Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 03:09:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716255.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_SRR9716255 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716255.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 03:09:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,623,162
Mapped reads	1,528,494 / 94.17%
Unmapped reads	94,668 / 5.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,641 / 2.07%
Read min/max/mean length	30 / 101 / 101.75
Duplicated reads (estimated)	64,463 / 3.97%
Duplication rate	3.29%
Clipped reads	1,559,818 / 96.1%

2.2. ACGT Content

Number/percentage of A's	29,218,590 / 24.71%
Number/percentage of C's	23,733,515 / 20.07%
Number/percentage of T's	34,643,932 / 29.29%
Number/percentage of G's	30,668,707 / 25.93%
Number/percentage of N's	4,661 / 0%
GC Percentage	46%

2.3. Coverage

Mean	0.0382

Standard Deviation	0.3118

2.4. Mapping Quality

Mean Mapping Quality	46.3

2.5. Mismatches and indels

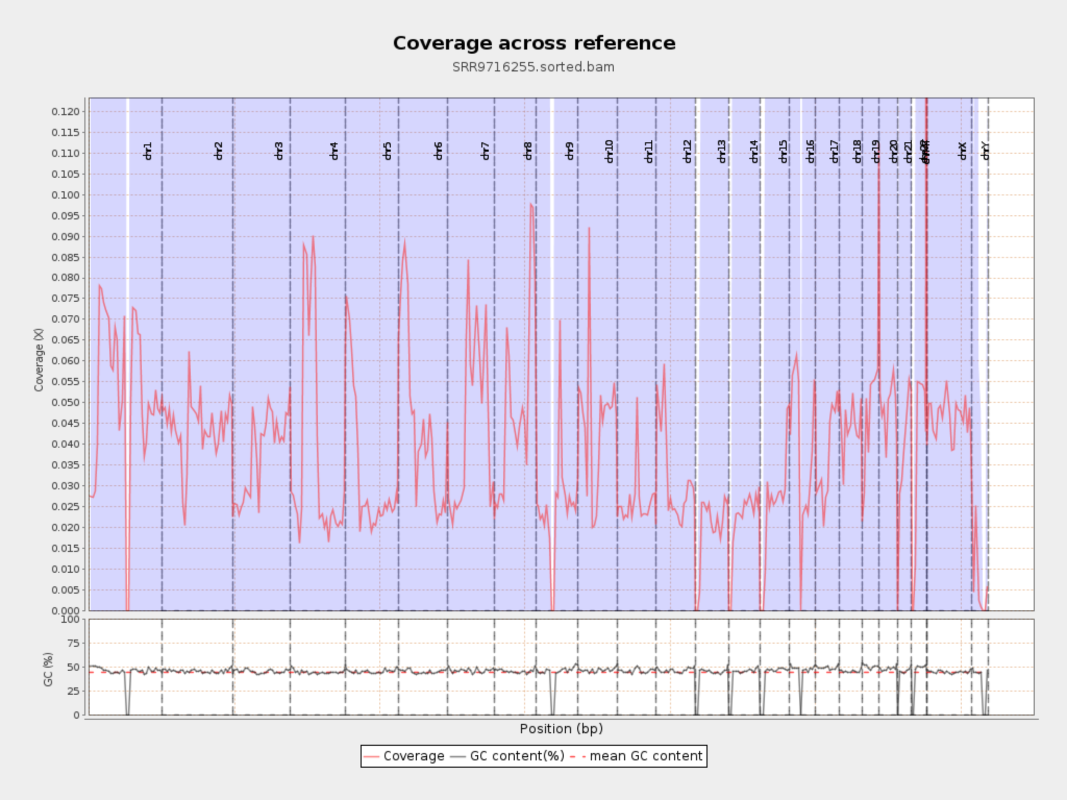
General error rate	0.65%
Mismatches	749,614
Insertions	9,913
Mapped reads with at least one insertion	0.64%
Deletions	21,557
Mapped reads with at least one deletion	1.39%
Homopolymer indels	38.35%

2.6. Chromosome stats

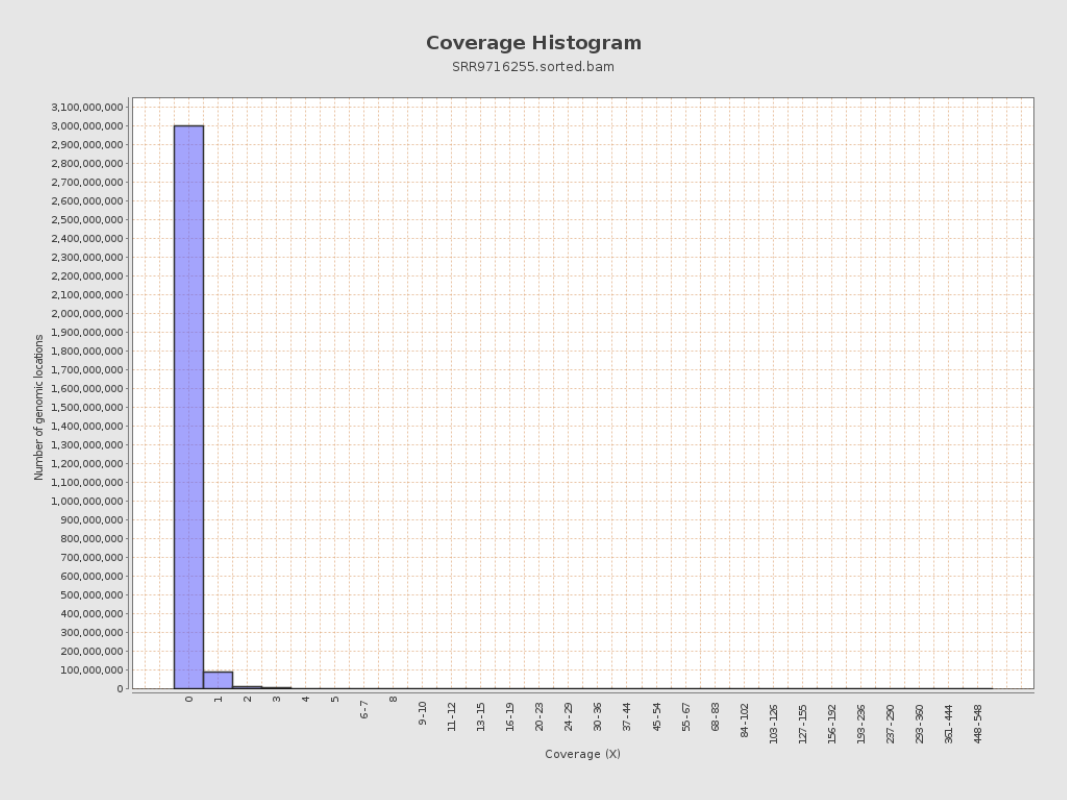
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12892866	0.0517	0.5468
chr2	243199373	10679014	0.0439	0.3361
chr3	198022430	7459060	0.0377	0.2242
chr4	191154276	7229285	0.0378	0.3013
chr5	180915260	5948225	0.0329	0.2079
chr6	171115067	7723867	0.0451	0.2553
chr7	159138663	7294407	0.0458	0.3945

chr8	146364022	7257117	0.0496	0.3463
chr9	141213431	3495217	0.0248	0.2287
chr10	135534747	6086678	0.0449	0.4395
chr11	135006516	3553556	0.0263	0.2323
chr12	133851895	4342353	0.0324	0.207
chr13	115169878	2219894	0.0193	0.1567
chr14	107349540	2280697	0.0212	0.186
chr15	102531392	2509727	0.0245	0.1783
chr16	90354753	3535094	0.0391	0.2449
chr17	81195210	2986068	0.0368	0.2417
chr18	78077248	3458293	0.0443	0.3315
chr19	59128983	2930690	0.0496	0.4243
chr20	63025520	3096369	0.0491	0.2681
chr21	48129895	1821392	0.0378	0.2664
chr22	51304566	1850059	0.0361	0.2267
chrMT	16571	15820	0.9547	1.2578
chrX	155270560	7250659	0.0467	0.2599
chrY	59373566	398367	0.0067	0.2285

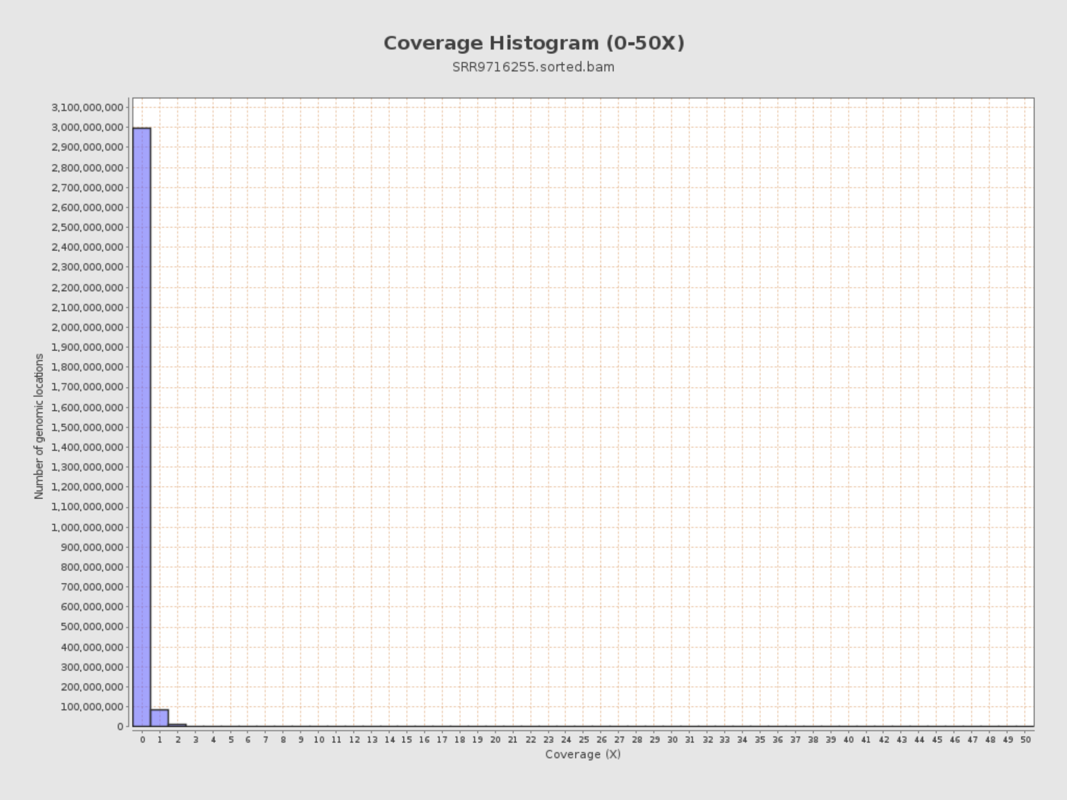
3. Results : Coverage across reference



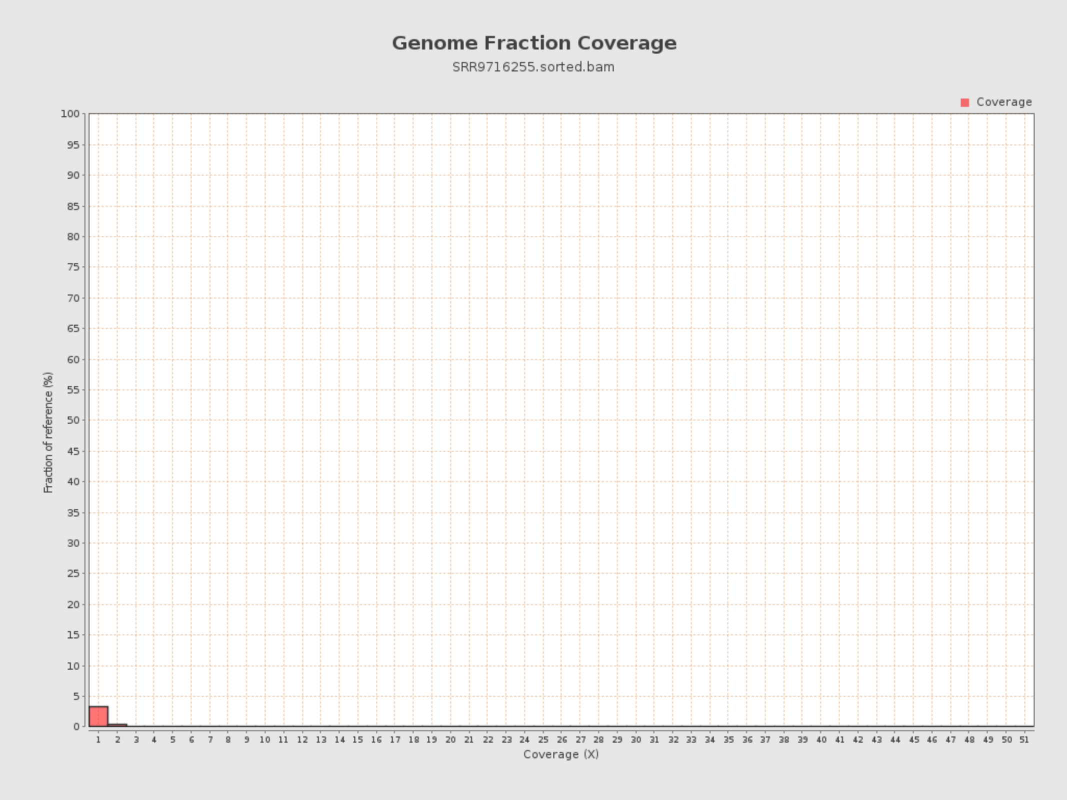
4. Results : Coverage Histogram



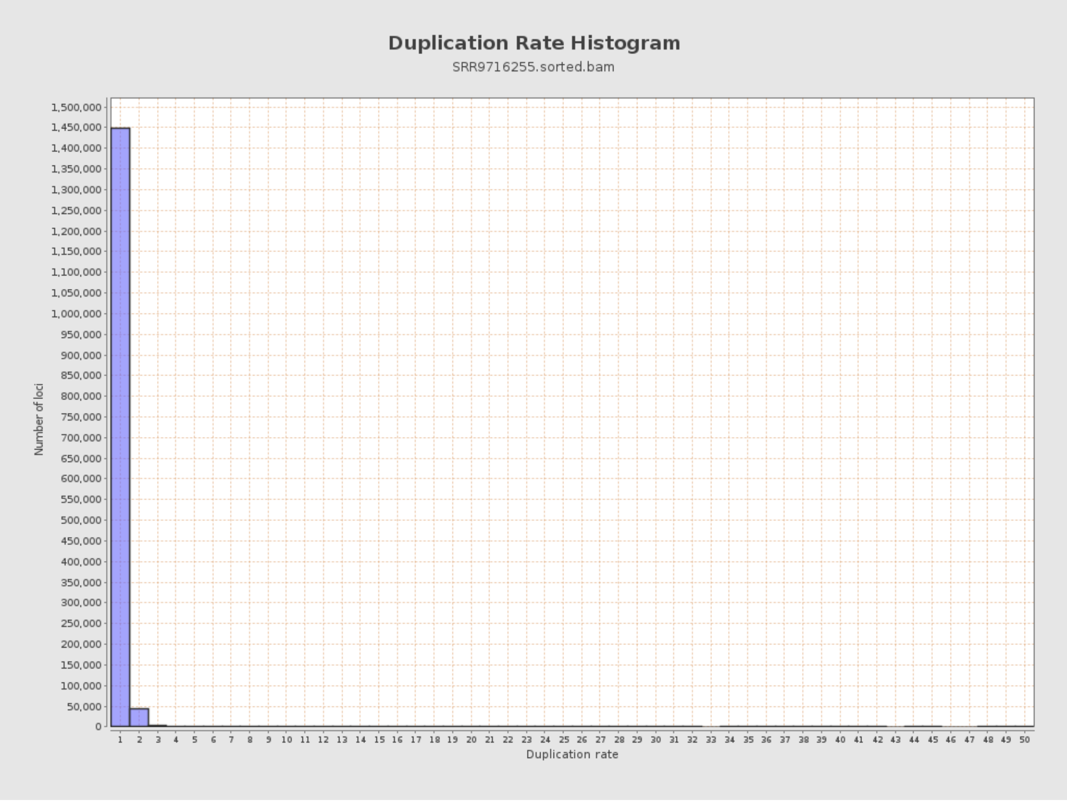
5. Results : Coverage Histogram (0-50X)



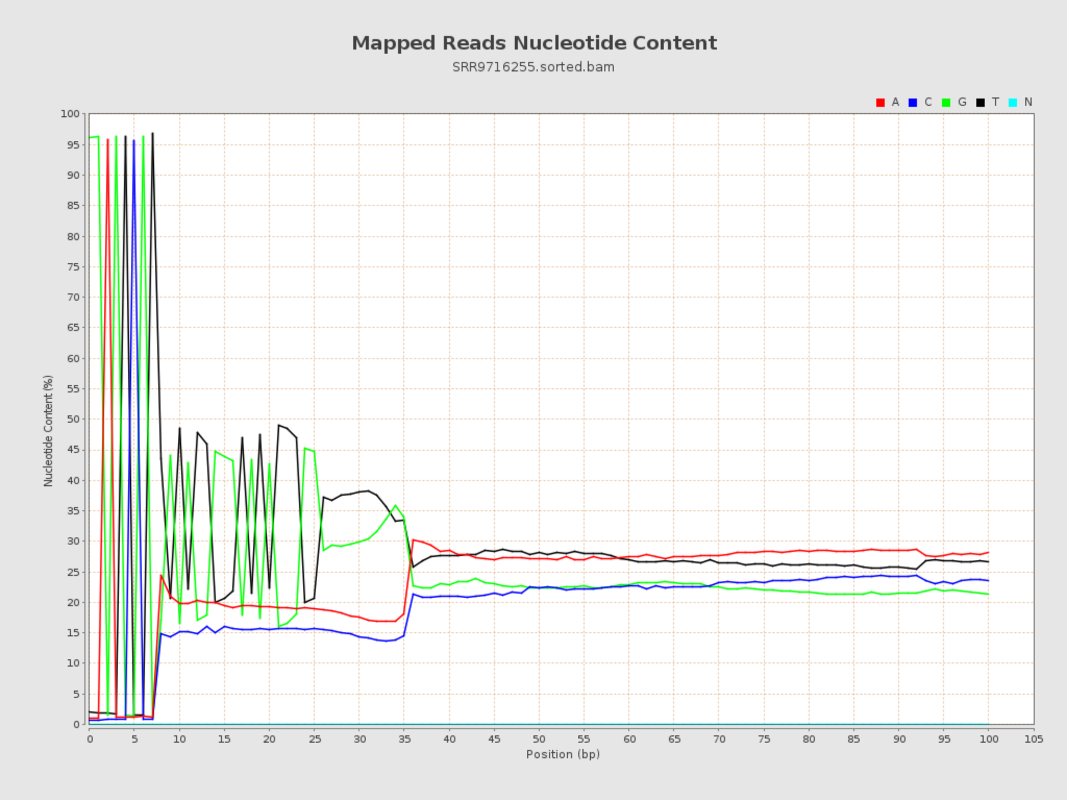
6. Results : Genome Fraction Coverage



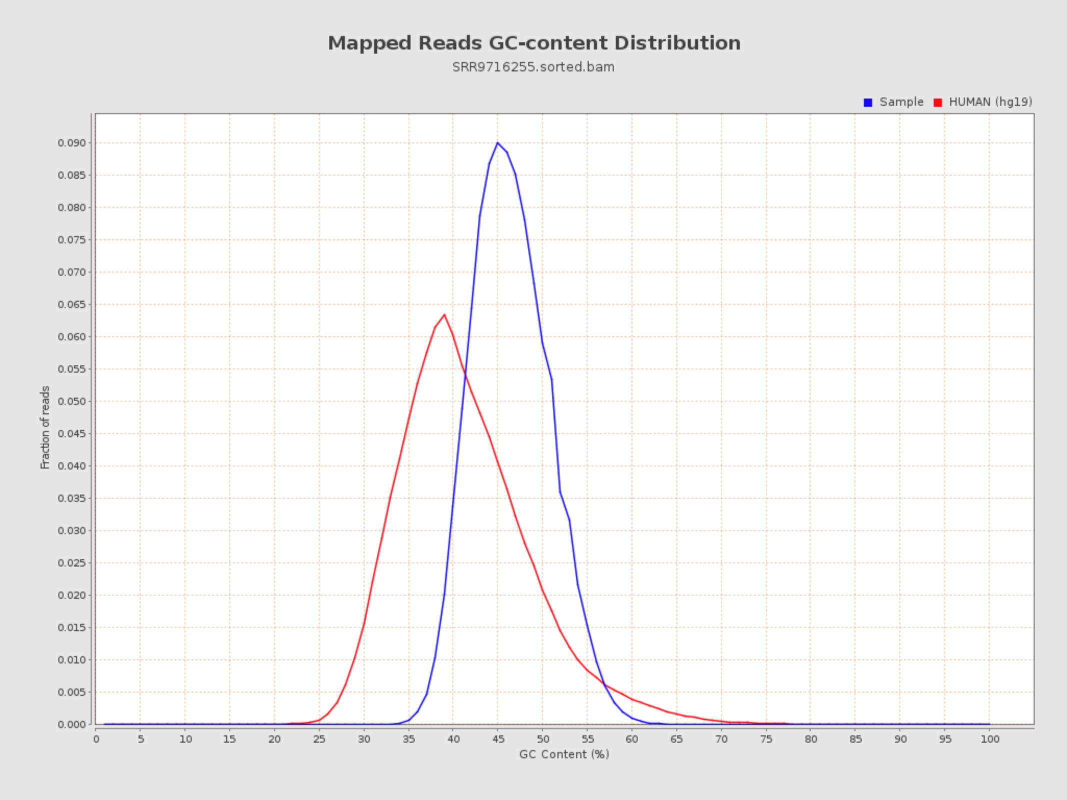
7. Results : Duplication Rate Histogram



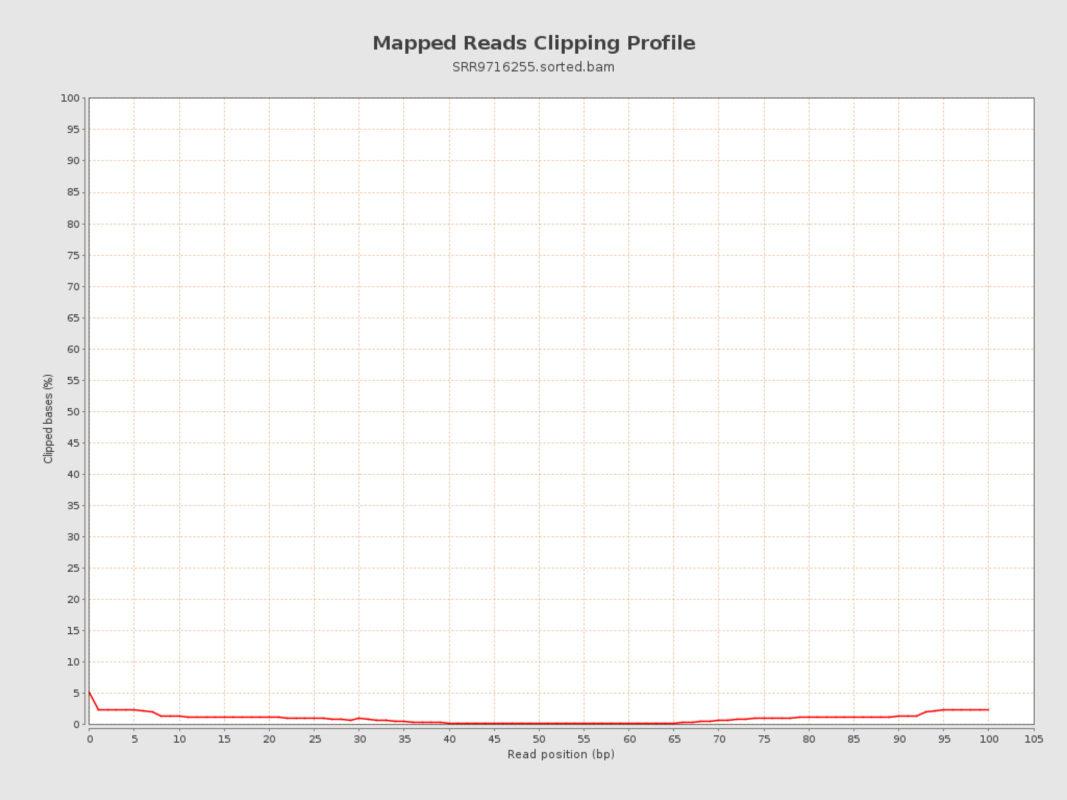
8. Results : Mapped Reads Nucleotide Content



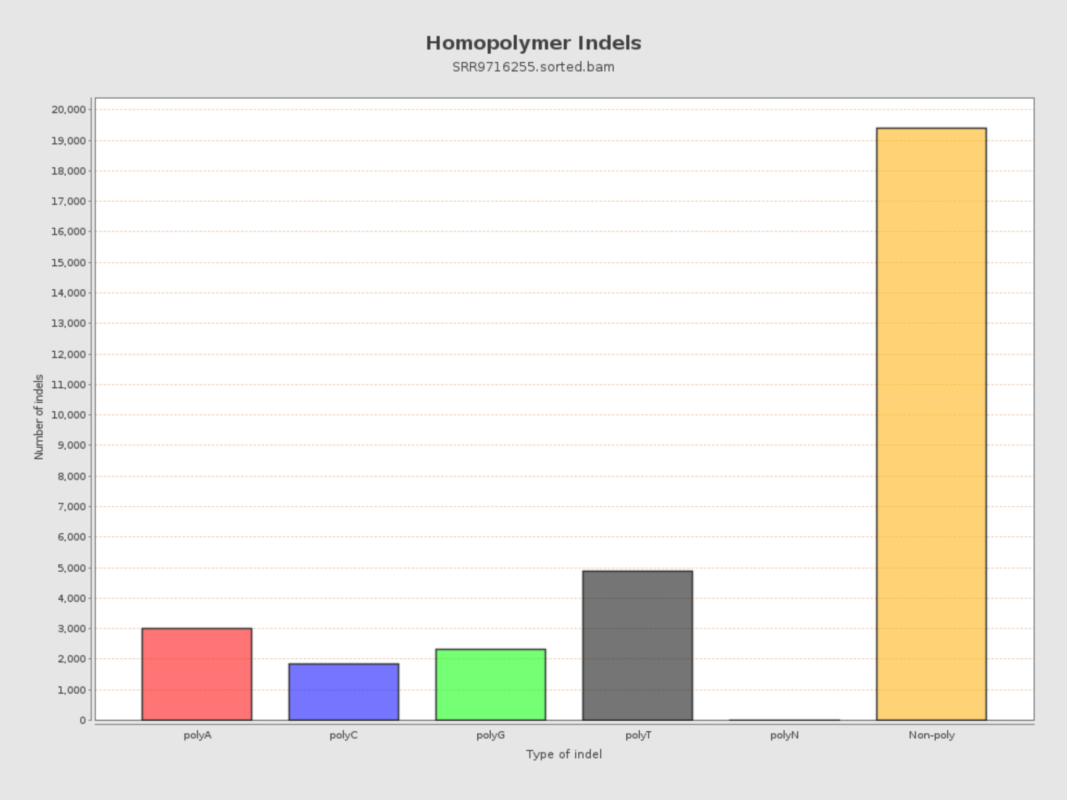
9. Results : Mapped Reads GC-content Distribution



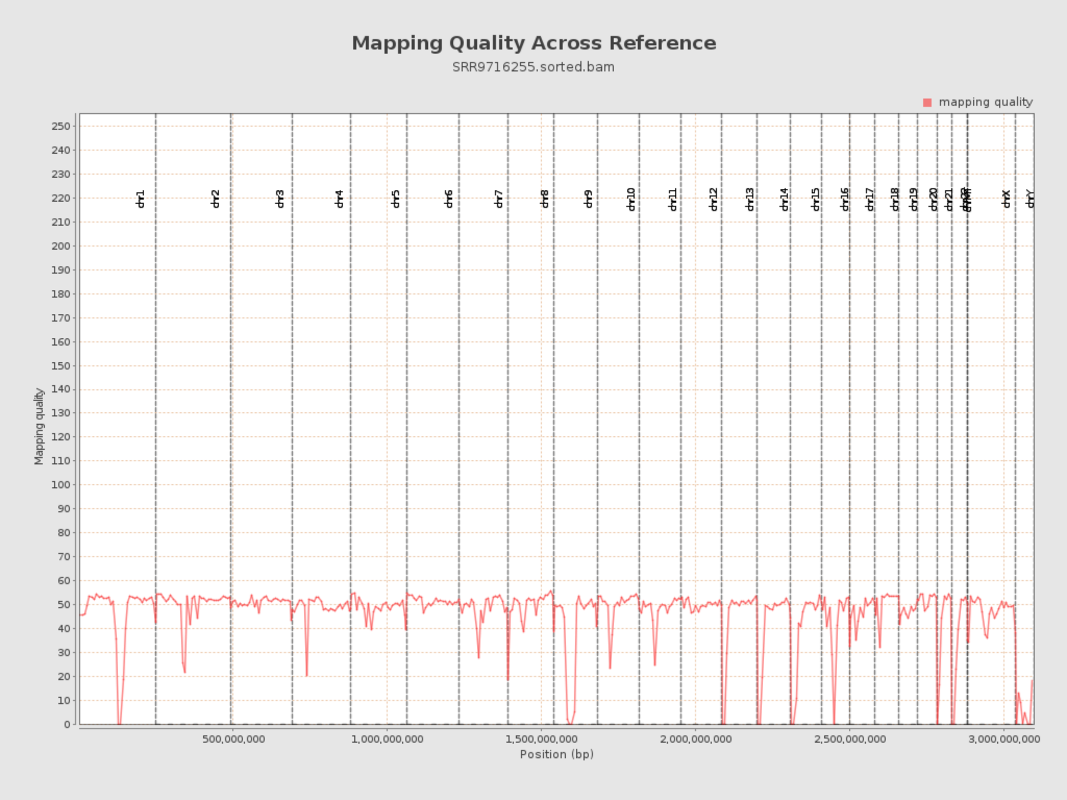
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram