

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:57:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081976.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_SRR3081976 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081976.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:57:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,884,460
Mapped reads	2,673,196 / 92.68%
Unmapped reads	211,264 / 7.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,397 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	129,765 / 4.5%
Duplication rate	3.69%
Clipped reads	941,889 / 32.65%

2.2. ACGT Content

Number/percentage of A's	52,584,939 / 28.65%
Number/percentage of C's	33,779,577 / 18.4%
Number/percentage of T's	58,353,365 / 31.79%
Number/percentage of G's	38,801,778 / 21.14%
Number/percentage of N's	23,751 / 0.01%
GC Percentage	39.54%

2.3. Coverage

Mean	0.0593

Standard Deviation	0.5264
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2.4. Mapping Quality

Mean Mapping Quality	46.76
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2.5. Mismatches and indels

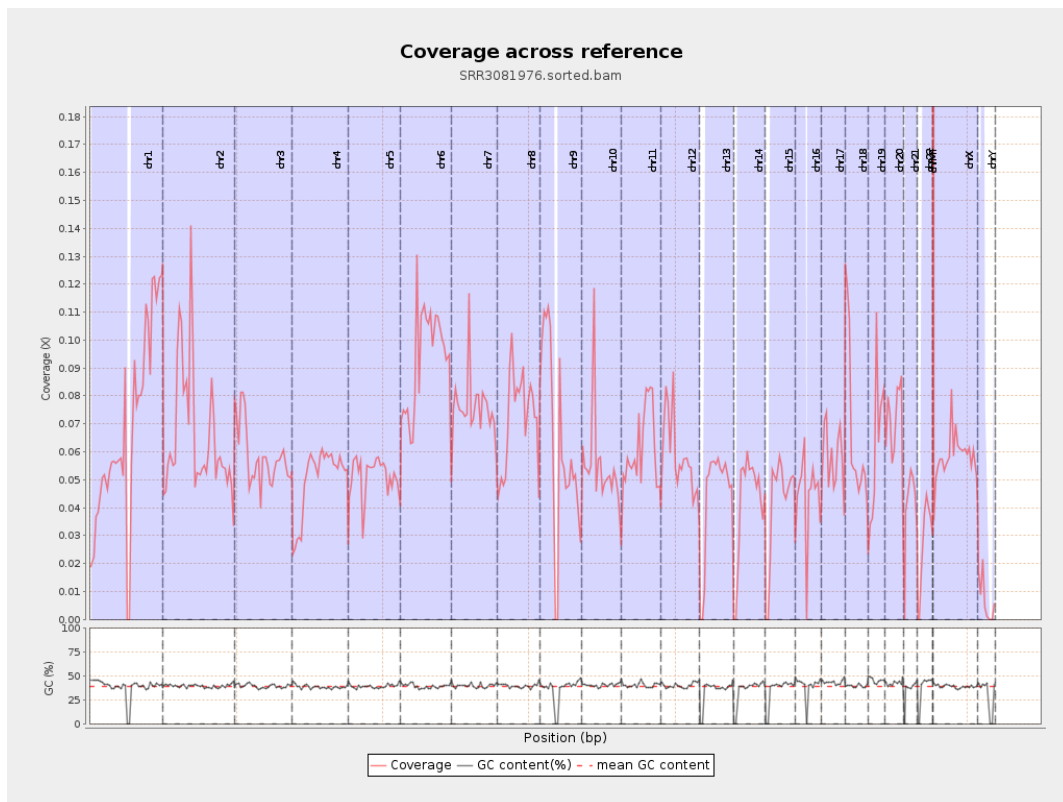
General error rate	0.77%
Mismatches	1,385,290
Insertions	13,196
Mapped reads with at least one insertion	0.49%
Deletions	38,363
Mapped reads with at least one deletion	1.42%
Homopolymer indels	48.39%

2.6. Chromosome stats

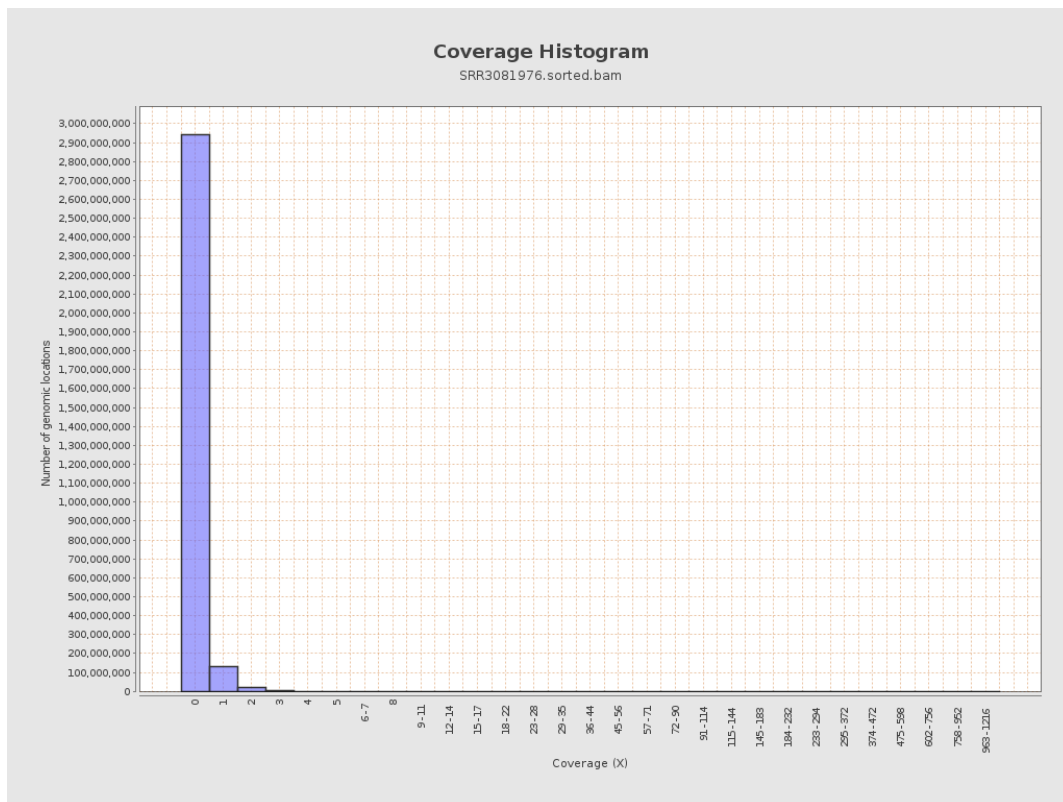
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16991372	0.0682	0.9252
chr2	243199373	16095886	0.0662	0.655
chr3	198022430	11586512	0.0585	0.2779
chr4	191154276	9655126	0.0505	0.2768
chr5	180915260	9210350	0.0509	0.2606
chr6	171115067	16028565	0.0937	0.4811
chr7	159138663	12050075	0.0757	0.7338

chr8	146364022	10542735	0.072	0.8289
chr9	141213431	8936301	0.0633	0.5304
chr10	135534747	7447252	0.0549	0.5451
chr11	135006516	8266988	0.0612	0.3783
chr12	133851895	7807911	0.0583	0.2938
chr13	115169878	5077856	0.0441	0.2378
chr14	107349540	4551011	0.0424	0.2657
chr15	102531392	4229300	0.0412	0.2308
chr16	90354753	3921091	0.0434	0.2944
chr17	81195210	4749157	0.0585	0.314
chr18	78077248	5236969	0.0671	0.8895
chr19	59128983	3682899	0.0623	0.725
chr20	63025520	4529867	0.0719	0.3151
chr21	48129895	1952909	0.0406	0.26
chr22	51304566	1423381	0.0277	0.1858
chrMT	16571	164496	9.9267	5.6488
chrX	155270560	9067063	0.0584	0.3346
chrY	59373566	406316	0.0068	0.1601

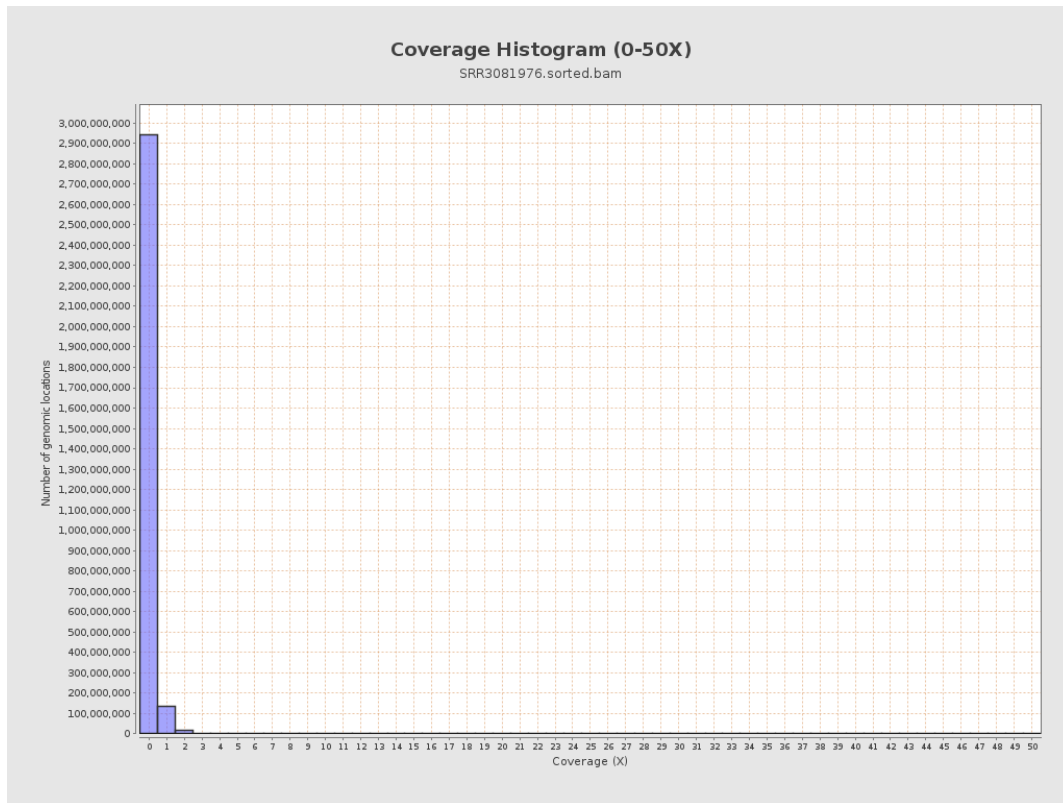
3. Results : Coverage across reference



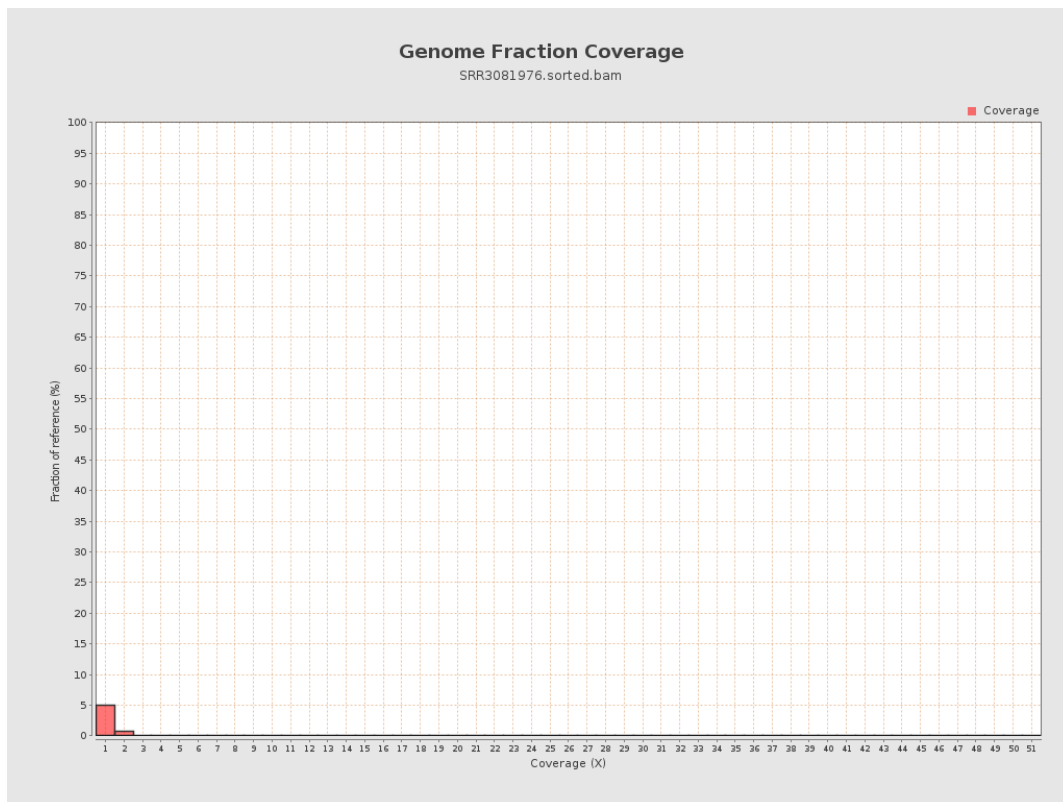
4. Results : Coverage Histogram



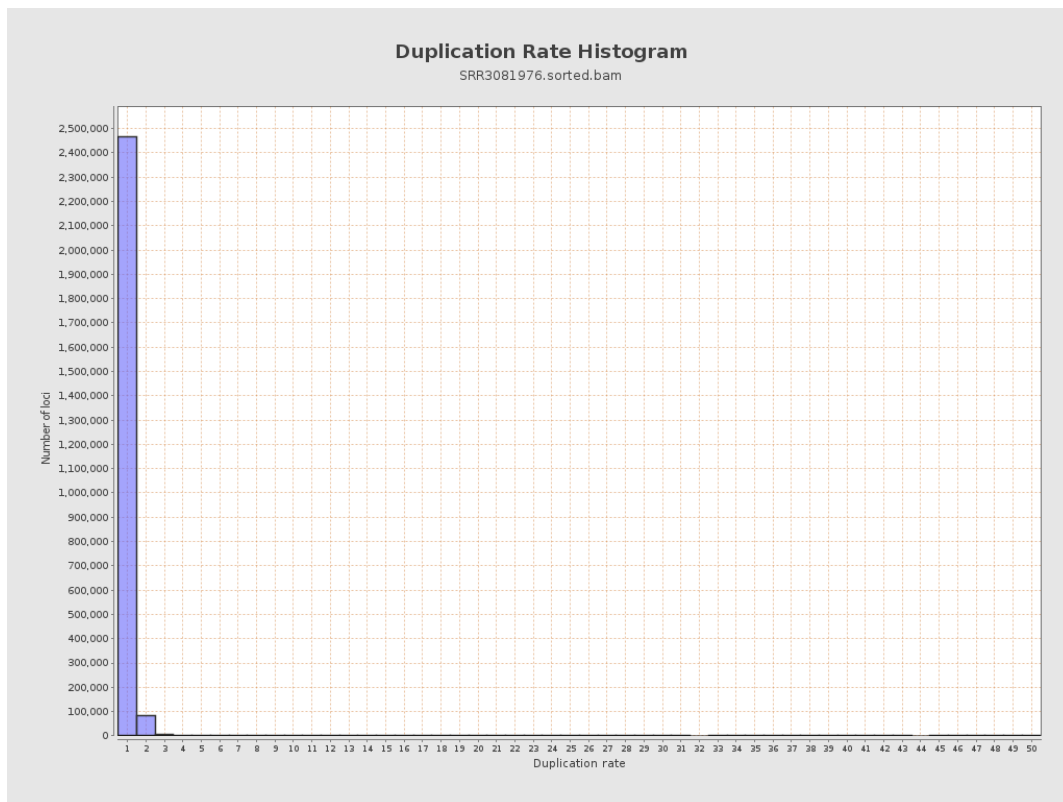
5. Results : Coverage Histogram (0-50X)



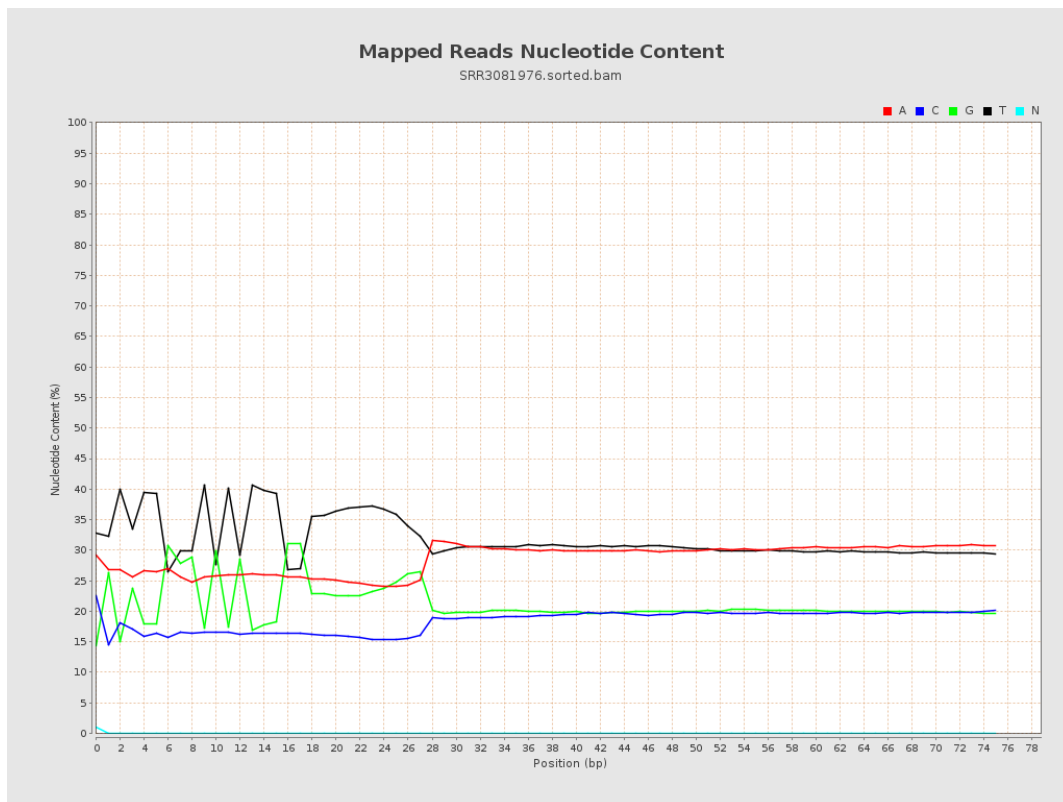
6. Results : Genome Fraction Coverage



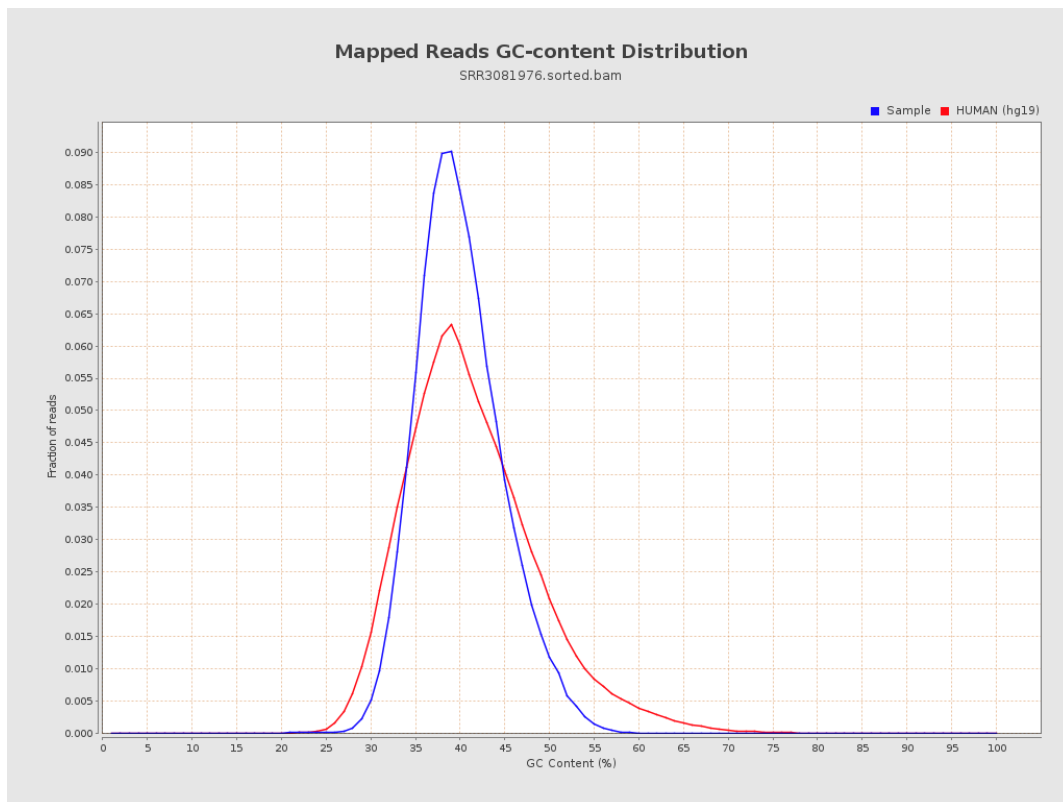
7. Results : Duplication Rate Histogram



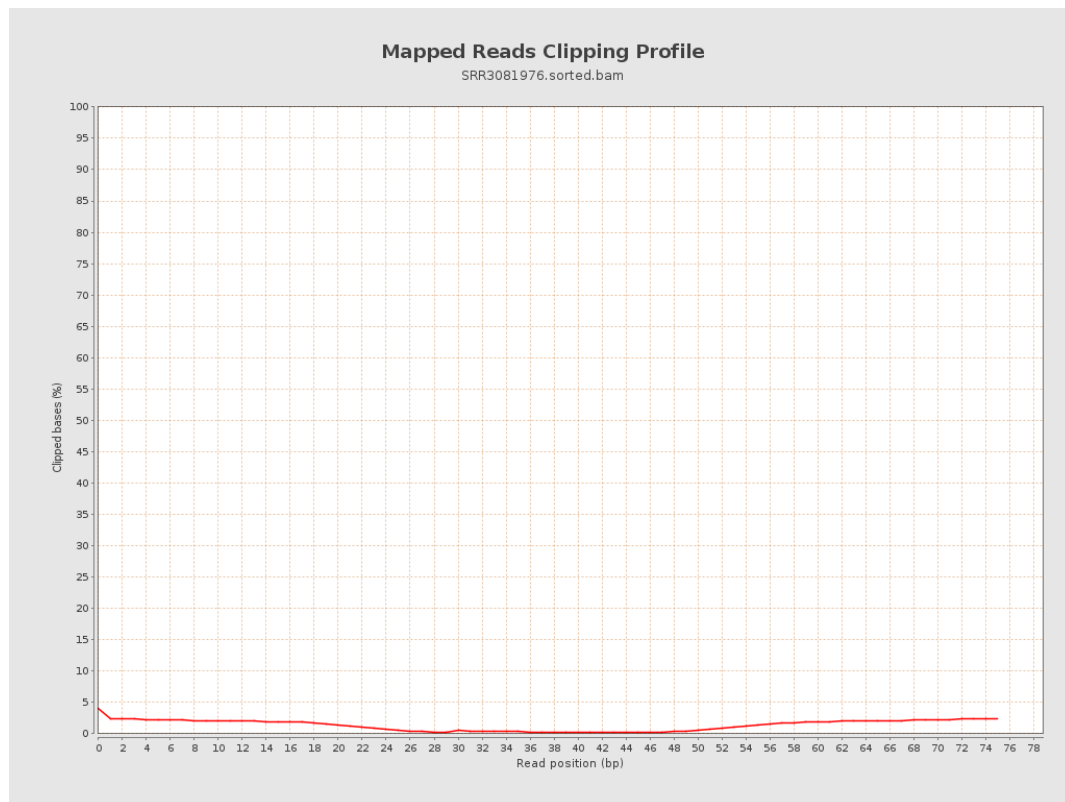
8. Results : Mapped Reads Nucleotide Content



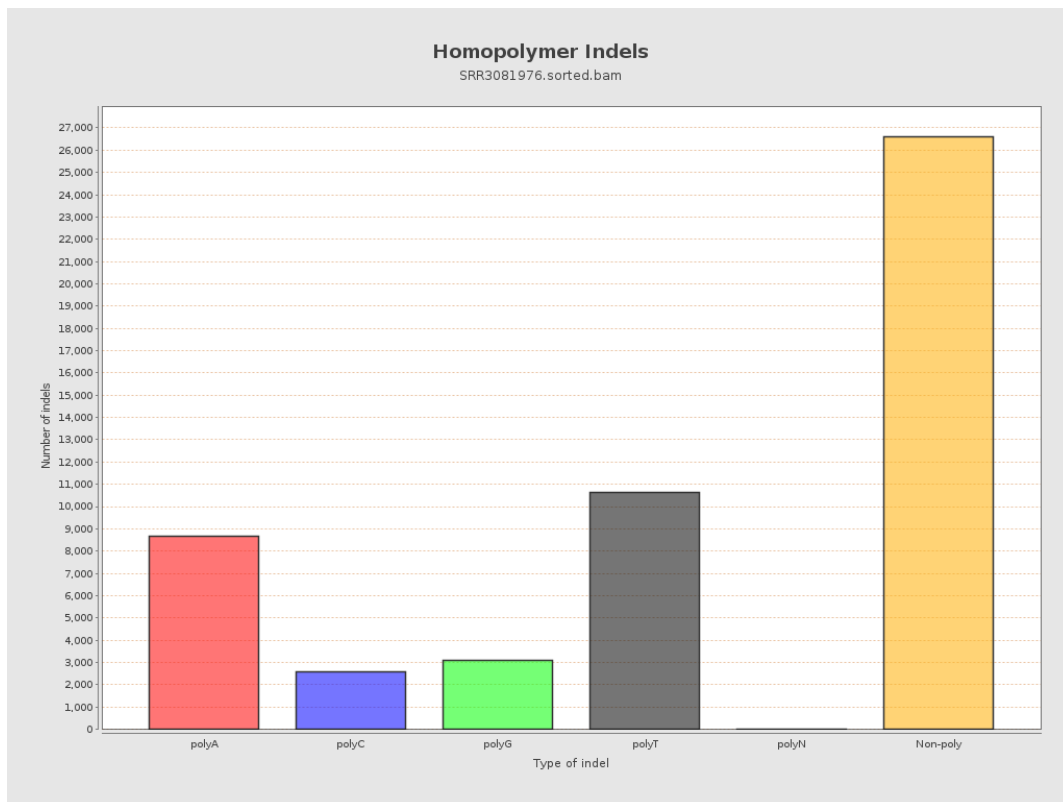
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

