Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:14:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236092.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_SRR6236092 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236092.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:14:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236092.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,281,582
Mapped reads	1,104,939 / 86.22%
Unmapped reads	176,643 / 13.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,916 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	54,721 / 4.27%
Duplication rate	4.18%
Clipped reads	519,911 / 40.57%

2.2. ACGT Content

Number/percentage of A's	20,065,877 / 27.62%
Number/percentage of C's	12,775,711 / 17.58%
Number/percentage of T's	23,713,997 / 32.64%
Number/percentage of G's	16,061,875 / 22.11%
Number/percentage of N's	39,827 / 0.05%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0235

Standard Deviation	0.2477

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

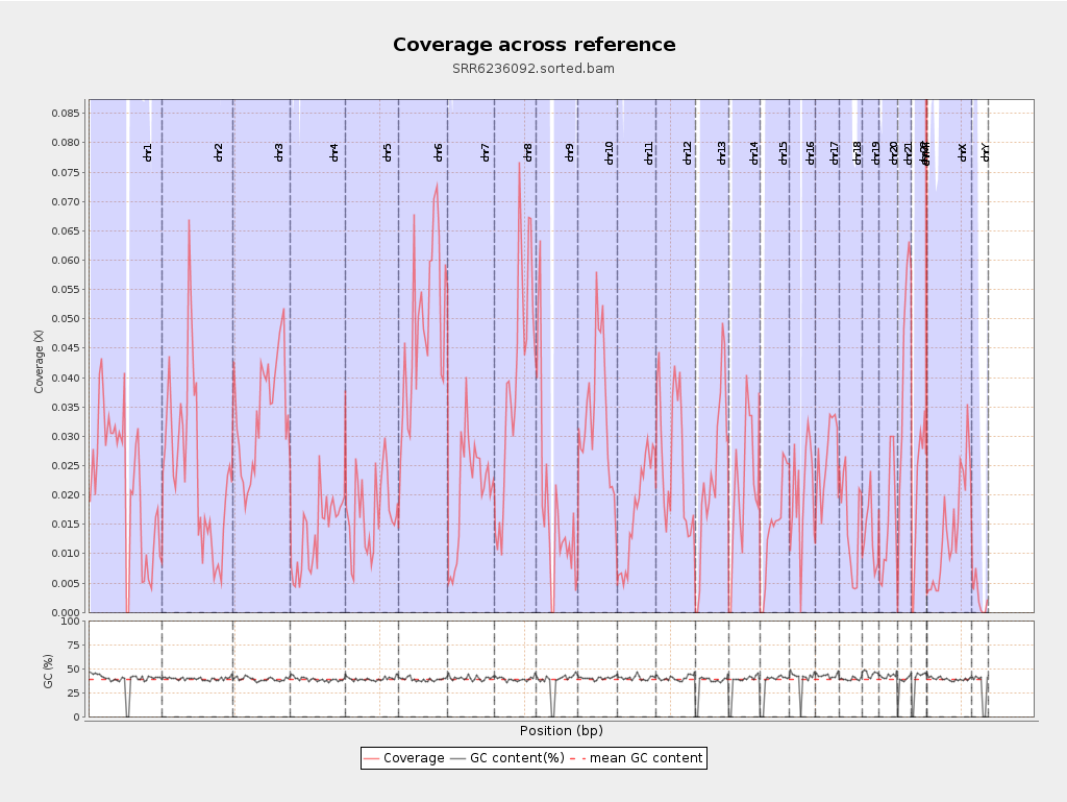
General error rate	0.82%
Mismatches	587,129
Insertions	5,145
Mapped reads with at least one insertion	0.46%
Deletions	22,619
Mapped reads with at least one deletion	2.02%
Homopolymer indels	46.65%

2.6. Chromosome stats

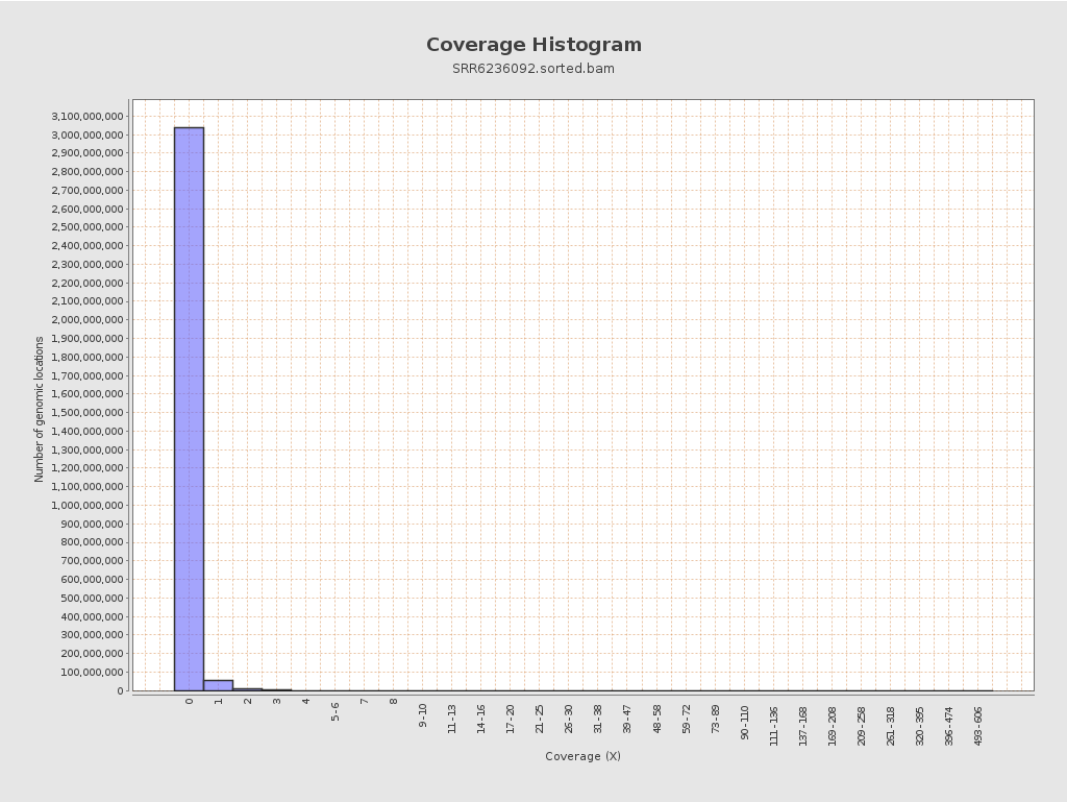
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5460903	0.0219	0.3906
chr2	243199373	5945784	0.0244	0.2613
chr3	198022430	6731426	0.034	0.2122
chr4	191154276	2556351	0.0134	0.1377
chr5	180915260	3094218	0.0171	0.1503
chr6	171115067	8168907	0.0477	0.3264
chr7	159138663	3331564	0.0209	0.2741

chr8	146364022	5733579	0.0392	0.449
chr9	141213431	2439155	0.0173	0.1825
chr10	135534747	4616026	0.0341	0.2625
chr11	135006516	2334201	0.0173	0.1661
chr12	133851895	3454584	0.0258	0.187
chr13	115169878	2672421	0.0232	0.176
chr14	107349540	2203552	0.0205	0.166
chr15	102531392	1524699	0.0149	0.1423
chr16	90354753	1838999	0.0204	0.1703
chr17	81195210	2143529	0.0264	0.1862
chr18	78077248	1150327	0.0147	0.299
chr19	59128983	806733	0.0136	0.2575
chr20	63025520	945996	0.015	0.1417
chr21	48129895	2000485	0.0416	0.2381
chr22	51304566	1060400	0.0207	0.1639
chrMT	16571	167235	10.092	6.8515
chrX	155270560	2171491	0.014	0.1424
chrY	59373566	143410	0.0024	0.0648

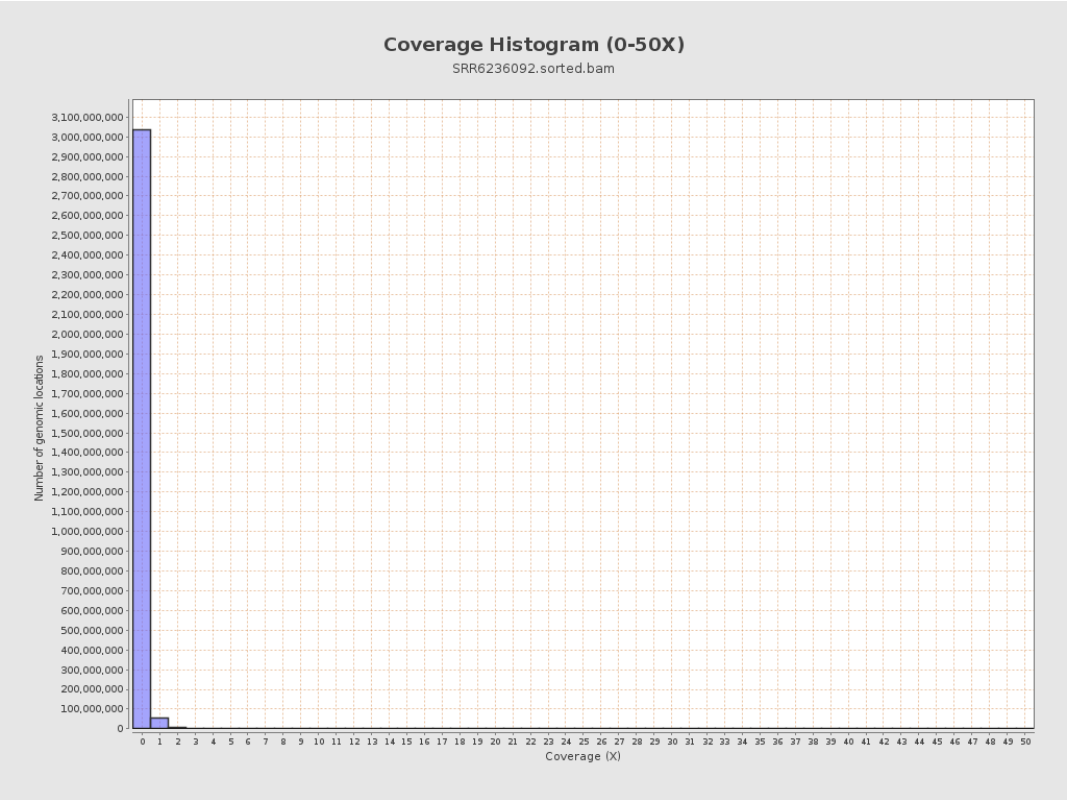
3. Results : Coverage across reference



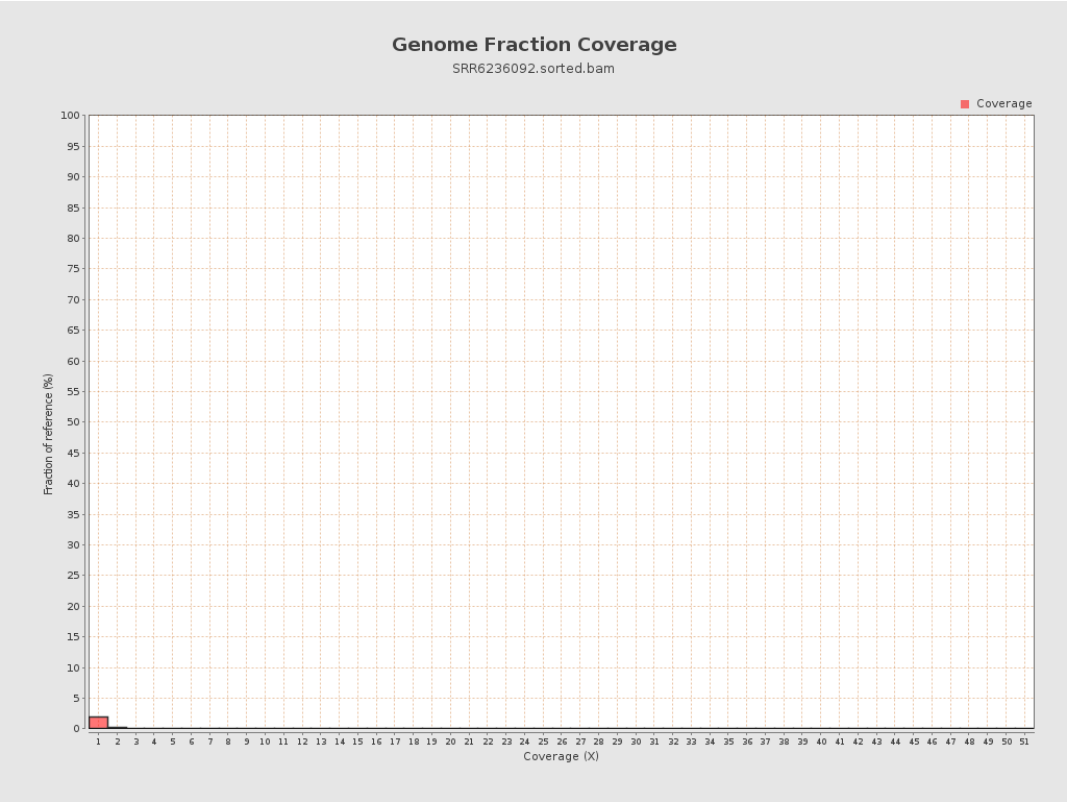
4. Results : Coverage Histogram



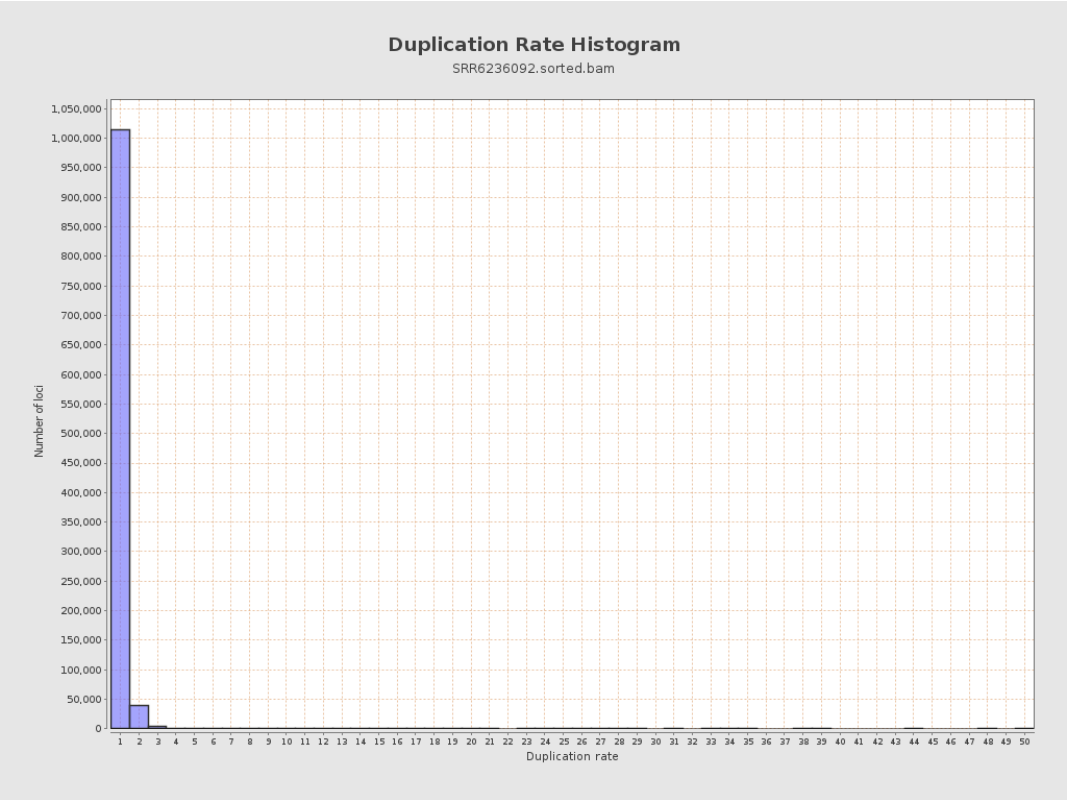
5. Results : Coverage Histogram (0-50X)



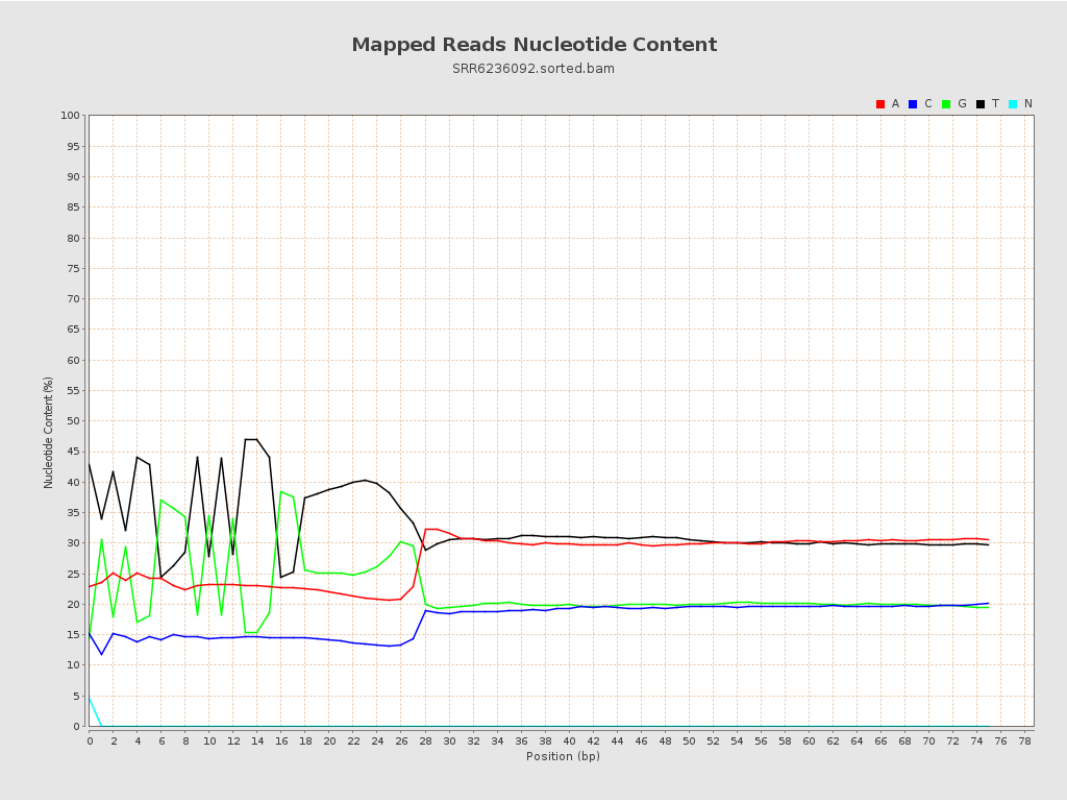
6. Results : Genome Fraction Coverage



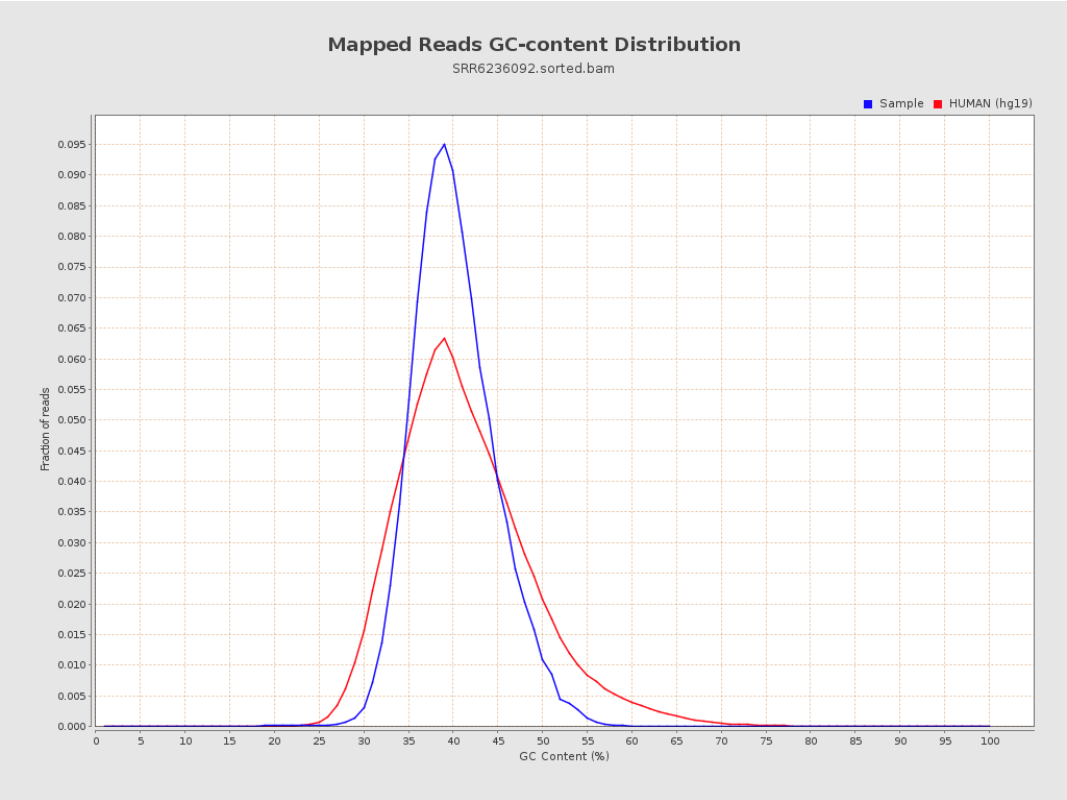
7. Results : Duplication Rate Histogram



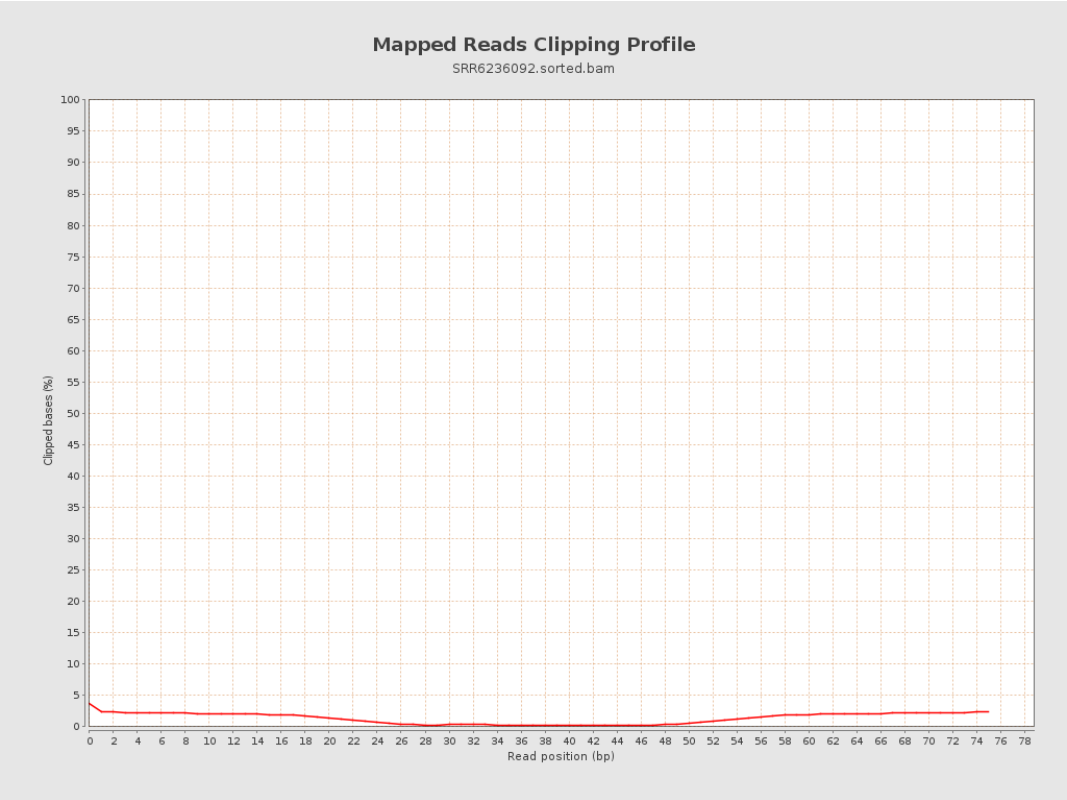
8. Results : Mapped Reads Nucleotide Content



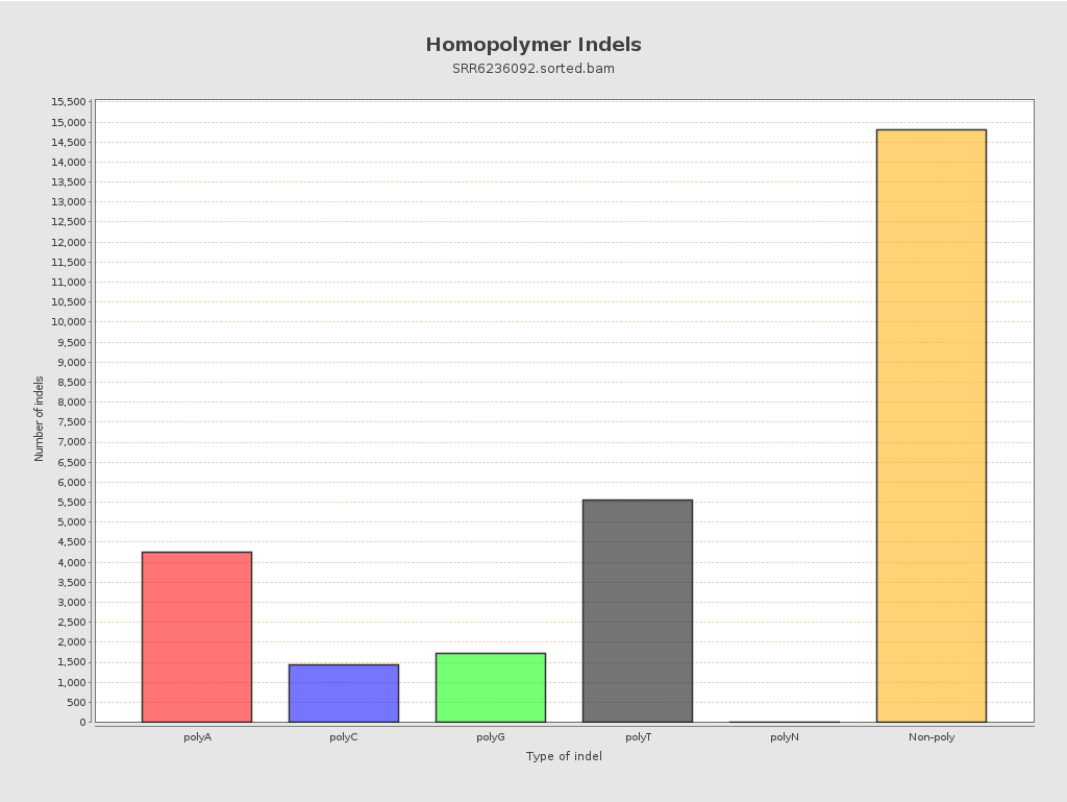
9. Results : Mapped Reads GC-content Distribution



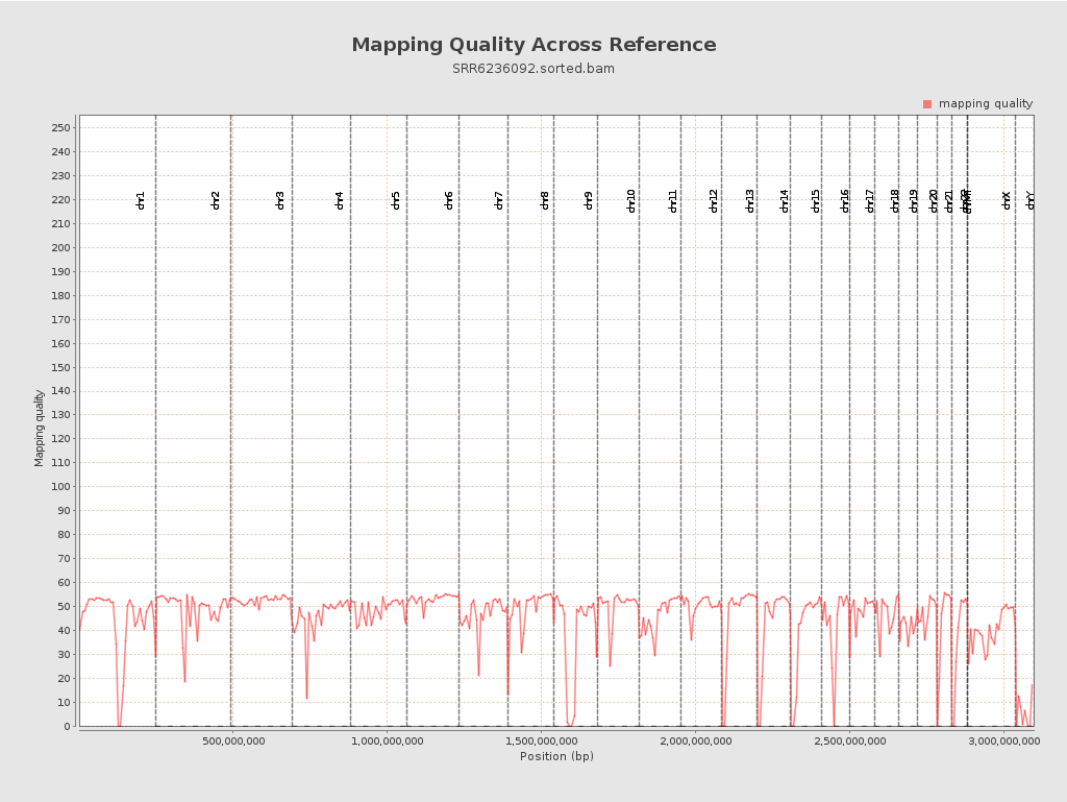
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram