



## SEQUENCING OF PARAINFLUENZA—BACKGROUND

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The International Gene Synthesis Consortium (IGSC) is composed of 11 companies, which together represent approximately 80% of commercial gene synthesis capacity worldwide.<sup>1</sup> The companies are:

- GINKGO BIOWORKS
- BGI
- BLUE HERON
- ATUM
- IDT
- THERMO FISHER SCIENTIFIC
- SGI-DNA
- GENSCRIPT
- TWIST BIOSCIENCE
- BIONEER CORP.
- EDINBURGH GENOME FOUNDRY

### HUMAN PARAINFLUENZA

Genome size: Negative sense RNA (~15,000 nucleotides) [15kb]<sup>2</sup>

- Estimated sequencing time: 1-2 days
- Estimated viral bioinformatics time for novel virus: ~1 week<sup>3</sup>
  - Read quality control
  - Reference strain determination
  - Read mapping to the reference strain
  - Single-nucleotide polymorphism (SNP) and small insertion or deletion (indel) detection
  - De novo genome assembly
  - Genome annotation
  - Phylogenetic tree construction
  - Phylogenetic analysis
    - Several software solutions are available for each step.

### REFERENCES

1. International Gene Synthesis Consortium. <https://genesynthesisconsortium.org/>. Accessed May 7, 2018.
2. [Henrickson KJ. Parainfluenza viruses. \*Clin Microbiol Rev\* 2003;16\(2\):242-264.](#)
3. Oakeson KF, Wagner JM, Mendenhall M, Rohrwasser A, Atkinson-Dunn R. Bioinformatic analyses of whole-genome sequence data in a public health laboratory. *Emerg Infect Dis* 2017;23(9):1441-1445.

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