Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:52:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081970.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_SRR3081970 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081970.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:52:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081970.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,962,015
Mapped reads	2,742,993 / 92.61%
Unmapped reads	219,022 / 7.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,442 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	134,773 / 4.55%
Duplication rate	4.04%
Clipped reads	1,029,633 / 34.76%

2.2. ACGT Content

Number/percentage of A's	53,256,228 / 28.51%
Number/percentage of C's	34,184,862 / 18.3%
Number/percentage of T's	59,595,170 / 31.91%
Number/percentage of G's	39,728,453 / 21.27%
Number/percentage of N's	24,165 / 0.01%
GC Percentage	39.57%

2.3. Coverage

Mean	0.0604

Standard Deviation	0.4391

2.4. Mapping Quality

Mean Mapping Quality	46.99

2.5. Mismatches and indels

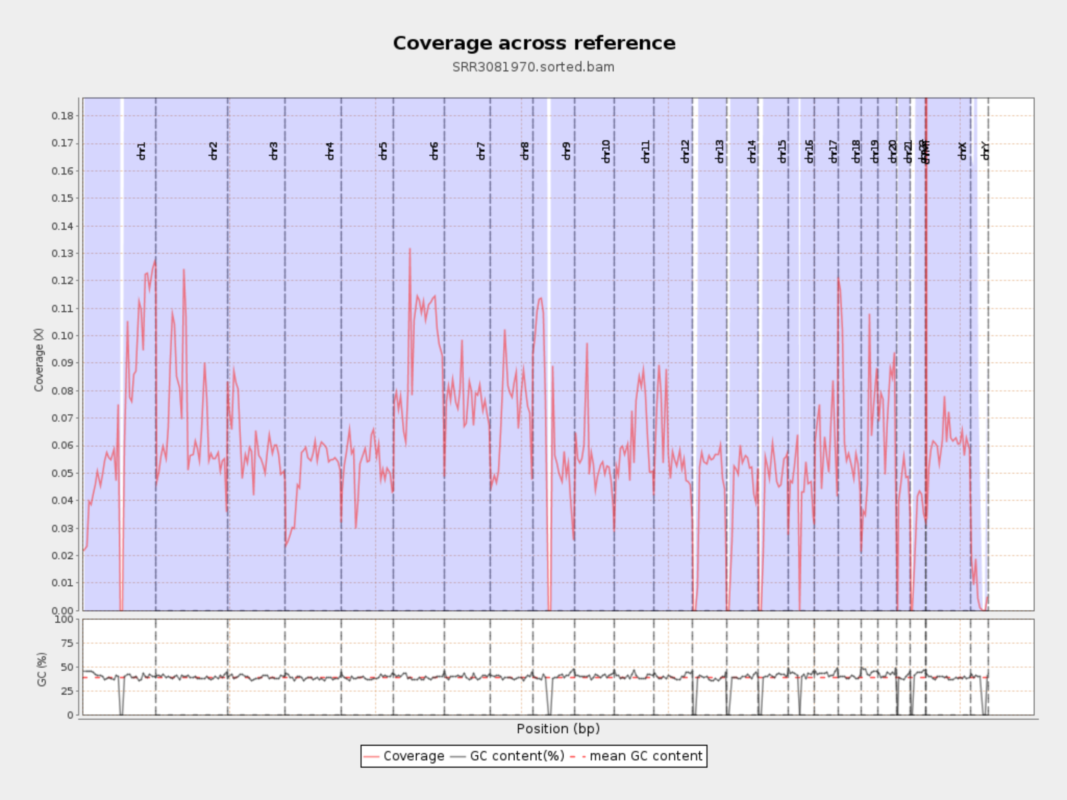
General error rate	0.76%
Mismatches	1,391,489
Insertions	12,888
Mapped reads with at least one insertion	0.47%
Deletions	39,400
Mapped reads with at least one deletion	1.42%
Homopolymer indels	48.67%

2.6. Chromosome stats

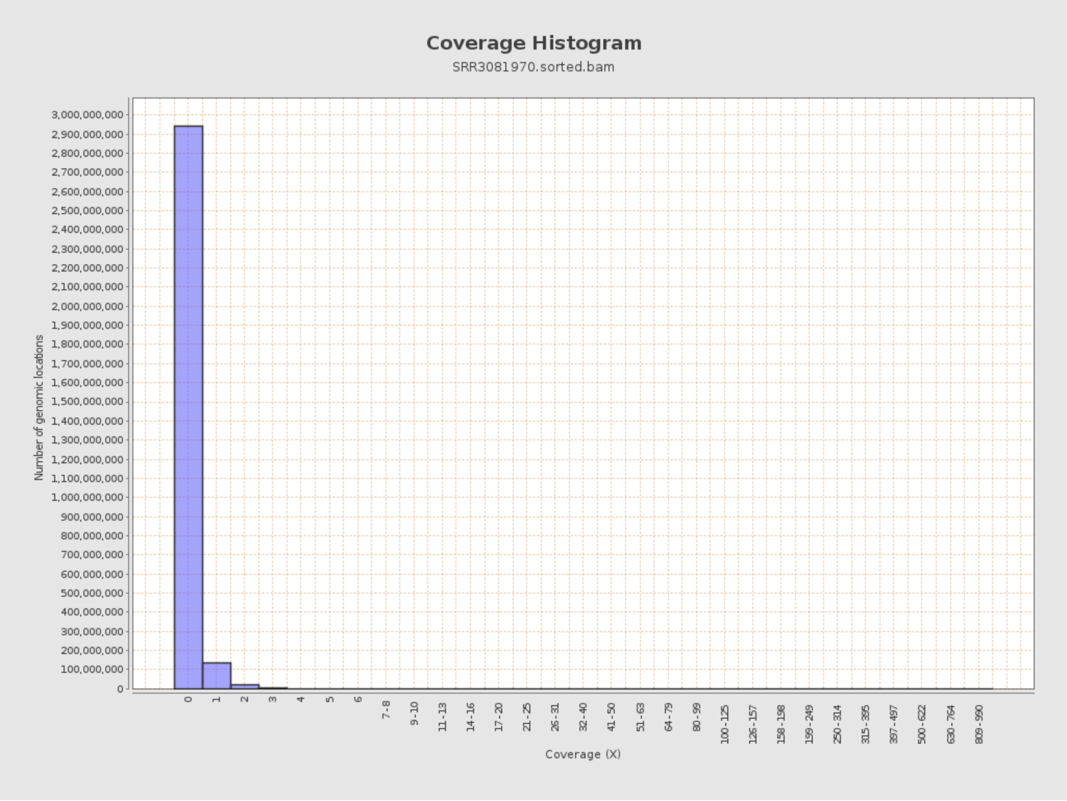
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17108121	0.0686	0.7003
chr2	243199373	16481326	0.0678	0.5637
chr3	198022430	12011272	0.0607	0.2836
chr4	191154276	9610150	0.0503	0.2681
chr5	180915260	9571537	0.0529	0.2664
chr6	171115067	16513122	0.0965	0.4476
chr7	159138663	12128225	0.0762	0.5611

chr8	146364022	10475679	0.0716	0.7017
chr9	141213431	8980929	0.0636	0.443
chr10	135534747	7466532	0.0551	0.4317
chr11	135006516	8509656	0.063	0.3515
chr12	133851895	7914927	0.0591	0.2857
chr13	115169878	5146888	0.0447	0.2416
chr14	107349540	4616147	0.043	0.2565
chr15	102531392	4354287	0.0425	0.2381
chr16	90354753	3845022	0.0426	0.2756
chr17	81195210	5049597	0.0622	0.3095
chr18	78077248	5305524	0.068	0.6882
chr19	59128983	3717218	0.0629	0.5388
chr20	63025520	4730862	0.0751	0.3198
chr21	48129895	2021867	0.042	0.2524
chr22	51304566	1437644	0.028	0.1885
chrMT	16571	114359	6.9012	4.1413
chrX	155270560	9355978	0.0603	0.3131
chrY	59373566	391349	0.0066	0.1329

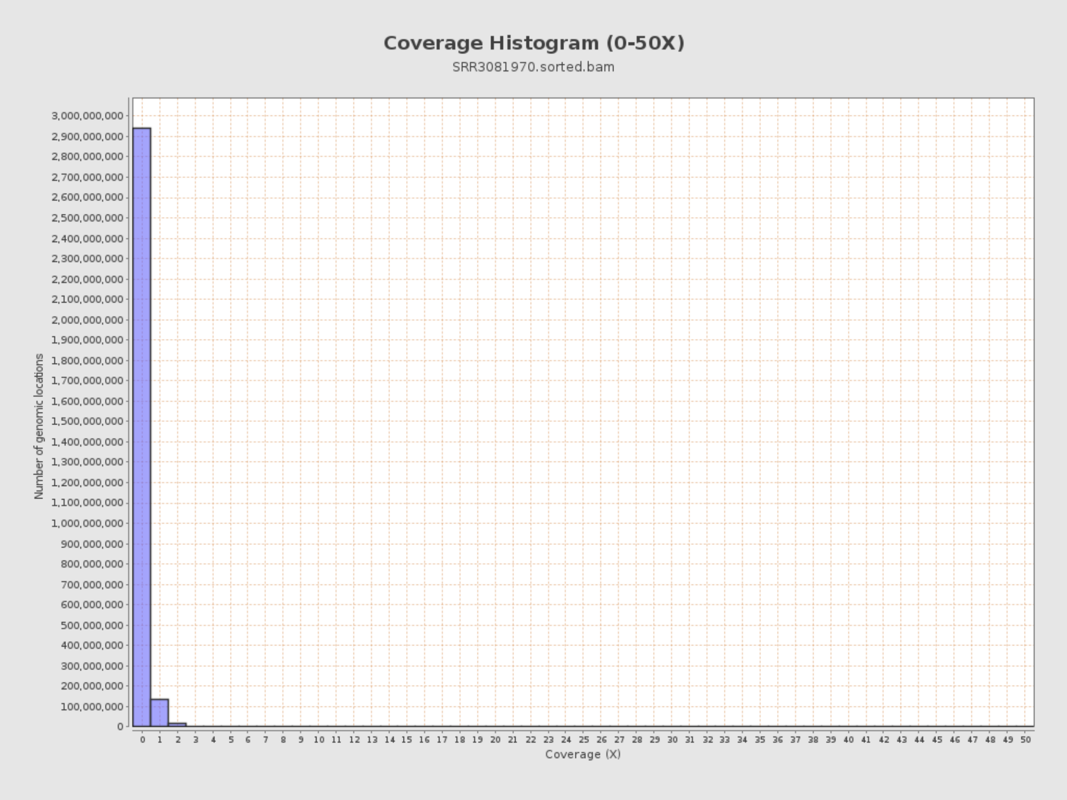
3. Results : Coverage across reference



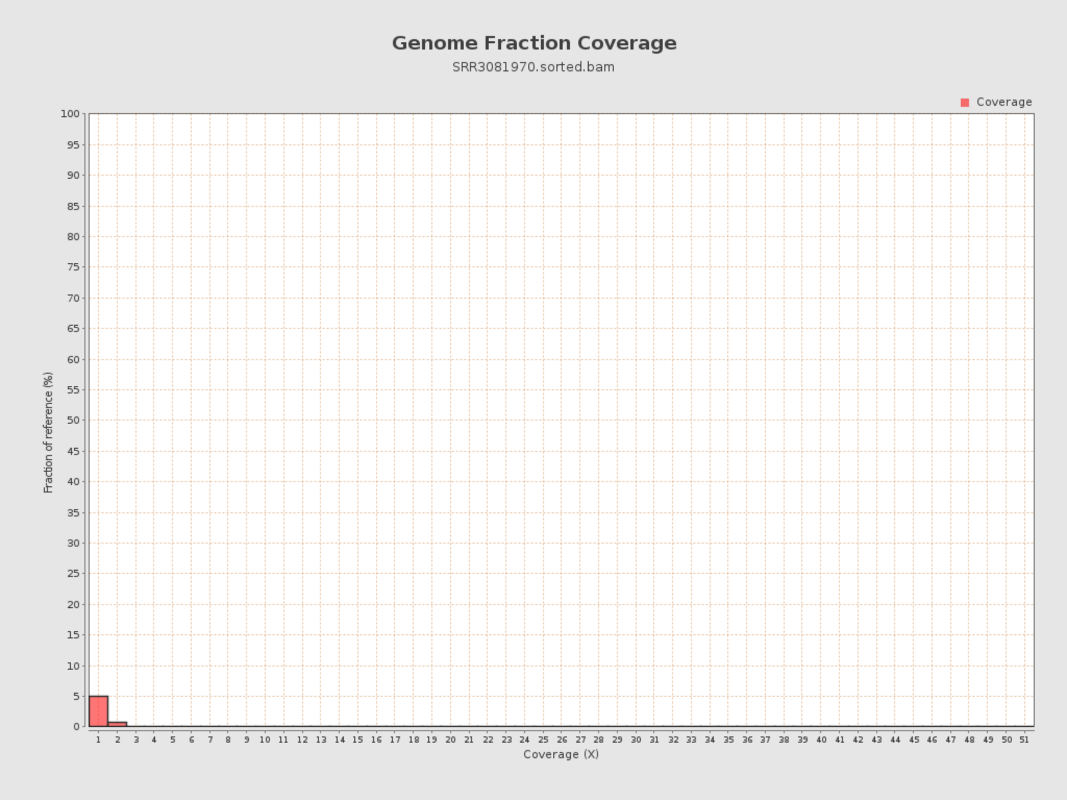
4. Results : Coverage Histogram



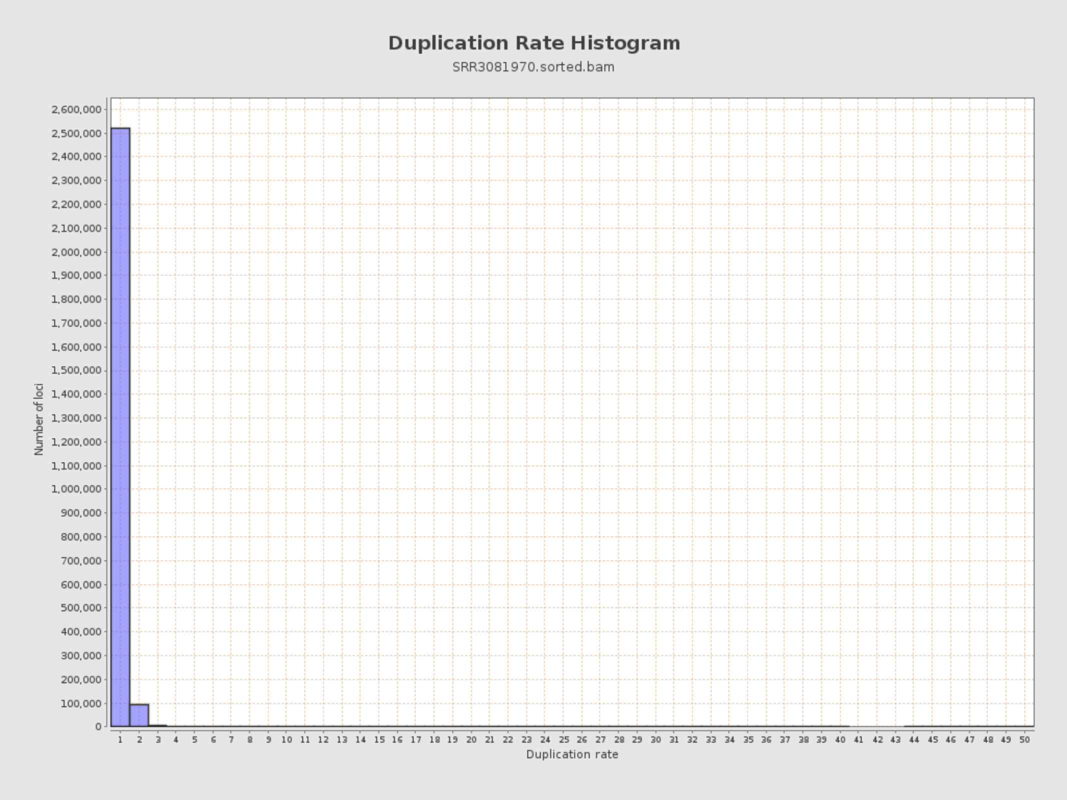
5. Results : Coverage Histogram (0-50X)



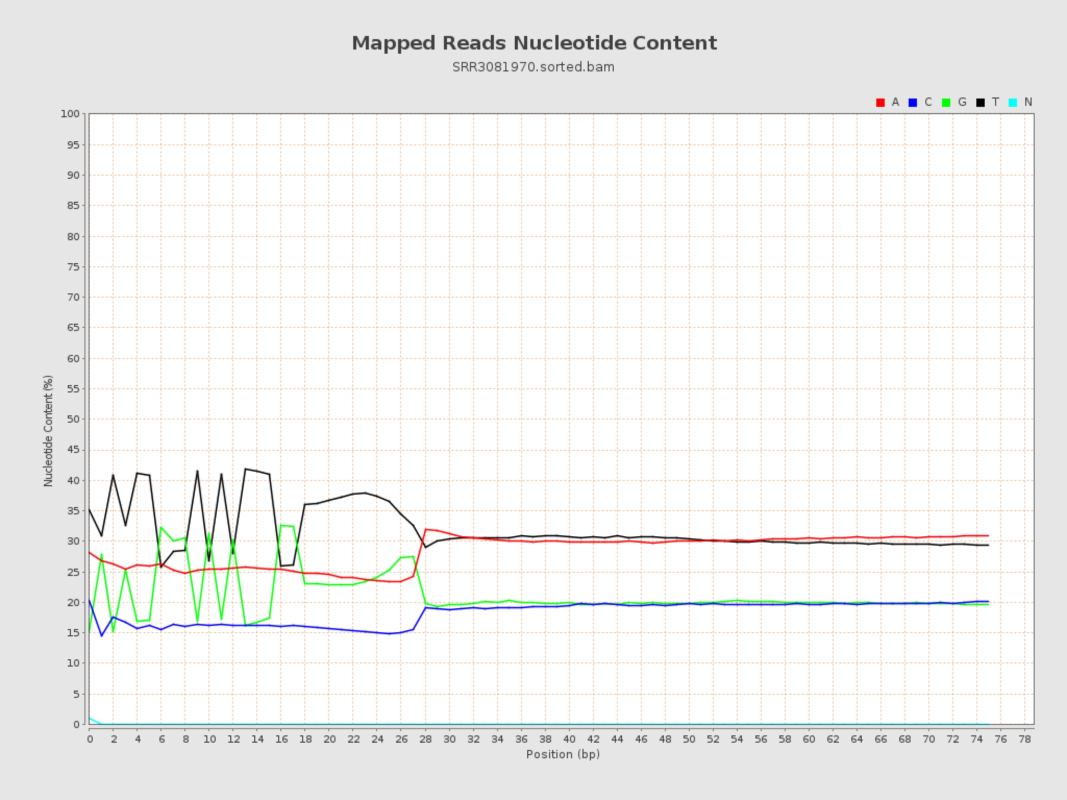
6. Results : Genome Fraction Coverage



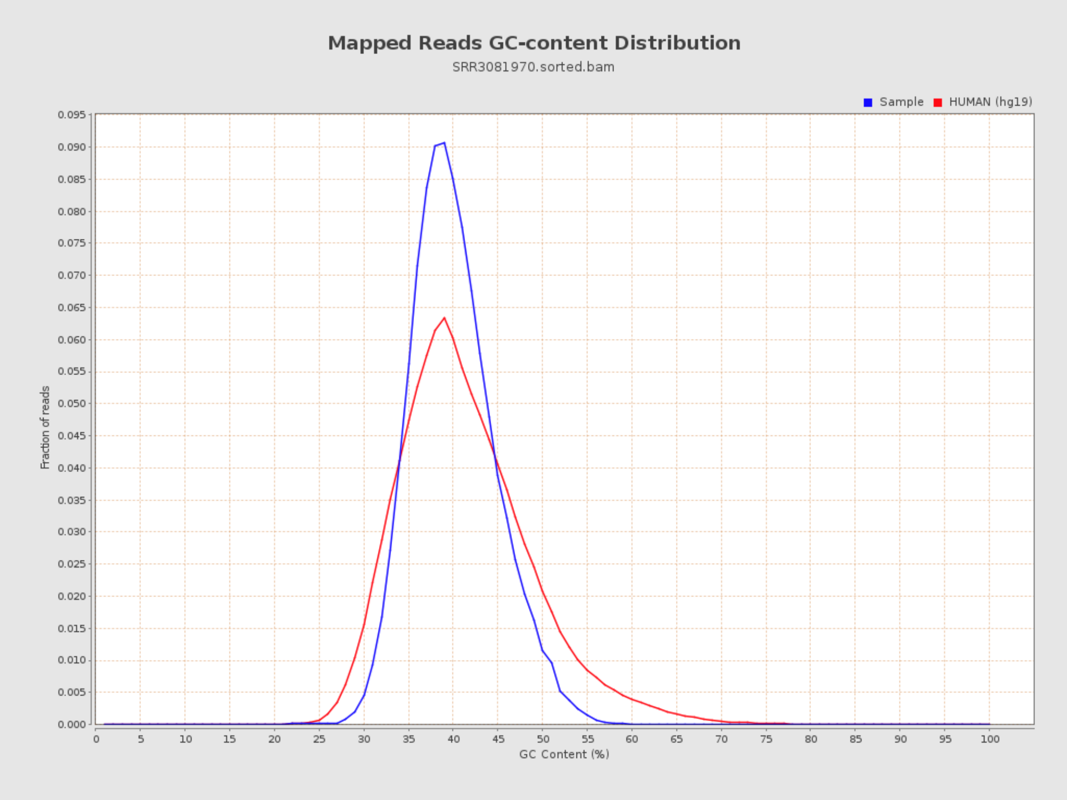
7. Results : Duplication Rate Histogram



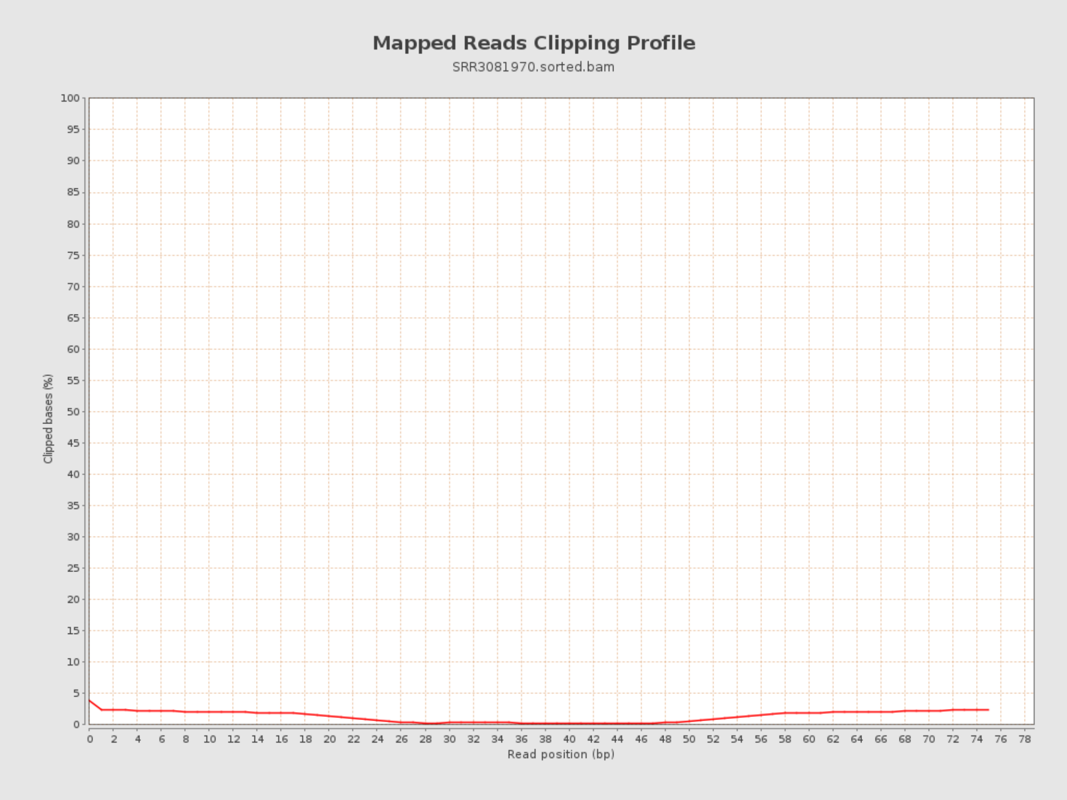
8. Results : Mapped Reads Nucleotide Content



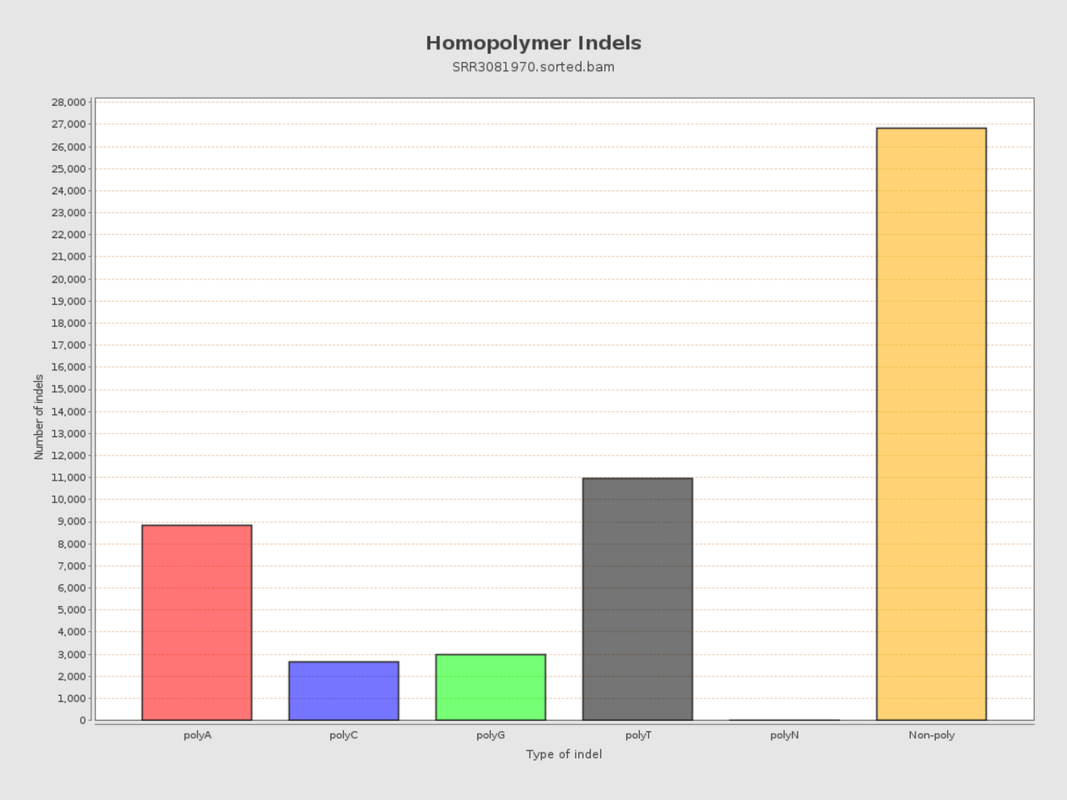
9. Results : Mapped Reads GC-content Distribution



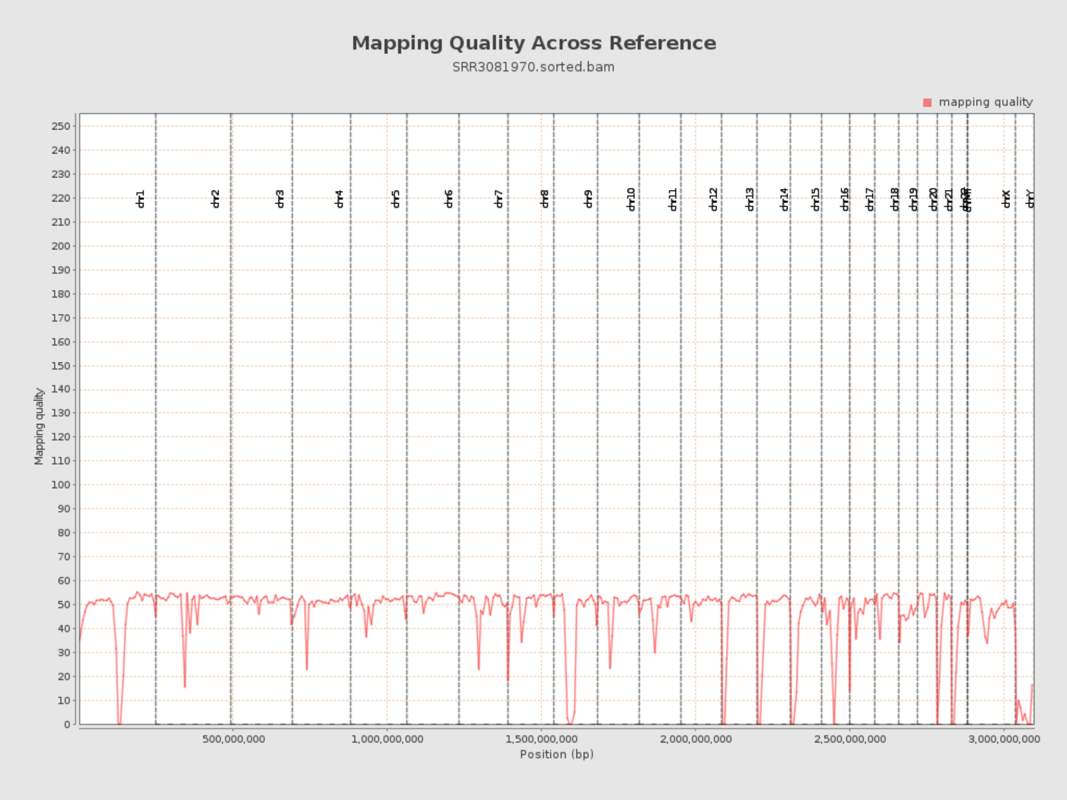
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram