Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:34:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081964.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_SRR3081964 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081964.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:34:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081964.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,908,995
Mapped reads	2,676,741 / 92.02%
Unmapped reads	232,254 / 7.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,567 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	102,046 / 3.51%
Duplication rate	2.89%
Clipped reads	724,924 / 24.92%

2.2. ACGT Content

Number/percentage of A's	56,070,181 / 29.58%
Number/percentage of C's	35,421,309 / 18.69%
Number/percentage of T's	59,975,750 / 31.64%
Number/percentage of G's	38,034,276 / 20.07%
Number/percentage of N's	25,530 / 0.01%
GC Percentage	38.76%

2.3. Coverage

Mean	0.0612

Standard Deviation	0.4969

2.4. Mapping Quality

Mean Mapping Quality	47.67

2.5. Mismatches and indels

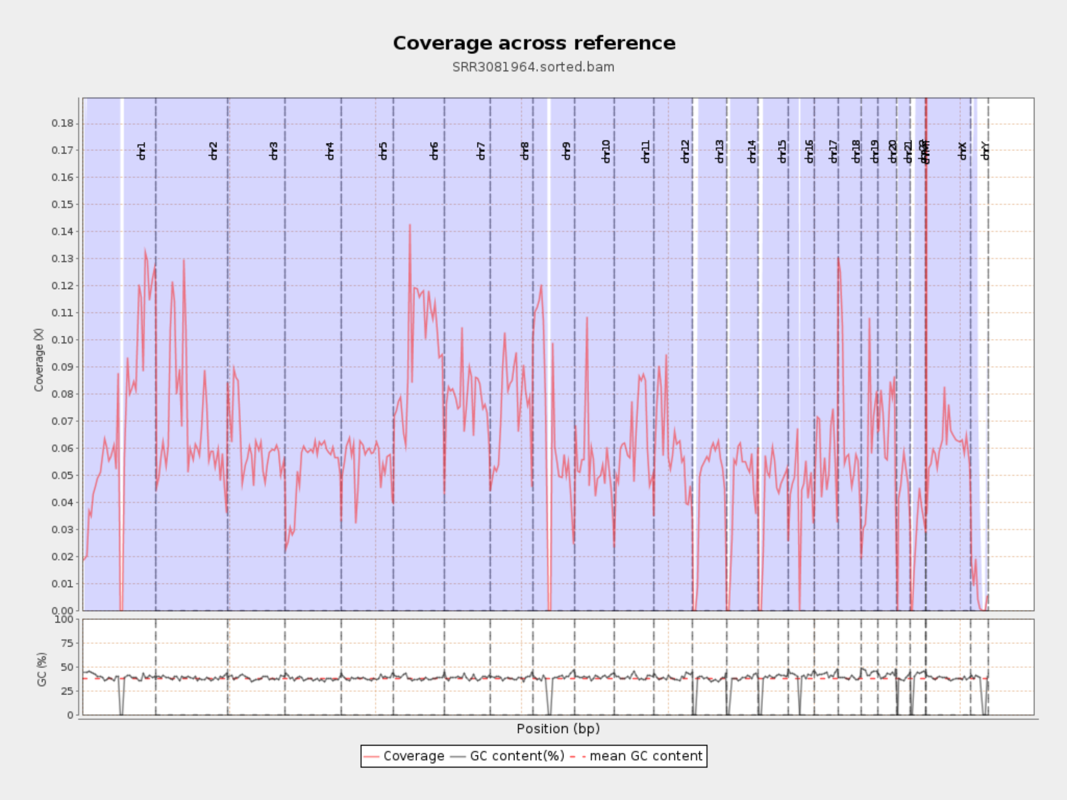
General error rate	0.78%
Mismatches	1,449,504
Insertions	14,184
Mapped reads with at least one insertion	0.52%
Deletions	39,234
Mapped reads with at least one deletion	1.45%
Homopolymer indels	48.27%

