

Supplementary material

***Terricaulis silvestris* gen. nov., sp. nov. a new prosthecate, budding member of the family *Caulobacteraceae* isolated from forest soil**

Selma Vieira^{1*}, Javier Pascual^{1,†}, Christian Boedeker¹, Alicia Geppert¹, Thomas Riedel¹,
Manfred Rohde², Jörg Overmann^{1,3}

¹ Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures,
Inhoffenstraße 7B, 38124 Braunschweig, Germany

² Helmholtz Centre for Infection Research, Inhoffenstraße 7, 38124 Braunschweig, Germany

³ Braunschweig University of Technology, Braunschweig, Germany

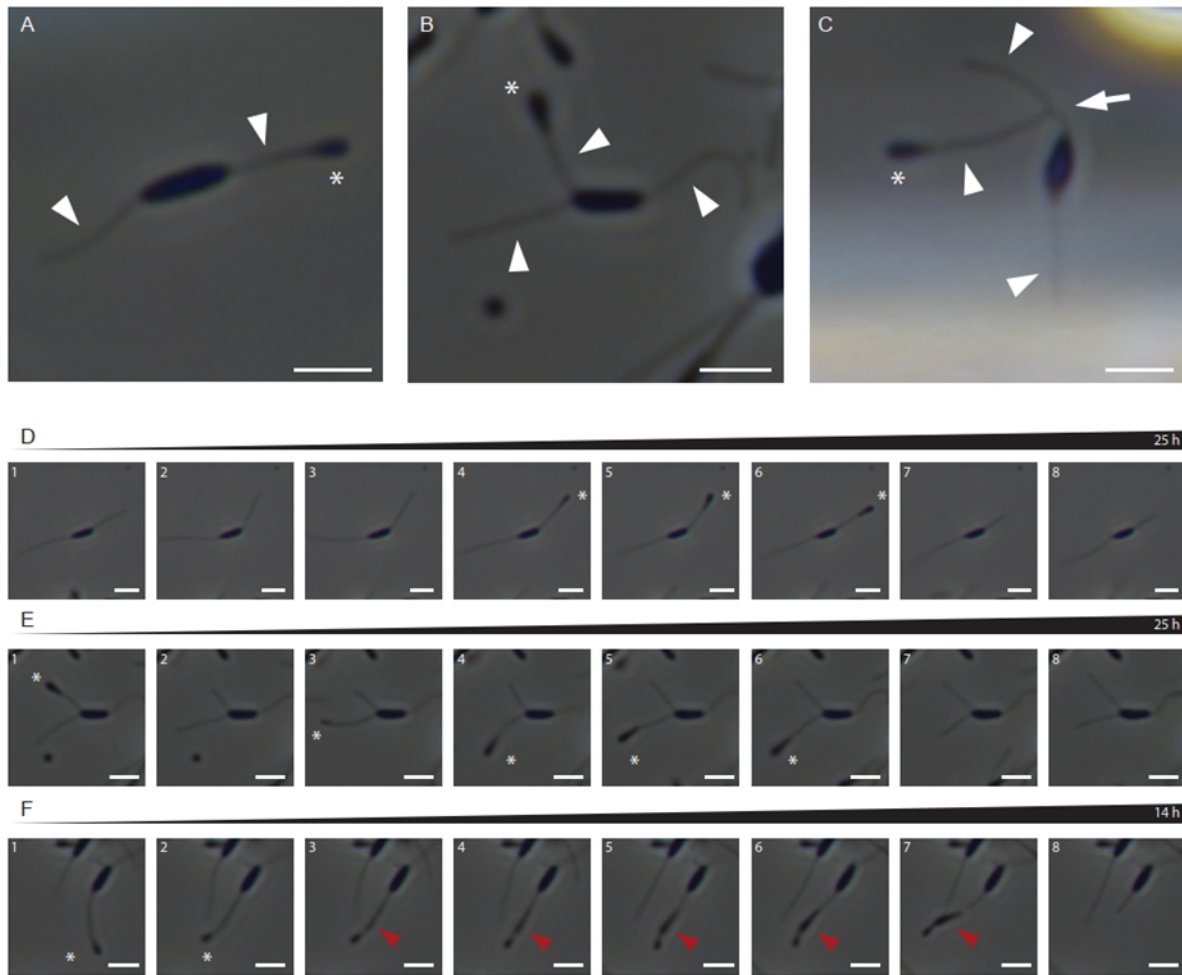
[†] Current adress: Darwin Bioprospecting, Parc Científic de la Universitat de València
c/Catedrático Agustín Escardino 9, 46980 Paterna (Valencia), Spain

Keywords: *Terricaulis*, *Terricaulis silvestris*, 0127_4, prosthecate

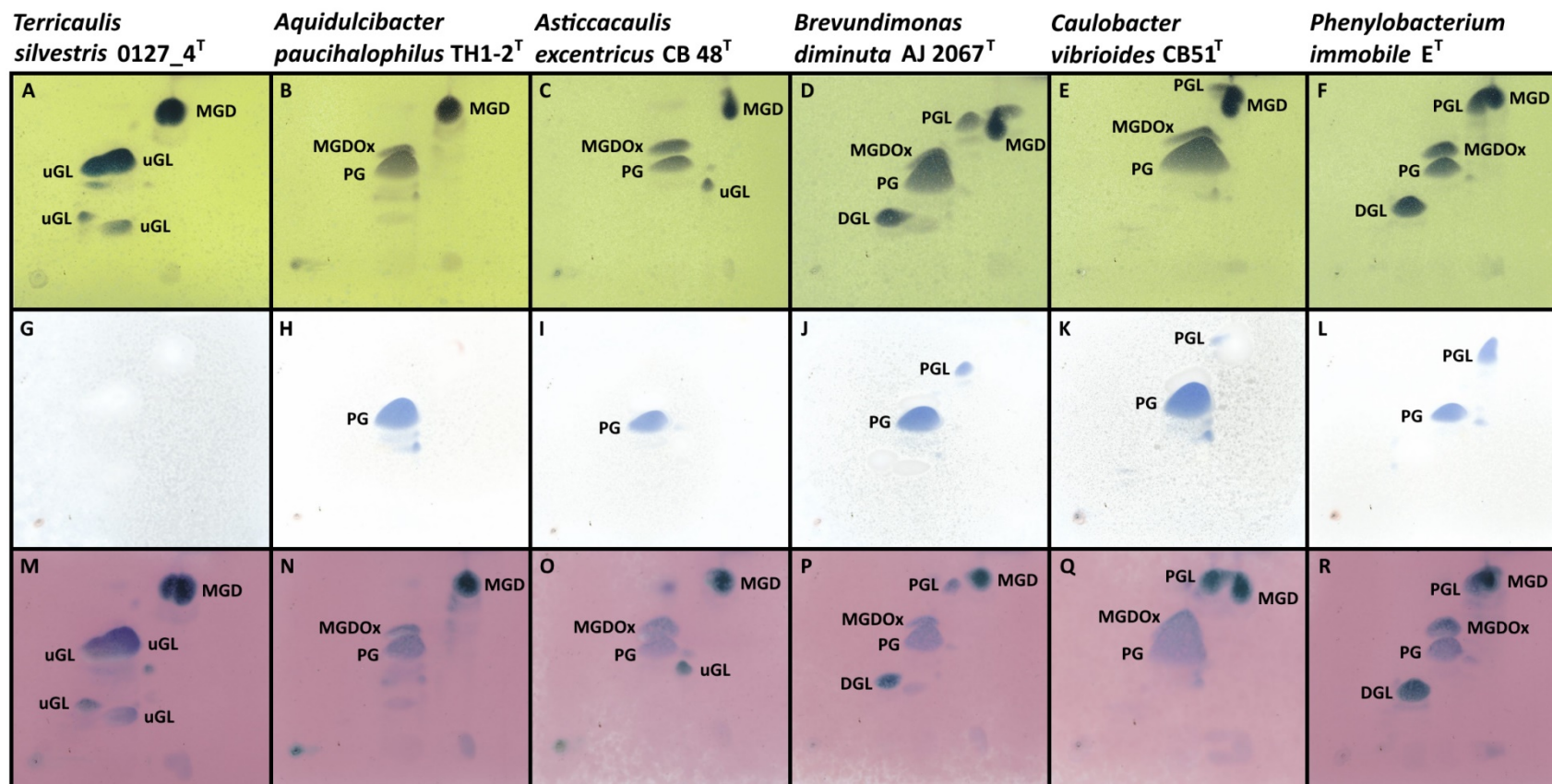
Repositories: The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence
of *Terricaulis silvestris* strain 0127_4^T is MN833493. The GenBank/EMBL/DDBJ accession
number for the genome sequence of strain 0127_4^T is CP047045.

* Correspondence: S. Vieira, Leibniz Institute DSMZ – German Collection of Microorganisms
and Cell Cultures, Inhoffenstraße 7B, 38124 Braunschweig, Germany.

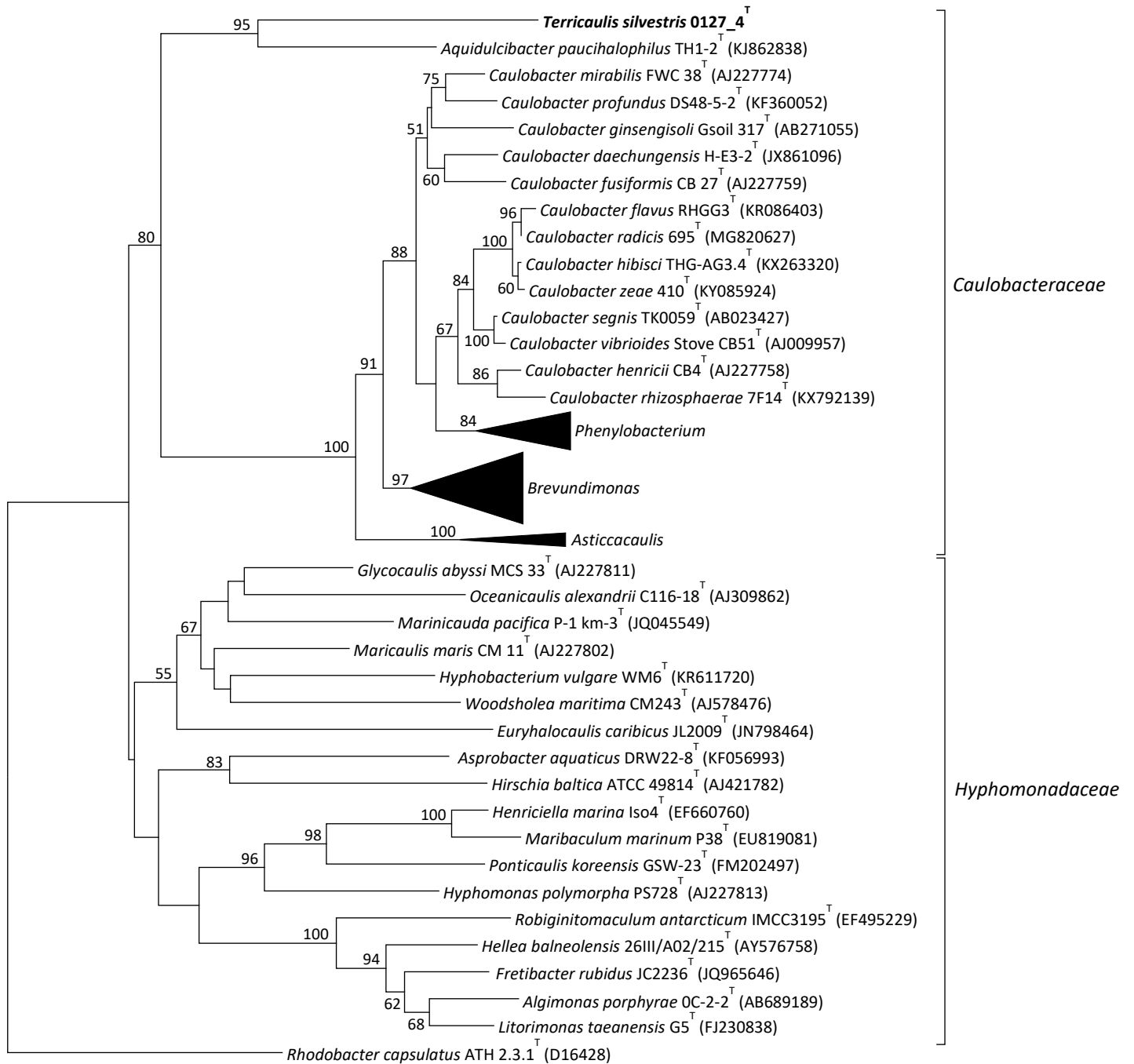
Tel. ++49-531-2616-364. Fax ++49-531-2616-418. E-mail: selma.gomes.vieira@dsmz.de



Supplementary Figure 1. Morphology and cell division of strain 0127_4^T by phase contrast (Phaco) microscopy (A-F). Cells are rod shaped and form up to three prosthecae (B, arrow head) which can be branched (C, arrow). (D) Time series over 25 h of the budding process of 0127_4^T show a formation of the daughter cell (asterisk) at the prosthecum. (E) Time series over 25 h of the budding process of 0127_4^T show a formation of the daughter cells at different prosthecae. (F) Time series over 14 h of the budding process of 0127_4^T show a formation of the daughter cell at the prosthecum and a bulge within the prosthecum before detachment (red arrow head). Scale bar 2 μm.

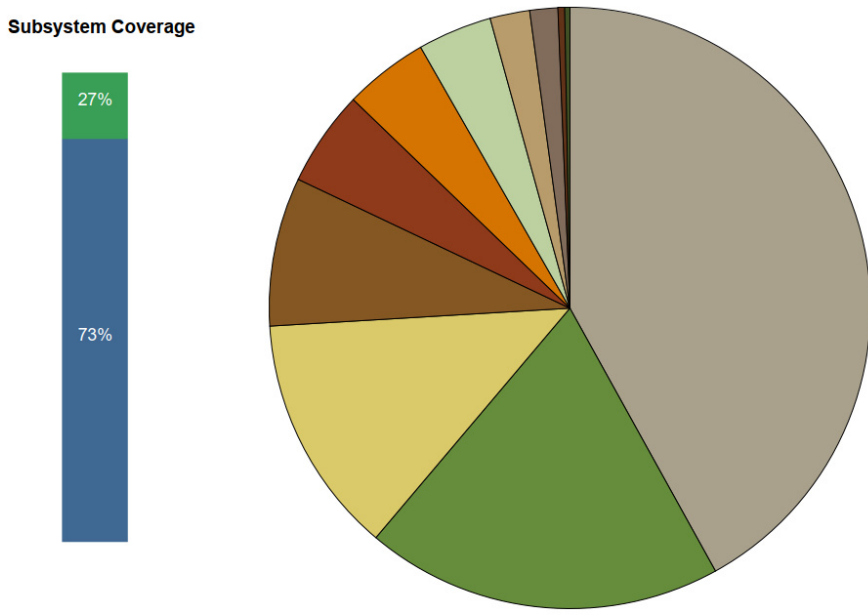


Supplementary Figure 2. Polar lipid composition of strain 0127_4^T and all type species of the genera which comprise the family *Caulobacteraceae* on thin layer chromatography. Data were generated in the present study and all strains were obtained from the German Collection of Microorganisms and Cell Cultures. Staining for determination of the polar lipids with dodecamolydophosphoric acid (A-F), molybdenum blue (G-L), anisaldehyde sulfuric acid (M-R). For lipid separation chloroform:methanol:water (65:25:4, v/v/v) was used in the first direction and chloroform:methanol:acetic acid:water (80:12:15:4, v/v/v/v) in the second direction. DGL: 1,2-di-*O*-acyl-3-*O*-[D-glucopyranosyl-(1→4)-α D-glucopyranuronosyl]glycerol, PG: phosphatidylglycerol, PGL: 1,2-diacyl-3-*O*-[6'-phosphatidyl-αD-glucopyranosyl]glycerol, MGD: 1,2-di-*O*-acyl-3-*O*-αD-glucopyranuronosylglycerol, MGDOx: 1,2-di-*O*-acyl-3-*O*-[αD-glucopyranosyl]-sn-glycerol, uGL: unidentified glycolipid.



0.01

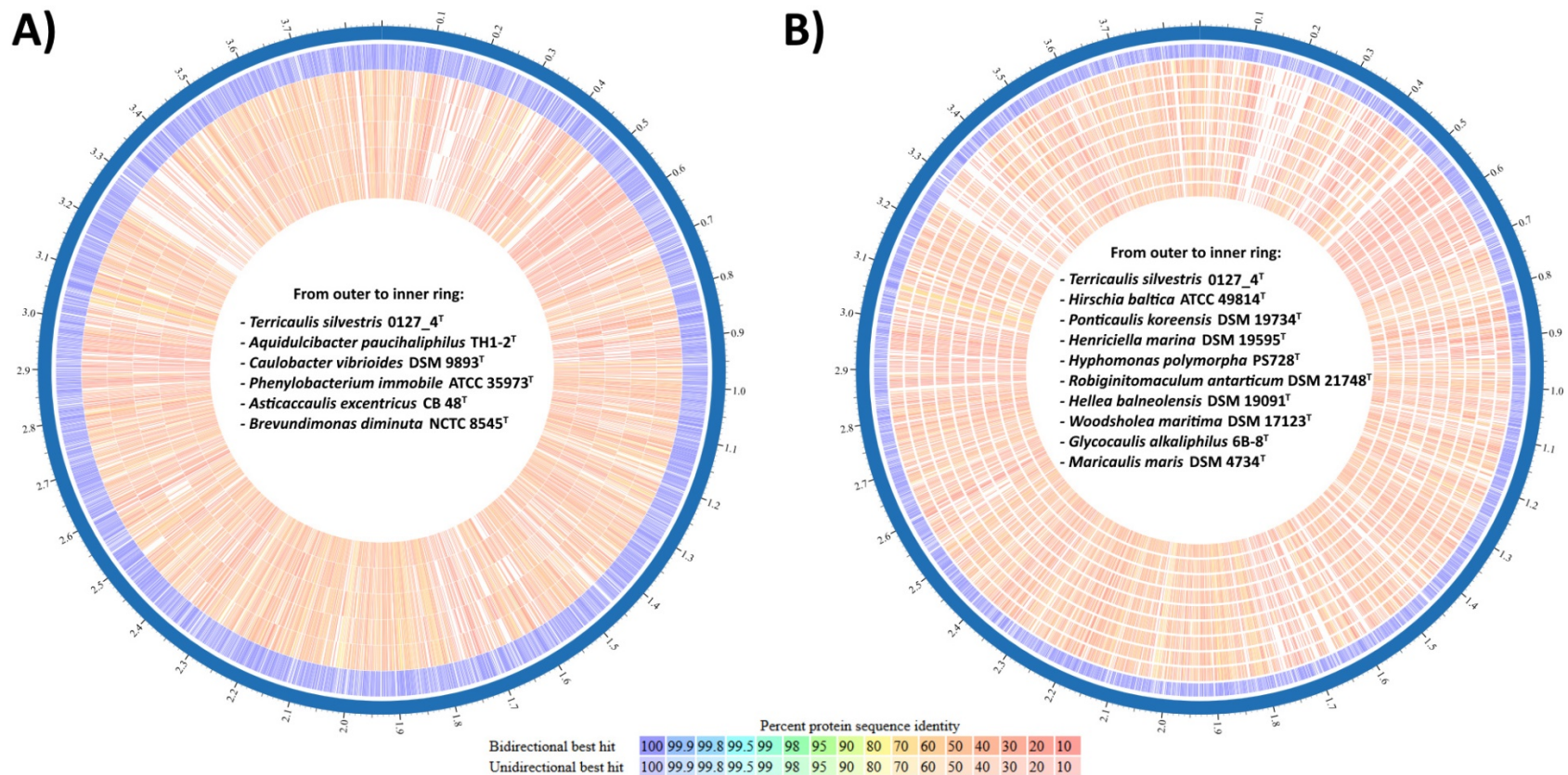
Supplementary Figure 3. Neighbor-joining (NJ) phylogenetic tree based on almost full length 16S rRNA gene sequences illustrating the phylogenetic position of *Terricaulis silvestris* 0127_4^T. The evolutionary distances were computed using the Kimura 2-parameter model. *Rhodobacter capsulatus* ATH 2.3.1^T (D16428) was used as outgroup. Bar indicates 1% nucleotide divergence. Only bootstrap values above 50% are indicated at the branches (1000 replicates).



Subsystem Counts (Subsystems, Genes)

- > METABOLISM (70, 472)
 - > Amino Acids and Derivatives (25, 157)
 - > Cofactors, Vitamins, Prosthetic Groups (16, 146)
 - > Fatty Acids, Lipids, and Isoprenoids (9, 66)
 - > Nucleosides and Nucleotides (6, 41)
 - > Carbohydrates (6, 20)
 - > Metabolite damage and its repair or mitigation (4, 19)
 - > Secondary Metabolism (2, 11)
 - > Phosphate Metabolism (1, 9)
 - > Sulfur Metabolism (1, 3)
- > PROTEIN PROCESSING (46, 216)
 - > Protein Synthesis (31, 168)
 - > Protein Fate (folding, modification, targeting, degradation) (15, 48)
- > ENERGY (21, 145)
 - > Energy and Precursor Metabolites Generation (13, 81)
 - > Respiration (8, 64)
- > CELLULAR PROCESSES (9, 58)
 - > Cell Cycle, Cell Division and Death (7, 50)
 - > Clustering-based subsystems (1, 7)
 - > Prokaryotic cell type differentiation (1, 1)
- > DNA PROCESSING (12, 51)
- > RNA PROCESSING (12, 45)
- > CELL ENVELOPE (5, 24)
- > MEMBRANE TRANSPORT (5, 17)
- > REGULATION AND CELL SIGNALING (2, 4)
- > MISCELLANEOUS (1, 3)

Supplementary Figure 4. Genome of strain 0127_4^T annotated using the RAST tool kit (RASTtk) implemented in the Pathosystems Resource Integration Center (PATRIC). The bar chart depicts the percentage of proteins assigned to a subsystem (subsystems represent collections of functionally related protein families). The pie chart reflects the distribution of the subsystems observed in the genome of strain 0127_4^T.



Supplementary Figure 5. Proteome comparison of *Terricaulis silvestris* 0127_4^T and the type strains of the genera of the family A) *Caulobacteraceae* or B) *Hyphomonadaceae*, based on RAST tool kit (RASTtk) genome annotation implemented in the Pathosystems Resource Integration Center (PATRIC). The exterior solid blue ring indicates the scaffold of the reference genome (one circular chromosome of *Terricaulis silvestris* 0127_4^T). Each ring represents one strain and it is comprised of lines indicating one protein homologous to a protein of the reference genome. Colours reflect the percentage of protein sequence identity with regards to the reference.