SUPPORTING INFORMATION

Supporting Figure Legends

Figure S1: Cell morphology of suppressor mutants was analyzed by electron microscopy. *A. oris* cells of various strains (**A**-**P**) were immobilized on nickel-coated carbon grids and stained with 1% uranyl acetated prior to microscopic examination. Scale bars indicate $0.5 \mu m$.

Figure S2: Transposon insertion at ANA_1289 caused a polar effect on downstream genes *acaC* and *lcp.* Expression levels of ANA_1289 (**A**), *acaC* (ANA_1291) (**B**), *lcp* (ANA_1292) (**C**) and *srtC2* (**D**) in wild-type MG-1 and two suppressor mutants Tn5-2 and Tn5-12 were analyzed by real-time PCR (RT-PCR). The data were presented here as average of three independent experiments and expressed relative to the transcript abundance of MG1, which was arbitrarily assigned a value of 1. All measured transcripts were normalized by using the 16S rRNA gene as a housekeeping control. Asterisk (*) indicates significance with P <0.001 by Student's *t* test.

Figure S3: Expression of AcaC in representative strains in each suppressor group was analyzed by immunoblotting. Cells of various strains grown to mid-log phase were normalized by optical density. Culture supernatant (S), cell wall (W), membrane (M), and cytoplasmic (C) fractions were obtained by cell fractionation. Equivalent protein samples were separated on 4- 12% Tris-Glycine gradient gels and detected by immunoblotting with antibodies against AcaC (α-AcaC) and SrtC2 (α-SrtC2). Molecular mass markers are shown in kDa.

Supporting Table S1: Bacterial strains and plasmids used

Supplementary Table S2: Bacterial strains and plasmids used

 $^(a)$ Underlined are the restriction sites in the primers.</sup>

Supporting Experimental Procedures

Plasmid construction

P*rpsJ*-SrtA, P*rpsJ*-SrtA-C216A, and P*ribo-*SrtA-C216A – The promoter region of the *rpsJ* gene and the *srtA* coding region were amplified from the MG-1 chromosome by PCR with the primer pairs rpsL-F/R and com-srtA-F/R, respectively (Table S2). PCR products were digested with appropriate restriction enzymes and ligated into the BamHI and EcoRI sites of *E. coli*/*Actinomyces* shuttle vector pJRD215 (Yeung & Kozelsky, 1994) to yield P*rpsJ*-SrtA.

To generate P*rpsJ*-SrtA-C216A, the BamHI and EcoRI fragment above was subcloned into pUC19. The generated plasmid was used as a template for site-directed mutagenesis by inverse PCR using primers srtA(C216A)-F/R as previously described (Wu *et al.*, 2012). The resulting mutagenized *srtA* fragment was cloned into pJRD215 between BamHI and EcoRI sites. The desired mutation was confirmed by DNA sequencing.

To construct P*ribo-*SrtA-C216A, the pUC19 vector harboring the *rpsJ*-SrtA-C216A fragment was used as a template for introduction of the riboswitch E* sequence(Topp *et al.*, 2010) upstream of the *srtA* coding sequence by inverse PCR using the primer pair Ribo-srtA-F and Ribo-PrpsJ-R. The generated plasmid was confirmed by DNA sequencing before it was digested with BamHI and EcoRI to release the *srtA*-containing fragment, which was then cloned into pJRD215.

pCWU2-∆*srtA* and pCWU3-∆*srtA* – One-kb fragments upstream and downstream of *srtA* were amplified from the MG-1 chromosome by PCR with primer sets srtAupF/srtAupR and srtAdnF/srtAdnR, respectively (Table S2). Generated fragments were digested with EcoRI/KpnI and KpnI/XbaI, respectively, and ligated into the *Actinomyces* deletion vector pCWU2 (Mishra et

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al., 2010) or pCWU3 (Wu & Ton-That, 2010) precut with EcoRI and XbaI. The resulting plasmids were confirmed by colony PCR and restrictive enzyme digestion.

pAcaC, pAcaC_{∆LPXTG} and pAcaC_{∆CWS} – A fragment encompassing the promoter region of the *acaC* gene and its open reading frame was PCR-amplified with primers com-AcaC-F/R. The PCR product treated with NdeI and EcoRI was cloned into pJRD215 pre-treated with the same enzymes to create pAcaC. To generate pAcaC∆LPXTG *and pAcaC∆*CWS, the treated *acaC* fragment above was cloned into pCWU2. The generated plasmid was used as a template for inverse PCR amplification using primers AcaC∆LPXTG-F/R and AcaC∆cws-F/R, respectively (Table S2). The resulting mutations were verified by DNA sequencing.

 $pAcaC_{H6-TEV}$ – pAcaC was used as a template for inverse PCR amplification using primers Rev-AcaC(H6)-F (5'-CACCACCACCACCACCACGGCAAGCCCCTGGCCCAGACCG-3') and Rev-AcaC(TEV)-R(5'-CGATTGGAAGTAGAGGTTCTCGGAGGTGGAGGCCGCCGGGGTGGCGTC-3'). This strategy allows insertion of a TEV-protease cleavage site (ENLYFQS), followed by a 6xHis-Tag upstream of the AcaC LPXTG motif. The obtained PCR product was circulated to generate pAac C_{H6-TEV} , which was further verified by DNA sequencing.

Generation of antibodies against AcaC

For antibody production, an expression vector for a recombinant AcaC protein lacking its signal peptide and cell wall sorting signal was generated as the following. The primers $AcaC_{Fcolir}F$ (5'aaaggatccaagatcgccgatgaccagc-3') and $Acc_{Ecoil}R$ (5'-aaactgcagttacttgccggaggtggagg-3') were used for PCR amplification of the *acaC* coding sequence from the chromosomal MG-1 DNA. The generated amplicon was treated with BamHI and BglII and cloned into the expression vector pQE30 (QIAGEN). The recombinant plasmid was transformed into *E. coli* XL1-Blue. Purification of the recombinant AcaC protein was carried out by affinity chromatography and the purified protein was used for antibody production accordingly (Mishra et al., 2007).

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Supporting References

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Figure S1: Wu et al.

Figure S2: Wu et al.

Figure S3: Wu et al.