

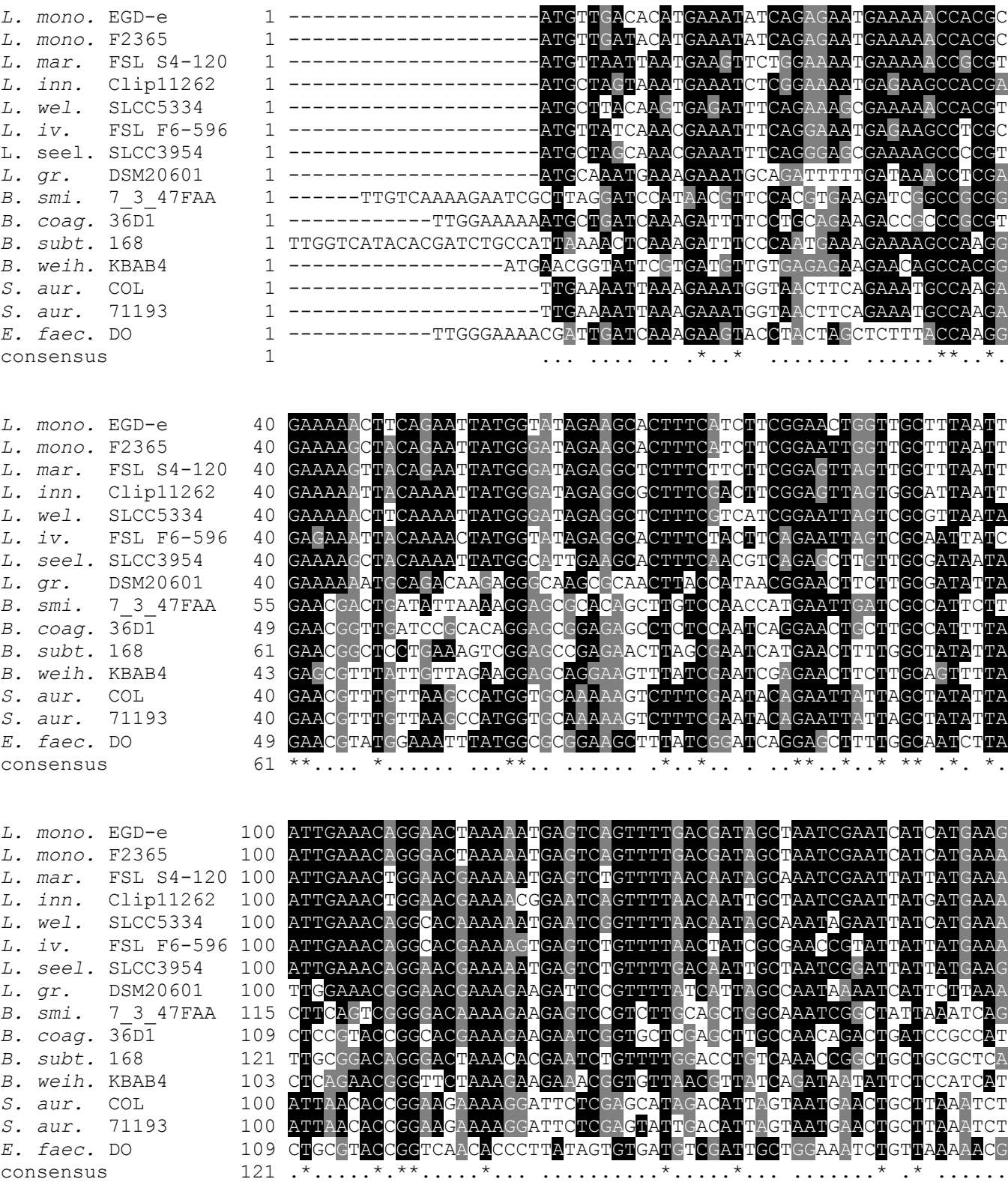
Title	Tn6188 - a novel transposon in <i>Listeria monocytogenes</i> responsible for tolerance to benzalkonium chloride
Authors	Mueller, Anneliese; Rychli, Kathrin; Muhterem-Uyar, Meryem; Zaiser, Andreas; Stessl, Beatrix; Guinane, Caitriona M.; Cotter, Paul D.; Wagner, Martin; Schmitz-Esser, Stephan
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Figure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



<i>L. mono.</i>	EGD-e	160	TTCAAAAATGTGGGTGAAATGCAATATGCTTCTATAGAAGAATTTC
<i>L. mono.</i>	F2365	160	TTCAAAAACGTGGGCGAAATGCAATATGCTTCTATAGAAGAATTTC
<i>L. mar.</i>	FSL S4-120	160	TTCAAAAATGTGGCAGAAATGCAGTATGCTTCTATTGAAGAATTTC
<i>L. inn.</i>	Clip11262	160	TTTAAACATATAGCTGAAATGCAGTACGCGTCTATTGAAGAATTTC
<i>L. wel.</i>	SLCC5334	160	TTTAAACATGTAGCAGAAATGCAATATGCTTCAATCGACGAATTC
<i>L. iv.</i>	FSL F6-596	160	TTCAAACATGTAGCTGAAATGCAATATGCTTCTTTGGAAGAGTTTC
<i>L. seel.</i>	SLCC3954	160	TTTAAACATGTAGCAGAAATGCAATATGCTTCTTTAGAAGAACTTC
<i>L. gr.</i>	DSM20601	160	TATAAATCGCTAGGAGATATCAAAGATCTGACTATCGAAGAATTGC
<i>B. smi.</i>	7_3_47FAA	175	TTTGAAGGATTACGAATGTTAAAAGATGCTACTTTAGAAGAAATTAC
<i>B. coag.</i>	36D1	169	TTTGAAGGCTTGCGGTTTTTAAAAGATGCTTCCCTTGAGGAATGAC
<i>B. subt.</i>	168	181	TTTGACGGGCTGCGCCTGCTCAAGGAAGCATCGGTTGAAGAGCTGT
<i>B. weih.</i>	KBAB4	163	TTTGACGGCTTACGAATGTTAAAGGATGCAACGTTAGAAGAGATGAT
<i>S. aur.</i>	COL	160	GCTTCGAATCTGAATGAATTGAAAAAATCTTCAATTAACGATTTGAT
<i>S. aur.</i>	71193	160	GCATCGAATCTGAATGAATTGAAAAAATCTTCAATTAACGATTTGAT
<i>E. faec.</i>	DO	169	TTTGGAGGACTGGCCTCTTTACGACAGGCTACTTTGCATGAGTTAGA
consensus		181	*.....*.....*.....*.....*.....*.....*.....**.

<i>L. mono.</i>	EGD-e	220	ATTGGAATAGCAAAAGCTTCTAAAATCATGGCTGCGATTGAACTAGGA
<i>L. mono.</i>	F2365	220	ATCGGAATAGCAAAAGCTTCTAAAATCATGGCTGCGATTGAACTTGG
<i>L. mar.</i>	FSL S4-120	220	ATCGGAATAGCTAAAGCATCTAAAATTATGGCTGCAGTTGAACTTGG
<i>L. inn.</i>	Clip11262	220	ATTGGAATTGCTAAAGCCTCAAAAATTATGGCAGCAGTCAAGCTTGG
<i>L. wel.</i>	SLCC5334	220	ATTGGAGTAGCAAAAGCCTCAAAAATAATGGCAGCAATTGAGCTGGG
<i>L. iv.</i>	FSL F6-596	220	ATTGGTATTGCTAAAGCTTCTAAAATAATGGCCGCTATTGAATTAGG
<i>L. seel.</i>	SLCC3954	220	ATAGGCTTTGCCAAGGCTTCAAAAATAATGGCAGCAGTAGAATTAGG
<i>L. gr.</i>	DSM20601	220	ATTGGACTTGCGAAAGCTACTAAAATCATGGCTGCGATCGAGATTGG
<i>B. smi.</i>	7_3_47FAA	235	ATTGGTTCGGGCGAAAGCTGTTCAAATCATGGCGGCGCTGGAAGTGG
<i>B. coag.</i>	36D1	229	ATCGGCACAGCAAAAGCGGTCCAGATTCTGGCCGCGATTGAACTCGG
<i>B. subt.</i>	168	241	ATCGGTATGGTAAAAGCGATTCAAATACTGGCAGCAGTTGAGCTTGG
<i>B. weih.</i>	KBAB4	223	GTTGGGATTGCAAAGCGCTCGCAGCTTATGGCTGCTTTTGAATTAGG
<i>S. aur.</i>	COL	220	ATTGGATTACAAAAGCAATTACTTTAAAAGCAGCATTGAGTTAGGGG
<i>S. aur.</i>	71193	220	ATTGGATTACAAAAGCAATTACATTAAAAGCGGCATTGAGTTAGGGG
<i>E. faec.</i>	DO	229	ATAGGACGCGTGAAAGCAATCGAAATCAAAGCCTTGATCGAATTAGG
consensus		241	.*.**.....**.*.....*.....*.....*.....*.....*.....*.....**..

<i>L. mono.</i>	EGD-e	280	ATCGTAACGGAGCAGGAAGAA-----GTGGTTGTTAGGTGTCCCGA
<i>L. mono.</i>	F2365	280	ATCGTAACGGAGCAGGAAGAA-----GTGGTAGTTAGGTGTCCCGA
<i>L. mar.</i>	FSL S4-120	280	TTAGTAACAGAACAAAGAGGAG-----GTTGTTGTTAGGTGCCCCGA
<i>L. inn.</i>	Clip11262	280	TTAGTTACGGAAACAAAAGAA-----ATTGTCATTAGATGTCCGGA
<i>L. wel.</i>	SLCC5334	280	ATTGTAACATAATCAAGAAGAA-----ATTGTTATTAGATGCCCTG
<i>L. iv.</i>	FSL F6-596	280	TTAGTAACGGAGCGTGAAGAA-----ATTGTCATTAGATGTCCAGG
<i>L. seel.</i>	SLCC3954	280	TTAGTGACAGAGCGCGAAGAA-----ATTGTAATAAGATGCCCTG
<i>L. gr.</i>	DSM20601	280	CTGCAAGTGAATCGAAAAAATAATATAGCGATCAGAACTCCACAAG
<i>B. smi.</i>	7_3_47FAA	295	AGTCTTTCATTAGACGAACGG-----TATGTTATCCGCTCTCCCGA
<i>B. coag.</i>	36D1	289	AATTTGCAGCACGATACACGT-----TATGTAATCCGCACGCCGA
<i>B. subt.</i>	168	301	AAATTAGCCACGAAGAACAT-----TTCGTTATTTCGCTCCCGGA
<i>B. weih.</i>	KBAB4	283	CGTTTAGAATATCAAATAGA-----TATAGTATTTCGAAGTCCGA
<i>S. aur.</i>	COL	280	AGAAGAGCTGAAAATAATCGT-----ATAAAAATAACGCAACCAAG
<i>S. aur.</i>	71193	280	AGAAGAGCTGAAAATAATCGT-----ATAAAAATAACGCAACCAAG
<i>E. faec.</i>	DO	288	-----GACGGATCATGAAAGAGCGGCTCCACCGTTTCGTACCAGCT
consensus		301	*.....*.....*.....*.....*.....*.....*.....

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).