

FUSIONCloud™

FusionCloud™ is a secure and compliant bioinformatics platform for analyzing next-generation sequencing (NGS) data from the ONETest™ assays developed by Fusion Genomics for sensitive multiplexed microbial identification. Operating behind FusionCloud™ is a proprietary bioinformatics pipeline to infer the type, subtype, and strain of microbes from NGS data.

FUSIONCloud™ offers:

- 1 Simple and intuitive data analysis workflow
- 2 Best-in-class project and run management tools
- 3 Bioinformatics applications for microbe typing, consensus sequence reconstruction, mutation calling, and geographical and phylogenetic analysis
- 4 Secure and compliant data storage

FusionCloud™, backed by the IBM SoftLayer® infrastructure, allows rapid on-demand scaling of computational power for data analysis. Where required by regulatory considerations FusionCloud™ also supports geographic segmentation of data. All data is stored in compliance with HIPPA, CLIA, 21 CFR parts 11, 58, and 493.

FusionCloud™ provides data encryption, discrete access control, auditing and monitoring. All analyses and results are version-controlled for reproducibility.

FusionCloud™ produces key QA/QC library metrics, type(s)/subtype(s)/strain(s) detected, consensus sequence(s) reconstructed per target region (e.g., hemagglutinin and neuraminidase genes in the case of the ONETest™ Influenza Sentinel assay), and mutations plus their corresponding amino acid substitutions (**Figures 1 and 2**). Additionally, heterogeneous data from widely used databases—including the NCBI Influenza Virus Resource—are integrated to facilitate downstream analysis (e.g., drug resistance variant annotation and phylogenetic analysis of outbreak strains).

