Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:15:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717041.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_SRR9717041 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717041.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:15:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717041.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,169,242
Mapped reads	3,608,989 / 86.56%
Unmapped reads	560,253 / 13.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	82,264 / 1.97%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	195,027 / 4.68%
Duplication rate	3.83%
Clipped reads	3,686,160 / 88.41%

2.2. ACGT Content

Number/percentage of A's	71,173,175 / 26.07%
Number/percentage of C's	54,867,169 / 20.1%
Number/percentage of T's	83,071,399 / 30.43%
Number/percentage of G's	63,858,436 / 23.39%
Number/percentage of N's	33,248 / 0.01%
GC Percentage	43.49%

2.3. Coverage

Mean	0.0882

Standard Deviation	0.7213

2.4. Mapping Quality

Mean Mapping Quality	45.97

2.5. Mismatches and indels

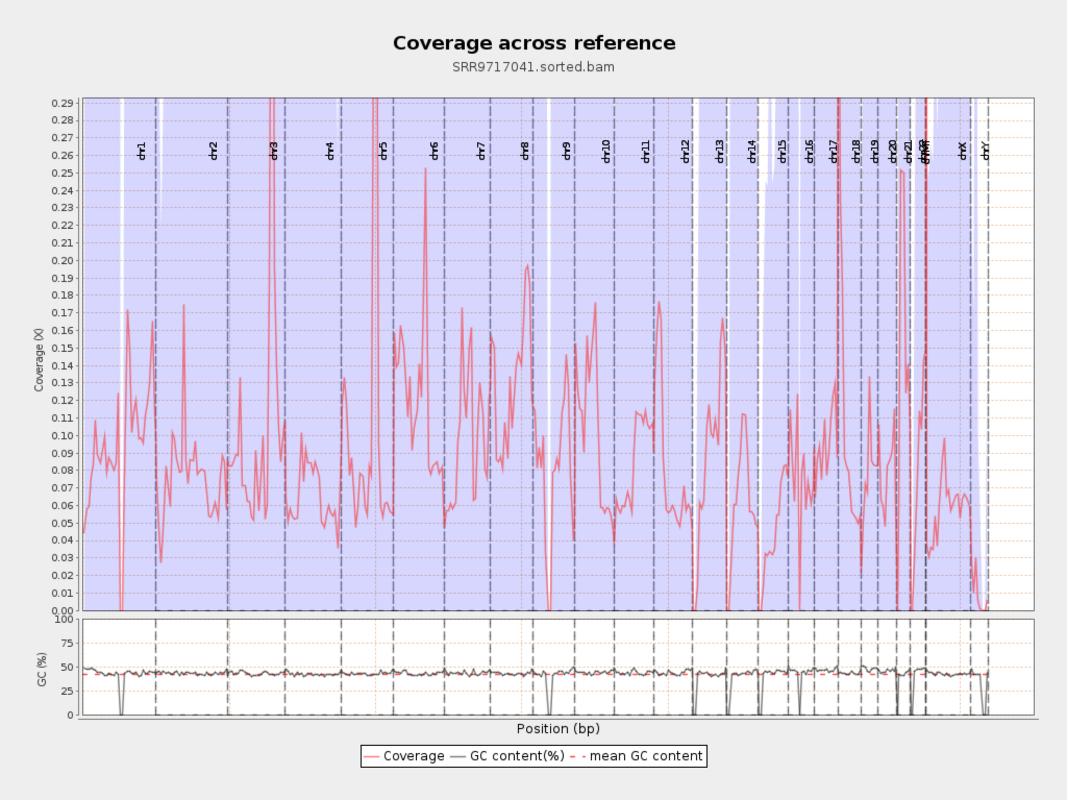
General error rate	0.74%
Mismatches	1,968,720
Insertions	21,938
Mapped reads with at least one insertion	0.6%
Deletions	57,562
Mapped reads with at least one deletion	1.57%
Homopolymer indels	41.66%

2.6. Chromosome stats

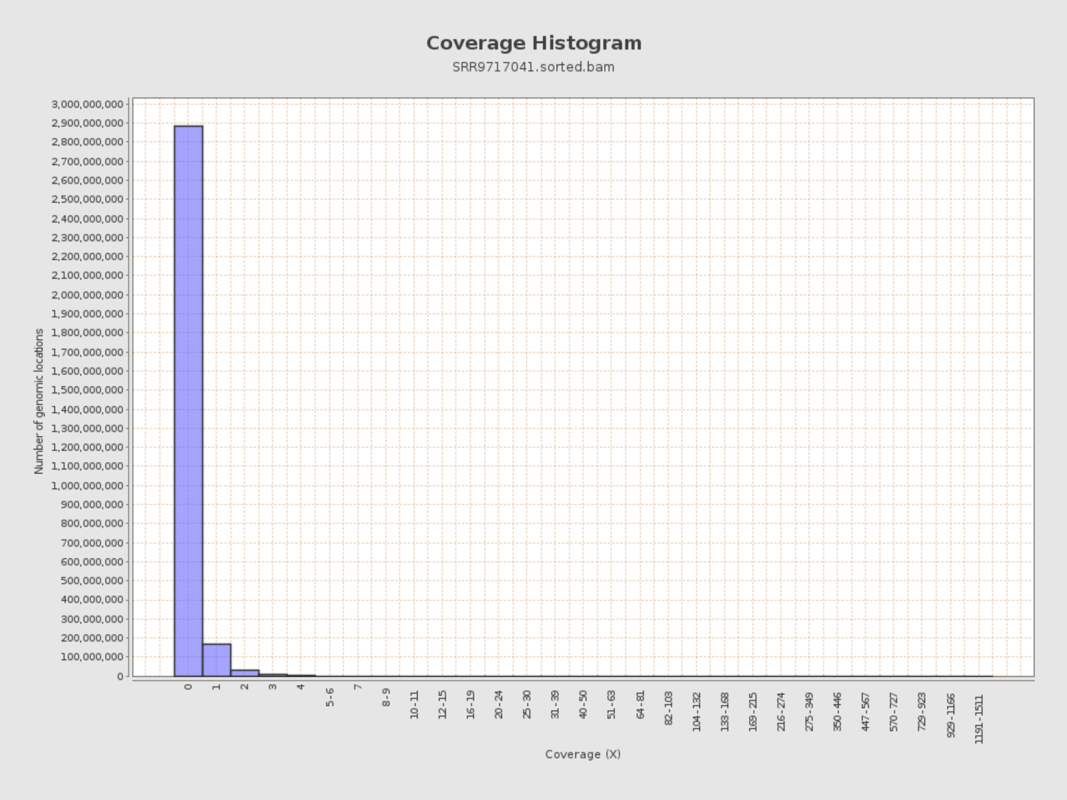
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23381528	0.0938	1.0077
chr2	243199373	18483466	0.076	1.1004
chr3	198022430	21910516	0.1106	0.4419
chr4	191154276	12638451	0.0661	0.3474
chr5	180915260	18217276	0.1007	0.4156
chr6	171115067	20787610	0.1215	0.5294
chr7	159138663	15458570	0.0971	1.3235

chr8	146364022	19208796	0.1312	0.8374
chr9	141213431	11448659	0.0811	0.6241
chr10	135534747	14281240	0.1054	0.653
chr11	135006516	11403344	0.0845	0.5517
chr12	133851895	11006844	0.0822	0.3663
chr13	115169878	10324588	0.0896	0.3703
chr14	107349540	6660312	0.062	0.3839
chr15	102531392	4299389	0.0419	0.2545
chr16	90354753	6729129	0.0745	0.4218
chr17	81195210	7767261	0.0957	0.4503
chr18	78077248	8779087	0.1124	1.5246
chr19	59128983	4693849	0.0794	0.8712
chr20	63025520	5038661	0.0799	0.4658
chr21	48129895	6881387	0.143	0.5151
chr22	51304566	3885535	0.0757	0.3443
chrMT	16571	163744	9.8814	7.6262
chrX	155270560	9097779	0.0586	0.4525
chrY	59373566	554314	0.0093	0.2312

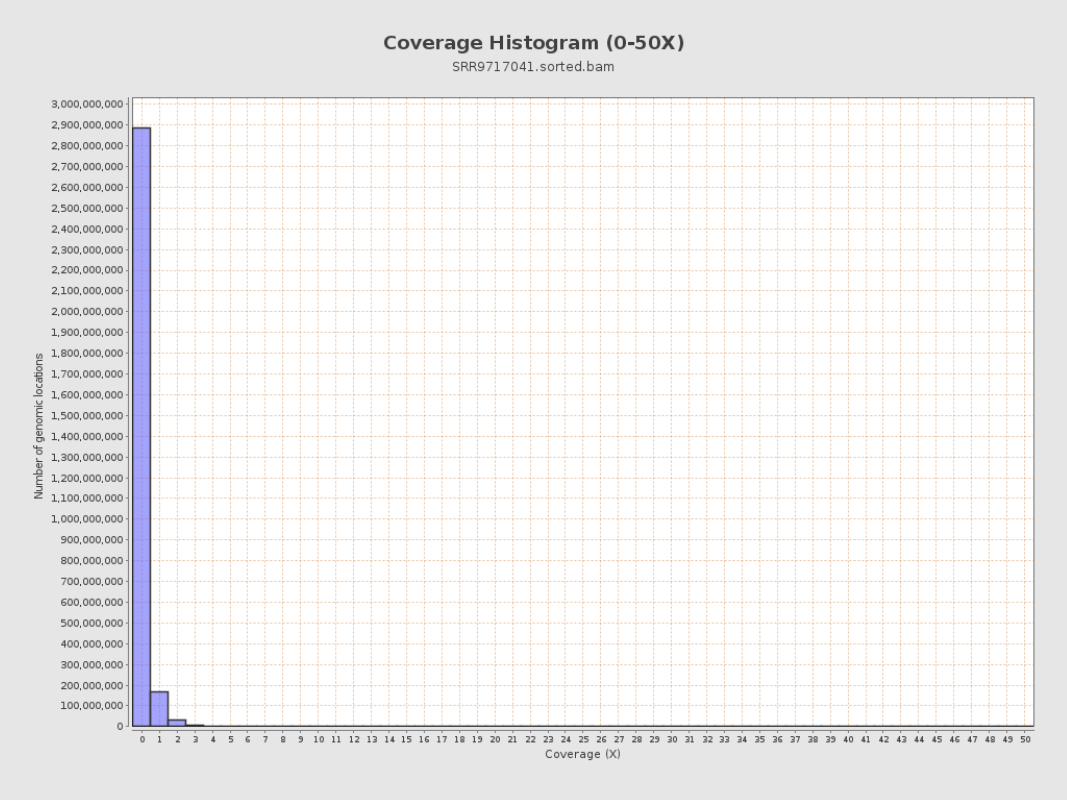
3. Results : Coverage across reference



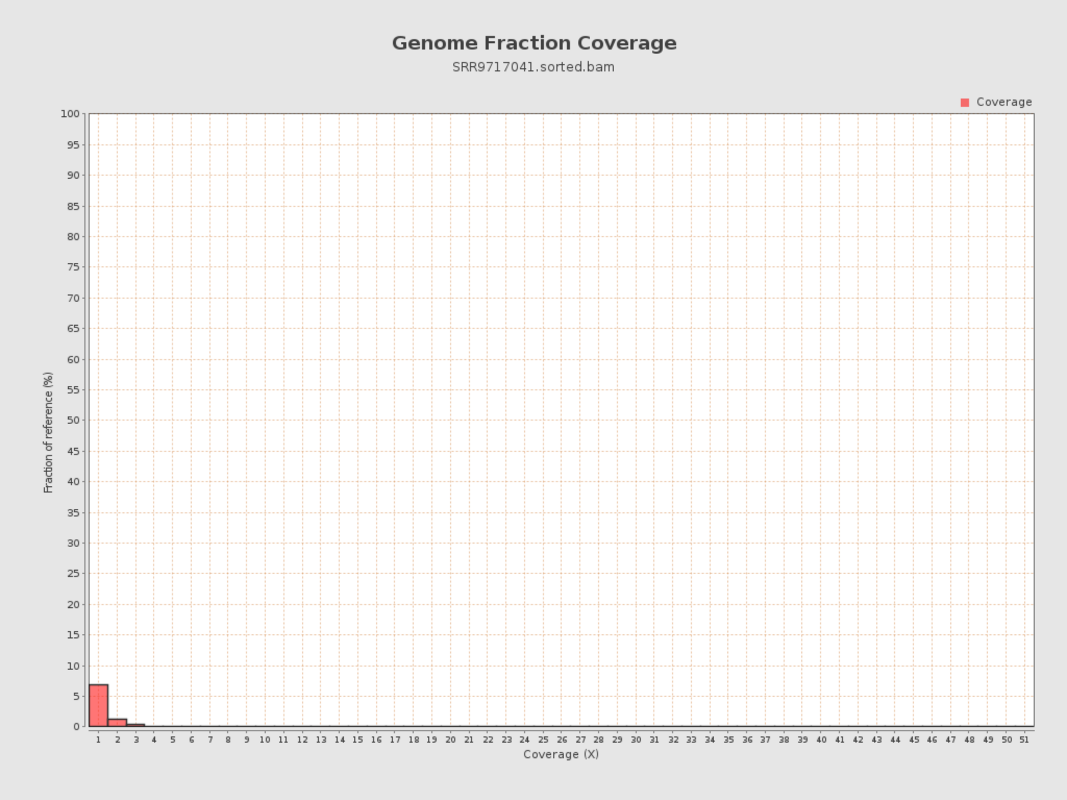
4. Results : Coverage Histogram



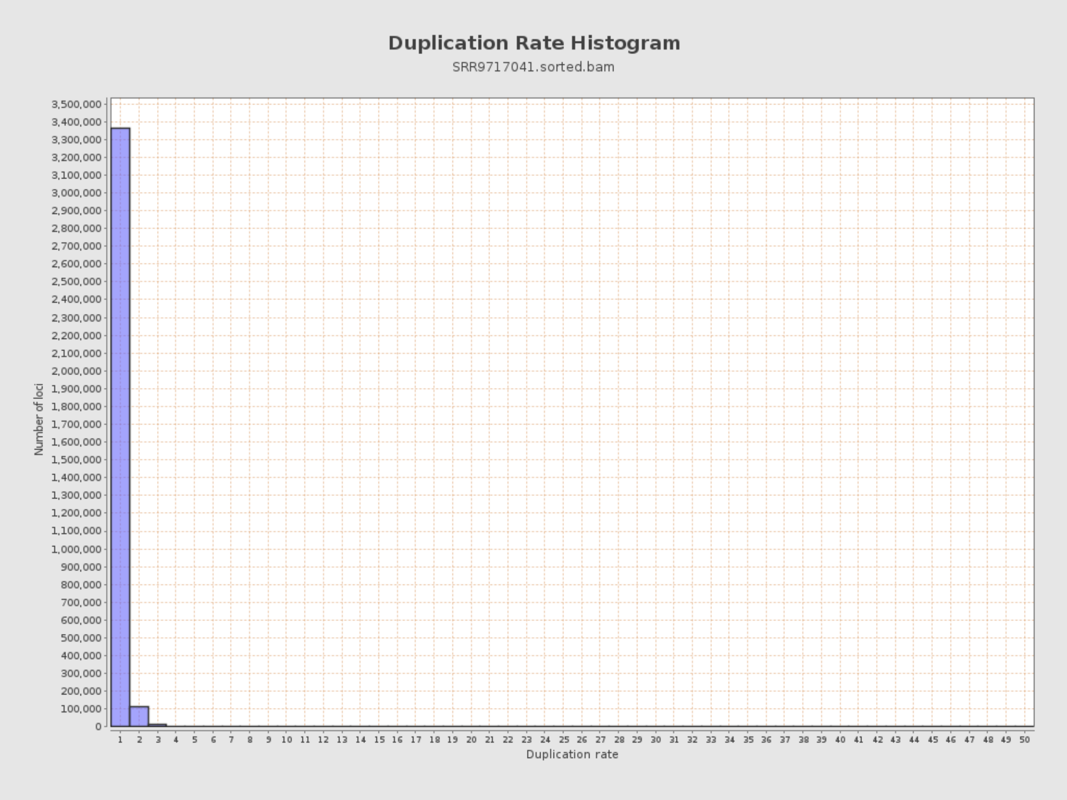
5. Results : Coverage Histogram (0-50X)



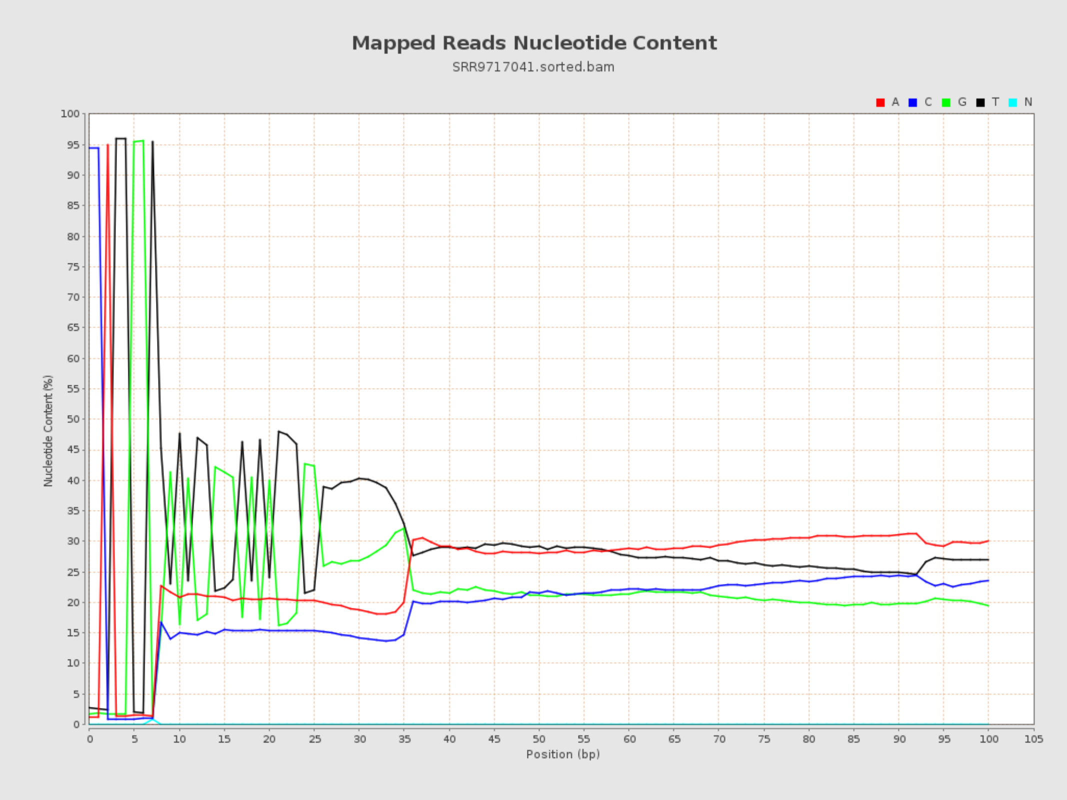
6. Results : Genome Fraction Coverage



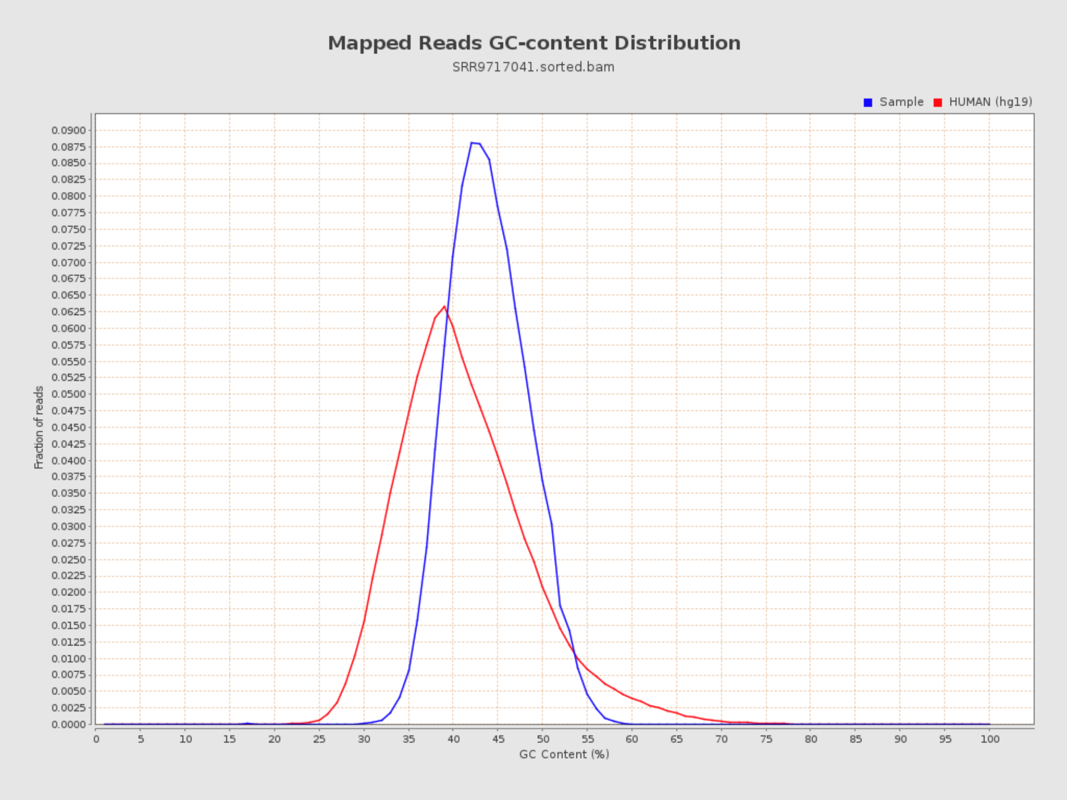
7. Results : Duplication Rate Histogram



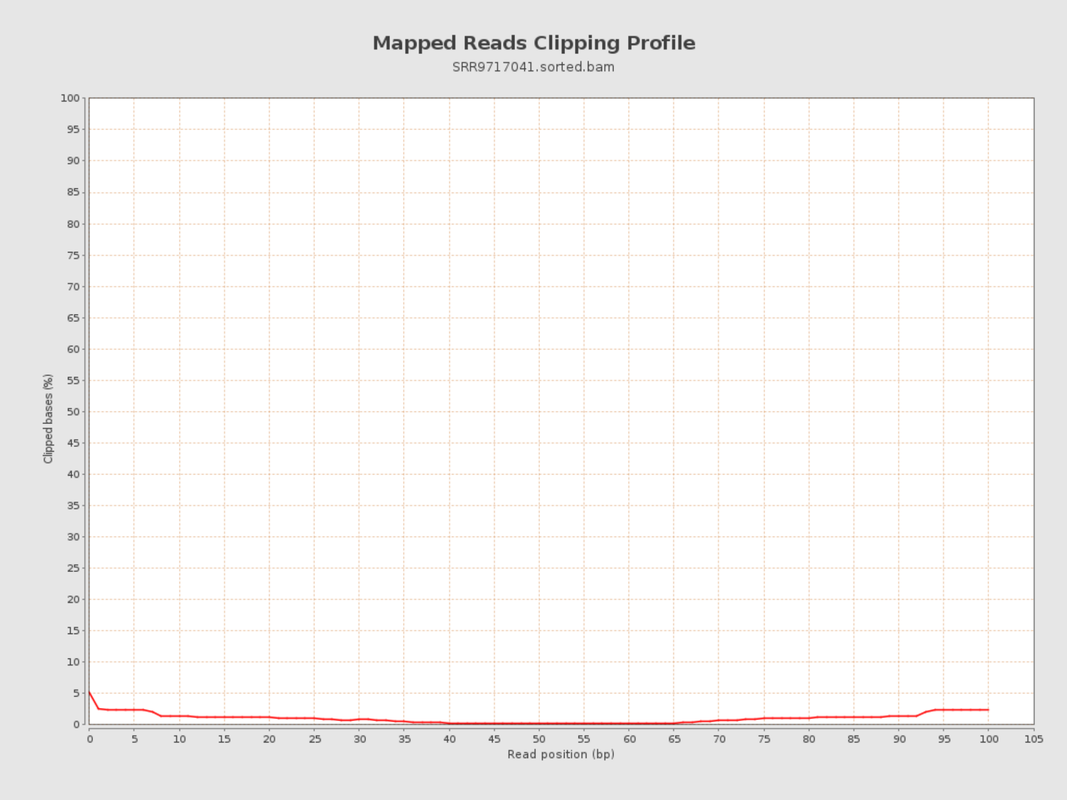
8. Results : Mapped Reads Nucleotide Content



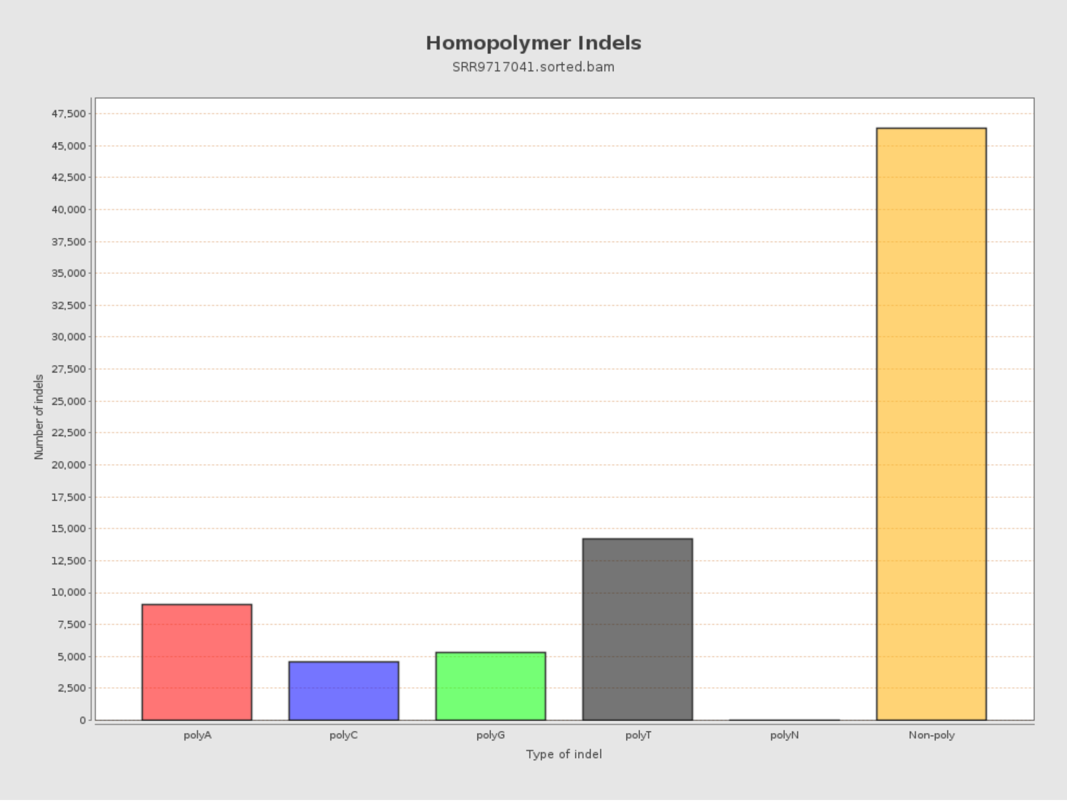
9. Results : Mapped Reads GC-content Distribution



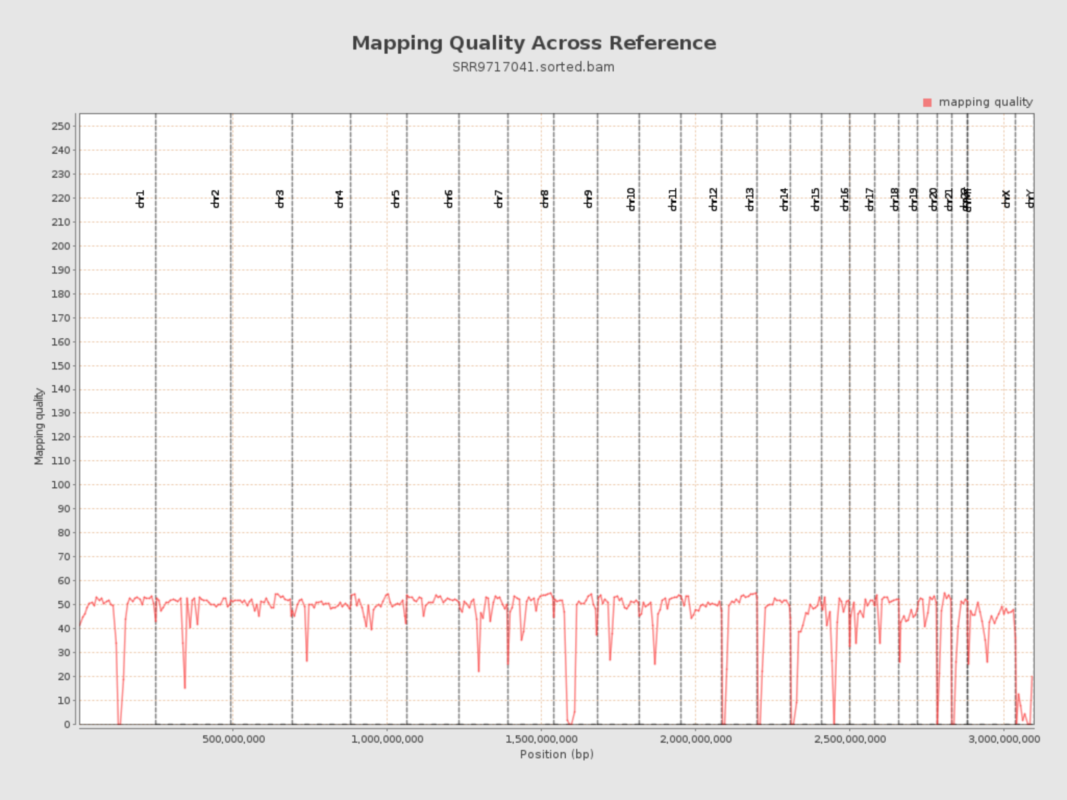
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram