Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:25:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716485.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_SRR9716485 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716485.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:25:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716485.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	656,491
Mapped reads	390,566 / 59.49%
Unmapped reads	265,925 / 40.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,715 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	7,198 / 1.1%
Duplication rate	1.44%
Clipped reads	391,429 / 59.62%

2.2. ACGT Content

Number/percentage of A's	5,678,874 / 25.51%
Number/percentage of C's	4,240,105 / 19.04%
Number/percentage of T's	7,065,128 / 31.73%
Number/percentage of G's	5,279,571 / 23.71%
Number/percentage of N's	314 / 0%
GC Percentage	42.76%

2.3. Coverage

Mean	0.0072

Standard Deviation	0.1007

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

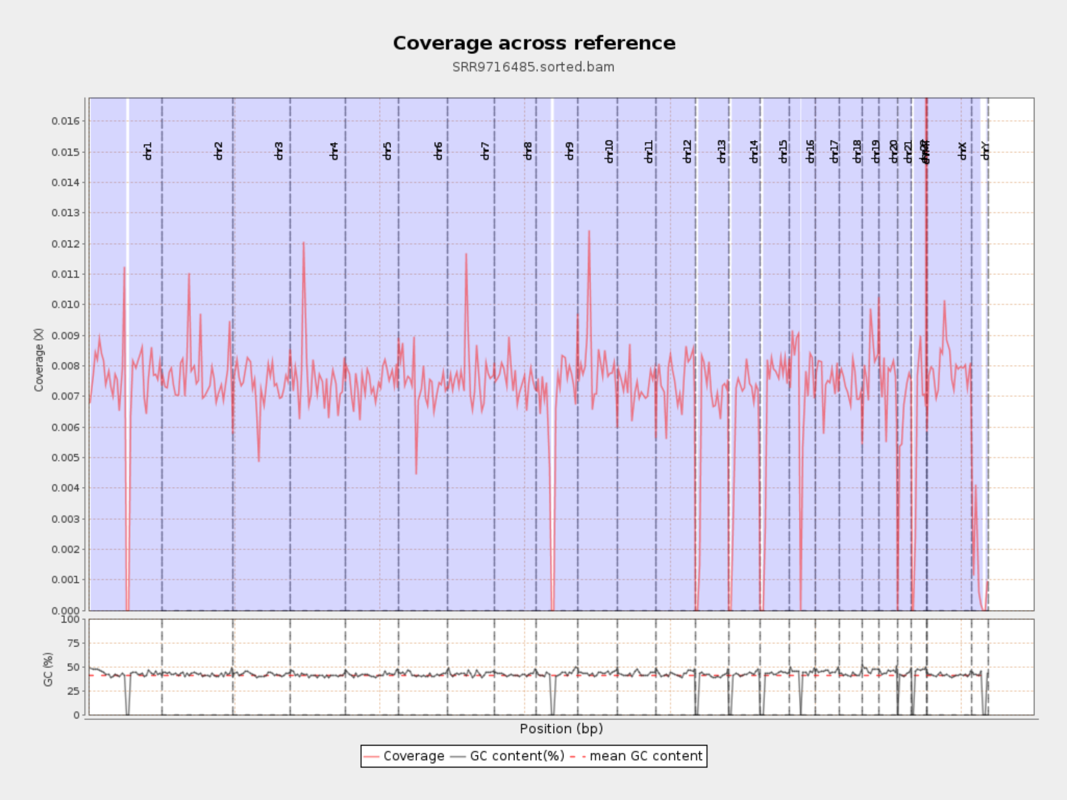
General error rate	0.52%
Mismatches	112,693
Insertions	1,498
Mapped reads with at least one insertion	0.38%
Deletions	3,981
Mapped reads with at least one deletion	1.01%
Homopolymer indels	40.23%

2.6. Chromosome stats

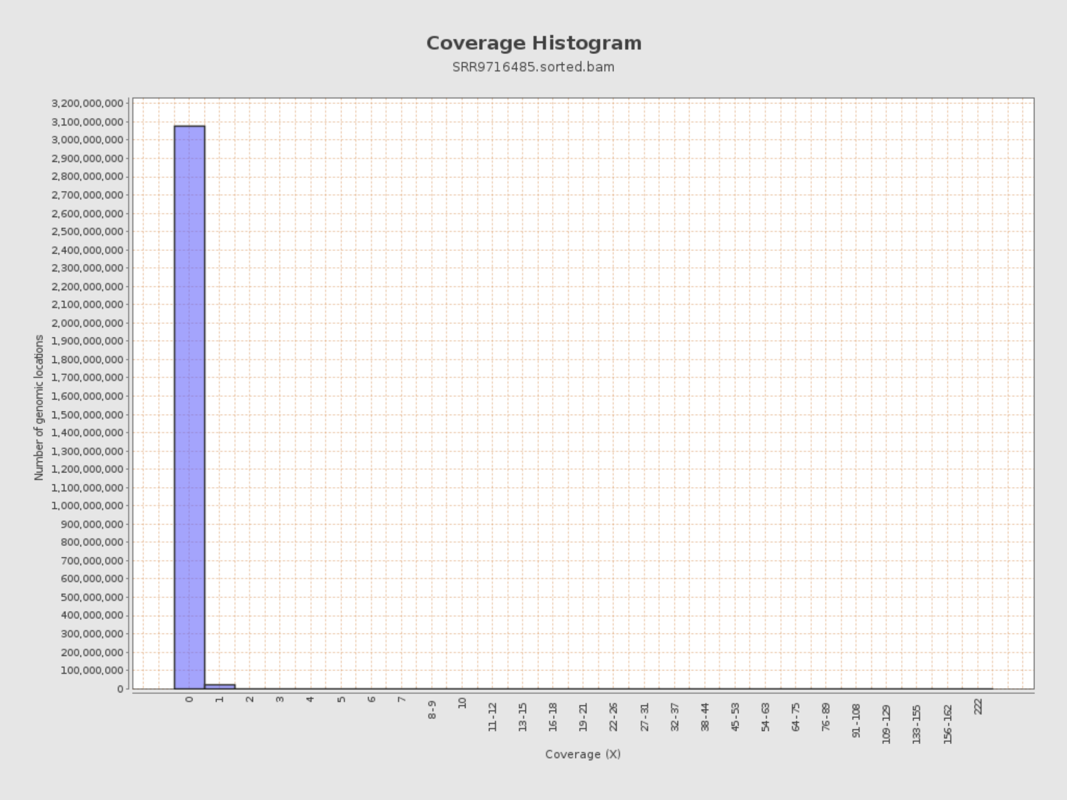
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1834827	0.0074	0.1428
chr2	243199373	1876941	0.0077	0.1274
chr3	198022430	1462826	0.0074	0.0889
chr4	191154276	1442739	0.0075	0.0919
chr5	180915260	1350625	0.0075	0.0892
chr6	171115067	1268490	0.0074	0.0932
chr7	159138663	1227730	0.0077	0.1103

chr8	146364022	1108381	0.0076	0.096
chr9	141213431	917696	0.0065	0.0892
chr10	135534747	1091786	0.0081	0.1025
chr11	135006516	991138	0.0073	0.0953
chr12	133851895	1013072	0.0076	0.09
chr13	115169878	706878	0.0061	0.0808
chr14	107349540	653848	0.0061	0.0818
chr15	102531392	656847	0.0064	0.0826
chr16	90354753	651948	0.0072	0.0884
chr17	81195210	610314	0.0075	0.0907
chr18	78077248	577795	0.0074	0.1164
chr19	59128983	486022	0.0082	0.1189
chr20	63025520	470838	0.0075	0.0895
chr21	48129895	290519	0.006	0.0823
chr22	51304566	270053	0.0053	0.0749
chrMT	16571	8583	0.518	0.8203
chrX	155270560	1231410	0.0079	0.0954
chrY	59373566	68824	0.0012	0.0422

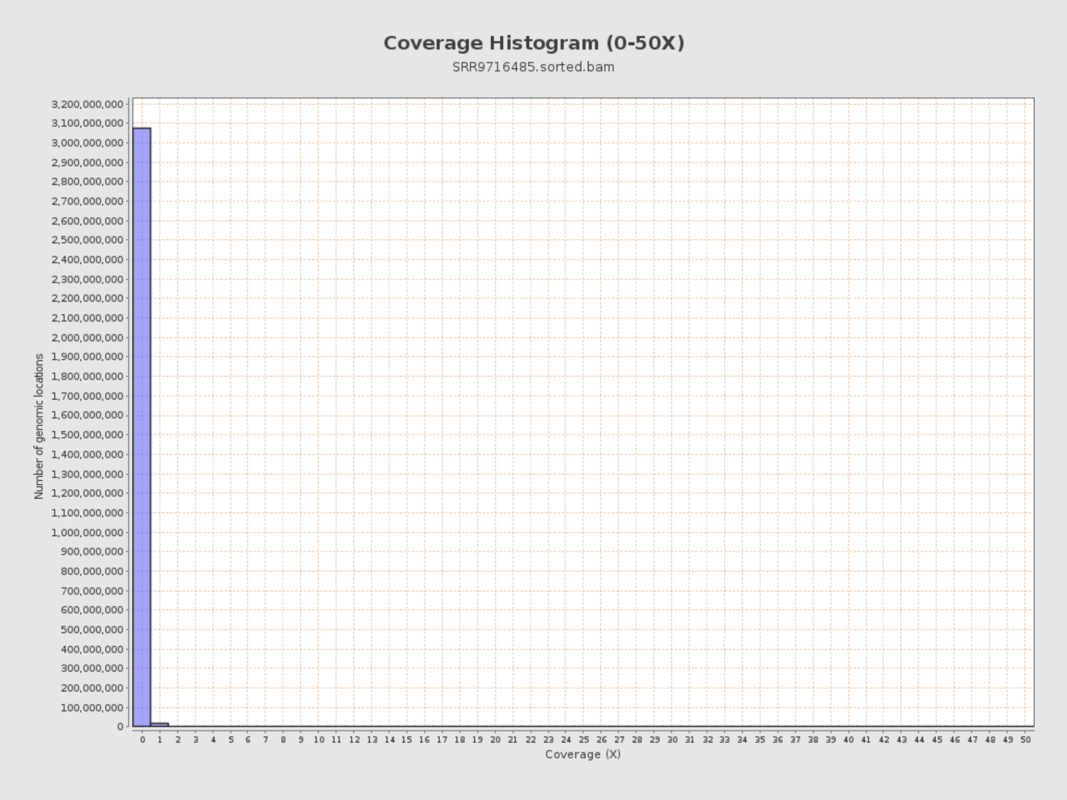
3. Results : Coverage across reference



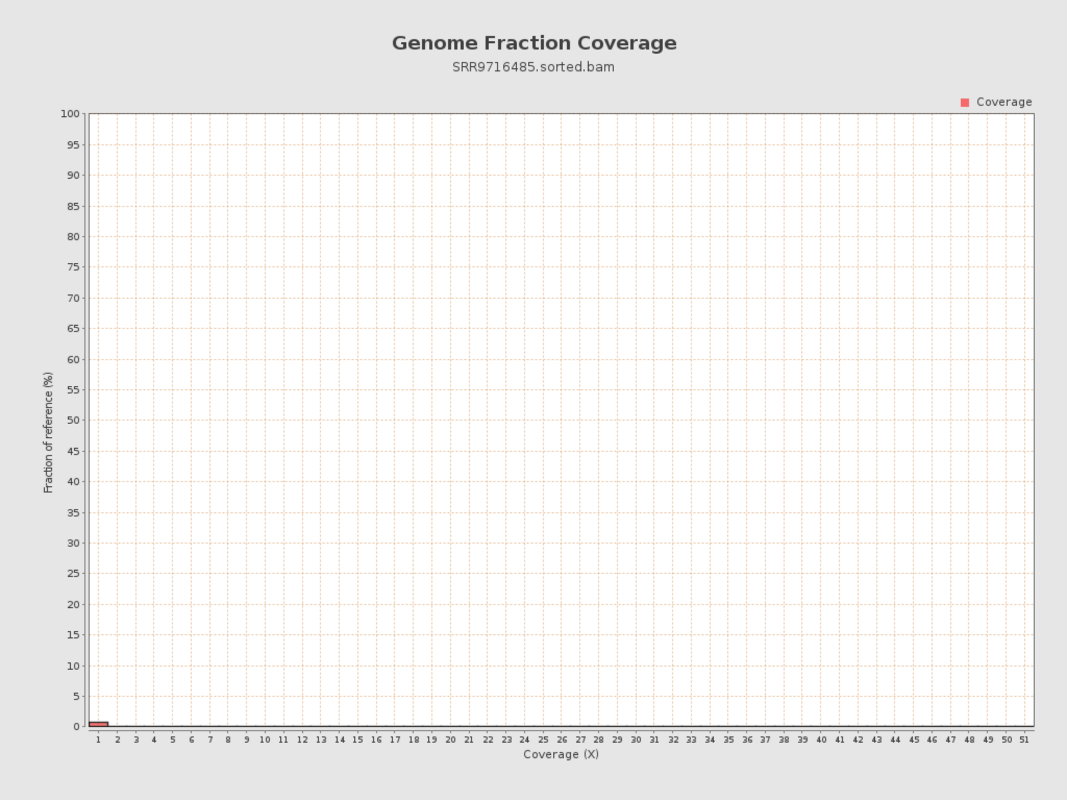
4. Results : Coverage Histogram



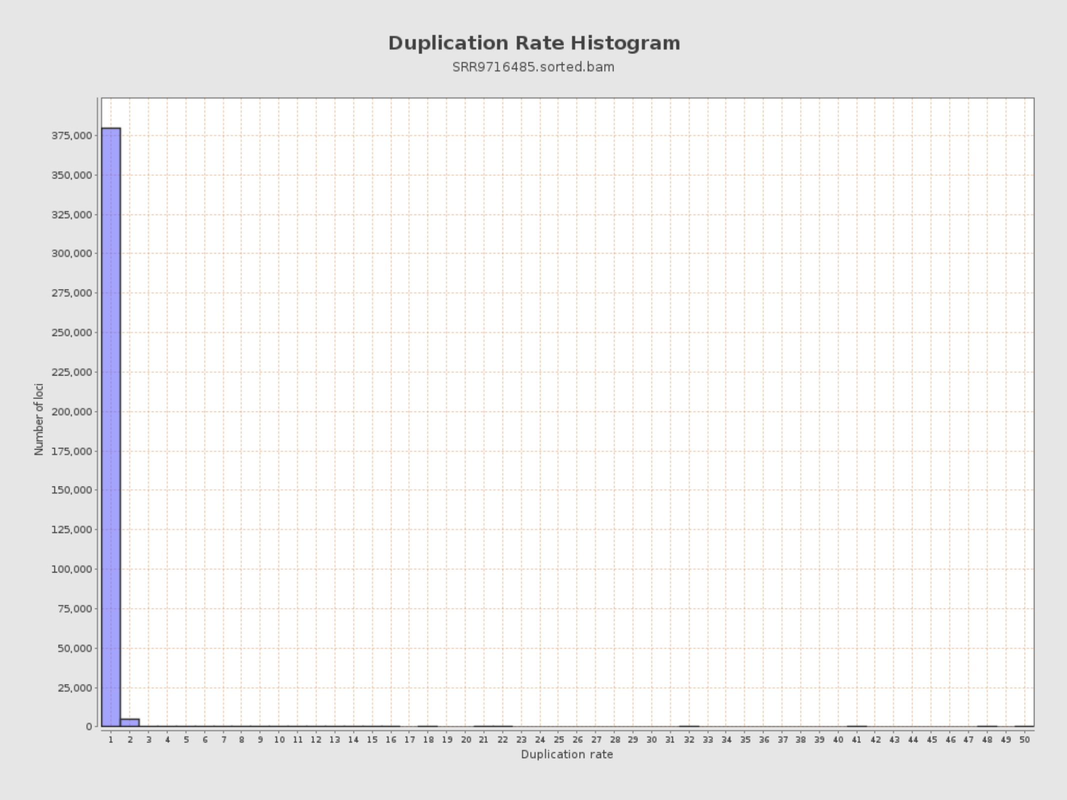
5. Results : Coverage Histogram (0-50X)



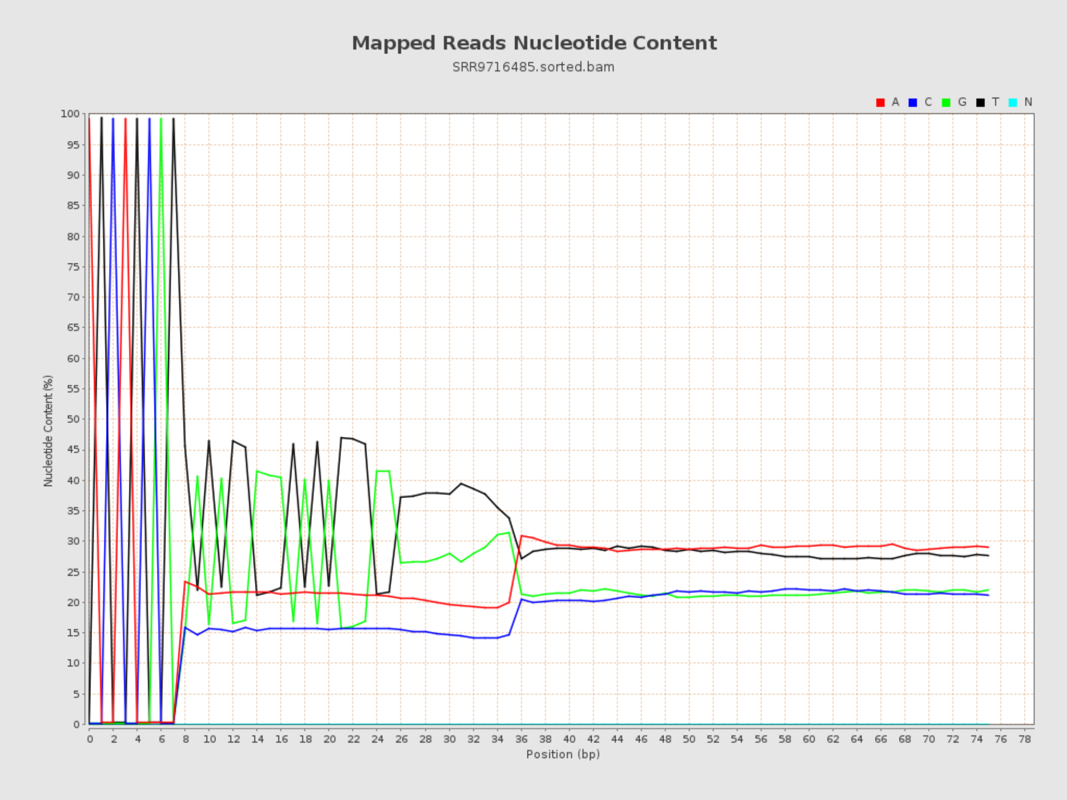
6. Results : Genome Fraction Coverage



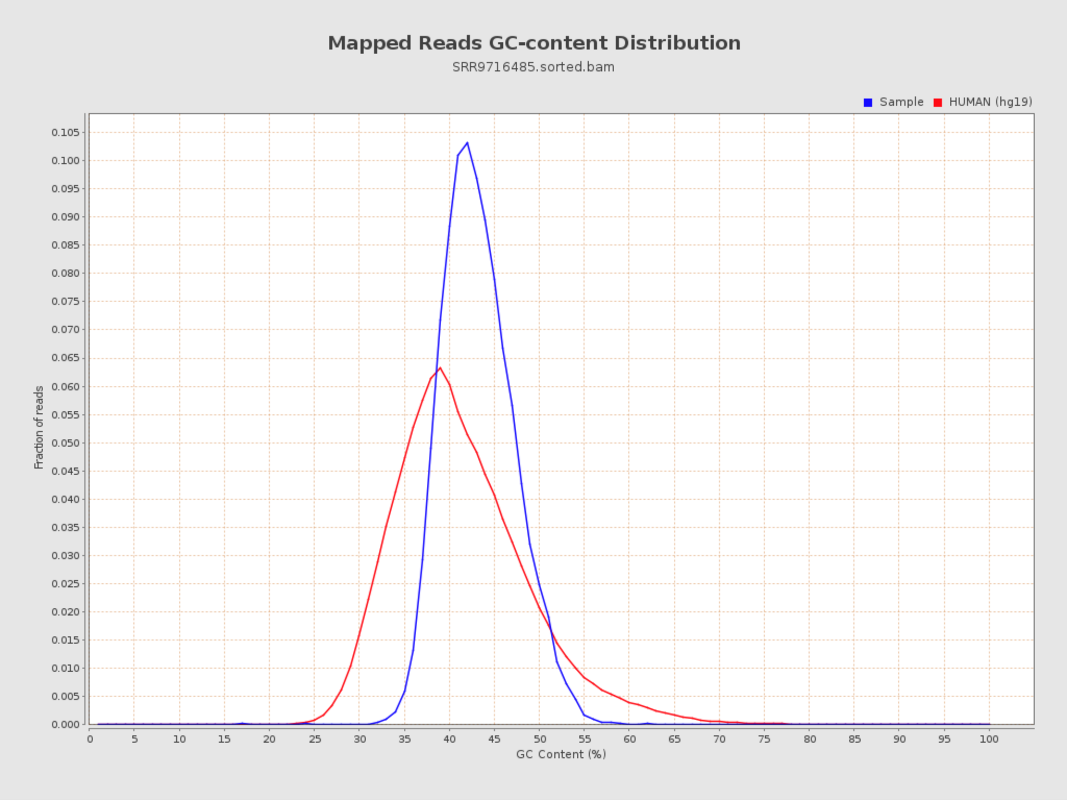
7. Results : Duplication Rate Histogram



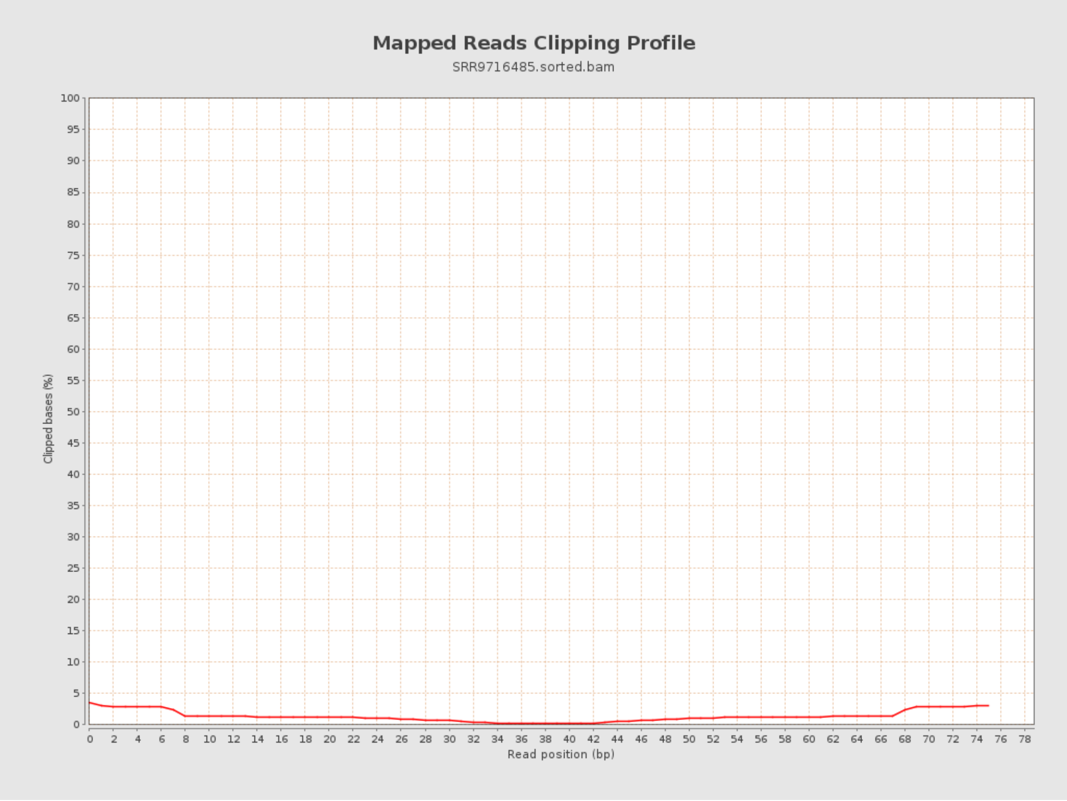
8. Results : Mapped Reads Nucleotide Content



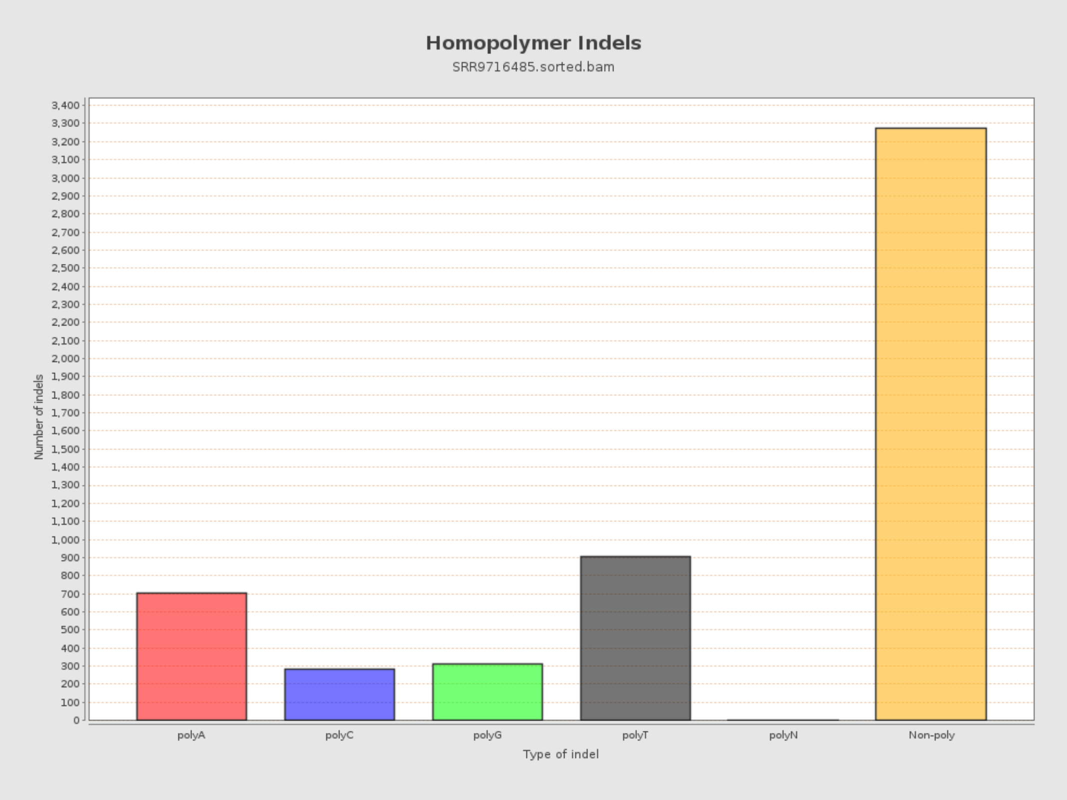
9. Results : Mapped Reads GC-content Distribution



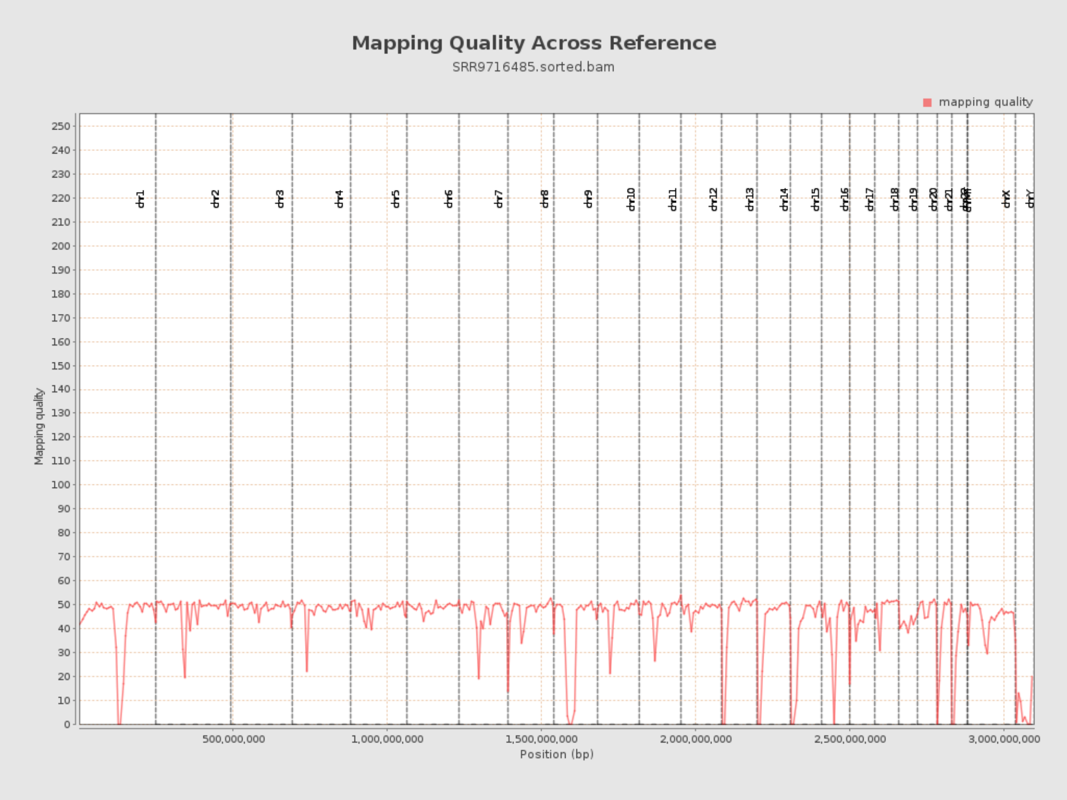
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram