

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:42:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173894.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_SRR10173894 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173894_1.fastq.gz SRR10173894_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:42:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173894.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,622,126
Mapped reads	1,581,819 / 97.52%
Unmapped reads	40,307 / 2.48%
Mapped paired reads	1,581,819 / 97.52%
Mapped reads, first in pair	791,881 / 48.82%
Mapped reads, second in pair	789,938 / 48.7%
Mapped reads, both in pair	1,557,558 / 96.02%
Mapped reads, singletons	24,261 / 1.5%
Secondary alignments	0
Supplementary alignments	151,433 / 9.34%
Read min/max/mean length	30 / 133 / 127.82
Duplicated reads (estimated)	1,147,063 / 70.71%
Duplication rate	60.88%
Clipped reads	619,142 / 38.17%

2.2. ACGT Content

Number/percentage of A's	56,960,565 / 30.46%
Number/percentage of C's	36,036,654 / 19.27%
Number/percentage of T's	56,754,715 / 30.34%
Number/percentage of G's	37,277,660 / 19.93%
Number/percentage of N's	2,258 / 0%

GC Percentage	39.2%
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2.3. Coverage

Mean	0.0605
Standard Deviation	1.0073

2.4. Mapping Quality

Mean Mapping Quality	53.18
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2.5. Insert size

Mean	919,873.89
Standard Deviation	8,861,162.08
P25/Median/P75	140 / 190 / 265

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	1,898,194
Insertions	20,942
Mapped reads with at least one insertion	1.28%
Deletions	47,772
Mapped reads with at least one deletion	2.95%
Homopolymer indels	42.33%

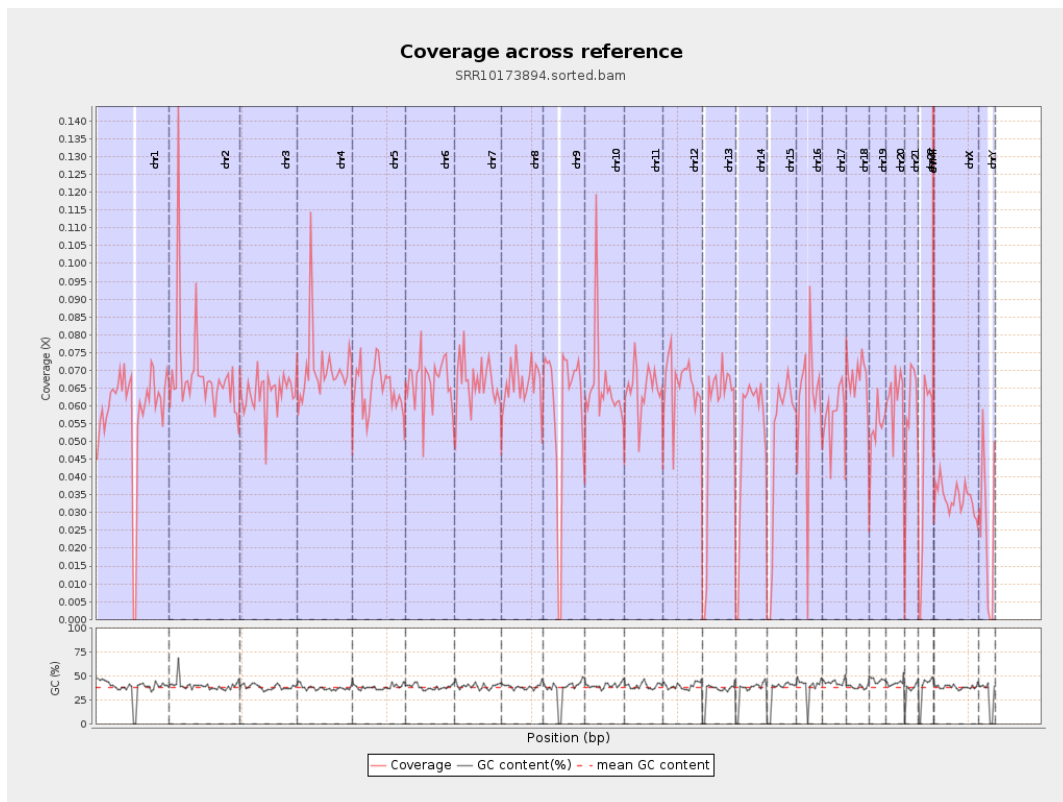
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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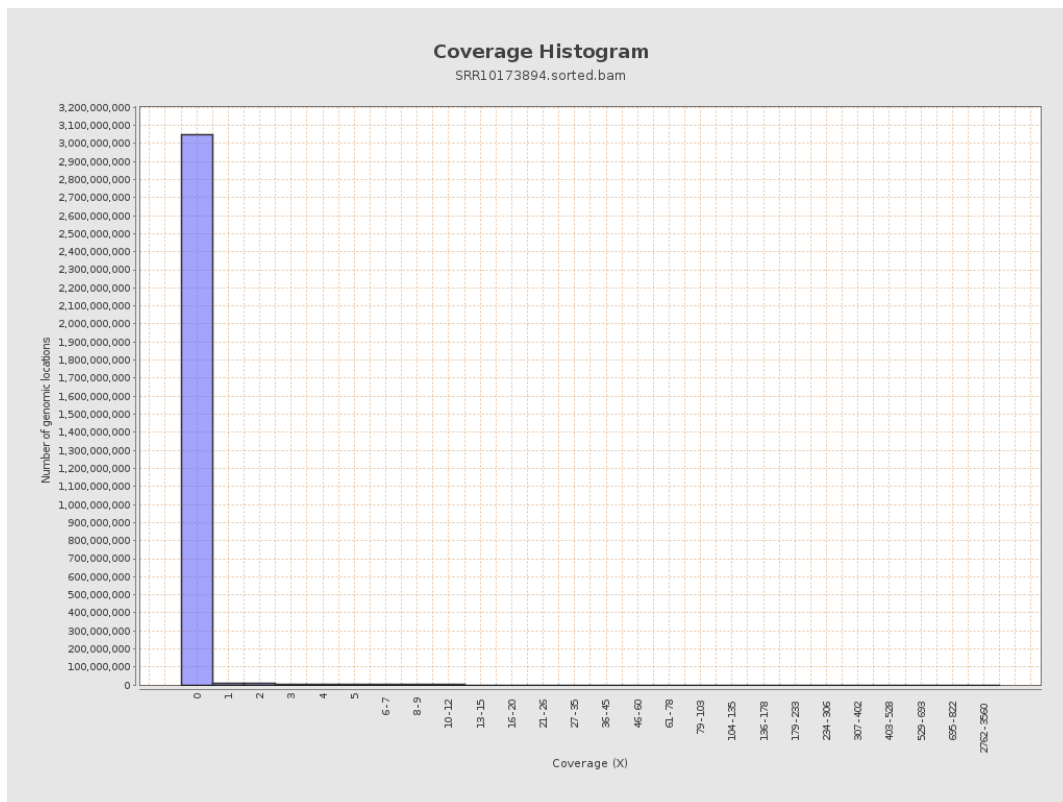
		bases	coverage	deviation
chr1	249250621	14565497	0.0584	0.7629
chr2	243199373	16744822	0.0689	2.5709
chr3	198022430	12628895	0.0638	0.7041
chr4	191154276	13414140	0.0702	0.8082
chr5	180915260	11721339	0.0648	0.7004
chr6	171115067	11412372	0.0667	0.7319
chr7	159138663	10671303	0.0671	0.7923
chr8	146364022	9680540	0.0661	0.8789
chr9	141213431	8453789	0.0599	0.778
chr10	135534747	8878834	0.0655	0.9329
chr11	135006516	8749988	0.0648	0.7015
chr12	133851895	8828071	0.066	0.702
chr13	115169878	6306032	0.0548	0.6522
chr14	107349540	5570489	0.0519	0.6292
chr15	102531392	5091750	0.0497	0.599
chr16	90354753	5463018	0.0605	0.7226
chr17	81195210	4615614	0.0568	0.6503
chr18	78077248	5346826	0.0685	0.9319
chr19	59128983	3182102	0.0538	0.6563
chr20	63025520	3900815	0.0619	0.6635
chr21	48129895	2694401	0.056	0.7162
chr22	51304566	2242241	0.0437	0.5728
chrMT	16571	293802	17.7299	17.0213
chrX	155270560	5244226	0.0338	0.4972

chrY	59373566	1442595	0.0243	0.5103
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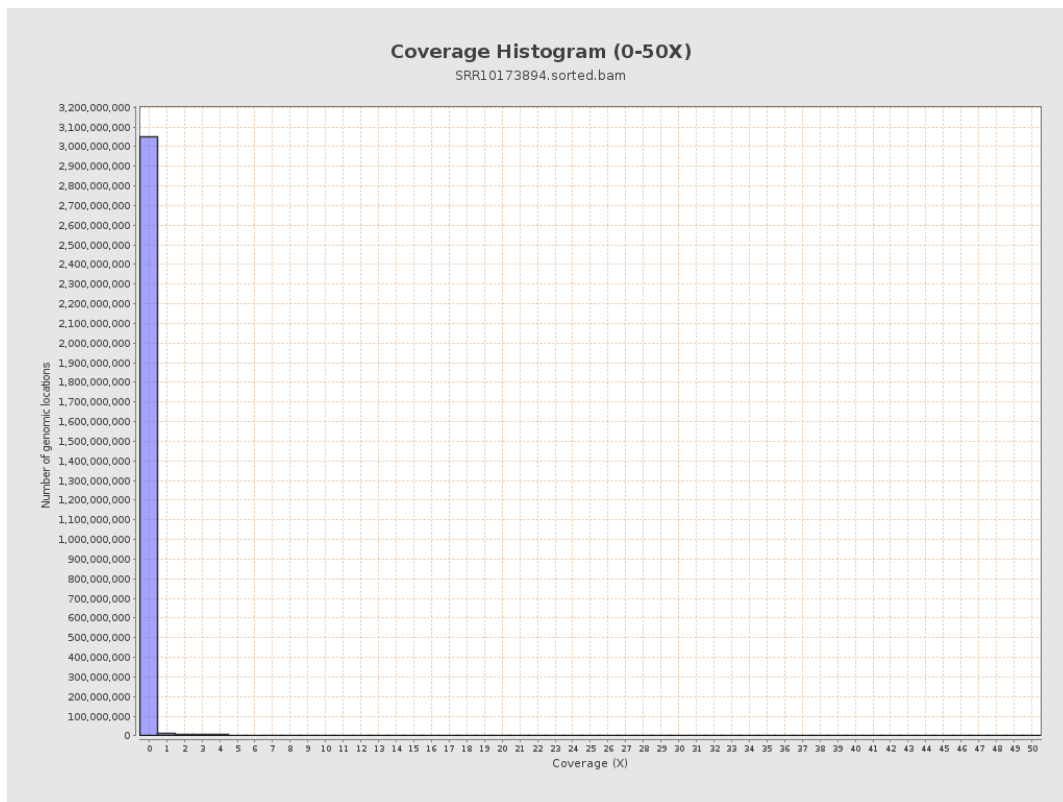
3. Results : Coverage across reference



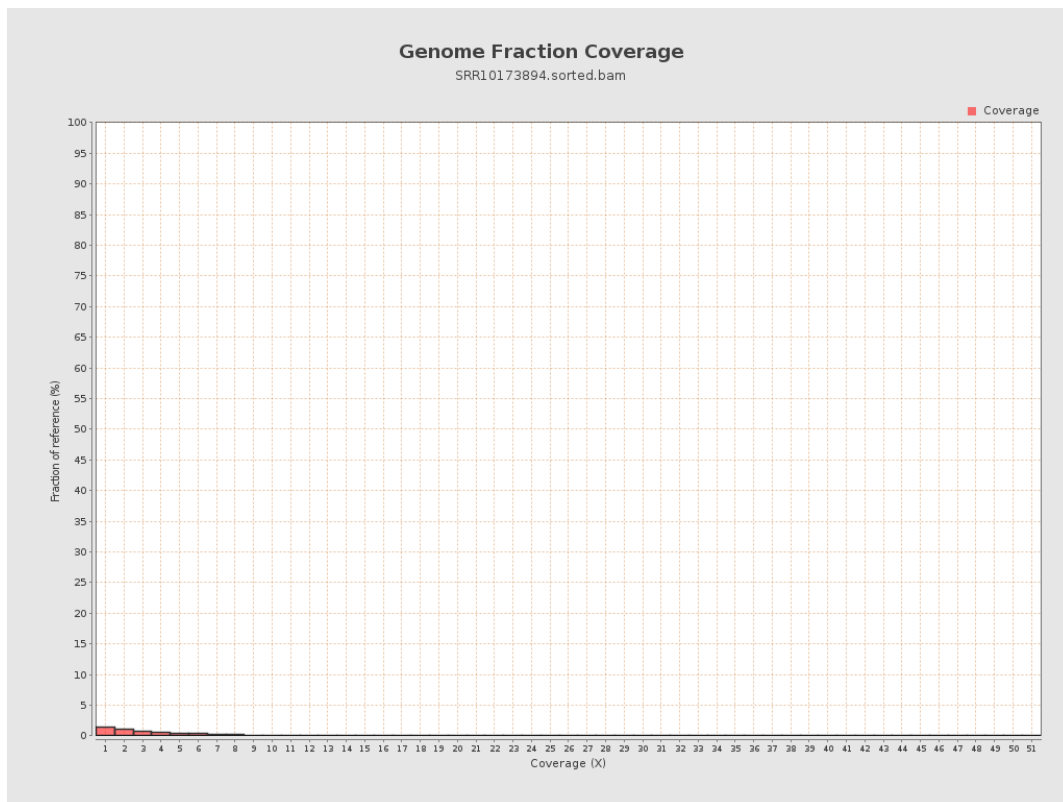
4. Results : Coverage Histogram



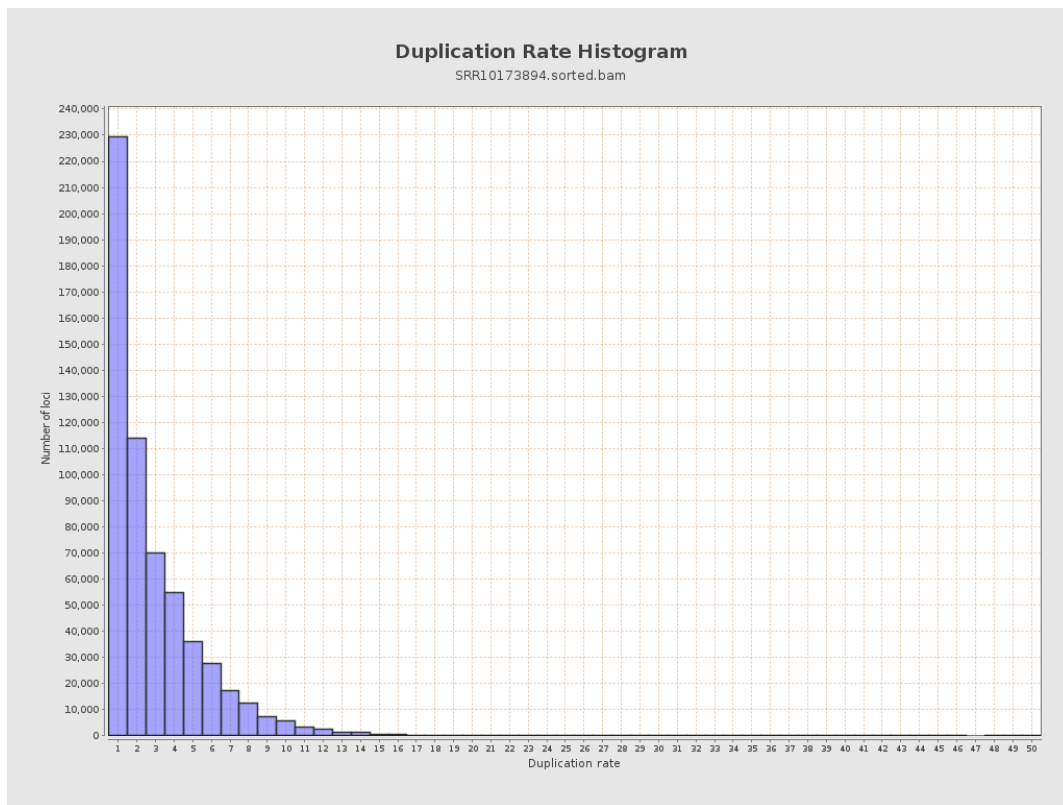
5. Results : Coverage Histogram (0-50X)



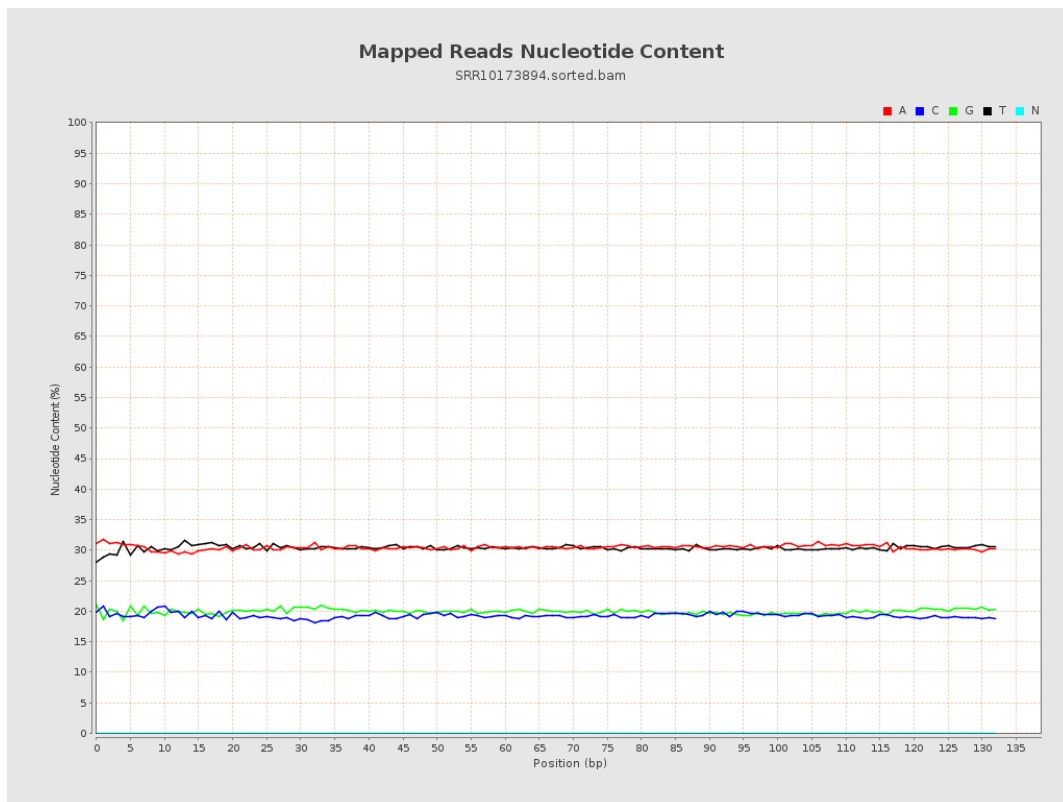
6. Results : Genome Fraction Coverage



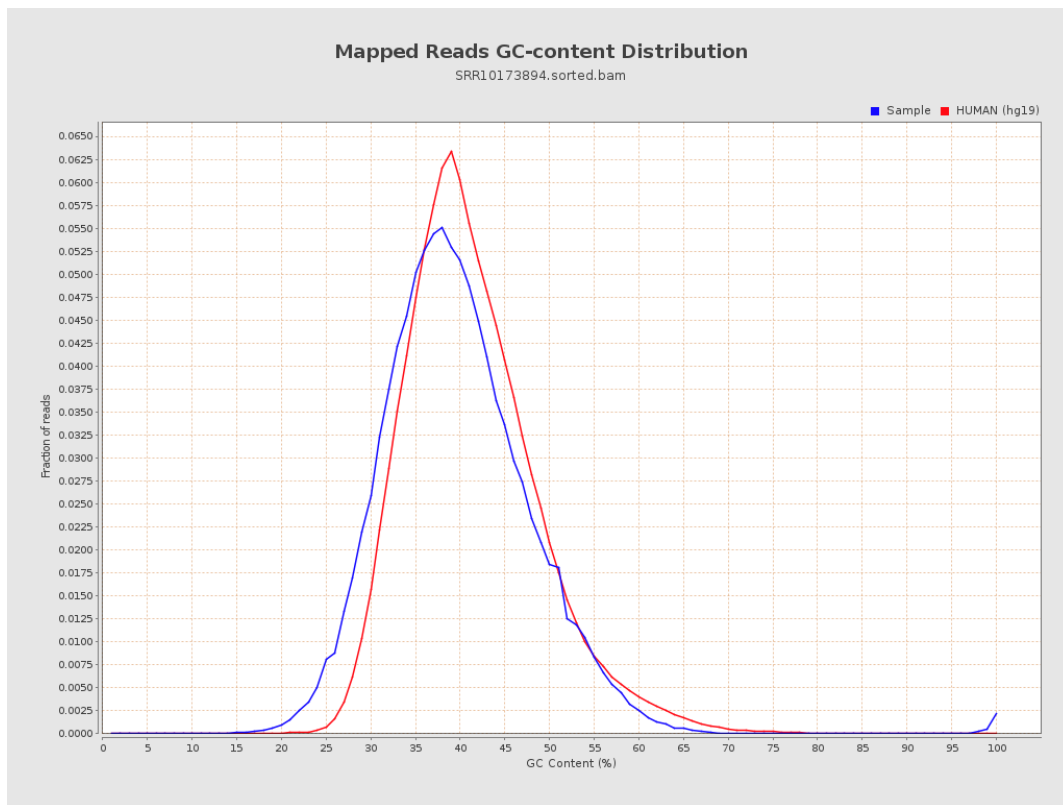
7. Results : Duplication Rate Histogram



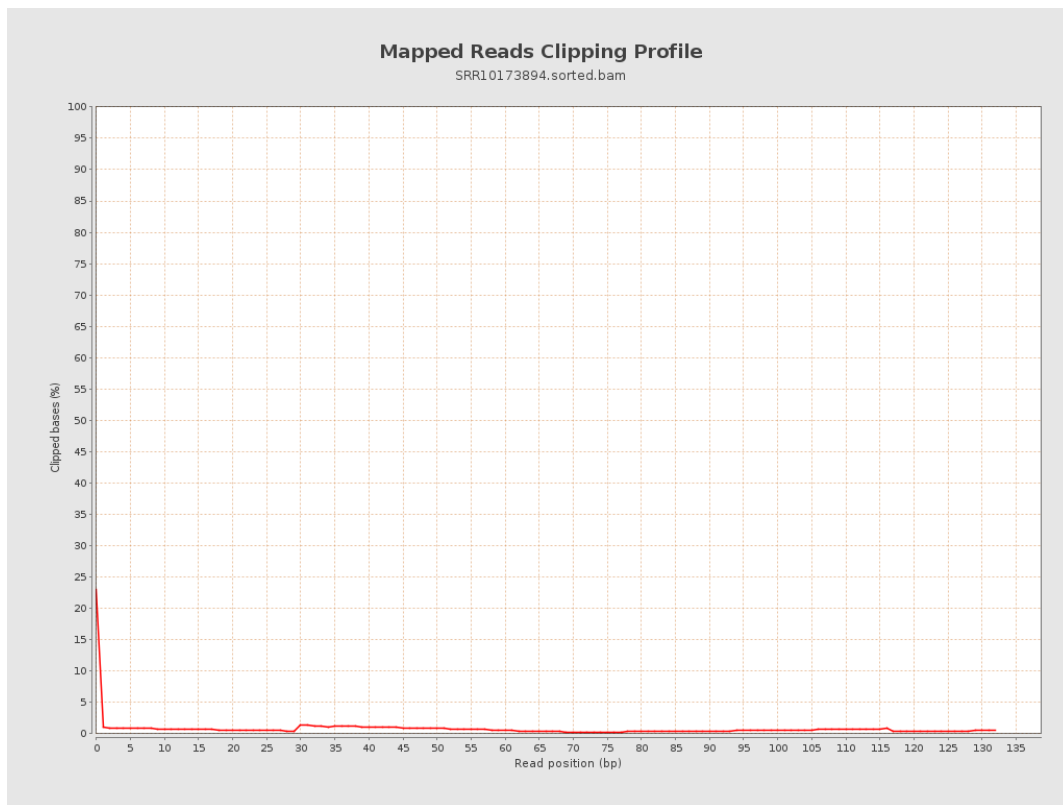
8. Results : Mapped Reads Nucleotide Content



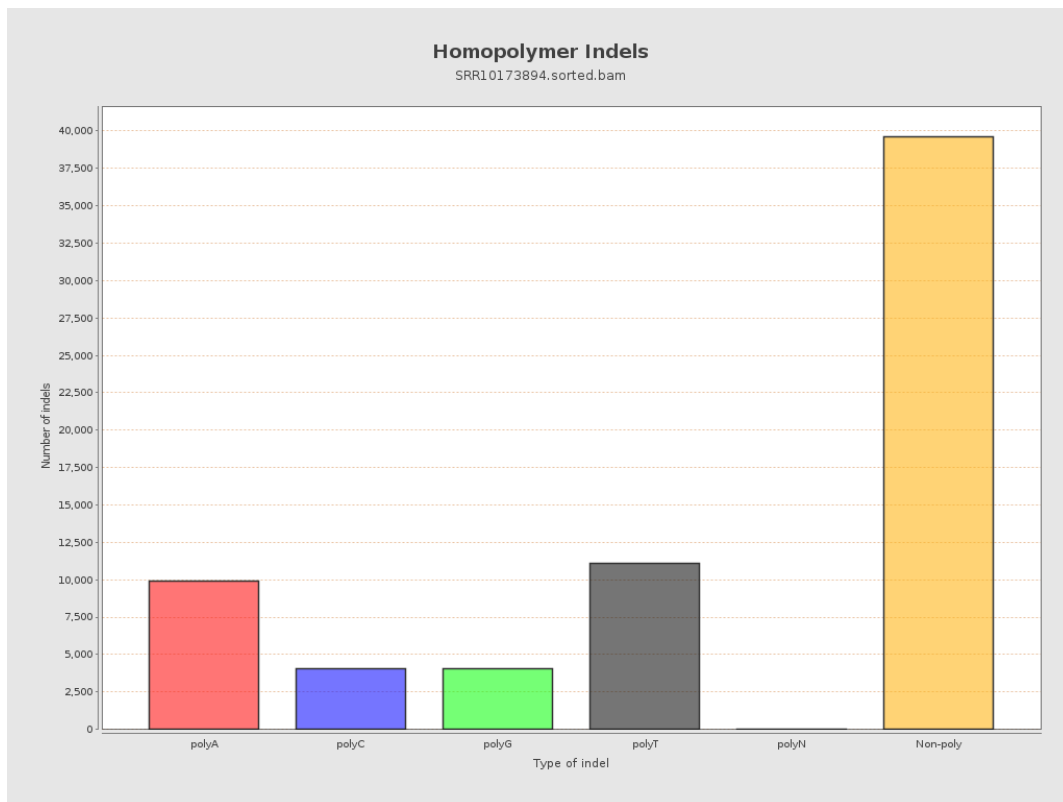
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



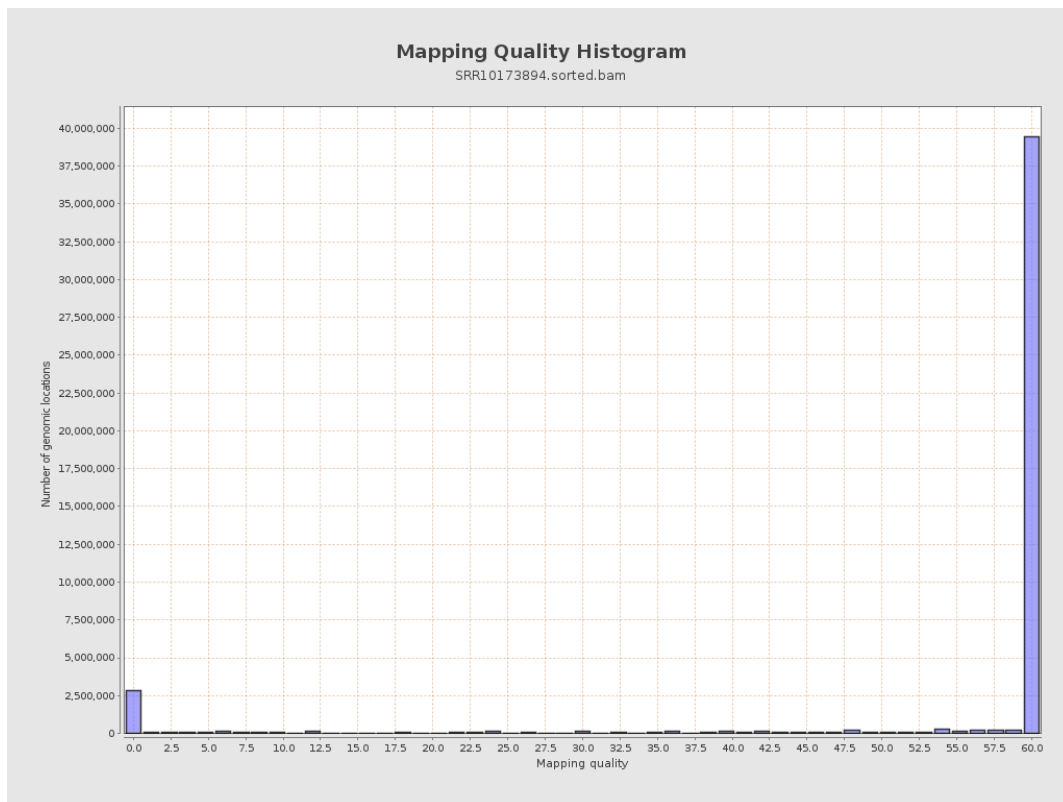
11. Results : Homopolymer Indels



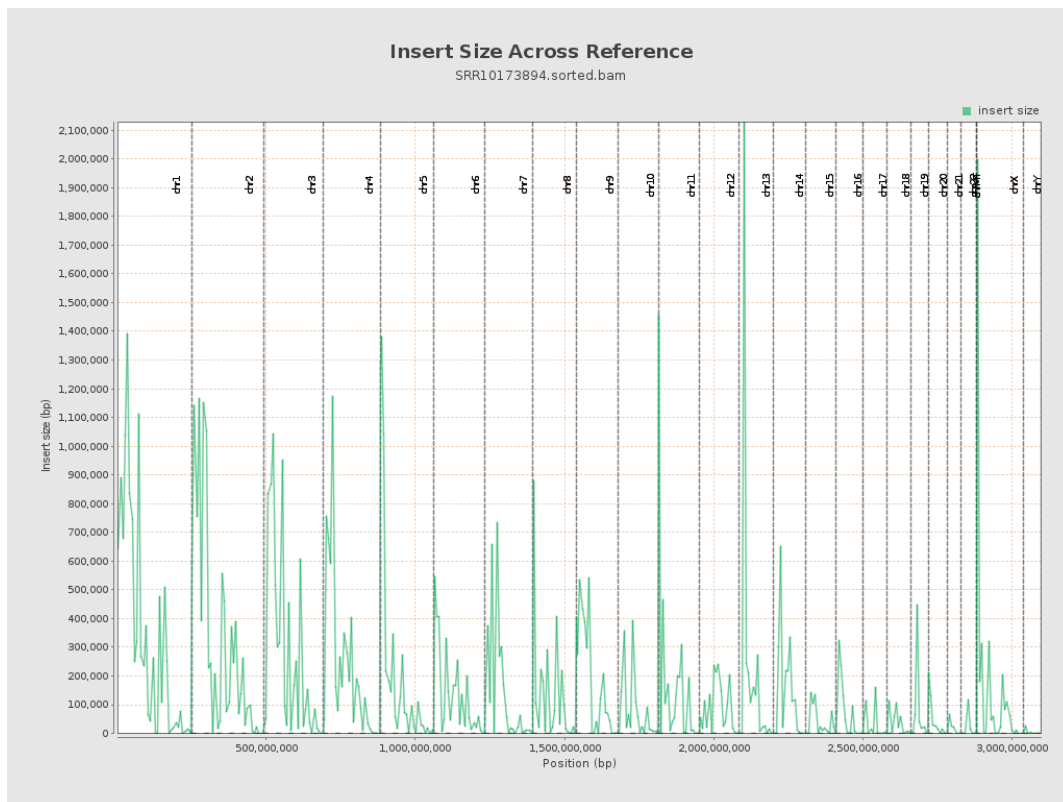
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

