Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 00:03:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716204.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_SRR9716204 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716204.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 00:03:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716204.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,701,185
Mapped reads	2,457,114 / 90.96%
Unmapped reads	244,071 / 9.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	62,024 / 2.3%
Read min/max/mean length	30 / 101 / 101.83
Duplicated reads (estimated)	93,363 / 3.46%
Duplication rate	2.61%
Clipped reads	2,514,924 / 93.1%

2.2. ACGT Content

Number/percentage of A's	47,463,712 / 26.21%
Number/percentage of C's	37,743,637 / 20.84%
Number/percentage of T's	53,442,797 / 29.51%
Number/percentage of G's	42,431,611 / 23.43%
Number/percentage of N's	21,432 / 0.01%
GC Percentage	44.27%

2.3. Coverage

Mean	0.0585

Standard Deviation	0.4527

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

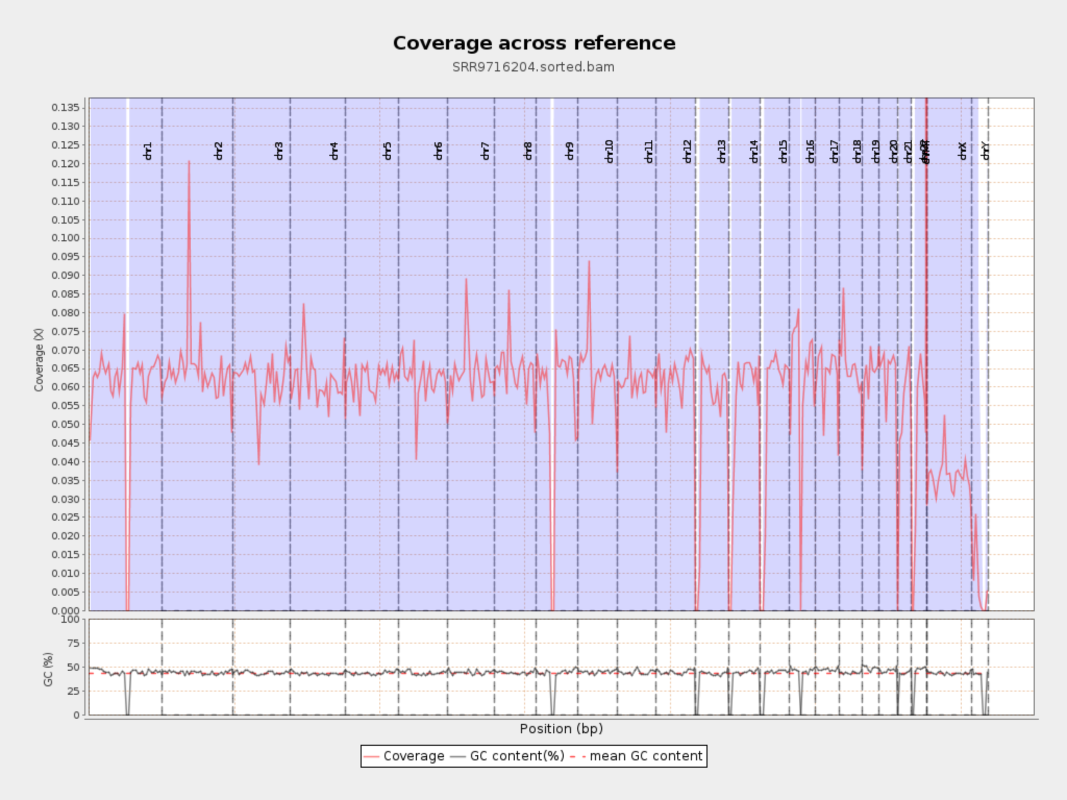
General error rate	0.73%
Mismatches	1,291,936
Insertions	15,190
Mapped reads with at least one insertion	0.61%
Deletions	36,776
Mapped reads with at least one deletion	1.47%
Homopolymer indels	40.4%

2.6. Chromosome stats

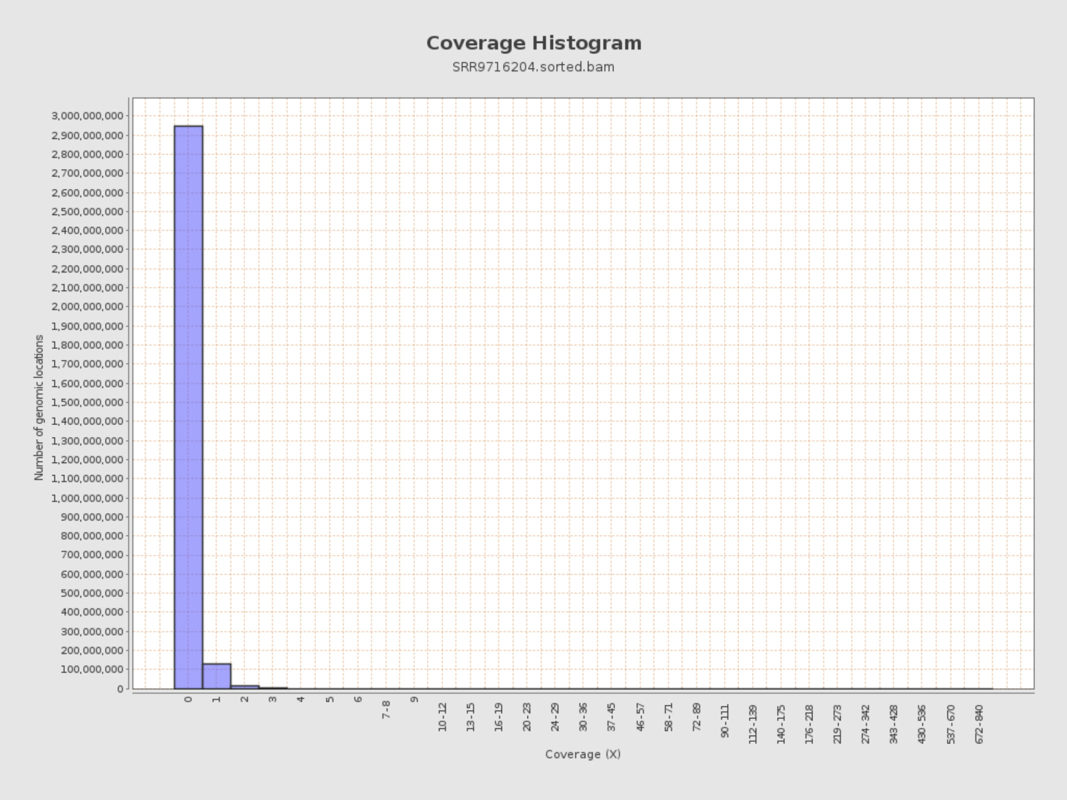
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14819332	0.0595	0.5498
chr2	243199373	15867963	0.0652	0.67
chr3	198022430	12251085	0.0619	0.2887
chr4	191154276	11843275	0.062	0.3216
chr5	180915260	11214156	0.062	0.2936
chr6	171115067	10659462	0.0623	0.3387
chr7	159138663	10208830	0.0642	0.5545

chr8	146364022	9472399	0.0647	0.5977
chr9	141213431	7973225	0.0565	0.4997
chr10	135534747	8825175	0.0651	0.4669
chr11	135006516	8323235	0.0617	0.4853
chr12	133851895	8410665	0.0628	0.2981
chr13	115169878	5853122	0.0508	0.2601
chr14	107349540	5639905	0.0525	0.3472
chr15	102531392	5397512	0.0526	0.2684
chr16	90354753	5616909	0.0622	0.3358
chr17	81195210	5112151	0.063	0.3251
chr18	78077248	5216463	0.0668	0.9699
chr19	59128983	3737522	0.0632	0.5173
chr20	63025520	4015245	0.0637	0.3135
chr21	48129895	2473221	0.0514	0.2958
chr22	51304566	2177329	0.0424	0.2398
chrMT	16571	14739	0.8894	1.3209
chrX	155270560	5636204	0.0363	0.3185
chrY	59373566	406825	0.0069	0.2247

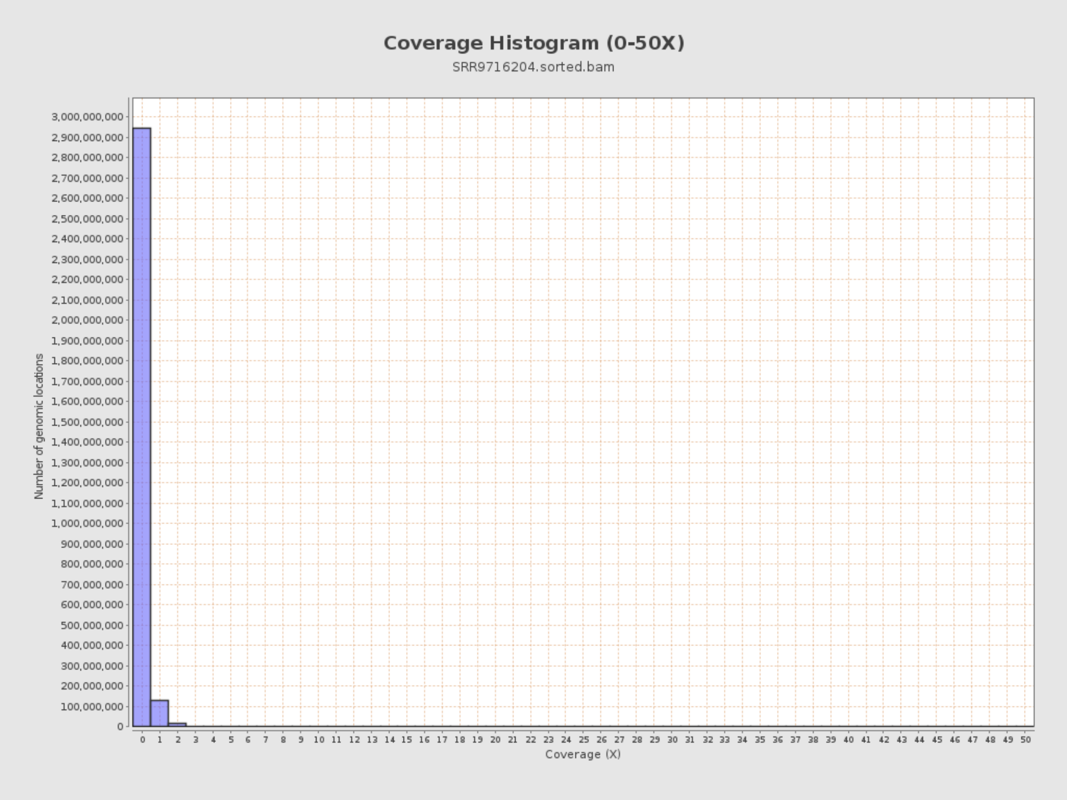
3. Results : Coverage across reference



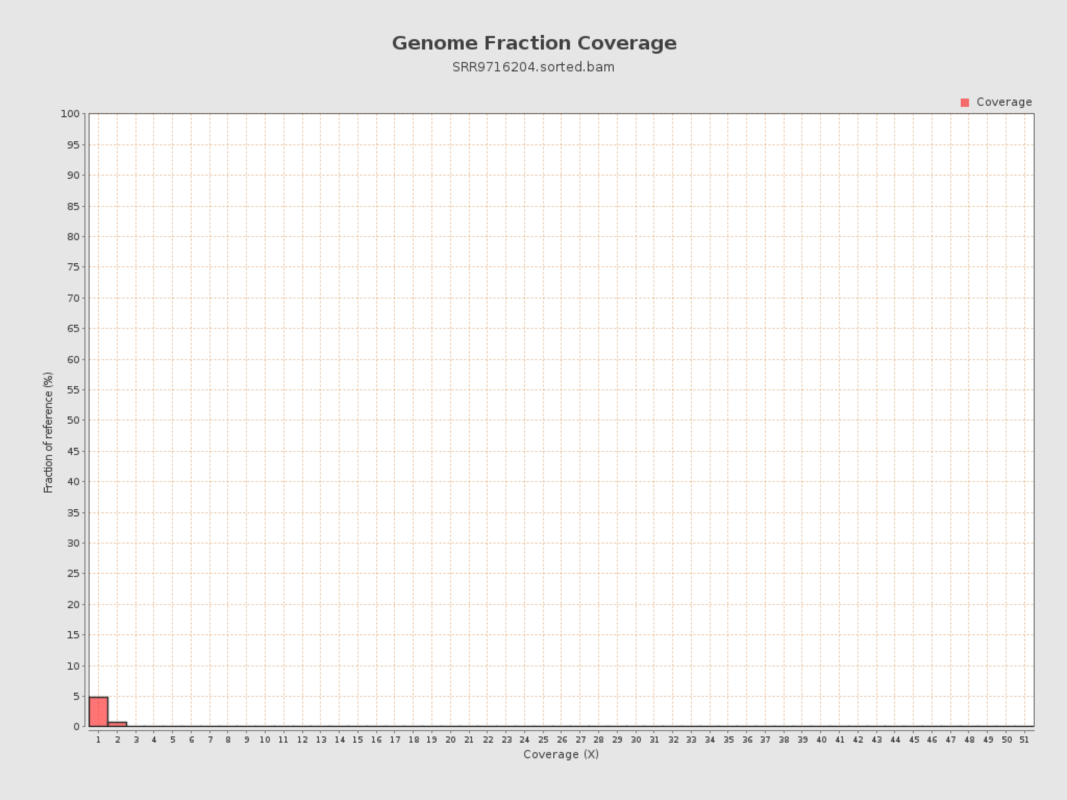
4. Results : Coverage Histogram



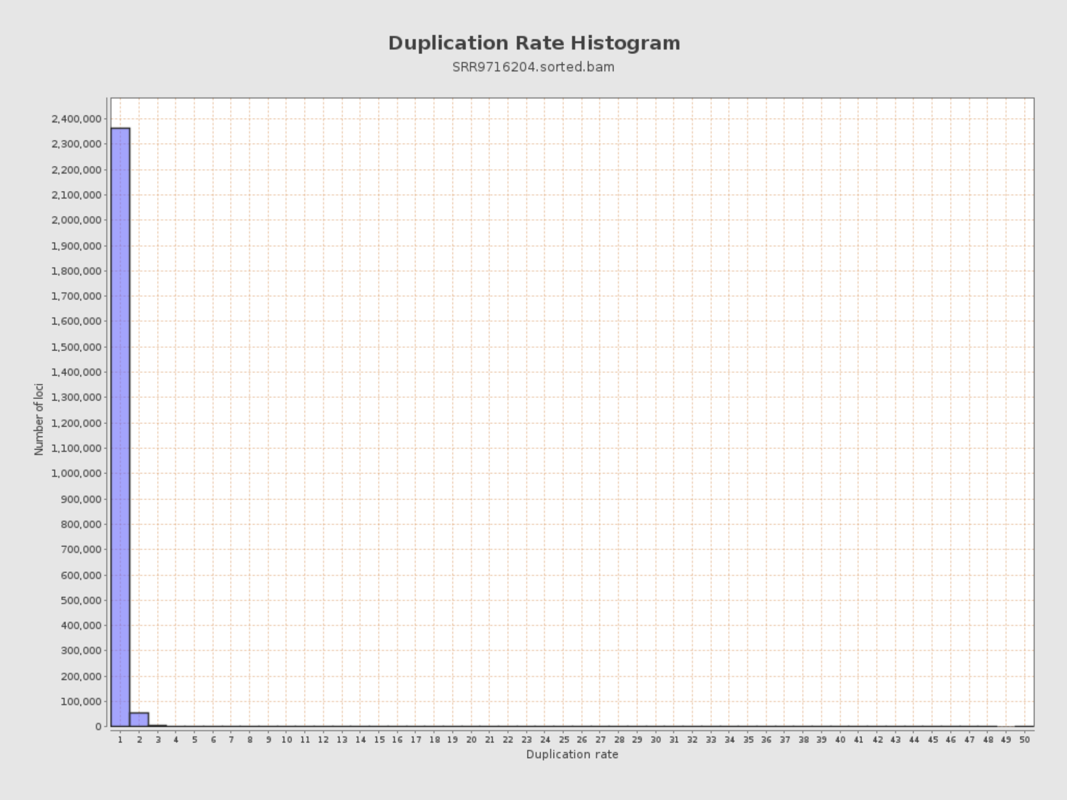
5. Results : Coverage Histogram (0-50X)



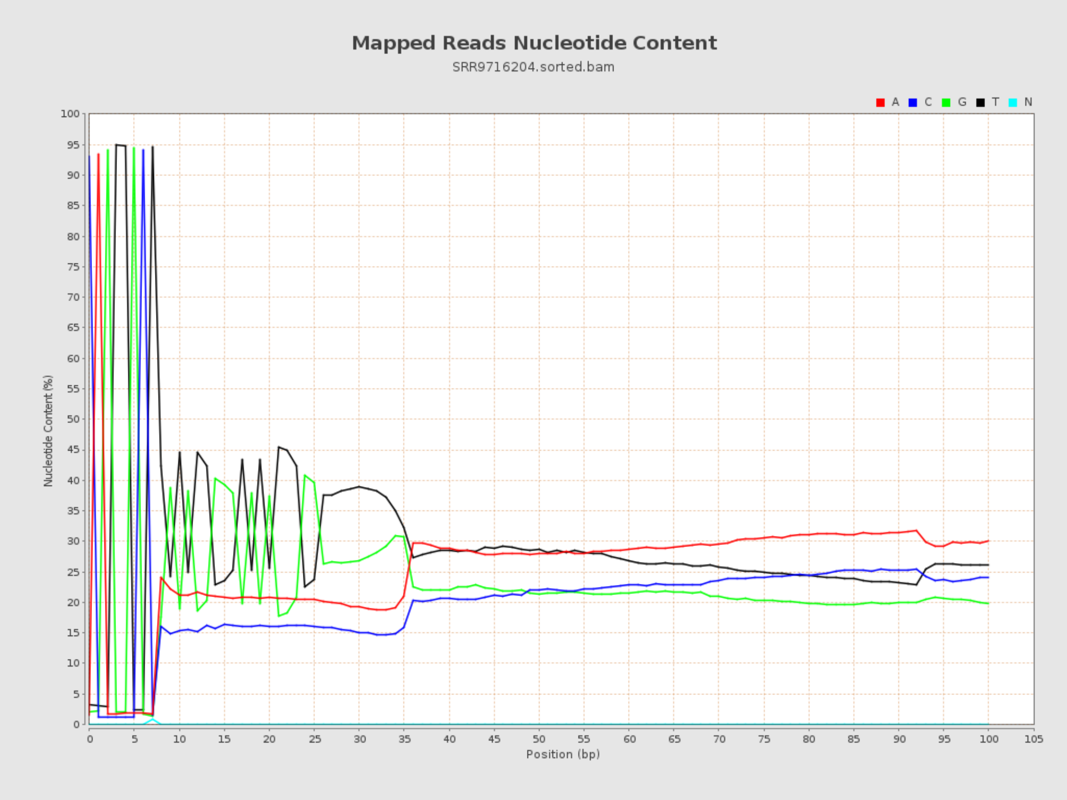
6. Results : Genome Fraction Coverage



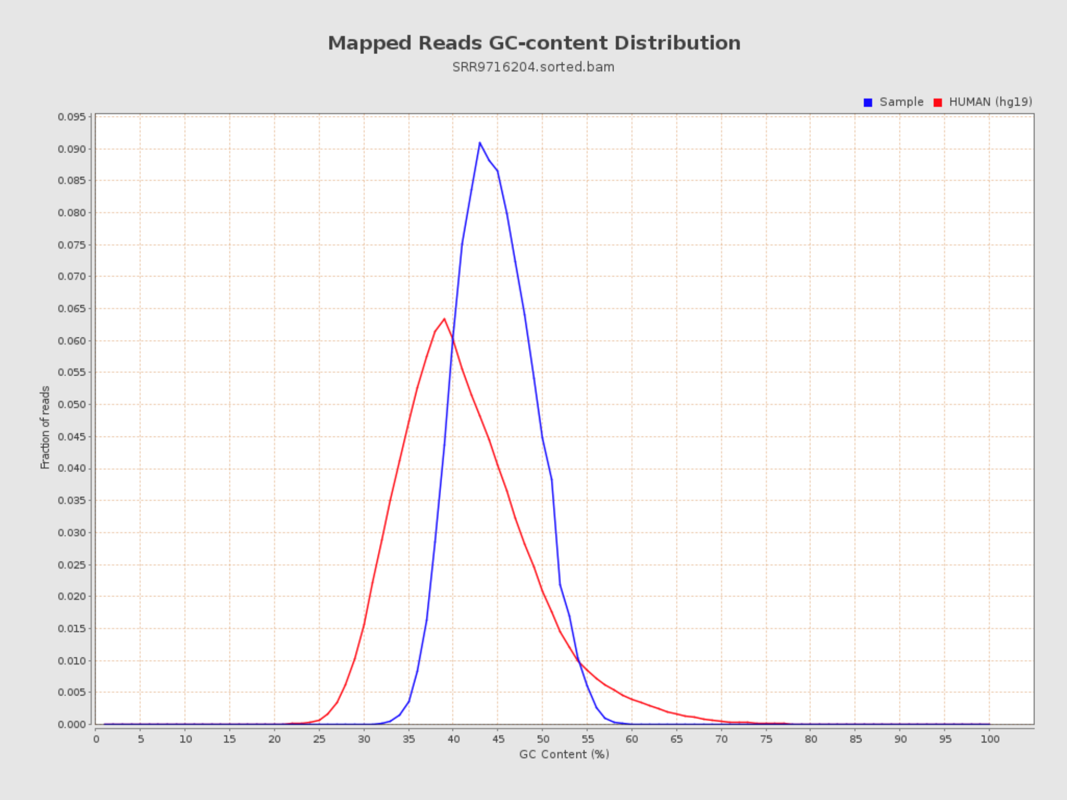
7. Results : Duplication Rate Histogram



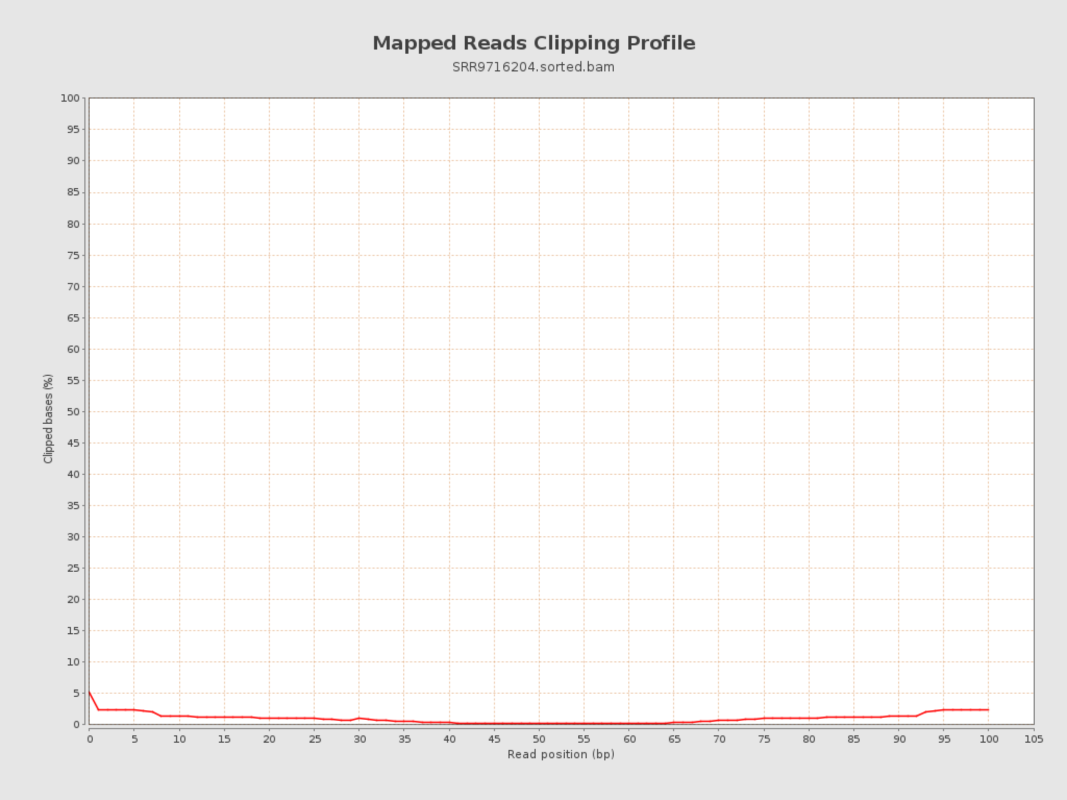
8. Results : Mapped Reads Nucleotide Content



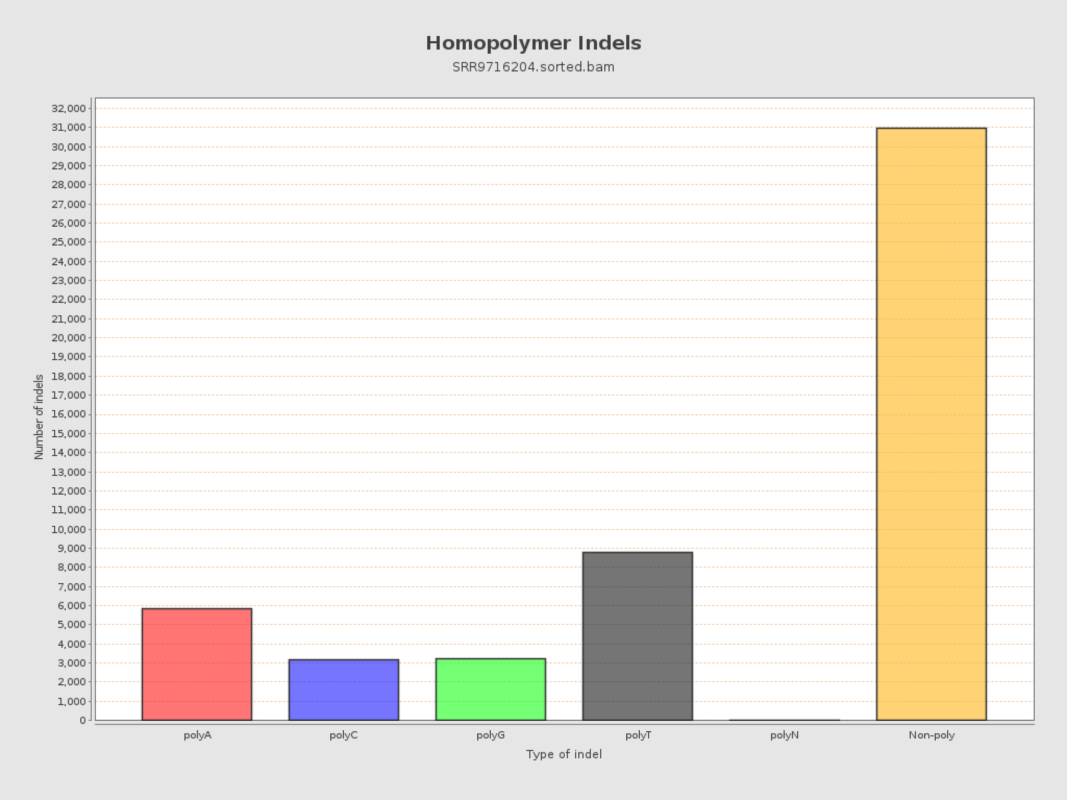
9. Results : Mapped Reads GC-content Distribution



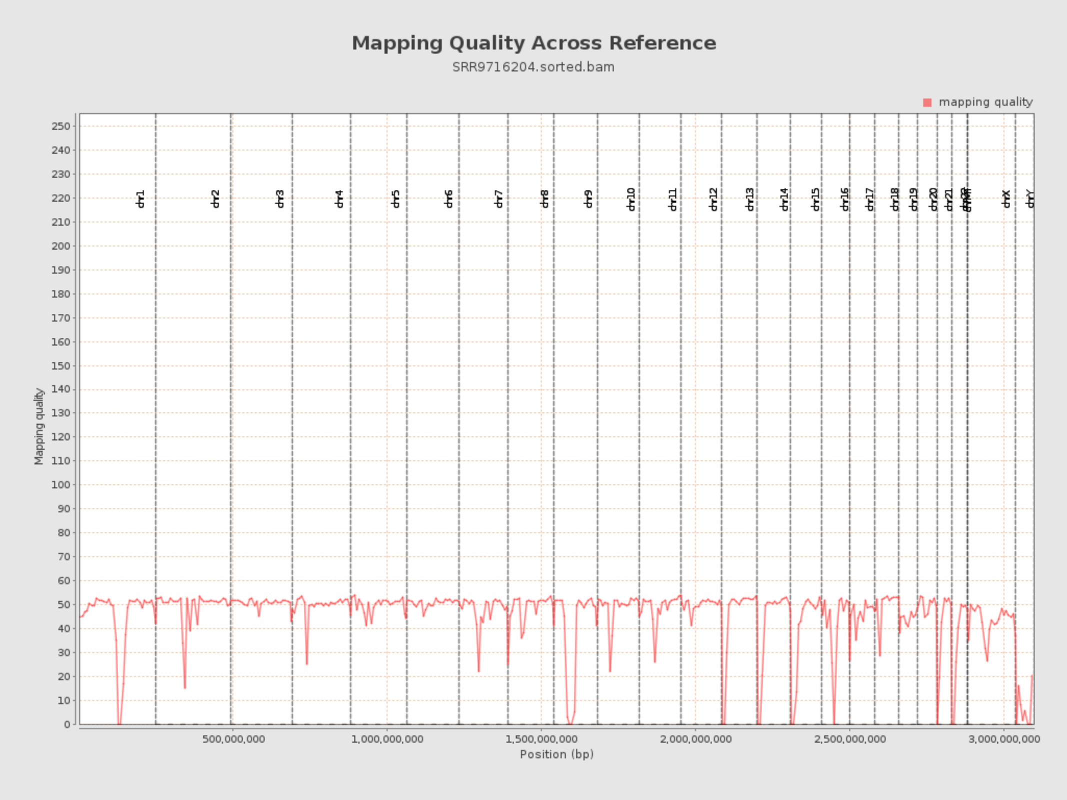
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram