Sequence: 59746783

Samples: 18053
Bases: 1359
Average spacing: 14.0
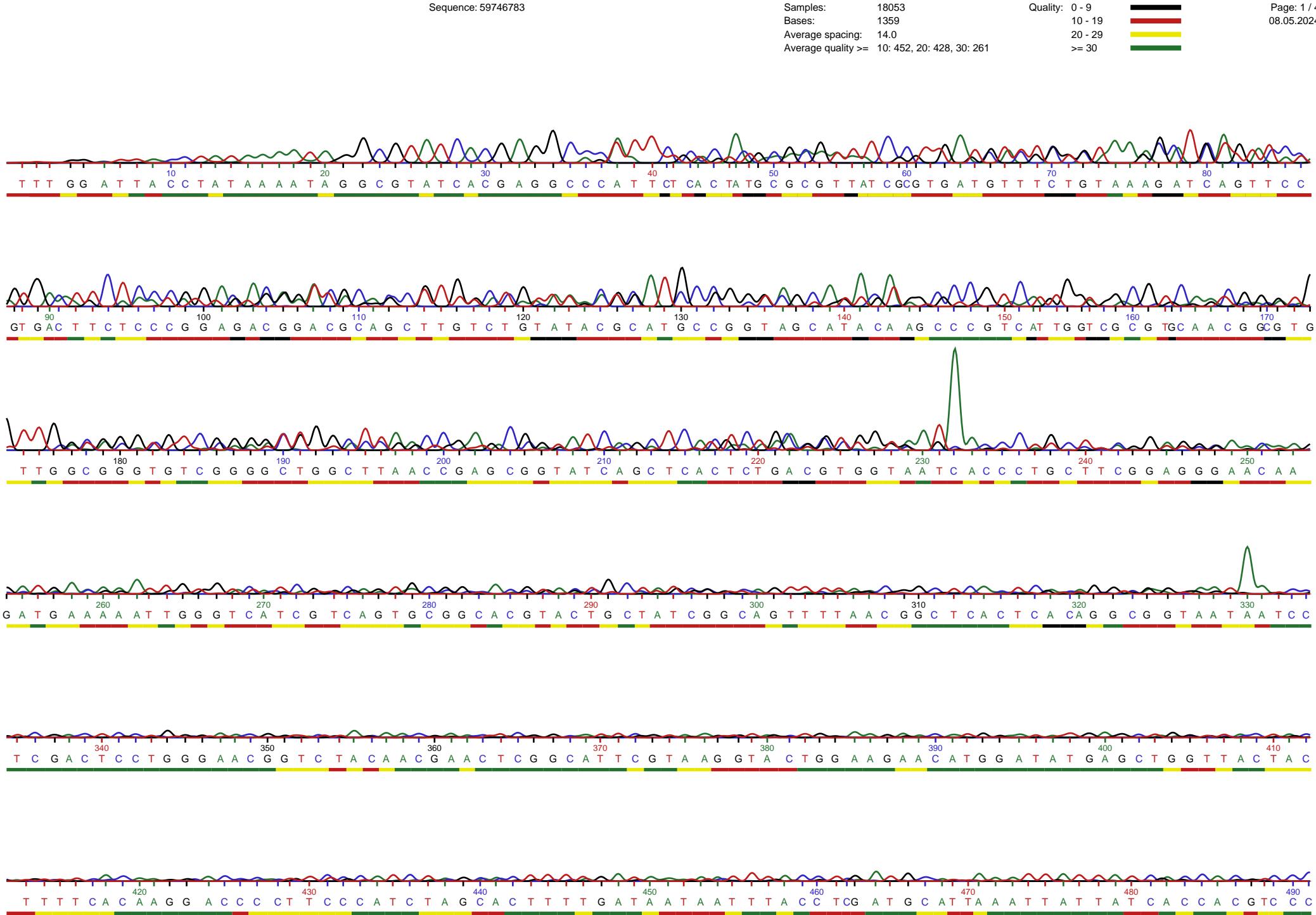Average quality >= 10: 452, 20: 428, 30: 261

Quality: 0 - 9
10 - 19
20 - 29
>= 30


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TTT GG ATTA CCTATAAAATAG G CGTATCACGAGG CCCATT CT CAC TATG C G CG T TAT CGCG TGATGTTT C TGTAAAGAT CAGTTCC
```

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GT GAC TTCTCCC A GAGACGGACGCAG CTTGTCTG TATACGCATG CCGGTAGCATACAAG CCCG TCAT TGGTCG CG TGCAACG GCG T G
```

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TTGGCGGGTGTCGGGGCTGGCTTAACCGAGCGGTATCAGCTCACTCTGACGTGGTAATCACCCTGCTTCGGAGGGACAA
```

```
GATGAAAATTGGGTCATCGTCAGTGCGGCACGTACTGCTATCGGCAGTTTTAACGCTCACTCAGGCGGTAATAATCC
```

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TCGACTCCTGGGAACGGTCTACAACGAACTCGGCATTCGTAAGGTACTGGAAGACATGGATATGAGCTGGTTACTAC
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TTTTCACAGGACCCCTTCCCATCTAGCACTTTTGATAATAATTTACCTCGATGCATTAAATTATTATCACCACGTCCC
```

Sequence: 59746783

Samples:	18053
Bases:	1359
Average spacing:	14.0
Average quality >=	10: 452, 20: 428, 30: 261

Quality: 0 - 9
10 - 19
20 - 29
>= 30

08.05.2024

TTCTTTCCGGCCTACGTGCACCAAGGTAGCGAATCGCATAAGCCCCAAAGACTCAAAGCTATGCGTTAACAGACCGGG

GTTAGAGGTCTGATACATTATGCACCCTGAATGCCATTGATGTGACTCGAGGCAATTGCCGTTCCTGAGAAGTTACGGGC

TCTAACGTATCAGAGTGTGGCGCAACACGTCTATTATAGACAATGCTAATTCCTGCTACGTAACTATGGAG

AAAGGTCACGCTCAGGCAACTCATAGGACTTGAGACATTGCTGCGGTTGCTAACGATGAGTTTG

ATATGGAAGGAATAAGGTGTTTGCGACTATCGGAGCAGGACGCATGGATATCGCATCCTCGA

GCGTCTAATCGCTTTTAACCCGATCAAATTACCTGTAACTAATGATTATCAAACCTCTACCG

Sequence: 59746783

Samples:	18053	Quality:	0 - 9
Bases:	1359		10 - 19
Average spacing:	14.0		20 - 29
Average quality >=	10: 452, 20: 428, 30: 261		>= 30
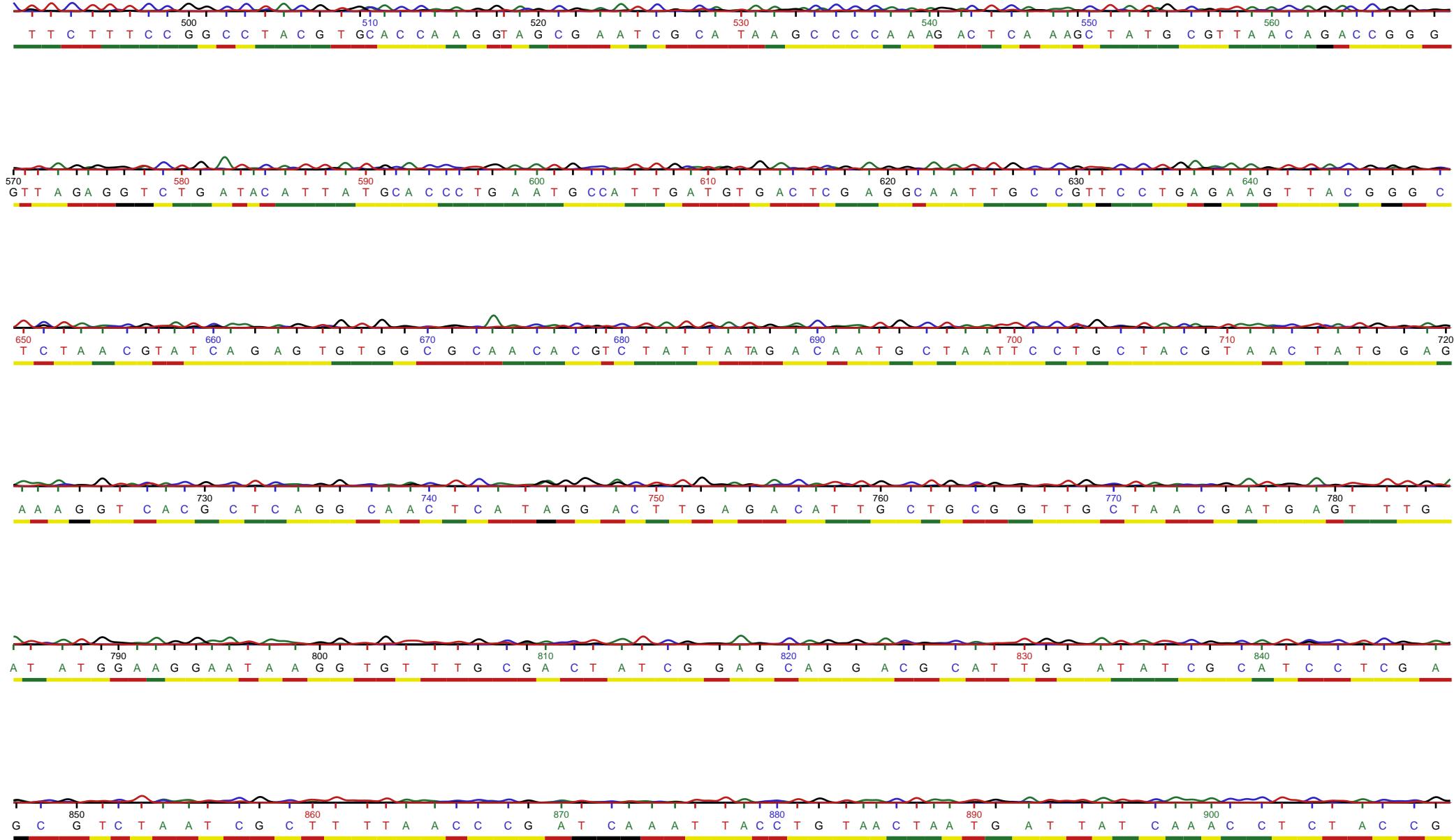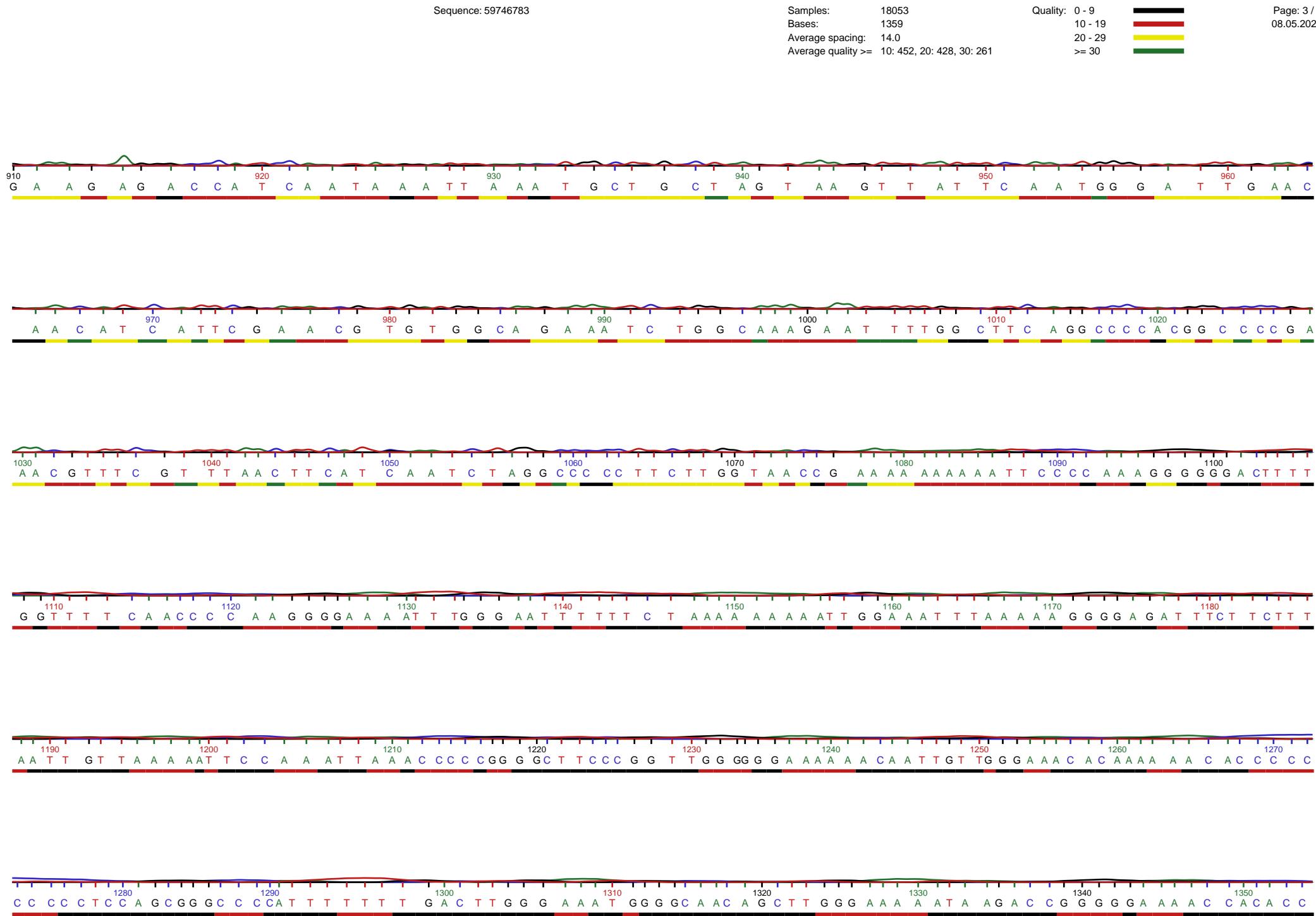
910 G A G A G A C C A T C A A T A A A T T A A A T G C T G C T A G T A A G T T A T T C A A T G G G A T T G A A C

A A C A T C A T T C G A A C G T G T G G C A G A A T C T G G C A A A G A A T T T T G G C T T C A G G C C C C A C G G C C C C G A

A A C G T T T C G T T T A A C T T C A T C A A T C T A G G C C C C C T T C T T G G T A A C C G A A A A A A A A A T T C C C C A A A G G G G G G A C T T T T

G G T T T T C A A C C C C A A G G G G A A A A T T T G G G A A T T T T T T C T A A A A A A A A A T T G G A A A T T T A A A A A G G G G A G A T T T C T T C T T T

A A T T G T T A A A A A T T C C A A A T T A A A C C C C C G G G G G C T T C C C G G T T T G G G G G G A A A A A A C A A T T G T T G G G A A A C A C A A A A A A C A C C C C C

C C C C C T C C A G C G G G C C C C C A T T T T T T T T G A C T T G G G A A A T G G G G C A A C A G C T T G G G A A A A A T A A G A C C G G G G G A A A A C C A C A C C C

A T T T