Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:34:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716506.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_SRR9716506 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716506.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:34:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716506.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	675,105
Mapped reads	607,091 / 89.93%
Unmapped reads	68,014 / 10.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,836 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	14,570 / 2.16%
Duplication rate	1.69%
Clipped reads	607,685 / 90.01%

2.2. ACGT Content

Number/percentage of A's	8,562,195 / 24.83%
Number/percentage of C's	6,248,320 / 18.12%
Number/percentage of T's	11,357,232 / 32.94%
Number/percentage of G's	8,313,993 / 24.11%
Number/percentage of N's	644 / 0%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0111

Standard Deviation	0.1384

2.4. Mapping Quality

Mean Mapping Quality	43.81

2.5. Mismatches and indels

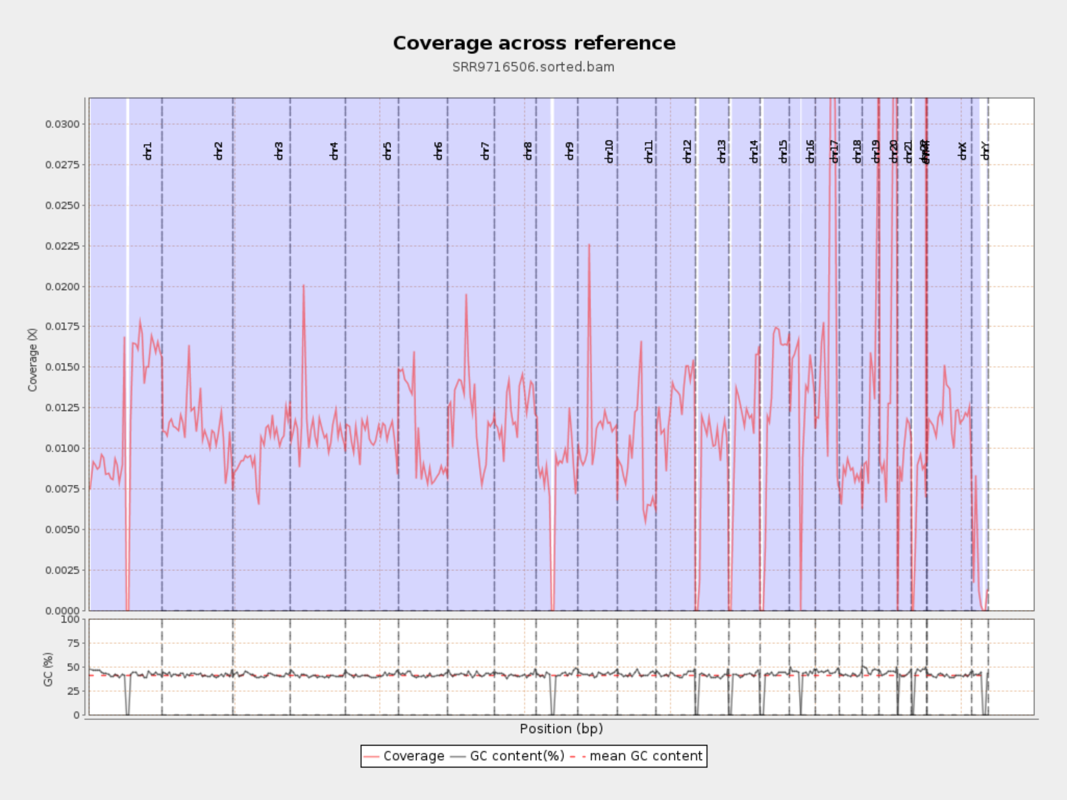
General error rate	0.54%
Mismatches	179,343
Insertions	2,585
Mapped reads with at least one insertion	0.42%
Deletions	6,750
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.73%

2.6. Chromosome stats

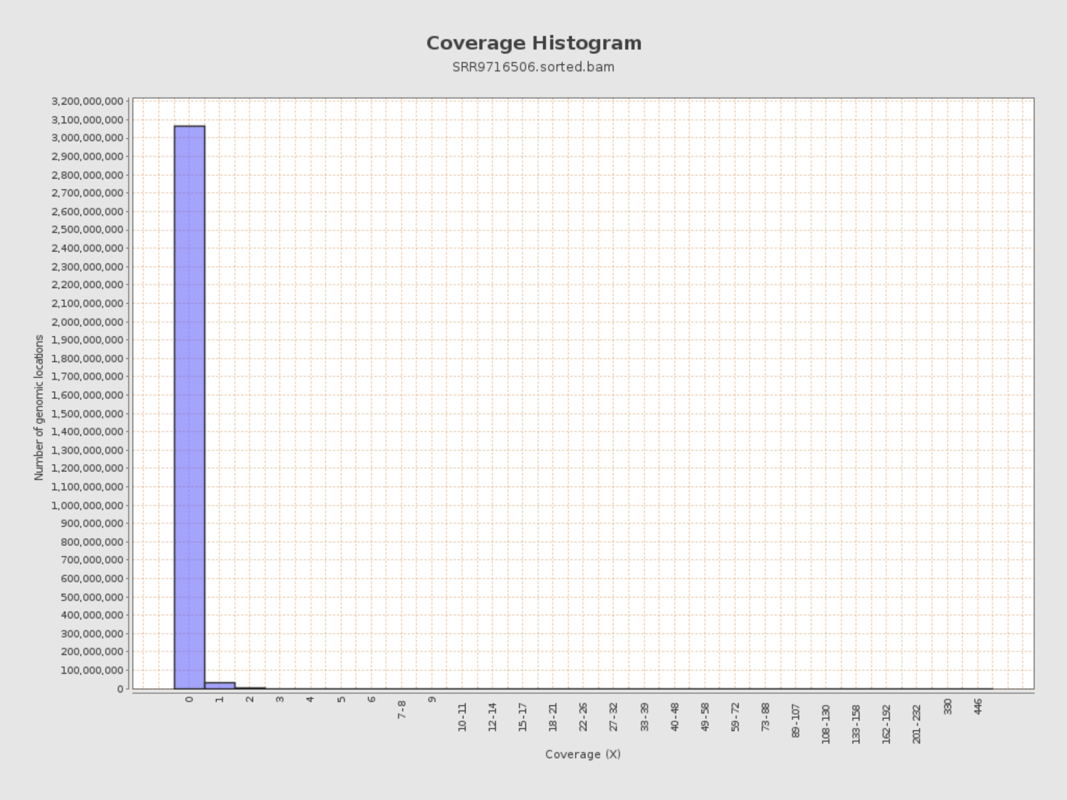
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2883106	0.0116	0.1804
chr2	243199373	2750305	0.0113	0.2081
chr3	198022430	1976274	0.01	0.1044
chr4	191154276	2158625	0.0113	0.121
chr5	180915260	1947709	0.0108	0.1081
chr6	171115067	1818606	0.0106	0.1171
chr7	159138663	1959841	0.0123	0.1641

chr8	146364022	1811550	0.0124	0.1697
chr9	141213431	1142634	0.0081	0.1026
chr10	135534747	1534987	0.0113	0.1418
chr11	135006516	1240110	0.0092	0.1147
chr12	133851895	1726849	0.0129	0.1189
chr13	115169878	1048619	0.0091	0.1002
chr14	107349540	1160652	0.0108	0.1096
chr15	102531392	1274277	0.0124	0.1169
chr16	90354753	1186371	0.0131	0.1232
chr17	81195210	1499876	0.0185	0.1435
chr18	78077248	649302	0.0083	0.1433
chr19	59128983	869477	0.0147	0.1587
chr20	63025520	1099905	0.0175	0.1395
chr21	48129895	440946	0.0092	0.1068
chr22	51304566	324675	0.0063	0.0835
chrMT	16571	5523	0.3333	0.6272
chrX	155270560	1857912	0.012	0.1199
chrY	59373566	124996	0.0021	0.0917

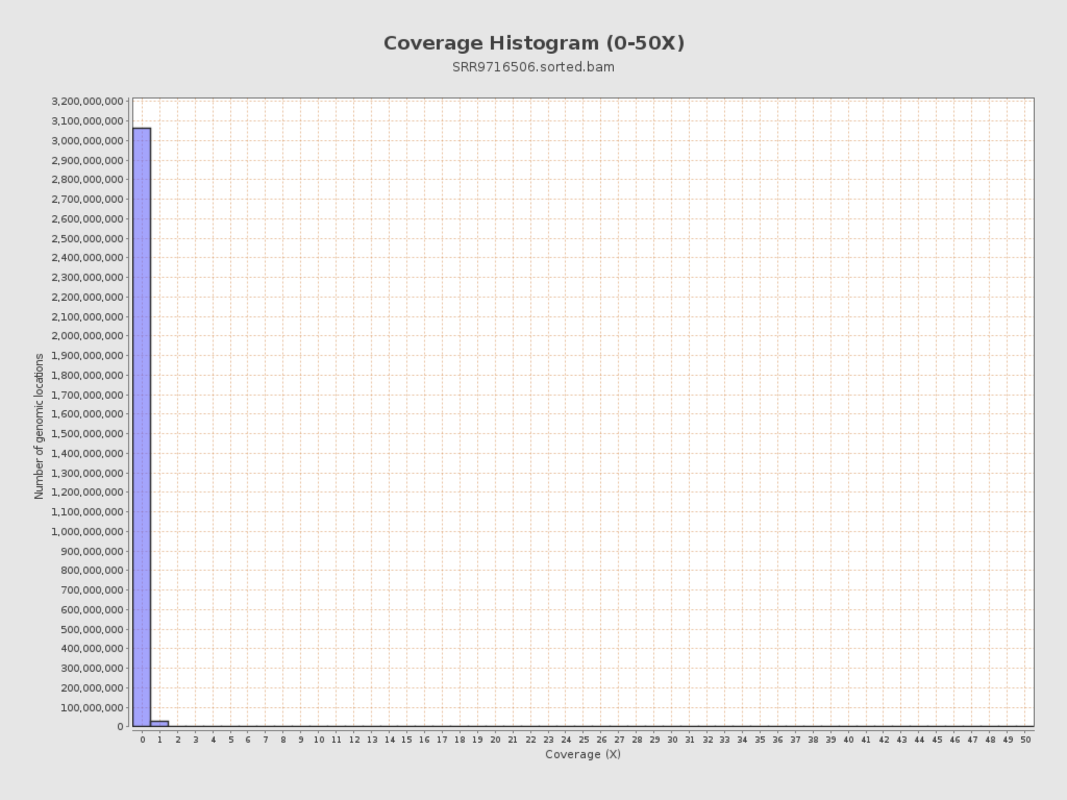
3. Results : Coverage across reference



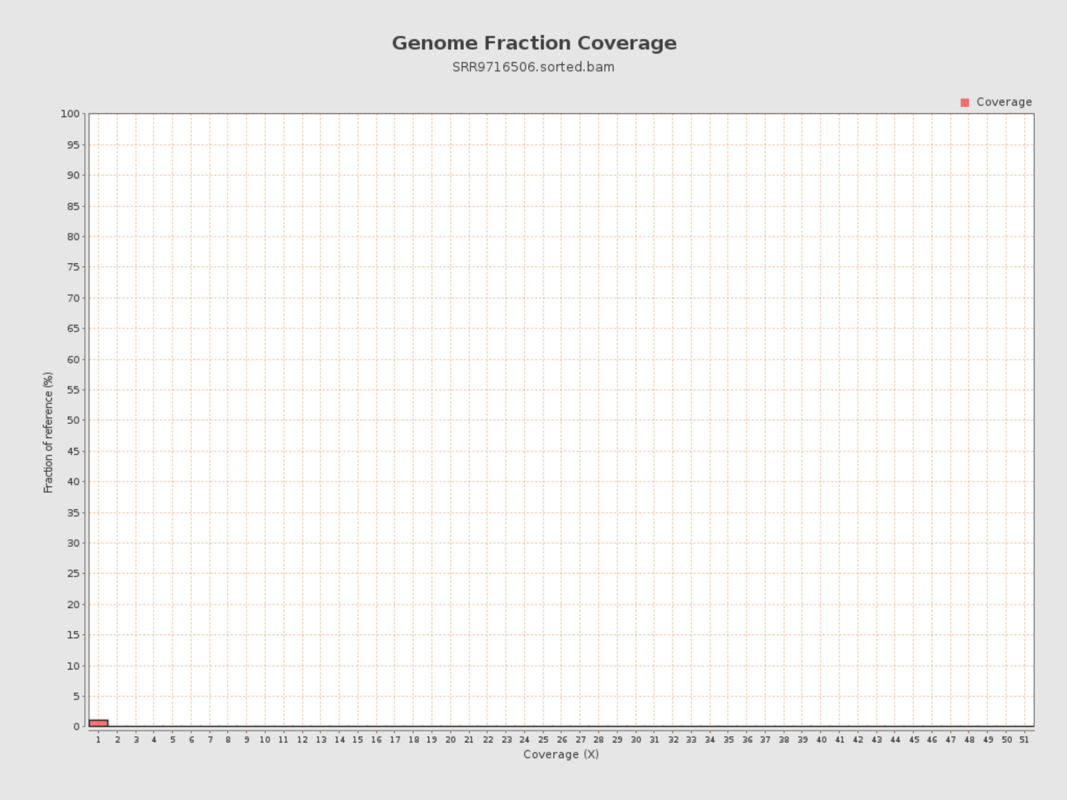
4. Results : Coverage Histogram



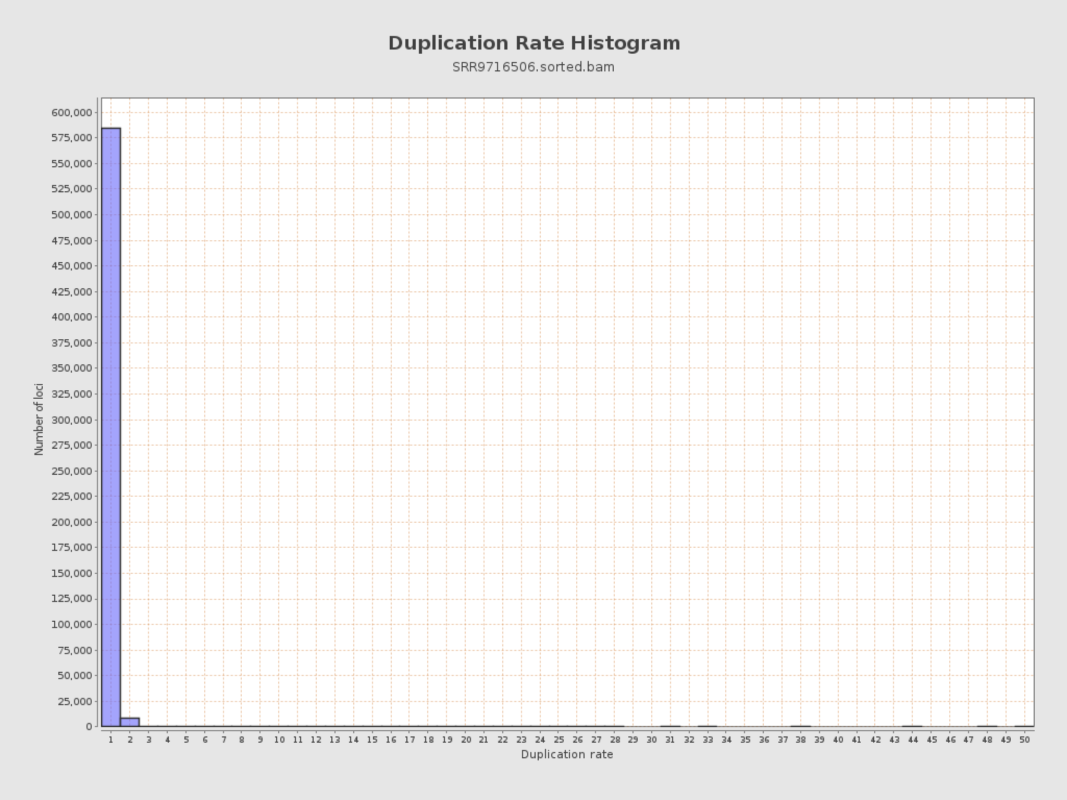
5. Results : Coverage Histogram (0-50X)



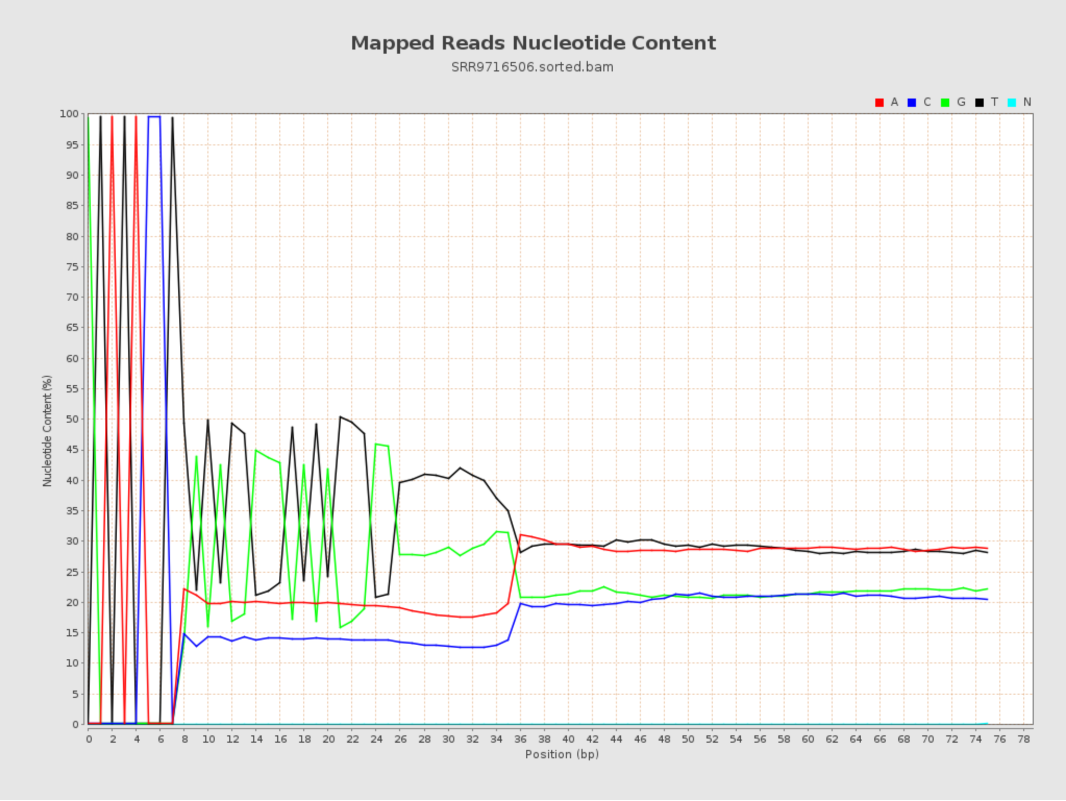
6. Results : Genome Fraction Coverage



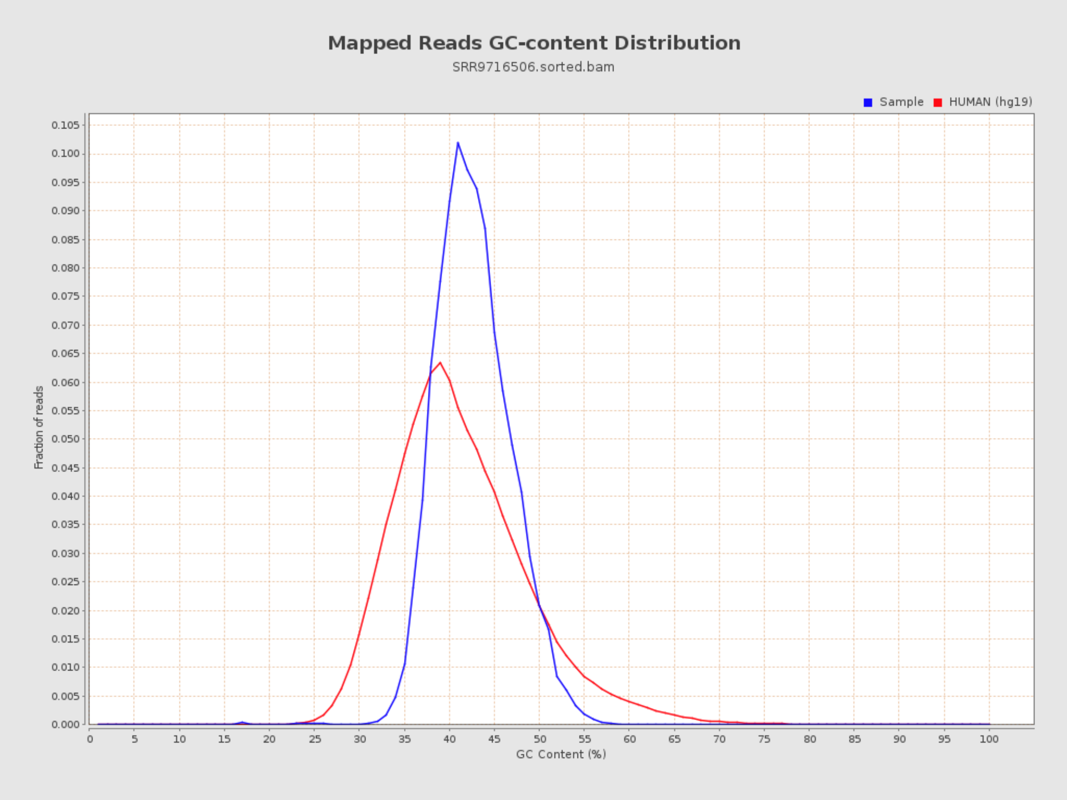
7. Results : Duplication Rate Histogram



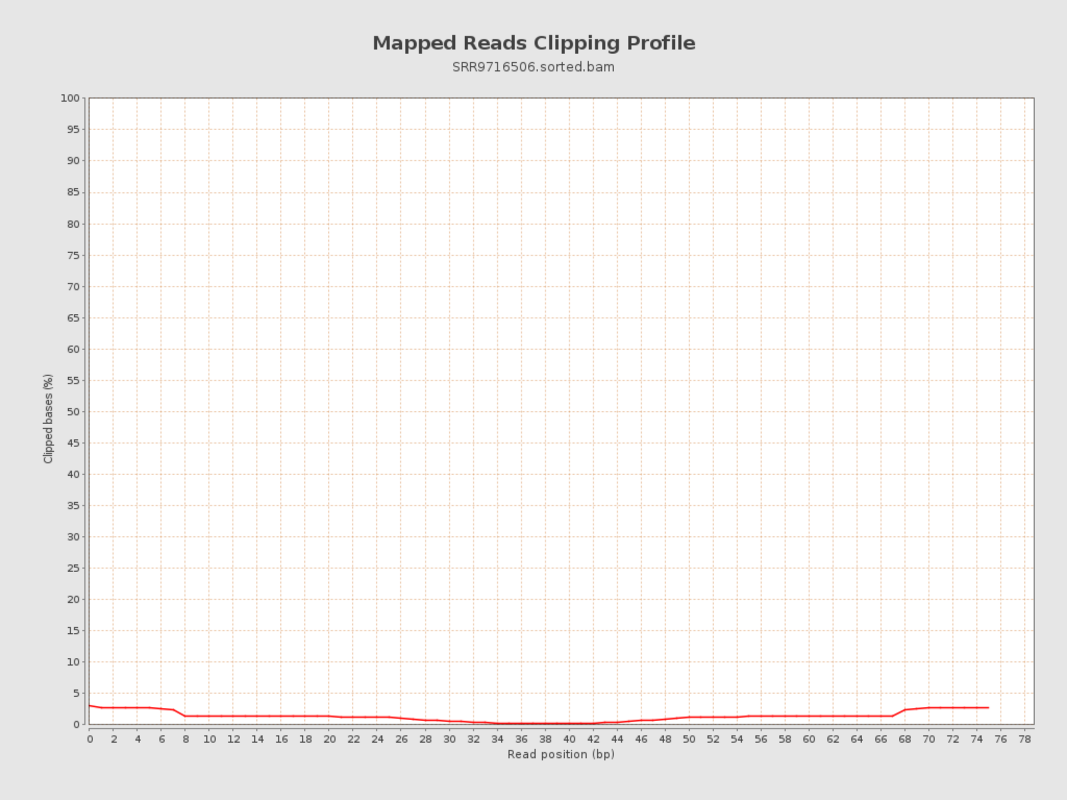
8. Results : Mapped Reads Nucleotide Content



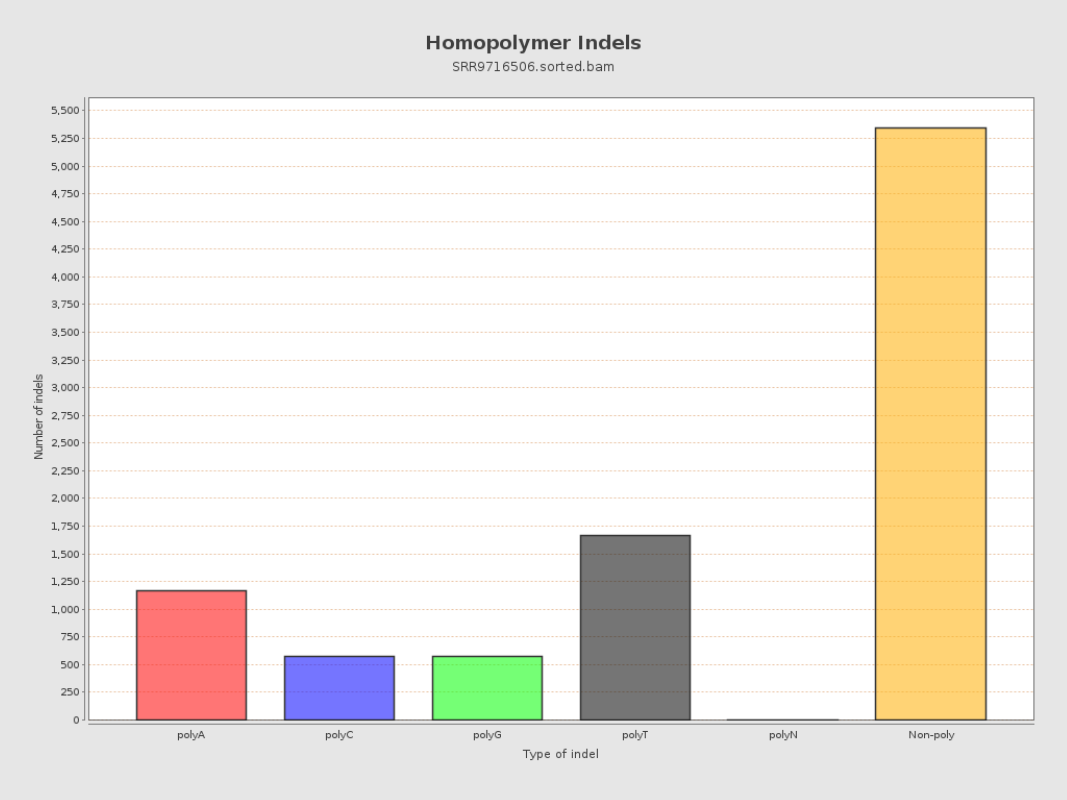
9. Results : Mapped Reads GC-content Distribution



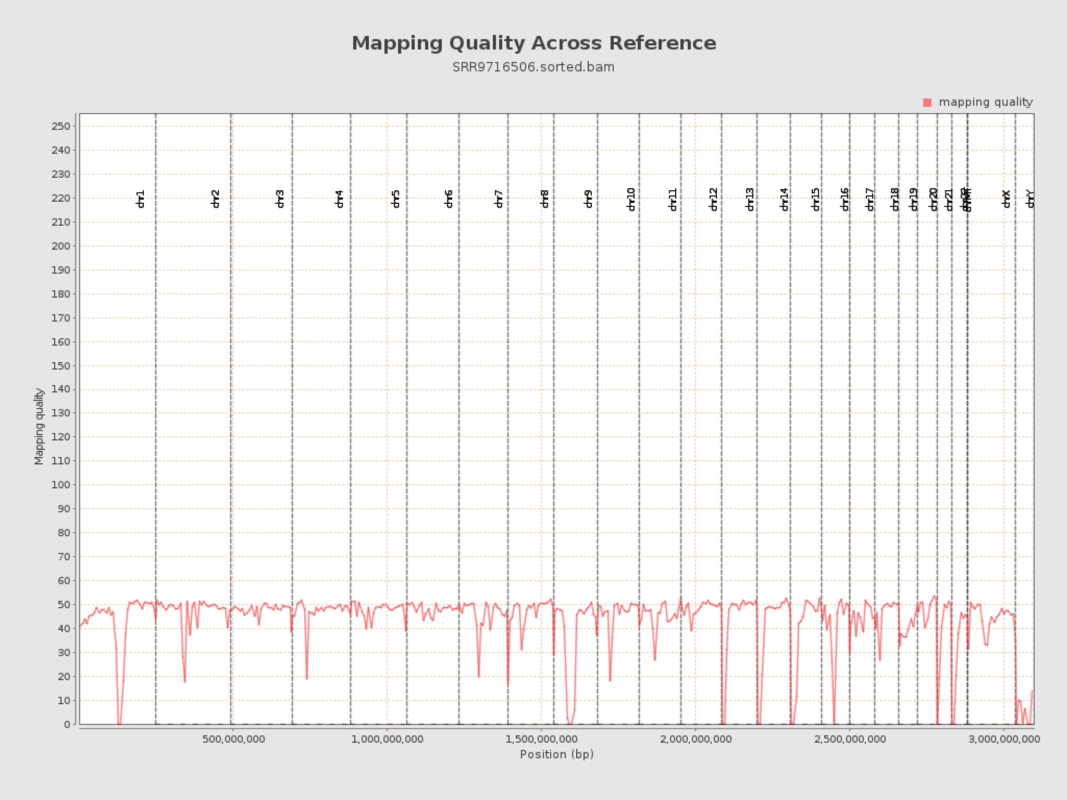
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram