Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:40:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716399.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_SRR9716399 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716399.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:40:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716399.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,937,019
Mapped reads	1,755,131 / 90.61%
Unmapped reads	181,888 / 9.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,196 / 1.35%
Read min/max/mean length	30 / 101 / 101.5
Duplicated reads (estimated)	83,475 / 4.31%
Duplication rate	3.24%
Clipped reads	1,777,913 / 91.79%

2.2. ACGT Content

Number/percentage of A's	35,170,195 / 25.35%
Number/percentage of C's	26,364,550 / 19.01%
Number/percentage of T's	43,747,802 / 31.54%
Number/percentage of G's	33,429,366 / 24.1%
Number/percentage of N's	8,210 / 0.01%
GC Percentage	43.1%

2.3. Coverage

Mean	0.0448

Standard Deviation	0.4538

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

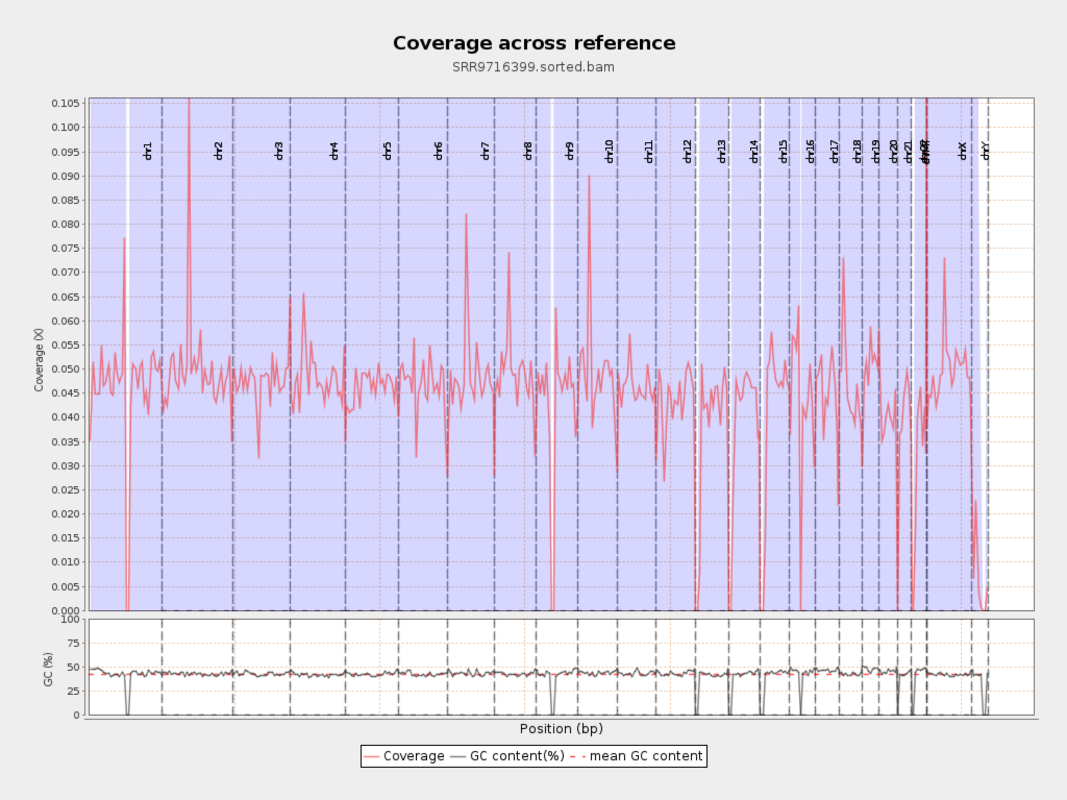
General error rate	0.83%
Mismatches	1,128,914
Insertions	13,091
Mapped reads with at least one insertion	0.74%
Deletions	32,459
Mapped reads with at least one deletion	1.82%
Homopolymer indels	43.78%

2.6. Chromosome stats

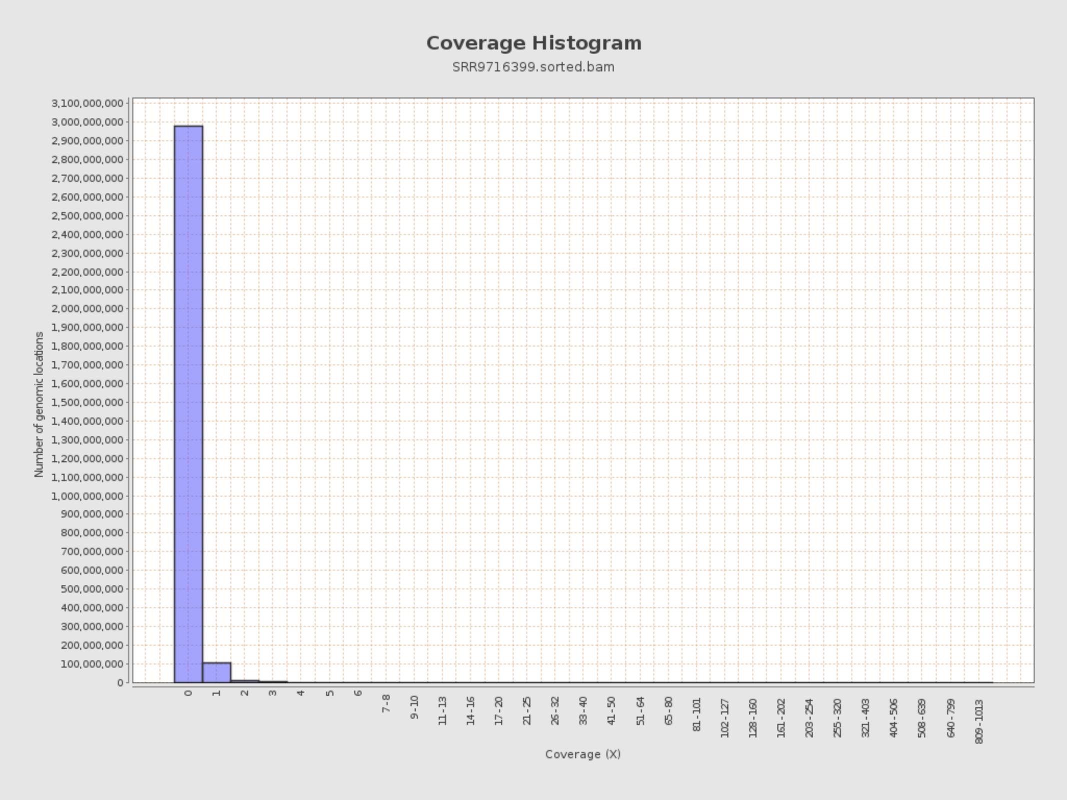
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11410347	0.0458	0.6987
chr2	243199373	12184473	0.0501	0.6904
chr3	198022430	9365154	0.0473	0.2531
chr4	191154276	9191441	0.0481	0.2857
chr5	180915260	8383693	0.0463	0.2522
chr6	171115067	7977373	0.0466	0.3018
chr7	159138663	7822355	0.0492	0.6096

chr8	146364022	7180383	0.0491	0.6147
chr9	141213431	5940024	0.0421	0.4858
chr10	135534747	6702777	0.0495	0.463
chr11	135006516	6230335	0.0461	0.4014
chr12	133851895	5814117	0.0434	0.2454
chr13	115169878	4272100	0.0371	0.2186
chr14	107349540	4082142	0.038	0.2974
chr15	102531392	4105599	0.04	0.2364
chr16	90354753	3903402	0.0432	0.2742
chr17	81195210	3626732	0.0447	0.2669
chr18	78077248	3698361	0.0474	0.8768
chr19	59128983	2991436	0.0506	0.5289
chr20	63025520	2513477	0.0399	0.2521
chr21	48129895	1825004	0.0379	0.2505
chr22	51304566	1445505	0.0282	0.1929
chrMT	16571	2568	0.155	0.4192
chrX	155270560	7720850	0.0497	0.3261
chrY	59373566	387645	0.0065	0.1965

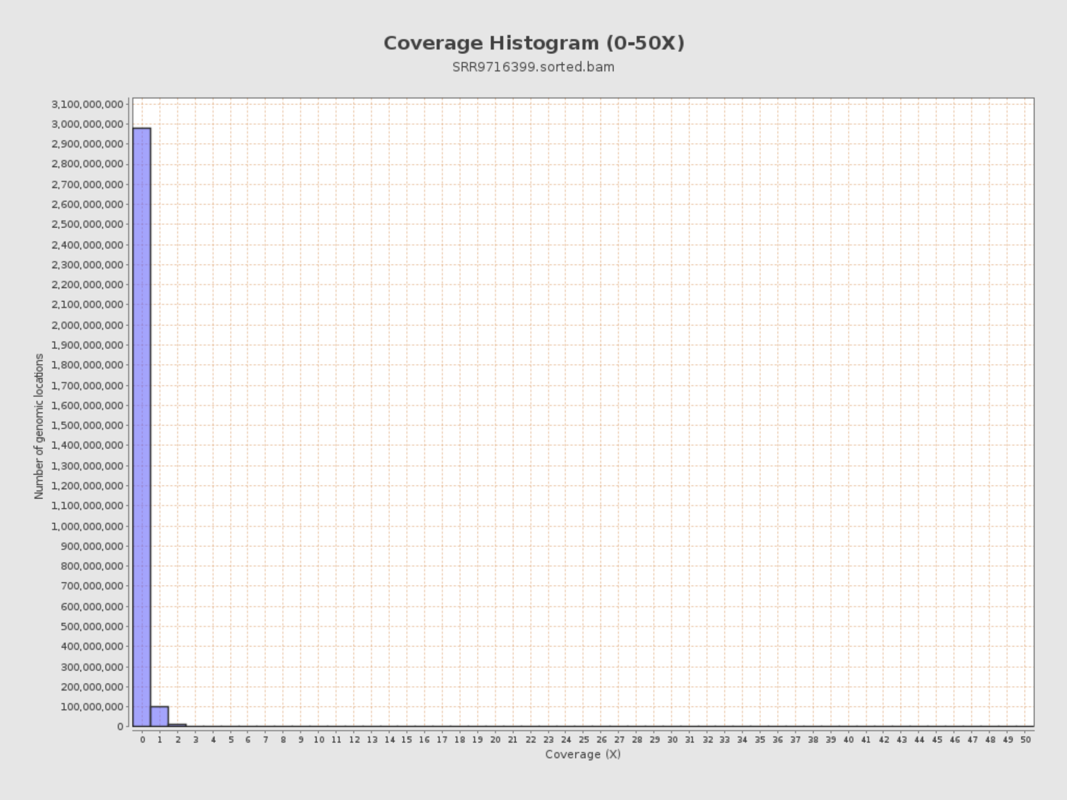
3. Results : Coverage across reference



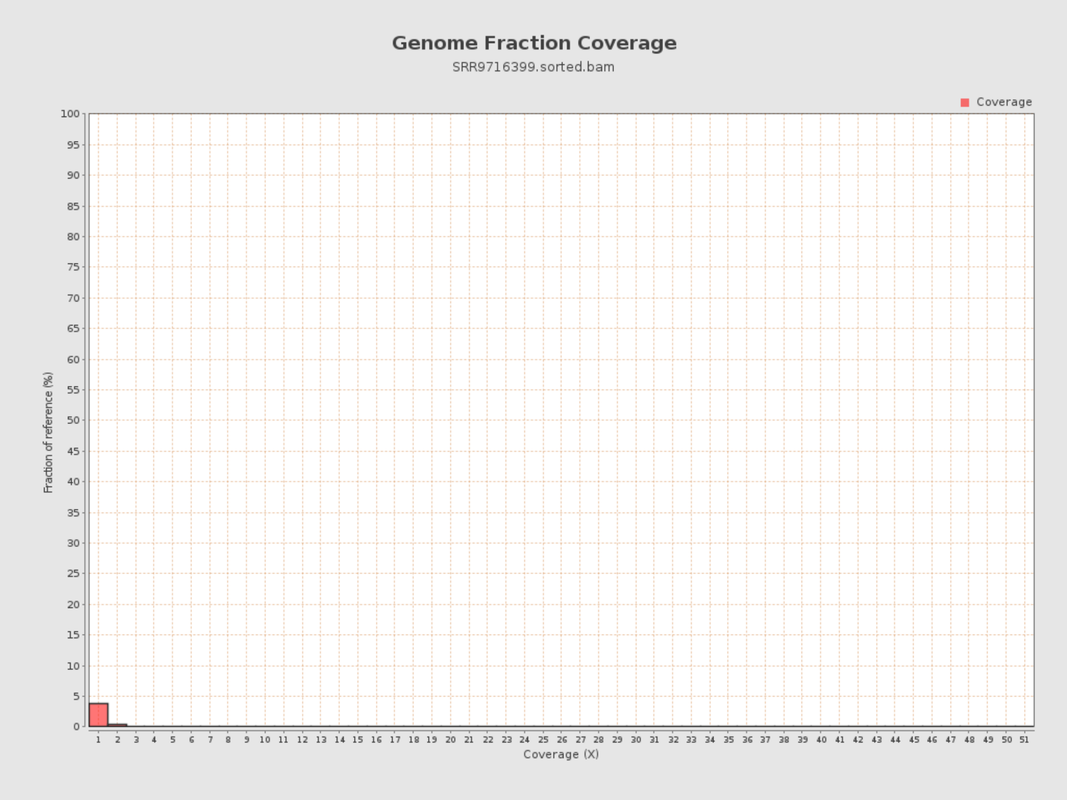
4. Results : Coverage Histogram



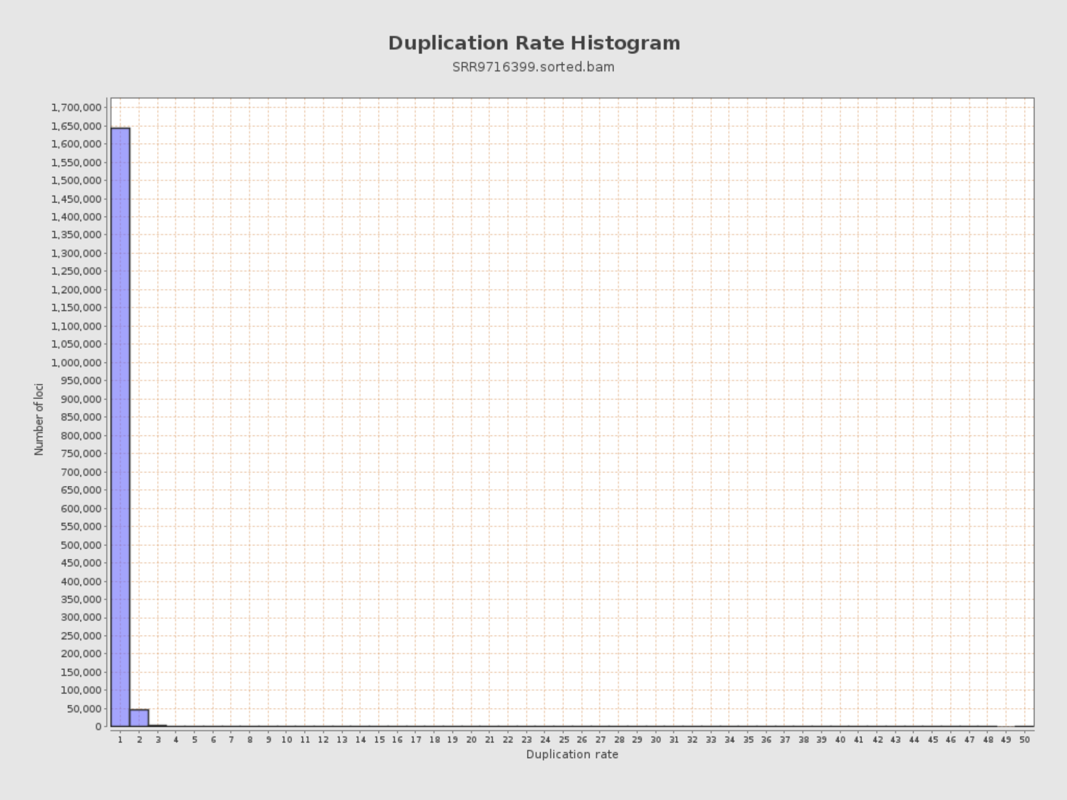
5. Results : Coverage Histogram (0-50X)



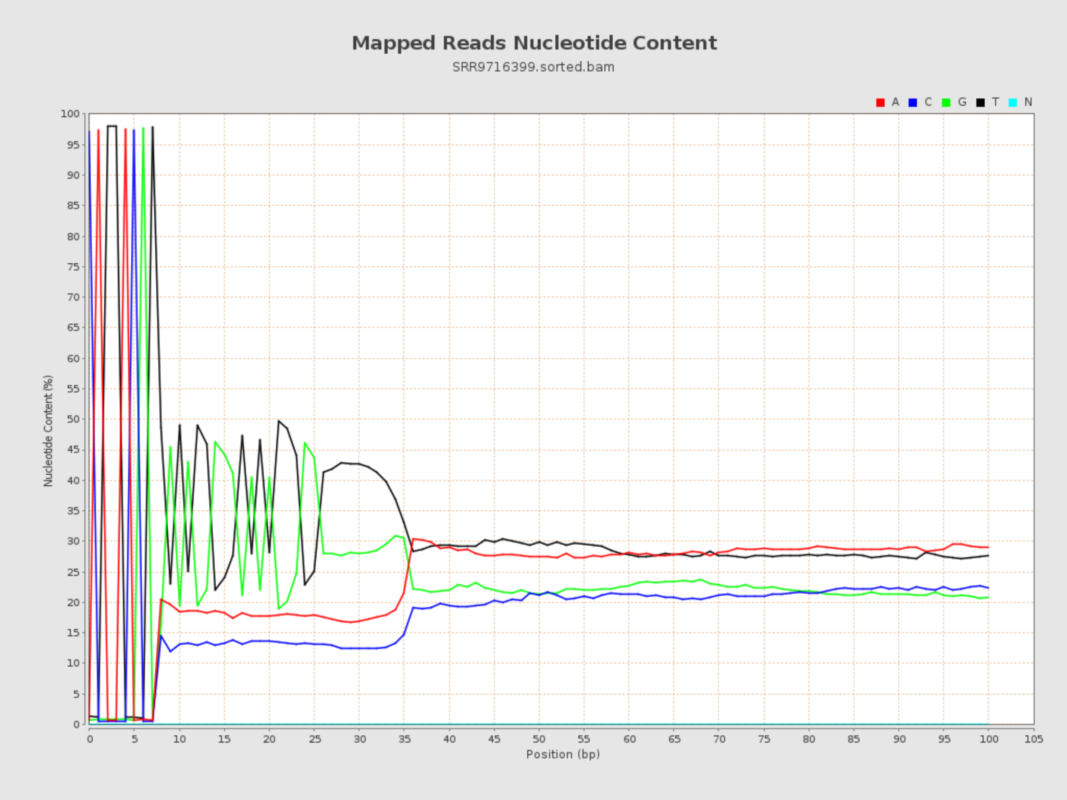
6. Results : Genome Fraction Coverage



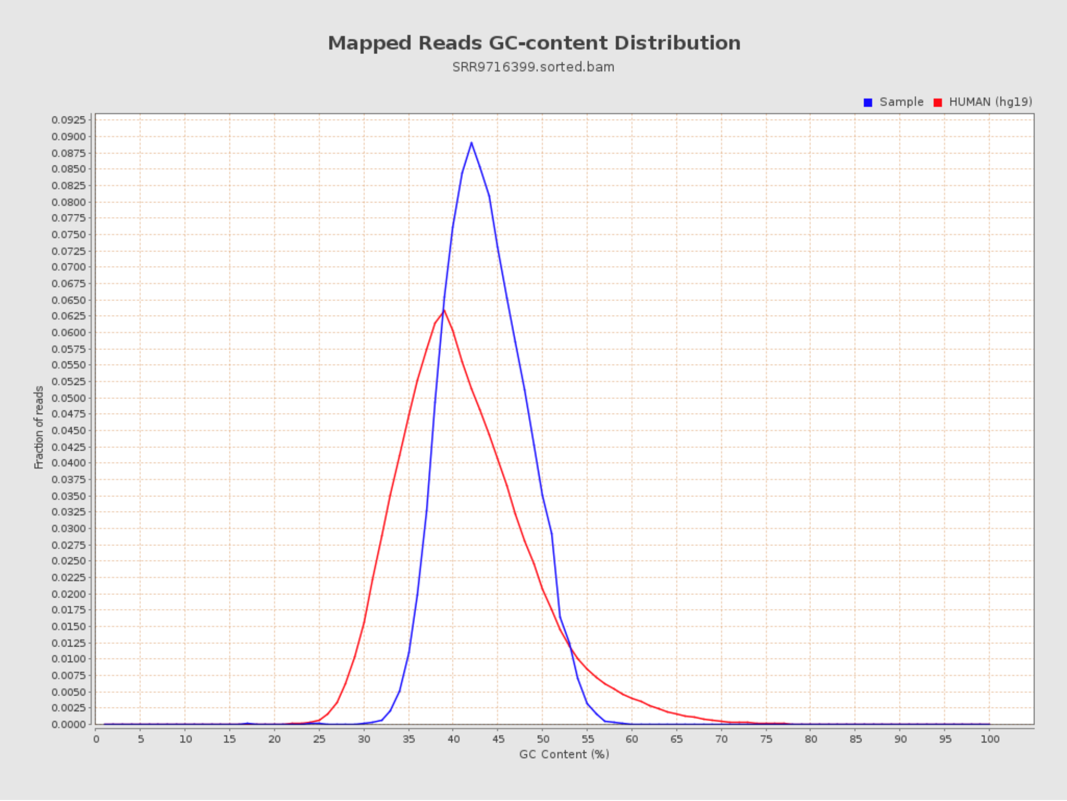
7. Results : Duplication Rate Histogram



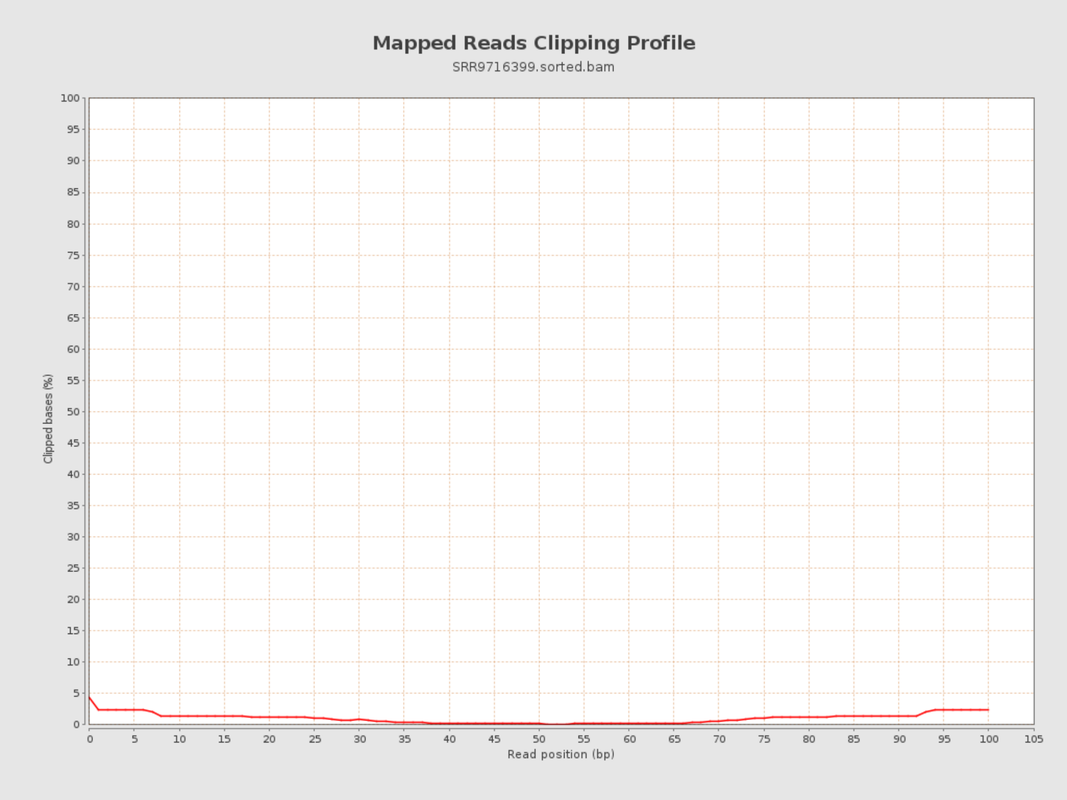
8. Results : Mapped Reads Nucleotide Content



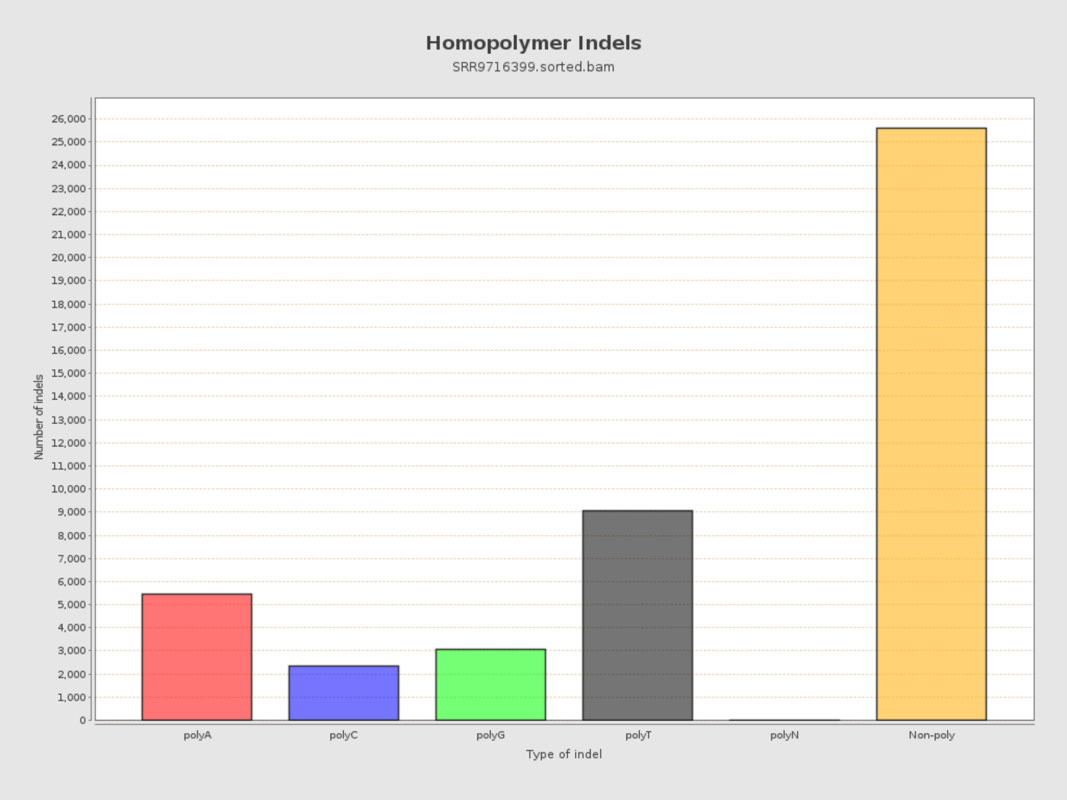
9. Results : Mapped Reads GC-content Distribution



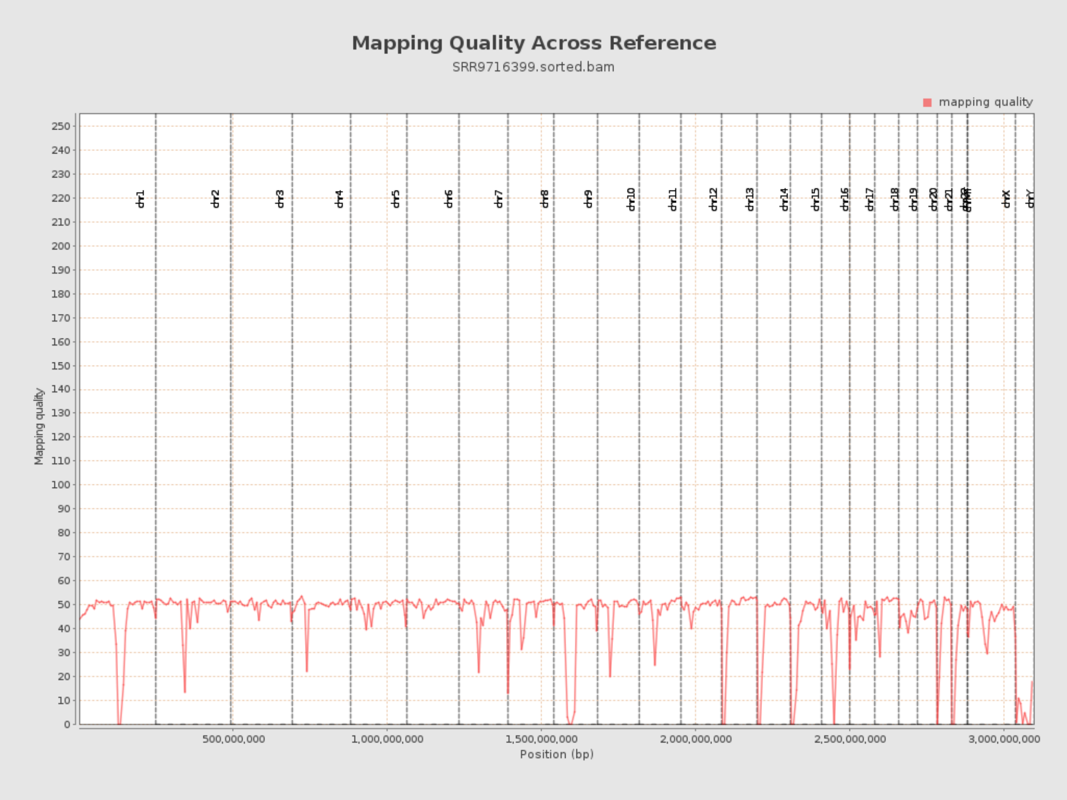
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram