

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:57:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472443.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_SRR3472443 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472443_1.fastq.gz SRR3472443_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:57:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472443.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,208,834
Mapped reads	19,046,979 / 99.16%
Unmapped reads	161,855 / 0.84%
Mapped paired reads	19,046,979 / 99.16%
Mapped reads, first in pair	9,547,749 / 49.7%
Mapped reads, second in pair	9,499,230 / 49.45%
Mapped reads, both in pair	18,962,224 / 98.72%
Mapped reads, singletons	84,755 / 0.44%
Secondary alignments	0
Supplementary alignments	64,347 / 0.33%
Read min/max/mean length	30 / 100 / 99.18
Duplicated reads (estimated)	12,778,087 / 66.52%
Duplication rate	48.47%
Clipped reads	1,520,785 / 7.92%

2.2. ACGT Content

Number/percentage of A's	491,655,369 / 26.42%
Number/percentage of C's	440,158,690 / 23.66%
Number/percentage of T's	492,348,957 / 26.46%
Number/percentage of G's	436,240,505 / 23.45%
Number/percentage of N's	238,241 / 0.01%

GC Percentage	47.1%
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2.3. Coverage

Mean	0.6011
Standard Deviation	21.2918

2.4. Mapping Quality

Mean Mapping Quality	53.84
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2.5. Insert size

Mean	19,263.91
Standard Deviation	1,434,132.41
P25/Median/P75	142 / 196 / 264

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	9,694,311
Insertions	105,265
Mapped reads with at least one insertion	0.55%
Deletions	84,622
Mapped reads with at least one deletion	0.44%
Homopolymer indels	45.88%

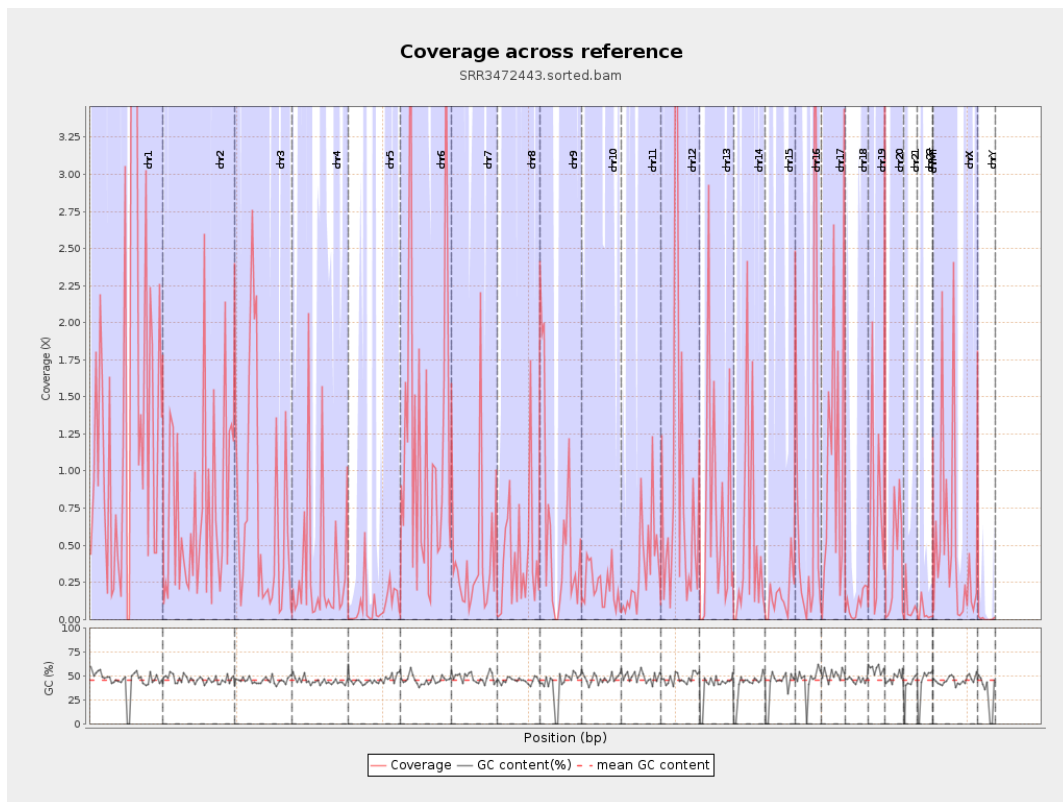
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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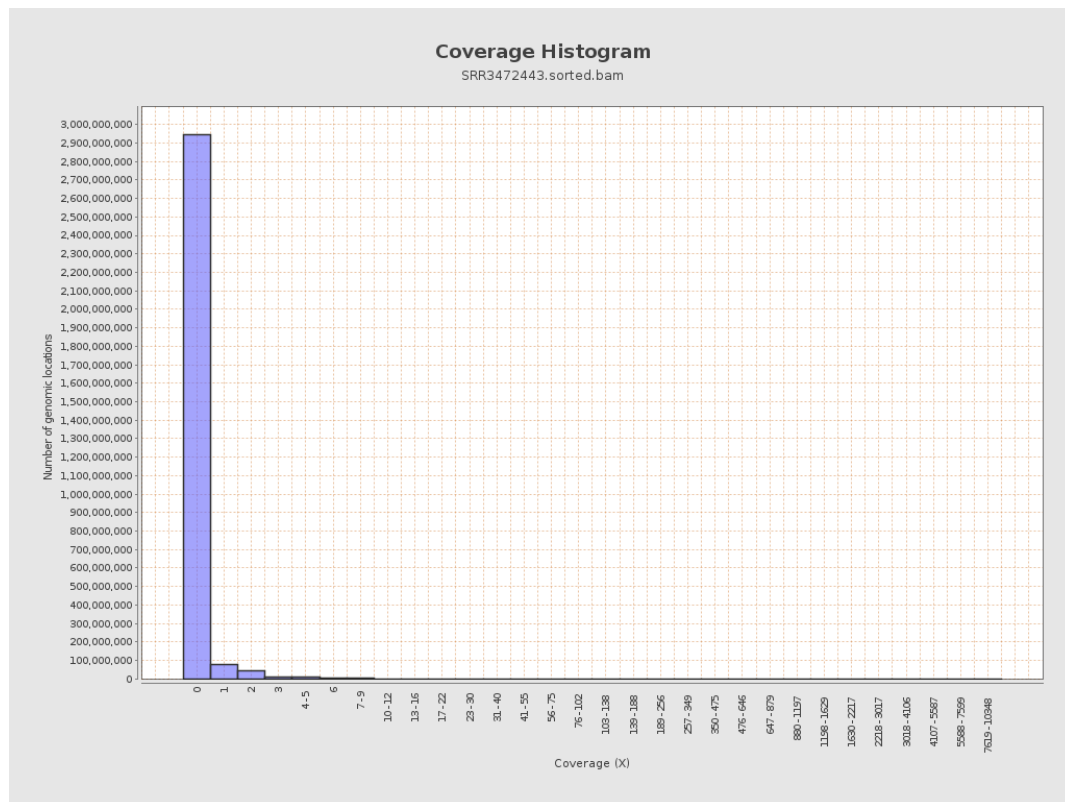
		bases	coverage	deviation
chr1	249250621	367738660	1.4754	39.2556
chr2	243199373	175326560	0.7209	21.2151
chr3	198022430	145021706	0.7323	19.7839
chr4	191154276	66712611	0.349	16.899
chr5	180915260	18162703	0.1004	4.7174
chr6	171115067	198390729	1.1594	31.0505
chr7	159138663	67836667	0.4263	16.6166
chr8	146364022	62190732	0.4249	14.3766
chr9	141213431	78346663	0.5548	14.8048
chr10	135534747	30578975	0.2256	8.2908
chr11	135006516	47515909	0.352	10.9072
chr12	133851895	123566600	0.9232	26.004
chr13	115169878	83018044	0.7208	22.9242
chr14	107349540	56586549	0.5271	20.7291
chr15	102531392	16269960	0.1587	5.4895
chr16	90354753	68845863	0.762	29.9746
chr17	81195210	84735813	1.0436	26.2919
chr18	78077248	8175586	0.1047	3.7253
chr19	59128983	49396096	0.8354	29.7123
chr20	63025520	24982901	0.3964	16.863
chr21	48129895	4703924	0.0977	6.7631
chr22	51304566	2091212	0.0408	2.8883
chrMT	16571	20377	1.2297	1.5322
chrX	155270560	80319390	0.5173	20.6713

chrY	59373566	303179	0.0051	0.3471
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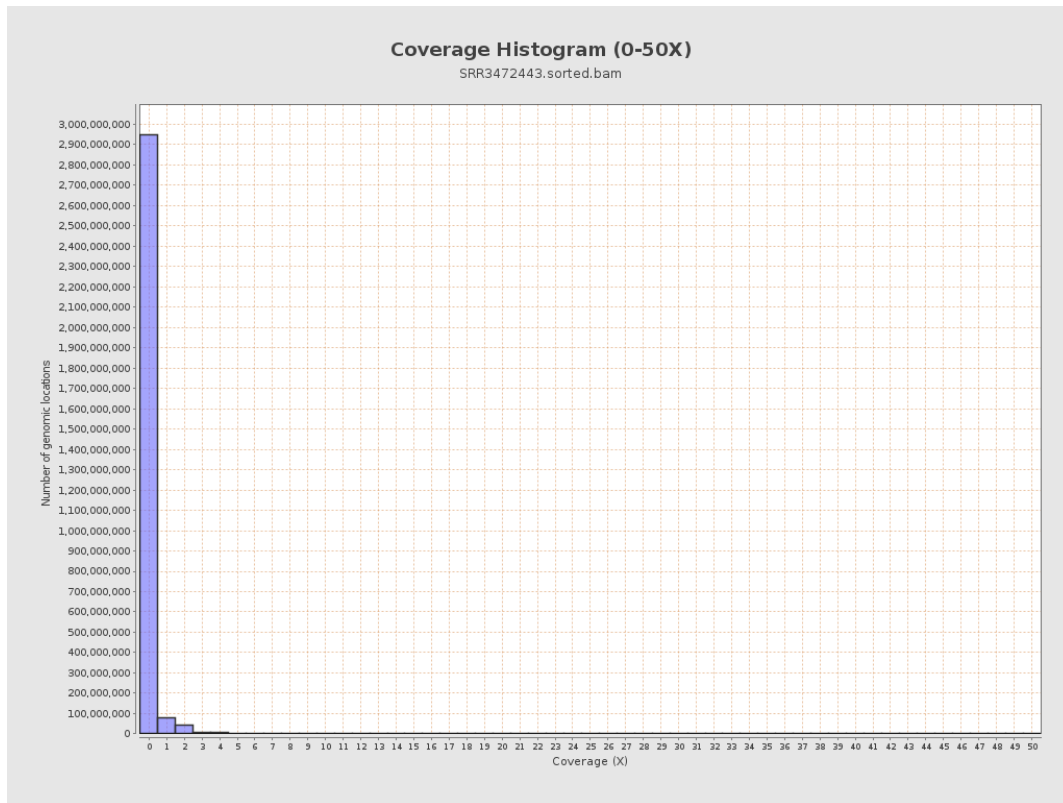
3. Results : Coverage across reference



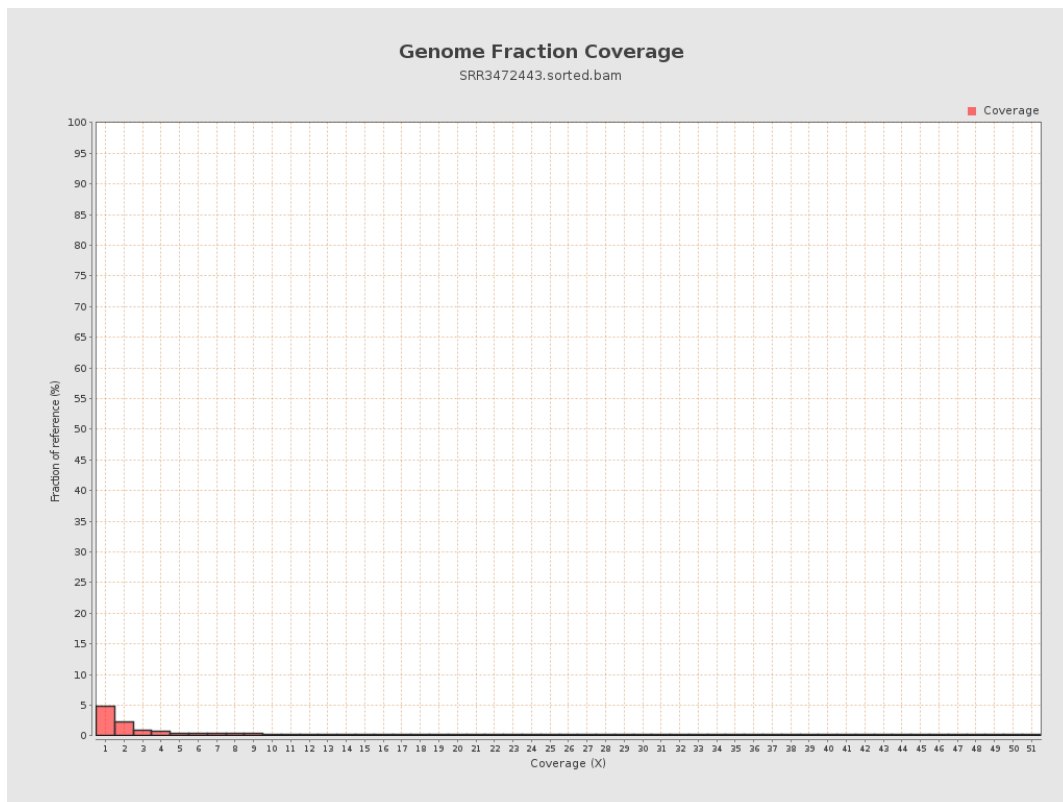
4. Results : Coverage Histogram



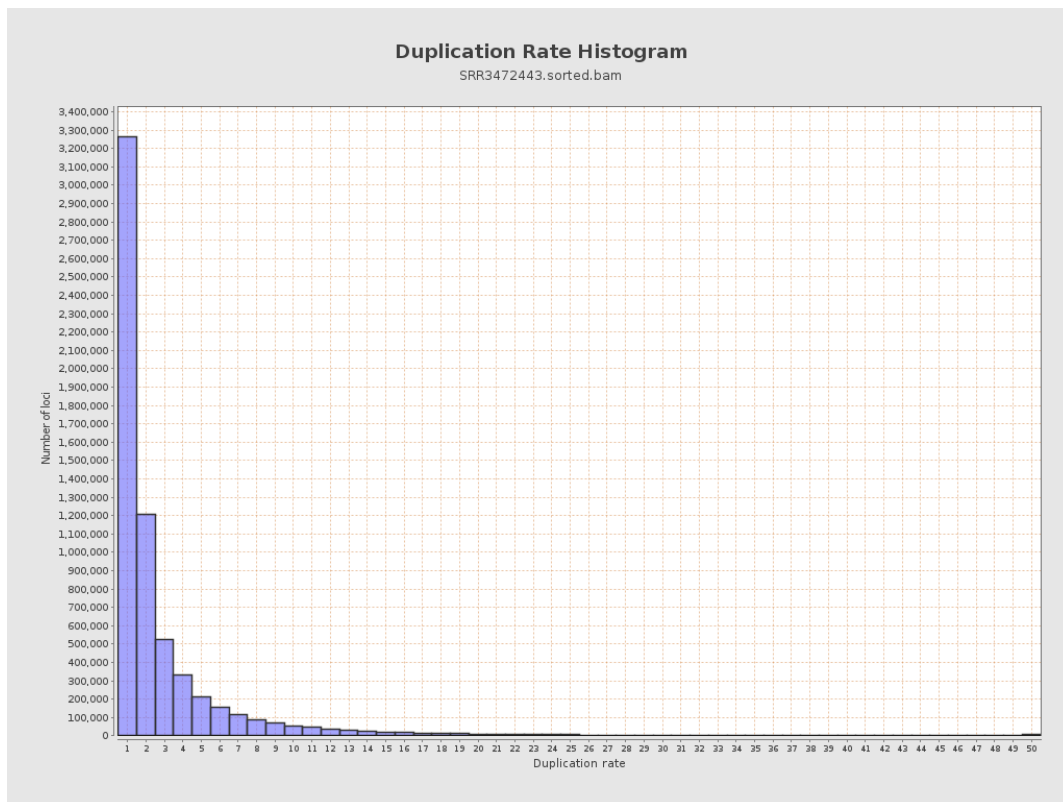
5. Results : Coverage Histogram (0-50X)



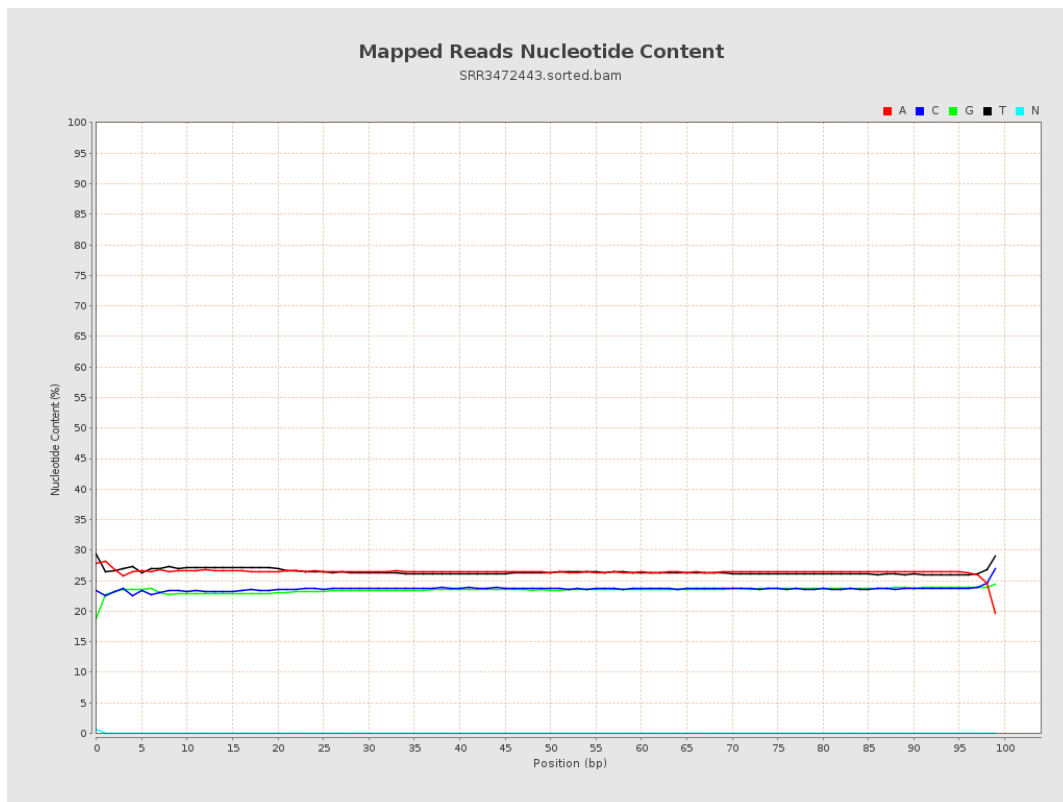
6. Results : Genome Fraction Coverage



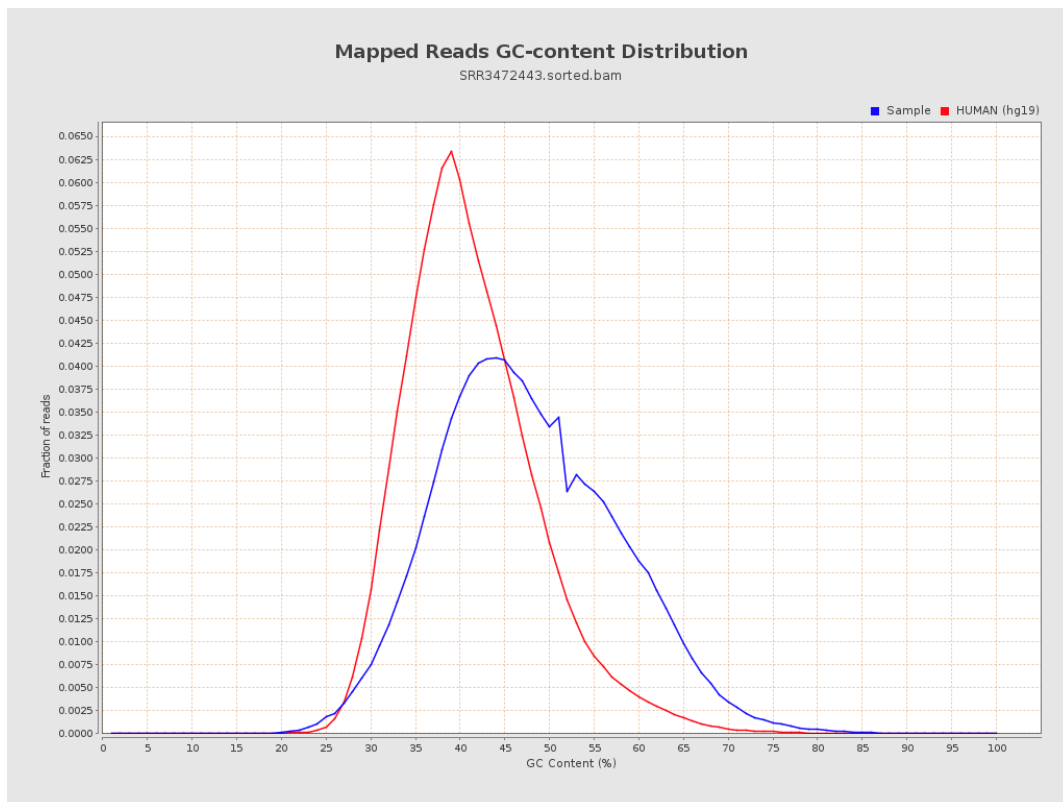
7. Results : Duplication Rate Histogram



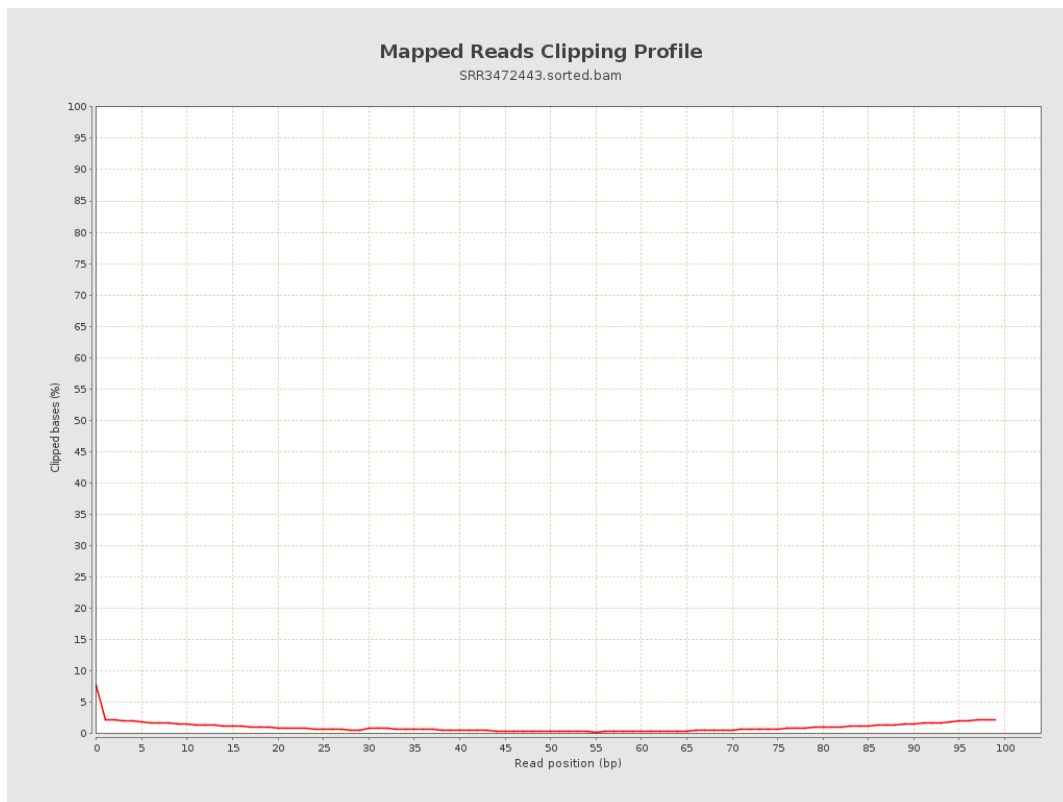
8. Results : Mapped Reads Nucleotide Content



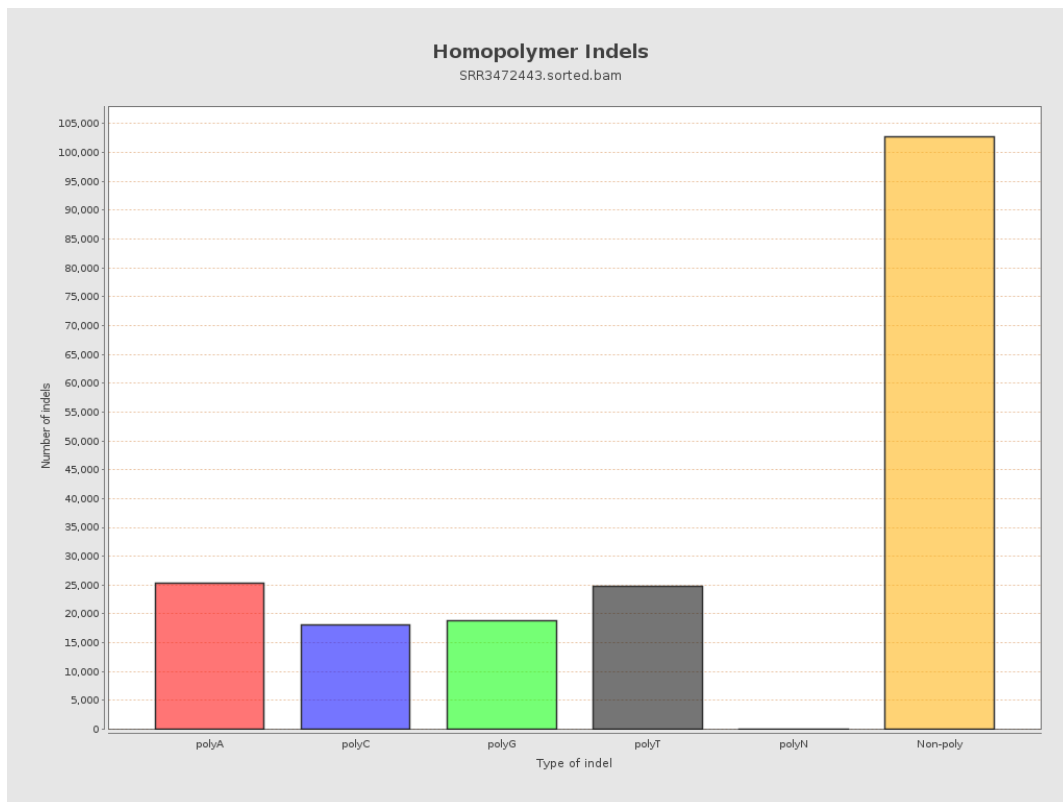
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



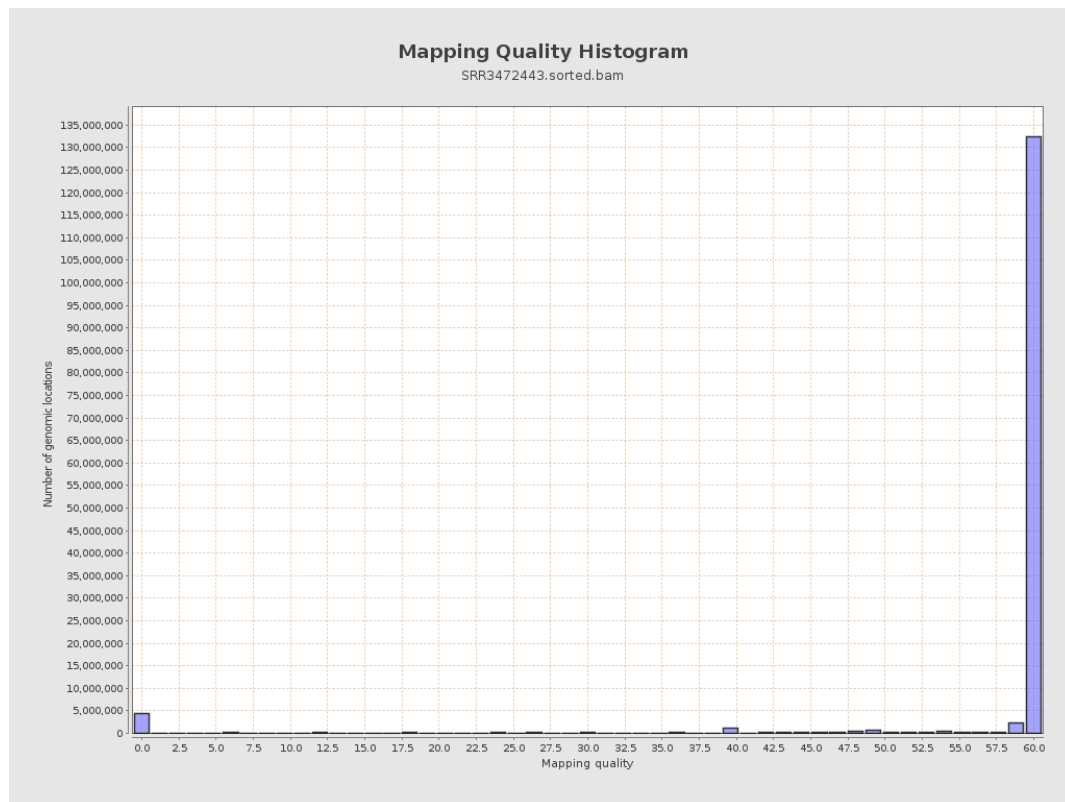
11. Results : Homopolymer Indels



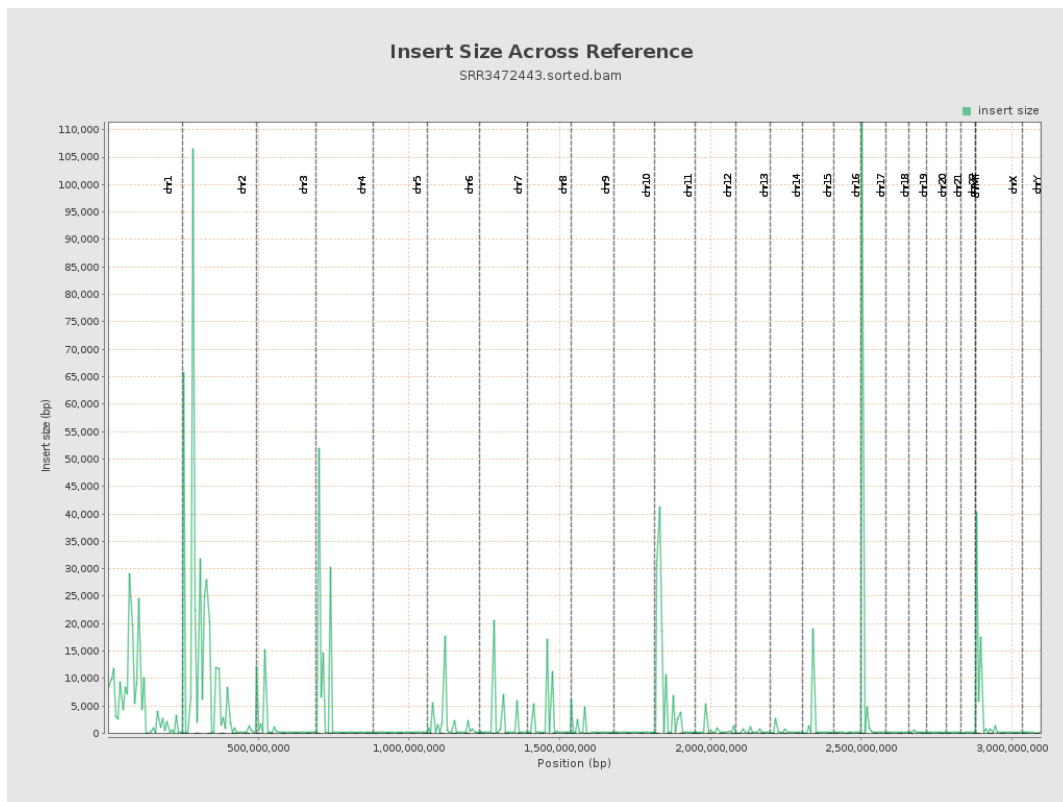
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

