

Mutation Calling

NGS Raw Data

Consensus Sequence



Calling iSNV

Lineage Feature  
Variations



Lineage Filtration

Candidate Within-host Lineage(s)



Hypergeometric Distribution

Credibility Evaluation

Statistical  
Significance

Mutation Frequency  
Uniformity

Mutation  
Concentration



Determined Within-host Lineage(s)



Pattern Determination

Co-infection

One Lineage  
Infection