Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 21:10:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716975.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_SRR9716975 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716975.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 21:10:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716975.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,847,297
Mapped reads	5,942,322 / 86.78%
Unmapped reads	904,975 / 13.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,495 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	339,639 / 4.96%
Duplication rate	4.09%
Clipped reads	5,952,505 / 86.93%

2.2. ACGT Content

Number/percentage of A's	81,752,476 / 24.4%
Number/percentage of C's	64,595,551 / 19.28%
Number/percentage of T's	105,777,543 / 31.57%
Number/percentage of G's	82,916,839 / 24.75%
Number/percentage of N's	5,009 / 0%
GC Percentage	44.03%

2.3. Coverage

Mean	0.1083

Standard Deviation	0.733

2.4. Mapping Quality

Mean Mapping Quality	41.99

2.5. Mismatches and indels

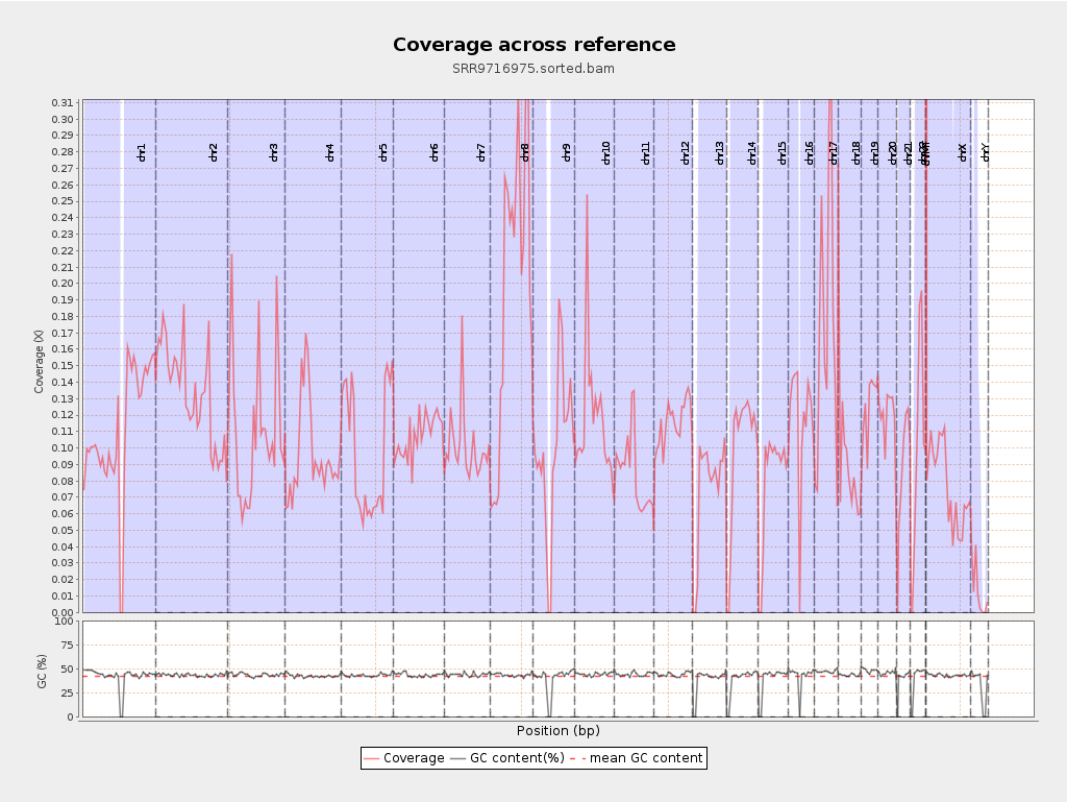
General error rate	0.53%
Mismatches	1,731,272
Insertions	22,918
Mapped reads with at least one insertion	0.38%
Deletions	60,369
Mapped reads with at least one deletion	1.01%
Homopolymer indels	40.09%

2.6. Chromosome stats

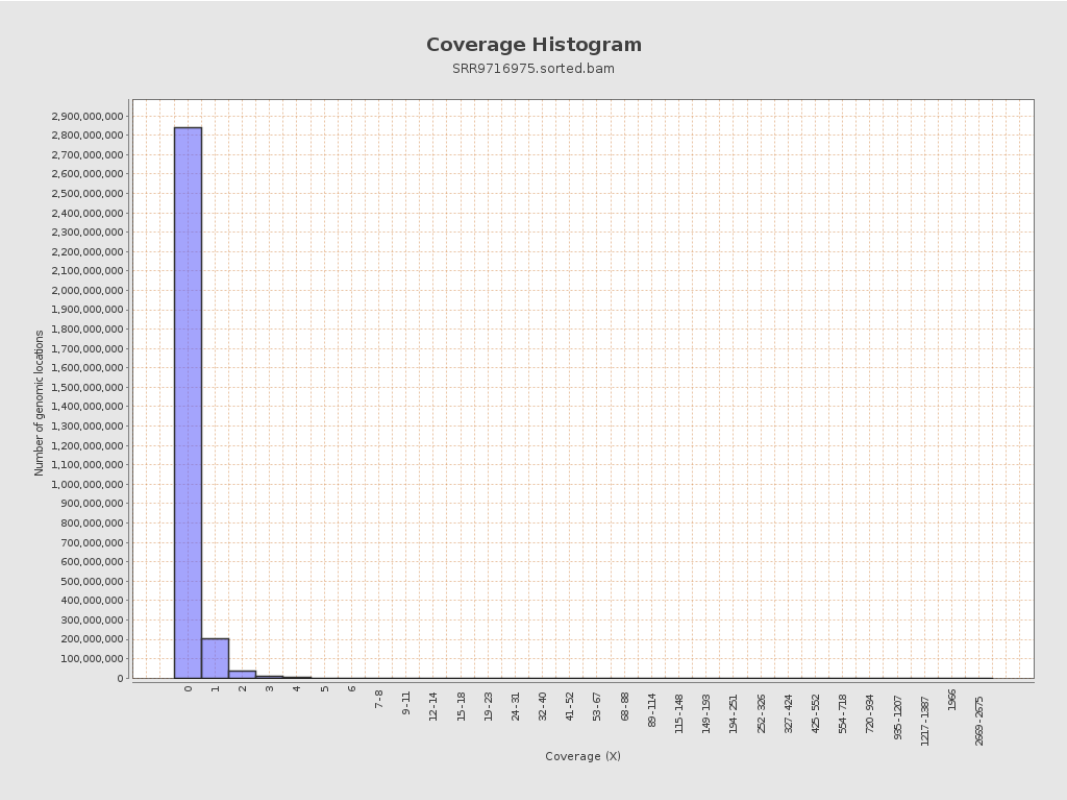
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	27701352	0.1111	1.0616
chr2	243199373	32439389	0.1334	1.2315
chr3	198022430	21656156	0.1094	0.4501
chr4	191154276	18492728	0.0967	0.46
chr5	180915260	17660838	0.0976	0.4006
chr6	171115067	18389899	0.1075	0.533
chr7	159138663	16112566	0.1012	1.2016

chr8	146364022	29488331	0.2015	0.7995
chr9	141213431	13898878	0.0984	0.5397
chr10	135534747	15833354	0.1168	0.9151
chr11	135006516	11403046	0.0845	0.5734
chr12	133851895	15500713	0.1158	0.459
chr13	115169878	8714957	0.0757	0.3473
chr14	107349540	10779281	0.1004	0.4415
chr15	102531392	8026569	0.0783	0.3871
chr16	90354753	10337997	0.1144	0.4853
chr17	81195210	14496216	0.1785	0.6202
chr18	78077248	7136106	0.0914	0.937
chr19	59128983	7342222	0.1242	0.9833
chr20	63025520	7526718	0.1194	0.456
chr21	48129895	4171000	0.0867	0.4191
chr22	51304566	5147685	0.1003	0.4207
chrMT	16571	210866	12.725	8.6734
chrX	155270560	11905324	0.0767	0.4671
chrY	59373566	772427	0.013	0.2902

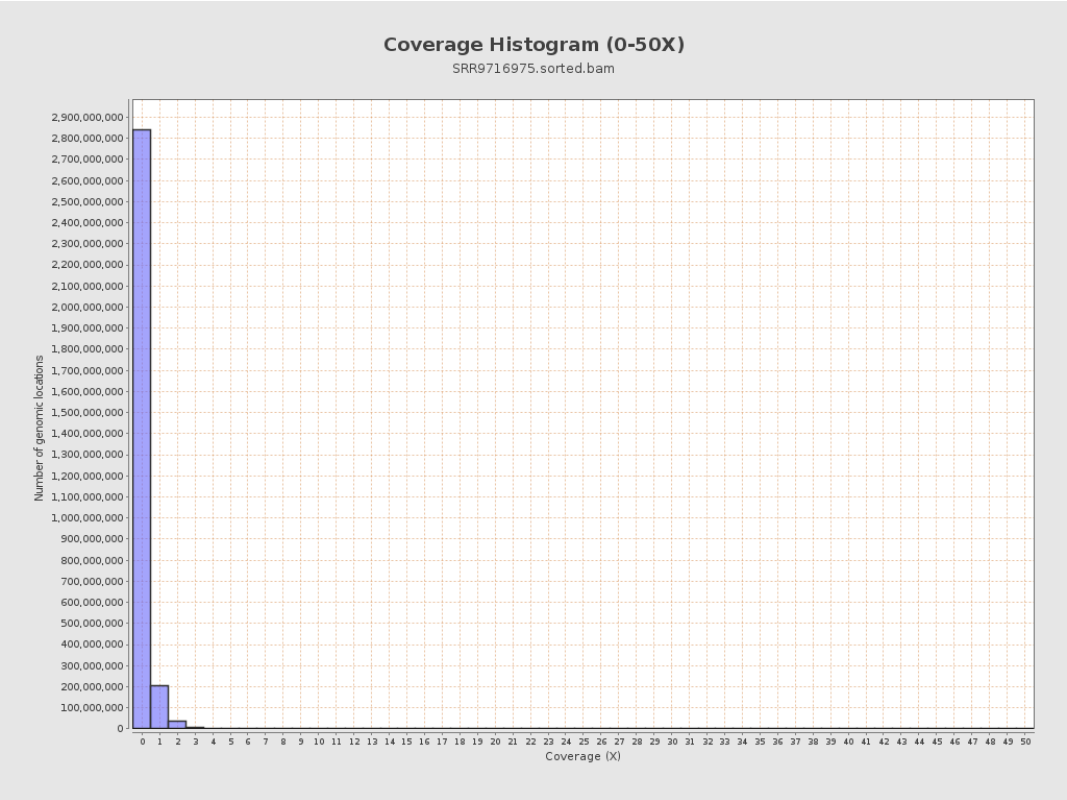
3. Results : Coverage across reference



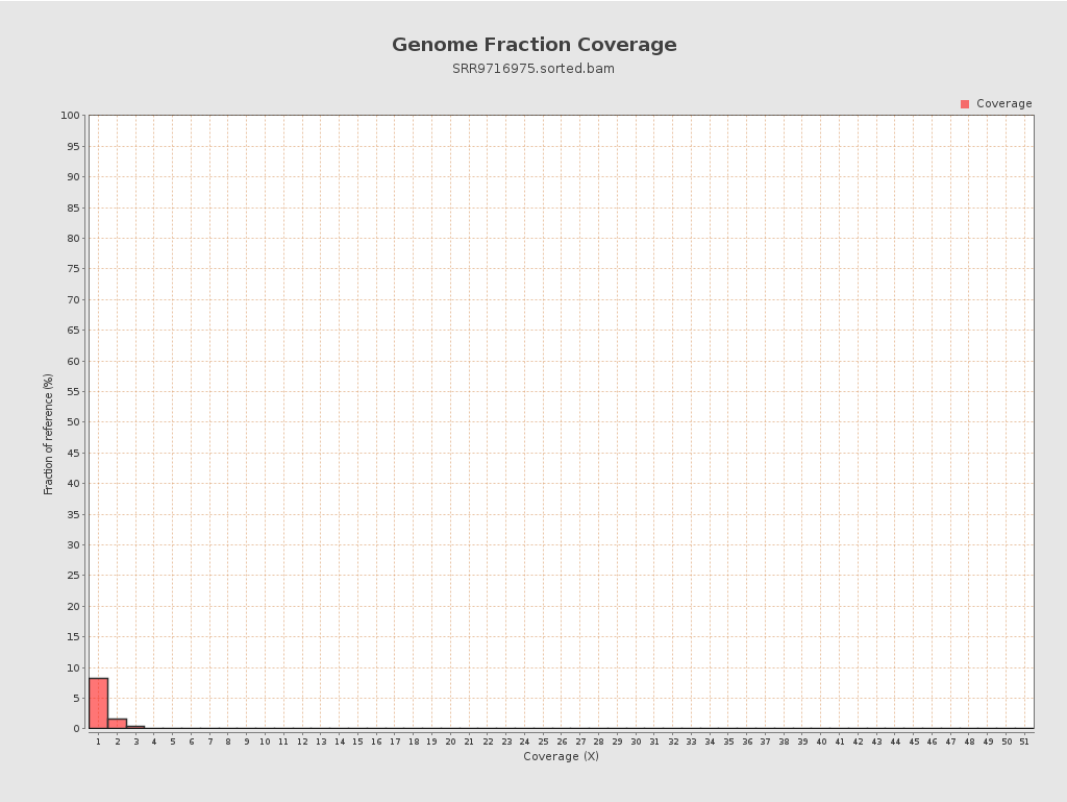
4. Results : Coverage Histogram



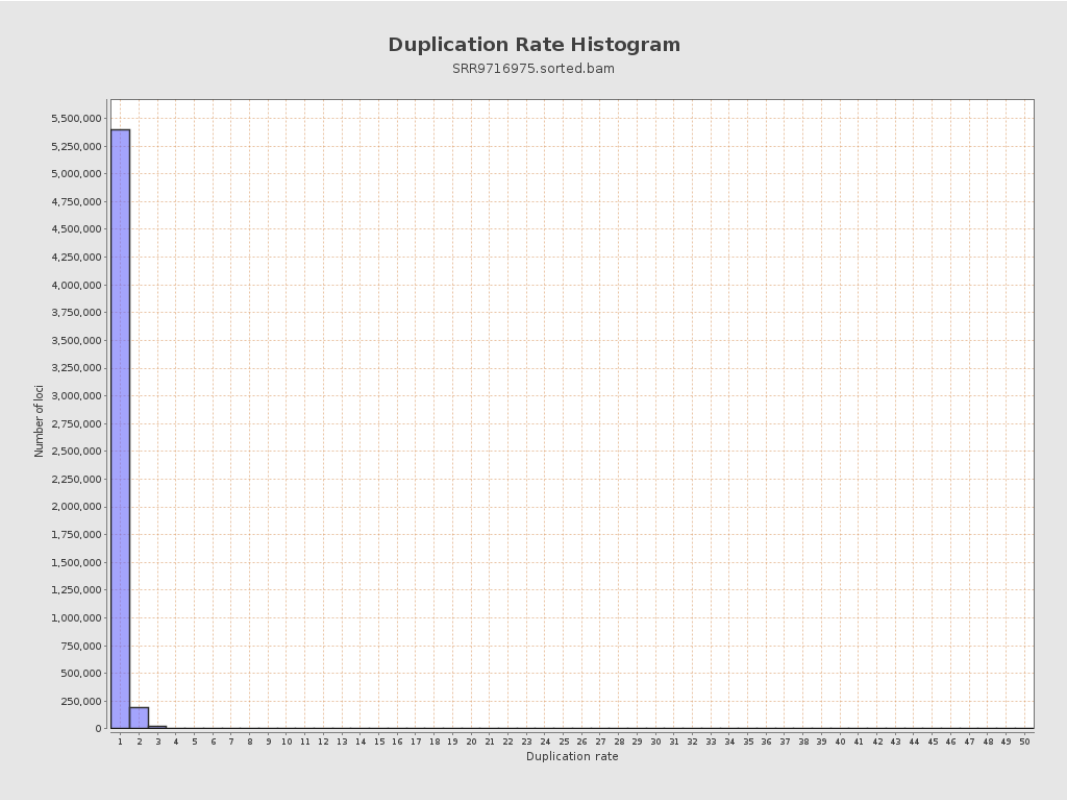
5. Results : Coverage Histogram (0-50X)



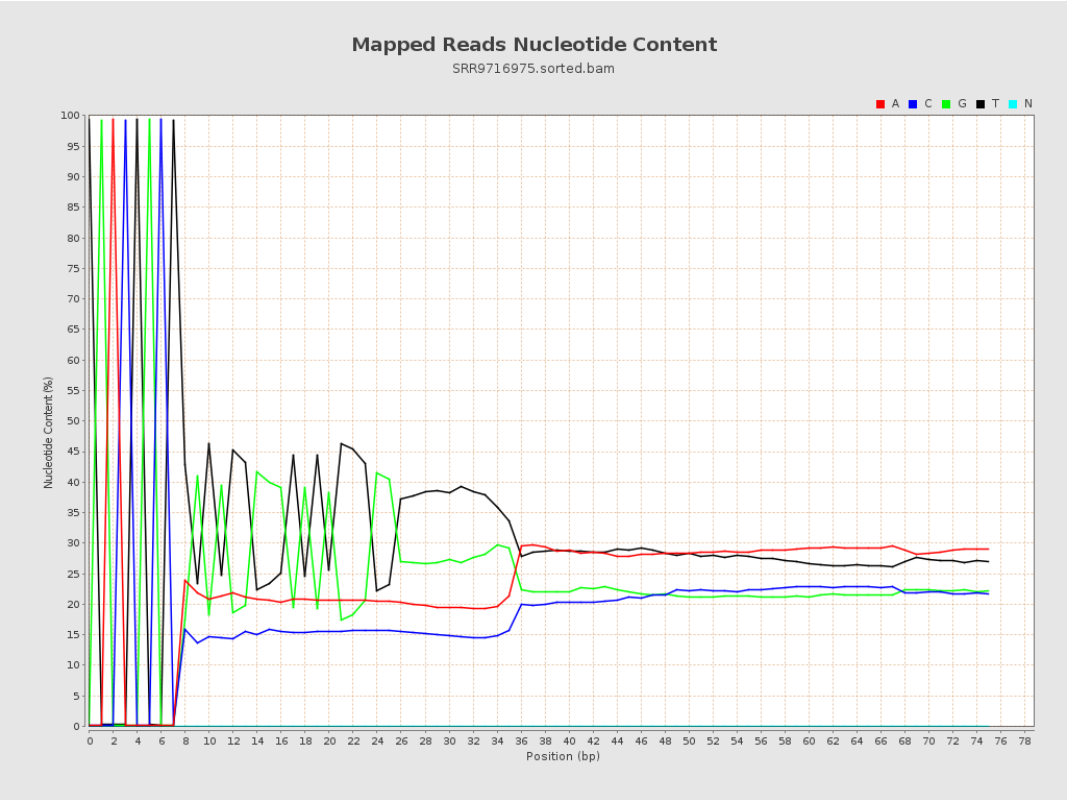
6. Results : Genome Fraction Coverage



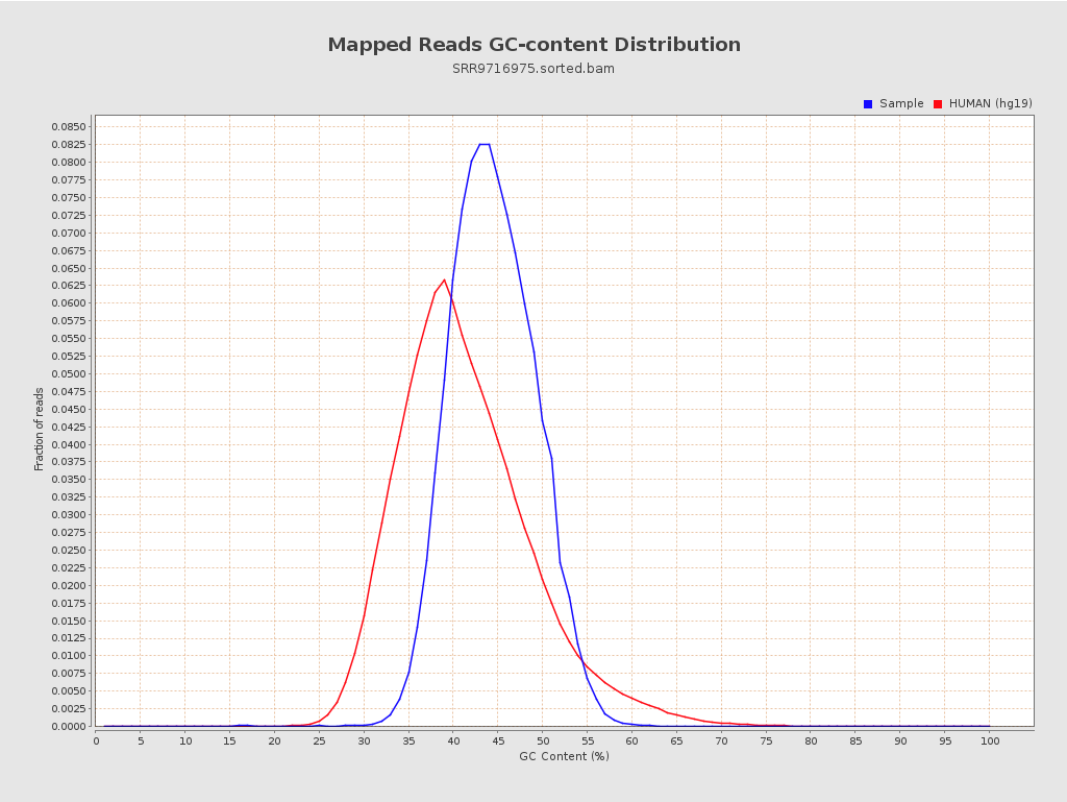
7. Results : Duplication Rate Histogram



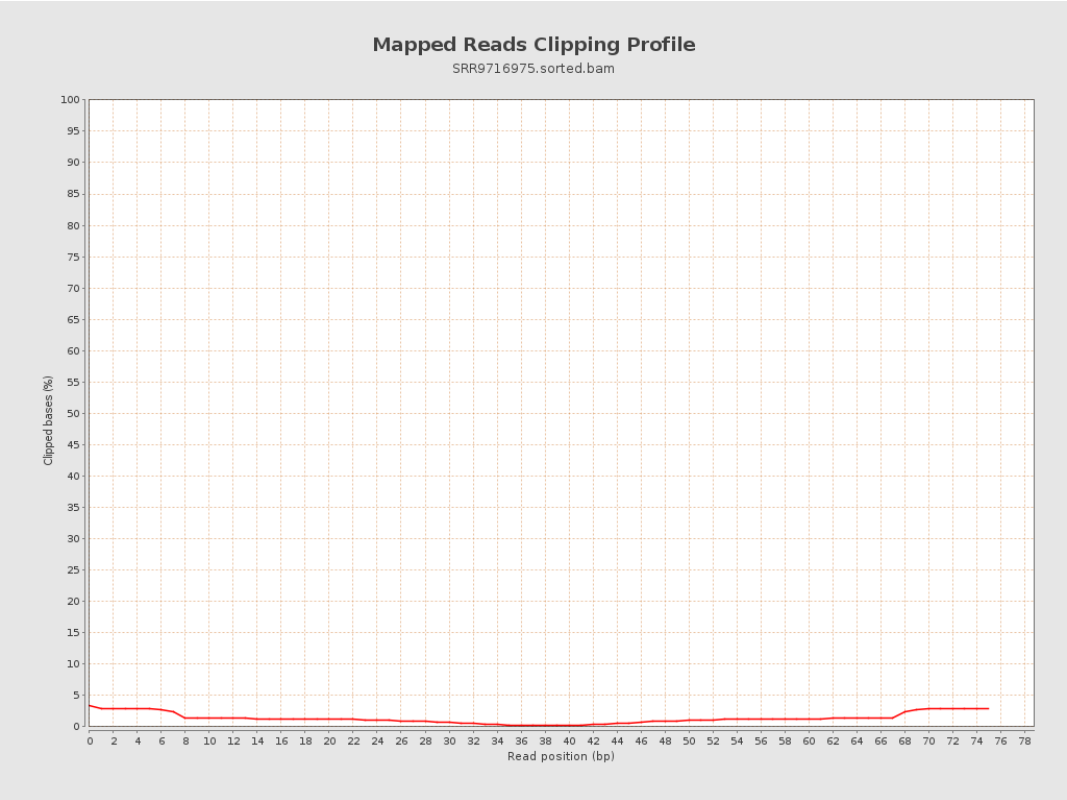
8. Results : Mapped Reads Nucleotide Content



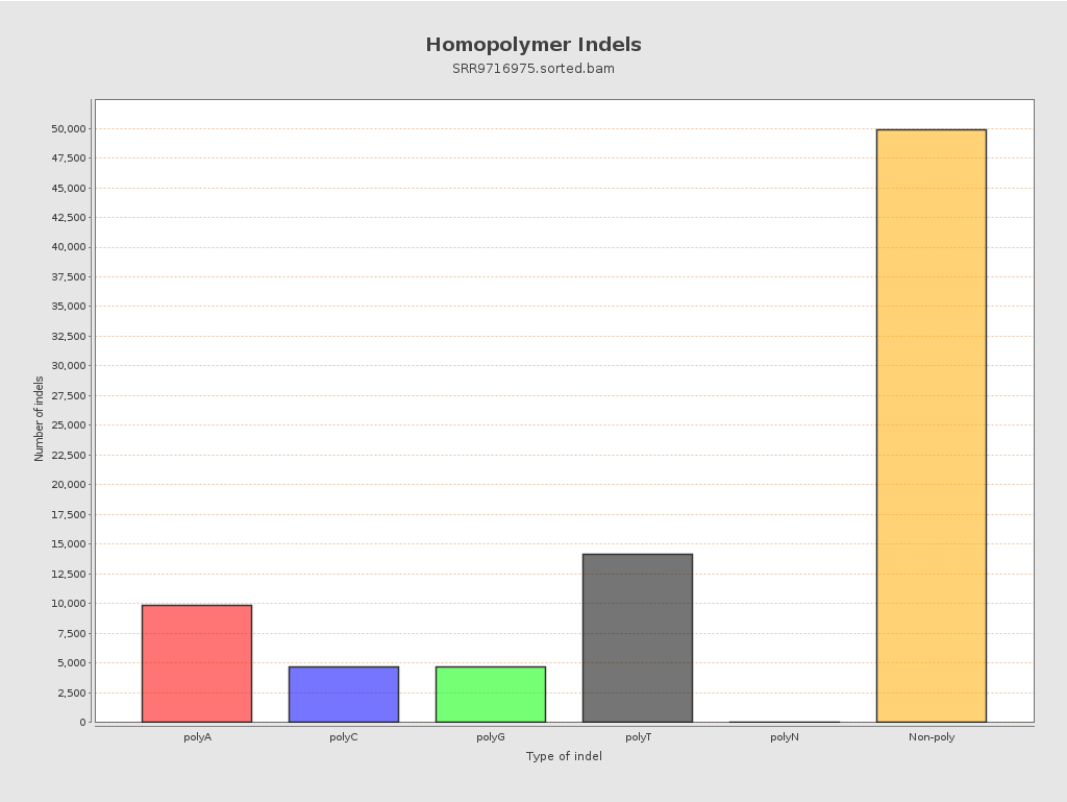
9. Results : Mapped Reads GC-content Distribution



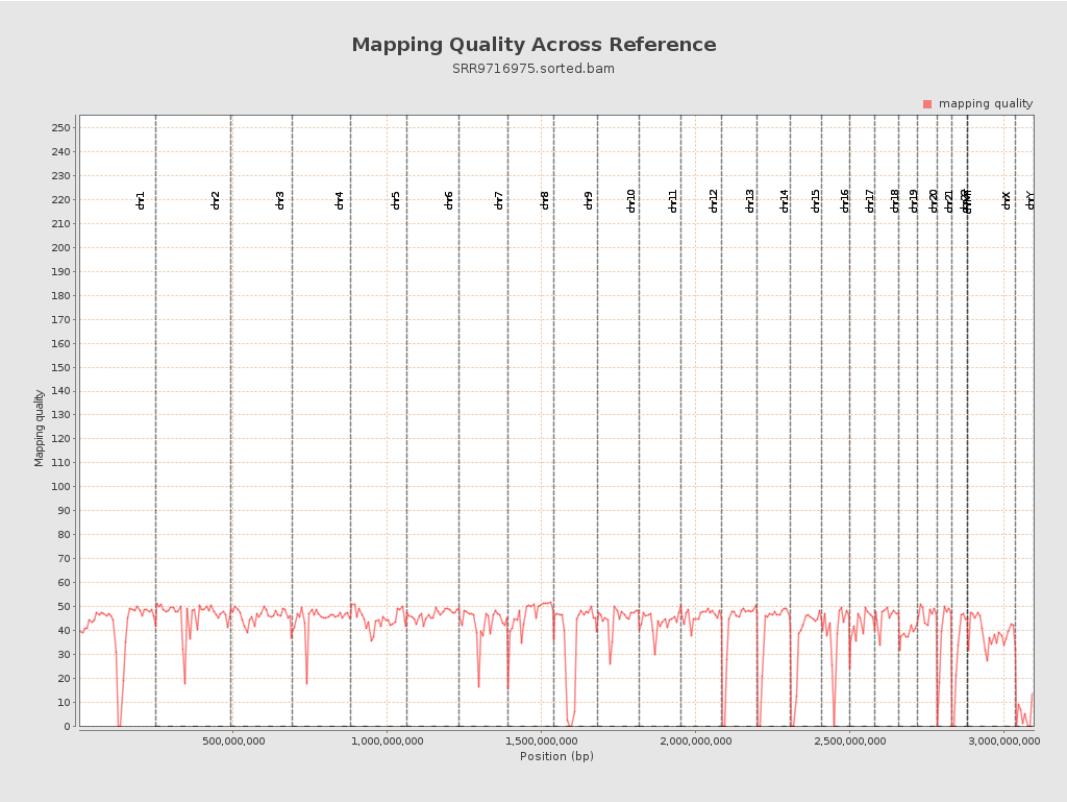
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram