Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:03:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716374.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_SRR9716374 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716374.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:03:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716374.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,070,991
Mapped reads	1,959,947 / 94.64%
Unmapped reads	111,044 / 5.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,557 / 1.91%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	87,645 / 4.23%
Duplication rate	3.21%
Clipped reads	1,997,913 / 96.47%

2.2. ACGT Content

Number/percentage of A's	40,788,145 / 26.15%
Number/percentage of C's	30,543,521 / 19.58%
Number/percentage of T's	46,180,094 / 29.61%
Number/percentage of G's	38,464,903 / 24.66%
Number/percentage of N's	10,389 / 0.01%
GC Percentage	44.24%

2.3. Coverage

Mean	0.0504

Standard Deviation	0.4663

2.4. Mapping Quality

Mean Mapping Quality	47.55

2.5. Mismatches and indels

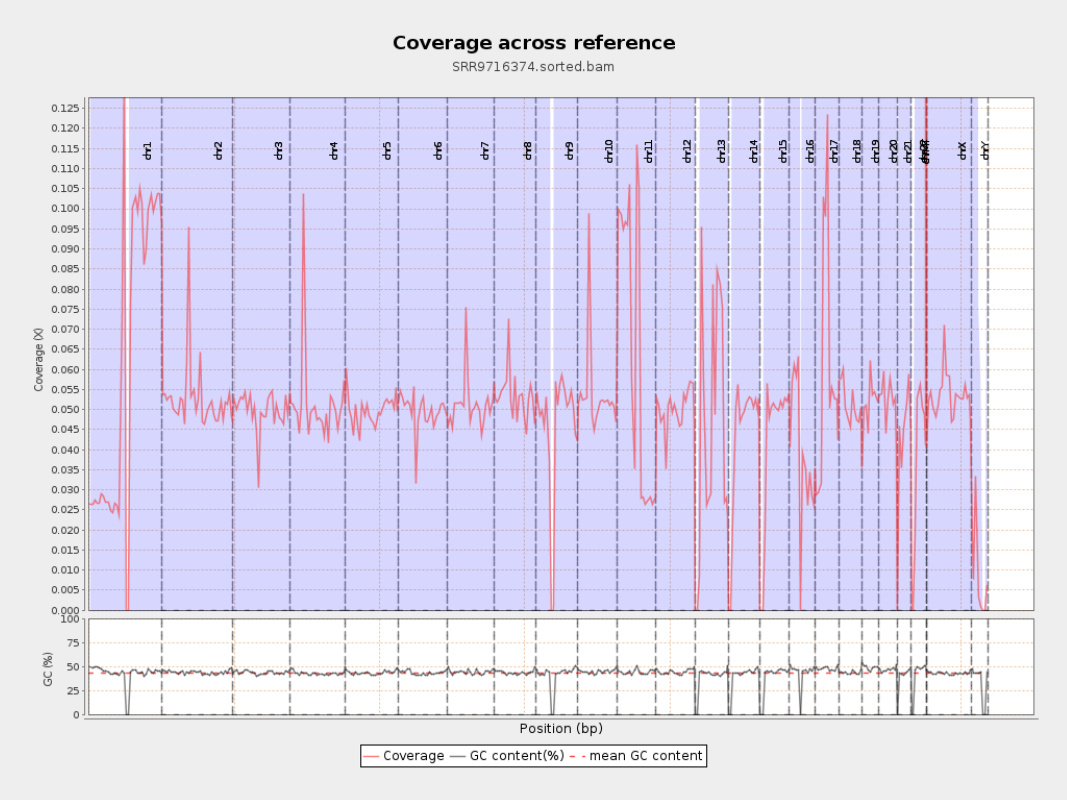
General error rate	0.63%
Mismatches	956,251
Insertions	12,585
Mapped reads with at least one insertion	0.63%
Deletions	35,885
Mapped reads with at least one deletion	1.8%
Homopolymer indels	43.37%

2.6. Chromosome stats

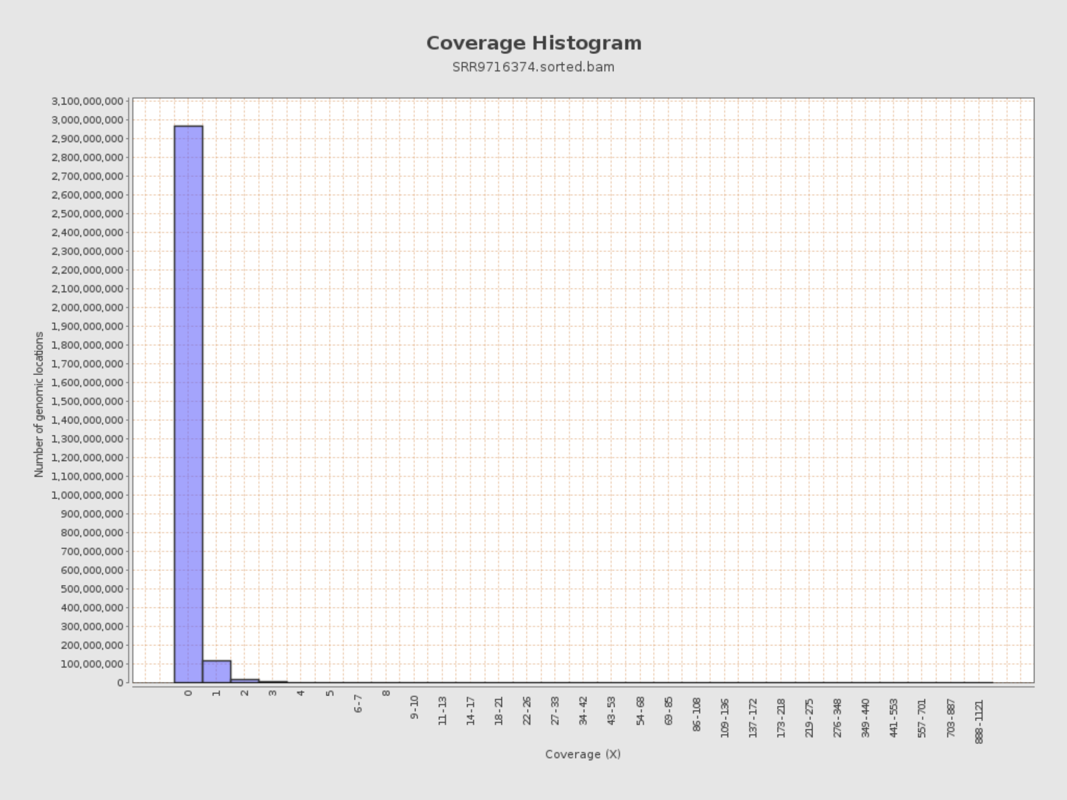
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15239960	0.0611	1.0049
chr2	243199373	12879490	0.053	0.4835
chr3	198022430	9828102	0.0496	0.2537
chr4	191154276	9788236	0.0512	0.3461
chr5	180915260	8990560	0.0497	0.2552
chr6	171115067	8479022	0.0496	0.2764
chr7	159138663	8156530	0.0513	0.5495

chr8	146364022	7790781	0.0532	0.517
chr9	141213431	6404773	0.0454	0.3798
chr10	135534747	7269647	0.0536	0.4627
chr11	135006516	8703299	0.0645	0.4966
chr12	133851895	6712777	0.0502	0.2561
chr13	115169878	5236723	0.0455	0.2438
chr14	107349540	4583367	0.0427	0.2574
chr15	102531392	4291093	0.0419	0.2309
chr16	90354753	3532526	0.0391	0.2546
chr17	81195210	5006806	0.0617	0.3512
chr18	78077248	4023718	0.0515	0.6398
chr19	59128983	3063705	0.0518	0.6636
chr20	63025520	3311697	0.0525	0.2802
chr21	48129895	2053639	0.0427	0.2894
chr22	51304566	1838263	0.0358	0.2165
chrMT	16571	91437	5.5179	3.726
chrX	155270560	8288707	0.0534	0.3122
chrY	59373566	492097	0.0083	0.2846

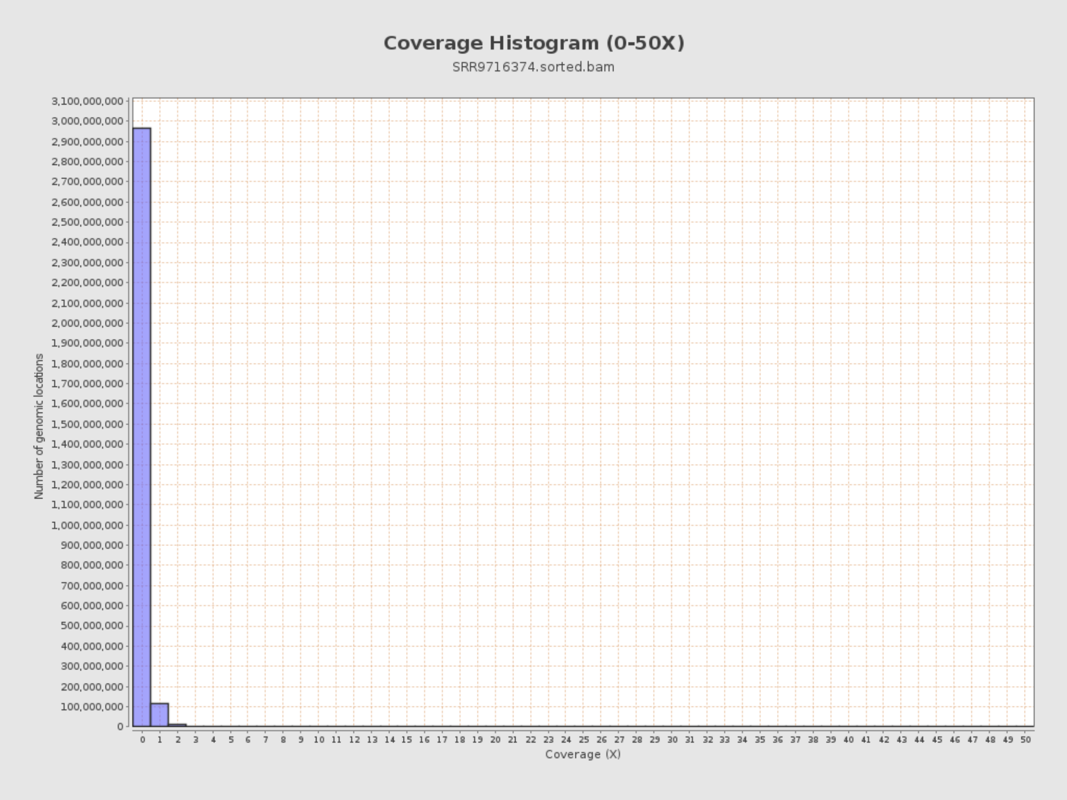
3. Results : Coverage across reference



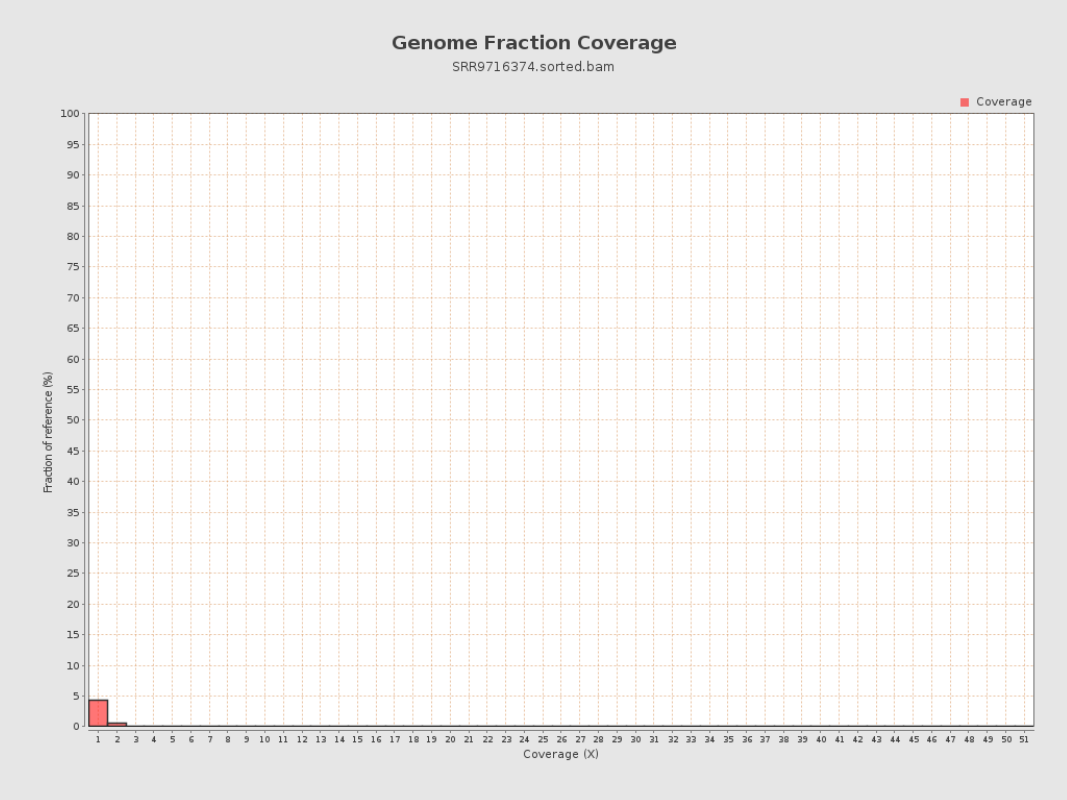
4. Results : Coverage Histogram



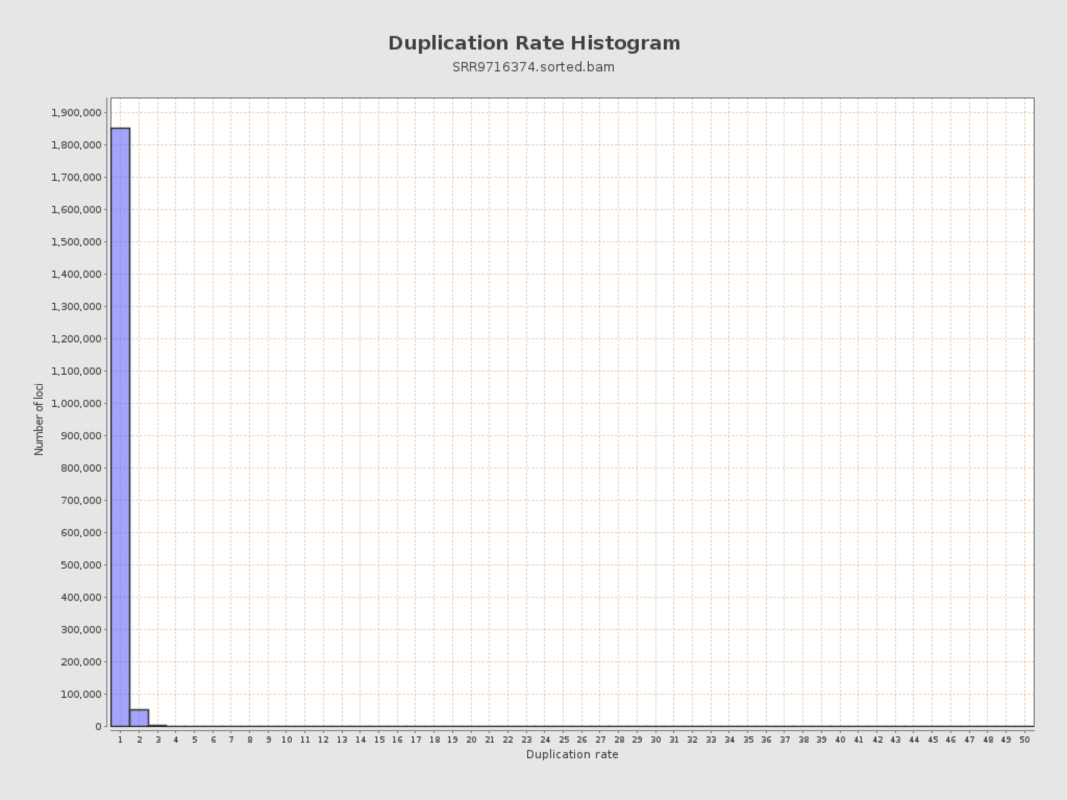
5. Results : Coverage Histogram (0-50X)



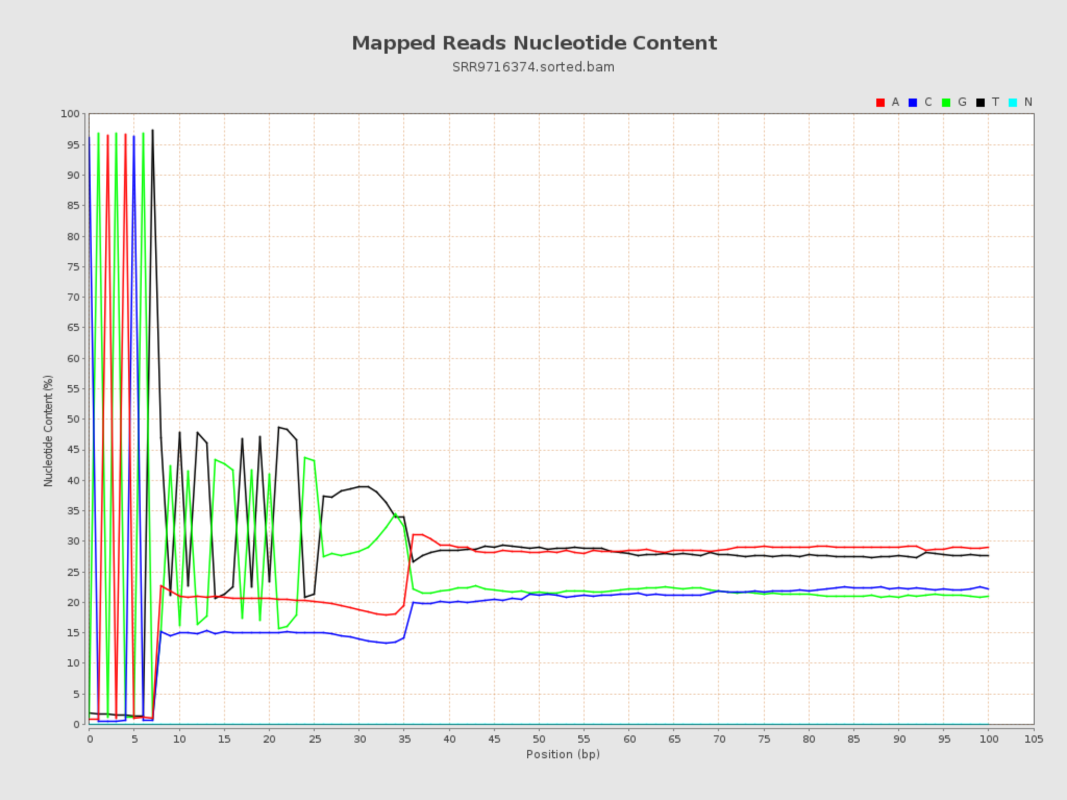
6. Results : Genome Fraction Coverage



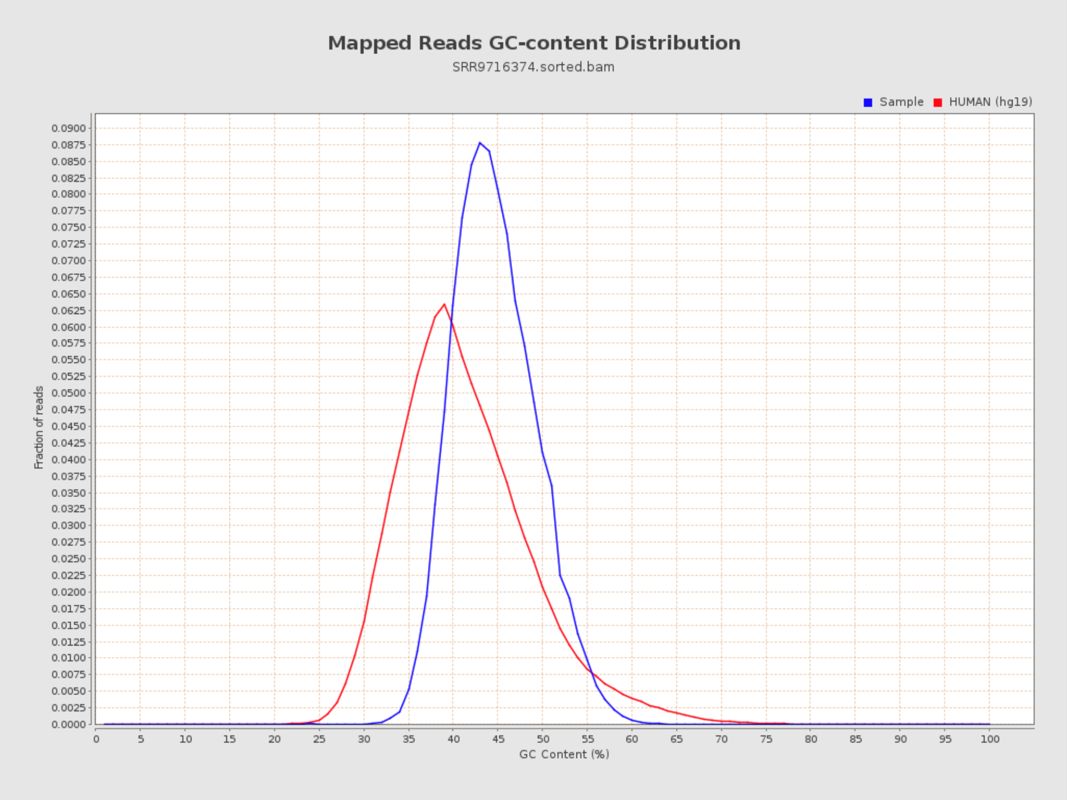
7. Results : Duplication Rate Histogram



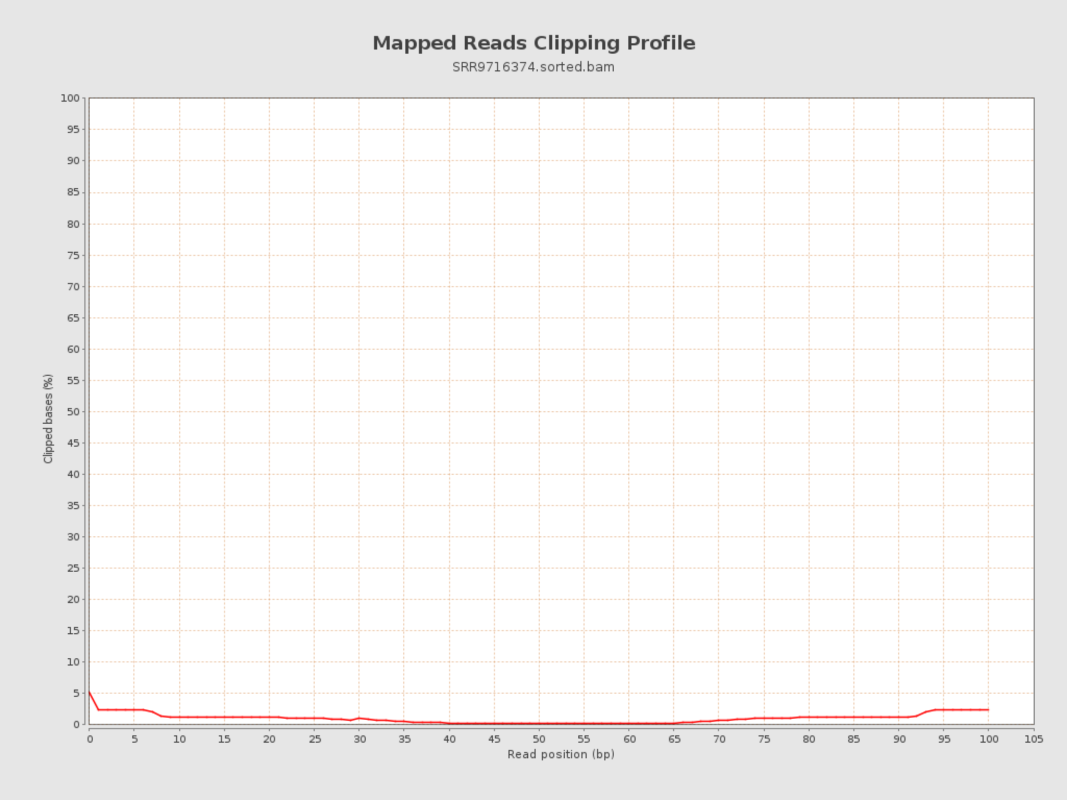
8. Results : Mapped Reads Nucleotide Content



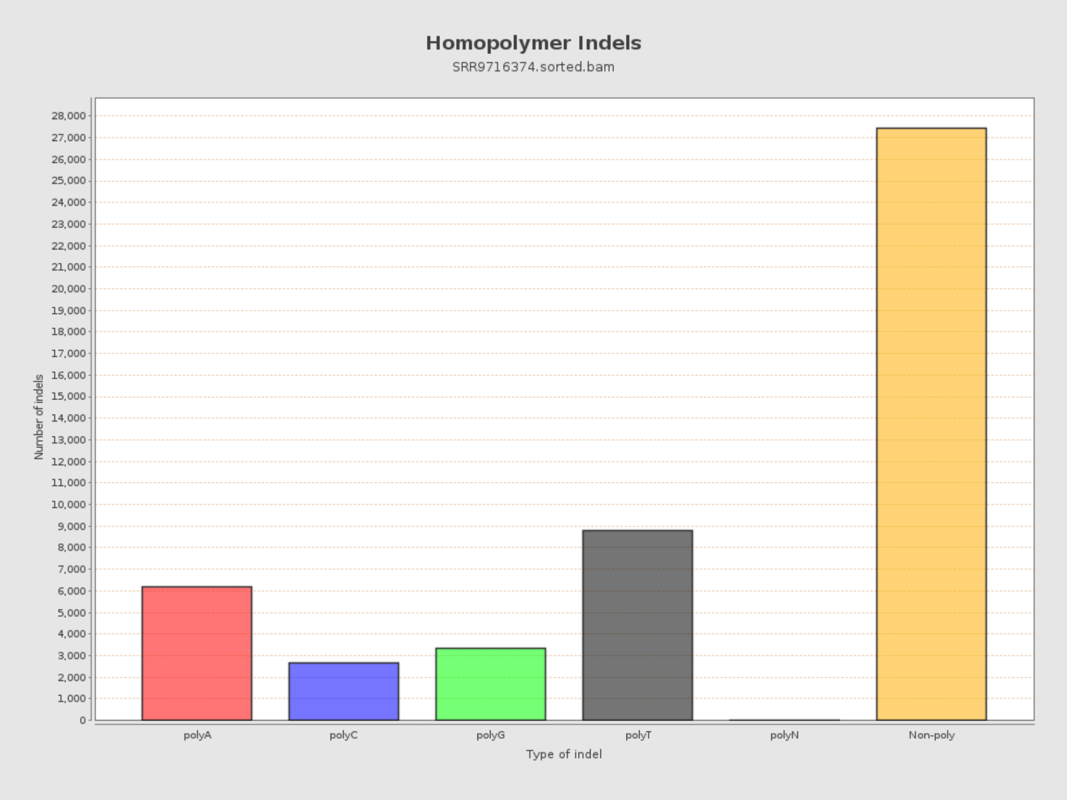
9. Results : Mapped Reads GC-content Distribution



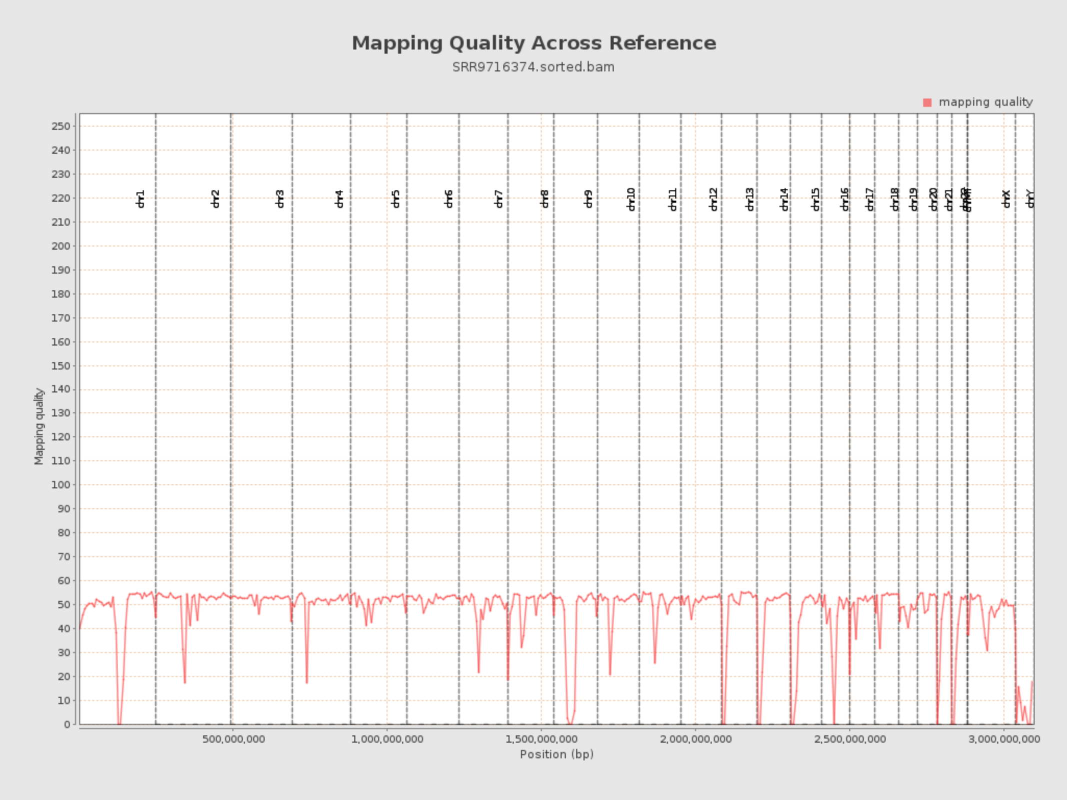
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram