Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:40:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716309.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_SRR9716309 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716309.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:40:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716309.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,134,741
Mapped reads	1,047,040 / 92.27%
Unmapped reads	87,701 / 7.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,775 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	39,321 / 3.47%
Duplication rate	2.77%
Clipped reads	1,047,372 / 92.3%

2.2. ACGT Content

Number/percentage of A's	15,423,918 / 25.28%
Number/percentage of C's	11,943,248 / 19.57%
Number/percentage of T's	19,172,810 / 31.42%
Number/percentage of G's	14,472,512 / 23.72%
Number/percentage of N's	1,300 / 0%
GC Percentage	43.29%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.2071

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

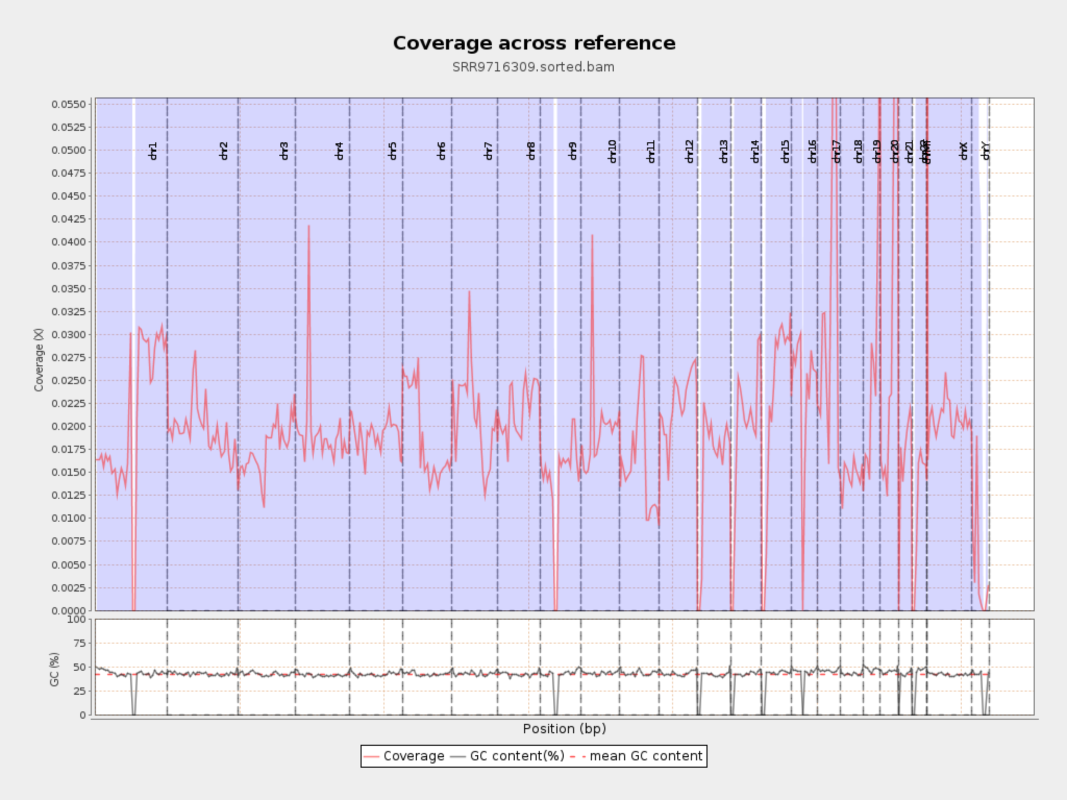
General error rate	0.52%
Mismatches	307,258
Insertions	5,278
Mapped reads with at least one insertion	0.5%
Deletions	12,402
Mapped reads with at least one deletion	1.18%
Homopolymer indels	42.32%

2.6. Chromosome stats

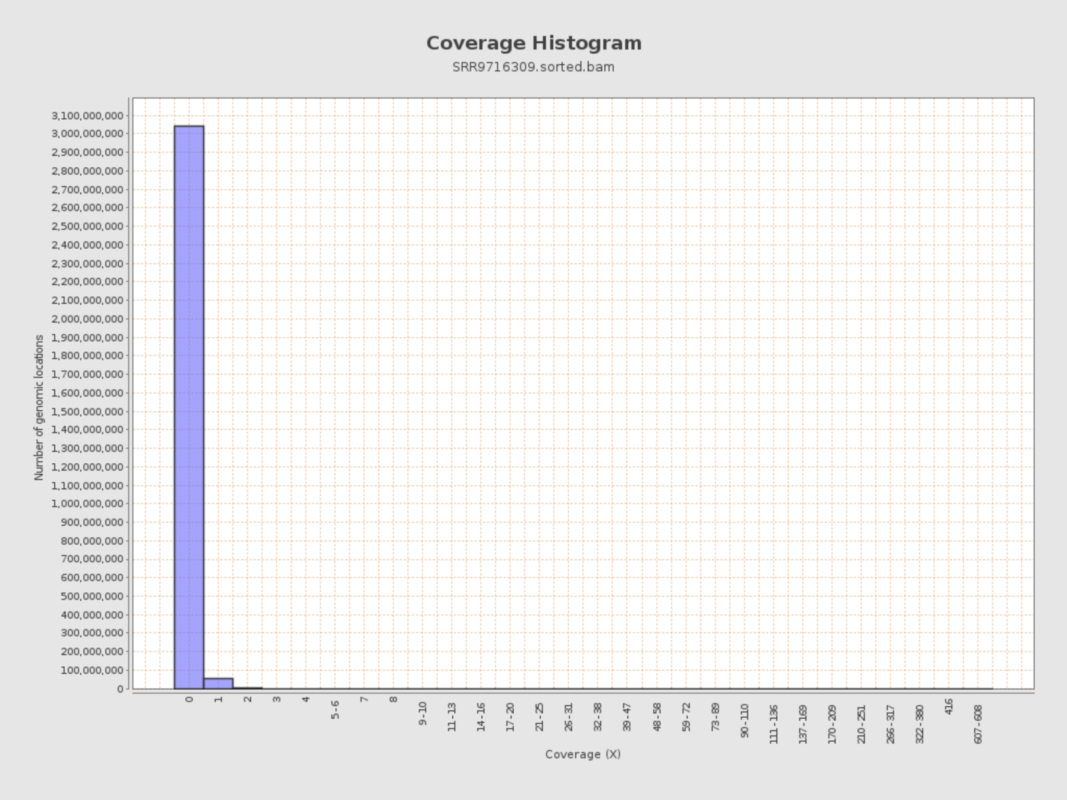
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5150334	0.0207	0.2941
chr2	243199373	4761315	0.0196	0.2947
chr3	198022430	3457132	0.0175	0.1405
chr4	191154276	3717319	0.0194	0.1872
chr5	180915260	3467323	0.0192	0.1485
chr6	171115067	3226827	0.0189	0.1647
chr7	159138663	3393142	0.0213	0.2385

chr8	146364022	3205318	0.0219	0.2733
chr9	141213431	2014713	0.0143	0.1511
chr10	135534747	2699569	0.0199	0.2384
chr11	135006516	2181485	0.0162	0.1667
chr12	133851895	3006431	0.0225	0.1615
chr13	115169878	1814082	0.0158	0.134
chr14	107349540	2065275	0.0192	0.15
chr15	102531392	2267994	0.0221	0.1583
chr16	90354753	2125365	0.0235	0.1703
chr17	81195210	2714976	0.0334	0.2038
chr18	78077248	1133375	0.0145	0.2275
chr19	59128983	1611263	0.0272	0.2462
chr20	63025520	2065261	0.0328	0.202
chr21	48129895	803486	0.0167	0.1737
chr22	51304566	583072	0.0114	0.1143
chrMT	16571	68282	4.1206	3.3335
chrX	155270560	3242976	0.0209	0.1629
chrY	59373566	257566	0.0043	0.2103

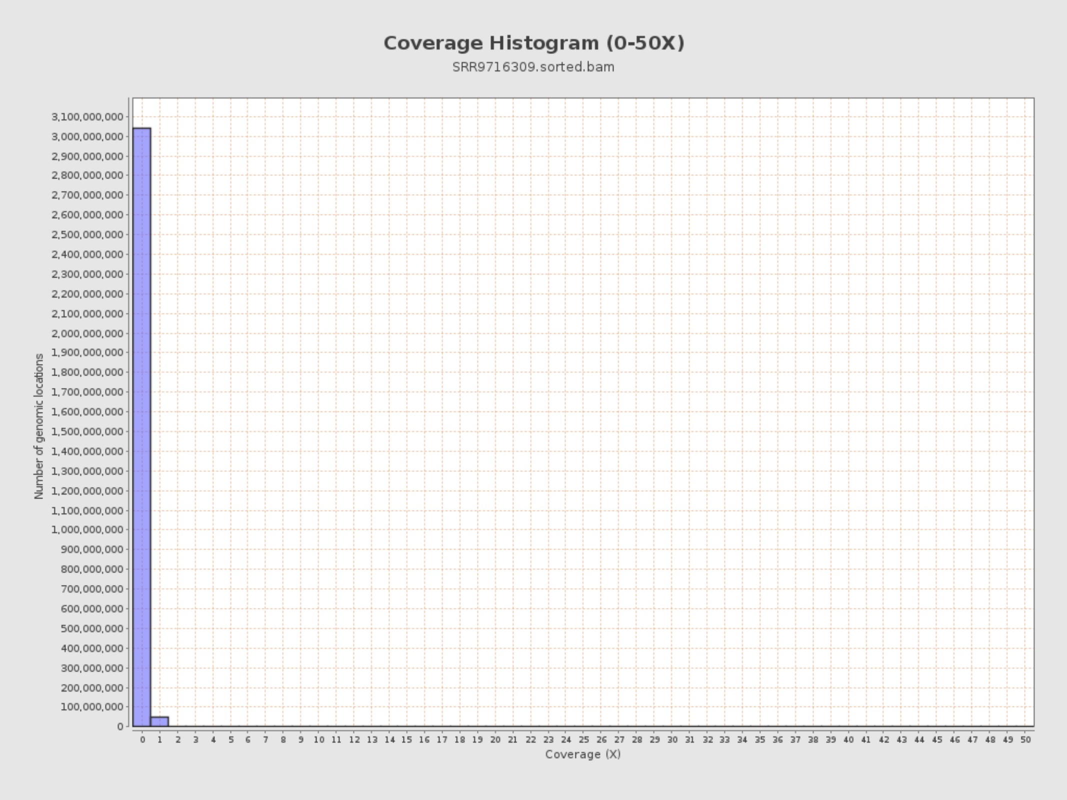
3. Results : Coverage across reference



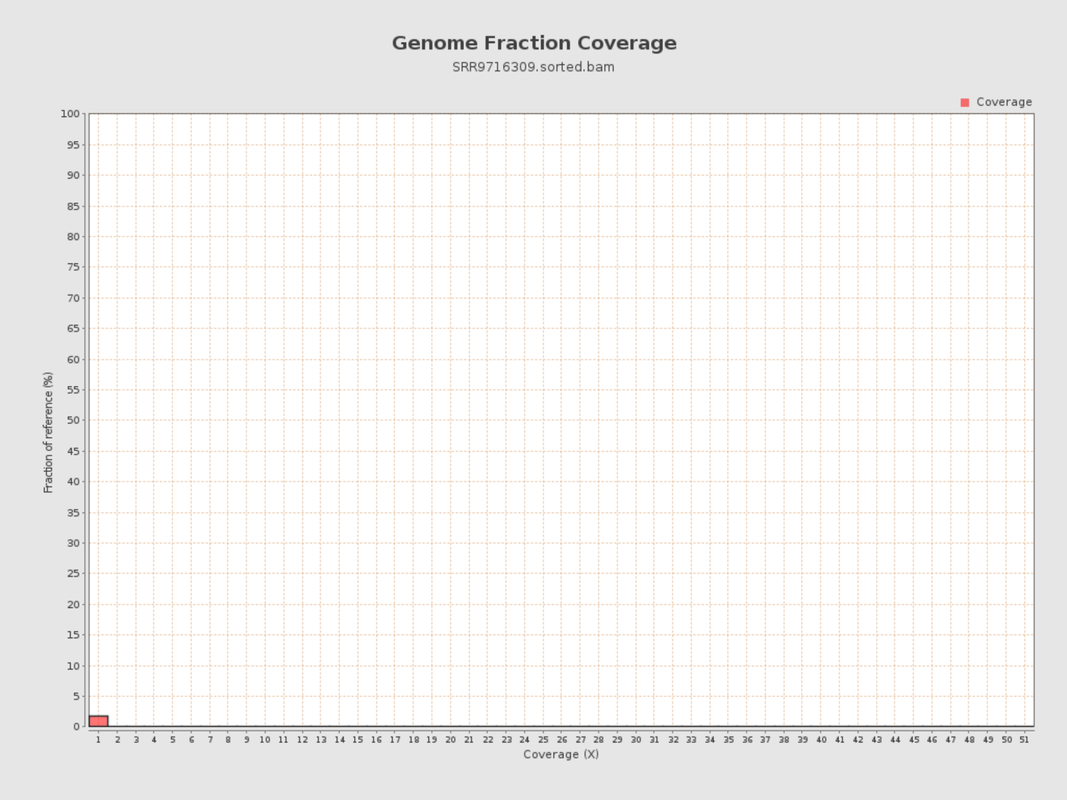
4. Results : Coverage Histogram



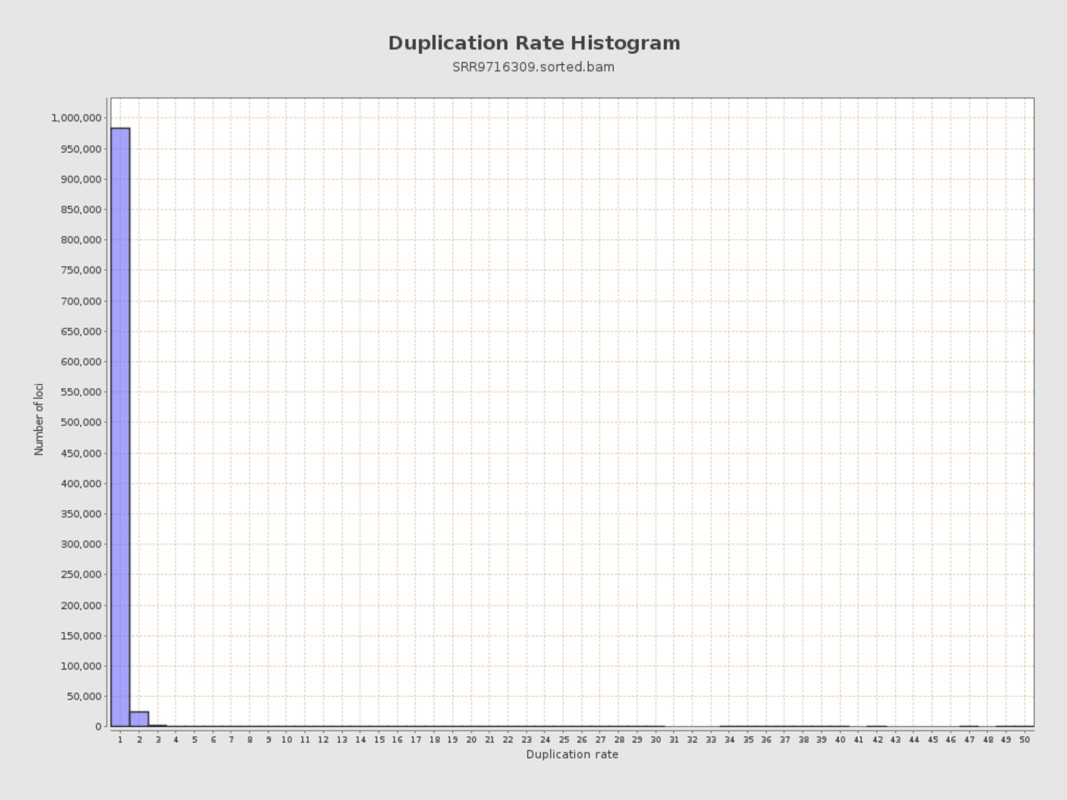
5. Results : Coverage Histogram (0-50X)



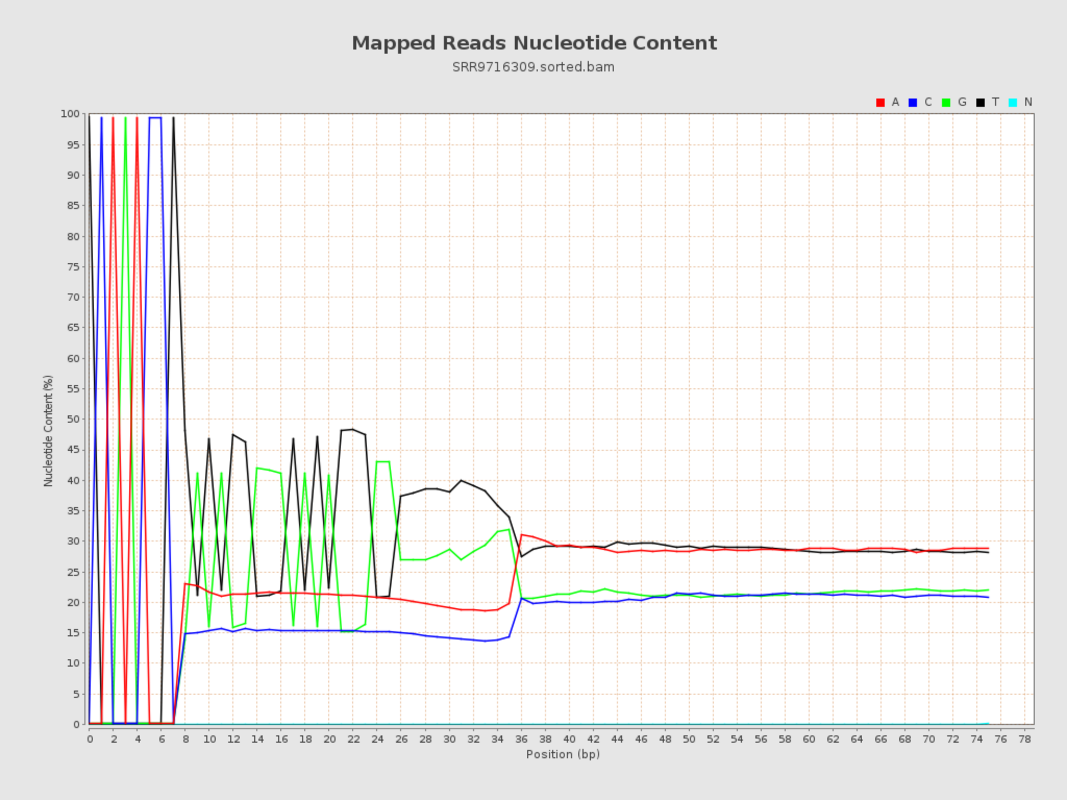
6. Results : Genome Fraction Coverage



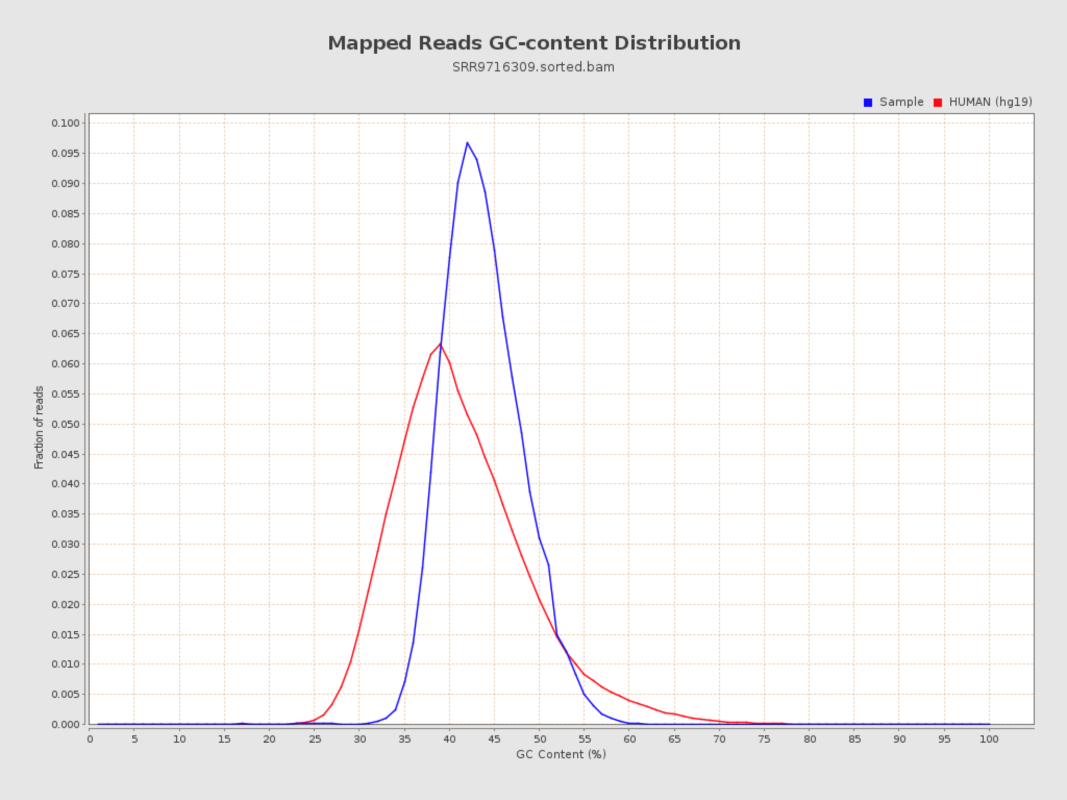
7. Results : Duplication Rate Histogram



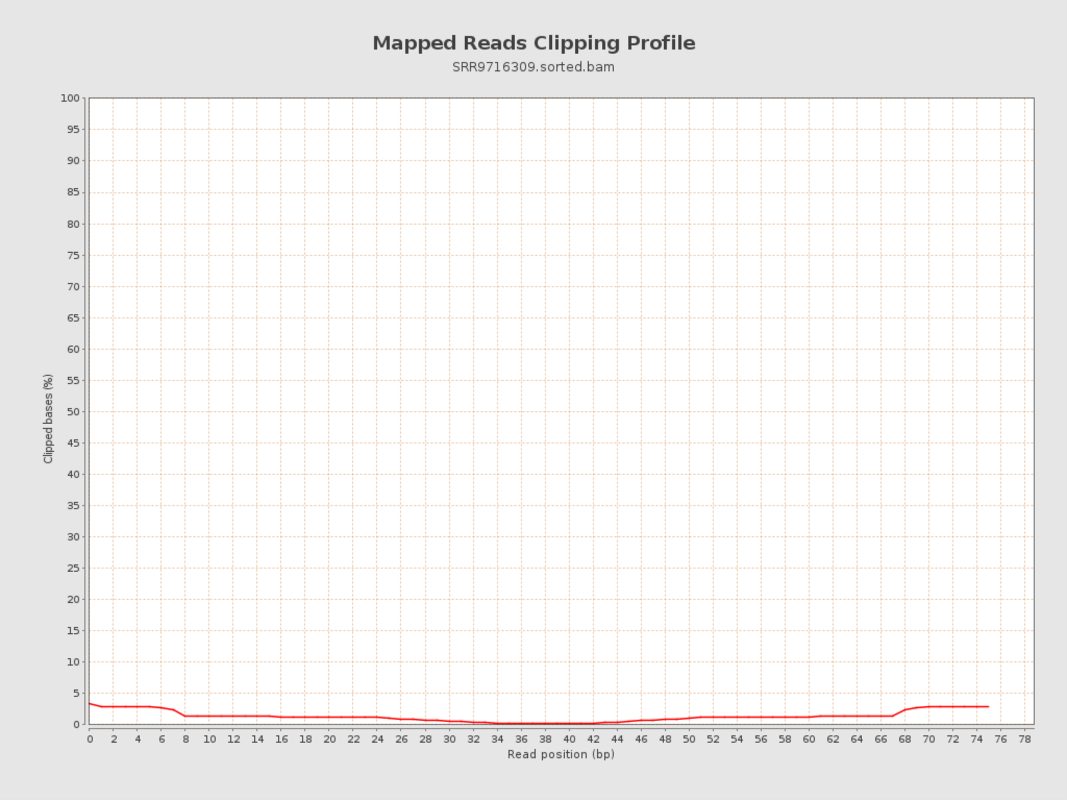
8. Results : Mapped Reads Nucleotide Content



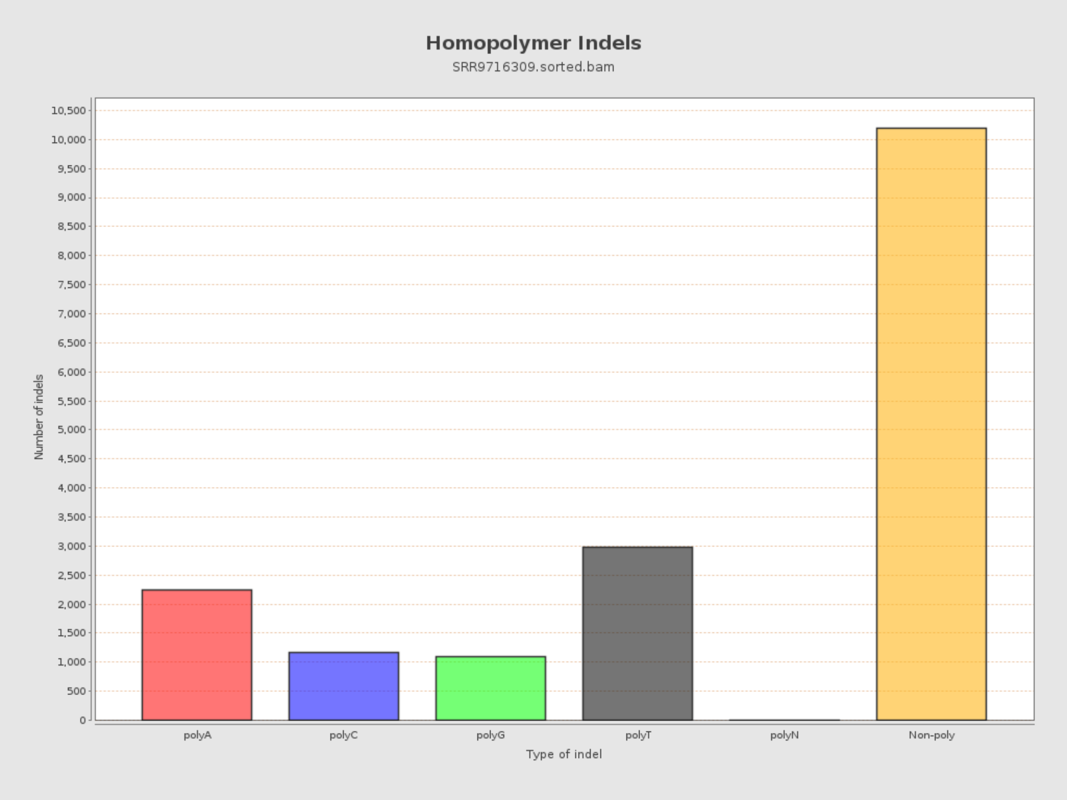
9. Results : Mapped Reads GC-content Distribution



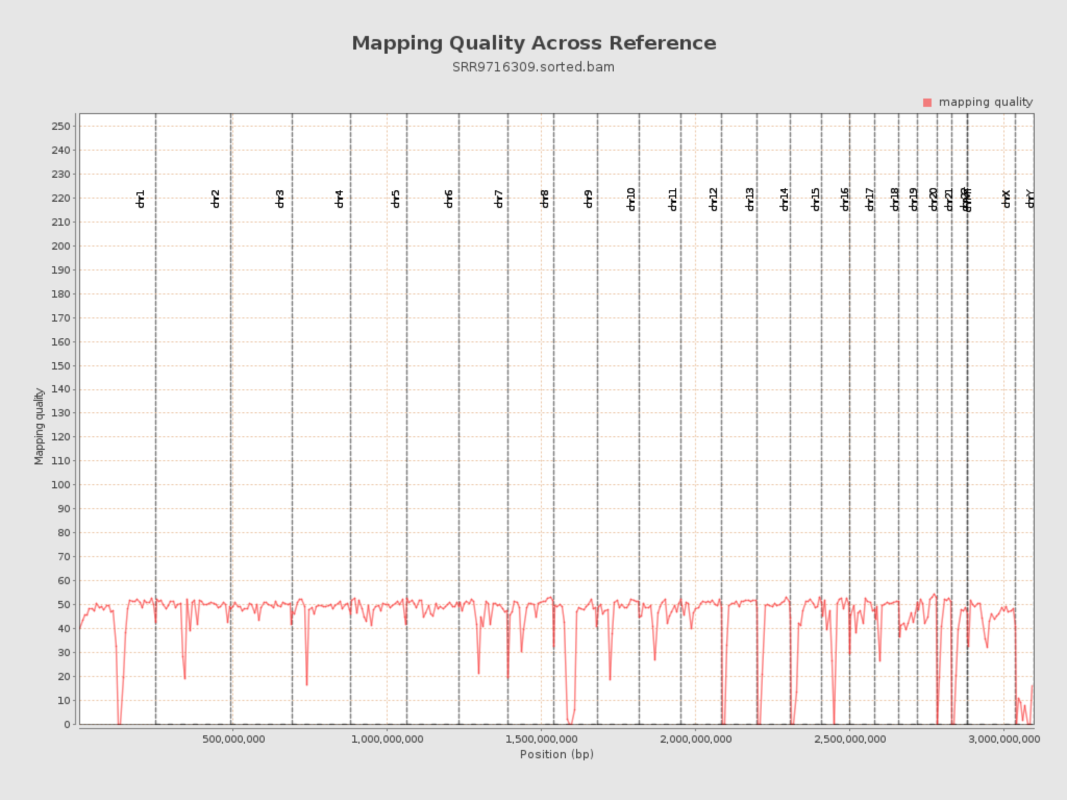
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram