Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 09:58:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231881.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_SRR6231881 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231881.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 09:58:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231881.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,724
Mapped reads	3,828 / 66.88%
Unmapped reads	1,896 / 33.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33 / 0.58%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	72 / 1.26%
Duplication rate	1.82%
Clipped reads	2,150 / 37.56%

2.2. ACGT Content

Number/percentage of A's	66,559 / 27.59%
Number/percentage of C's	39,987 / 16.57%
Number/percentage of T's	83,513 / 34.61%
Number/percentage of G's	51,209 / 21.22%
Number/percentage of N's	9 / 0%
GC Percentage	37.8%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.009

2.4. Mapping Quality

Mean Mapping Quality	42.44

2.5. Mismatches and indels

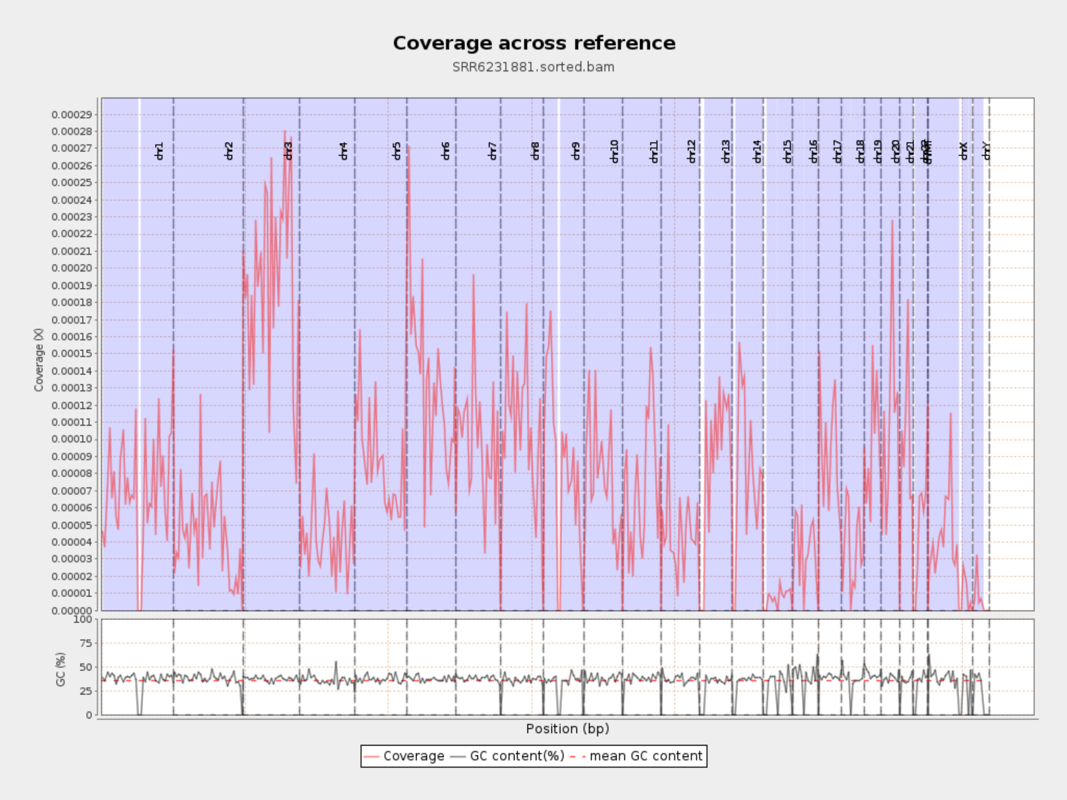
General error rate	1.23%
Mismatches	2,944
Insertions	19
Mapped reads with at least one insertion	0.47%
Deletions	71
Mapped reads with at least one deletion	1.83%
Homopolymer indels	50%

2.6. Chromosome stats

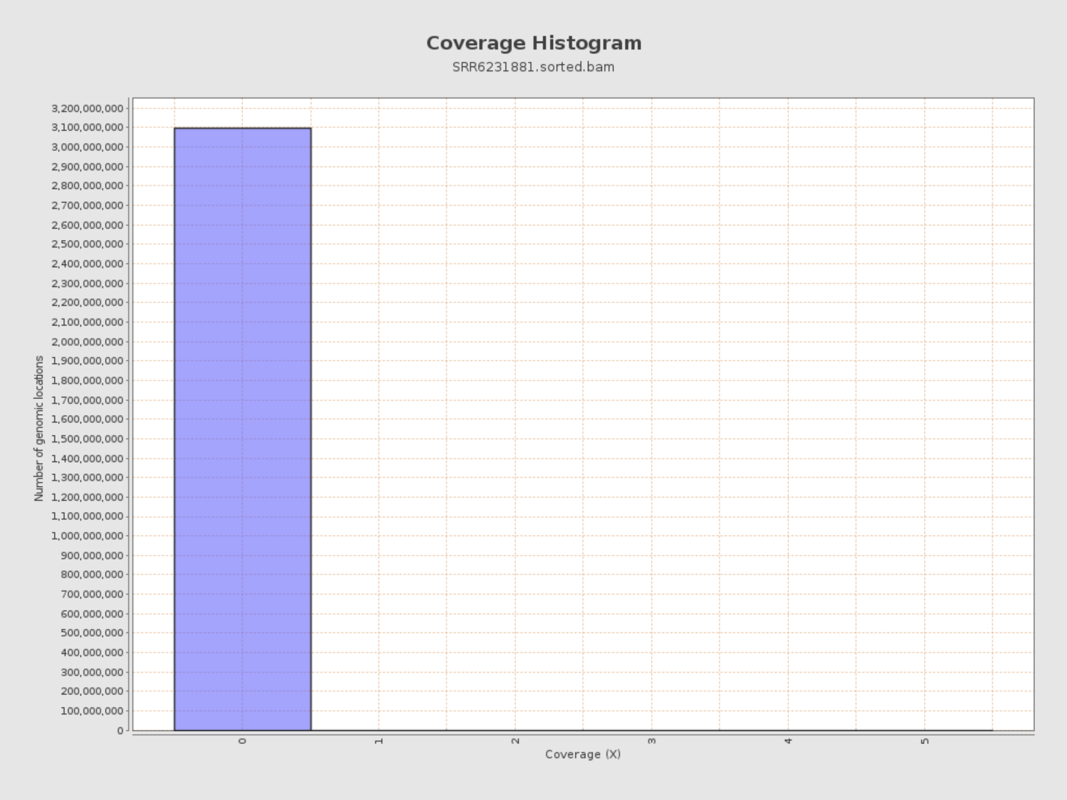
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17497	0.0001	0.0086
chr2	243199373	10876	0	0.0071
chr3	198022430	38657	0.0002	0.0141
chr4	191154276	7865	0	0.0064
chr5	180915260	15704	0.0001	0.0095
chr6	171115067	23107	0.0001	0.012
chr7	159138663	15633	0.0001	0.0101

chr8	146364022	15858	0.0001	0.0109
chr9	141213431	11837	0.0001	0.0093
chr10	135534747	10432	0.0001	0.0089
chr11	135006516	10062	0.0001	0.0089
chr12	133851895	6109	0	0.0069
chr13	115169878	9856	0.0001	0.0093
chr14	107349540	8394	0.0001	0.009
chr15	102531392	781	0	0.0028
chr16	90354753	3136	0	0.006
chr17	81195210	7561	0.0001	0.0097
chr18	78077248	2743	0	0.0064
chr19	59128983	5713	0.0001	0.0101
chr20	63025520	7037	0.0001	0.0107
chr21	48129895	4653	0.0001	0.01
chr22	51304566	2455	0	0.0071
chrMT	16571	0	0	0
chrX	155270560	5031	0	0.0058
chrY	59373566	395	0	0.0026

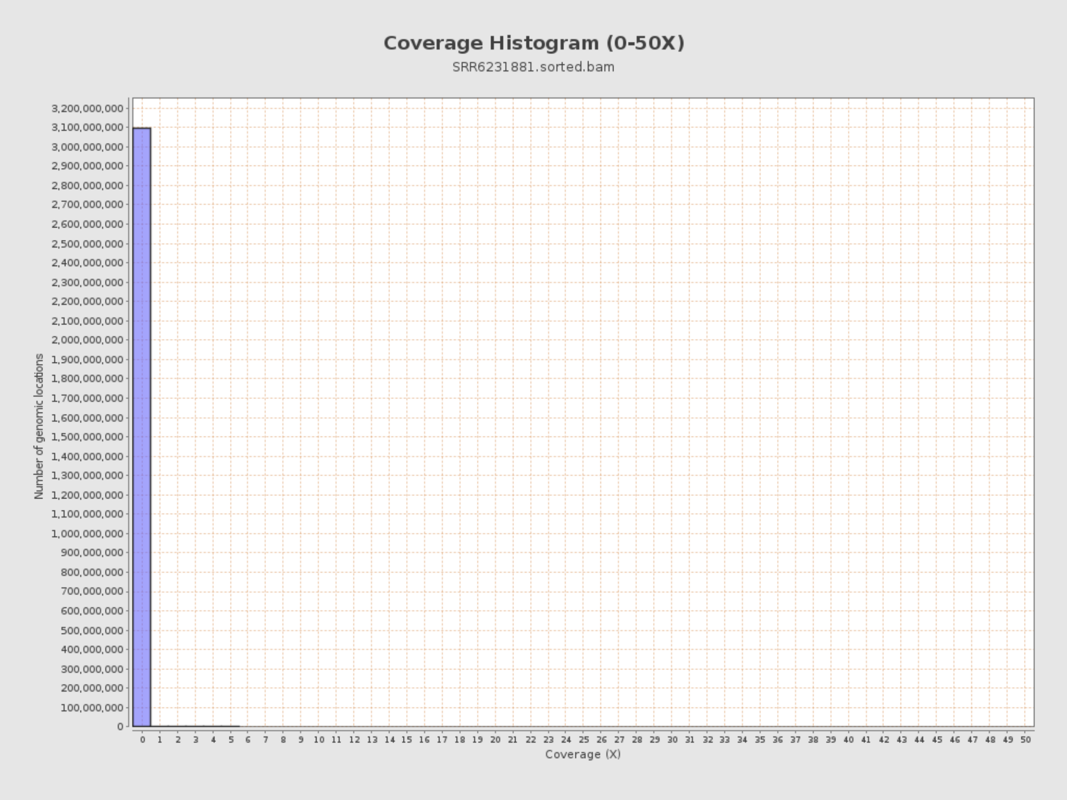
3. Results : Coverage across reference



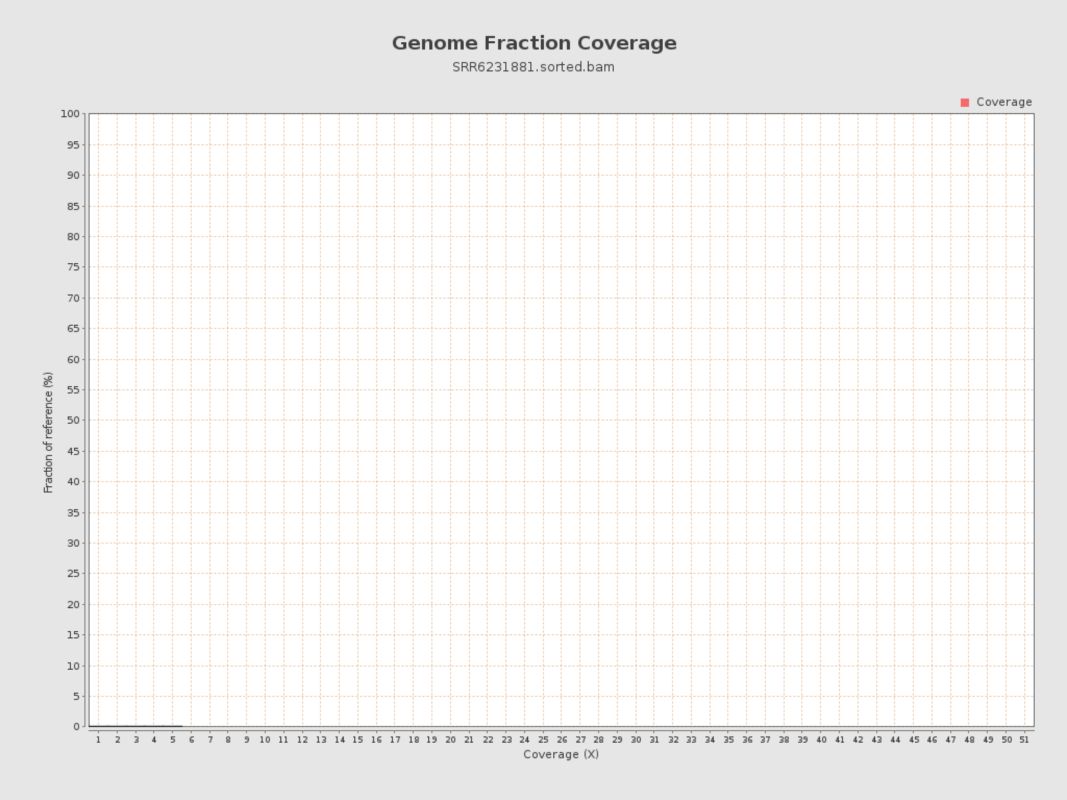
4. Results : Coverage Histogram



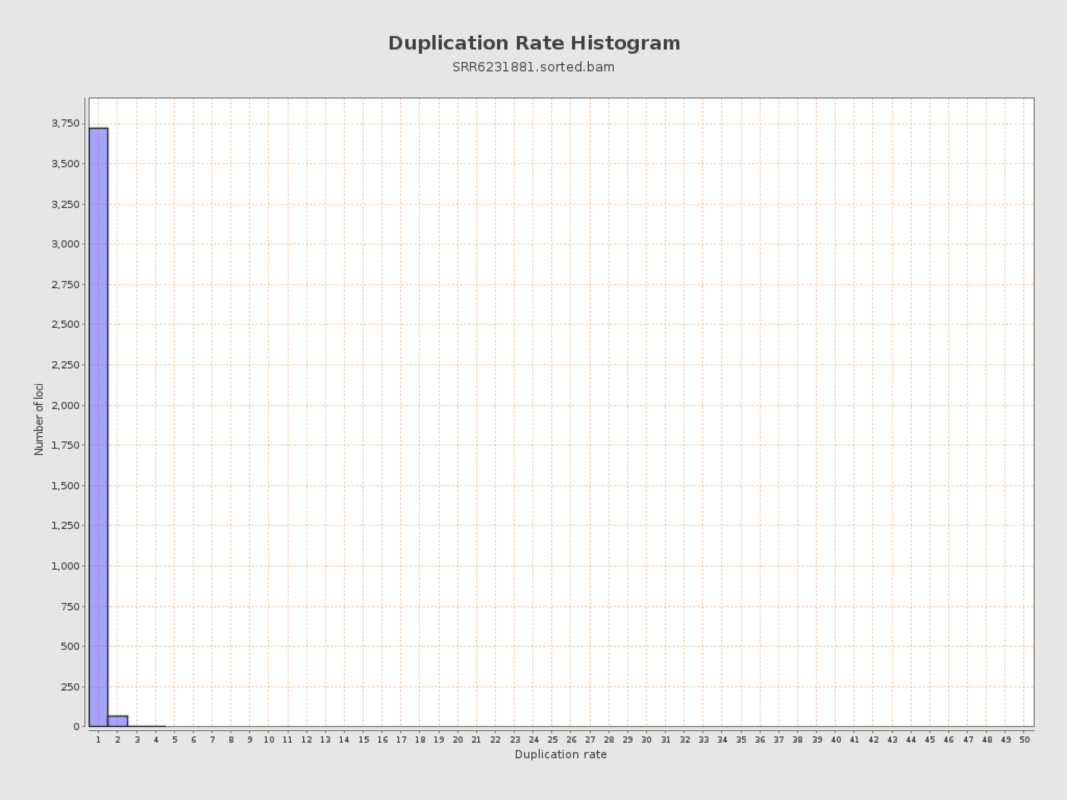
5. Results : Coverage Histogram (0-50X)



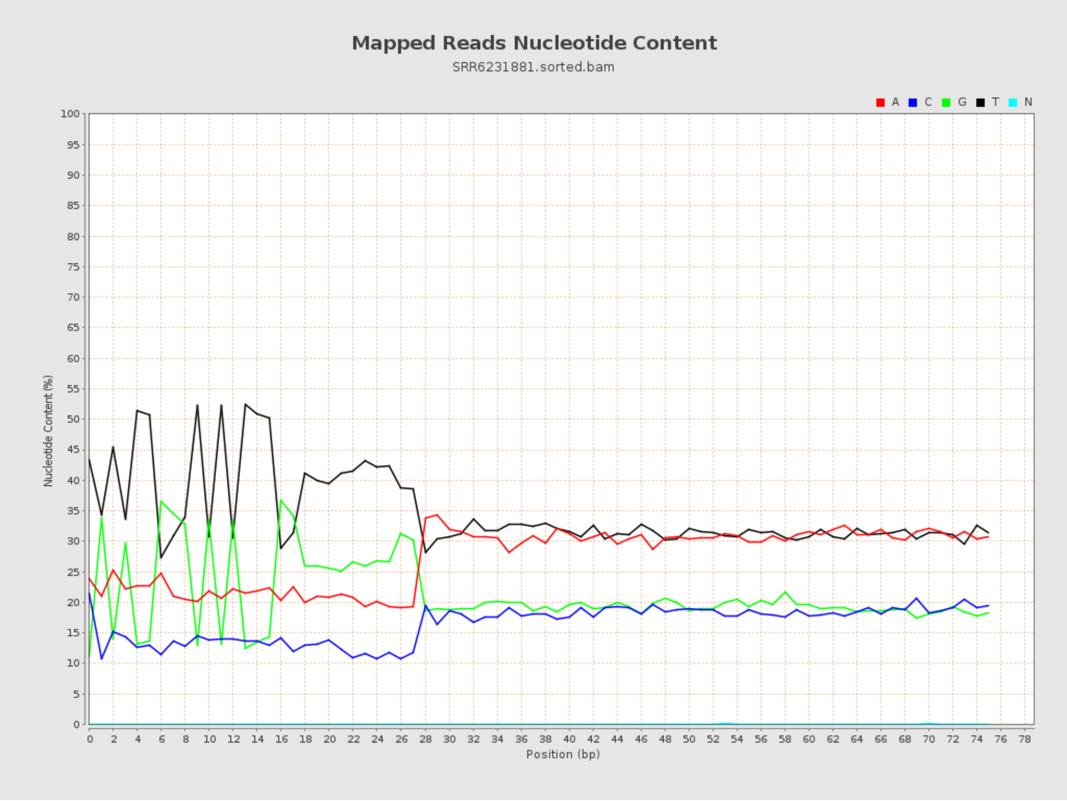
6. Results : Genome Fraction Coverage



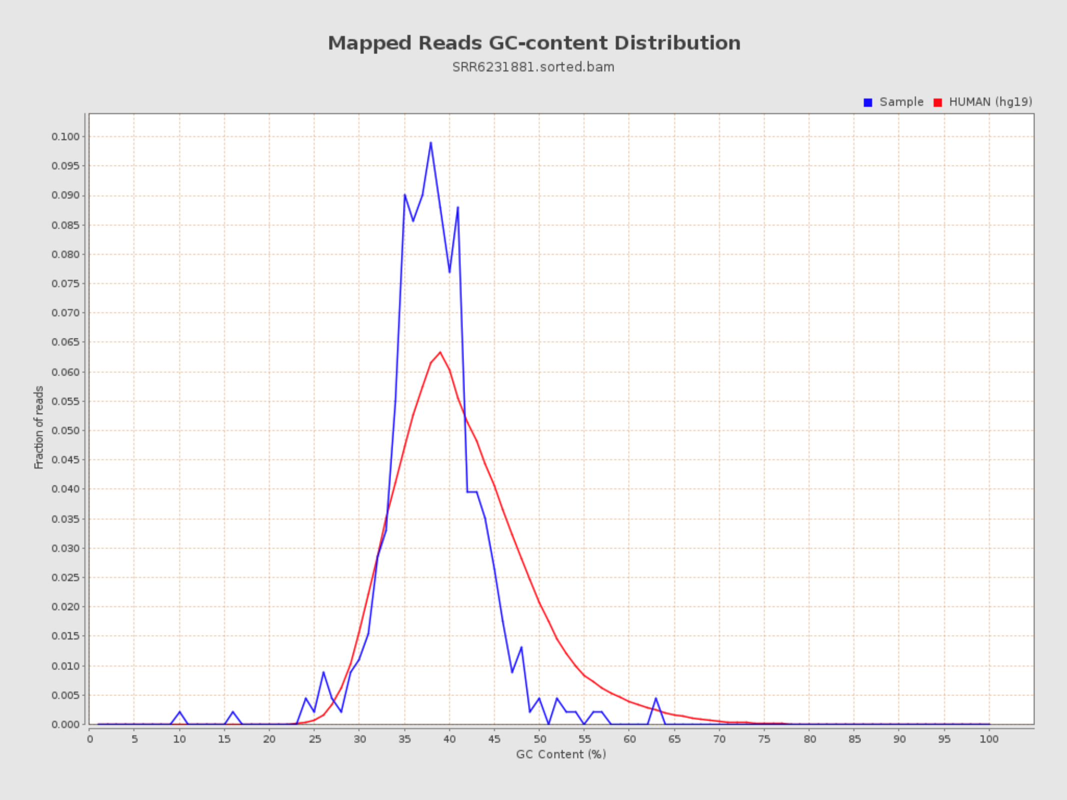
7. Results : Duplication Rate Histogram



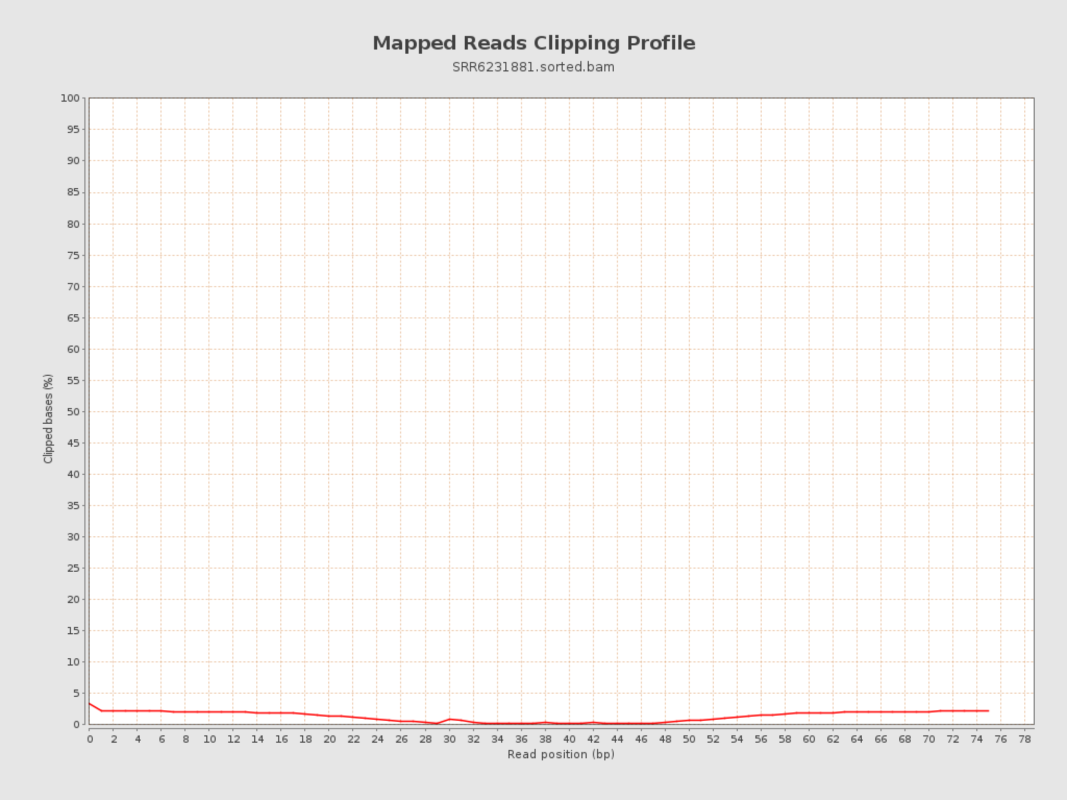
8. Results : Mapped Reads Nucleotide Content



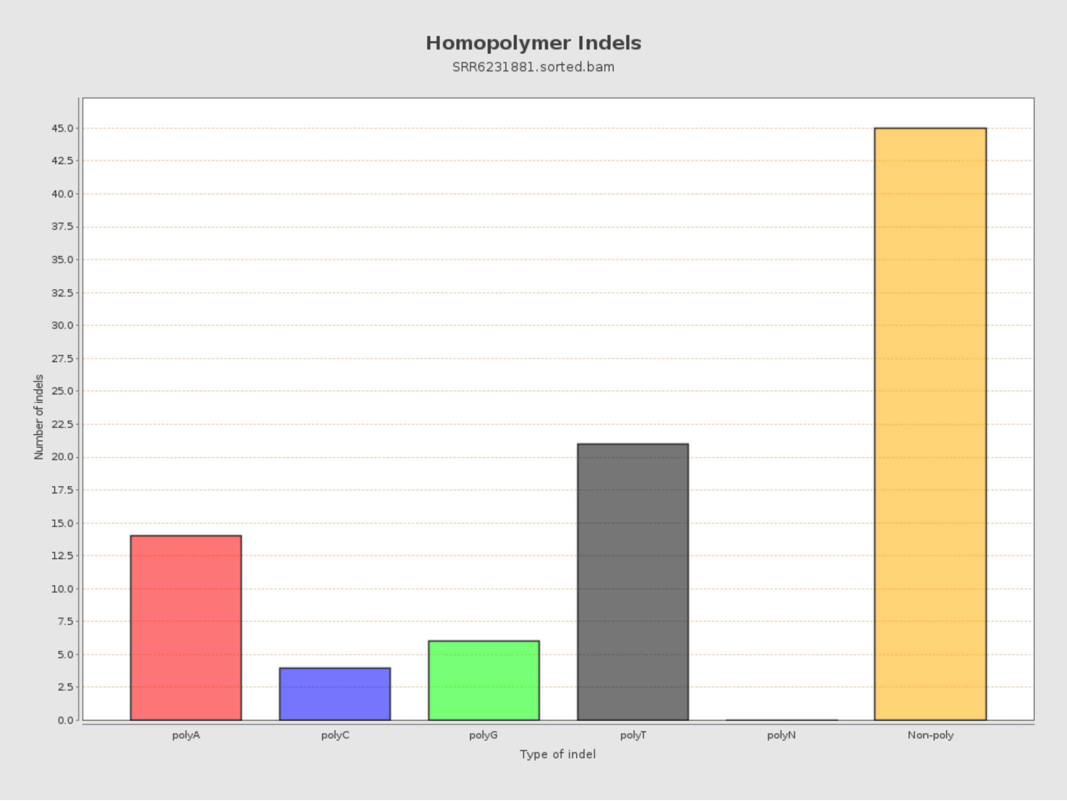
9. Results : Mapped Reads GC-content Distribution



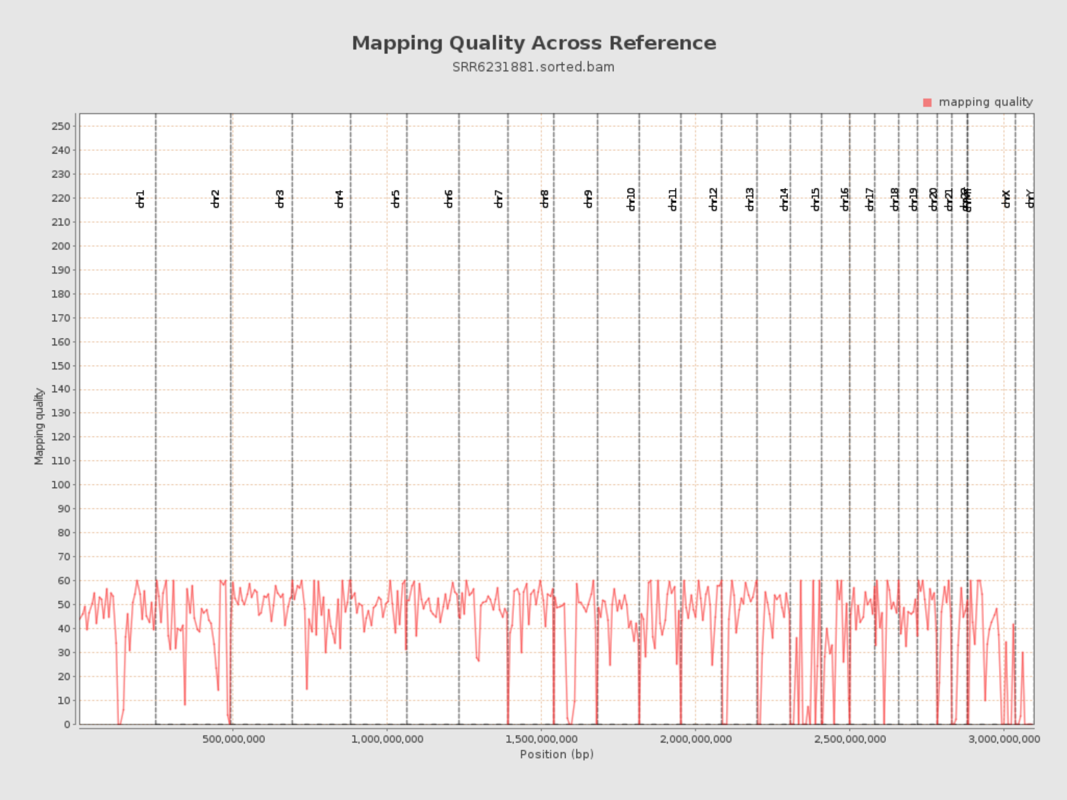
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram