Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:22:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716630.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_SRR9716630 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716630.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:22:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716630.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	596,201
Mapped reads	533,036 / 89.41%
Unmapped reads	63,165 / 10.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,687 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	9,576 / 1.61%
Duplication rate	1.44%
Clipped reads	534,019 / 89.57%

2.2. ACGT Content

Number/percentage of A's	8,271,174 / 26.19%
Number/percentage of C's	6,100,091 / 19.31%
Number/percentage of T's	9,401,533 / 29.77%
Number/percentage of G's	7,810,085 / 24.73%
Number/percentage of N's	888 / 0%
GC Percentage	44.04%

2.3. Coverage

Mean	0.0102

Standard Deviation	0.119

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

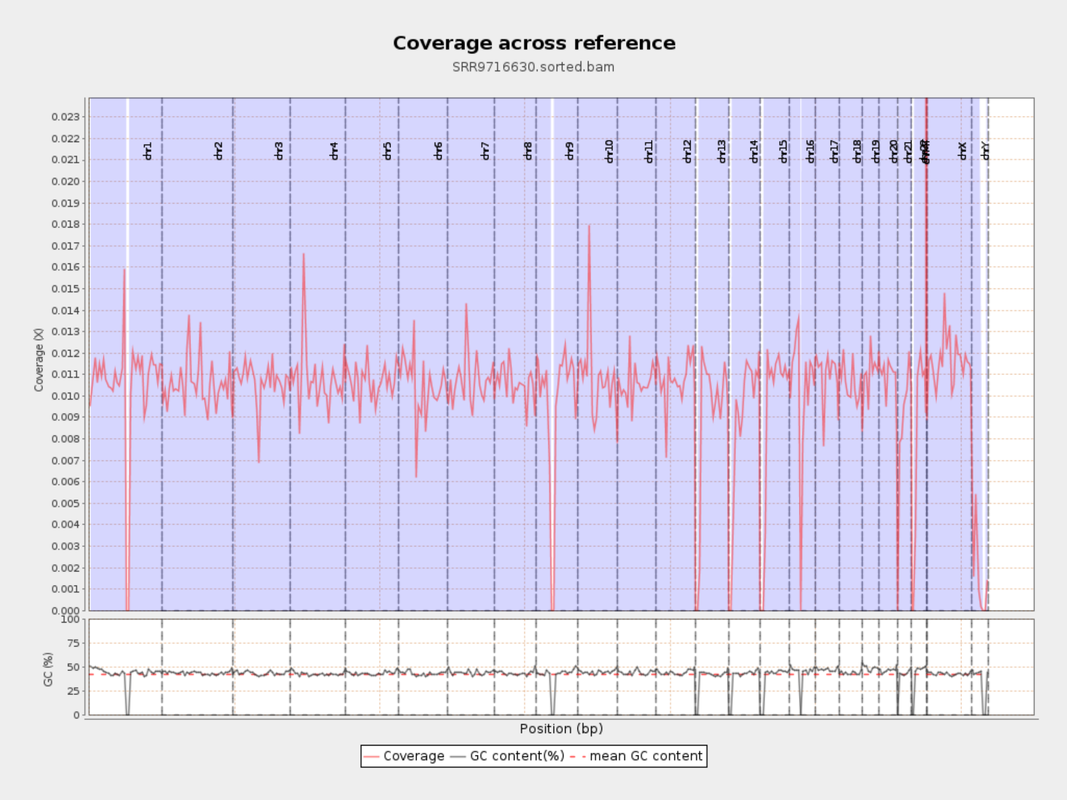
General error rate	0.51%
Mismatches	156,073
Insertions	2,434
Mapped reads with at least one insertion	0.45%
Deletions	6,021
Mapped reads with at least one deletion	1.12%
Homopolymer indels	40.76%

2.6. Chromosome stats

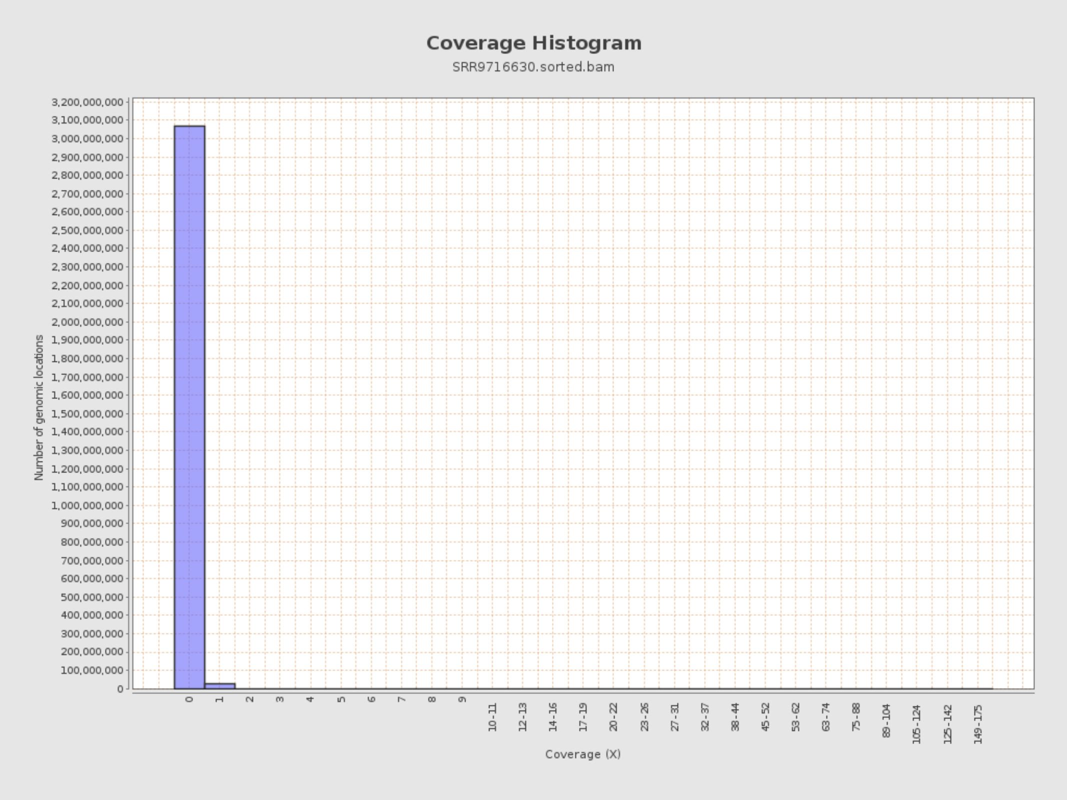
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2597435	0.0104	0.1667
chr2	243199373	2573305	0.0106	0.1303
chr3	198022430	2109444	0.0107	0.107
chr4	191154276	2063137	0.0108	0.1115
chr5	180915260	1937290	0.0107	0.1075
chr6	171115067	1797529	0.0105	0.1137
chr7	159138663	1711420	0.0108	0.1294

chr8	146364022	1547907	0.0106	0.1204
chr9	141213431	1337859	0.0095	0.1088
chr10	135534747	1477058	0.0109	0.1236
chr11	135006516	1423344	0.0105	0.1151
chr12	133851895	1447287	0.0108	0.1079
chr13	115169878	1013880	0.0088	0.0973
chr14	107349540	915773	0.0085	0.0981
chr15	102531392	932356	0.0091	0.0993
chr16	90354753	925807	0.0102	0.1077
chr17	81195210	884360	0.0109	0.1102
chr18	78077248	832356	0.0107	0.1537
chr19	59128983	653508	0.0111	0.1336
chr20	63025520	688686	0.0109	0.1089
chr21	48129895	422226	0.0088	0.1019
chr22	51304566	395084	0.0077	0.0913
chrMT	16571	4757	0.2871	0.5824
chrX	155270560	1805283	0.0116	0.1145
chrY	59373566	96672	0.0016	0.0553

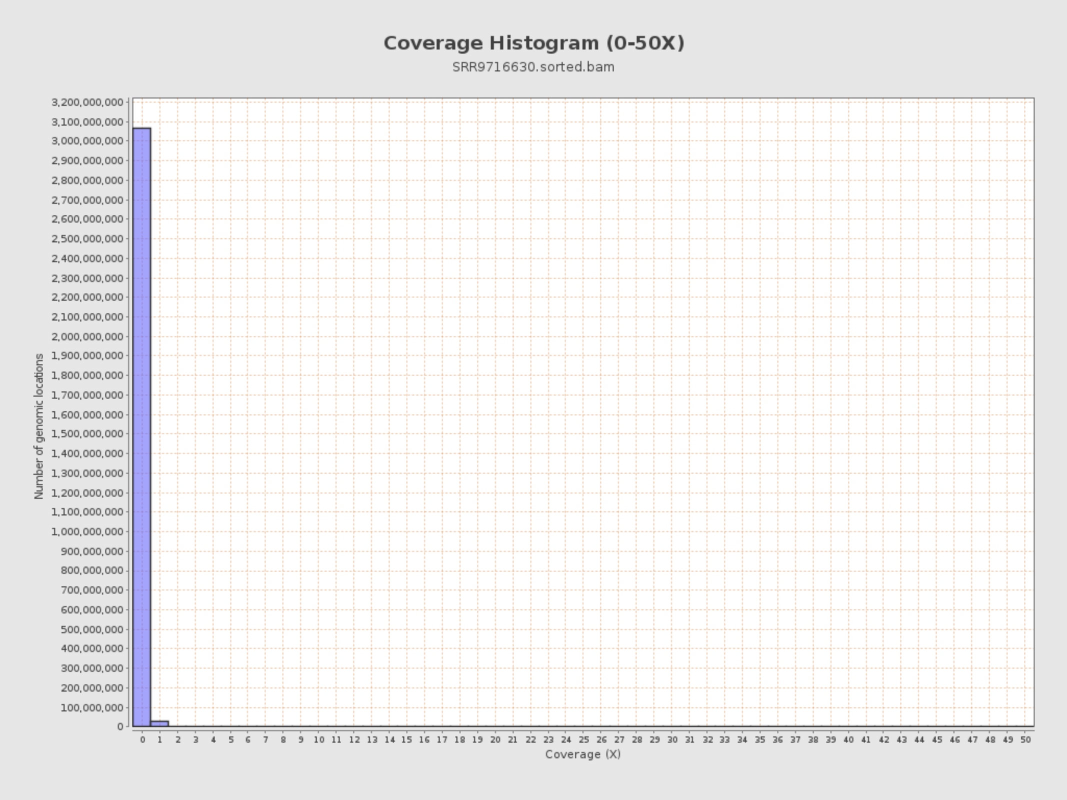
3. Results : Coverage across reference



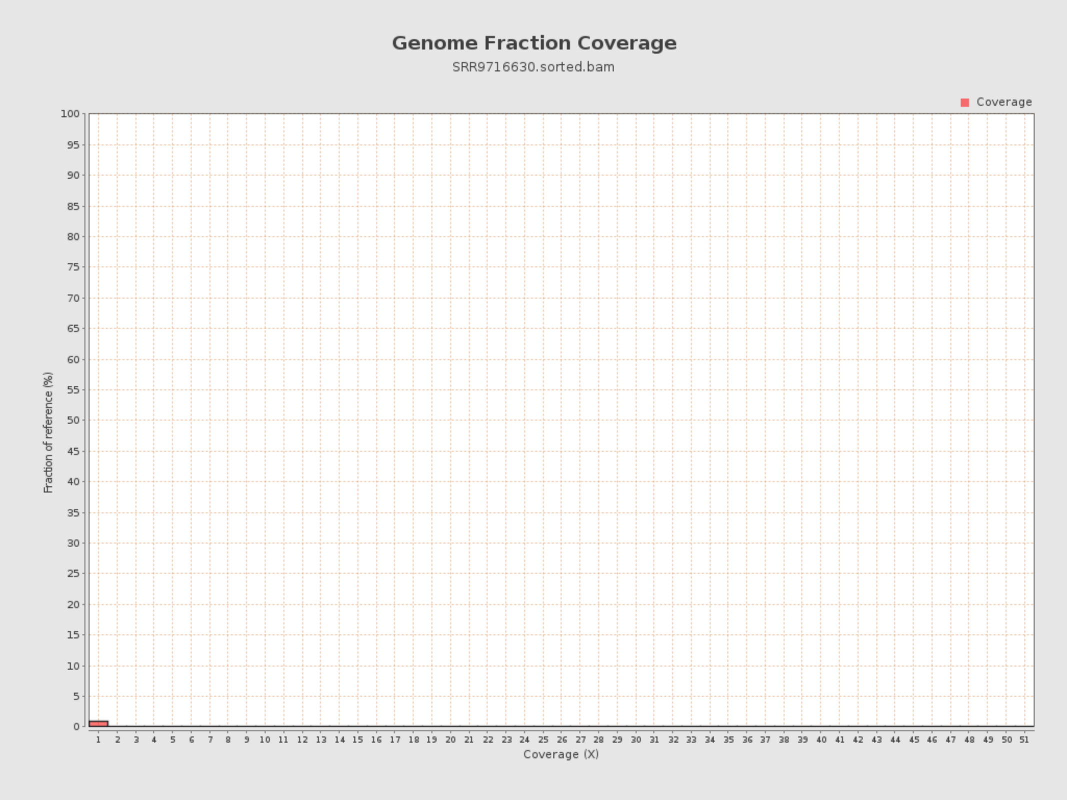
4. Results : Coverage Histogram



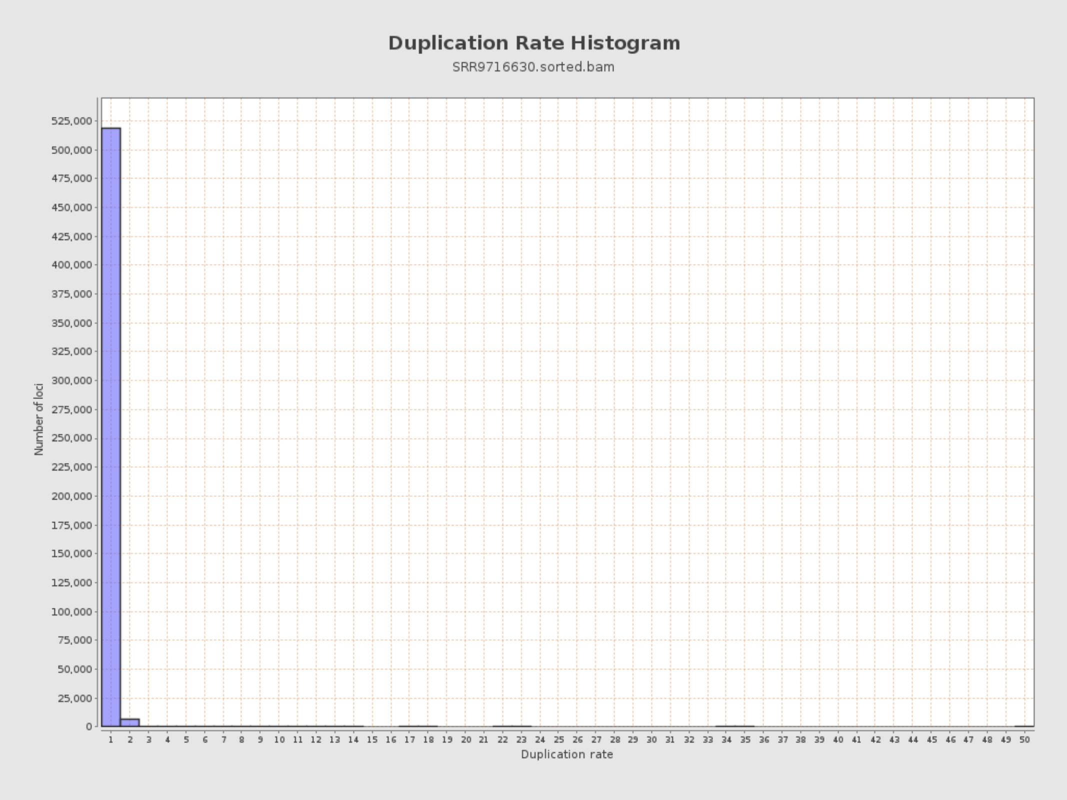
5. Results : Coverage Histogram (0-50X)



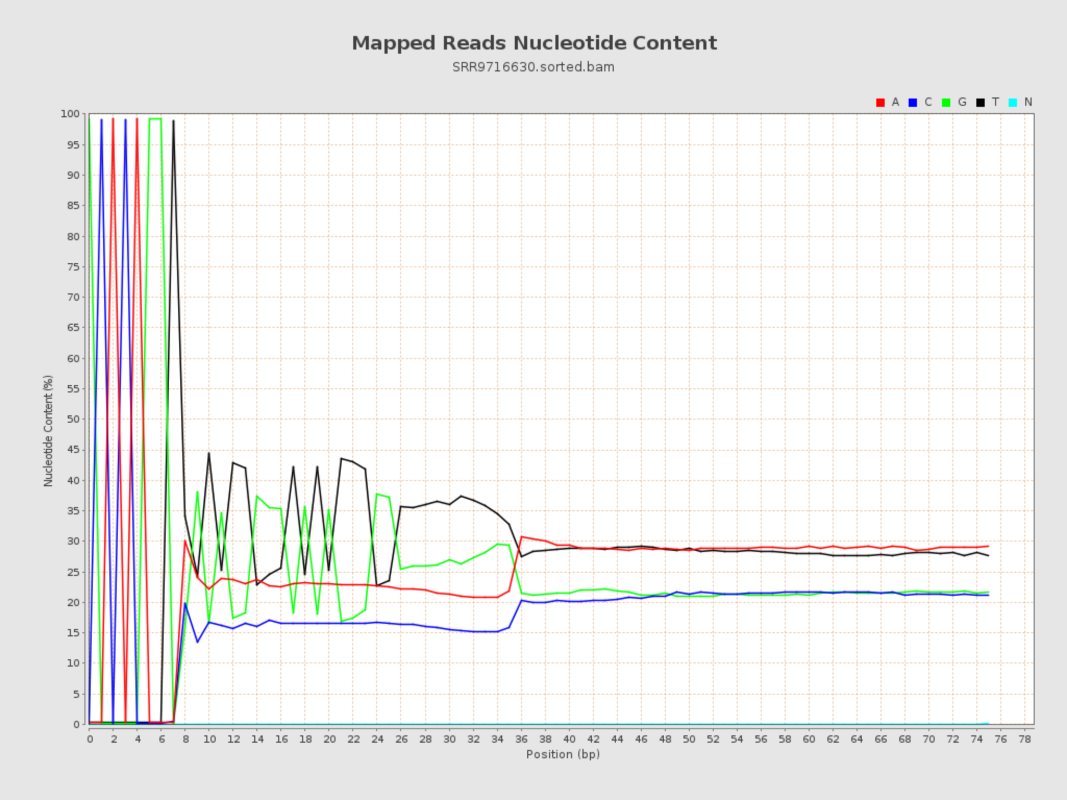
6. Results : Genome Fraction Coverage



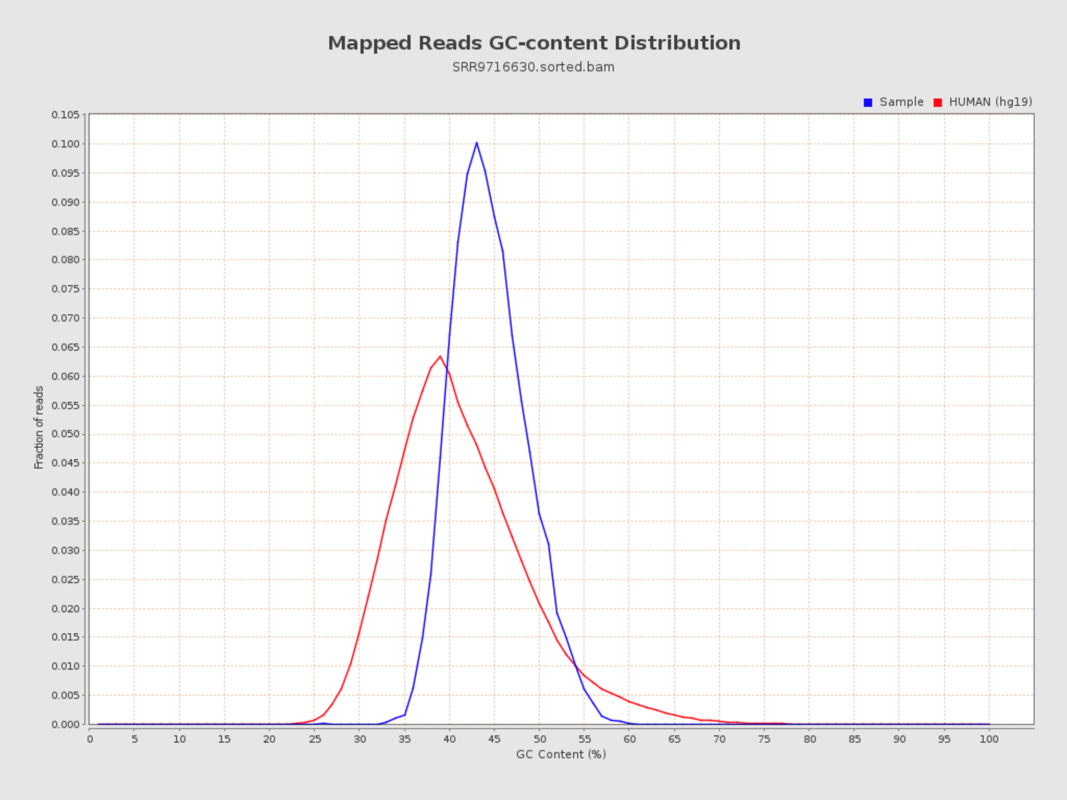
7. Results : Duplication Rate Histogram



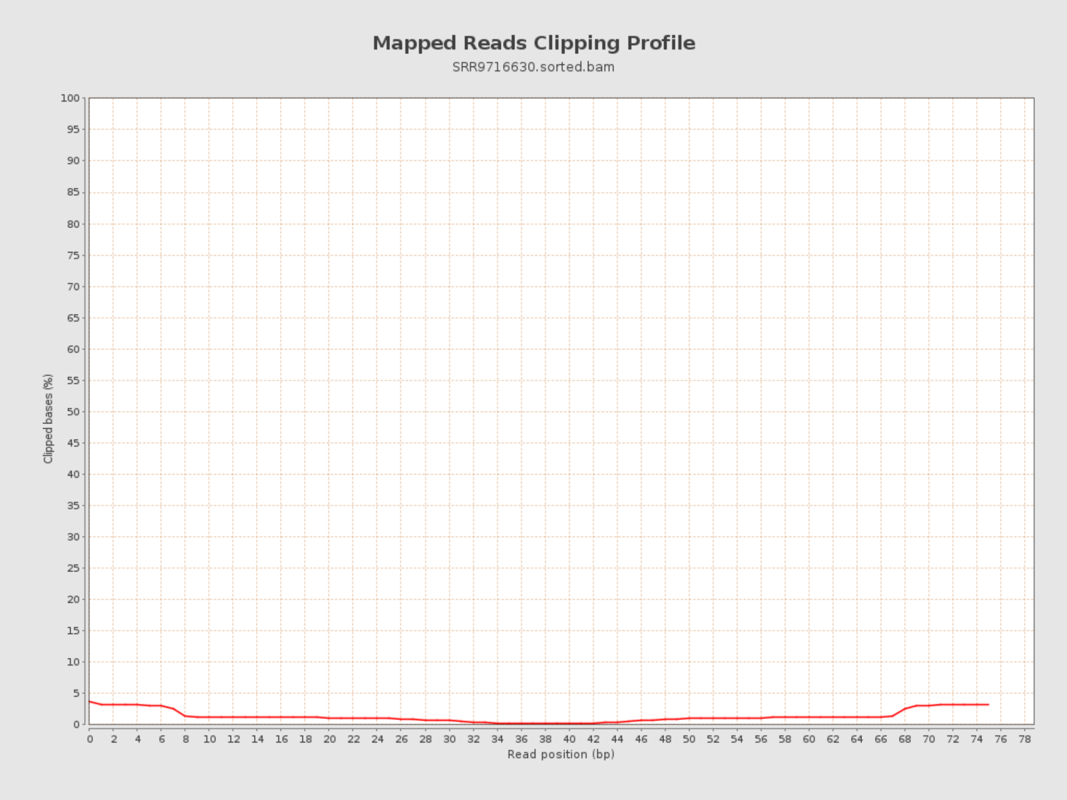
8. Results : Mapped Reads Nucleotide Content



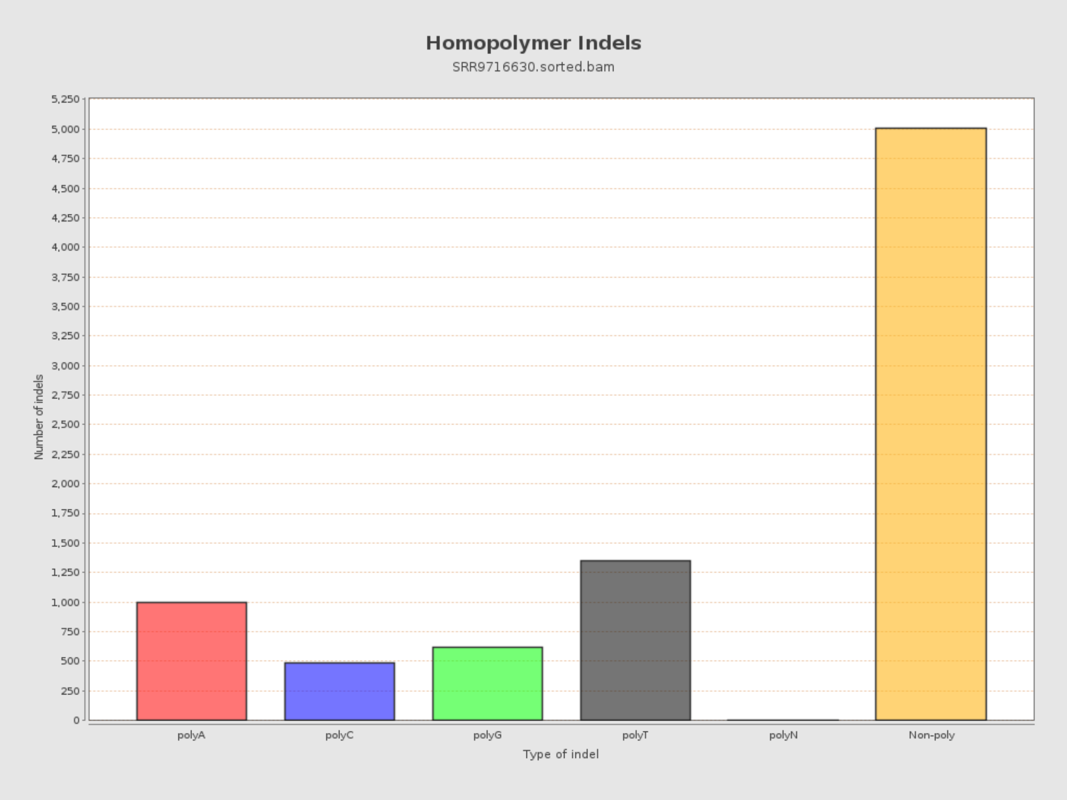
9. Results : Mapped Reads GC-content Distribution



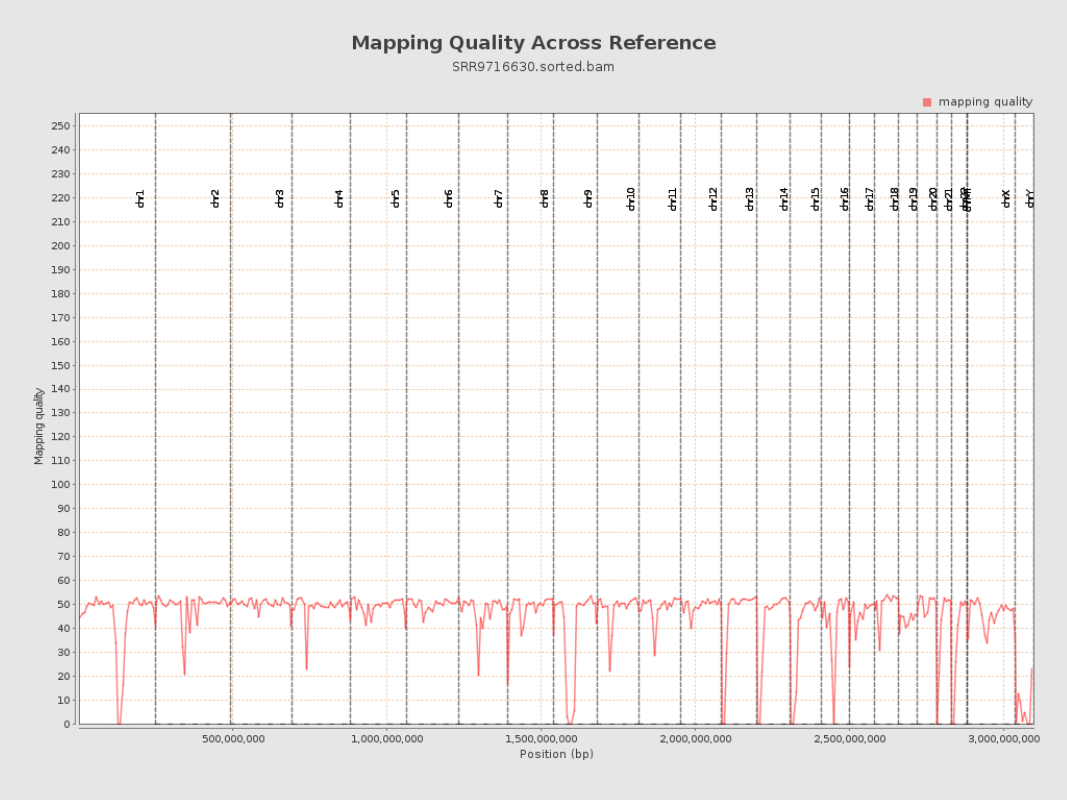
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram