Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:00:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238496.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_SRR6238496 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238496.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:00:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238496.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,023,154
Mapped reads	3,061,348 / 76.09%
Unmapped reads	961,806 / 23.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,349 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	1,238,853 / 30.79%
Duplication rate	22.38%
Clipped reads	1,956,579 / 48.63%

2.2. ACGT Content

Number/percentage of A's	46,425,693 / 24.76%
Number/percentage of C's	33,073,216 / 17.64%
Number/percentage of T's	62,726,019 / 33.45%
Number/percentage of G's	45,286,095 / 24.15%
Number/percentage of N's	4,251 / 0%
GC Percentage	41.79%

2.3. Coverage

Mean	0.0606

Standard Deviation	1.1387

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

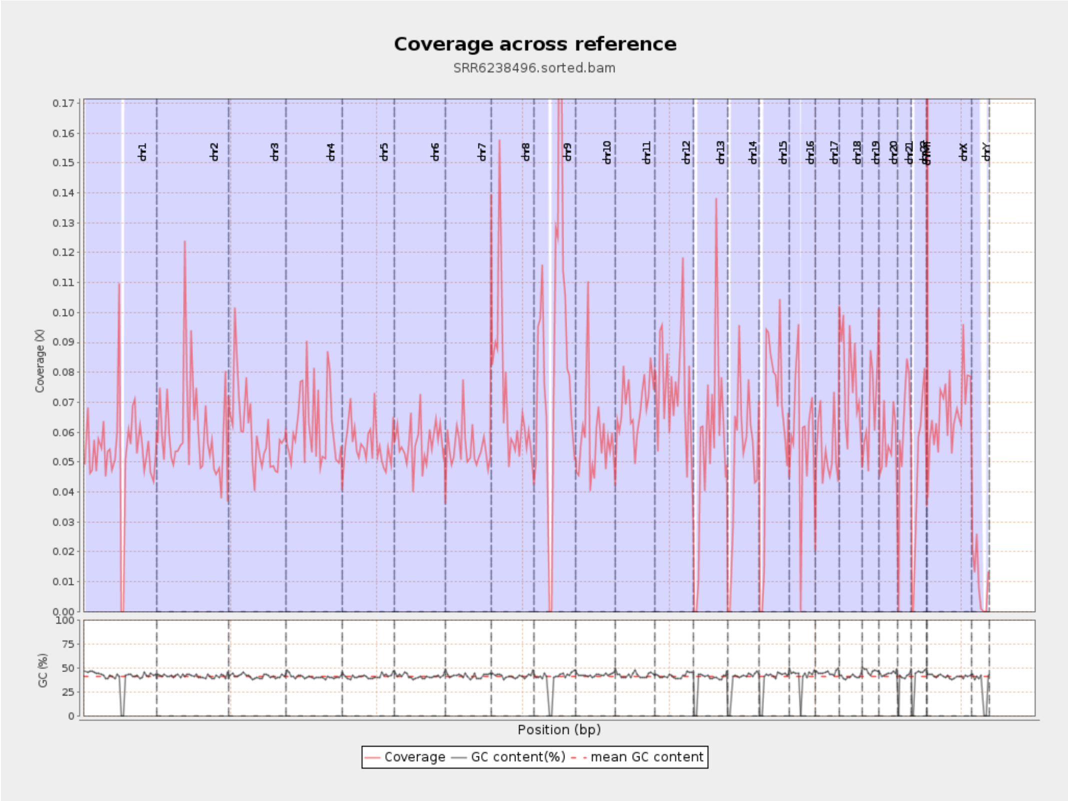
General error rate	0.57%
Mismatches	1,053,667
Insertions	12,399
Mapped reads with at least one insertion	0.4%
Deletions	42,241
Mapped reads with at least one deletion	1.37%
Homopolymer indels	42.74%

2.6. Chromosome stats

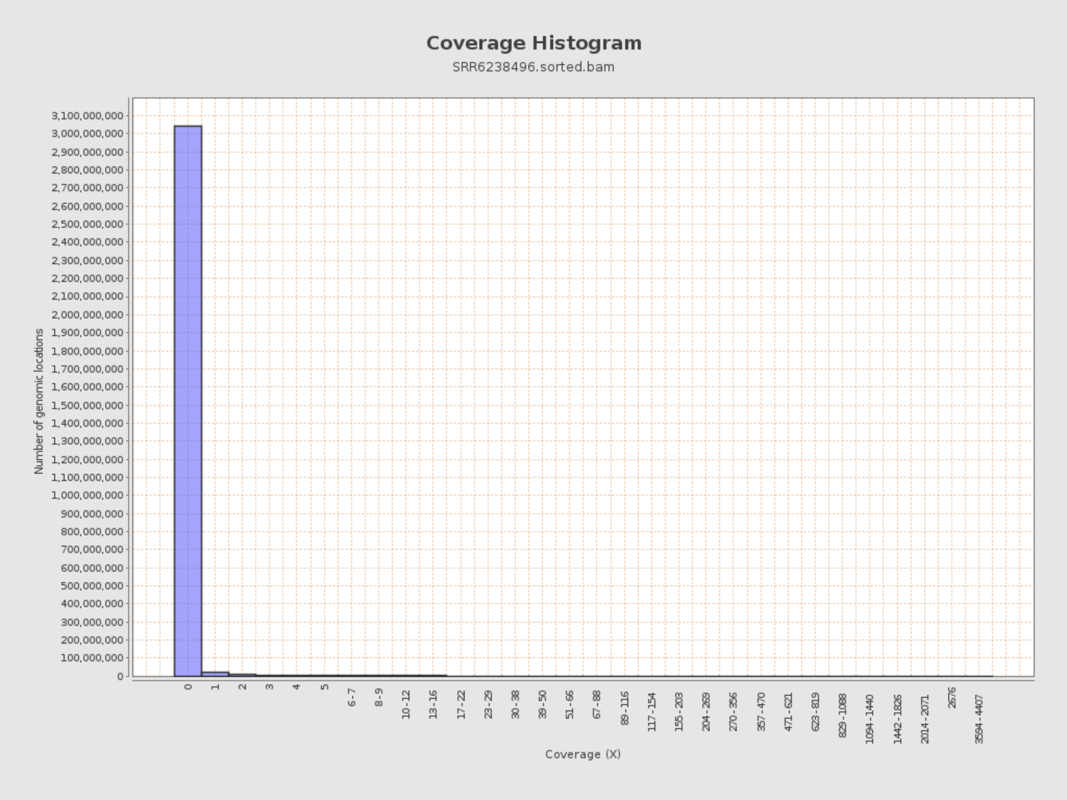
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13183300	0.0529	1.6219
chr2	243199373	14704631	0.0605	2.1828
chr3	198022430	11923752	0.0602	0.7665
chr4	191154276	11914473	0.0623	0.7827
chr5	180915260	10098512	0.0558	0.7054
chr6	171115067	9627530	0.0563	0.9621
chr7	159138663	8685797	0.0546	0.8877

chr8	146364022	10407553	0.0711	0.9944
chr9	141213431	12301318	0.0871	0.9578
chr10	135534747	7764975	0.0573	0.863
chr11	135006516	9237385	0.0684	0.8113
chr12	133851895	9957856	0.0744	0.8656
chr13	115169878	6362671	0.0552	0.8695
chr14	107349540	5563110	0.0518	1.0512
chr15	102531392	6351480	0.0619	1.4731
chr16	90354753	5153229	0.057	0.749
chr17	81195210	4406929	0.0543	0.7184
chr18	78077248	6070814	0.0778	1.6106
chr19	59128983	4056624	0.0686	1.1424
chr20	63025520	3562562	0.0565	0.7289
chr21	48129895	2932433	0.0609	0.7558
chr22	51304566	2374270	0.0463	0.9125
chrMT	16571	35554	2.1456	3.6432
chrX	155270560	10327752	0.0665	0.8615
chrY	59373566	583481	0.0098	0.369

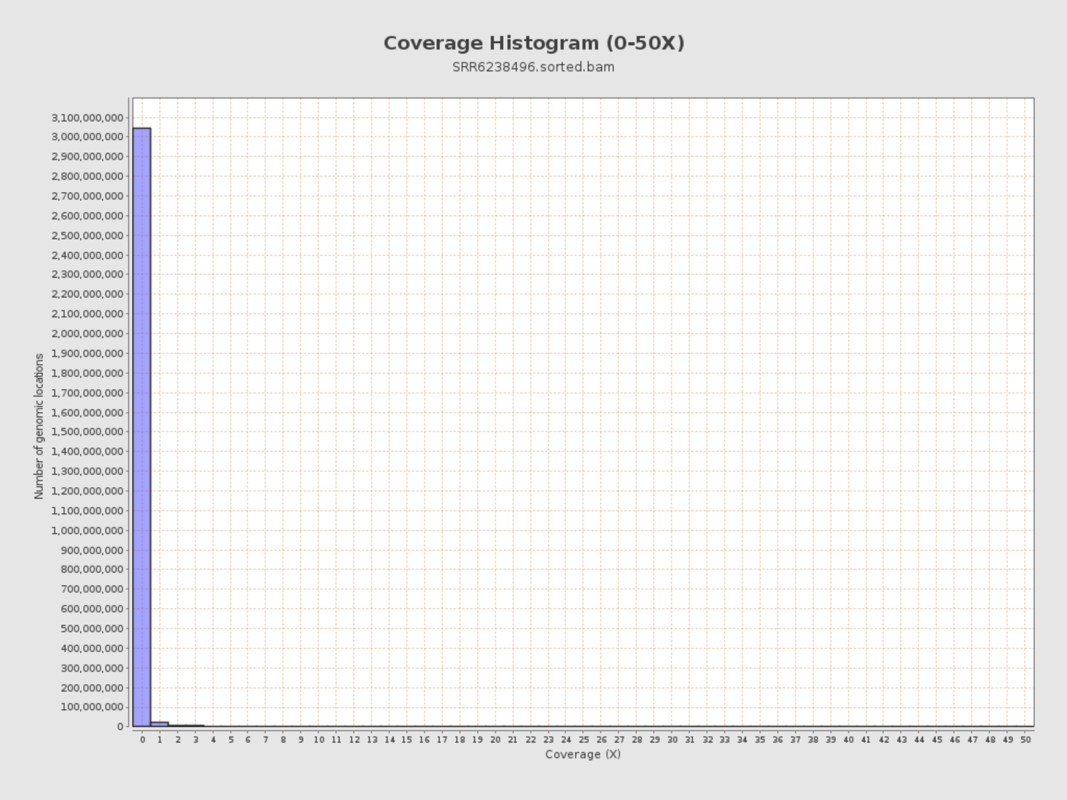
3. Results : Coverage across reference



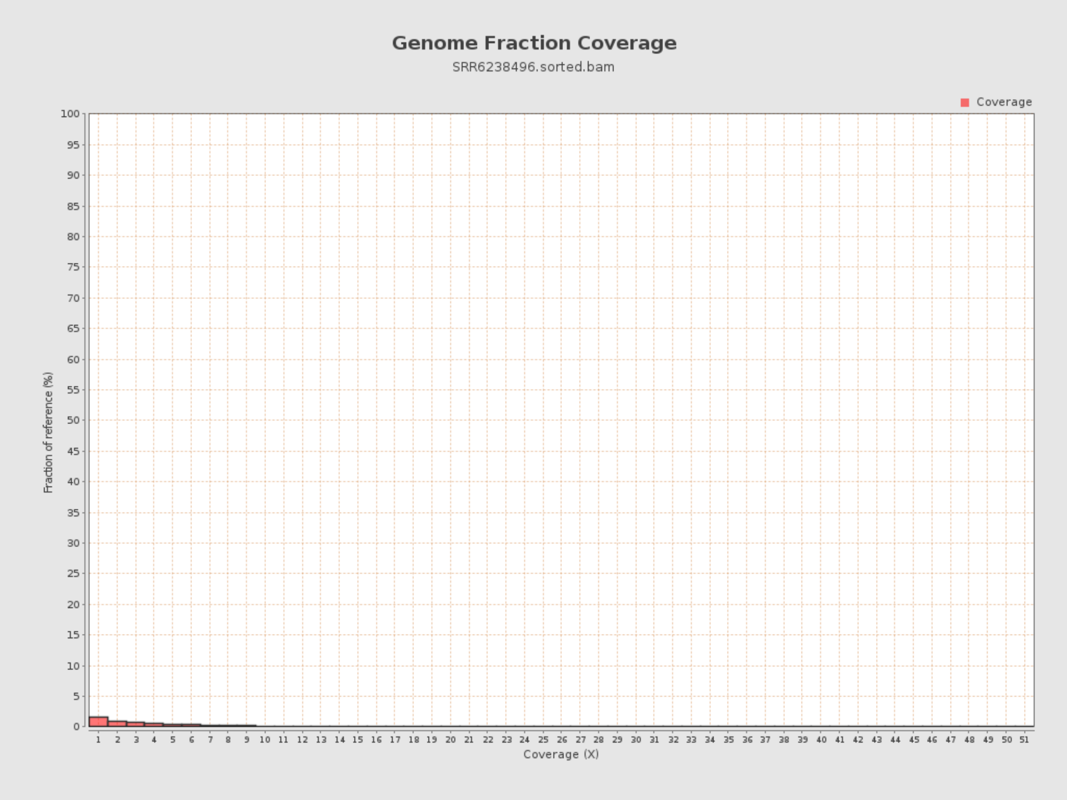
4. Results : Coverage Histogram



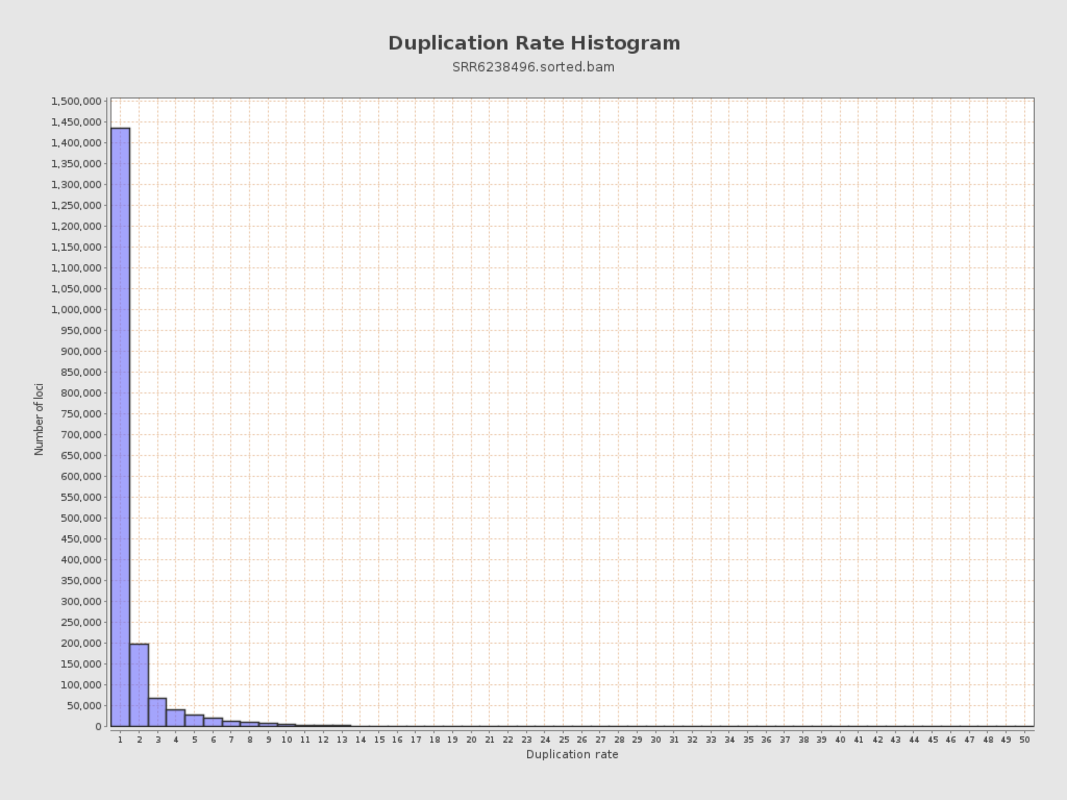
5. Results : Coverage Histogram (0-50X)



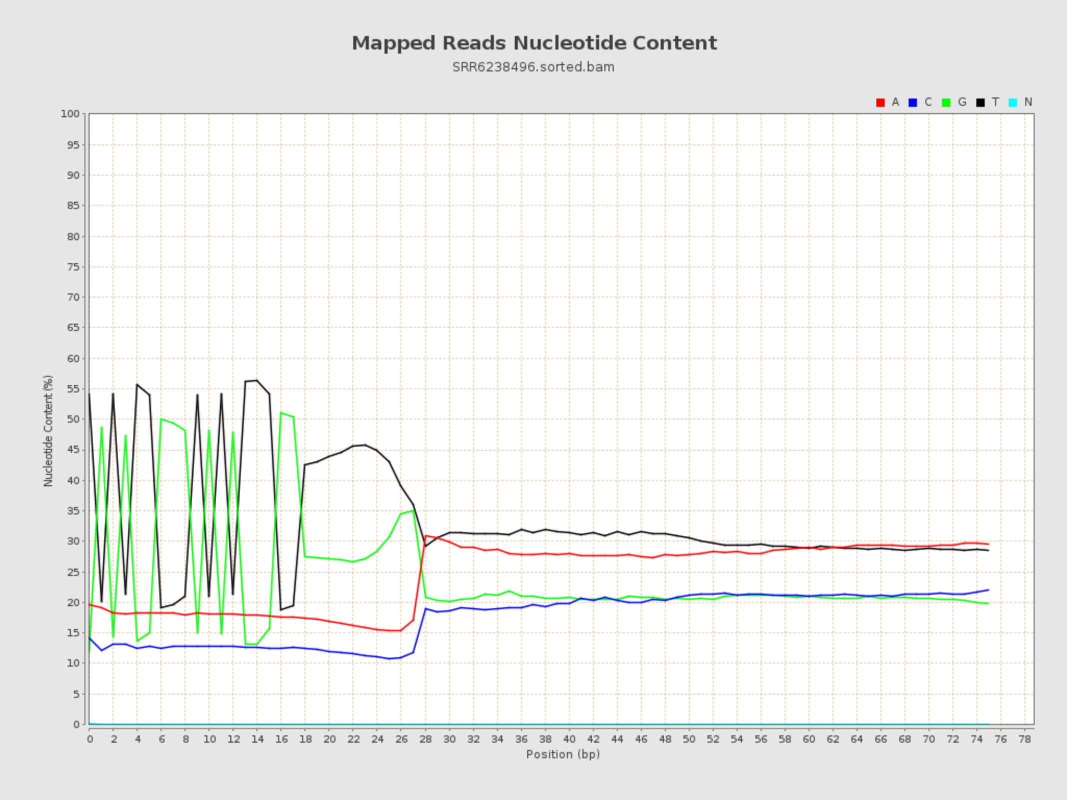
6. Results : Genome Fraction Coverage



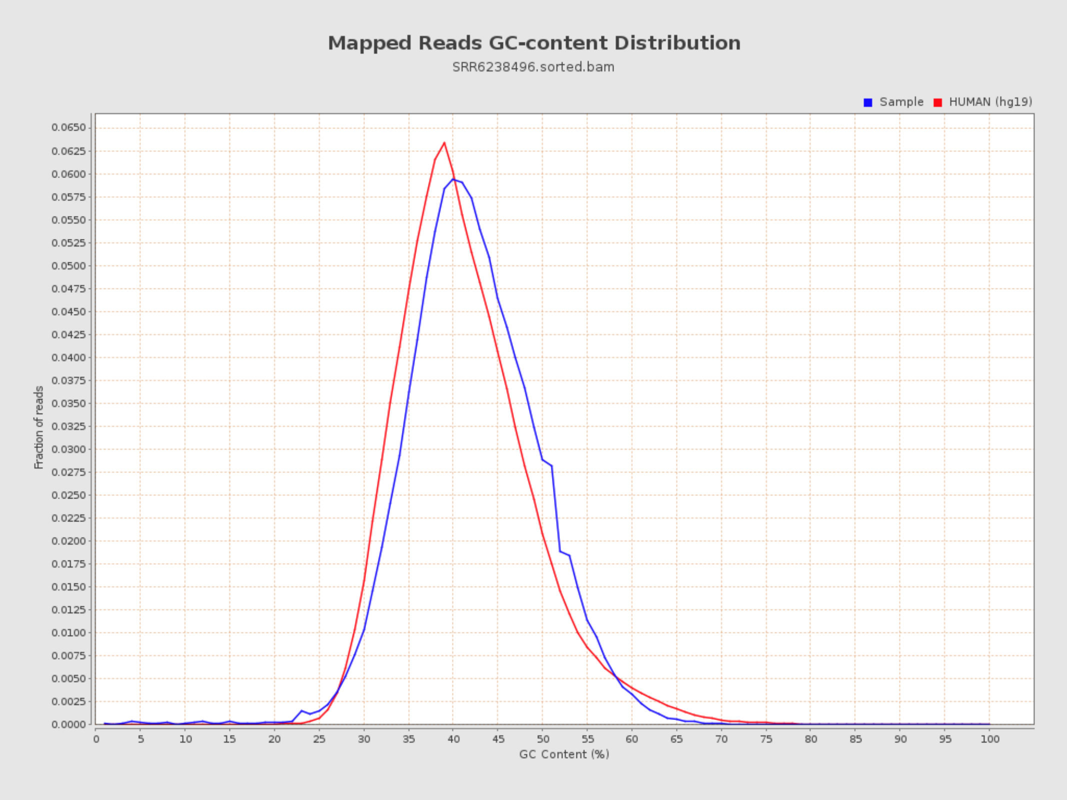
7. Results : Duplication Rate Histogram



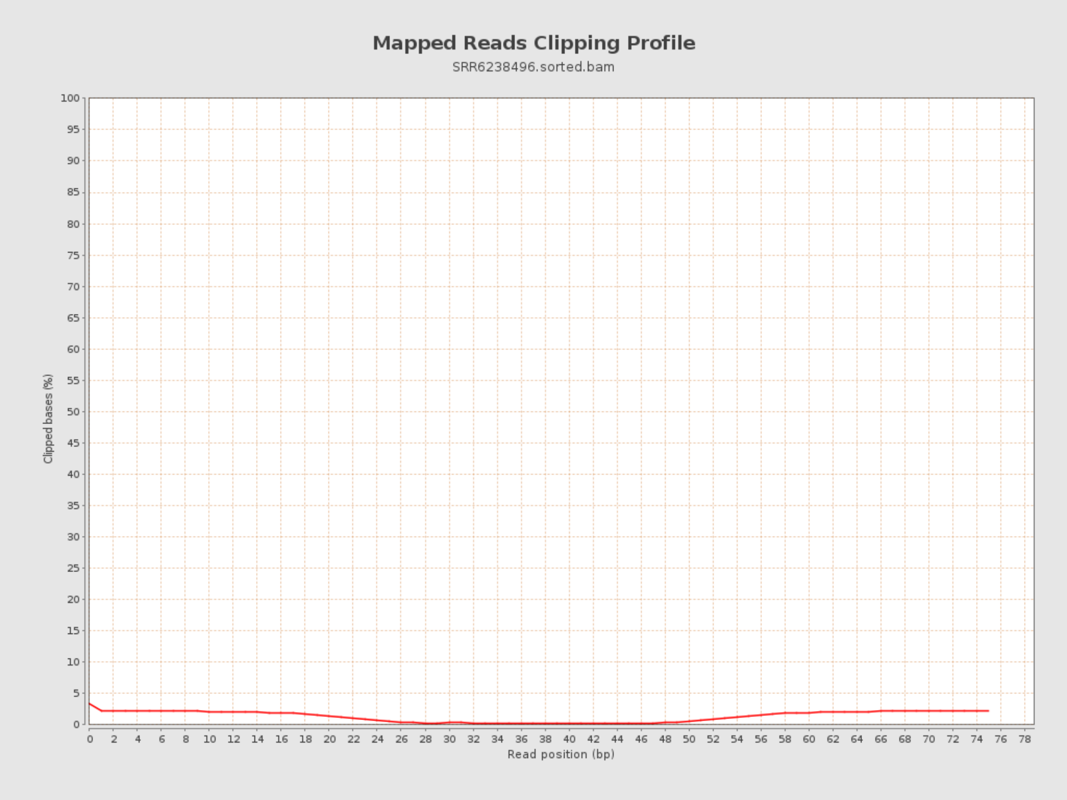
8. Results : Mapped Reads Nucleotide Content



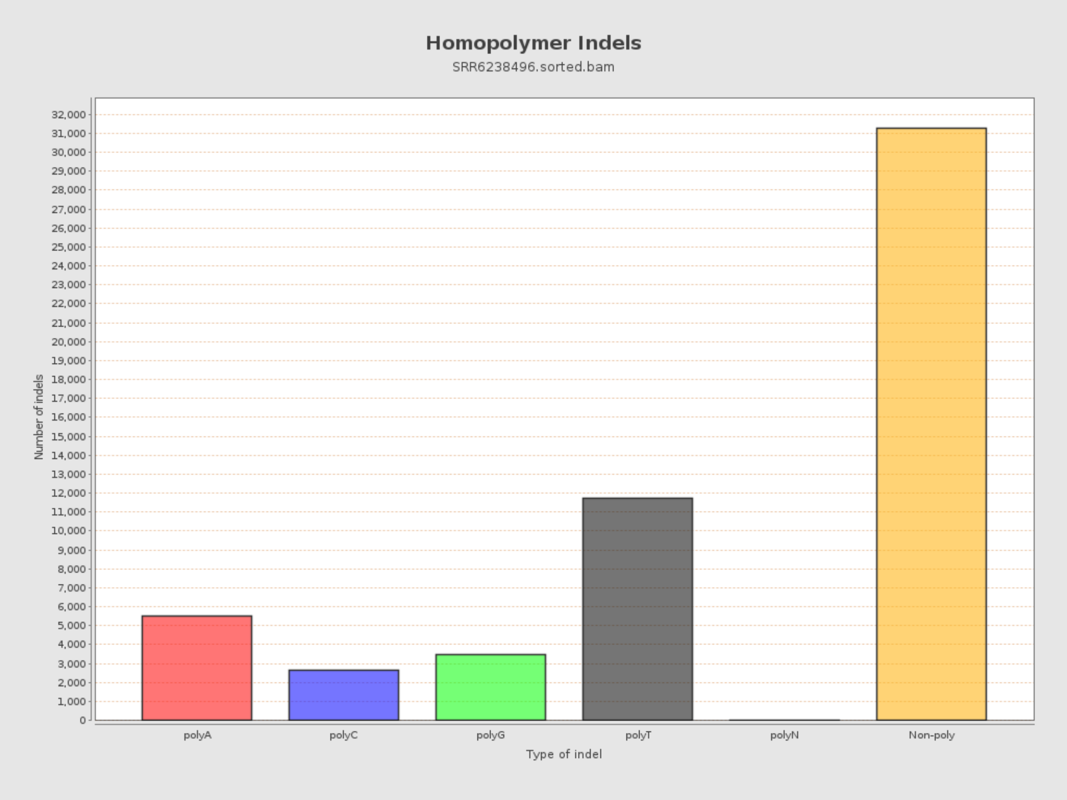
9. Results : Mapped Reads GC-content Distribution



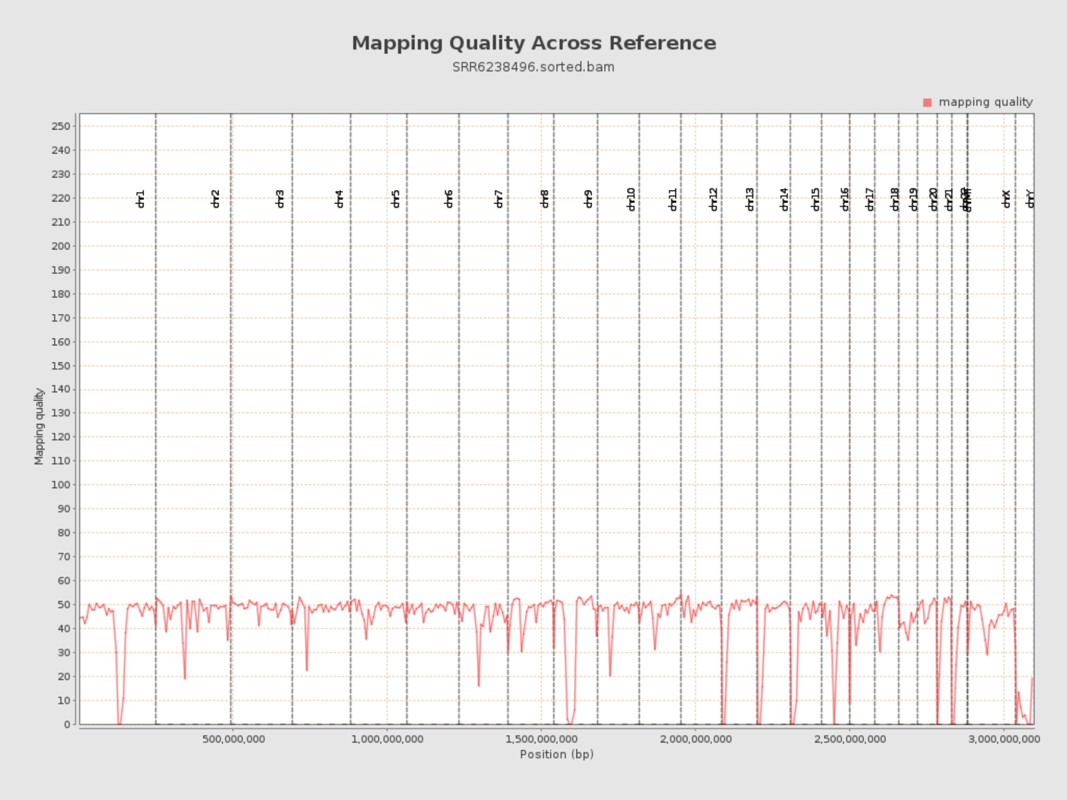
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram