



**Next Generation Analysis  
for  
Re-sequencing and Mapping of  
Microbial and Viral Genomes  
using NGS technologies**

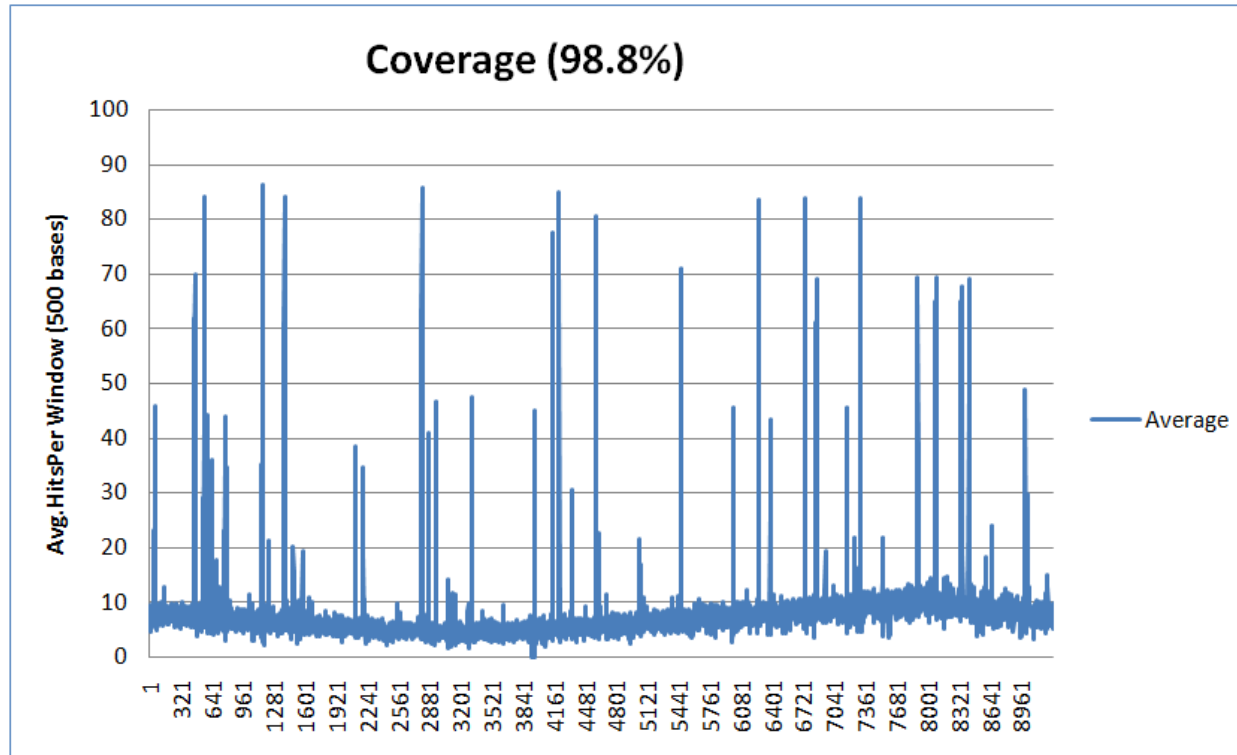


**EUREKAGENOMICS<sup>SM</sup>**



# Re-sequencing of Microbial and Viral Genomes

## Escherichia coli str. K-12 substr. MG1655



### Coverage

Reference Length: 4,639,675  
# of Unmapped Positions: 57,722  
Genome covered: 98.7559%

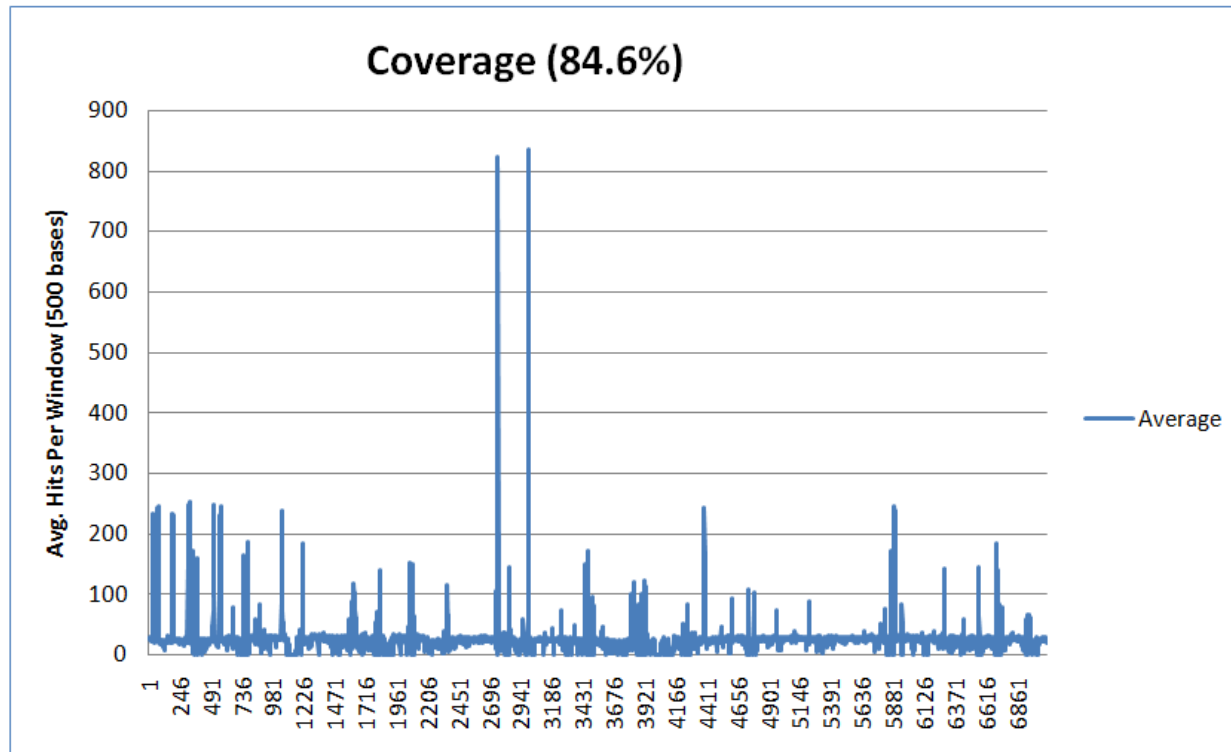
### Gaps

# of Gaps: 4,798  
Min Gap Length: 1  
Max Gap Length: 8,614  
Median Gap Length: 6



# Re-sequencing of Microbial and Viral Genomes

## Geobacillus kaustophilus HTA426



### Coverage

Reference Length: 3,544,776  
# of Unmapped Positions: 546,305  
Genome covered: 84.5884%

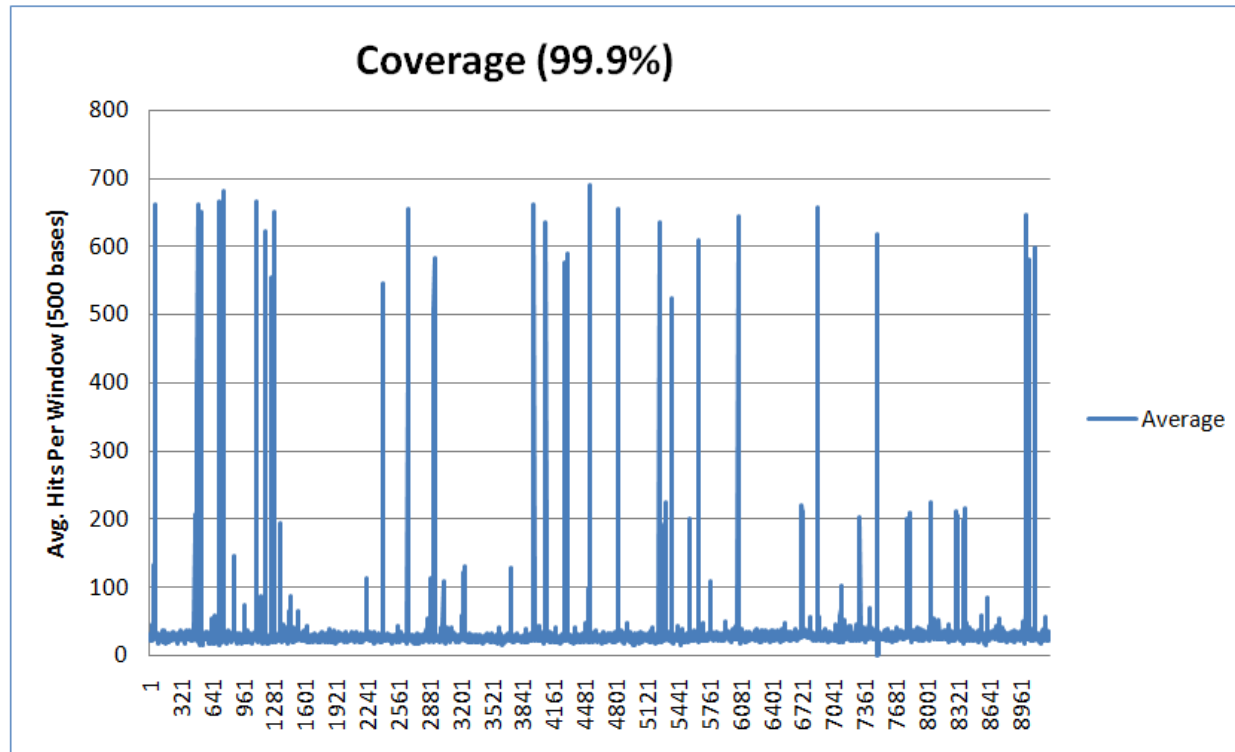
### Gaps

# of Gaps: 5,015  
Min Gap Length: 1  
Max Gap Length: 23,078  
Median Gap Length: 17



# Re-sequencing of Microbial and Viral Genomes

## E. coli. REL606



### Coverage

Reference Length: 4,629,813  
# of Unmapped Positions: 3,020  
Genome covered: 0.999347

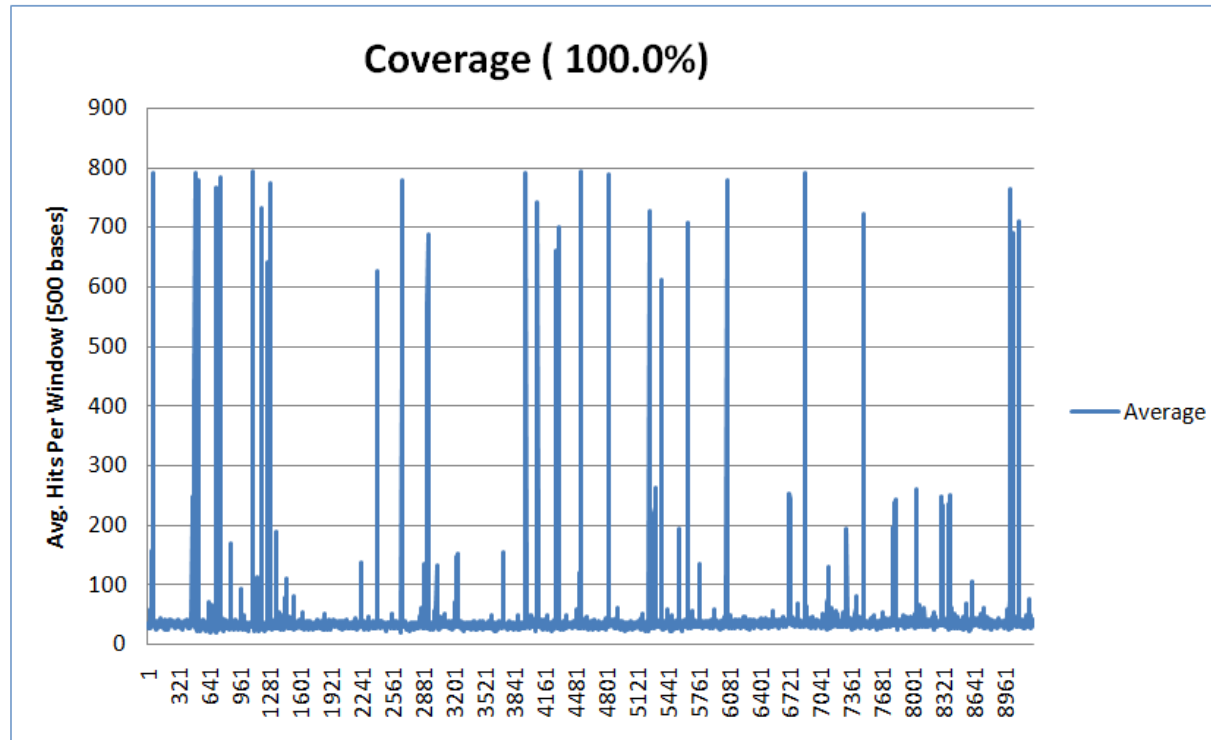
### Gaps

# of Gaps: 5  
Min Gap Length: 1  
Max Gap Length: 2,987  
Median Gap Length: 12



# Re-sequencing of Microbial and Viral Genomes

## E. coli REL606 (2)



### Coverage

Reference Length: 4,629,813  
# of Unmapped Positions: 0  
Genome covered: 1.000000

### Gaps

# of Gaps: 0  
Min Gap Length: 0  
Max Gap Length: 0  
Median Gap Length: 0