

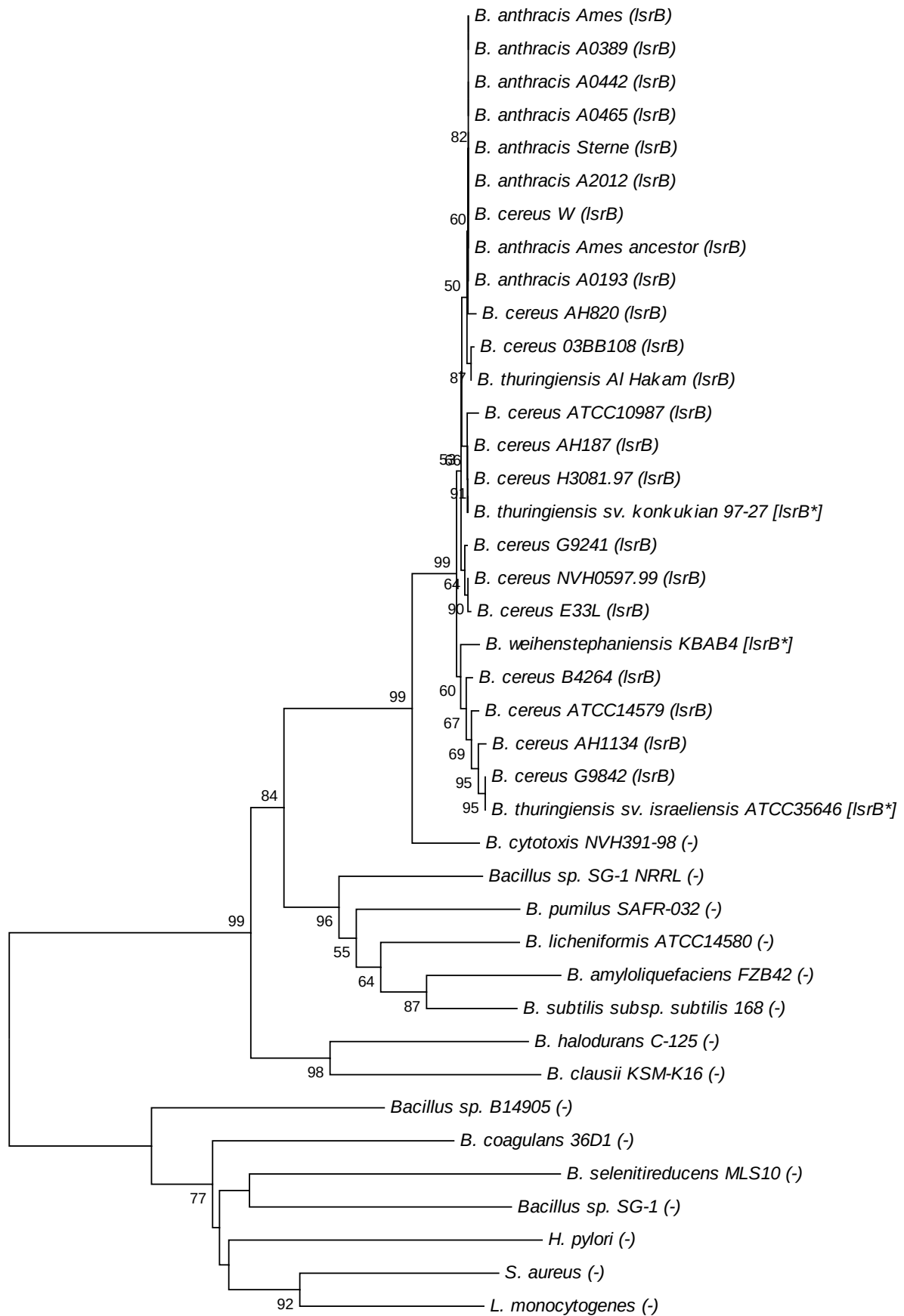


Figure 1s. Phylogenetic relationships among sequenced *Bacillus* species on the basis of complete *luxS* sequences and presence of the *lsrB* receptor gene in the respective genomes. The distance tree was generated by the NJ method with the JC formula, without choosing any outgroup. Nodal supports were assessed by 1000 bootstrap replicates. Only bootstrap values greater than 50% are shown. The scale bar represents the number of substitutions per site. The presence of *lsrB* is indicated between parentheses. The asterisk shows the strains in which one or more genes encoding the Lsr-receptor complex present frameshift or rearrangement leading to truncated proteins. The *luxS* sequences of other Gram-positive bacteria *Helicobacter pylori* (NC_008086) , *Listeria monocytogenes* (NC_002973) and *Staphylococcus aureus* (NC_003923) were used as comparison. All genomes were retrieved at the NCBI database, accession numbers are: *Bacillus amyloliquefaciens* FZB42 (NC_009725); *Bacillus anthracis* str. Ames (NC_003997), Ames Ancestor (NC_007530), Sterne (NC_005945), A0193 (NZ_ABKF000000000), A0389 (NZ_ABLB000000000), A0442 (NZ_ABKG000000000), A2012 (NZ_AAAC000000000); *Bacillus cereus* str. 03BB108 (NZ_ABDM000000000), E33L (NC_006274), AH187 (NZ_AAUF000000000), AH820 (NZ_AAUE000000000), AH1134 (NZ_ABDA000000000), ATCC 10987 (NC_005707), ATCC 14579 (NC_004722), B4264 (NZ_ABDI000000000), G9241 (NZ_AAEK000000000), G9842 (NZ_ABDJ000000000), H3081.97 (NZ_ABDL000000000), NVH0597-99 (NZ_ABDK000000000), W (NZ_ABCZ000000000); *Bacillus cereus* subsp. *cytotoxis* NVH 391-98 (NC_009674); *Bacillus clausii* KSM-K16 (NC_006582); *Bacillus coagulans* 36D1 (NZ_AAWV000000000); *Bacillus halodurans* C-125 (NC_002570); *Bacillus licheniformis* ATCC 14580 (NC_006322); *Bacillus pumilus* SAFR-032 (NC_009848); *Bacillus selenitireducens* MLS10 (NZ_ABHZ000000000); *Bacillus subtilis* subsp. *subtilis* str. 168 (NC_000964); *Bacillus thuringensis* serovar *israelensis* ATCC 35646 (NZ_AAJM000000000), serovar *konkukian* str. 97-27 (NC_005957), Al Hakam (NC_008600); *Bacillus weihenstephanensis* KBAB4 (NC_010184); *Bacillus* sp. B14905 (NZ_AAXV000000000), NRRL B-14911 (NZ_AAOX000000000), SG-1 (NZ_ABCF000000000).