Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:38:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716230.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_SRR9716230 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716230.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:38:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716230.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,699,355
Mapped reads	1,526,254 / 89.81%
Unmapped reads	173,101 / 10.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,552 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	55,145 / 3.25%
Duplication rate	2.74%
Clipped reads	1,529,751 / 90.02%

2.2. ACGT Content

Number/percentage of A's	22,069,867 / 25.28%
Number/percentage of C's	15,480,300 / 17.73%
Number/percentage of T's	28,567,442 / 32.72%
Number/percentage of G's	21,199,589 / 24.28%
Number/percentage of N's	1,388 / 0%
GC Percentage	42.01%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.258

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

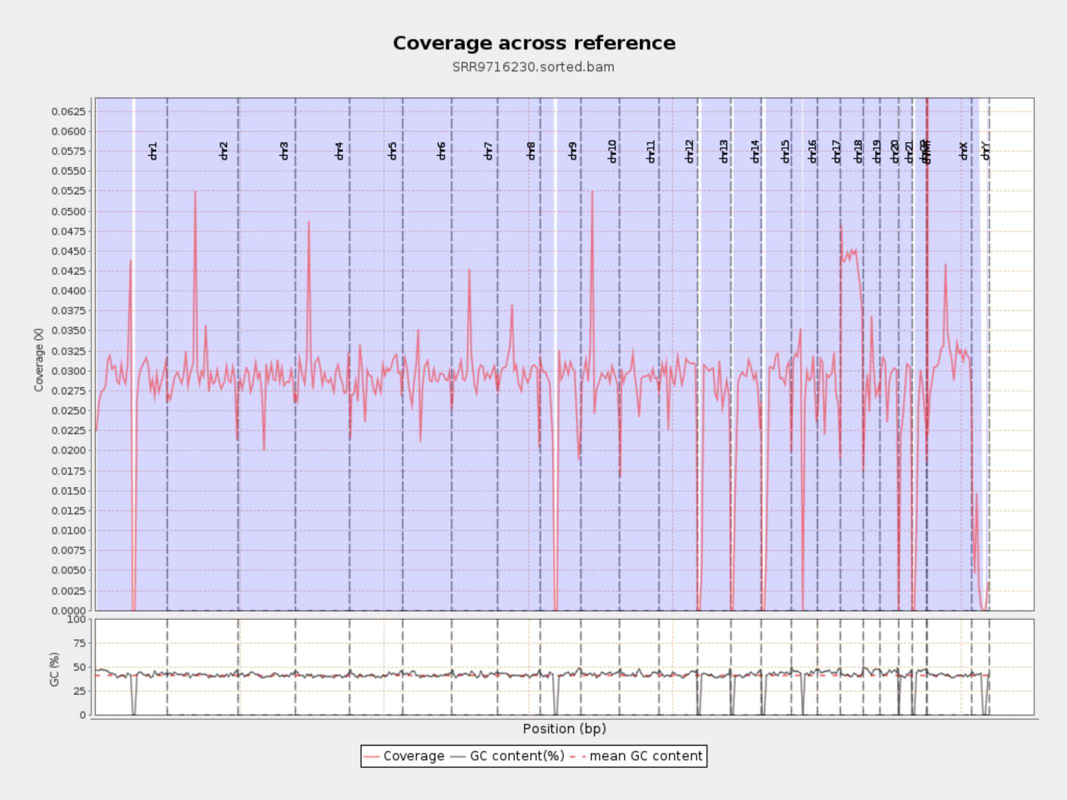
General error rate	0.55%
Mismatches	468,464
Insertions	6,695
Mapped reads with at least one insertion	0.44%
Deletions	13,936
Mapped reads with at least one deletion	0.91%
Homopolymer indels	41.59%

2.6. Chromosome stats

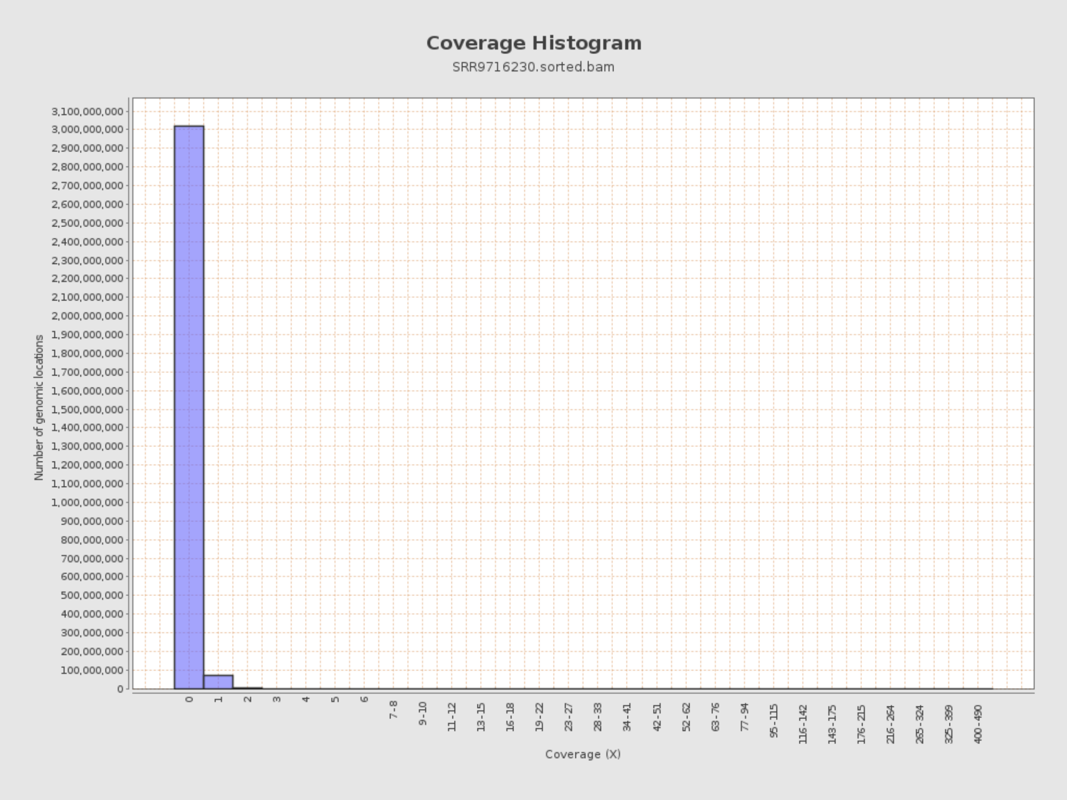
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6899520	0.0277	0.4206
chr2	243199373	7270125	0.0299	0.3054
chr3	198022430	5701846	0.0288	0.1842
chr4	191154276	5752066	0.0301	0.2082
chr5	180915260	5265078	0.0291	0.1871
chr6	171115067	4985526	0.0291	0.2026
chr7	159138663	4803588	0.0302	0.2837

chr8	146364022	4380233	0.0299	0.2874
chr9	141213431	3582477	0.0254	0.2595
chr10	135534747	4106370	0.0303	0.2589
chr11	135006516	3898847	0.0289	0.2547
chr12	133851895	3961744	0.0296	0.1927
chr13	115169878	2750298	0.0239	0.167
chr14	107349540	2596655	0.0242	0.1815
chr15	102531392	2486150	0.0242	0.1689
chr16	90354753	2432947	0.0269	0.1968
chr17	81195210	2272551	0.028	0.1921
chr18	78077248	3404983	0.0436	0.4655
chr19	59128983	1675280	0.0283	0.3316
chr20	63025520	1813439	0.0288	0.1888
chr21	48129895	1164675	0.0242	0.1872
chr22	51304566	941844	0.0184	0.1469
chrMT	16571	11484	0.693	0.9594
chrX	155270560	4917463	0.0317	0.2312
chrY	59373566	266906	0.0045	0.1108

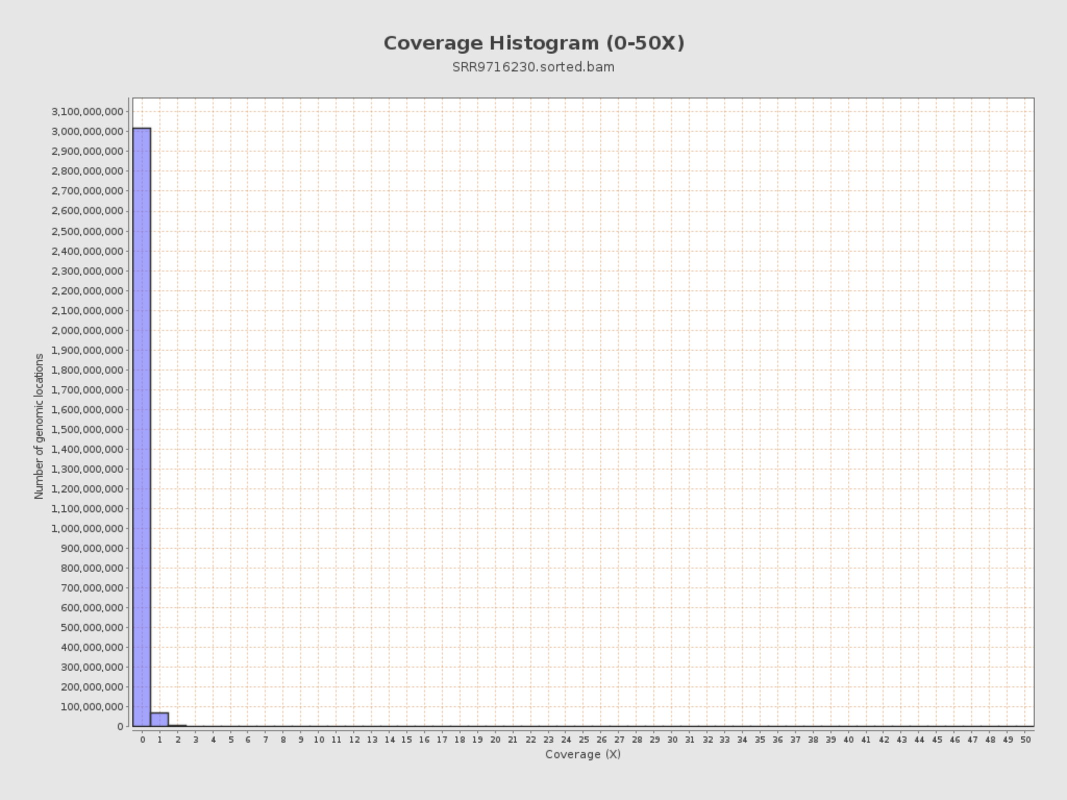
3. Results : Coverage across reference



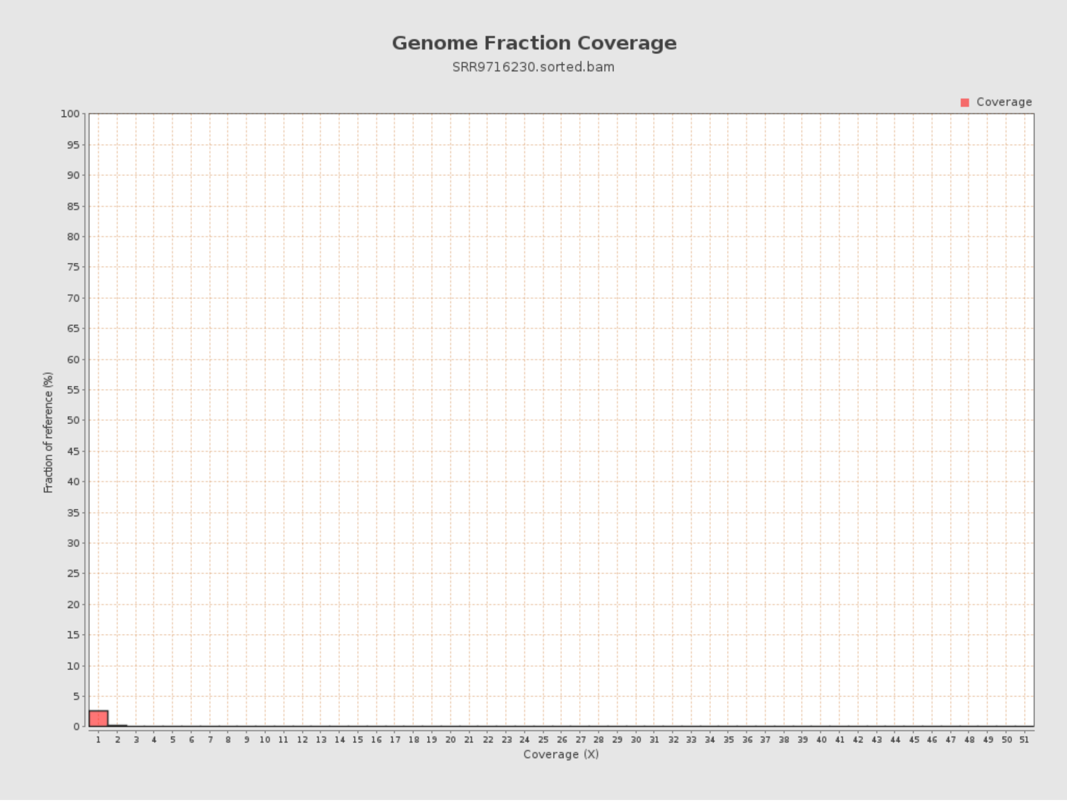
4. Results : Coverage Histogram



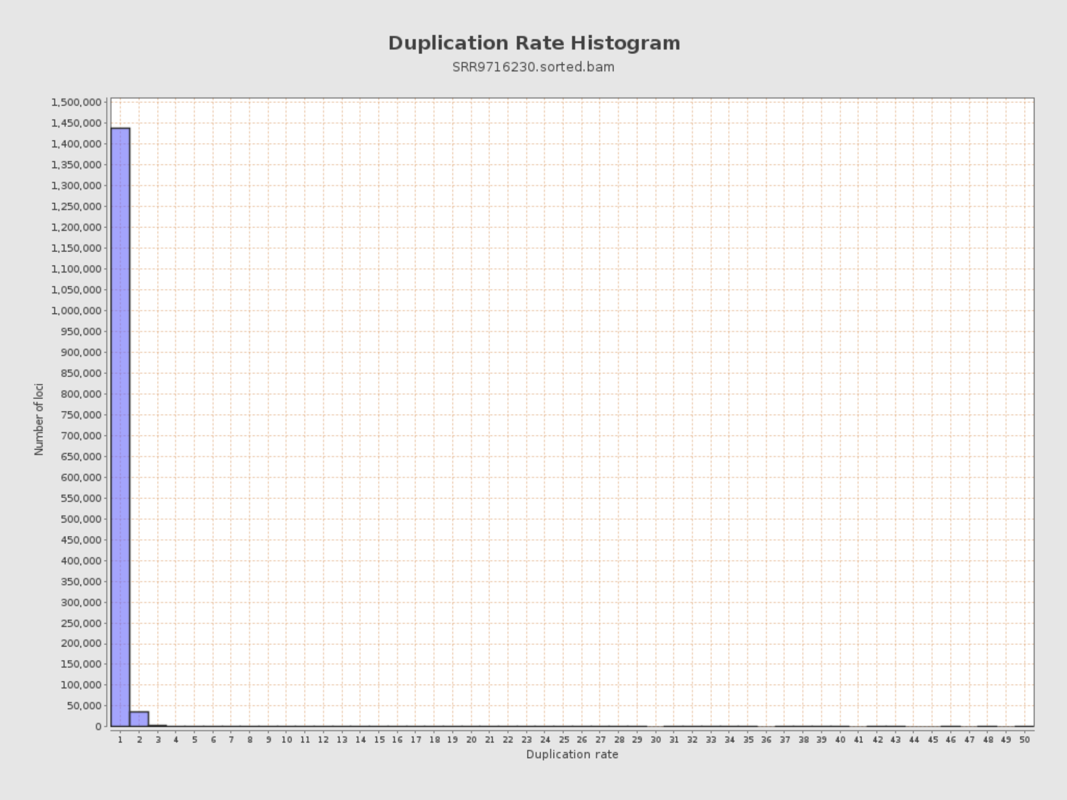
5. Results : Coverage Histogram (0-50X)



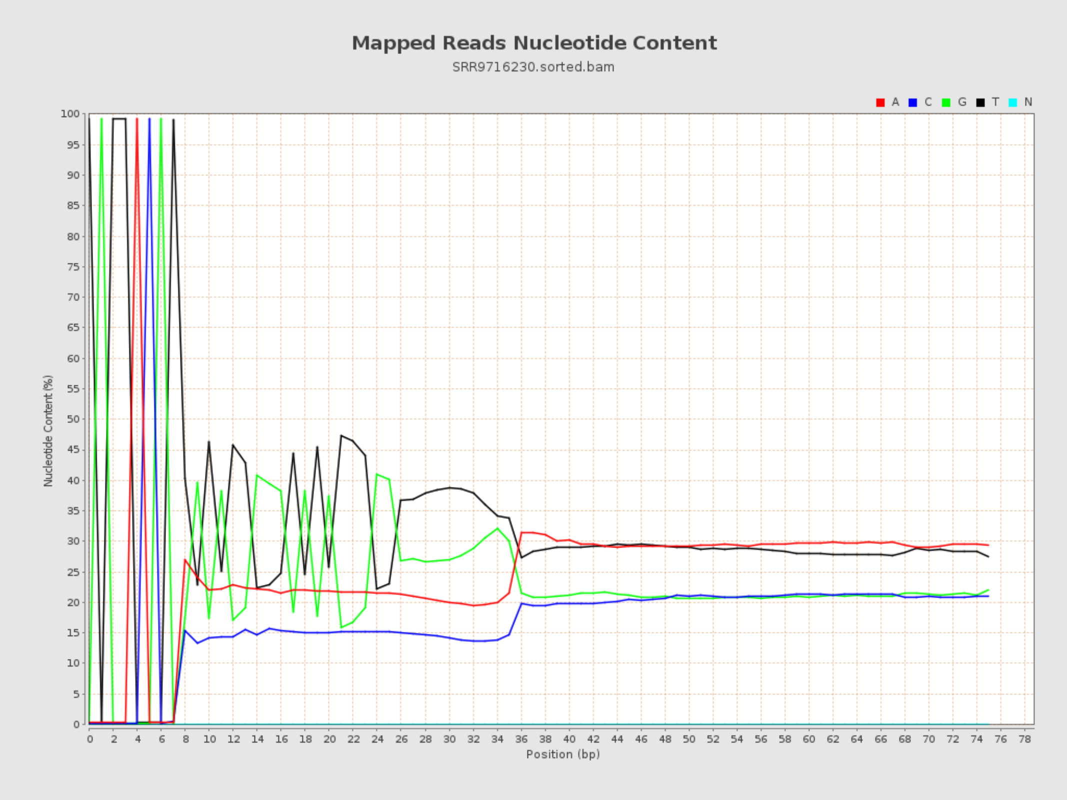
6. Results : Genome Fraction Coverage



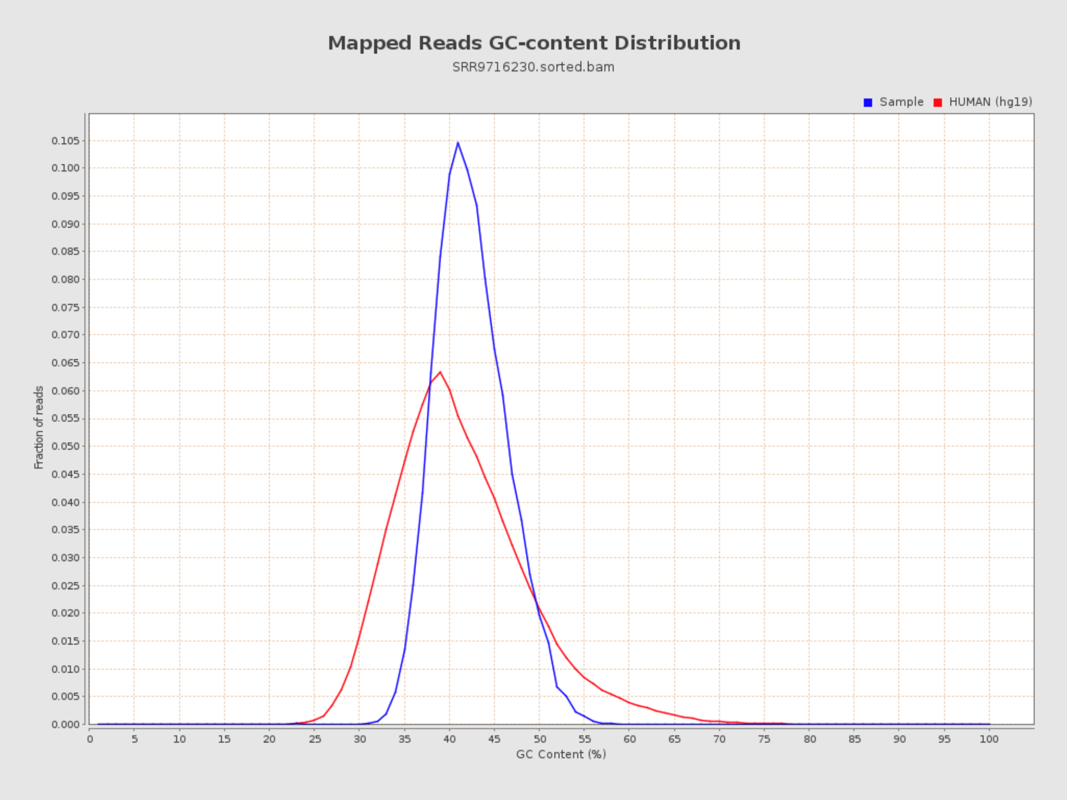
7. Results : Duplication Rate Histogram



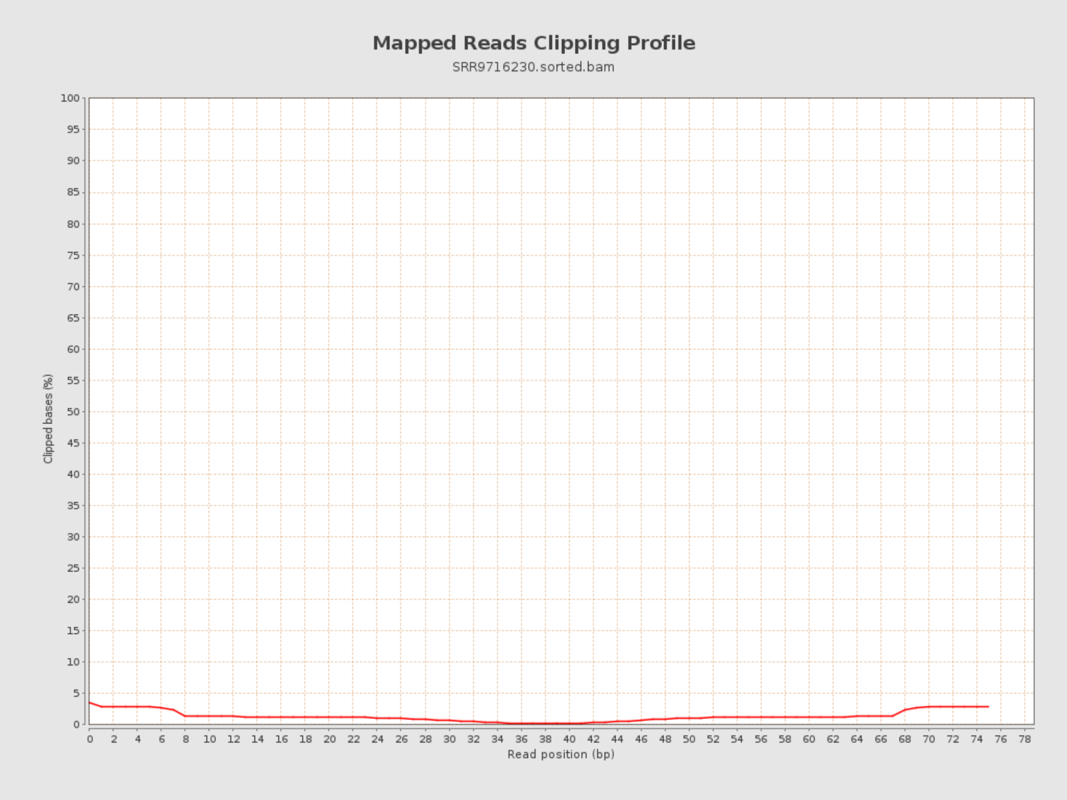
8. Results : Mapped Reads Nucleotide Content



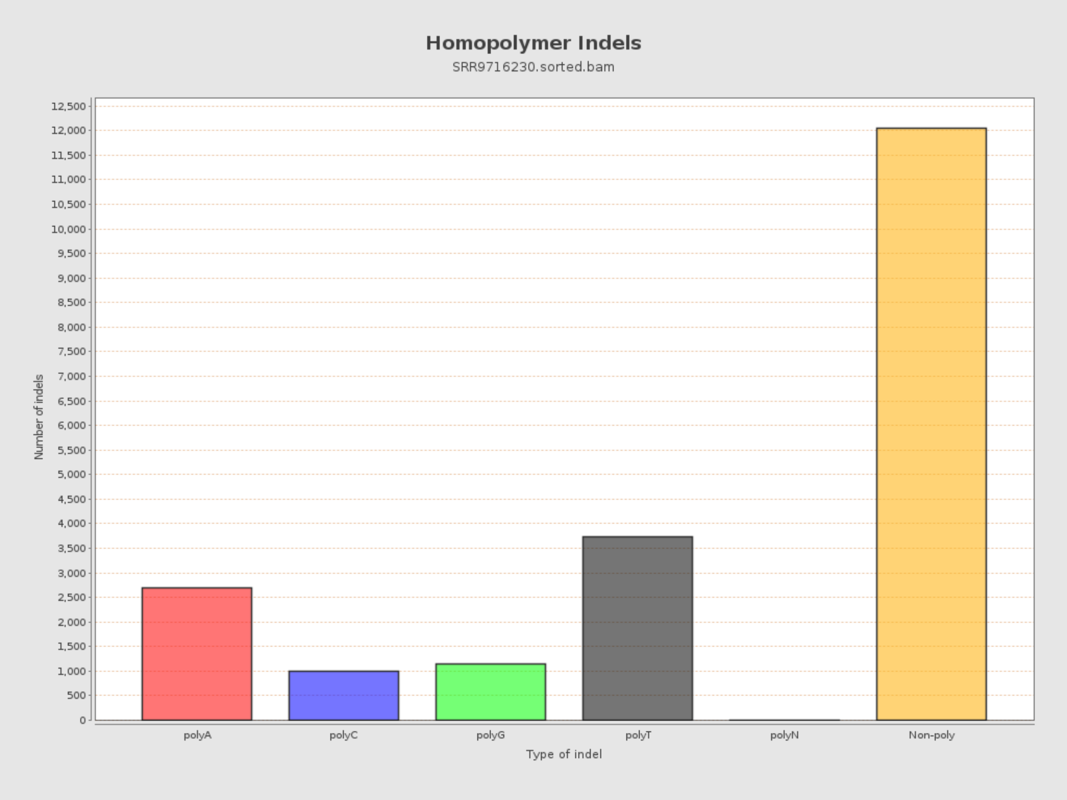
9. Results : Mapped Reads GC-content Distribution



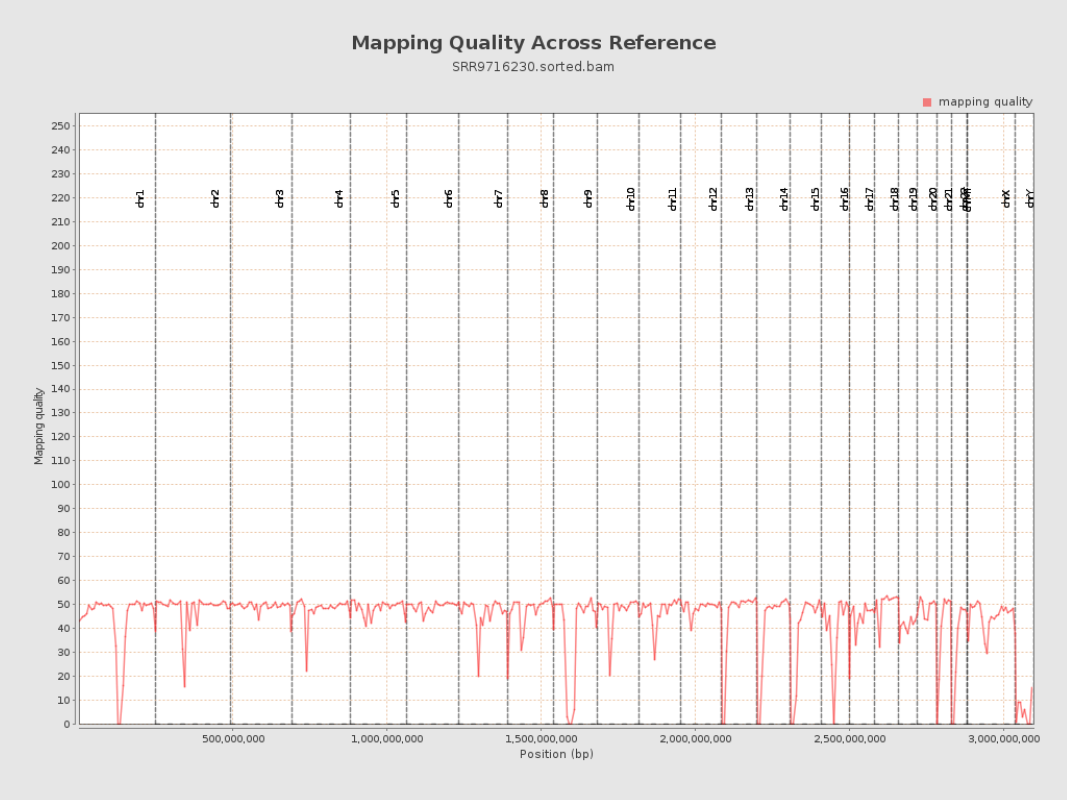
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram