More than 75 species or species-level phylotypes of spirochete bacteria reside within the human oral cavity; all of which belong to the genus *Treponema*. Several oral treponeme species/phylotypes have been associated with periodontitis and other infectious-inflammatory diseases. Here we report the genome sequencing of the oral phylgroup 1 treponeme strain OMZ 835, which was originally isolated from a necrotizing ulcerative gingivitis lesion, using only the ONT MinION sequencer.

**Method**
- *Treponema* sp. OMZ 835 culture in TYGVS medium
- Genomic DNA extraction and sequencing library preparation
- Genomic sequencing (SQK-MAP006) on ONT MinION Mk1
- 2D Bascalling on Metrichor v2.39.1

**Data Process**
- 2D Reads extraction using poretools
- *De novo* assembly of the 2D reads using canu
- Nanopolish
- Alignment with the closest reference in Mauve
- Scaffolding using CONTIGuator

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**Results**
- 11,425 2D Reads, 76,000,000 bases
- 11 Contigs, 2,511,414 bp with an NG50 of 305,969 bp
- 1 Final scaffold, 2,518,618 bp
- 2D Reads coverage: 29X
- Rotol reads coverage: 84X

**Evaluation**
- 16S rRNA gene accuracy 97.3% (0.1% Insertion; 2.4% Deletion; 0.1% substitution)
- 4 Other gene markers mean accuracy 96.7% (95.7%-97.9%)
- 1 Scaffold but prone to error

**Future plan**
- Correct with HiSeq reads

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