

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 18:26:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173994.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_SRR10173994 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173994_1.fastq.gz SRR10173994_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 18:26:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173994.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,621,850
Mapped reads	3,547,171 / 97.94%
Unmapped reads	74,679 / 2.06%
Mapped paired reads	3,547,171 / 97.94%
Mapped reads, first in pair	1,774,555 / 49%
Mapped reads, second in pair	1,772,616 / 48.94%
Mapped reads, both in pair	3,502,322 / 96.7%
Mapped reads, singletons	44,849 / 1.24%
Secondary alignments	0
Supplementary alignments	455,719 / 12.58%
Read min/max/mean length	30 / 133 / 123.97
Duplicated reads (estimated)	2,780,311 / 76.76%
Duplication rate	62.58%
Clipped reads	1,799,338 / 49.68%

2.2. ACGT Content

Number/percentage of A's	119,779,965 / 30.13%
Number/percentage of C's	78,238,239 / 19.68%
Number/percentage of T's	118,591,122 / 29.83%
Number/percentage of G's	80,897,276 / 20.35%
Number/percentage of N's	2,847 / 0%

GC Percentage	40.03%
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2.3. Coverage

Mean	0.1285
Standard Deviation	2.3235

2.4. Mapping Quality

Mean Mapping Quality	52.65
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2.5. Insert size

Mean	931,558.57
Standard Deviation	8,588,174.16
P25/Median/P75	100 / 142 / 215

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	3,287,630
Insertions	42,062
Mapped reads with at least one insertion	1.14%
Deletions	114,352
Mapped reads with at least one deletion	3.15%
Homopolymer indels	40.57%

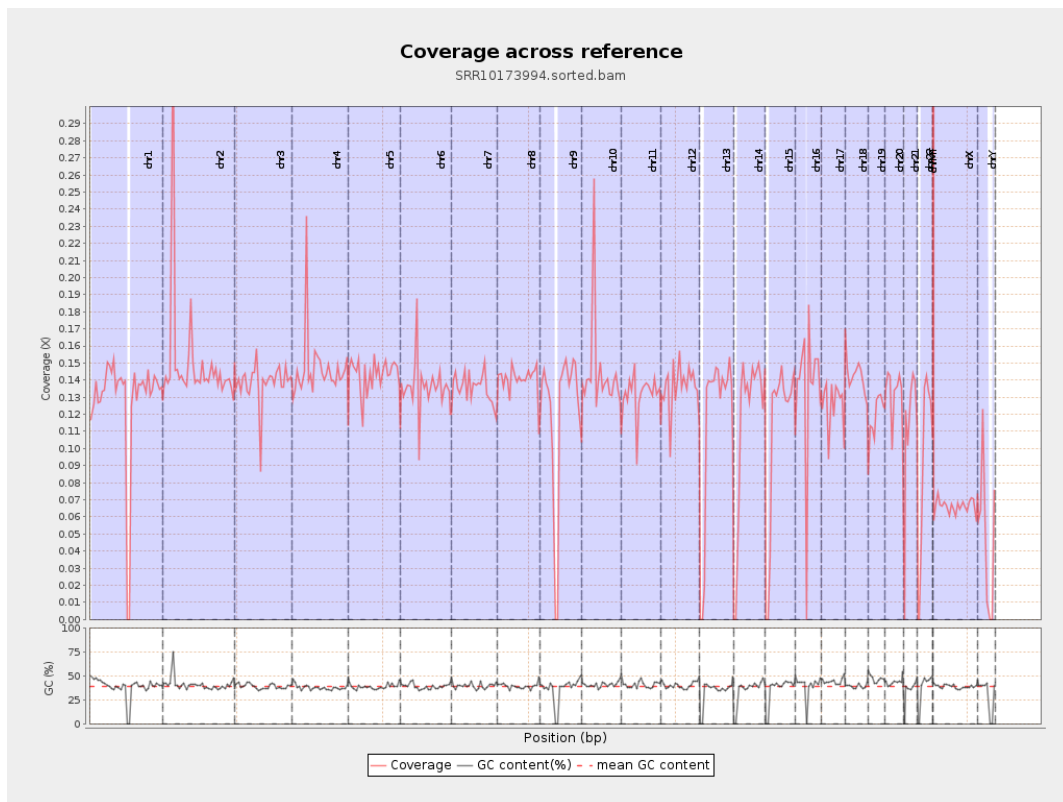
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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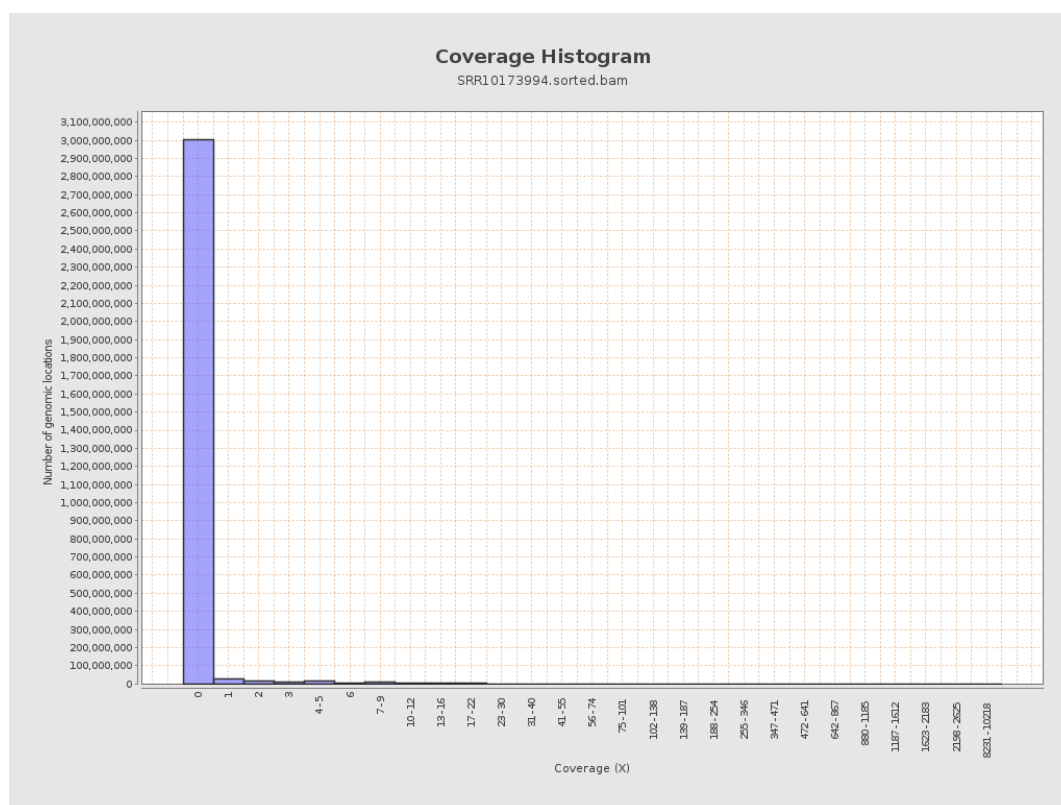
		bases	coverage	deviation
chr1	249250621	31938510	0.1281	1.2625
chr2	243199373	36394556	0.1496	7.1857
chr3	198022430	27454441	0.1386	1.1298
chr4	191154276	28048774	0.1467	1.365
chr5	180915260	25863948	0.143	1.1532
chr6	171115067	23335432	0.1364	1.2017
chr7	159138663	21529332	0.1353	1.2682
chr8	146364022	20531745	0.1403	1.462
chr9	141213431	17165812	0.1216	1.2071
chr10	135534747	19474283	0.1437	1.5623
chr11	135006516	17781755	0.1317	1.1118
chr12	133851895	18285530	0.1366	1.1494
chr13	115169878	13400129	0.1164	1.0366
chr14	107349540	12525396	0.1167	1.0318
chr15	102531392	11150313	0.1088	0.9922
chr16	90354753	12110856	0.134	1.2545
chr17	81195210	10254444	0.1263	1.0934
chr18	78077248	11097779	0.1421	1.5772
chr19	59128983	7057346	0.1194	1.0868
chr20	63025520	8350582	0.1325	1.1113
chr21	48129895	5518826	0.1147	1.2031
chr22	51304566	4753773	0.0927	0.9941
chrMT	16571	571374	34.4804	32.3875
chrX	155270560	10279598	0.0662	0.7645

chrY	59373566	2906166	0.0489	0.8471
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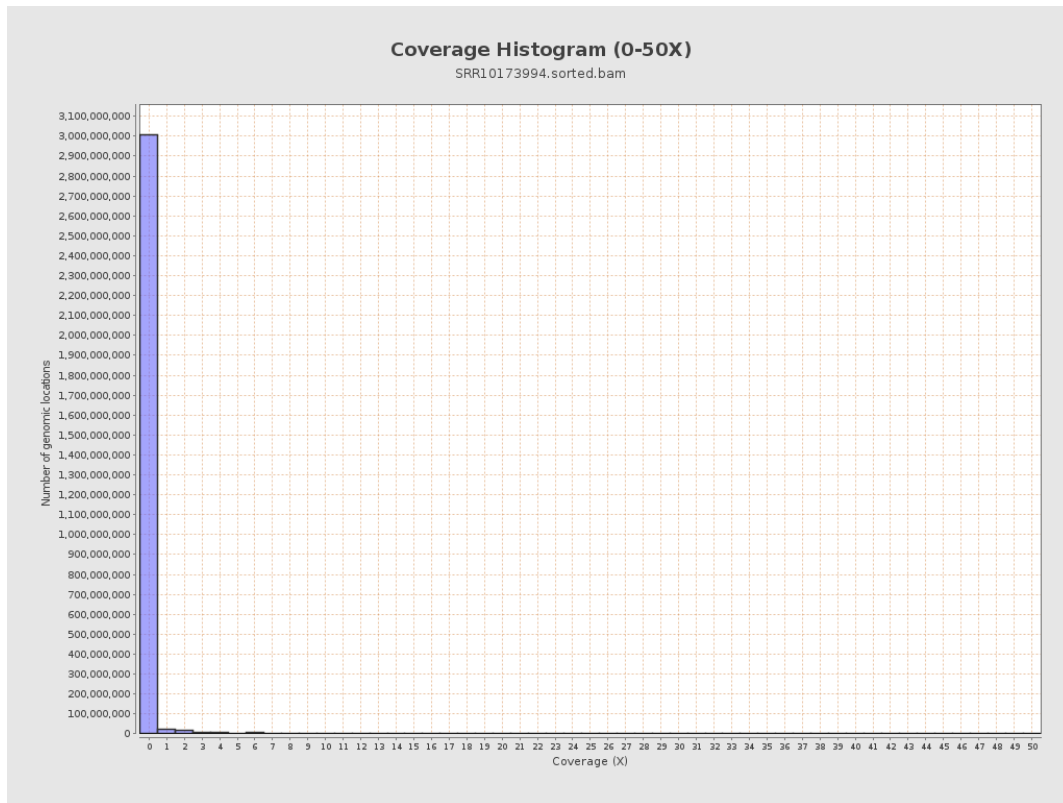
3. Results : Coverage across reference



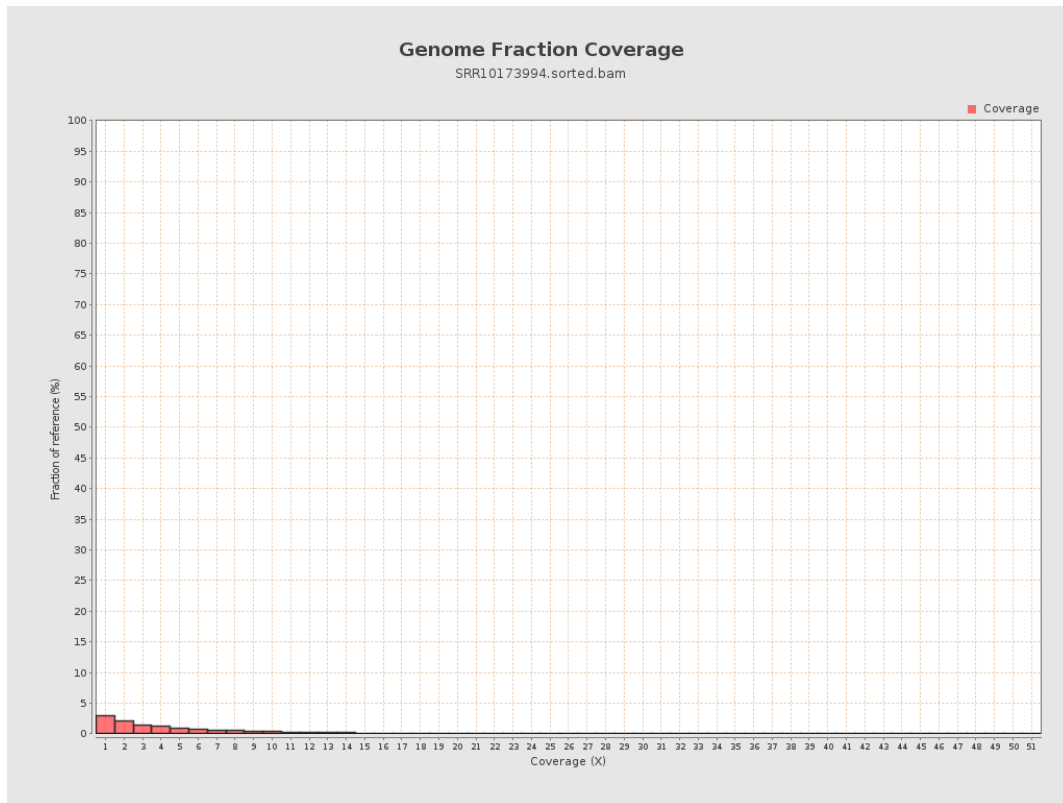
4. Results : Coverage Histogram



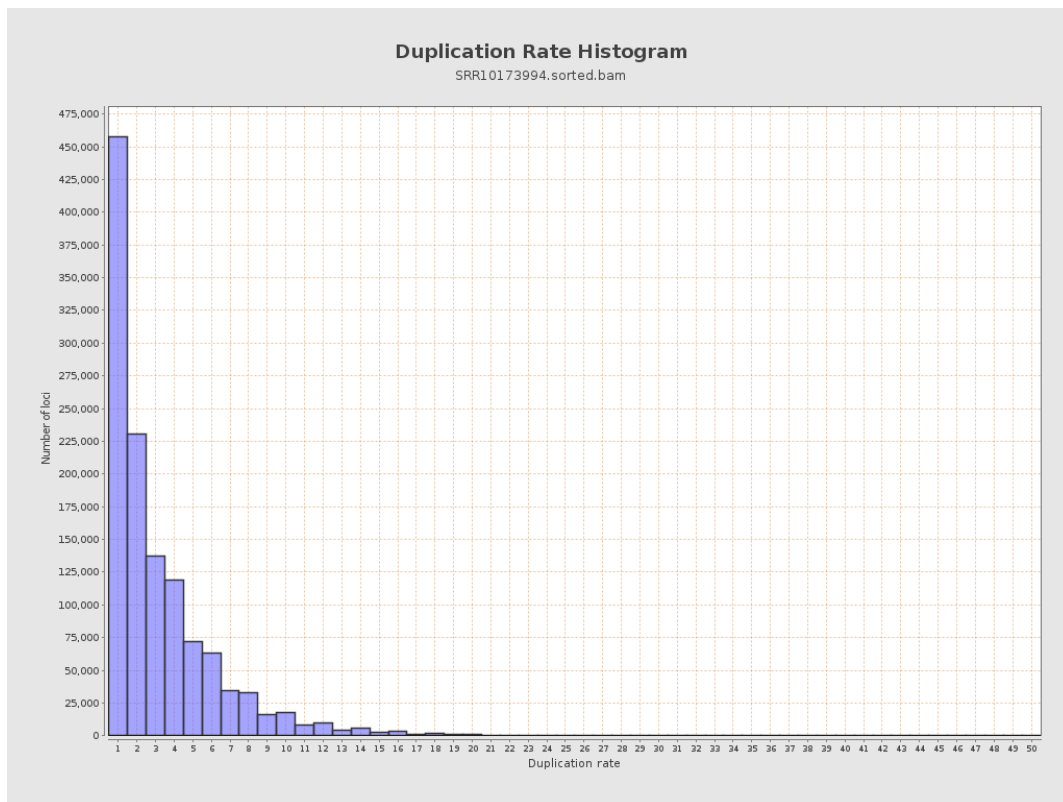
5. Results : Coverage Histogram (0-50X)



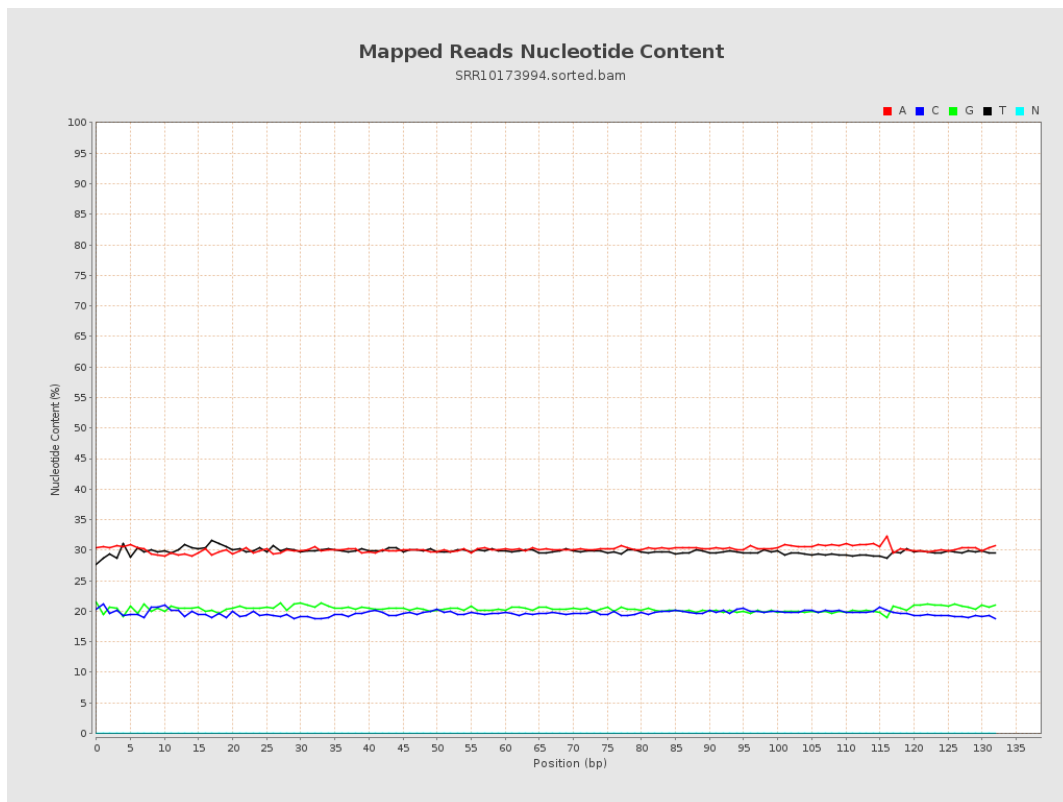
6. Results : Genome Fraction Coverage



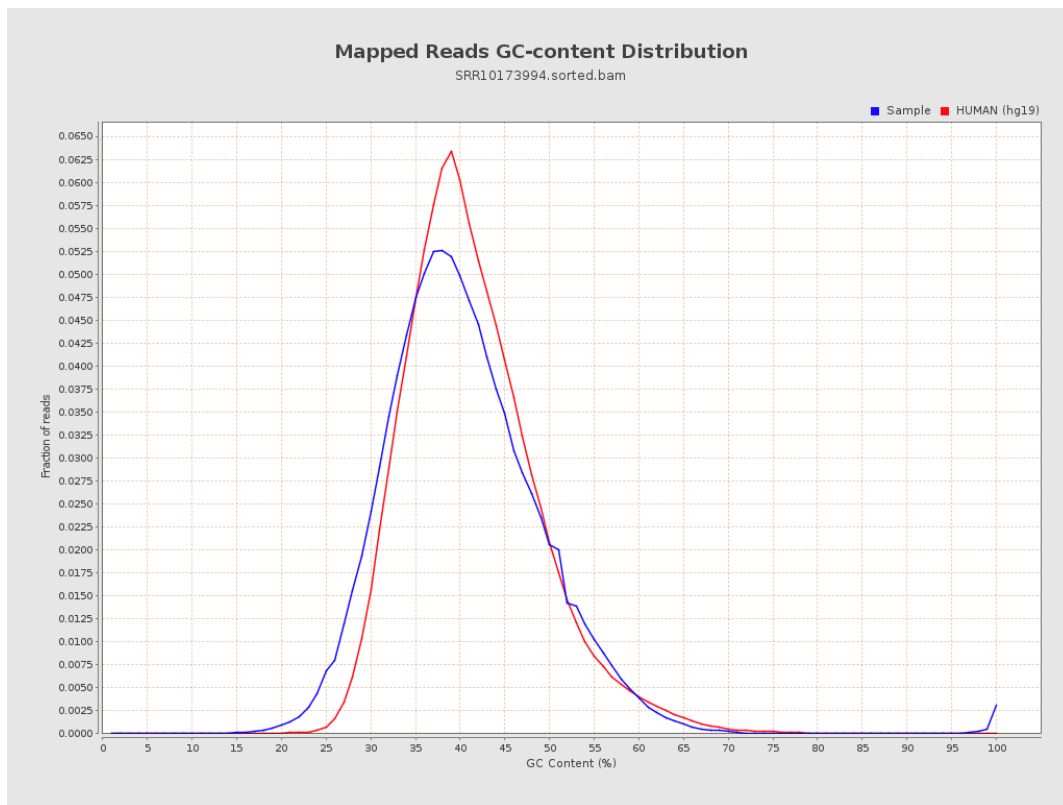
7. Results : Duplication Rate Histogram



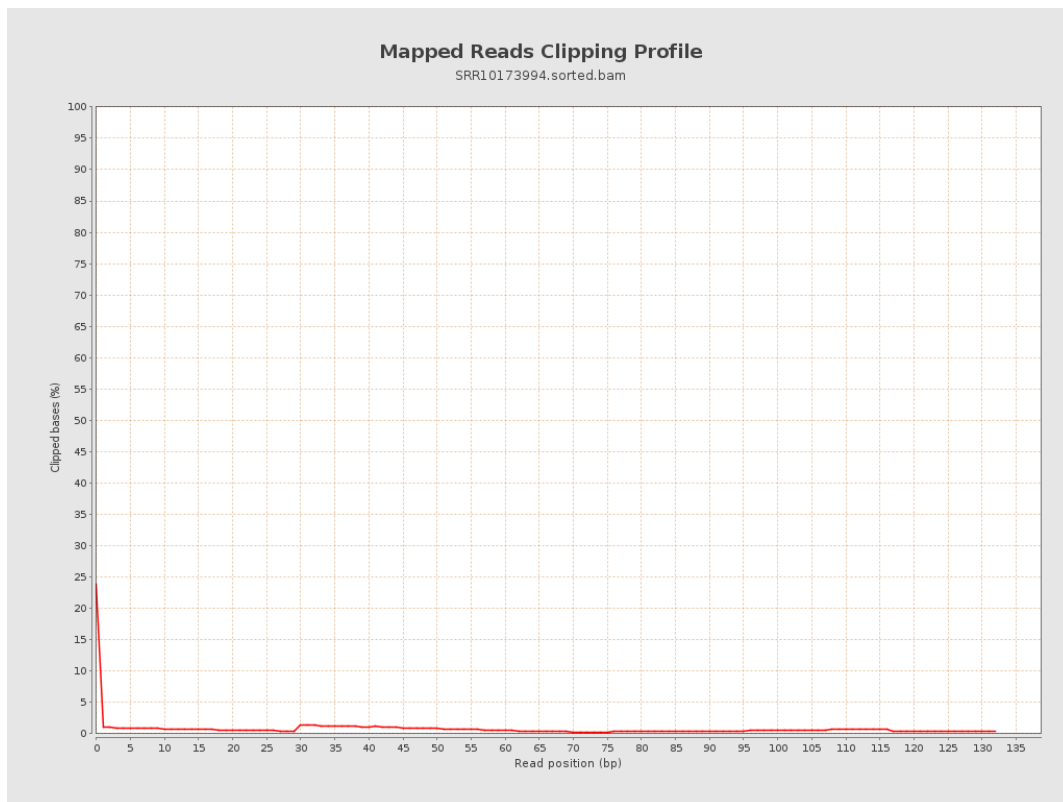
8. Results : Mapped Reads Nucleotide Content



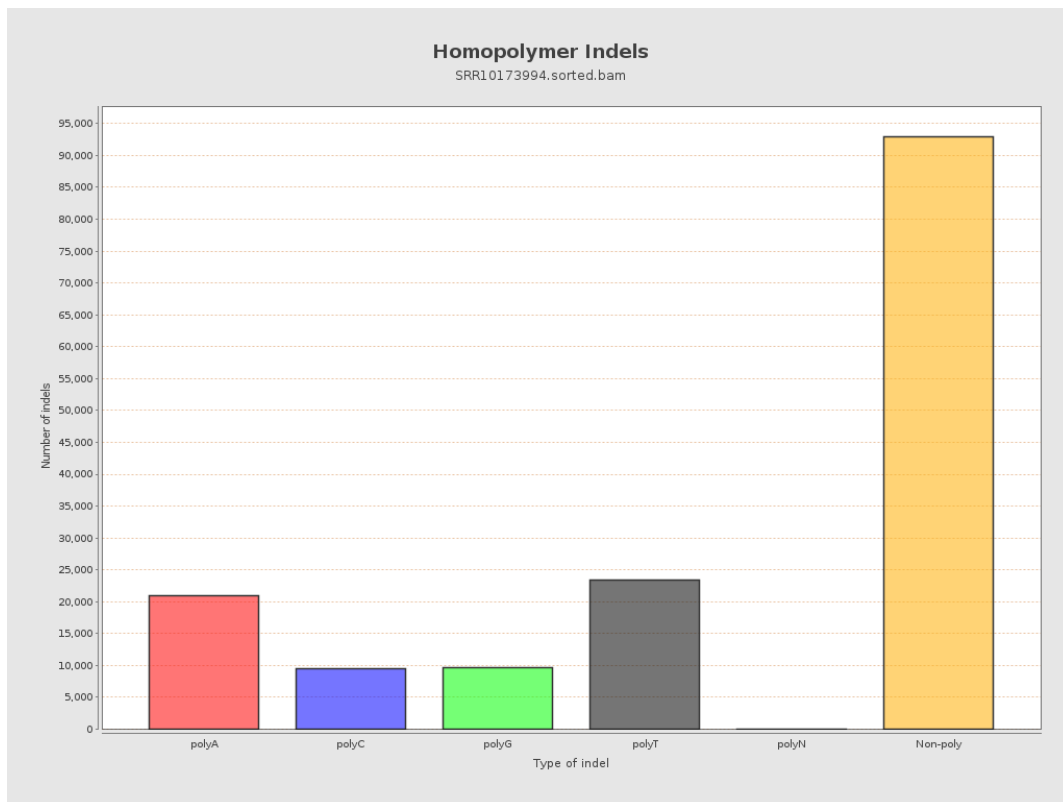
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



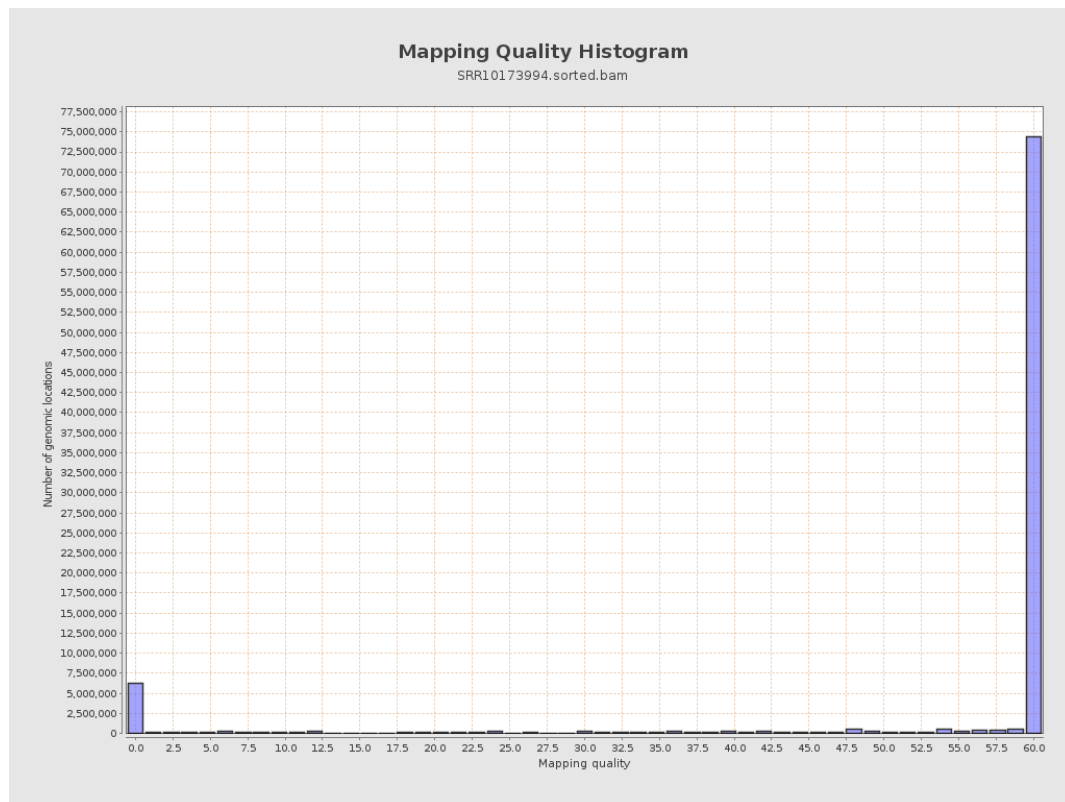
11. Results : Homopolymer Indels



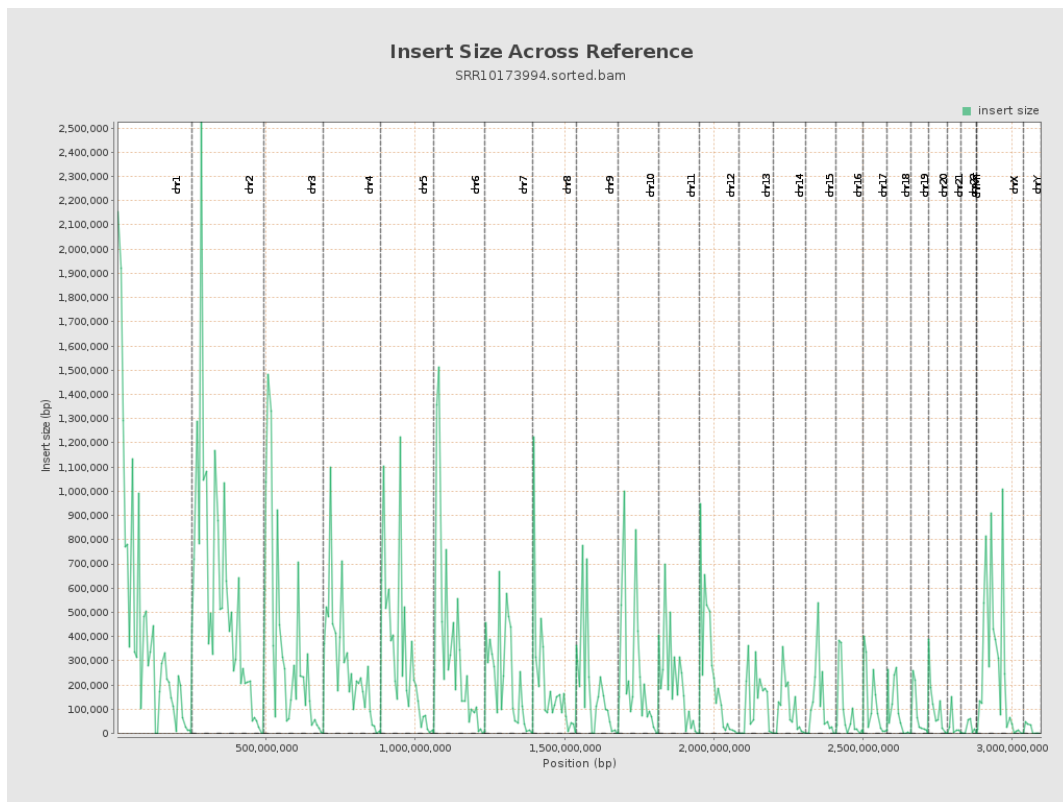
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

