Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:31:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717069.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_SRR9717069 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717069.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:31:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	553,561
Mapped reads	505,327 / 91.29%
Unmapped reads	48,234 / 8.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,227 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	11,089 / 2%
Duplication rate	1.79%
Clipped reads	505,595 / 91.34%

2.2. ACGT Content

Number/percentage of A's	7,043,982 / 24.26%
Number/percentage of C's	5,132,139 / 17.67%
Number/percentage of T's	9,212,050 / 31.73%
Number/percentage of G's	7,648,428 / 26.34%
Number/percentage of N's	256 / 0%
GC Percentage	44.01%

2.3. Coverage

Mean	0.0094

Standard Deviation	0.1139

2.4. Mapping Quality

Mean Mapping Quality	45.2

2.5. Mismatches and indels

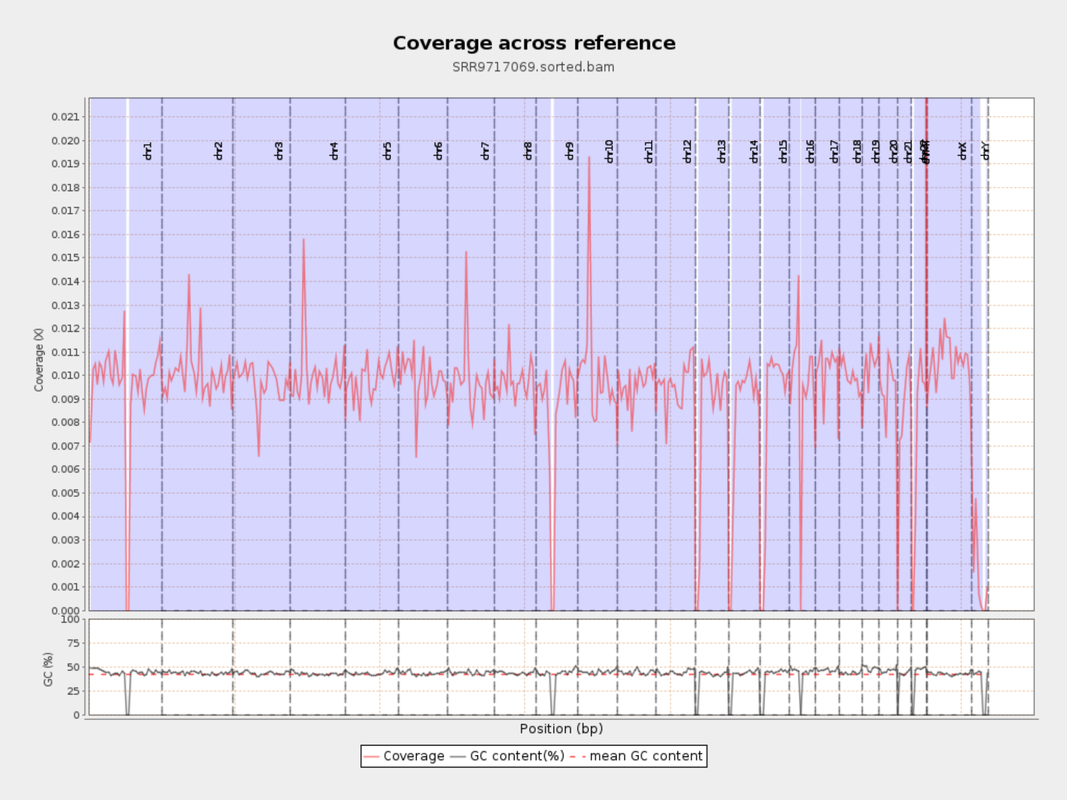
General error rate	0.5%
Mismatches	141,696
Insertions	1,935
Mapped reads with at least one insertion	0.38%
Deletions	5,737
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.53%

2.6. Chromosome stats

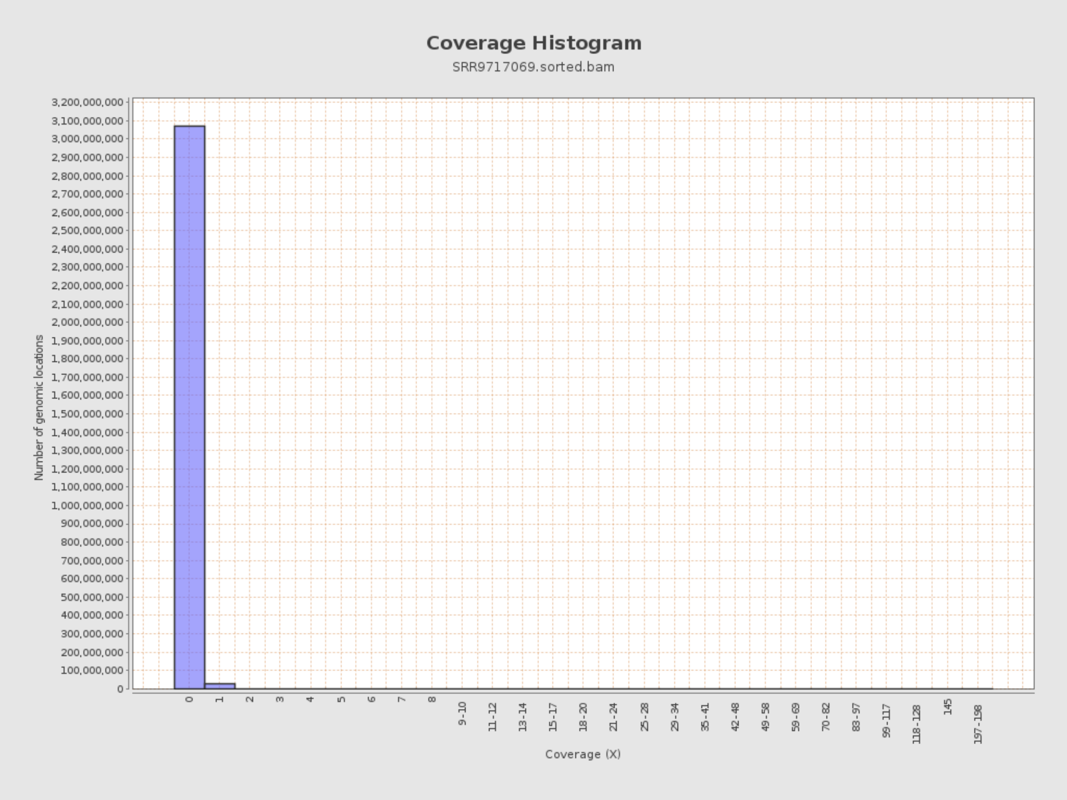
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2349446	0.0094	0.1331
chr2	243199373	2454363	0.0101	0.1388
chr3	198022430	1922754	0.0097	0.1027
chr4	191154276	1915895	0.01	0.1077
chr5	180915260	1780034	0.0098	0.1032
chr6	171115067	1697559	0.0099	0.1098
chr7	159138663	1547987	0.0097	0.1384

chr8	146364022	1423197	0.0097	0.1129
chr9	141213431	1168648	0.0083	0.1011
chr10	135534747	1381962	0.0102	0.1272
chr11	135006516	1300086	0.0096	0.1102
chr12	133851895	1286077	0.0096	0.1023
chr13	115169878	938844	0.0082	0.0939
chr14	107349540	866898	0.0081	0.0949
chr15	102531392	845201	0.0082	0.0942
chr16	90354753	860349	0.0095	0.1068
chr17	81195210	832716	0.0103	0.1086
chr18	78077248	781137	0.01	0.1522
chr19	59128983	616324	0.0104	0.1262
chr20	63025520	593737	0.0094	0.1021
chr21	48129895	388382	0.0081	0.0969
chr22	51304566	354871	0.0069	0.0867
chrMT	16571	4300	0.2595	0.5501
chrX	155270560	1648578	0.0106	0.1107
chrY	59373566	86633	0.0015	0.0504

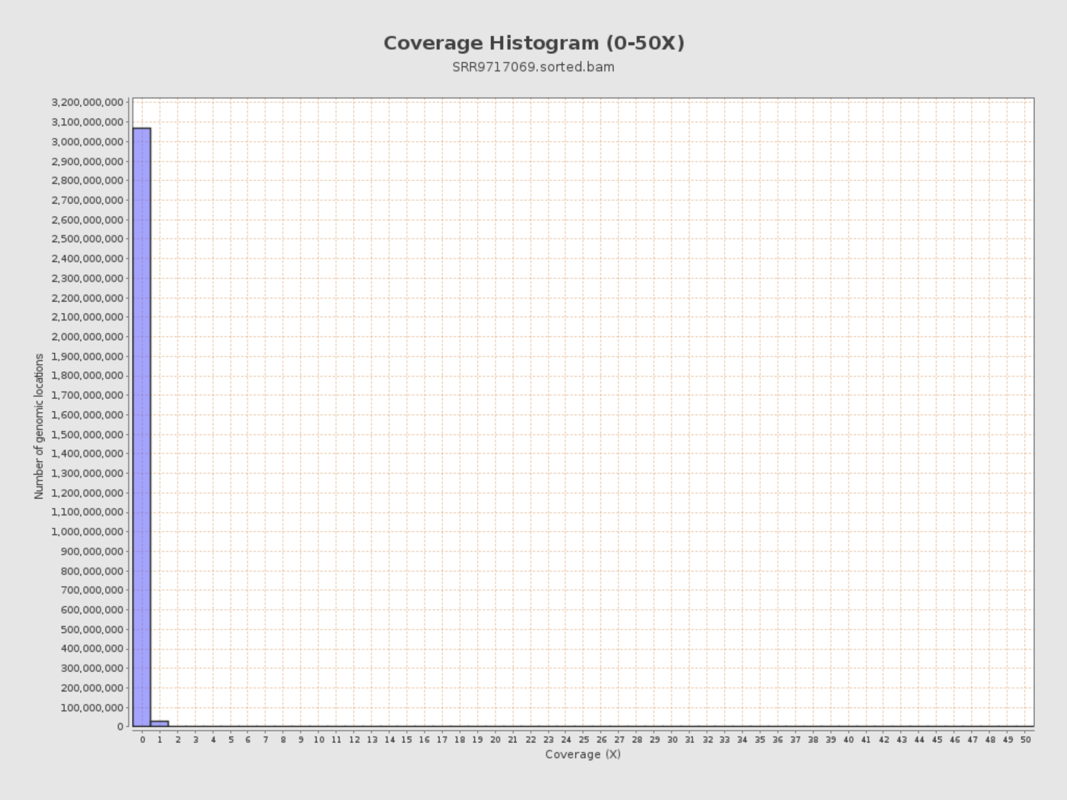
3. Results : Coverage across reference



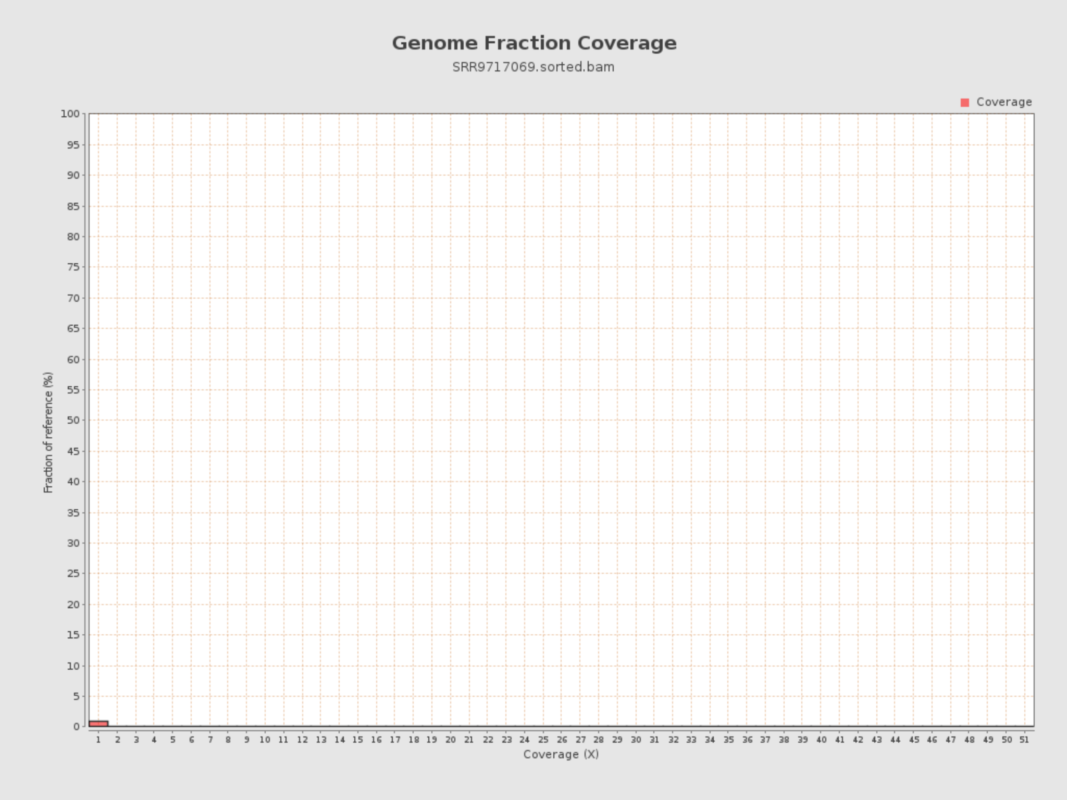
4. Results : Coverage Histogram



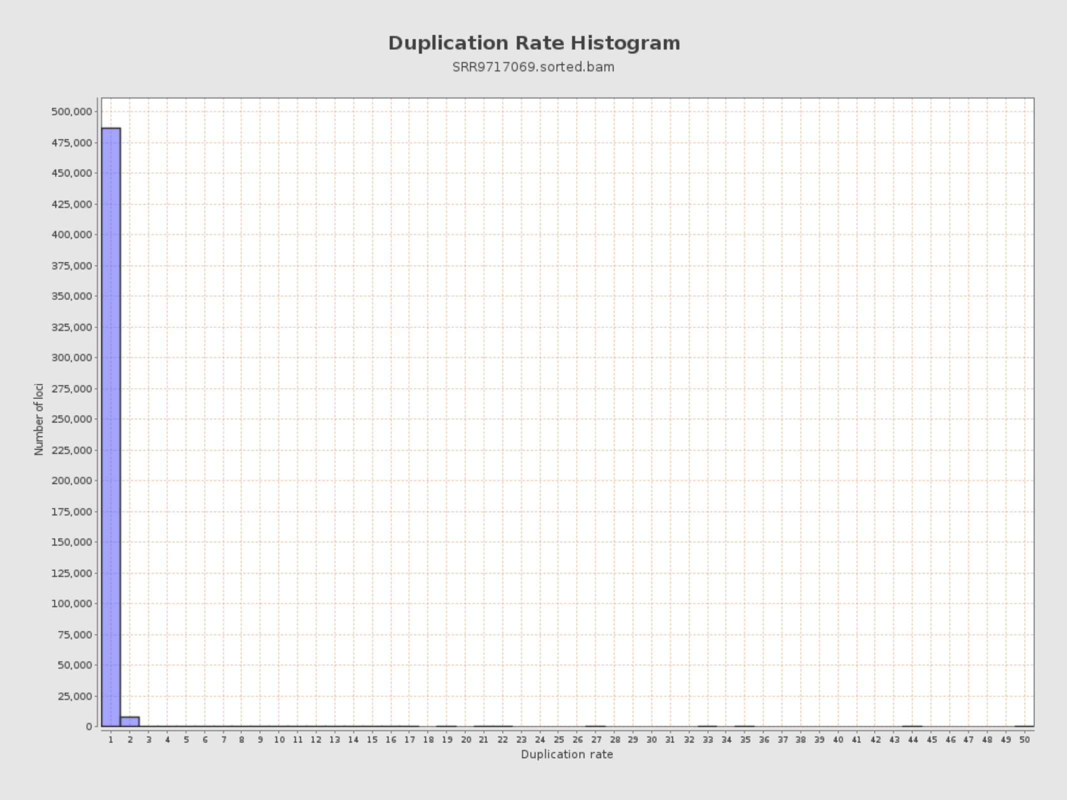
5. Results : Coverage Histogram (0-50X)



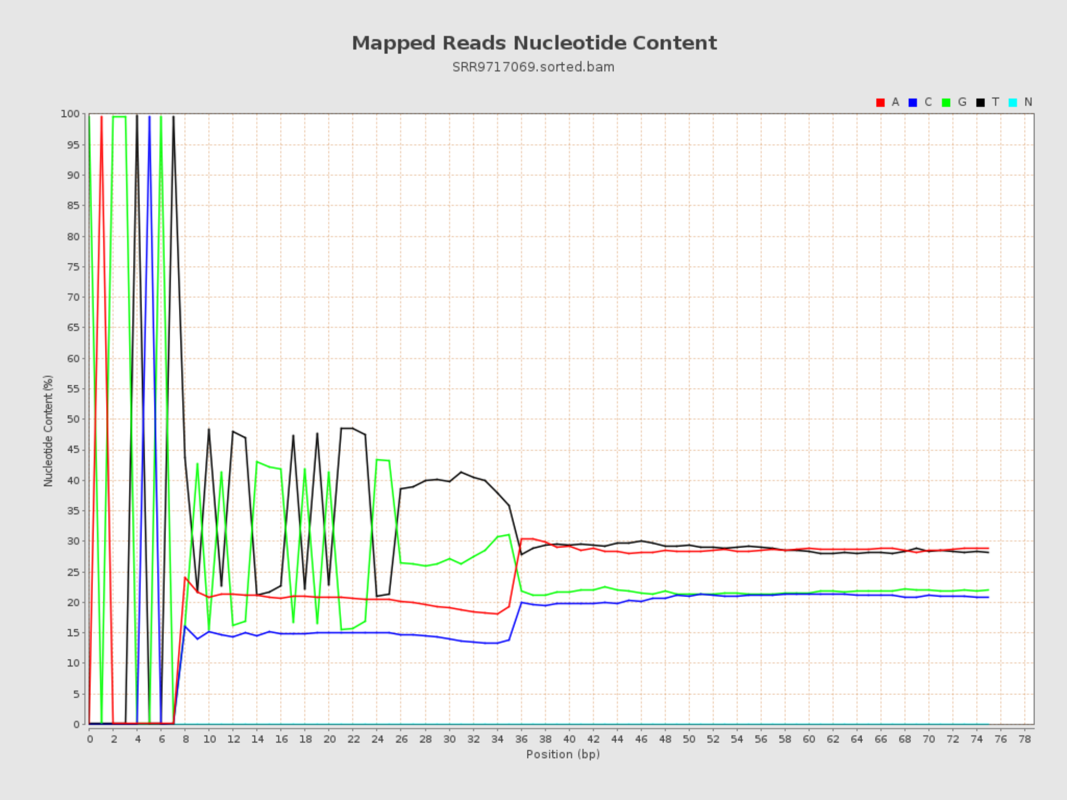
6. Results : Genome Fraction Coverage



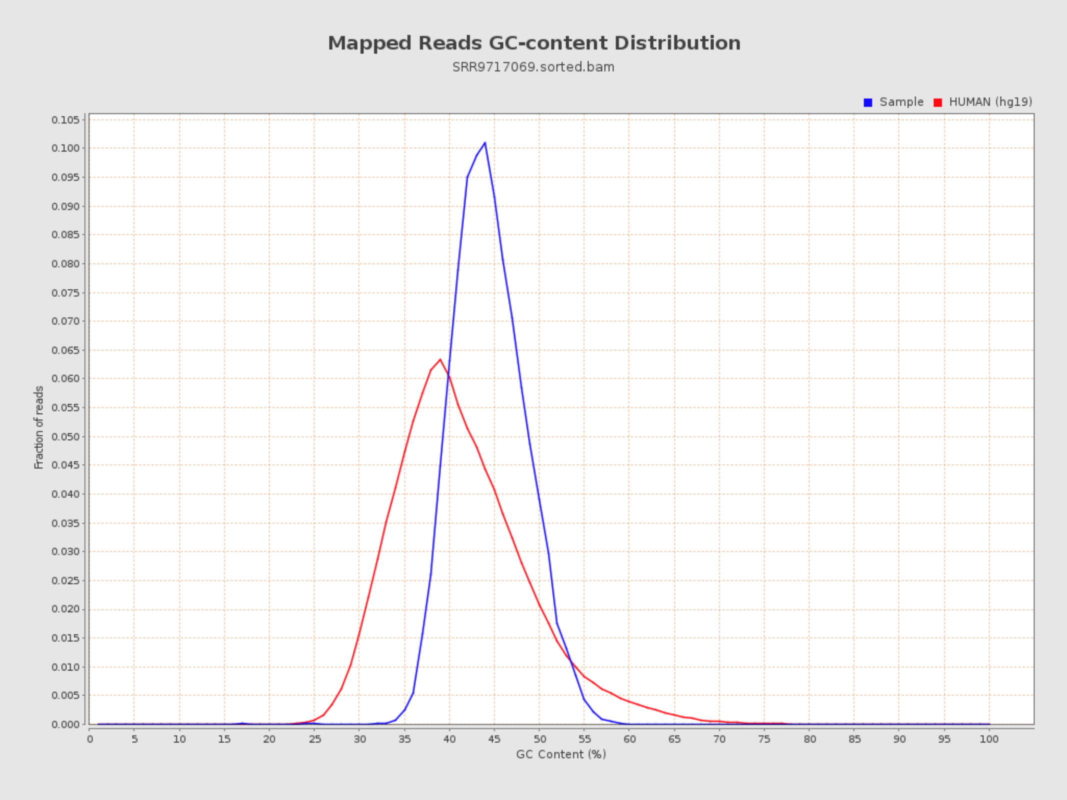
7. Results : Duplication Rate Histogram



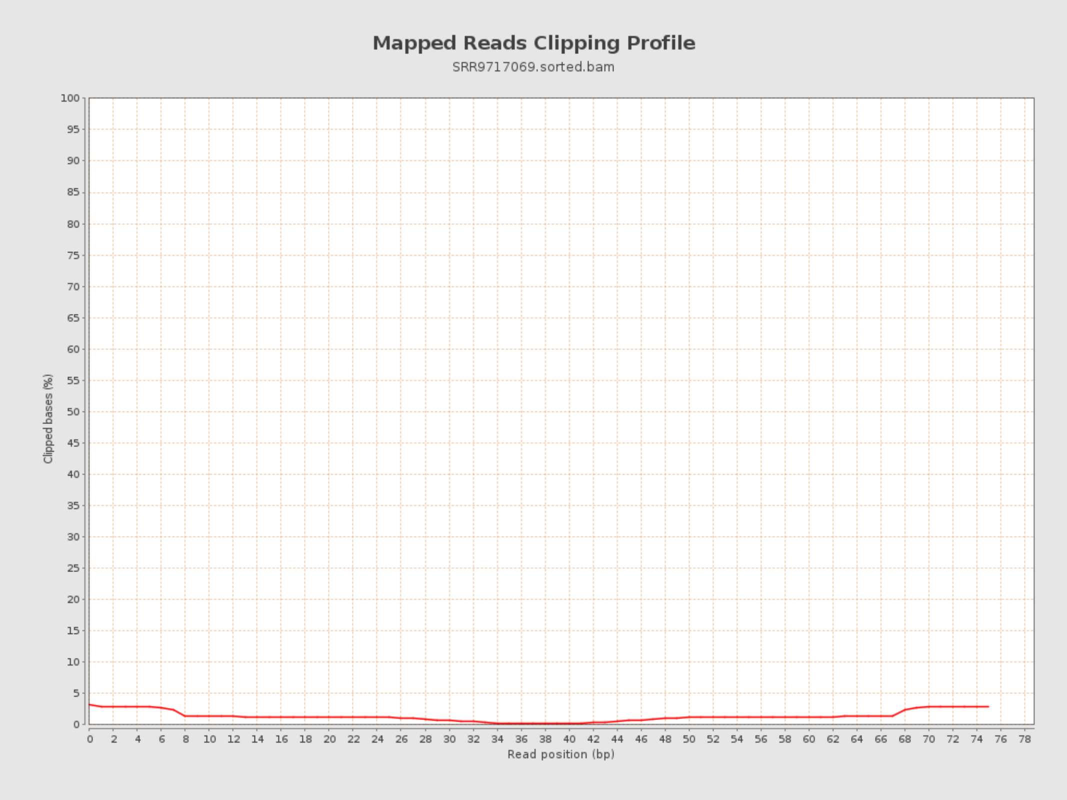
8. Results : Mapped Reads Nucleotide Content



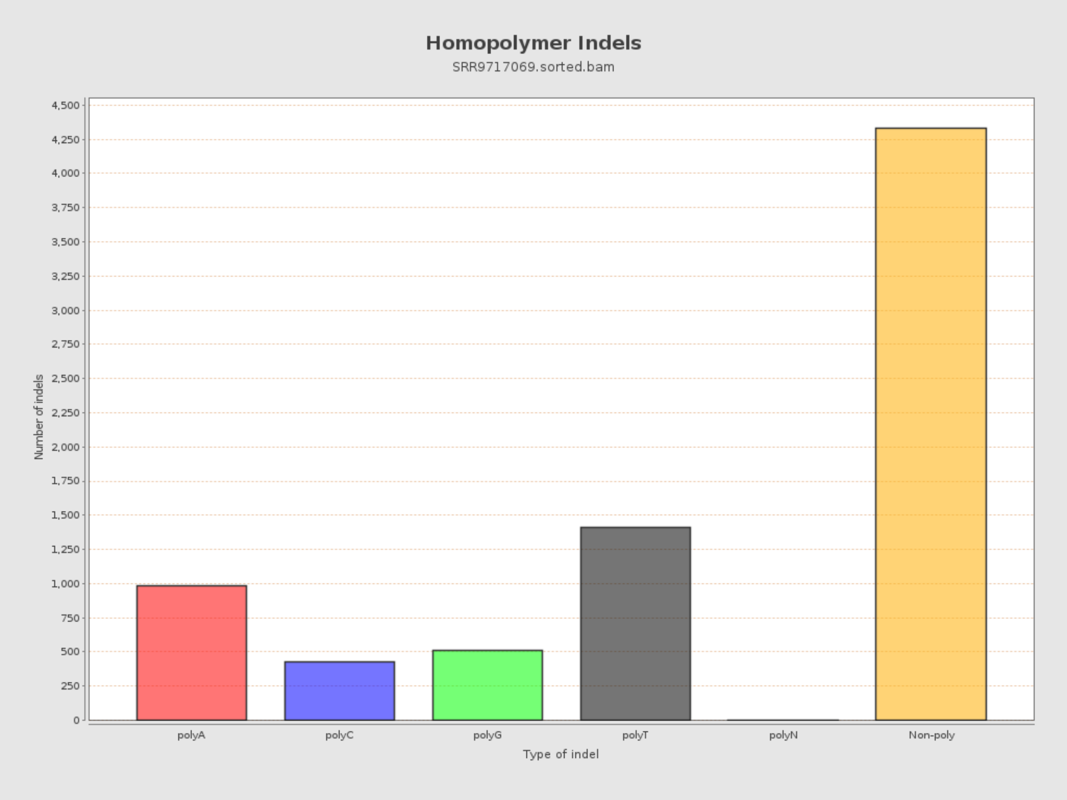
9. Results : Mapped Reads GC-content Distribution



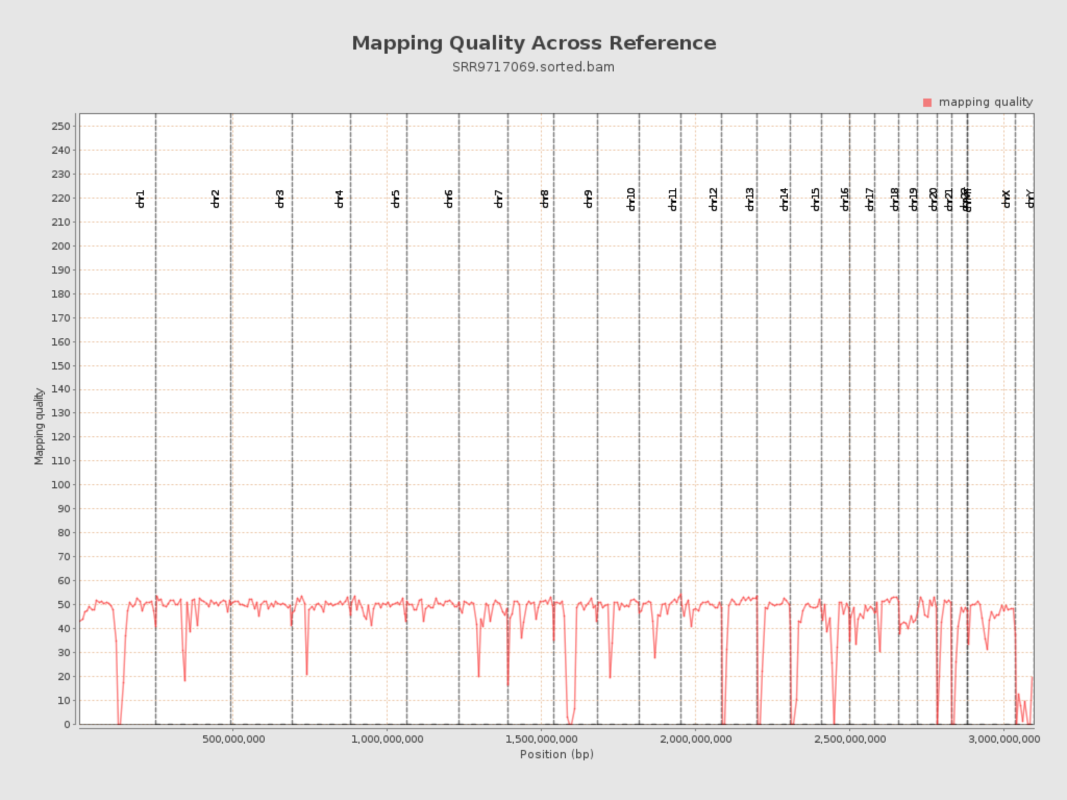
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram