

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:54:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506023.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1506023 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506023.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:54:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506023.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,102,974
Mapped reads	4,524,431 / 74.13%
Unmapped reads	1,578,543 / 25.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	170 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	368,563 / 6.04%
Duplication rate	5.92%
Clipped reads	751,969 / 12.32%

2.2. ACGT Content

Number/percentage of A's	62,136,050 / 29.6%
Number/percentage of C's	43,443,265 / 20.7%
Number/percentage of T's	60,292,578 / 28.72%
Number/percentage of G's	43,325,027 / 20.64%
Number/percentage of N's	701,192 / 0.33%
GC Percentage	41.34%

2.3. Coverage

Mean	0.0678

Standard Deviation	0.669
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2.4. Mapping Quality

Mean Mapping Quality	44.08
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2.5. Mismatches and indels

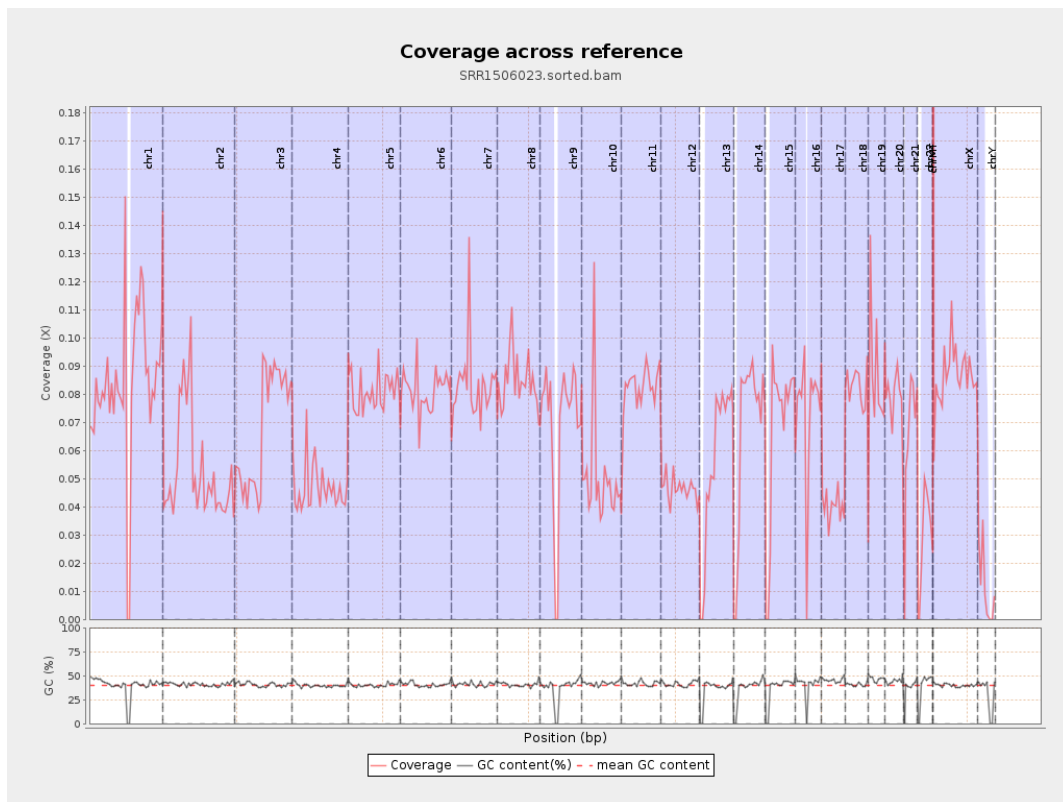
General error rate	0.81%
Mismatches	1,681,540
Insertions	8,809
Mapped reads with at least one insertion	0.19%
Deletions	29,448
Mapped reads with at least one deletion	0.65%
Homopolymer indels	45.56%

2.6. Chromosome stats

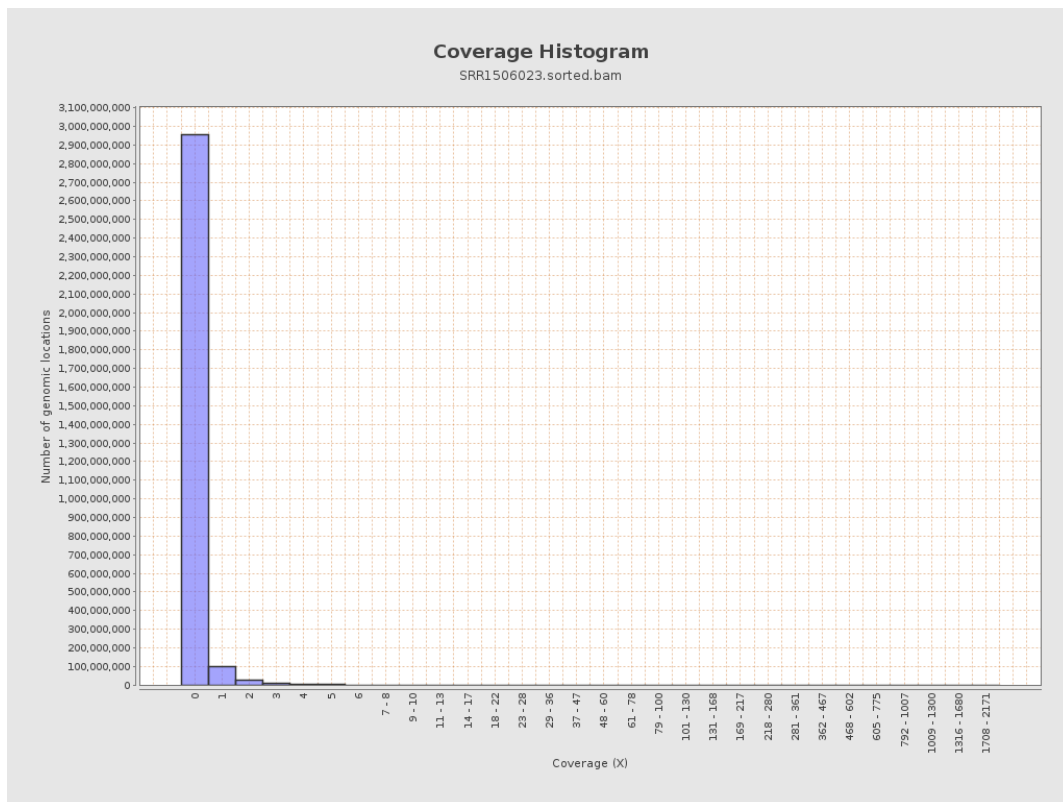
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20923617	0.0839	1.5122
chr2	243199373	12878316	0.053	0.494
chr3	198022430	13301693	0.0672	0.3713
chr4	191154276	8929978	0.0467	0.3215
chr5	180915260	14641568	0.0809	0.4057
chr6	171115067	13912710	0.0813	0.4742
chr7	159138663	13257404	0.0833	0.8822

chr8	146364022	12400372	0.0847	0.8135
chr9	141213431	9835673	0.0697	0.4788
chr10	135534747	6748945	0.0498	0.6718
chr11	135006516	11073710	0.082	0.5345
chr12	133851895	6212651	0.0464	0.3223
chr13	115169878	6506043	0.0565	0.3329
chr14	107349540	7380468	0.0688	0.7212
chr15	102531392	6774883	0.0661	0.36
chr16	90354753	6522075	0.0722	0.4346
chr17	81195210	3273536	0.0403	0.319
chr18	78077248	6451053	0.0826	0.7434
chr19	59128983	5125069	0.0867	1.0428
chr20	63025520	4969107	0.0788	0.4047
chr21	48129895	3153496	0.0655	0.4025
chr22	51304566	1515437	0.0295	0.238
chrMT	16571	27562	1.6633	2.0917
chrX	155270560	13450454	0.0866	0.4721
chrY	59373566	673368	0.0113	0.2205

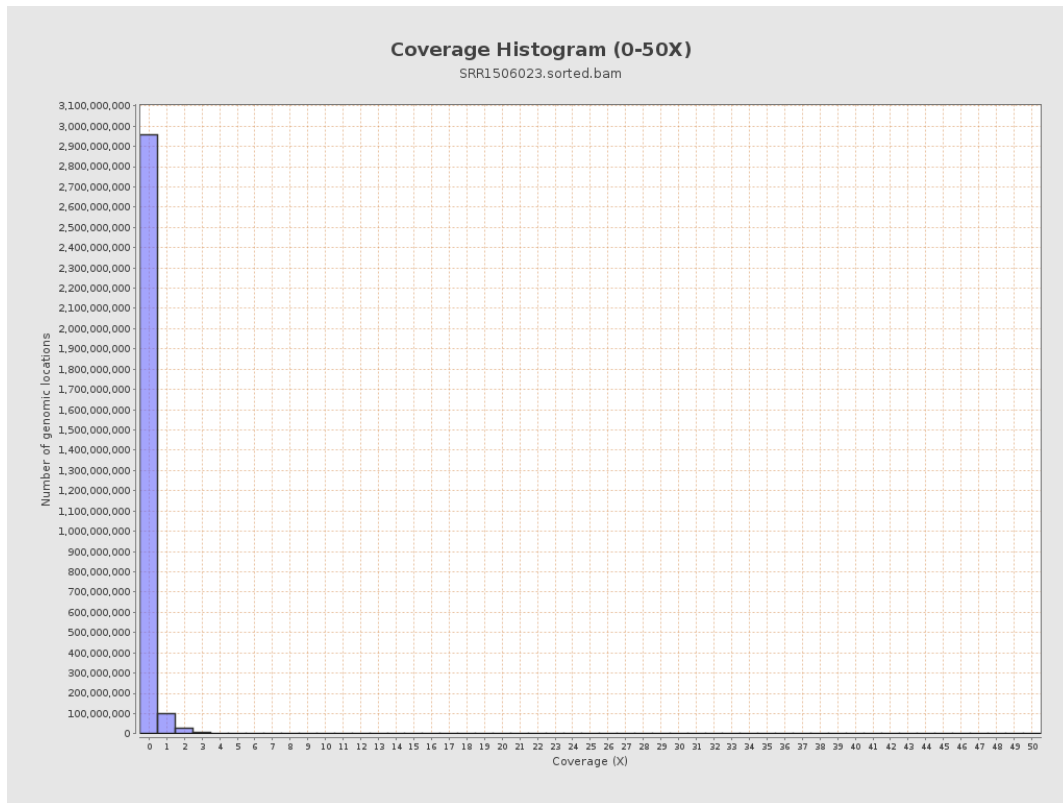
3. Results : Coverage across reference



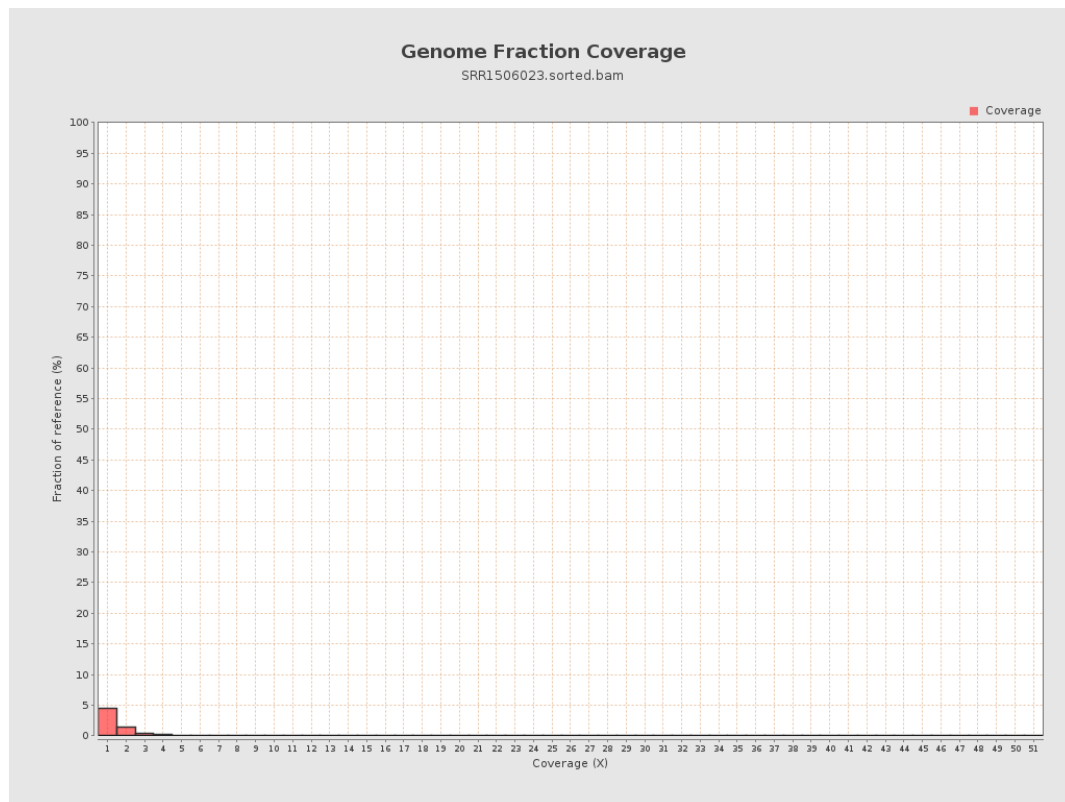
4. Results : Coverage Histogram



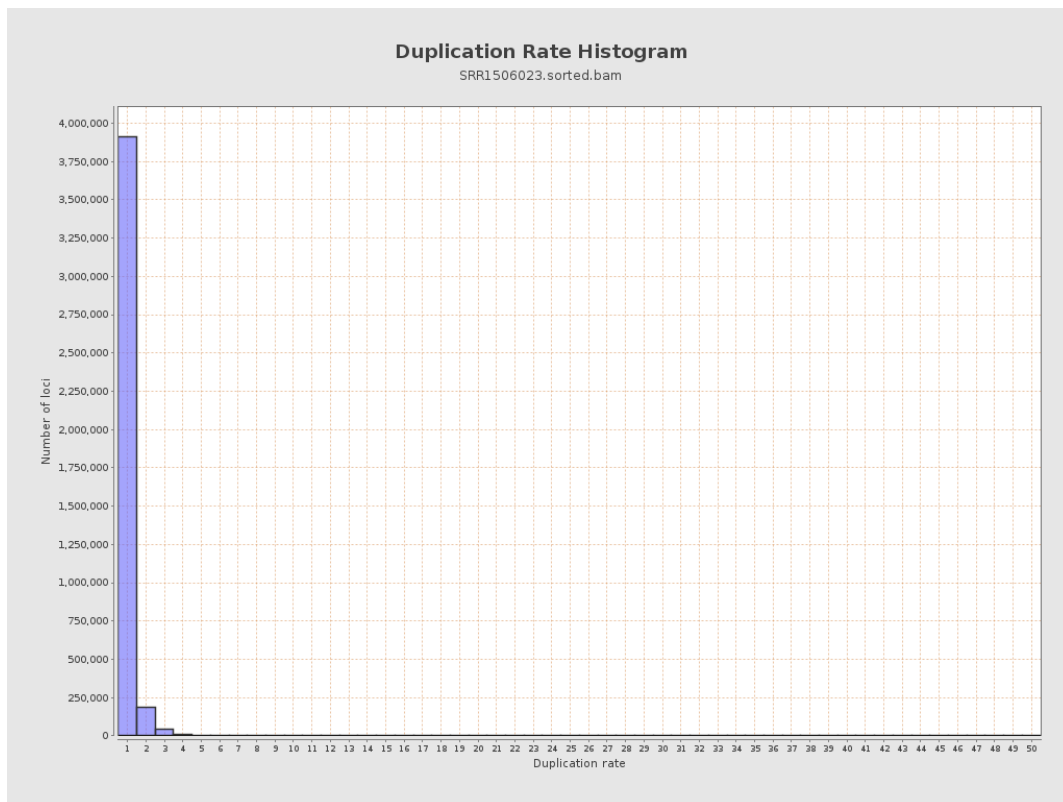
5. Results : Coverage Histogram (0-50X)



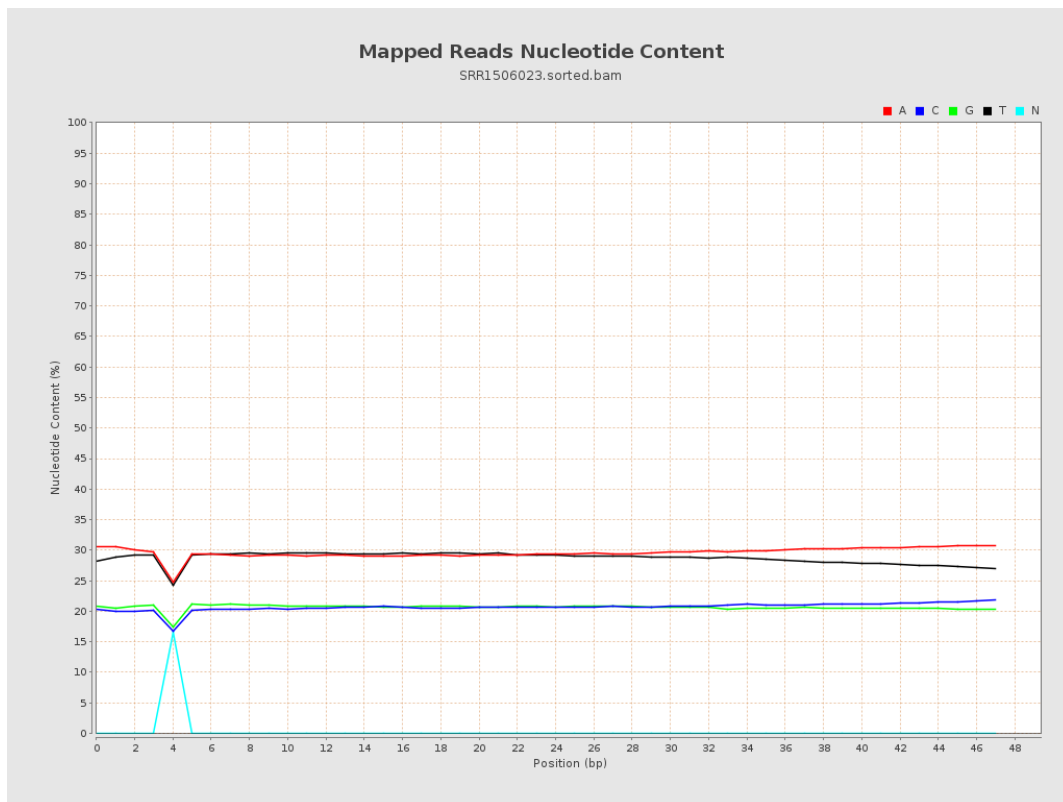
6. Results : Genome Fraction Coverage



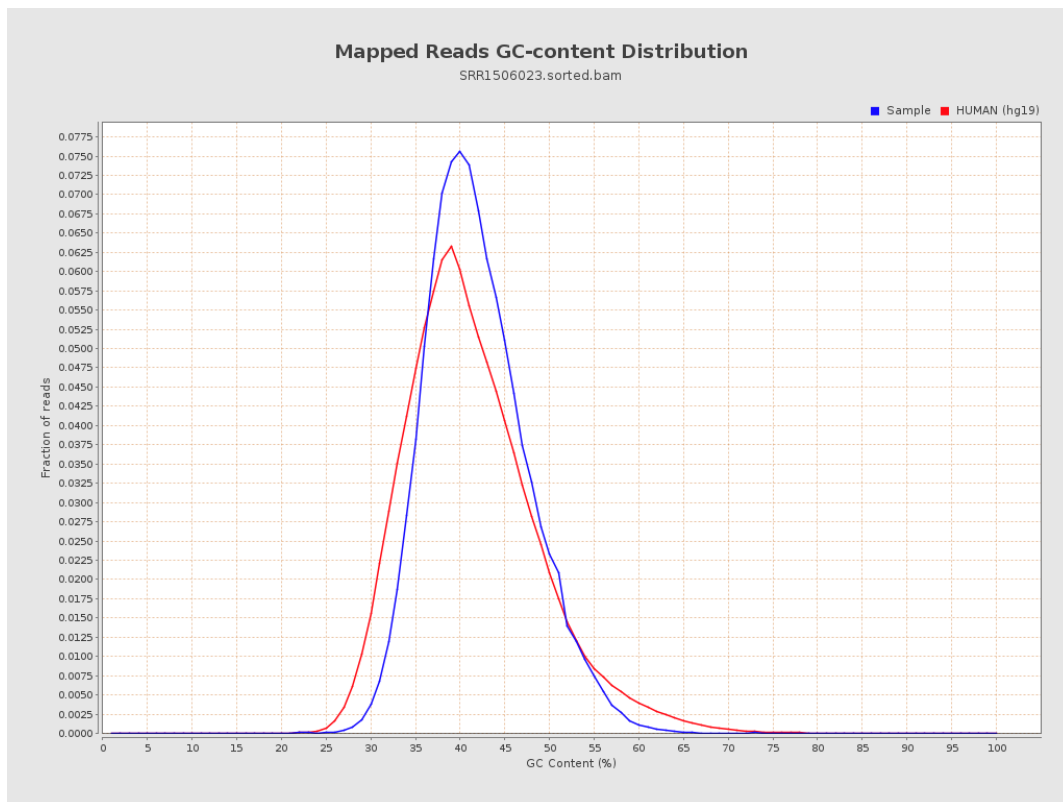
7. Results : Duplication Rate Histogram



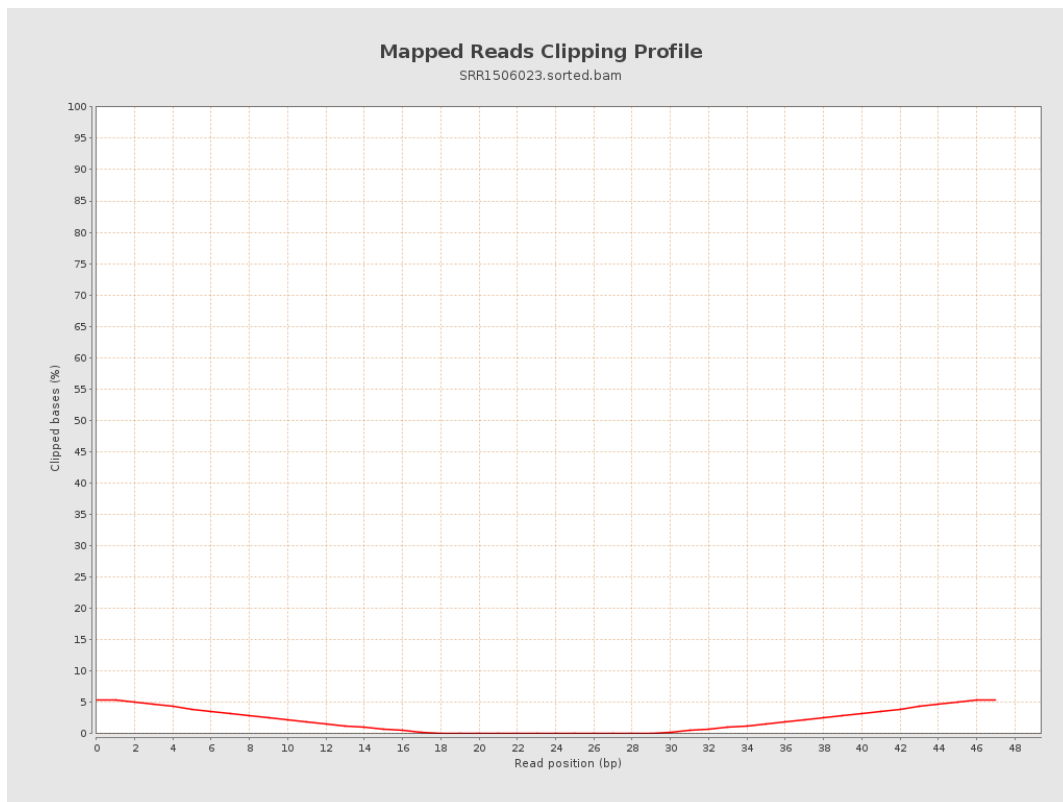
8. Results : Mapped Reads Nucleotide Content



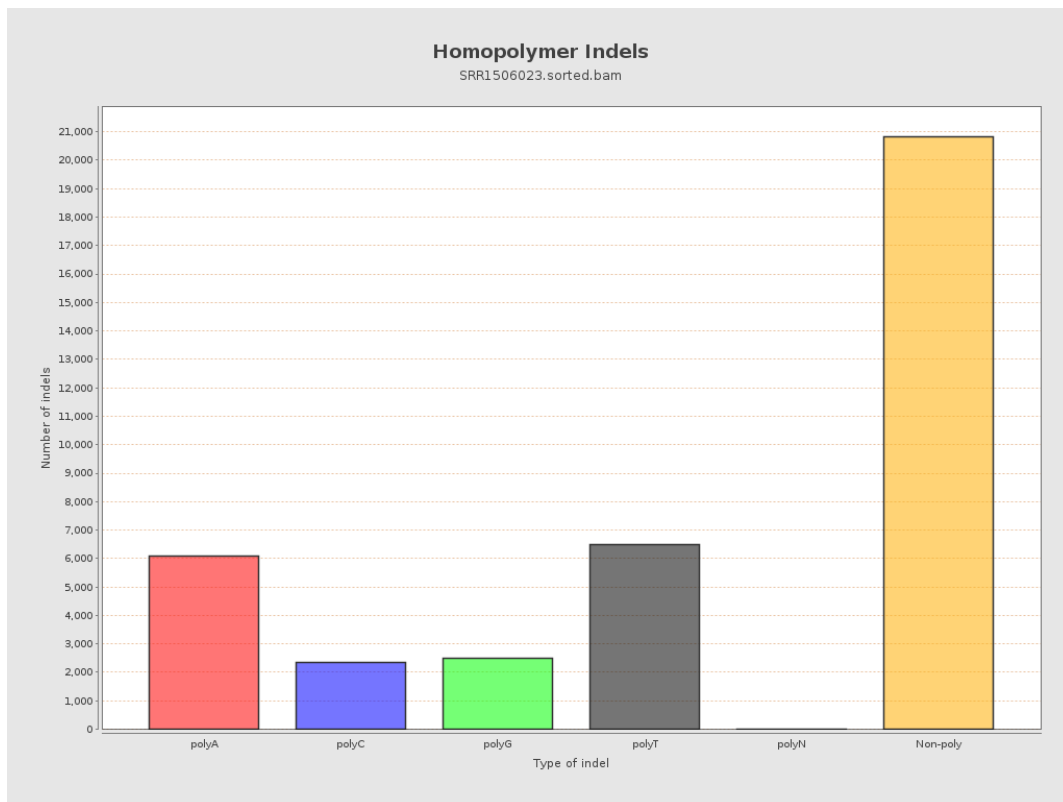
9. Results : Mapped Reads GC-content Distribution



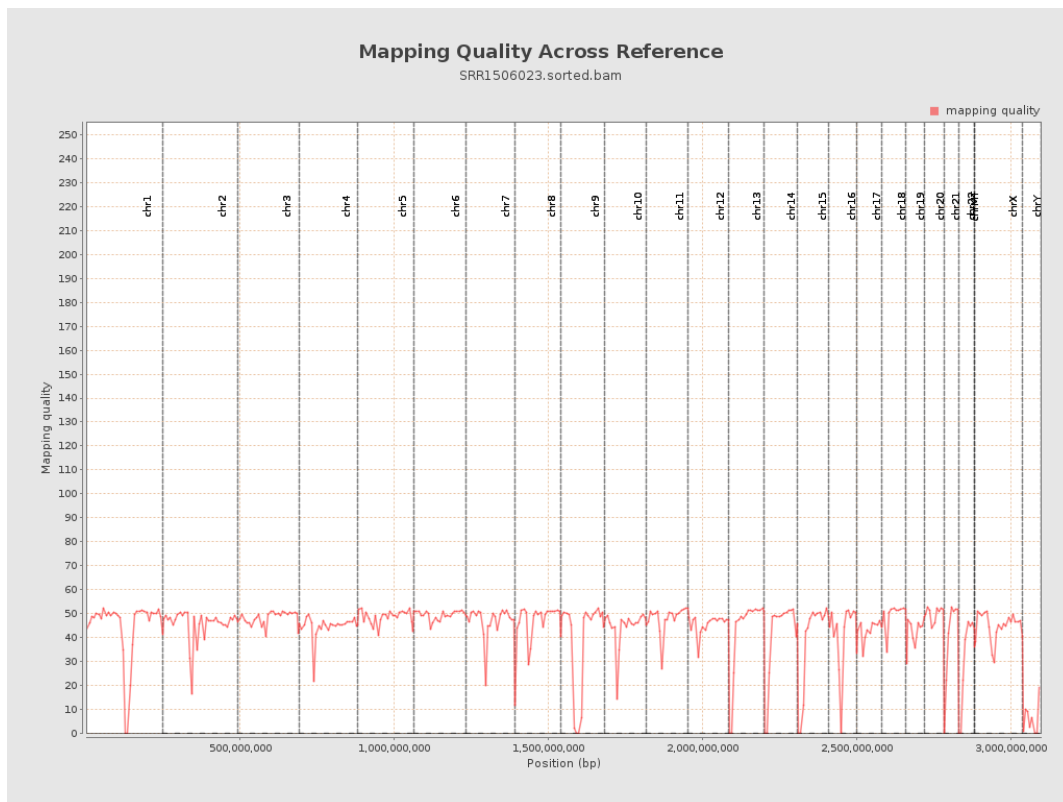
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

