Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:08:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716479.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_SRR9716479 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716479.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:08:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716479.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,509,986
Mapped reads	1,345,840 / 89.13%
Unmapped reads	164,146 / 10.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,104 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	29,776 / 1.97%
Duplication rate	1.52%
Clipped reads	1,350,009 / 89.41%

2.2. ACGT Content

Number/percentage of A's	18,248,405 / 23.82%
Number/percentage of C's	15,538,773 / 20.28%
Number/percentage of T's	23,441,398 / 30.59%
Number/percentage of G's	19,392,547 / 25.31%
Number/percentage of N's	543 / 0%
GC Percentage	45.59%

2.3. Coverage

Mean	0.0248

Standard Deviation	0.2159

2.4. Mapping Quality

Mean Mapping Quality	42.3

2.5. Mismatches and indels

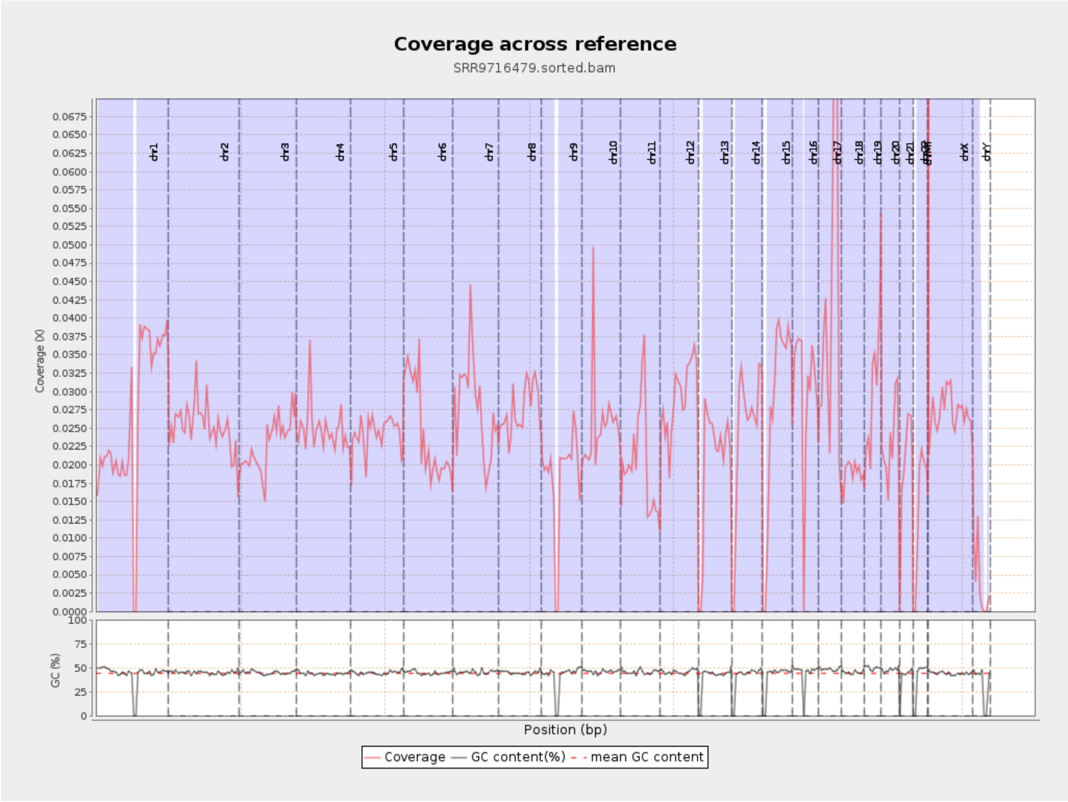
General error rate	0.54%
Mismatches	403,098
Insertions	4,449
Mapped reads with at least one insertion	0.33%
Deletions	14,452
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.03%

2.6. Chromosome stats

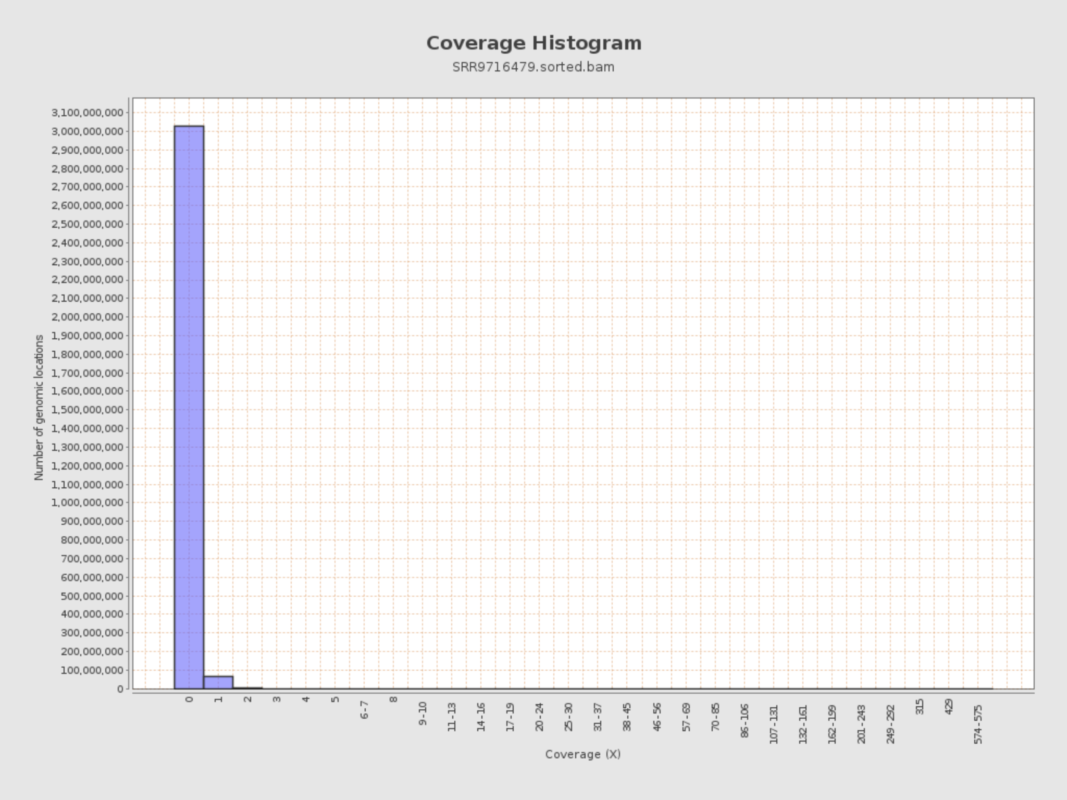
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6575959	0.0264	0.279
chr2	243199373	6130644	0.0252	0.2958
chr3	198022430	4495313	0.0227	0.1642
chr4	191154276	4752139	0.0249	0.1789
chr5	180915260	4434032	0.0245	0.1667
chr6	171115067	4188118	0.0245	0.1923
chr7	159138663	4451421	0.028	0.3043

chr8	146364022	4030369	0.0275	0.2148
chr9	141213431	2595989	0.0184	0.1685
chr10	135534747	3450202	0.0255	0.268
chr11	135006516	2754773	0.0204	0.1847
chr12	133851895	3895472	0.0291	0.1835
chr13	115169878	2334511	0.0203	0.1525
chr14	107349540	2622272	0.0244	0.1722
chr15	102531392	2875827	0.028	0.1817
chr16	90354753	2685464	0.0297	0.1949
chr17	81195210	3491153	0.043	0.2321
chr18	78077248	1468425	0.0188	0.2566
chr19	59128983	1771299	0.03	0.2638
chr20	63025520	1455064	0.0231	0.1652
chr21	48129895	971143	0.0202	0.1609
chr22	51304566	731228	0.0143	0.1285
chrMT	16571	24684	1.4896	1.6404
chrX	155270560	4228407	0.0272	0.1862
chrY	59373566	230928	0.0039	0.1107

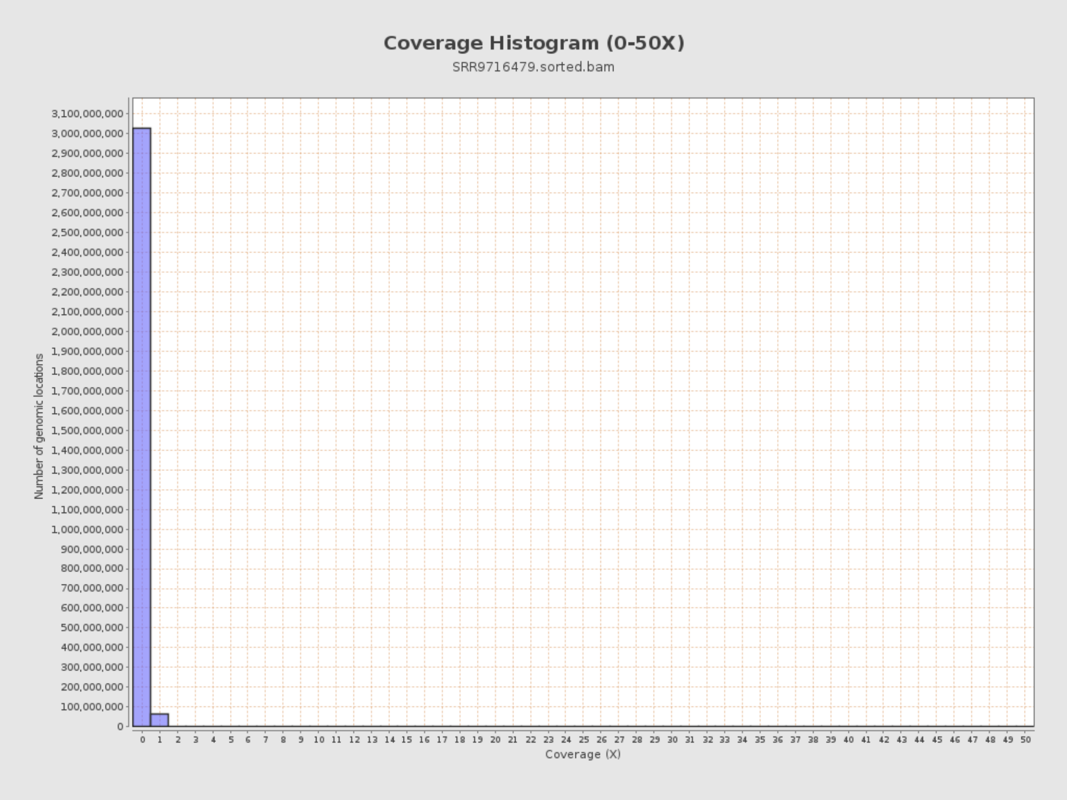
3. Results : Coverage across reference



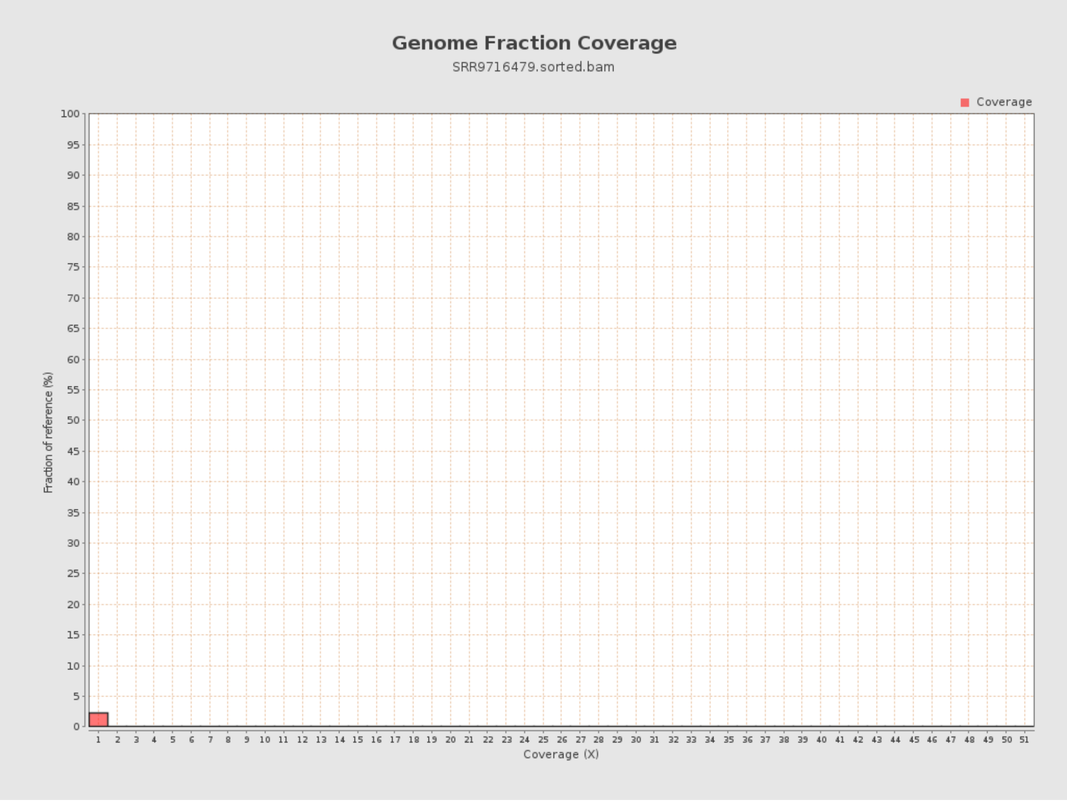
4. Results : Coverage Histogram



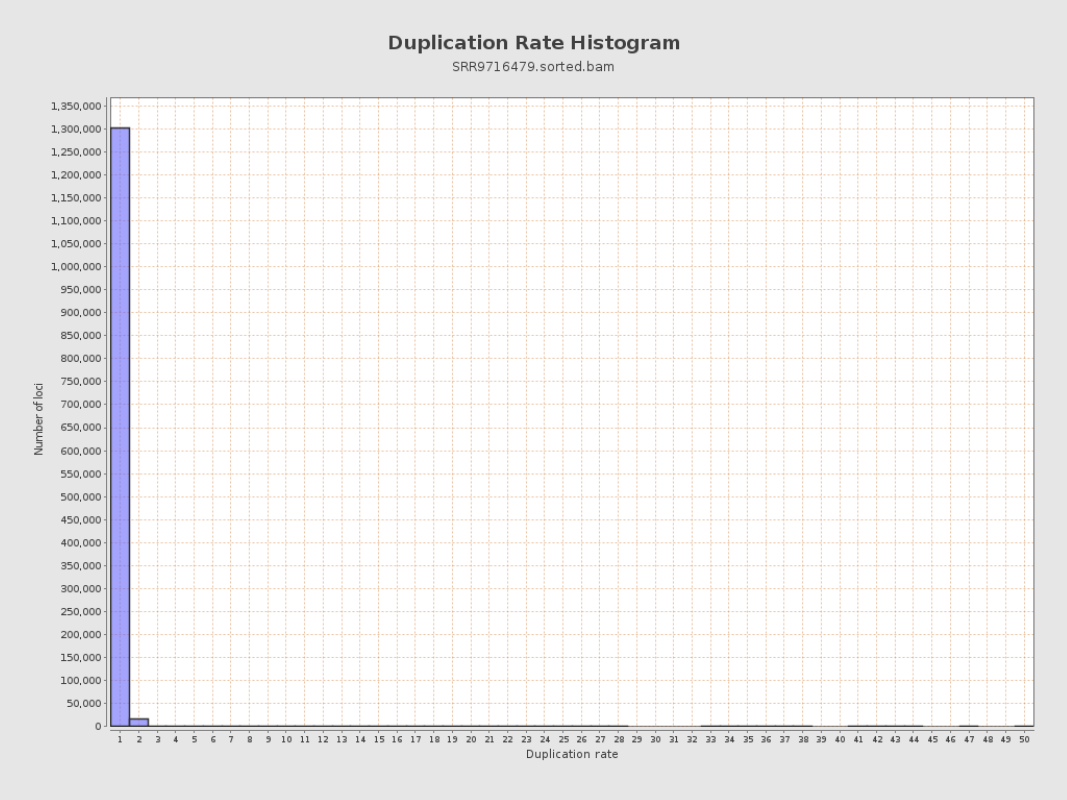
5. Results : Coverage Histogram (0-50X)



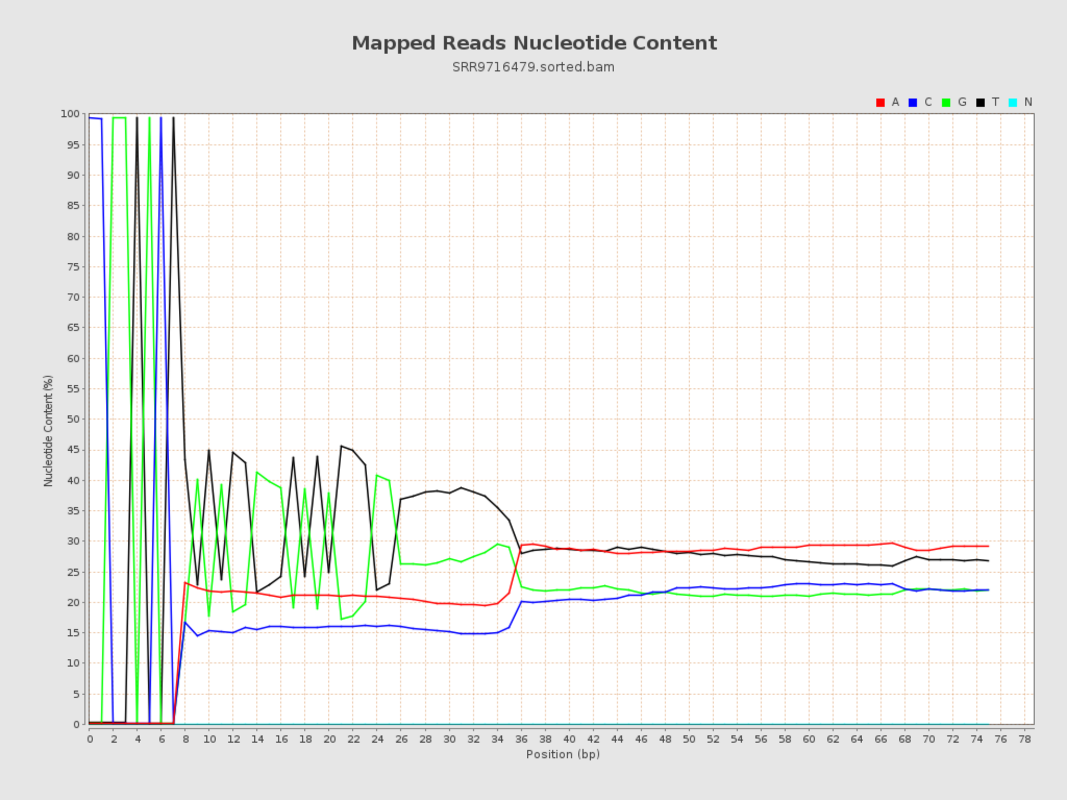
6. Results : Genome Fraction Coverage



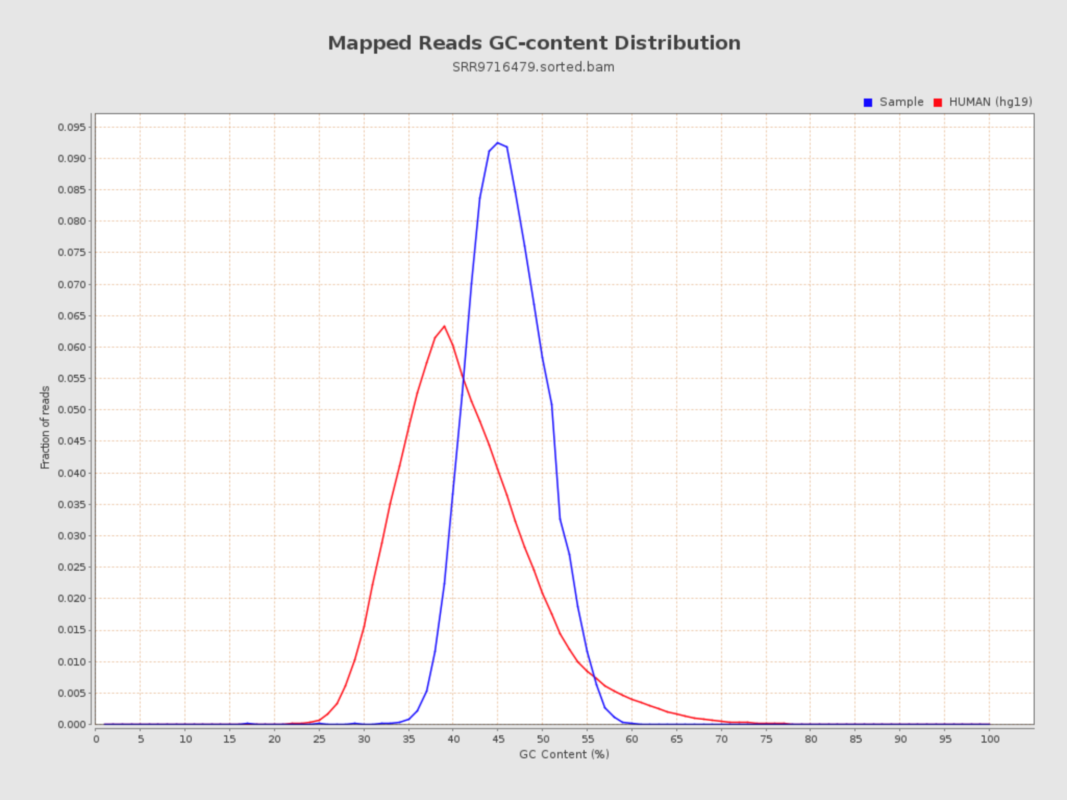
7. Results : Duplication Rate Histogram



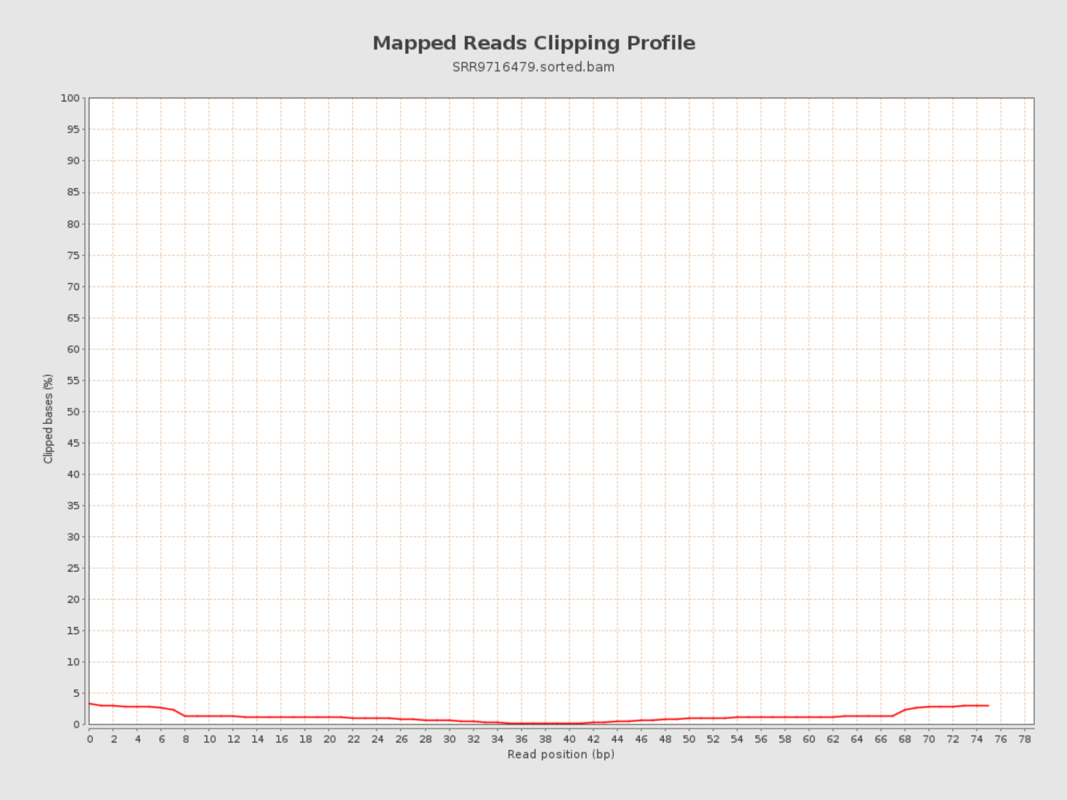
8. Results : Mapped Reads Nucleotide Content



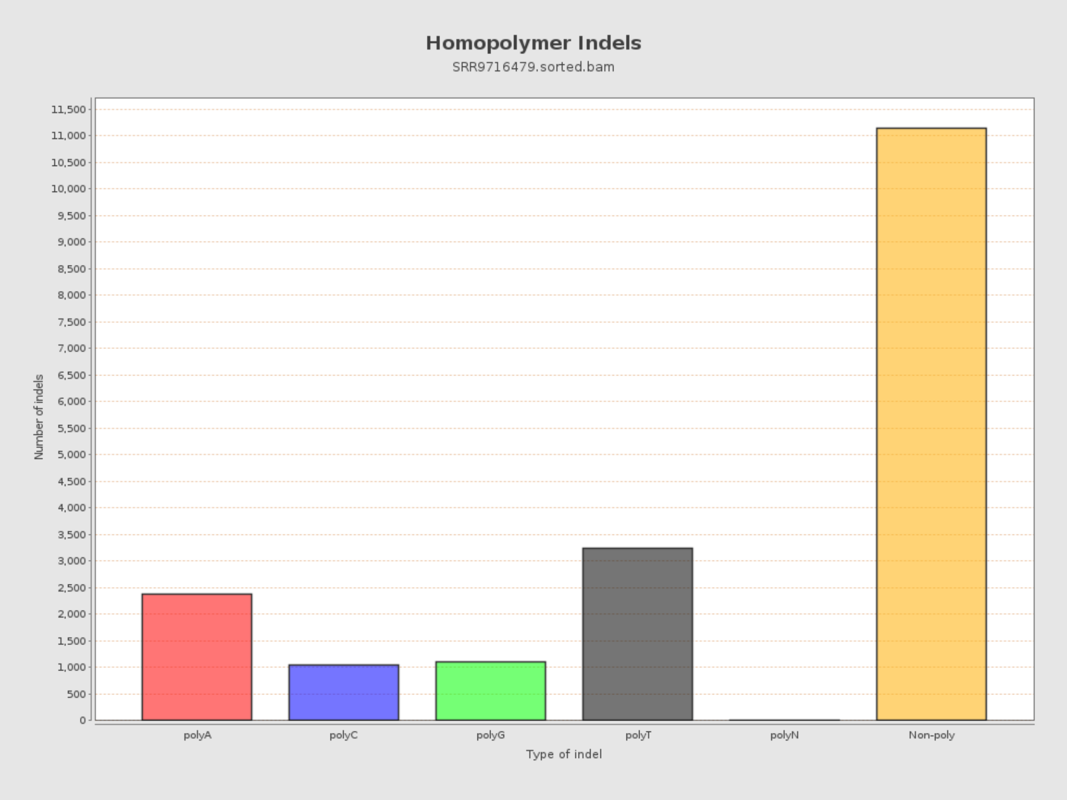
9. Results : Mapped Reads GC-content Distribution



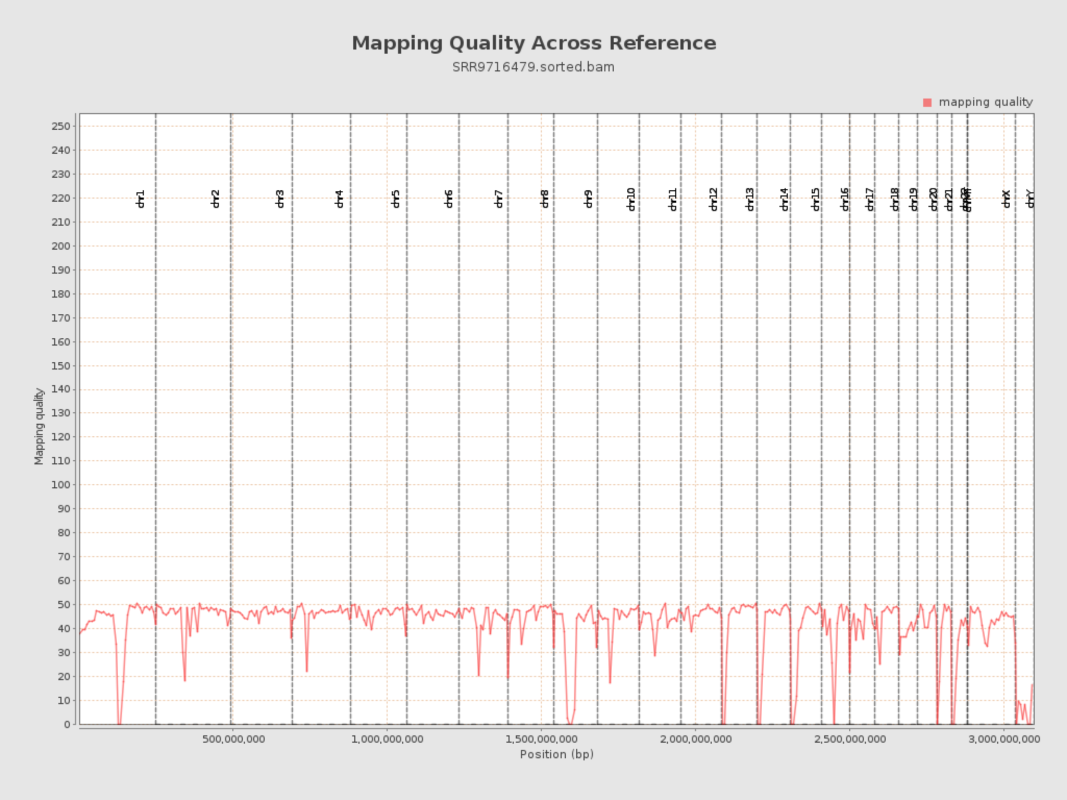
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram