

Subcutaneous Nodules Caused by *Tropheryma whipplei* Infection

Appendix

Details about Shotgun Metagenomic Sequencing

Sample Information

Sample number: B2030406_TIS

Sample type: Biopsy sample

Receipt day: December 9, 2020

Report day: December 11, 2020

Report Information

Bacterium: *Tropheryma whipplei*

Reads: 28

Total bases: 4,149 bp sequence length

3,145 bp reads

Coverage: 0.34% average depth: 1.3×

Estimated concentration: 1.1×10^1 copies/mL

PCR was performed to amplify partial sequence for *T. whipplei* and products was purified and sequenced by using first-generation sequencing technology.

Primers

TW-F: 5'-caggaagaagcgaagtga-3'

TW- R: 5'-accacctgtataccgacctt-3'

Tropheryma whipplei 16S rRNA (partial sequence: 1,478 bases)

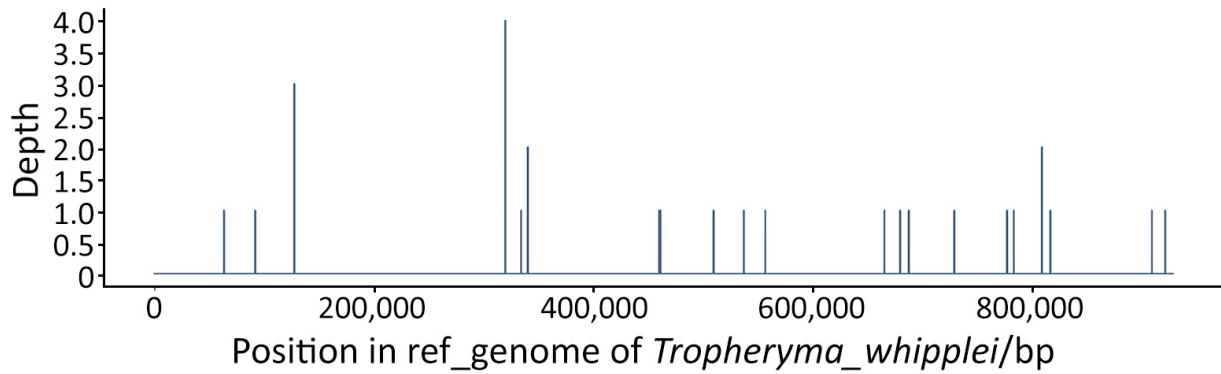
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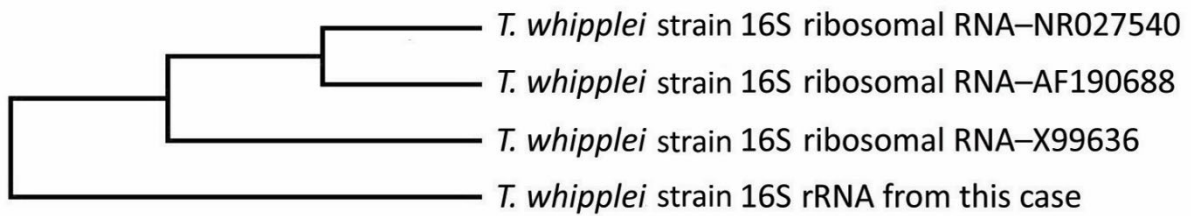
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1381 gtcataaagctggtaacaccgaagccggtgacttaaccttttggagagagccgctcga
1441 aggtgggattggtgattgggactaagtcgtaacaaggt

Conclusion

Phylogenetic analysis indicated that the obtained partial sequence was from *T. whipplei*.



Appendix Figure 1. Mapping of *Tropheryma whipplei* reads.



Appendix Figure 2. Phylogenetic tree of *Tropheryma whipplei* 16S rRNA sequence.