

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:48:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472496.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_SRR3472496 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472496_1.fastq.gz SRR3472496_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:48:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472496.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,700,968
Mapped reads	20,449,760 / 98.79%
Unmapped reads	251,208 / 1.21%
Mapped paired reads	20,449,760 / 98.79%
Mapped reads, first in pair	10,254,771 / 49.54%
Mapped reads, second in pair	10,194,989 / 49.25%
Mapped reads, both in pair	20,324,882 / 98.18%
Mapped reads, singletons	124,878 / 0.6%
Secondary alignments	0
Supplementary alignments	69,790 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	13,290,181 / 64.2%
Duplication rate	46.87%
Clipped reads	1,773,384 / 8.57%

2.2. ACGT Content

Number/percentage of A's	550,981,020 / 27.42%
Number/percentage of C's	457,508,800 / 22.77%
Number/percentage of T's	546,792,478 / 27.21%
Number/percentage of G's	453,969,957 / 22.59%
Number/percentage of N's	310,936 / 0.02%

GC Percentage	45.36%
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2.3. Coverage

Mean	0.6492
Standard Deviation	23.21

2.4. Mapping Quality

Mean Mapping Quality	55.14
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2.5. Insert size

Mean	27,852.55
Standard Deviation	1,655,912.8
P25/Median/P75	167 / 236 / 319

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	12,160,532
Insertions	109,082
Mapped reads with at least one insertion	0.53%
Deletions	102,795
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.13%

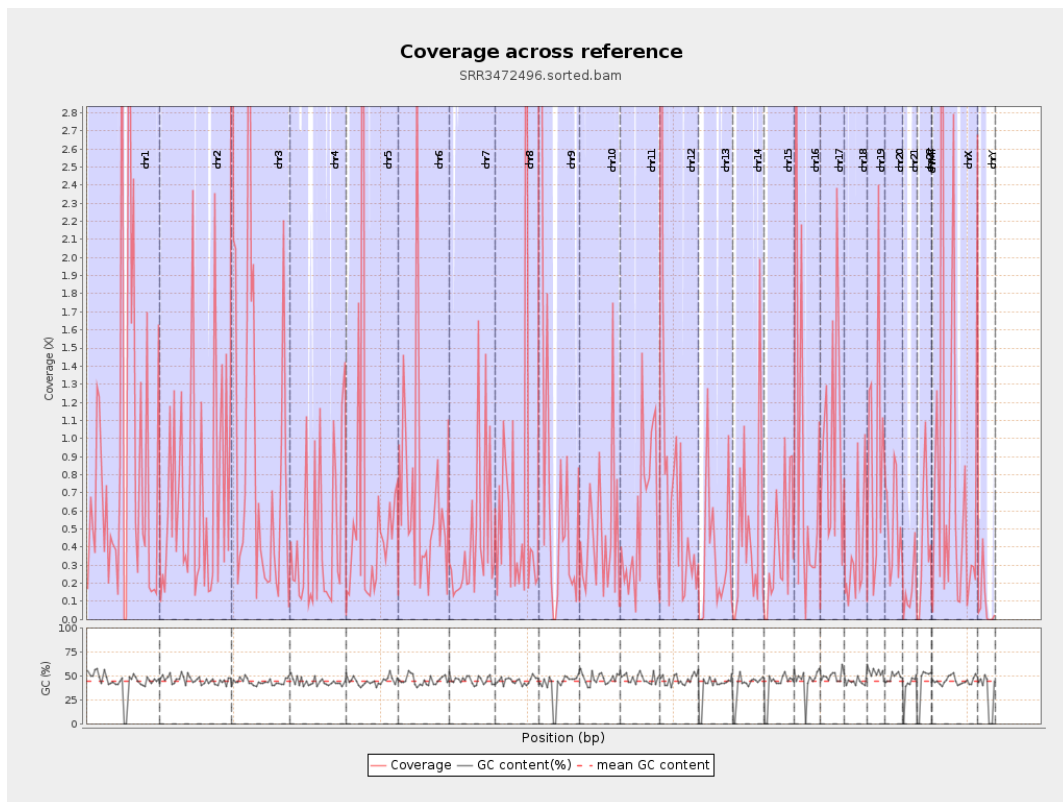
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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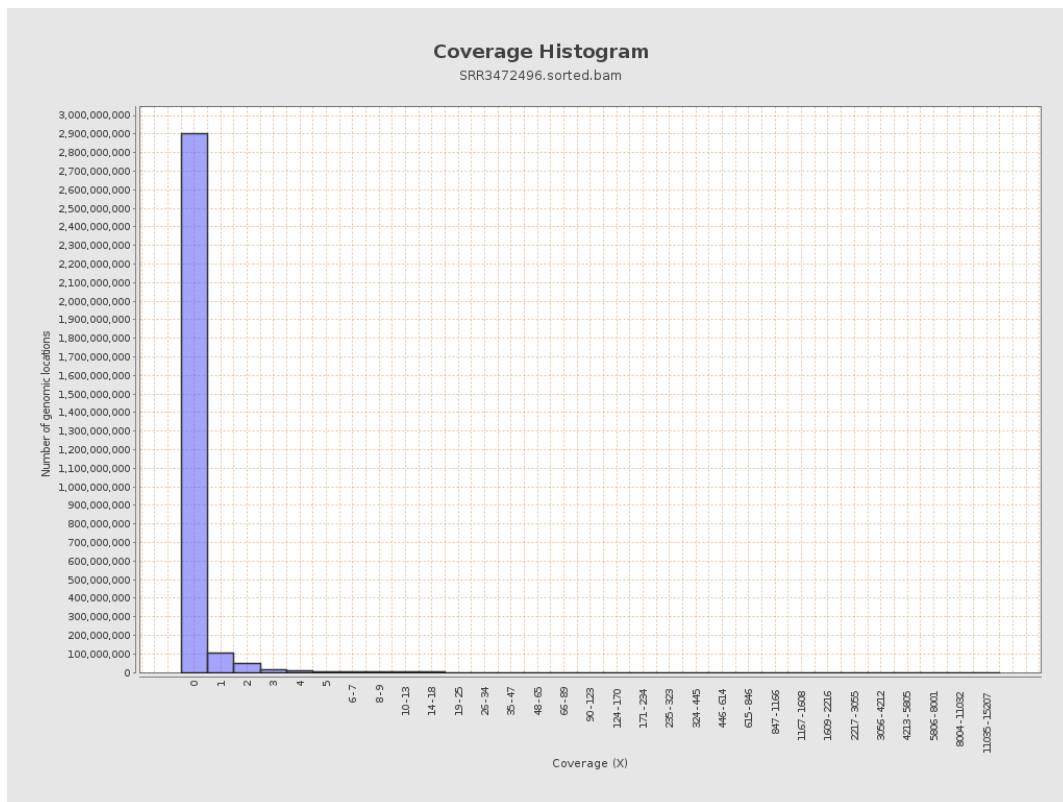
		bases	coverage	deviation
chr1	249250621	216811746	0.8699	30.6393
chr2	243199373	167071306	0.687	22.2221
chr3	198022430	200433628	1.0122	21.7049
chr4	191154276	85625771	0.4479	15.0642
chr5	180915260	116984975	0.6466	20.0663
chr6	171115067	115878926	0.6772	19.7867
chr7	159138663	70090101	0.4404	15.0828
chr8	146364022	99987963	0.6831	31.6326
chr9	141213431	109970953	0.7788	20.5751
chr10	135534747	65143935	0.4806	20.4533
chr11	135006516	76800038	0.5689	22.7414
chr12	133851895	114807895	0.8577	36.5742
chr13	115169878	43003999	0.3734	13.8805
chr14	107349540	48763935	0.4543	18.978
chr15	102531392	40650058	0.3965	11.3464
chr16	90354753	76387531	0.8454	33.8563
chr17	81195210	79369490	0.9775	24.1442
chr18	78077248	30727849	0.3936	13.6455
chr19	59128983	56905444	0.9624	44.5494
chr20	63025520	33468707	0.531	14.1207
chr21	48129895	7996607	0.1661	6.4782
chr22	51304566	21863097	0.4261	11.9452
chrMT	16571	2048	0.1236	0.4126
chrX	155270560	125554033	0.8086	26.4876

chrY	59373566	5520232	0.093	4.538
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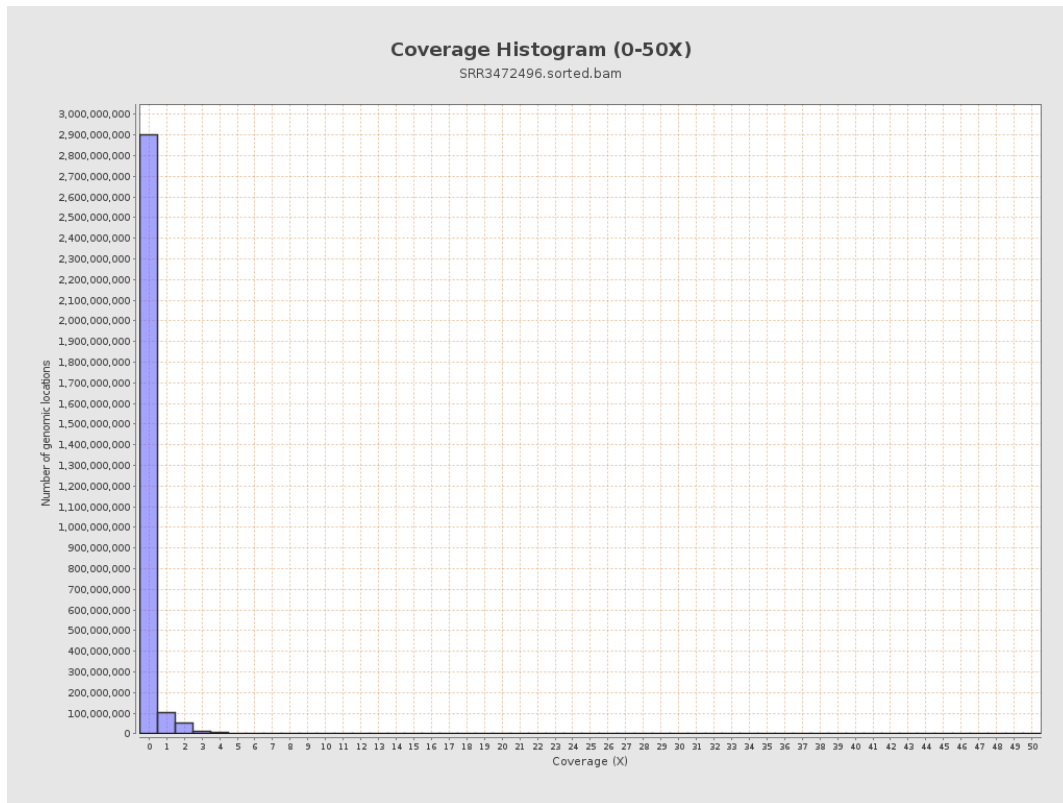
3. Results : Coverage across reference



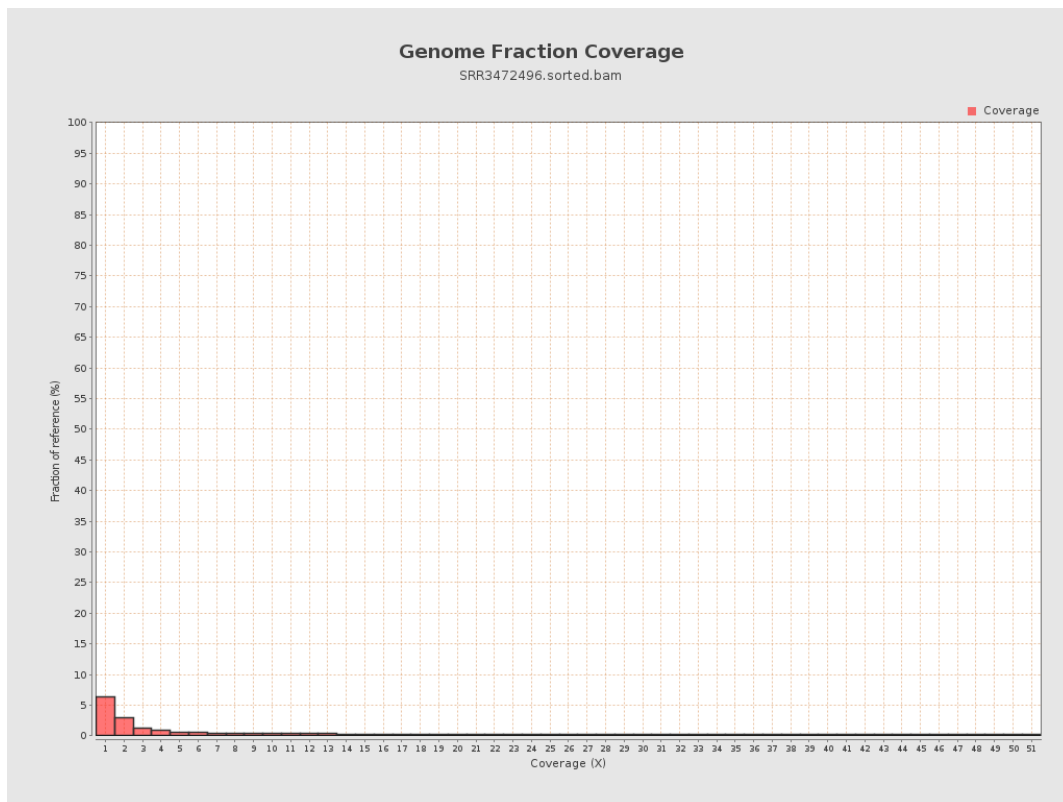
4. Results : Coverage Histogram



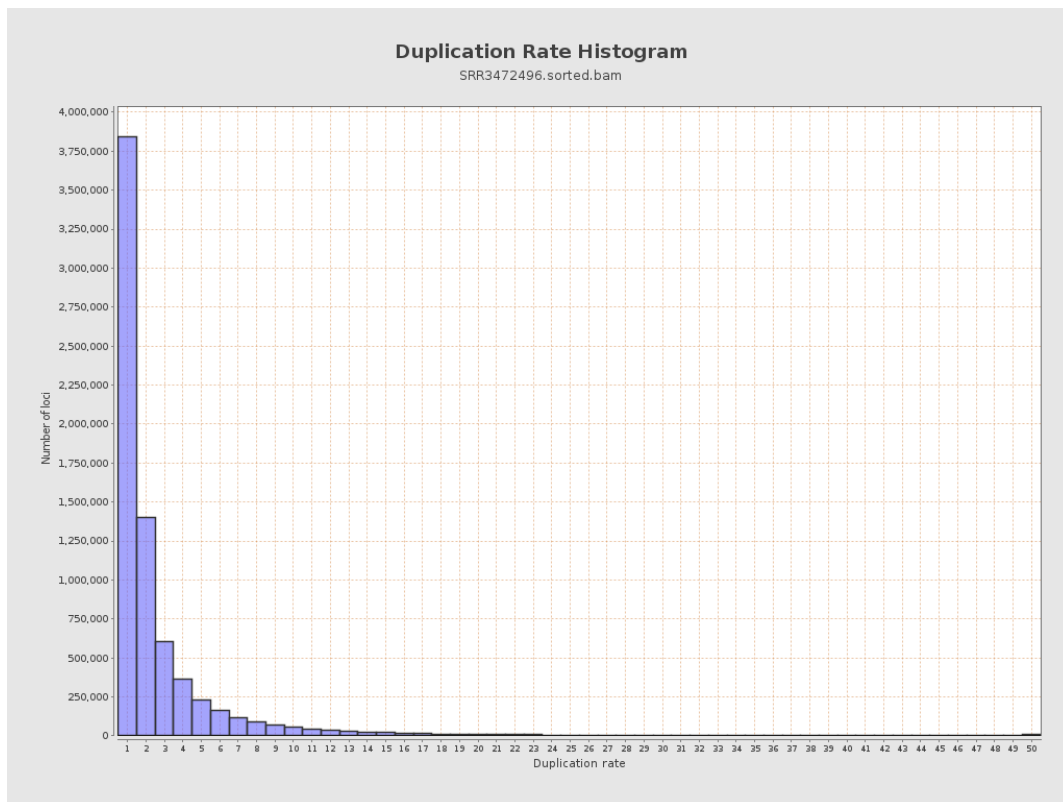
5. Results : Coverage Histogram (0-50X)



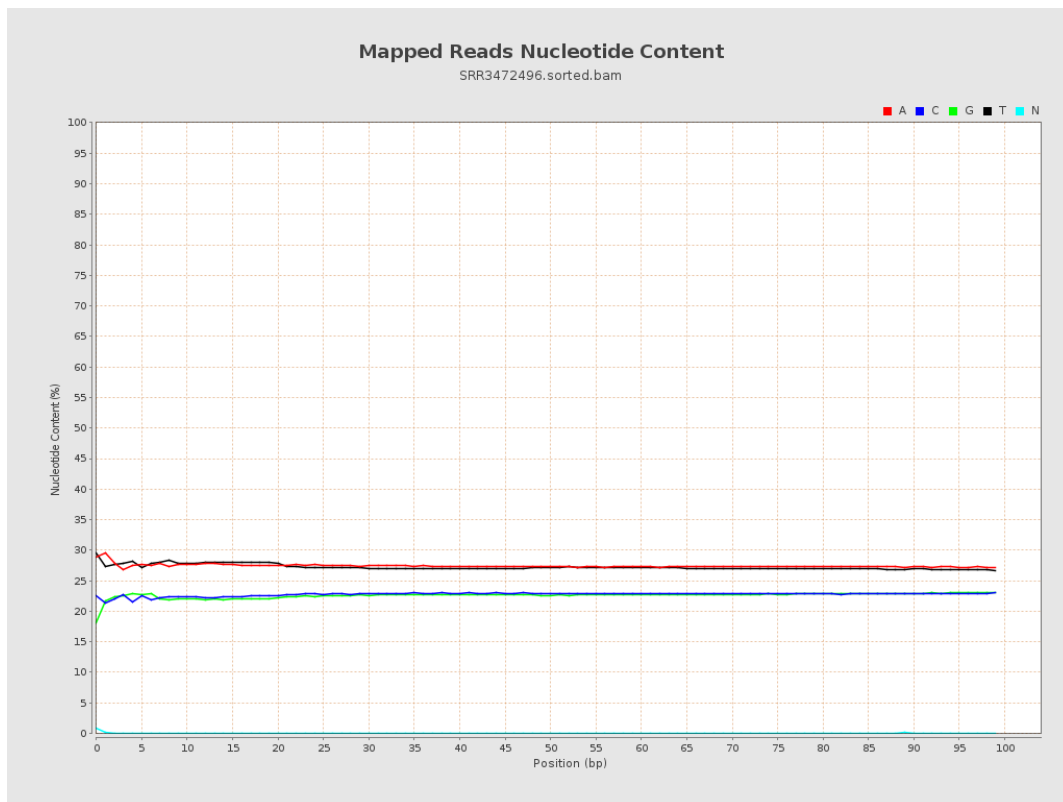
6. Results : Genome Fraction Coverage



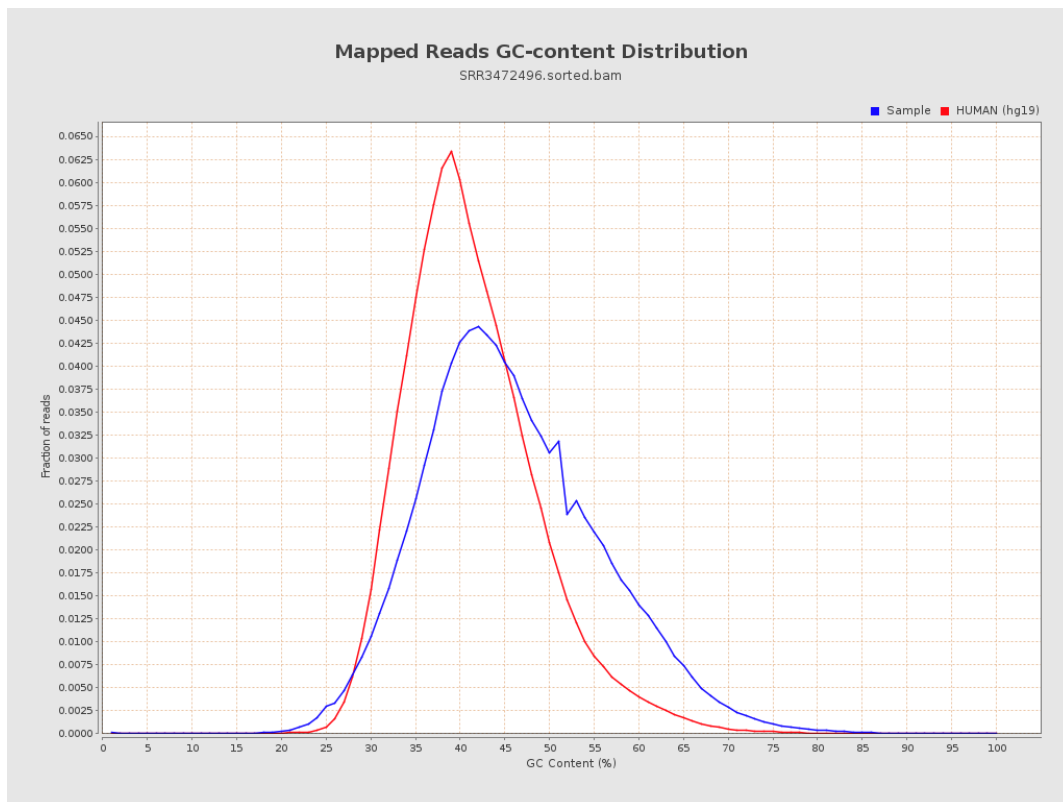
7. Results : Duplication Rate Histogram



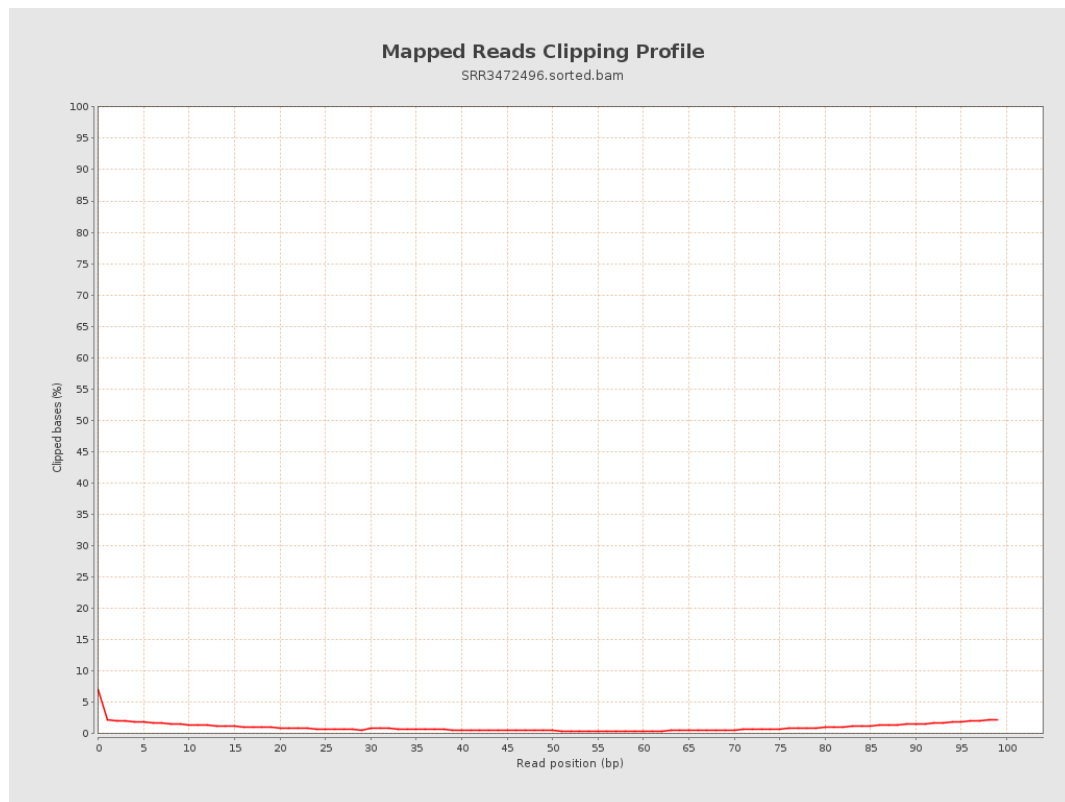
8. Results : Mapped Reads Nucleotide Content



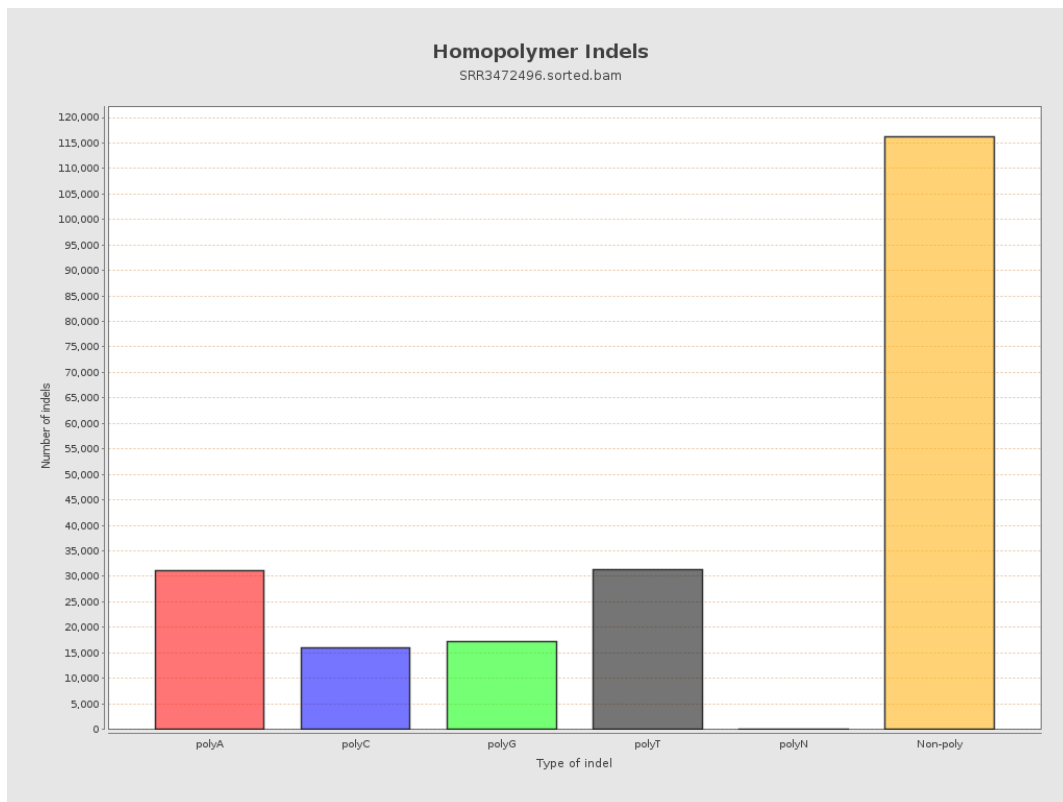
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



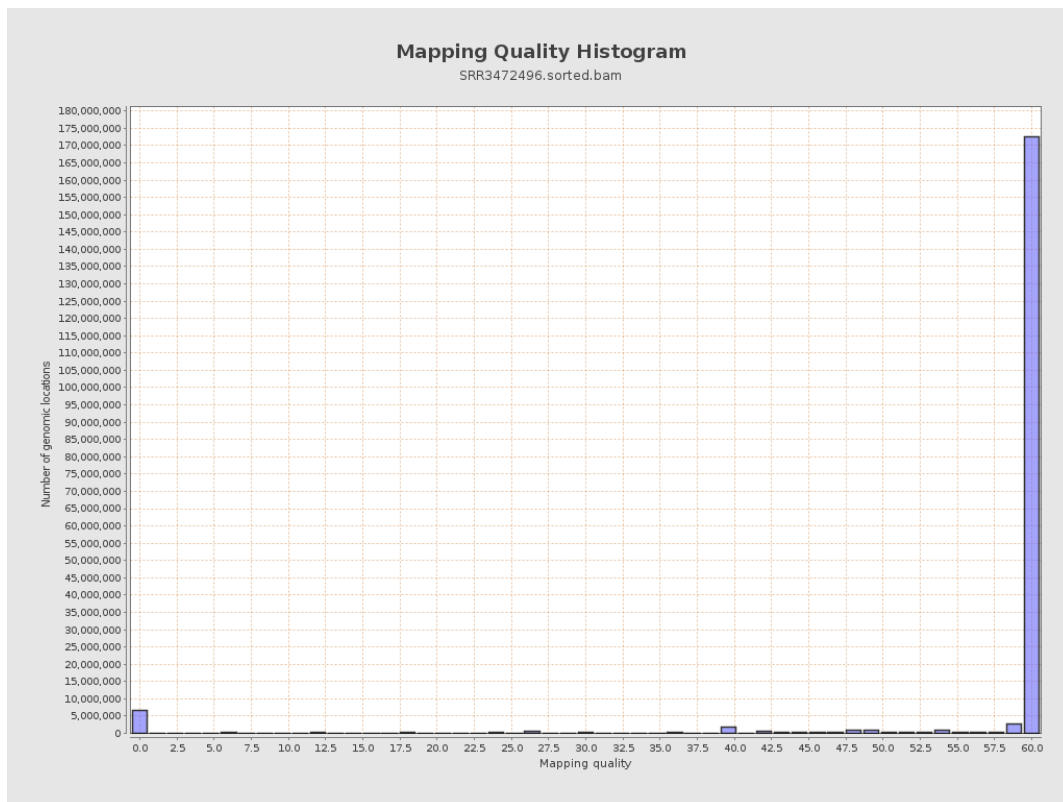
11. Results : Homopolymer Indels



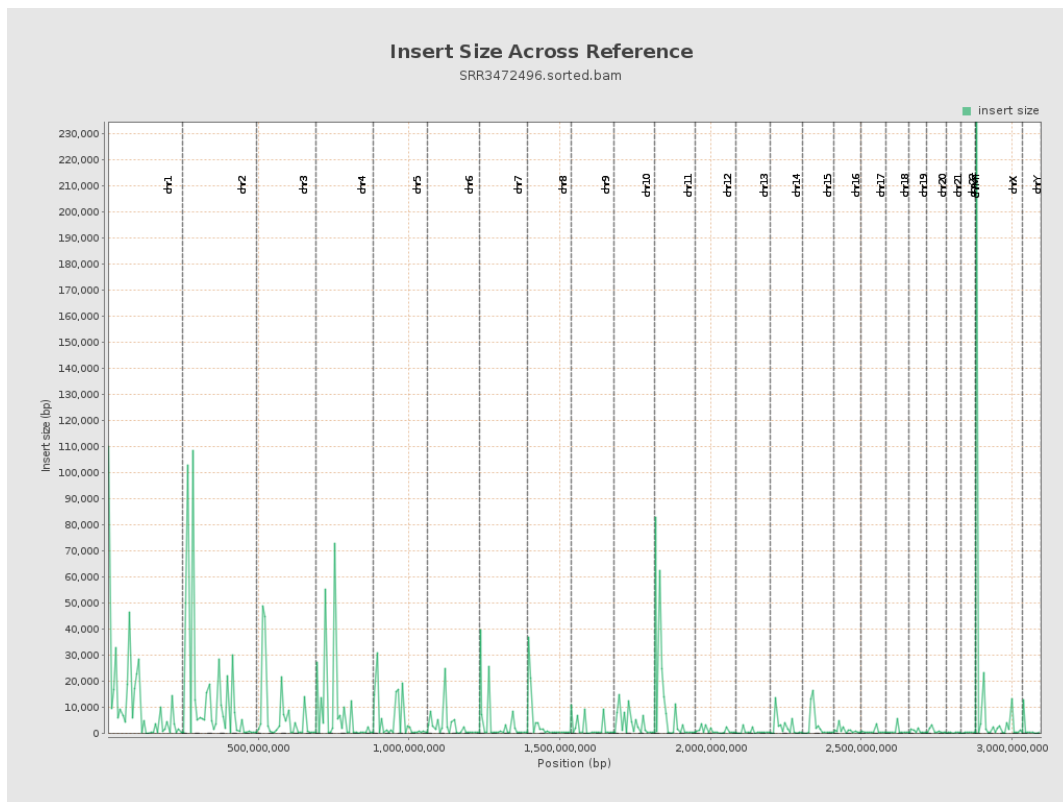
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

