

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:52:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237575.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_SRR6237575 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237575.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:52:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237575.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,915,474
Mapped reads	1,543,153 / 80.56%
Unmapped reads	372,321 / 19.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,530 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	94,516 / 4.93%
Duplication rate	4.14%
Clipped reads	964,052 / 50.33%

2.2. ACGT Content

Number/percentage of A's	24,817,878 / 25.58%
Number/percentage of C's	18,194,607 / 18.75%
Number/percentage of T's	29,515,764 / 30.42%
Number/percentage of G's	24,480,158 / 25.23%
Number/percentage of N's	22,668 / 0.02%
GC Percentage	43.98%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.3103
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2.4. Mapping Quality

Mean Mapping Quality	39.78
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2.5. Mismatches and indels

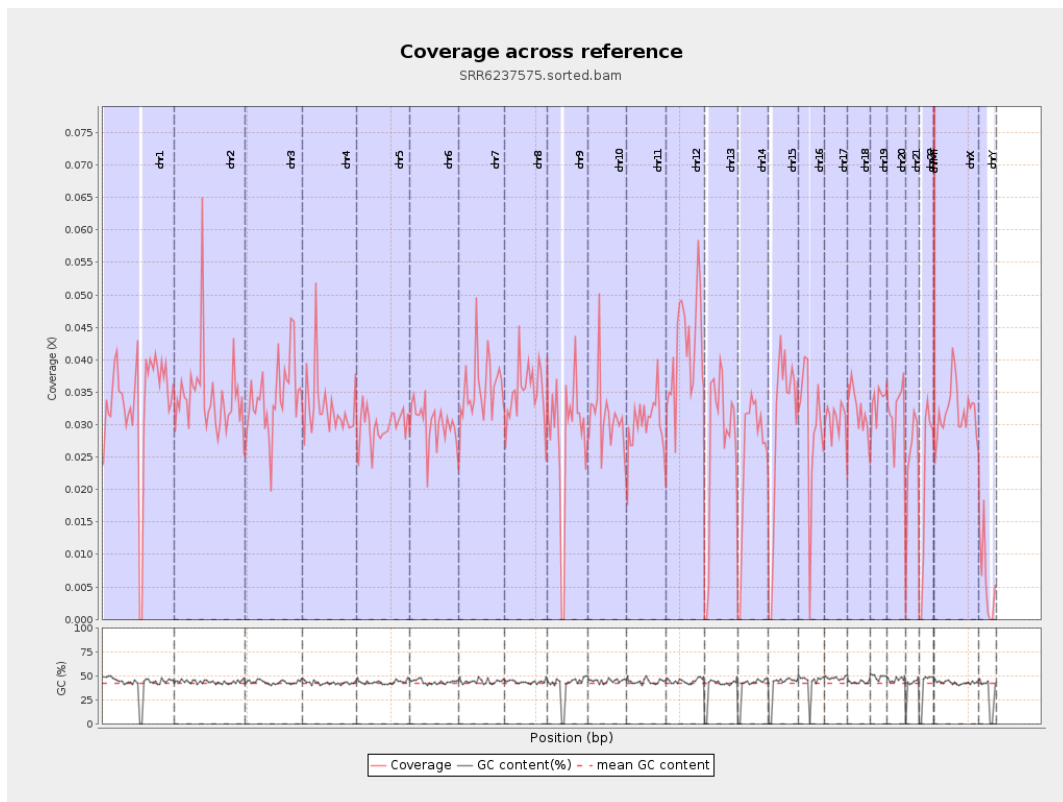
General error rate	0.98%
Mismatches	932,222
Insertions	9,195
Mapped reads with at least one insertion	0.59%
Deletions	34,762
Mapped reads with at least one deletion	2.22%
Homopolymer indels	46.09%

2.6. Chromosome stats

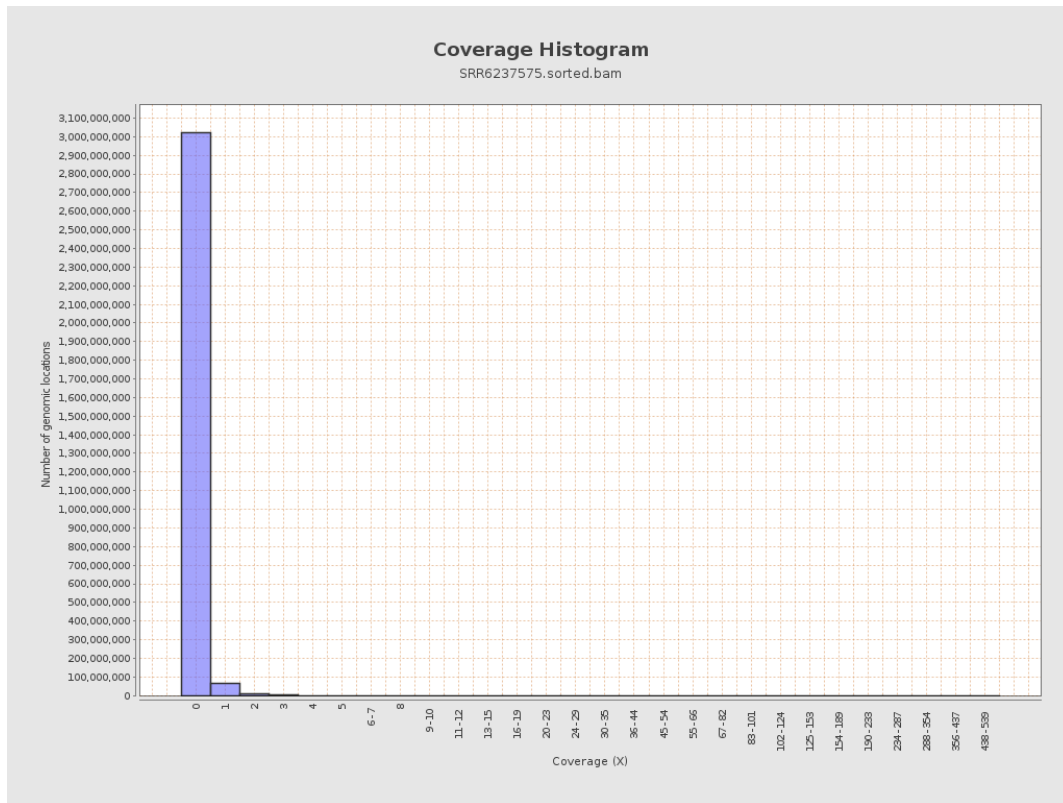
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8291347	0.0333	0.3661
chr2	243199373	8334099	0.0343	0.4494
chr3	198022430	6764757	0.0342	0.2512
chr4	191154276	6223603	0.0326	0.2564
chr5	180915260	5404809	0.0299	0.225
chr6	171115067	5146189	0.0301	0.2511
chr7	159138663	5669100	0.0356	0.4192

chr8	146364022	5097255	0.0348	0.3002
chr9	141213431	3962339	0.0281	0.3343
chr10	135534747	4210846	0.0311	0.3081
chr11	135006516	4111728	0.0305	0.3364
chr12	133851895	5551562	0.0415	0.287
chr13	115169878	3122149	0.0271	0.2251
chr14	107349540	2736048	0.0255	0.2501
chr15	102531392	3053382	0.0298	0.2425
chr16	90354753	2685445	0.0297	0.2607
chr17	81195210	2492757	0.0307	0.258
chr18	78077248	2525869	0.0324	0.4569
chr19	59128983	1981974	0.0335	0.3193
chr20	63025520	2012425	0.0319	0.2478
chr21	48129895	1188160	0.0247	0.2352
chr22	51304566	1088698	0.0212	0.1967
chrMT	16571	95019	5.7341	5.0893
chrX	155270560	4984017	0.0321	0.2678
chrY	59373566	354871	0.006	0.1439

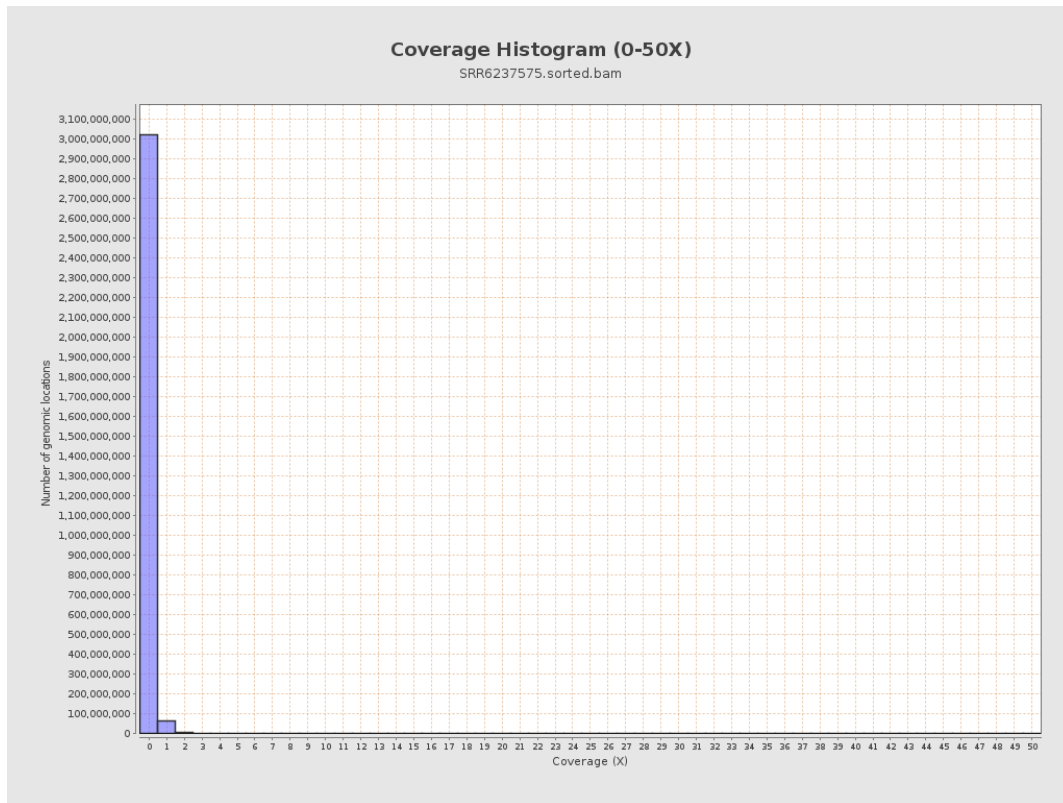
3. Results : Coverage across reference



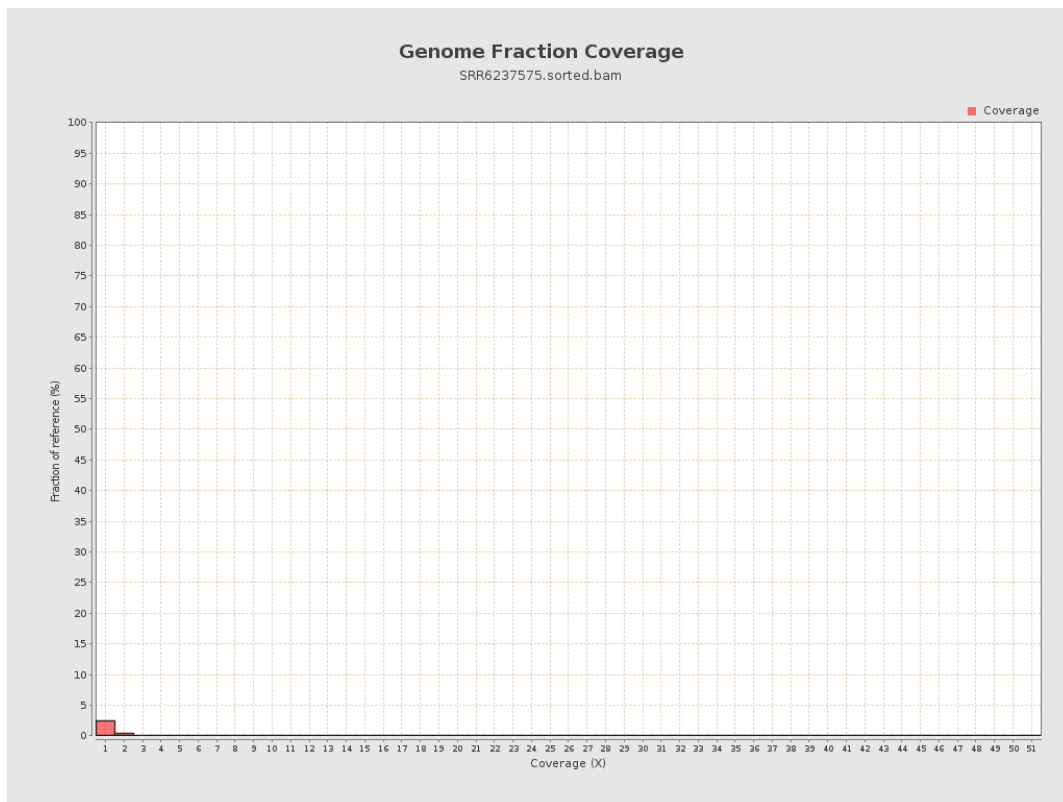
4. Results : Coverage Histogram



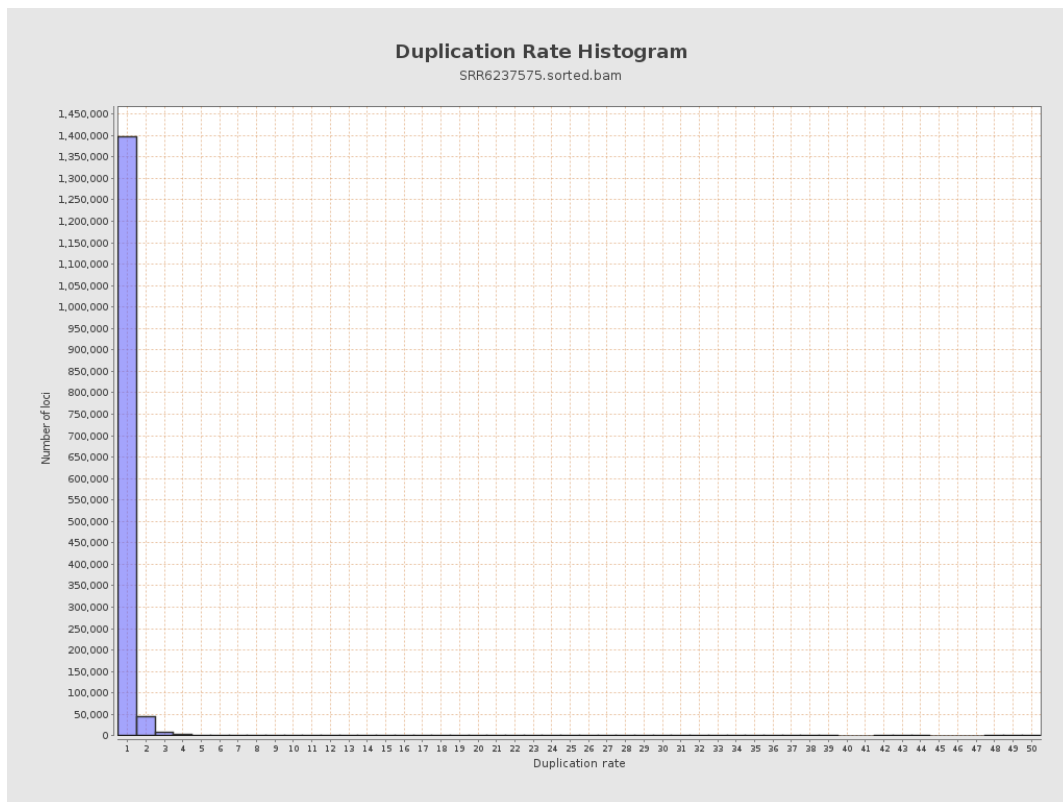
5. Results : Coverage Histogram (0-50X)



