

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 05:35:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124921.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_SRR3124921 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124921_1.fastq.gz SRR3124921_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 05:35:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,278,406
Mapped reads	4,210,844 / 98.42%
Unmapped reads	67,562 / 1.58%
Mapped paired reads	4,210,844 / 98.42%
Mapped reads, first in pair	2,109,371 / 49.3%
Mapped reads, second in pair	2,101,473 / 49.12%
Mapped reads, both in pair	4,193,582 / 98.02%
Mapped reads, singletons	17,262 / 0.4%
Secondary alignments	0
Supplementary alignments	53,335 / 1.25%
Read min/max/mean length	30 / 151 / 151.6
Duplicated reads (estimated)	652,239 / 15.24%
Duplication rate	14.37%
Clipped reads	3,107,462 / 72.63%

2.2. ACGT Content

Number/percentage of A's	164,152,905 / 28.94%
Number/percentage of C's	115,491,978 / 20.36%
Number/percentage of T's	166,477,785 / 29.35%
Number/percentage of G's	121,132,808 / 21.35%
Number/percentage of N's	24,732 / 0%

GC Percentage	41.71%
---------------	--------

2.3. Coverage

Mean	0.1834
Standard Deviation	2.1055

2.4. Mapping Quality

Mean Mapping Quality	53.45
----------------------	-------

2.5. Insert size

Mean	63,577.74
Standard Deviation	2,415,012.4
P25/Median/P75	136 / 167 / 209

2.6. Mismatches and indels

General error rate	1.44%
Mismatches	7,880,396
Insertions	107,534
Mapped reads with at least one insertion	2.42%
Deletions	207,343
Mapped reads with at least one deletion	4.74%
Homopolymer indels	45.56%

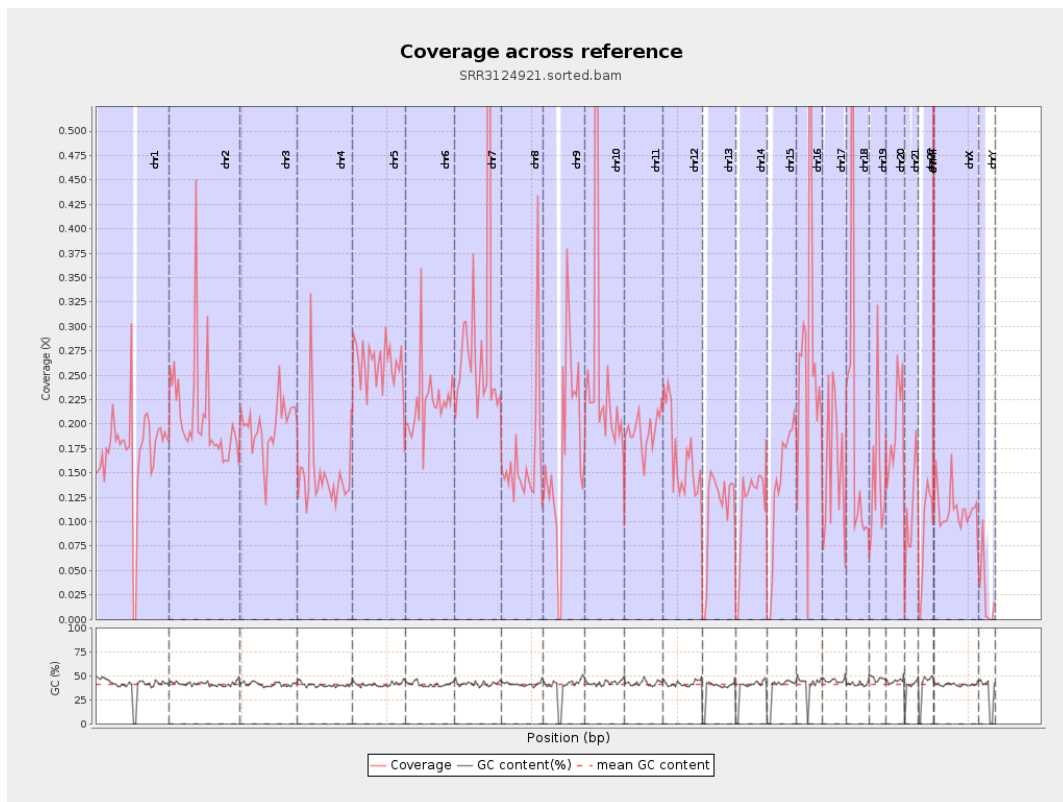
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

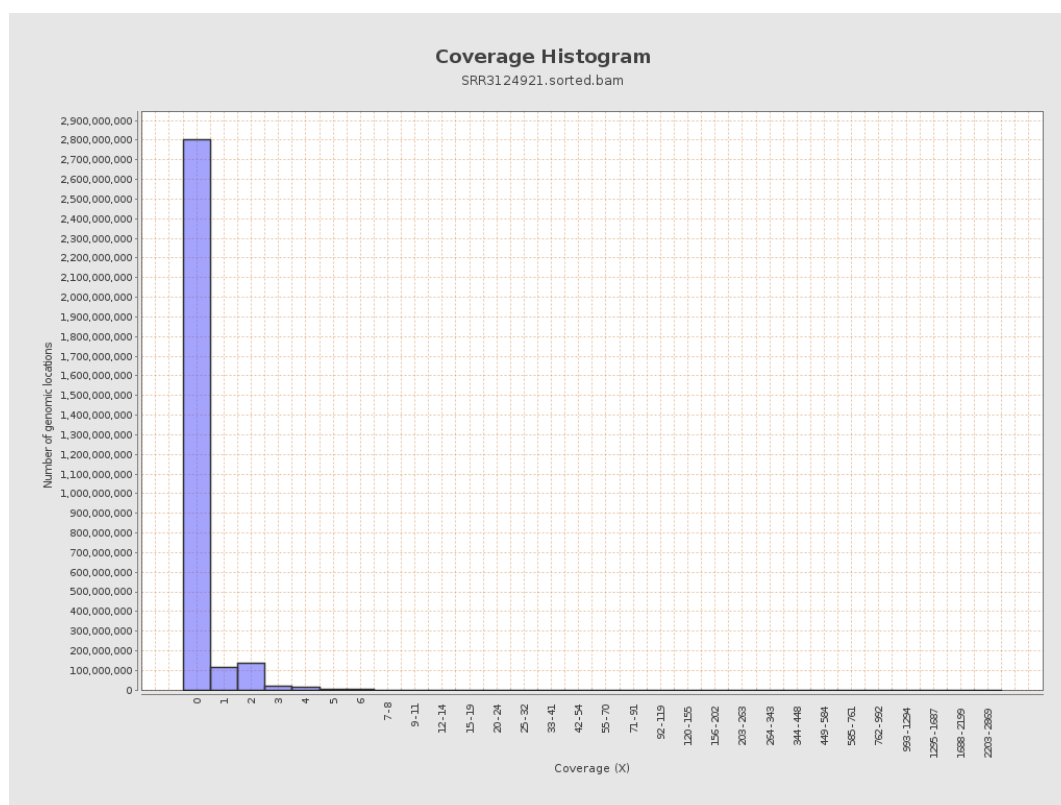
		bases	coverage	deviation
chr1	249250621	42859859	0.172	2.1809
chr2	243199373	50627019	0.2082	2.0157
chr3	198022430	39234122	0.1981	0.6915
chr4	191154276	28286181	0.148	1.3514
chr5	180915260	47187818	0.2608	0.7686
chr6	171115067	38047416	0.2223	1.7646
chr7	159138663	48087372	0.3022	3.0373
chr8	146364022	24114990	0.1648	0.755
chr9	141213431	24704533	0.1749	2.7447
chr10	135534747	34171764	0.2521	5.9743
chr11	135006516	25762621	0.1908	1.3372
chr12	133851895	22370409	0.1671	0.6017
chr13	115169878	12719938	0.1104	0.4754
chr14	107349540	12223058	0.1139	0.5202
chr15	102531392	13878718	0.1354	0.5368
chr16	90354753	24555099	0.2718	3.9573
chr17	81195210	12541314	0.1545	2.0167
chr18	78077248	16264383	0.2083	2.4656
chr19	59128983	8851185	0.1497	1.3798
chr20	63025520	12305955	0.1953	0.8003
chr21	48129895	5333715	0.1108	0.7716
chr22	51304566	4466169	0.0871	0.4531
chrMT	16571	20521	1.2384	1.5816
chrX	155270560	17617289	0.1135	0.669

chrY	59373566	1453858	0.0245	1.5755
------	----------	---------	--------	--------

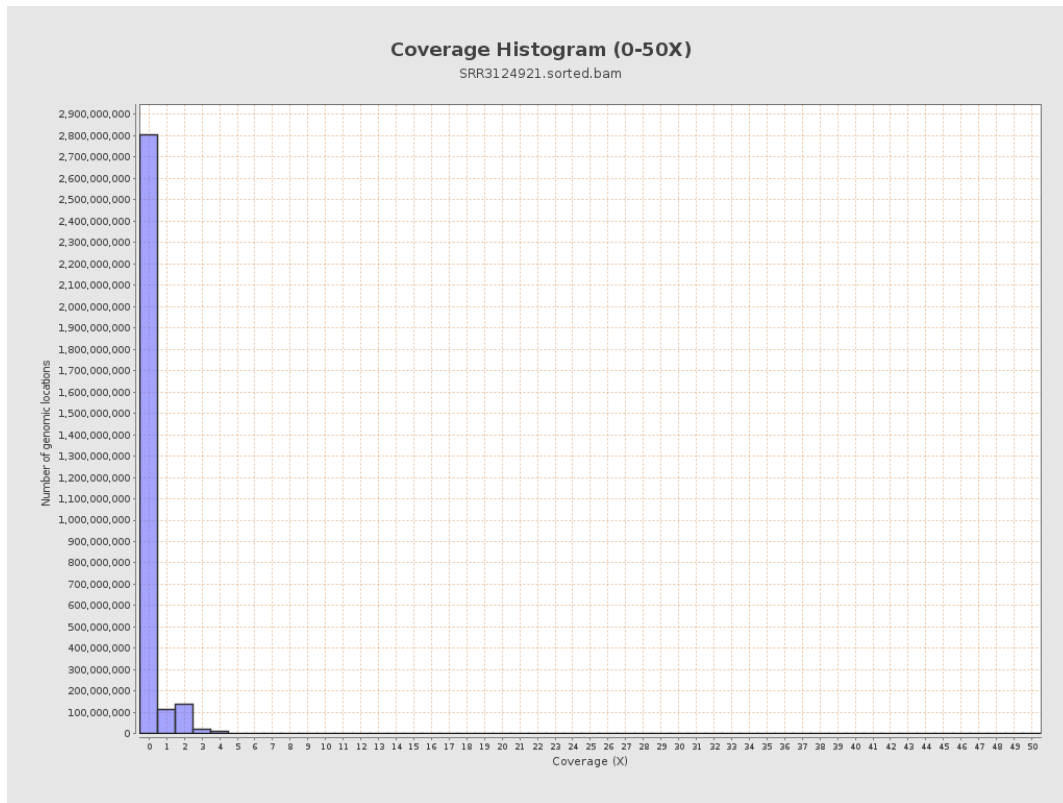
3. Results : Coverage across reference



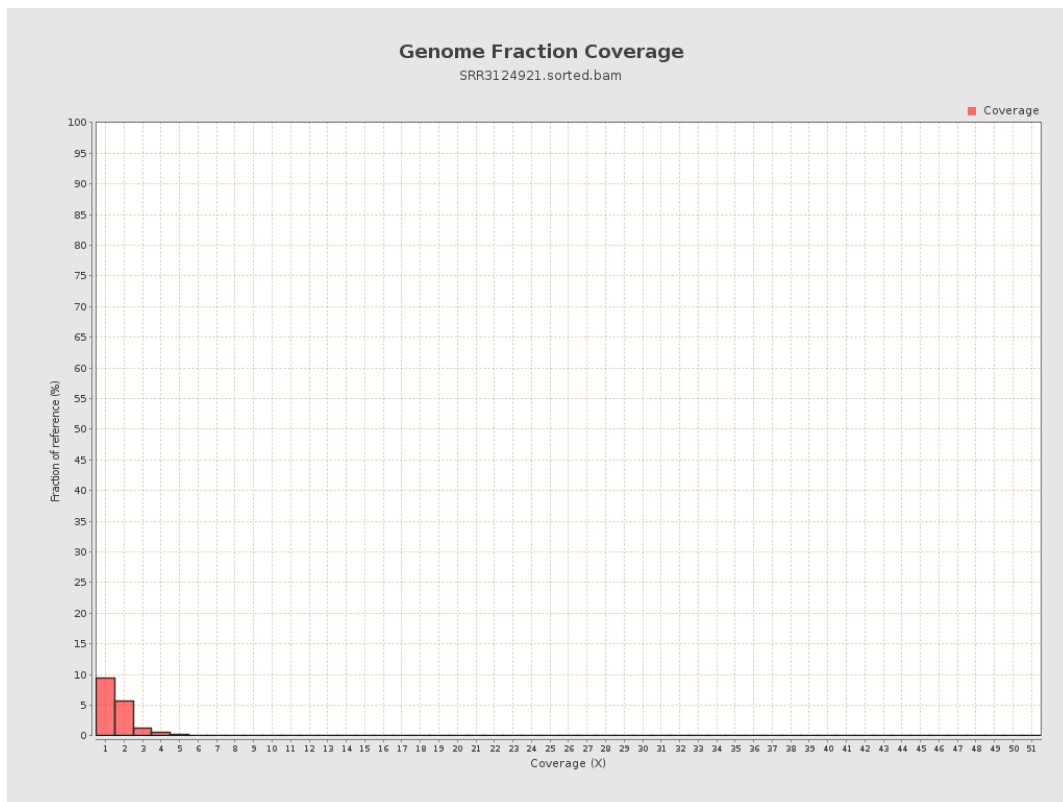
4. Results : Coverage Histogram



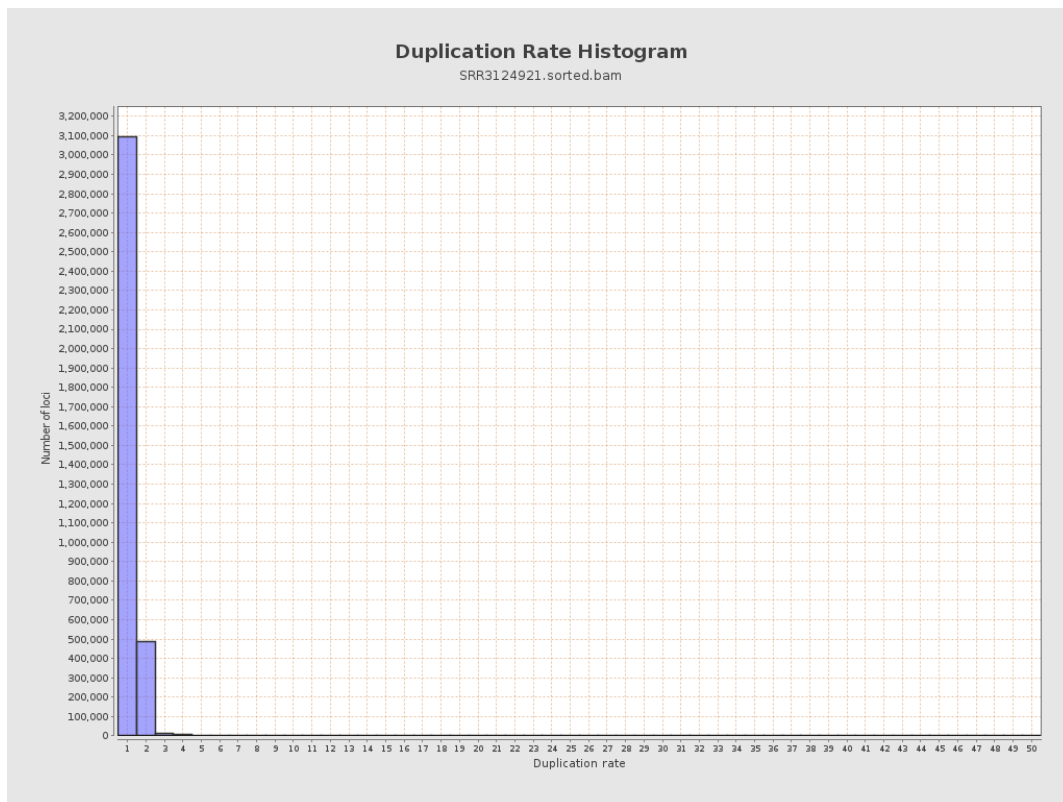
5. Results : Coverage Histogram (0-50X)



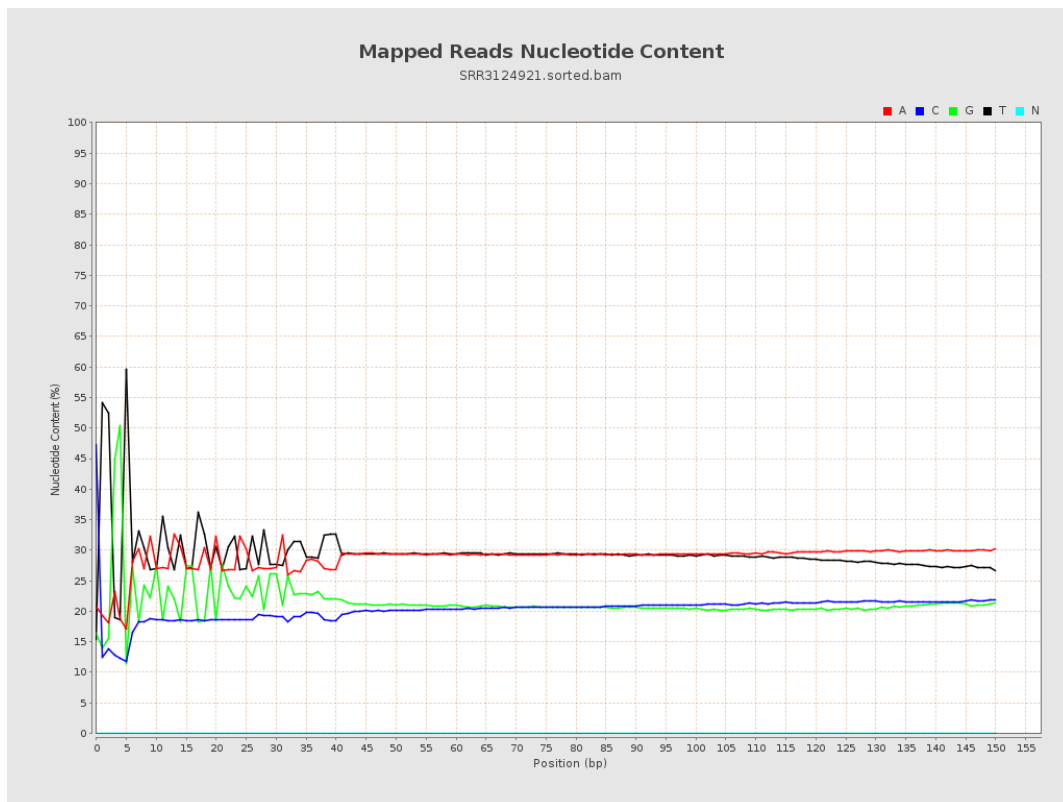
6. Results : Genome Fraction Coverage



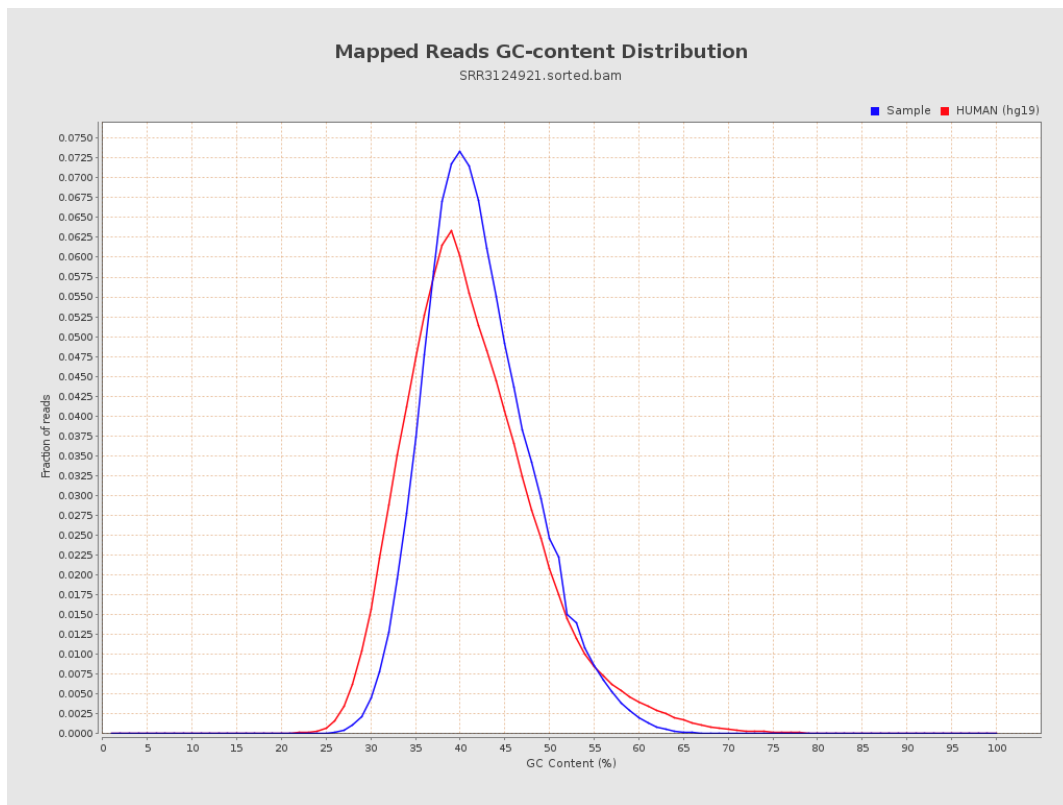
7. Results : Duplication Rate Histogram



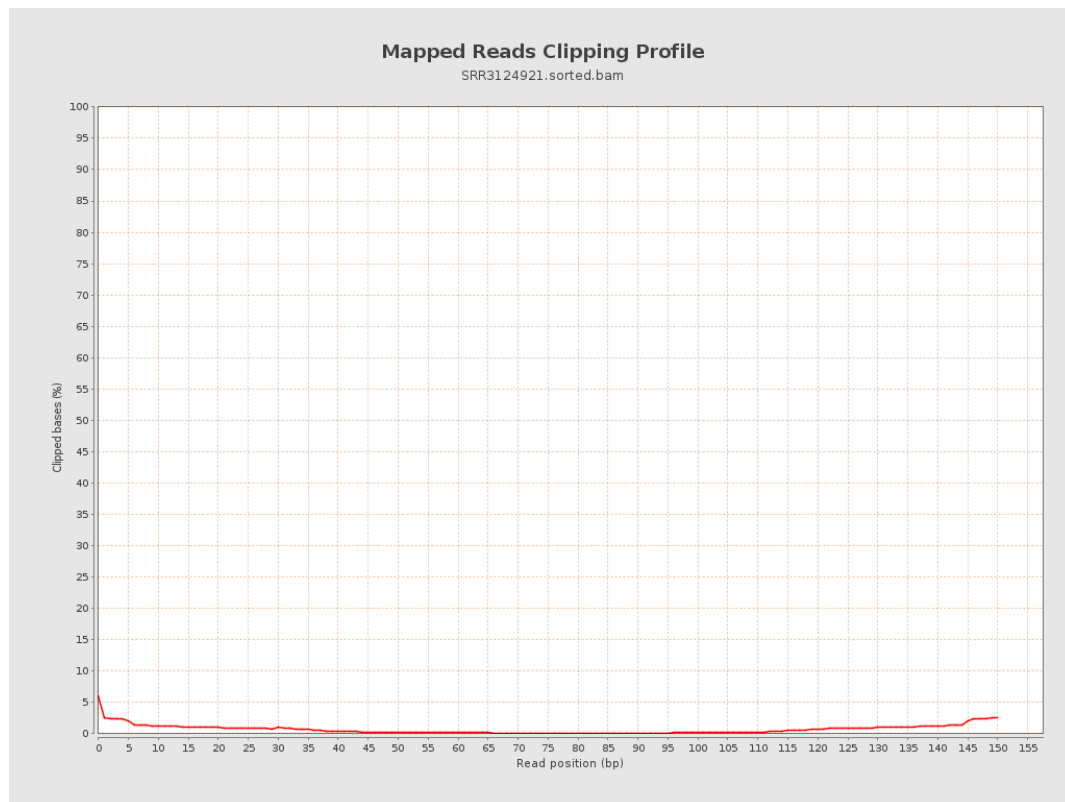
8. Results : Mapped Reads Nucleotide Content



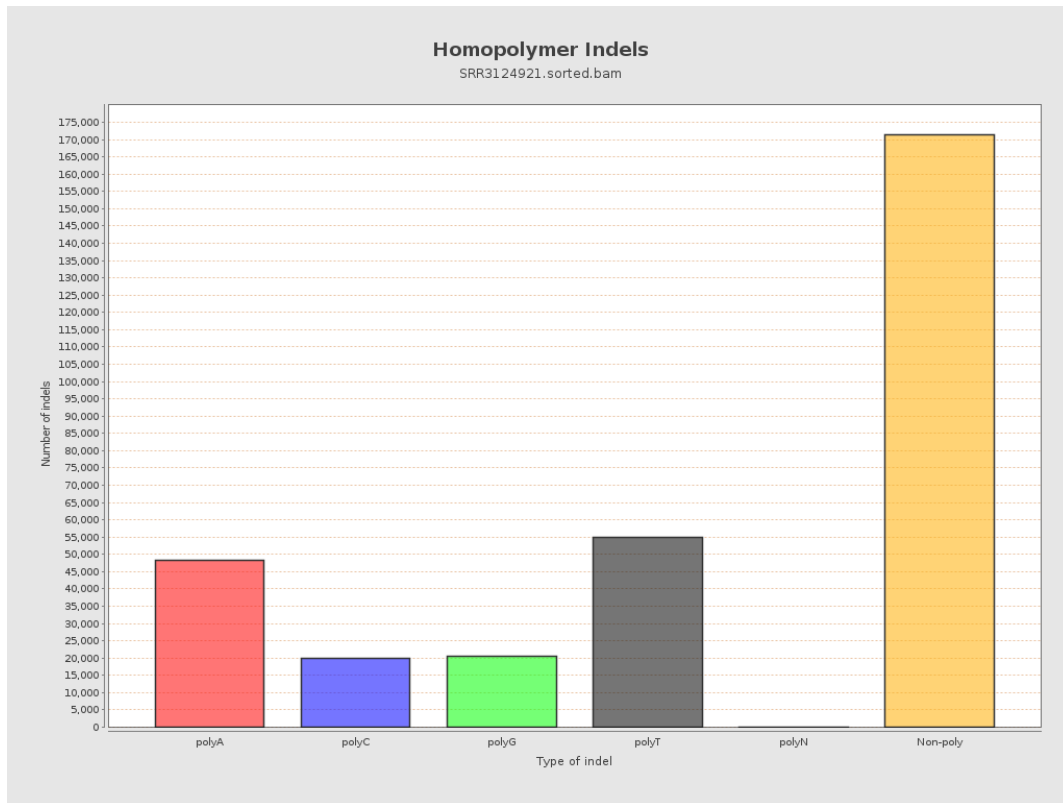
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



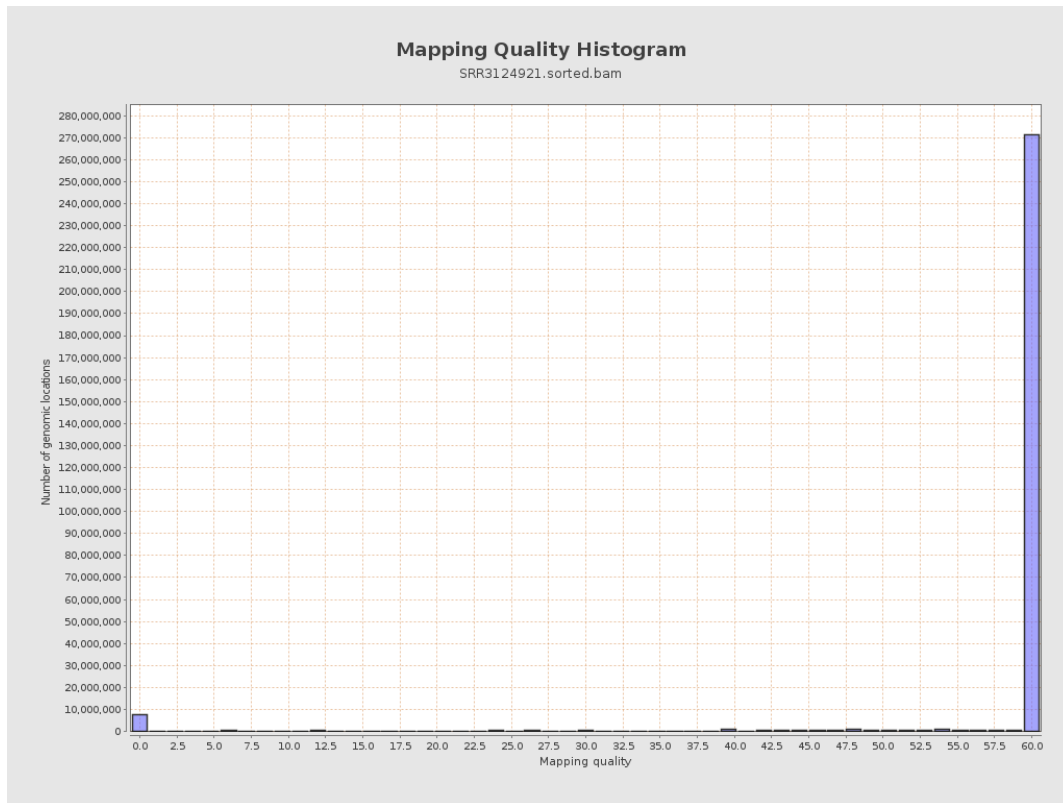
11. Results : Homopolymer Indels



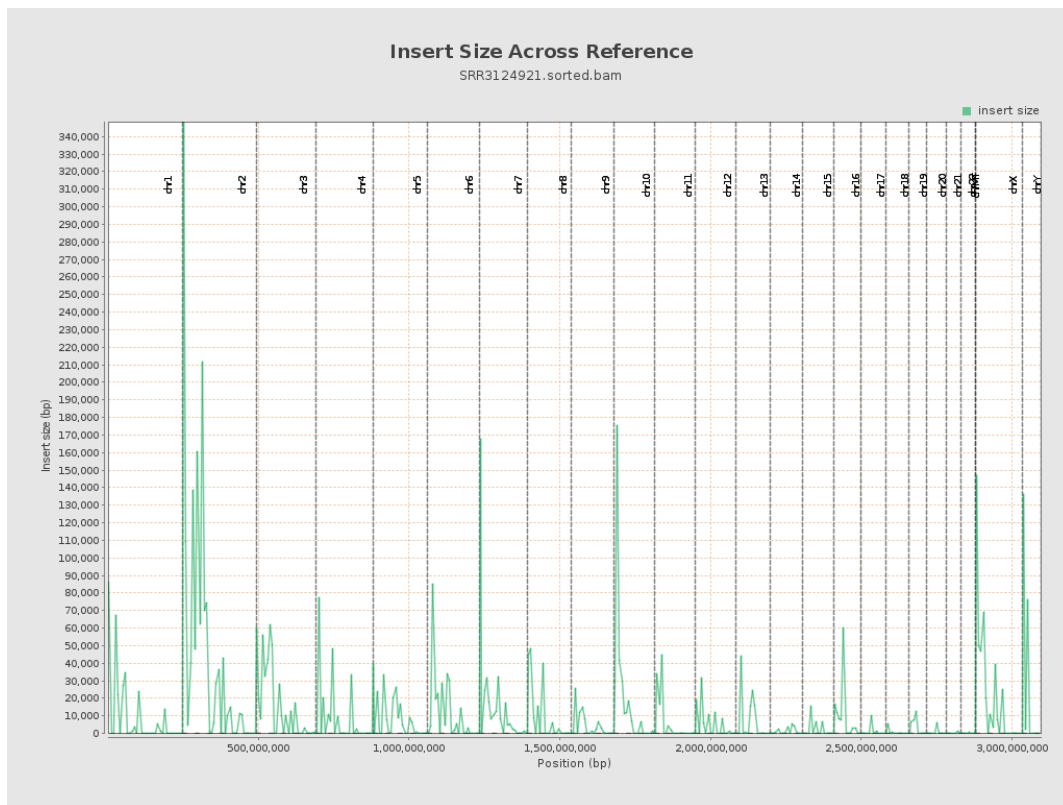
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

