Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:36:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716421.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_SRR9716421 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716421.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:36:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716421.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,347,571
Mapped reads	1,237,848 / 91.86%
Unmapped reads	109,723 / 8.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,431 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	44,287 / 3.29%
Duplication rate	2.56%
Clipped reads	1,238,151 / 91.88%

2.2. ACGT Content

Number/percentage of A's	18,631,903 / 25.99%
Number/percentage of C's	14,502,293 / 20.23%
Number/percentage of T's	22,070,830 / 30.78%
Number/percentage of G's	16,490,043 / 23%
Number/percentage of N's	1,340 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2337

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

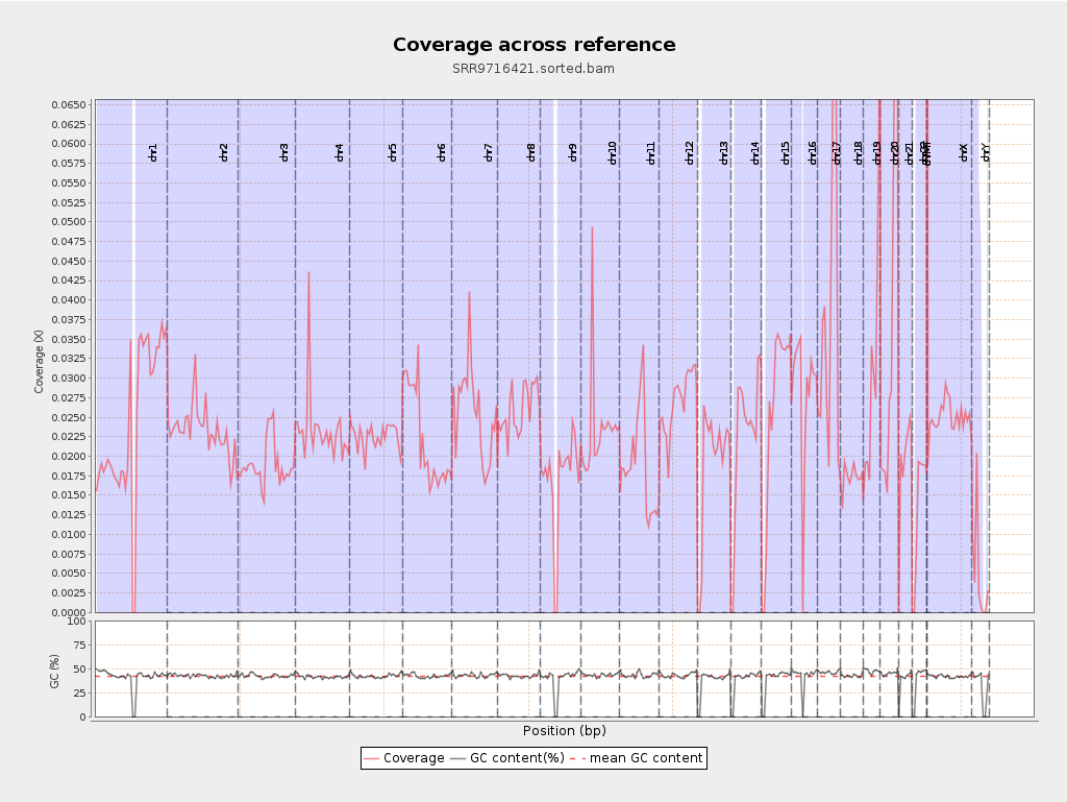
General error rate	0.52%
Mismatches	358,526
Insertions	5,911
Mapped reads with at least one insertion	0.48%
Deletions	13,784
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.24%

2.6. Chromosome stats

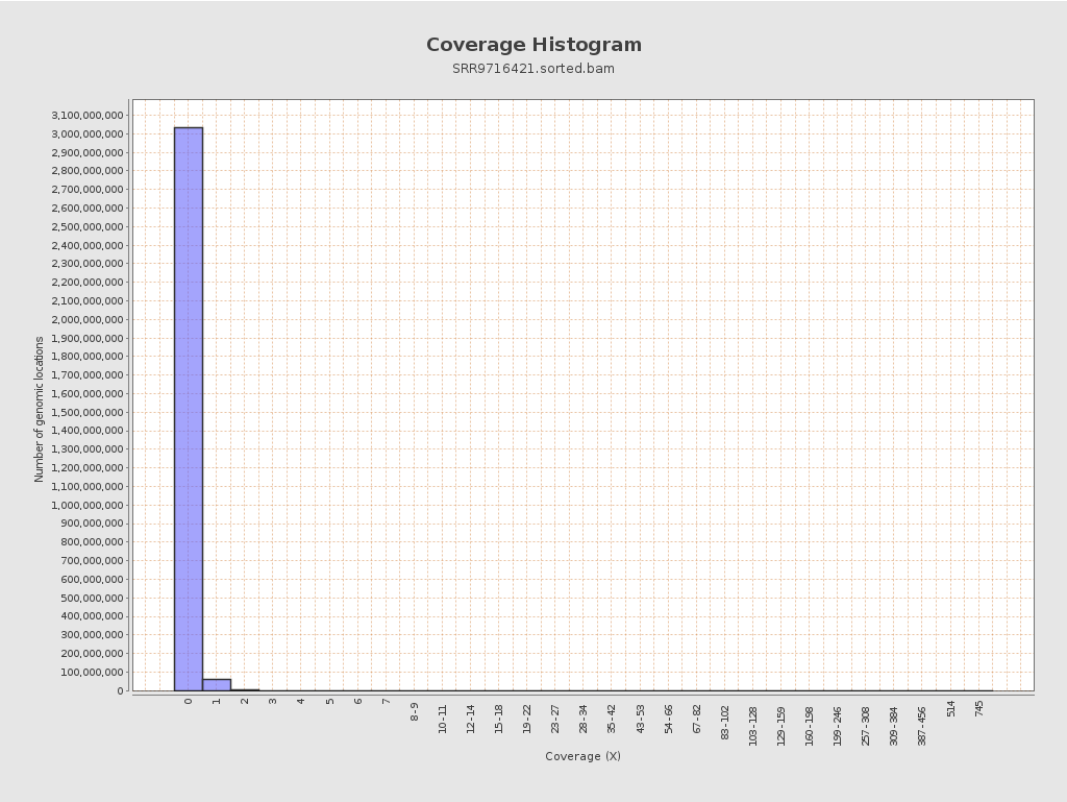
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6035985	0.0242	0.3522
chr2	243199373	5659363	0.0233	0.3437
chr3	198022430	3736045	0.0189	0.1491
chr4	191154276	4455655	0.0233	0.1989
chr5	180915260	4073731	0.0225	0.161
chr6	171115067	3798071	0.0222	0.1834
chr7	159138663	4091904	0.0257	0.2824

chr8	146364022	3806752	0.026	0.3019
chr9	141213431	2407086	0.017	0.1633
chr10	135534747	3172564	0.0234	0.2551
chr11	135006516	2559641	0.019	0.184
chr12	133851895	3603985	0.0269	0.1775
chr13	115169878	2170961	0.0189	0.1484
chr14	107349540	2410470	0.0225	0.1627
chr15	102531392	2628447	0.0256	0.1721
chr16	90354753	2505489	0.0277	0.1875
chr17	81195210	3205185	0.0395	0.2226
chr18	78077248	1343600	0.0172	0.2646
chr19	59128983	1874186	0.0317	0.2943
chr20	63025520	2386798	0.0379	0.2173
chr21	48129895	931576	0.0194	0.1817
chr22	51304566	685559	0.0134	0.1242
chrMT	16571	9163	0.553	0.8757
chrX	155270560	3884014	0.025	0.1826
chrY	59373566	282523	0.0048	0.217

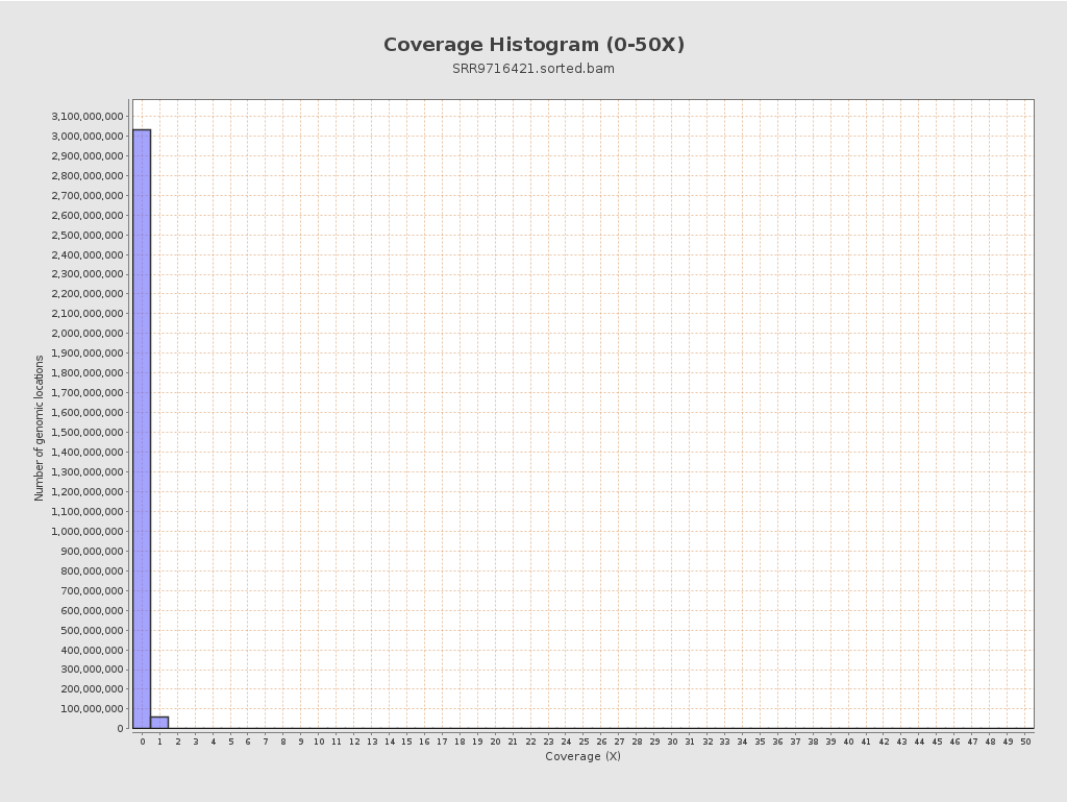
3. Results : Coverage across reference



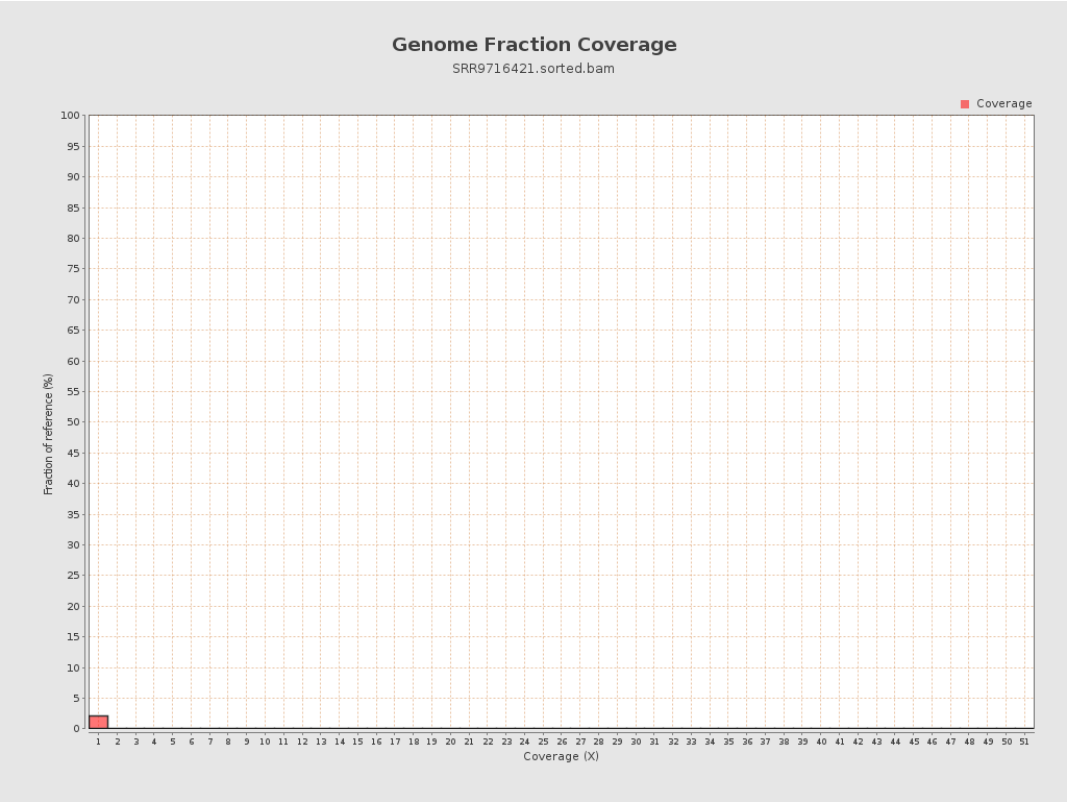
4. Results : Coverage Histogram



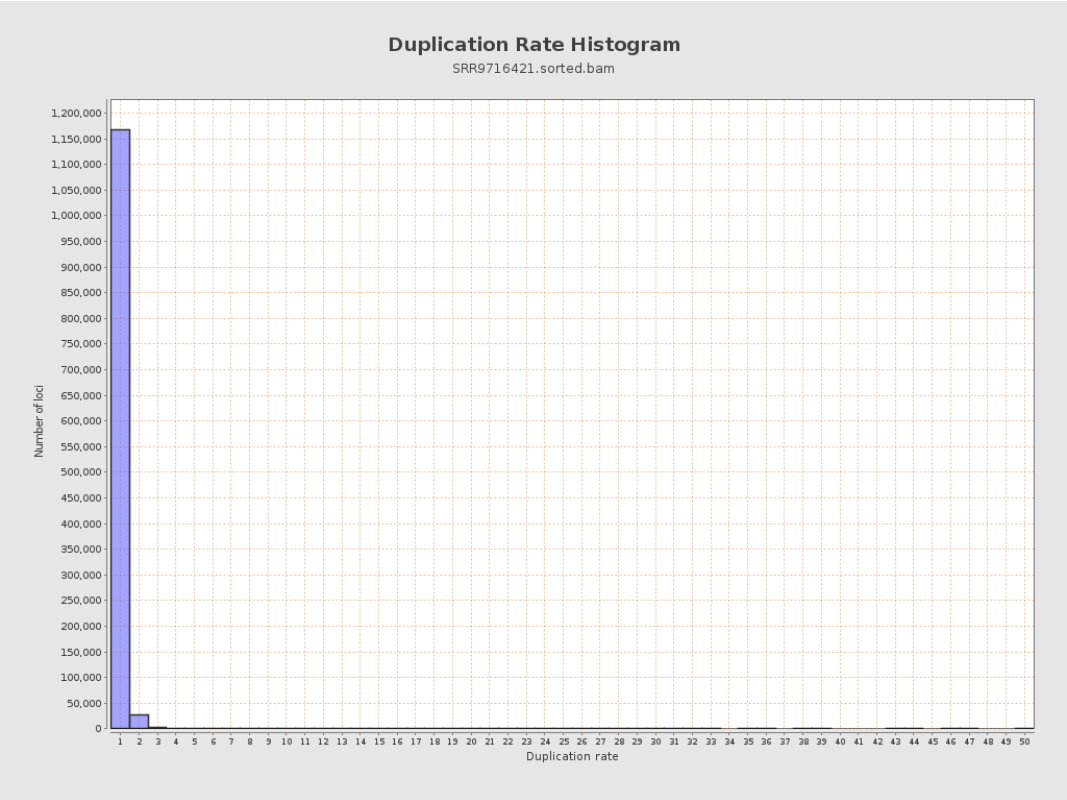
5. Results : Coverage Histogram (0-50X)



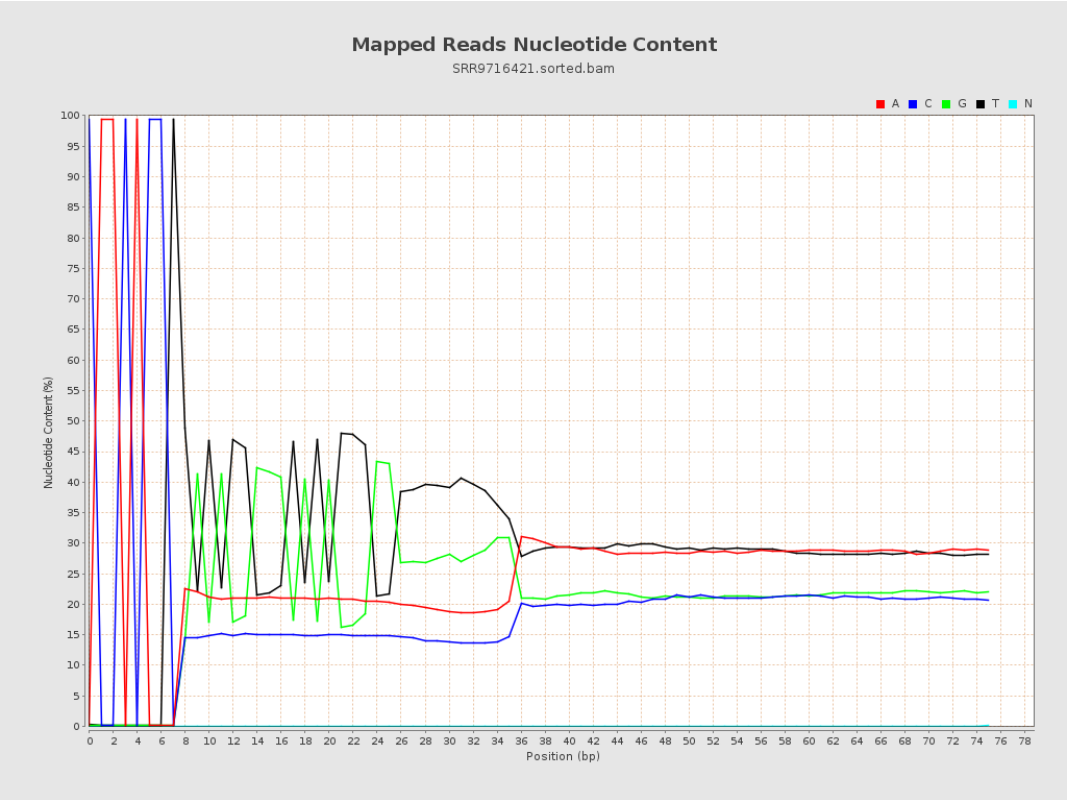
6. Results : Genome Fraction Coverage



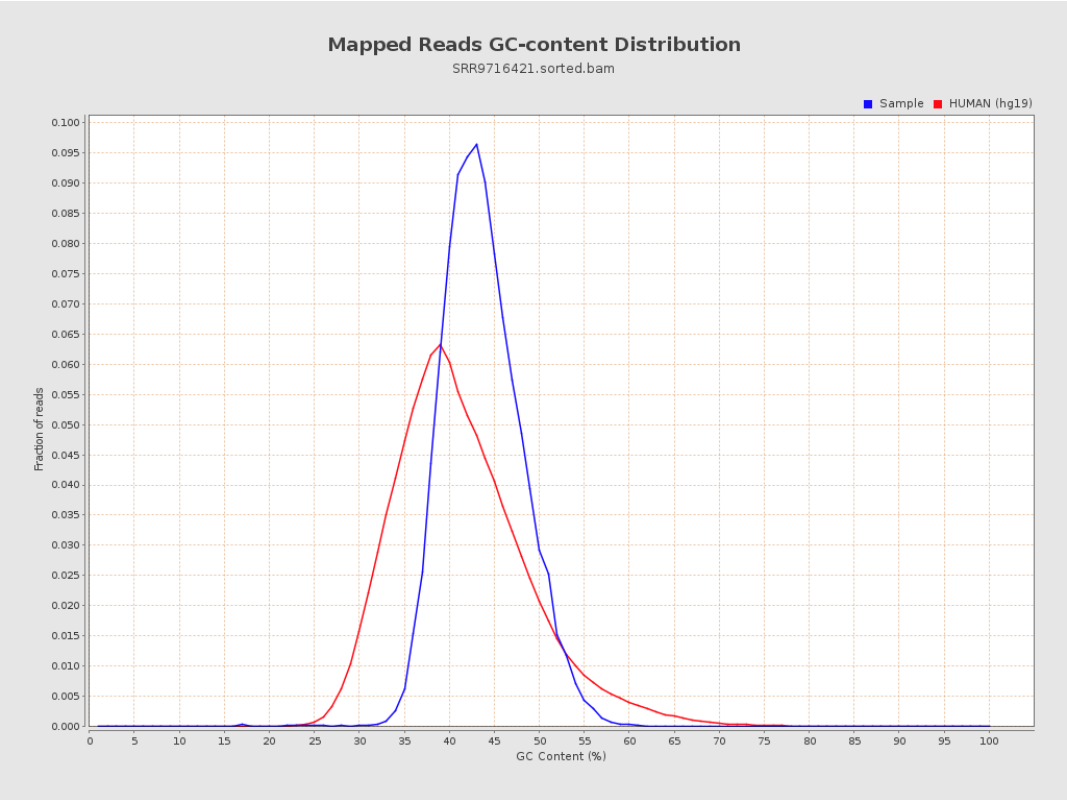
7. Results : Duplication Rate Histogram



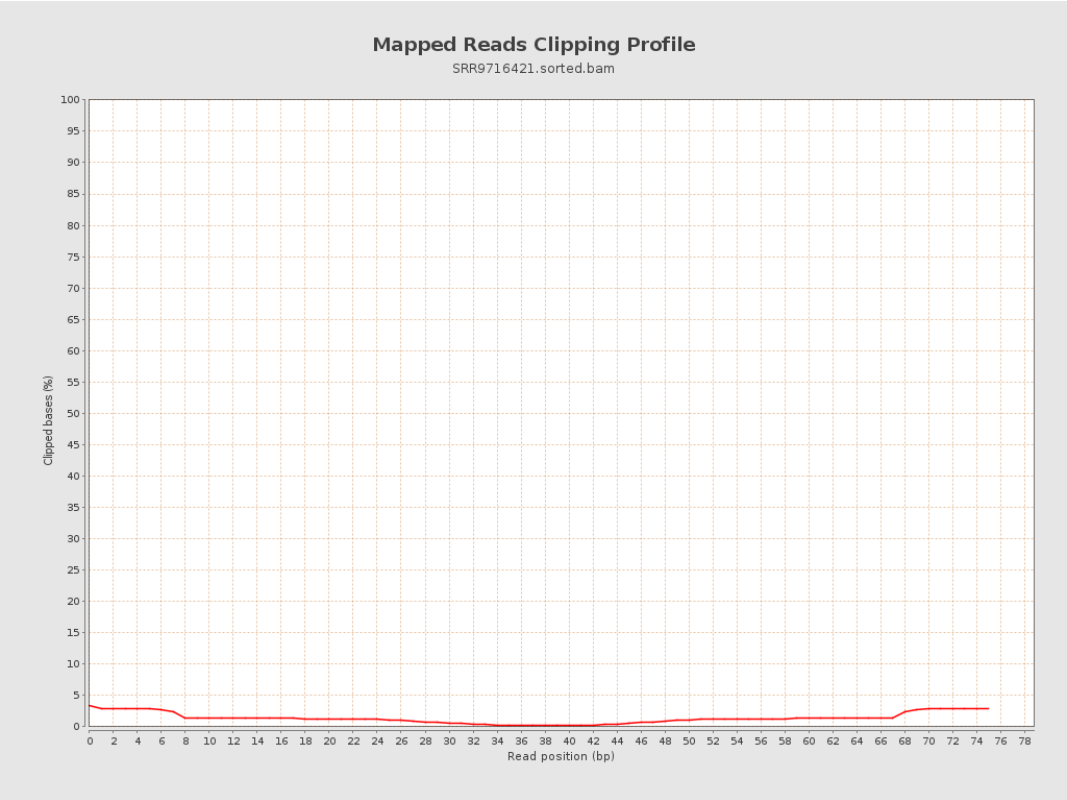
8. Results : Mapped Reads Nucleotide Content



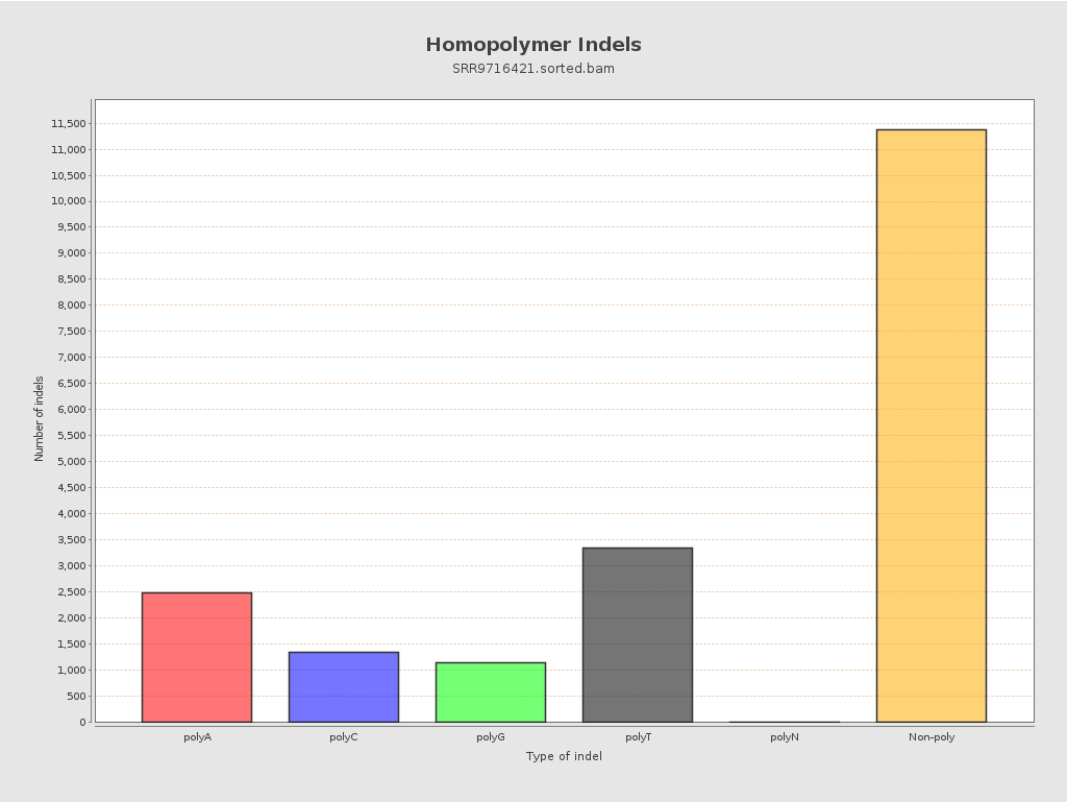
9. Results : Mapped Reads GC-content Distribution



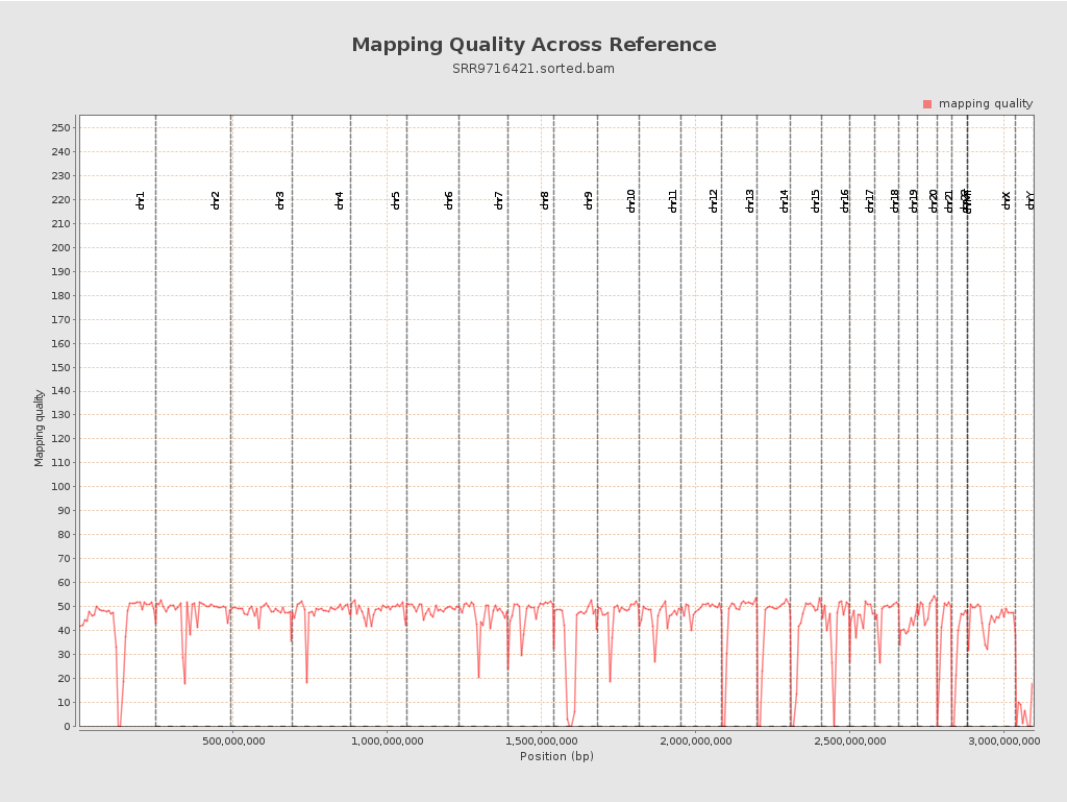
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram