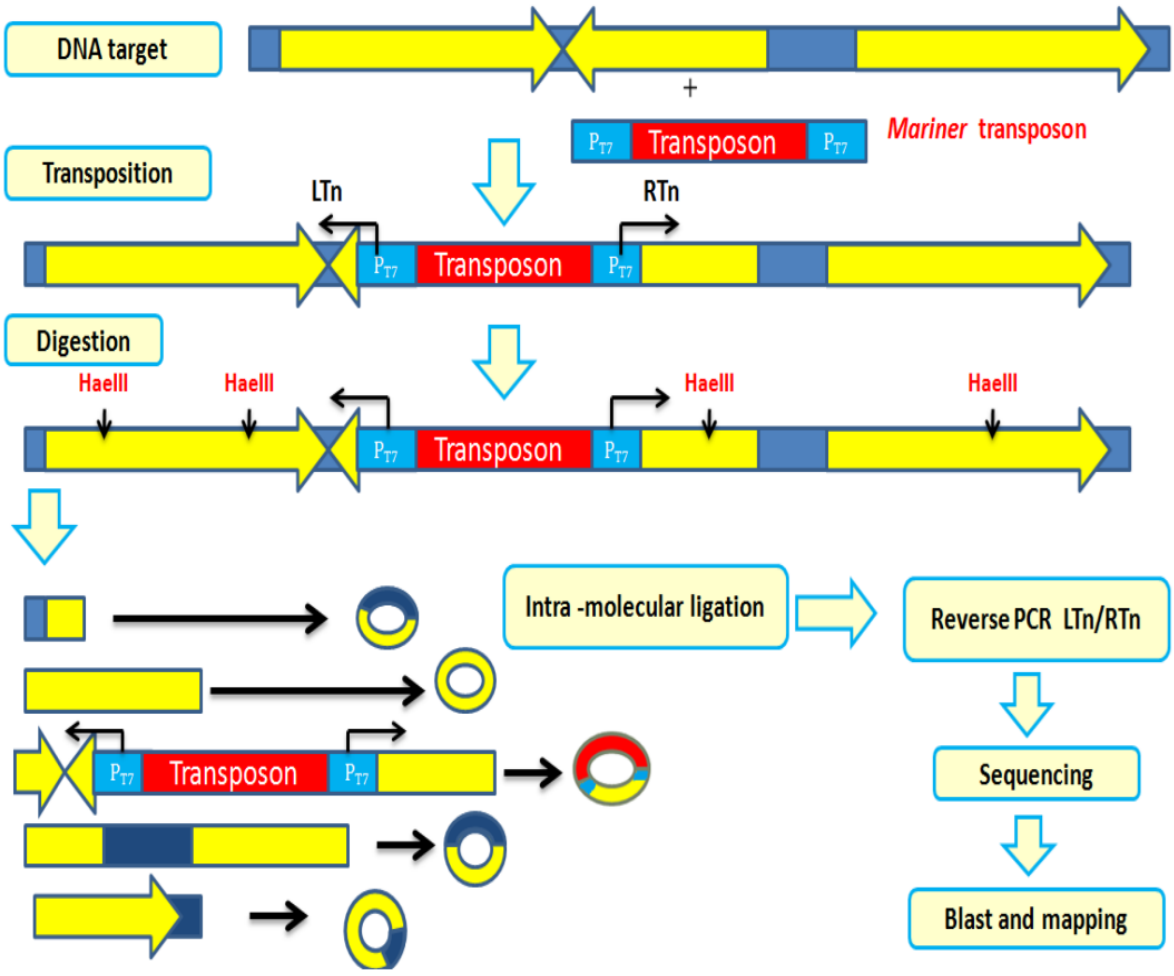

Fig. S1. Schematic presentation of the mapping method for the transposon insertion sites. To map the sites of transposon insertion, genomic DNA of mutants with partially restored tolerance screened from the transposon library was extracted and digested with *Hae*III endonuclease. The chromosomal parts attached to the transposon were amplified by PCR using the transposon specific primer pair LTn/RTn after circularization of the restriction fragments by ligation. The PCR products were purified and sequenced and the obtained sequences were blasted against the genome of *E. faecalis* strain OG1RF to locate the transposition sites.

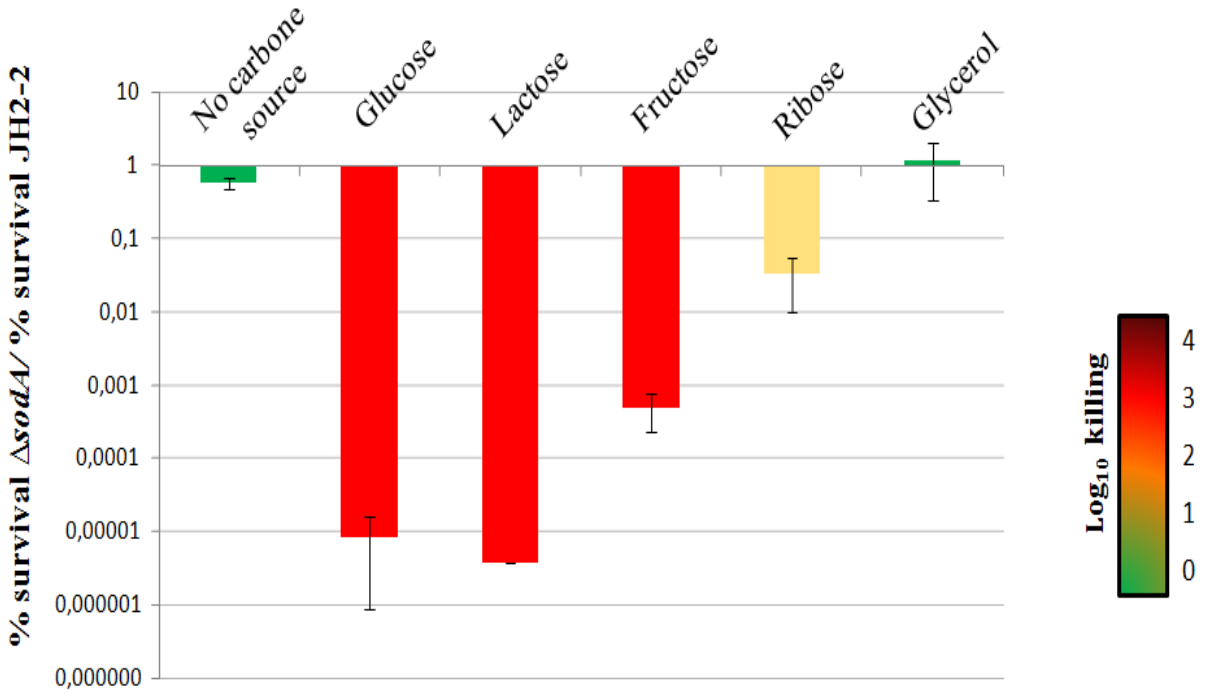

Fig. S2. Bactericidal activity of penicillin is dependent on the energy source in *E. faecalis* JH2-2 Δ*sodA* mutant. Ratio of relative survival of *E. faecalis* JH2-2 and its derivative JH2-2 Δ*sodA* mutant after 24 hours of exposure to 20 µg/mL of penicillin in ccM17 MOPS medium supplemented with glucose, lactose, fructose, ribose or glycerol. Mean values of at least three different experiments are represented with error bars indicating standard deviations..

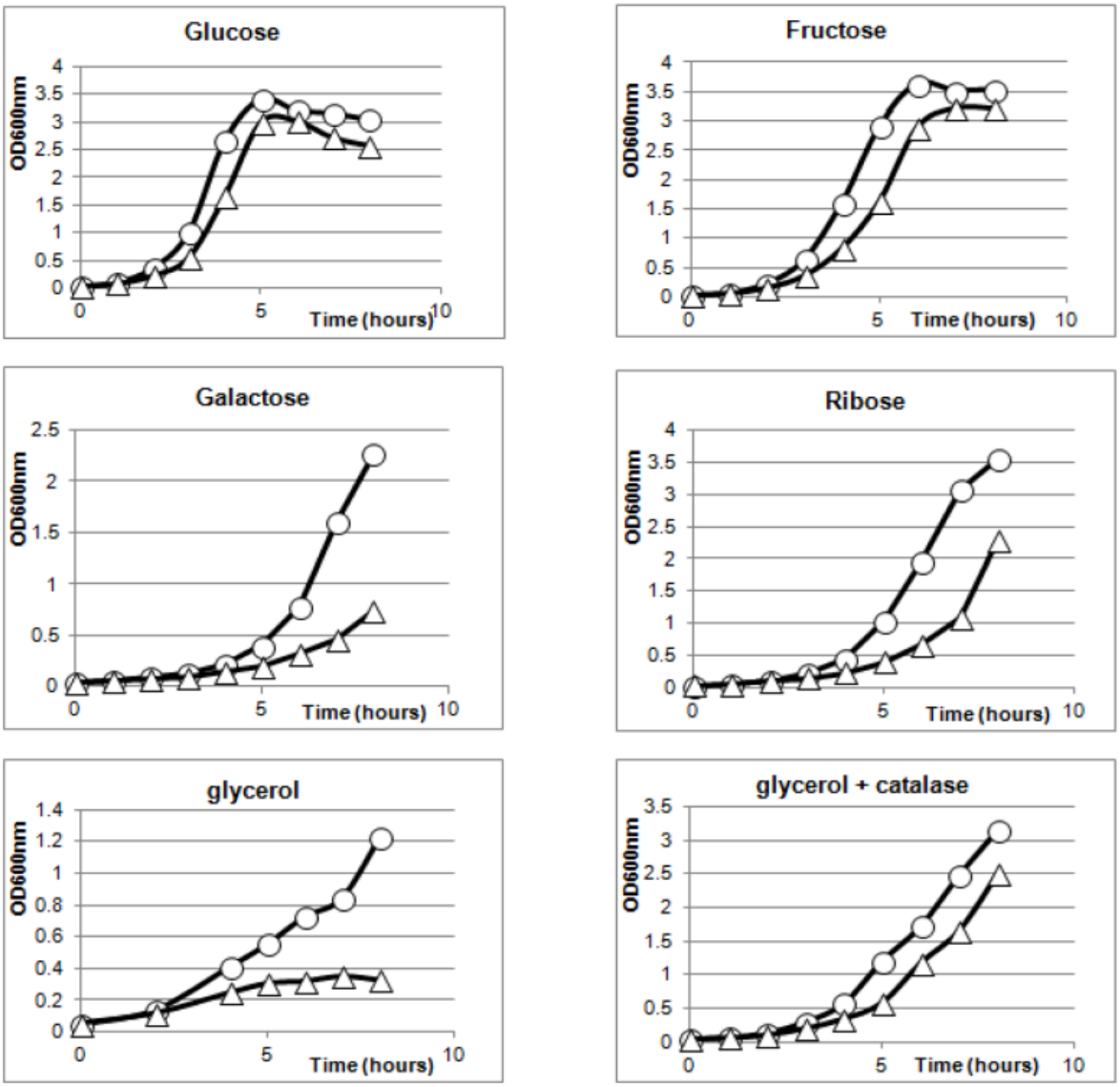

Fig. S3. Growth of *E. faecalis* strains on different substrates. Growth curves of *E. faecalis* JH2-2 wild-type (O) and its isogenic Δ*sodA* mutant (Δ) under aerobic conditions (60 rpm) on ccM17MOPS medium supplemented with 0.5% of glucose, fructose, galactose, ribose or glycerol in presence or absence of catalase from bovine liver added to the medium at a final concentration of 500 U/ml are shown.

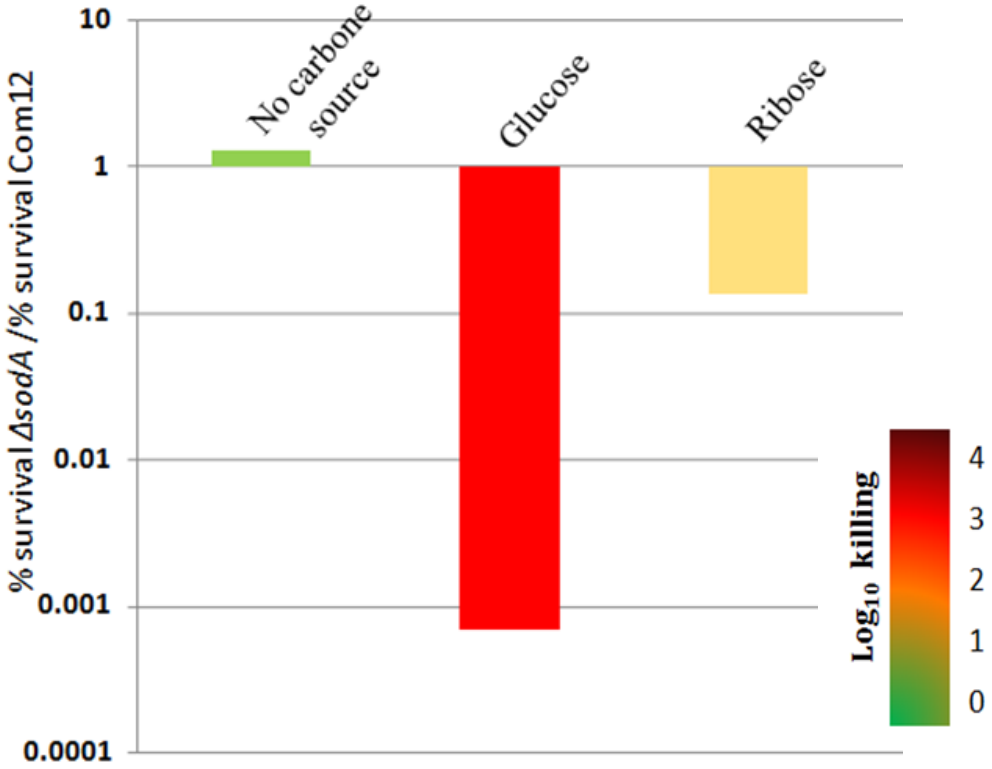

Fig. S4. Bactericidal activity of vancomycin is dependent on the energy source in *E. faecium* Com12 Δ*sodA* mutant. Ratio of relative survival of *E. faecium* Com12 and its derivative Com12 Δ*sodA* mutant after 24 hours of exposure to 20 µg/mL of vancomycin in ccM17 MOPS medium supplemented with glucose or ribose. Only one experiment has been carried out for these results.

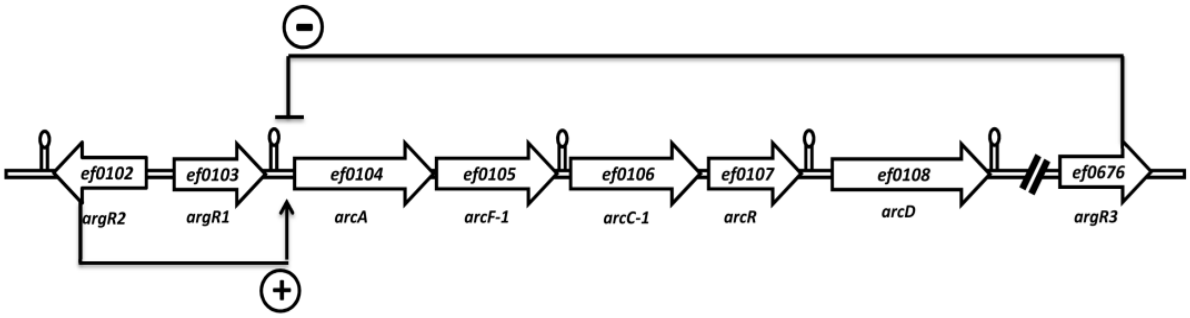

Fig S5. Organization of ADI operon and its regulation in *E. faecalis*. Structure and proposed regulation of expression by ArgR2 and ArgR3 of the arginine deiminase operon in *E. faecalis.*

Table S1. Primers used in this study

Primer pair	Sequence (5' – 3')*		Use
	Forward	Reverse	
PU/ PR	GTAAAACGACGGCCAGT	CAGGAAACAGCTATGAC	Cloning verification
pZXL5 for/pZXL5 Rev	TTCAAGCGTGGTGAAATGAG	TACTTTGCCAGCGGACTTTT	Screen the presence of pZXL5
LTn/RTn	GCCCCCTGAAATCCTTACAT	AAACAGGAATTTATCGAAAATGGT	Reverse PCR for transposon mapping
104ForPst/104RevEco	AAAAAA<u>CTGCAG</u>CACAAGCAGAA CATGATGCA *(Pst1)*	AAAAAA<u>GAATTC</u>AATTGACGCAGC ATCCGTTC *(EcoR1)*	Cloning in pUCB30
104verifF/104verifR	GCCAGATTATCTGGAGAGAC	GAATTTACGATGTTCACCGA	Cloning verification
ef0102L/ef0102R	TTCTCGTGACATTCGTGAGC	TATTTTGGACGAAGGGCAGA	RT-qPCR
ef0103L/ef0103R	GCGAGATAAATGTCGCACAA	AAATCGTTAACCGCATCTCG	RT-qPCR
ef0104L/ef0104R	CGGTGAACACCGTAAATTCAT	AAACAACCAAACCACCTTCG	RT-qPCR
ef0105L/ef0105R	ACTGTTTGCCAGCCTTTCAT	GCGGAAGACTTCATCCGTAA	RT-qPCR
ef0106L/ef0106R	TTGTCCAATGCGCTTAATCA	ATGCCTCATCTGCTGGATCT	RT-qPCR
ef0107L/ef0107R	CATTACGACTCCGCGATTG	TGAATCAATTGCTGGGGATT	RT-qPCR
ef0676L/ef0676R	CAGAAGTGGCTGGTACAGTGG	TCATATTTTCGATGCGTTCG	RT-qPCR

*Underlined sequences correspond to the recognition sites of the restriction endonucleases reported in parentheses