Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:52:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238494.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_SRR6238494 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238494.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:52:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238494.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,432,750
Mapped reads	1,855,558 / 76.27%
Unmapped reads	577,192 / 23.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,567 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	913,899 / 37.57%
Duplication rate	22.4%
Clipped reads	1,266,077 / 52.04%

2.2. ACGT Content

Number/percentage of A's	27,574,366 / 24.7%
Number/percentage of C's	19,013,656 / 17.04%
Number/percentage of T's	38,623,091 / 34.6%
Number/percentage of G's	26,401,246 / 23.65%
Number/percentage of N's	2,303 / 0%
GC Percentage	40.69%

2.3. Coverage

Mean	0.0361

Standard Deviation	1.3028

2.4. Mapping Quality

Mean Mapping Quality	39.51

2.5. Mismatches and indels

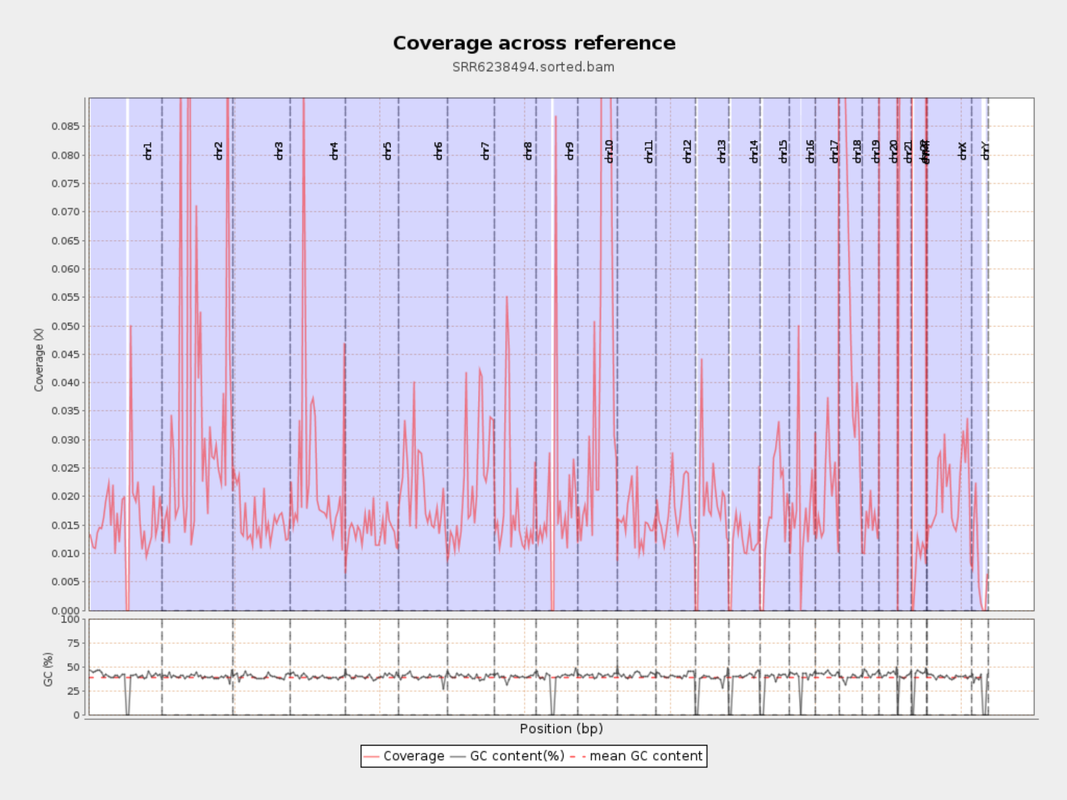
General error rate	0.74%
Mismatches	811,858
Insertions	9,139
Mapped reads with at least one insertion	0.49%
Deletions	33,657
Mapped reads with at least one deletion	1.79%
Homopolymer indels	40.22%

2.6. Chromosome stats

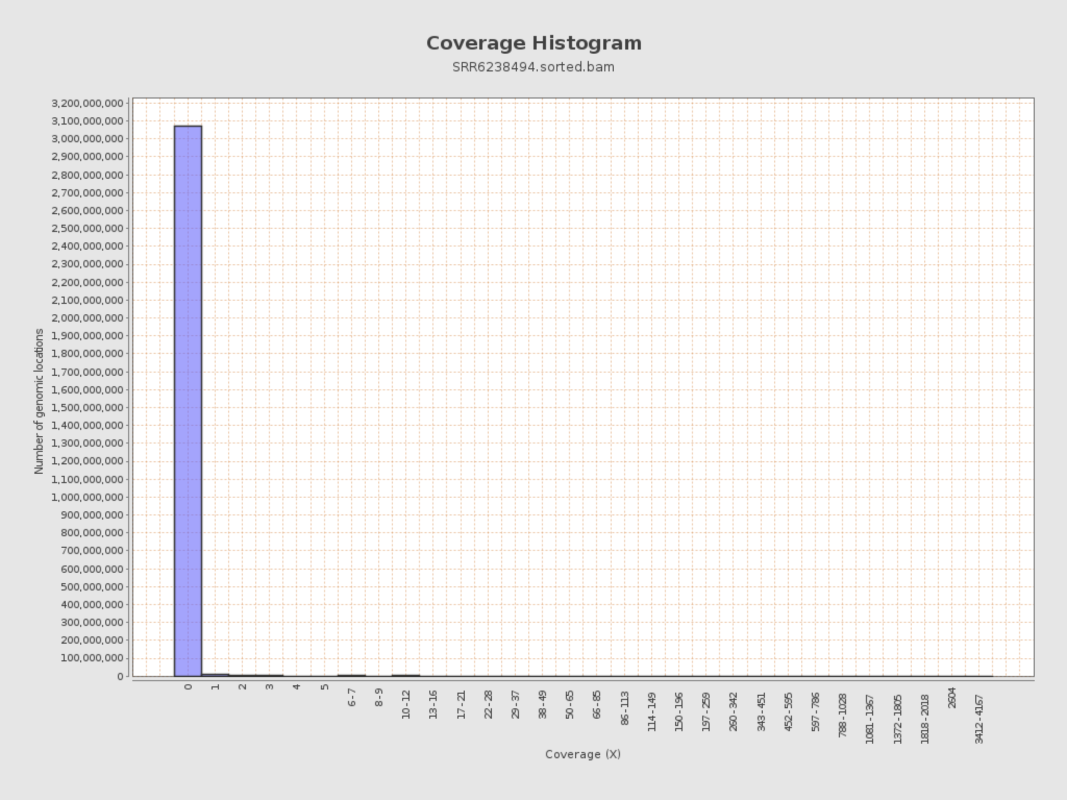
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3953035	0.0159	0.456
chr2	243199373	8802834	0.0362	2.3833
chr3	198022430	3141337	0.0159	0.4704
chr4	191154276	4678597	0.0245	0.5798
chr5	180915260	2554843	0.0141	0.4251
chr6	171115067	3509015	0.0205	0.9239
chr7	159138663	3559297	0.0224	0.7312

chr8	146364022	2680238	0.0183	1.2539
chr9	141213431	2690500	0.0191	0.8402
chr10	135534747	7181356	0.053	0.8572
chr11	135006516	2116074	0.0157	0.5119
chr12	133851895	2412815	0.018	0.5011
chr13	115169878	2157165	0.0187	0.82
chr14	107349540	1199189	0.0112	0.4786
chr15	102531392	1806564	0.0176	0.6016
chr16	90354753	1601763	0.0177	0.5665
chr17	81195210	1641137	0.0202	0.517
chr18	78077248	8023780	0.1028	5.041
chr19	59128983	896052	0.0152	0.5567
chr20	63025520	28609666	0.4539	2.6731
chr21	48129895	14358708	0.2983	2.1413
chr22	51304566	410996	0.008	0.2777
chrMT	16571	21924	1.323	3.693
chrX	155270560	3245949	0.0209	0.582
chrY	59373566	417399	0.007	0.5075

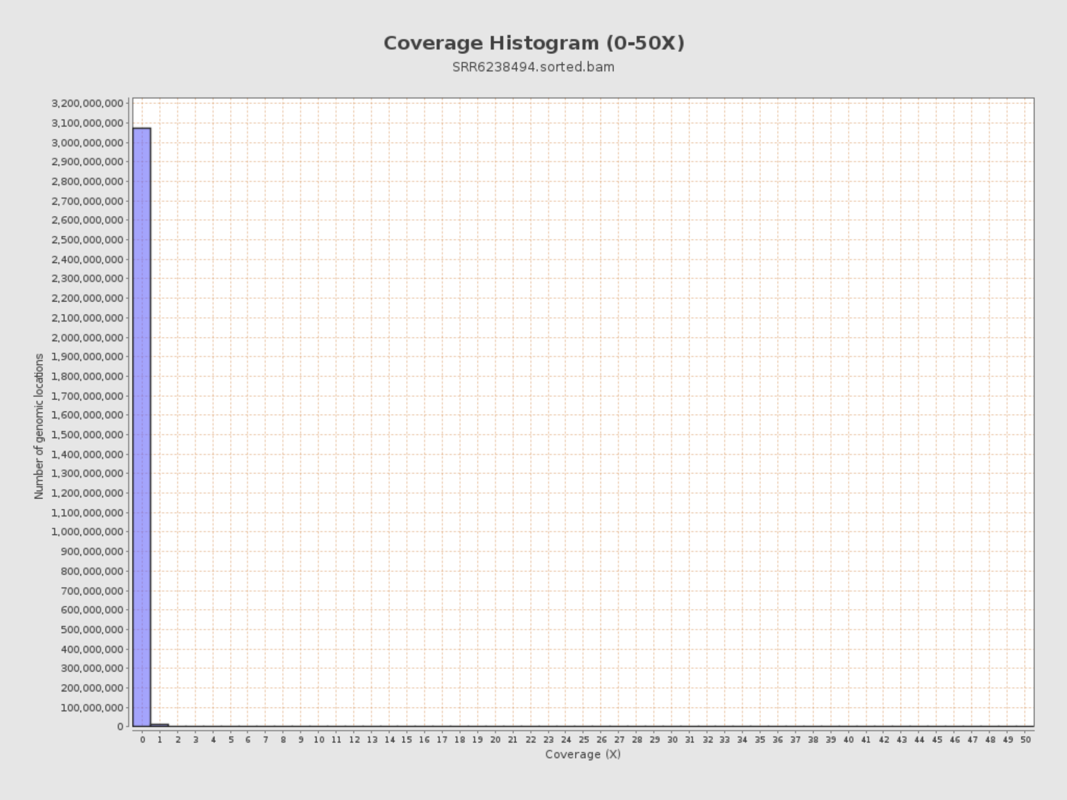
3. Results : Coverage across reference



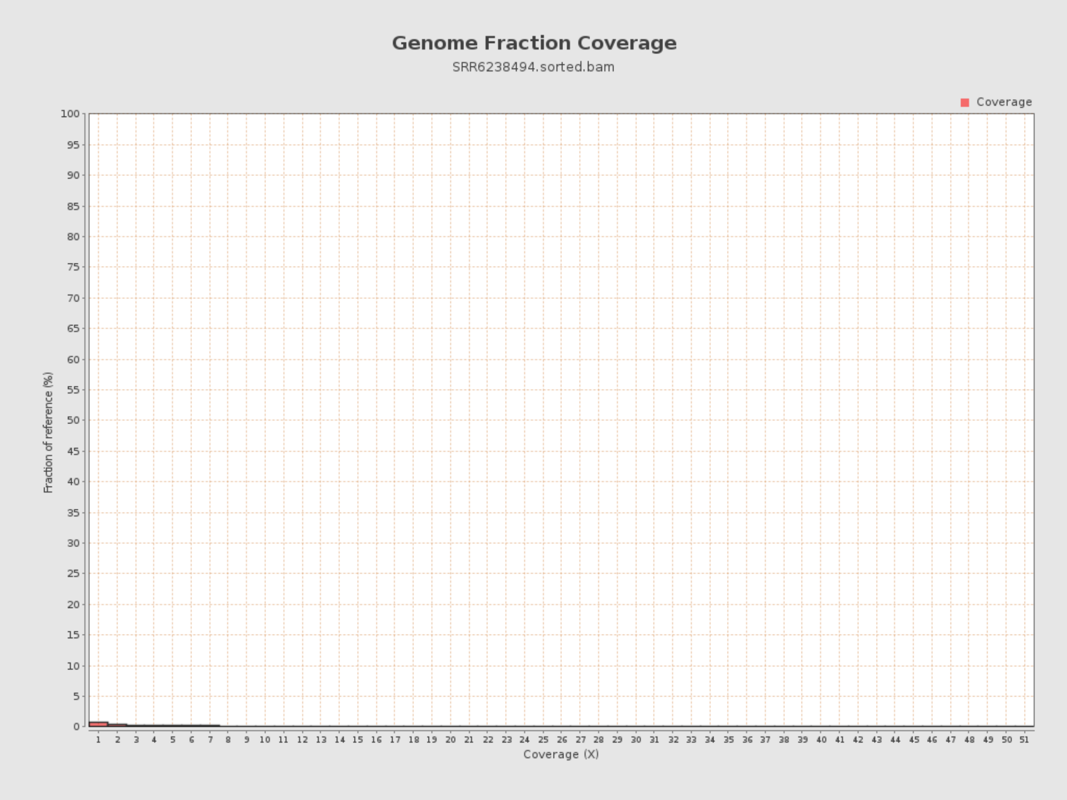
4. Results : Coverage Histogram



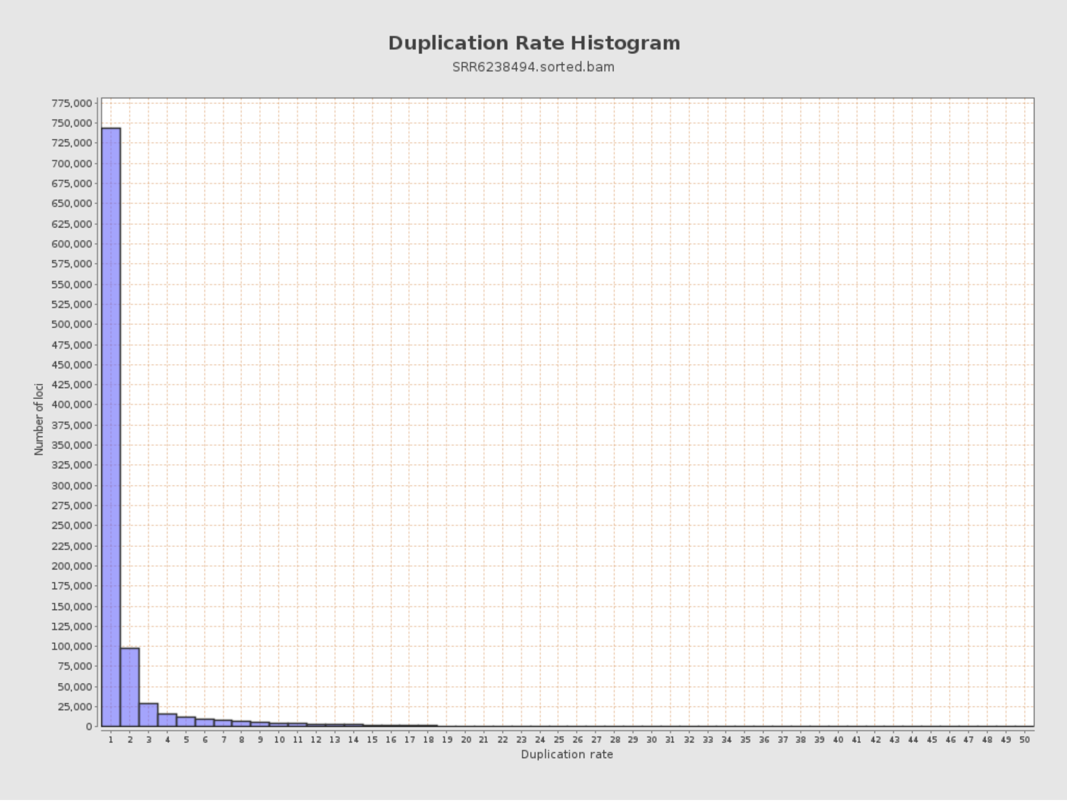
5. Results : Coverage Histogram (0-50X)



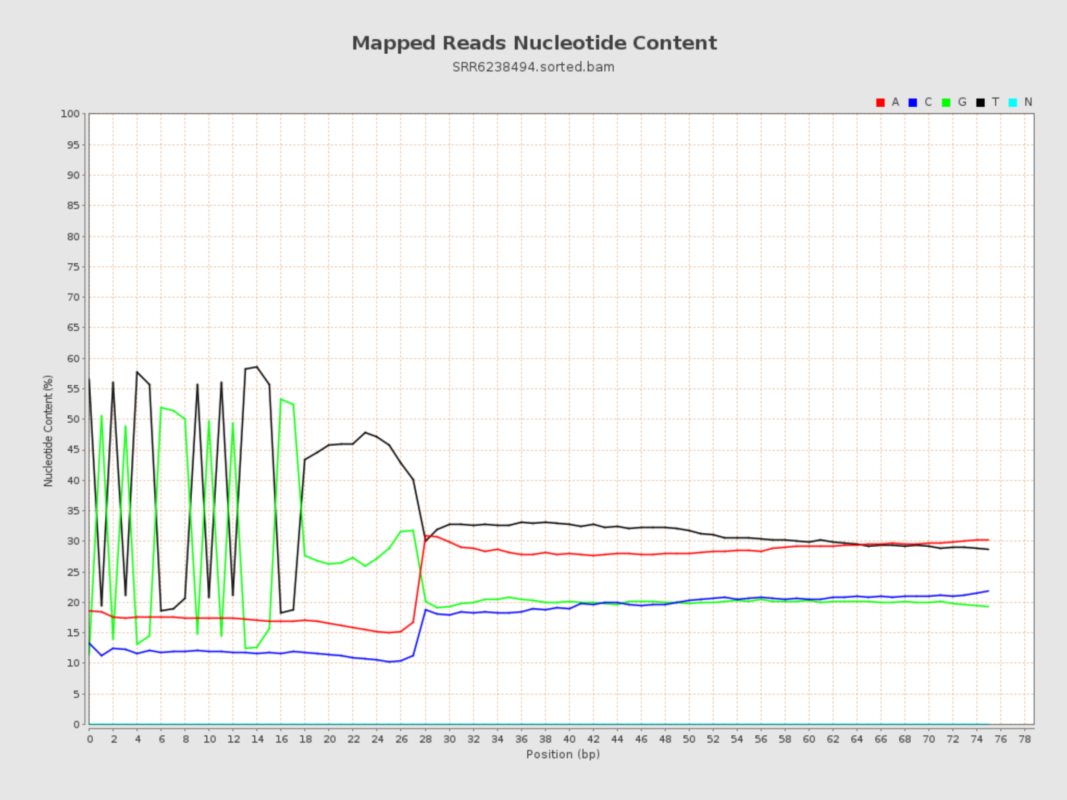
6. Results : Genome Fraction Coverage



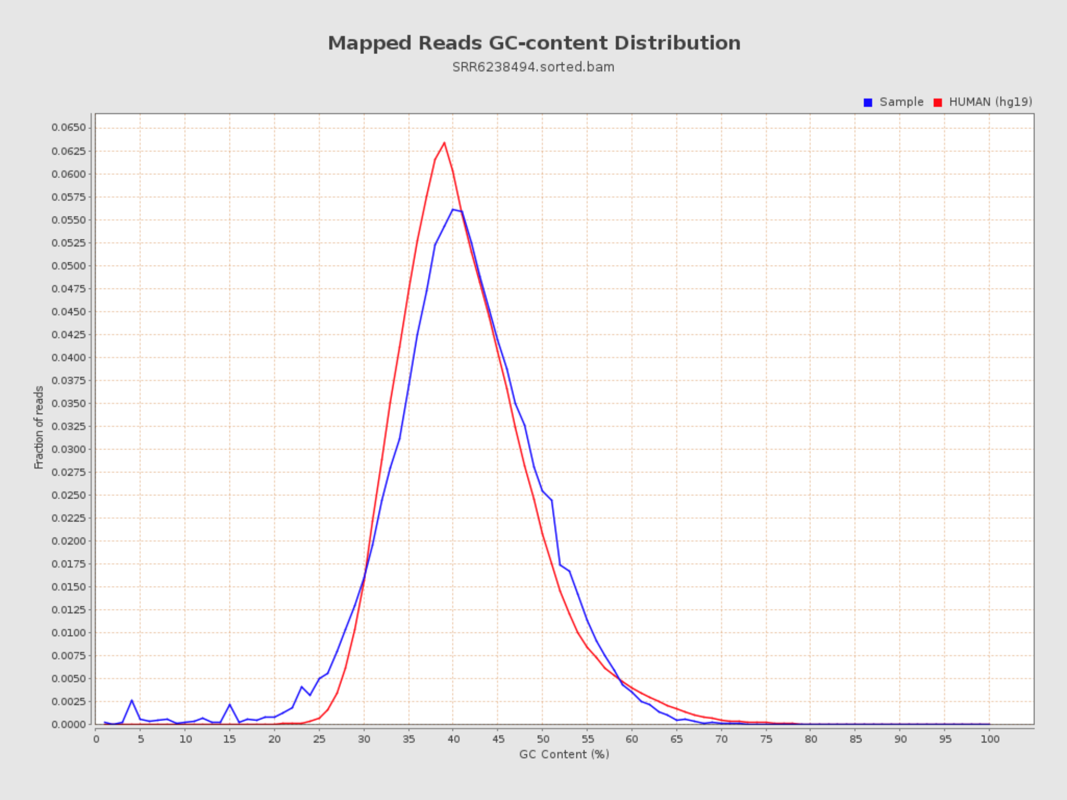
7. Results : Duplication Rate Histogram



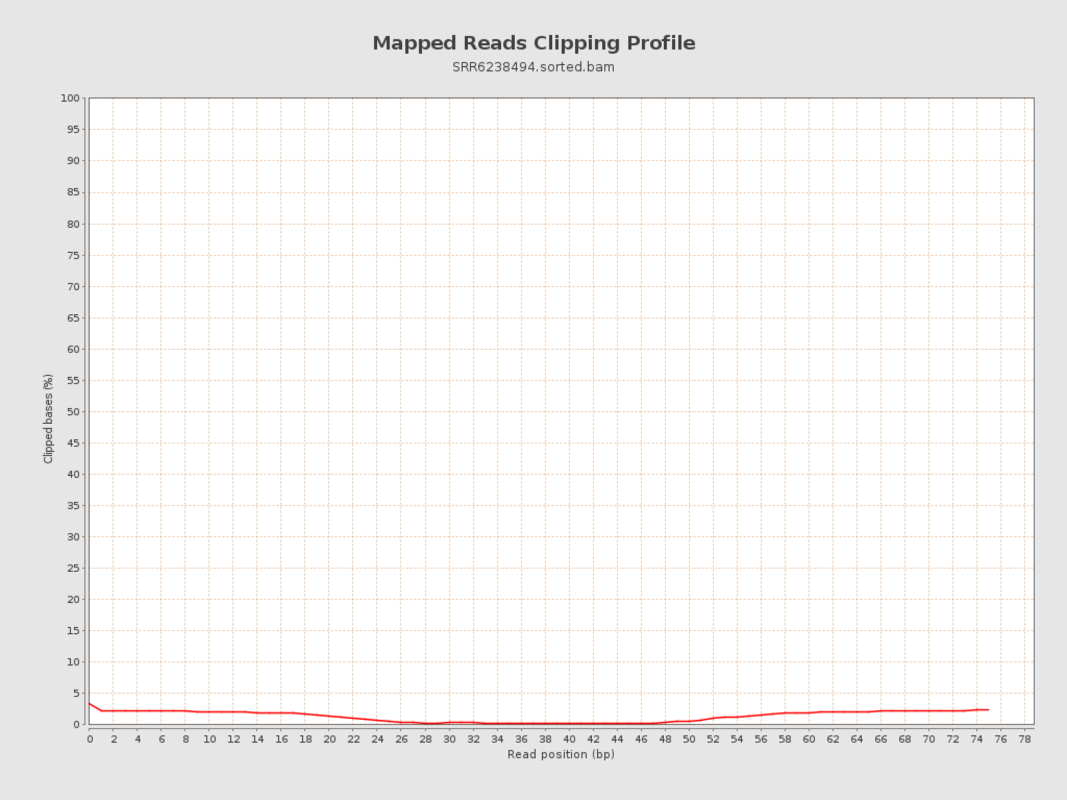
8. Results : Mapped Reads Nucleotide Content



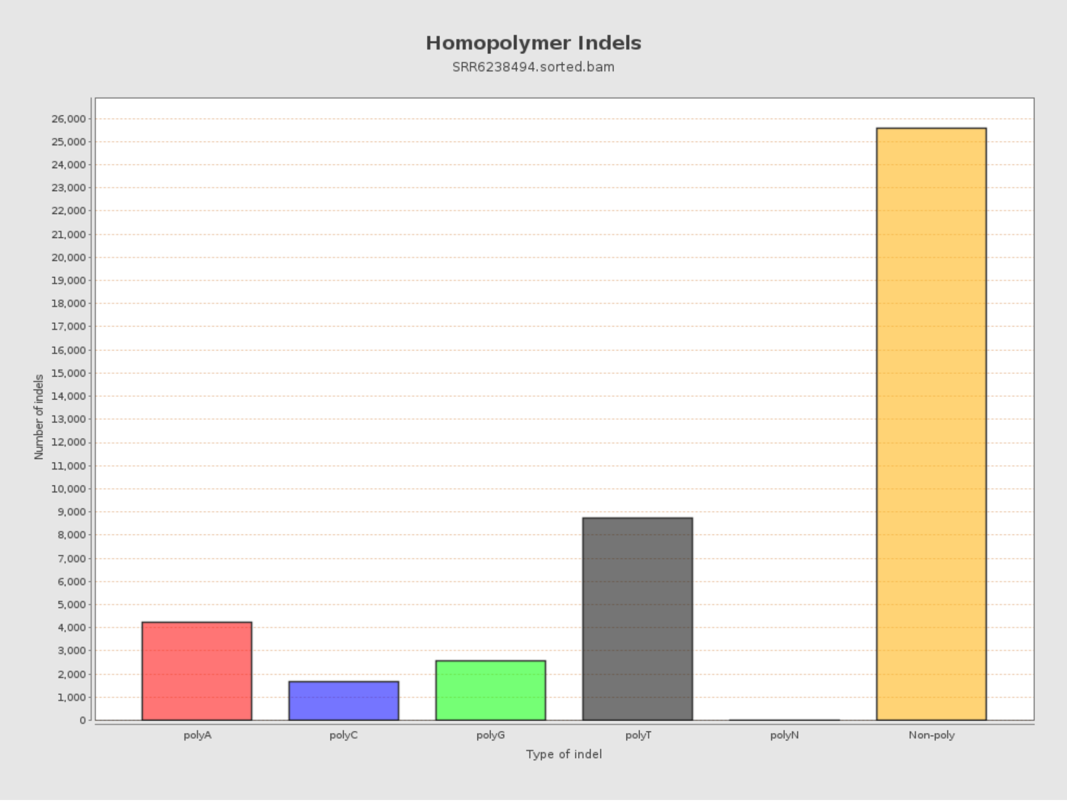
9. Results : Mapped Reads GC-content Distribution



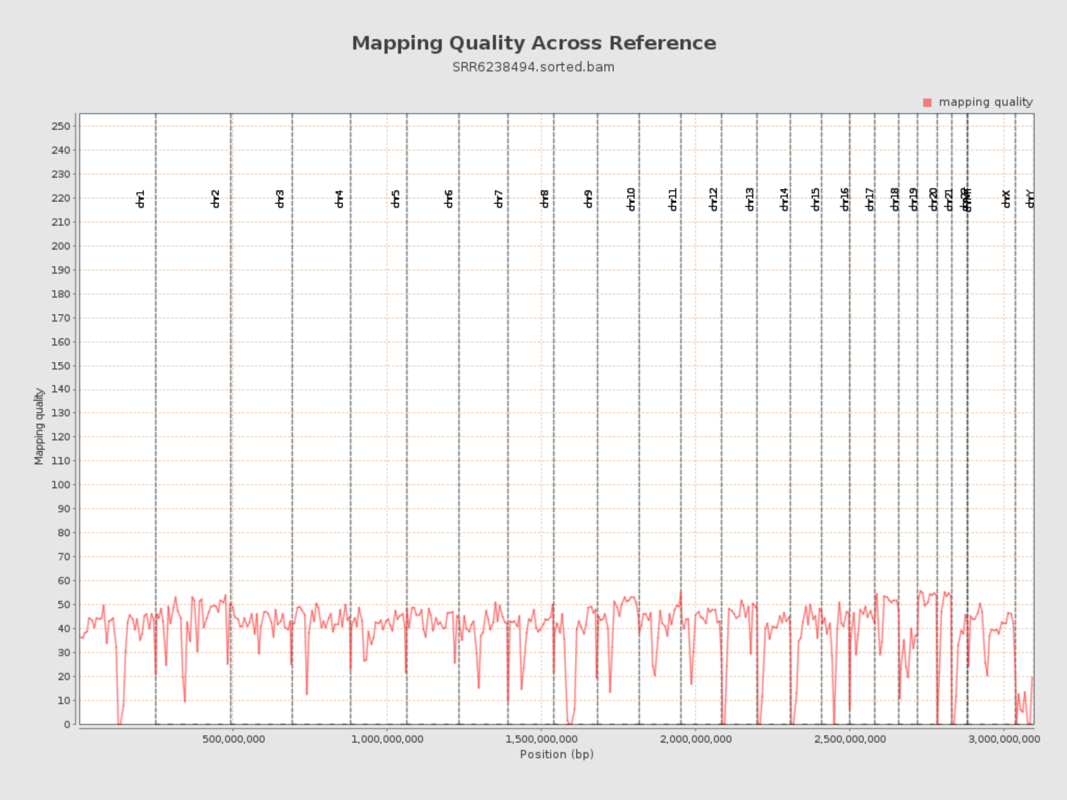
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram