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 ×10¹ 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′-cagggagaagcgaaagtga-3′

TW- R: 5′-accacctgtataccgacctt-3′

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

1  agagtttgatctgctgcctcaggacgaacgcgtgactggcgggtcggtaaacatgcagaagtgaac

61  ggaatcagggagctgtgctcctgtgattatgtagtaaacacgtgagcaaa
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.