Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:41:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716780.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_SRR9716780 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716780.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:41:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716780.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,679,964
Mapped reads	3,606,472 / 77.06%
Unmapped reads	1,073,492 / 22.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	82,431 / 1.76%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	191,655 / 4.1%
Duplication rate	3.77%
Clipped reads	3,683,320 / 78.7%

2.2. ACGT Content

Number/percentage of A's	71,589,238 / 26.3%
Number/percentage of C's	55,001,843 / 20.21%
Number/percentage of T's	82,567,798 / 30.34%
Number/percentage of G's	62,967,815 / 23.14%
Number/percentage of N's	34,779 / 0.01%
GC Percentage	43.35%

2.3. Coverage

Mean	0.0879

Standard Deviation	0.6593

2.4. Mapping Quality

Mean Mapping Quality	46.4

2.5. Mismatches and indels

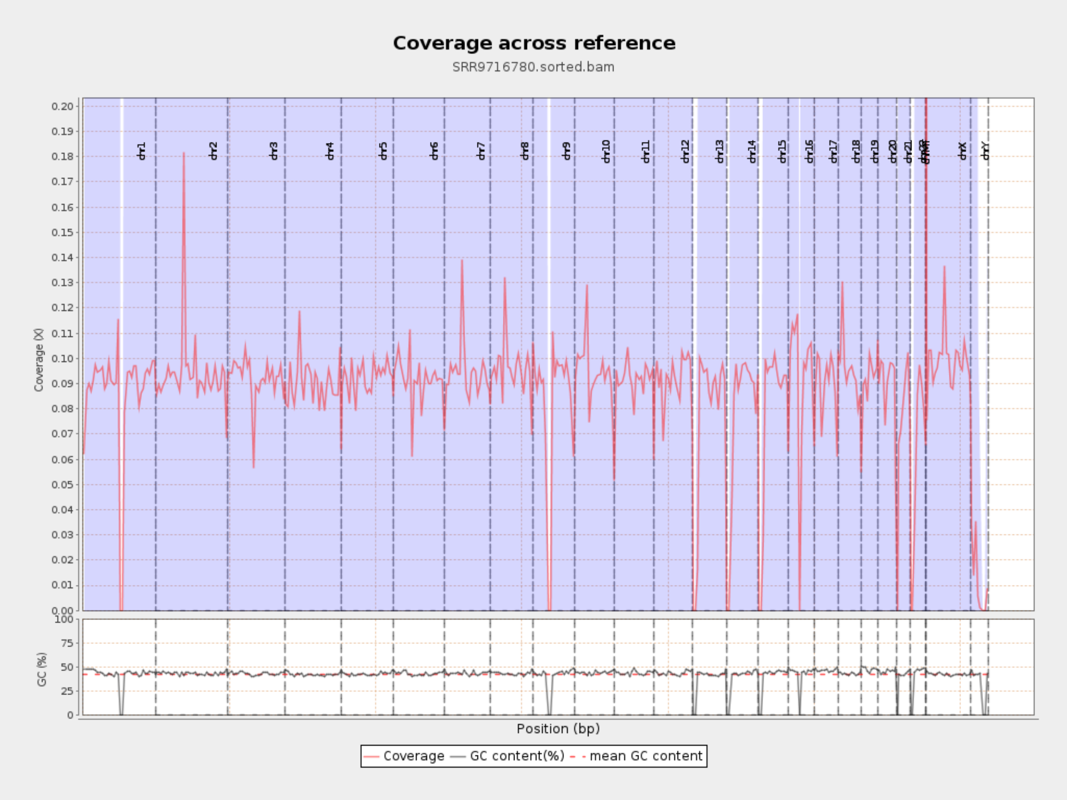
General error rate	0.78%
Mismatches	2,064,717
Insertions	23,498
Mapped reads with at least one insertion	0.64%
Deletions	57,239
Mapped reads with at least one deletion	1.57%
Homopolymer indels	40.6%

2.6. Chromosome stats

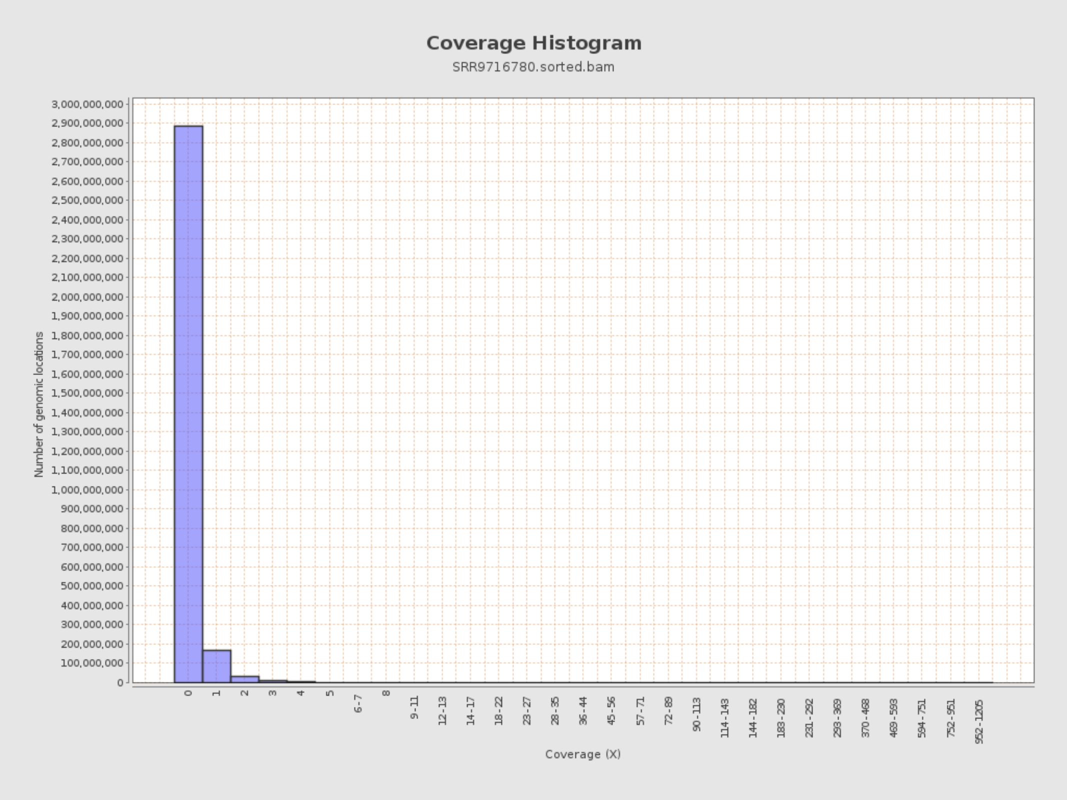
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21480480	0.0862	0.7534
chr2	243199373	23044965	0.0948	1.0066
chr3	198022430	18241372	0.0921	0.3761
chr4	191154276	17306996	0.0905	0.4236
chr5	180915260	16714878	0.0924	0.3859
chr6	171115067	15695209	0.0917	0.4589
chr7	159138663	15044016	0.0945	0.9273

chr8	146364022	13980366	0.0955	0.8633
chr9	141213431	11459247	0.0811	0.7366
chr10	135534747	12848881	0.0948	0.6025
chr11	135006516	12324699	0.0913	0.7669
chr12	133851895	12381727	0.0925	0.3909
chr13	115169878	8775341	0.0762	0.3412
chr14	107349540	8238433	0.0767	0.4779
chr15	102531392	7831444	0.0764	0.3502
chr16	90354753	8041786	0.089	0.4477
chr17	81195210	7365384	0.0907	0.4435
chr18	78077248	7531552	0.0965	1.4693
chr19	59128983	5423844	0.0917	0.6745
chr20	63025520	5729510	0.0909	0.4055
chr21	48129895	3607053	0.0749	0.3849
chr22	51304566	3102741	0.0605	0.3072
chrMT	16571	17659	1.0657	1.7439
chrX	155270560	15393853	0.0991	0.5857
chrY	59373566	676331	0.0114	0.2841

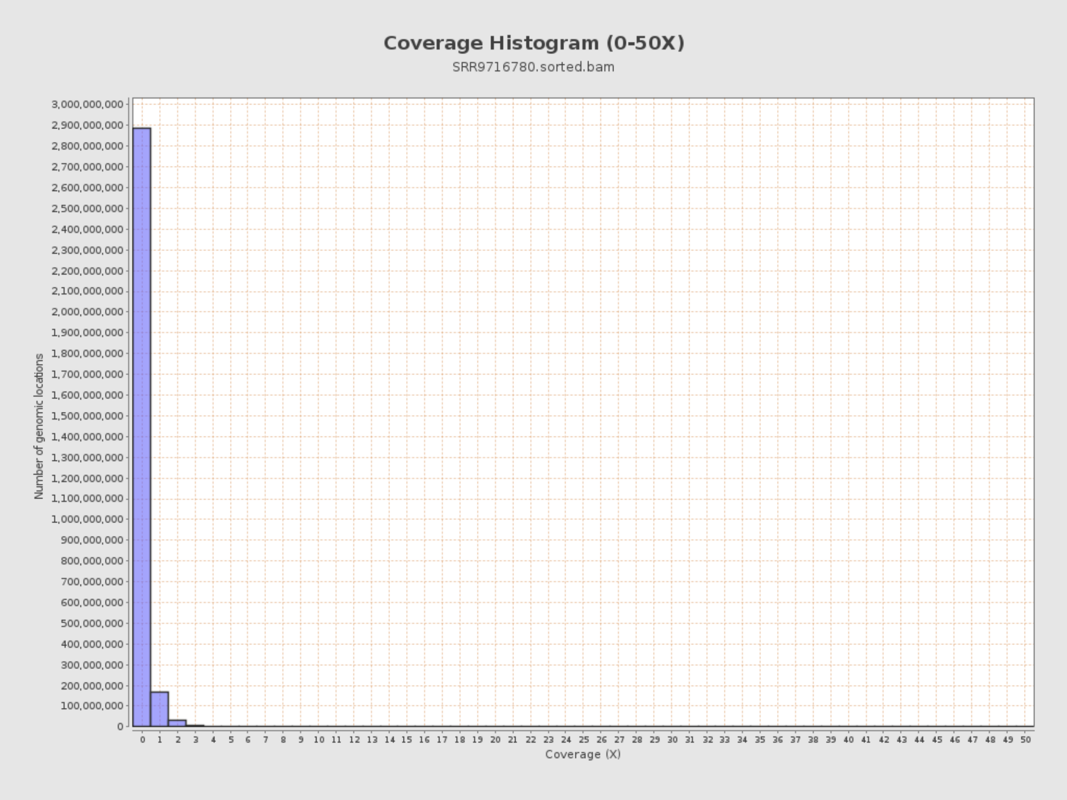
3. Results : Coverage across reference



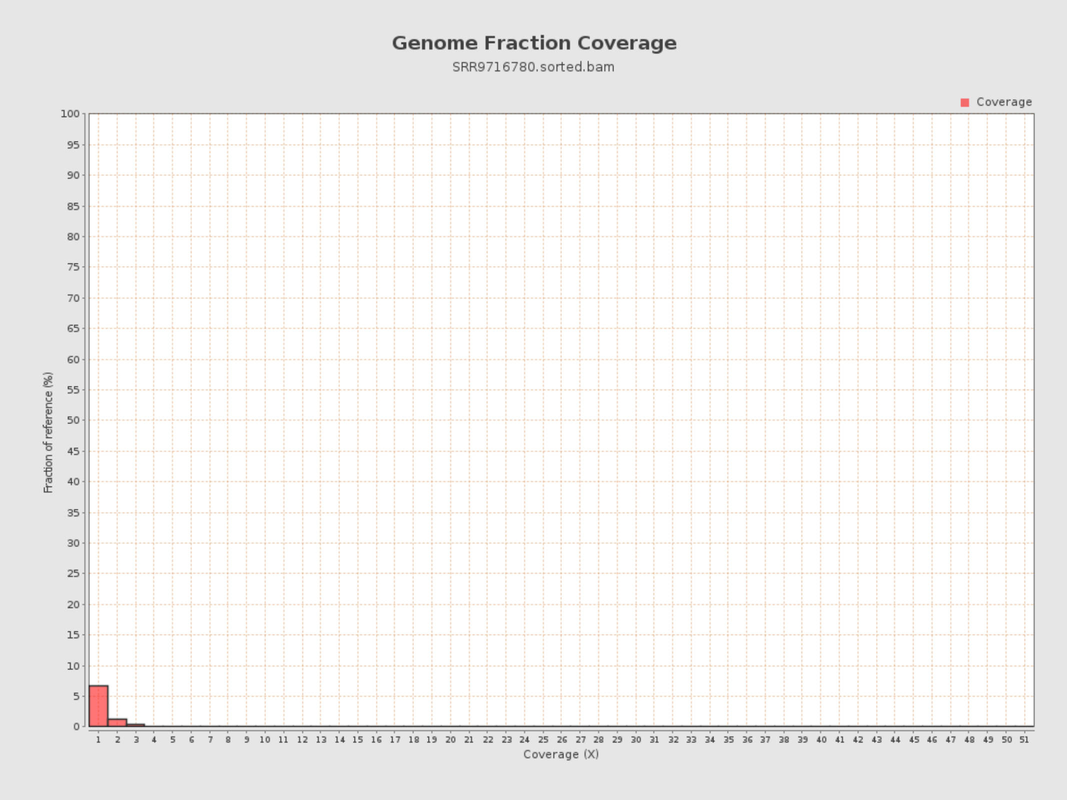
4. Results : Coverage Histogram



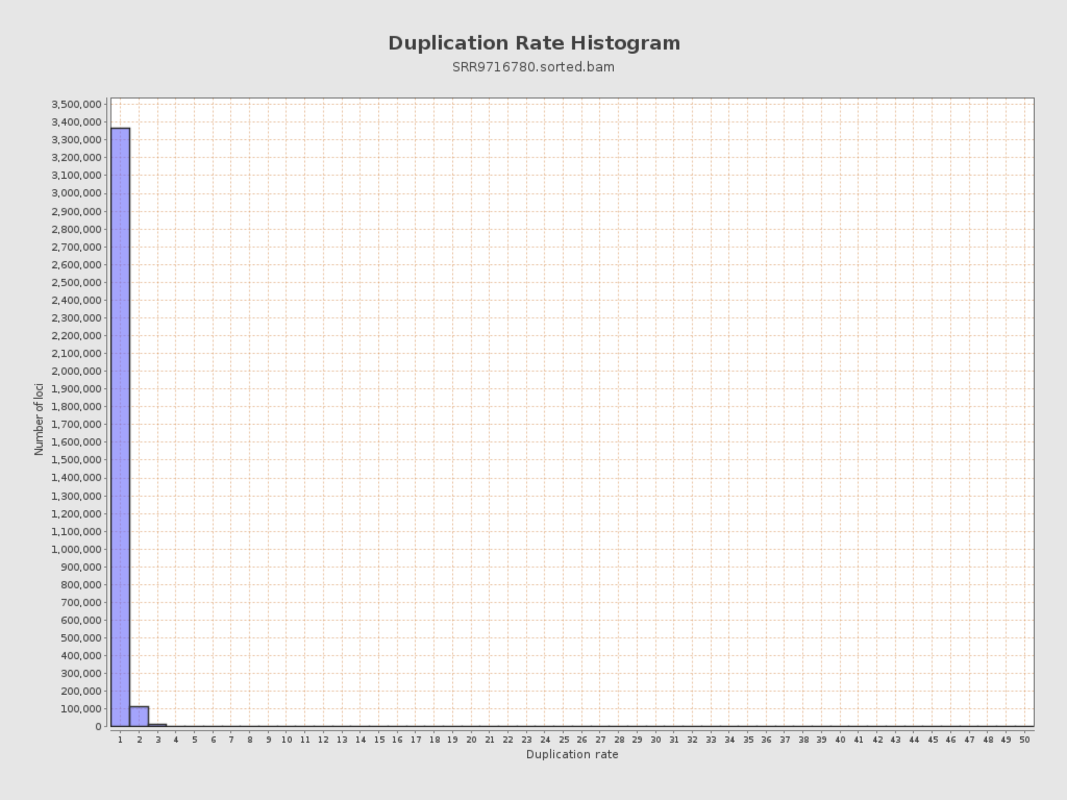
5. Results : Coverage Histogram (0-50X)



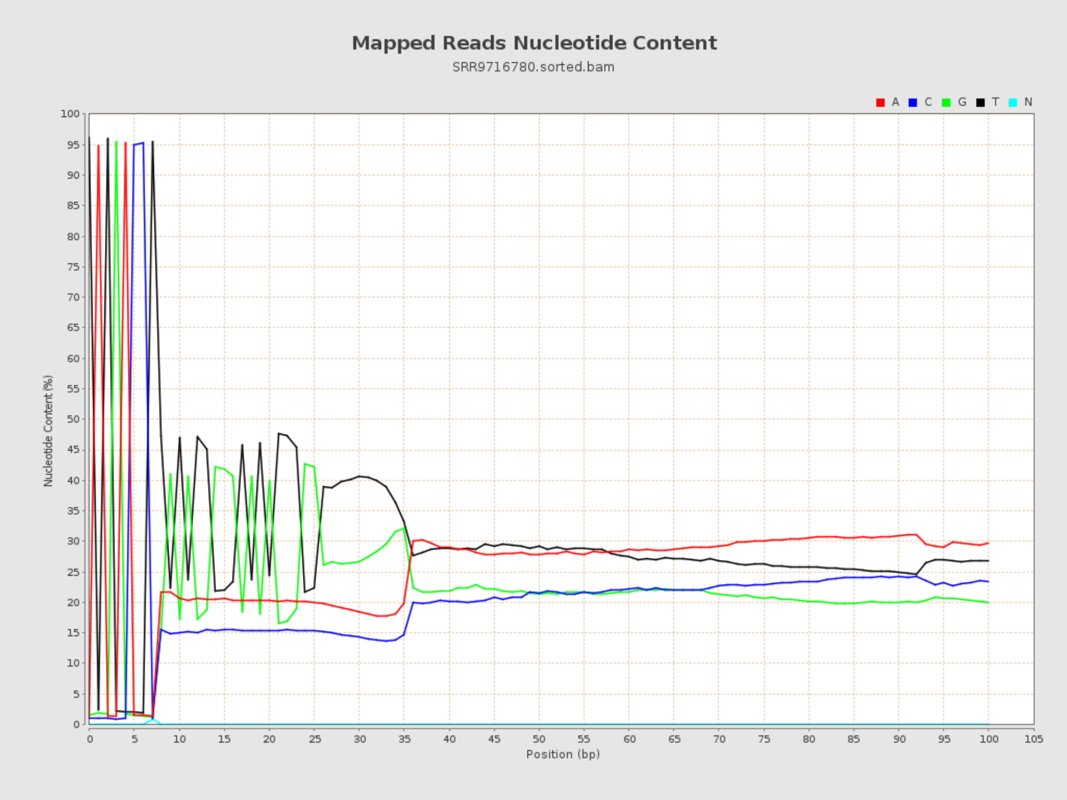
6. Results : Genome Fraction Coverage



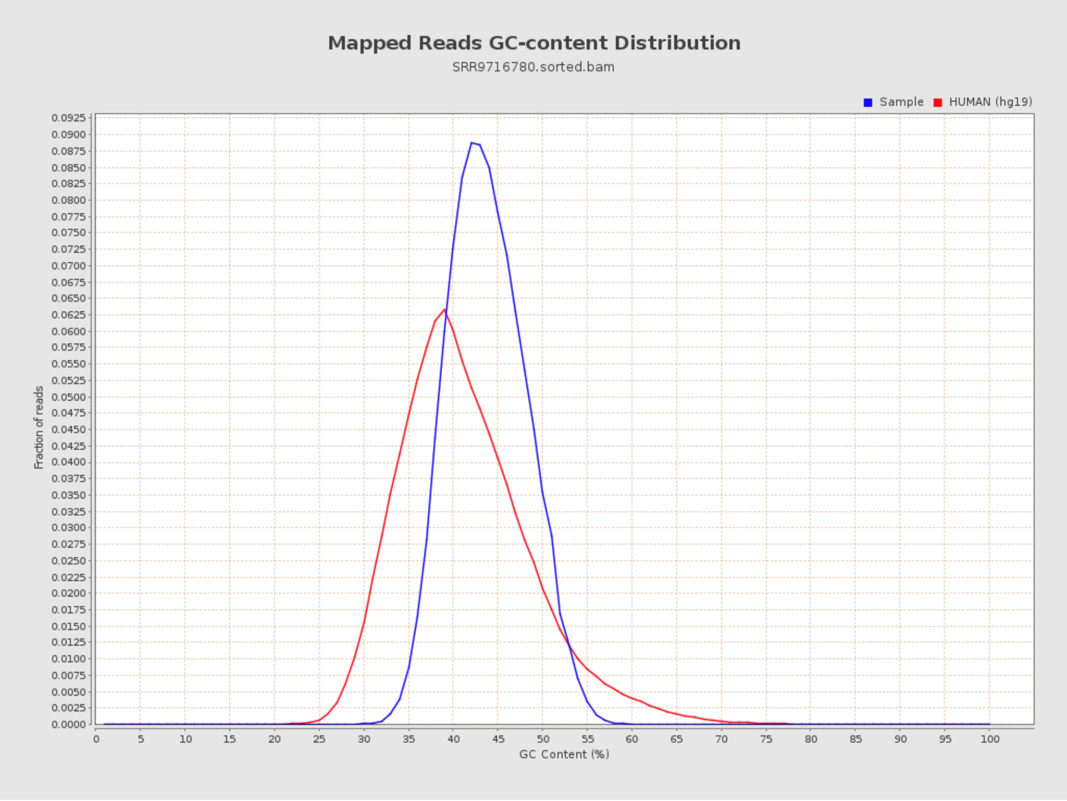
7. Results : Duplication Rate Histogram



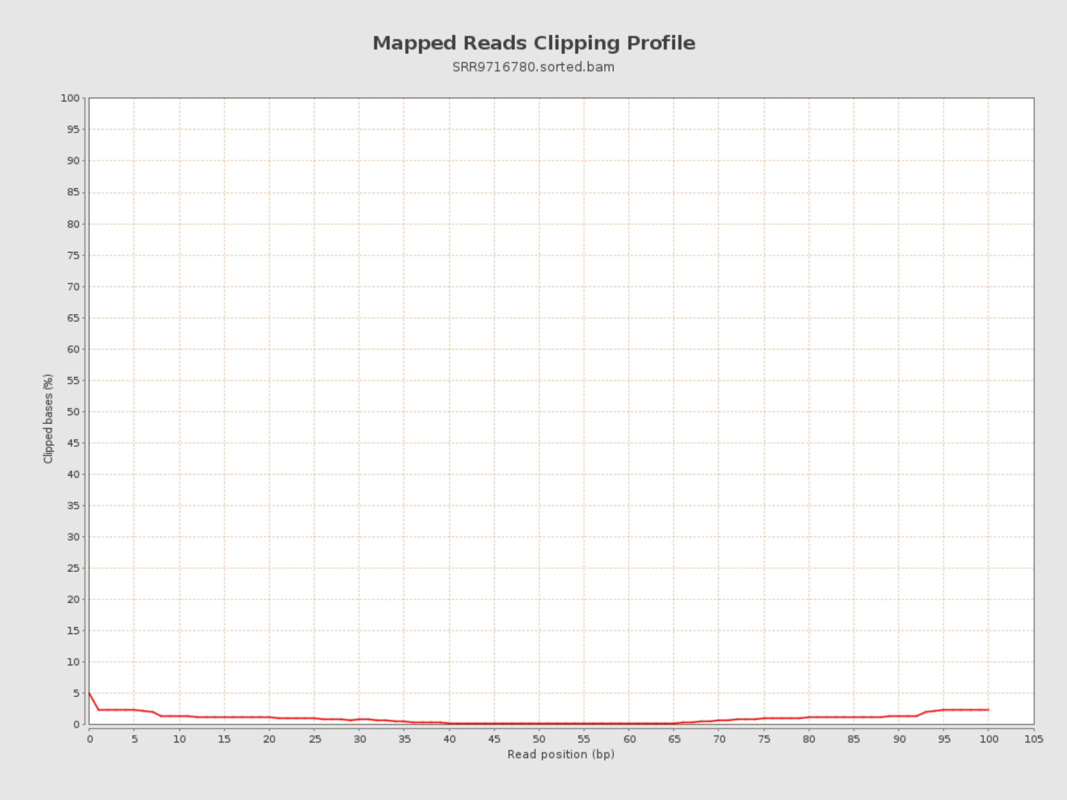
8. Results : Mapped Reads Nucleotide Content



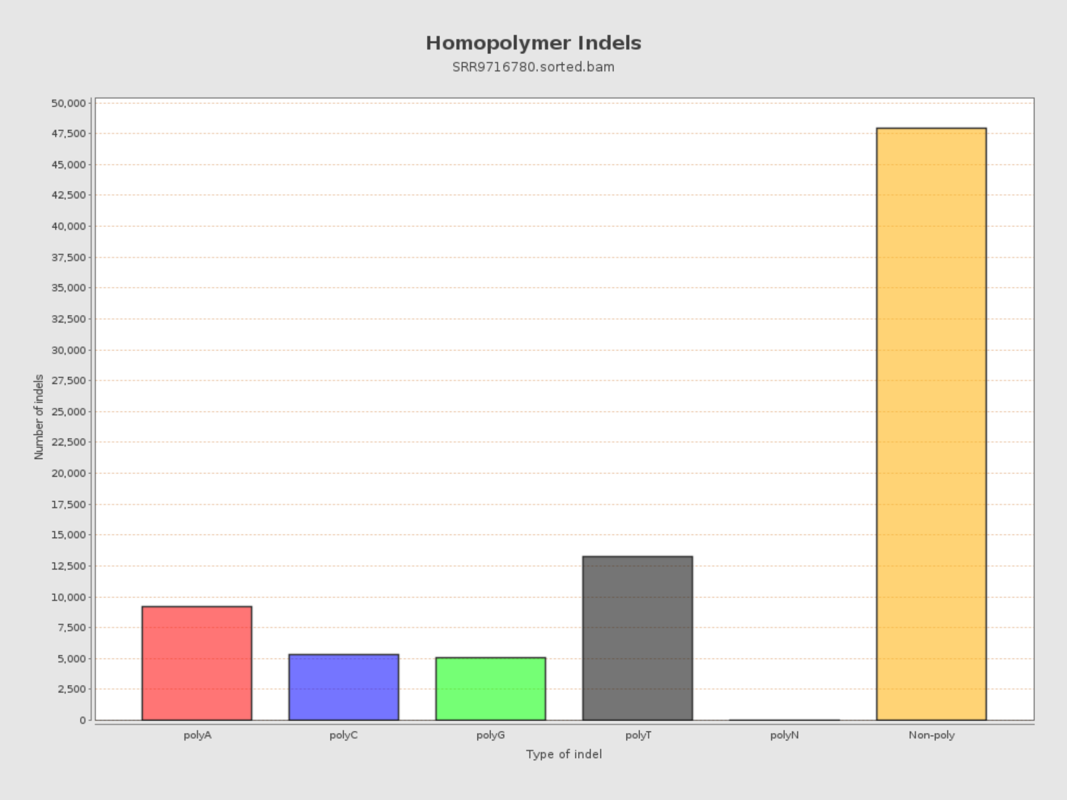
9. Results : Mapped Reads GC-content Distribution



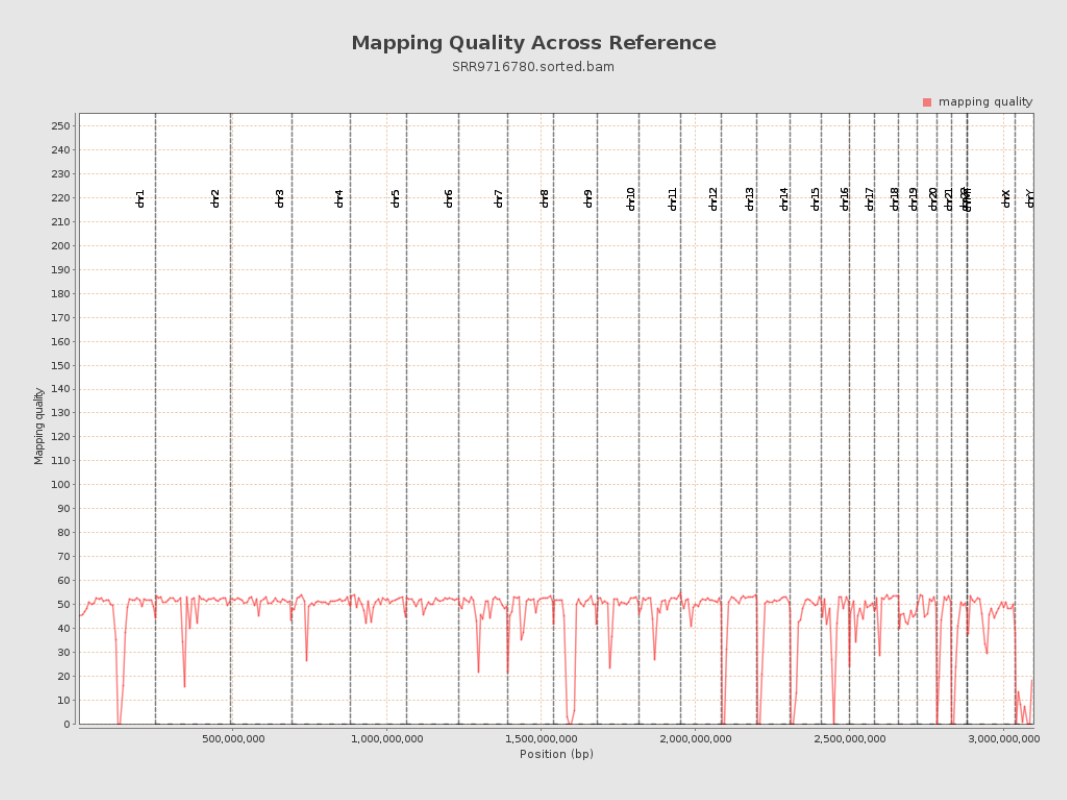
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram