ИЛЬЯ

SRR5462773

SRA   [SRA]   **Search**

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SRX2750583: DNA_Seq of S.cerevisiae: clone Q_I_6
1 ILLUMINA (Illumina HiSeq 2000) run: 1.5M spots, 300.3M bases, 176Mb downloads

Design: Nextera

Submitted by: Jagiellonian University

Study: Whole genome sequences of S.cerevisiae clones from Q and NQ cells enriched lines
     PRJNA383491 • SRP104610 • All experiments • All runs
     show Abstract

Sample:
     SAMN06766204 • SRS2136569 • All experiments • All runs
     Organism: Saccharomyces cerevisiae S288C

Library:
     Name: CGAGGCTG - CTCTCTAT
     Instrument: Illumina HiSeq 2000
     Strategy: WGS
     Source: GENOMIC
     Selection: RANDOM
     Layout: PAIRED

Runs: 1 run, 1.5M spots, 300.3M bases, 176Mb

Run	# of Spots	# of Bases	Size	Published
SRR5462773	1,486,392	300.3M	176Mb	2017-04-21

ID: 3962036

Related information

BioProject

BioSample

Taxonomy

Recent activity

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🔍 5462773[uid] (1)
                                          SRA

📄 Escherichia coli O8:H36 strain MOD1-
     EC6081, whole genome shotgun   Nucleotide

🔍 Escherichia coli serovar (1042013)
                                          Nucleotide

🔍 Escherichia coli serovar O8 : H36 (0)
                                          Nucleotide

🔍 SRR6427360 AND srcdb_refseq[PROP]
     (0)   Nucleotide

See more...

```
spospots read      :  1,486,392
reads read       :  2,972,784
reads written    :  2,972,784
```

```
null
null
Started analysis of raw_fastq_1.fastq
Approx 5% complete for raw_fastq_1.fastq
Approx 10% complete for raw_fastq_1.fastq
Approx 15% complete for raw_fastq_1.fastq
Approx 20% complete for raw_fastq_1.fastq
Approx 25% complete for raw_fastq_1.fastq
Approx 30% complete for raw_fastq_1.fastq
Approx 35% complete for raw_fastq_1.fastq
Approx 40% complete for raw_fastq_1.fastq
Approx 45% complete for raw_fastq_1.fastq
Approx 50% complete for raw_fastq_1.fastq
Approx 55% complete for raw_fastq_1.fastq
Approx 60% complete for raw_fastq_1.fastq
Approx 65% complete for raw_fastq_1.fastq
Approx 70% complete for raw_fastq_1.fastq
Approx 75% complete for raw_fastq_1.fastq
Approx 80% complete for raw_fastq_1.fastq
Approx 85% complete for raw_fastq_1.fastq
Approx 90% complete for raw_fastq_1.fastq
```

```
Approx 95% complete for raw_fastq_1.fastq
Analysis complete for raw_fastq_1.fastq
```
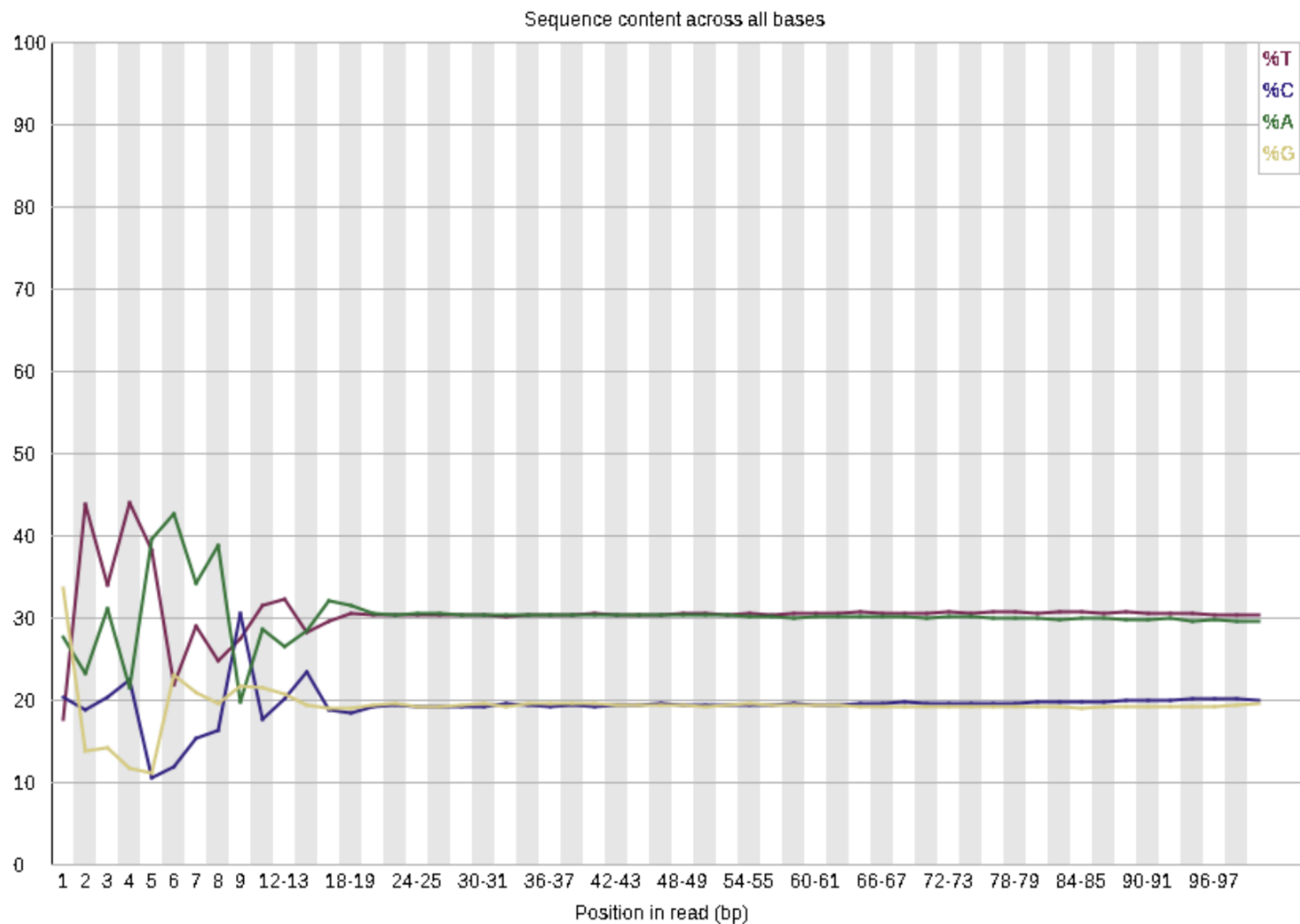
```
Started analysis of raw_fastq_2.fastq
Approx 5% complete for raw_fastq_2.fastq
Approx 10% complete for raw_fastq_2.fastq
Approx 15% complete for raw_fastq_2.fastq
Approx 20% complete for raw_fastq_2.fastq
Approx 25% complete for raw_fastq_2.fastq
Approx 30% complete for raw_fastq_2.fastq
Approx 35% complete for raw_fastq_2.fastq
Approx 40% complete for raw_fastq_2.fastq
Approx 45% complete for raw_fastq_2.fastq
Approx 50% complete for raw_fastq_2.fastq
Approx 55% complete for raw_fastq_2.fastq
Approx 60% complete for raw_fastq_2.fastq
Approx 65% complete for raw_fastq_2.fastq
Approx 70% complete for raw_fastq_2.fastq
Approx 75% complete for raw_fastq_2.fastq
Approx 80% complete for raw_fastq_2.fastq
Approx 85% complete for raw_fastq_2.fastq
Approx 90% complete for raw_fastq_2.fastq
Approx 95% complete for raw_fastq_2.fastq
Analysis complete for raw_fastq_2.fastq
```

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

⚠️ [Per tile sequence quality](#)

✅ [Per sequence quality scores](#)

❌ [Per base sequence content](#)

✅ [Per sequence GC content](#)

✅ [Per base N content](#)

✅ [Sequence Length Distribution](#)

✅ [Sequence Duplication Levels](#)

✅ [Overrepresented sequences](#)

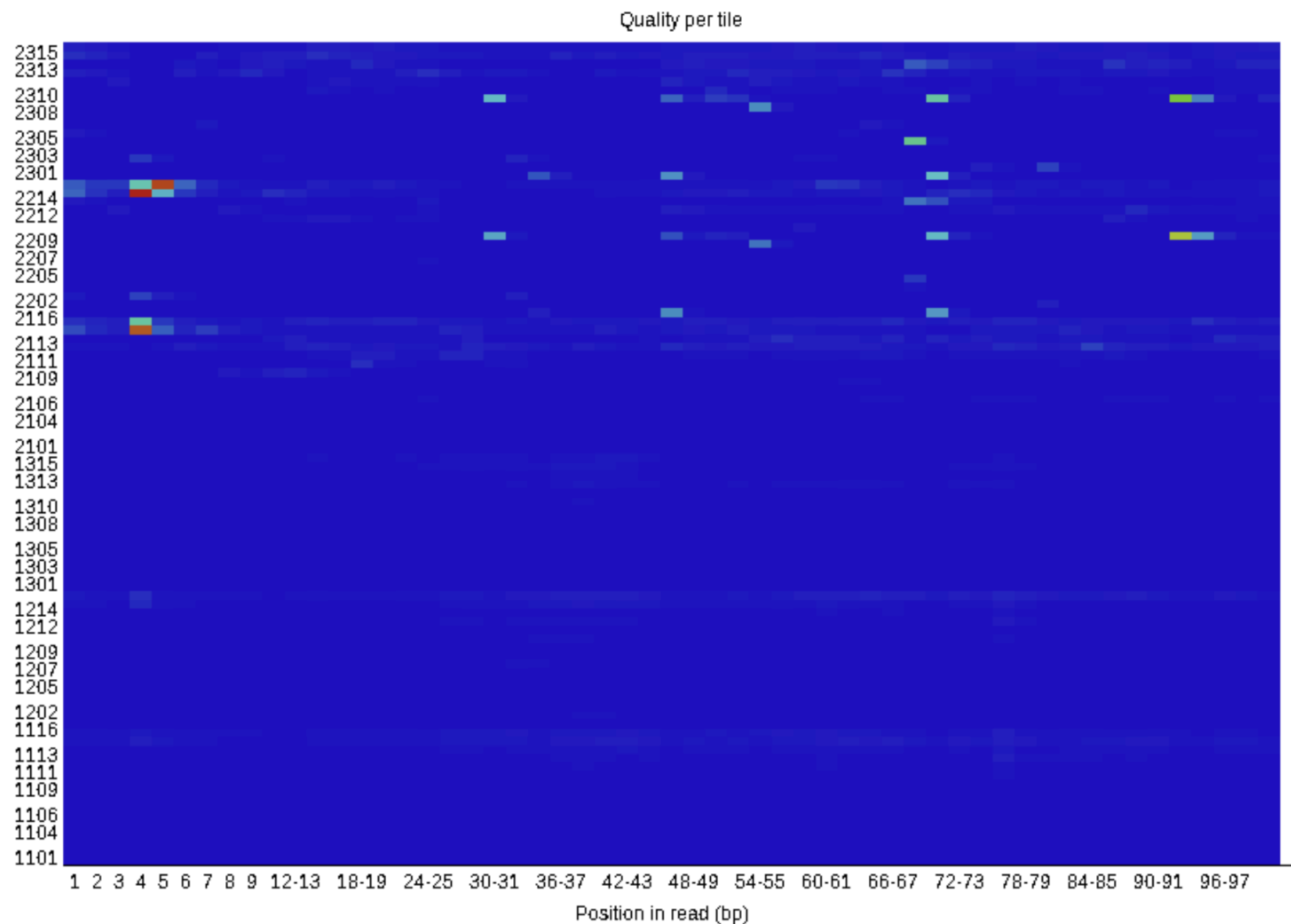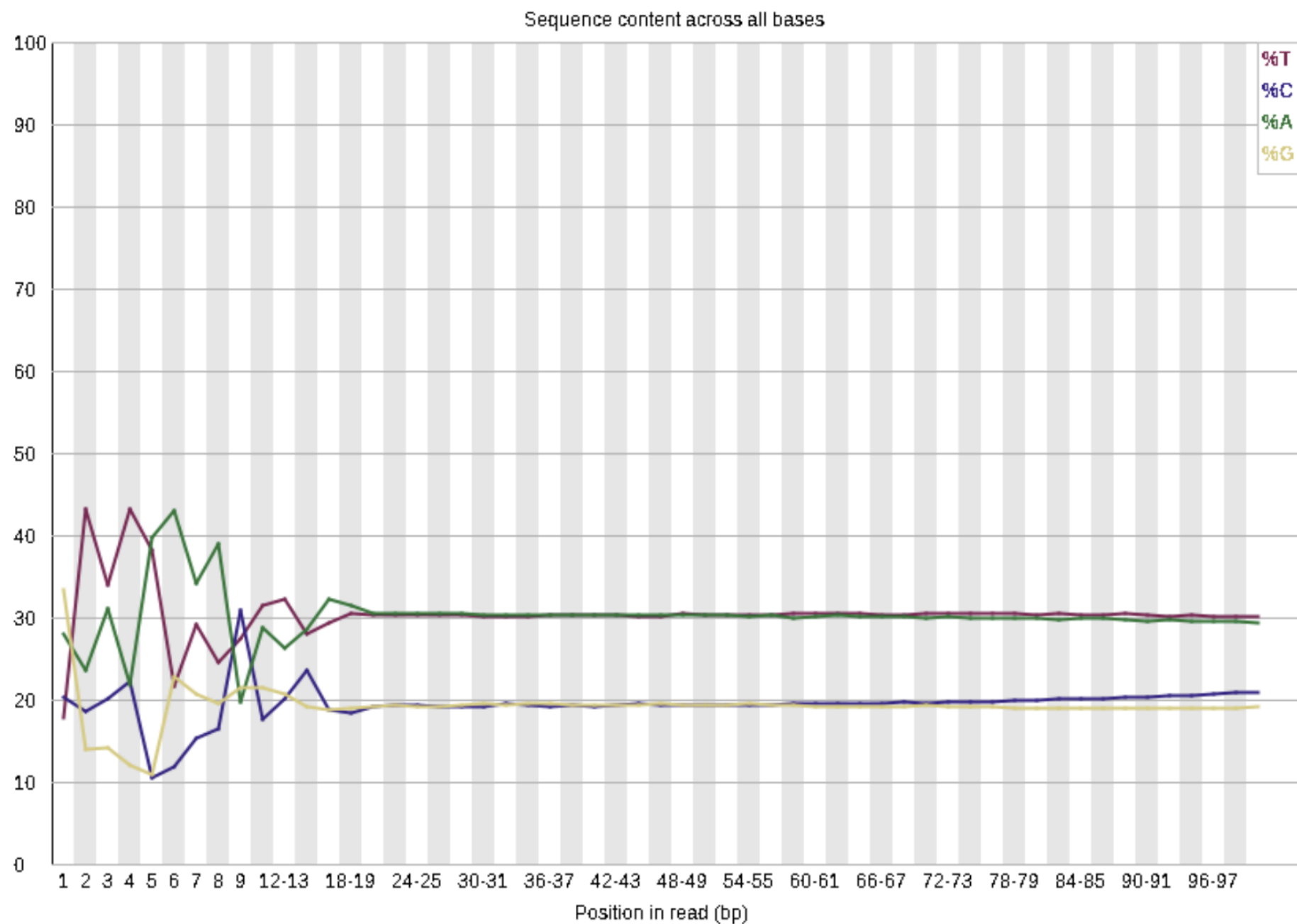⚠️ [Adapter Content](#)

✅ Basic Statistics

Measure	Value
Filename	raw_fastq_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1486392
Total Bases	150.1 Mbp
Sequences flagged as poor quality	0
Sequence length	101
%GC	39

✅ Per base sequence quality

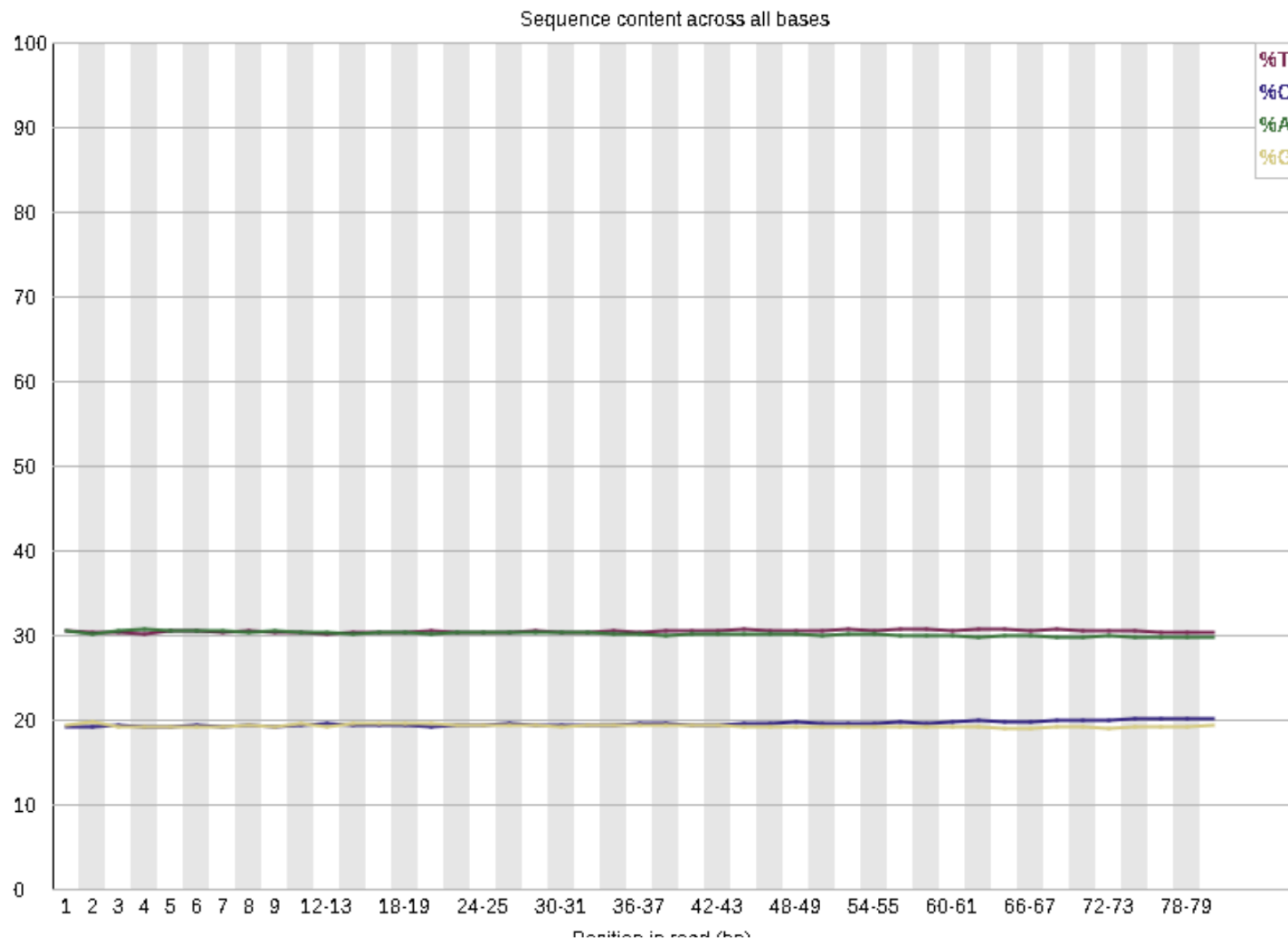# Per base sequence content

Sequence content across all bases

Summary

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✅ Basic Statistics

Measure	Value
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Total Sequences	1486392
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✅ Per base sequence quality

Per tile sequence quality

Quality per tile

Per base sequence content

Sequence content across all bases

Summary

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✅ Basic Statistics

Measure	Value
Filename	SRR5462773_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1456579
Total Bases	117.6 Mbp
Sequences flagged as poor quality	0
Sequence length	50-81
%GC	39

✅ Per base sequence quality

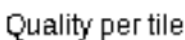# Per base sequence content

Sequence content across all bases

Summary

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 [Per sequence quality scores](#)

 [Per base sequence content](#)

 [Per sequence GC content](#)

 [Per base N content](#)

 [Sequence Length Distribution](#)

 [Sequence Duplication Levels](#)

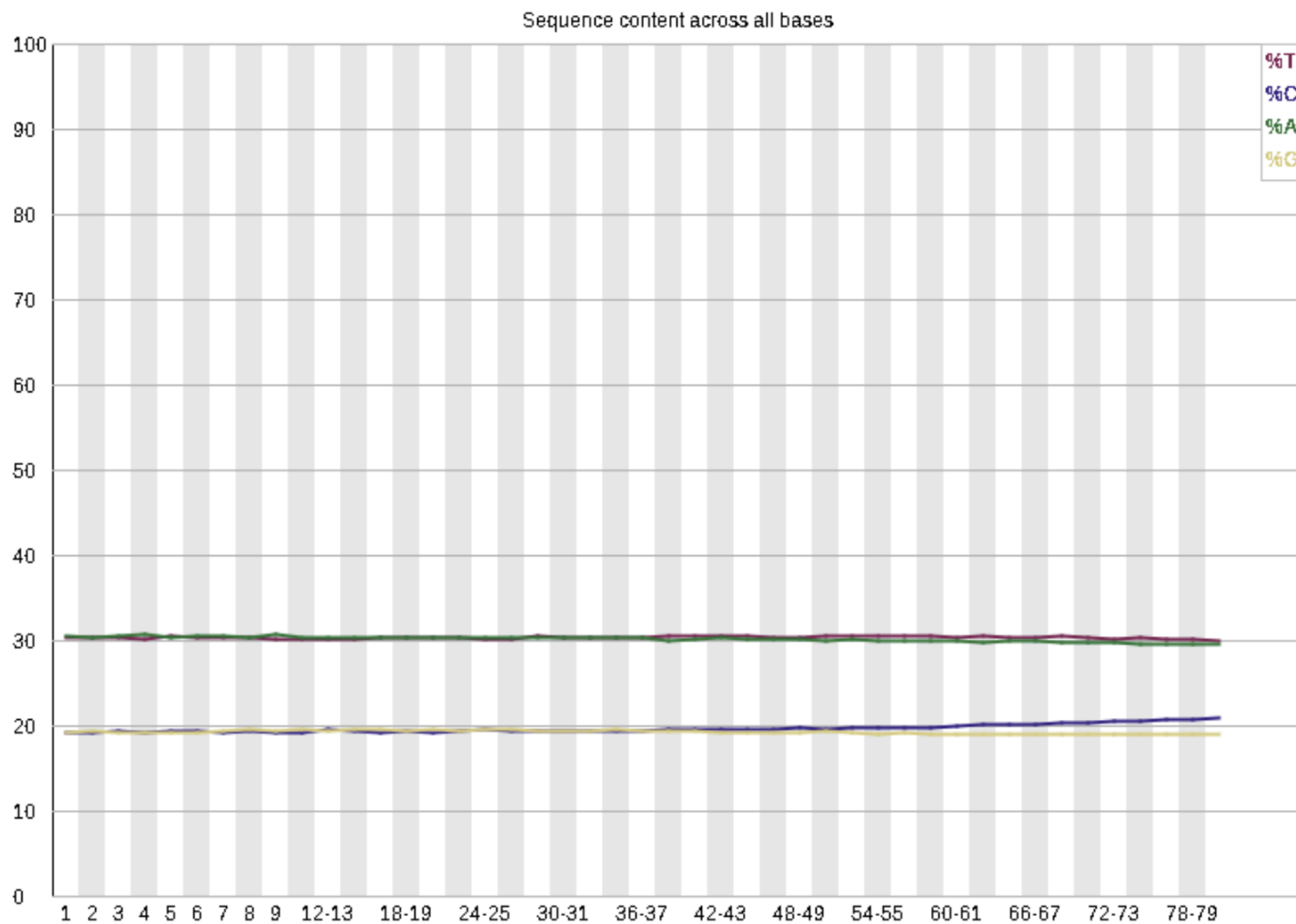 [Overrepresented sequences](#)

 [Adapter Content](#)

Basic Statistics

Measure	Value
Filename	SRR5462773_2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1456579
Total Bases	117.7 Mbp
Sequences flagged as poor quality	0
Sequence length	50-81
%GC	39

Per base sequence quality

Per tile sequence quality

Quality per tile

Position in read (bp)

Per base sequence content

Position in read (bp)