Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 00:55:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716214.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_SRR9716214 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716214.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 00:55:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716214.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	555,549
Mapped reads	486,115 / 87.5%
Unmapped reads	69,434 / 12.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,198 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	6,726 / 1.21%
Duplication rate	1.05%
Clipped reads	487,845 / 87.81%

2.2. ACGT Content

Number/percentage of A's	6,971,548 / 25.28%
Number/percentage of C's	5,336,257 / 19.35%
Number/percentage of T's	8,192,846 / 29.71%
Number/percentage of G's	7,075,063 / 25.66%
Number/percentage of N's	575 / 0%
GC Percentage	45.01%

2.3. Coverage

Mean	0.0089

Standard Deviation	0.1077

2.4. Mapping Quality

Mean Mapping Quality	43.89

2.5. Mismatches and indels

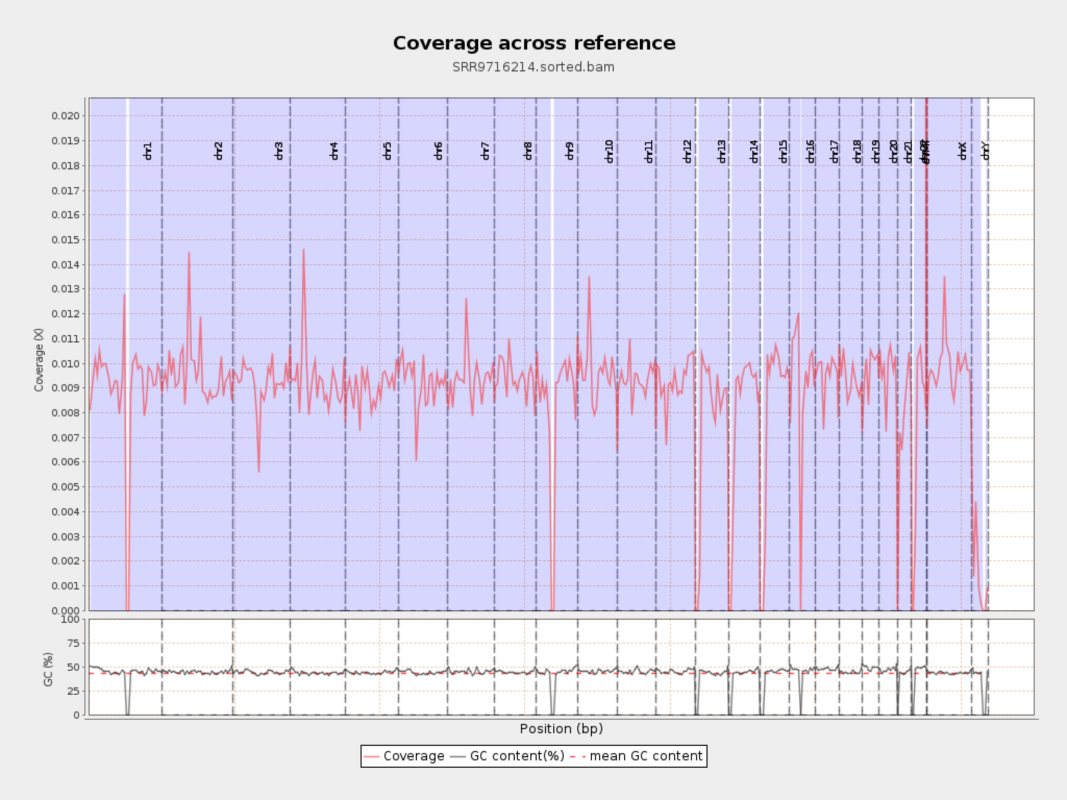
General error rate	0.52%
Mismatches	139,800
Insertions	1,584
Mapped reads with at least one insertion	0.32%
Deletions	4,802
Mapped reads with at least one deletion	0.98%
Homopolymer indels	40.31%

2.6. Chromosome stats

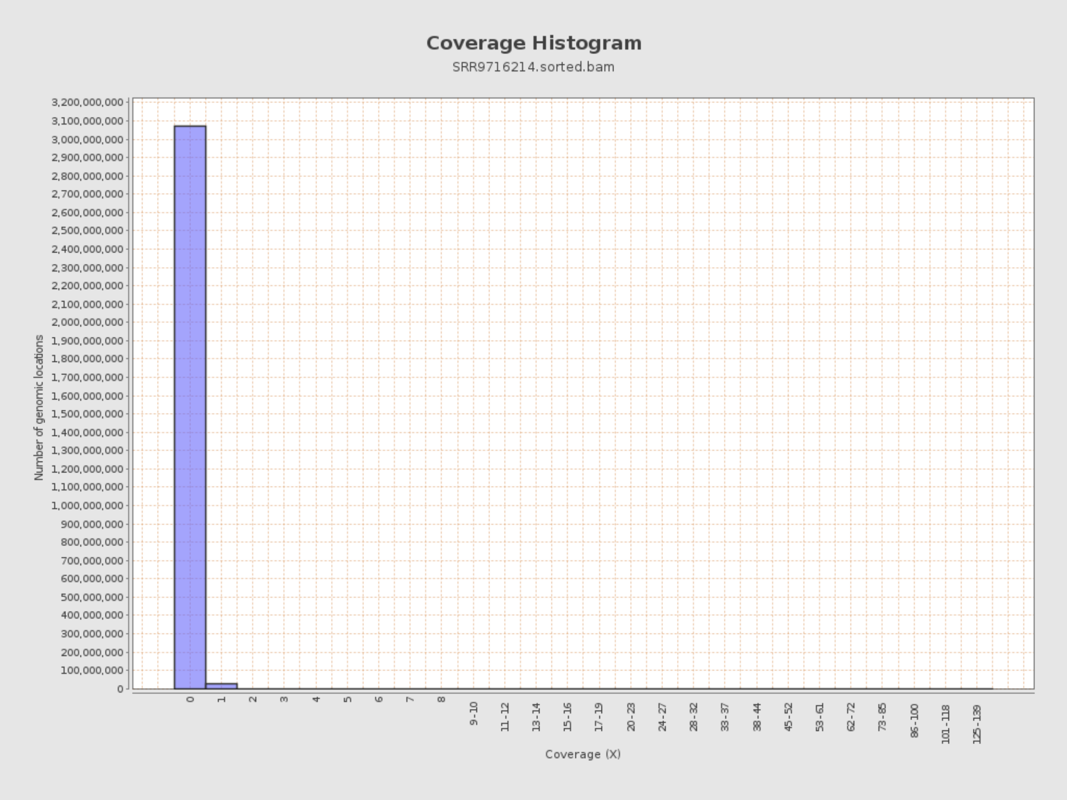
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2224955	0.0089	0.1399
chr2	243199373	2338173	0.0096	0.1167
chr3	198022430	1823631	0.0092	0.0986
chr4	191154276	1783555	0.0093	0.102
chr5	180915260	1631173	0.009	0.098
chr6	171115067	1579198	0.0092	0.1002
chr7	159138663	1498923	0.0094	0.1143

chr8	146364022	1380764	0.0094	0.104
chr9	141213431	1151918	0.0082	0.1061
chr10	135534747	1305591	0.0096	0.1087
chr11	135006516	1256192	0.0093	0.11
chr12	133851895	1239855	0.0093	0.0994
chr13	115169878	865712	0.0075	0.0888
chr14	107349540	841721	0.0078	0.0936
chr15	102531392	820006	0.008	0.0921
chr16	90354753	831569	0.0092	0.1016
chr17	81195210	770493	0.0095	0.1014
chr18	78077248	734381	0.0094	0.1511
chr19	59128983	575289	0.0097	0.1234
chr20	63025520	607773	0.0096	0.1016
chr21	48129895	362502	0.0075	0.0929
chr22	51304566	342590	0.0067	0.0839
chrMT	16571	6140	0.3705	0.6438
chrX	155270560	1531761	0.0099	0.1071
chrY	59373566	80693	0.0014	0.0447

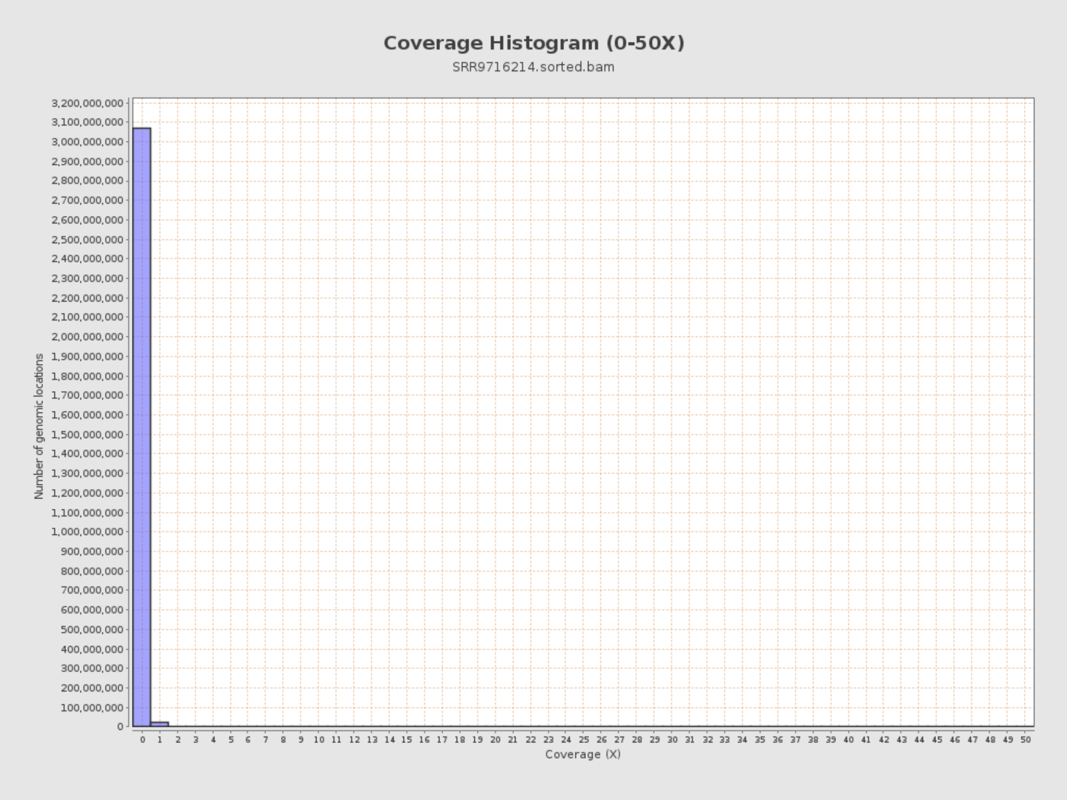
3. Results : Coverage across reference



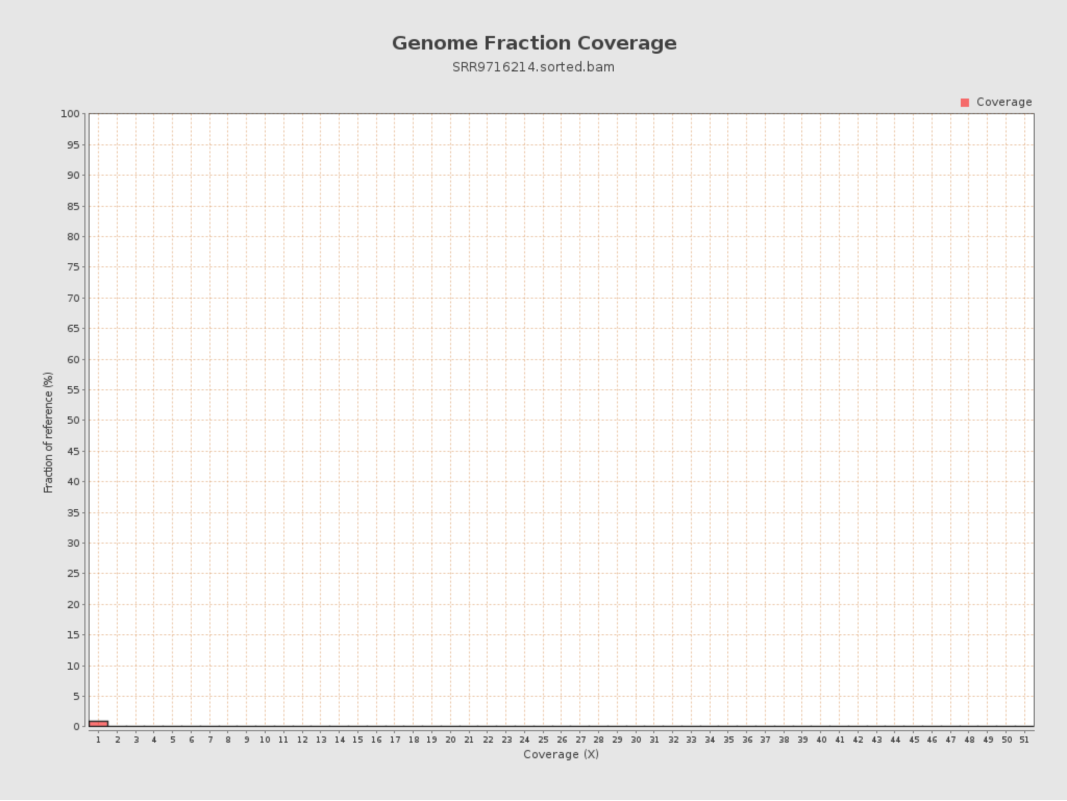
4. Results : Coverage Histogram



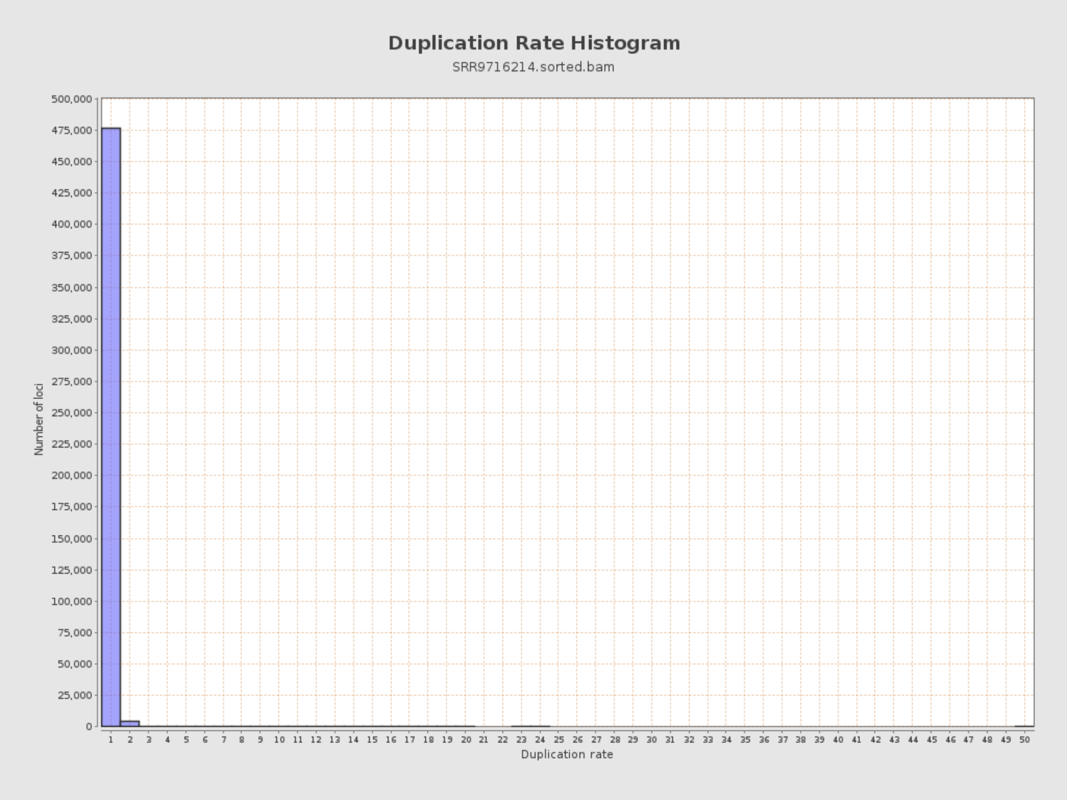
5. Results : Coverage Histogram (0-50X)



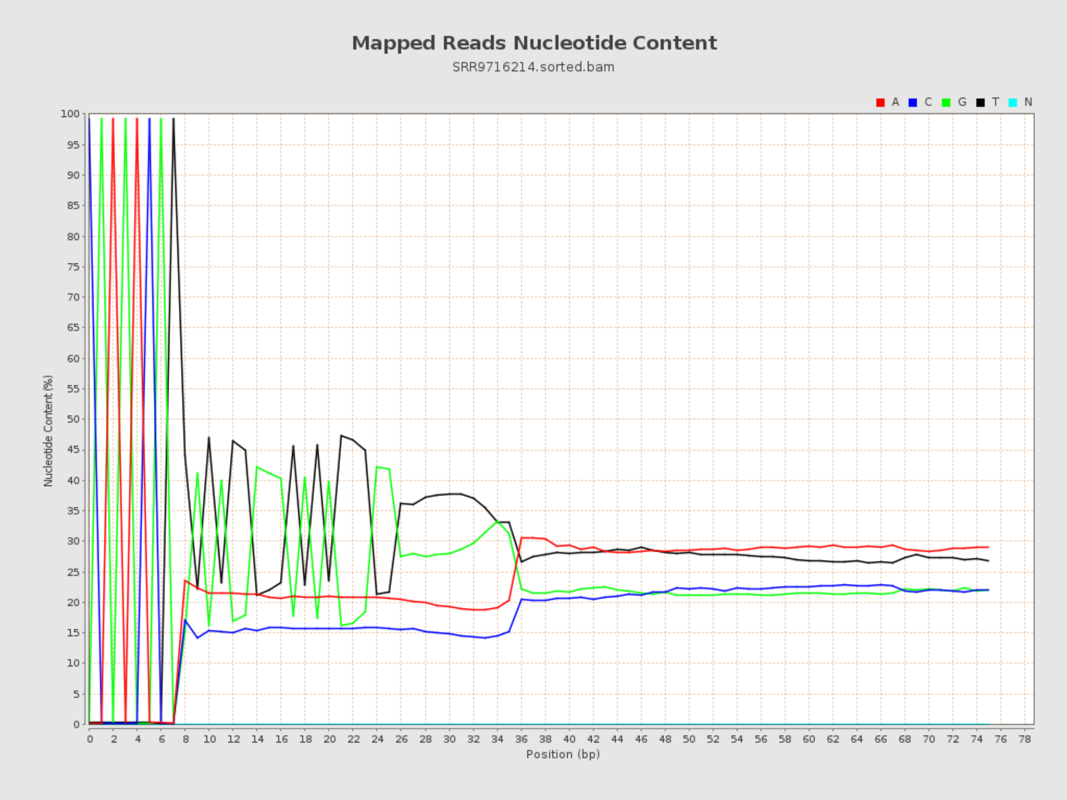
6. Results : Genome Fraction Coverage



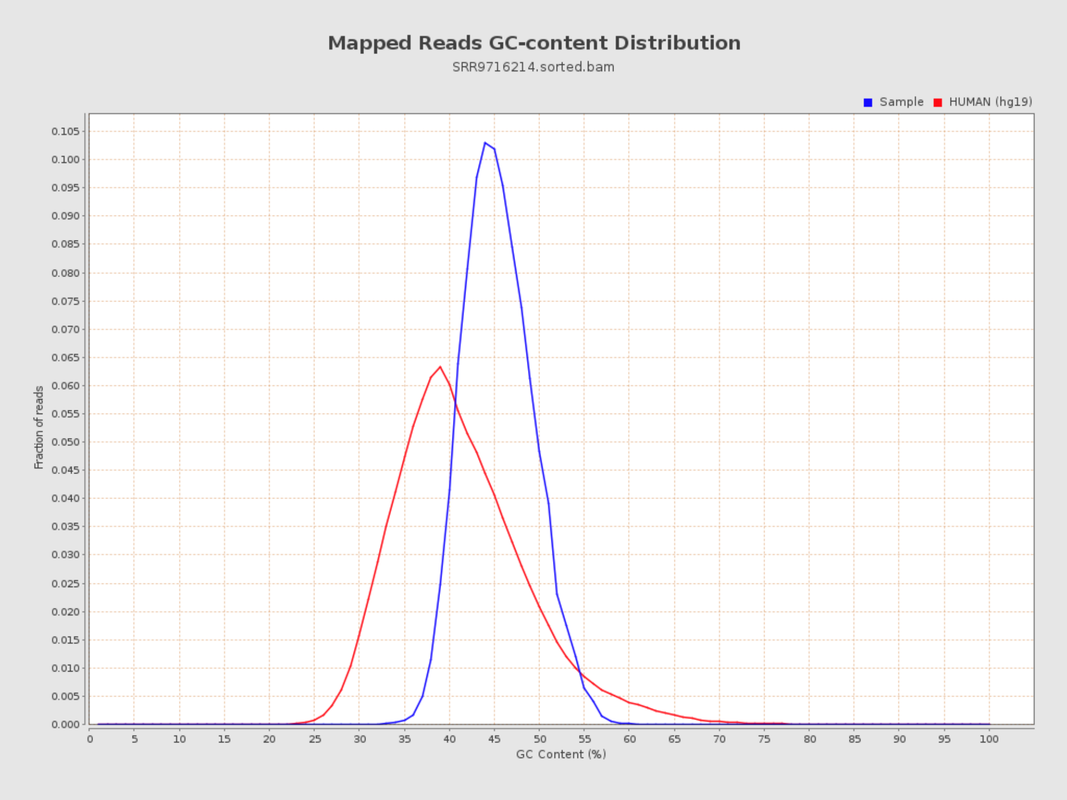
7. Results : Duplication Rate Histogram



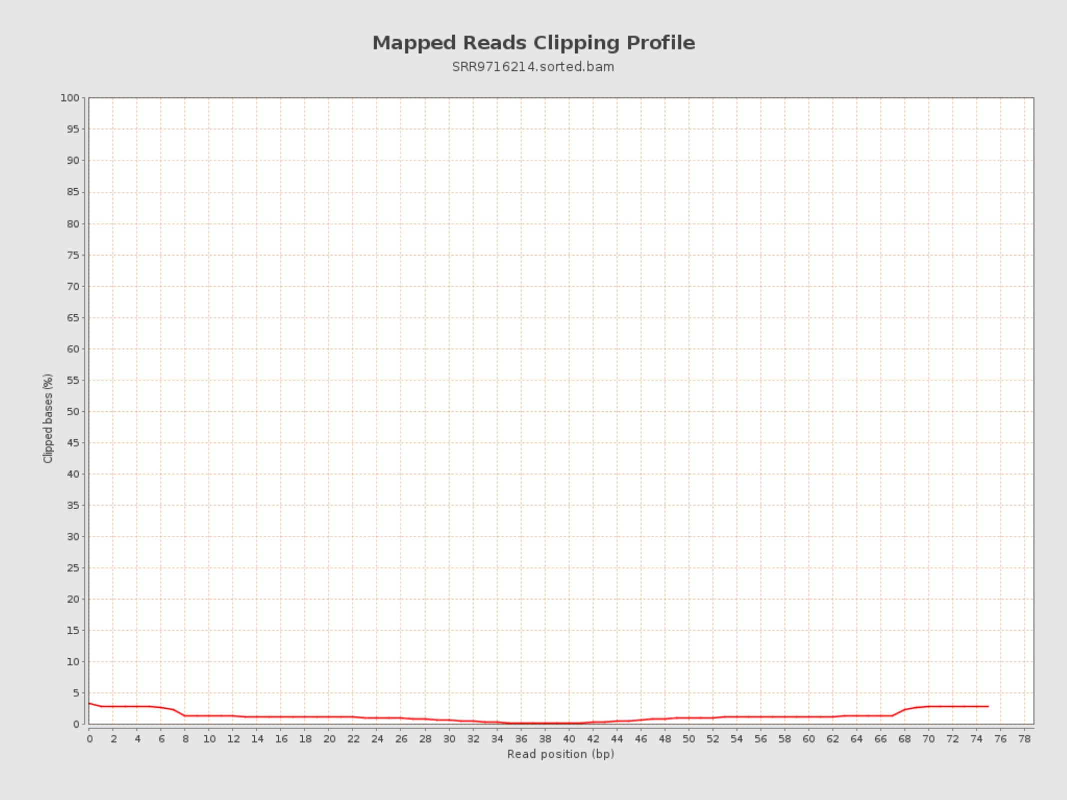
8. Results : Mapped Reads Nucleotide Content



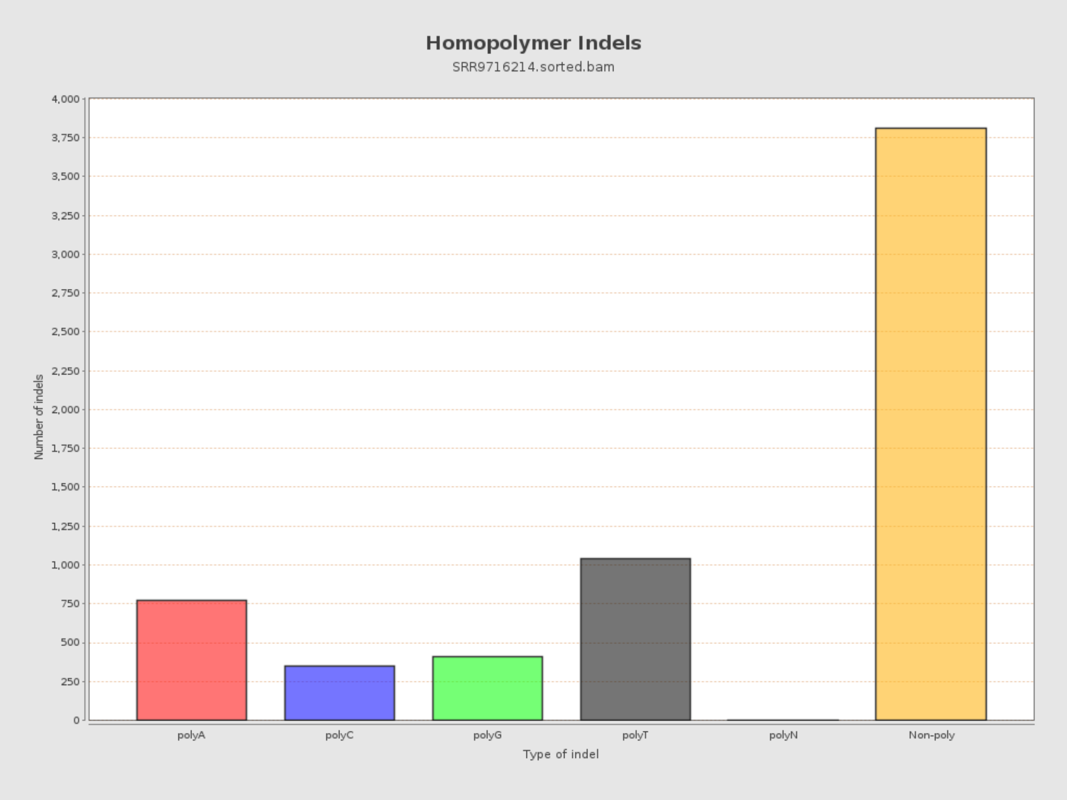
9. Results : Mapped Reads GC-content Distribution



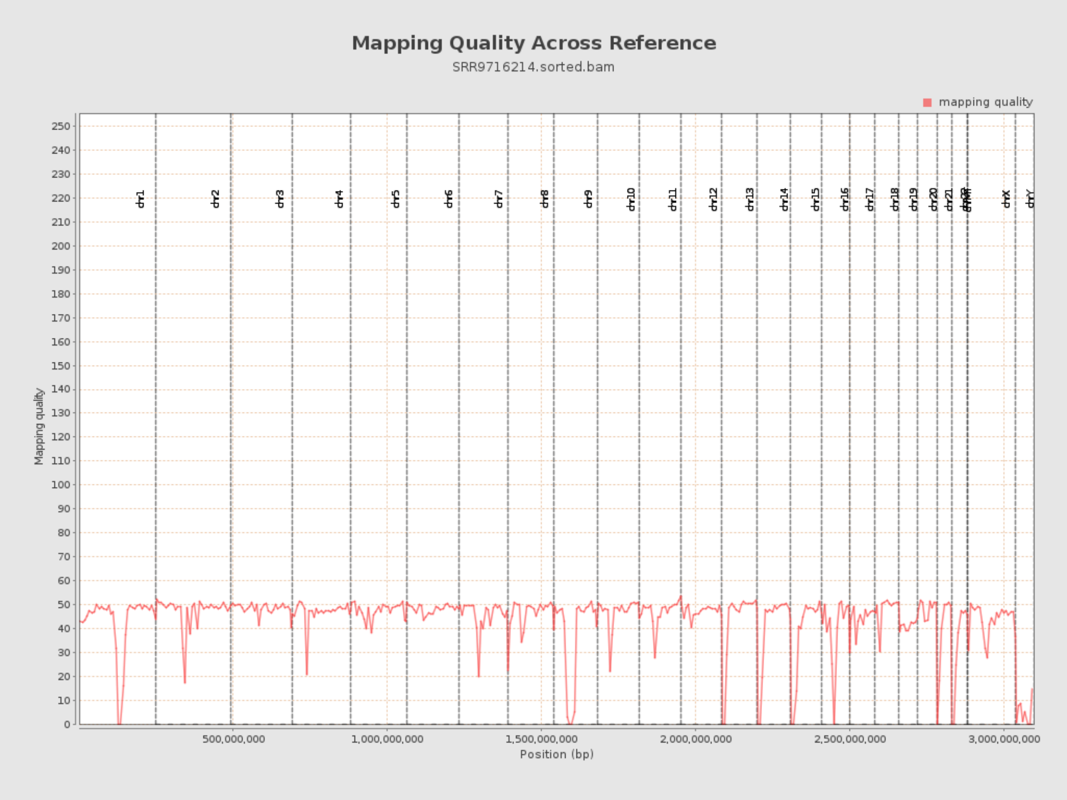
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram