Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 00:07:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716205.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_SRR9716205 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716205.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 00:07:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716205.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,472,017
Mapped reads	2,279,433 / 92.21%
Unmapped reads	192,584 / 7.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	56,471 / 2.28%
Read min/max/mean length	30 / 101 / 101.83
Duplicated reads (estimated)	86,705 / 3.51%
Duplication rate	2.71%
Clipped reads	2,333,852 / 94.41%

2.2. ACGT Content

Number/percentage of A's	43,966,749 / 26.1%
Number/percentage of C's	34,483,275 / 20.47%
Number/percentage of T's	49,108,375 / 29.16%
Number/percentage of G's	40,848,948 / 24.25%
Number/percentage of N's	20,084 / 0.01%
GC Percentage	44.73%

2.3. Coverage

Mean	0.0544

Standard Deviation	0.4091

2.4. Mapping Quality

Mean Mapping Quality	46.01

2.5. Mismatches and indels

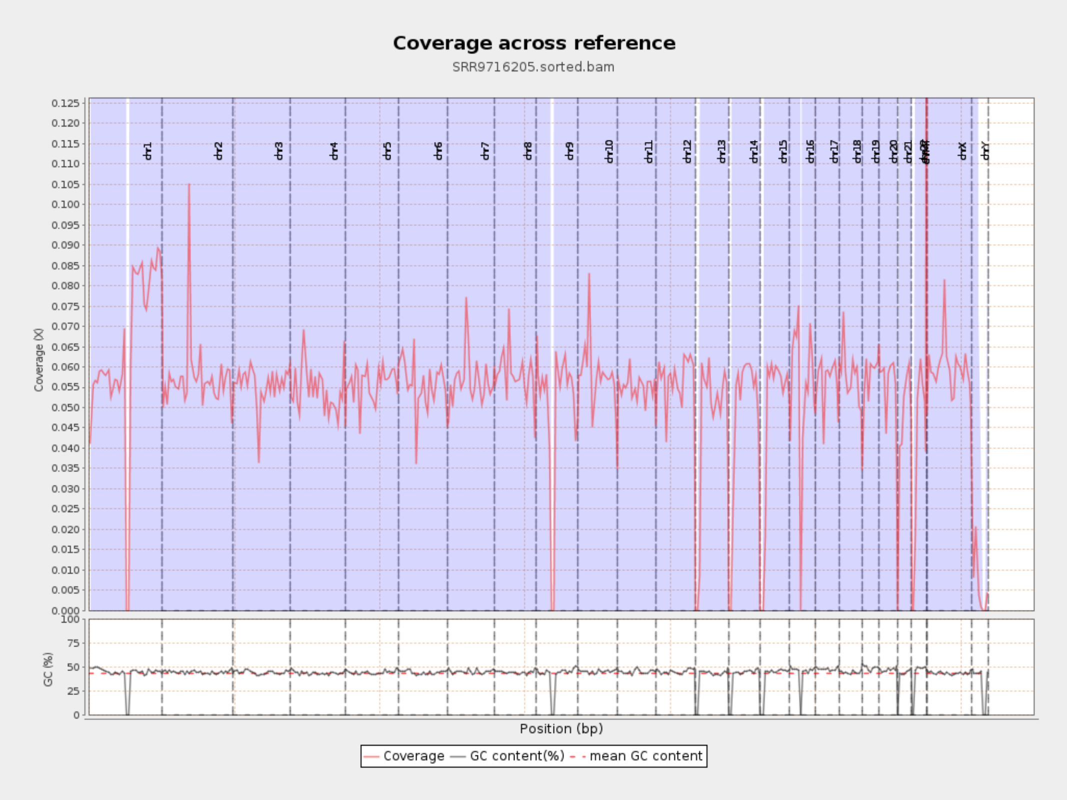
General error rate	0.75%
Mismatches	1,230,071
Insertions	13,516
Mapped reads with at least one insertion	0.59%
Deletions	33,898
Mapped reads with at least one deletion	1.47%
Homopolymer indels	40.15%

2.6. Chromosome stats

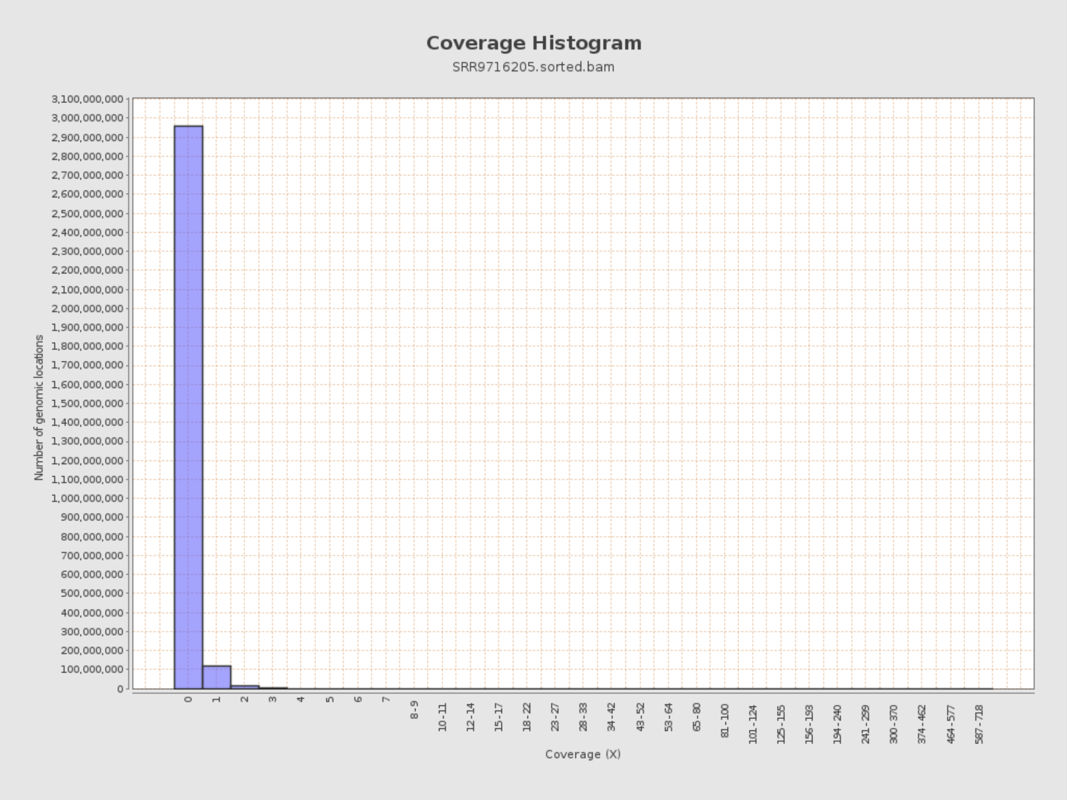
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15976709	0.0641	0.4776
chr2	243199373	13992781	0.0575	0.597
chr3	198022430	10988294	0.0555	0.276
chr4	191154276	10403700	0.0544	0.2946
chr5	180915260	10138287	0.056	0.2804
chr6	171115067	9570976	0.0559	0.3201
chr7	159138663	9053970	0.0569	0.4956

chr8	146364022	8492425	0.058	0.5183
chr9	141213431	6990385	0.0495	0.4489
chr10	135534747	7925489	0.0585	0.4324
chr11	135006516	7386531	0.0547	0.4567
chr12	133851895	7626316	0.057	0.2831
chr13	115169878	5227687	0.0454	0.2468
chr14	107349540	5082169	0.0473	0.3044
chr15	102531392	4787077	0.0467	0.2559
chr16	90354753	4962644	0.0549	0.3152
chr17	81195210	4569251	0.0563	0.3129
chr18	78077248	4559914	0.0584	0.8281
chr19	59128983	3400996	0.0575	0.4297
chr20	63025520	3528894	0.056	0.29
chr21	48129895	2195293	0.0456	0.2768
chr22	51304566	1933793	0.0377	0.2274
chrMT	16571	5884	0.3551	0.7171
chrX	155270560	9290241	0.0598	0.3721
chrY	59373566	395619	0.0067	0.1674

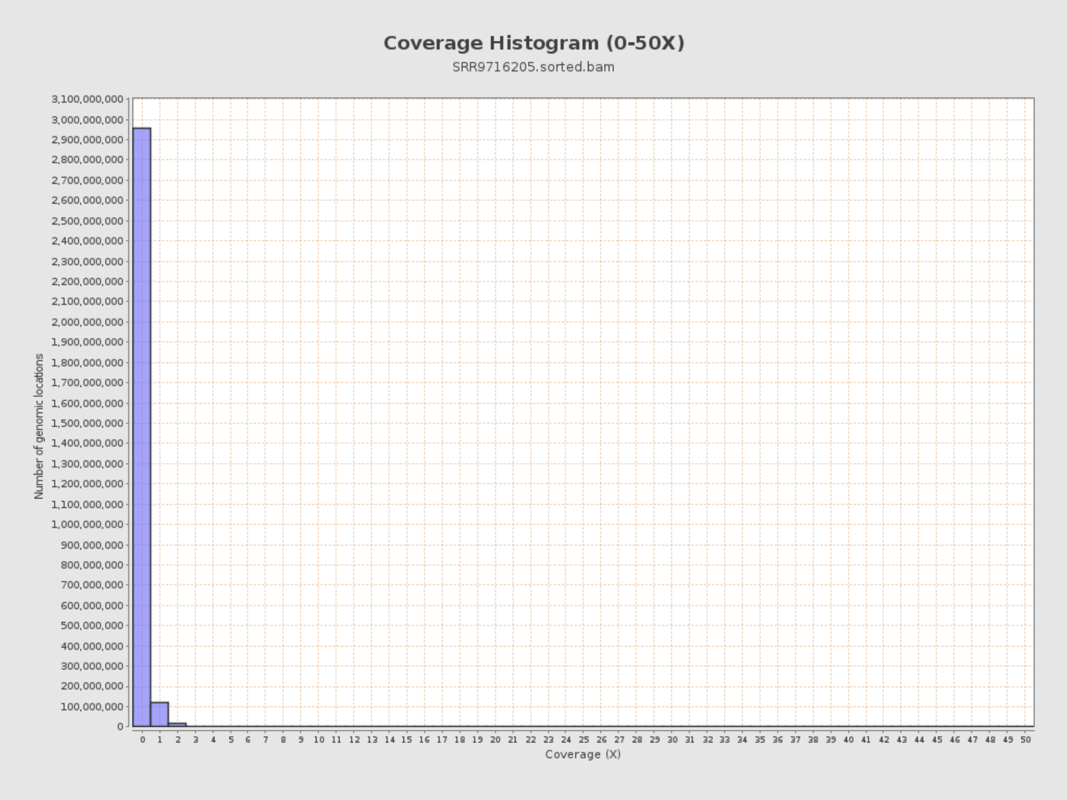
3. Results : Coverage across reference



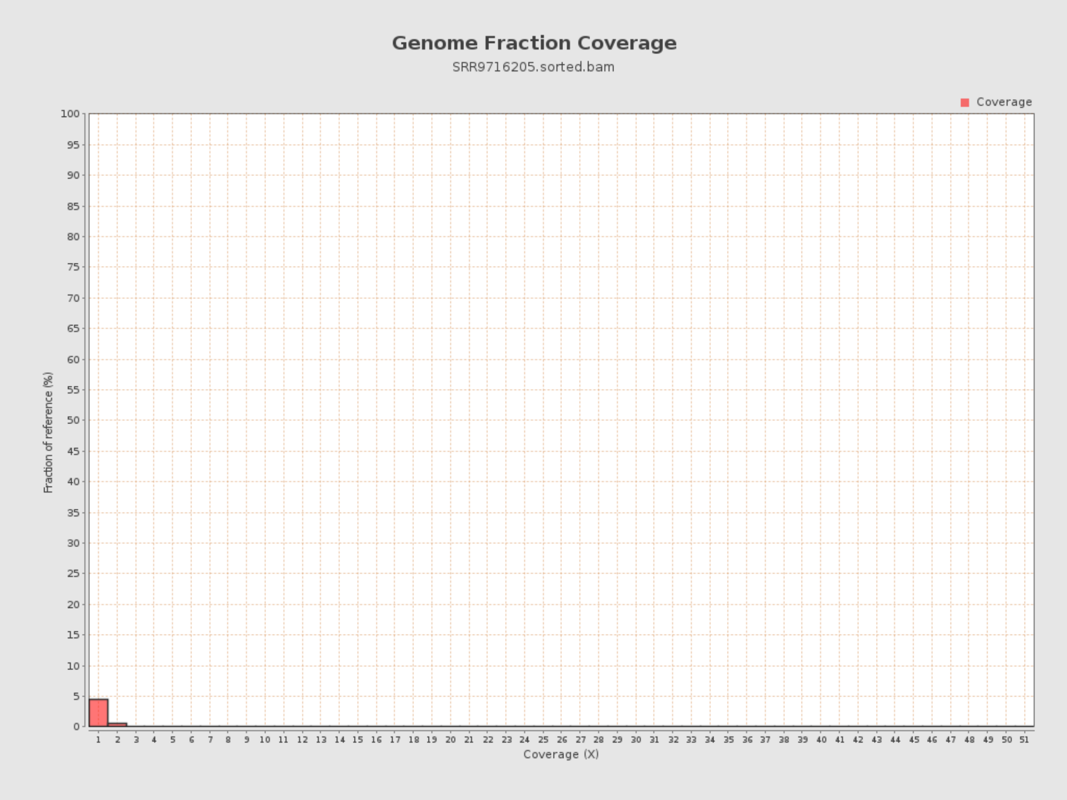
4. Results : Coverage Histogram



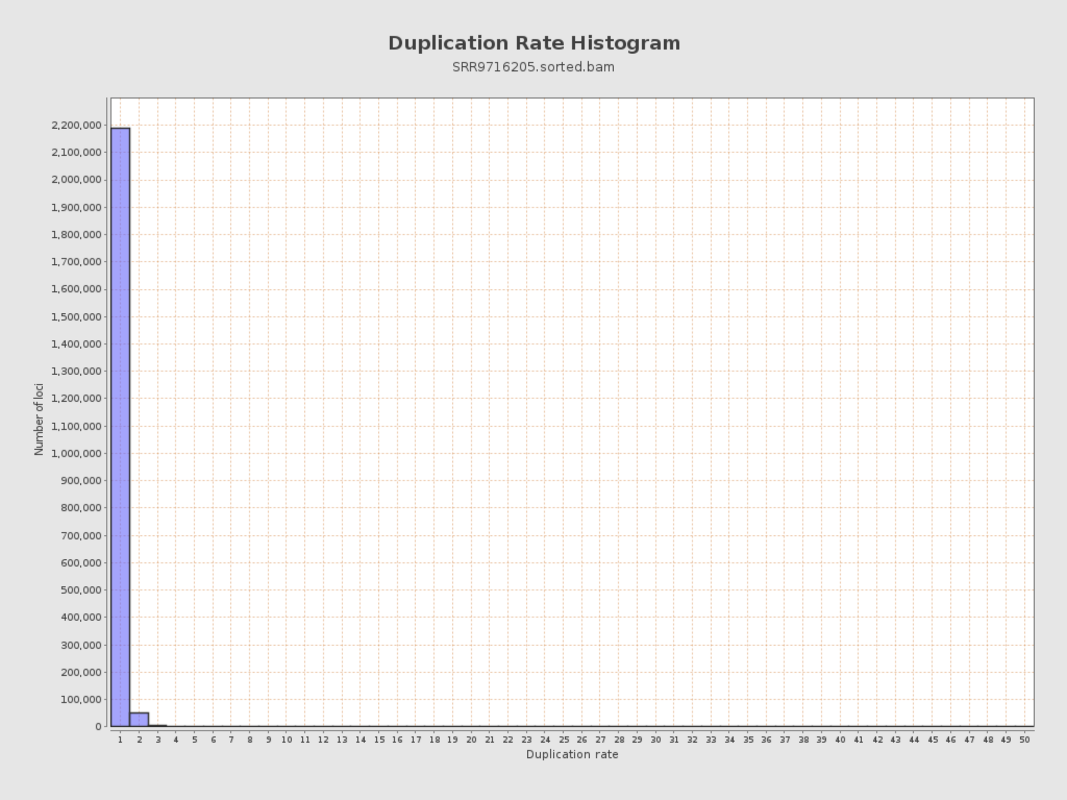
5. Results : Coverage Histogram (0-50X)



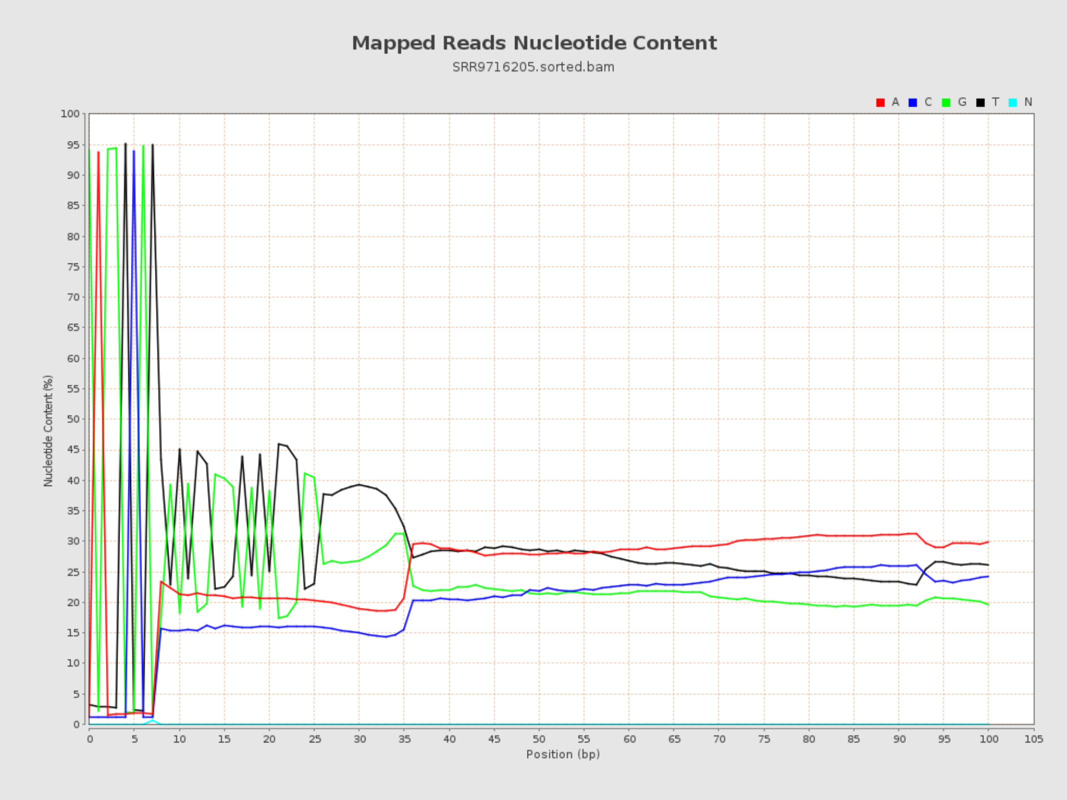
6. Results : Genome Fraction Coverage



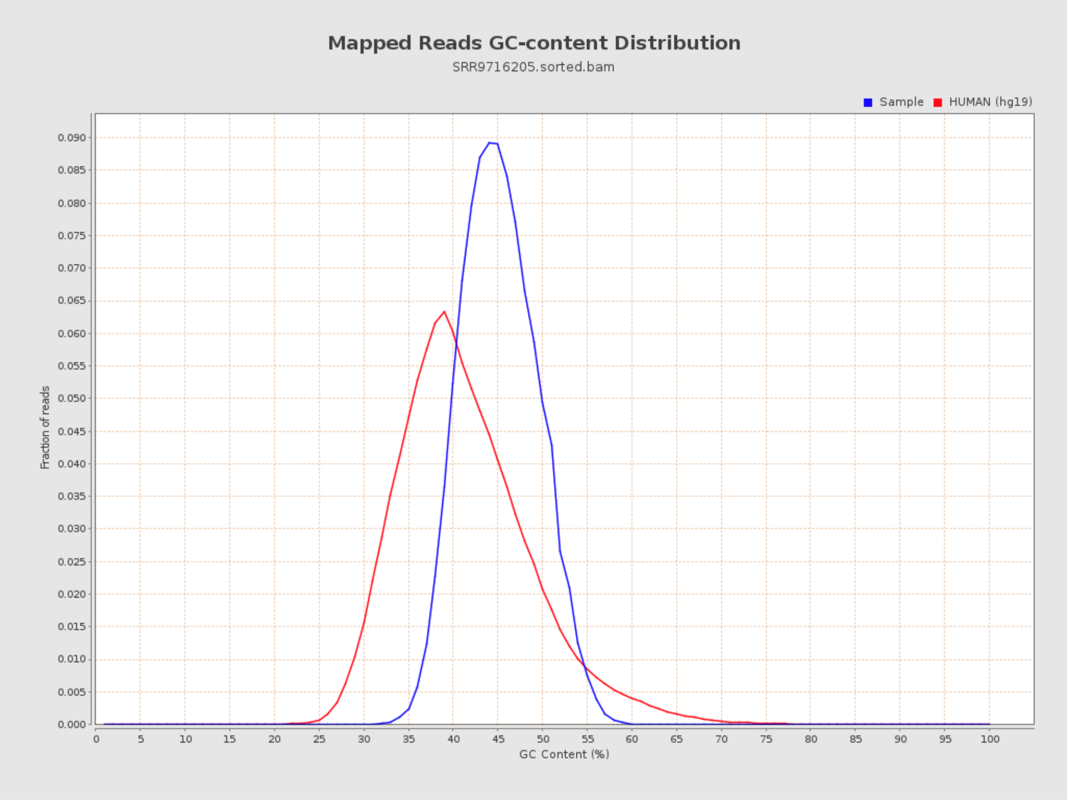
7. Results : Duplication Rate Histogram



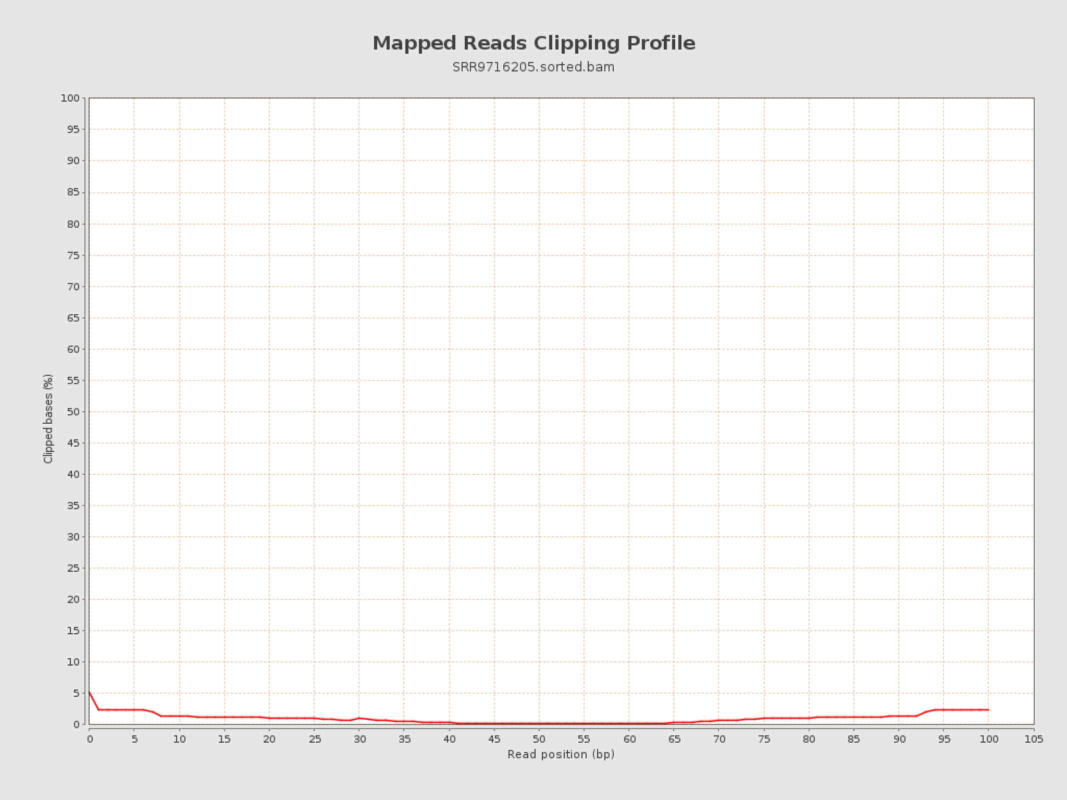
8. Results : Mapped Reads Nucleotide Content



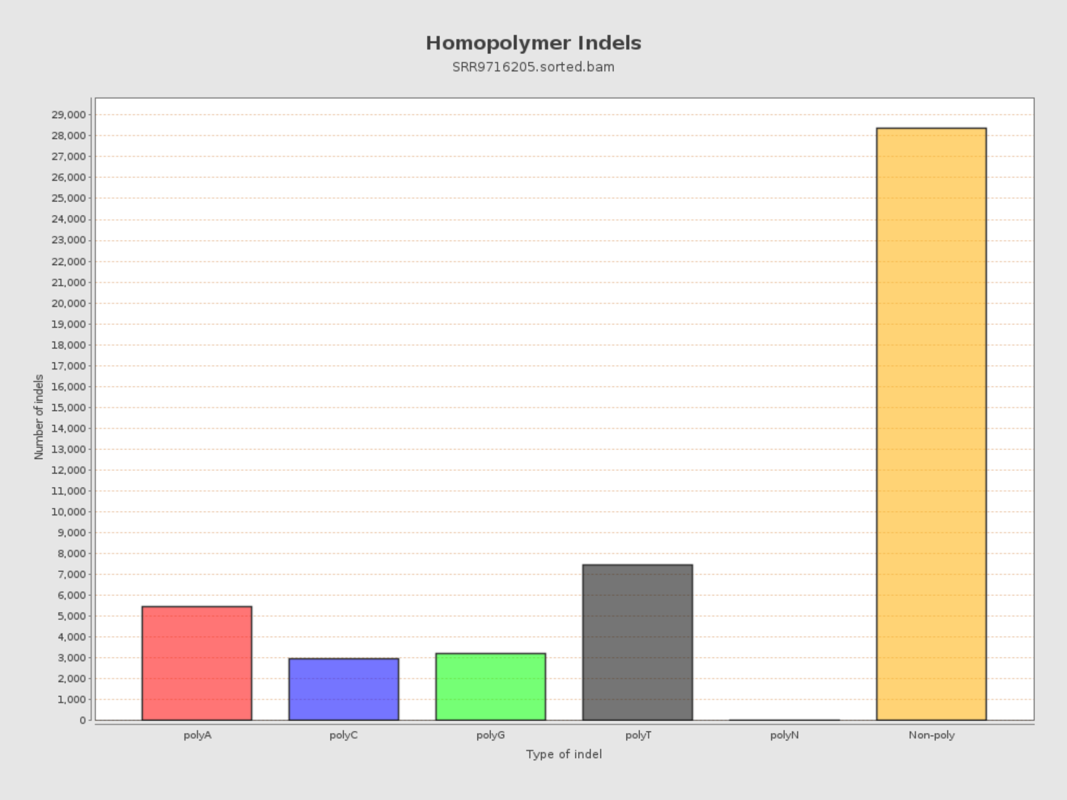
9. Results : Mapped Reads GC-content Distribution



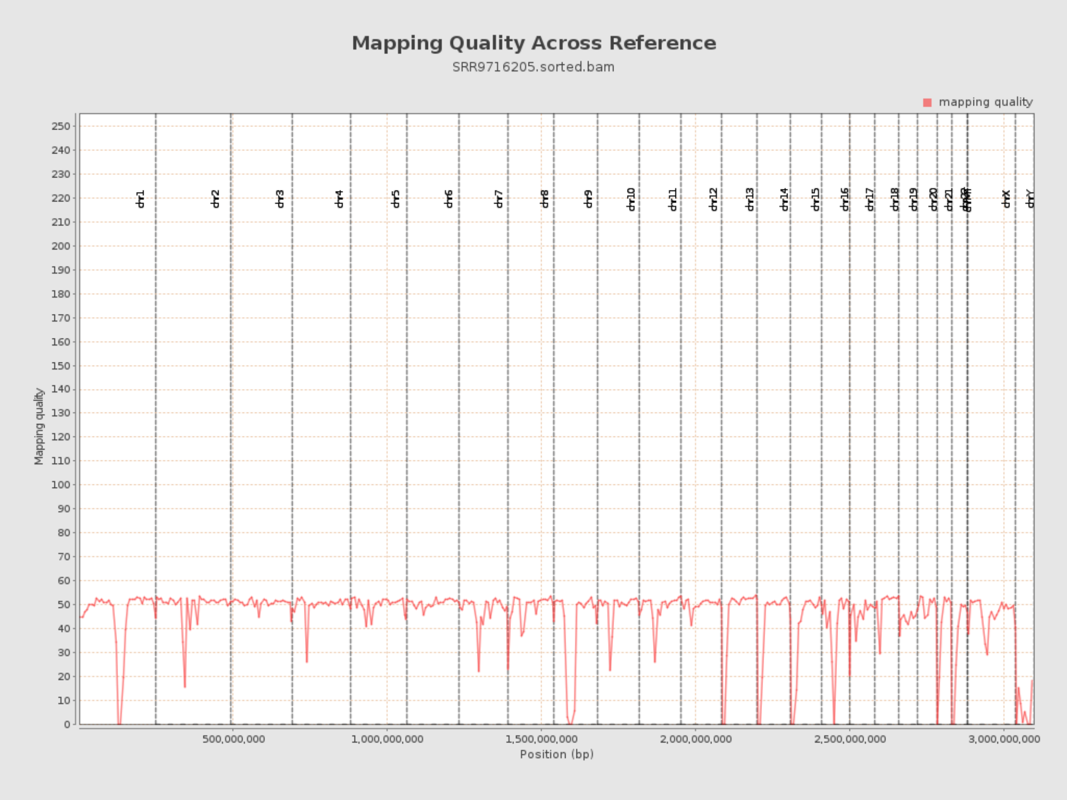
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram