Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:52:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716782.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_SRR9716782 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716782.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:52:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716782.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,426,397
Mapped reads	2,102,561 / 86.65%
Unmapped reads	323,836 / 13.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	53,277 / 2.2%
Read min/max/mean length	30 / 101 / 101.8
Duplicated reads (estimated)	74,530 / 3.07%
Duplication rate	2.4%
Clipped reads	2,152,198 / 88.7%

2.2. ACGT Content

Number/percentage of A's	41,314,549 / 26.16%
Number/percentage of C's	31,513,265 / 19.95%
Number/percentage of T's	48,117,035 / 30.47%
Number/percentage of G's	36,975,297 / 23.41%
Number/percentage of N's	19,283 / 0.01%
GC Percentage	43.36%

2.3. Coverage

Mean	0.051

Standard Deviation	0.4126

2.4. Mapping Quality

Mean Mapping Quality	46.19

2.5. Mismatches and indels

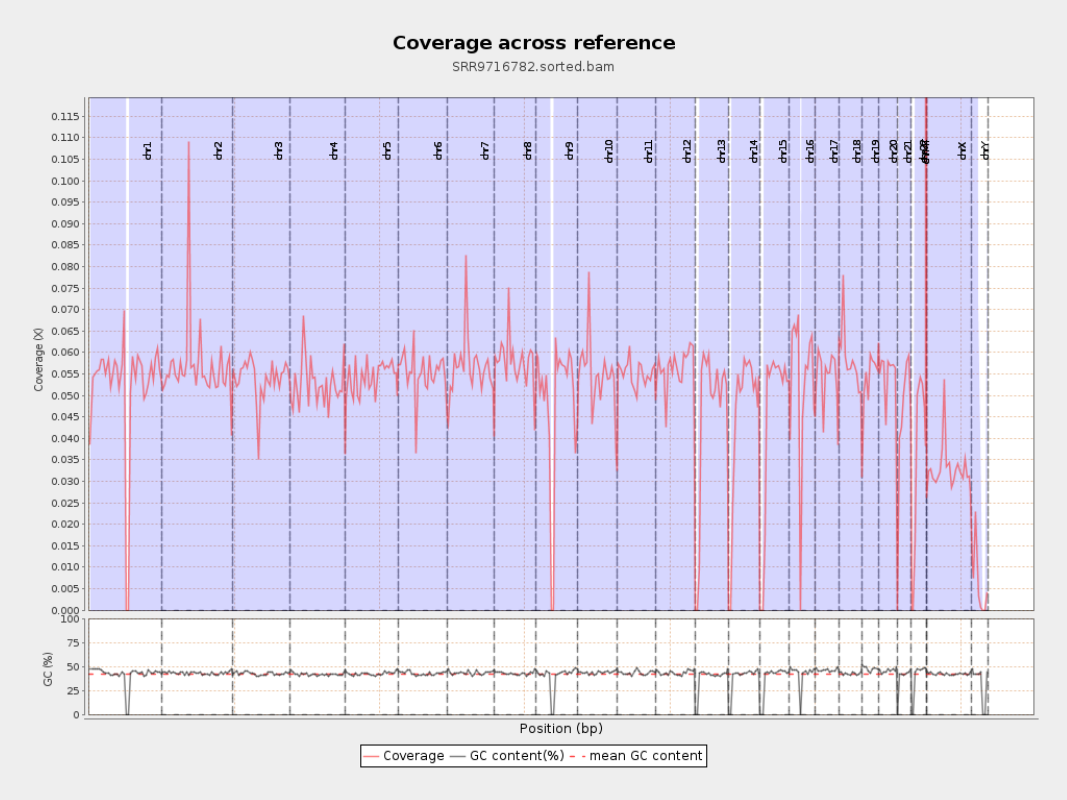
General error rate	0.76%
Mismatches	1,168,103
Insertions	14,582
Mapped reads with at least one insertion	0.69%
Deletions	32,576
Mapped reads with at least one deletion	1.53%
Homopolymer indels	39.76%

2.6. Chromosome stats

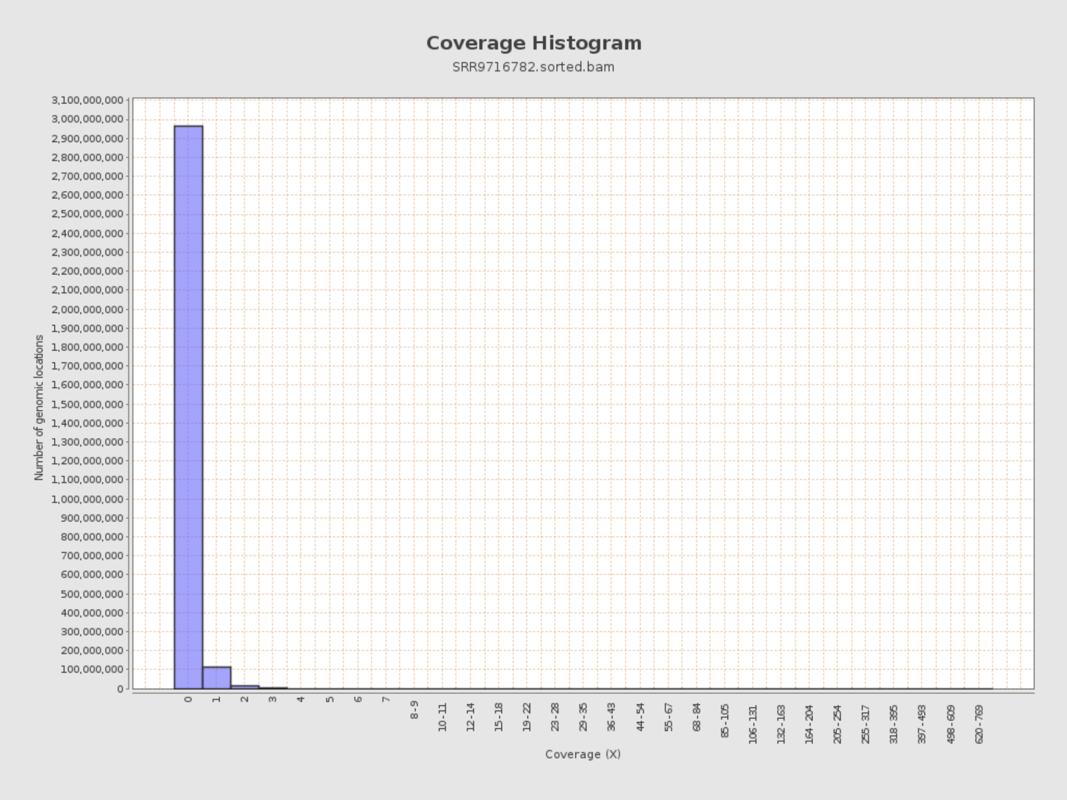
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12987002	0.0521	0.4862
chr2	243199373	13866630	0.057	0.6208
chr3	198022430	10676027	0.0539	0.266
chr4	191154276	10049434	0.0526	0.2879
chr5	180915260	9821889	0.0543	0.2724
chr6	171115067	9461364	0.0553	0.316
chr7	159138663	9057375	0.0569	0.5342

chr8	146364022	8482334	0.058	0.5225
chr9	141213431	6764522	0.0479	0.4459
chr10	135534747	7465606	0.0551	0.4148
chr11	135006516	7394813	0.0548	0.4659
chr12	133851895	7534405	0.0563	0.2773
chr13	115169878	5178243	0.045	0.2408
chr14	107349540	4790727	0.0446	0.2988
chr15	102531392	4606935	0.0449	0.246
chr16	90354753	4816492	0.0533	0.3033
chr17	81195210	4385342	0.054	0.2975
chr18	78077248	4584670	0.0587	0.8852
chr19	59128983	3211632	0.0543	0.4214
chr20	63025520	3416535	0.0542	0.2878
chr21	48129895	2156663	0.0448	0.2682
chr22	51304566	1785228	0.0348	0.2136
chrMT	16571	17369	1.0482	1.2676
chrX	155270560	5128531	0.033	0.3043
chrY	59373566	355572	0.006	0.1982

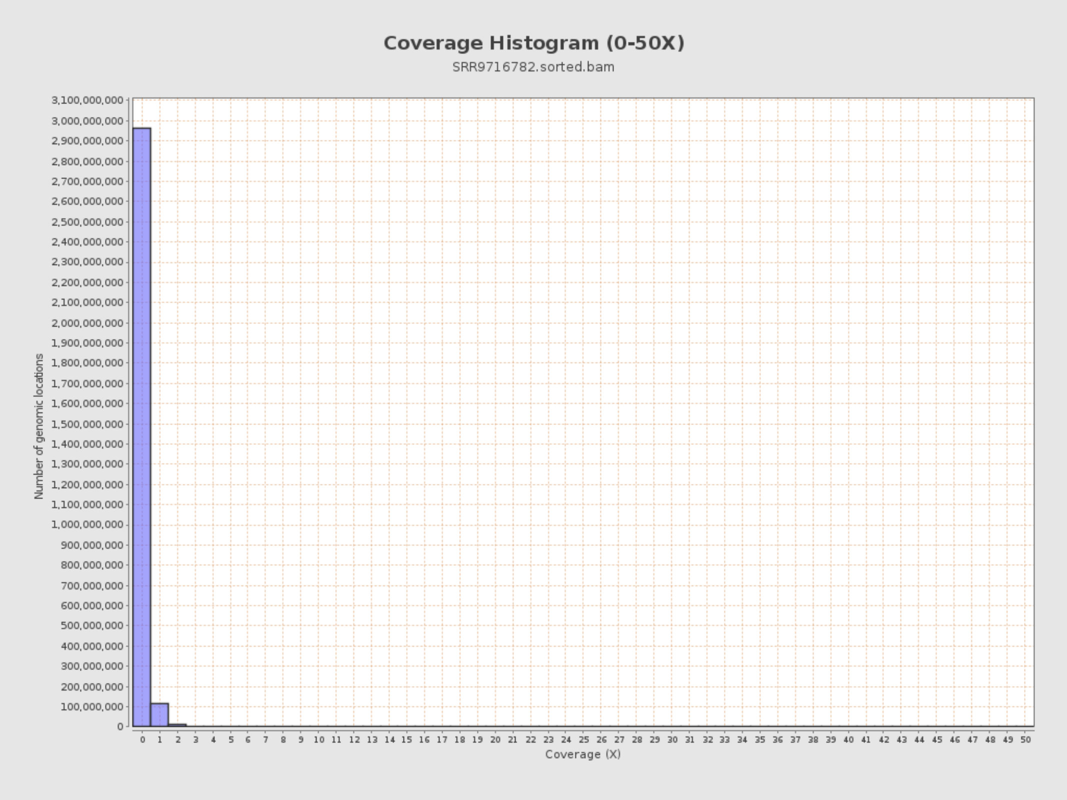
3. Results : Coverage across reference



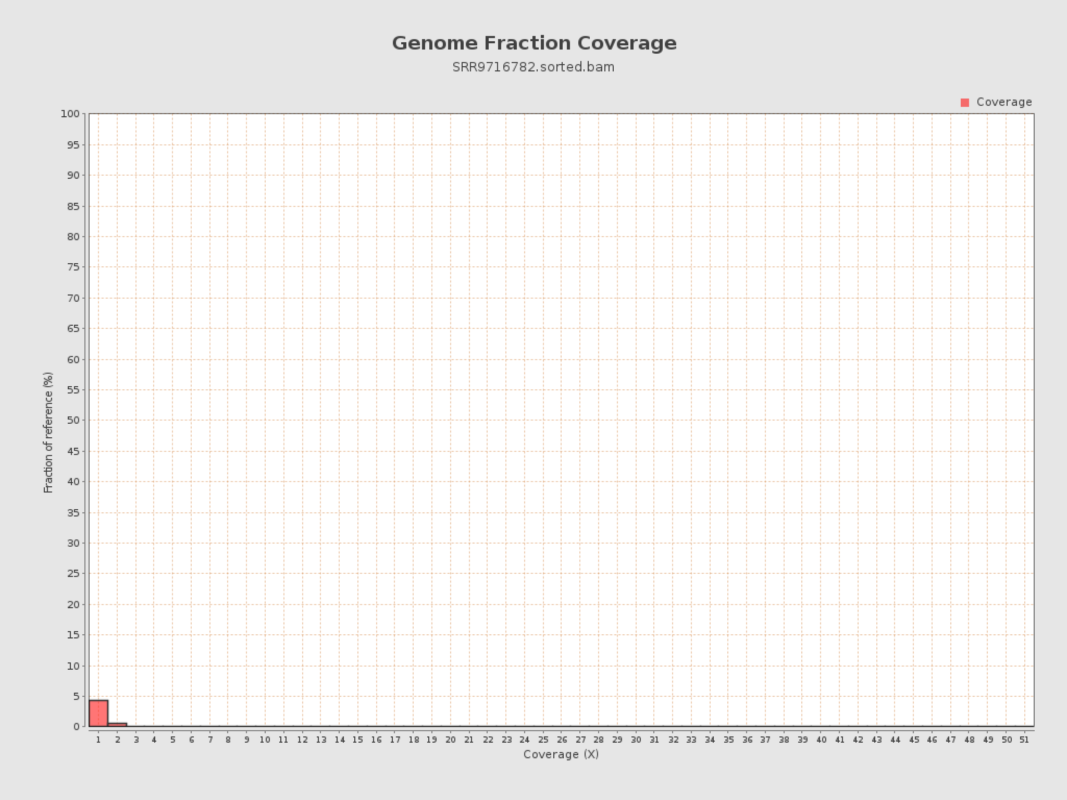
4. Results : Coverage Histogram



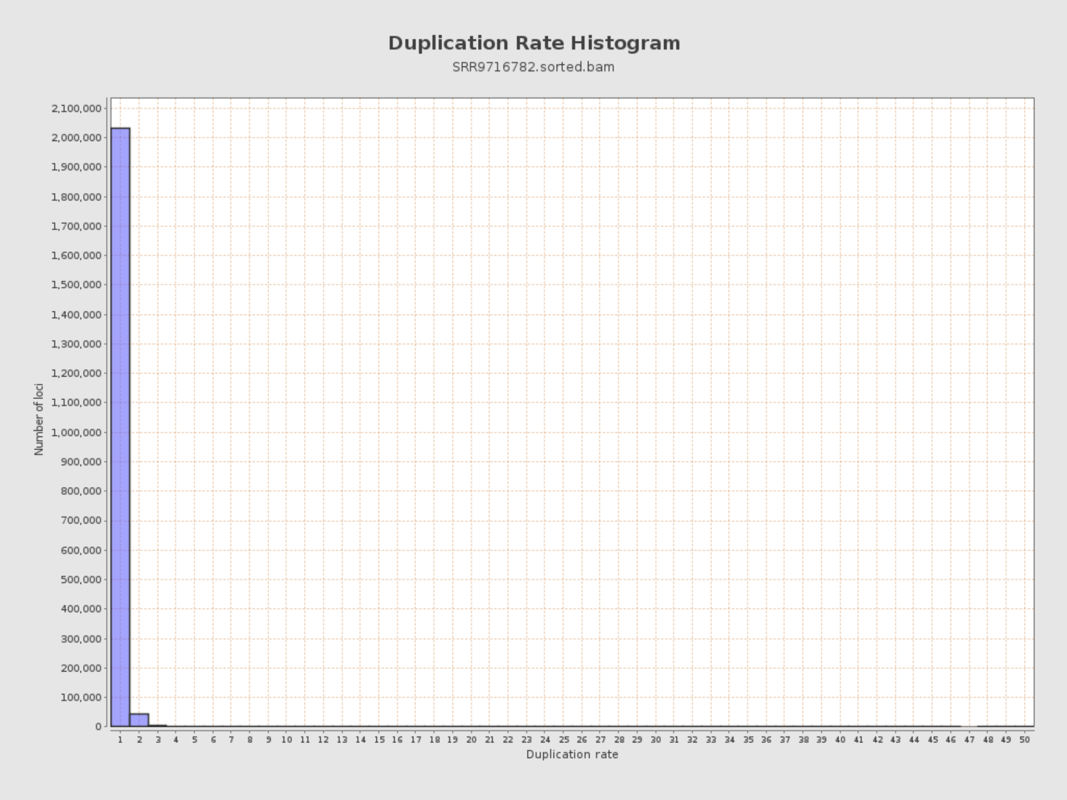
5. Results : Coverage Histogram (0-50X)



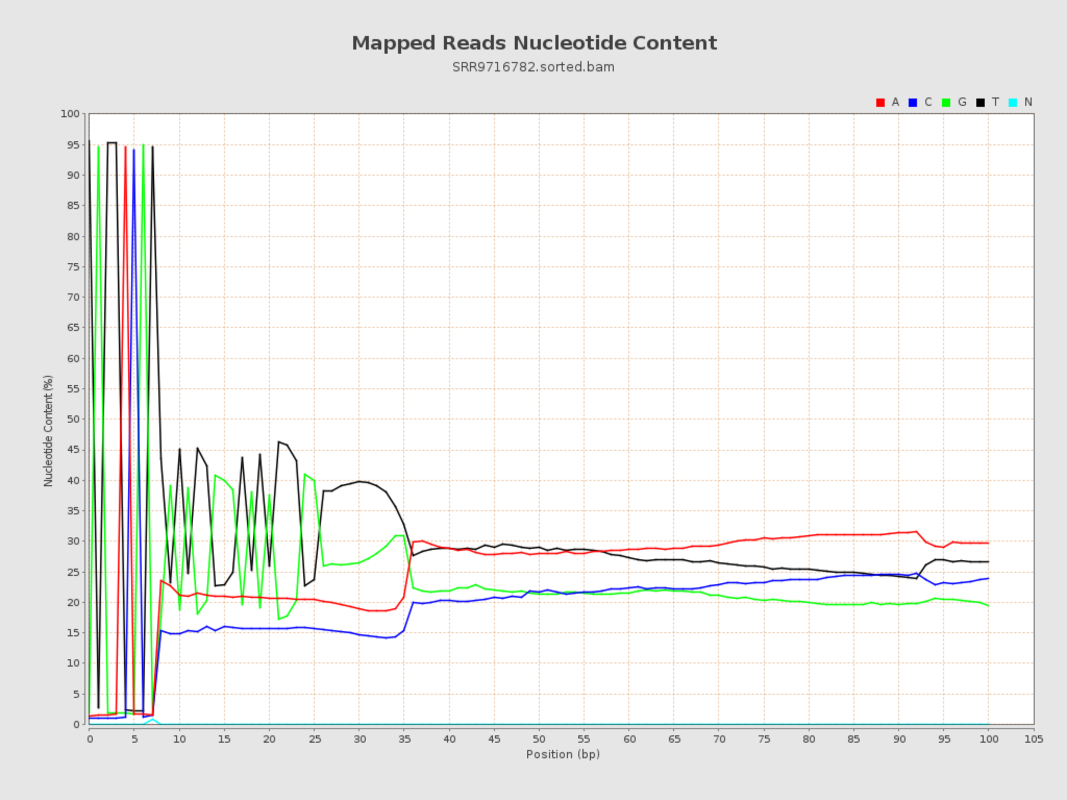
6. Results : Genome Fraction Coverage



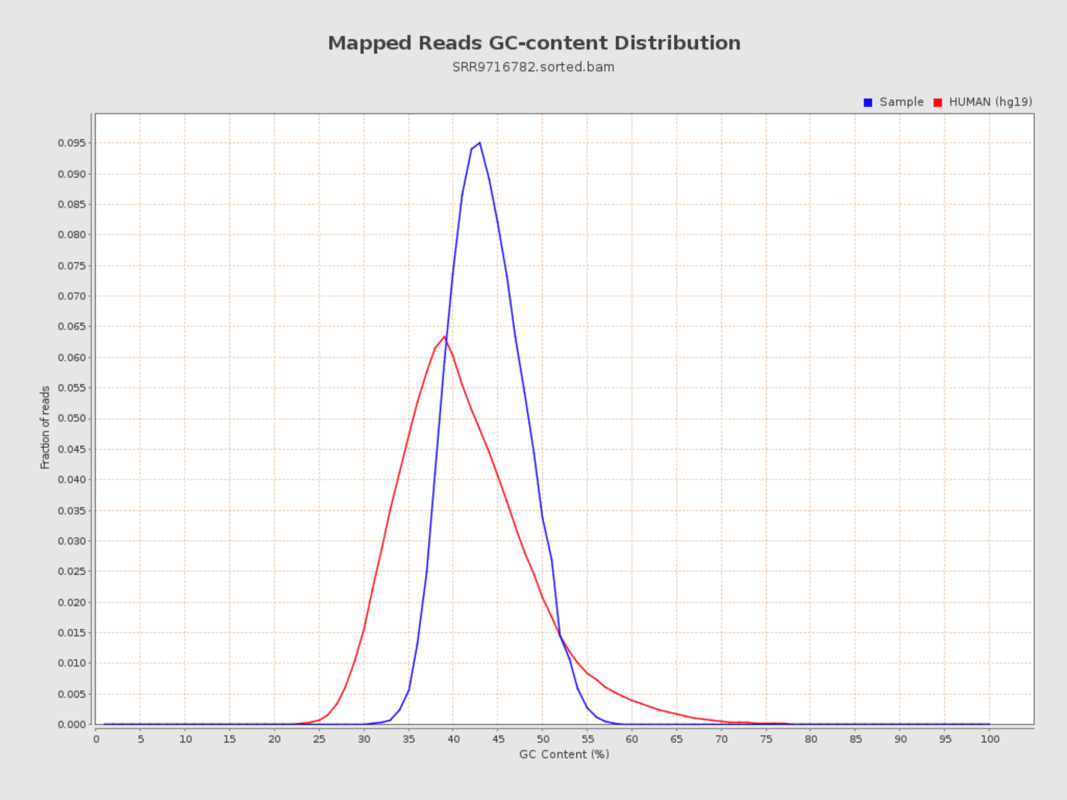
7. Results : Duplication Rate Histogram



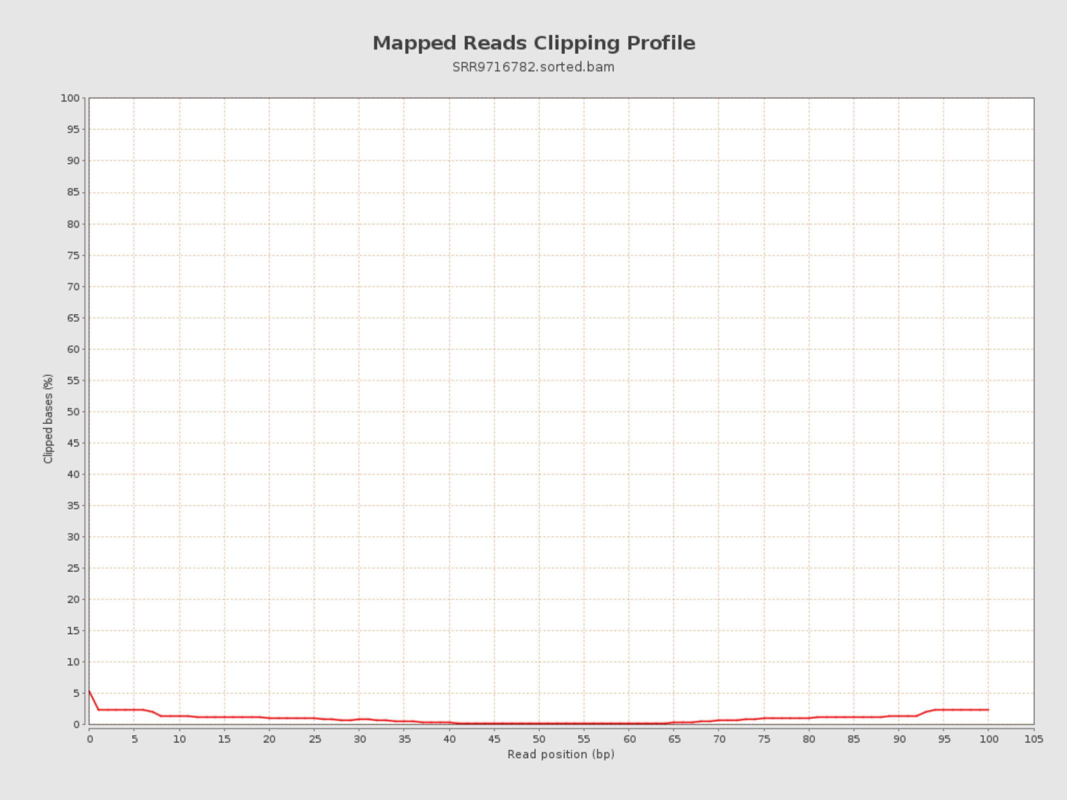
8. Results : Mapped Reads Nucleotide Content



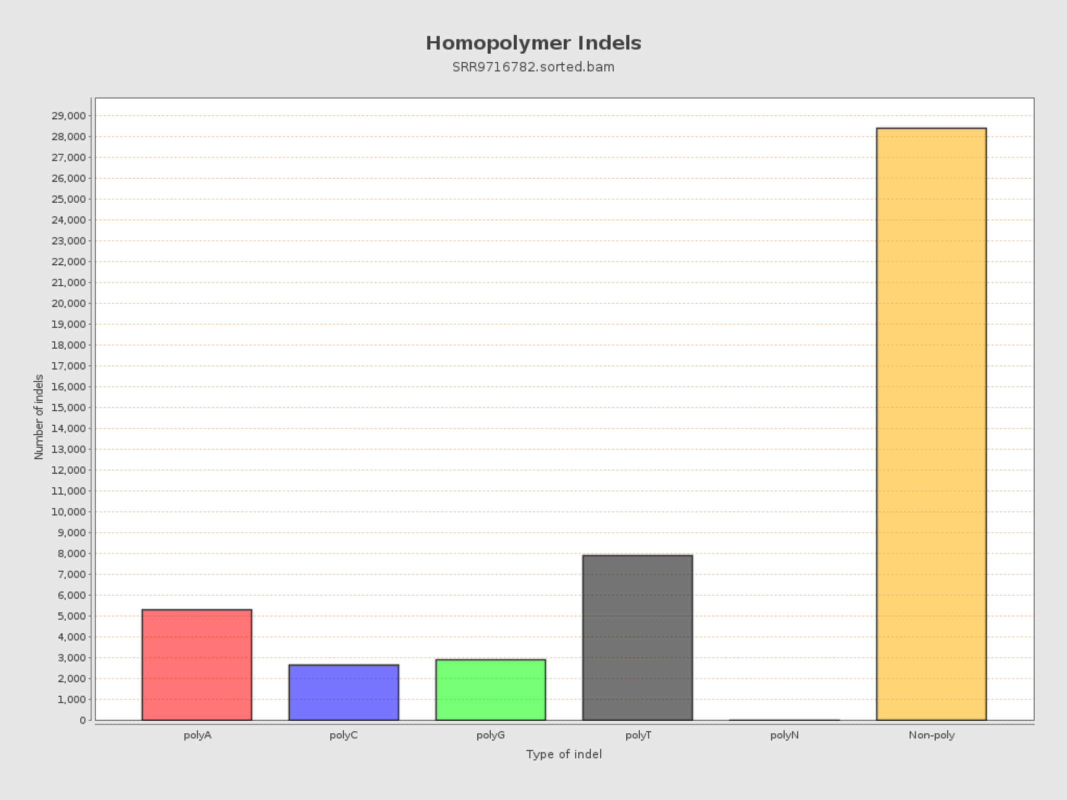
9. Results : Mapped Reads GC-content Distribution



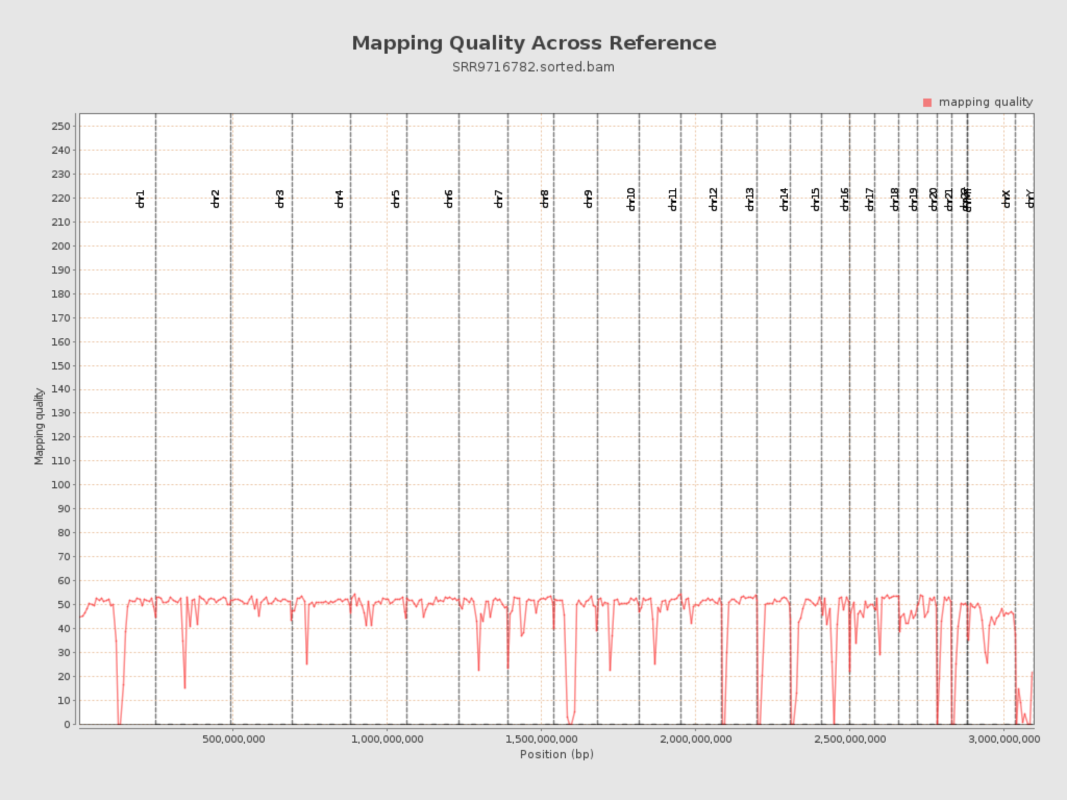
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram