

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 01:11:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085108.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_SRR3085108 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085108.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 01:11:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085108.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,952,359
Mapped reads	2,477,057 / 83.9%
Unmapped reads	475,302 / 16.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,962 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	92,336 / 3.13%
Duplication rate	2.89%
Clipped reads	1,738,601 / 58.89%

2.2. ACGT Content

Number/percentage of A's	42,843,793 / 28.81%
Number/percentage of C's	30,799,458 / 20.71%
Number/percentage of T's	41,905,510 / 28.18%
Number/percentage of G's	33,165,658 / 22.3%
Number/percentage of N's	3,139 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0481

Standard Deviation	0.3697
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2.4. Mapping Quality

Mean Mapping Quality	42.56
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2.5. Mismatches and indels

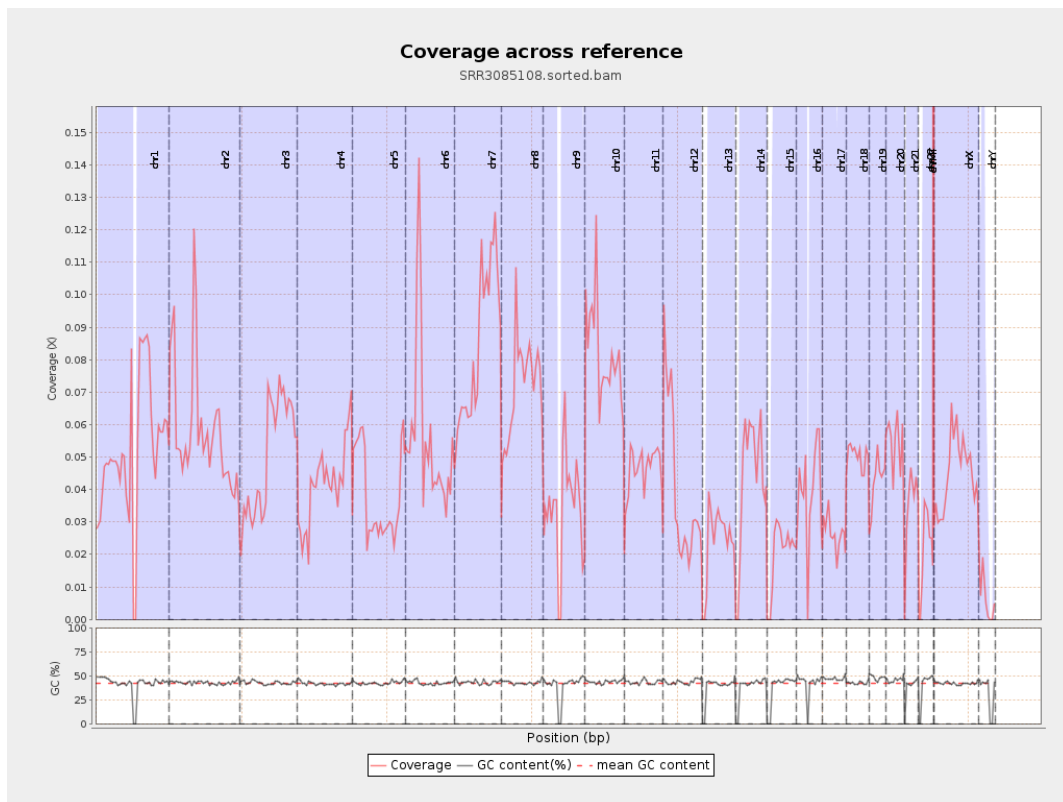
General error rate	0.87%
Mismatches	1,282,764
Insertions	10,955
Mapped reads with at least one insertion	0.44%
Deletions	30,701
Mapped reads with at least one deletion	1.23%
Homopolymer indels	43.7%

2.6. Chromosome stats

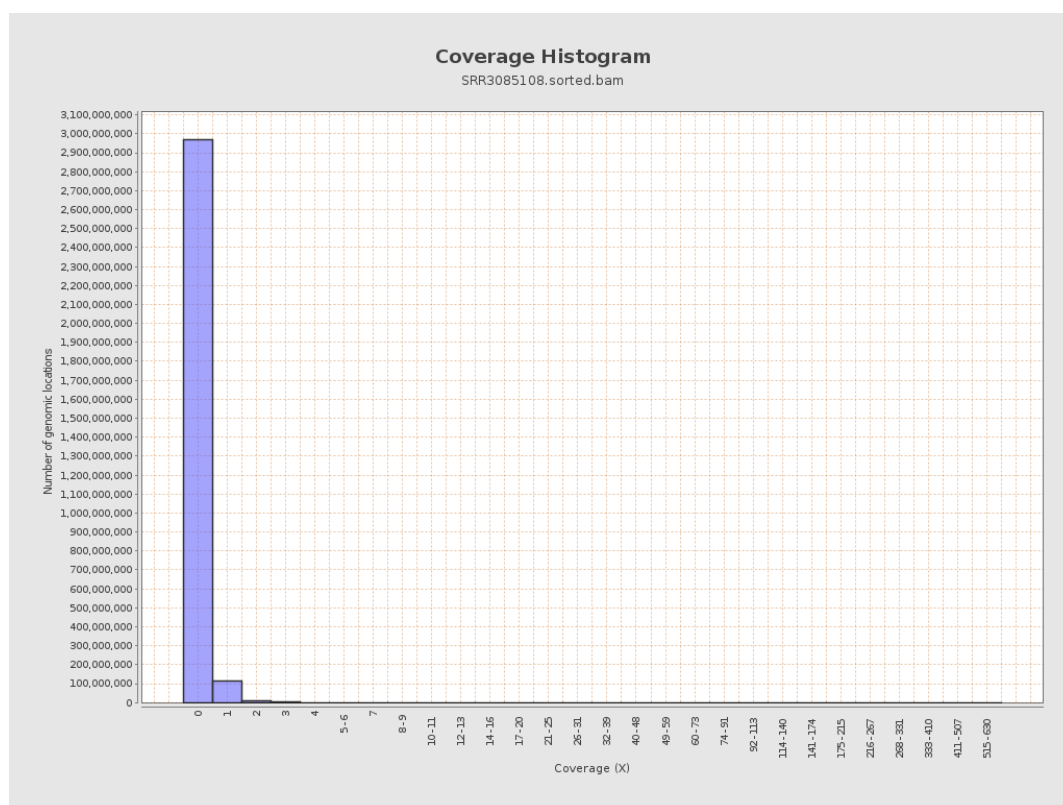
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13018676	0.0522	0.5658
chr2	243199373	14218842	0.0585	0.4759
chr3	198022430	9895728	0.05	0.2585
chr4	191154276	8015789	0.0419	0.2439
chr5	180915260	6886904	0.0381	0.2186
chr6	171115067	9647704	0.0564	0.3765
chr7	159138663	13625706	0.0856	0.4585

chr8	146364022	10550667	0.0721	0.5117
chr9	141213431	4916454	0.0348	0.3332
chr10	135534747	11078734	0.0817	0.5652
chr11	135006516	6216820	0.046	0.3339
chr12	133851895	5324997	0.0398	0.2303
chr13	115169878	2775325	0.0241	0.1701
chr14	107349540	4715812	0.0439	0.2453
chr15	102531392	2117884	0.0207	0.1611
chr16	90354753	3584163	0.0397	0.2478
chr17	81195210	2139544	0.0264	0.2177
chr18	78077248	3933598	0.0504	0.5431
chr19	59128983	2564200	0.0434	0.406
chr20	63025520	3413901	0.0542	0.2654
chr21	48129895	1693370	0.0352	0.2249
chr22	51304566	1072388	0.0209	0.1591
chrMT	16571	12536	0.7565	1.0309
chrX	155270560	6981097	0.045	0.2921
chrY	59373566	365874	0.0062	0.1219

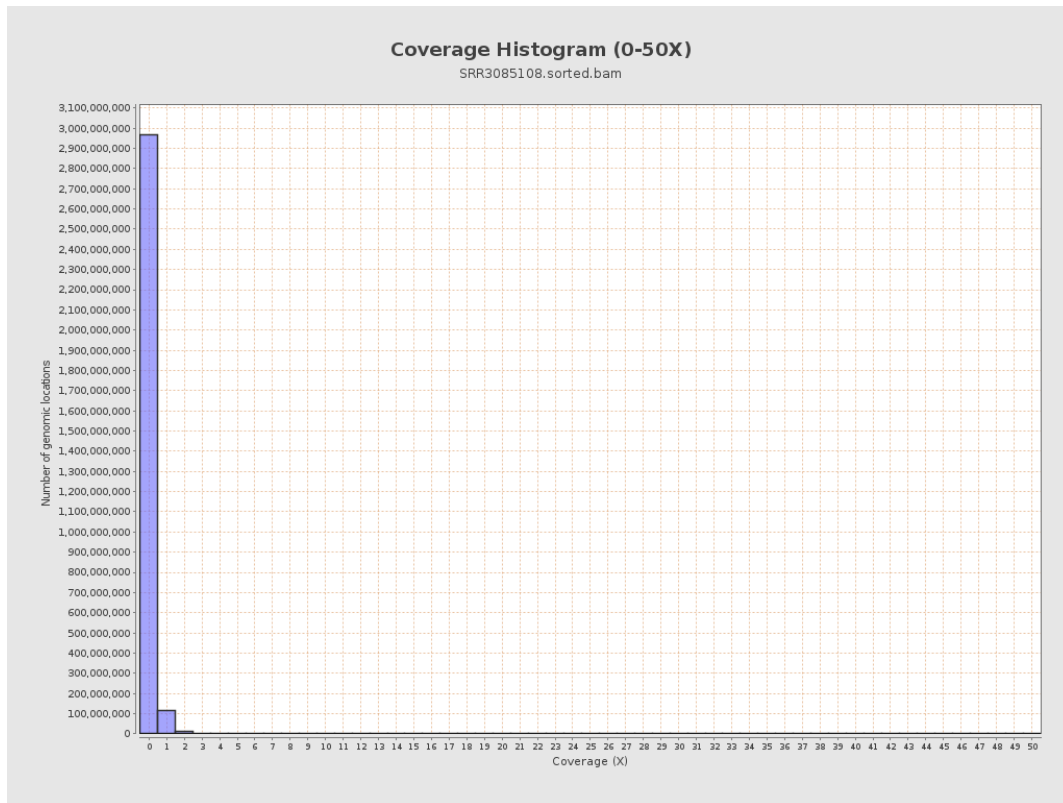
3. Results : Coverage across reference



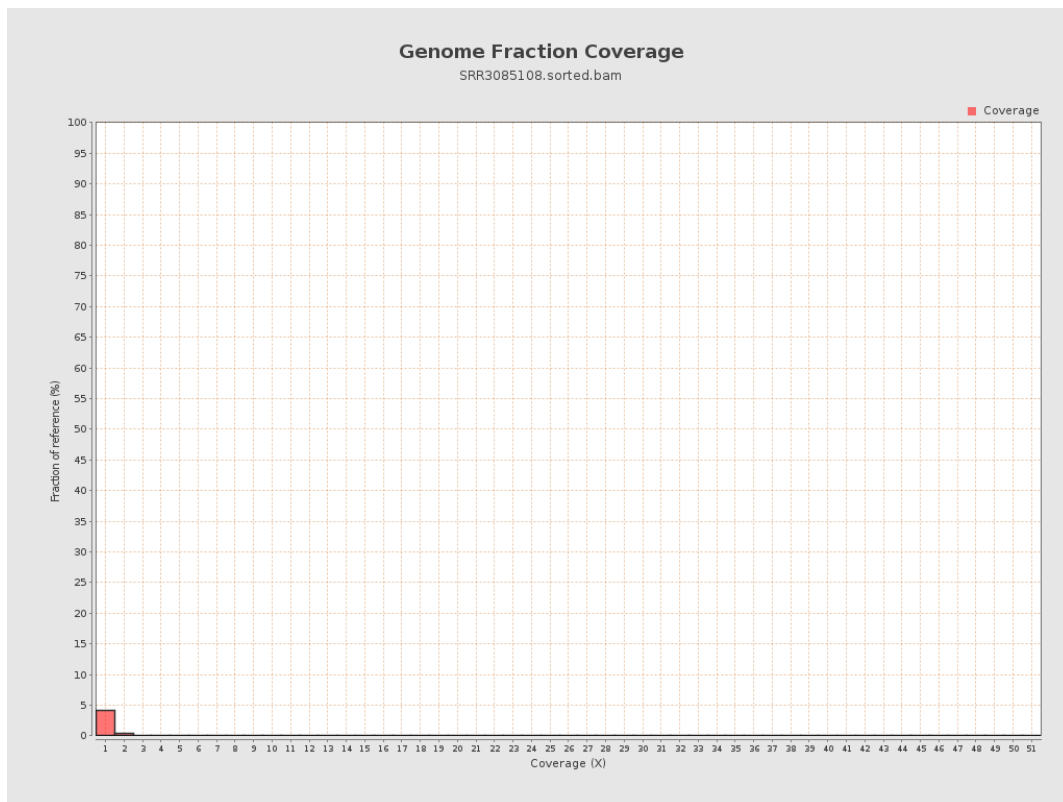
4. Results : Coverage Histogram



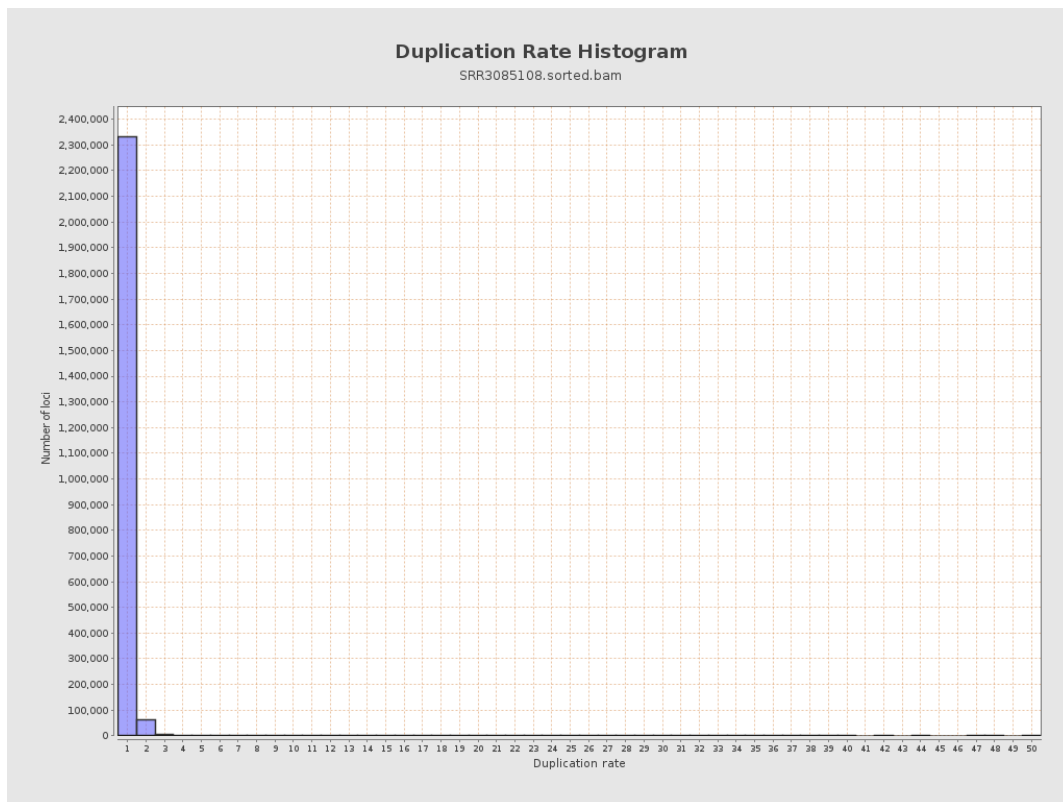
5. Results : Coverage Histogram (0-50X)



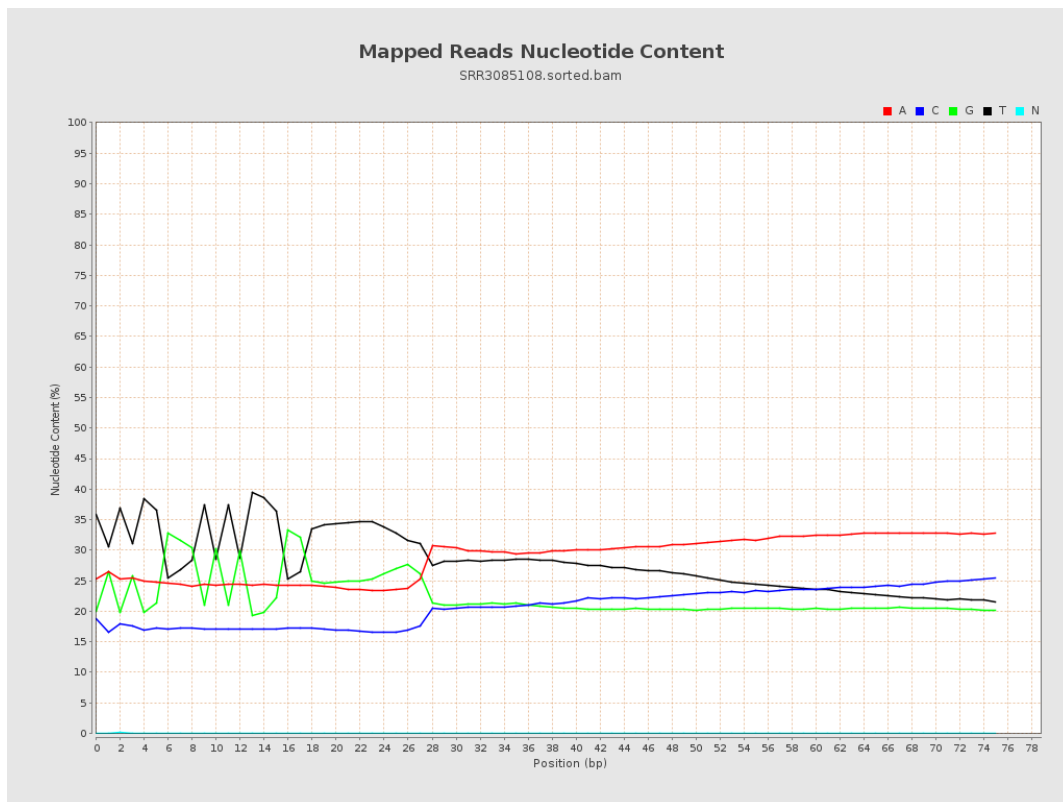
6. Results : Genome Fraction Coverage



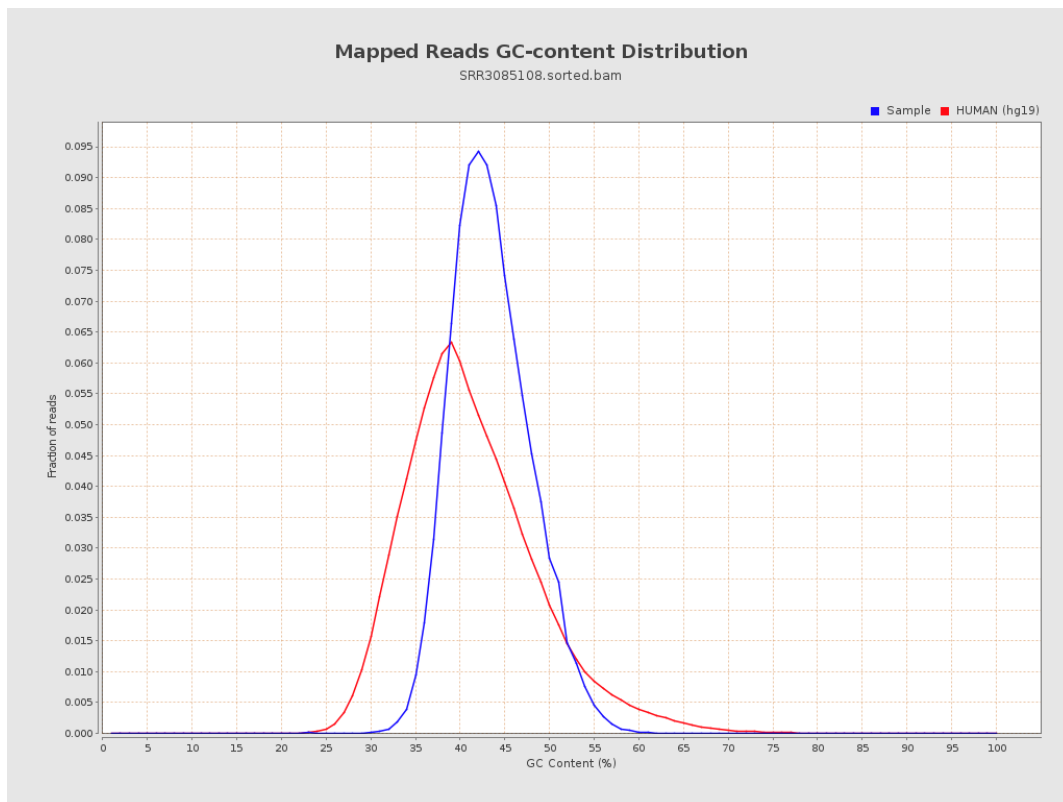
7. Results : Duplication Rate Histogram



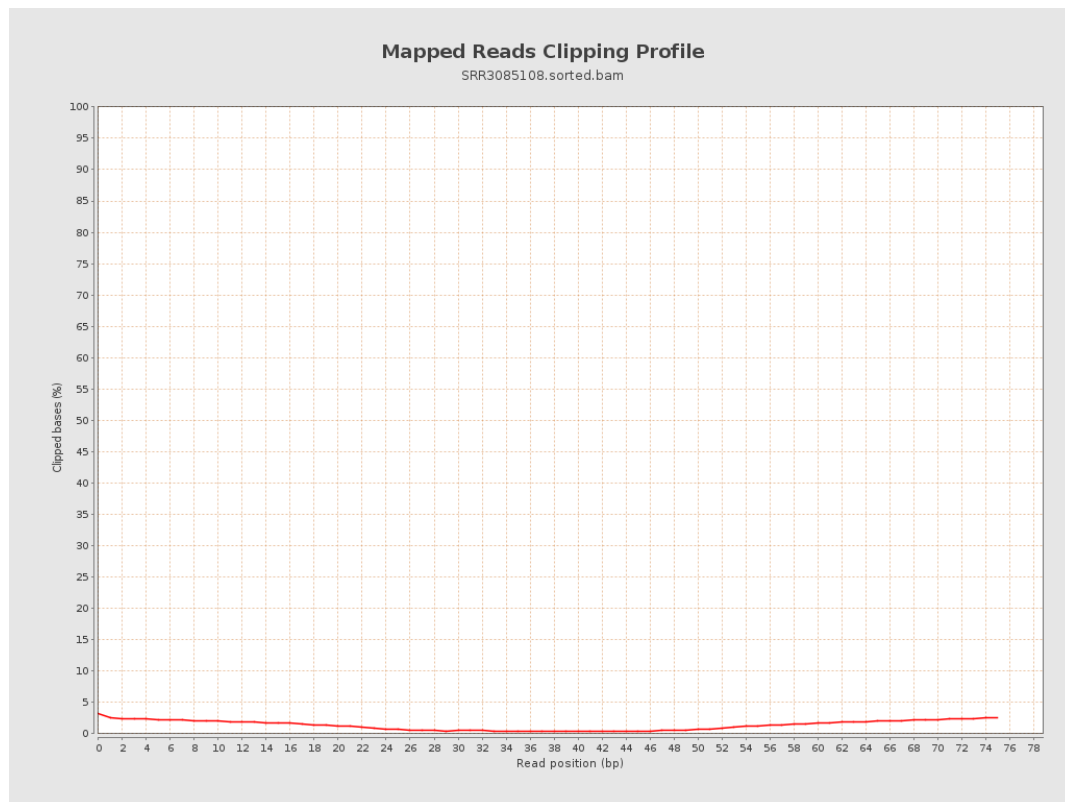
8. Results : Mapped Reads Nucleotide Content



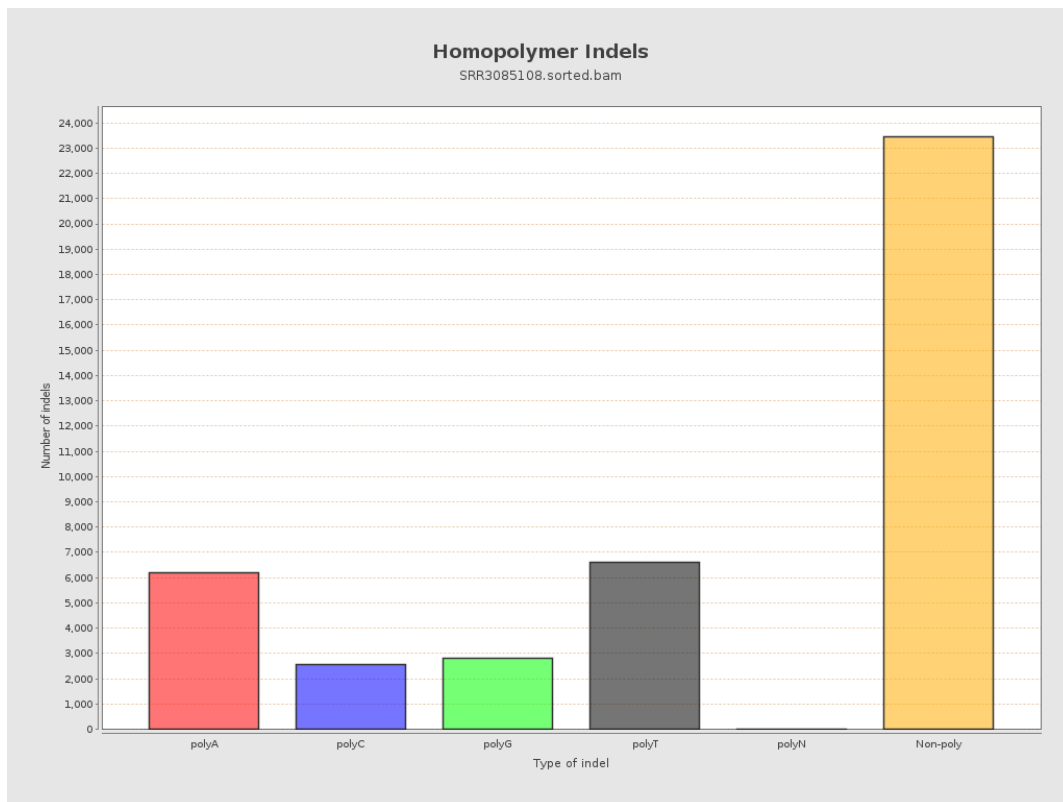
9. Results : Mapped Reads GC-content Distribution



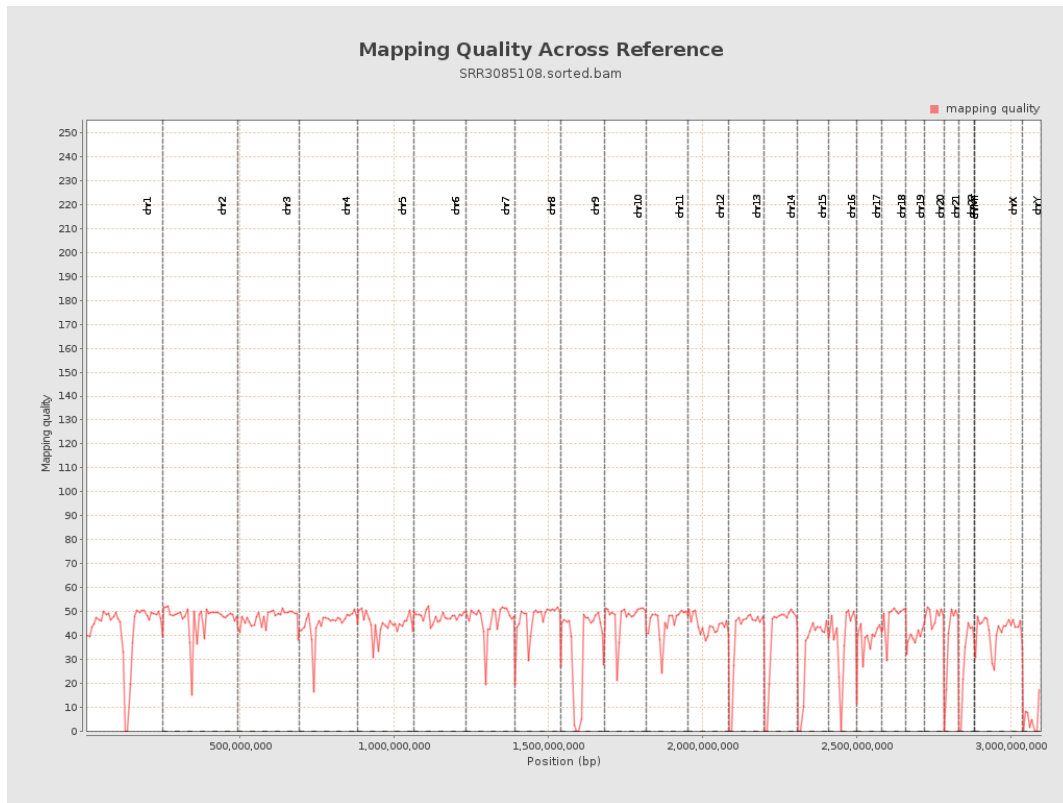
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

