Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:27:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716960.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_SRR9716960 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716960.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:27:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716960.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	735,262
Mapped reads	593,795 / 80.76%
Unmapped reads	141,467 / 19.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,336 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	10,167 / 1.38%
Duplication rate	1.2%
Clipped reads	594,454 / 80.85%

2.2. ACGT Content

Number/percentage of A's	8,588,142 / 25.6%
Number/percentage of C's	6,278,707 / 18.71%
Number/percentage of T's	10,811,228 / 32.22%
Number/percentage of G's	7,872,535 / 23.46%
Number/percentage of N's	508 / 0%
GC Percentage	42.18%

2.3. Coverage

Mean	0.0108

Standard Deviation	0.1335

2.4. Mapping Quality

Mean Mapping Quality	42.93

2.5. Mismatches and indels

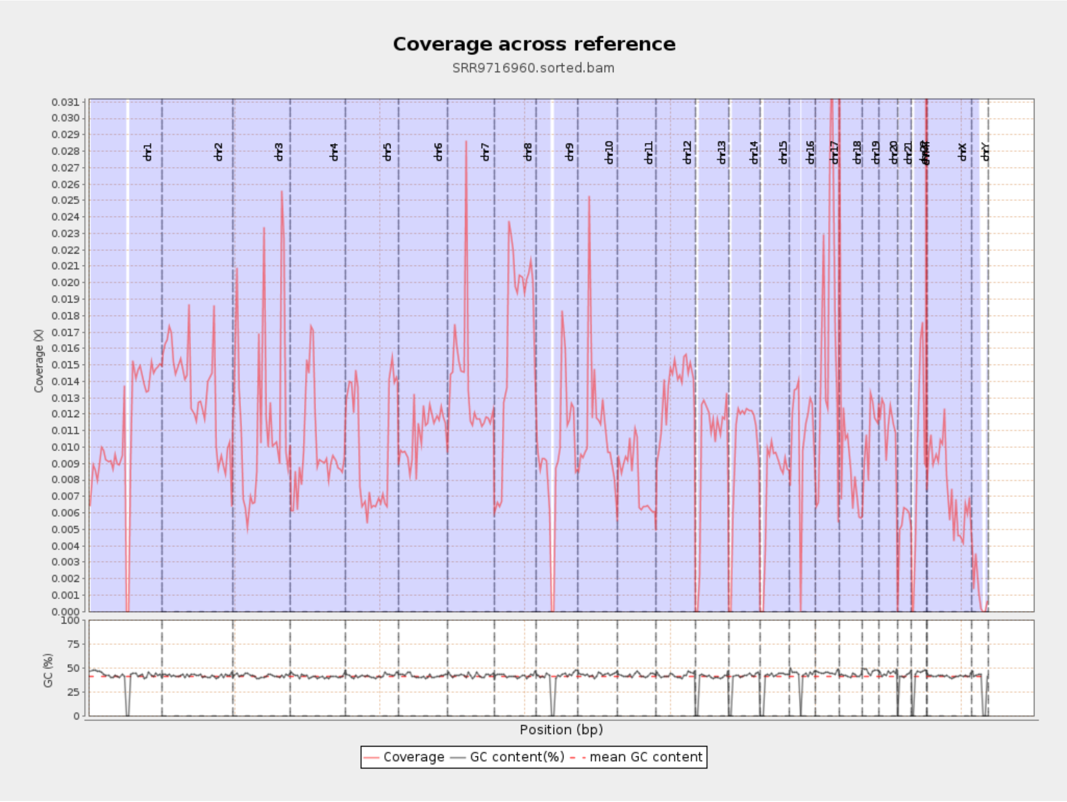
General error rate	0.53%
Mismatches	171,379
Insertions	2,744
Mapped reads with at least one insertion	0.46%
Deletions	6,802
Mapped reads with at least one deletion	1.14%
Homopolymer indels	40.26%

2.6. Chromosome stats

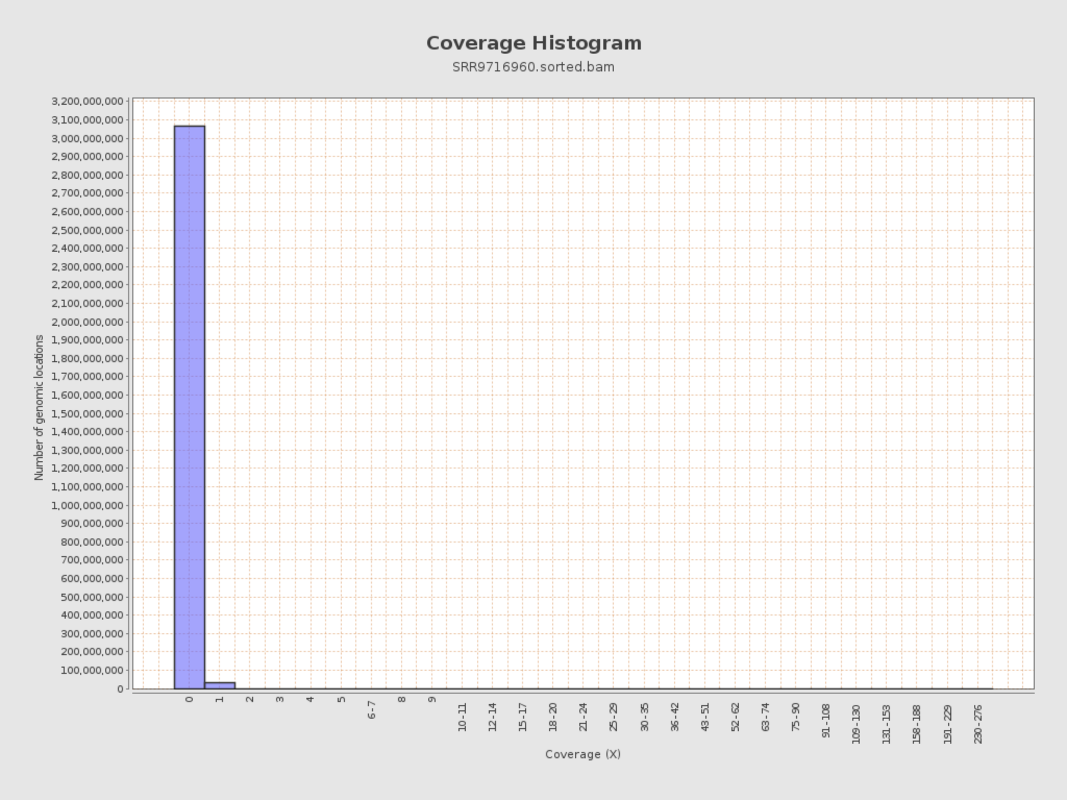
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2695872	0.0108	0.1504
chr2	243199373	3235807	0.0133	0.1662
chr3	198022430	2343362	0.0118	0.1144
chr4	191154276	1886578	0.0099	0.1042
chr5	180915260	1781638	0.0098	0.1025
chr6	171115067	1857818	0.0109	0.114
chr7	159138663	2198009	0.0138	0.2678

chr8	146364022	2439714	0.0167	0.148
chr9	141213431	1340239	0.0095	0.1089
chr10	135534747	1530389	0.0113	0.1454
chr11	135006516	1074835	0.008	0.1028
chr12	133851895	1814965	0.0136	0.1221
chr13	115169878	1135167	0.0099	0.1023
chr14	107349540	1060898	0.0099	0.1042
chr15	102531392	775903	0.0076	0.0905
chr16	90354753	981608	0.0109	0.1113
chr17	81195210	1326915	0.0163	0.1348
chr18	78077248	747464	0.0096	0.1308
chr19	59128983	639252	0.0108	0.1408
chr20	63025520	712413	0.0113	0.1106
chr21	48129895	247612	0.0051	0.0754
chr22	51304566	461173	0.009	0.0982
chrMT	16571	15318	0.9244	1.0828
chrX	155270560	1188043	0.0077	0.0974
chrY	59373566	70719	0.0012	0.0415

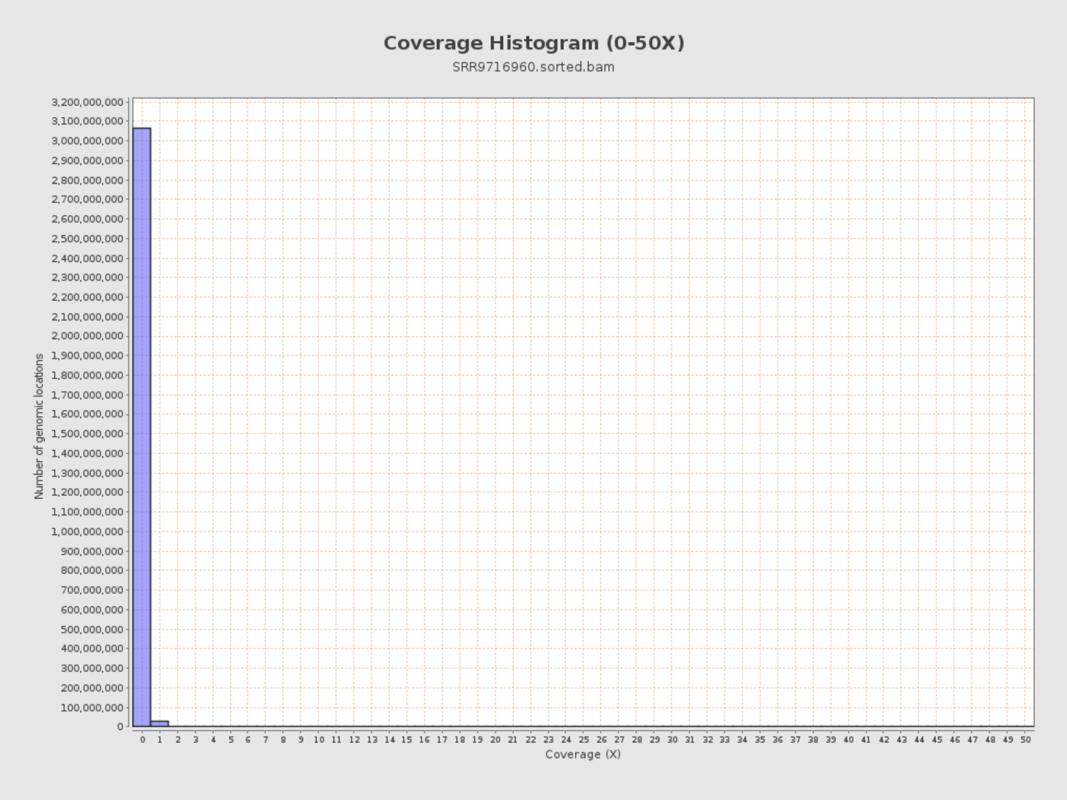
3. Results : Coverage across reference



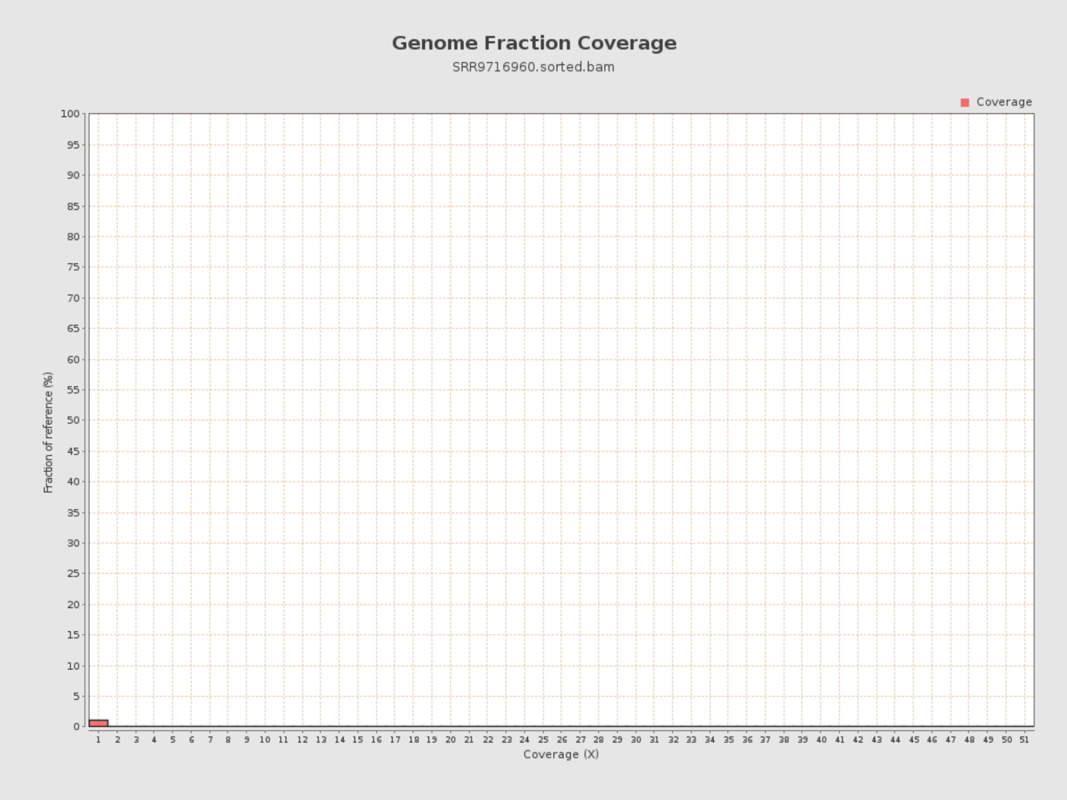
4. Results : Coverage Histogram



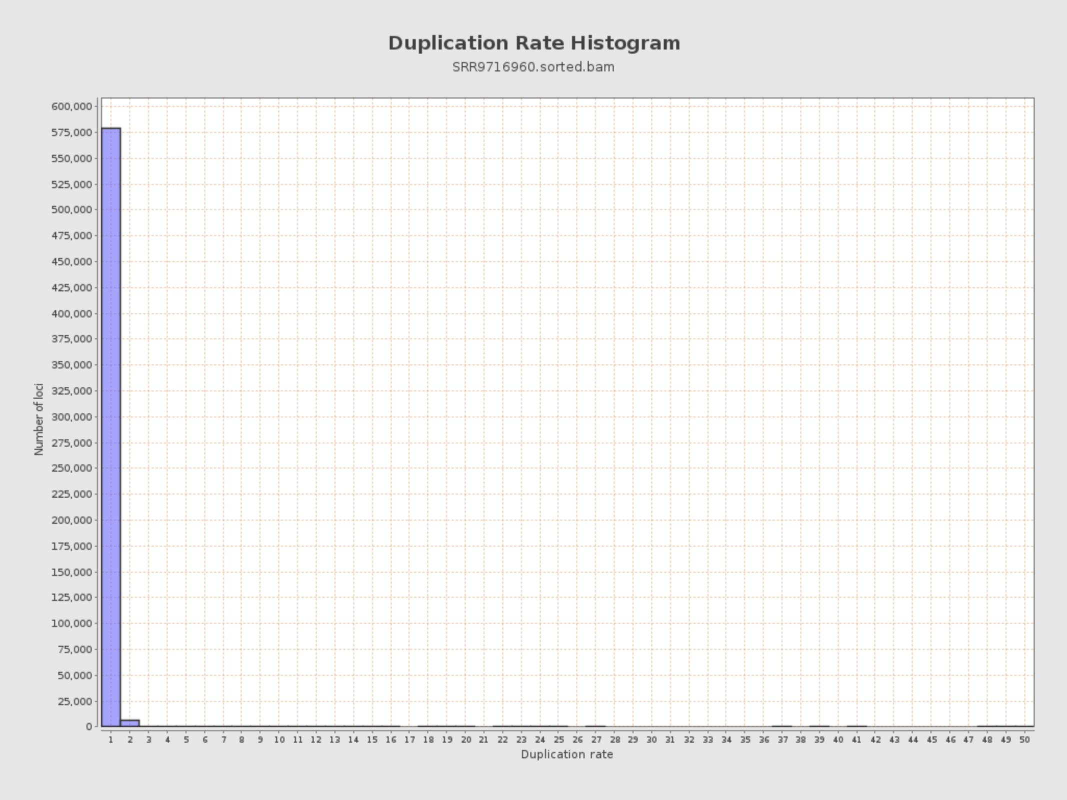
5. Results : Coverage Histogram (0-50X)



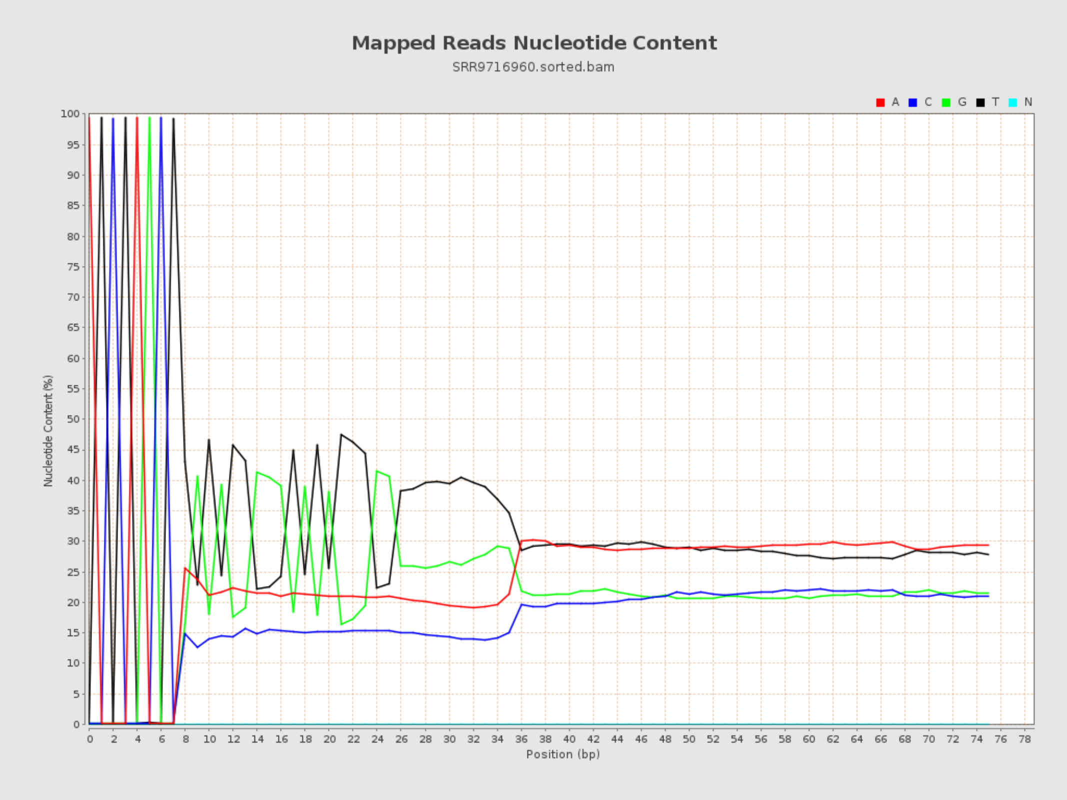
6. Results : Genome Fraction Coverage



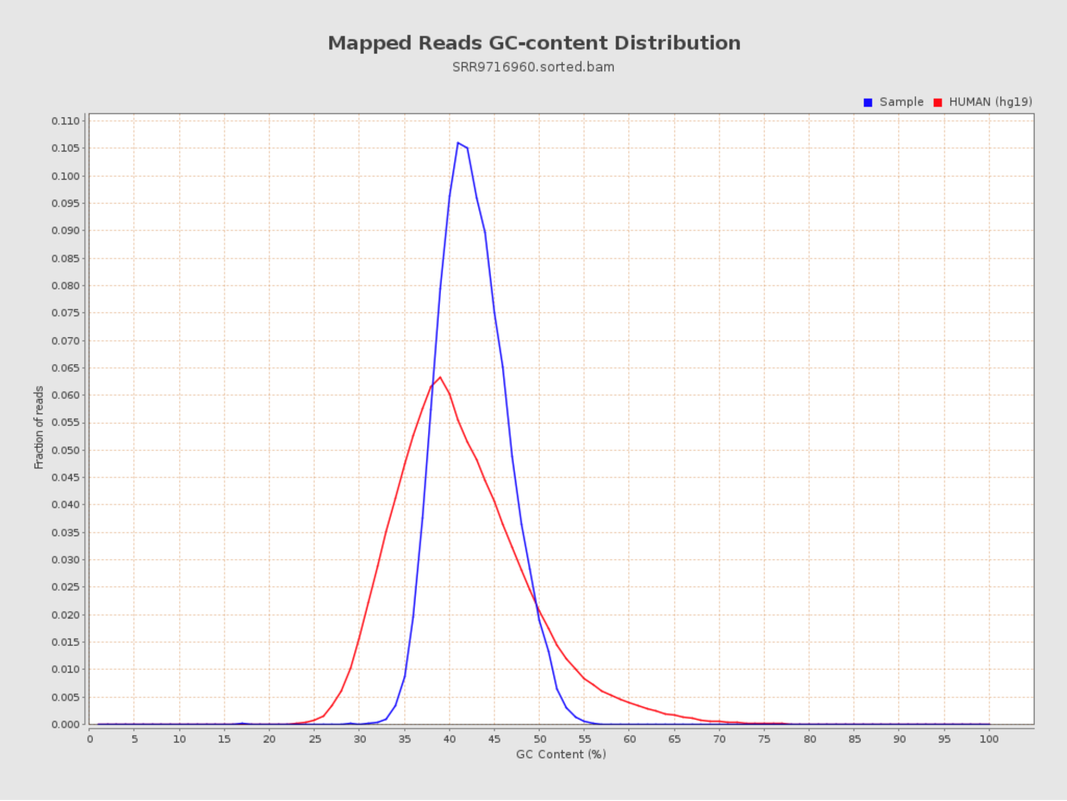
7. Results : Duplication Rate Histogram



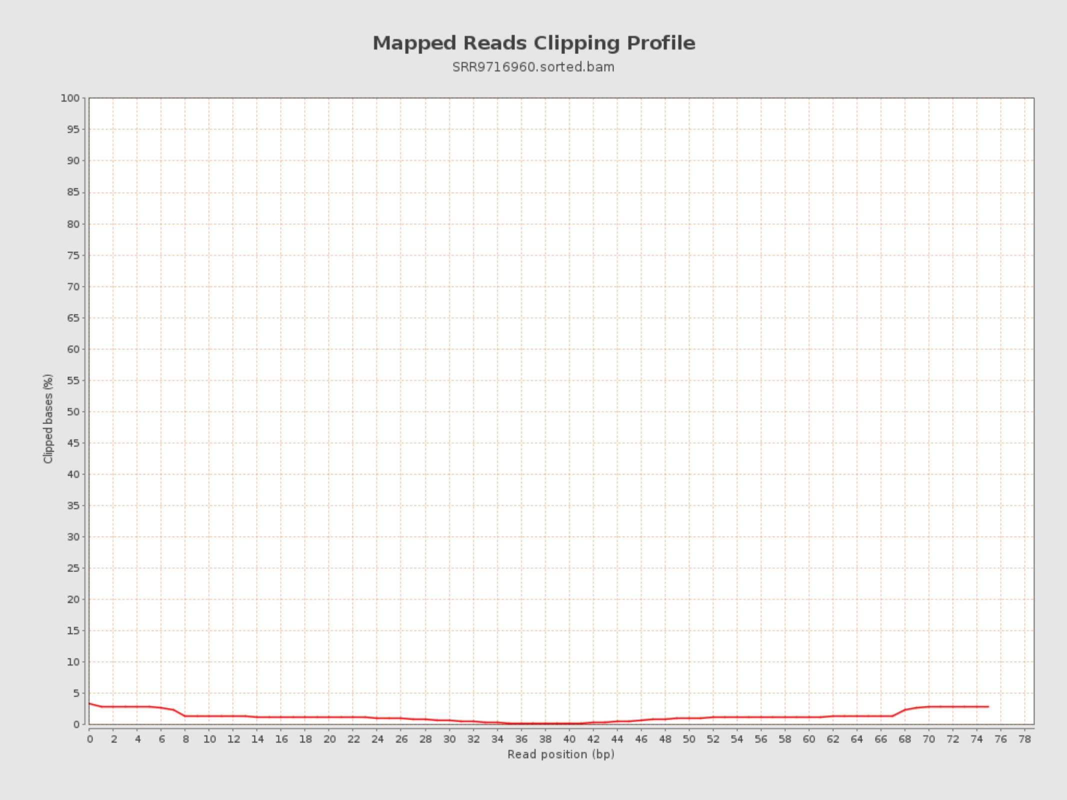
8. Results : Mapped Reads Nucleotide Content



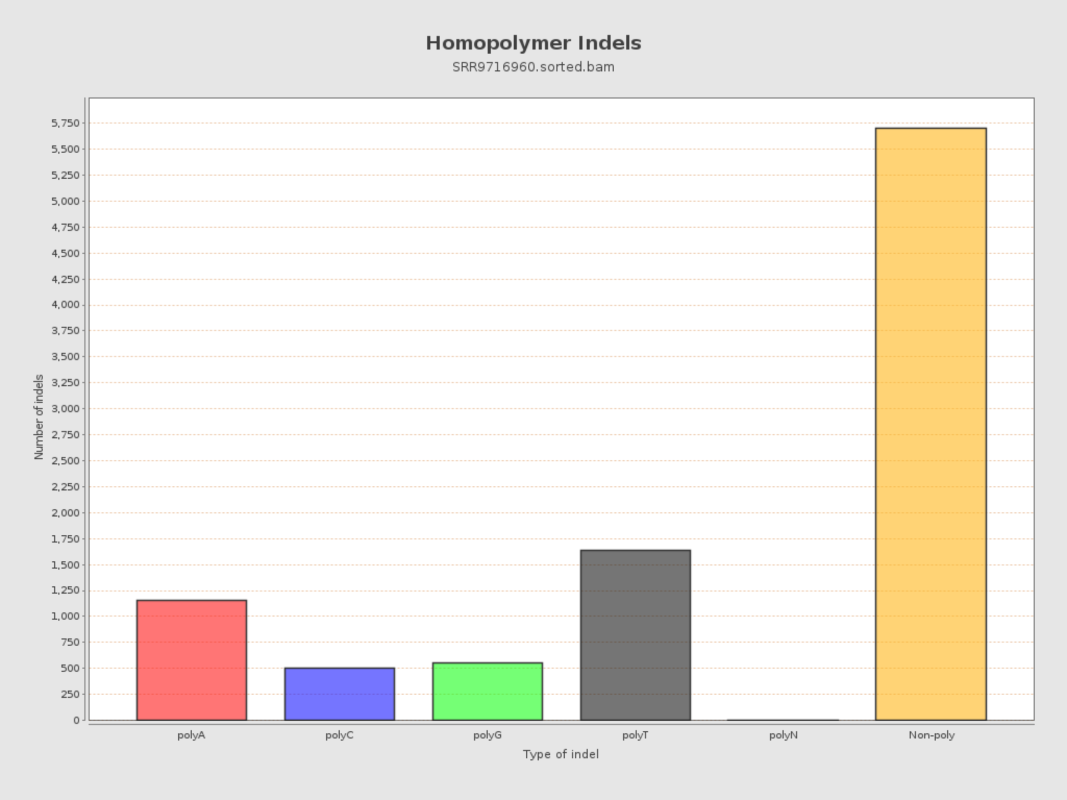
9. Results : Mapped Reads GC-content Distribution



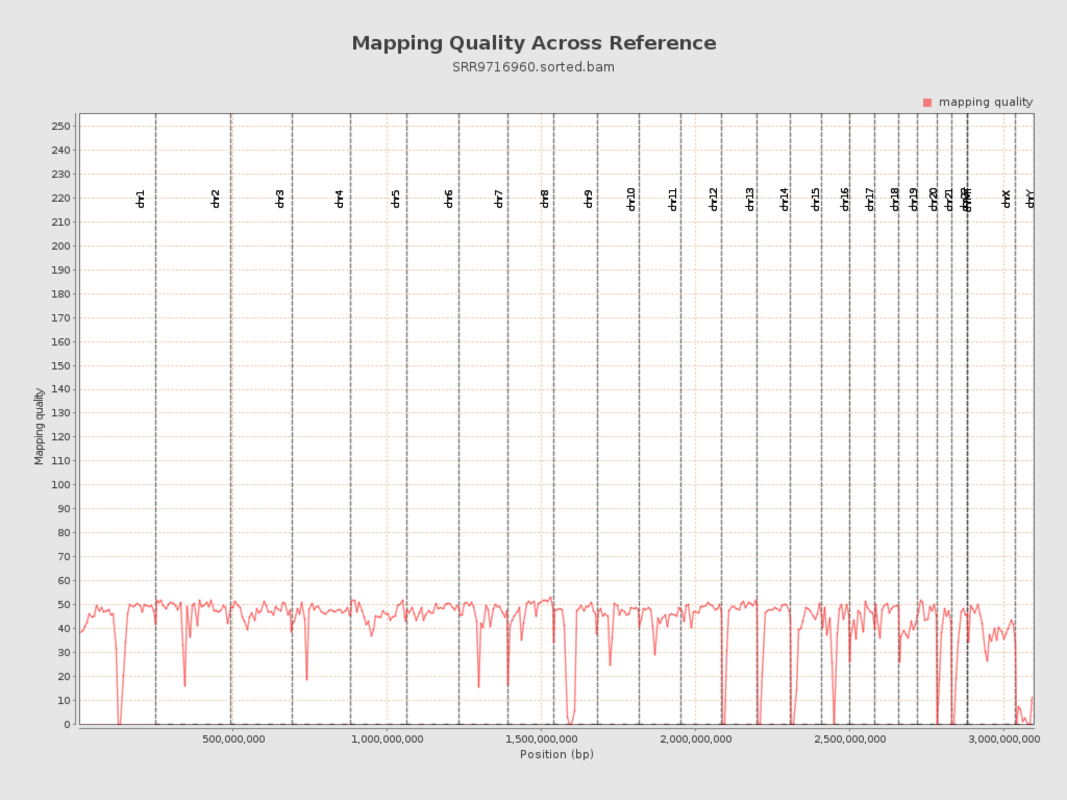
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram