

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 16:25:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234106.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_SRR6234106 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234106.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 16:25:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234106.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,463,668
Mapped reads	5,171,093 / 94.65%
Unmapped reads	292,575 / 5.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,641 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	476,547 / 8.72%
Duplication rate	4.59%
Clipped reads	1,809,481 / 33.12%

2.2. ACGT Content

Number/percentage of A's	95,074,846 / 26.72%
Number/percentage of C's	67,267,584 / 18.9%
Number/percentage of T's	103,419,242 / 29.06%
Number/percentage of G's	90,032,820 / 25.3%
Number/percentage of N's	79,271 / 0.02%
GC Percentage	44.2%

2.3. Coverage

Mean	0.115

Standard Deviation	26.0194
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2.4. Mapping Quality

Mean Mapping Quality	46.26
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2.5. Mismatches and indels

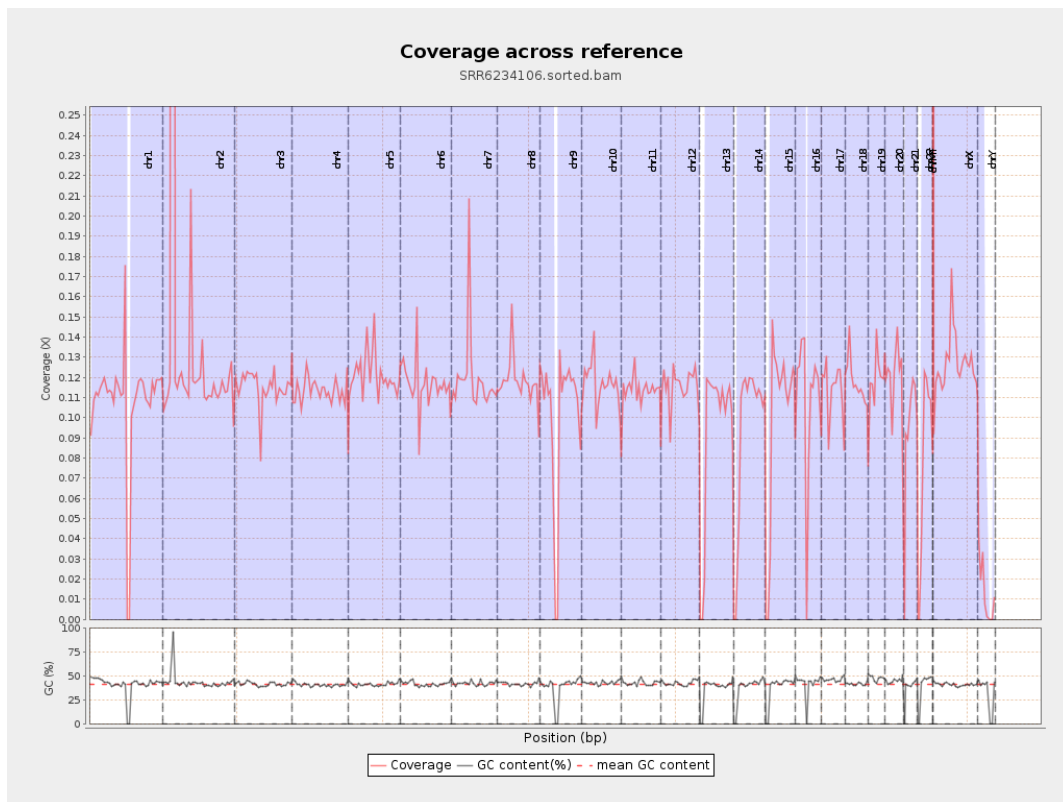
General error rate	0.63%
Mismatches	2,189,522
Insertions	23,596
Mapped reads with at least one insertion	0.45%
Deletions	71,048
Mapped reads with at least one deletion	1.36%
Homopolymer indels	47.84%

2.6. Chromosome stats

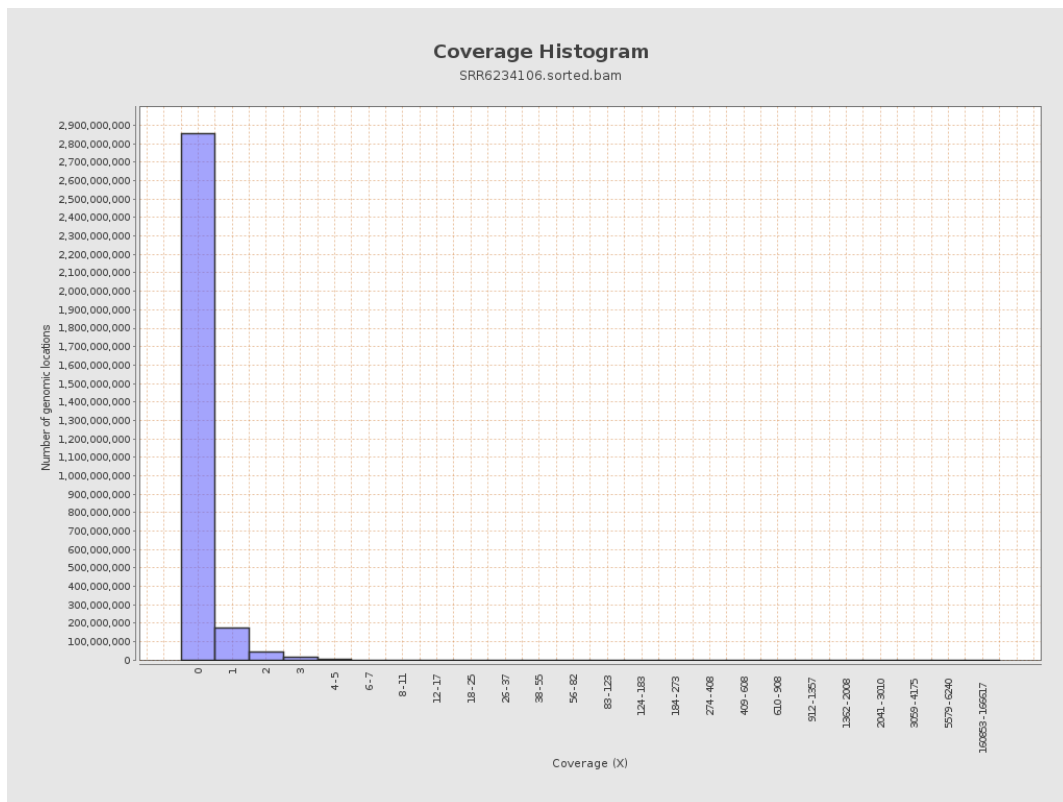
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	26855881	0.1077	1.5889
chr2	243199373	41933023	0.1724	92.7842
chr3	198022430	22791692	0.1151	0.4561
chr4	191154276	21752829	0.1138	0.4854
chr5	180915260	21963498	0.1214	0.4706
chr6	171115067	19976522	0.1167	0.6162
chr7	159138663	19052020	0.1197	1.6084

chr8	146364022	17247422	0.1178	0.8652
chr9	141213431	14300558	0.1013	0.8178
chr10	135534747	15828897	0.1168	0.6902
chr11	135006516	15355078	0.1137	0.7832
chr12	133851895	15561135	0.1163	0.4778
chr13	115169878	10761573	0.0934	0.4108
chr14	107349540	10216056	0.0952	0.5895
chr15	102531392	10137282	0.0989	0.425
chr16	90354753	9657218	0.1069	0.5176
chr17	81195210	9309357	0.1147	0.5658
chr18	78077248	9235387	0.1183	1.6428
chr19	59128983	7074955	0.1197	1.1294
chr20	63025520	7577222	0.1202	0.4925
chr21	48129895	4564753	0.0948	0.5047
chr22	51304566	4020448	0.0784	0.3763
chrMT	16571	334600	20.1919	11.8072
chrX	155270560	19697790	0.1269	0.5752
chrY	59373566	784493	0.0132	0.2255

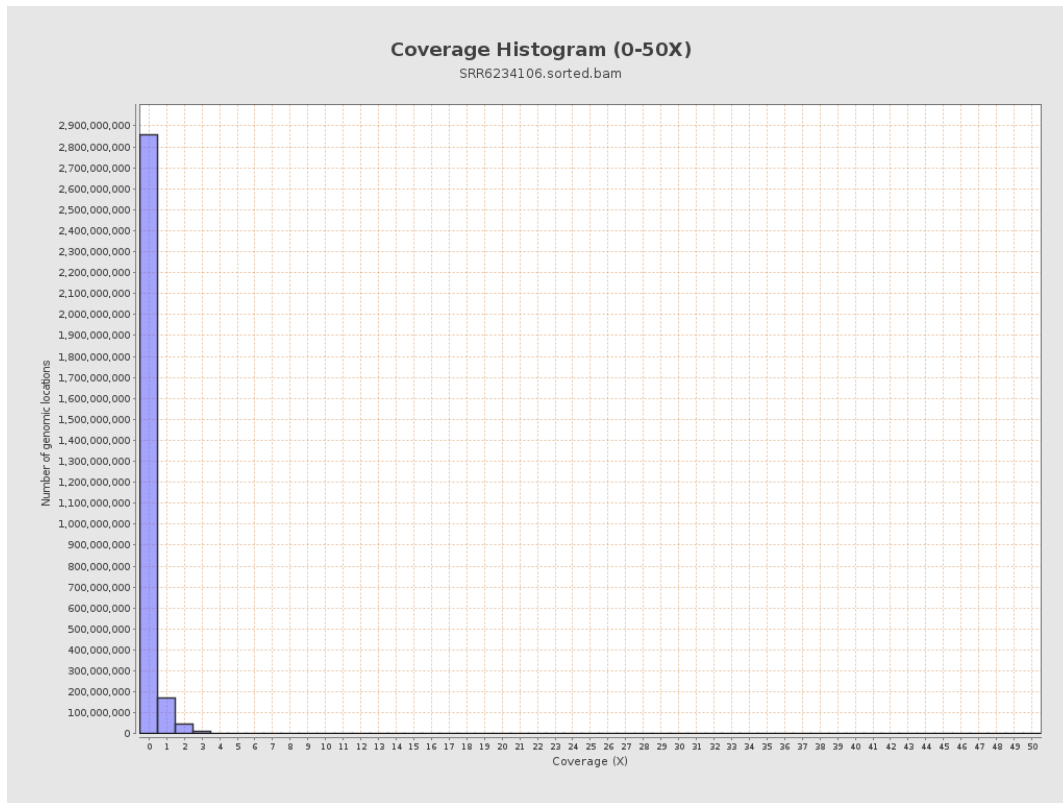
3. Results : Coverage across reference



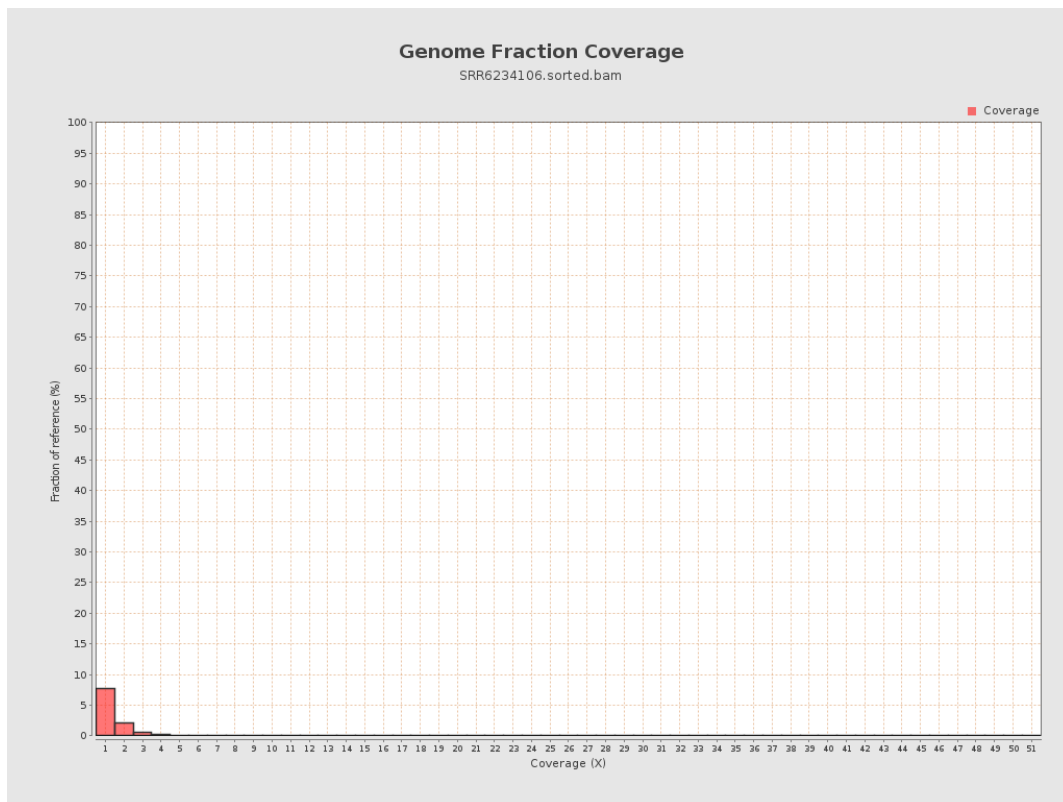
4. Results : Coverage Histogram



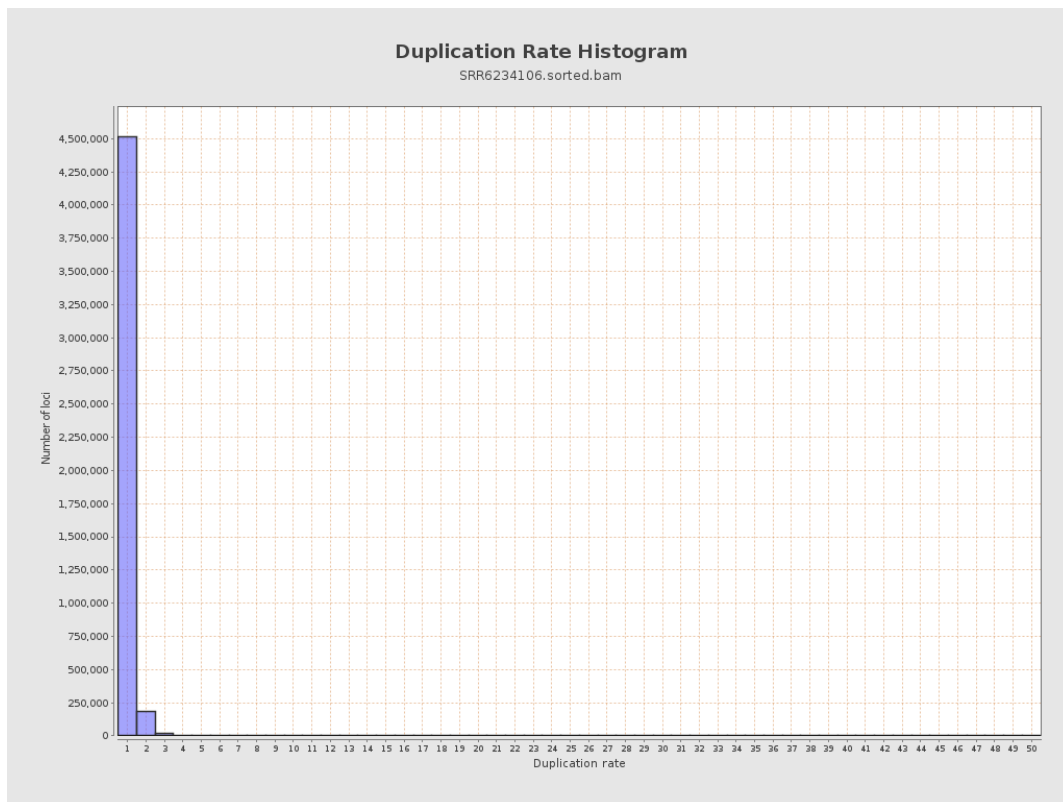
5. Results : Coverage Histogram (0-50X)



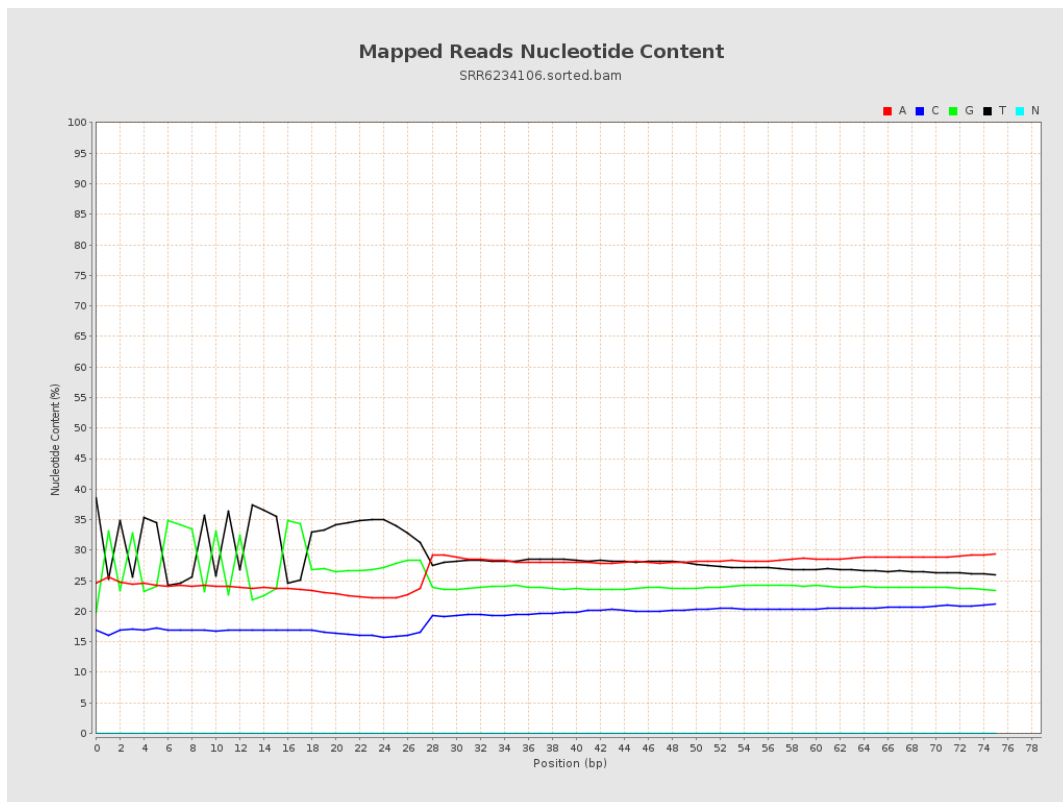
6. Results : Genome Fraction Coverage



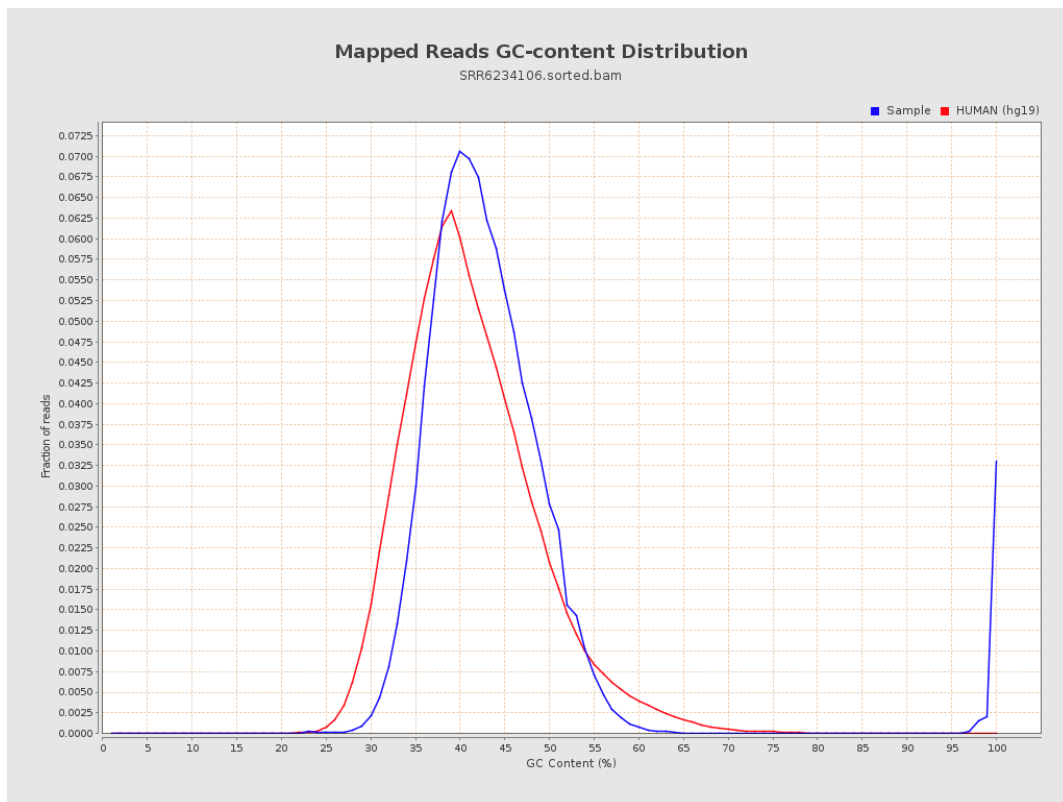
7. Results : Duplication Rate Histogram



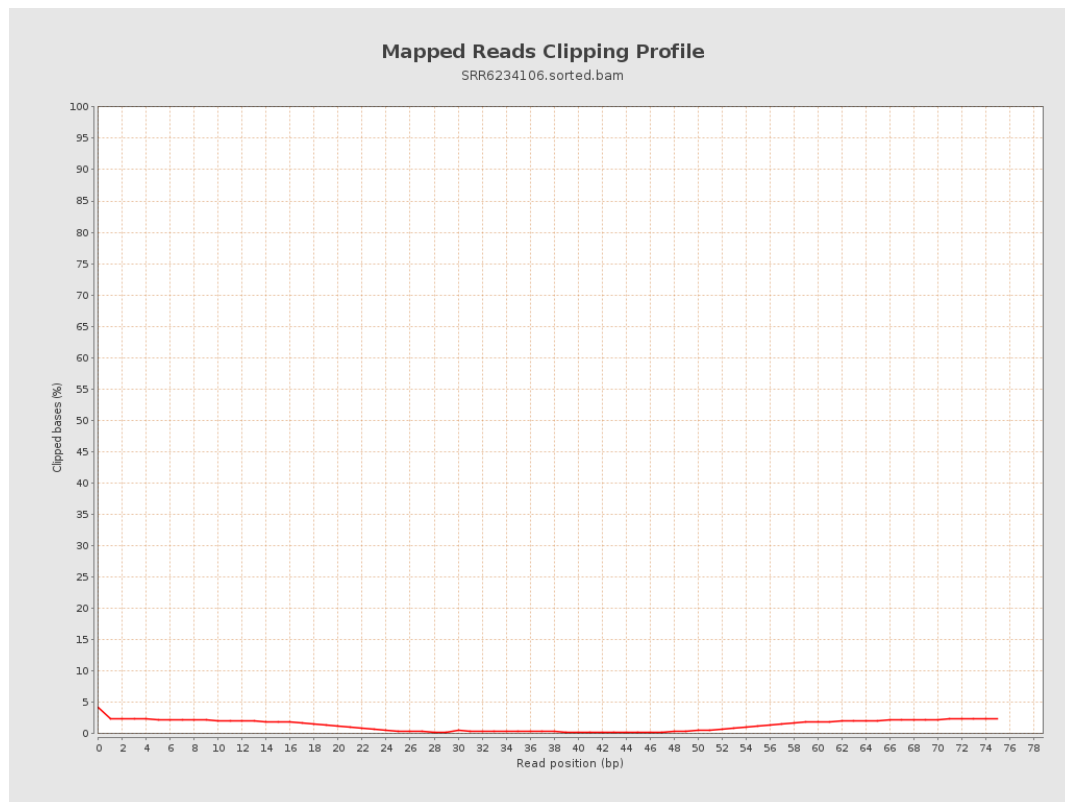
8. Results : Mapped Reads Nucleotide Content



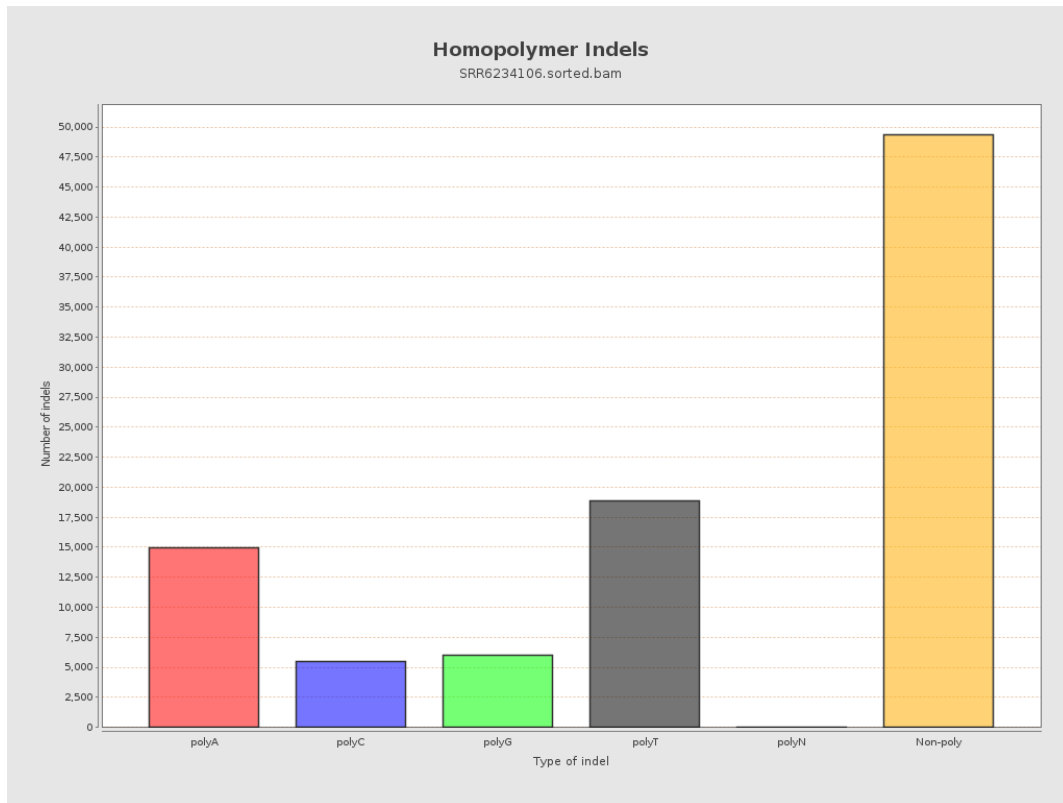
9. Results : Mapped Reads GC-content Distribution



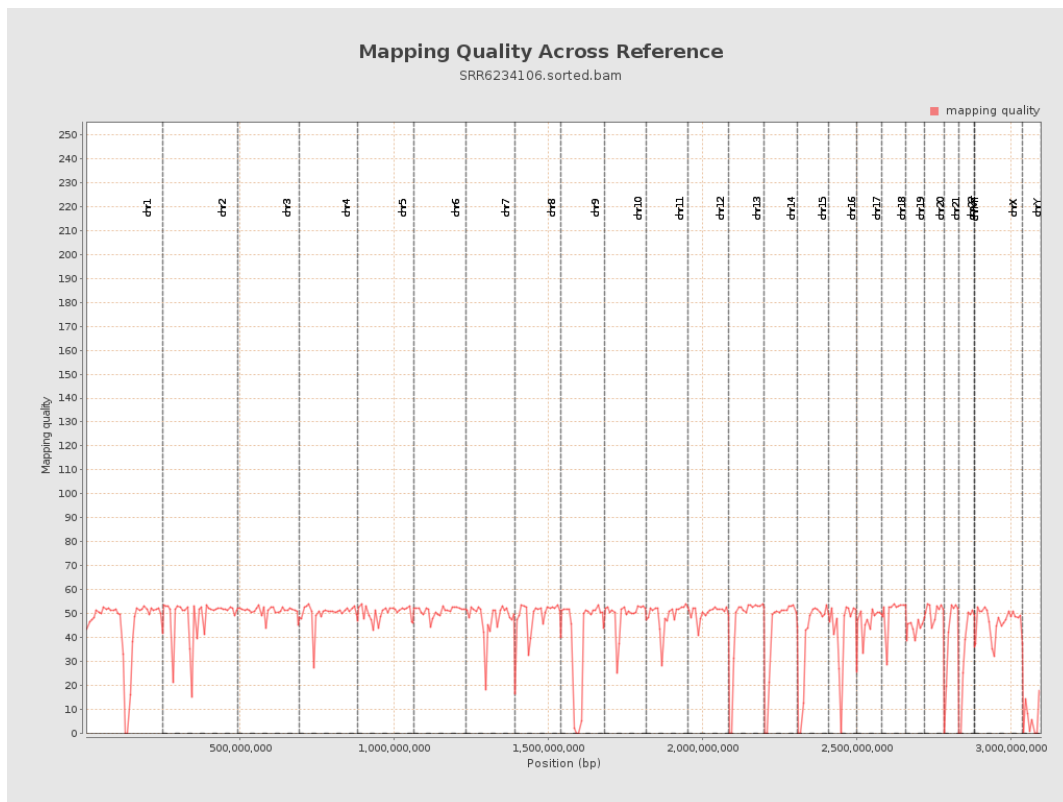
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

