Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:31:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716227.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_SRR9716227 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716227.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:31:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716227.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,595,338
Mapped reads	2,334,759 / 89.96%
Unmapped reads	260,579 / 10.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,424 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	102,040 / 3.93%
Duplication rate	3.04%
Clipped reads	2,345,065 / 90.36%

2.2. ACGT Content

Number/percentage of A's	34,840,078 / 26.06%
Number/percentage of C's	24,629,285 / 18.42%
Number/percentage of T's	40,860,676 / 30.56%
Number/percentage of G's	33,369,151 / 24.96%
Number/percentage of N's	2,076 / 0%
GC Percentage	43.38%

2.3. Coverage

Mean	0.0432

Standard Deviation	0.4111

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Mismatches and indels

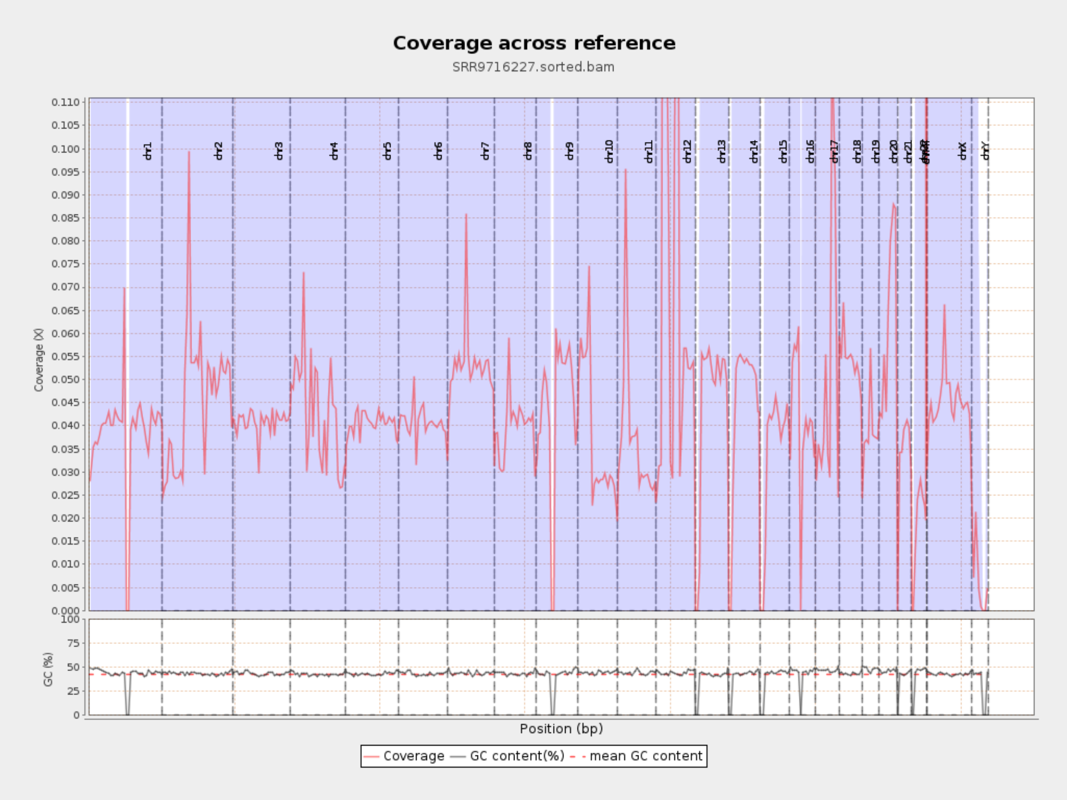
General error rate	0.56%
Mismatches	727,809
Insertions	7,895
Mapped reads with at least one insertion	0.34%
Deletions	22,497
Mapped reads with at least one deletion	0.96%
Homopolymer indels	43.03%

2.6. Chromosome stats

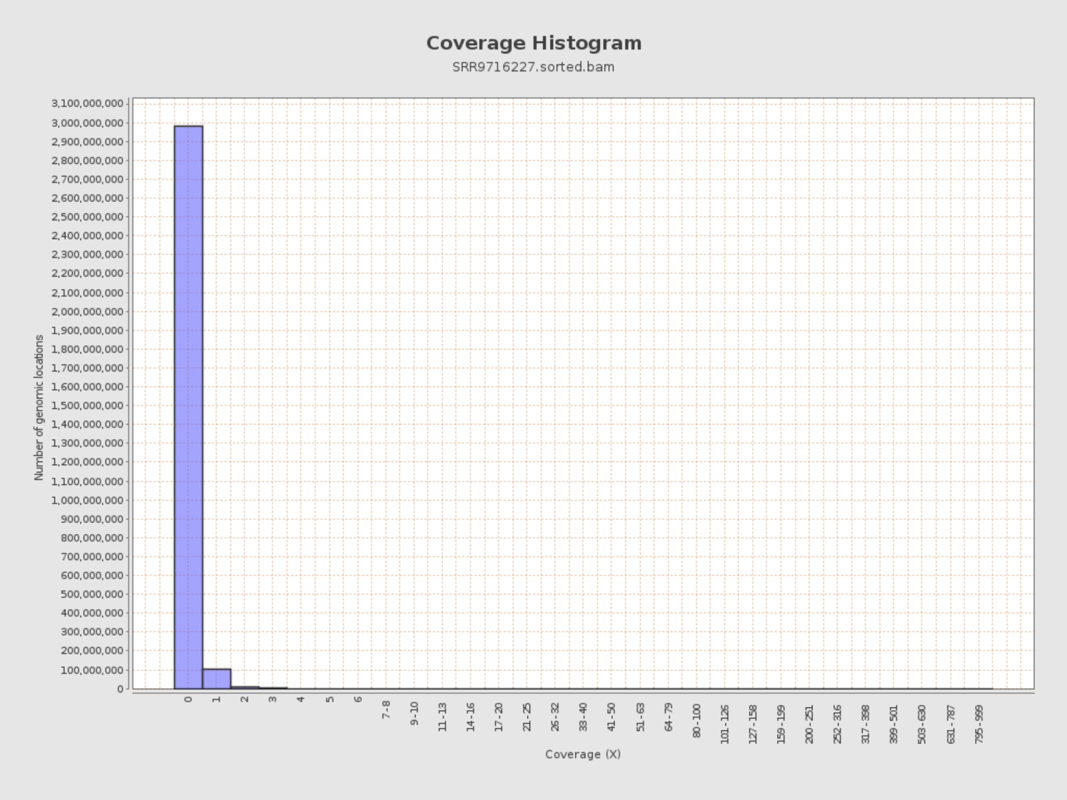
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9560864	0.0384	0.7545
chr2	243199373	11237828	0.0462	0.4677
chr3	198022430	8074250	0.0408	0.2246
chr4	191154276	8288007	0.0434	0.2629
chr5	180915260	7334565	0.0405	0.2304
chr6	171115067	6955314	0.0406	0.2647
chr7	159138663	8540223	0.0537	0.555

chr8	146364022	5843640	0.0399	0.3716
chr9	141213431	6210582	0.044	0.4488
chr10	135534747	5142507	0.0379	0.3945
chr11	135006516	5089382	0.0377	0.3326
chr12	133851895	9942839	0.0743	0.3519
chr13	115169878	5067917	0.044	0.2302
chr14	107349540	4719590	0.044	0.273
chr15	102531392	3435853	0.0335	0.2036
chr16	90354753	3724275	0.0412	0.2617
chr17	81195210	4024489	0.0496	0.2627
chr18	78077248	4272779	0.0547	0.8419
chr19	59128983	2312039	0.0391	0.5875
chr20	63025520	3964354	0.0629	0.2923
chr21	48129895	1607244	0.0334	0.257
chr22	51304566	915398	0.0178	0.1452
chrMT	16571	51903	3.1322	2.4734
chrX	155270560	7041288	0.0453	0.3167
chrY	59373566	382157	0.0064	0.1461

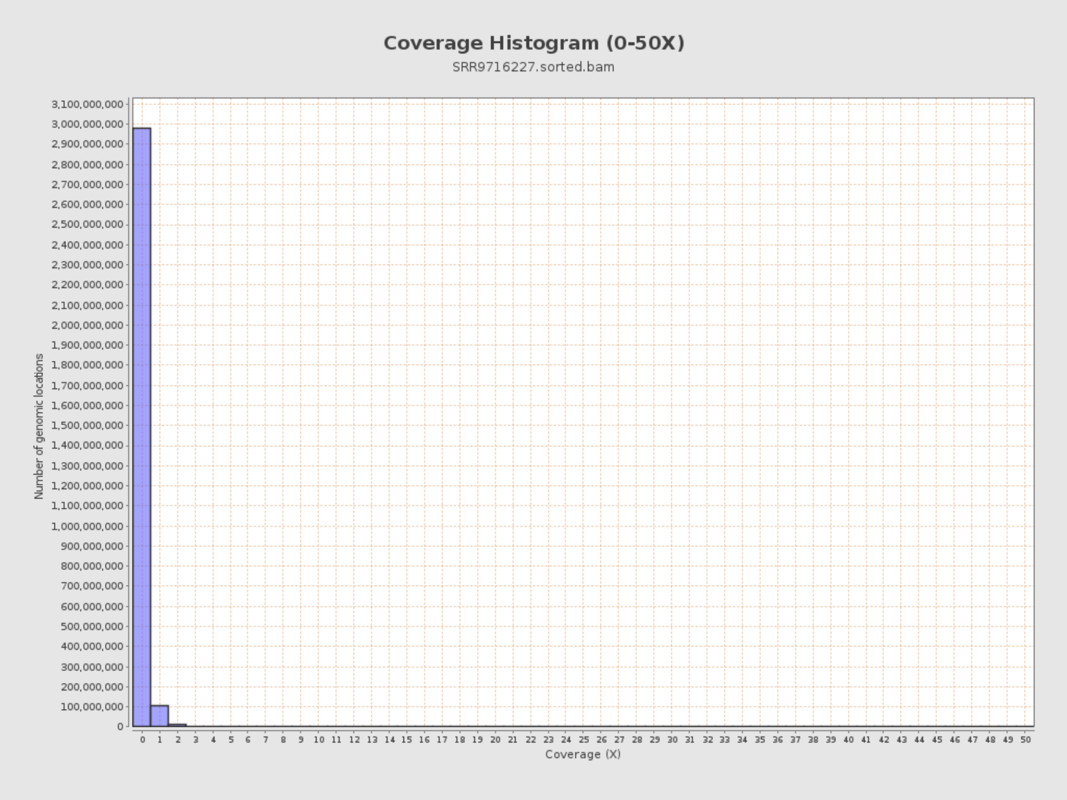
3. Results : Coverage across reference



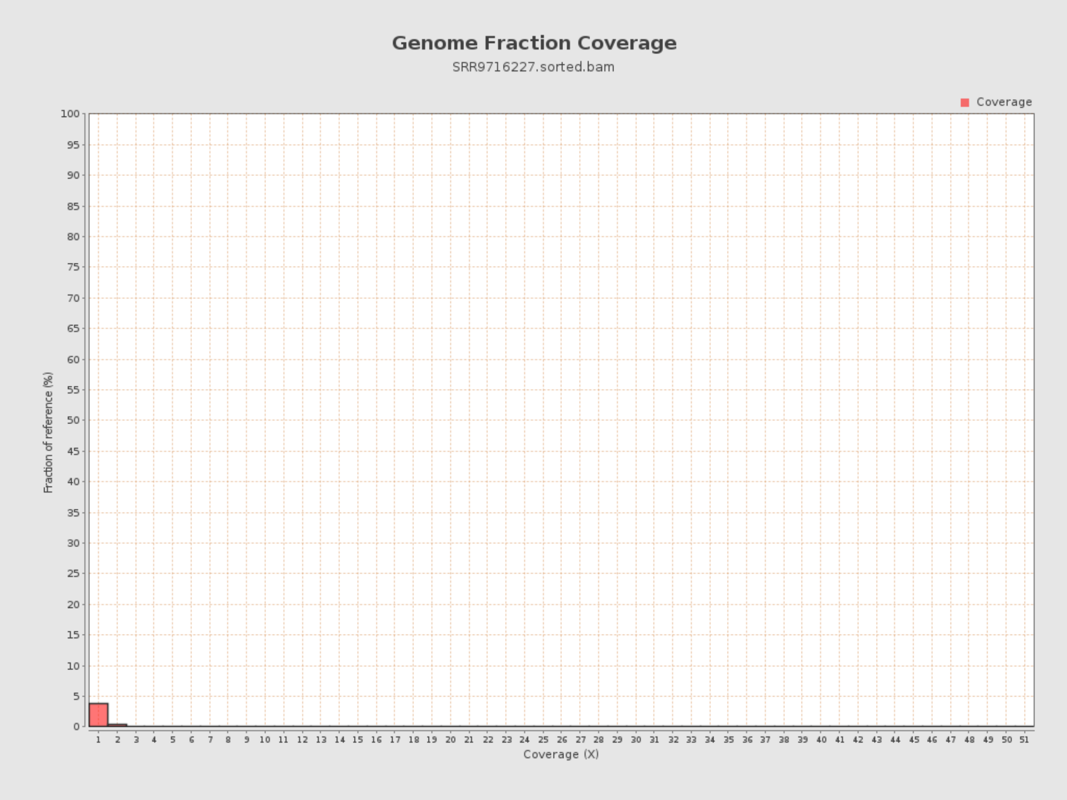
4. Results : Coverage Histogram



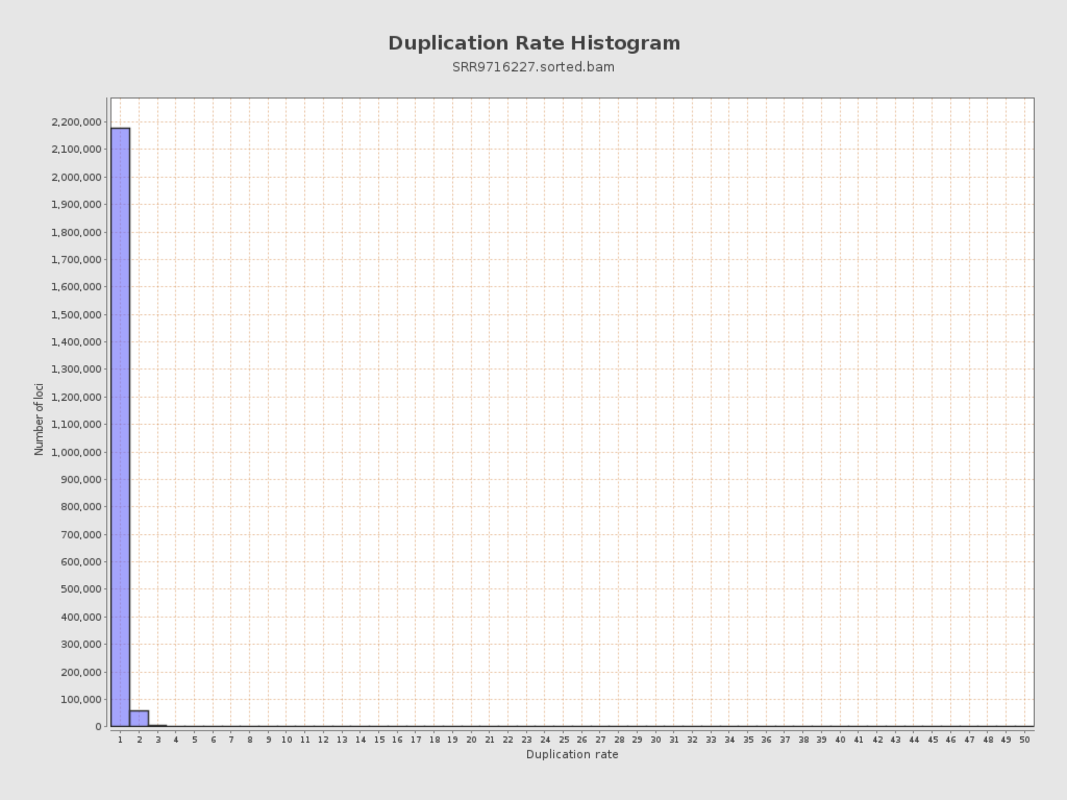
5. Results : Coverage Histogram (0-50X)



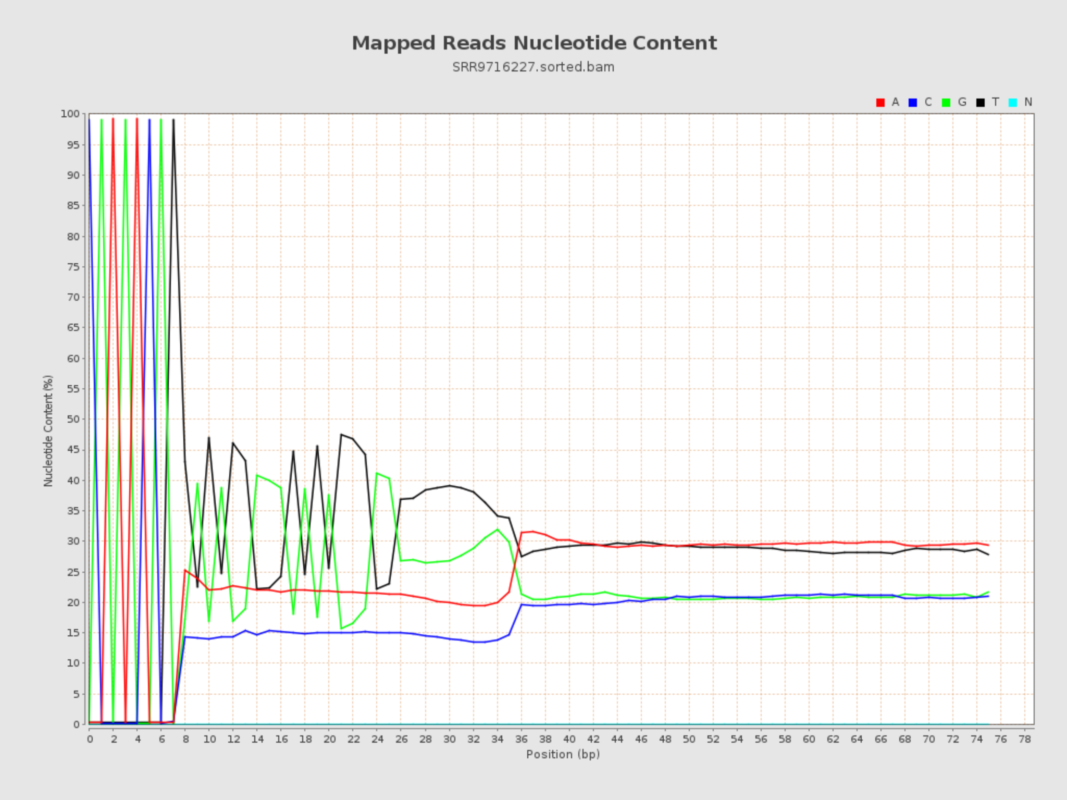
6. Results : Genome Fraction Coverage



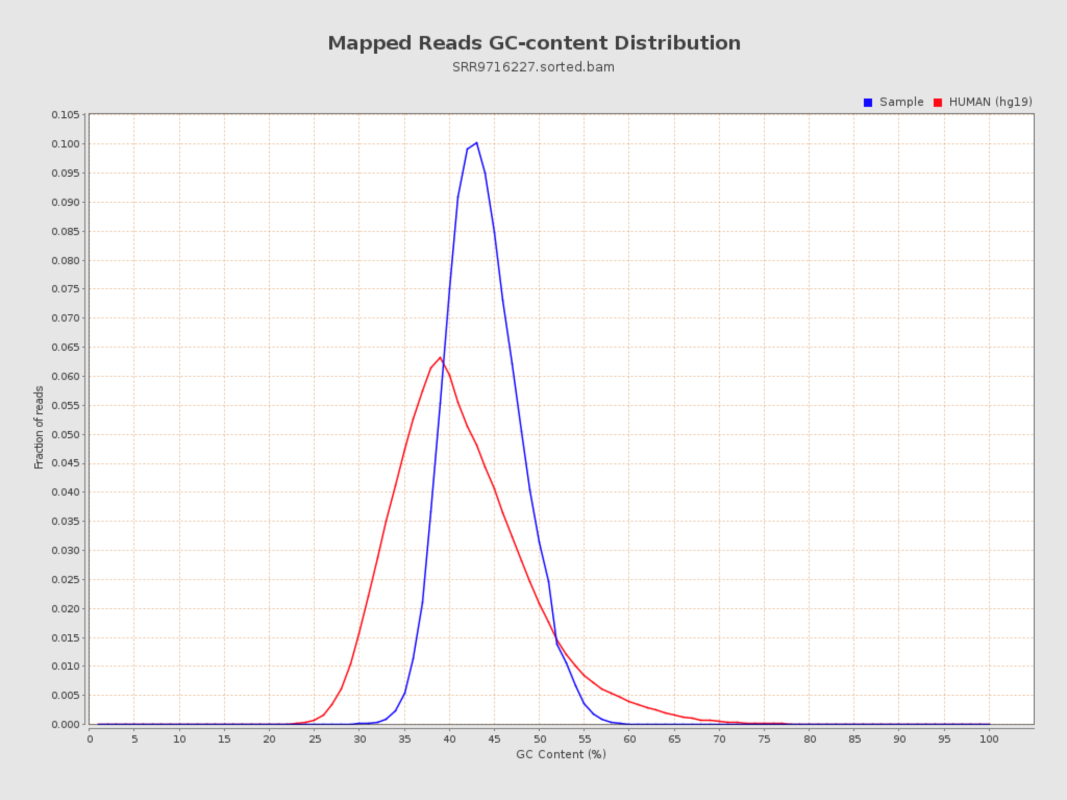
7. Results : Duplication Rate Histogram



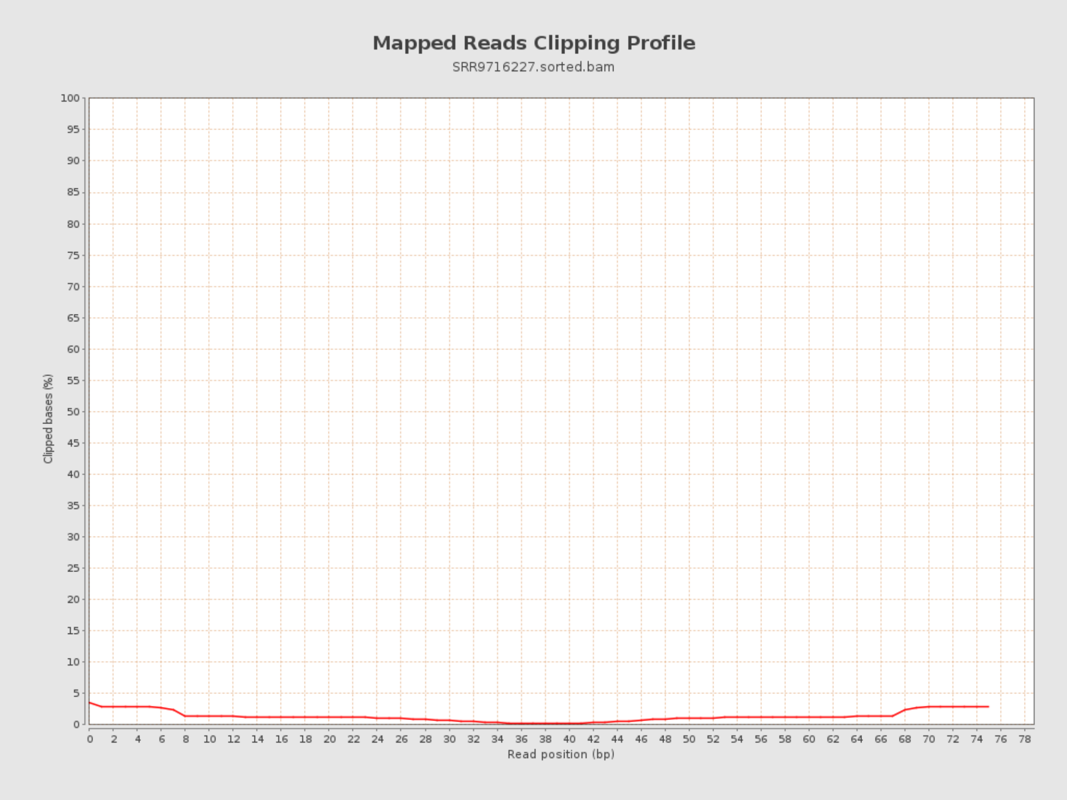
8. Results : Mapped Reads Nucleotide Content



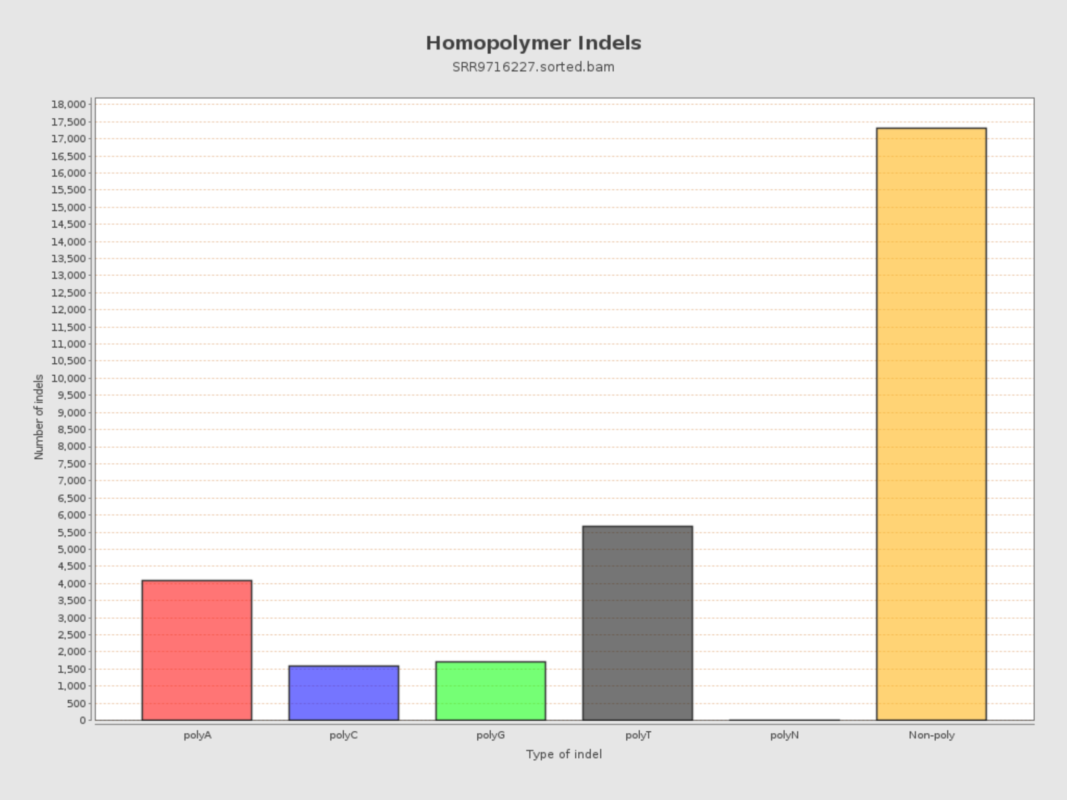
9. Results : Mapped Reads GC-content Distribution



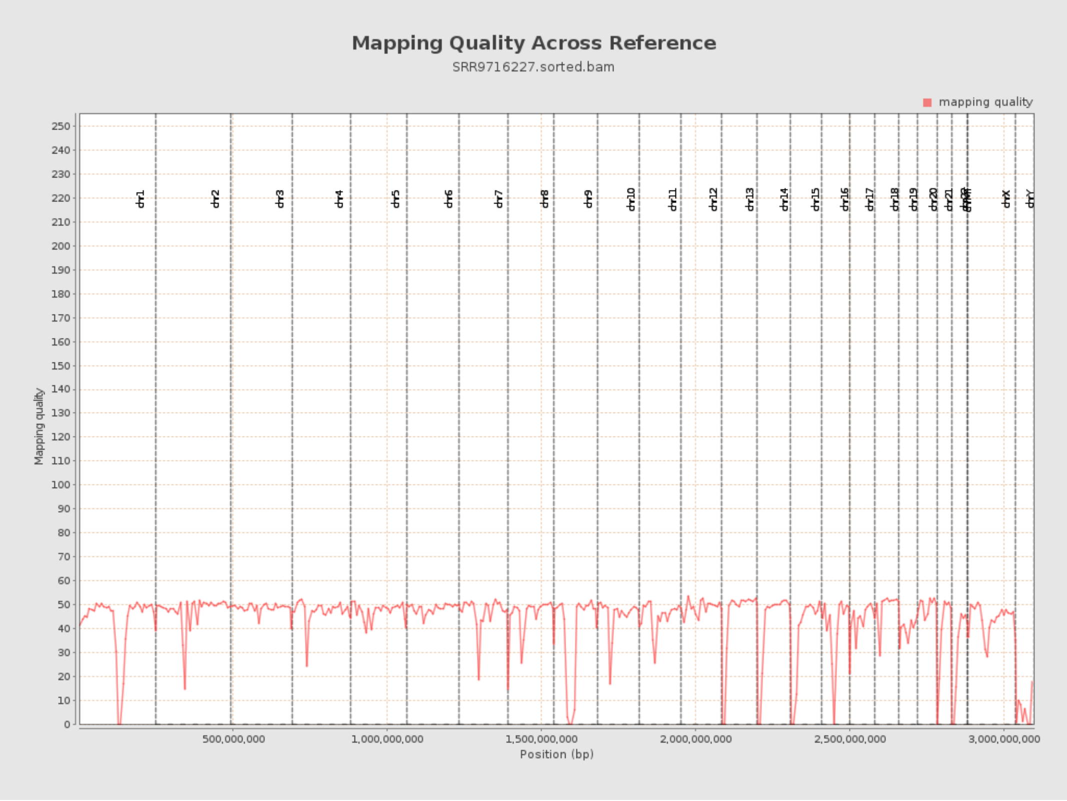
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram