Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:58:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238031.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_SRR6238031 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238031.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:58:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,898,760
Mapped reads	72,297 / 3.81%
Unmapped reads	1,826,463 / 96.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	800 / 0.04%
Read min/max/mean length	30 / 76 / 76.01
Duplicated reads (estimated)	7,363 / 0.39%
Duplication rate	1.55%
Clipped reads	43,089 / 2.27%

2.2. ACGT Content

Number/percentage of A's	1,168,244 / 26.18%
Number/percentage of C's	852,119 / 19.1%
Number/percentage of T's	1,375,175 / 30.82%
Number/percentage of G's	1,065,873 / 23.89%
Number/percentage of N's	387 / 0.01%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0014

Standard Deviation	0.6942

2.4. Mapping Quality

Mean Mapping Quality	41.53

2.5. Mismatches and indels

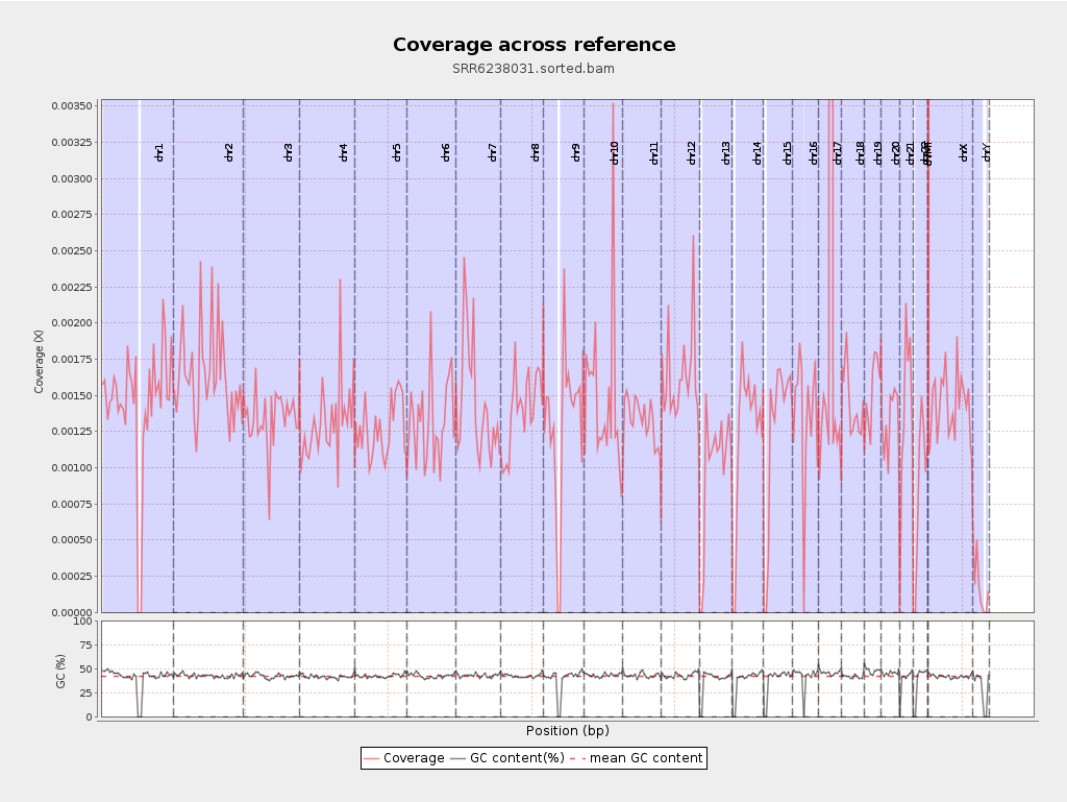
General error rate	1.31%
Mismatches	57,724
Insertions	633
Mapped reads with at least one insertion	0.87%
Deletions	1,008
Mapped reads with at least one deletion	1.37%
Homopolymer indels	37.29%

2.6. Chromosome stats

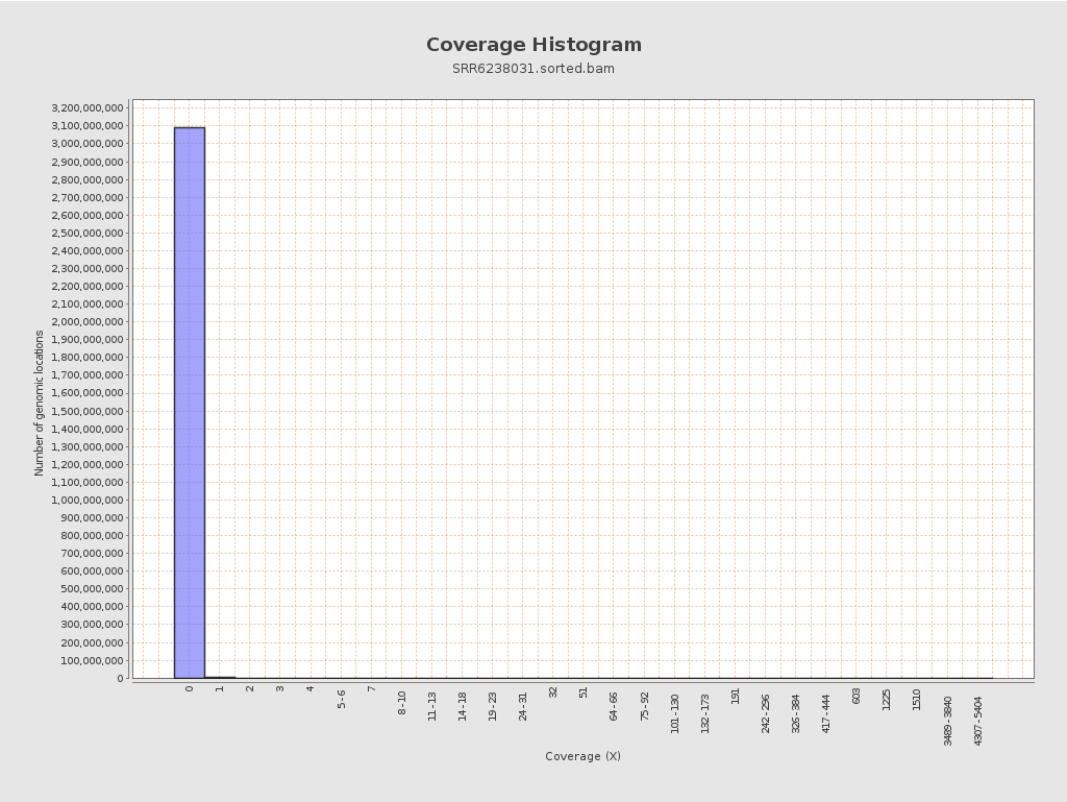
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	364064	0.0015	0.0425
chr2	243199373	398386	0.0016	0.047
chr3	198022430	265406	0.0013	0.0378
chr4	191154276	251696	0.0013	0.0728
chr5	180915260	229729	0.0013	0.0373
chr6	171115067	224317	0.0013	0.0396
chr7	159138663	227029	0.0014	0.0422

chr8	146364022	205142	0.0014	0.0404
chr9	141213431	180763	0.0013	0.0377
chr10	135534747	200965	0.0015	0.2198
chr11	135006516	179545	0.0013	0.0381
chr12	133851895	219019	0.0016	0.0417
chr13	115169878	114103	0.001	0.0326
chr14	107349540	133813	0.0012	0.037
chr15	102531392	126734	0.0012	0.0381
chr16	90354753	121652	0.0013	0.0378
chr17	81195210	386778	0.0048	4.2697
chr18	78077248	111964	0.0014	0.0445
chr19	59128983	90798	0.0015	0.0426
chr20	63025520	83140	0.0013	0.0379
chr21	48129895	68737	0.0014	0.04
chr22	51304566	44808	0.0009	0.0307
chrMT	16571	1515	0.0914	0.2983
chrX	155270560	221728	0.0014	0.0394
chrY	59373566	11646	0.0002	0.0145

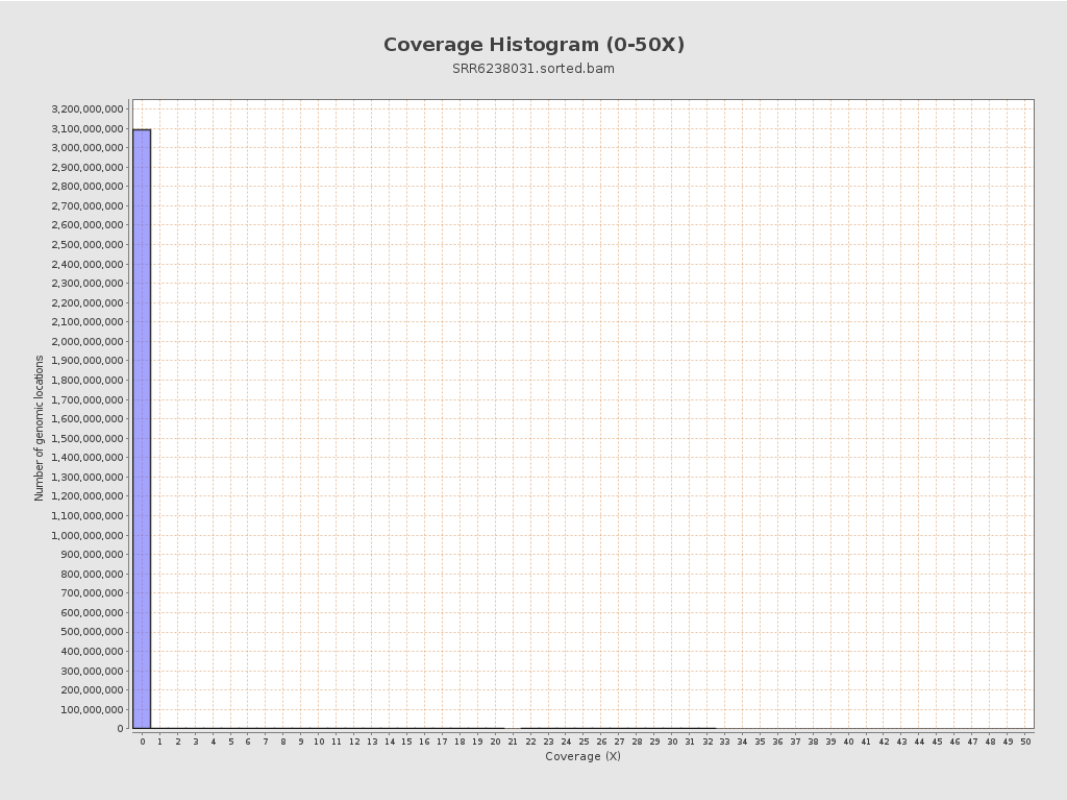
3. Results : Coverage across reference



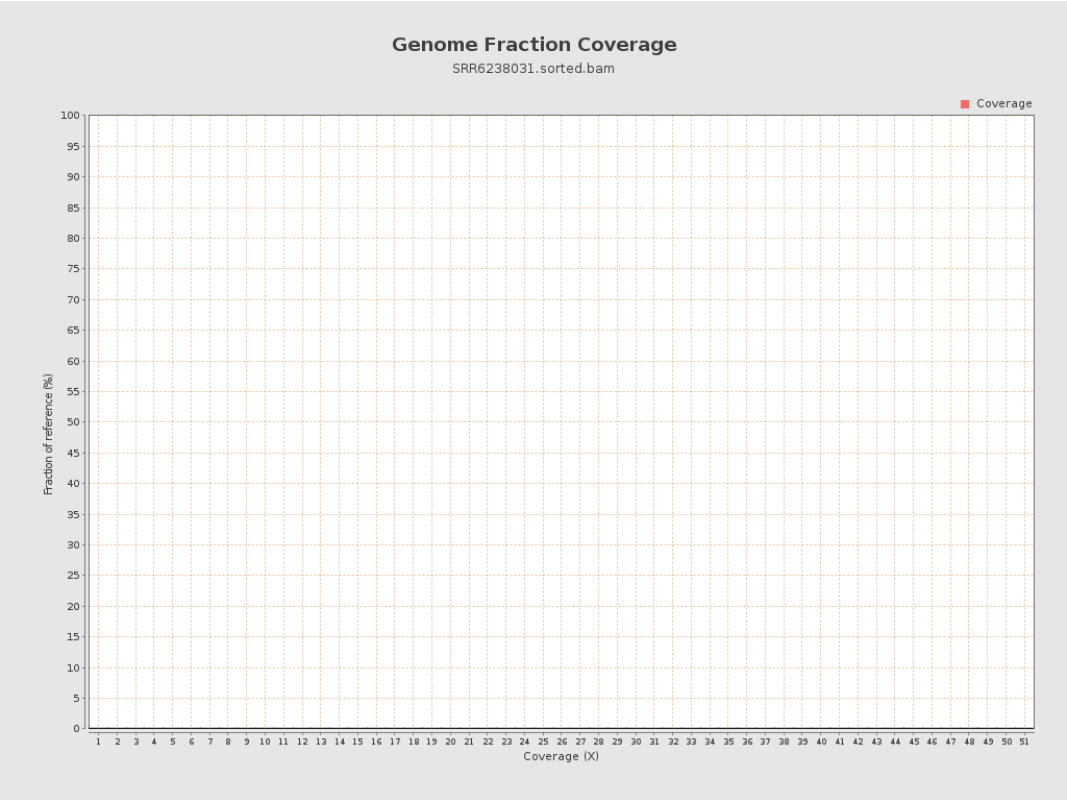
4. Results : Coverage Histogram



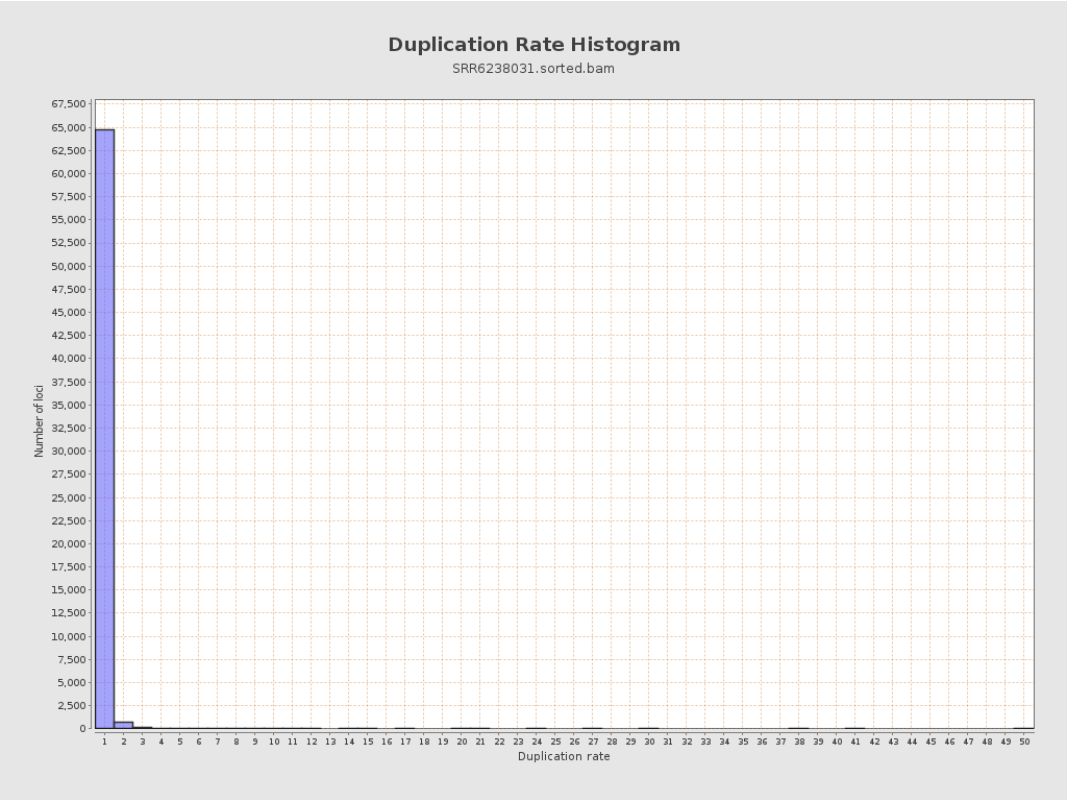
5. Results : Coverage Histogram (0-50X)



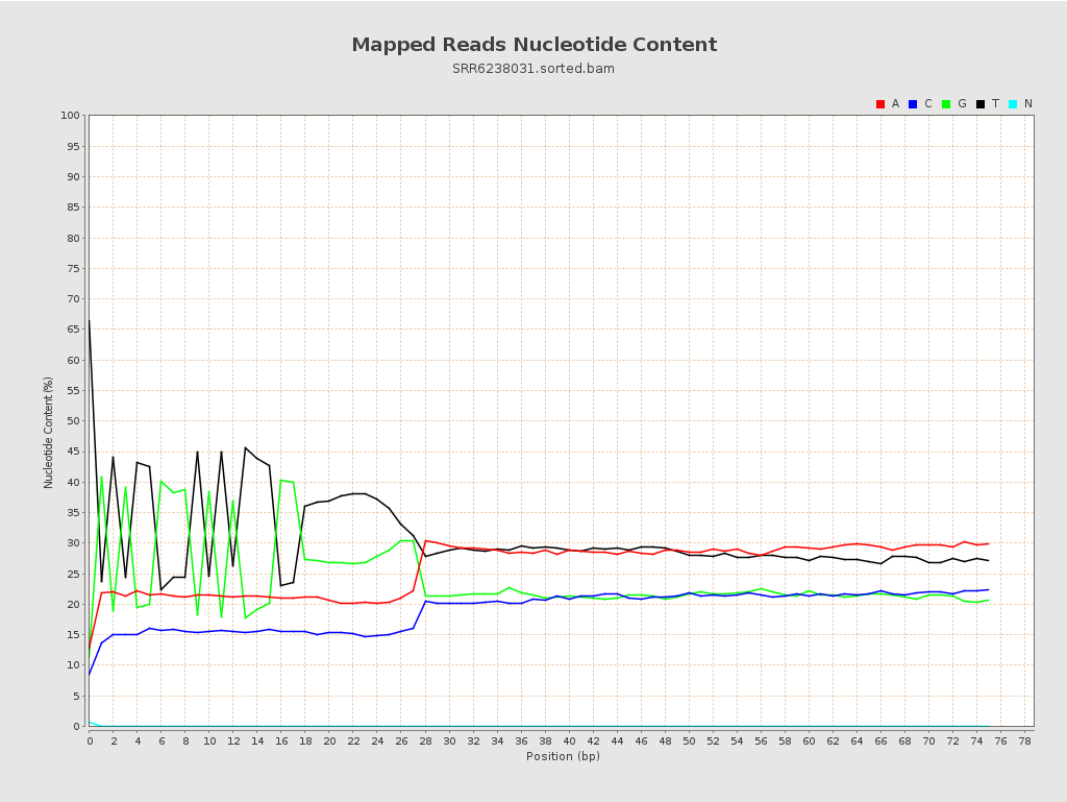
6. Results : Genome Fraction Coverage



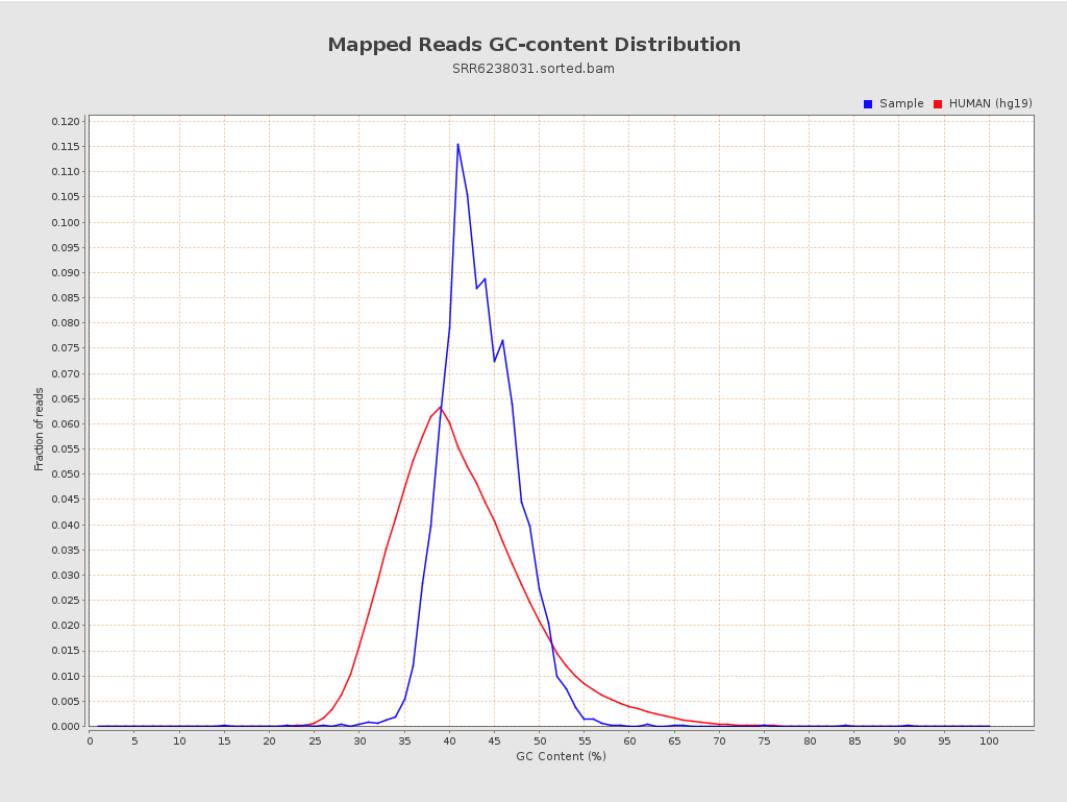
7. Results : Duplication Rate Histogram



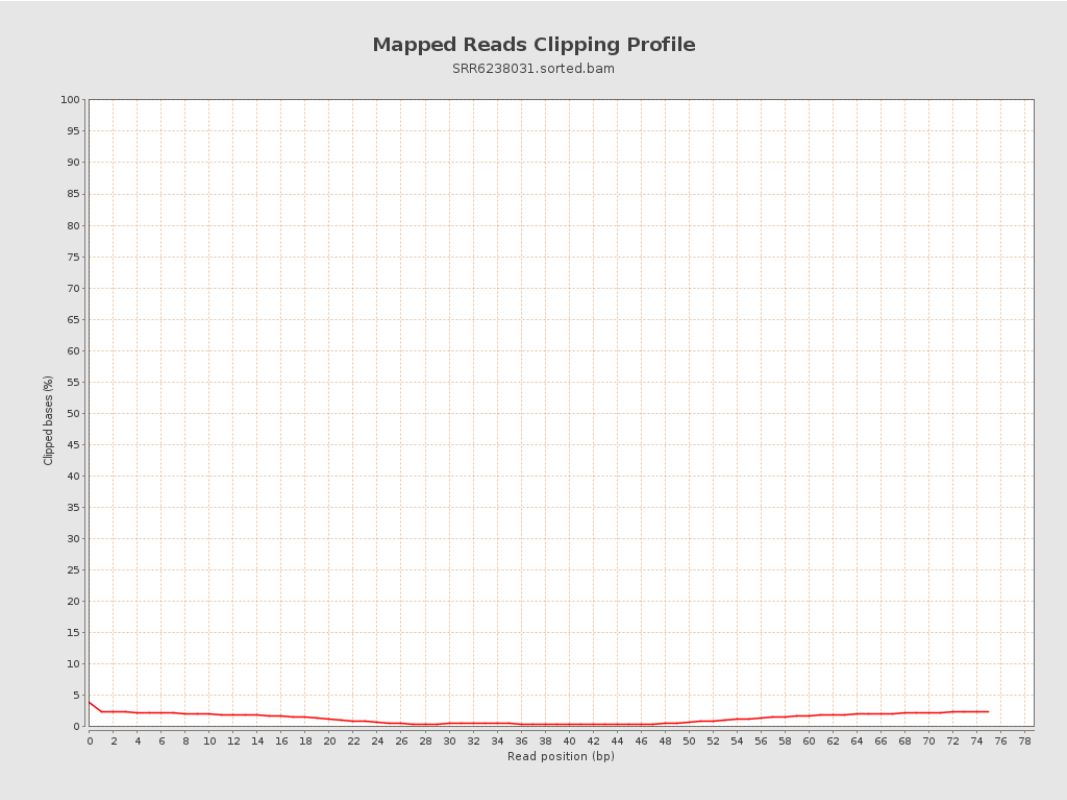
8. Results : Mapped Reads Nucleotide Content



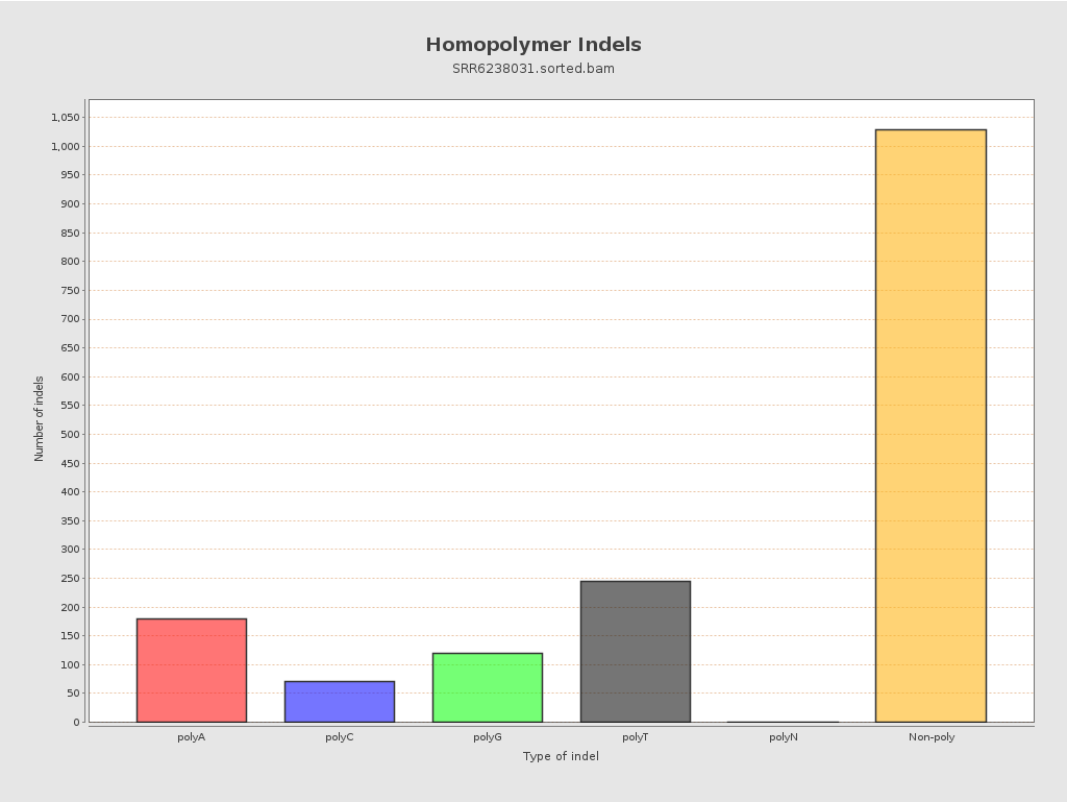
9. Results : Mapped Reads GC-content Distribution



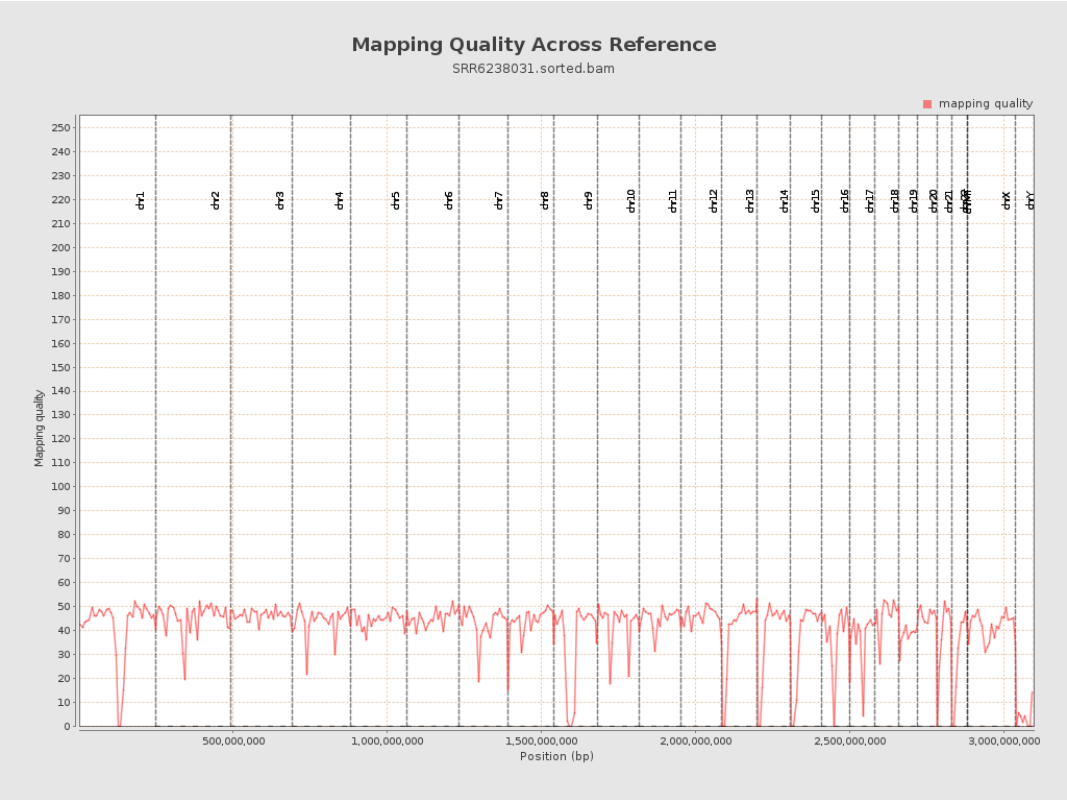
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram