Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:10:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236072.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_SRR6236072 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236072.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:10:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,704,526
Mapped reads	1,336,148 / 78.39%
Unmapped reads	368,378 / 21.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,164 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	110,533 / 6.48%
Duplication rate	6.94%
Clipped reads	641,710 / 37.65%

2.2. ACGT Content

Number/percentage of A's	23,804,770 / 27.19%
Number/percentage of C's	15,398,033 / 17.59%
Number/percentage of T's	28,707,098 / 32.79%
Number/percentage of G's	19,598,455 / 22.38%
Number/percentage of N's	50,643 / 0.06%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0283

Standard Deviation	0.3107

2.4. Mapping Quality

Mean Mapping Quality	45.46

2.5. Mismatches and indels

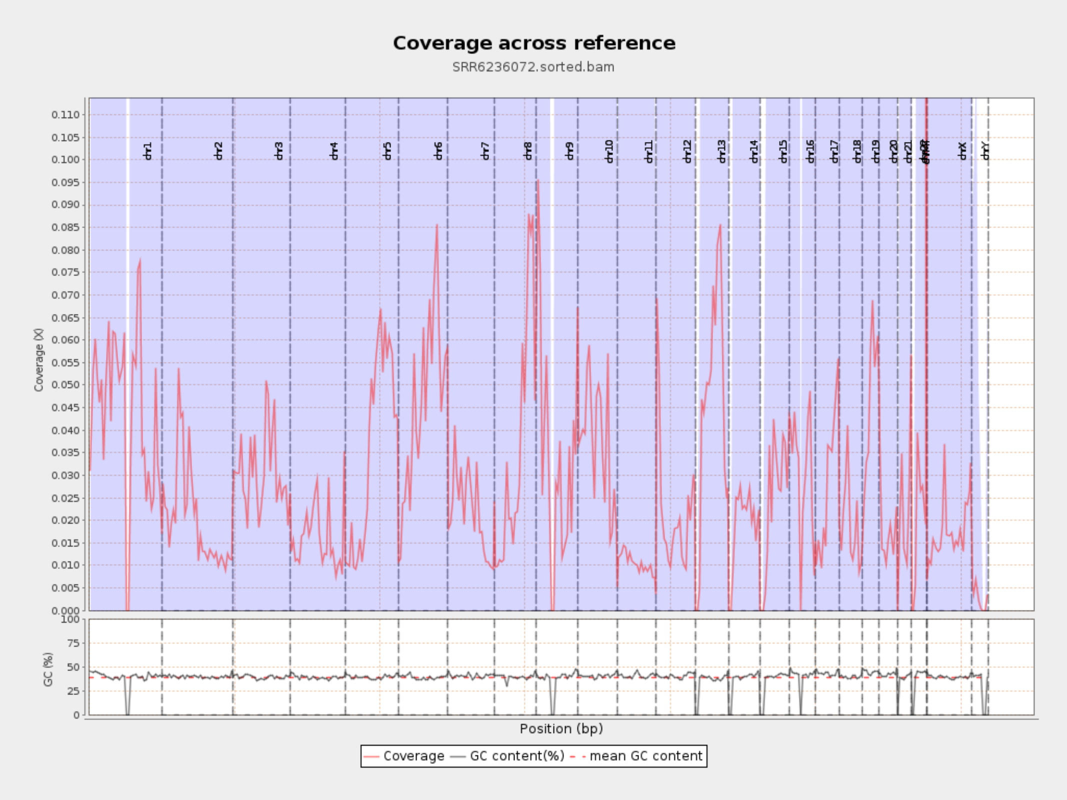
General error rate	0.82%
Mismatches	708,733
Insertions	6,175
Mapped reads with at least one insertion	0.46%
Deletions	24,805
Mapped reads with at least one deletion	1.84%
Homopolymer indels	48.09%

2.6. Chromosome stats

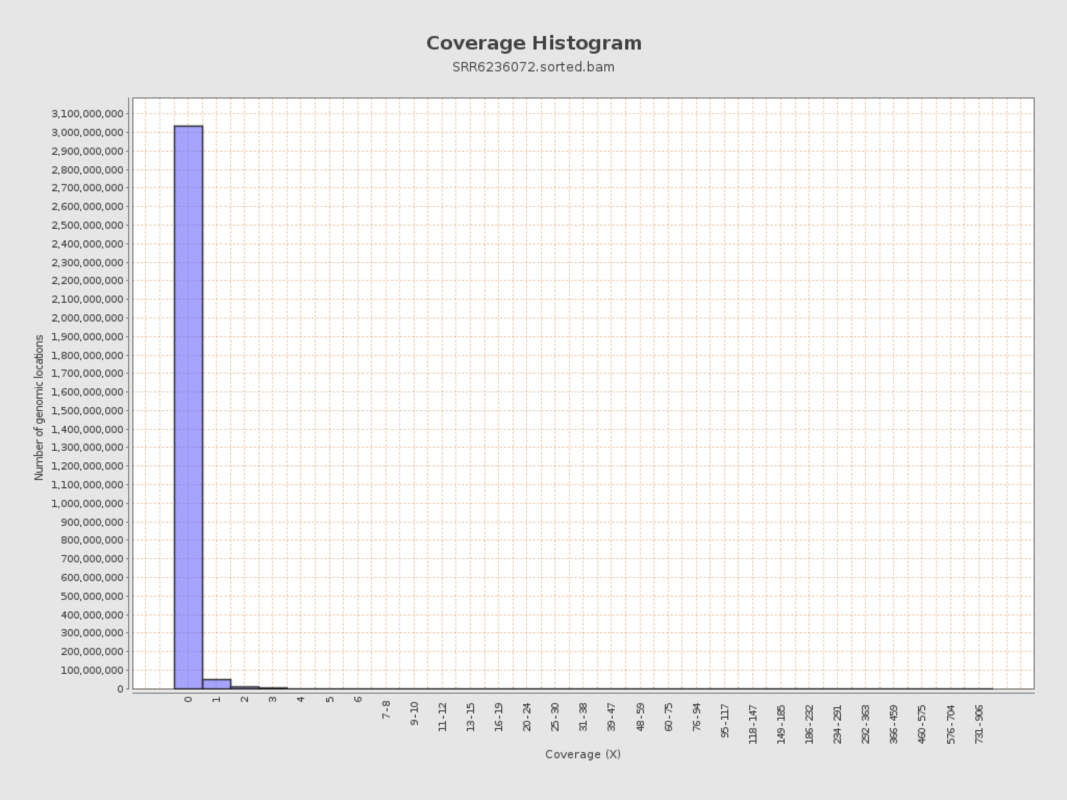
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10969634	0.044	0.5954
chr2	243199373	4919750	0.0202	0.2803
chr3	198022430	6106575	0.0308	0.2364
chr4	191154276	3136696	0.0164	0.1716
chr5	180915260	6580499	0.0364	0.2531
chr6	171115067	7867251	0.046	0.2998
chr7	159138663	3517984	0.0221	0.2215

chr8	146364022	5290778	0.0361	0.6321
chr9	141213431	4660865	0.033	0.2629
chr10	135534747	5092546	0.0376	0.2771
chr11	135006516	1402302	0.0104	0.151
chr12	133851895	2965830	0.0222	0.198
chr13	115169878	5230405	0.0454	0.2829
chr14	107349540	2033756	0.0189	0.185
chr15	102531392	2510069	0.0245	0.2083
chr16	90354753	2710442	0.03	0.2265
chr17	81195210	2353868	0.029	0.219
chr18	78077248	1493582	0.0191	0.3086
chr19	59128983	2747272	0.0465	0.3822
chr20	63025520	1083965	0.0172	0.1728
chr21	48129895	1078470	0.0224	0.1964
chr22	51304566	973607	0.019	0.1781
chrMT	16571	20873	1.2596	1.6198
chrX	155270560	2701332	0.0174	0.177
chrY	59373566	153891	0.0026	0.0682

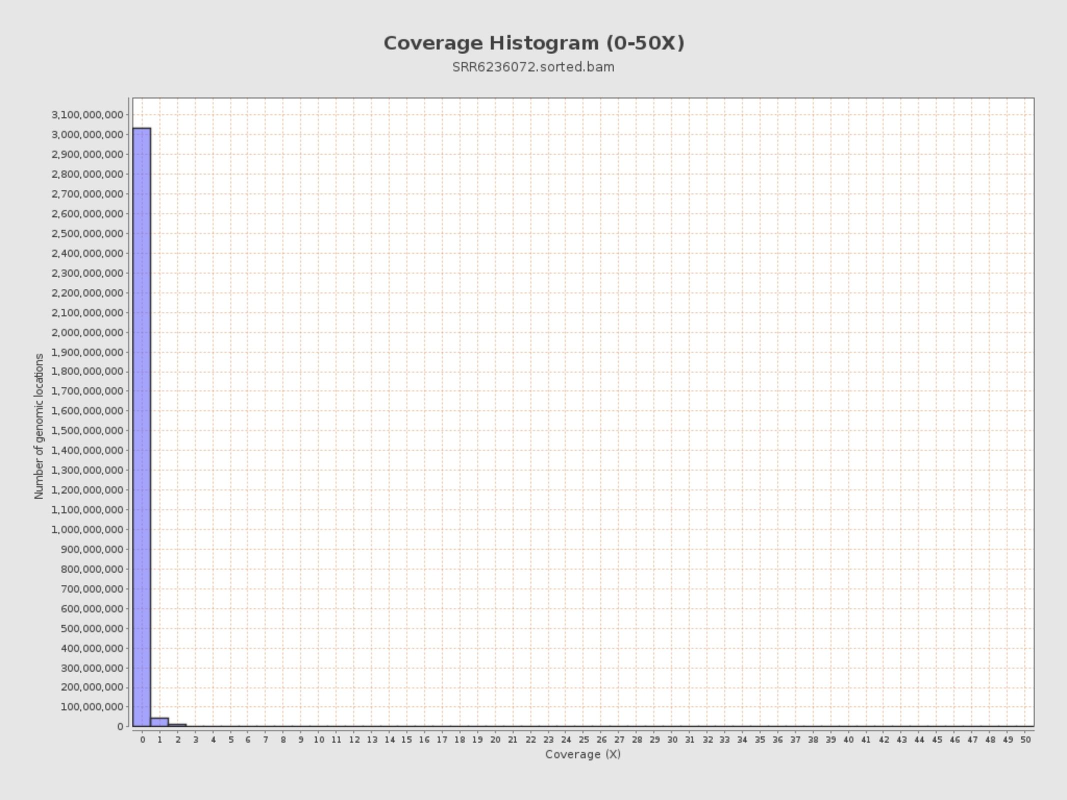
3. Results : Coverage across reference



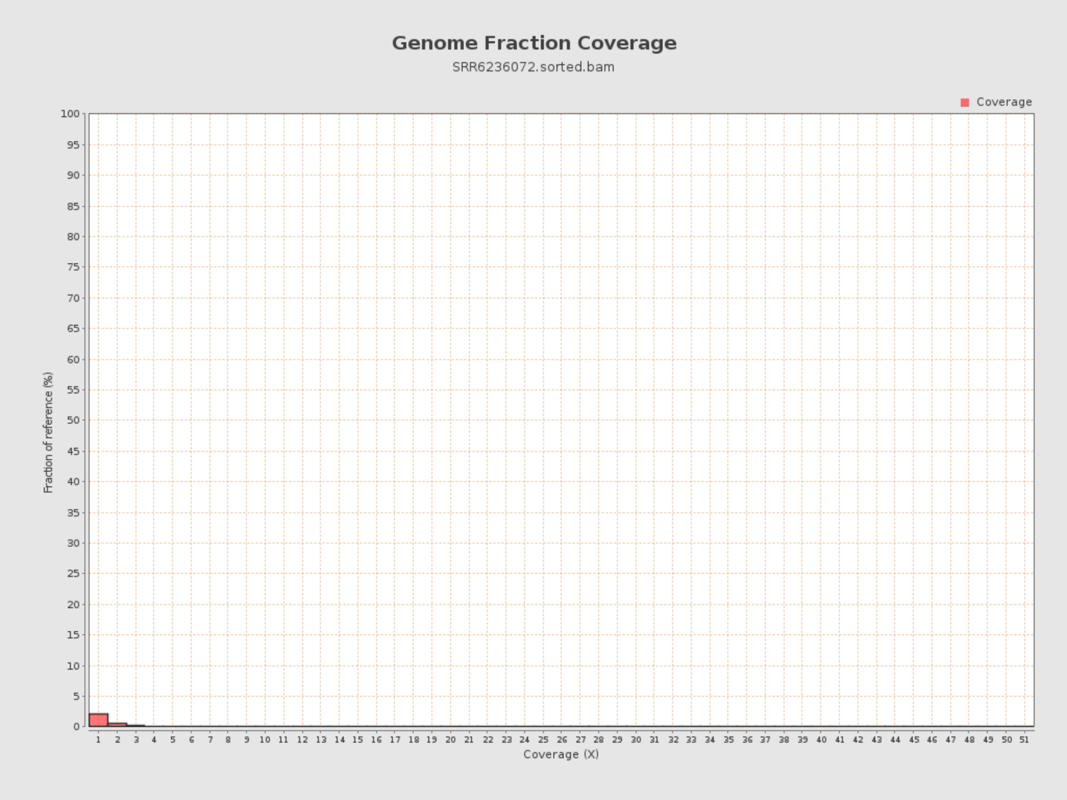
4. Results : Coverage Histogram



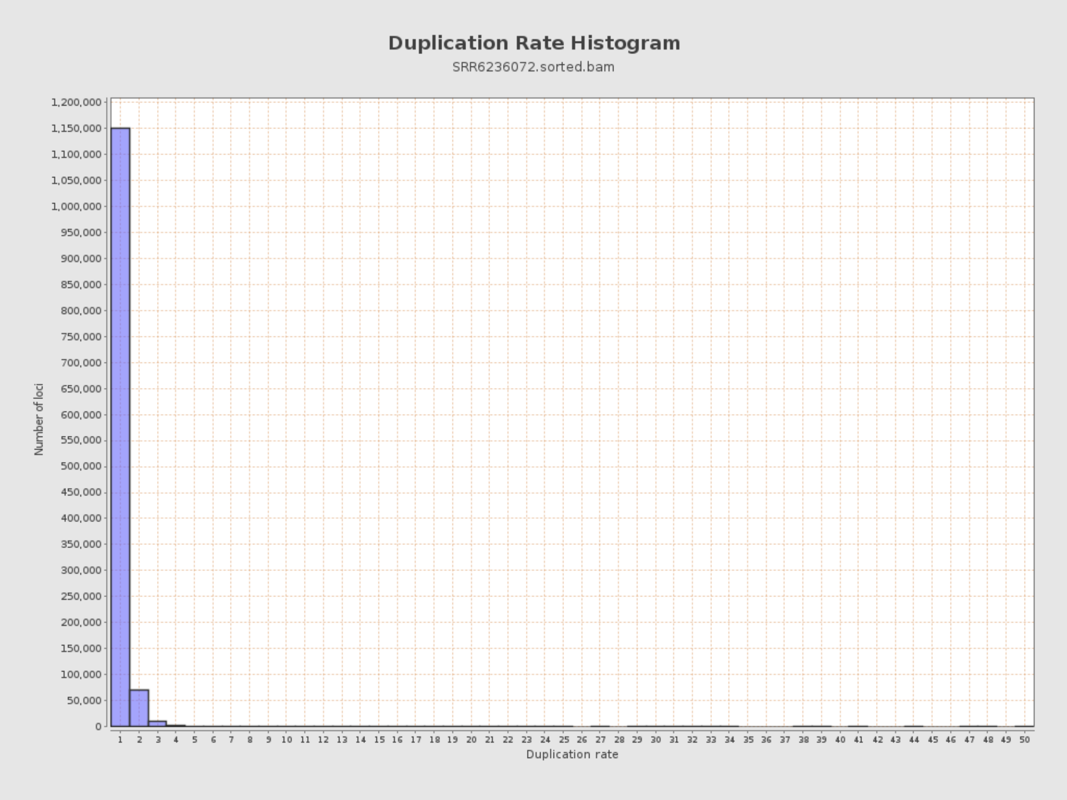
5. Results : Coverage Histogram (0-50X)



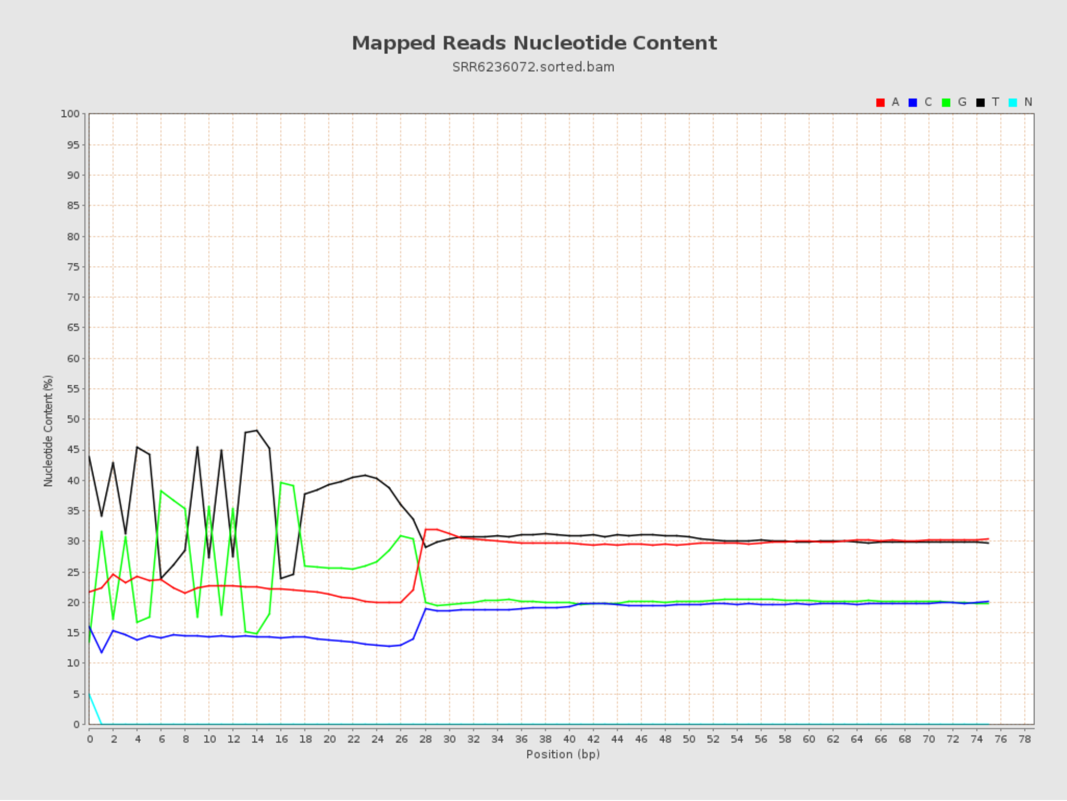
6. Results : Genome Fraction Coverage



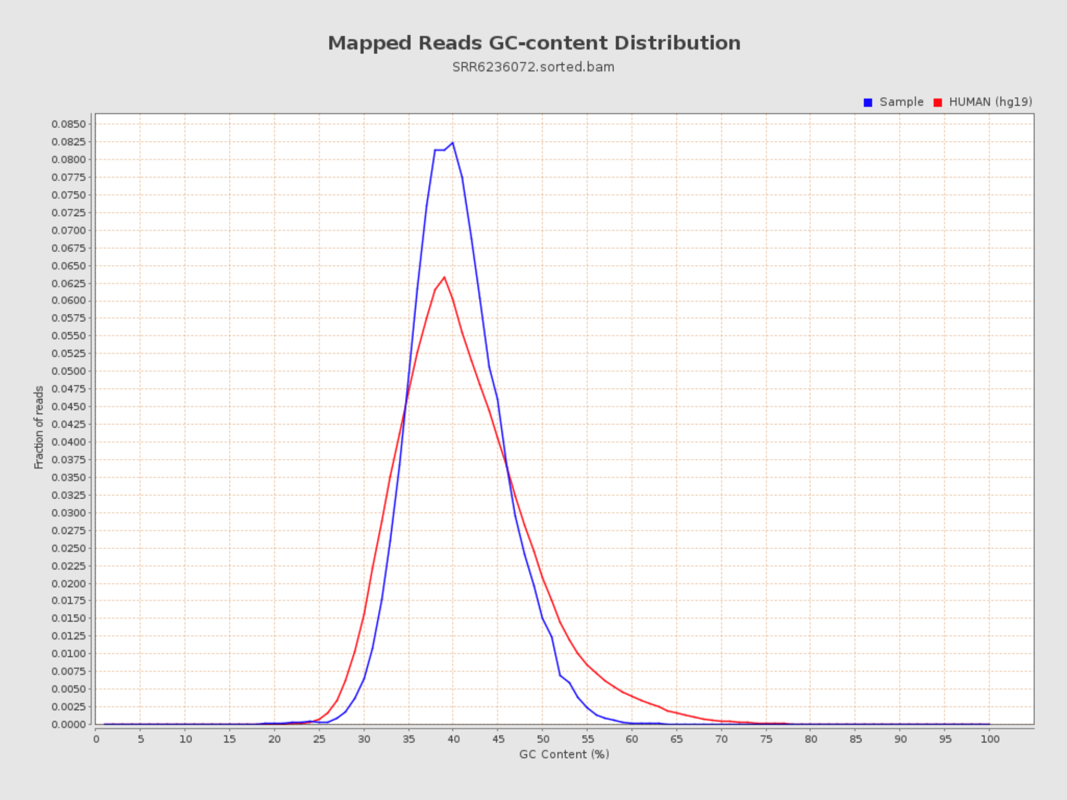
7. Results : Duplication Rate Histogram



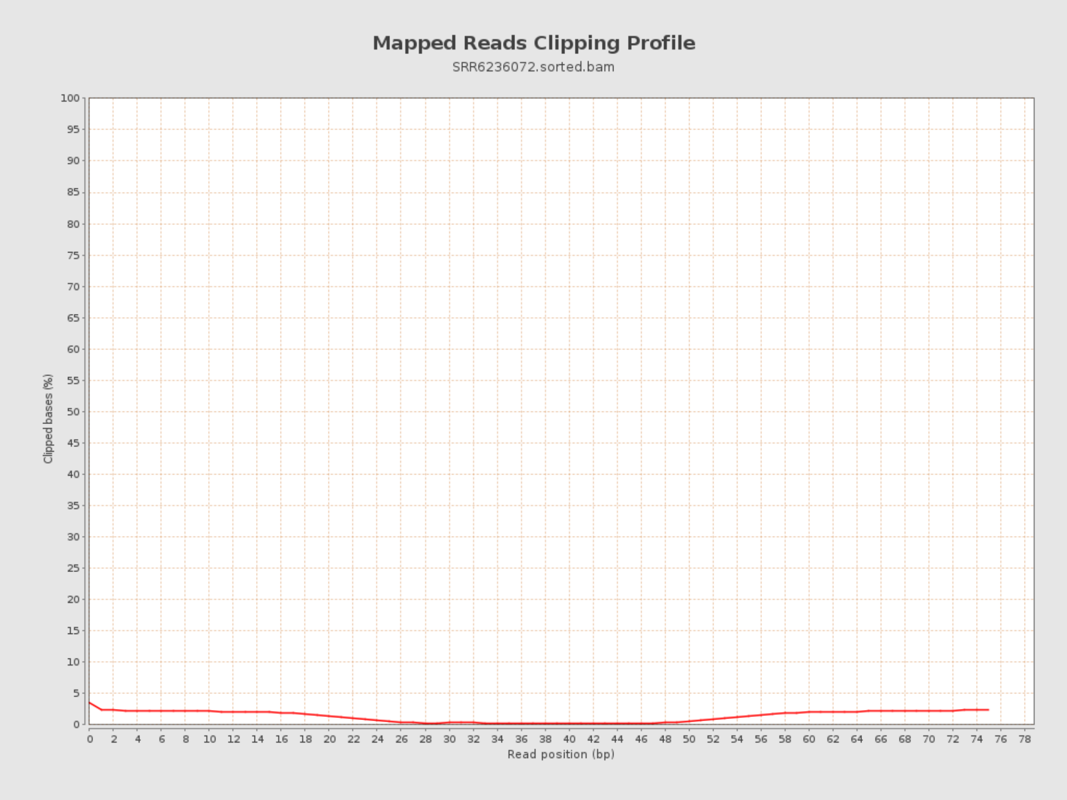
8. Results : Mapped Reads Nucleotide Content



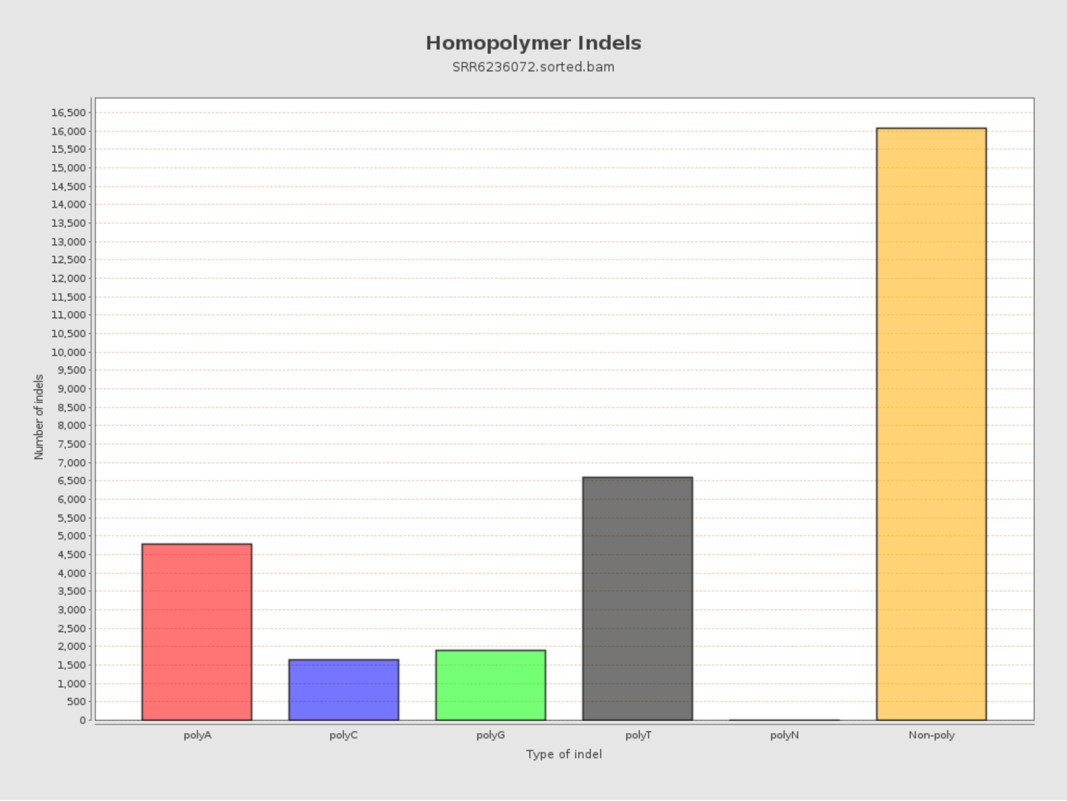
9. Results : Mapped Reads GC-content Distribution



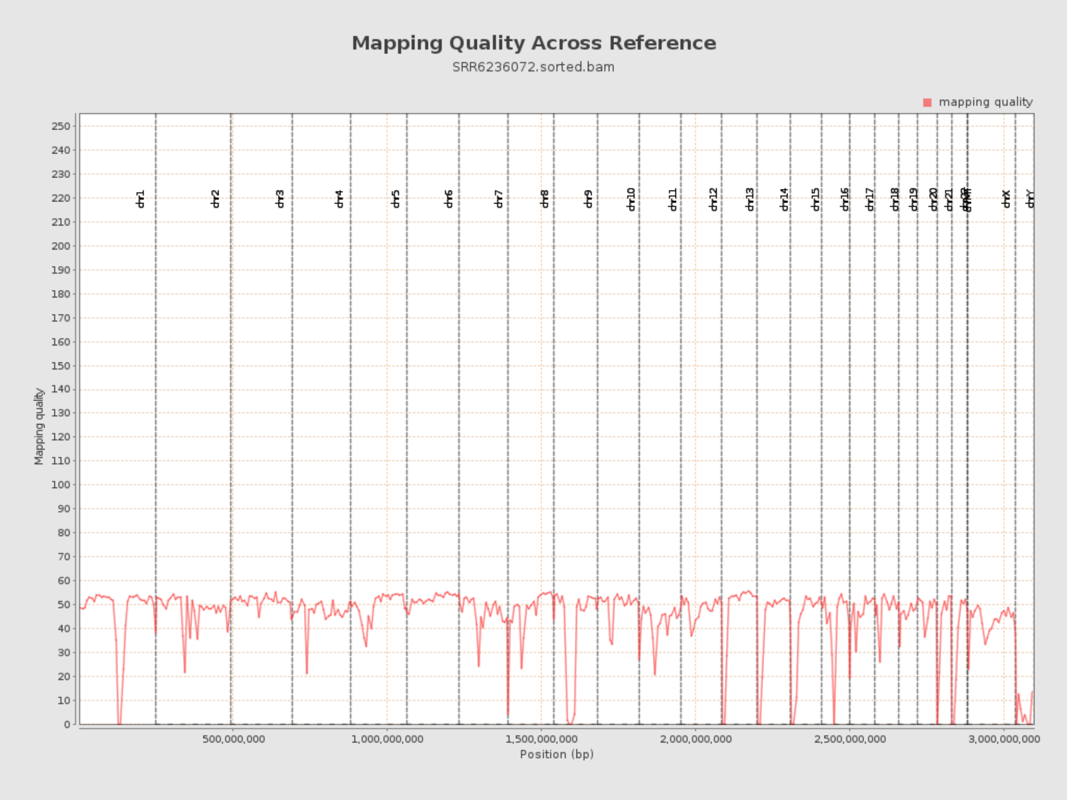
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram