Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:16:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717087.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_SRR9717087 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717087.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:16:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717087.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,628,354
Mapped reads	1,458,571 / 89.57%
Unmapped reads	169,783 / 10.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,602 / 1.45%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	65,317 / 4.01%
Duplication rate	2.68%
Clipped reads	1,479,537 / 90.86%

2.2. ACGT Content

Number/percentage of A's	28,891,455 / 25.29%
Number/percentage of C's	21,862,528 / 19.14%
Number/percentage of T's	35,854,396 / 31.39%
Number/percentage of G's	27,610,767 / 24.17%
Number/percentage of N's	6,839 / 0.01%
GC Percentage	43.31%

2.3. Coverage

Mean	0.0369

Standard Deviation	0.4544

2.4. Mapping Quality

Mean Mapping Quality	44.26

2.5. Mismatches and indels

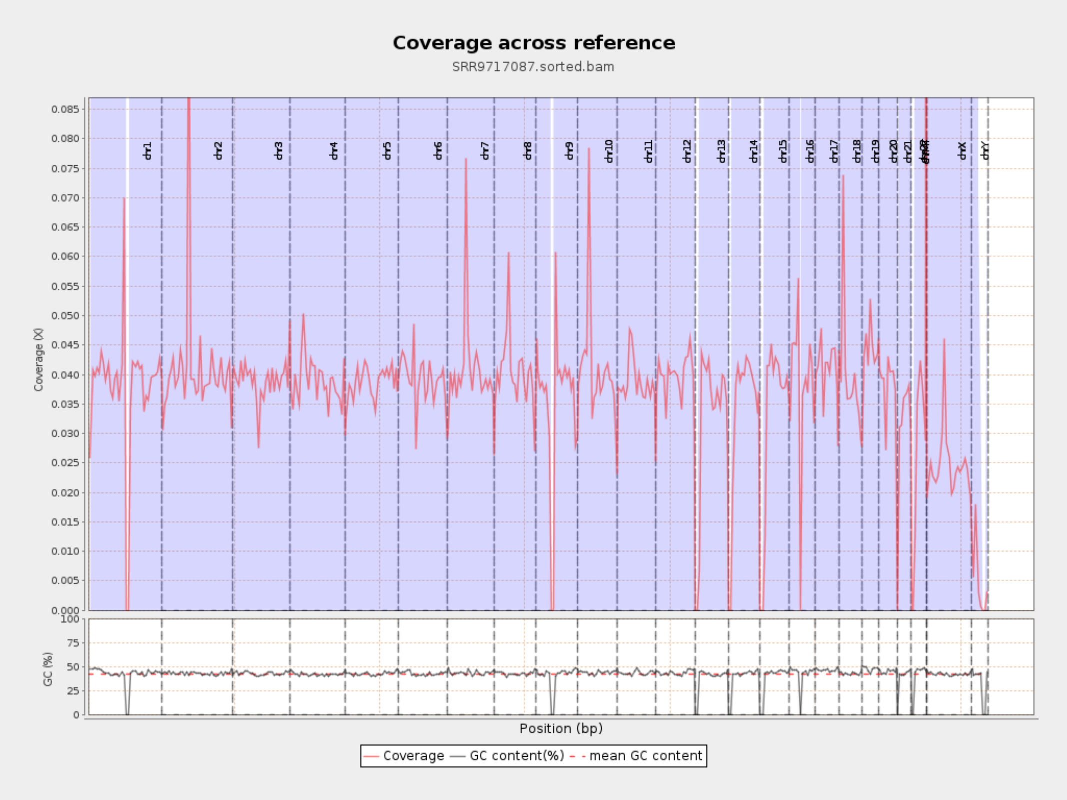
General error rate	0.88%
Mismatches	980,545
Insertions	11,038
Mapped reads with at least one insertion	0.75%
Deletions	27,662
Mapped reads with at least one deletion	1.87%
Homopolymer indels	43.61%

2.6. Chromosome stats

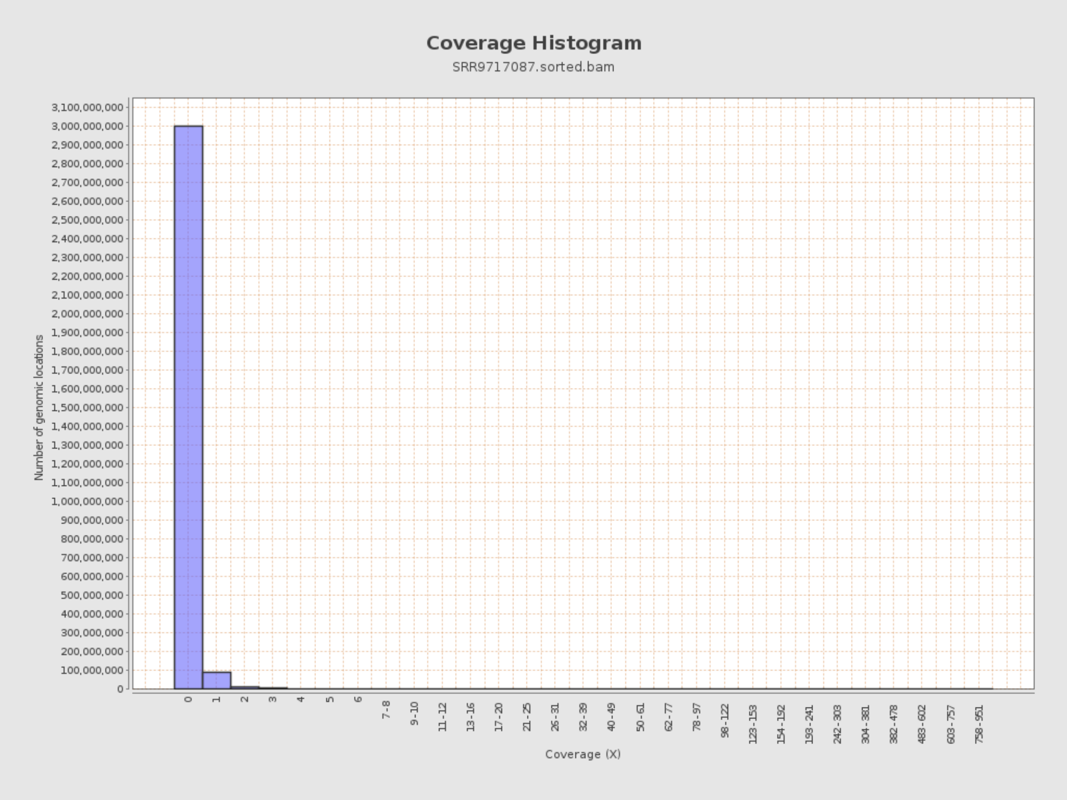
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9397270	0.0377	0.7195
chr2	243199373	10075643	0.0414	0.7106
chr3	198022430	7701192	0.0389	0.2266
chr4	191154276	7420605	0.0388	0.2416
chr5	180915260	7009586	0.0387	0.2266
chr6	171115067	6715863	0.0392	0.2786
chr7	159138663	6552096	0.0412	0.5908

chr8	146364022	5903661	0.0403	0.6095
chr9	141213431	4940322	0.035	0.5055
chr10	135534747	5587187	0.0412	0.4299
chr11	135006516	5192314	0.0385	0.4061
chr12	133851895	5328111	0.0398	0.2341
chr13	115169878	3679683	0.032	0.1984
chr14	107349540	3553700	0.0331	0.2852
chr15	102531392	3347599	0.0326	0.2069
chr16	90354753	3451283	0.0382	0.2594
chr17	81195210	3303340	0.0407	0.2606
chr18	78077248	3179021	0.0407	0.9758
chr19	59128983	2614351	0.0442	0.5535
chr20	63025520	2371837	0.0376	0.2382
chr21	48129895	1491052	0.031	0.2143
chr22	51304566	1309288	0.0255	0.1787
chrMT	16571	11723	0.7074	0.9808
chrX	155270560	3851509	0.0248	0.2788
chrY	59373566	285695	0.0048	0.1493

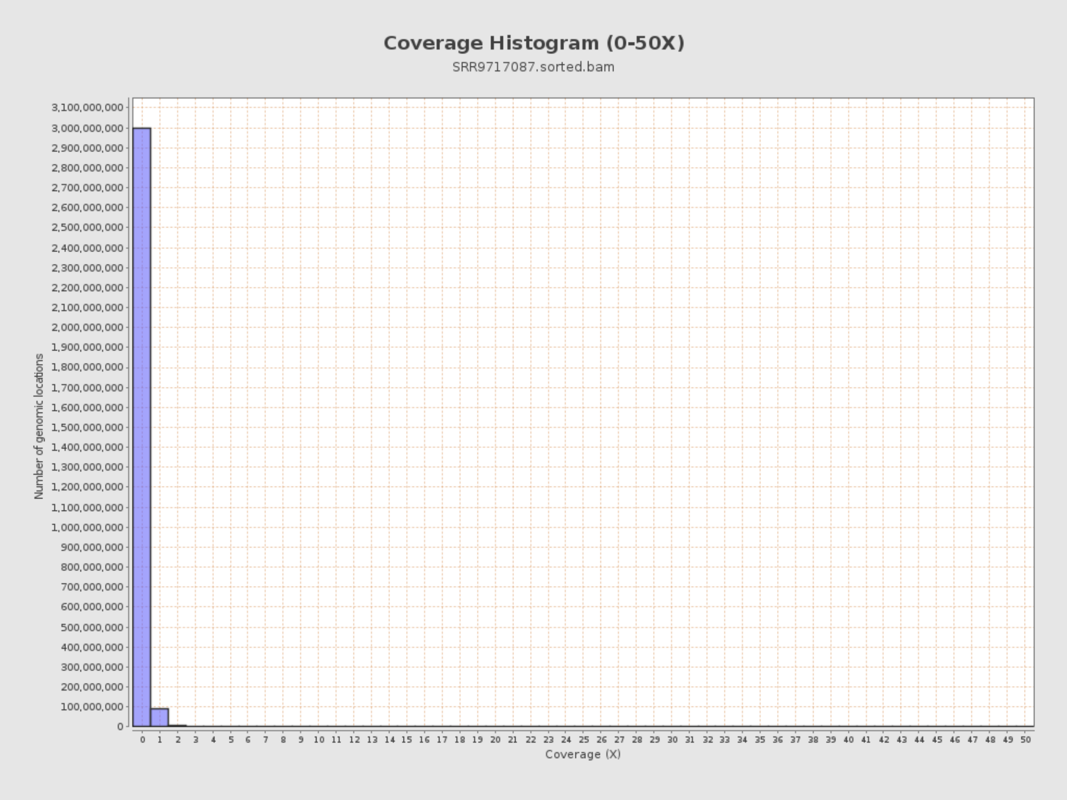
3. Results : Coverage across reference



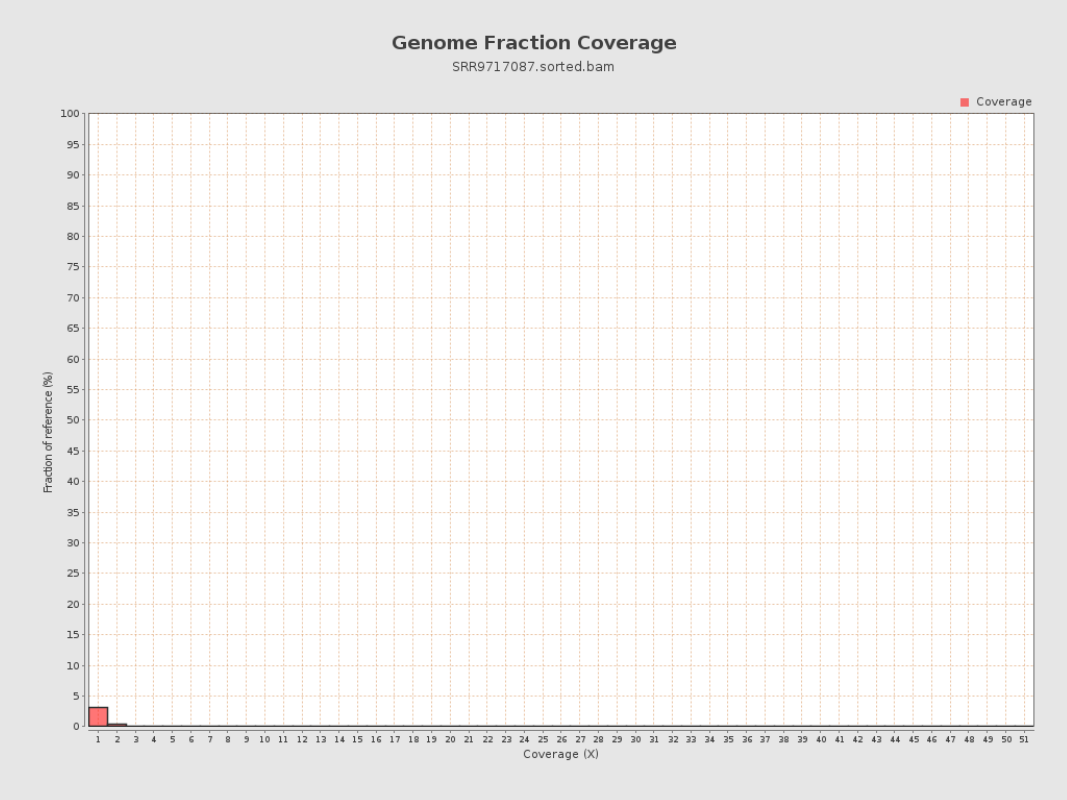
4. Results : Coverage Histogram



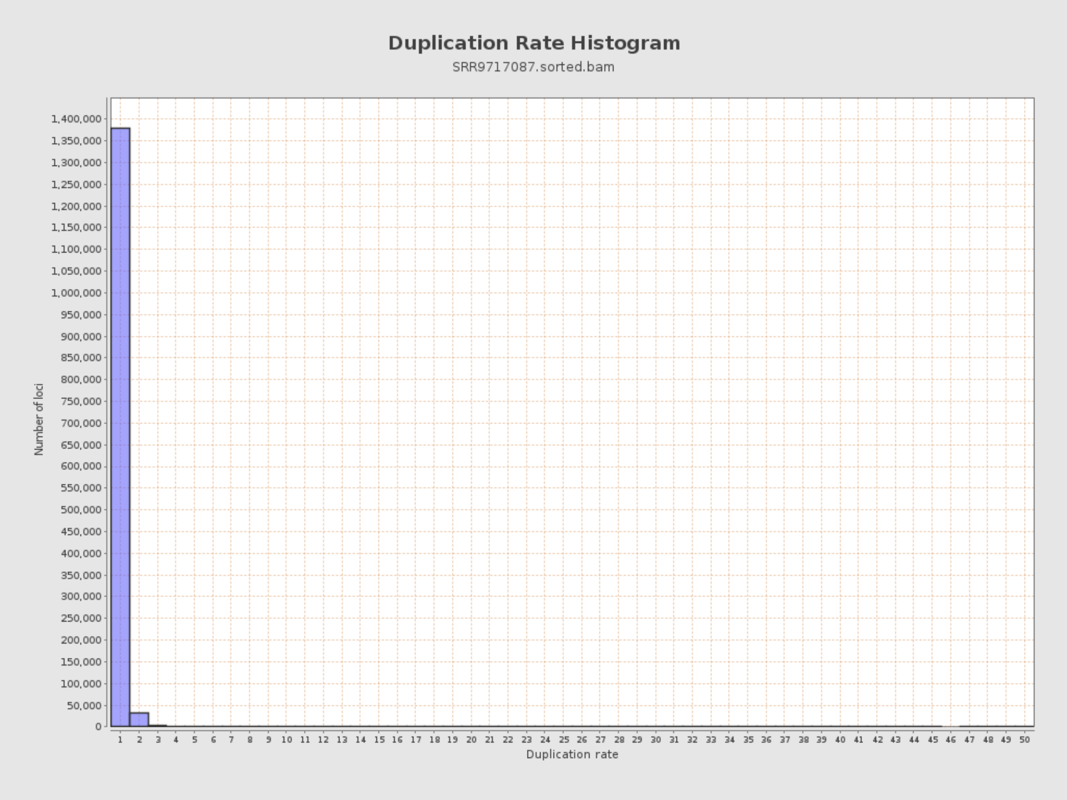
5. Results : Coverage Histogram (0-50X)



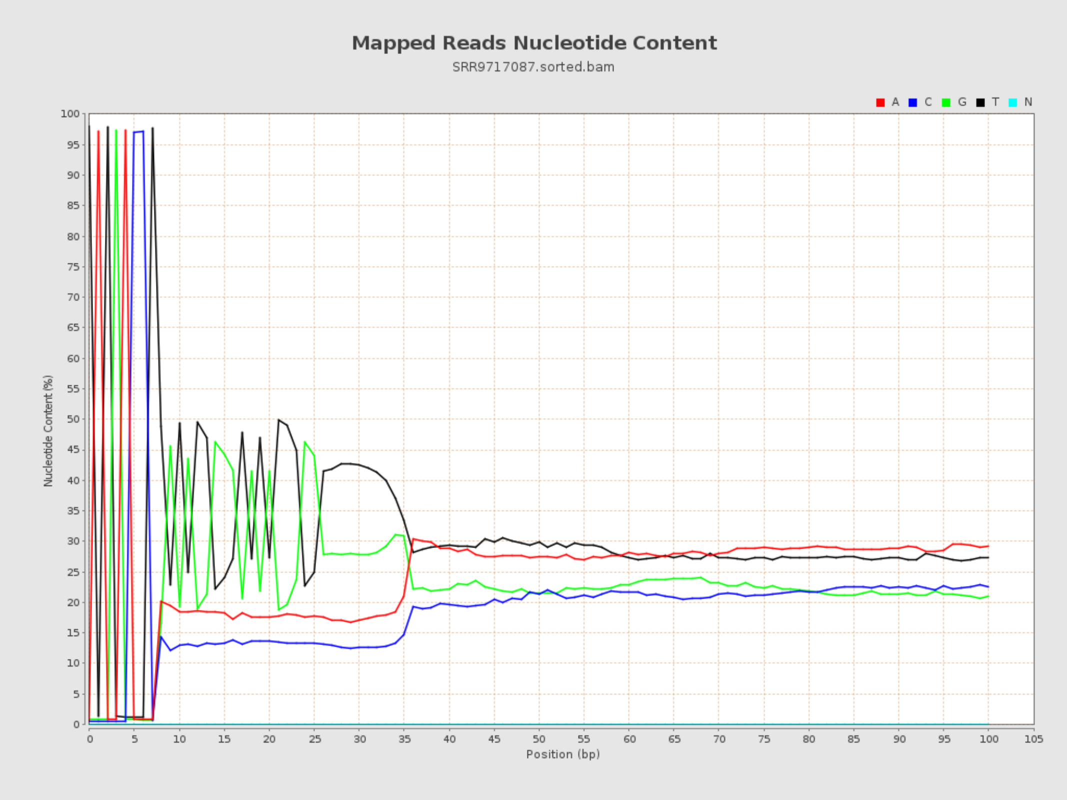
6. Results : Genome Fraction Coverage



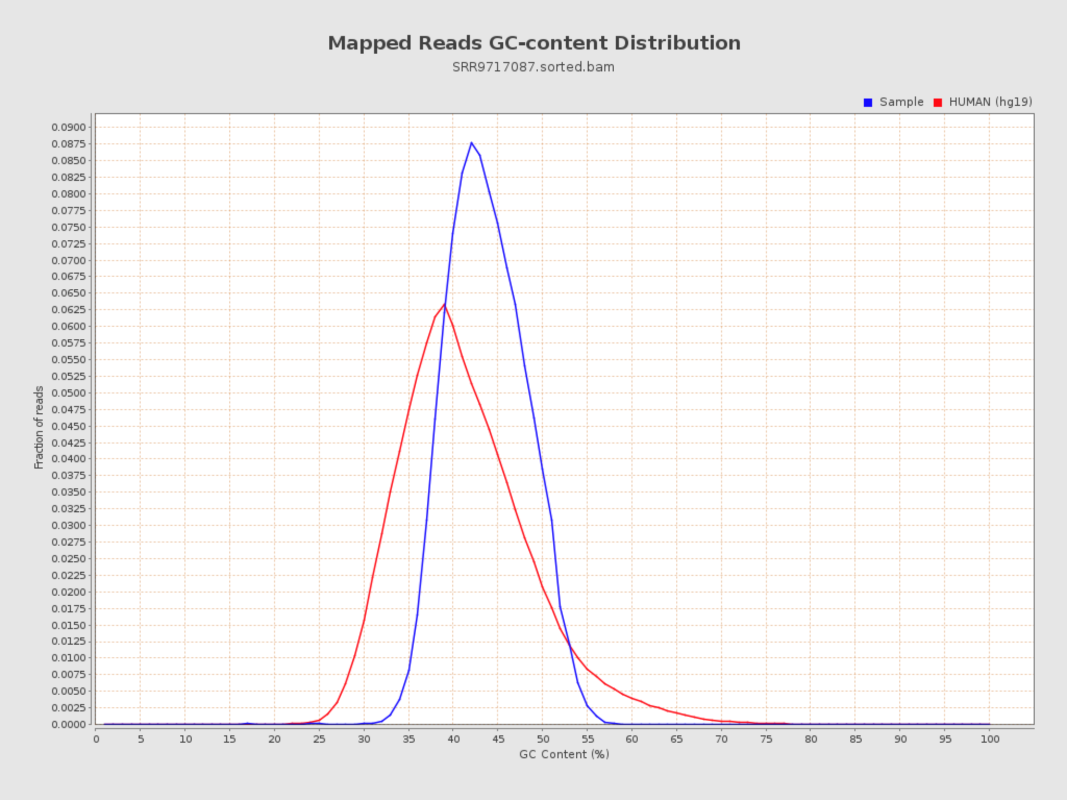
7. Results : Duplication Rate Histogram



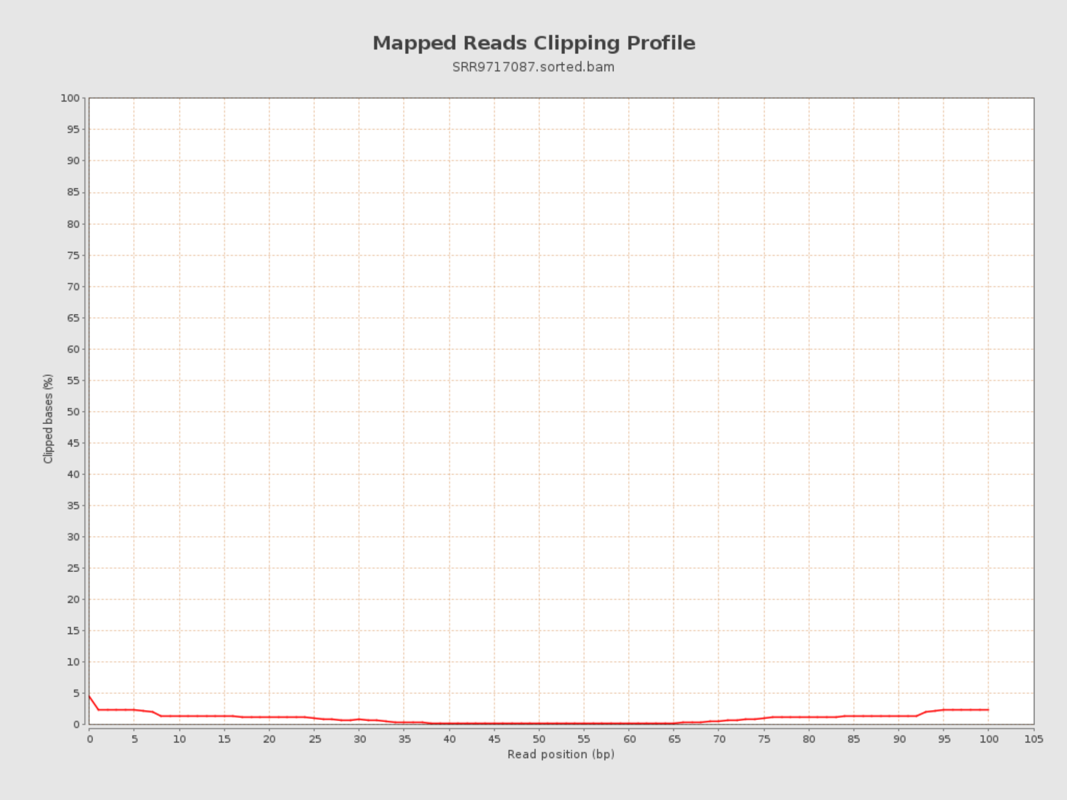
8. Results : Mapped Reads Nucleotide Content



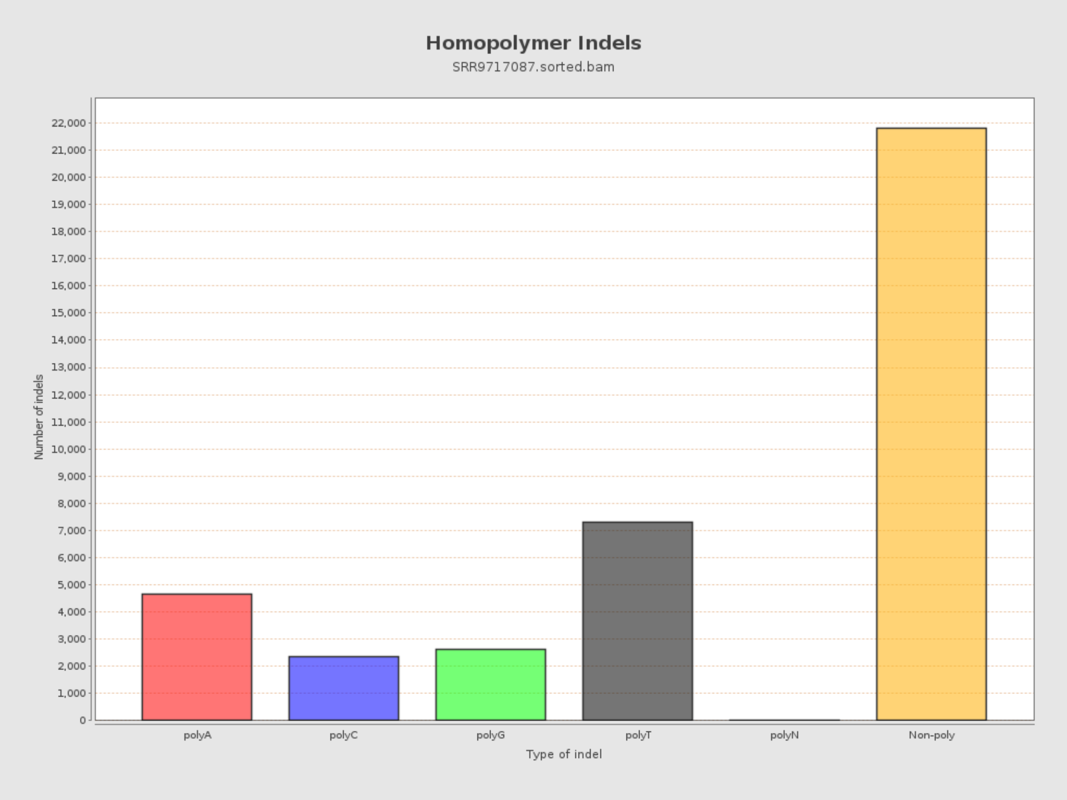
9. Results : Mapped Reads GC-content Distribution



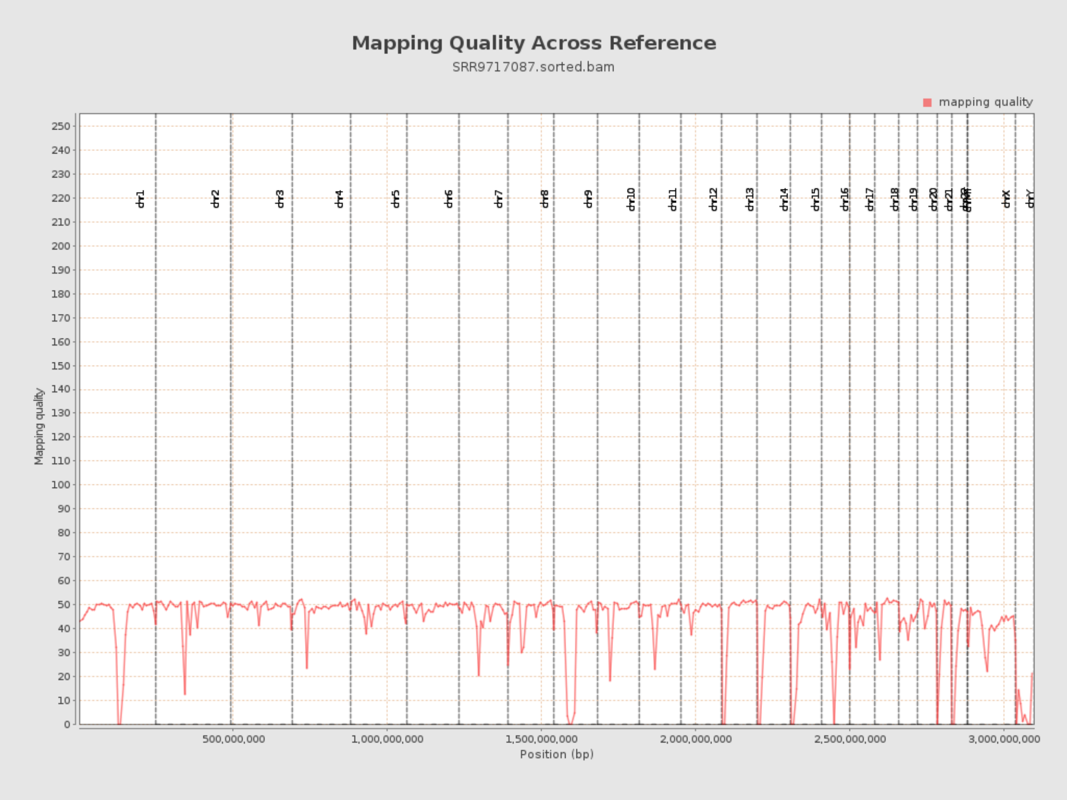
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram