

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:34:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472430.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_SRR3472430 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472430_1.fastq.gz SRR3472430_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:34:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472430.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,613,544
Mapped reads	19,338,231 / 98.6%
Unmapped reads	275,313 / 1.4%
Mapped paired reads	19,338,231 / 98.6%
Mapped reads, first in pair	9,724,791 / 49.58%
Mapped reads, second in pair	9,613,440 / 49.01%
Mapped reads, both in pair	19,170,092 / 97.74%
Mapped reads, singletons	168,139 / 0.86%
Secondary alignments	0
Supplementary alignments	68,375 / 0.35%
Read min/max/mean length	30 / 100 / 99.25
Duplicated reads (estimated)	12,650,304 / 64.5%
Duplication rate	48.44%
Clipped reads	1,479,595 / 7.54%

2.2. ACGT Content

Number/percentage of A's	508,808,238 / 26.89%
Number/percentage of C's	438,463,899 / 23.18%
Number/percentage of T's	509,419,403 / 26.93%
Number/percentage of G's	434,982,382 / 22.99%
Number/percentage of N's	238,127 / 0.01%

GC Percentage	46.17%
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2.3. Coverage

Mean	0.6112
Standard Deviation	19.832

2.4. Mapping Quality

Mean Mapping Quality	54.86
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2.5. Insert size

Mean	18,670.9
Standard Deviation	1,353,165.04
P25/Median/P75	145 / 200 / 269

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	10,226,789
Insertions	102,208
Mapped reads with at least one insertion	0.52%
Deletions	89,892
Mapped reads with at least one deletion	0.45%
Homopolymer indels	44.37%

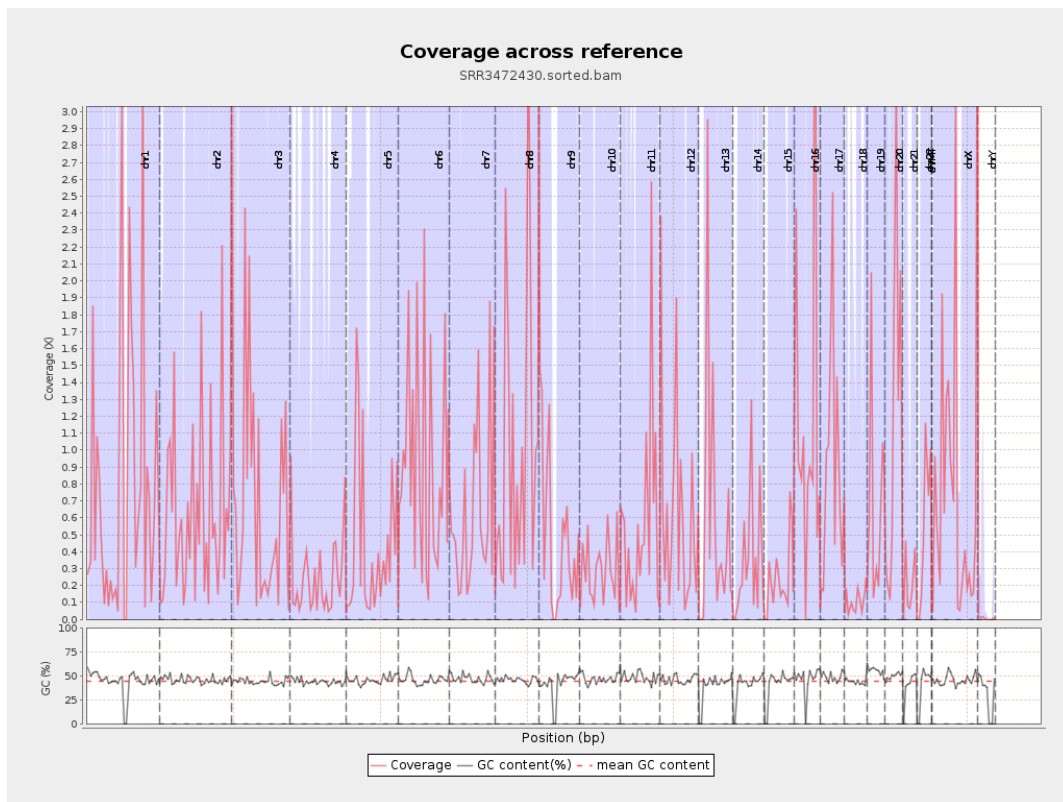
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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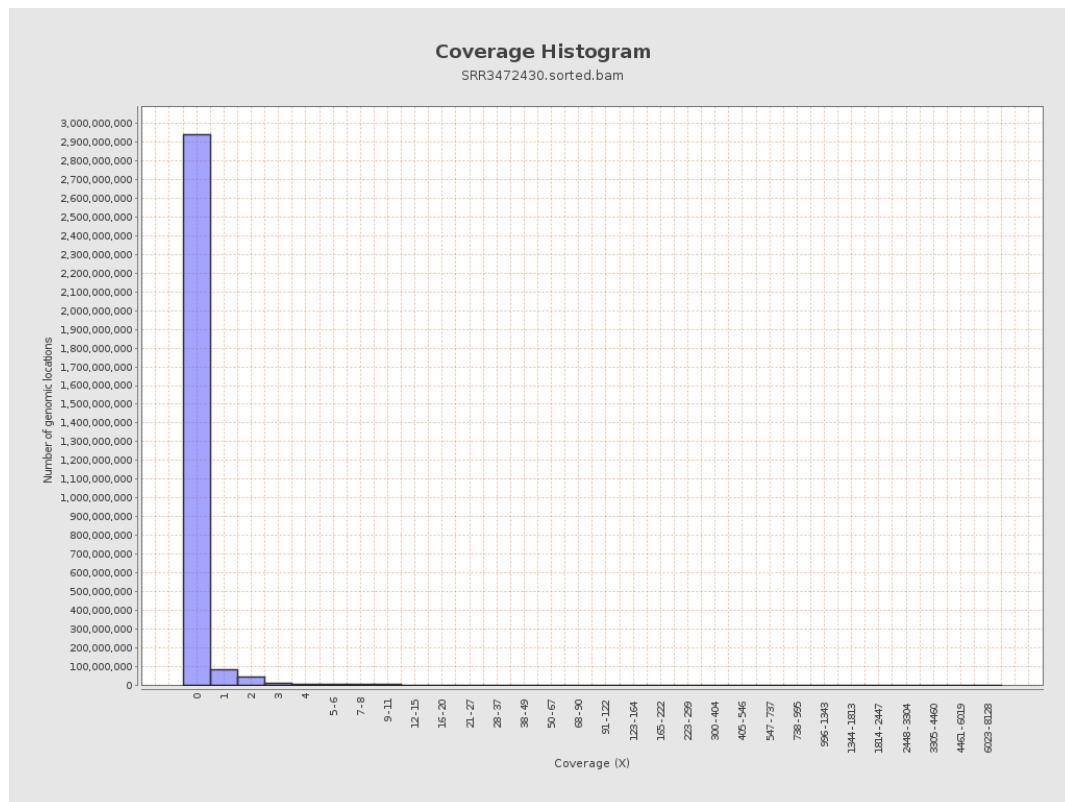
		bases	coverage	deviation
chr1	249250621	204256469	0.8195	26.4623
chr2	243199373	153187831	0.6299	18.5916
chr3	198022430	139203770	0.703	21.9339
chr4	191154276	46013666	0.2407	10.3943
chr5	180915260	77603064	0.4289	15.8224
chr6	171115067	153150066	0.895	21.1506
chr7	159138663	105807654	0.6649	17.7322
chr8	146364022	149054019	1.0184	26.3727
chr9	141213431	71536149	0.5066	13.8845
chr10	135534747	38876856	0.2868	10.2707
chr11	135006516	75316254	0.5579	19.3964
chr12	133851895	85820923	0.6412	21.1259
chr13	115169878	66786798	0.5799	23.9275
chr14	107349540	35219495	0.3281	10.8389
chr15	102531392	25095120	0.2448	6.9438
chr16	90354753	110597881	1.224	32.5039
chr17	81195210	75735447	0.9328	20.2227
chr18	78077248	8579976	0.1099	3.6463
chr19	59128983	40587440	0.6864	17.2875
chr20	63025520	74640978	1.1843	30.1302
chr21	48129895	10263521	0.2132	8.1952
chr22	51304566	26930238	0.5249	19.1794
chrMT	16571	5322	0.3212	0.7848
chrX	155270560	117490594	0.7567	26.2353

chrY	59373566	368562	0.0062	0.4895
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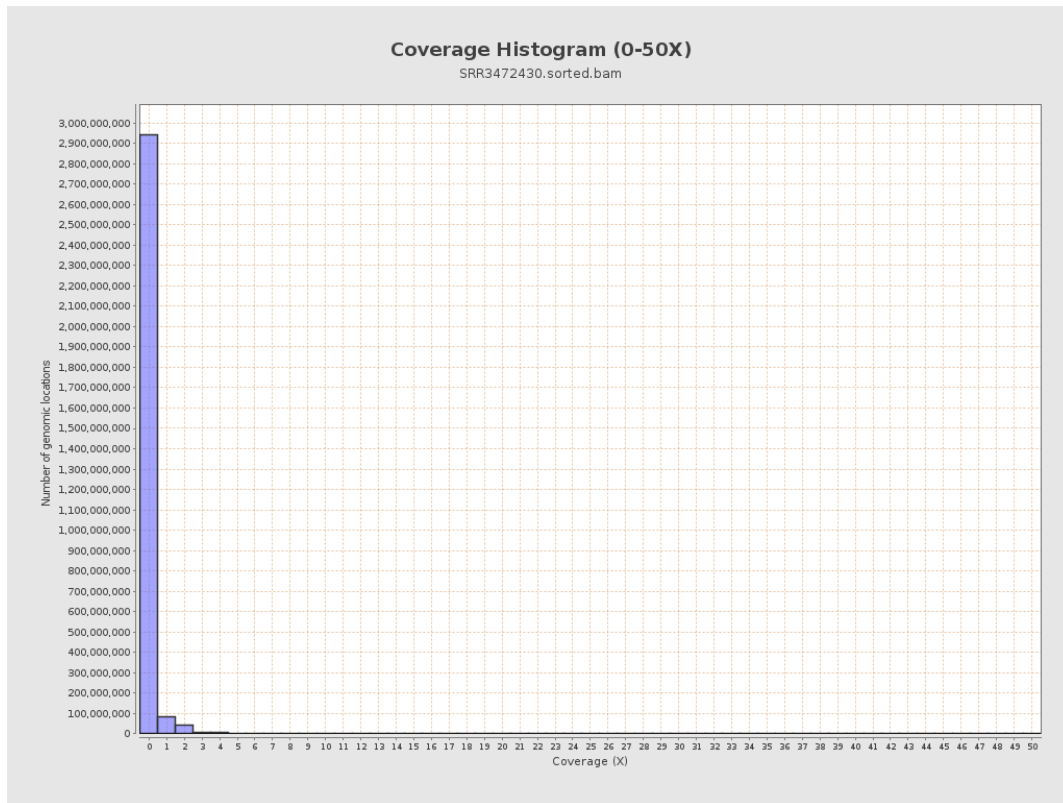
3. Results : Coverage across reference



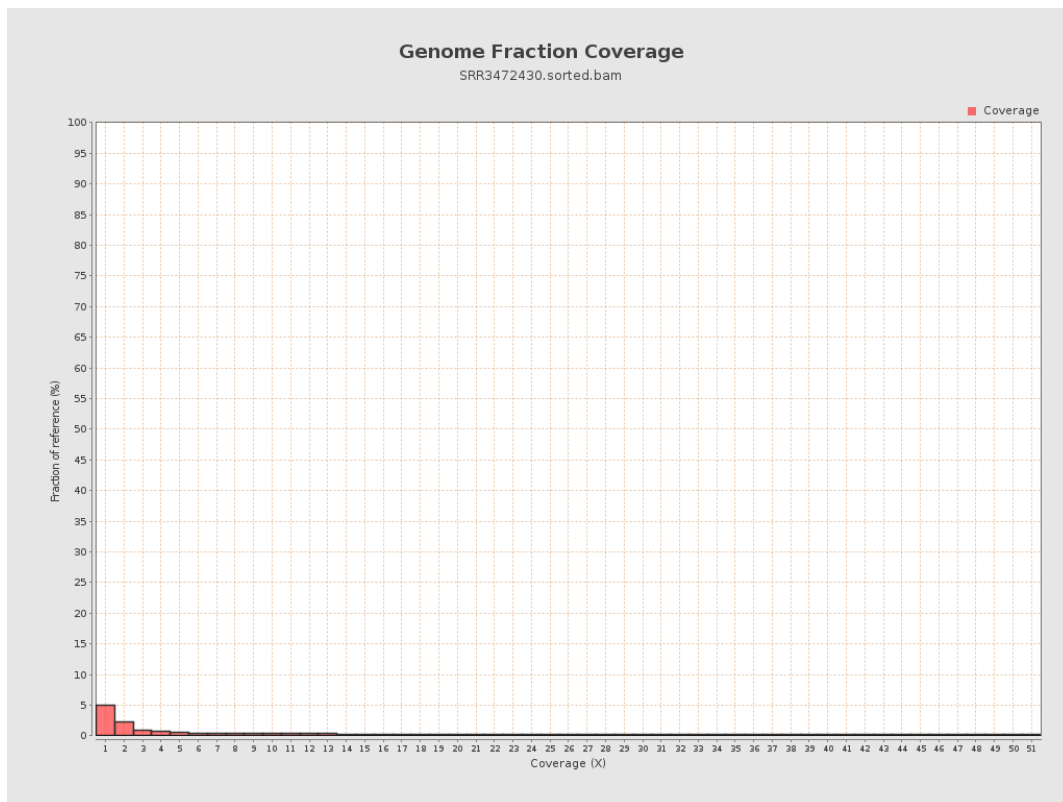
4. Results : Coverage Histogram



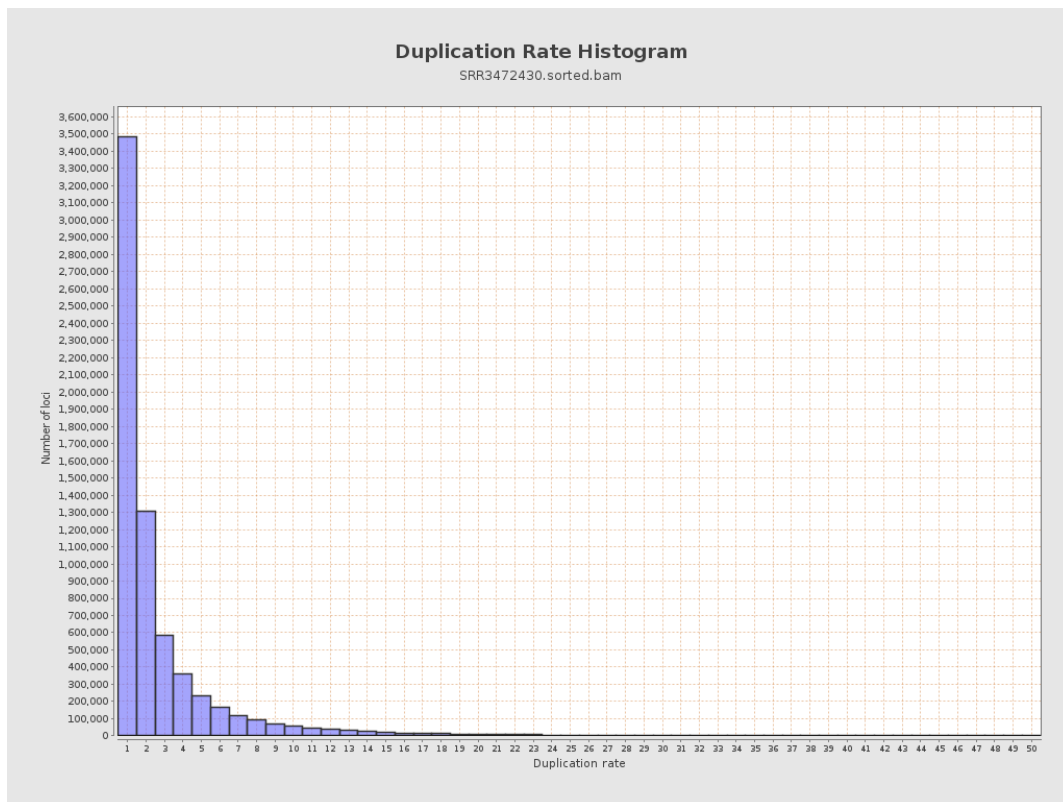
5. Results : Coverage Histogram (0-50X)



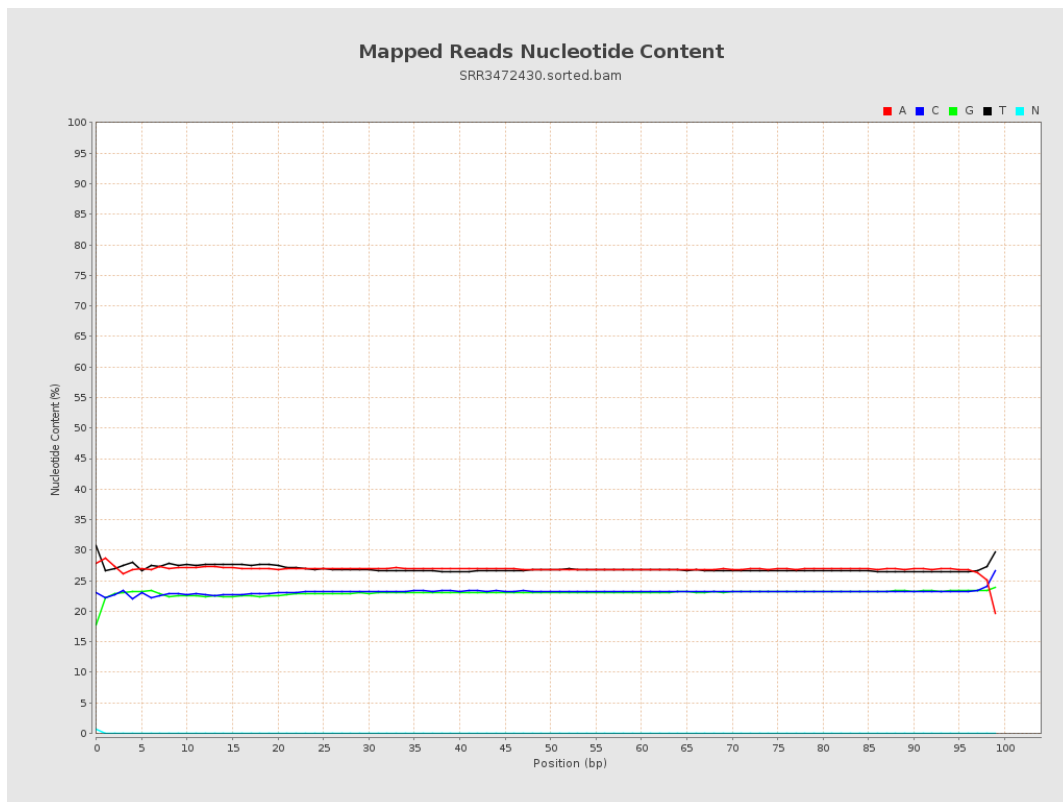
6. Results : Genome Fraction Coverage



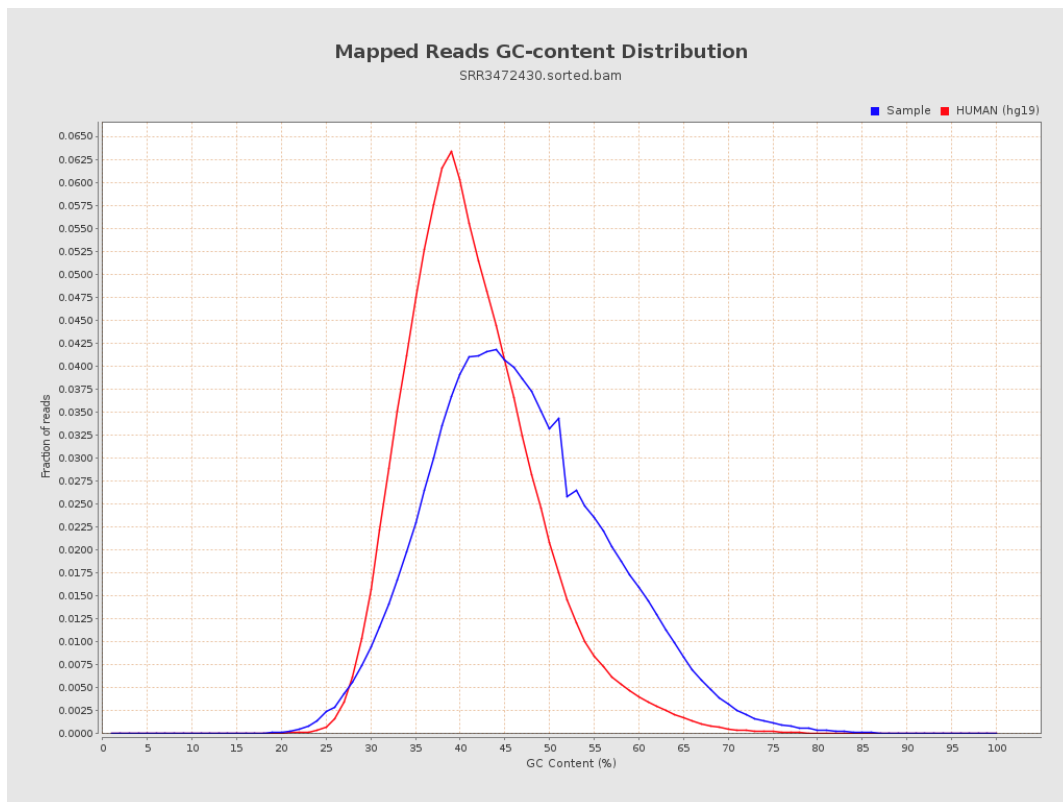
7. Results : Duplication Rate Histogram



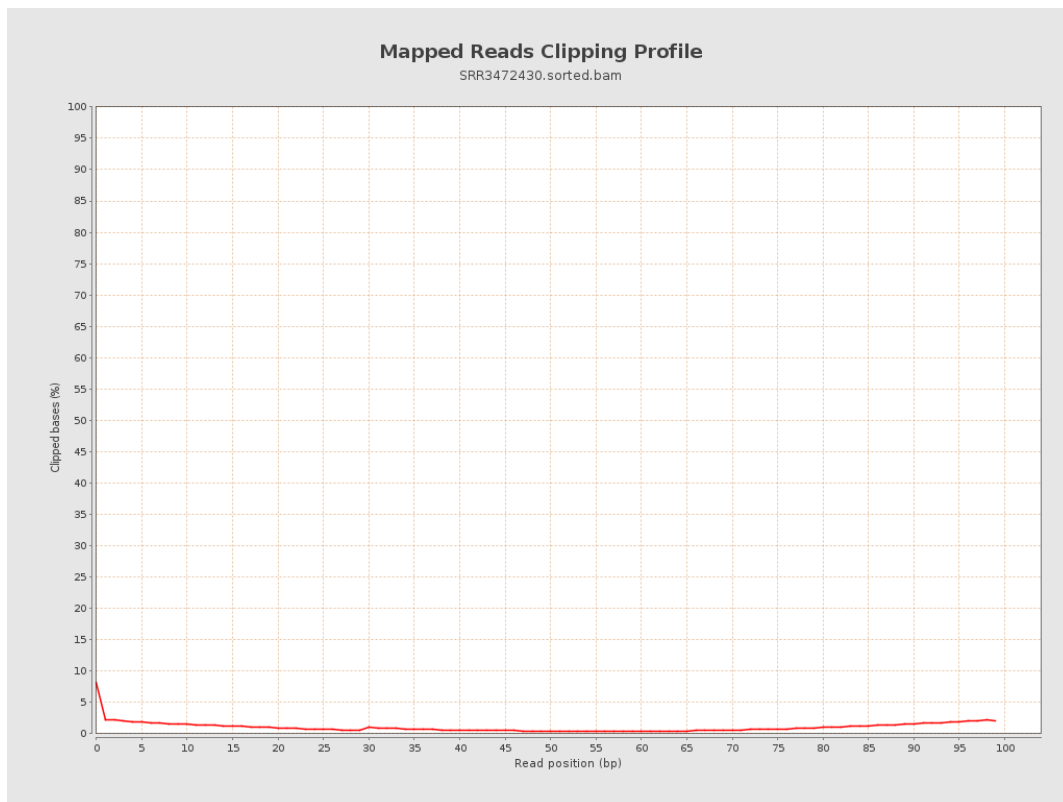
8. Results : Mapped Reads Nucleotide Content



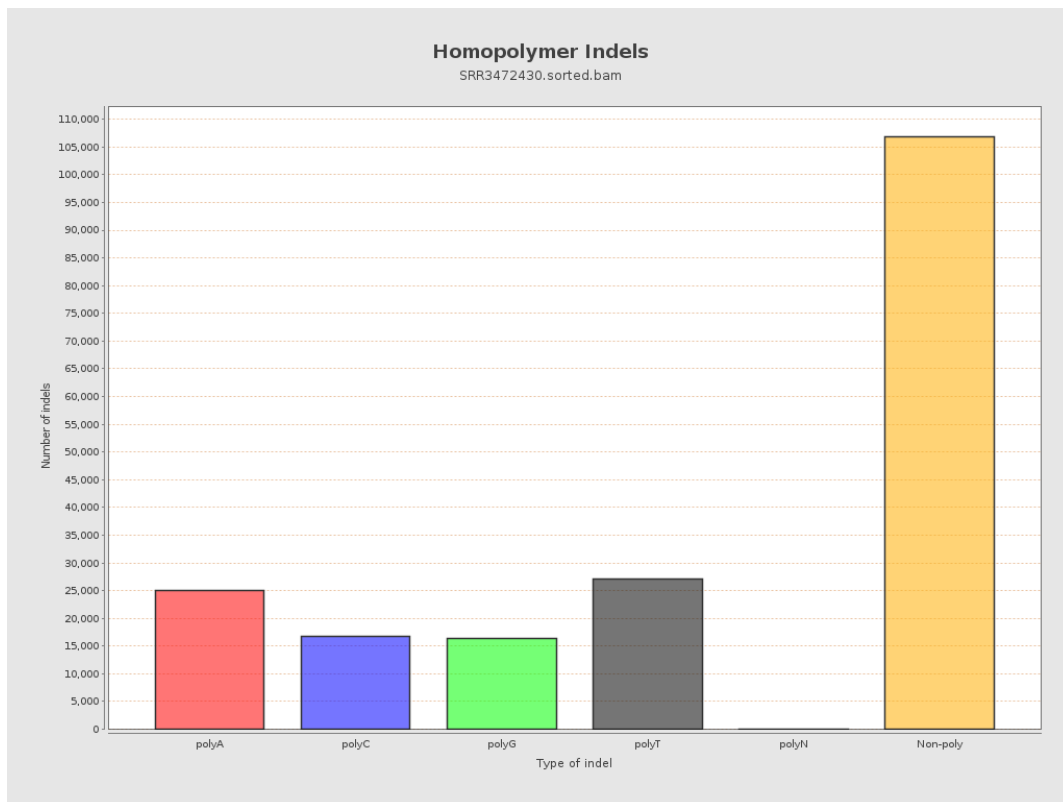
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



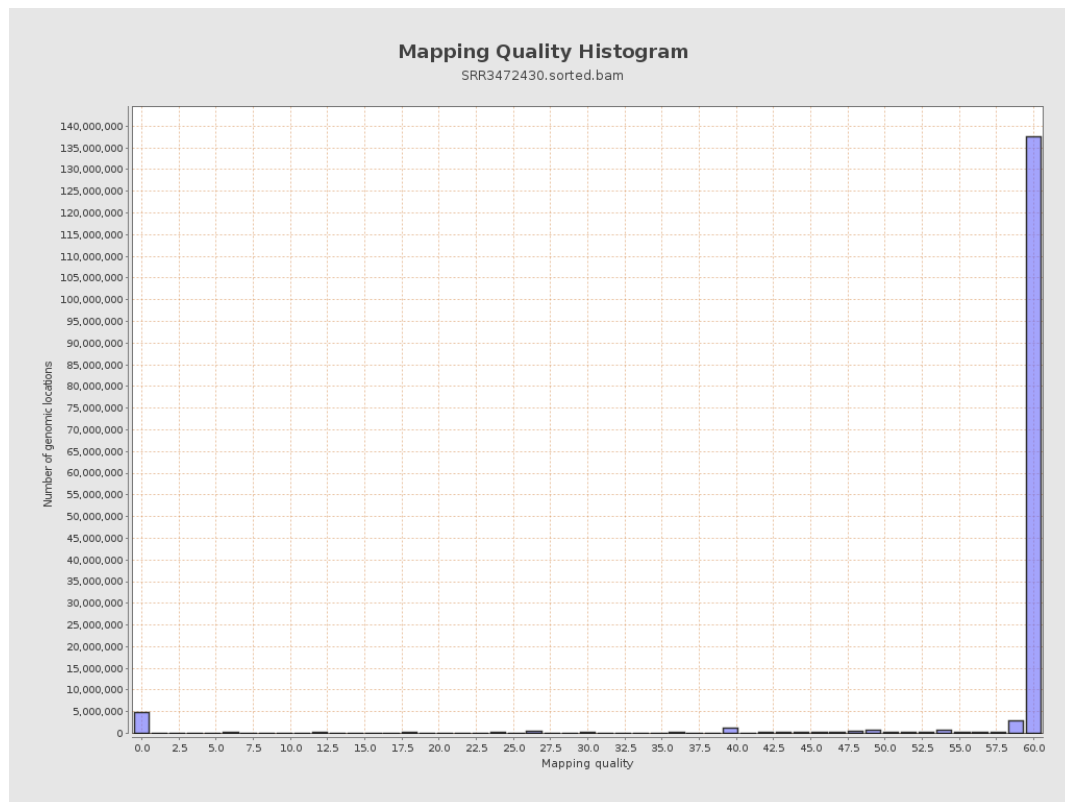
11. Results : Homopolymer Indels



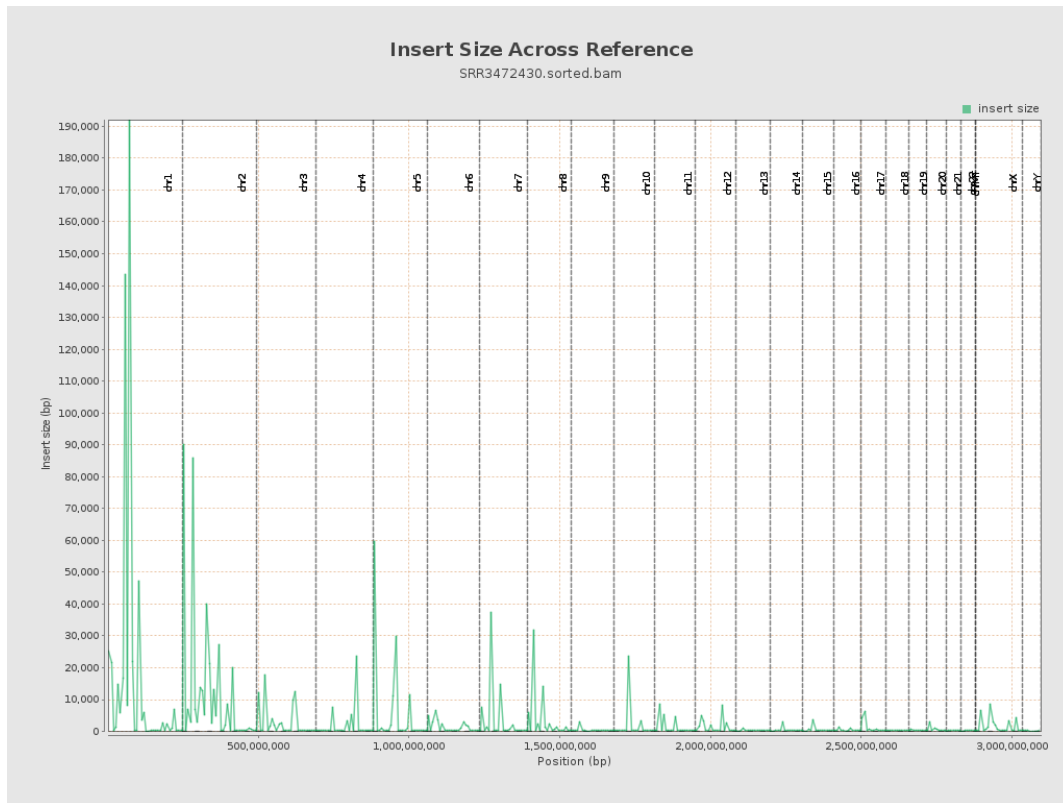
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

