Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:12:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716499.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_SRR9716499 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716499.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:12:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716499.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	778,912
Mapped reads	708,943 / 91.02%
Unmapped reads	69,969 / 8.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,307 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	17,737 / 2.28%
Duplication rate	1.83%
Clipped reads	710,439 / 91.21%

2.2. ACGT Content

Number/percentage of A's	9,929,582 / 24.19%
Number/percentage of C's	7,278,707 / 17.73%
Number/percentage of T's	13,615,104 / 33.16%
Number/percentage of G's	10,229,977 / 24.92%
Number/percentage of N's	995 / 0%
GC Percentage	42.65%

2.3. Coverage

Mean	0.0133

Standard Deviation	0.1623

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

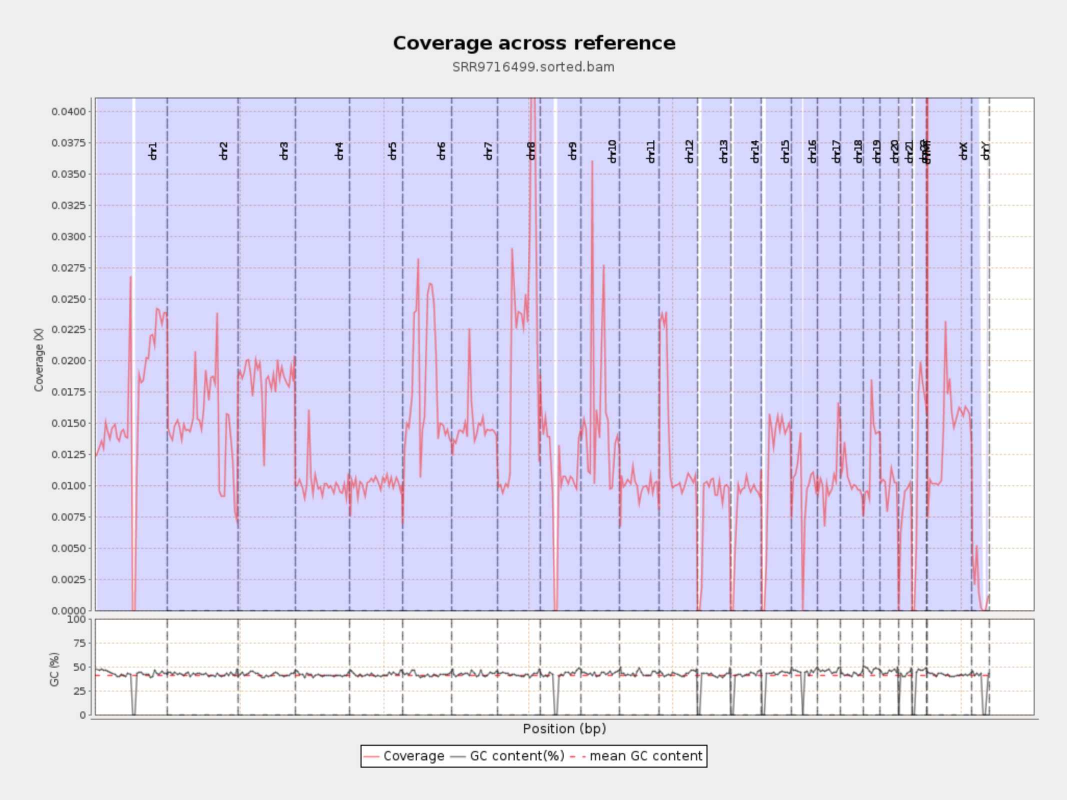
General error rate	0.5%
Mismatches	201,011
Insertions	2,650
Mapped reads with at least one insertion	0.37%
Deletions	6,726
Mapped reads with at least one deletion	0.94%
Homopolymer indels	44.22%

2.6. Chromosome stats

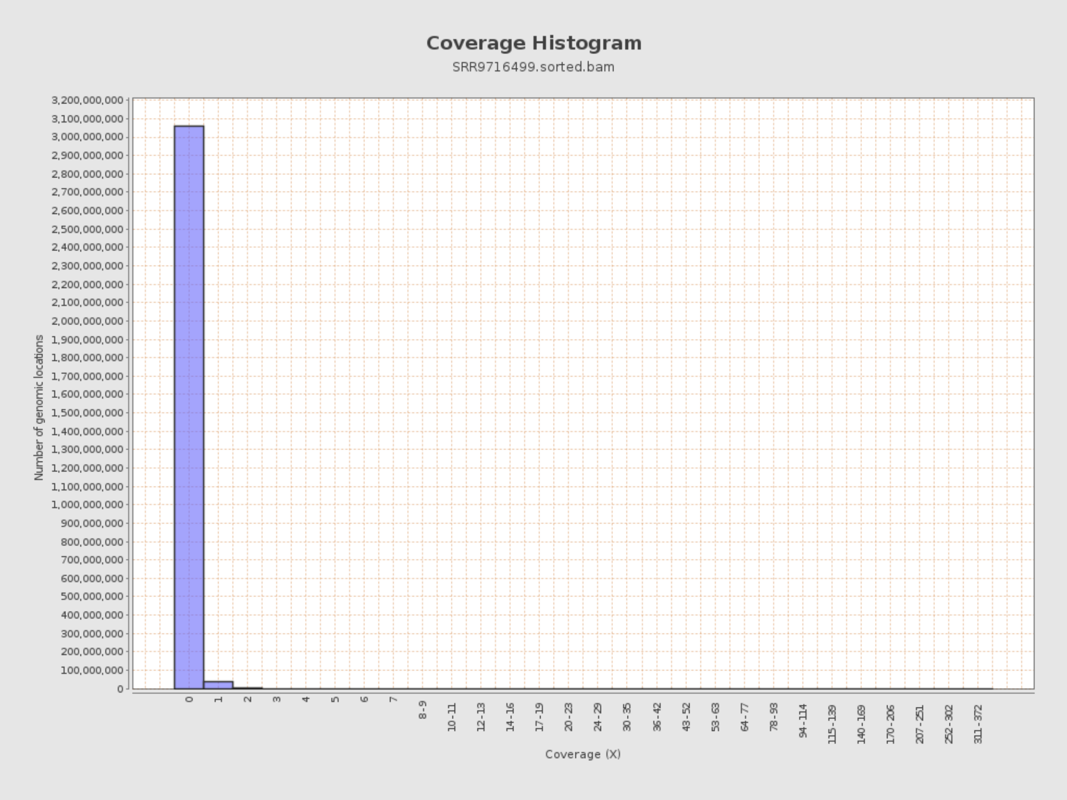
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4122895	0.0165	0.293
chr2	243199373	3613190	0.0149	0.1811
chr3	198022430	3680479	0.0186	0.144
chr4	191154276	1945388	0.0102	0.1092
chr5	180915260	1845644	0.0102	0.107
chr6	171115067	3065674	0.0179	0.1789
chr7	159138663	2358783	0.0148	0.1851

chr8	146364022	3208854	0.0219	0.1646
chr9	141213431	1528049	0.0108	0.1327
chr10	135534747	2139130	0.0158	0.1904
chr11	135006516	1354551	0.01	0.1279
chr12	133851895	1810244	0.0135	0.1232
chr13	115169878	947954	0.0082	0.0947
chr14	107349540	882717	0.0082	0.1
chr15	102531392	1212550	0.0118	0.114
chr16	90354753	862509	0.0095	0.1133
chr17	81195210	864698	0.0106	0.1103
chr18	78077248	817689	0.0105	0.2156
chr19	59128983	748291	0.0127	0.1994
chr20	63025520	625520	0.0099	0.1044
chr21	48129895	382640	0.008	0.1024
chr22	51304566	631840	0.0123	0.1163
chrMT	16571	90735	5.4755	3.647
chrX	155270560	2223599	0.0143	0.1345
chrY	59373566	101191	0.0017	0.0519

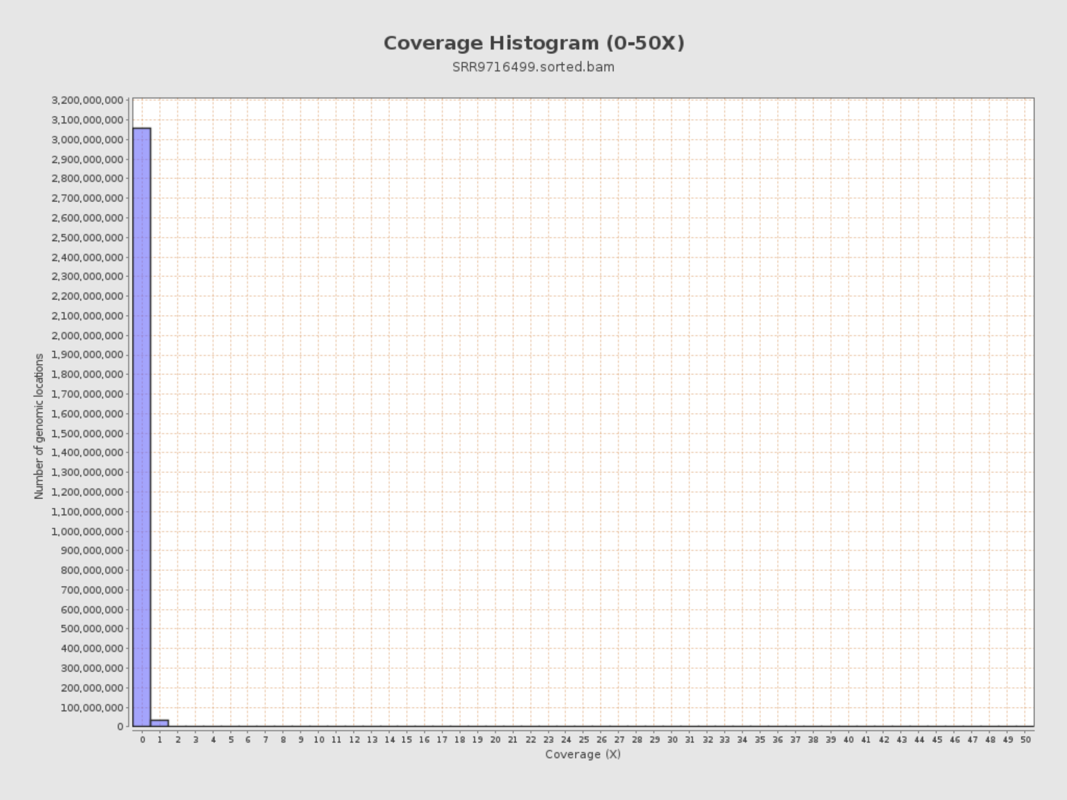
3. Results : Coverage across reference



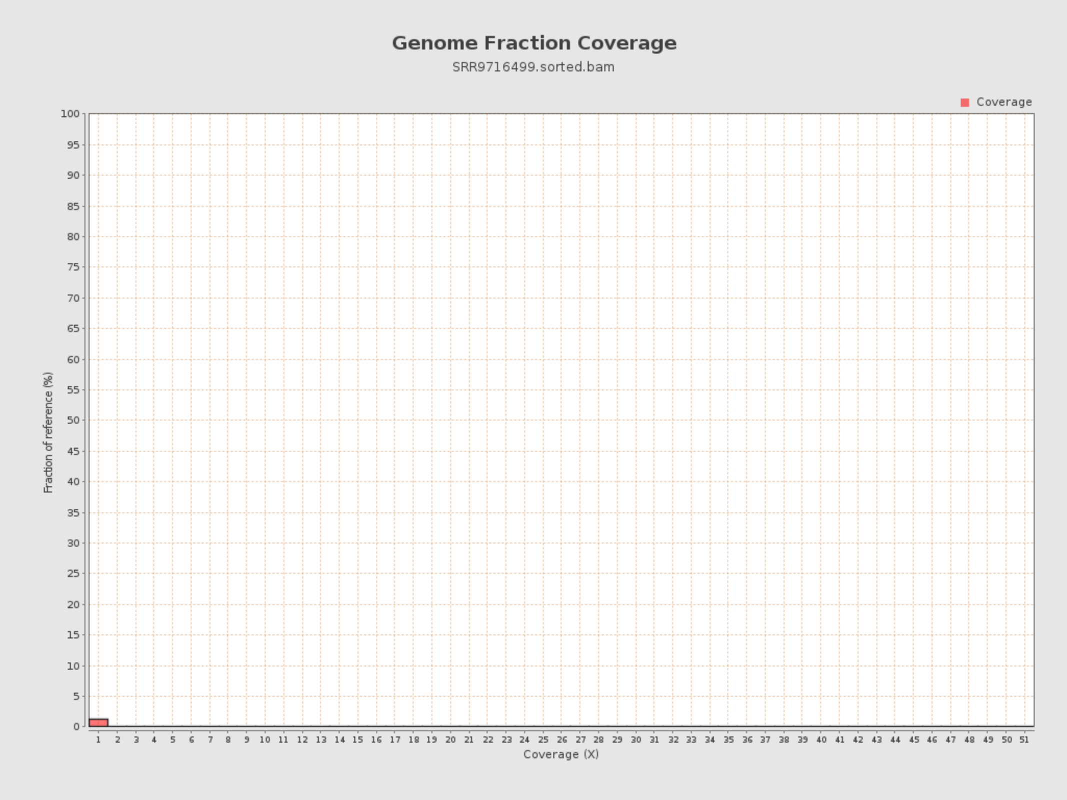
4. Results : Coverage Histogram



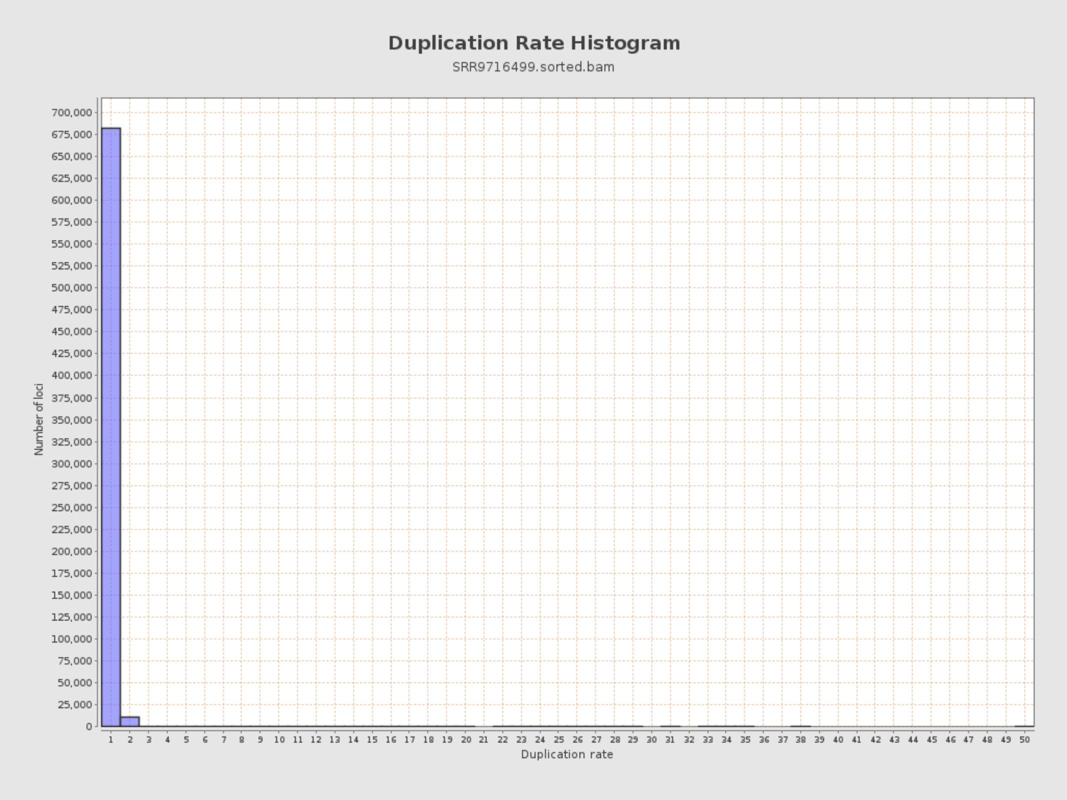
5. Results : Coverage Histogram (0-50X)



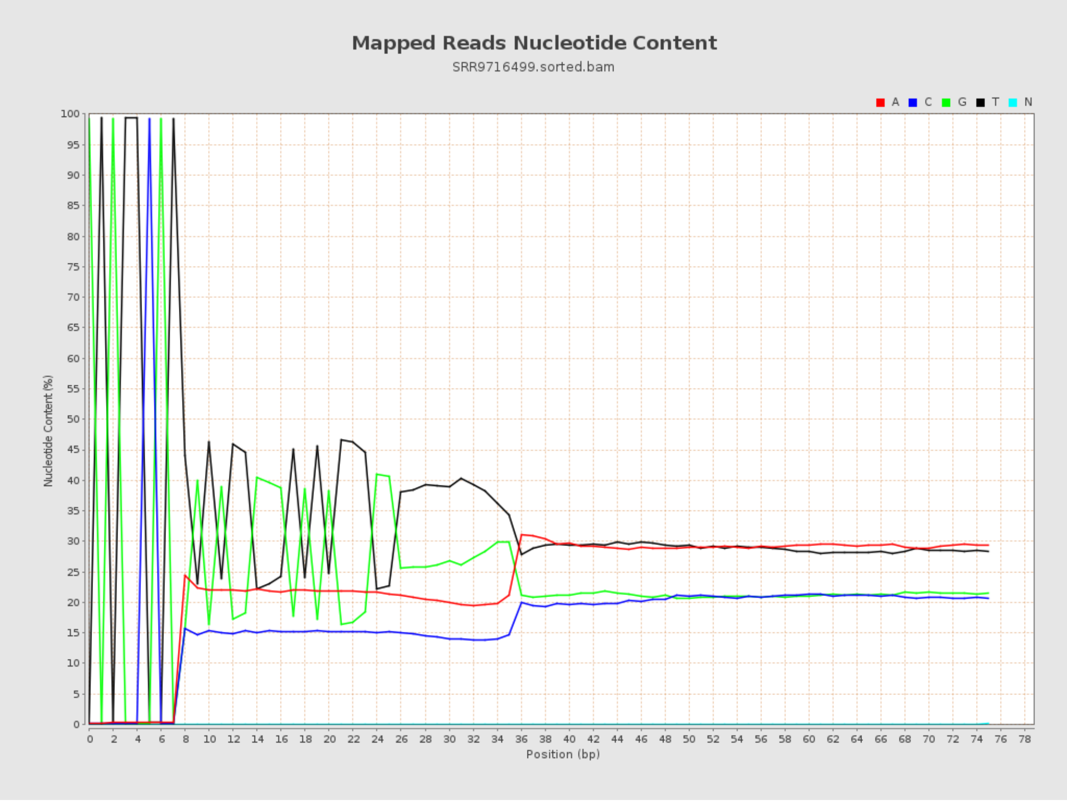
6. Results : Genome Fraction Coverage



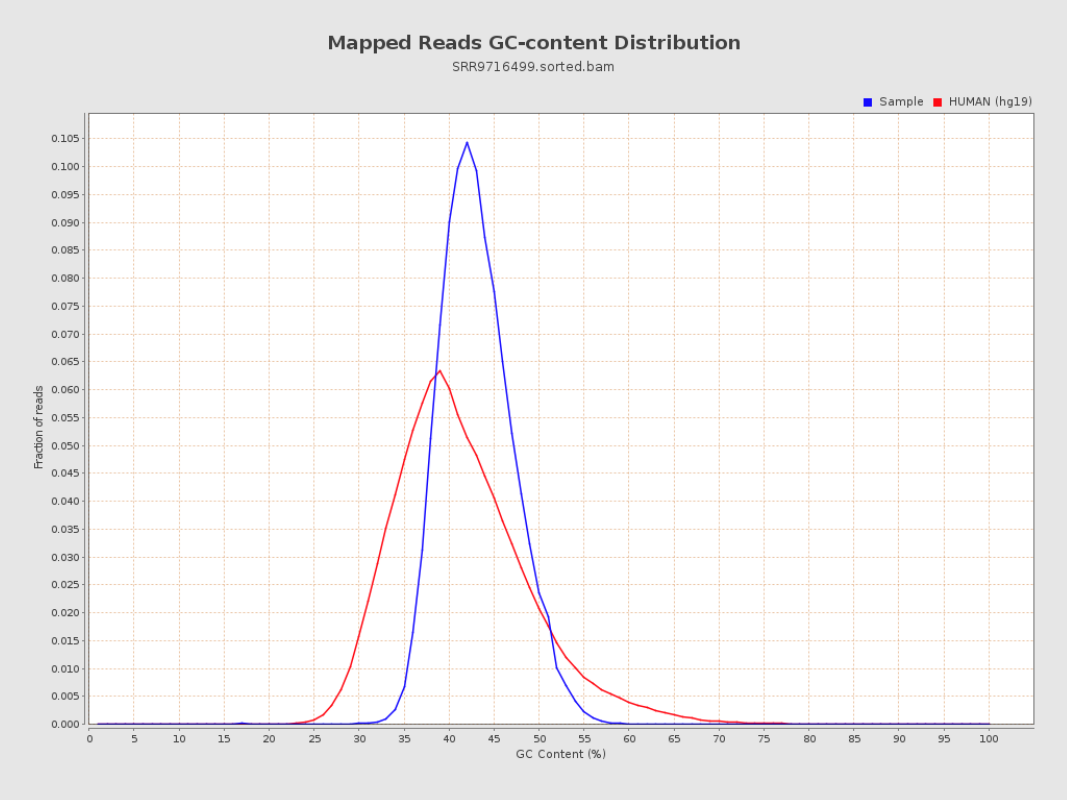
7. Results : Duplication Rate Histogram



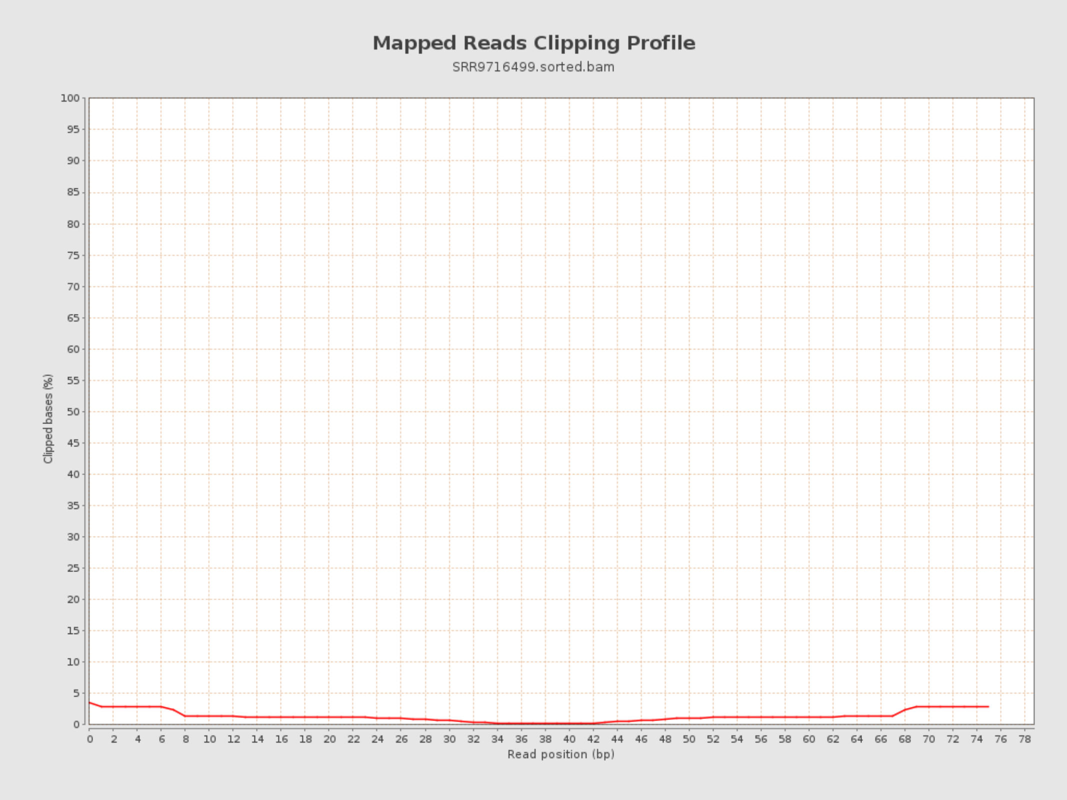
8. Results : Mapped Reads Nucleotide Content



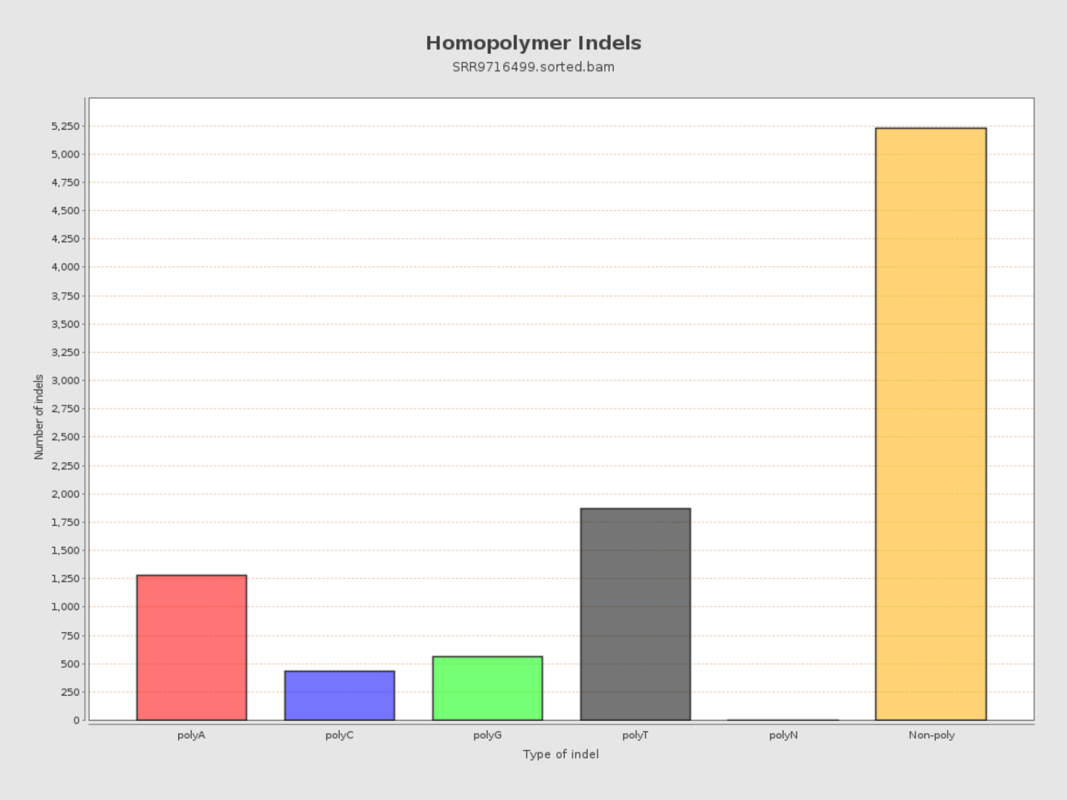
9. Results : Mapped Reads GC-content Distribution



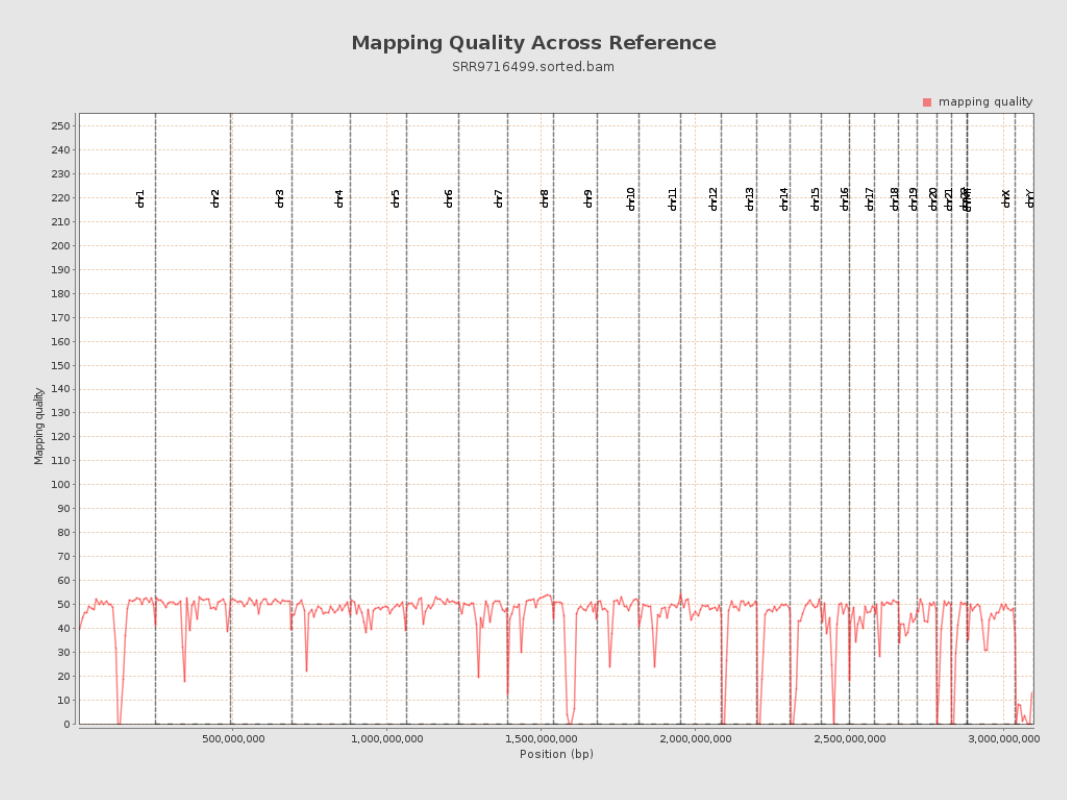
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram