**Suppl. Data Table 1.** Summary of the resources provided as Supplementary Data through the Landcare Research Datastore, https://doi.org/10.7931/J2V98678)

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| **File names** | **Description** |
| 454 run samples and MID summary.xlsx | list of the 454 run file names, samples, and MID numbers |
| HOAU3XK01.fna and .qual | Site 3, 454 raw data following Roche 454 Amplicon pipeline |
| HOPKTW301.fna and .qual | Site 3 run 2, 454 raw data following Roche 454 Amplicon pipeline |
| HO95TPY01.fna and .qual | Site 4, 454 raw data following Roche 454 Amplicon pipeline |
| F\_allsites\_OTUs.fasta | Forward read OTU sequences |
| R\_allsites\_OTUs.fasta | Reverse read OTU sequences |
| Suppl. Data Table 1.docx | Number of raw wells in each 454 run, number of reads retained following Roche 454 amplicon pipeline, average read length, and number of reads retained for Uparse OTU clustering |
| Suppl. Data Table 2.xlsx | Forward read OTUs, their taxonomic assignment, and number of reads across samples |
| Suppl. DataTable 3.xlsx | Reverse read OTUs, their taxonomic assignment, and number of reads across samples |
| Suppl. Data Table 4.docx | Frequency of 454 detection for those species also detected in culture. |
| Suppl. Data Table 5.docx | Number of samples from which each reverse read OTU was detected, across each host. |
| Suppl. Data Fig 1.pdf | Example of the Uparse quality score report from one of the 454 runs. |
| Suppl. Data Fig 2.jpg | Comparative frequency at which the same reverse read OTU was detected in separate 454 runs using the same DNA extract from Site 3. |