Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:42:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716921.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_SRR9716921 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716921.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:42:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,364,851
Mapped reads	2,156,158 / 91.18%
Unmapped reads	208,693 / 8.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,149 / 0.6%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	117,934 / 4.99%
Duplication rate	4.32%
Clipped reads	2,162,229 / 91.43%

2.2. ACGT Content

Number/percentage of A's	32,607,646 / 25.91%
Number/percentage of C's	25,428,112 / 20.21%
Number/percentage of T's	38,460,319 / 30.56%
Number/percentage of G's	29,347,836 / 23.32%
Number/percentage of N's	925 / 0%
GC Percentage	43.53%

2.3. Coverage

Mean	0.0407

Standard Deviation	0.3376

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

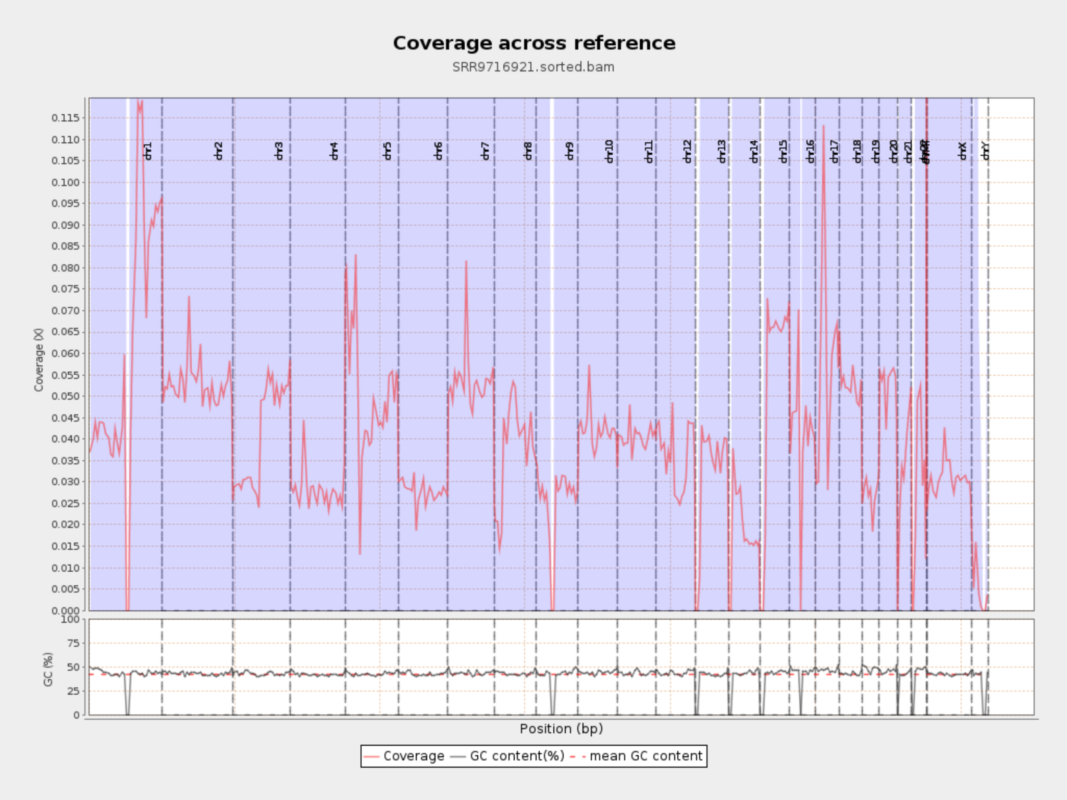
General error rate	0.51%
Mismatches	627,512
Insertions	10,142
Mapped reads with at least one insertion	0.47%
Deletions	22,709
Mapped reads with at least one deletion	1.05%
Homopolymer indels	40.72%

2.6. Chromosome stats

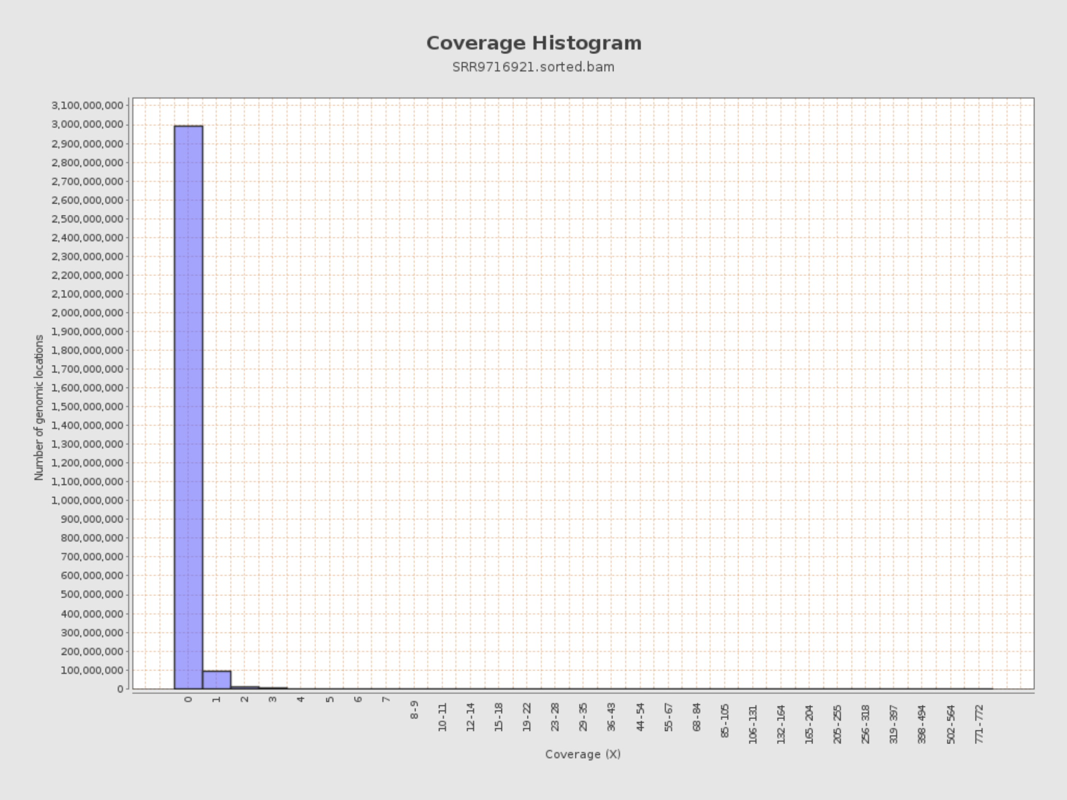
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15055457	0.0604	0.5438
chr2	243199373	12926488	0.0532	0.4575
chr3	198022430	8058740	0.0407	0.2327
chr4	191154276	5343573	0.028	0.2213
chr5	180915260	9101964	0.0503	0.2603
chr6	171115067	4761287	0.0278	0.2173
chr7	159138663	8581245	0.0539	0.5626

chr8	146364022	5590469	0.0382	0.3139
chr9	141213431	3497589	0.0248	0.2586
chr10	135534747	5743254	0.0424	0.2937
chr11	135006516	5455650	0.0404	0.3237
chr12	133851895	4804294	0.0359	0.2212
chr13	115169878	3650273	0.0317	0.2061
chr14	107349540	1979202	0.0184	0.1715
chr15	102531392	5531041	0.0539	0.2699
chr16	90354753	3759246	0.0416	0.2484
chr17	81195210	4812526	0.0593	0.3084
chr18	78077248	4123707	0.0528	0.5568
chr19	59128983	1603144	0.0271	0.3919
chr20	63025520	3349890	0.0532	0.2706
chr21	48129895	1620275	0.0337	0.2272
chr22	51304566	1437704	0.028	0.1928
chrMT	16571	2735	0.165	0.434
chrX	155270560	4800761	0.0309	0.2351
chrY	59373566	289897	0.0049	0.121

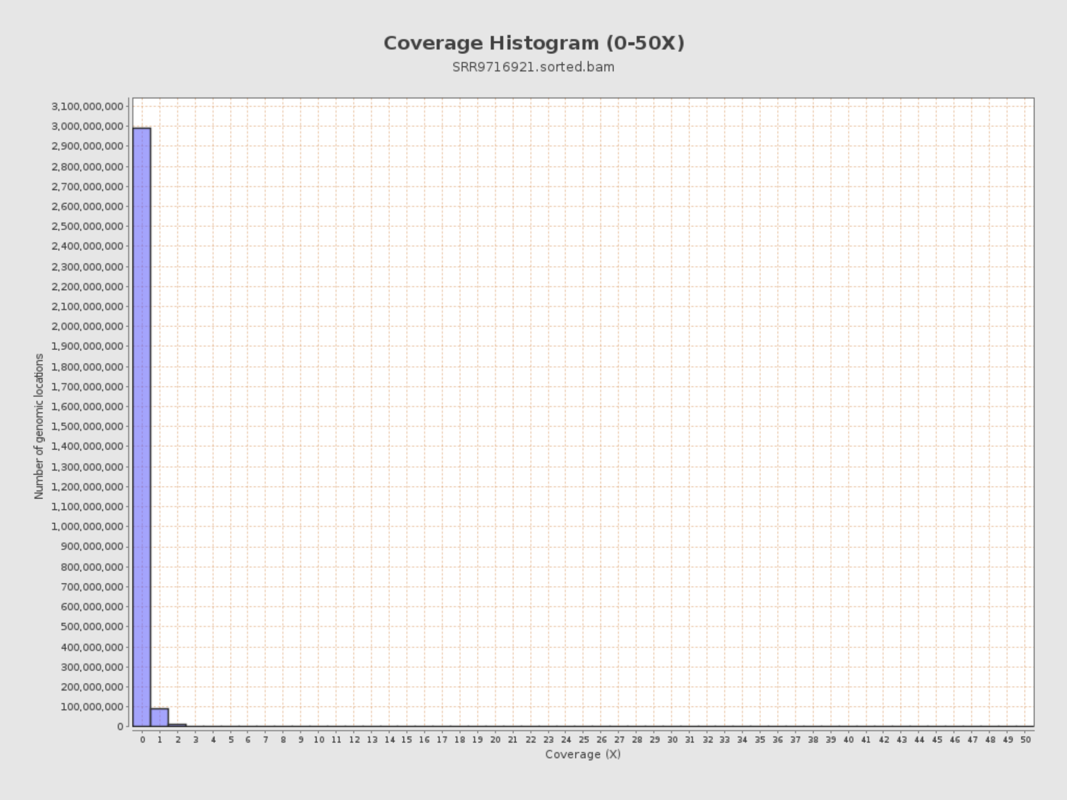
3. Results : Coverage across reference



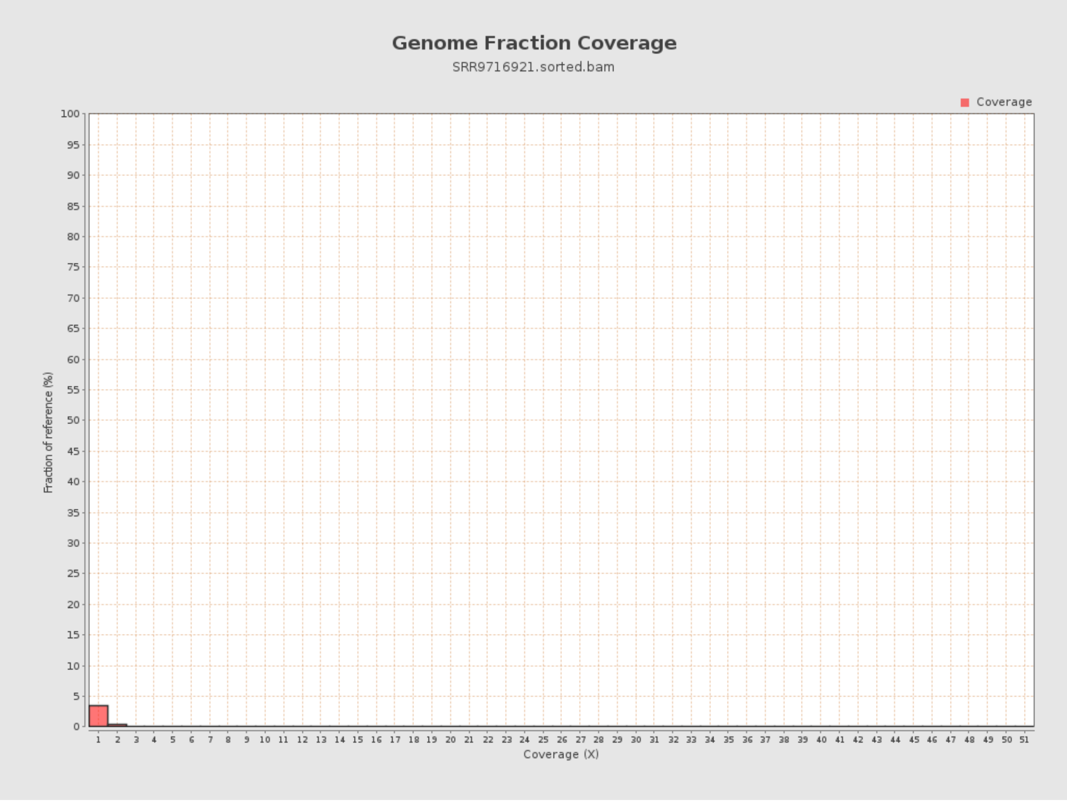
4. Results : Coverage Histogram



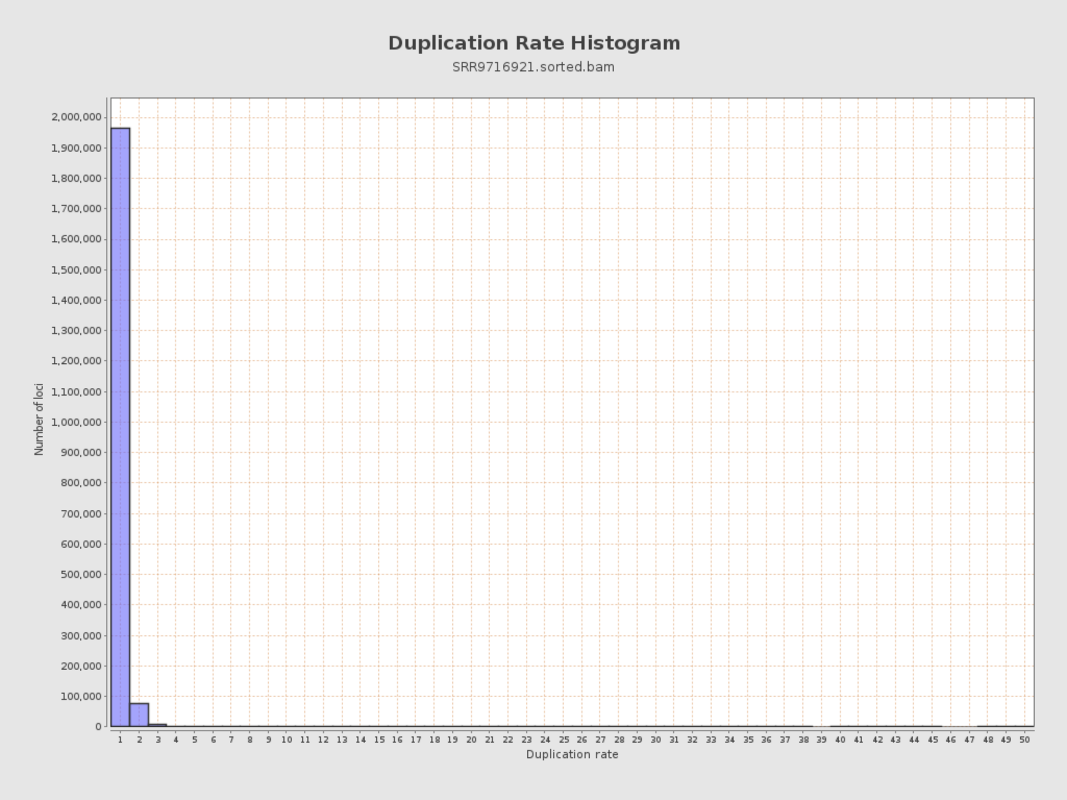
5. Results : Coverage Histogram (0-50X)



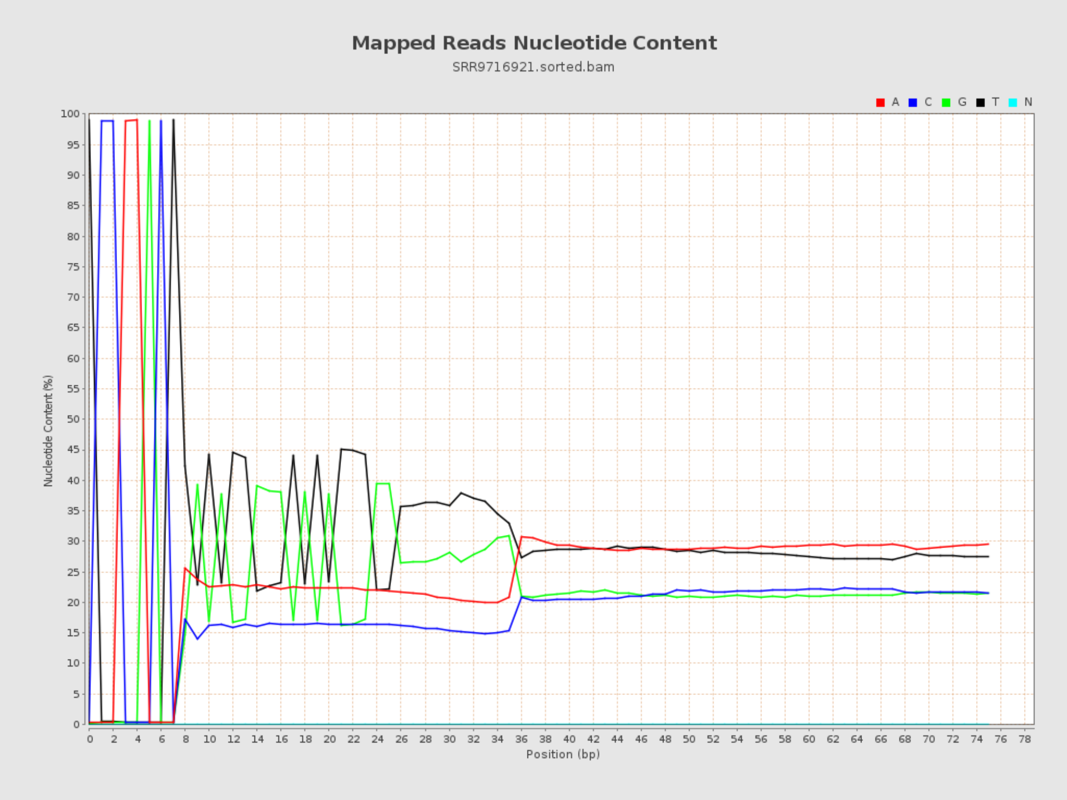
6. Results : Genome Fraction Coverage



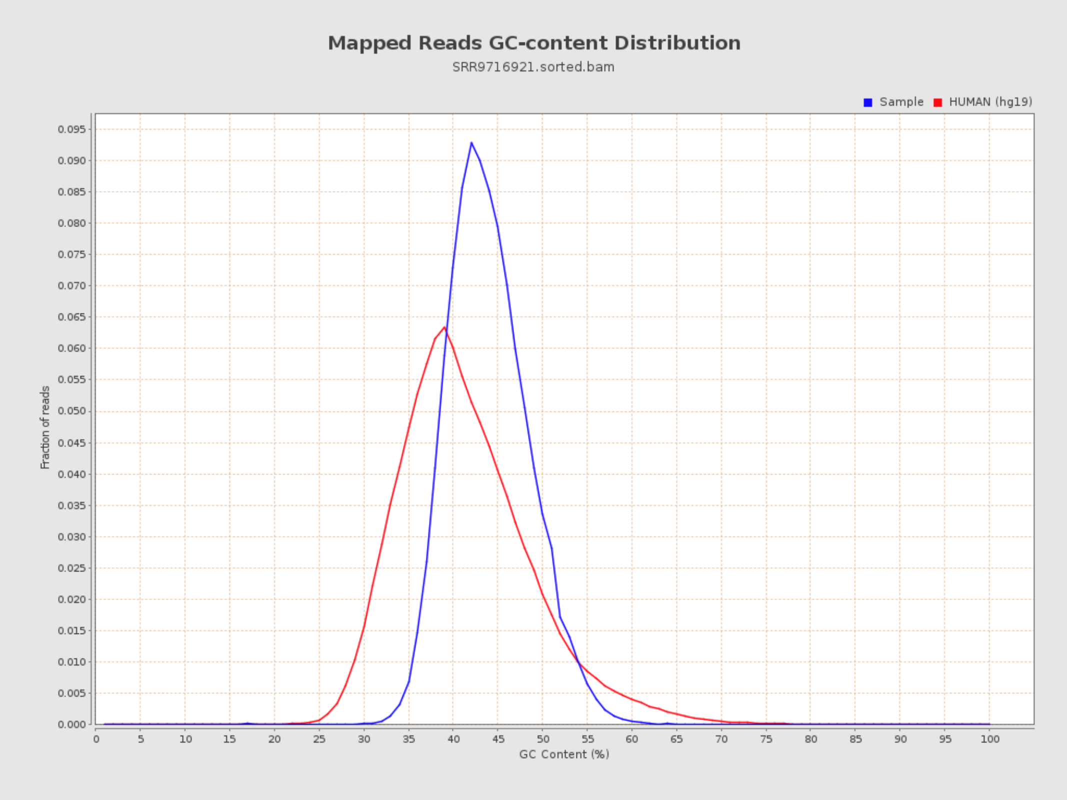
7. Results : Duplication Rate Histogram



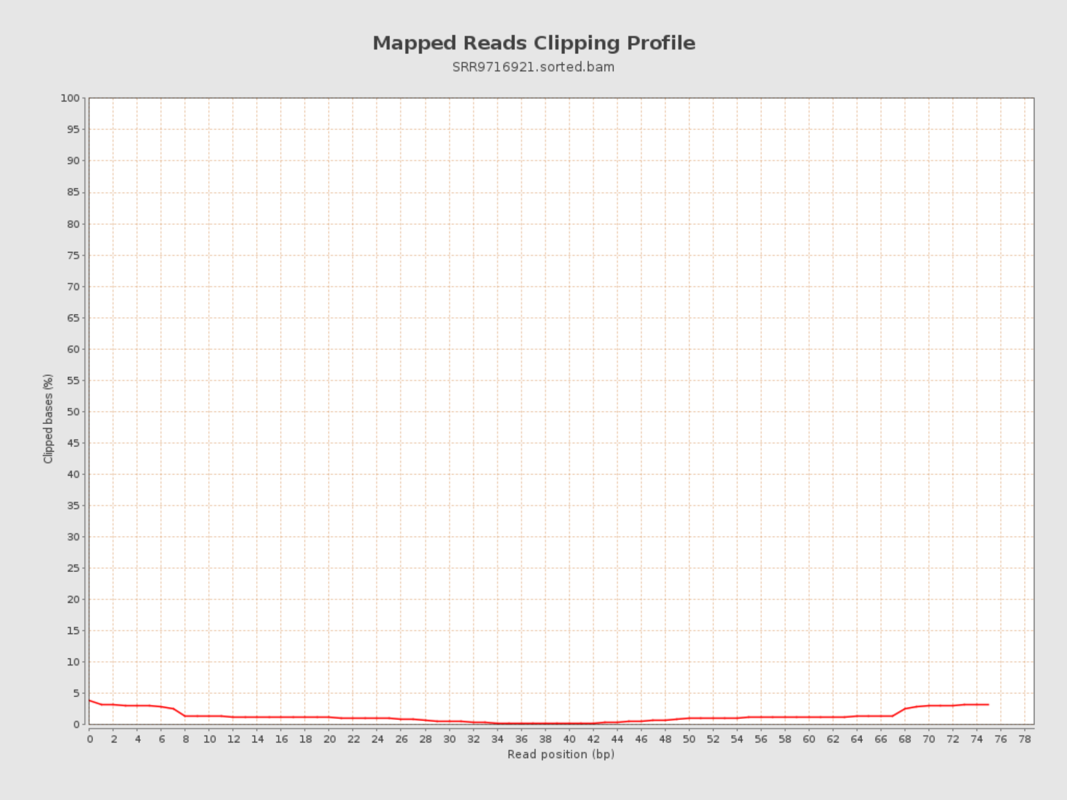
8. Results : Mapped Reads Nucleotide Content



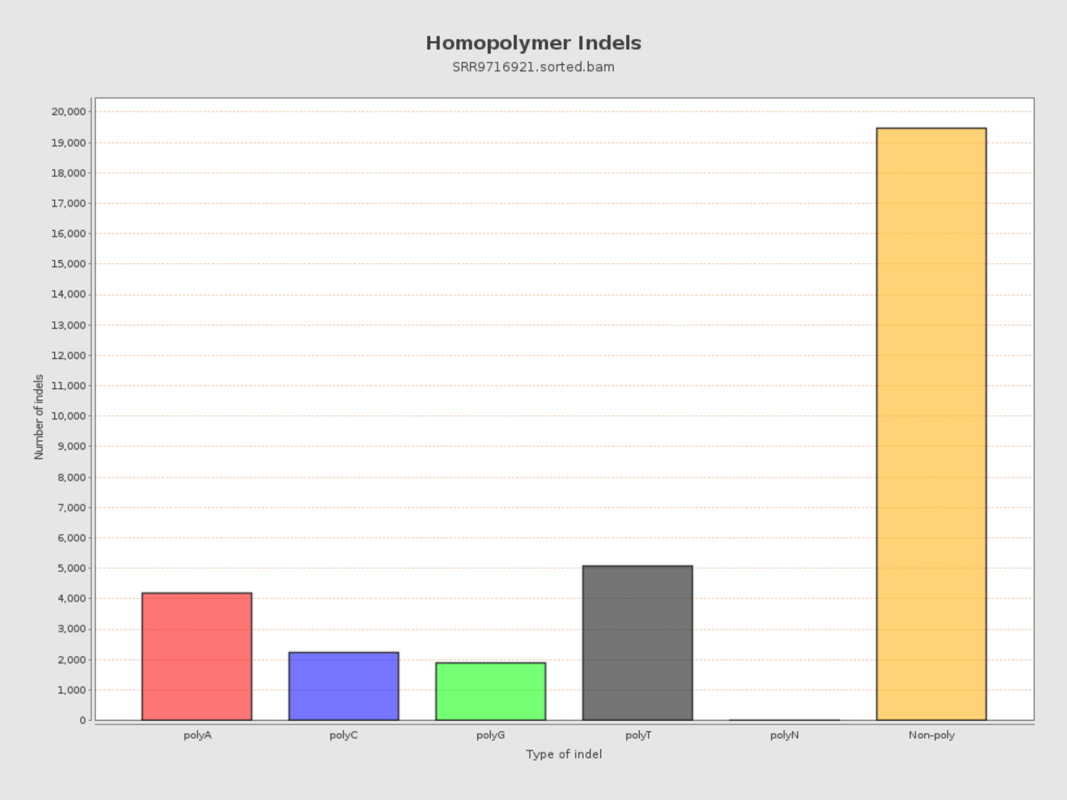
9. Results : Mapped Reads GC-content Distribution



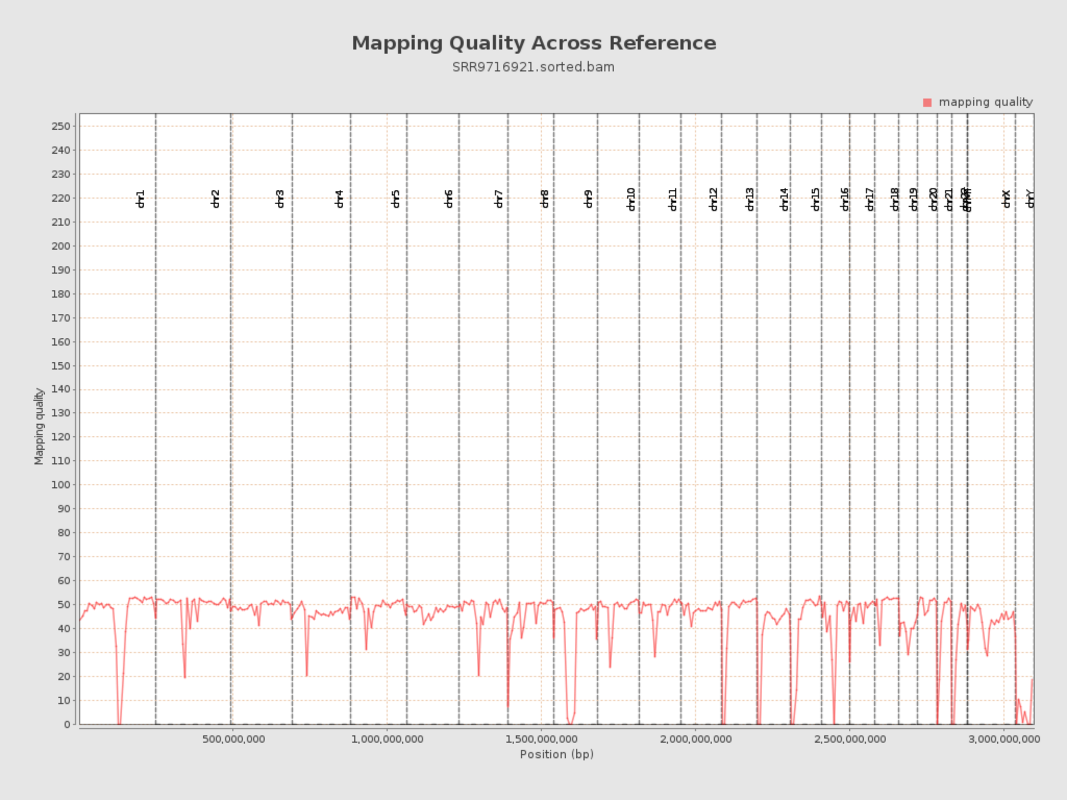
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram