

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 15:42:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124810.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_SRR3124810 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124810_1.fastq.gz SRR3124810_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 15:42:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124810.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	71,393,276
Mapped reads	71,330,973 / 99.91%
Unmapped reads	62,303 / 0.09%
Mapped paired reads	71,330,973 / 99.91%
Mapped reads, first in pair	35,668,230 / 49.96%
Mapped reads, second in pair	35,662,743 / 49.95%
Mapped reads, both in pair	71,301,464 / 99.87%
Mapped reads, singletons	29,509 / 0.04%
Secondary alignments	0
Supplementary alignments	20,165 / 0.03%
Read min/max/mean length	30 / 101 / 101.01
Duplicated reads (estimated)	29,927,086 / 41.92%
Duplication rate	40.94%
Clipped reads	35,320,180 / 49.47%

2.2. ACGT Content

Number/percentage of A's	1,845,274,456 / 26.39%
Number/percentage of C's	1,658,141,118 / 23.71%
Number/percentage of T's	1,828,714,676 / 26.15%
Number/percentage of G's	1,638,414,616 / 23.43%
Number/percentage of N's	21,612,674 / 0.31%

GC Percentage	47.15%
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2.3. Coverage

Mean	2.2589
Standard Deviation	15.2202

2.4. Mapping Quality

Mean Mapping Quality	56.47
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2.5. Insert size

Mean	102,806.29
Standard Deviation	3,179,111.87
P25/Median/P75	158 / 195 / 246

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	38,691,336
Insertions	432,228
Mapped reads with at least one insertion	0.6%
Deletions	333,779
Mapped reads with at least one deletion	0.46%
Homopolymer indels	37.13%

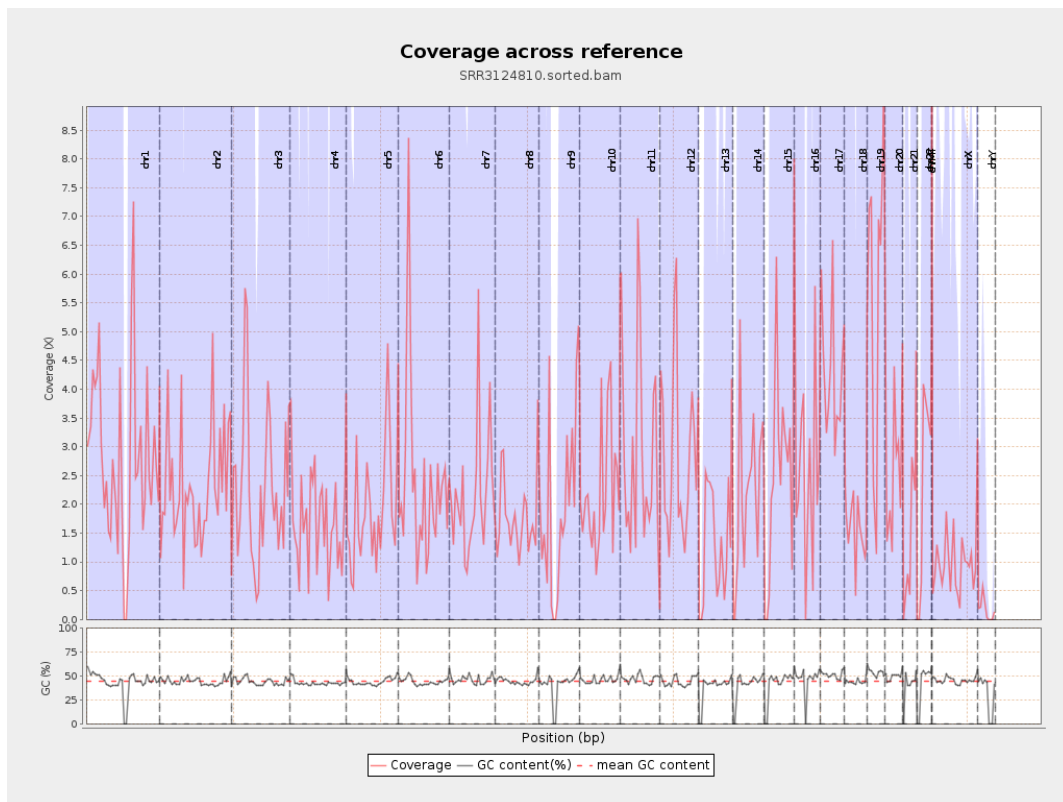
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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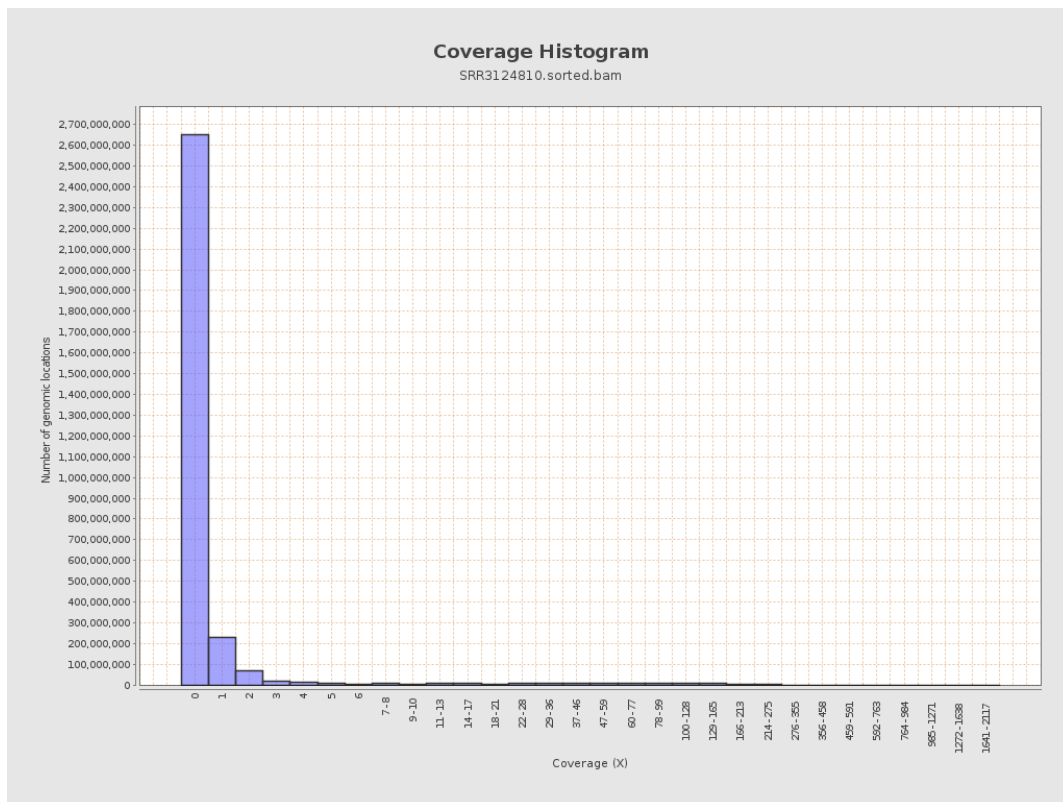
		bases	coverage	deviation
chr1	249250621	701181854	2.8132	17.2222
chr2	243199373	564282417	2.3202	15.756
chr3	198022430	450414729	2.2746	15.4575
chr4	191154276	324081325	1.6954	13.5099
chr5	180915260	355973843	1.9676	14.553
chr6	171115067	399647496	2.3355	16.0391
chr7	159138663	347394373	2.183	15.0468
chr8	146364022	261633242	1.7876	13.4316
chr9	141213431	279912692	1.9822	14.1396
chr10	135534747	297553321	2.1954	15.0276
chr11	135006516	408122541	3.023	17.9143
chr12	133851895	381826400	2.8526	17.0237
chr13	115169878	151011198	1.3112	11.9138
chr14	107349540	231795850	2.1593	14.9727
chr15	102531392	244852568	2.3881	15.674
chr16	90354753	251013488	2.7781	16.3233
chr17	81195210	351823019	4.3331	20.3805
chr18	78077248	121897405	1.5612	12.6301
chr19	59128983	340805071	5.7638	23.1227
chr20	63025520	165584830	2.6273	16.2512
chr21	48129895	74811032	1.5544	12.884
chr22	51304566	128430413	2.5033	14.9752
chrMT	16571	200429	12.0952	28.9485
chrX	155270560	148136400	0.9541	7.4844

chrY	59373566	10522984	0.1772	2.7316
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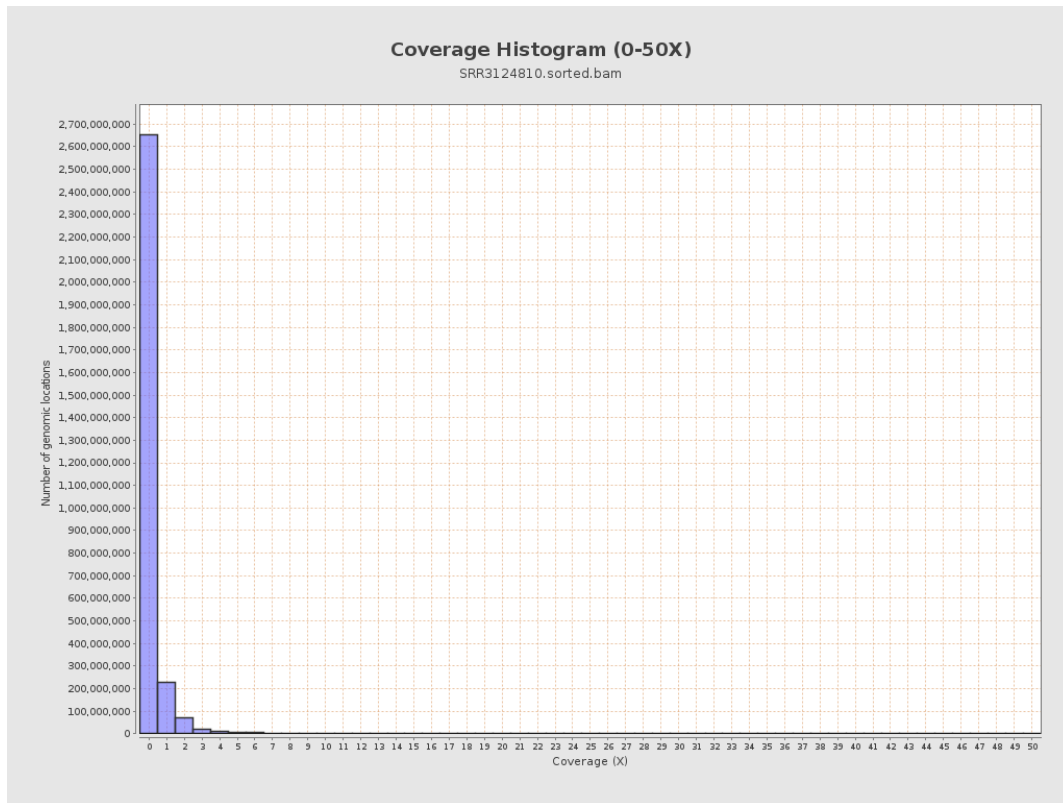
3. Results : Coverage across reference



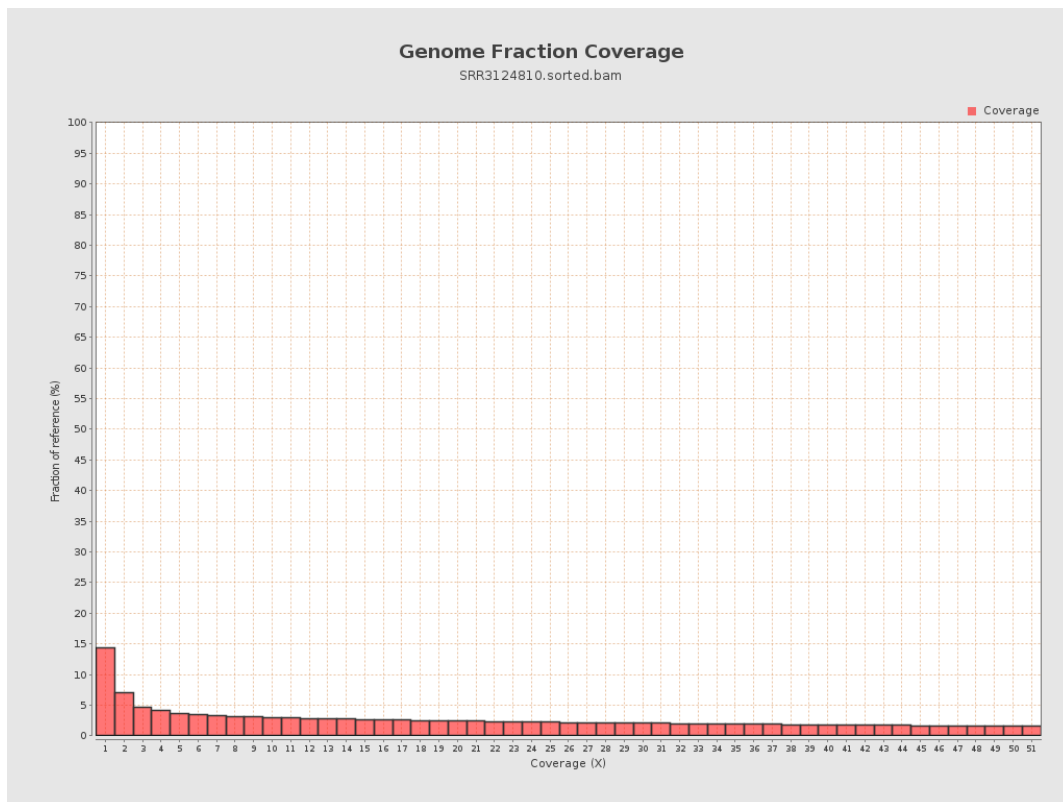
4. Results : Coverage Histogram



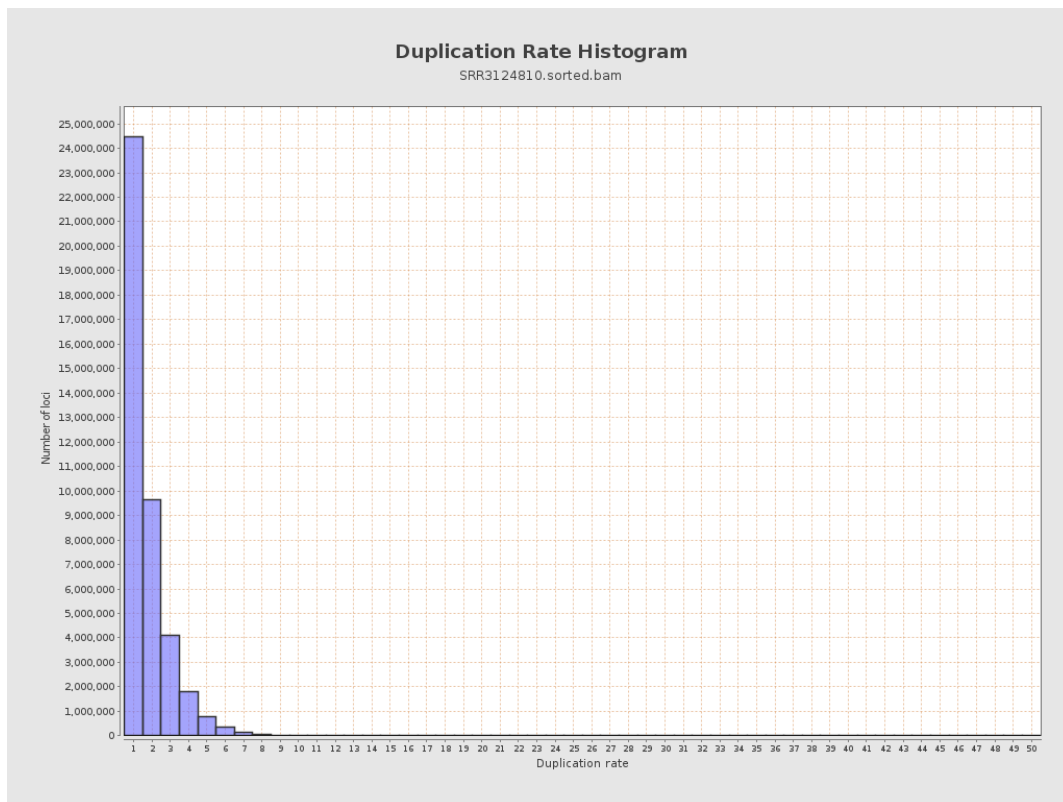
5. Results : Coverage Histogram (0-50X)



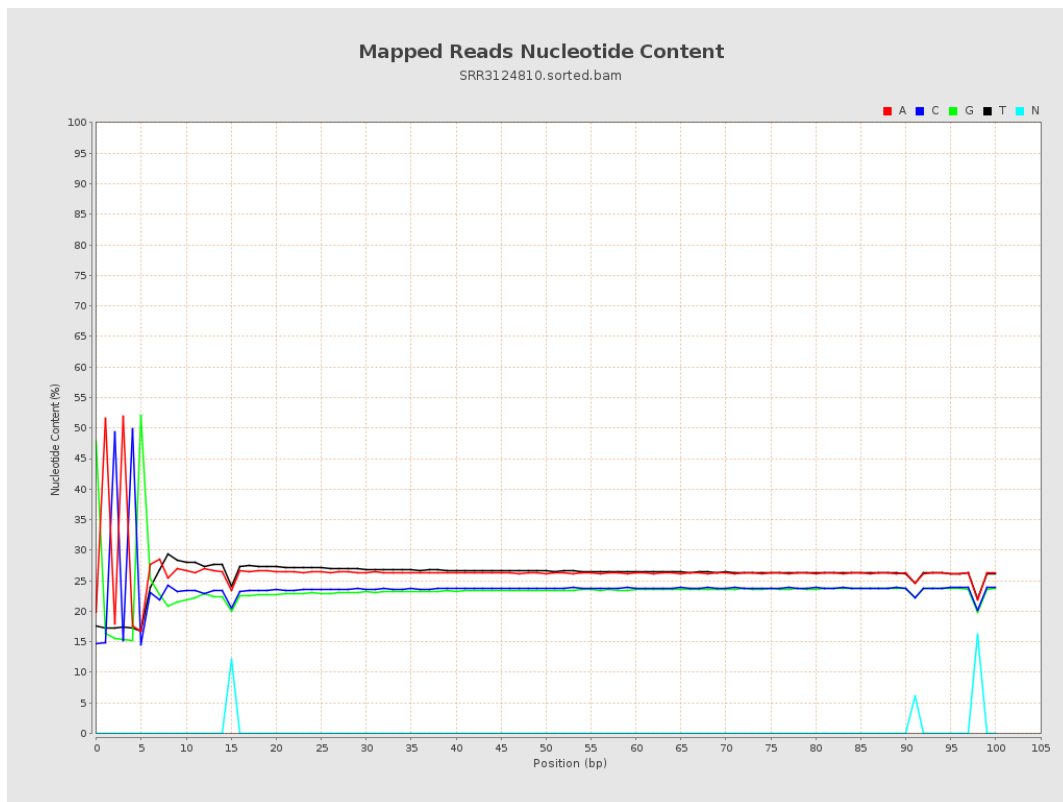
6. Results : Genome Fraction Coverage



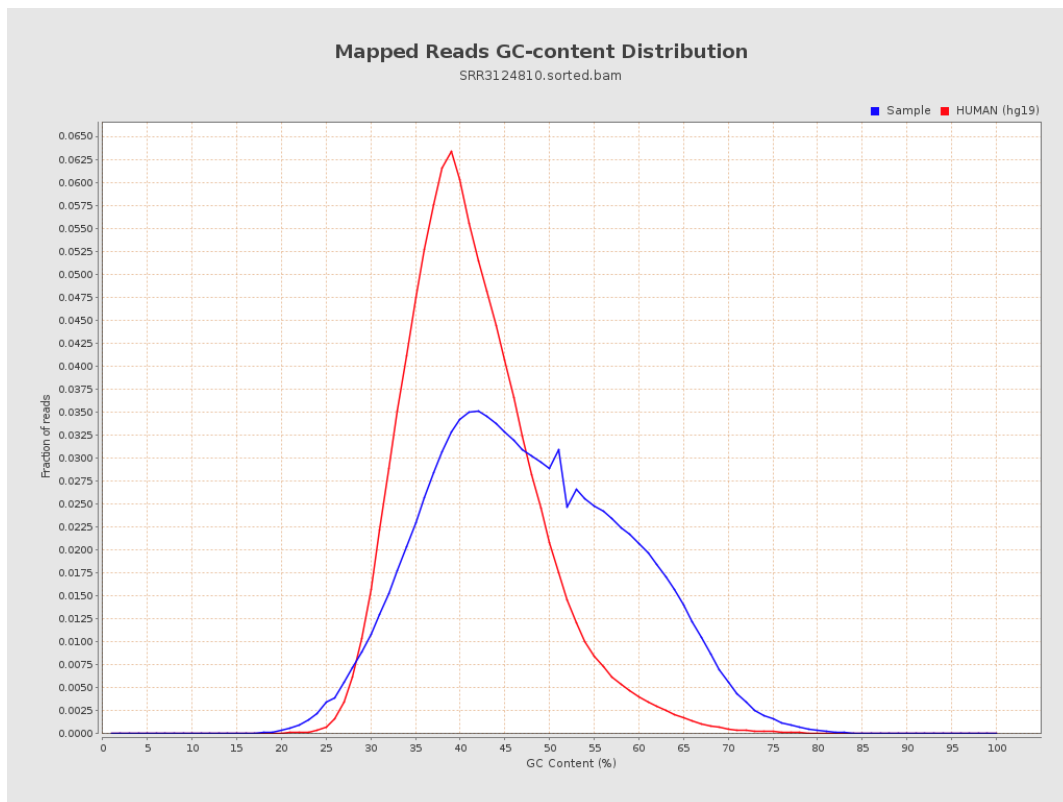
7. Results : Duplication Rate Histogram



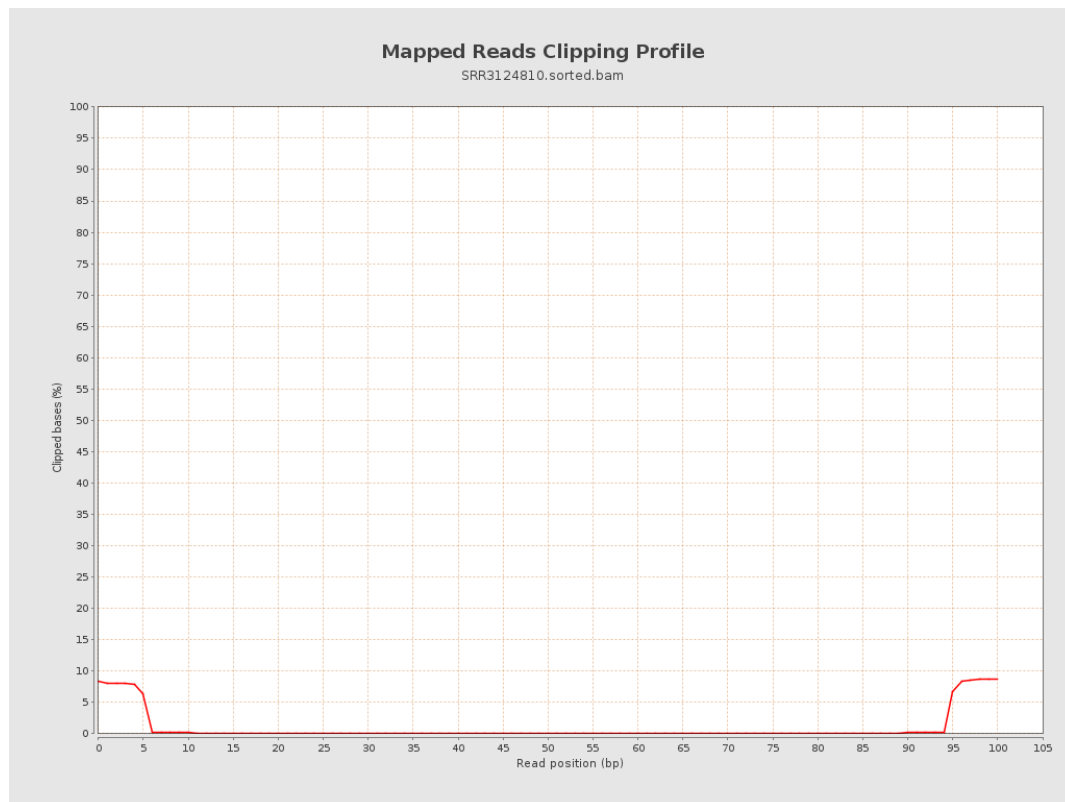
8. Results : Mapped Reads Nucleotide Content



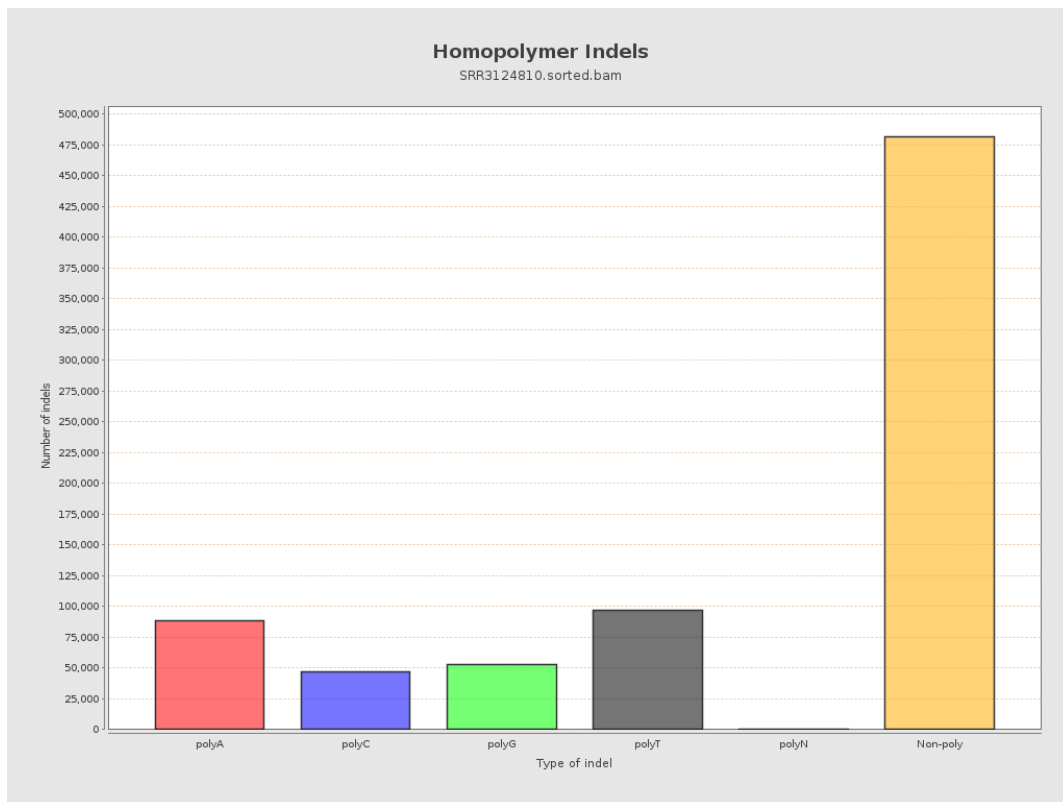
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



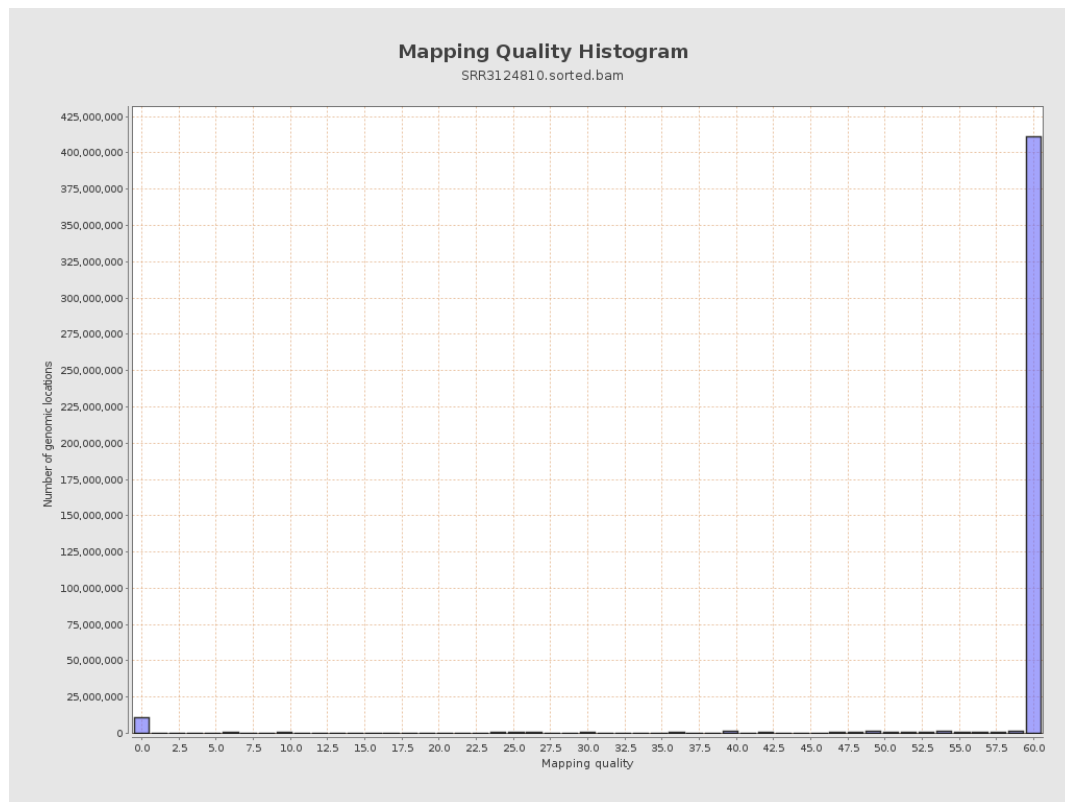
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

