Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:59:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240238.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_SRR6240238 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240238.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:59:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240238.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,820,144
Mapped reads	2,053,235 / 72.81%
Unmapped reads	766,909 / 27.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,023 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	317,254 / 11.25%
Duplication rate	11.45%
Clipped reads	972,105 / 34.47%

2.2. ACGT Content

Number/percentage of A's	38,302,377 / 28.18%
Number/percentage of C's	24,983,227 / 18.38%
Number/percentage of T's	43,515,714 / 32.01%
Number/percentage of G's	29,071,721 / 21.39%
Number/percentage of N's	52,056 / 0.04%
GC Percentage	39.77%

2.3. Coverage

Mean	0.0439

Standard Deviation	0.5121

2.4. Mapping Quality

Mean Mapping Quality	46.96

2.5. Mismatches and indels

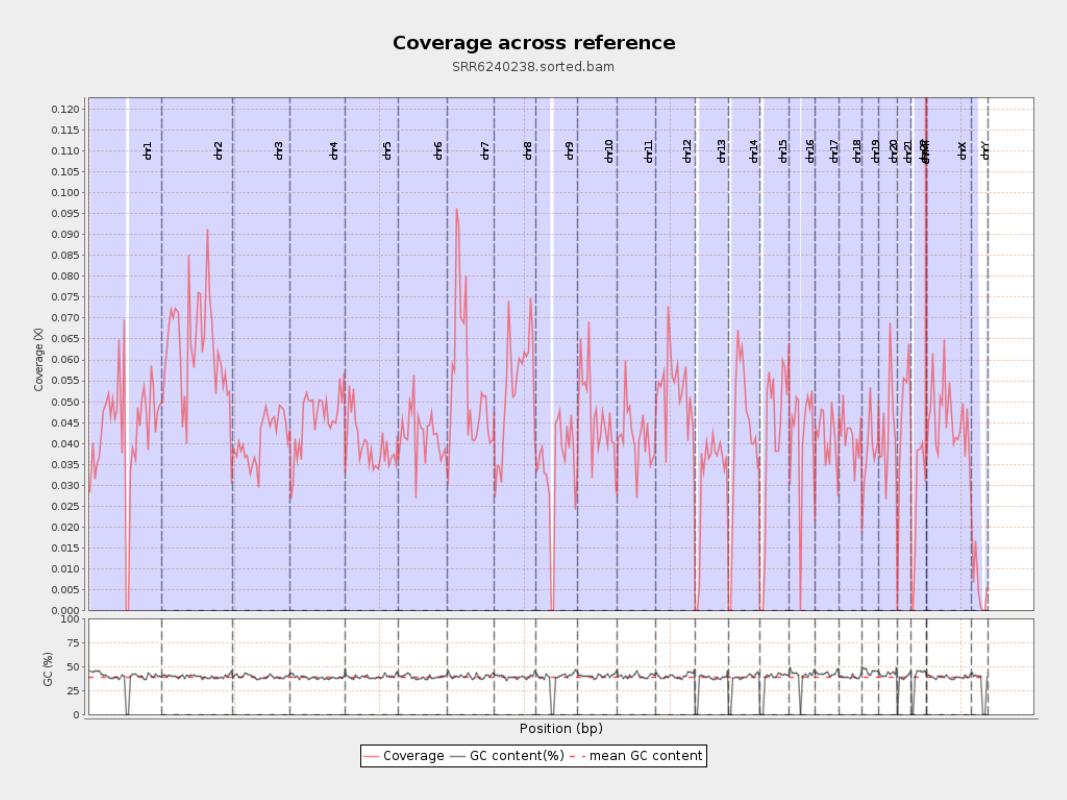
General error rate	0.88%
Mismatches	1,178,765
Insertions	9,987
Mapped reads with at least one insertion	0.48%
Deletions	36,151
Mapped reads with at least one deletion	1.74%
Homopolymer indels	47.52%

2.6. Chromosome stats

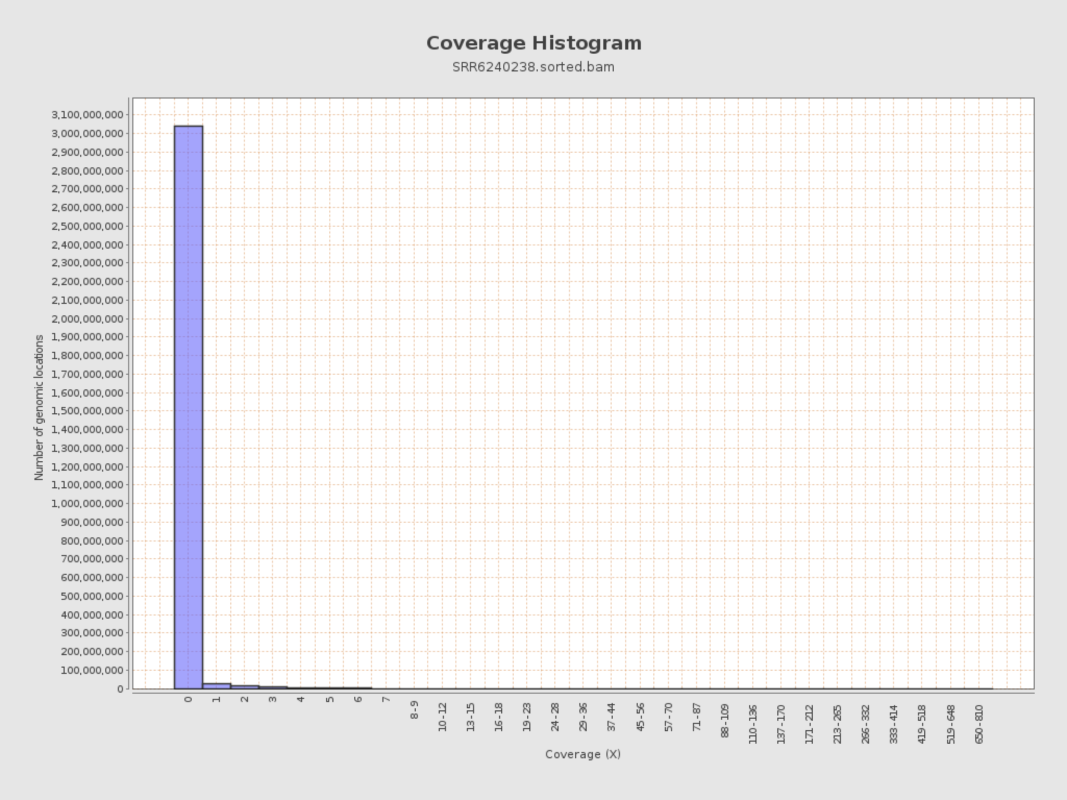
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10677821	0.0428	0.7678
chr2	243199373	15219308	0.0626	0.6136
chr3	198022430	8163503	0.0412	0.4022
chr4	191154276	8731625	0.0457	0.4301
chr5	180915260	7157408	0.0396	0.3926
chr6	171115067	7176447	0.0419	0.4286
chr7	159138663	8699901	0.0547	0.7083

chr8	146364022	7762697	0.053	0.6733
chr9	141213431	4793069	0.0339	0.4276
chr10	135534747	6372002	0.047	0.4823
chr11	135006516	5614959	0.0416	0.4519
chr12	133851895	7085016	0.0529	0.4575
chr13	115169878	3577940	0.0311	0.3541
chr14	107349540	4474484	0.0417	0.416
chr15	102531392	4218922	0.0411	0.4102
chr16	90354753	3735652	0.0413	0.4004
chr17	81195210	3306334	0.0407	0.411
chr18	78077248	3265491	0.0418	0.6954
chr19	59128983	2296967	0.0388	0.5219
chr20	63025520	2674408	0.0424	0.4103
chr21	48129895	2190186	0.0455	0.4255
chr22	51304566	1340792	0.0261	0.3096
chrMT	16571	15378	0.928	1.9431
chrX	155270560	7089644	0.0457	0.4354
chrY	59373566	348356	0.0059	0.1389

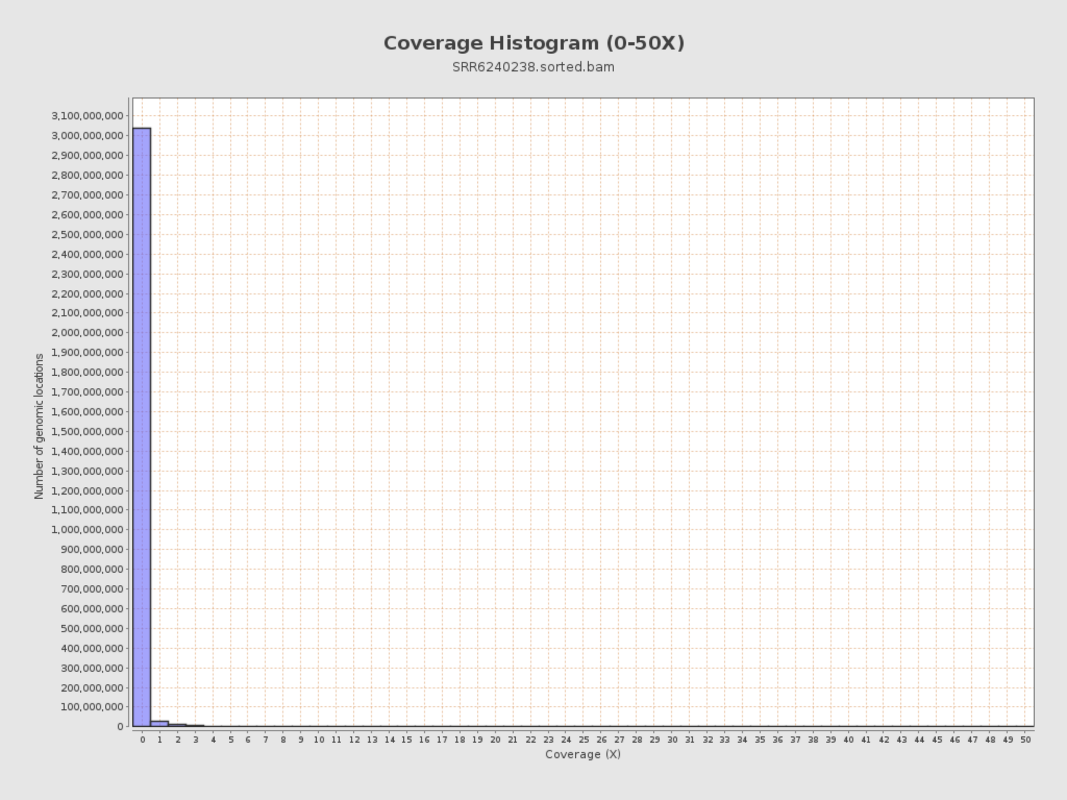
3. Results : Coverage across reference



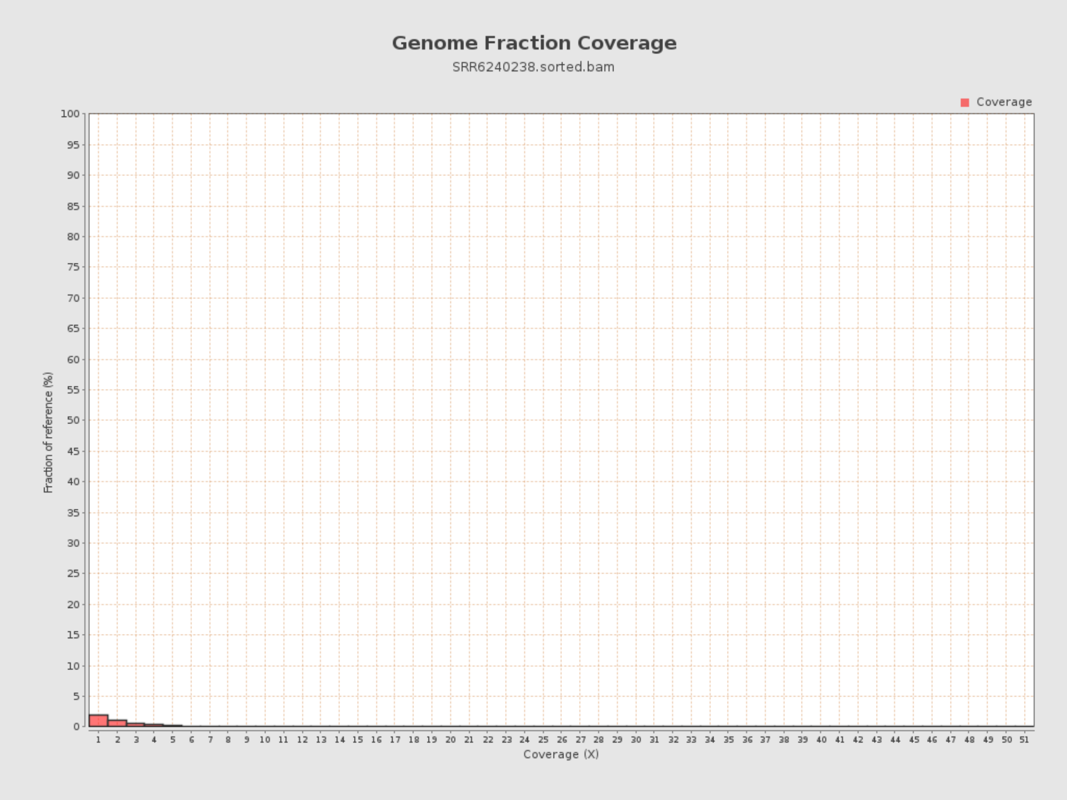
4. Results : Coverage Histogram



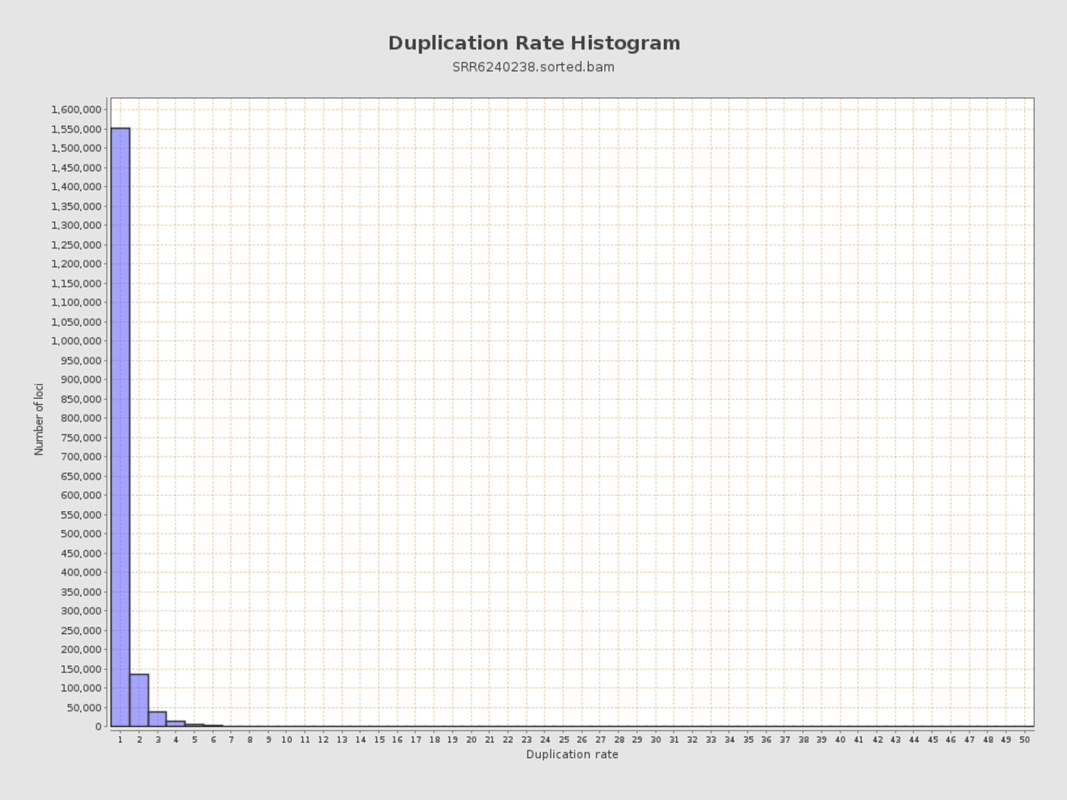
5. Results : Coverage Histogram (0-50X)



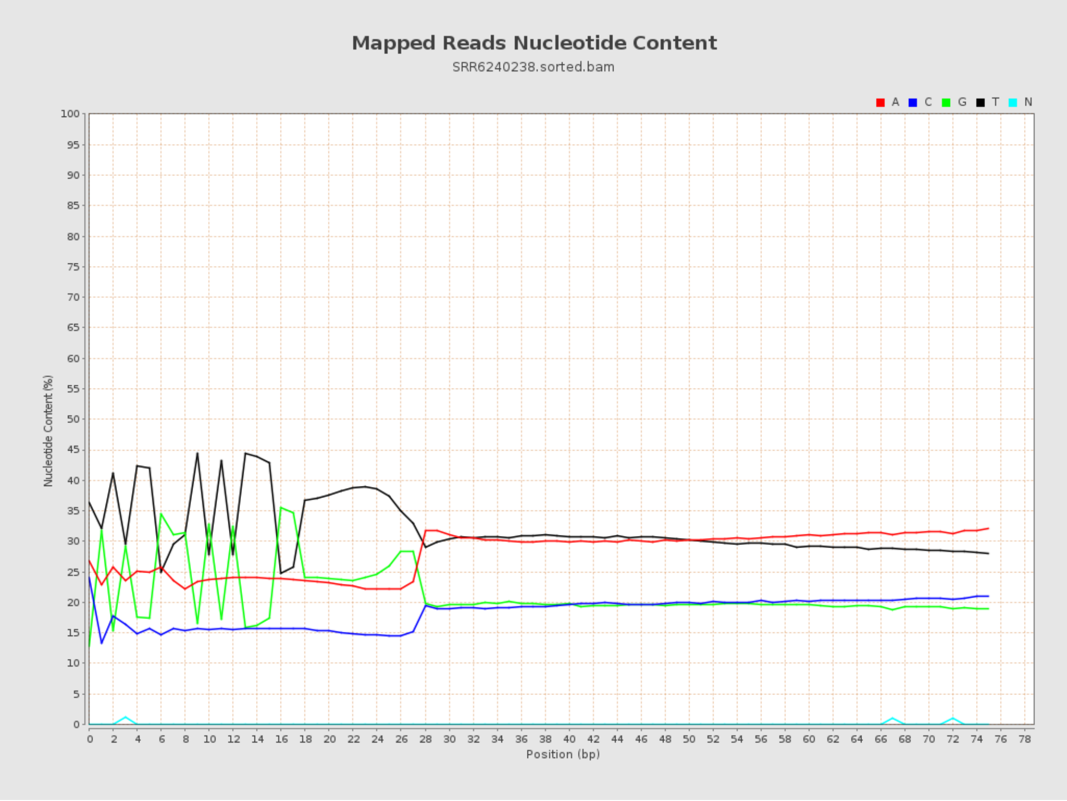
6. Results : Genome Fraction Coverage



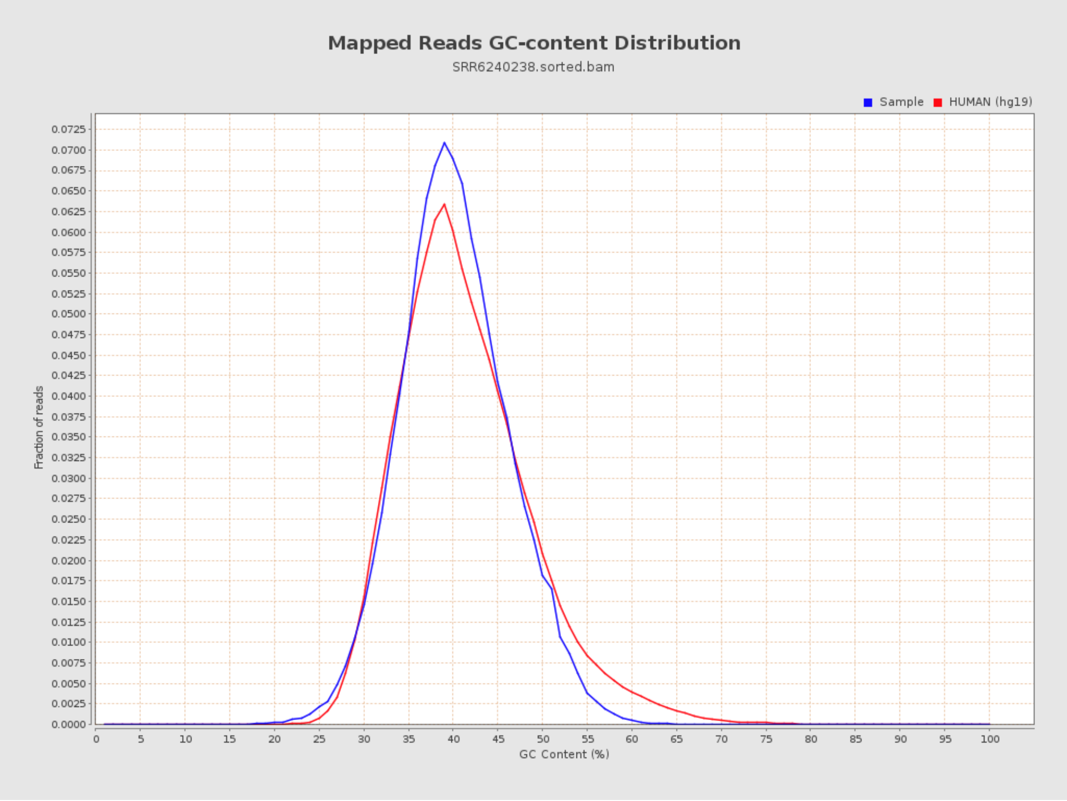
7. Results : Duplication Rate Histogram



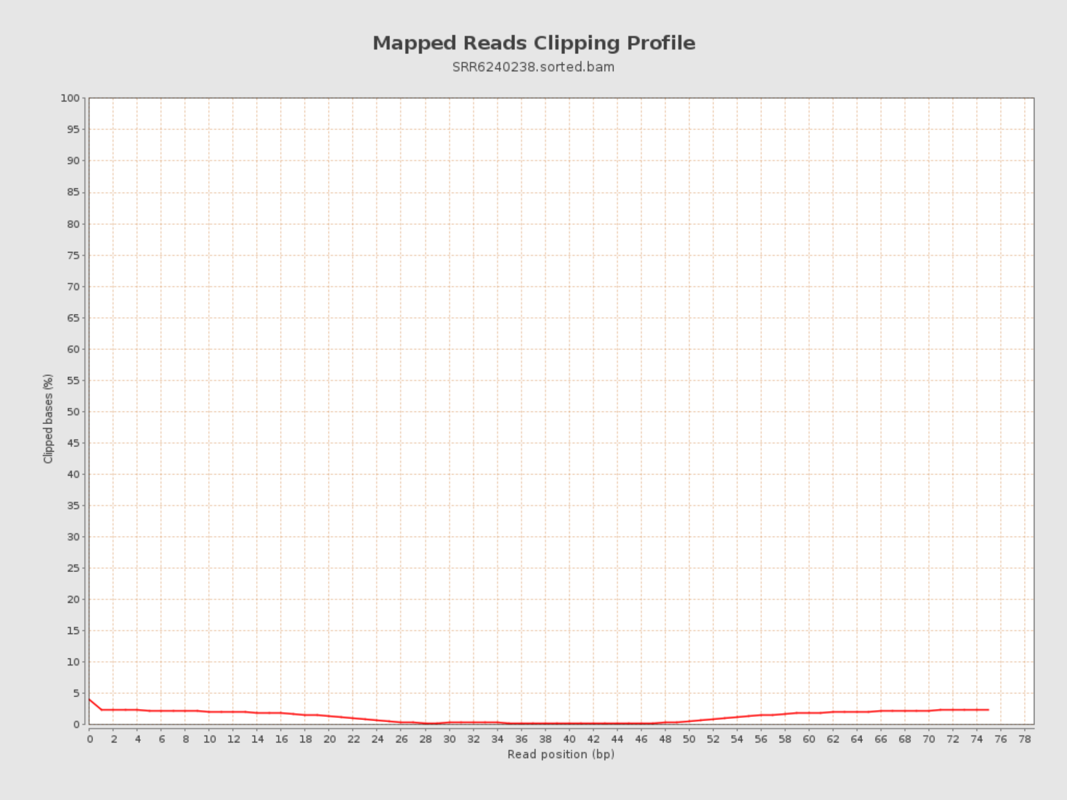
8. Results : Mapped Reads Nucleotide Content



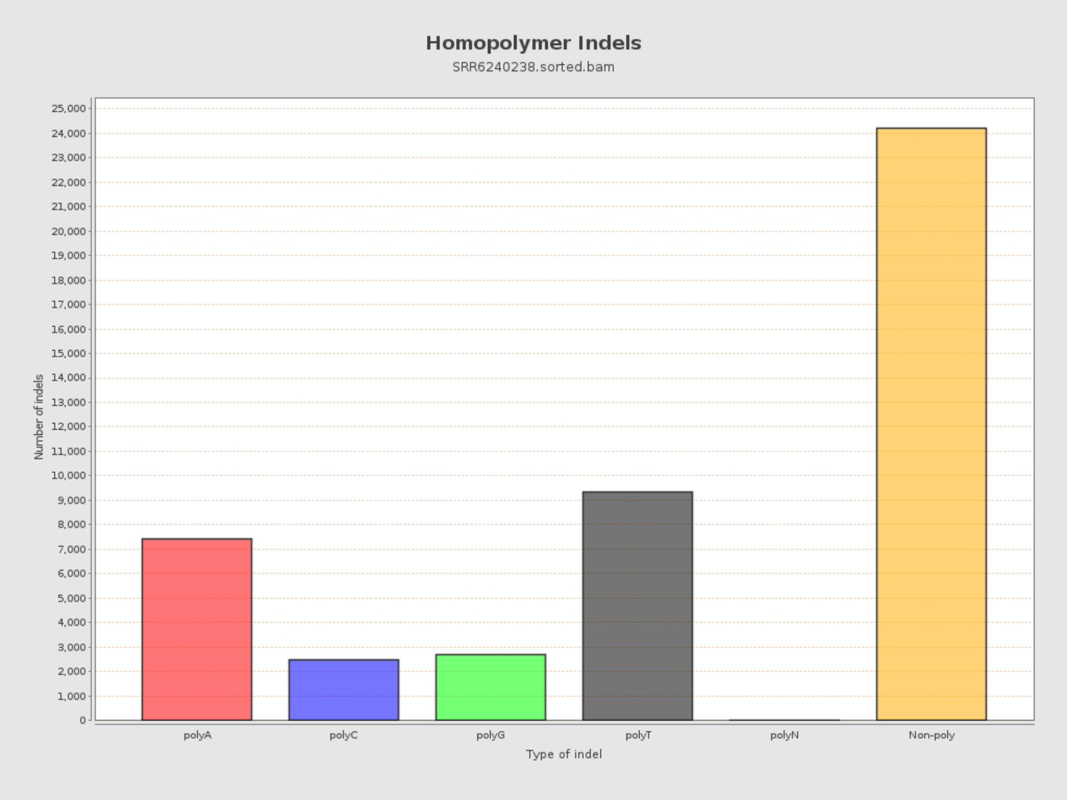
9. Results : Mapped Reads GC-content Distribution



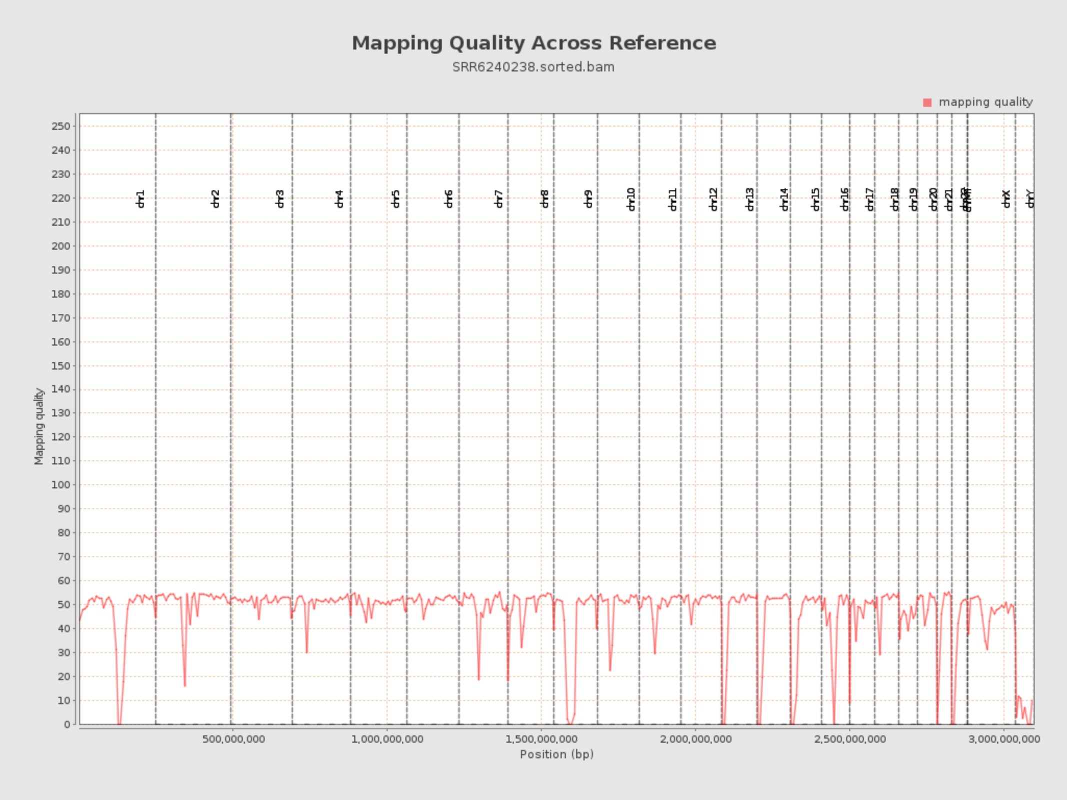
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram