Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:06:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716102.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_SRR9716102 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716102.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:06:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716102.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,672,820
Mapped reads	1,518,901 / 90.8%
Unmapped reads	153,919 / 9.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,325 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	61,743 / 3.69%
Duplication rate	3.13%
Clipped reads	1,522,174 / 90.99%

2.2. ACGT Content

Number/percentage of A's	21,437,000 / 24.54%
Number/percentage of C's	17,640,125 / 20.2%
Number/percentage of T's	28,214,602 / 32.3%
Number/percentage of G's	20,054,682 / 22.96%
Number/percentage of N's	2,343 / 0%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.2596

2.4. Mapping Quality

Mean Mapping Quality	44.41

2.5. Mismatches and indels

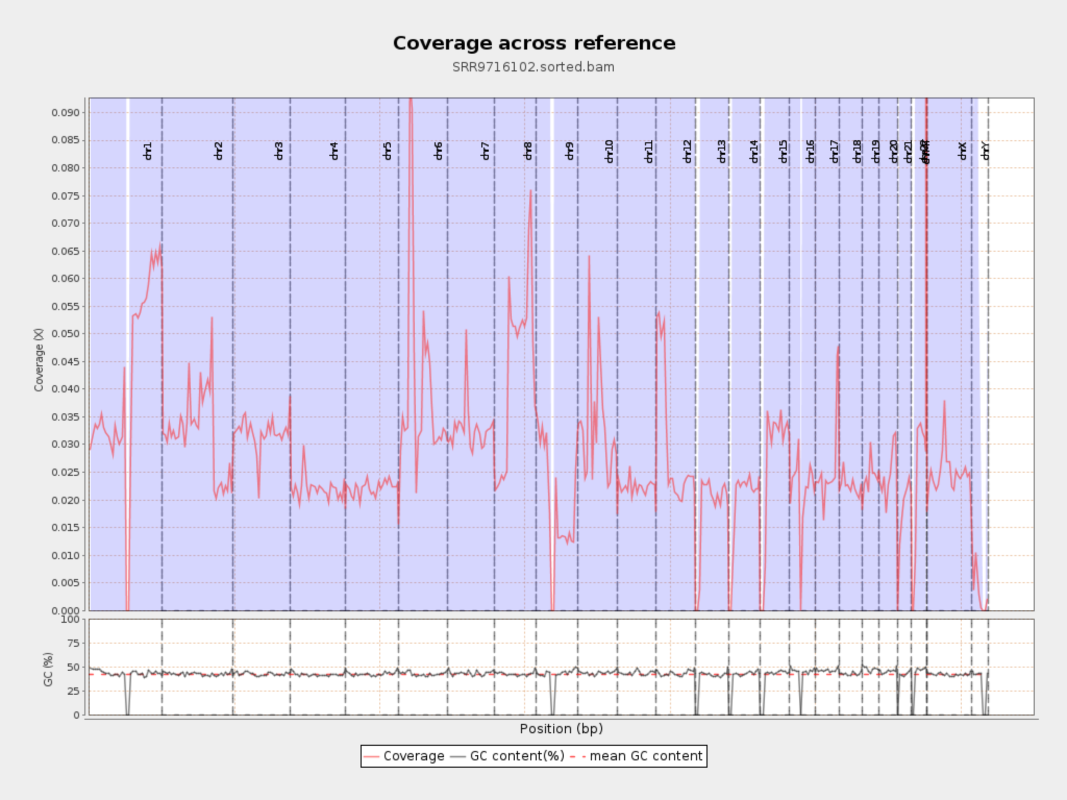
General error rate	0.5%
Mismatches	430,363
Insertions	5,639
Mapped reads with at least one insertion	0.37%
Deletions	14,668
Mapped reads with at least one deletion	0.96%
Homopolymer indels	44.43%

2.6. Chromosome stats

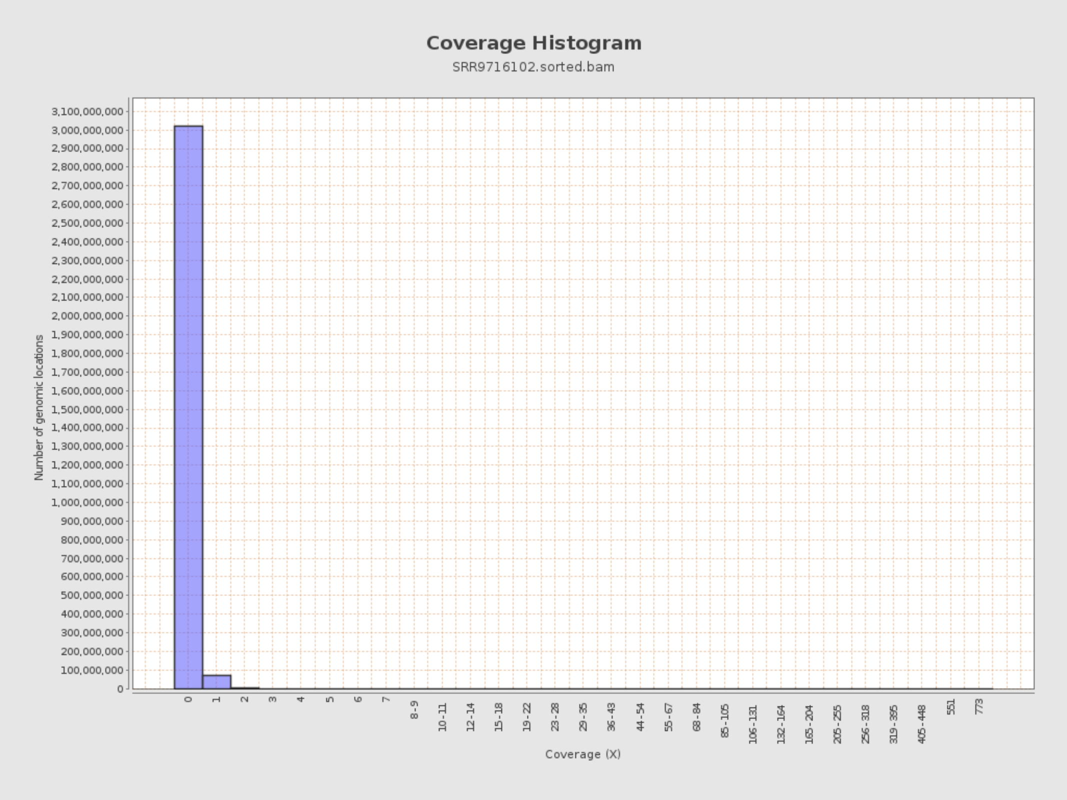
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10246218	0.0411	0.3948
chr2	243199373	7792825	0.032	0.3658
chr3	198022430	6312697	0.0319	0.2009
chr4	191154276	4202385	0.022	0.1716
chr5	180915260	4012088	0.0222	0.1662
chr6	171115067	6891180	0.0403	0.2664
chr7	159138663	5252038	0.033	0.3607

chr8	146364022	6504662	0.0444	0.2593
chr9	141213431	2621553	0.0186	0.2051
chr10	135534747	4588732	0.0339	0.3218
chr11	135006516	3017843	0.0224	0.2083
chr12	133851895	4016789	0.03	0.1958
chr13	115169878	2071100	0.018	0.149
chr14	107349540	2024189	0.0189	0.1666
chr15	102531392	2740509	0.0267	0.1835
chr16	90354753	1954182	0.0216	0.1852
chr17	81195210	2130268	0.0262	0.1861
chr18	78077248	1764197	0.0226	0.3674
chr19	59128983	1435968	0.0243	0.3076
chr20	63025520	1565410	0.0248	0.1746
chr21	48129895	839726	0.0174	0.1596
chr22	51304566	1136388	0.0221	0.1644
chrMT	16571	179774	10.8487	5.9777
chrX	155270560	3867366	0.0249	0.1998
chrY	59373566	203162	0.0034	0.0846

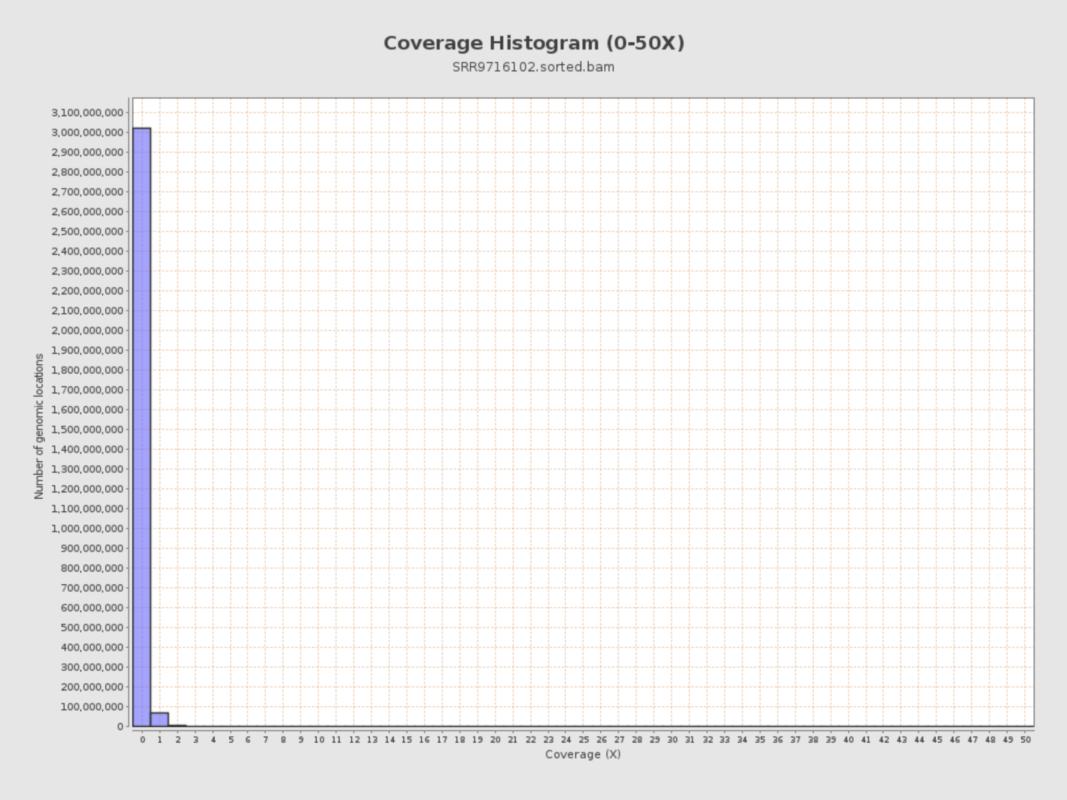
3. Results : Coverage across reference



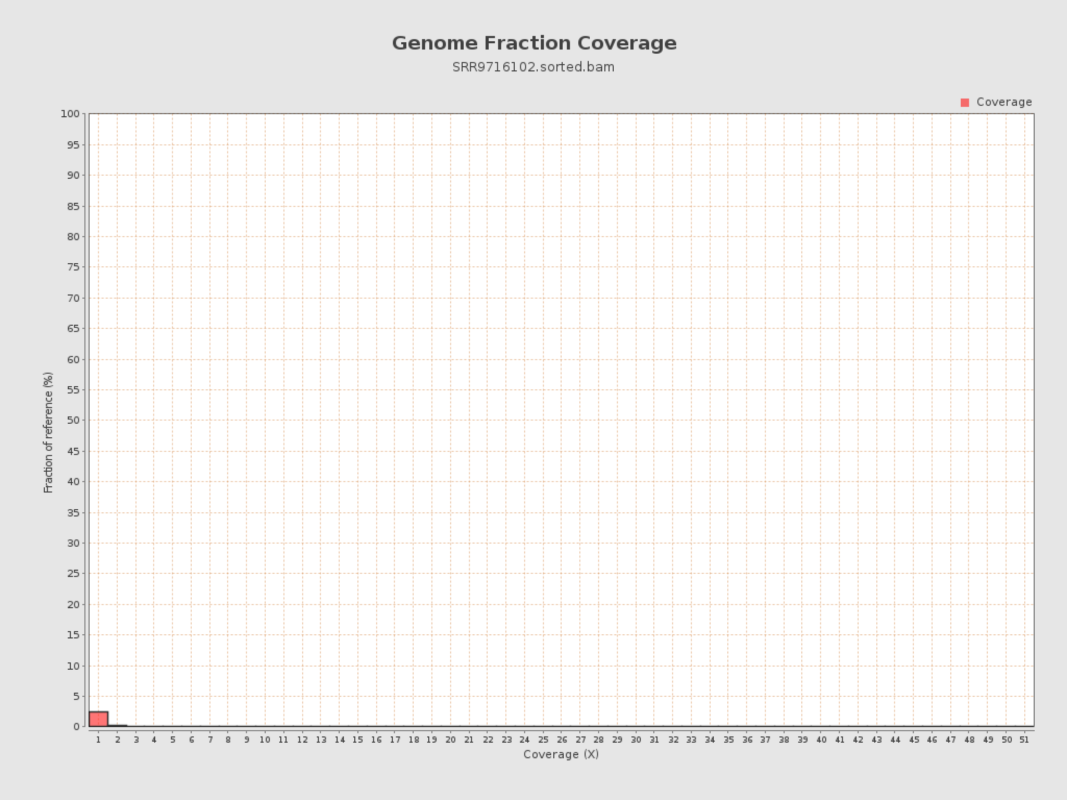
4. Results : Coverage Histogram



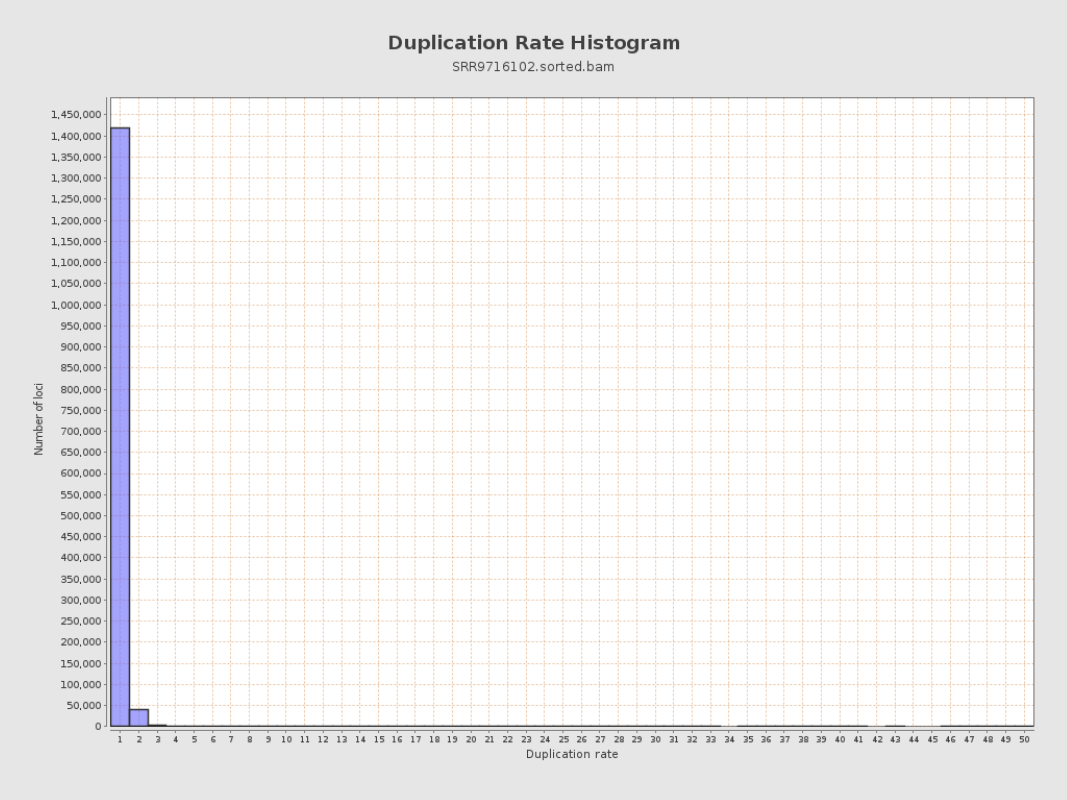
5. Results : Coverage Histogram (0-50X)



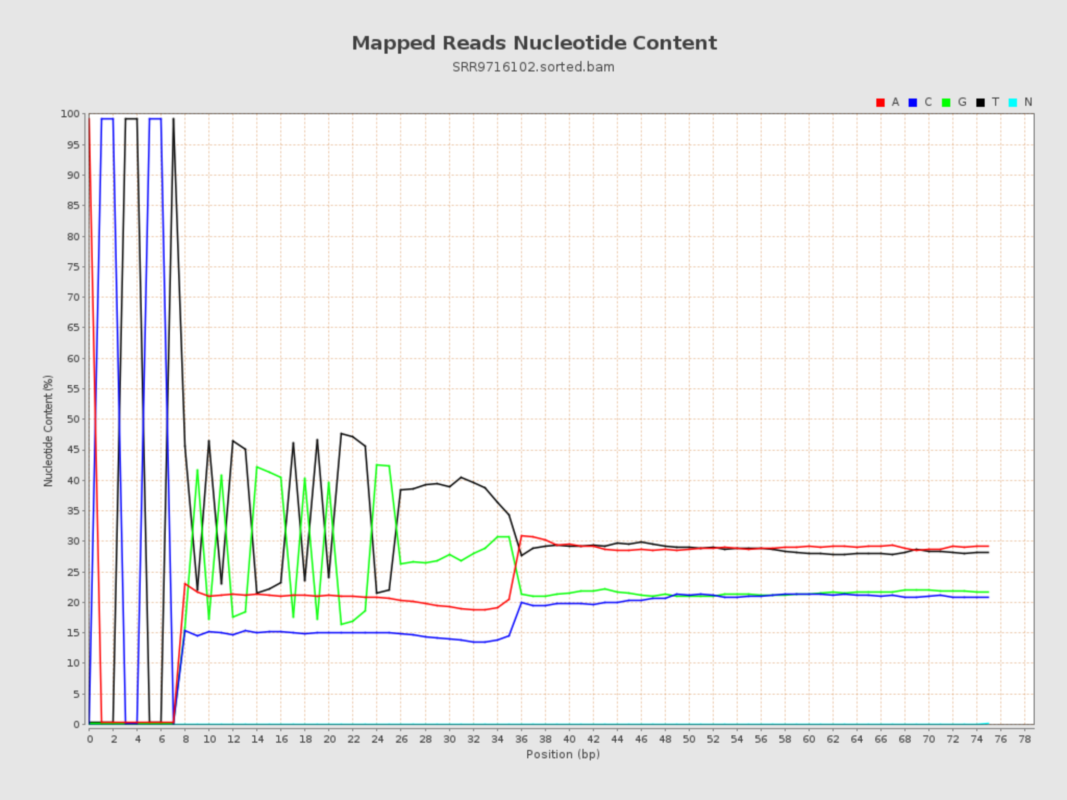
6. Results : Genome Fraction Coverage



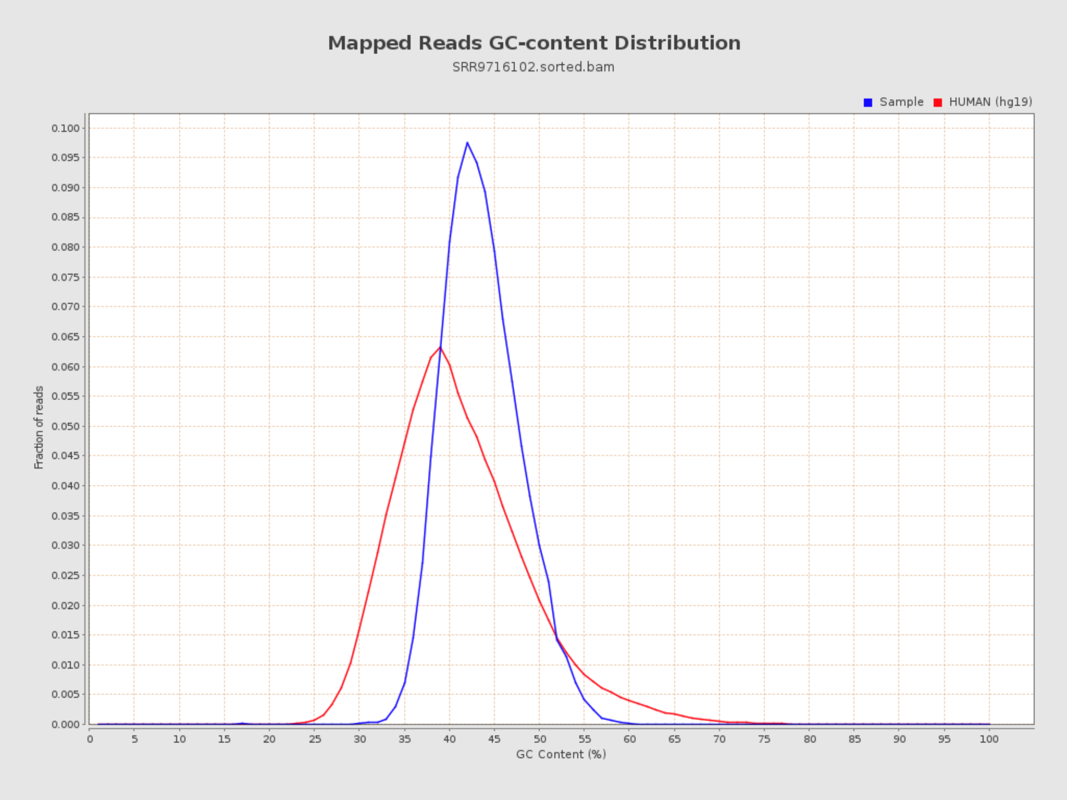
7. Results : Duplication Rate Histogram



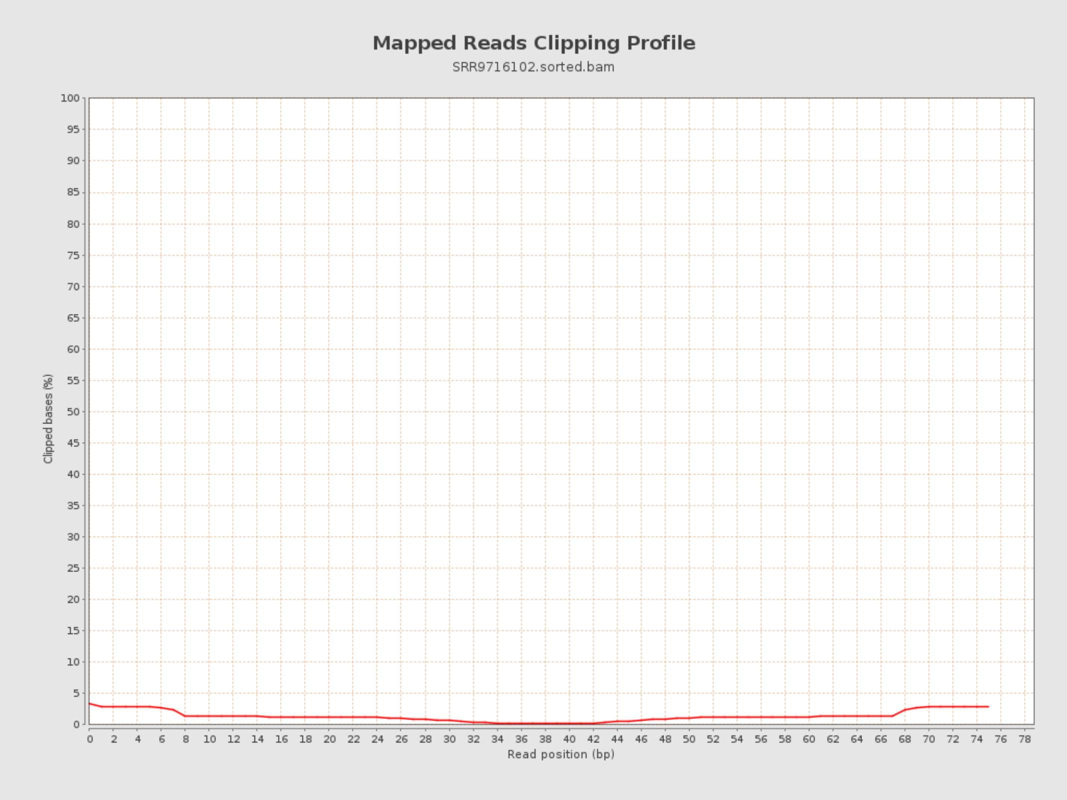
8. Results : Mapped Reads Nucleotide Content



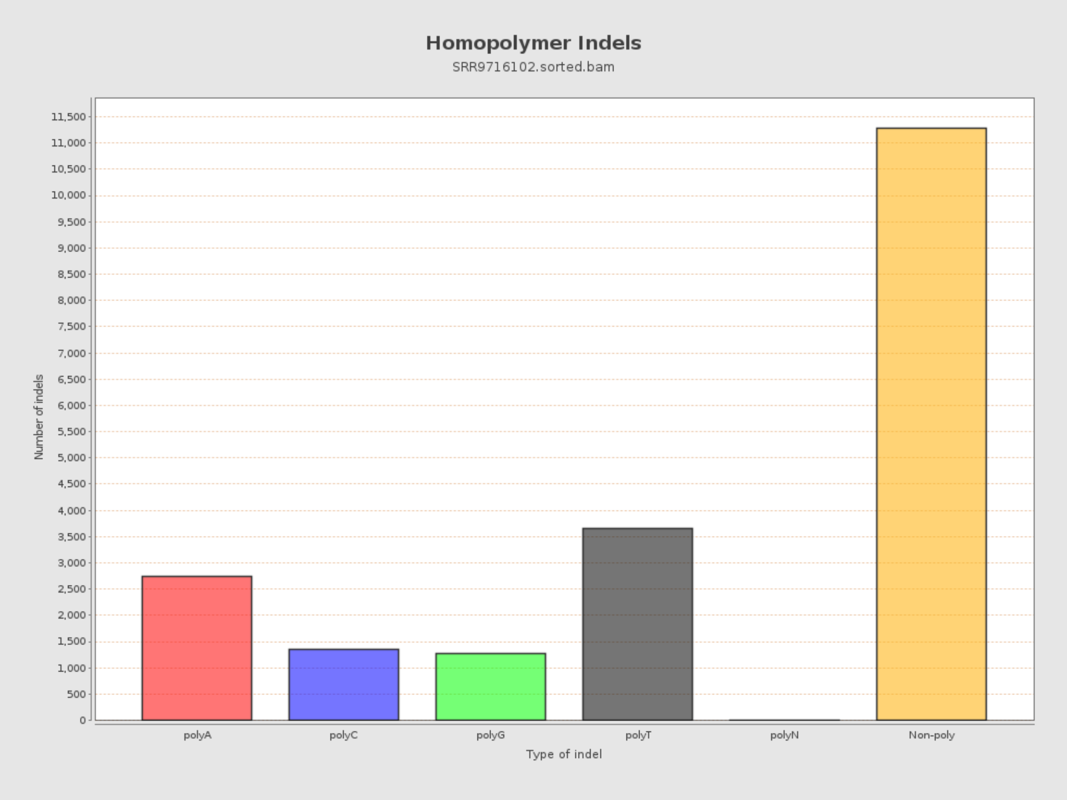
9. Results : Mapped Reads GC-content Distribution



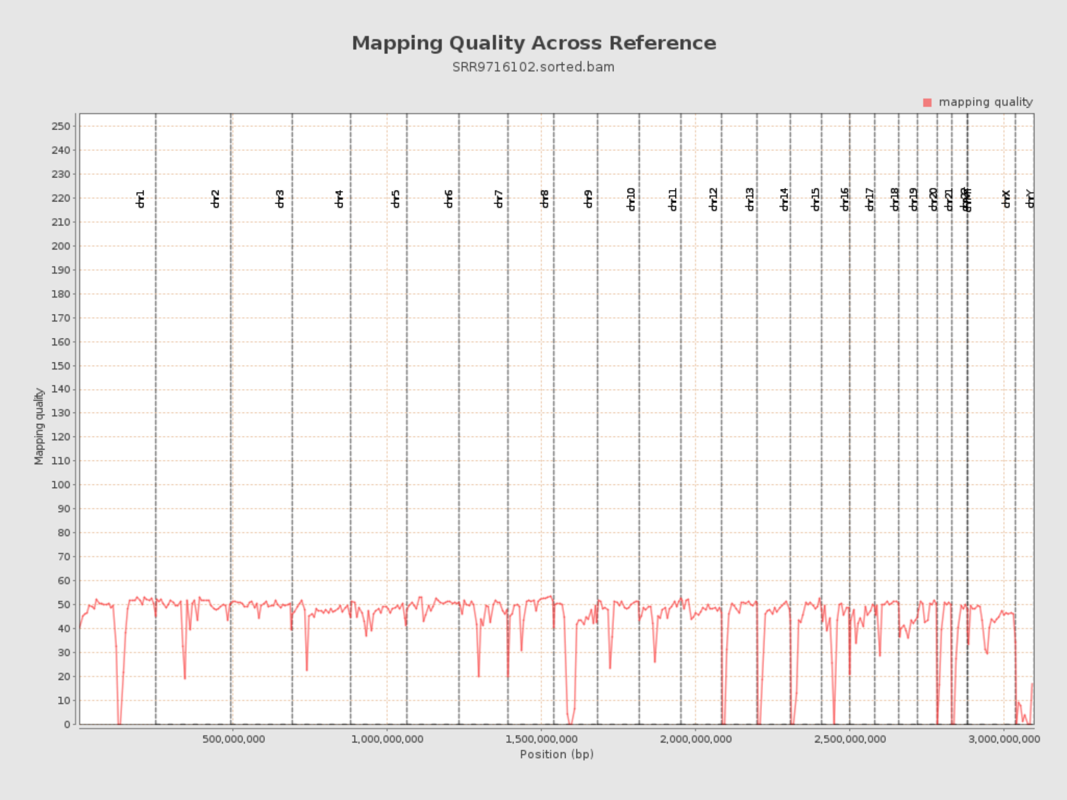
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram