Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:53:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238250.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_SRR6238250 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238250.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:53:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238250.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,430,638
Mapped reads	3,014,364 / 87.87%
Unmapped reads	416,274 / 12.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,021 / 0.9%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	171,147 / 4.99%
Duplication rate	4.17%
Clipped reads	1,618,897 / 47.19%

2.2. ACGT Content

Number/percentage of A's	55,252,253 / 28.25%
Number/percentage of C's	37,120,887 / 18.98%
Number/percentage of T's	60,457,019 / 30.91%
Number/percentage of G's	42,689,644 / 21.83%
Number/percentage of N's	49,366 / 0.03%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0632

Standard Deviation	0.6419

2.4. Mapping Quality

Mean Mapping Quality	43.16

2.5. Mismatches and indels

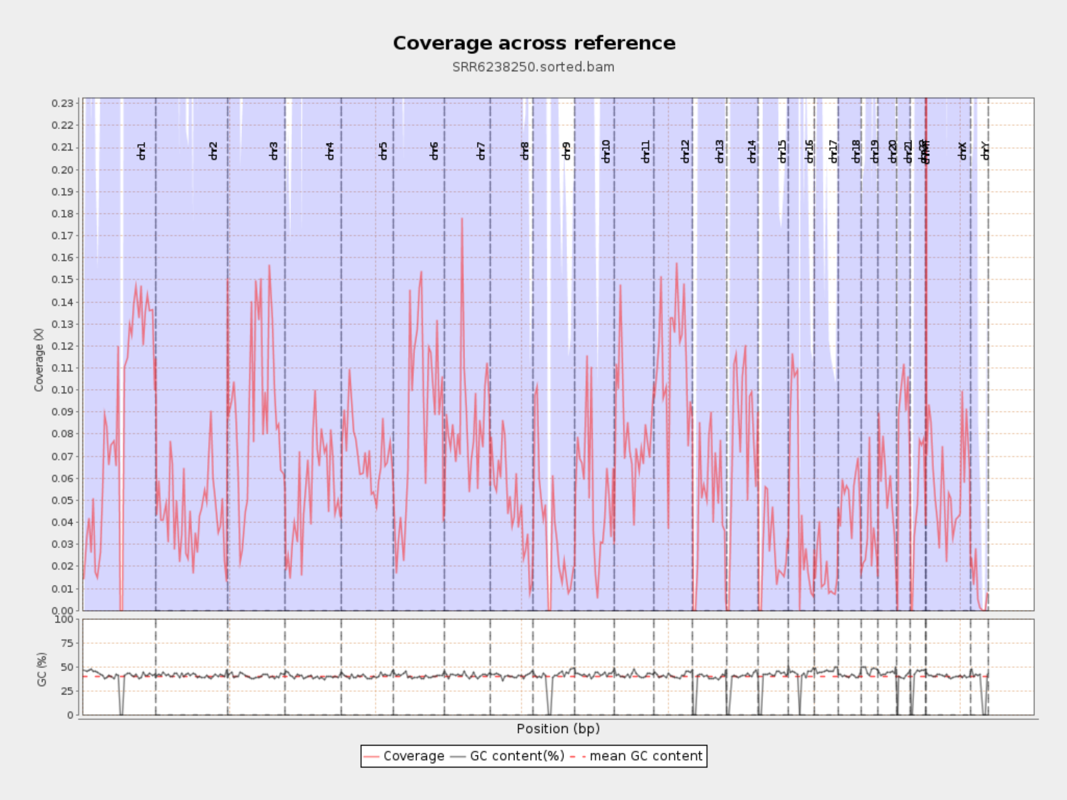
General error rate	0.9%
Mismatches	1,738,693
Insertions	15,908
Mapped reads with at least one insertion	0.52%
Deletions	54,262
Mapped reads with at least one deletion	1.78%
Homopolymer indels	45.21%

2.6. Chromosome stats

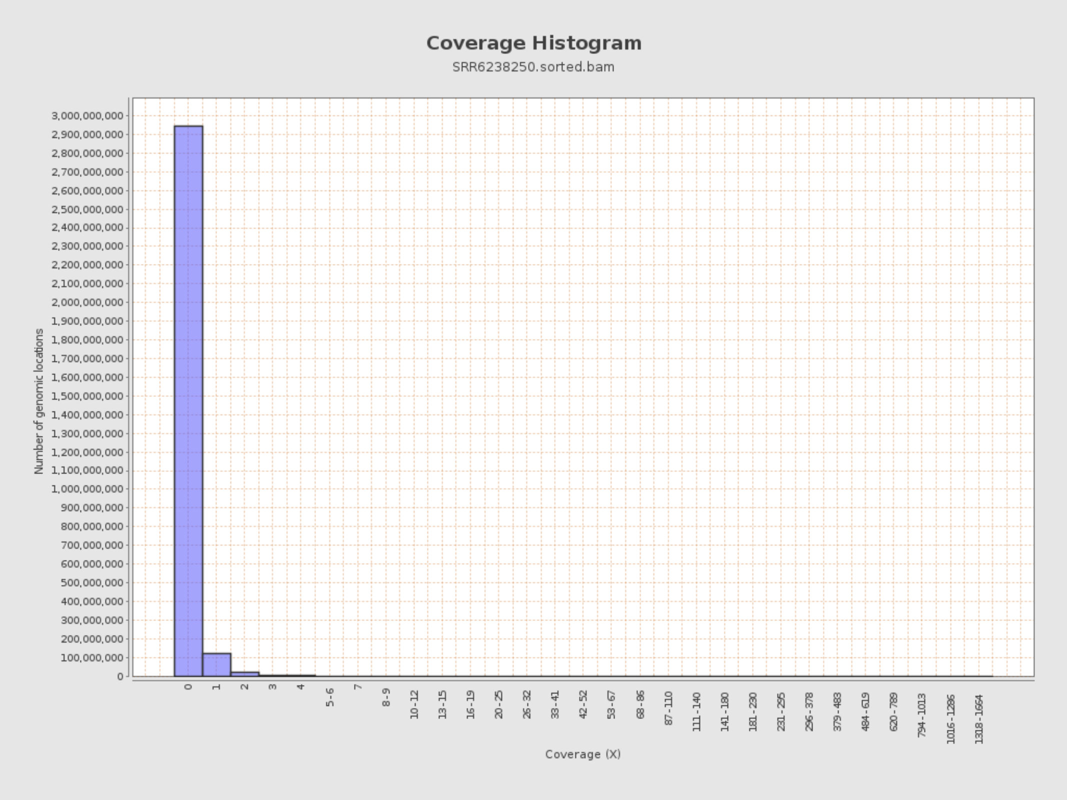
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20872335	0.0837	1.1754
chr2	243199373	10761386	0.0442	0.5453
chr3	198022430	18113593	0.0915	0.3791
chr4	191154276	10284974	0.0538	0.3157
chr5	180915260	12875521	0.0712	0.3307
chr6	171115067	15213276	0.0889	0.8189
chr7	159138663	13722367	0.0862	1.1222

chr8	146364022	7077719	0.0484	1.0474
chr9	141213431	4990526	0.0353	0.342
chr10	135534747	7367846	0.0544	0.6112
chr11	135006516	11012745	0.0816	0.4911
chr12	133851895	15244019	0.1139	0.4236
chr13	115169878	5781043	0.0502	0.2772
chr14	107349540	8300969	0.0773	0.3652
chr15	102531392	2654760	0.0259	0.2304
chr16	90354753	4367965	0.0483	0.3282
chr17	81195210	1310240	0.0161	0.2022
chr18	78077248	4137984	0.053	0.9593
chr19	59128983	1923251	0.0325	0.822
chr20	63025520	3599156	0.0571	0.3146
chr21	48129895	4133330	0.0859	0.391
chr22	51304566	2494660	0.0486	0.2706
chrMT	16571	18526	1.118	1.4746
chrX	155270560	8860404	0.0571	0.3365
chrY	59373566	539911	0.0091	0.1781

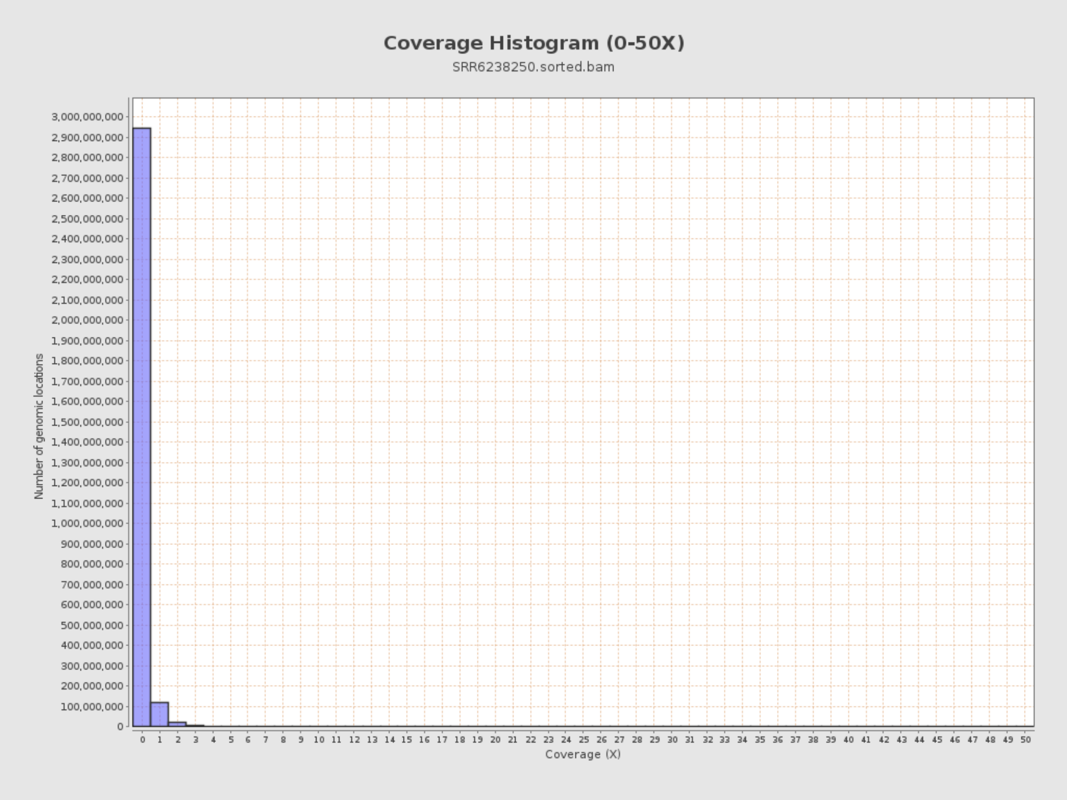
3. Results : Coverage across reference



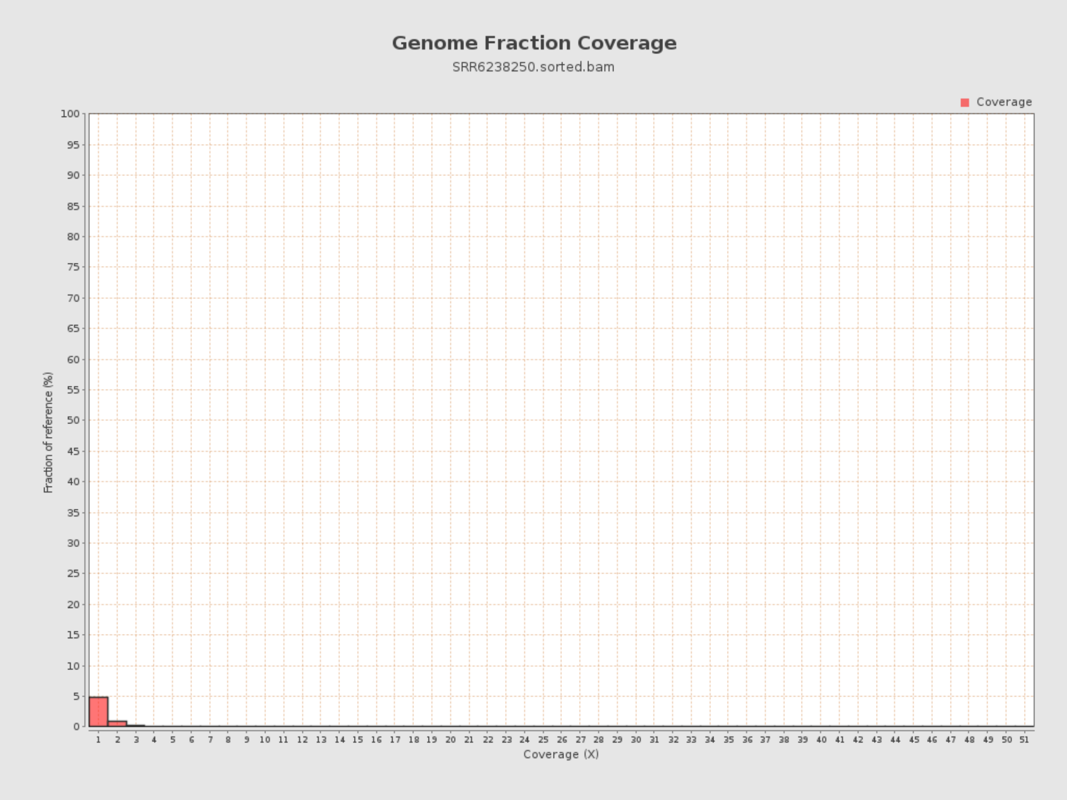
4. Results : Coverage Histogram



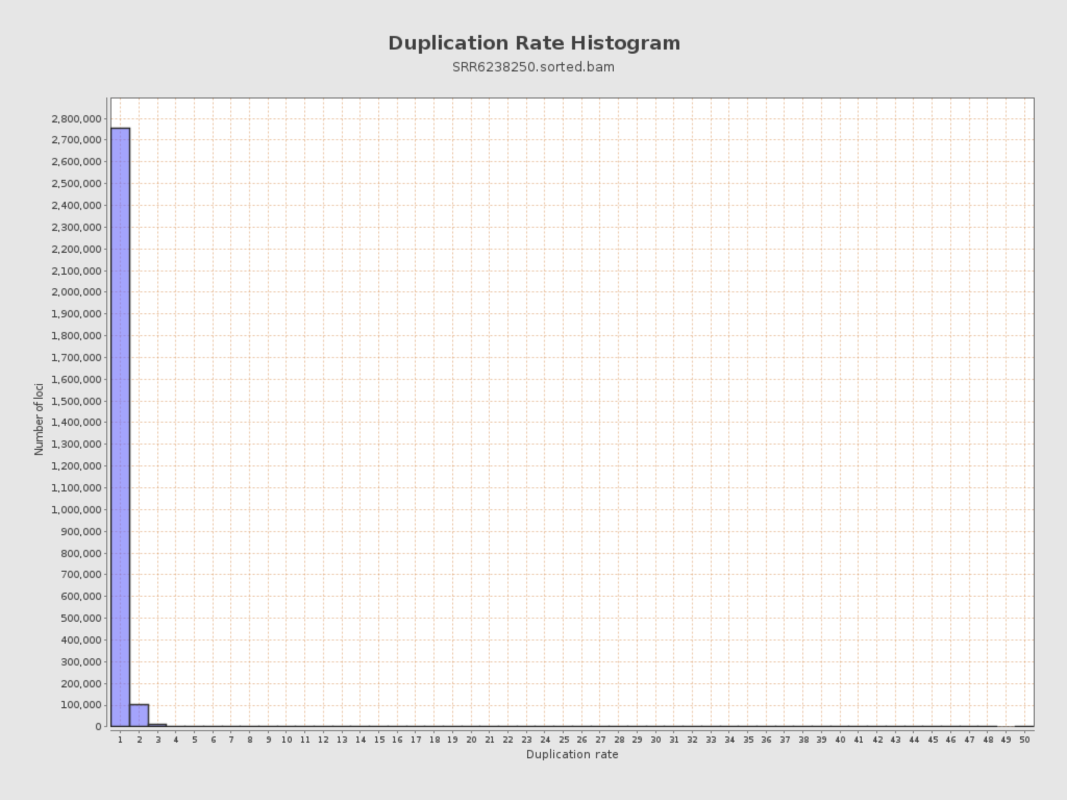
5. Results : Coverage Histogram (0-50X)



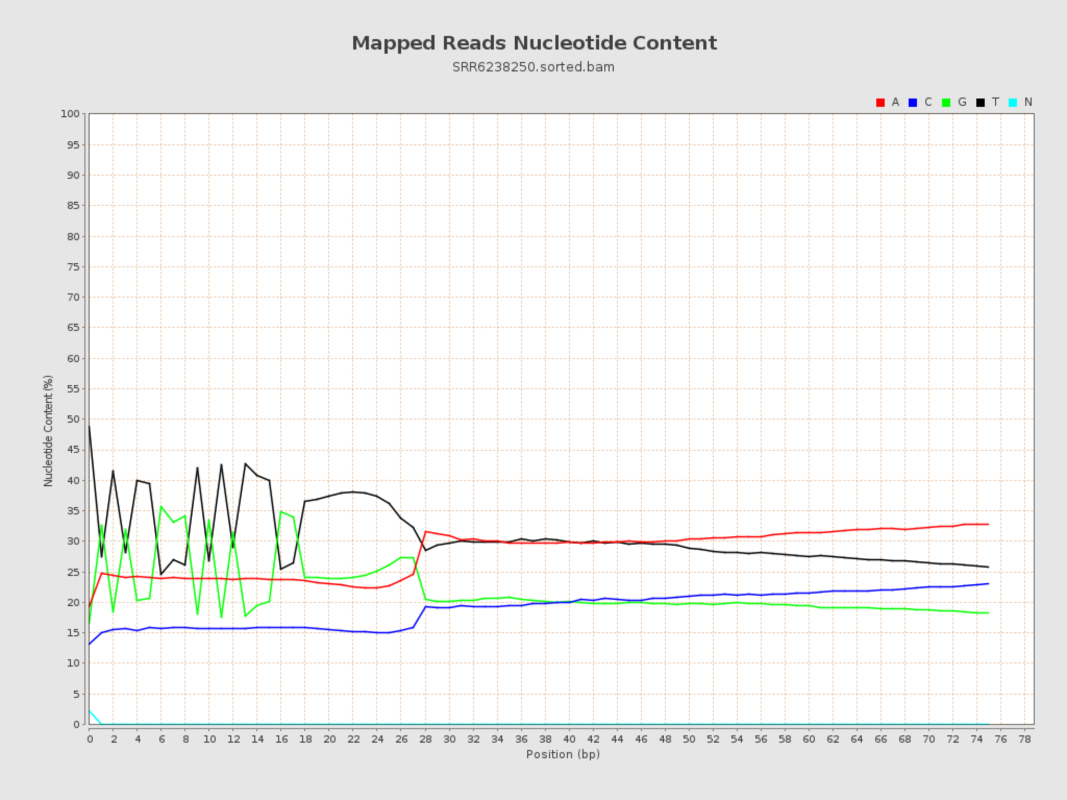
6. Results : Genome Fraction Coverage



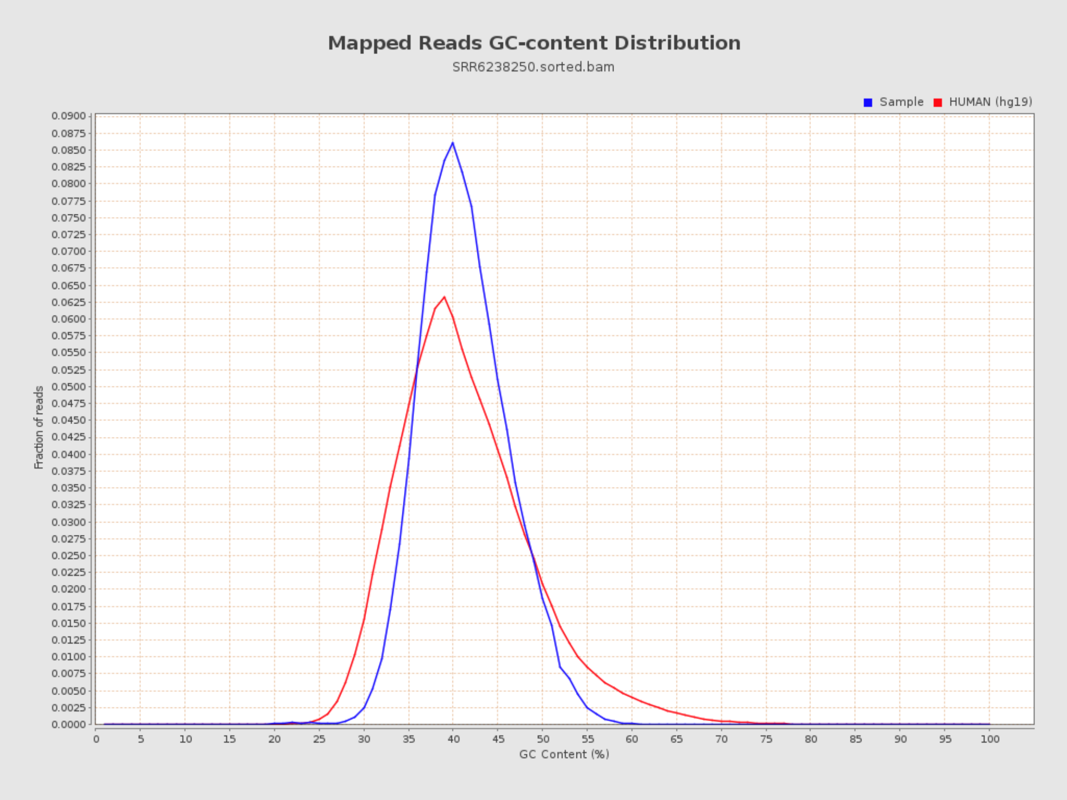
7. Results : Duplication Rate Histogram



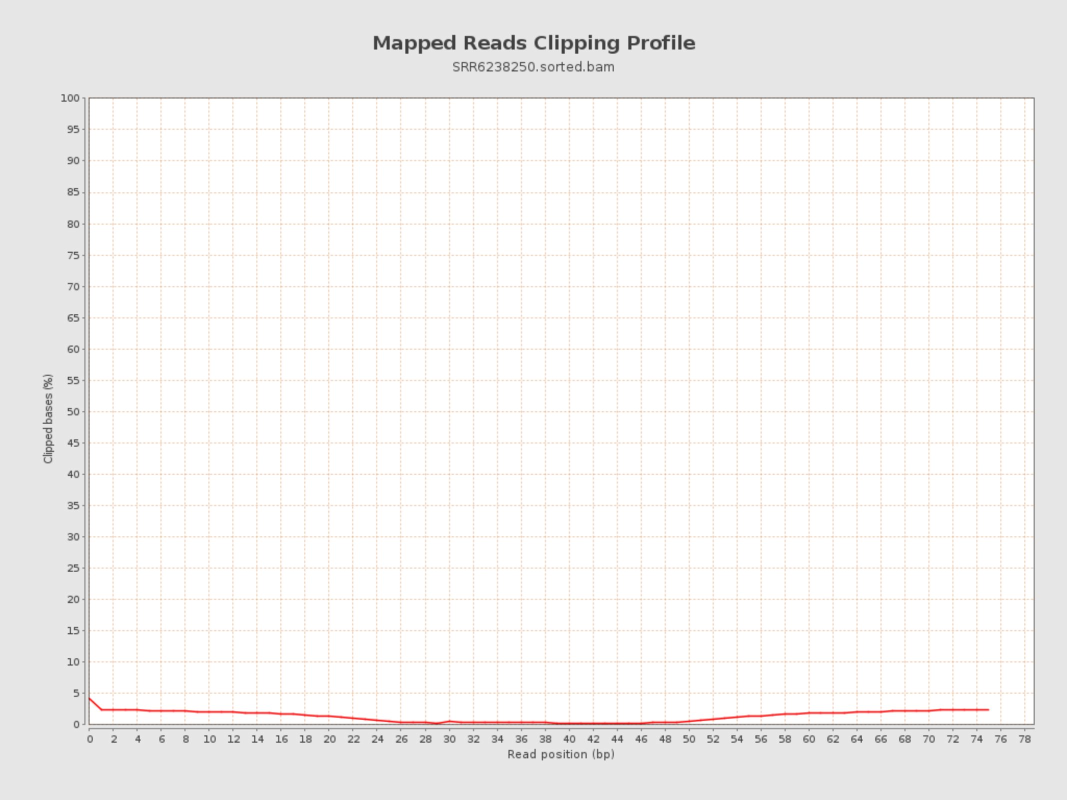
8. Results : Mapped Reads Nucleotide Content



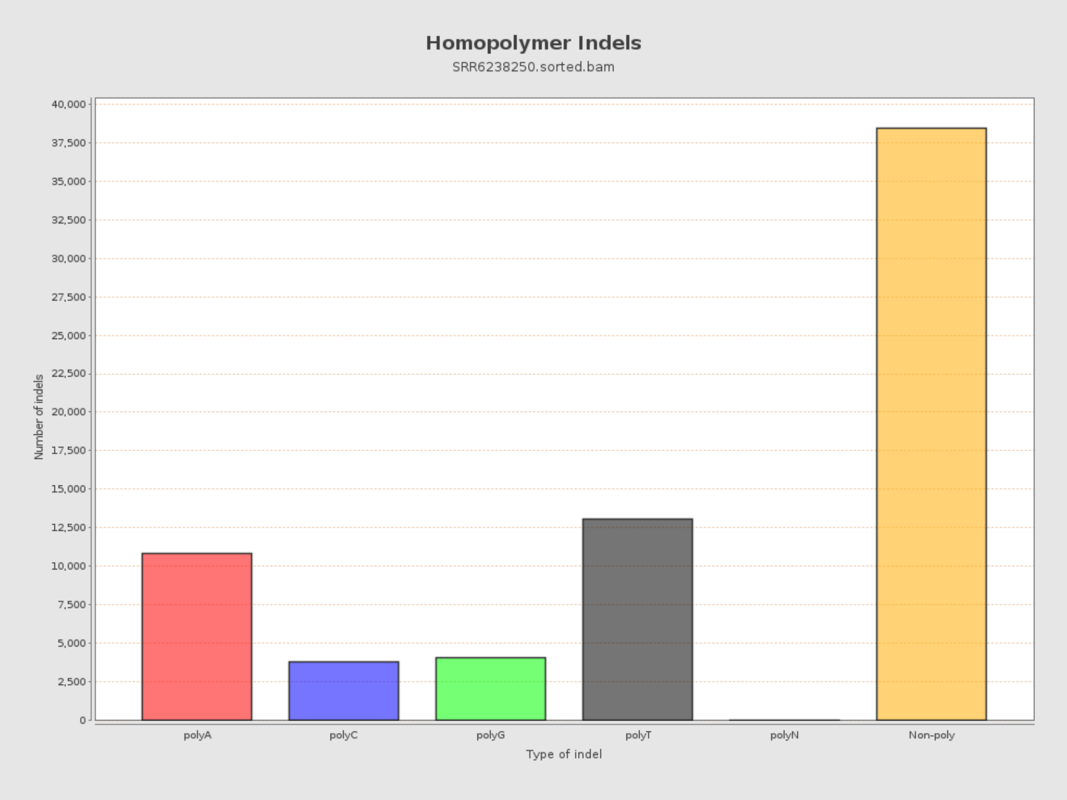
9. Results : Mapped Reads GC-content Distribution



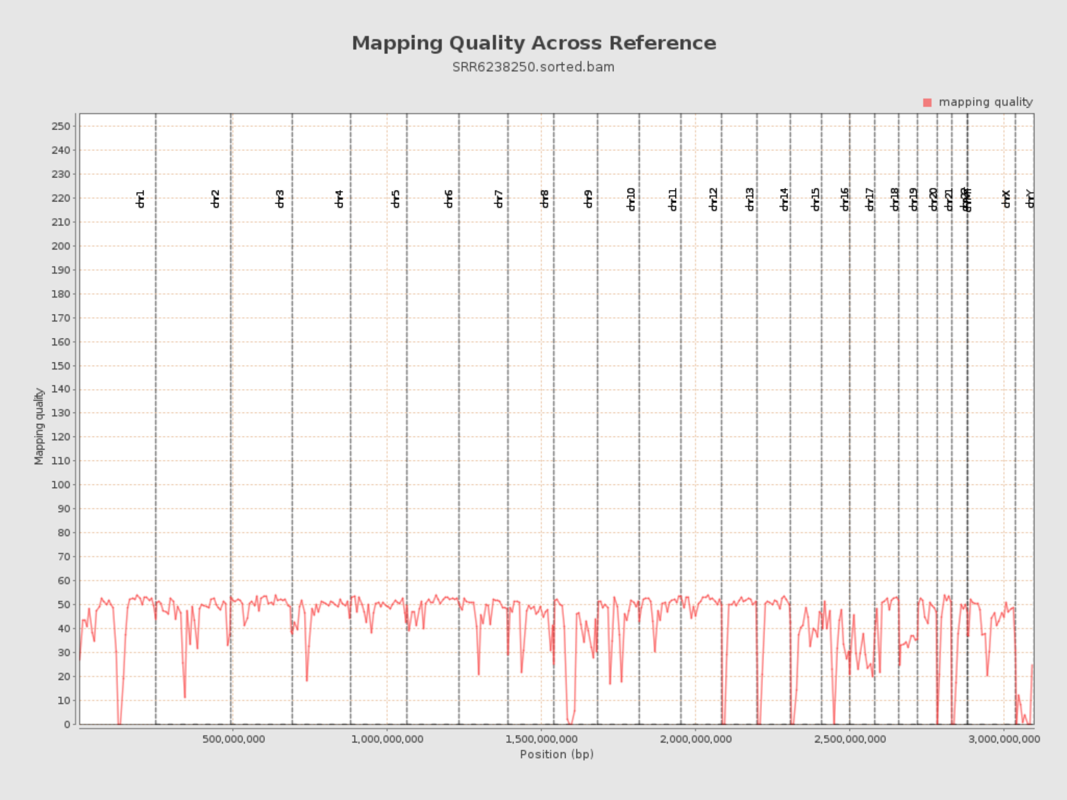
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram