Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:40:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081111.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_SRR3081111 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081111.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:40:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081111.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,433,123
Mapped reads	2,214,603 / 91.02%
Unmapped reads	218,520 / 8.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,499 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	99,201 / 4.08%
Duplication rate	3.41%
Clipped reads	956,181 / 39.3%

2.2. ACGT Content

Number/percentage of A's	40,339,970 / 27.14%
Number/percentage of C's	28,706,515 / 19.31%
Number/percentage of T's	45,395,742 / 30.54%
Number/percentage of G's	34,188,140 / 23%
Number/percentage of N's	1,631 / 0%
GC Percentage	42.32%

2.3. Coverage

Mean	0.048

Standard Deviation	0.4266

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

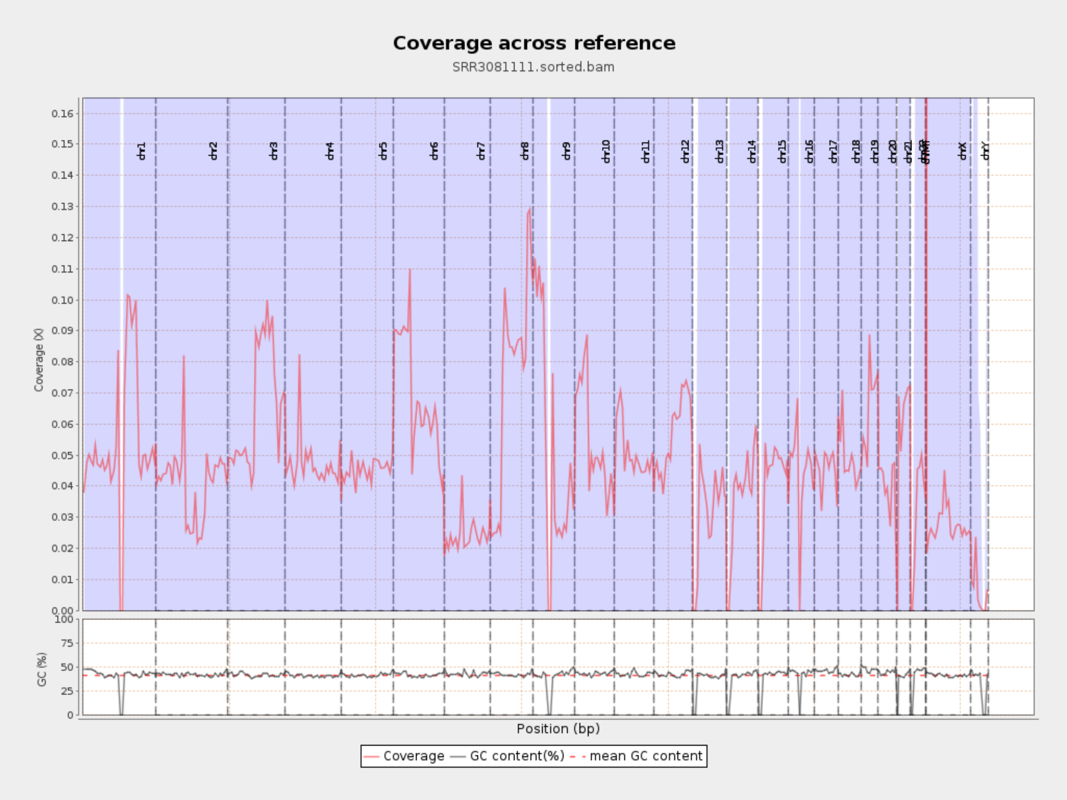
General error rate	0.89%
Mismatches	1,307,553
Insertions	11,211
Mapped reads with at least one insertion	0.5%
Deletions	33,961
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46.61%

2.6. Chromosome stats

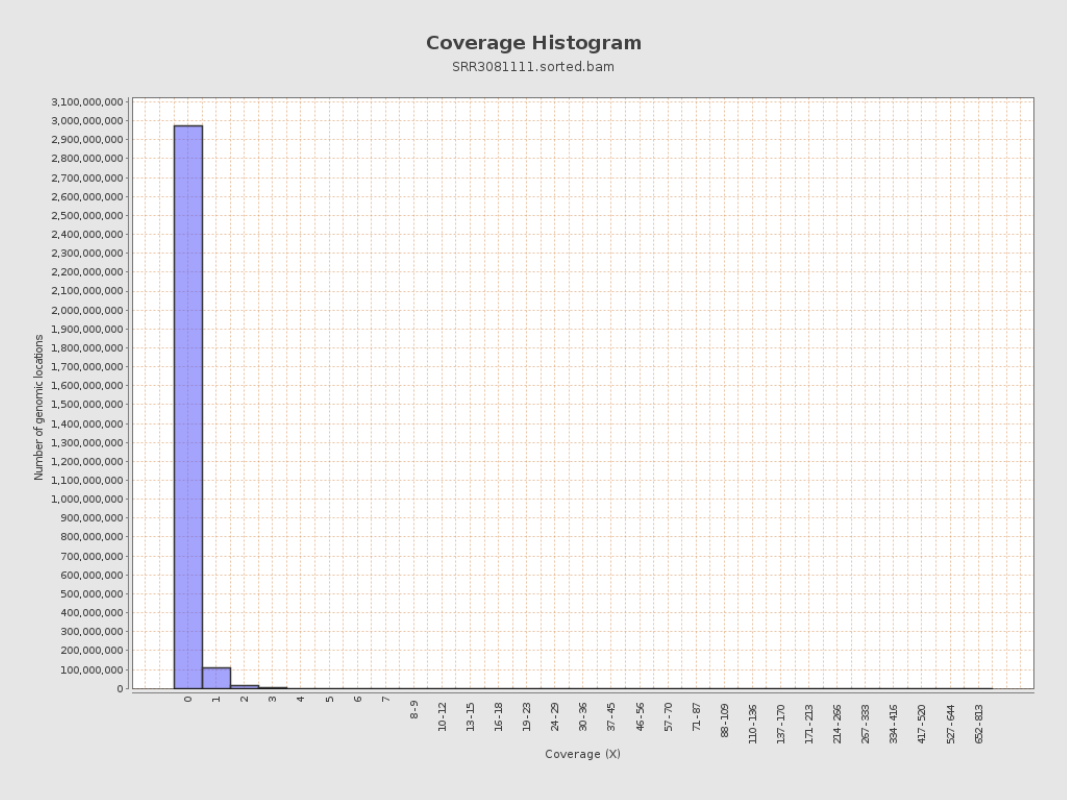
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13512840	0.0542	0.7397
chr2	243199373	9984416	0.0411	0.4693
chr3	198022430	12886665	0.0651	0.295
chr4	191154276	9037189	0.0473	0.2828
chr5	180915260	8231773	0.0455	0.2471
chr6	171115067	11928243	0.0697	0.4523
chr7	159138663	3859691	0.0243	0.2875

chr8	146364022	11009952	0.0752	0.4442
chr9	141213431	7422412	0.0526	0.5399
chr10	135534747	7424498	0.0548	0.4208
chr11	135006516	6926973	0.0513	0.381
chr12	133851895	7668665	0.0573	0.3016
chr13	115169878	3658269	0.0318	0.2023
chr14	107349540	3946446	0.0368	0.3295
chr15	102531392	4032213	0.0393	0.2354
chr16	90354753	3937397	0.0436	0.3248
chr17	81195210	3732639	0.046	0.259
chr18	78077248	3829999	0.0491	0.9768
chr19	59128983	3856503	0.0652	0.5768
chr20	63025520	2575830	0.0409	0.263
chr21	48129895	2893448	0.0601	0.359
chr22	51304566	1597041	0.0311	0.1997
chrMT	16571	80986	4.8872	3.4776
chrX	155270560	4276514	0.0275	0.2387
chrY	59373566	382559	0.0064	0.1838

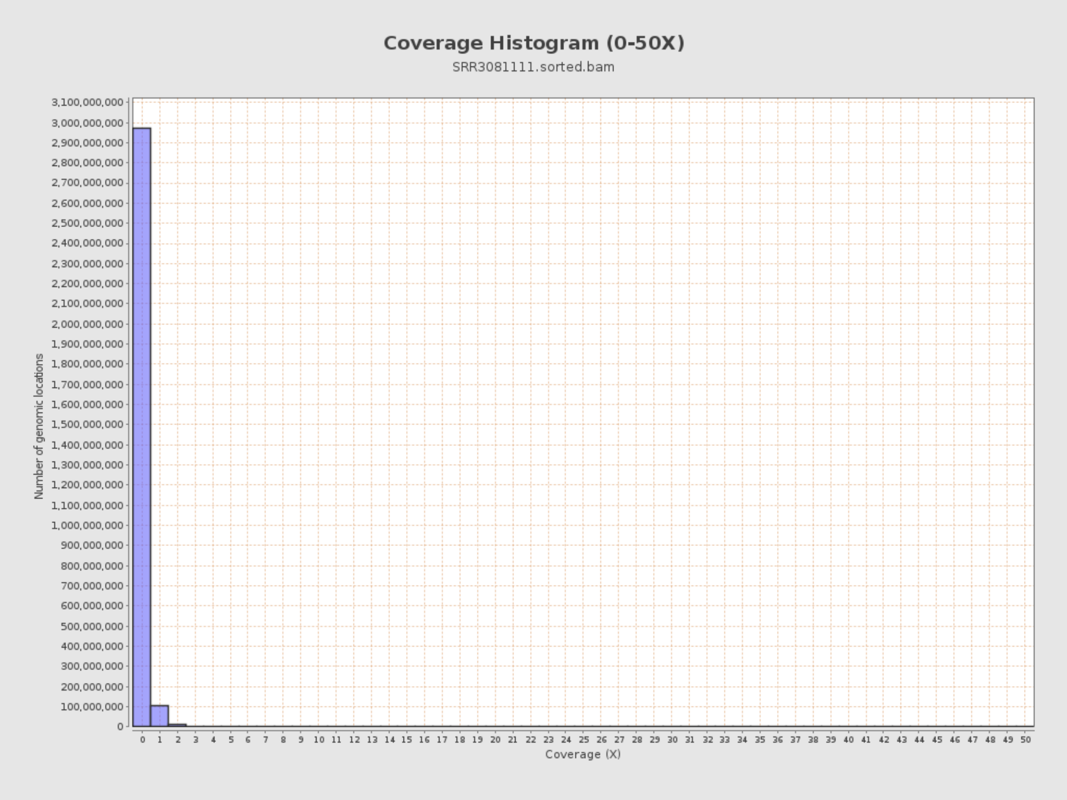
3. Results : Coverage across reference



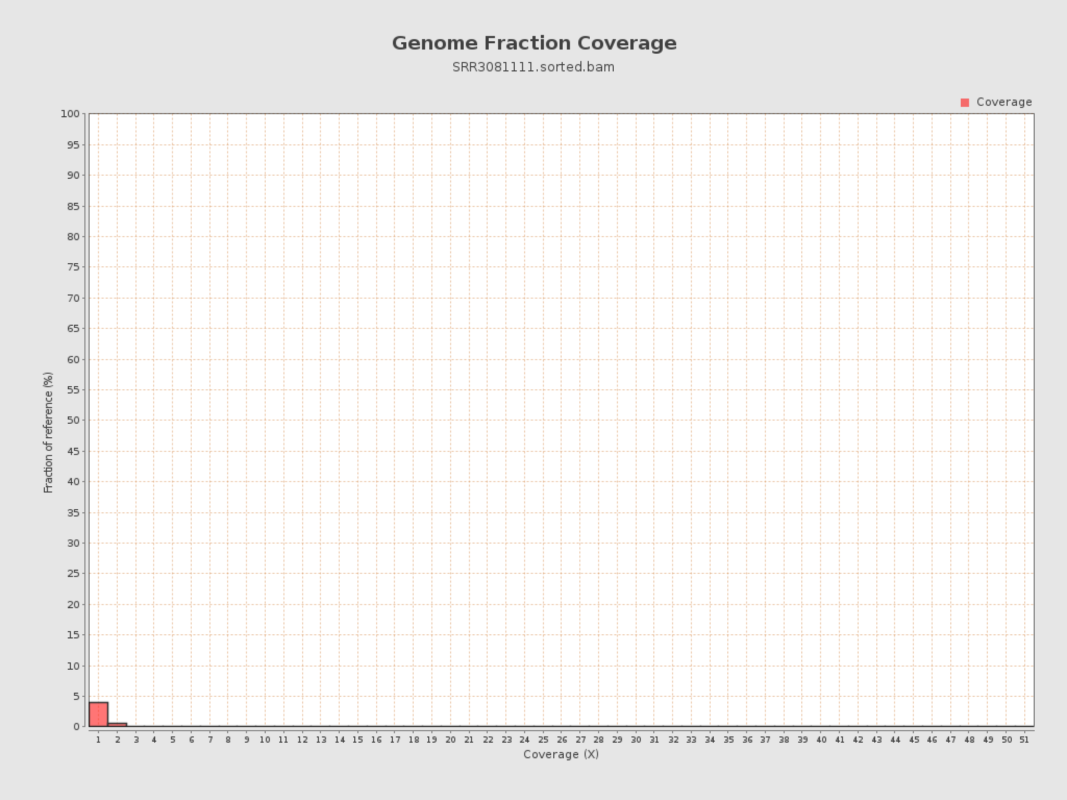
4. Results : Coverage Histogram



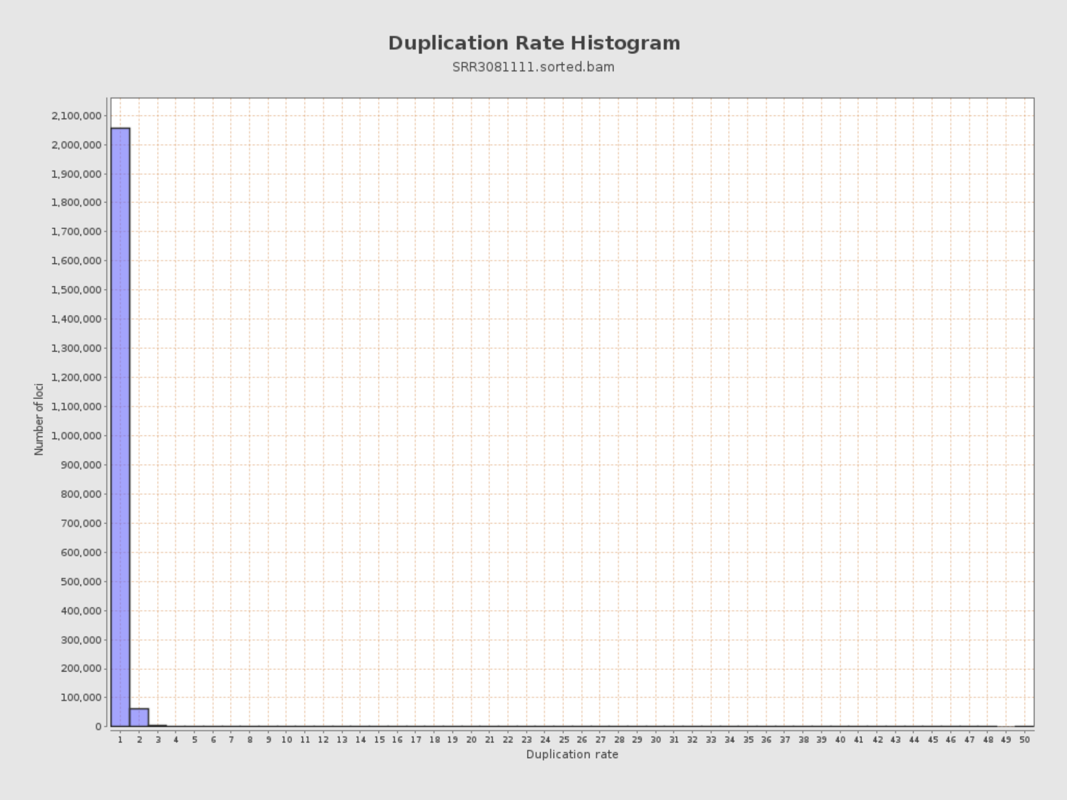
5. Results : Coverage Histogram (0-50X)



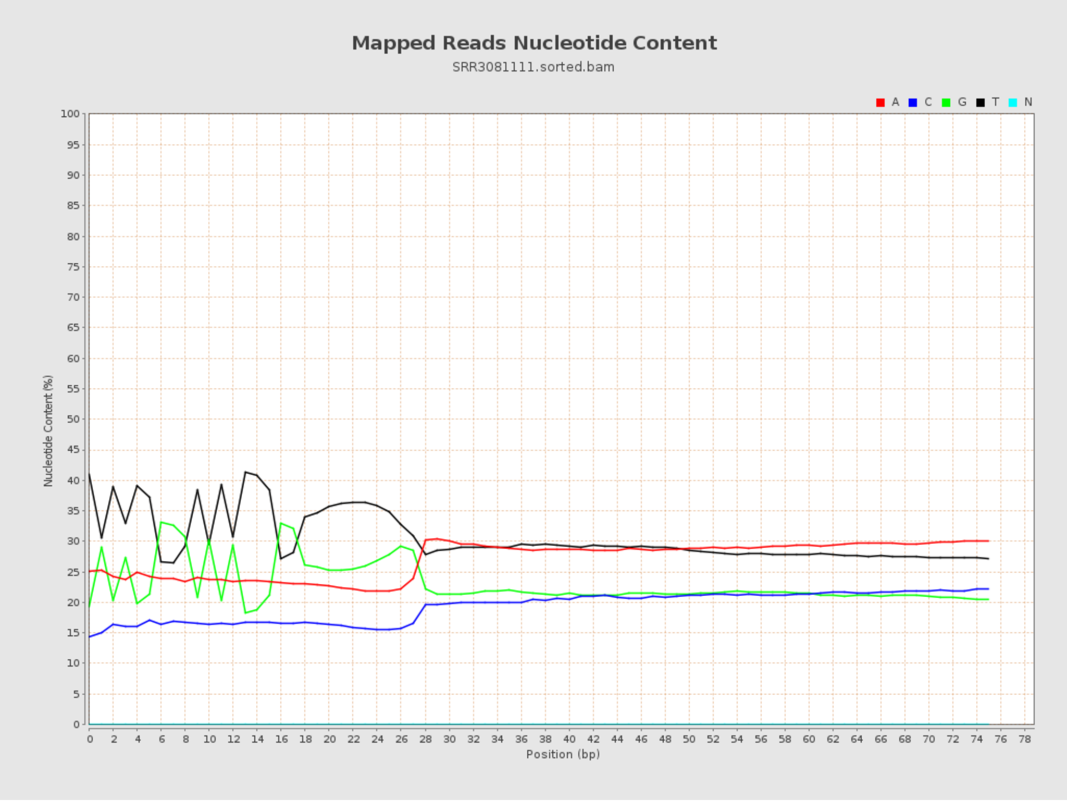
6. Results : Genome Fraction Coverage



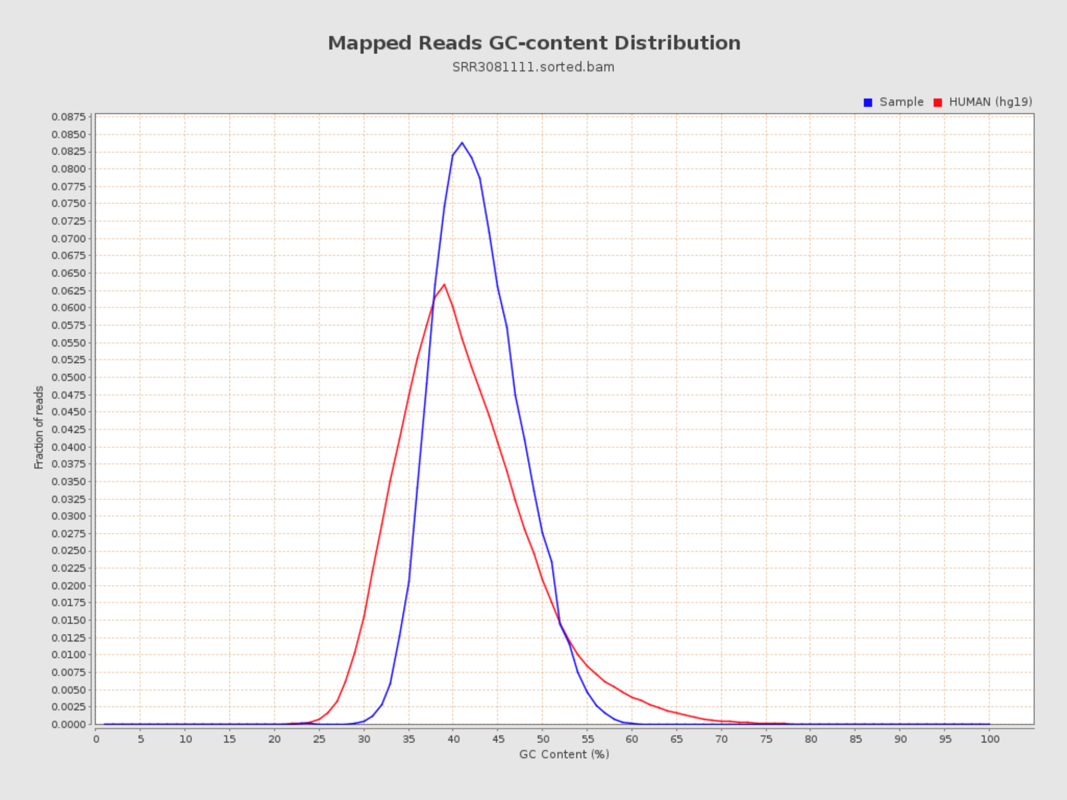
7. Results : Duplication Rate Histogram



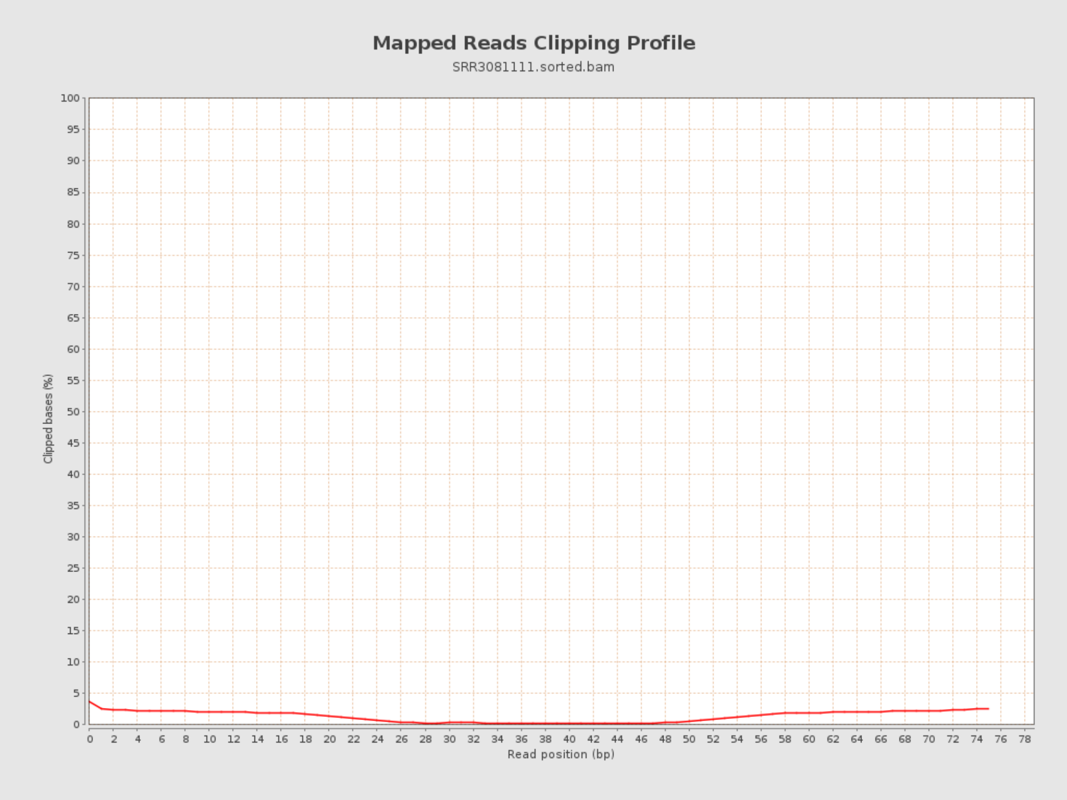
8. Results : Mapped Reads Nucleotide Content



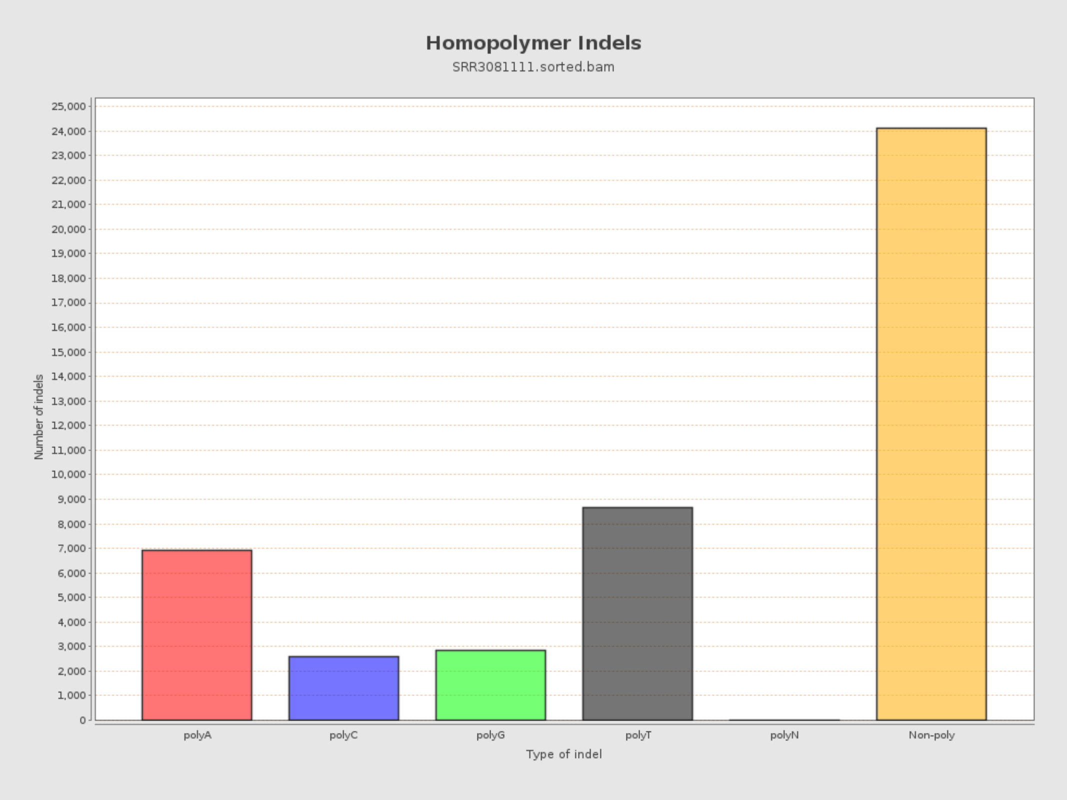
9. Results : Mapped Reads GC-content Distribution



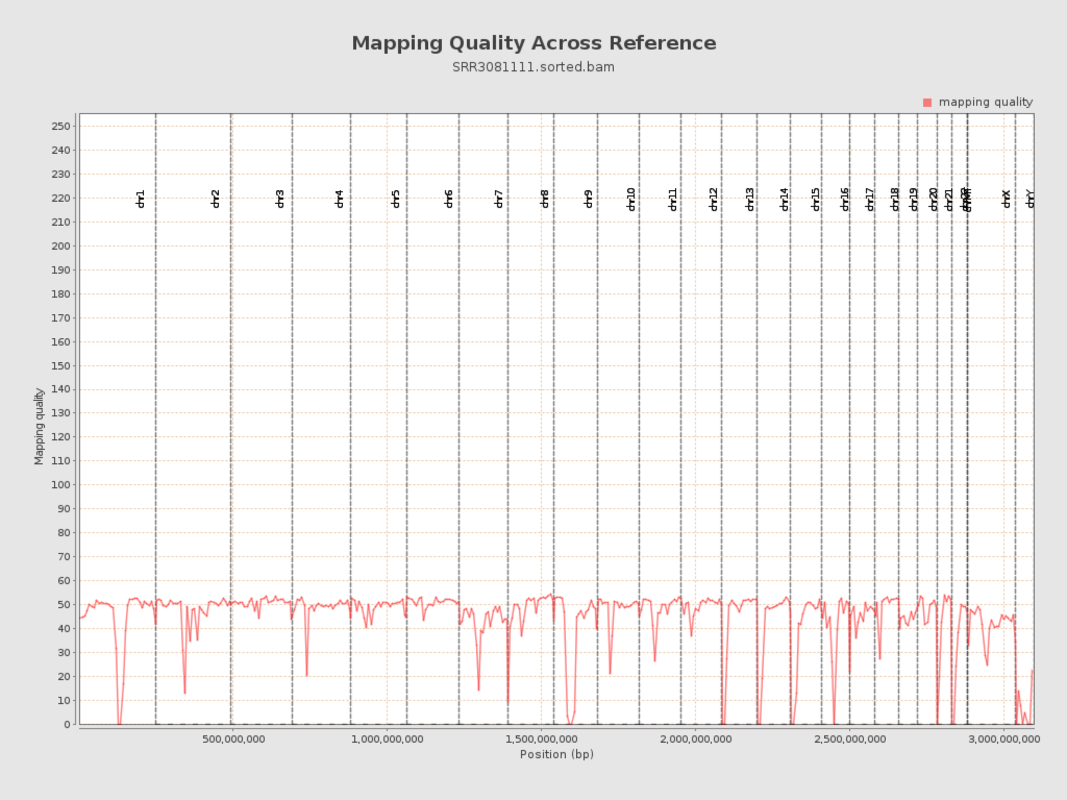
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram