Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:28:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717090.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_SRR9717090 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717090.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:28:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717090.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,818,468
Mapped reads	1,593,134 / 87.61%
Unmapped reads	225,334 / 12.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,629 / 1.3%
Read min/max/mean length	30 / 101 / 101.48
Duplicated reads (estimated)	74,281 / 4.08%
Duplication rate	2.9%
Clipped reads	1,614,109 / 88.76%

2.2. ACGT Content

Number/percentage of A's	31,427,972 / 25.17%
Number/percentage of C's	23,723,059 / 19%
Number/percentage of T's	39,338,532 / 31.51%
Number/percentage of G's	30,347,514 / 24.31%
Number/percentage of N's	7,067 / 0.01%
GC Percentage	43.31%

2.3. Coverage

Mean	0.0403

Standard Deviation	0.4685

2.4. Mapping Quality

Mean Mapping Quality	44.57

2.5. Mismatches and indels

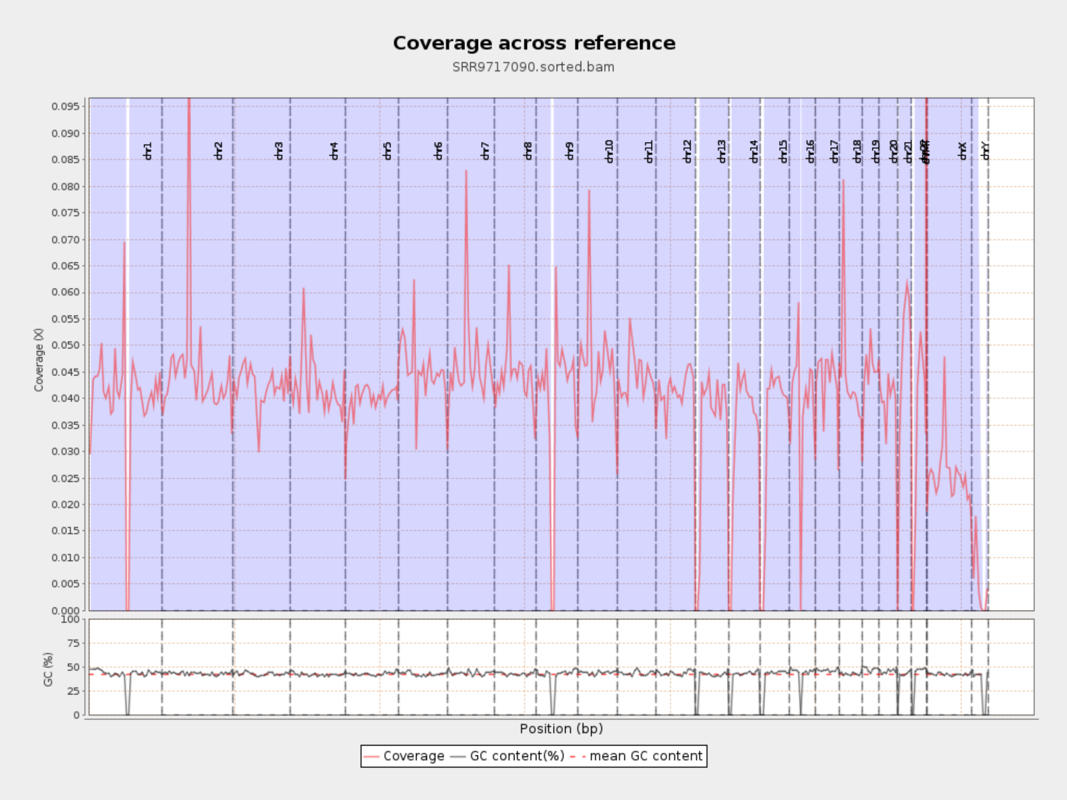
General error rate	0.87%
Mismatches	1,061,126
Insertions	11,619
Mapped reads with at least one insertion	0.72%
Deletions	29,966
Mapped reads with at least one deletion	1.85%
Homopolymer indels	43.55%

2.6. Chromosome stats

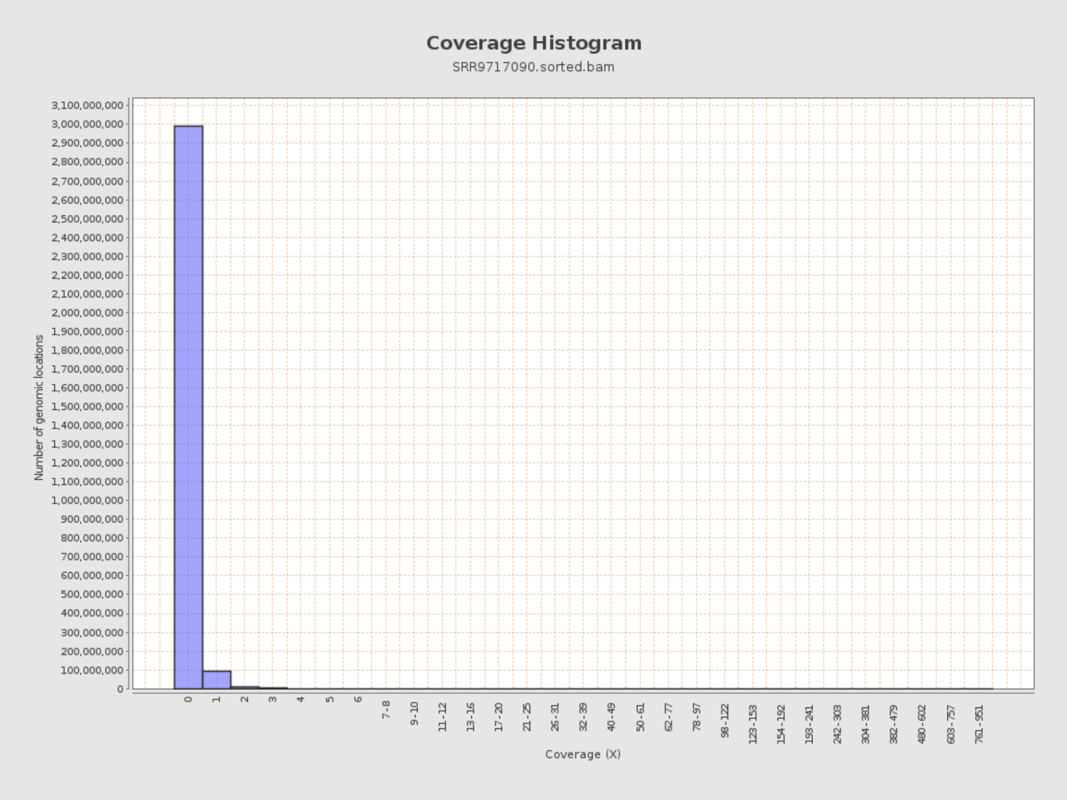
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9936369	0.0399	0.6805
chr2	243199373	11114222	0.0457	0.7173
chr3	198022430	8375560	0.0423	0.2353
chr4	191154276	8103543	0.0424	0.2579
chr5	180915260	7247876	0.0401	0.2359
chr6	171115067	7784335	0.0455	0.3171
chr7	159138663	7484738	0.047	0.6165

chr8	146364022	6490640	0.0443	0.6359
chr9	141213431	5670864	0.0402	0.5309
chr10	135534747	6354136	0.0469	0.4378
chr11	135006516	5918581	0.0438	0.4625
chr12	133851895	5533815	0.0413	0.2398
chr13	115169878	3857243	0.0335	0.2059
chr14	107349540	3657291	0.0341	0.2982
chr15	102531392	3480205	0.0339	0.2145
chr16	90354753	3514598	0.0389	0.2801
chr17	81195210	3527686	0.0434	0.2668
chr18	78077248	3511620	0.045	1.0743
chr19	59128983	2688051	0.0455	0.5411
chr20	63025520	2470985	0.0392	0.2568
chr21	48129895	2226195	0.0463	0.267
chr22	51304566	1632110	0.0318	0.2036
chrMT	16571	7483	0.4516	0.7912
chrX	155270560	4014594	0.0259	0.3138
chrY	59373566	293572	0.0049	0.1494

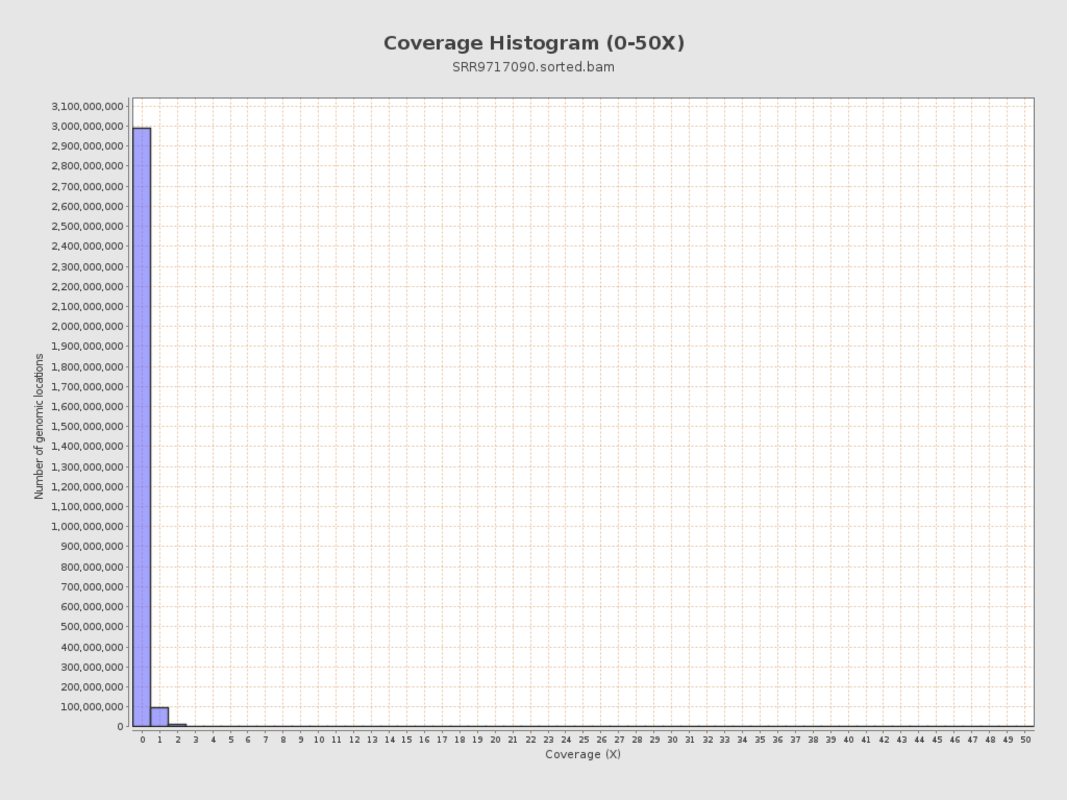
3. Results : Coverage across reference



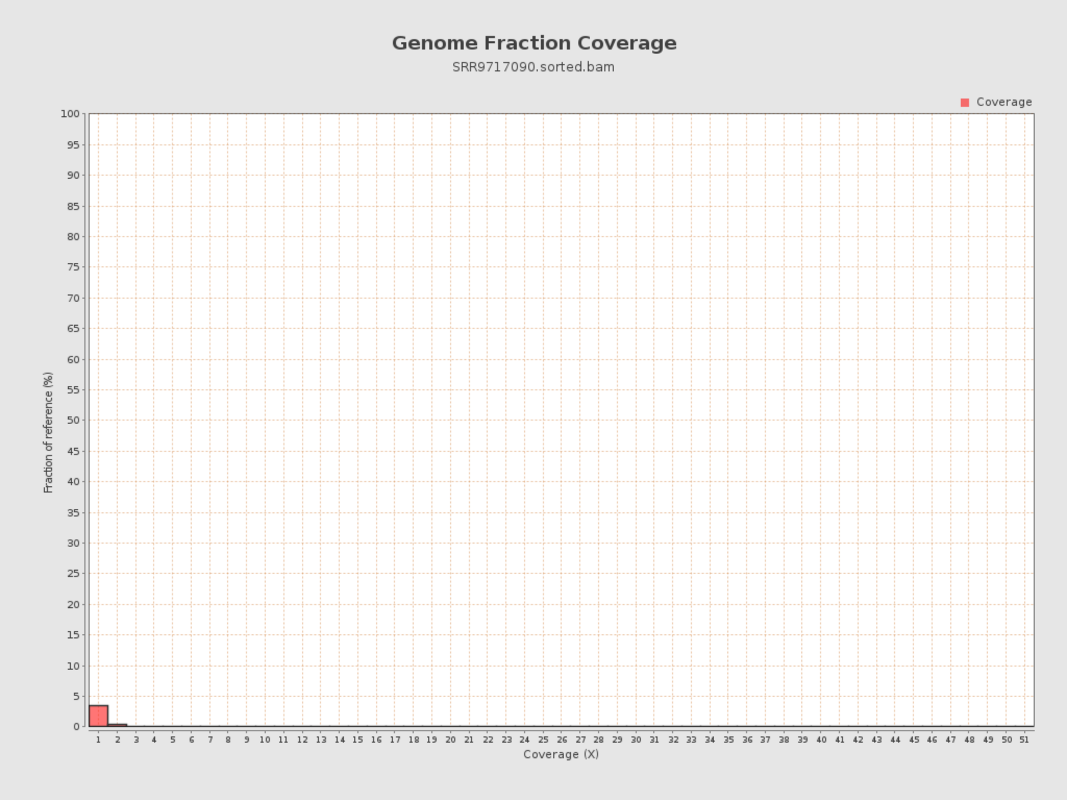
4. Results : Coverage Histogram



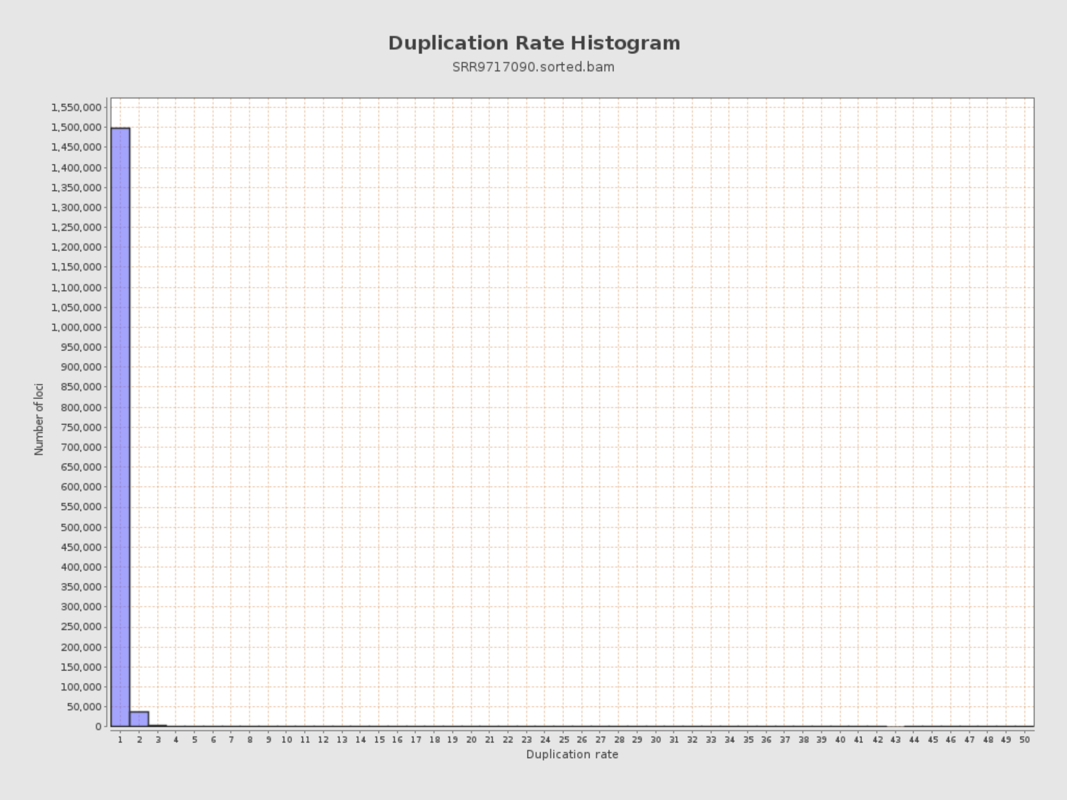
5. Results : Coverage Histogram (0-50X)



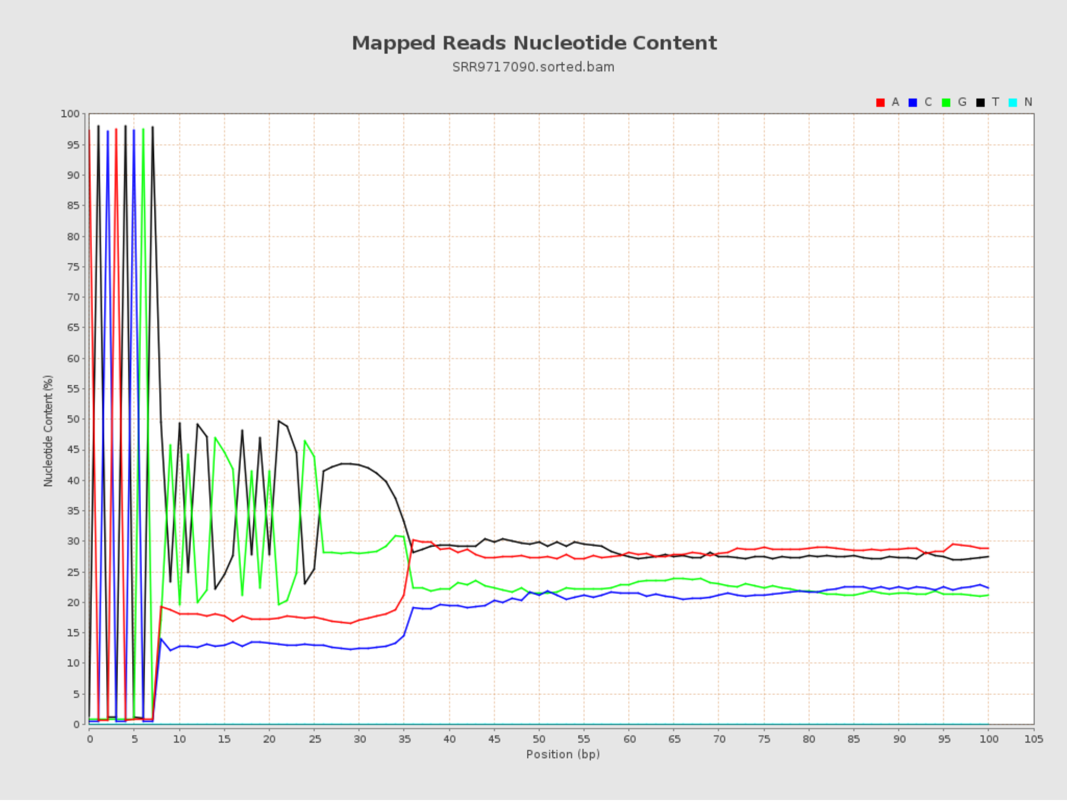
6. Results : Genome Fraction Coverage



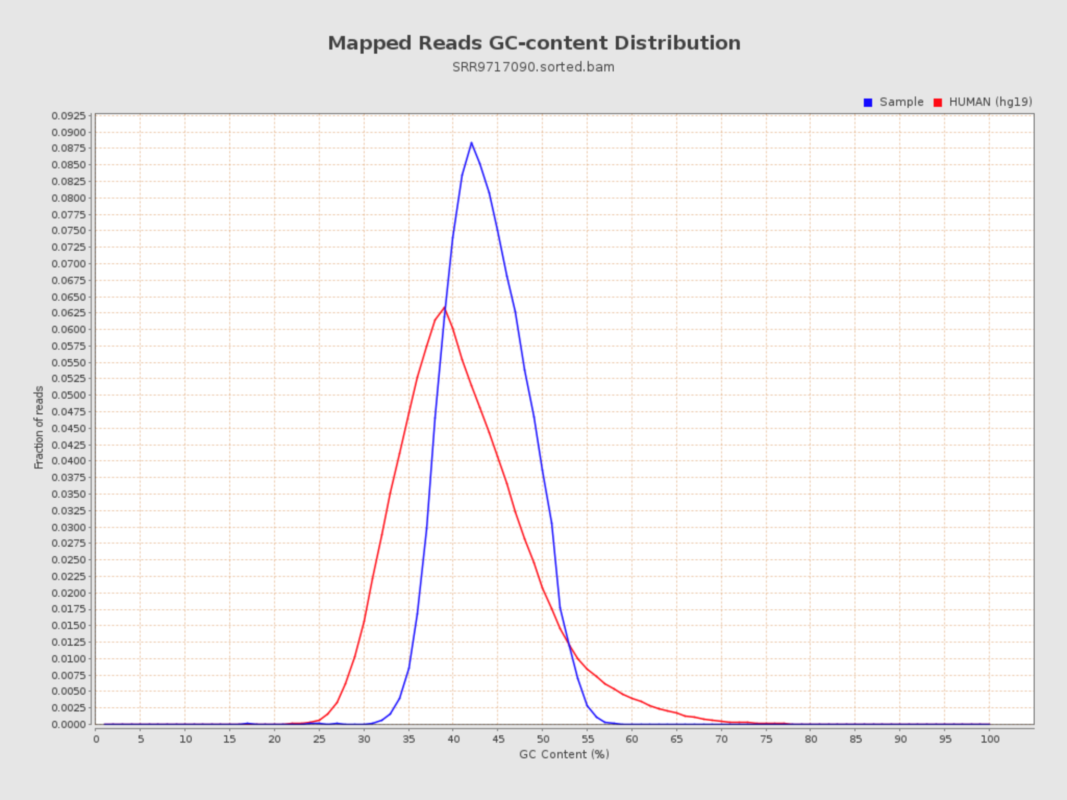
7. Results : Duplication Rate Histogram



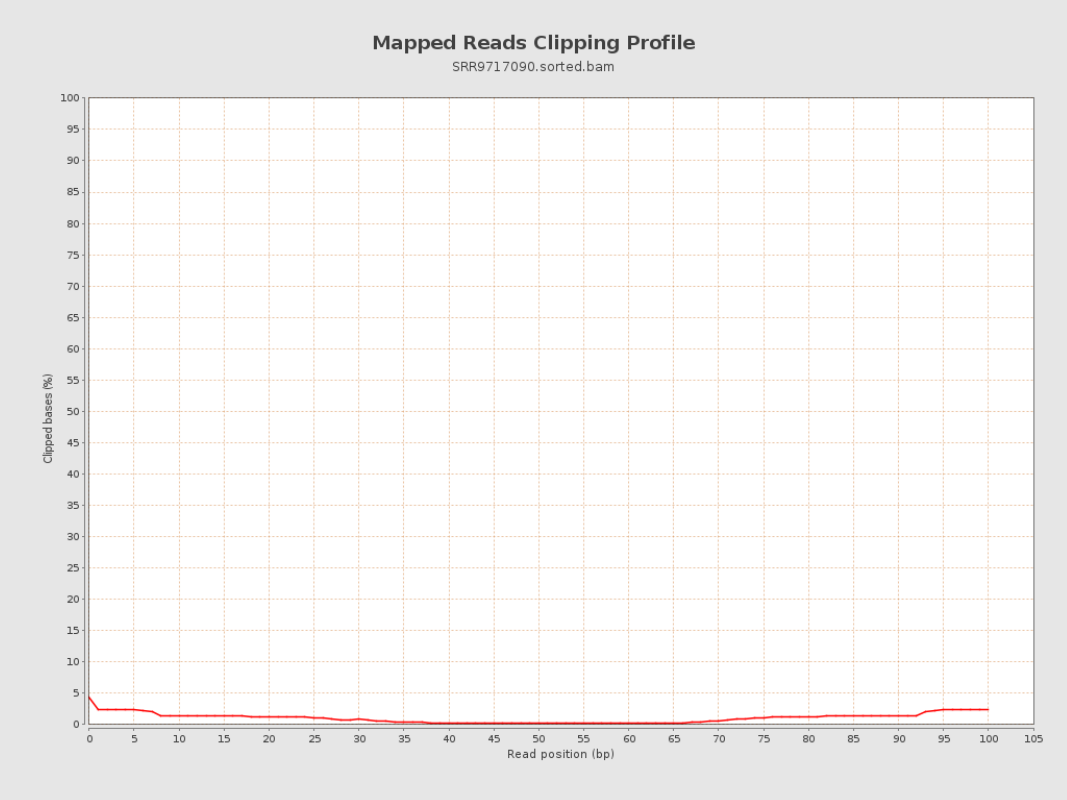
8. Results : Mapped Reads Nucleotide Content



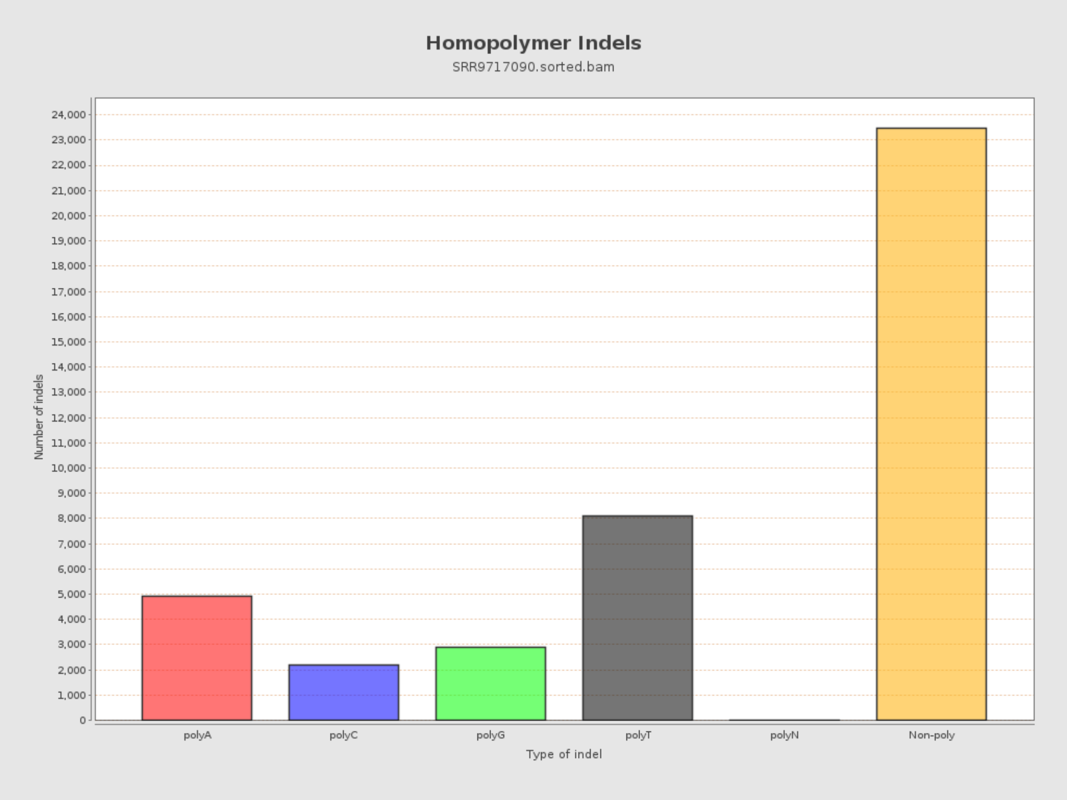
9. Results : Mapped Reads GC-content Distribution



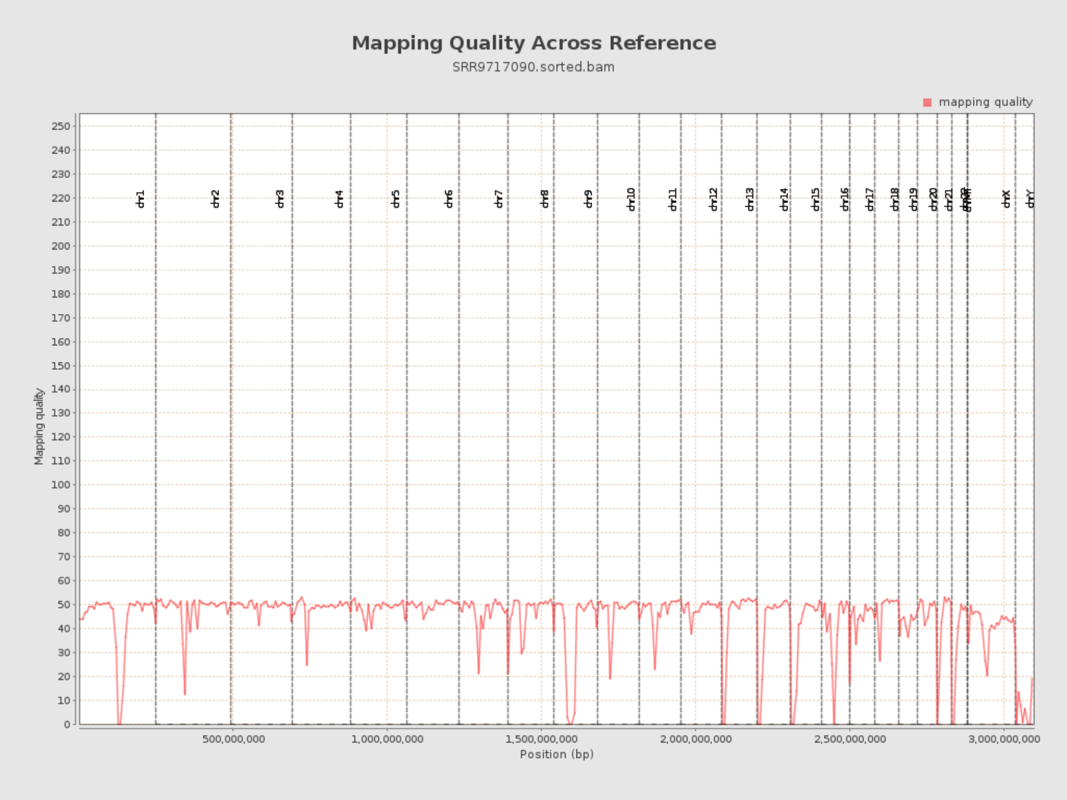
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram