Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:05:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236089.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_SRR6236089 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236089.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:05:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236089.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,974,384
Mapped reads	2,591,464 / 87.13%
Unmapped reads	382,920 / 12.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,776 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	154,698 / 5.2%
Duplication rate	4.62%
Clipped reads	1,118,524 / 37.61%

2.2. ACGT Content

Number/percentage of A's	48,506,456 / 28.1%
Number/percentage of C's	30,372,952 / 17.59%
Number/percentage of T's	56,287,603 / 32.61%
Number/percentage of G's	37,360,503 / 21.64%
Number/percentage of N's	95,509 / 0.06%
GC Percentage	39.24%

2.3. Coverage

Mean	0.0558

Standard Deviation	0.6284

2.4. Mapping Quality

Mean Mapping Quality	46.13

2.5. Mismatches and indels

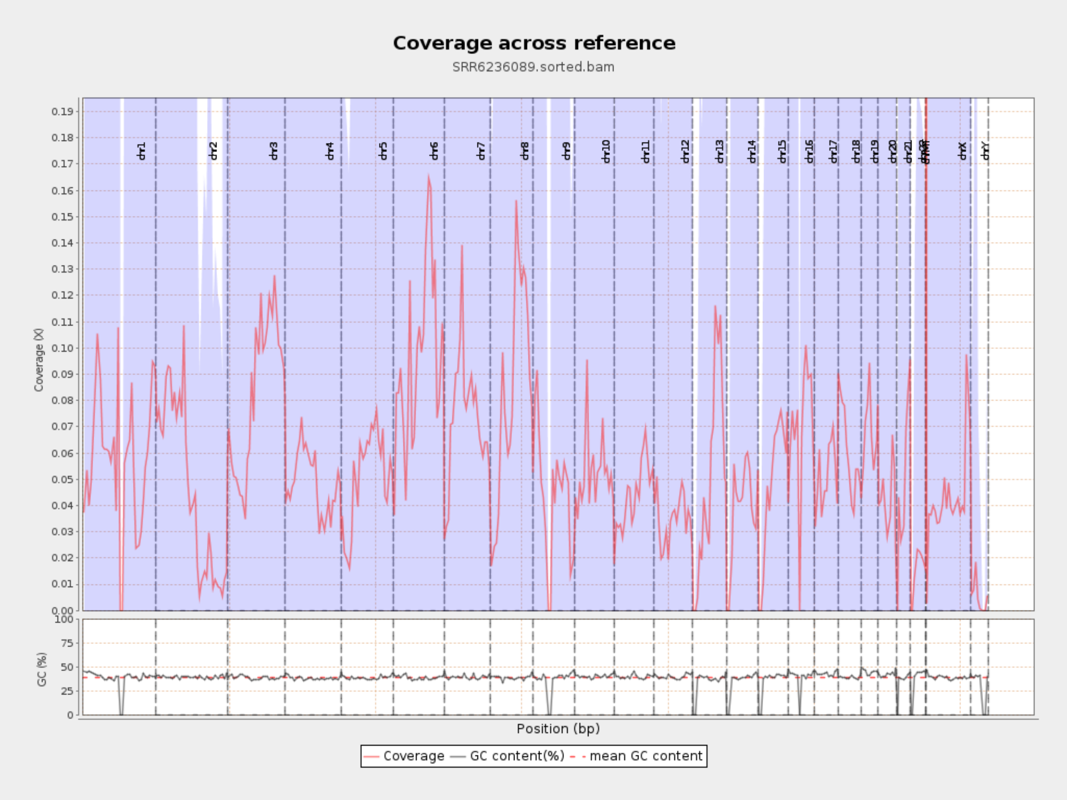
General error rate	0.85%
Mismatches	1,447,166
Insertions	12,344
Mapped reads with at least one insertion	0.47%
Deletions	55,624
Mapped reads with at least one deletion	2.12%
Homopolymer indels	46.21%

2.6. Chromosome stats

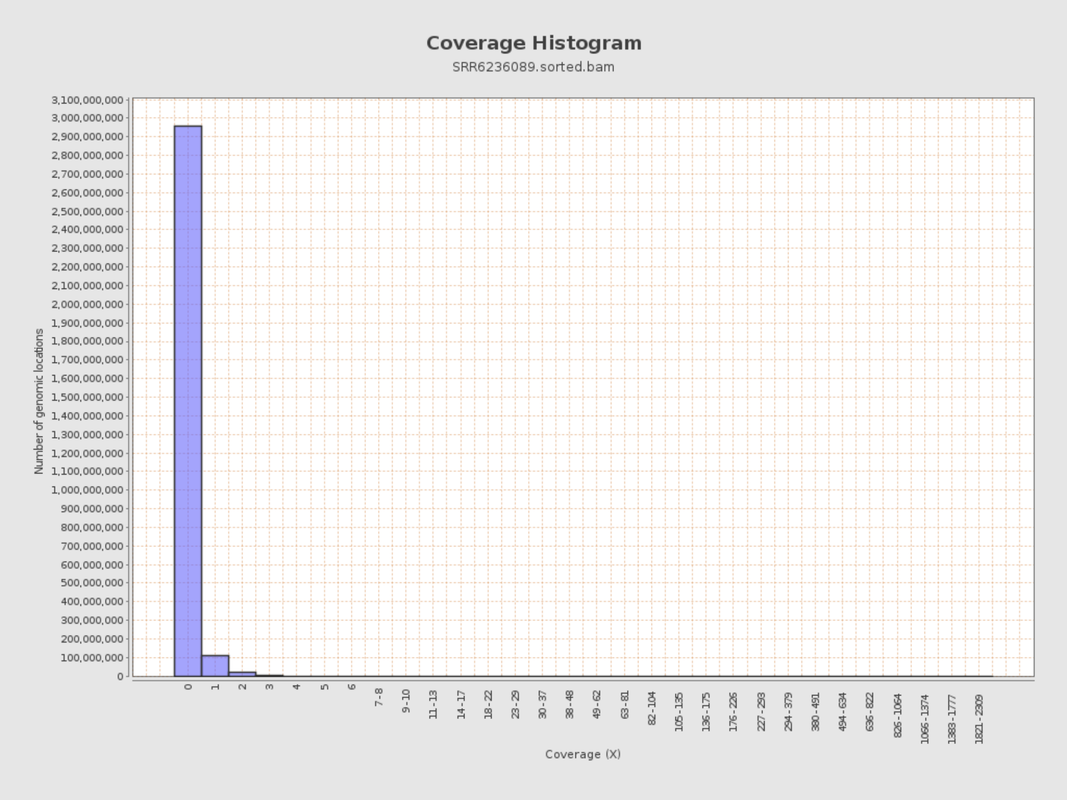
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14499964	0.0582	1.271
chr2	243199373	11232913	0.0462	0.4754
chr3	198022430	16411598	0.0829	0.3484
chr4	191154276	9298911	0.0486	0.2762
chr5	180915260	9252557	0.0511	0.2753
chr6	171115067	16650047	0.0973	0.5408
chr7	159138663	11794367	0.0741	0.9342

chr8	146364022	12393706	0.0847	1.4525
chr9	141213431	6290711	0.0445	0.4177
chr10	135534747	7080944	0.0522	0.4756
chr11	135006516	5999669	0.0444	0.3444
chr12	133851895	4677994	0.0349	0.2403
chr13	115169878	5827950	0.0506	0.2727
chr14	107349540	4114491	0.0383	0.2493
chr15	102531392	4798678	0.0468	0.2641
chr16	90354753	6221249	0.0689	0.331
chr17	81195210	4185526	0.0515	0.312
chr18	78077248	4770013	0.0611	0.5919
chr19	59128983	4022645	0.068	0.8302
chr20	63025520	2748976	0.0436	0.2565
chr21	48129895	2429084	0.0505	0.2874
chr22	51304566	785310	0.0153	0.1423
chrMT	16571	227322	13.7181	8.6075
chrX	155270560	6689808	0.0431	0.278
chrY	59373566	314999	0.0053	0.1254

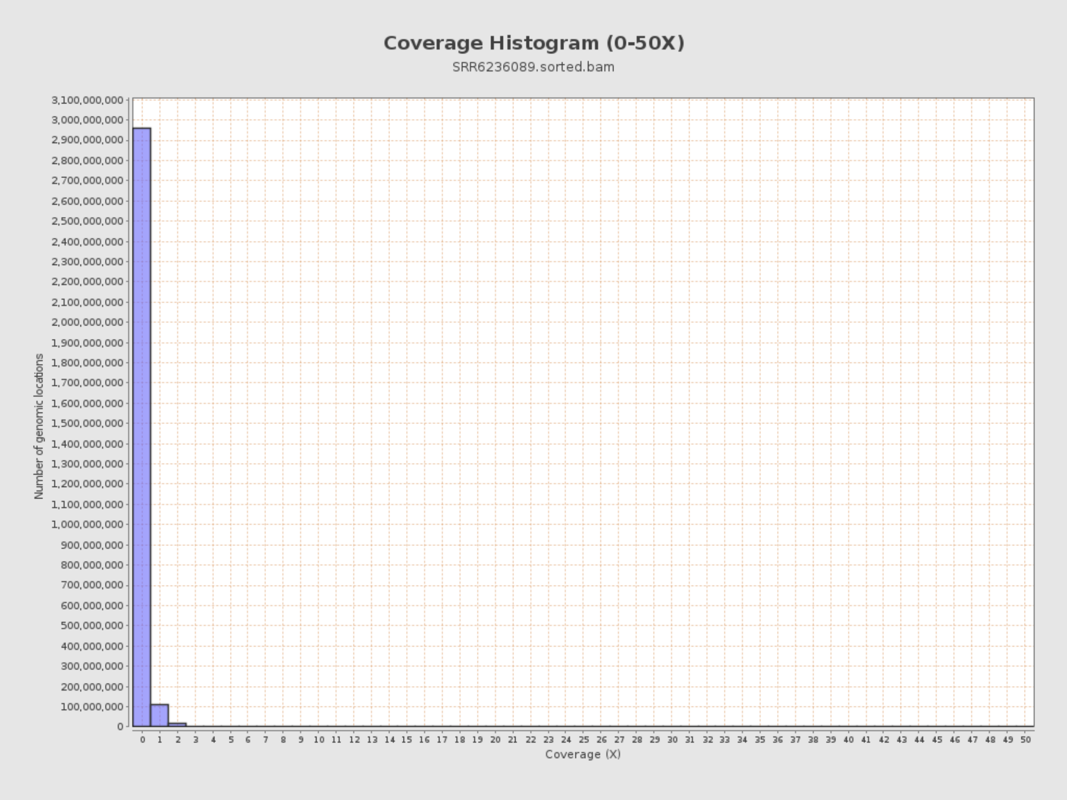
3. Results : Coverage across reference



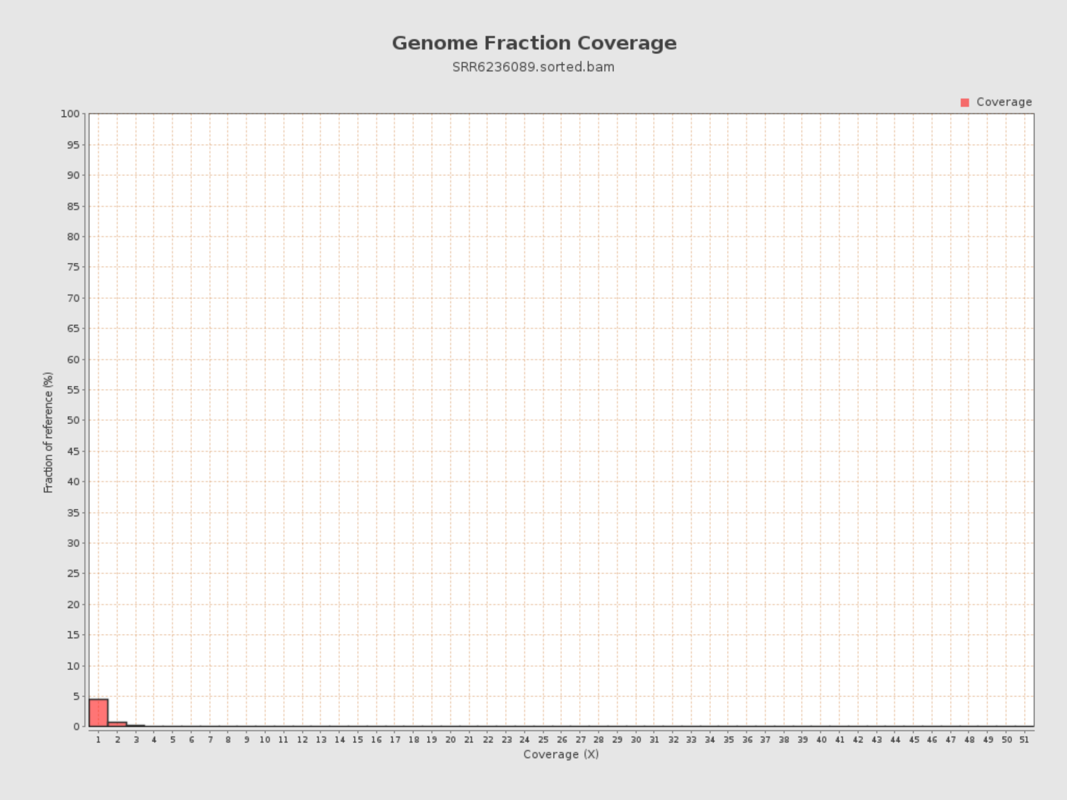
4. Results : Coverage Histogram



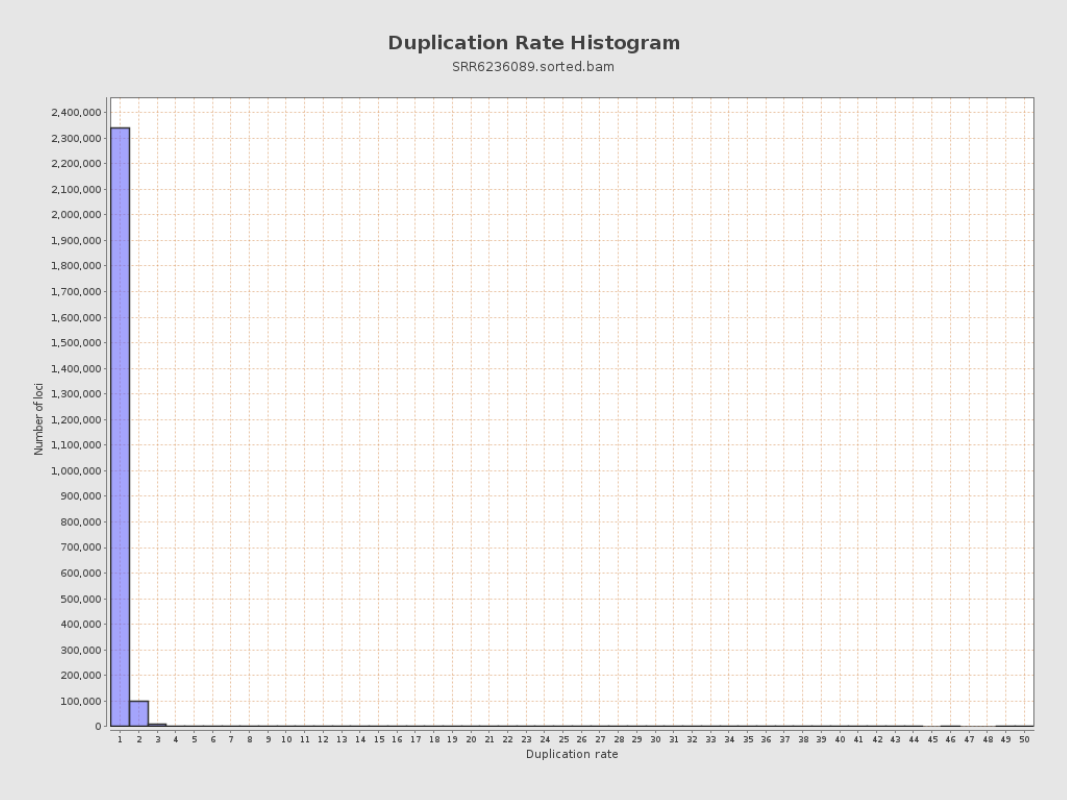
5. Results : Coverage Histogram (0-50X)



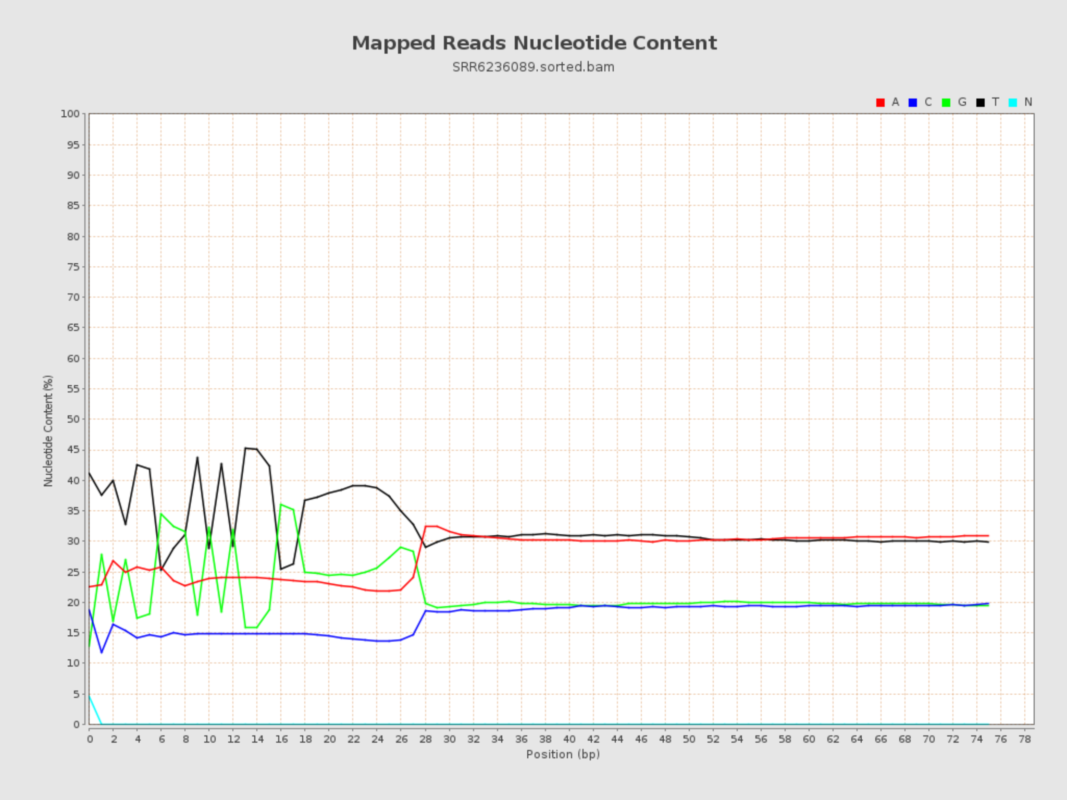
6. Results : Genome Fraction Coverage



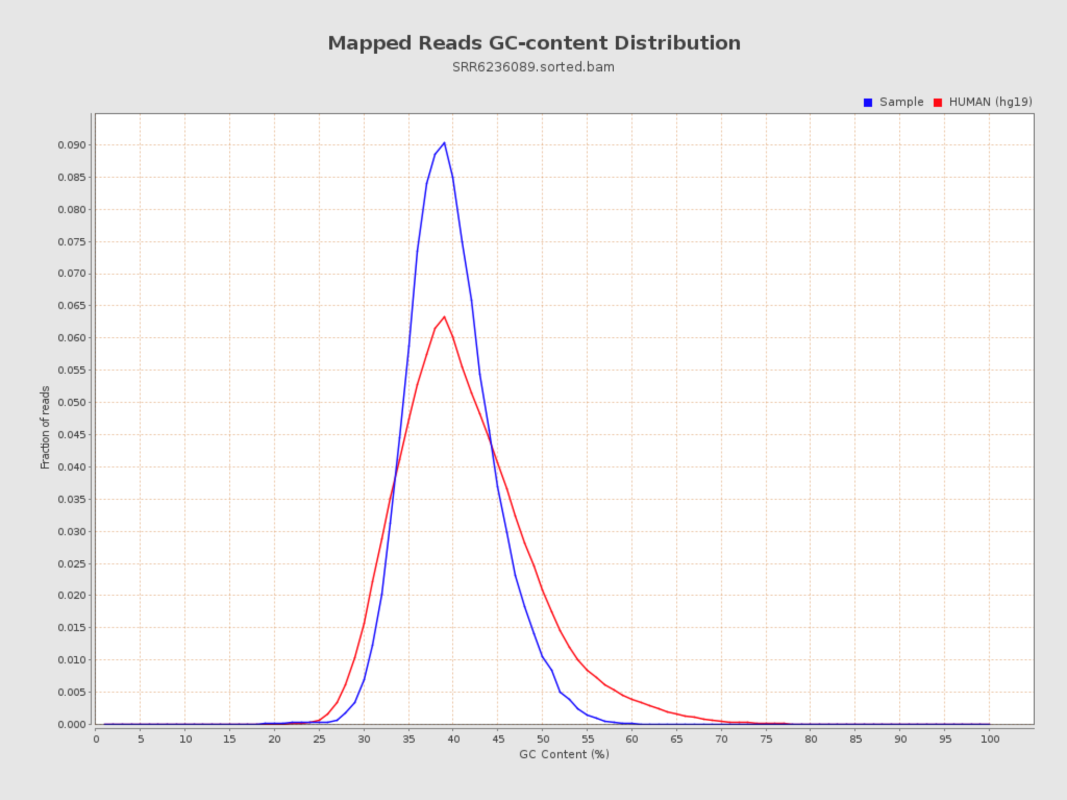
7. Results : Duplication Rate Histogram



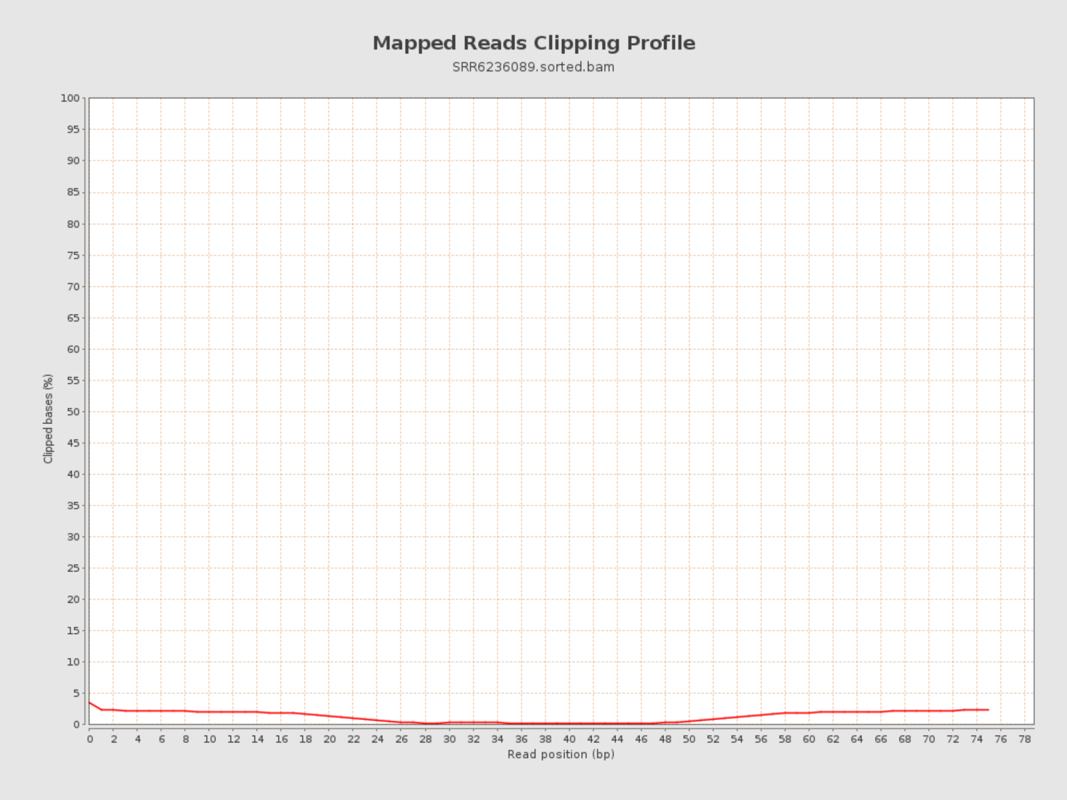
8. Results : Mapped Reads Nucleotide Content



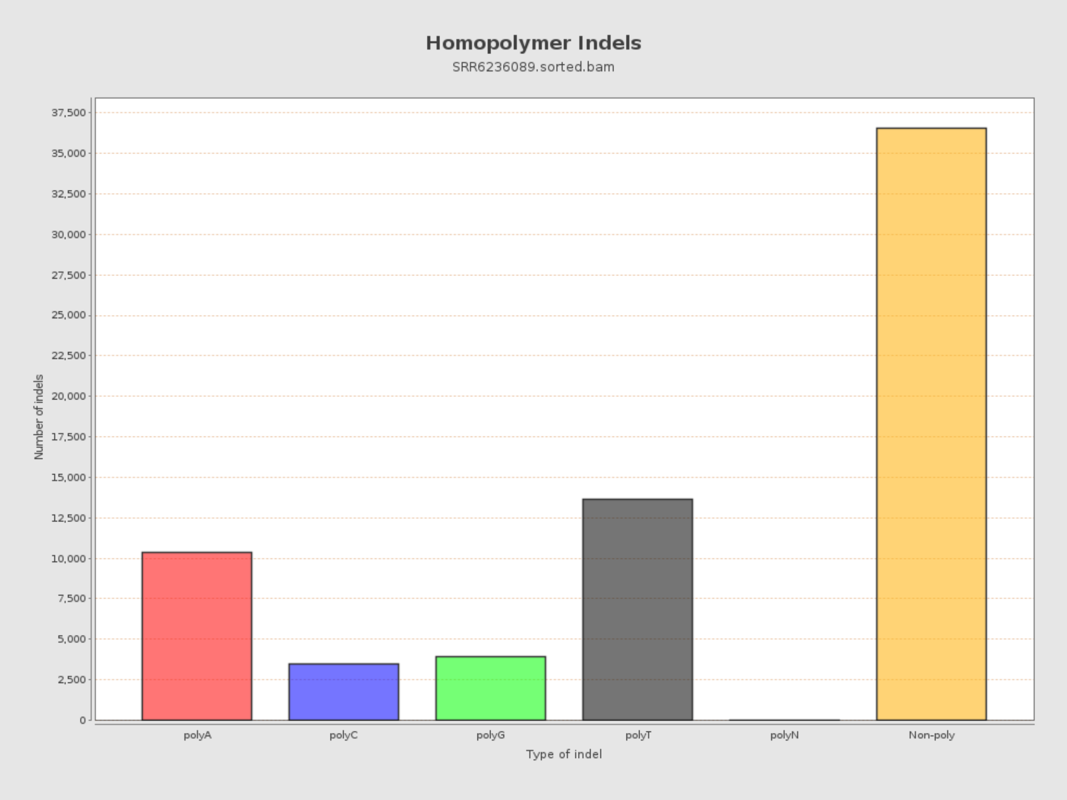
9. Results : Mapped Reads GC-content Distribution



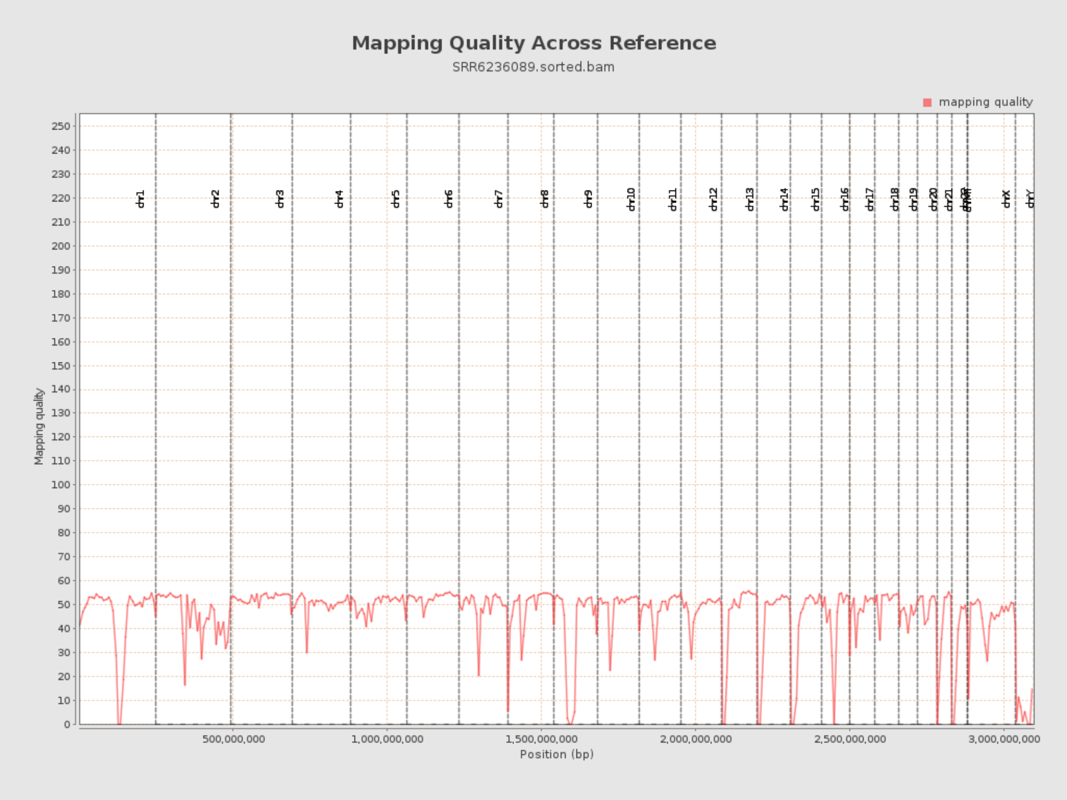
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram