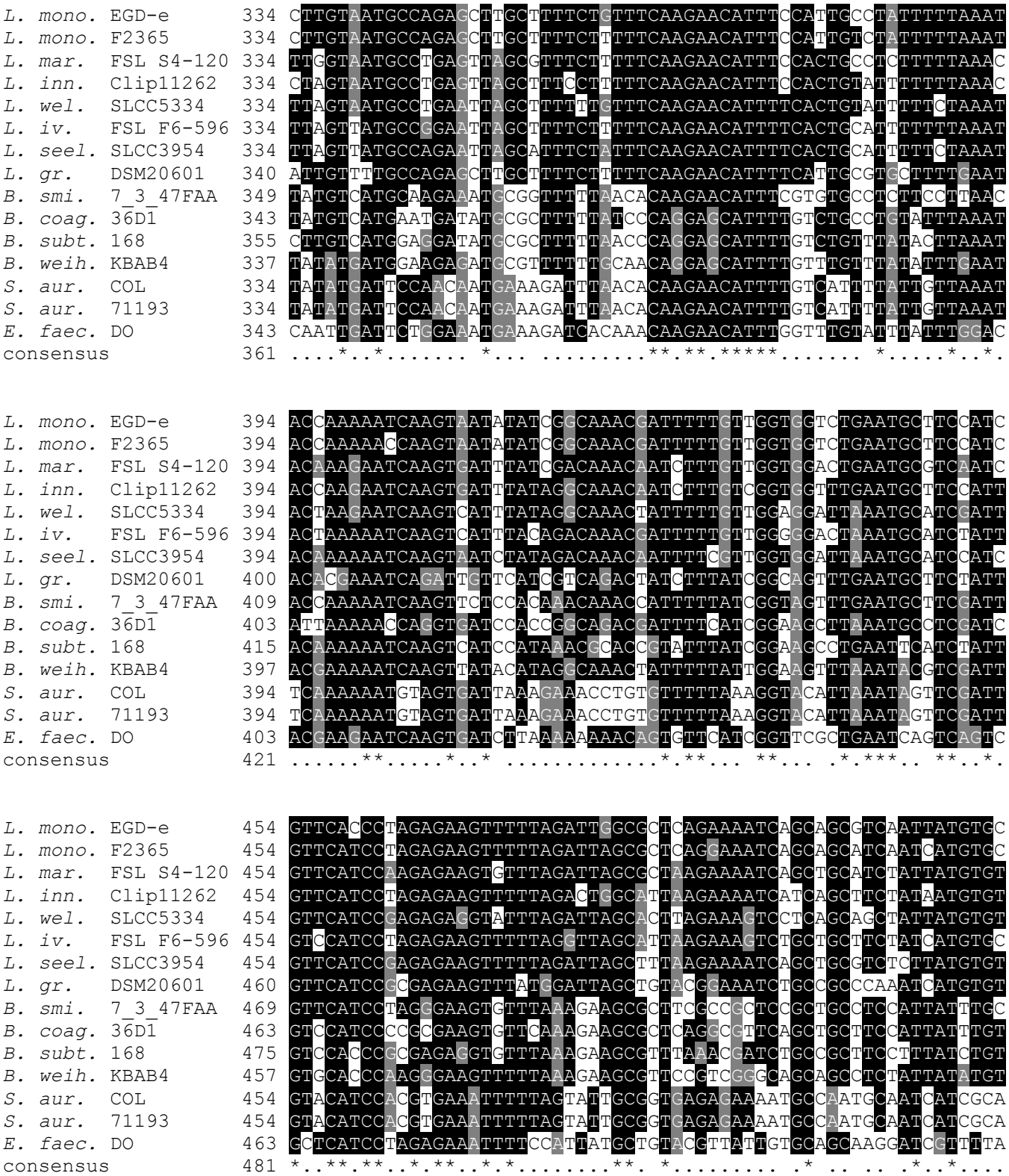
Title	Tn6188 - a novel transposon in Listeria monocytogenes responsible for tolerance to benzalkonium chloride
Authors	Mueller, Anneliese;Rychli, Kathrin;Muhterem-Uyar, Meryem;Zaiser, Andreas;Stessl, Beatrix;Guinane, Caitriona M.;Cotter, Paul D.;Wagner, Martin;Schmitz-Esser, Stephan
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Figure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


L. mono. EGD-e
L. mono. F2365
L. mar. FSL S4-120
L. inn. Clip11262
L. wel. SLCC5334
L. iv. FSL F6-596
L. seel. SLCC3954
L. gr. DSM20601
B. smi. 7_3_47FAA
B. coag. 36D1
B. subt. 168
B. weih. KBAB4
S. aur. COL
S. aur. 71193
E. faec. DO
consensus


L. mono. EGD-e 160
L. mono. F2365 160
L. mar. FSL S4-120 160
L. inn. Clip11262 160
L. wel. SLCC5334 160
L. iv. FSL F6-596 160
L. seel. SLCC3954 160
L. gr. DSM20601 160
B. smi. 7_3_47FAA 175
B. coag. 36D1 169
B. subt. 168 181
B. weih. KBAB4 163
S. aur. COL 160
S. aur. 71193 160
E. faec. DO 169
consensus 181
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L. mono. F2365 220
L. mar. FSL S4-120 220
L. inn. Clip11262 220
L. wel. SLCC5334 220
L. iv. FSL F6-596 220
L. seel. SLCC3954 220
L. gr. DSM20601 220
B. smi. 7_3_47FAA 235
B. coag. 36D1 229
B. subt. 168 241
B. weih. KBAB4 223
S. aur. COL 220
S. aur. 71193 220
E. faec. DO 229
consensus 241
L. mono. EGD-e 280
L. mono. F2365 280
L. mar. FSL S4-120 280
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L. wel. SLCC5334 280
L. iv. FSL F6-596 280
L. seel. SLCC3954 280
L. gr. DSM20601 280
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B. coag. 36D1 289
B. subt. 168 301
B. weih. KBAB4 283
S. aur. COL 280
S. aur. 71193 280
E. faec. DO 288
consensus 301


L. mono. EGD-e 334 CTTGTAATGCCAGAGCTTGCTTTTCTGTTTCAAGAACATTTCCATTGCCTATTTTTAAAT
L. mono. F2365 334 CTTGTAATGCCAGAGCTTGCTTTTCTTTTTCAAGAACATTTCCATTGTCTATTTTTAAAT
L. mar. FSL S4-120 334 TTGGTAATGCCTGAGTTAGCGTTTCTTTTTCAAGAACATTTCCACTGCCTCTTTTTAAAC
L. inn. Clip11262 334 CTAGTAATGCCTGAGTTAGCTTTCCTTTTTCAAGAACATTTCCACTGTATTTTTTAAAC
L. wel. SLCC5334 334 TTAGTAATGCCTGAATTAGCTTTTTTGTTTCAAGAACATTTTCACTGTATTTTTCTAAAT
L. iv. FSL F6-596 334 TTAGTTATGCCGGAATTAGCTTTTCTTTTTCAAGAACATTTTCACTGCATTTTTTTAAAT
L. seel. SLCC3954 334 TTAGTTATGCCAGAATTAGCATTTCTATTTCAAGAACATTTTCACTGCATTTTTCTAAAT
L. gr. DSM20601 340 ATTGTTTTGCCAGAGCTTGCTTTTCTTTTTCAAGAACATTTTCATTGCGTGCTTTTGAAT
B. smi. 7_3_47FAA 349 TATGTCATGCAAGAAATCCGGTTTTTAACACAAGAACATTTCGTGTGCCTCTTCCTTAAC
B. coag. 36D1 343 TATGTCATGAATGATATCGCGTTTTTATCCCAGGAGCATTTTGTCTGCCTGTATTTAAAT
B. subt. 168 355 CTTGTCATGGAGGATATCGCGTTTTTAACCCAGGAGCATTTTGTCTGTTTATACTTAAAT
B. weih. KBAB4 337 TATATGATGGAAGAGATCGTTTTTTGCAACAGGAGCATTTTGTTTGTTTATATTTGAAT
S. aur. COL 334 TATATGATTCCAACAATGAAAGATTTAACACAAGAACATTTTGTCATTTTATTGTTAAAT
S. aur. 71193 334 TATATGATTCCAACAATGAAAGATTTAACACAAGAACATTTTGTCATTTTATTGTTAAAT
E. faec. DO 343 CAATTGATTCTGGAAATGAAAGATCACAAACAAGAACATTTGGTTTGTATTTATTTGGAC
consensus 361 ....*..*..... *... .....**.**.*****..... *.....*..*.
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L. mono. F2365 394 ACCAAAAACCAAGTAATATATCGGCAAACGATTTTTGTTGGTGGTCTGAATGCTTCCATC
L. mar. FSL S4-120 394 ACAAAGAATCAAGTGATTTATCGACAAACAATCTTTGTTGGTGGACTGAATGCGTCAATC
L. inn. Clip11262 394 ACCAAGAATCAAGTGATTTATAGGCAAACAATCTTTGTCGGTGGTTTGAATGCTTCCATT
L. wel. SLCC5334 394 ACTAAGAATCAAGTCATTTATAGGCAAACTATTTTTGTTGGAGGATTAAATGCATCGATT
L. iv. FSL F6-596 394 ACTAAAAATCAAGTCATTTACAGACAAACGATTTTTGTTGGGGGACTAAATGCATCTATT
L. seel. SLCC3954 394 ACAAAAAATCAAGTAATCTATAGACAAACAATTTTCGTTGGTGGATTAAATGCATCCATC
L. gr. DSM20601 400 ACACGAAATCAGATTGTTCATCGTCAGACTATCTTTATCGGCAGTTTGAATGCTTCTATT
B. smi. 7_3_47FAA 409 ACCAAAAATCAAGTTCTCCACAAACAAACCATTTTTATCGGTAGTTTGAATGCTTCGATT
B. coag. 36D1 403 ATTAAAAACCAGGTGATCCACCGGCAGACGATTTTCATCGGAAGCTTAAATGCCTCGATC
B. subt. 168 415 ACAAAAAATCAAGTCATCCATAAACGCACCGTATTTATCGGAAGCCTGAATTCATCTATT
B. weih. KBAB4 397 ACGAAAAATCAAGTTATACATAGGCAAACTATTTTTATTGGAAGTTTAAATACGTCGATT
S. aur. COL 394 TCAAAAAATGTAGTGATTAAAGAAACCTGTGTTTTTAAAGGTACATTAAATAGTTCGATT
S. aur. 71193 394 TCAAAAAATGTAGTGATTAAAGAAACCTGTGTTTTTAAAGGTACATTAAATAGTTCGATT
E. faec. DO 403 ACGAAGAATCAAGTGATCTTAAAAAAAACAGTGTTCATCGGTTCGCTGAATCAGTCAGTC
consensus 421 ......**.....*..* .............*.**... **... .*.***.. **..*.
L. mono. EGD-e 454 GTTCACCCTAGAGAAGTTTTTAGATTGGCGCTCAGAAAATCAGCAGCGTCAATTATGTGC
L. mono. F2365 454 GTTCATCCTAGAGAAGTTTTTAGATTAGCGCTCAGGAAATCAGCAGCATCAATCATGTGC
L. mar. FSL S4-120 454 GTTCATCCAAGAGAAGTGTTTAGATTAGCGCTAAGAAAATCAGCTGCATCTATTATGTGT
L. inn. Clip11262 454 GTTCATCCTAGAGAAGTTTTTAGACTGGCATTAAGAAAATCATCAGCTTCTATAATGTGT
L. wel. SLCC5334 454 GTTCATCCGAGAGAGGTATTTAGATTAGCACTTAGAAAGTCCTCAGCAGCTATTATGTGT
L. iv. FSL F6-596 454 GTCCATCCTAGAGAAGTTTTTAGGTTAGCATTAAGAAAGTCTGCTGCTTCTATCATGTGC
L. seel. SLCC3954 454 GTTCATCCGAGAGAAGTTTTTAGATTAGCTTTAAGAAAATCAGCTGCGTCTCTTATGTGT
L. gr. DSM20601 460 GTTCATCCGCGAGAAGTTTATGGATTAGCTGTACGGAAATCTGCCGCCCAAATCATGTGT
B. smi. 7_3_47FAA 469 GTTCATCCTAGGGAAGTGTTTAAAGAAGCGCTTCGCCGCTCCGCTGCCTCCATTATTTGC
B. coag. 36D1 463 GTCCATCCCCGCGAAGTGTTCAAAGAAGCGCTCAGGCGTTCAGCTGCTTCCATTATTTGT
B. subt. 168 475 GTCCACCCGCGAGAGGTGTTTAAAGAAGCGTTTAAACGATCTGCCGCTTCCTTTATCTGT
B. weih. KBAB4 457 GTGCACCCAAGGGAAGTTTTTAAAGAAGCGTTCCGTCGGGCAGCAGCCTCTATTATATGT
S. aur. COL 454 GTACATCCACGTGAAATTTTTAGTATTGCGGTGAGAGAAAATGCCAATGCAATCATCGCA
S. aur. 71193 454 GTACATCCACGTGAAATTTTTAGTATTGCGGTGAGAGAAAATGCCAATGCAATCATCGCA
E. faec. DO 463 GCTCATCCTAGAGAAATTTTCCATTATGCTGTACGTTATTGTGCAGCAAGGATCGTTTTA
consensus 481 *..**.**..*.**..*.*........**. *......... .* .. .. .*..*....

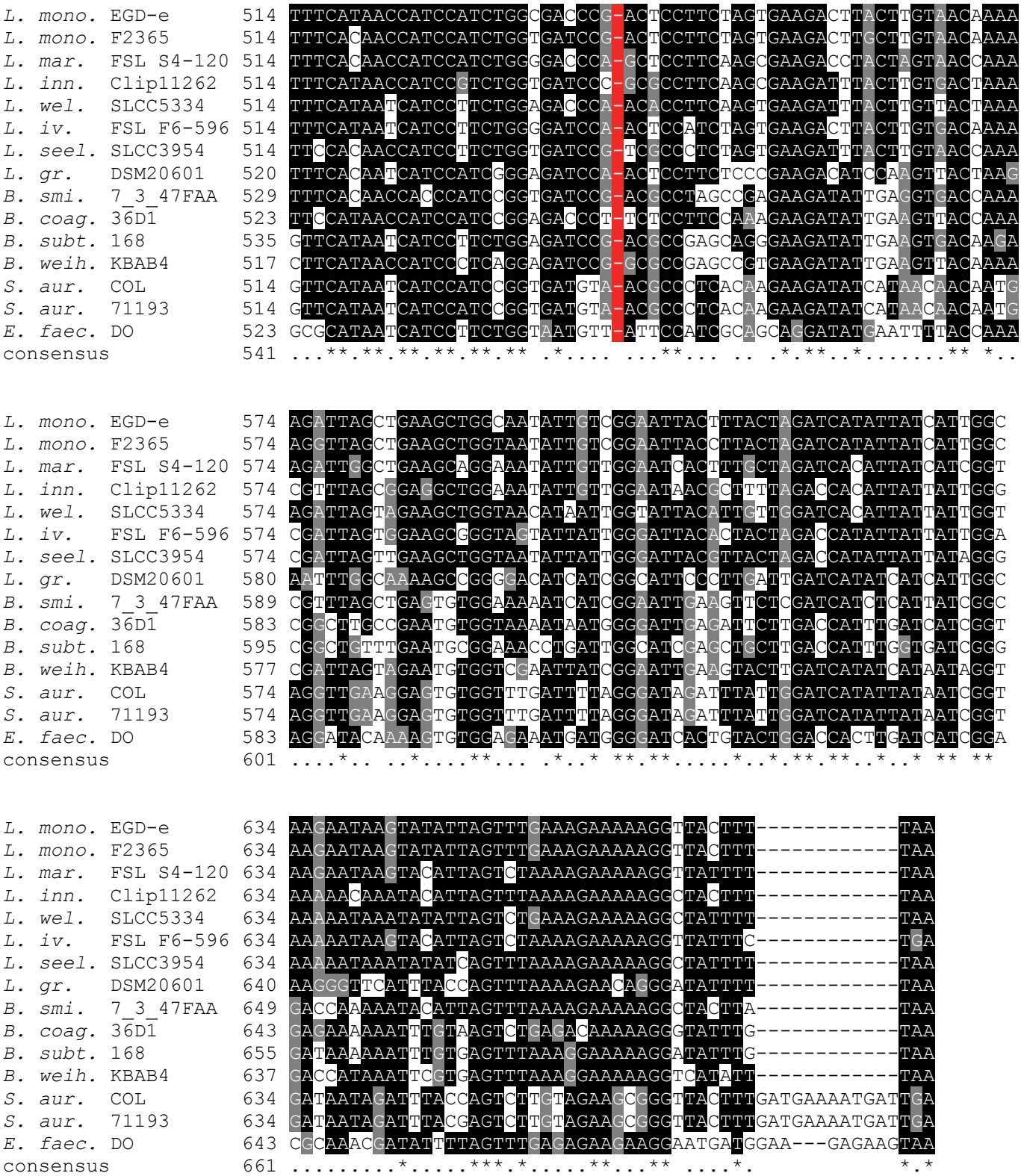

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L. mono. F2365 514 TTTCACAACCATCCATCTGGTGATCCG-ACTCCTTCTAGTGAAGACTTGCTTGTAACAAAA
L. mar. FSL S4-120 514 TTTCACAACCATCCATCTGGGGACCCA-GCTCCTTCAAGCGAAGACCTACTAGTAACCAAA
L. inn. Clip11262 514 TTTCATAACCATCCGTCTGGTGATCCC-GCGCCTTCAAGCGAAGATTTACTTGTGACTAAA
L. wel. SLCC5334 514 TTTCATAATCATCCTTCTGGAGACCCA-ACACCTTCAAGTGAAGATTTACTTGTTACTAAA
L. iv. FSL F6-596 514 TTTCATAATCATCCTTCTGGGGATCCA-ACTCCATCTAGTGAAGACTTACTTGTGACAAAA
L. seel. SLCC3954 514 TTCCACAACCATCCTTCTGGTGATCCG-TCGCCCTCTAGTGAAGATTTACTTGTAACCAAA
L. gr. DSM20601 520 TTTCACAATCATCCATCGGGAGATCCA-ACTCCTTCTCCCGAAGACATCCAAGTTACTAAG
B. smi. 7_3_47FAA 529 TTTCACAACCACCCATCCGGTGATCCG-ACGCCTAGCCGAGAAGATATTGAGGTGACCAAA
B. coag. 36D1 523 TTCCATAACCATCCATCCGGAGACCCT-TCTCCTTCCAAAGAAGATATTGAAGTTACCAAA
B. subt. 168 535 GTTCATAATCATCCTTCTGGAGATCCG-ACGCCGAGCAGGGAAGATATTGAAGTGACAAGA
B. weih. KBAB4 517 CTTCATAACCATCCCTCAGGAGATCCG-GCGCCGAGCCGTGAAGATATTGAAGTTACAAAA
S. aur. COL 514 GTTCATAATCATCCATCCGGTGATGTA-ACGCCCTCACAAGAAGATATCATAACAACAATG
S. aur. 71193 514 GTTCATAATCATCCATCCGGTGATGTA-ACGCCCTCACAAGAAGATATCATAACAACAATG
E. faec. DO 523 GCGCATAATCATCCTTCTGGTAATGTT-ATTCCATCGCAGCAGGATATGAATTTTACCAAA
consensus 541 ...**.**.**.**.**.** .*.... ...**... .. .*.**..*.......** *..
L. mono. EGD-e 574 AGATTAGCTGAAGCTGGCAATATTGTCGGAATTACTTTACTAGATCATATTATCATTGGC
L. mono. F2365 574 AGGTTAGCTGAAGCTGGTAATATTGTCGGAATTACCTTACTAGATCATATTATCATTGGC
L. mar. FSL S4-120 574 AGATTGGCTGAAGCAGGAAATATTGTTGGAATCACTTTGCTAGATCACATTATCATCGGT
L. inn. Clip11262 574 CGTTTAGCGGAGGCTGGAAATATTGTTGGAATAACGCTTTTAGACCACATTATTATTGGG
L. wel. SLCC5334 574 AGATTAGTAGAAGCTGGTAACATAATTGGTATTACATTGTTGGATCACATTATTATTGGT
L. iv. FSL F6-596 574 CGATTAGTGGAAGCGGGTAGTATTATTGGGATTACACTACTAGACCATATTATTATTGGA
L. seel. SLCC3954 574 CGATTAGTTGAAGCTGGTAATATTATTGGGATTACGTTACTAGACCATATTATTATAGGG
L. gr. DSM20601 580 AATTTGGCAAAAGCCGGGGACATCATCGGCATTCCCTTCATTGATCATATCATCATTGGC
B. smi. 7_3_47FAA 589 CGTTTAGCTGAGTGTGGAAAAATCATCGGAATTGAAGTTCTCGATCATCTCATTATCGGC
B. coag. 36D1 583 CGGCTTGCCGAATGTGGTAAAATAATGGGGATTGAGATTCTTGACCATTTGATCATCGGT
B. subt. 168 595 CGGCTGTTTGAATGCGGAAACCTGATTGGCATCGAGCTGCTTGACCATTTGGTGATCGGG
B. weih. KBAB4 577 CGATTAGTAGAATGTGGTCGAATTATCGGAATTGAAGTACTTGATCATATCATAATAGGT
S. aur. COL 574 AGGTTGAAGGAGTGTGGTTTGATTTTAGGGATAGATTTATTGGATCATATTATAATCGGT
S. aur. 71193 574 AGGTTGAAGGAGTGTGGTTTGATTTTAGGGATAGATTTATTGGATCATATTATAATCGGT
E. faec. DO 583 AGGATACAAAAGTGTGGAGAAATGATGGGGATCACTGTACTGGACCACTTGATCATCGGA
consensus 601 ....*.. ..*....**... .*..* **.**.....*..*.**.**..*..* ** **
L. mono. EGD-e 634 AAGAATAAGTATATTAGTTTGAAAGAAAAAGGTTACTTT----------TAA
L. mono. F2365 634 AAGAATAAGTATATTAGTTTGAAAGAAAAAGGTTACTTT----------TAA
L. mar. FSL S4-120 634 AAGAATAAGTACATTAGTCTAAAAGAAAAAGGTTATTTT----------TAA
L. inn. Clip11262 634 AAAAACAAATACATTAGTTTAAAAGAAAAAGGCTACTTT----------TAA
L. wel. SLCC5334 634 AAAAATAAATATATTAGTCTGAAAGAAAAAGGCTATTTT----------TAA
L. iv. FSL F6-596 634 AAAAATAAGTACATTAGTCTAAAAGAAAAAGGTTATTTC----------TGA
L. seel. SLCC3954 634 AAAAATAAATATATCAGTTTAAAAGAAAAAGGCTATTTT----------TAA
L. gr. DSM20601 640 AAGGGTTCATTTACCAGTTTAAAAGAACAGGGATATTTT----------TAA
B. smi. 7_3_47FAA 649 GACCAAAAATACATTAGTTTAAAAGAAAAAGGCTACTTA----------TAA
B. coag. 36D1 643 GAGAAAAAATTTGTAAGTCTGAGACAAAAAGGGTATTTG----------TAA
B. subt. 168 655 GATAAAAAATTTGTGAGTTTAAAGGAAAAAGGATATTTG----------TAA
B. weih. KBAB4 637 GACCATAAATTCGTGAGTTTAAAGGAAAAAGGTCATATT----------TAA
S. aur. COL 634 GATAATAGATTTACCAGTCTTGTAGAAGCGGGTTACTTTGATGAAAATGATTGA
S. aur. 71193 634 GATAATAGATTTACGAGTCTTGTAGAAGCGGGTTACTTTGATGAAAATGATTGA
E. faec. DO 643 CGCAAACGATATTTTAGTTTGAGAGAAGAAGGAATGATGGAA---GAGAAGTAA
consensus 661 .........*.....***.*.....**...** ....*. *.*

Figure S2: Nucleic acid based alignment of *radC* sequences from various *Firmicutes*.
The alignment was done with MAFFT (Katoh K, Toh H (2008), Brief Bioinform 9: 286-298), shading of conserved residues was performed with Boxshade. The insertion site of Tn*6188* and other Tn*554*-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).