Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:18:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971319.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_SRR2971319 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971319.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:18:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971319.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	75,490,972
Mapped reads	65,369,404 / 86.59%
Unmapped reads	10,121,568 / 13.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	11,165,595 / 14.79%
Duplication rate	14.17%
Clipped reads	4,203,249 / 5.57%

2.2. ACGT Content

Number/percentage of A's	783,372,867 / 30.24%
Number/percentage of C's	501,426,485 / 19.36%
Number/percentage of T's	796,021,937 / 30.73%
Number/percentage of G's	509,412,587 / 19.66%
Number/percentage of N's	248,795 / 0.01%
GC Percentage	39.02%

2.3. Coverage

Mean	0.8369
Standard Deviation	4.7398

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Mismatches and indels

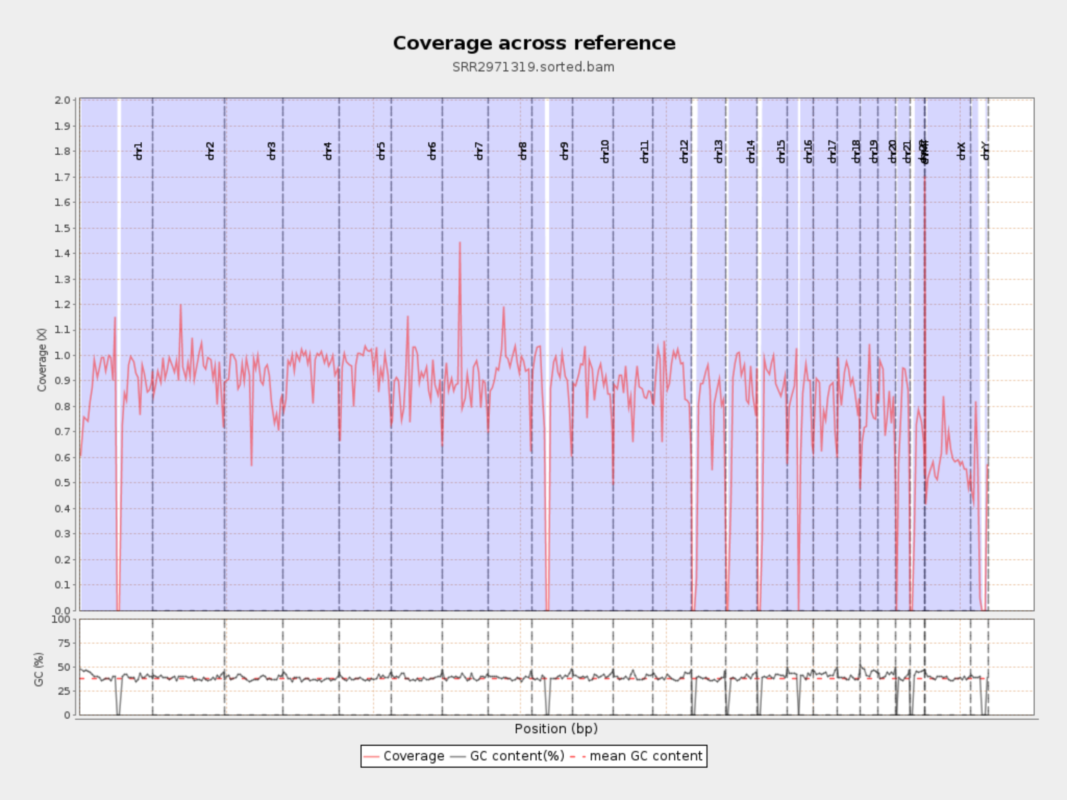
General error rate	0.28%
Mismatches	7,113,816
Insertions	84,363
Mapped reads with at least one insertion	0.13%
Deletions	258,127
Mapped reads with at least one deletion	0.39%
Homopolymer indels	47.11%

2.6. Chromosome stats

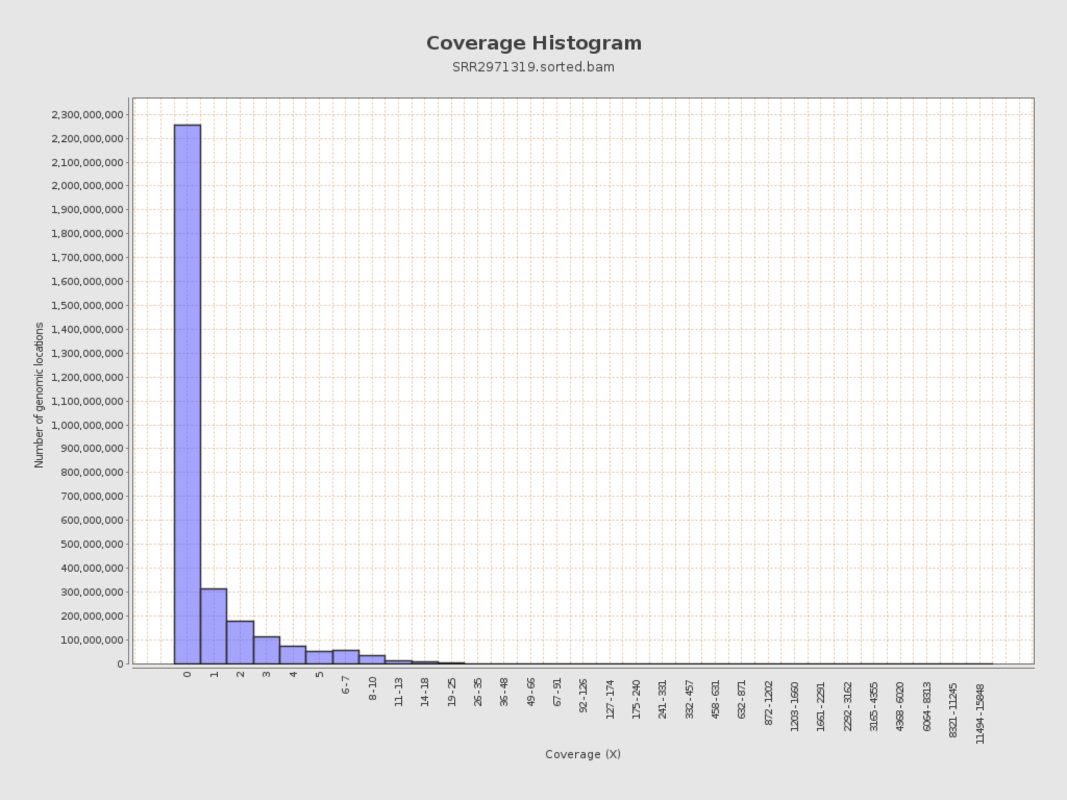
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	209122217	0.839	9.3824
chr2	243199373	230551384	0.948	4.0219
chr3	198022430	176522814	0.8914	2.2085
chr4	191154276	184432678	0.9648	2.4324
chr5	180915260	170870706	0.9445	2.3411
chr6	171115067	154661297	0.9038	3.2462
chr7	159138663	143256503	0.9002	7.801
chr8	146364022	139666486	0.9542	8.2957

chr9	141213431	113710806	0.8052	3.6346
chr10	135534747	122419002	0.9032	3.4102
chr11	135006516	115455671	0.8552	3.8971
chr12	133851895	122175407	0.9128	2.4174
chr13	115169878	80620001	0.7	1.905
chr14	107349540	81509953	0.7593	2.9313
chr15	102531392	75867757	0.7399	1.9629
chr16	90354753	68228168	0.7551	2.3624
chr17	81195210	64164553	0.7903	2.4436
chr18	78077248	69221510	0.8866	7.1957
chr19	59128983	45166015	0.7639	7.6521
chr20	63025520	51222113	0.8127	2.2365
chr21	48129895	34736562	0.7217	2.5724
chr22	51304566	25819468	0.5033	2.1952
chrMT	16571	28209	1.7023	2.1807
chrX	155270560	90140960	0.5805	2.6647
chrY	59373566	21240450	0.3577	2.8658

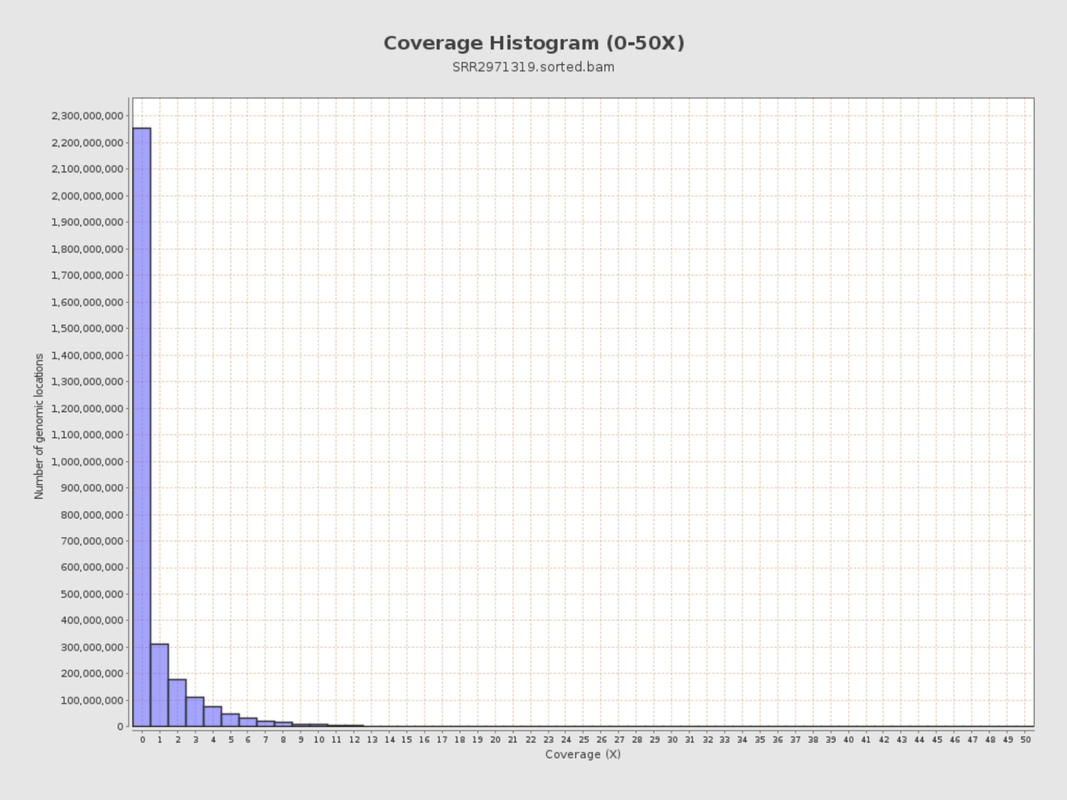
3. Results : Coverage across reference



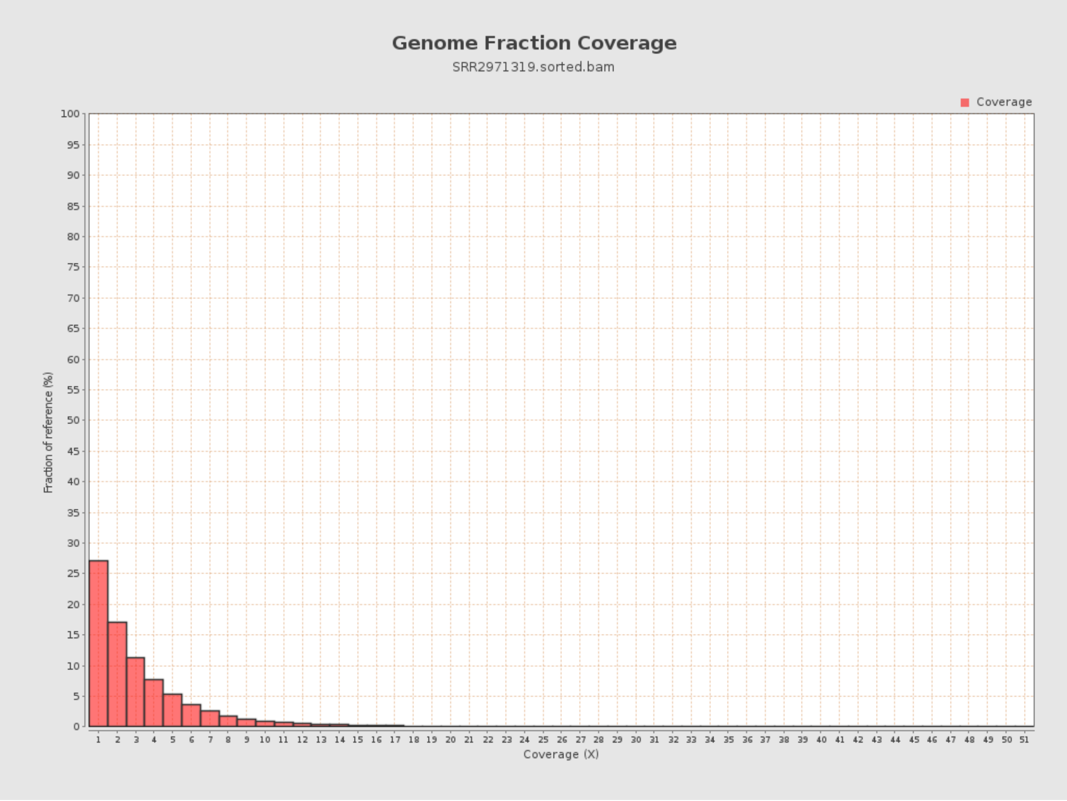
4. Results : Coverage Histogram



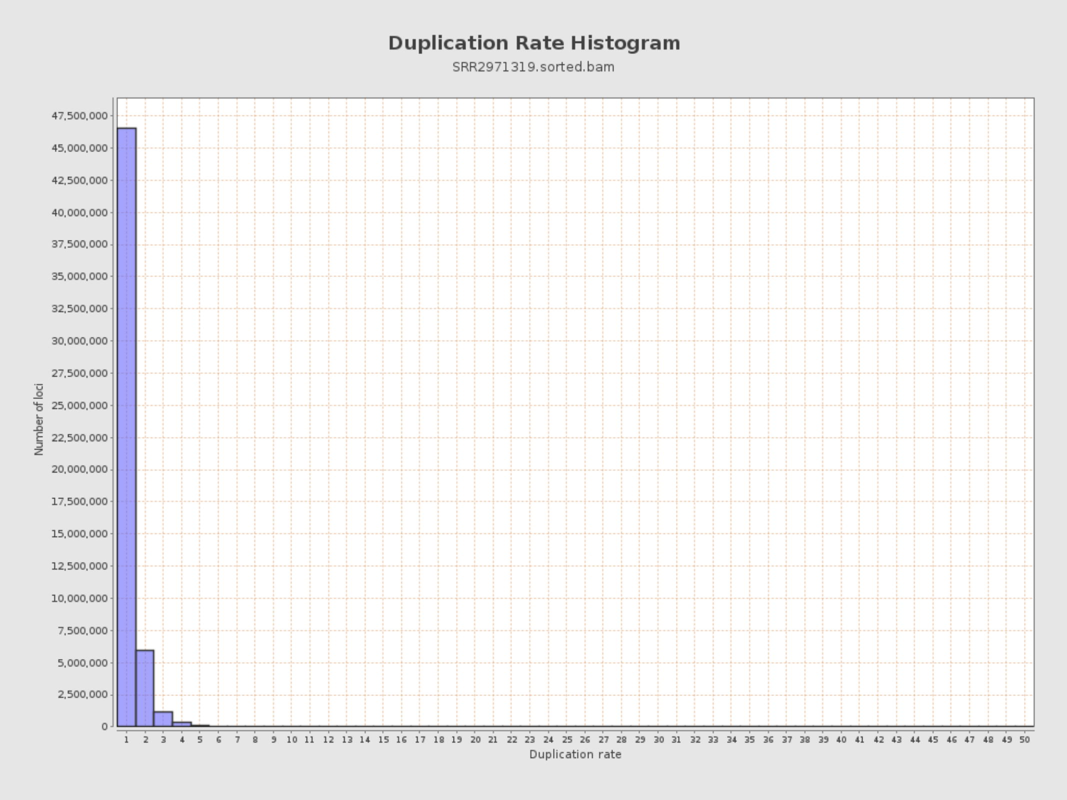
5. Results : Coverage Histogram (0-50X)



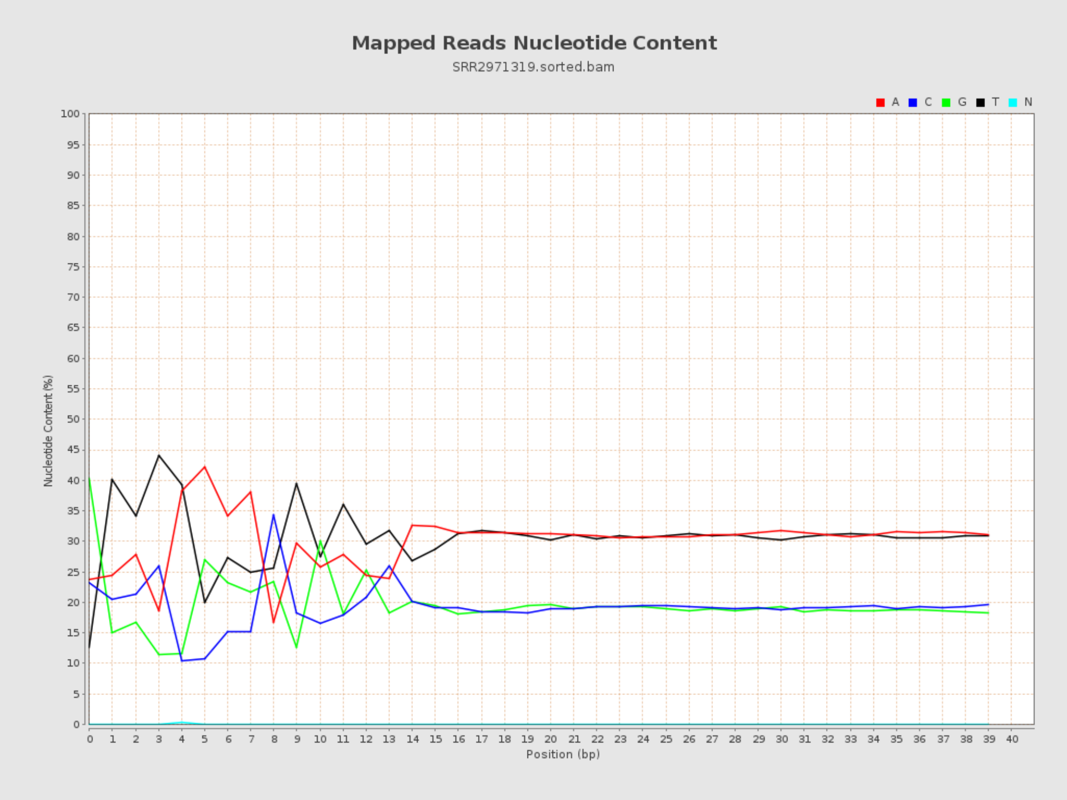
6. Results : Genome Fraction Coverage



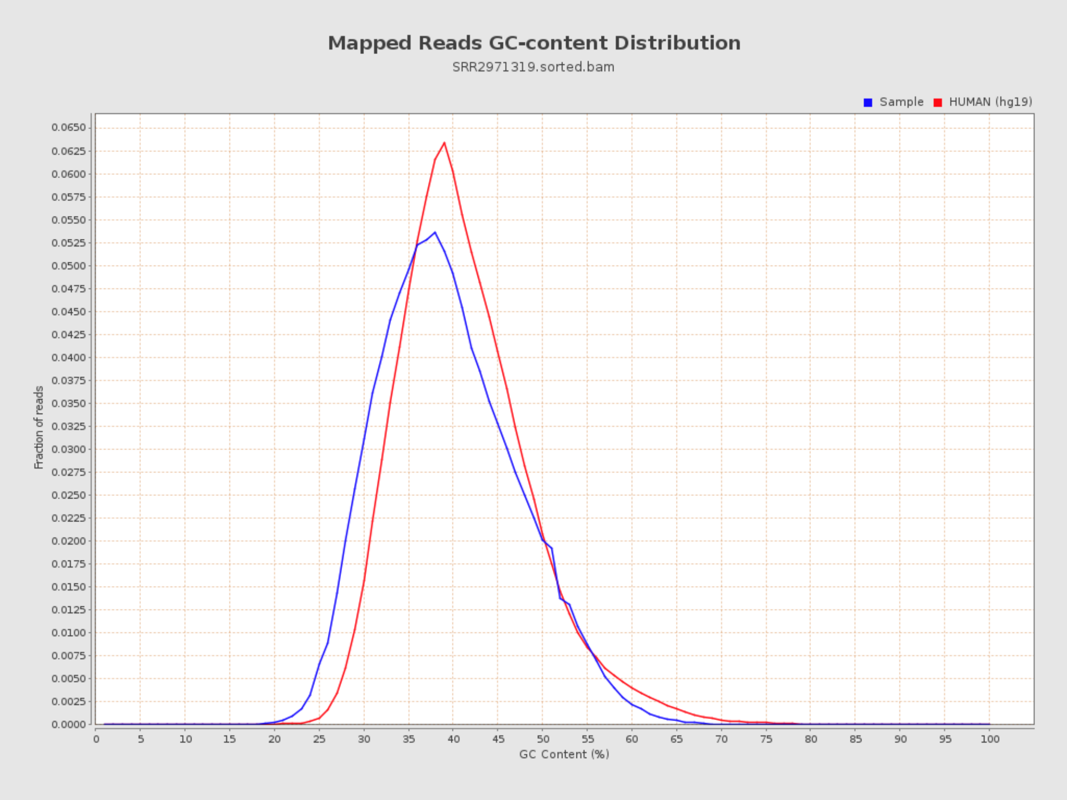
7. Results : Duplication Rate Histogram



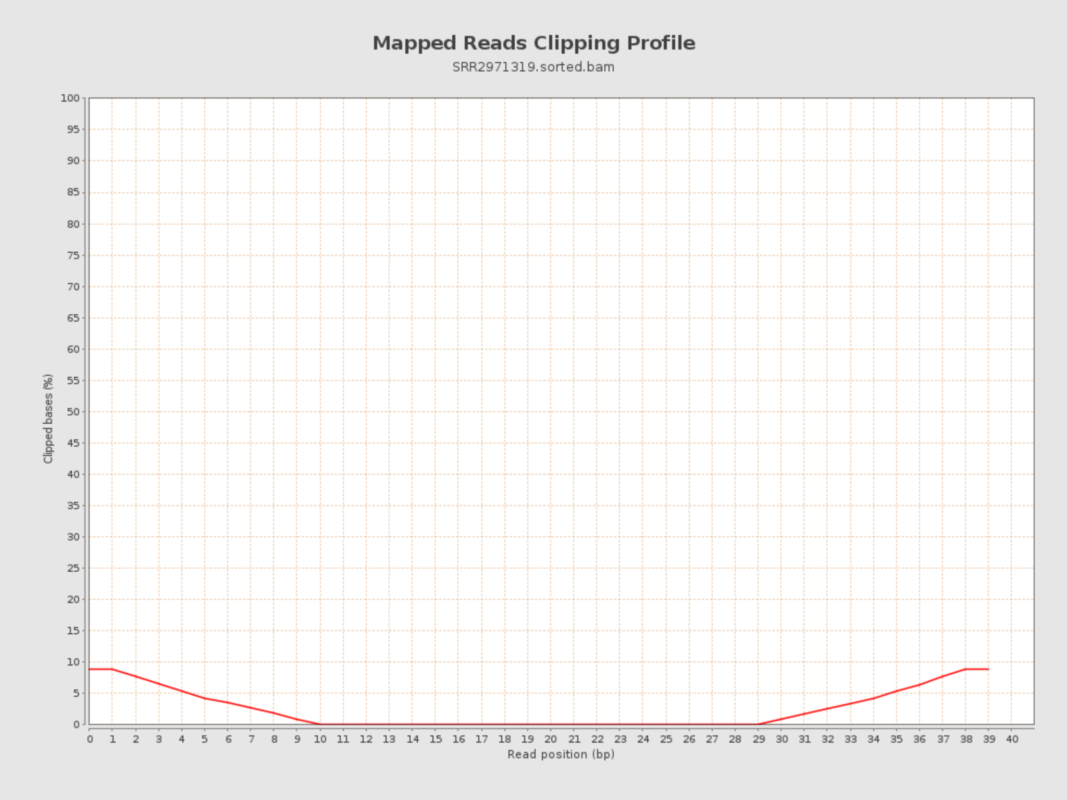
8. Results : Mapped Reads Nucleotide Content



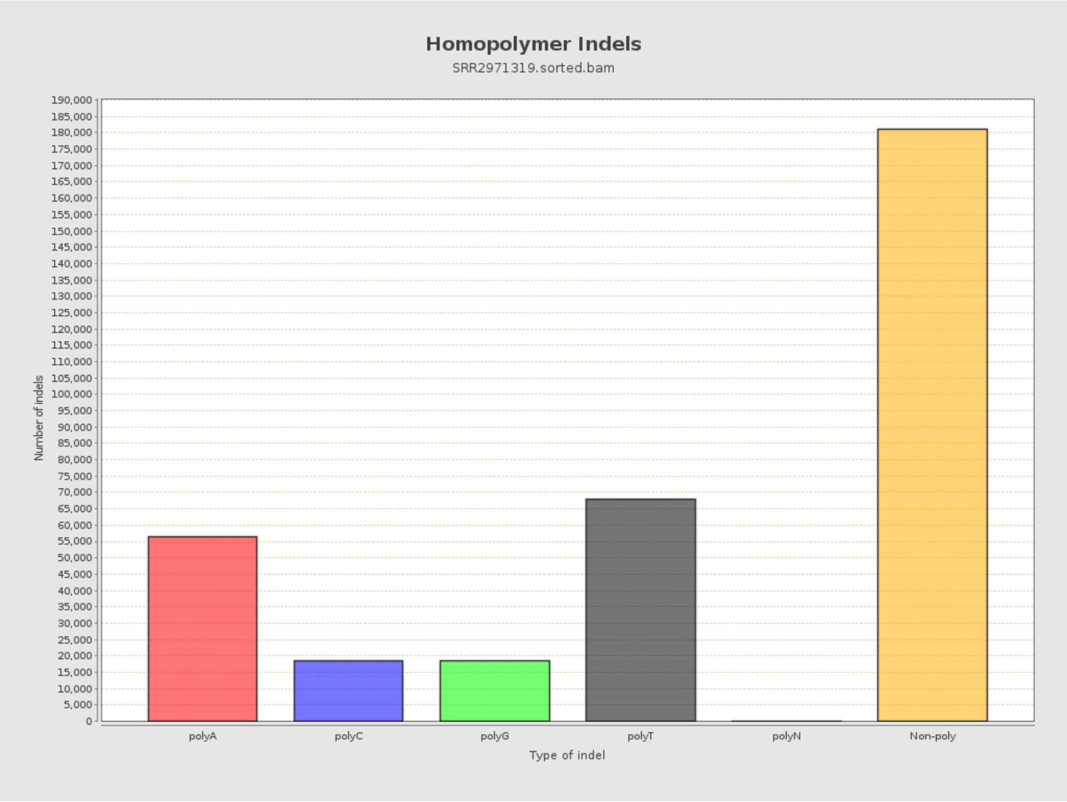
9. Results : Mapped Reads GC-content Distribution



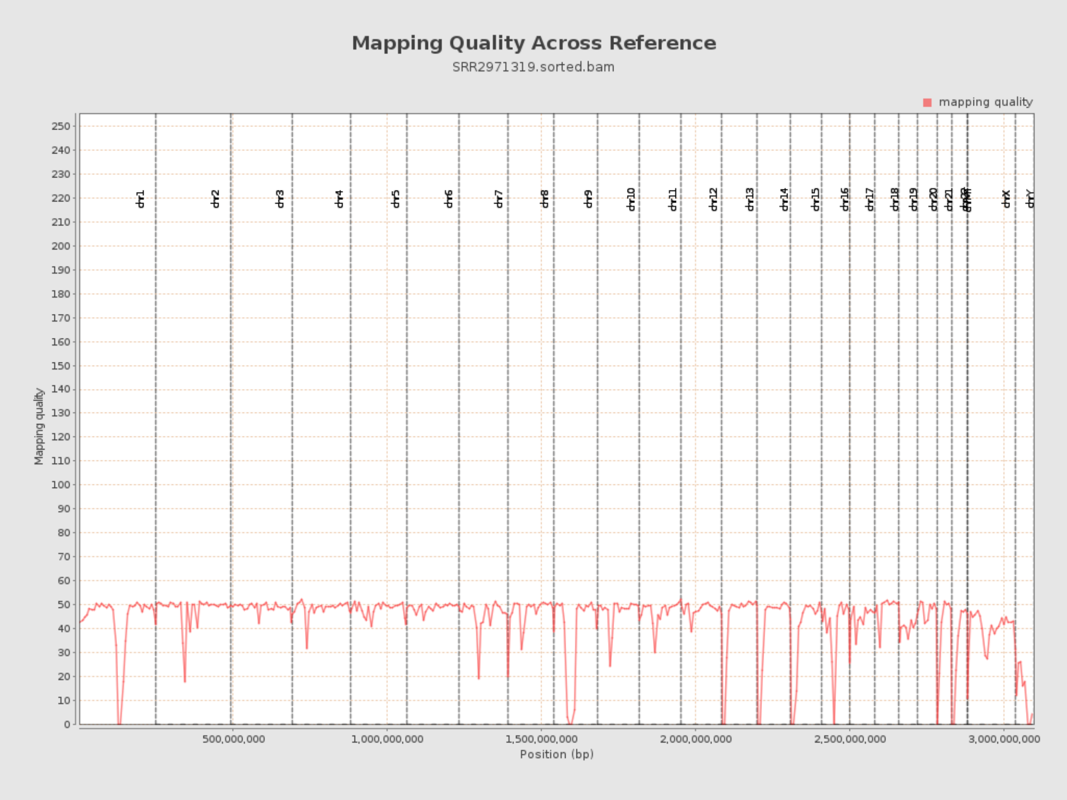
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram