Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 07:12:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716702.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_SRR9716702 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716702.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 07:12:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716702.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,574,924
Mapped reads	1,448,037 / 91.94%
Unmapped reads	126,887 / 8.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,385 / 1.42%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	61,969 / 3.93%
Duplication rate	2.42%
Clipped reads	1,467,679 / 93.19%

2.2. ACGT Content

Number/percentage of A's	27,327,681 / 23.86%
Number/percentage of C's	21,930,973 / 19.15%
Number/percentage of T's	35,811,278 / 31.26%
Number/percentage of G's	29,471,495 / 25.73%
Number/percentage of N's	6,838 / 0.01%
GC Percentage	44.87%

2.3. Coverage

Mean	0.037

Standard Deviation	0.5002

2.4. Mapping Quality

Mean Mapping Quality	42.76

2.5. Mismatches and indels

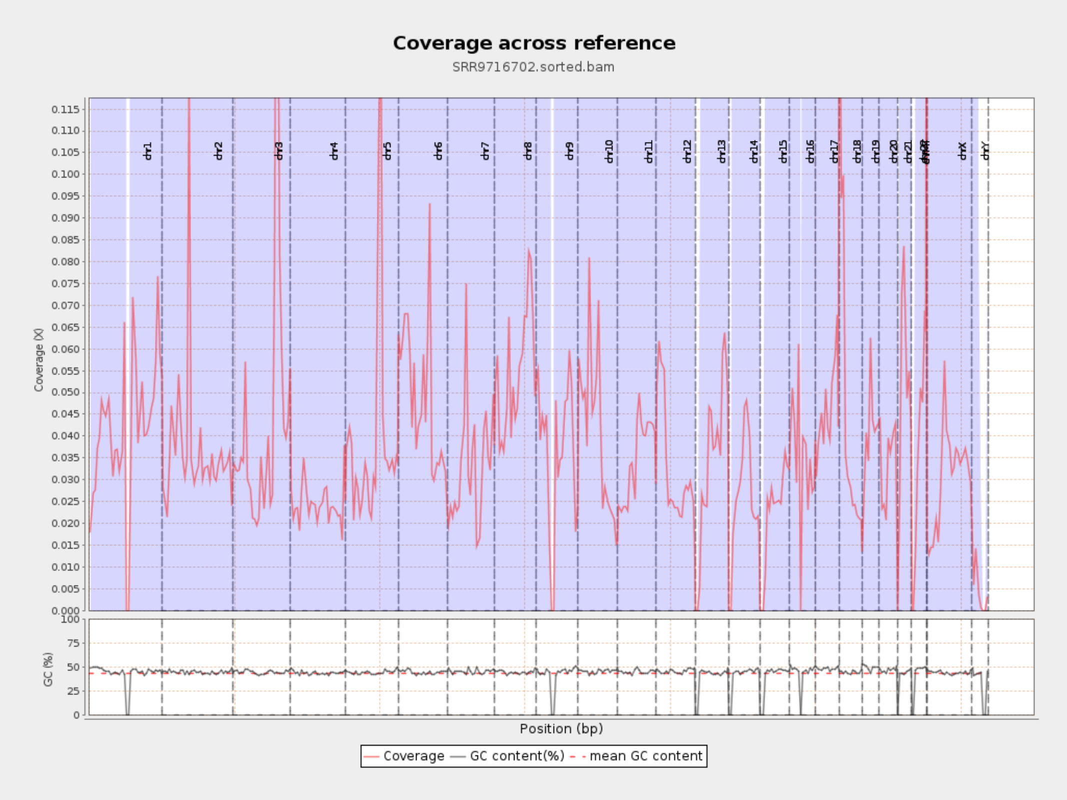
General error rate	0.85%
Mismatches	955,859
Insertions	10,619
Mapped reads with at least one insertion	0.72%
Deletions	27,999
Mapped reads with at least one deletion	1.9%
Homopolymer indels	43.76%

2.6. Chromosome stats

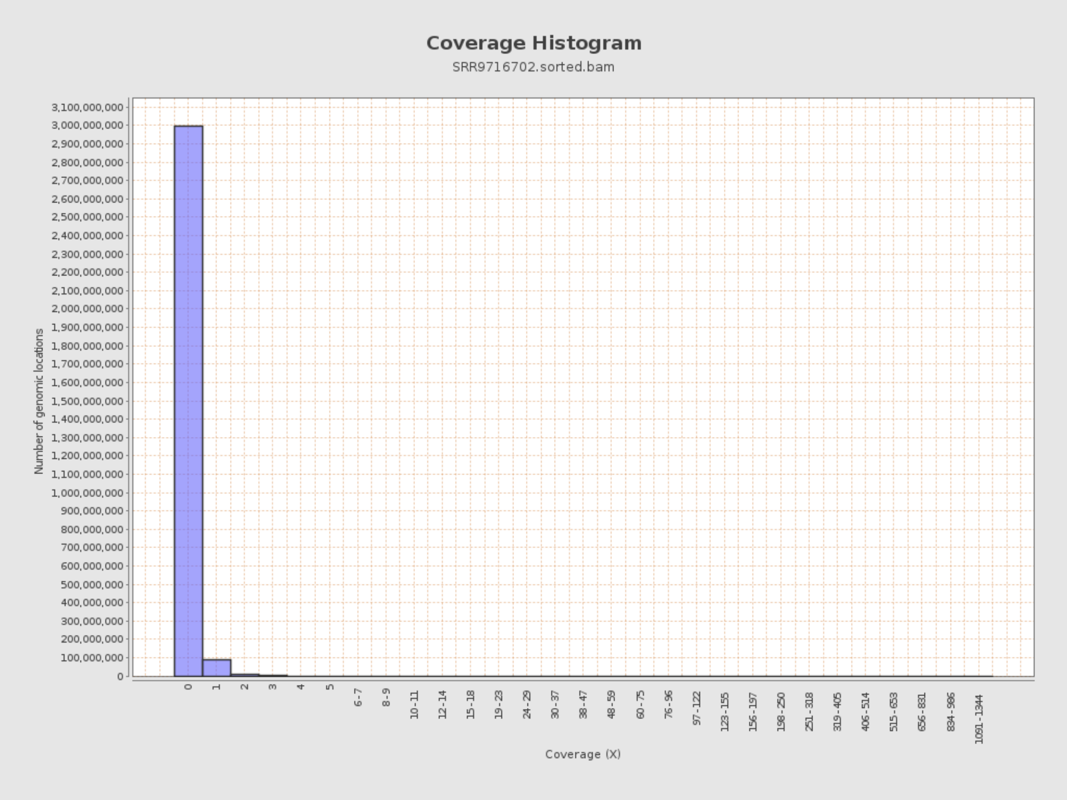
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10319864	0.0414	0.7074
chr2	243199373	8985030	0.0369	0.9289
chr3	198022430	8621141	0.0435	0.2476
chr4	191154276	4662376	0.0244	0.1933
chr5	180915260	7124210	0.0394	0.2292
chr6	171115067	8355101	0.0488	0.3131
chr7	159138663	5278518	0.0332	0.6632

chr8	146364022	8067445	0.0551	0.6985
chr9	141213431	5107112	0.0362	0.4934
chr10	135534747	5679082	0.0419	0.4337
chr11	135006516	4681257	0.0347	0.3357
chr12	133851895	4377626	0.0327	0.2114
chr13	115169878	3990786	0.0347	0.2086
chr14	107349540	2778112	0.0259	0.2344
chr15	102531392	2300552	0.0224	0.1744
chr16	90354753	3119868	0.0345	0.2551
chr17	81195210	3747407	0.0462	0.2953
chr18	78077248	3681910	0.0472	1.1305
chr19	59128983	2403517	0.0406	0.579
chr20	63025520	2093503	0.0332	0.2657
chr21	48129895	2417956	0.0502	0.2652
chr22	51304566	1768330	0.0345	0.211
chrMT	16571	4204	0.2537	0.6818
chrX	155270560	4744672	0.0306	0.2985
chrY	59373566	287848	0.0048	0.1475

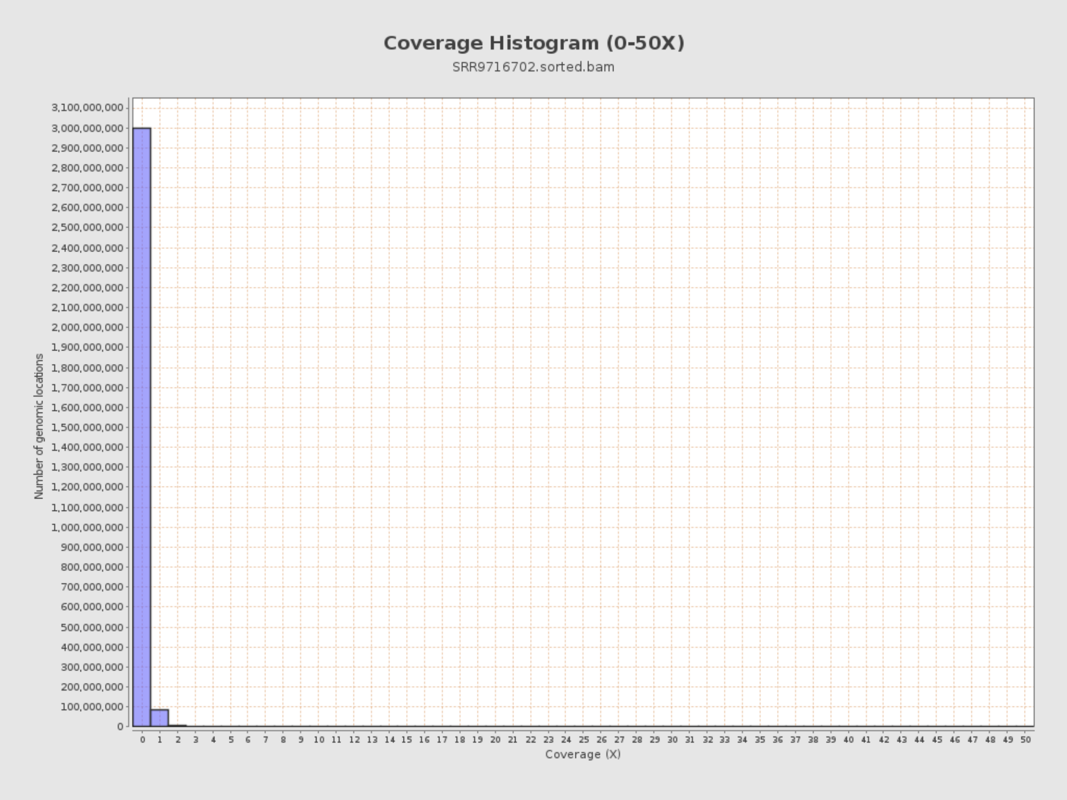
3. Results : Coverage across reference



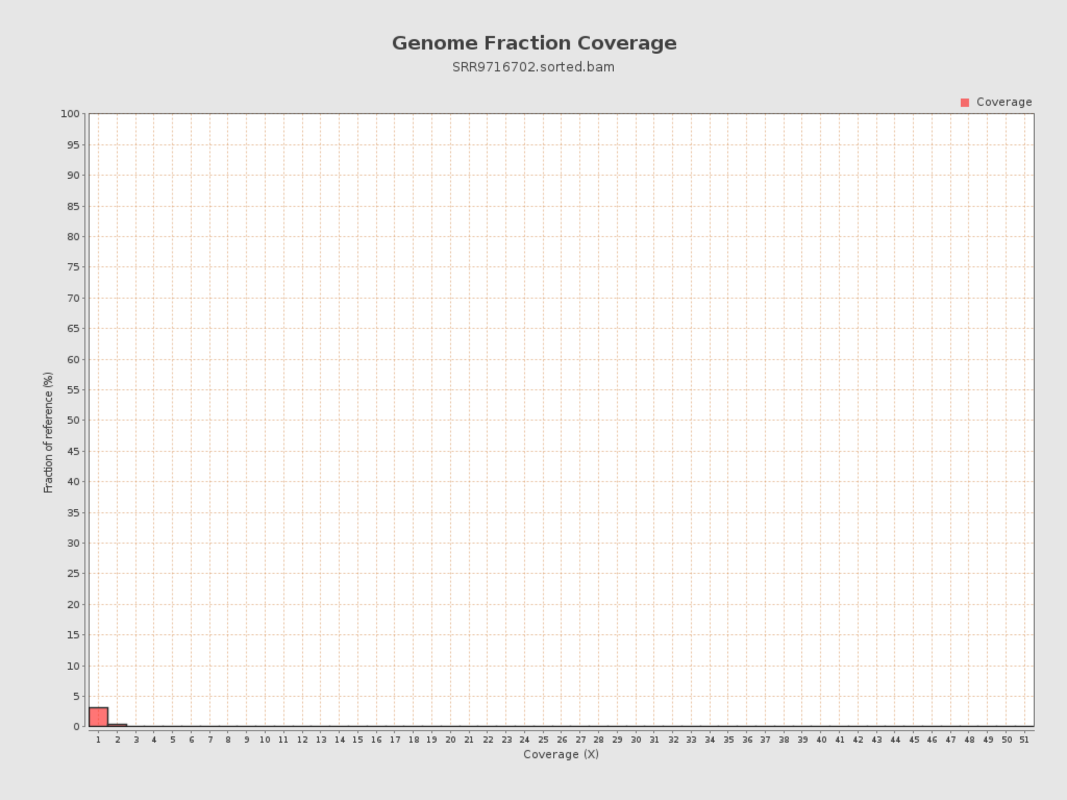
4. Results : Coverage Histogram



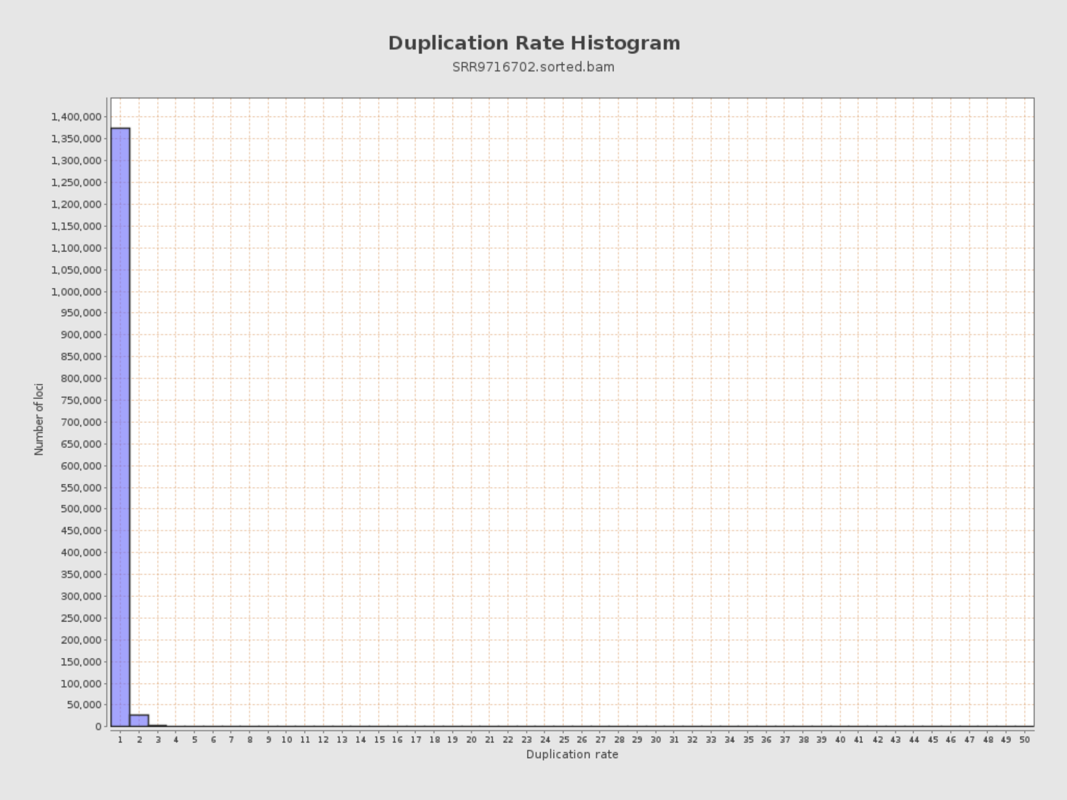
5. Results : Coverage Histogram (0-50X)



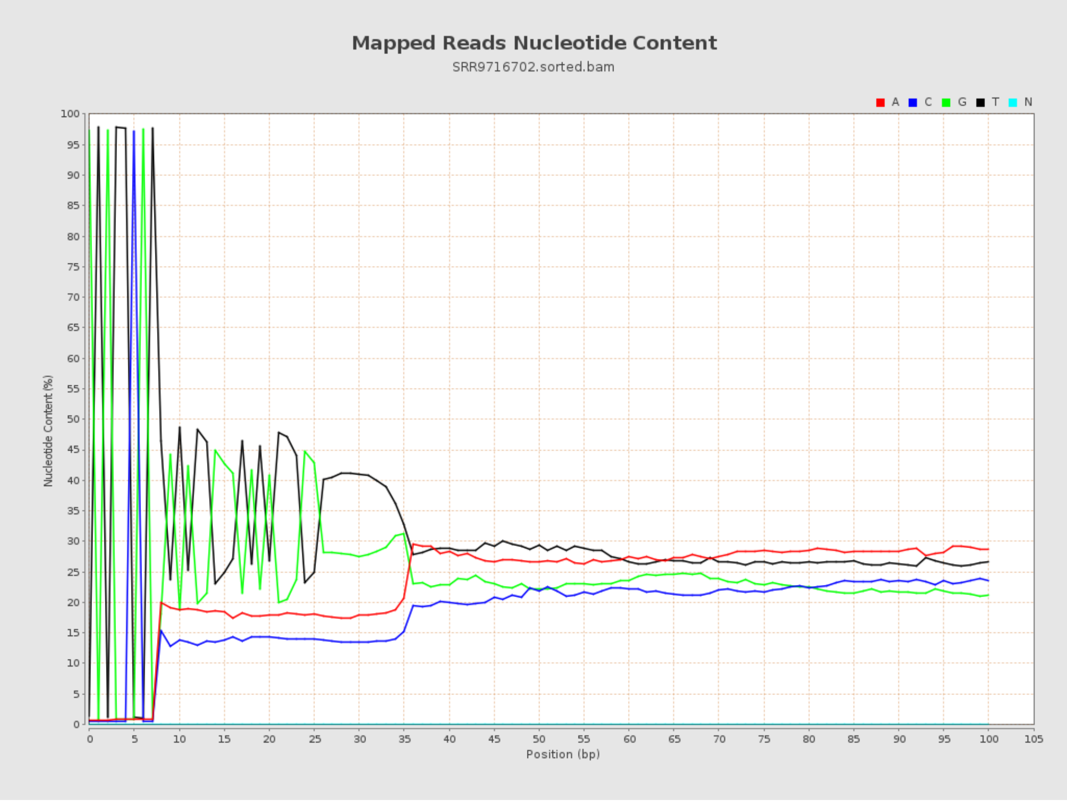
6. Results : Genome Fraction Coverage



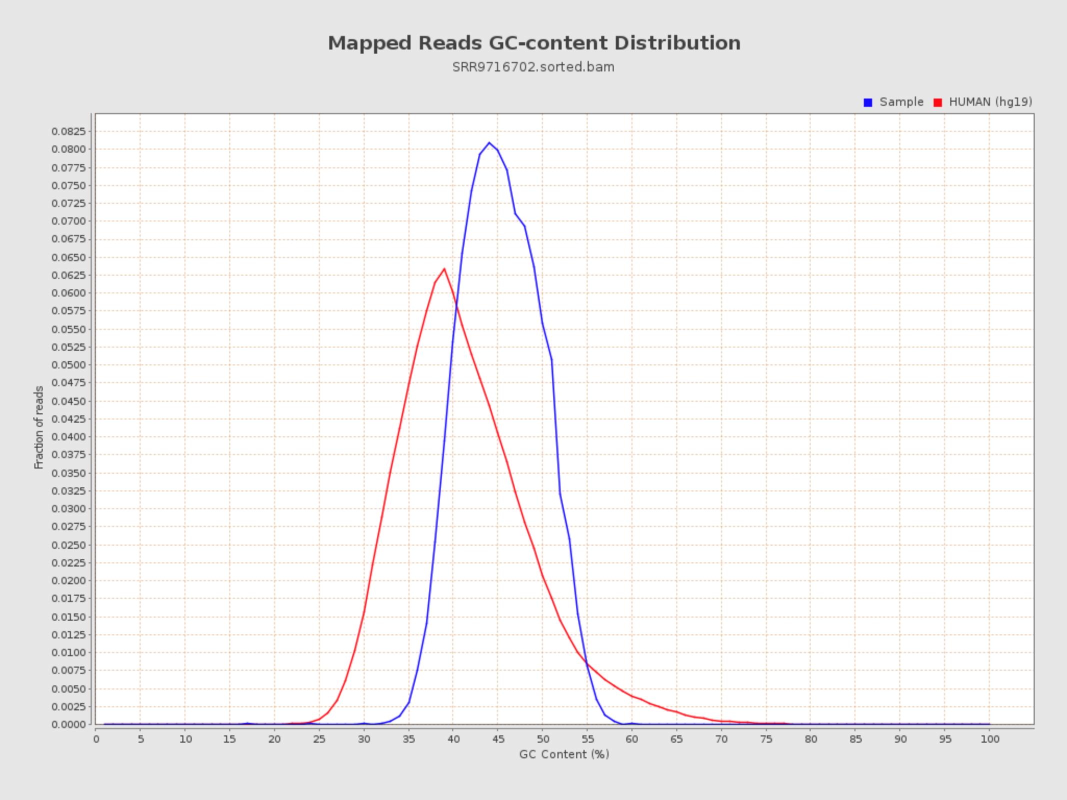
7. Results : Duplication Rate Histogram



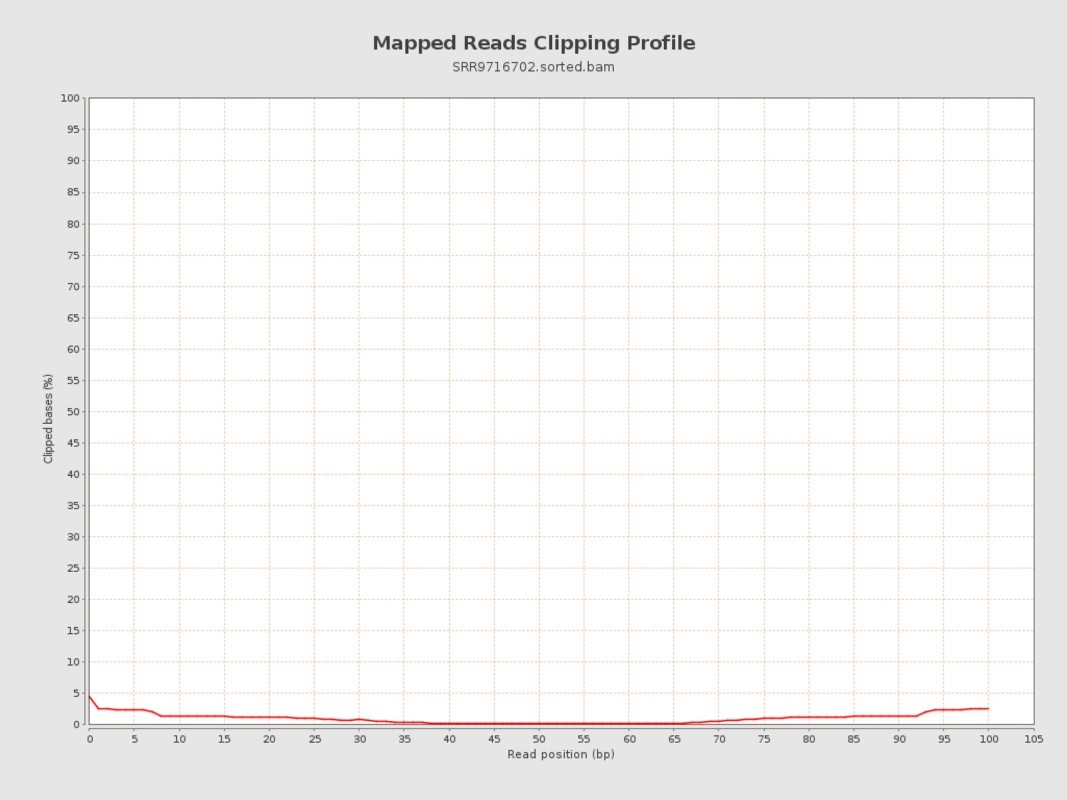
8. Results : Mapped Reads Nucleotide Content



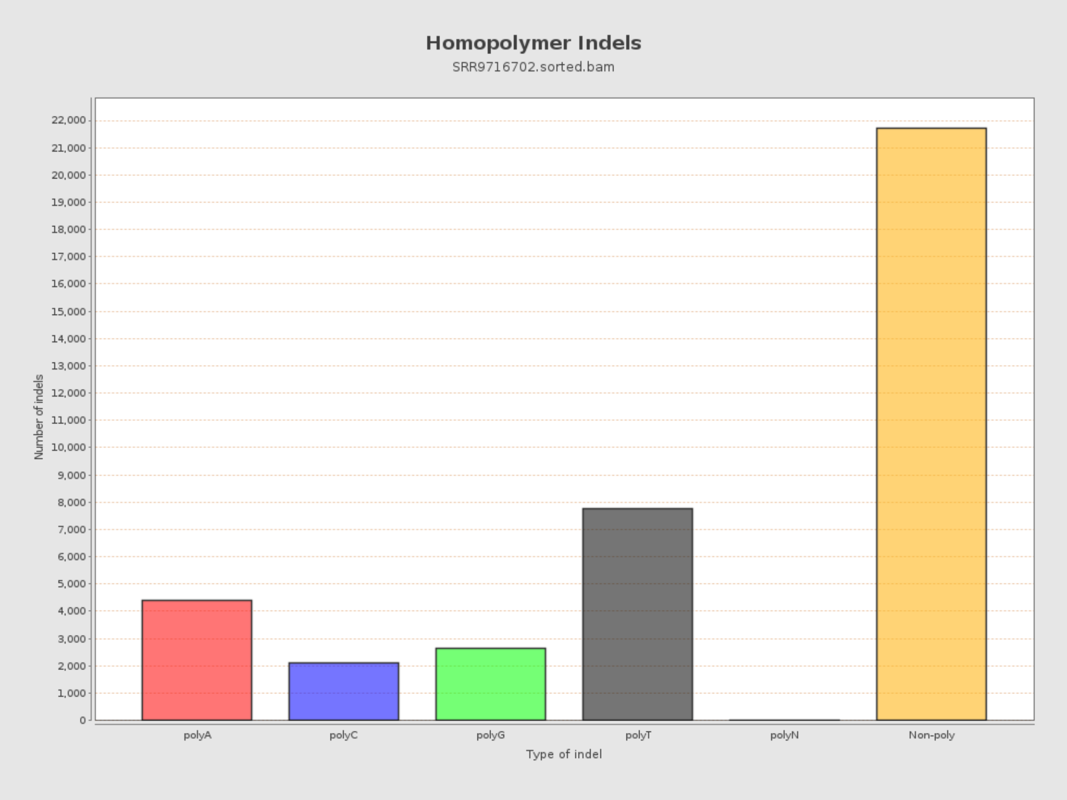
9. Results : Mapped Reads GC-content Distribution



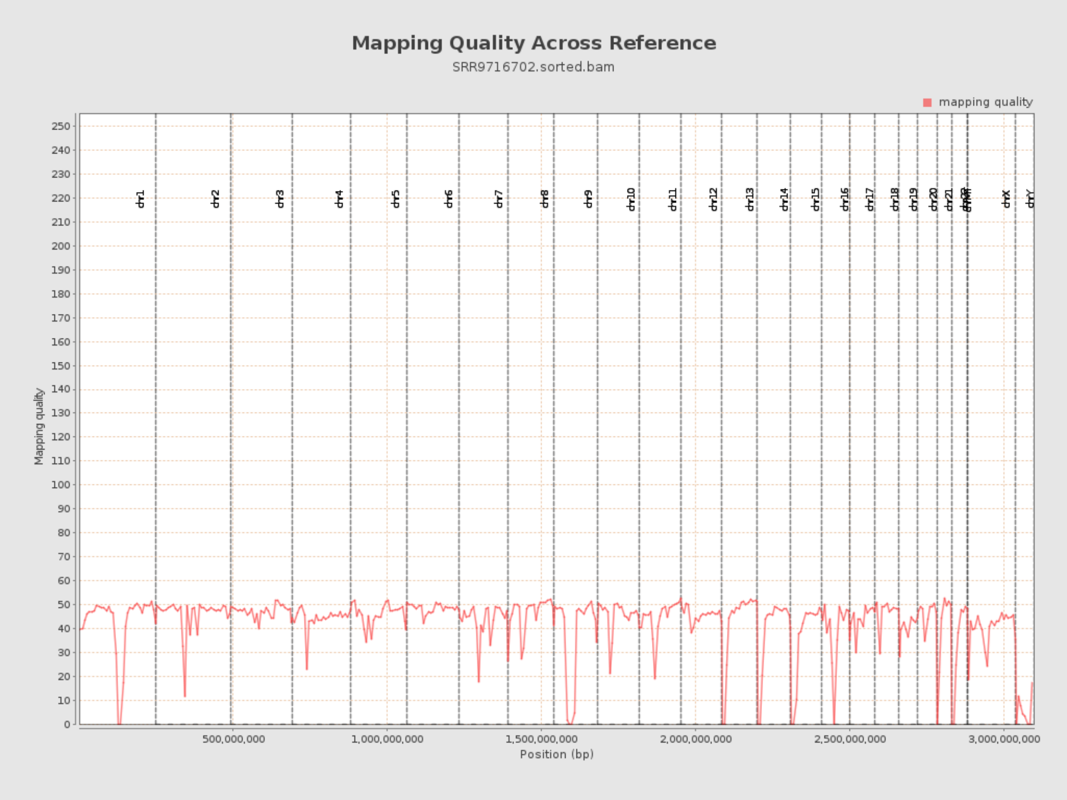
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram