Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:33:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238634.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_SRR6238634 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238634.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:33:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238634.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,010,214
Mapped reads	1,676,722 / 83.41%
Unmapped reads	333,492 / 16.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,981 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	720,981 / 35.87%
Duplication rate	23.23%
Clipped reads	1,142,513 / 56.84%

2.2. ACGT Content

Number/percentage of A's	25,464,383 / 25.08%
Number/percentage of C's	16,719,606 / 16.46%
Number/percentage of T's	35,803,361 / 35.26%
Number/percentage of G's	23,561,864 / 23.2%
Number/percentage of N's	2,101 / 0%
GC Percentage	39.67%

2.3. Coverage

Mean	0.0328

Standard Deviation	0.8303

2.4. Mapping Quality

Mean Mapping Quality	42.4

2.5. Mismatches and indels

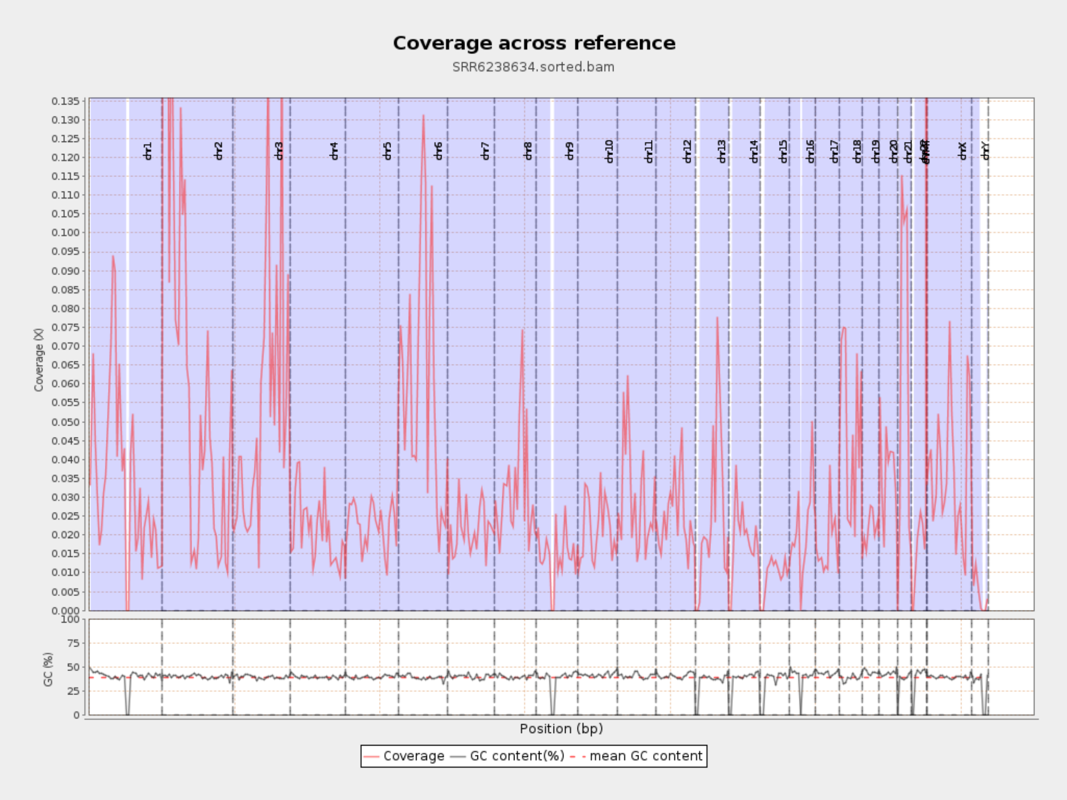
General error rate	0.66%
Mismatches	653,108
Insertions	7,008
Mapped reads with at least one insertion	0.41%
Deletions	35,003
Mapped reads with at least one deletion	2.06%
Homopolymer indels	41.08%

2.6. Chromosome stats

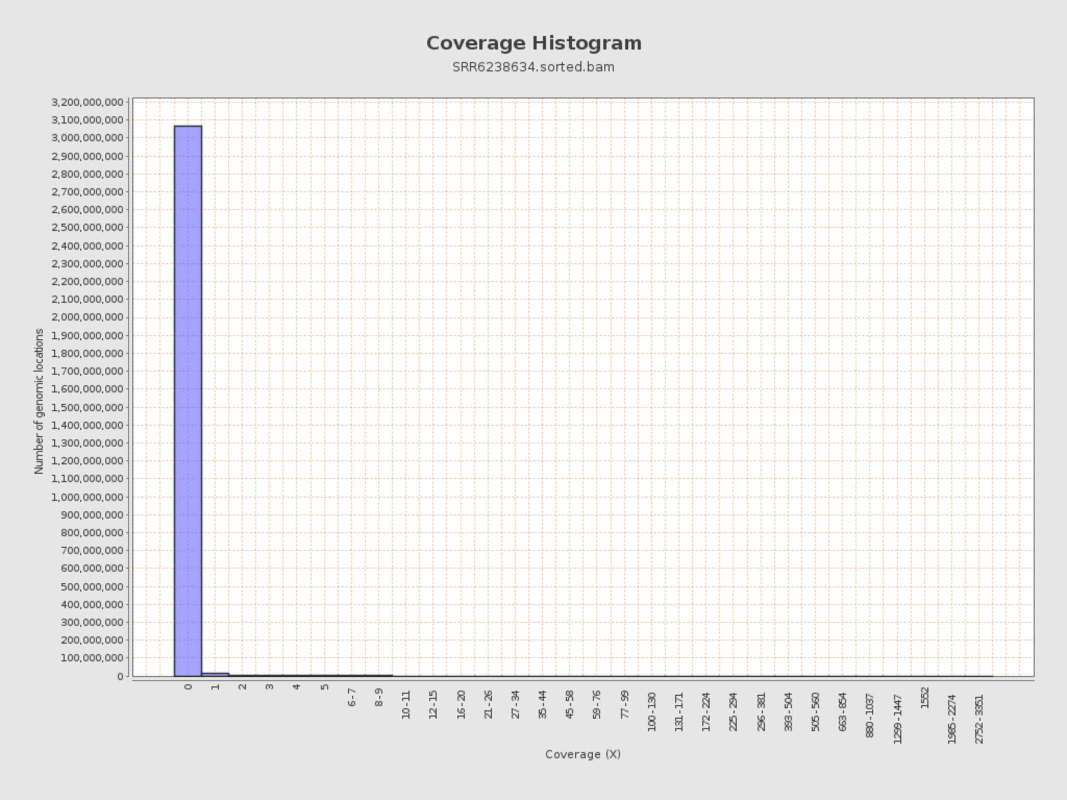
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8582897	0.0344	0.5614
chr2	243199373	16893021	0.0695	1.6735
chr3	198022430	10719184	0.0541	0.687
chr4	191154276	4073002	0.0213	0.4006
chr5	180915260	4137537	0.0229	0.4224
chr6	171115067	10396850	0.0608	0.899
chr7	159138663	3386135	0.0213	0.5551

chr8	146364022	4614336	0.0315	0.647
chr9	141213431	2009064	0.0142	0.3439
chr10	135534747	2932407	0.0216	0.4304
chr11	135006516	4087272	0.0303	0.5124
chr12	133851895	3350073	0.025	0.4517
chr13	115169878	2788435	0.0242	0.5986
chr14	107349540	1964004	0.0183	0.3839
chr15	102531392	959053	0.0094	0.4048
chr16	90354753	1989910	0.022	0.4322
chr17	81195210	1388100	0.0171	0.3713
chr18	78077248	3853521	0.0494	2.8754
chr19	59128983	1287881	0.0218	0.4628
chr20	63025520	2344535	0.0372	0.5498
chr21	48129895	2937255	0.061	0.7162
chr22	51304566	773833	0.0151	0.3352
chrMT	16571	80558	4.8614	8.6769
chrX	155270560	5788809	0.0373	0.5581
chrY	59373566	272474	0.0046	0.2752

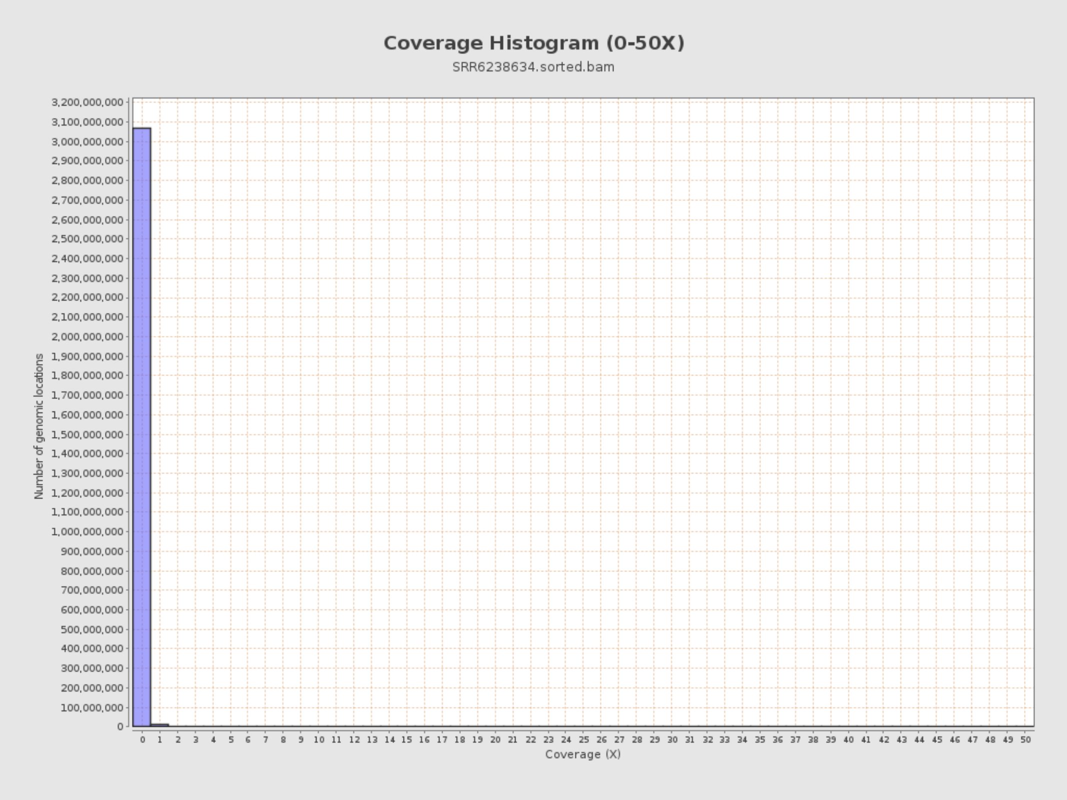
3. Results : Coverage across reference



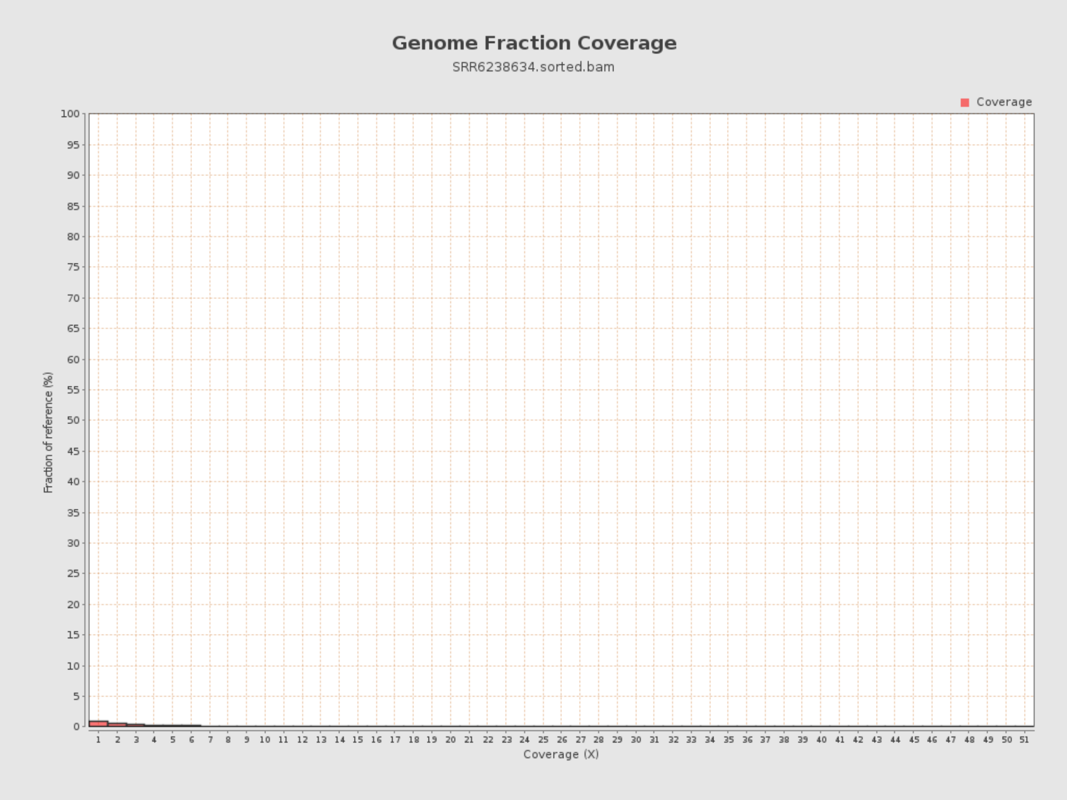
4. Results : Coverage Histogram



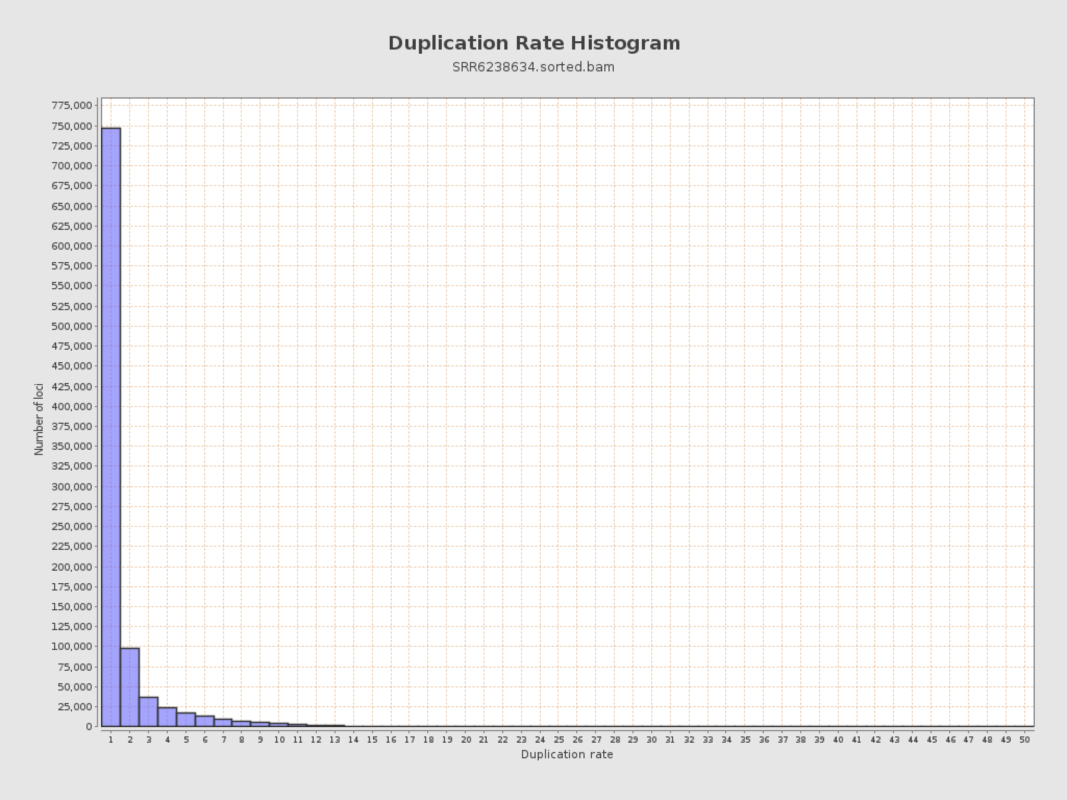
5. Results : Coverage Histogram (0-50X)



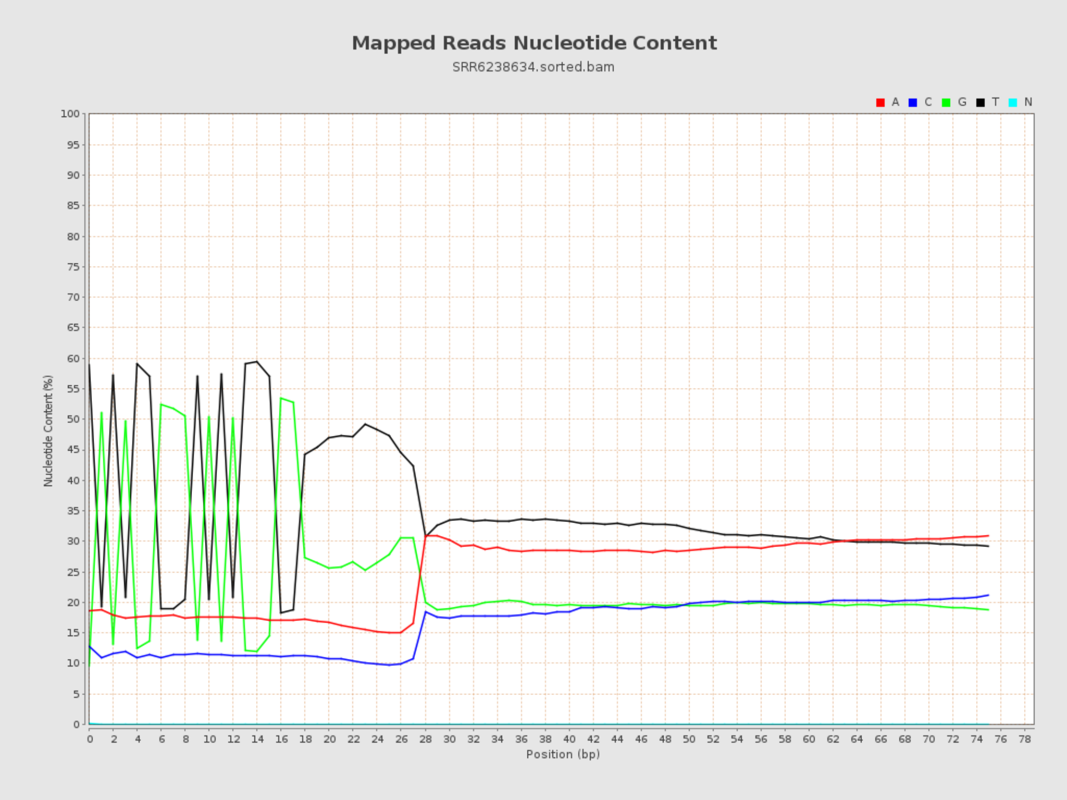
6. Results : Genome Fraction Coverage



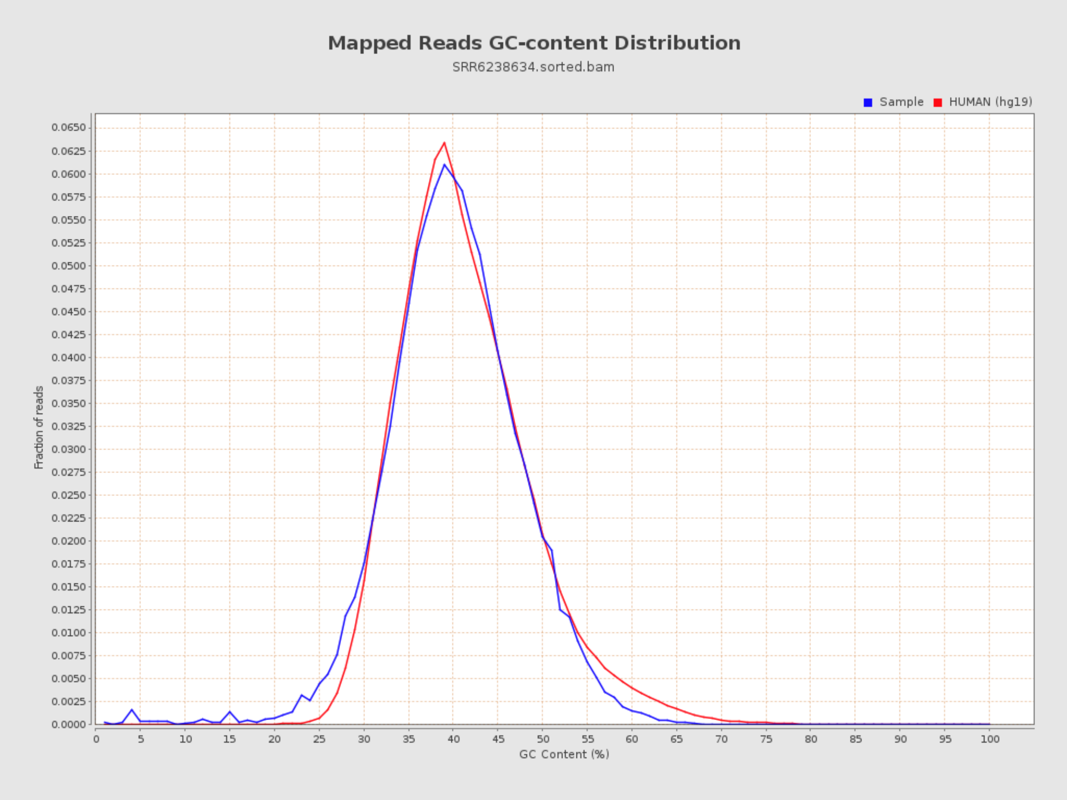
7. Results : Duplication Rate Histogram



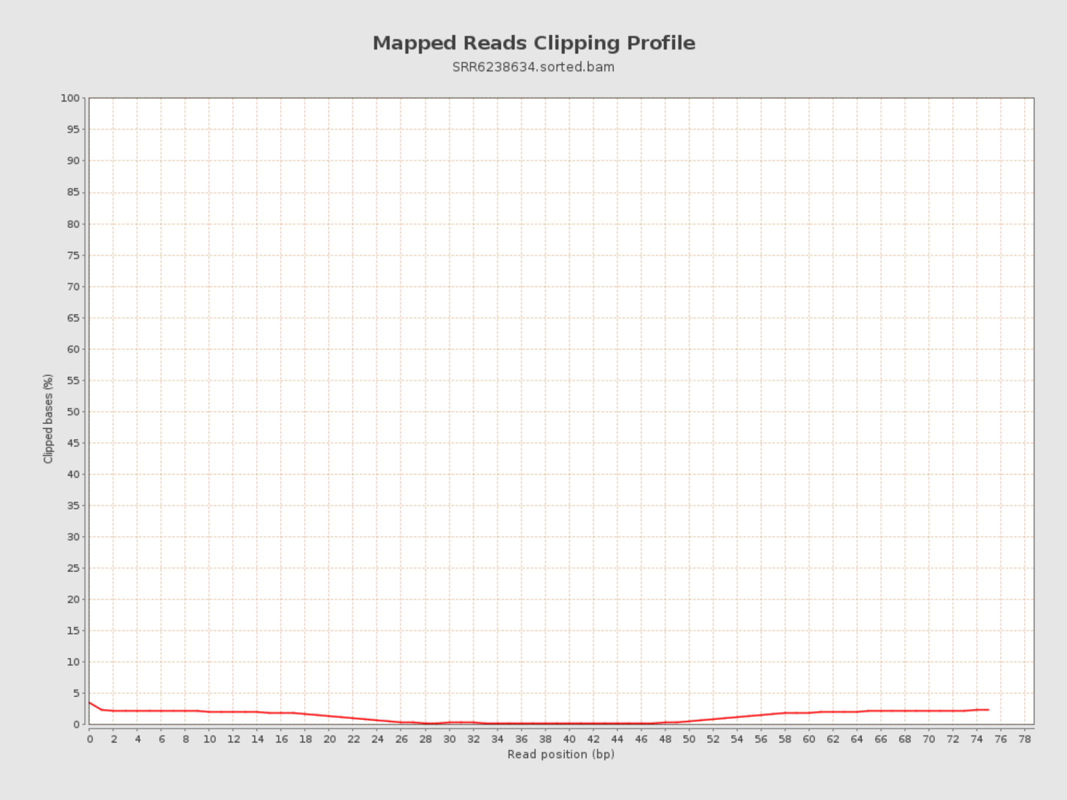
8. Results : Mapped Reads Nucleotide Content



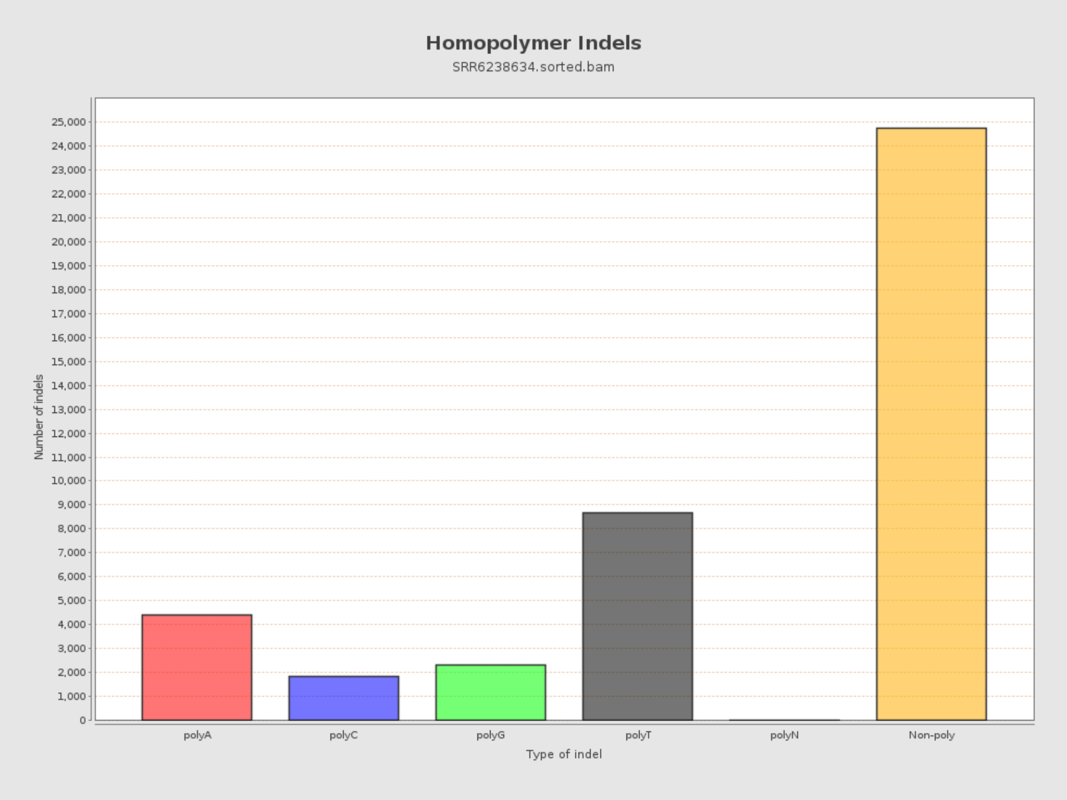
9. Results : Mapped Reads GC-content Distribution



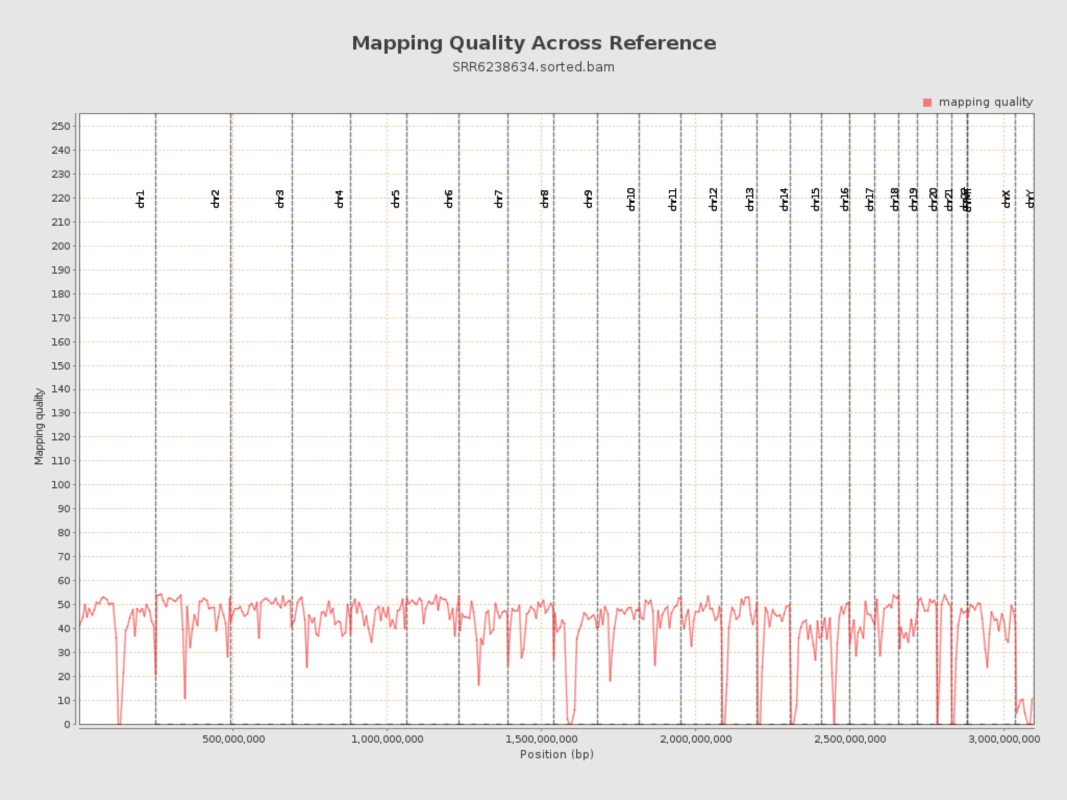
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram