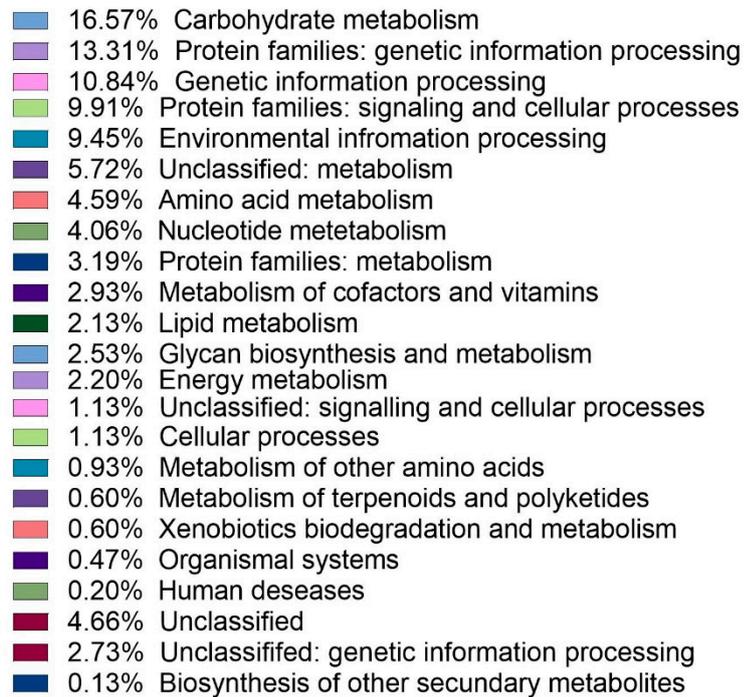
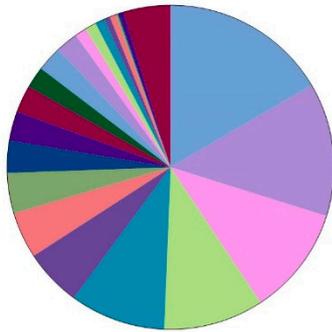


A) VB4



B) VB1

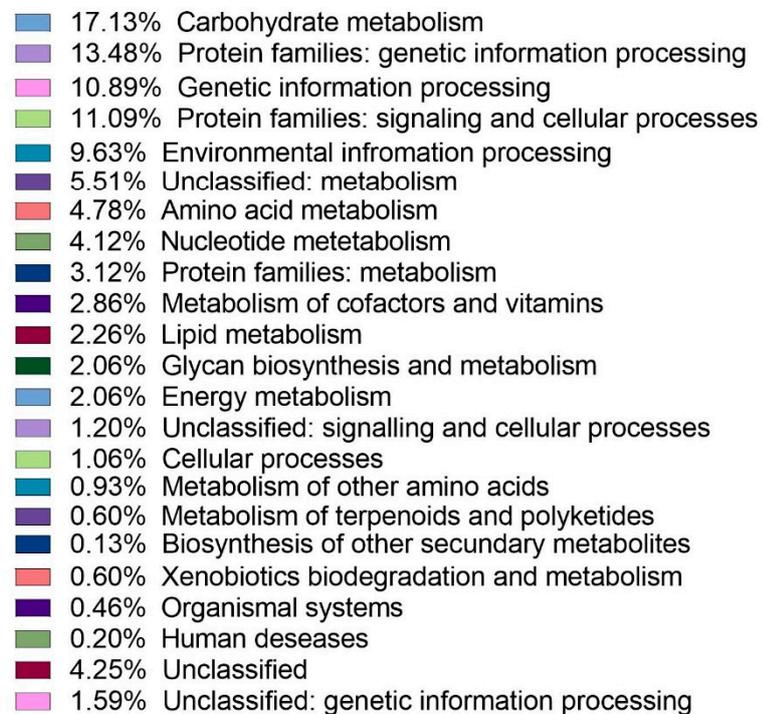
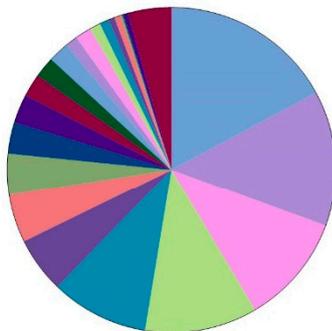
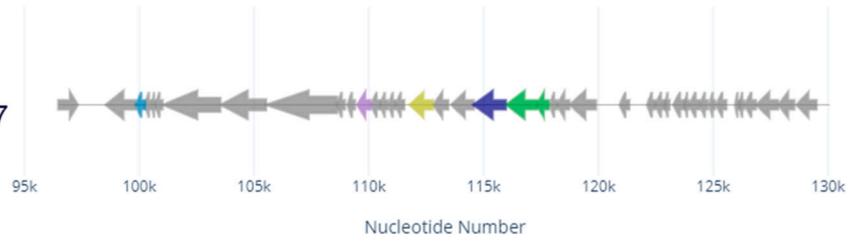


Figure S2. Distribution of KEGG orthology (KO) categories of identified protein-coding genes in the *Lacticaseibacillus rhamnosus* VB4 (A) and VB1 (B) genomes, respectively.

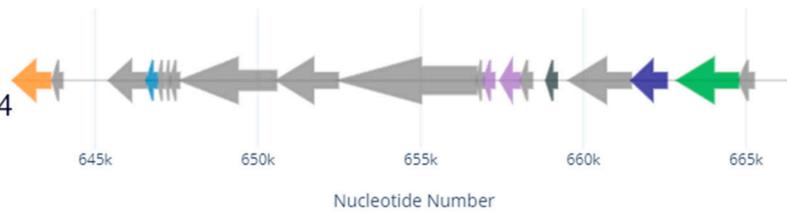
(A)

VB4_Contig 2
96478..130067



(B)

VB1_Contig 1
642460..666284



- Lysis
- Integration
- Terminase
- Tail
- Portal
- Other (structural)
- Other
- Coat

Figure S3. Organization of the main prophage regions in VB4 (A) and VB1 (B) genomes.

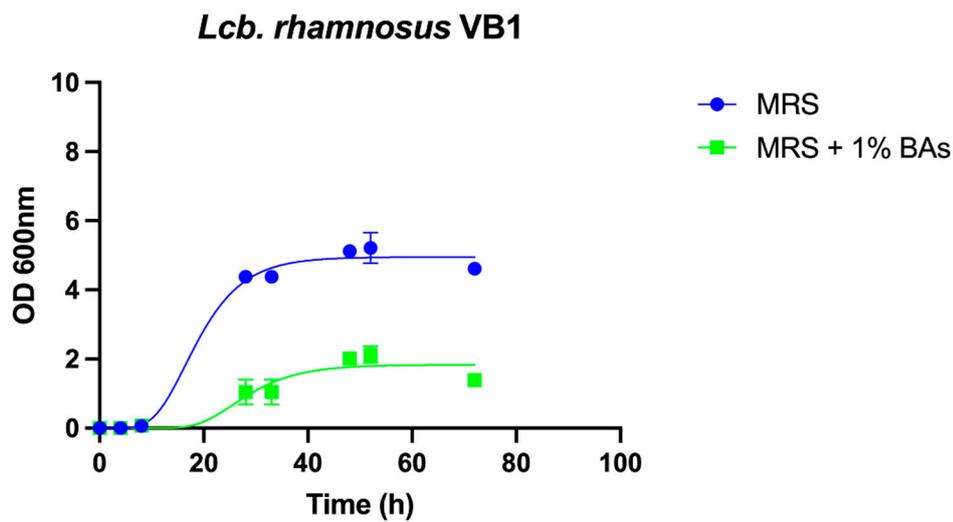
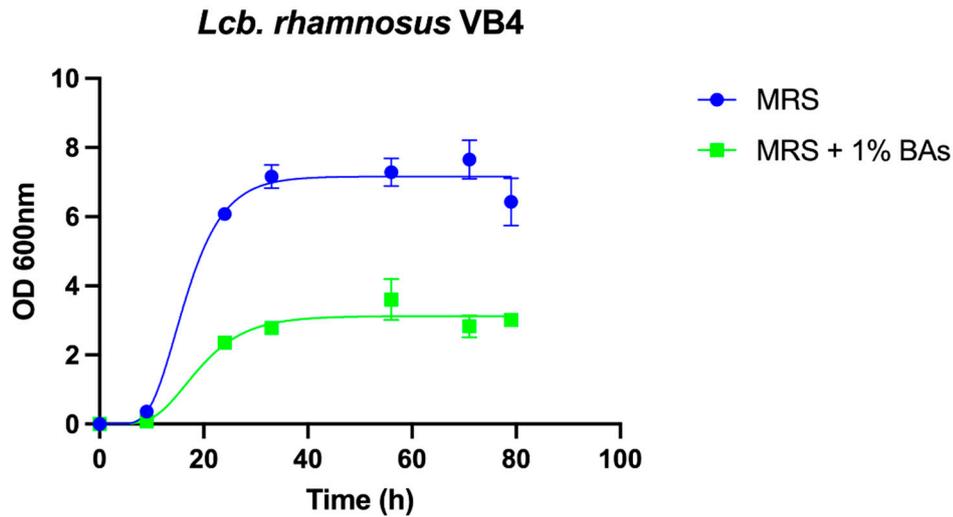


Figure S4. Growth curves of VB4 and VB1 strains in presence of 1% (w/v) BAs mixture (green) compared with control growth conditions (MRS medium; blue). Growth was monitored over the time as mean of OD_{600nm} values in three different biological replicates. Bars (when visible) indicate standard deviation (SD) values of OD_{600nm} measurements. The curves were fitted by non-linear Gompertz model and plotted using GraphPad v.8.00 software (San Diego, CA, USA).

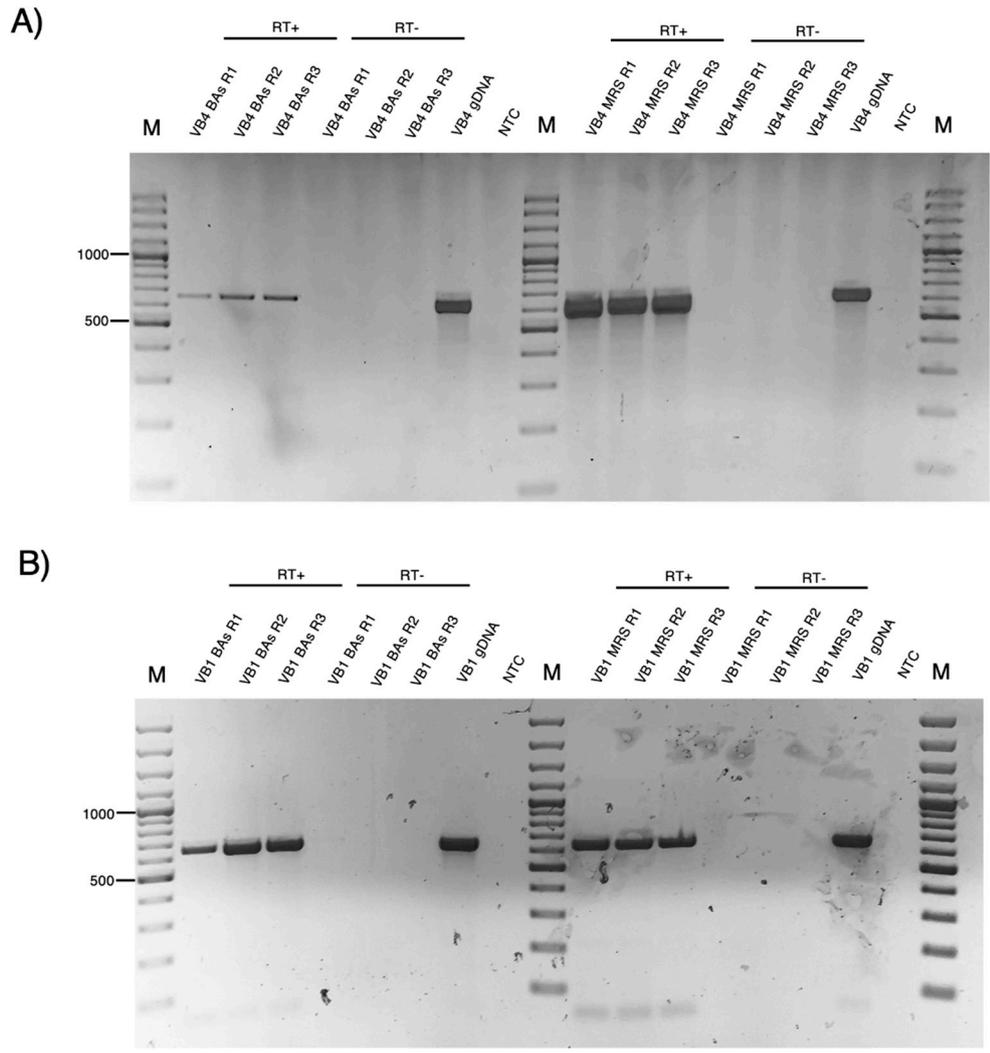


Figure S5. End-point RT-PCR targeting *bsh* gene in BAS-stressed (MRS medium supplemented with 1% (w/v) BAS) and non-stressed (MRS medium) stationary cells of *Lactocaseibacillus rhamnosus* VB4 (A) and VB1 (B), respectively. Three independent replicates, numbered from R1 to R3, were used. +/- RT indicates addition of reverse transcriptase to the cDNA synthesis reaction. The expected PCR product length was established for each amplicon by using 100 bp DNA Gene Ruler Plus as molecular weight marker. For each RT-PCR reaction gDNA was used as positive control. 16S rRNA gene PCR reactions used as control were omitted. Abbreviations: M, molecular-weight size marker; NTC, negative control.