# Table 1. The distribution of butyric acid production genes.

The final stage of butyric acid production can be undertaken by 2 gene groups: butyrate kinase or butyryl-CoA:acetate CoA-transferase. The presence of each gene within a Lachnospiraceae genome is marked with a +.

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| **Name** | **Butyrate Kinase** | **BCoAT** |
| *Anaerostipes caccae* DSM 14662 |  | + |
| *Anaerostipes* sp. 3\_2\_56FAA |  | + |
| *Butyrivibrio crossotus* DSM 2876 | + |  |
| *Butyrivibrio proteoclasticus* B316 | + |  |
| *Catonella morbi* ATCC 51271 |  |  |
| *Cellulosilyticum lentocellum* DSM 5427 |  |  |
| *Coprococcus comes* ATCC 27758 | + |  |
| *Coprococcus eutactus* ATCC 27759 | + |  |
| *Dorea formicigenerans* ATCC 27755 |  |  |
| *Dorea longicatena* DSM 13814 |  |  |
| *Lachnospiraceae* bacterium 1\_1\_57FAA |  |  |
| *Lachnospiraceae* bacterium 1\_4\_56FAA | + |  |
| *Lachnospiraceae* bacterium 2\_1\_46FAA |  |  |
| *Lachnospiraceae* bacterium 2\_1\_58FAA |  |  |
| *Lachnospiraceae* bacterium 3\_1\_46FAA |  |  |
| *Lachnospiraceae* bacterium 3\_1\_57FAA\_CT1 | + |  |
| *Lachnospiraceae* bacterium 4\_1\_37FAA |  |  |
| *Lachnospiraceae* bacterium 5\_1\_57FAA |  |  |
| *Lachnospiraceae* bacterium 5\_1\_63FAA |  | + |
| *Lachnospiraceae* bacterium 6\_1\_63FAA |  |  |
| *Lachnospiraceae* bacterium 8\_1\_57FAA |  |  |
| *Lachnospiraceae* bacterium 9\_1\_43BFAA |  |  |
| *Lachnospiraceae* oral taxon 107 str. F0167 |  |  |
| *Marvinbryantia formatexigens* DSM 14469 |  |  |
| *Oribacterium sinus* F0268 |  |  |
| *Oribacterium* sp. oral taxon 078 str. F0262 |  |  |
| *Oribacterium* sp. oral taxon 108 str. F0425 |  |  |
| *Roseburia intestinalis* L1-82 |  | + |
| *Roseburia inulinivorans* DSM 16841 |  | + |
| *Shuttleworthia satelles* DSM 14600 | + |  |