Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:38:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717071.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_SRR9717071 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717071.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:38:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,038,023
Mapped reads	943,098 / 90.86%
Unmapped reads	94,925 / 9.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,855 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	31,728 / 3.06%
Duplication rate	2.52%
Clipped reads	944,515 / 90.99%

2.2. ACGT Content

Number/percentage of A's	13,338,379 / 24.39%
Number/percentage of C's	10,235,521 / 18.72%
Number/percentage of T's	17,610,412 / 32.2%
Number/percentage of G's	13,502,254 / 24.69%
Number/percentage of N's	946 / 0%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0177

Standard Deviation	0.187

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

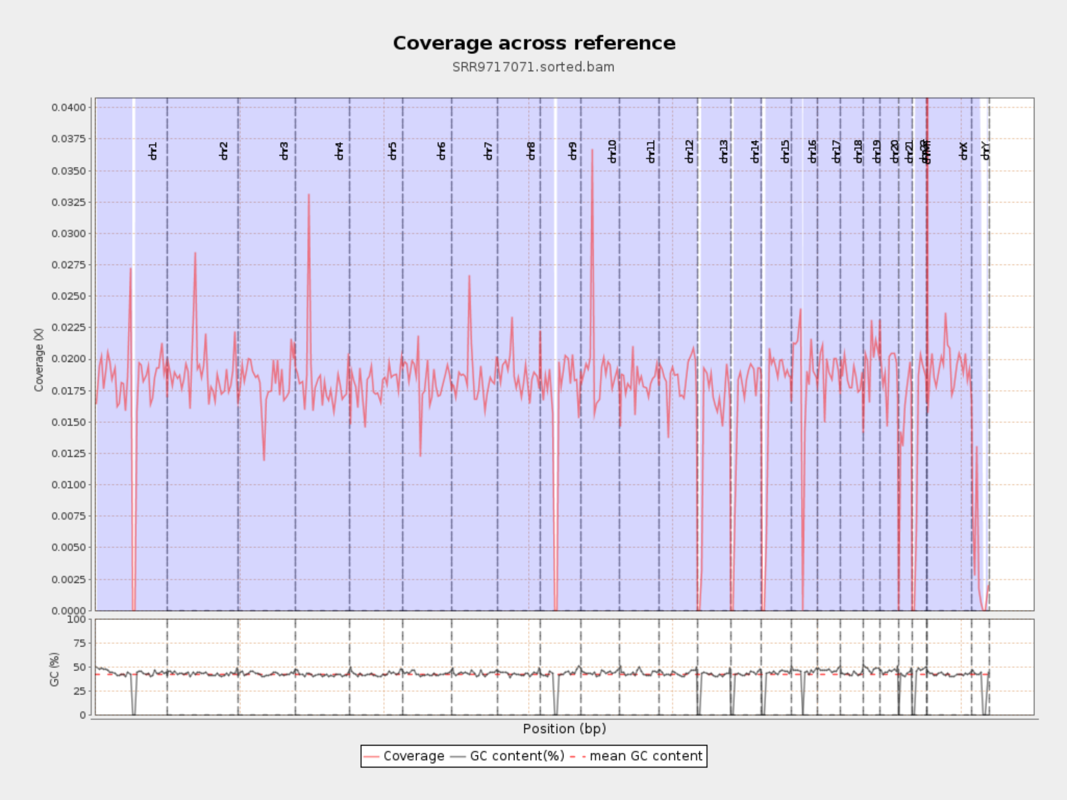
General error rate	0.52%
Mismatches	277,168
Insertions	4,149
Mapped reads with at least one insertion	0.44%
Deletions	11,253
Mapped reads with at least one deletion	1.18%
Homopolymer indels	42.46%

2.6. Chromosome stats

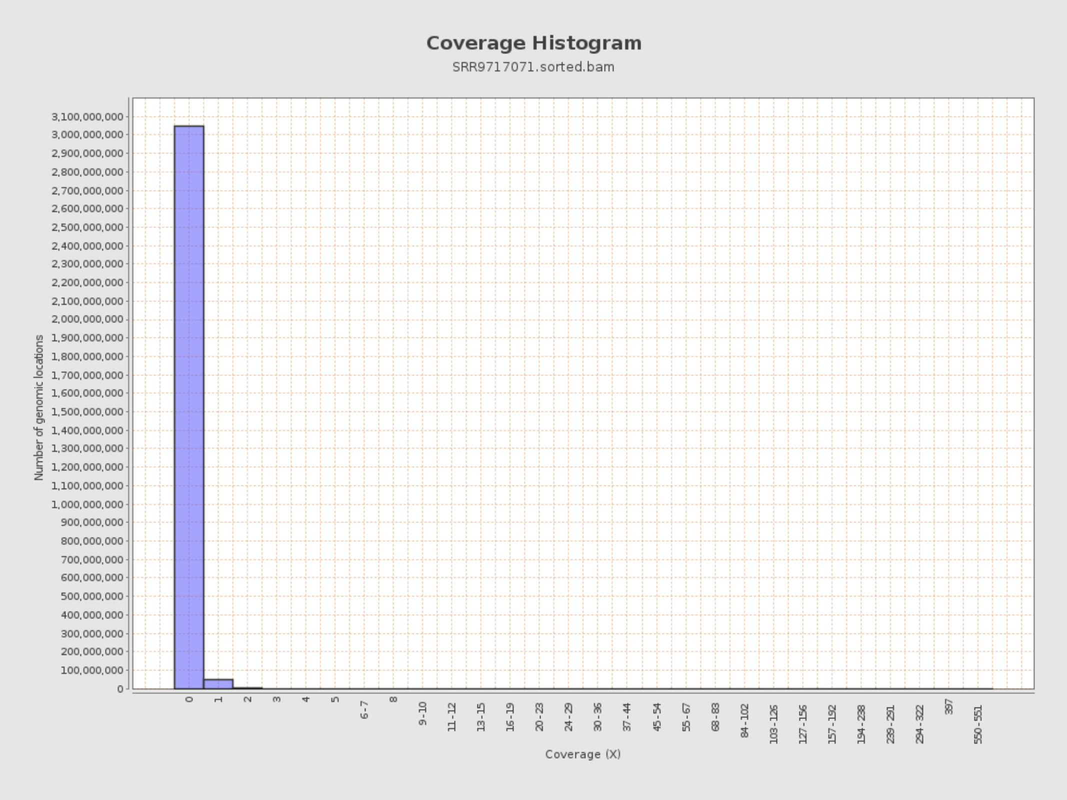
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4386960	0.0176	0.2701
chr2	243199373	4618481	0.019	0.275
chr3	198022430	3605422	0.0182	0.1442
chr4	191154276	3514456	0.0184	0.1643
chr5	180915260	3268380	0.0181	0.1432
chr6	171115067	3134629	0.0183	0.1574
chr7	159138663	2956777	0.0186	0.2045

chr8	146364022	2753775	0.0188	0.2165
chr9	141213431	2312364	0.0164	0.1566
chr10	135534747	2660335	0.0196	0.2081
chr11	135006516	2455462	0.0182	0.1633
chr12	133851895	2478502	0.0185	0.1466
chr13	115169878	1684896	0.0146	0.1298
chr14	107349540	1663271	0.0155	0.1362
chr15	102531392	1604052	0.0156	0.1362
chr16	90354753	1623230	0.018	0.1508
chr17	81195210	1553247	0.0191	0.1532
chr18	78077248	1445725	0.0185	0.2326
chr19	59128983	1188029	0.0201	0.2229
chr20	63025520	1189743	0.0189	0.1504
chr21	48129895	717021	0.0149	0.1458
chr22	51304566	680439	0.0133	0.1238
chrMT	16571	3939	0.2377	0.5002
chrX	155270560	3008200	0.0194	0.1582
chrY	59373566	198235	0.0033	0.1341

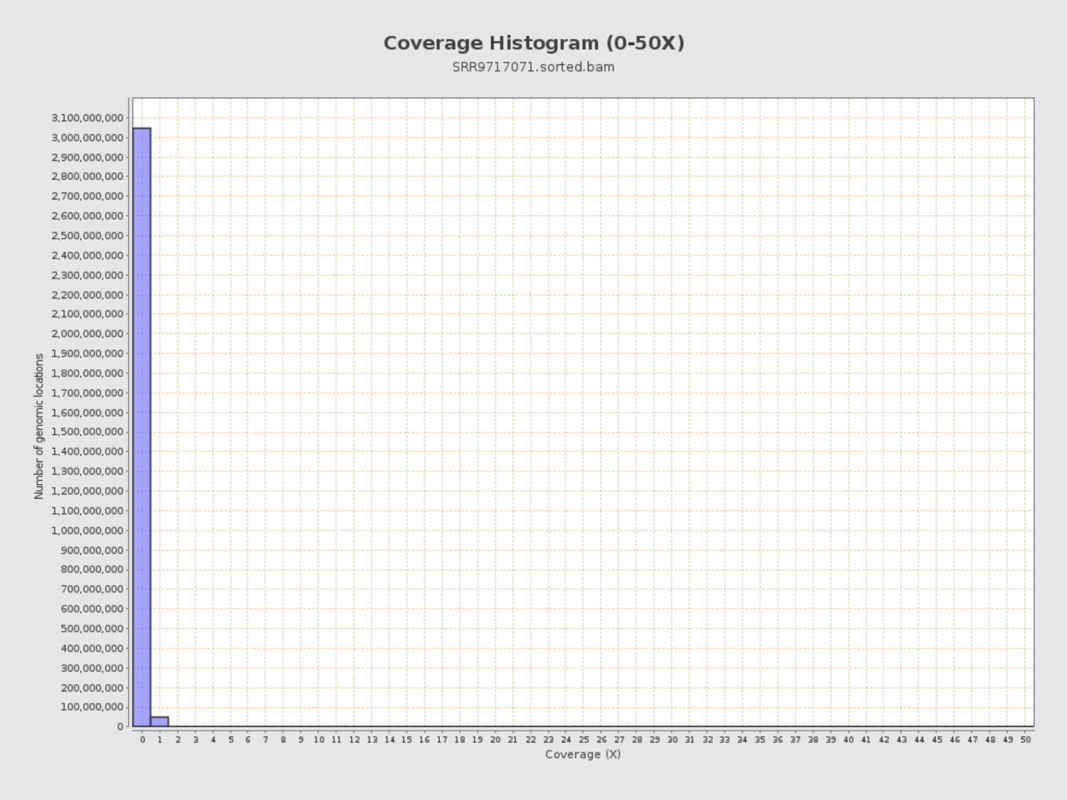
3. Results : Coverage across reference



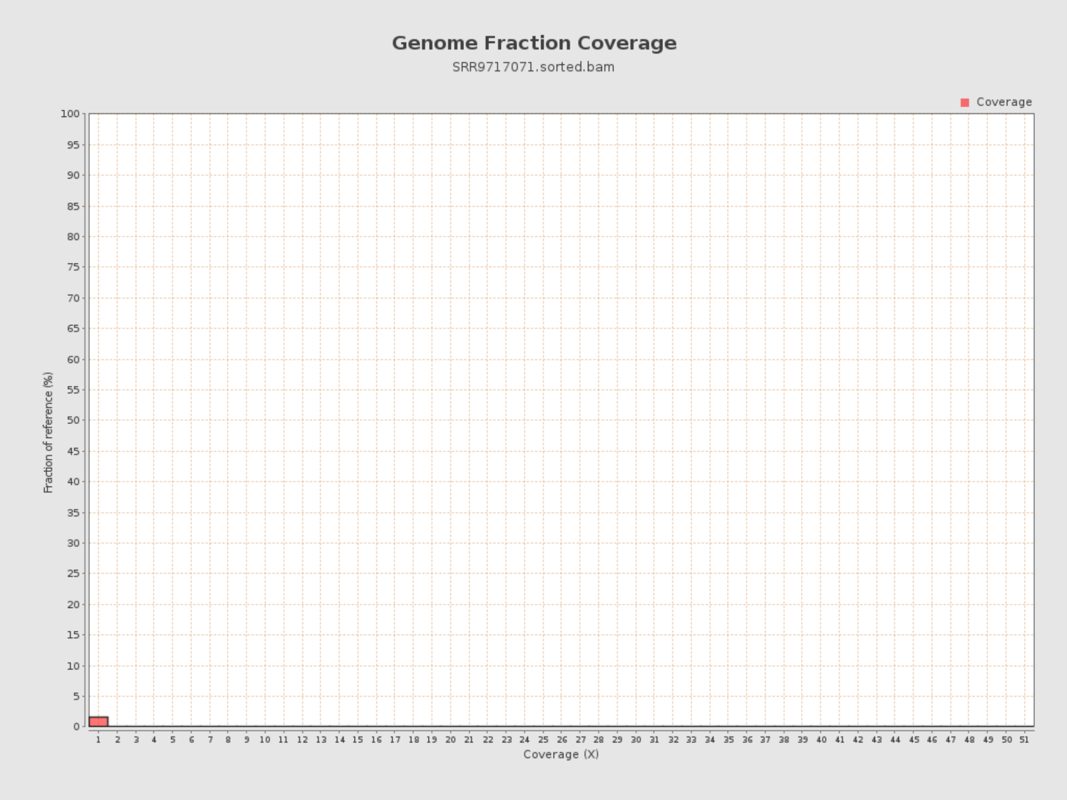
4. Results : Coverage Histogram



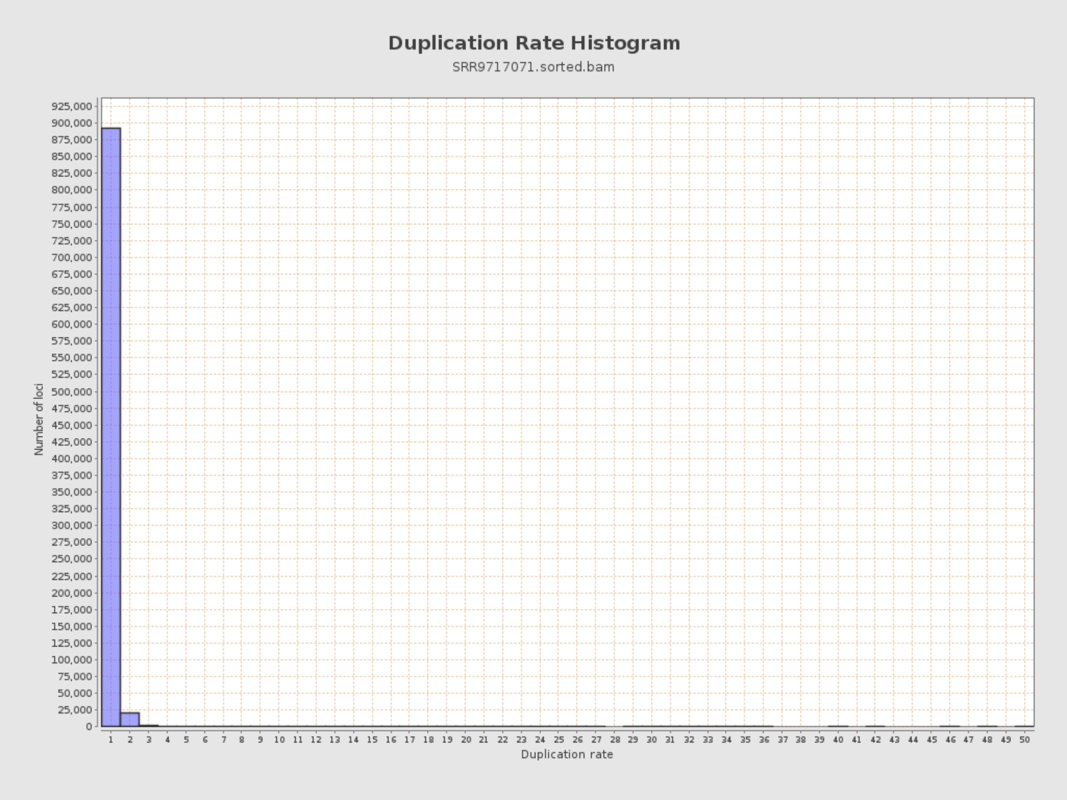
5. Results : Coverage Histogram (0-50X)



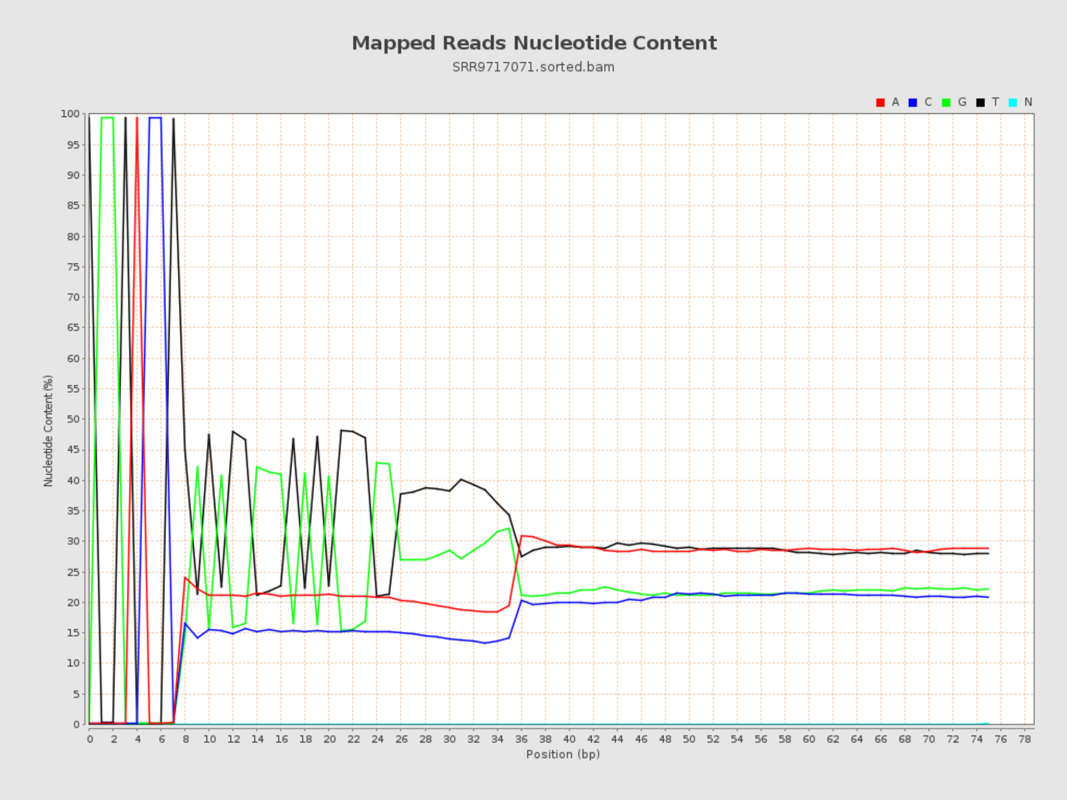
6. Results : Genome Fraction Coverage



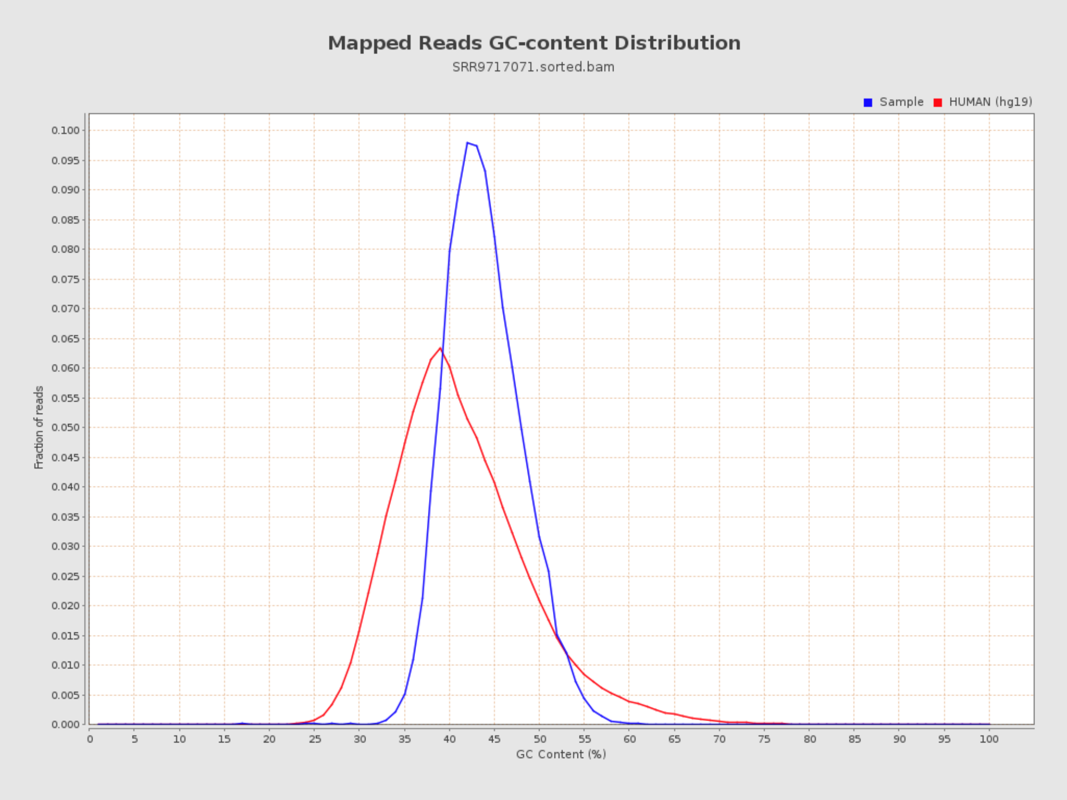
7. Results : Duplication Rate Histogram



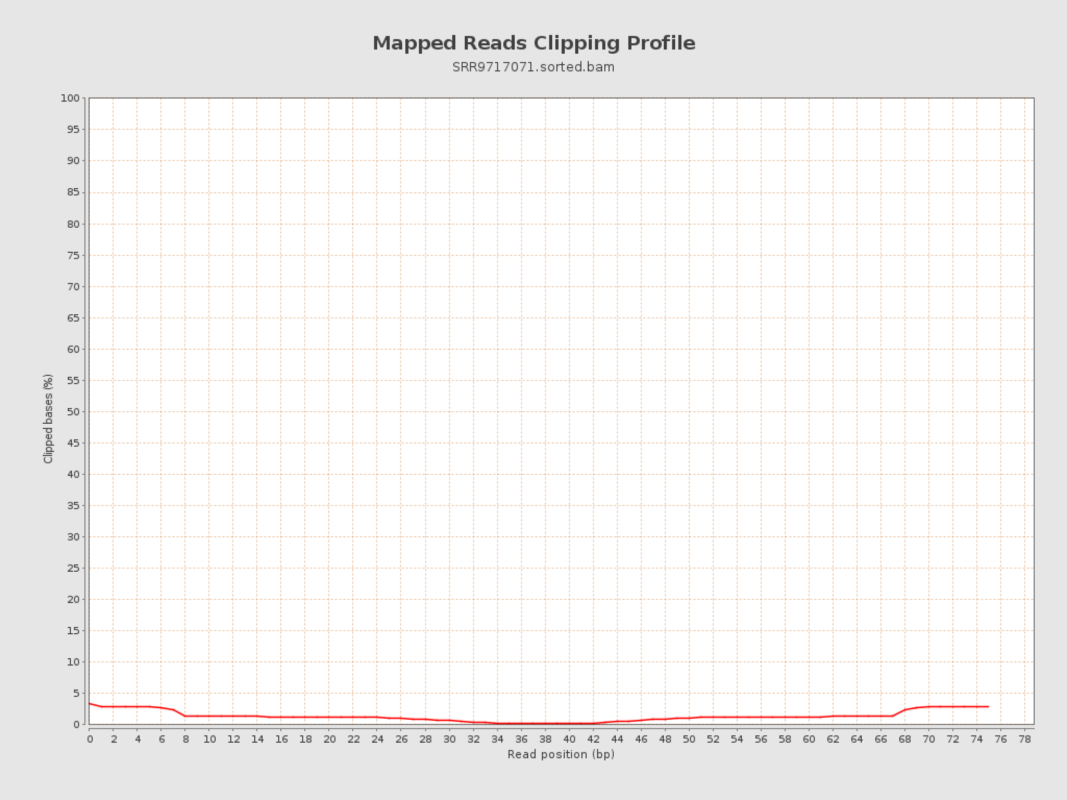
8. Results : Mapped Reads Nucleotide Content



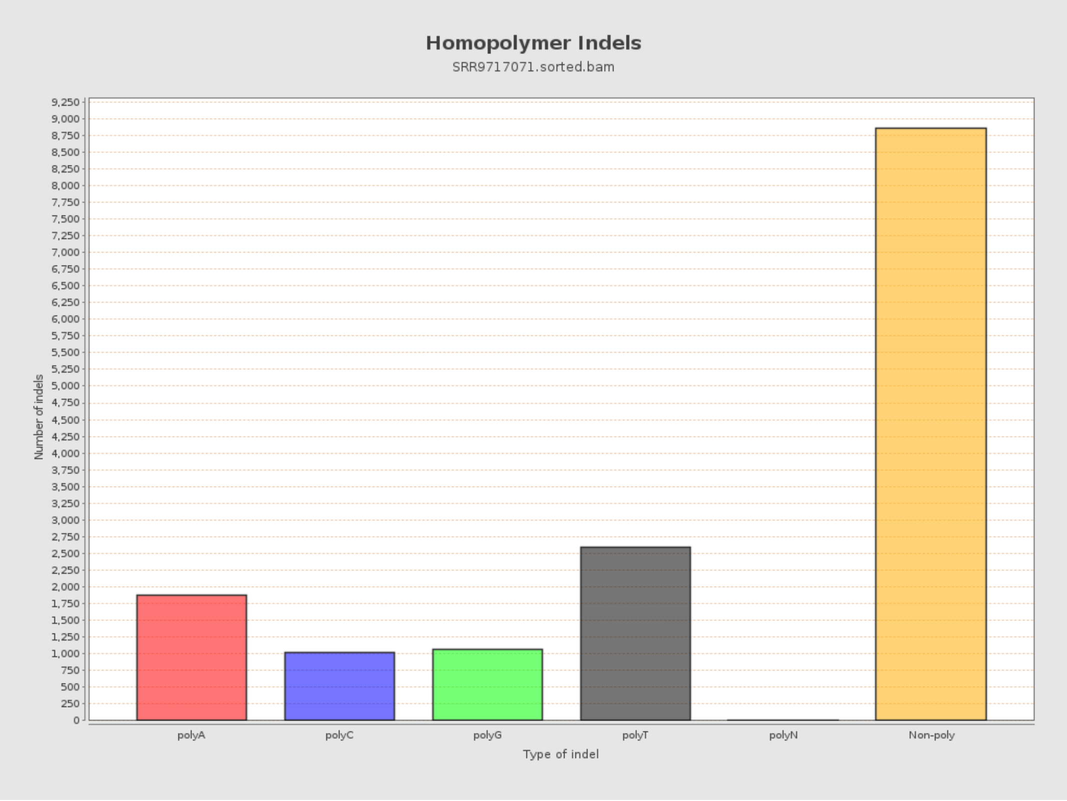
9. Results : Mapped Reads GC-content Distribution



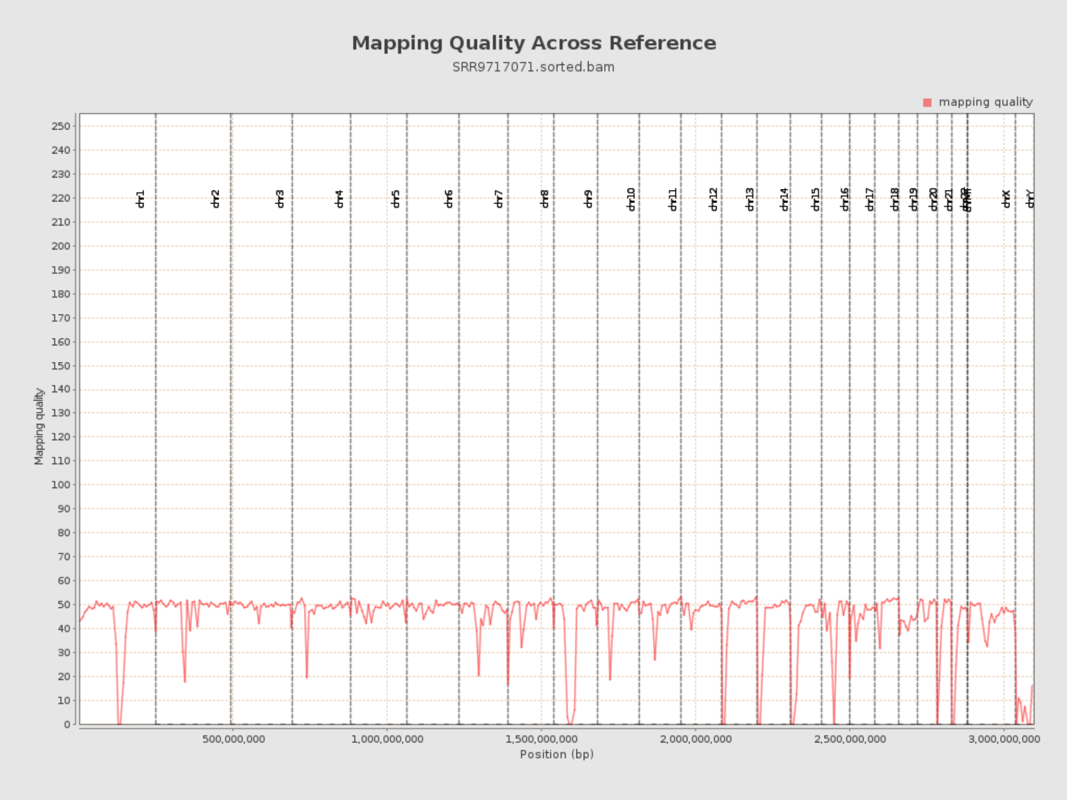
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram