Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 00:10:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716206.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_SRR9716206 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716206.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 00:10:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716206.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,333,061
Mapped reads	1,118,779 / 83.93%
Unmapped reads	214,282 / 16.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,889 / 1.87%
Read min/max/mean length	30 / 101 / 101.67
Duplicated reads (estimated)	26,627 / 2%
Duplication rate	1.63%
Clipped reads	1,141,549 / 85.63%

2.2. ACGT Content

Number/percentage of A's	21,252,234 / 25.33%
Number/percentage of C's	17,927,122 / 21.37%
Number/percentage of T's	25,105,442 / 29.93%
Number/percentage of G's	19,594,910 / 23.36%
Number/percentage of N's	10,408 / 0.01%
GC Percentage	44.73%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.2367

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

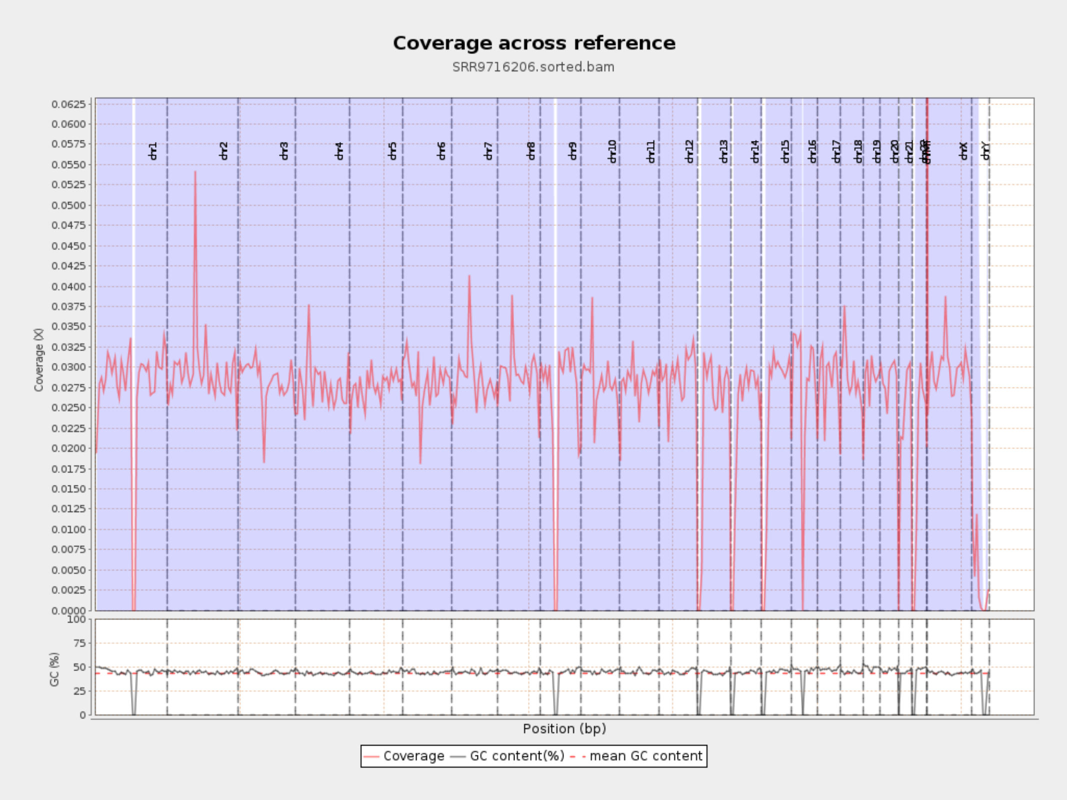
General error rate	0.77%
Mismatches	631,925
Insertions	7,136
Mapped reads with at least one insertion	0.63%
Deletions	17,338
Mapped reads with at least one deletion	1.53%
Homopolymer indels	40.59%

2.6. Chromosome stats

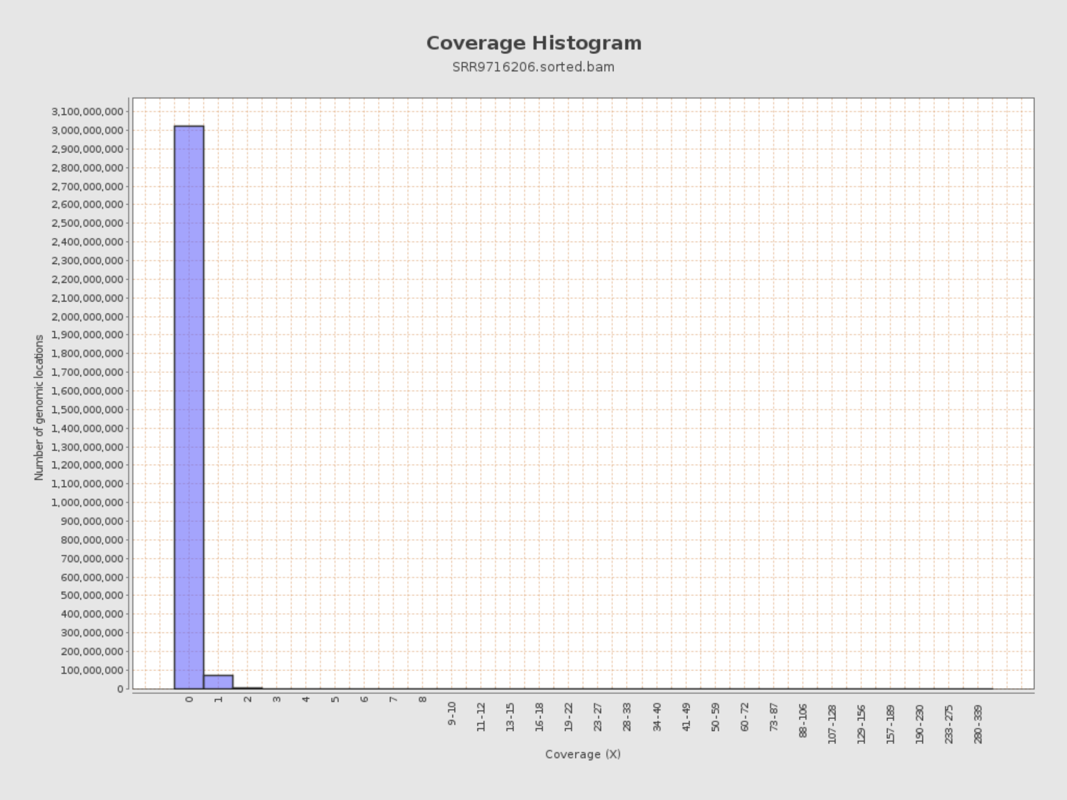
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6814932	0.0273	0.2577
chr2	243199373	7227219	0.0297	0.3272
chr3	198022430	5627168	0.0284	0.1823
chr4	191154276	5300005	0.0277	0.1909
chr5	180915260	5028144	0.0278	0.1817
chr6	171115067	4824437	0.0282	0.1977
chr7	159138663	4555261	0.0286	0.2969

chr8	146364022	4280957	0.0292	0.3015
chr9	141213431	3639382	0.0258	0.239
chr10	135534747	3830689	0.0283	0.2387
chr11	135006516	3810734	0.0282	0.2543
chr12	133851895	3886734	0.029	0.1862
chr13	115169878	2709068	0.0235	0.1668
chr14	107349540	2494979	0.0232	0.1892
chr15	102531392	2485910	0.0242	0.1703
chr16	90354753	2462088	0.0272	0.1934
chr17	81195210	2304129	0.0284	0.1966
chr18	78077248	2264747	0.029	0.4423
chr19	59128983	1689927	0.0286	0.2401
chr20	63025520	1768149	0.0281	0.1878
chr21	48129895	1105504	0.023	0.1764
chr22	51304566	962718	0.0188	0.1502
chrMT	16571	6383	0.3852	0.7317
chrX	155270560	4626575	0.0298	0.2174
chrY	59373566	213618	0.0036	0.11

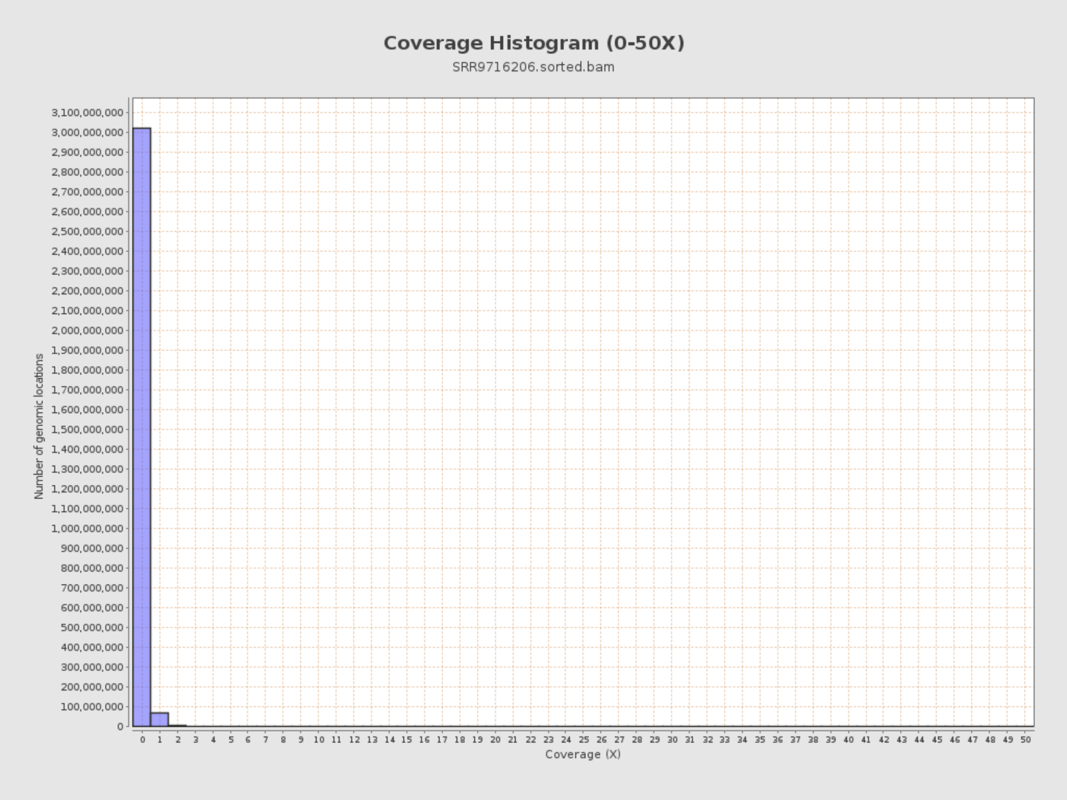
3. Results : Coverage across reference



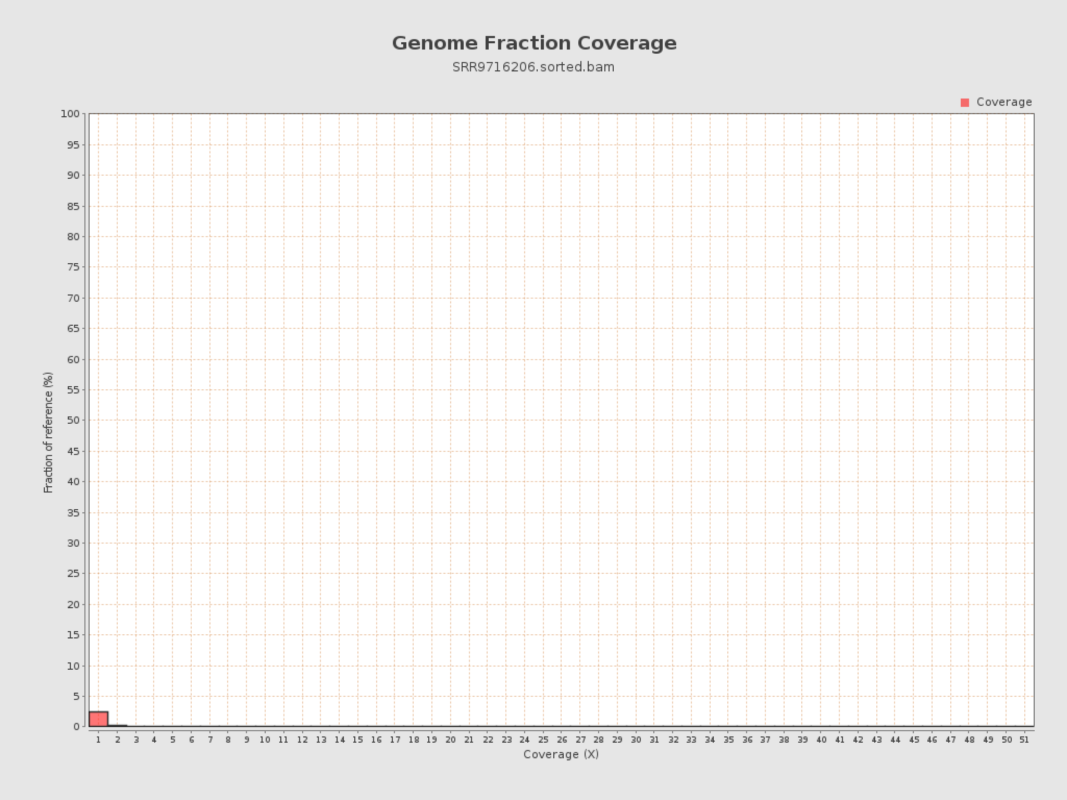
4. Results : Coverage Histogram



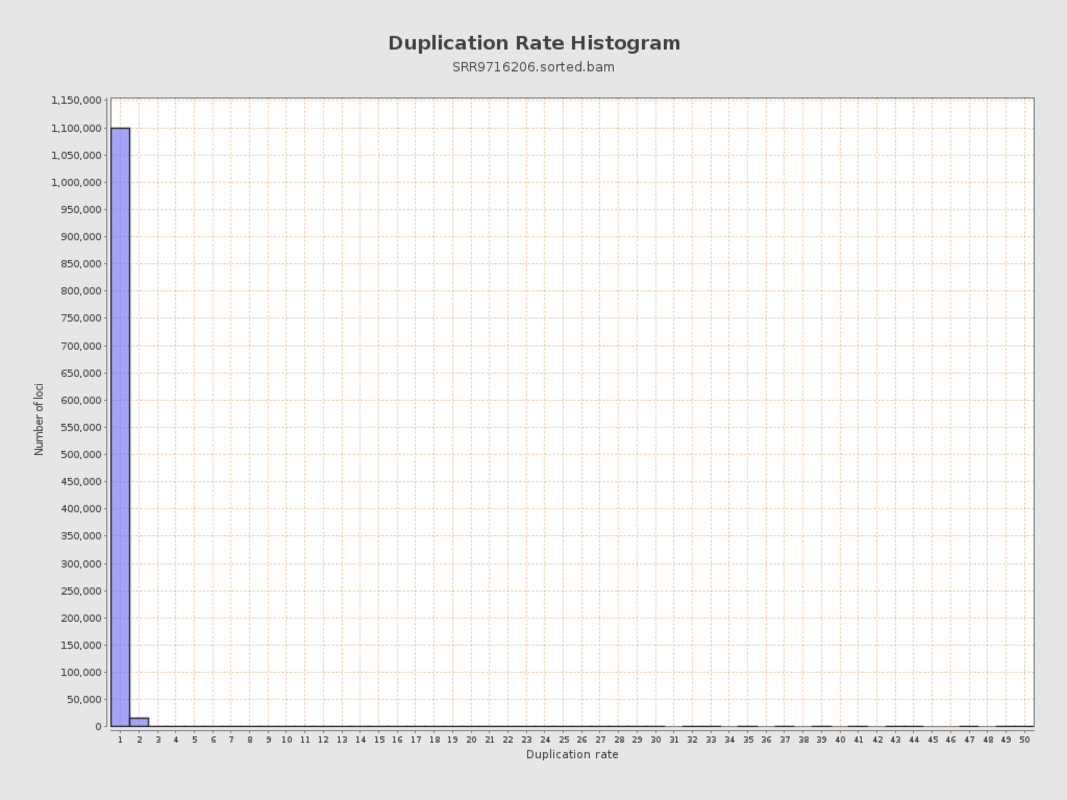
5. Results : Coverage Histogram (0-50X)



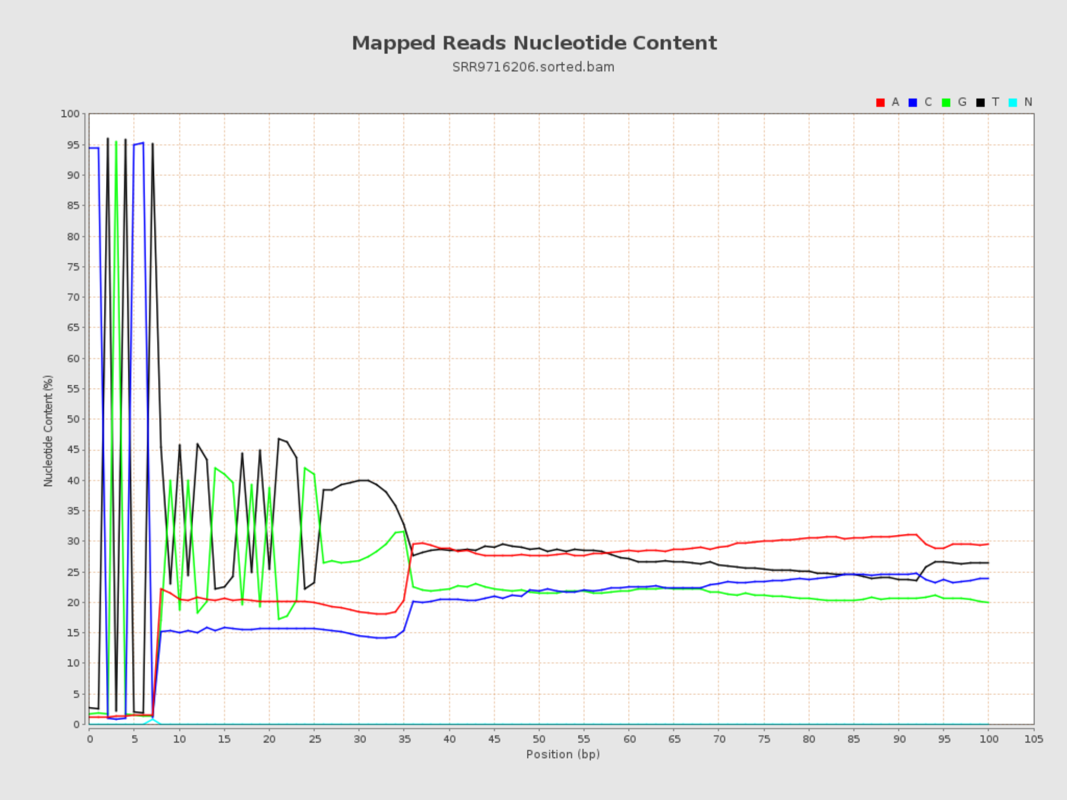
6. Results : Genome Fraction Coverage



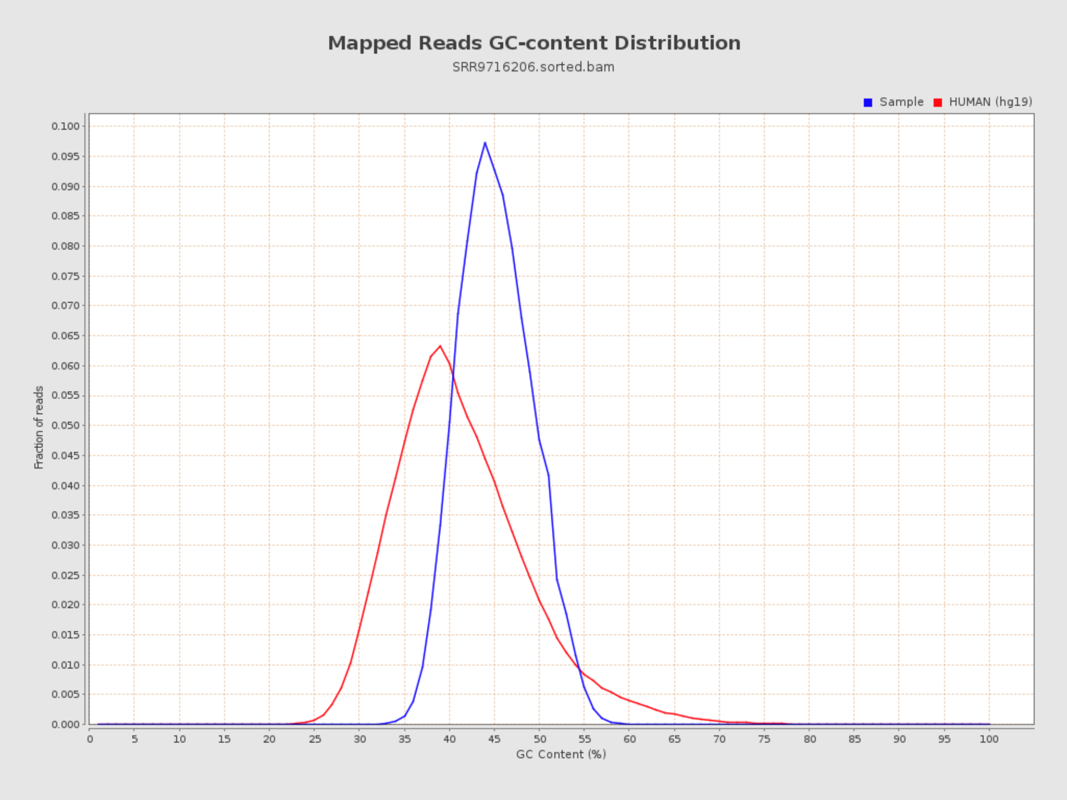
7. Results : Duplication Rate Histogram



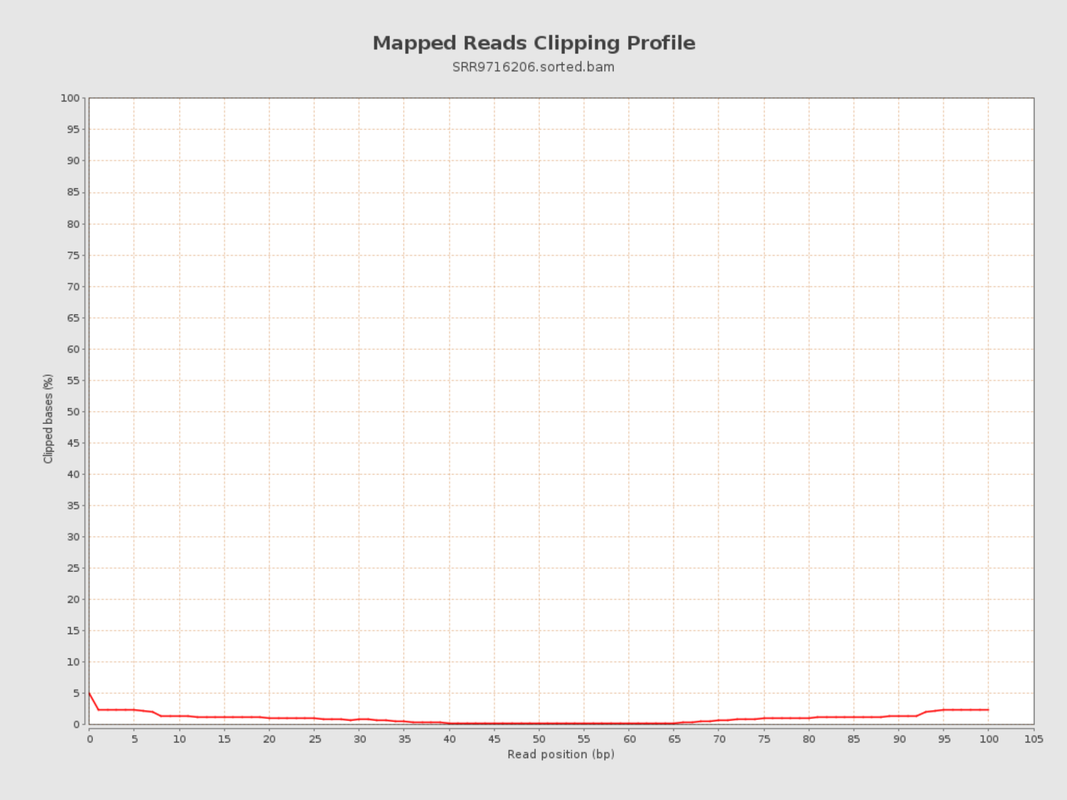
8. Results : Mapped Reads Nucleotide Content



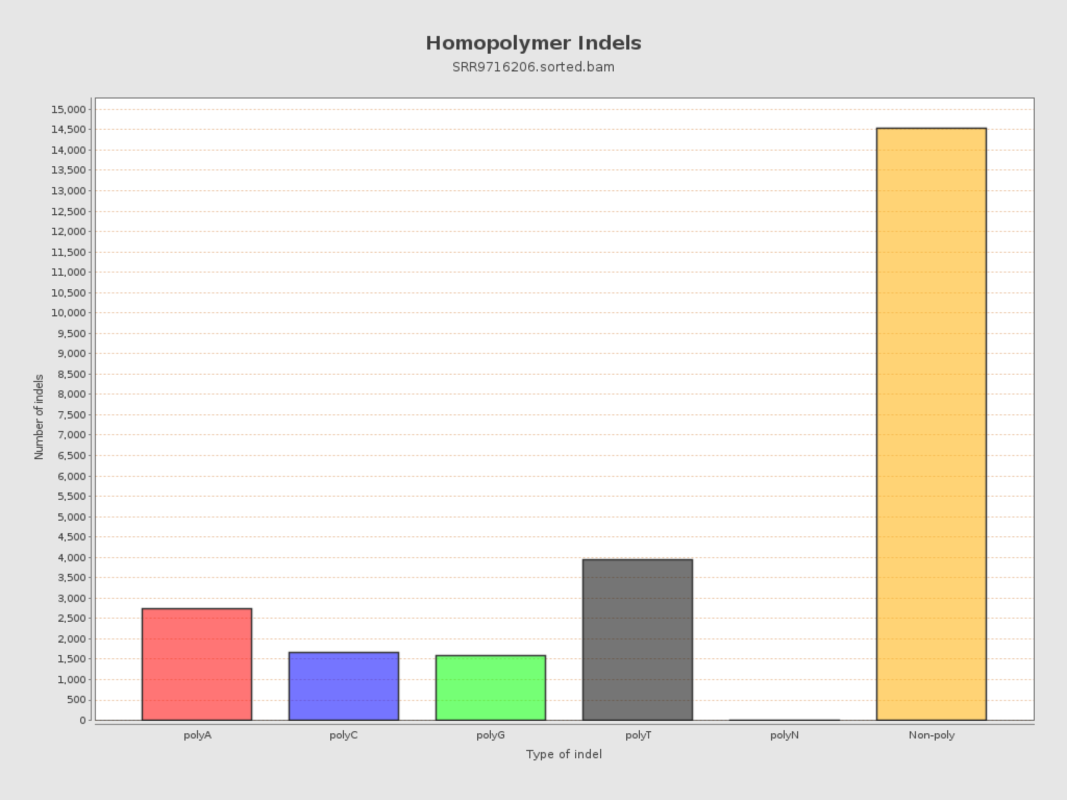
9. Results : Mapped Reads GC-content Distribution



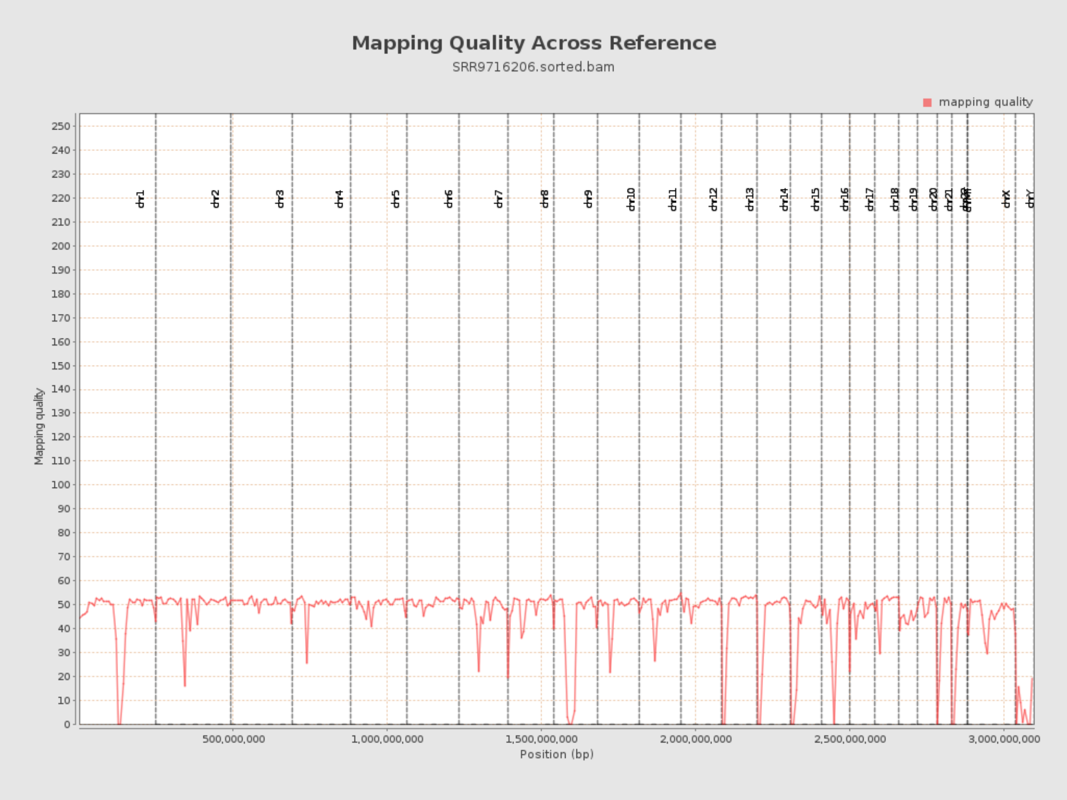
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram