Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:31:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081696.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_SRR3081696 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081696.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:31:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081696.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,798,984
Mapped reads	1,566,659 / 87.09%
Unmapped reads	232,325 / 12.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,968 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	74,427 / 4.14%
Duplication rate	4.04%
Clipped reads	656,274 / 36.48%

2.2. ACGT Content

Number/percentage of A's	29,910,899 / 28.33%
Number/percentage of C's	18,633,506 / 17.65%
Number/percentage of T's	34,427,877 / 32.61%
Number/percentage of G's	22,530,435 / 21.34%
Number/percentage of N's	76,088 / 0.07%
GC Percentage	38.99%

2.3. Coverage

Mean	0.0341

Standard Deviation	0.2795

2.4. Mapping Quality

Mean Mapping Quality	47.61

2.5. Mismatches and indels

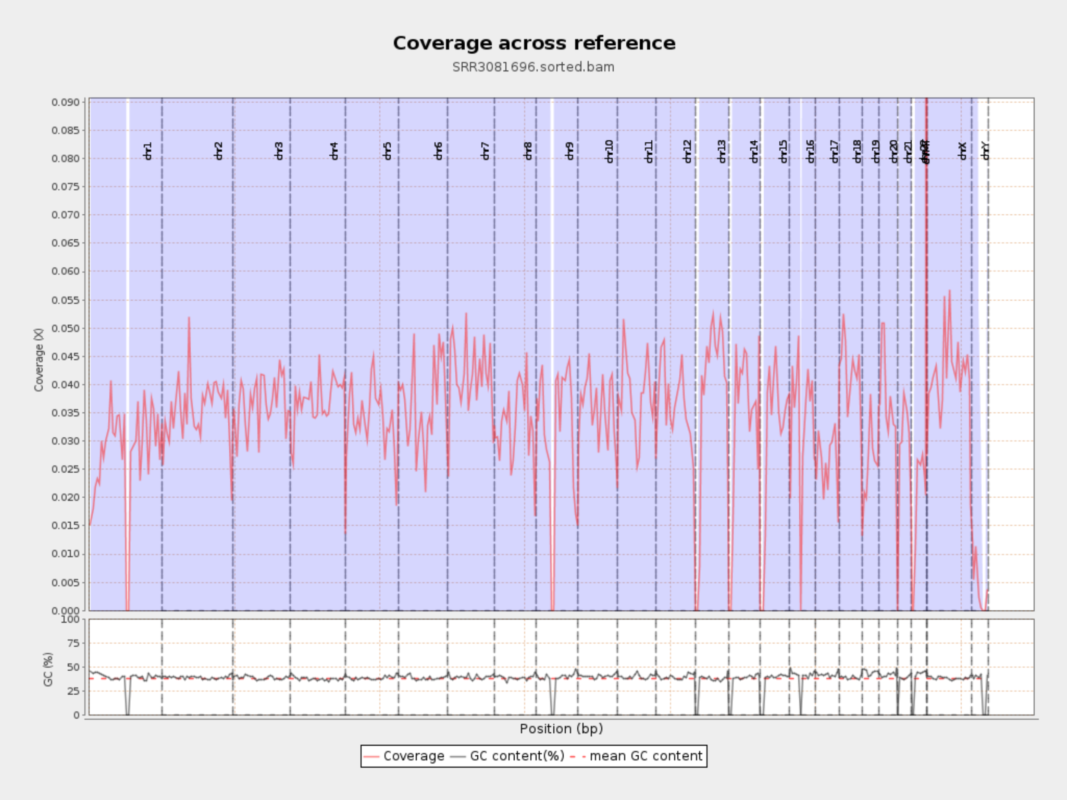
General error rate	0.86%
Mismatches	893,149
Insertions	8,594
Mapped reads with at least one insertion	0.54%
Deletions	24,119
Mapped reads with at least one deletion	1.52%
Homopolymer indels	49.31%

2.6. Chromosome stats

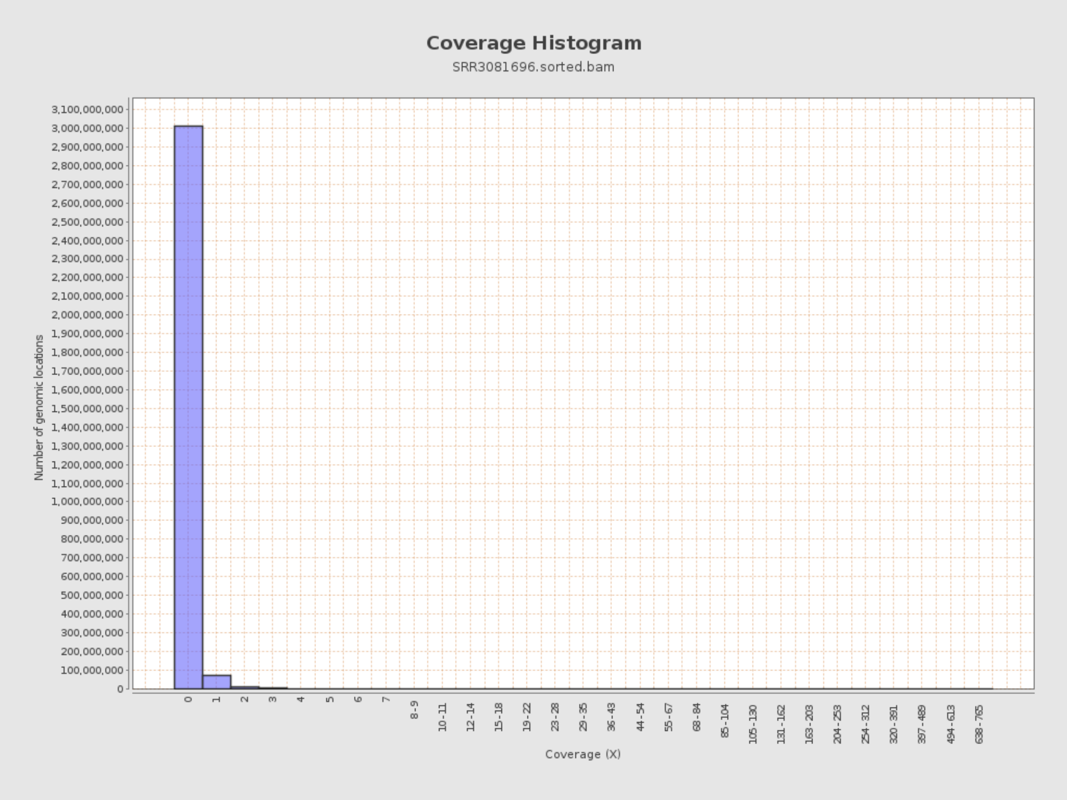
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6952965	0.0279	0.297
chr2	243199373	8676202	0.0357	0.3098
chr3	198022430	7280104	0.0368	0.2269
chr4	191154276	7099899	0.0371	0.2305
chr5	180915260	6127881	0.0339	0.2185
chr6	171115067	6251372	0.0365	0.2619
chr7	159138663	6673035	0.0419	0.3392

chr8	146364022	4839141	0.0331	0.5138
chr9	141213431	4416773	0.0313	0.278
chr10	135534747	4910104	0.0362	0.2626
chr11	135006516	5137744	0.0381	0.2525
chr12	133851895	4875814	0.0364	0.2296
chr13	115169878	4348194	0.0378	0.23
chr14	107349540	3463416	0.0323	0.2197
chr15	102531392	3123126	0.0305	0.2069
chr16	90354753	3049806	0.0338	0.2259
chr17	81195210	2098457	0.0258	0.1967
chr18	78077248	3346317	0.0429	0.4576
chr19	59128983	1568515	0.0265	0.3118
chr20	63025520	2359569	0.0374	0.2339
chr21	48129895	1360974	0.0283	0.2062
chr22	51304566	926903	0.0181	0.1583
chrMT	16571	11291	0.6814	0.9881
chrX	155270560	6473335	0.0417	0.2531
chrY	59373566	246706	0.0042	0.0899

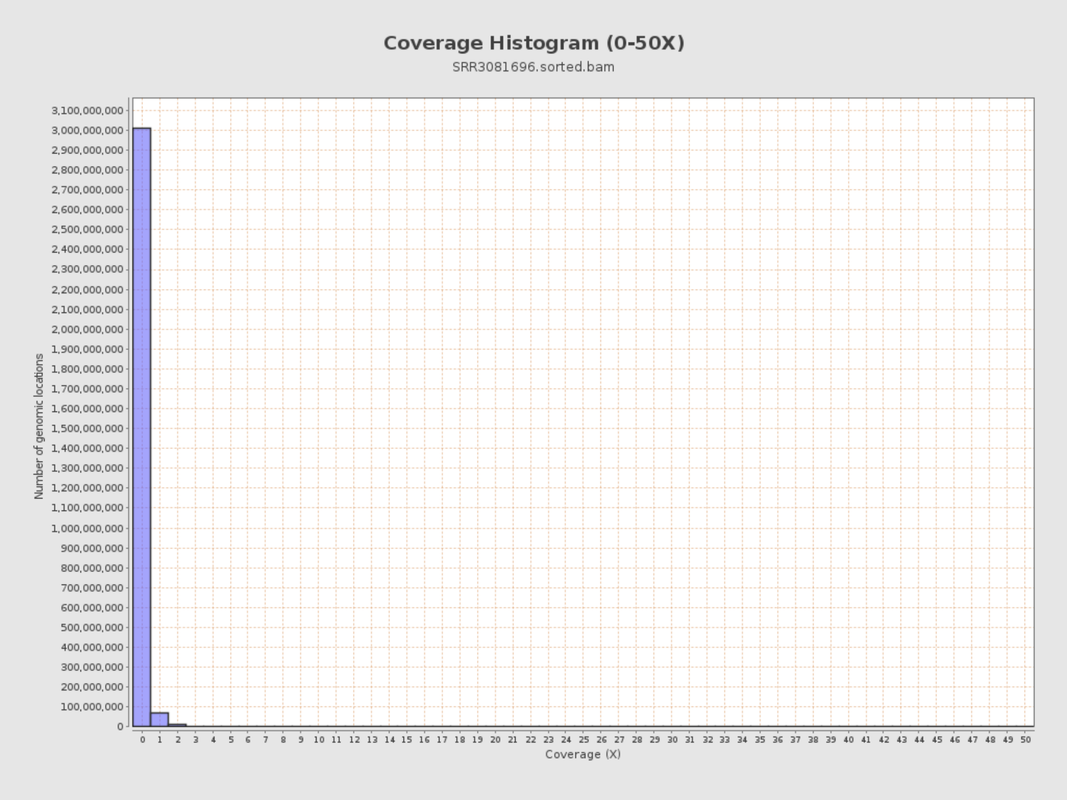
3. Results : Coverage across reference



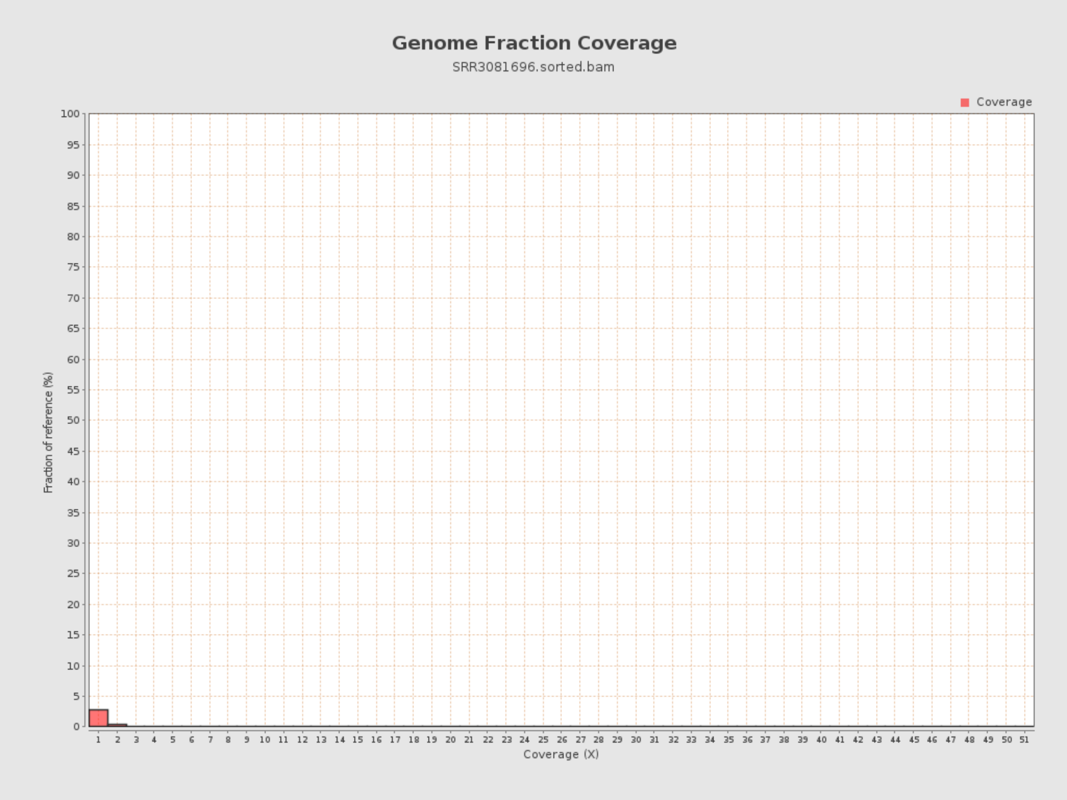
4. Results : Coverage Histogram



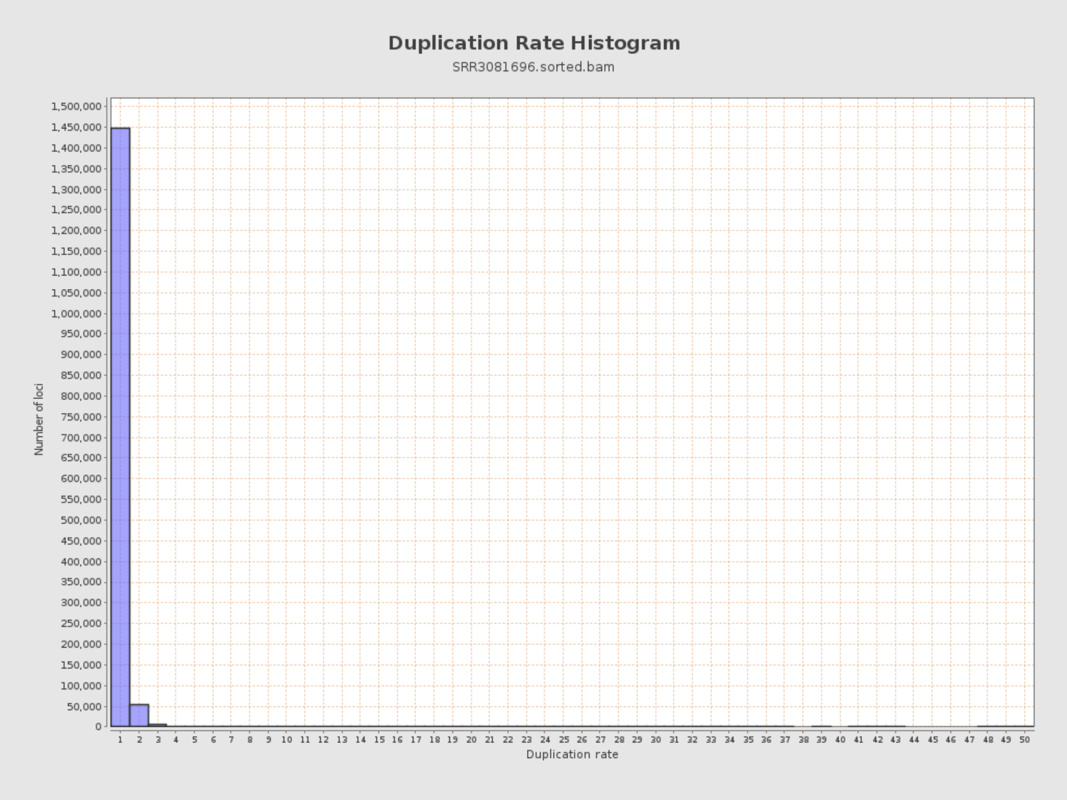
5. Results : Coverage Histogram (0-50X)



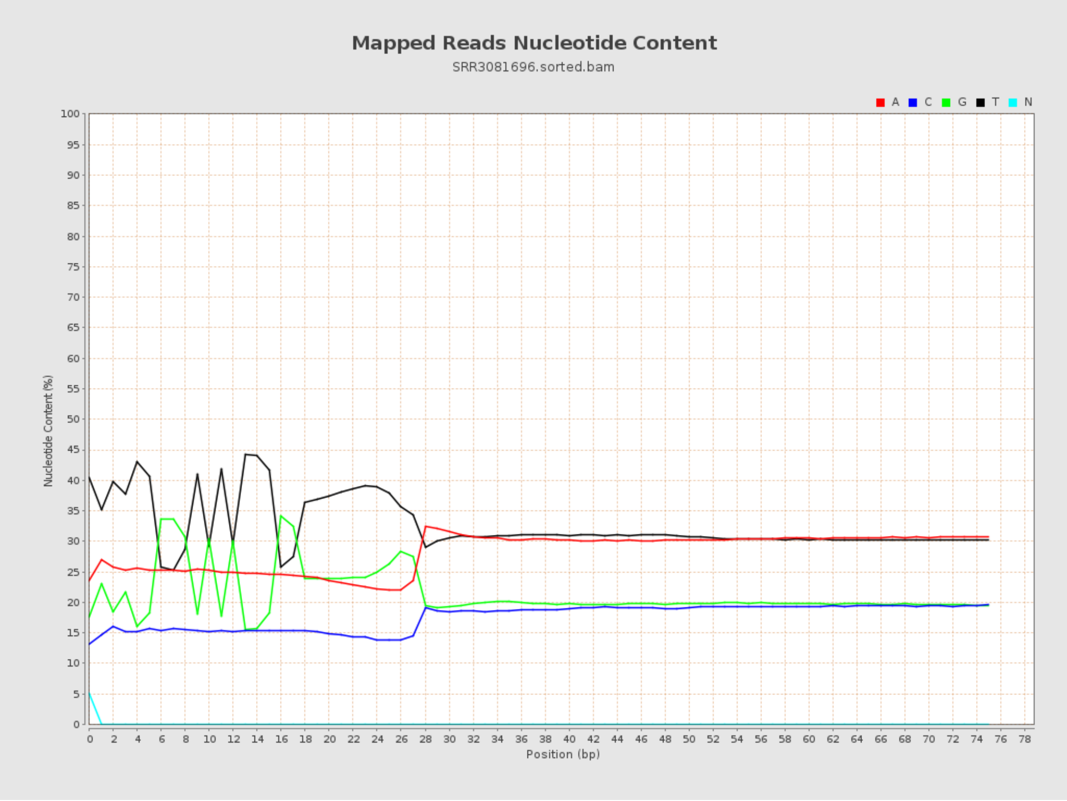
6. Results : Genome Fraction Coverage



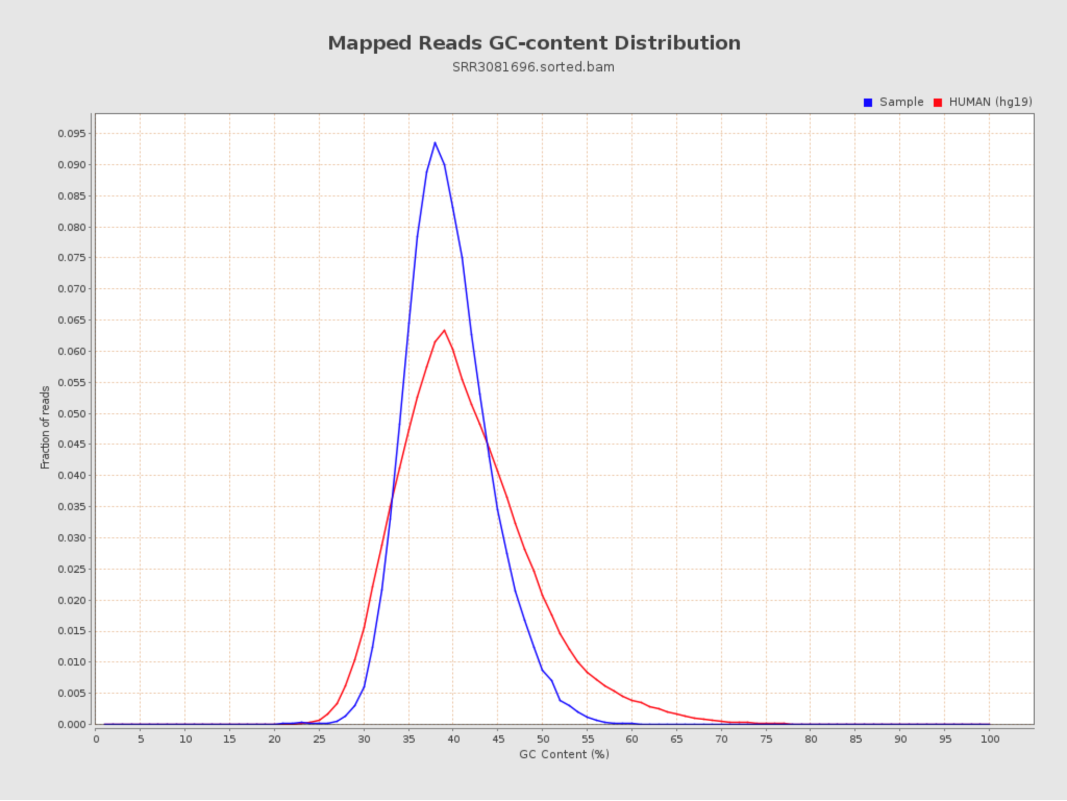
7. Results : Duplication Rate Histogram



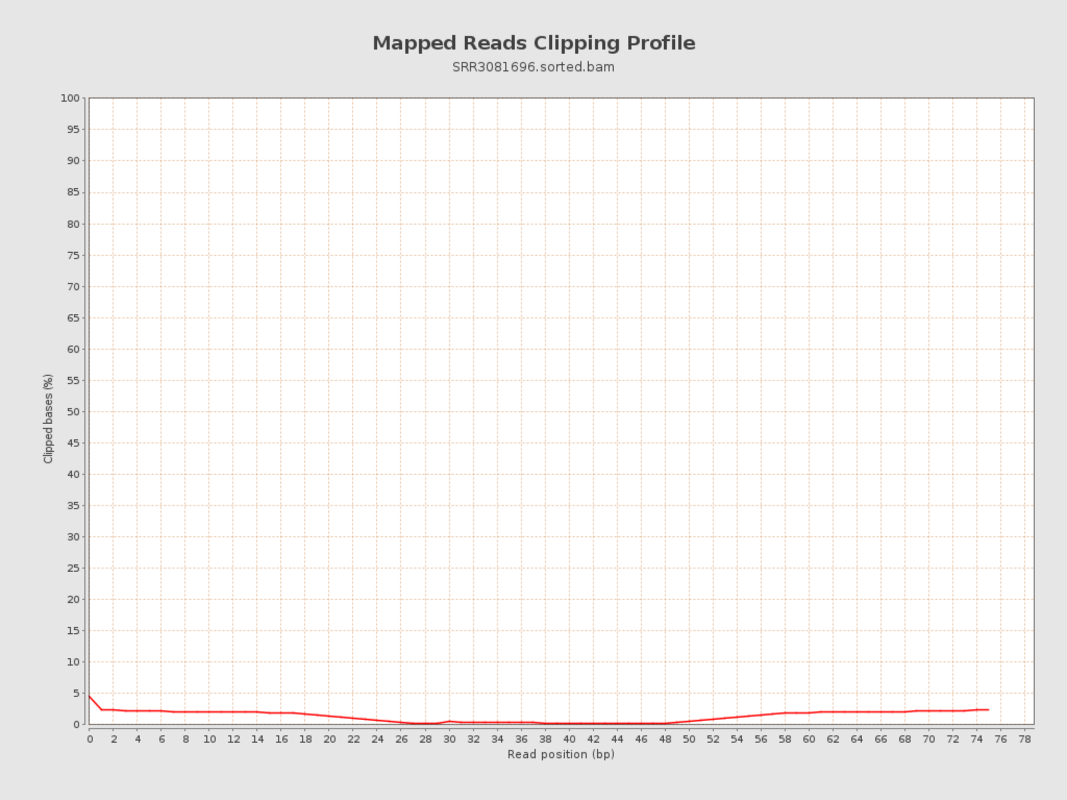
8. Results : Mapped Reads Nucleotide Content



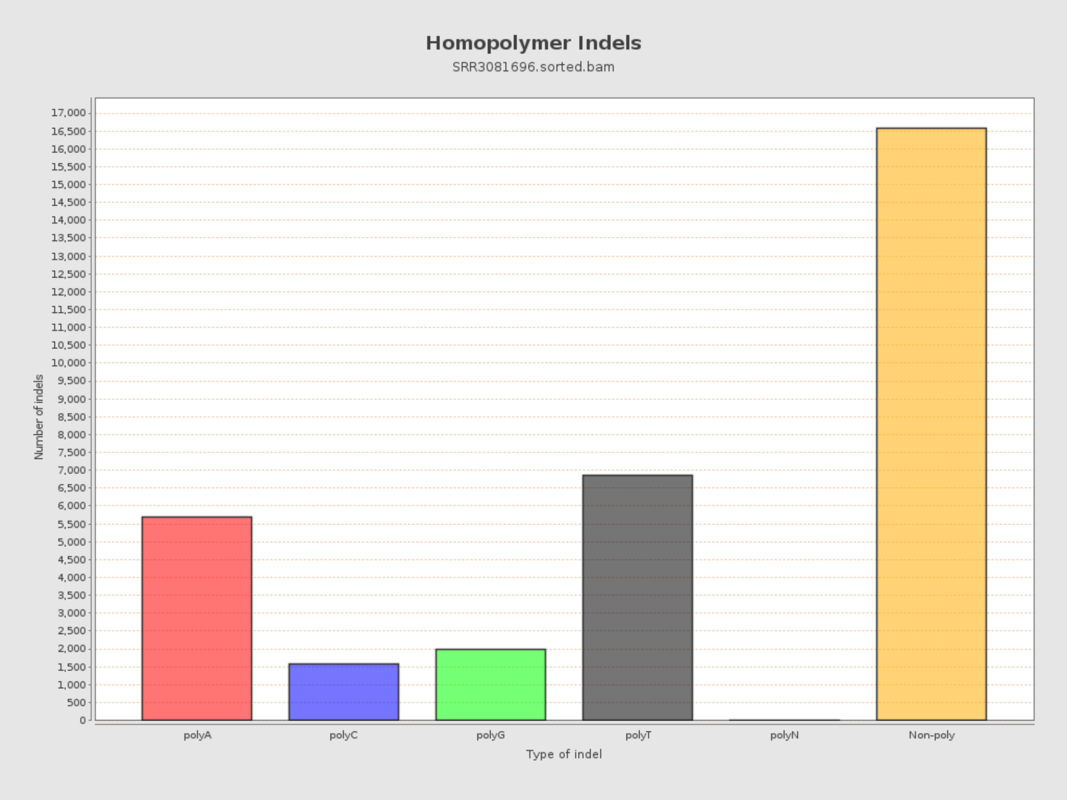
9. Results : Mapped Reads GC-content Distribution



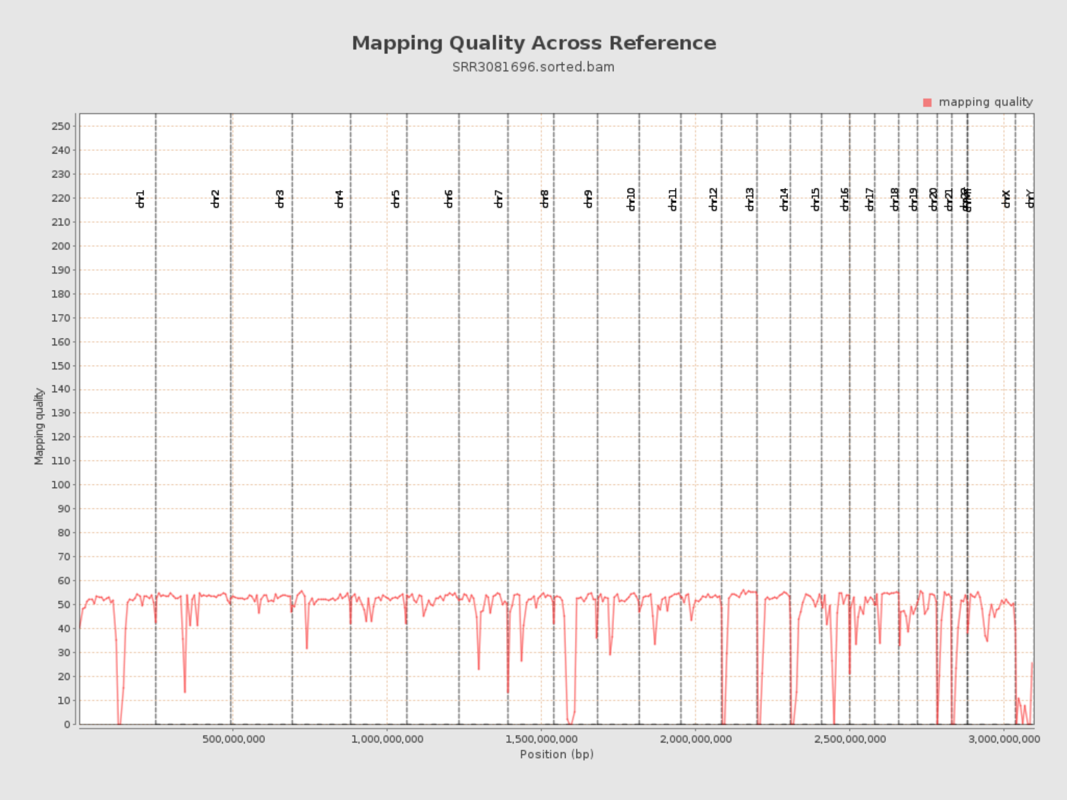
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram