Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 07:31:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231846.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_SRR6231846 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231846.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 07:31:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231846.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,958,840
Mapped reads	2,695,796 / 91.11%
Unmapped reads	263,044 / 8.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,660 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	143,896 / 4.86%
Duplication rate	3.09%
Clipped reads	1,149,500 / 38.85%

2.2. ACGT Content

Number/percentage of A's	51,775,851 / 28.57%
Number/percentage of C's	34,390,760 / 18.98%
Number/percentage of T's	53,879,942 / 29.73%
Number/percentage of G's	41,171,188 / 22.72%
Number/percentage of N's	13,576 / 0.01%
GC Percentage	41.69%

2.3. Coverage

Mean	0.0586

Standard Deviation	4.7544

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

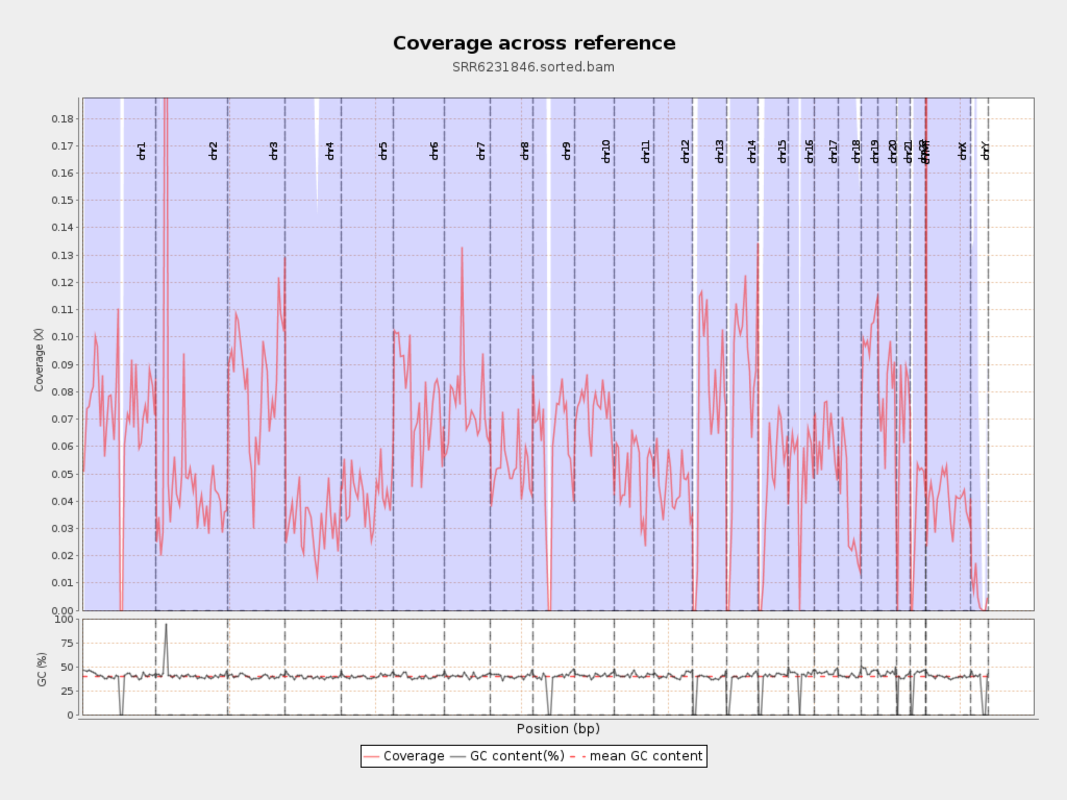
General error rate	0.62%
Mismatches	1,092,755
Insertions	13,088
Mapped reads with at least one insertion	0.48%
Deletions	42,746
Mapped reads with at least one deletion	1.57%
Homopolymer indels	47.14%

2.6. Chromosome stats

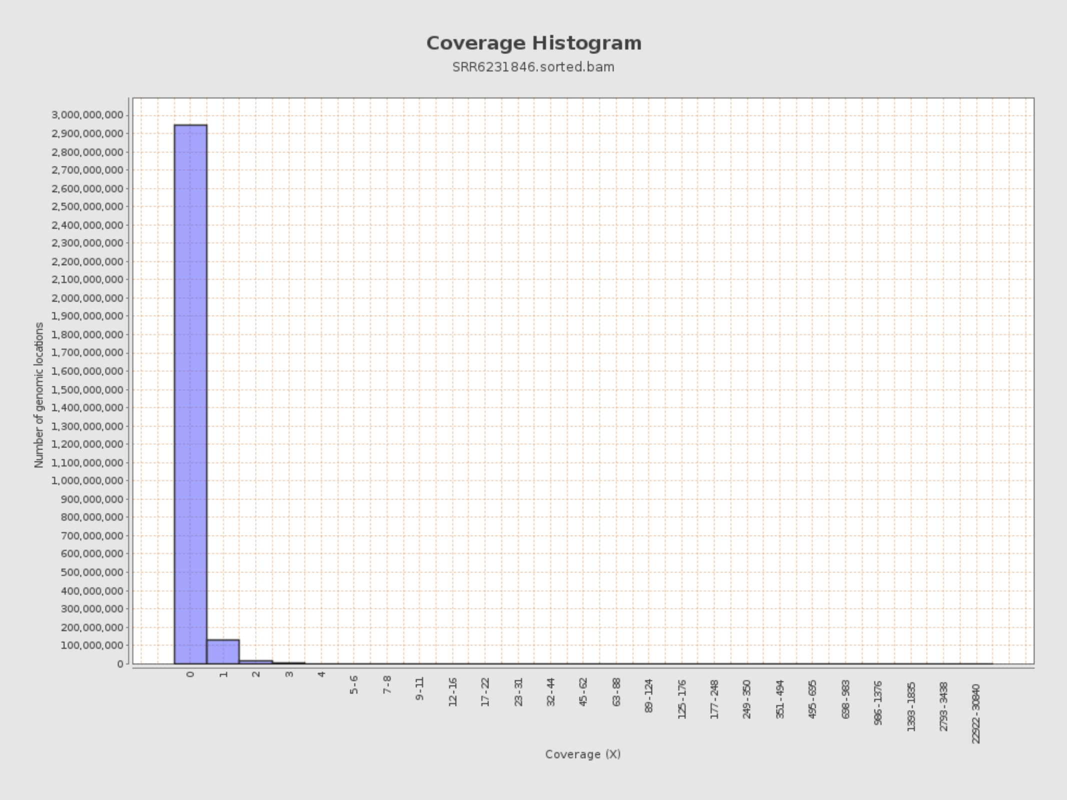
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17733365	0.0711	1.2049
chr2	243199373	12600477	0.0518	16.8568
chr3	198022430	16479729	0.0832	0.3423
chr4	191154276	5991364	0.0313	0.2151
chr5	180915260	7701646	0.0426	0.2403
chr6	171115067	13192860	0.0771	0.3863
chr7	159138663	11929510	0.075	0.8709

chr8	146364022	7640233	0.0522	0.7763
chr9	141213431	8272927	0.0586	0.4149
chr10	135534747	9997111	0.0738	0.4341
chr11	135006516	6685381	0.0495	0.3451
chr12	133851895	6200034	0.0463	0.2533
chr13	115169878	8620469	0.0749	0.3125
chr14	107349540	8590876	0.08	0.3704
chr15	102531392	4601654	0.0449	0.2438
chr16	90354753	4523634	0.0501	0.2954
chr17	81195210	5096524	0.0628	0.3028
chr18	78077248	2933414	0.0376	0.7952
chr19	59128983	5937210	0.1004	0.74
chr20	63025520	4873485	0.0773	0.3271
chr21	48129895	3174989	0.066	0.3037
chr22	51304566	1842225	0.0359	0.266
chrMT	16571	130671	7.8855	4.9482
chrX	155270560	6222091	0.0401	0.2619
chrY	59373566	331644	0.0056	0.1118

