Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:56:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238495.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_SRR6238495 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238495.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:56:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238495.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,781,269
Mapped reads	3,315,958 / 87.69%
Unmapped reads	465,311 / 12.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,773 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,423,386 / 37.64%
Duplication rate	22.53%
Clipped reads	2,135,475 / 56.48%

2.2. ACGT Content

Number/percentage of A's	50,520,279 / 24.81%
Number/percentage of C's	34,235,993 / 16.81%
Number/percentage of T's	70,914,250 / 34.83%
Number/percentage of G's	47,948,240 / 23.55%
Number/percentage of N's	4,562 / 0%
GC Percentage	40.36%

2.3. Coverage

Mean	0.0658

Standard Deviation	1.2545

2.4. Mapping Quality

Mean Mapping Quality	38.03

2.5. Mismatches and indels

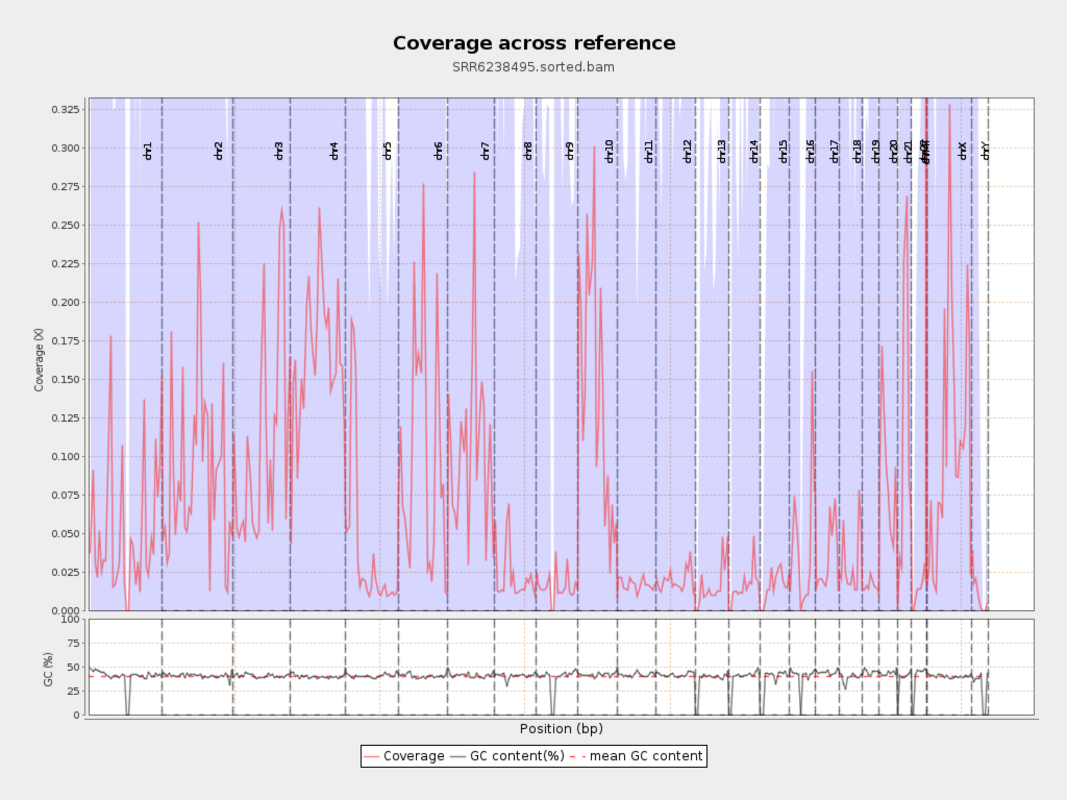
General error rate	0.59%
Mismatches	1,178,606
Insertions	13,463
Mapped reads with at least one insertion	0.4%
Deletions	56,760
Mapped reads with at least one deletion	1.7%
Homopolymer indels	41.63%

2.6. Chromosome stats

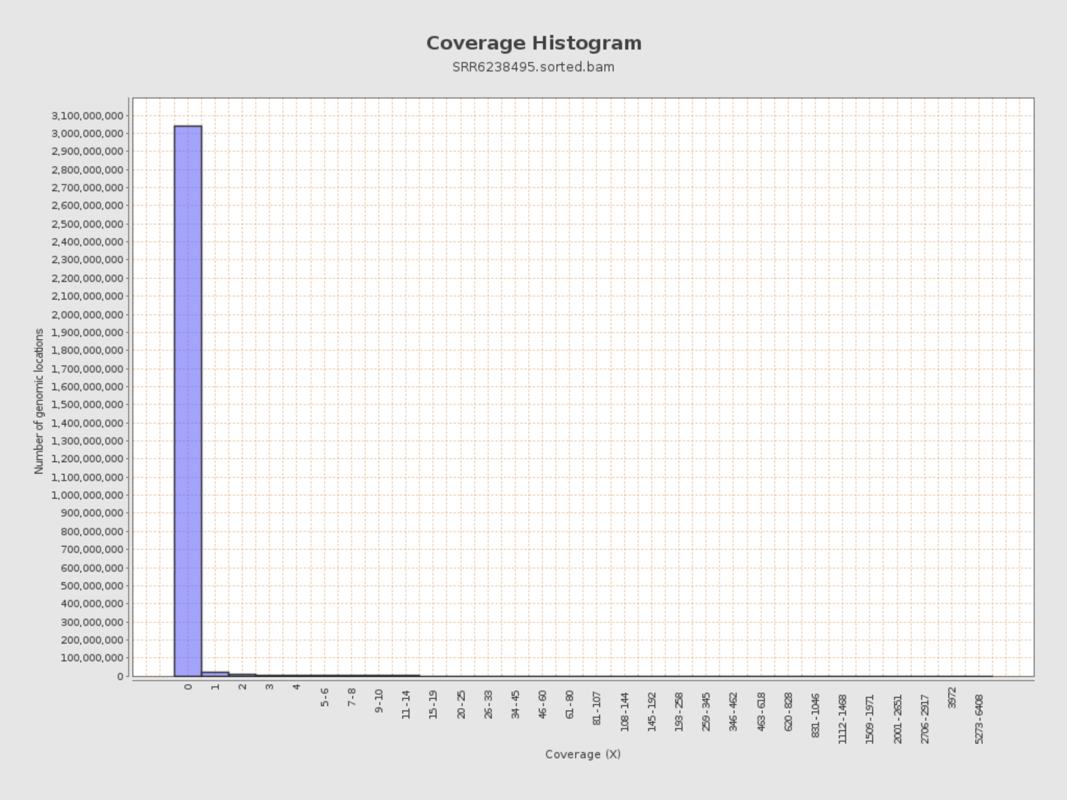
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12578799	0.0505	0.6484
chr2	243199373	22046590	0.0907	2.8884
chr3	198022430	21062936	0.1064	0.9663
chr4	191154276	31579728	0.1652	1.1995
chr5	180915260	7201491	0.0398	0.581
chr6	171115067	17529460	0.1024	1.513
chr7	159138663	16796527	0.1055	1.3698

chr8	146364022	3314746	0.0226	1.6684
chr9	141213431	2120319	0.015	0.453
chr10	135534747	19584187	0.1445	1.3547
chr11	135006516	2245214	0.0166	0.3446
chr12	133851895	2597477	0.0194	0.4276
chr13	115169878	1876492	0.0163	0.651
chr14	107349540	1702721	0.0159	0.4344
chr15	102531392	1637308	0.016	0.6036
chr16	90354753	3948334	0.0437	0.6485
chr17	81195210	2737499	0.0337	0.5279
chr18	78077248	2440985	0.0313	2.0997
chr19	59128983	966037	0.0163	0.5209
chr20	63025520	5832053	0.0925	0.9089
chr21	48129895	5285826	0.1098	1.0033
chr22	51304566	696953	0.0136	0.3028
chrMT	16571	87311	5.2689	6.9186
chrX	155270560	17246137	0.1111	0.9818
chrY	59373566	603240	0.0102	0.431

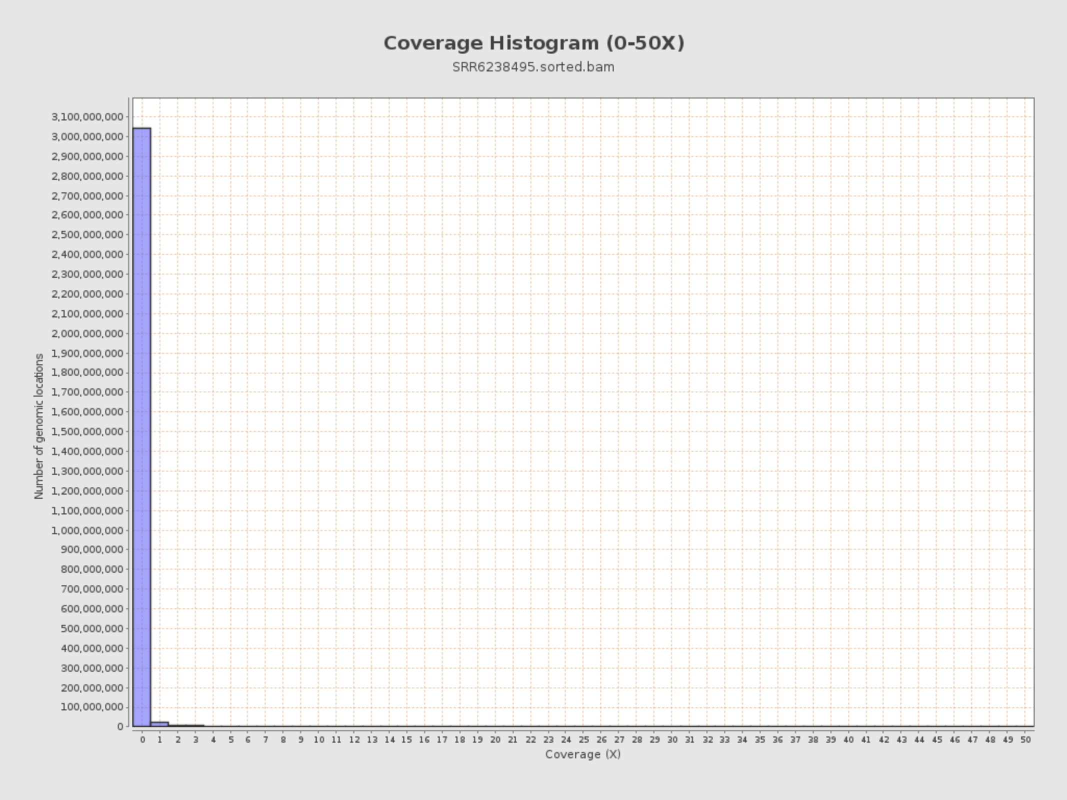
3. Results : Coverage across reference



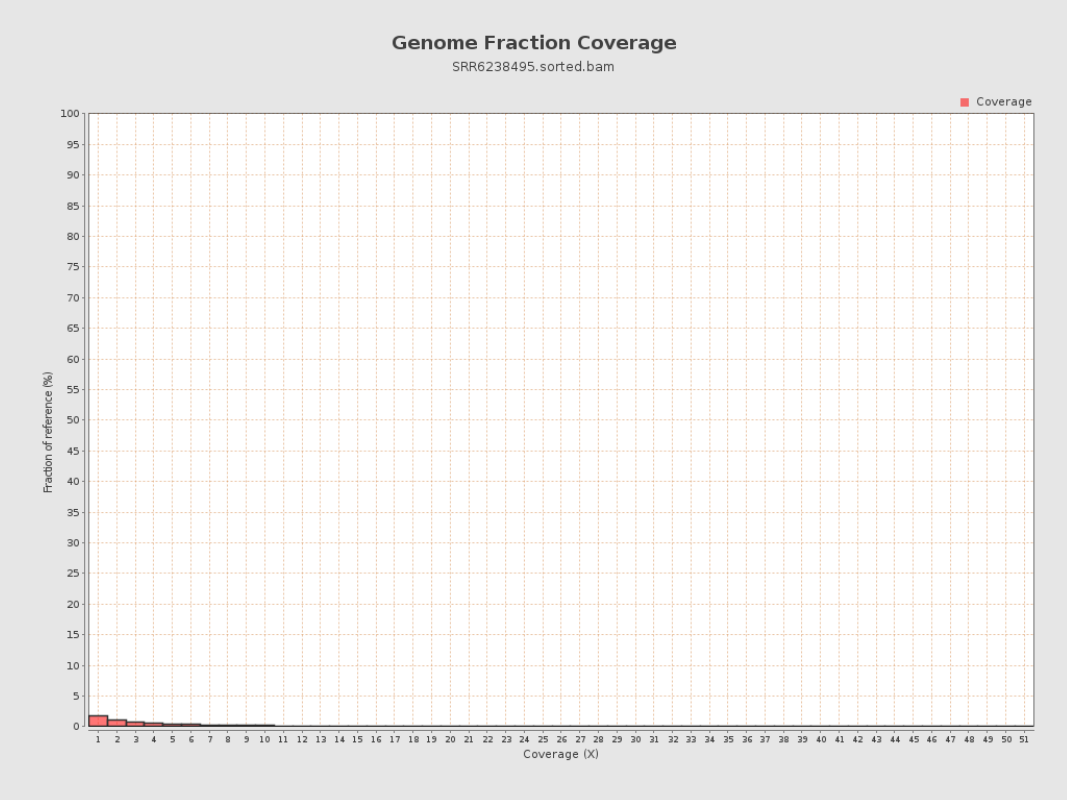
4. Results : Coverage Histogram



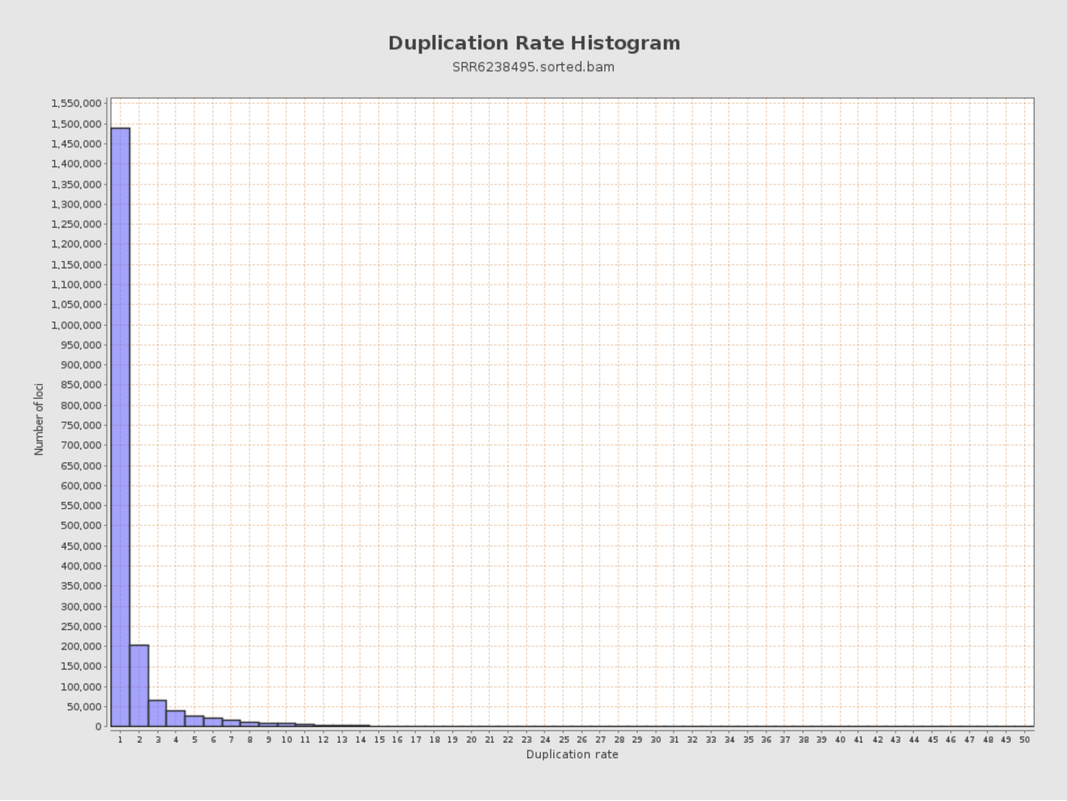
5. Results : Coverage Histogram (0-50X)



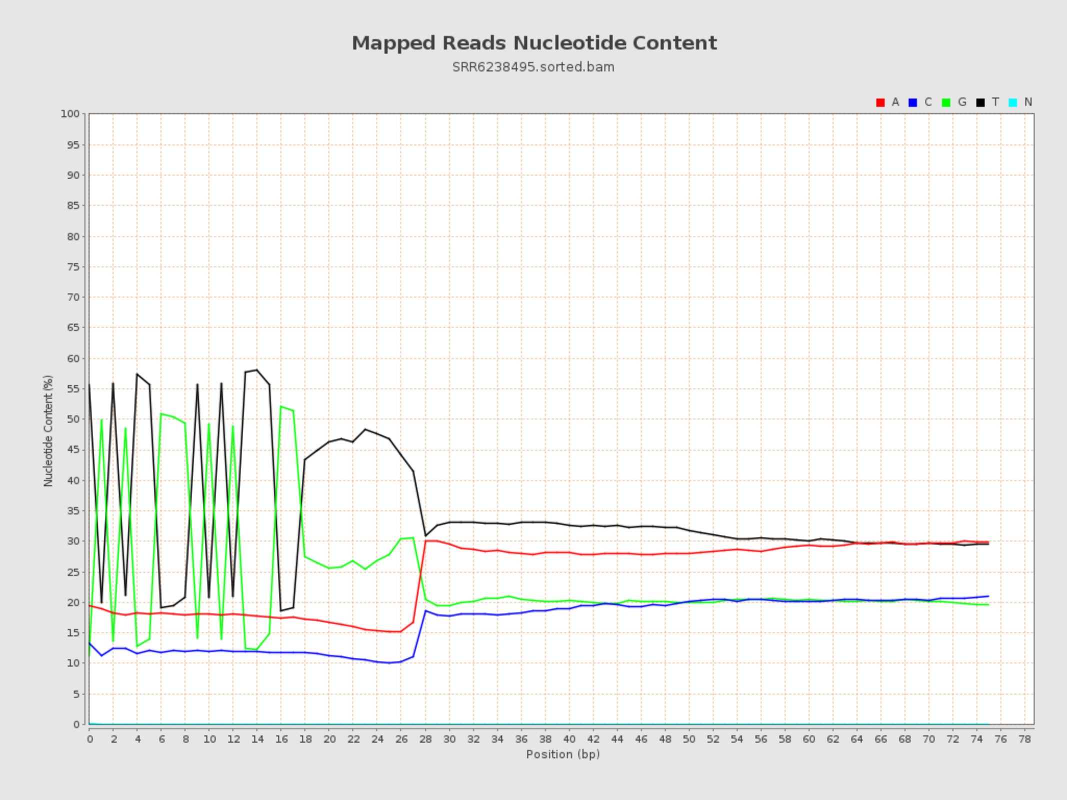
6. Results : Genome Fraction Coverage



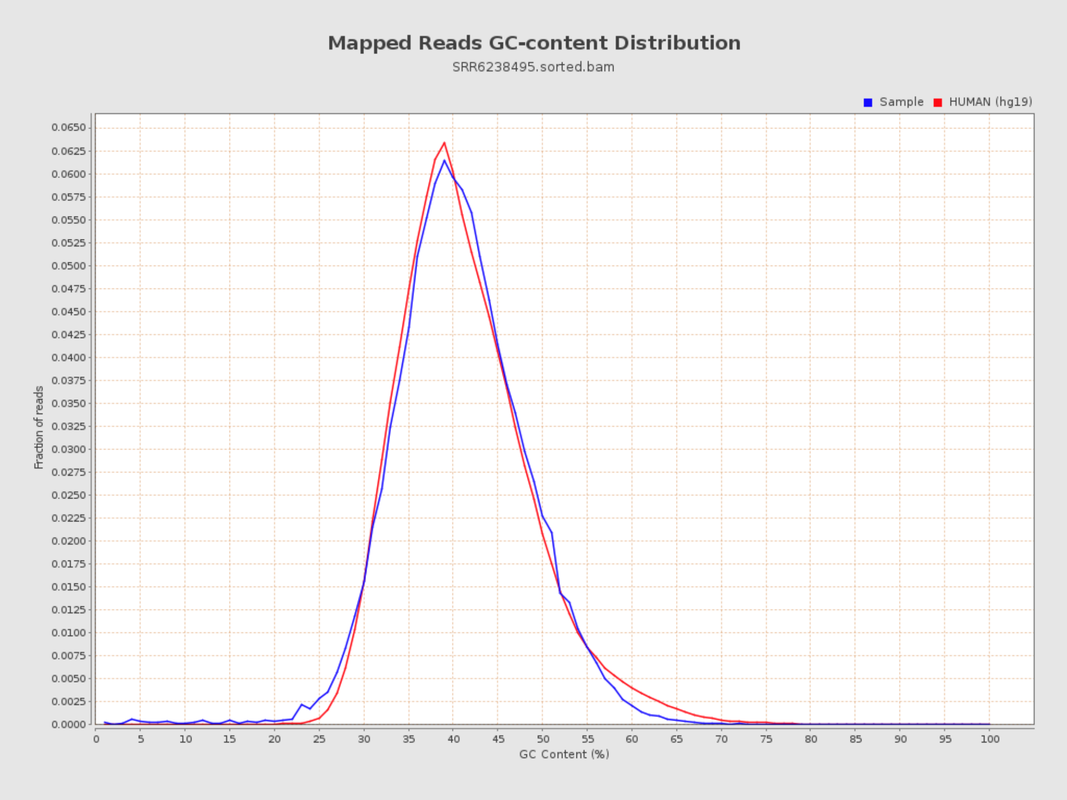
7. Results : Duplication Rate Histogram



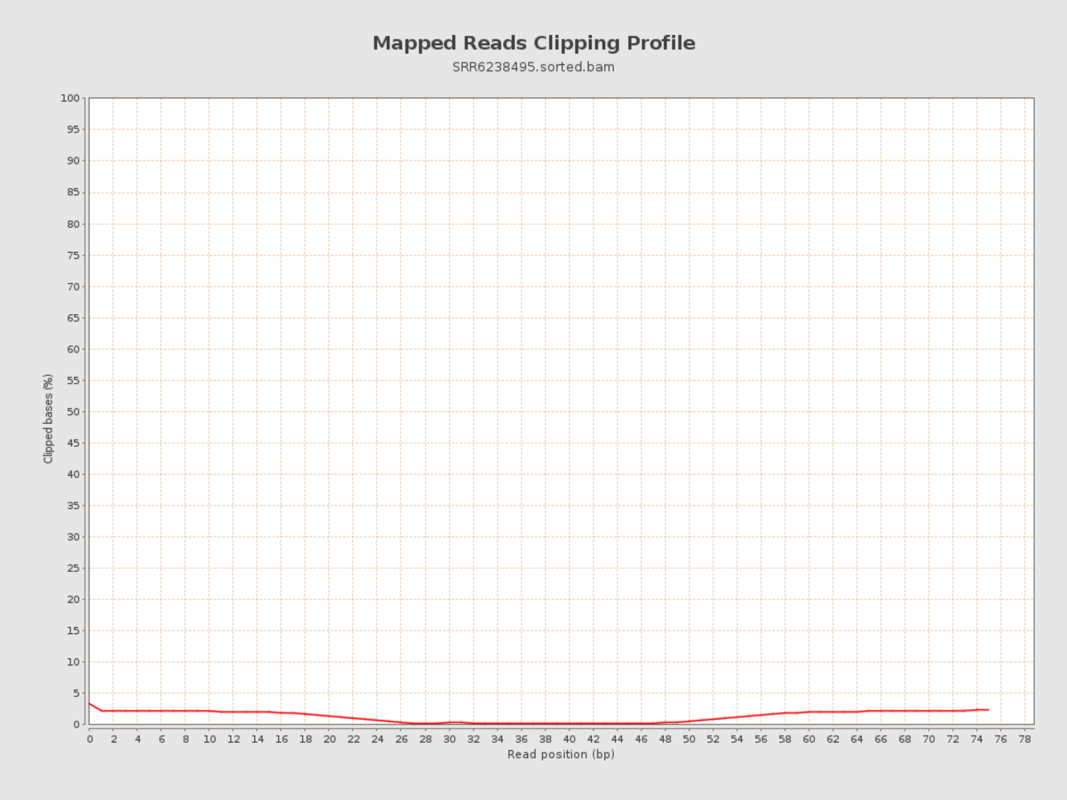
8. Results : Mapped Reads Nucleotide Content



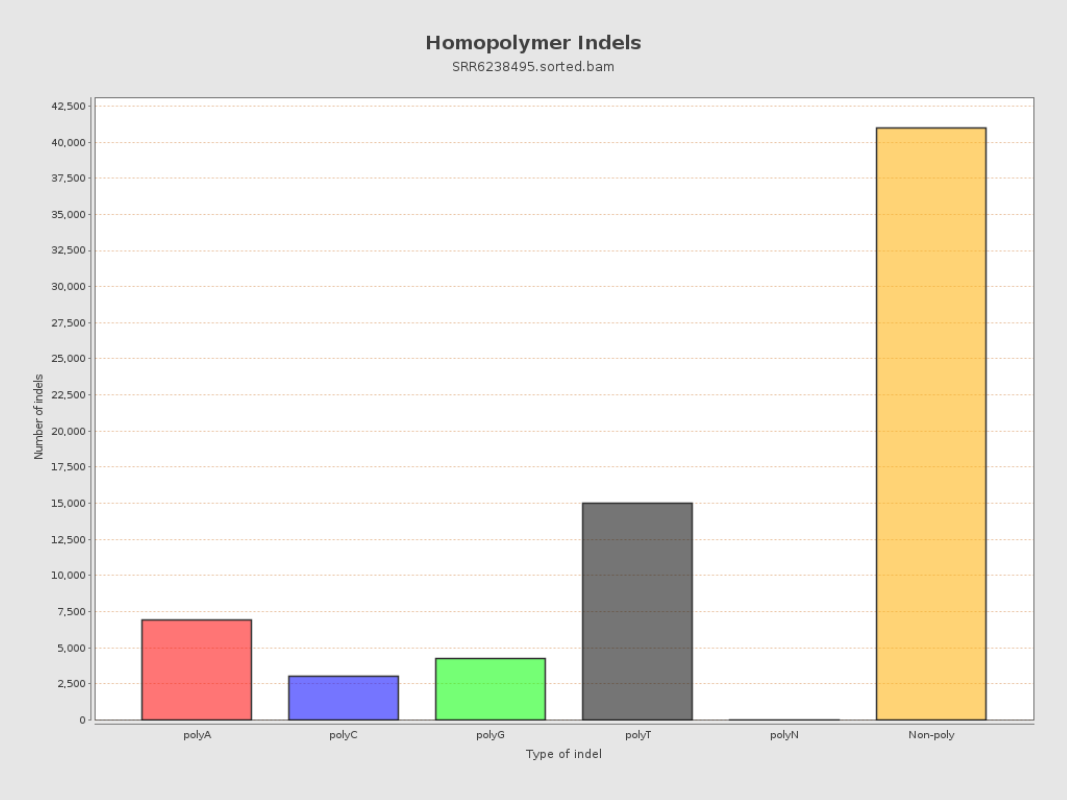
9. Results : Mapped Reads GC-content Distribution



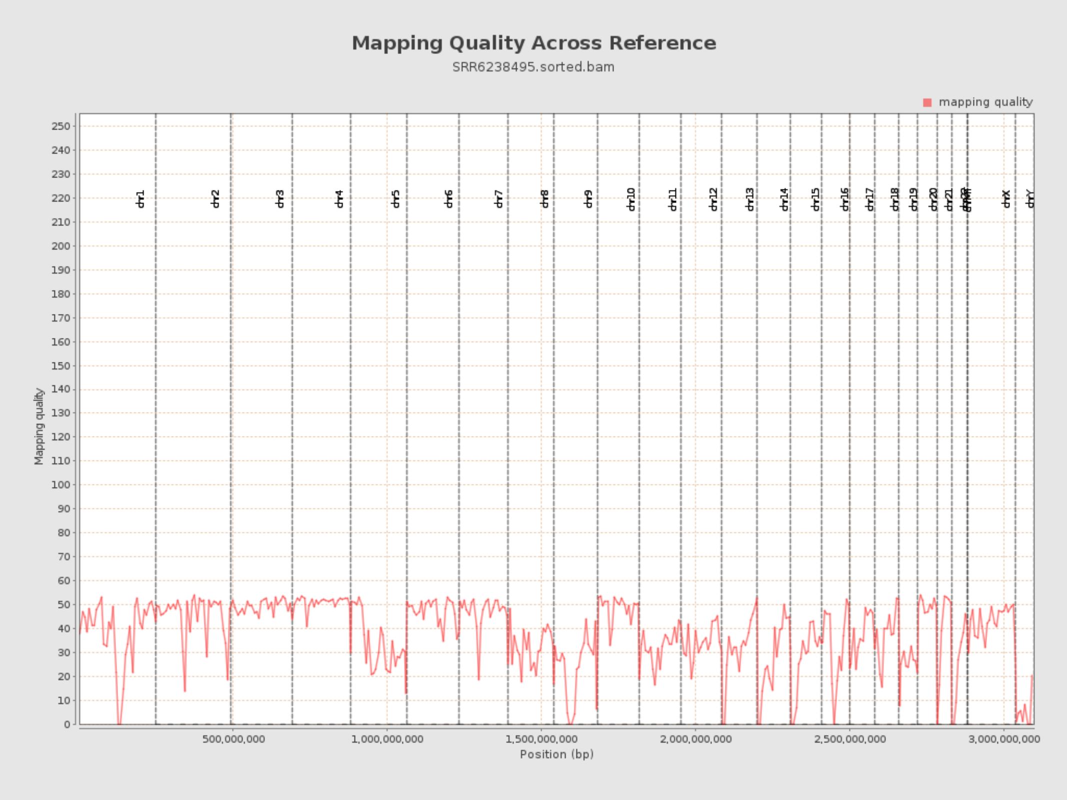
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram