

Supplementary Tables:

Supplementary Table 1. The copy numbers of *dsrB* and *mcrA* genes in Outokumpu fractures.

Fracture depth m	<i>dsrB</i>				<i>mcrA</i>			
	DNA	SEM ¹	RNA	SEM ¹	DNA	SEM ¹	RNA	SEM ¹
180	5,92E+02	4,55E+02	5,82E+00	1,05E+00	3,42E+01	8,51E+00	8,34E+00	6,55E+00
500	7,39E+03	1,79E+03	8,28E+01	3,51E+01	3,73E+01	1,83E+01	b.d	n.a
967	1,52E+01	7,31E-01	2,77E+00	4,42E-02	3,07E+01	0,00E+00	2,05E+02	1,02E+02
1820	2,96E+02	1,86E+01	7,07E+02	1,44E+01	b.d	n.a	b.d	n.a
2260	4,98E+02	2,26E+02	3,82E+01	8,51E+00	b.d	n.a	b.d	n.a
2300	3,29E+02	3,54E+01	6,01E+02	3,52E+01	b.d	n.a	b.d	n.a

¹SEM = standard error of mean

b.d = below detection limit

n.a = not available

Supplementary Table 2. The phylogenetic affiliation and relative abundance of the bacterial OTUs representing more than 0,1% abundance in the communities in the six fractures.

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Supplementary Table 3. The phylogenetic affiliation of archaeal OTUs and their relative abundance in the communities in Outokumpu fractures.

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Supplementary Table 4. The diversity and richness indexes of the communities and sequencing coverage of A) bacteria and B) archaea.

A)

BACTERIA

	180 m		500 m		967 m		1820 m		2260 m		2300 m	
Diversity index	DNA	RNA	DNA	RNA	DNA	RNA	DNA	RNA	DNA	RNA	DNA	RNA
Shannon H'	2.9	2.6	3.4	4.9	5.3	5.1	6.3	3.5	2.7	5.1	6.3	1.8
Chao1	208	125	428	461	326	363	523	538	394	492	495	209
Observed %												
Chao	69	72	77	86	84	88	83	77	73	91	86	56
Observed species	143	90	329	395	274	318	432	412	286	446	424	116

B)

ARCHAEA

	180 m		500 m		967 m		1820 m		2260 m		2300 m	
Diversity index	DNA	RNA	DNA	RNA	DNA	RNA	DNA	RNA	DNA	RNA	DNA	RNA
Shannon H'	2.4	2.1	0.9	0.8	2.3	1.2	n.d	n.d	0.6	0.8	0.8	n.d
Chao1	45	32	3	3	58	32	n.d	n.d	7	8	5	n.d
Observed %												
Chao	98	92	100	100	100	94	n.a	n.a	100	97	80	n.a
Observed species	44	29	3	3	58	30	n.d	n.d	7	8	4	n.d

n.d = not detected

n.a = not available

Supplementary Table 5. The average nearest sequenced taxon indexes of bacterial and archaeal communities in Outokumpu bedrock fractures.

	180 m		500 m		967 m		1820 m		2260 m		2300 m	
	DNA	RNA	DNA	RNA	DNA	RNA	DNA	RNA	DNA	RNA	DNA	RNA
Bacteria	0.22	0.10	0.13	0.07	0.21	0.10	0.07	0.07	0.30	0.24	0.07	0.12
Archaea	0.04	0.07	0.05	0.05	0.29	0.04	n.a	n.a	0.04	0.04	0.04	n.a

Supplementary Table 6. The abundance of amino acid metabolism, carbon metabolism and energy metabolism genes predicted from metagenomes of (A) bacteria and (B) archaea.

	180 m DNA	180 m RNA	500 m DNA	500 m RNA	967 m DNA	967 m RNA	1820 m DNA	1820 m RNA	2260 m DNA	2260 m RNA	2300 m DNA
A) Bacteria											
Amino acid metabolism											
Amino acid related enzymes	14%	15%	13%	11%	12%	12%	11%	11%	11%	13%	11%
Arginine and proline metabolism	12%	12%	12%	11%	11%	13%	11%	12%	12%	11%	12%
Valine, leucine and isoleucine degradation	5%	4%	10%	11%	10%	7%	11%	9%	10%	10%	10%
Glycine, serine and threonine metabolism	9%	9%	9%	10%	8%	9%	8%	8%	8%	9%	9%
Alanine, aspartate and glutamate metabolism	11%	11%	8%	8%	8%	9%	8%	9%	8%	7%	8%
Tryptophan metabolism	3%	3%	7%	8%	6%	4%	7%	6%	7%	7%	7%
Cysteine and methionine metabolism	8%	9%	7%	6%	7%	9%	7%	8%	8%	7%	7%
Valine, leucine and isoleucine biosynthesis	7%	7%	6%	6%	7%	7%	6%	8%	7%	7%	6%
Lysine degradation	2%	2%	6%	7%	5%	4%	6%	5%	5%	6%	6%
Phenylalanine, tyrosine and tryptophan biosynthesis	9%	9%	5%	5%	7%	8%	6%	6%	7%	5%	6%
Histidine metabolism	7%	7%	5%	5%	6%	5%	5%	5%	6%	5%	5%
Lysine biosynthesis	8%	8%	5%	5%	6%	6%	5%	6%	5%	6%	5%
Tyrosine metabolism	3%	3%	4%	4%	4%	3%	5%	3%	3%	4%	5%
Phenylalanine metabolism	2%	2%	3%	4%	4%	3%	4%	3%	4%	3%	4%
Carbohydrate metabolism											
Propanoate metabolism	6%	7%	11%	13%	11%	10%	12%	11%	11%	11%	12%
Butanoate metabolism	7%	8%	11%	13%	12%	10%	13%	11%	12%	12%	13%
Pyruvate metabolism	10%	11%	12%	12%	12%	12%	12%	11%	12%	11%	12%
Glycolysis / Gluconeogenesis	10%	11%	11%	10%	10%	11%	10%	11%	13%	11%	10%
Glyoxylate and dicarboxylate metabolism	6%	7%	9%	10%	9%	7%	9%	8%	6%	10%	10%
Amino sugar and nucleotide sugar metabolism	13%	12%	8%	8%	9%	10%	8%	12%	9%	8%	8%
Citrate cycle (TCA cycle)	9%	8%	7%	7%	9%	10%	8%	10%	11%	10%	8%
Pentose phosphate pathway	6%	8%	7%	6%	6%	7%	6%	6%	7%	6%	6%
Fructose and mannose metabolism	6%	7%	5%	5%	5%	5%	5%	5%	6%	5%	5%
Starch and sucrose metabolism	8%	6%	4%	4%	5%	6%	4%	4%	2%	4%	4%
Pentose and glucuronate interconversions	4%	4%	4%	4%	3%	3%	3%	2%	3%	3%	3%
C5-Branched dibasic acid metabolism	3%	3%	2%	3%	3%	4%	3%	3%	2%	3%	3%
Galactose metabolism	7%	4%	3%	2%	3%	3%	3%	3%	2%	2%	2%
Inositol phosphate metabolism	1%	2%	2%	2%	1%	2%	2%	1%	2%	2%	2%
Ascorbate and aldarate metabolism	1%	1%	2%	2%	2%	1%	2%	2%	1%	2%	2%
Energy metabolism											
Oxidative phosphorylation	24%	20%	22%	22%	22%	21%	24%	28%	26%	27%	24%
Carbon fixation pathways in prokaryotes	20%	19%	18%	20%	22%	22%	21%	21%	22%	17%	20%
Methane metabolism	20%	21%	17%	18%	17%	22%	18%	18%	23%	16%	18%
Nitrogen metabolism	11%	14%	14%	17%	13%	15%	15%	11%	8%	11%	16%
Carbon fixation in photosynthetic organisms	9%	9%	10%	8%	9%	7%	7%	8%	8%	9%	8%
Photosynthesis proteins	6%	7%	8%	6%	6%	4%	5%	5%	5%	8%	5%
Sulfur metabolism	4%	4%	5%	5%	6%	5%	6%	4%	2%	5%	6%

Photosynthesis	6%	6%	6%	4%	5%	4%	4%	5%	5%	8%	4%
	180 m DNA	180 m RNA	500 m DNA	500 m RNA	967 m DNA	967 m RNA	1820 m DNA	1820 m RNA	2260 m DNA	2260 m RNA	2300 m DNA
B) Archaea											
Amino acid metabolism											
Amino acid related enzymes	16%	16%	17%	17%	17%	16%			16%	16%	16%
Valine, leucine and isoleucine biosynthesis	12%	12%	13%	13%	9%	12%			12%	12%	12%
Phenylalanine, tyrosine and tryptophan biosynthesis	11%	11%	11%	11%	12%	11%			11%	11%	11%
Arginine and proline metabolism	10%	10%	9%	9%	11%	11%			11%	11%	11%
Cysteine and methionine metabolism	9%	8%	8%	8%	9%	9%			9%	9%	9%
Alanine, aspartate and glutamate metabolism	9%	9%	9%	9%	11%	9%			9%	9%	9%
Lysine biosynthesis	8%	9%	9%	9%	7%	8%			8%	8%	8%
Glycine, serine and threonine metabolism	7%	8%	8%	8%	8%	7%			7%	7%	7%
Histidine metabolism	7%	6%	6%	6%	5%	6%			6%	6%	6%
Phenylalanine metabolism	3%	3%	2%	2%	3%	3%			3%	3%	3%
Valine, leucine and isoleucine degradation	3%	4%	4%	4%	3%	4%			4%	4%	4%
Tyrosine metabolism	3%	3%	2%	2%	2%	2%			2%	2%	2%
Tryptophan metabolism	1%	1%	1%	1%	2%	2%			2%	2%	2%
Lysine degradation	1%	1%	1%	1%	1%	1%			1%	1%	1%
Carbohydrate metabolism											
Citrate cycle (TCA cycle)	15%	15%	16%	16%	14%	16%			16%	16%	16%
Glycolysis / Gluconeogenesis	14%	13%	11%	11%	14%	13%			13%	13%	13%
Pyruvate metabolism	12%	11%	11%	11%	12%	10%			10%	10%	10%
Amino sugar and nucleotide sugar metabolism	9%	9%	10%	10%	10%	11%			11%	11%	11%
Butanoate metabolism	8%	8%	8%	8%	8%	8%			8%	8%	8%
Propanoate metabolism	8%	7%	7%	7%	9%	7%			7%	7%	7%
C5-Branched dibasic acid metabolism	8%	9%	10%	10%	7%	10%			10%	10%	10%
Fructose and mannose metabolism	5%	5%	5%	5%	4%	4%			4%	4%	4%
Glyoxylate and dicarboxylate metabolism	5%	6%	6%	6%	5%	5%			5%	5%	5%
Pentose phosphate pathway	5%	5%	5%	5%	5%	4%			4%	4%	4%
Pentose and glucuronate interconversions	4%	4%	4%	4%	4%	5%			5%	5%	5%
Starch and sucrose metabolism	3%	3%	3%	3%	3%	2%			2%	2%	2%
Galactose metabolism	2%	2%	2%	2%	2%	2%			2%	2%	2%
Inositol phosphate metabolism	2%	2%	2%	2%	2%	2%			2%	2%	2%
Ascorbate and aldarate metabolism	0%	0%	0%	0%	1%	1%			1%	1%	1%
Energy metabolism											
Methane metabolism	61%	64%	68%	68%	52%	69%			69%	69%	69%
Carbon fixation pathways in prokaryotes	16%	14%	12%	12%	17%	12%			12%	12%	12%
Oxidative phosphorylation	8%	9%	8%	8%	16%	8%			8%	8%	8%
Nitrogen metabolism	8%	7%	7%	7%	6%	6%			6%	6%	6%
Carbon fixation in photosynthetic organisms	6%	5%	4%	4%	8%	4%			4%	4%	4%
Sulfur metabolism	1%	1%	0%	0%	1%	2%			2%	2%	2%
Photosynthesis	0%	0%	0%	0%	0%	0%			0%	0%	0%

Supplementary Table 7. The relative abundance and coverage of selected KEGG modules in total and active predicted bacterial metagenomes in Outokumpu fractures located at six different depths.

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Supplementary Table 8. The relative abundance and coverage of selected KEGG modules in total and active predicted archaeal metagenomes in Outokumpu fractures located at six different depths.

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