San Diego county Nanopore SARS-Cov2 sequencing data shows metagenomic *Prevotella*, *Haemophilus parainfluenzae*, a lot of unknown species and chimeric reads

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Letter

Prevotella was definitely a dominant factor in the the SARS-Cov2 [1, 2] patient [3], playing a key role in immune suppression [4]. The same immune suppressive proteins from the same bacteria (elongation factor Tu) was also observed in low amounts in two other patients [5].

Prevotella is known to cause ground glass opacity [6] being used to identify SARS-Cov2 patients [7]. It is also known to increase IL-6 in plasma [8–10], which is correlated with severity/fatalities [11]. In 2003 SARS-Cov1 outbreak, secondary infection and IL-6 was highly correlated with hospitalization and deaths [12].

Metagenomic presence - known bacteria, and many (10% of reads) unknown species

Here, sequencing data (Accid:SRR11347377, Reads=2.64million, Nanopore) from San Diego show *Prevotella*, *Haemophilus parainfluenzae* (which can have the same ground glass in CT [13]) and other bacteria in small amounts (SI/bacteria.fa, N=23). More intriguingly, there are significant amount of reads with no known matches (SI/nomatches.fa, N=200K, about 10%).

Chimeric reads (10% of reads) involving SARS-Cov2

Like previous, data (N=3) showing SARS-Cov2 integration in bacteria [14], there are a significant percentage of chimeric reads (SI/integrated.fa, N=250K, ~10%) having both SARS-Cov2 and something else (sometimes known bacterial reads). Is this sequencing artifact - or is the virus infecting both bacterial and human cells (which would be a first) [15]? It would explain the long incubations and false negatives.

References

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Table 1: **Bacterial species with number of reads:** Prevotellamassilia is a new bacterial species isolated from the human gut [16].

Species	Number of reads
Prevotella	7
Haemophilus	7
Prevotellamassilia	2
Veillonella	3

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