

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:42:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716202.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_SRR9716202 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716202.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:42:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716202.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,048,109
Mapped reads	1,765,957 / 86.22%
Unmapped reads	282,152 / 13.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	45,232 / 2.21%
Read min/max/mean length	30 / 101 / 101.8
Duplicated reads (estimated)	53,440 / 2.61%
Duplication rate	2.07%
Clipped reads	1,808,076 / 88.28%

2.2. ACGT Content

Number/percentage of A's	34,184,670 / 25.97%
Number/percentage of C's	27,356,939 / 20.78%
Number/percentage of T's	40,144,128 / 30.49%
Number/percentage of G's	29,952,472 / 22.75%
Number/percentage of N's	16,293 / 0.01%
GC Percentage	43.53%

2.3. Coverage

Mean	0.0425

Standard Deviation	0.3364
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2.4. Mapping Quality

Mean Mapping Quality	46.03
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2.5. Mismatches and indels

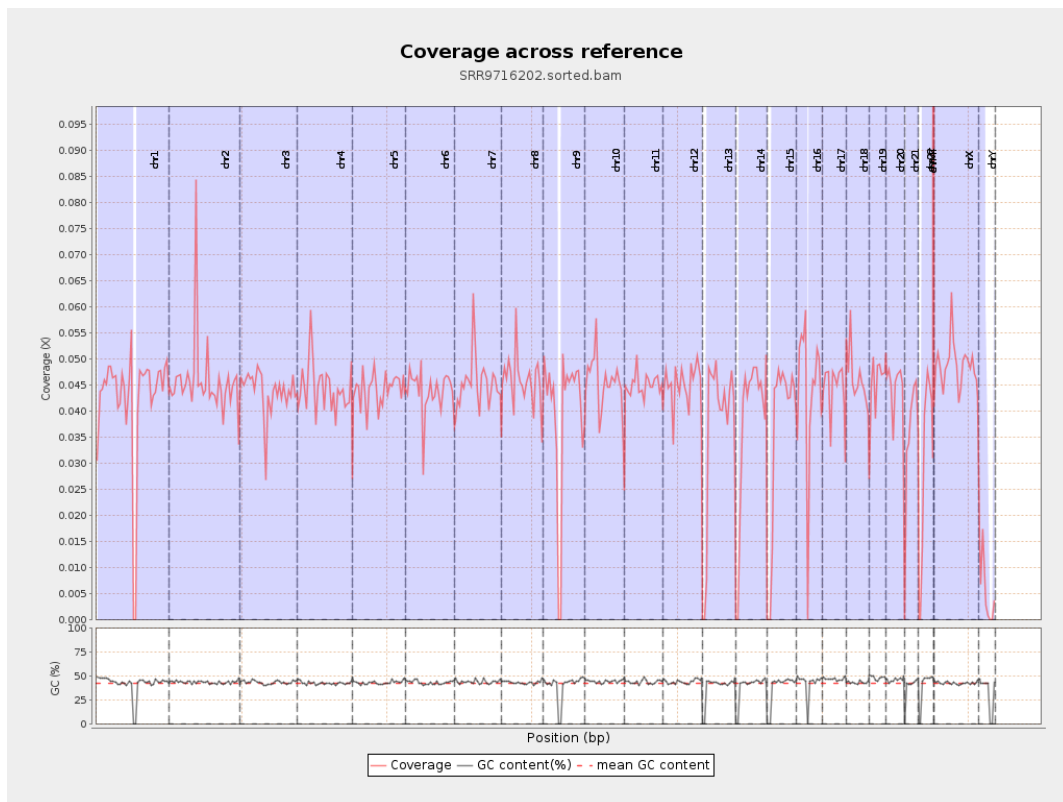
General error rate	0.78%
Mismatches	999,544
Insertions	10,651
Mapped reads with at least one insertion	0.6%
Deletions	27,037
Mapped reads with at least one deletion	1.51%
Homopolymer indels	40.18%

2.6. Chromosome stats

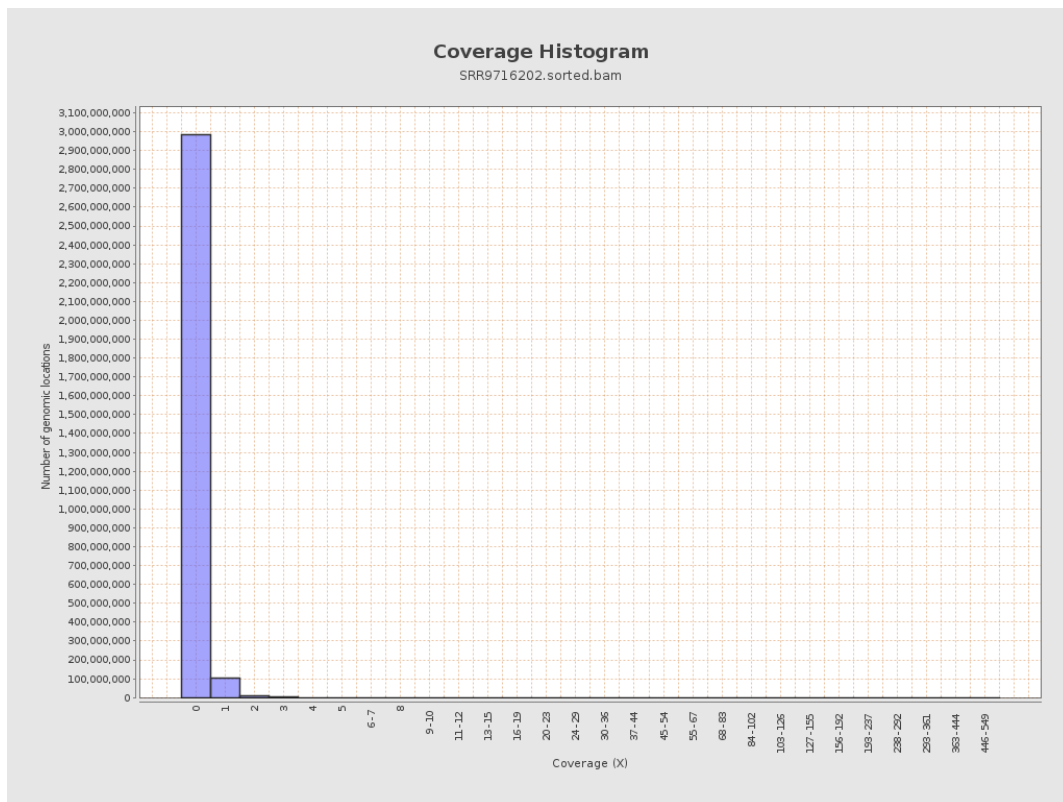
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10557493	0.0424	0.385
chr2	243199373	11116757	0.0457	0.4935
chr3	198022430	8668016	0.0438	0.2338
chr4	191154276	8468609	0.0443	0.2562
chr5	180915260	7973720	0.0441	0.2362
chr6	171115067	7500827	0.0438	0.2622
chr7	159138663	7237454	0.0455	0.4245

chr8	146364022	6697751	0.0458	0.4267
chr9	141213431	5567337	0.0394	0.3648
chr10	135534747	6183096	0.0456	0.3133
chr11	135006516	6026635	0.0446	0.3627
chr12	133851895	6022051	0.045	0.2427
chr13	115169878	4217285	0.0366	0.2129
chr14	107349540	3998239	0.0372	0.2618
chr15	102531392	3717875	0.0363	0.2156
chr16	90354753	3970897	0.0439	0.2623
chr17	81195210	3574558	0.044	0.2581
chr18	78077248	3626761	0.0465	0.6662
chr19	59128983	2705142	0.0457	0.3515
chr20	63025520	2768984	0.0439	0.25
chr21	48129895	1698364	0.0353	0.2307
chr22	51304566	1518636	0.0296	0.194
chrMT	16571	8709	0.5256	0.8628
chrX	155270560	7554245	0.0487	0.3127
chrY	59373566	320841	0.0054	0.1387

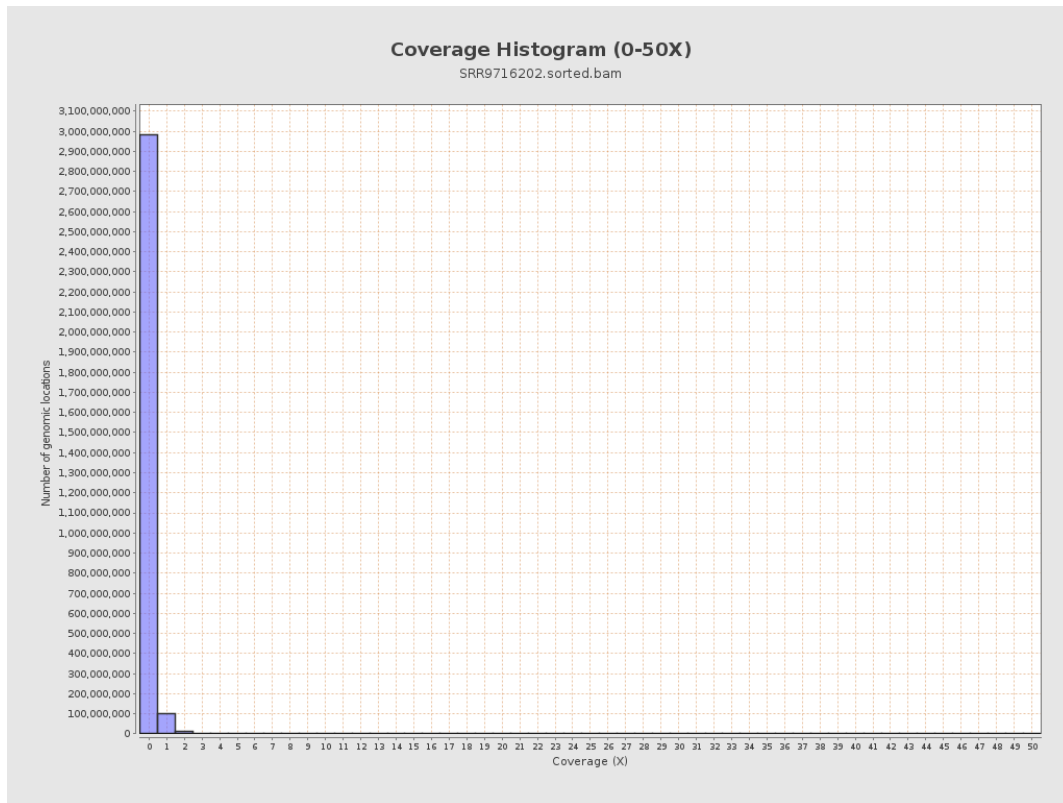
3. Results : Coverage across reference



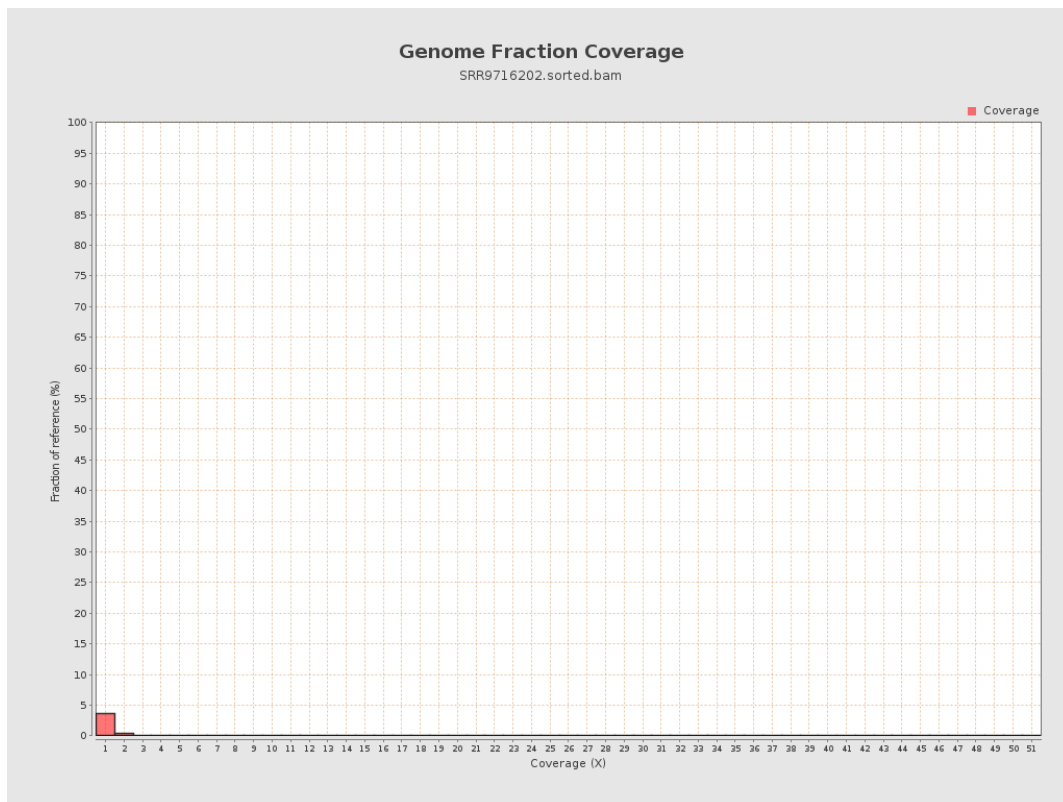
4. Results : Coverage Histogram



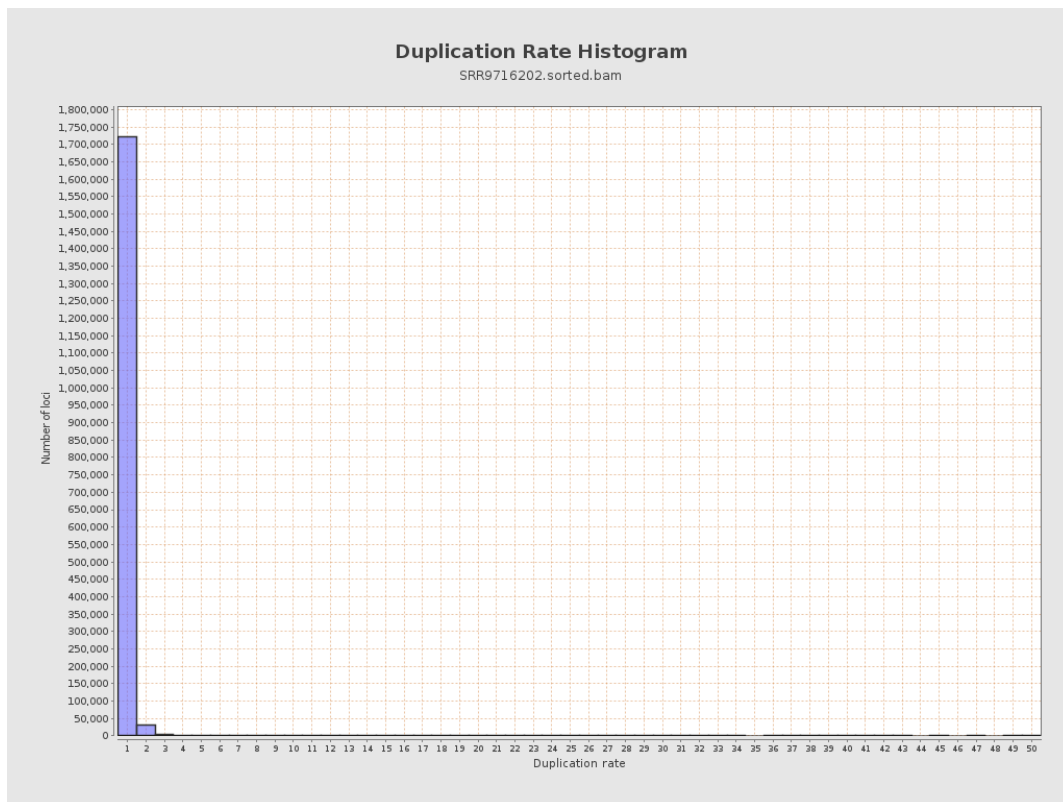
5. Results : Coverage Histogram (0-50X)



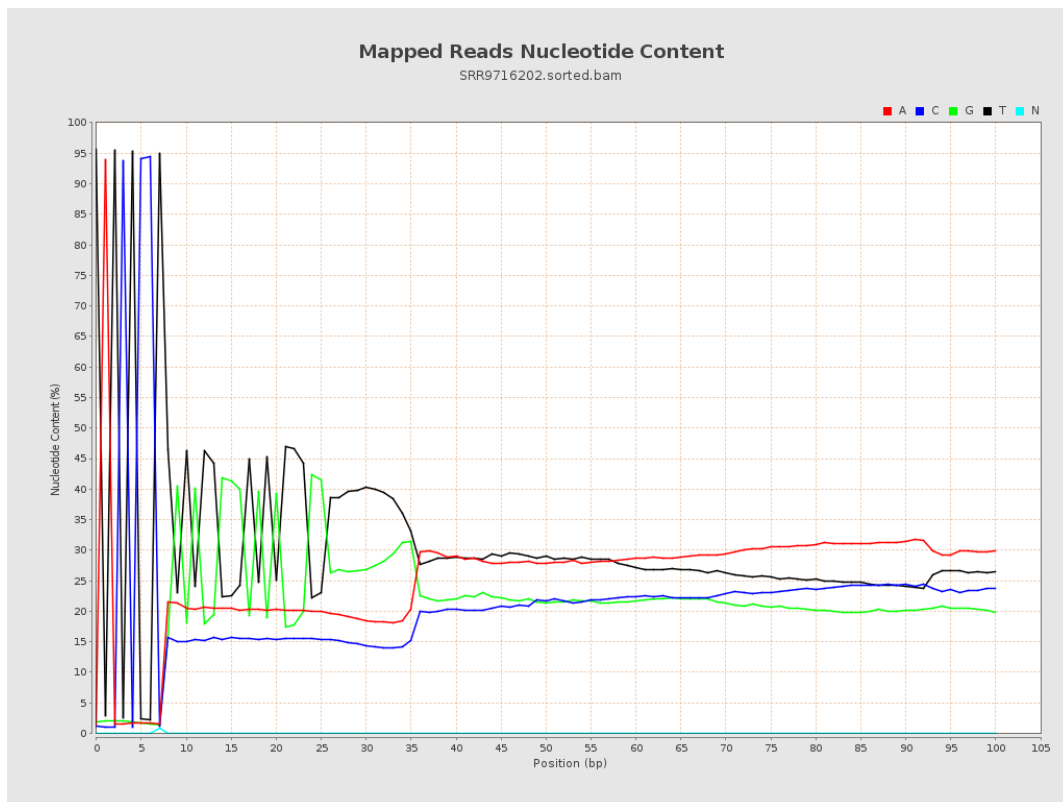
6. Results : Genome Fraction Coverage



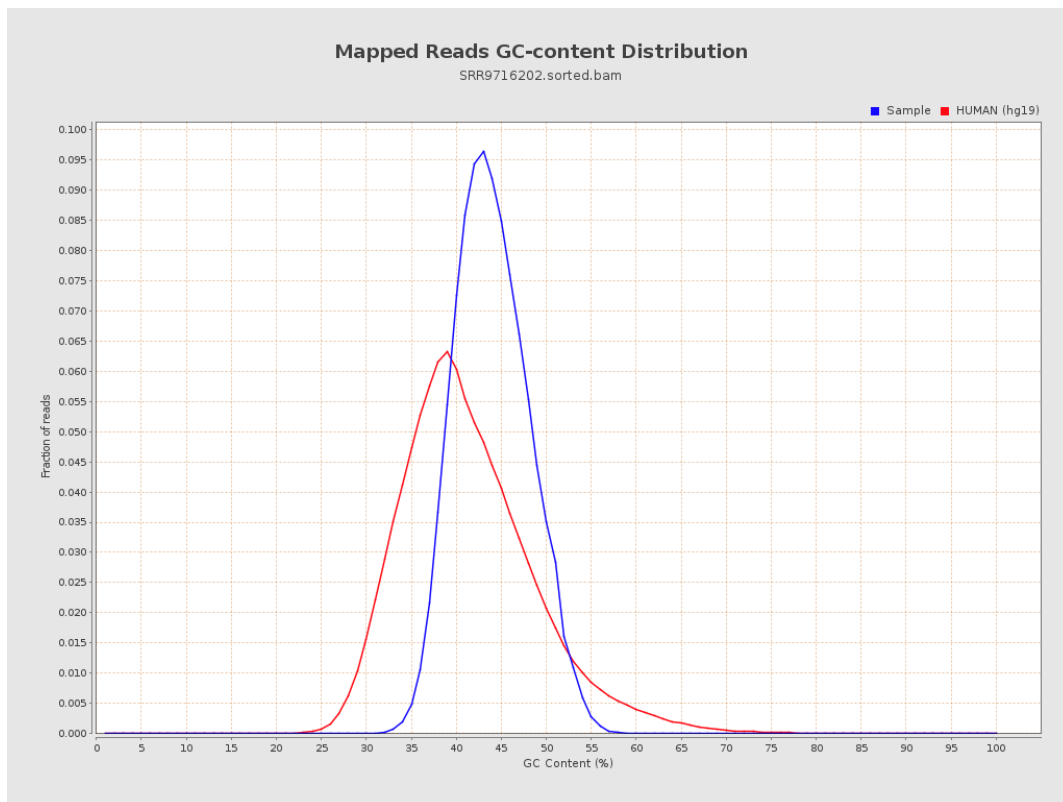
7. Results : Duplication Rate Histogram



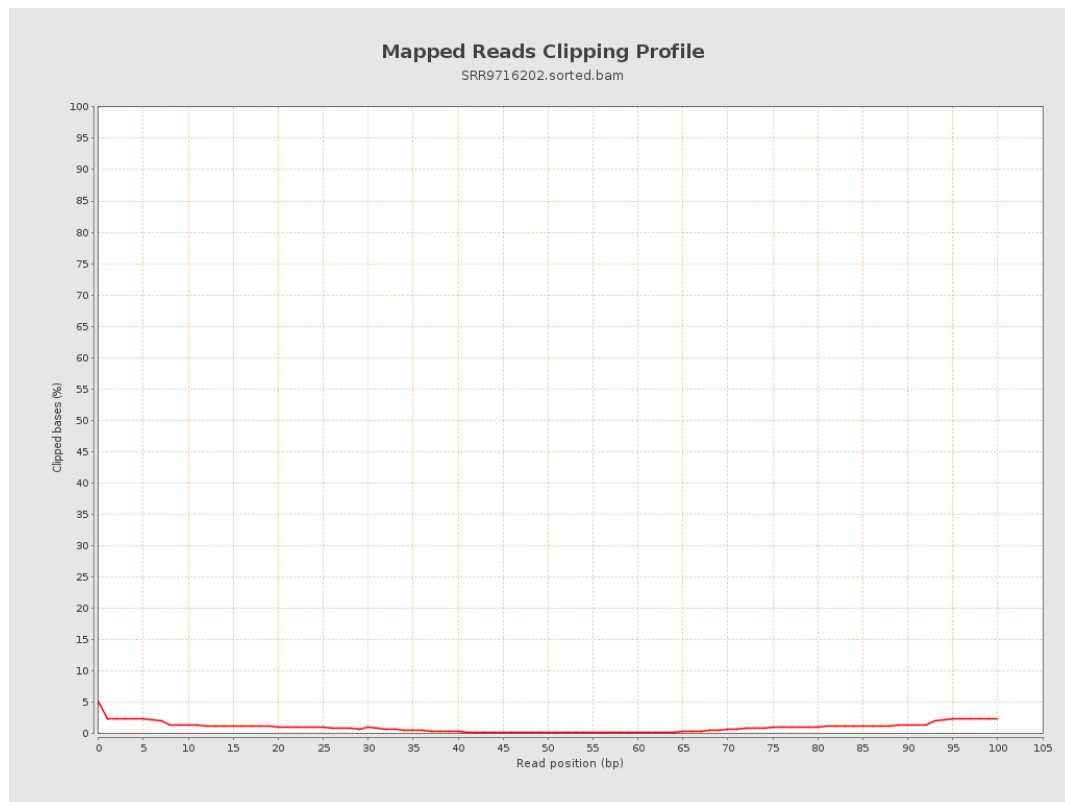
8. Results : Mapped Reads Nucleotide Content



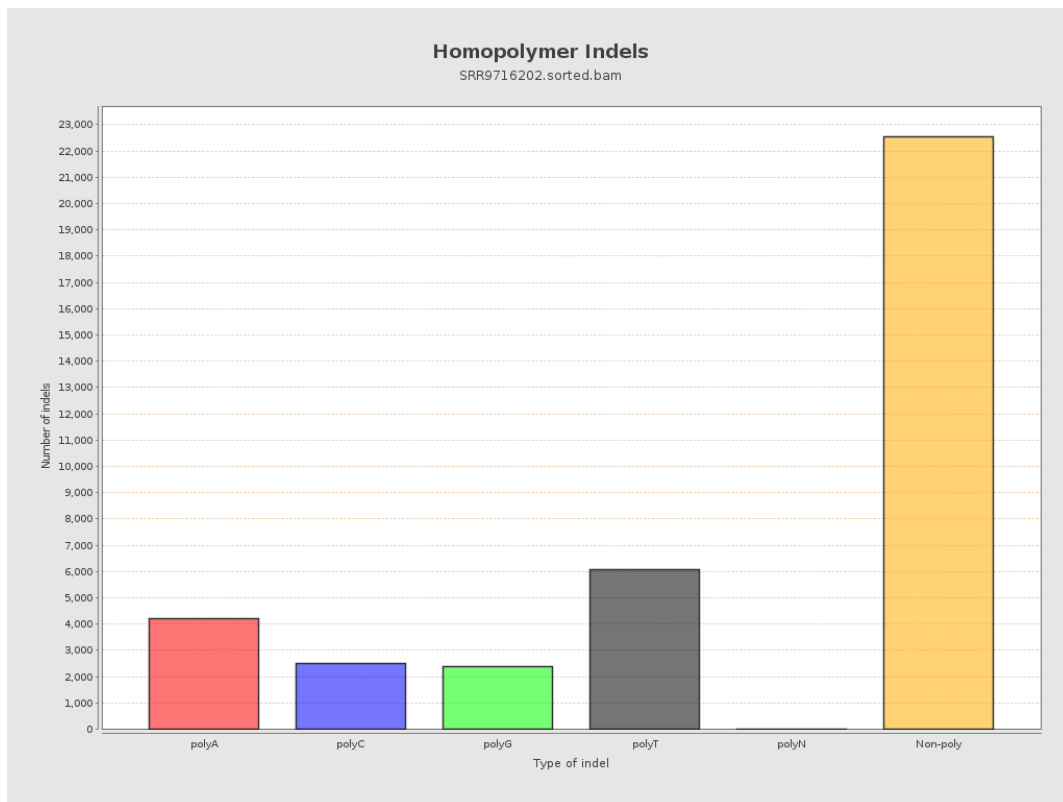
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

