

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 23:52:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124874.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_SRR3124874 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124874_1.fastq.gz SRR3124874_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 23:52:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124874.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,821,730
Mapped reads	4,770,822 / 98.94%
Unmapped reads	50,908 / 1.06%
Mapped paired reads	4,770,822 / 98.94%
Mapped reads, first in pair	2,386,709 / 49.5%
Mapped reads, second in pair	2,384,113 / 49.45%
Mapped reads, both in pair	4,754,274 / 98.6%
Mapped reads, singletons	16,548 / 0.34%
Secondary alignments	0
Supplementary alignments	19,330 / 0.4%
Read min/max/mean length	30 / 101 / 101.16
Duplicated reads (estimated)	289,657 / 6.01%
Duplication rate	3.88%
Clipped reads	1,960,933 / 40.67%

2.2. ACGT Content

Number/percentage of A's	122,778,243 / 28.61%
Number/percentage of C's	81,678,372 / 19.04%
Number/percentage of T's	127,835,661 / 29.79%
Number/percentage of G's	96,784,957 / 22.56%
Number/percentage of N's	6,356 / 0%

GC Percentage	41.59%
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2.3. Coverage

Mean	0.1387
Standard Deviation	1.3552

2.4. Mapping Quality

Mean Mapping Quality	53.22
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2.5. Insert size

Mean	41,950.09
Standard Deviation	1,893,356.41
P25/Median/P75	146 / 191 / 260

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	3,124,081
Insertions	54,451
Mapped reads with at least one insertion	1.11%
Deletions	136,630
Mapped reads with at least one deletion	2.81%
Homopolymer indels	47.01%

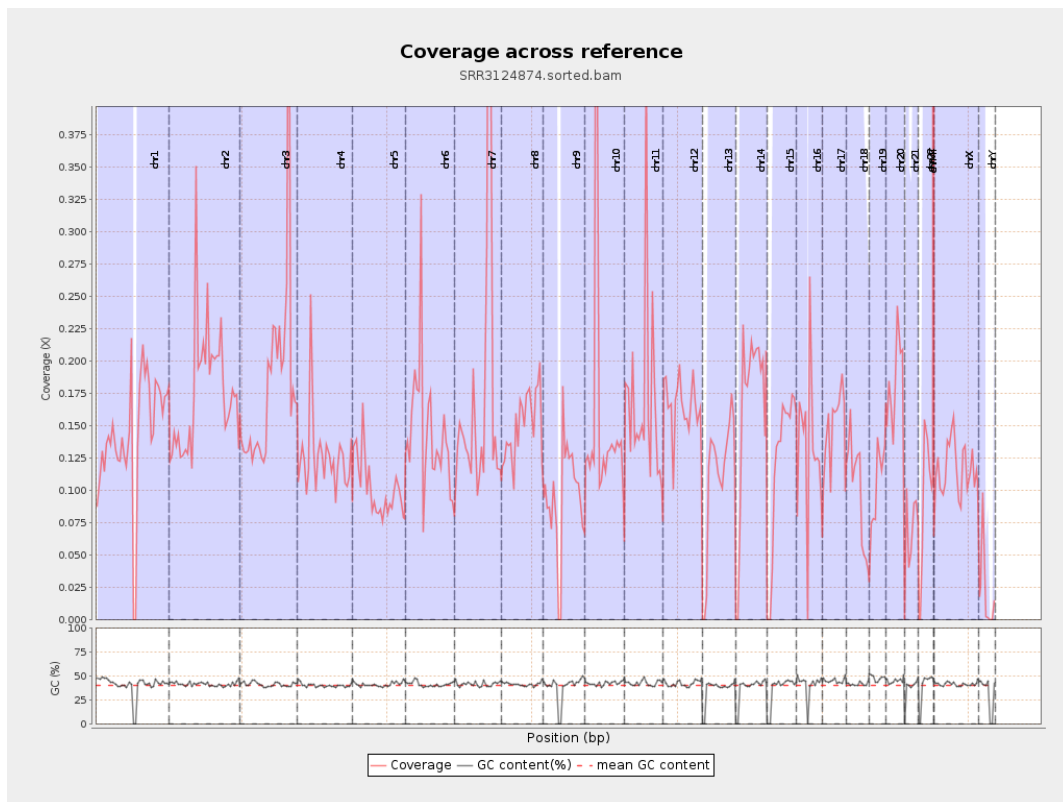
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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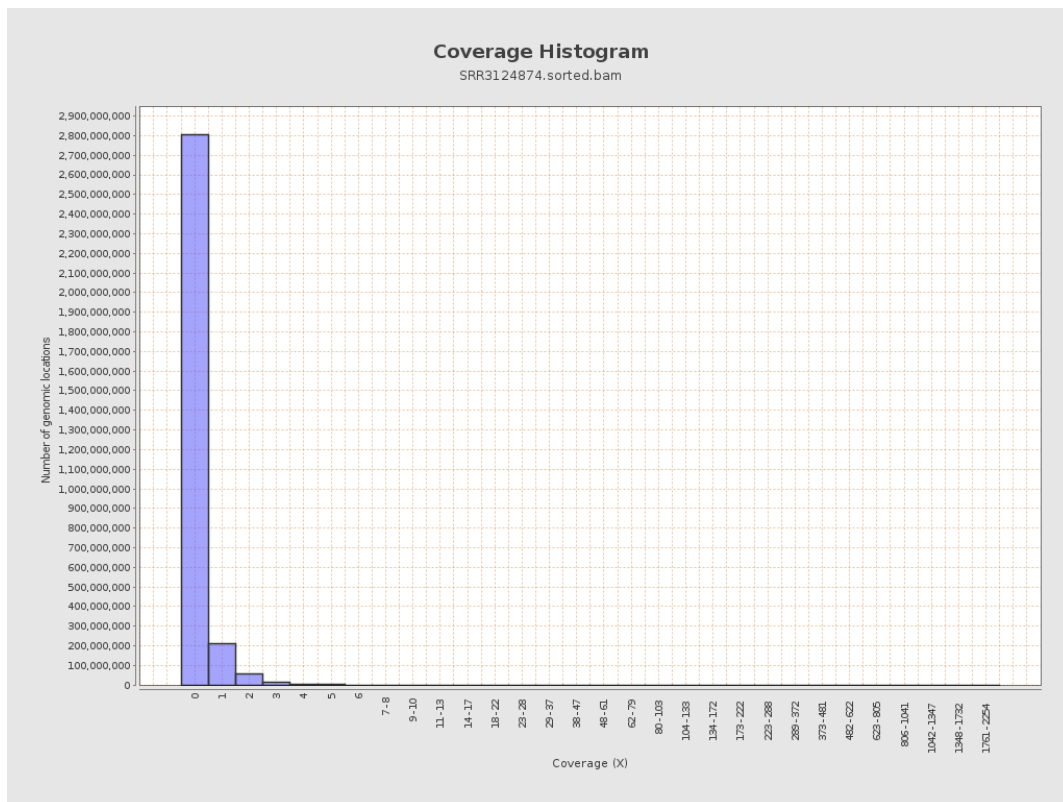
		bases	coverage	deviation
chr1	249250621	35633738	0.143	1.371
chr2	243199373	42688932	0.1755	1.3951
chr3	198022430	36159656	0.1826	0.605
chr4	191154276	23845994	0.1247	0.9283
chr5	180915260	18332859	0.1013	0.438
chr6	171115067	24532908	0.1434	1.6804
chr7	159138663	28262085	0.1776	1.6647
chr8	146364022	22069332	0.1508	0.6566
chr9	141213431	13364914	0.0946	1.6013
chr10	135534747	20614776	0.1521	4.0075
chr11	135006516	22536617	0.1669	0.9465
chr12	133851895	22093676	0.1651	0.559
chr13	115169878	12648895	0.1098	0.4305
chr14	107349540	17509317	0.1631	0.5695
chr15	102531392	12437296	0.1213	0.4689
chr16	90354753	11988949	0.1327	1.2749
chr17	81195210	12001294	0.1478	1.0501
chr18	78077248	7809656	0.1	1.5064
chr19	59128983	6228392	0.1053	0.9434
chr20	63025520	11444120	0.1816	0.6499
chr21	48129895	3263654	0.0678	0.5105
chr22	51304566	4605058	0.0898	0.4261
chrMT	16571	42555	2.568	1.8021
chrX	155270560	17989409	0.1159	0.6295

chrY	59373566	1204515	0.0203	1.4458
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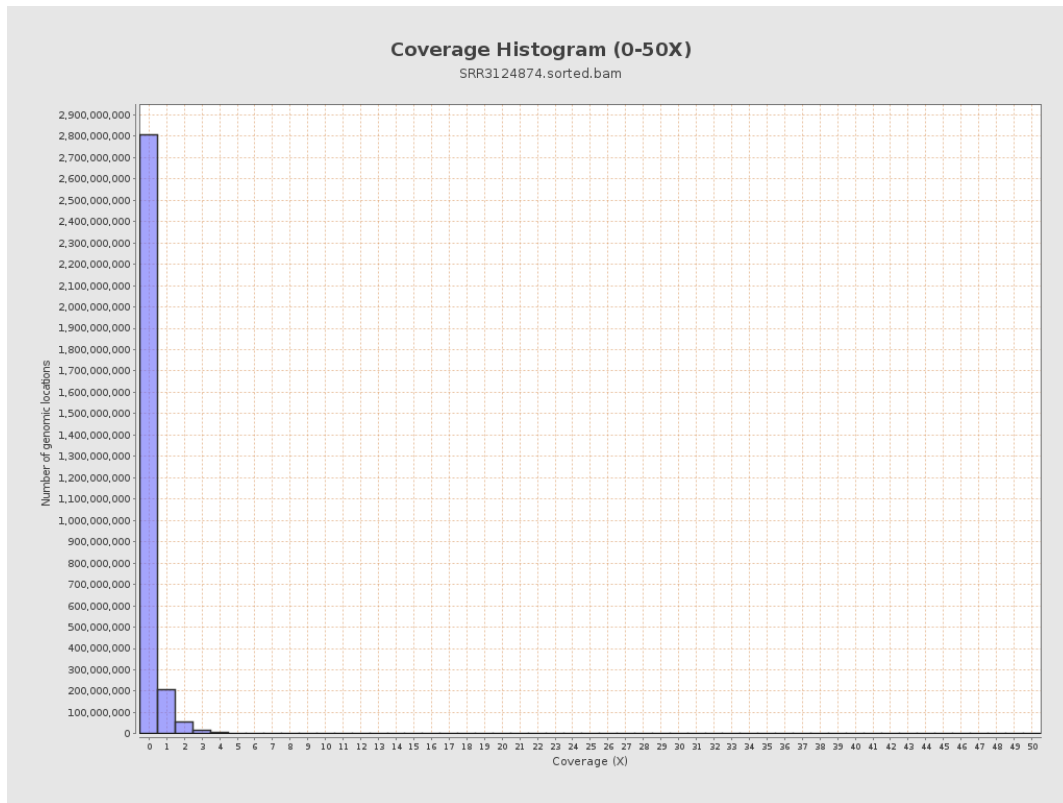
3. Results : Coverage across reference



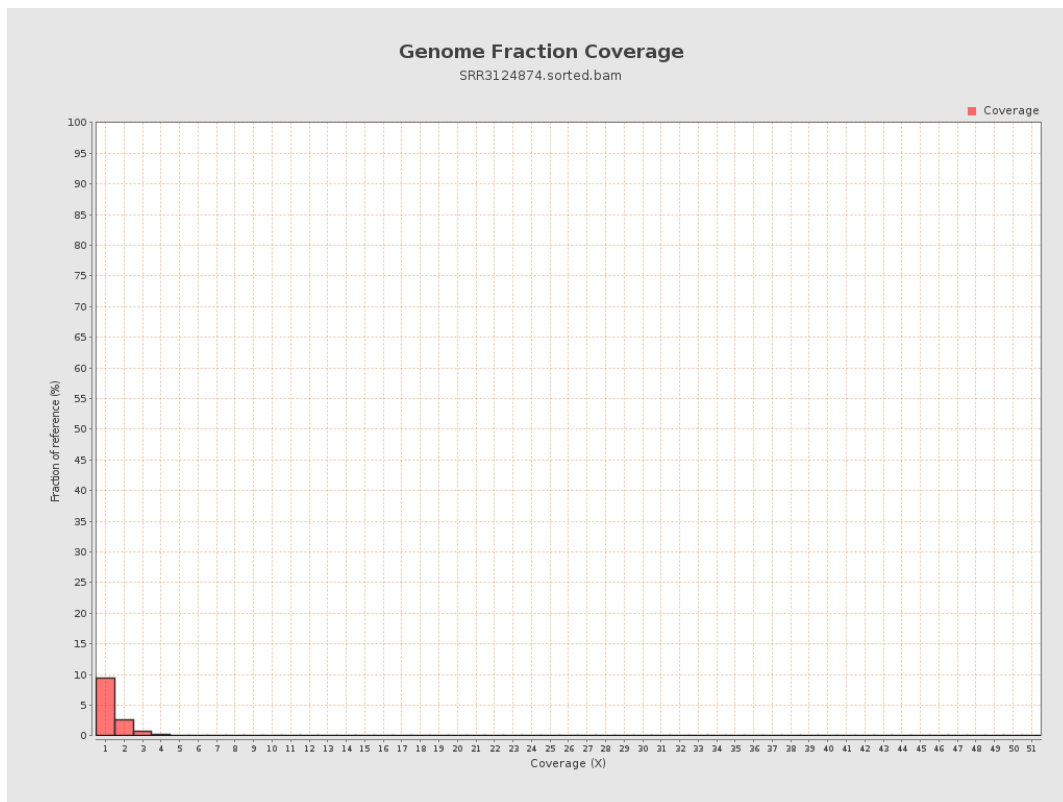
4. Results : Coverage Histogram



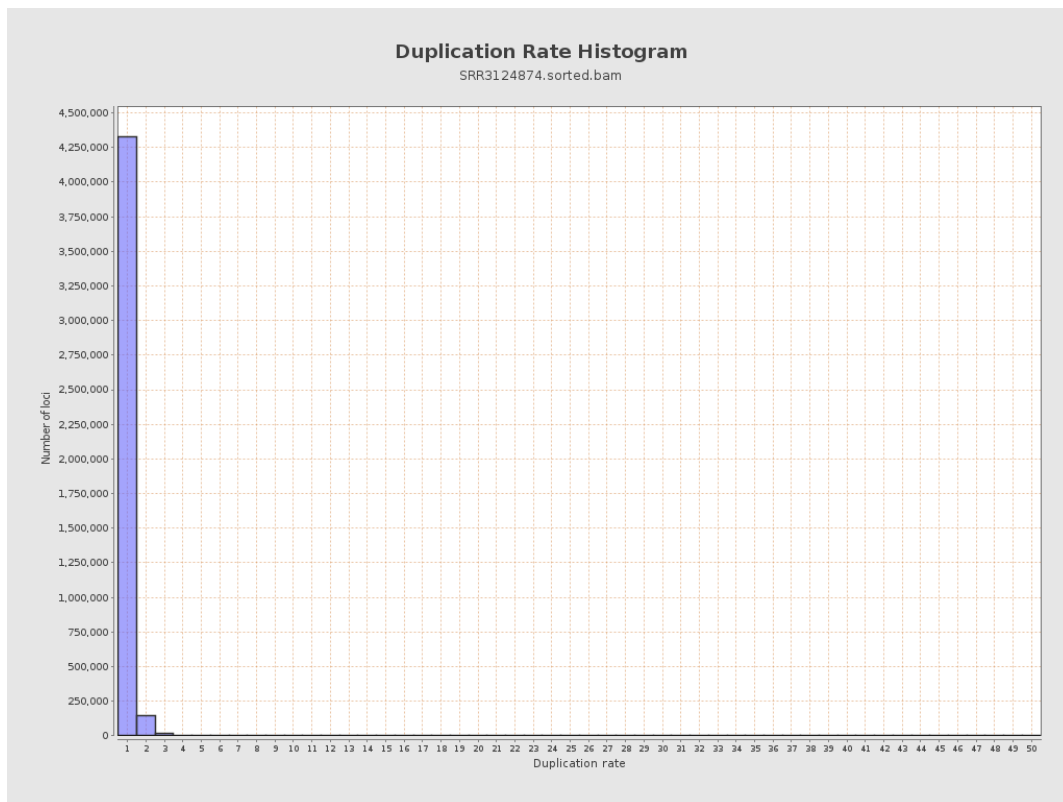
5. Results : Coverage Histogram (0-50X)



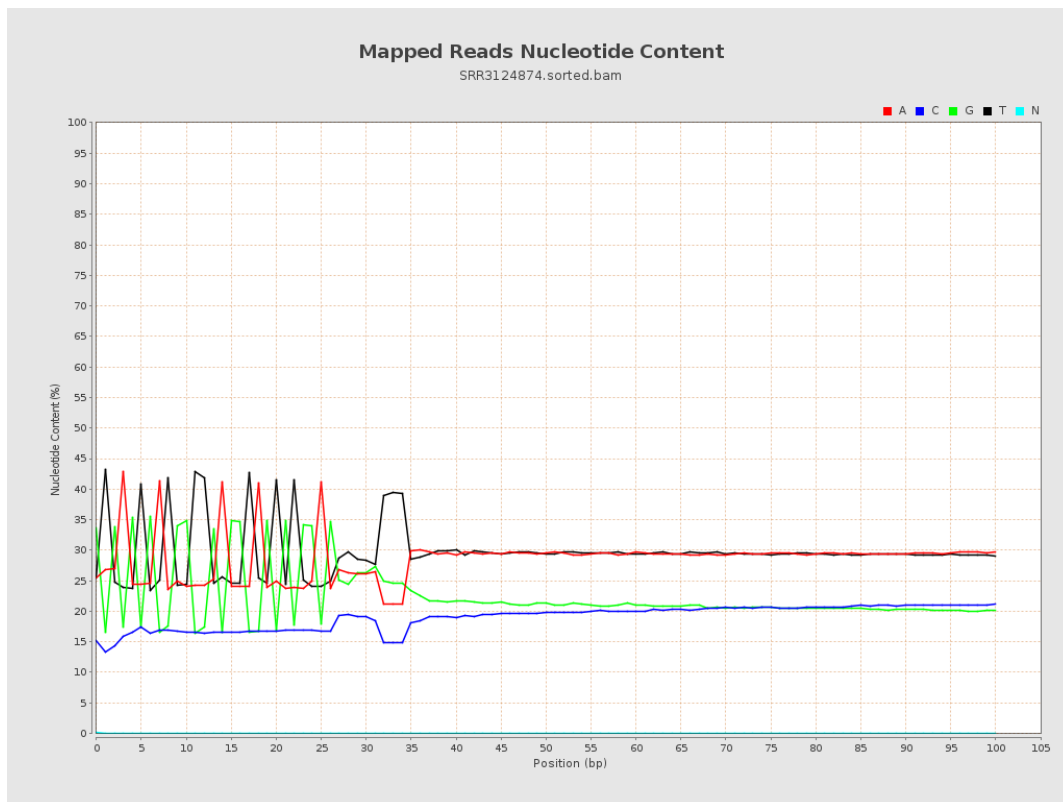
6. Results : Genome Fraction Coverage



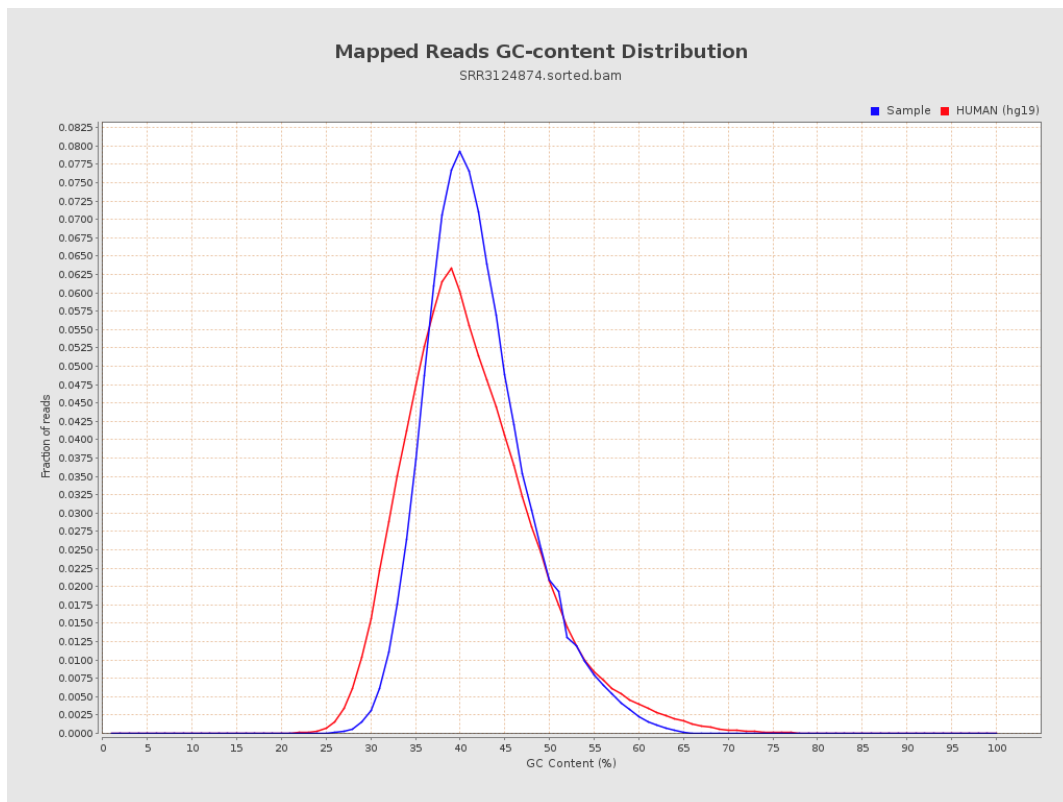
7. Results : Duplication Rate Histogram



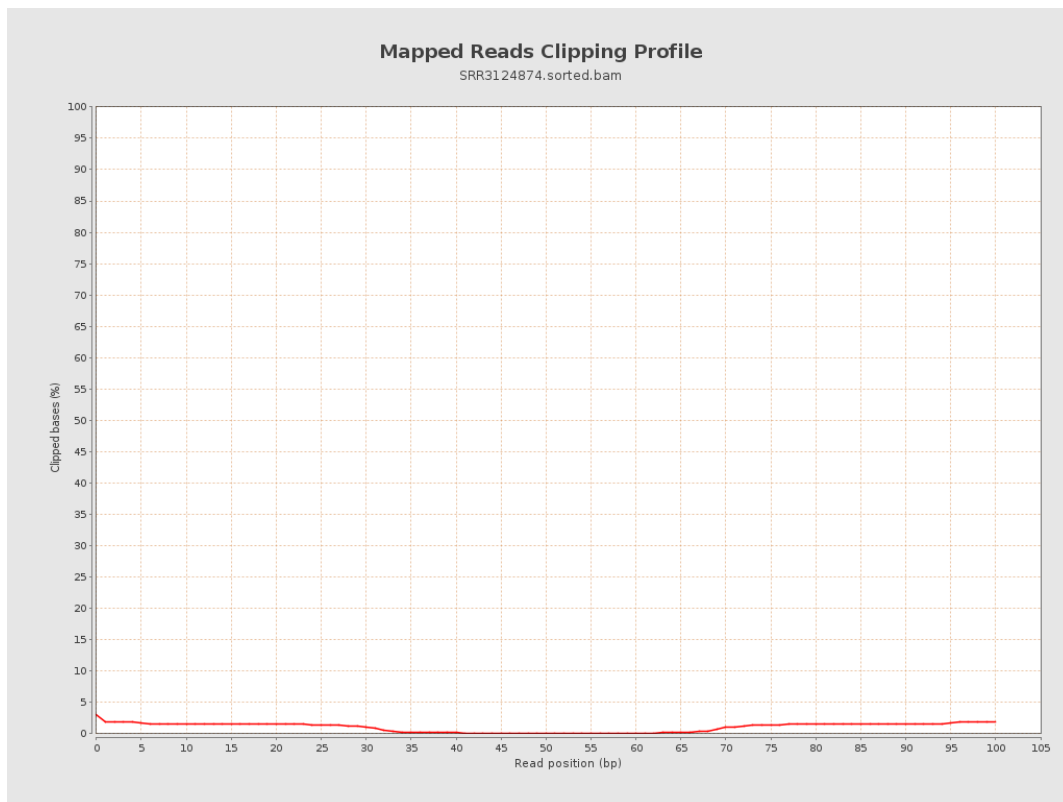
8. Results : Mapped Reads Nucleotide Content



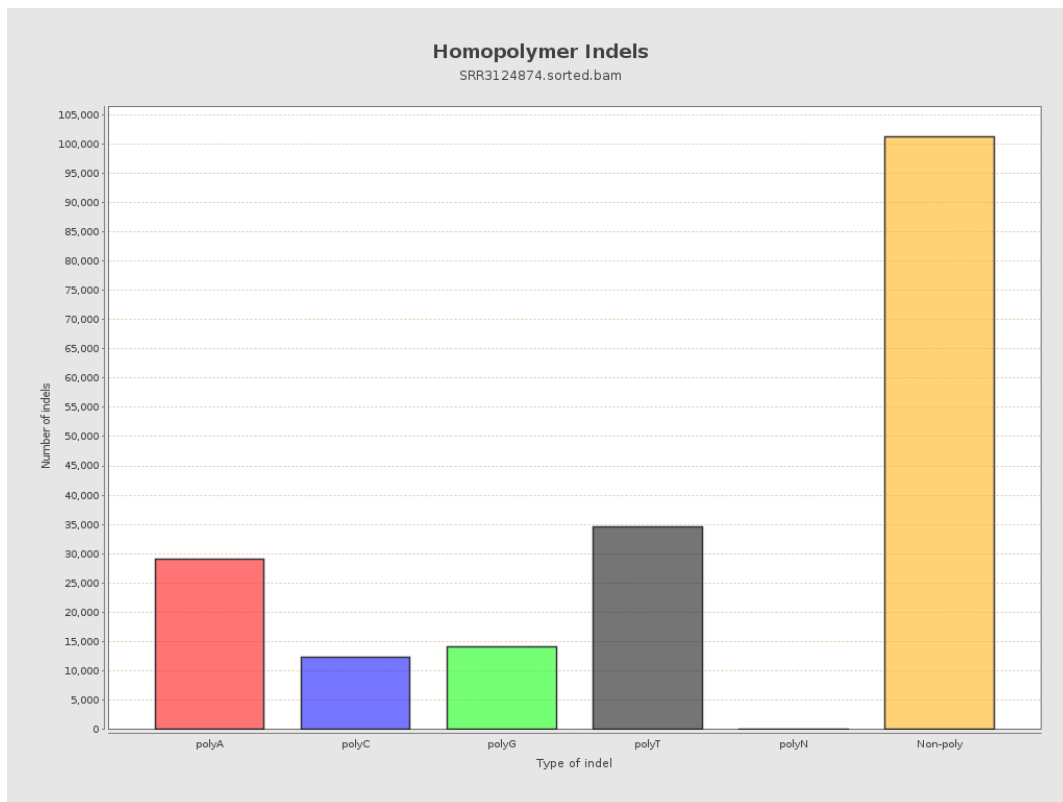
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



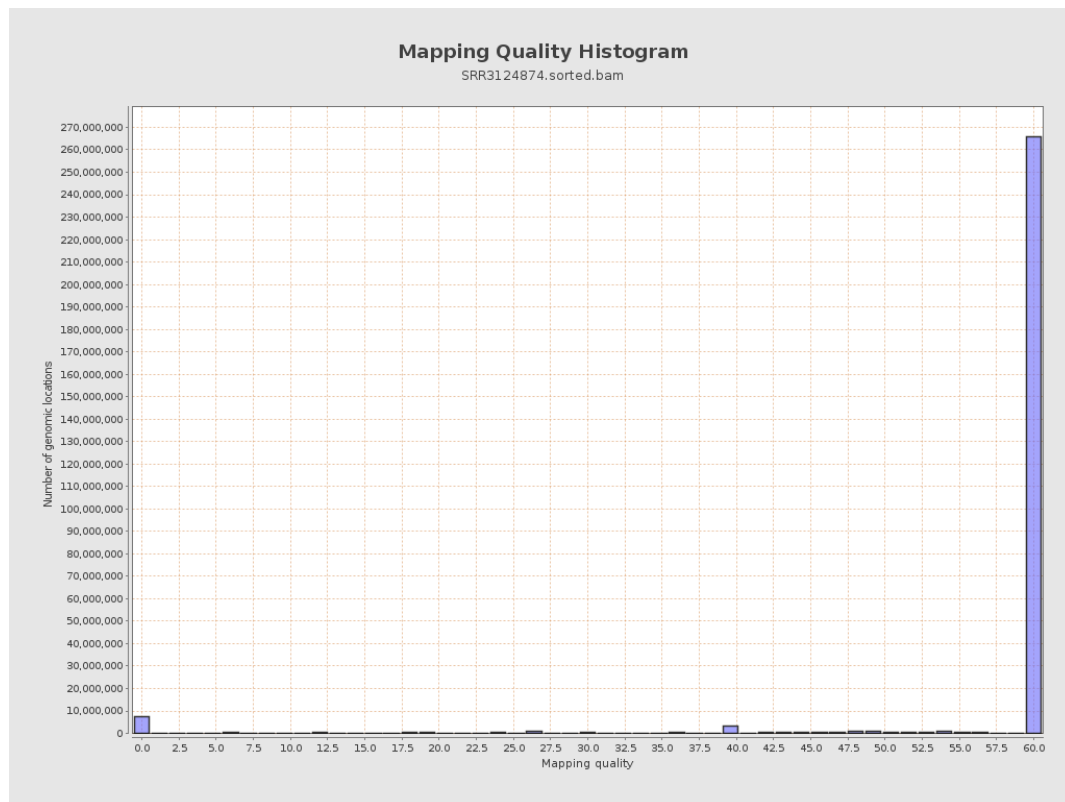
11. Results : Homopolymer Indels



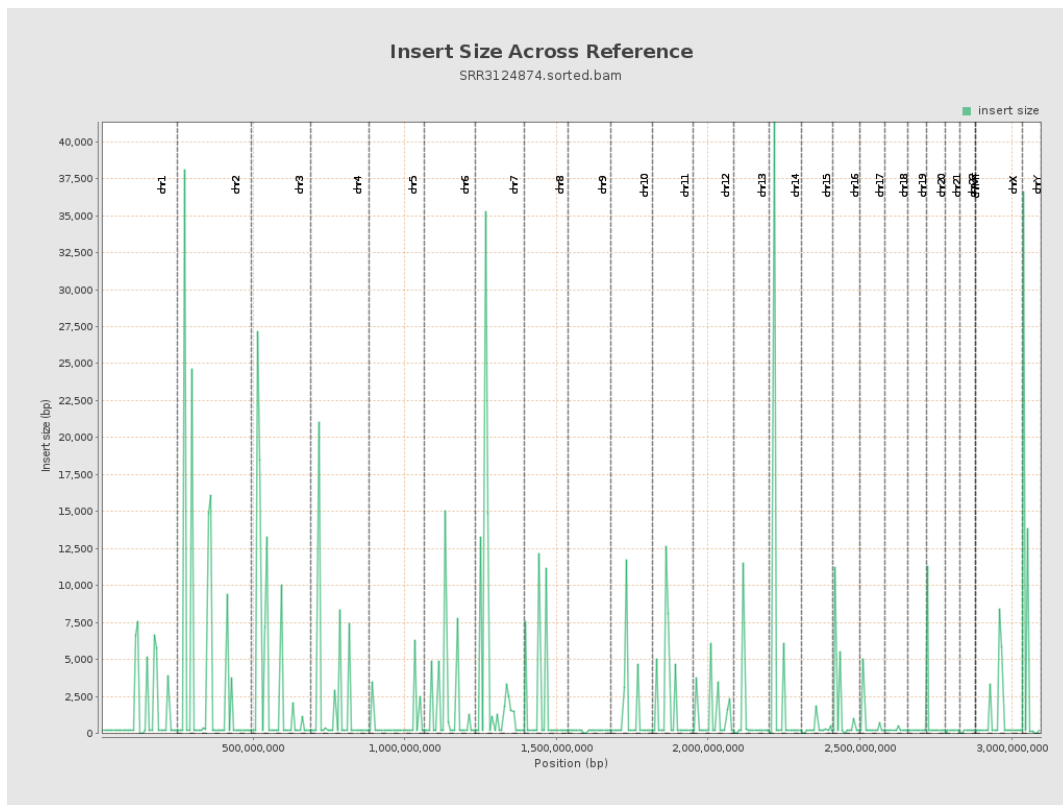
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

