Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:57:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717052.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_SRR9717052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717052.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:57:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717052.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,004,164
Mapped reads	797,245 / 79.39%
Unmapped reads	206,919 / 20.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,001 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	14,868 / 1.48%
Duplication rate	1.33%
Clipped reads	798,536 / 79.52%

2.2. ACGT Content

Number/percentage of A's	10,835,552 / 24.22%
Number/percentage of C's	9,610,714 / 21.49%
Number/percentage of T's	13,051,490 / 29.18%
Number/percentage of G's	11,230,193 / 25.11%
Number/percentage of N's	1,219 / 0%
GC Percentage	46.59%

2.3. Coverage

Mean	0.0145

Standard Deviation	0.1474

2.4. Mapping Quality

Mean Mapping Quality	39.75

2.5. Mismatches and indels

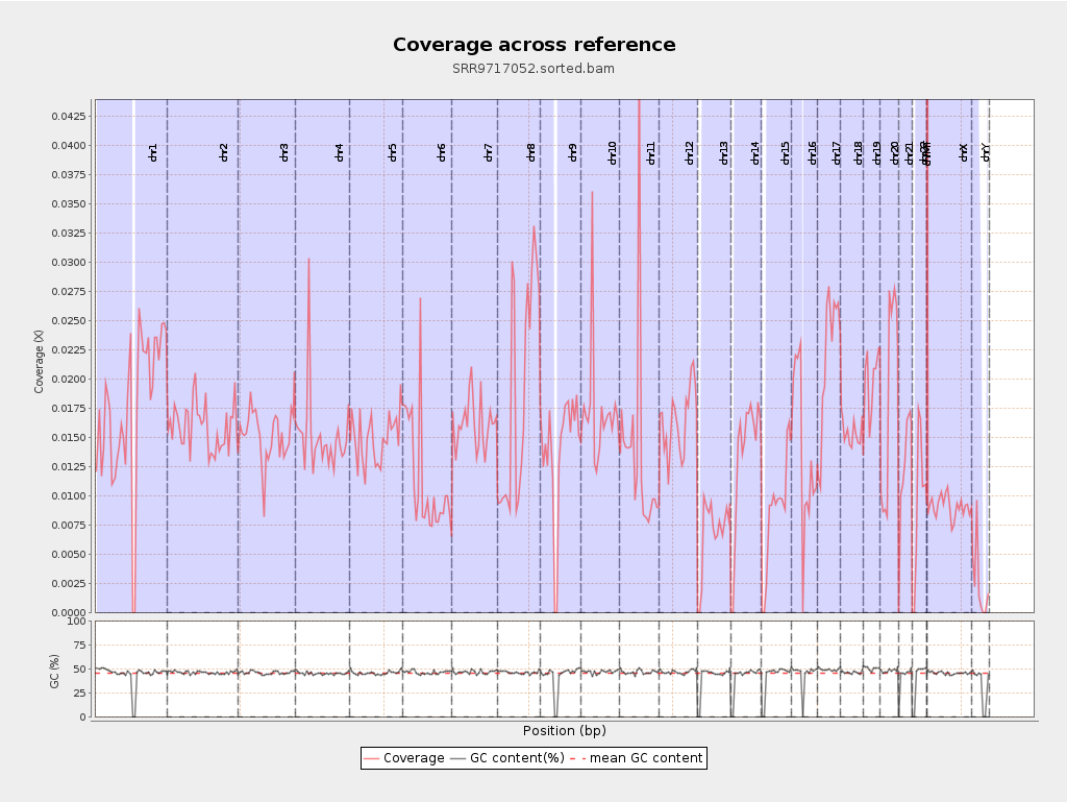
General error rate	0.54%
Mismatches	236,011
Insertions	3,593
Mapped reads with at least one insertion	0.45%
Deletions	7,315
Mapped reads with at least one deletion	0.91%
Homopolymer indels	33.44%

2.6. Chromosome stats

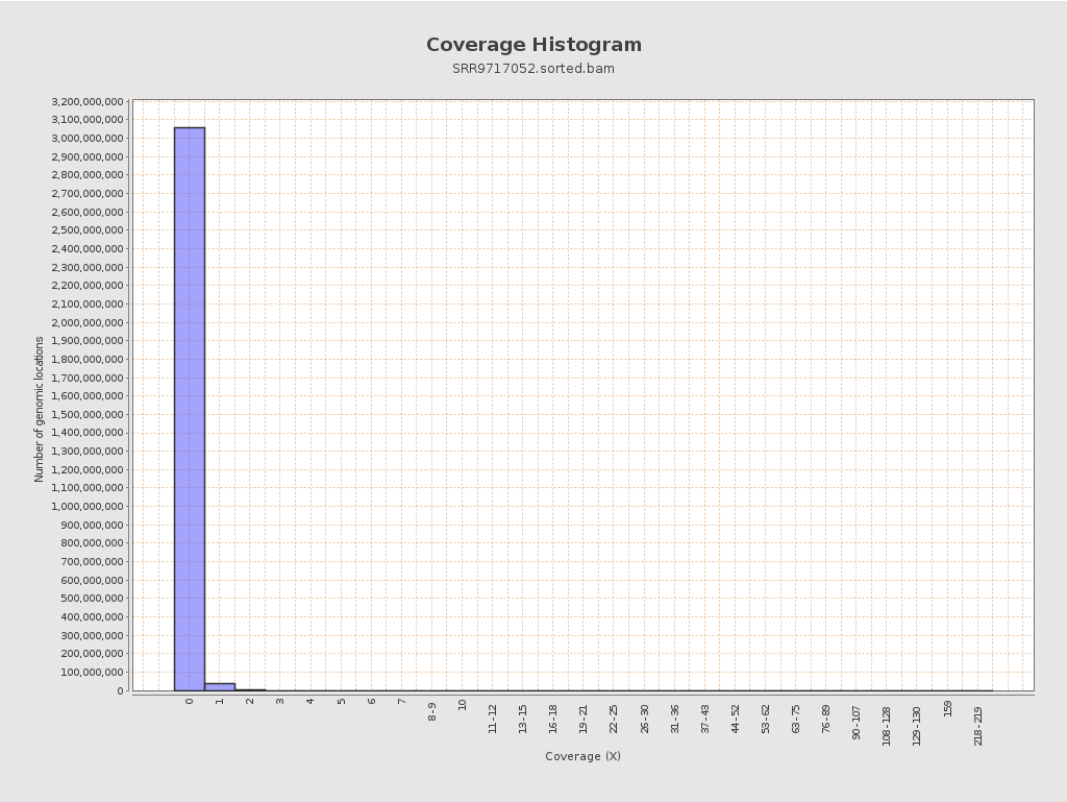
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4384815	0.0176	0.1759
chr2	243199373	3863078	0.0159	0.177
chr3	198022430	3007406	0.0152	0.1367
chr4	191154276	2889932	0.0151	0.1469
chr5	180915260	2713442	0.015	0.132
chr6	171115067	1945463	0.0114	0.117
chr7	159138663	2572875	0.0162	0.1638

chr8	146364022	2756562	0.0188	0.1529
chr9	141213431	1951197	0.0138	0.1332
chr10	135534747	2330511	0.0172	0.2188
chr11	135006516	1860759	0.0138	0.1457
chr12	133851895	2189061	0.0164	0.1388
chr13	115169878	776310	0.0067	0.0889
chr14	107349540	1429972	0.0133	0.1253
chr15	102531392	893330	0.0087	0.1006
chr16	90354753	1223565	0.0135	0.1344
chr17	81195210	1773899	0.0218	0.1656
chr18	78077248	1200175	0.0154	0.163
chr19	59128983	1169068	0.0198	0.1706
chr20	63025520	1159688	0.0184	0.1511
chr21	48129895	603879	0.0125	0.13
chr22	51304566	494326	0.0096	0.1078
chrMT	16571	5157	0.3112	0.626
chrX	155270560	1403988	0.009	0.1089
chrY	59373566	143293	0.0024	0.0845

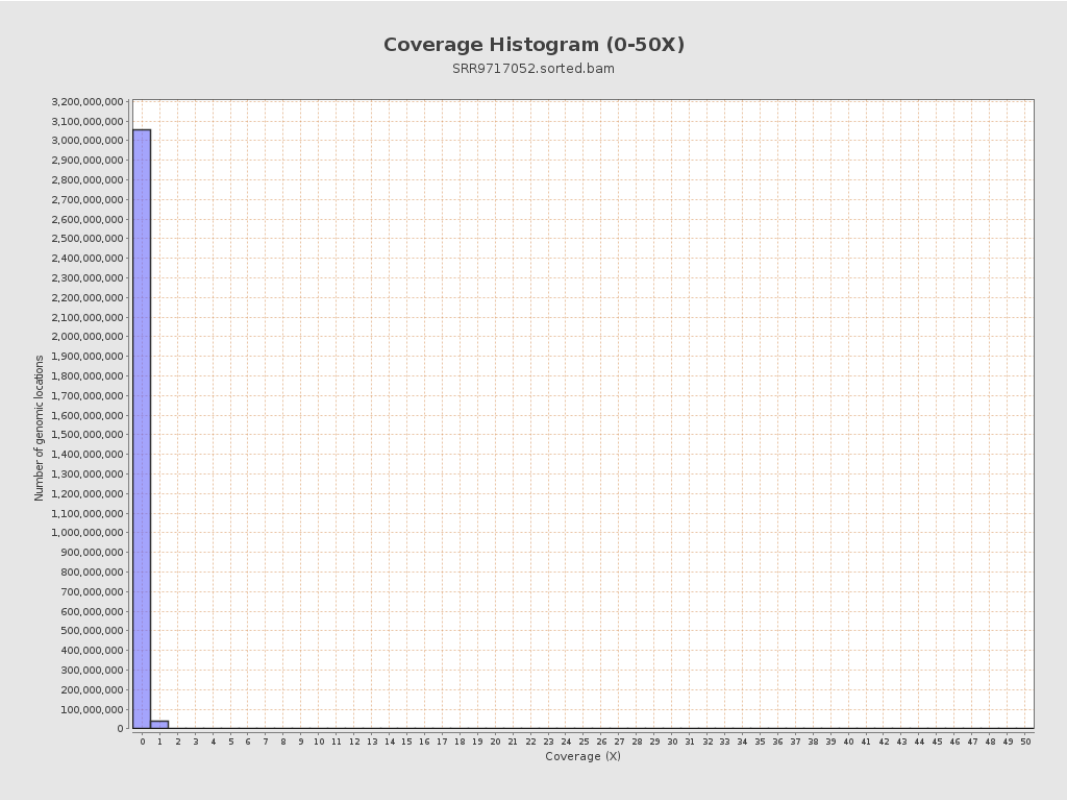
3. Results : Coverage across reference



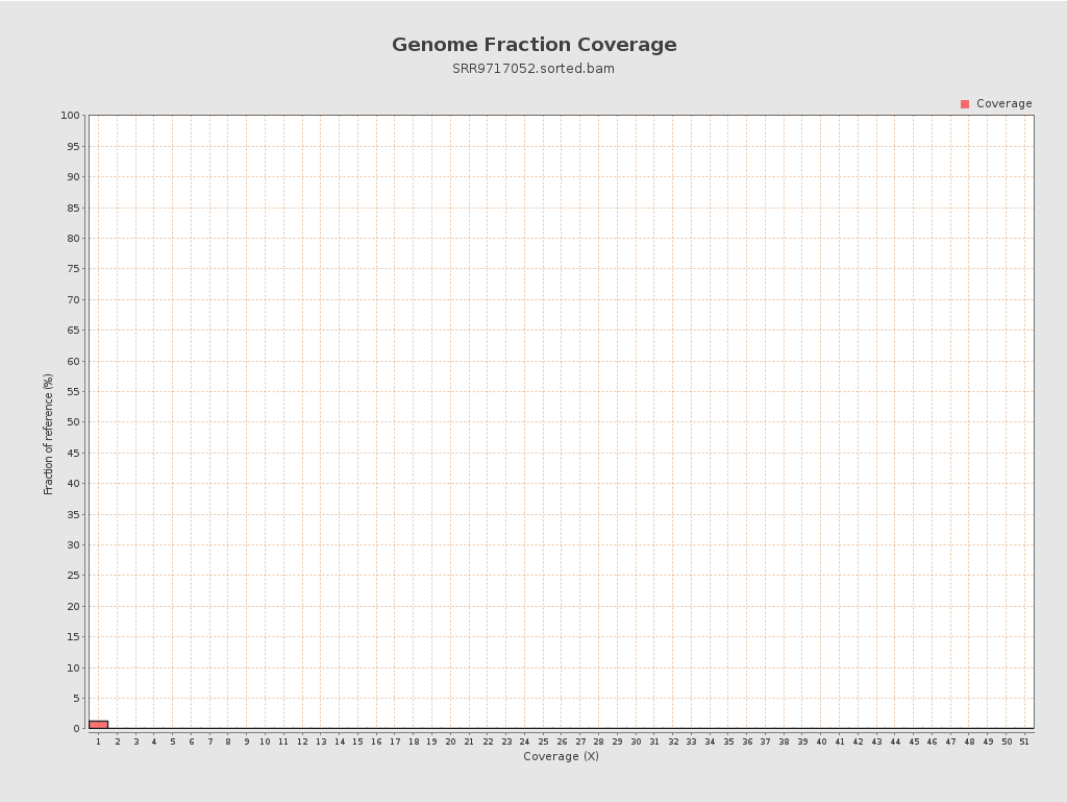
4. Results : Coverage Histogram



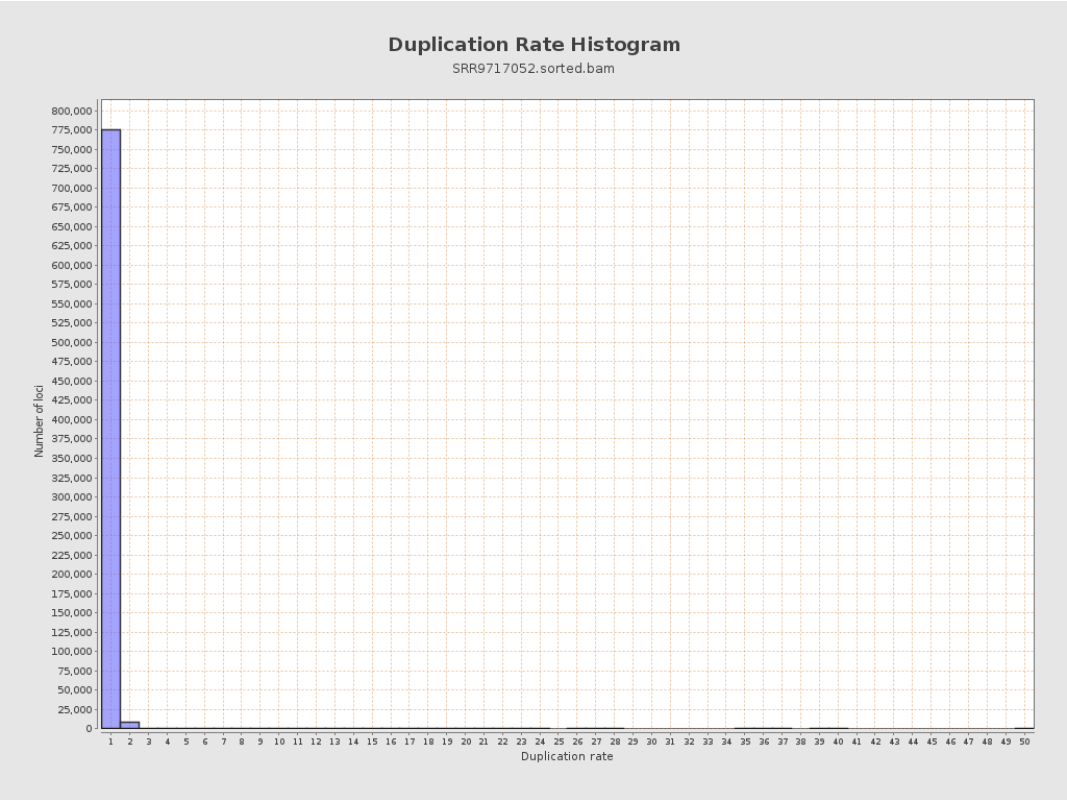
5. Results : Coverage Histogram (0-50X)



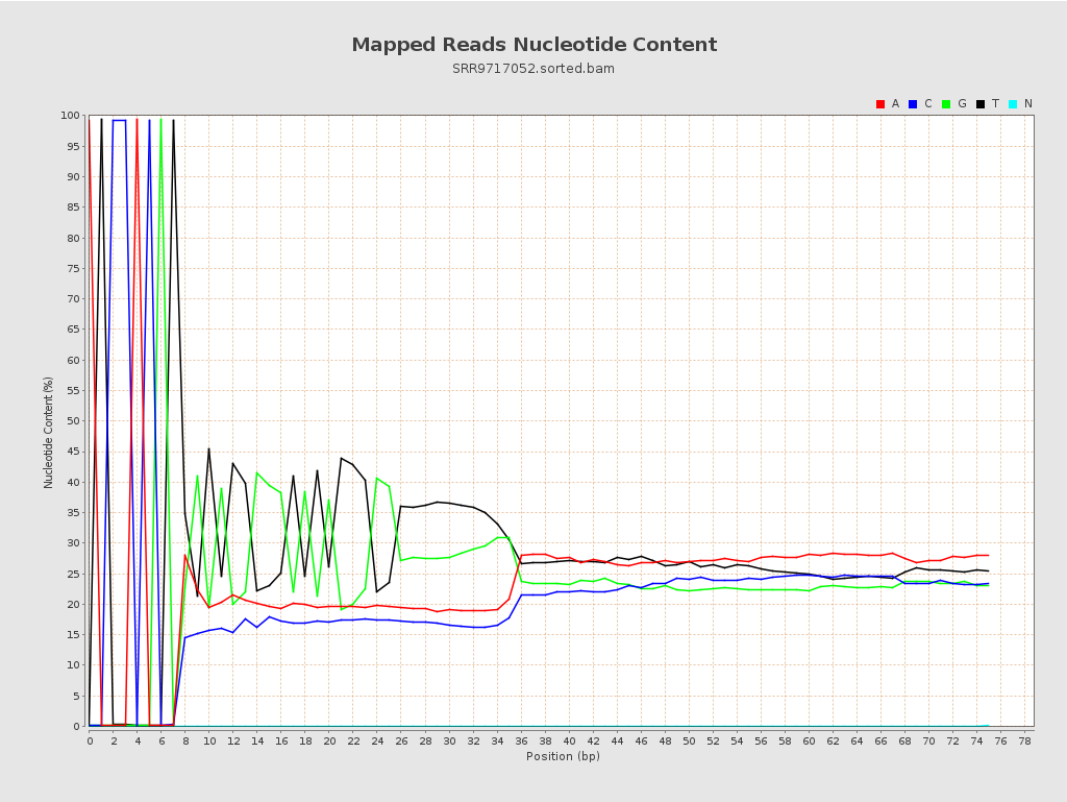
6. Results : Genome Fraction Coverage



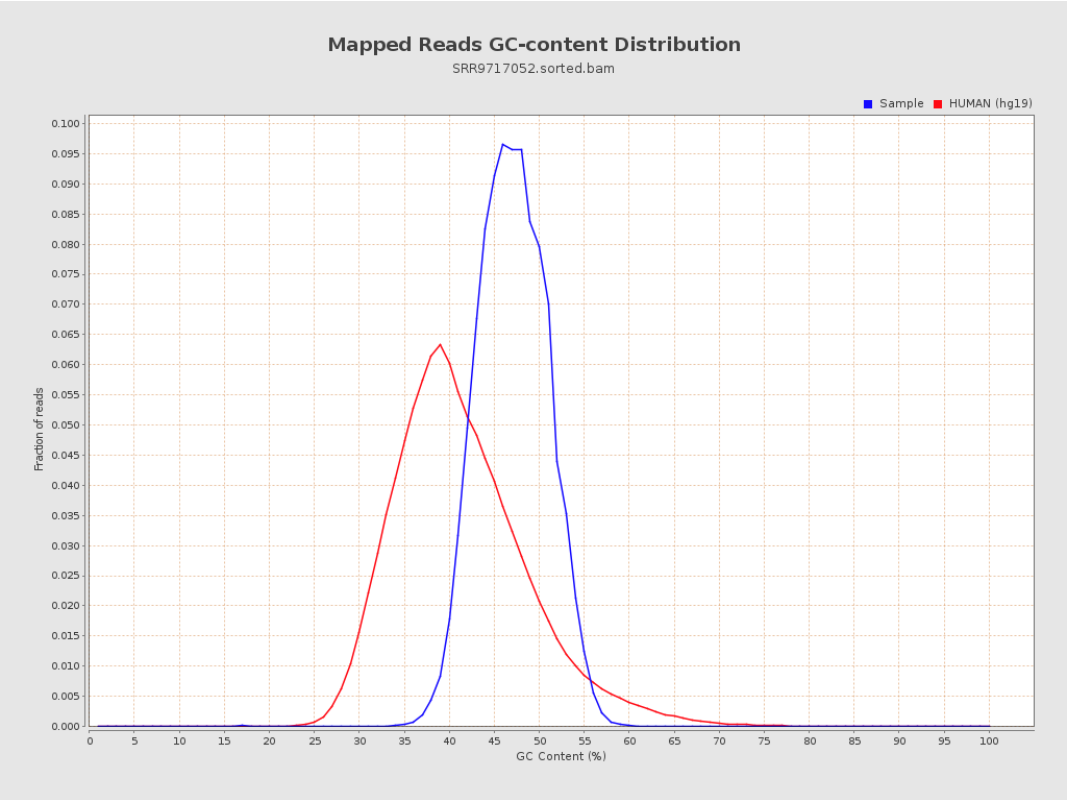
7. Results : Duplication Rate Histogram



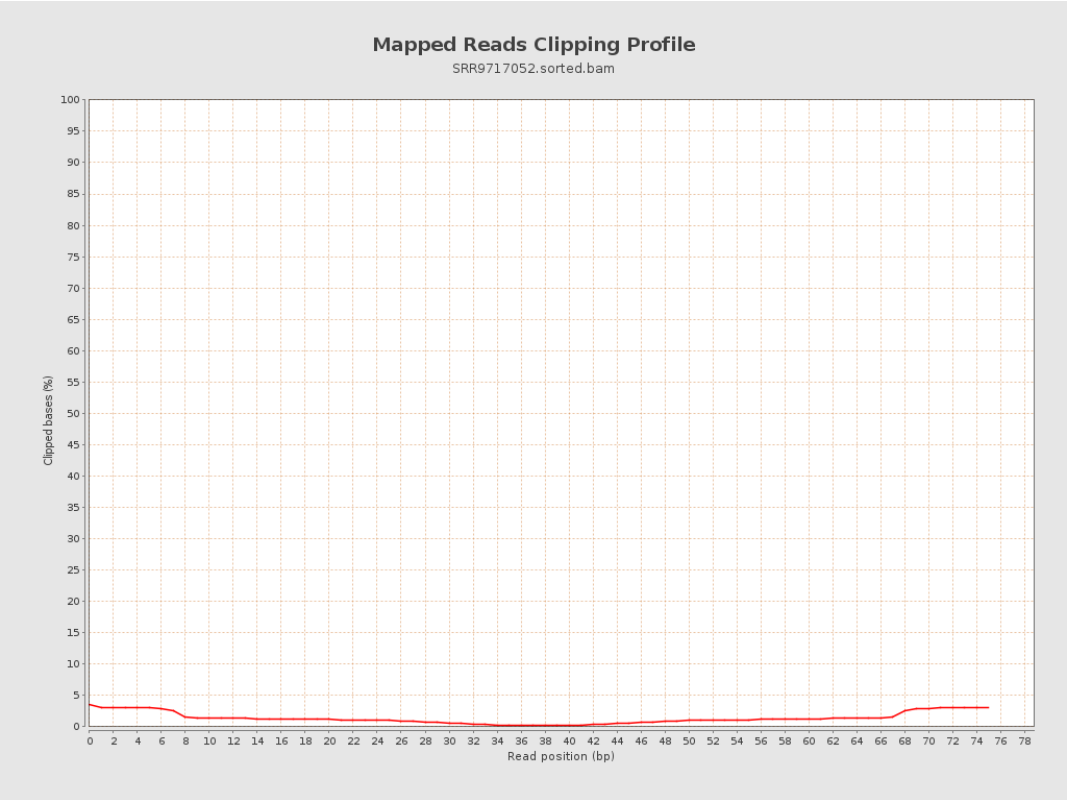
8. Results : Mapped Reads Nucleotide Content



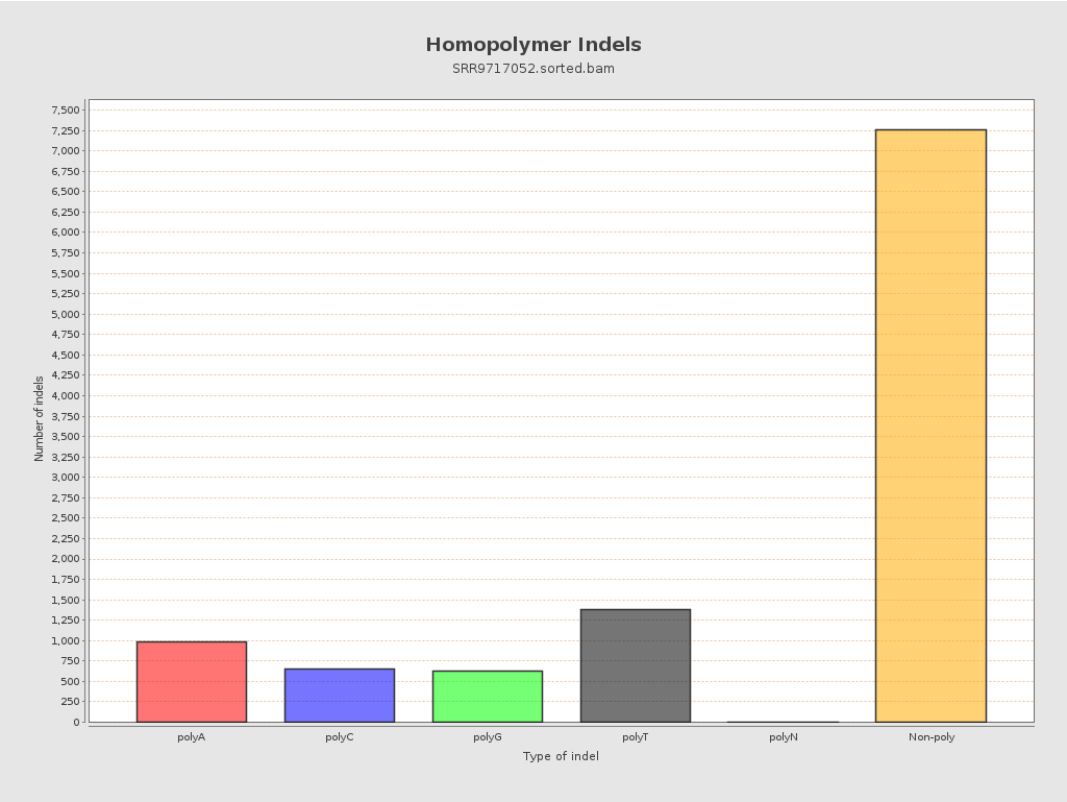
9. Results : Mapped Reads GC-content Distribution



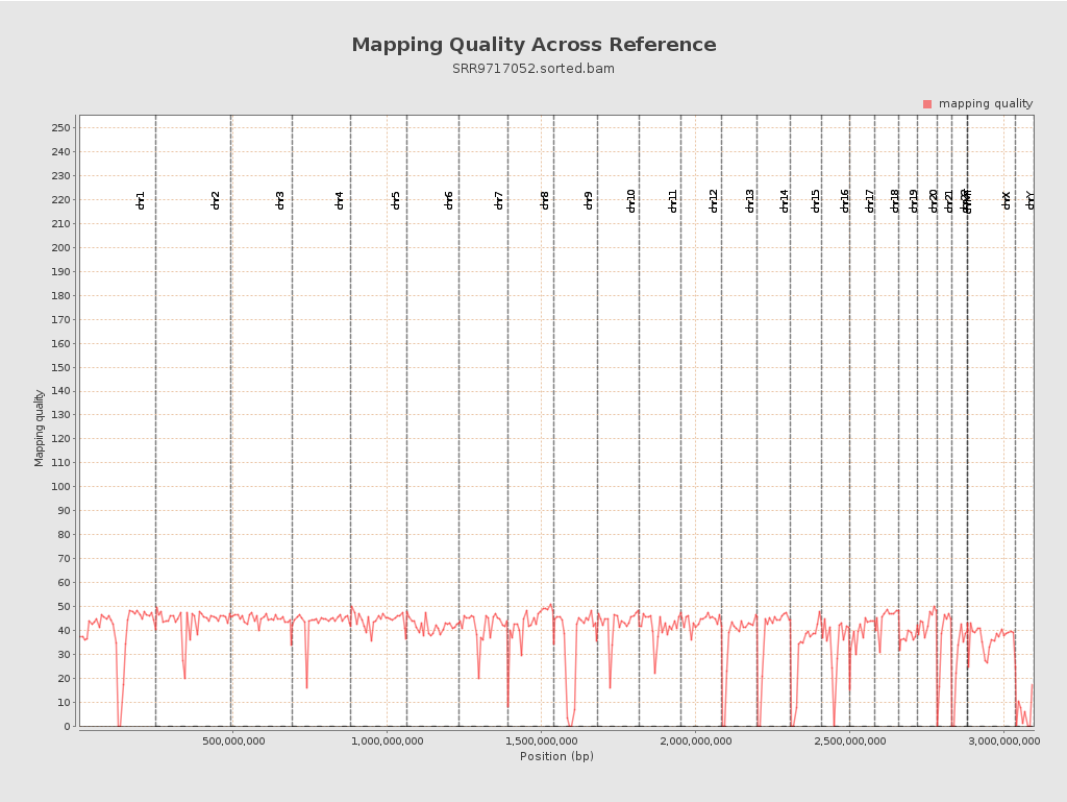
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram