Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:22:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716224.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_SRR9716224 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716224.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:22:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716224.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,419,047
Mapped reads	1,271,221 / 89.58%
Unmapped reads	147,826 / 10.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,120 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	41,312 / 2.91%
Duplication rate	2.52%
Clipped reads	1,272,639 / 89.68%

2.2. ACGT Content

Number/percentage of A's	19,110,628 / 26.15%
Number/percentage of C's	12,348,075 / 16.9%
Number/percentage of T's	23,333,462 / 31.93%
Number/percentage of G's	18,276,246 / 25.01%
Number/percentage of N's	1,099 / 0%
GC Percentage	41.91%

2.3. Coverage

Mean	0.0236

Standard Deviation	0.2241

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Mismatches and indels

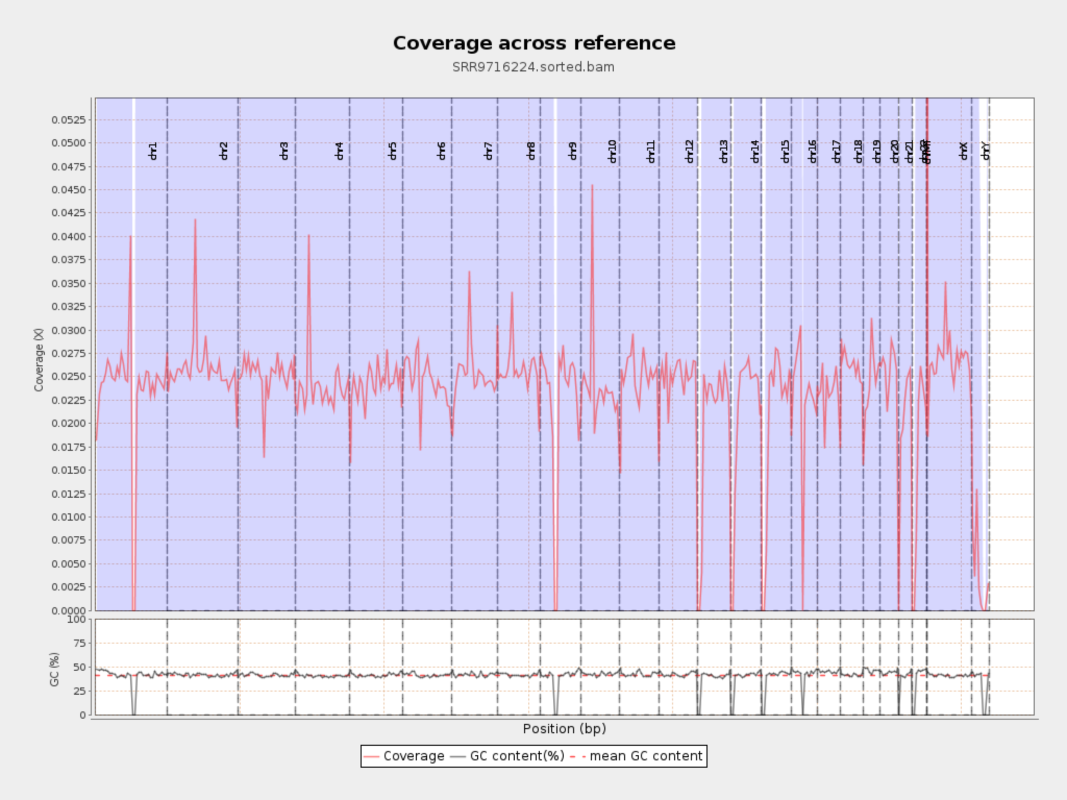
General error rate	0.55%
Mismatches	391,393
Insertions	5,164
Mapped reads with at least one insertion	0.4%
Deletions	11,866
Mapped reads with at least one deletion	0.93%
Homopolymer indels	42.77%

2.6. Chromosome stats

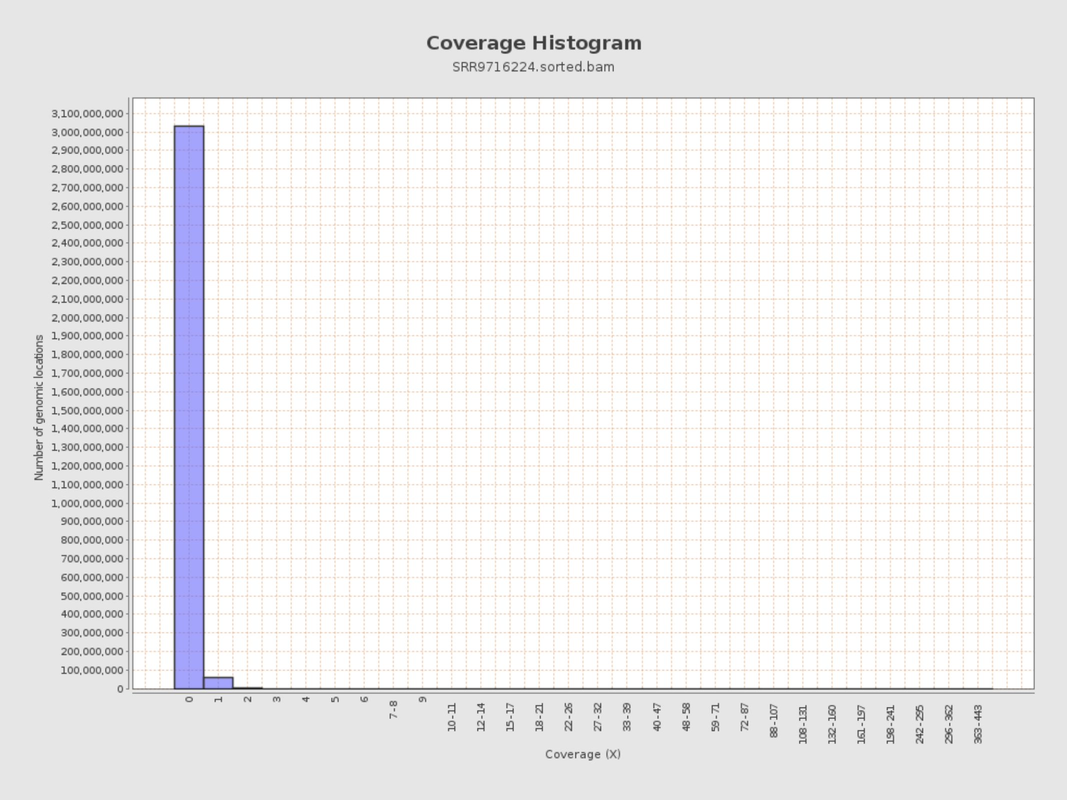
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5872018	0.0236	0.382
chr2	243199373	6321662	0.026	0.2477
chr3	198022430	4993758	0.0252	0.1701
chr4	191154276	4599901	0.0241	0.1823
chr5	180915260	4425822	0.0245	0.1686
chr6	171115067	4194032	0.0245	0.1778
chr7	159138663	4018227	0.0252	0.237

chr8	146364022	3768600	0.0257	0.2429
chr9	141213431	3119692	0.0221	0.2187
chr10	135534747	3252065	0.024	0.237
chr11	135006516	3401289	0.0252	0.2117
chr12	133851895	3349206	0.025	0.1738
chr13	115169878	2273861	0.0197	0.1502
chr14	107349540	2239396	0.0209	0.1643
chr15	102531392	2071565	0.0202	0.1525
chr16	90354753	2004841	0.0222	0.1751
chr17	81195210	1884102	0.0232	0.17
chr18	78077248	2051622	0.0263	0.371
chr19	59128983	1459685	0.0247	0.2881
chr20	63025520	1593868	0.0253	0.1767
chr21	48129895	963731	0.02	0.1674
chr22	51304566	832940	0.0162	0.1359
chrMT	16571	10626	0.6412	0.8937
chrX	155270560	4166826	0.0268	0.1943
chrY	59373566	220076	0.0037	0.1045

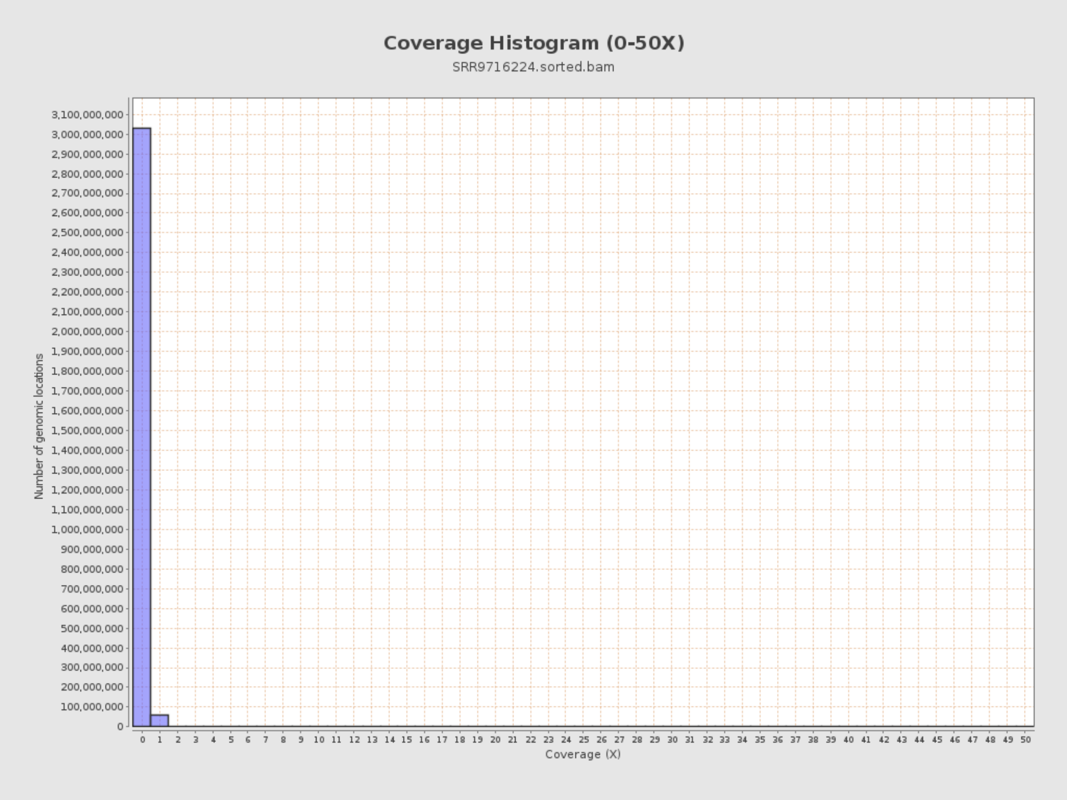
3. Results : Coverage across reference



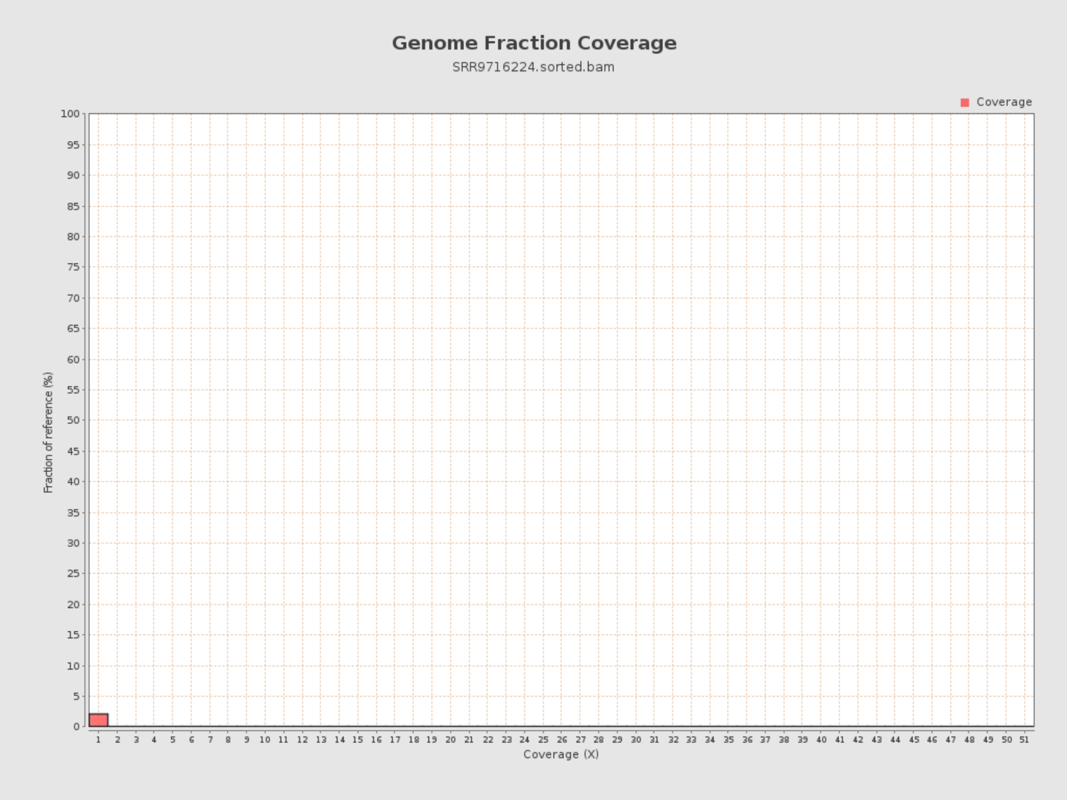
4. Results : Coverage Histogram



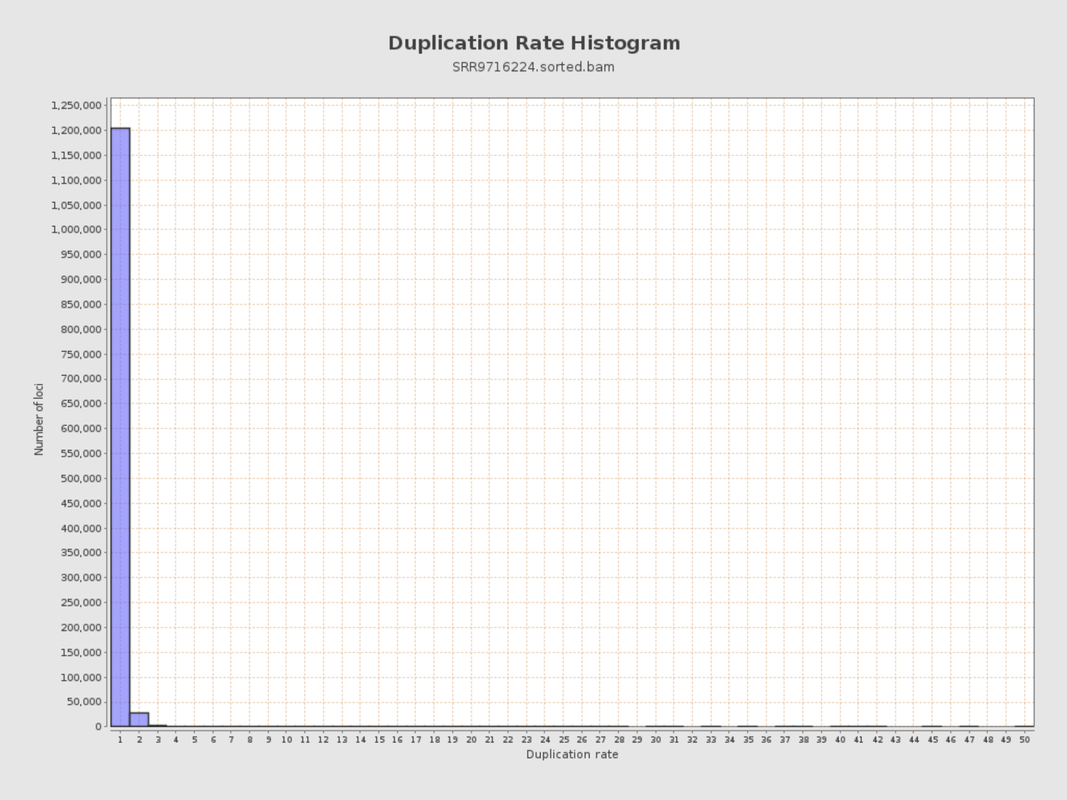
5. Results : Coverage Histogram (0-50X)



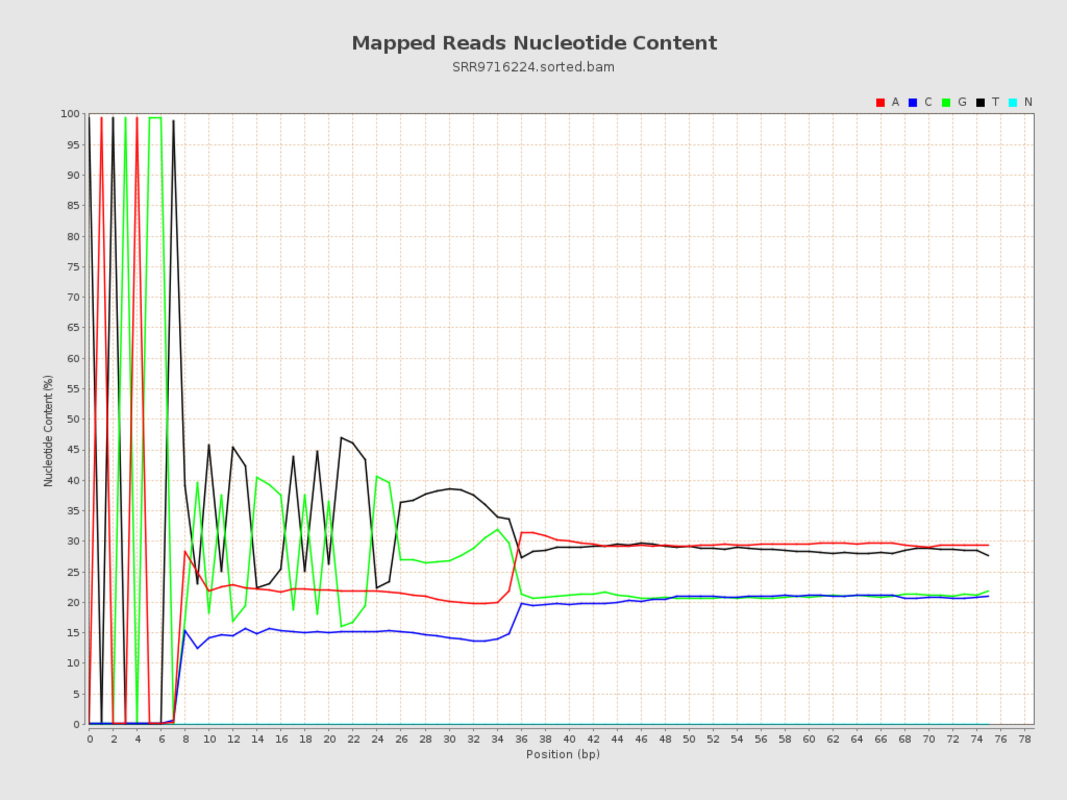
6. Results : Genome Fraction Coverage



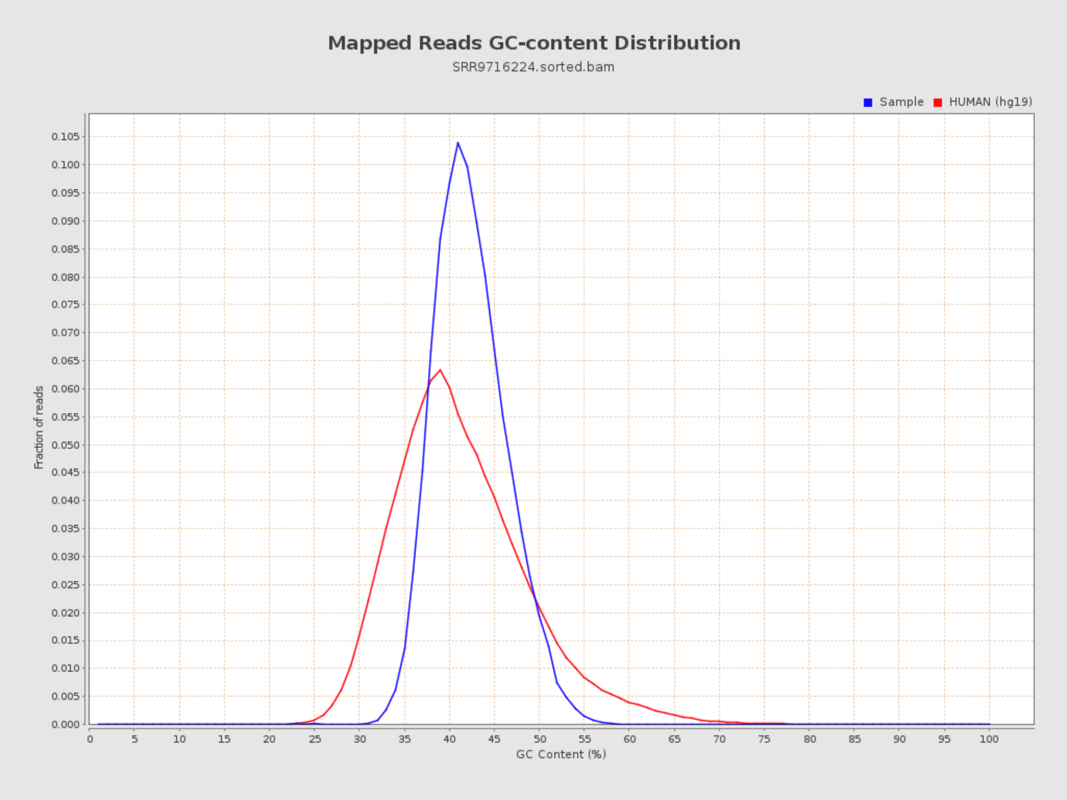
7. Results : Duplication Rate Histogram



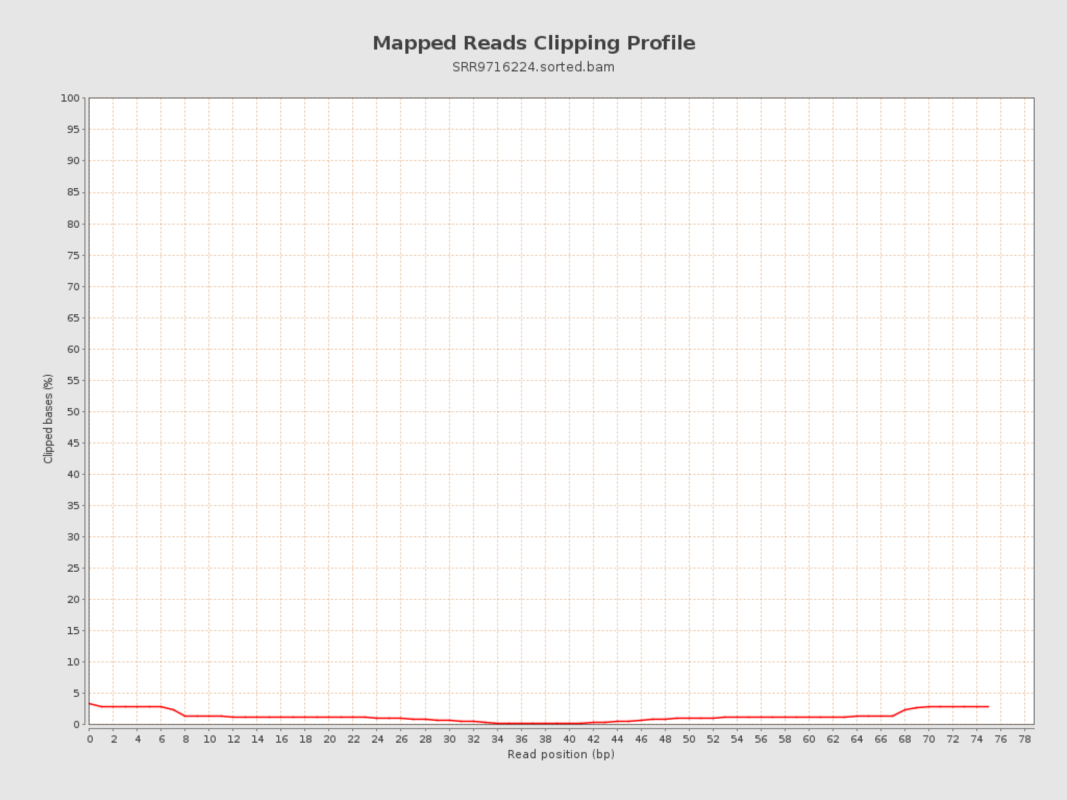
8. Results : Mapped Reads Nucleotide Content



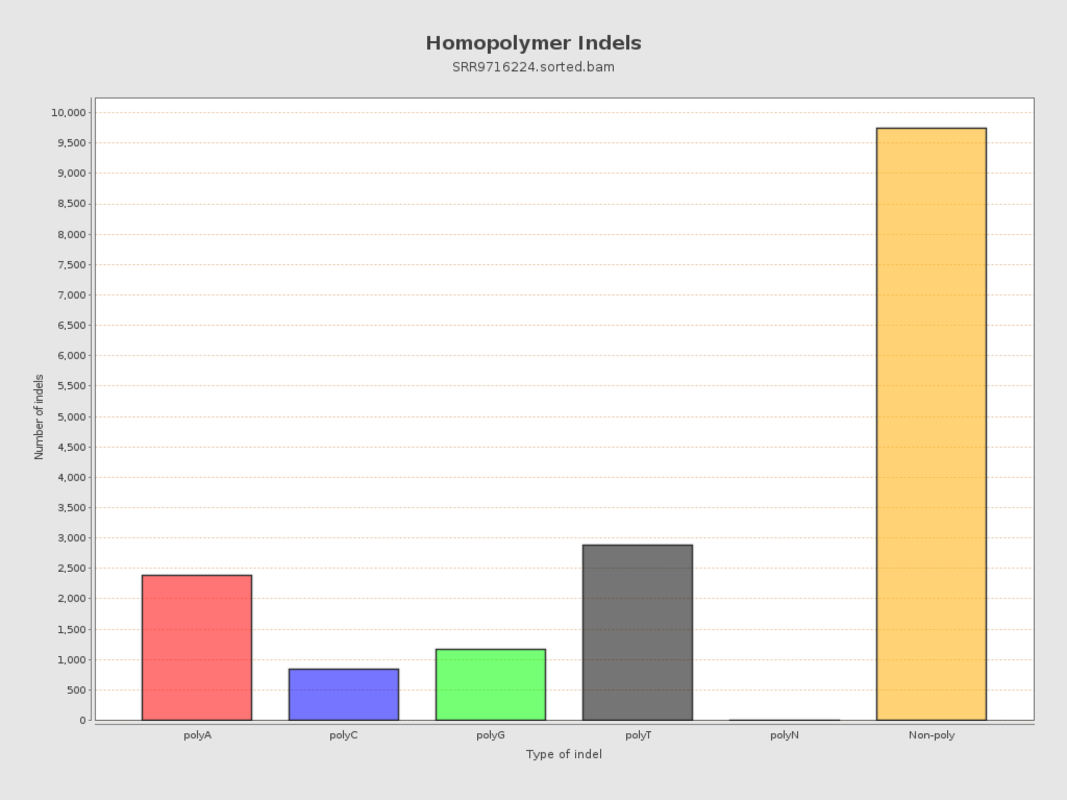
9. Results : Mapped Reads GC-content Distribution



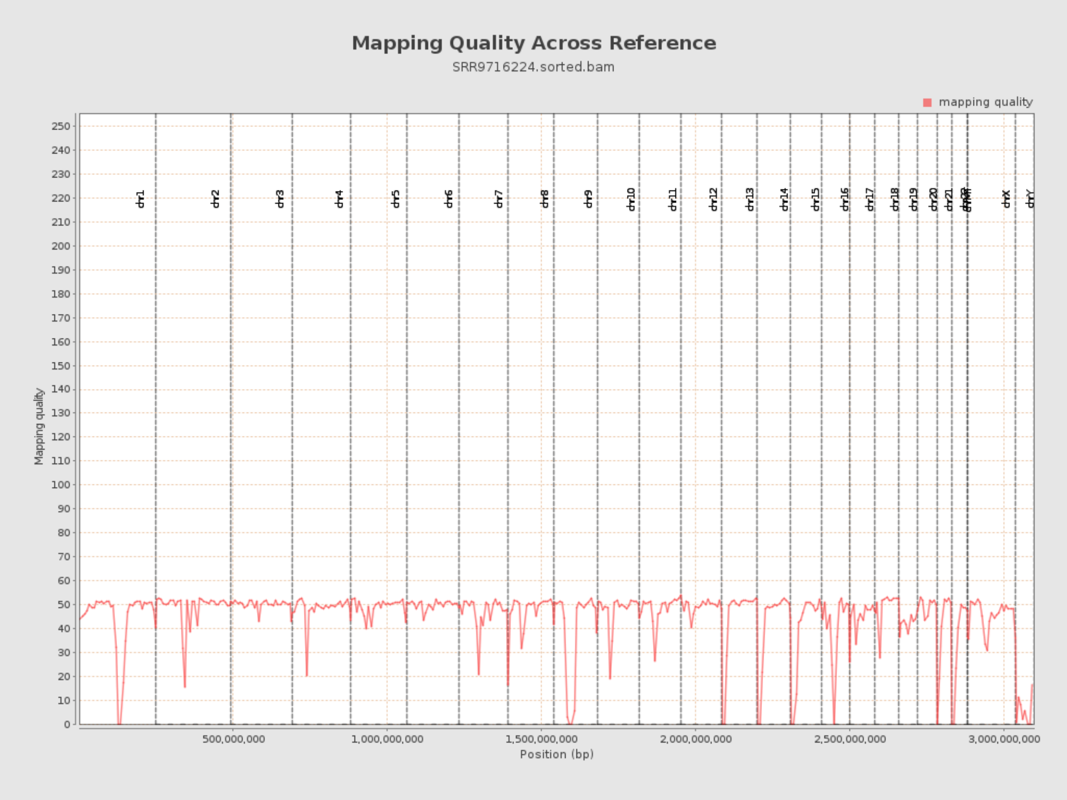
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram