Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:00:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236069.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_SRR6236069 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236069.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:00:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,890,937
Mapped reads	1,662,145 / 87.9%
Unmapped reads	228,792 / 12.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,057 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	76,592 / 4.05%
Duplication rate	3.61%
Clipped reads	761,394 / 40.27%

2.2. ACGT Content

Number/percentage of A's	30,158,819 / 27.44%
Number/percentage of C's	19,728,341 / 17.95%
Number/percentage of T's	35,332,054 / 32.15%
Number/percentage of G's	24,632,064 / 22.41%
Number/percentage of N's	57,557 / 0.05%
GC Percentage	40.36%

2.3. Coverage

Mean	0.0355

Standard Deviation	0.3746

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

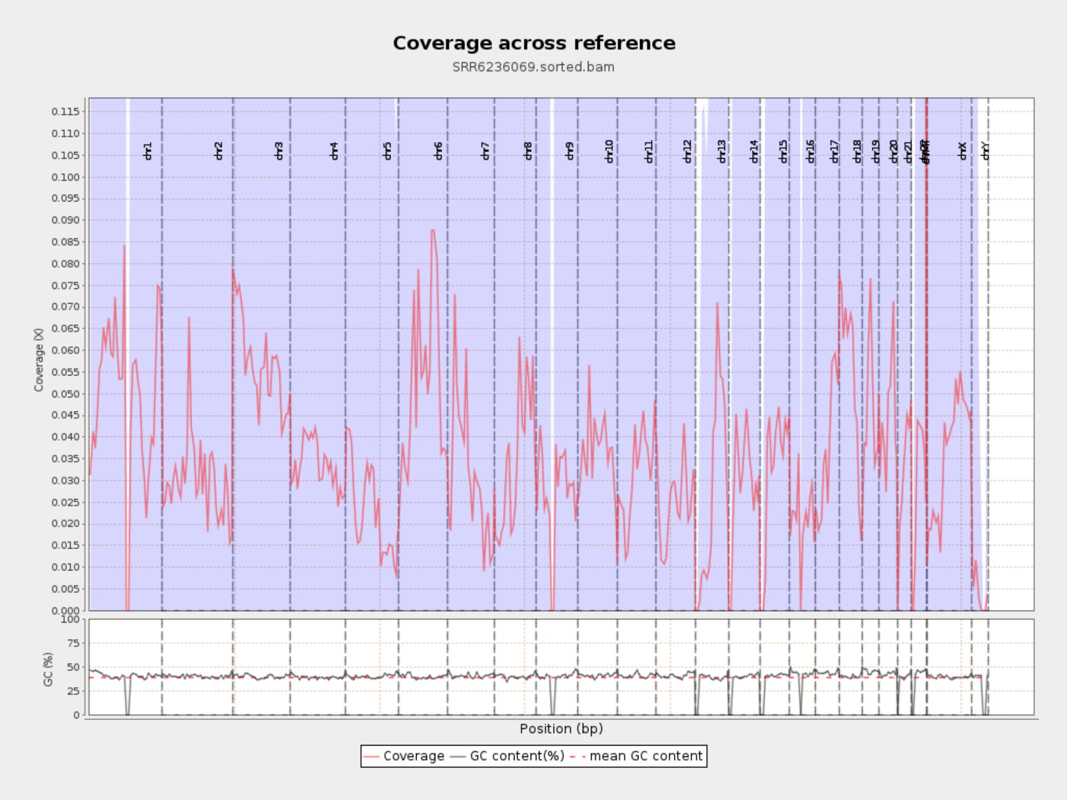
General error rate	0.8%
Mismatches	863,069
Insertions	7,853
Mapped reads with at least one insertion	0.47%
Deletions	29,516
Mapped reads with at least one deletion	1.76%
Homopolymer indels	47.76%

2.6. Chromosome stats

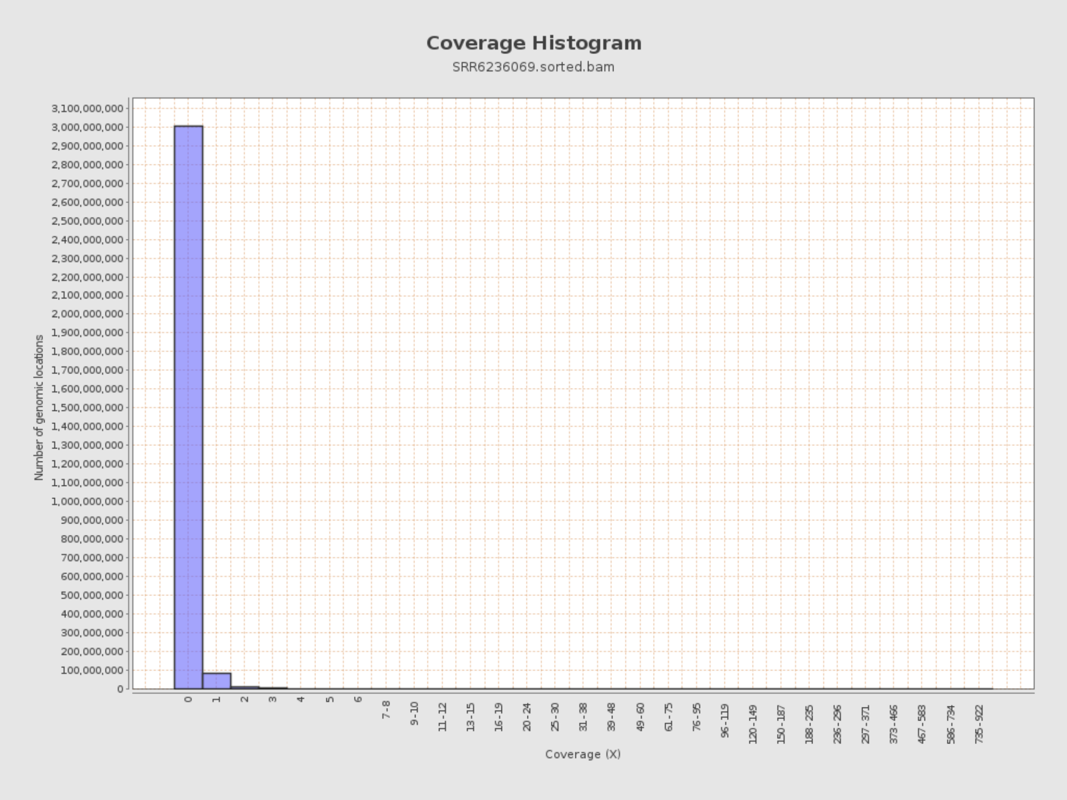
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12224578	0.049	0.8268
chr2	243199373	7325846	0.0301	0.3886
chr3	198022430	11304280	0.0571	0.2728
chr4	191154276	6419904	0.0336	0.2213
chr5	180915260	4123376	0.0228	0.1764
chr6	171115067	8917651	0.0521	0.3509
chr7	159138663	5059687	0.0318	0.4413

chr8	146364022	5030707	0.0344	0.5054
chr9	141213431	3851885	0.0273	0.2985
chr10	135534747	5020955	0.037	0.3171
chr11	135006516	4231199	0.0313	0.2566
chr12	133851895	3384871	0.0253	0.1923
chr13	115169878	3078678	0.0267	0.1869
chr14	107349540	3046865	0.0284	0.2049
chr15	102531392	3259296	0.0318	0.209
chr16	90354753	1895498	0.021	0.1776
chr17	81195210	3071182	0.0378	0.2299
chr18	78077248	4367683	0.0559	0.4749
chr19	59128983	2792045	0.0472	0.4597
chr20	63025520	2778143	0.0441	0.244
chr21	48129895	1519002	0.0316	0.2154
chr22	51304566	1422298	0.0277	0.1873
chrMT	16571	44911	2.7102	2.2844
chrX	155270560	5554569	0.0358	0.2363
chrY	59373566	234911	0.004	0.1086

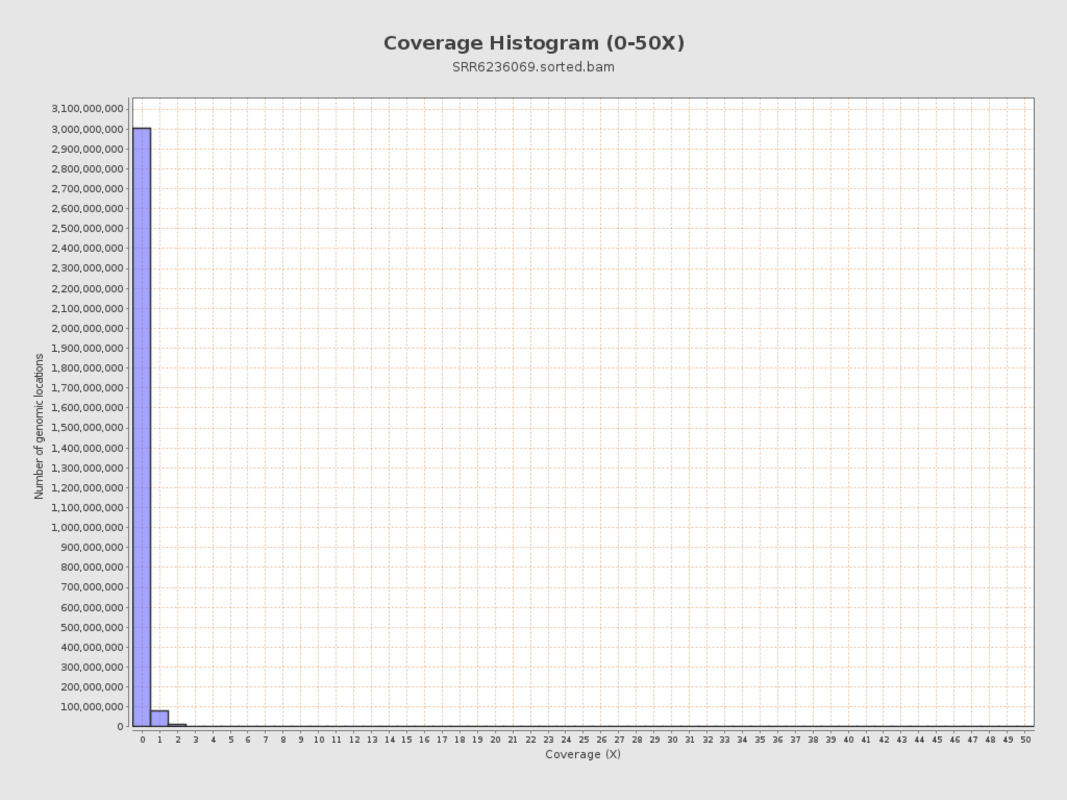
3. Results : Coverage across reference



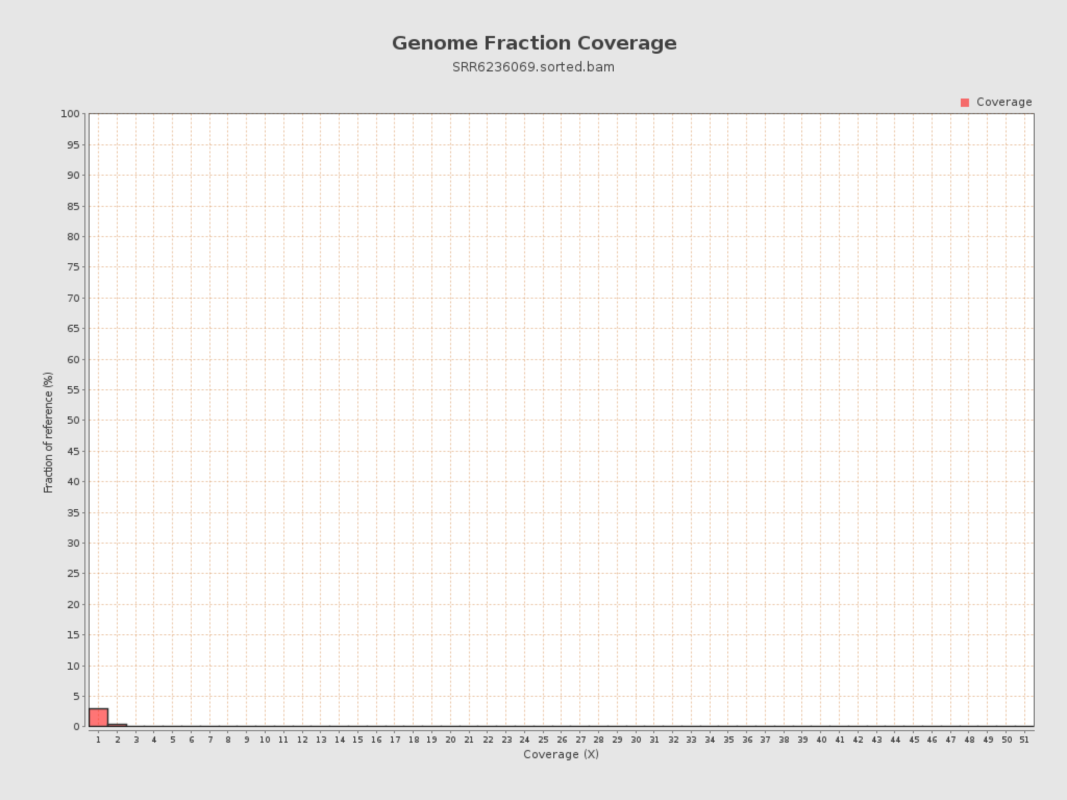
4. Results : Coverage Histogram



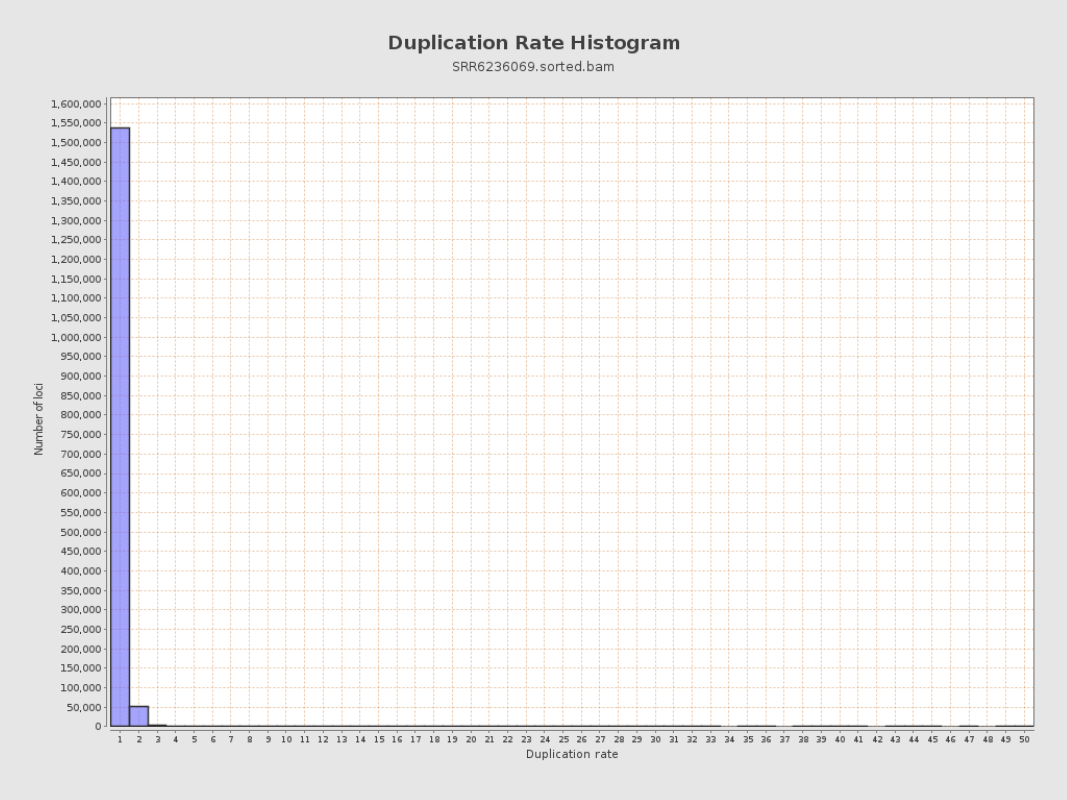
5. Results : Coverage Histogram (0-50X)



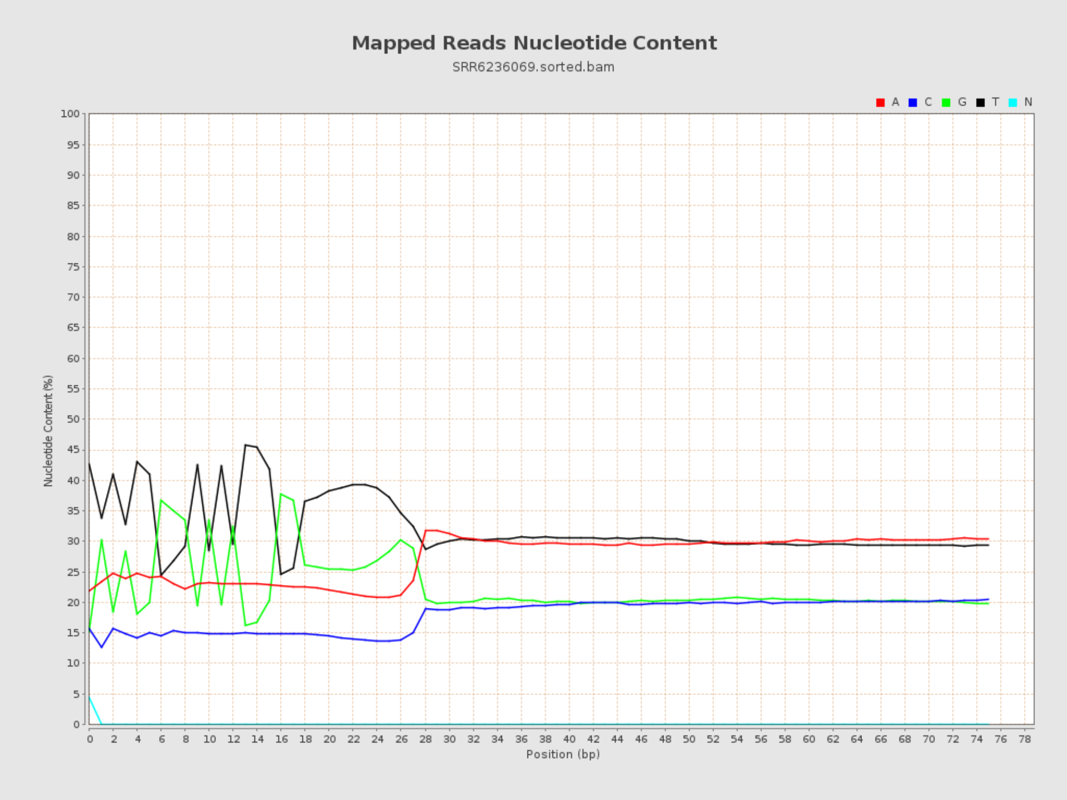
6. Results : Genome Fraction Coverage



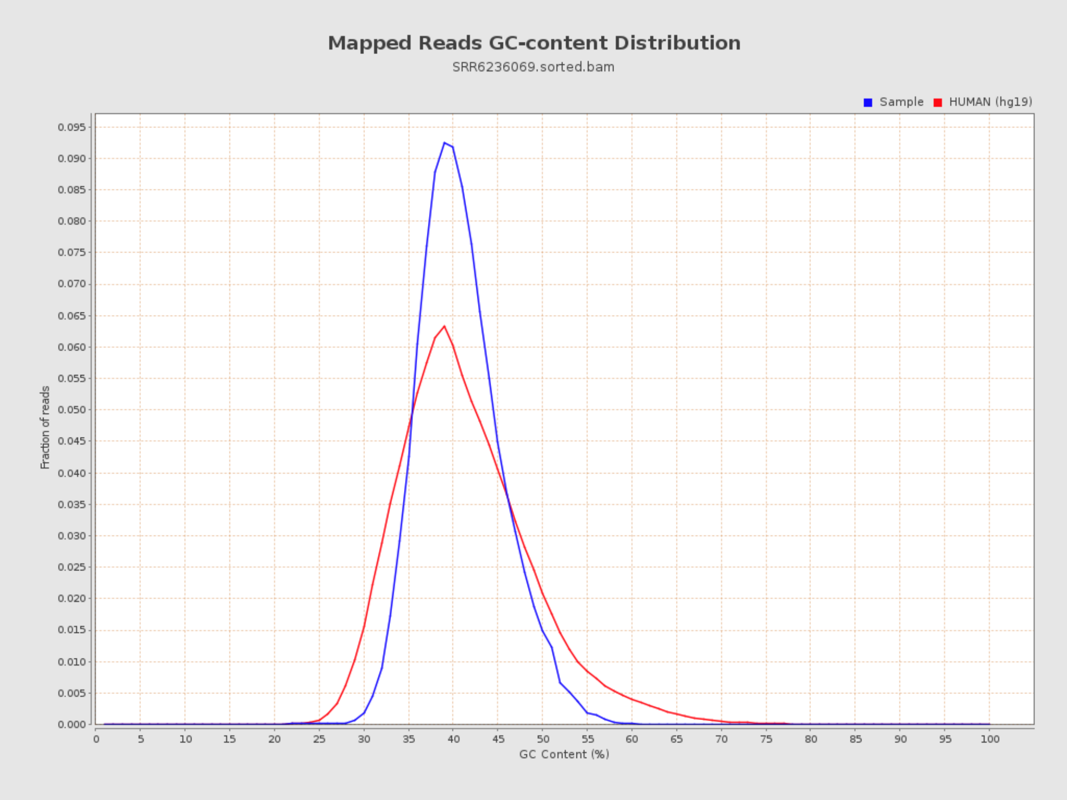
7. Results : Duplication Rate Histogram



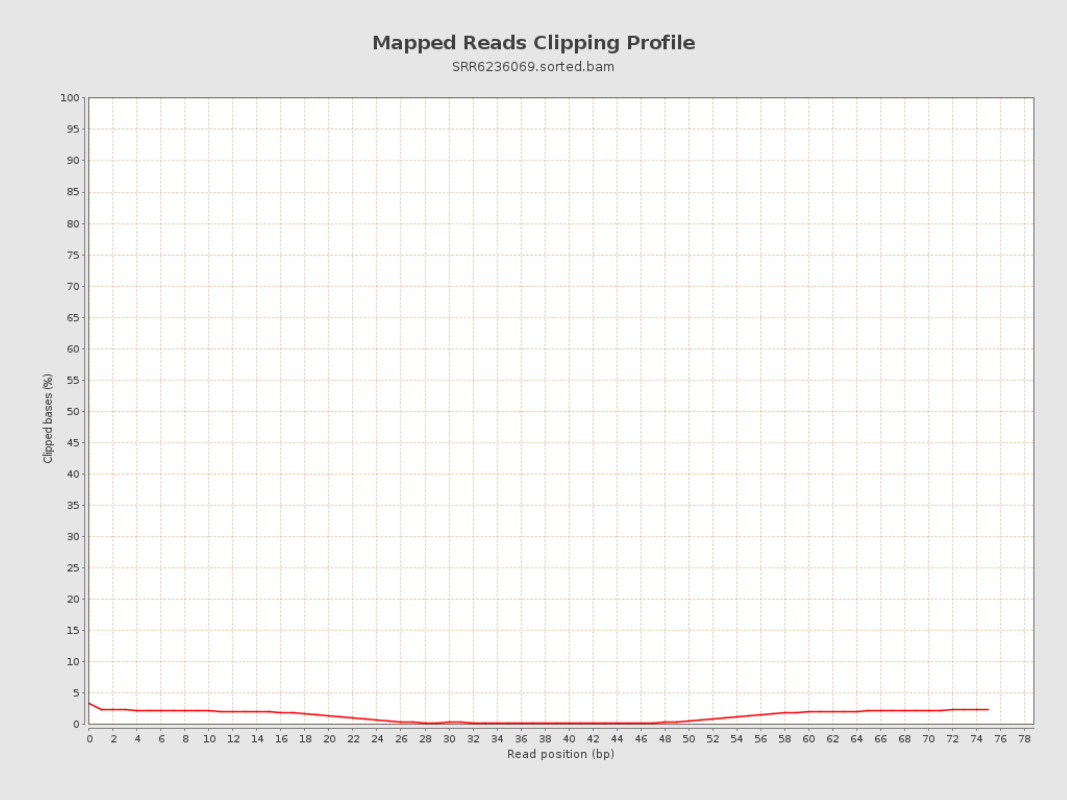
8. Results : Mapped Reads Nucleotide Content



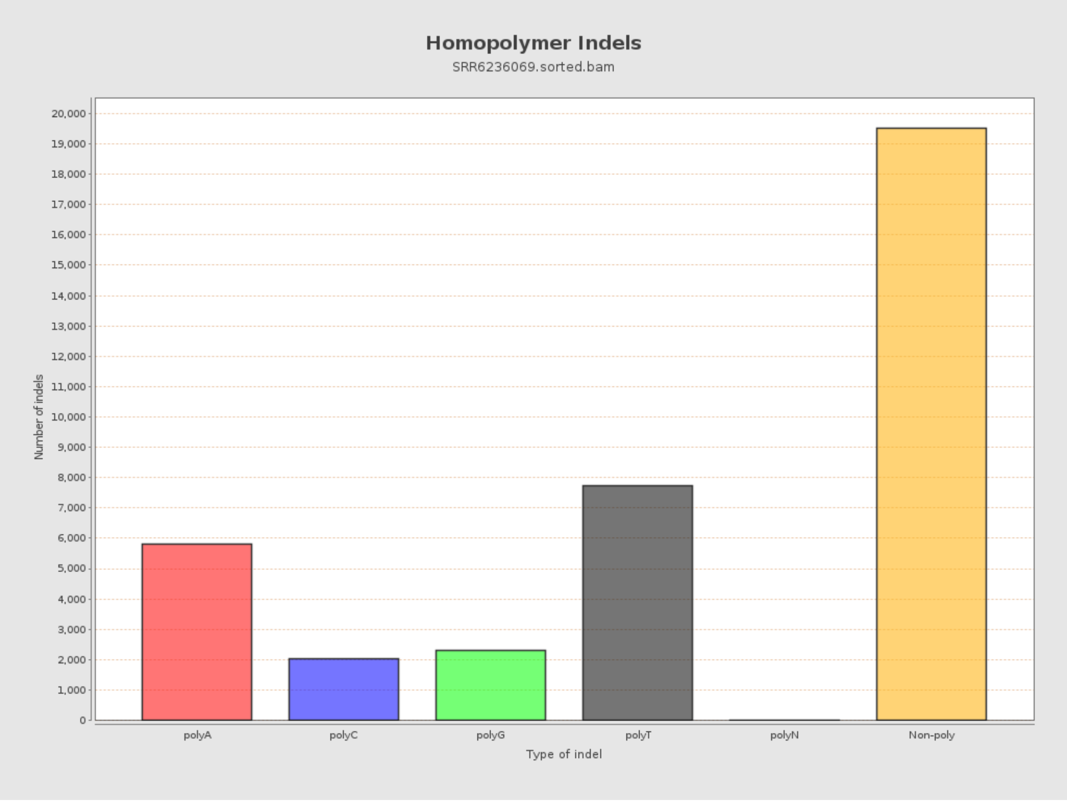
9. Results : Mapped Reads GC-content Distribution



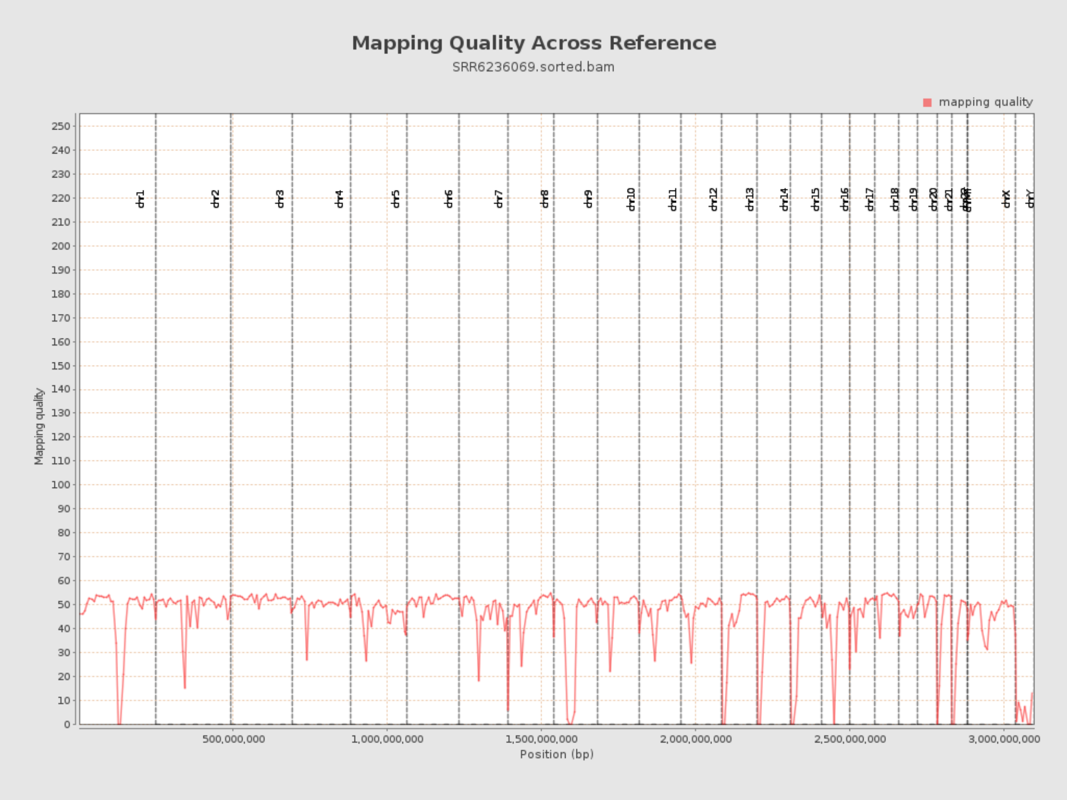
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram