

Dec 10, 2025

Version 1

Molecular Inversion Probes _User Friendly SOP_12-10-2025 V.1

DOI

dx.doi.org/10.17504/protocols.io.yxmvmmbb96g3p/v1



Azeza Falghoush¹, Luis Gamboal², Brandi Torrevillas¹, Lea Starita², Allison Black³, ksnek¹, Thomas Waltzek¹

¹Washington State University College of Veterinary Medicine, Pullman, WA, United States;

²UW Genome Sciences, University of Washington, Seattle, WA, United States;

³Washington State Department of Health, Shoreline, WA, United States

PGCoE_NW_WADDL



Azeza Falghoush

Washington State University

Create & collaborate more with a free account

Edit and publish protocols, collaborate in communities, share insights through comments, and track progress with run records.

Create free account

OPEN  ACCESS



DOI: <https://dx.doi.org/10.17504/protocols.io.yxmvmmbb96g3p/v1>

Protocol Citation: Azeza Falghoush, Luis Gamboal, Brandi Torrevillas, Lea Starita, Allison Black, ksnek , Thomas Waltzek 2025. Molecular Inversion Probes _User Friendly SOP_12-10-2025. **protocols.io**
<https://dx.doi.org/10.17504/protocols.io.yxmvmmbb96g3p/v1>

License: This is an open access protocol distributed under the terms of the **[Creative Commons Attribution License](#)**, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Protocol status: Working

This protocol is currently in use at the Washington Animal Disease Diagnostic Laboratory

Created: October 23, 2025

Last Modified: December 19, 2025

Protocol Integer ID: 230612

Keywords: Molecular Inversion Probes, User Friendly SOP, H5N1, viral RNA, WGS, genome of highly pathogenic avian influenza h5n1 clade, highly pathogenic avian influenza h5n1 clade, tm viral rna target capture kit, samples with high viral load, samples with lower viral load, rna virus, high viral load, sequencing library, lower viral load, genome, libraries for whole genome, whole genome, complete hpai, hpai

Funders Acknowledgements:

Washington State Department of Health Northwest Pathogen Genomics Center of Excellence (WA DOH contract number HED29191

Grant ID: NU50CK000630

Disclaimer

DISCLAIMER – FOR INFORMATIONAL PURPOSES ONLY; USE AT YOUR OWN RISK

The protocol content here is for informational purposes only and does not constitute legal, medical, clinical, or safety advice, or otherwise; content added to **protocols.io** is not peer reviewed and may not have undergone a formal approval of any kind. Information presented in this protocol should not substitute for independent professional judgment, advice, diagnosis, or treatment. Any action you take or refrain from taking using or relying upon the information presented here is strictly at your own risk. You agree that neither the Company nor any of the authors, contributors, administrators, or anyone else associated with **protocols.io**, can be held responsible for your use of the information contained in or linked to this protocol or any of our Sites/Apps and Services.



Abstract

TM Viral RNA Target Capture Kit is used to prepare next-generation sequencing libraries for whole genome or targeted sequencing of RNA viruses. This protocol contains instructions for library preparation for sequencing on Illumina platforms. Users should refer to product labeling for the probe design code as well as the probe fill size and the design version number. The authors have tested this protocol using a probe panel designed to cover the genome of Highly Pathogenic Avian Influenza H5N1 clade 2.3.4.4b genotype B3.13. The authors have had good success recovering the complete, or nearly complete, HPAI genomes from samples with high viral loads (e.g., when Ct values are ≤ 30). Samples with lower viral loads are unlikely to yield the complete HPAI genome using this protocol.

Attachments



Molecular Inversion ...

272KB

Troubleshooting



- 1 This protocol is recommended for higher amounts of input RNA Ct ≤ 29 . It was found to produce superior results. However, the results may not be as expected if the RNA input is too low and/or the Ct values are high (≥ 30). For whole genome RNA (host and pathogen) sequencing, best results will be achieved if reactions contain at least 10,000 copies of RNA.

* The probe panel of the kit was designed to cover the genome of Highly Pathogenic Avian Influenza H5N1 clade 2.3.4.4b, genotype B3.13

For all kit reagents and part numbers, see the attached ordering sheet in page (7).

1-