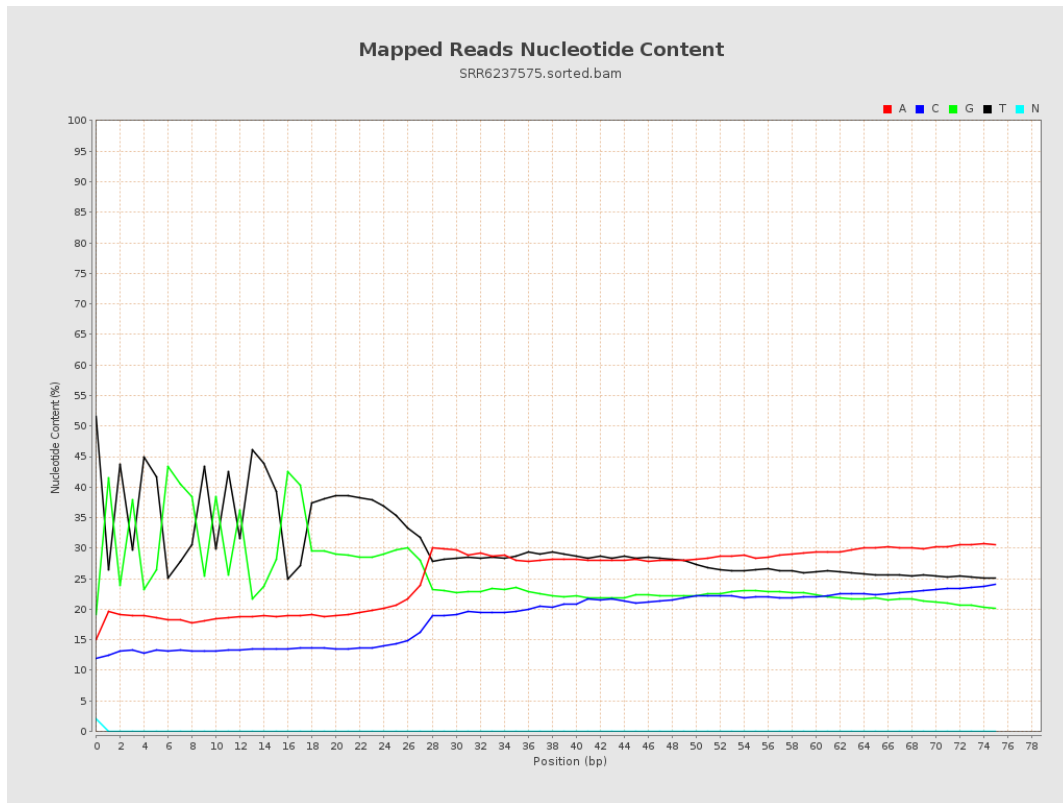
6. Results : Genome Fraction Coverage



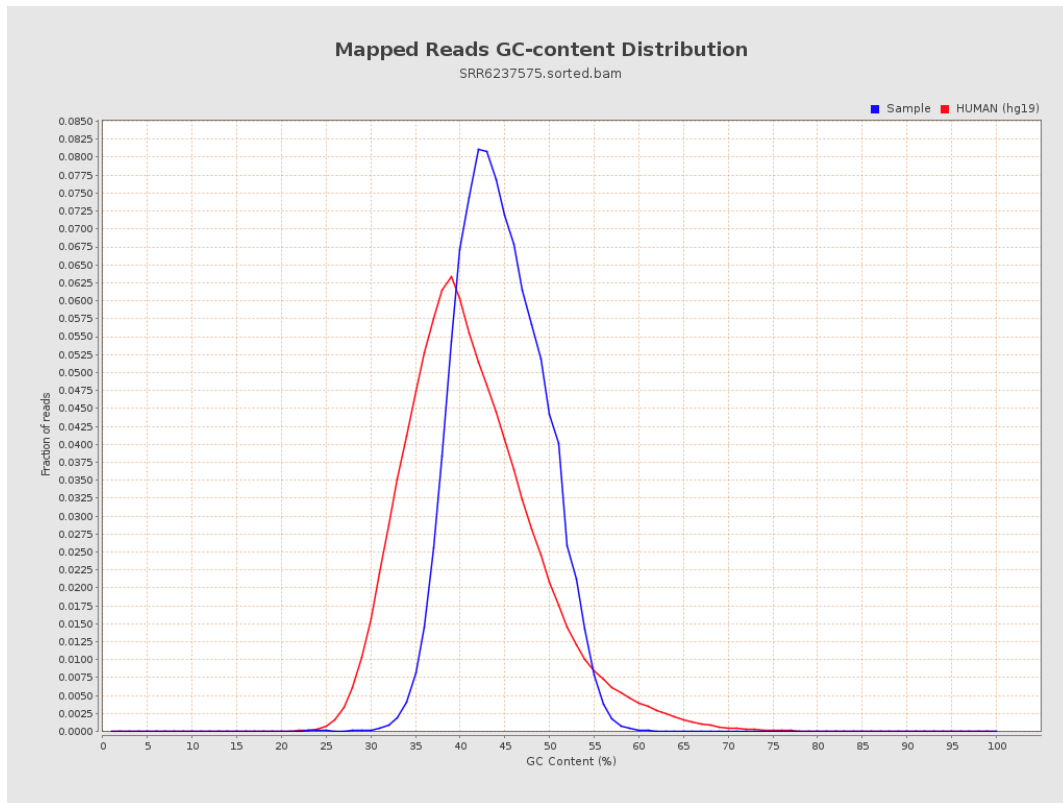
7. Results : Duplication Rate Histogram



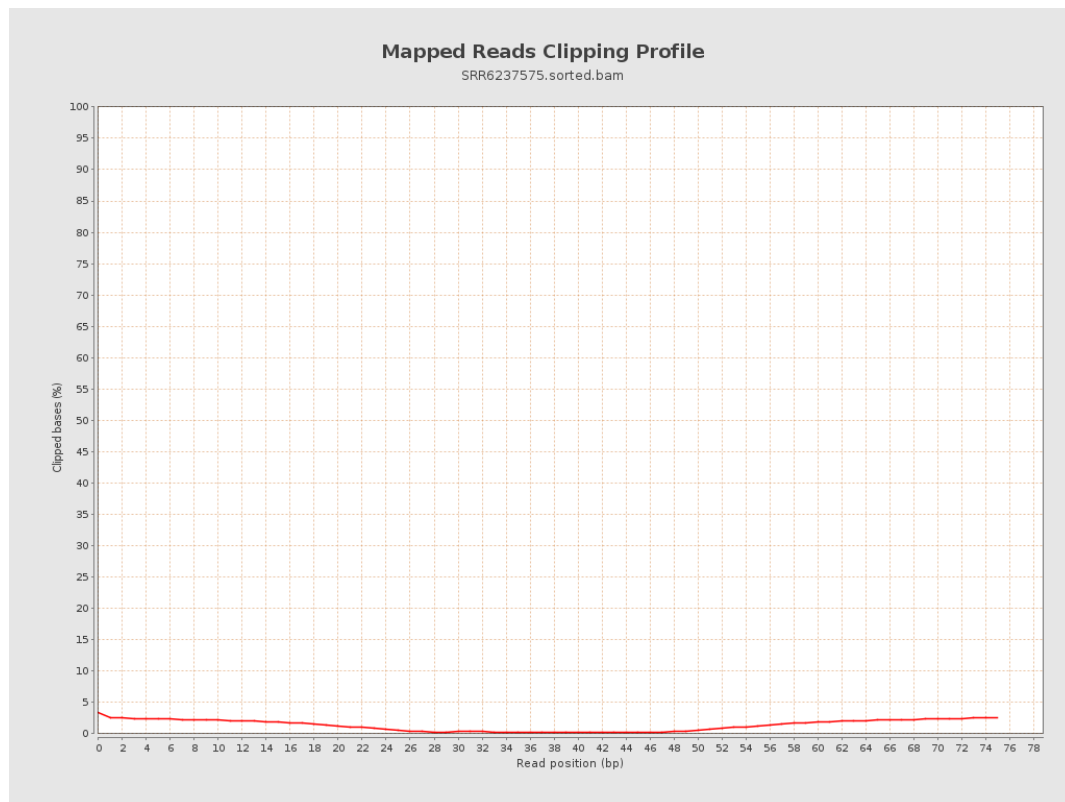
8. Results : Mapped Reads Nucleotide Content



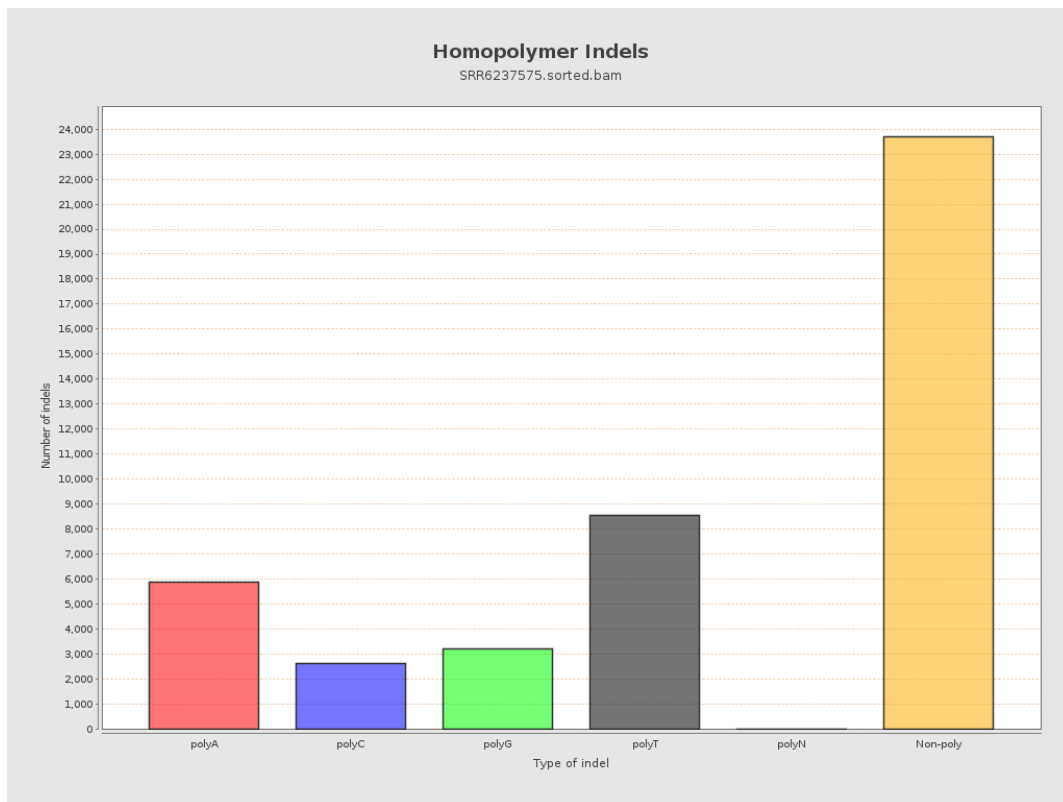
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

