

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:16:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237320.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_SRR6237320 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237320.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:16:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237320.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,286,486
Mapped reads	1,929,655 / 84.39%
Unmapped reads	356,831 / 15.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,374 / 0.85%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	599,039 / 26.2%
Duplication rate	20.94%
Clipped reads	1,258,599 / 55.05%

2.2. ACGT Content

Number/percentage of A's	29,560,485 / 24.92%
Number/percentage of C's	20,440,825 / 17.23%
Number/percentage of T's	39,836,108 / 33.58%
Number/percentage of G's	28,764,667 / 24.25%
Number/percentage of N's	11,660 / 0.01%
GC Percentage	41.48%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.6018
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2.4. Mapping Quality

Mean Mapping Quality	43.95
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2.5. Mismatches and indels

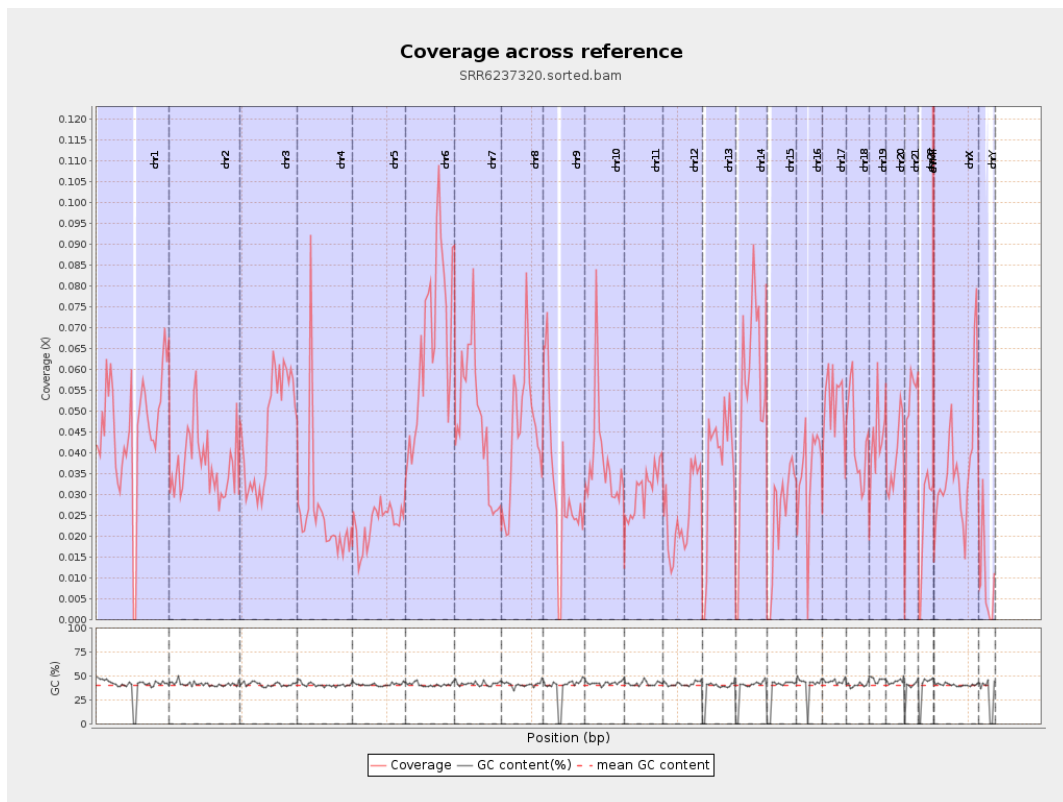
General error rate	0.68%
Mismatches	786,793
Insertions	9,394
Mapped reads with at least one insertion	0.48%
Deletions	33,213
Mapped reads with at least one deletion	1.7%
Homopolymer indels	43.34%

2.6. Chromosome stats

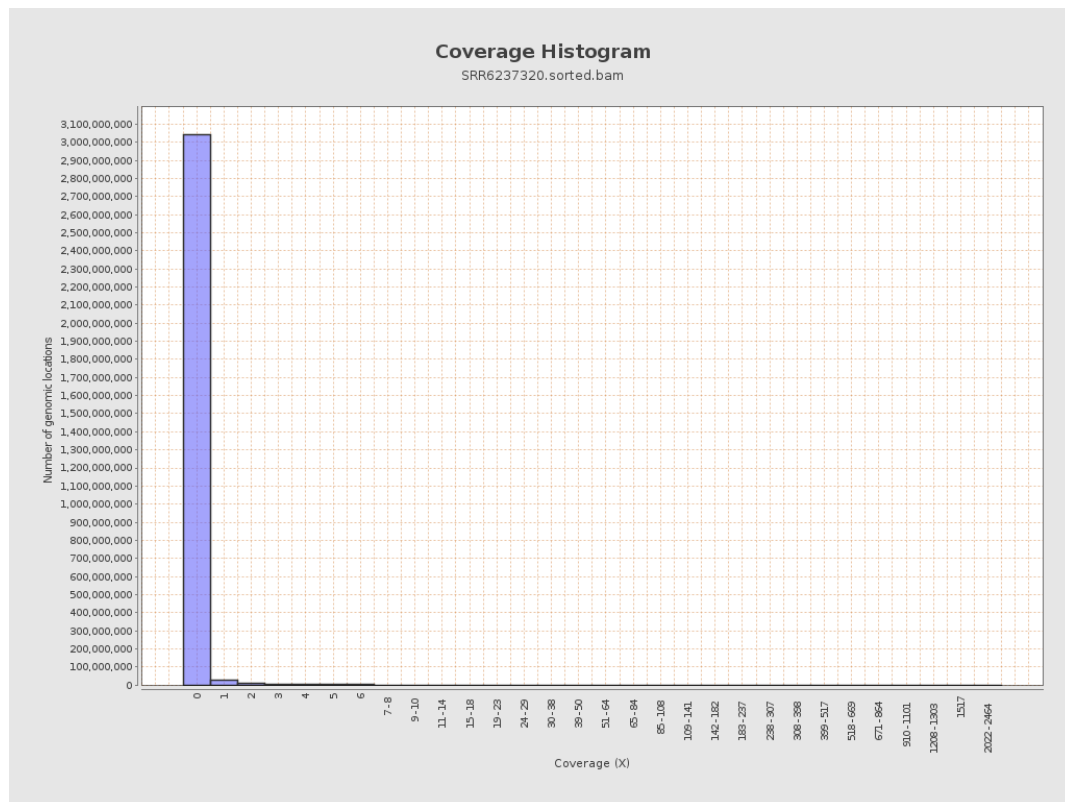
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11385757	0.0457	0.6417
chr2	243199373	9071155	0.0373	1.2268
chr3	198022430	9030538	0.0456	0.4057
chr4	191154276	4739174	0.0248	0.3892
chr5	180915260	4161003	0.023	0.3024
chr6	171115067	11303580	0.0661	0.6133
chr7	159138663	7455379	0.0468	0.5905

chr8	146364022	6443952	0.044	0.8869
chr9	141213431	4404371	0.0312	0.3991
chr10	135534747	5121475	0.0378	0.5432
chr11	135006516	4146983	0.0307	0.3808
chr12	133851895	3380567	0.0253	0.3253
chr13	115169878	4237280	0.0368	0.4228
chr14	107349540	5753411	0.0536	0.4343
chr15	102531392	2555049	0.0249	0.3119
chr16	90354753	3166754	0.035	0.3708
chr17	81195210	4166001	0.0513	0.4805
chr18	78077248	3371805	0.0432	1.0827
chr19	59128983	2585431	0.0437	0.4854
chr20	63025520	2429511	0.0385	0.3926
chr21	48129895	2374790	0.0493	0.4478
chr22	51304566	1204879	0.0235	0.3055
chrMT	16571	17967	1.0842	2.4714
chrX	155270560	5671782	0.0365	0.4051
chrY	59373566	493518	0.0083	0.3069

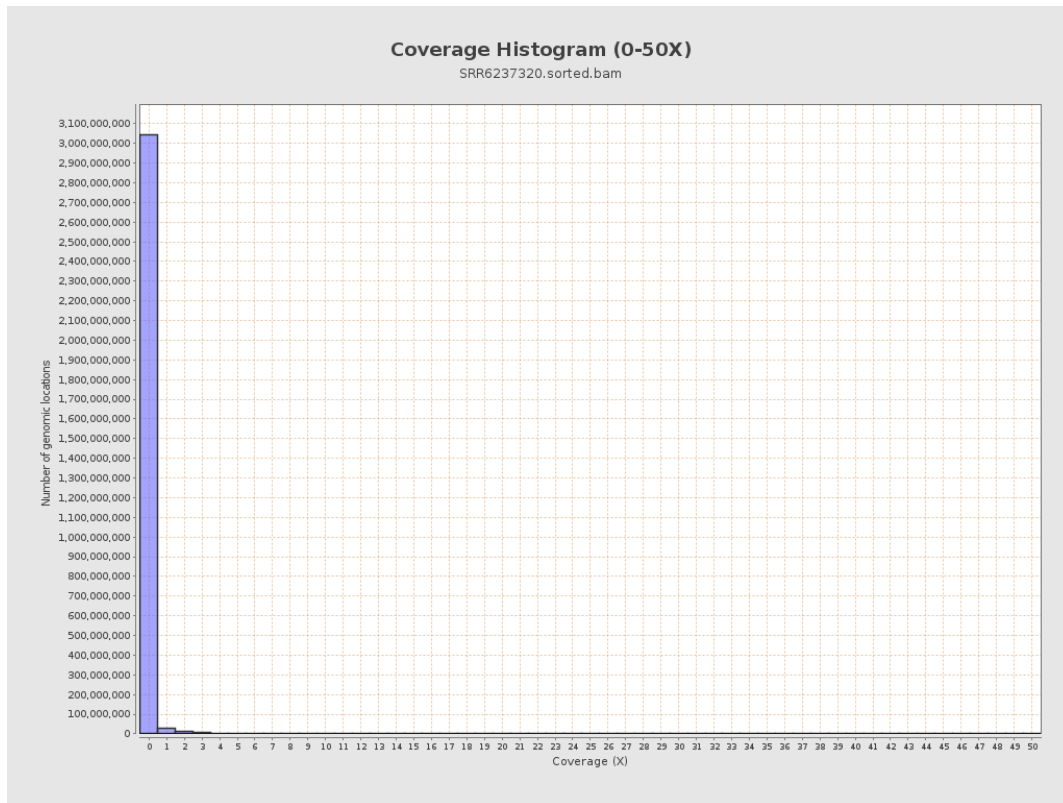
3. Results : Coverage across reference



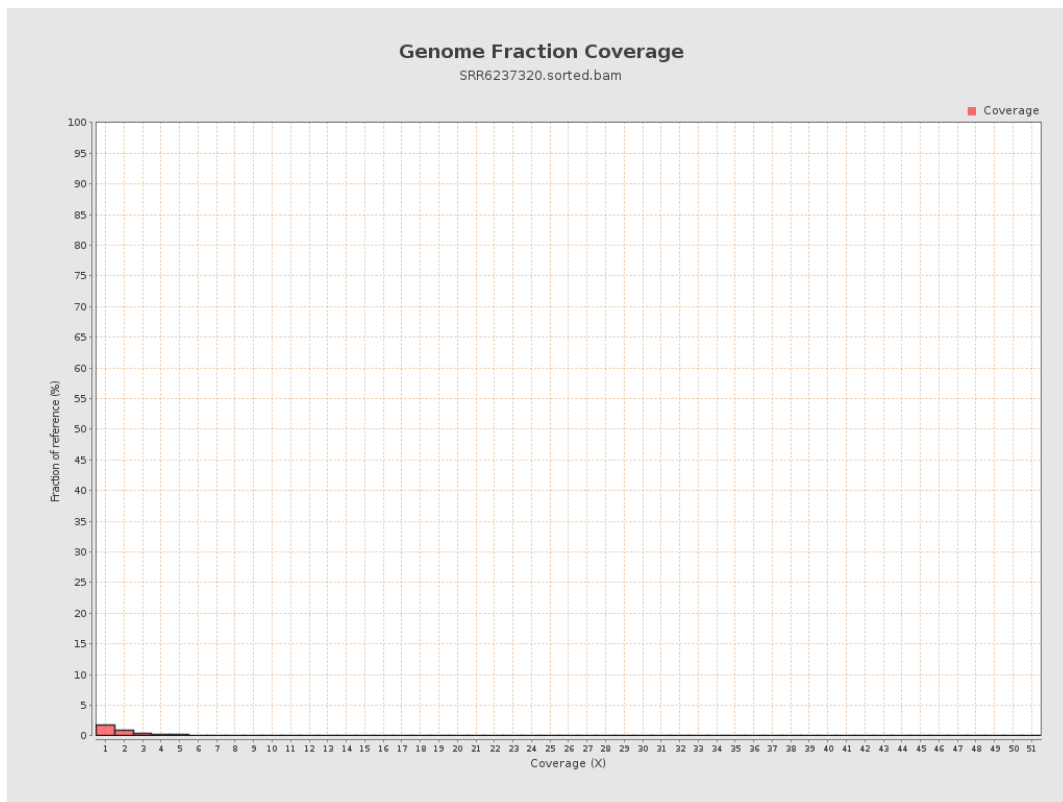
4. Results : Coverage Histogram



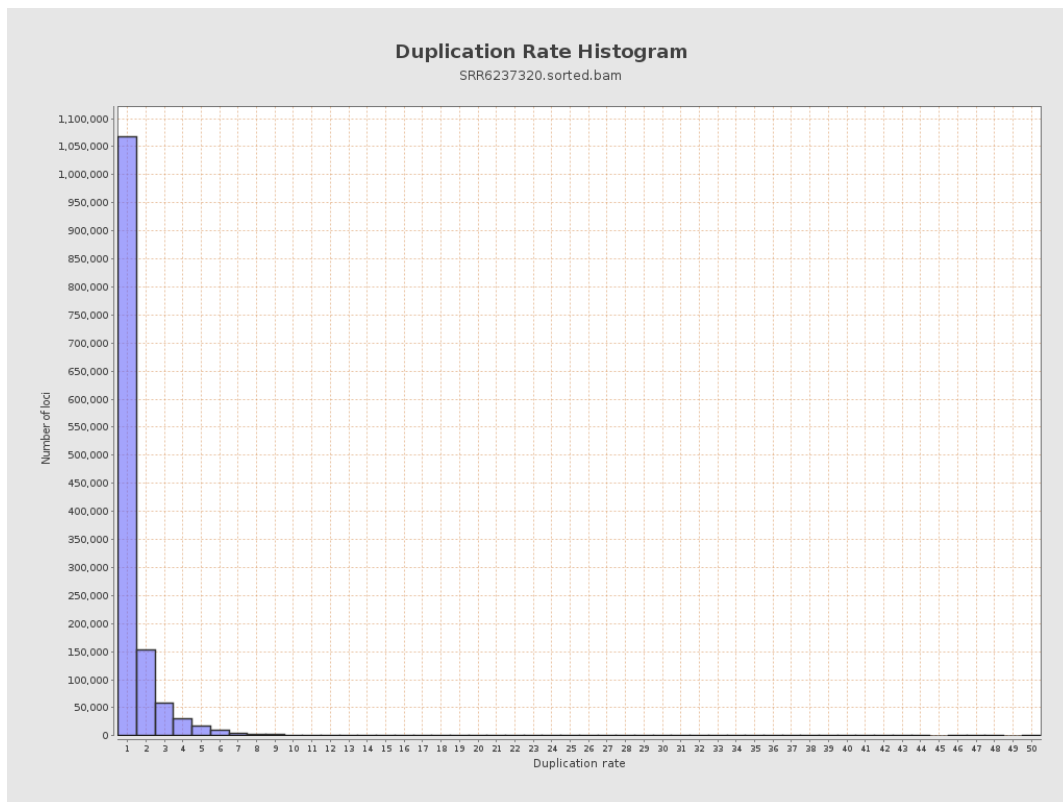
5. Results : Coverage Histogram (0-50X)



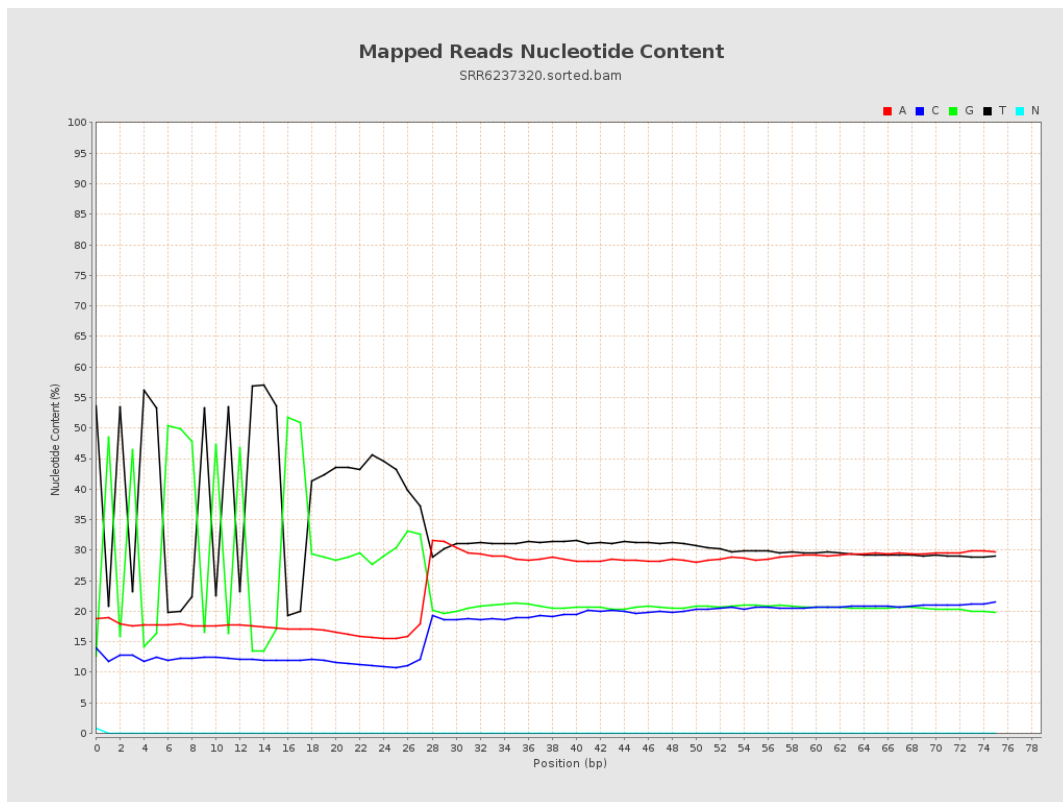
6. Results : Genome Fraction Coverage



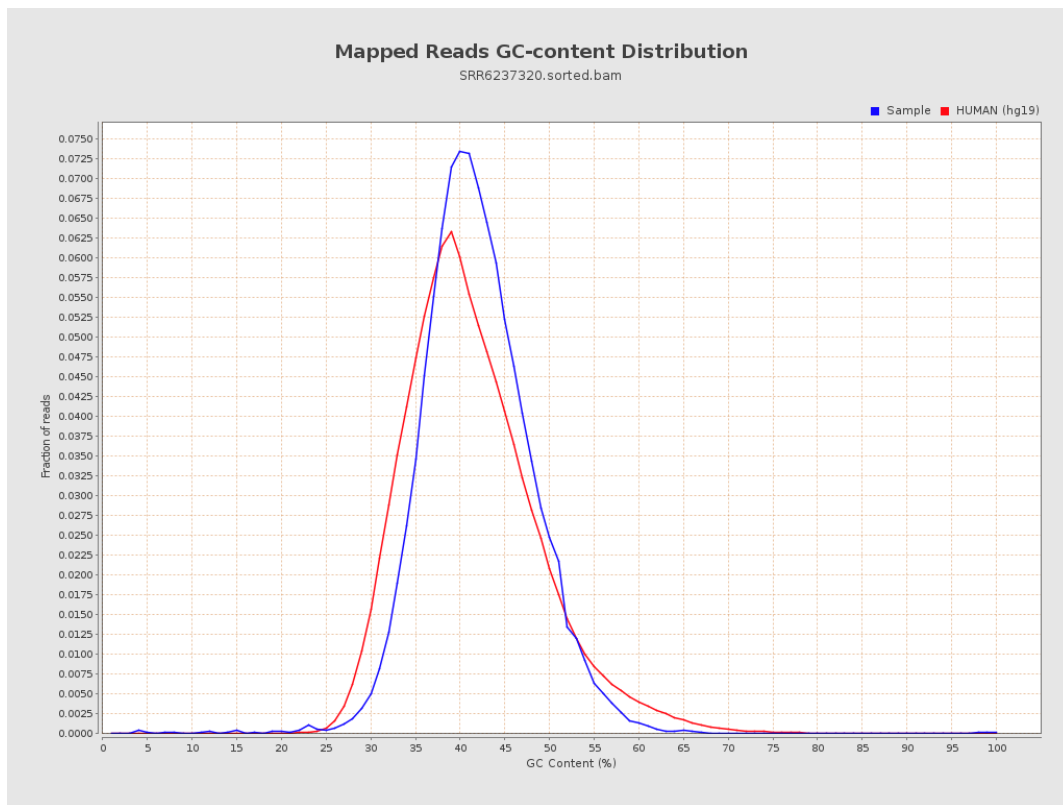
7. Results : Duplication Rate Histogram



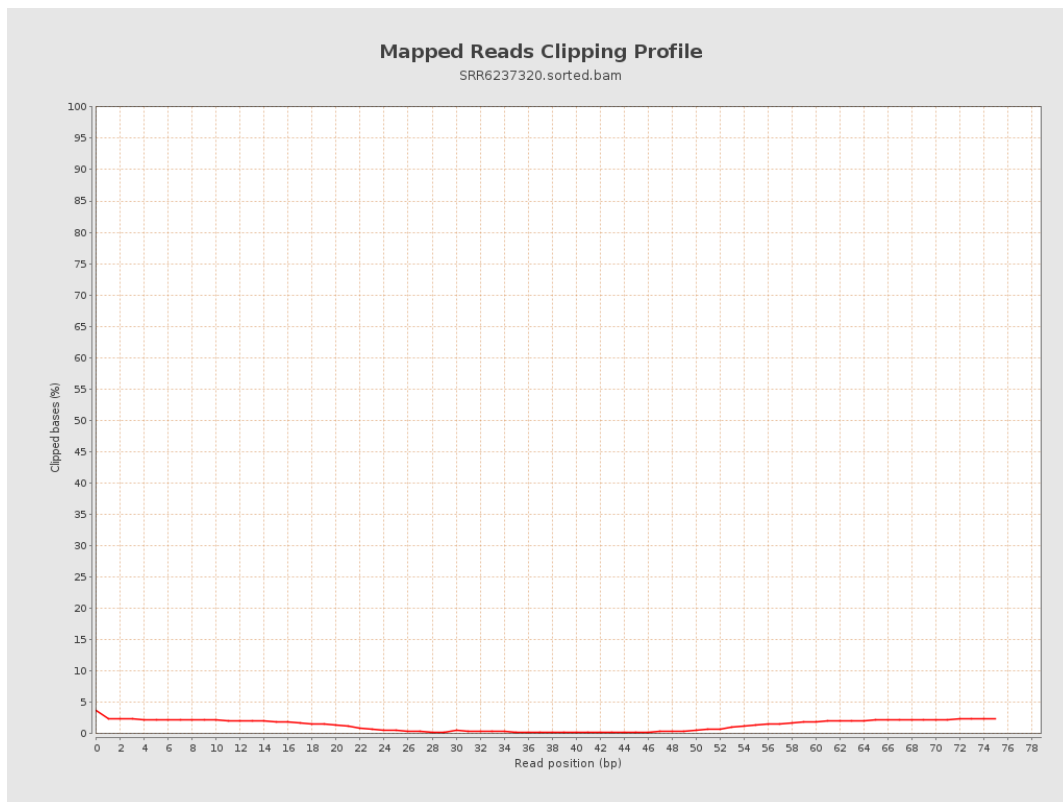
8. Results : Mapped Reads Nucleotide Content



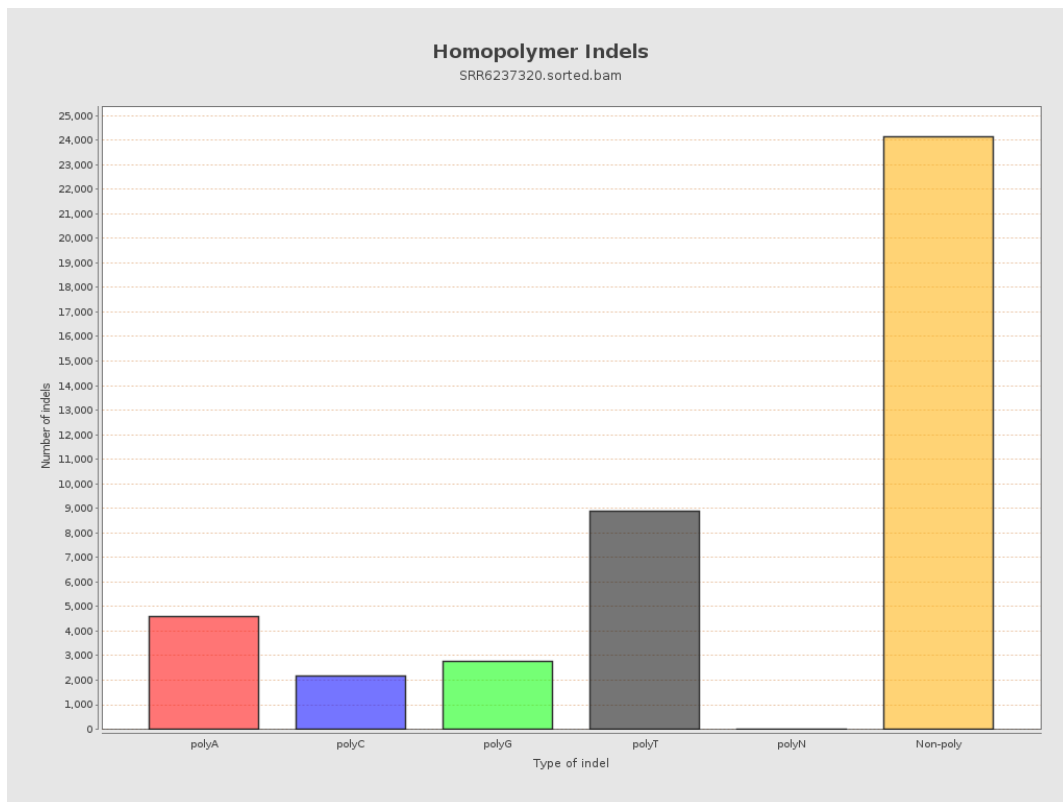
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

