Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:40:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716575.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_SRR9716575 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716575.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:40:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716575.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,414,920
Mapped reads	1,294,848 / 91.51%
Unmapped reads	120,072 / 8.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,731 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	49,115 / 3.47%
Duplication rate	2.82%
Clipped reads	1,301,969 / 92.02%

2.2. ACGT Content

Number/percentage of A's	19,043,010 / 25.32%
Number/percentage of C's	15,767,819 / 20.96%
Number/percentage of T's	22,427,812 / 29.82%
Number/percentage of G's	17,974,584 / 23.9%
Number/percentage of N's	876 / 0%
GC Percentage	44.86%

2.3. Coverage

Mean	0.0243

Standard Deviation	0.2437

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Mismatches and indels

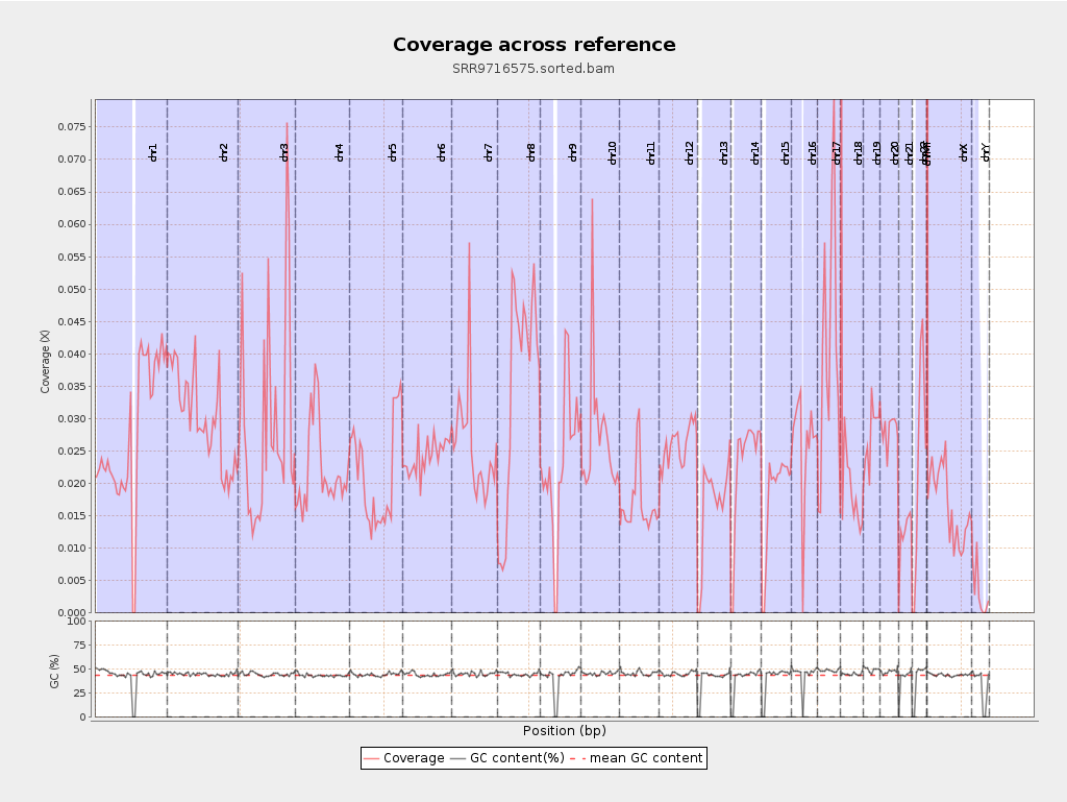
General error rate	0.5%
Mismatches	366,337
Insertions	4,731
Mapped reads with at least one insertion	0.36%
Deletions	13,125
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.52%

2.6. Chromosome stats

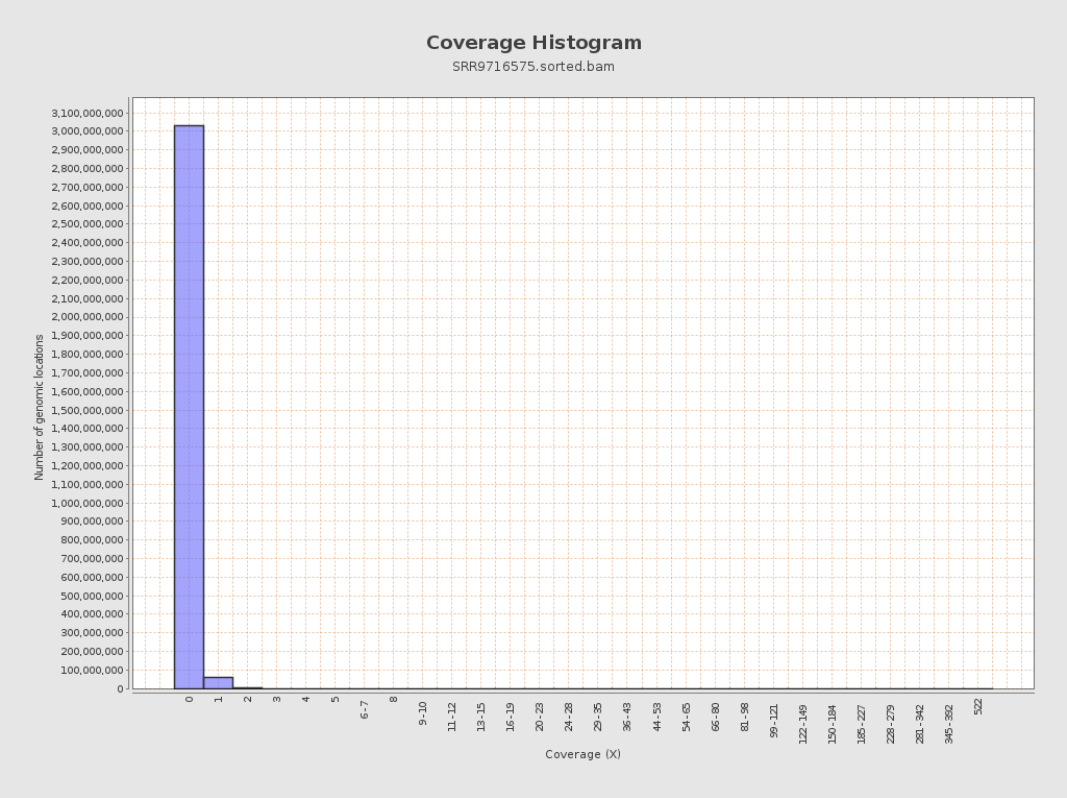
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6878288	0.0276	0.3469
chr2	243199373	7336921	0.0302	0.2955
chr3	198022430	5618666	0.0284	0.1925
chr4	191154276	4188980	0.0219	0.1833
chr5	180915260	3802433	0.021	0.1578
chr6	171115067	4138793	0.0242	0.1799
chr7	159138663	4089971	0.0257	0.4826

chr8	146364022	5116596	0.035	0.2495
chr9	141213431	3216499	0.0228	0.1836
chr10	135534747	3637366	0.0268	0.3268
chr11	135006516	2292537	0.017	0.1706
chr12	133851895	3460072	0.0259	0.1885
chr13	115169878	1894720	0.0165	0.1381
chr14	107349540	2425786	0.0226	0.1673
chr15	102531392	1806655	0.0176	0.1449
chr16	90354753	2323405	0.0257	0.1811
chr17	81195210	3273707	0.0403	0.2272
chr18	78077248	1711756	0.0219	0.2484
chr19	59128983	1623836	0.0275	0.3179
chr20	63025520	1780697	0.0283	0.1871
chr21	48129895	583040	0.0121	0.1341
chr22	51304566	1206109	0.0235	0.1673
chrMT	16571	75581	4.561	3.4105
chrX	155270560	2569569	0.0165	0.1555
chrY	59373566	182730	0.0031	0.0958

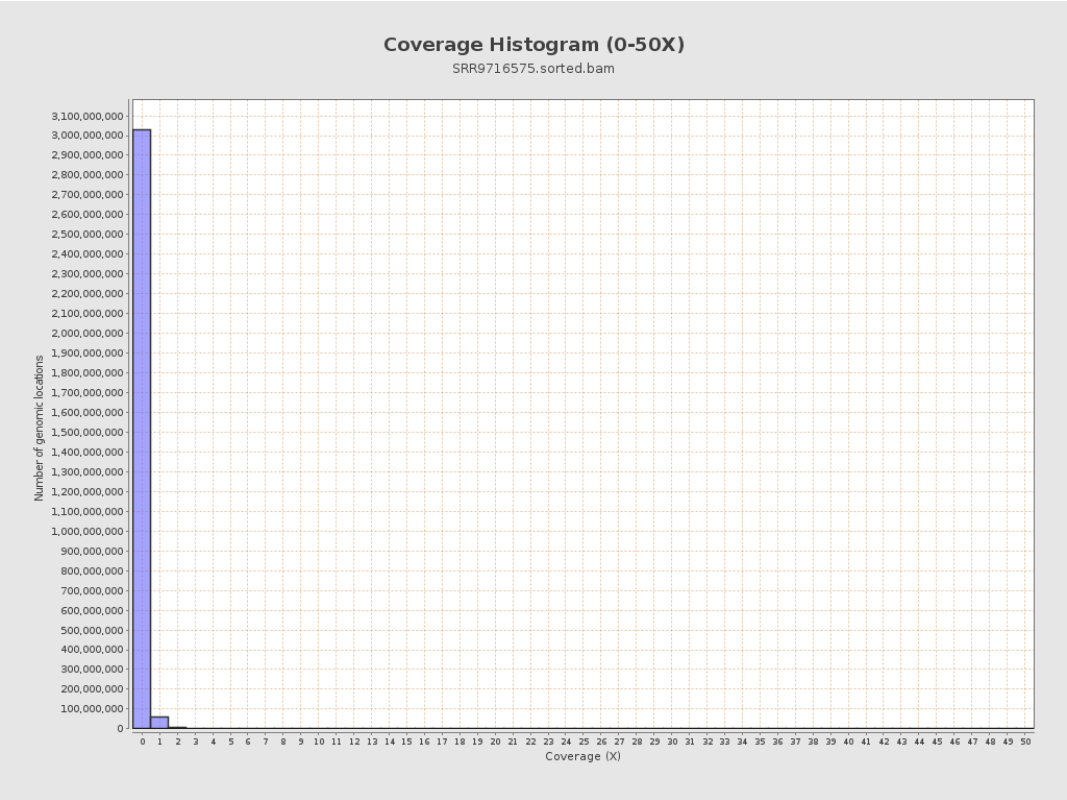
3. Results : Coverage across reference



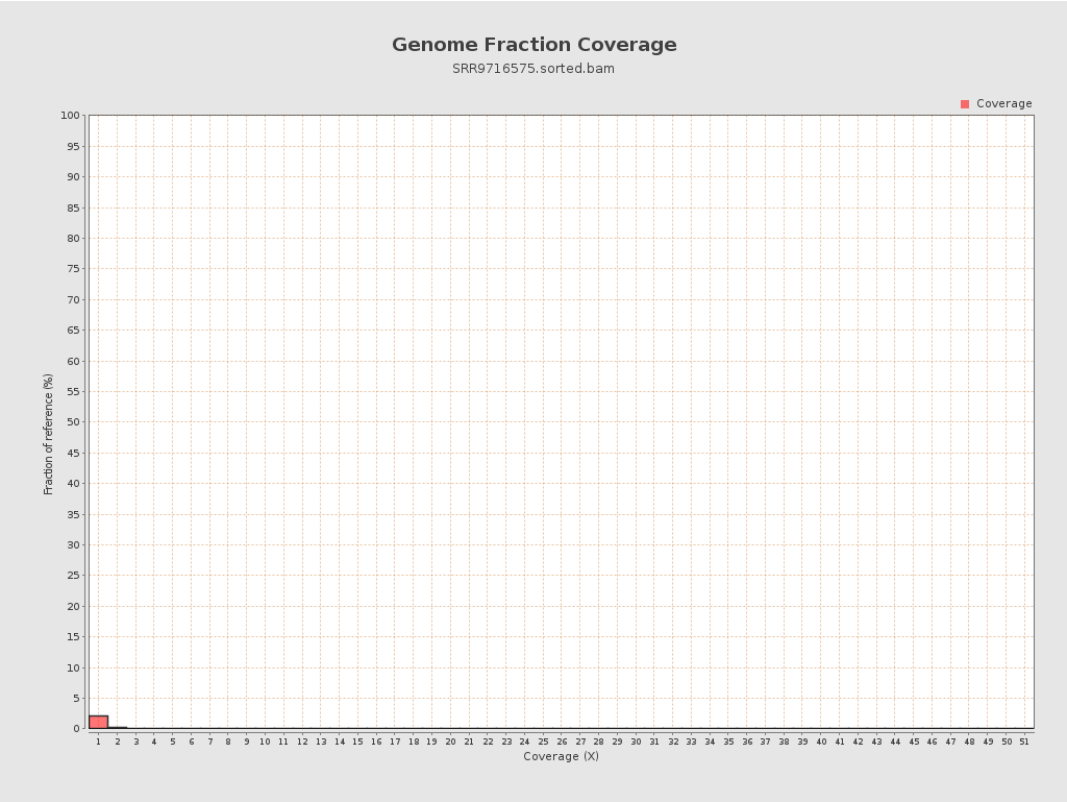
4. Results : Coverage Histogram



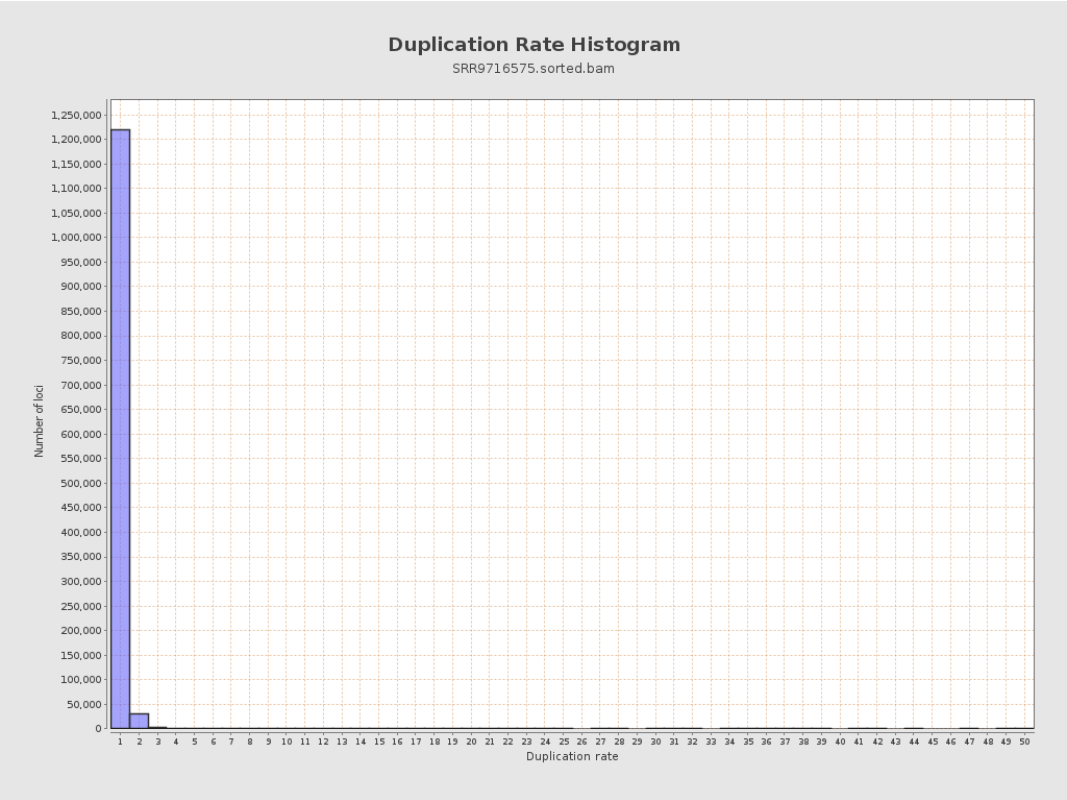
5. Results : Coverage Histogram (0-50X)



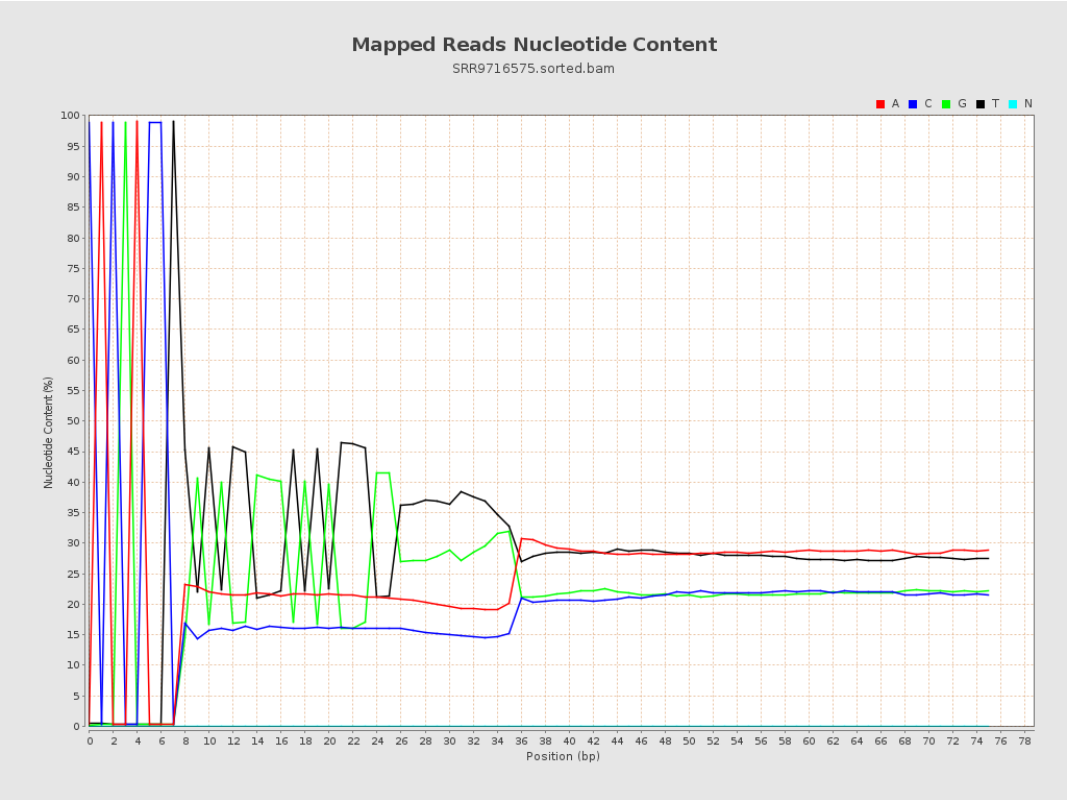
6. Results : Genome Fraction Coverage



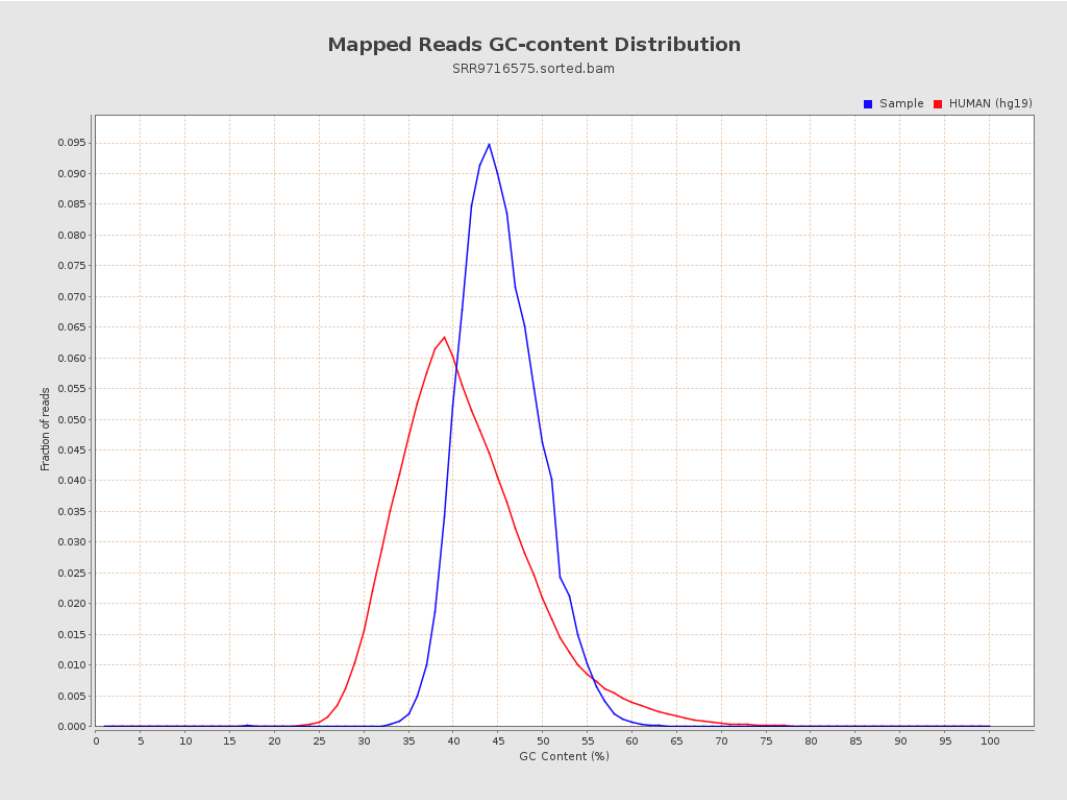
7. Results : Duplication Rate Histogram



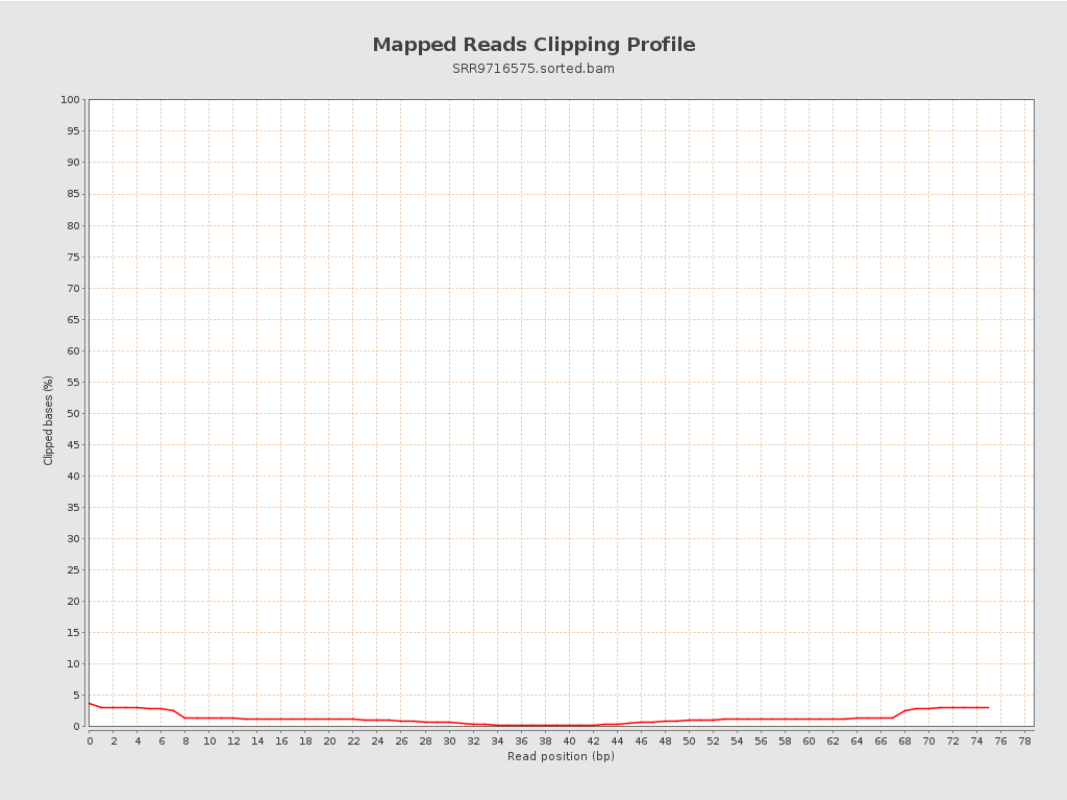
8. Results : Mapped Reads Nucleotide Content



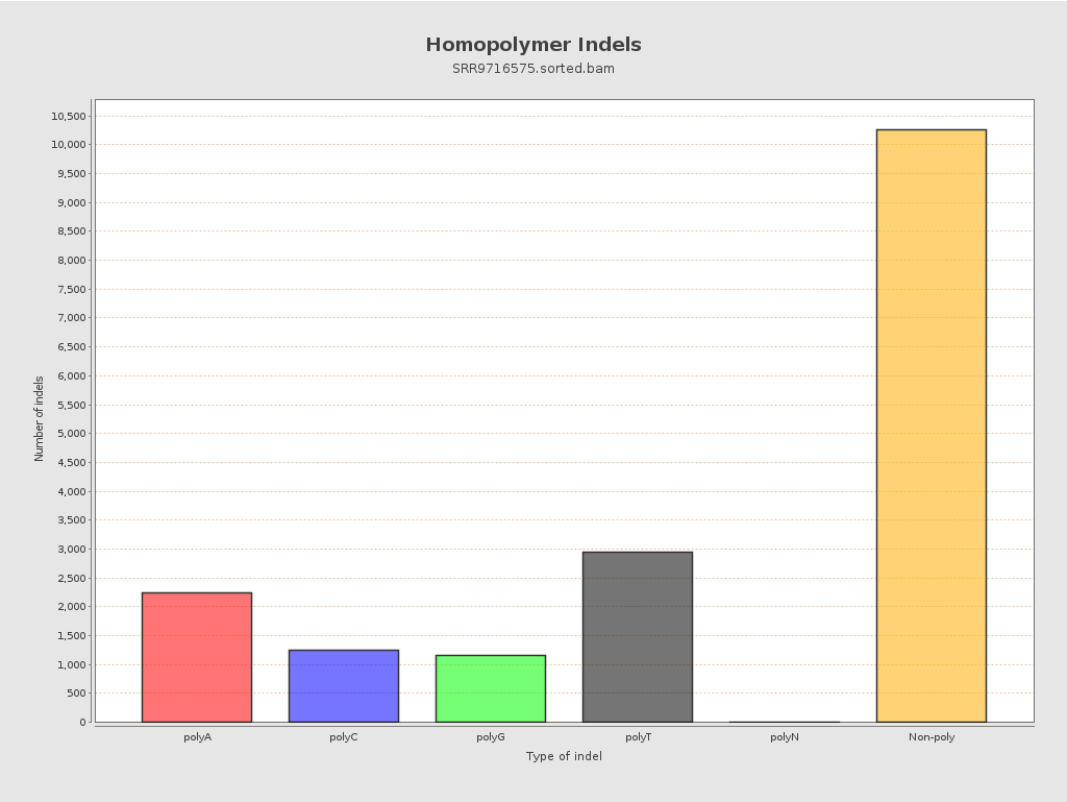
9. Results : Mapped Reads GC-content Distribution



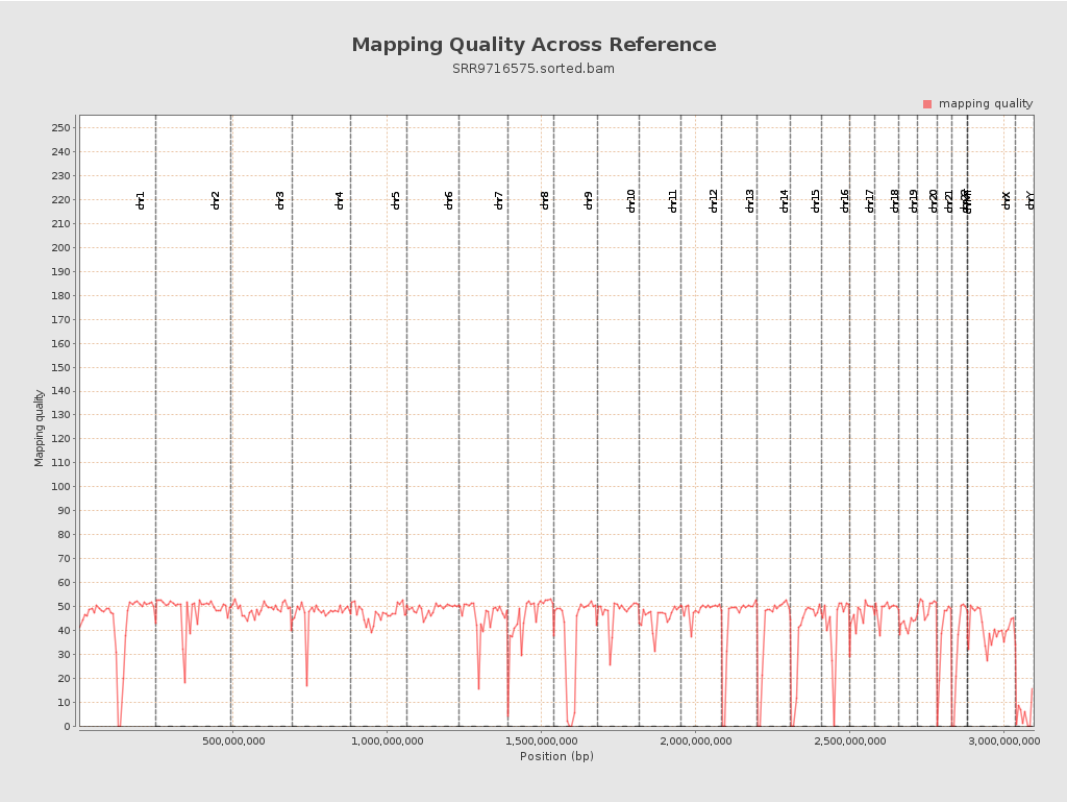
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram