Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:03:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971309.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_SRR2971309 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971309.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:03:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971309.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,499,942
Mapped reads	5,474,529 / 84.22%
Unmapped reads	1,025,413 / 15.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	281,348 / 4.33%
Duplication rate	3.77%
Clipped reads	573,205 / 8.82%

2.2. ACGT Content

Number/percentage of A's	61,933,961 / 28.72%
Number/percentage of C's	44,706,855 / 20.73%
Number/percentage of T's	63,295,946 / 29.35%
Number/percentage of G's	45,693,911 / 21.19%
Number/percentage of N's	12,245 / 0.01%
GC Percentage	41.92%

2.3. Coverage

Mean	0.0697
Standard Deviation	0.6185

2.4. Mapping Quality

Mean Mapping Quality	37.73

2.5. Mismatches and indels

General error rate	0.33%
Mismatches	708,327
Insertions	8,277
Mapped reads with at least one insertion	0.15%
Deletions	18,011
Mapped reads with at least one deletion	0.33%
Homopolymer indels	38.86%

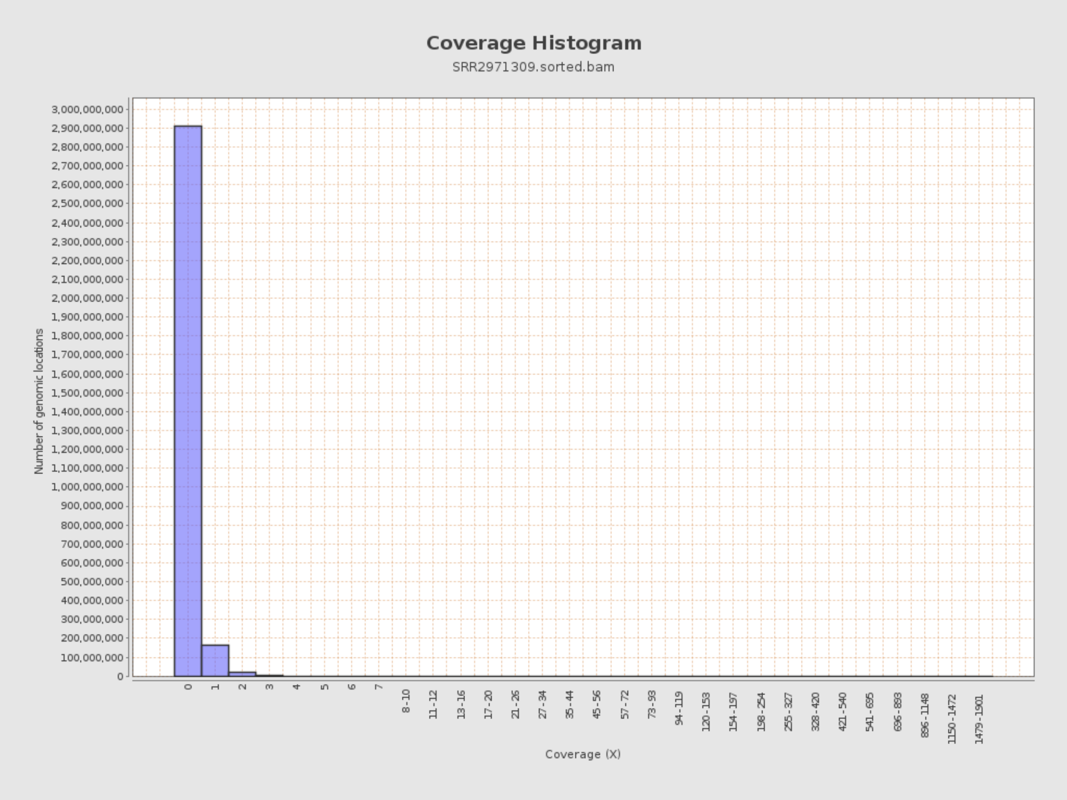
2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17068736	0.0685	1.1972
chr2	243199373	17526558	0.0721	0.541
chr3	198022430	14537807	0.0734	0.3092
chr4	191154276	14631024	0.0765	0.3766
chr5	180915260	13344637	0.0738	0.3155
chr6	171115067	12602123	0.0736	0.3656
chr7	159138663	12090670	0.076	0.8441
chr8	146364022	11129408	0.076	1.0088

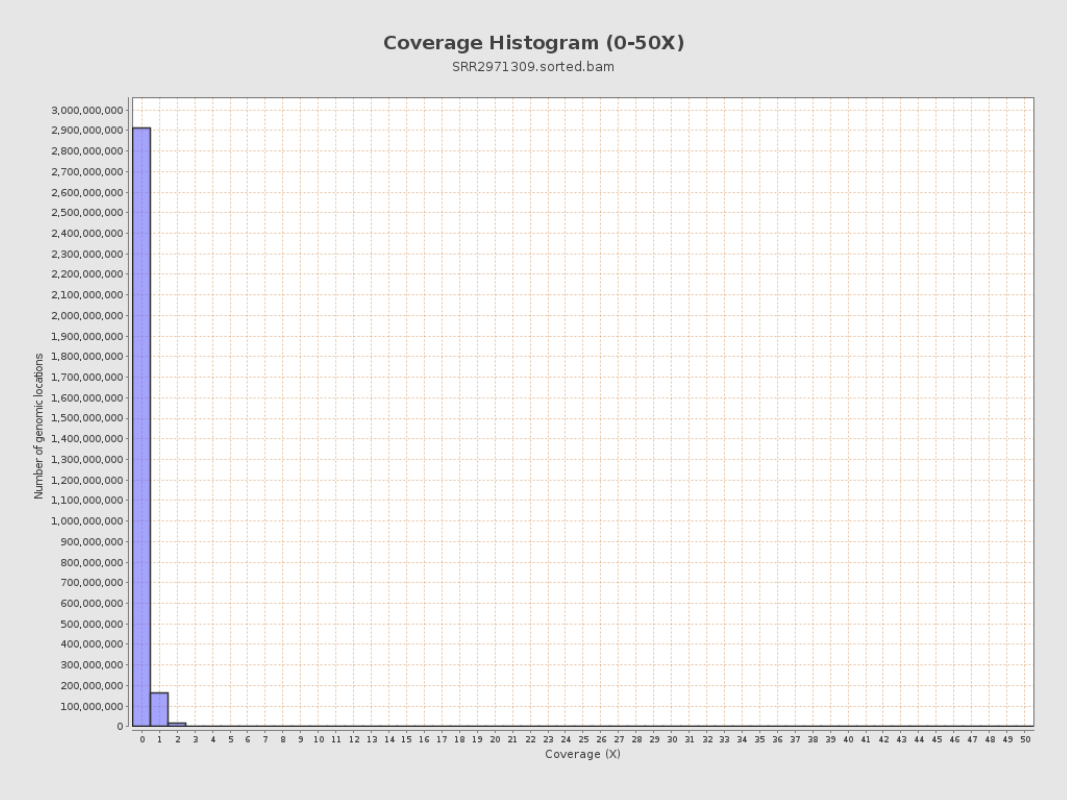
chr9	141213431	8952504	0.0634	0.5491
chr10	135534747	10367222	0.0765	0.7117
chr11	135006516	9779963	0.0724	0.453
chr12	133851895	9850747	0.0736	0.3248
chr13	115169878	6899482	0.0599	0.2707
chr14	107349540	6556592	0.0611	0.3713
chr15	102531392	5991165	0.0584	0.2727
chr16	90354753	6032435	0.0668	0.3921
chr17	81195210	5492445	0.0676	0.34
chr18	78077248	5690864	0.0729	0.9757
chr19	59128983	4315357	0.073	1.1608
chr20	63025520	4224781	0.067	0.3144
chr21	48129895	2745819	0.0571	0.3556
chr22	51304566	2247566	0.0438	0.2409
chrMT	16571	9809	0.5919	0.9397
chrX	155270560	12662577	0.0816	0.4037
chrY	59373566	915018	0.0154	0.2713

3. Results : Coverage across reference

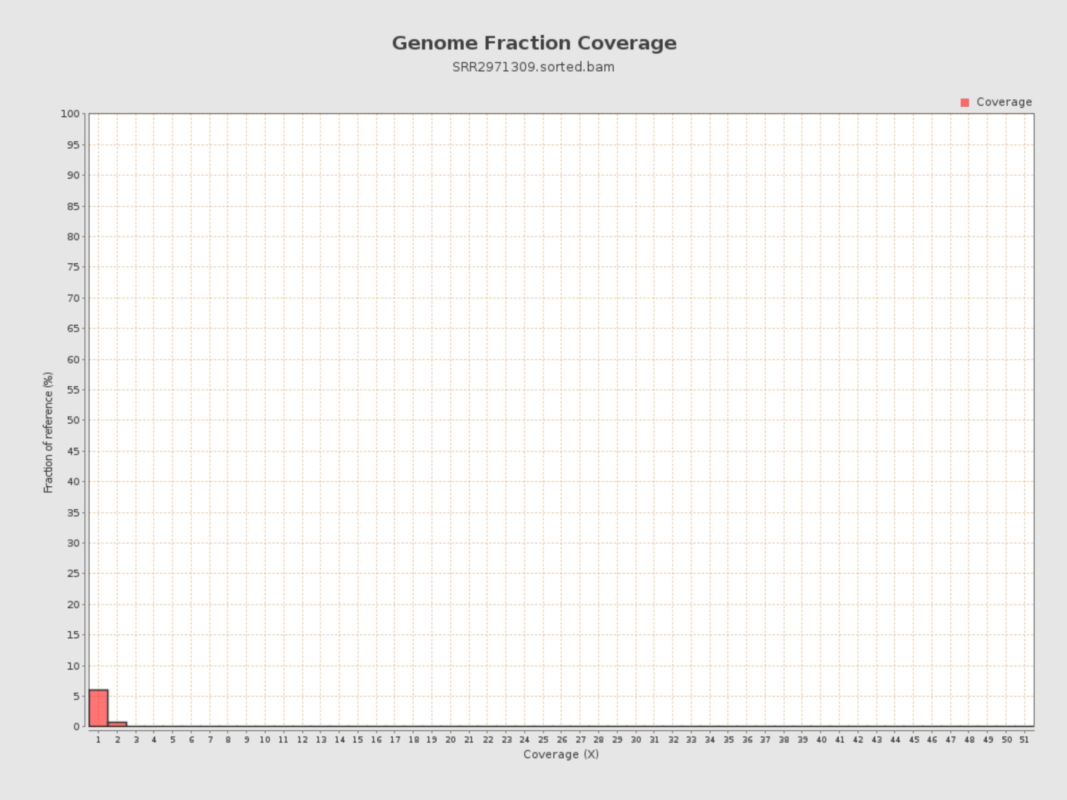
4. Results : Coverage Histogram



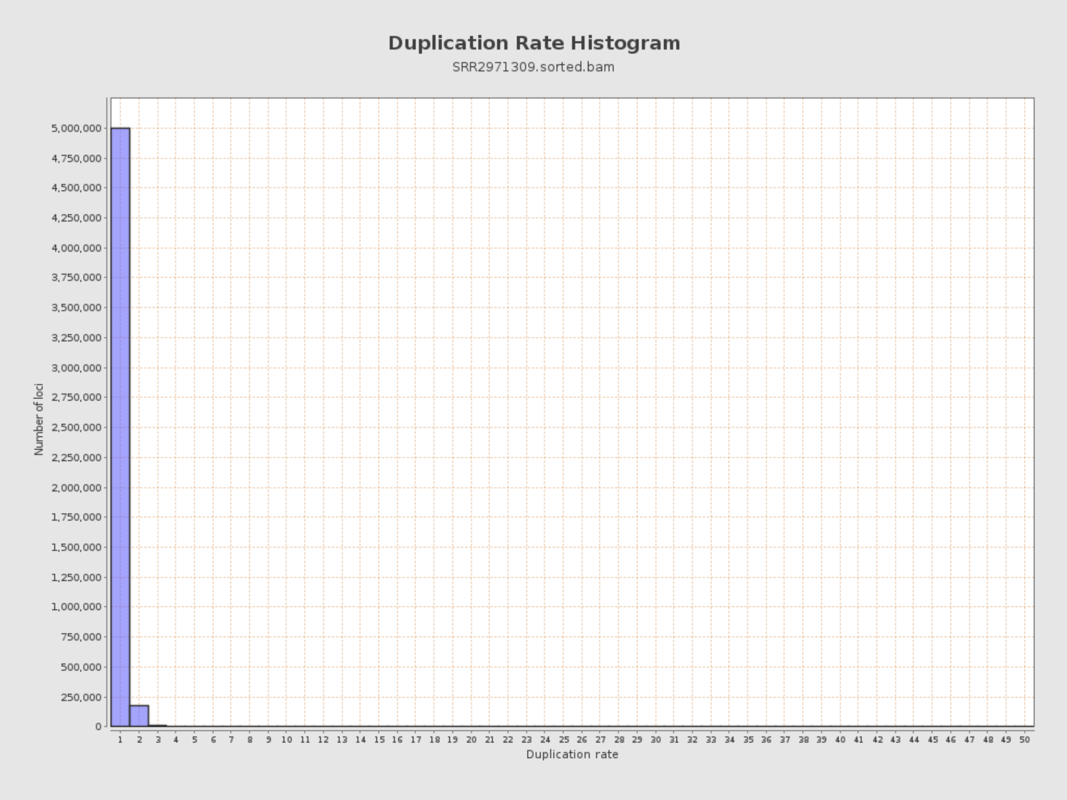
5. Results : Coverage Histogram (0-50X)



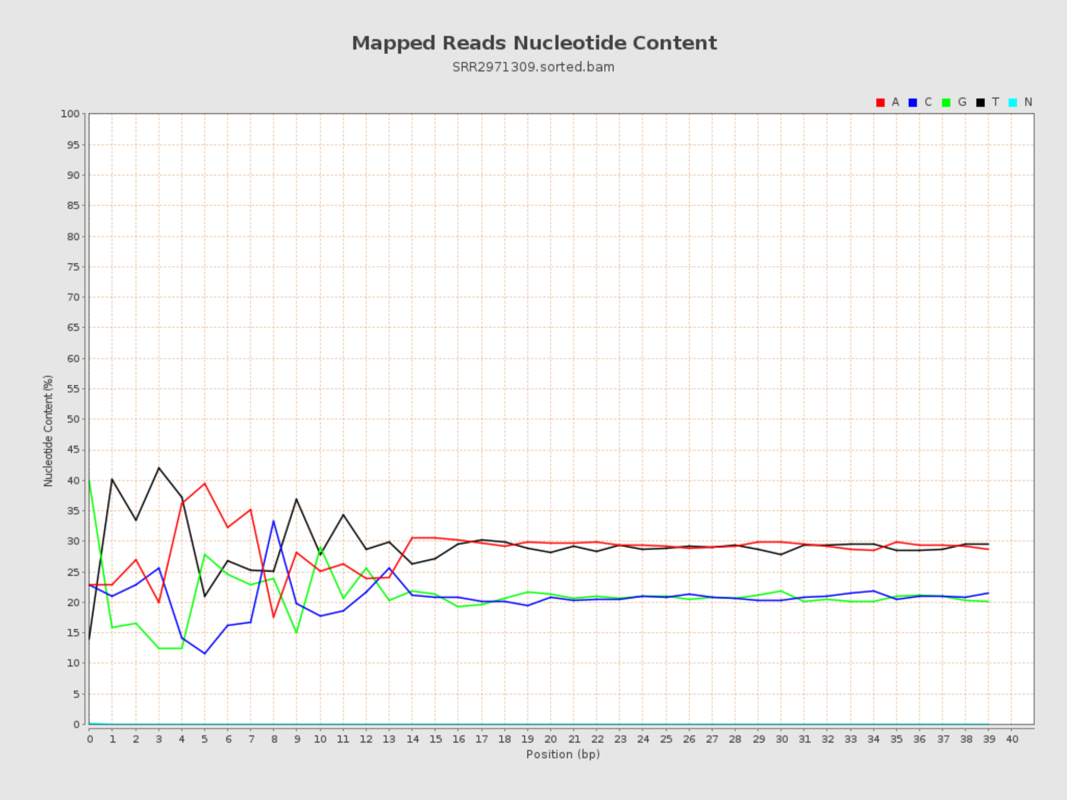
6. Results : Genome Fraction Coverage



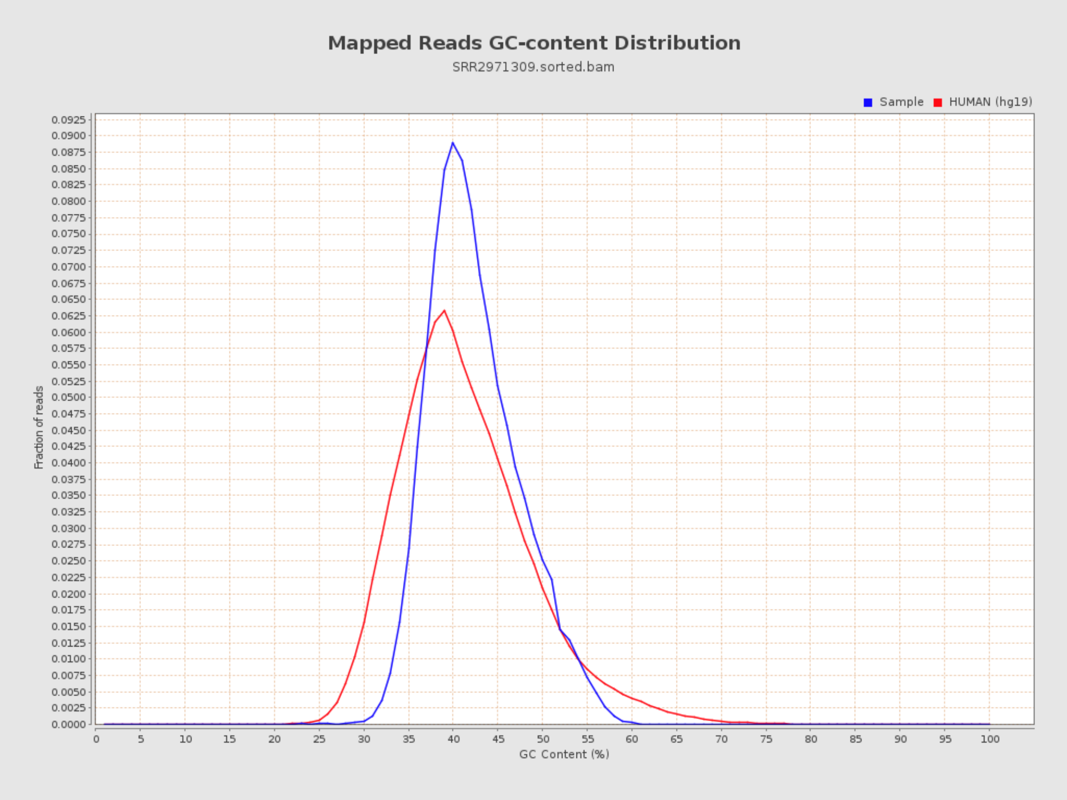
7. Results : Duplication Rate Histogram



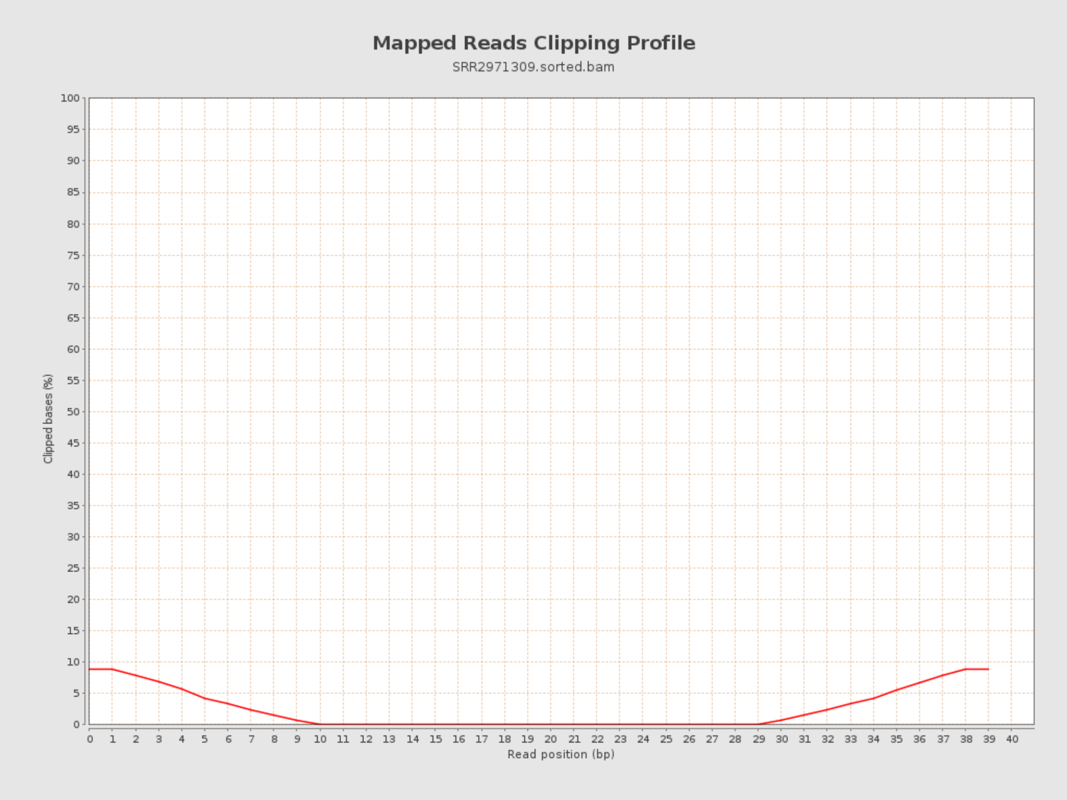
8. Results : Mapped Reads Nucleotide Content



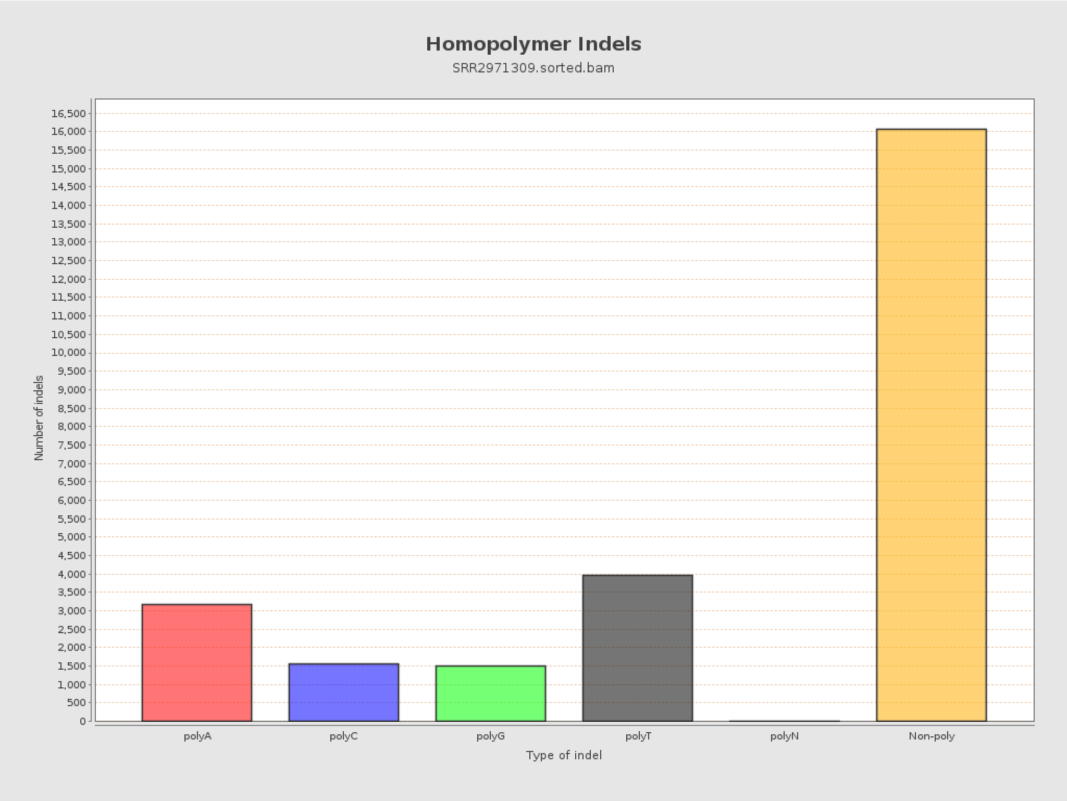
9. Results : Mapped Reads GC-content Distribution



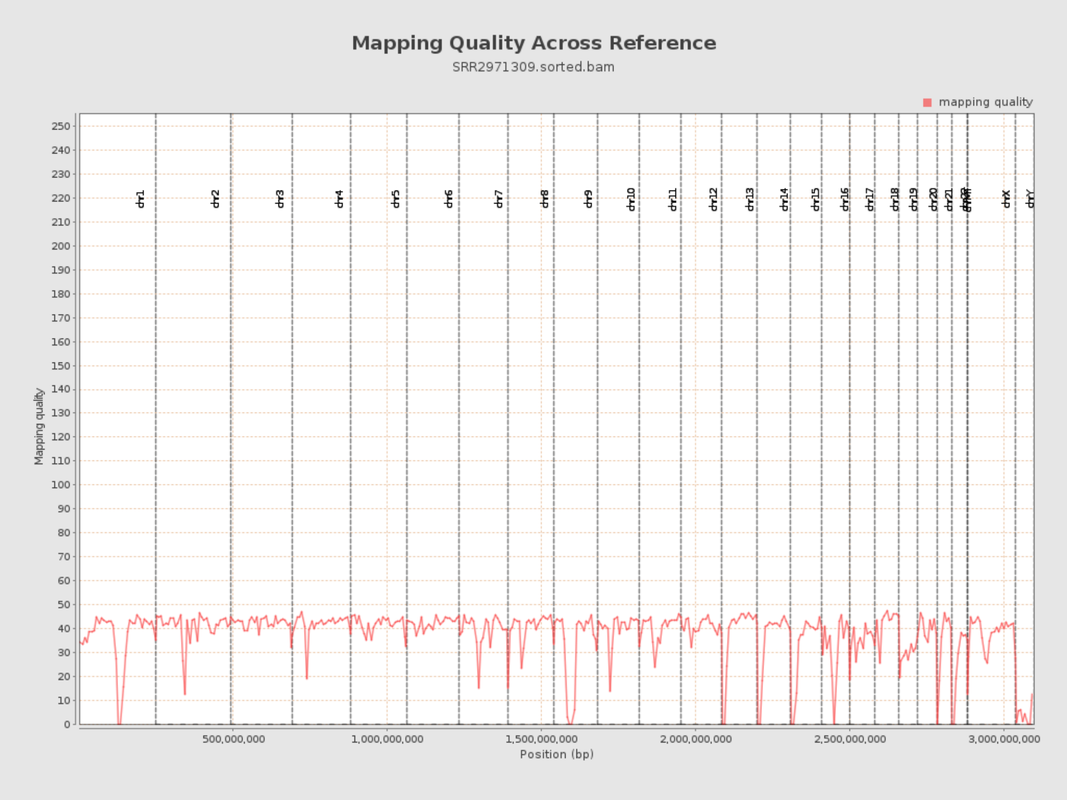
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram