

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 23:30:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472733.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_SRR3472733 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472733_1.fastq.gz SRR3472733_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 23:30:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472733.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,243,874
Mapped reads	18,078,924 / 99.1%
Unmapped reads	164,950 / 0.9%
Mapped paired reads	18,078,924 / 99.1%
Mapped reads, first in pair	9,073,600 / 49.74%
Mapped reads, second in pair	9,005,324 / 49.36%
Mapped reads, both in pair	17,974,752 / 98.52%
Mapped reads, singletons	104,172 / 0.57%
Secondary alignments	0
Supplementary alignments	66,611 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	11,668,839 / 63.96%
Duplication rate	47.58%
Clipped reads	1,239,787 / 6.8%

2.2. ACGT Content

Number/percentage of A's	497,208,092 / 27.84%
Number/percentage of C's	398,283,044 / 22.3%
Number/percentage of T's	494,680,584 / 27.7%
Number/percentage of G's	395,124,420 / 22.13%
Number/percentage of N's	342,822 / 0.02%

GC Percentage	44.43%
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2.3. Coverage

Mean	0.5769
Standard Deviation	20.0152

2.4. Mapping Quality

Mean Mapping Quality	55.26
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2.5. Insert size

Mean	23,605.55
Standard Deviation	1,533,822.77
P25/Median/P75	184 / 255 / 343

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	11,343,740
Insertions	107,716
Mapped reads with at least one insertion	0.59%
Deletions	99,516
Mapped reads with at least one deletion	0.54%
Homopolymer indels	45.53%

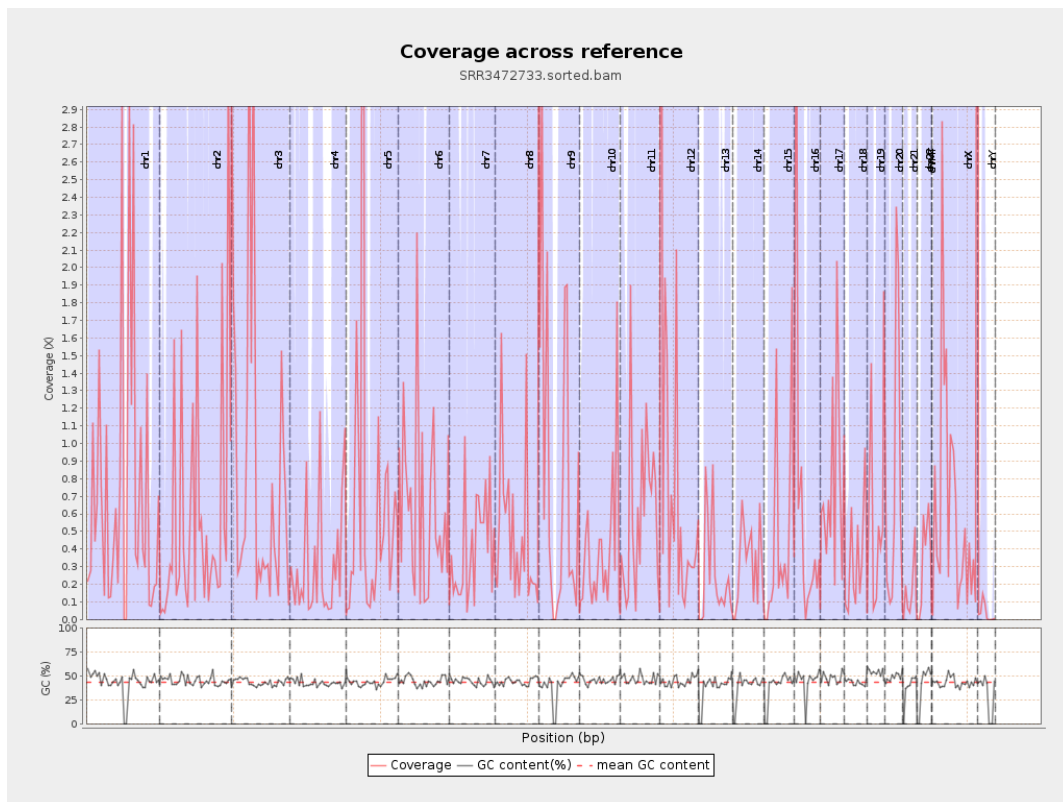
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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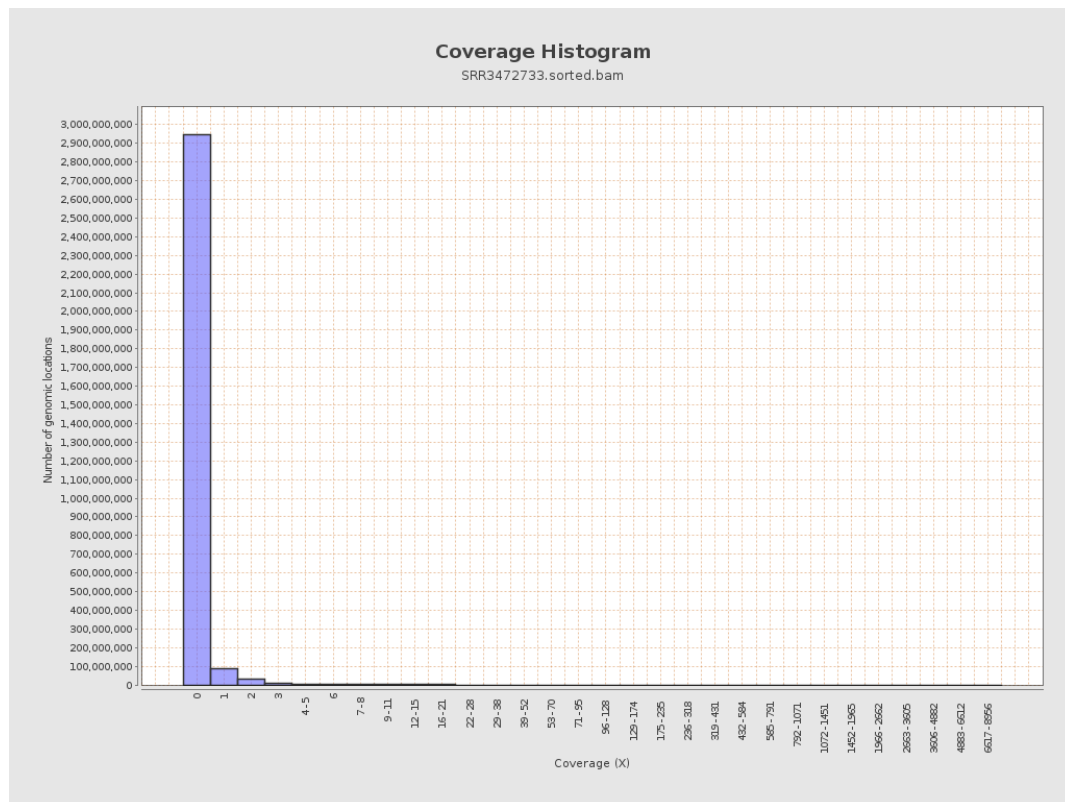
		bases	coverage	deviation
chr1	249250621	182417605	0.7319	22.3091
chr2	243199373	145733929	0.5992	27.5078
chr3	198022430	174097484	0.8792	21.1218
chr4	191154276	57407459	0.3003	11.8624
chr5	180915260	127964331	0.7073	23.7039
chr6	171115067	105232776	0.615	16.0807
chr7	159138663	64957346	0.4082	13.1399
chr8	146364022	71254667	0.4868	14.0571
chr9	141213431	116644676	0.826	20.3001
chr10	135534747	54286791	0.4005	16.1175
chr11	135006516	81896858	0.6066	25.7154
chr12	133851895	124980737	0.9337	33.3421
chr13	115169878	29409581	0.2554	9.4707
chr14	107349540	34134174	0.318	9.9402
chr15	102531392	46810048	0.4565	18.028
chr16	90354753	56198080	0.622	18.1799
chr17	81195210	61497785	0.7574	15.6031
chr18	78077248	26604061	0.3407	10.5604
chr19	59128983	33806849	0.5717	13.9272
chr20	63025520	49367589	0.7833	32.74
chr21	48129895	7829181	0.1627	7.508
chr22	51304566	16714288	0.3258	10.3344
chrMT	16571	1947	0.1175	0.5897
chrX	155270560	114237818	0.7357	23.1109

chrY	59373566	2407430	0.0405	1.7044
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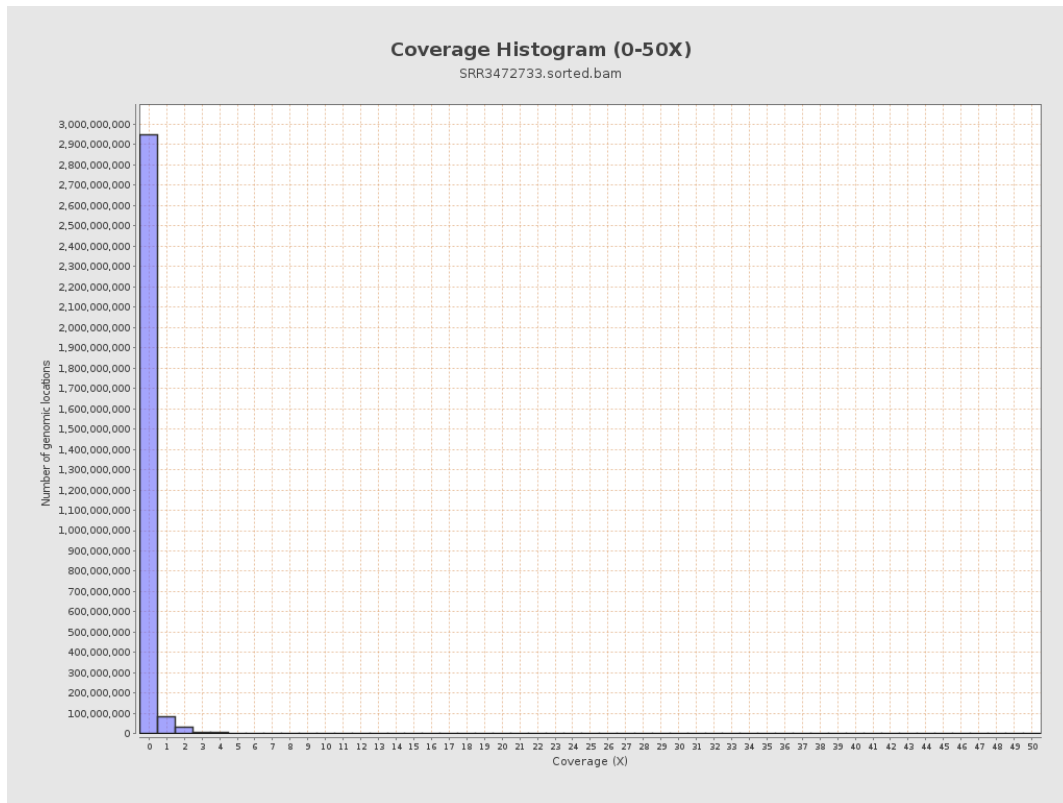
3. Results : Coverage across reference



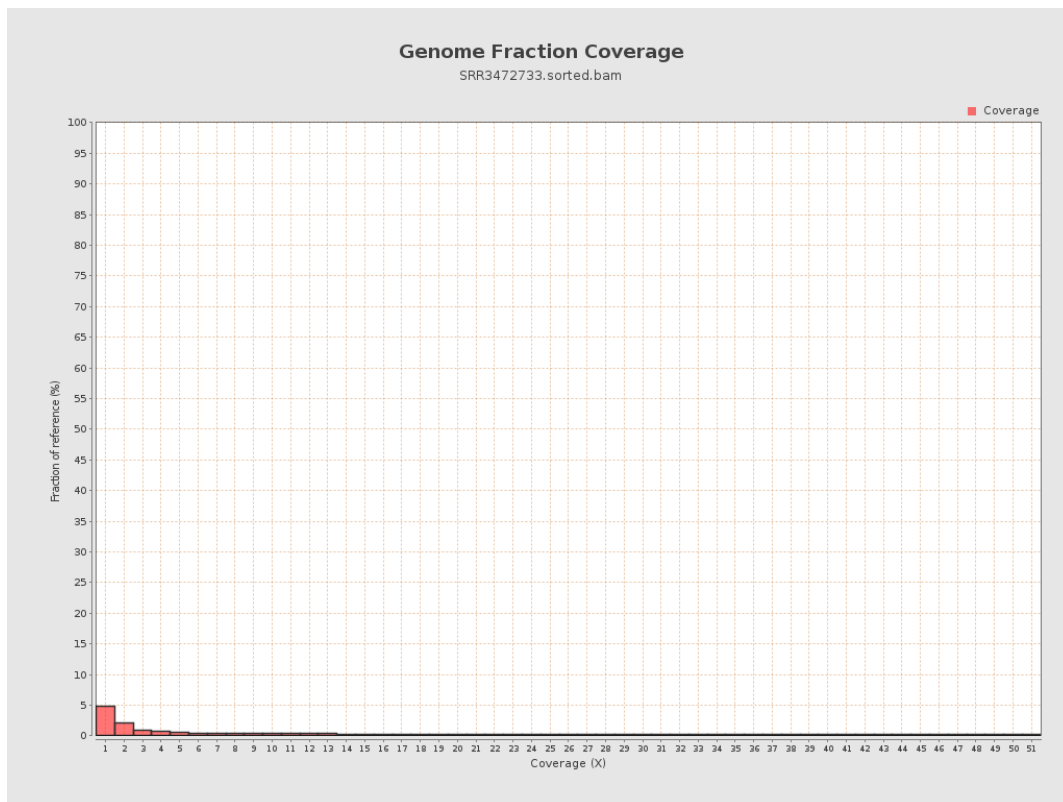
4. Results : Coverage Histogram



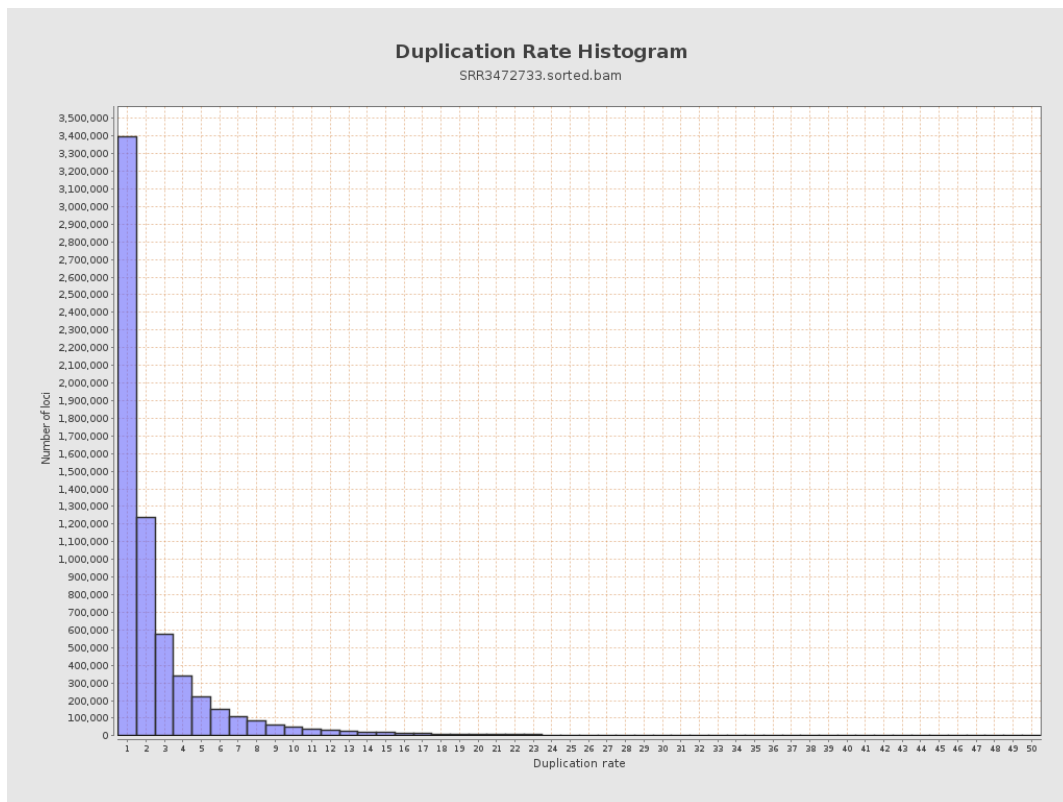
5. Results : Coverage Histogram (0-50X)



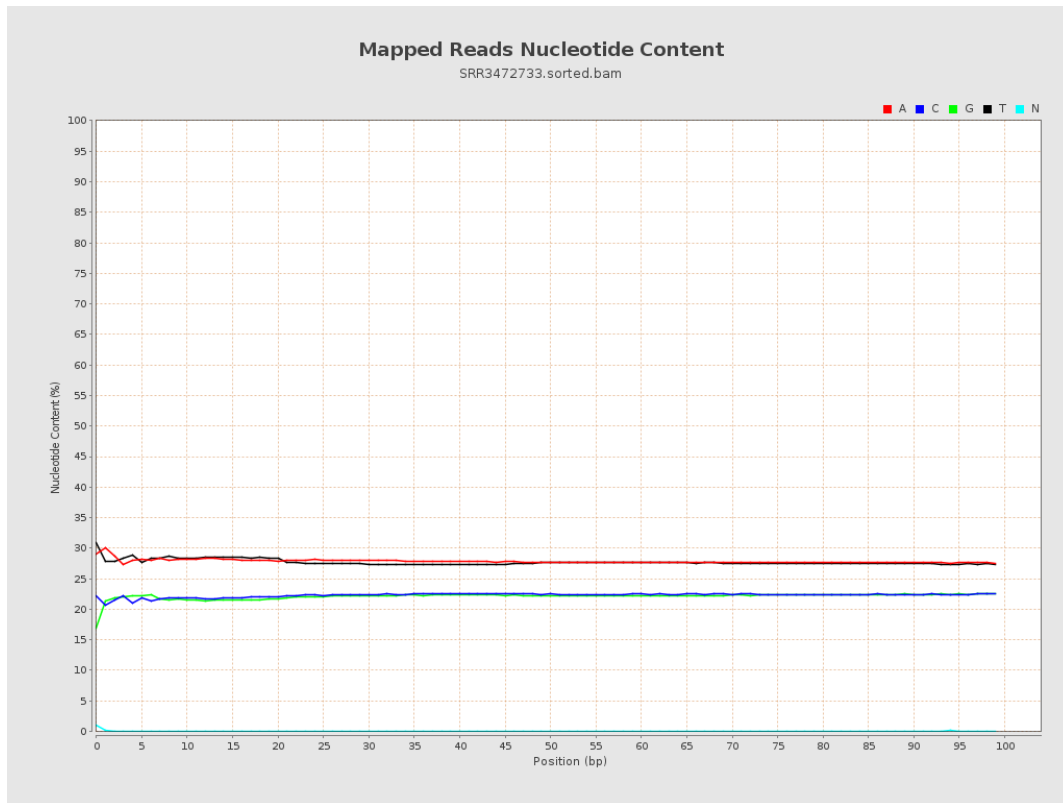
6. Results : Genome Fraction Coverage



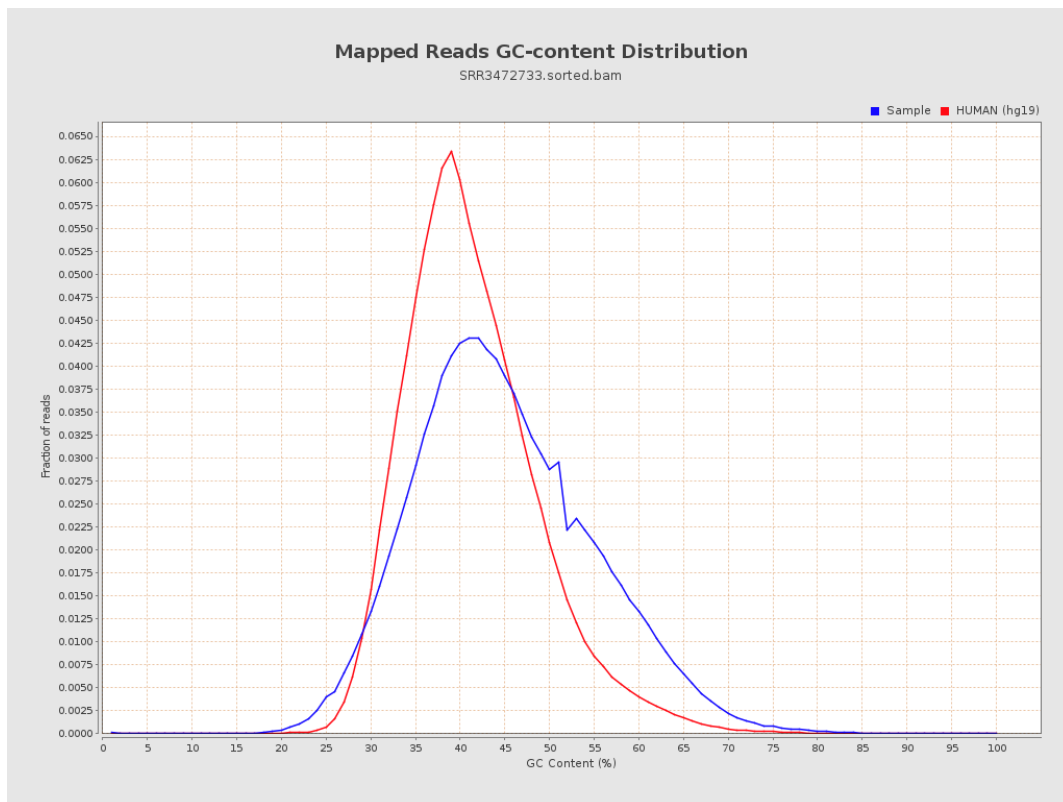
7. Results : Duplication Rate Histogram



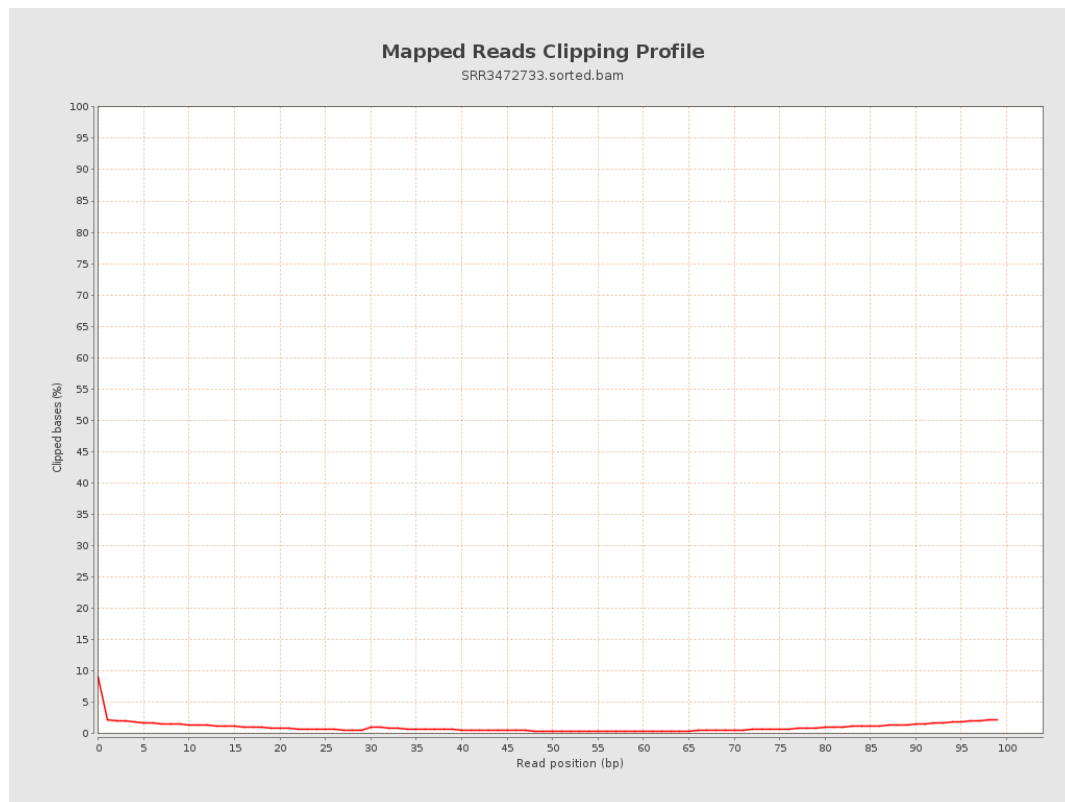
8. Results : Mapped Reads Nucleotide Content



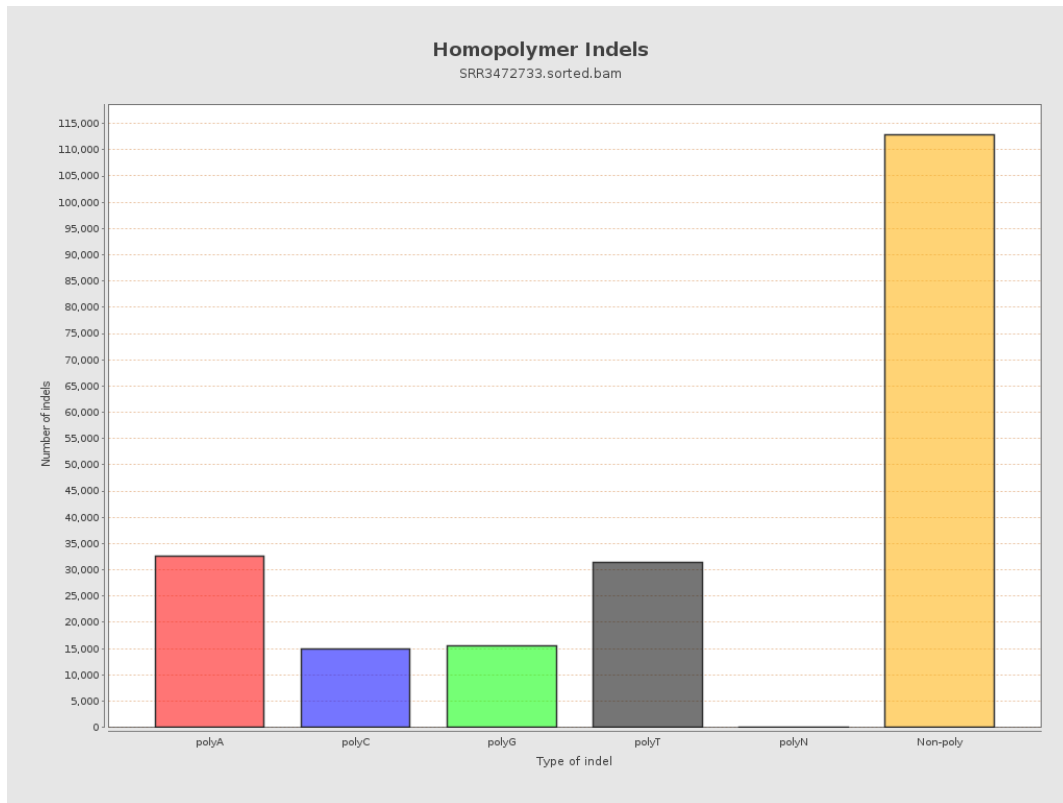
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



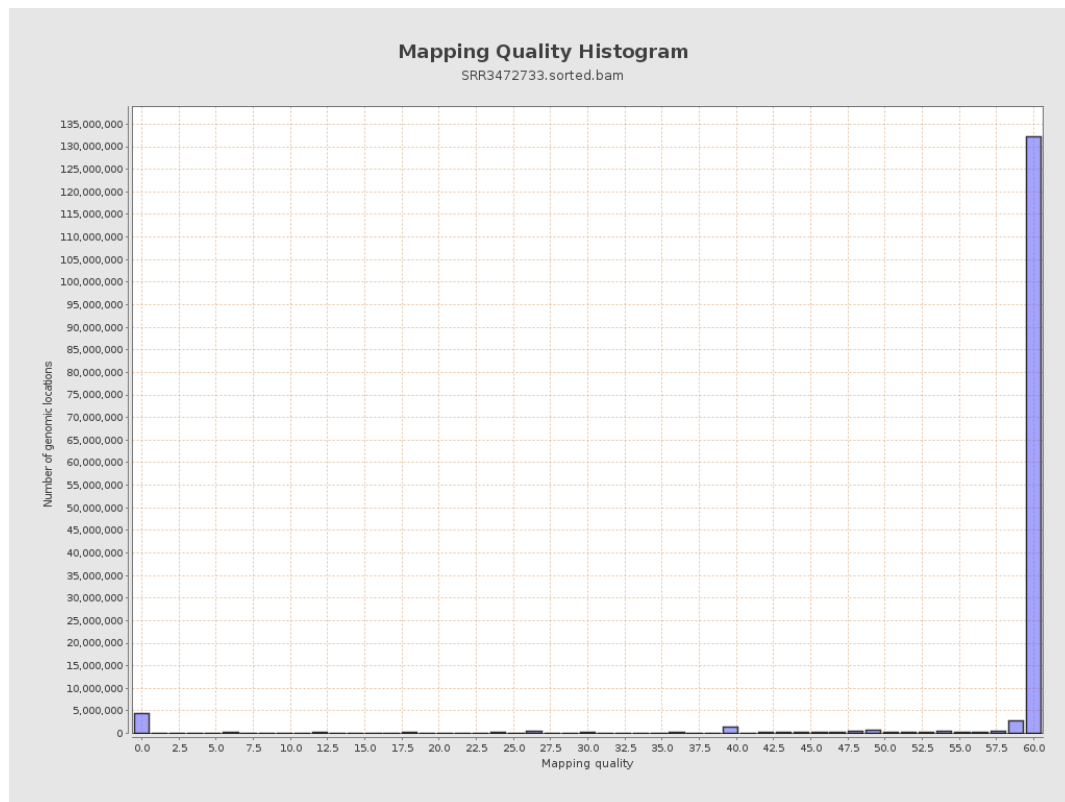
11. Results : Homopolymer Indels



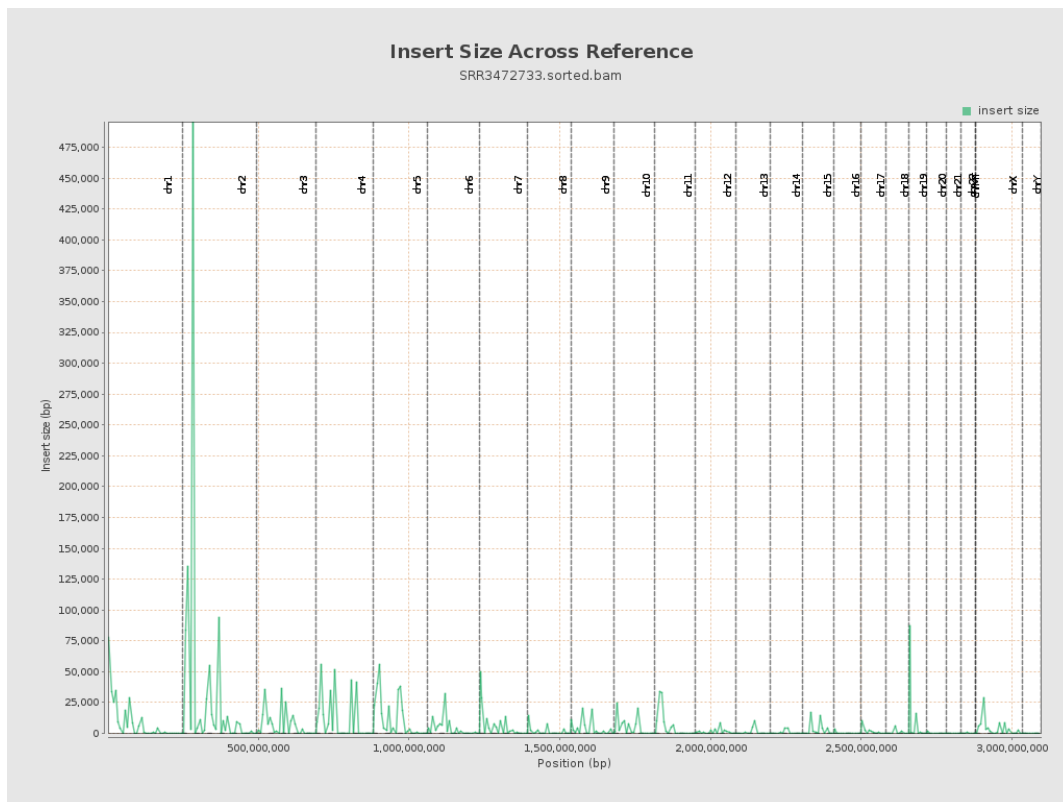
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

