Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 13:09:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716433.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_SRR9716433 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716433.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 13:09:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716433.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,481,324
Mapped reads	728,126 / 49.15%
Unmapped reads	753,198 / 50.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,985 / 0.13%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	17,047 / 1.15%
Duplication rate	1.66%
Clipped reads	728,987 / 49.21%

2.2. ACGT Content

Number/percentage of A's	9,711,042 / 24.46%
Number/percentage of C's	7,151,240 / 18.01%
Number/percentage of T's	13,114,946 / 33.03%
Number/percentage of G's	9,727,491 / 24.5%
Number/percentage of N's	595 / 0%
GC Percentage	42.51%

2.3. Coverage

Mean	0.0128

Standard Deviation	0.1534

2.4. Mapping Quality

Mean Mapping Quality	42.13

2.5. Mismatches and indels

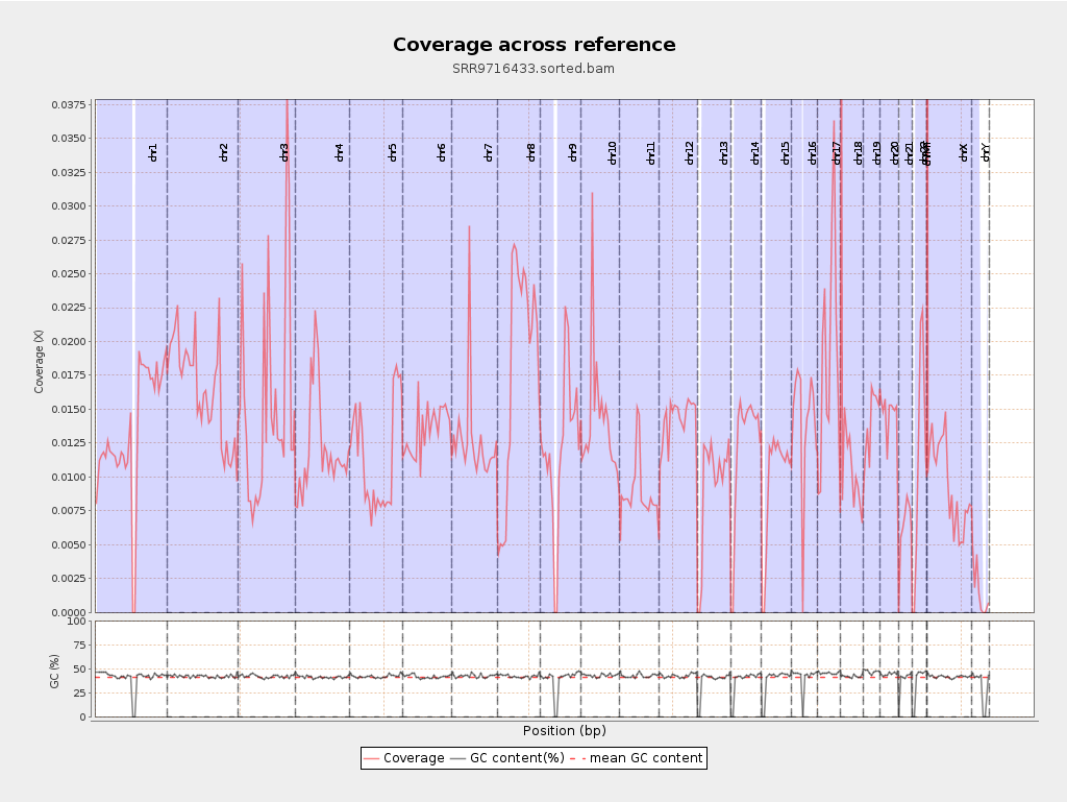
General error rate	0.54%
Mismatches	208,475
Insertions	2,694
Mapped reads with at least one insertion	0.37%
Deletions	7,218
Mapped reads with at least one deletion	0.98%
Homopolymer indels	40.23%

2.6. Chromosome stats

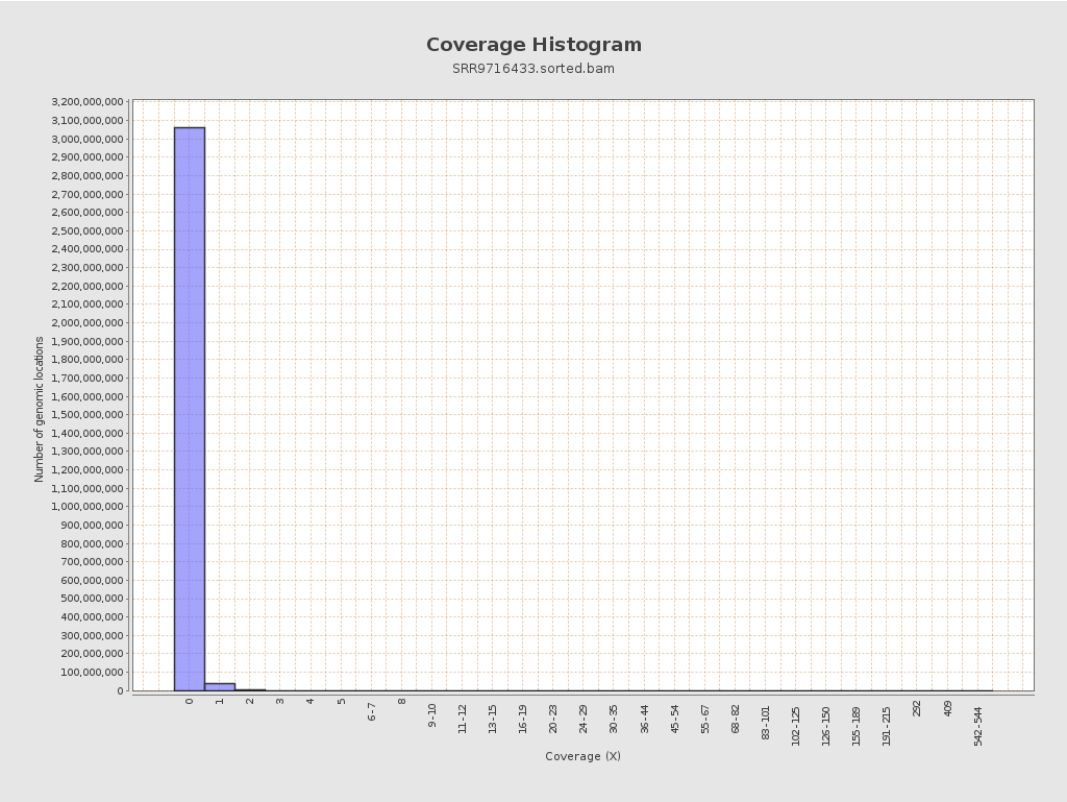
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3340109	0.0134	0.157
chr2	243199373	4002710	0.0165	0.2534
chr3	198022430	3005198	0.0152	0.1337
chr4	191154276	2311107	0.0121	0.1173
chr5	180915260	2049296	0.0113	0.1123
chr6	171115067	2295852	0.0134	0.1358
chr7	159138663	2028888	0.0127	0.2656

chr8	146364022	2674654	0.0183	0.1525
chr9	141213431	1701567	0.012	0.1243
chr10	135534747	1912639	0.0141	0.1735
chr11	135006516	1212231	0.009	0.1091
chr12	133851895	1901183	0.0142	0.1278
chr13	115169878	1072983	0.0093	0.1026
chr14	107349540	1304140	0.0121	0.1165
chr15	102531392	987356	0.0096	0.1075
chr16	90354753	1255017	0.0139	0.1278
chr17	81195210	1532226	0.0189	0.1466
chr18	78077248	936983	0.012	0.1583
chr19	59128983	833818	0.0141	0.1619
chr20	63025520	911057	0.0145	0.1277
chr21	48129895	303217	0.0063	0.0852
chr22	51304566	580914	0.0113	0.1123
chrMT	16571	4689	0.283	0.5513
chrX	155270560	1468041	0.0095	0.1143
chrY	59373566	90713	0.0015	0.0466

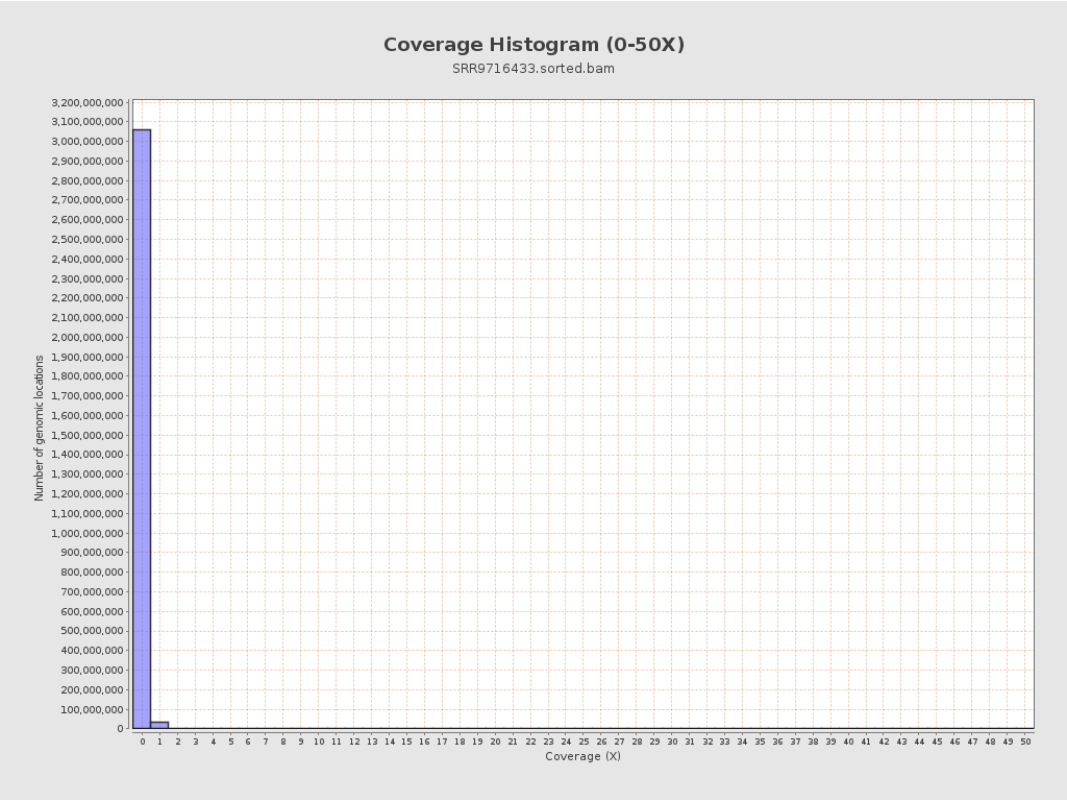
3. Results : Coverage across reference



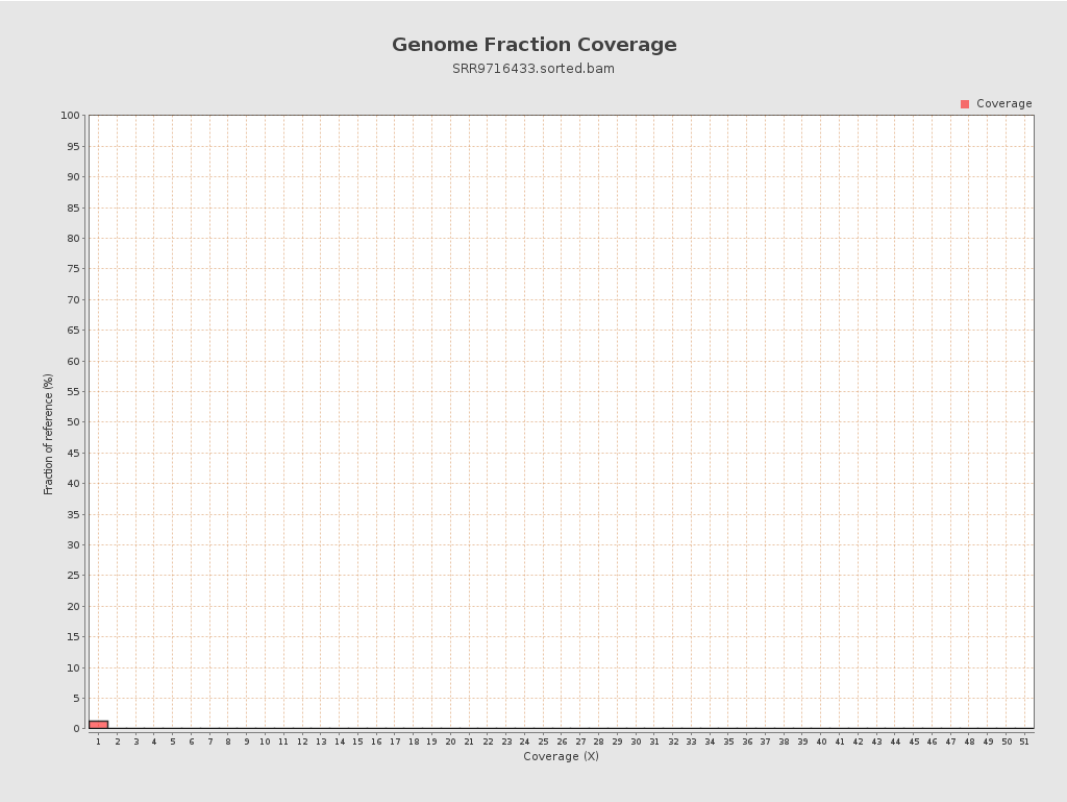
4. Results : Coverage Histogram



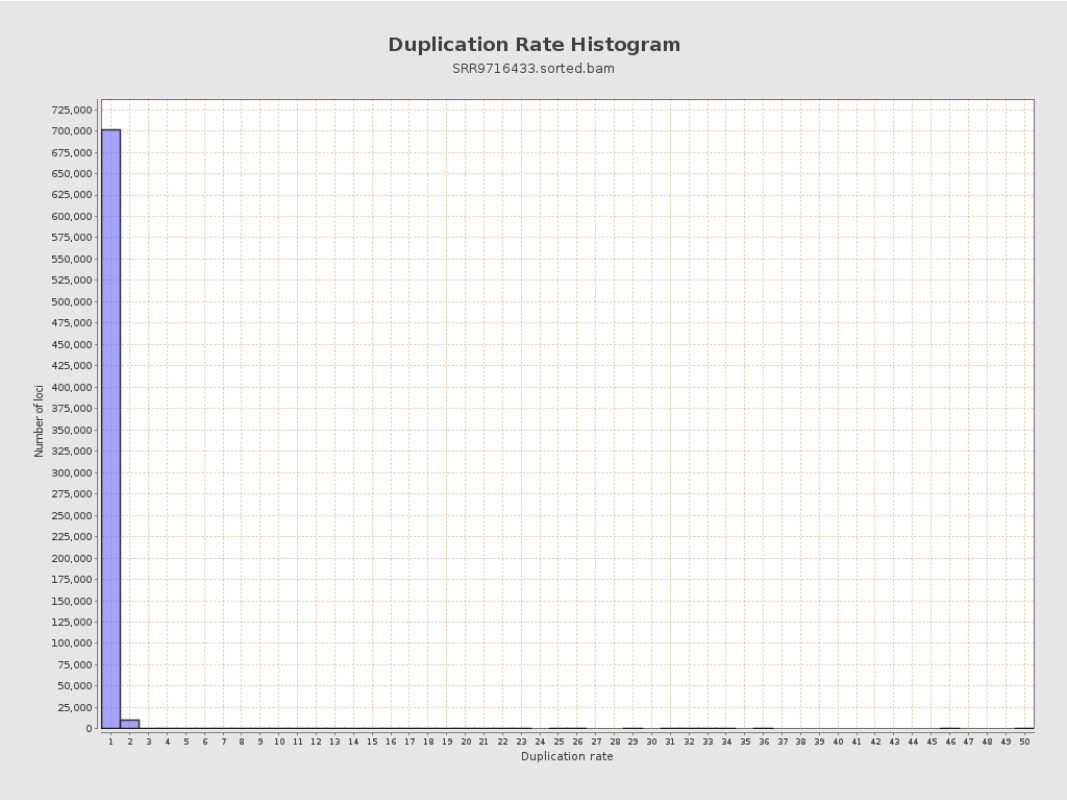
5. Results : Coverage Histogram (0-50X)



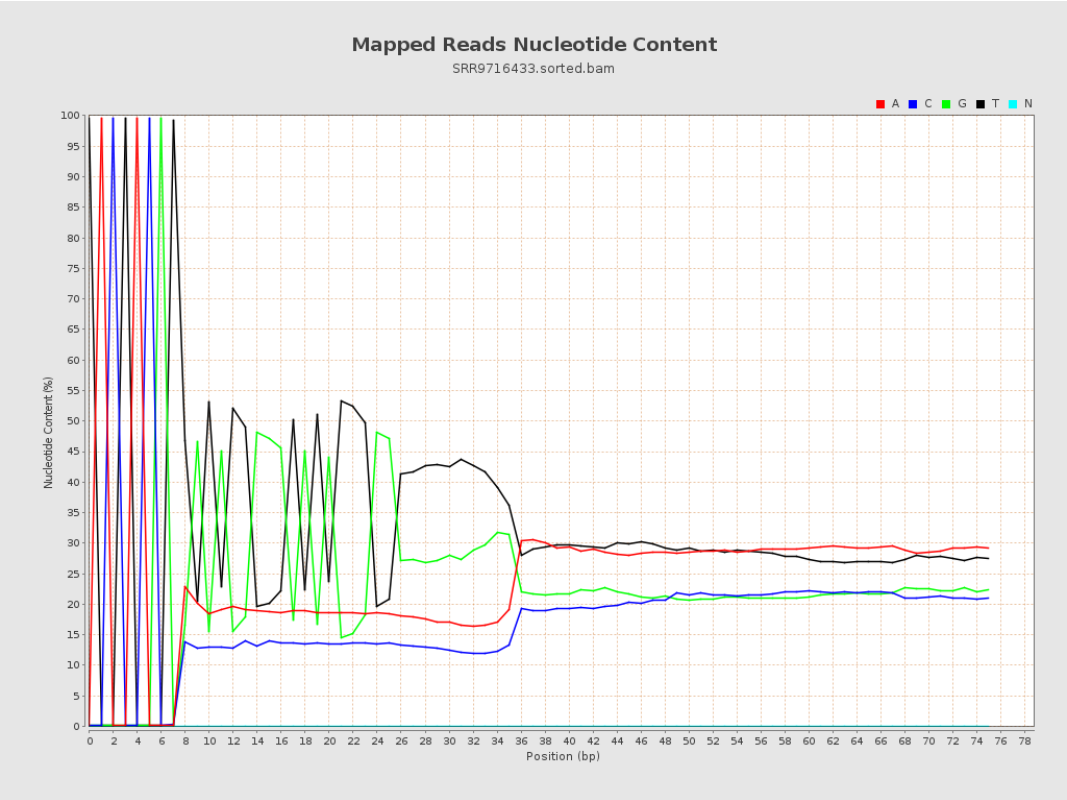
6. Results : Genome Fraction Coverage



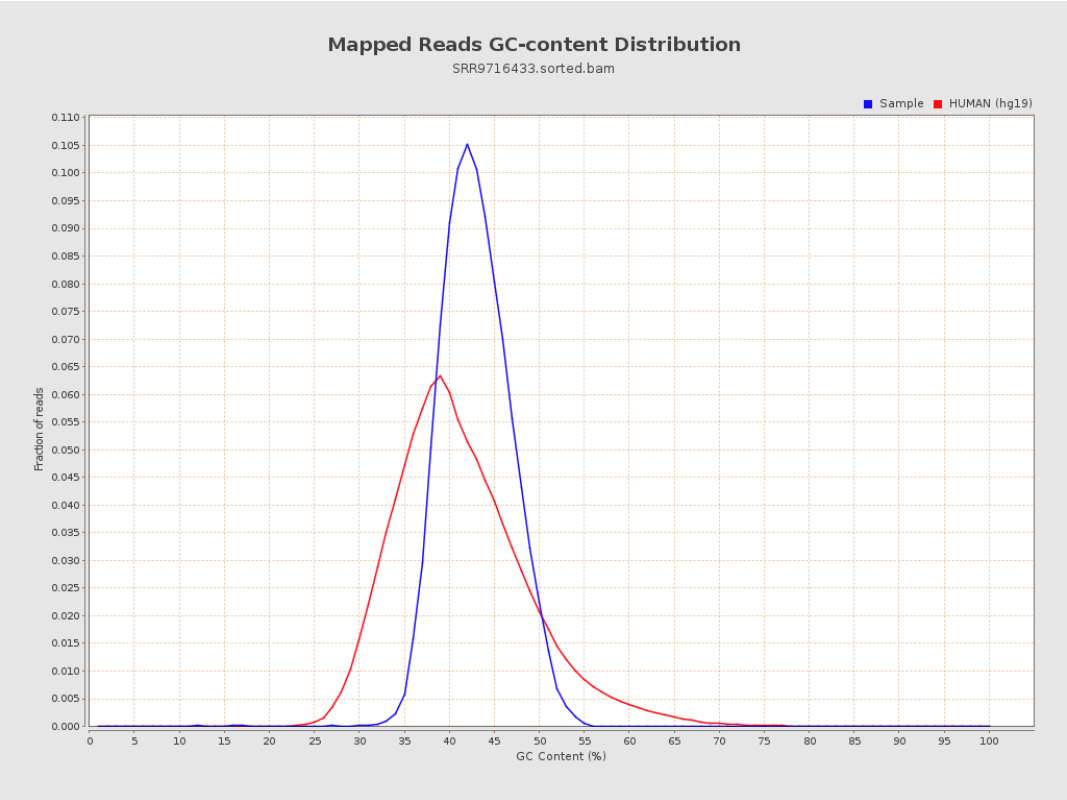
7. Results : Duplication Rate Histogram



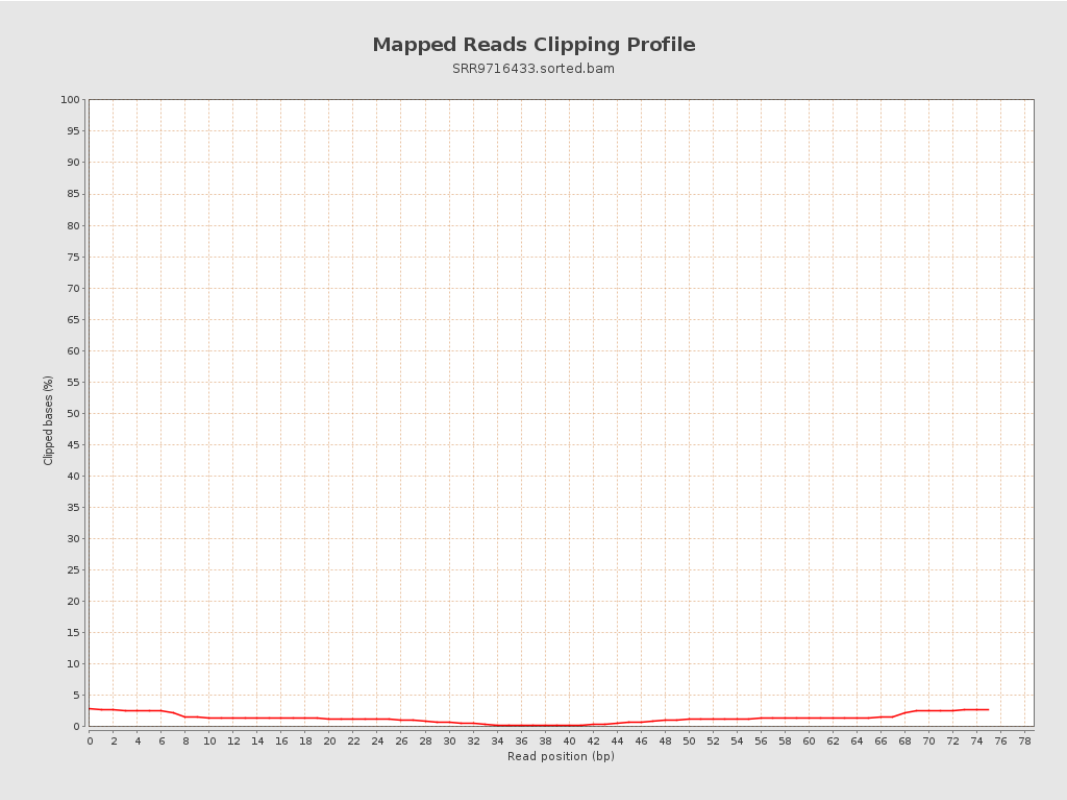
8. Results : Mapped Reads Nucleotide Content



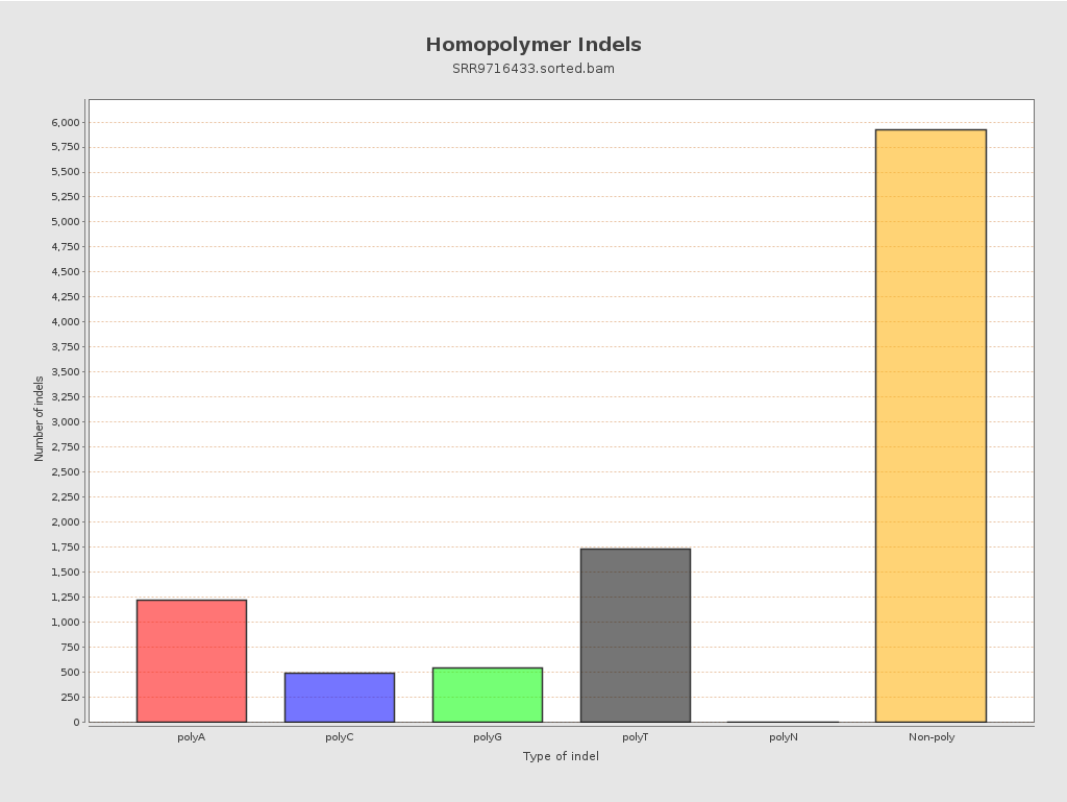
9. Results : Mapped Reads GC-content Distribution



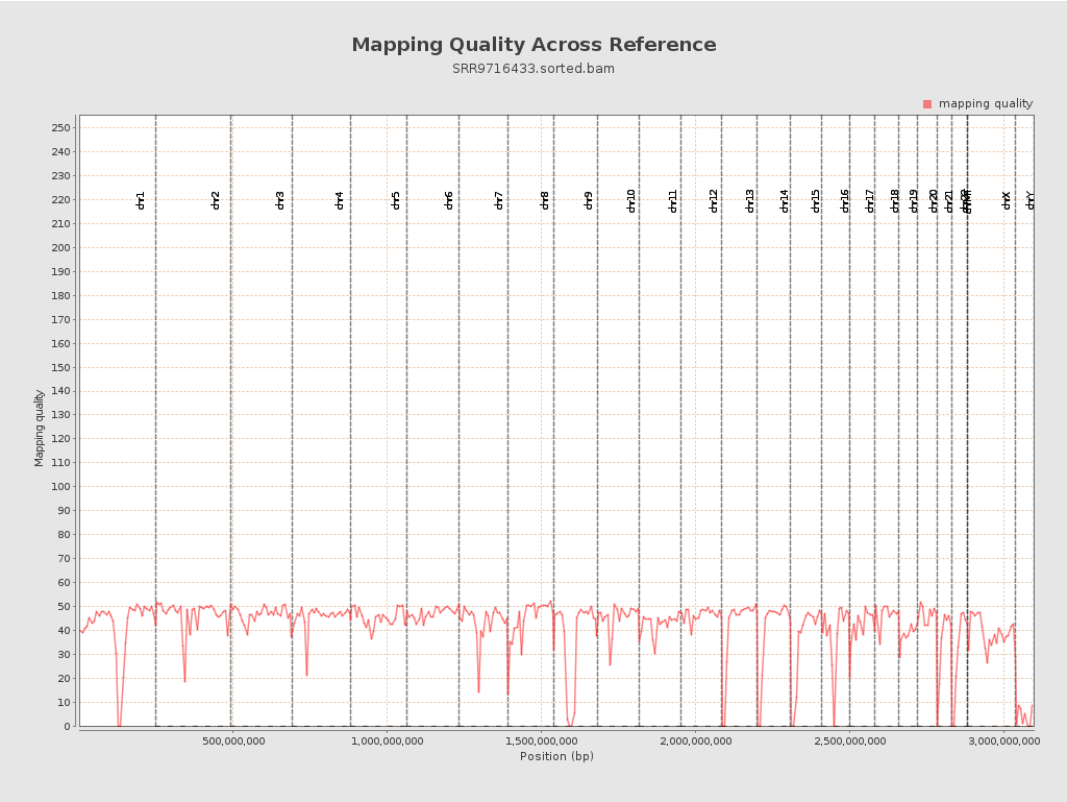
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram