

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.

→ as .zip

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

→ as .zip

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% |