Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 04:46:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716671.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_SRR9716671 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716671.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 04:46:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716671.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,844,556
Mapped reads	2,595,107 / 91.23%
Unmapped reads	249,449 / 8.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,037 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	192,540 / 6.77%
Duplication rate	5.84%
Clipped reads	2,602,759 / 91.5%

2.2. ACGT Content

Number/percentage of A's	39,141,746 / 25.88%
Number/percentage of C's	30,668,128 / 20.28%
Number/percentage of T's	45,893,371 / 30.34%
Number/percentage of G's	35,554,354 / 23.51%
Number/percentage of N's	1,047 / 0%
GC Percentage	43.78%

2.3. Coverage

Mean	0.0489

Standard Deviation	0.3972

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

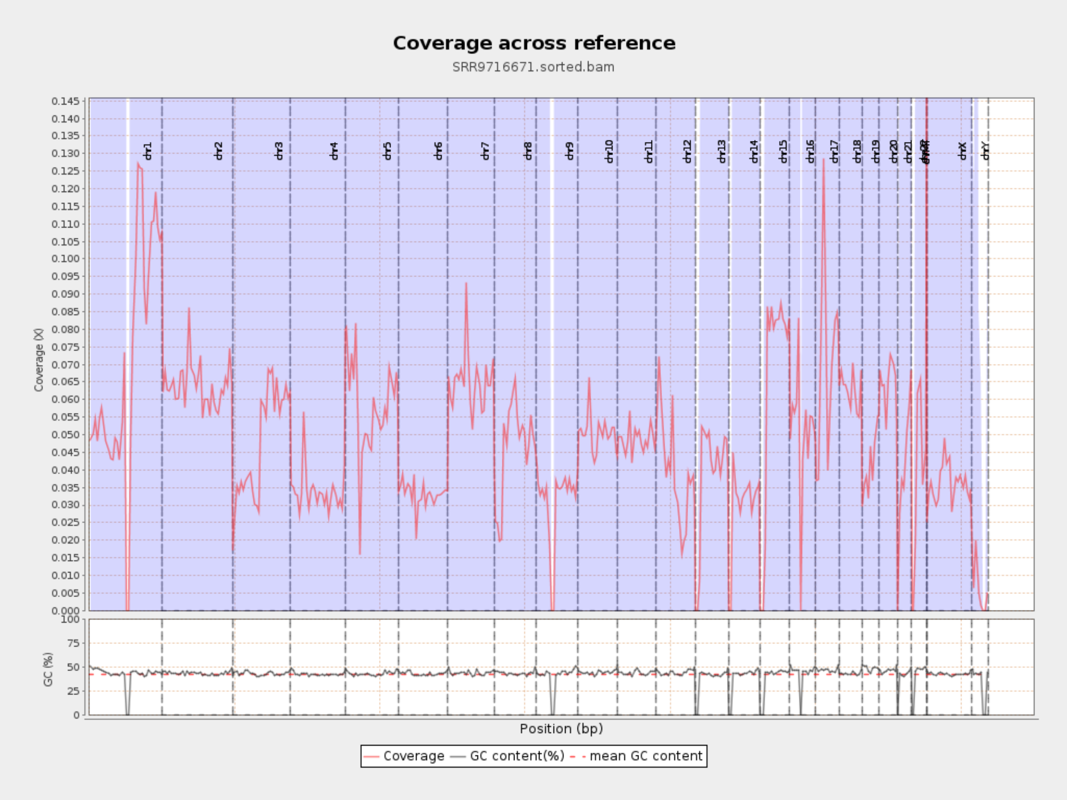
General error rate	0.5%
Mismatches	735,911
Insertions	12,612
Mapped reads with at least one insertion	0.48%
Deletions	26,137
Mapped reads with at least one deletion	1%
Homopolymer indels	40.4%

2.6. Chromosome stats

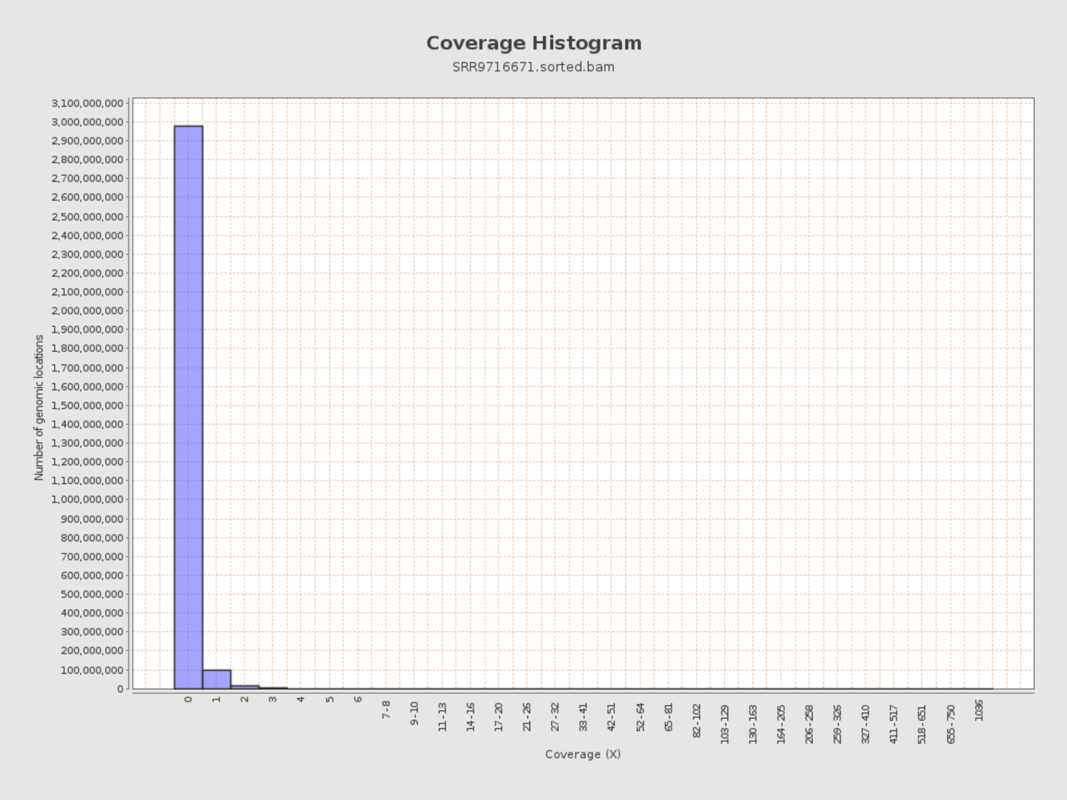
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17536678	0.0704	0.6494
chr2	243199373	15611049	0.0642	0.5663
chr3	198022430	9447818	0.0477	0.2657
chr4	191154276	6420273	0.0336	0.271
chr5	180915260	10446790	0.0577	0.2934
chr6	171115067	5660567	0.0331	0.2502
chr7	159138663	10381932	0.0652	0.6264

chr8	146364022	6805860	0.0465	0.3848
chr9	141213431	4269646	0.0302	0.3013
chr10	135534747	6857985	0.0506	0.3482
chr11	135006516	6560284	0.0486	0.3676
chr12	133851895	5294453	0.0396	0.246
chr13	115169878	4418867	0.0384	0.24
chr14	107349540	3153611	0.0294	0.2255
chr15	102531392	6788543	0.0662	0.3159
chr16	90354753	4611805	0.051	0.2912
chr17	81195210	5827069	0.0718	0.3596
chr18	78077248	4901851	0.0628	0.6464
chr19	59128983	2466815	0.0417	0.4614
chr20	63025520	4086315	0.0648	0.3182
chr21	48129895	1957883	0.0407	0.2701
chr22	51304566	1834871	0.0358	0.2306
chrMT	16571	3234	0.1952	0.4854
chrX	155270560	5593857	0.036	0.2646
chrY	59373566	361336	0.0061	0.1563

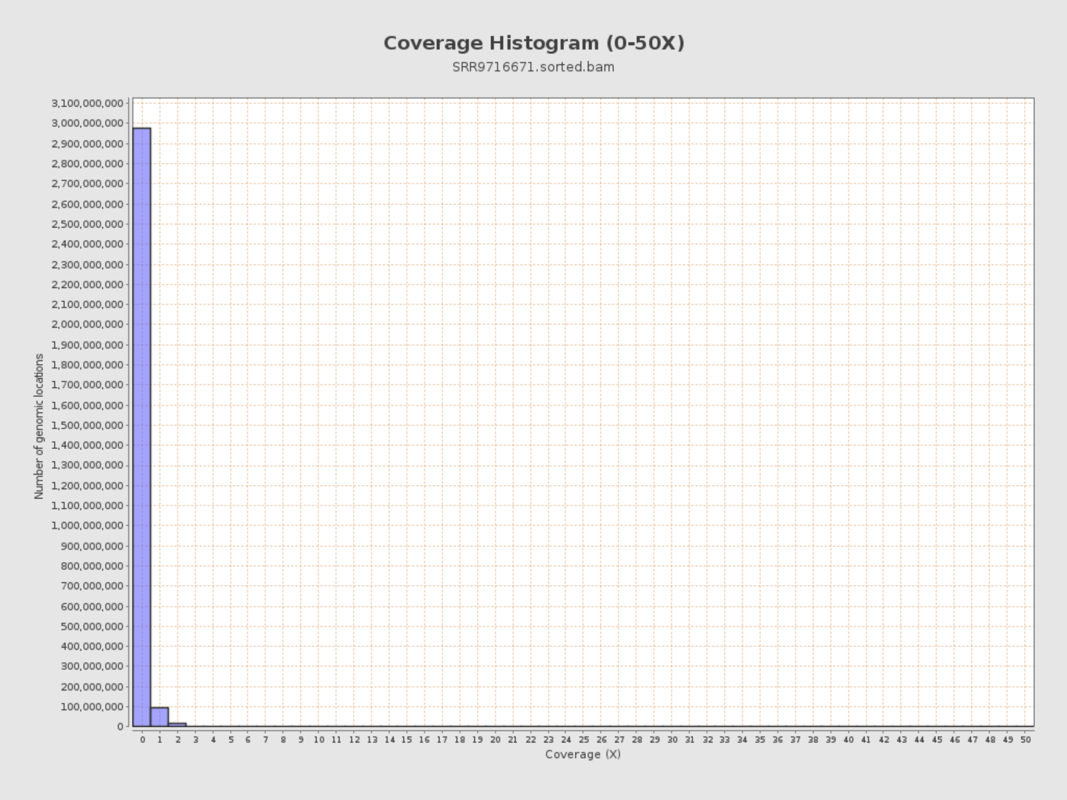
3. Results : Coverage across reference



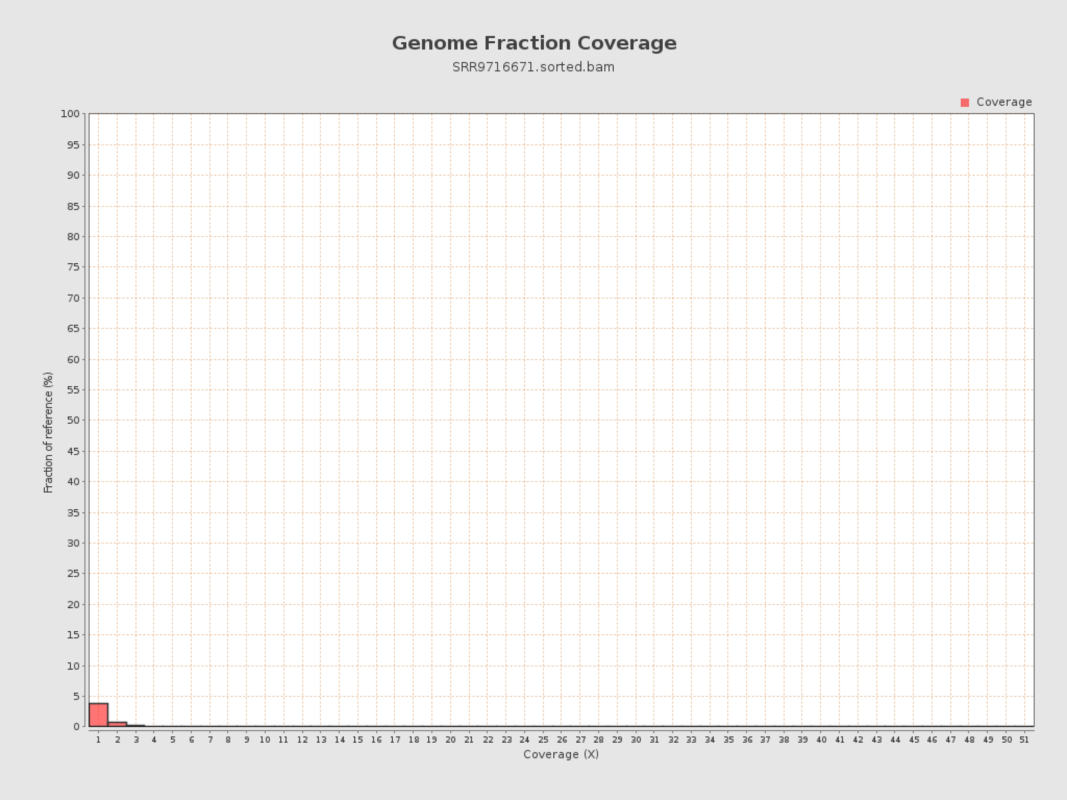
4. Results : Coverage Histogram



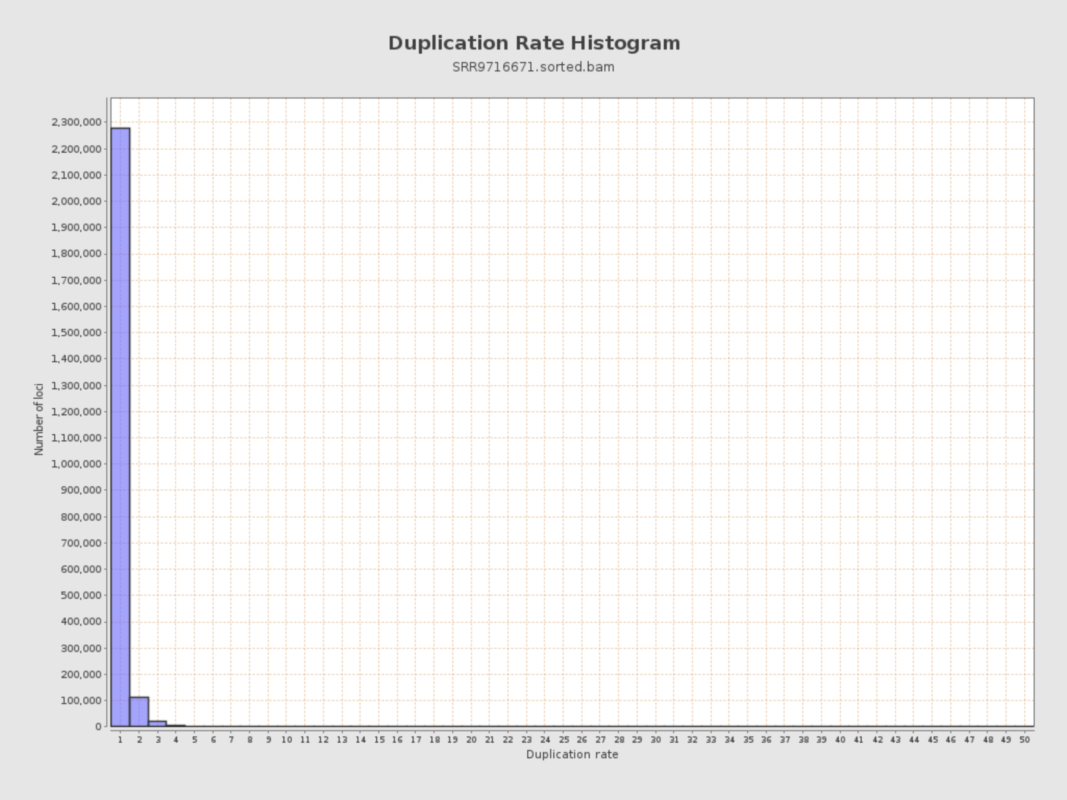
5. Results : Coverage Histogram (0-50X)



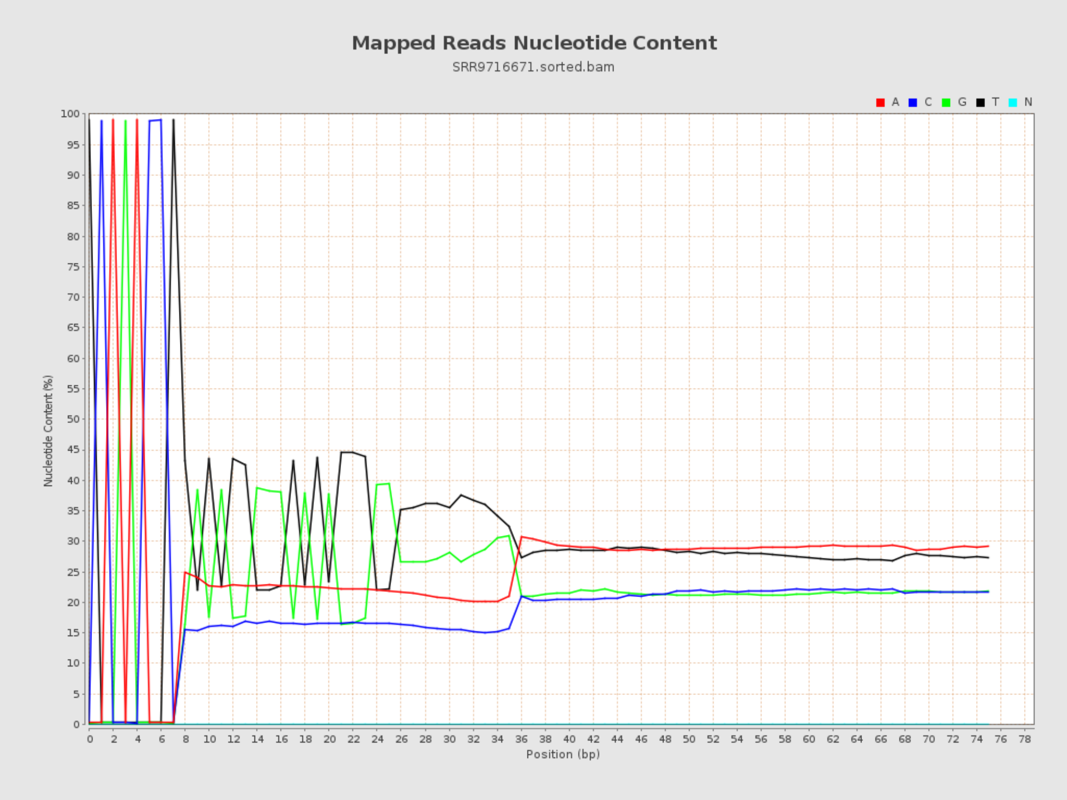
6. Results : Genome Fraction Coverage



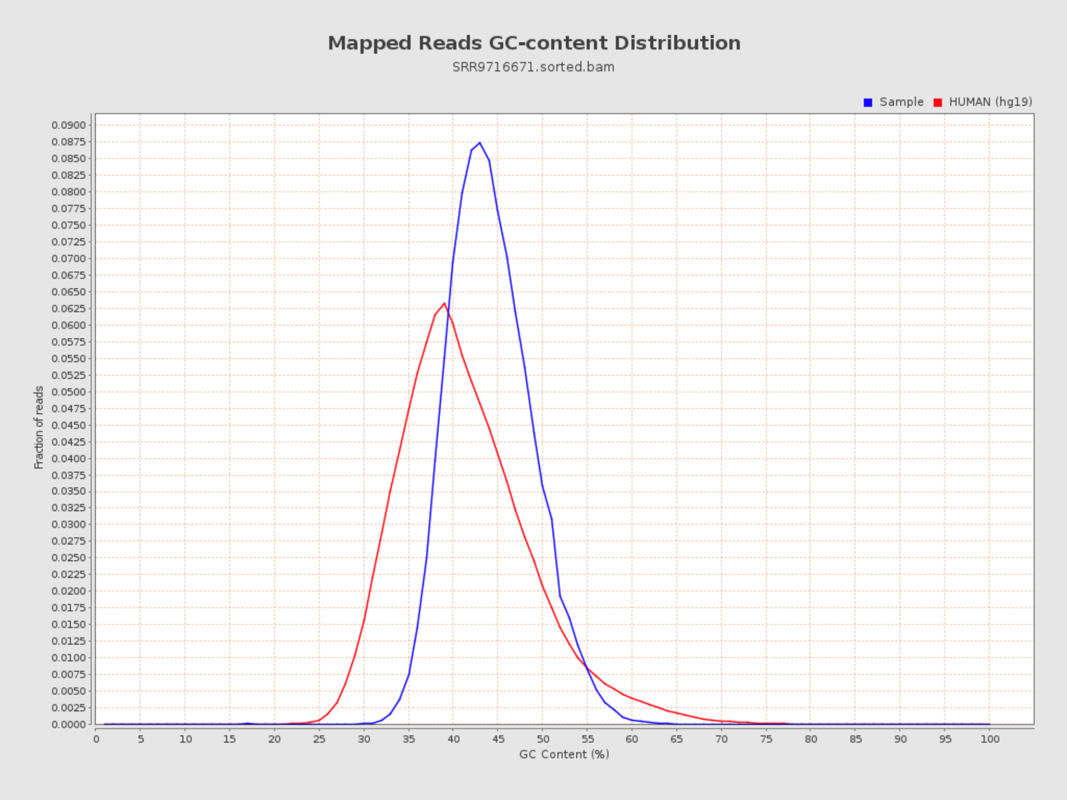
7. Results : Duplication Rate Histogram



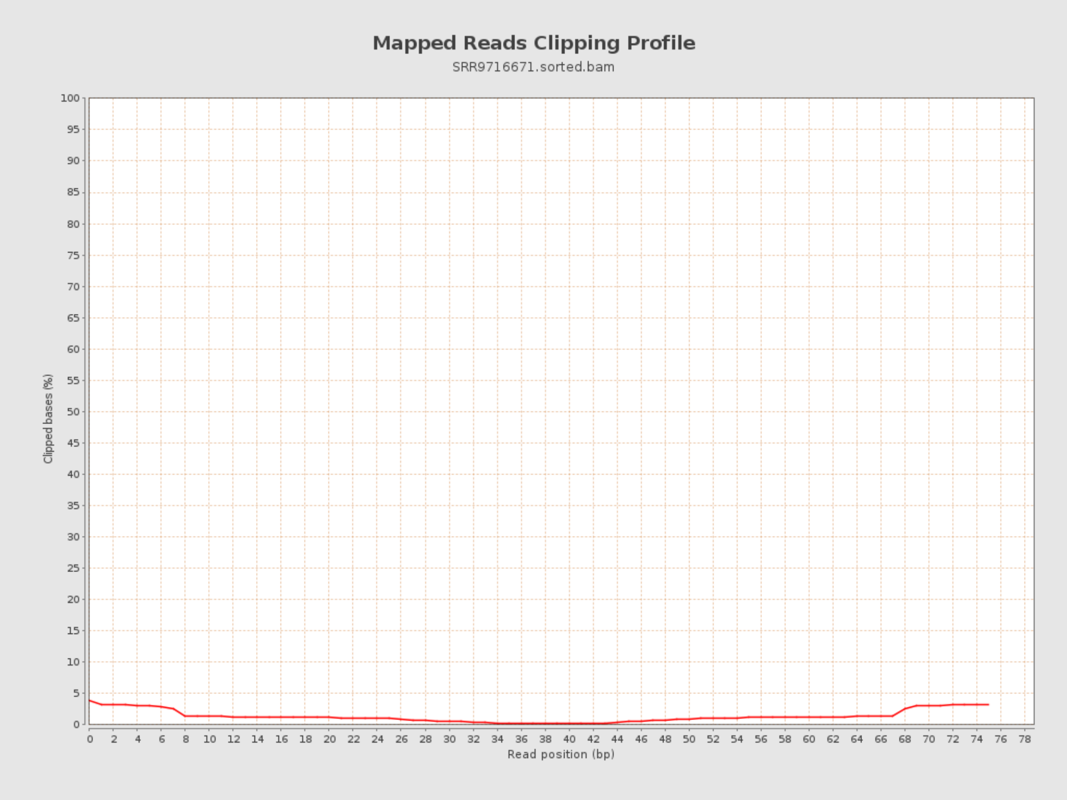
8. Results : Mapped Reads Nucleotide Content



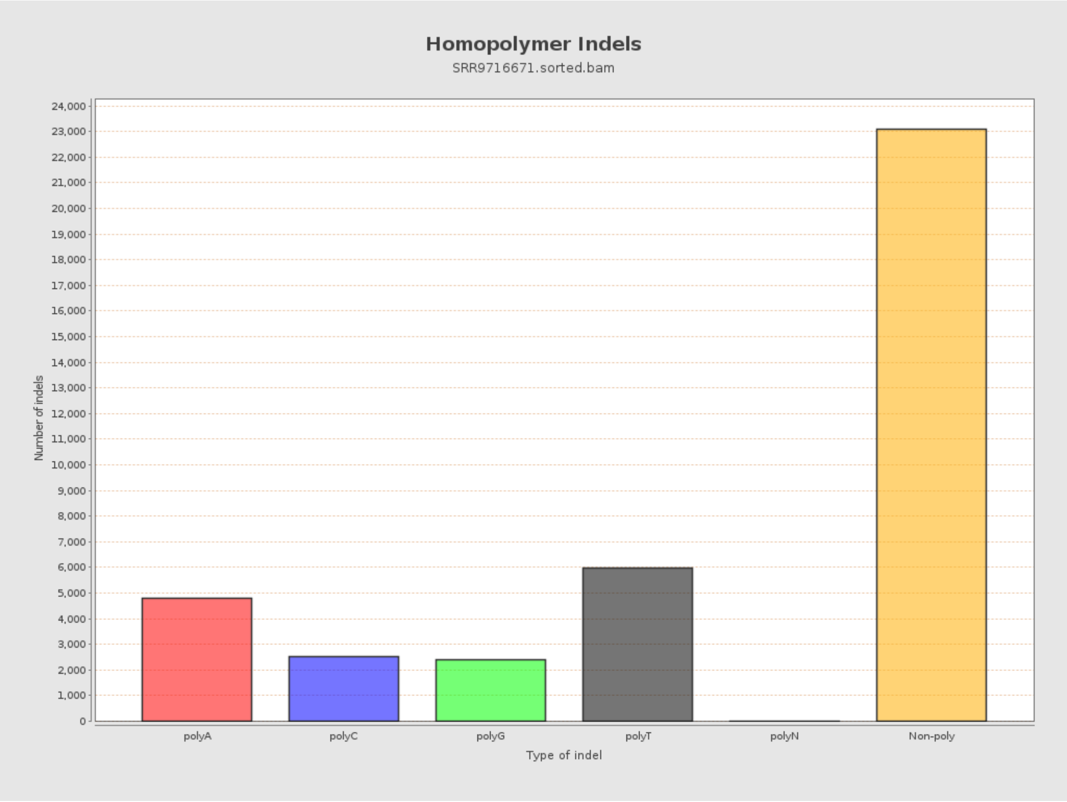
9. Results : Mapped Reads GC-content Distribution



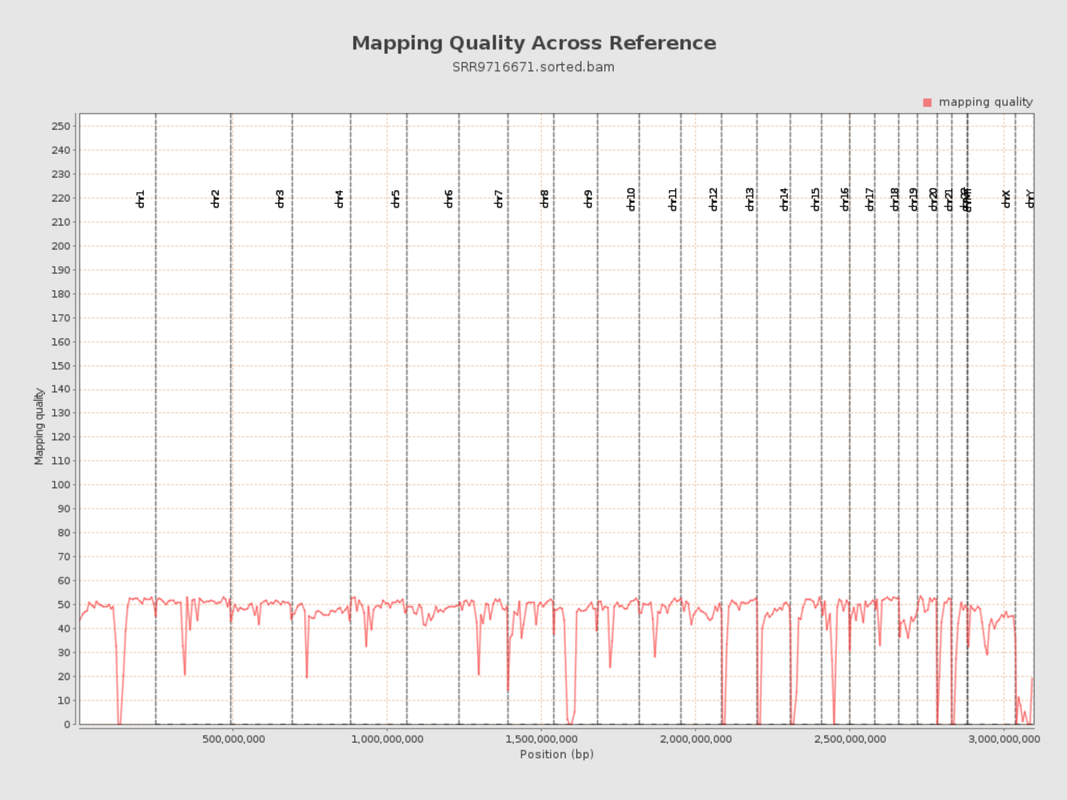
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram