Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:36:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236080.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_SRR6236080 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236080.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:36:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,489,976
Mapped reads	6,712,612 / 89.62%
Unmapped reads	777,364 / 10.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	58,584 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	837,116 / 11.18%
Duplication rate	8.96%
Clipped reads	3,002,905 / 40.09%

2.2. ACGT Content

Number/percentage of A's	126,155,028 / 28.13%
Number/percentage of C's	83,181,426 / 18.55%
Number/percentage of T's	141,670,093 / 31.59%
Number/percentage of G's	97,444,911 / 21.73%
Number/percentage of N's	4,211 / 0%
GC Percentage	40.28%

2.3. Coverage

Mean	0.1449

Standard Deviation	1.4537

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

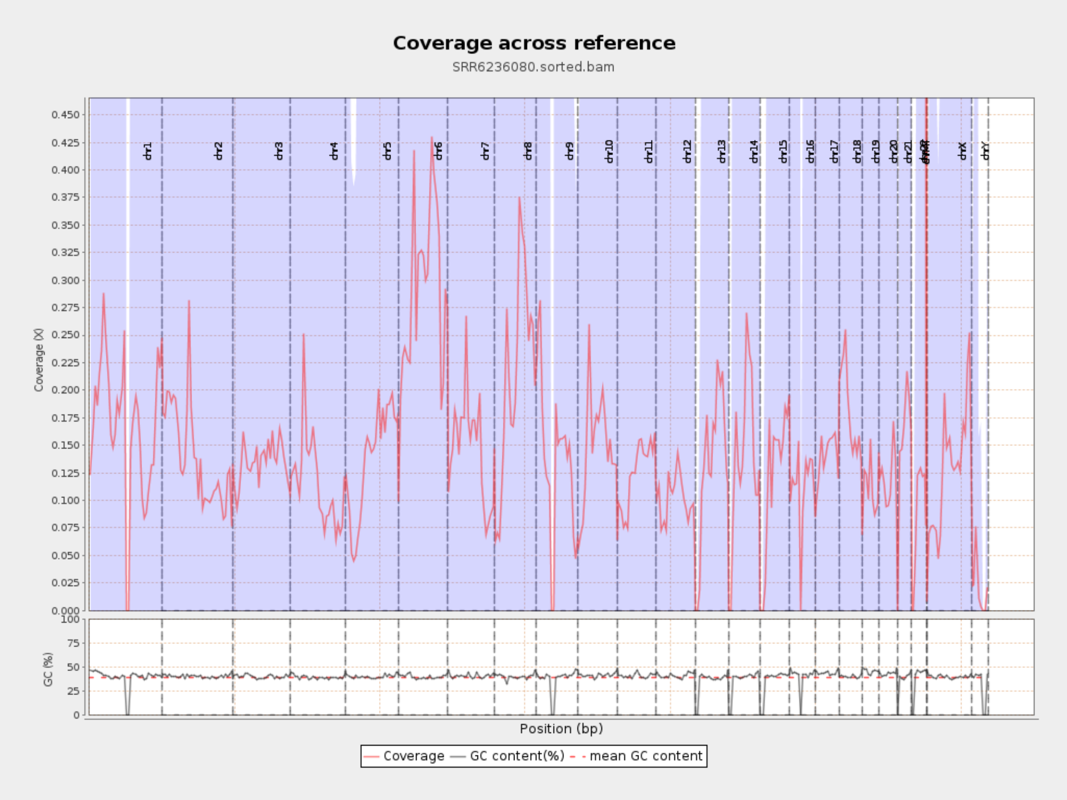
General error rate	0.75%
Mismatches	3,310,437
Insertions	35,721
Mapped reads with at least one insertion	0.53%
Deletions	124,285
Mapped reads with at least one deletion	1.83%
Homopolymer indels	47.06%

2.6. Chromosome stats

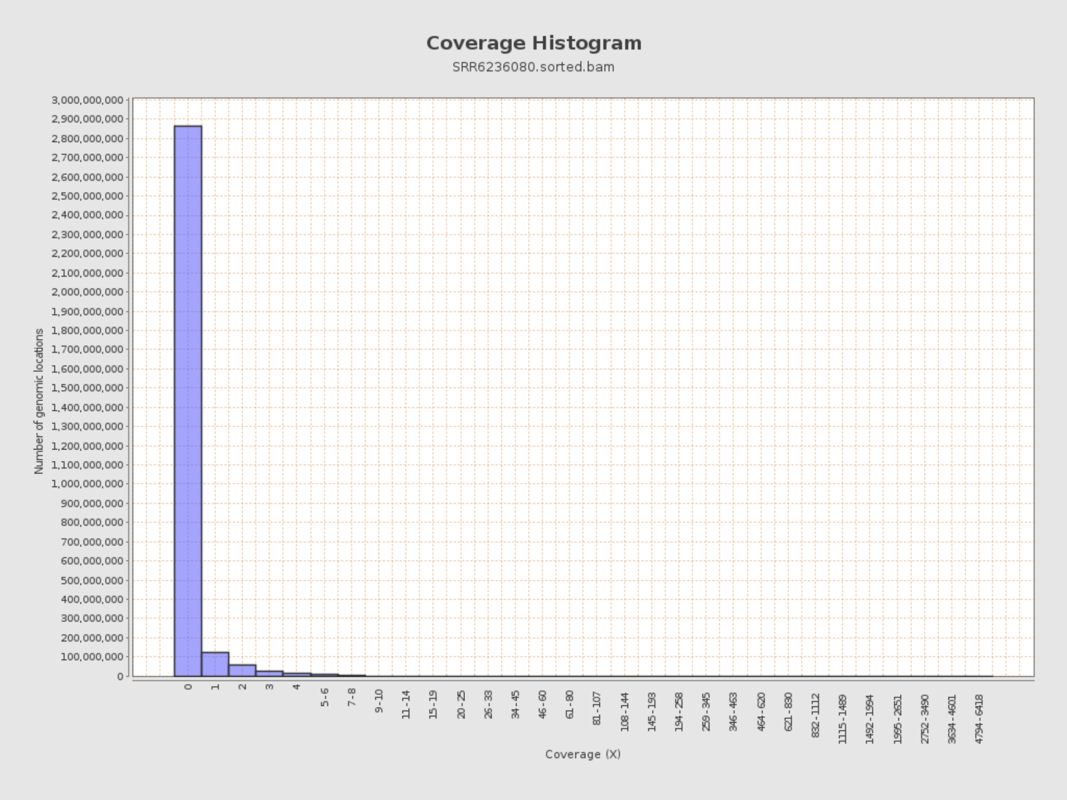
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	41437750	0.1662	1.9794
chr2	243199373	34068048	0.1401	1.5811
chr3	198022430	26831717	0.1355	0.6018
chr4	191154276	22143428	0.1158	0.8642
chr5	180915260	24648712	0.1362	0.6213
chr6	171115067	49841756	0.2913	1.3961
chr7	159138663	23288294	0.1463	1.5409

chr8	146364022	31075367	0.2123	4.1048
chr9	141213431	19149961	0.1356	1.1976
chr10	135534747	20167919	0.1488	1.2566
chr11	135006516	16727099	0.1239	1.013
chr12	133851895	13679118	0.1022	0.5861
chr13	115169878	15358257	0.1334	0.6128
chr14	107349540	14661178	0.1366	0.7159
chr15	102531392	12254231	0.1195	0.6037
chr16	90354753	10070474	0.1115	0.6648
chr17	81195210	11368323	0.14	0.8209
chr18	78077248	14268517	0.1827	2.1256
chr19	59128983	6627102	0.1121	1.2905
chr20	63025520	7538265	0.1196	0.6278
chr21	48129895	7522242	0.1563	0.8435
chr22	51304566	4377191	0.0853	0.4583
chrMT	16571	588756	35.5293	26.5432
chrX	155270560	19817080	0.1276	0.7221
chrY	59373566	1162084	0.0196	0.622

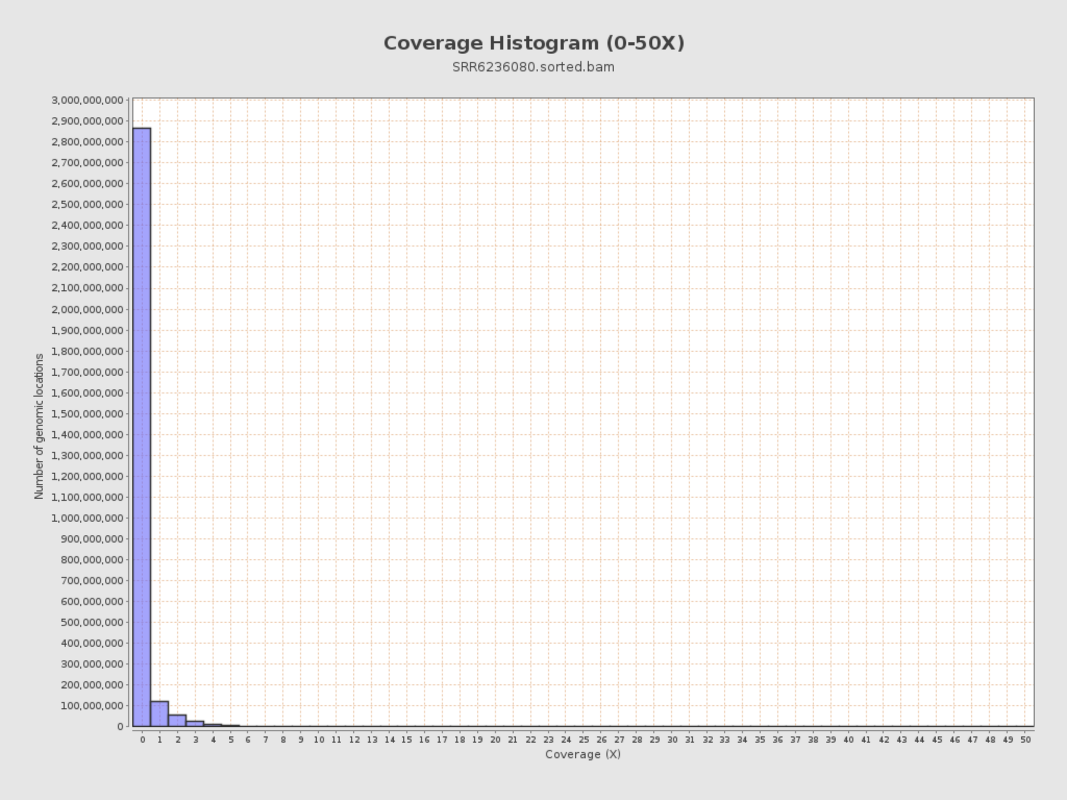
3. Results : Coverage across reference



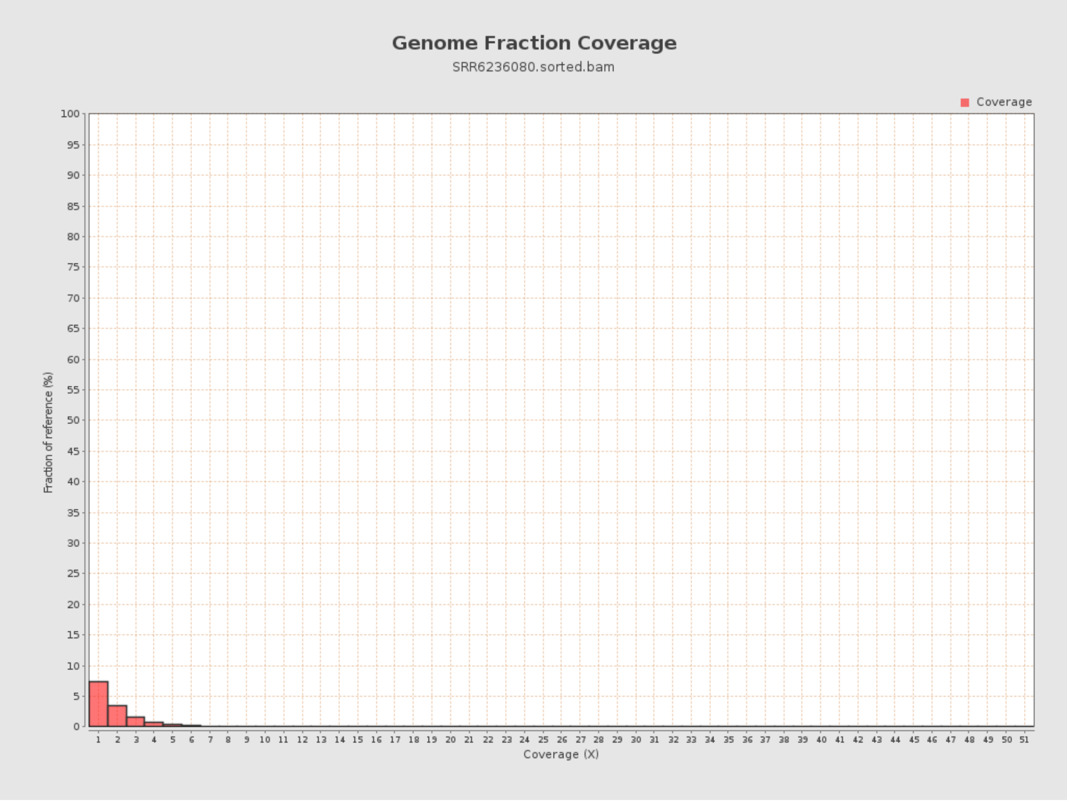
4. Results : Coverage Histogram



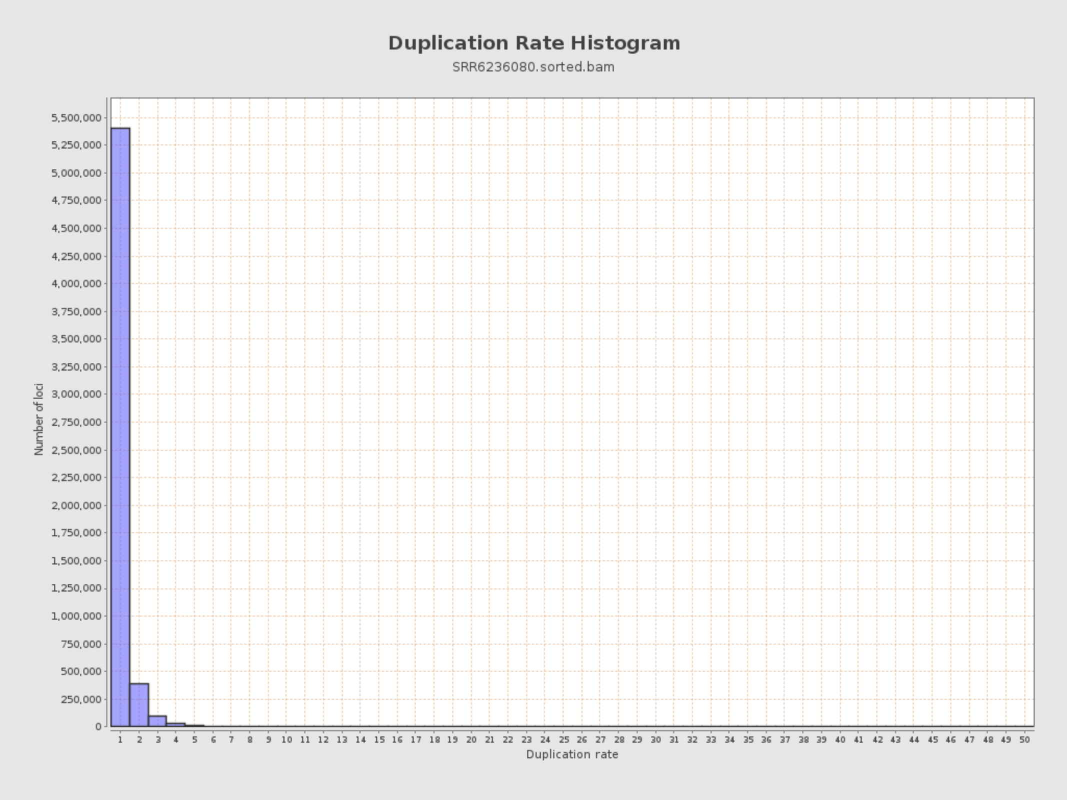
5. Results : Coverage Histogram (0-50X)



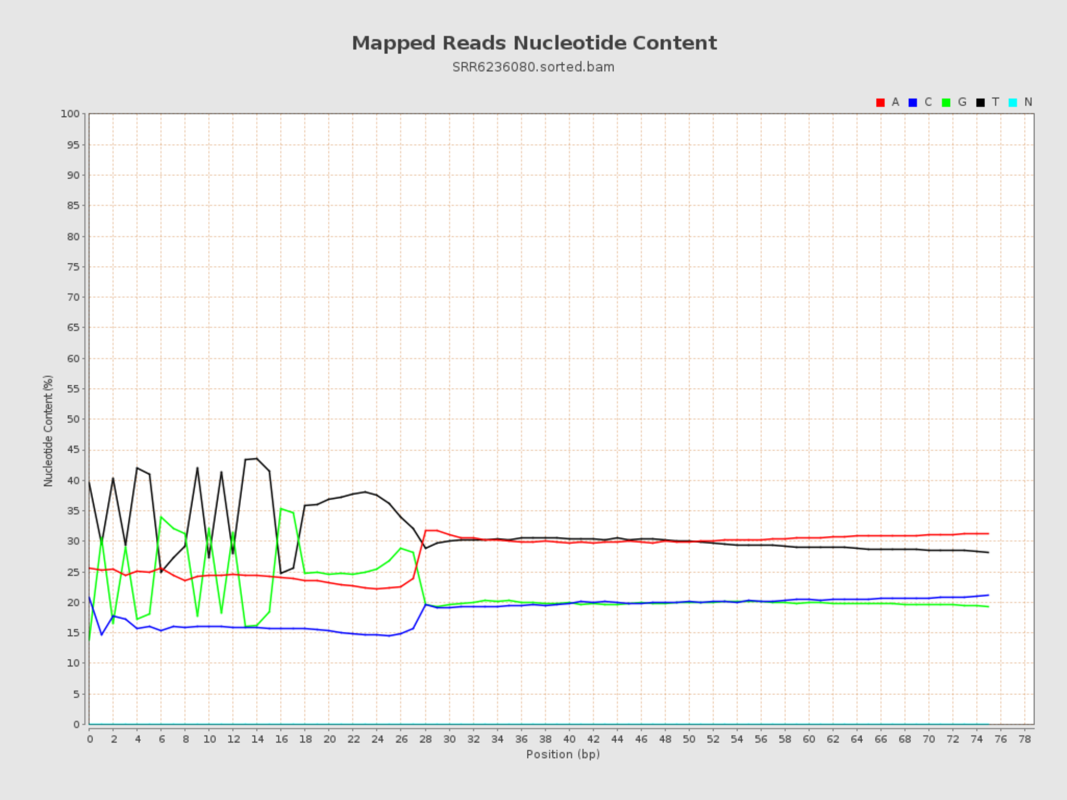
6. Results : Genome Fraction Coverage



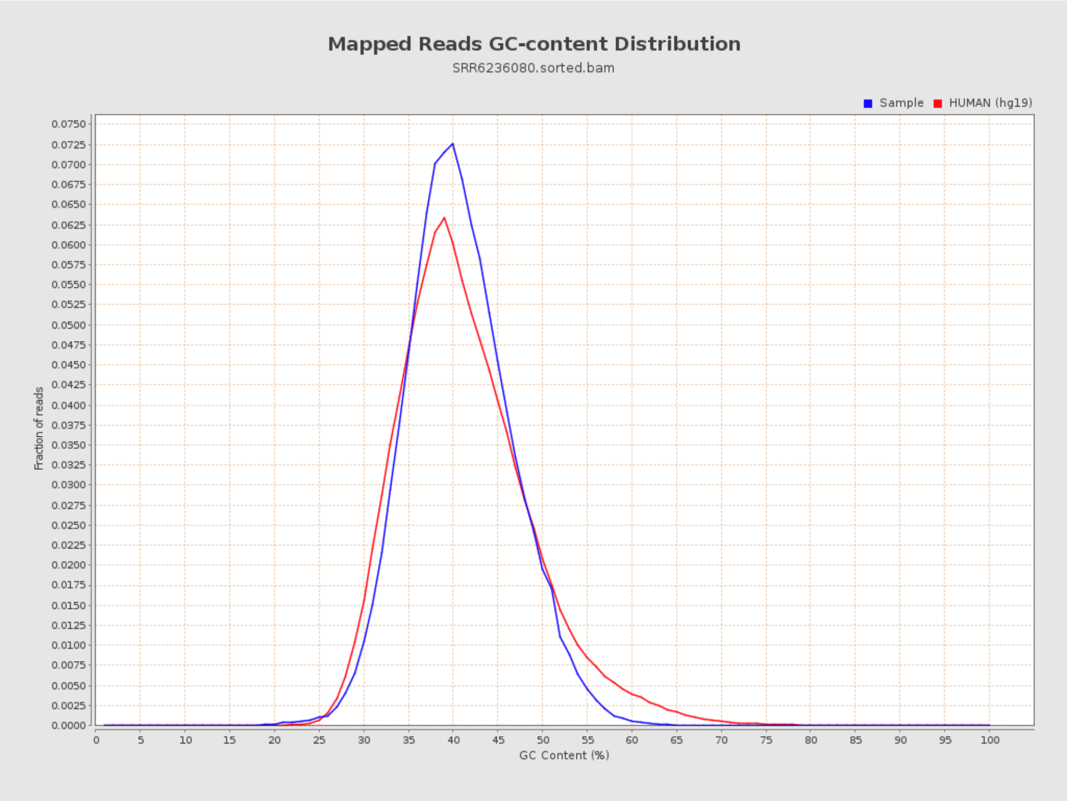
7. Results : Duplication Rate Histogram



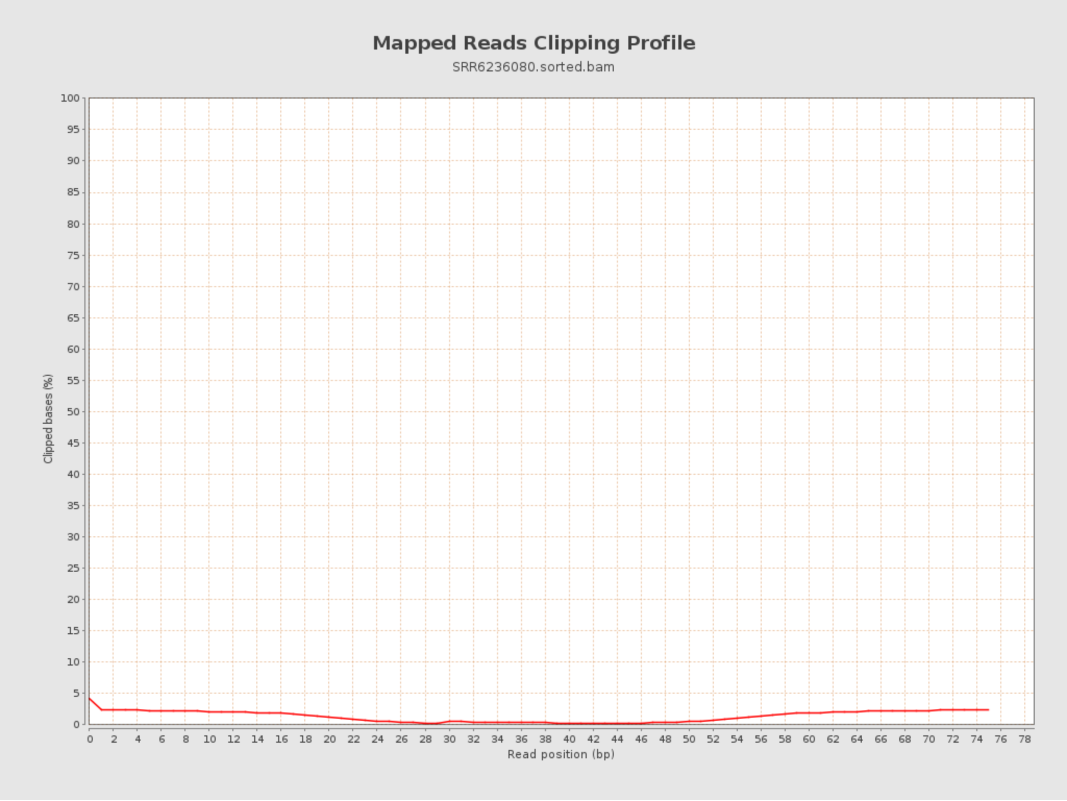
8. Results : Mapped Reads Nucleotide Content



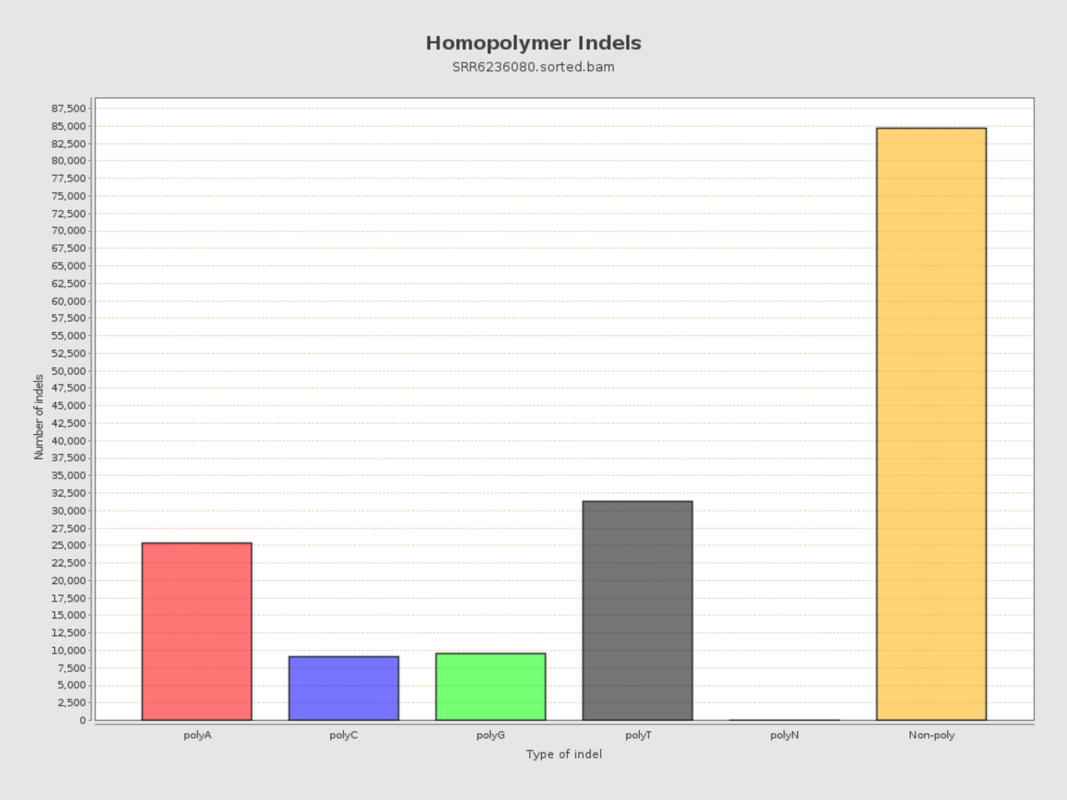
9. Results : Mapped Reads GC-content Distribution



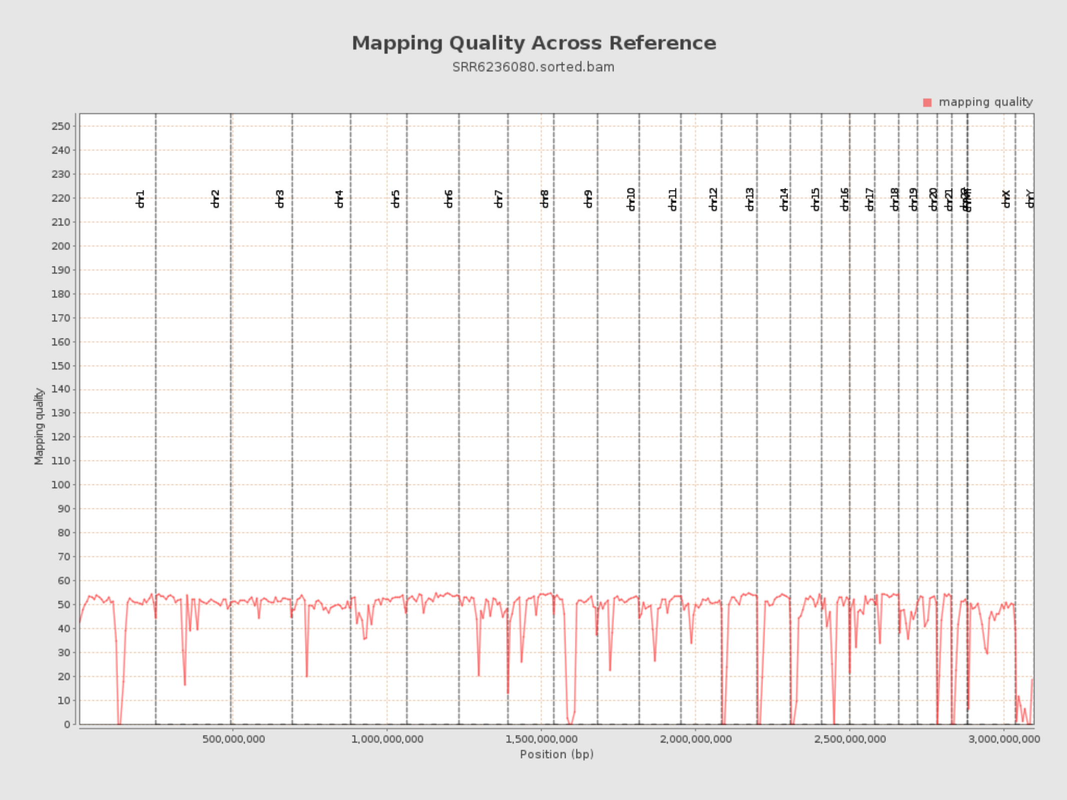
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram