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## Sample-sequence-interpretation pipeline

**WORLD  
CHANGING  
GLASGOW**

**A WORLD  
TOP 100  
UNIVERSITY**

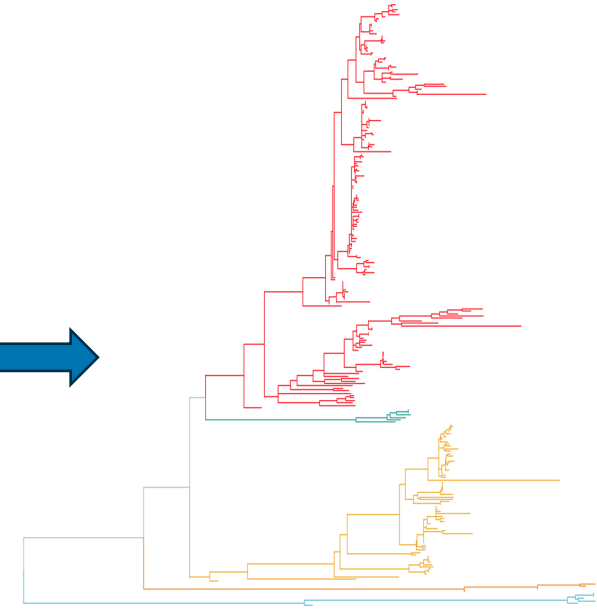




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# Sampling – Rabies samples

Sample collection (brain sample)+ rapid test is performed in the field

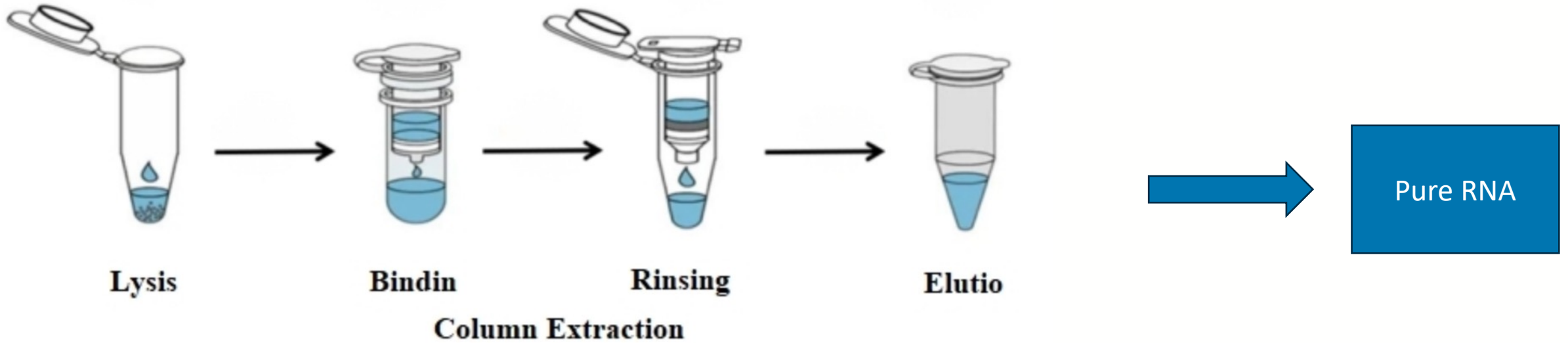


Molecular tech (PCR Sequencing - WGS)



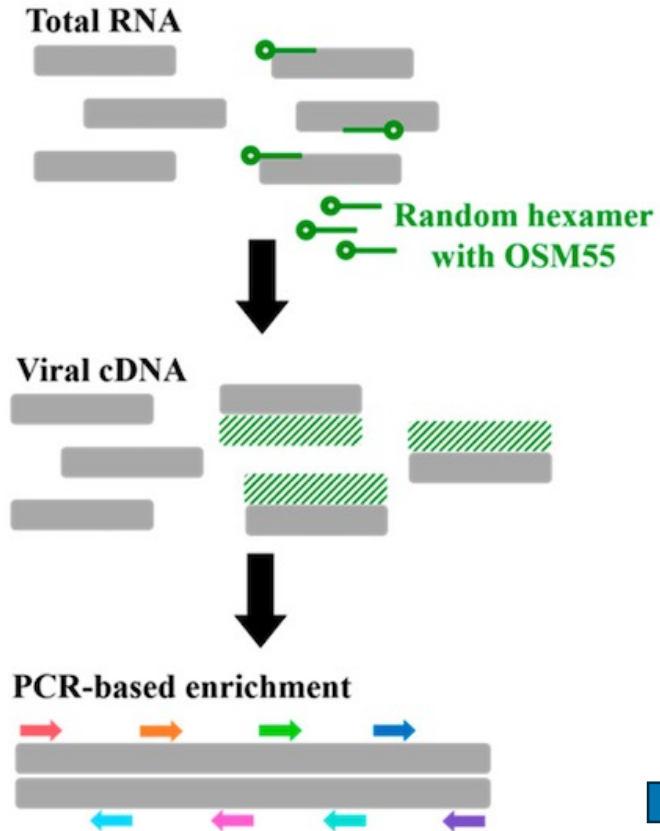
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## RNA-extraction – using zymo kit





# cDNA- multiplex PCR



REGIONS

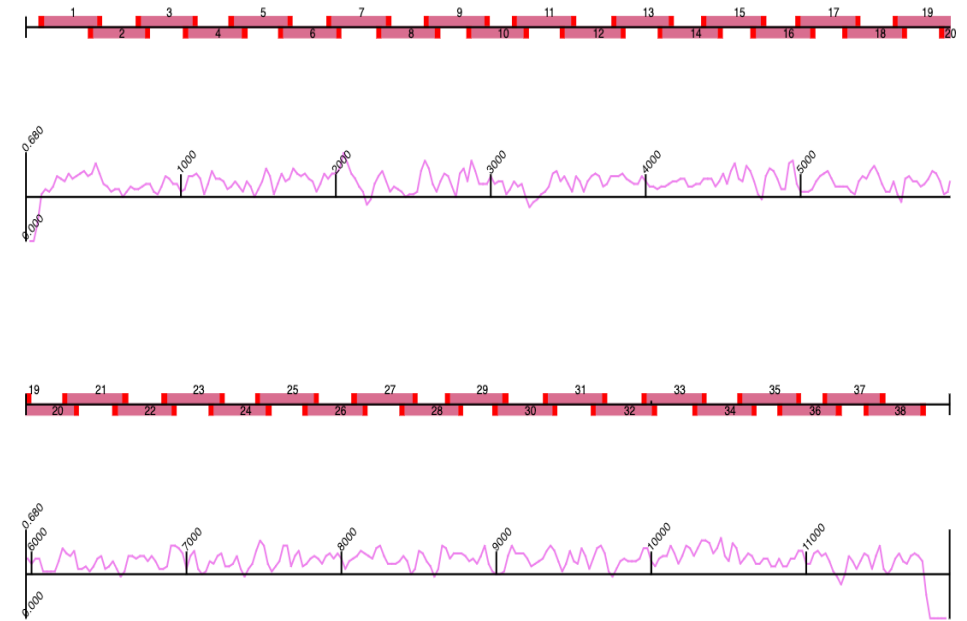
**38**

GAPS

**0**

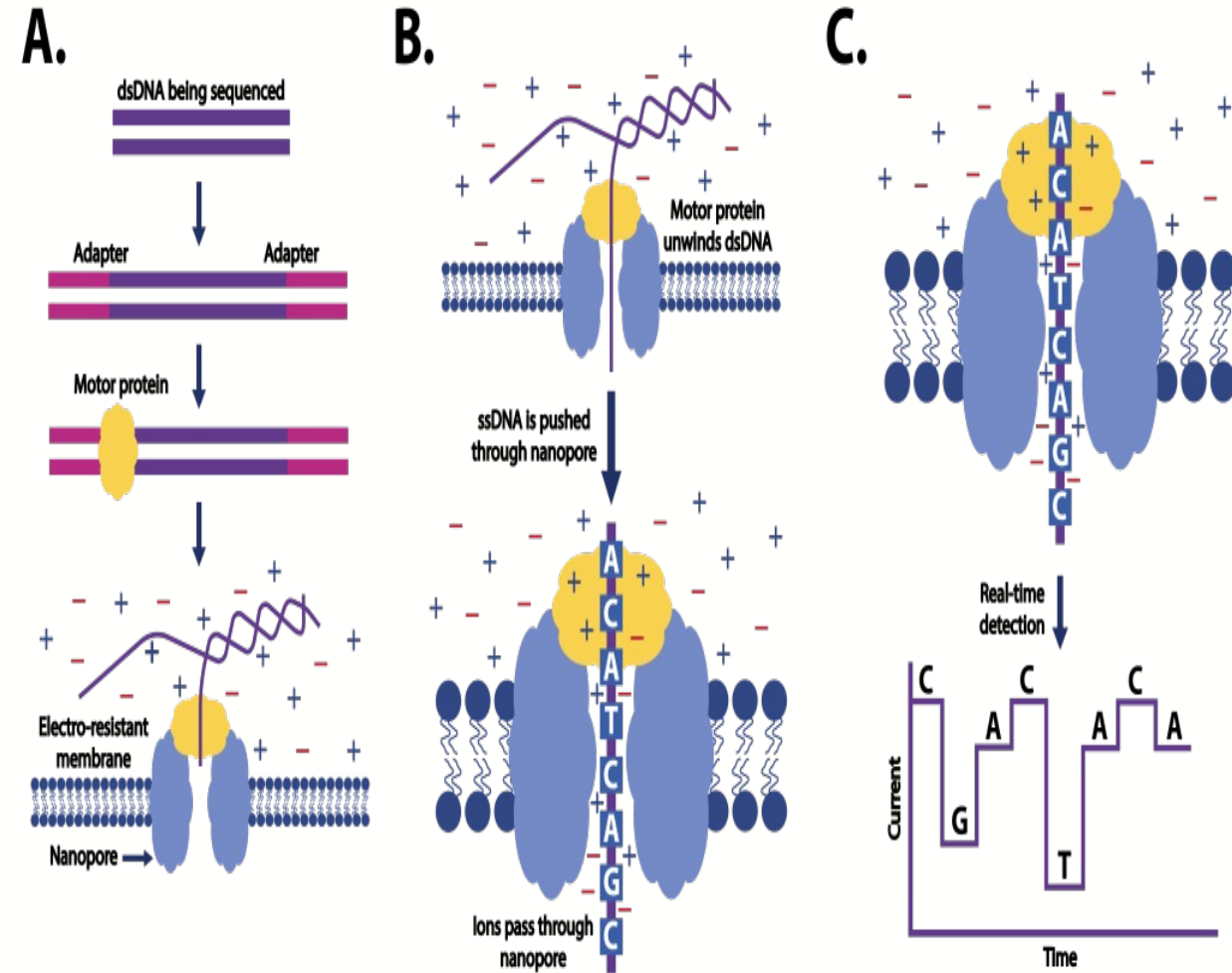
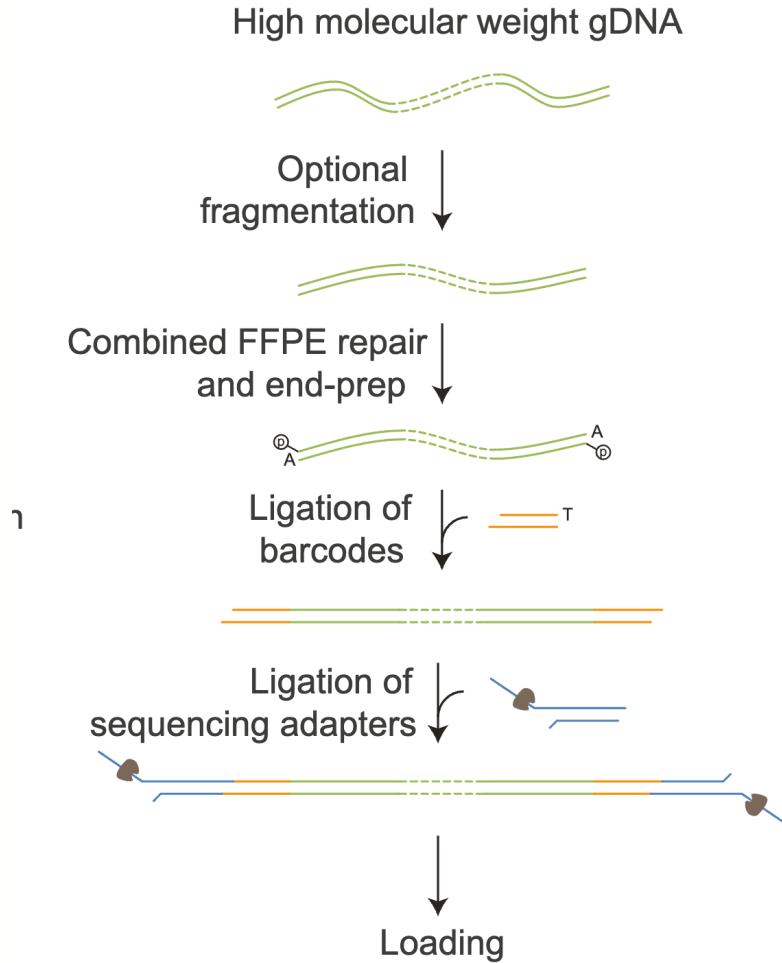
COVERAGE

**97.51%**



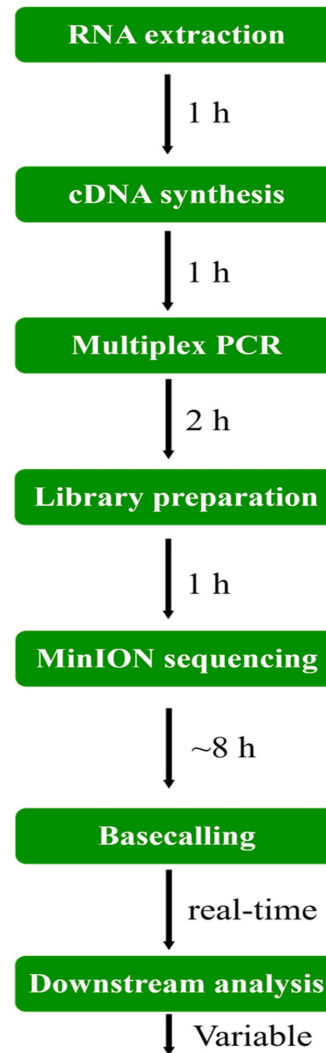
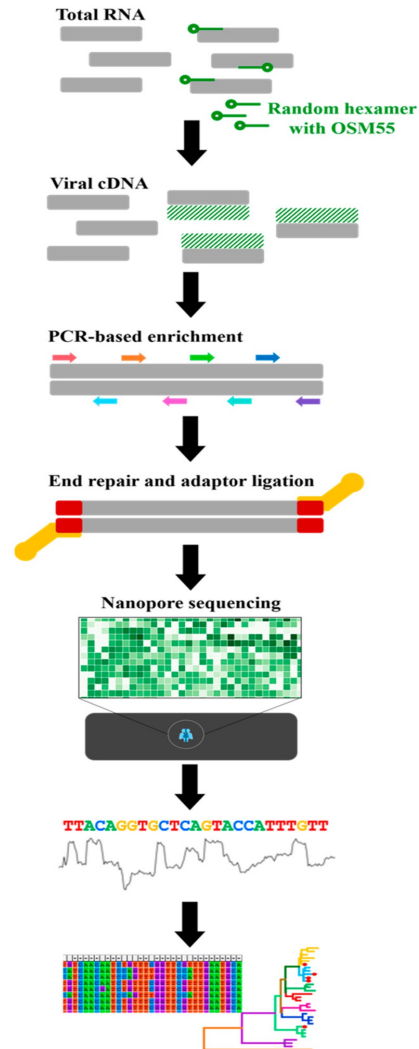
Primal scheme– using tiling approach

# Minlon loading and sequencing





## Summary



### Multiplex PCR-Based Nanopore Sequencing and Epidemiological Surveillance of *Hantaan orthohantavirus* in *Apodemus agrarius*, Republic of Korea

by Kyungmin Park <sup>1,2</sup> , Seung-Ho Lee <sup>2</sup> , Jongwoo Kim <sup>1,2</sup> , Jingyeong Lee <sup>2</sup> , Geum-Young Lee <sup>2</sup> , Seungchan Cho <sup>2</sup> , Seung Ho Lee <sup>2</sup> , Kkothanahreum Park <sup>2</sup> , Jin Sun No <sup>3</sup> , Shailesh Budhathoki <sup>4</sup> , Yu-Jin Kim <sup>5</sup> , Young-Su Kim <sup>6</sup> , Heung-Chul Kim <sup>7</sup> , Terry A. Klein <sup>7</sup> , Won-Keun Kim <sup>4,8</sup> and Jin-Won Song <sup>1,2,\*</sup>



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# Minlon interpretation



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## Rampart- run





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# Consensus generation



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**Closing slide – You can add  
contact details, a call to action or  
a simple thank you**

**#UofGWorldChangers**



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