

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:56:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472414.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_SRR3472414 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472414_1.fastq.gz SRR3472414_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:56:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472414.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,256,516
Mapped reads	18,100,468 / 99.15%
Unmapped reads	156,048 / 0.85%
Mapped paired reads	18,100,468 / 99.15%
Mapped reads, first in pair	9,082,260 / 49.75%
Mapped reads, second in pair	9,018,208 / 49.4%
Mapped reads, both in pair	17,998,378 / 98.59%
Mapped reads, singletons	102,090 / 0.56%
Secondary alignments	0
Supplementary alignments	71,951 / 0.39%
Read min/max/mean length	30 / 100 / 99.45
Duplicated reads (estimated)	11,626,725 / 63.69%
Duplication rate	47.1%
Clipped reads	1,260,814 / 6.91%

2.2. ACGT Content

Number/percentage of A's	478,547,873 / 26.95%
Number/percentage of C's	410,109,710 / 23.09%
Number/percentage of T's	479,966,501 / 27.03%
Number/percentage of G's	407,002,351 / 22.92%
Number/percentage of N's	217,457 / 0.01%

GC Percentage	46.01%
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2.3. Coverage

Mean	0.5737
Standard Deviation	19.4546

2.4. Mapping Quality

Mean Mapping Quality	55.16
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2.5. Insert size

Mean	19,713.1
Standard Deviation	1,443,213.26
P25/Median/P75	159 / 222 / 298

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	9,935,851
Insertions	104,333
Mapped reads with at least one insertion	0.57%
Deletions	87,929
Mapped reads with at least one deletion	0.48%
Homopolymer indels	46.47%

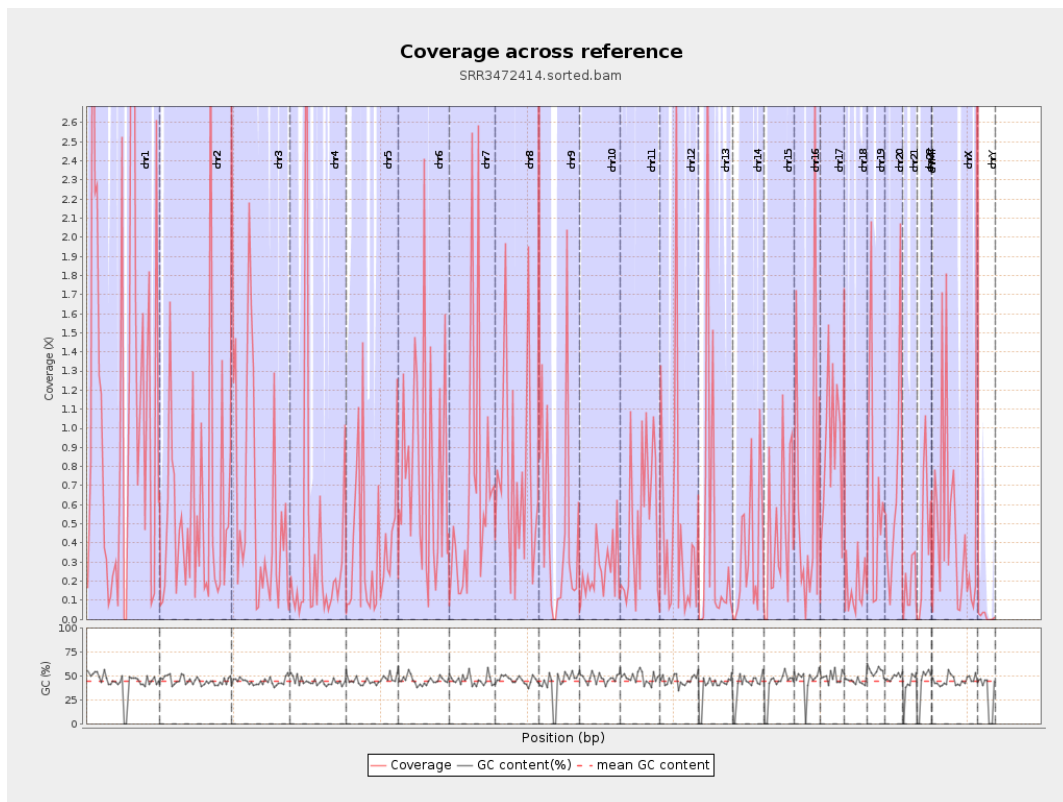
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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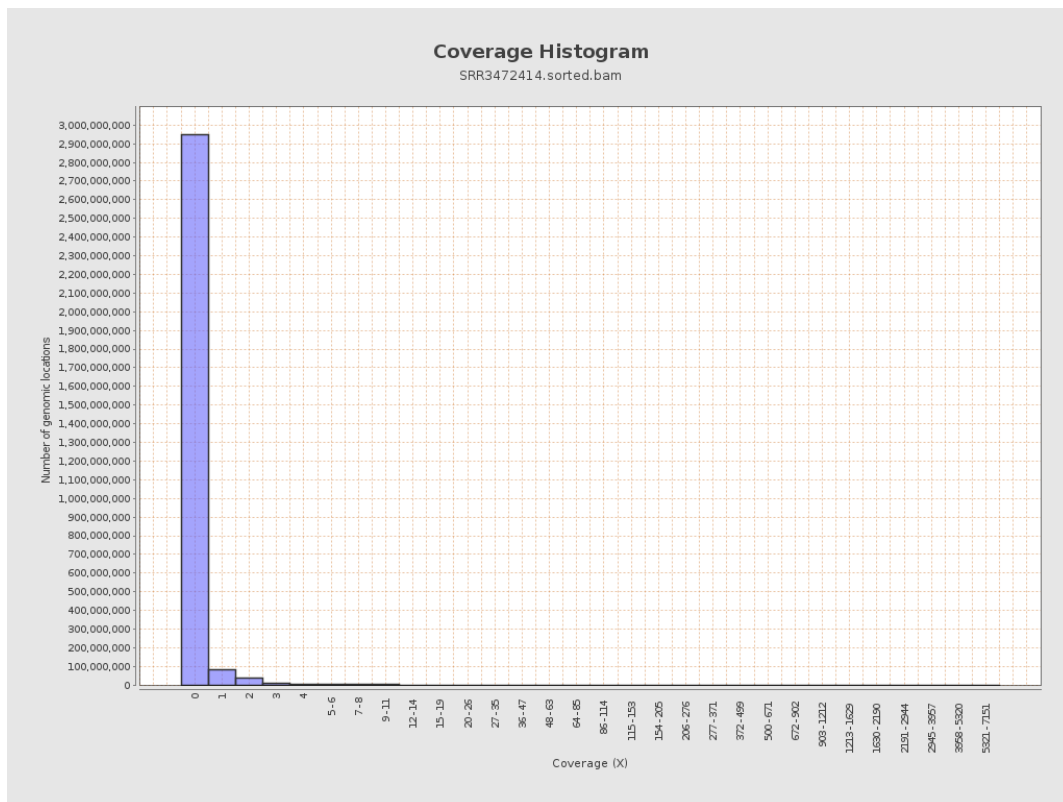
		bases	coverage	deviation
chr1	249250621	298949192	1.1994	33.8987
chr2	243199373	136625321	0.5618	19.8425
chr3	198022430	126139869	0.637	14.2471
chr4	191154276	68091067	0.3562	19.5713
chr5	180915260	70952811	0.3922	11.9192
chr6	171115067	134118340	0.7838	21.4
chr7	159138663	105496883	0.6629	25.474
chr8	146364022	112696803	0.77	24.2272
chr9	141213431	69093705	0.4893	13.9007
chr10	135534747	34651828	0.2557	7.788
chr11	135006516	69751264	0.5167	17.5043
chr12	133851895	65133744	0.4866	20.1599
chr13	115169878	50546962	0.4389	18.9218
chr14	107349540	35348998	0.3293	9.5976
chr15	102531392	48165439	0.4698	17.6051
chr16	90354753	62492218	0.6916	19.2241
chr17	81195210	76599742	0.9434	19.8
chr18	78077248	13350700	0.171	5.3133
chr19	59128983	43008311	0.7274	16.1507
chr20	63025520	41518574	0.6588	20.4304
chr21	48129895	8807425	0.183	7.2132
chr22	51304566	22670746	0.4419	12.6177
chrMT	16571	11152	0.673	1.2198
chrX	155270560	80898107	0.521	17.6938

chrY	59373566	934067	0.0157	0.4436
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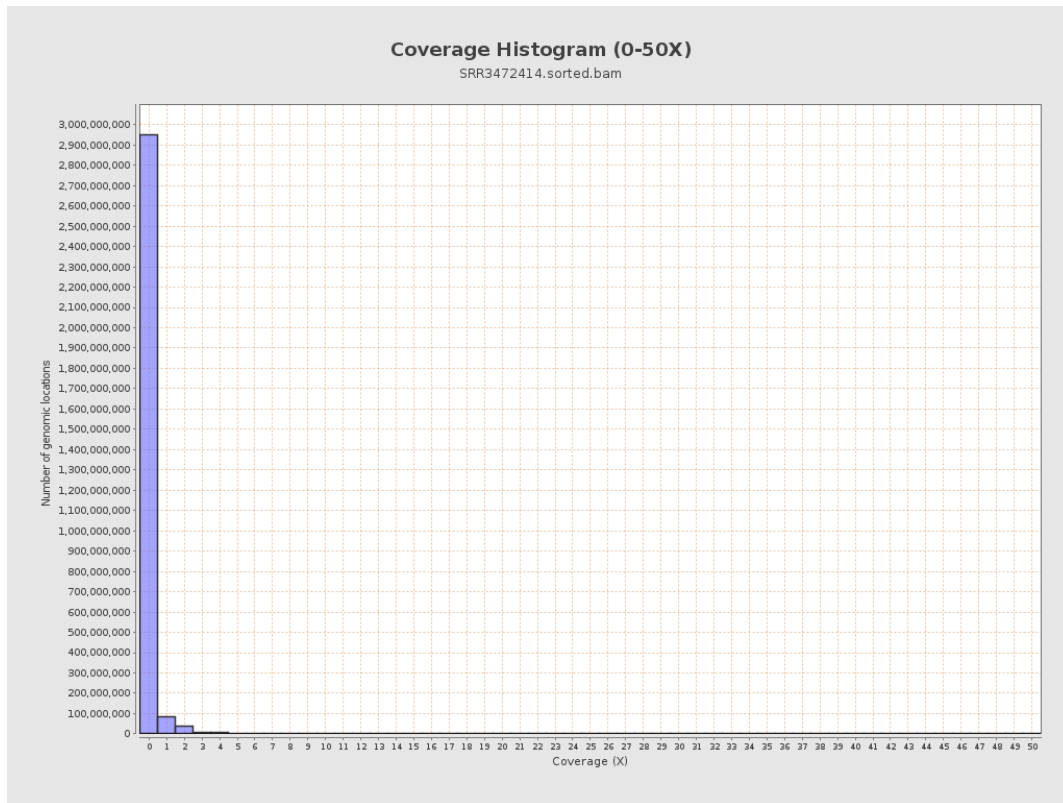
3. Results : Coverage across reference



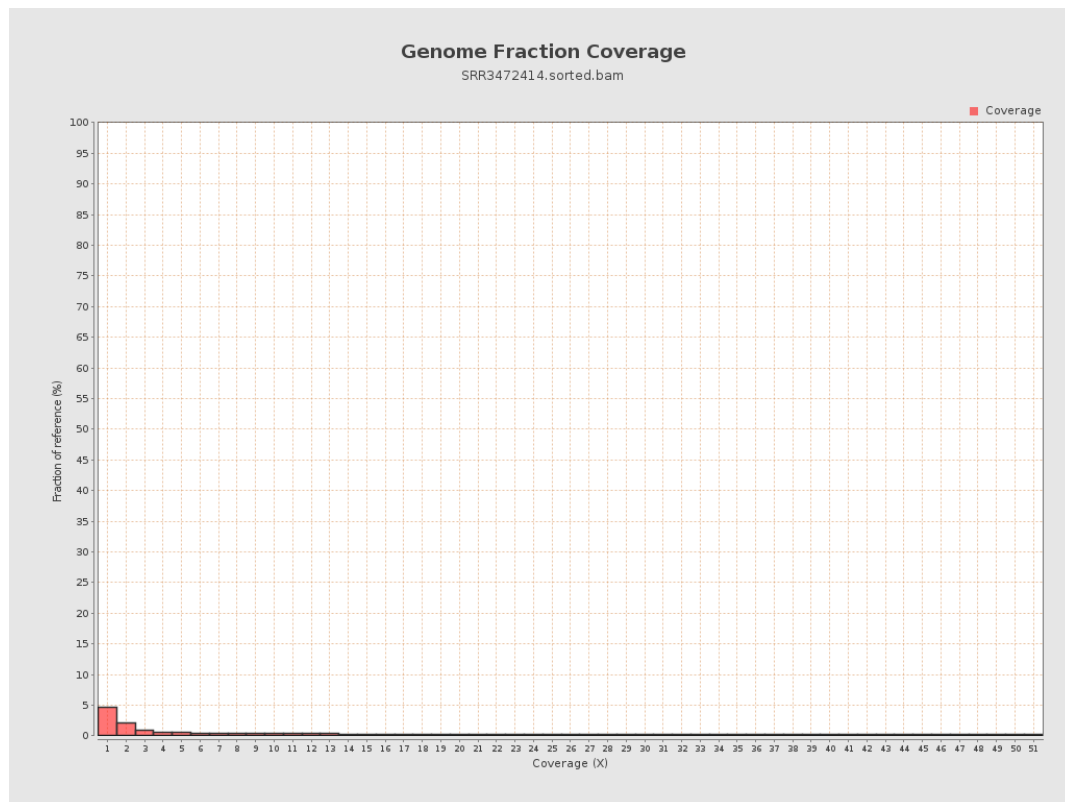
4. Results : Coverage Histogram



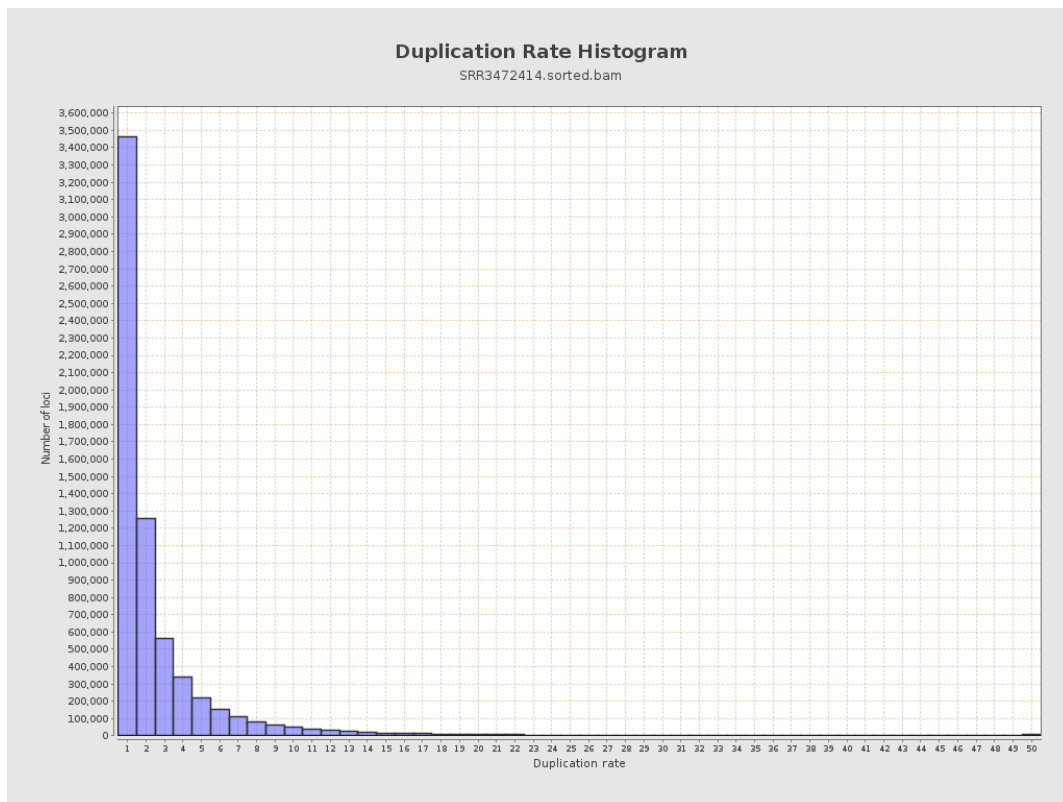
5. Results : Coverage Histogram (0-50X)



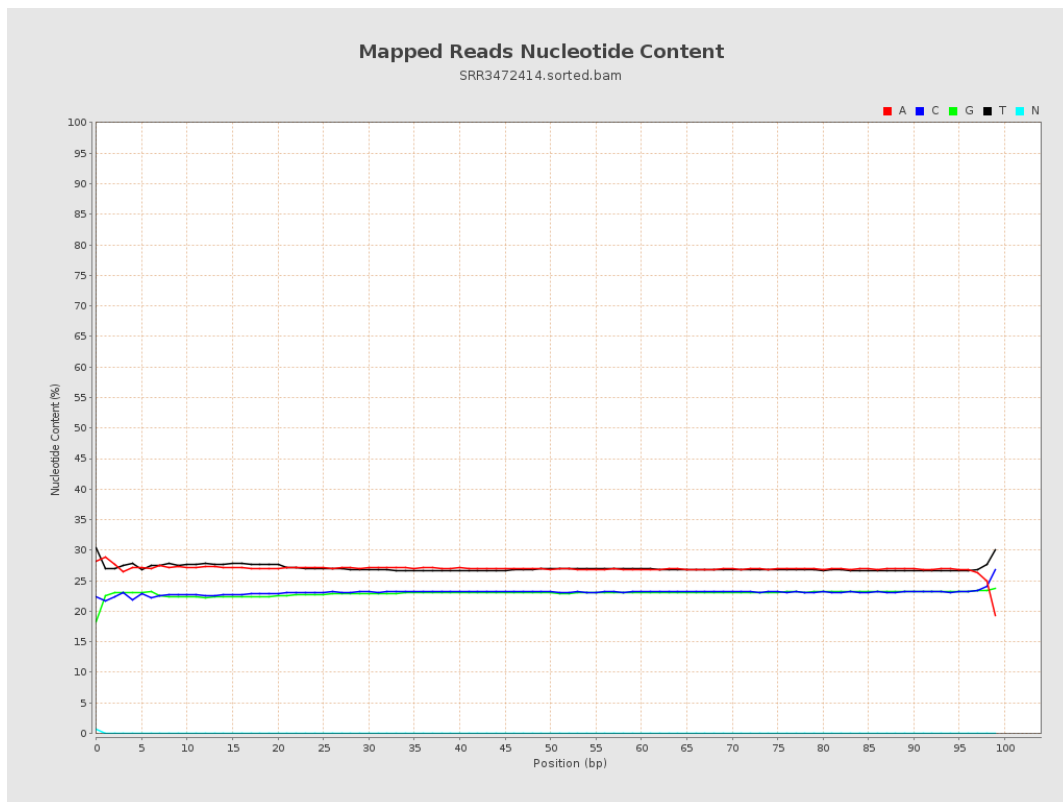
6. Results : Genome Fraction Coverage



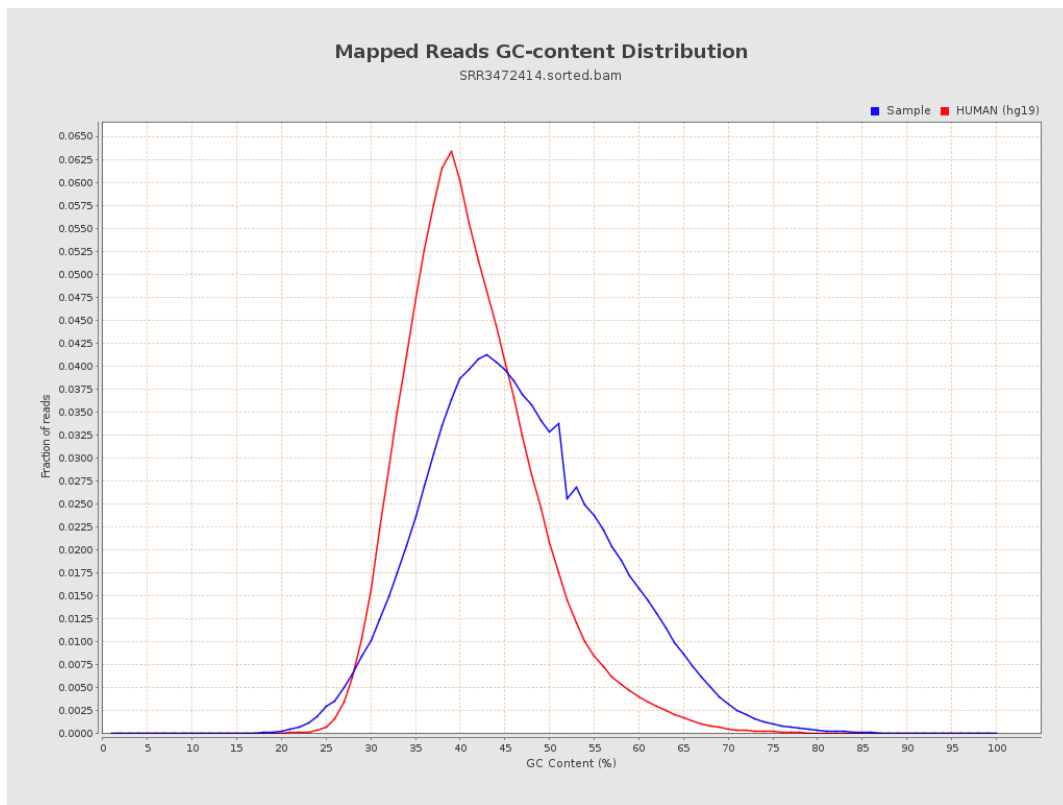
7. Results : Duplication Rate Histogram



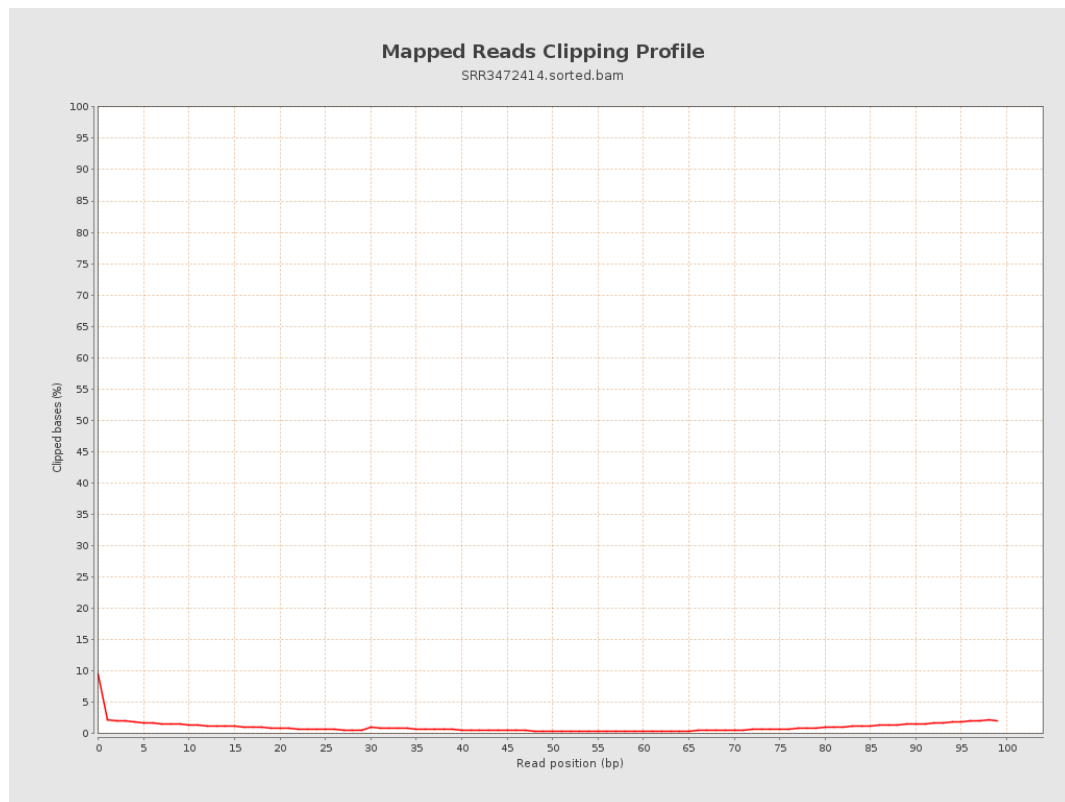
8. Results : Mapped Reads Nucleotide Content



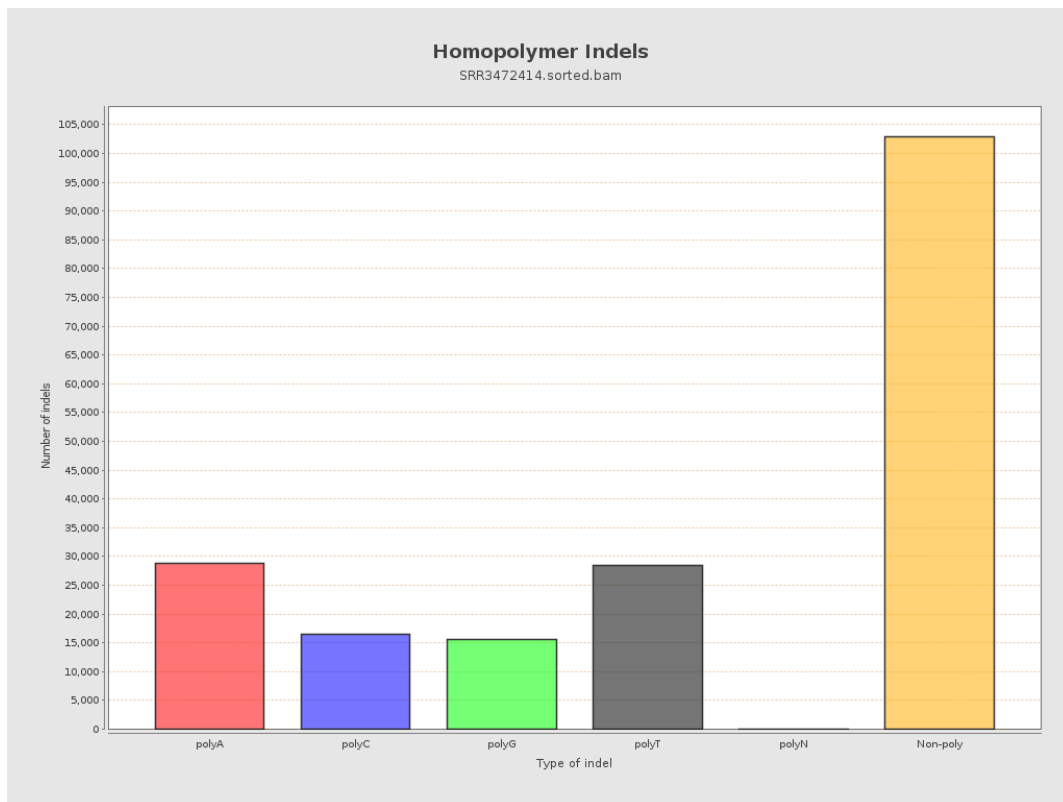
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



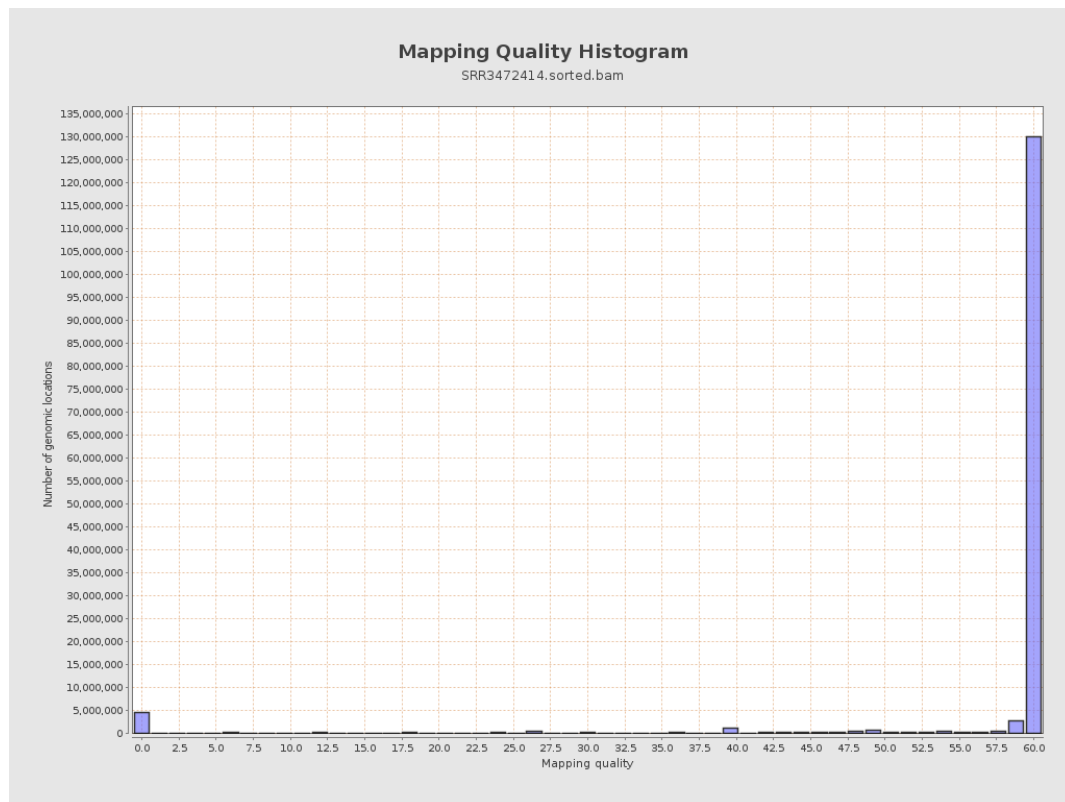
11. Results : Homopolymer Indels



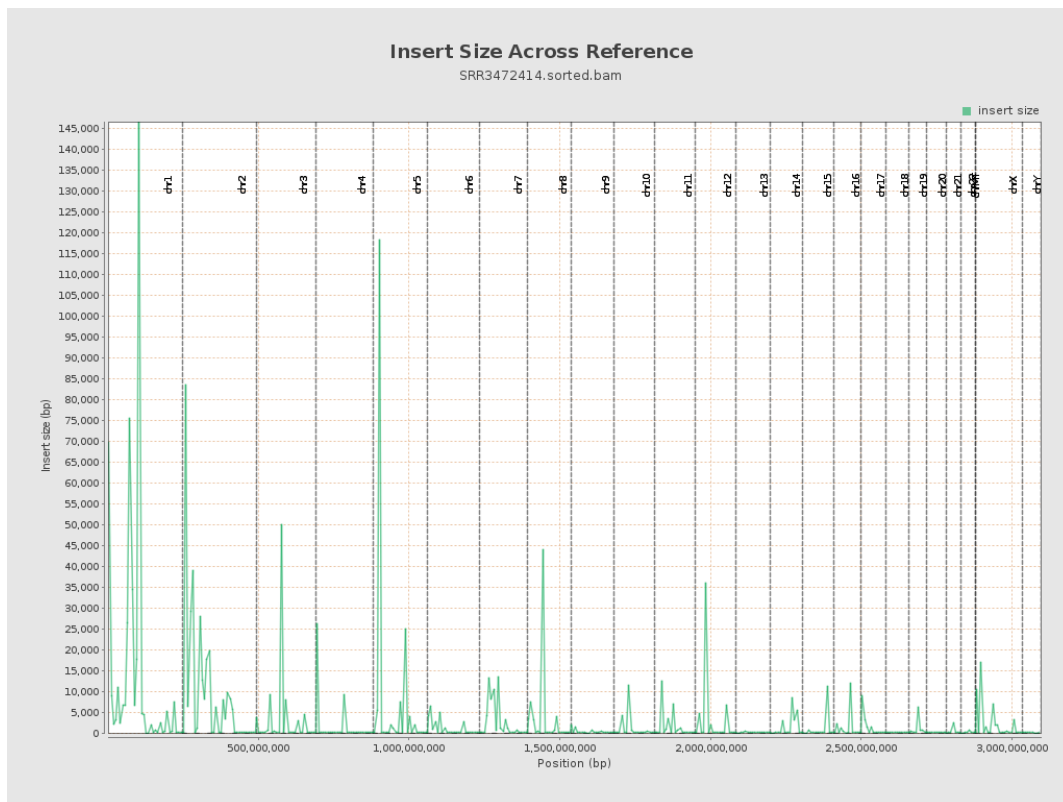
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

