Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:13:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237284.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_SRR6237284 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237284.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:13:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237284.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,051,564
Mapped reads	2,819,897 / 92.41%
Unmapped reads	231,667 / 7.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,812 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	1,242,921 / 40.73%
Duplication rate	22.89%
Clipped reads	1,850,075 / 60.63%

2.2. ACGT Content

Number/percentage of A's	44,284,834 / 25.47%
Number/percentage of C's	29,784,842 / 17.13%
Number/percentage of T's	58,331,959 / 33.55%
Number/percentage of G's	41,462,169 / 23.85%
Number/percentage of N's	17,913 / 0.01%
GC Percentage	40.97%

2.3. Coverage

Mean	0.0562

Standard Deviation	0.8878

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

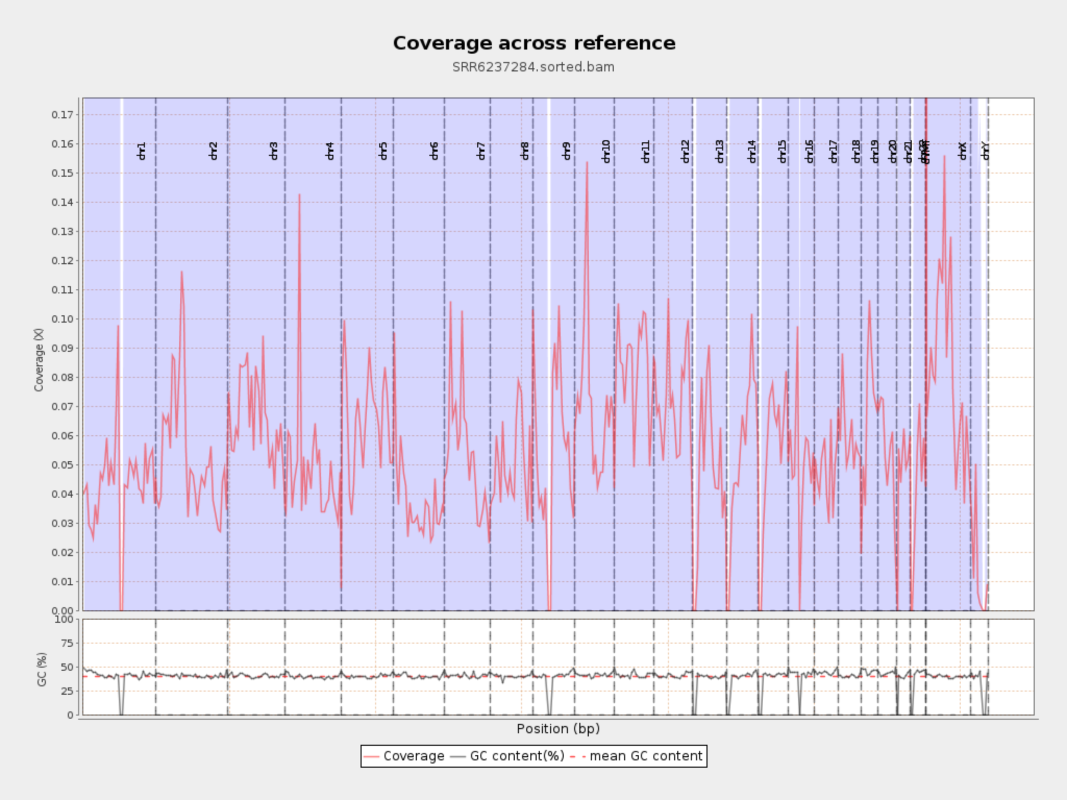
General error rate	0.63%
Mismatches	1,068,518
Insertions	14,041
Mapped reads with at least one insertion	0.49%
Deletions	51,145
Mapped reads with at least one deletion	1.79%
Homopolymer indels	43.09%

2.6. Chromosome stats

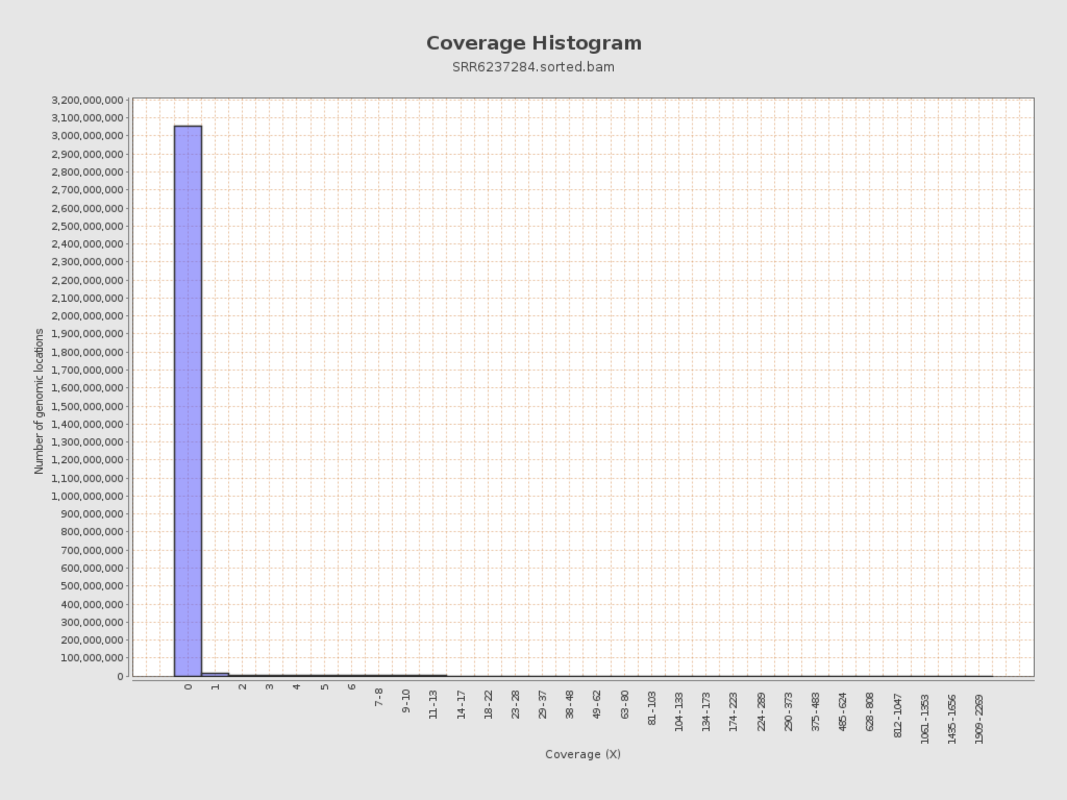
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10768409	0.0432	0.9658
chr2	243199373	12998061	0.0534	1.2866
chr3	198022430	13079185	0.066	0.7471
chr4	191154276	9352414	0.0489	0.7573
chr5	180915260	11917257	0.0659	0.7462
chr6	171115067	6336497	0.037	0.6354
chr7	159138663	8562041	0.0538	0.8776

chr8	146364022	7288626	0.0498	1.1451
chr9	141213431	7466646	0.0529	0.7927
chr10	135534747	9518347	0.0702	1.0534
chr11	135006516	11281679	0.0836	0.9751
chr12	133851895	9738002	0.0728	0.8021
chr13	115169878	5538141	0.0481	0.6467
chr14	107349540	5893178	0.0549	0.7084
chr15	102531392	5470409	0.0534	0.6719
chr16	90354753	4504891	0.0499	0.6897
chr17	81195210	3824550	0.0471	0.6528
chr18	78077248	4699971	0.0602	1.4341
chr19	59128983	4146127	0.0701	0.9197
chr20	63025520	3451974	0.0548	0.7191
chr21	48129895	2327007	0.0483	0.711
chr22	51304566	2040956	0.0398	0.5726
chrMT	16571	111623	6.736	10.0066
chrX	155270560	12874749	0.0829	0.8652
chrY	59373566	780086	0.0131	0.5382

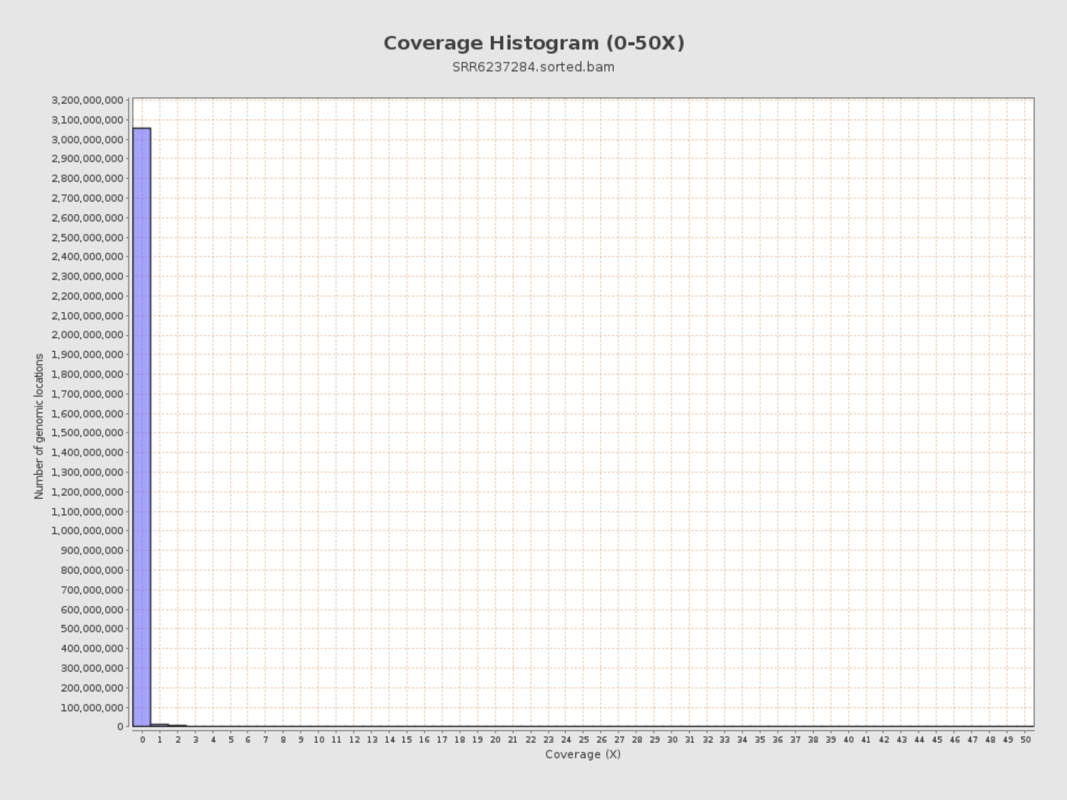
3. Results : Coverage across reference



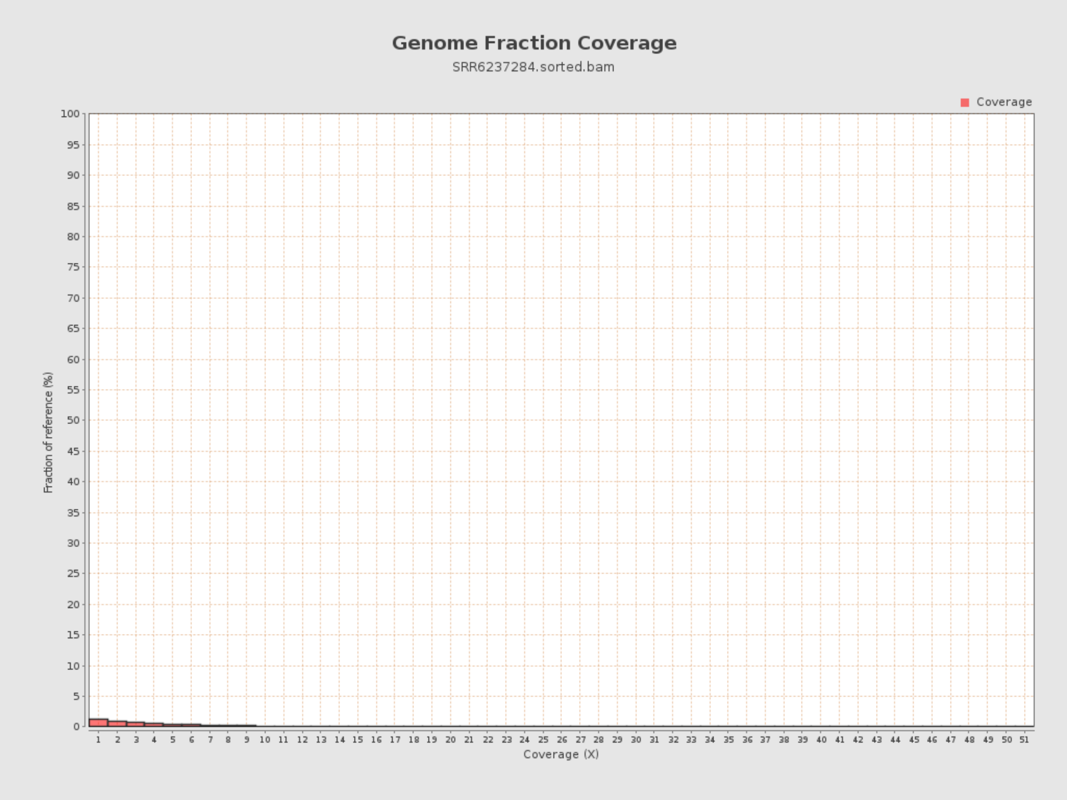
4. Results : Coverage Histogram



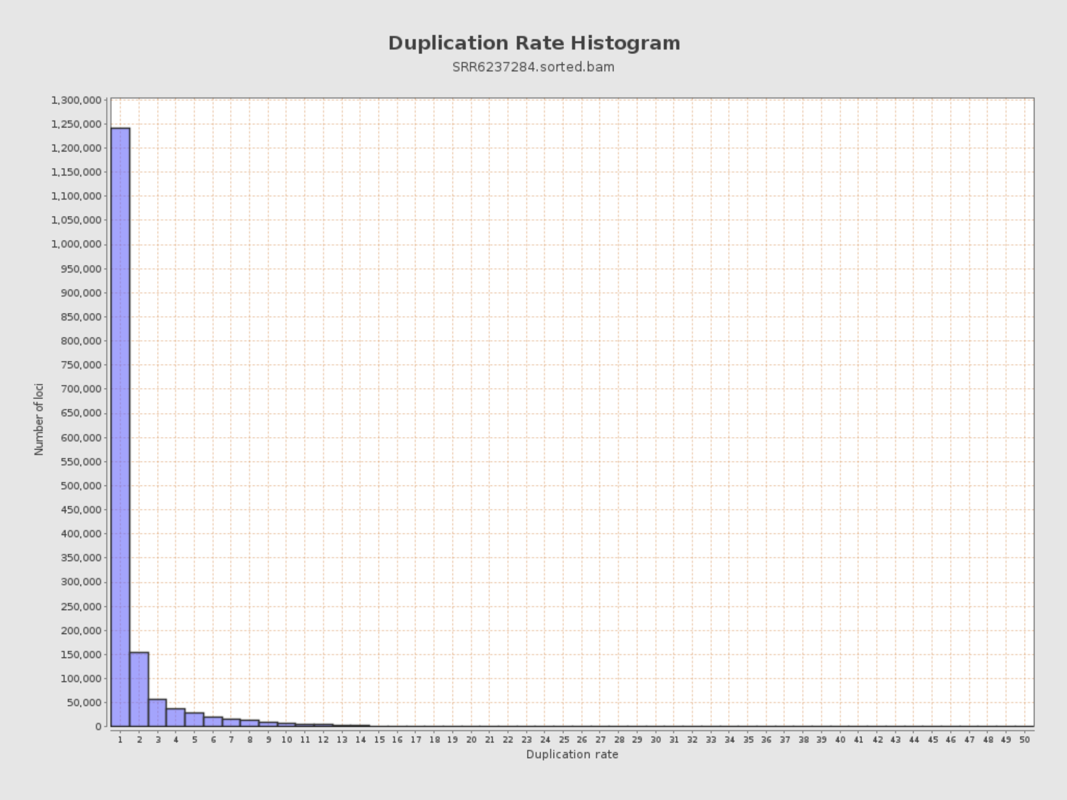
5. Results : Coverage Histogram (0-50X)



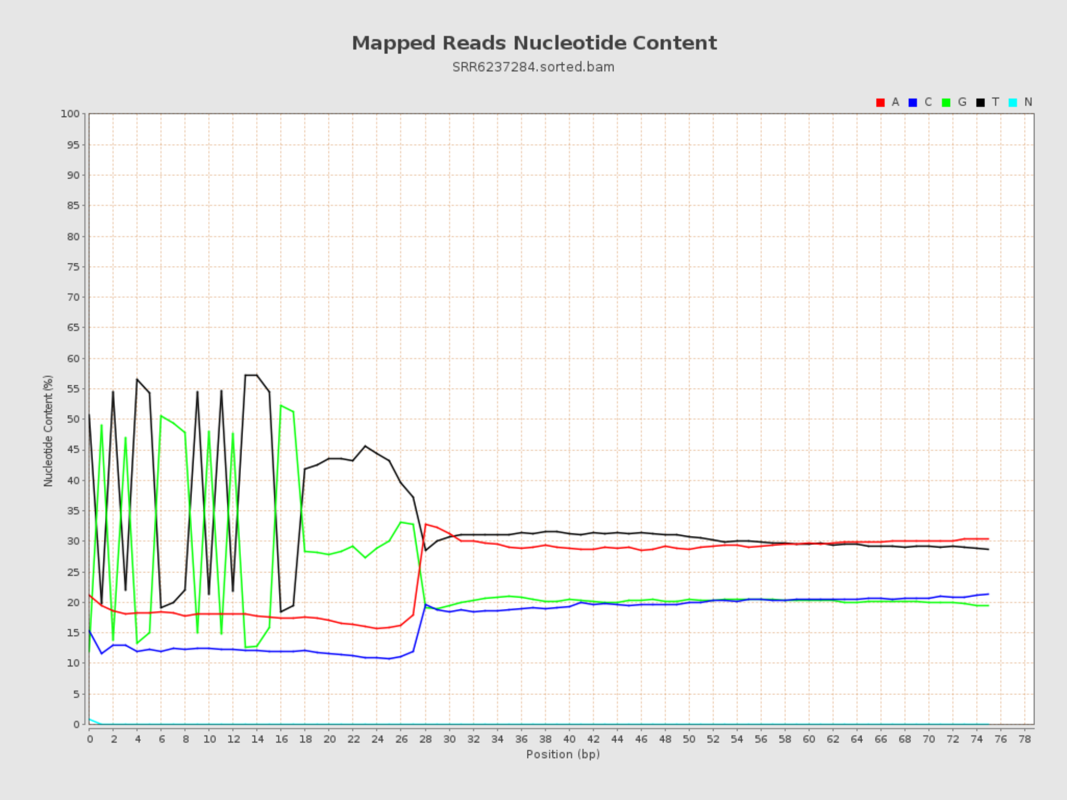
6. Results : Genome Fraction Coverage



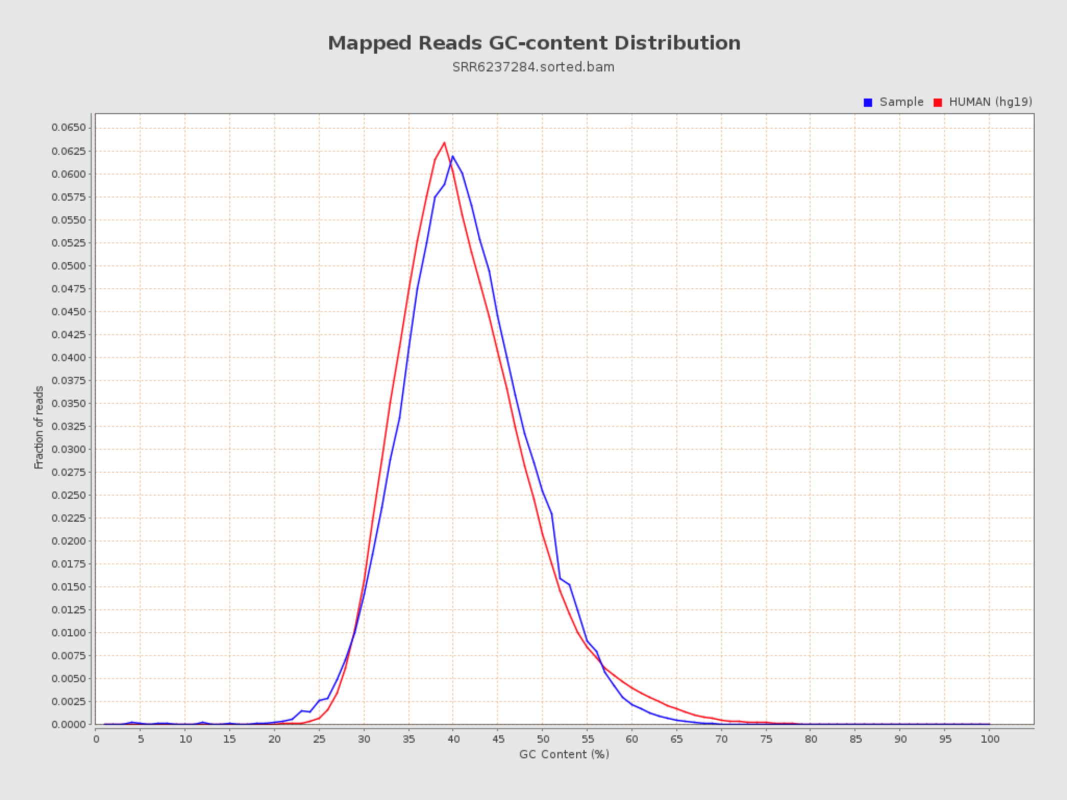
7. Results : Duplication Rate Histogram



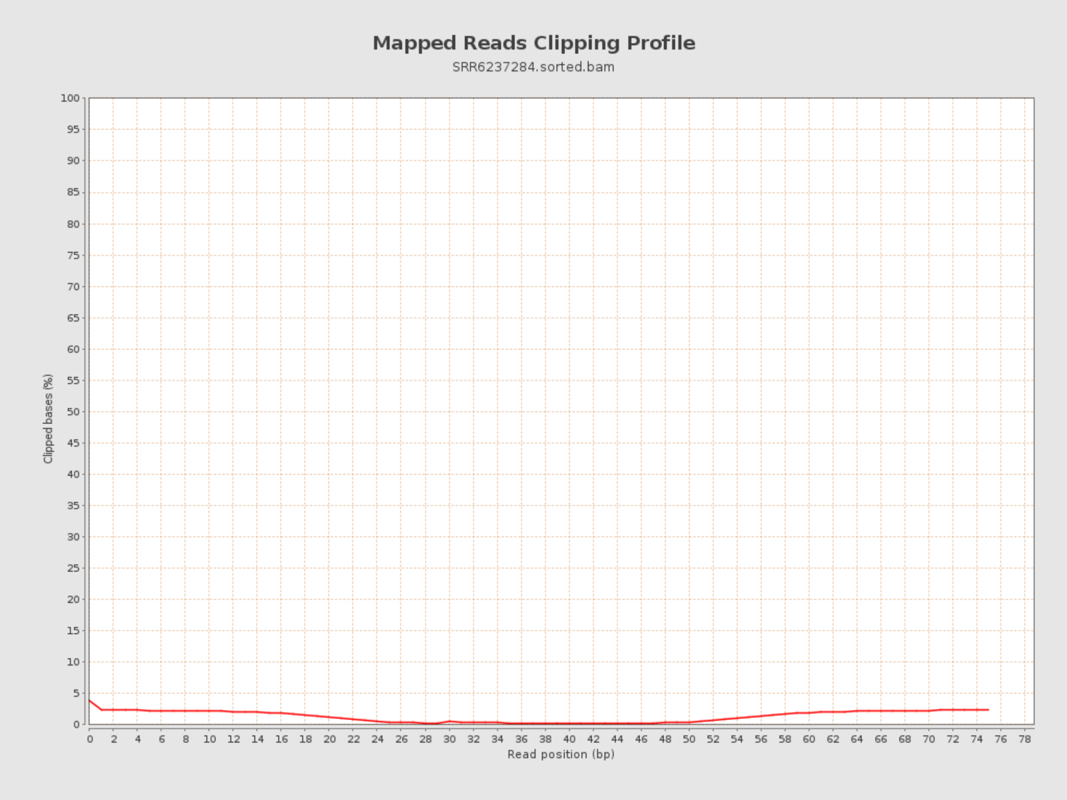
8. Results : Mapped Reads Nucleotide Content



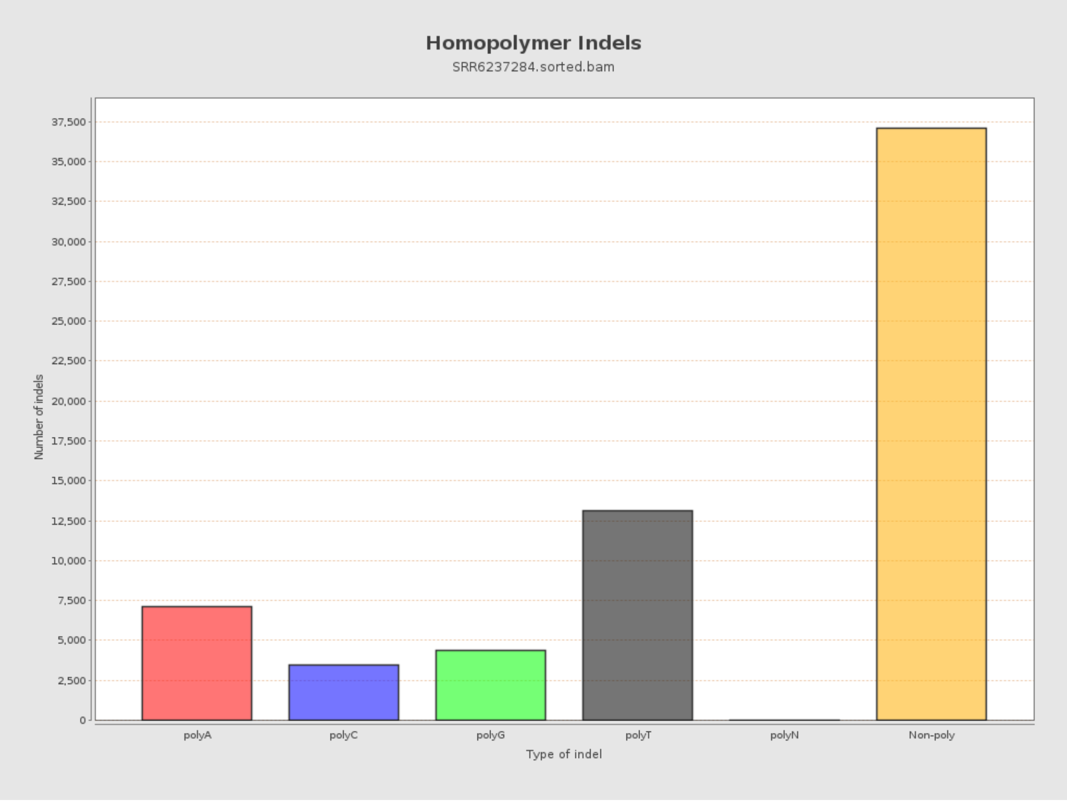
9. Results : Mapped Reads GC-content Distribution



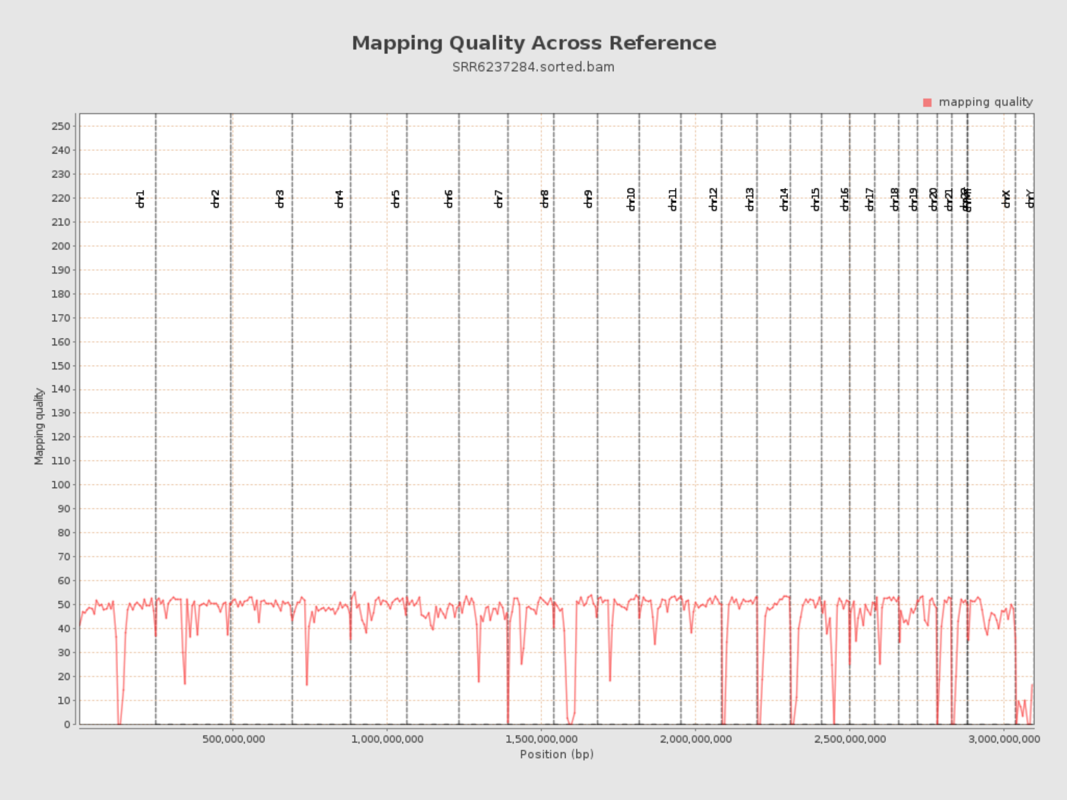
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram