Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 05:19:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716676.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_SRR9716676 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716676.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 05:19:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716676.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,326,049
Mapped reads	2,099,109 / 90.24%
Unmapped reads	226,940 / 9.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,863 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	101,603 / 4.37%
Duplication rate	3.72%
Clipped reads	2,105,697 / 90.53%

2.2. ACGT Content

Number/percentage of A's	31,031,898 / 25.63%
Number/percentage of C's	22,277,215 / 18.4%
Number/percentage of T's	37,337,773 / 30.84%
Number/percentage of G's	30,433,760 / 25.13%
Number/percentage of N's	784 / 0%
GC Percentage	43.53%

2.3. Coverage

Mean	0.0391

Standard Deviation	0.3348

2.4. Mapping Quality

Mean Mapping Quality	44.41

2.5. Mismatches and indels

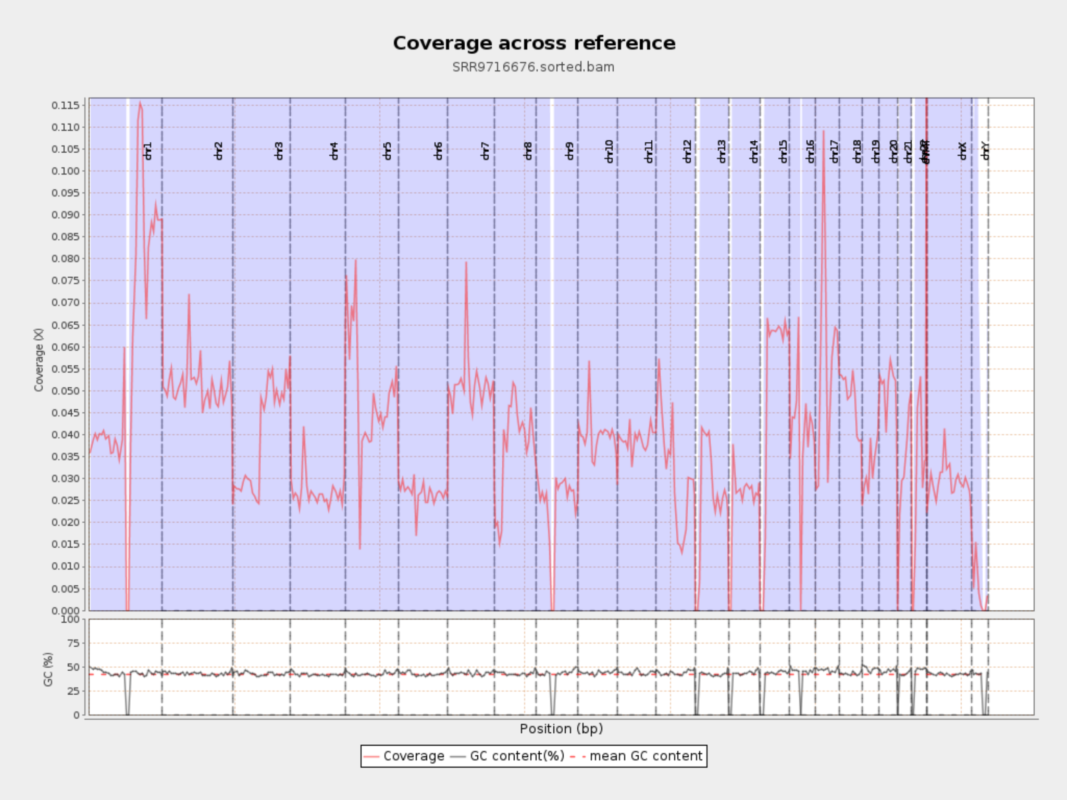
General error rate	0.5%
Mismatches	593,399
Insertions	8,094
Mapped reads with at least one insertion	0.38%
Deletions	20,425
Mapped reads with at least one deletion	0.97%
Homopolymer indels	40.59%

2.6. Chromosome stats

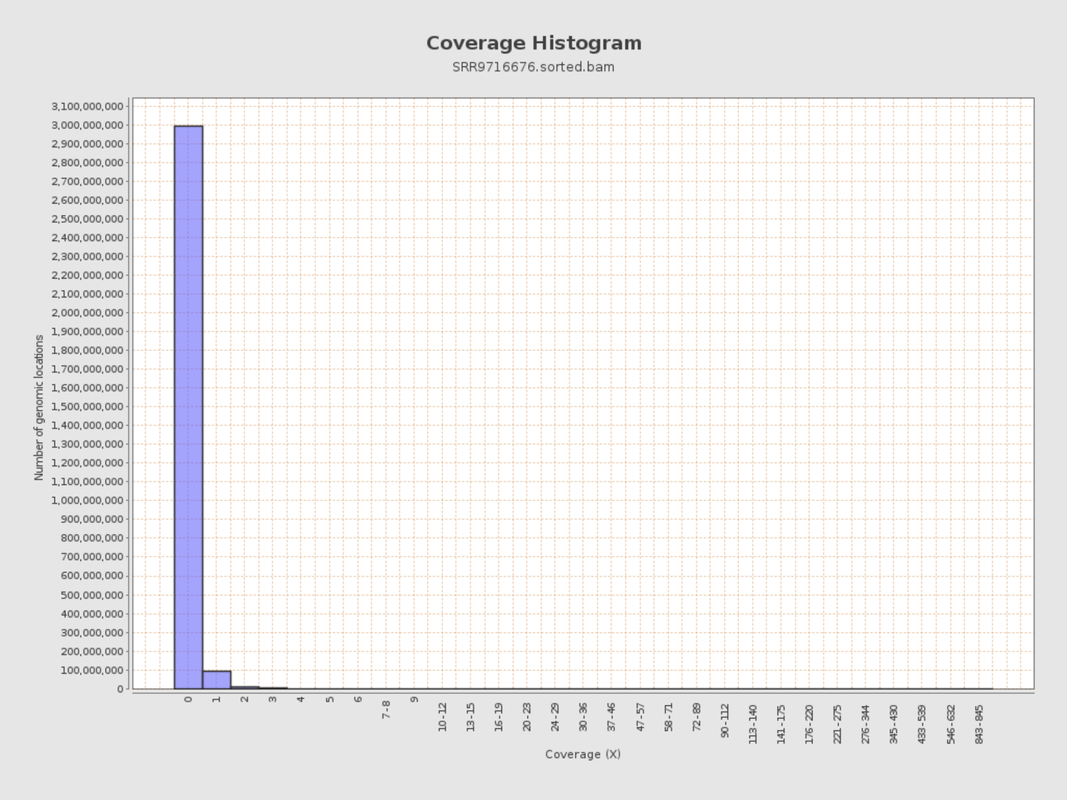
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14338229	0.0575	0.5542
chr2	243199373	12484576	0.0513	0.4651
chr3	198022430	7796897	0.0394	0.2246
chr4	191154276	5131166	0.0268	0.2106
chr5	180915260	8894347	0.0492	0.2517
chr6	171115067	4565722	0.0267	0.2092
chr7	159138663	8250162	0.0518	0.561

chr8	146364022	5476465	0.0374	0.2919
chr9	141213431	3345682	0.0237	0.2429
chr10	135534747	5436976	0.0401	0.2845
chr11	135006516	5240998	0.0388	0.3228
chr12	133851895	4194620	0.0313	0.2039
chr13	115169878	2978914	0.0259	0.1836
chr14	107349540	2621747	0.0244	0.1907
chr15	102531392	5256530	0.0513	0.2601
chr16	90354753	3642468	0.0403	0.2426
chr17	81195210	4673053	0.0576	0.3
chr18	78077248	3773623	0.0483	0.557
chr19	59128983	1943030	0.0329	0.4083
chr20	63025520	3216175	0.051	0.2589
chr21	48129895	1542025	0.032	0.2125
chr22	51304566	1438167	0.028	0.1885
chrMT	16571	3667	0.2213	0.5152
chrX	155270560	4582986	0.0295	0.2255
chrY	59373566	285351	0.0048	0.1175

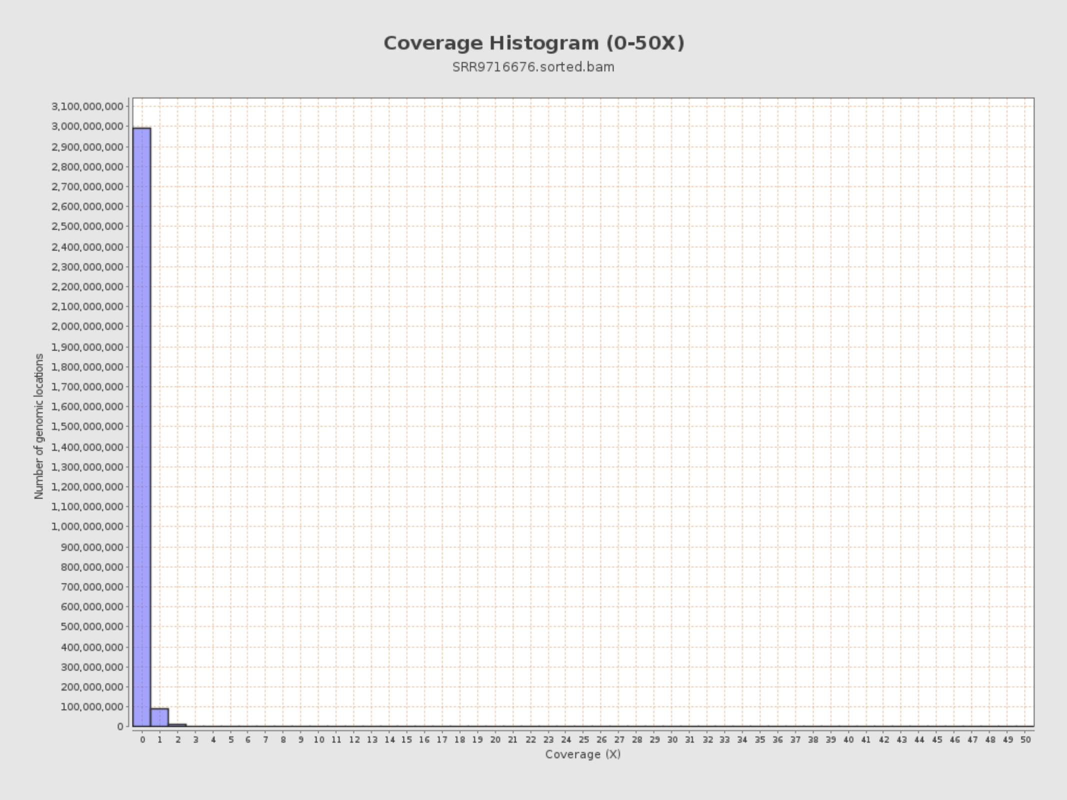
3. Results : Coverage across reference



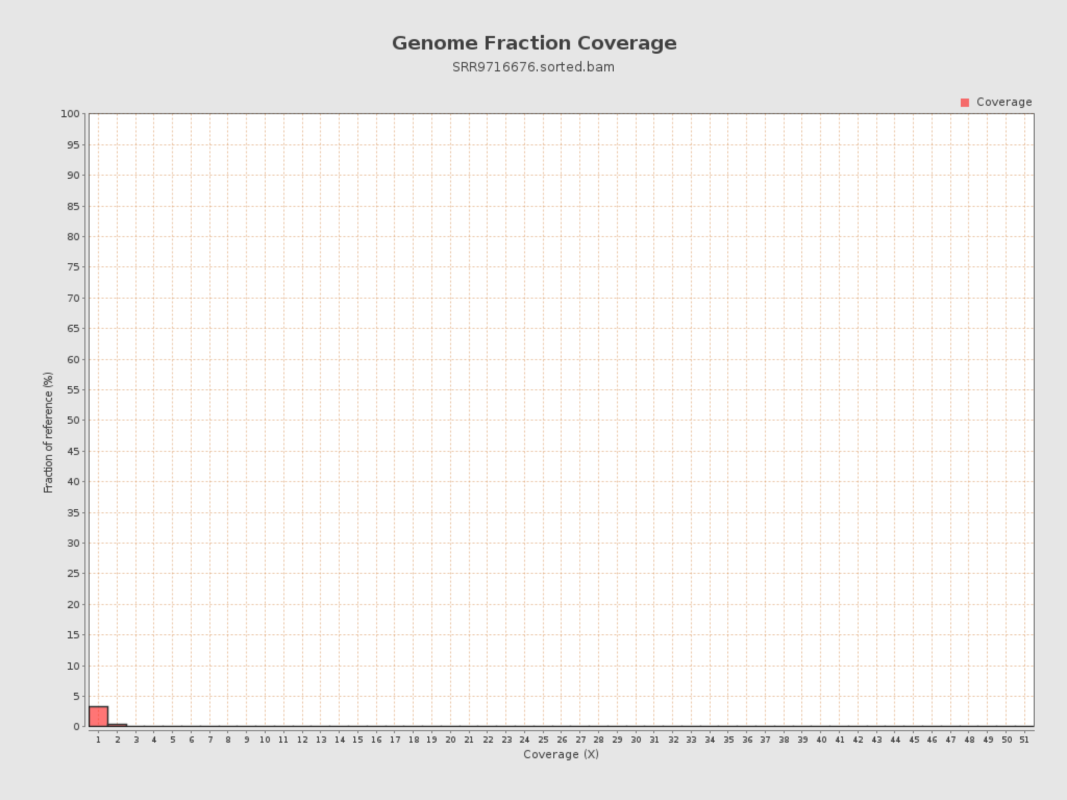
4. Results : Coverage Histogram



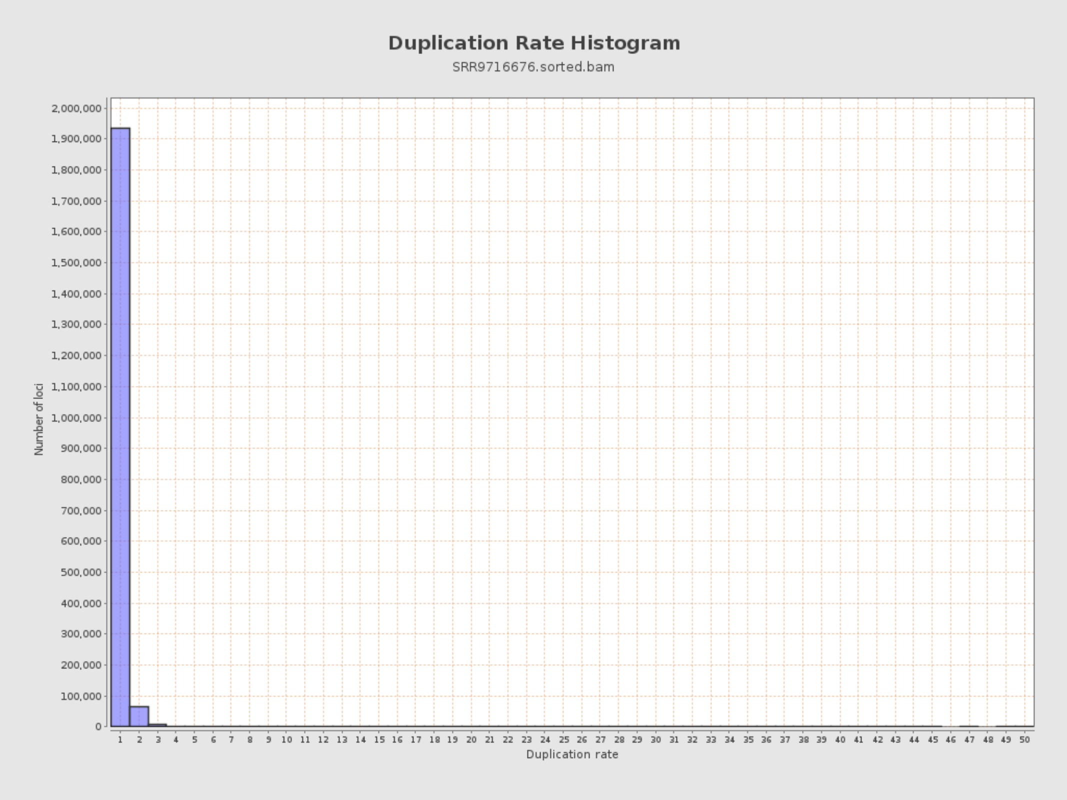
5. Results : Coverage Histogram (0-50X)



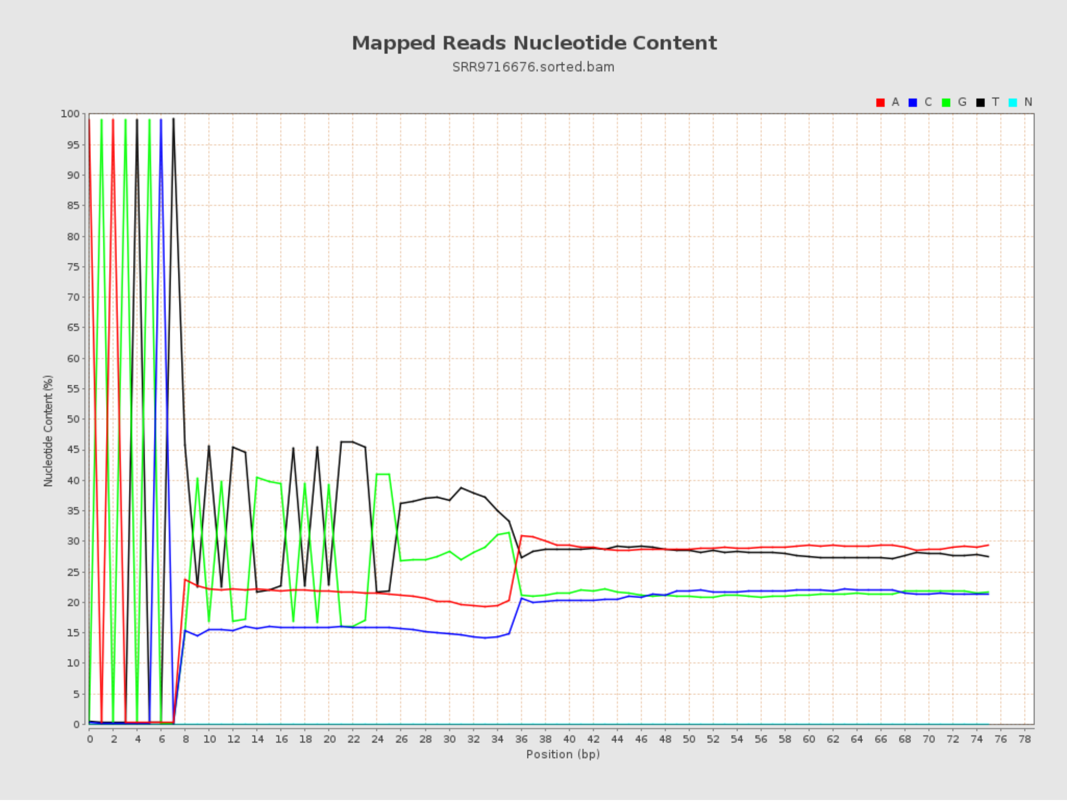
6. Results : Genome Fraction Coverage



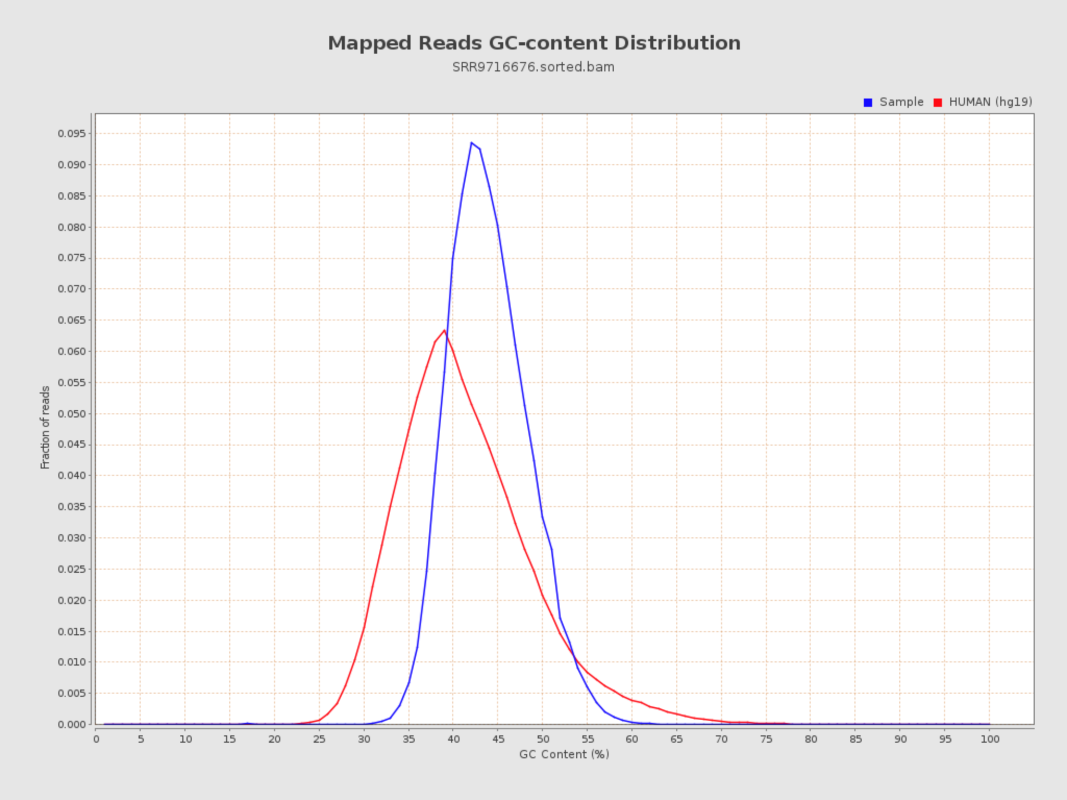
7. Results : Duplication Rate Histogram



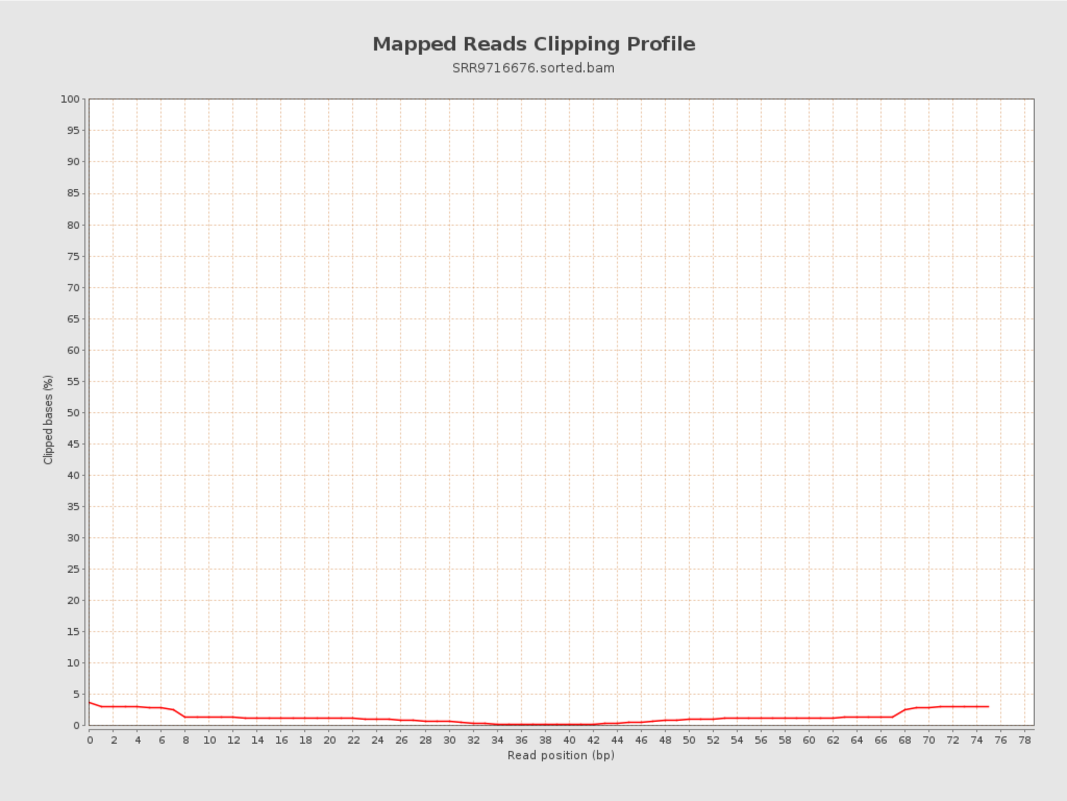
8. Results : Mapped Reads Nucleotide Content



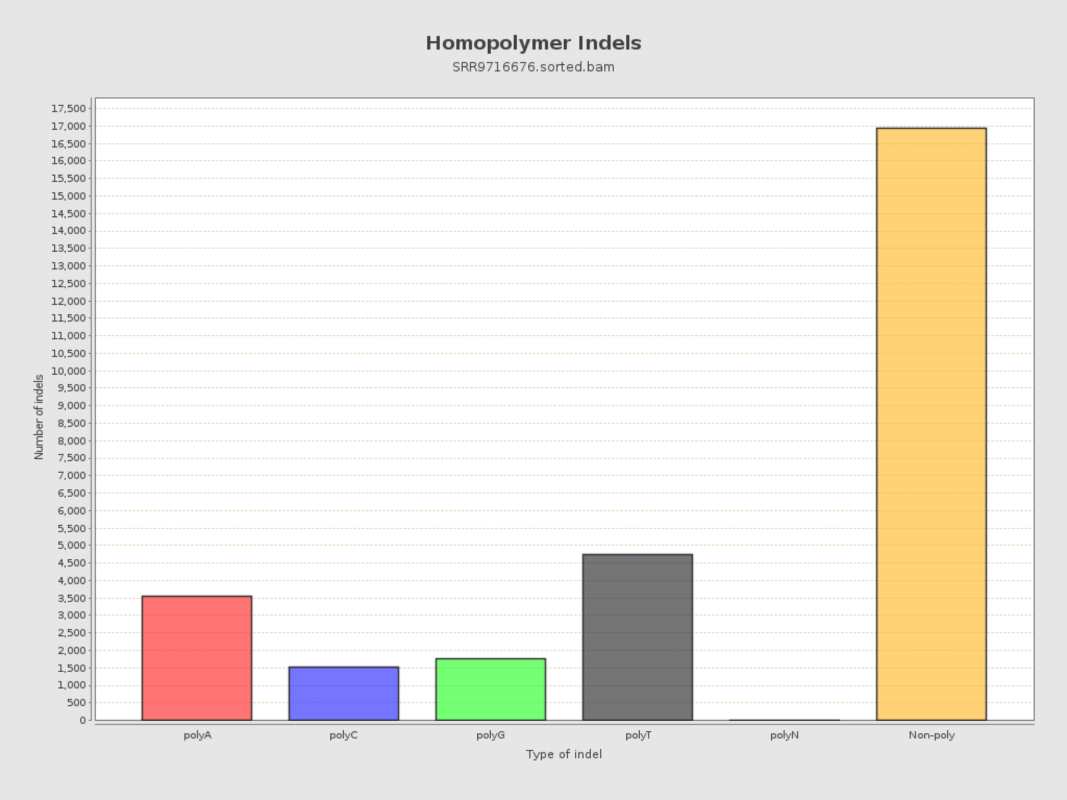
9. Results : Mapped Reads GC-content Distribution



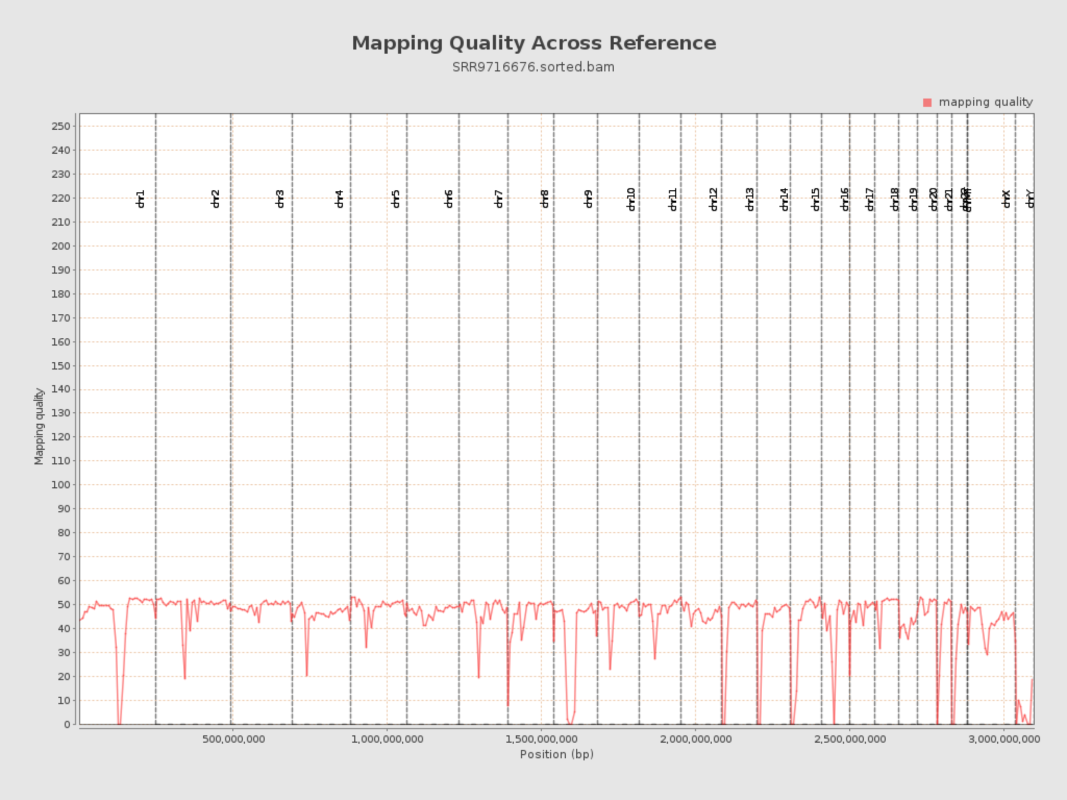
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram