



WHO Collaborating Centre
for Reference and
Research on Influenza
VIDRL



**World Health
Organization**
Philippines



KDCA
Korea Disease Control and
Prevention Agency

Case Study

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<Name>

<Affiliation>



**CENTRE FOR
PATHOGEN
GENOMICS**



**Doherty
Institute**



THE UNIVERSITY OF
MELBOURNE



**The Royal
Melbourne
Hospital**

A joint venture between The University of Melbourne and The Royal Melbourne Hospital

Quality Assessment of FASTQ files

- Describe the quality of your sequence data.
- Is the quality of your sequence high or low?
- What is the median Q score of your sequence?

Genome Assembly



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- Summarize the results of genome assembly on your sequence.
- What is the coverage depth, breadth of coverage?

Quality Assessment of Consensus Sequence



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- Describe the quality of your consensus sequence

Annotation



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- Which clade/lineage your samples belong to? What are the characteristic amino acid substitutions of this clade/lineage?
- What amino acid substitutions of epidemiological interest (e.g. antiviral resistance, vaccine effectiveness, pathogenicity, etc.) are present in your samples?

Phylogenetic analysis



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- Describe the topology of your phylogenetic tree.
- Which reference virus (or vaccine strain) your samples clustered together?

Discussion

- Interpret and discuss your results



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