

## Supplemental Material

### 1) NETPATH input parameters

Flowpath: **HTL H-31 to HTL H-41**

Used constraints: Carbon, Nitrogen, Potassium

Phases: "CH<sub>2</sub>O", Calcite, Exchange (Na/K), K-Mica, NH<sub>3</sub>-Gas

Initial C-14: 56.75 pmC

Model: Tamers

Flowpath: **HTL H-41 to HTL H-51**

Used constraints: Carbon, Nitrogen, Potassium

Phases: "CH<sub>2</sub>O", Calcite, Exchange (Na/K), K-Mica, NH<sub>3</sub>-Gas

Initial C-14: 56.42 pmC

<sup>14</sup>C Model: Tamers

Flowpath: **HTU H-32 to HTL H-43**

Used constraints: Carbon, Sulfur, Iron, Redox, Calcium

Phases: "CH<sub>2</sub>O", Calcite, Exchange (Na/K), Goethite, Gypsum, Pyrite

Initial C-14: 55.86 pmC

<sup>14</sup>C Model: Tamers

Flowpath: **HTU H-32 to HTL H-52**

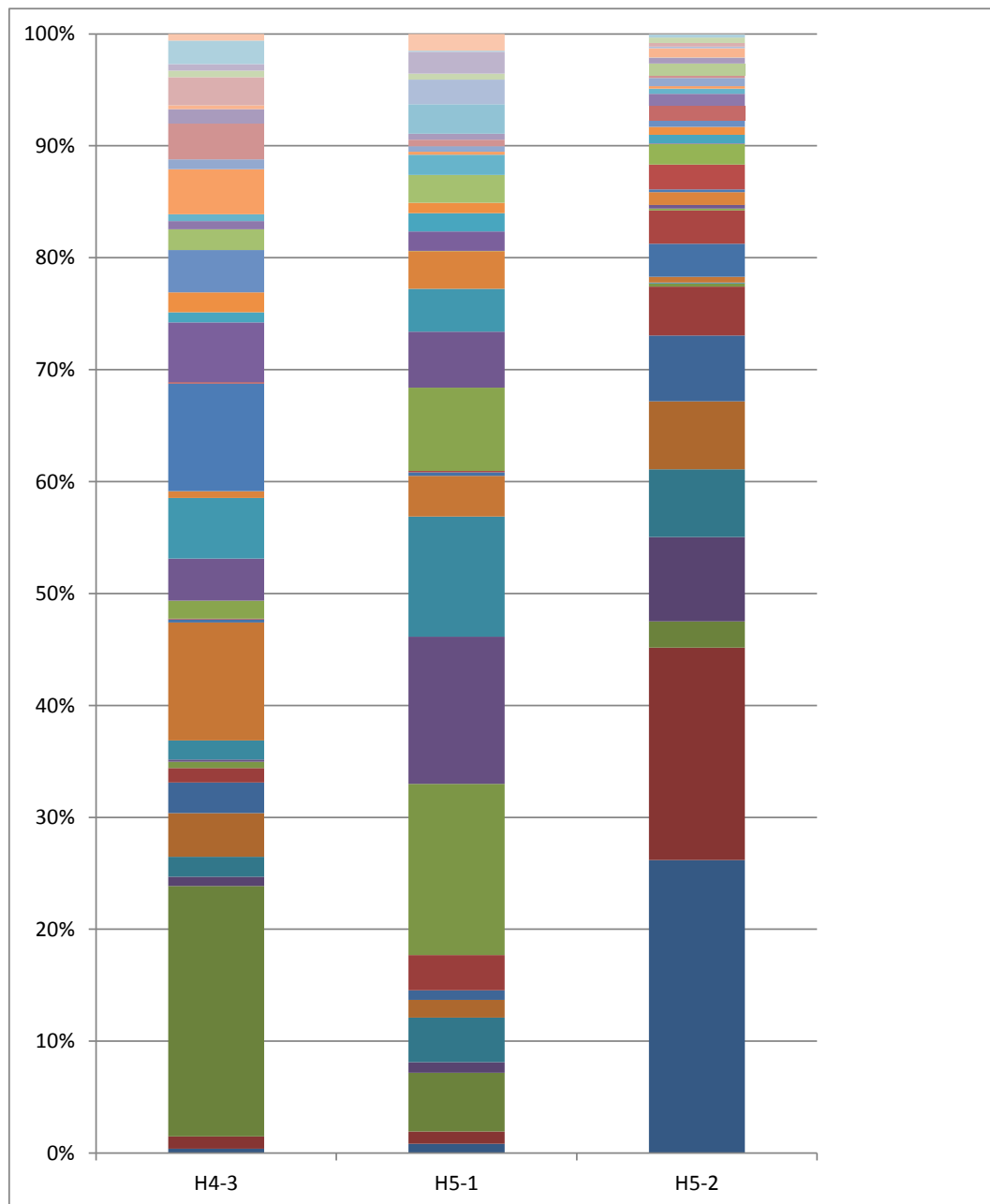
Used constraints: Carbon, Sulfur, Nitrogen, Calcium, Magnesium, C-14, Carbon-13, Potassium

Phases: "CH<sub>2</sub>O", Calcite, Dolomite, Gypsum, Pyrite, N<sub>2</sub> Gas, NH<sub>3</sub> Gas, NH<sub>4</sub>/CAEX, CO<sub>2</sub> Gas, CH<sub>4</sub> Gas

Initial C-14: 55.86 pmC

<sup>14</sup>C Model: Rev. Fontes & Garnier solid ex

## 2) Abundance of bacterial OTU's at genus level



**Figure S1: Abundance of bacterial OTU's at genus level:**

- BSV26\_unclassified; BSV26; Ignavibacteriales; Ignavibacteria; Chlorobi
- Candidate\_division\_TM7\_unclassified; Candidate\_division\_TM7\_unclassified; Candidate\_division\_TM7\_unclassified; Candidate\_division\_TM7\_unclassified; Candidate\_division\_TM7
- Candidate\_division\_OD1\_unclassified; Candidate\_division\_OD1\_unclassified; Candidate\_division\_OD1\_unclassified; Candidate\_division\_OD1\_unclassified; Candidate\_division\_OD1
- Nitrospiraceae\_unclassified; Nitrospiraceae; Nitrospirales; Nitrospira; Nitrospirae
- BSV13\_unclassified; BSV13\_unclassified; BSV13\_unclassified; BSV13; Bacteroidetes
- Betaproteobacteria\_unclassified; Betaproteobacteria\_unclassified; Betaproteobacteria\_unclassified; Betaproteobacteria; Proteobacteria
- Syntrophus; Syntrophaceae; Syntrophobacteriales; Deltaproteobacteria; Proteobacteria
- Gammaproteobacteria\_unclassified; Gammaproteobacteria\_unclassified; Gammaproteobacteria\_unclassified; Gammaproteobacteria; Proteobacteria
- Albidiferax; Comamonadaceae; Burkholderiales; Betaproteobacteria; Proteobacteria
- Actinobacteria\_unclassified; Actinobacteria\_unclassified; Actinobacteria\_unclassified; Actinobacteria\_unclassified; Actinobacteria
- Nitrospira; Nitrospiraceae; Nitrospirales; Nitrospira; Nitrospirae
- Candidate\_division\_OP3\_unclassified; Candidate\_division\_OP3\_unclassified; Candidate\_division\_OP3\_unclassified; Candidate\_division\_OP3\_unclassified; Candidate\_division\_OP3
- Sulfuritalea; Rhodocyclaceae; Rhodocyclales; Betaproteobacteria; Proteobacteria
- Ignavibacteriales\_unclassified; Ignavibacteriales\_unclassified; Ignavibacteriales; Ignavibacteria; Chlorobi
- Caulobacteraceae\_unclassified; Caulobacteraceae; Caulobacterales; Alphaproteobacteria; Proteobacteria
- Subgroup\_6\_unclassified; Subgroup\_6\_unclassified; Subgroup\_6; Acidobacteria; Acidobacteria
- O319-6A21\_unclassified; O319-6A21; Nitrospirales; Nitrospira; Nitrospirae
- Deltaproteobacteria\_unclassified; Deltaproteobacteria\_unclassified; Deltaproteobacteria\_unclassified; Deltaproteobacteria; Proteobacteria
- Desulfosporosinus; Peptococcaceae; Clostridiales; Clostridia; Firmicutes
- Desulfurivibrio; Desulfobulbaceae; Desulfobacteriales; Deltaproteobacteria; Proteobacteria
- TM146\_unclassified; TM146; Solirubrobacteriales; Thermoleophila; Actinobacteria
- NPL-UPA2\_unclassified; NPL-UPA2\_unclassified; NPL-UPA2\_unclassified; NPL-UPA2\_unclassified; NPL-UPA2
- Proteobacteria\_unclassified; Proteobacteria\_unclassified; Proteobacteria\_unclassified; Proteobacteria\_unclassified; Proteobacteria
- DTB120\_unclassified; DTB120\_unclassified; DTB120; Deltaproteobacteria; Proteobacteria
- TRA3-20\_unclassified; TRA3-20\_unclassified; TRA3-20; Betaproteobacteria; Proteobacteria
- Candidatus\_Magnetoovum; Nitrospiraceae; Nitrospirales; Nitrospira; Nitrospirae
- Aquicella; Coxiellaceae; Legionellales; Gammaproteobacteria; Proteobacteria
- Sulfuricum; Helicobacteraceae; Campylobacteriales; Epsilonproteobacteria; Proteobacteria
- Comamonadaceae\_unclassified; Comamonadaceae; Burkholderiales; Betaproteobacteria; Proteobacteria
- Gallionellaceae\_unclassified; Gallionellaceae; Nitrosomonadales; Betaproteobacteria; Proteobacteria
- Lineage\_IV\_unclassified; Lineage\_IV\_unclassified; Lineage\_IV; Elusimicrobia; Elusimicrobia
- Pedobacter; Sphingobacteriaceae; Sphingobacteriales; Sphingobacteriia; Bacteroidetes
- Desulfocapsa; Desulfobulbaceae; Desulfobacteriales; Deltaproteobacteria; Proteobacteria
- BD1-5\_unclassified; BD1-5\_unclassified; BD1-5\_unclassified; BD1-5\_unclassified; BD1-5
- Caldilineaceae\_unclassified; Caldilineaceae; Caldilineales; Caldilineae; Chloroflexi
- WCHB1-32\_unclassified; WCHB1-32\_unclassified; WCHB1-32\_unclassified; WCHB1-32; Bacteroidetes
- Acidiferrobacter; Ectothiorhodospiraceae; Chromatiales; Gammaproteobacteria; Proteobacteria
- 43F-1404R\_unclassified; 43F-1404R\_unclassified; 43F-1404R; Deltaproteobacteria; Proteobacteria
- Bacteroidetes\_unclassified; Bacteroidetes\_unclassified; Bacteroidetes\_unclassified; Bacteroidetes\_unclassified; Bacteroidetes
- NKB5\_unclassified; NKB5\_unclassified; NKB5; Gammaproteobacteria; Proteobacteria
- TM6\_unclassified; TM6\_unclassified; TM6\_unclassified; TM6\_unclassified; TM6
- Anaerolineaceae\_unclassified; Anaerolineaceae; Anaerolineales; Anaerolineae; Chloroflexi

**Figure S2: Abundance of bacterial OTU's at genus level (legend).**