Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:10:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716241.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_SRR9716241 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716241.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:10:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716241.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,212,583
Mapped reads	2,022,807 / 91.42%
Unmapped reads	189,776 / 8.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,437 / 1.6%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	101,139 / 4.57%
Duplication rate	3.05%
Clipped reads	2,054,343 / 92.85%

2.2. ACGT Content

Number/percentage of A's	40,011,412 / 25.39%
Number/percentage of C's	31,546,108 / 20.02%
Number/percentage of T's	48,097,681 / 30.52%
Number/percentage of G's	37,905,243 / 24.06%
Number/percentage of N's	8,722 / 0.01%
GC Percentage	44.08%

2.3. Coverage

Mean	0.0509

Standard Deviation	0.5835

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

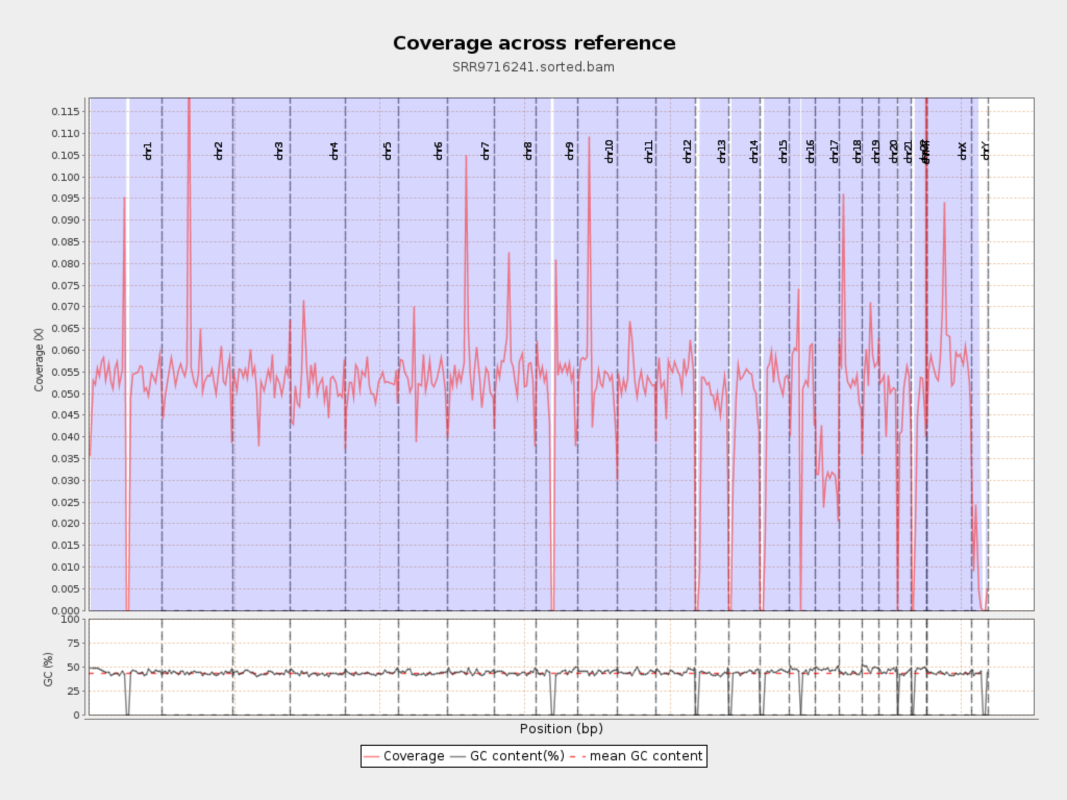
General error rate	0.85%
Mismatches	1,306,255
Insertions	15,469
Mapped reads with at least one insertion	0.75%
Deletions	40,182
Mapped reads with at least one deletion	1.96%
Homopolymer indels	43.81%

2.6. Chromosome stats

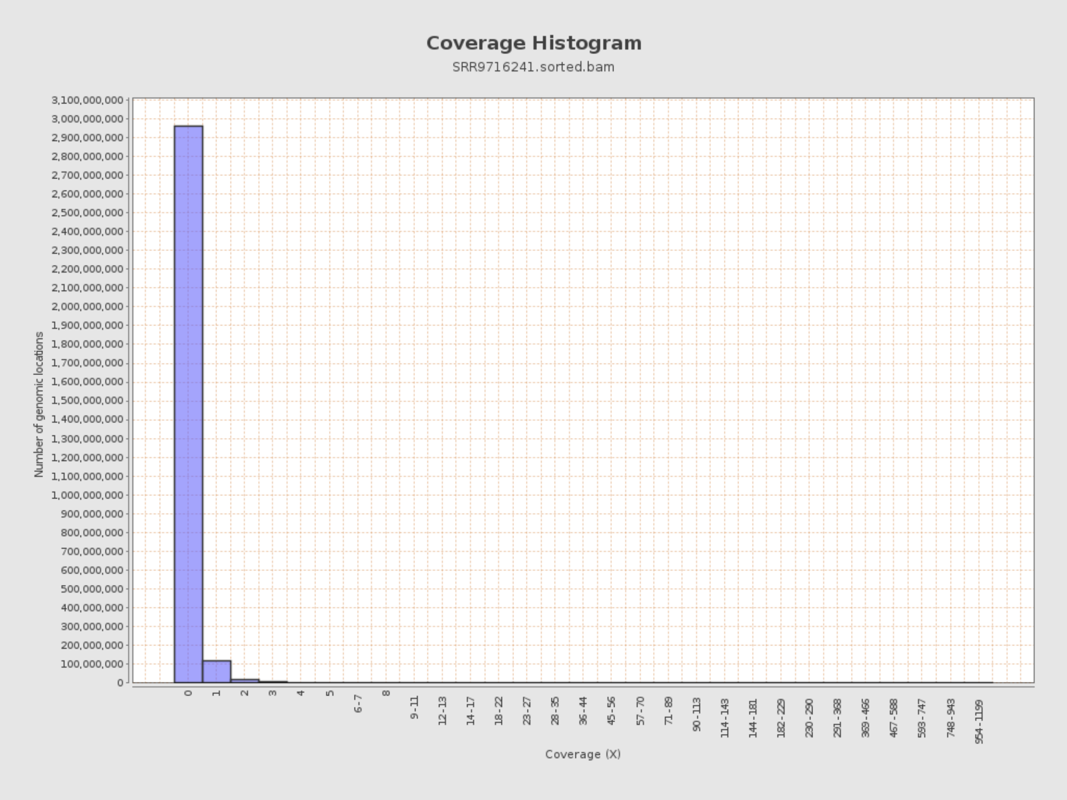
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12848127	0.0515	0.9377
chr2	243199373	13809273	0.0568	0.8935
chr3	198022430	10556696	0.0533	0.2735
chr4	191154276	9927081	0.0519	0.2981
chr5	180915260	9500873	0.0525	0.2739
chr6	171115067	9213618	0.0538	0.3608
chr7	159138663	8923753	0.0561	0.7642

chr8	146364022	8198417	0.056	0.743
chr9	141213431	6912619	0.049	0.6567
chr10	135534747	7592710	0.056	0.5936
chr11	135006516	7179002	0.0532	0.5625
chr12	133851895	7300398	0.0545	0.2818
chr13	115169878	4822122	0.0419	0.2323
chr14	107349540	4731955	0.0441	0.3559
chr15	102531392	4515442	0.044	0.2496
chr16	90354753	4661901	0.0516	0.332
chr17	81195210	2483381	0.0306	0.2302
chr18	78077248	4473542	0.0573	1.2557
chr19	59128983	3409497	0.0577	0.7337
chr20	63025520	3131725	0.0497	0.2925
chr21	48129895	2082298	0.0433	0.2674
chr22	51304566	1754062	0.0342	0.2138
chrMT	16571	21233	1.2813	1.5298
chrX	155270560	9145762	0.0589	0.425
chrY	59373566	443915	0.0075	0.1961

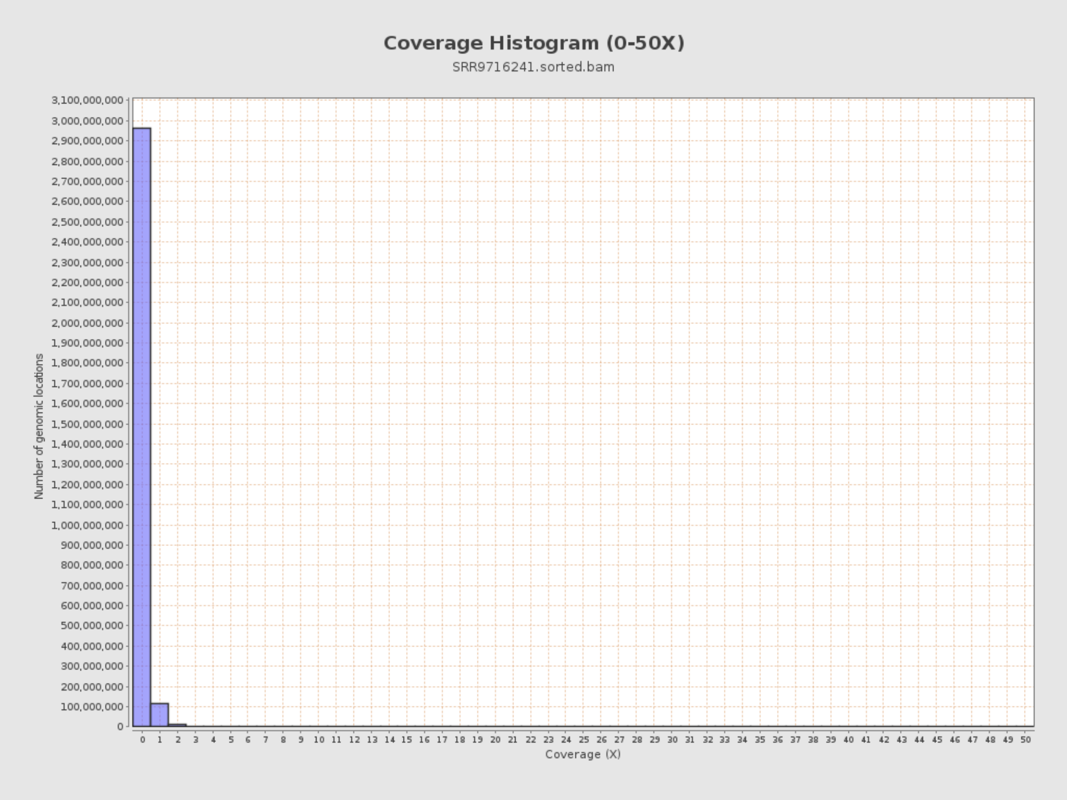
3. Results : Coverage across reference



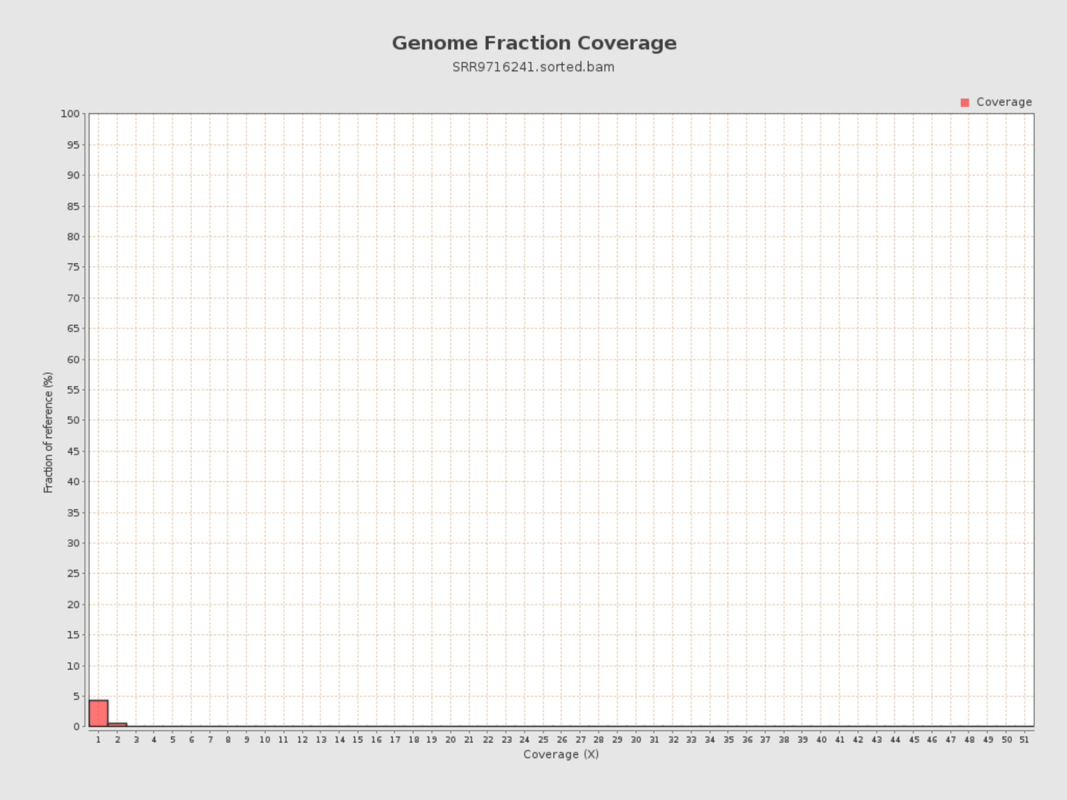
4. Results : Coverage Histogram



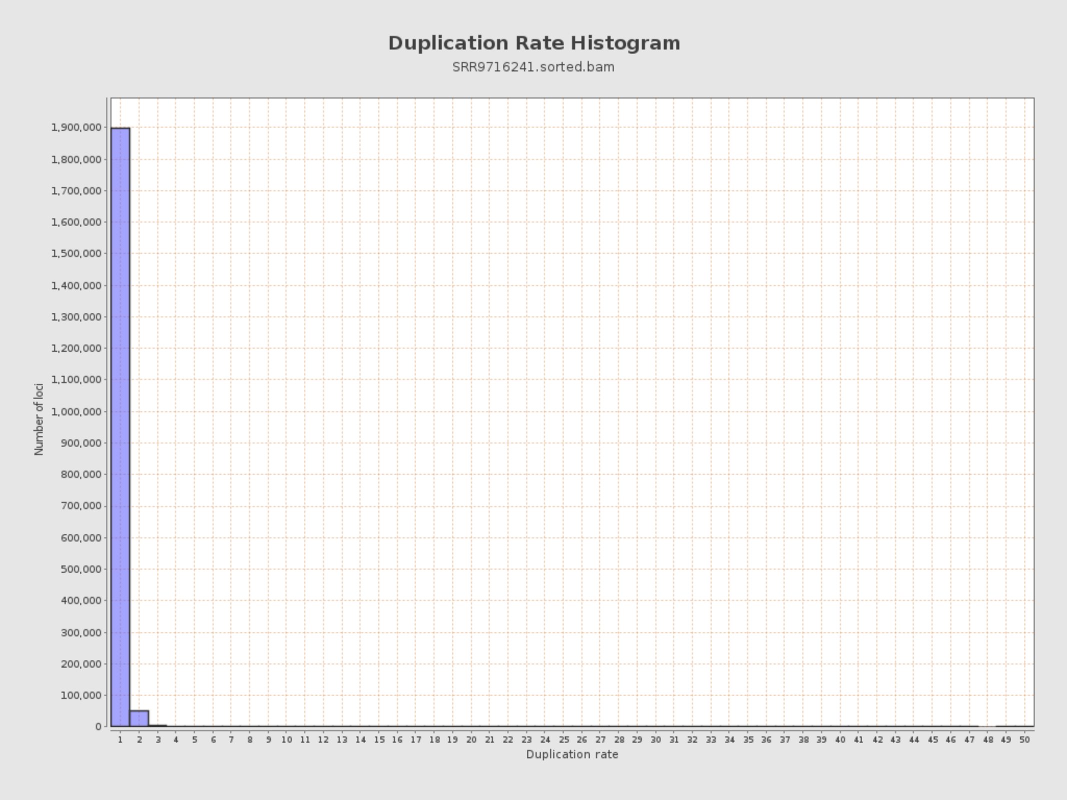
5. Results : Coverage Histogram (0-50X)



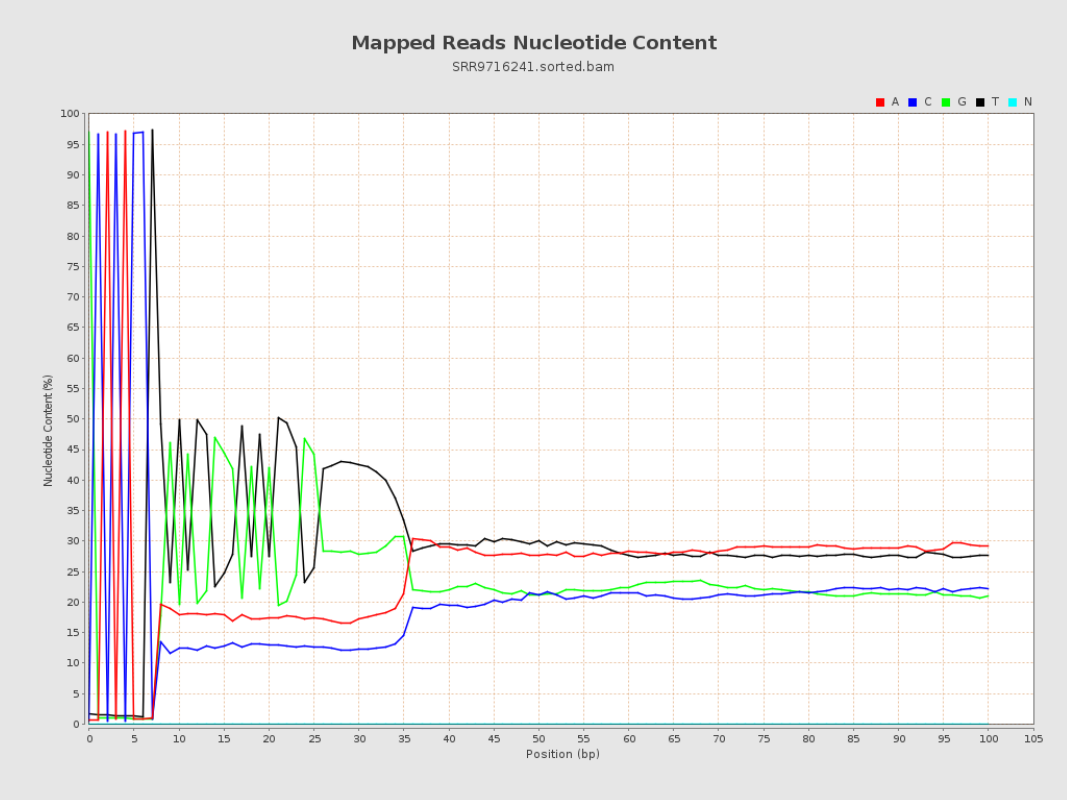
6. Results : Genome Fraction Coverage



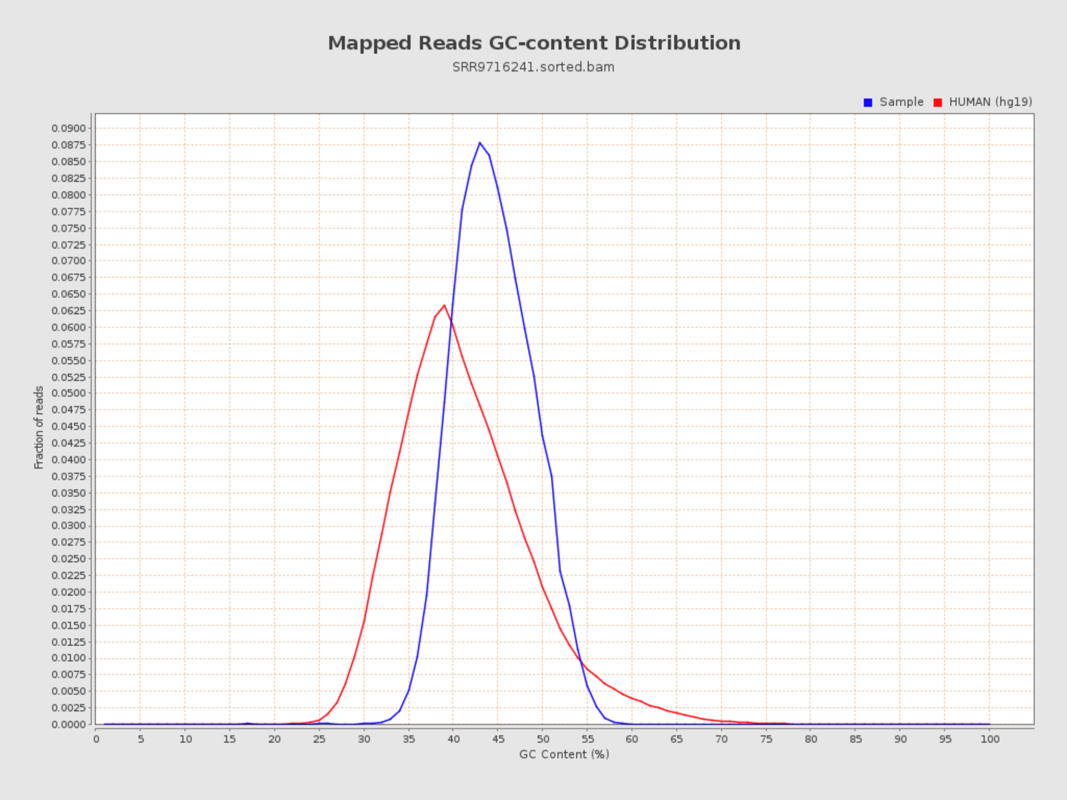
7. Results : Duplication Rate Histogram



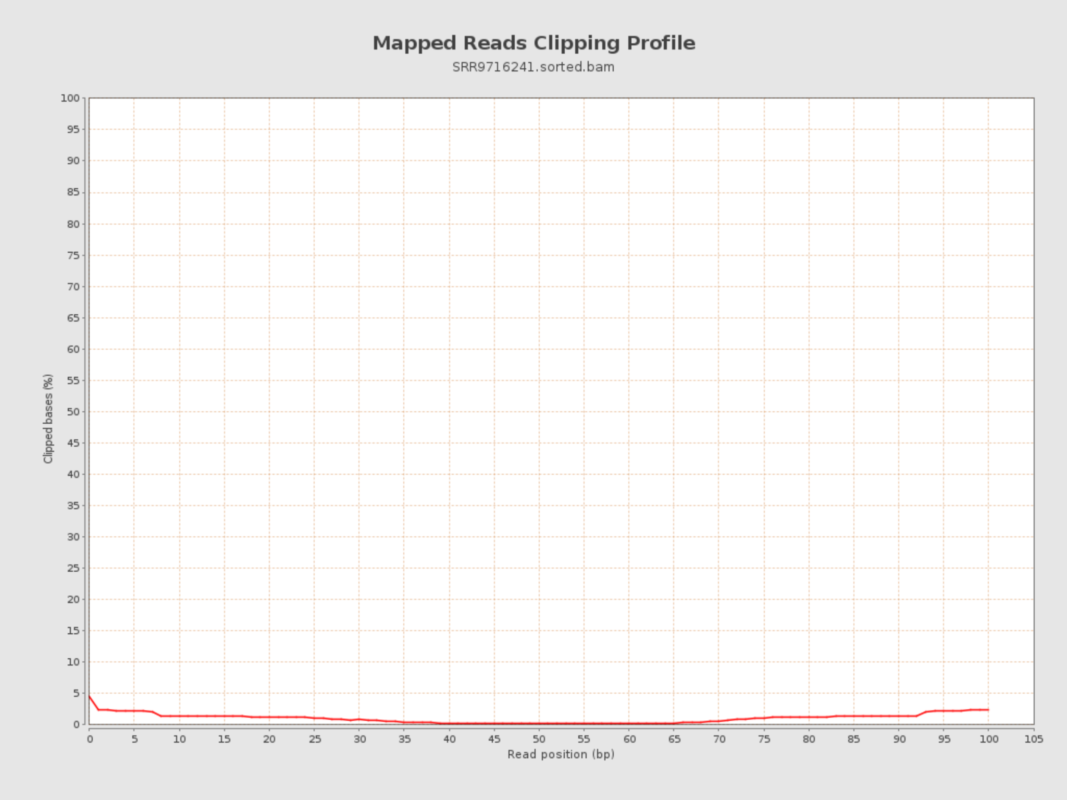
8. Results : Mapped Reads Nucleotide Content



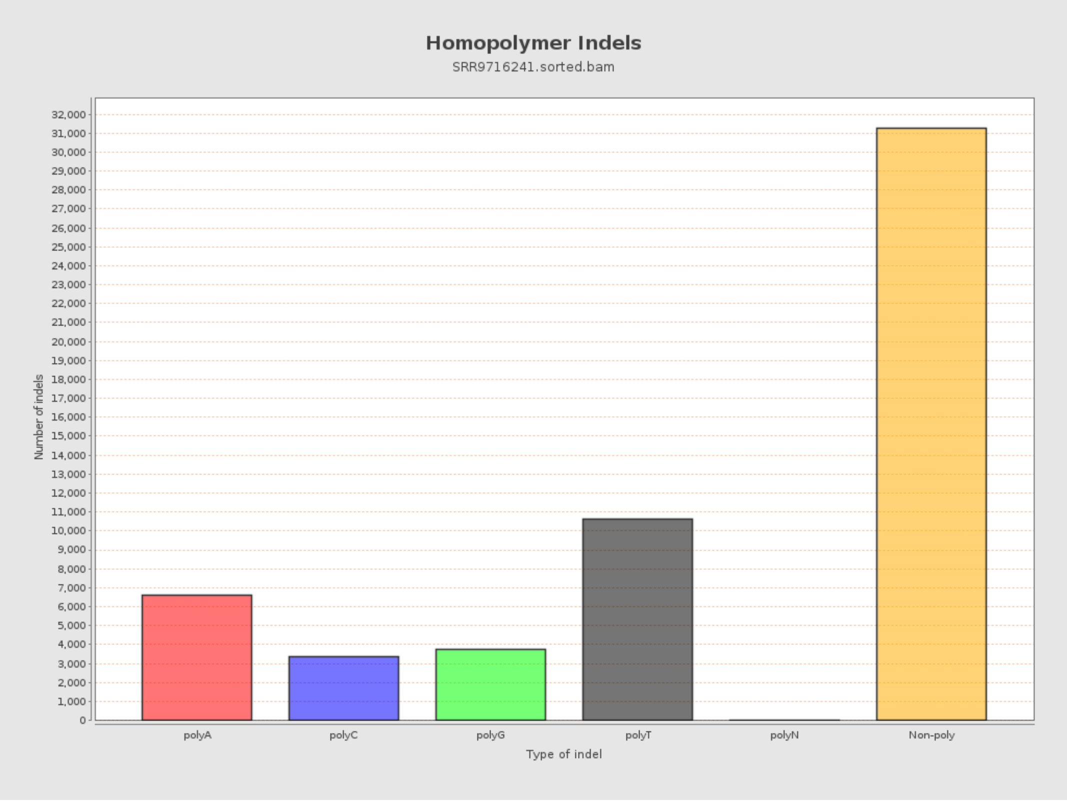
9. Results : Mapped Reads GC-content Distribution



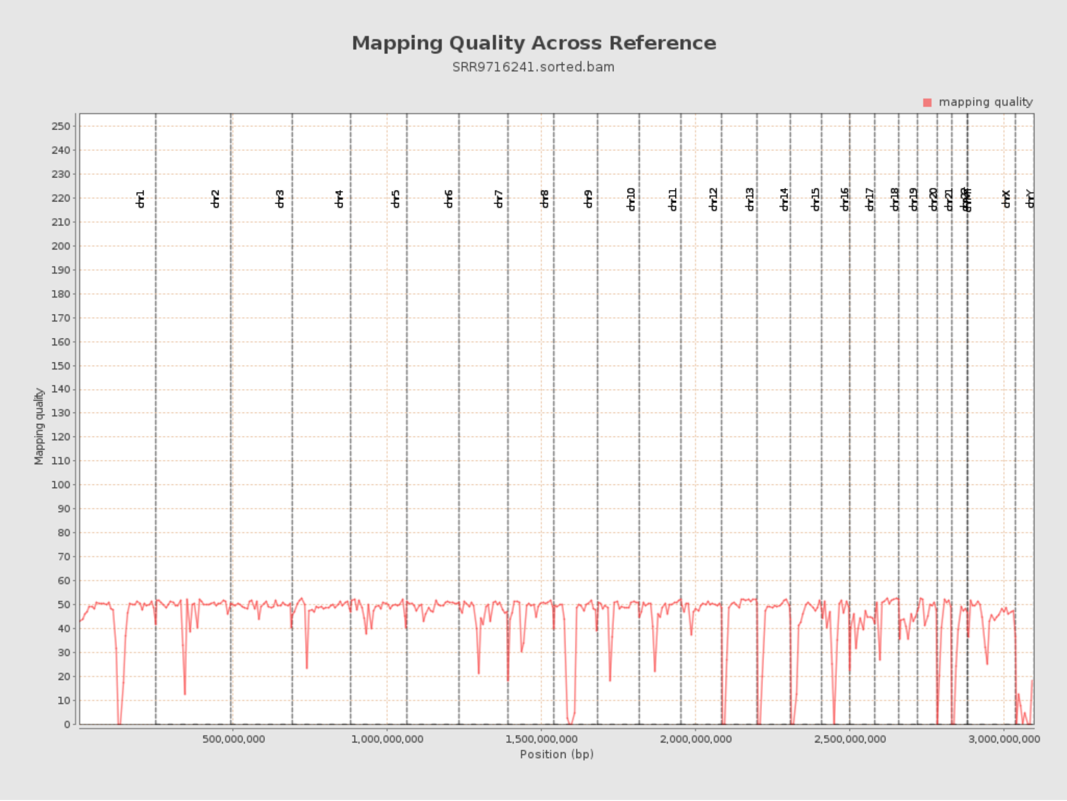
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram