

Ceriani-Nakamurakare E., Ramos S., Robles C.A., Novas M.V., D'Jonsiles M.F., Gonzalez-Audino P., Carmaran C. (2018). Metagenomic approach of associated fungi with *Megaplatypus mutatus* (Coleoptera: Platypodinae). *Silva Fennica* vol. 52 no. 3 article id 9940.
<https://doi.org/10.14214/sf.9940>

Supplementary file S2. Additional statistics data of the metagenomic analysis. Pyrosequencing data was processed using QIIME 1.8.0 (Caporaso et al. 2010).

PRINSEQ-graphs v0.6 HTML Report

[Generated: 05/15/2017

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Input Information	# Sequences: 102,830	Total bases: 58,287,977
Length Distribution	Mean sequence length: 566.84 ± 96.40 bp Maximum length: 818 bp Mode length: 474 bp with 3,729 sequences	Minimum length: 251 bp Length range: 568 bp
GC Content Distribution	Mean GC content: 49.46 ± 5.03 % Maximum GC content: 60 % Mode GC content: 50 % with 21,060 sequences	Minimum GC content: 35 % GC content range: 26 %
Sequence Duplication	# Sequences Exact duplicates: 26,875 (26.14 %) Exact duplicates with reverse complements: 0 5' duplicates 11,886 (11.56 %) 3' duplicates 16 (0.02 %) 5'/3' duplicates with reverse complements 0 Total: 38,777 (37.71 %)	Max duplicates 2023 0 8 1 0 -
Tag Sequence Check	5'-end Probability of tag sequence: 19 % GSMIDs or RLMIDs:	3'-end 26% none

Reference

Caporaso, J.G., Kuczynski, J., Stombaugh, J. *et al.* 2010. QIIME allows analysis of highthroughput community sequencing data. *Nat. Methods* 7(5):335-336.