

Figure S2

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L. mono. EGD-e           1  -----ATGTTGACACATGAAATATCAGAGAATGAAAAACCACGC
L. mono. F2365          1  -----ATGTTGATACATGAAATATCAGAGAATGAAAAACCACGC
L. mar. FSL S4-120     1  -----ATGTTAATTAATGAAGTTCTGGAAAATGAAAAACCGCGT
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  -----TTGGAAAAATGCTGATCAAAGATTTTCTGCAGAAAGACCGCCCGCGT
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  GAGAAATTACAAAATTATGGTATAGAGGCACTTTCCTACTTCAGAATTAGTCGCAATTATC
L. seel. SLCC3954     40  GAAAAGCTACAAAATTATGGCATTGAAGCACTTTCACGTCAGAGCTTGTTCGCATAATA
L. gr. DSM20601       40  GAAAAATGCAGACAAGAGGGCAAGCCGCAACTTACCATAACGGAACCTCTTGCATATTA
B. smi. 7_3_47FAA     55  GAACGACTGATATTAAGAGGAGCGCACAGCTTGTCCAACCATGAATTGATCGCCATTCTT
B. coag. 36D1         49  GAACGGTTGATCCGCACAGGAGCGGAGAGCTCTCTCCAATCAGGAATTTGCTGCCATTTTA
B. subt. 168          61  GAACGGCTCCTGAAGTCGGAGCCGAGAACTTAGCGAATCATGAACTTTTGGCTATATTA
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  ATTGAAACAGGAAC TAAAAATGAGTCAGTTTTGACGATAGCTAATCGAATCATCATGAAG
L. mono. F2365          100  ATTGAAACAGGGACT TAAAAATGAGTCAGTTTTGACGATAGCTAATCGAATCATCATGAAA
L. mar. FSL S4-120     100  ATTGAAACTGGAACGAAAAATGAGTCTGTTTTAACAATAGCAAATCGAATTATTATGAAA
L. inn. Clip11262      100  ATTGAAACTGGAACGAAAAATGAGTCTGTTTTAACAATAGCAAATCGAATTATTATGAAA
L. wel. SLCC5334       100  ATTGAAACAGGCACAAAAAATGAATCGGTTTTAACAATAGCAAATAGAATTATCATGAAA
L. iv. FSL F6-596     100  ATTGAAACAGGCACGAAAAGTGAATCGGTTTTAACAATAGCAAATAGAATTATTATGAAA
L. seel. SLCC3954     100  ATTGAAACAGGAACGAAAAATGAGTCTGTTTTGACAATTGCTAATCGGATTATTATGAAG
L. gr. DSM20601       100  TTGGAAACGGGAACGAAAGAAGATTCGGTTTTATCATTAGCCAATAAAATCATTCTTAAA
B. smi. 7_3_47FAA     115  CTCAGTACGGGACAAAAGAAGATCCGTCTTGCAGCTGGCAAATCGGCTATTAATCAG
B. coag. 36D1         109  CTCCTTACCGGCACGAAAGAAGAAATCGTGTGCTCGAGCTTGCCAACAGACTGATCCGCCAT
B. subt. 168          121  TTGCGGACAGGGACTAAAACACGAATCTGTTTTGGACCTGTCAAACCGGCTGCTGCGCTCA
B. weih. KBAB4        103  CTCAGAACGGGTTCTAAAGAAGAAACGGTGTAAACGTTATCAGATAAATATTCTCCATCAT
S. aur. COL           100  ATTAACACCGGAAGAAAAGGATTCTCGAGCATAGACATTAGTAATGAACTGCTTAAATCT
S. aur. 71193         100  ATTAACACCGGAAGAAAAGGATTCTCGAGTATTACATTAGTAATGAACTGCTTAAATCT
E. faec. DO           109  CTGCGTACCGGTCAACACCCTTATAGTGTGATGTGATGCTGGAAATCTGTTAAAAACG
consensus              121  . * . . . . * . . . . . * . . . . . * . . . . . * . . . . . * . . . . .

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L. mono. EGD-e 334 CTTGTAATGCCAGAGCTTGCTTTTCTGTTTCAAGAACATTTCCATTGCCTATTTTTAAAT
L. mono. F2365 334 CTTGTAATGCCAGAGCTTGCTTTTCTTTTCAAGAACATTTCCATTGTCTATTTTTAAAT
L. mar. FSL S4-120 334 TTGGTAATGCCTGAGTTAGCGTTTCTTTTCAAGAACATTTCCACTGCCTCTTTTTAAAC
L. inn. Clip11262 334 CTAGTAATGCCTGAGTTAGCTTTCTTTTCAAGAACATTTCCACTGTATTTTTTAAAC
L. wel. SLCC5334 334 TTAGTAATGCCTGAATTAGCTTTTTTTGTTTCAAGAACATTTTCACTGTATTTTTCTAAAT
L. iv. FSL F6-596 334 TTAGTTATGCCGGAATTAGCTTTTCTTTTCAAGAACATTTTCACTGCATTTTTTAAAT
L. seel. SLCC3954 334 TTAGTTATGCCAGAAATAGCATTTCTATTTCAGAAGACATTTTCACTGCATTTTTCTAAAT
L. gr. DSM20601 340 ATTGTTTTGCCAGAGCTTGCTTTTCTTTTCAAGAACATTTTCCATTGCGTGCCTTTTGAAT
B. smi. 7_3_47FAA 349 TATGTCATGCAAGAAATGCGGTTTTTTAACACAAGAACATTTTCGTGTGCCTCTTCCTTAAC
B. coag. 36D1 343 TATGTCATGAATGATATGCGCTTTTTTATCCCAGGAGCATTTTTGTCTGCCTGTATTTAAAT
B. subt. 168 355 CTTGTCATGGAGGATATGCGCTTTTTTAAACCAGGAGCATTTTTGTCTGTTTATACTTAAAT
B. weih. KBAB4 337 TATATGATGGAAGAGATGCGTTTTTTGCAACAGGAGCATTTTTGTGTTTATATTTGAAT
S. aur. COL 334 TATATGATTTCCAACAATGAAAGATTTAACAACAAGAACATTTTGTGATTTTATTGTTAAAT
S. aur. 71193 334 TATATGATTTCCAACAATGAAAGATTTAACAACAAGAACATTTTGTGATTTTATTGTTAAAT
E. faec. DO 343 CAATGATTTCTGGAATGAAAGATCACAACAAGAACATTTGGTTGTTATTATTGGAAC
consensus 361*..*.....*.....**..**.....*.....*..*..*

L. mono. EGD-e 394 ACCAAAAATCAAGTAATATATCGGCAAACGATTTTTGTTGGTGGTCTGAATGCTTCCATC
L. mono. F2365 394 ACCAAAAATCAAGTAATATATCGGCAAACGATTTTTGTTGGTGGTCTGAATGCTTCCATC
L. mar. FSL S4-120 394 ACAAGAATCAAGTATTTATCGACAACAATCTTTGTTGGTGGACTGAATGCGTCAATC
L. inn. Clip11262 394 ACCAAGAATCAAGTATTTATAGGCAAACAATCTTTGTCGGTGGTTGAATGCTTCCATT
L. wel. SLCC5334 394 ACTAAGAATCAAGTATTTATAGCAAACTATTTTTGTTGGAGGATTAATGCATCGATT
L. iv. FSL F6-596 394 ACTAAAAATCAAGTATTTACAGACAACGATTTTTGTTGGGGACTAAATGCATCTATT
L. seel. SLCC3954 394 ACAAAAAATCAAGTAATCTATAGACAACAATTTTTGTTGGTGGATTAATGCATCCATC
L. gr. DSM20601 400 ACACGAAATCAGATTGTTTCATCGTCAGACTATCTTTATCGGCAGTTTGAATGCTTCTATT
B. smi. 7_3_47FAA 409 ACCAAAAATCAAGTCTCCACAACAACCATTTTTATCGGTAGTTTGAATGCTTCGATT
B. coag. 36D1 403 ATTAATAATCAAGTATCCACCGGCAGACGATTTTCATCGGAAGCTTAAATGCCTCGATC
B. subt. 168 415 ACAAAAAATCAAGTATCCATAAACGCACCGTATTTATCGGAAGCCTGAATTCATCTATT
B. weih. KBAB4 397 ACGAAAAATCAAGTTATACATAGGCAAACATTTTTATTGGAAGTTAAATACGTCGATT
S. aur. COL 394 TCAAAAAATGTAGTGATTAAGAAACCTGTGTTTTTAAAGGTACATTAAATAGTTCGATT
S. aur. 71193 394 TCAAAAAATGTAGTGATTAAGAAACCTGTGTTTTTAAAGGTACATTAAATAGTTCGATT
E. faec. DO 403 ACGAAGAATCAAGTATCTTAAAAAACAAGTGTTCATCGGTTCGCTGAATCAGTCAGTC
consensus 421**.....*..*.....*..**....**....*..***...***..*

L. mono. EGD-e 454 GTTCACCTAGAGAAGTTTTAGATTGCGCTCAGAAAATCAGCAGCGTCAATTATGTGC
L. mono. F2365 454 GTTCATCCTAGAGAAGTTTTAGATTAGCGCTCAGAAAATCAGCAGCATCAATCATGTGC
L. mar. FSL S4-120 454 GTTCATCCAAGAGAAGTTTATAGATTAGCGCTAAGAAAATCAGCTGCATCTATTATGTGT
L. inn. Clip11262 454 GTTCATCCTAGAGAAGTTTTAGACTGCAATTAAGAAAATCAGCTGCATCTATTATGTGT
L. wel. SLCC5334 454 GTTCATCCGAGAGAGTTATTTAGATTAGCACTTAAAGAAAGTCTGCTGCTTCTATCATGTGC
L. iv. FSL F6-596 454 GTTCATCCTAGAGAAGTTTTAGGTTAGCATTAAAGAAAGTCTGCTGCTTCTATCATGTGC
L. seel. SLCC3954 454 GTTCATCCGAGAGAAGTTTTATAGATTAGCTTTAAGAAAATCAGCTGCGTCTCTTATGTGT
L. gr. DSM20601 460 GTTCATCCGCGAGAAGTTTTATGGATTAGCTGTACGGAAATCTGCCGCCAAATCATGTGT
B. smi. 7_3_47FAA 469 GTTCATCCTAGGGAAGTGTTTAAAGAAGCGCTTCGCCGCTCCGCTGCCTCCATTATTTGC
B. coag. 36D1 463 GTCCATCCCGCGAAGTGTTCAAAGAAGCGCTCAGGCGTTTCAGCTGCTTCCATTATTTGT
B. subt. 168 475 GTCCACCCGCGAGAGGTGTTTAAAGAAGCGTTTAAACGATCTGCCGCTTCTTTATCTGT
B. weih. KBAB4 457 GTGCACCCAGGGAAGTTTTTAAAGAAGCGTTCCGTCGGGCAGCAGCCTCTATTATATGT
S. aur. COL 454 GTACATCCACGTGAAATTTTTAGTATTGCGGTGAGAGAAAATGCCAATGCAATCATCGCA
S. aur. 71193 454 GTACATCCACGTGAAATTTTTAGTATTGCGGTGAGAGAAAATGCCAATGCAATCATCGCA
E. faec. DO 463 GCTCATCCTAGAGAAATTTTCCATTATGCTGTACGTTATTGTGCAGCAAGGATCGTTTTTA
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).