Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:42:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717000.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_SRR9717000 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717000.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:42:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717000.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,997,524
Mapped reads	4,624,518 / 92.54%
Unmapped reads	373,006 / 7.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,766 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	356,167 / 7.13%
Duplication rate	5.9%
Clipped reads	4,634,139 / 92.73%

2.2. ACGT Content

Number/percentage of A's	68,878,419 / 25.44%
Number/percentage of C's	55,019,177 / 20.32%
Number/percentage of T's	81,873,191 / 30.24%
Number/percentage of G's	64,942,203 / 23.99%
Number/percentage of N's	4,152 / 0%
GC Percentage	44.31%

2.3. Coverage

Mean	0.0875

Standard Deviation	0.6877

2.4. Mapping Quality

Mean Mapping Quality	45.9

2.5. Mismatches and indels

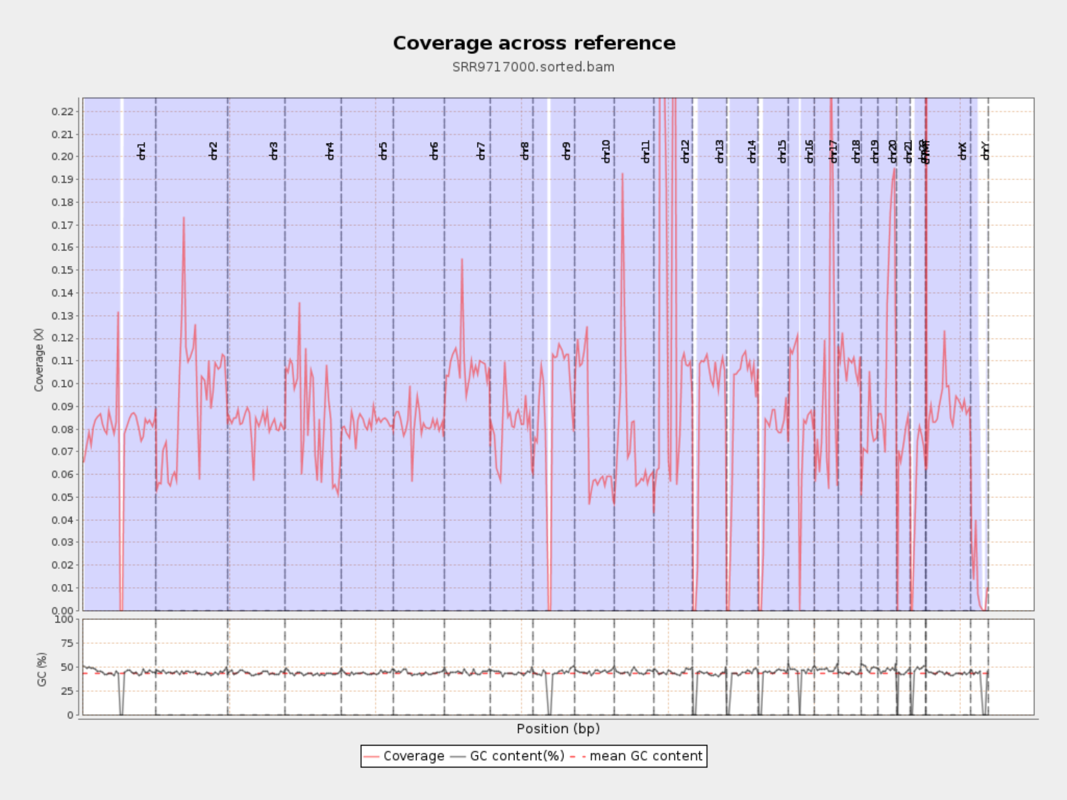
General error rate	0.54%
Mismatches	1,430,640
Insertions	17,710
Mapped reads with at least one insertion	0.38%
Deletions	42,617
Mapped reads with at least one deletion	0.92%
Homopolymer indels	43.2%

2.6. Chromosome stats

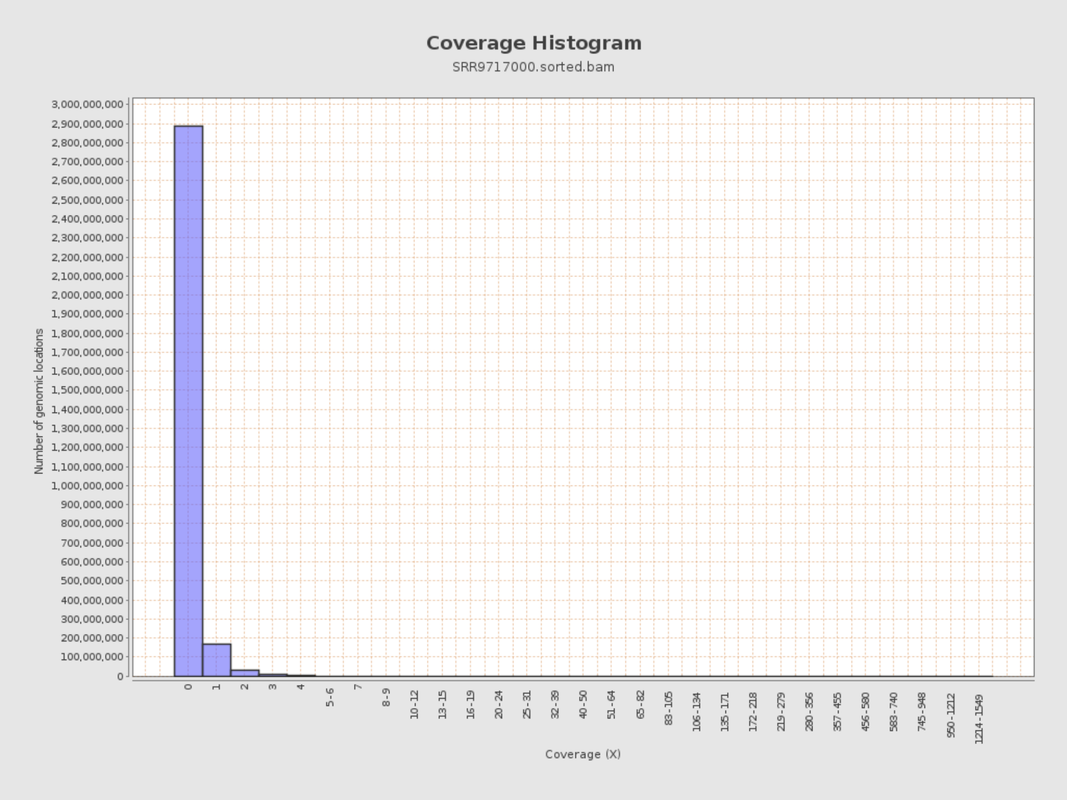
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19356595	0.0777	1.2639
chr2	243199373	22642751	0.0931	0.7673
chr3	198022430	16346271	0.0825	0.3517
chr4	191154276	16544359	0.0865	0.4529
chr5	180915260	14904350	0.0824	0.3628
chr6	171115067	14117947	0.0825	0.4322
chr7	159138663	17273621	0.1085	0.9632

chr8	146364022	11824478	0.0808	0.7495
chr9	141213431	12637260	0.0895	0.7144
chr10	135534747	10215093	0.0754	0.6452
chr11	135006516	10443622	0.0774	0.5678
chr12	133851895	19994204	0.1494	0.5996
chr13	115169878	10203406	0.0886	0.3717
chr14	107349540	9542256	0.0889	0.4414
chr15	102531392	6933095	0.0676	0.3222
chr16	90354753	7707510	0.0853	0.4193
chr17	81195210	8154208	0.1004	0.4316
chr18	78077248	8545916	0.1095	1.3978
chr19	59128983	4562179	0.0772	0.9404
chr20	63025520	8120613	0.1288	0.4697
chr21	48129895	3255855	0.0676	0.3972
chr22	51304566	2728990	0.0532	0.2775
chrMT	16571	24703	1.4907	1.5942
chrX	155270560	13987996	0.0901	0.5015
chrY	59373566	720417	0.0121	0.2578

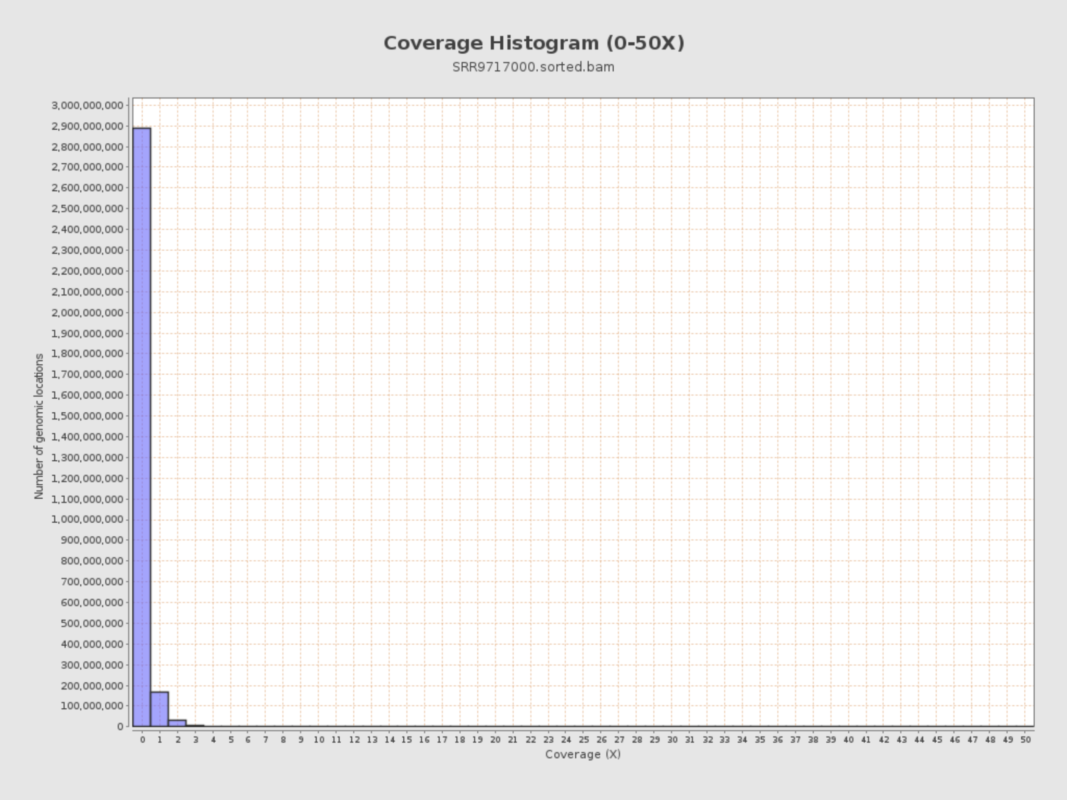
3. Results : Coverage across reference



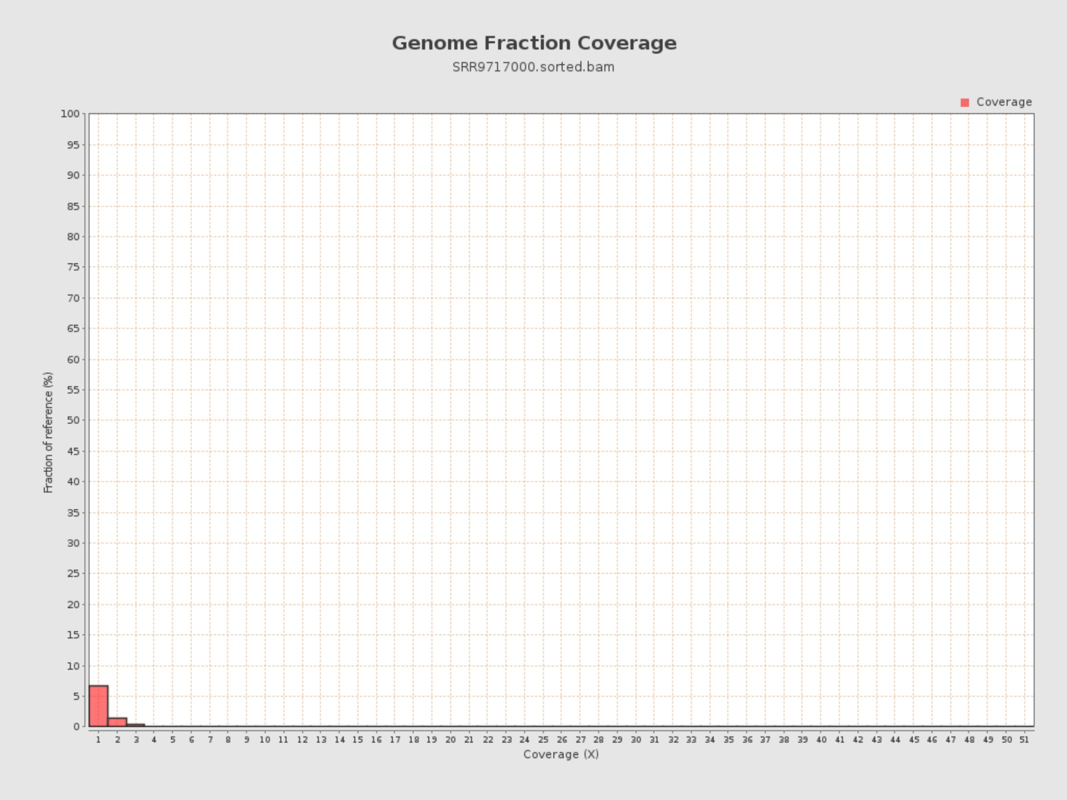
4. Results : Coverage Histogram



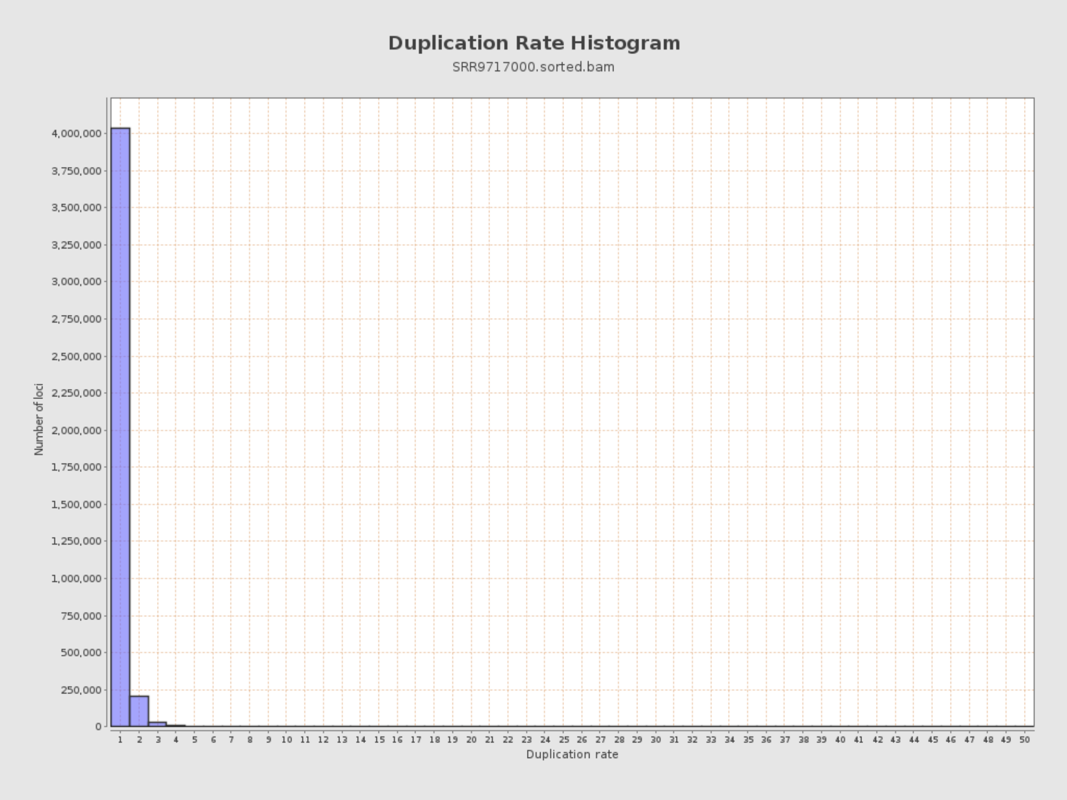
5. Results : Coverage Histogram (0-50X)



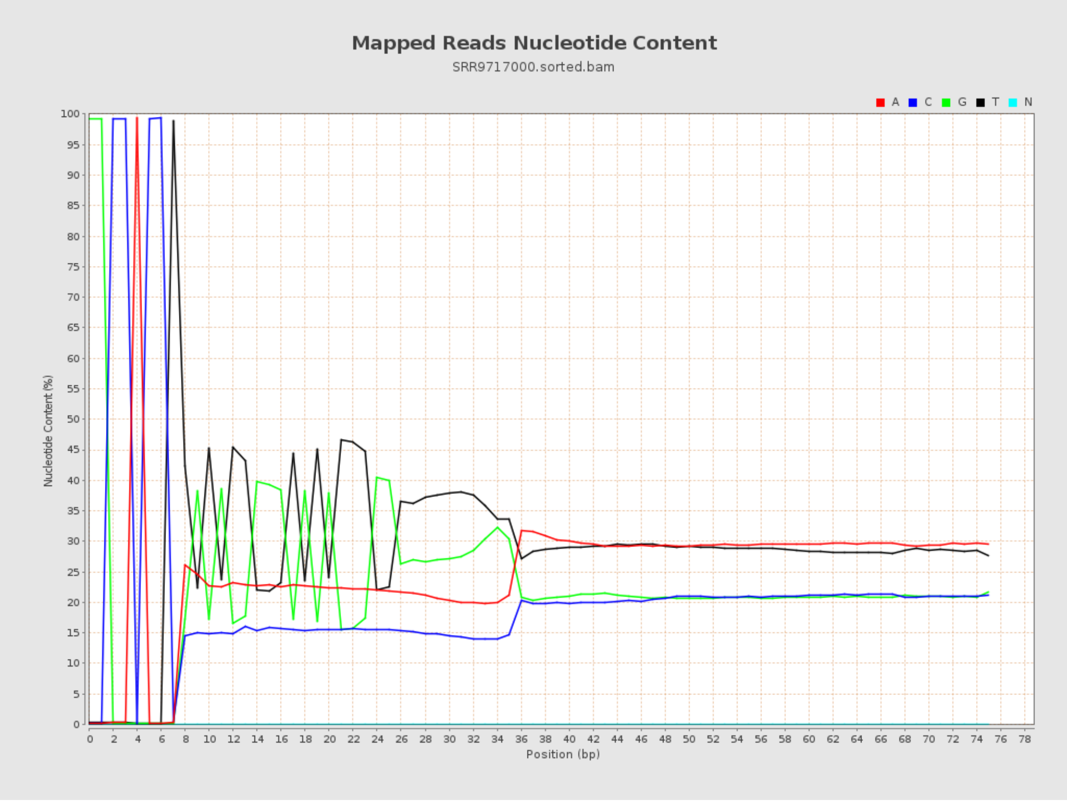
6. Results : Genome Fraction Coverage



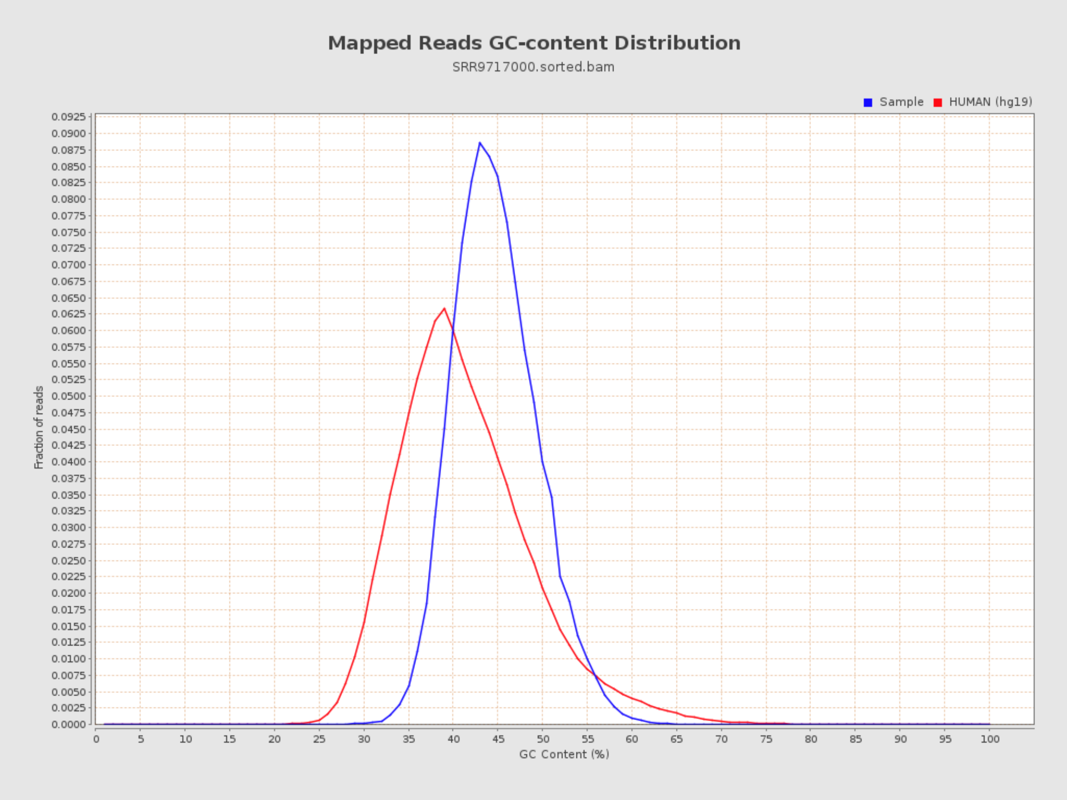
7. Results : Duplication Rate Histogram



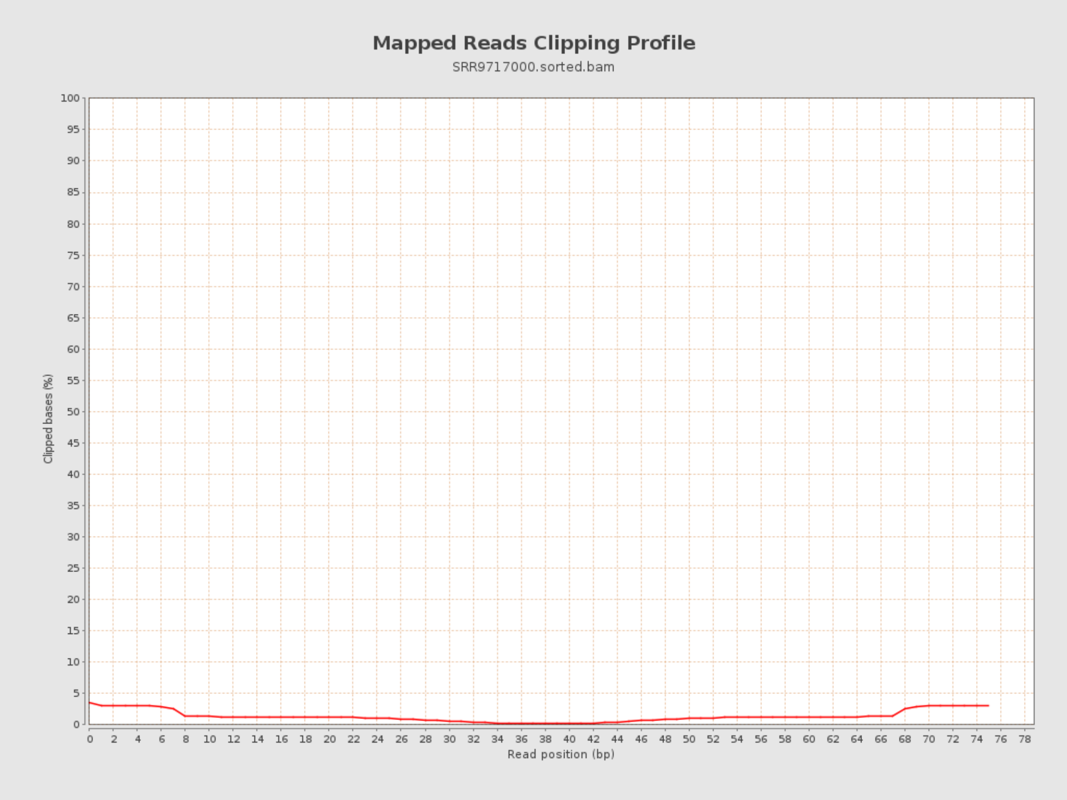
8. Results : Mapped Reads Nucleotide Content



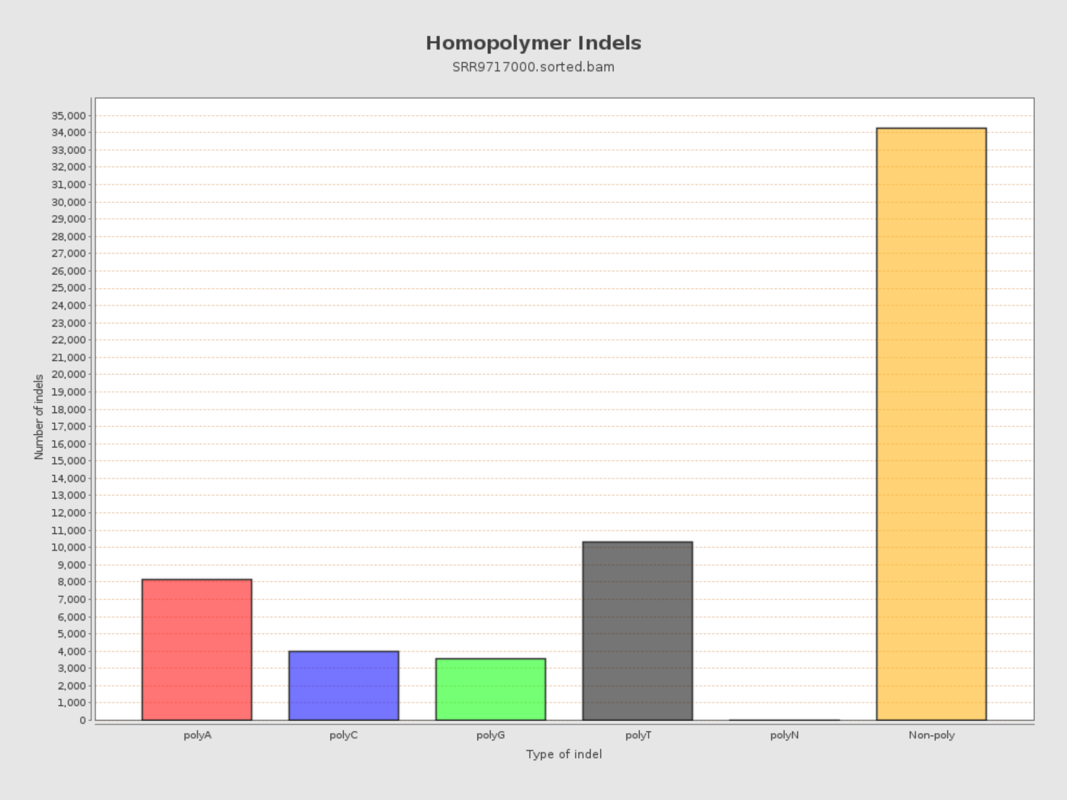
9. Results : Mapped Reads GC-content Distribution



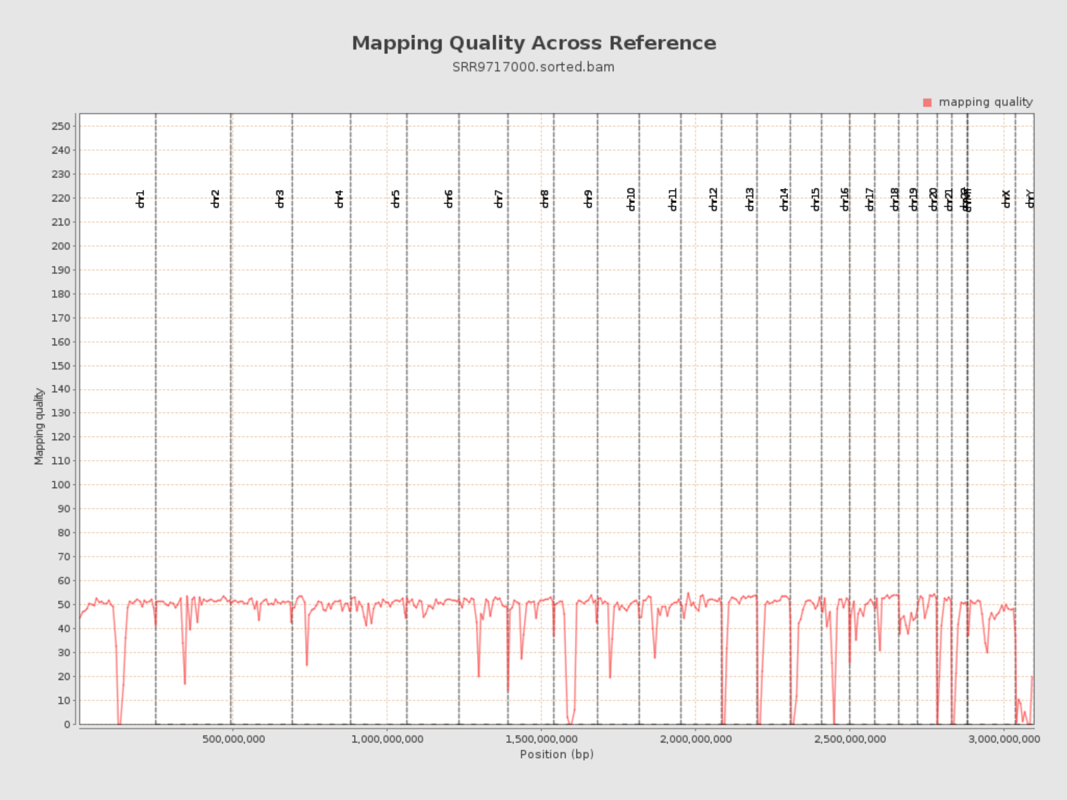
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram