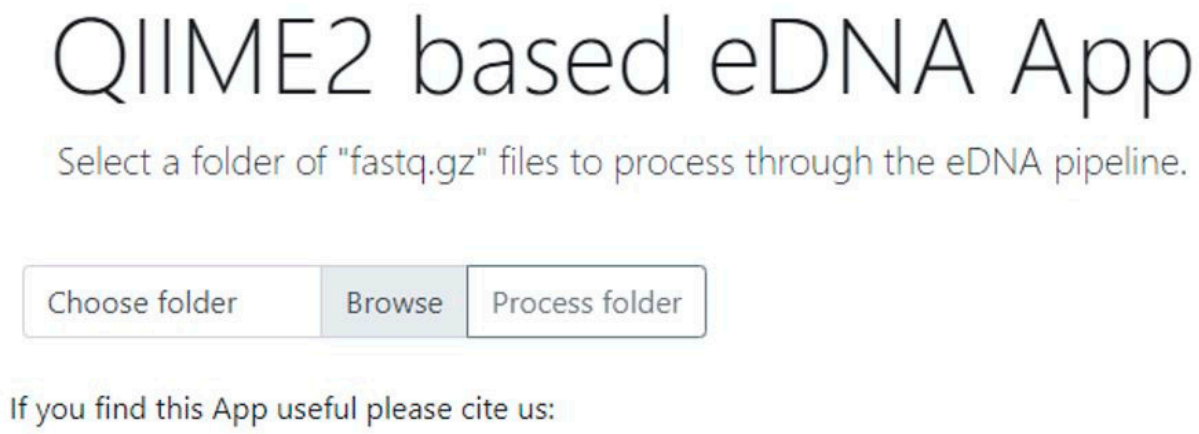

Figure S1. The *eDNA-container app* main GUI homepage with the sequencing folder selection buttons.

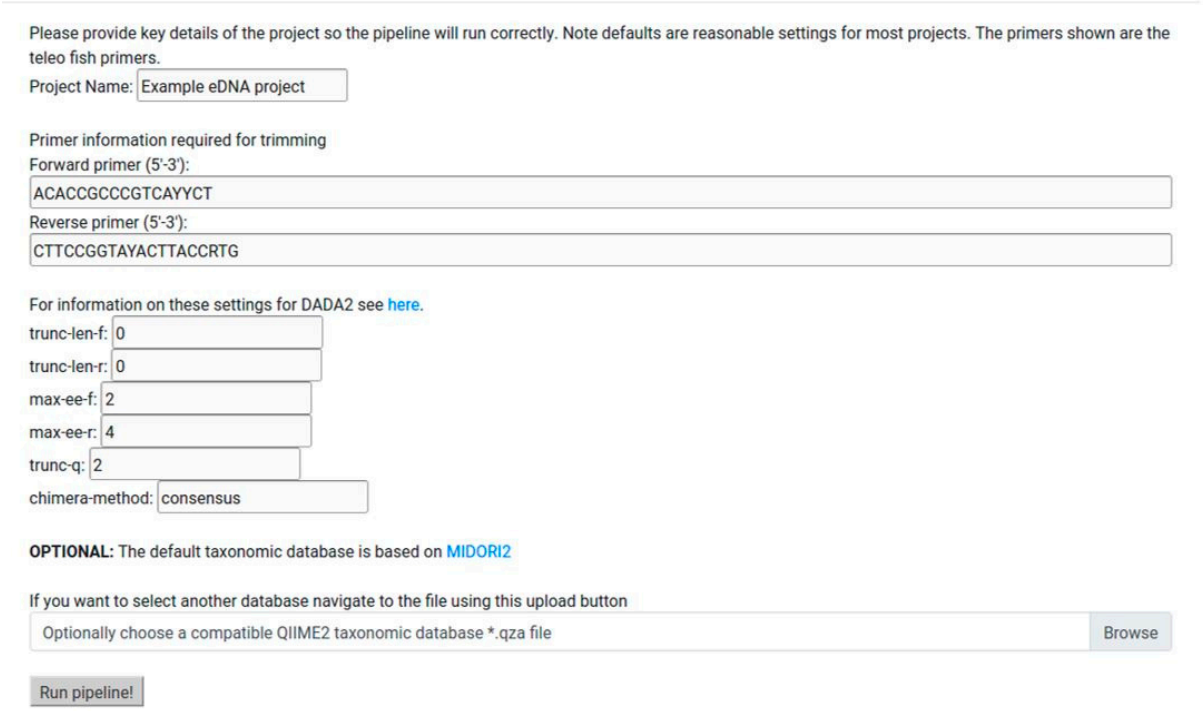

Figure S2. The *eDNA-container app* settings screen. The project name will be included in the final PDF report as the project title. The primer sequences are used for trimming using the *cutadapt* plugin. Key *DADA2* parameters can be adjusted to improve the number and quality of ASVs generated. The user can select a compatible a *QIIME2* database (QZA file) or use the default which is based on MIDORI 12S rRNA.

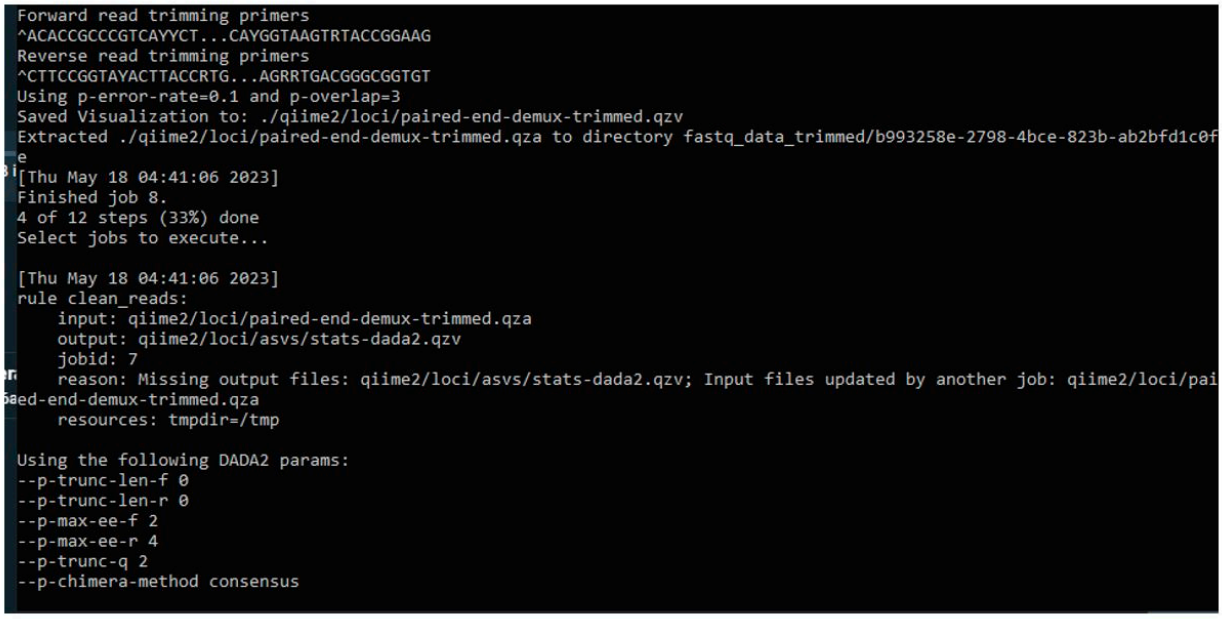

Figure S3. Outputs from each step of the *Snakemake* pipeline are logged to the Docker terminal window. These outputs are important for troubleshooting any pipeline failures.