

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:05:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004108.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_SRR6004108 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004108.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:05:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004108.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,287,254
Mapped reads	3,792,607 / 88.46%
Unmapped reads	494,647 / 11.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,531 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	214,982 / 5.01%
Duplication rate	4.25%
Clipped reads	1,387,543 / 32.36%

2.2. ACGT Content

Number/percentage of A's	73,756,148 / 28.26%
Number/percentage of C's	48,952,822 / 18.76%
Number/percentage of T's	83,014,636 / 31.81%
Number/percentage of G's	55,238,235 / 21.16%
Number/percentage of N's	35,622 / 0.01%
GC Percentage	39.92%

2.3. Coverage

Mean	0.0843

Standard Deviation	0.7507
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2.4. Mapping Quality

Mean Mapping Quality	47.11
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2.5. Mismatches and indels

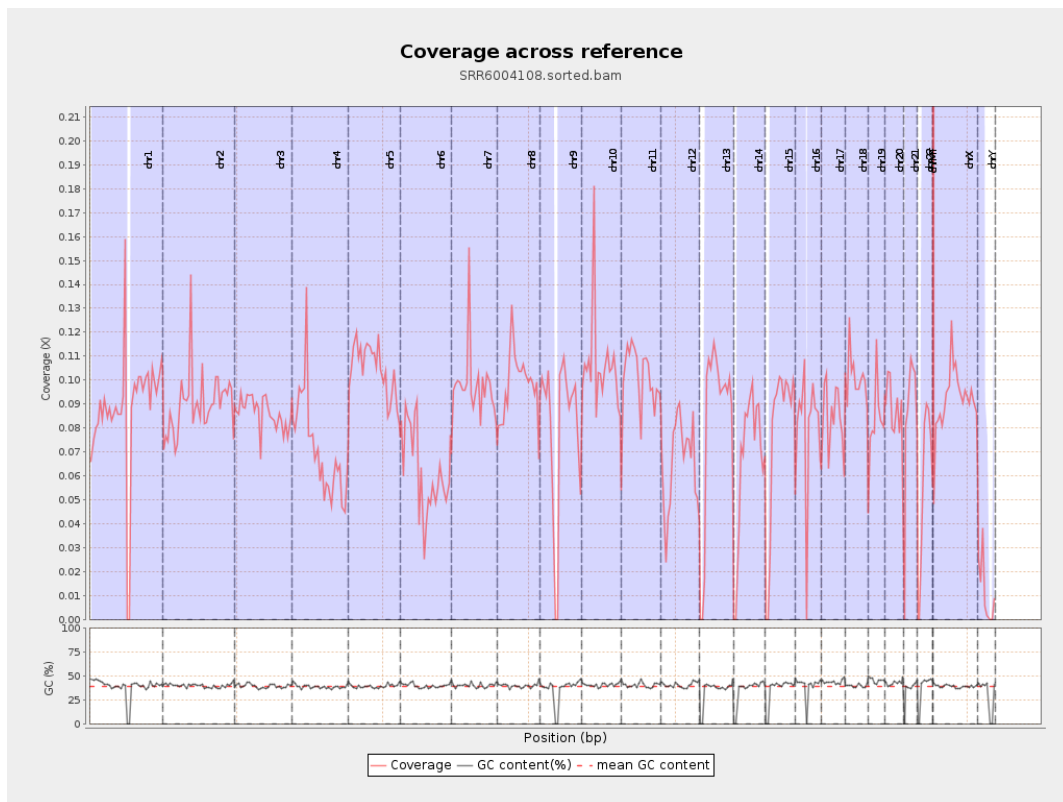
General error rate	0.96%
Mismatches	2,453,051
Insertions	22,698
Mapped reads with at least one insertion	0.59%
Deletions	70,502
Mapped reads with at least one deletion	1.84%
Homopolymer indels	46.71%

2.6. Chromosome stats

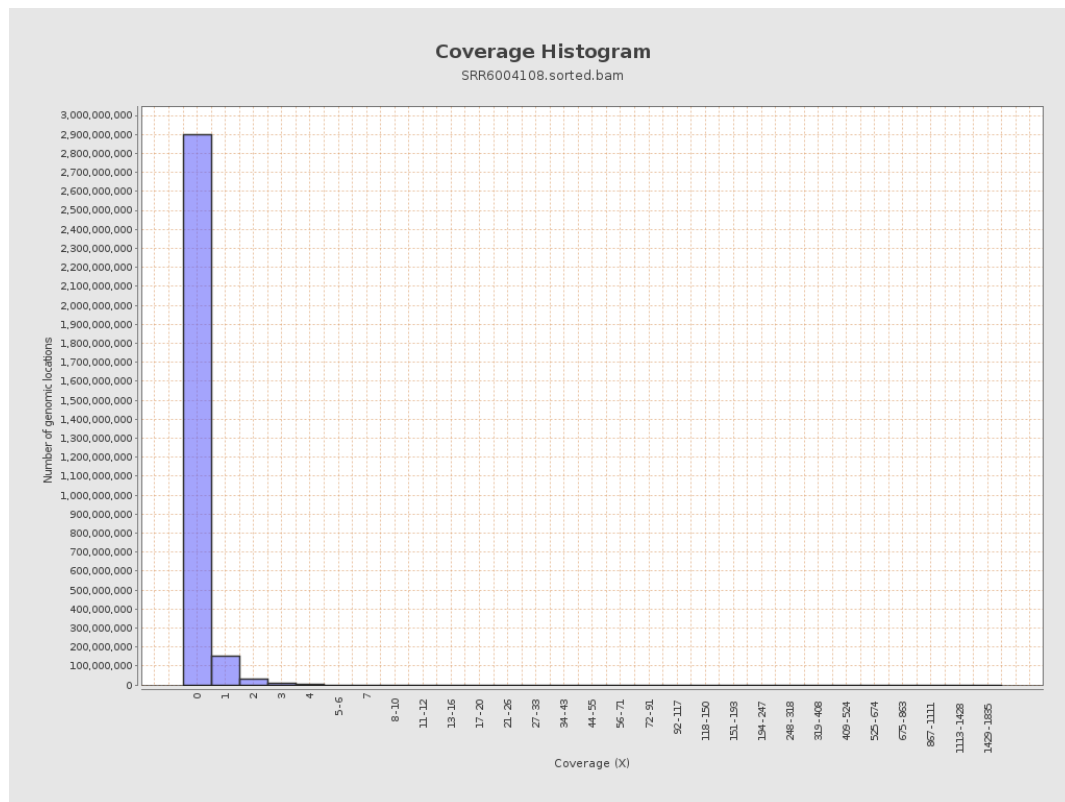
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21905442	0.0879	1.5505
chr2	243199373	21877011	0.09	0.7671
chr3	198022430	17085074	0.0863	0.3802
chr4	191154276	13605869	0.0712	0.4071
chr5	180915260	18771189	0.1038	0.4123
chr6	171115067	10559429	0.0617	0.357
chr7	159138663	15467088	0.0972	0.9996

chr8	146364022	14355106	0.0981	1.0046
chr9	141213431	11446777	0.0811	0.7127
chr10	135534747	14328016	0.1057	0.7739
chr11	135006516	13643880	0.1011	0.6564
chr12	133851895	8767811	0.0655	0.3457
chr13	115169878	9684482	0.0841	0.3629
chr14	107349540	7244805	0.0675	0.3963
chr15	102531392	7851350	0.0766	0.3488
chr16	90354753	7096586	0.0785	0.4783
chr17	81195210	6922849	0.0853	0.4262
chr18	78077248	7917691	0.1014	1.4318
chr19	59128983	4983014	0.0843	0.9694
chr20	63025520	5552783	0.0881	0.3917
chr21	48129895	4144044	0.0861	0.4498
chr22	51304566	2948352	0.0575	0.3004
chrMT	16571	31112	1.8775	1.7809
chrX	155270560	14255109	0.0918	0.4422
chrY	59373566	671727	0.0113	0.2752

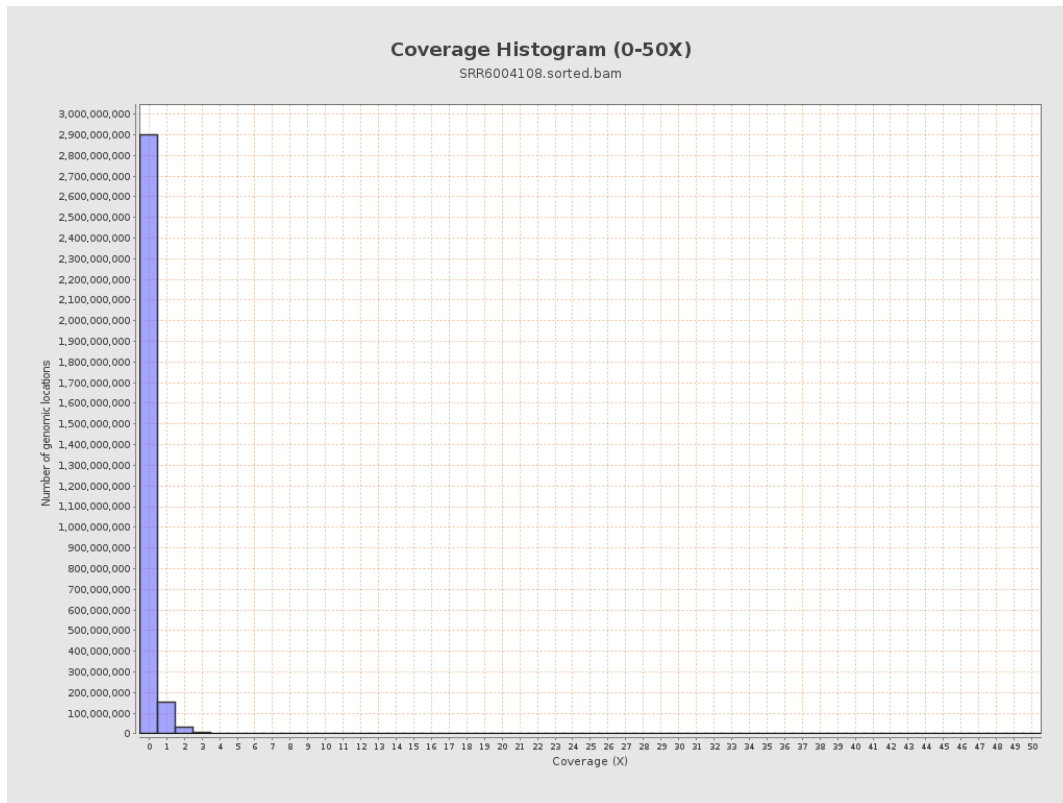
3. Results : Coverage across reference



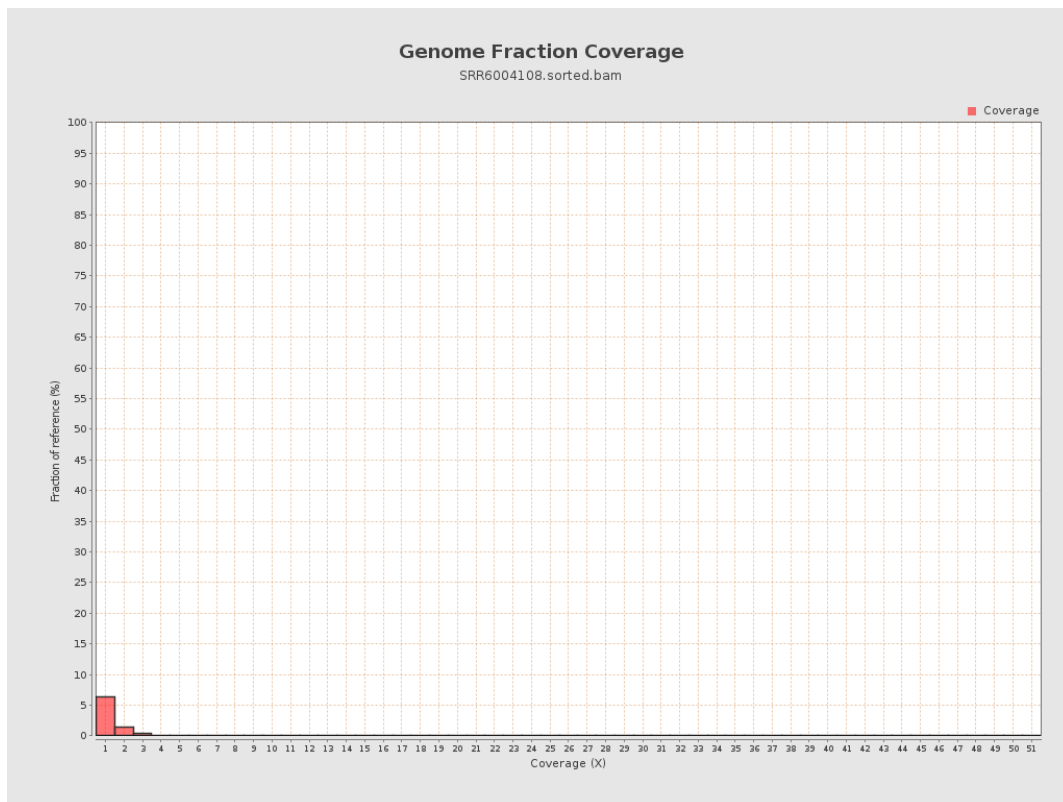
4. Results : Coverage Histogram



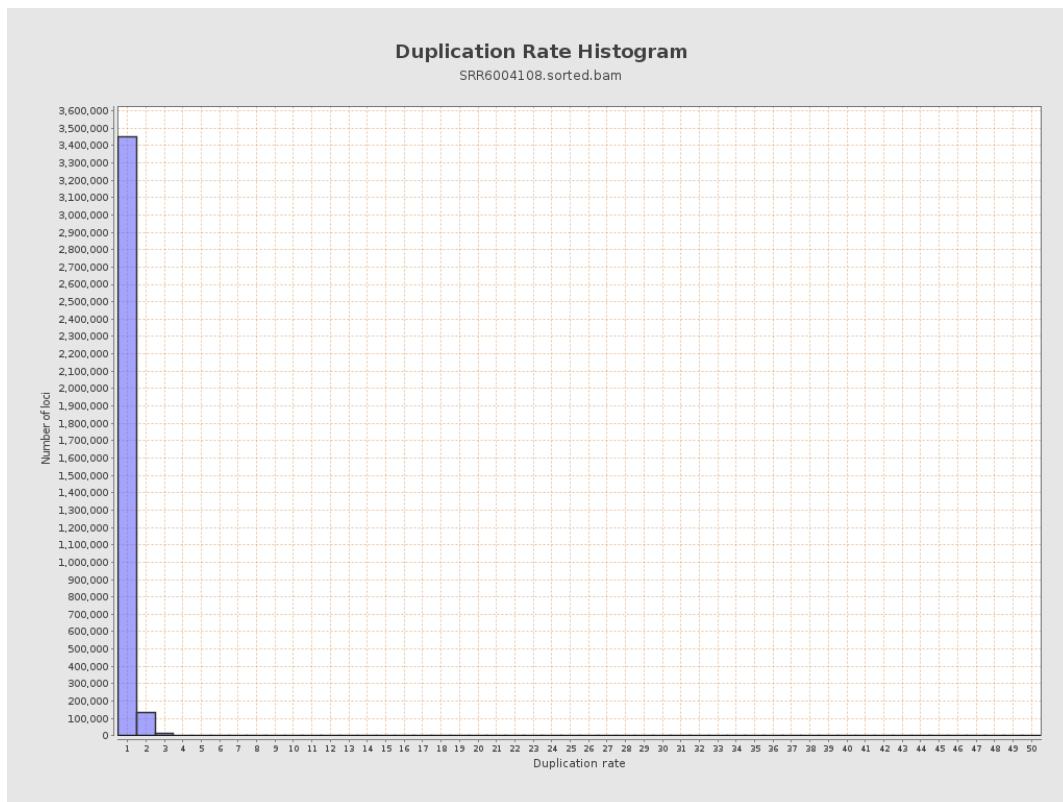
5. Results : Coverage Histogram (0-50X)



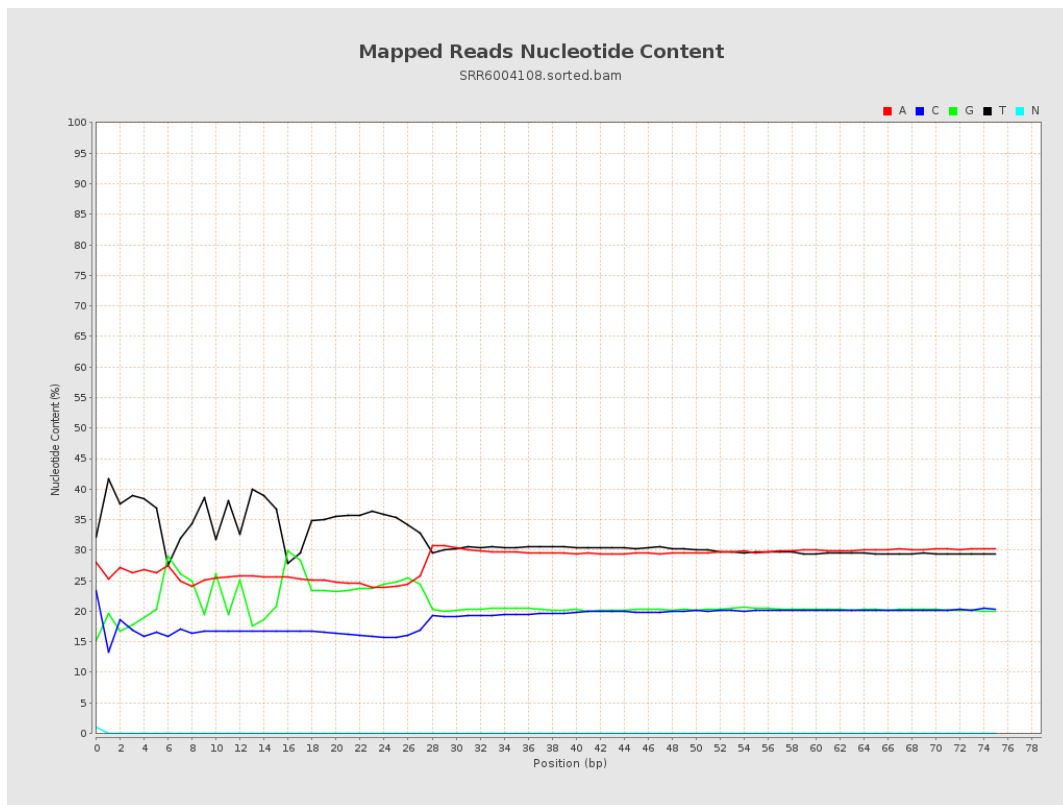
6. Results : Genome Fraction Coverage



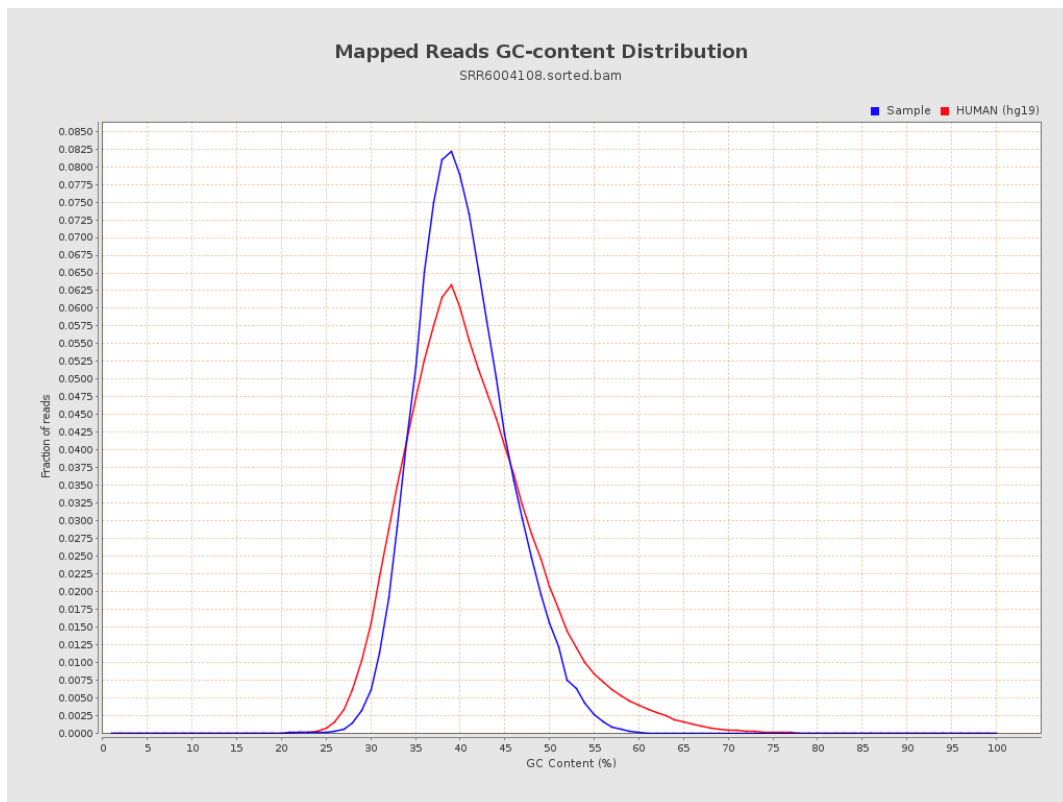
7. Results : Duplication Rate Histogram



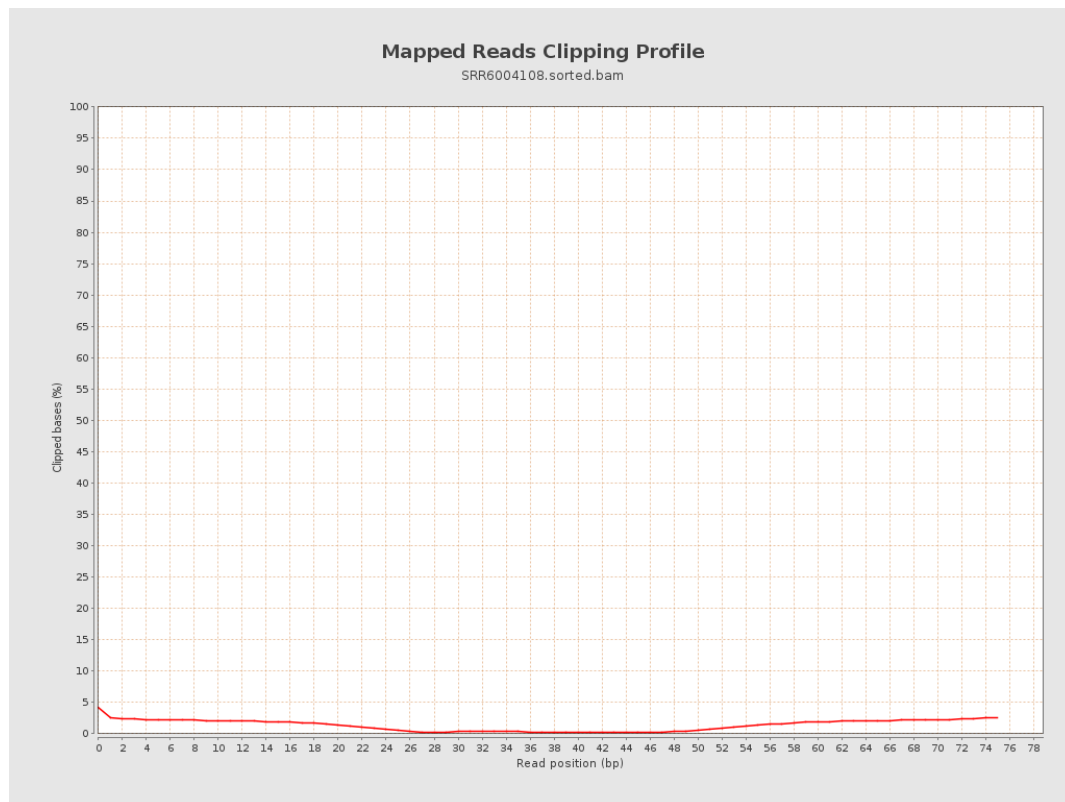
8. Results : Mapped Reads Nucleotide Content



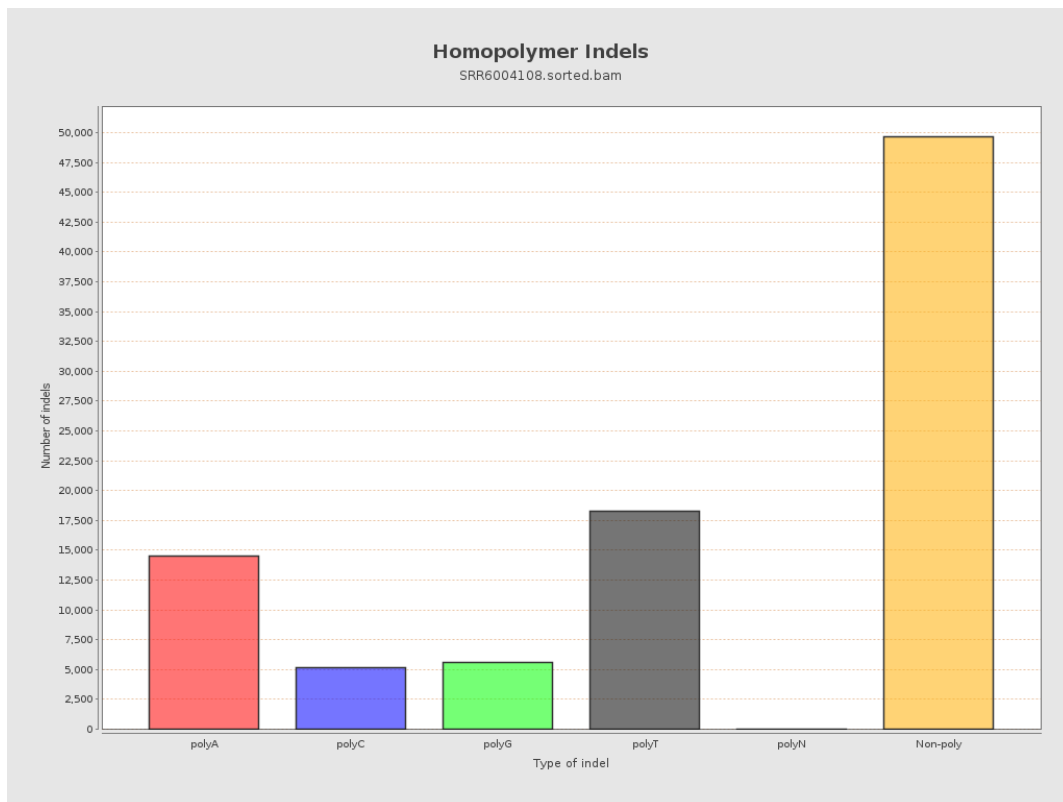
9. Results : Mapped Reads GC-content Distribution



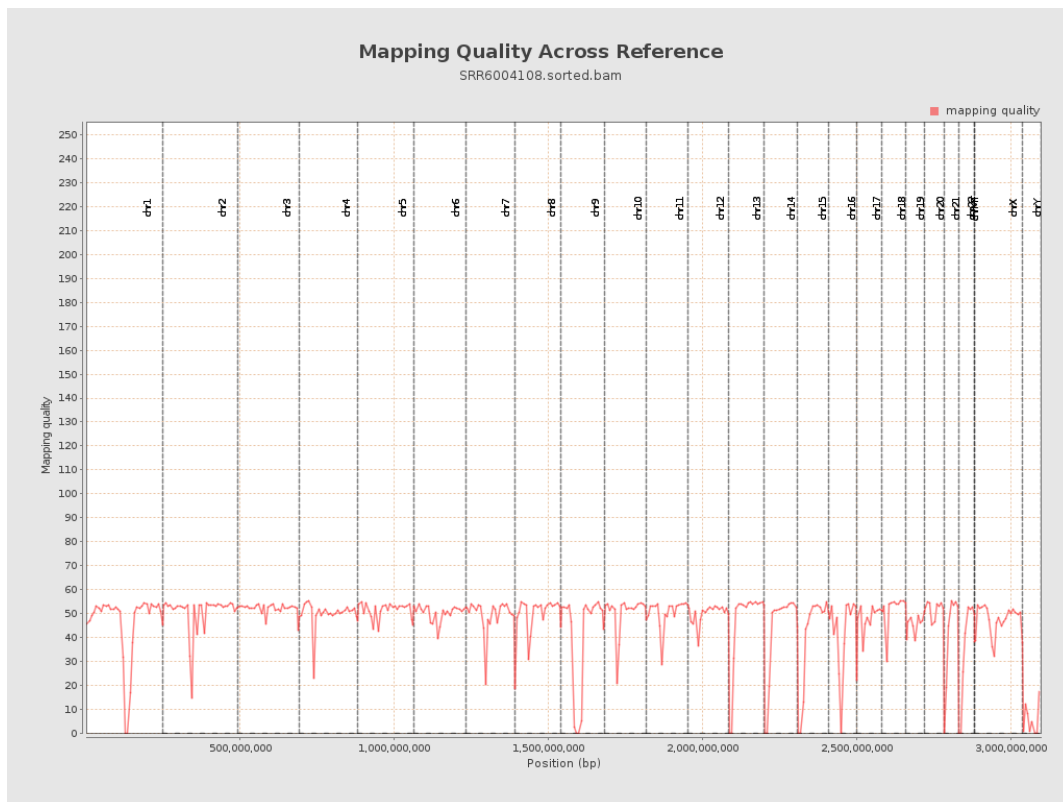
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