2.6. Chromosome stats

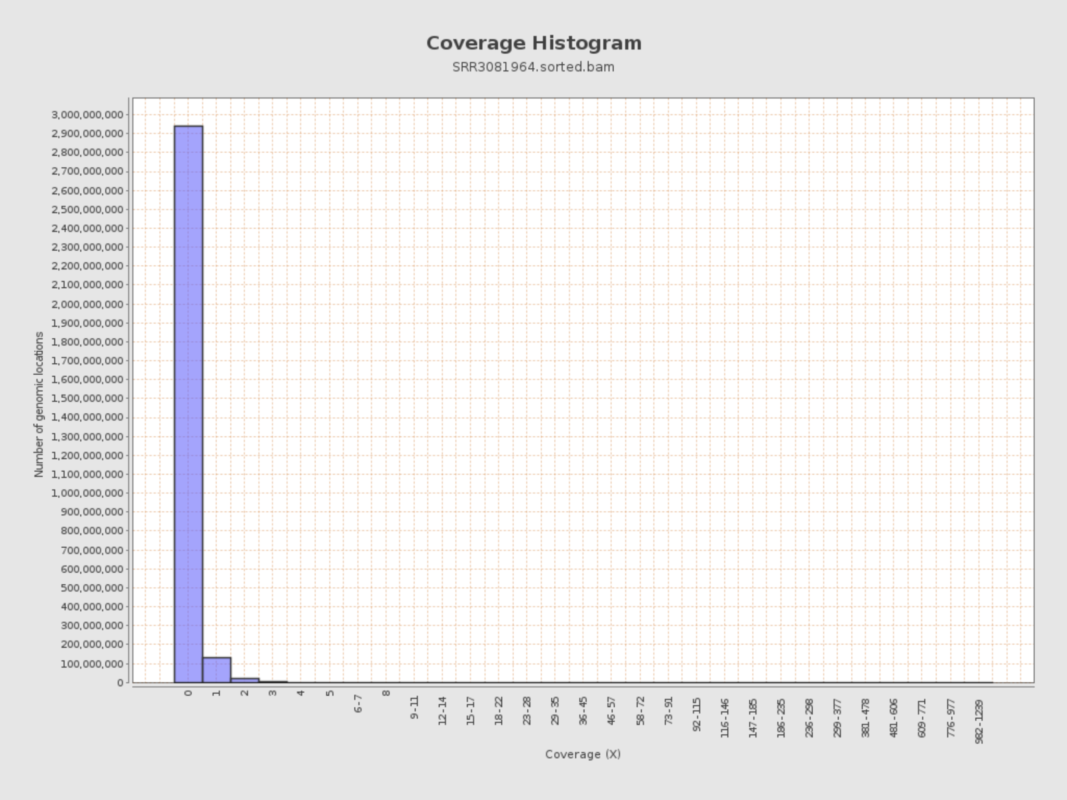
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17405423	0.0698	0.8659
chr2	243199373	16775572	0.069	0.577
chr3	198022430	12161402	0.0614	0.2881
chr4	191154276	9959671	0.0521	0.2772
chr5	180915260	9934989	0.0549	0.2733
chr6	171115067	16889651	0.0987	0.4915
chr7	159138663	12396092	0.0779	0.6034

chr8	146364022	10965976	0.0749	0.8508
chr9	141213431	9332959	0.0661	0.5231
chr10	135534747	7478105	0.0552	0.4812
chr11	135006516	8474524	0.0628	0.3723
chr12	133851895	8210590	0.0613	0.2969
chr13	115169878	5280362	0.0458	0.2457
chr14	107349540	4777741	0.0445	0.2675
chr15	102531392	4270479	0.0417	0.2353
chr16	90354753	3841054	0.0425	0.3001
chr17	81195210	4662120	0.0574	0.314
chr18	78077248	5355860	0.0686	0.8471
chr19	59128983	3488621	0.059	0.588
chr20	63025520	4506789	0.0715	0.3141
chr21	48129895	2054276	0.0427	0.2694
chr22	51304566	1364523	0.0266	0.1838
chrMT	16571	188312	11.3639	7.5712
chrX	155270560	9434340	0.0608	0.3263
chrY	59373566	387758	0.0065	0.1453

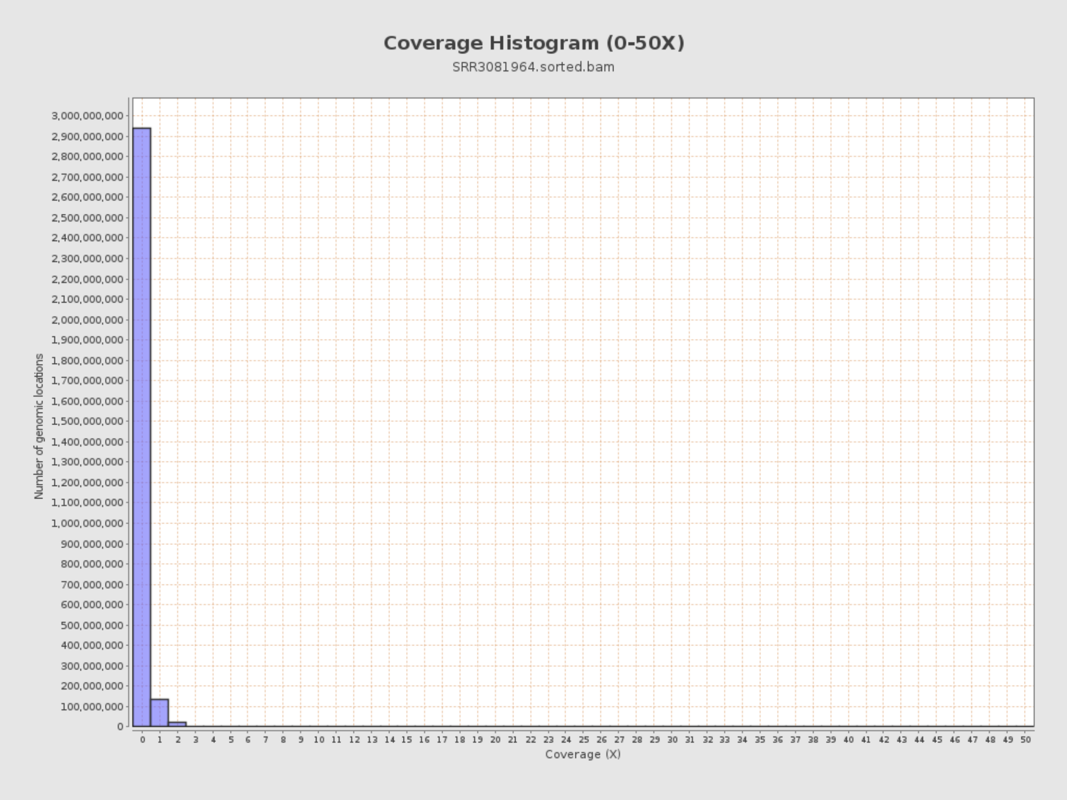
3. Results : Coverage across reference



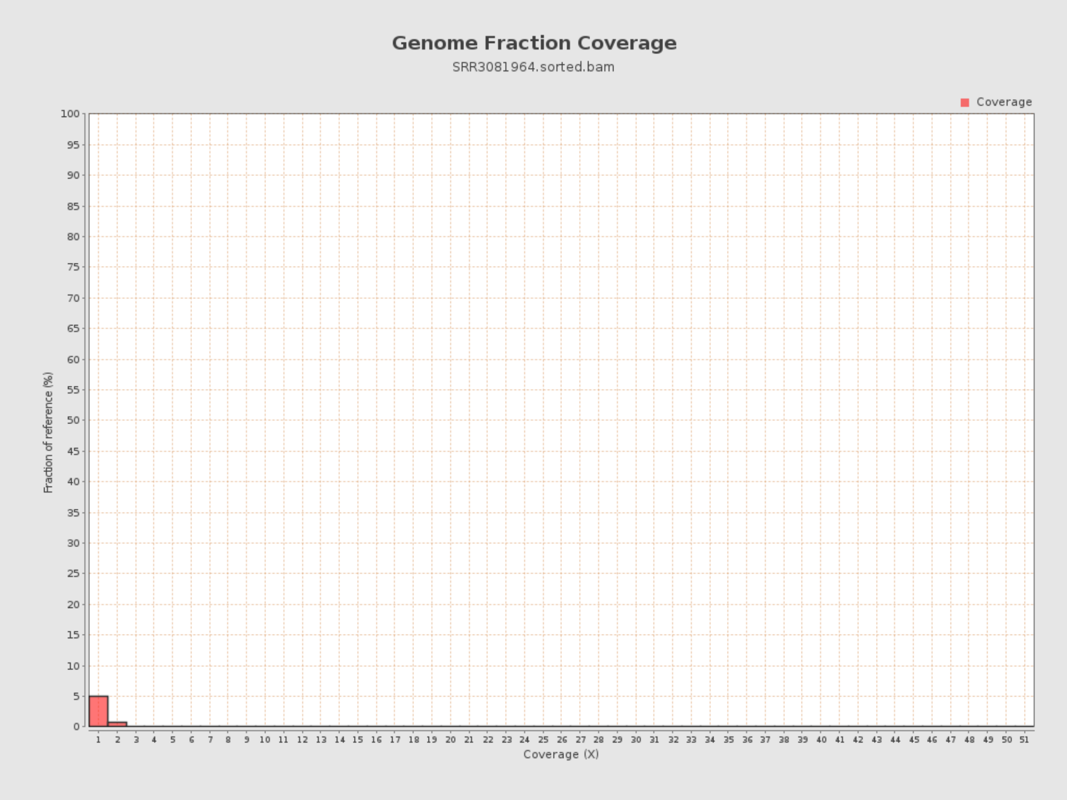
4. Results : Coverage Histogram



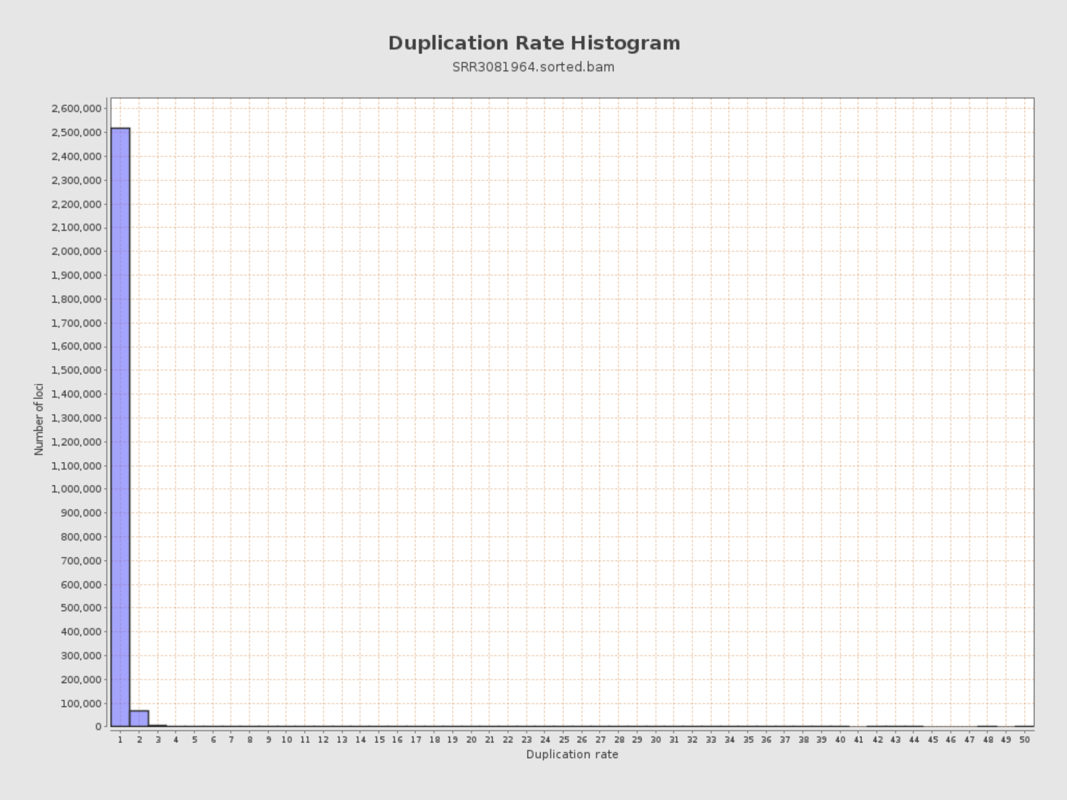
5. Results : Coverage Histogram (0-50X)



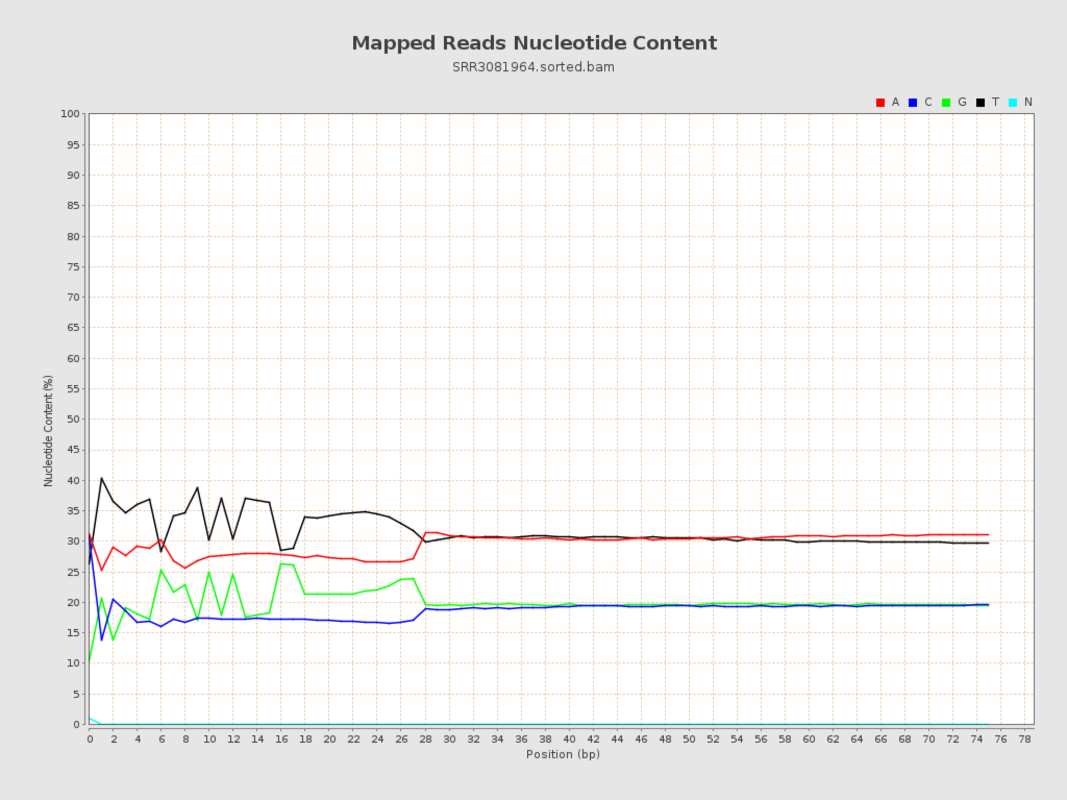
6. Results : Genome Fraction Coverage



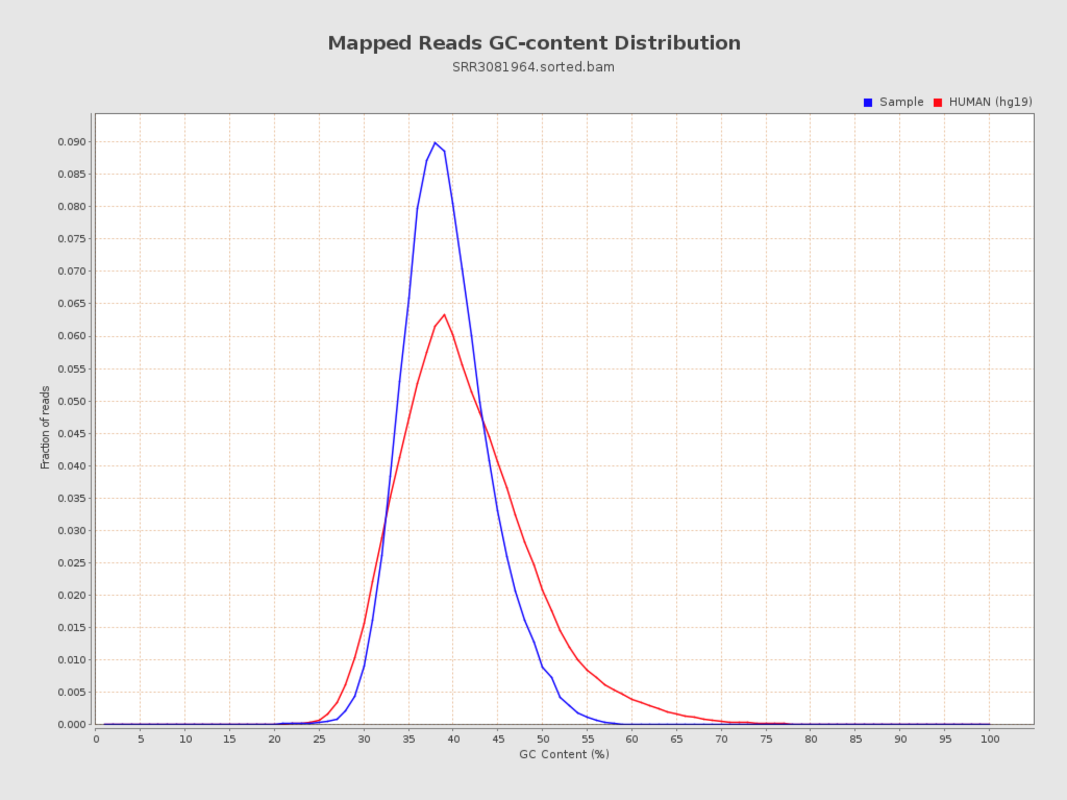
7. Results : Duplication Rate Histogram



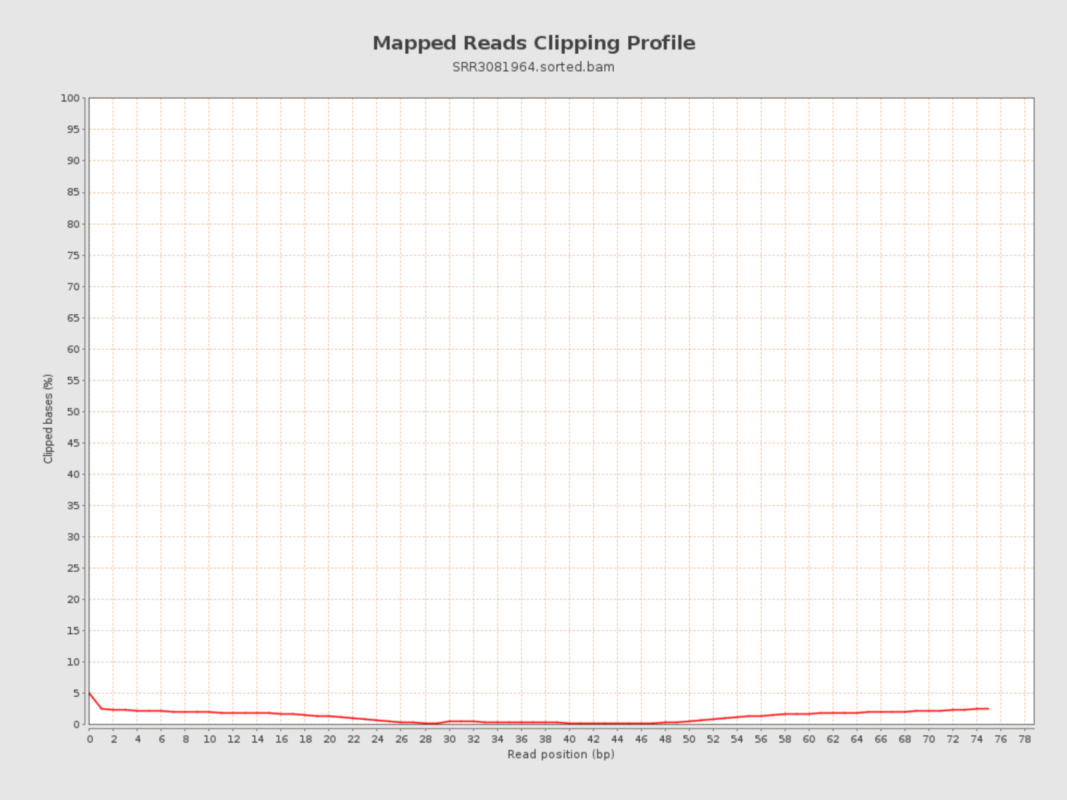
8. Results : Mapped Reads Nucleotide Content



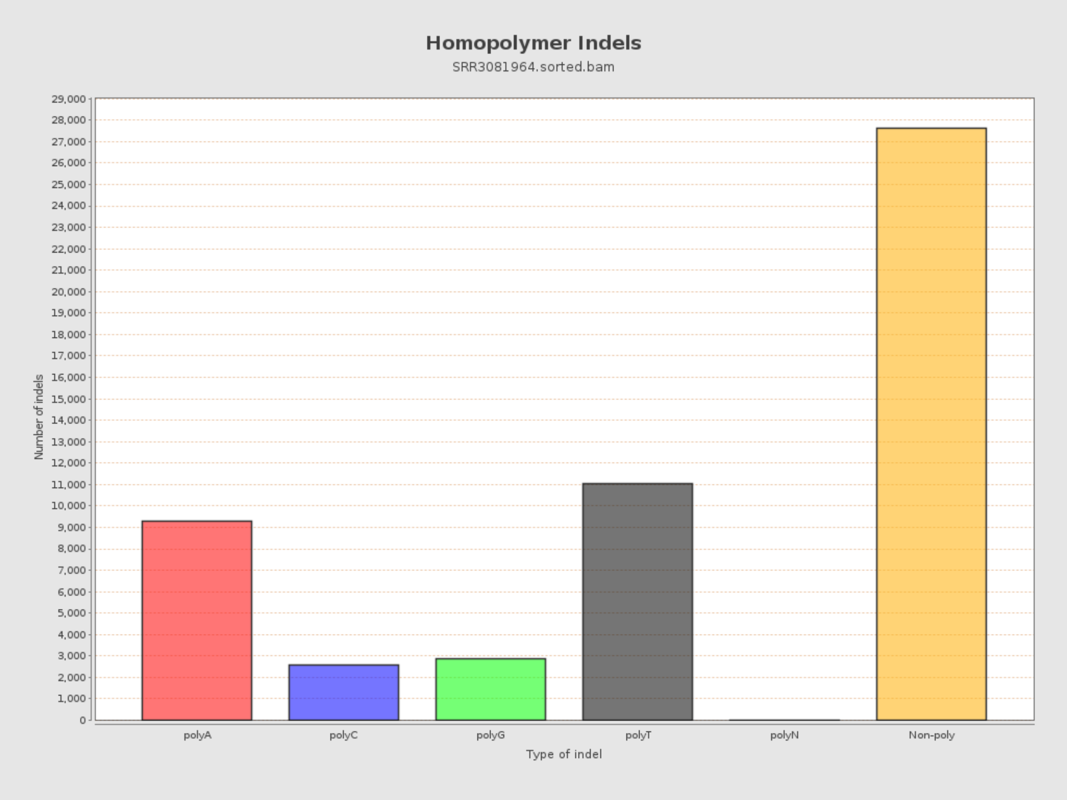
9. Results : Mapped Reads GC-content Distribution



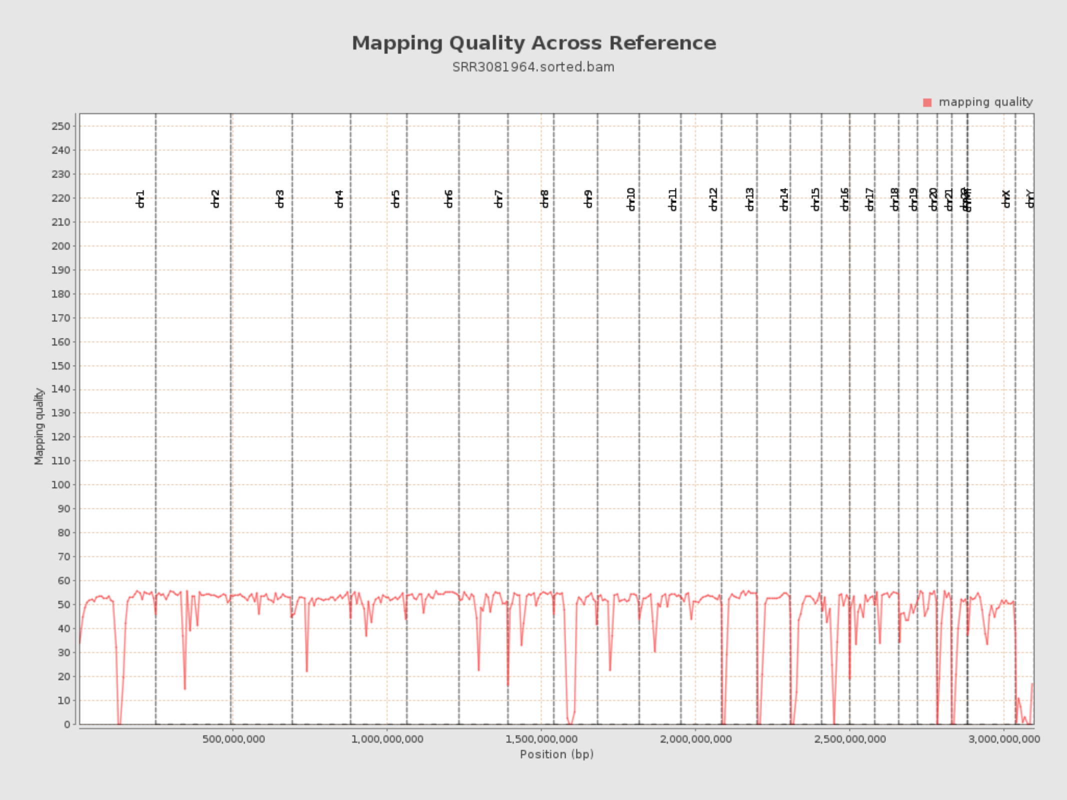
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram