Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:59:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716700.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_SRR9716700 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716700.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:59:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716700.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,474,686
Mapped reads	1,306,355 / 88.59%
Unmapped reads	168,331 / 11.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,707 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	29,343 / 1.99%
Duplication rate	1.57%
Clipped reads	1,307,948 / 88.69%

2.2. ACGT Content

Number/percentage of A's	18,594,659 / 25.04%
Number/percentage of C's	14,960,651 / 20.15%
Number/percentage of T's	22,966,152 / 30.93%
Number/percentage of G's	17,734,445 / 23.88%
Number/percentage of N's	599 / 0%
GC Percentage	44.03%

2.3. Coverage

Mean	0.024

Standard Deviation	0.2122

2.4. Mapping Quality

Mean Mapping Quality	42.29

2.5. Mismatches and indels

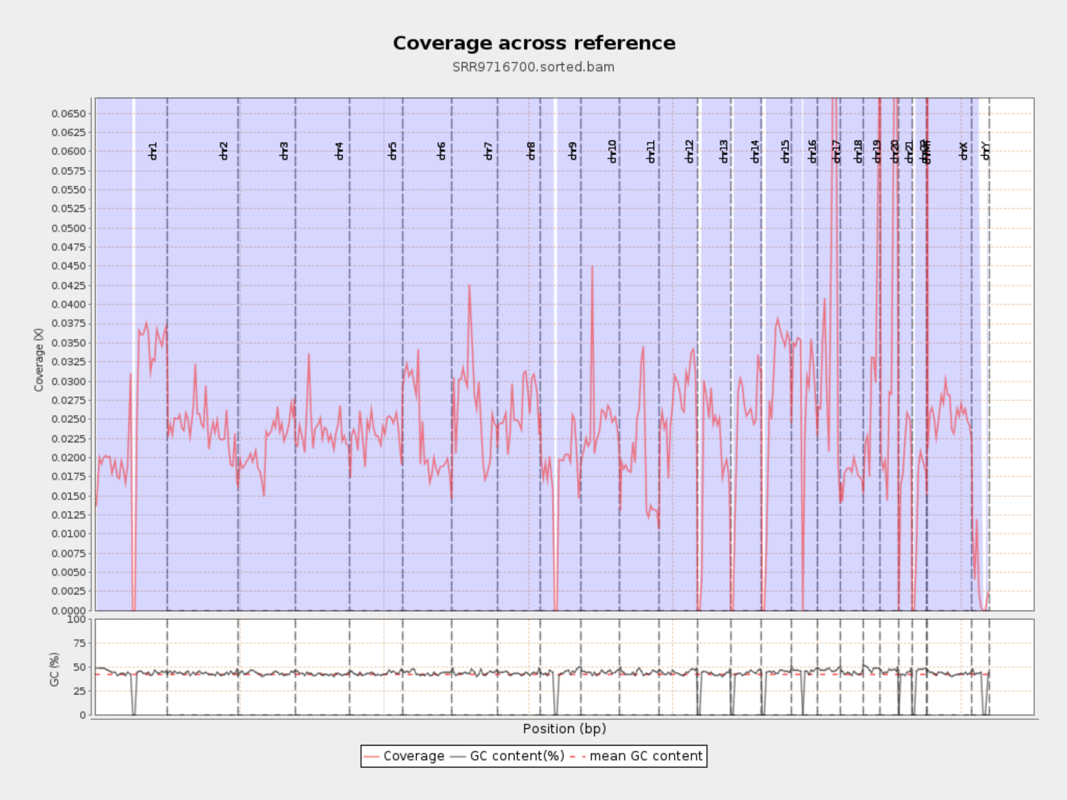
General error rate	0.53%
Mismatches	388,554
Insertions	4,846
Mapped reads with at least one insertion	0.37%
Deletions	14,242
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.29%

2.6. Chromosome stats

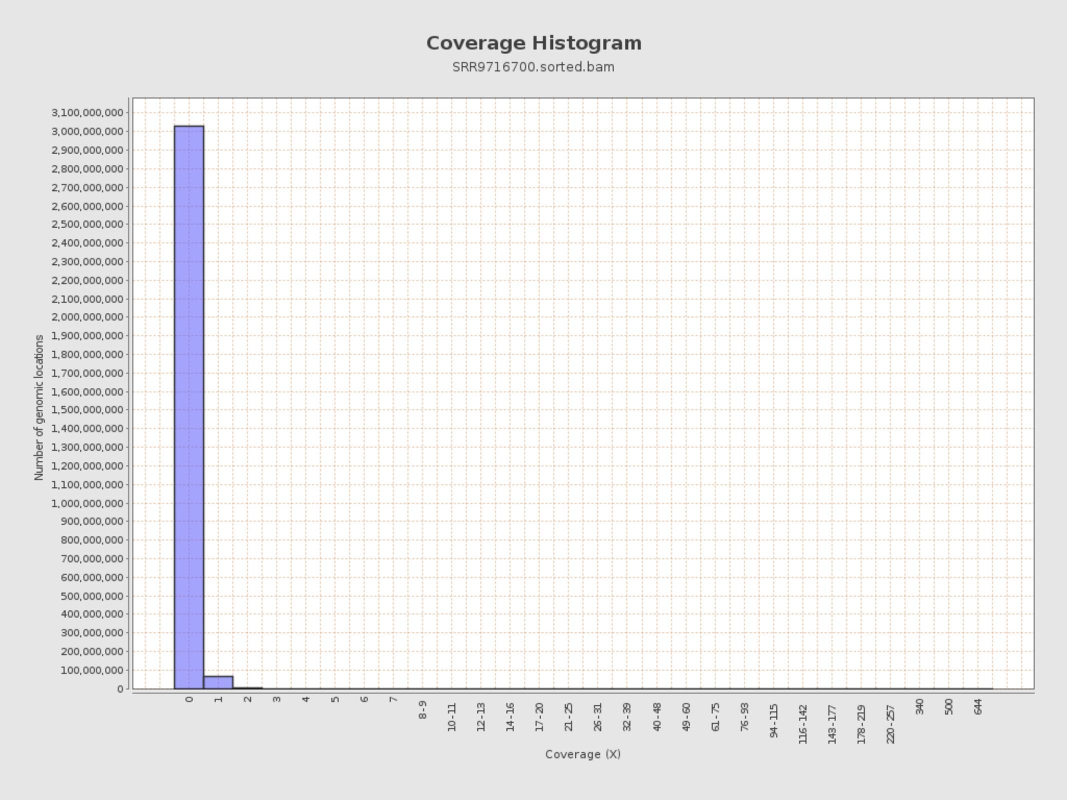
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6207181	0.0249	0.2718
chr2	243199373	5831453	0.024	0.3098
chr3	198022430	4285718	0.0216	0.16
chr4	191154276	4514418	0.0236	0.1728
chr5	180915260	4247563	0.0235	0.1631
chr6	171115067	3966225	0.0232	0.186
chr7	159138663	4288837	0.027	0.2932

chr8	146364022	3856915	0.0264	0.209
chr9	141213431	2476857	0.0175	0.1605
chr10	135534747	3357585	0.0248	0.2455
chr11	135006516	2612799	0.0194	0.1838
chr12	133851895	3678049	0.0275	0.1781
chr13	115169878	2259761	0.0196	0.1509
chr14	107349540	2506017	0.0233	0.1696
chr15	102531392	2766335	0.027	0.1804
chr16	90354753	2582900	0.0286	0.1915
chr17	81195210	3271629	0.0403	0.2261
chr18	78077248	1392463	0.0178	0.2331
chr19	59128983	1978553	0.0335	0.2596
chr20	63025520	2351902	0.0373	0.2149
chr21	48129895	934352	0.0194	0.1571
chr22	51304566	688934	0.0134	0.1248
chrMT	16571	9229	0.5569	0.9825
chrX	155270560	3994657	0.0257	0.1809
chrY	59373566	218737	0.0037	0.1019

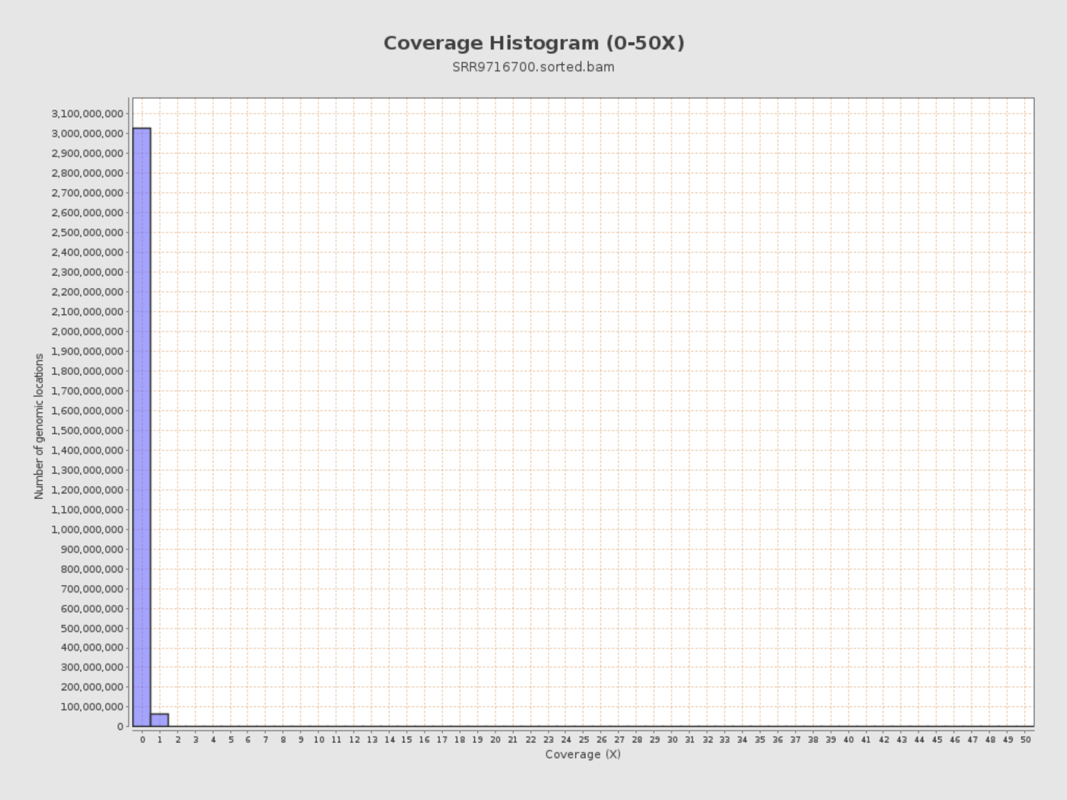
3. Results : Coverage across reference



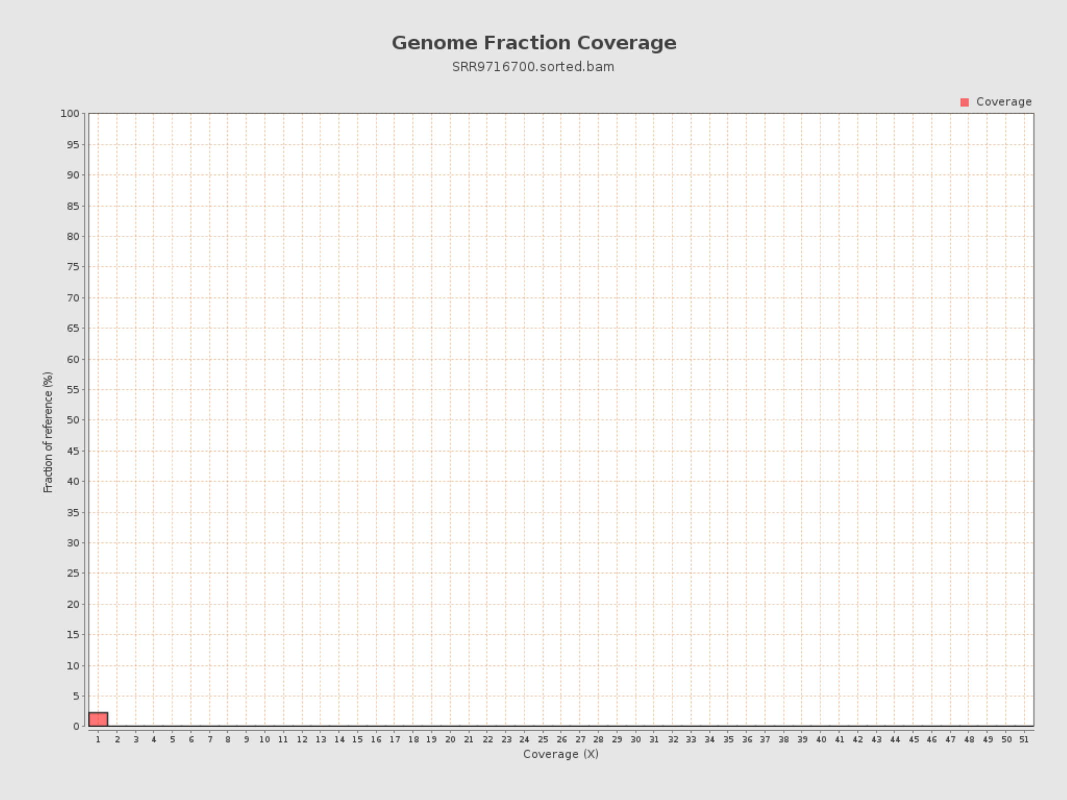
4. Results : Coverage Histogram



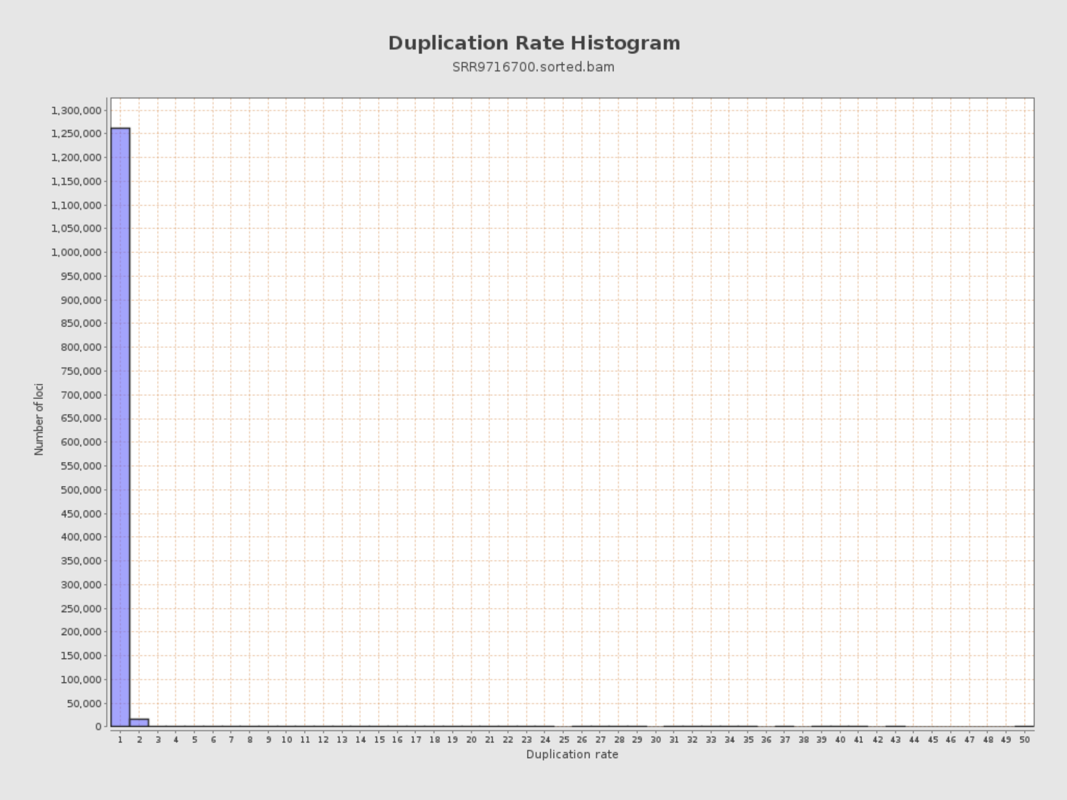
5. Results : Coverage Histogram (0-50X)



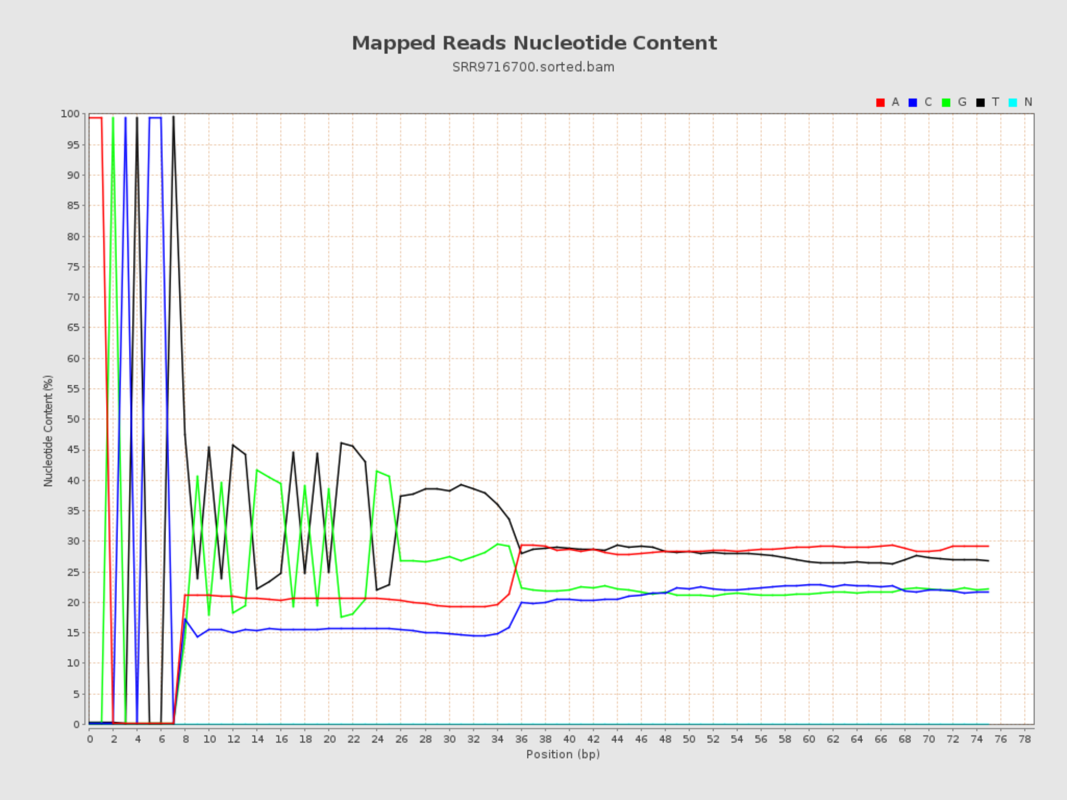
6. Results : Genome Fraction Coverage



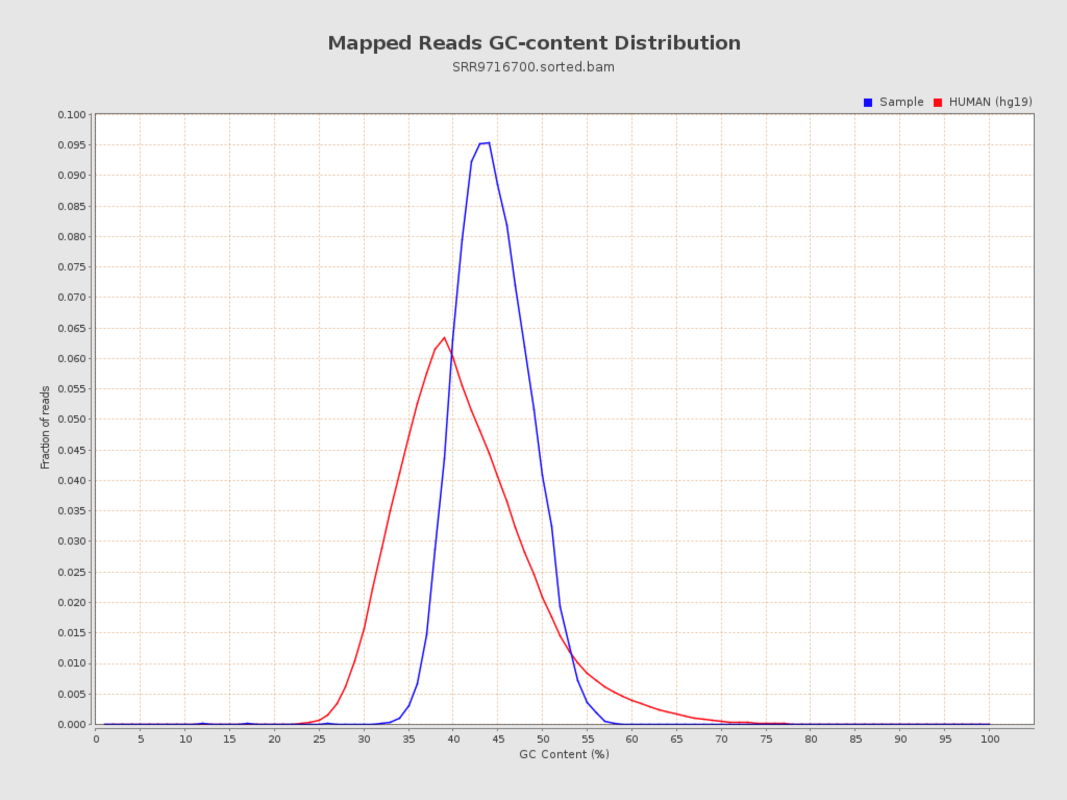
7. Results : Duplication Rate Histogram



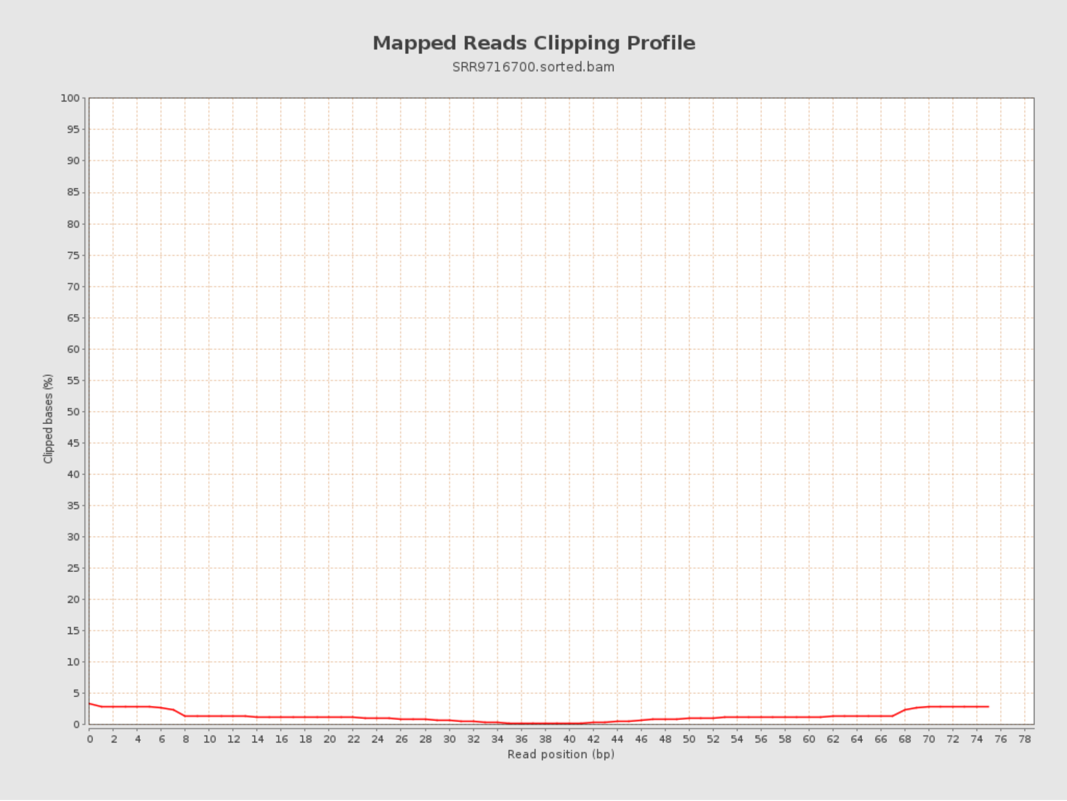
8. Results : Mapped Reads Nucleotide Content



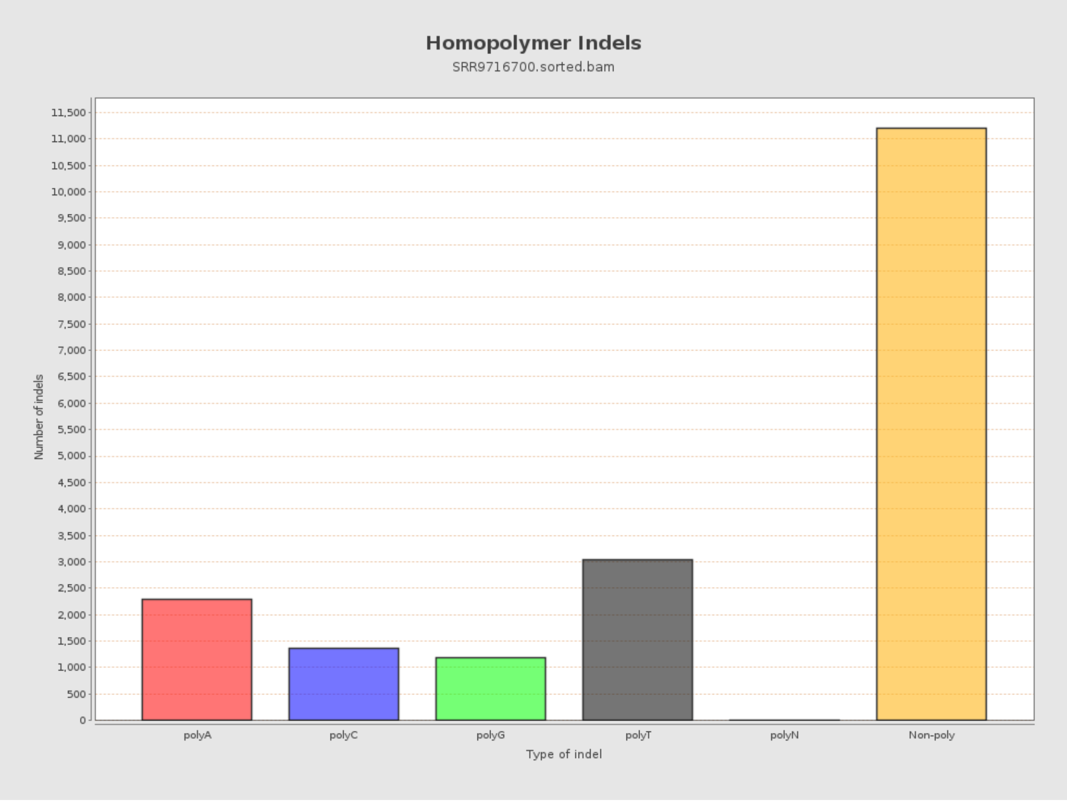
9. Results : Mapped Reads GC-content Distribution



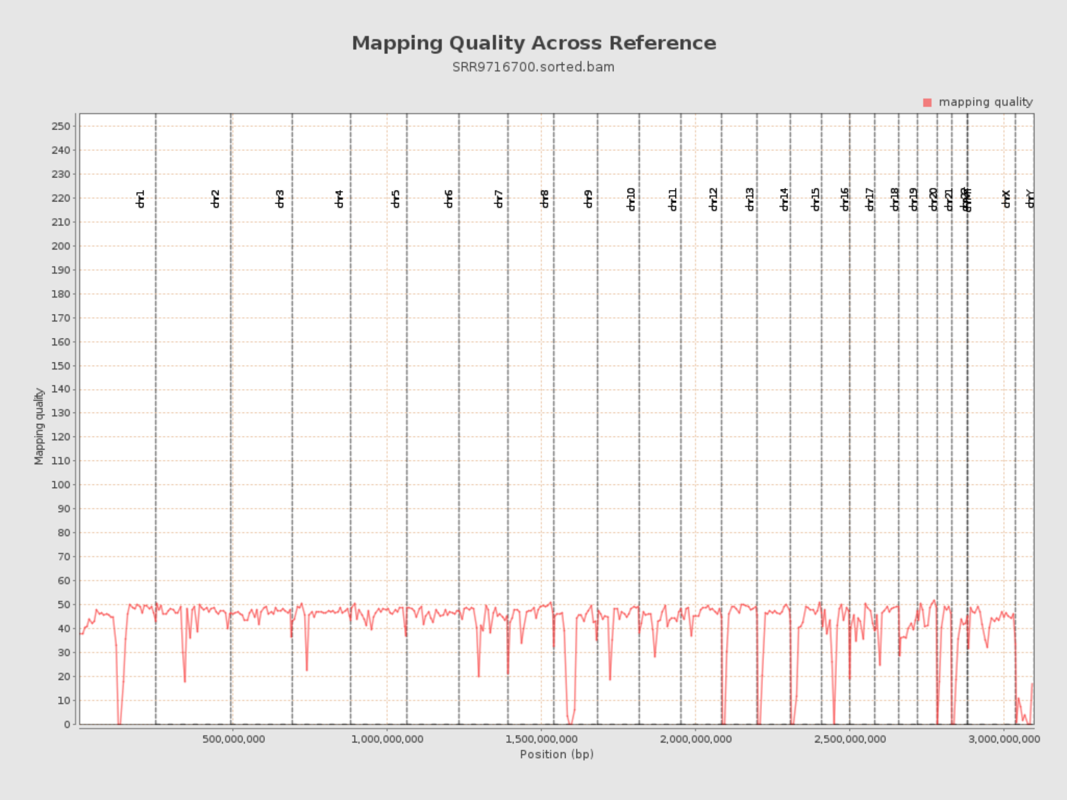
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram