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	*Flavobacterium 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)

Tab. S2: Strains isolated from rock (r), groundwater (gw) and soil (s) samples from Middle Muschelkalk (MM) or Lower (LM) identified by 16S rDNA sequencing. The affiliations to kingdoms (classes for Proteobacteria) are given.

Strain	Organism	Affiliation	Strain	Organism	Affiliation	Strain	Organism	Affiliation
Rock Lower Muschelkalk, outcrop Jena Formation (51125583, 11707340/57)			Groundwater Lower Muschelkalk, Stöben (5660183, 4478864)			Soil Lower Muschelkalk, quarry Bad Kösen on Jena formation (51125376/427, 11709132/319)		
rLM1.4	*Bacillus niacini*	Firmicutes	S_1.1	*Pseudomonas* sp.	Gamma-proteobacteria	sLM2	*Streptomyces* sp.	Actinobacteria
rLM1.5	*Bacillus flexus*	Firmicutes	S_1.13	*Microbacterium* sp.	Actinobacteria	sLM5	*Streptomyces* sp.	Actinobacteria
rLM1.6	*Bacillus pumilus*	Firmicutes	S_1.16	*Pantoea ananatis*	Gamma-proteobacteria	sLM6	*Rhodococcus* sp.	Actinobacteria
rLM1.9	*Bacillus altitudinis*	Firmicutes	S_1.18	*Paenibacillus glycanilyticus*	Firmicutes	sLM8	*Streptomyces* sp.	Actinobacteria
rLM2.3	*Bacillus anthracis*	Firmicutes	S_2.5	*Pseudomonas migulae*	Gamma-proteobacteria	sLM10	*Agromyces cerinus*	Actinobacteria
rLM2.4	*Bacillus subtilis*	Firmicutes	S_2.6	*Pseudomonas fluorescens*	Gamma-proteobacteria	sLM11	*Bacillus badius*	Firmicutes
rLM2.6	*Bacillus massiliensis*	Firmicutes	S_2.9	*Pseudomonas* sp.	Gamma-proteobacteria	sLM13	*Bacillus simplex*	Firmicutes
rLM2.7	*Bacillus strato-sphericus*	Firmicutes	S_2.10	*Microbacterium* sp.	Actinobacteria	sLM15	*Bacillus pumilus*	Firmicutes
rLM4.3	*Kocuria* sp.		S_3.1	*Aeromonas sharmana*	Gamma-proteobacteria	sLM17	*Streptomyces* sp.	Actinobacteria
rLM3.1F	*Bacillus pumilus*	Firmicutes	S_3.6	*Aeromonas salmonicida*	Gamma-proteobacteria	sLM18	*Phyllobacterium* sp.	Alphaproteo-bacteria
rLM3.2F	*Paeni-bacillus* sp.	Firmicutes	S_3.7	*Pseudomonas protegens*	Gamma-proteobacteria	sLM29	*Paenibacillus* sp.	Firmicutes
rLM3.3F	*Bacillus simplex*	Firmicutes	S_3.8	*Acinetobacter calcoaceticus*	Gamma-proteobacteria	sLM39	*Streptomyces* sp.	Actinobacteria
rLM3.5F	*Bacillus* sp.	Firmicutes	S_4.1a	*Rhizobium* sp.	Alphaproteo-bacteria	sLM41	*Streptomyces phaeochromogenes*	Actinobacteria
rLM3.6F	*Paeni-bacillus amylolyticus*	Firmicutes	S_5.2	*Janthinobac-terium lividum*	Actinobacteria	sLM42	*Bacillus* sp.	Firmicutes
rLM4.1F	*Bacillus cereus*	Firmicutes	S_5.3	*Flavobacterium limicola*	Bacteroidetes	sLM43	*Bacillus* sp.	Firmicutes
rLMa	*Bacillus* sp.	Firmicutes	S_Sd4	*Massilia aurea*	Betaproteo-bacteria	sLM47	*Bacillus pumilus*	Firmicutes
rLMc	*Micrococcus luteus*	Actinobacteria	S_Sd8	*Acidovorax facilis*	Betaproteo-bacteria	sLM48	*Streptomyces anulatus*	Actinobacteria
rLMd	*Bacillus muralis*	Firmicutes	S_Sd9	*Pseudomonas peli*	Gamma-proteobacteria	sLM50	*Bacillus pumilus*	Firmicutes
			S_Sd13	*Aeromonas* sp.	Gamma-proteobacteria	sLM1E4	*Caballeronia glathei*	Firmicutes
			S_Sd16	*Pseudomonas* sp.	Gamma-proteobacteria	sLM2A3	*Pseudomonas brenneri*	Gammaproteo-bacteria
			Sd20	*Microbacterium* sp.	Actinobacteria			
			S_A2	*Pseudomonas*	Gamma-			

ID	Species	Class
	baetica	proteobacteria
S_B2	*Agrobacterium* sp.	Alphaproteobacteria
S_G4	*Pseudomonas umsongensis*	Gammaproteobacteria
S_H1	*Rahnella* sp.	Gammaproteobacteria
S_H3	*Lelliottia amnigena*	Gammaproteobacteria
S_H4	*Pseudomonas* sp.	Gammaproteobacteria

Rock Middle Muschelkalk, outcrop Kartstadt formation (51126206, 11704266-11704280)

ID	Species	Class
rMM4	*Arthrobacter phenantrenivorans*	Actinobacteria
rMM7	*Ramlibacter tataouinensis*	Betaproteobacteria
rMM8	*Bacillus* sp.	Firmicutes
rMM9	*Bacillus* sp.	Firmicutes
rMM10	*Bacillus* sp.	Firmicutes
rMM11	*Streptomyces* sp.	Actinobacteria
rMM12	*Arthrobacter* sp.	Actinobacteria
rMM13	*Arthrobacter phenantrenivorans*	Actinobacteria
rMM14	*Bacillus* sp.	Firmicutes
rMM16	*Bacillus niabensis*	Firmicutes
rMM17	*Arthrobacter phenantrenivorans*	Actinobacteria
rMM19	*Arthrobacter pascens*	Actinobacteria
rMM20	*Psychrobacillus psychrodurans*	Firmicutes
rMM21	*Cryocola* sp.	Actinobacteria
rMM23	*Ochrobactrum intermedium*	Alphaproteobacteria

Groundwater Middle Muschelkalk, Wichmar (5655906, 4478030)

ID	Species	Class
W_1.1	*Staphylococcus succinus*	Firmicutes
W_1.3	*Staphylococcus xylosus*	Firmicutes
W_2.1	*Arthrobacter* sp.	Actinobacteria
W_3.1b	*Sporosarcina aquimarina*	Firmicutes
W_3.2	*Glucamicibacter arilaitensis*	Actinobacteria
W_3.7	*Pantoea* sp.	Gammaproteobacteria
W_4.1a	*Pseudomonas* sp.	Gammaproteobacteria
W_4.1b	*Lelliottia amnigena*	Gammaproteobacteria
W_5.1a	*Stenotrophomonas rhizophila*	Gammaproteobacteria
W_5.3a	*Sphingobacterium kitahiroshimense*	Bacteroidetes
W_5.3b	*Comamonas koreensis*	Betaproteobacteria
W_5.4	*Flavobacterium* sp.	Bacteroidetes
W_6.5b	*Pseudomonas* sp.	Gammaproteobacteria
W_Sd1	*Glaciihabitans tibetensis*	Actinobacteria
W_Sd2	*Rathayibacter* sp.	Actinobacteria
W_Sd3	*Advenella* sp.	Betaproteobacteria
W_Sd4	*Pseudomonas* sp.	Gammaproteobacteria
W_Sd5	*Rhodococcus erythropolis*	Actinobacteria
W_Sd8	*Mycoplana* sp.	Alphaproteobacteria
W_Sd9	*Enterobacter* sp.	Gammaproteobacteria
W_Sd11	*Stenotrophomonas rhizophila*	Gammaproteobacteria
W_Sd13	*Rhodococcus* sp.	Actinobacteria
W_B4	*Pedobacter daejeonensis*	Bacteroidetes
W_B5	*Chryseobacterium* sp.	Bacteroidetes
W_B6	*Stenotrophomonas humi*	Gammaproteobacteria
W_B10	*Serratia proteamaculans*	Gammaproteobacteria

Soil Middel Muschelkalk, quarry Bad Kösen, Kartstadt formation (5665596-5665733_4479366-4479449)

ID	Species	Class
sMM5	*Bacillus* sp.	Firmicutes
sMM6	*Kocuria rhizophila*	Actinobacteria
sMM7	*Rathayibacter caricis*	Actinobacteria
sMM10	*Streptomyces* sp.	Actinobacteria
sMM13	*Paracoccus yeei*	Alphaproteobacteria
sMM16	*Moraxella osloensis*	Gammaproteobacteria
sMM17	*Promicromonospora umidemergens*	Actinobacteria
sMM19	*Streptomyces beijiangensis*	Actinobacteria
sMM21	*Dermacoccus* sp.	Actinobacteria
sMM23	*Arthrobacter pascens*	Actinobacteria
sMM27	*Promicromonospora sukumoe*	Actinobacteria
sMM28	*Ramlibacter tataouinensis*	Betaproteobacteria
sMM31	*Stenotrophomonas maltophilia*	Gammaproteobacteria
sMM32	*Micrococcus* sp.	Actinobacteria
sMM33	*Stenotrophomonas* sp.	Gammaproteobacteria
sMM35	*Micrococcus luteus*	Actinobacteria
sMM36	*Arthrobacter* sp.	Actinobacteria
sMM40	*Streptomyces astrooliviaceus*	Actinobacteria
sMM41	*Sphingopyxis bauzanensis*	Alphaproteobacteria
sMM43	*Micrococcus yunnanensis*	Actinobacteria
sMM44	*Streptomyces ederensis*	Actinobacteria
sMM45	*Streptomyces spororaveus*	Actinobacteria
sMM46	*Bacillus* sp.	Firmicutes
sMM47	*Kocuria palustris*	Actinobacteria
sMM48	*Streptomyces atratus*	Actinobacteria
sMM49	*Micrococcus yunnanensis*	Actinobacteria
sMM51	*Agrococcus jejunensis*	Actinobacteria
sMMB1	*Pseudomonas* sp.	Gammaproteobacteria
sMMB2	*Serratia proteamaculans*	Gammaproteobacteria

sMMB6	*Enterobacter* sp.	Gammaproteo-bacteria
sMMB10	*Enterobacter ludwigii*	Gammaproteo-bacteria
sMMB14	*Bacillus tequilensis*	Firmicutes
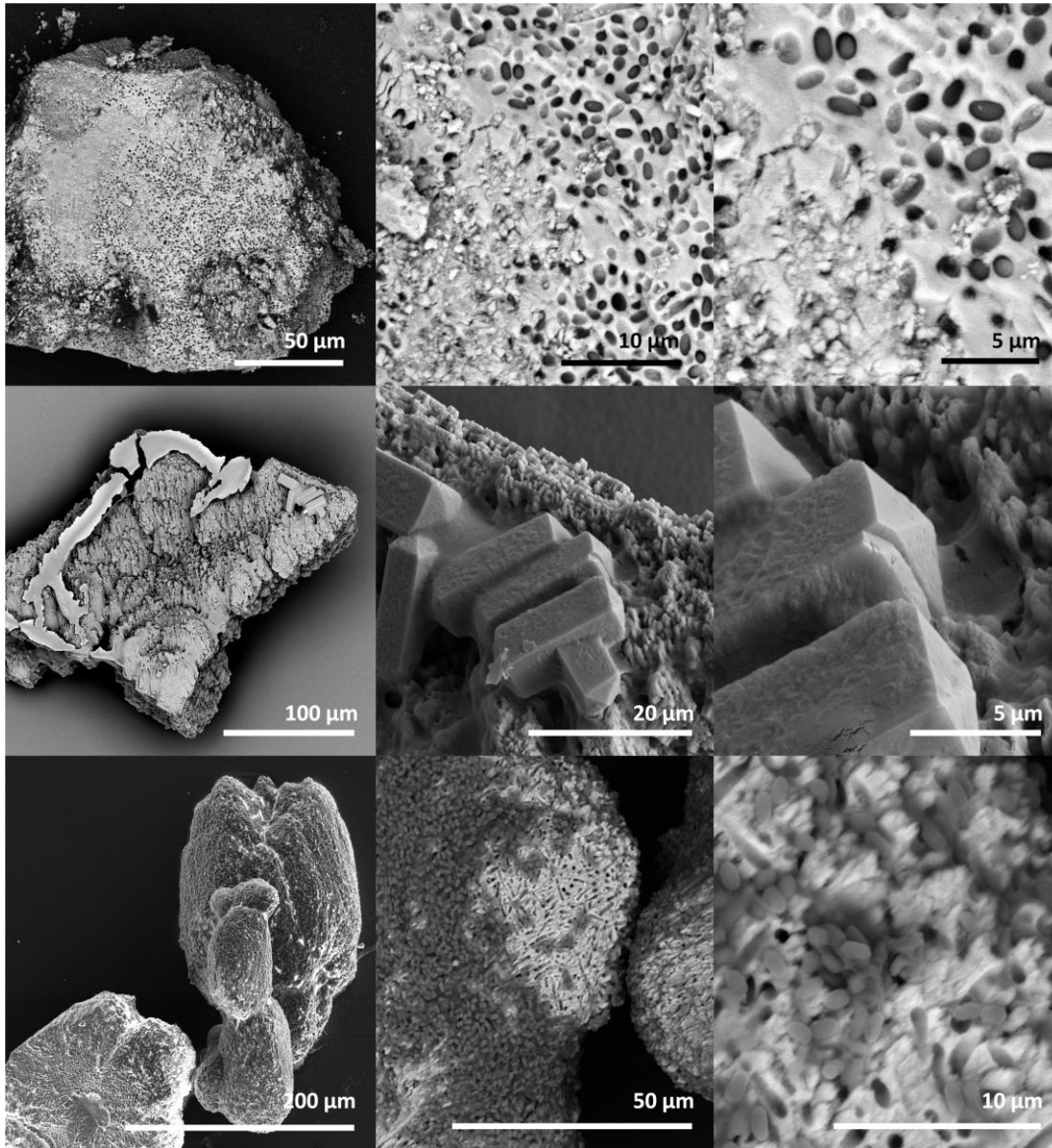
Fig. S1: Biominerals visualized by scanning electron microscopy. *Bacillus flexus* rLM1.5 (A), *Comamonas koreensis* W_5.3b (B), *Bacillus* sp. rMM10 (C) are shown, each for an overview of crystal shapes, partly covered with organic matrix, and high magnification to give insight into surface and microcrystalline structures. Some minerals are settled by bacterial cells leaving holes after lysis.
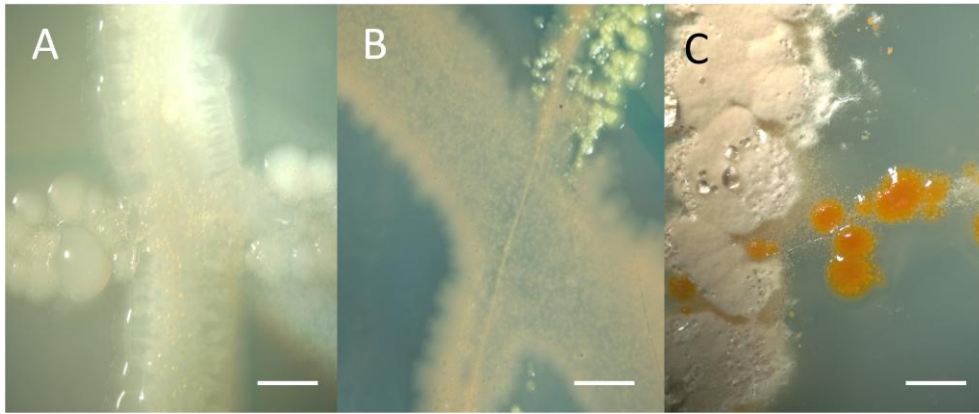
Fig. S2: Interactions with effects on formation of biominerals. More crystals were produced in the interaction zone between *L. amnigena* S_H3 and *Pseudomonas* sp. (A), crystal formation was reduced at the contact zone between *Micrococcus luteus* rLMc and *Bacillus muralis* rLMd (B). *Moraxella olsoensis* sMM16 *vs. Agrococcus jejunensis* sMM51 showed overgrowth (C).