**Supplementary Tables**

**Table S1.** Known acetogens according to Drake, Gößner and Daniel (2008); used for multiple sequence alignment to deduce amino acid sequence residue sequence conservation and for profile HMM analysis

|  |  |
| --- | --- |
| **No.** | **Acetogen** |
| 1 | *Acetitomaculum ruminis* |
| 2 | *Acetoanaerobium noterae* |
| 3 | *Acetobacterium bakii* |
| 4 | *Acetobacterium dehalogenans* |
| 5 | *Acetobacterium wieringae* |
| 6 | *Acetobacterium woodii* |
| 7 | *Acetohalobium arabaticum* |
| 8 | *Acetonema longum* |
| 9 | *Blautia hydrogenotrophica* |
| 10 | *Blautia producta* |
| 11 | *Butyribacterium methylotrophicum* |
| 12 | *Caloramator fervidus* |
| 13 | *Clostridioides difficile* |
| 14 | *Clostridium aceticum* |
| 15 | *Clostridium autoethanogenum* |
| 16 | *Clostridium carboxidivorans* |
| 17 | *Clostridium drakei* |
| 18 | *Clostridium formicaceticum* |
| 19 | *Clostridium ljungdahlii* |
| 20 | *Clostridium magnum* |
| 21 | *Clostridium scatologenes* |
| 22 | *Clostridium ultunense* |
| 23 | *Eubacterium aggregans* |
| 24 | *Eubacterium limosum* |
| 25 | *Holophaga foetida* |
| 26 | *Marvinbryantia formatexigens* |
| 27 | *Moorella glycerini* |
| 28 | *Moorella mulderi* |
| 29 | *Moorella thermoacetica* |
| 30 | *Oxobacter pfennigii* |
| 31 | *Sporomusa acidovorans* |
| 32 | *Sporomusa malonica* |
| 33 | *Sporomusa silvacetica* |
| 34 | *Sporomusa sphaeroides* |
| 35 | *Terrisporobacter glycolicus* |
| 36 | *Thermacetogenium phaeum* |
| 37 | *Thermoanaerobacter kivui* |
| 38 | *Tindallia californiensis* |
| 39 | *Treponema azotonutricium* |
| 40 | *Treponema primitia* |

**Table S2.** KEGG pathway module and list of enzymes involved in the Wood-Ljungdahl pathway

|  |  |  |  |
| --- | --- | --- | --- |
| KEGG Module | M00377 | | |
| Name | Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway) | | |
| KEGG Orthology | Enzyme: | EC number | Gene |
| K01491 | methylenetetrahydrofolate dehydrogenase (NADP+) | EC:1.5.1.5 | folD |
| K01491 | methenyltetrahydrofolate cyclohydrolase | EC:1.5.1.5 | folD |
| K00197/K00194 | acetyl-CoA decarbonylase | EC:2.1.1.245 | cdh |
| K15023 | 5-methyltetrahydrofolate corrinoid/iron sulfur protein methyltransferase | EC:2.1.1.258 | acsE |
| K14138 | acetyl-CoA synthase | EC:2.3.1.169 | acsB |
| K00297 | methylenetetrahydrofolate reductase (NADPH) | EC:1.5.1.20 | metF |
| K00198 | anaerobic carbon-monoxide dehydrogenase | EC:1.2.7.4 | acsA |
| K01938 | formate--tetrahydrofolate ligase/formyltetrahydrofolate synthetase | EC:6.3.4.3 | fhs |
| K00925 | acetate kinase | EC:2.7.2.1 | ack |