Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:40:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716596.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_SRR9716596 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716596.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:40:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716596.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,479,344
Mapped reads	2,122,661 / 85.61%
Unmapped reads	356,683 / 14.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,903 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	85,744 / 3.46%
Duplication rate	3.02%
Clipped reads	2,127,083 / 85.79%

2.2. ACGT Content

Number/percentage of A's	30,336,571 / 24.76%
Number/percentage of C's	22,193,154 / 18.12%
Number/percentage of T's	40,101,318 / 32.73%
Number/percentage of G's	29,872,329 / 24.38%
Number/percentage of N's	1,578 / 0%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0396

Standard Deviation	0.3233

2.4. Mapping Quality

Mean Mapping Quality	44.25

2.5. Mismatches and indels

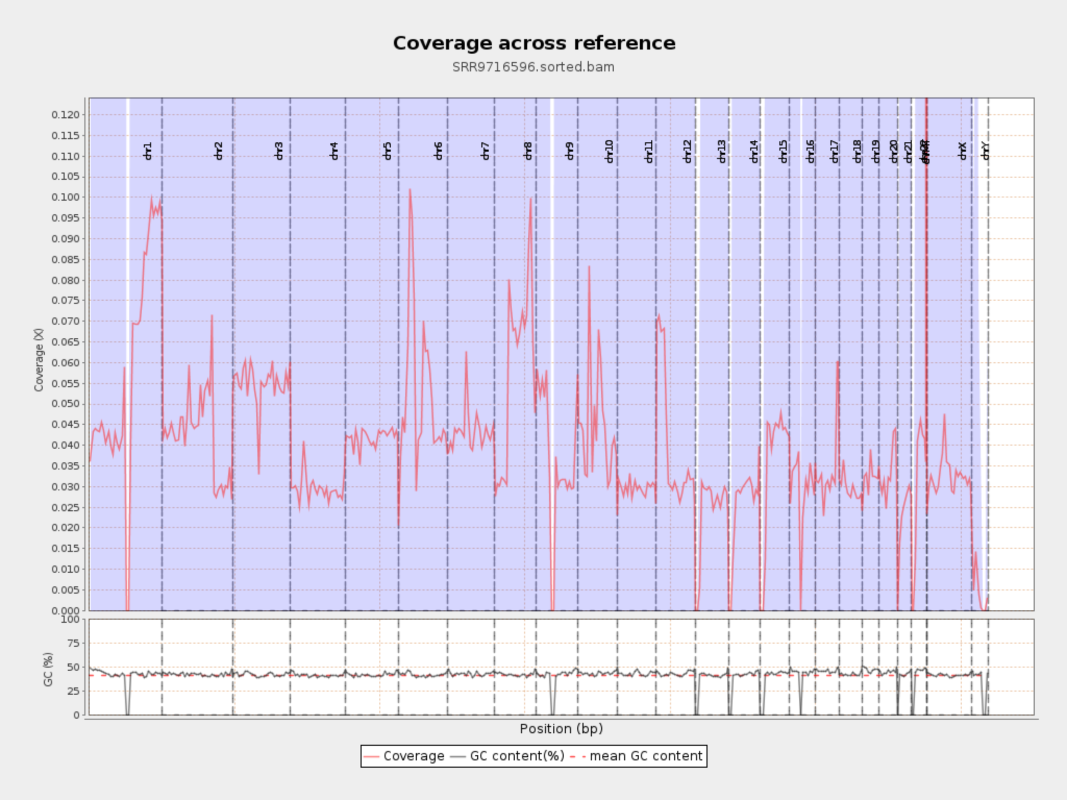
General error rate	0.51%
Mismatches	609,575
Insertions	8,396
Mapped reads with at least one insertion	0.39%
Deletions	22,041
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.69%

2.6. Chromosome stats

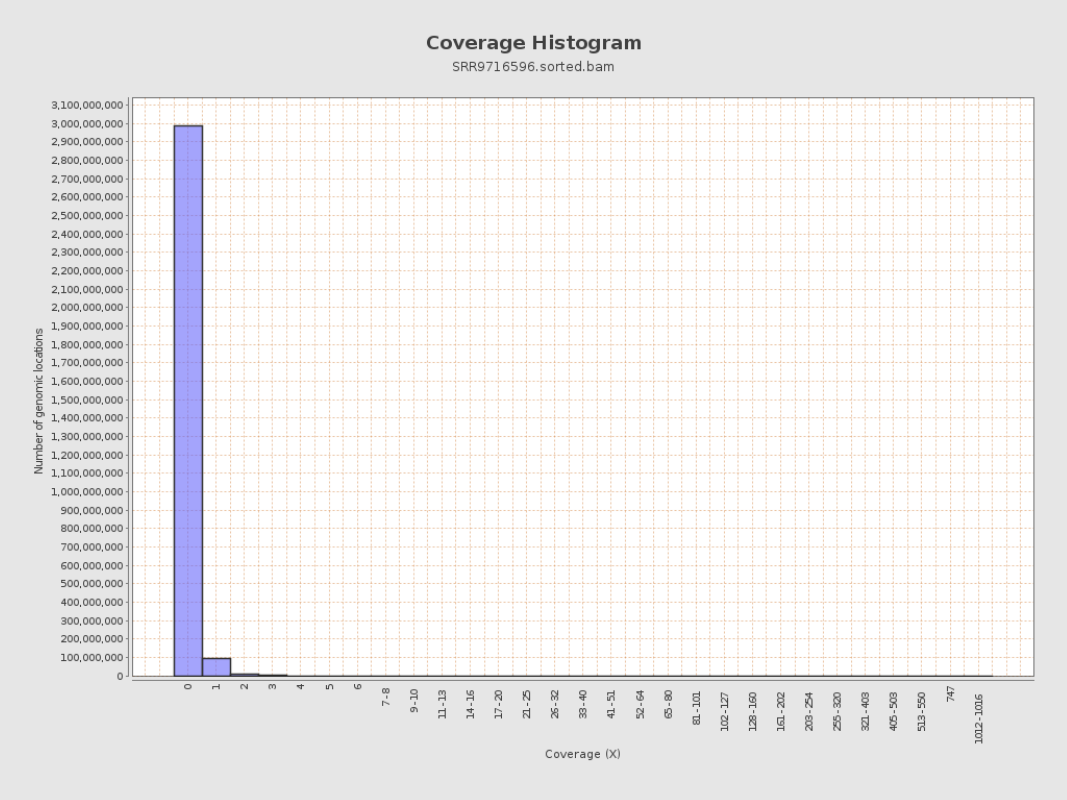
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14333317	0.0575	0.5011
chr2	243199373	10367663	0.0426	0.4737
chr3	198022430	10837392	0.0547	0.2642
chr4	191154276	5631686	0.0295	0.2084
chr5	180915260	7577407	0.0419	0.231
chr6	171115067	9013643	0.0527	0.3384
chr7	159138663	6939062	0.0436	0.4222

chr8	146364022	8607067	0.0588	0.3031
chr9	141213431	5002483	0.0354	0.2827
chr10	135534747	6121822	0.0452	0.3782
chr11	135006516	4001315	0.0296	0.2629
chr12	133851895	5354826	0.04	0.2308
chr13	115169878	2708957	0.0235	0.1731
chr14	107349540	2644987	0.0246	0.2107
chr15	102531392	3632461	0.0354	0.2144
chr16	90354753	2618633	0.029	0.2302
chr17	81195210	2819945	0.0347	0.2196
chr18	78077248	2321515	0.0297	0.4945
chr19	59128983	1917668	0.0324	0.3715
chr20	63025520	2107787	0.0334	0.2088
chr21	48129895	1094249	0.0227	0.1967
chr22	51304566	1488816	0.029	0.1907
chrMT	16571	55116	3.3261	2.5942
chrX	155270560	5068805	0.0326	0.2451
chrY	59373566	272671	0.0046	0.1125

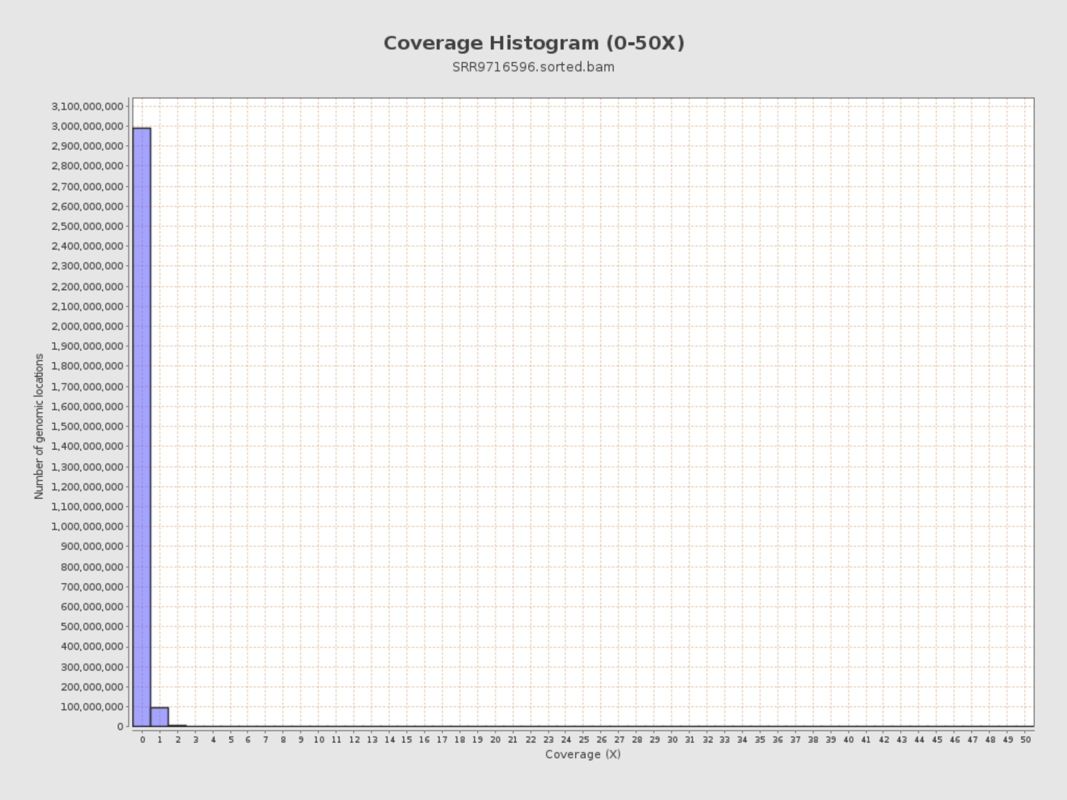
3. Results : Coverage across reference



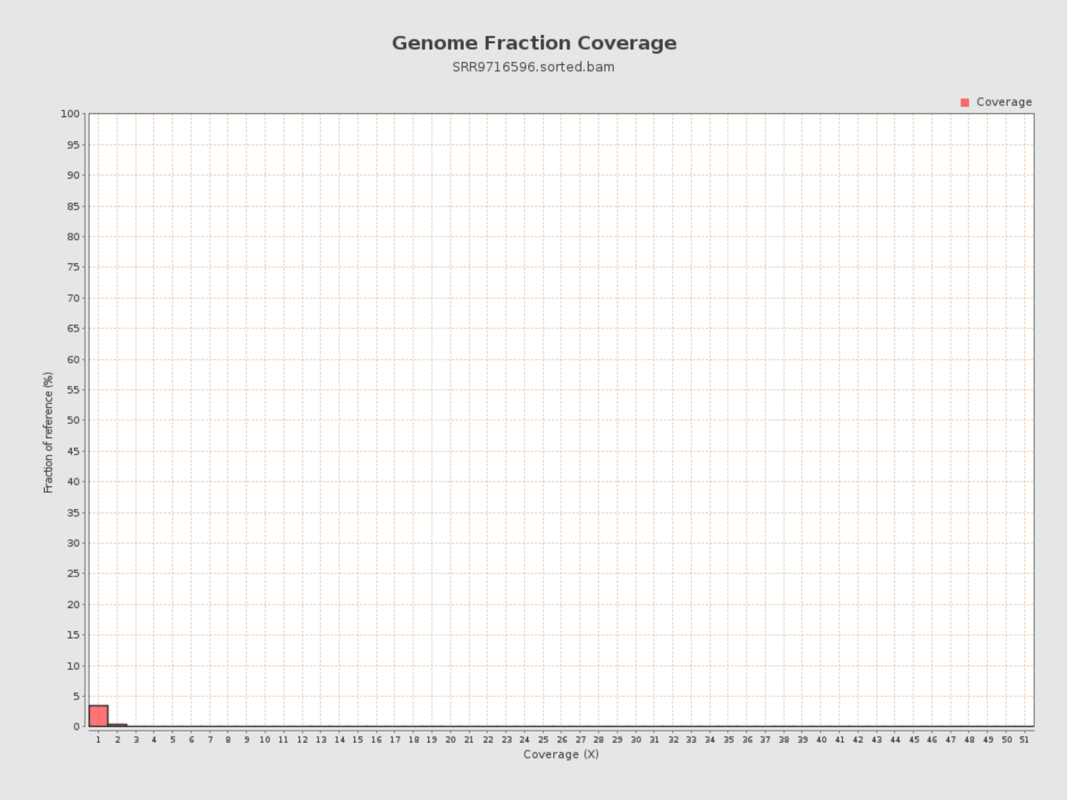
4. Results : Coverage Histogram



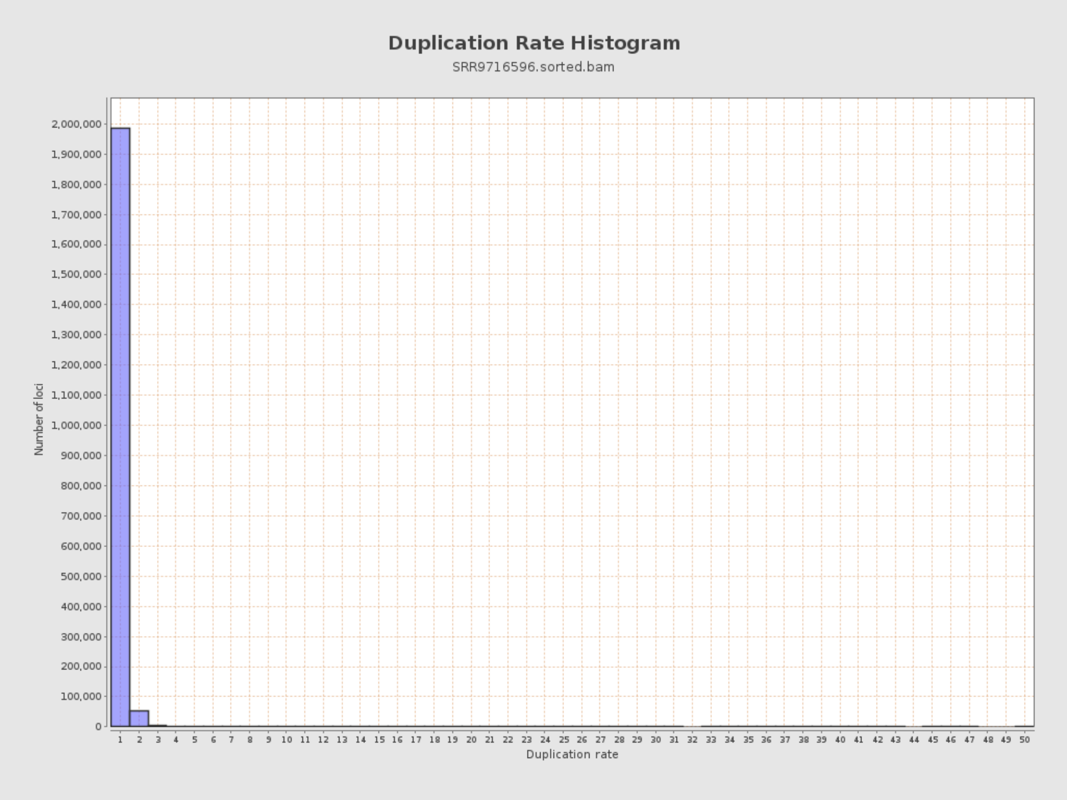
5. Results : Coverage Histogram (0-50X)



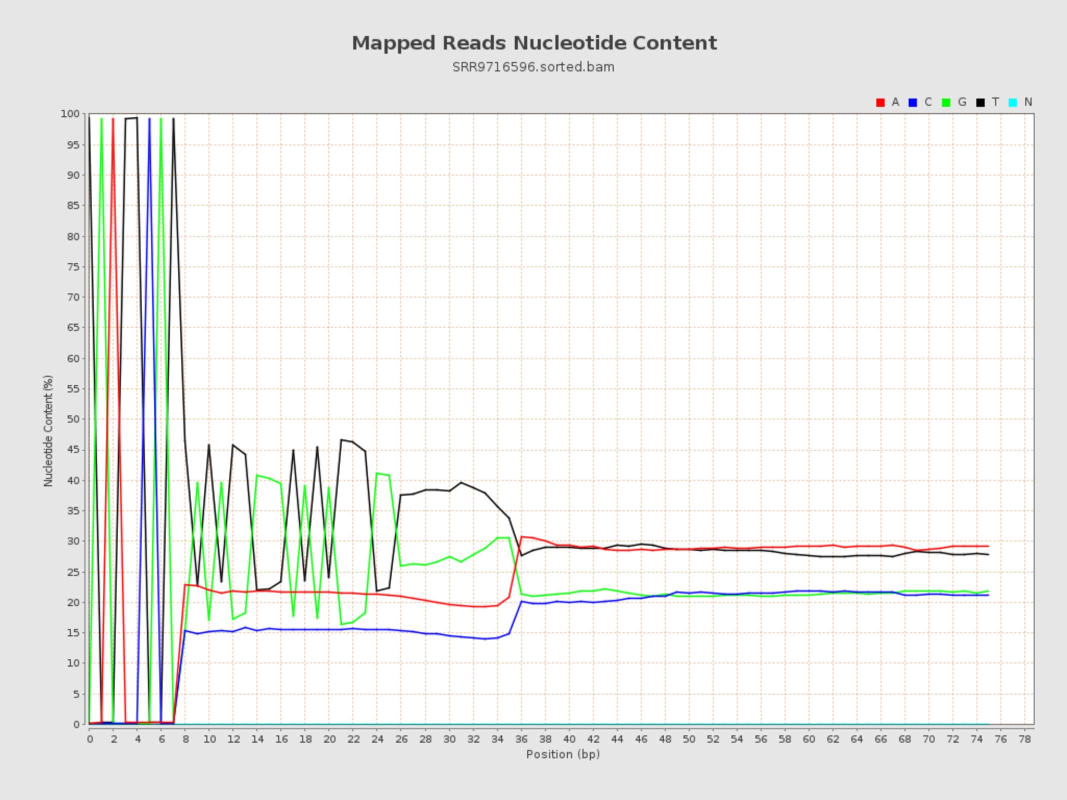
6. Results : Genome Fraction Coverage



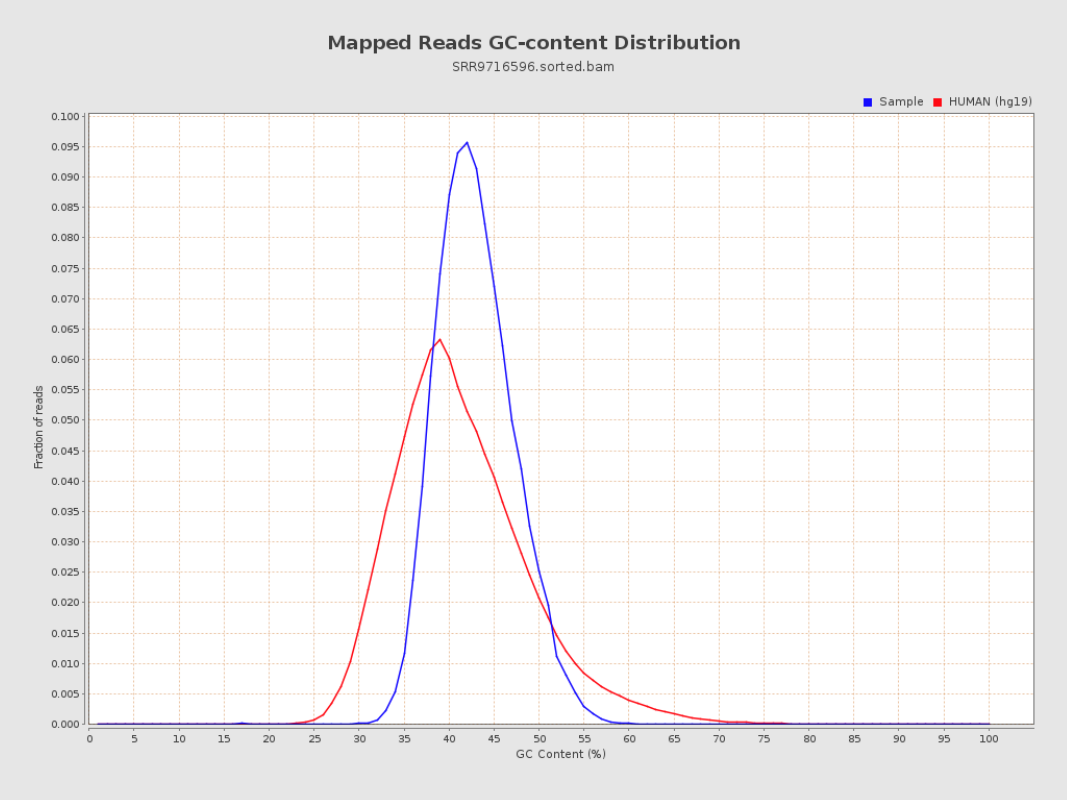
7. Results : Duplication Rate Histogram



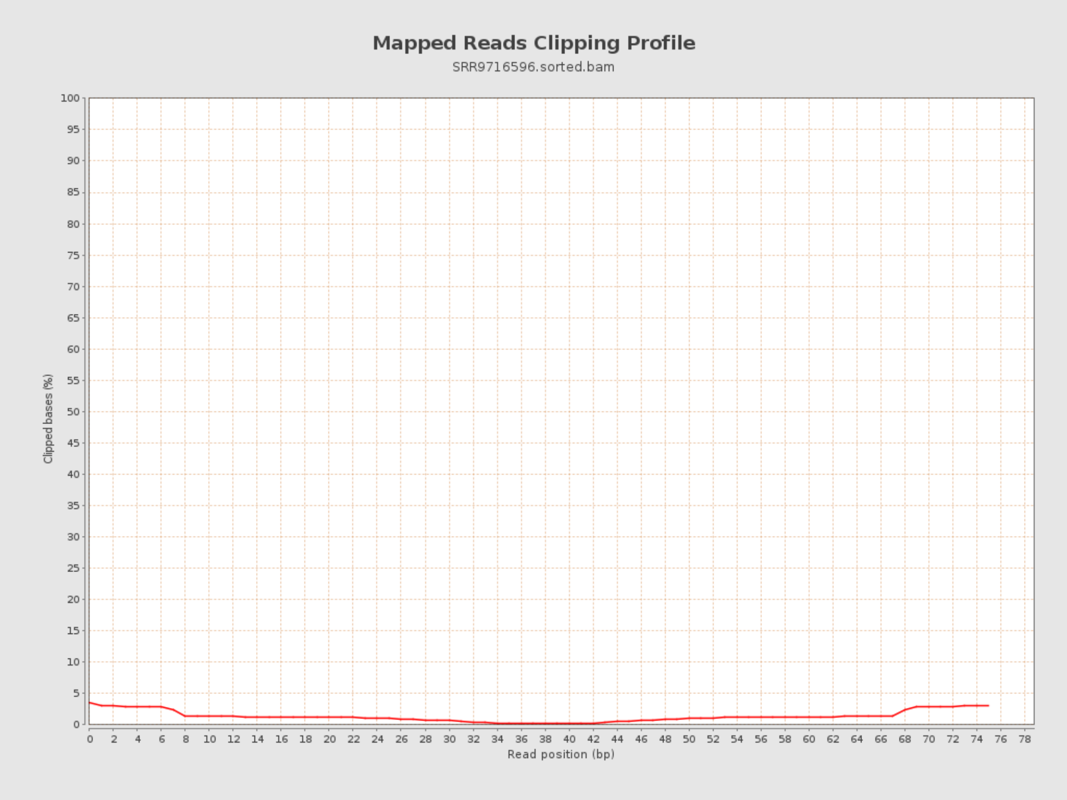
8. Results : Mapped Reads Nucleotide Content



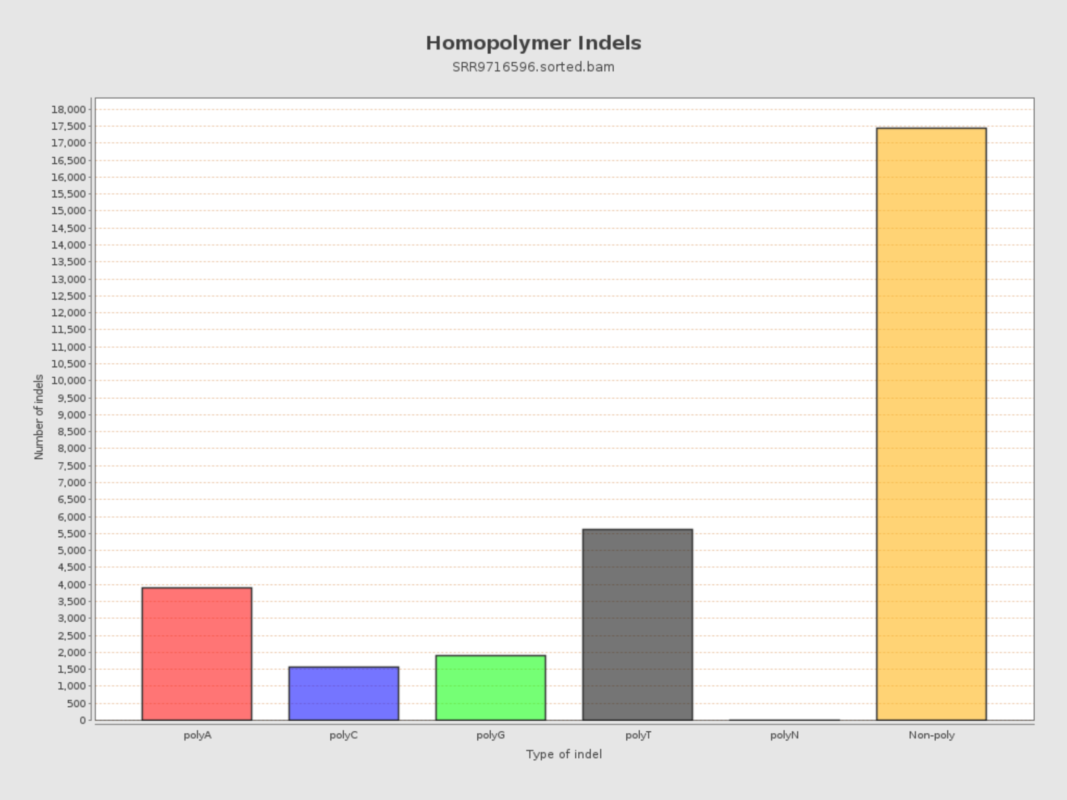
9. Results : Mapped Reads GC-content Distribution



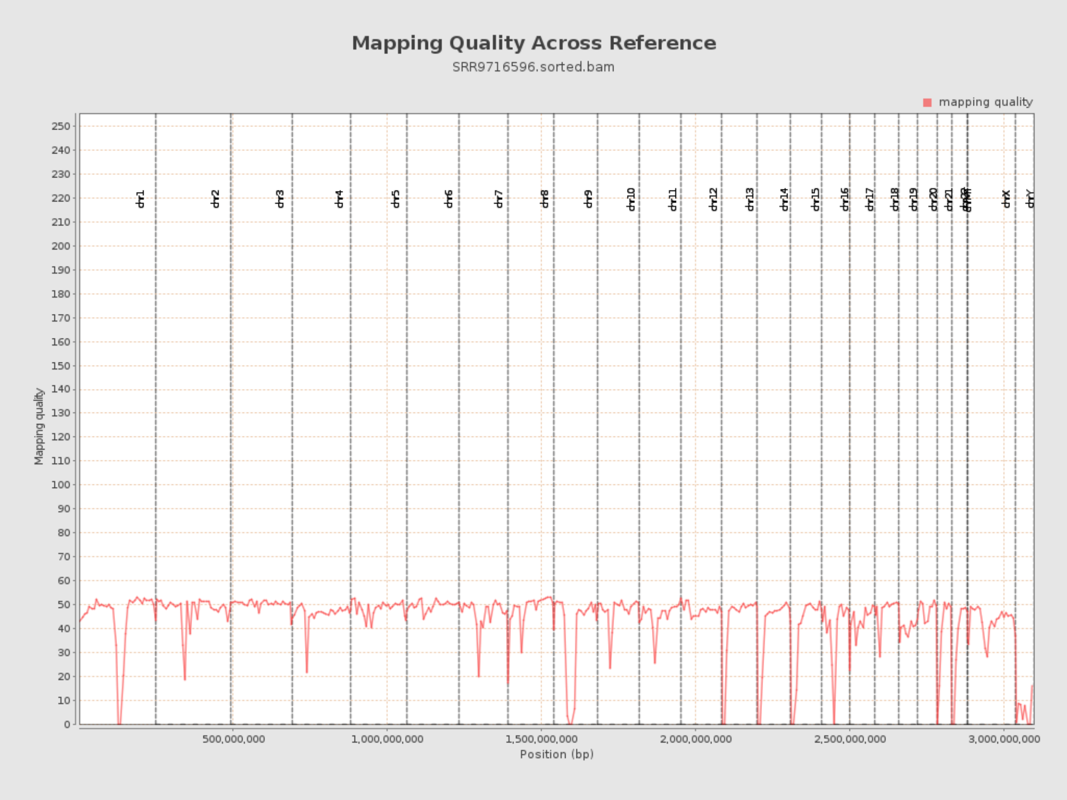
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram