Supplemental Material

Tab. S1: Strains selected from each habitat used in this study. The four most representative strains from isolation plates for rock (r), groundwater (gw) and soil (s) samples from Middle Muschelkalk (MM) or Lower (LM) were selected. 16S rDNA sequence accession numbers are given in parentheses (Genbank).

rLM	rMM	gwLM	gwMM	sLM	sMM
Bacillus sp. rLMa (KX527723.1)	*Arthrobacter pascens* rMM19	*Flavobac-terium limicola* S_5.3 (KR088468.1)	*Arthrobacter sp.* W_2.1 (KX570903.1)	*Agromyces cerinus* sLM10 (KX536506.1)	*Agrococcus jejuensis* sMM51 (KX527688.1)
Bacillus muralis rLMd (KX527725.1)	*Bacillus sp.* rMM8 (KX527696.1)	*Lelliottia amni-gena* S_H3 (KR088478.1)	*Planococcus sp.* W_1.2 (KR088481.1)	*Bacillus sp.* sLM42 (KX536514.1)	*Moraxella osloensis* sMM16 (KX527667.1)
Bacillus simplex 3.3F (KX527719.1)	*Psychrobacillus psychrodurans* rMM20 (KX527705.1)	*Pseudomonas sp.* S_H4 (KX573101.1)	*Rhodococcus erythropolis* W_Sd5 (KX570908.1)	*Streptomyces sp.* sLM17	*Sphingopyxis bauzanensis* sMM41 (KX527680.1)
Micrococcus luteus rLMc (KX527724.1)	*Ochrobactrum intermedium* rMM23 (KX527707.1)	*Rhizobium sp.* S_4.1a	*Advenella sp.* W_Sd3 (KR088492.1)	*Streptomyces sp.*sLM8 (KX536505.1)	*Streptomyces sp.* sMM10 (KX527665.1)
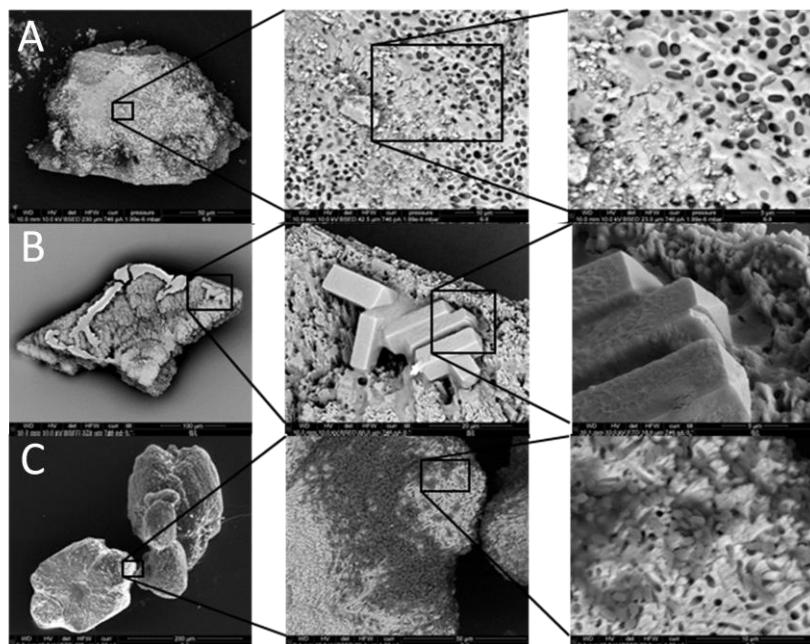
Fig. S1: Biominerals visualized by scanning electron microscopy. *Bacillus flexus* rLM1.5 (A), *Comamonas koreensis* W_5.3b (B), *Bacillus sp.* rMM10 (C) are shown, each for an overview of crystal shapes, partly covered with organic matrix, and high magnification to give insight into surface and microcrystalline structures. Some minerals are settled by bacterial cells leaving holes after lysis.