Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:11:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717085.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_SRR9717085 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717085.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:10:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717085.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,072,377
Mapped reads	1,877,843 / 90.61%
Unmapped reads	194,534 / 9.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,817 / 1.44%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	89,227 / 4.31%
Duplication rate	3.02%
Clipped reads	1,902,382 / 91.8%

2.2. ACGT Content

Number/percentage of A's	38,527,923 / 26.09%
Number/percentage of C's	27,161,613 / 18.39%
Number/percentage of T's	45,749,656 / 30.98%
Number/percentage of G's	36,230,754 / 24.53%
Number/percentage of N's	8,541 / 0.01%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.5163

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

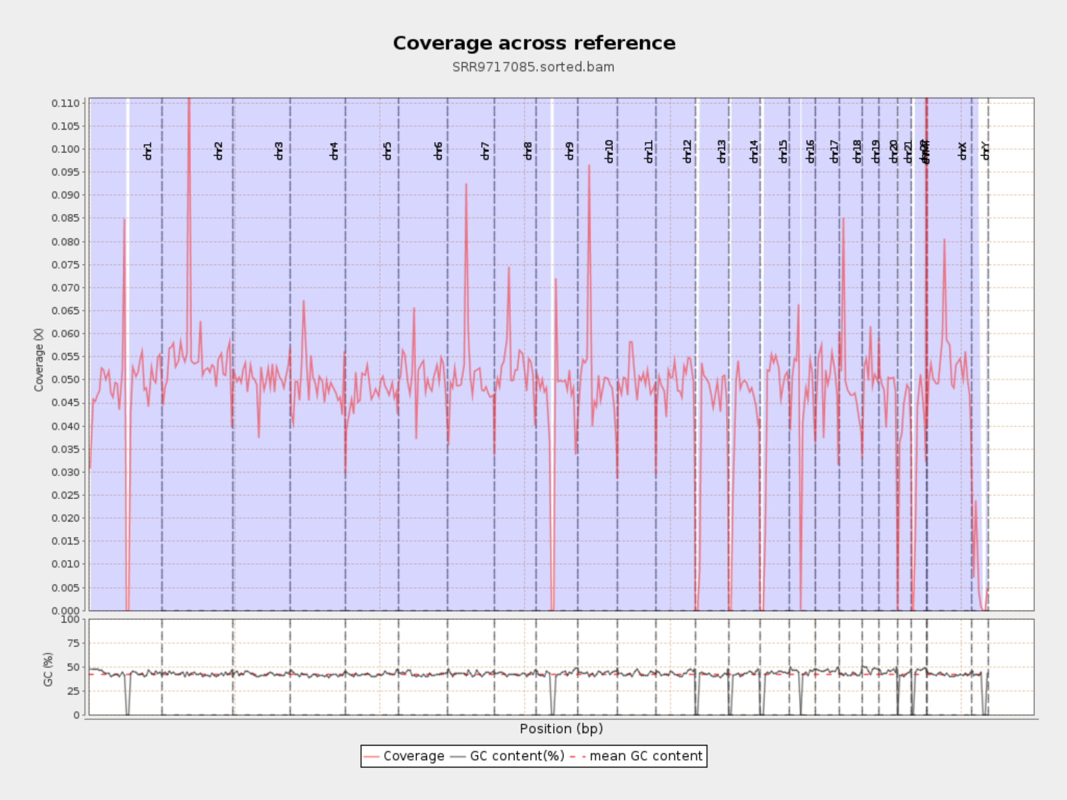
General error rate	0.86%
Mismatches	1,234,306
Insertions	15,065
Mapped reads with at least one insertion	0.79%
Deletions	35,565
Mapped reads with at least one deletion	1.86%
Homopolymer indels	43.03%

2.6. Chromosome stats

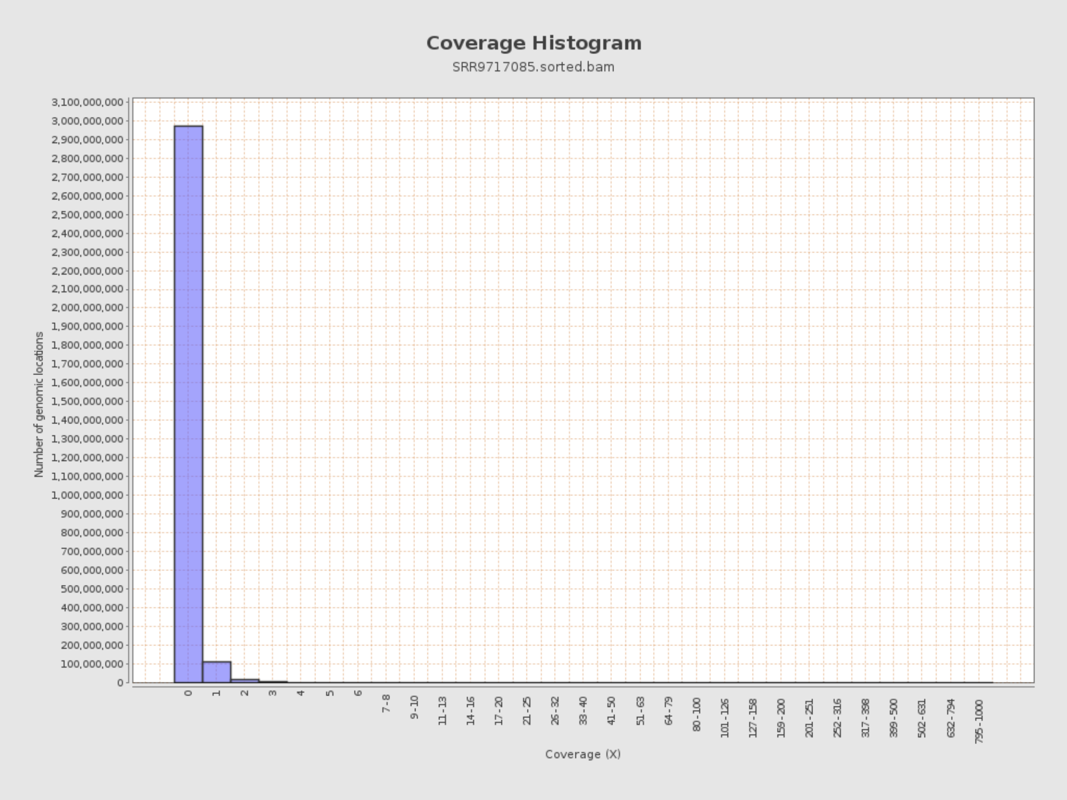
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11745812	0.0471	0.8254
chr2	243199373	13575199	0.0558	0.7483
chr3	198022430	9925413	0.0501	0.26
chr4	191154276	9393344	0.0491	0.2822
chr5	180915260	8566934	0.0474	0.2547
chr6	171115067	8724098	0.051	0.3374
chr7	159138663	8206137	0.0516	0.6598

chr8	146364022	7725967	0.0528	0.6906
chr9	141213431	6133230	0.0434	0.6011
chr10	135534747	6877752	0.0507	0.522
chr11	135006516	6703555	0.0497	0.4917
chr12	133851895	6631258	0.0495	0.2658
chr13	115169878	4631134	0.0402	0.2276
chr14	107349540	4323401	0.0403	0.3438
chr15	102531392	4281033	0.0418	0.2386
chr16	90354753	4125372	0.0457	0.2881
chr17	81195210	3994741	0.0492	0.2958
chr18	78077248	3975093	0.0509	1.0992
chr19	59128983	3070017	0.0519	0.613
chr20	63025520	2972475	0.0472	0.2717
chr21	48129895	1864900	0.0387	0.2534
chr22	51304566	1597747	0.0311	0.2013
chrMT	16571	15786	0.9526	1.1655
chrX	155270560	8268830	0.0533	0.3779
chrY	59373566	411674	0.0069	0.2083

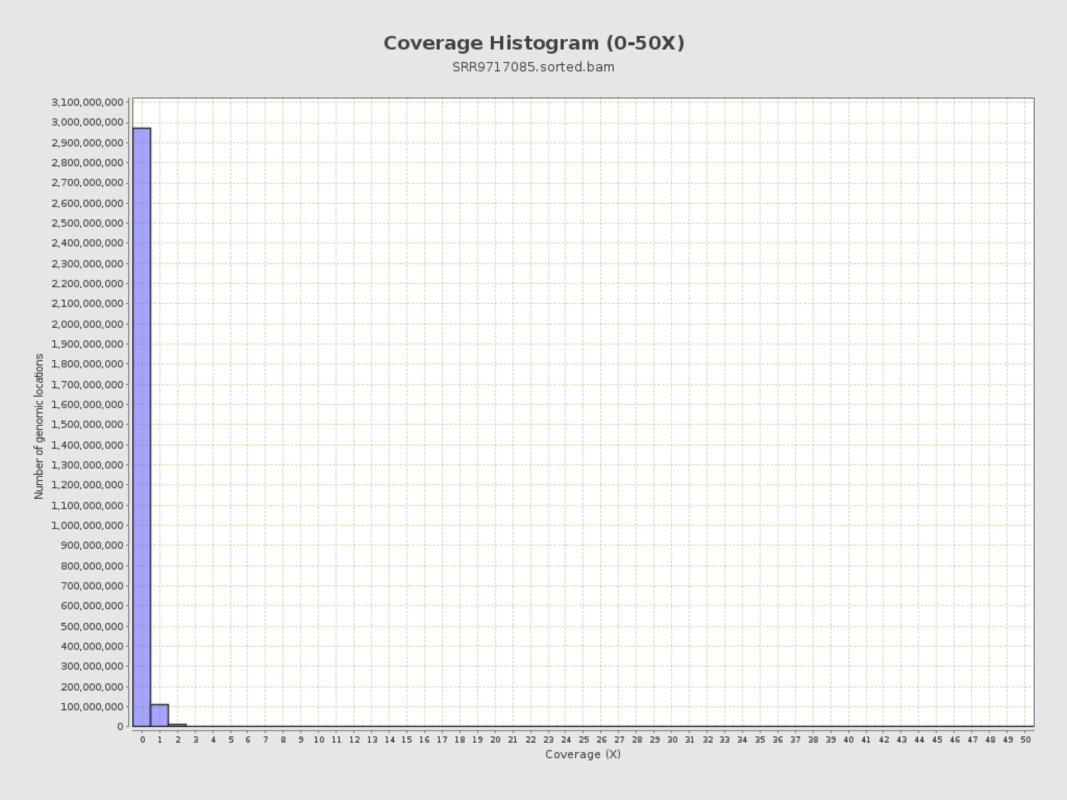
3. Results : Coverage across reference



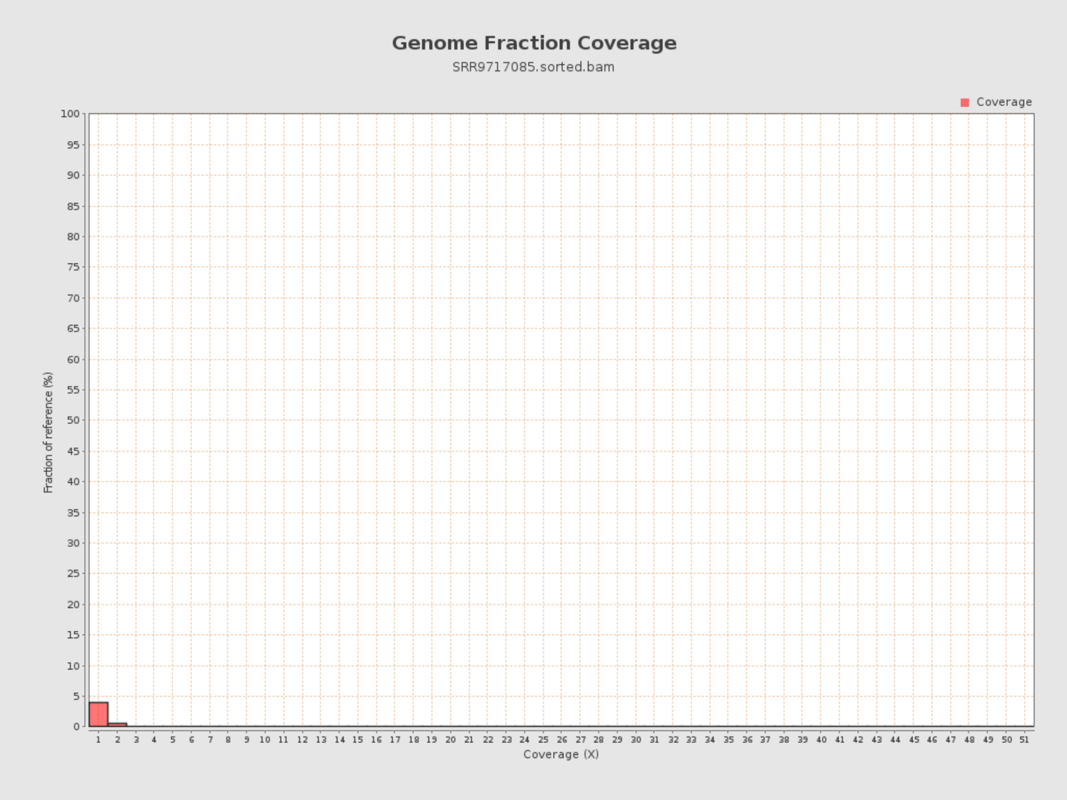
4. Results : Coverage Histogram



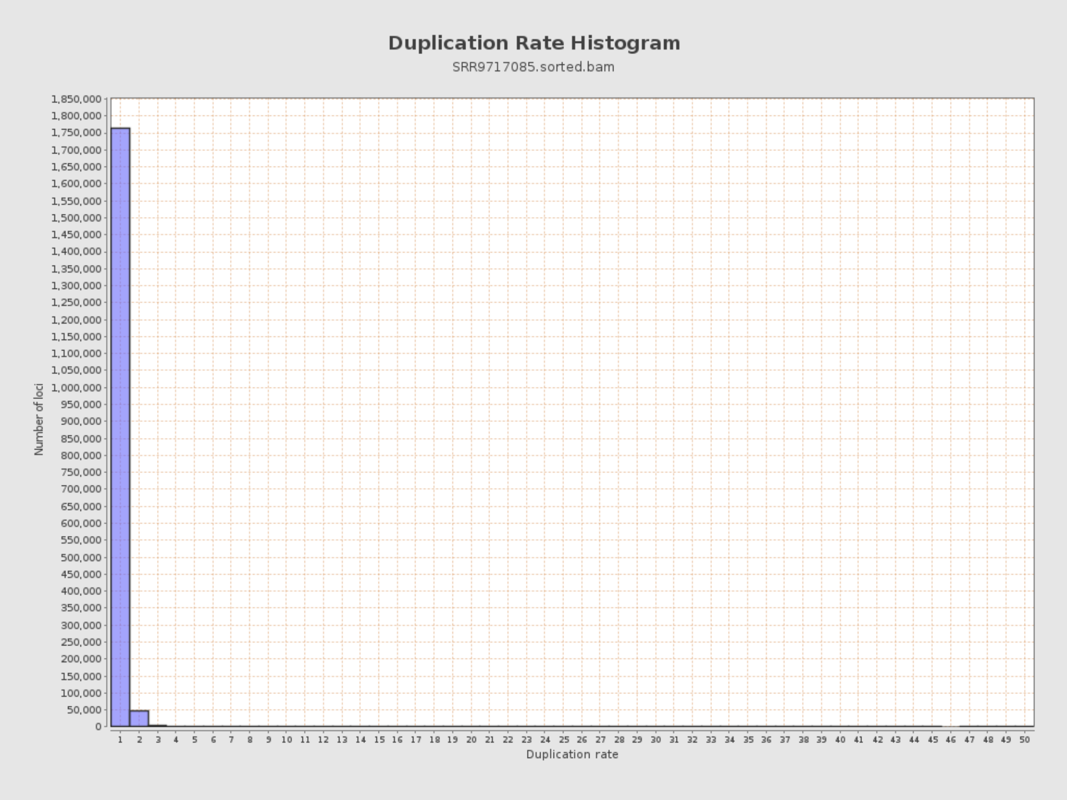
5. Results : Coverage Histogram (0-50X)



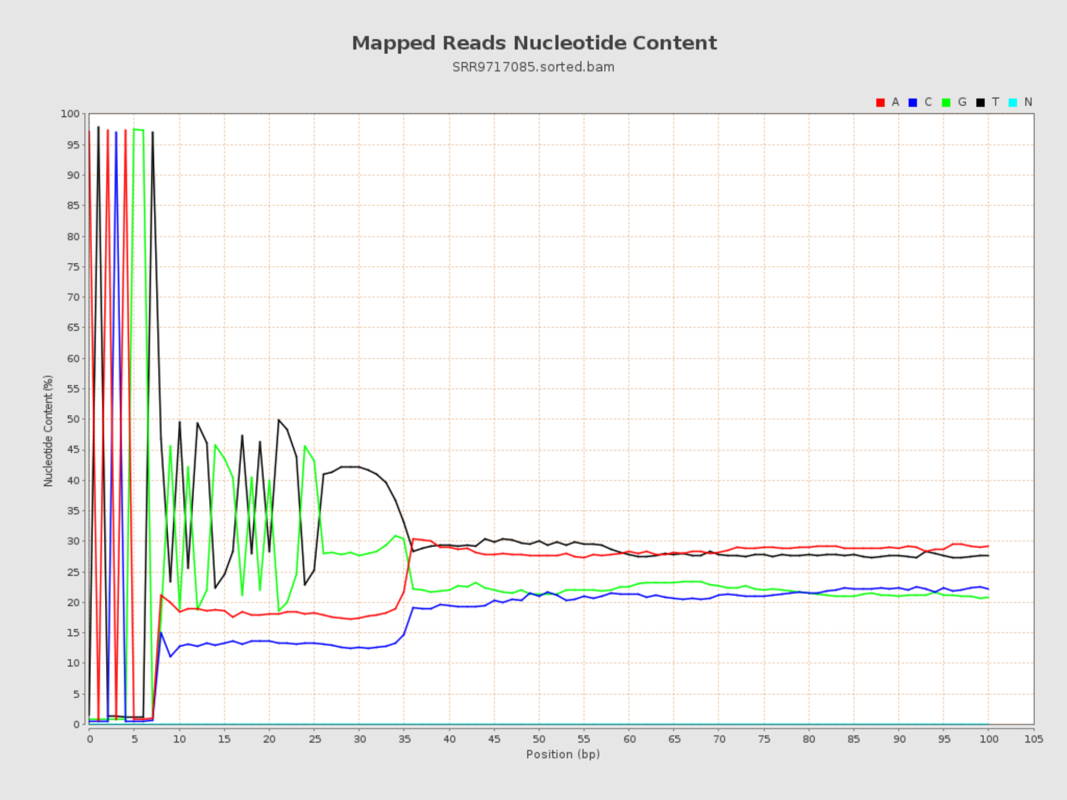
6. Results : Genome Fraction Coverage



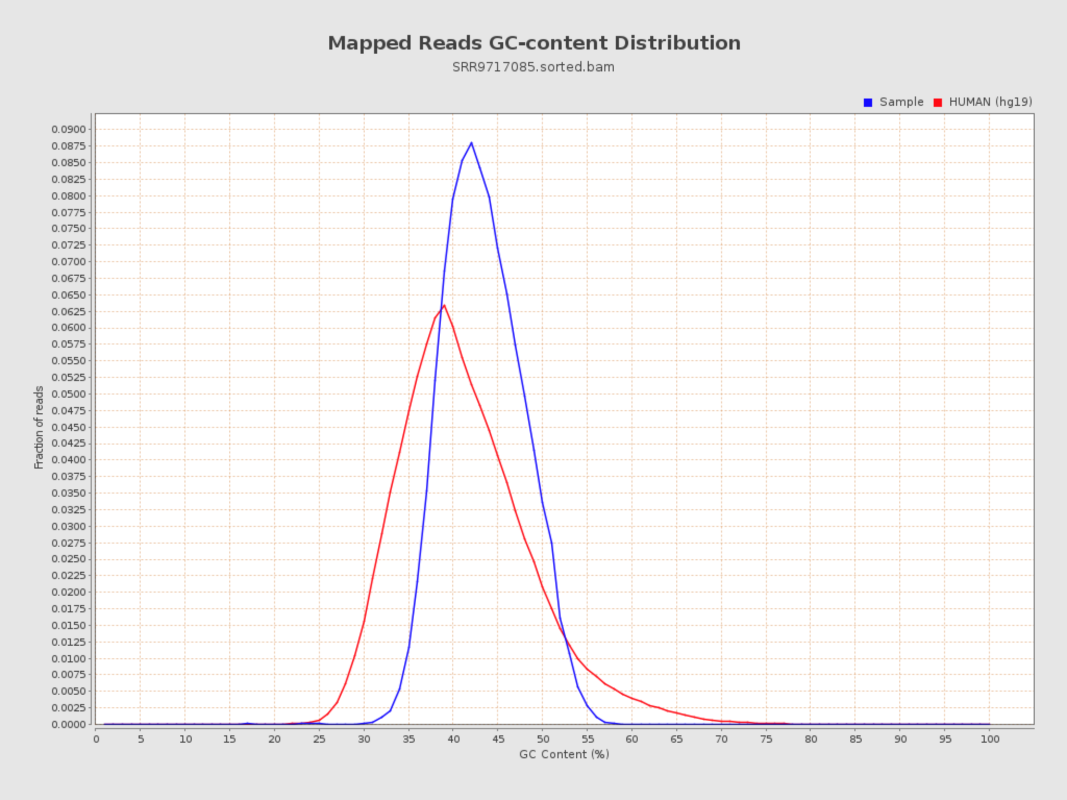
7. Results : Duplication Rate Histogram



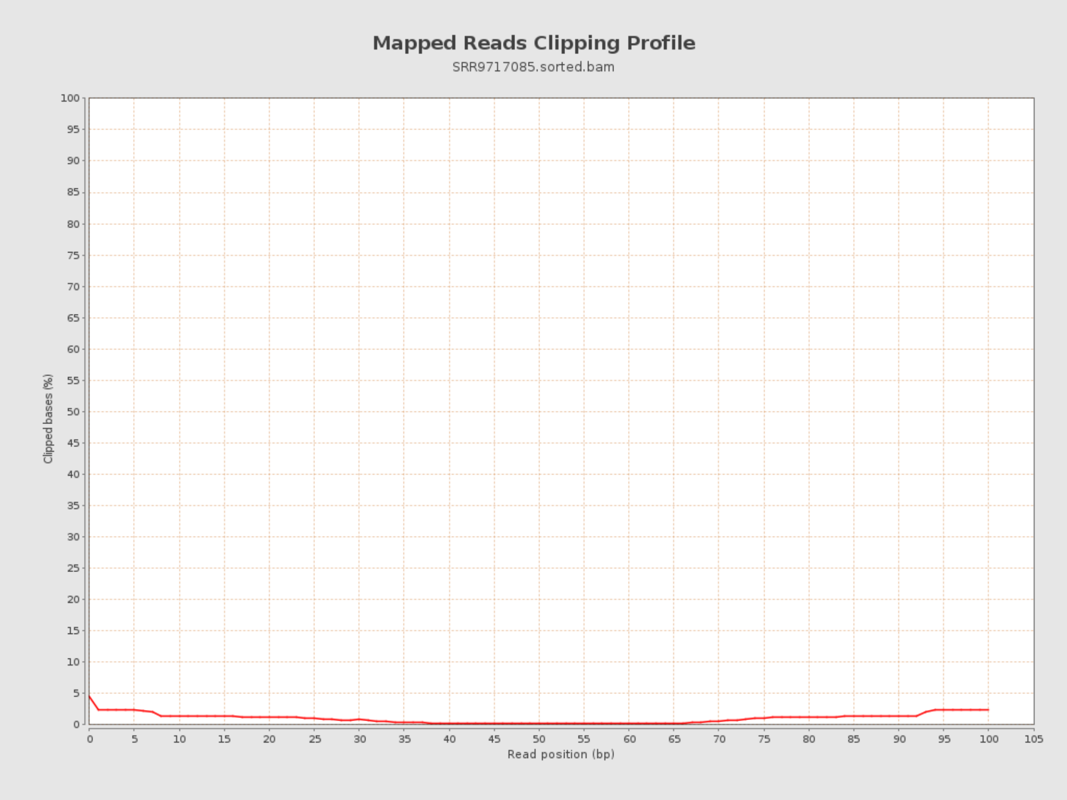
8. Results : Mapped Reads Nucleotide Content



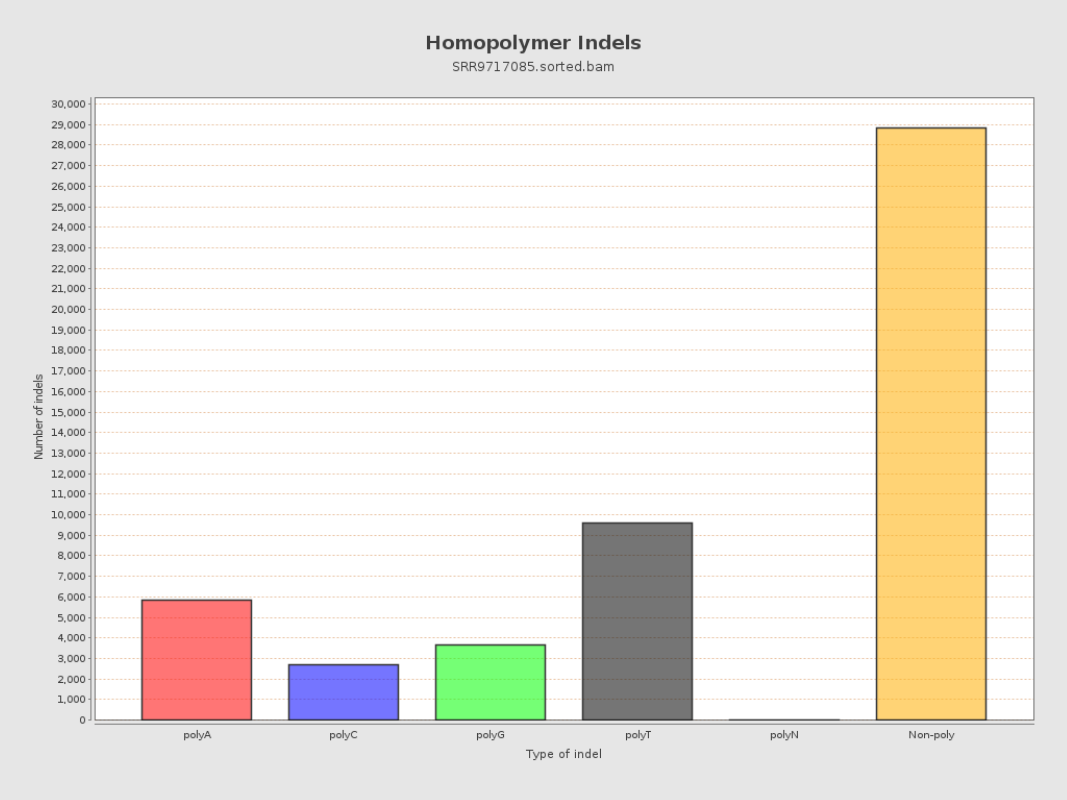
9. Results : Mapped Reads GC-content Distribution



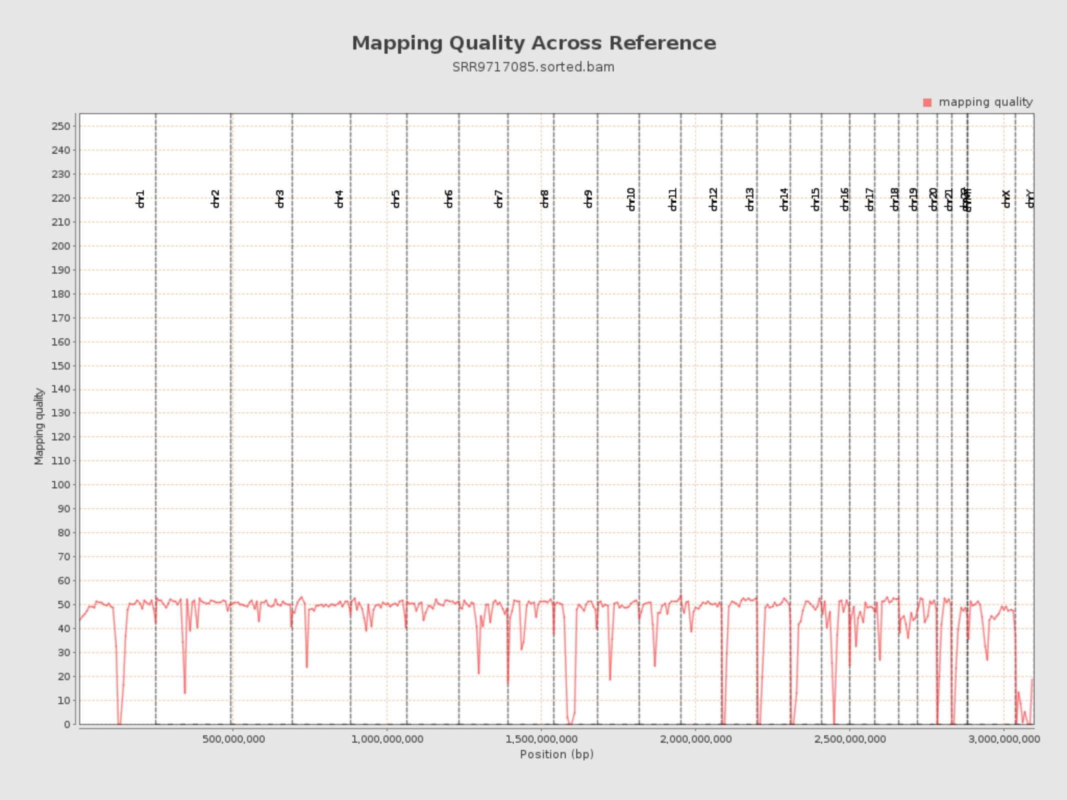
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram