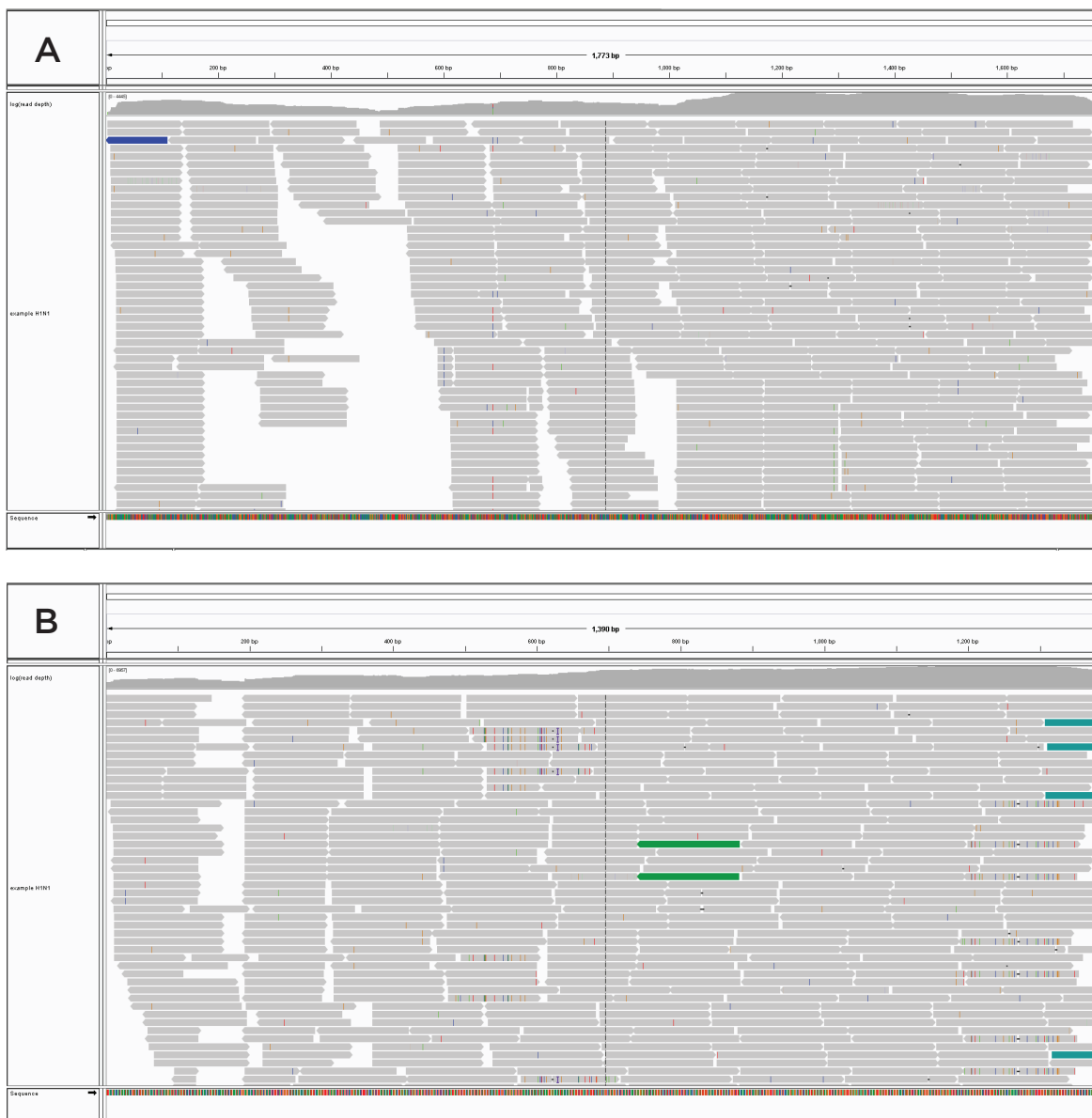# **ONE**Test™ Influenza Sentinel

The **ONETest™ Influenza Sentinel** assay allows sensitive and scalable identification of all major circulating influenza viruses. The assay provides more information than all widely employed conventional tests combined (i.e., RT-PCR assays and Sanger sequencing), including estimates of viral load and quasi-species. The assay enables various types of epidemiological investigation—from routine surveillance to vaccine effectiveness studies—in a single simple-to-perform assay.

The **ONETest™** system when used in conjunction with most next-generation sequencing machines offers a complete benchtop-to-desktop solution. It consists of the UniPrep™ universal library preparation kit, patent-pending QuantumProbes™ designed to capture over 95% of known influenza virus strain diversity, and comprehensive bioinformatics analysis in the FusionCloud™, a secure and compliant cloud computing environment.

ONETest™ Influenza Sentinel assay allows:

1 Capture of the entire hemagglutinin (HA) and neuraminidase (NA) segments as well as conserved regions of the matrix segment

2 Simultaneous identification of all major circulating influenza viruses (A/H1N1, A/H3N2, B/Victoria, and B/Yamagata) in a single reaction

3 Detection of multiple co-occurring types, subtypes, and strains

4 Discovery of mutations possibly associated with antigenic drift or virulence as well as quasi-species within a sample

5 Semi-quantitative estimation of viral load

The ONETest™ Influenza Sentinel assay was applied on a H1N1 influenza virus-positive sample. Example data demonstrates the assay's capability to (1) identify influenza type, subtype, and strain correctly, (2) recover the entire sequences of HA and NA, and (3) mutations and quasi-species.

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Figure: Example read coverage over the (A) hemagglutinin (HA) and (B) neuraminidase (NA) segments. Data was generated using an Illumina NextSeq® machine from a H1N1 influenza virus-positive sample processed using the ONETest™ Influenza Sentinel protocol. Influenza typing and reconstruction of the HA and NA consensus sequences were performed on the FusionCloud™. The reads were aligned to the consensus sequences, and their alignments were visualized using IGV[1,2].

References

1. Robinson JT, Thorvaldsdóttir H, Winckler W, Guttman M, Lander ES, Getz G, & Mesirov JP. 2011. Integrative Genomics Viewer. Nature Biotechnology 29: 24–26

2. Thorvaldsdóttir H, Robinson JT, & Mesirov JP. 2013. Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration. Briefings in Bioinformatics 14: 178-192.

Learn more

For more information about the **ONE**Test™ Influenza Sentinel assay and the
ONETest™ system, please visit: **WWW.FUSIONGENOMICS.COM**

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