Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:51:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717076.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_SRR9717076 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717076.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:51:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717076.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	723,411
Mapped reads	663,009 / 91.65%
Unmapped reads	60,402 / 8.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,292 / 0.18%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	14,569 / 2.01%
Duplication rate	1.71%
Clipped reads	662,032 / 91.52%

2.2. ACGT Content

Number/percentage of A's	9,850,423 / 25.57%
Number/percentage of C's	6,799,526 / 17.65%
Number/percentage of T's	12,195,373 / 31.65%
Number/percentage of G's	9,683,088 / 25.13%
Number/percentage of N's	382 / 0%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0124

Standard Deviation	0.1396

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

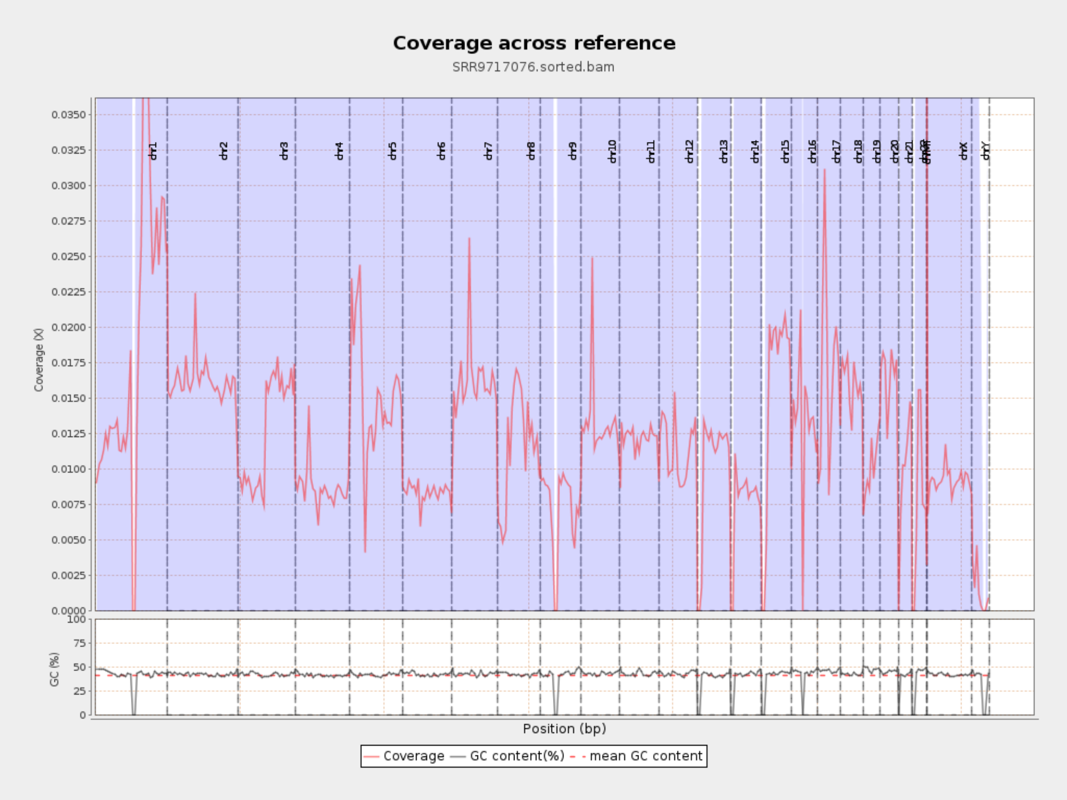
General error rate	0.49%
Mismatches	183,061
Insertions	3,097
Mapped reads with at least one insertion	0.47%
Deletions	7,821
Mapped reads with at least one deletion	1.17%
Homopolymer indels	40.99%

2.6. Chromosome stats

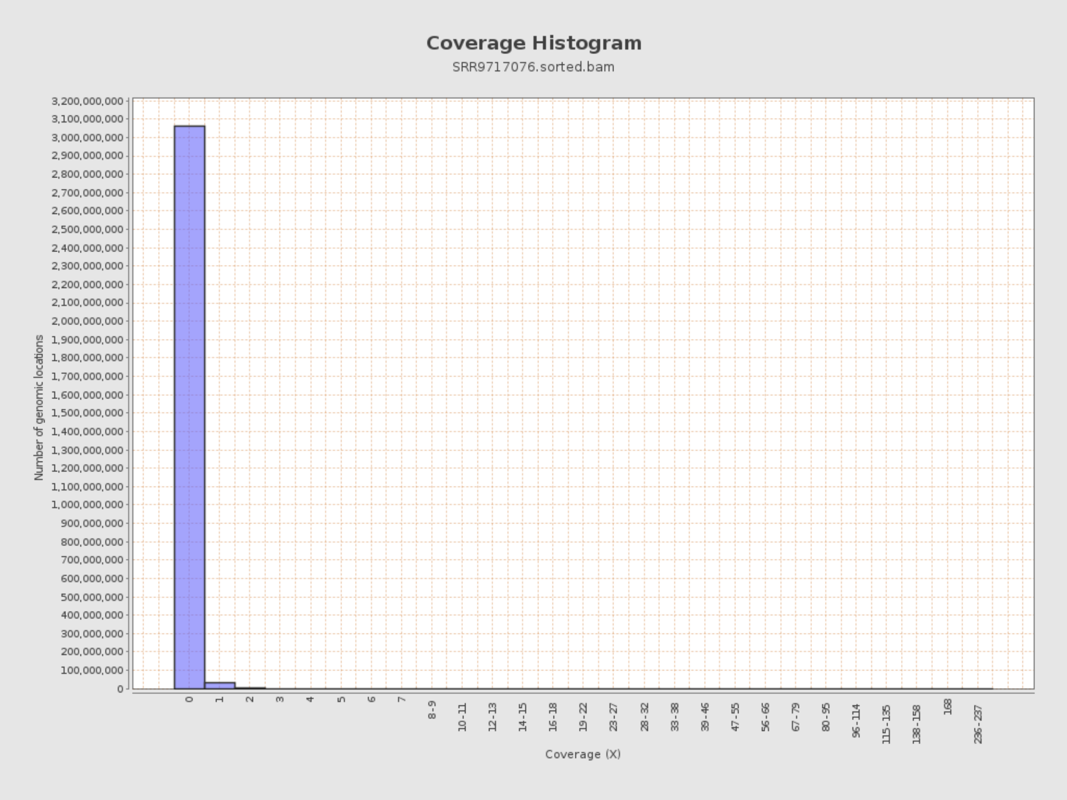
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4538118	0.0182	0.1865
chr2	243199373	3941577	0.0162	0.1767
chr3	198022430	2495365	0.0126	0.1187
chr4	191154276	1659120	0.0087	0.0997
chr5	180915260	2783850	0.0154	0.1294
chr6	171115067	1428228	0.0083	0.0998
chr7	159138663	2587548	0.0163	0.225

chr8	146364022	1717705	0.0117	0.123
chr9	141213431	1010931	0.0072	0.1045
chr10	135534747	1804404	0.0133	0.1631
chr11	135006516	1645346	0.0122	0.1341
chr12	133851895	1516206	0.0113	0.1116
chr13	115169878	1160358	0.0101	0.1049
chr14	107349540	806545	0.0075	0.0925
chr15	102531392	1594031	0.0155	0.1305
chr16	90354753	1179693	0.0131	0.1263
chr17	81195210	1391407	0.0171	0.1416
chr18	78077248	1250612	0.016	0.1923
chr19	59128983	601032	0.0102	0.1415
chr20	63025520	1028096	0.0163	0.1335
chr21	48129895	486491	0.0101	0.1078
chr22	51304566	401636	0.0078	0.0923
chrMT	16571	664	0.0401	0.1961
chrX	155270560	1428126	0.0092	0.1079
chrY	59373566	84101	0.0014	0.0458

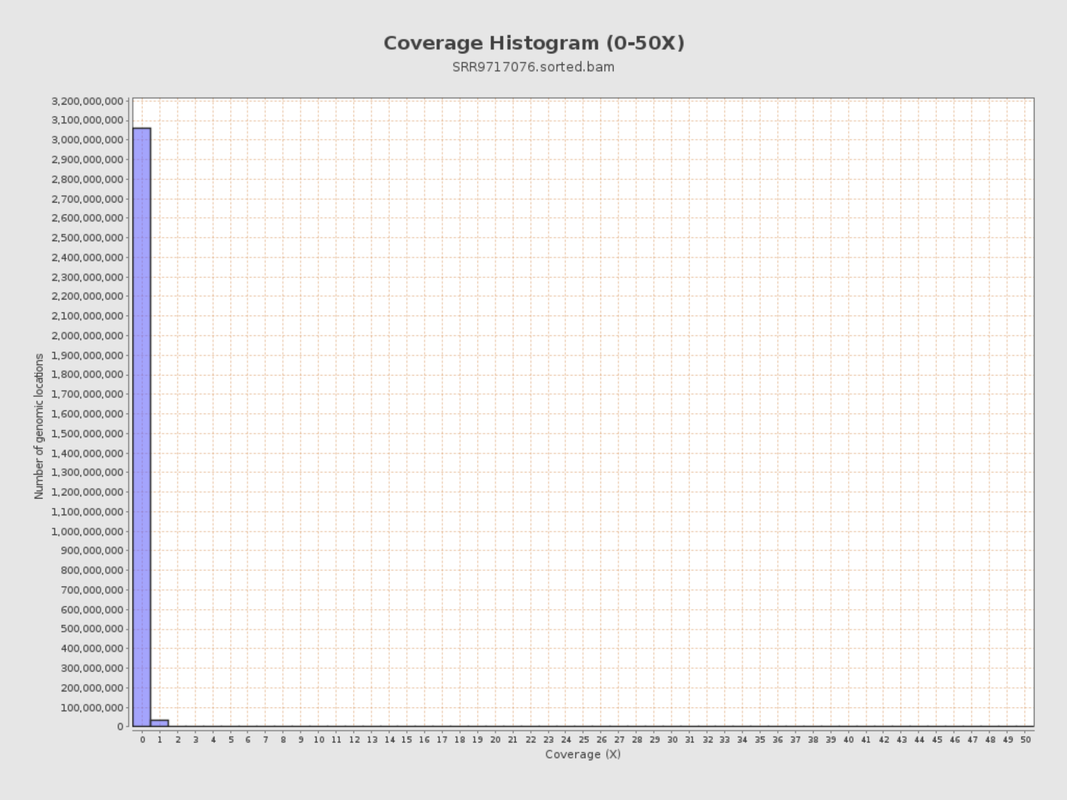
3. Results : Coverage across reference



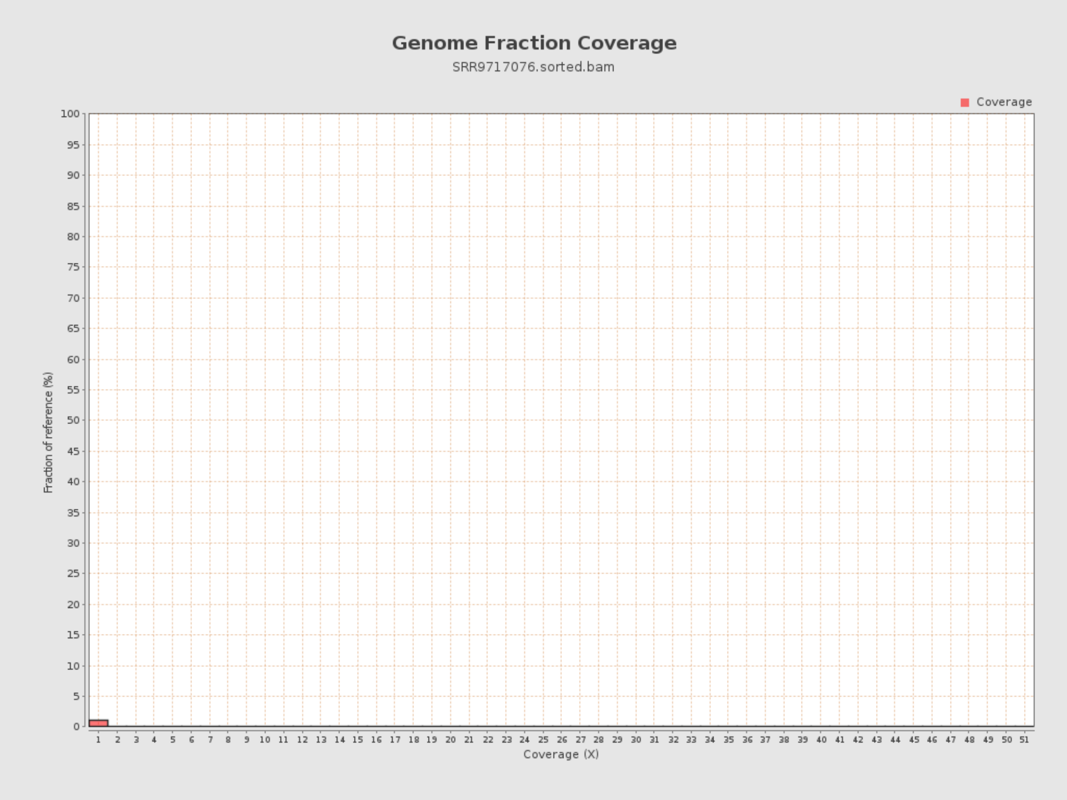
4. Results : Coverage Histogram



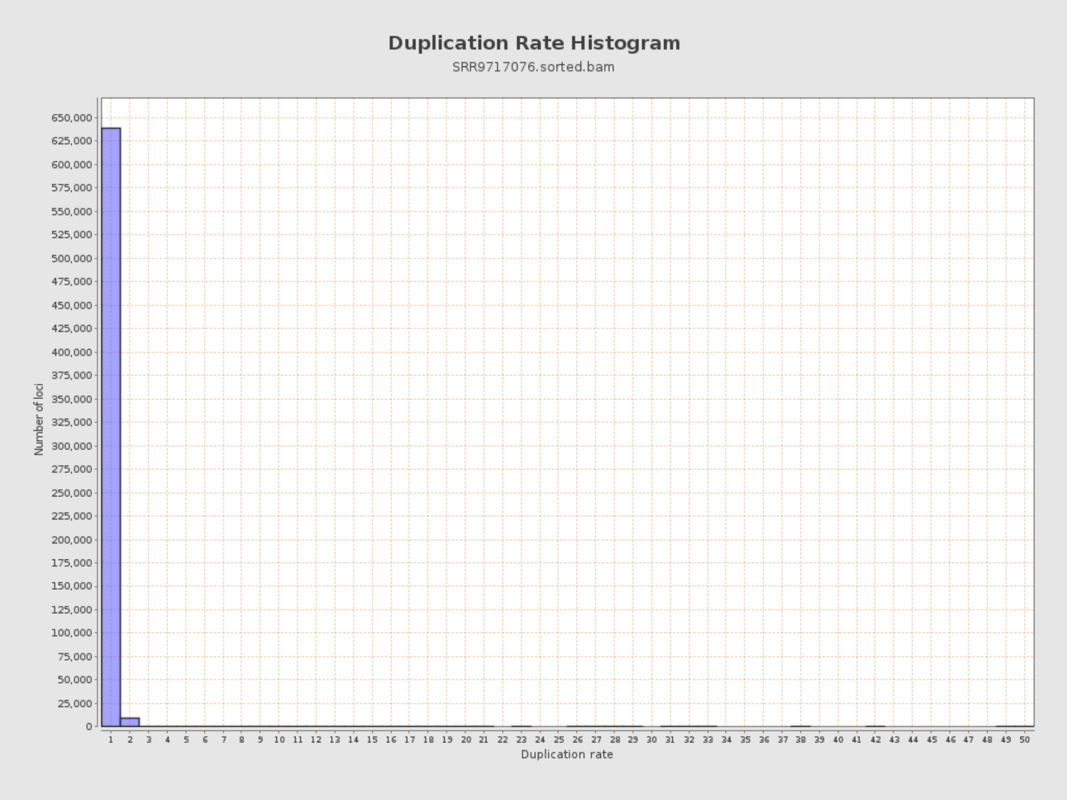
5. Results : Coverage Histogram (0-50X)



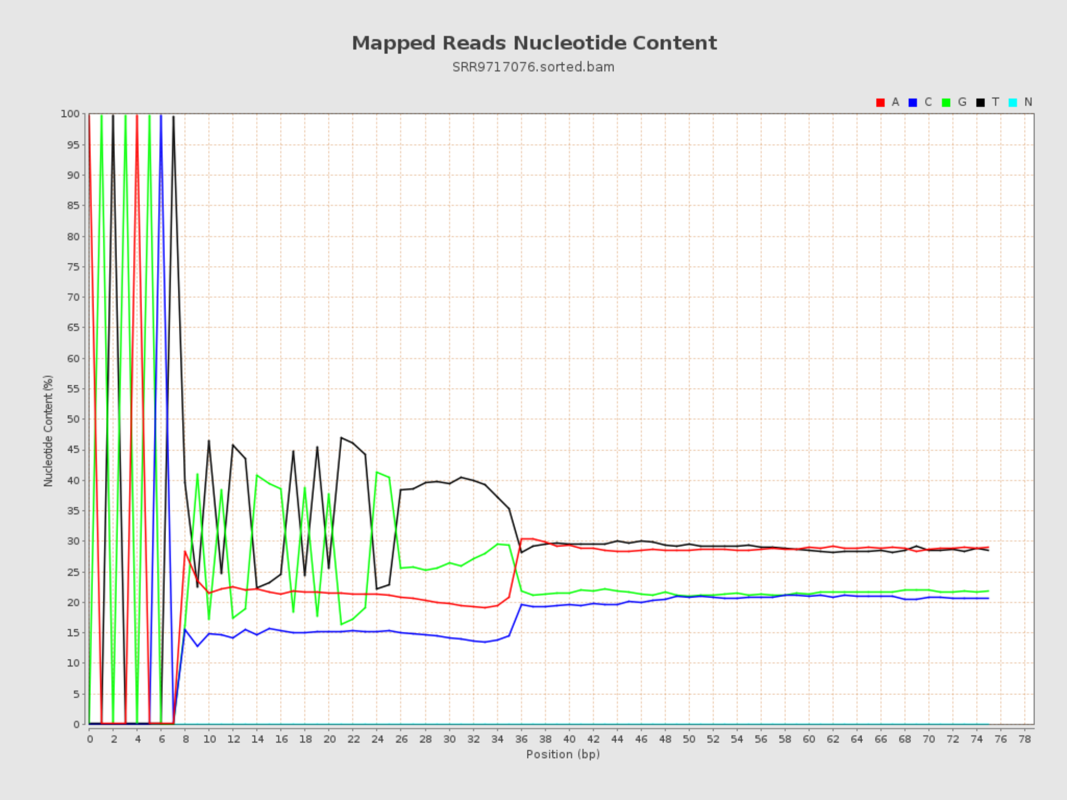
6. Results : Genome Fraction Coverage



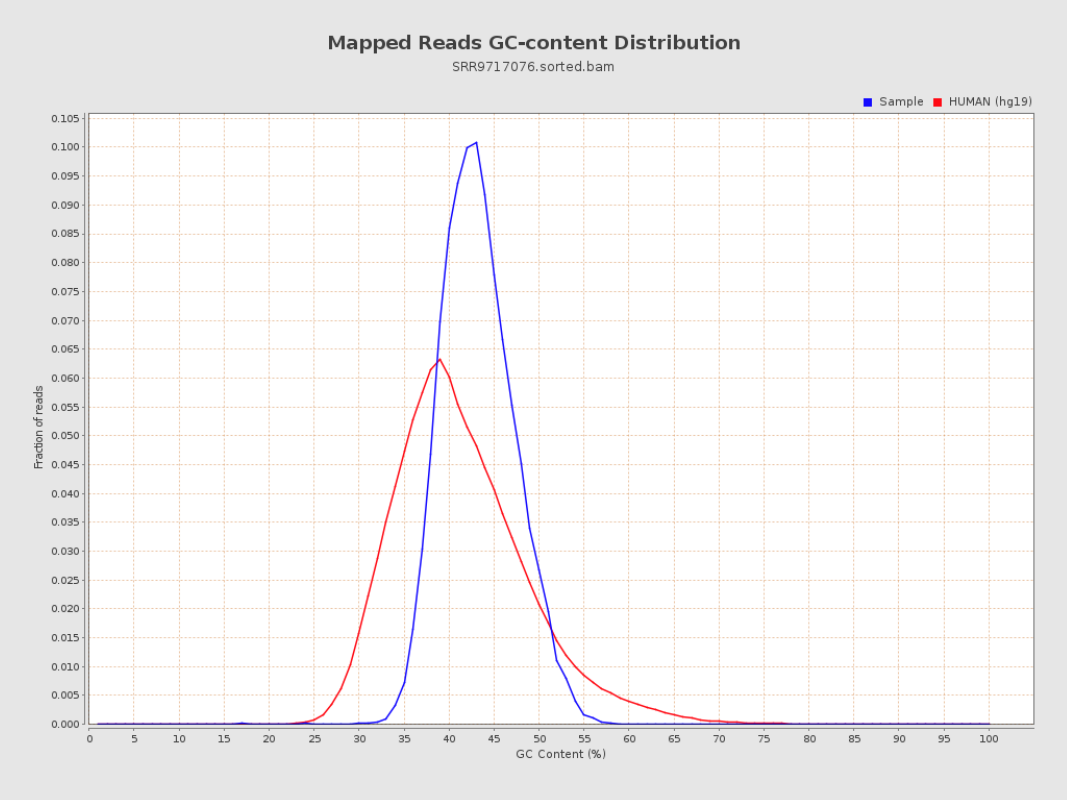
7. Results : Duplication Rate Histogram



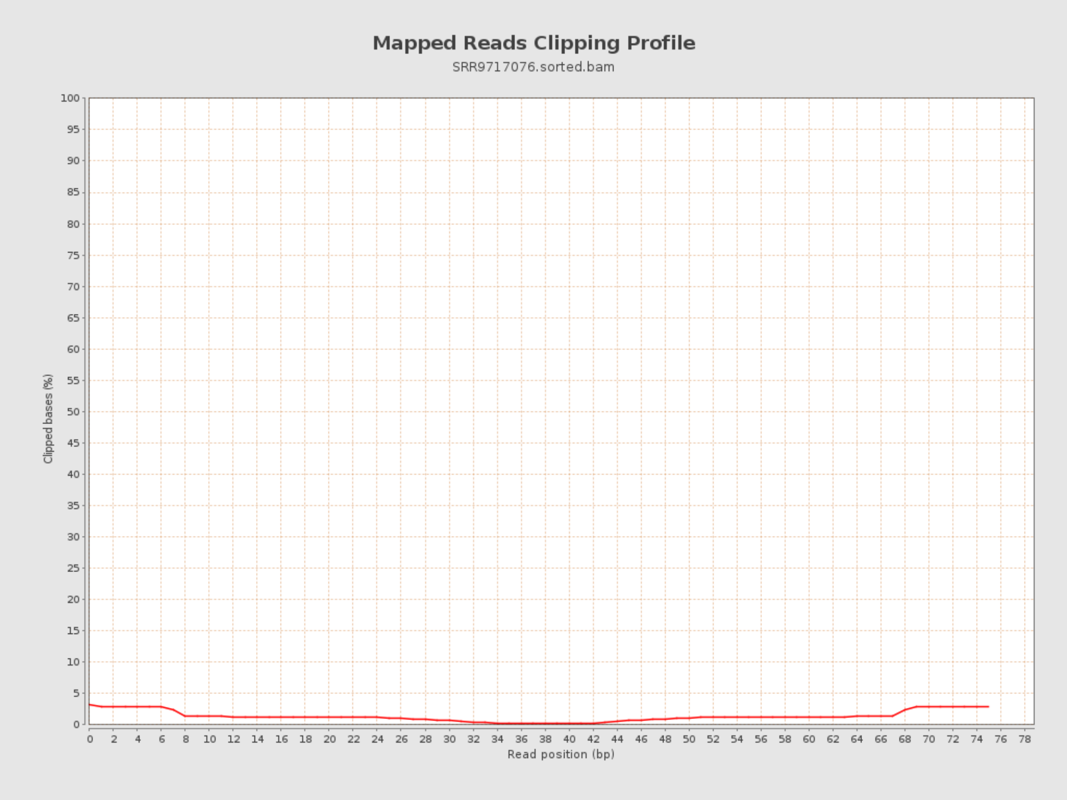
8. Results : Mapped Reads Nucleotide Content



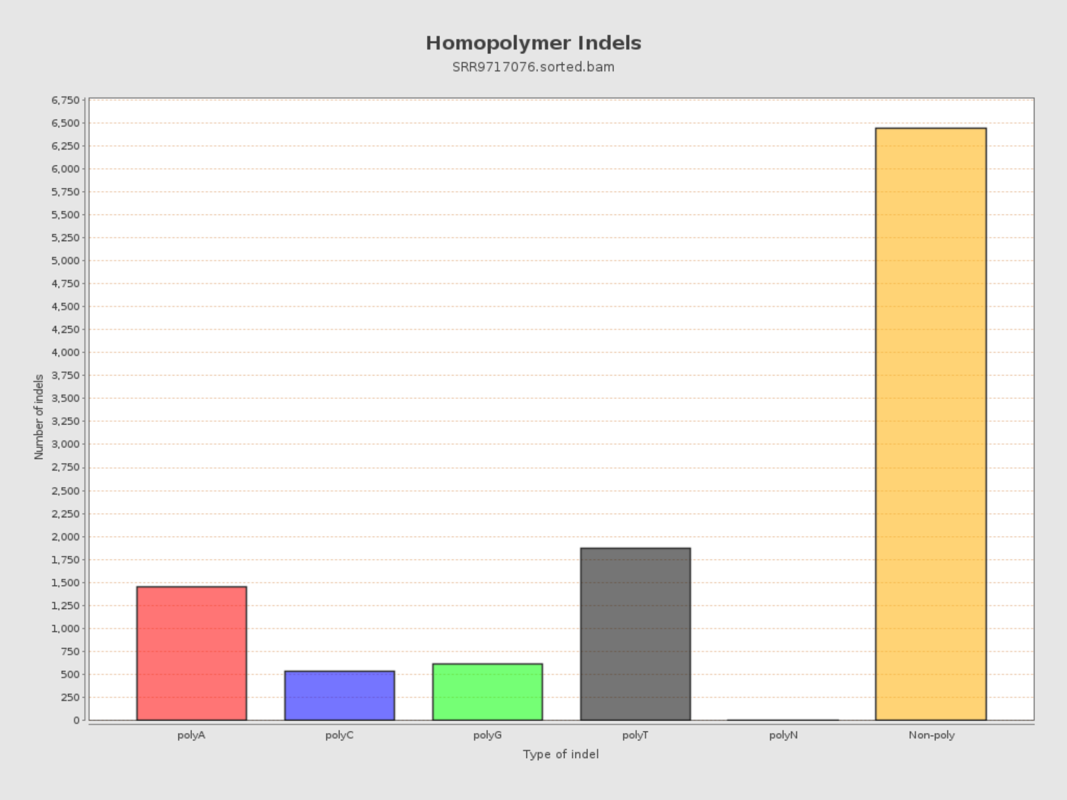
9. Results : Mapped Reads GC-content Distribution



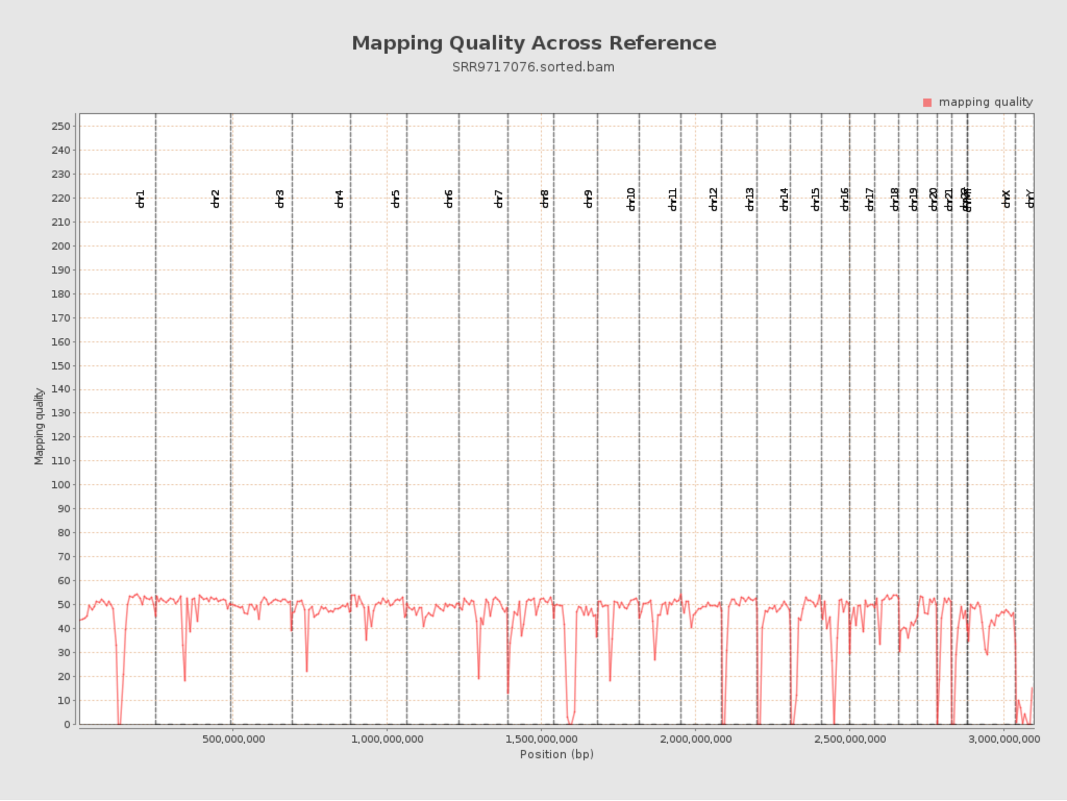
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram