Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:40:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081096.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_SRR3081096 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081096.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:40:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081096.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,566,998
Mapped reads	2,332,120 / 90.85%
Unmapped reads	234,878 / 9.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,695 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	106,603 / 4.15%
Duplication rate	3.63%
Clipped reads	1,054,289 / 41.07%

2.2. ACGT Content

Number/percentage of A's	43,592,256 / 27.9%
Number/percentage of C's	29,757,904 / 19.05%
Number/percentage of T's	48,589,884 / 31.1%
Number/percentage of G's	34,292,474 / 21.95%
Number/percentage of N's	1,712 / 0%
GC Percentage	41%

2.3. Coverage

Mean	0.0505

Standard Deviation	0.4009

2.4. Mapping Quality

Mean Mapping Quality	45.59

2.5. Mismatches and indels

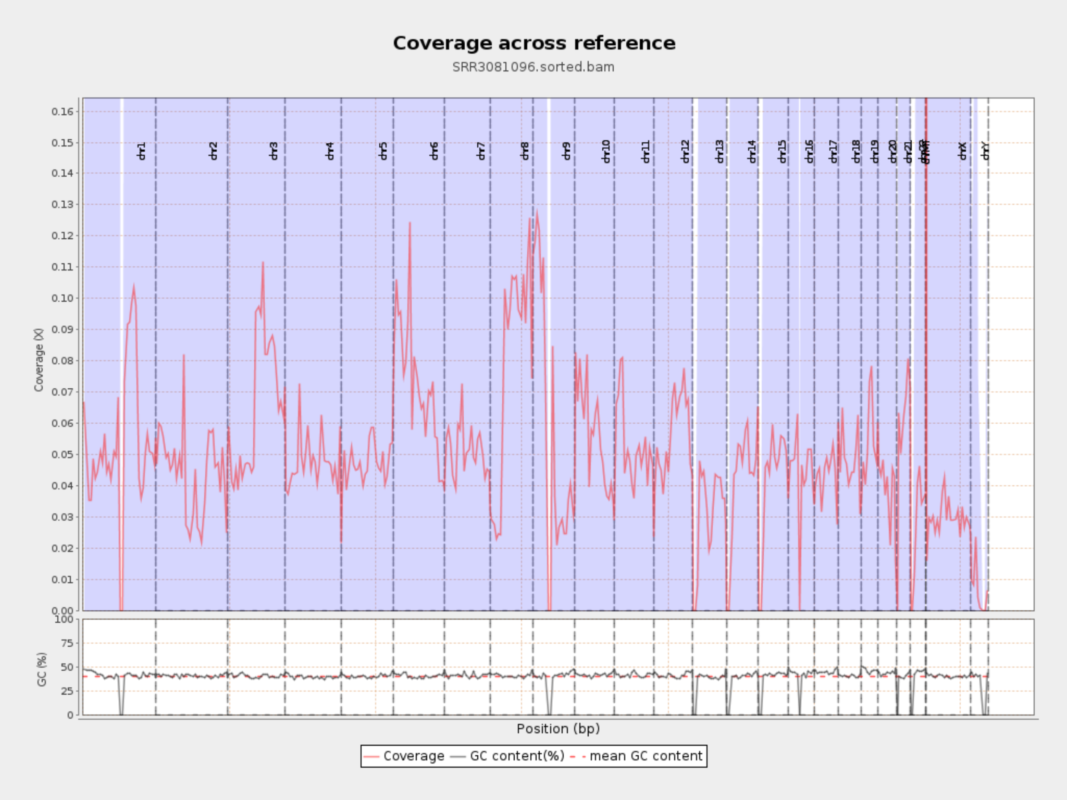
General error rate	0.93%
Mismatches	1,428,947
Insertions	12,308
Mapped reads with at least one insertion	0.52%
Deletions	34,500
Mapped reads with at least one deletion	1.46%
Homopolymer indels	46.1%

2.6. Chromosome stats

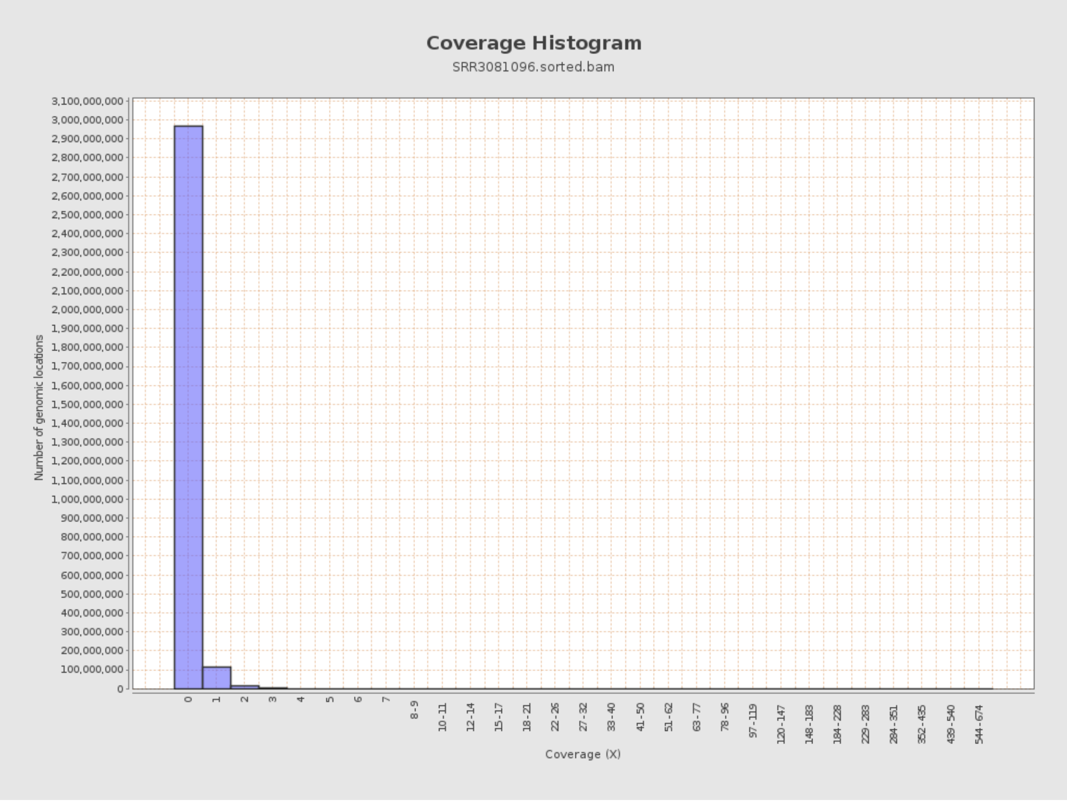
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13313378	0.0534	0.622
chr2	243199373	10791078	0.0444	0.4404
chr3	198022430	12933770	0.0653	0.2968
chr4	191154276	9124697	0.0477	0.2748
chr5	180915260	8646734	0.0478	0.2539
chr6	171115067	12565911	0.0734	0.4479
chr7	159138663	8187918	0.0515	0.4584

chr8	146364022	11560085	0.079	0.4598
chr9	141213431	7937425	0.0562	0.4926
chr10	135534747	7679216	0.0567	0.4096
chr11	135006516	7144247	0.0529	0.3192
chr12	133851895	7626529	0.057	0.297
chr13	115169878	3562532	0.0309	0.2062
chr14	107349540	4424949	0.0412	0.3318
chr15	102531392	4184887	0.0408	0.2329
chr16	90354753	3883903	0.043	0.3207
chr17	81195210	3568124	0.0439	0.2501
chr18	78077248	3841392	0.0492	0.7935
chr19	59128983	3236974	0.0547	0.4549
chr20	63025520	2486556	0.0395	0.2443
chr21	48129895	2871891	0.0597	0.3319
chr22	51304566	1379060	0.0269	0.1858
chrMT	16571	354830	21.4127	11.3693
chrX	155270560	4600022	0.0296	0.2321
chrY	59373566	384635	0.0065	0.1646

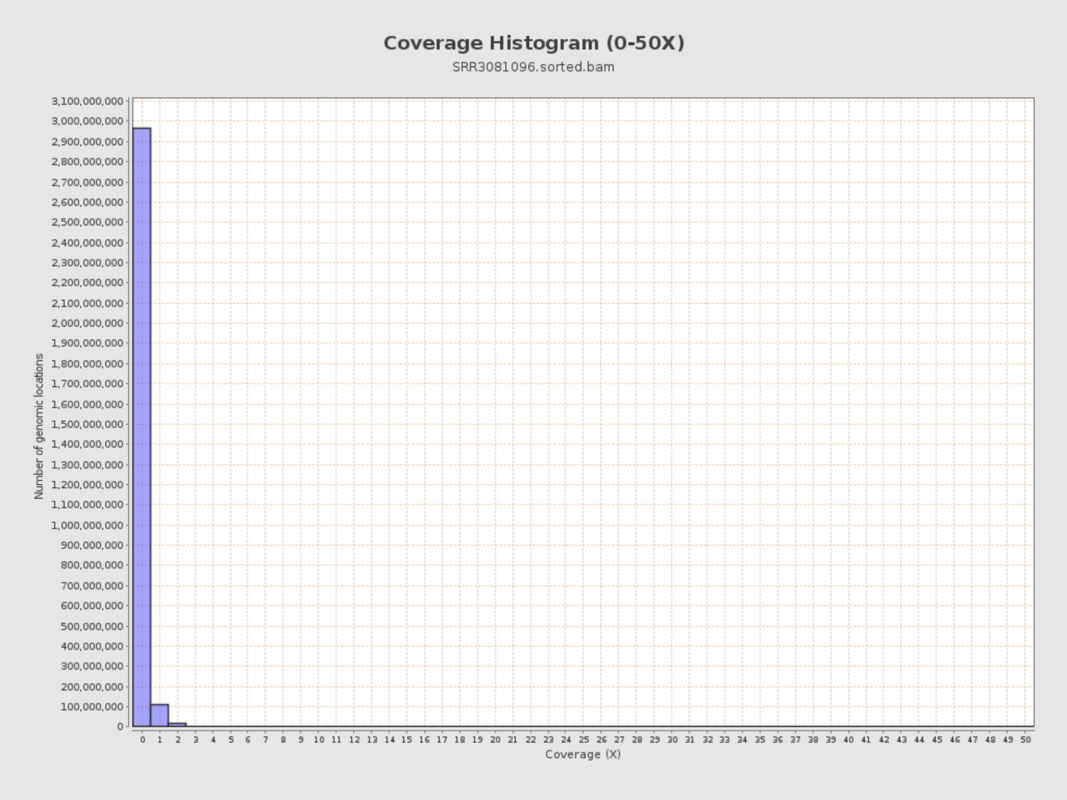
3. Results : Coverage across reference



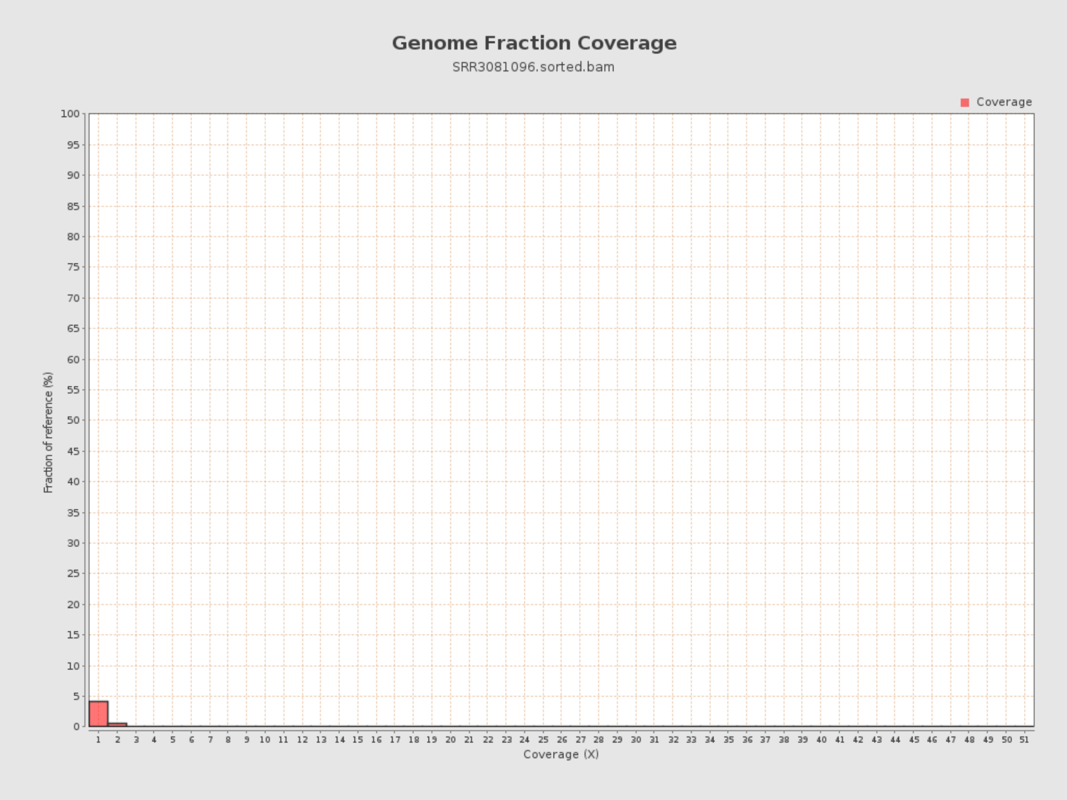
4. Results : Coverage Histogram



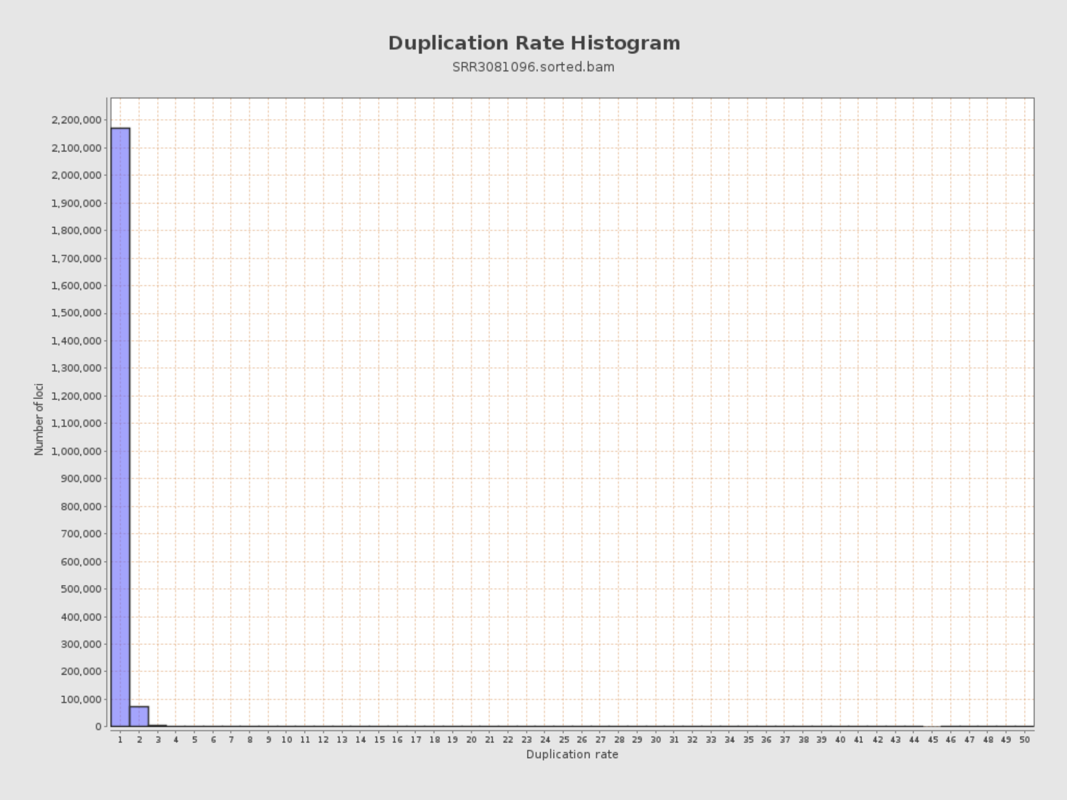
5. Results : Coverage Histogram (0-50X)



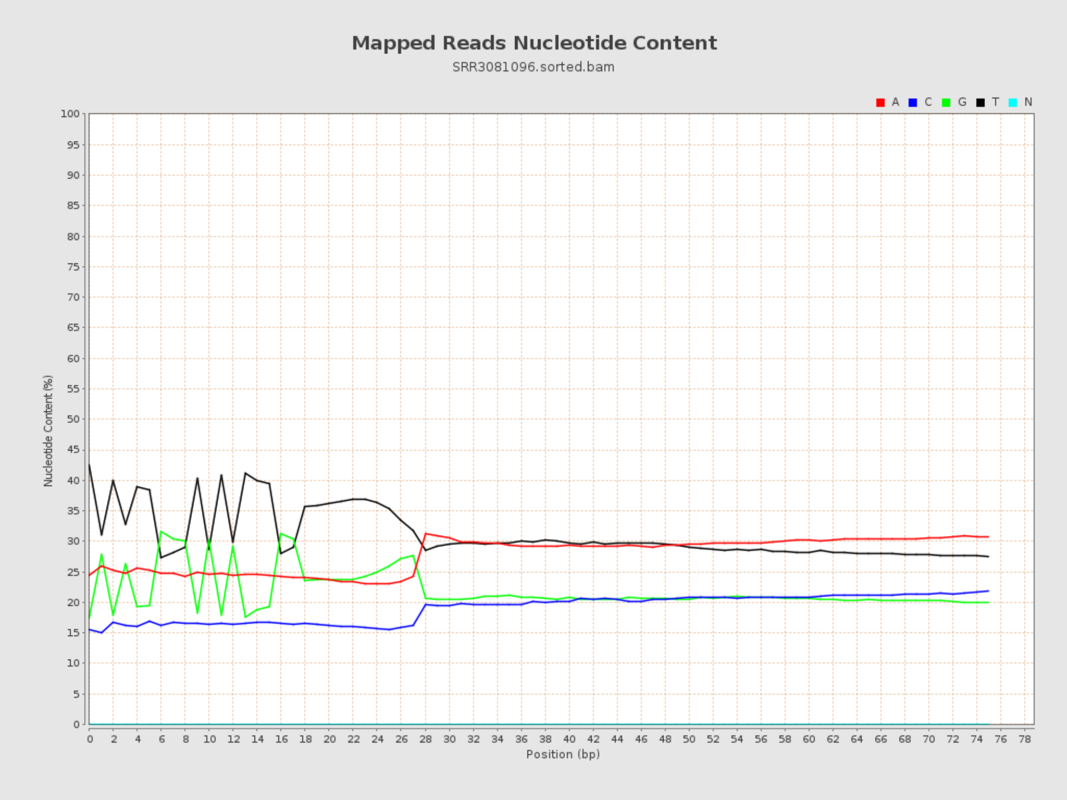
6. Results : Genome Fraction Coverage



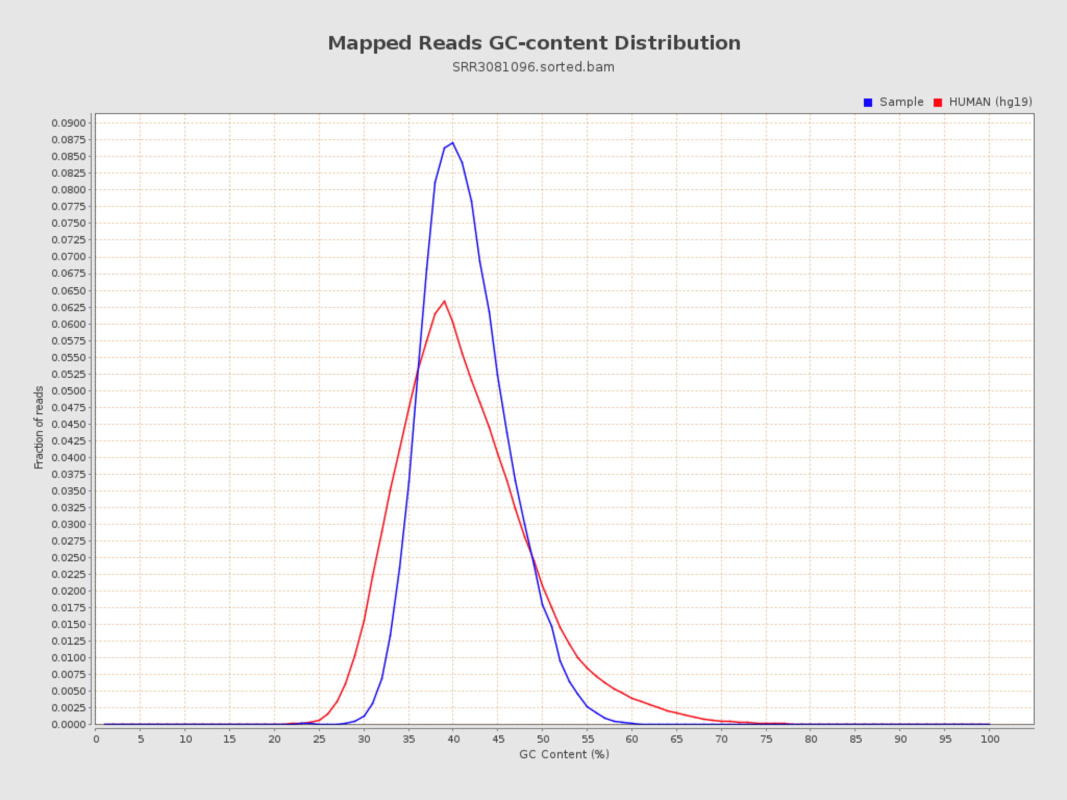
7. Results : Duplication Rate Histogram



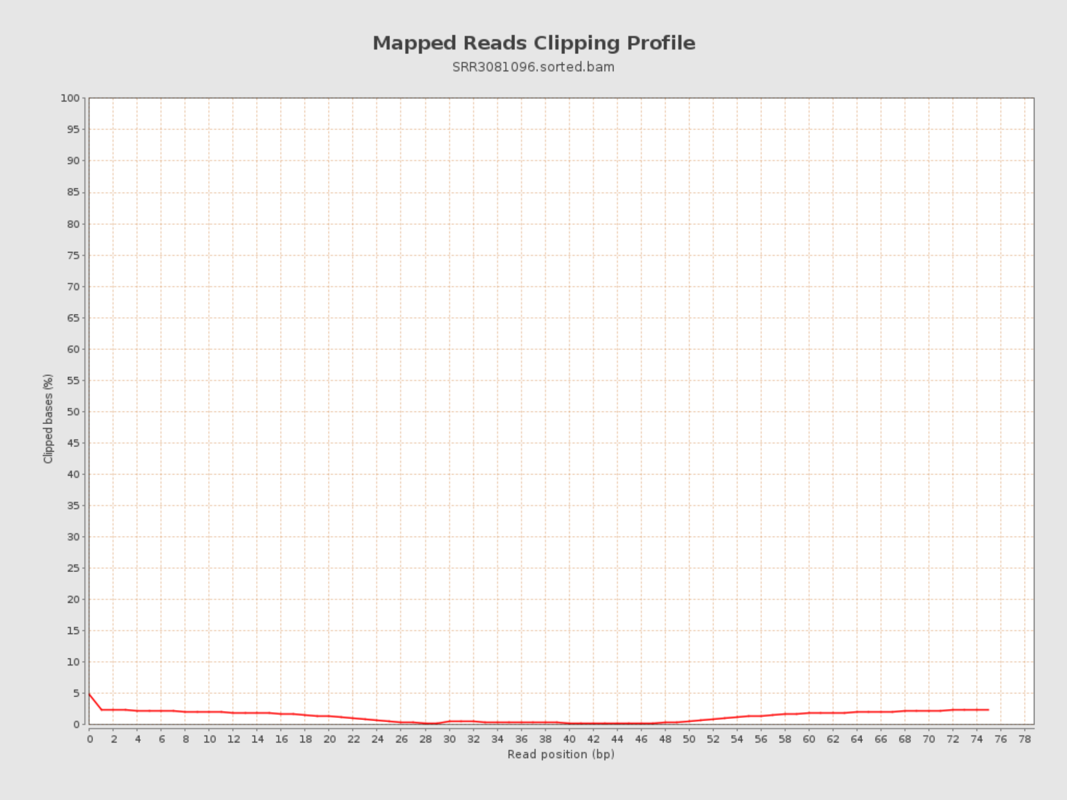
8. Results : Mapped Reads Nucleotide Content



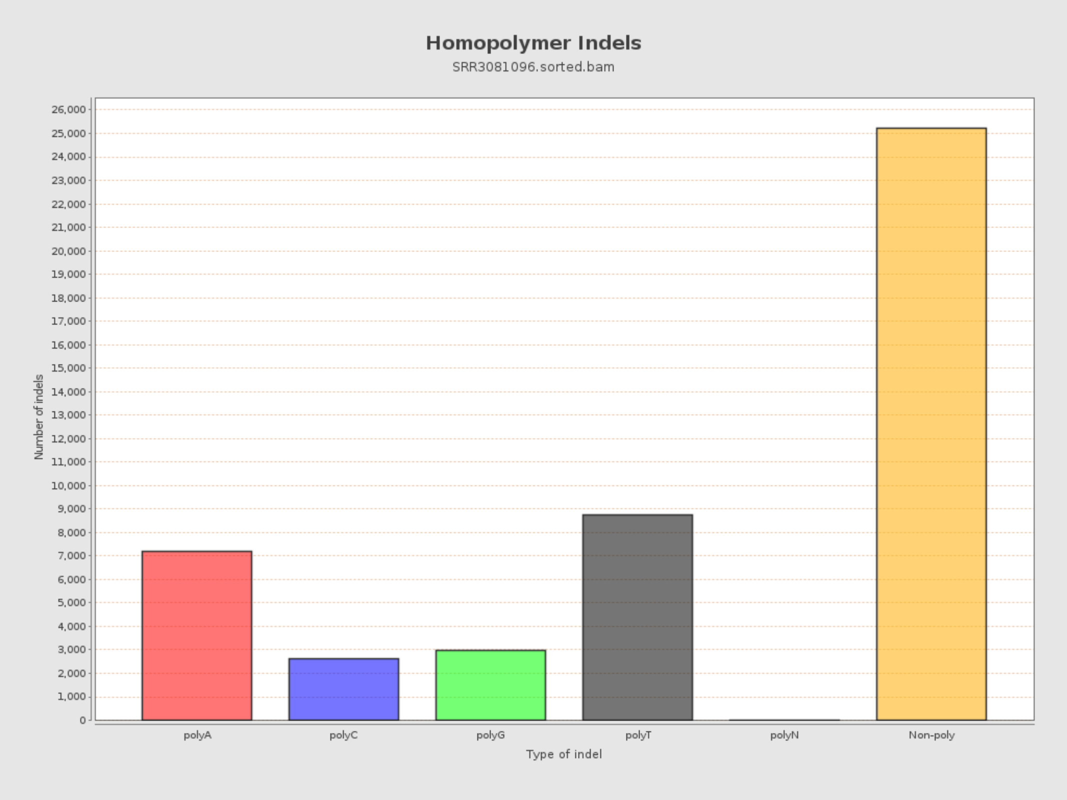
9. Results : Mapped Reads GC-content Distribution



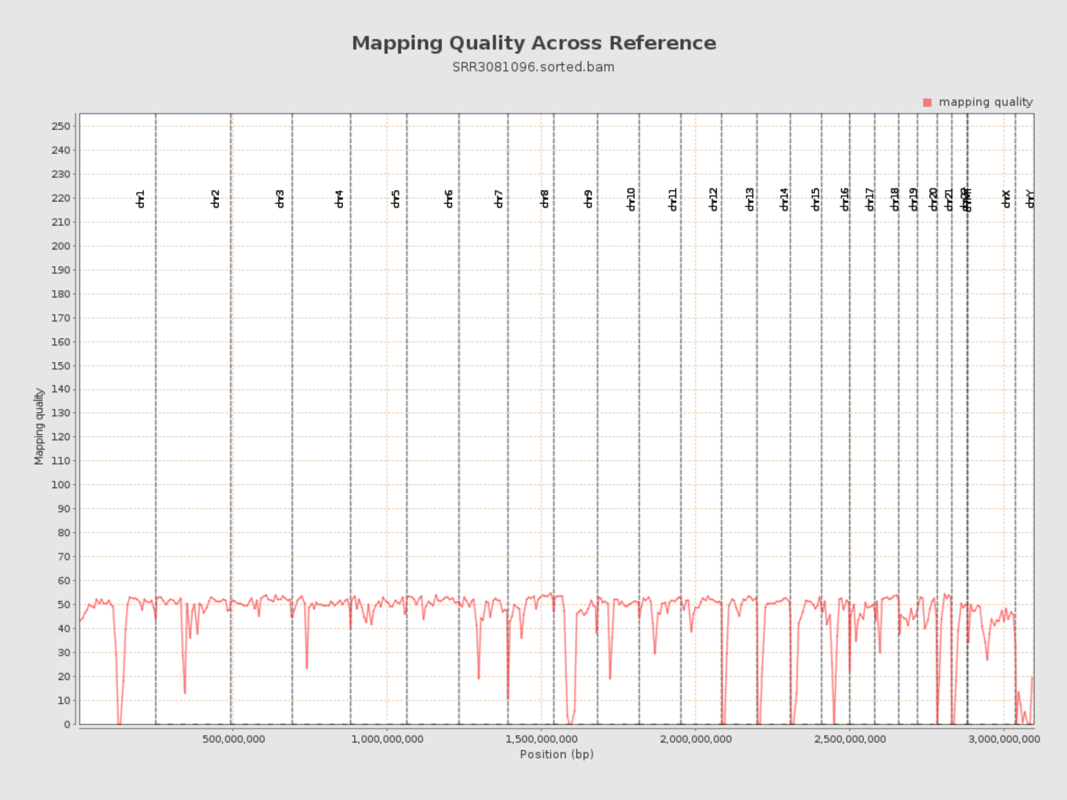
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram