Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:28:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237323.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_SRR6237323 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237323.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:28:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237323.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,373,913
Mapped reads	2,912,223 / 86.32%
Unmapped reads	461,690 / 13.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,877 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	1,193,382 / 35.37%
Duplication rate	21.51%
Clipped reads	1,927,014 / 57.12%

2.2. ACGT Content

Number/percentage of A's	45,737,551 / 25.73%
Number/percentage of C's	31,096,630 / 17.49%
Number/percentage of T's	59,285,520 / 33.35%
Number/percentage of G's	41,607,615 / 23.41%
Number/percentage of N's	18,728 / 0.01%
GC Percentage	40.9%

2.3. Coverage

Mean	0.0574

Standard Deviation	0.9746

2.4. Mapping Quality

Mean Mapping Quality	42.75

2.5. Mismatches and indels

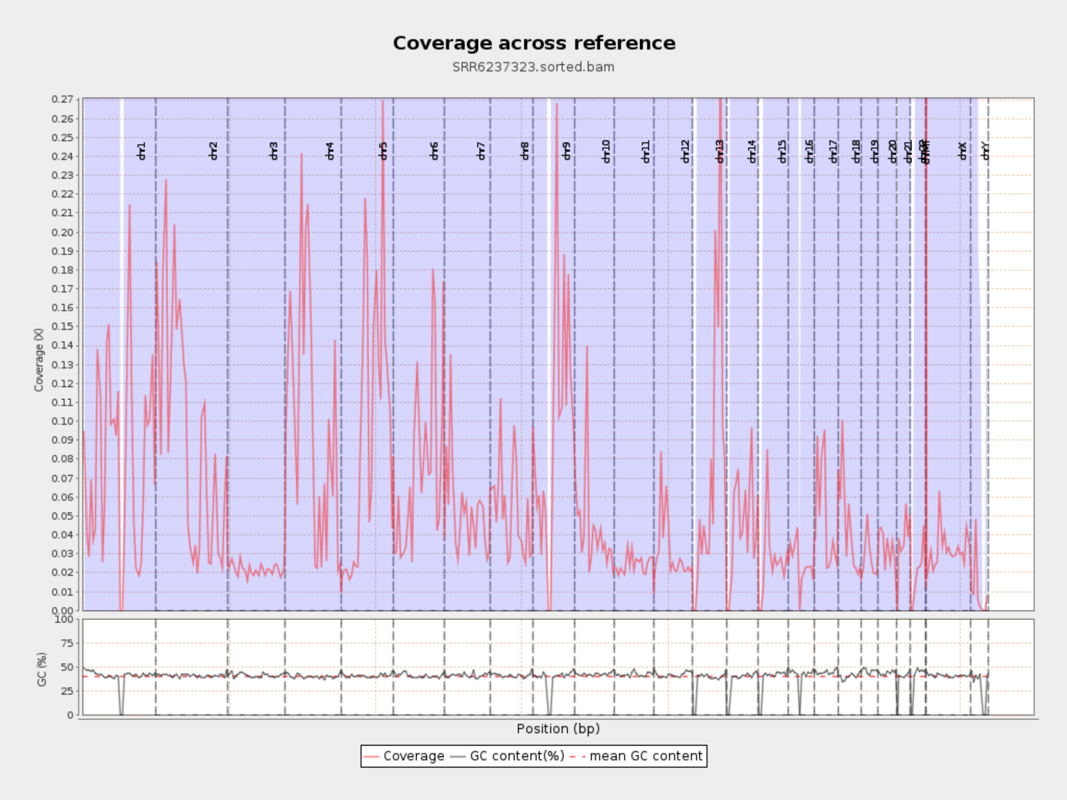
General error rate	0.61%
Mismatches	1,052,347
Insertions	13,203
Mapped reads with at least one insertion	0.45%
Deletions	48,485
Mapped reads with at least one deletion	1.64%
Homopolymer indels	41.77%

2.6. Chromosome stats

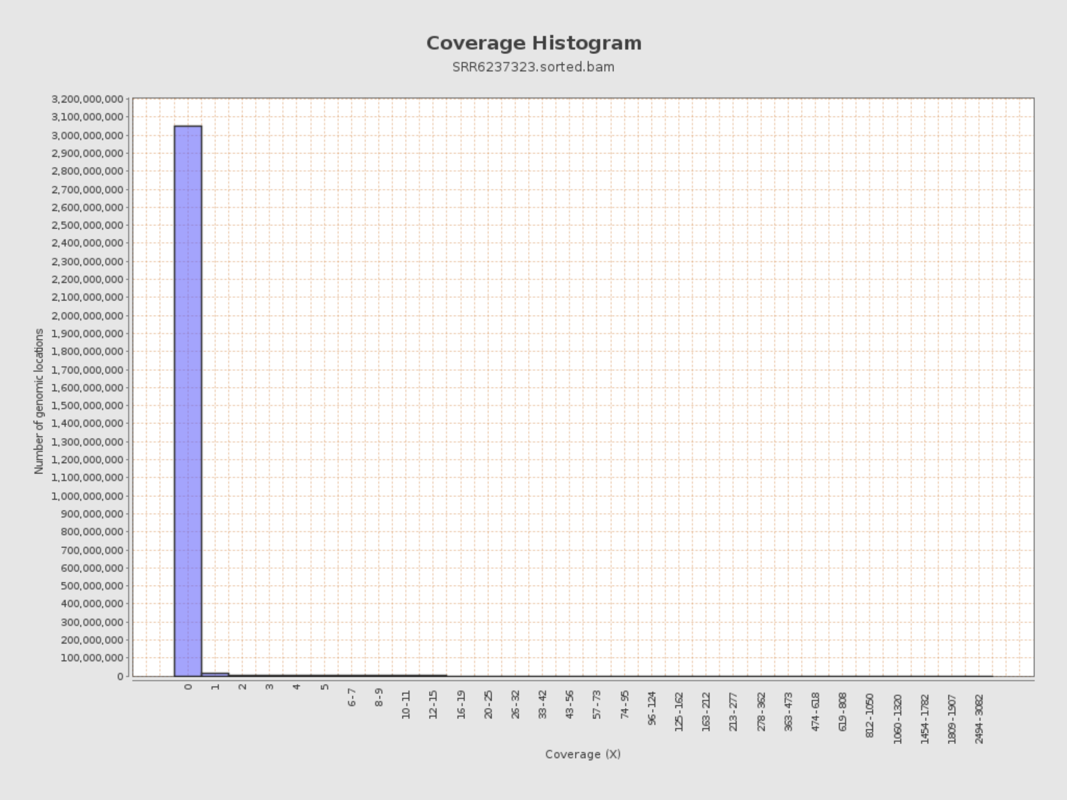
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19919589	0.0799	1.0219
chr2	243199373	22348080	0.0919	1.7754
chr3	198022430	4317851	0.0218	0.4277
chr4	191154276	19563157	0.1023	1.0387
chr5	180915260	17000423	0.094	0.888
chr6	171115067	12840344	0.075	0.9773
chr7	159138663	8316787	0.0523	0.7392

chr8	146364022	7849927	0.0536	0.8006
chr9	141213431	13731889	0.0972	0.9355
chr10	135534747	5831325	0.043	1.0233
chr11	135006516	3307029	0.0245	0.4881
chr12	133851895	4252637	0.0318	0.528
chr13	115169878	9089920	0.0789	0.8843
chr14	107349540	4925389	0.0459	0.6521
chr15	102531392	2765574	0.027	0.5193
chr16	90354753	2181445	0.0241	0.4848
chr17	81195210	3928132	0.0484	0.6506
chr18	78077248	3532031	0.0452	2.5082
chr19	59128983	1699028	0.0287	0.6124
chr20	63025520	2112338	0.0335	0.5651
chr21	48129895	1792916	0.0373	0.6411
chr22	51304566	984002	0.0192	0.4129
chrMT	16571	18452	1.1135	3.7666
chrX	155270560	4911223	0.0316	0.5213
chrY	59373566	612347	0.0103	0.6292

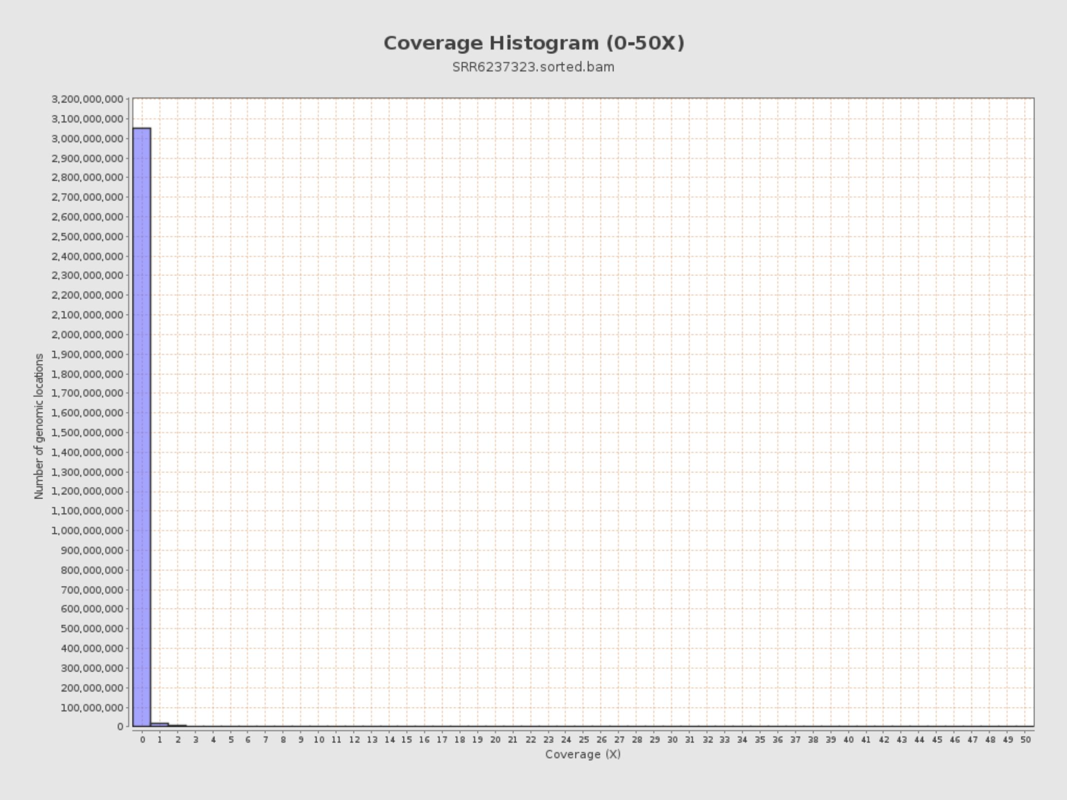
3. Results : Coverage across reference



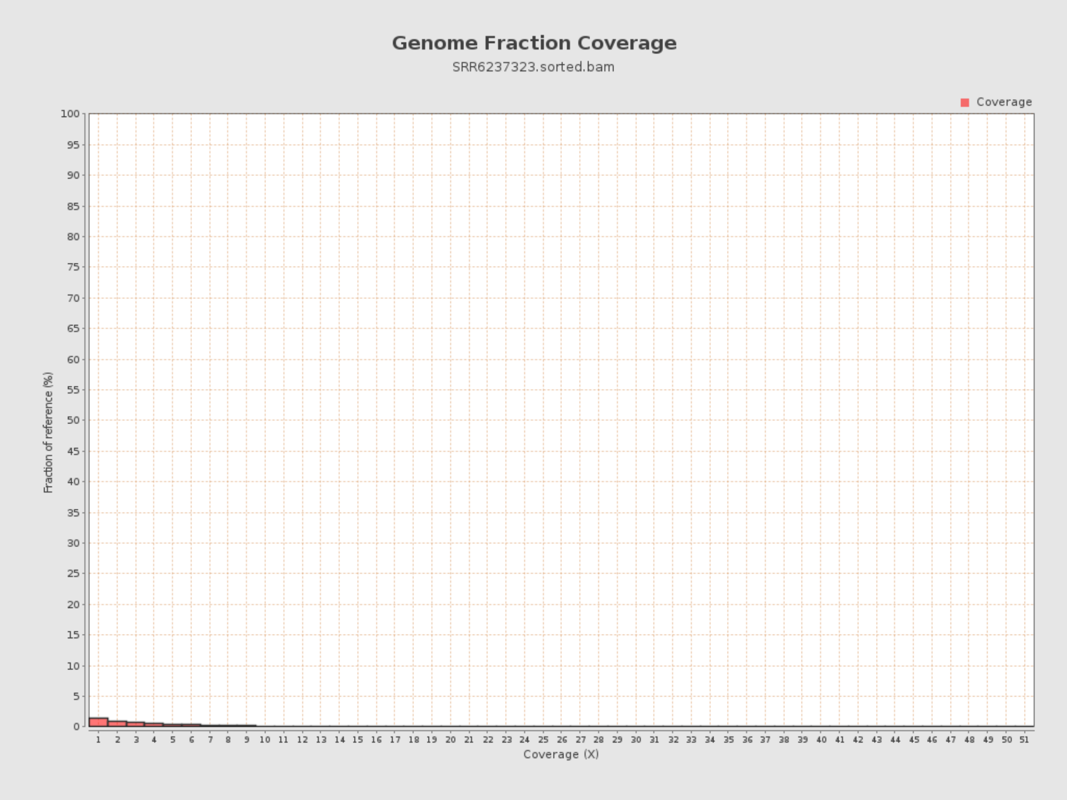
4. Results : Coverage Histogram



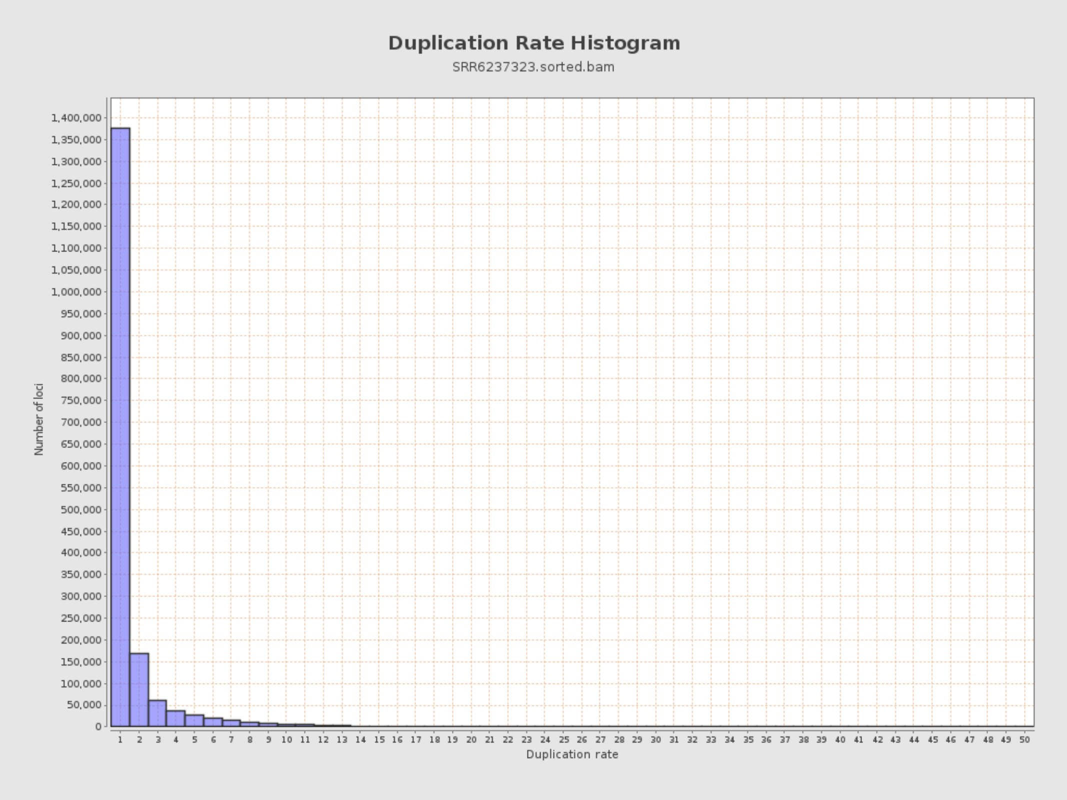
5. Results : Coverage Histogram (0-50X)



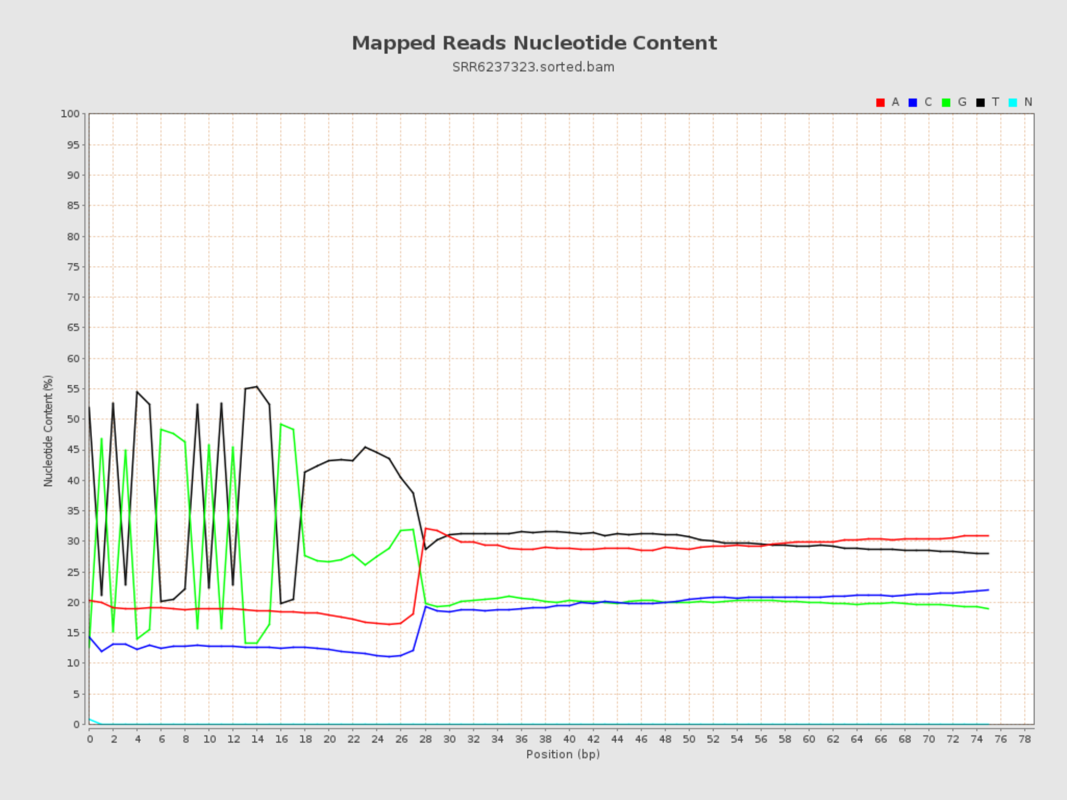
6. Results : Genome Fraction Coverage



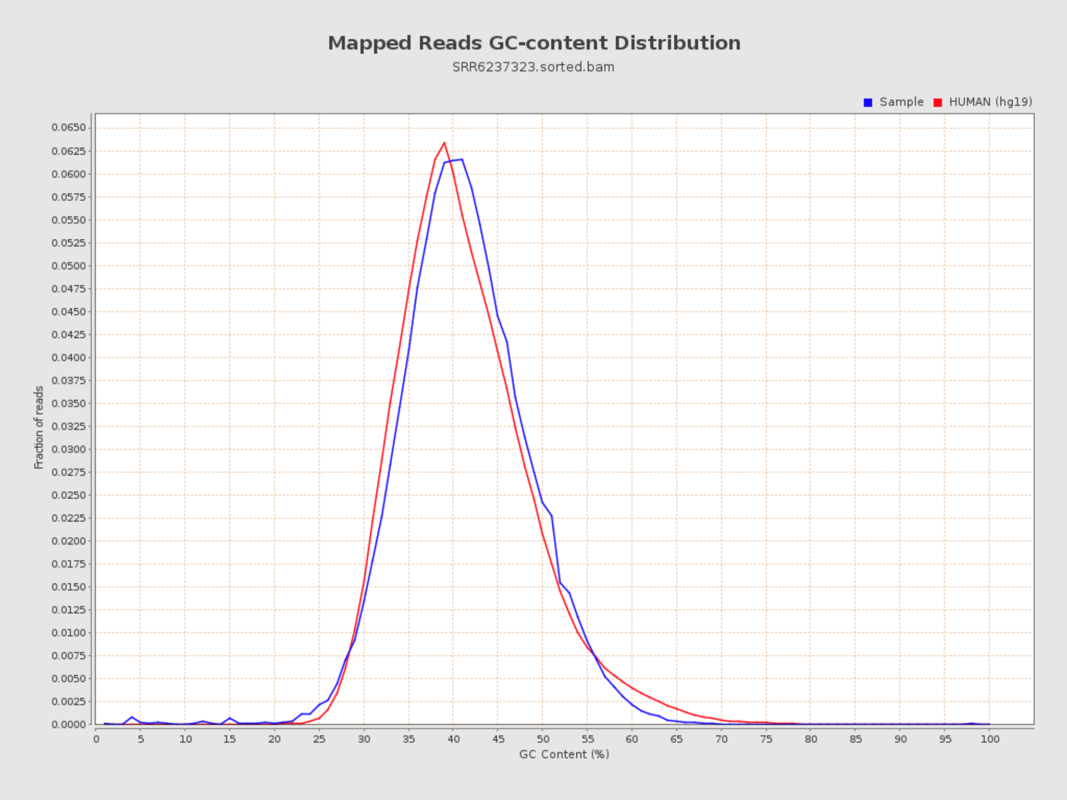
7. Results : Duplication Rate Histogram



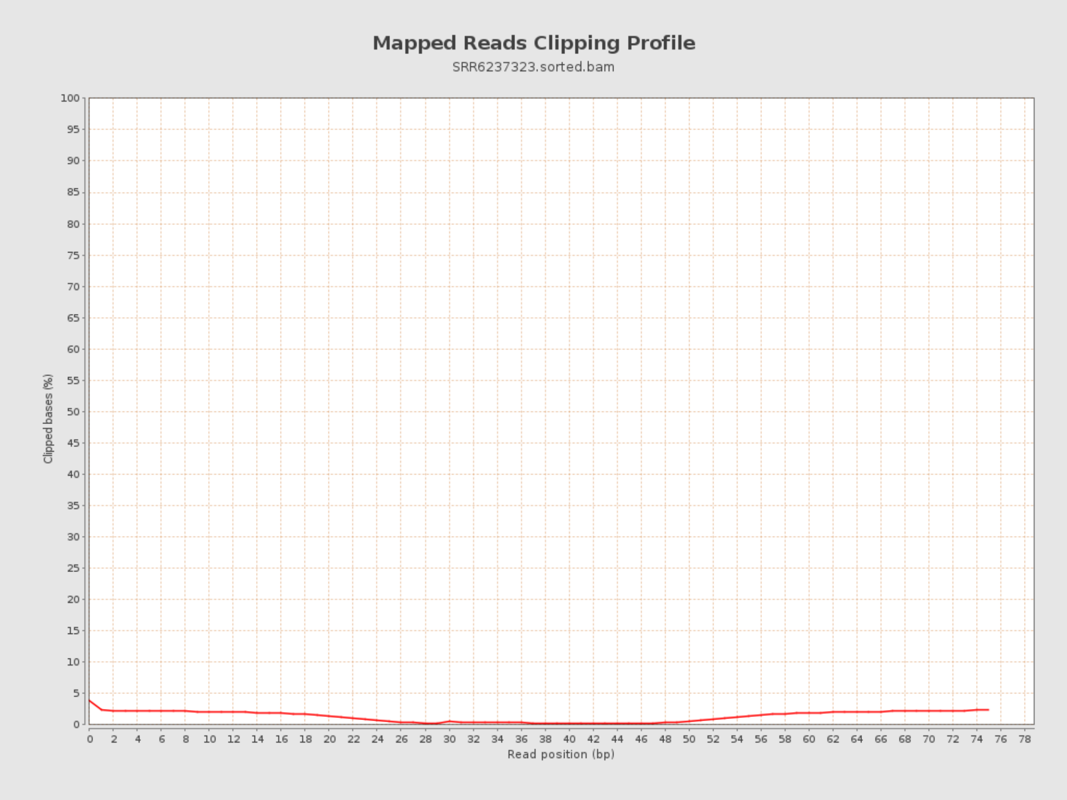
8. Results : Mapped Reads Nucleotide Content



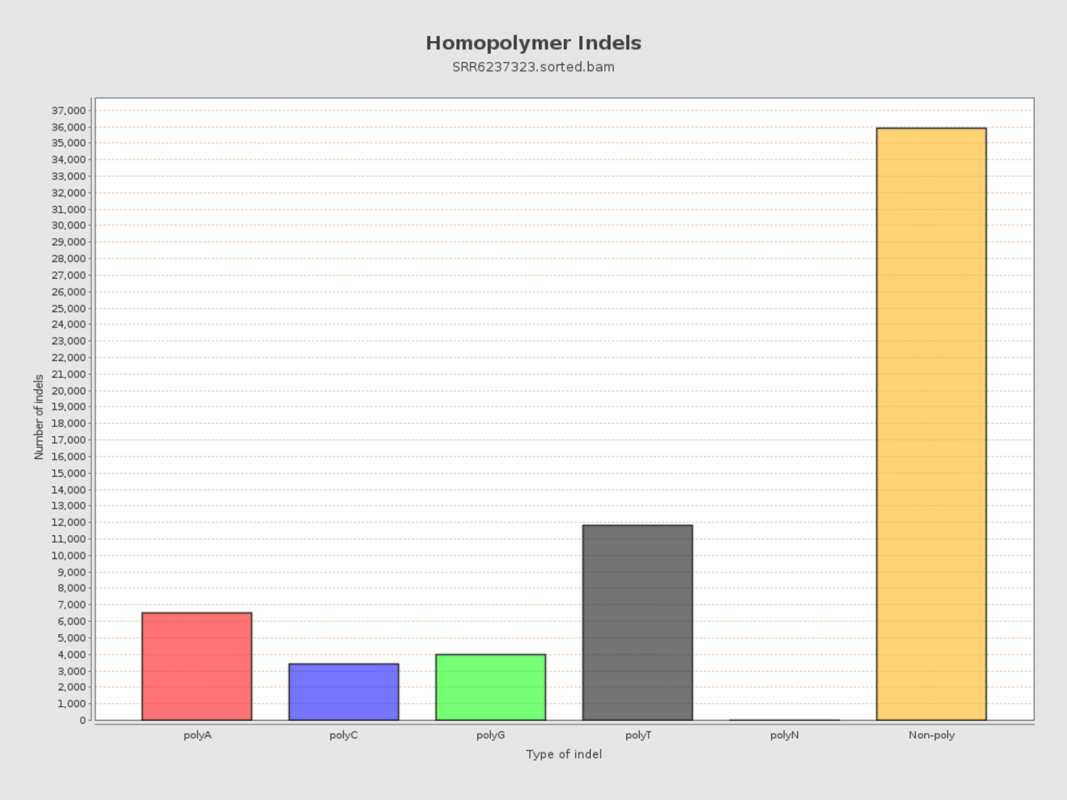
9. Results : Mapped Reads GC-content Distribution



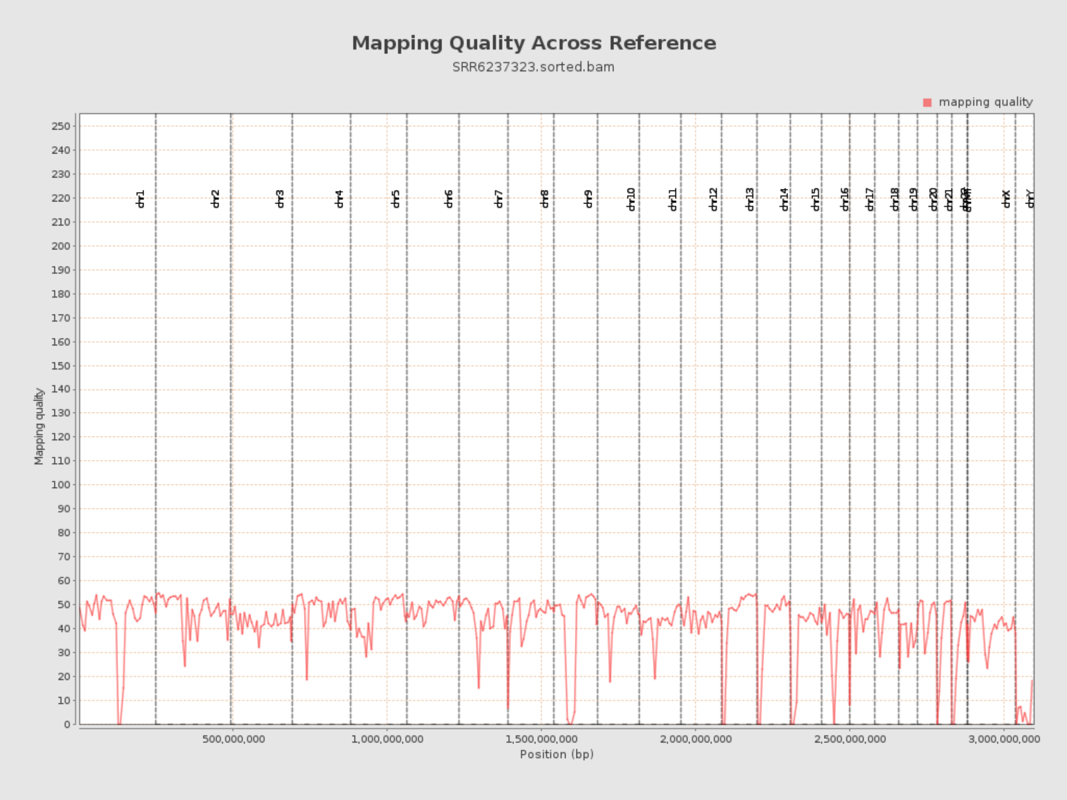
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram