

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:07:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240072.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_SRR6240072 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240072.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:07:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,274,370
Mapped reads	2,077,181 / 91.33%
Unmapped reads	197,189 / 8.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,141 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	87,162 / 3.83%
Duplication rate	2.85%
Clipped reads	743,229 / 32.68%

2.2. ACGT Content

Number/percentage of A's	41,697,870 / 29.1%
Number/percentage of C's	26,803,595 / 18.7%
Number/percentage of T's	45,297,448 / 31.61%
Number/percentage of G's	29,499,212 / 20.58%
Number/percentage of N's	14,058 / 0.01%
GC Percentage	39.29%

2.3. Coverage

Mean	0.0463

Standard Deviation	0.59
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2.4. Mapping Quality

Mean Mapping Quality	47.61
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2.5. Mismatches and indels

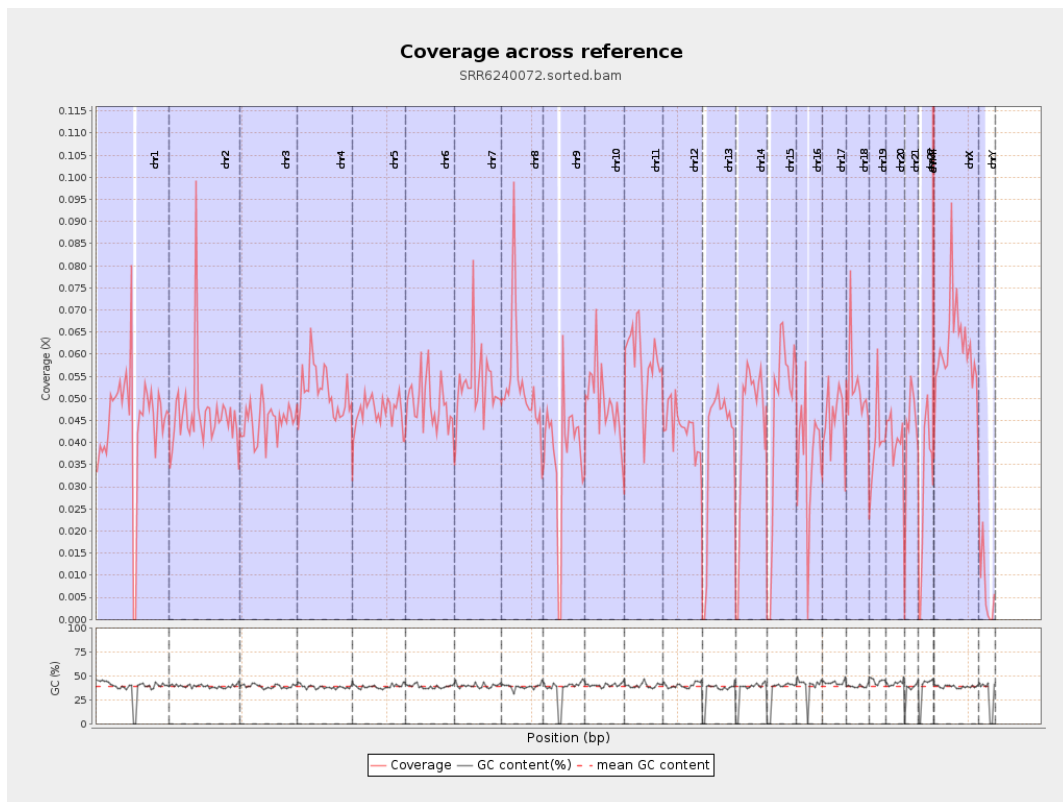
General error rate	0.81%
Mismatches	1,141,810
Insertions	11,303
Mapped reads with at least one insertion	0.54%
Deletions	31,311
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.28%

2.6. Chromosome stats

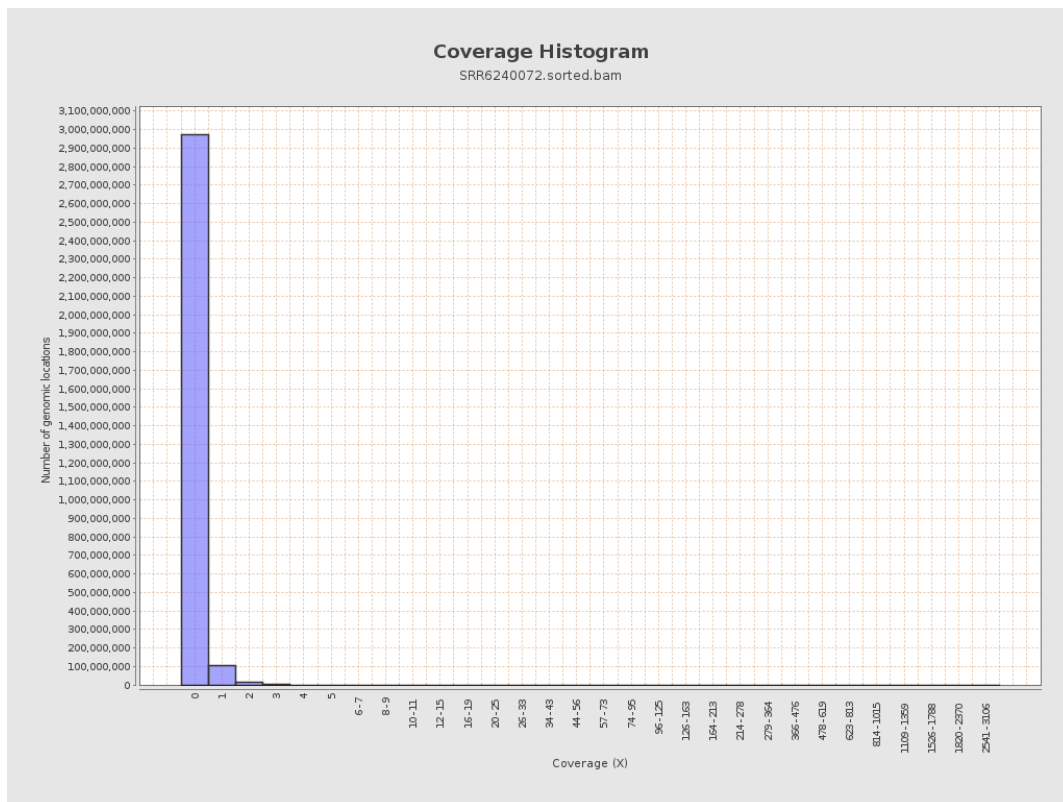
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11124486	0.0446	0.81
chr2	243199373	11279703	0.0464	0.4923
chr3	198022430	8895168	0.0449	0.2375
chr4	191154276	9833974	0.0514	0.277
chr5	180915260	8504454	0.047	0.2498
chr6	171115067	8296729	0.0485	0.3072
chr7	159138663	8498601	0.0534	0.4794

chr8	146364022	7731769	0.0528	1.8661
chr9	141213431	5340330	0.0378	0.4575
chr10	135534747	6672504	0.0492	0.3503
chr11	135006516	7799659	0.0578	0.4888
chr12	133851895	5783028	0.0432	0.2455
chr13	115169878	4527057	0.0393	0.2217
chr14	107349540	4691660	0.0437	0.2727
chr15	102531392	4735216	0.0462	0.2416
chr16	90354753	3352237	0.0371	0.2792
chr17	81195210	3665189	0.0451	0.3103
chr18	78077248	4124937	0.0528	1.0574
chr19	59128983	2379803	0.0402	0.519
chr20	63025520	2578898	0.0409	0.2455
chr21	48129895	2019639	0.042	0.2637
chr22	51304566	1513826	0.0295	0.1901
chrMT	16571	79127	4.775	3.739
chrX	155270560	9535009	0.0614	0.3558
chrY	59373566	404332	0.0068	0.1729

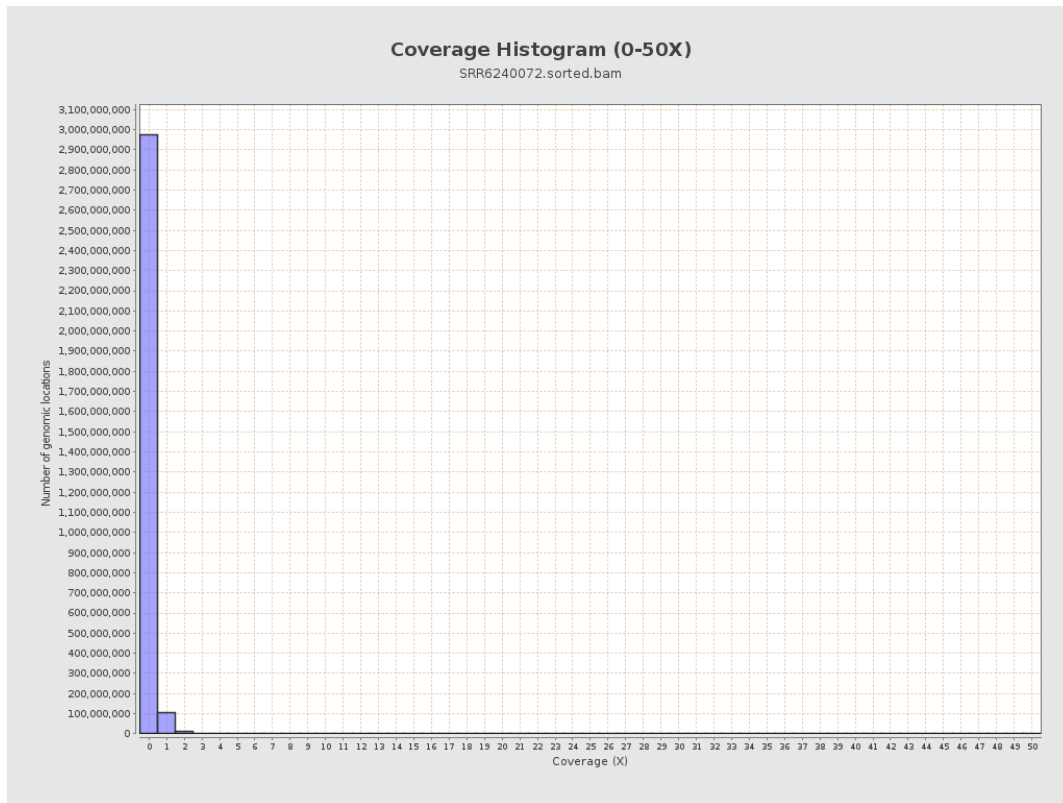
3. Results : Coverage across reference



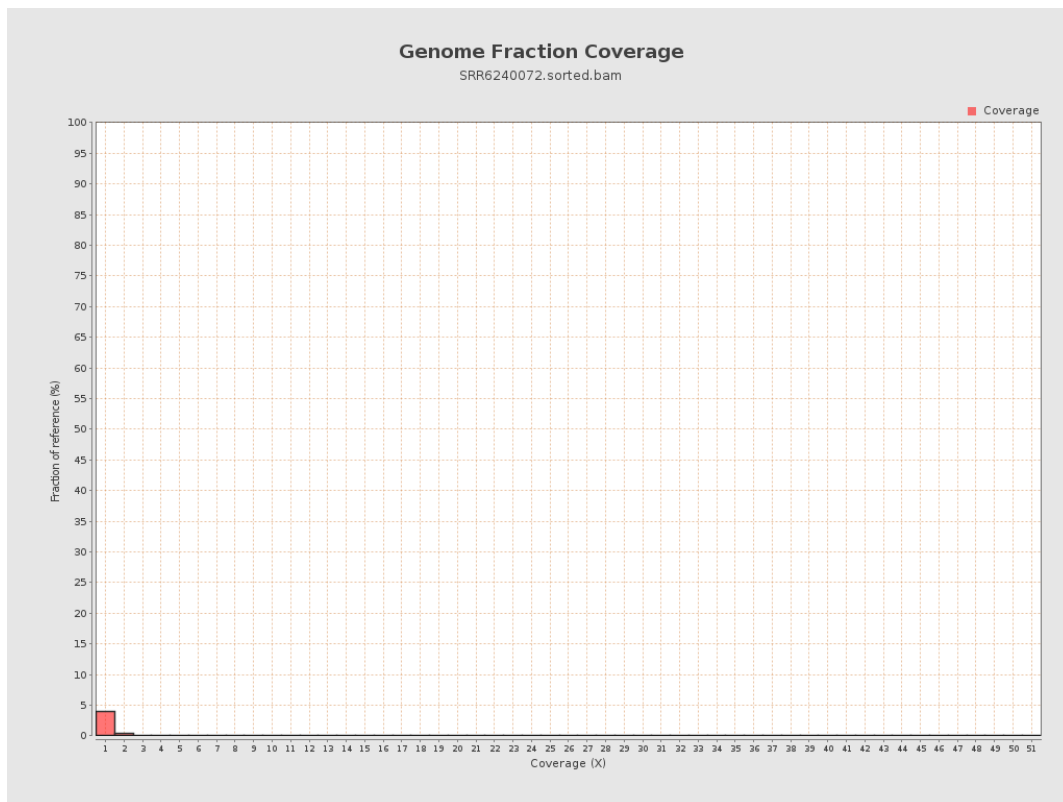
4. Results : Coverage Histogram



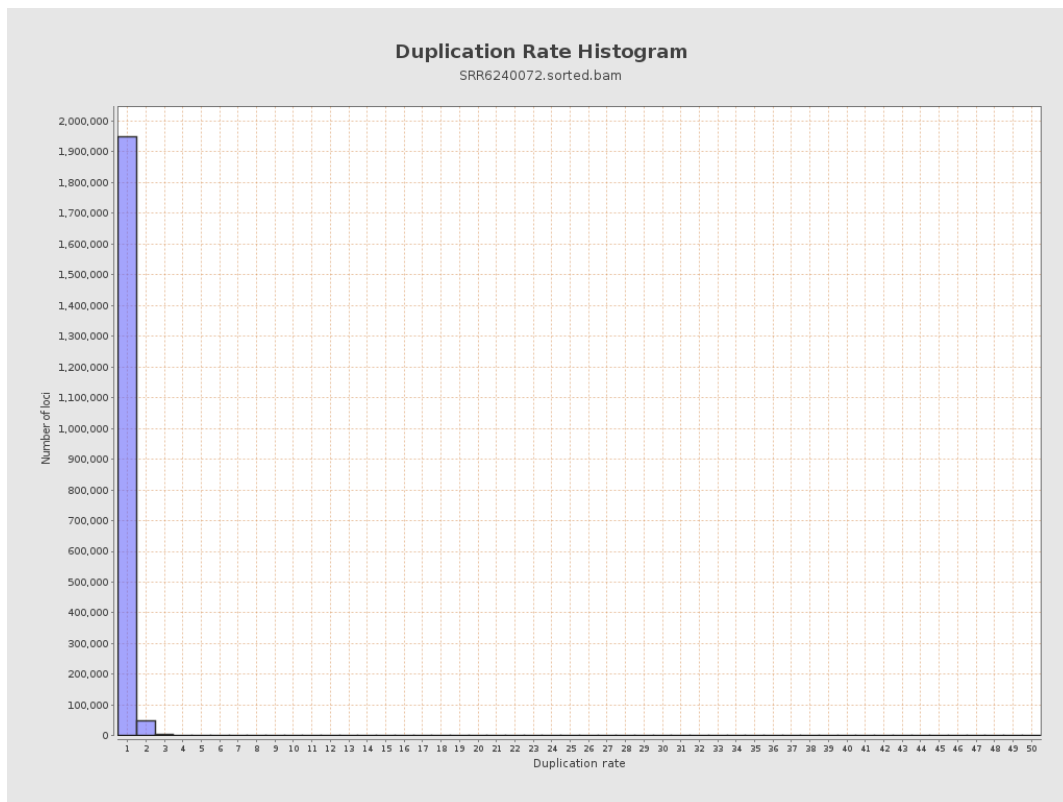
5. Results : Coverage Histogram (0-50X)



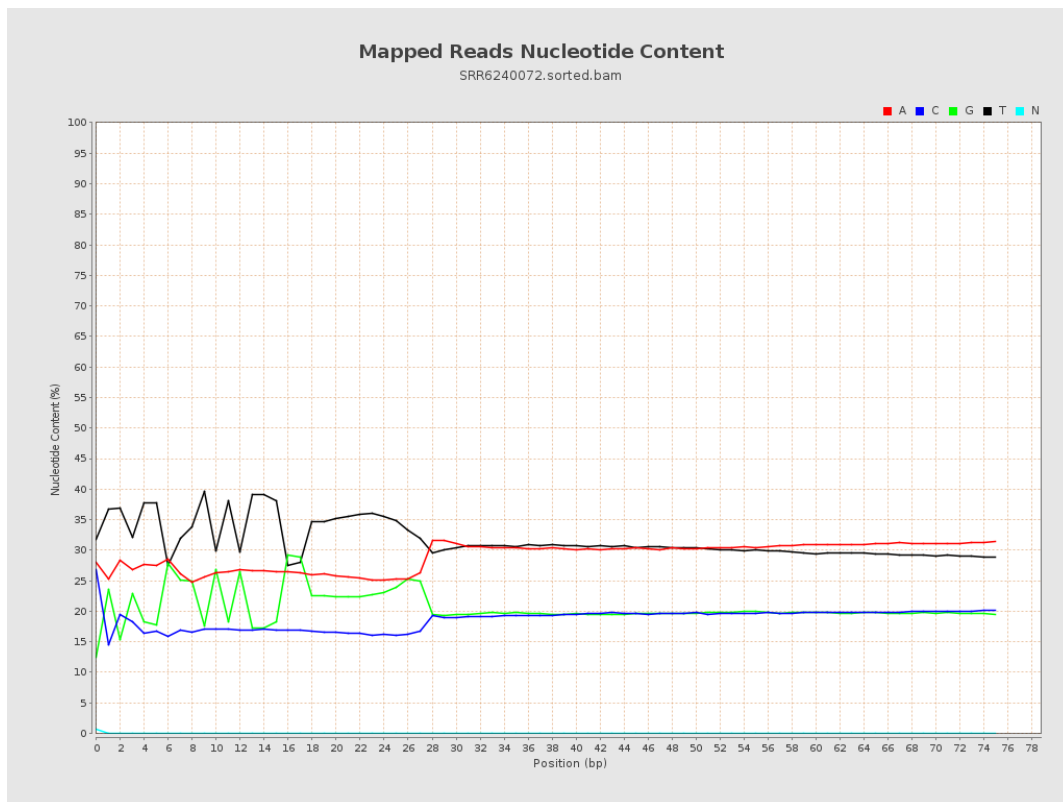
6. Results : Genome Fraction Coverage



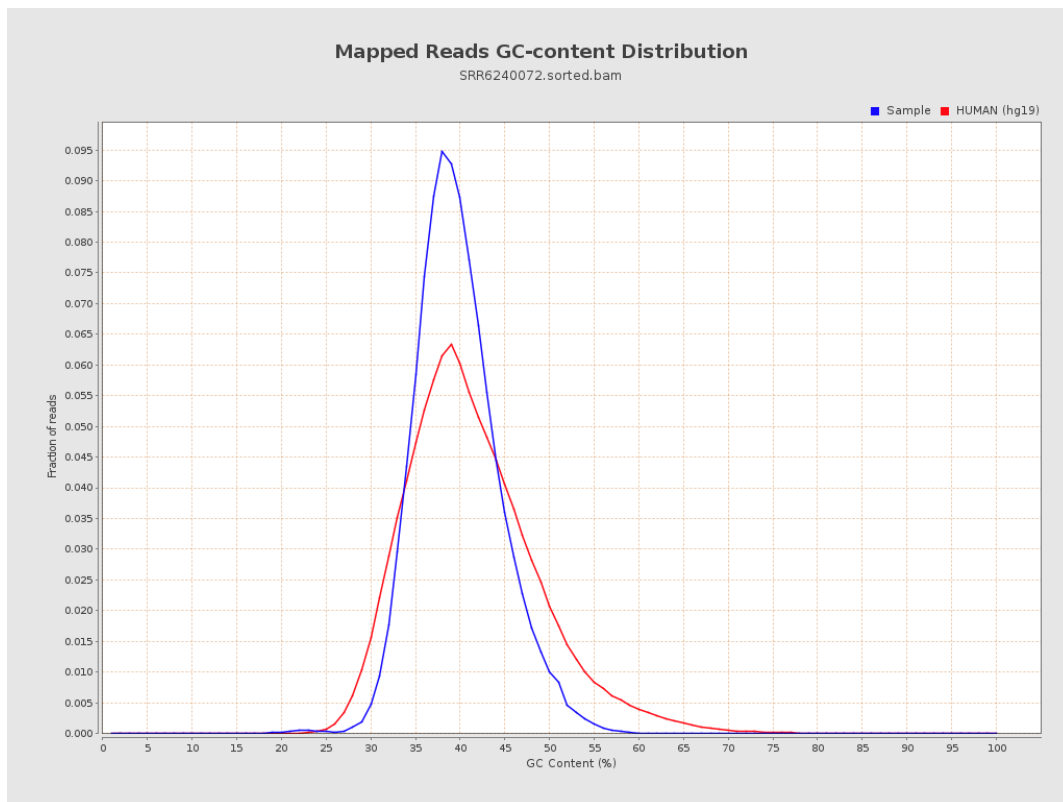
7. Results : Duplication Rate Histogram



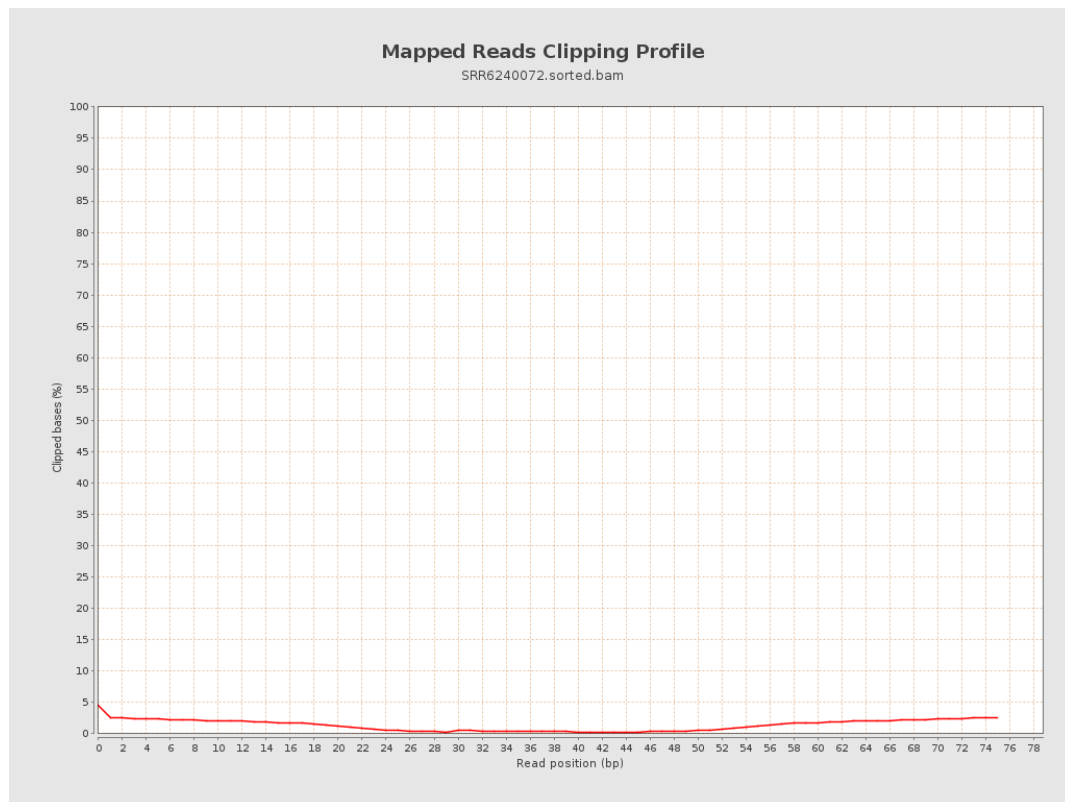
8. Results : Mapped Reads Nucleotide Content



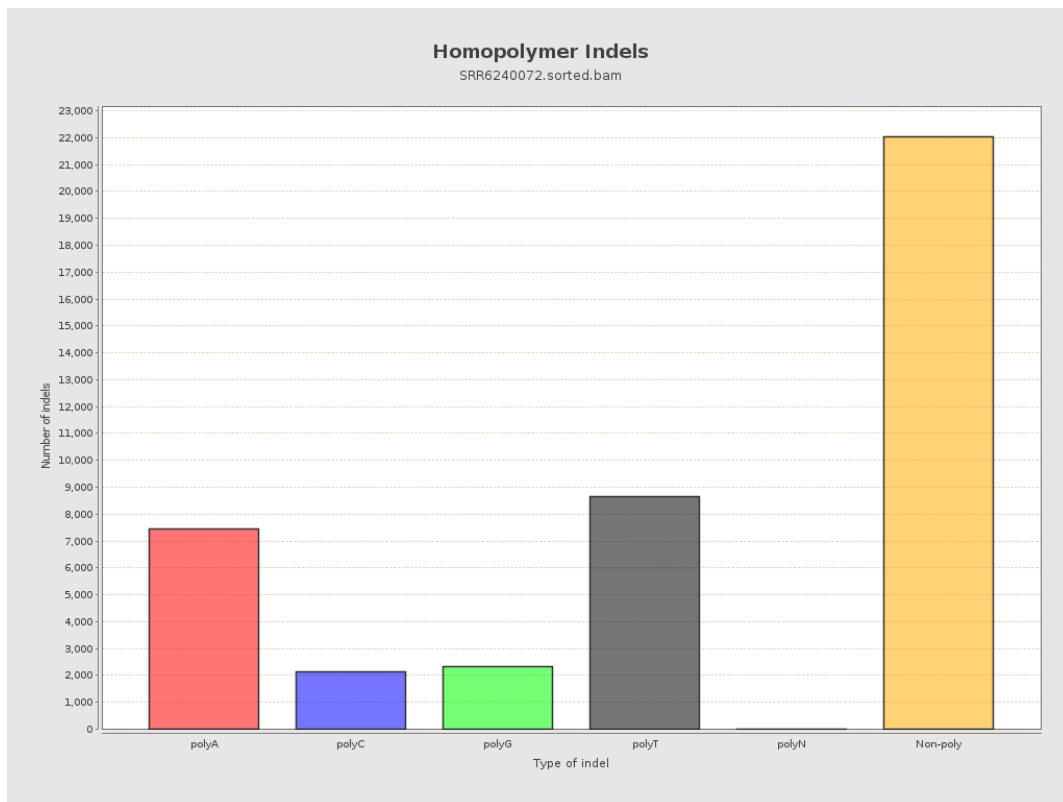
9. Results : Mapped Reads GC-content Distribution



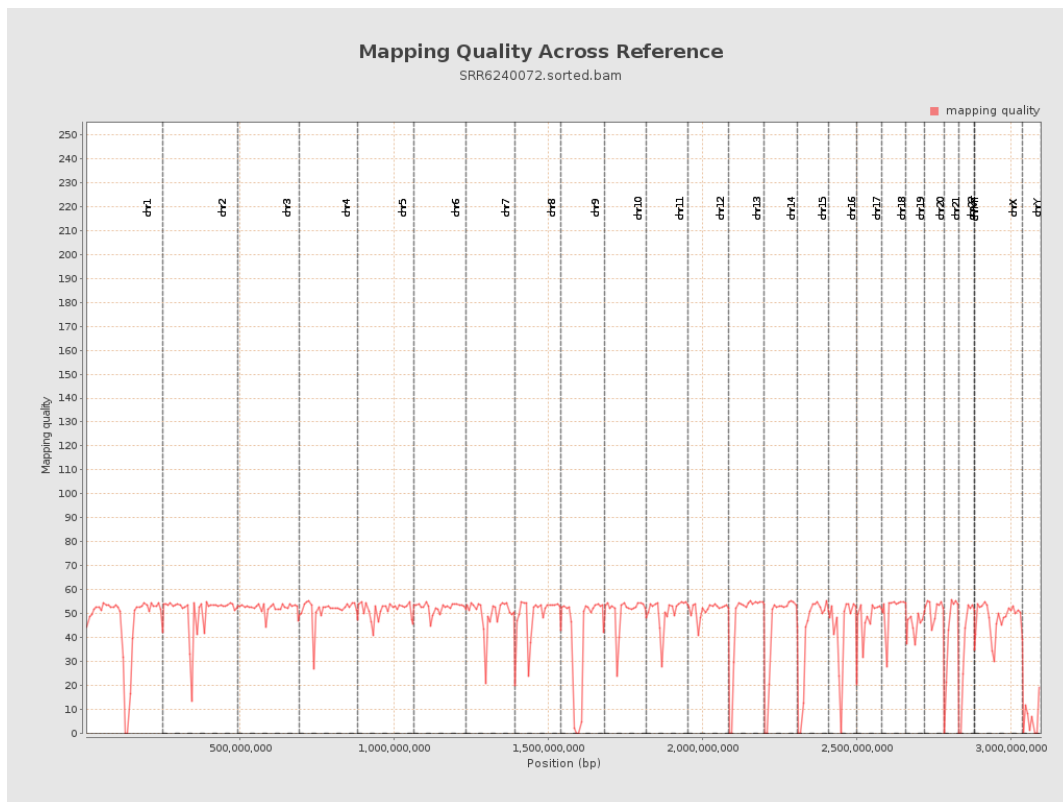
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

