Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:35:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716944.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_SRR9716944 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716944.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:35:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716944.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,488,877
Mapped reads	1,322,065 / 88.8%
Unmapped reads	166,812 / 11.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,217 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	39,246 / 2.64%
Duplication rate	2.2%
Clipped reads	1,325,423 / 89.02%

2.2. ACGT Content

Number/percentage of A's	19,474,370 / 25.18%
Number/percentage of C's	14,317,061 / 18.51%
Number/percentage of T's	23,709,568 / 30.65%
Number/percentage of G's	19,853,828 / 25.67%
Number/percentage of N's	1,028 / 0%
GC Percentage	44.17%

2.3. Coverage

Mean	0.025

Standard Deviation	0.2381

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

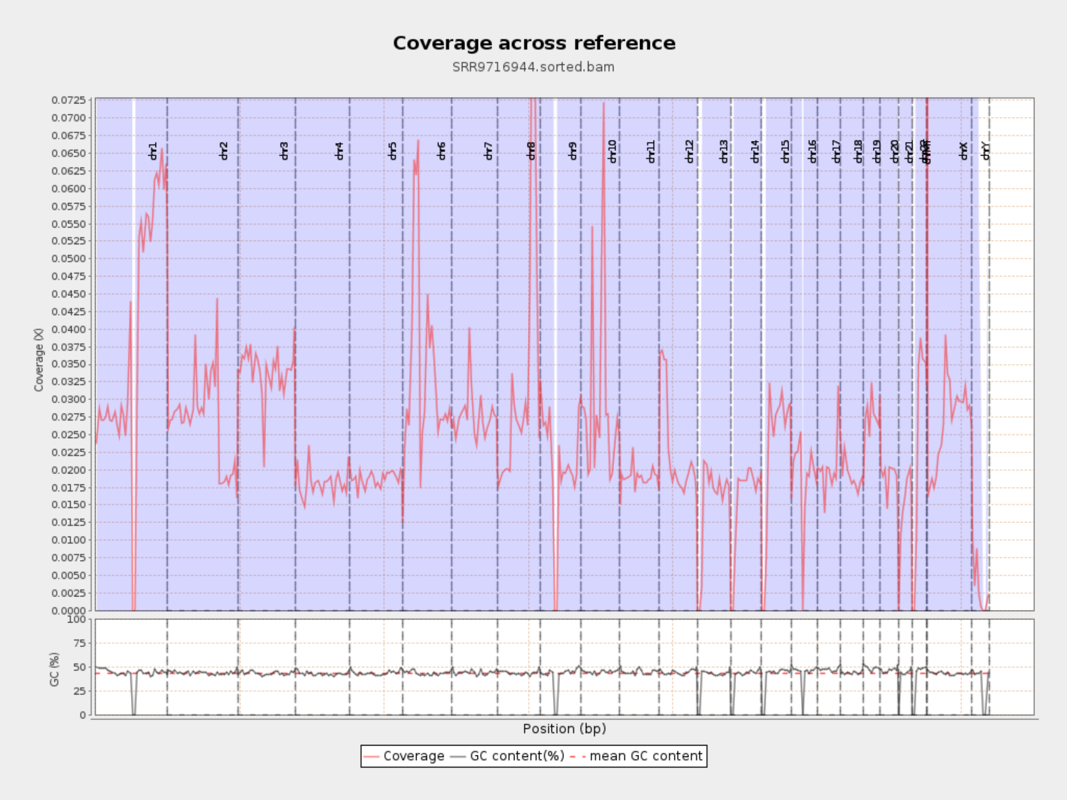
General error rate	0.5%
Mismatches	374,903
Insertions	5,114
Mapped reads with at least one insertion	0.39%
Deletions	13,382
Mapped reads with at least one deletion	1.01%
Homopolymer indels	41.8%

2.6. Chromosome stats

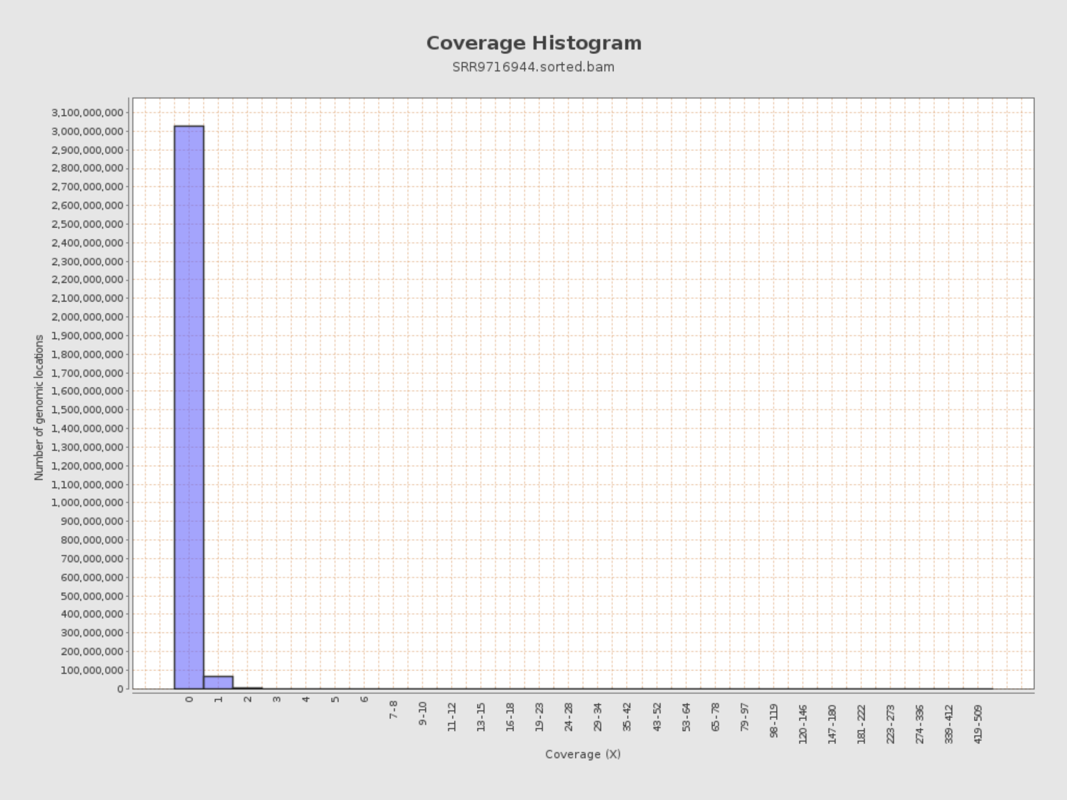
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9632875	0.0386	0.4383
chr2	243199373	6589861	0.0271	0.2782
chr3	198022430	6732516	0.034	0.2033
chr4	191154276	3471896	0.0182	0.151
chr5	180915260	3393979	0.0188	0.1486
chr6	171115067	5852088	0.0342	0.2911
chr7	159138663	4436988	0.0279	0.2856

chr8	146364022	4883970	0.0334	0.2167
chr9	141213431	2870424	0.0203	0.1885
chr10	135534747	4116921	0.0304	0.2719
chr11	135006516	2574846	0.0191	0.1835
chr12	133851895	3072835	0.023	0.1656
chr13	115169878	1746092	0.0152	0.1319
chr14	107349540	1675506	0.0156	0.1456
chr15	102531392	2353201	0.023	0.1636
chr16	90354753	1682173	0.0186	0.1667
chr17	81195210	1667769	0.0205	0.159
chr18	78077248	1492592	0.0191	0.3169
chr19	59128983	1626472	0.0275	0.2966
chr20	63025520	1197269	0.019	0.1478
chr21	48129895	706768	0.0147	0.1404
chr22	51304566	1261784	0.0246	0.1691
chrMT	16571	4413	0.2663	0.5103
chrX	155270560	4147215	0.0267	0.1905
chrY	59373566	186313	0.0031	0.0749

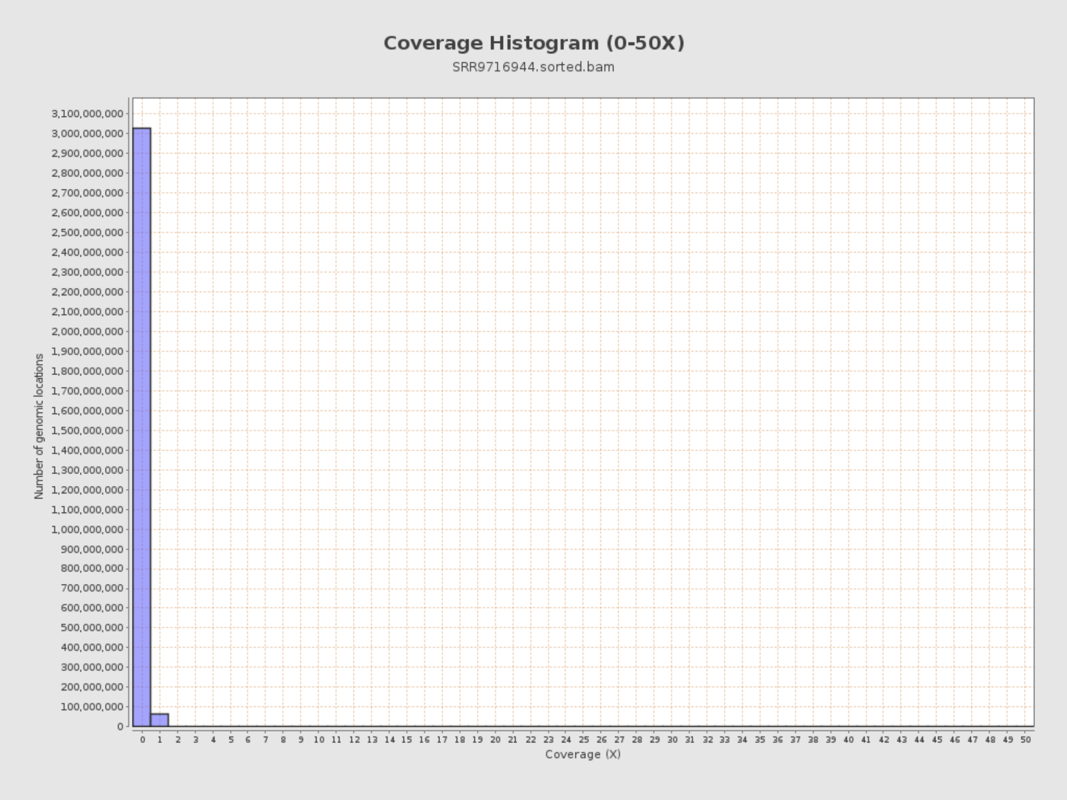
3. Results : Coverage across reference



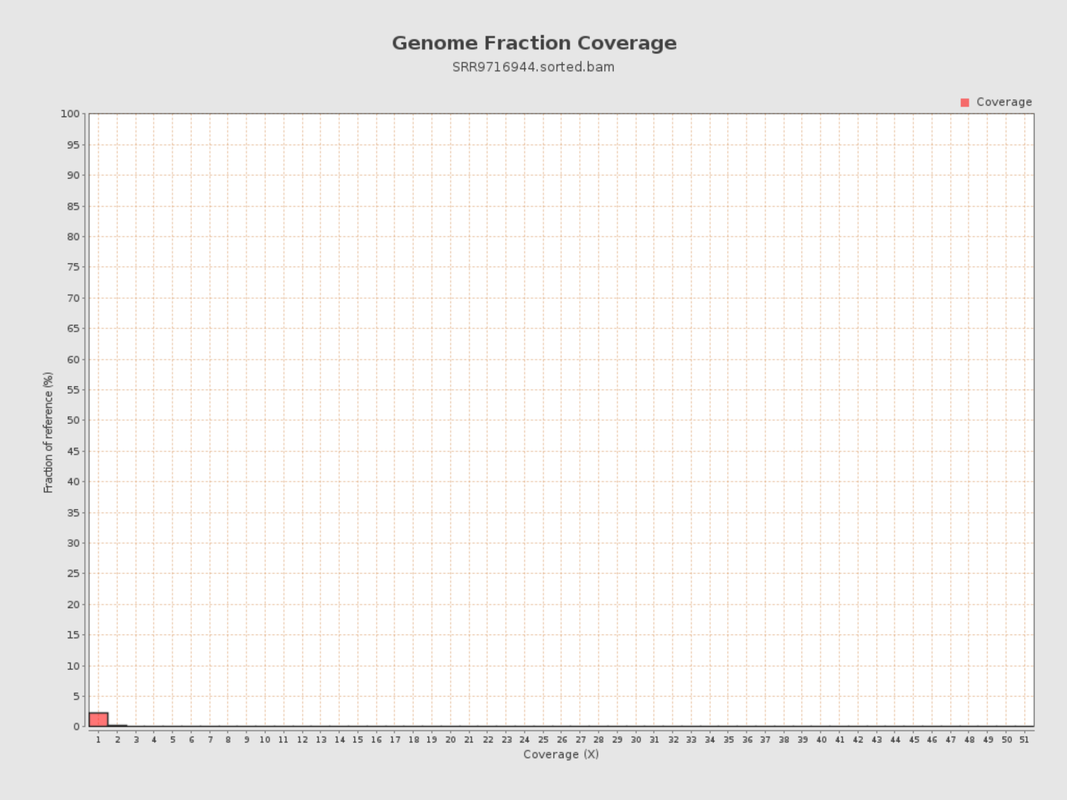
4. Results : Coverage Histogram



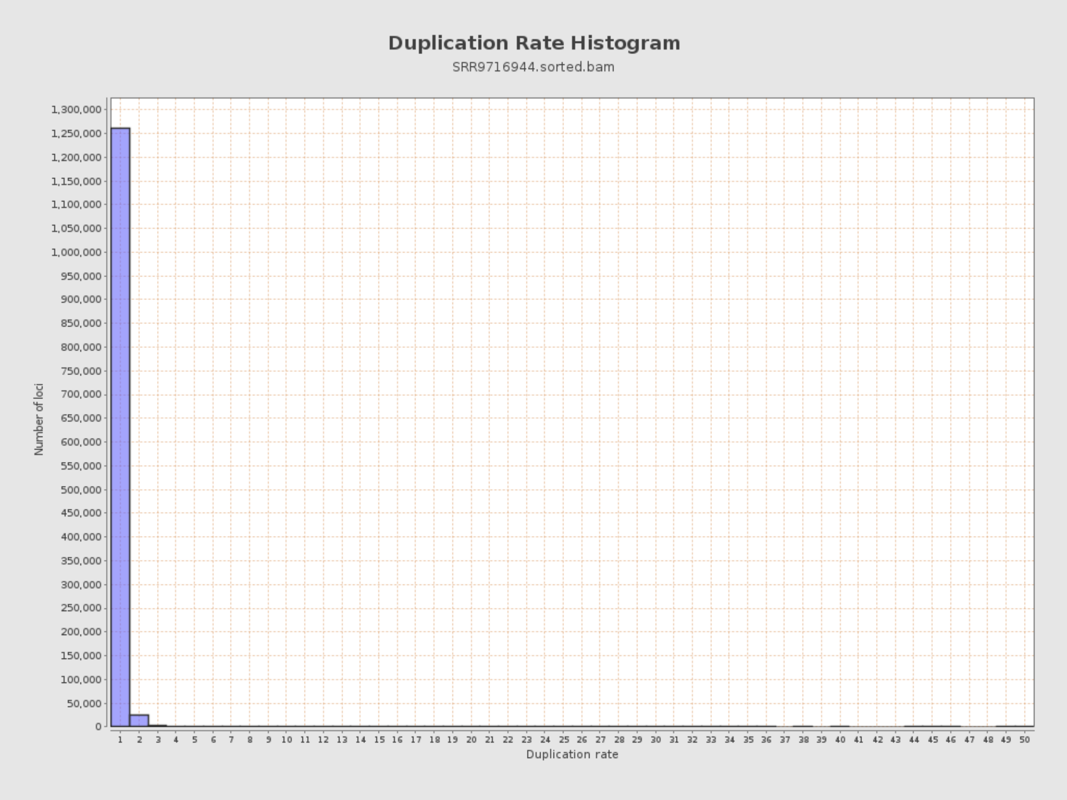
5. Results : Coverage Histogram (0-50X)



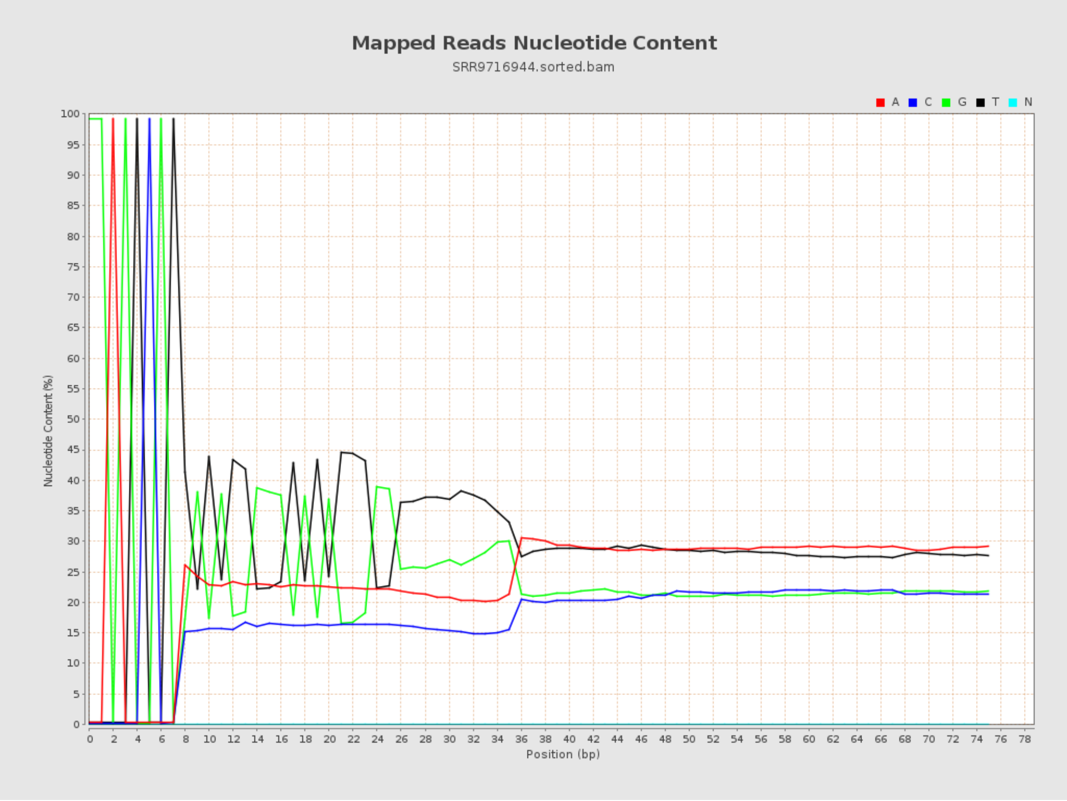
6. Results : Genome Fraction Coverage



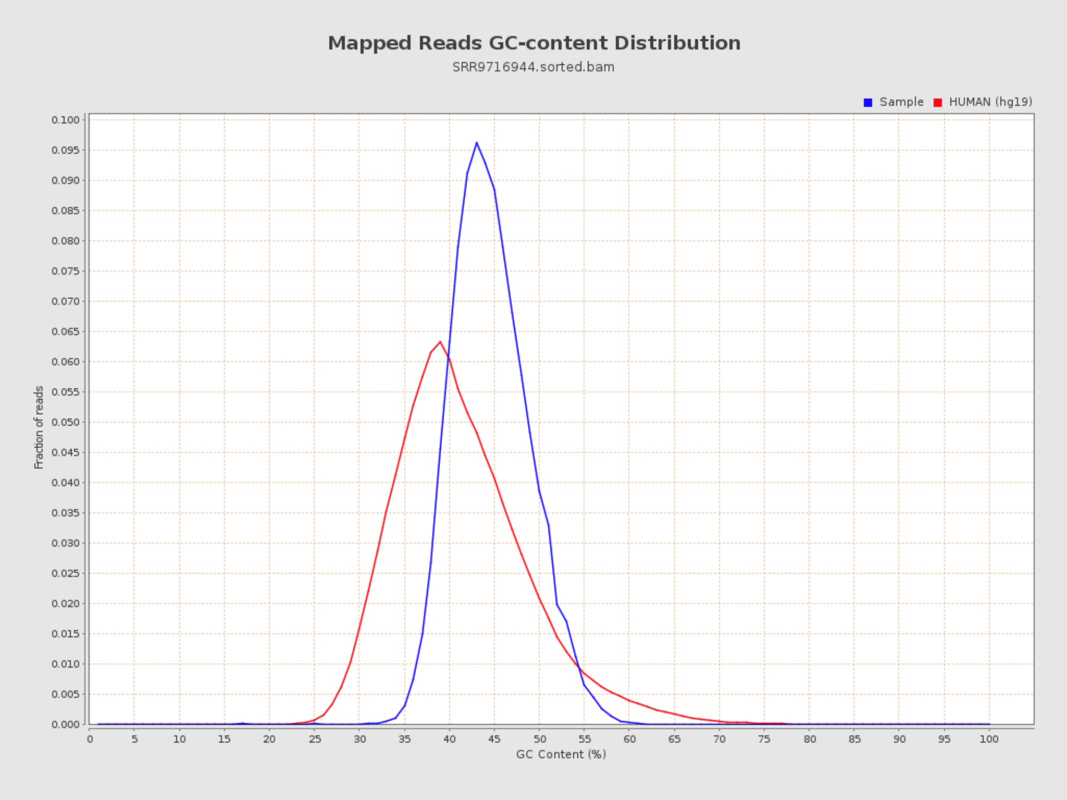
7. Results : Duplication Rate Histogram



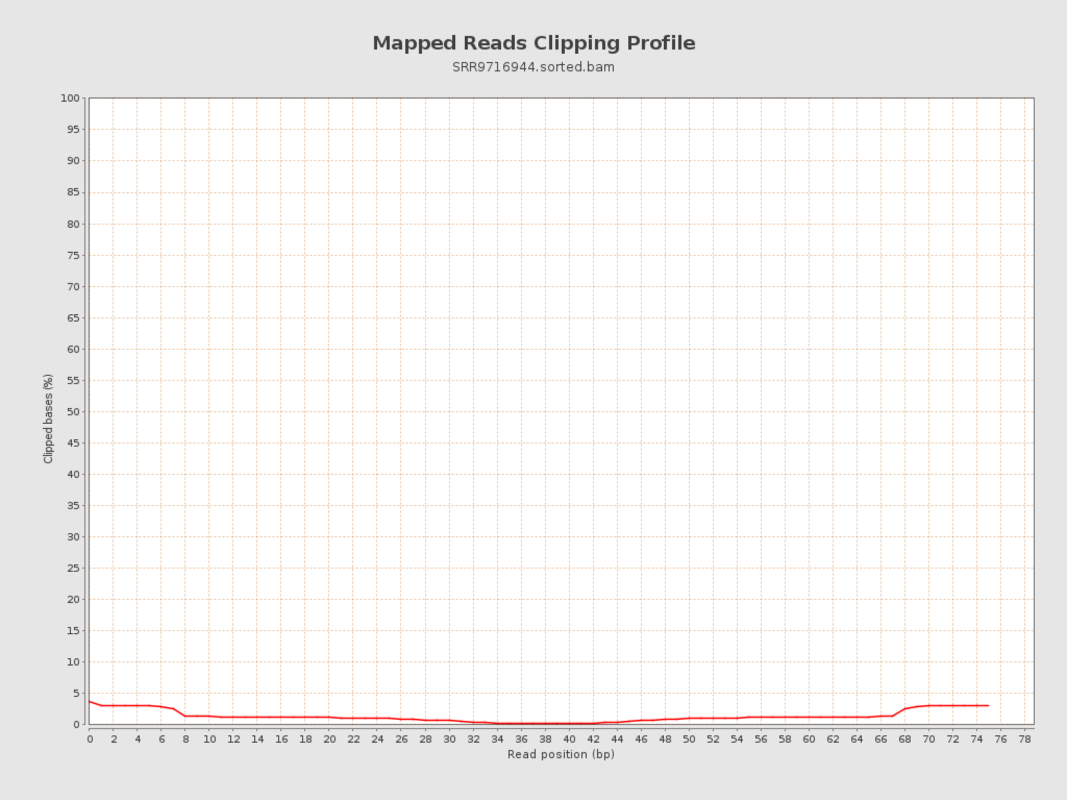
8. Results : Mapped Reads Nucleotide Content



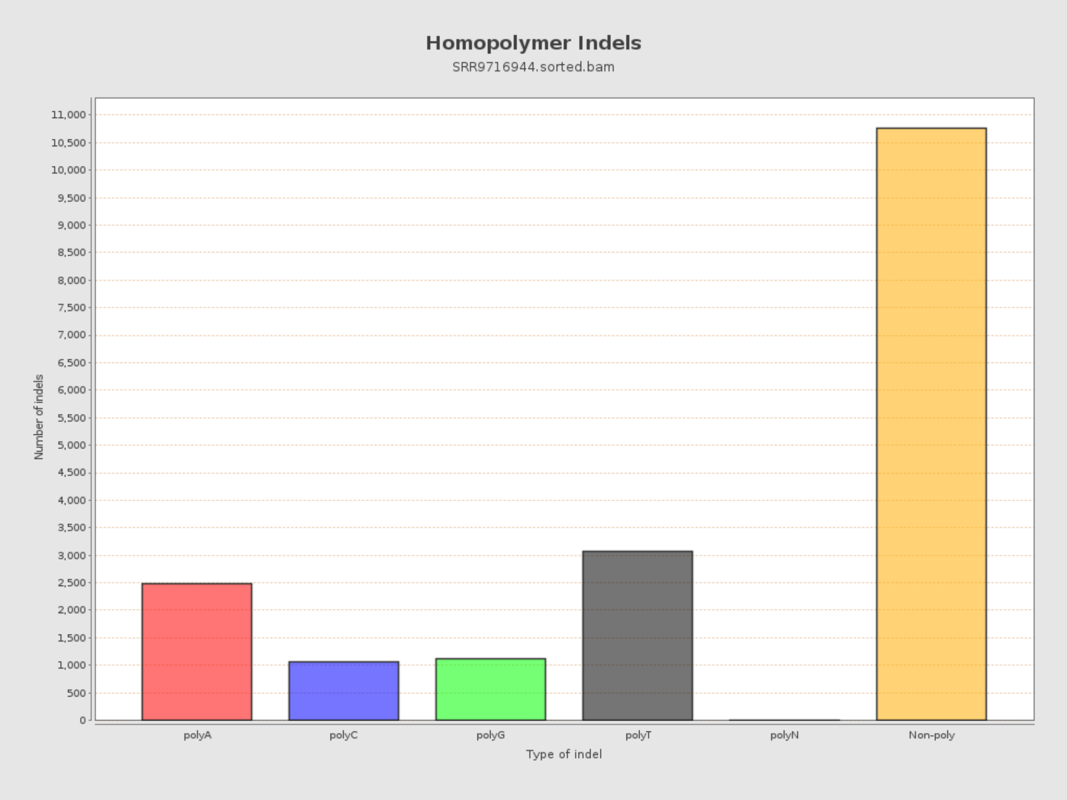
9. Results : Mapped Reads GC-content Distribution



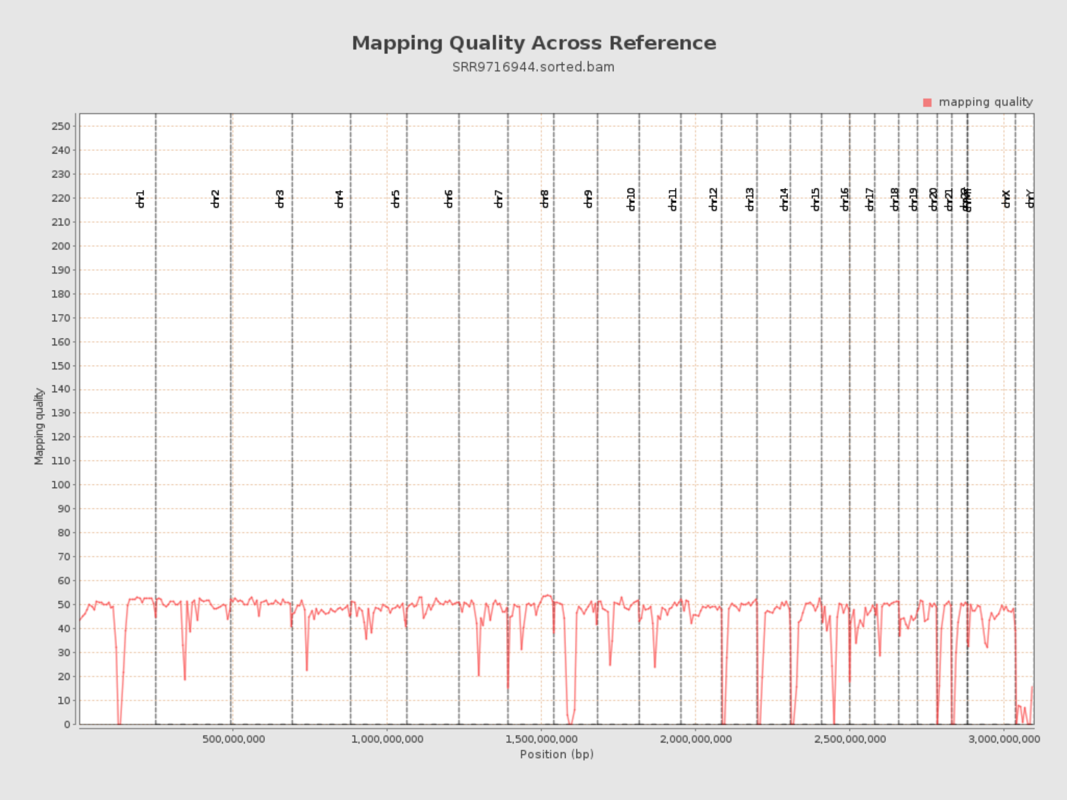
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram