Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:07:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716391.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_SRR9716391 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716391.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:07:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716391.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,272,191
Mapped reads	3,027,703 / 92.53%
Unmapped reads	244,488 / 7.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	46,354 / 1.42%
Read min/max/mean length	30 / 101 / 101.52
Duplicated reads (estimated)	164,405 / 5.02%
Duplication rate	3.49%
Clipped reads	3,068,533 / 93.78%

2.2. ACGT Content

Number/percentage of A's	59,265,776 / 24.57%
Number/percentage of C's	46,941,250 / 19.46%
Number/percentage of T's	75,041,565 / 31.11%
Number/percentage of G's	59,932,503 / 24.85%
Number/percentage of N's	14,556 / 0.01%
GC Percentage	44.31%

2.3. Coverage

Mean	0.0779

Standard Deviation	0.8126

2.4. Mapping Quality

Mean Mapping Quality	43.91

2.5. Mismatches and indels

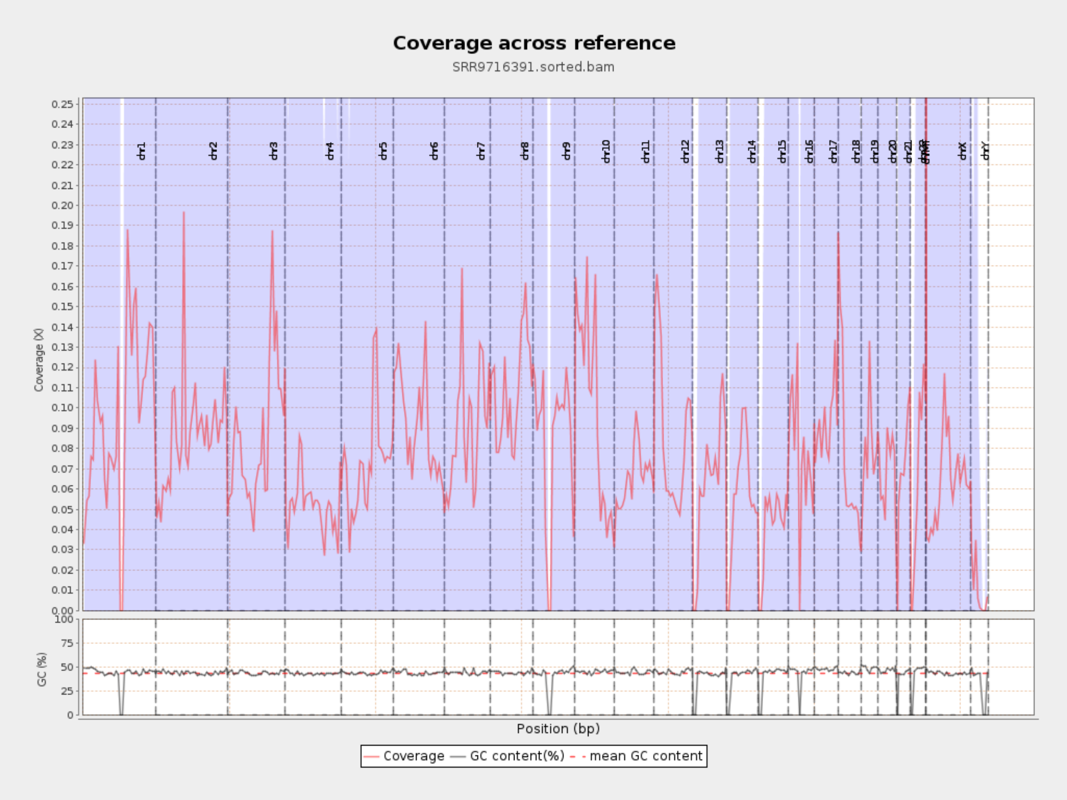
General error rate	0.82%
Mismatches	1,934,938
Insertions	22,732
Mapped reads with at least one insertion	0.74%
Deletions	58,073
Mapped reads with at least one deletion	1.89%
Homopolymer indels	43.94%

2.6. Chromosome stats

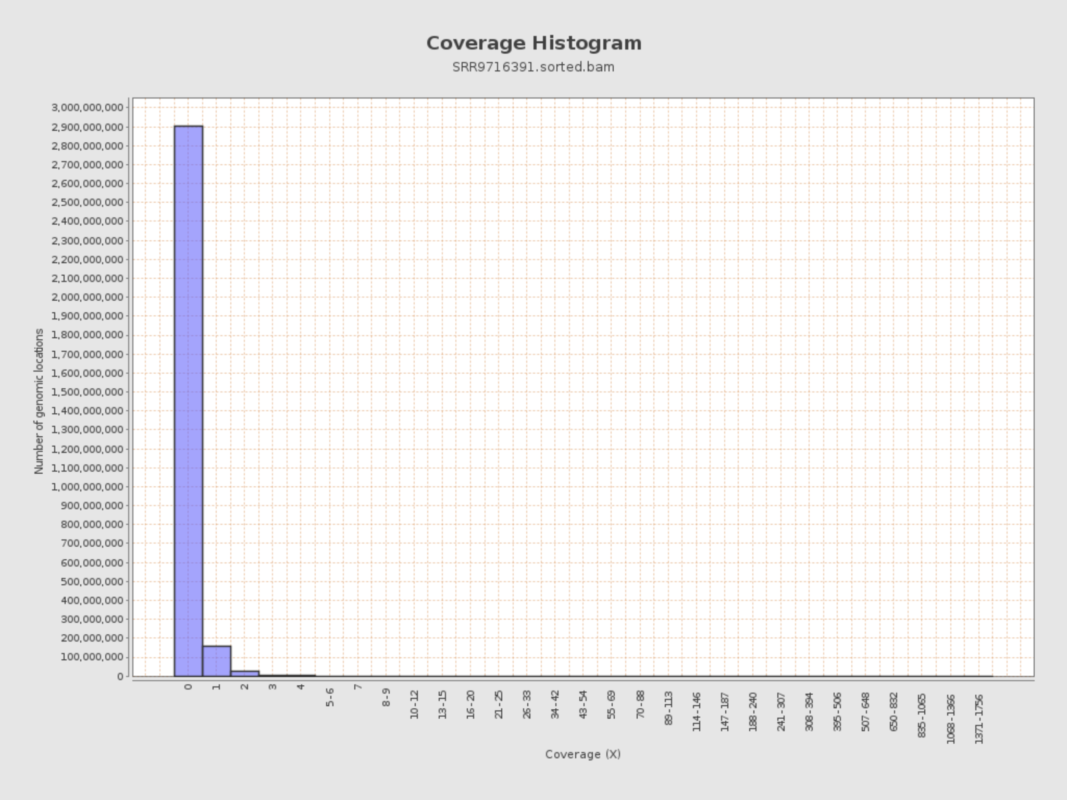
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23631393	0.0948	1.37
chr2	243199373	21214722	0.0872	1.3388
chr3	198022430	16857810	0.0851	0.3598
chr4	191154276	9979704	0.0522	0.3623
chr5	180915260	13065857	0.0722	0.33
chr6	171115067	15645612	0.0914	0.4397
chr7	159138663	14318515	0.09	1.4066

chr8	146364022	15903031	0.1087	1.096
chr9	141213431	11828664	0.0838	0.755
chr10	135534747	13737075	0.1014	0.7967
chr11	135006516	8861313	0.0656	0.6217
chr12	133851895	11820632	0.0883	0.371
chr13	115169878	7388961	0.0642	0.3022
chr14	107349540	6146135	0.0573	0.3724
chr15	102531392	4178006	0.0407	0.2584
chr16	90354753	6824495	0.0755	0.3872
chr17	81195210	7504568	0.0924	0.4423
chr18	78077248	5957320	0.0763	1.2434
chr19	59128983	4774354	0.0807	1.0804
chr20	63025520	4385512	0.0696	0.3647
chr21	48129895	3414292	0.0709	0.364
chr22	51304566	3307475	0.0645	0.3154
chrMT	16571	12367	0.7463	1.3354
chrX	155270560	9926094	0.0639	0.4437
chrY	59373566	613416	0.0103	0.3227

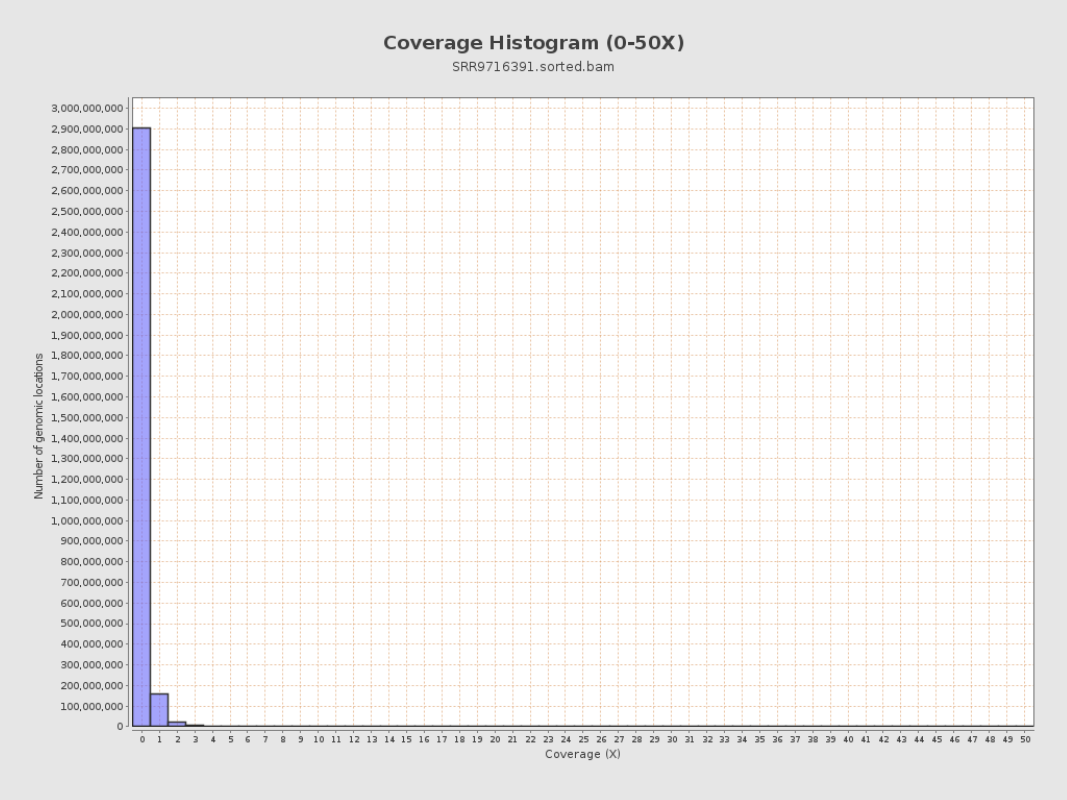
3. Results : Coverage across reference



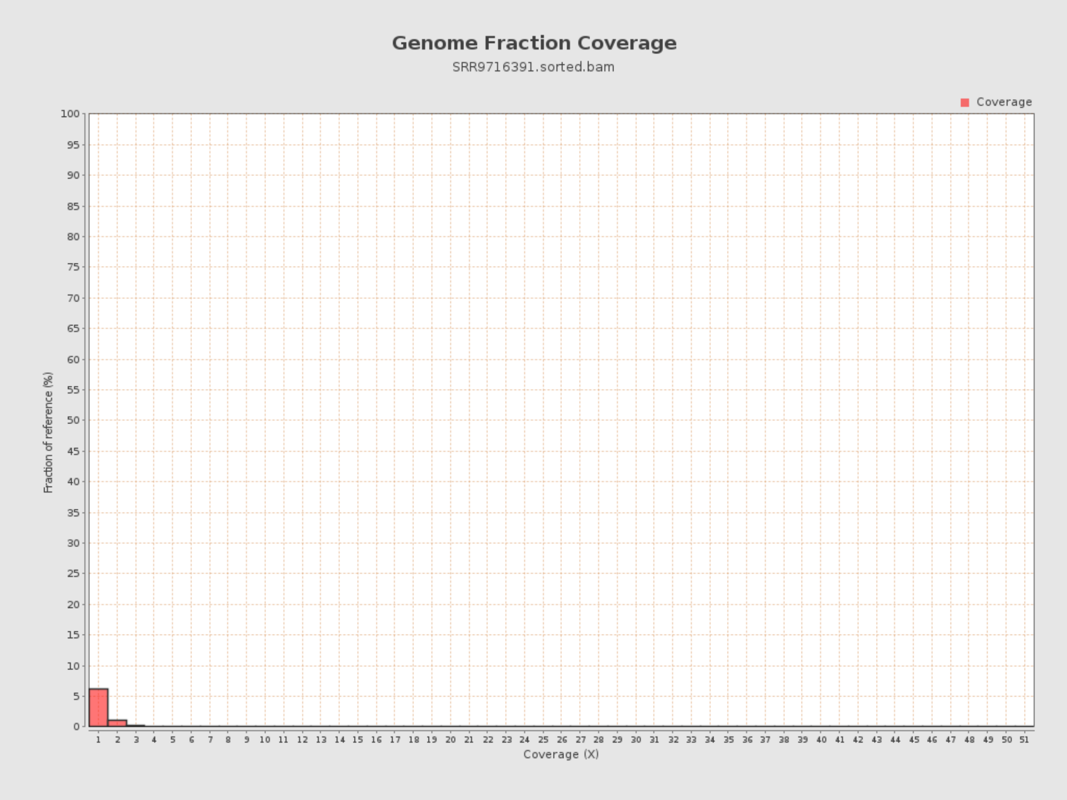
4. Results : Coverage Histogram



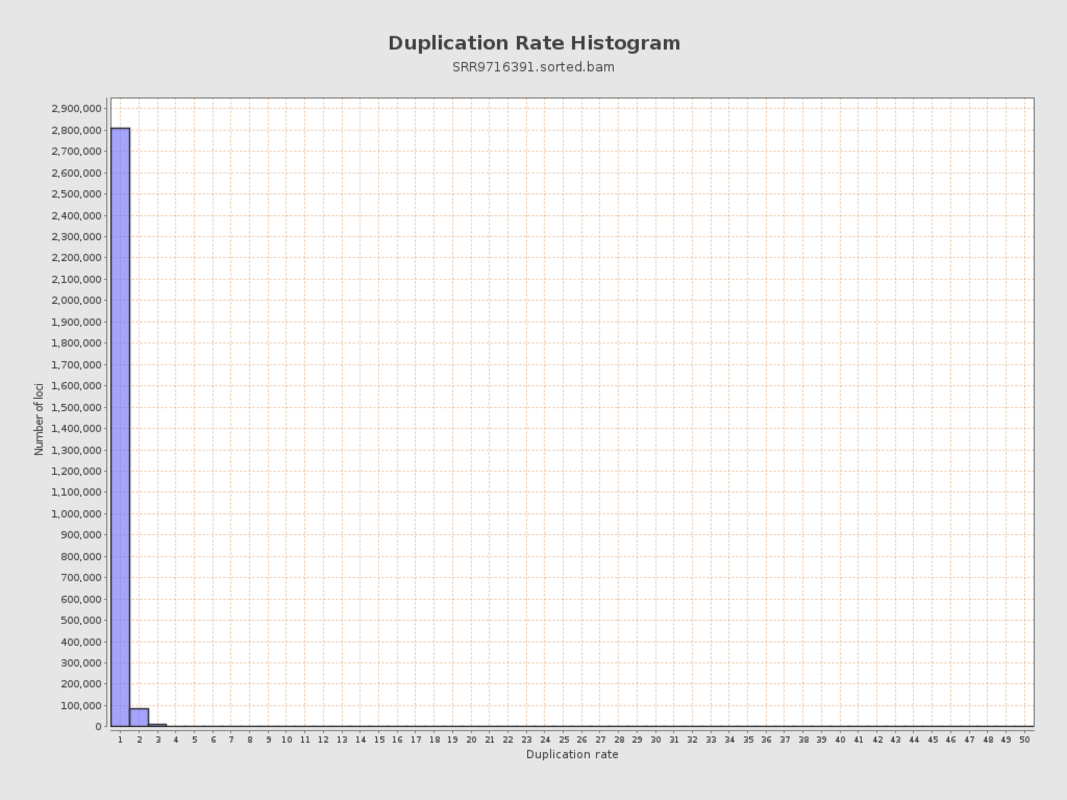
5. Results : Coverage Histogram (0-50X)



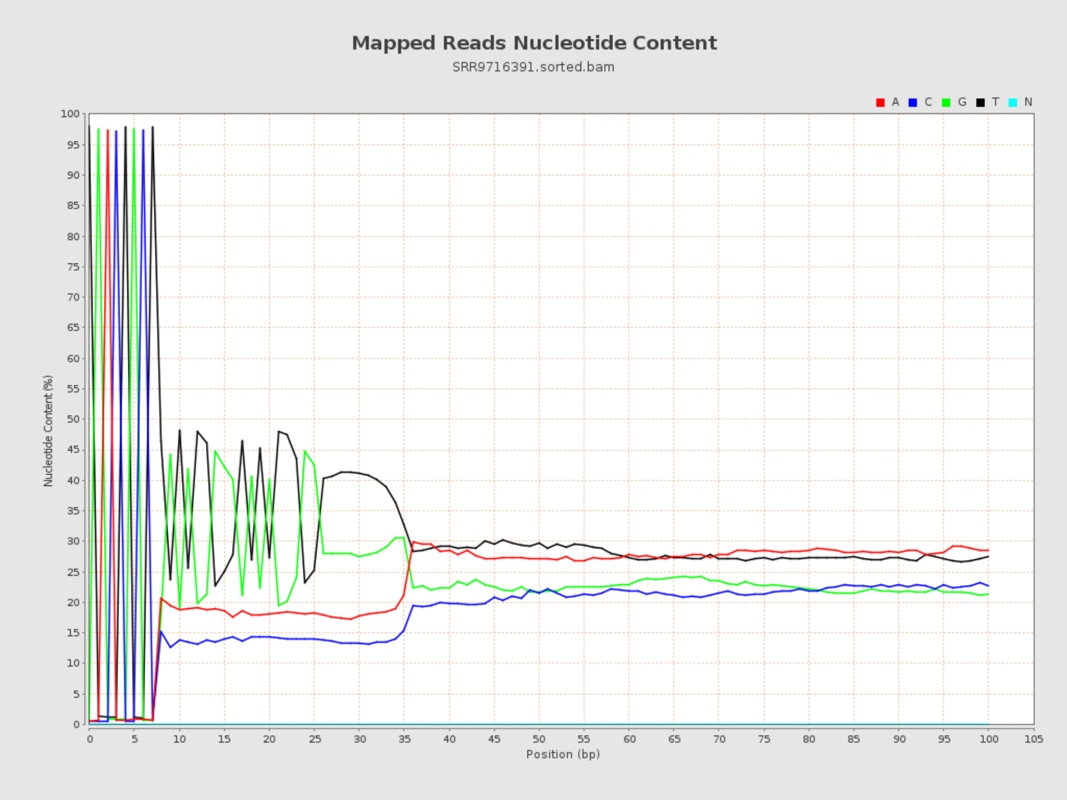
6. Results : Genome Fraction Coverage



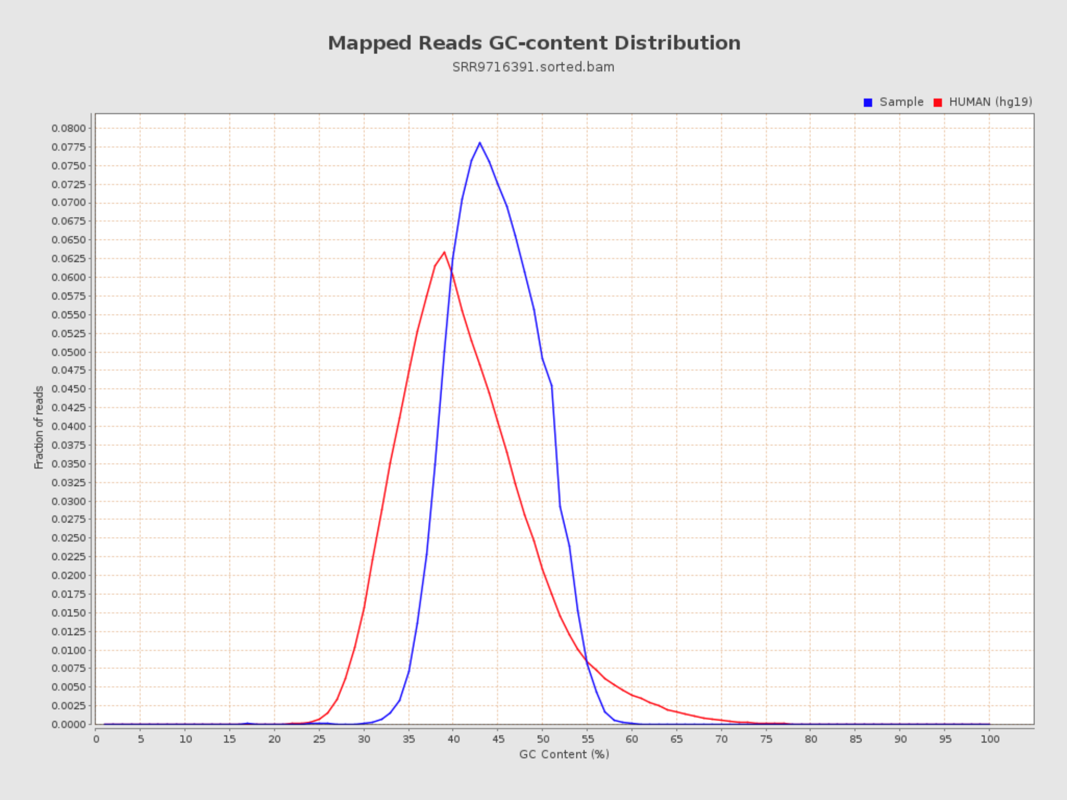
7. Results : Duplication Rate Histogram



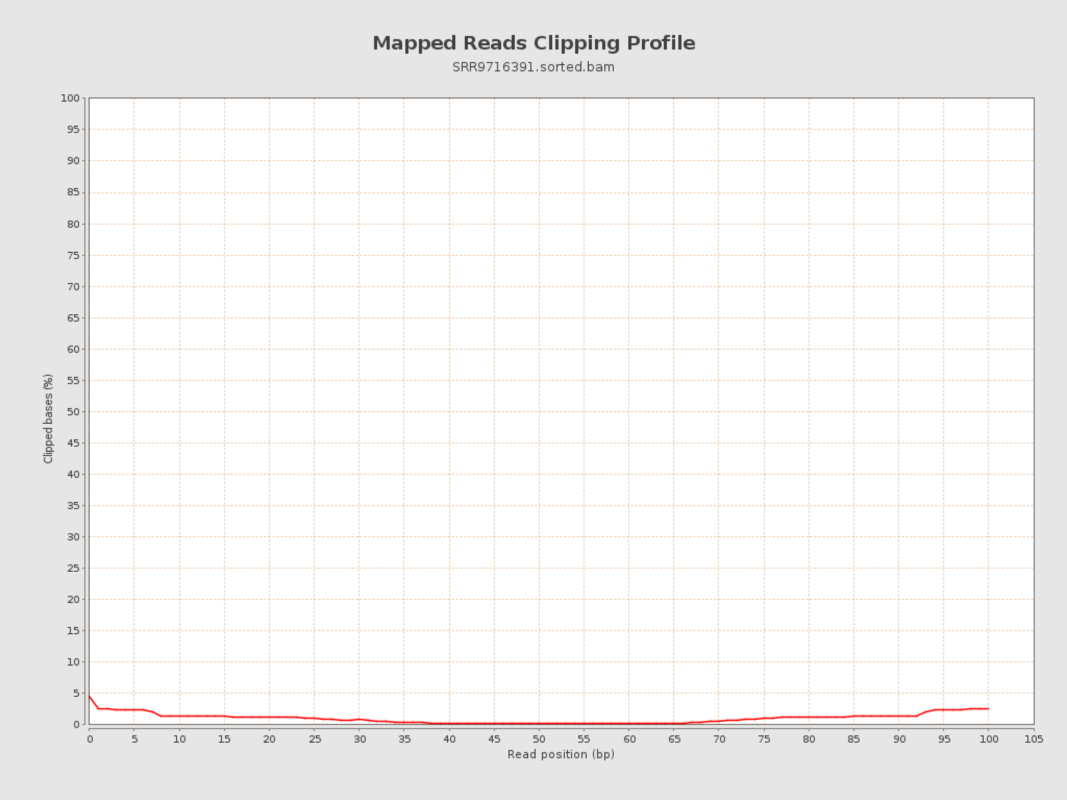
8. Results : Mapped Reads Nucleotide Content



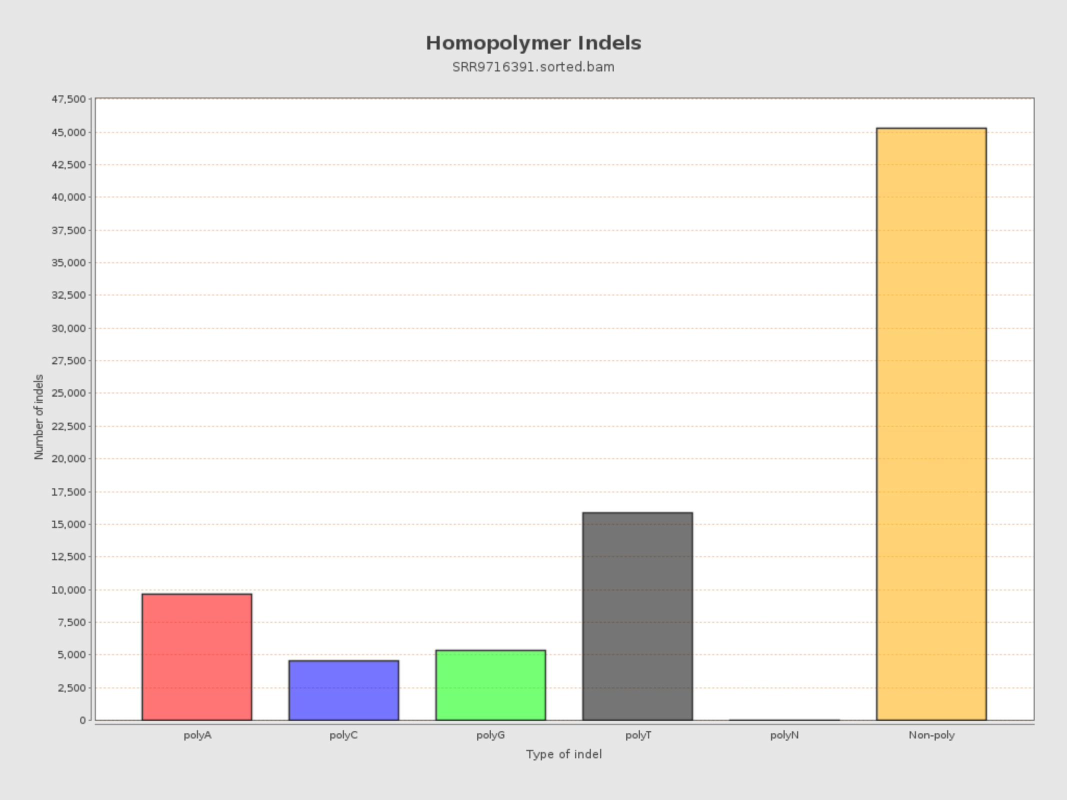
9. Results : Mapped Reads GC-content Distribution



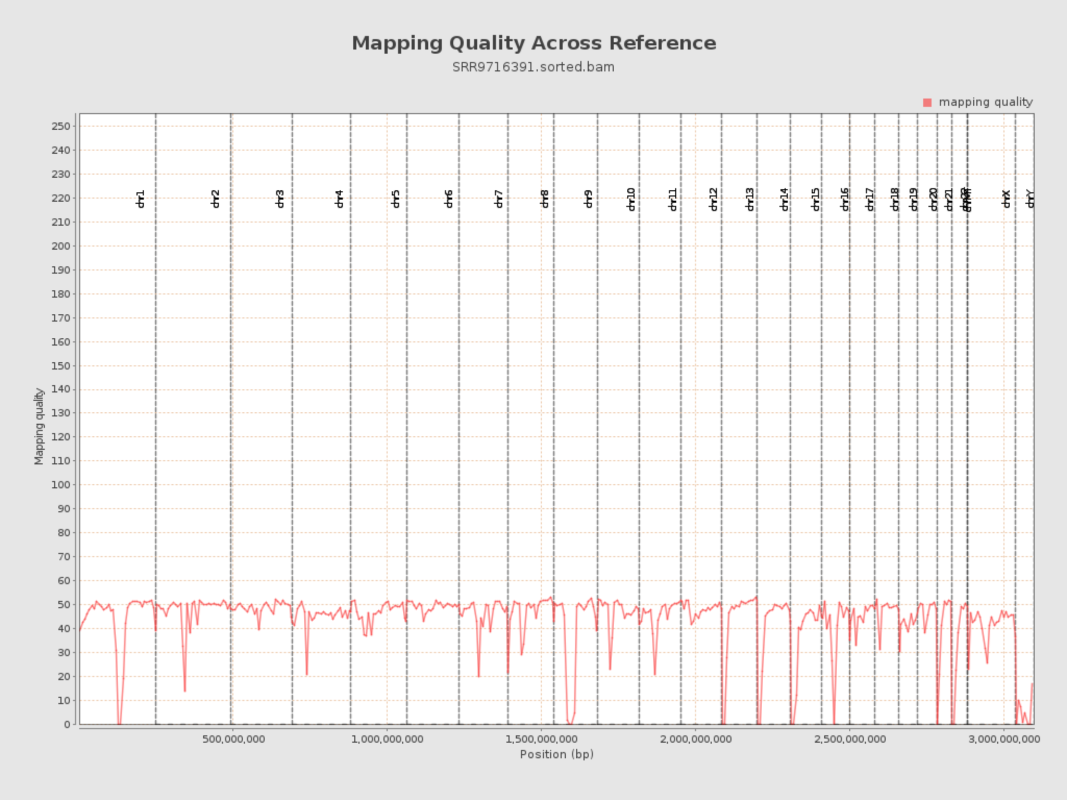
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram