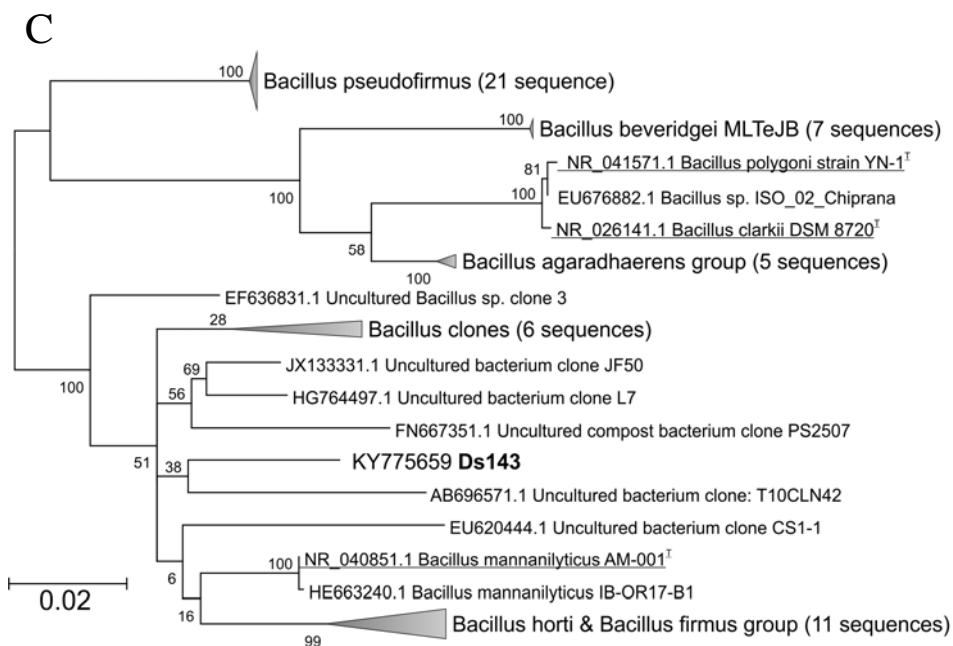
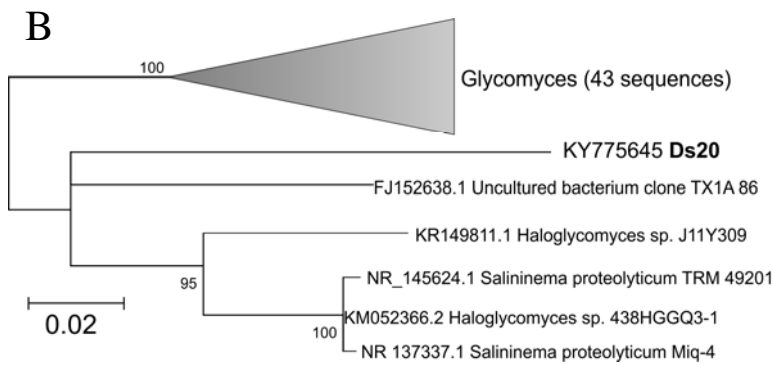
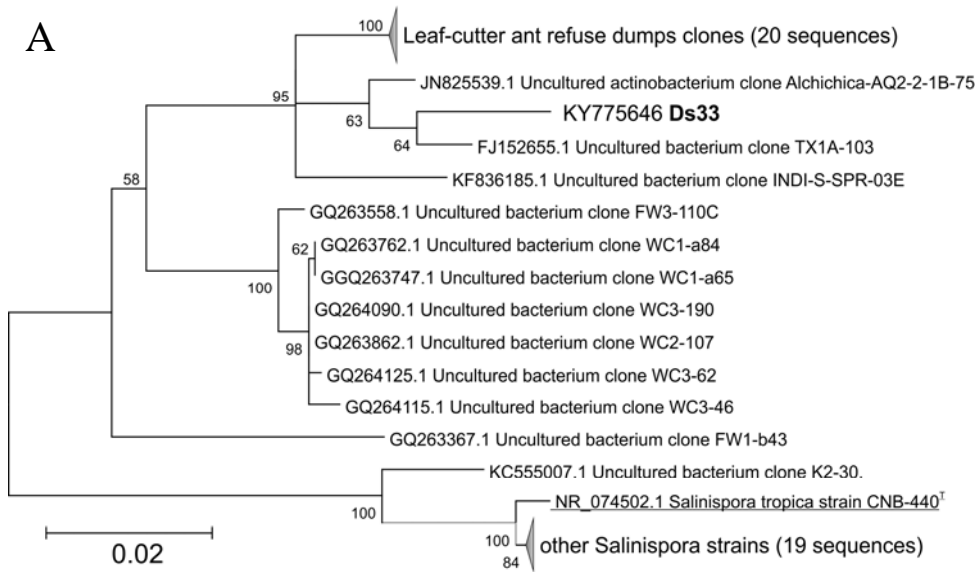


**Supplementary Table S1.** SILVAngs Project Summary and Project Settings.

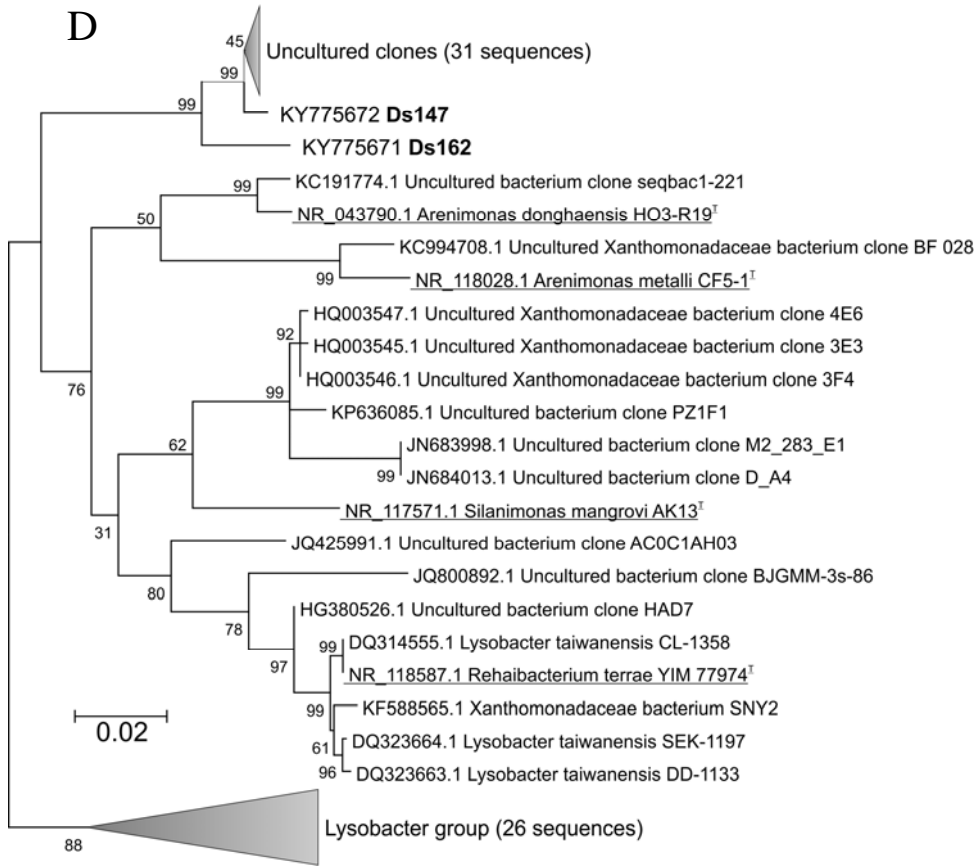
<b>Project Summary</b>	
Project Name:	DS collection
Project Description:	Default configuration
Sequence Type:	SSU
Number of Samples:	1
Number of Sequences:	179
Number of Rejected Sequences:	0 (0.00%)
<b>Raw Sequence Information</b>	
Min. Length:	441
Avg. Length:	1101
Max. Length:	1497
<b>Aligned Sequence Information</b>	
Min. Length:	441
Avg. Length:	1101
Max. Length:	1497
<b>Clustering information</b>	
Number of OTUs:	45 (25.14 %)
Number of Clustered Sequences:	95 (53.07 %)
Number of Replicates:	39 (21.79 %)
Classification Information	
Number of Classified Sequences:	179 (100.00 %)
Number of "No Relative":	0 (0.00 %)
<b>Project Settings</b>	
SINA Version:	SINA v1.2.10 for ARB SVN (revision 21008)
Min Align. Identity (%):	50
Min Align. Score:	40
Min Basepair Score (%):	30
<b>Quality Control</b>	
Min. Sequence Quality (%):	30
Min. Length (aligned nuc.):	50
Max. Ambiguities (%):	2
Max. Homopolymers (%):	2
<b>Clustering</b>	
CD-Hit Version:	3.1.2
Min. OTU Identity (%):	98
<b>Classification</b>	
BLAST Version:	2.2.30+
Reference:	SILVA
Reference Version:	128
Similarity (%):	93

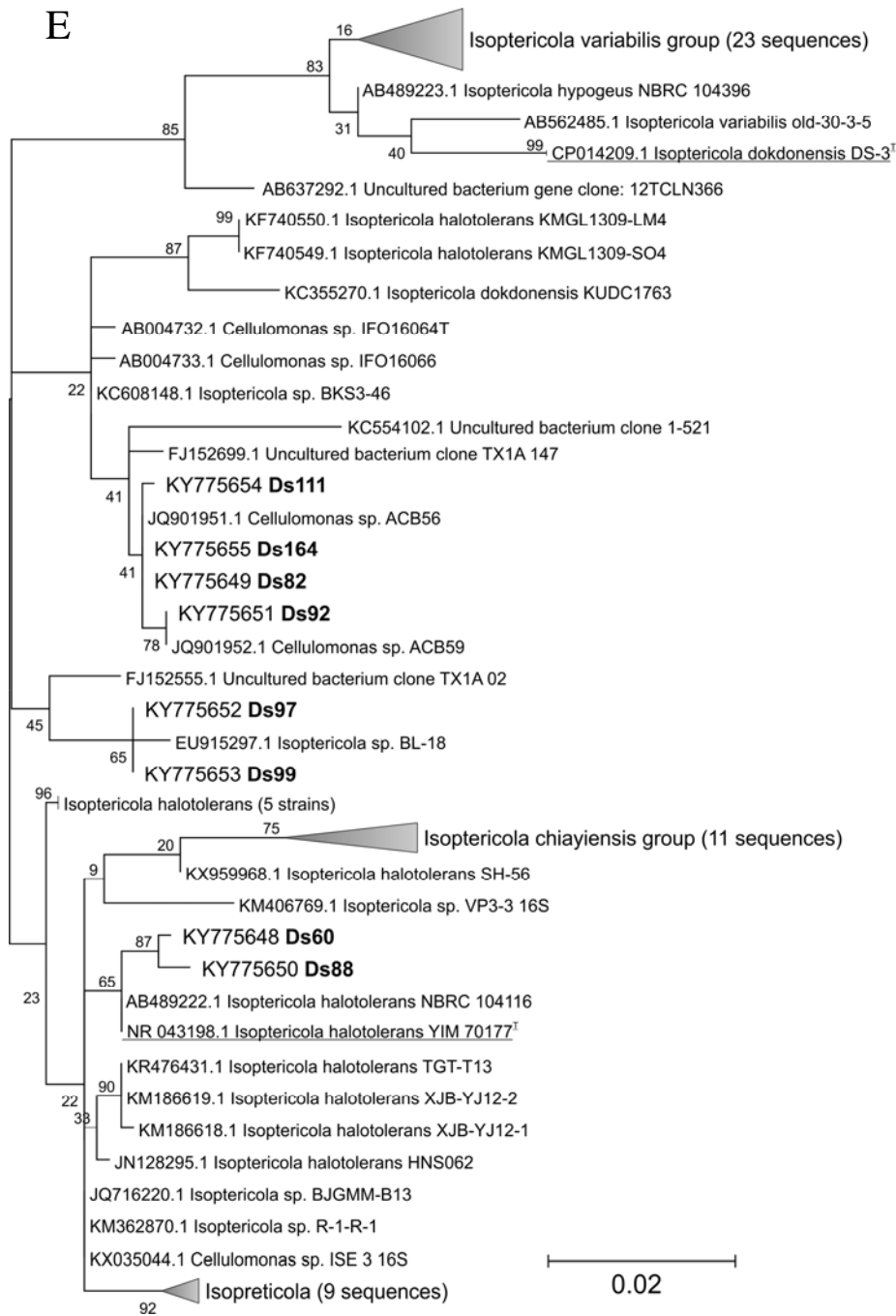
**Suppl. Table S2.** Site-specific taxonomic distribution of isolates different locations

Group	Armenia	s-w Siberia		s-e Siberia	n-e Mongolia	Kenya- Tanzania	Egypt	California
	AA	KS	BS	KUS	MS	KT	EWN	MLC
<b>Actinobacteria</b>								
<i>Nocardiopsis alba</i>	4							
<i>Nocardiopsis</i> YIM80133	3	4		2	5	1		
<i>Nocardiopsis</i> E-143	6	6		4	8	3		
<i>Nocardiopsis</i> AACH2	1	1		4				
<i>Nocardiopsis exhalans</i>			1	1				
<i>Streptomyces sodiiphilus</i>	1	4	3	1				
<i>Streptomyces alkaliphilus</i>	2	2				1		
<i>Streptomyces</i> E-070		2				1	2	1
<i>Streptomyces alkalithermotolerans</i>	1	1				1		
<i>Streptomyces</i> YIM80244						1		1
<i>Isoptericola halotolerance</i>		3			3	2		
<b>Bacillales</b>								
<i>B. pseudofirmus</i>		6	5		5	7		
<i>B. akibai</i>					6	1		
<i>B. halodurans</i>					3	2		
<i>B. horikoshii</i>		2	1			2		
<i>B. polygonii</i>						4		
<i>B. cellulolyticus</i>						3		
<i>Bacillus daliensis</i>		2			2			
<i>Bacillus alkalisediminis</i>					5			
<i>B. vedderii</i>						1		
<i>B. bogoriensis</i>						1		
<i>B. clarkii</i>						1		
<i>Bacillus alkalinitrilicus</i>					1			
<i>Bacillus</i> E-141				1				
<i>Anaerobacillus alkalidiazotrophicus</i>						2		
<b>Gammaproteobacteria</b>								
<i>Aliidiomarina</i>			1		4			
<i>Alkalimonas amylolytica</i>		2	2	1	1			
<i>Xanthomonadaceae</i>		3			1			



D





**Suppl. Figure S1.** Unrooted 16S rRNA gene sequence Maximum likelihood phylogenetic trees of the haloalkaliphilic isolates, possibly representing novel taxa, and its nearest relatives. All positions with less than 95 % site coverage were eliminated. There were a total of 1338 (A), 1394 (B), 1442 (C), 1373 (D) and 1103 (E) positions in the final datasets. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site with corrections, associated with the model. Bootstrap values as percentages of 1000 repetitions are shown next to the branches. Type strains of validly published species are underlined. Genbank numbers are indicated at the beginning of each sequence designation.