Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 17:34:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716894.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_SRR9716894 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716894.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 17:34:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716894.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,489,145
Mapped reads	3,770,756 / 84%
Unmapped reads	718,389 / 16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	76,052 / 1.69%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	194,580 / 4.33%
Duplication rate	3.74%
Clipped reads	3,842,566 / 85.6%

2.2. ACGT Content

Number/percentage of A's	73,151,695 / 27.01%
Number/percentage of C's	55,706,285 / 20.57%
Number/percentage of T's	80,496,123 / 29.72%
Number/percentage of G's	61,438,961 / 22.69%
Number/percentage of N's	32,168 / 0.01%
GC Percentage	43.25%

2.3. Coverage

Mean	0.0875

Standard Deviation	0.6196

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

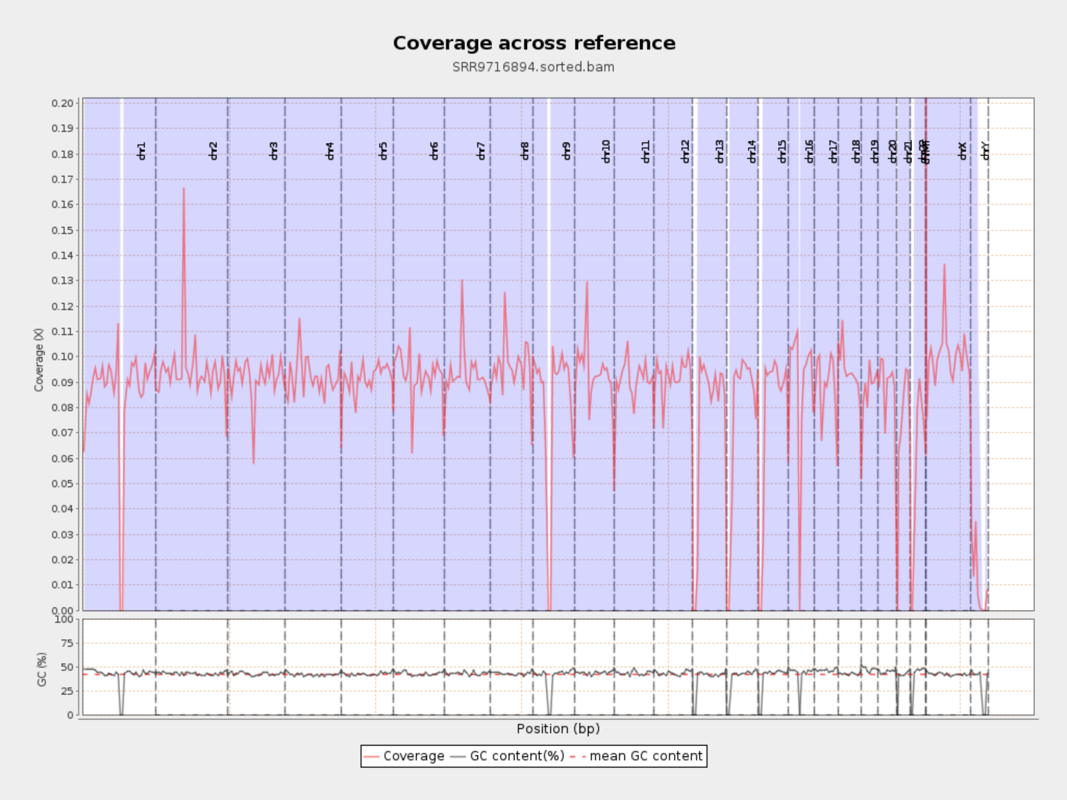
General error rate	0.71%
Mismatches	1,884,195
Insertions	22,872
Mapped reads with at least one insertion	0.6%
Deletions	51,550
Mapped reads with at least one deletion	1.35%
Homopolymer indels	39.99%

2.6. Chromosome stats

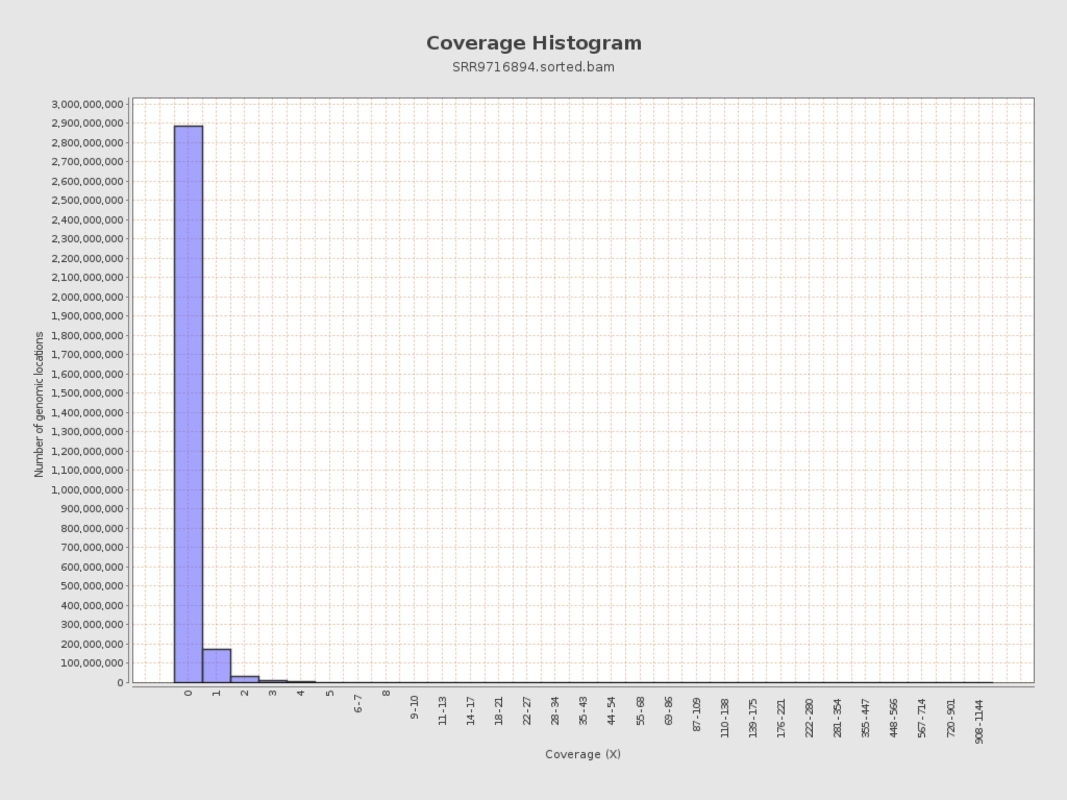
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21300853	0.0855	0.773
chr2	243199373	23179311	0.0953	0.9196
chr3	198022430	18145415	0.0916	0.3731
chr4	191154276	17702006	0.0926	0.4154
chr5	180915260	16534451	0.0914	0.3785
chr6	171115067	15953191	0.0932	0.467
chr7	159138663	14862381	0.0934	0.8395

chr8	146364022	13999263	0.0956	0.8354
chr9	141213431	11405084	0.0808	0.6677
chr10	135534747	12784758	0.0943	0.6112
chr11	135006516	12244904	0.0907	0.6325
chr12	133851895	12380021	0.0925	0.3861
chr13	115169878	8667024	0.0753	0.3367
chr14	107349540	8243322	0.0768	0.4598
chr15	102531392	7679176	0.0749	0.3404
chr16	90354753	7833949	0.0867	0.434
chr17	81195210	7246189	0.0892	0.4219
chr18	78077248	7420992	0.095	1.2806
chr19	59128983	5171120	0.0875	0.71
chr20	63025520	5560842	0.0882	0.3929
chr21	48129895	3490263	0.0725	0.3726
chr22	51304566	2893455	0.0564	0.294
chrMT	16571	4074	0.2459	0.7854
chrX	155270560	15541992	0.1001	0.5417
chrY	59373566	668350	0.0113	0.2718

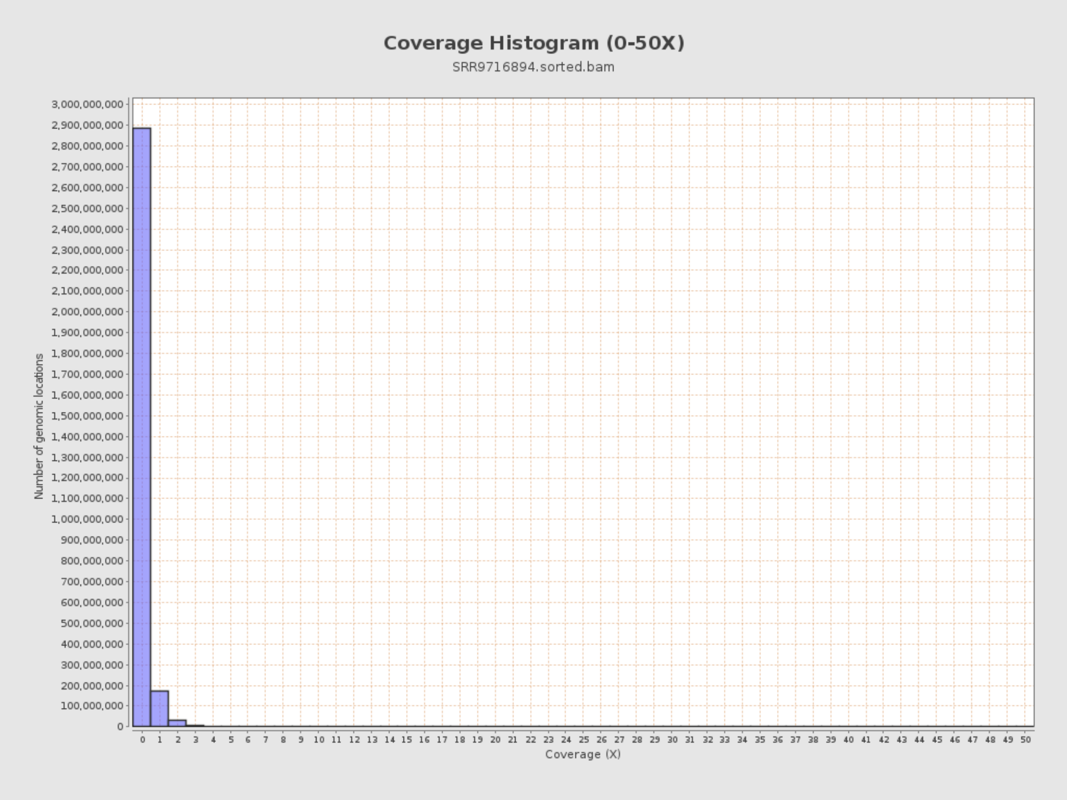
3. Results : Coverage across reference



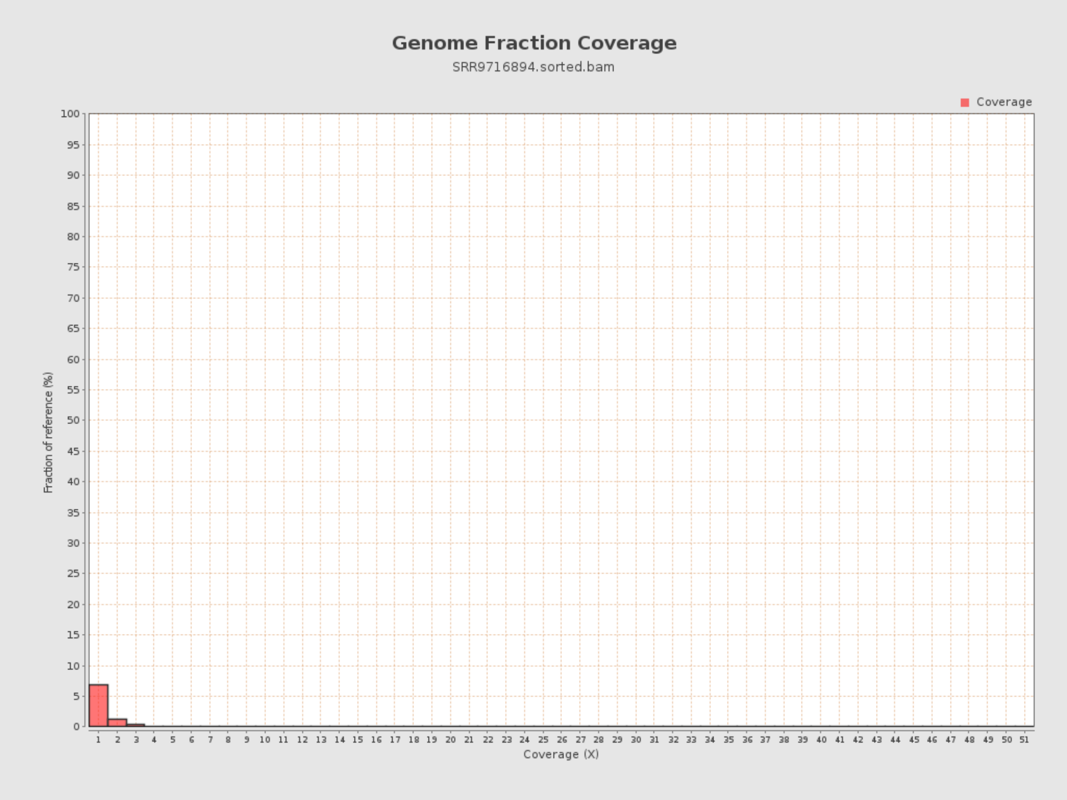
4. Results : Coverage Histogram



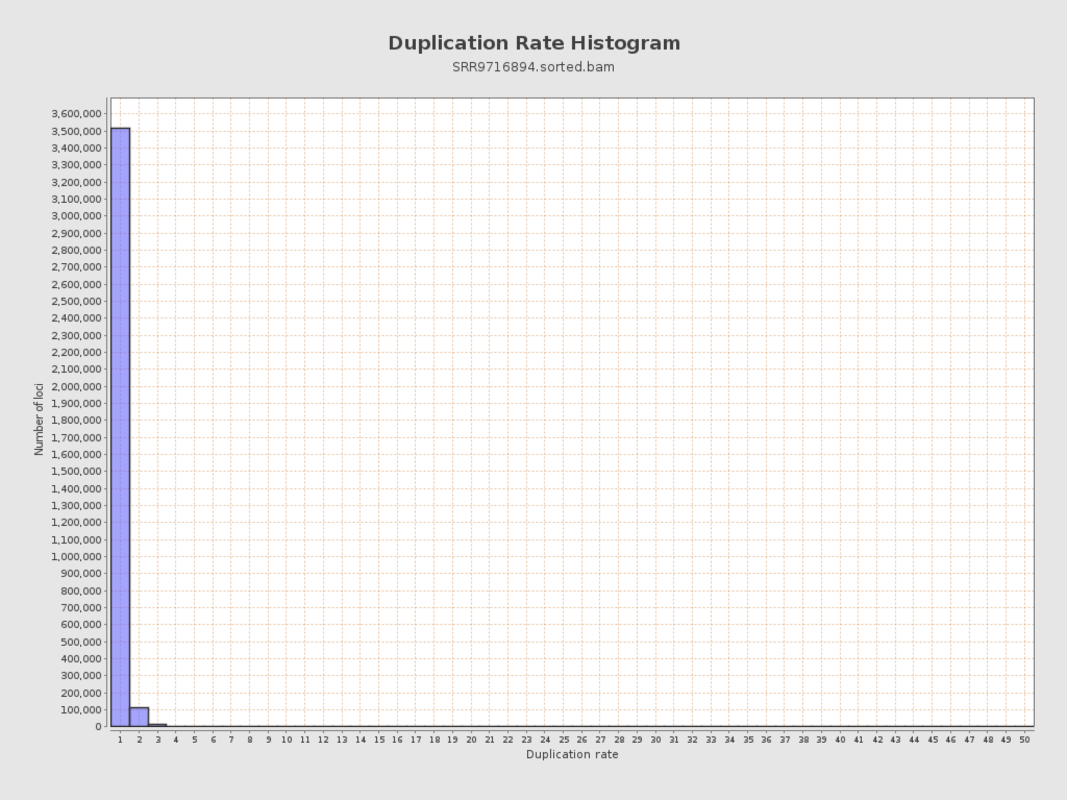
5. Results : Coverage Histogram (0-50X)



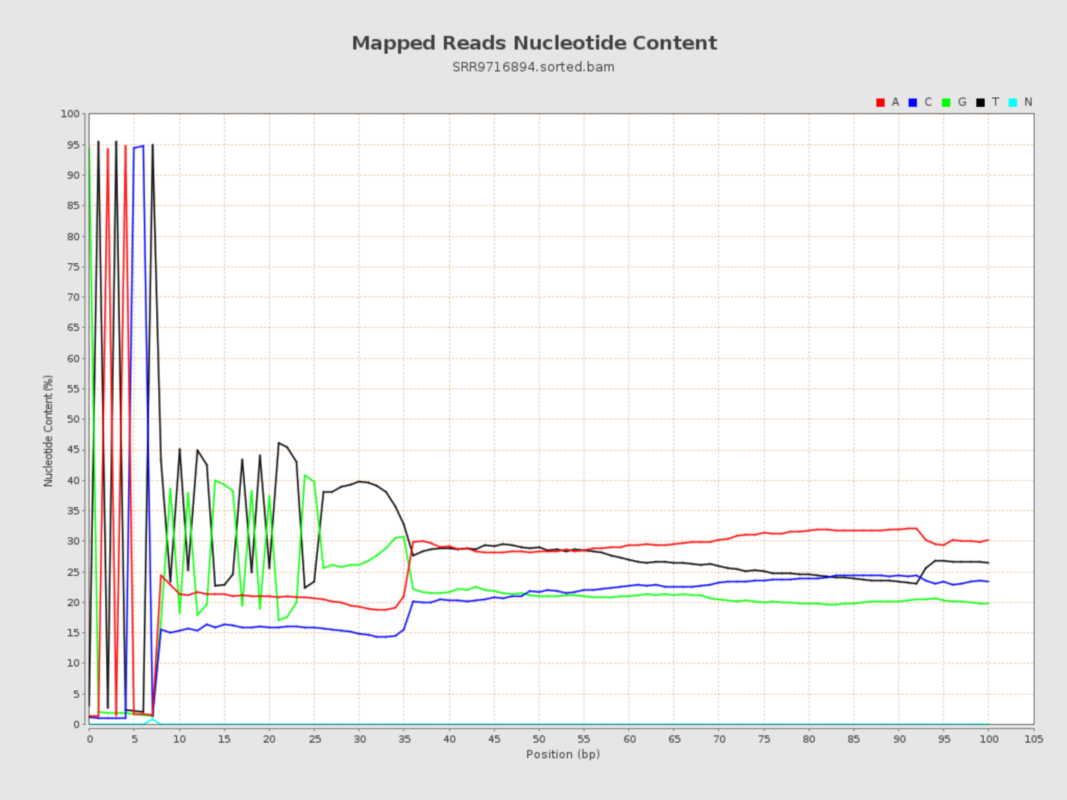
6. Results : Genome Fraction Coverage



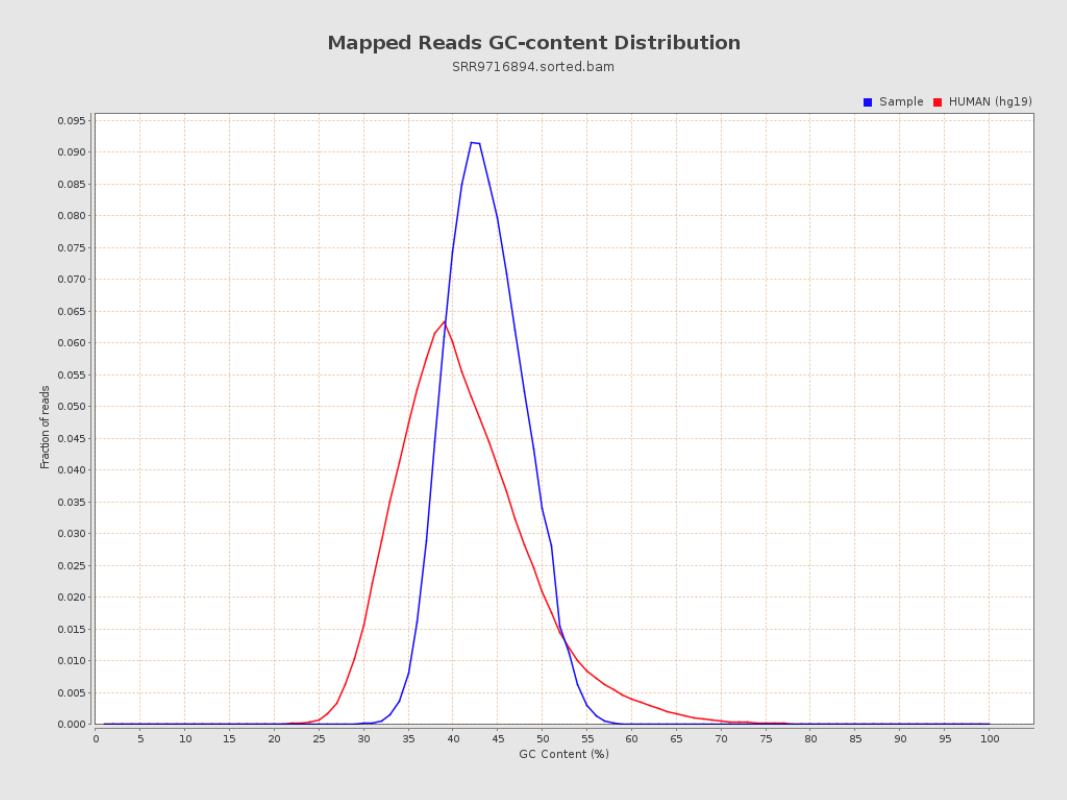
7. Results : Duplication Rate Histogram



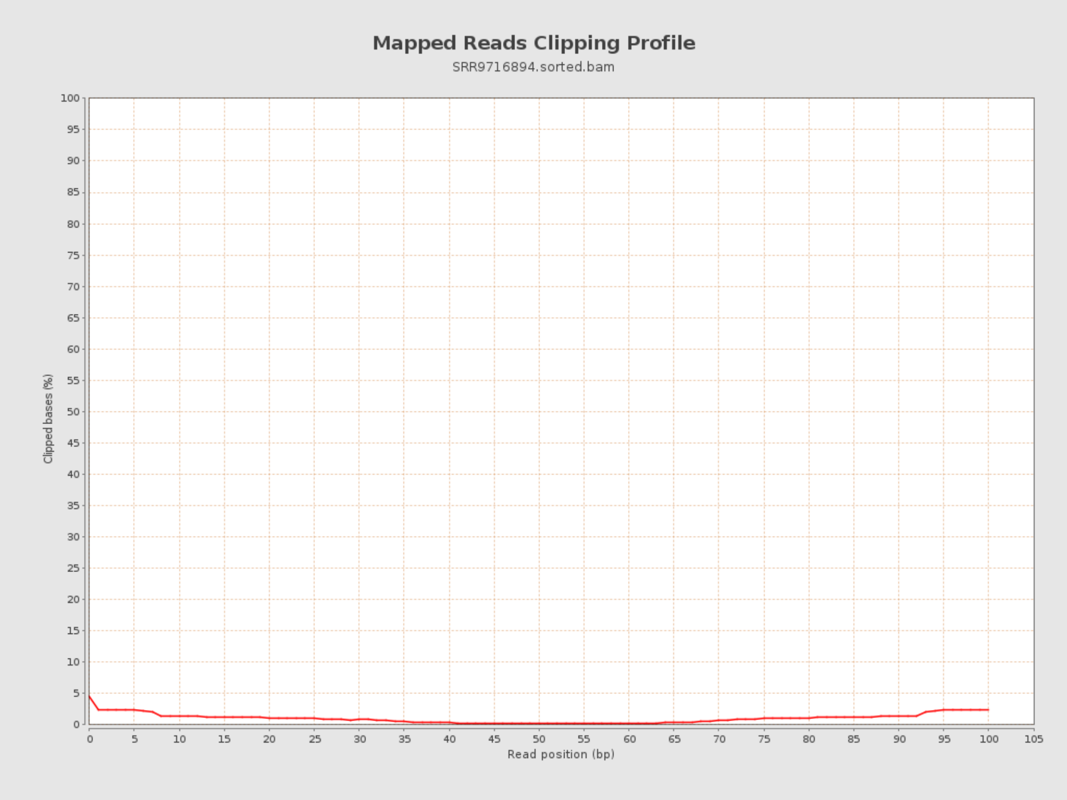
8. Results : Mapped Reads Nucleotide Content



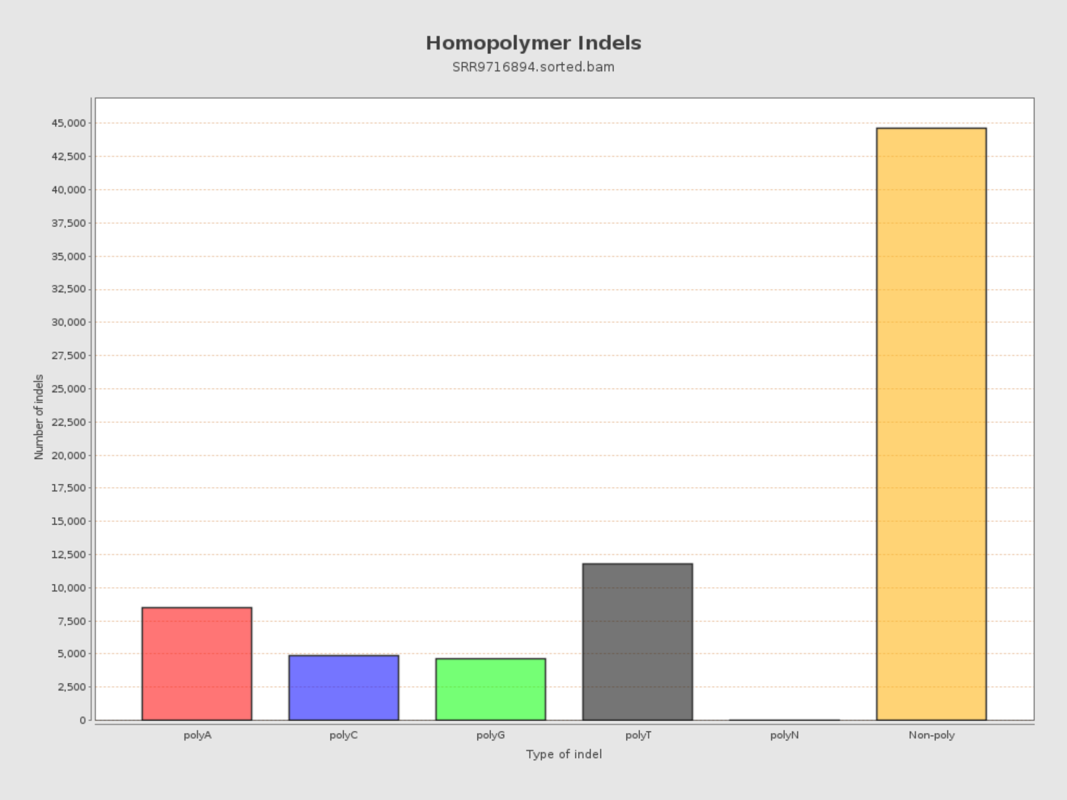
9. Results : Mapped Reads GC-content Distribution



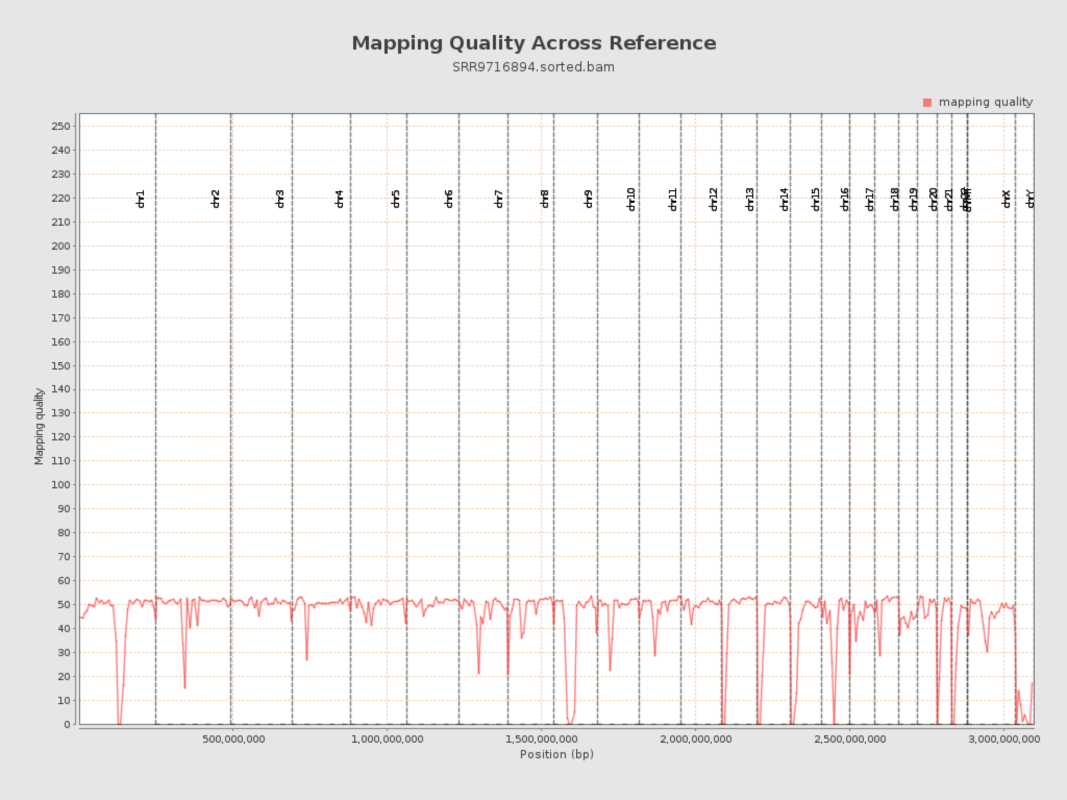
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram