Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:11:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472497.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_SRR3472497 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472497_1.fastq.gz SRR3472497_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:11:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472497.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,221,156
Mapped reads	18,990,745 / 98.8%
Unmapped reads	230,411 / 1.2%
Mapped paired reads	18,990,745 / 98.8%
Mapped reads, first in pair	9,525,066 / 49.56%
Mapped reads, second in pair	9,465,679 / 49.25%
Mapped reads, both in pair	18,877,162 / 98.21%
Mapped reads, singletons	113,583 / 0.59%
Secondary alignments	0
Supplementary alignments	67,344 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	12,504,916 / 65.06%
Duplication rate	45.77%
Clipped reads	1,663,212 / 8.65%

2.2. ACGT Content

Number/percentage of A's	502,602,768 / 26.93%
Number/percentage of C's	433,336,341 / 23.22%
Number/percentage of T's	499,341,179 / 26.75%
Number/percentage of G's	430,834,817 / 23.08%
Number/percentage of N's	290,669 / 0.02%

GC Percentage	46.3%

2.3. Coverage

Mean	0.603
Standard Deviation	23.5467

2.4. Mapping Quality

Mean Mapping Quality	54.98

2.5. Insert size

Mean	24,716.36
Standard Deviation	1,573,263.85
P25/Median/P75	163 / 227 / 306

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	11,026,169
Insertions	99,956
Mapped reads with at least one insertion	0.52%
Deletions	95,816
Mapped reads with at least one deletion	0.49%
Homopolymer indels	44.16%

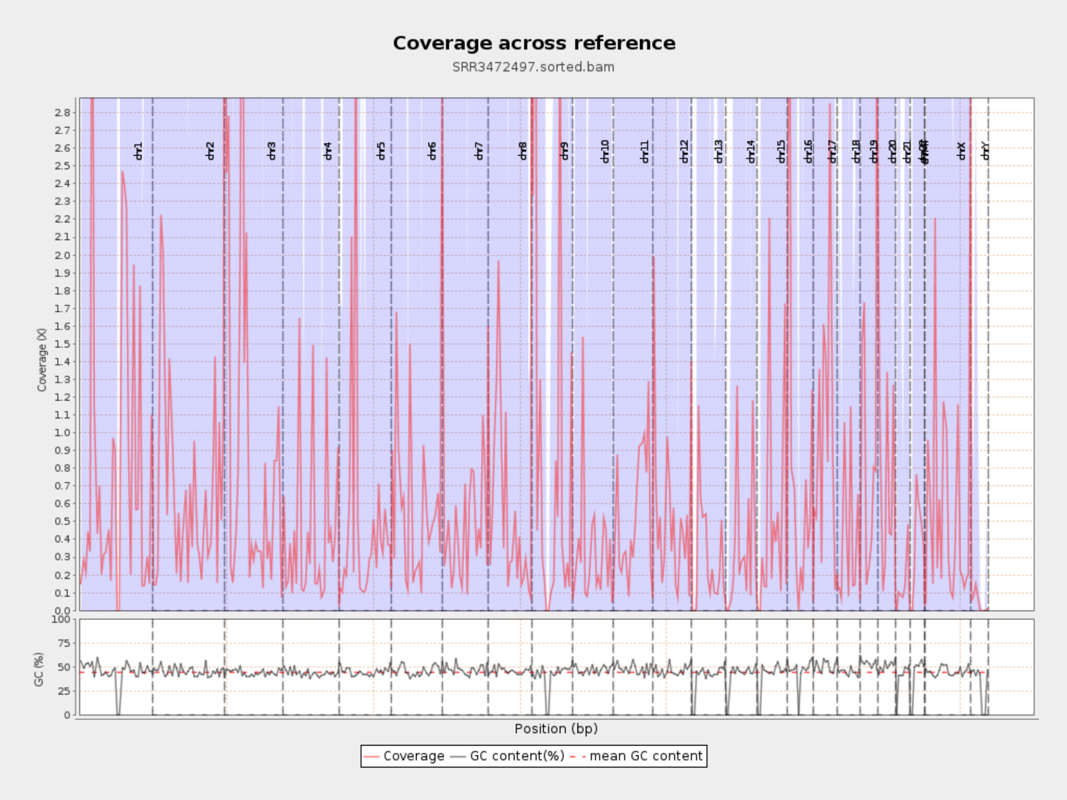
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

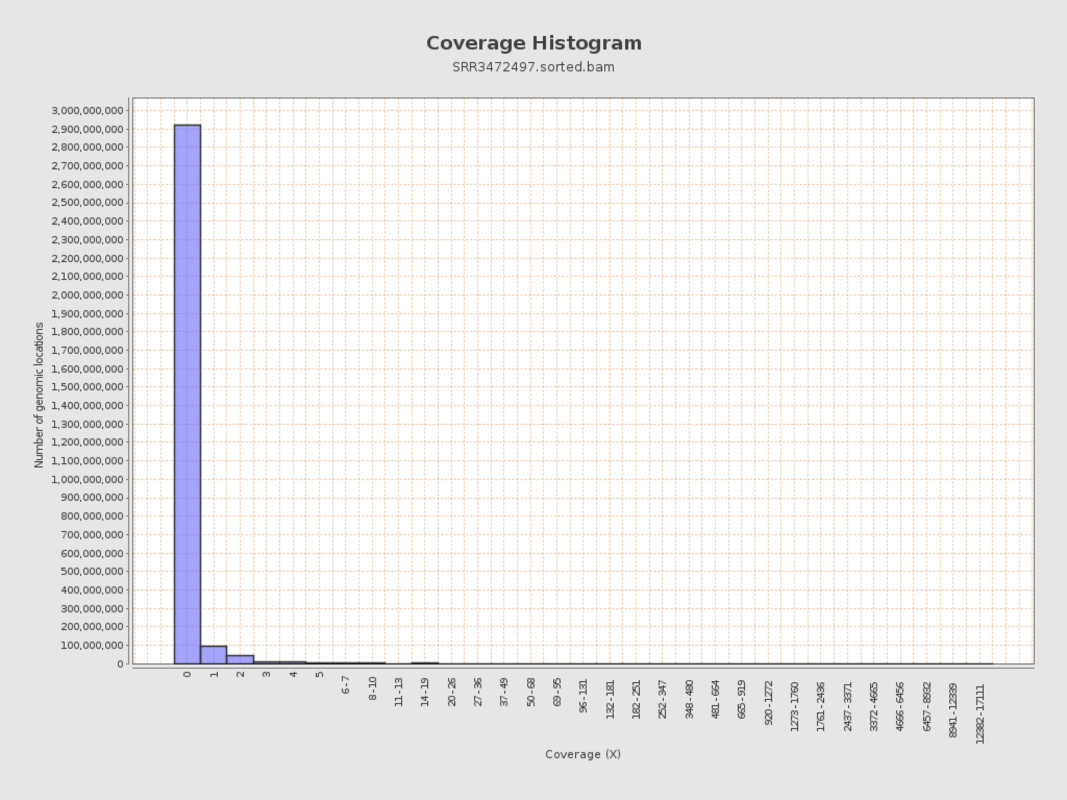
		bases	coverage	deviation
chr1	249250621	205285238	0.8236	36.2419
chr2	243199373	162387431	0.6677	27.6097
chr3	198022430	200735457	1.0137	23.4939
chr4	191154276	82154973	0.4298	18.8867
chr5	180915260	94688107	0.5234	21.9616
chr6	171115067	97929716	0.5723	16.4415
chr7	159138663	83263067	0.5232	20.9067
chr8	146364022	77702872	0.5309	21.889
chr9	141213431	144673654	1.0245	38.2395
chr10	135534747	45610293	0.3365	14.1938
chr11	135006516	72780391	0.5391	18.1018
chr12	133851895	70443396	0.5263	16.8855
chr13	115169878	34141836	0.2964	13.963
chr14	107349540	37665032	0.3509	14.1764
chr15	102531392	56524873	0.5513	32.2397
chr16	90354753	74422559	0.8237	25.758
chr17	81195210	80732855	0.9943	23.4873
chr18	78077248	32025579	0.4102	17.4663
chr19	59128983	50966616	0.862	26.9118
chr20	63025520	47760938	0.7578	29.907
chr21	48129895	7162736	0.1488	5.2821
chr22	51304566	18965663	0.3697	11.2404
chrMT	16571	1767	0.1066	0.3507
chrX	155270560	85852972	0.5529	18.0011

chrY	59373566	2780507	0.0468	1.1756

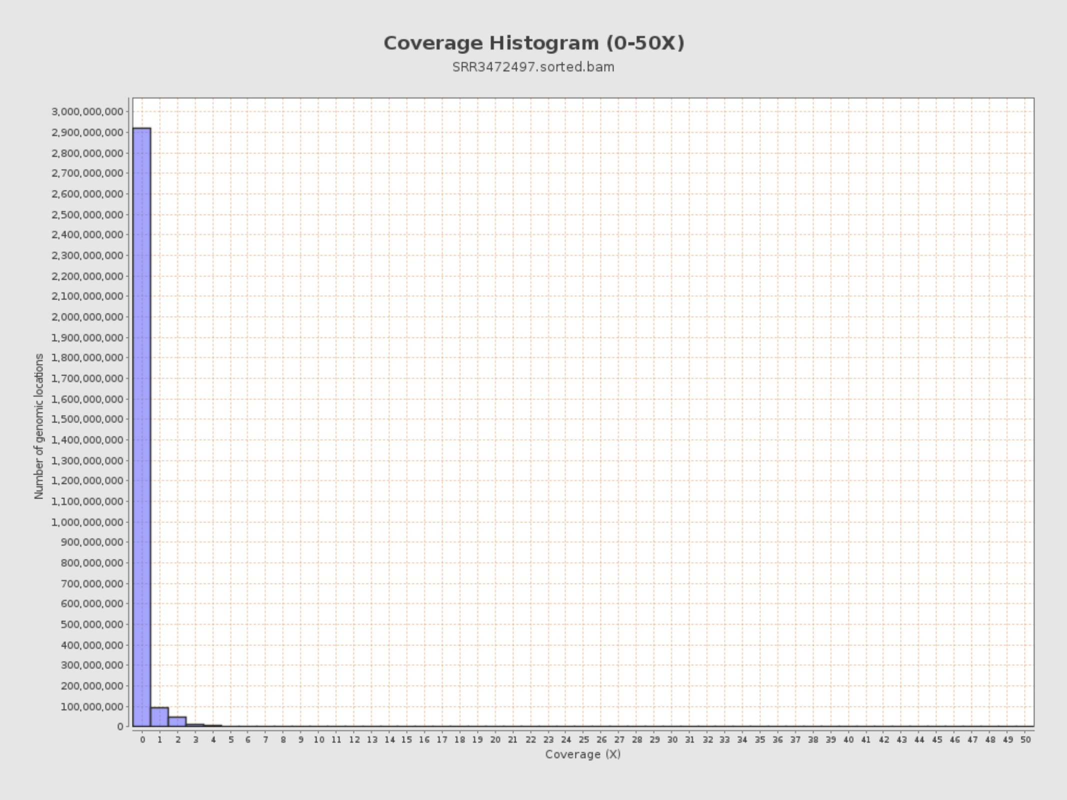
3. Results : Coverage across reference



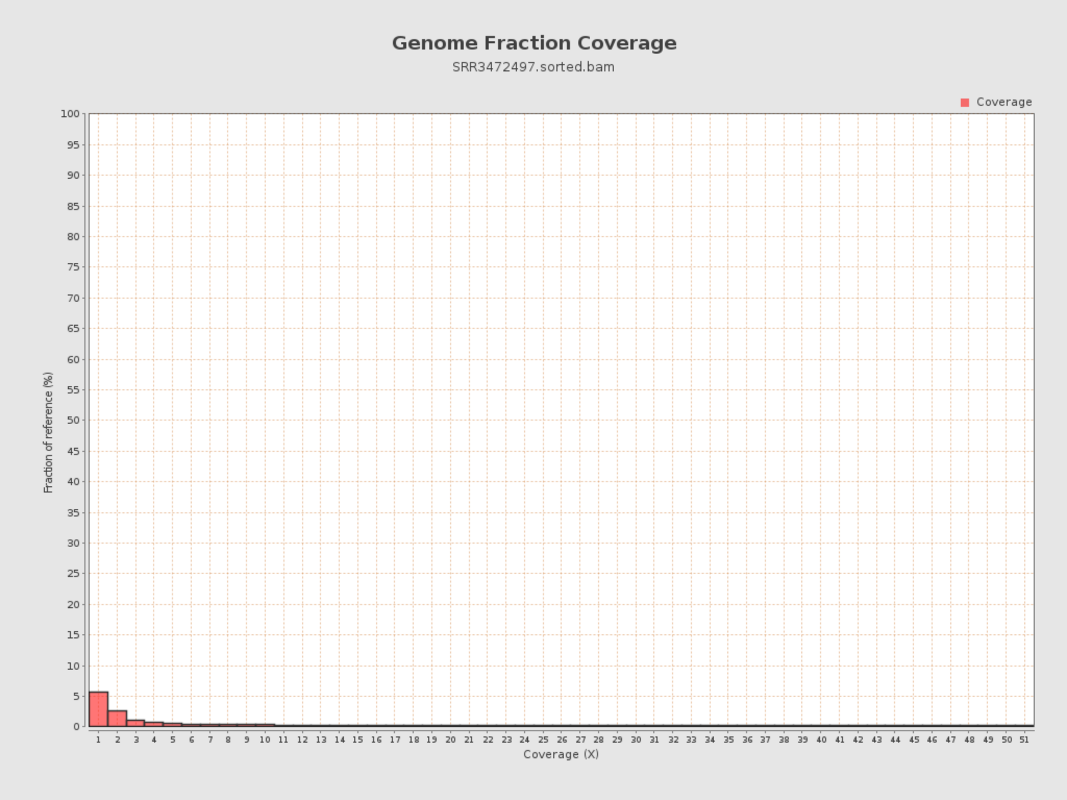
4. Results : Coverage Histogram



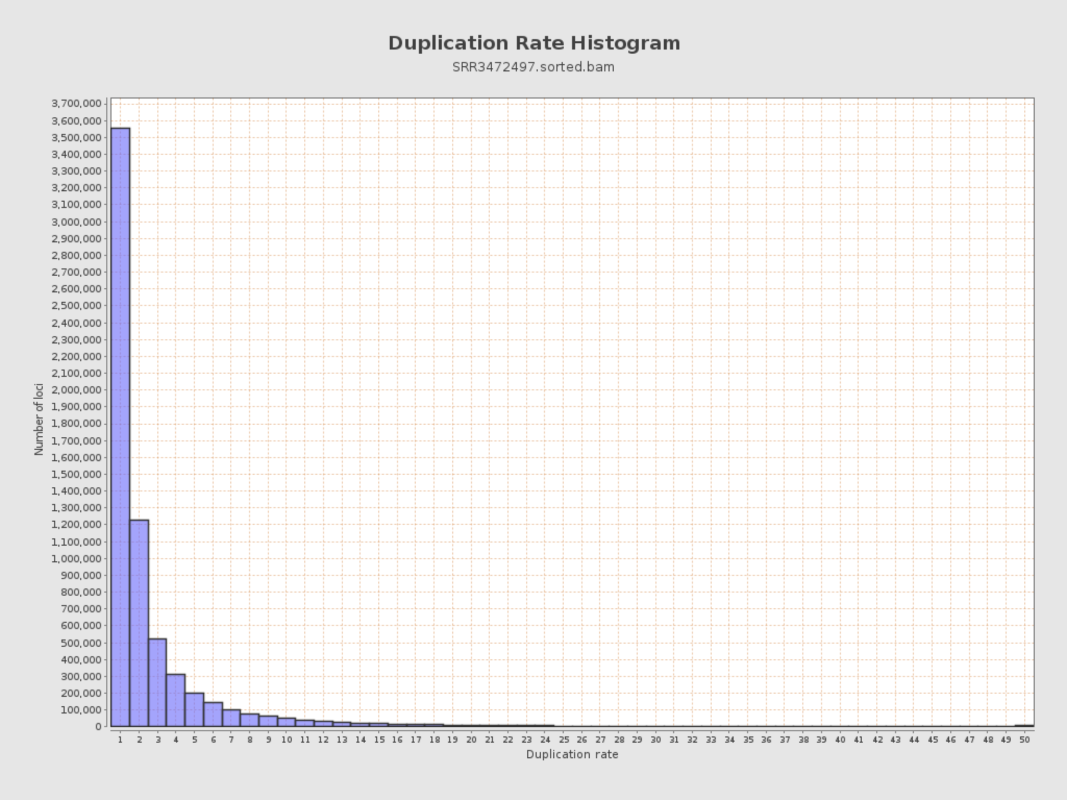
5. Results : Coverage Histogram (0-50X)



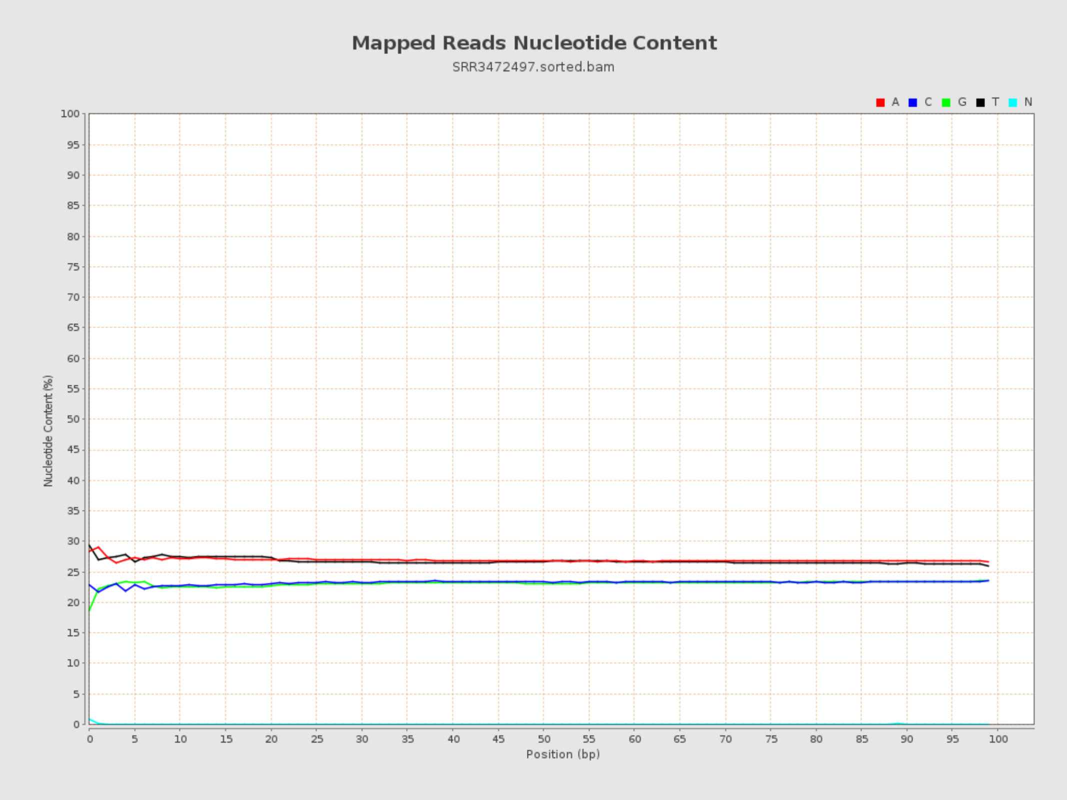
6. Results : Genome Fraction Coverage



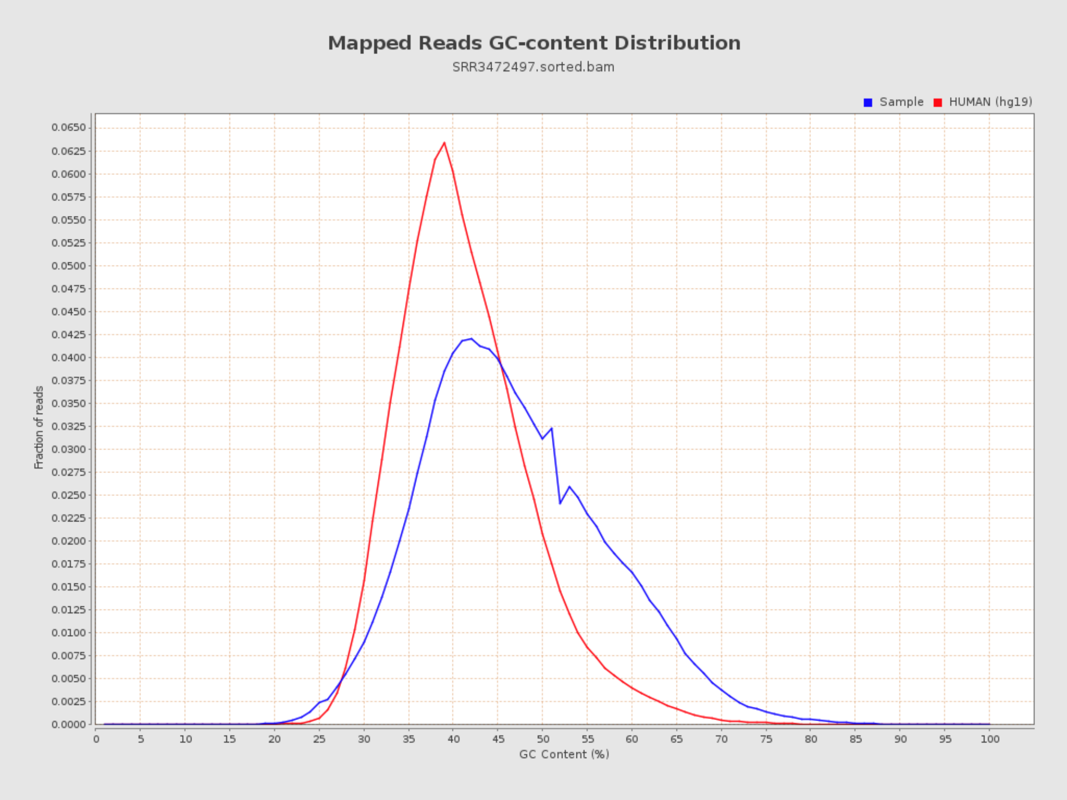
7. Results : Duplication Rate Histogram



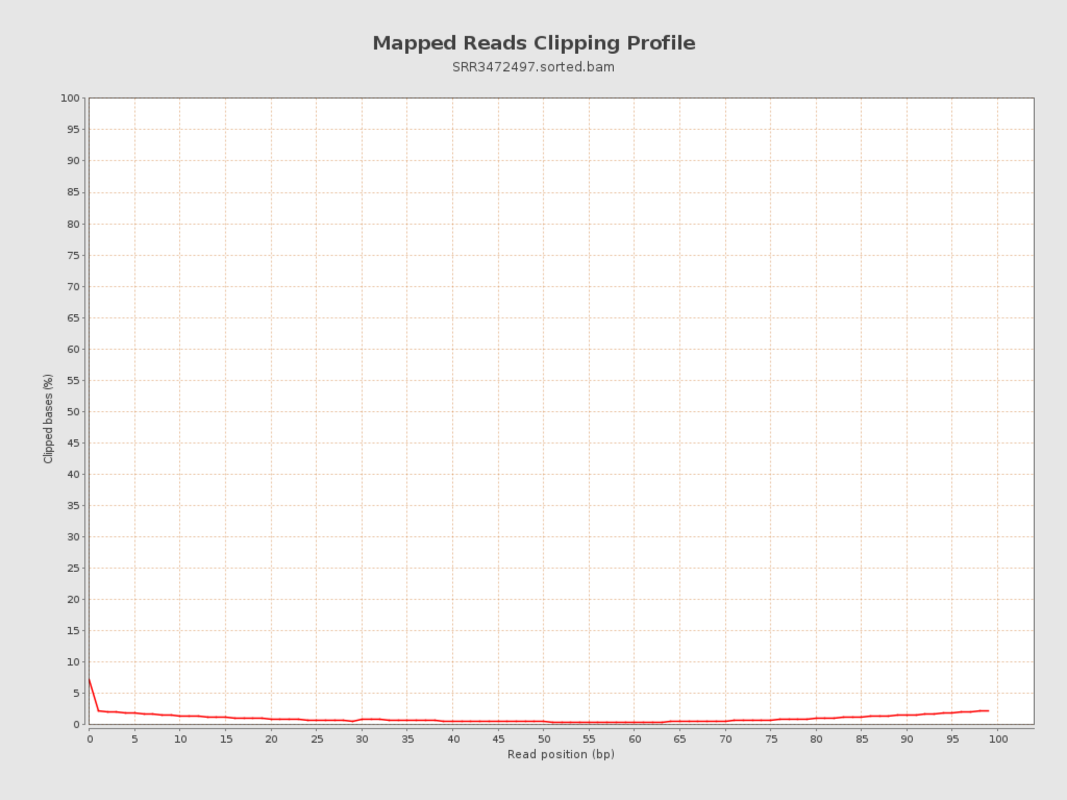
8. Results : Mapped Reads Nucleotide Content



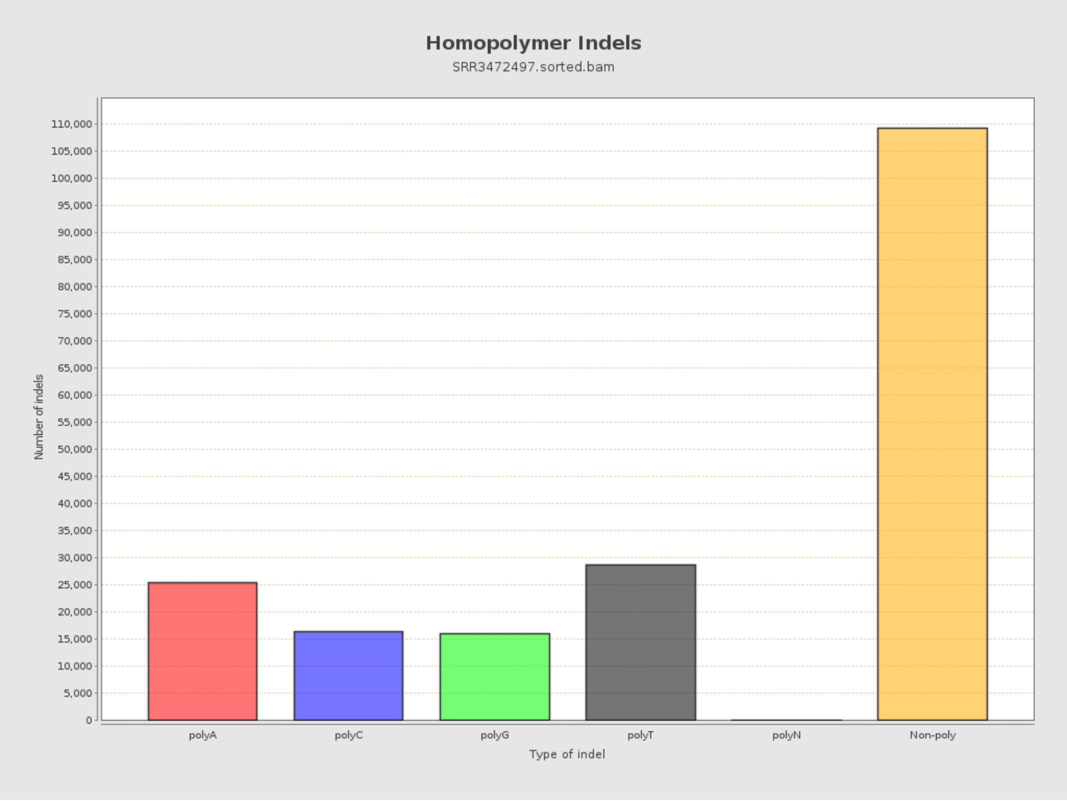
9. Results : Mapped Reads GC-content Distribution



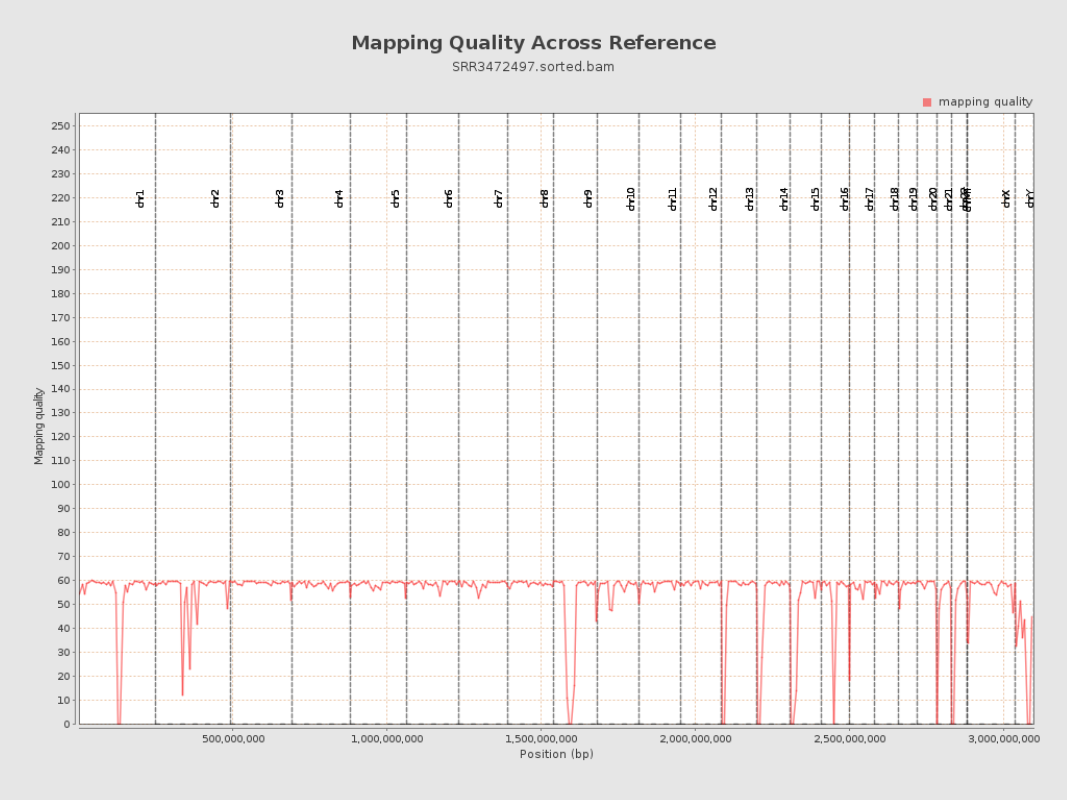
10. Results : Mapped Reads Clipping Profile



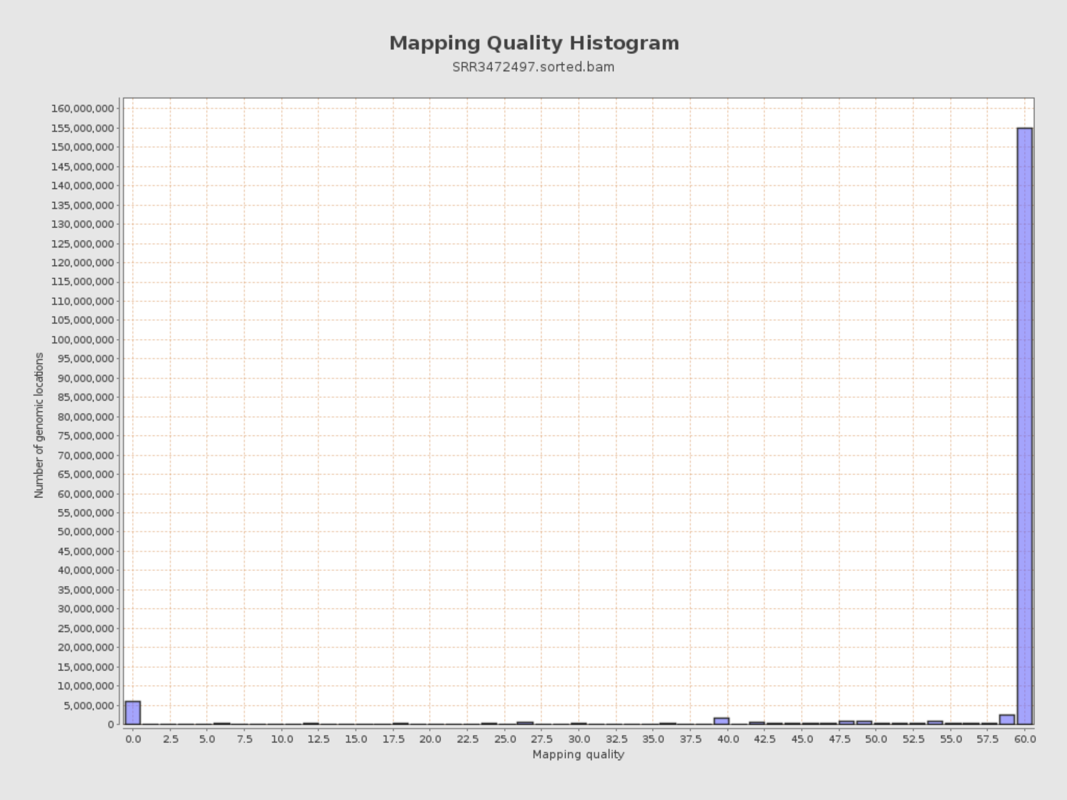
11. Results : Homopolymer Indels



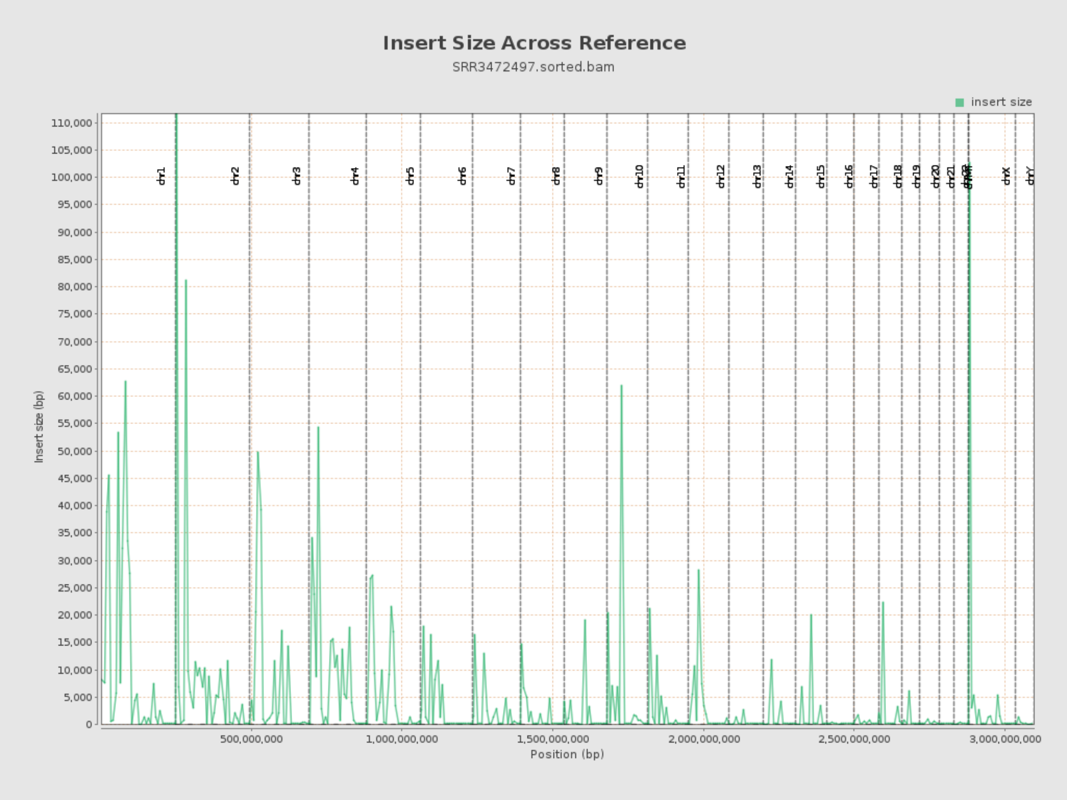
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram