

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:38:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472492.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_SRR3472492 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472492_1.fastq.gz SRR3472492_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:38:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472492.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,448,592
Mapped reads	17,117,552 / 98.1%
Unmapped reads	331,040 / 1.9%
Mapped paired reads	17,117,552 / 98.1%
Mapped reads, first in pair	8,619,615 / 49.4%
Mapped reads, second in pair	8,497,937 / 48.7%
Mapped reads, both in pair	16,938,096 / 97.07%
Mapped reads, singletons	179,456 / 1.03%
Secondary alignments	0
Supplementary alignments	80,713 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	10,947,850 / 62.74%
Duplication rate	44.92%
Clipped reads	1,403,014 / 8.04%

2.2. ACGT Content

Number/percentage of A's	472,867,373 / 28.06%
Number/percentage of C's	371,559,055 / 22.05%
Number/percentage of T's	470,694,536 / 27.93%
Number/percentage of G's	369,845,085 / 21.95%
Number/percentage of N's	259,271 / 0.02%

GC Percentage	43.99%
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2.3. Coverage

Mean	0.5445
Standard Deviation	20.8234

2.4. Mapping Quality

Mean Mapping Quality	54.85
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2.5. Insert size

Mean	33,242.66
Standard Deviation	1,782,040.36
P25/Median/P75	176 / 246 / 334

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	11,077,378
Insertions	96,129
Mapped reads with at least one insertion	0.55%
Deletions	97,604
Mapped reads with at least one deletion	0.56%
Homopolymer indels	45.38%

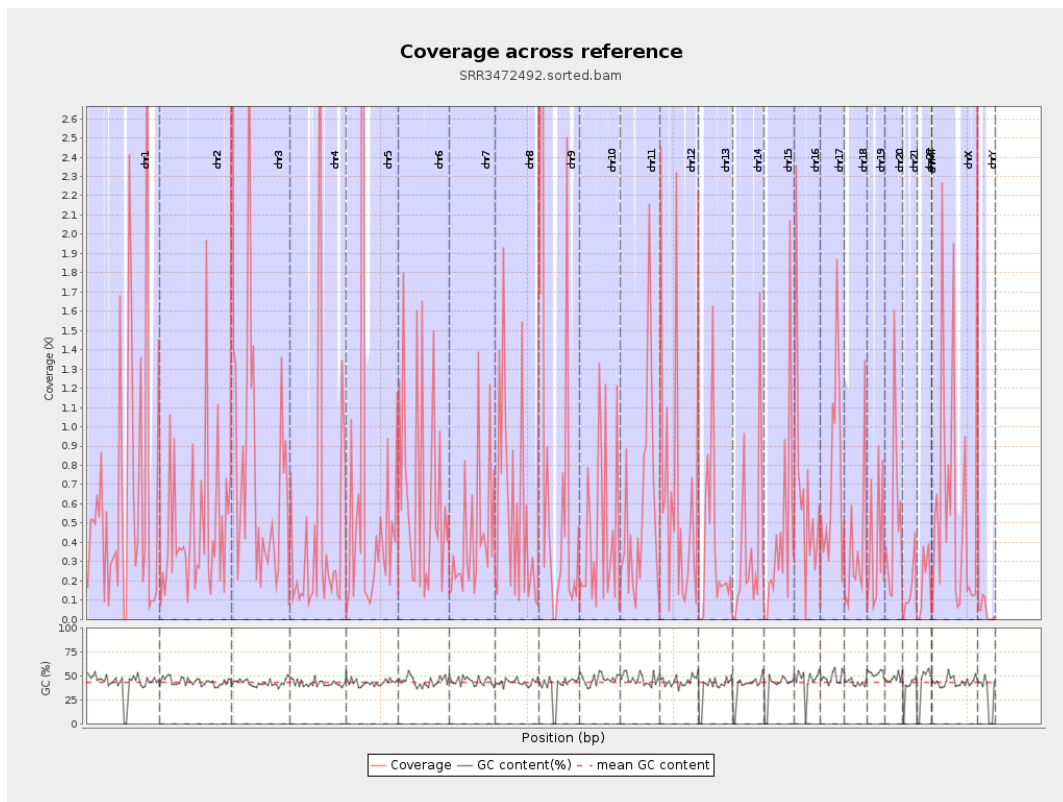
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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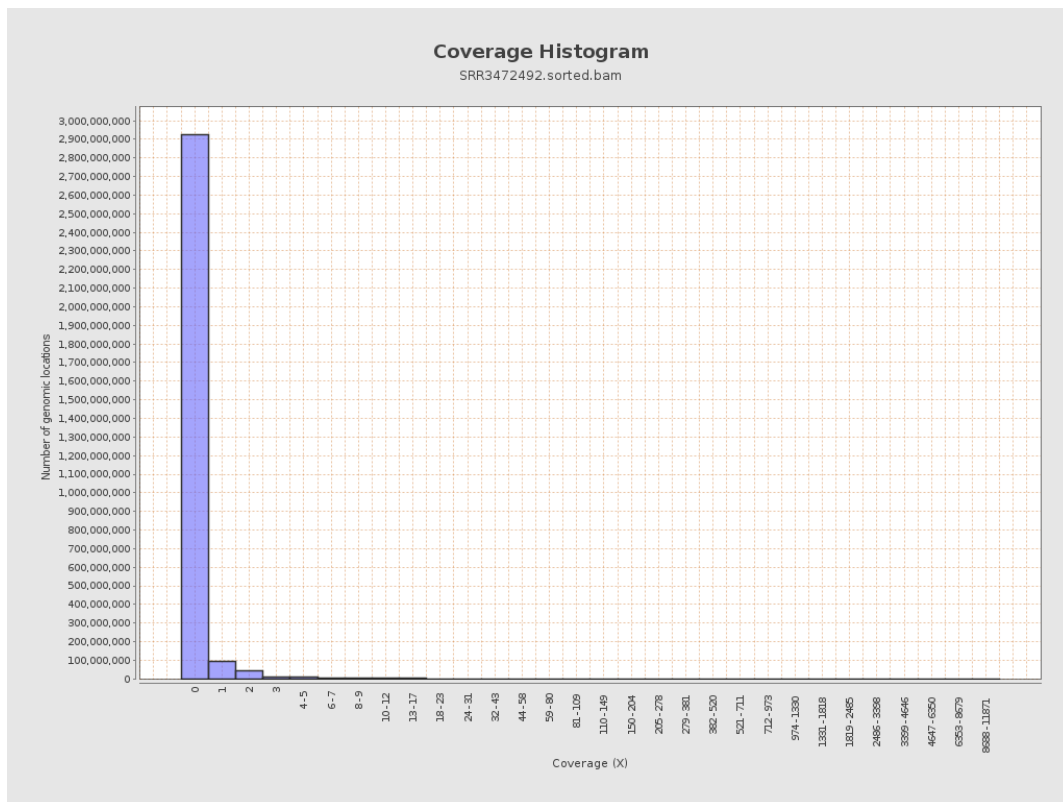
		bases	coverage	deviation
chr1	249250621	161899082	0.6495	27.0598
chr2	243199373	114274317	0.4699	21.7292
chr3	198022430	162938333	0.8228	19.2287
chr4	191154276	81243911	0.425	19.9575
chr5	180915260	116301067	0.6428	26.2393
chr6	171115067	112684691	0.6585	22.3092
chr7	159138663	68964606	0.4334	13.0249
chr8	146364022	83053570	0.5674	21.1259
chr9	141213431	118048835	0.836	26.9001
chr10	135534747	62925557	0.4643	22.4598
chr11	135006516	77994641	0.5777	26.4991
chr12	133851895	88566829	0.6617	20.224
chr13	115169878	40246108	0.3494	19.919
chr14	107349540	38297757	0.3568	13.3939
chr15	102531392	44752663	0.4365	17.1088
chr16	90354753	57738728	0.639	19.0583
chr17	81195210	59373895	0.7312	17.555
chr18	78077248	27349932	0.3503	13.5979
chr19	59128983	24554610	0.4153	14.9758
chr20	63025520	34395321	0.5457	18.5609
chr21	48129895	7253171	0.1507	6.8189
chr22	51304566	9313205	0.1815	5.1448
chrMT	16571	4290	0.2589	0.9024
chrX	155270560	90622486	0.5836	20.8356

chrY	59373566	2662602	0.0448	1.768
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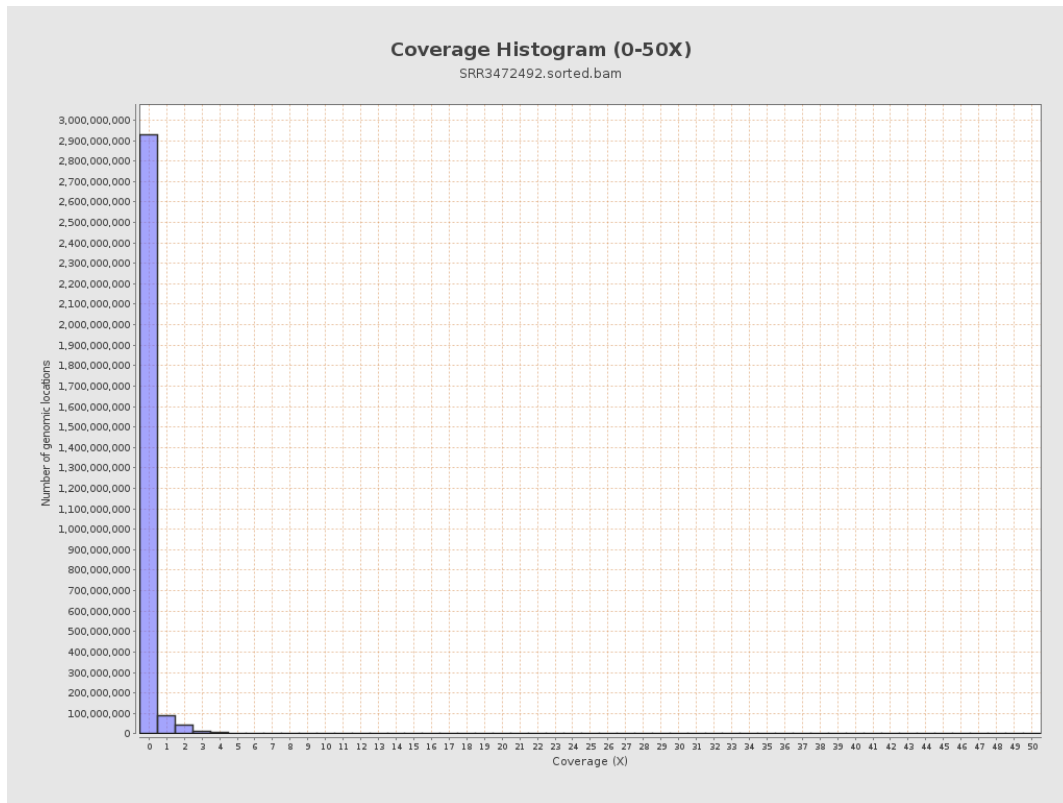
3. Results : Coverage across reference



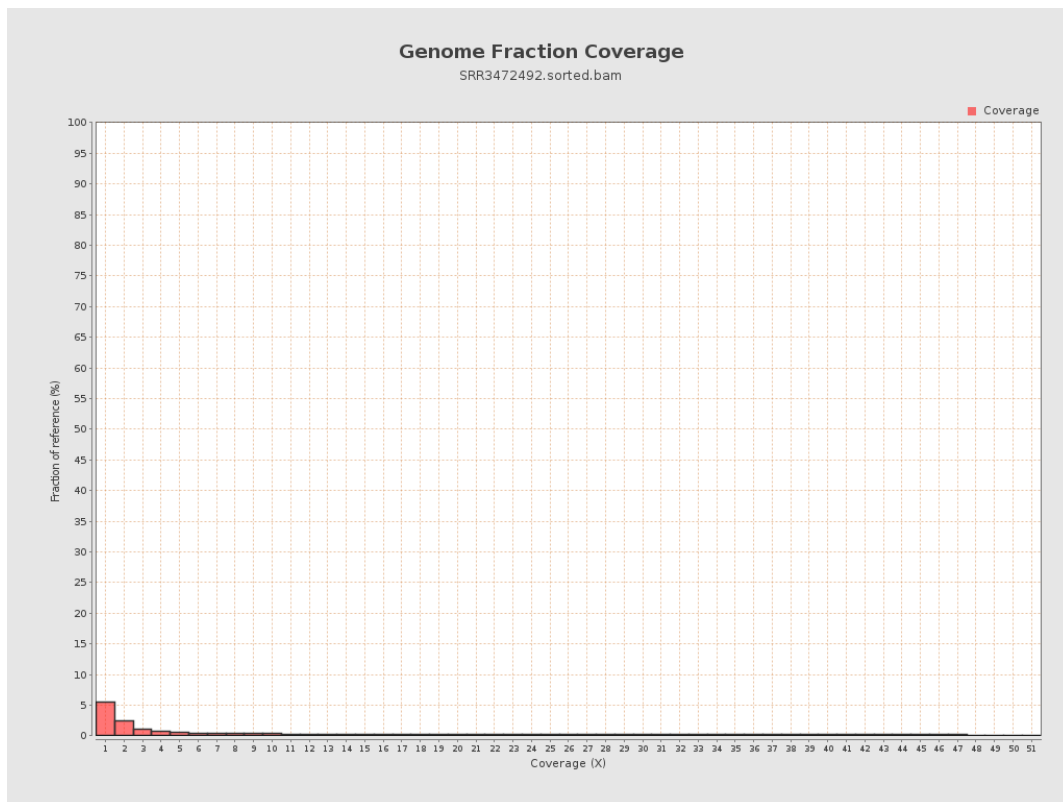
4. Results : Coverage Histogram



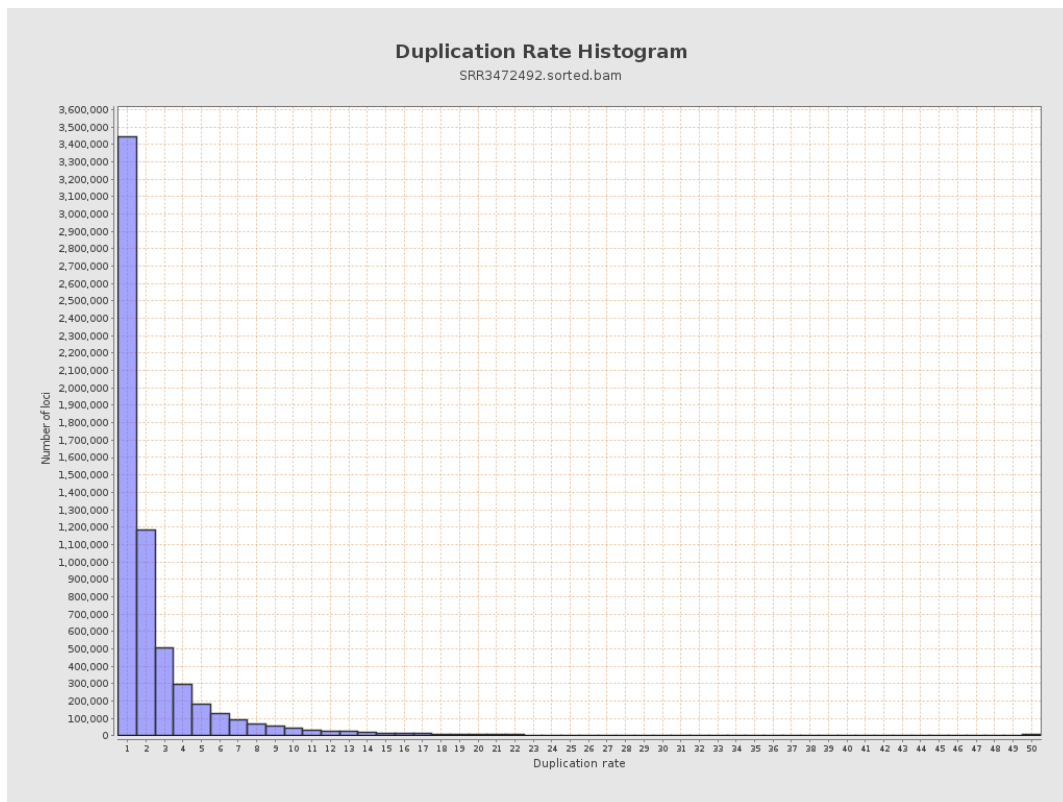
5. Results : Coverage Histogram (0-50X)



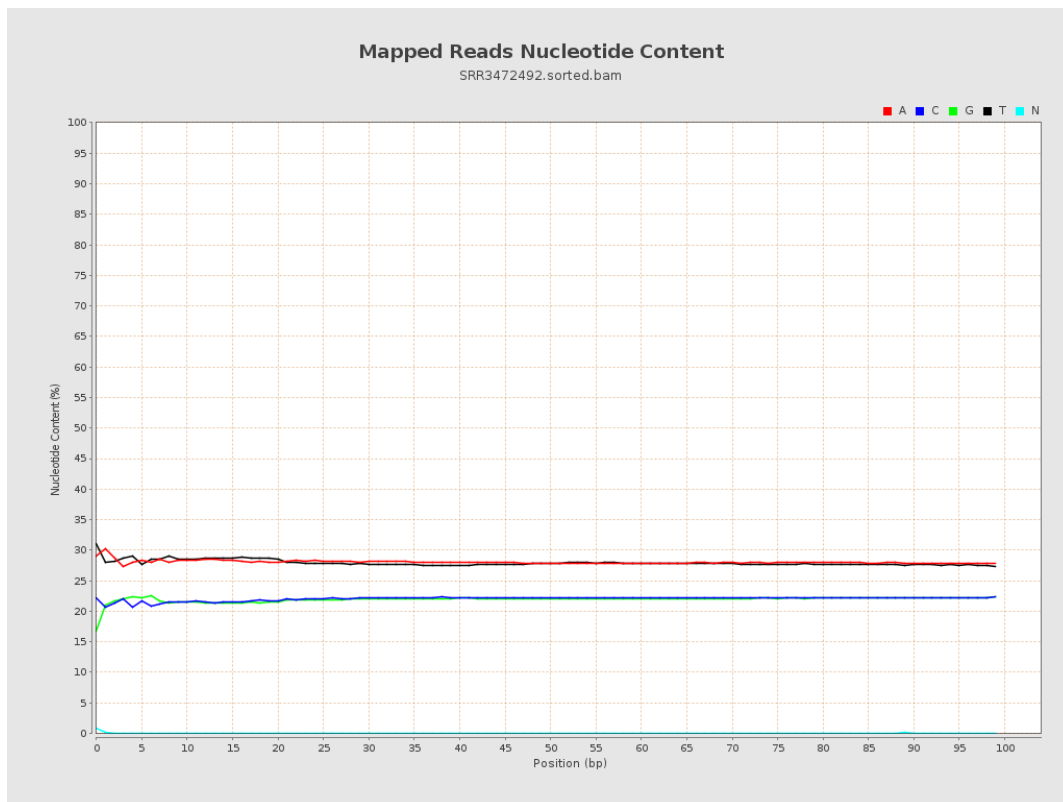
6. Results : Genome Fraction Coverage



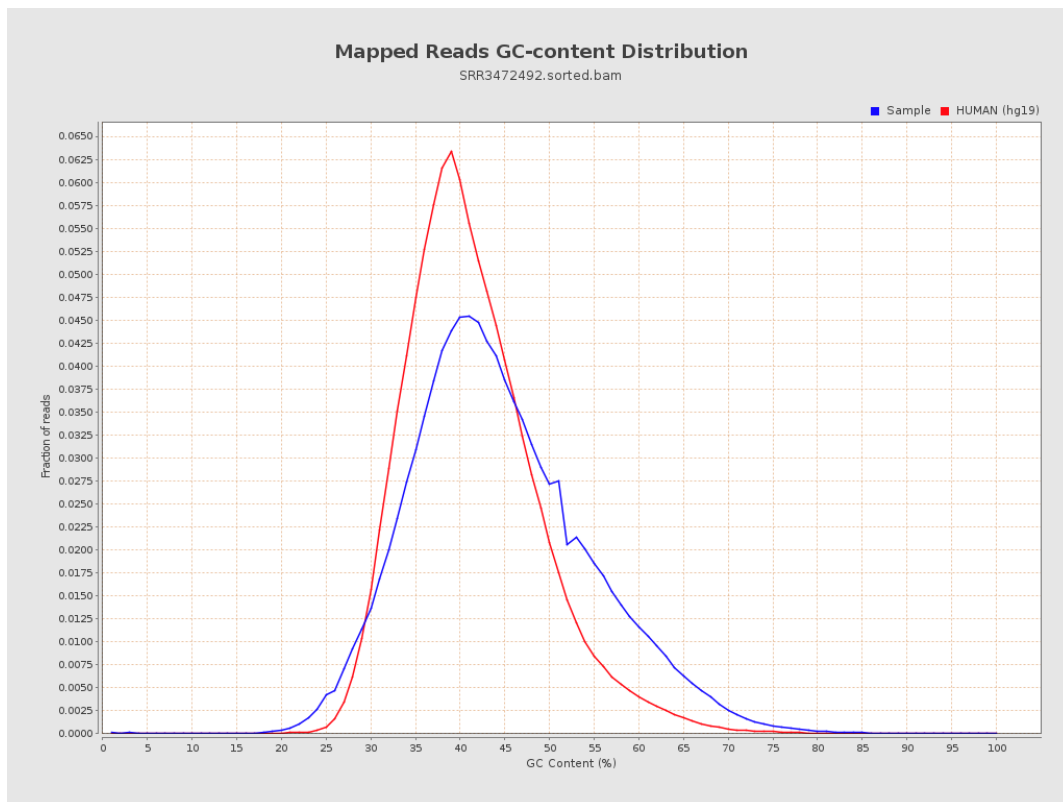
7. Results : Duplication Rate Histogram



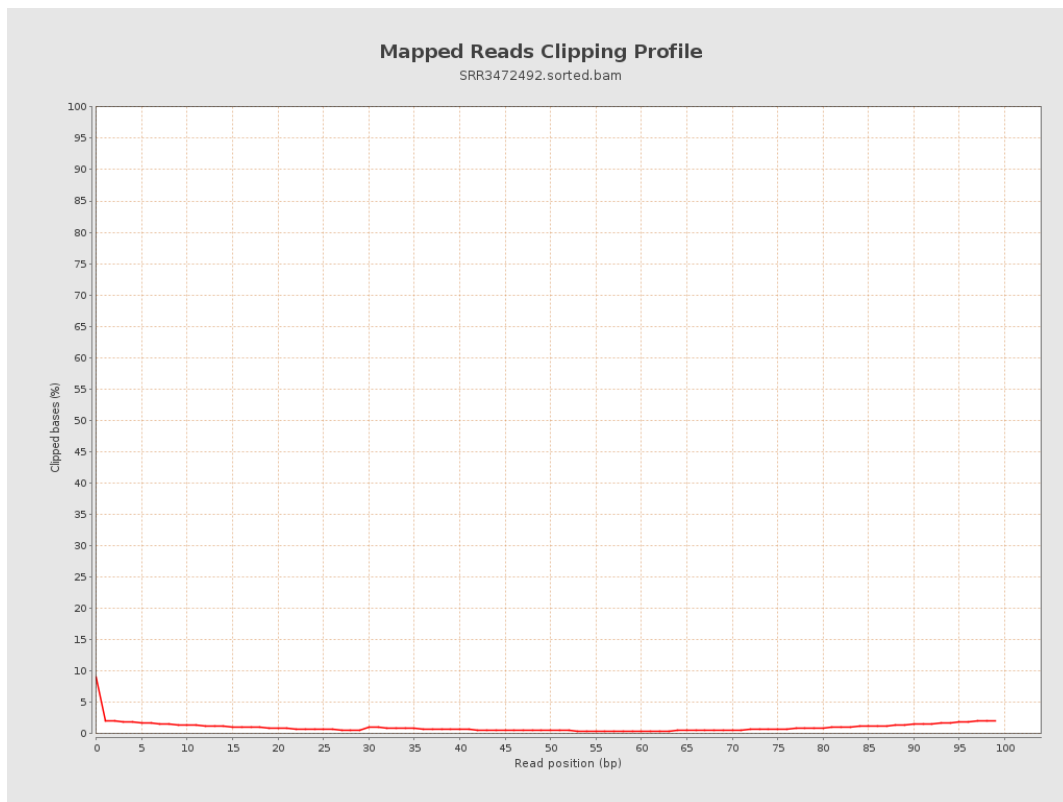
8. Results : Mapped Reads Nucleotide Content



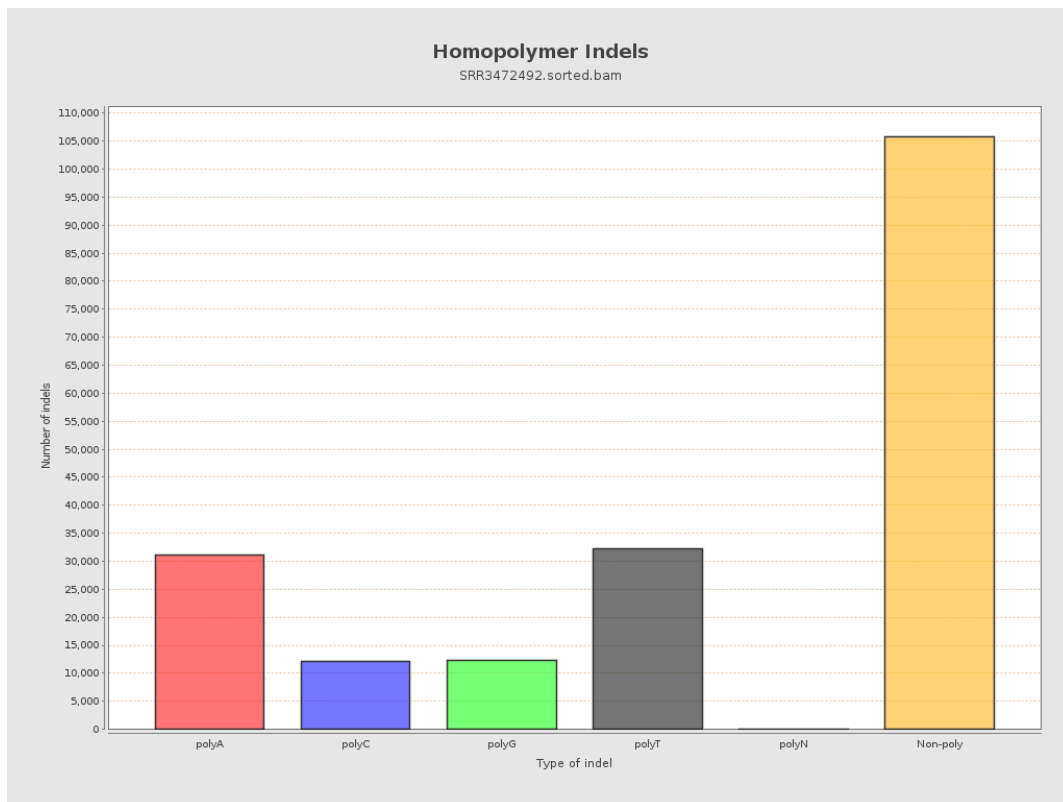
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



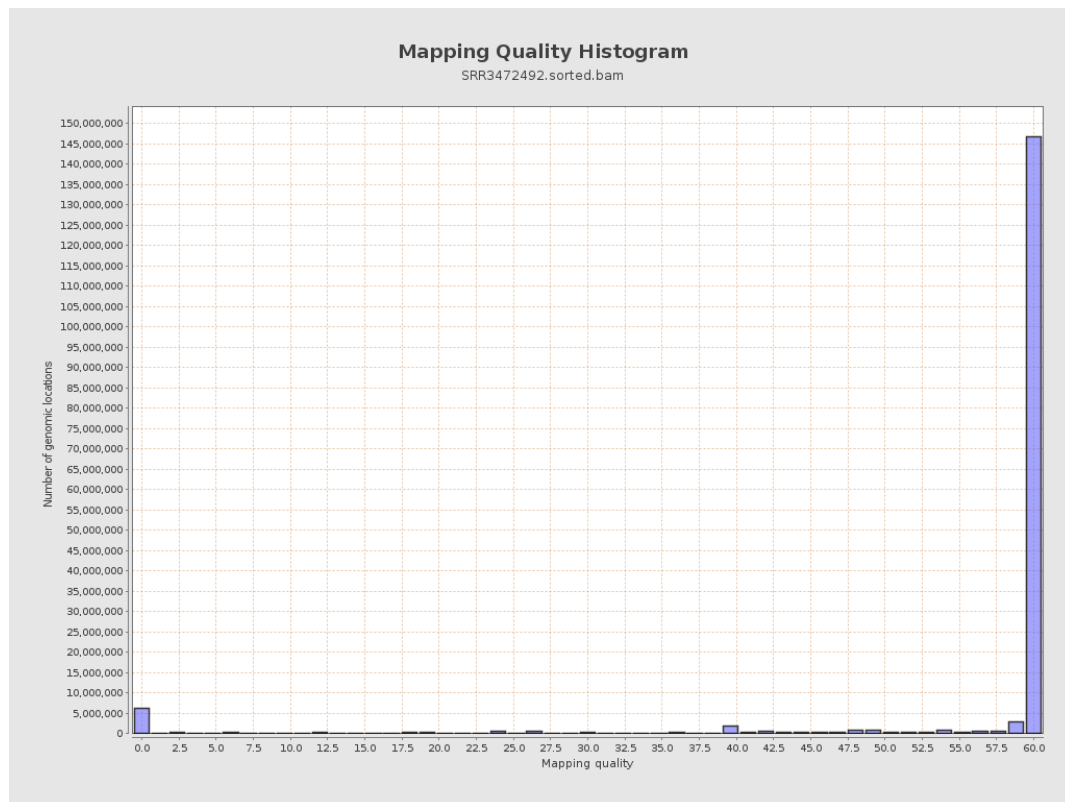
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

