

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:08:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004076.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_SRR6004076 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004076.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:08:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004076.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,101,743
Mapped reads	1,921,272 / 91.41%
Unmapped reads	180,471 / 8.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,833 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	79,395 / 3.78%
Duplication rate	3.28%
Clipped reads	801,778 / 38.15%

2.2. ACGT Content

Number/percentage of A's	36,751,497 / 28.38%
Number/percentage of C's	23,794,264 / 18.38%
Number/percentage of T's	41,098,042 / 31.74%
Number/percentage of G's	27,814,424 / 21.48%
Number/percentage of N's	23,244 / 0.02%
GC Percentage	39.86%

2.3. Coverage

Mean	0.0418

Standard Deviation	0.3629
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2.4. Mapping Quality

Mean Mapping Quality	46.29
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2.5. Mismatches and indels

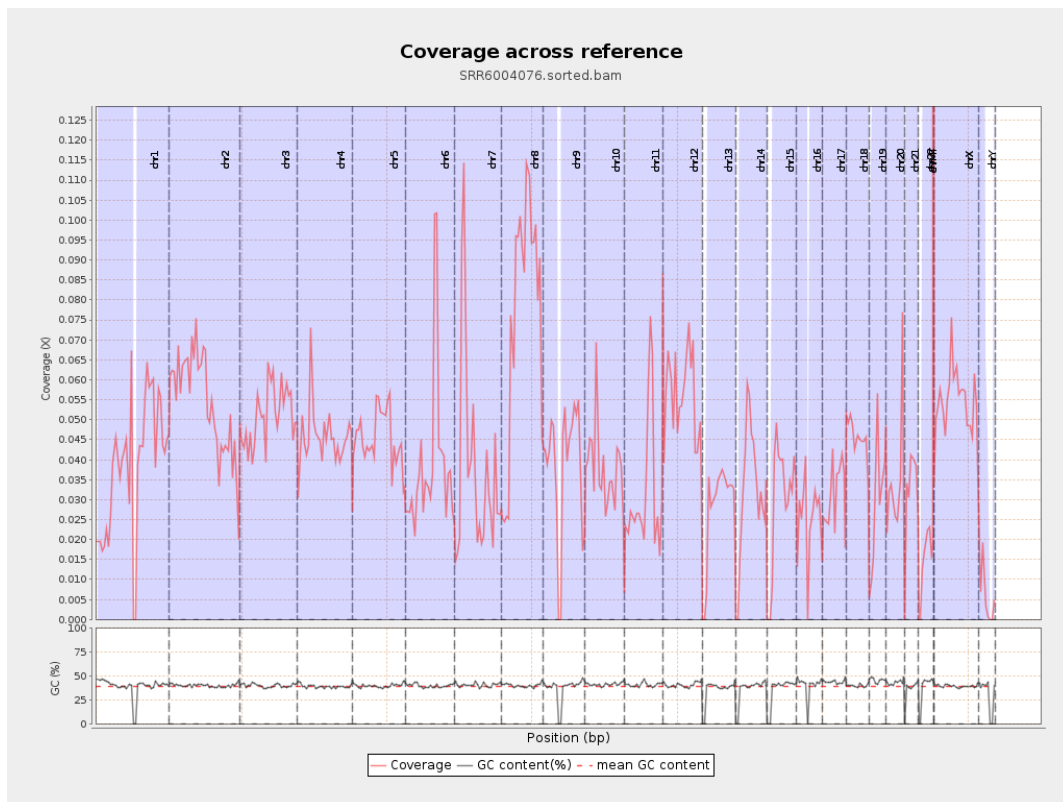
General error rate	0.87%
Mismatches	1,108,710
Insertions	9,423
Mapped reads with at least one insertion	0.49%
Deletions	31,702
Mapped reads with at least one deletion	1.63%
Homopolymer indels	46.69%

2.6. Chromosome stats

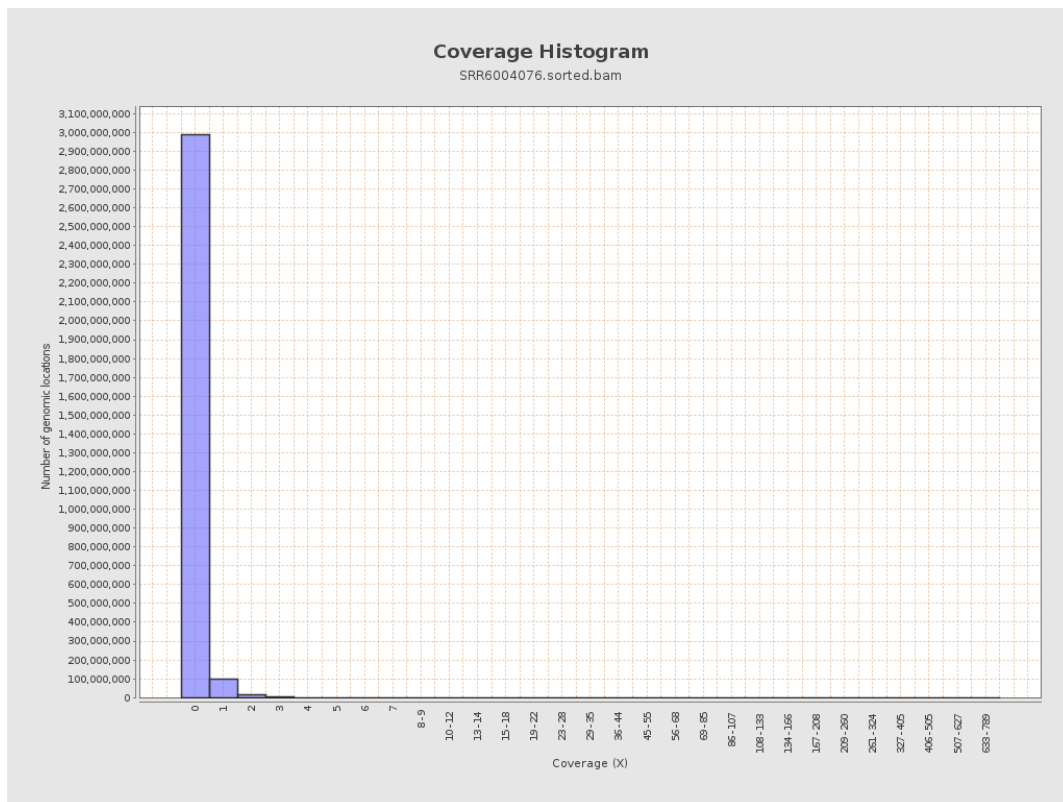
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9602760	0.0385	0.7143
chr2	243199373	13223296	0.0544	0.3898
chr3	198022430	10093130	0.051	0.2555
chr4	191154276	8730306	0.0457	0.2679
chr5	180915260	8244413	0.0456	0.2442
chr6	171115067	6688178	0.0391	0.2426
chr7	159138663	6105553	0.0384	0.4038

chr8	146364022	11117379	0.076	0.5061
chr9	141213431	5465753	0.0387	0.3255
chr10	135534747	5132131	0.0379	0.3509
chr11	135006516	4296460	0.0318	0.2408
chr12	133851895	7490423	0.056	0.2755
chr13	115169878	3219378	0.028	0.1927
chr14	107349540	3440053	0.032	0.2202
chr15	102531392	3071390	0.03	0.1991
chr16	90354753	2306253	0.0255	0.2089
chr17	81195210	2551275	0.0314	0.2127
chr18	78077248	3581787	0.0459	0.5948
chr19	59128983	1803579	0.0305	0.4603
chr20	63025520	2224599	0.0353	0.2244
chr21	48129895	1549191	0.0322	0.2298
chr22	51304566	740969	0.0144	0.133
chrMT	16571	24660	1.4881	1.703
chrX	155270560	8479895	0.0546	0.2897
chrY	59373566	354210	0.006	0.1538

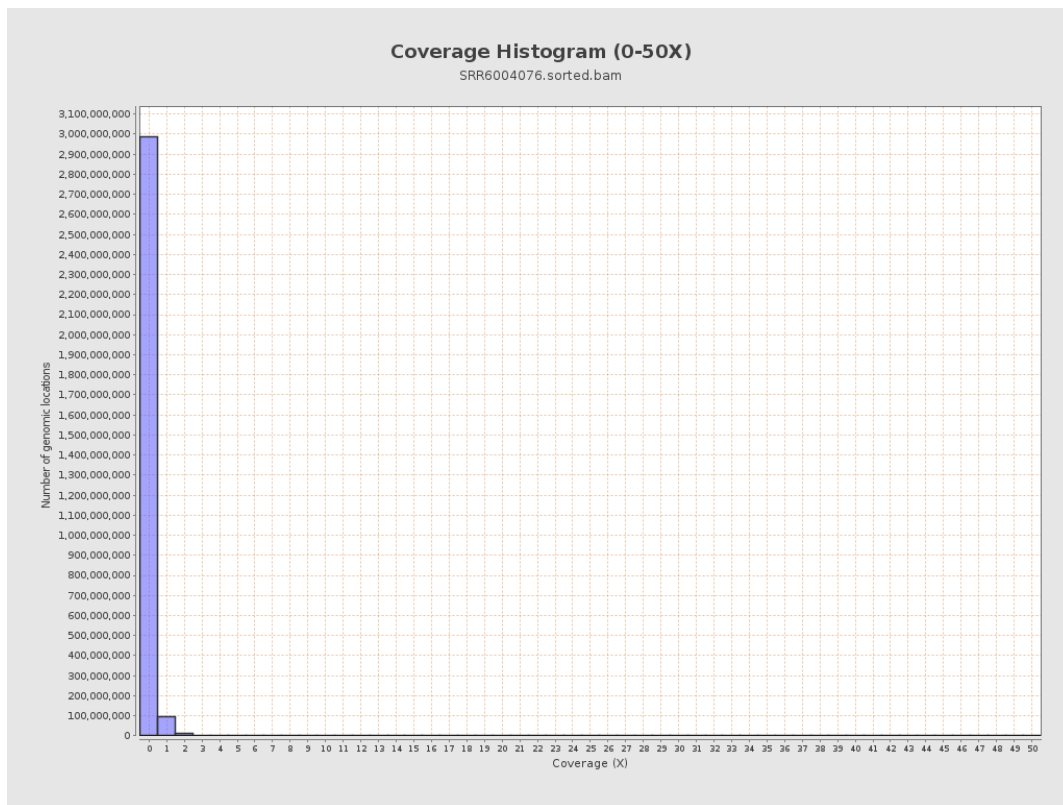
3. Results : Coverage across reference



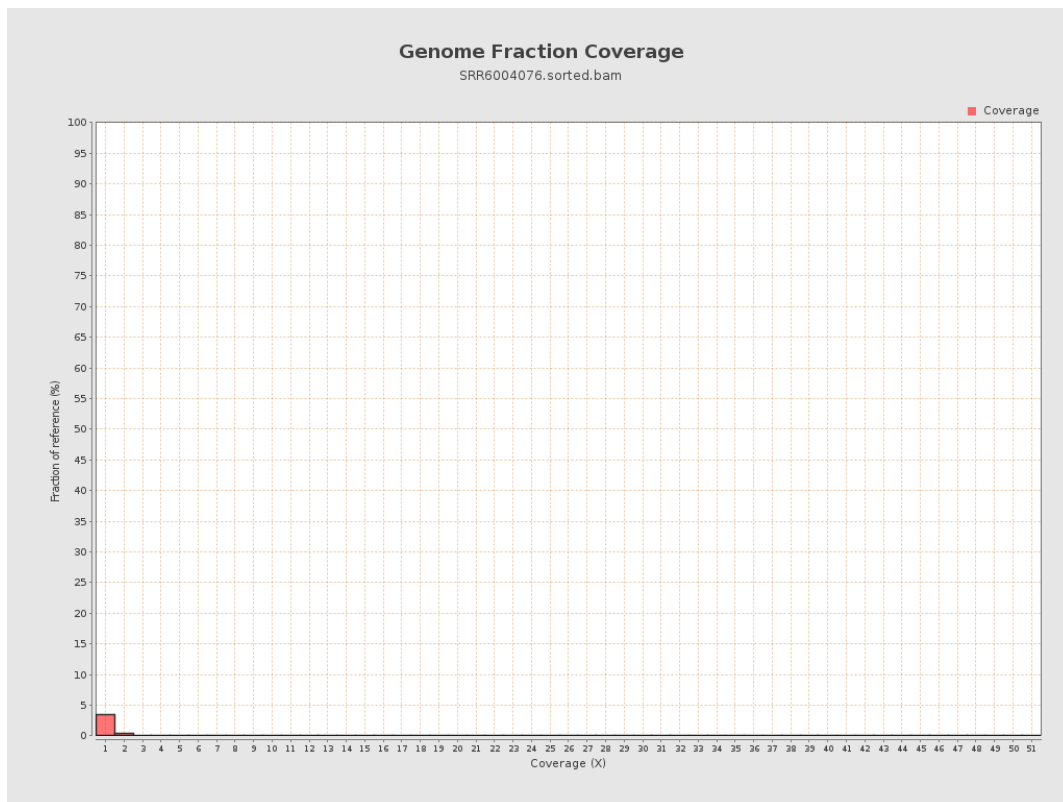
4. Results : Coverage Histogram



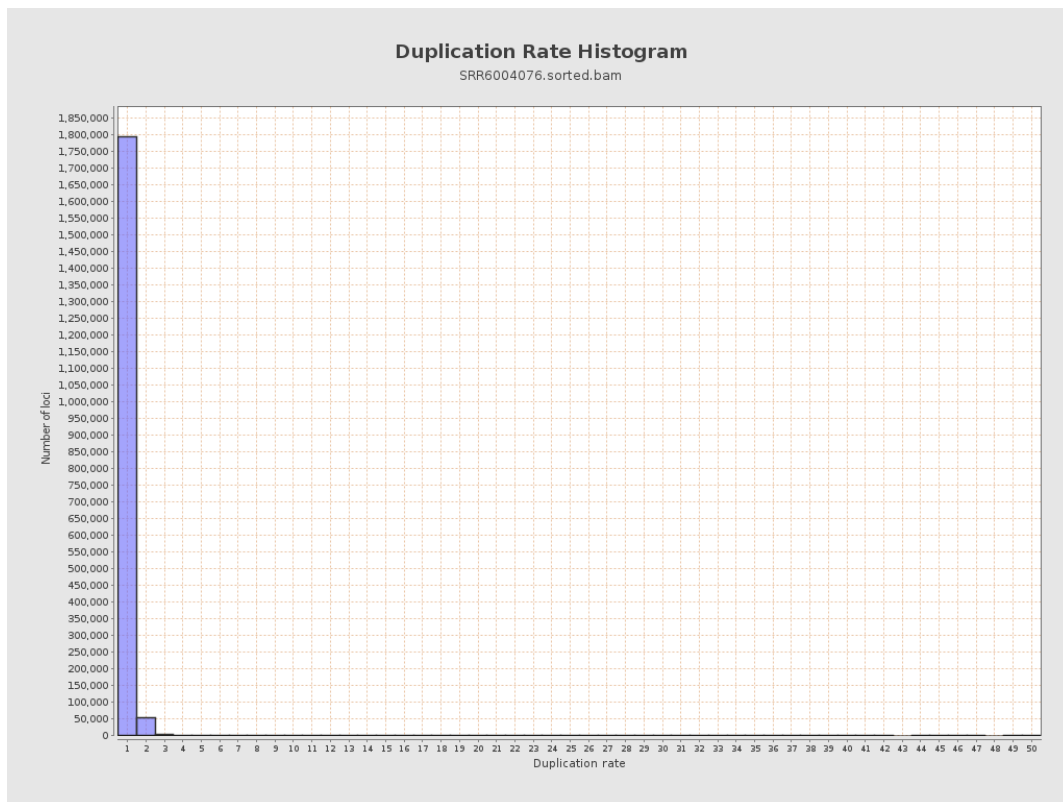
5. Results : Coverage Histogram (0-50X)



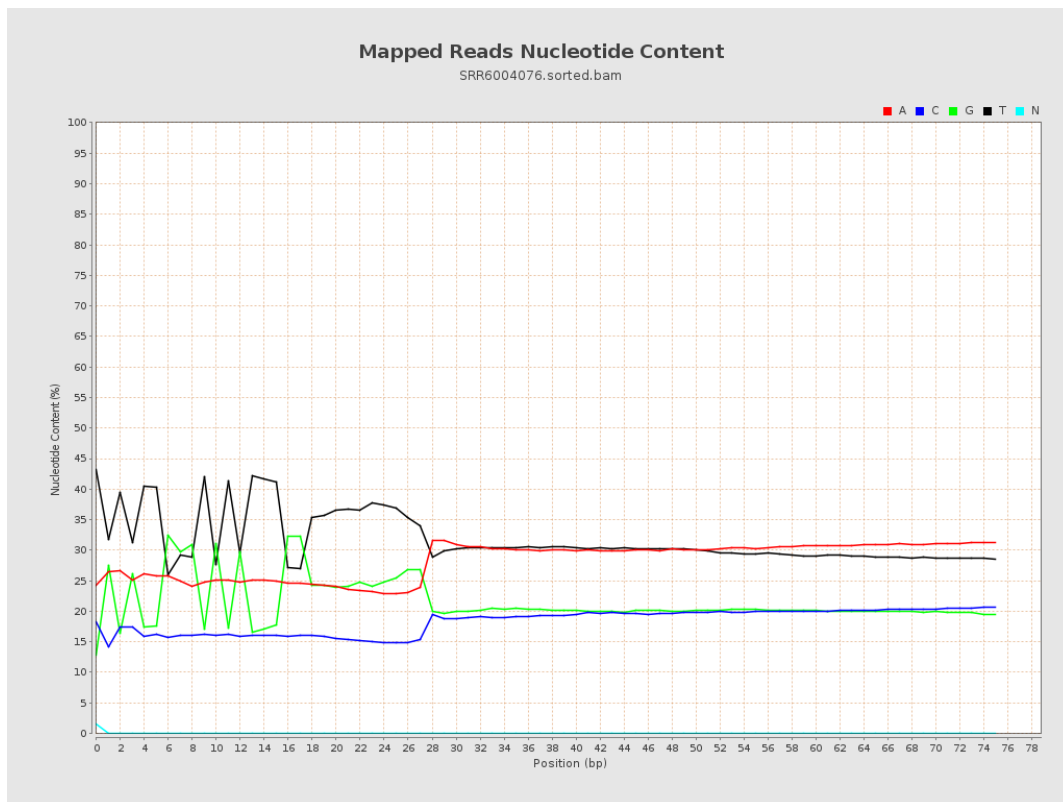
6. Results : Genome Fraction Coverage



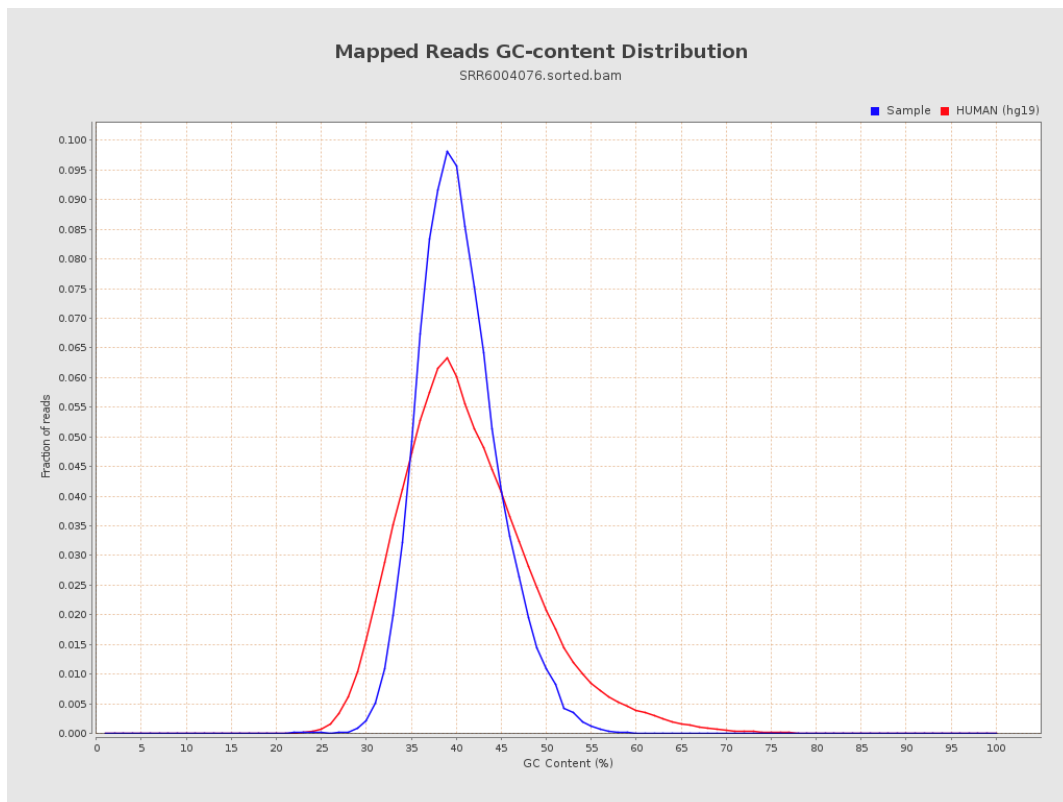
7. Results : Duplication Rate Histogram



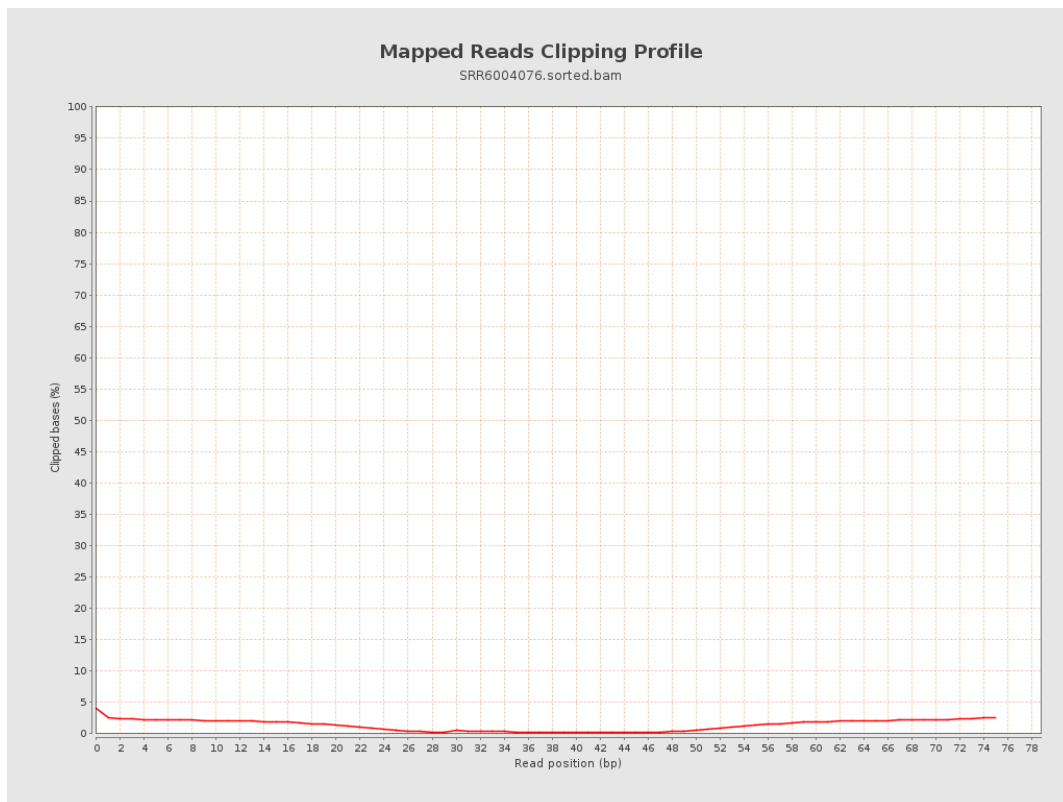
8. Results : Mapped Reads Nucleotide Content



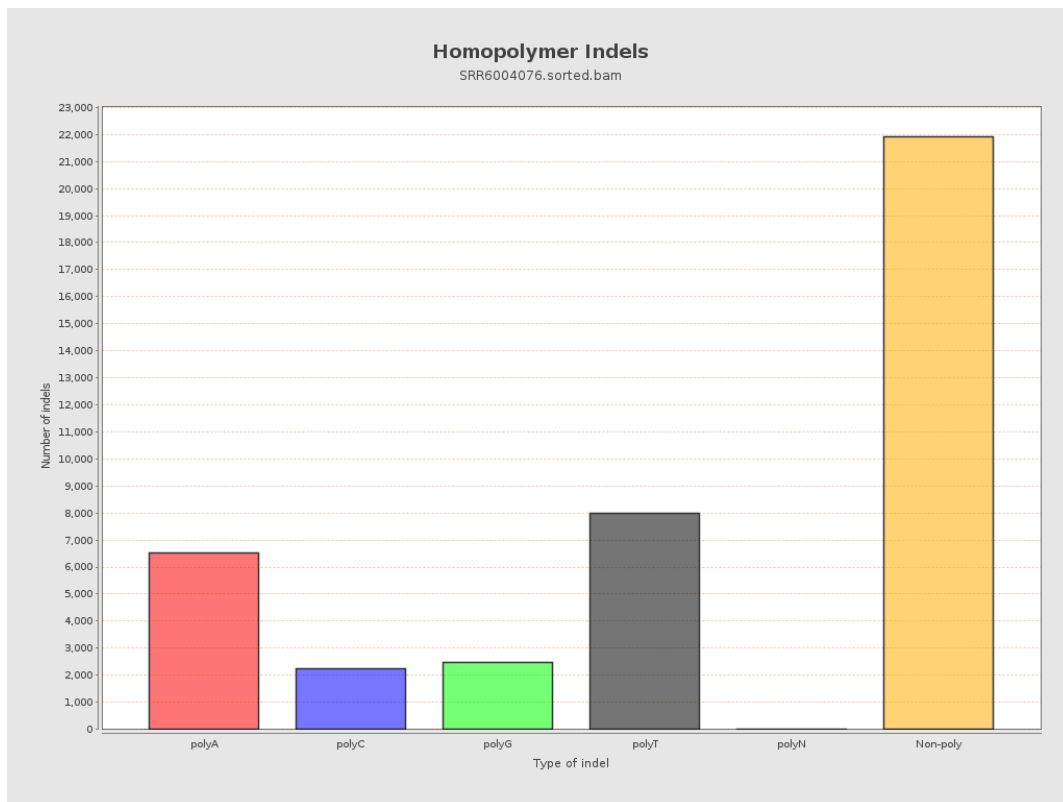
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

