



Raw signal

Basecalling  
Guppy

Demultiplexing  
Guppy

Raw reads  
MultiQC

Trimming  
Fastp

Trimmed reads  
MultiQC

Decontamination  
Minimap2/SAMtools

Host-depleted reads  
MultiQC

Viral classification  
MetaMaps

Viral reads  
Seqtk

Reference-based  
assembly

1. Mapping  
Medaka

2. Sequencing depth  
bamread-count/SAMtools

3. Variant calling  
ivar

4. Polish indels  
homopolish

viral consensus

Final report

Sample	Virus (Acc/TaxID)
Read count	Coverage
Average depth	Consensus cov.
%N	Read identity
Read length	Base quality

Input/Output  
Process