Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:32:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717092.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_SRR9717092 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717092.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:32:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717092.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	695,844
Mapped reads	584,191 / 83.95%
Unmapped reads	111,653 / 16.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,506 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	9,883 / 1.42%
Duplication rate	1.2%
Clipped reads	586,101 / 84.23%

2.2. ACGT Content

Number/percentage of A's	7,959,744 / 24.29%
Number/percentage of C's	6,317,503 / 19.28%
Number/percentage of T's	10,323,095 / 31.5%
Number/percentage of G's	8,167,804 / 24.93%
Number/percentage of N's	501 / 0%
GC Percentage	44.2%

2.3. Coverage

Mean	0.0106

Standard Deviation	0.1264

2.4. Mapping Quality

Mean Mapping Quality	41.54

2.5. Mismatches and indels

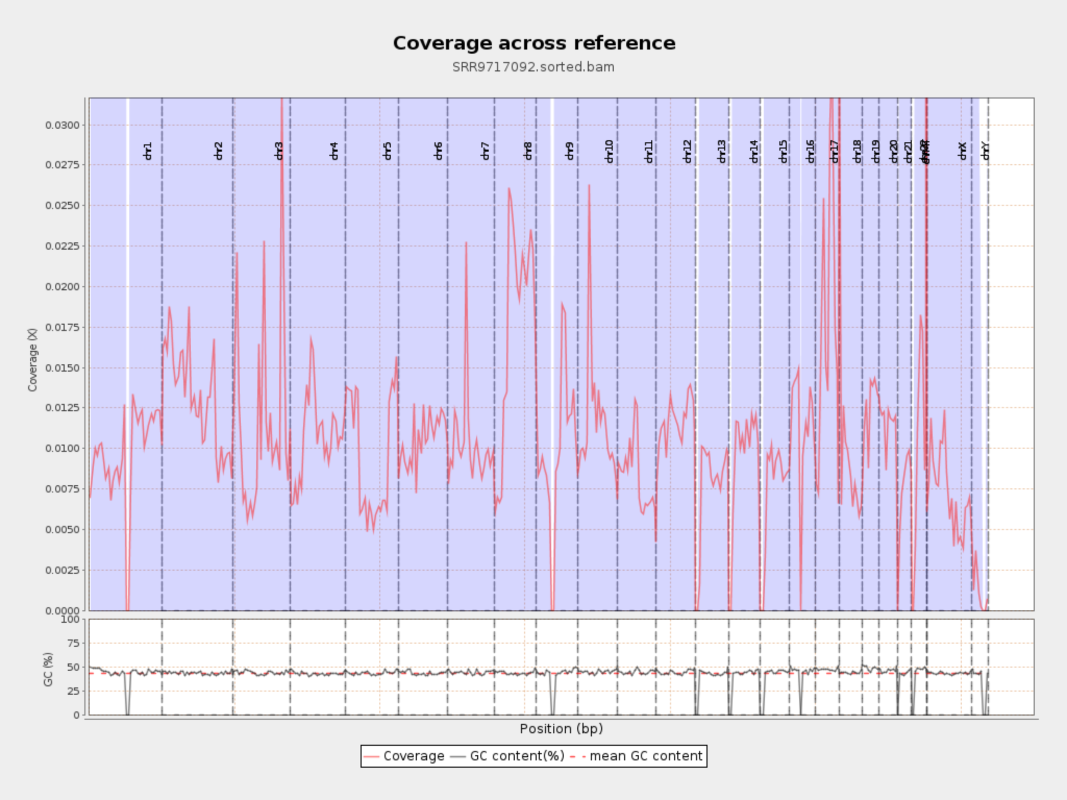
General error rate	0.54%
Mismatches	172,795
Insertions	1,906
Mapped reads with at least one insertion	0.32%
Deletions	6,040
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.02%

2.6. Chromosome stats

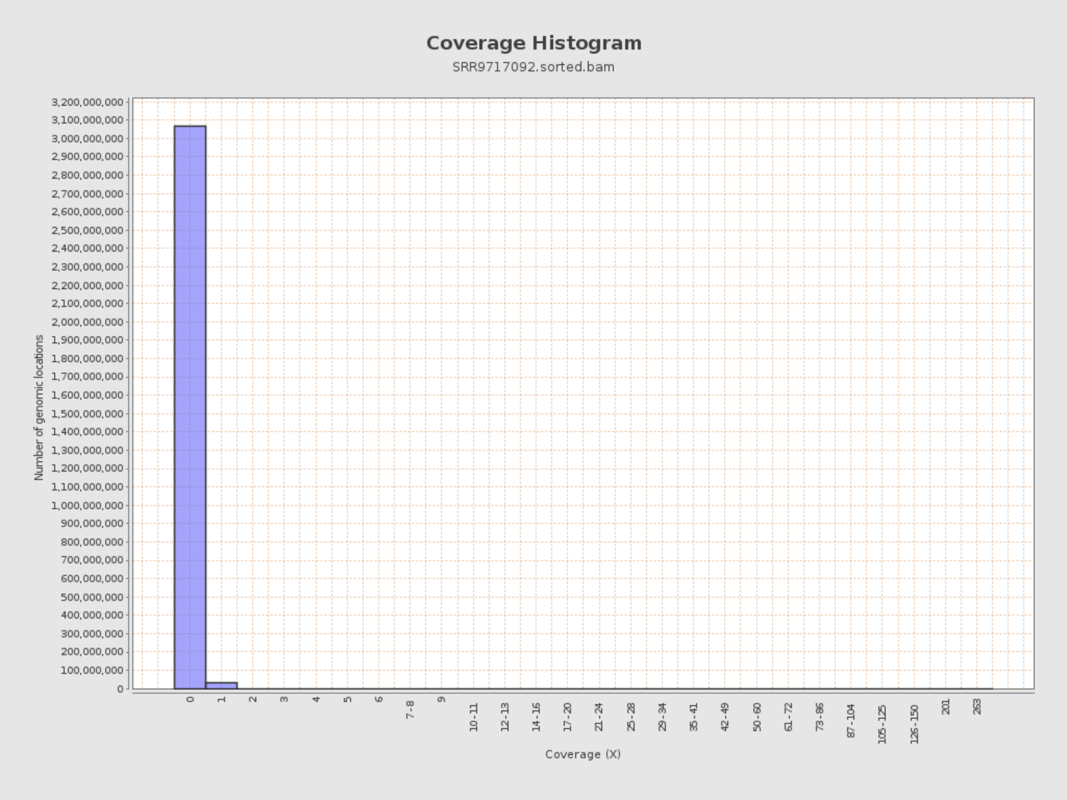
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2393782	0.0096	0.1392
chr2	243199373	3232302	0.0133	0.1658
chr3	198022430	2332696	0.0118	0.1154
chr4	191154276	2044423	0.0107	0.1096
chr5	180915260	1712062	0.0095	0.1009
chr6	171115067	1815182	0.0106	0.1114
chr7	159138663	1649423	0.0104	0.2025

chr8	146364022	2609148	0.0178	0.1475
chr9	141213431	1377756	0.0098	0.1094
chr10	135534747	1584366	0.0117	0.1464
chr11	135006516	1119454	0.0083	0.104
chr12	133851895	1557135	0.0116	0.1144
chr13	115169878	861563	0.0075	0.0895
chr14	107349540	995656	0.0093	0.101
chr15	102531392	751458	0.0073	0.0895
chr16	90354753	1028875	0.0114	0.113
chr17	81195210	1448118	0.0178	0.1418
chr18	78077248	742820	0.0095	0.1289
chr19	59128983	736588	0.0125	0.1452
chr20	63025520	724912	0.0115	0.1118
chr21	48129895	349421	0.0073	0.0889
chr22	51304566	478256	0.0093	0.1007
chrMT	16571	11199	0.6758	0.8855
chrX	155270560	1149901	0.0074	0.0975
chrY	59373566	71720	0.0012	0.0444

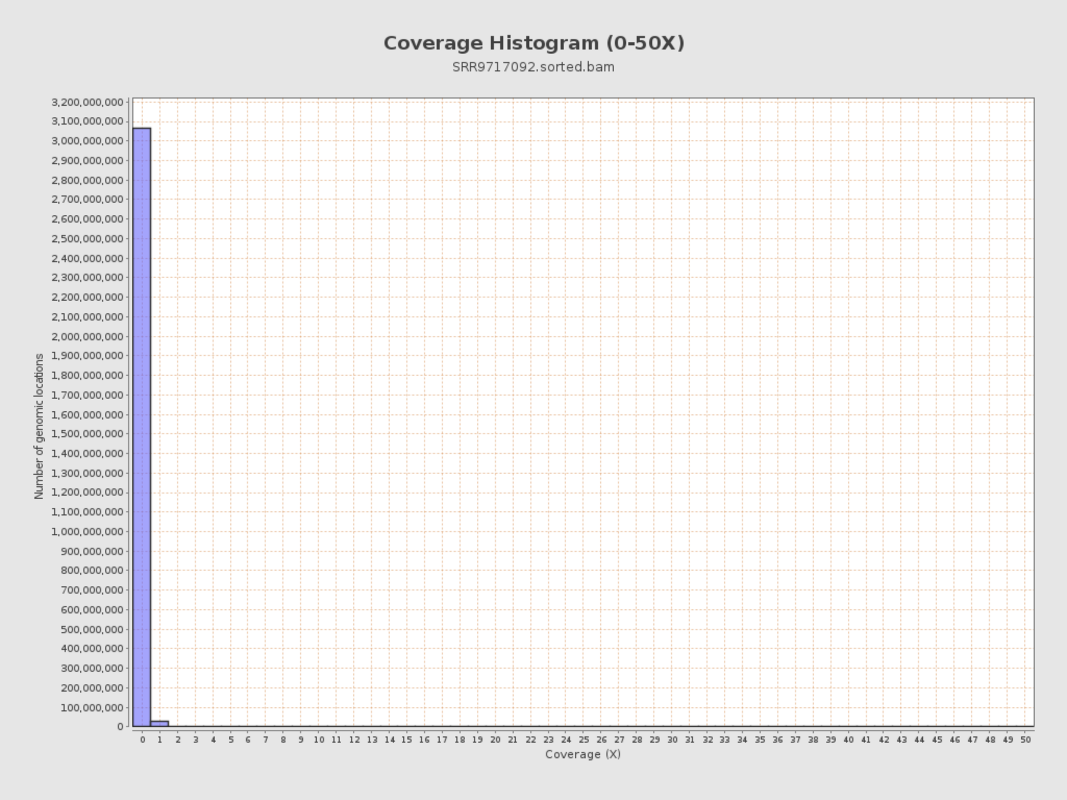
3. Results : Coverage across reference



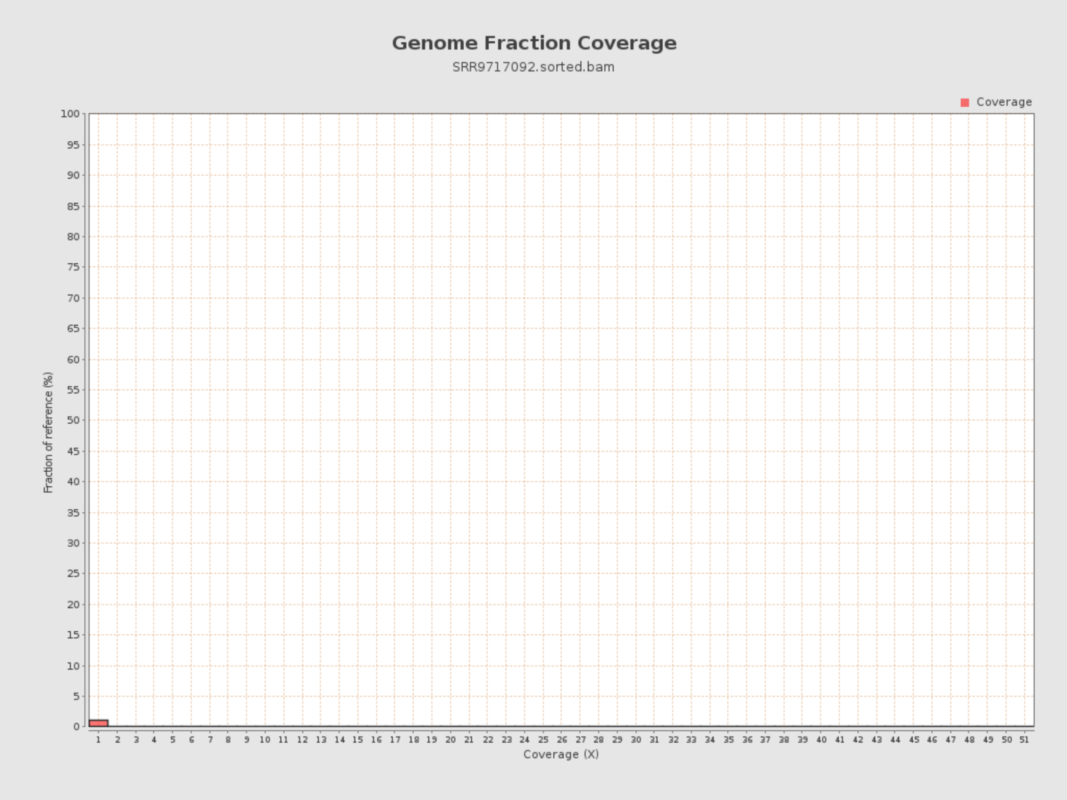
4. Results : Coverage Histogram



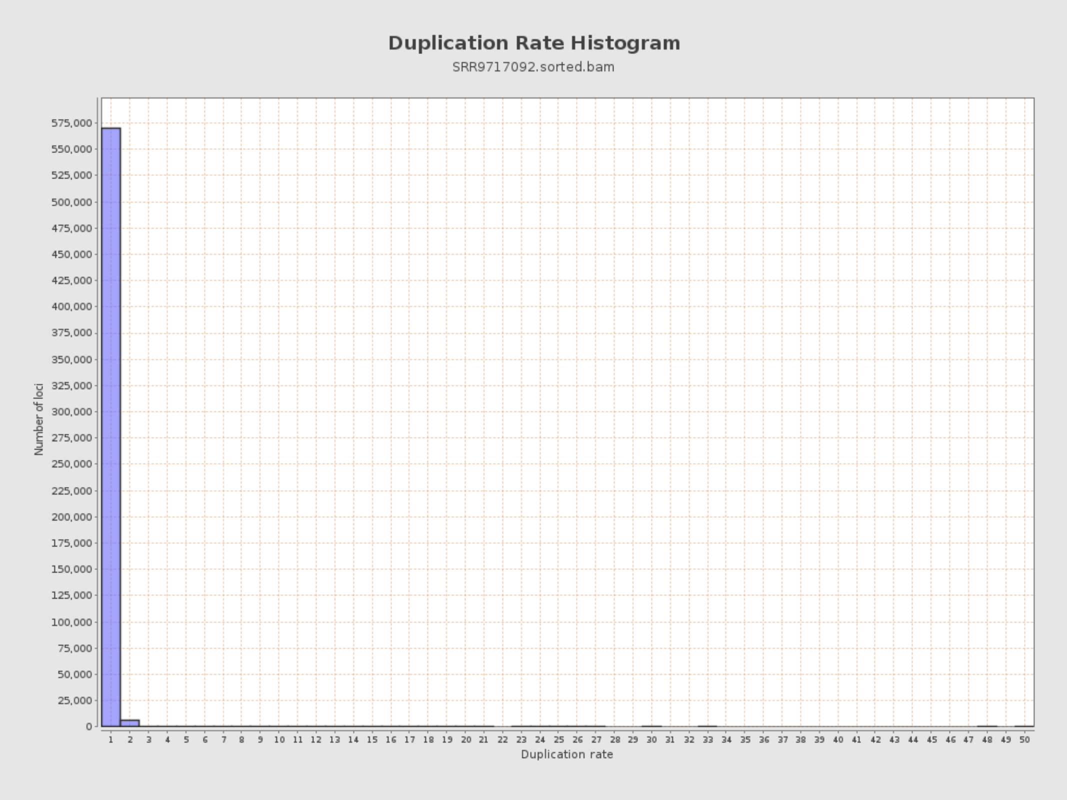
5. Results : Coverage Histogram (0-50X)



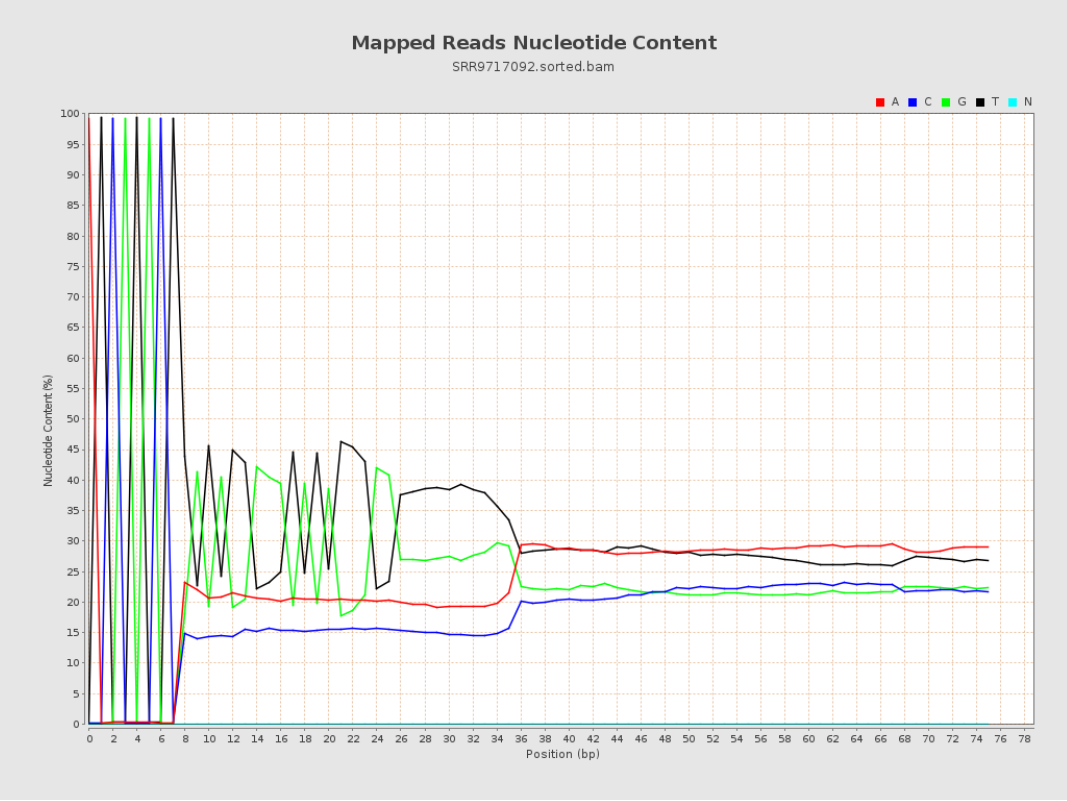
6. Results : Genome Fraction Coverage



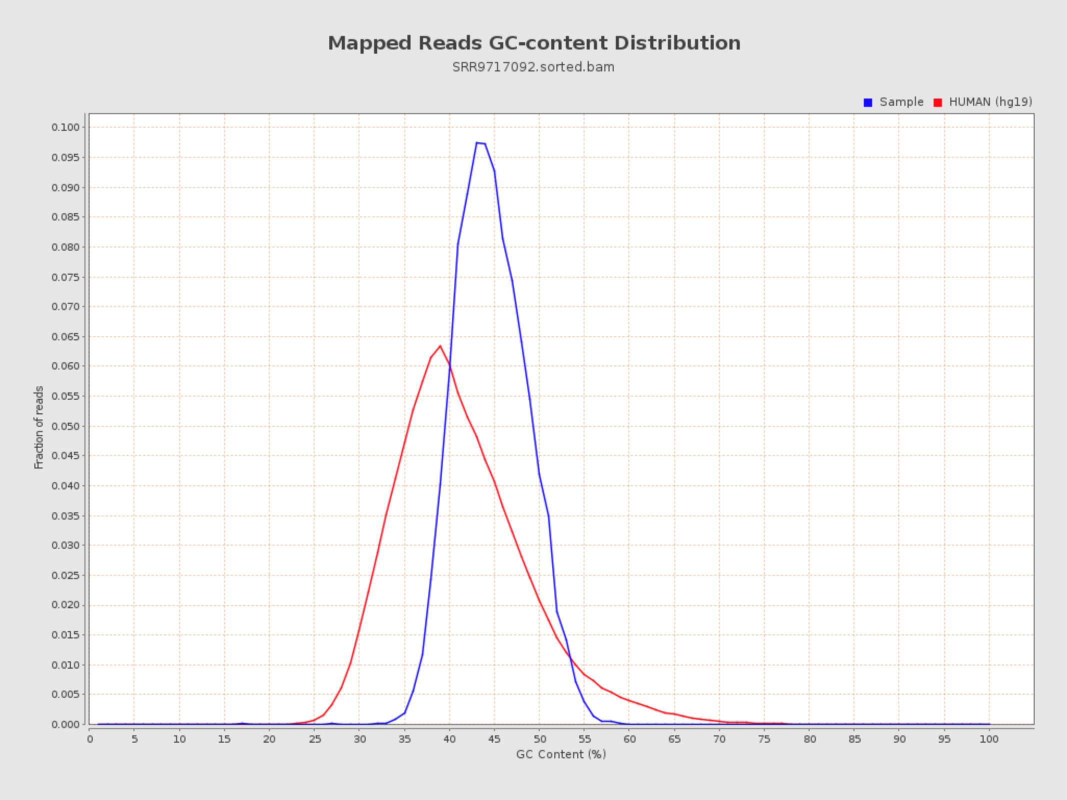
7. Results : Duplication Rate Histogram



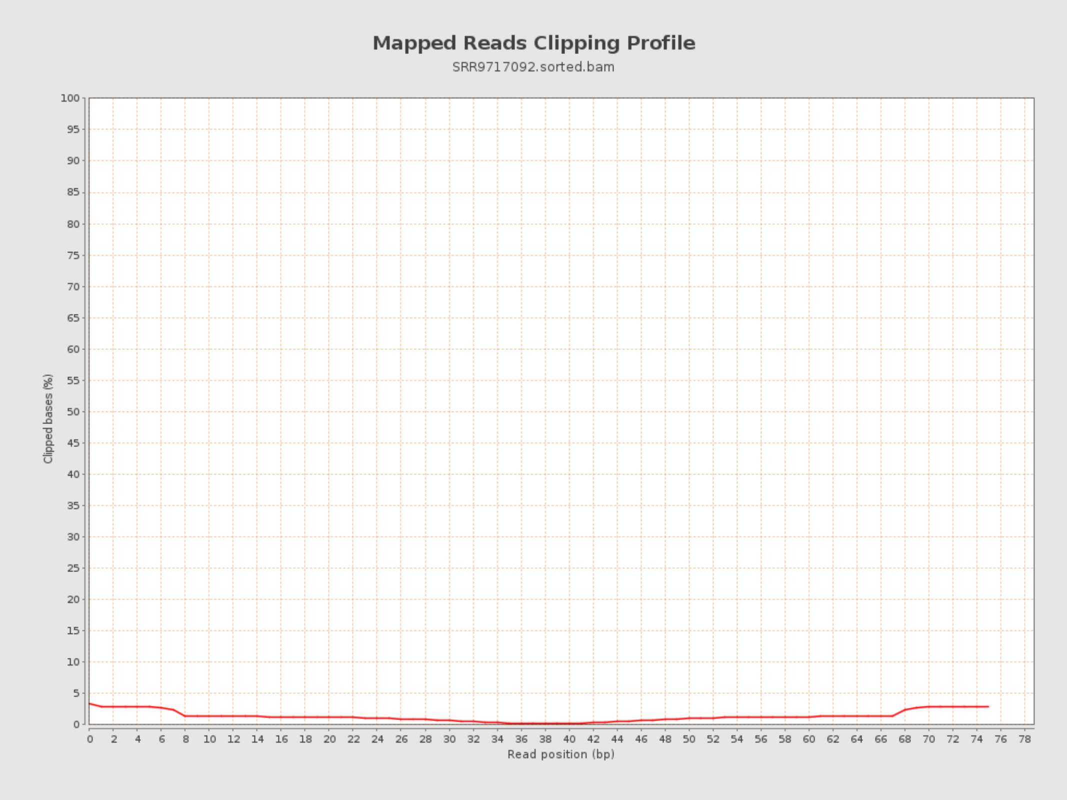
8. Results : Mapped Reads Nucleotide Content



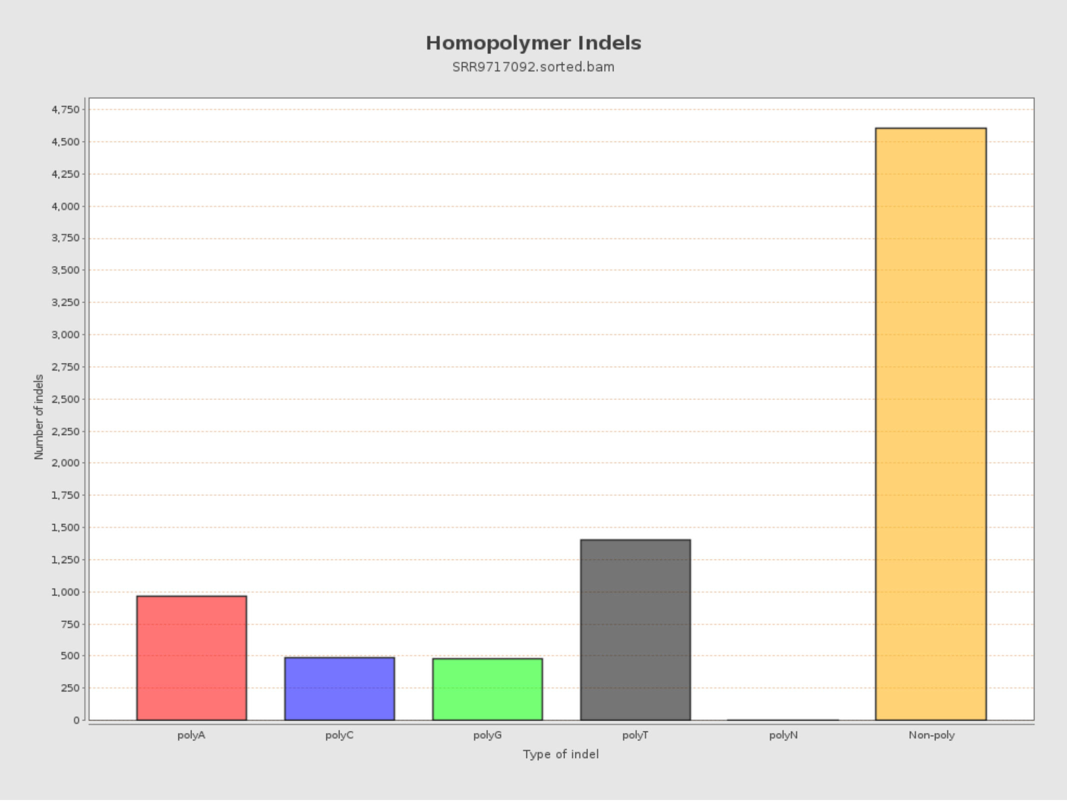
9. Results : Mapped Reads GC-content Distribution



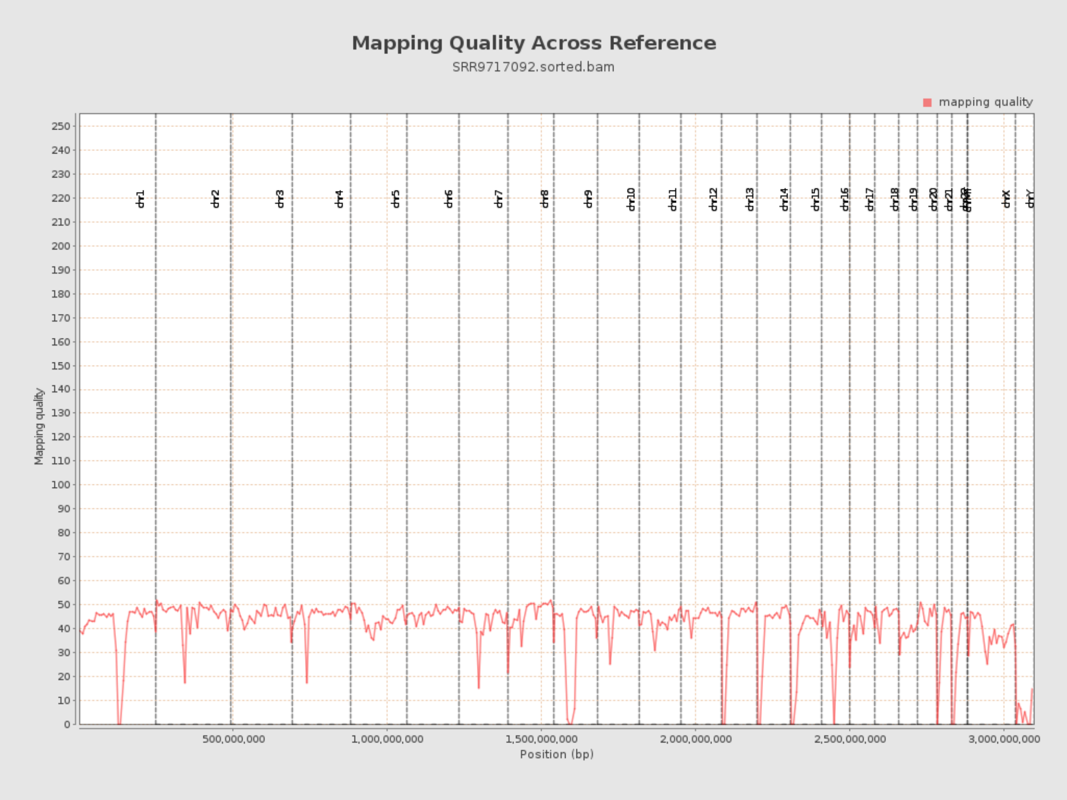
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram