Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:26:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238239.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_SRR6238239 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238239.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:26:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238239.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,177,587
Mapped reads	1,837,305 / 84.37%
Unmapped reads	340,282 / 15.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,379 / 1.26%
Read min/max/mean length	30 / 76 / 76.44
Duplicated reads (estimated)	260,817 / 11.98%
Duplication rate	9.88%
Clipped reads	967,103 / 44.41%

2.2. ACGT Content

Number/percentage of A's	34,431,583 / 28.69%
Number/percentage of C's	23,750,665 / 19.79%
Number/percentage of T's	36,073,681 / 30.06%
Number/percentage of G's	25,715,143 / 21.43%
Number/percentage of N's	20,590 / 0.02%
GC Percentage	41.22%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.4331

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

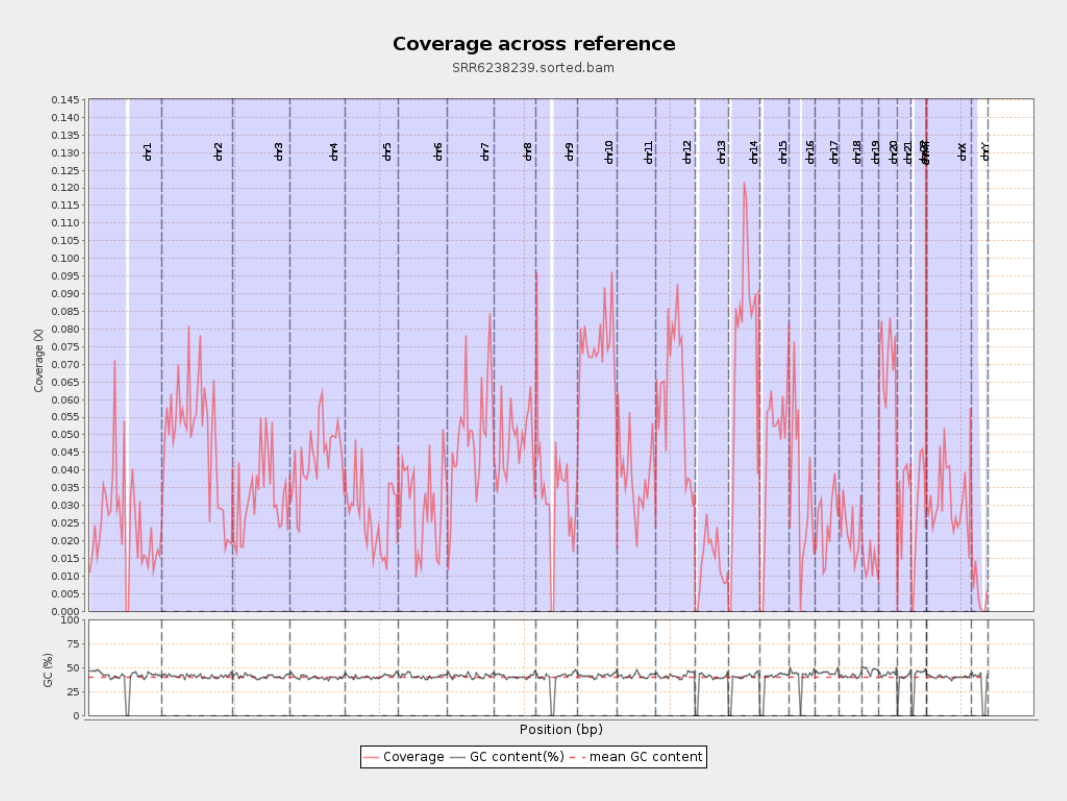
General error rate	0.87%
Mismatches	1,031,098
Insertions	9,956
Mapped reads with at least one insertion	0.54%
Deletions	34,150
Mapped reads with at least one deletion	1.84%
Homopolymer indels	45.32%

2.6. Chromosome stats

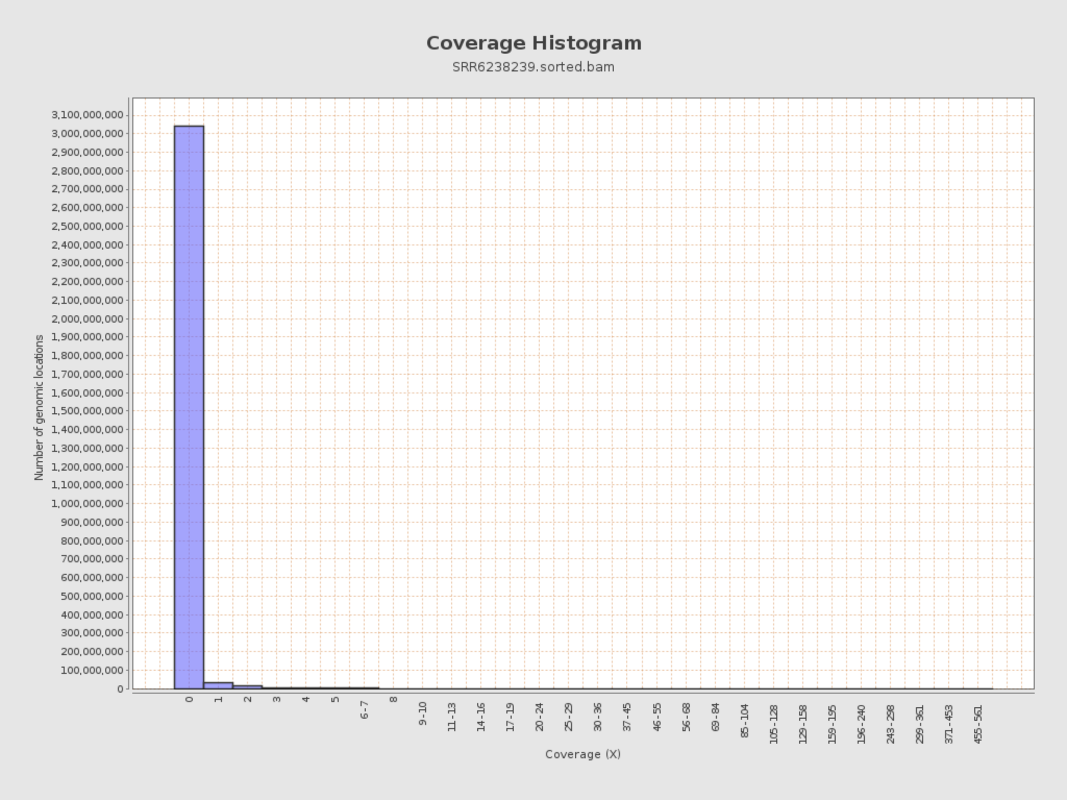
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5972671	0.024	0.3666
chr2	243199373	11845461	0.0487	0.5383
chr3	198022430	6571364	0.0332	0.3437
chr4	191154276	8273163	0.0433	0.3946
chr5	180915260	4898166	0.0271	0.3086
chr6	171115067	5272418	0.0308	0.3536
chr7	159138663	7981397	0.0502	0.6012

chr8	146364022	7020404	0.048	0.5378
chr9	141213431	4403491	0.0312	0.3917
chr10	135534747	10212341	0.0753	0.5893
chr11	135006516	5125273	0.038	0.4171
chr12	133851895	8204327	0.0613	0.4715
chr13	115169878	1540612	0.0134	0.2256
chr14	107349540	7764749	0.0723	0.5671
chr15	102531392	4707132	0.0459	0.4747
chr16	90354753	3077162	0.0341	0.3538
chr17	81195210	2004226	0.0247	0.2949
chr18	78077248	1825798	0.0234	0.5998
chr19	59128983	800542	0.0135	0.3026
chr20	63025520	4462118	0.0708	0.5142
chr21	48129895	1521129	0.0316	0.3281
chr22	51304566	1400038	0.0273	0.3068
chrMT	16571	7579	0.4574	1.1161
chrX	155270560	4859485	0.0313	0.3518
chrY	59373566	297350	0.005	0.1251

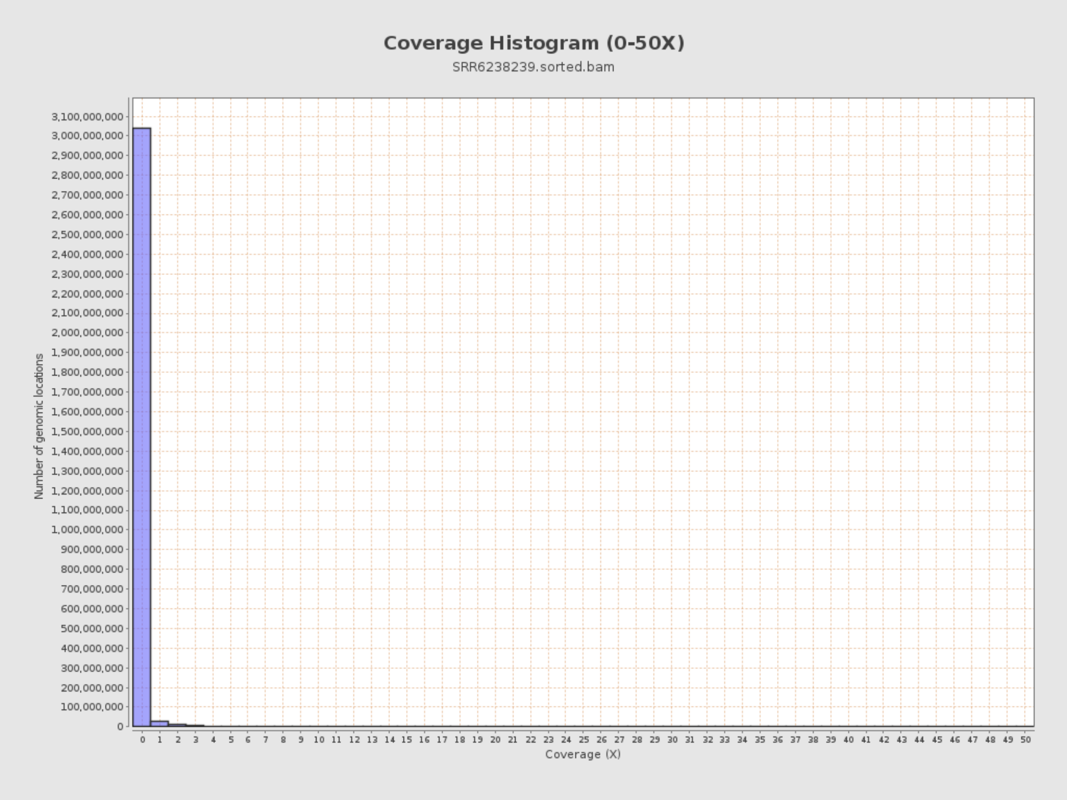
3. Results : Coverage across reference



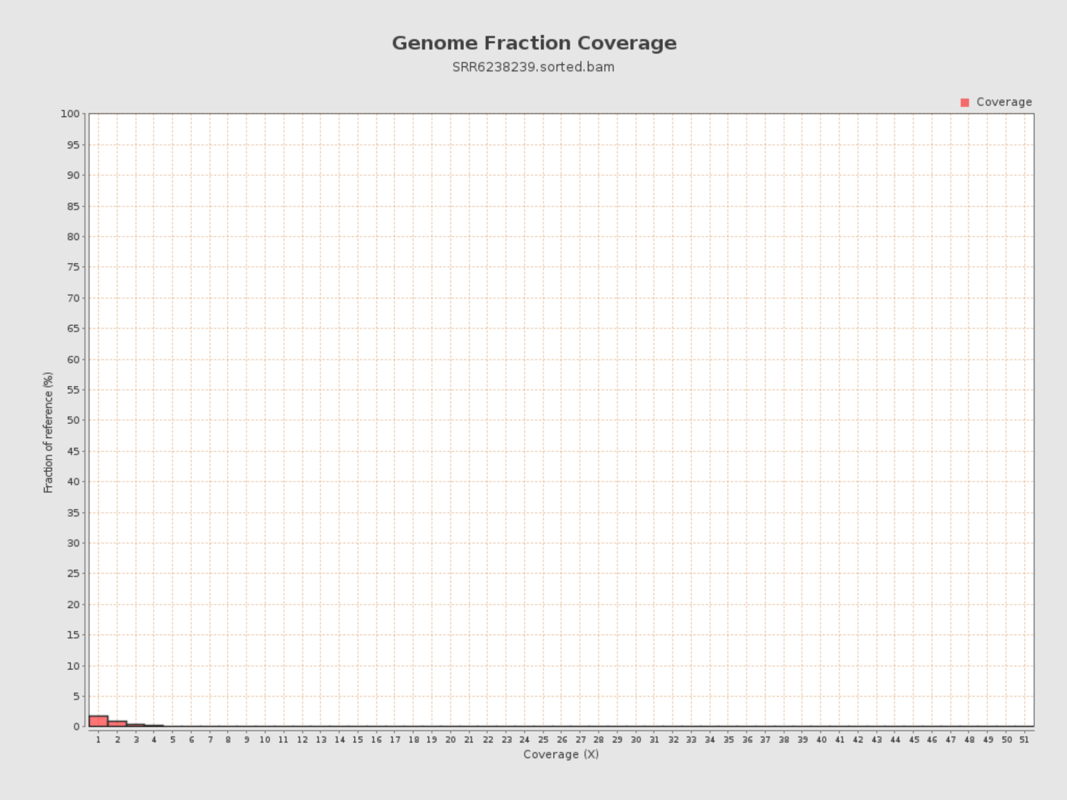
4. Results : Coverage Histogram



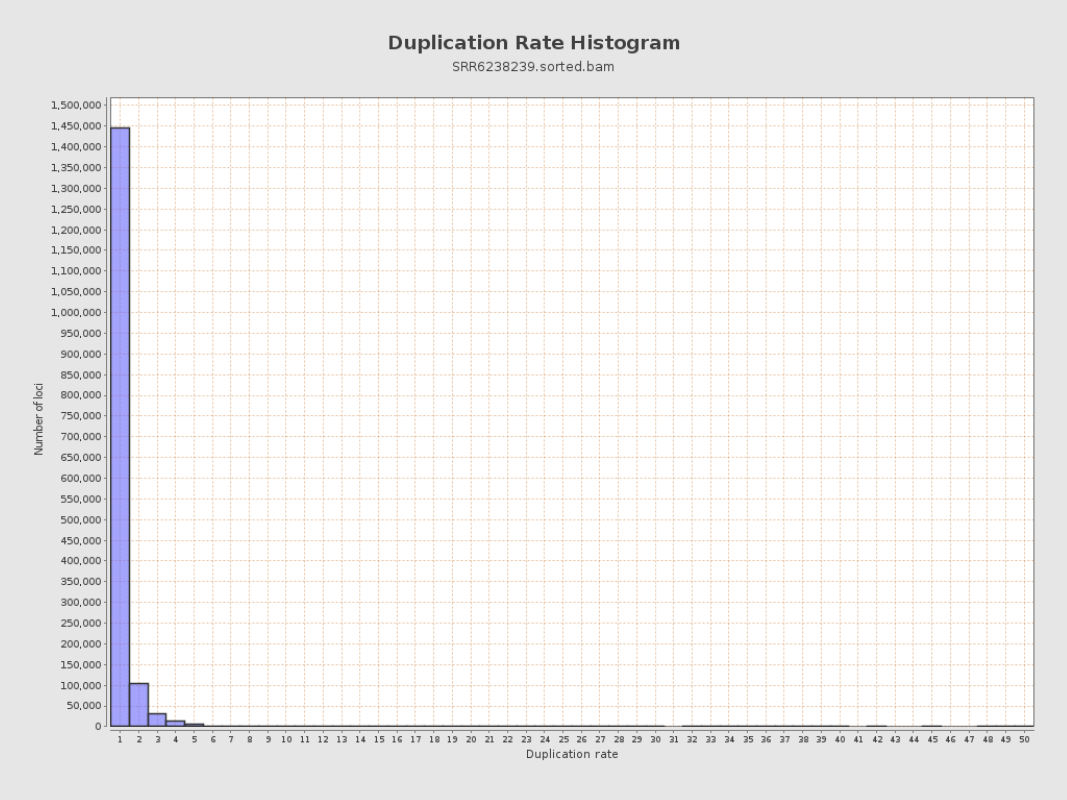
5. Results : Coverage Histogram (0-50X)



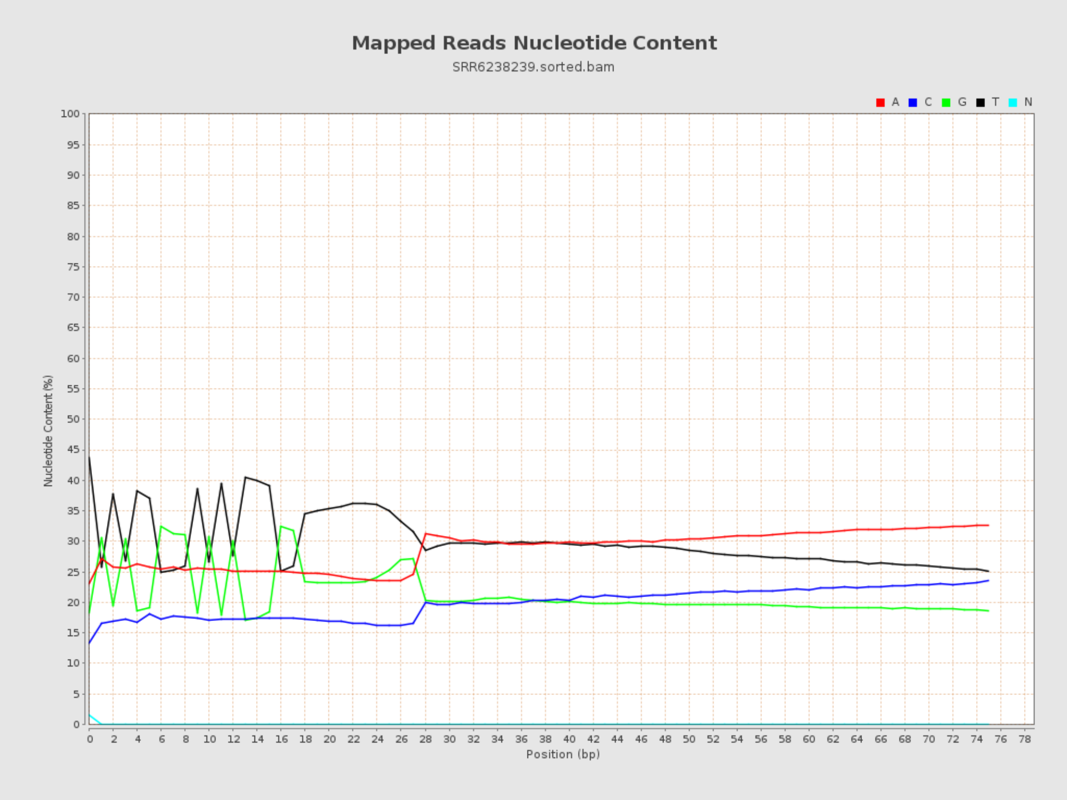
6. Results : Genome Fraction Coverage



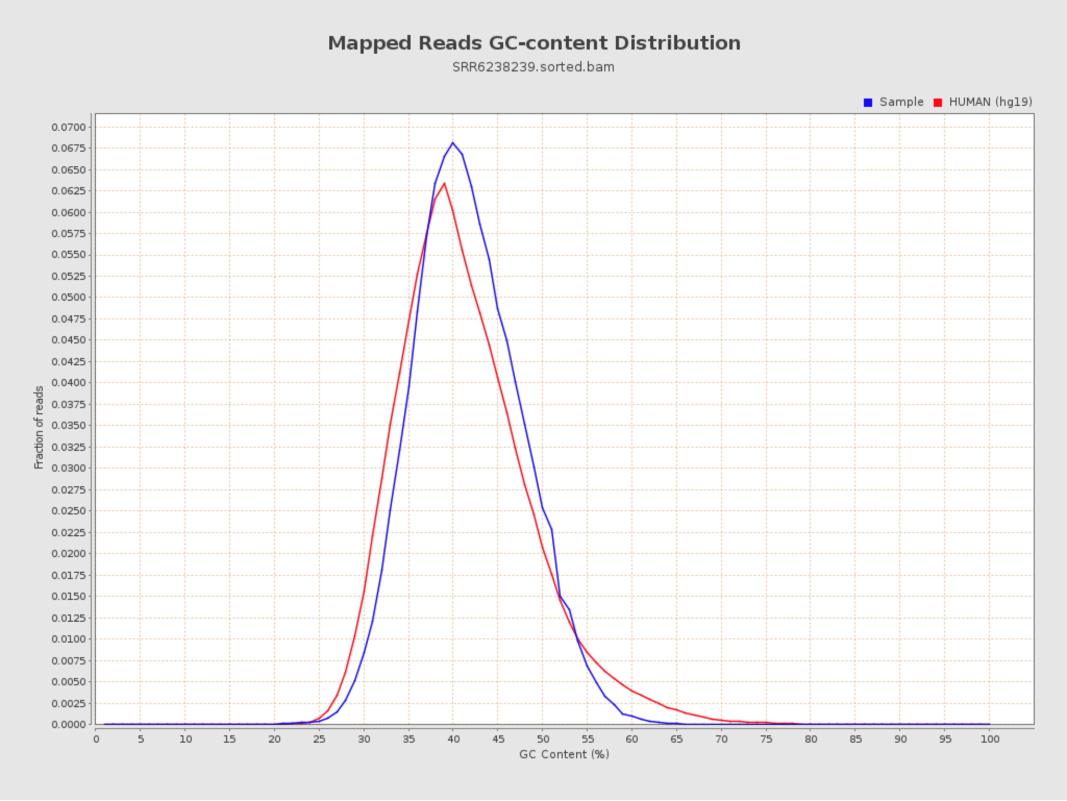
7. Results : Duplication Rate Histogram



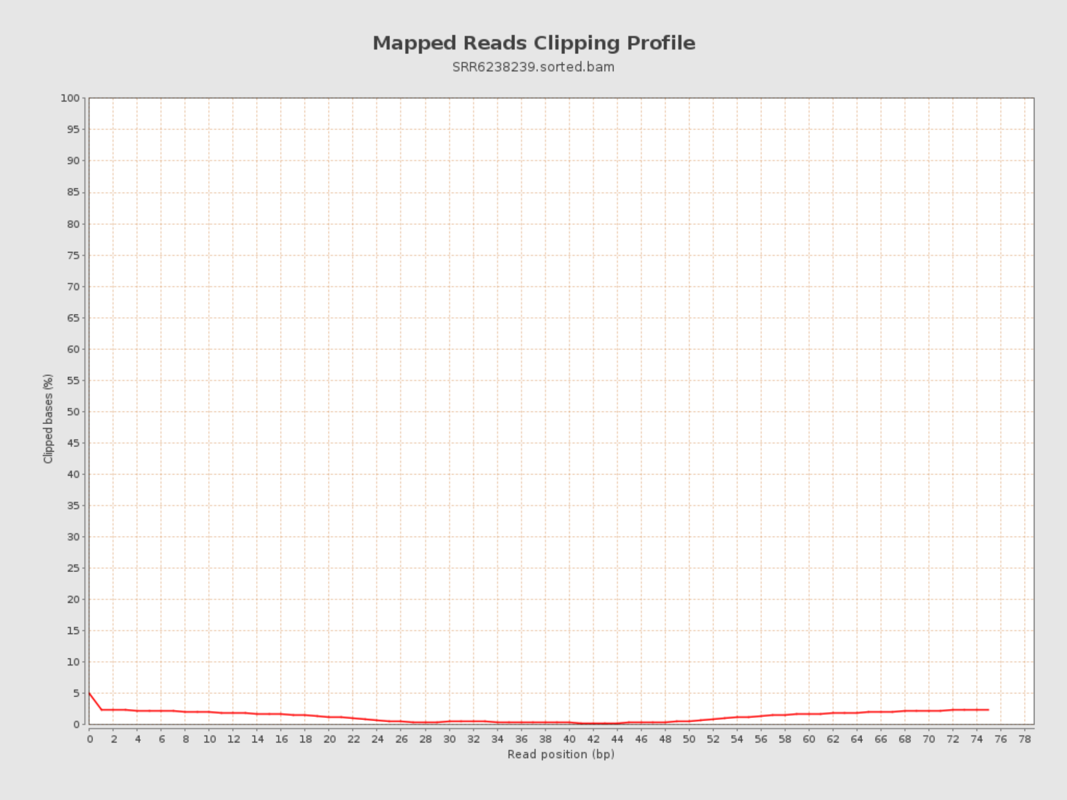
8. Results : Mapped Reads Nucleotide Content



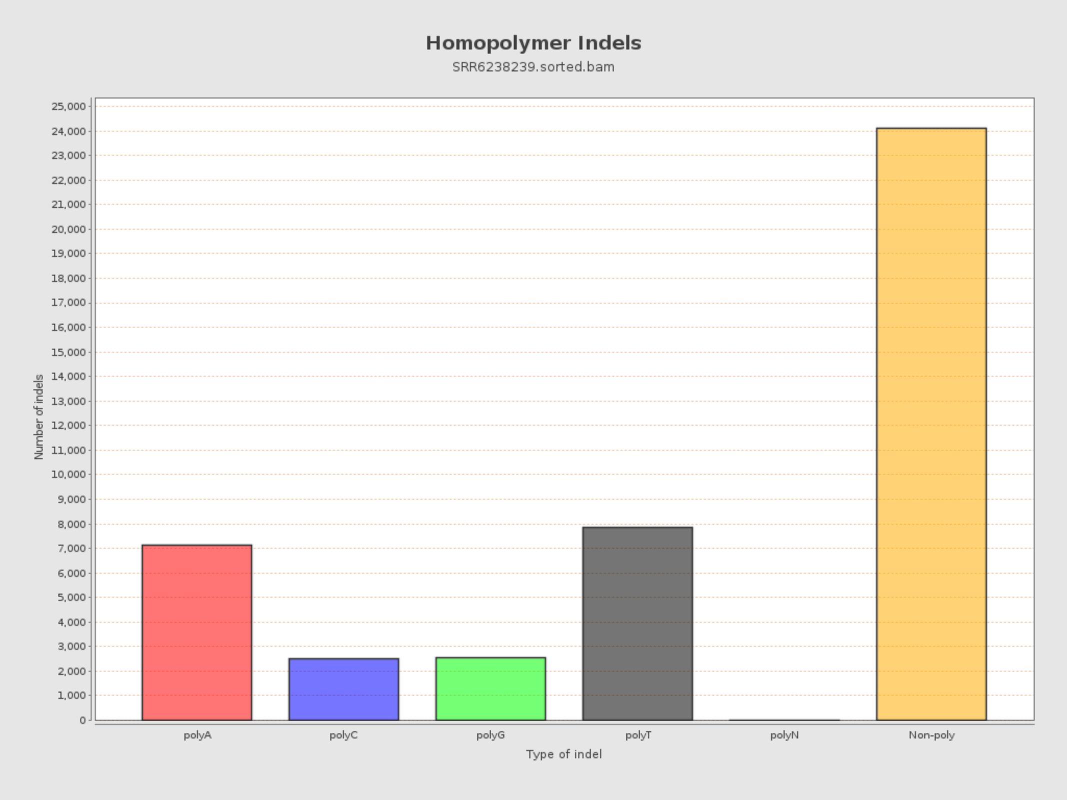
9. Results : Mapped Reads GC-content Distribution



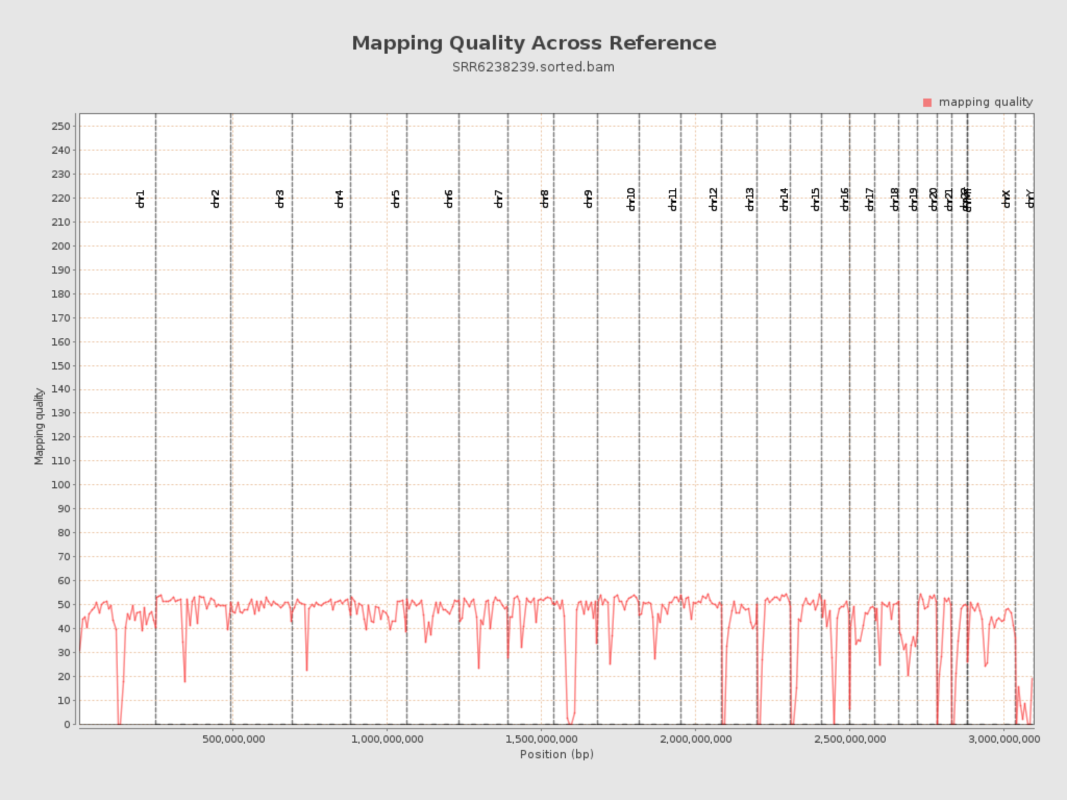
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram