	Statistics

Nucleotide Statistics:
Length: 16,661 bp
Sequences: 918
Identical Sites: 15,510 (95.6%)
Pairwise Identity: 98.8%

Coverage (restricted):
Mean: -   Std Dev: -
Minimum: -   Maximum: -
Forward: -   Reverse: -
Ref-Seq: 97.3% (16,215 of 16,660)

Read Lengths (restricted):
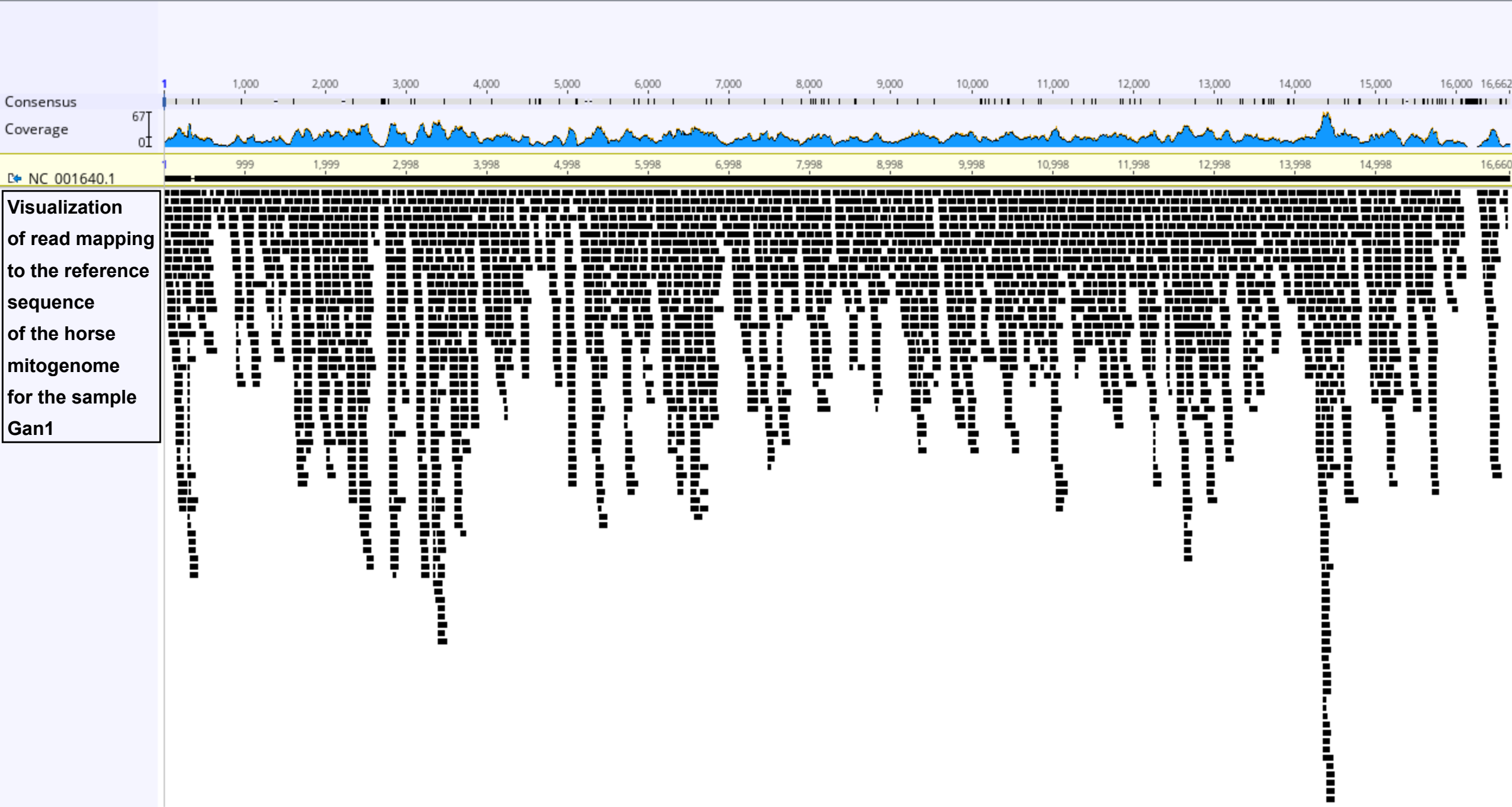Mean: -   Std Dev: -
Minimum: -   Maximum: -

Confidence Mean: (restricted)
Expected Errors: (restricted)
Error Free Odds: (restricted)
At least Q20: (restricted)
At least Q30: (restricted)

Consensus

Coverage   23
           0

NC_001640.1

Visualization of read mapping to the reference sequence of the horse mitogenome for the sample Er1

Visualization of read mapping to the reference sequence of the horse mitogenome for the sample Gan1

Statistics

Stats include 1 hidden columns

Nucleotide Statistics:
Length: 16,662 bp
Sequences: 3,144
Identical Sites: 13,578 (82.2%)
Pairwise Identity: 97.5%

Coverage (restricted):
Mean: -   Std Dev: -
Minimum: -   Maximum: -
Forward: - Reverse: -
Ref-Seq: 99.1% (16,515 of 16,660)

Read Lengths (restricted):
Mean: -   Std Dev: -
Minimum: -   Maximum: -

Confidence Mean: (restricted)
Expected Errors: (restricted)
Error Free Odds: (restricted)
At least Q20: (restricted)
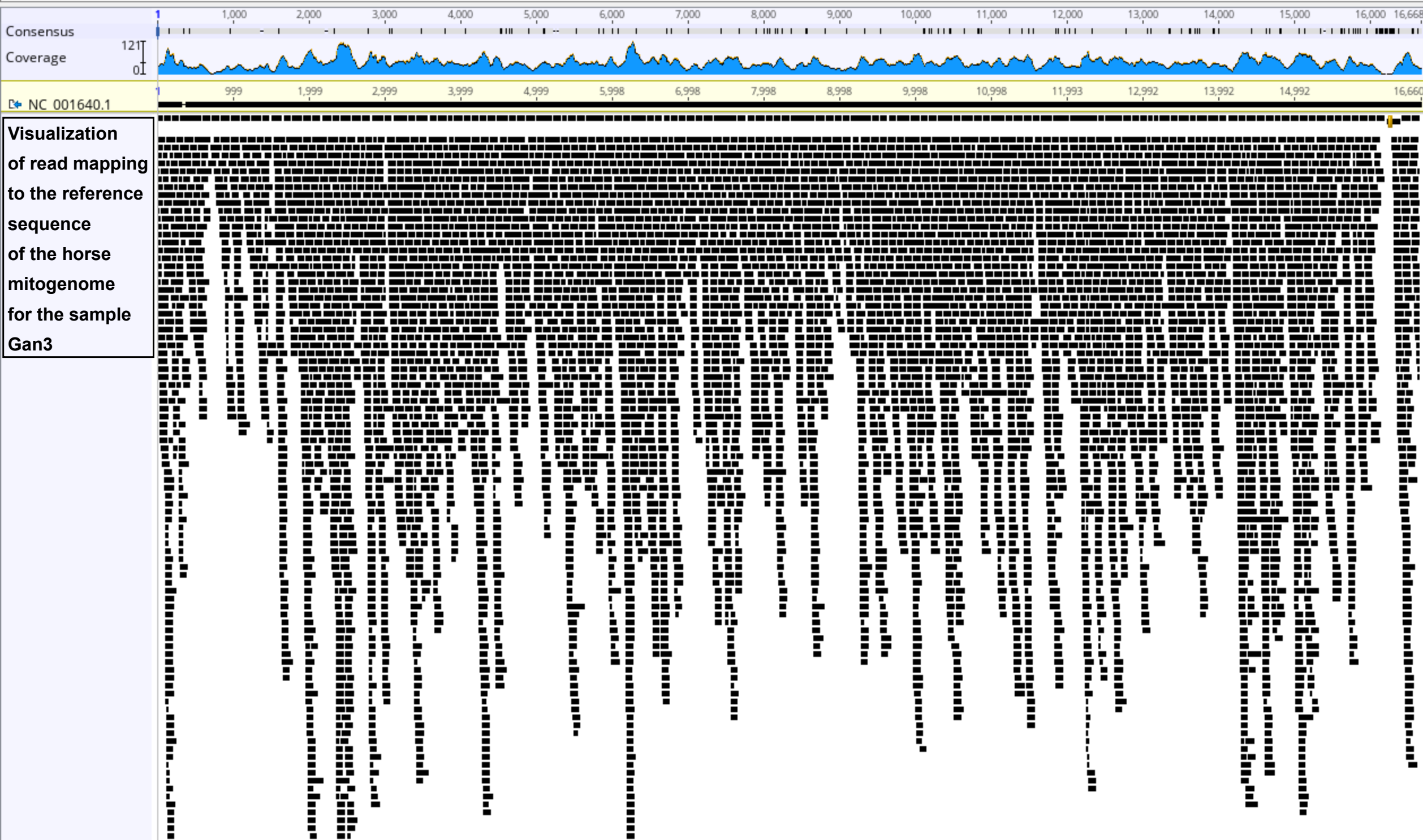At least Q30: (restricted)
At least Q40: (restricted)
Rough Tm: (restricted)

	Freq	% of non-gaps
A:	105,747	32.4%
C:	90,273	27.6%
G:	43,262	13.2%
T:	87,395	26.8%
GC:	133,535	40.9%
All:	326,677	100.0%
-:	106	0.0% (of any)

Consensus

Coverage 67 / 0

NC_001640.1

Visualization of read mapping to the reference sequence of the horse mitogenome for the sample Gan3

Statistics

Nucleotide Statistics:

Length: 16,668 bp
Sequences: 6,920
Identical Sites: 11,653 (70.1%)
Pairwise Identity: 97.0%

Coverage (restricted):
  Mean: -   Std Dev: -
  Minimum: -   Maximum: -
  Forward: - Reverse: -
  Ref-Seq: 99.8% (16,624 of 16,660)

Read Lengths (restricted):
  Mean: -   Std Dev: -
  Minimum: -   Maximum: -

Confidence Mean: (restricted)
Expected Errors: (restricted)
Error Free Odds: (restricted)
At least Q20: (restricted)
At least Q30: (restricted)
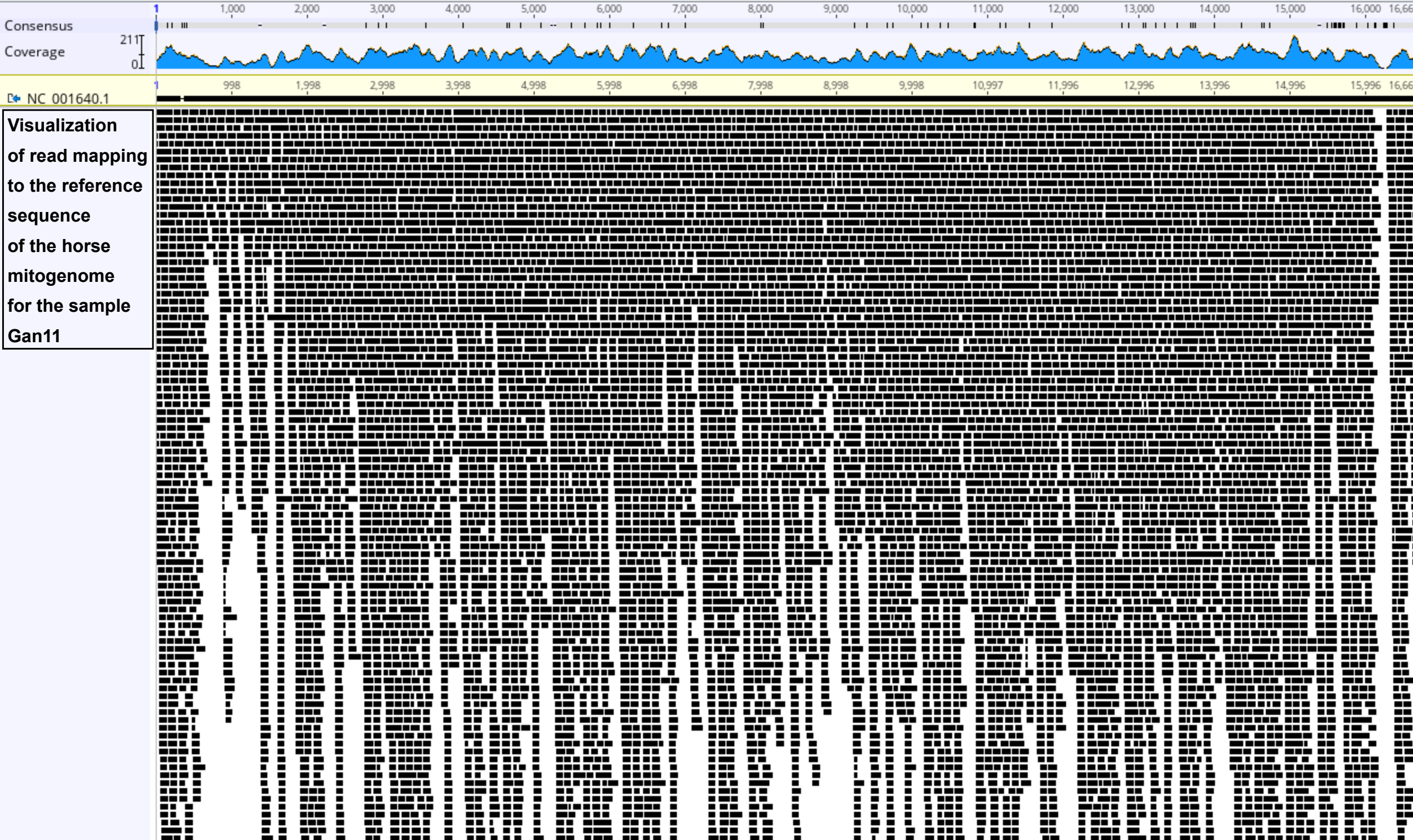At least Q40: (restricted)
Rough Tm: (restricted)

	Freq	% of non-gaps
A:	230,136	32.3%
C:	201,204	28.2%
G:	93,652	13.1%
T:	188,039	26.4%
R:	2	0.0%
GC:	294,856	41.4%
All:	713,033	100.0%
-:	679	0.1% (of any)

Visualization of read mapping to the reference sequence of the horse mitogenome for the sample Gan11

Statistics

Stats include 4 hidden columns

Nucleotide Statistics:
Length: 16,665 bp
Sequences: 13,894
Identical Sites: 10,378 (62.4%)
Pairwise Identity: 96.9%

Coverage (restricted):
  Mean: -   Std Dev: -
  Minimum: - Maximum: -
  Forward: - Reverse: -
  Ref-Seq: 99.7% (16,618 of 16,660)

Read Lengths (restricted):
  Mean: -   Std Dev: -
  Minimum: - Maximum: -

Confidence Mean: (restricted)
Expected Errors: (restricted)
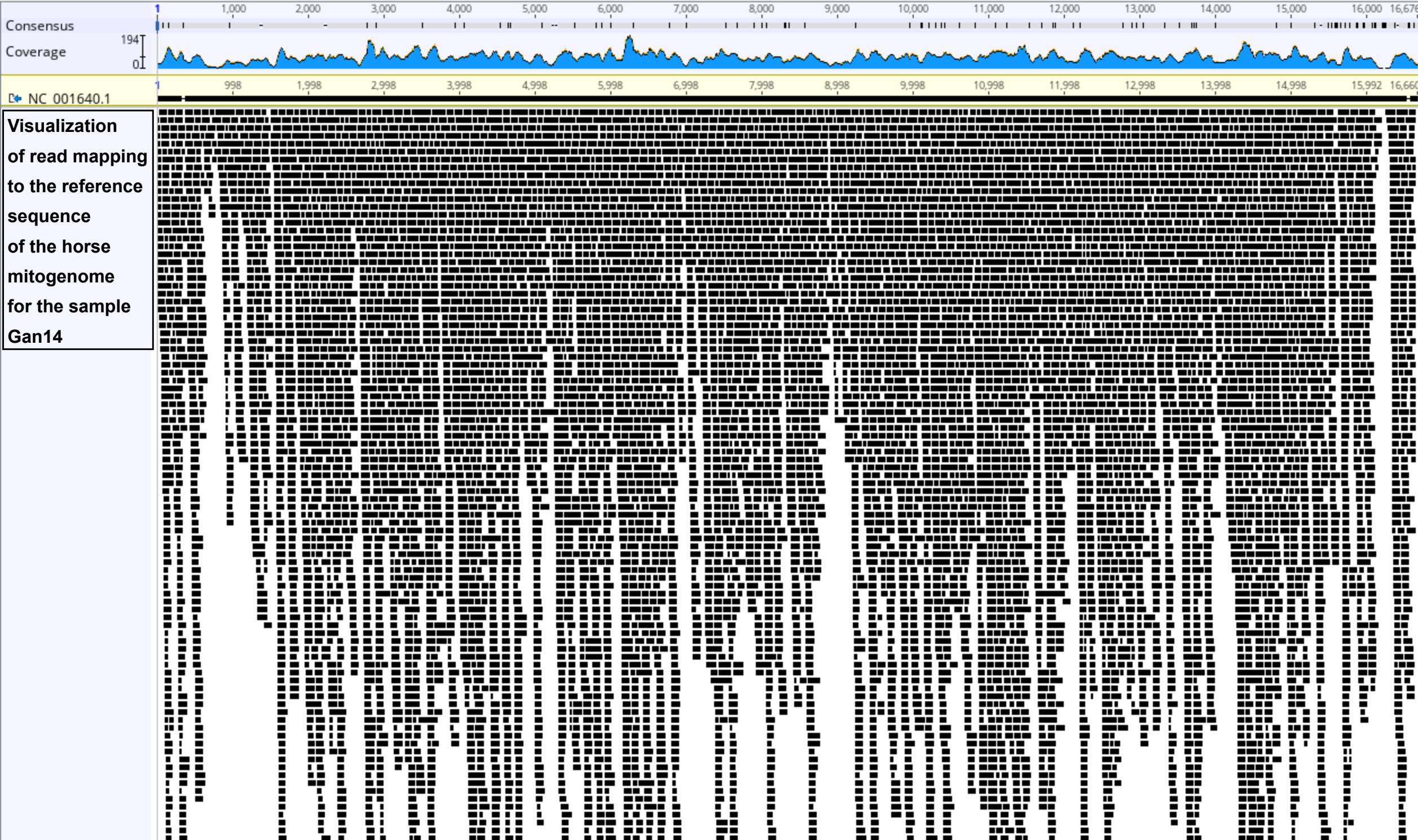Error Free Odds: (restricted)
At least Q20: (restricted)
At least Q30: (restricted)
At least Q40: (restricted)
Rough Tm: (restricted)

	Freq	% of non-gaps
A:	468,982	32.4%
C:	410,694	28.4%
G:	185,192	12.8%
T:	383,016	26.5%
GC:	595,886	41.2%
All:	1,447,884	100.0%
-:	741	0.1% (of any)

Visualization of read mapping to the reference sequence of the horse mitogenome for the sample Gan14

Statistics

Nucleotide Statistics:
Length: 16,676 bp
Sequences: 11,644
Identical Sites: 10,523 (63.2%)
Pairwise Identity: 96.7%

Coverage (restricted):
Mean: -   Std Dev: -
Minimum: -   Maximum: -
Forward: - Reverse: -
Ref-Seq: 99.8% (16,622 of 16,660)

Read Lengths (restricted):
Mean: -   Std Dev: -
Minimum: -   Maximum: -

Confidence Mean: (restricted)
Expected Errors: (restricted)
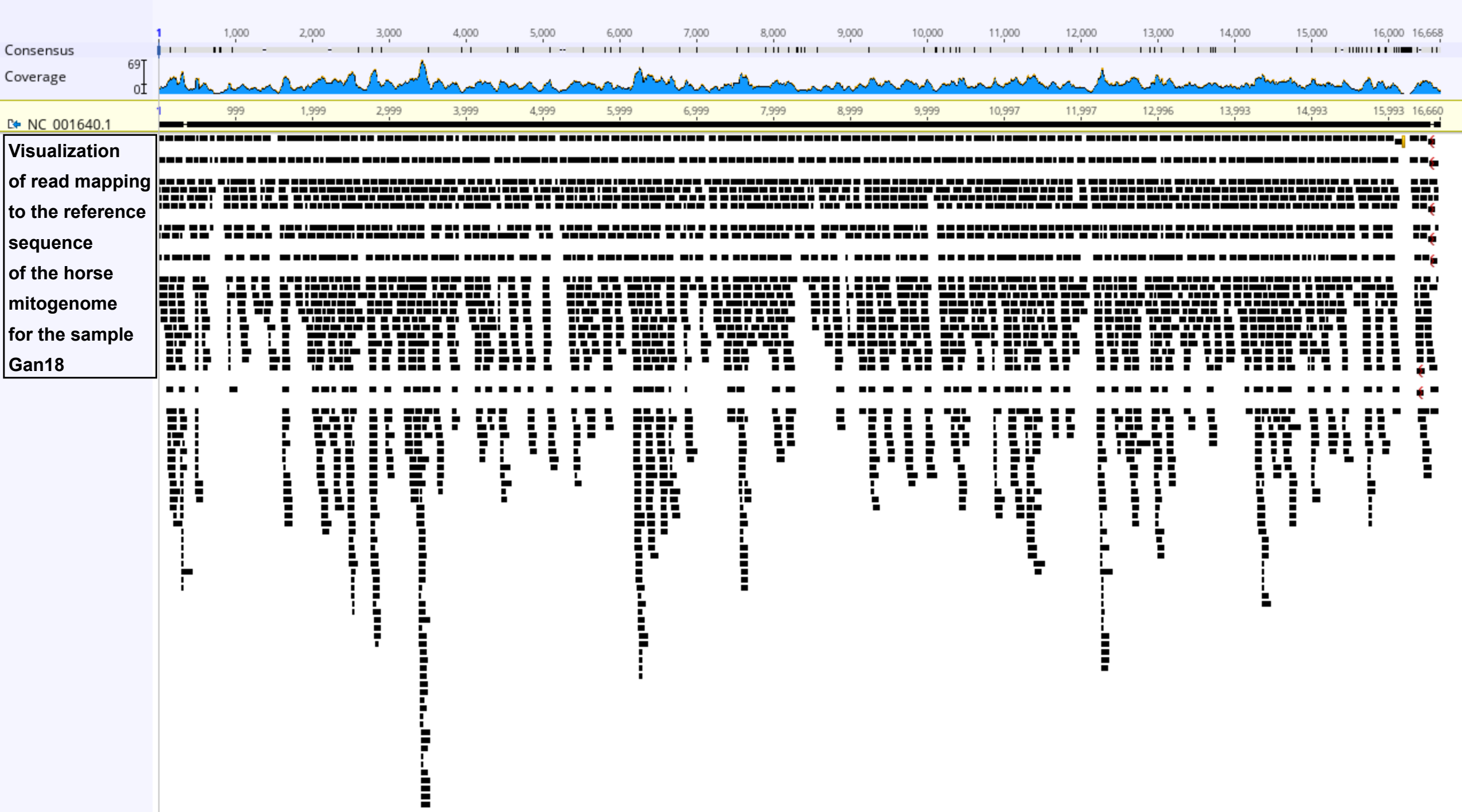Error Free Odds: (restricted)
At least Q20: (restricted)
At least Q30: (restricted)
At least Q40: (restricted)
Rough Tm: (restricted)

	Freq	% of non-gaps
A:	367,495	32.6%
C:	314,396	27.9%
G:	144,211	12.8%
T:	301,502	26.7%
GC:	458,607	40.7%
All:	1,127,604	100.0%
-:	1,152	0.1% (of any)

Consensus

Coverage

69
0

NC_001640.1

Visualization of read mapping to the reference sequence of the horse mitogenome for the sample Gan18