

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 16:57:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971301.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_SRR2971301 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971301.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 16:57:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971301.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,308,239
Mapped reads	8,744,770 / 84.83%
Unmapped reads	1,563,469 / 15.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	590,626 / 5.73%
Duplication rate	5.43%
Clipped reads	783,600 / 7.6%

2.2. ACGT Content

Number/percentage of A's	99,114,034 / 28.73%
Number/percentage of C's	70,171,129 / 20.34%
Number/percentage of T's	102,605,981 / 29.74%
Number/percentage of G's	73,089,223 / 21.19%
Number/percentage of N's	2,552 / 0%
GC Percentage	41.53%

2.3. Coverage

Mean	0.1115
Standard Deviation	0.9031

2.4. Mapping Quality

Mean Mapping Quality	39.95
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2.5. Mismatches and indels

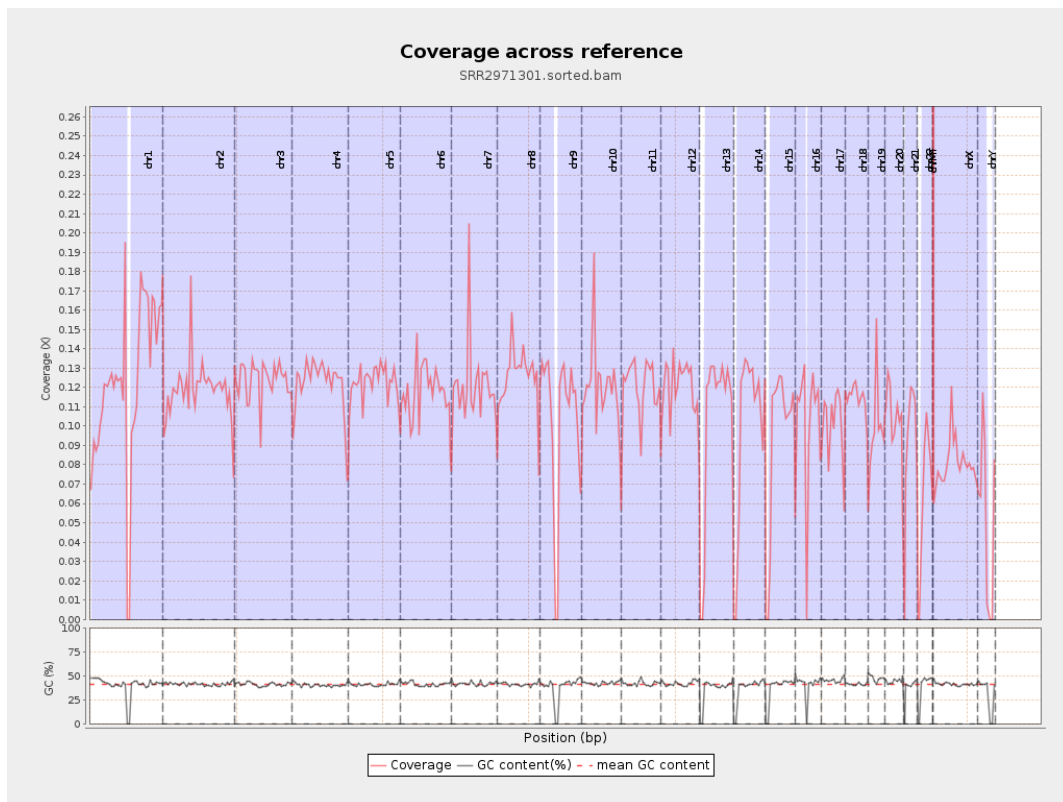
General error rate	0.28%
Mismatches	938,060
Insertions	11,425
Mapped reads with at least one insertion	0.13%
Deletions	26,681
Mapped reads with at least one deletion	0.3%
Homopolymer indels	40.36%

2.6. Chromosome stats

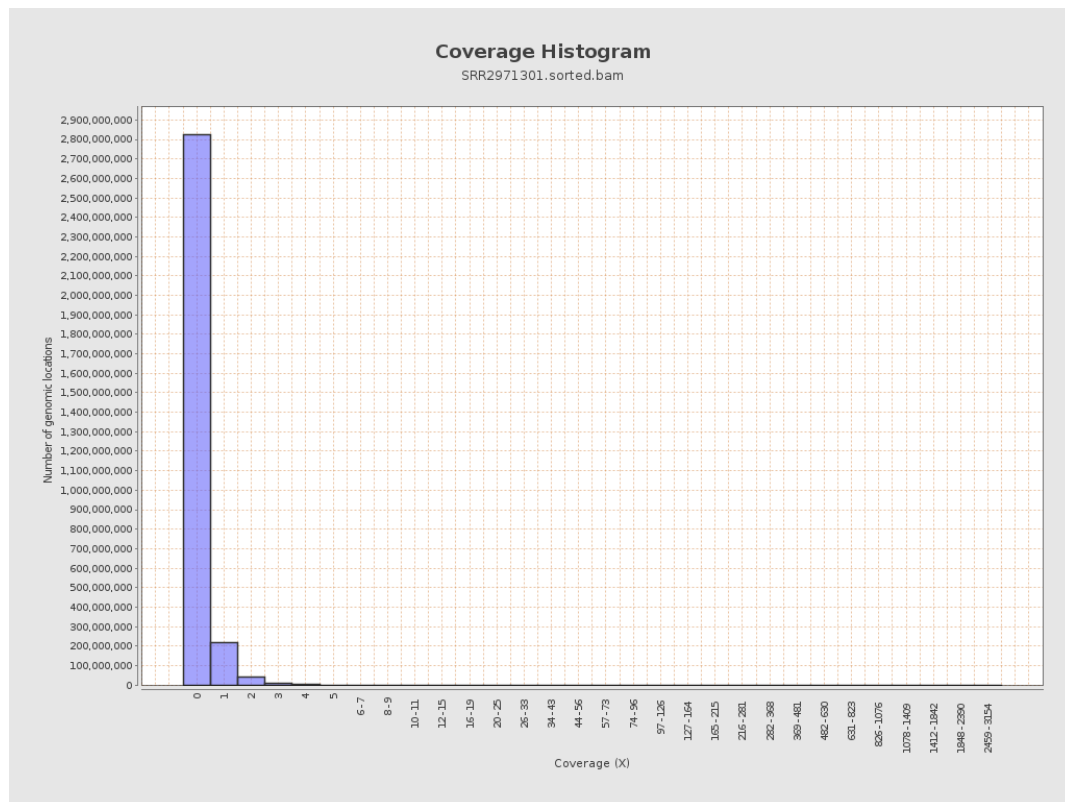
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	30577778	0.1227	1.9379
chr2	243199373	28884013	0.1188	0.6993
chr3	198022430	24548938	0.124	0.4322
chr4	191154276	23346782	0.1221	0.4547
chr5	180915260	22043273	0.1218	0.4446
chr6	171115067	20230866	0.1182	0.533
chr7	159138663	19186094	0.1206	1.1755
chr8	146364022	18424311	0.1259	1.6174

chr9	141213431	14702744	0.1041	0.7239
chr10	135534747	16371664	0.1208	0.8002
chr11	135006516	16255636	0.1204	0.7169
chr12	133851895	16123711	0.1205	0.4426
chr13	115169878	11813274	0.1026	0.3834
chr14	107349540	10775942	0.1004	0.485
chr15	102531392	9467861	0.0923	0.3675
chr16	90354753	9007816	0.0997	0.4593
chr17	81195210	8267880	0.1018	0.4567
chr18	78077248	8984042	0.1151	1.3111
chr19	59128983	5926142	0.1002	1.5835
chr20	63025520	6651992	0.1055	0.437
chr21	48129895	4410865	0.0916	0.4561
chr22	51304566	3285090	0.064	0.3885
chrMT	16571	49493	2.9867	3.4283
chrX	155270560	12517337	0.0806	0.4571
chrY	59373566	3163032	0.0533	0.4484

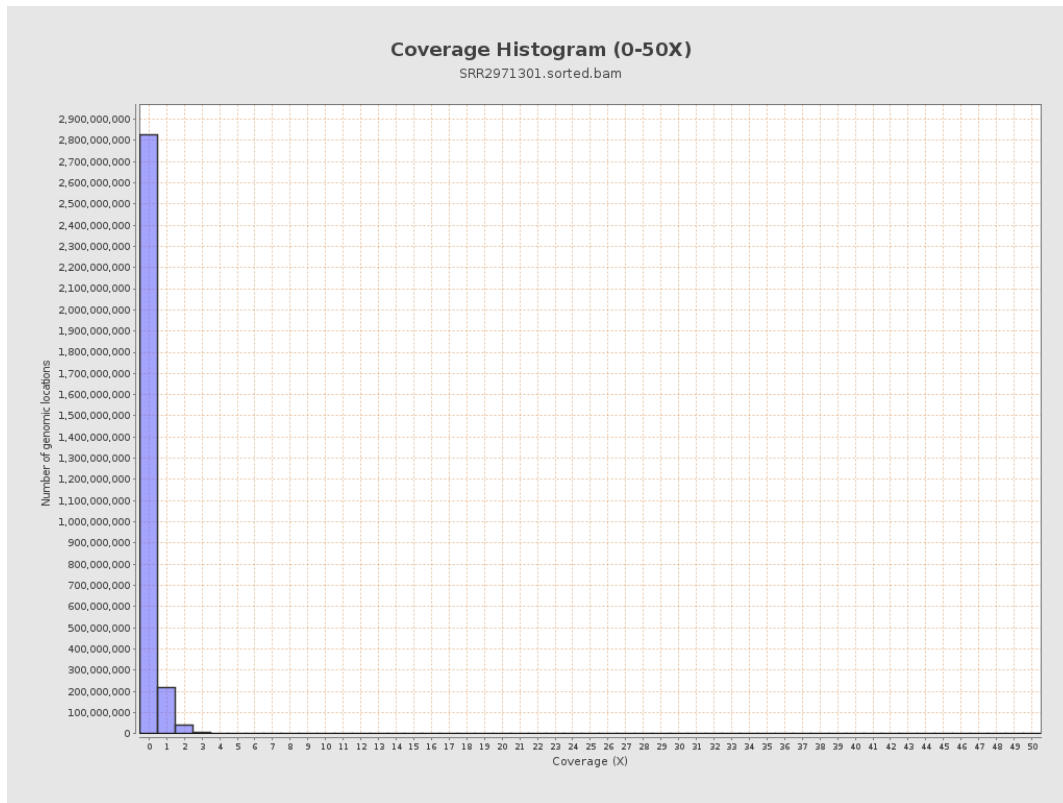
3. Results : Coverage across reference



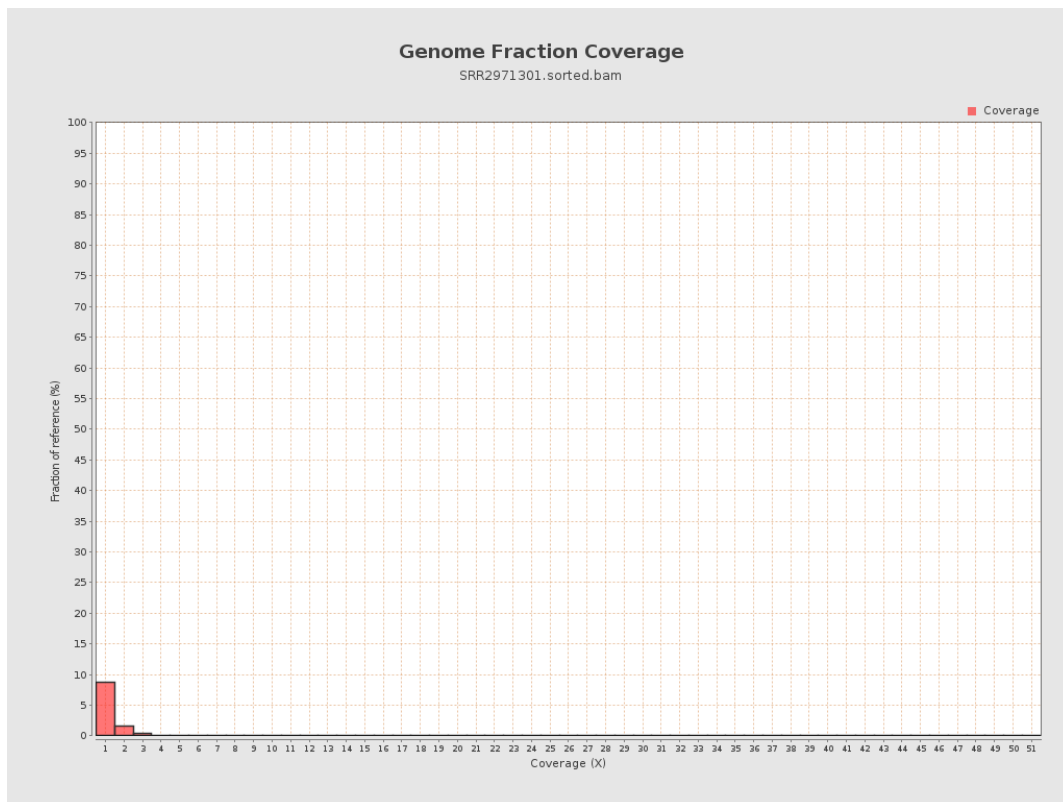
4. Results : Coverage Histogram



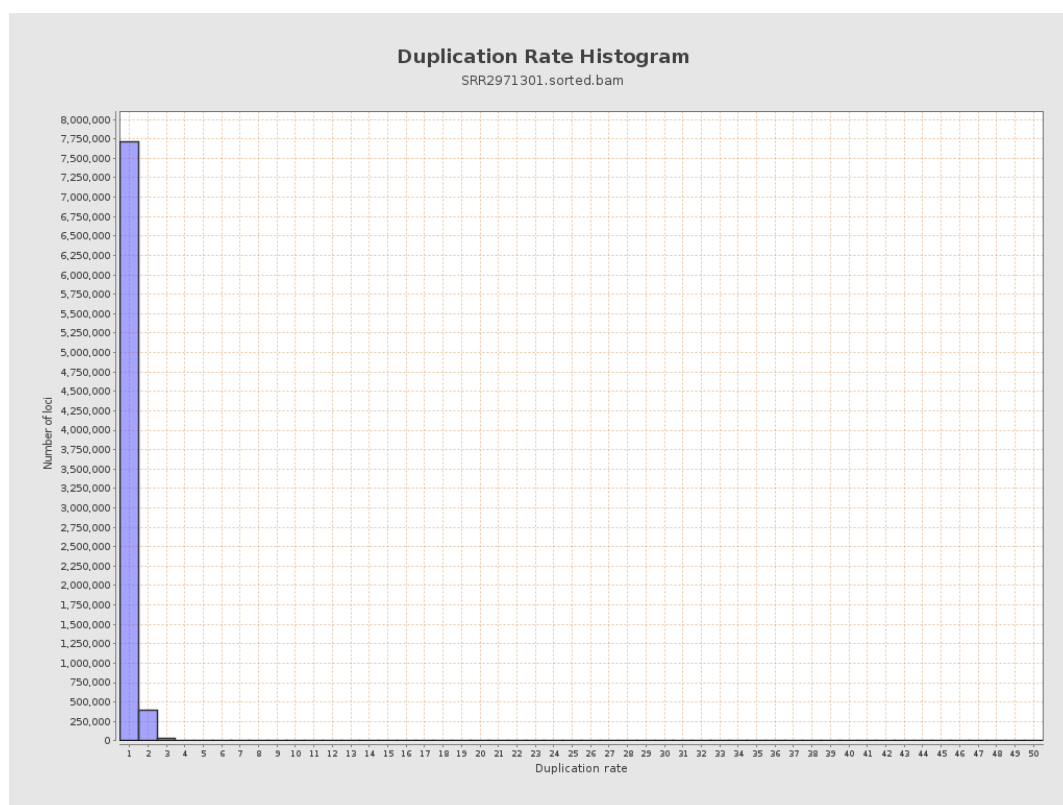
5. Results : Coverage Histogram (0-50X)



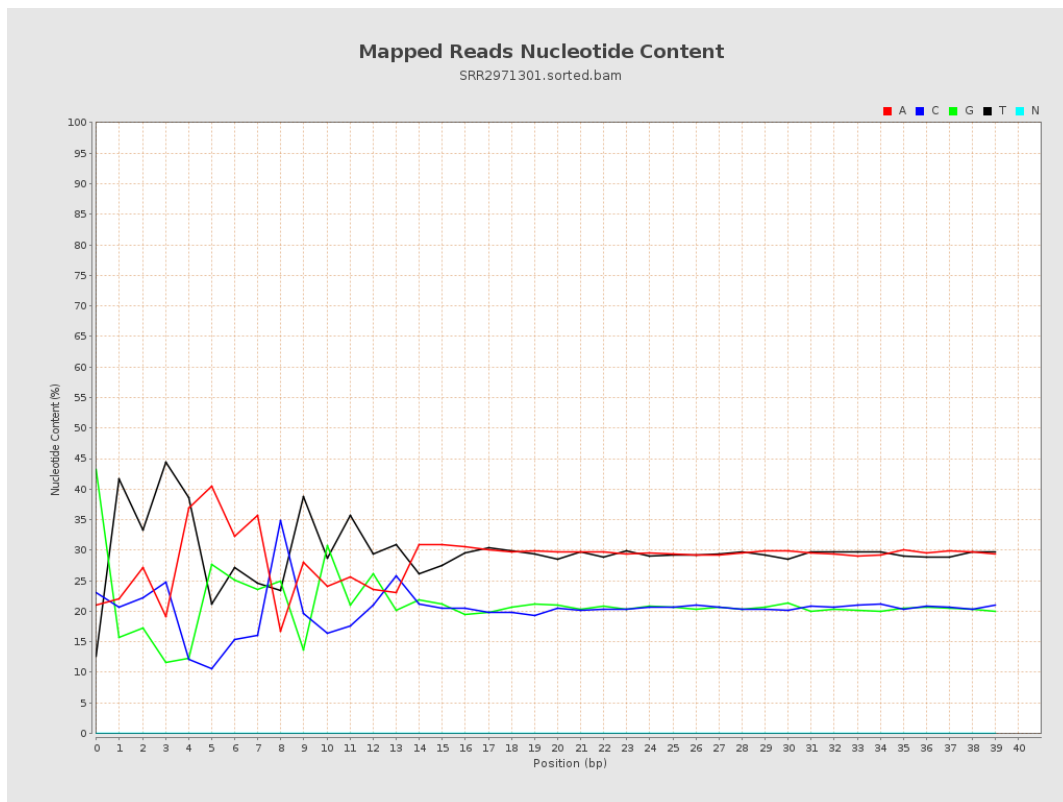
6. Results : Genome Fraction Coverage



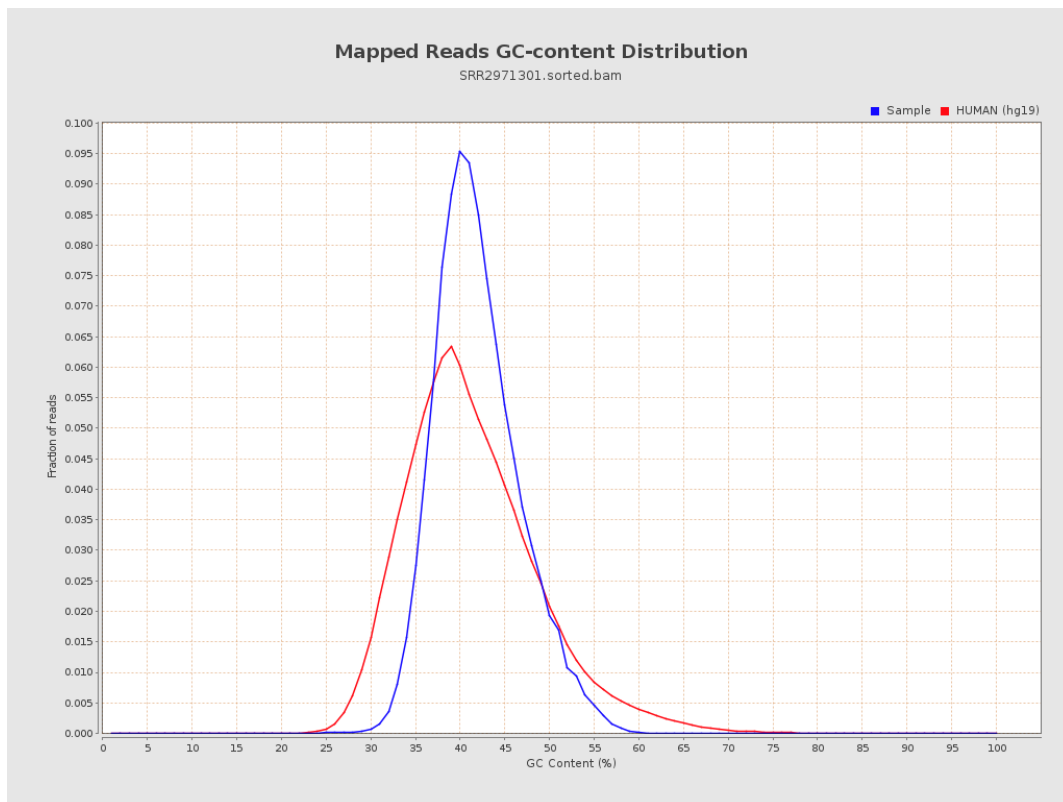
7. Results : Duplication Rate Histogram



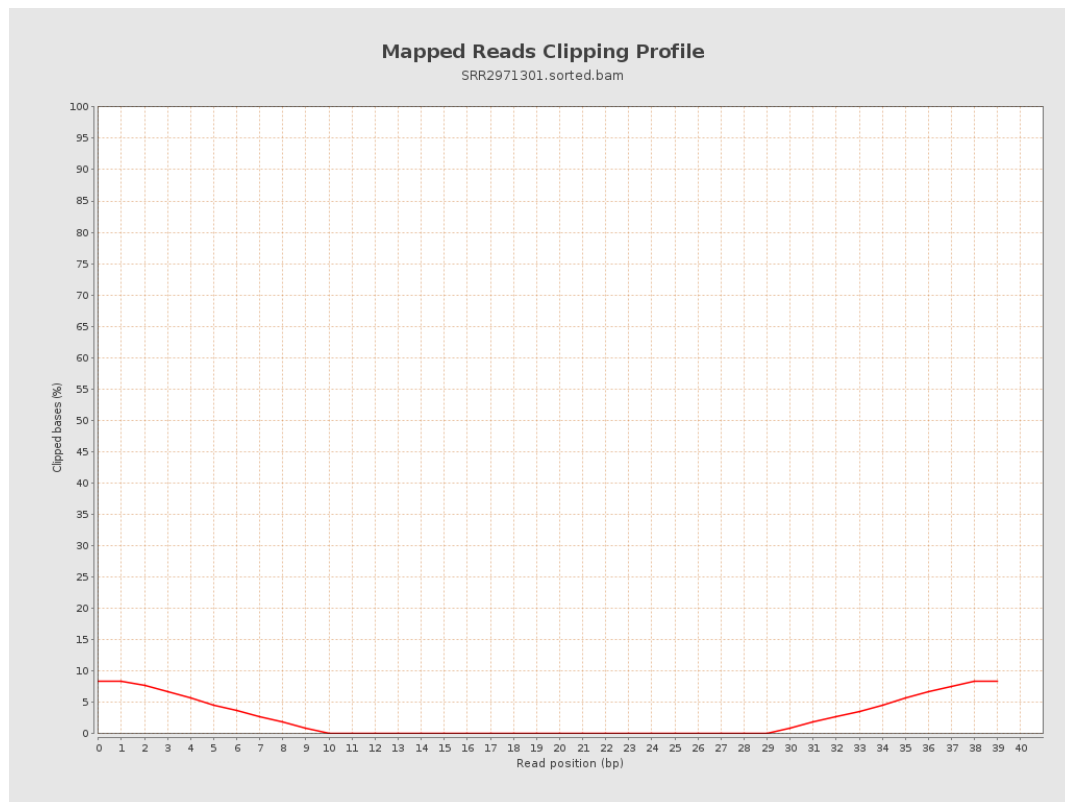
8. Results : Mapped Reads Nucleotide Content



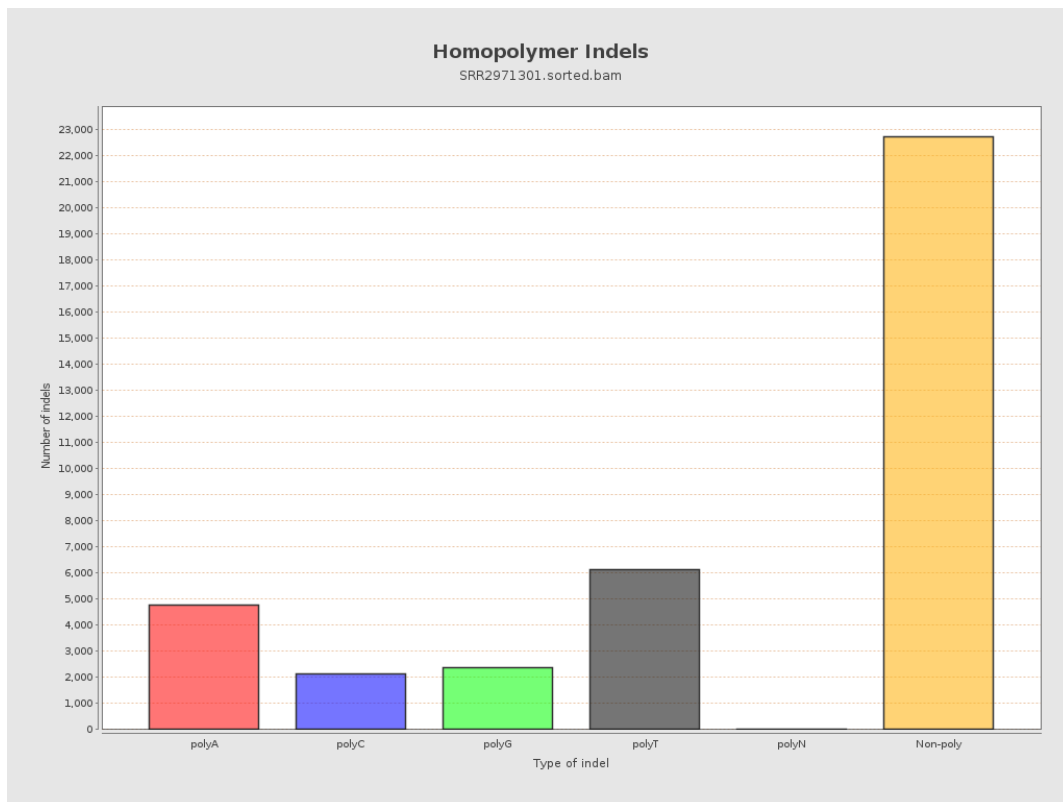
9. Results : Mapped Reads GC-content Distribution



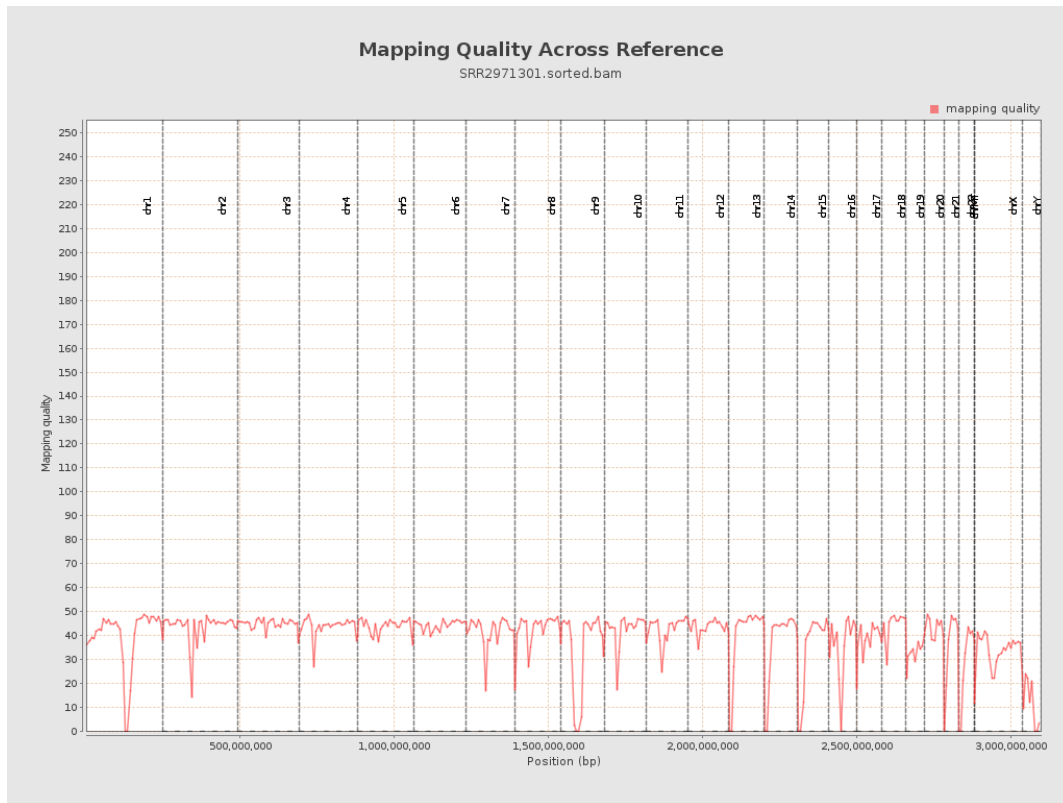
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