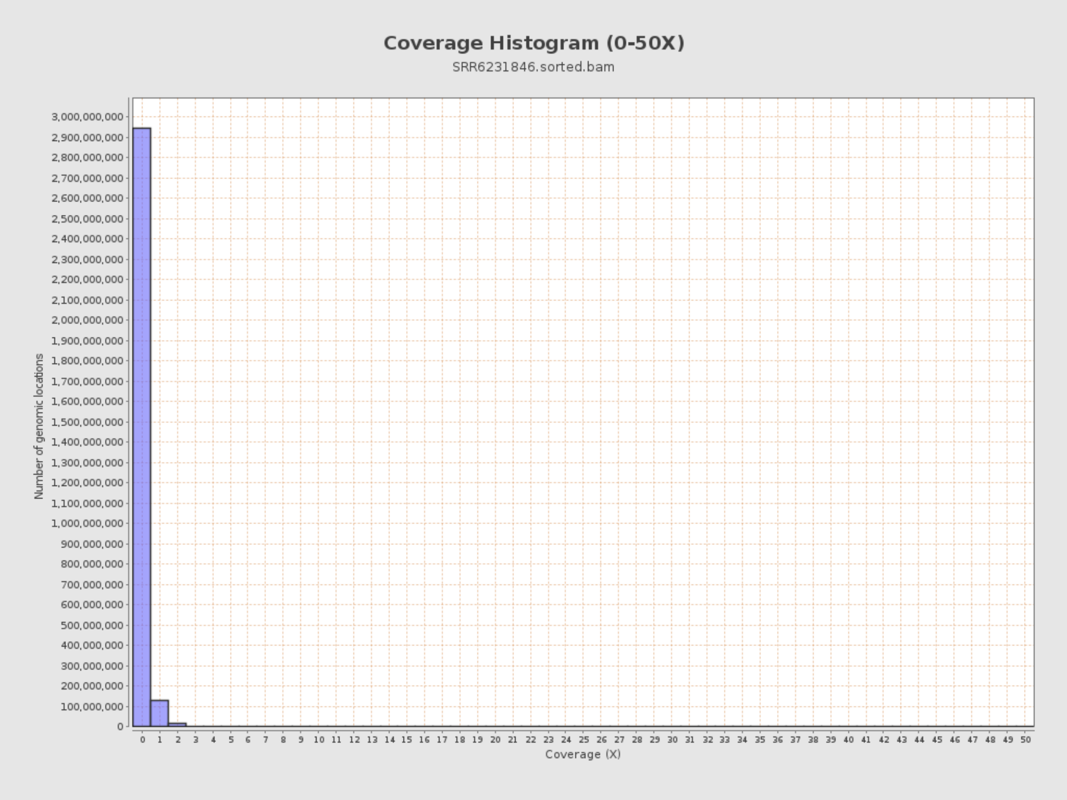
3. Results : Coverage across reference



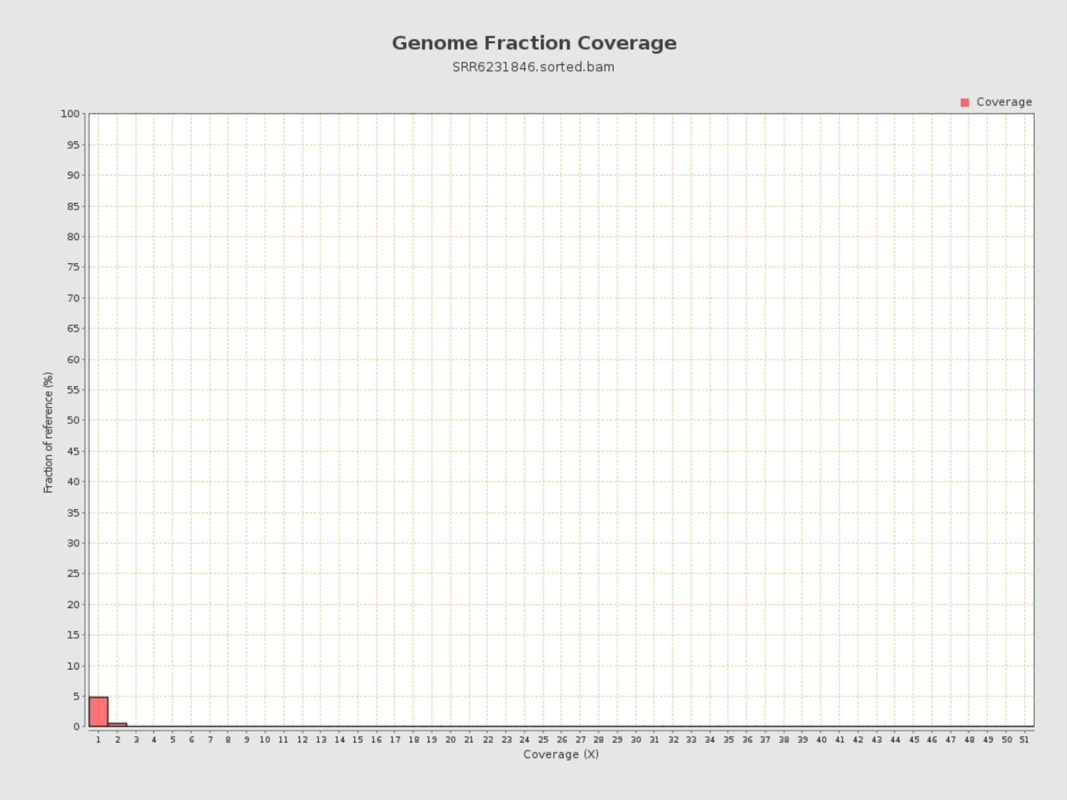
4. Results : Coverage Histogram



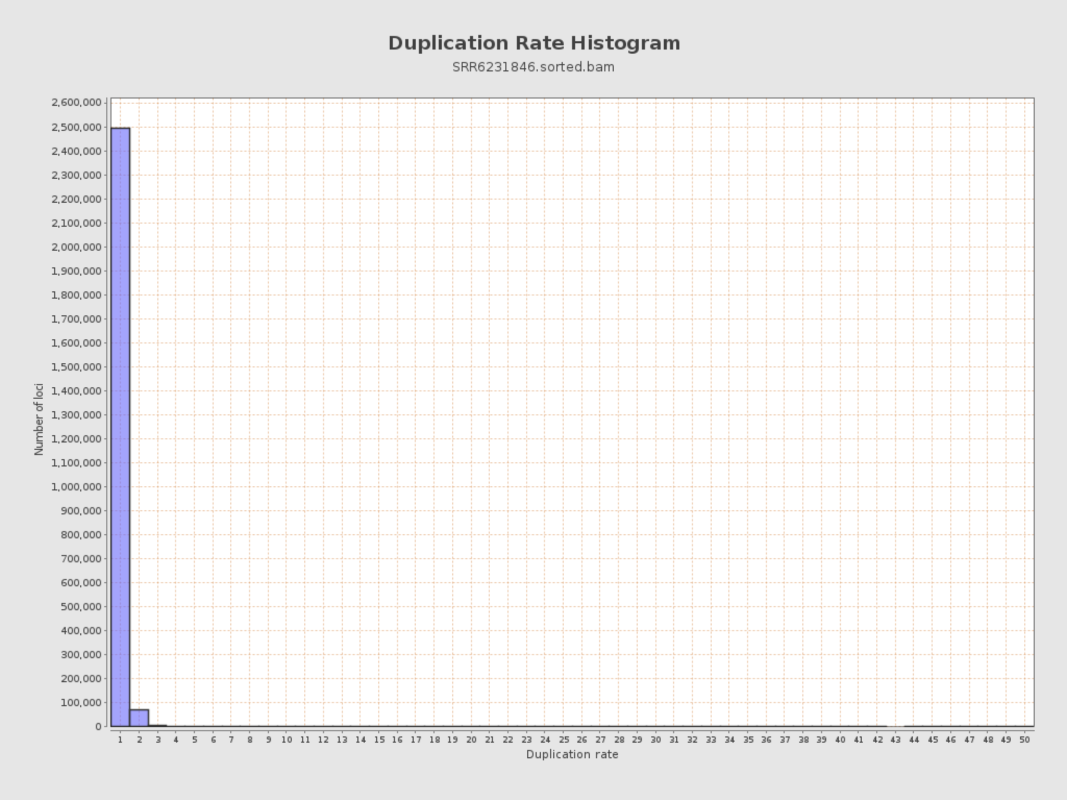
5. Results : Coverage Histogram (0-50X)



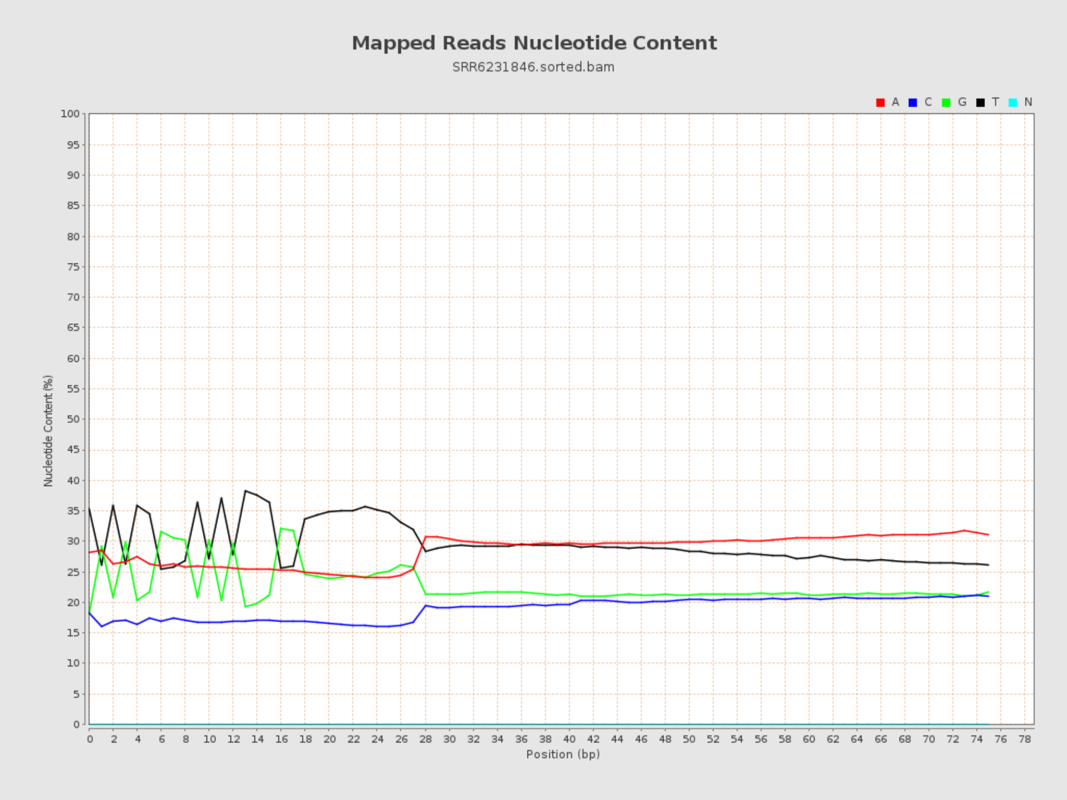
6. Results : Genome Fraction Coverage



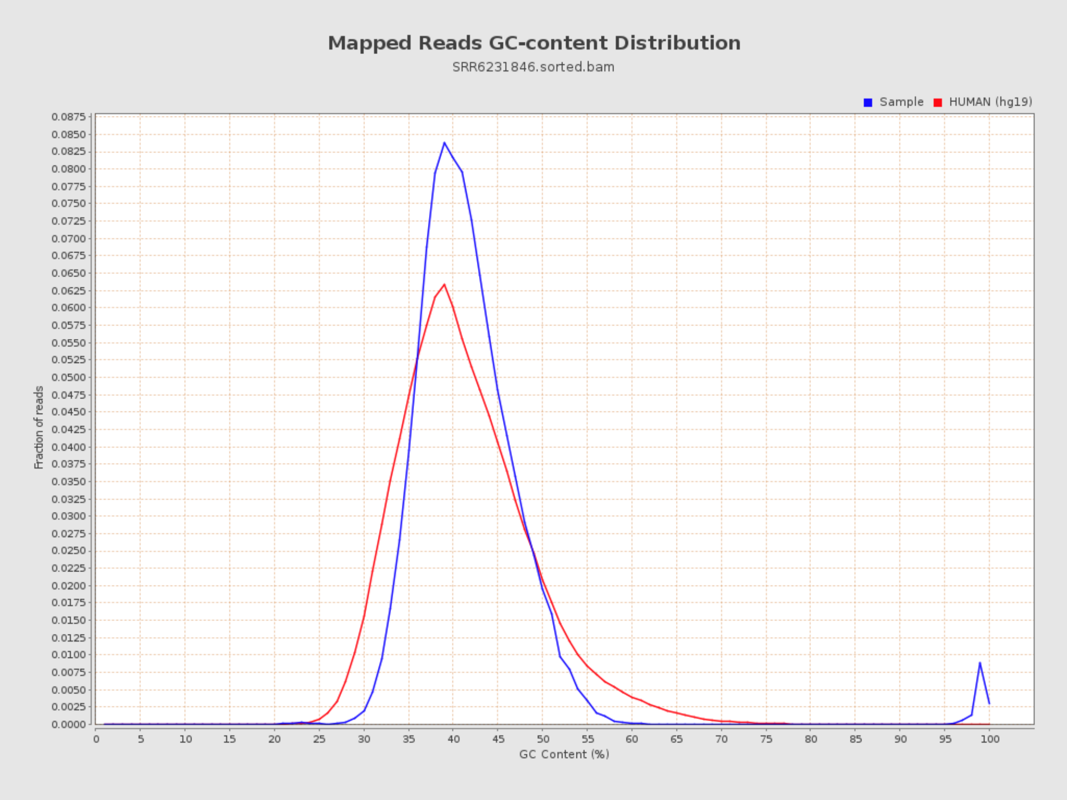
7. Results : Duplication Rate Histogram



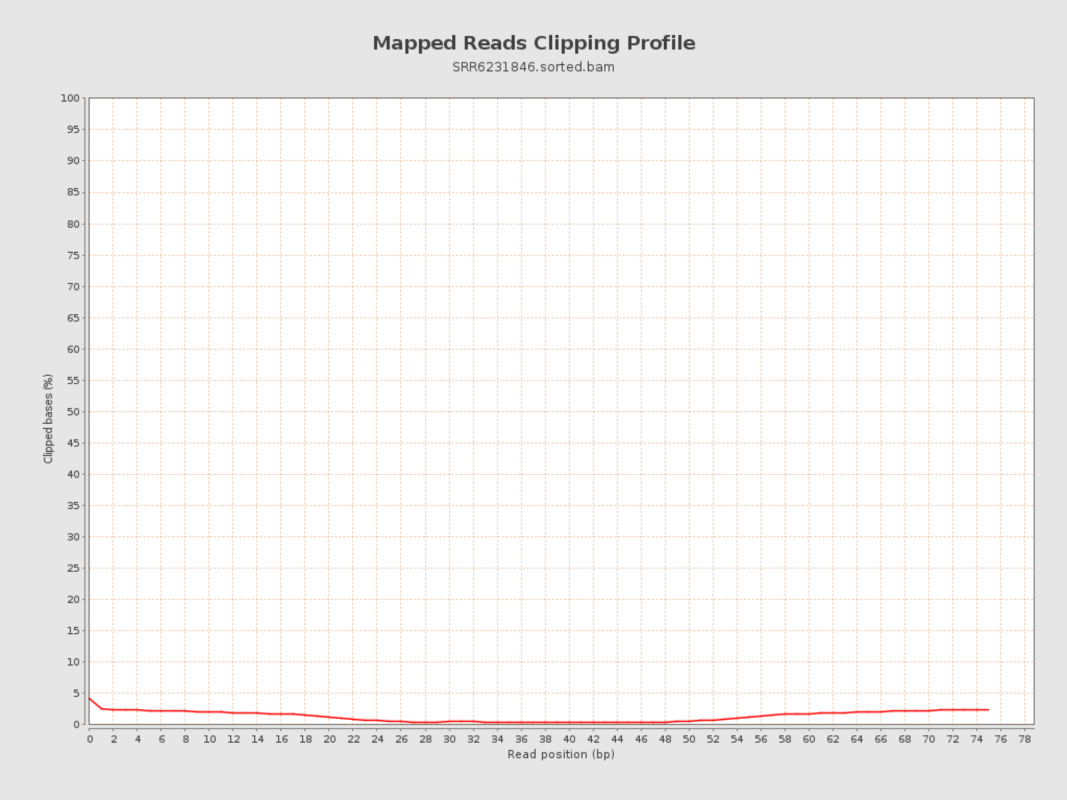
8. Results : Mapped Reads Nucleotide Content



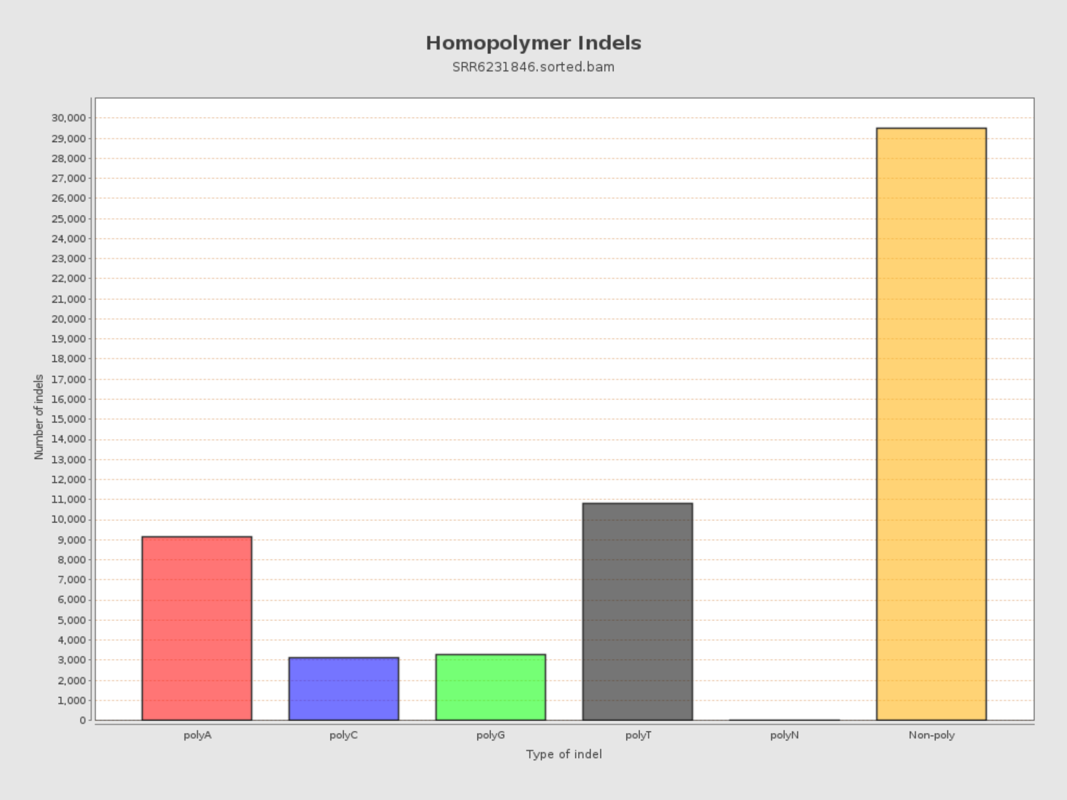
9. Results : Mapped Reads GC-content Distribution



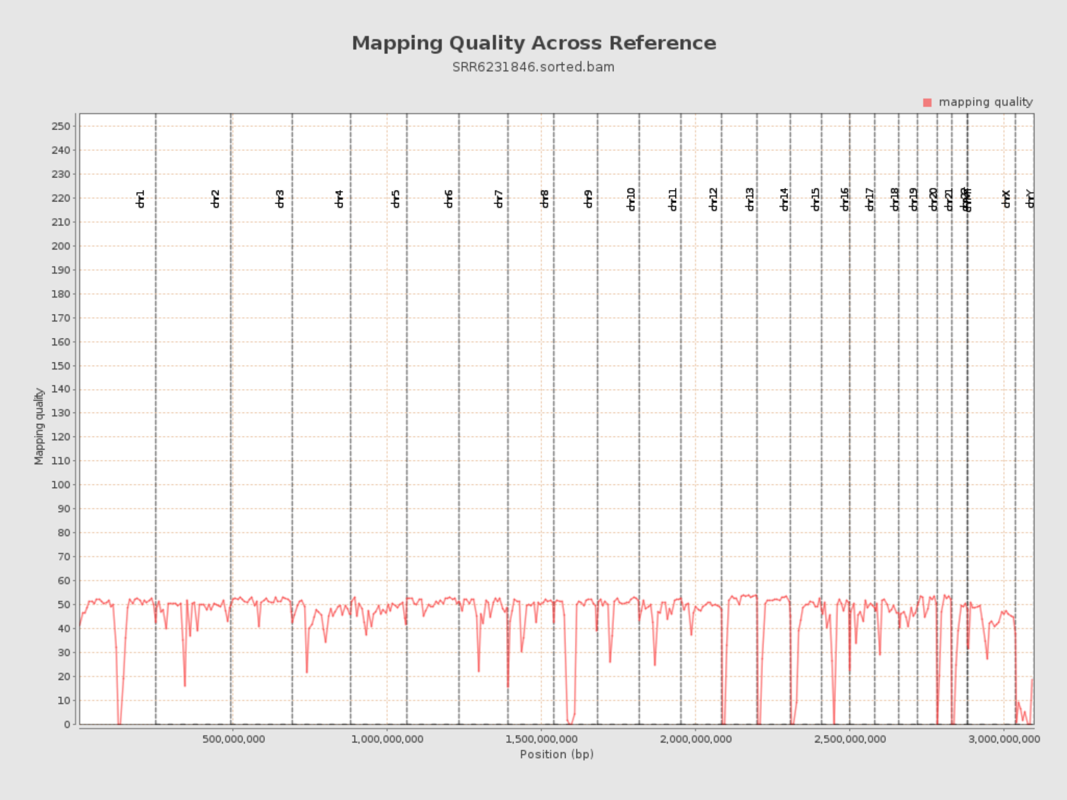
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram