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L. mono. EGD-e      172 FHNHPSGDP-TPSSEDLIVTKRLAEAGNIVGITLLDHIIGKNKYISLKEKGYF----
L. mono. F2365     172 FHNHPSGDP-TPSSEDLIVTKRLAEAGNIVGITLLDHIIGKNKYISLKEKGYF----
L. mar.           172 FHNHPSGDP-APSSSEDLIVTKRLAEAGNIVGITLLDHIIGKNKYISLKEKGYF----
L. inn. Clip11262 172 FHNHPSGDP-APSSSEDLIVTKRLAEAGNIVGITLLDHIIGKNKYISLKEKGYF----
L. wel. SLCC5334   172 FHNHPSGDP-TPSSEDLIVTKRLVEAGNIIGITLLDHIIGKNKYISLKEKGYF----
L. iv. FSL F6-596 172 FHNHPSGDP-TPSSEDLIVTKRLVEAGSIIGITLLDHIIGKNKYISLKEKGYF----
L. seel. SLCC3954  172 FHNHPSGDP-SPSSSEDLIVTKRLVEAGNIIGITLLDHIIGKNKYISLKEKGYF----
L. gr.           174 FHNHPSGDP-TPSPEDIQVTKNLAKAGDIIGIPLIDHIIGKGSFTSLKEQGYF----
B. smi. 7_3_47FAA 177 FHNHPSGDP-TPSREDIEVTKRLAECGKIIGIEVLDHLIIGDQKYISLKEKGYL----
B. coag. 36D1     175 FHNHPSGDP-SPSKEDIEVTKRLAECGKIMGIEILDHLIIGDKKFVSLRQKGYL----
B. subt. 168     179 VHNHPSGDP-TPSREDIEVTRRLFECGNLIGIELLDHLVIGDKKFVSLKEKGYL----
B. weih. KBAB4   173 LHNHPSGDP-APSREDIEVTKRLVECGRIIGIEVLDHIIGDGHKHFVSLKEKCHI----
S. aur. 71193    172 VHNHPSGDV-TPSQEDIITMRLKECGLILGIDLLDHIIGDNRFTSLVEAGYFDEND
S. aur. COL      172 VHNHPSGDV-TPSQEDIITMRLKECGLILGIDLLDHIIGDNRFTSLVEAGYFDEND
E. faec. DO      175 AHNHPSGNV-IPSQODMNFVKRIQKCGEMMGITVLDHLIIGRKRYFSLREEGMMEEK-
consensus        181 .*****... ** *...*... ..* ..**...**..**.....**...*..

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**Figure S1: Amino acid based alignment of RadC proteins from various *Firmicutes*.**

The alignment was done with MAFFT (Kato H, Toh H (2008), *Brief Bioinform* 9: 286-298), shading of conserved amino acid 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, NP\_465074), *L. mono.* F2365 (*L. monocytogenes* F2365, YP\_014167), *L. mar.* (*L. marthii*, WP\_008947916), *L. inn.* Clip11262 (*L. innocua* Clip11262, NP\_470920), *L. wel.* SLCC5334 (*L. welshimeri* SLCC5334, YP\_849759), *L. iv.* FSL F6-596 (*L. ivanovii* FSL F6-596, ZP\_07873944), *L. seel.* SLCC3954 (*L. seeligeri* SLCC3954, YP\_003464701), *L. gr.* (*L. grayi*, WP\_003755617), *B. smi.* 7\_3\_47FAA (*Bacillus smithii* 7\_3\_47FAA, ZP\_09354272), *B. coag.* 36D1 (*Bacillus coagulans* 36D1, YP\_004860597), *B. subt.* 168 (*Bacillus subtilis* 168, NP\_390682), *B. weih.* KBAB4 (*Bacillus weihenstephanensis* KBAB4, YP\_001647086), *S. aur.* 71193 (*Staphylococcus aureus* 71193, AFH69892), *S. aur.* COL (*Staphylococcus aureus* COL, YP\_186546), *E. faec.* DO (*Enterococcus faecium* DO, AFK59806)