Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:08:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716990.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_SRR9716990 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716990.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:08:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716990.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,430,946
Mapped reads	1,219,828 / 85.25%
Unmapped reads	211,118 / 14.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,300 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	27,612 / 1.93%
Duplication rate	1.24%
Clipped reads	1,223,375 / 85.49%

2.2. ACGT Content

Number/percentage of A's	16,583,391 / 24.1%
Number/percentage of C's	13,705,290 / 19.91%
Number/percentage of T's	21,309,967 / 30.96%
Number/percentage of G's	17,224,013 / 25.03%
Number/percentage of N's	554 / 0%
GC Percentage	44.94%

2.3. Coverage

Mean	0.0222

Standard Deviation	0.2279

2.4. Mapping Quality

Mean Mapping Quality	40.08

2.5. Mismatches and indels

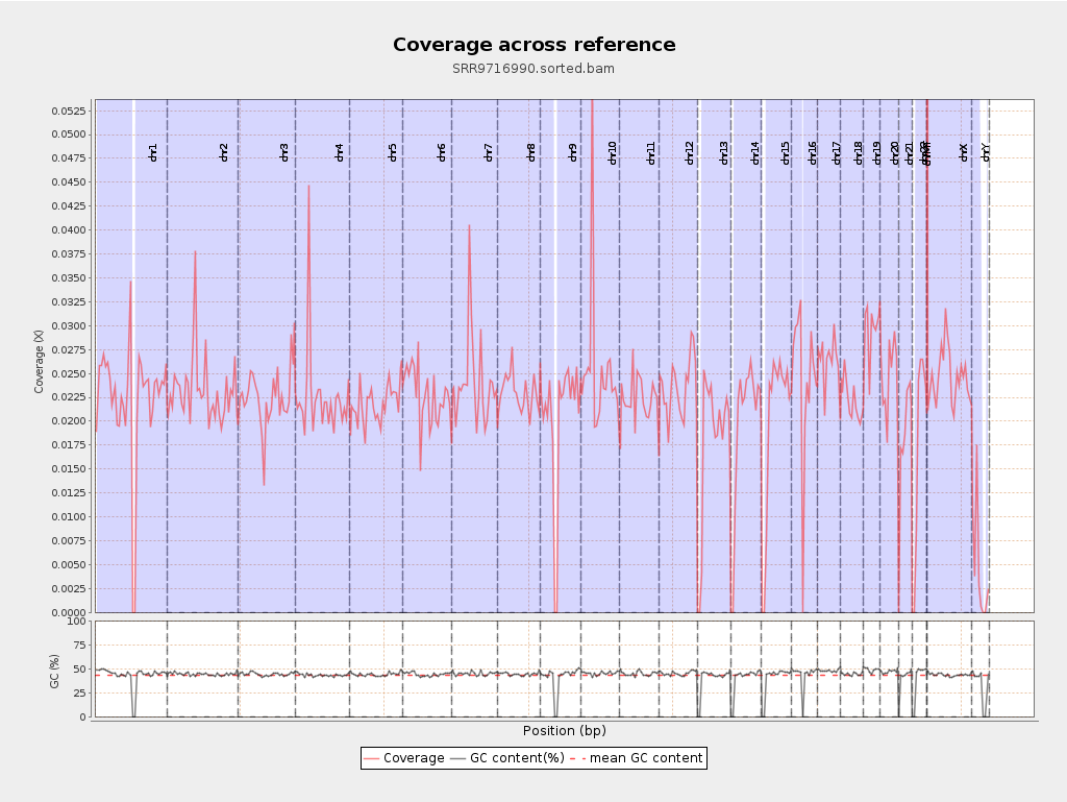
General error rate	0.53%
Mismatches	356,796
Insertions	5,517
Mapped reads with at least one insertion	0.45%
Deletions	11,143
Mapped reads with at least one deletion	0.9%
Homopolymer indels	38.32%

2.6. Chromosome stats

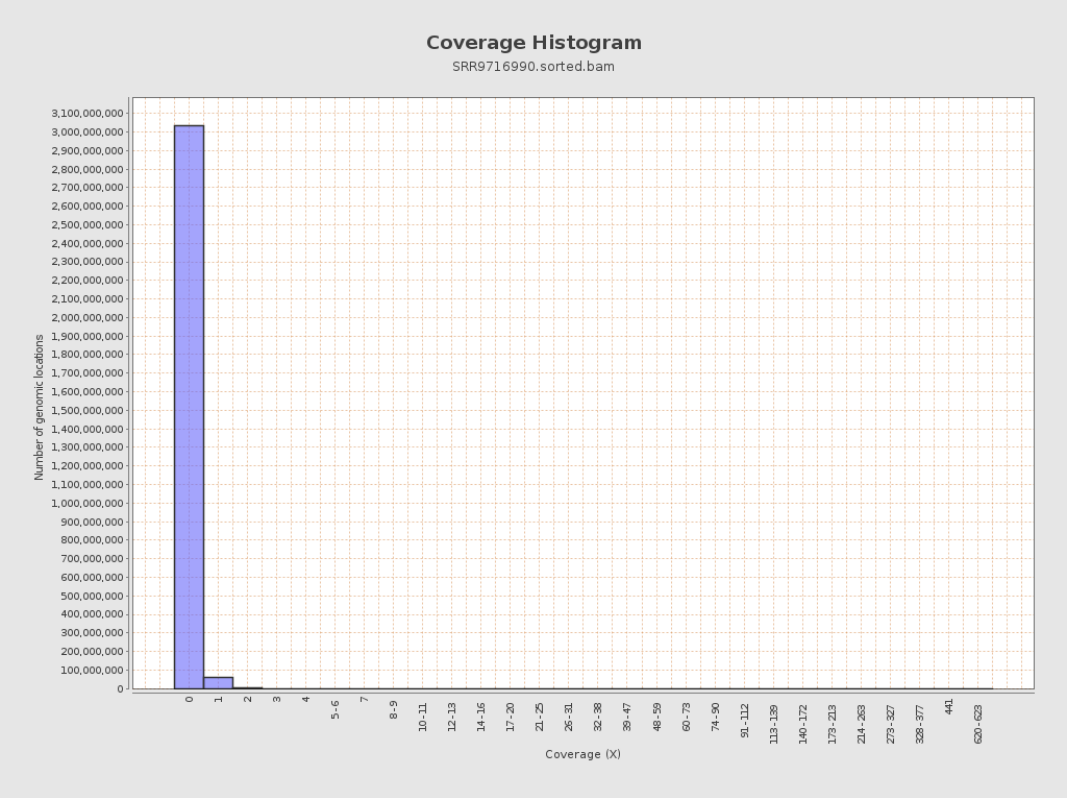
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5541681	0.0222	0.3433
chr2	243199373	5646637	0.0232	0.3282
chr3	198022430	4443672	0.0224	0.1613
chr4	191154276	4308408	0.0225	0.1871
chr5	180915260	3969851	0.0219	0.1562
chr6	171115067	3872441	0.0226	0.1811
chr7	159138663	3833781	0.0241	0.2876

chr8	146364022	3359242	0.023	0.213
chr9	141213431	2859570	0.0202	0.1923
chr10	135534747	3439407	0.0254	0.3062
chr11	135006516	3042068	0.0225	0.1931
chr12	133851895	3147010	0.0235	0.1635
chr13	115169878	2045308	0.0178	0.1398
chr14	107349540	2099453	0.0196	0.1596
chr15	102531392	2027456	0.0198	0.1534
chr16	90354753	2175184	0.0241	0.183
chr17	81195210	2131981	0.0263	0.1796
chr18	78077248	1725241	0.0221	0.3017
chr19	59128983	1738786	0.0294	0.3001
chr20	63025520	1546137	0.0245	0.1744
chr21	48129895	879225	0.0183	0.1664
chr22	51304566	889536	0.0173	0.1399
chrMT	16571	19646	1.1856	1.3444
chrX	155270560	3833236	0.0247	0.1839
chrY	59373566	266606	0.0045	0.1805

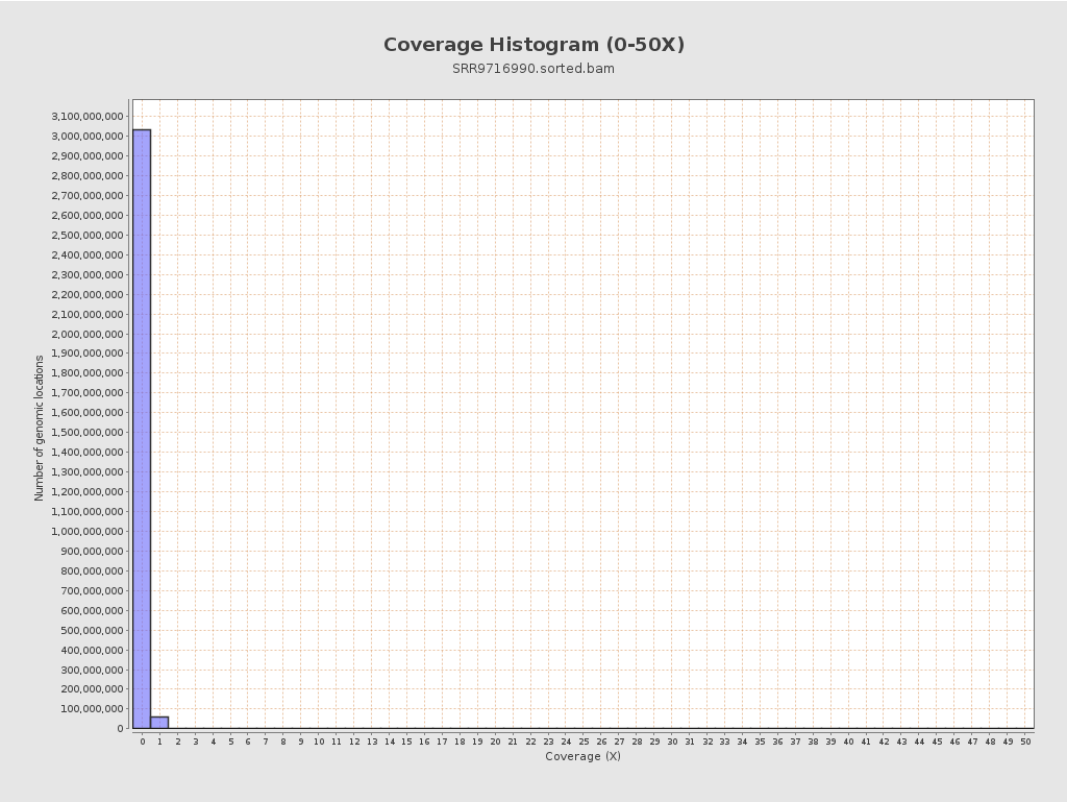
3. Results : Coverage across reference



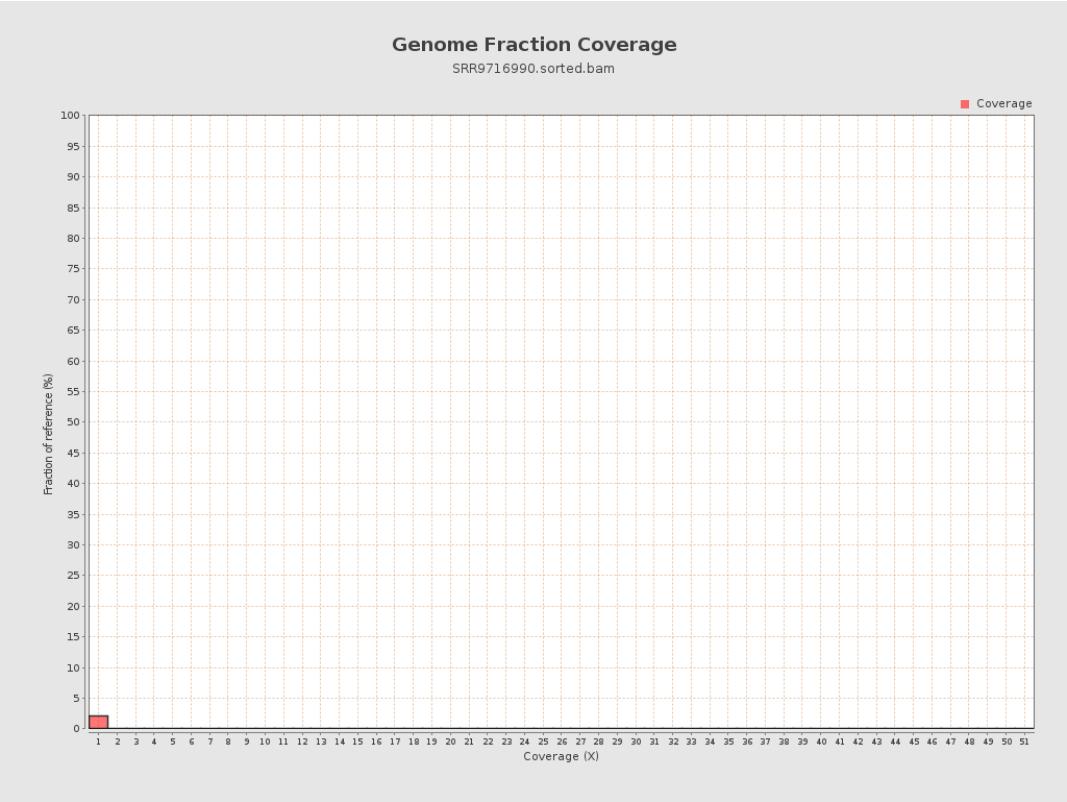
4. Results : Coverage Histogram



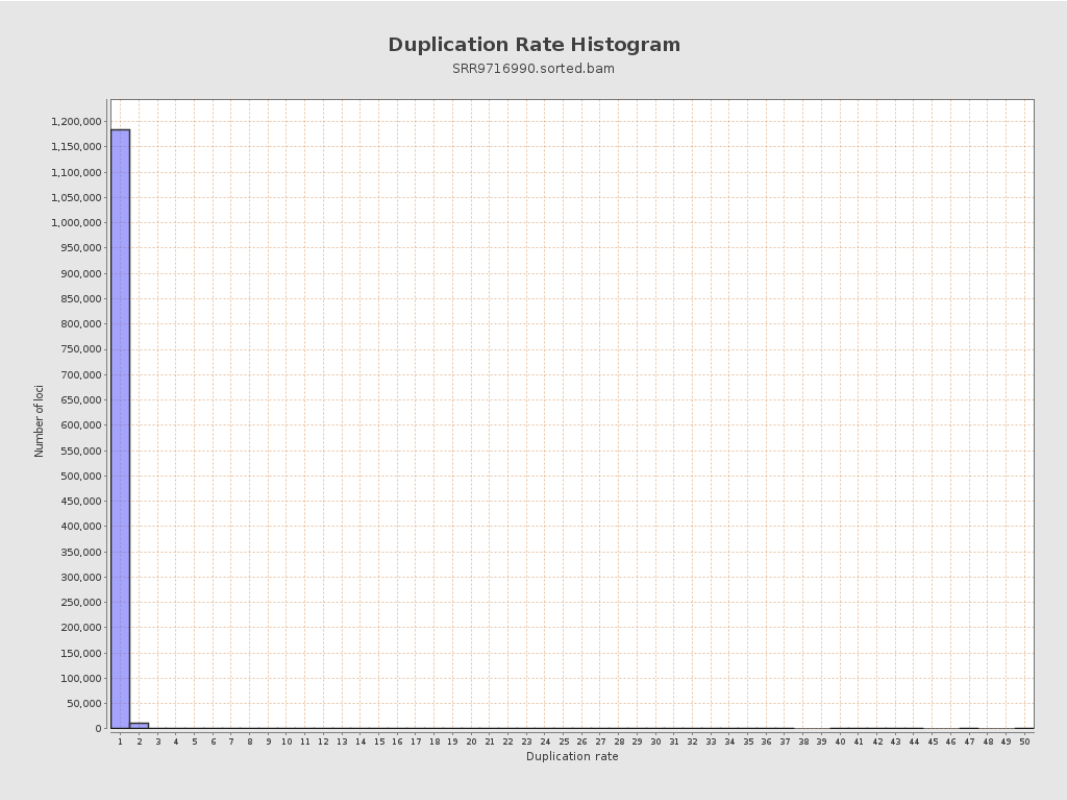
5. Results : Coverage Histogram (0-50X)



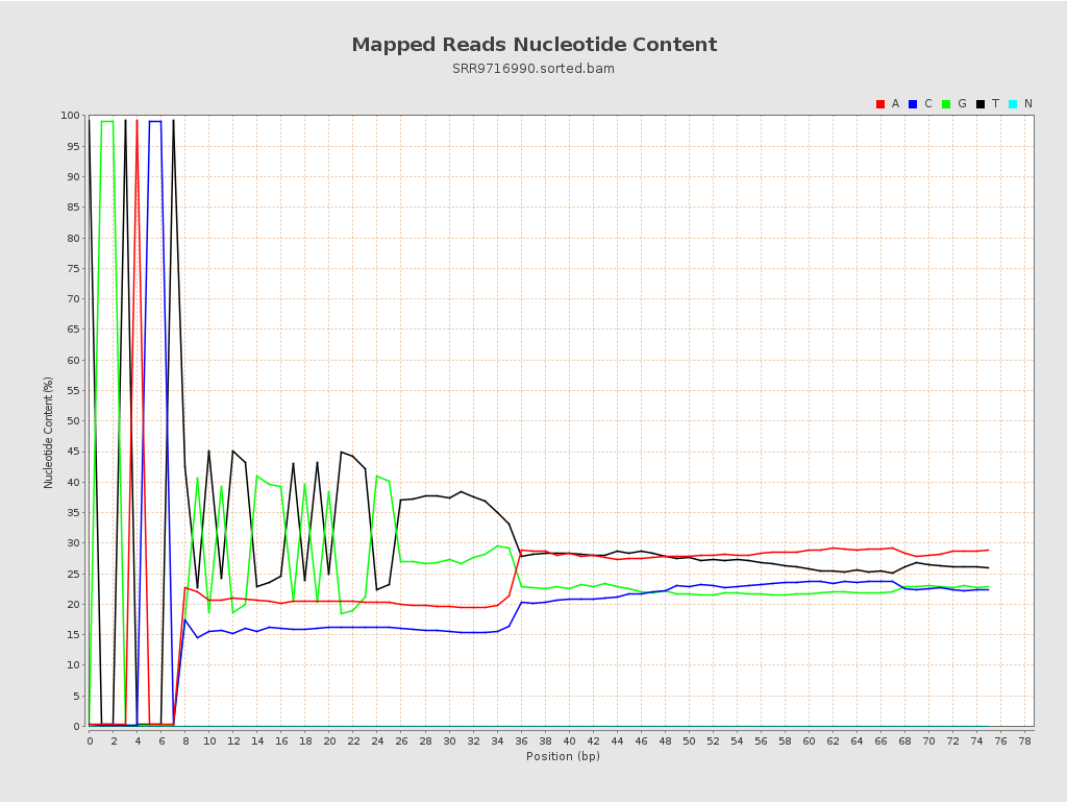
6. Results : Genome Fraction Coverage



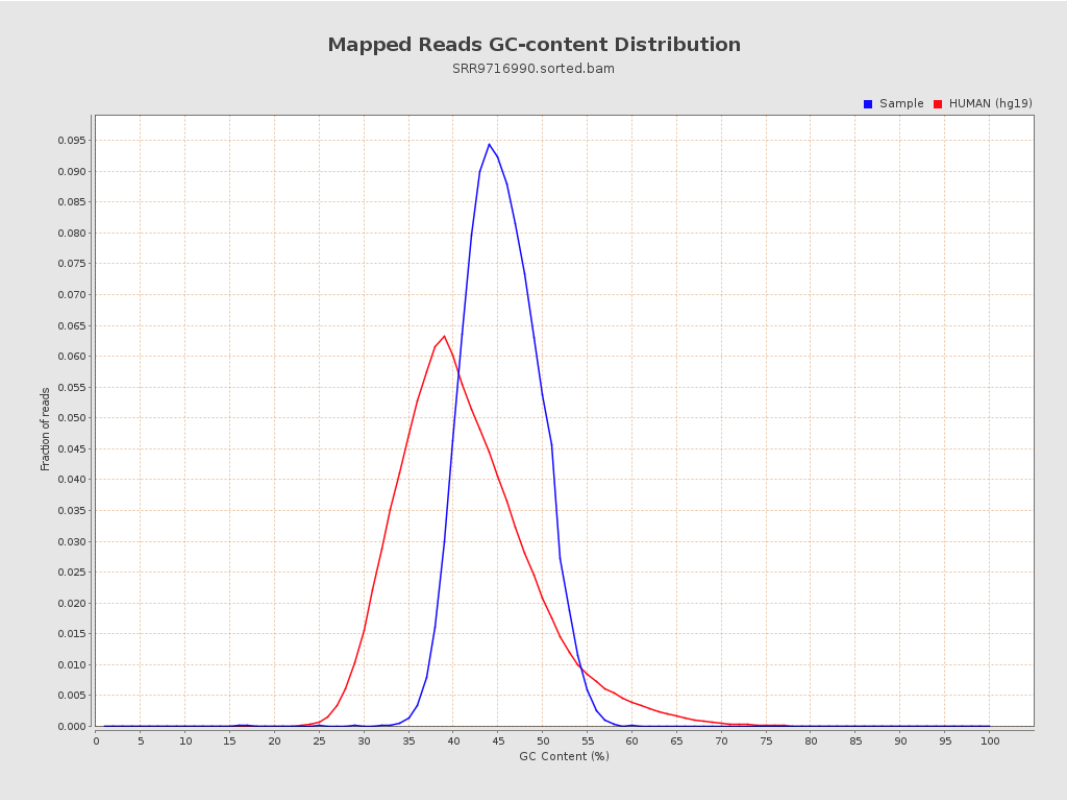
7. Results : Duplication Rate Histogram



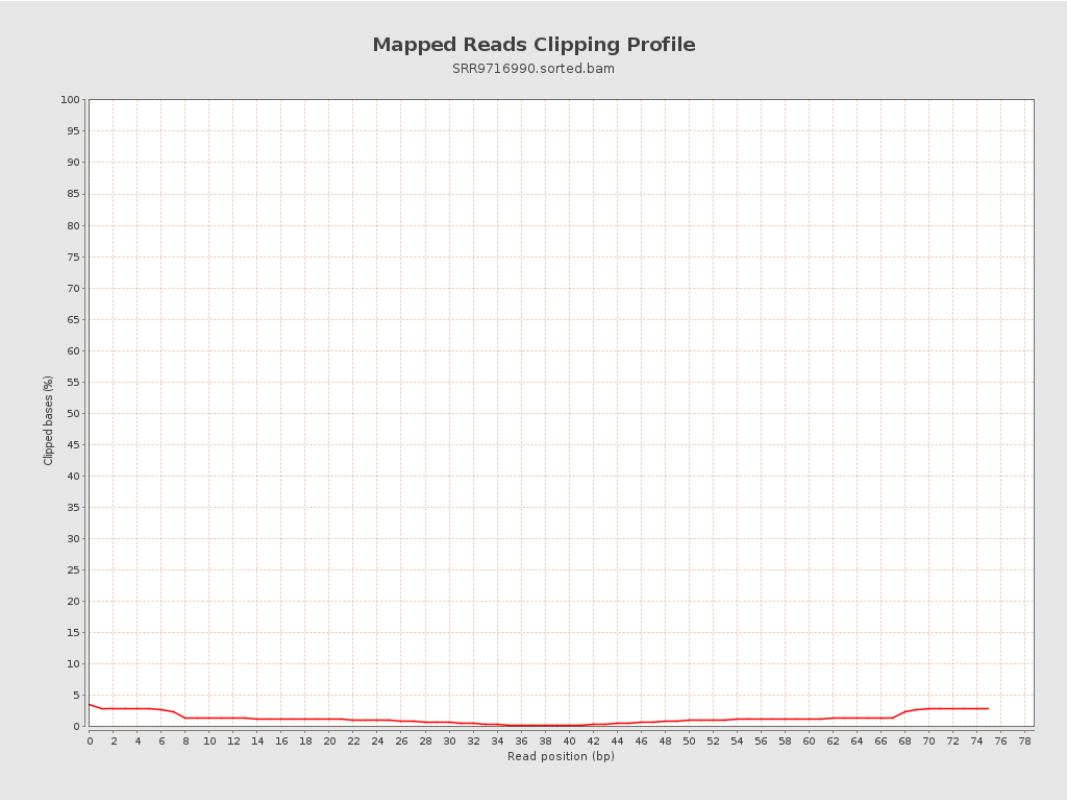
8. Results : Mapped Reads Nucleotide Content



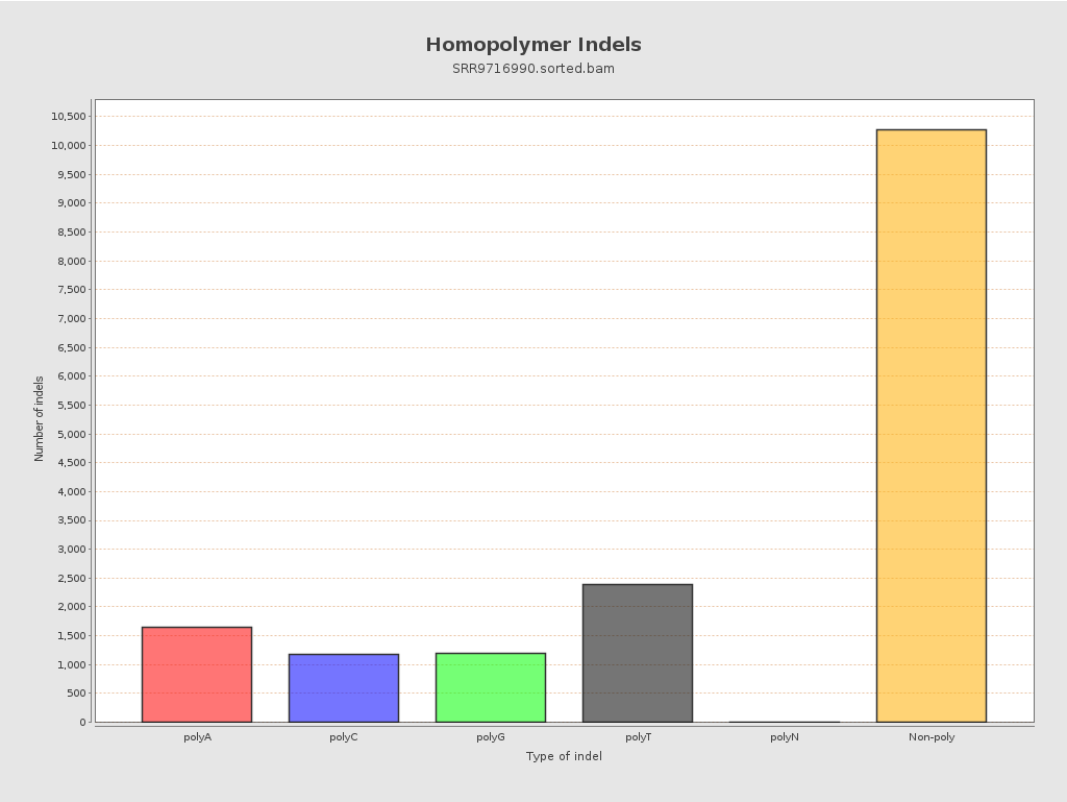
9. Results : Mapped Reads GC-content Distribution



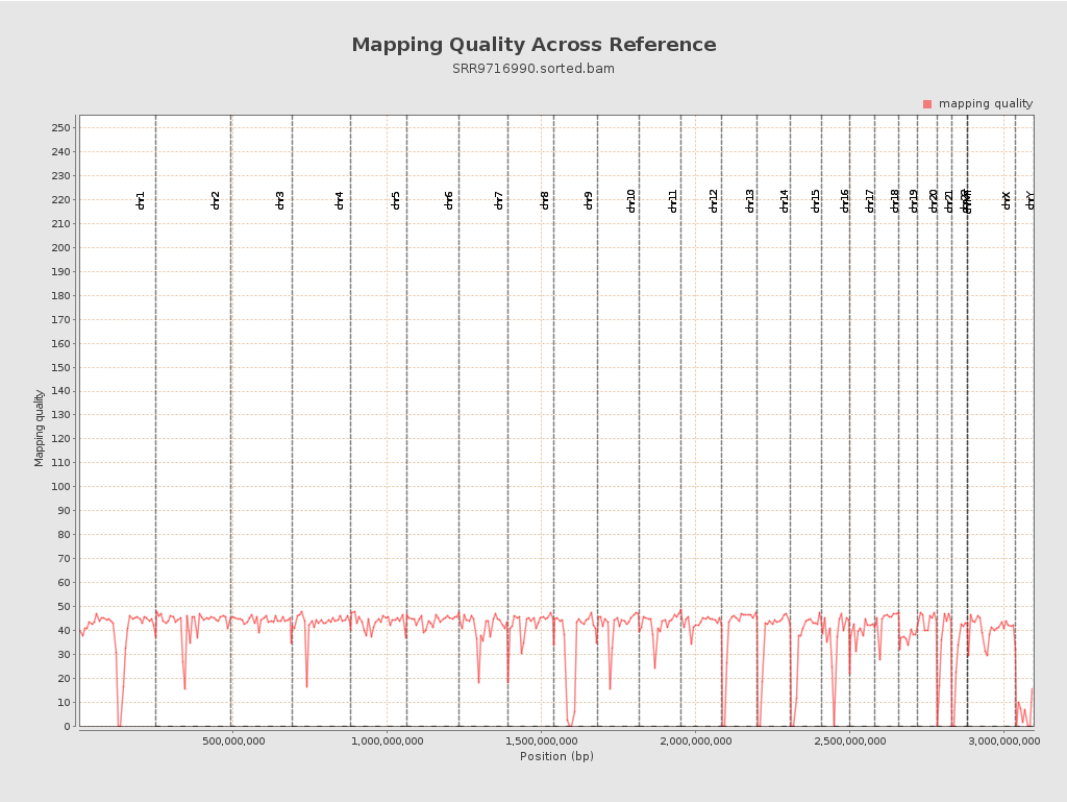
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram