Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 02:14:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231782.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_SRR6231782 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231782.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 02:14:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231782.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,612,720
Mapped reads	4,109,963 / 89.1%
Unmapped reads	502,757 / 10.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,930 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	274,948 / 5.96%
Duplication rate	2.57%
Clipped reads	2,118,958 / 45.94%

2.2. ACGT Content

Number/percentage of A's	77,289,038 / 28.78%
Number/percentage of C's	52,063,475 / 19.39%
Number/percentage of T's	73,759,833 / 27.47%
Number/percentage of G's	65,385,722 / 24.35%
Number/percentage of N's	18,677 / 0.01%
GC Percentage	43.74%

2.3. Coverage

Mean	0.0868

Standard Deviation	16.9627

2.4. Mapping Quality

Mean Mapping Quality	42.95

2.5. Mismatches and indels

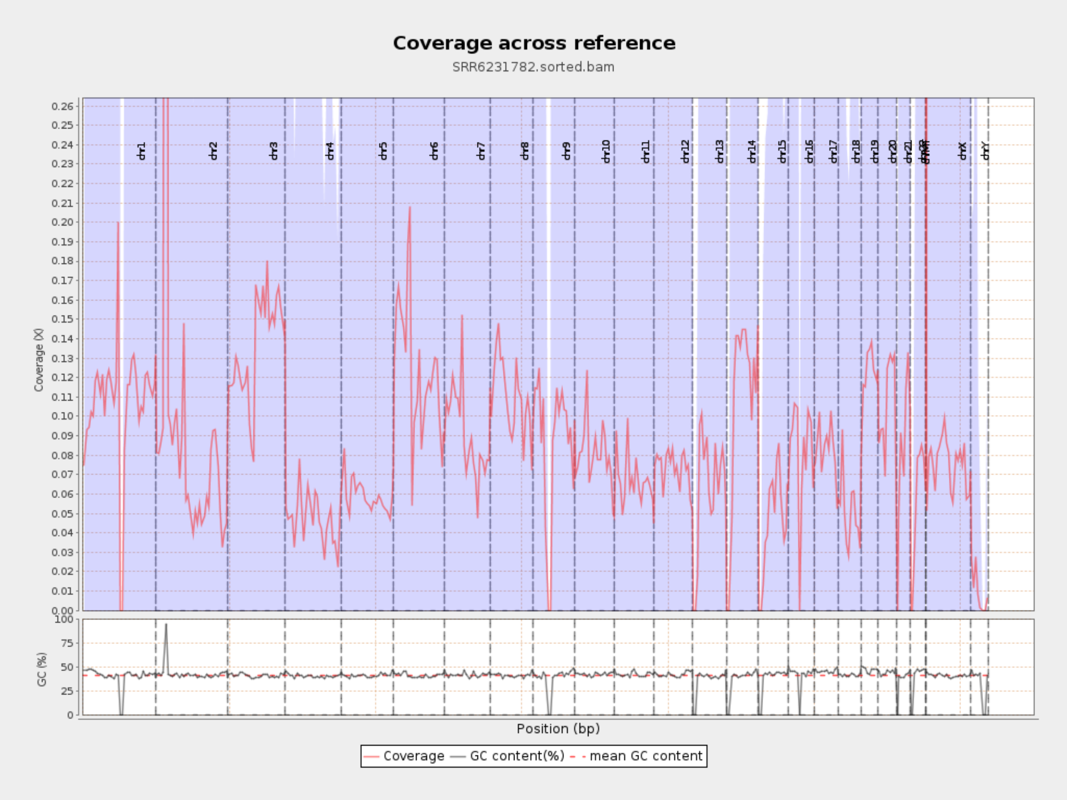
General error rate	0.69%
Mismatches	1,808,717
Insertions	19,658
Mapped reads with at least one insertion	0.47%
Deletions	64,123
Mapped reads with at least one deletion	1.54%
Homopolymer indels	43.66%

2.6. Chromosome stats

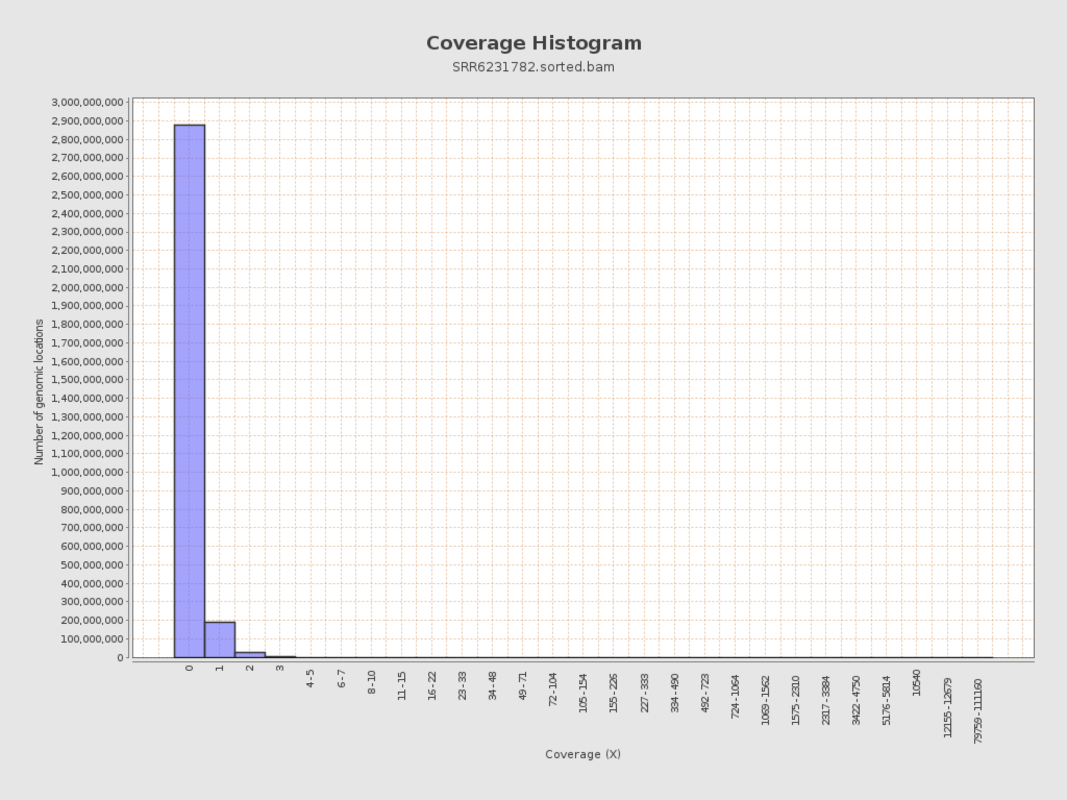
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26661000	0.107	2.0249
chr2	243199373	26597812	0.1094	60.4528
chr3	198022430	26783787	0.1353	0.4187
chr4	191154276	9058986	0.0474	0.2799
chr5	180915260	10751516	0.0594	0.291
chr6	171115067	21347757	0.1248	0.6583
chr7	159138663	14426210	0.0907	1.015

chr8	146364022	16091082	0.1099	0.9863
chr9	141213431	12223786	0.0866	0.5936
chr10	135534747	10964649	0.0809	0.6513
chr11	135006516	9022859	0.0668	0.5672
chr12	133851895	9908568	0.074	0.3181
chr13	115169878	7244534	0.0629	0.2811
chr14	107349540	11554594	0.1076	0.5596
chr15	102531392	4590113	0.0448	0.248
chr16	90354753	7162345	0.0793	0.4129
chr17	81195210	6878533	0.0847	0.4408
chr18	78077248	4000338	0.0512	1.2294
chr19	59128983	7292024	0.1233	1.1581
chr20	63025520	6748972	0.1071	0.398
chr21	48129895	4050621	0.0842	0.3615
chr22	51304566	2846269	0.0555	0.2665
chrMT	16571	109971	6.6364	4.2911
chrX	155270560	11743745	0.0756	0.3833
chrY	59373566	564630	0.0095	0.1767

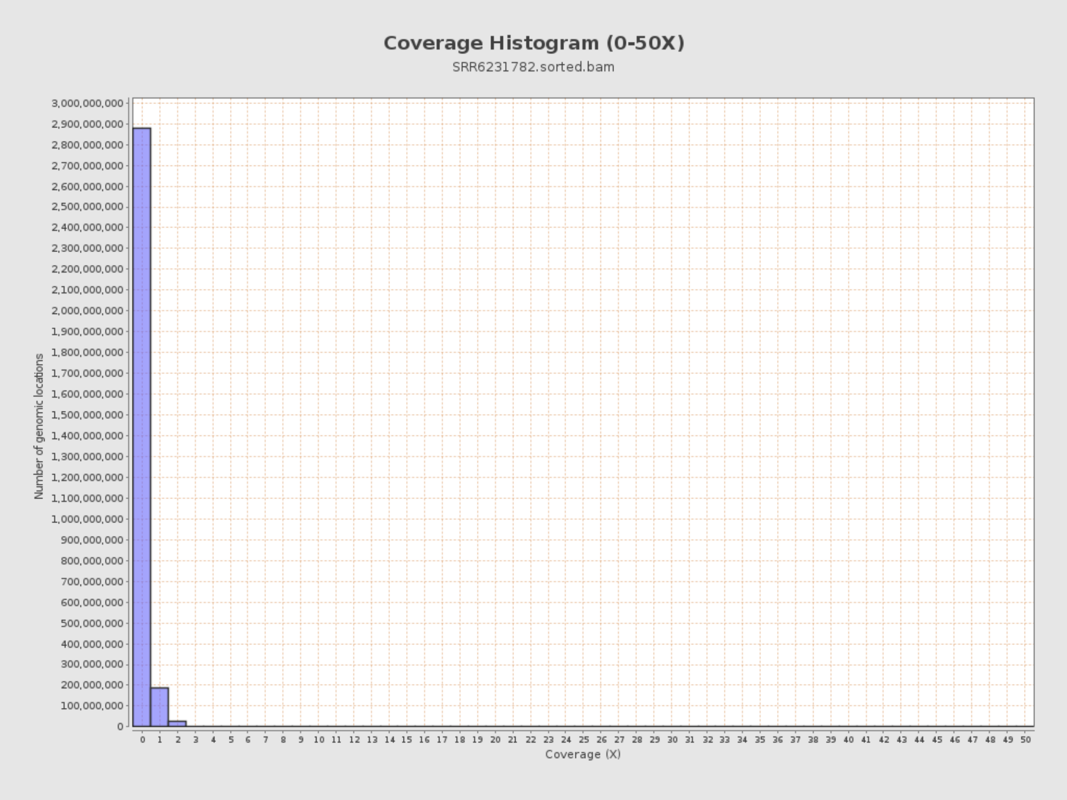
3. Results : Coverage across reference



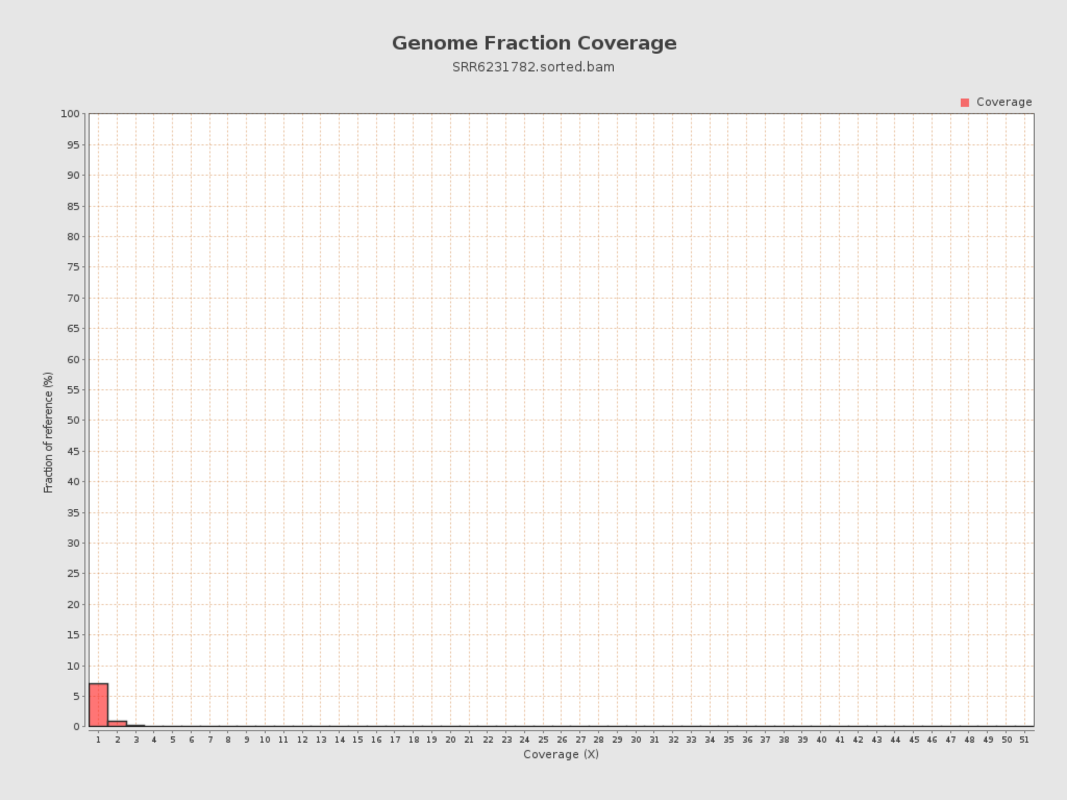
4. Results : Coverage Histogram



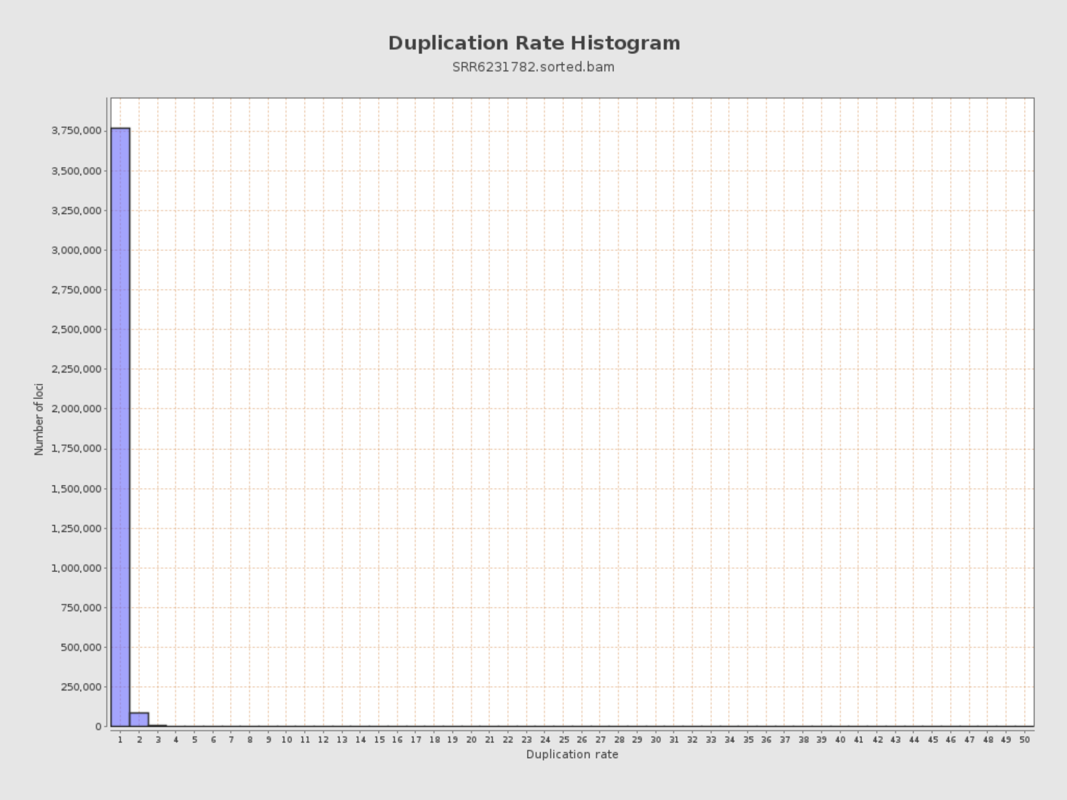
5. Results : Coverage Histogram (0-50X)



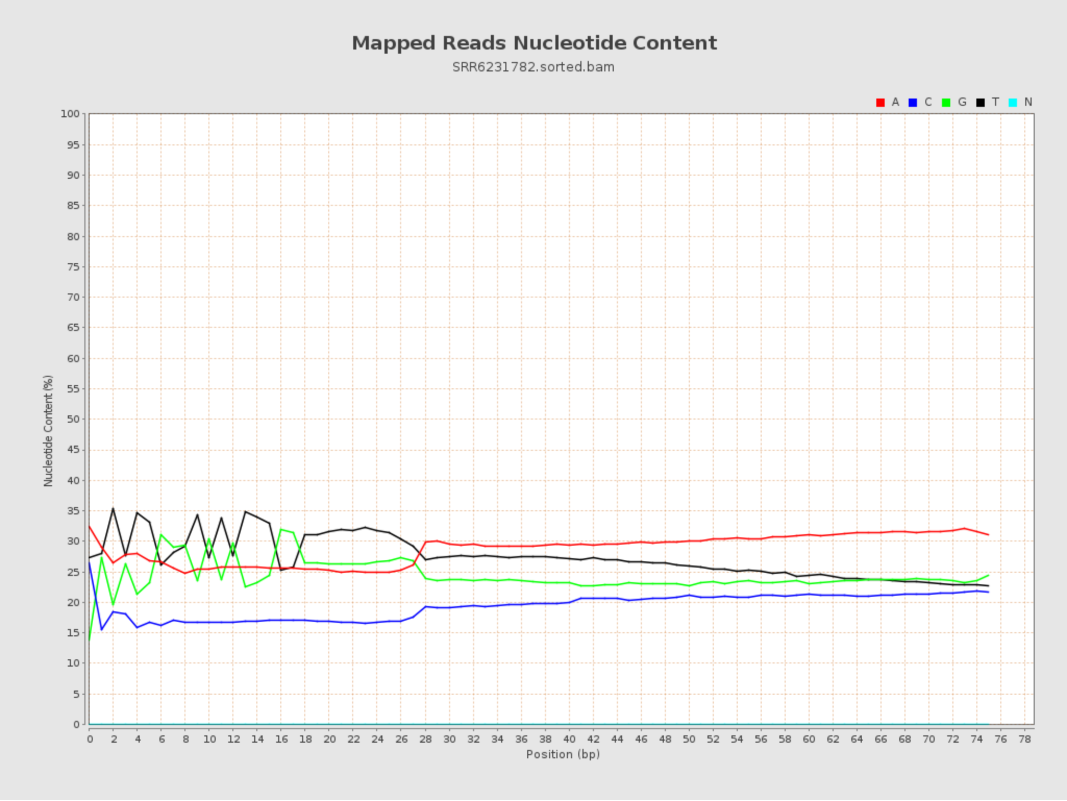
6. Results : Genome Fraction Coverage



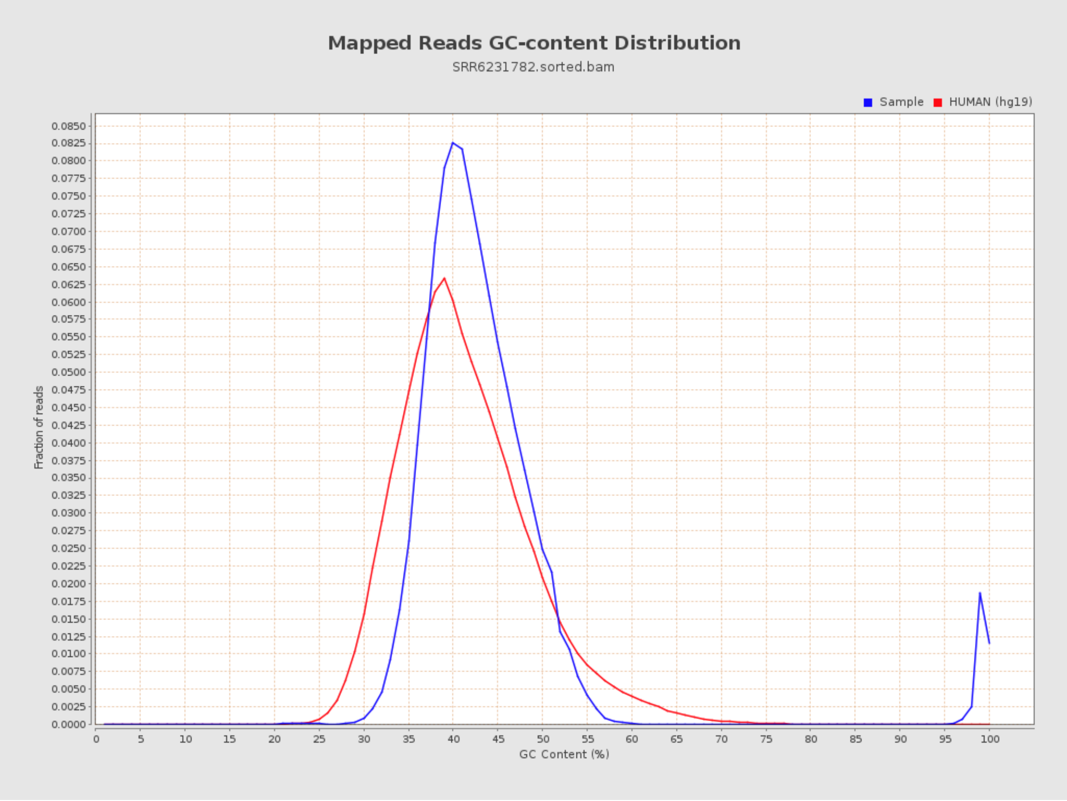
7. Results : Duplication Rate Histogram



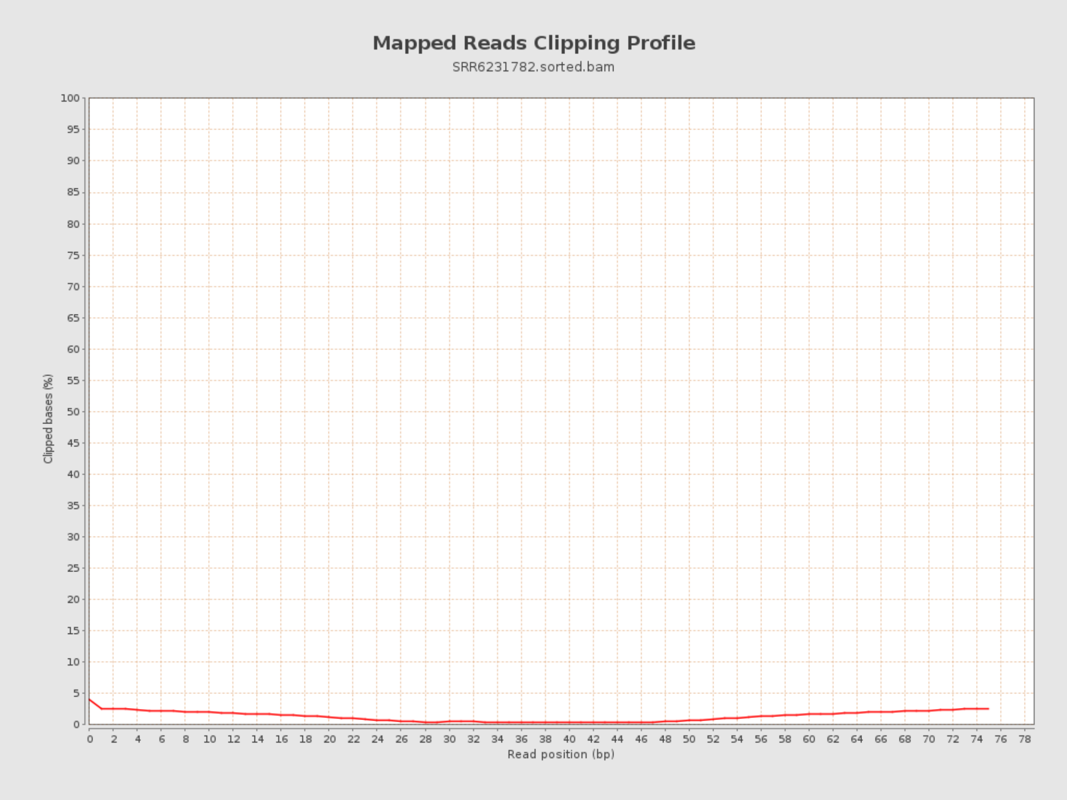
8. Results : Mapped Reads Nucleotide Content



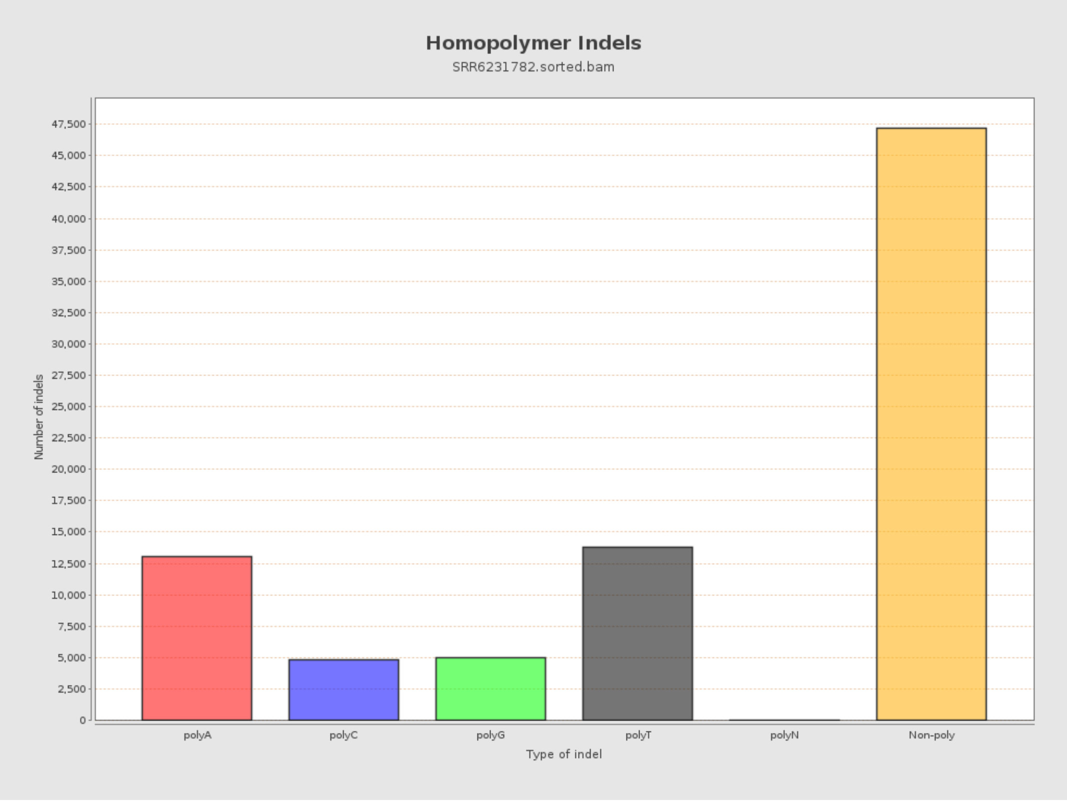
9. Results : Mapped Reads GC-content Distribution



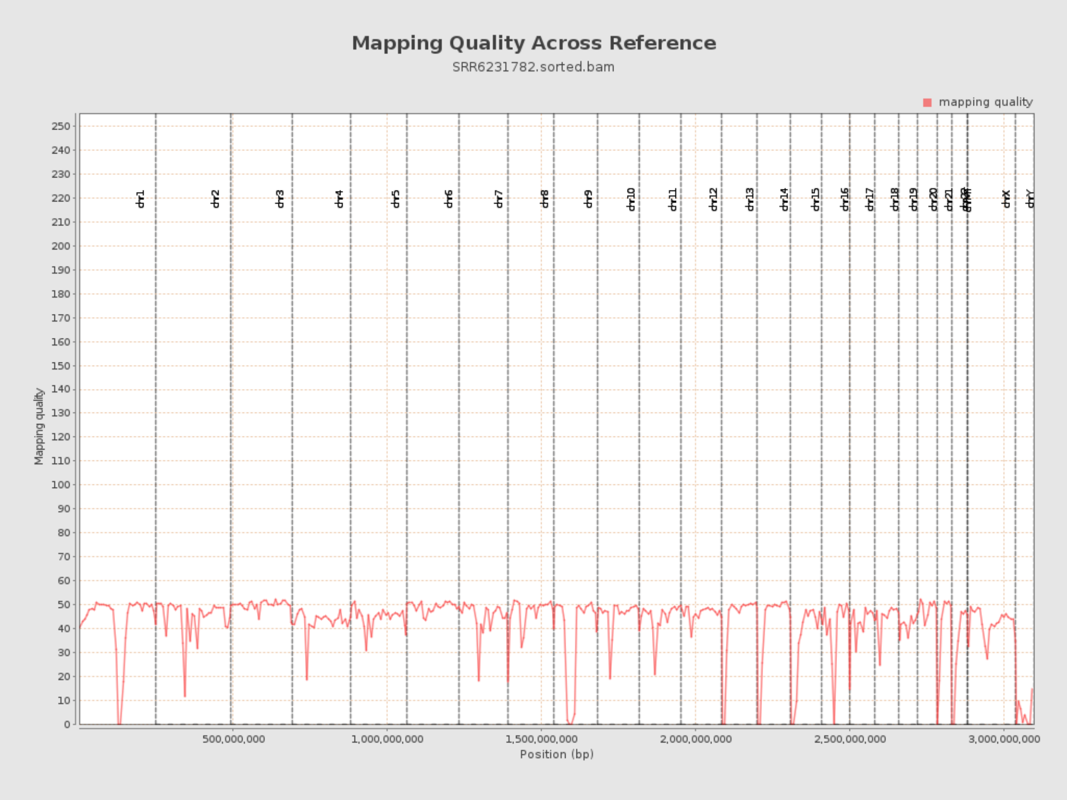
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram