

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:02:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240239.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_SRR6240239 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240239.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:02:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240239.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,934,812
Mapped reads	2,187,842 / 74.55%
Unmapped reads	746,970 / 25.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,837 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	344,436 / 11.74%
Duplication rate	11.82%
Clipped reads	1,130,015 / 38.5%

2.2. ACGT Content

Number/percentage of A's	39,992,516 / 28.07%
Number/percentage of C's	25,594,836 / 17.96%
Number/percentage of T's	46,301,786 / 32.5%
Number/percentage of G's	30,533,040 / 21.43%
Number/percentage of N's	53,414 / 0.04%
GC Percentage	39.39%

2.3. Coverage

Mean	0.046

Standard Deviation	0.5103
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2.4. Mapping Quality

Mean Mapping Quality	46.76
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2.5. Mismatches and indels

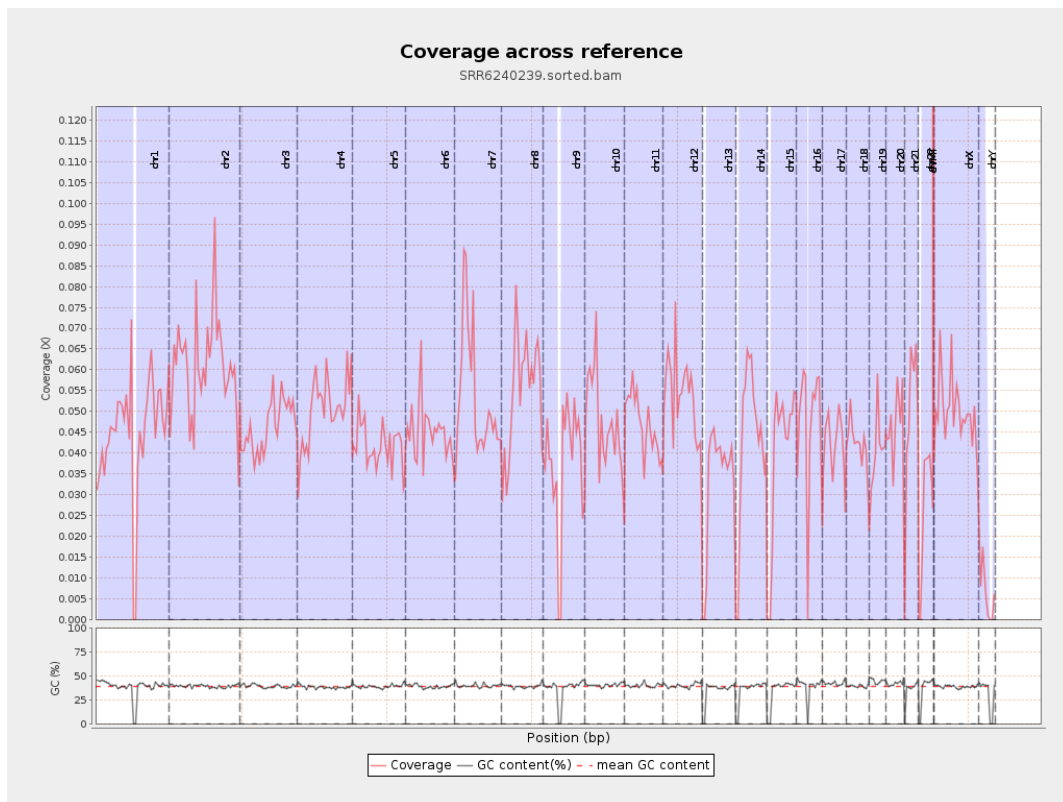
General error rate	0.92%
Mismatches	1,291,136
Insertions	10,887
Mapped reads with at least one insertion	0.49%
Deletions	41,420
Mapped reads with at least one deletion	1.87%
Homopolymer indels	48.44%

2.6. Chromosome stats

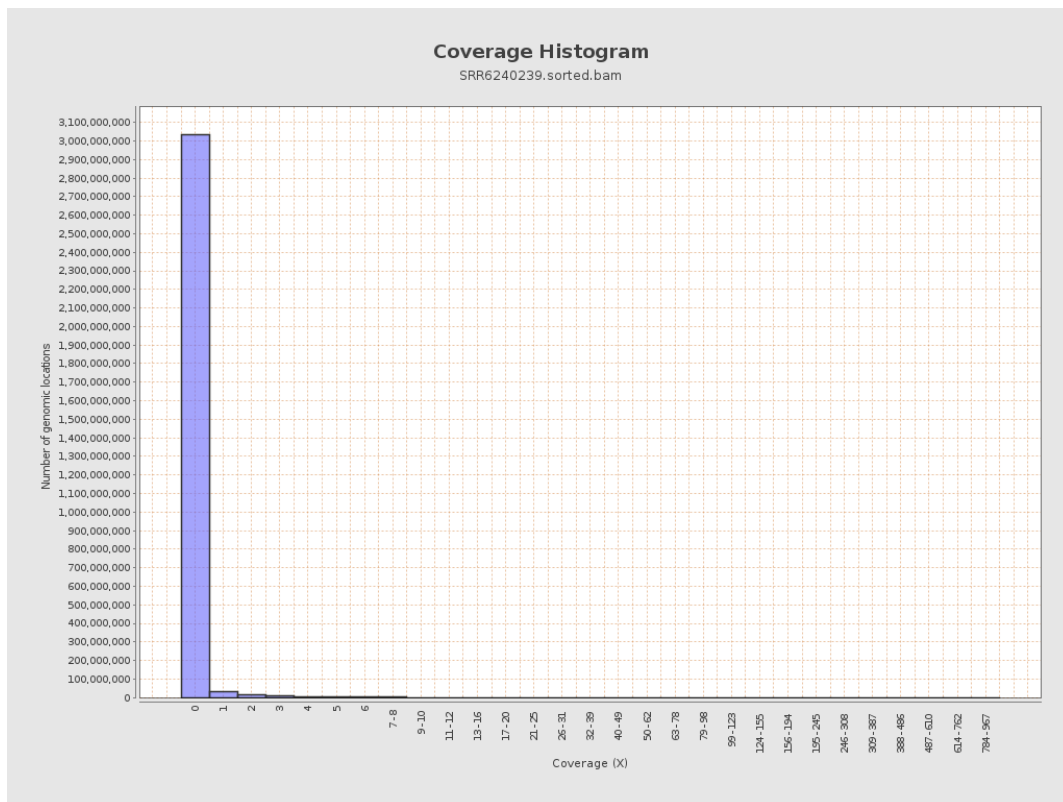
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11203098	0.0449	0.7408
chr2	243199373	14824909	0.061	0.5741
chr3	198022430	9209072	0.0465	0.4091
chr4	191154276	9628588	0.0504	0.4355
chr5	180915260	7554448	0.0418	0.385
chr6	171115067	7699419	0.045	0.4543
chr7	159138663	8546016	0.0537	0.688

chr8	146364022	8015983	0.0548	0.7448
chr9	141213431	5290058	0.0375	0.4317
chr10	135534747	6495914	0.0479	0.4762
chr11	135006516	6266061	0.0464	0.5102
chr12	133851895	7186395	0.0537	0.4462
chr13	115169878	3812496	0.0331	0.3468
chr14	107349540	4619275	0.043	0.4023
chr15	102531392	4082817	0.0398	0.3835
chr16	90354753	4242894	0.047	0.4226
chr17	81195210	3383118	0.0417	0.3981
chr18	78077248	3324171	0.0426	0.6774
chr19	59128983	2398079	0.0406	0.5205
chr20	63025520	2915101	0.0463	0.4047
chr21	48129895	2363880	0.0491	0.4303
chr22	51304566	1336441	0.026	0.2981
chrMT	16571	36543	2.2052	2.8393
chrX	155270560	7727870	0.0498	0.436
chrY	59373566	384844	0.0065	0.1448

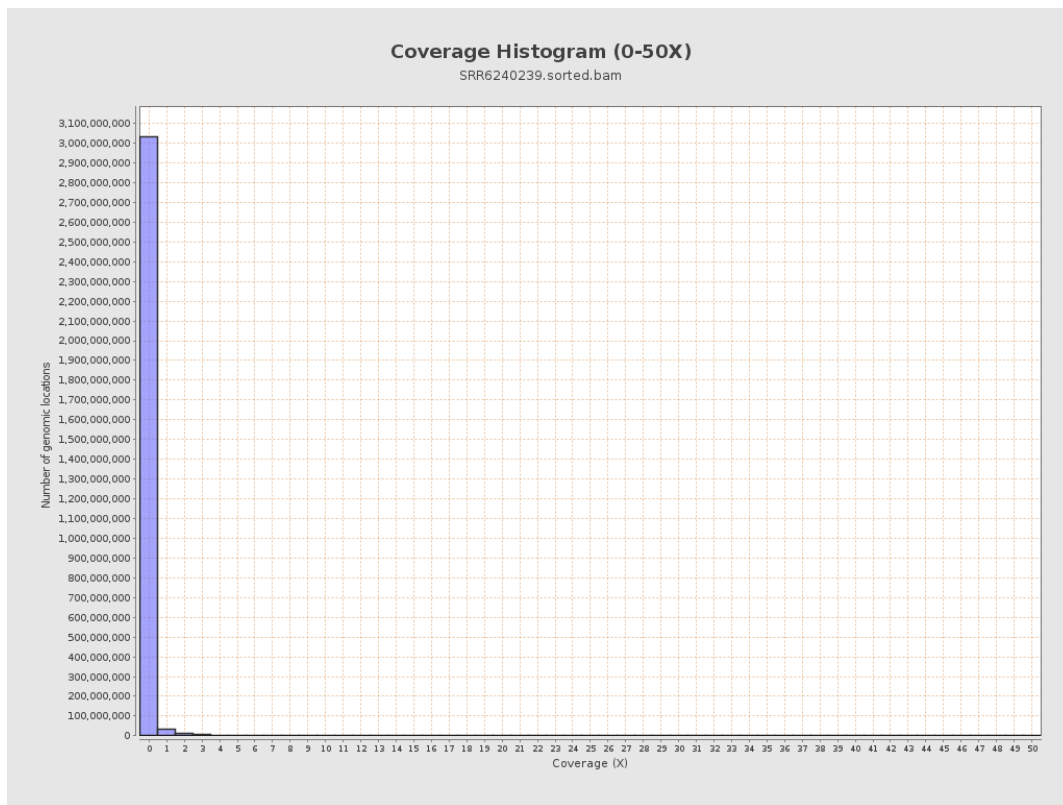
3. Results : Coverage across reference



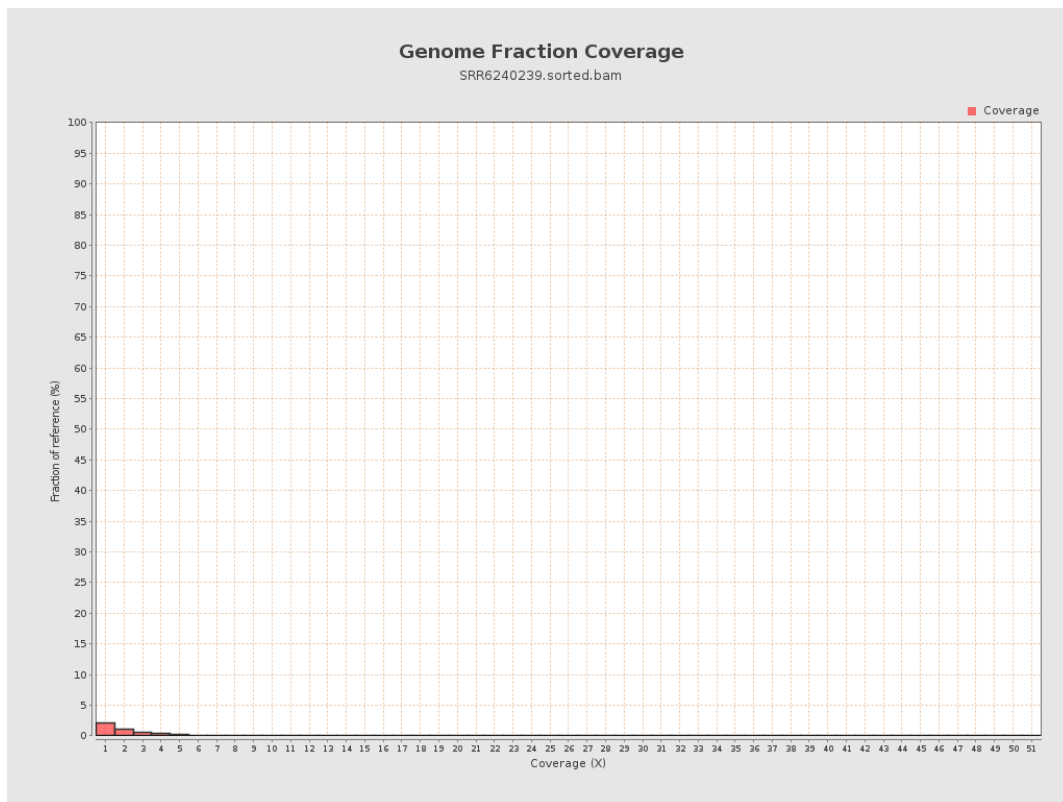
4. Results : Coverage Histogram



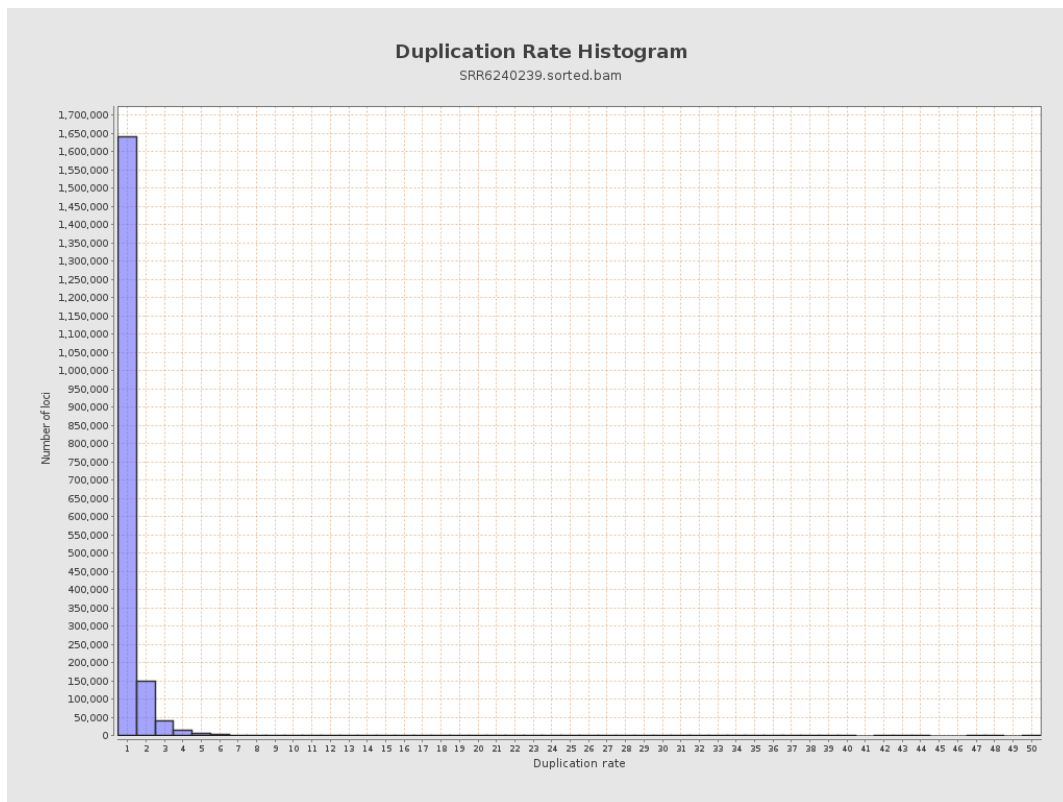
5. Results : Coverage Histogram (0-50X)



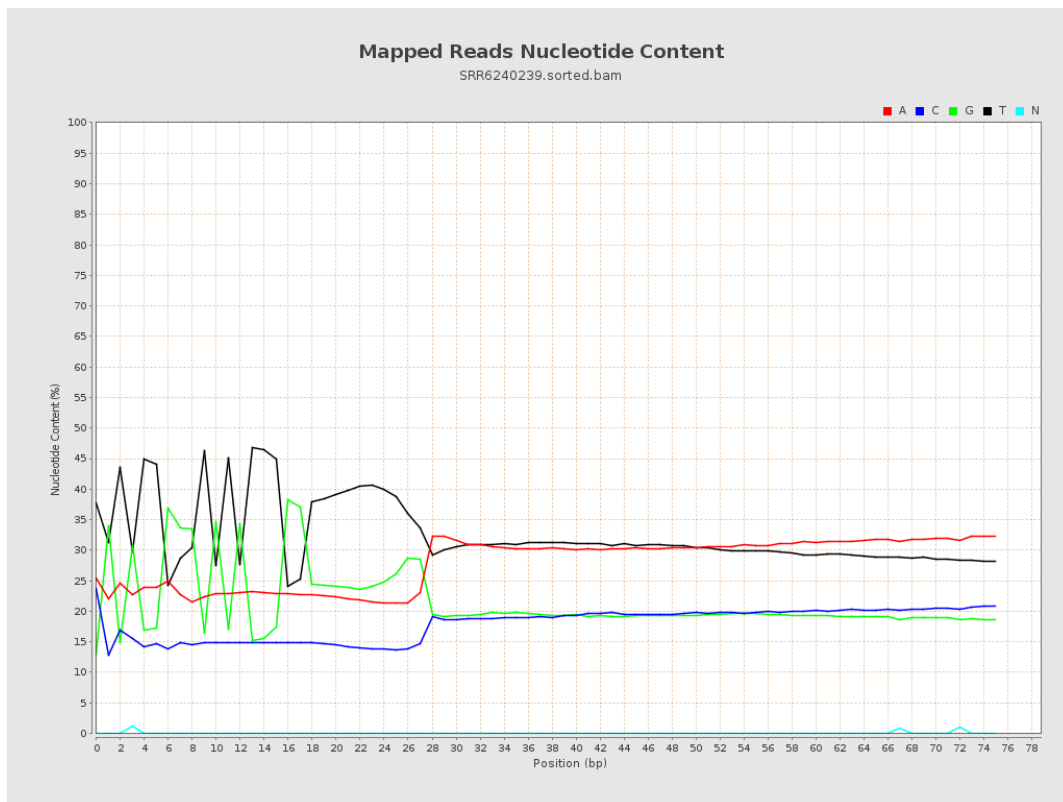
6. Results : Genome Fraction Coverage



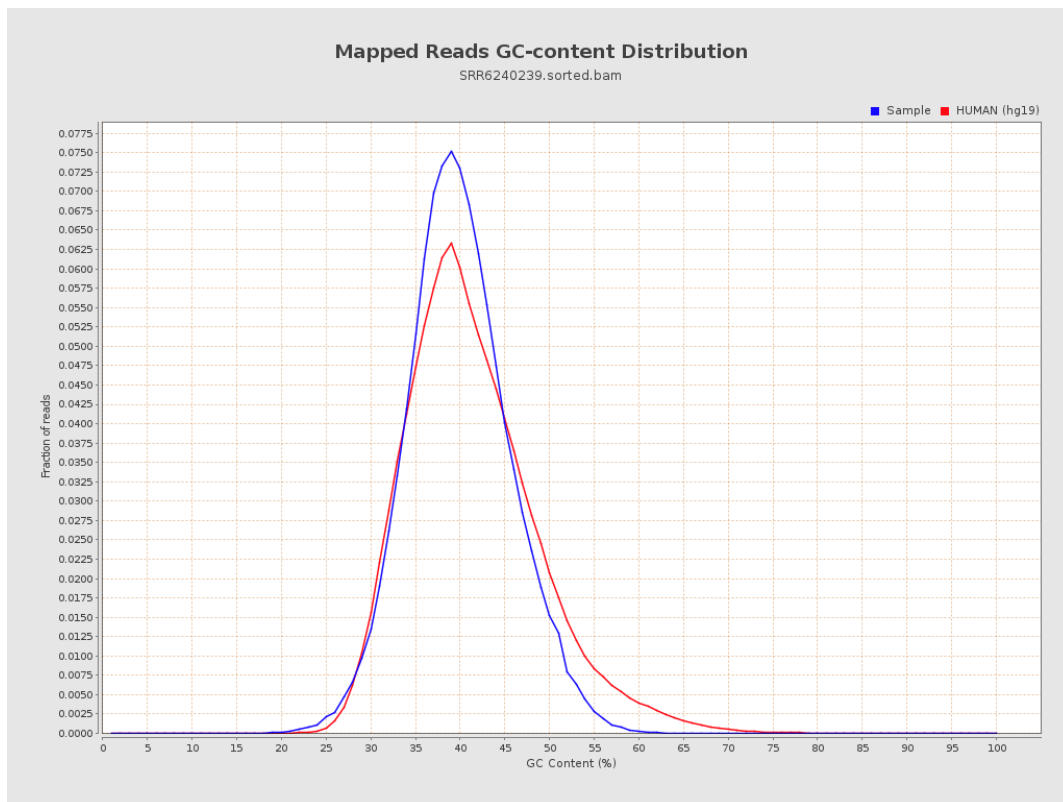
7. Results : Duplication Rate Histogram



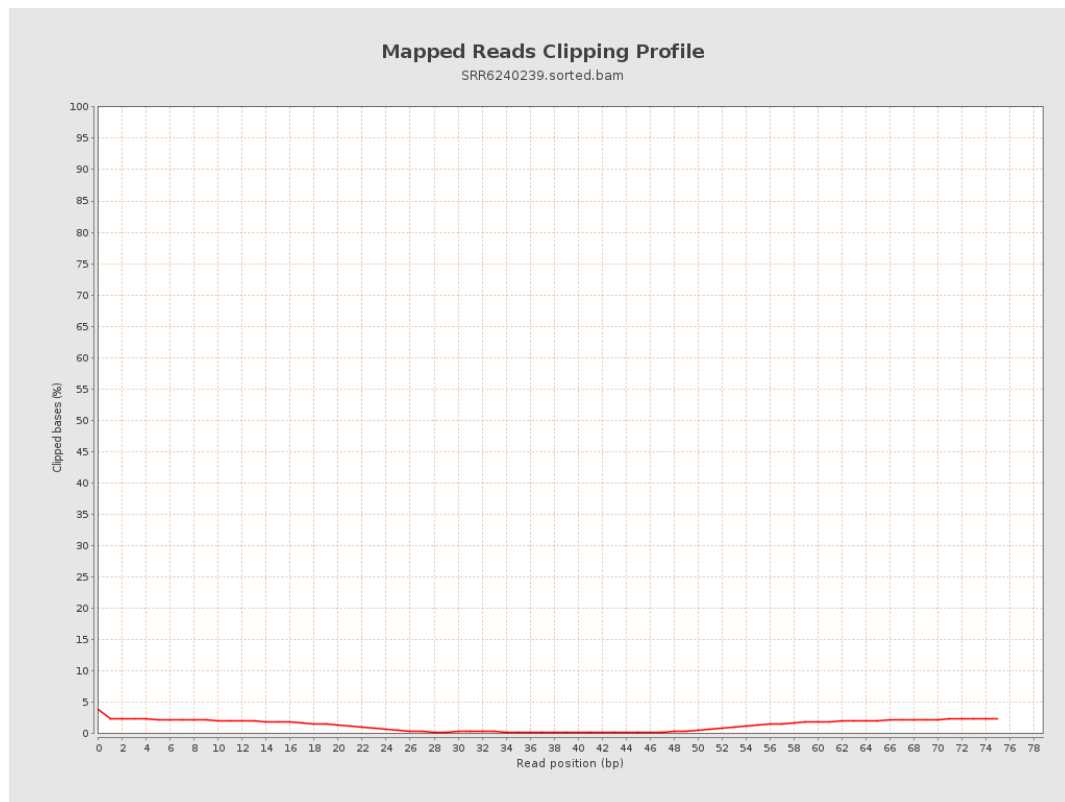
8. Results : Mapped Reads Nucleotide Content



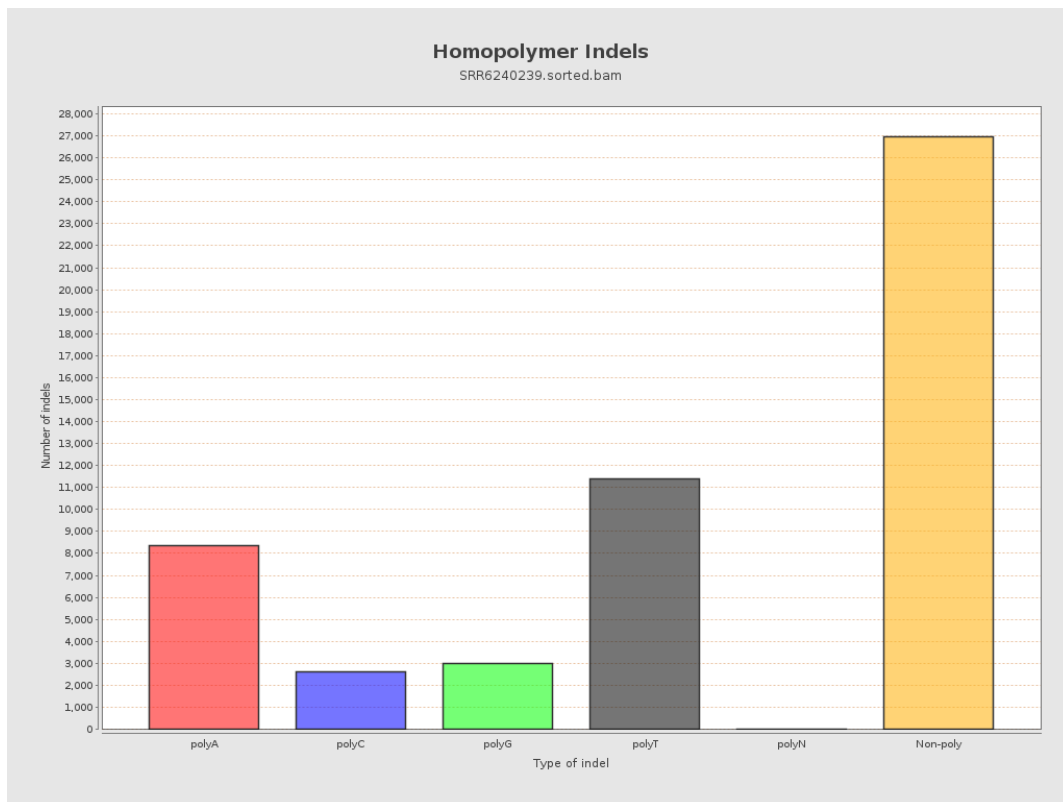
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

