

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 03:48:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124908.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_SRR3124908 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124908_1.fastq.gz SRR3124908_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 03:48:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124908.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,824,708
Mapped reads	4,758,317 / 98.62%
Unmapped reads	66,391 / 1.38%
Mapped paired reads	4,758,317 / 98.62%
Mapped reads, first in pair	2,380,806 / 49.35%
Mapped reads, second in pair	2,377,511 / 49.28%
Mapped reads, both in pair	4,736,634 / 98.17%
Mapped reads, singletons	21,683 / 0.45%
Secondary alignments	0
Supplementary alignments	28,052 / 0.58%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	304,558 / 6.31%
Duplication rate	3.24%
Clipped reads	2,892,088 / 59.94%

2.2. ACGT Content

Number/percentage of A's	125,527,021 / 28.98%
Number/percentage of C's	85,341,937 / 19.7%
Number/percentage of T's	127,089,760 / 29.34%
Number/percentage of G's	95,154,699 / 21.97%
Number/percentage of N's	7,309 / 0%

GC Percentage	41.67%
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2.3. Coverage

Mean	0.14
Standard Deviation	1.7046

2.4. Mapping Quality

Mean Mapping Quality	52.66
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2.5. Insert size

Mean	100,849.46
Standard Deviation	3,038,362.34
P25/Median/P75	137 / 170 / 216

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	3,604,296
Insertions	81,254
Mapped reads with at least one insertion	1.66%
Deletions	158,534
Mapped reads with at least one deletion	3.26%
Homopolymer indels	44.43%

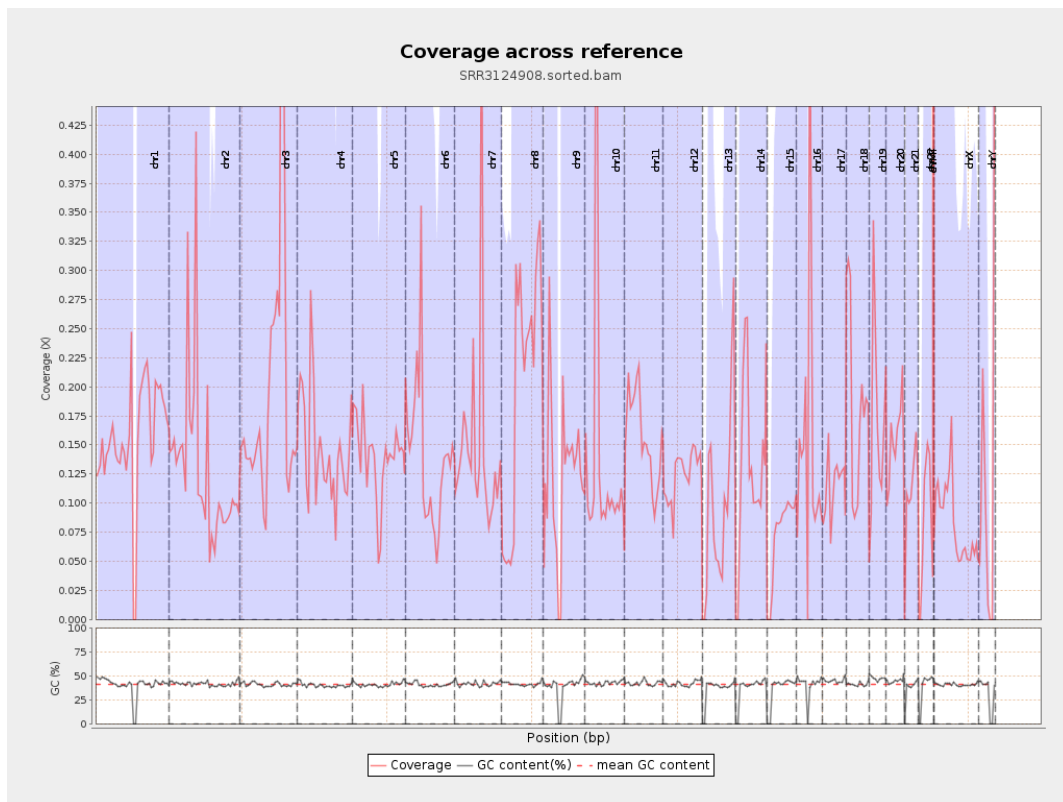
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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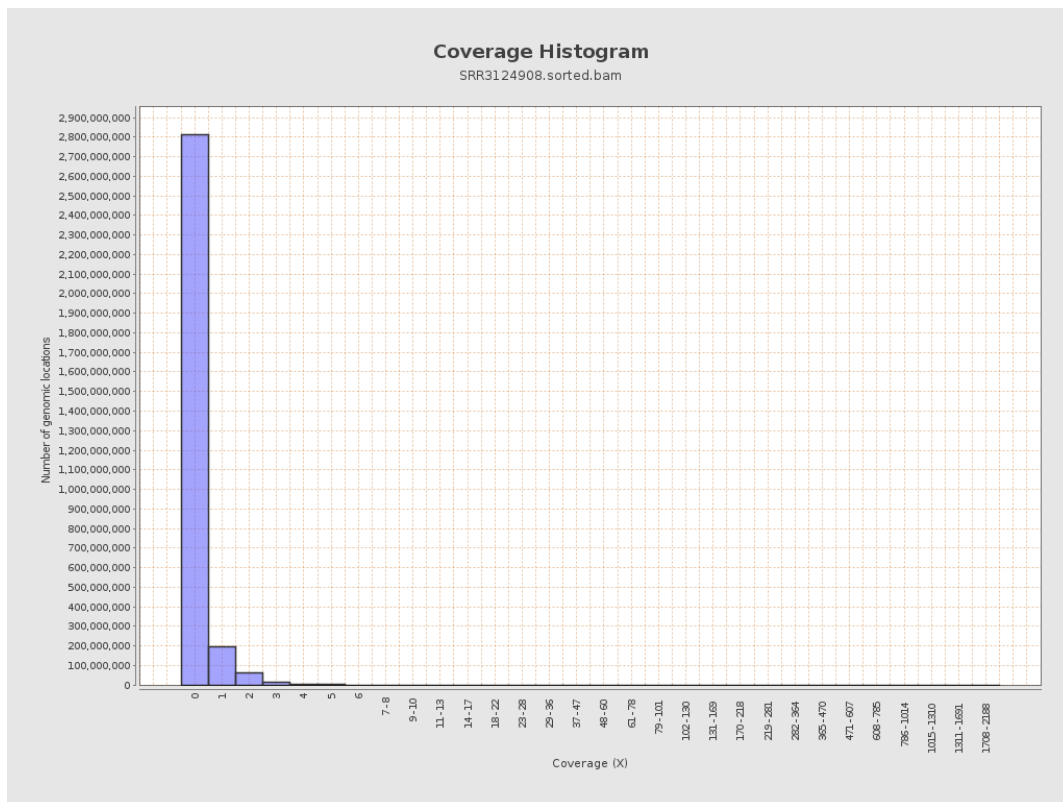
		bases	coverage	deviation
chr1	249250621	38985652	0.1564	1.6723
chr2	243199373	32026047	0.1317	1.9579
chr3	198022430	38894496	0.1964	0.6634
chr4	191154276	27891090	0.1459	1.2116
chr5	180915260	25130576	0.1389	0.5025
chr6	171115067	24143912	0.1411	1.9655
chr7	159138663	24135010	0.1517	1.9643
chr8	146364022	29478660	0.2014	0.7795
chr9	141213431	17874233	0.1266	2.1806
chr10	135534747	18108247	0.1336	4.3954
chr11	135006516	20912644	0.1549	1.4298
chr12	133851895	16674436	0.1246	0.463
chr13	115169878	11348935	0.0985	0.4168
chr14	107349540	13849516	0.129	0.5533
chr15	102531392	7450819	0.0727	0.3433
chr16	90354753	13360481	0.1479	2.8037
chr17	81195210	9196305	0.1133	1.1617
chr18	78077248	14507183	0.1858	2.4028
chr19	59128983	10416321	0.1762	1.1306
chr20	63025520	9743262	0.1546	0.603
chr21	48129895	5317731	0.1105	0.6617
chr22	51304566	4166414	0.0812	0.4076
chrMT	16571	142176	8.5798	5.0712
chrX	155270560	12956133	0.0834	0.7327

chrY	59373566	6690925	0.1127	2.7293
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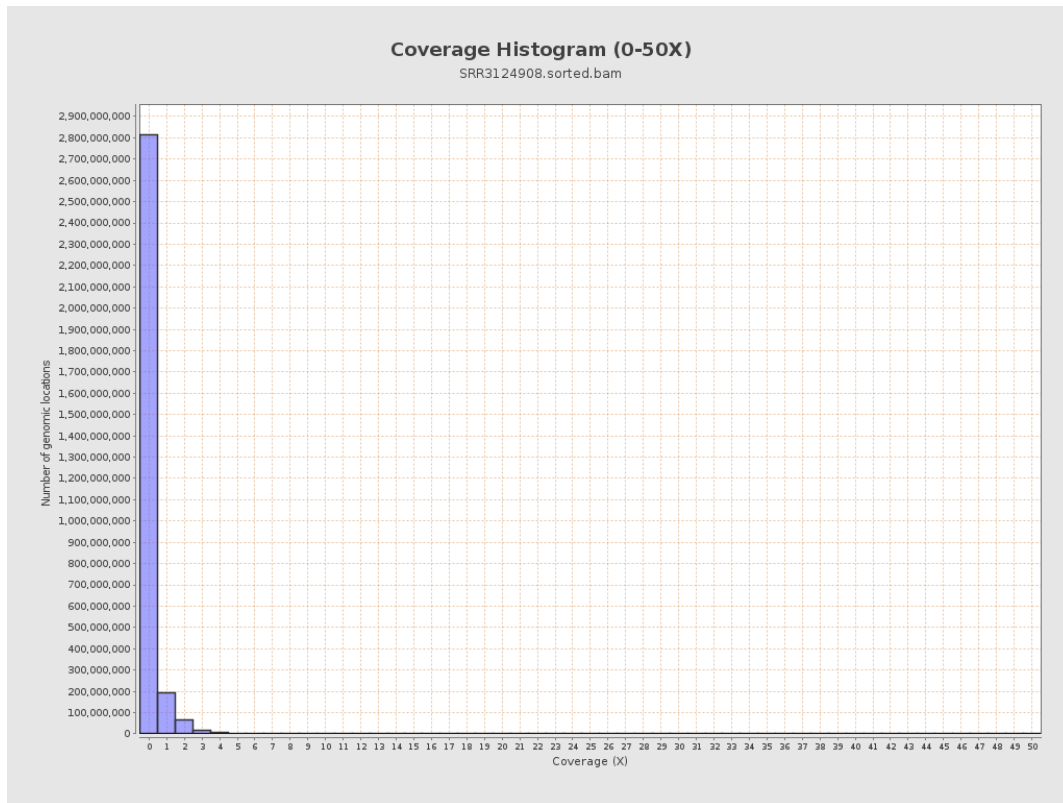
3. Results : Coverage across reference



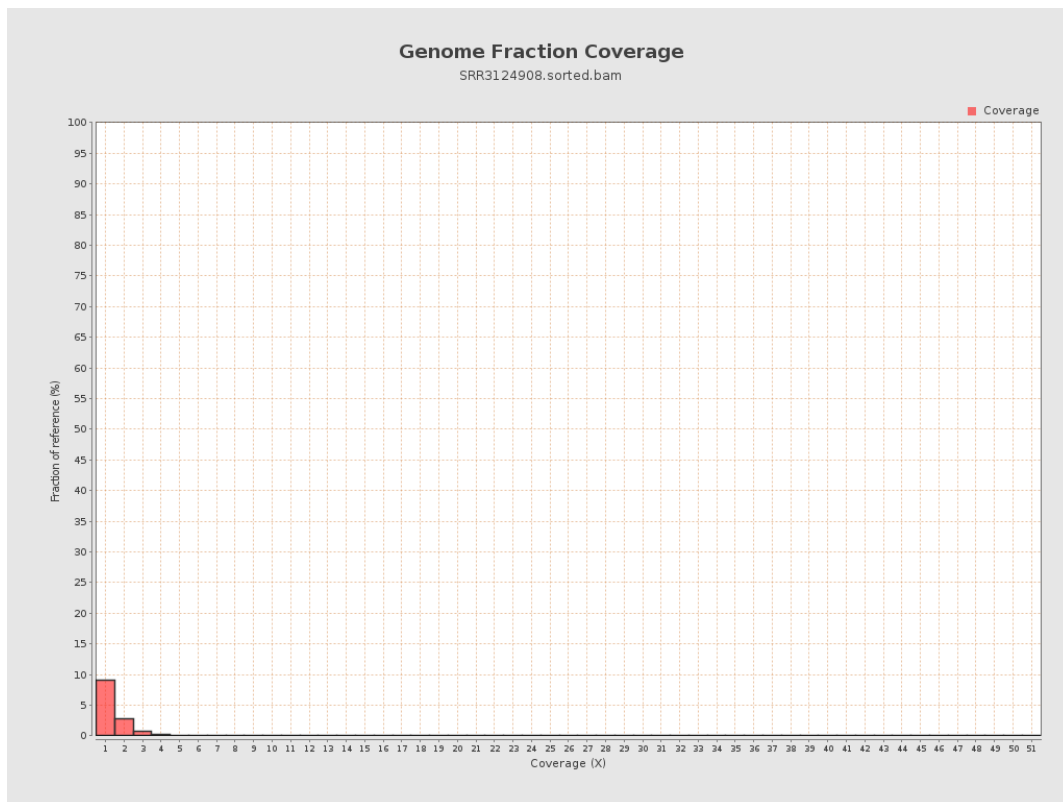
4. Results : Coverage Histogram



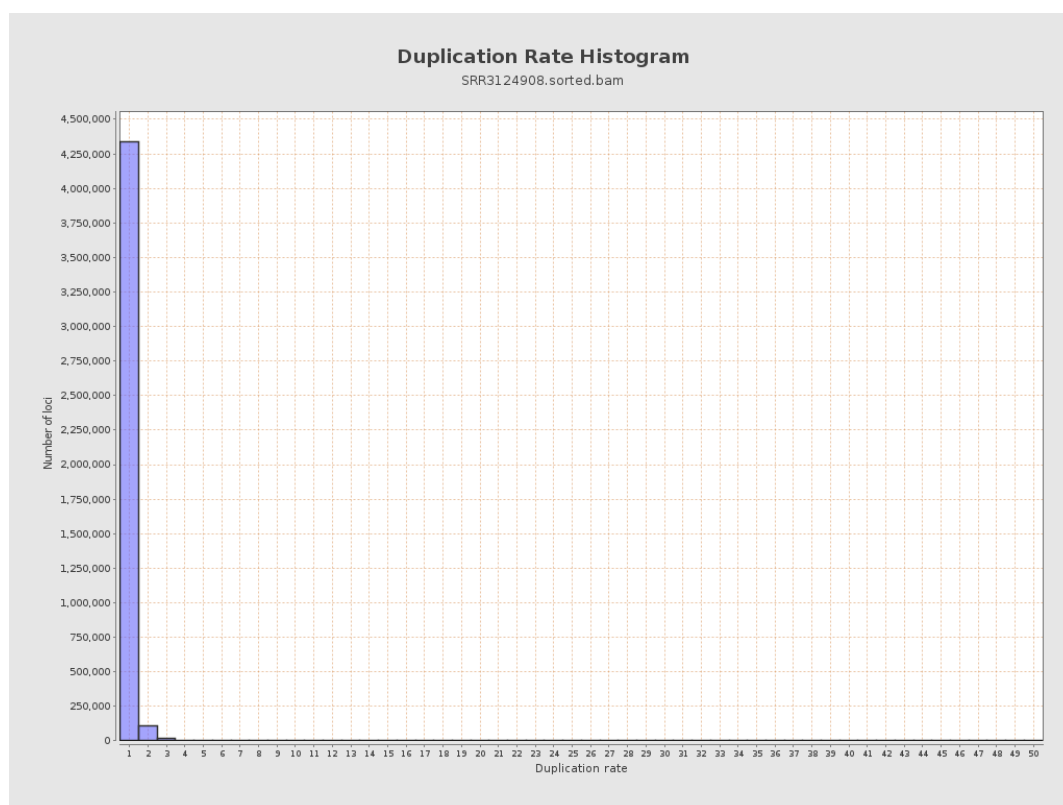
5. Results : Coverage Histogram (0-50X)



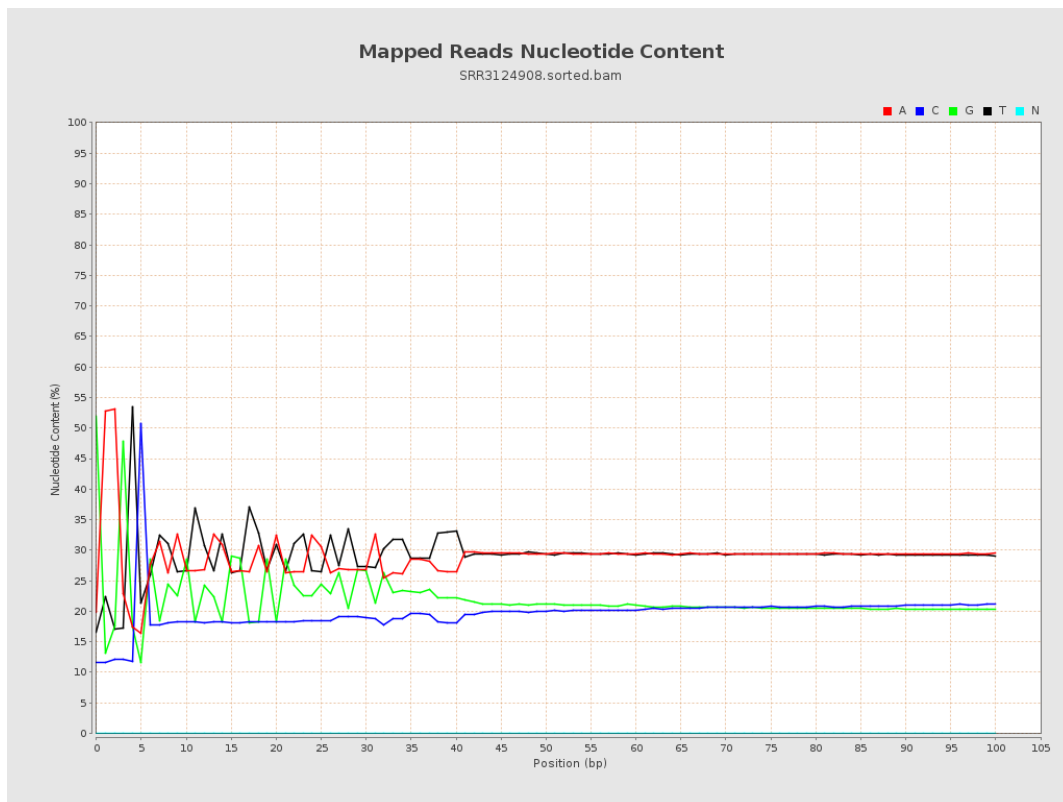
6. Results : Genome Fraction Coverage



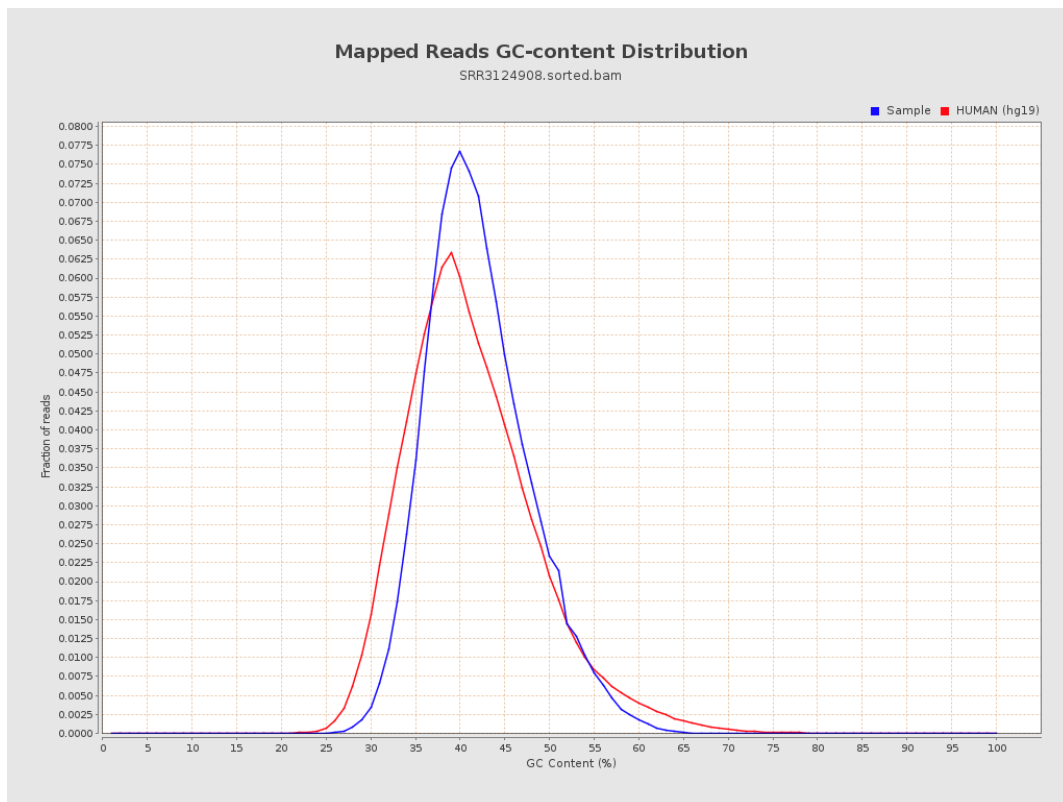
7. Results : Duplication Rate Histogram



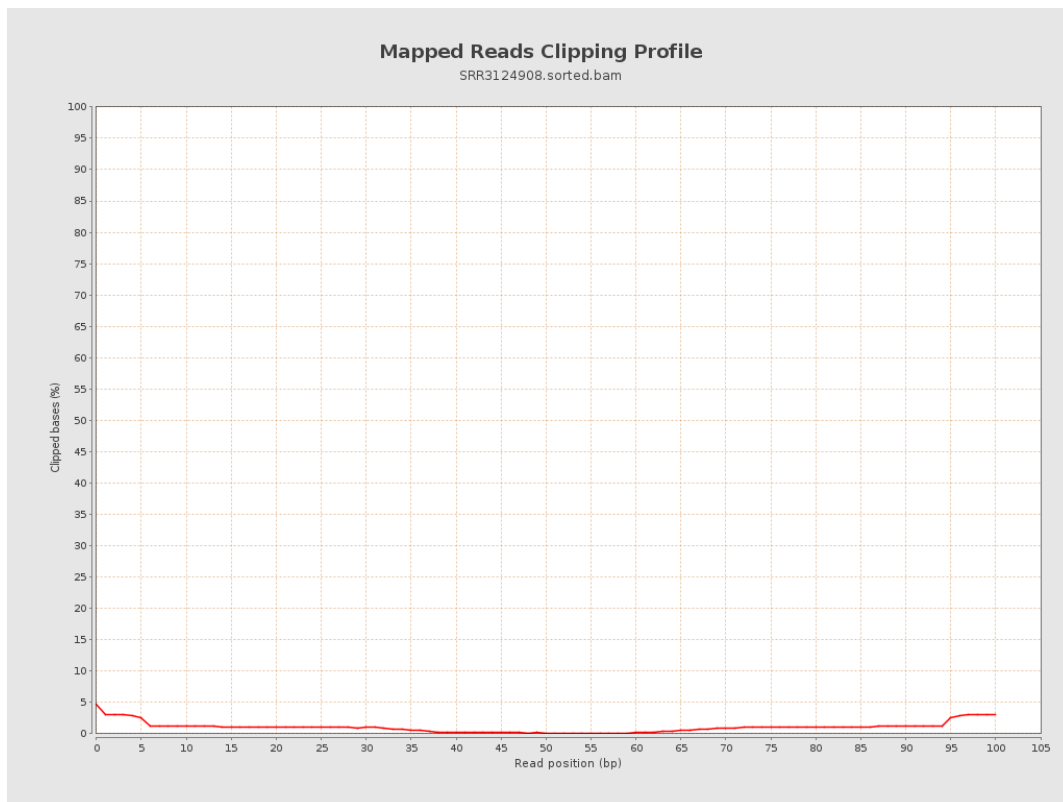
8. Results : Mapped Reads Nucleotide Content



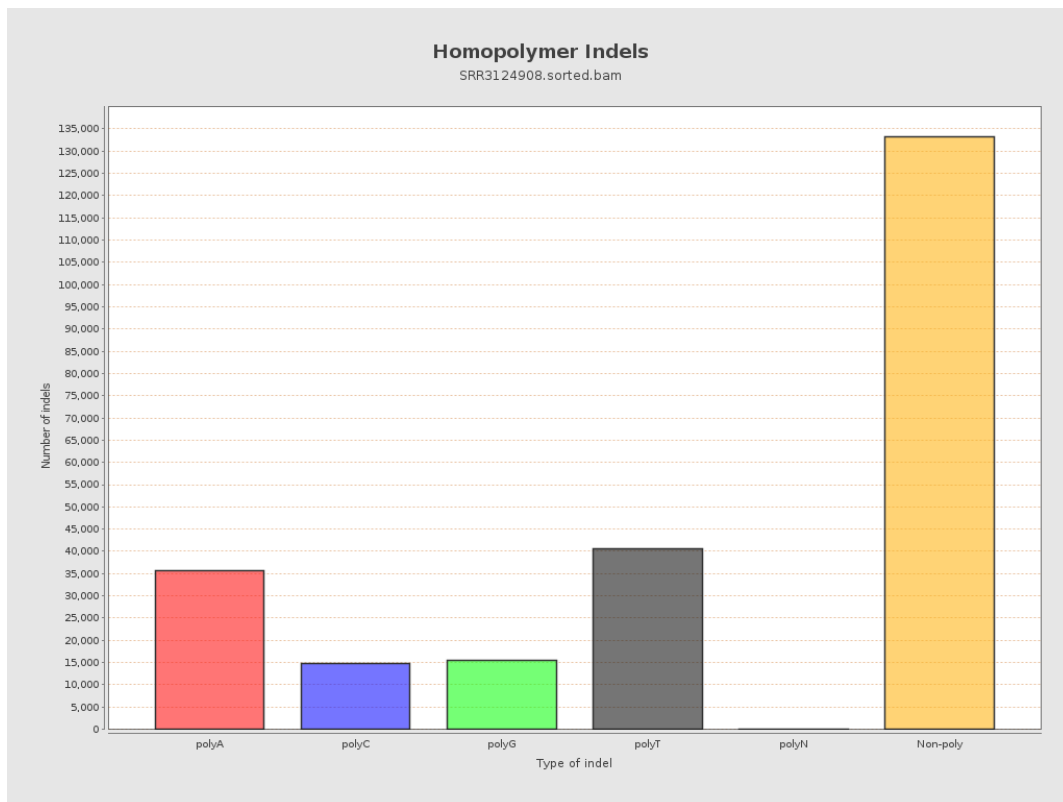
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



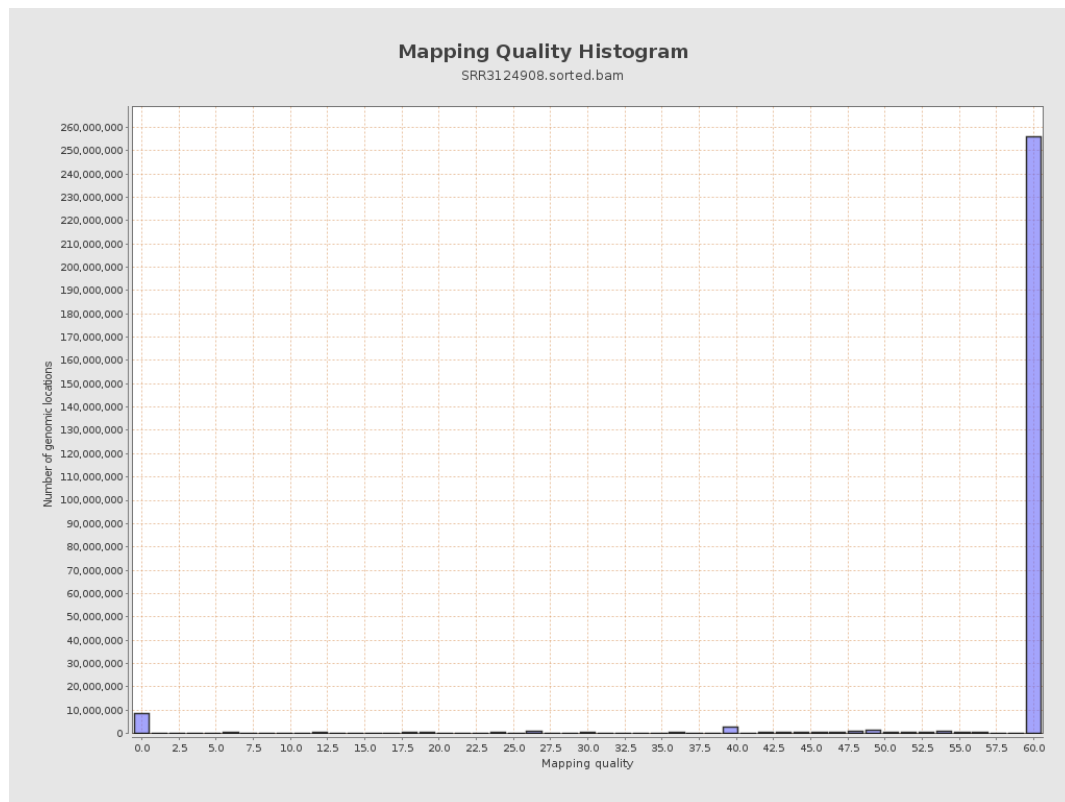
11. Results : Homopolymer Indels



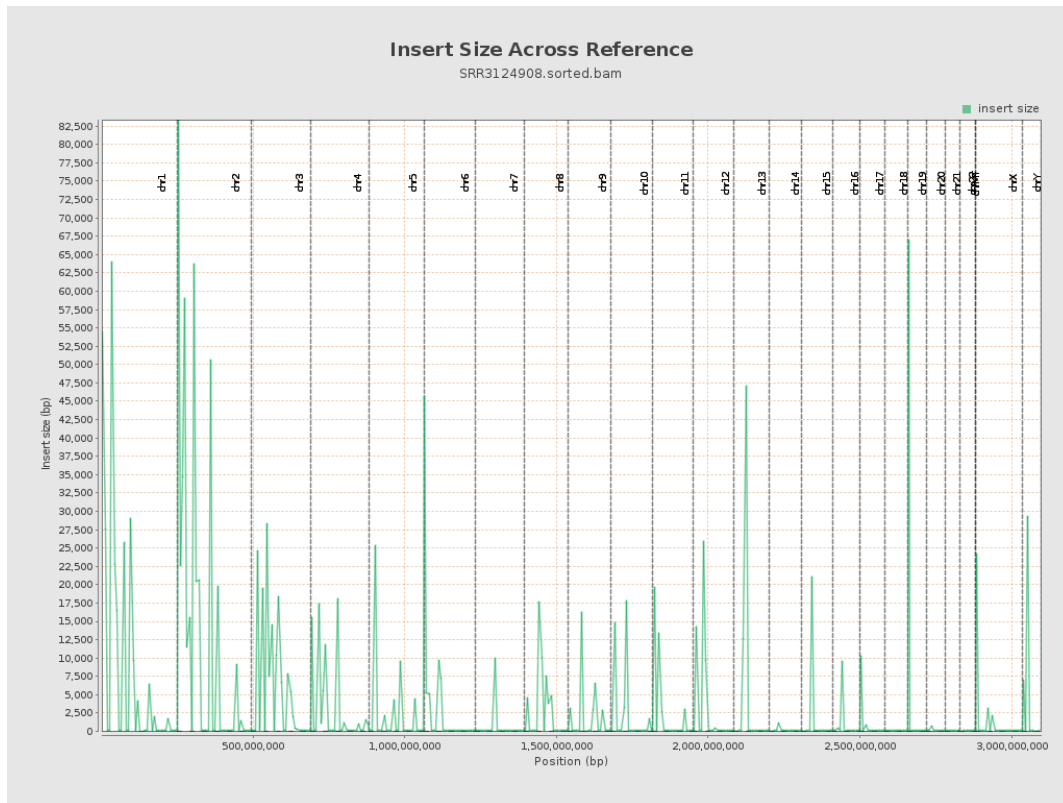
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

