Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:00:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716871.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_SRR9716871 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716871.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:00:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716871.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,443,683
Mapped reads	1,303,411 / 90.28%
Unmapped reads	140,272 / 9.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,095 / 0.49%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	37,438 / 2.59%
Duplication rate	2.09%
Clipped reads	1,308,191 / 90.61%

2.2. ACGT Content

Number/percentage of A's	18,215,168 / 24.12%
Number/percentage of C's	14,160,317 / 18.75%
Number/percentage of T's	24,191,249 / 32.04%
Number/percentage of G's	18,937,660 / 25.08%
Number/percentage of N's	1,938 / 0%
GC Percentage	43.83%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.2311

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

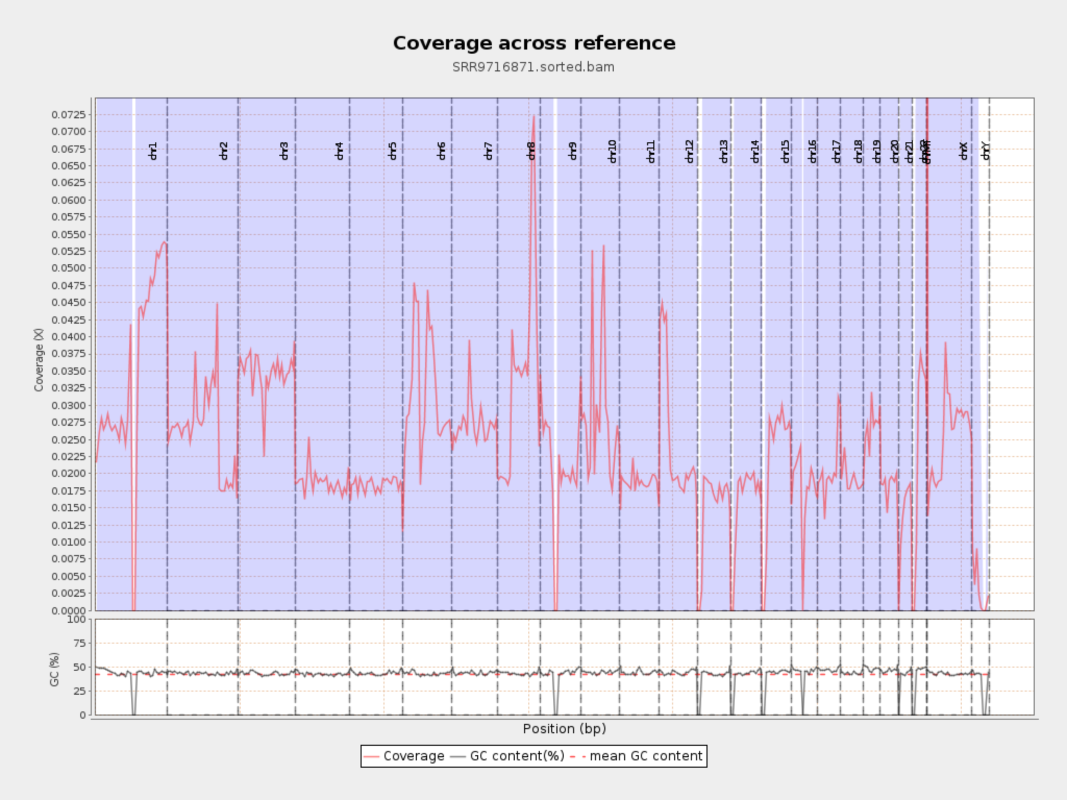
General error rate	0.51%
Mismatches	379,387
Insertions	4,874
Mapped reads with at least one insertion	0.37%
Deletions	13,924
Mapped reads with at least one deletion	1.06%
Homopolymer indels	44.21%

2.6. Chromosome stats

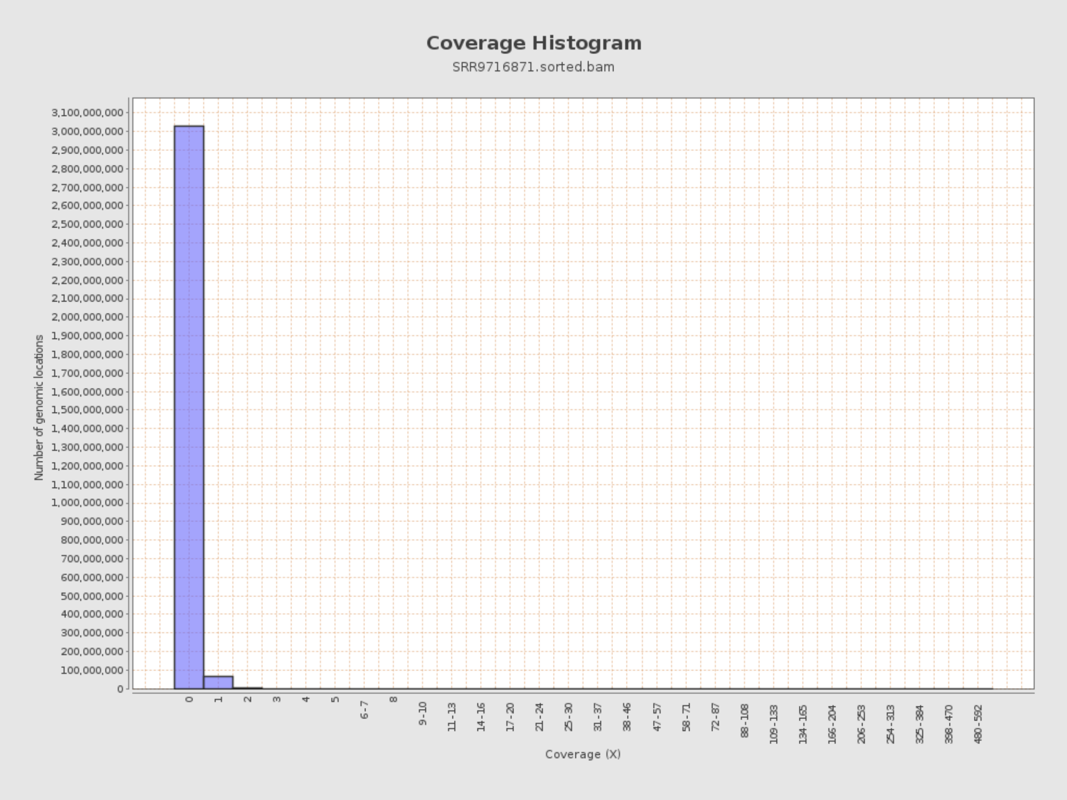
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8569111	0.0344	0.3944
chr2	243199373	6421862	0.0264	0.2998
chr3	198022430	6888331	0.0348	0.2024
chr4	191154276	3592921	0.0188	0.1533
chr5	180915260	3351478	0.0185	0.1472
chr6	171115067	5423554	0.0317	0.25
chr7	159138663	4357571	0.0274	0.2807

chr8	146364022	5020880	0.0343	0.2191
chr9	141213431	2860873	0.0203	0.1986
chr10	135534747	3926283	0.029	0.259
chr11	135006516	2550858	0.0189	0.1875
chr12	133851895	3375549	0.0252	0.1726
chr13	115169878	1703223	0.0148	0.1308
chr14	107349540	1681146	0.0157	0.1446
chr15	102531392	2250230	0.0219	0.1617
chr16	90354753	1588658	0.0176	0.164
chr17	81195210	1665939	0.0205	0.1594
chr18	78077248	1499698	0.0192	0.3315
chr19	59128983	1579135	0.0267	0.2813
chr20	63025520	1151439	0.0183	0.1452
chr21	48129895	664061	0.0138	0.1406
chr22	51304566	1217066	0.0237	0.1655
chrMT	16571	10890	0.6572	0.8414
chrX	155270560	3993553	0.0257	0.1924
chrY	59373566	183945	0.0031	0.076

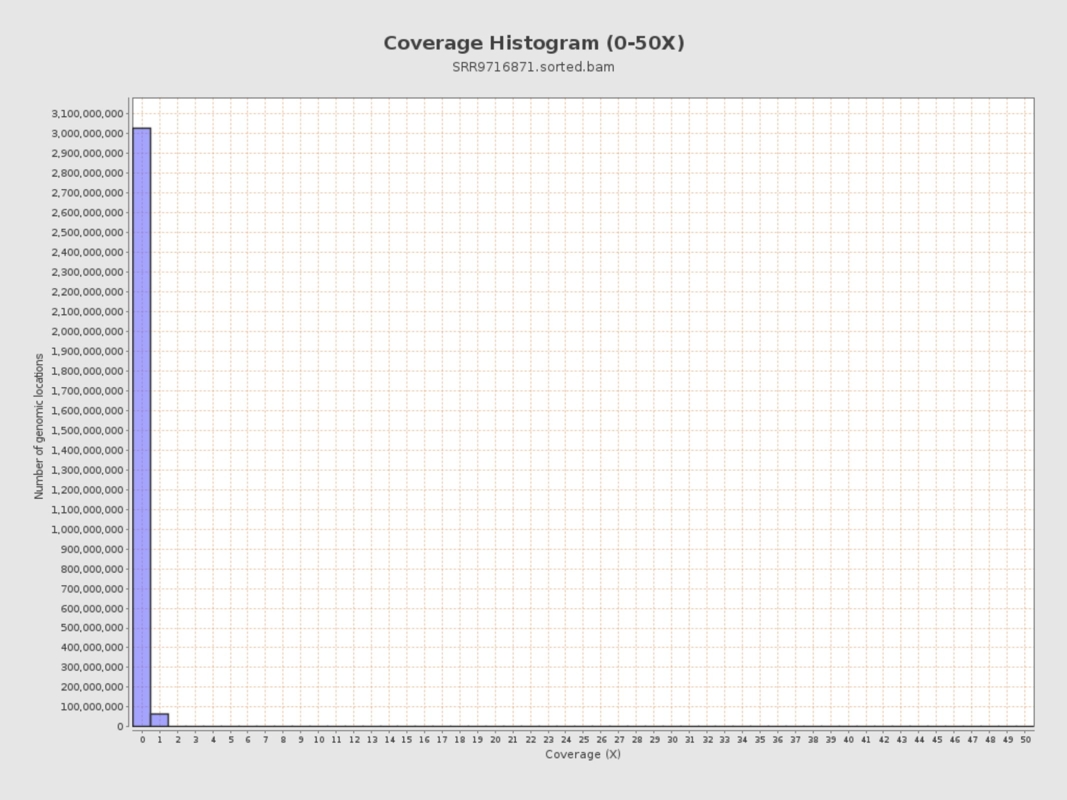
3. Results : Coverage across reference



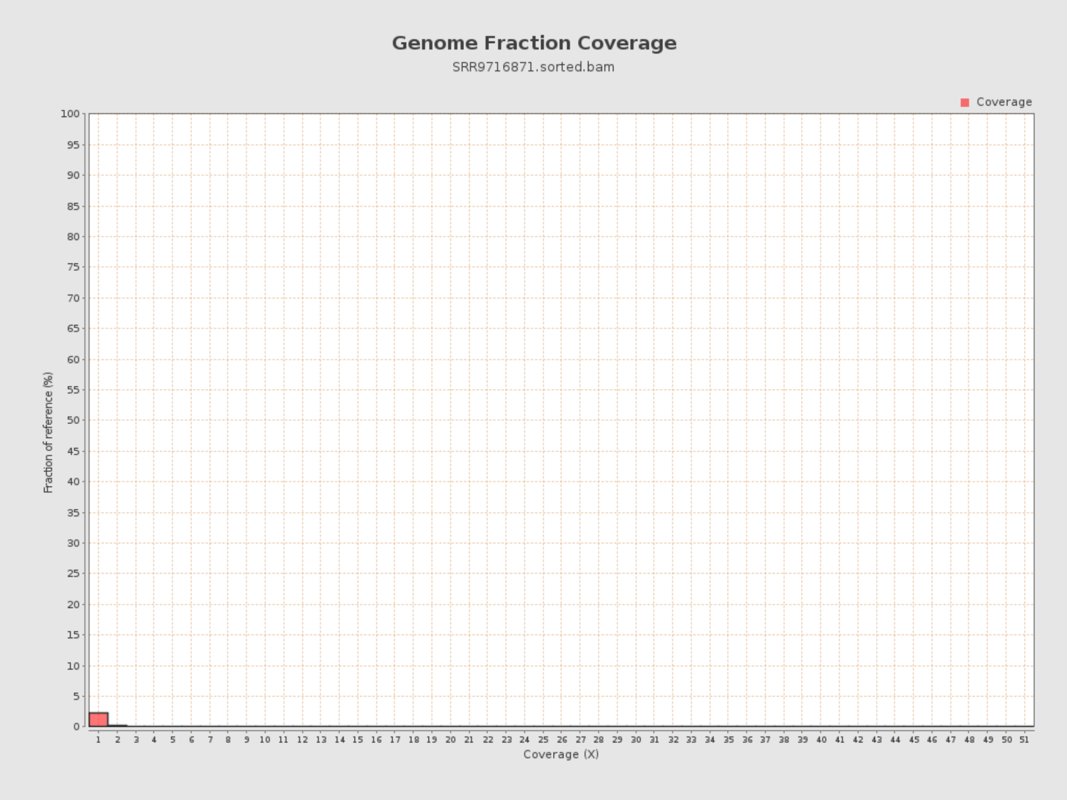
4. Results : Coverage Histogram



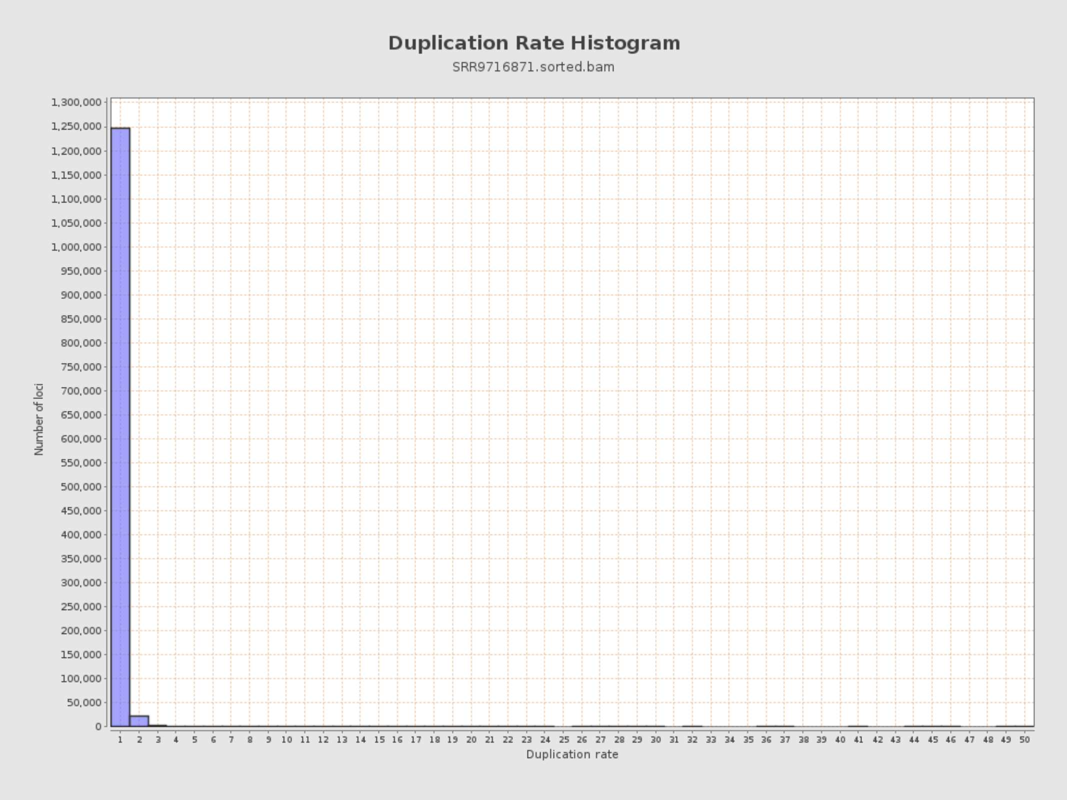
5. Results : Coverage Histogram (0-50X)



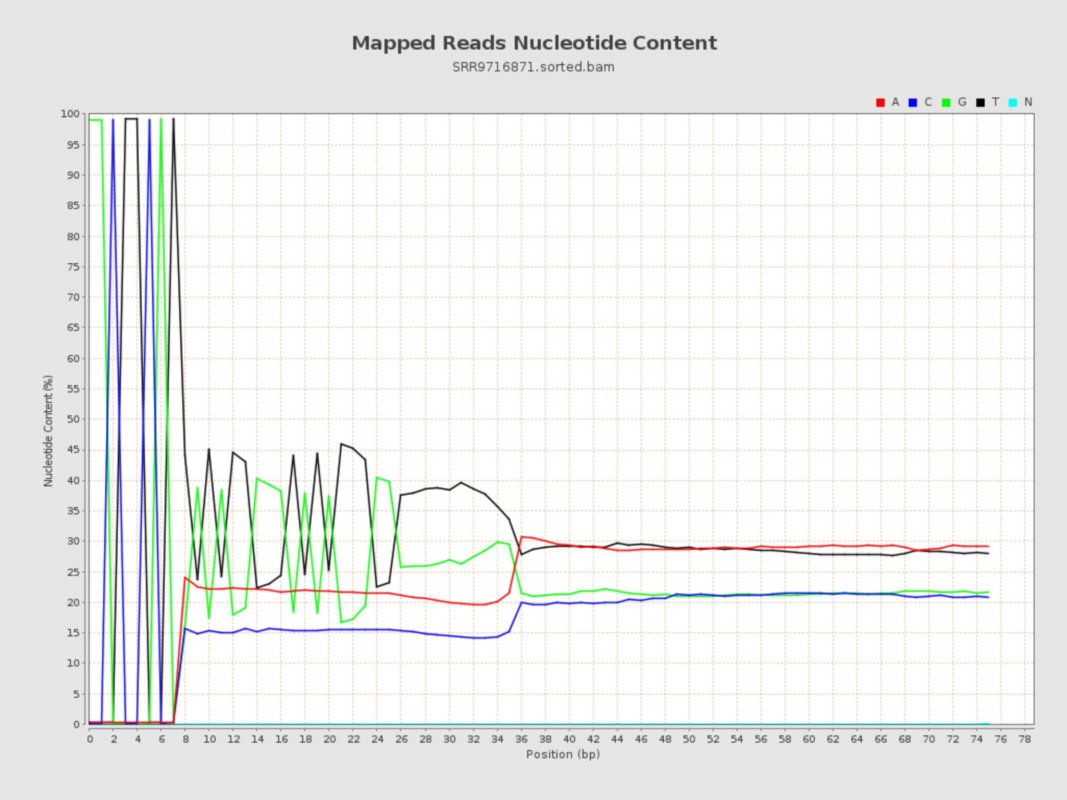
6. Results : Genome Fraction Coverage



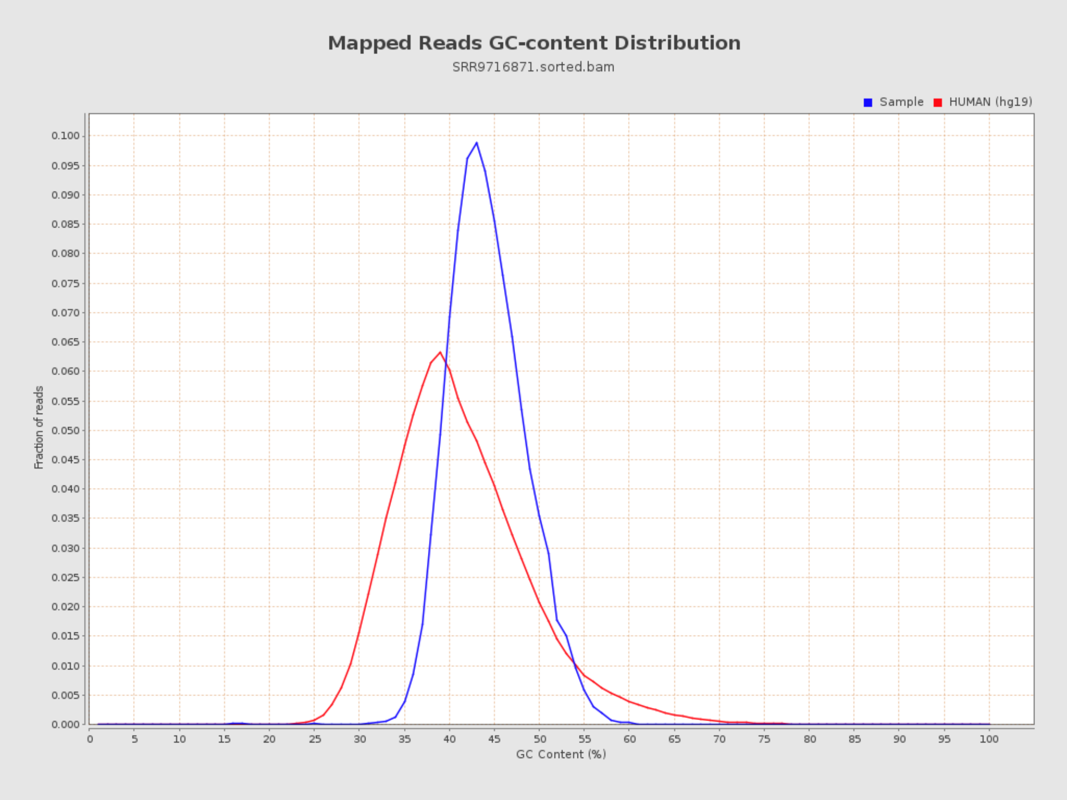
7. Results : Duplication Rate Histogram



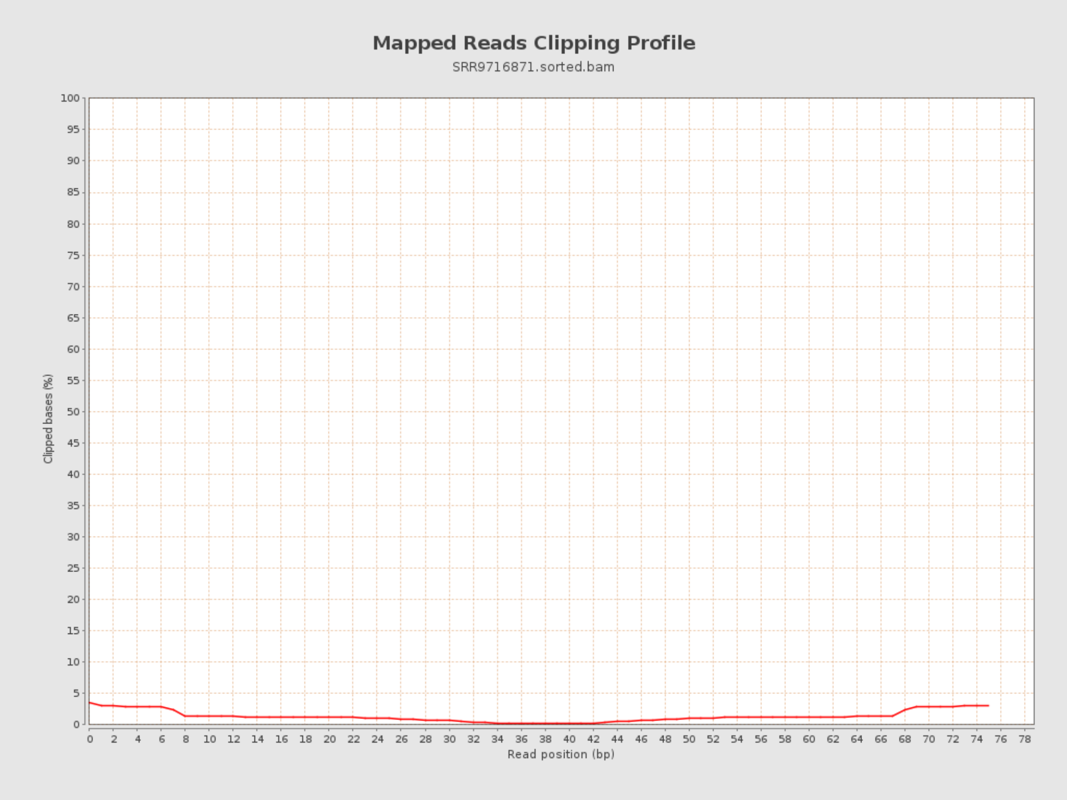
8. Results : Mapped Reads Nucleotide Content



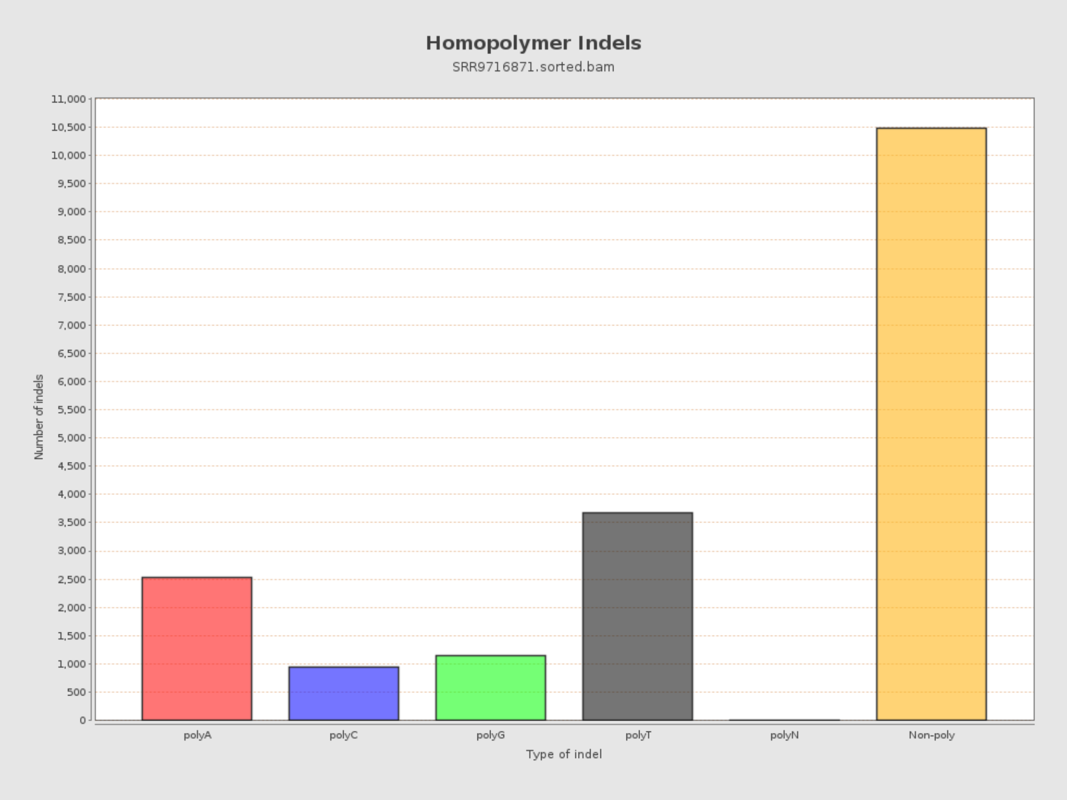
9. Results : Mapped Reads GC-content Distribution



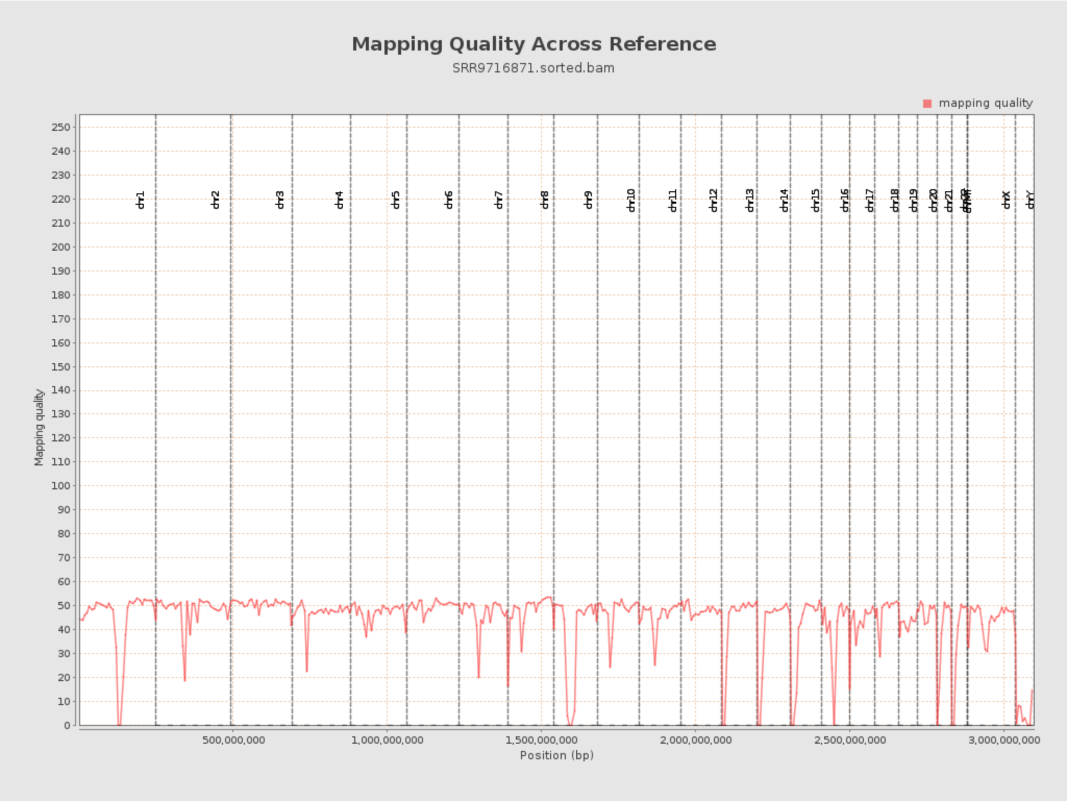
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram