Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:24:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716760.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_SRR9716760 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716760.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:24:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716760.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,010,192
Mapped reads	846,759 / 83.82%
Unmapped reads	163,433 / 16.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,116 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	15,566 / 1.54%
Duplication rate	1.33%
Clipped reads	847,060 / 83.85%

2.2. ACGT Content

Number/percentage of A's	11,292,500 / 23.95%
Number/percentage of C's	9,346,681 / 19.82%
Number/percentage of T's	14,044,885 / 29.79%
Number/percentage of G's	12,466,823 / 26.44%
Number/percentage of N's	1,311 / 0%
GC Percentage	46.26%

2.3. Coverage

Mean	0.0152

Standard Deviation	0.1488

2.4. Mapping Quality

Mean Mapping Quality	40.22

2.5. Mismatches and indels

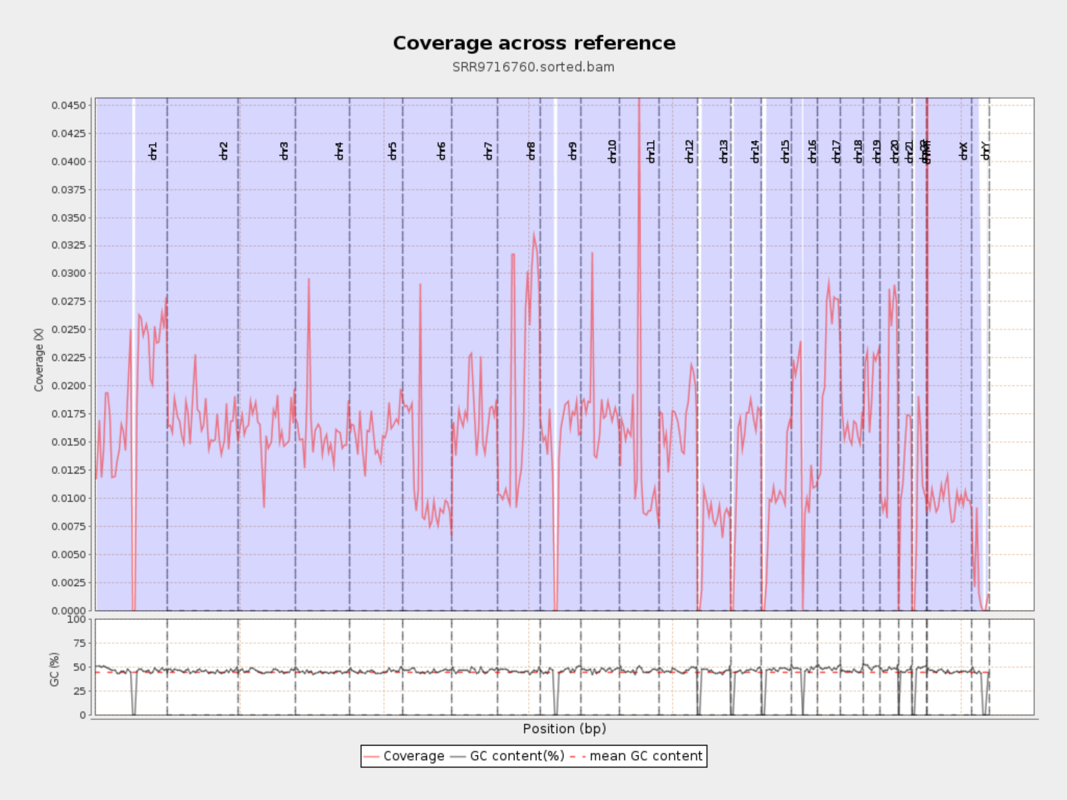
General error rate	0.53%
Mismatches	243,600
Insertions	3,381
Mapped reads with at least one insertion	0.4%
Deletions	7,760
Mapped reads with at least one deletion	0.91%
Homopolymer indels	35.66%

2.6. Chromosome stats

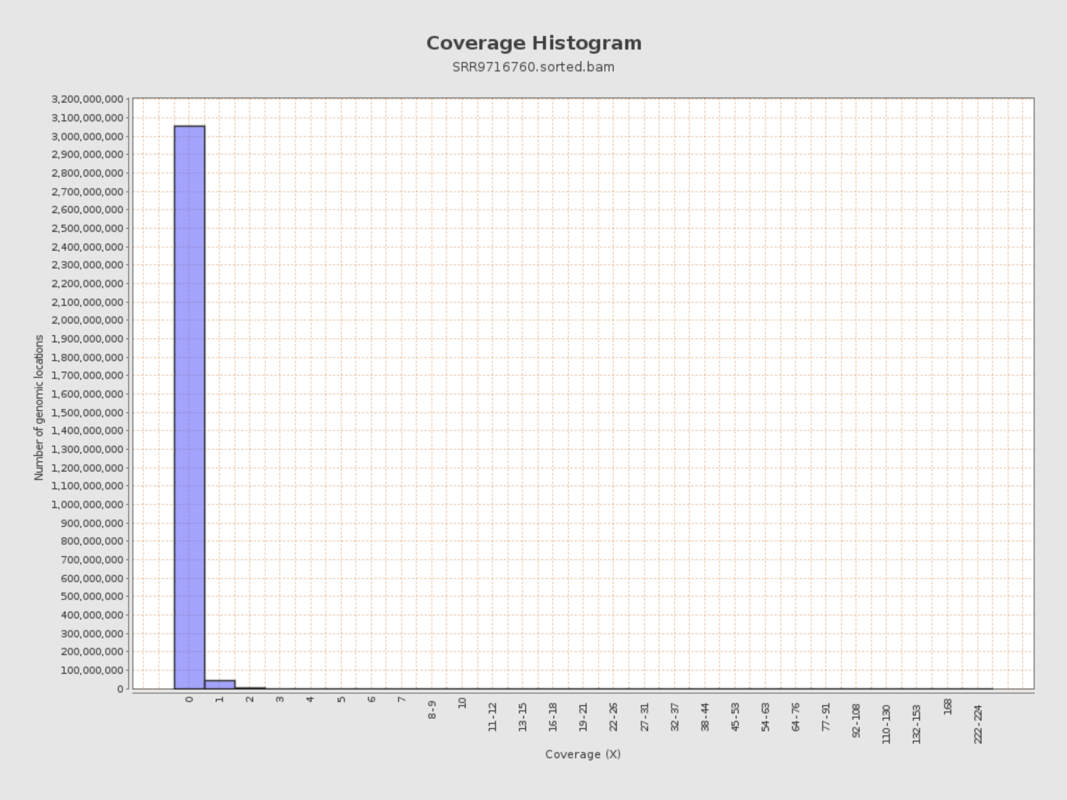
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4615613	0.0185	0.1787
chr2	243199373	4076154	0.0168	0.1802
chr3	198022430	3196080	0.0161	0.138
chr4	191154276	3069842	0.0161	0.146
chr5	180915260	2880830	0.0159	0.1345
chr6	171115067	2022474	0.0118	0.1197
chr7	159138663	2772219	0.0174	0.1781

chr8	146364022	2920609	0.02	0.1578
chr9	141213431	2050971	0.0145	0.1367
chr10	135534747	2451127	0.0181	0.196
chr11	135006516	1943598	0.0144	0.147
chr12	133851895	2274683	0.017	0.1386
chr13	115169878	839708	0.0073	0.0915
chr14	107349540	1507721	0.014	0.1293
chr15	102531392	945631	0.0092	0.1038
chr16	90354753	1256196	0.0139	0.1315
chr17	81195210	1861656	0.0229	0.1688
chr18	78077248	1264317	0.0162	0.1701
chr19	59128983	1235613	0.0209	0.1781
chr20	63025520	1184674	0.0188	0.1504
chr21	48129895	623107	0.0129	0.1293
chr22	51304566	497889	0.0097	0.1058
chrMT	16571	3352	0.2023	0.4583
chrX	155270560	1529442	0.0099	0.1143
chrY	59373566	141361	0.0024	0.0786

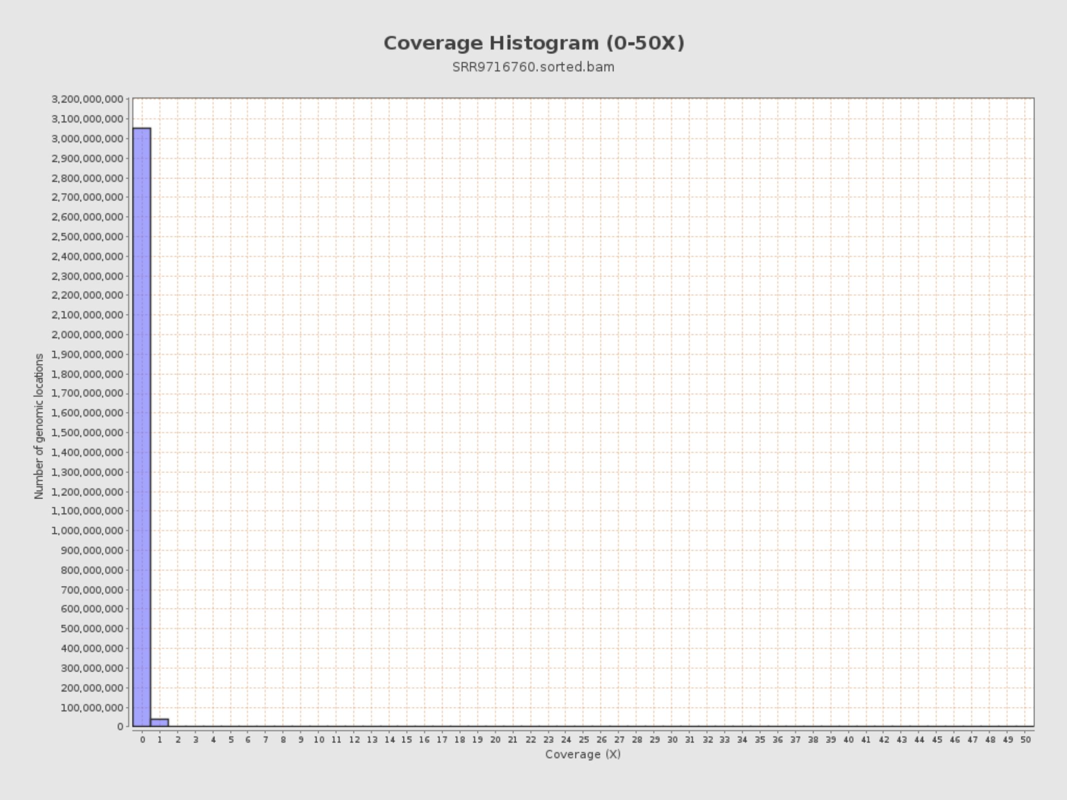
3. Results : Coverage across reference



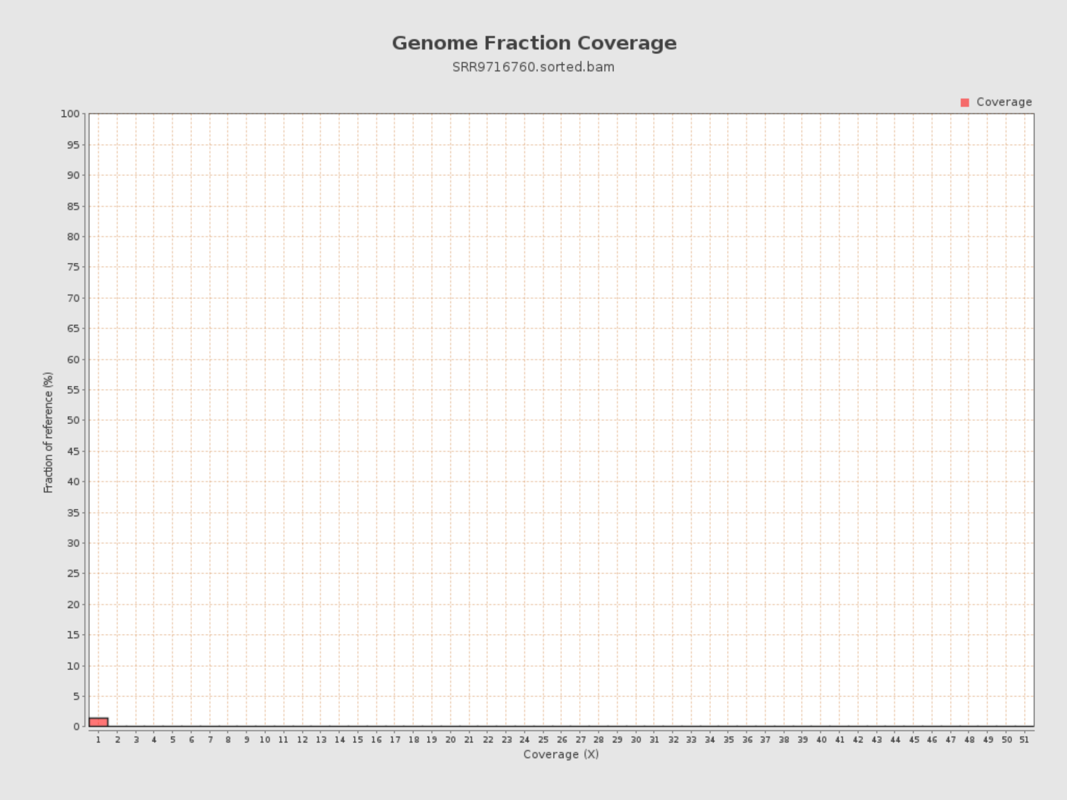
4. Results : Coverage Histogram



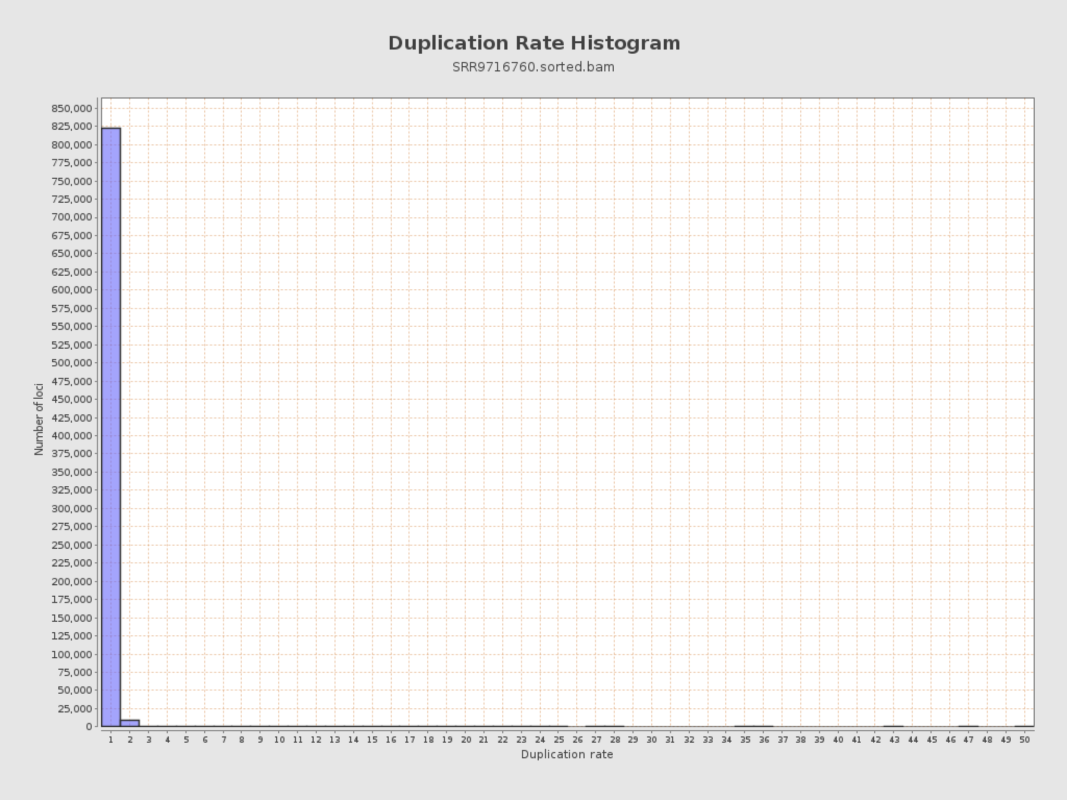
5. Results : Coverage Histogram (0-50X)



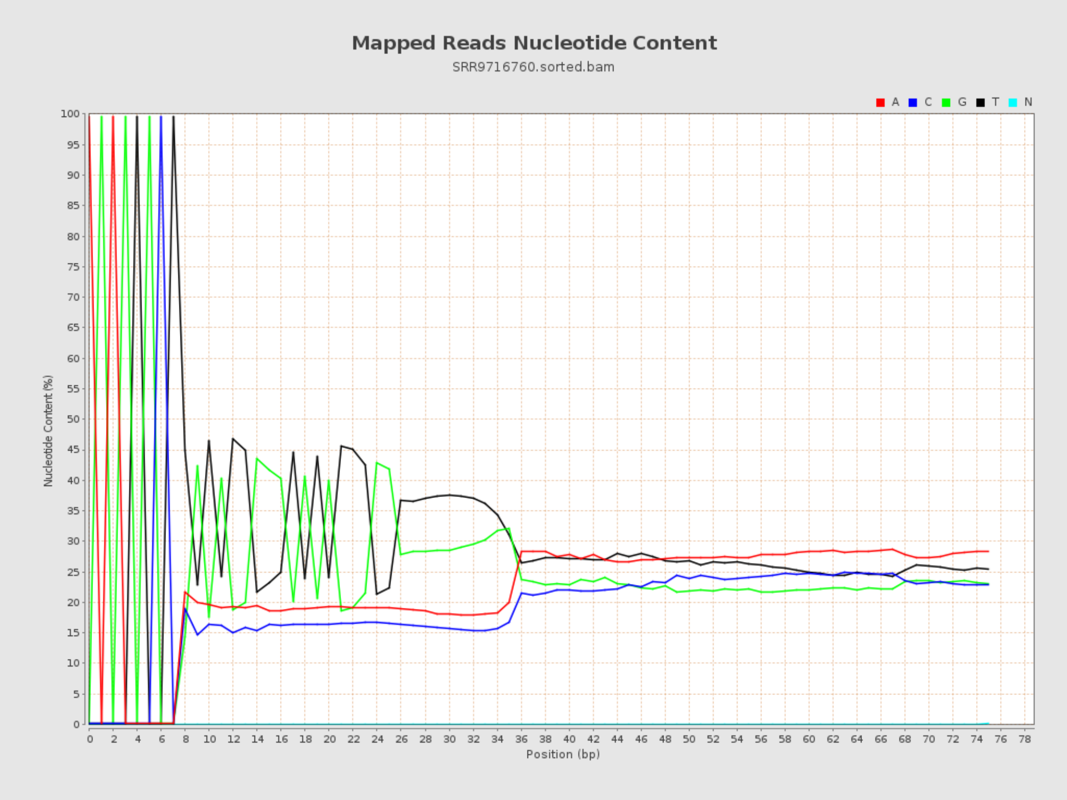
6. Results : Genome Fraction Coverage



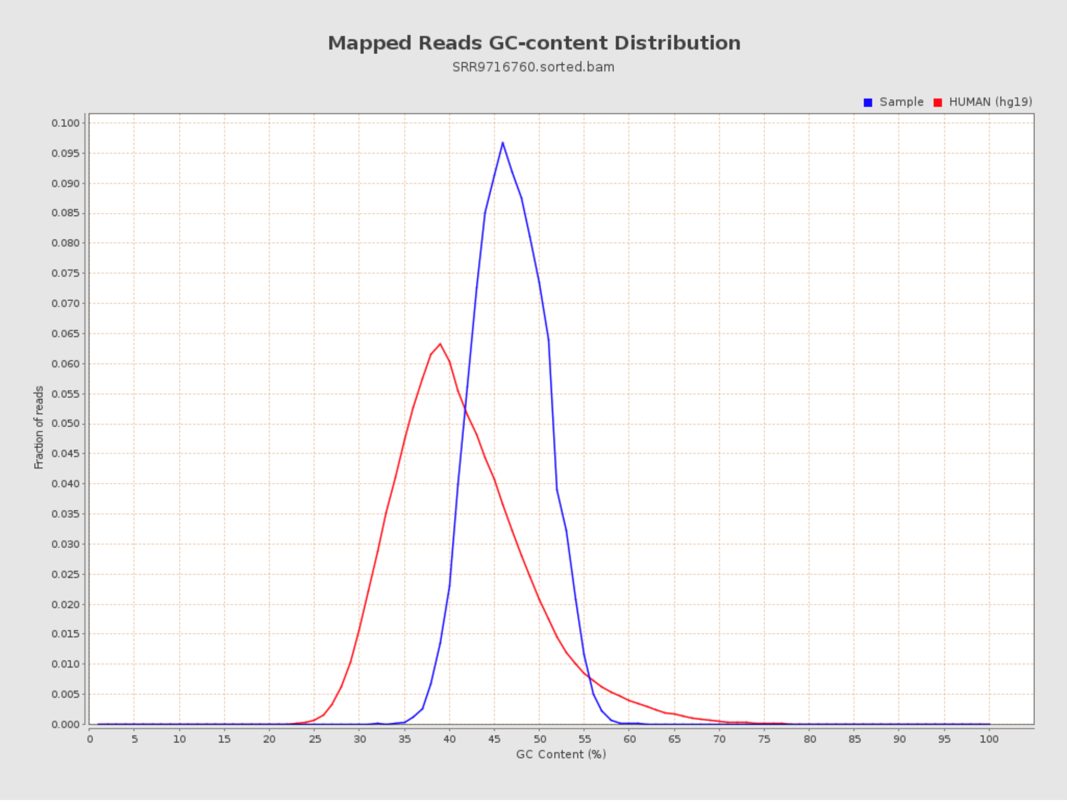
7. Results : Duplication Rate Histogram



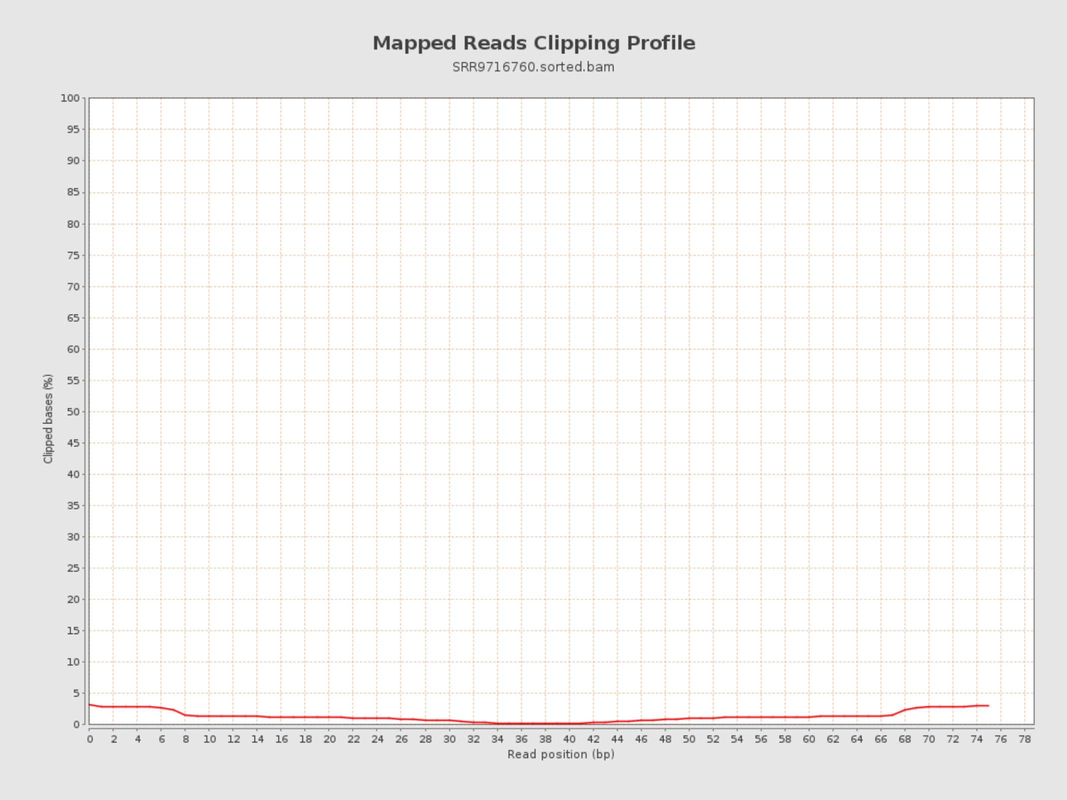
8. Results : Mapped Reads Nucleotide Content



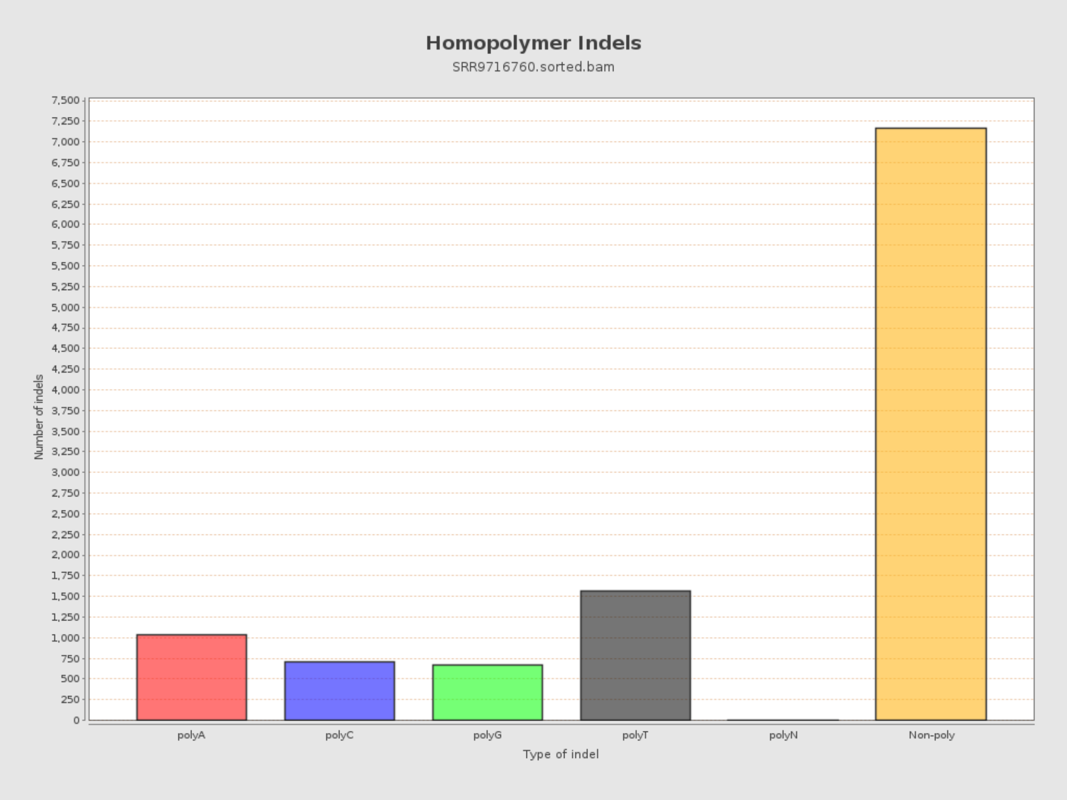
9. Results : Mapped Reads GC-content Distribution



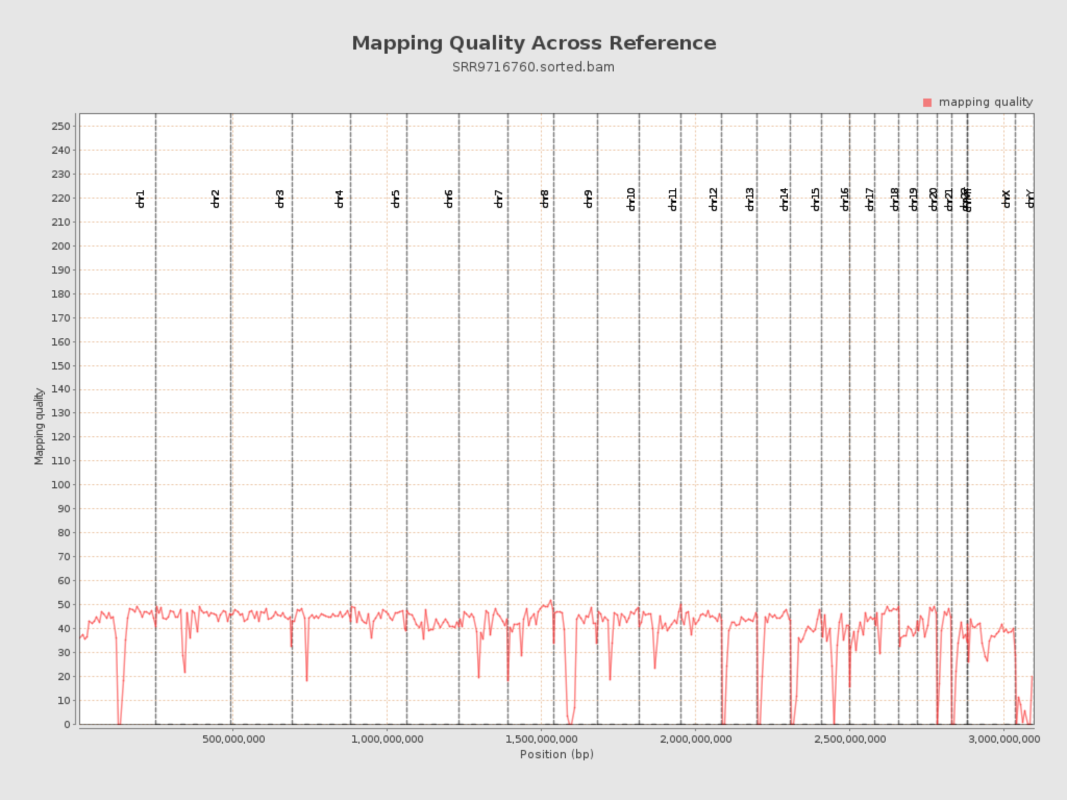
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram