**Bioinformatic Tools Used for the Spekboom Genome Sequencing Bioinformatic analyses:**

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| **Program name** | **Link** | **Function** |
| **Guppy (6.3.7 and 6.3.8)** | <https://nanoporetech.com/> | Basecalling - High Accuracy (HAC) and Super Accuracy (SUP) |
| **Nanoplot 1.40.2** | <https://nanoplot.bioinf.be/> | Read quality assessment. |
| **Abyss 1.3.6** | <https://github.com/bcgsc/abyss> | Read quality assessment. |
| **Flye 2.9.1** | <https://github.com/fenderglass/Flye> | *De novo* Assembly |
| **Wtdbg2-2.3** | <https://github.com/ruanjue/wtdbg2> | *De novo* Assembly |
| **Quast 5.0.2**  **(Quality assessment tool)** | <https://github.com/ablab/quast> | Assembly quality assessment |
| **BUSCO 5.3.2**  **(Benchmarking Universal Single-Copy Orthologs)** | <https://github.com/WenchaoLin/BUSCO-Mod> | Assembly quality assessment |
| **BlobTools V1.1** | <https://blobtools.readme.io/docs> | Assembly quality assessment |