

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:44:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237256.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_SRR6237256 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237256.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:44:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237256.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,506,939
Mapped reads	2,238,868 / 89.31%
Unmapped reads	268,071 / 10.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,742 / 1.19%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	631,704 / 25.2%
Duplication rate	20.83%
Clipped reads	1,608,749 / 64.17%

2.2. ACGT Content

Number/percentage of A's	34,526,073 / 25.73%
Number/percentage of C's	22,437,529 / 16.72%
Number/percentage of T's	46,075,293 / 34.33%
Number/percentage of G's	31,155,209 / 23.21%
Number/percentage of N's	13,657 / 0.01%
GC Percentage	39.93%

2.3. Coverage

Mean	0.0434

Standard Deviation	0.6309
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.67
----------------------	-------

2.5. Mismatches and indels

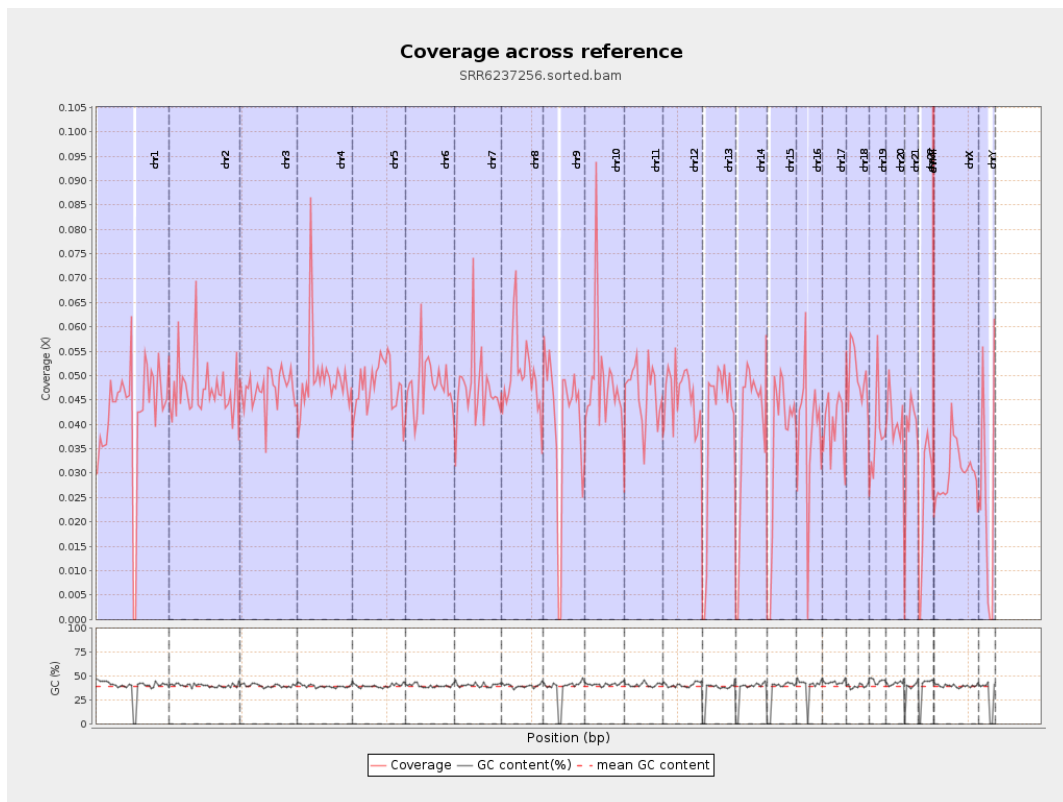
General error rate	0.69%
Mismatches	911,185
Insertions	9,206
Mapped reads with at least one insertion	0.41%
Deletions	45,425
Mapped reads with at least one deletion	2.01%
Homopolymer indels	40.95%

2.6. Chromosome stats

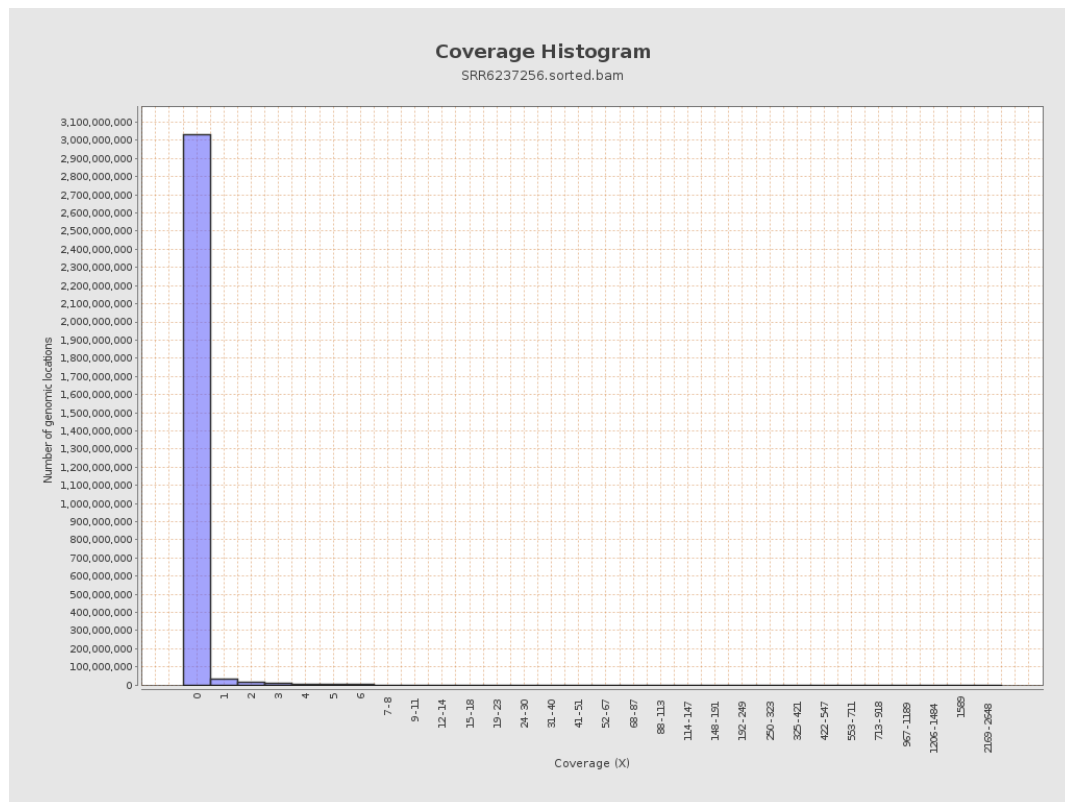
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10548220	0.0423	0.684
chr2	243199373	11496528	0.0473	1.3125
chr3	198022430	9367291	0.0473	0.4004
chr4	191154276	9422235	0.0493	0.4479
chr5	180915260	8654045	0.0478	0.4038
chr6	171115067	8220165	0.048	0.575
chr7	159138663	7564125	0.0475	0.5934

chr8	146364022	7301132	0.0499	0.8467
chr9	141213431	5725429	0.0405	0.4318
chr10	135534747	6602451	0.0487	0.5601
chr11	135006516	6255477	0.0463	0.4365
chr12	133851895	6130356	0.0458	0.3963
chr13	115169878	4555459	0.0396	0.4238
chr14	107349540	4162421	0.0388	0.3698
chr15	102531392	3699286	0.0361	0.3739
chr16	90354753	3496854	0.0387	0.3781
chr17	81195210	3180961	0.0392	0.3811
chr18	78077248	3911379	0.0501	1.2578
chr19	59128983	2261898	0.0383	0.5656
chr20	63025520	2569987	0.0408	0.3779
chr21	48129895	1798795	0.0374	0.376
chr22	51304566	1232507	0.024	0.2835
chrMT	16571	41825	2.524	3.2802
chrX	155270560	4676197	0.0301	0.3231
chrY	59373566	1410103	0.0237	0.4226

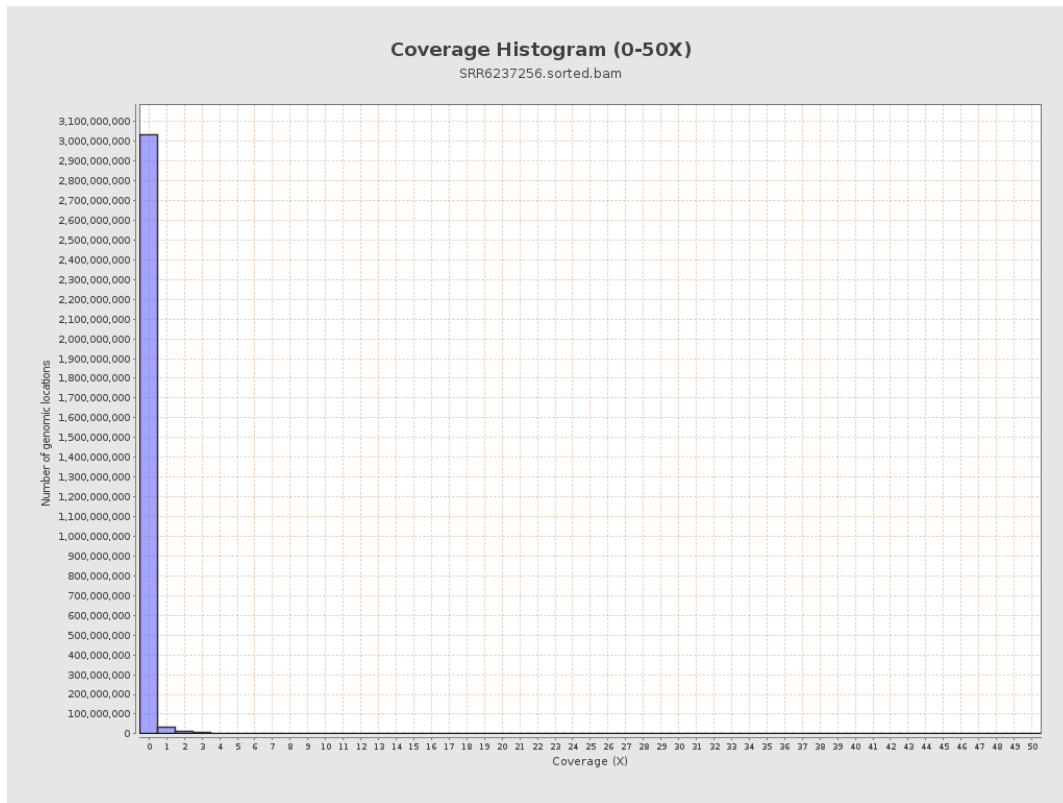
3. Results : Coverage across reference



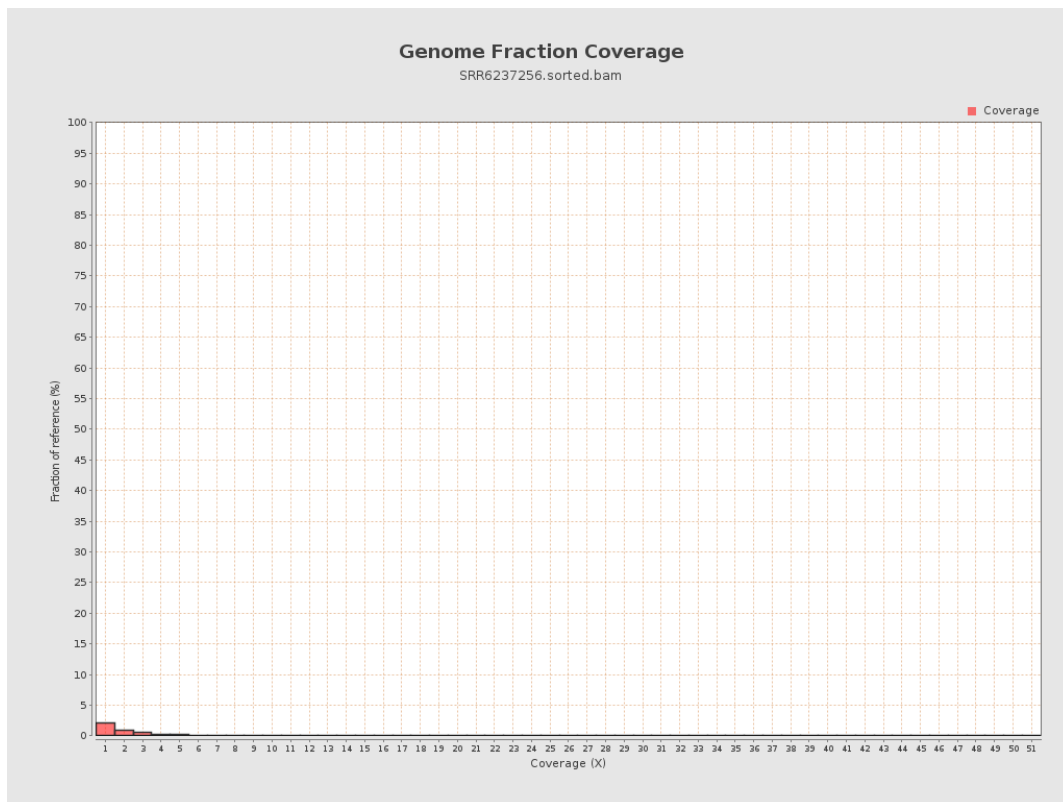
4. Results : Coverage Histogram



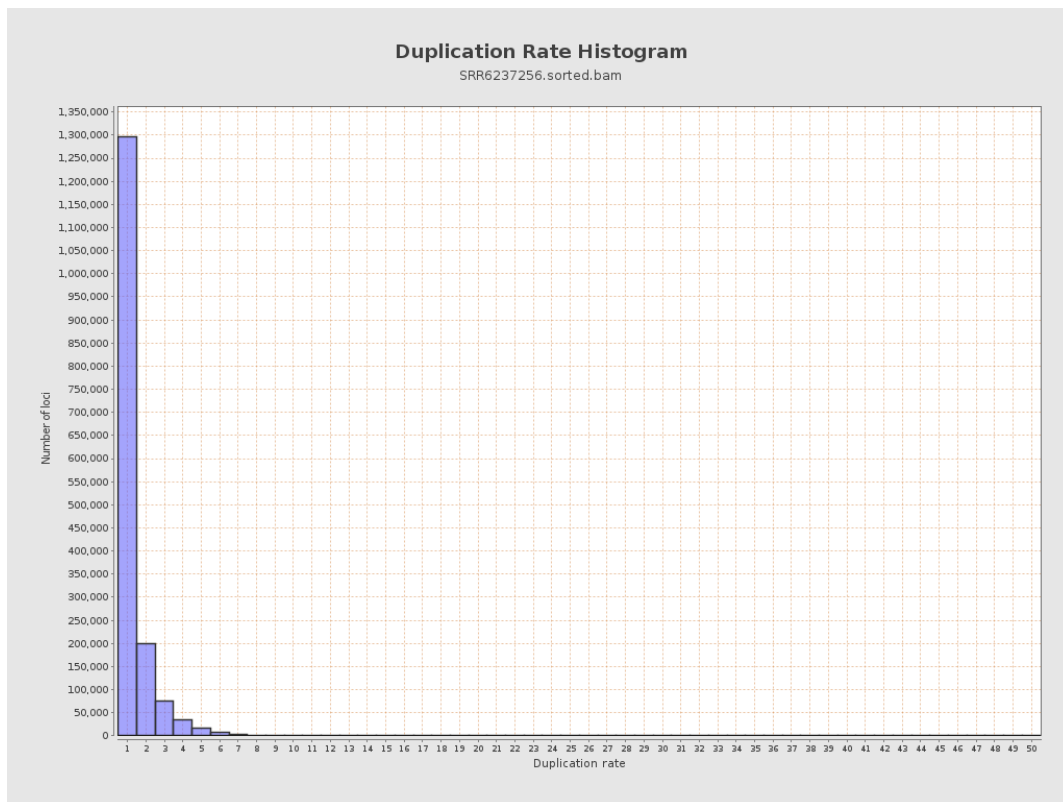
5. Results : Coverage Histogram (0-50X)



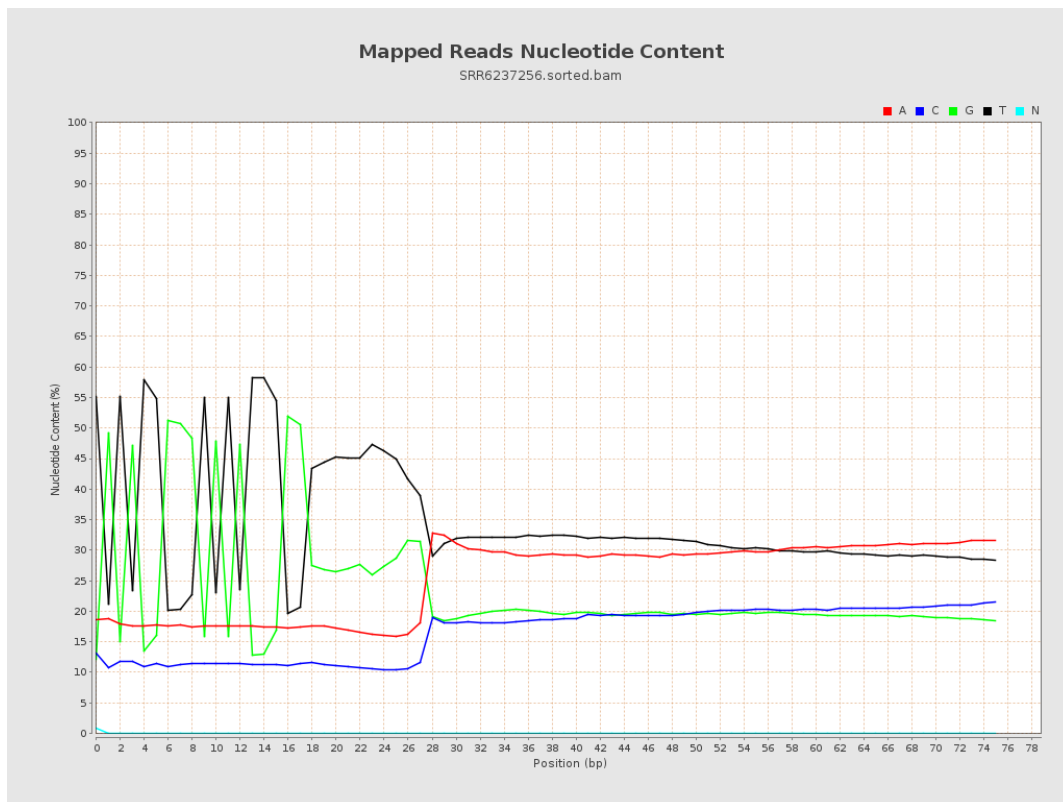
6. Results : Genome Fraction Coverage



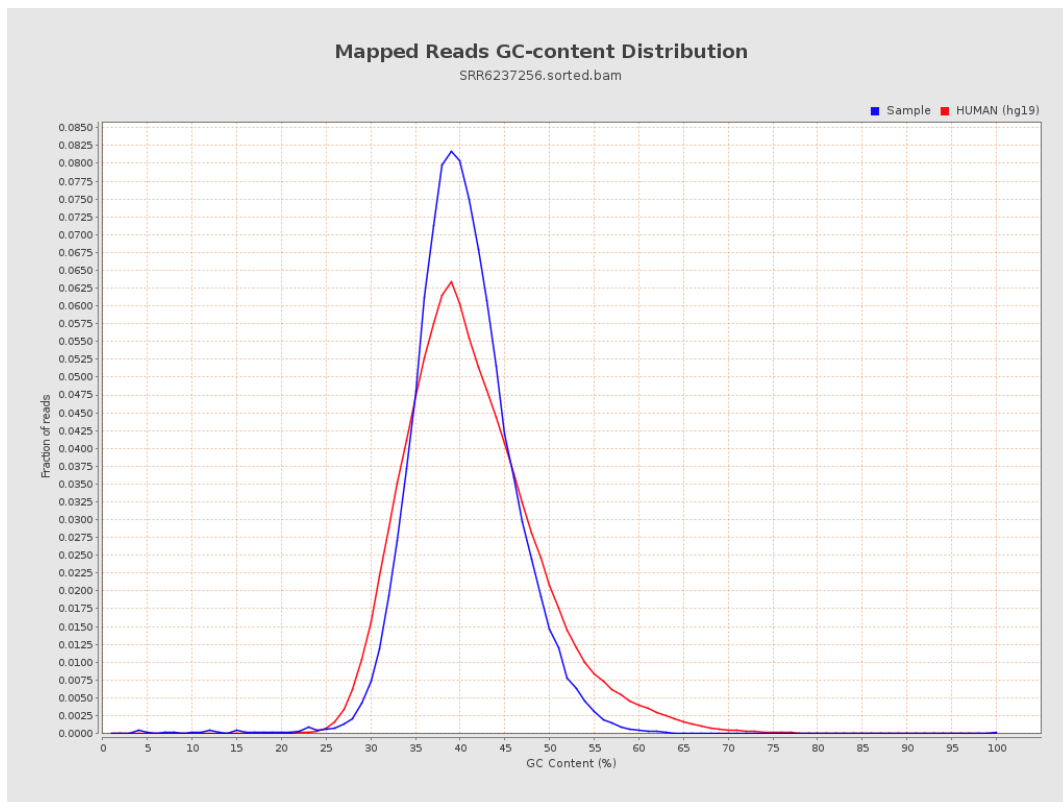
7. Results : Duplication Rate Histogram



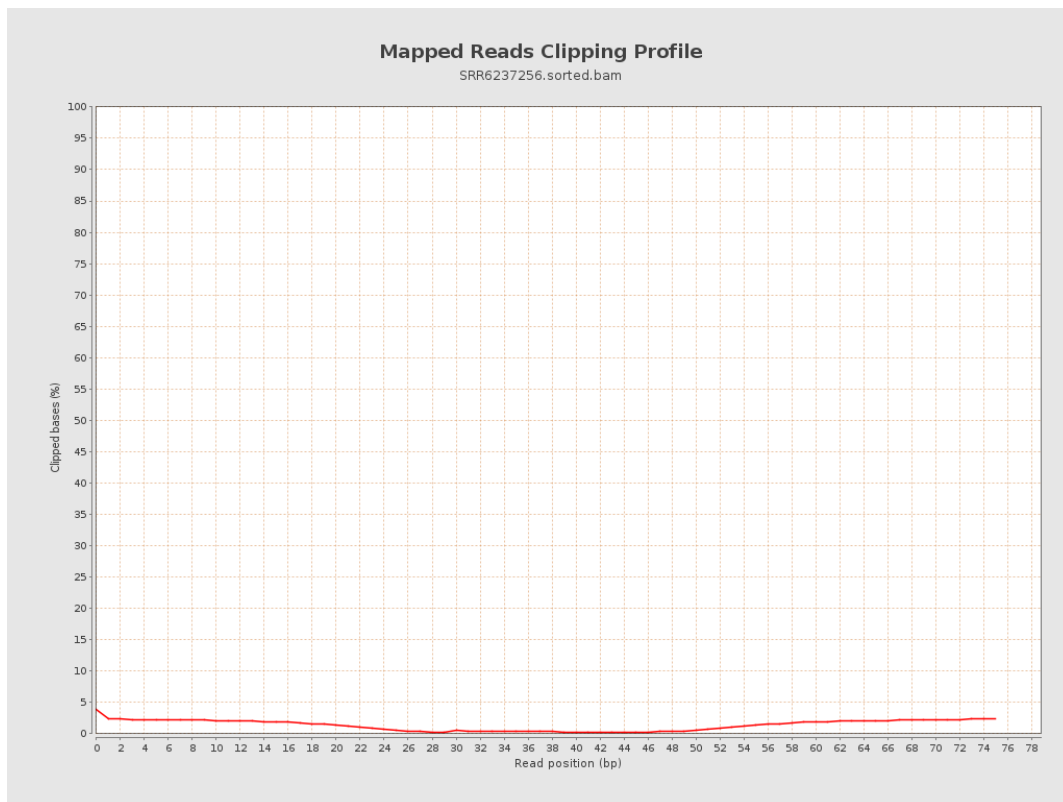
8. Results : Mapped Reads Nucleotide Content



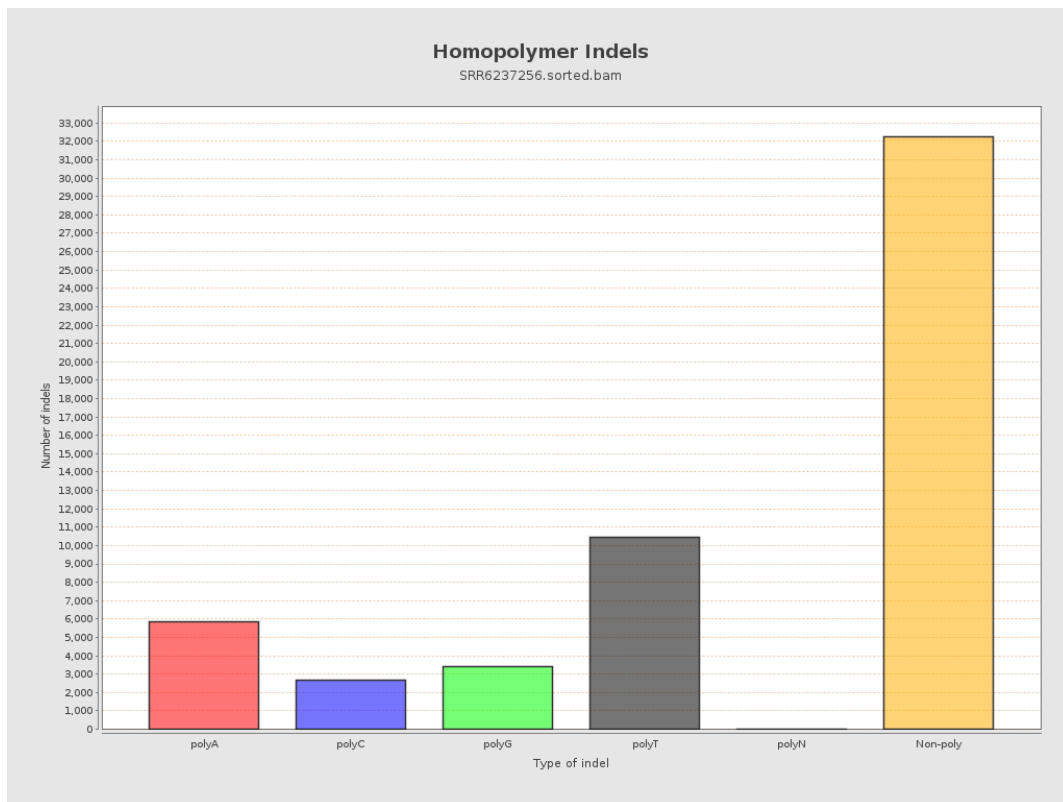
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

