Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:38:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716422.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_SRR9716422 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716422.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:38:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716422.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,568,182
Mapped reads	1,452,772 / 92.64%
Unmapped reads	115,410 / 7.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,138 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	54,517 / 3.48%
Duplication rate	2.7%
Clipped reads	1,454,658 / 92.76%

2.2. ACGT Content

Number/percentage of A's	20,772,585 / 24.51%
Number/percentage of C's	17,281,227 / 20.39%
Number/percentage of T's	25,930,762 / 30.6%
Number/percentage of G's	20,767,599 / 24.5%
Number/percentage of N's	1,788 / 0%
GC Percentage	44.89%

2.3. Coverage

Mean	0.0274

Standard Deviation	0.2629

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

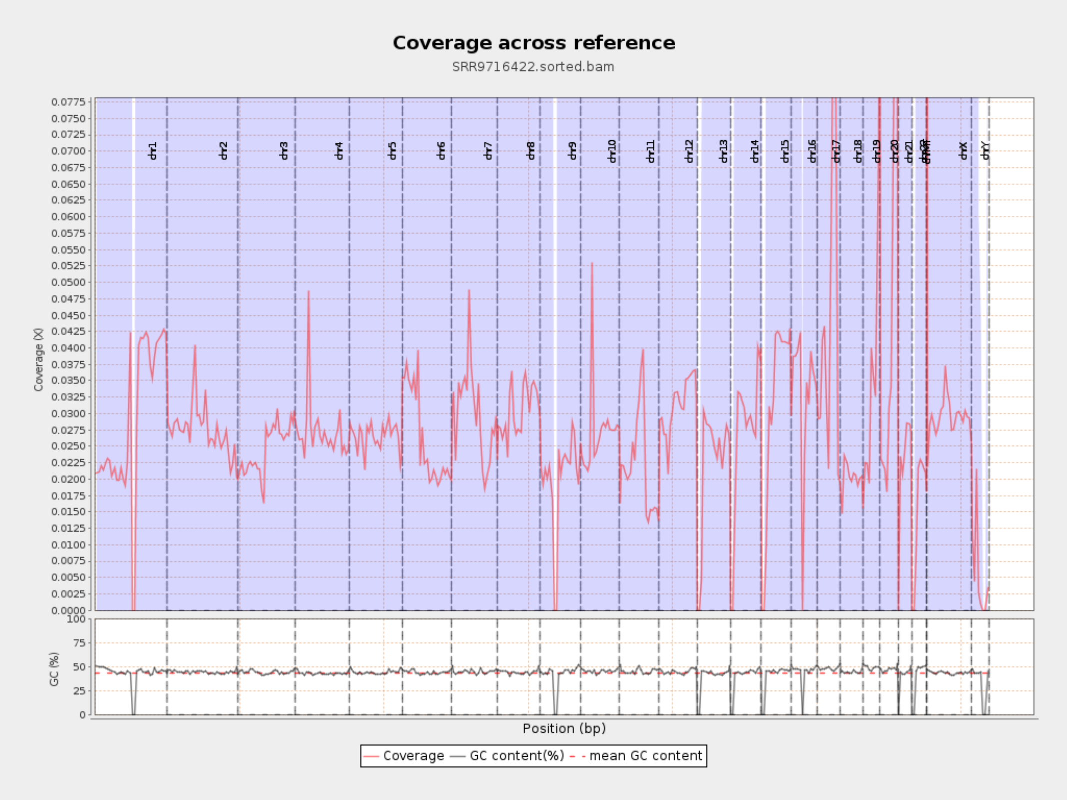
General error rate	0.51%
Mismatches	422,331
Insertions	6,283
Mapped reads with at least one insertion	0.43%
Deletions	16,384
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.38%

2.6. Chromosome stats

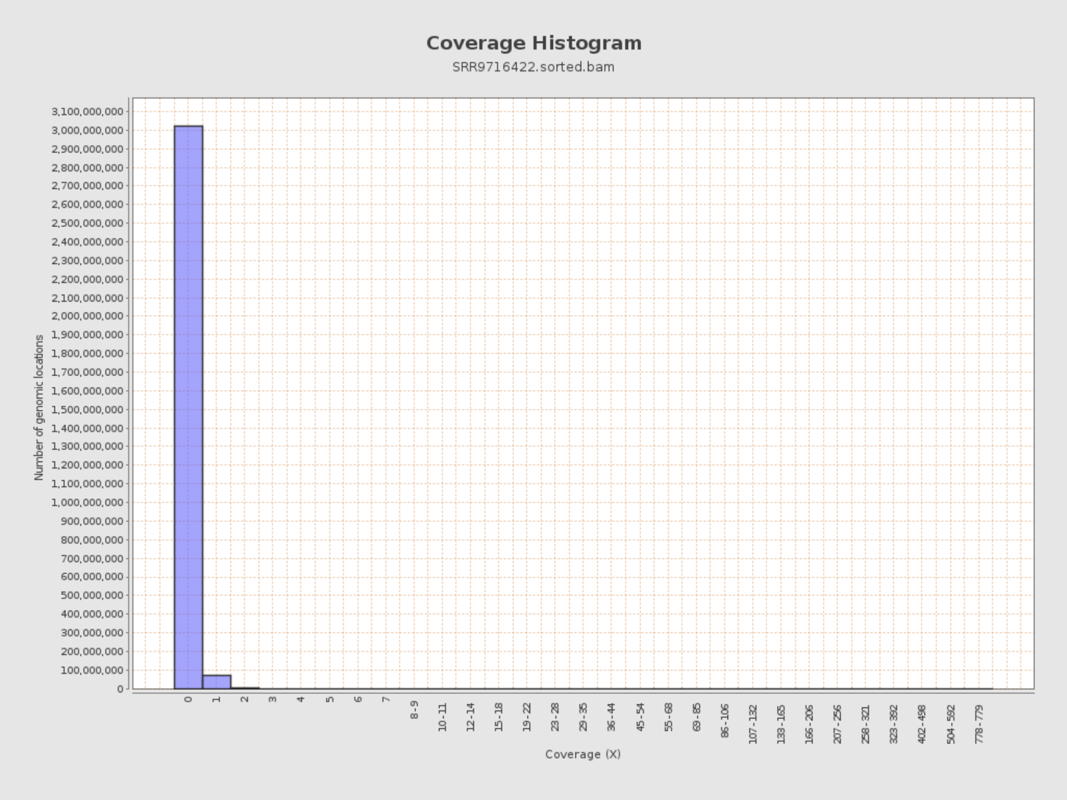
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7158225	0.0287	0.4167
chr2	243199373	6692637	0.0275	0.3686
chr3	198022430	4852940	0.0245	0.1704
chr4	191154276	5220319	0.0273	0.2114
chr5	180915260	4805804	0.0266	0.1768
chr6	171115067	4505261	0.0263	0.2049
chr7	159138663	4789258	0.0301	0.3312

chr8	146364022	4484070	0.0306	0.3533
chr9	141213431	2803048	0.0198	0.185
chr10	135534747	3698575	0.0273	0.2716
chr11	135006516	3010552	0.0223	0.2049
chr12	133851895	4182043	0.0312	0.1923
chr13	115169878	2543551	0.0221	0.1621
chr14	107349540	2846082	0.0265	0.179
chr15	102531392	3147960	0.0307	0.1911
chr16	90354753	2940198	0.0325	0.2058
chr17	81195210	3679790	0.0453	0.2408
chr18	78077248	1562376	0.02	0.3177
chr19	59128983	2162617	0.0366	0.3237
chr20	63025520	2841516	0.0451	0.2409
chr21	48129895	1102649	0.0229	0.2059
chr22	51304566	785800	0.0153	0.1338
chrMT	16571	58734	3.5444	2.6765
chrX	155270560	4589771	0.0296	0.1994
chrY	59373566	316660	0.0053	0.2342

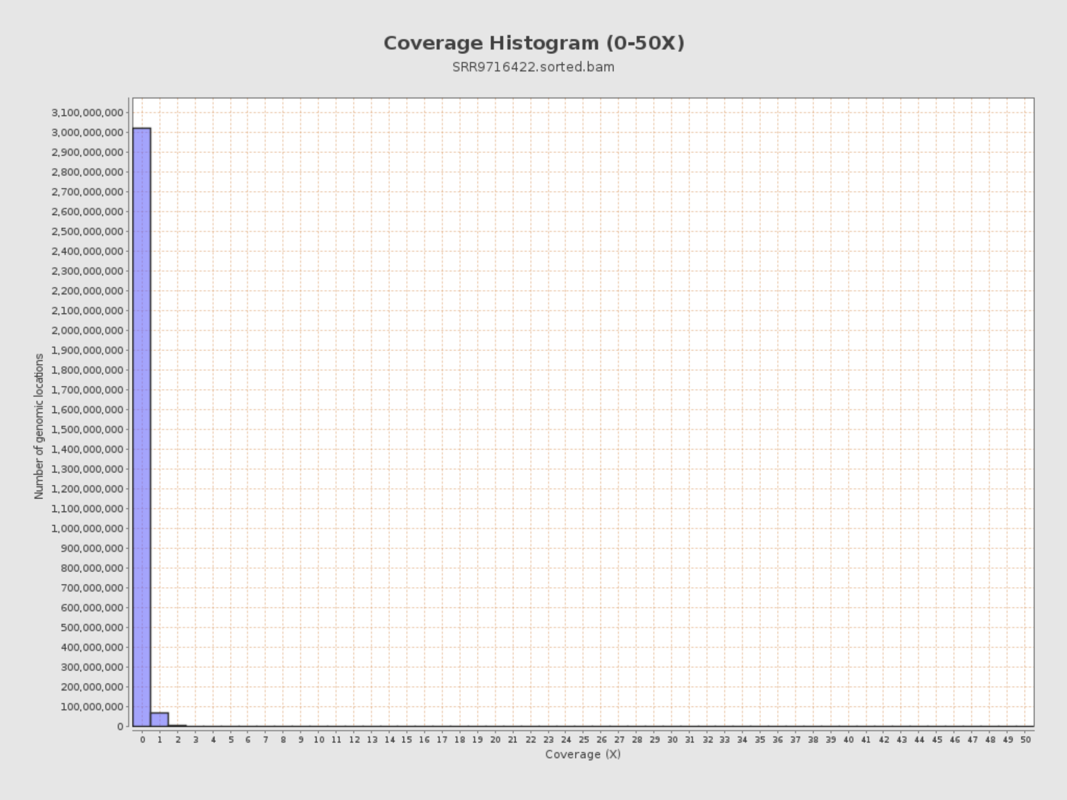
3. Results : Coverage across reference



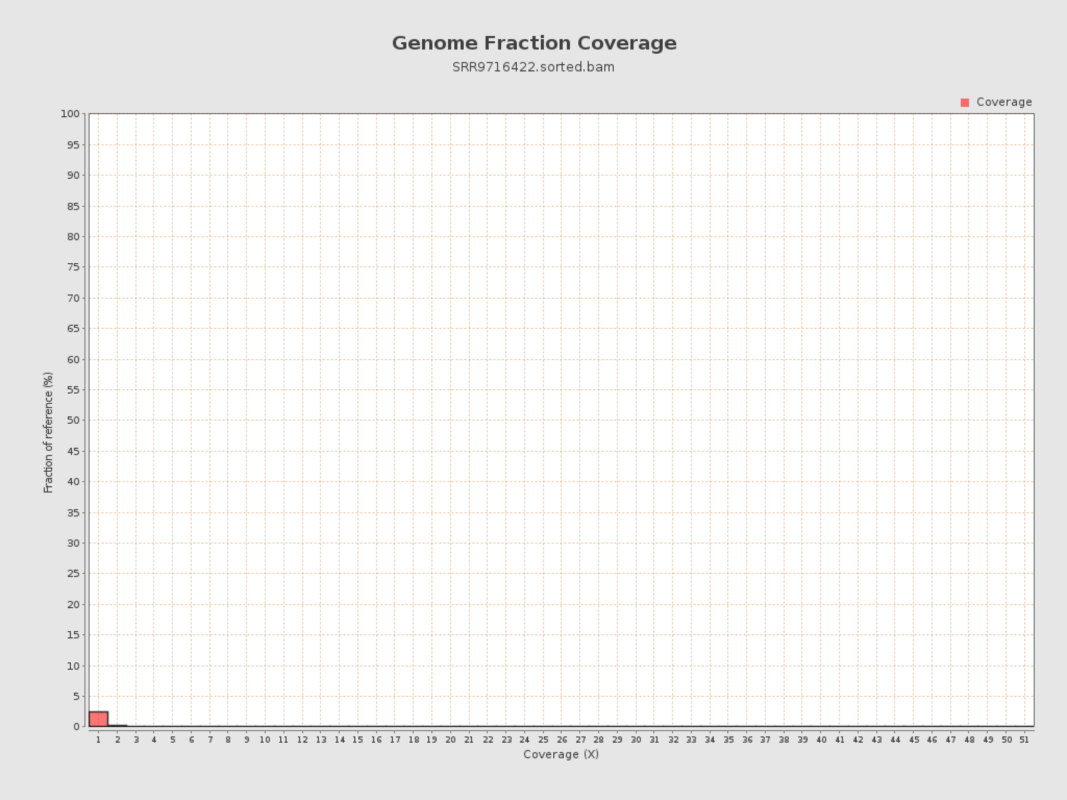
4. Results : Coverage Histogram



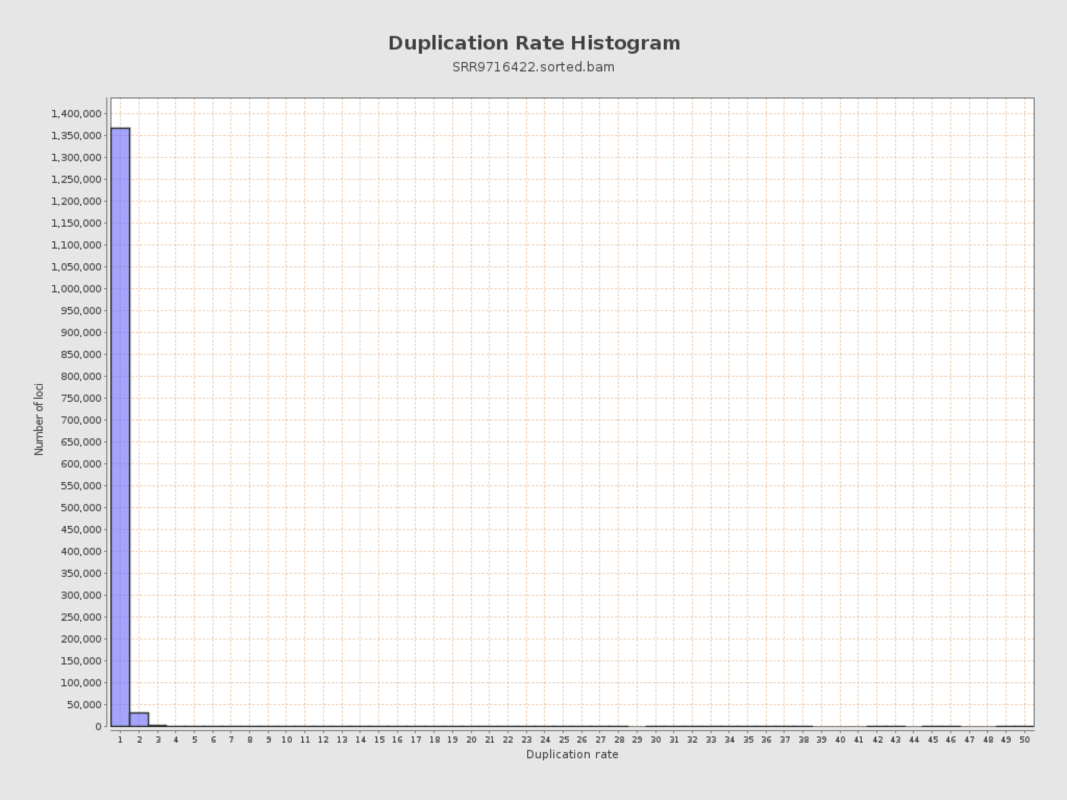
5. Results : Coverage Histogram (0-50X)



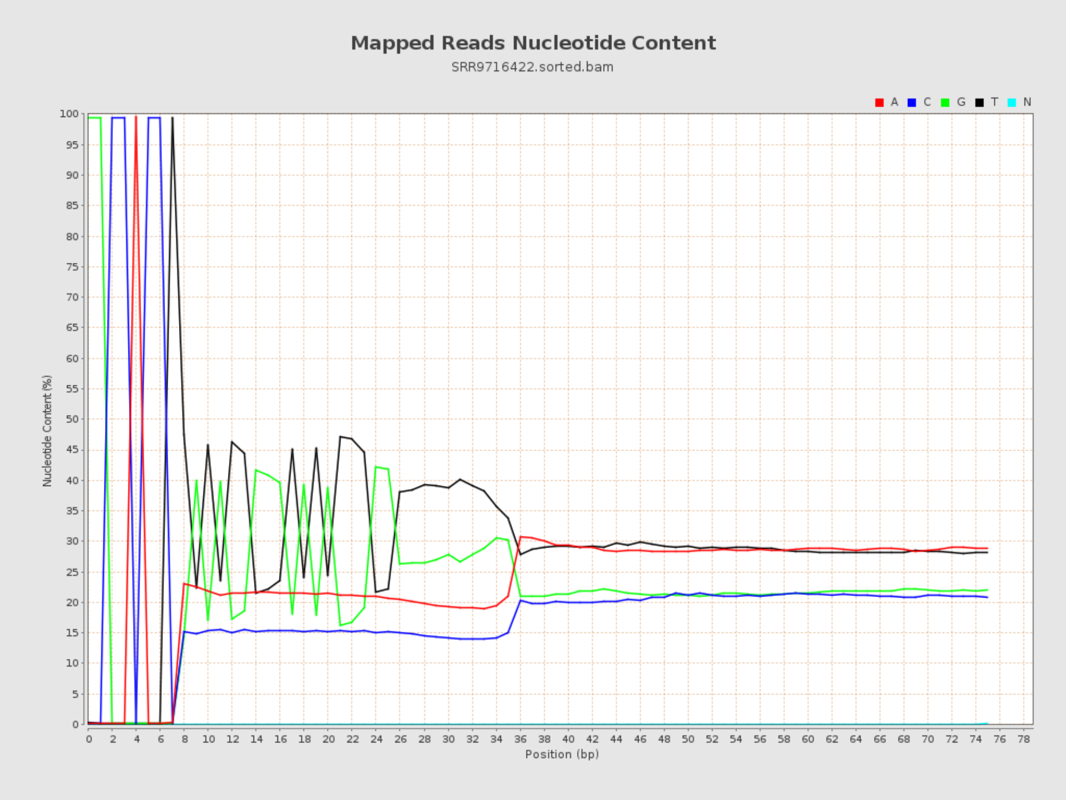
6. Results : Genome Fraction Coverage



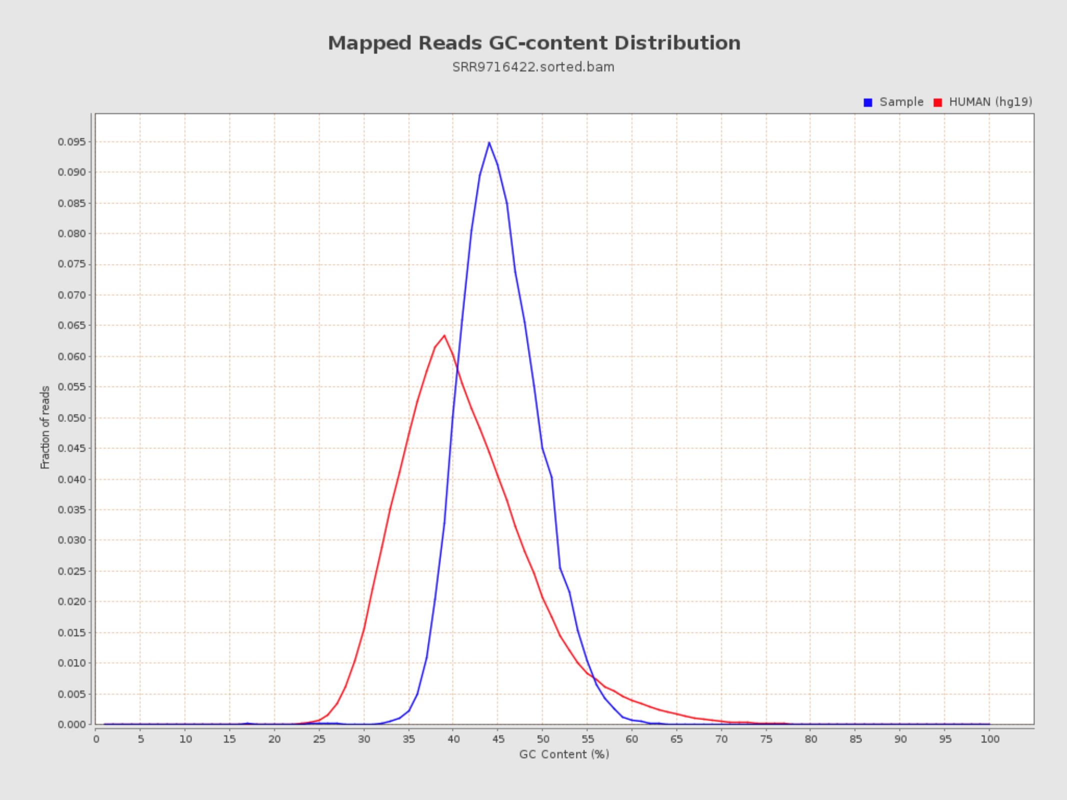
7. Results : Duplication Rate Histogram



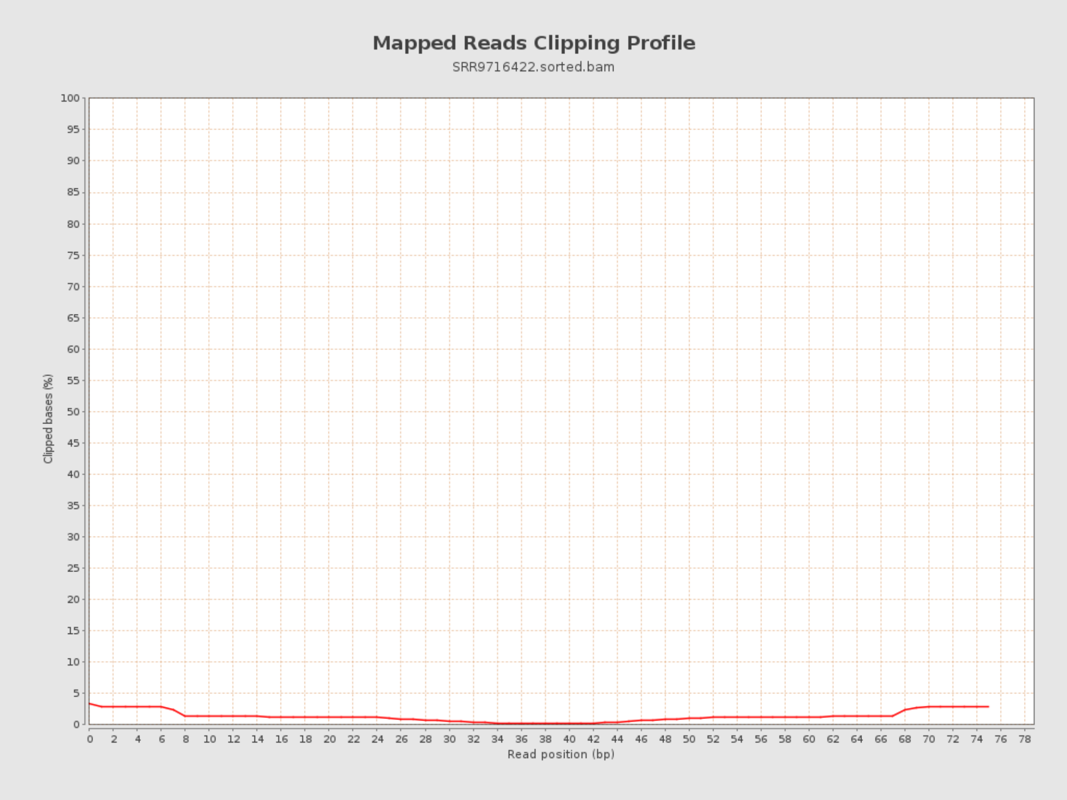
8. Results : Mapped Reads Nucleotide Content



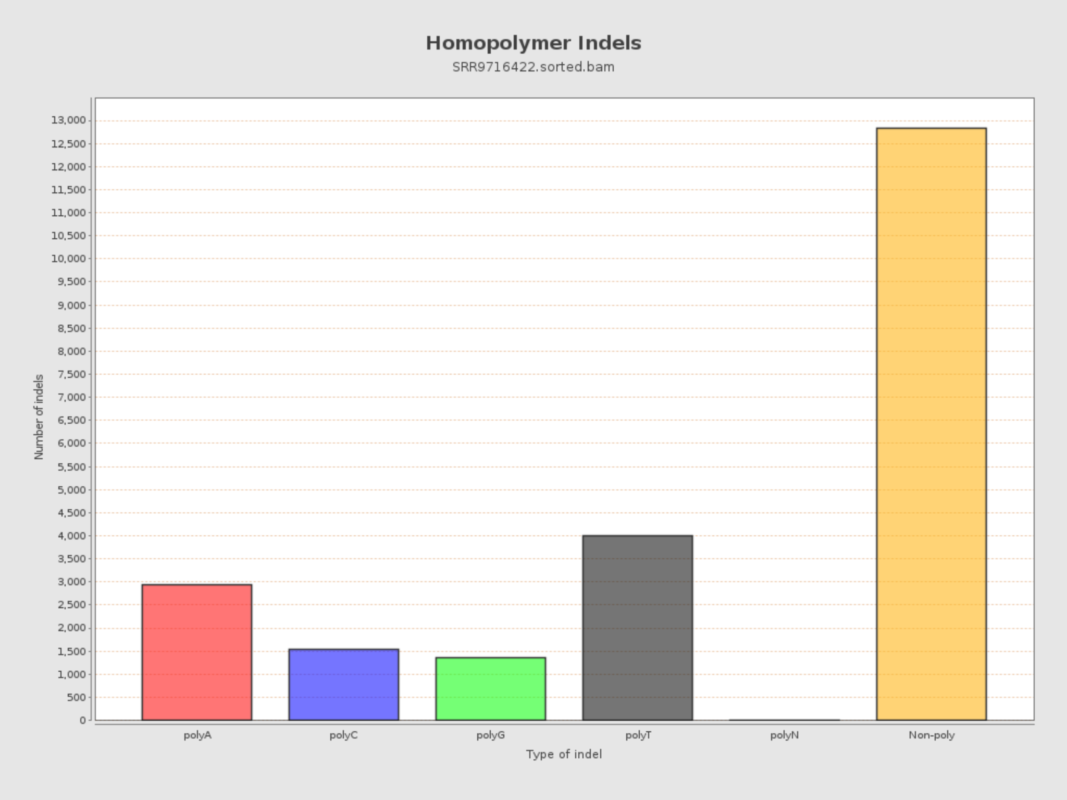
9. Results : Mapped Reads GC-content Distribution



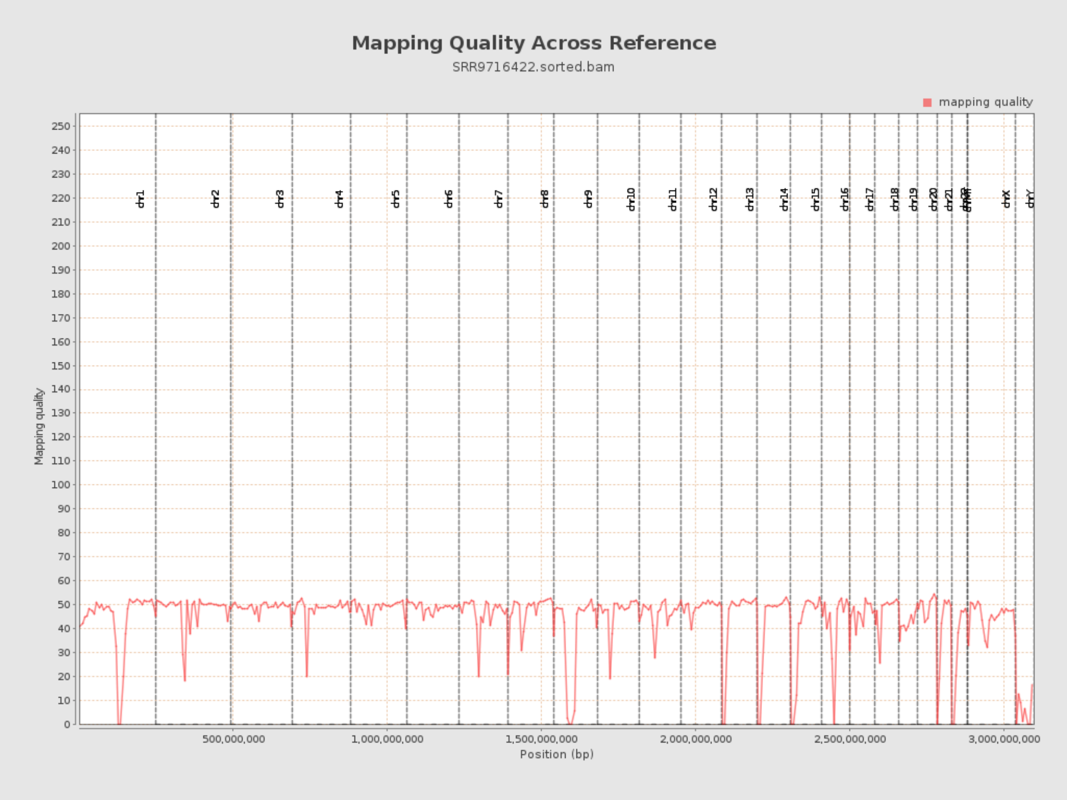
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram