Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:17:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230393.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_SRR6230393 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230393.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:17:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230393.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,726,226
Mapped reads	2,374,368 / 87.09%
Unmapped reads	351,858 / 12.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,376 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	151,594 / 5.56%
Duplication rate	5.12%
Clipped reads	1,334,022 / 48.93%

2.2. ACGT Content

Number/percentage of A's	41,517,352 / 27.41%
Number/percentage of C's	26,976,632 / 17.81%
Number/percentage of T's	48,695,853 / 32.15%
Number/percentage of G's	34,213,623 / 22.59%
Number/percentage of N's	67,807 / 0.04%
GC Percentage	40.4%

2.3. Coverage

Mean	0.0489

Standard Deviation	0.4343

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

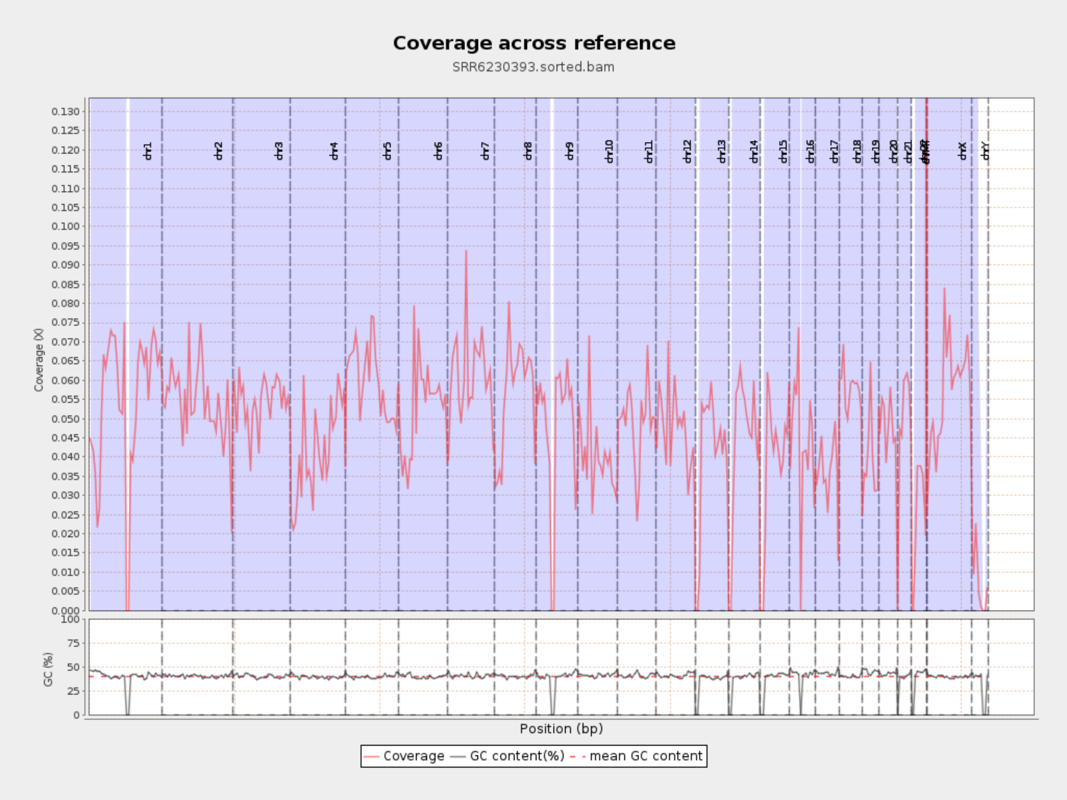
General error rate	0.88%
Mismatches	1,304,763
Insertions	11,744
Mapped reads with at least one insertion	0.49%
Deletions	37,899
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.4%

2.6. Chromosome stats

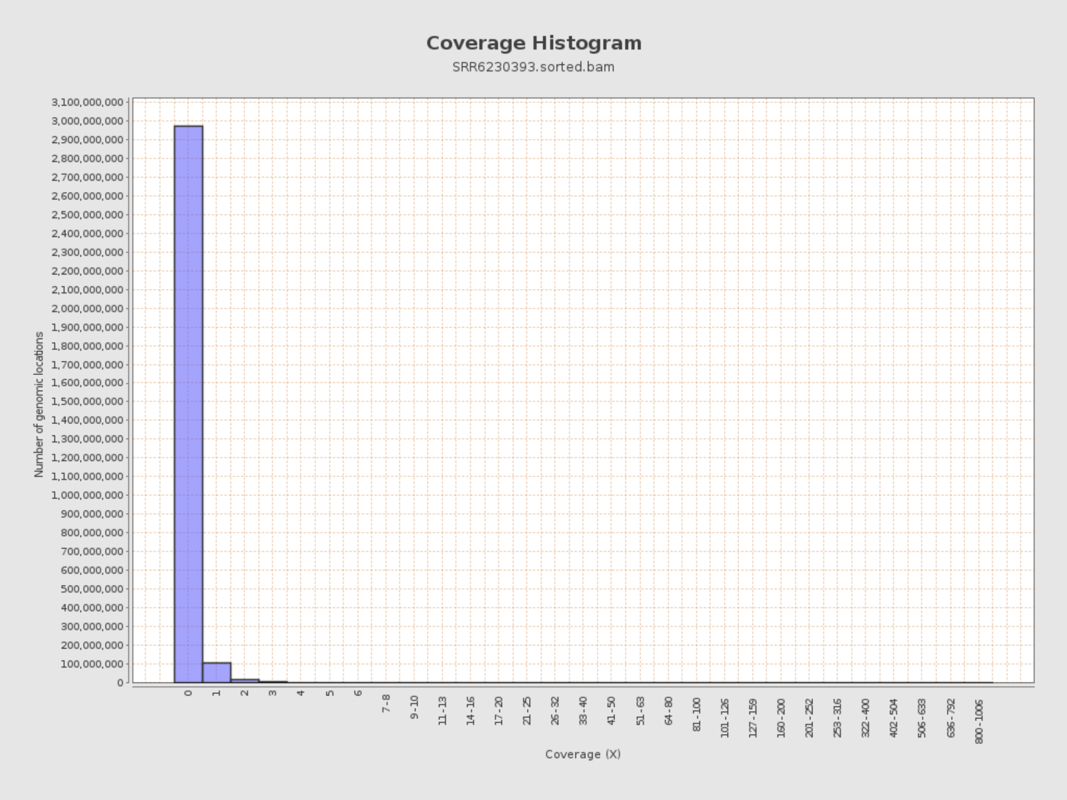
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13602676	0.0546	0.8115
chr2	243199373	13243202	0.0545	0.4947
chr3	198022430	10770056	0.0544	0.2759
chr4	191154276	7948990	0.0416	0.2652
chr5	180915260	10871484	0.0601	0.2907
chr6	171115067	9074749	0.053	0.3454
chr7	159138663	9853340	0.0619	0.6102

chr8	146364022	8269908	0.0565	0.5186
chr9	141213431	6714062	0.0475	0.4162
chr10	135534747	5456314	0.0403	0.3779
chr11	135006516	6568240	0.0487	0.3634
chr12	133851895	6332048	0.0473	0.2662
chr13	115169878	4625564	0.0402	0.2358
chr14	107349540	4731185	0.0441	0.2708
chr15	102531392	3908991	0.0381	0.2397
chr16	90354753	3975634	0.044	0.2914
chr17	81195210	2902034	0.0357	0.2492
chr18	78077248	4553643	0.0583	0.768
chr19	59128983	2362489	0.04	0.5672
chr20	63025520	2984352	0.0474	0.2753
chr21	48129895	2333594	0.0485	0.2833
chr22	51304566	1228447	0.0239	0.1818
chrMT	16571	11108	0.6703	0.9617
chrX	155270560	8802276	0.0567	0.3218
chrY	59373566	409650	0.0069	0.1547

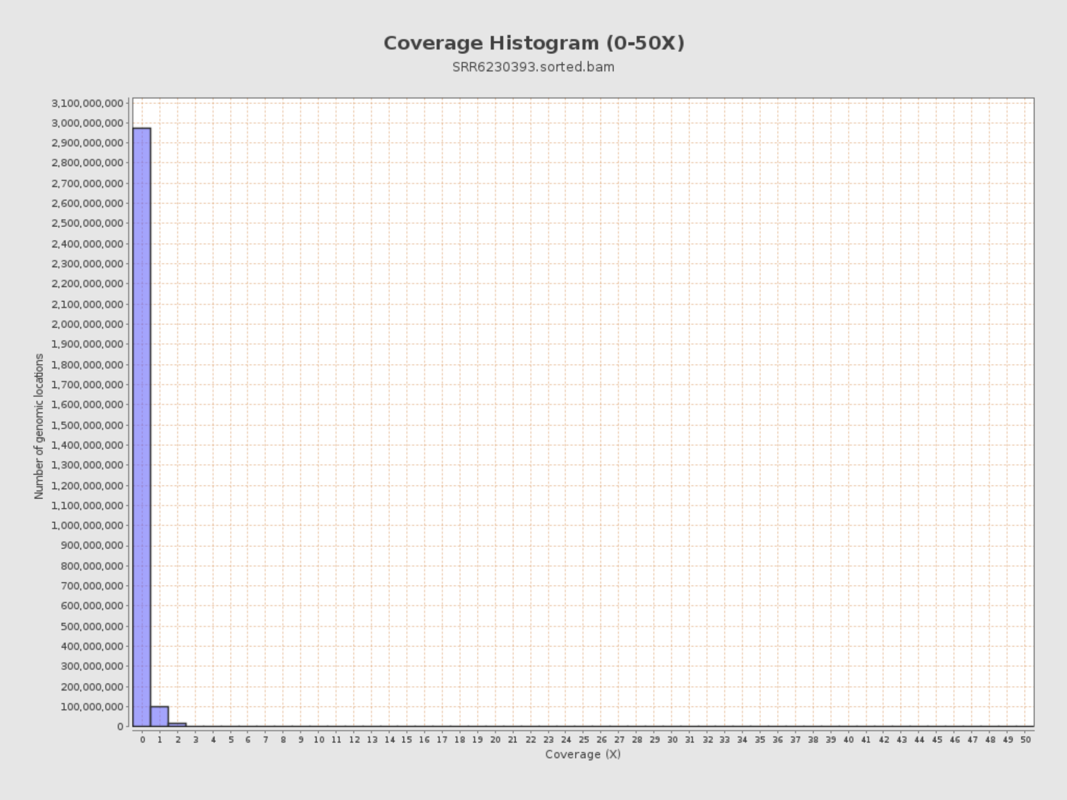
3. Results : Coverage across reference



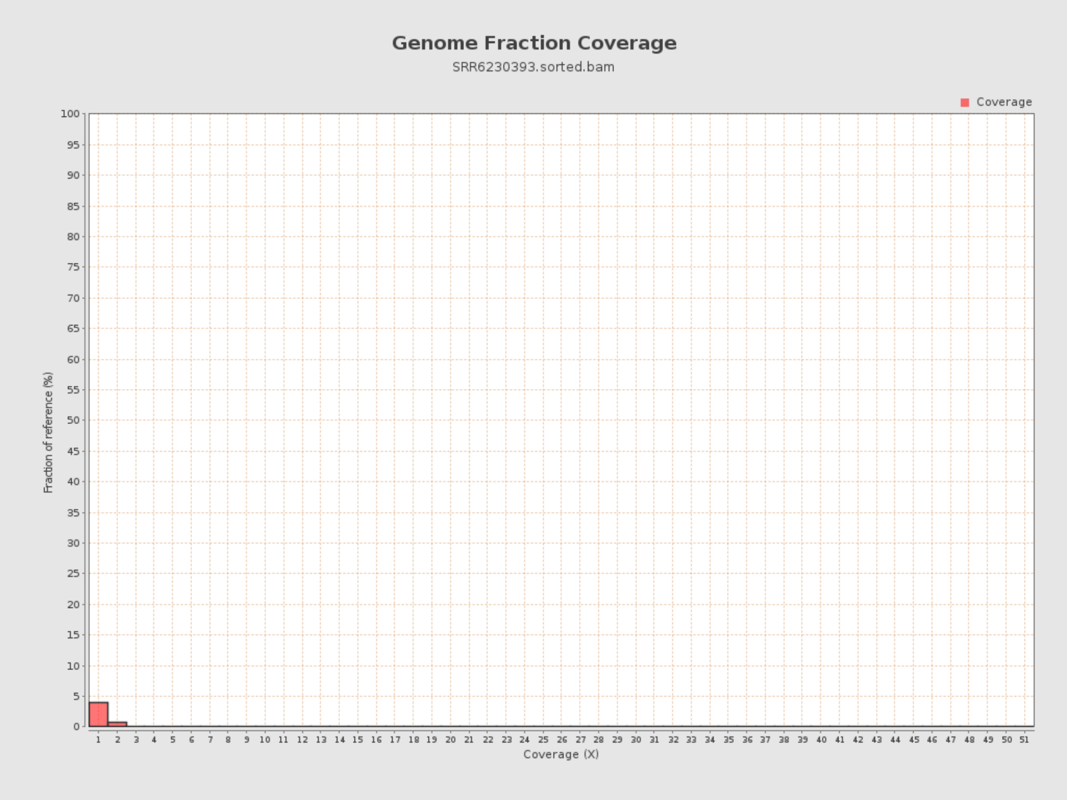
4. Results : Coverage Histogram



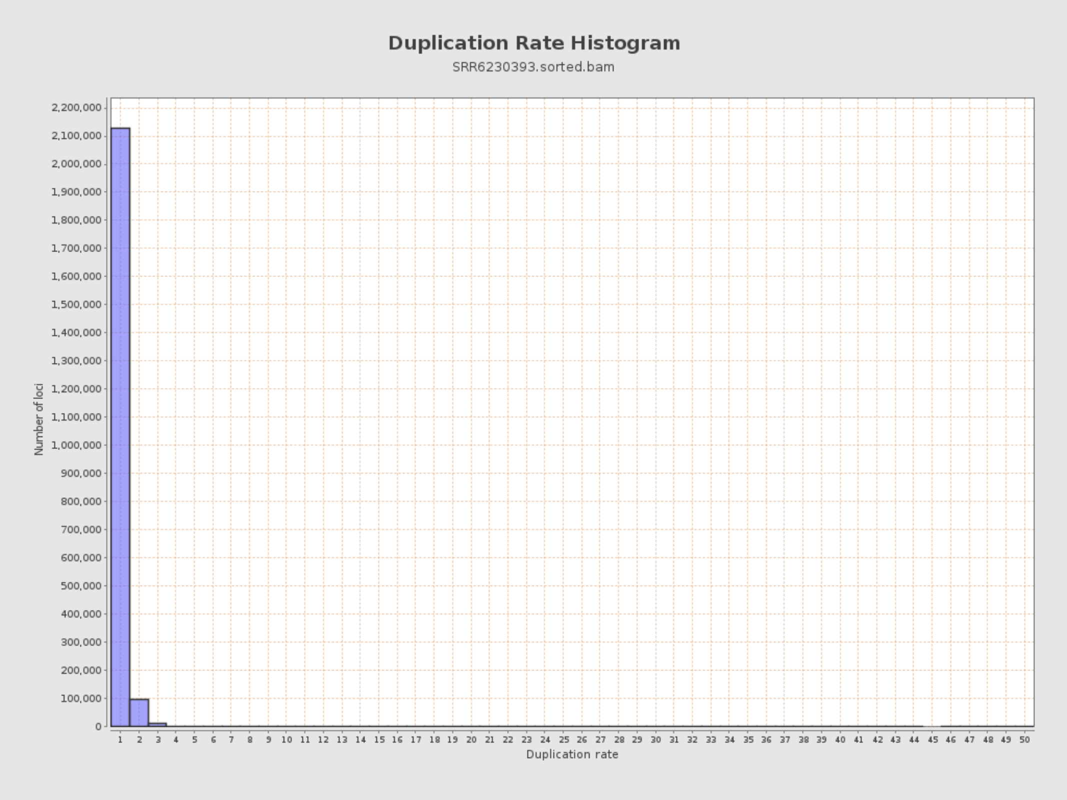
5. Results : Coverage Histogram (0-50X)



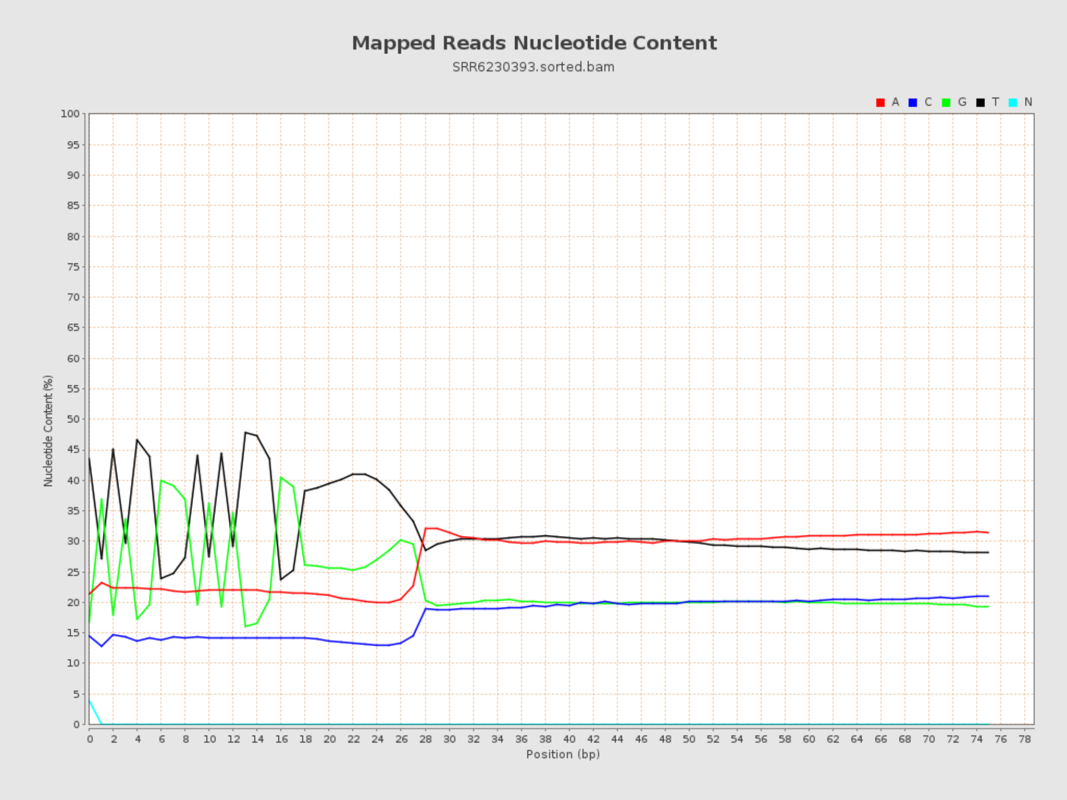
6. Results : Genome Fraction Coverage



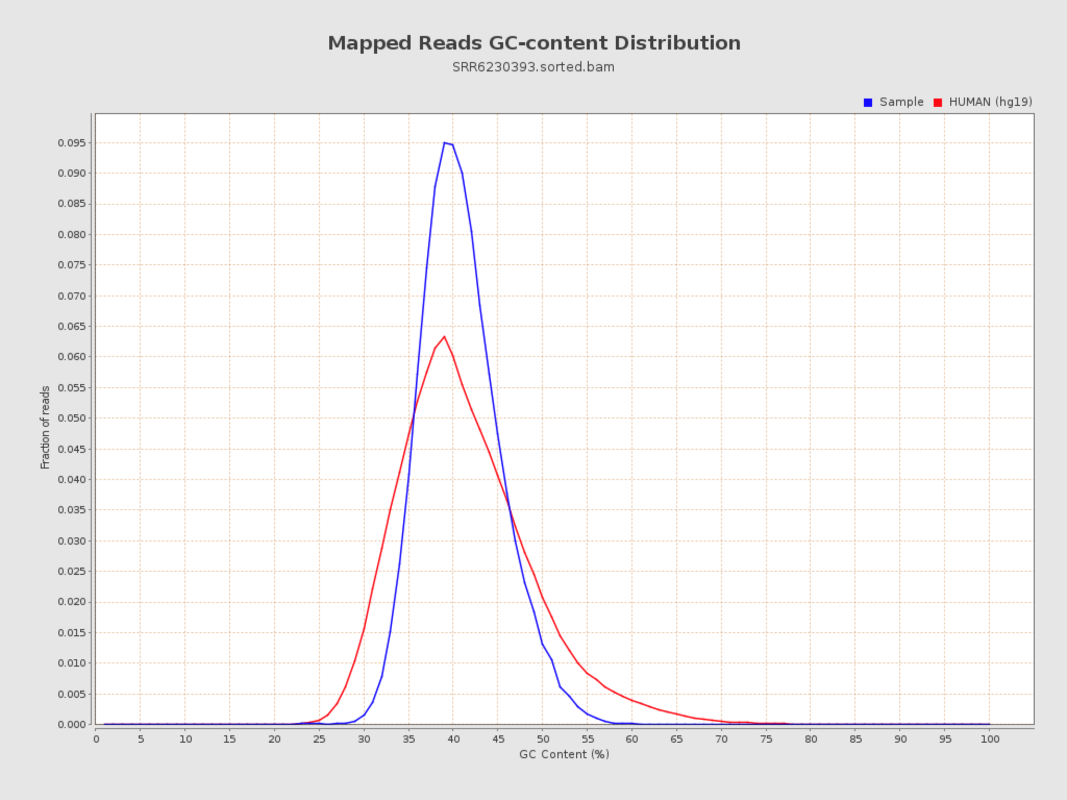
7. Results : Duplication Rate Histogram



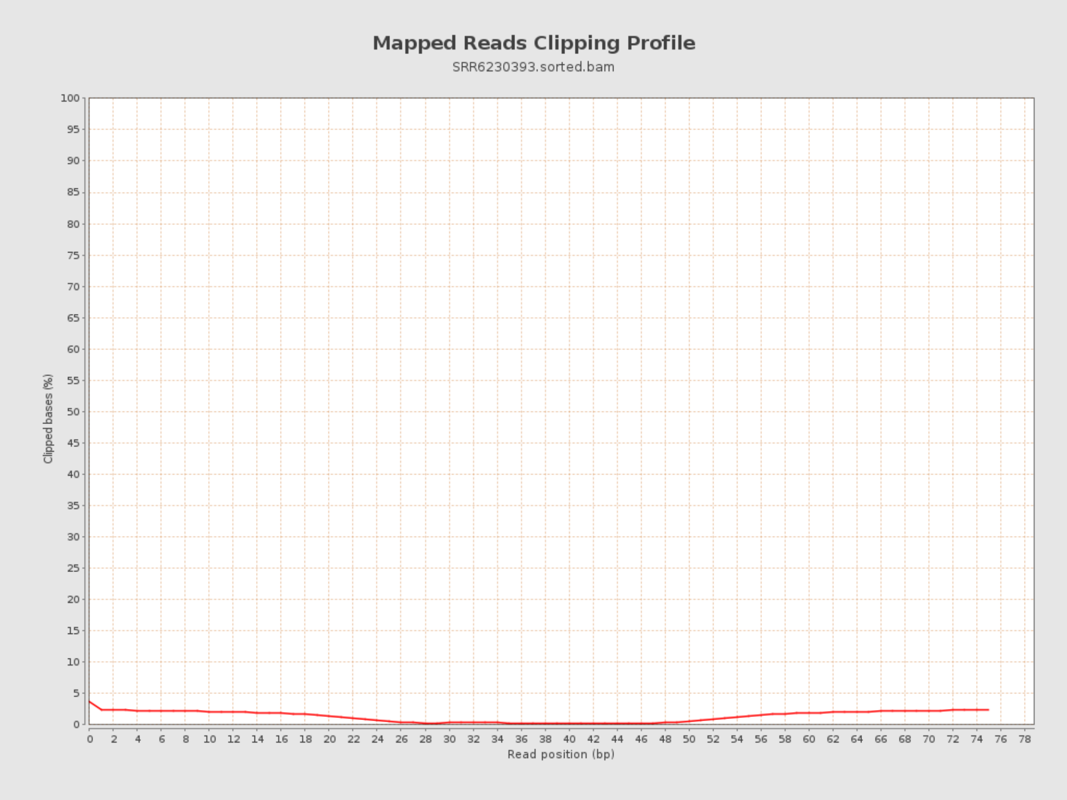
8. Results : Mapped Reads Nucleotide Content



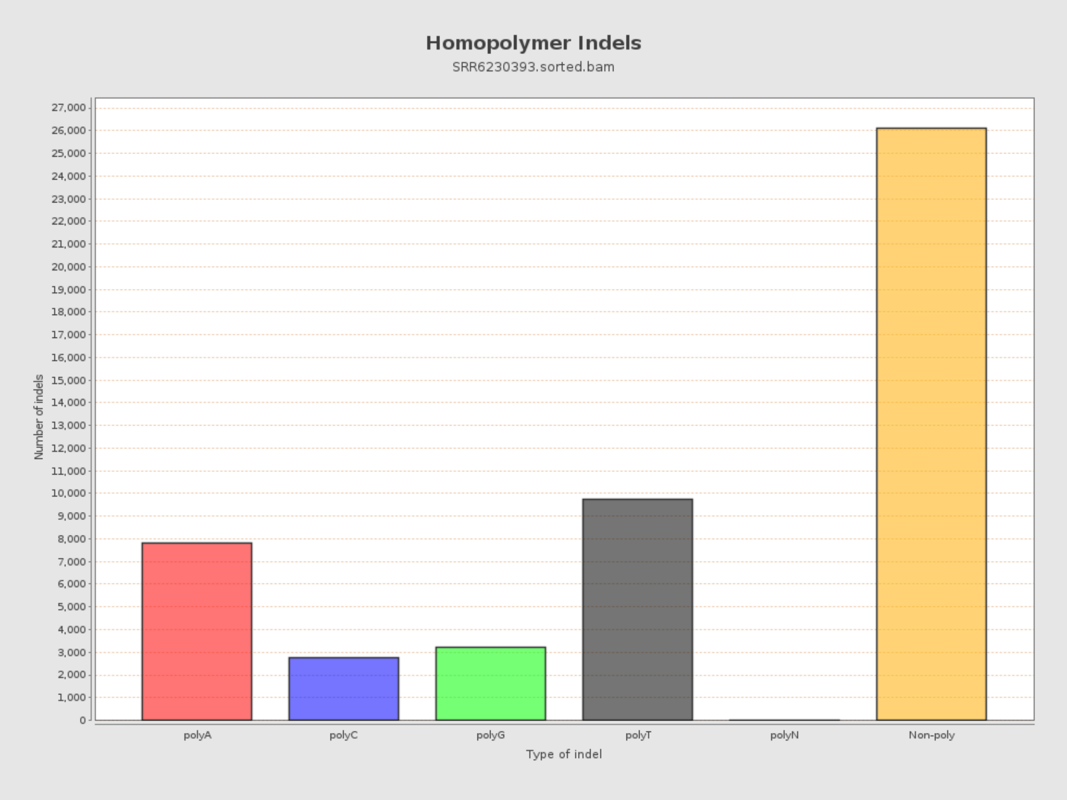
9. Results : Mapped Reads GC-content Distribution



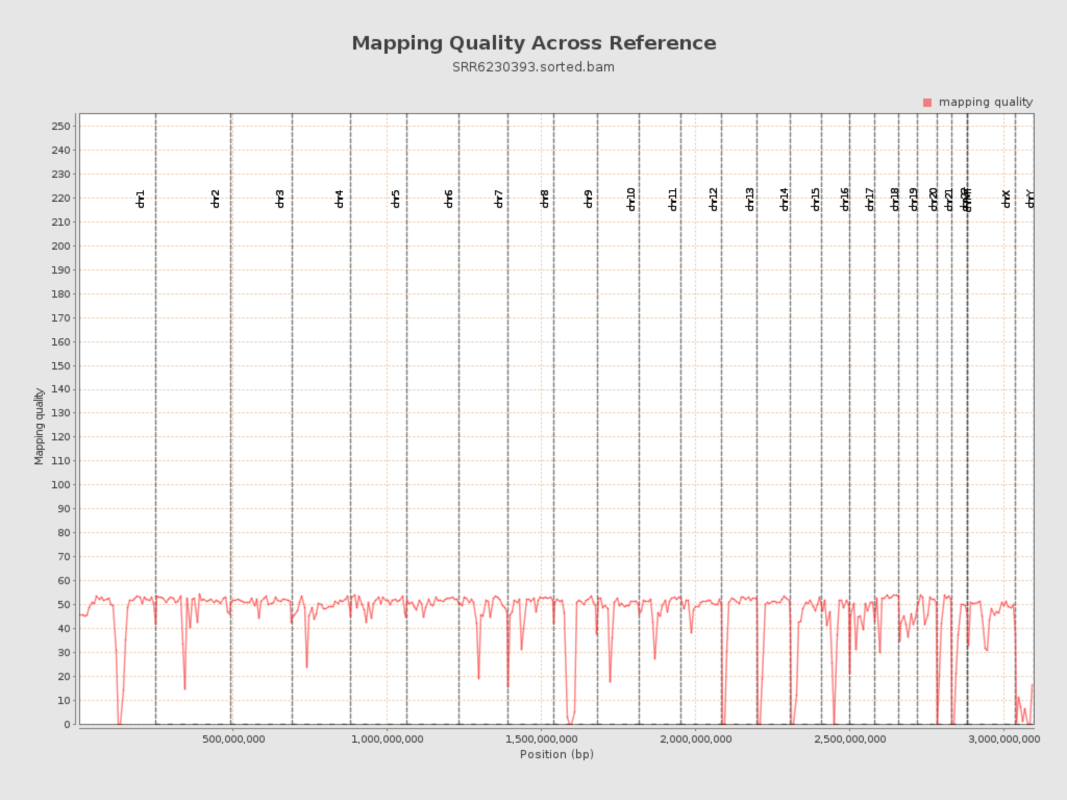
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram