Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:42:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716471.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_SRR9716471 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716471.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:42:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716471.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	524,490
Mapped reads	477,458 / 91.03%
Unmapped reads	47,032 / 8.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,502 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	8,155 / 1.55%
Duplication rate	1.17%
Clipped reads	478,346 / 91.2%

2.2. ACGT Content

Number/percentage of A's	7,005,525 / 25.1%
Number/percentage of C's	5,220,259 / 18.7%
Number/percentage of T's	8,504,981 / 30.47%
Number/percentage of G's	7,183,595 / 25.73%
Number/percentage of N's	548 / 0%
GC Percentage	44.43%

2.3. Coverage

Mean	0.009

Standard Deviation	0.1177

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

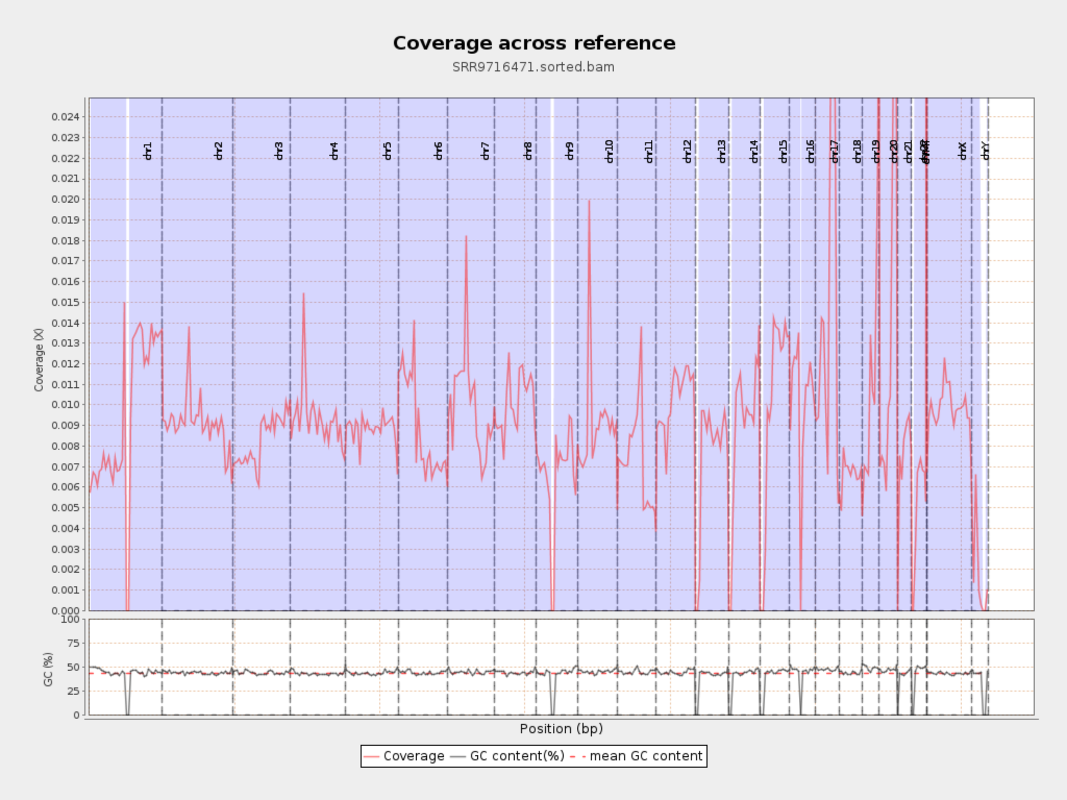
General error rate	0.56%
Mismatches	151,957
Insertions	1,739
Mapped reads with at least one insertion	0.36%
Deletions	5,215
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.16%

2.6. Chromosome stats

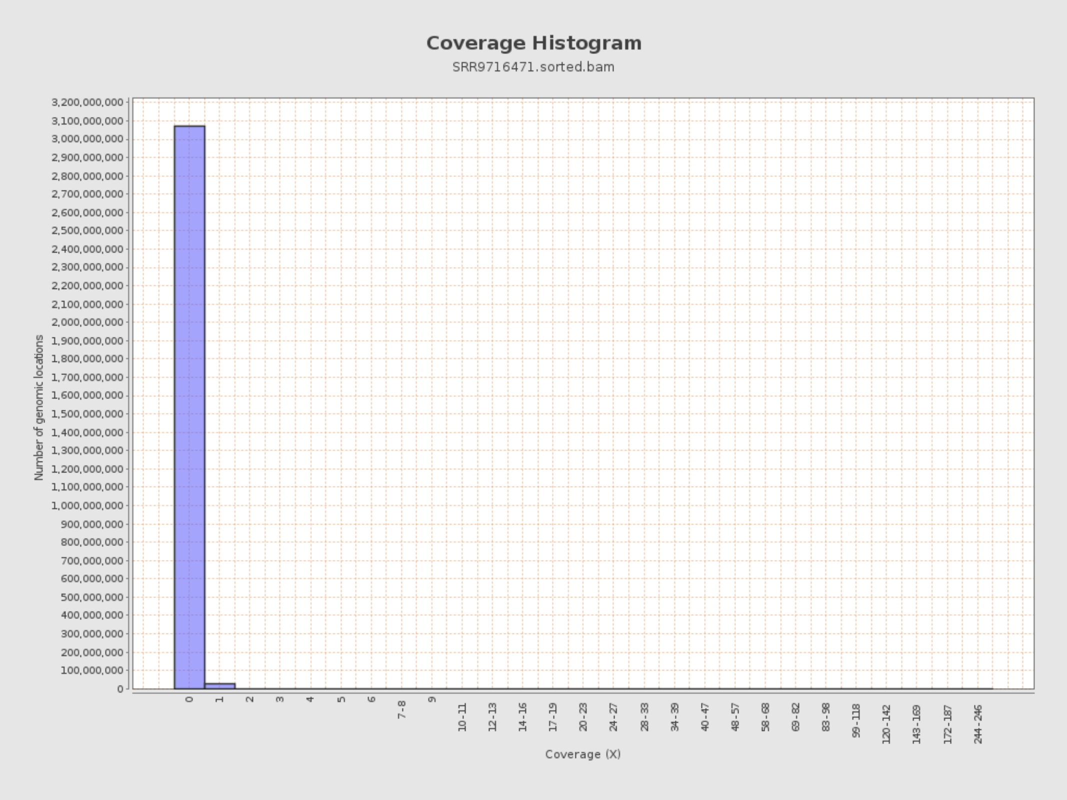
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2331141	0.0094	0.1662
chr2	243199373	2221495	0.0091	0.1425
chr3	198022430	1631534	0.0082	0.093
chr4	191154276	1778350	0.0093	0.104
chr5	180915260	1601509	0.0089	0.0964
chr6	171115067	1516149	0.0089	0.103
chr7	159138663	1596177	0.01	0.1463

chr8	146364022	1481374	0.0101	0.1368
chr9	141213431	917352	0.0065	0.0902
chr10	135534747	1231739	0.0091	0.1243
chr11	135006516	995887	0.0074	0.1004
chr12	133851895	1378135	0.0103	0.1046
chr13	115169878	855694	0.0074	0.0884
chr14	107349540	935320	0.0087	0.0966
chr15	102531392	1018990	0.0099	0.103
chr16	90354753	922295	0.0102	0.1072
chr17	81195210	1181903	0.0146	0.1261
chr18	78077248	519537	0.0067	0.1286
chr19	59128983	681323	0.0115	0.1463
chr20	63025520	896185	0.0142	0.1239
chr21	48129895	355779	0.0074	0.0952
chr22	51304566	247419	0.0048	0.0712
chrMT	16571	1546	0.0933	0.2972
chrX	155270560	1529634	0.0099	0.1048
chrY	59373566	96746	0.0016	0.076

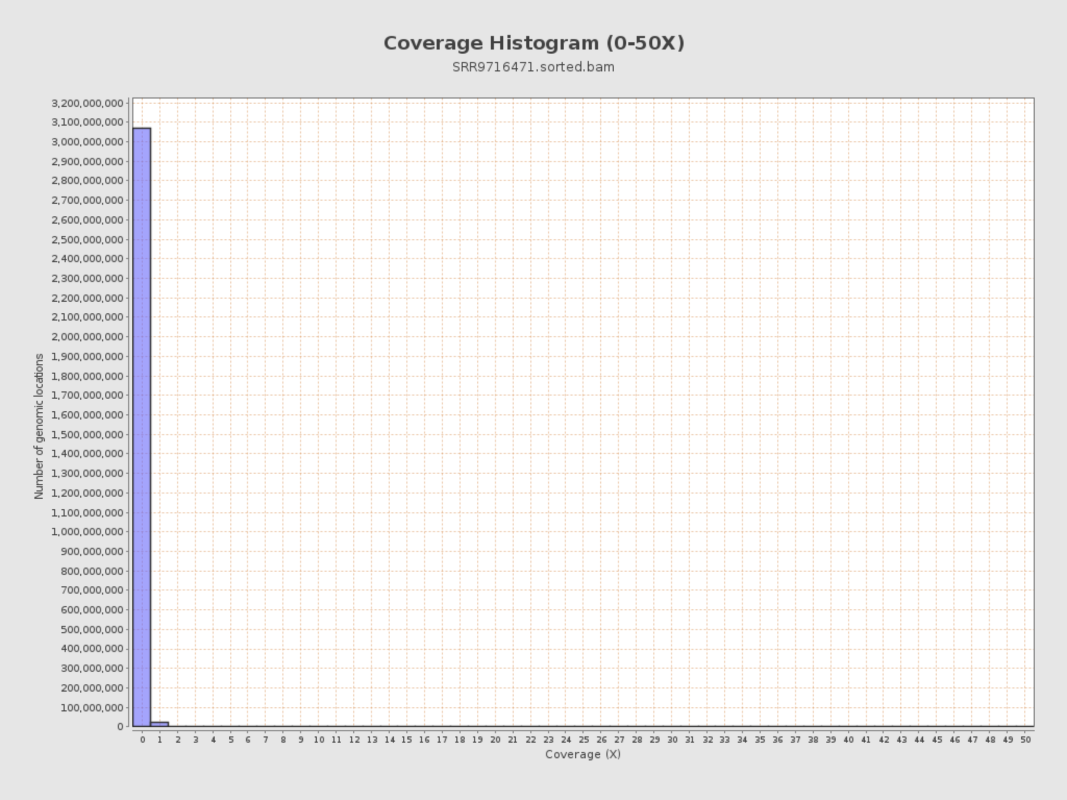
3. Results : Coverage across reference



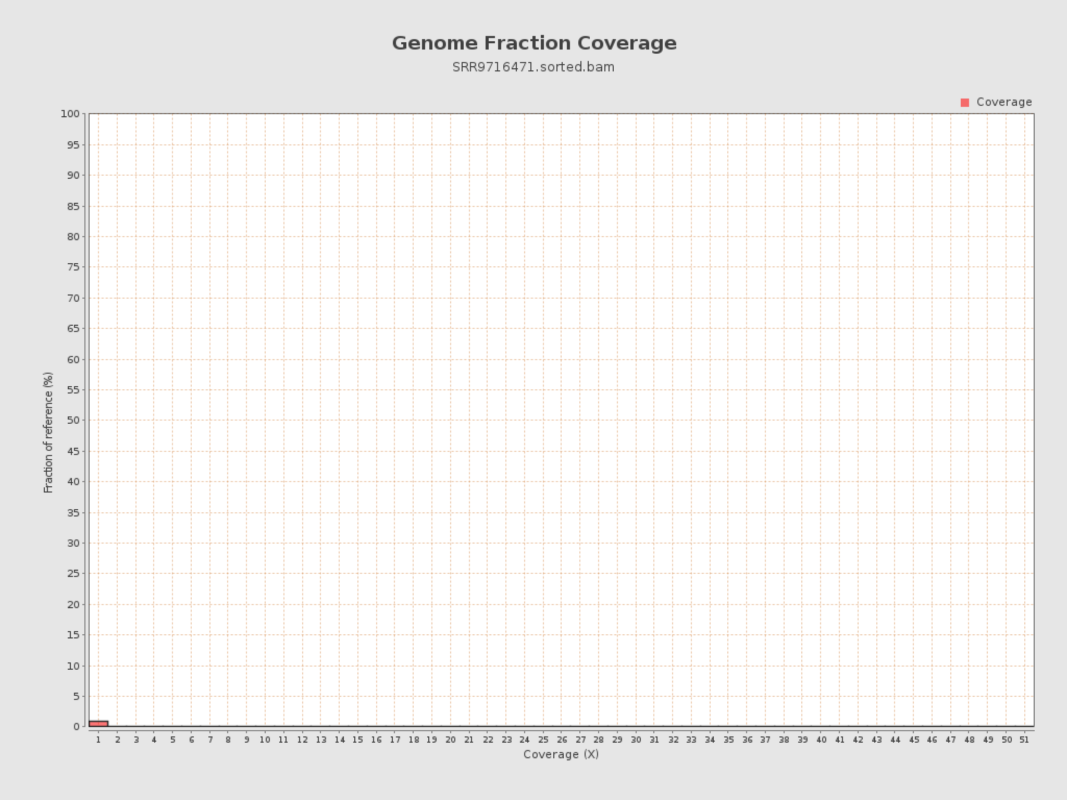
4. Results : Coverage Histogram



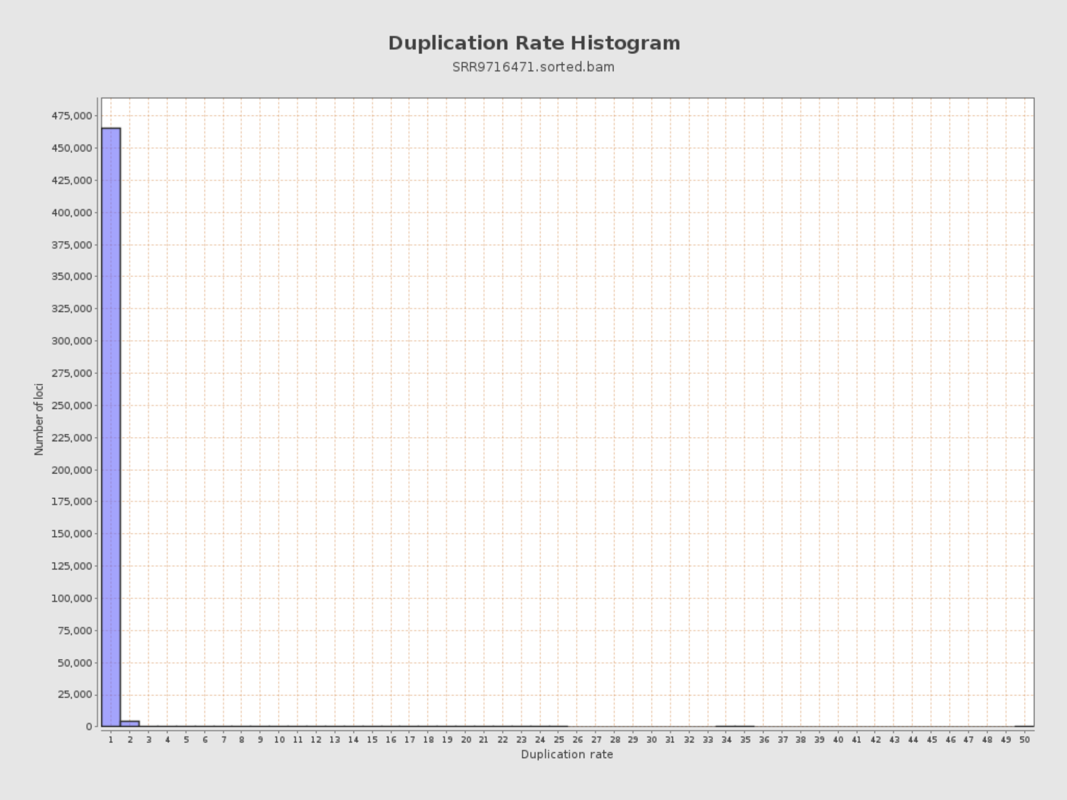
5. Results : Coverage Histogram (0-50X)



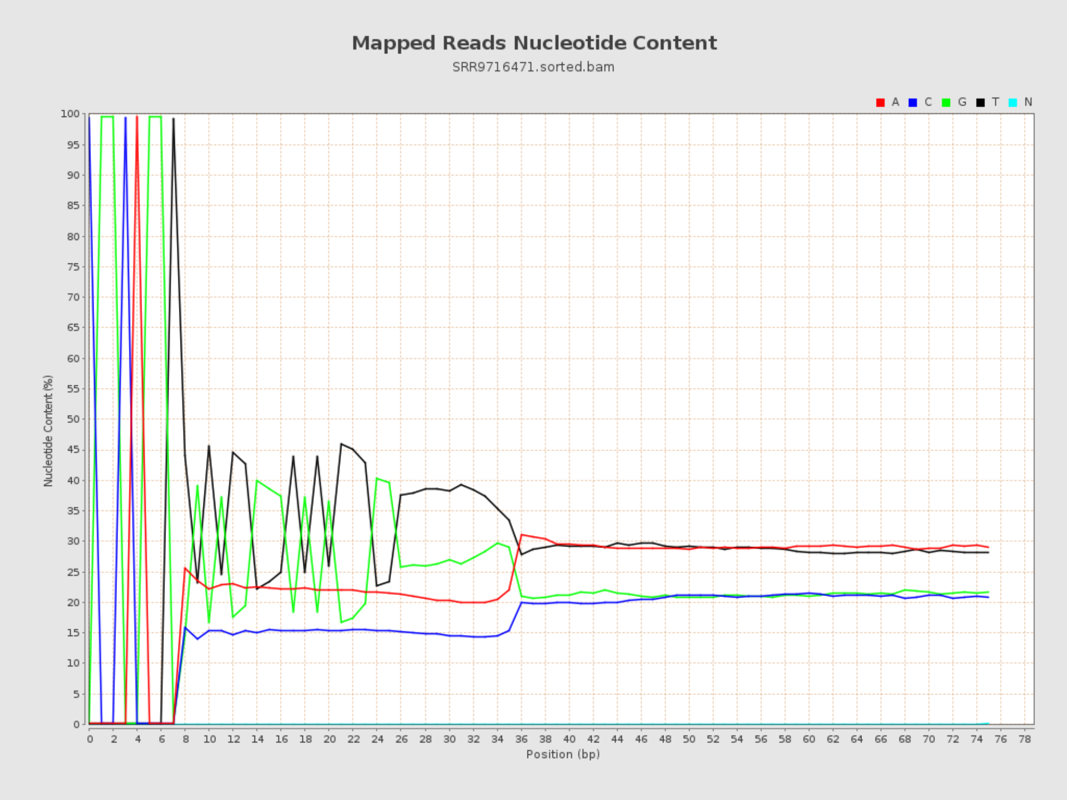
6. Results : Genome Fraction Coverage



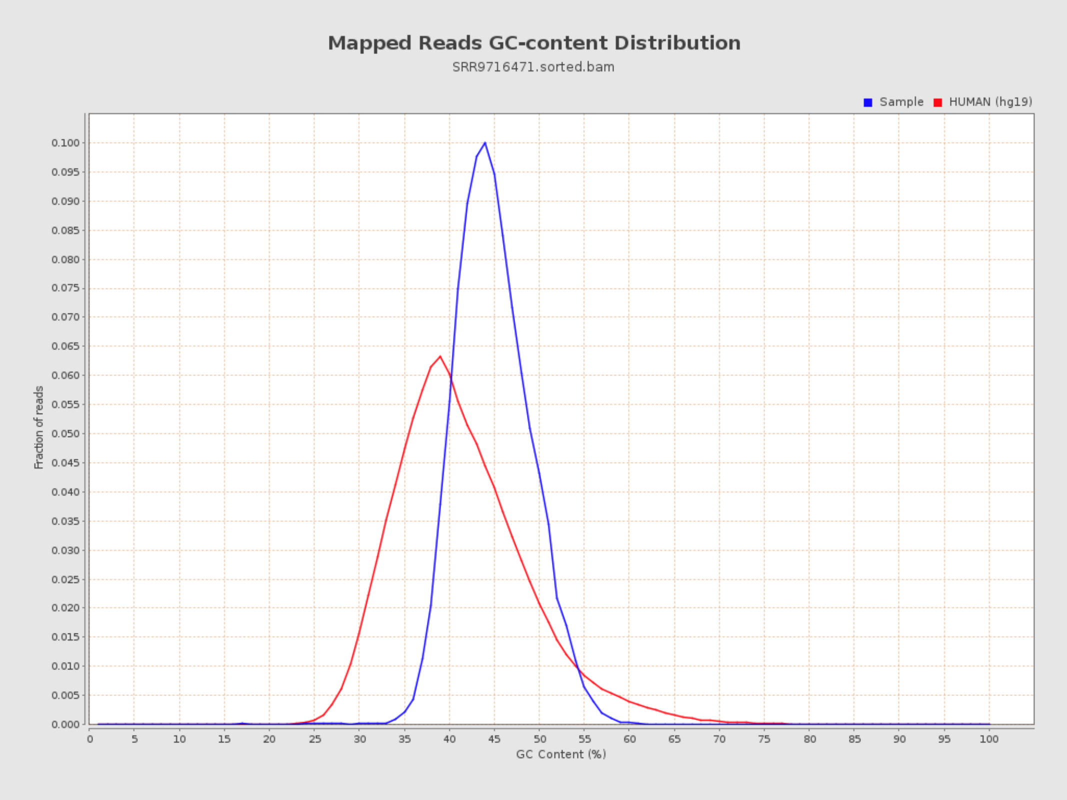
7. Results : Duplication Rate Histogram



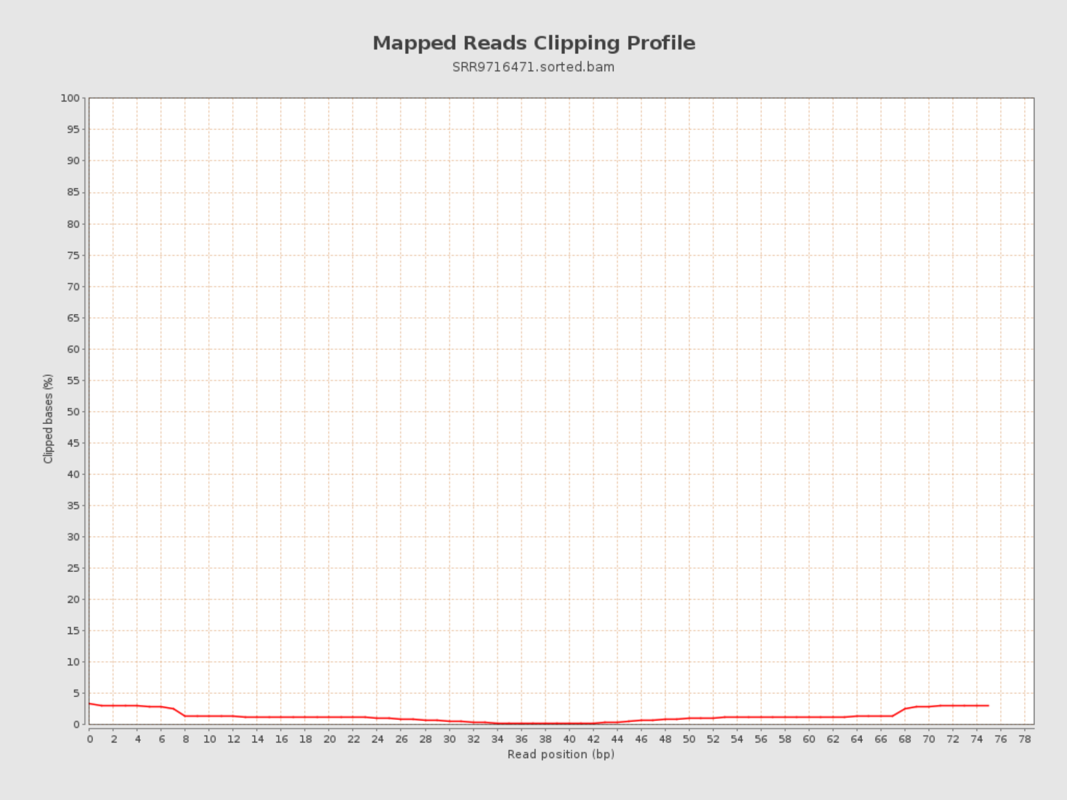
8. Results : Mapped Reads Nucleotide Content



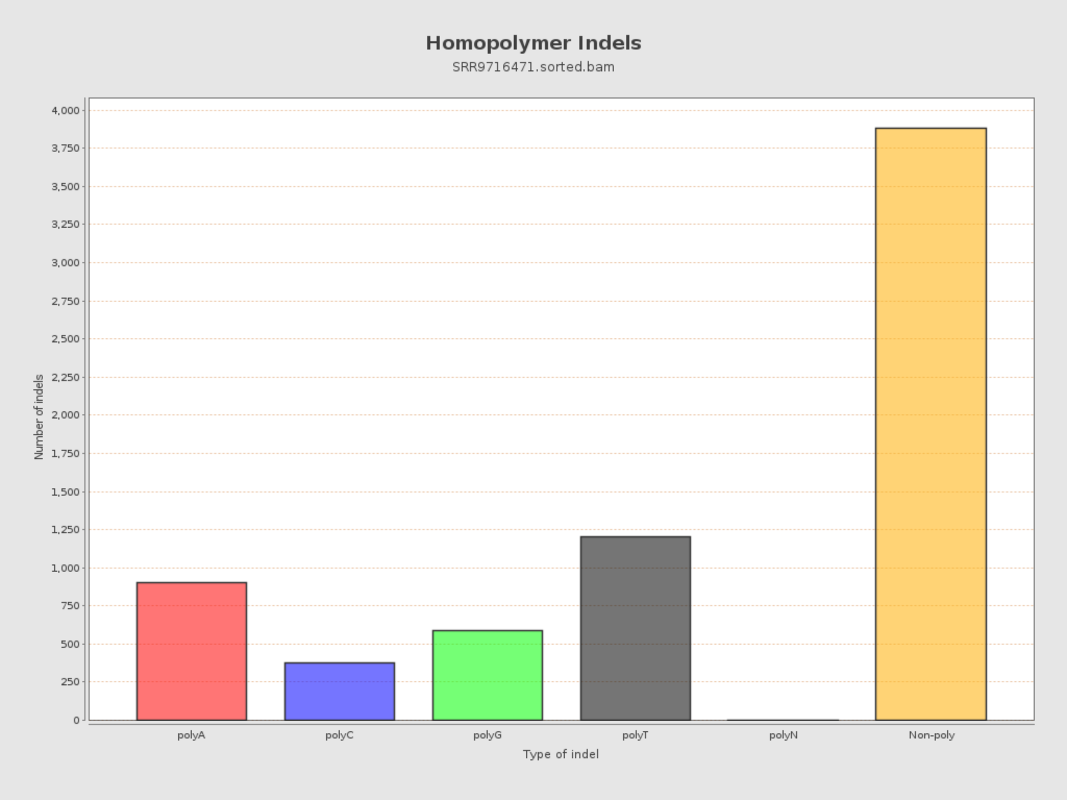
9. Results : Mapped Reads GC-content Distribution



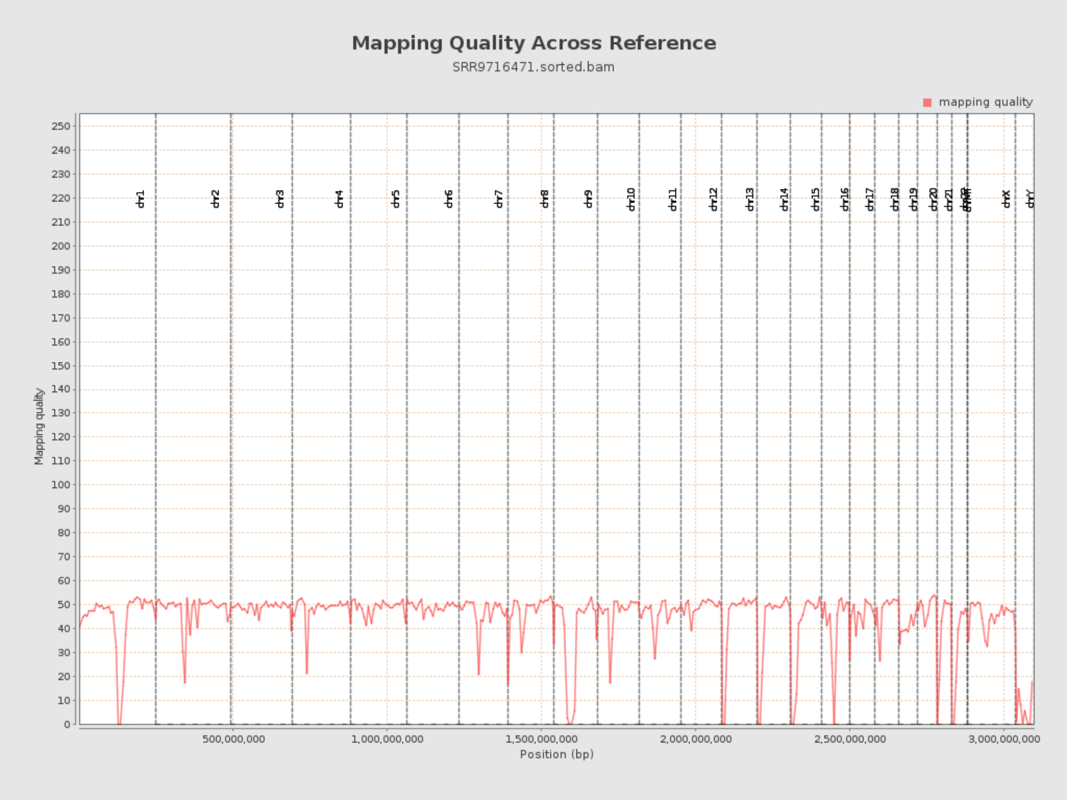
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram