

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:18:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472410.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_SRR3472410 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472410_1.fastq.gz SRR3472410_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:18:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472410.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,745,754
Mapped reads	18,589,291 / 99.17%
Unmapped reads	156,463 / 0.83%
Mapped paired reads	18,589,291 / 99.17%
Mapped reads, first in pair	9,319,881 / 49.72%
Mapped reads, second in pair	9,269,410 / 49.45%
Mapped reads, both in pair	18,493,892 / 98.66%
Mapped reads, singletons	95,399 / 0.51%
Secondary alignments	0
Supplementary alignments	76,983 / 0.41%
Read min/max/mean length	30 / 100 / 99.3
Duplicated reads (estimated)	12,041,174 / 64.23%
Duplication rate	46.72%
Clipped reads	1,292,477 / 6.89%

2.2. ACGT Content

Number/percentage of A's	493,983,747 / 27.12%
Number/percentage of C's	417,828,208 / 22.94%
Number/percentage of T's	494,779,806 / 27.17%
Number/percentage of G's	414,540,971 / 22.76%
Number/percentage of N's	215,772 / 0.01%

GC Percentage	45.7%
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2.3. Coverage

Mean	0.5884
Standard Deviation	20.4107

2.4. Mapping Quality

Mean Mapping Quality	54.63
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2.5. Insert size

Mean	19,408.61
Standard Deviation	1,369,521.45
P25/Median/P75	156 / 219 / 295

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	9,988,926
Insertions	113,976
Mapped reads with at least one insertion	0.61%
Deletions	95,854
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.75%

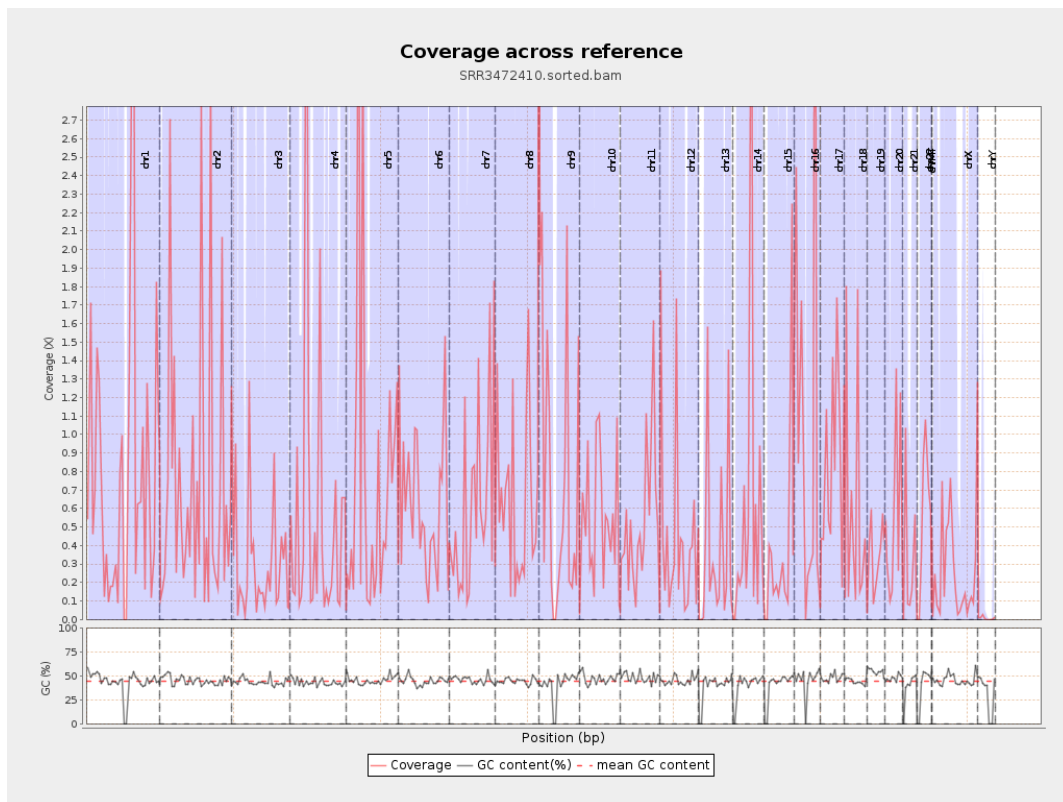
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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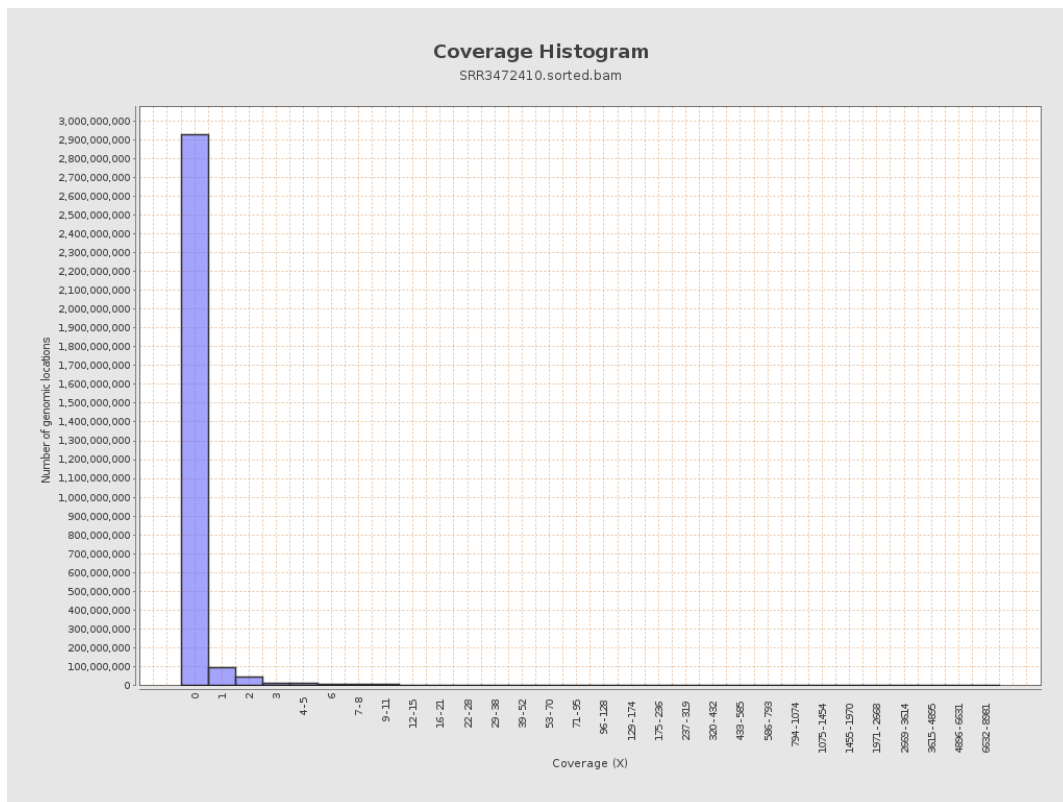
		bases	coverage	deviation
chr1	249250621	207207314	0.8313	22.2657
chr2	243199373	179035914	0.7362	27.8013
chr3	198022430	63070578	0.3185	8.99
chr4	191154276	107047971	0.56	24.4424
chr5	180915260	145149249	0.8023	28.6742
chr6	171115067	104419374	0.6102	14.6717
chr7	159138663	100710782	0.6328	18.6212
chr8	146364022	96130486	0.6568	15.9966
chr9	141213431	111403948	0.7889	19.0592
chr10	135534747	74489054	0.5496	20.1799
chr11	135006516	73231278	0.5424	18.4156
chr12	133851895	61388004	0.4586	21.1706
chr13	115169878	43397135	0.3768	17.2235
chr14	107349540	62695522	0.584	24.2055
chr15	102531392	42333769	0.4129	18.1039
chr16	90354753	98665638	1.092	32.4282
chr17	81195210	68158927	0.8394	16.7065
chr18	78077248	45483504	0.5825	25.8993
chr19	59128983	21001883	0.3552	8.2546
chr20	63025520	35171556	0.5581	14.8861
chr21	48129895	15631089	0.3248	14.8348
chr22	51304566	27893115	0.5437	15.2127
chrMT	16571	8316	0.5018	0.9223
chrX	155270560	37420513	0.241	10.176

chrY	59373566	423556	0.0071	0.746
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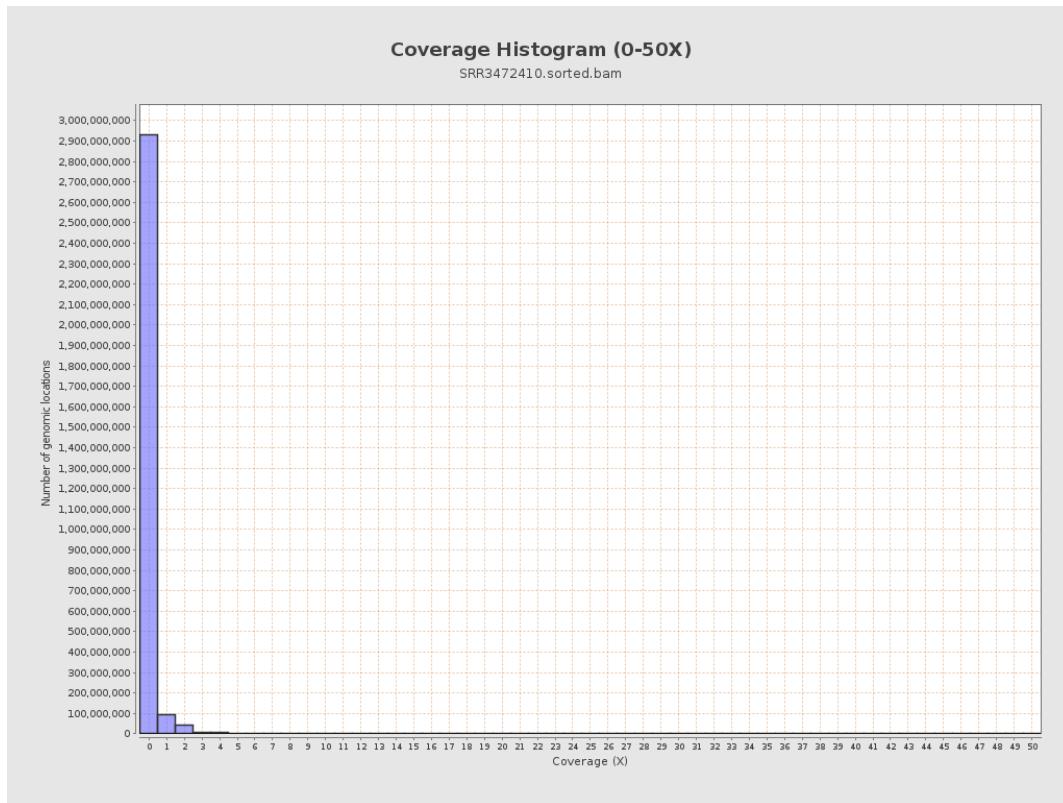
3. Results : Coverage across reference



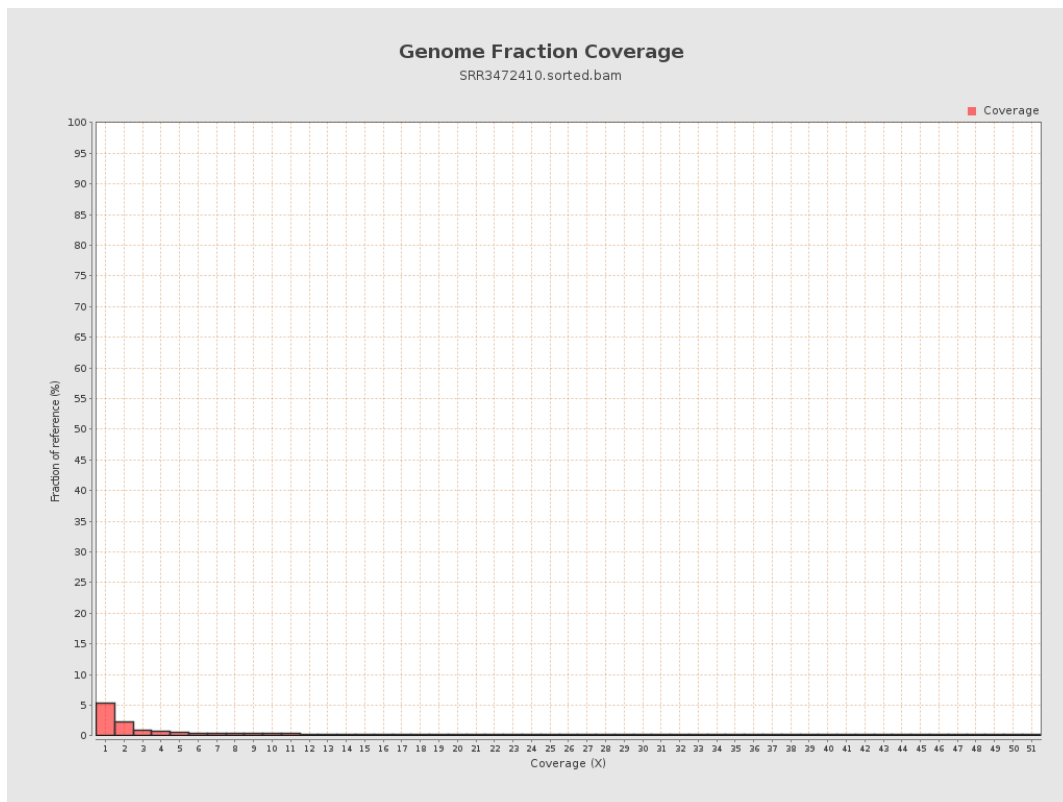
4. Results : Coverage Histogram



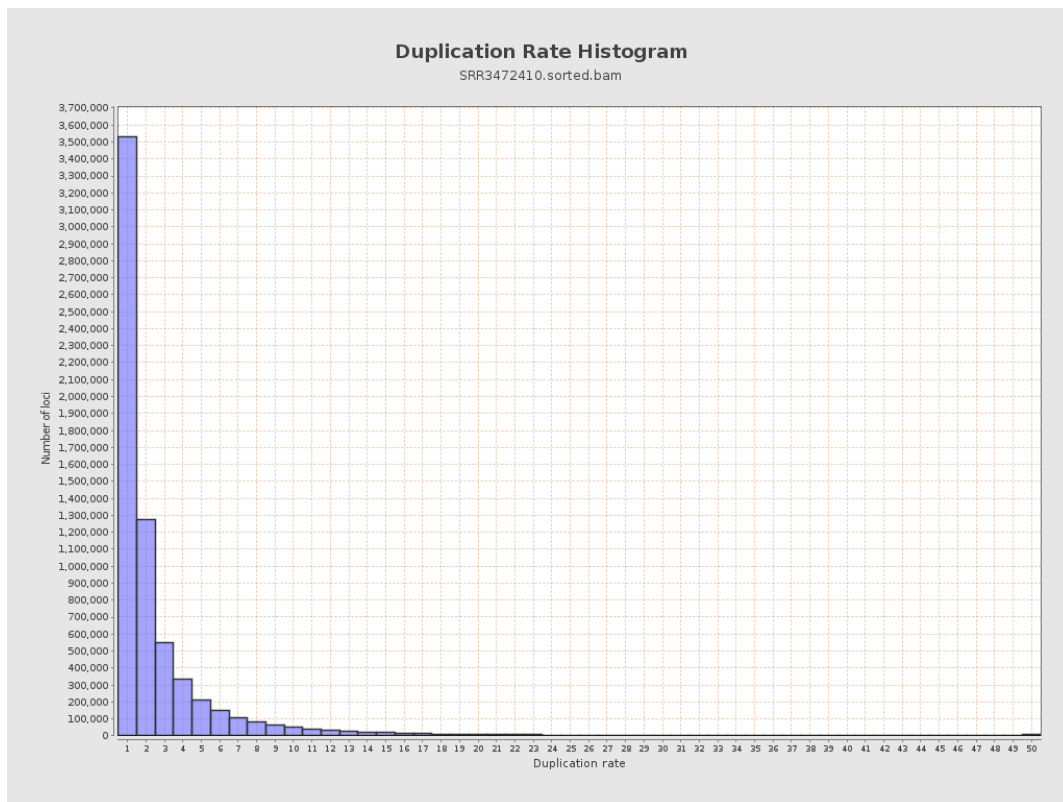
5. Results : Coverage Histogram (0-50X)



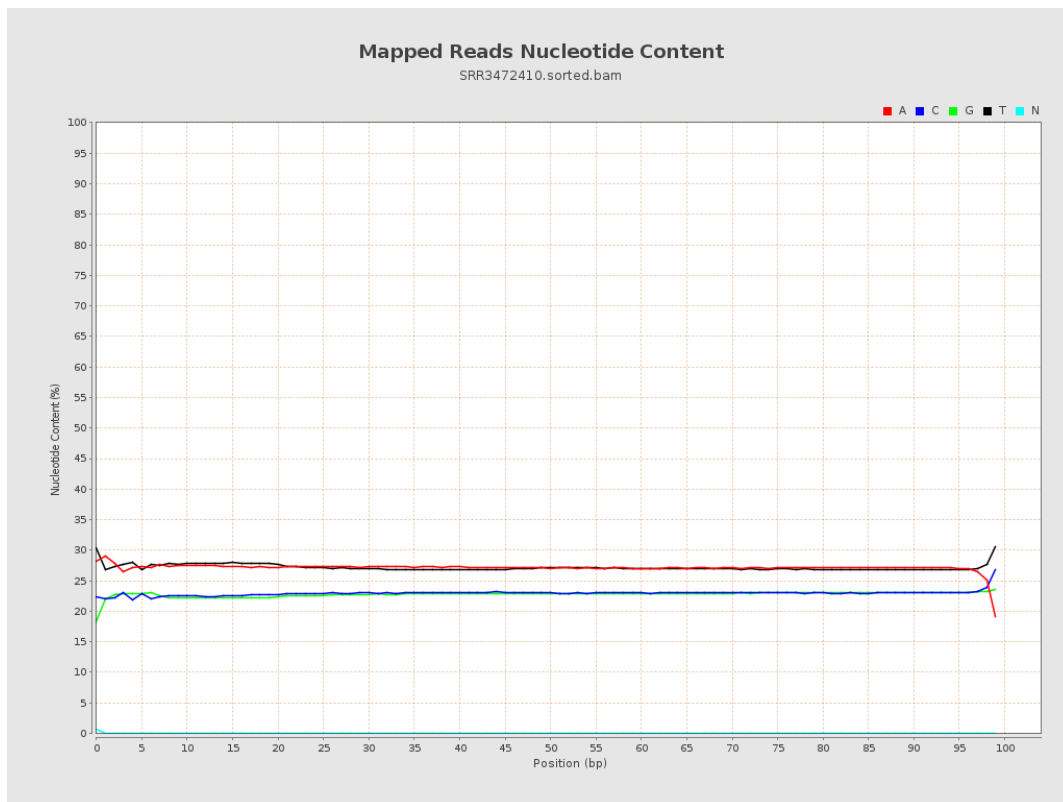
6. Results : Genome Fraction Coverage



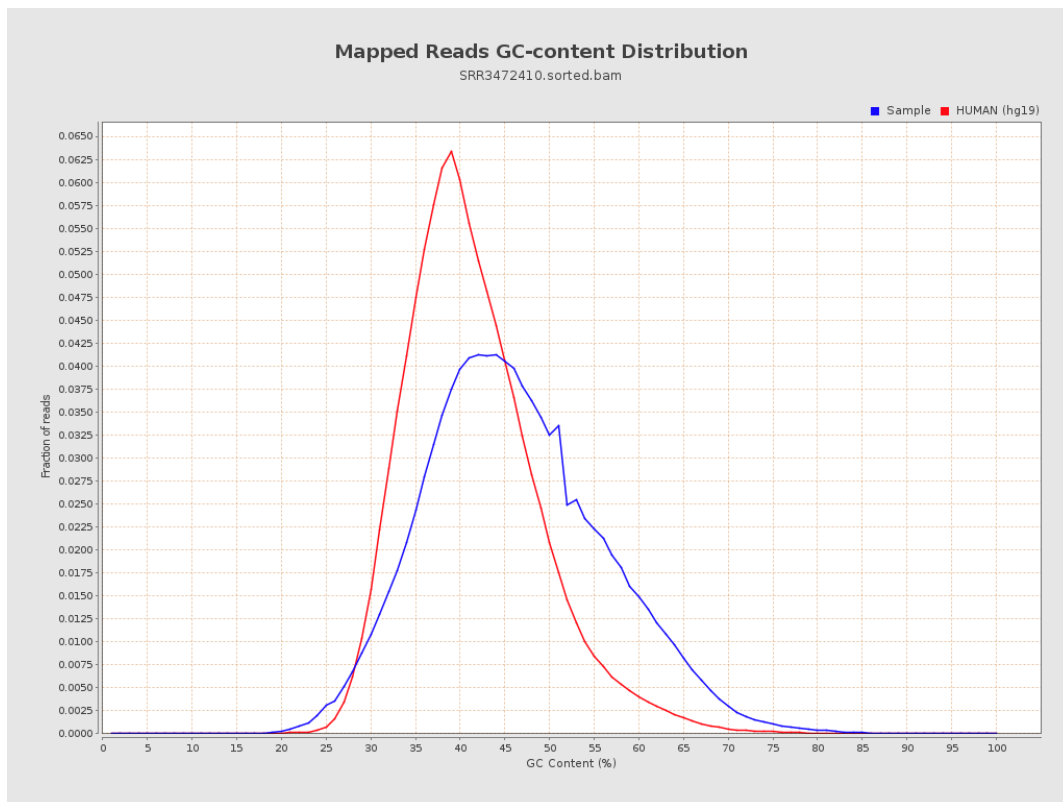
7. Results : Duplication Rate Histogram



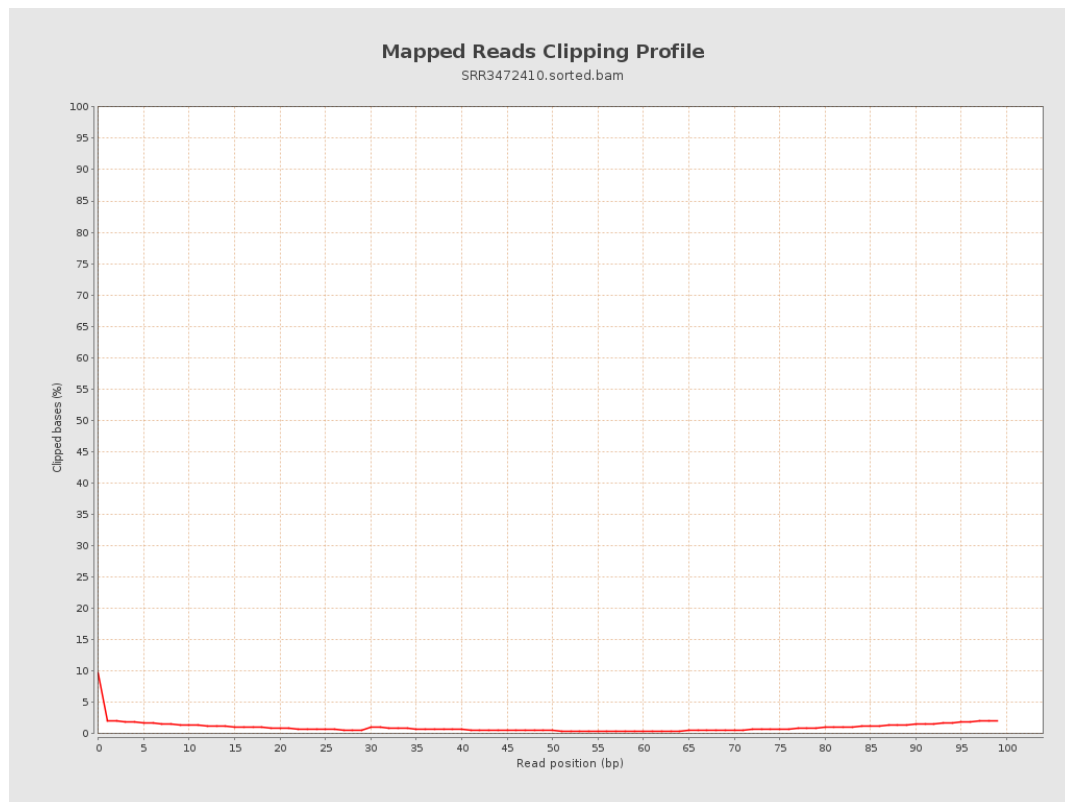
8. Results : Mapped Reads Nucleotide Content



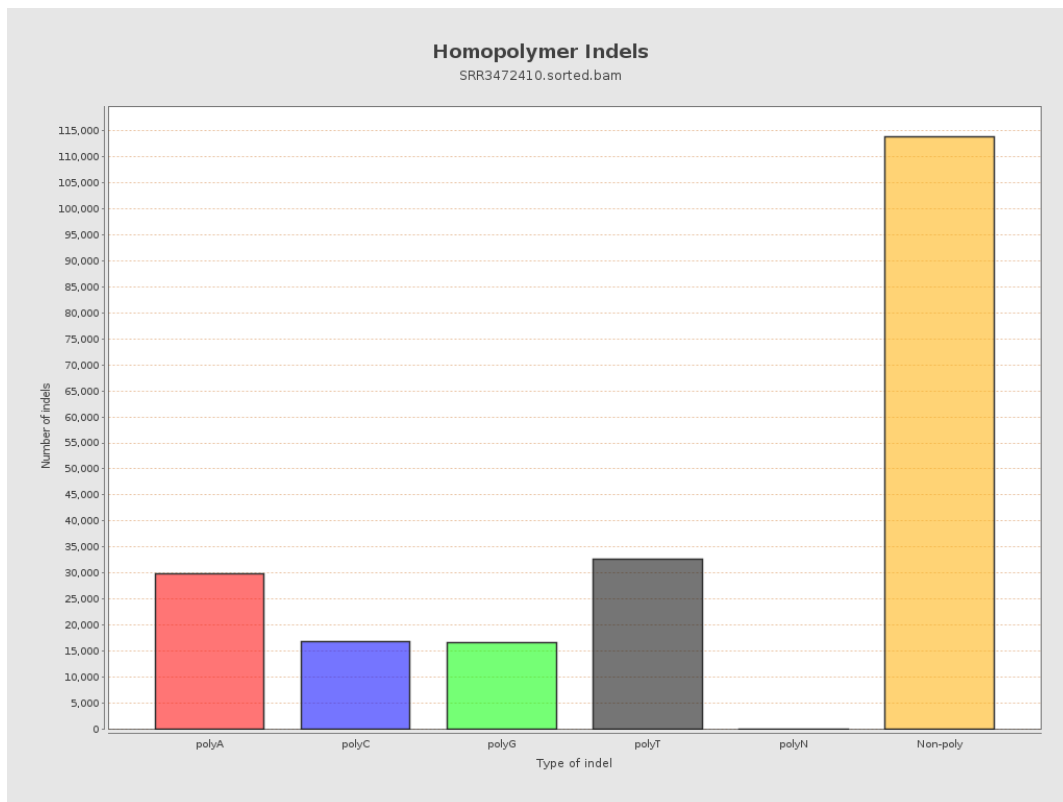
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



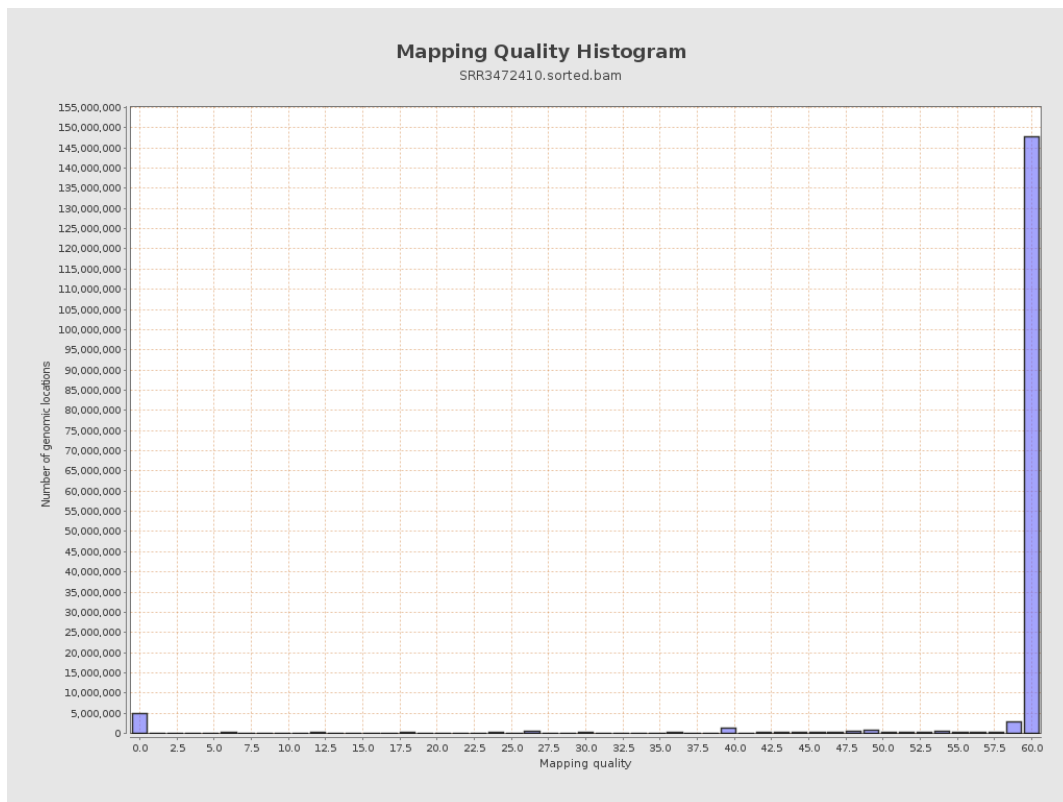
11. Results : Homopolymer Indels



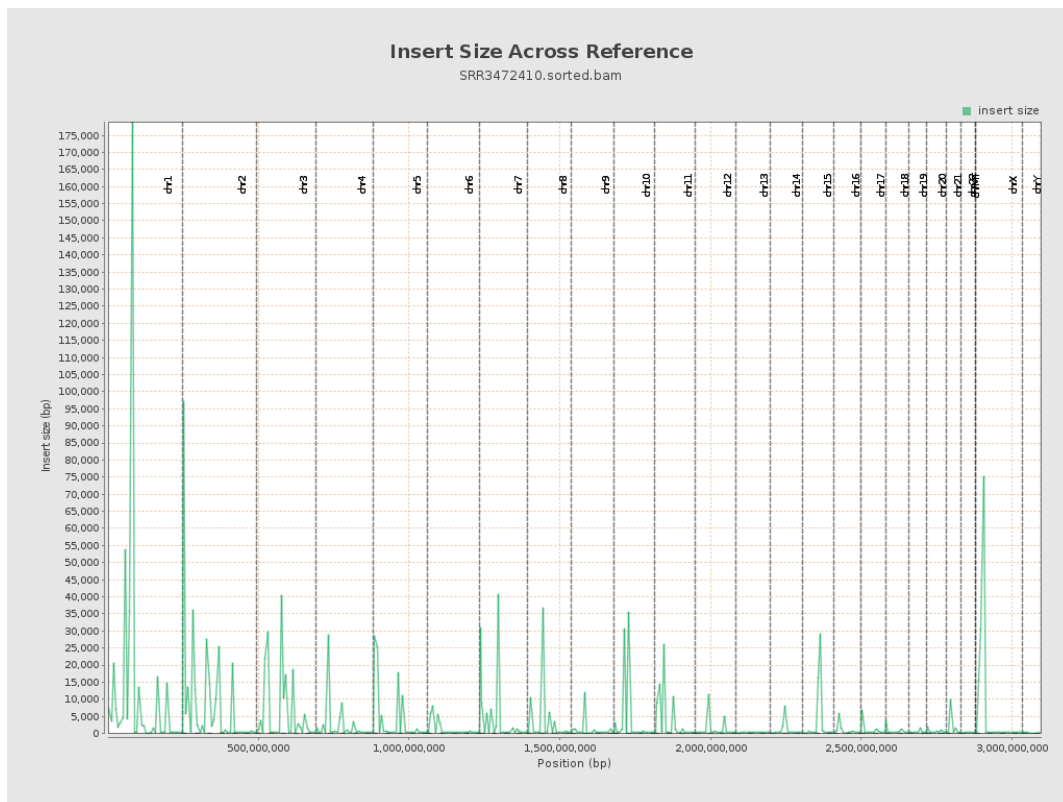
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

