Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 00:15:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716207.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_SRR9716207 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716207.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 00:15:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716207.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,726,156
Mapped reads	4,295,674 / 90.89%
Unmapped reads	430,482 / 9.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	101,084 / 2.14%
Read min/max/mean length	30 / 101 / 101.78
Duplicated reads (estimated)	240,333 / 5.09%
Duplication rate	3.91%
Clipped reads	4,389,977 / 92.89%

2.2. ACGT Content

Number/percentage of A's	85,061,358 / 26.43%
Number/percentage of C's	65,020,736 / 20.2%
Number/percentage of T's	97,854,252 / 30.41%
Number/percentage of G's	73,831,712 / 22.94%
Number/percentage of N's	39,391 / 0.01%
GC Percentage	43.15%

2.3. Coverage

Mean	0.104

Standard Deviation	0.7755

2.4. Mapping Quality

Mean Mapping Quality	46.13

2.5. Mismatches and indels

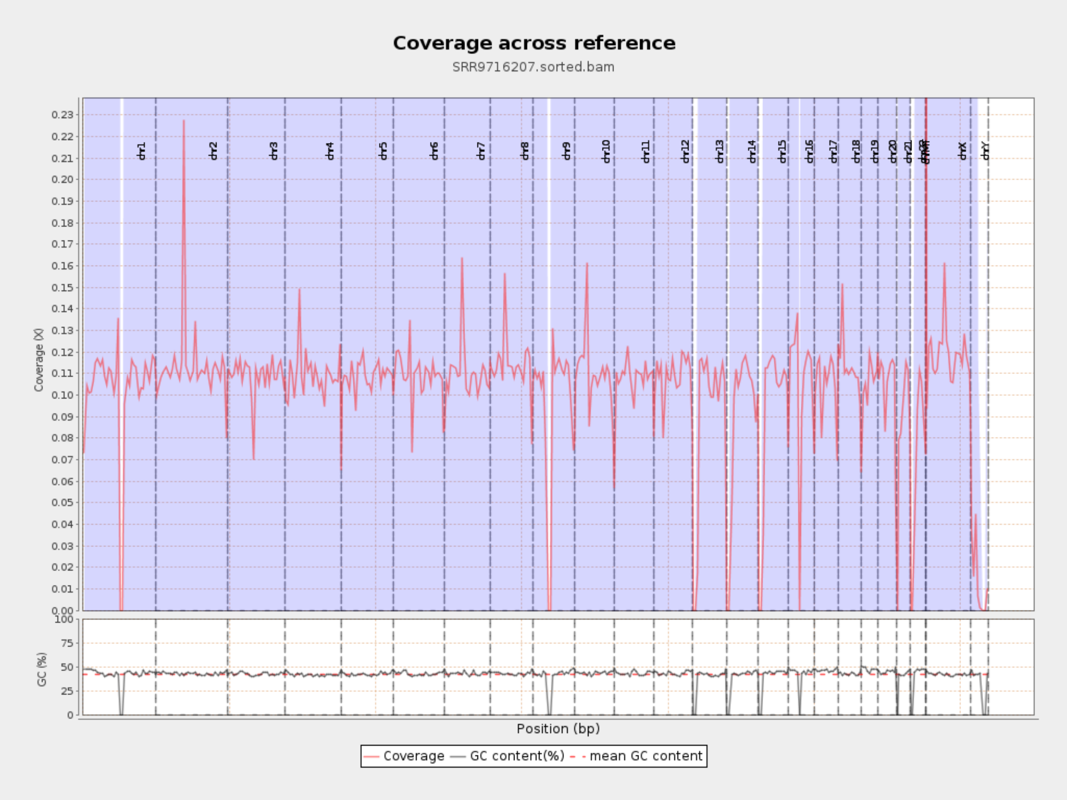
General error rate	0.77%
Mismatches	2,416,207
Insertions	27,495
Mapped reads with at least one insertion	0.63%
Deletions	68,045
Mapped reads with at least one deletion	1.56%
Homopolymer indels	39.72%

2.6. Chromosome stats

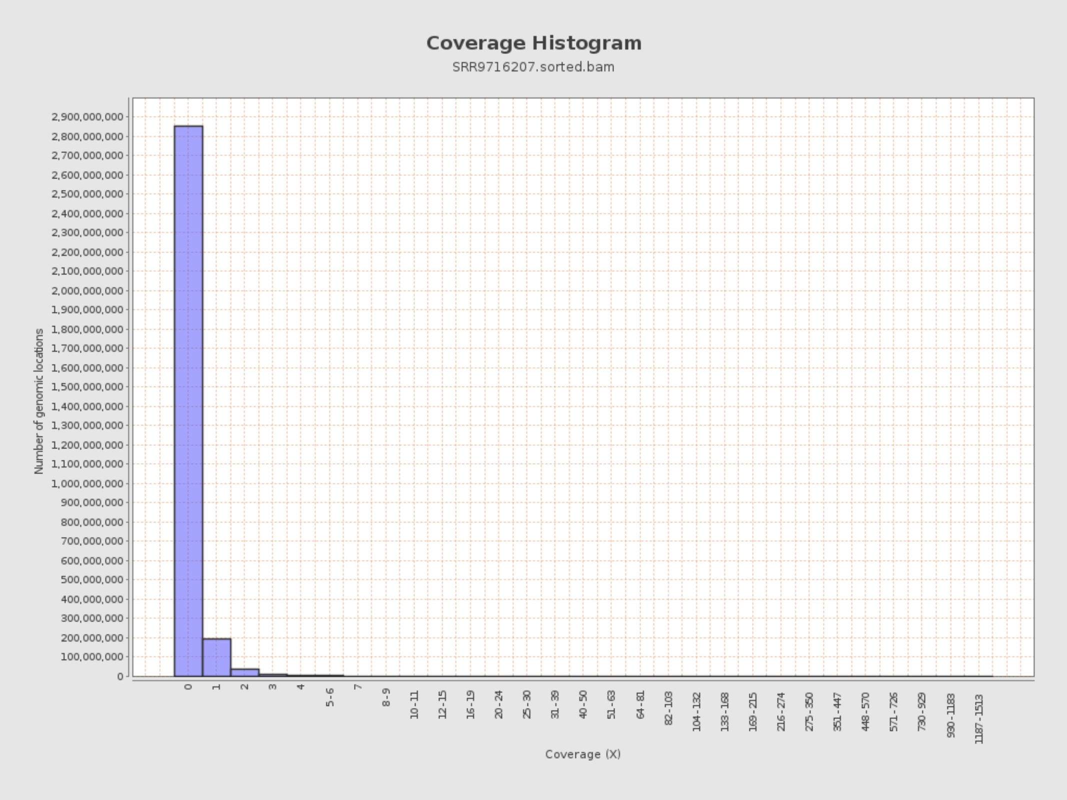
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25369513	0.1018	0.9025
chr2	243199373	27808698	0.1143	1.2398
chr3	198022430	21555775	0.1089	0.419
chr4	191154276	21004552	0.1099	0.4923
chr5	180915260	19688850	0.1088	0.4298
chr6	171115067	18742535	0.1095	0.5366
chr7	159138663	17574055	0.1104	1.0286

chr8	146364022	16684182	0.114	1.0757
chr9	141213431	13489402	0.0955	0.8595
chr10	135534747	15018620	0.1108	0.7295
chr11	135006516	14545343	0.1077	0.8738
chr12	133851895	14624479	0.1093	0.4388
chr13	115169878	10351884	0.0899	0.3792
chr14	107349540	9568670	0.0891	0.5531
chr15	102531392	9177237	0.0895	0.3866
chr16	90354753	9287304	0.1028	0.4959
chr17	81195210	8609441	0.106	0.4971
chr18	78077248	8958562	0.1147	1.722
chr19	59128983	6264173	0.1059	0.7753
chr20	63025520	6679581	0.106	0.4604
chr21	48129895	4186969	0.087	0.4435
chr22	51304566	3512677	0.0685	0.3318
chrMT	16571	16429	0.9914	1.5901
chrX	155270560	18405314	0.1185	0.6568
chrY	59373566	799720	0.0135	0.3643

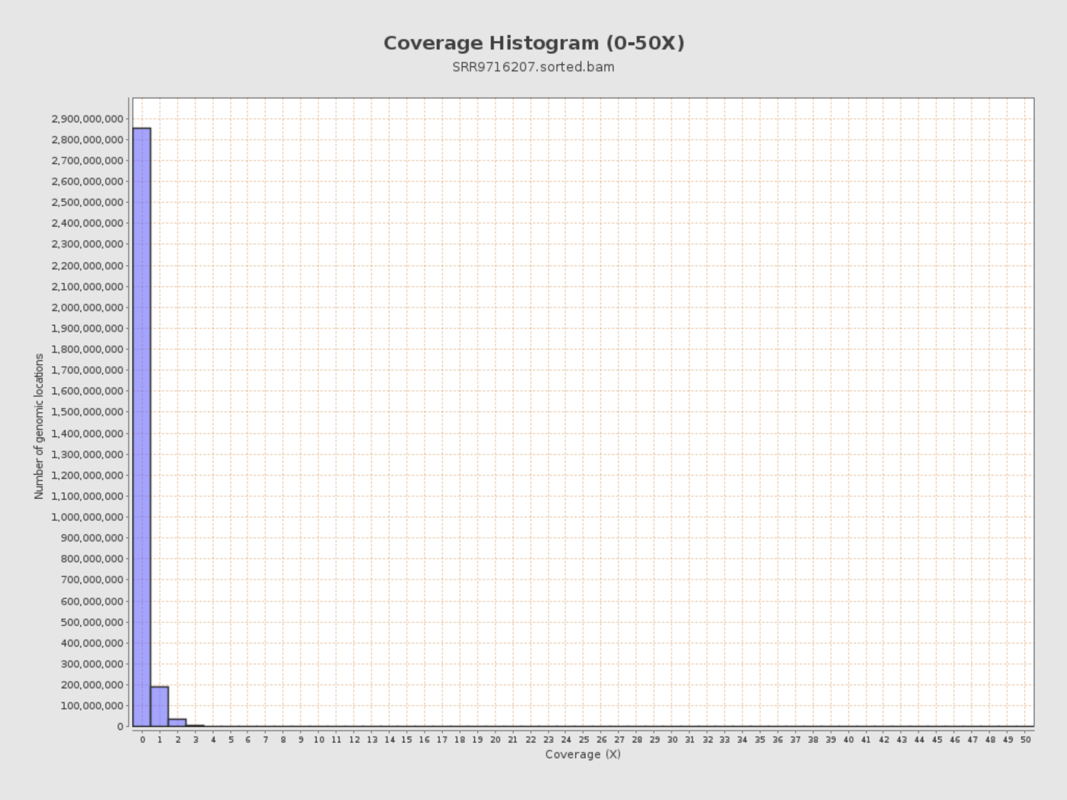
3. Results : Coverage across reference



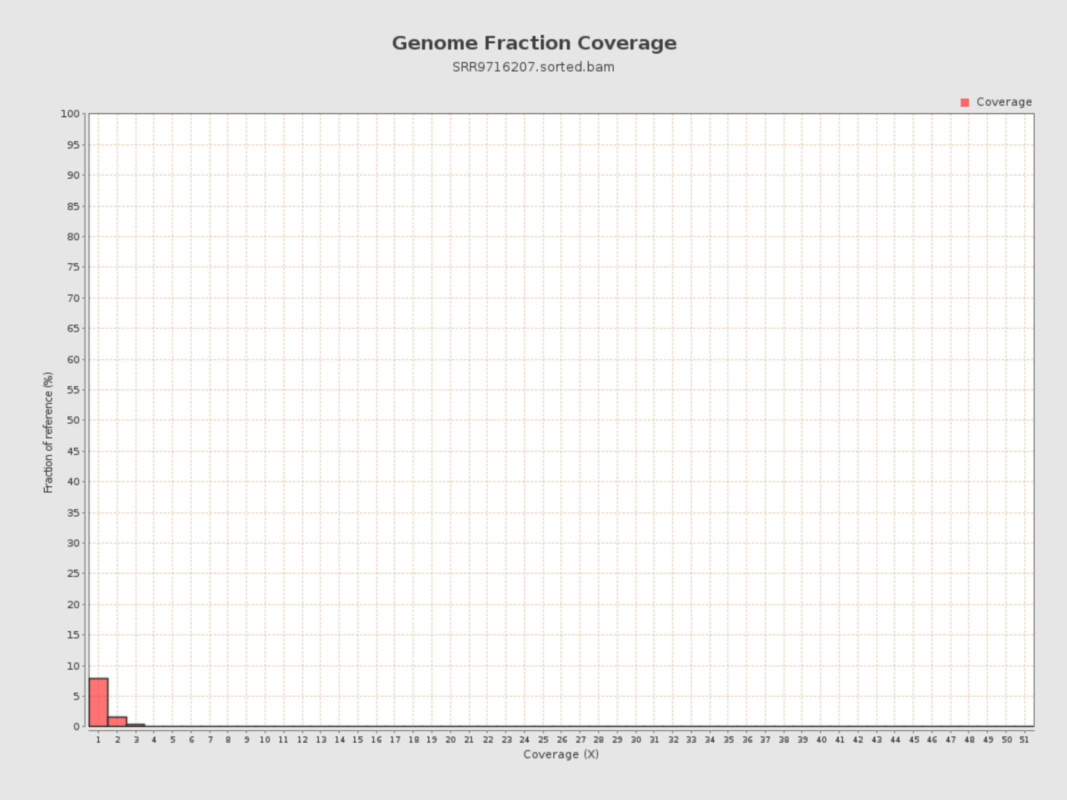
4. Results : Coverage Histogram



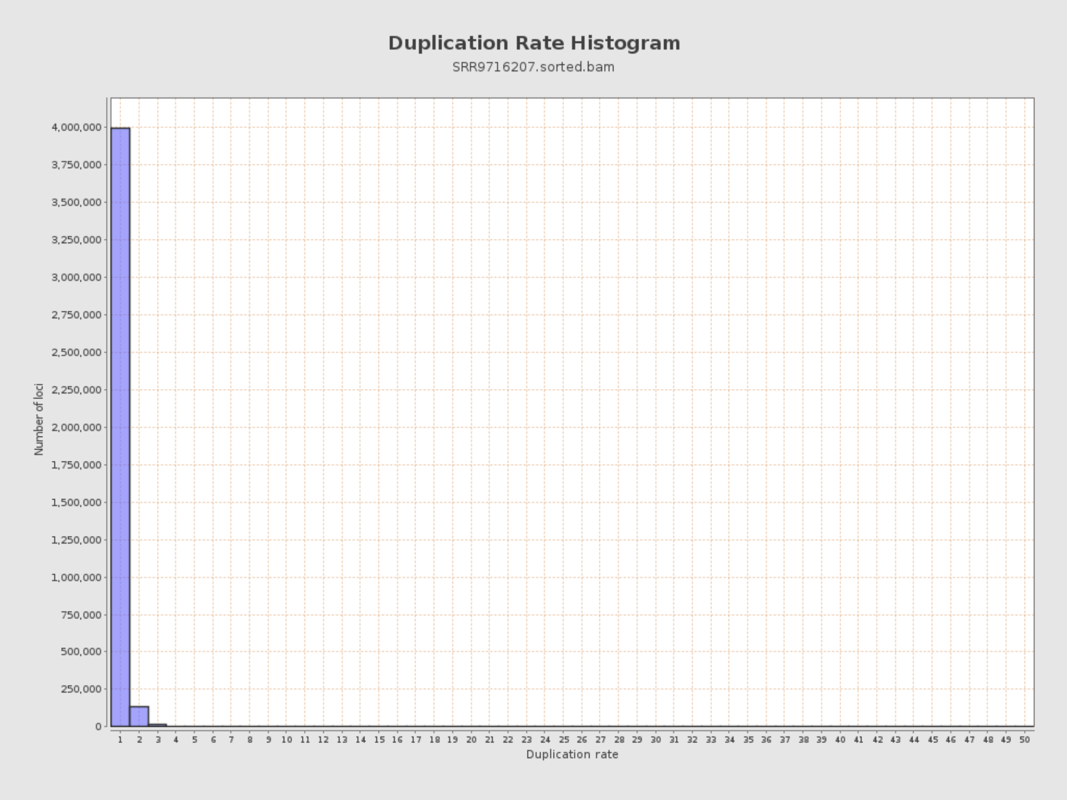
5. Results : Coverage Histogram (0-50X)



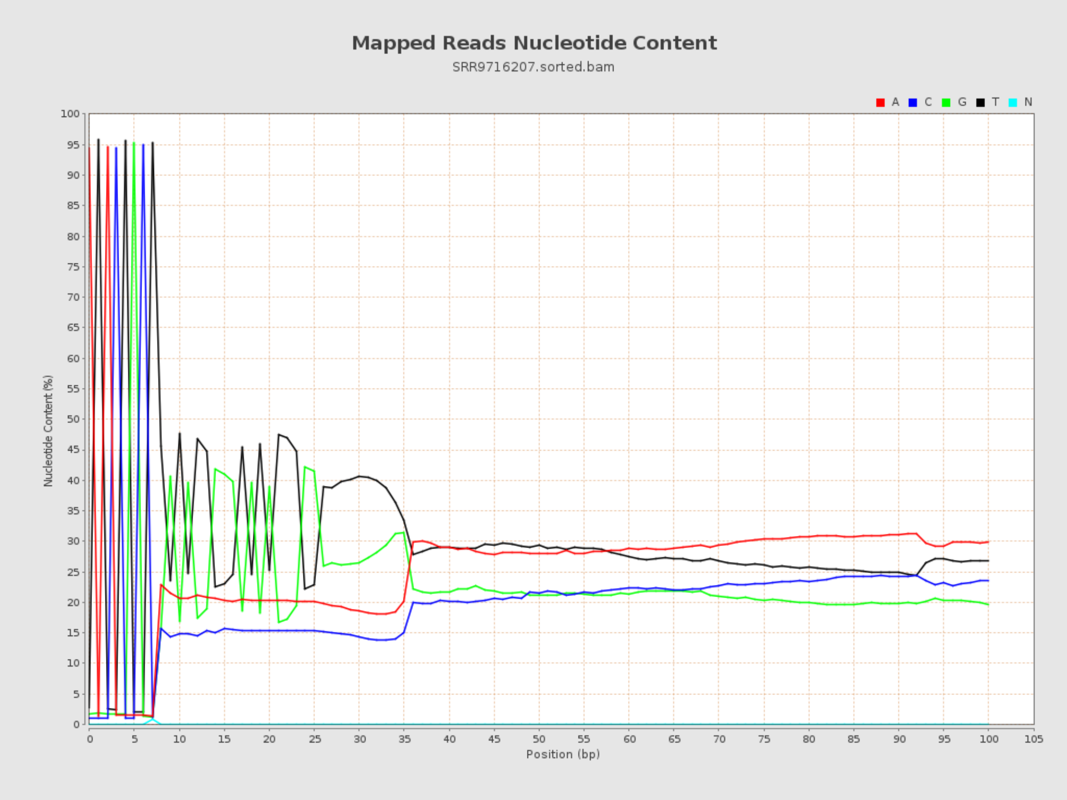
6. Results : Genome Fraction Coverage



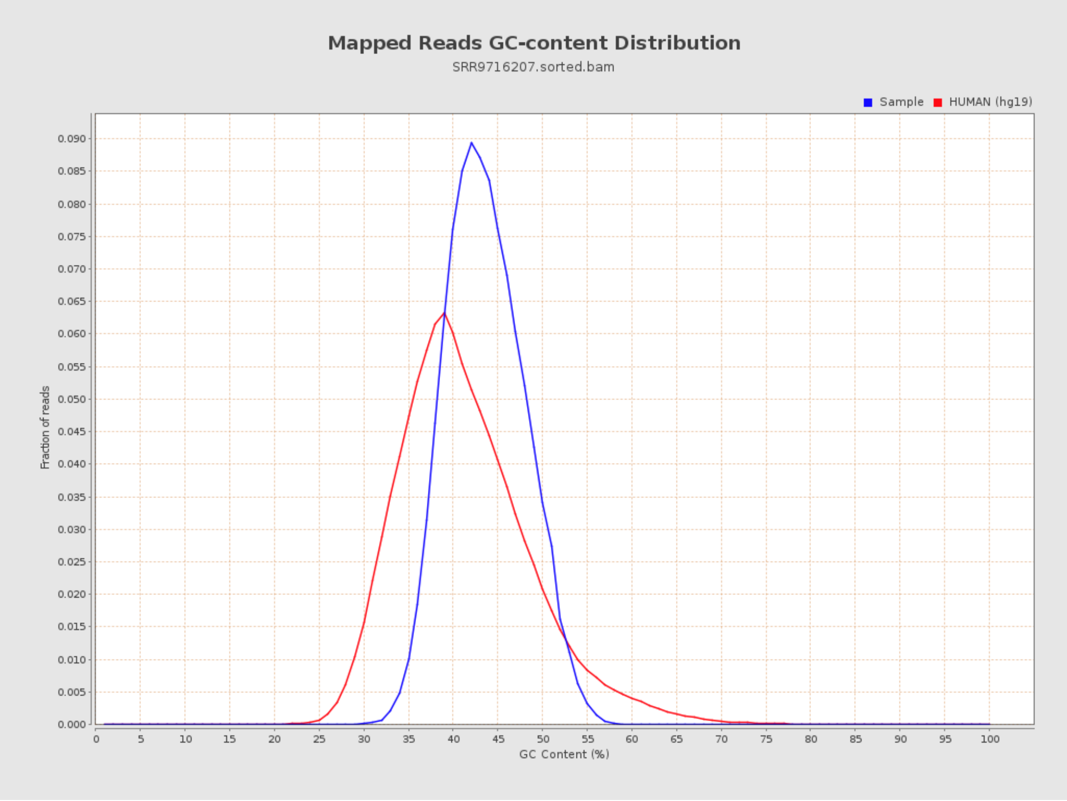
7. Results : Duplication Rate Histogram



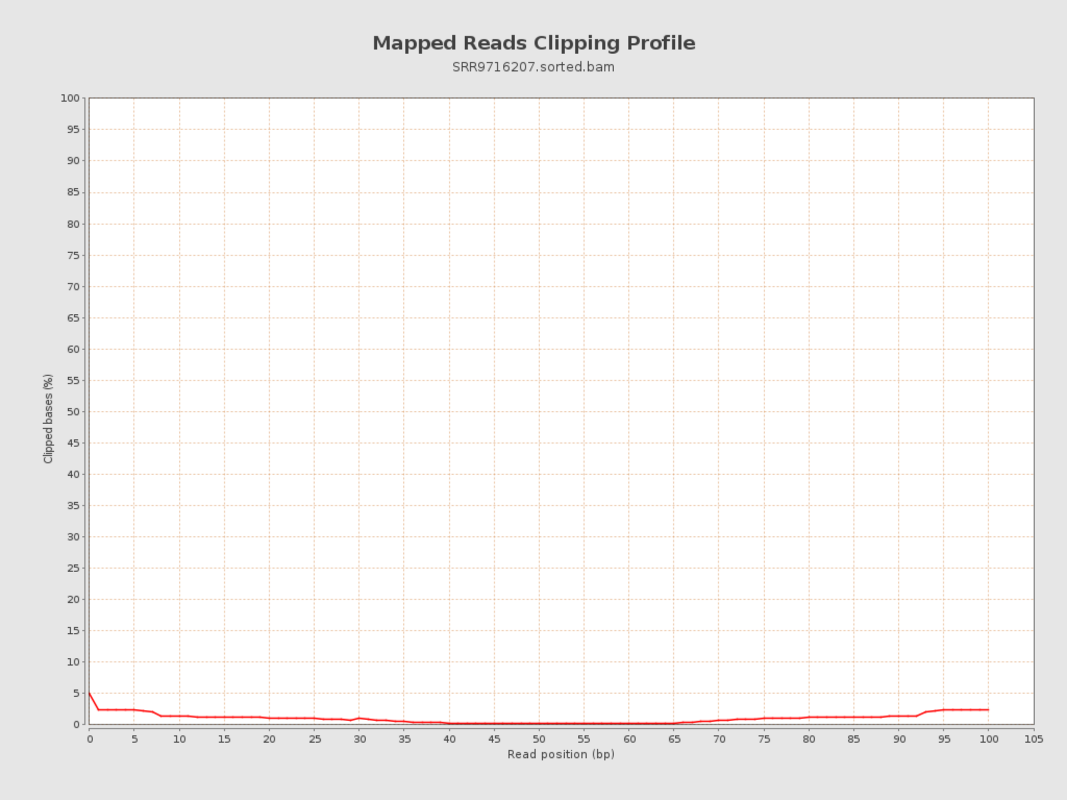
8. Results : Mapped Reads Nucleotide Content



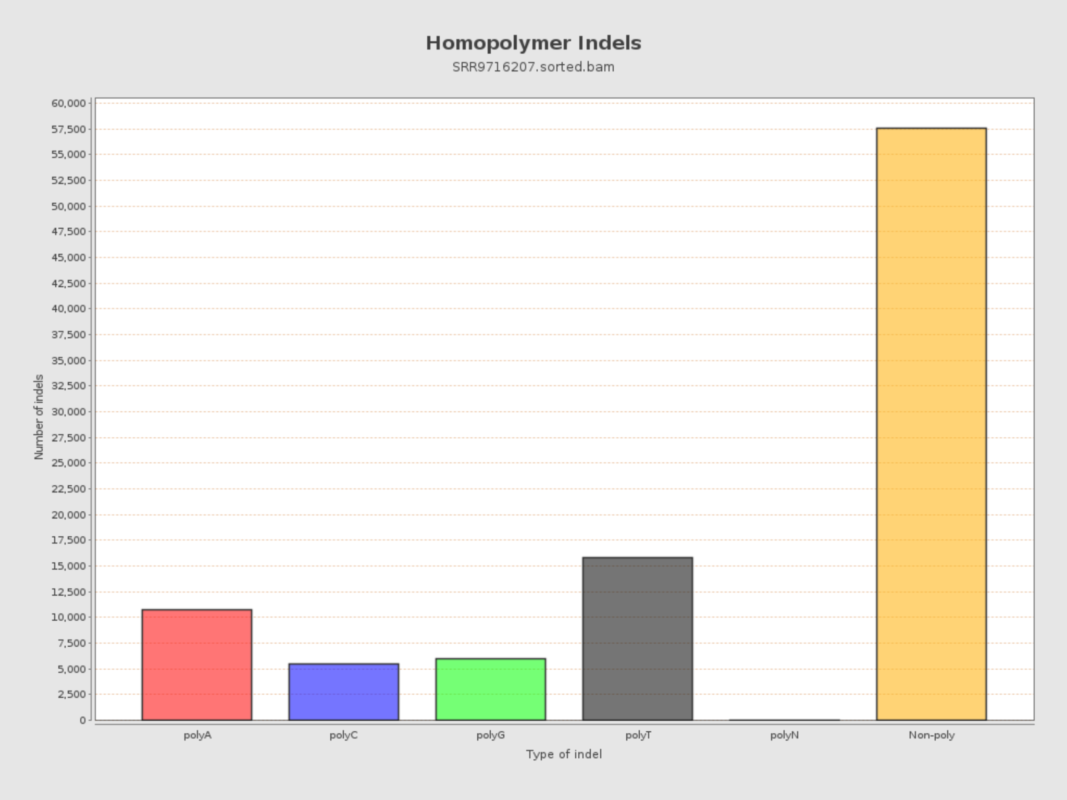
9. Results : Mapped Reads GC-content Distribution



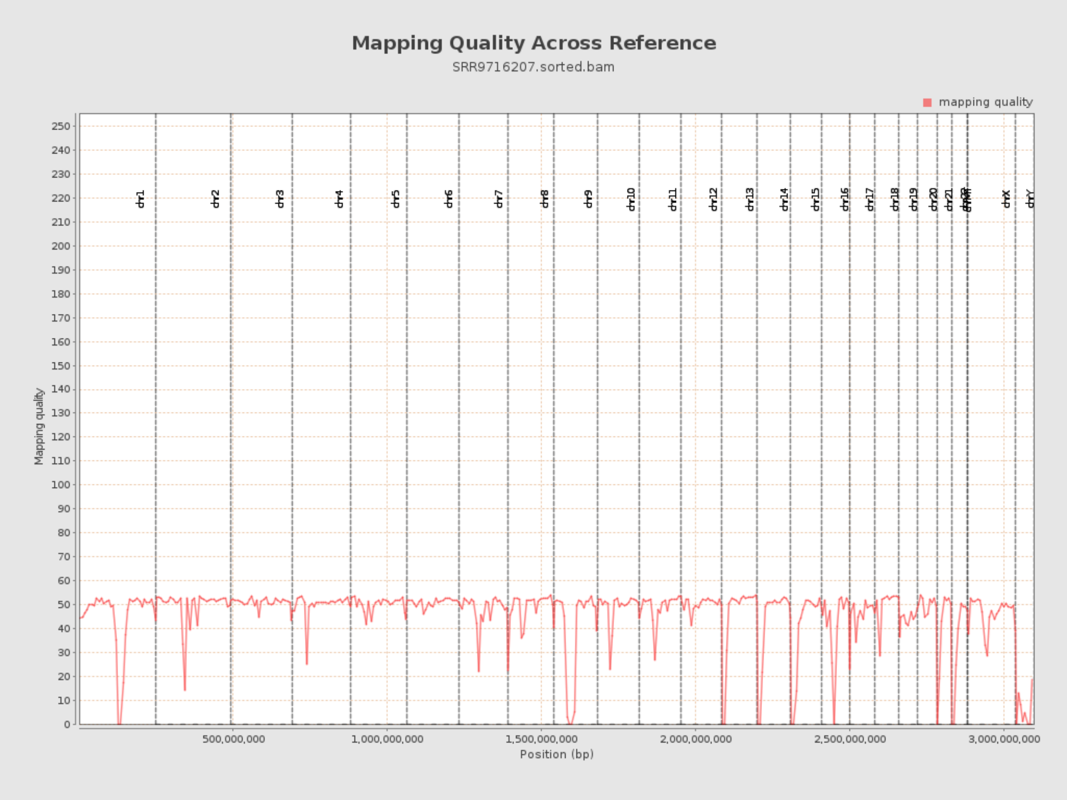
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram