Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:24:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238631.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_SRR6238631 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238631.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:24:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238631.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,100,073
Mapped reads	3,793,120 / 92.51%
Unmapped reads	306,953 / 7.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,649 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	478,279 / 11.67%
Duplication rate	10.61%
Clipped reads	2,333,325 / 56.91%

2.2. ACGT Content

Number/percentage of A's	58,371,606 / 24.81%
Number/percentage of C's	41,504,600 / 17.64%
Number/percentage of T's	78,338,441 / 33.3%
Number/percentage of G's	57,033,749 / 24.24%
Number/percentage of N's	12,048 / 0.01%
GC Percentage	41.88%

2.3. Coverage

Mean	0.076

Standard Deviation	0.787

2.4. Mapping Quality

Mean Mapping Quality	43.39

2.5. Mismatches and indels

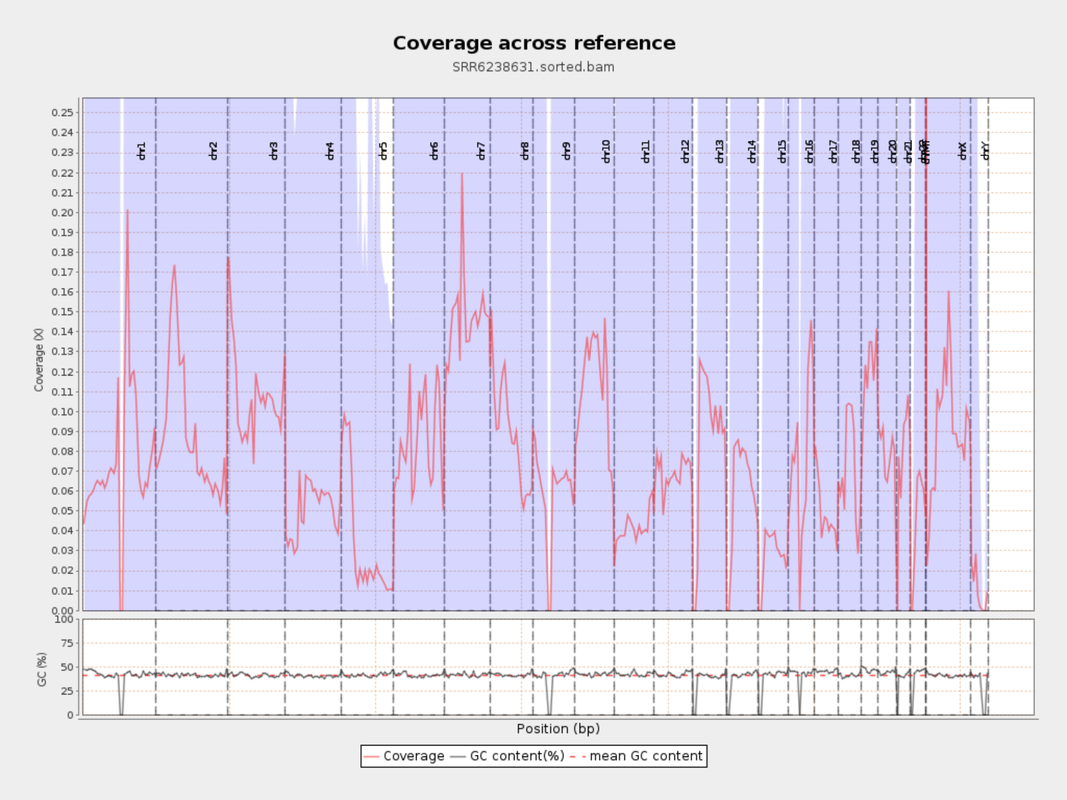
General error rate	0.59%
Mismatches	1,350,640
Insertions	14,876
Mapped reads with at least one insertion	0.39%
Deletions	72,208
Mapped reads with at least one deletion	1.88%
Homopolymer indels	42.09%

2.6. Chromosome stats

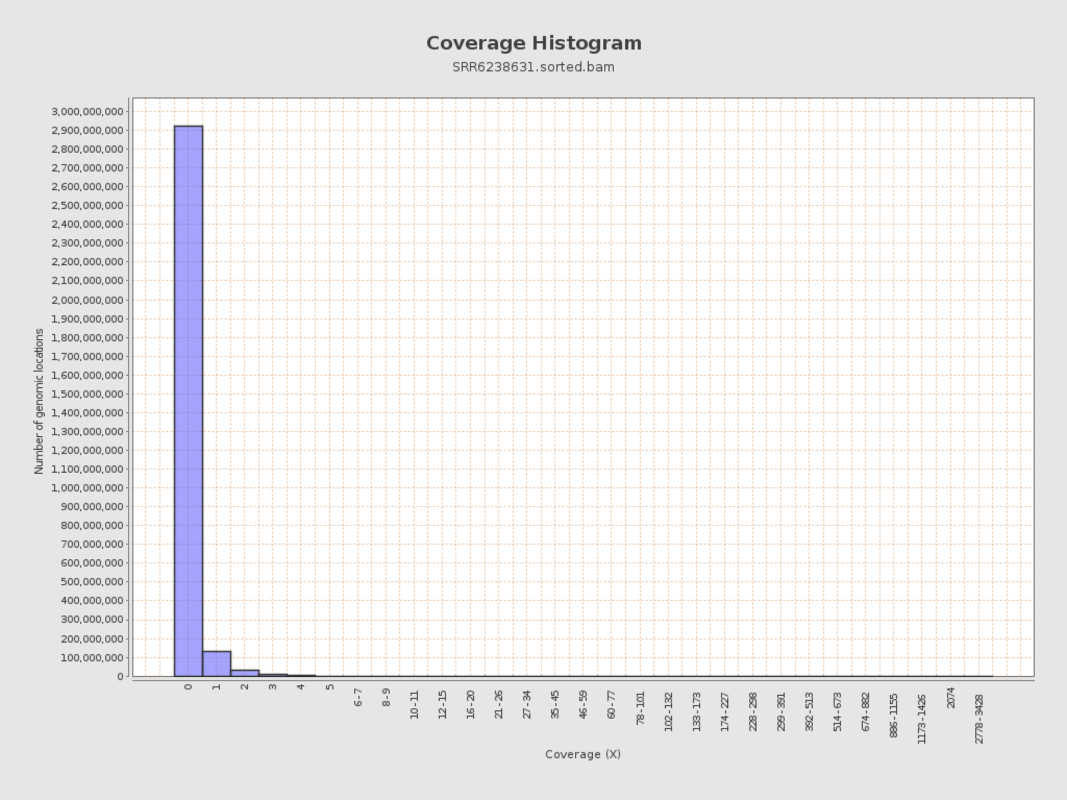
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18577707	0.0745	1.1518
chr2	243199373	21887015	0.09	1.5568
chr3	198022430	21433368	0.1082	0.4348
chr4	191154276	9755807	0.051	0.3181
chr5	180915260	5943318	0.0329	0.2563
chr6	171115067	14634537	0.0855	0.684
chr7	159138663	23365024	0.1468	1.516

chr8	146364022	12880547	0.088	0.7465
chr9	141213431	8304965	0.0588	0.4903
chr10	135534747	15351874	0.1133	0.6229
chr11	135006516	5622646	0.0416	0.3408
chr12	133851895	9262593	0.0692	0.3599
chr13	115169878	10046138	0.0872	0.4705
chr14	107349540	6519664	0.0607	0.3481
chr15	102531392	2786533	0.0272	0.3799
chr16	90354753	6698258	0.0741	0.4454
chr17	81195210	4054810	0.0499	0.3039
chr18	78077248	5509427	0.0706	1.1997
chr19	59128983	7059032	0.1194	0.7555
chr20	63025520	4955882	0.0786	0.3771
chr21	48129895	3771167	0.0784	0.4003
chr22	51304566	2305573	0.0449	0.2725
chrMT	16571	12744	0.7691	1.2015
chrX	155270560	14044387	0.0905	0.4333
chrY	59373566	602727	0.0102	0.2706

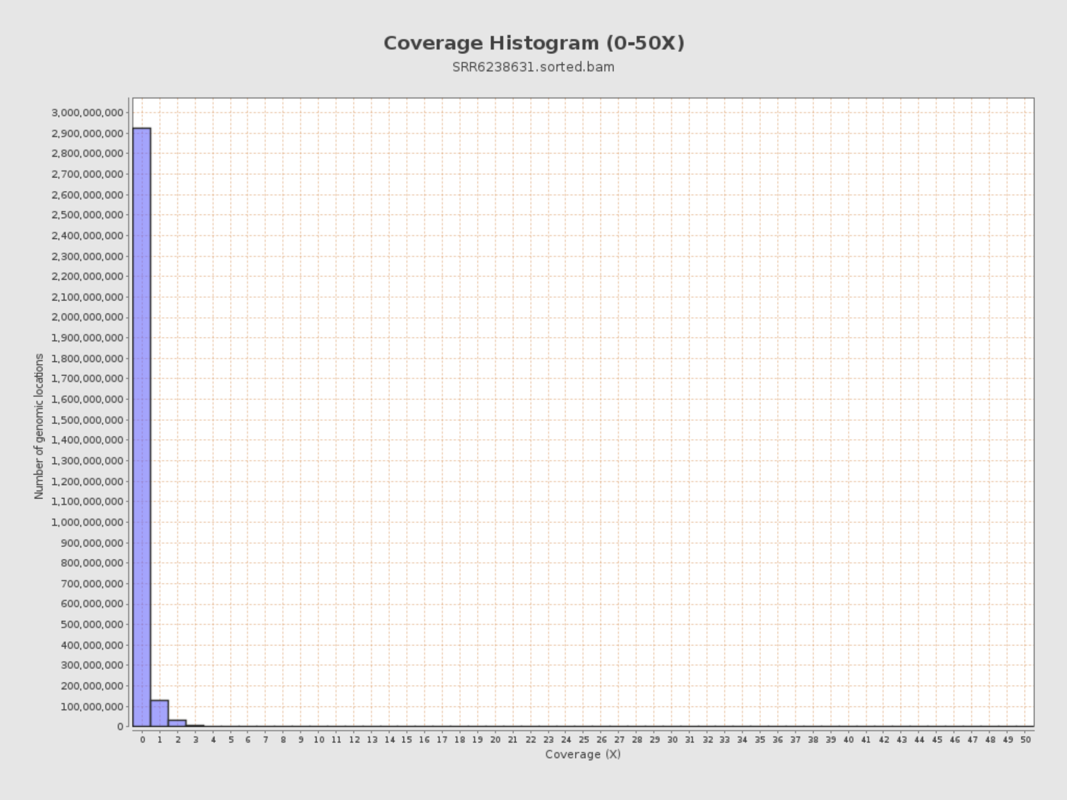
3. Results : Coverage across reference



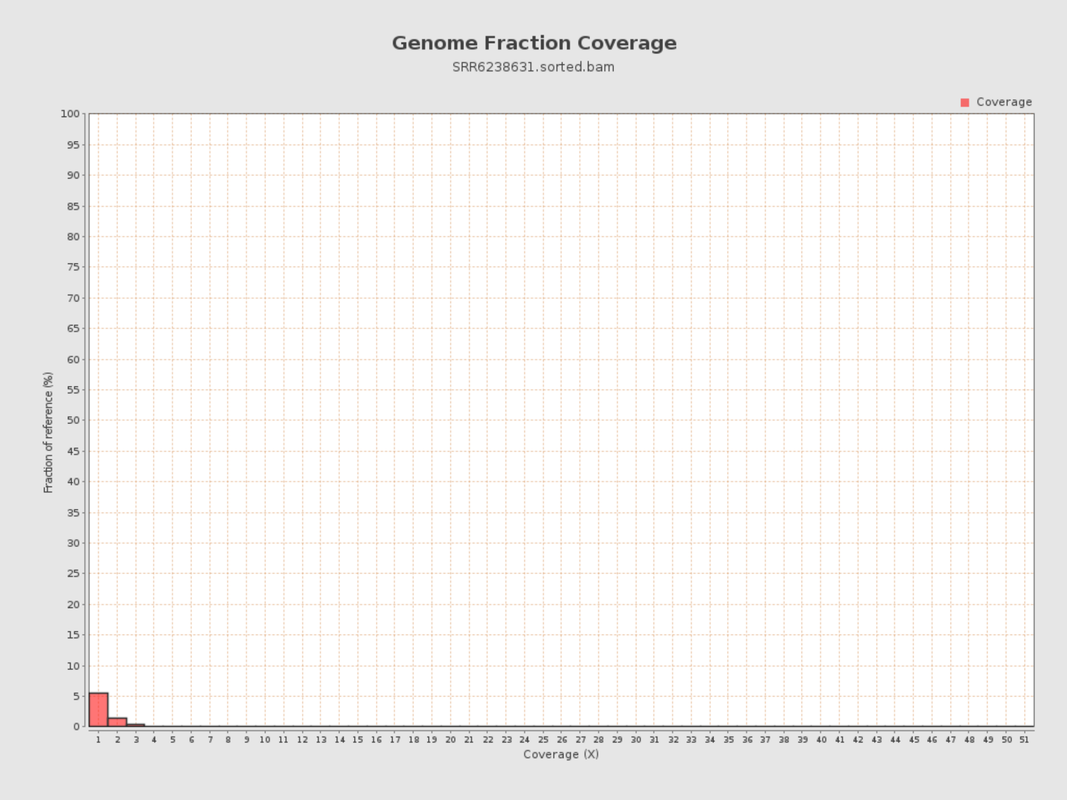
4. Results : Coverage Histogram



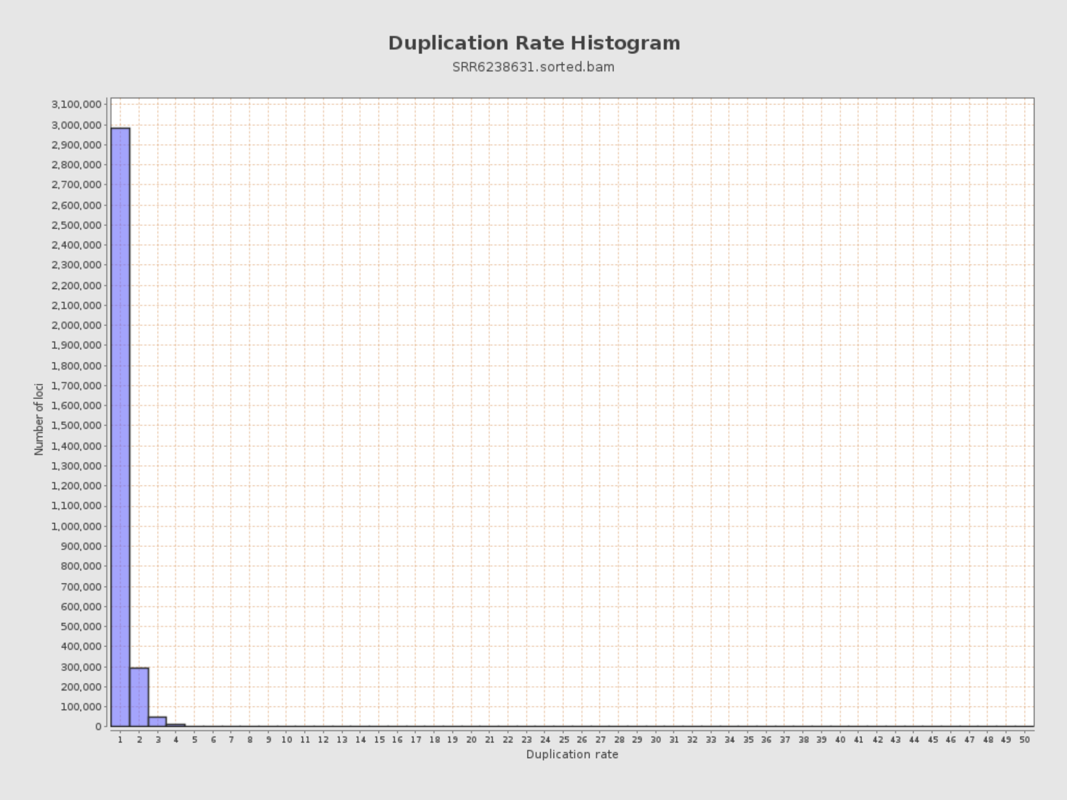
5. Results : Coverage Histogram (0-50X)



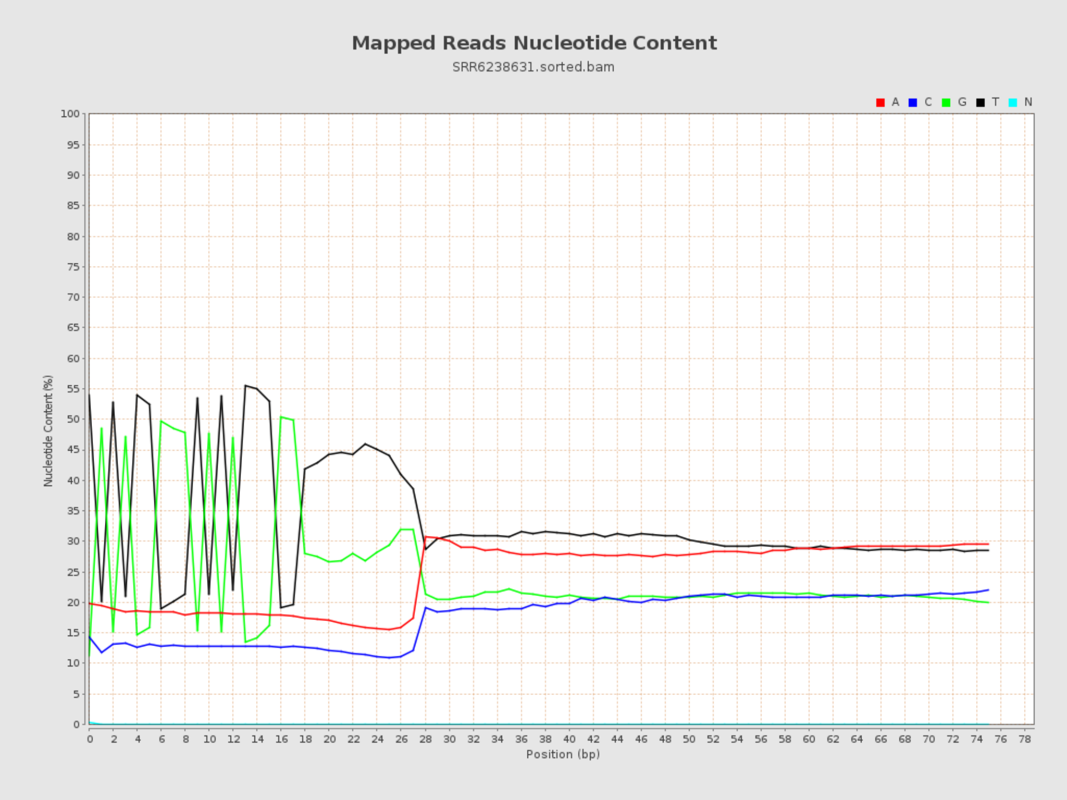
6. Results : Genome Fraction Coverage



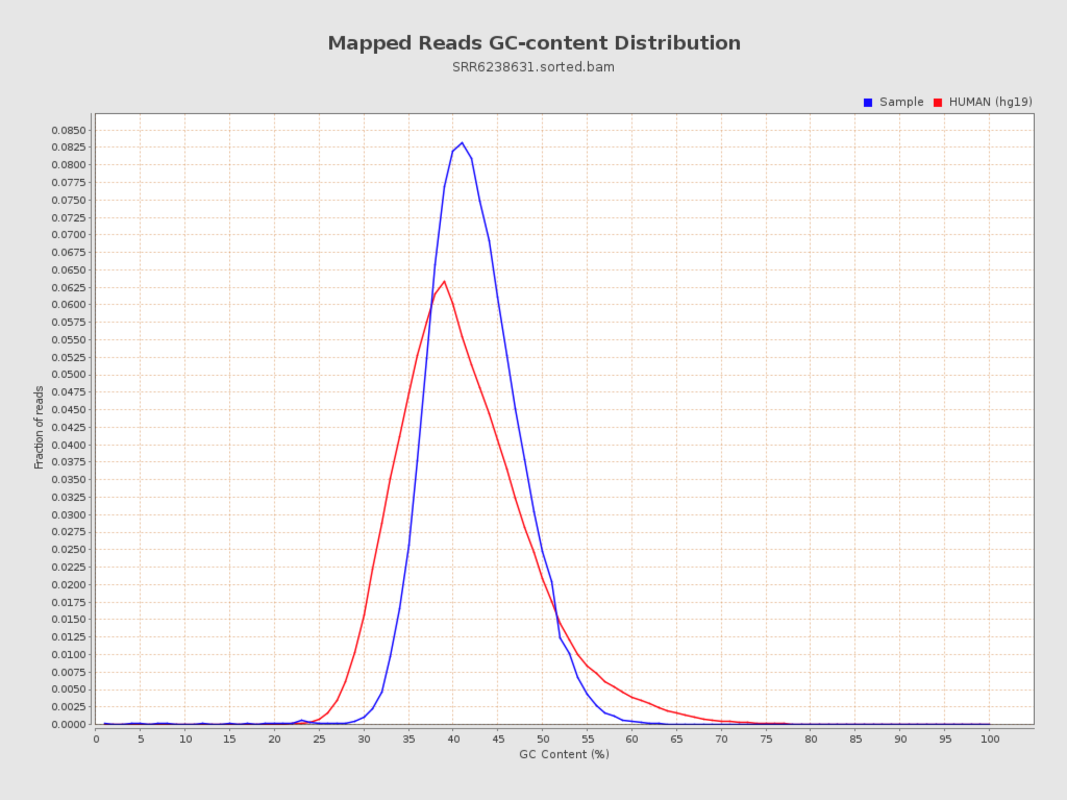
7. Results : Duplication Rate Histogram



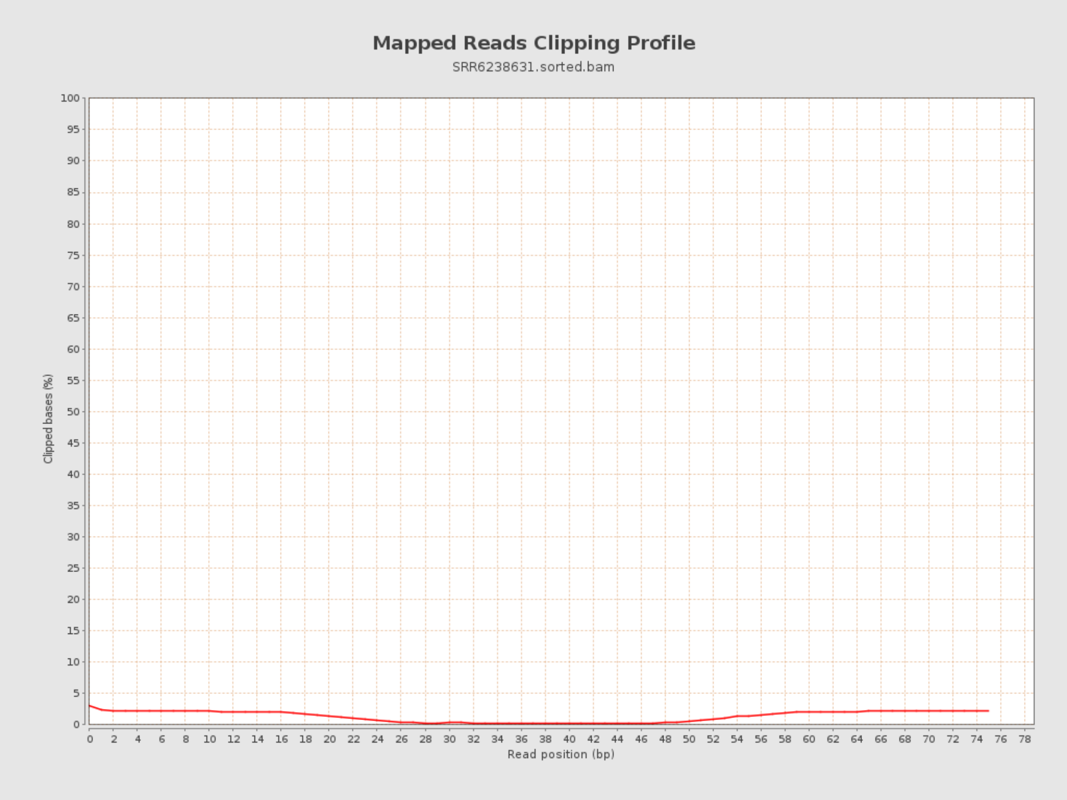
8. Results : Mapped Reads Nucleotide Content



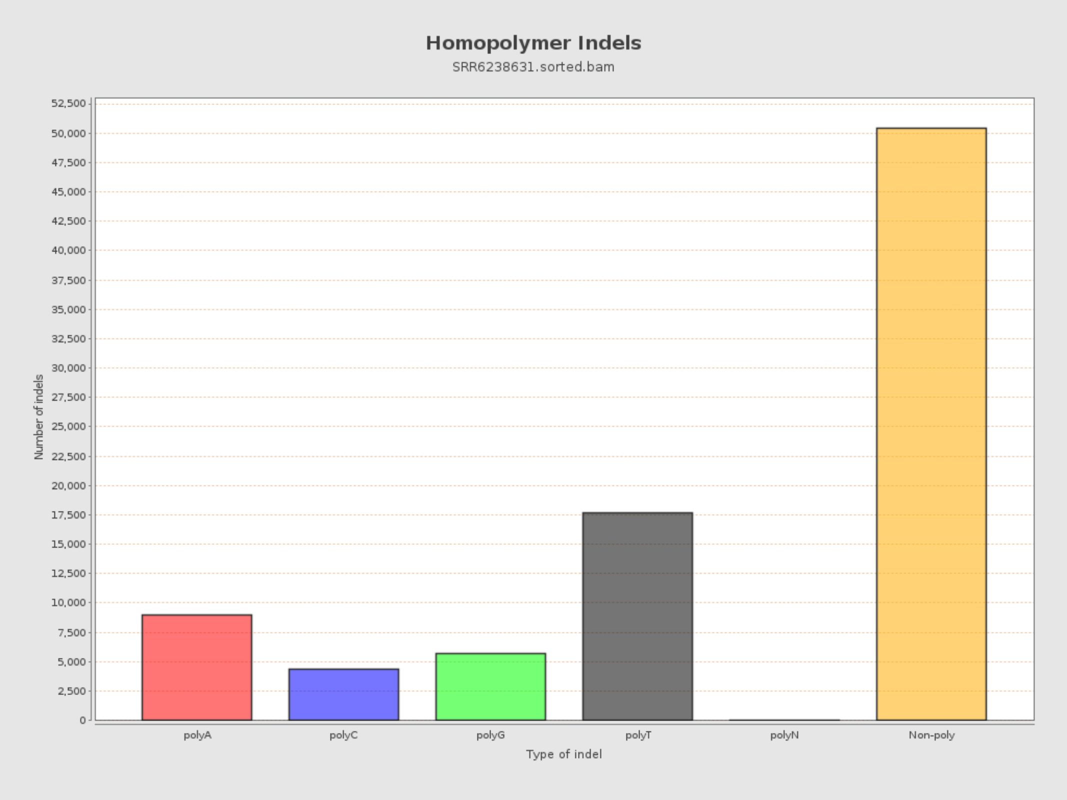
9. Results : Mapped Reads GC-content Distribution



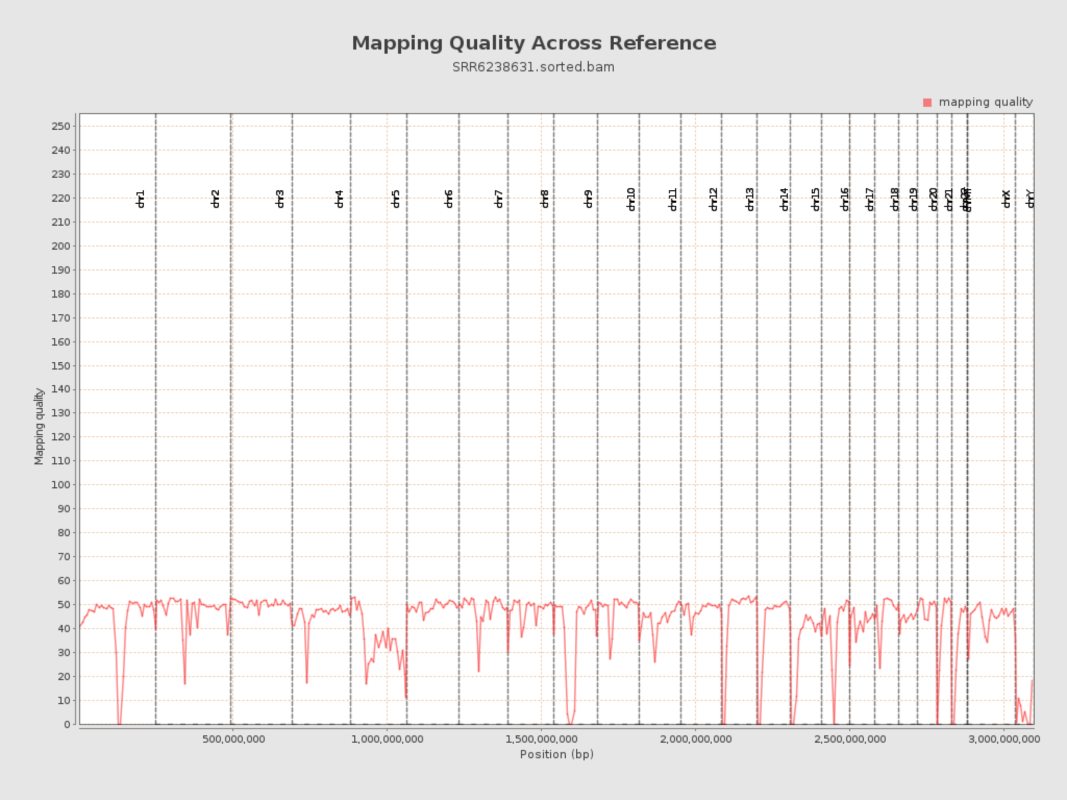
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram