

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:50:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472523.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_SRR3472523 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472523_1.fastq.gz SRR3472523_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:50:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472523.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,473,544
Mapped reads	14,352,221 / 99.16%
Unmapped reads	121,323 / 0.84%
Mapped paired reads	14,352,221 / 99.16%
Mapped reads, first in pair	7,197,869 / 49.73%
Mapped reads, second in pair	7,154,352 / 49.43%
Mapped reads, both in pair	14,279,836 / 98.66%
Mapped reads, singletons	72,385 / 0.5%
Secondary alignments	0
Supplementary alignments	51,805 / 0.36%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	8,946,440 / 61.81%
Duplication rate	45.12%
Clipped reads	1,083,542 / 7.49%

2.2. ACGT Content

Number/percentage of A's	398,207,621 / 28.14%
Number/percentage of C's	311,245,022 / 22%
Number/percentage of T's	395,785,653 / 27.97%
Number/percentage of G's	309,495,505 / 21.87%
Number/percentage of N's	219,505 / 0.02%

GC Percentage	43.87%
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2.3. Coverage

Mean	0.4571
Standard Deviation	18.5238

2.4. Mapping Quality

Mean Mapping Quality	55.05
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2.5. Insert size

Mean	25,112.49
Standard Deviation	1,554,560.91
P25/Median/P75	175 / 245 / 332

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	8,558,184
Insertions	78,808
Mapped reads with at least one insertion	0.54%
Deletions	74,691
Mapped reads with at least one deletion	0.51%
Homopolymer indels	44.88%

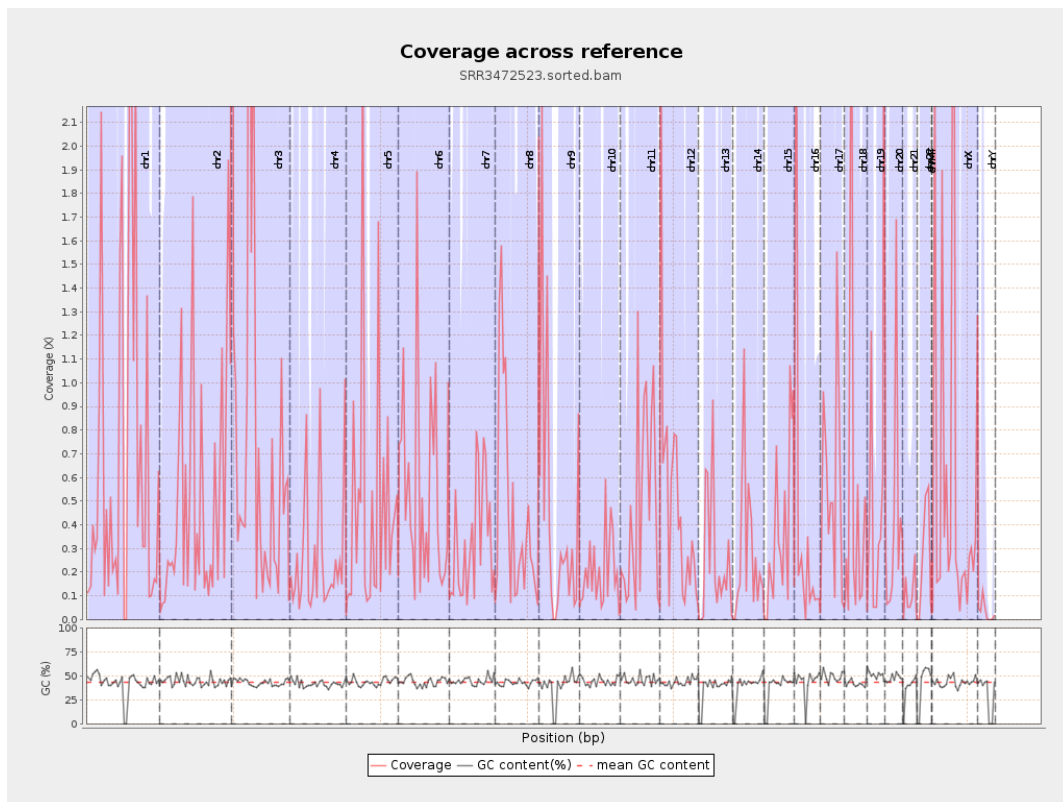
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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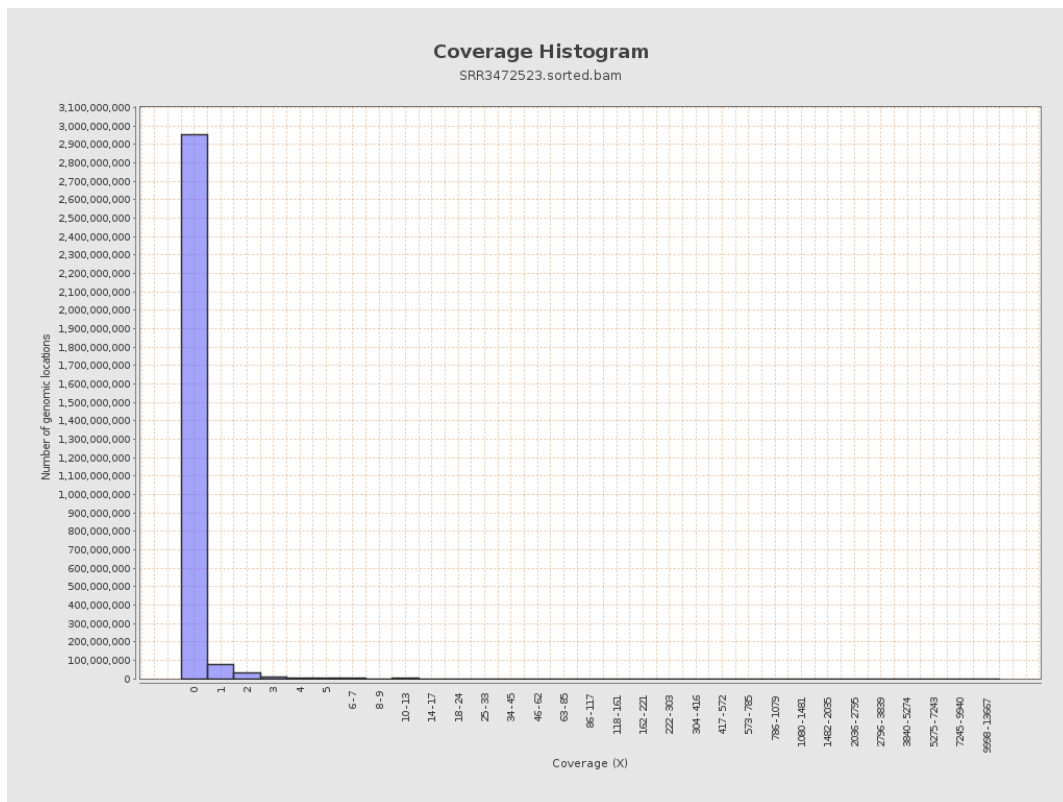
		bases	coverage	deviation
chr1	249250621	171849737	0.6895	32.4034
chr2	243199373	122767635	0.5048	19.7068
chr3	198022430	166158208	0.8391	18.9924
chr4	191154276	48423512	0.2533	10.9308
chr5	180915260	88140147	0.4872	20.2061
chr6	171115067	92259831	0.5392	16.0057
chr7	159138663	51435757	0.3232	10.4151
chr8	146364022	67270173	0.4596	16.1105
chr9	141213431	61498538	0.4355	11.6086
chr10	135534747	27985094	0.2065	7.4894
chr11	135006516	64824892	0.4802	21.2086
chr12	133851895	69434690	0.5187	14.9006
chr13	115169878	28468132	0.2472	9.2155
chr14	107349540	30171791	0.2811	9.7172
chr15	102531392	37792631	0.3686	10.6629
chr16	90354753	34809216	0.3853	12.7653
chr17	81195210	43450002	0.5351	12.8439
chr18	78077248	40208536	0.515	42.29
chr19	59128983	28570811	0.4832	14.6727
chr20	63025520	26322066	0.4176	16.2958
chr21	48129895	5193141	0.1079	5.0492
chr22	51304566	12875226	0.251	8.1883
chrMT	16571	4091	0.2469	0.6457
chrX	155270560	93183119	0.6001	23.8235

chrY	59373566	2048295	0.0345	1.2237
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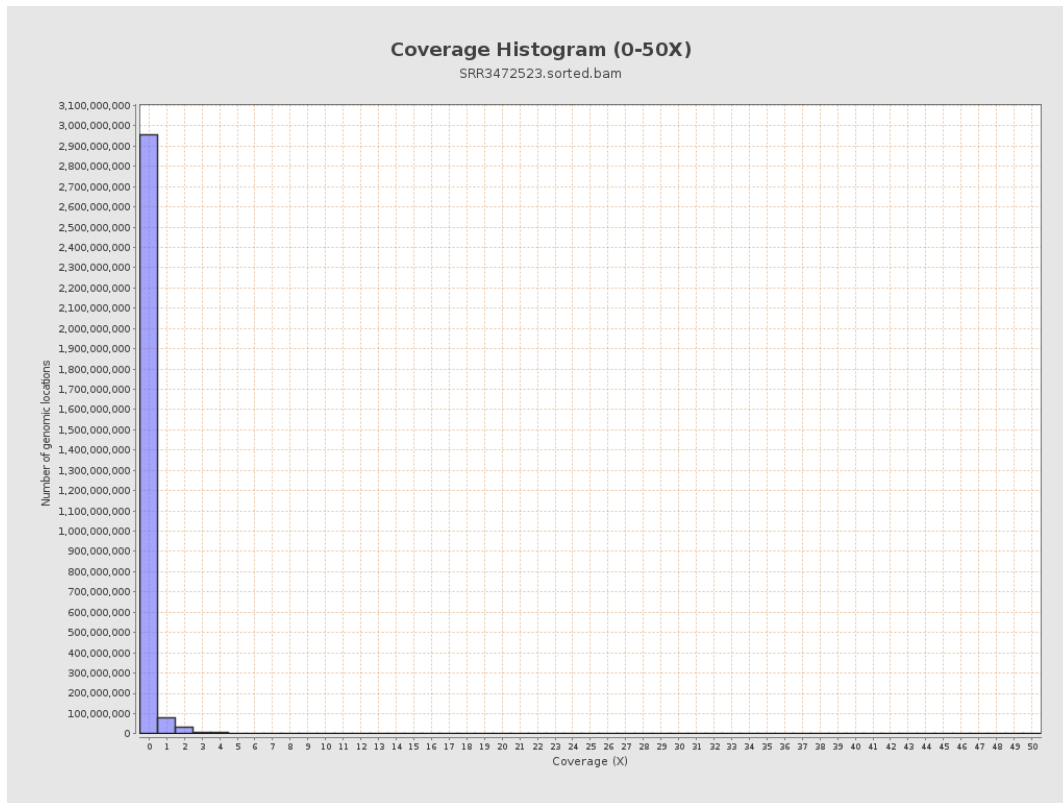
3. Results : Coverage across reference



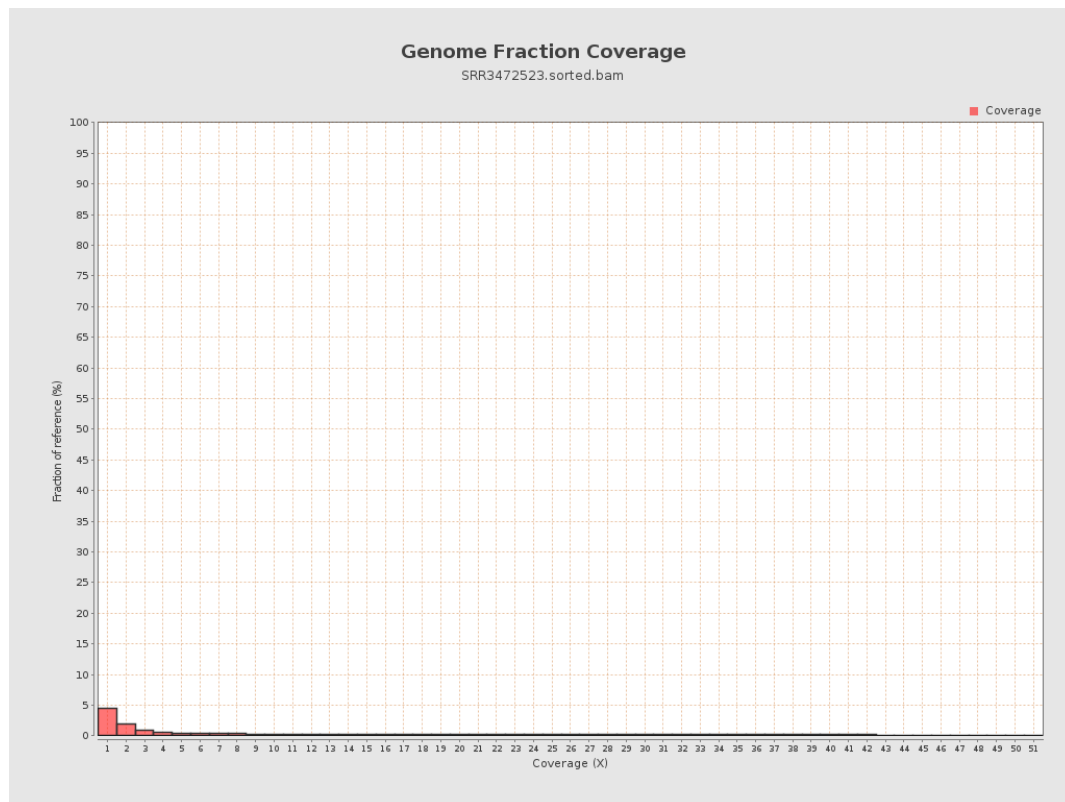
4. Results : Coverage Histogram



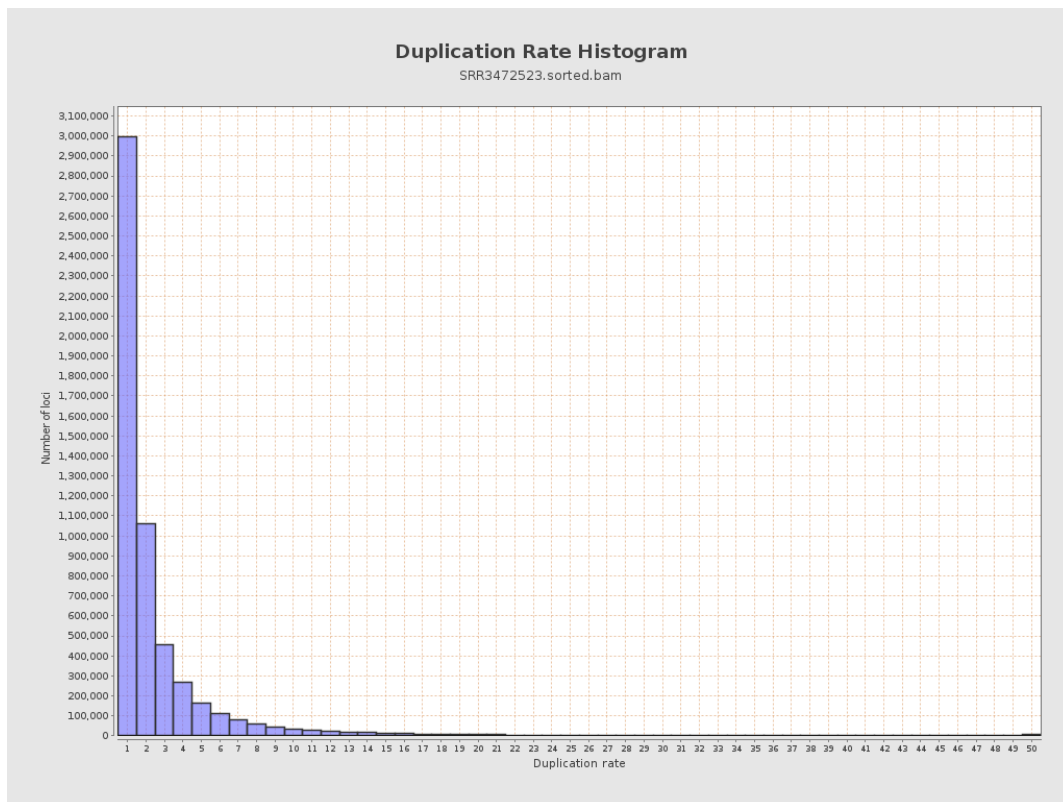
5. Results : Coverage Histogram (0-50X)



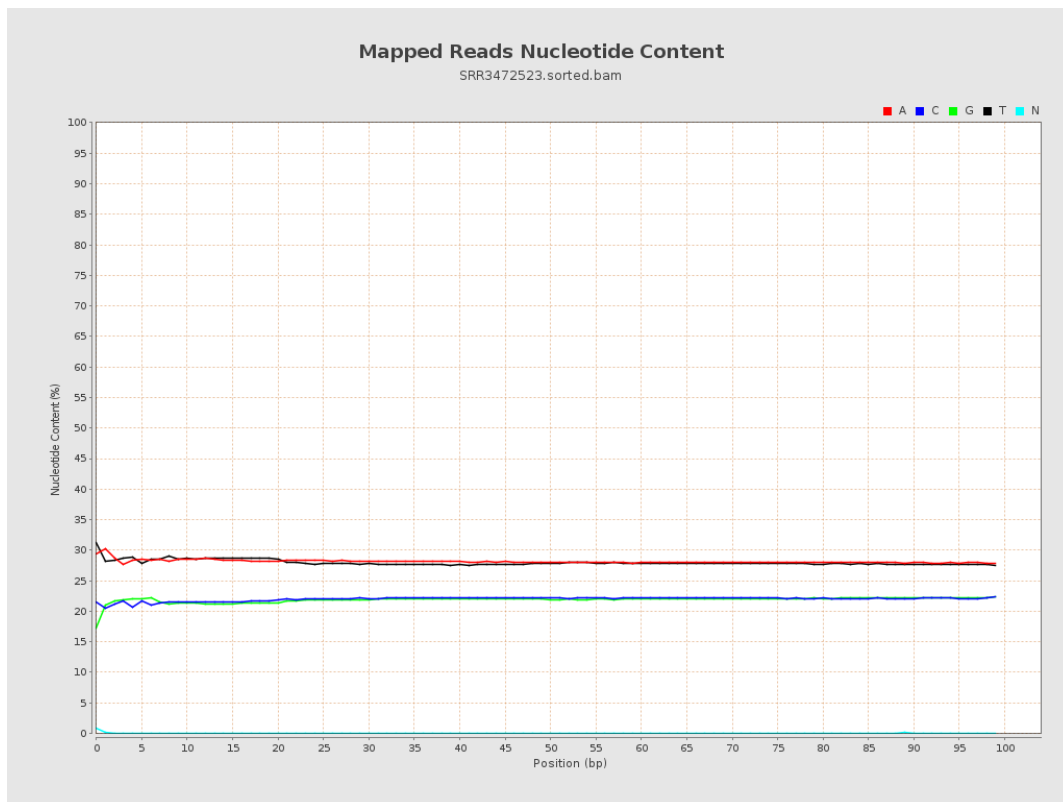
6. Results : Genome Fraction Coverage



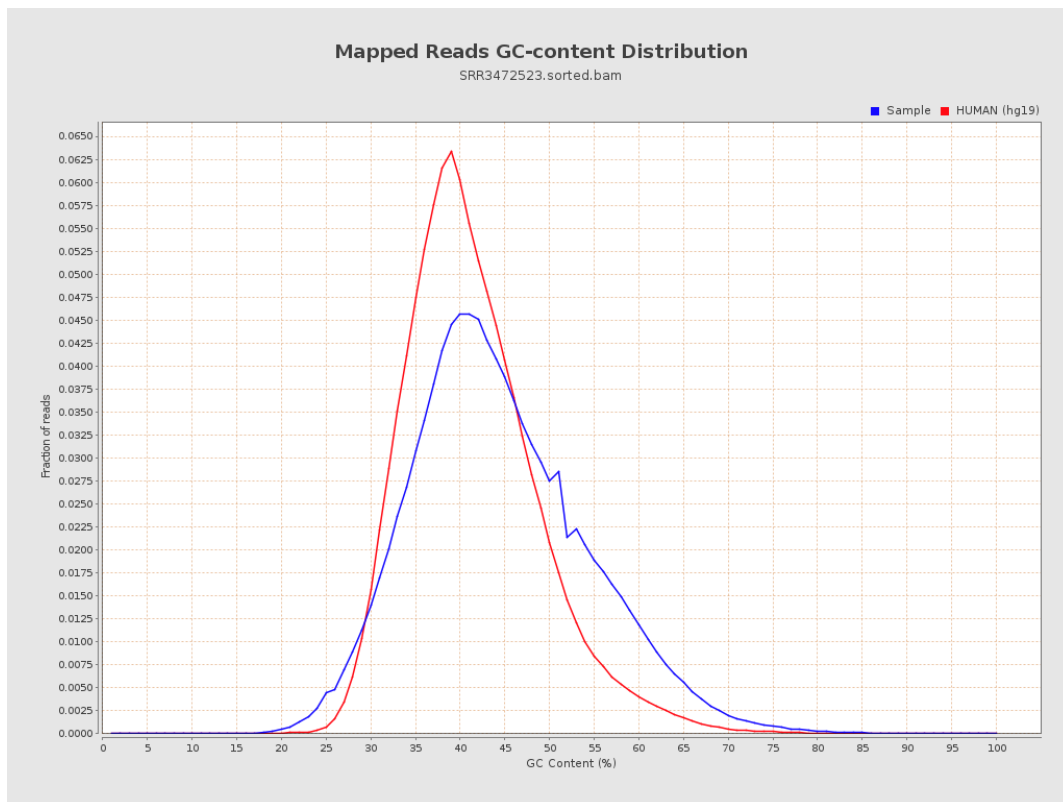
7. Results : Duplication Rate Histogram



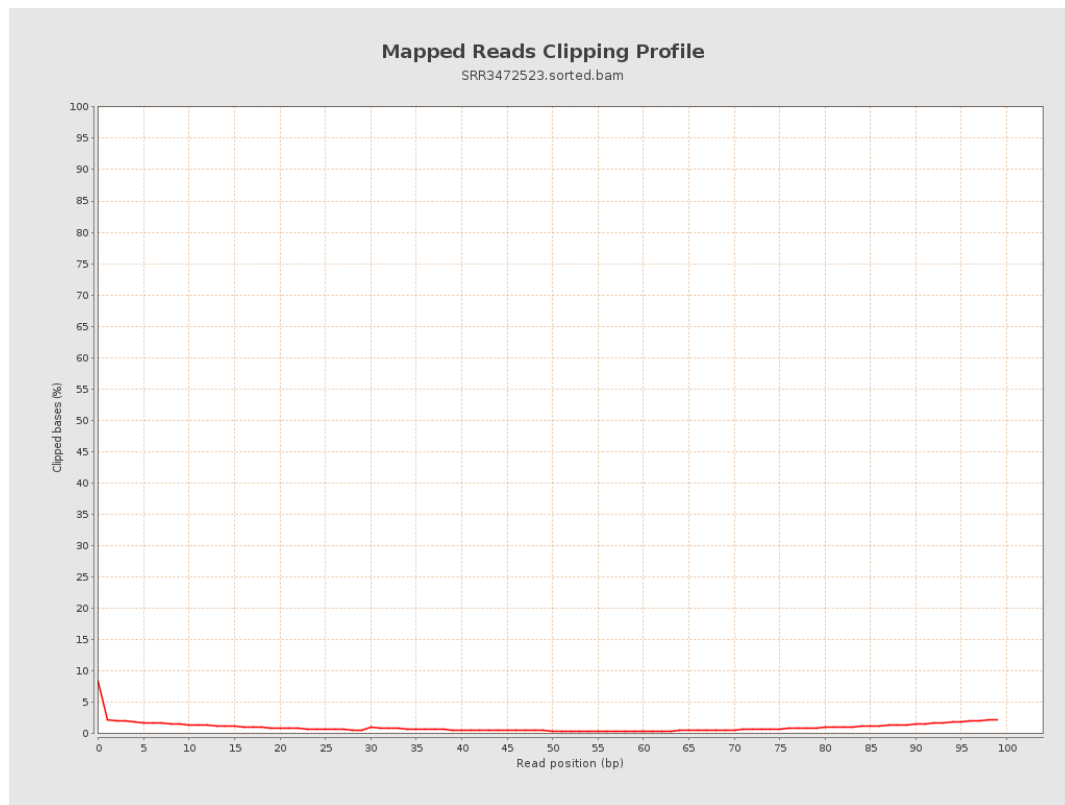
8. Results : Mapped Reads Nucleotide Content



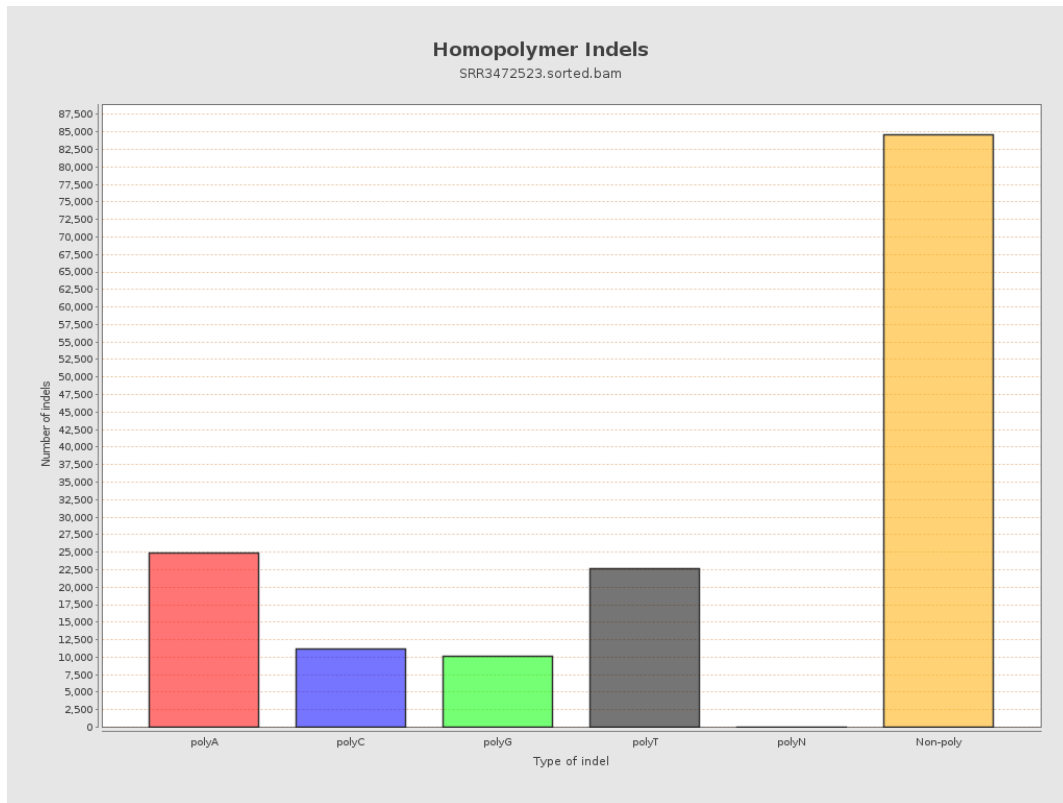
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



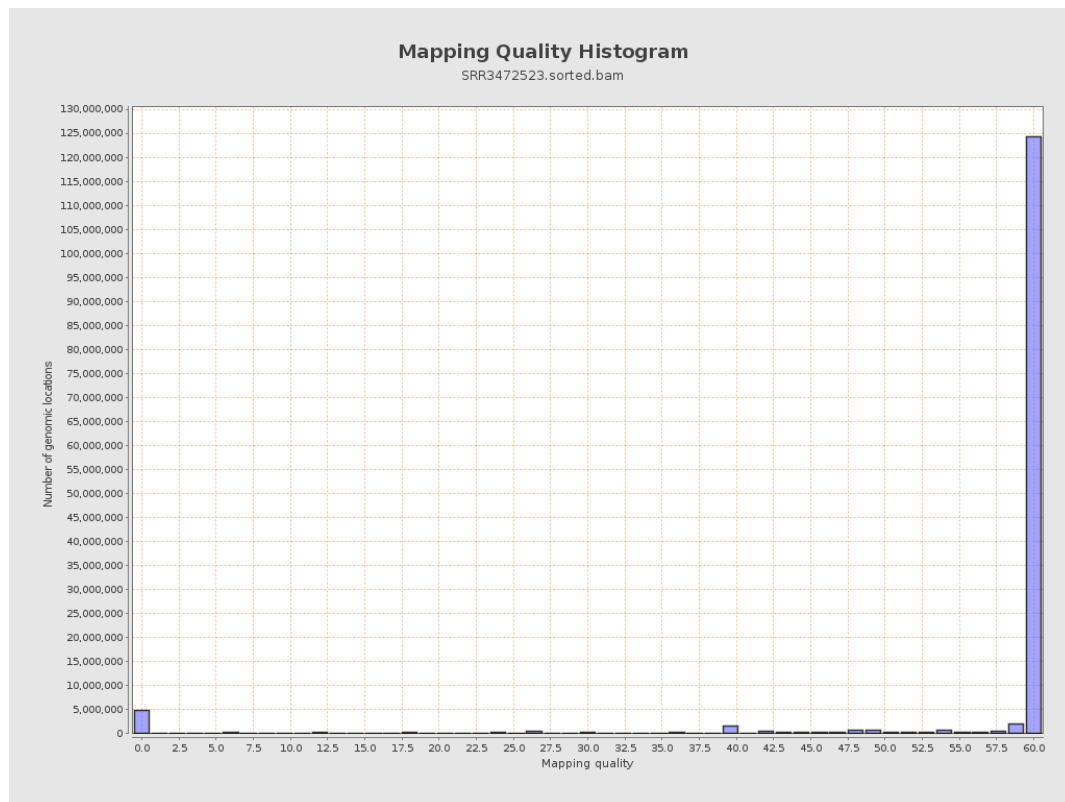
11. Results : Homopolymer Indels



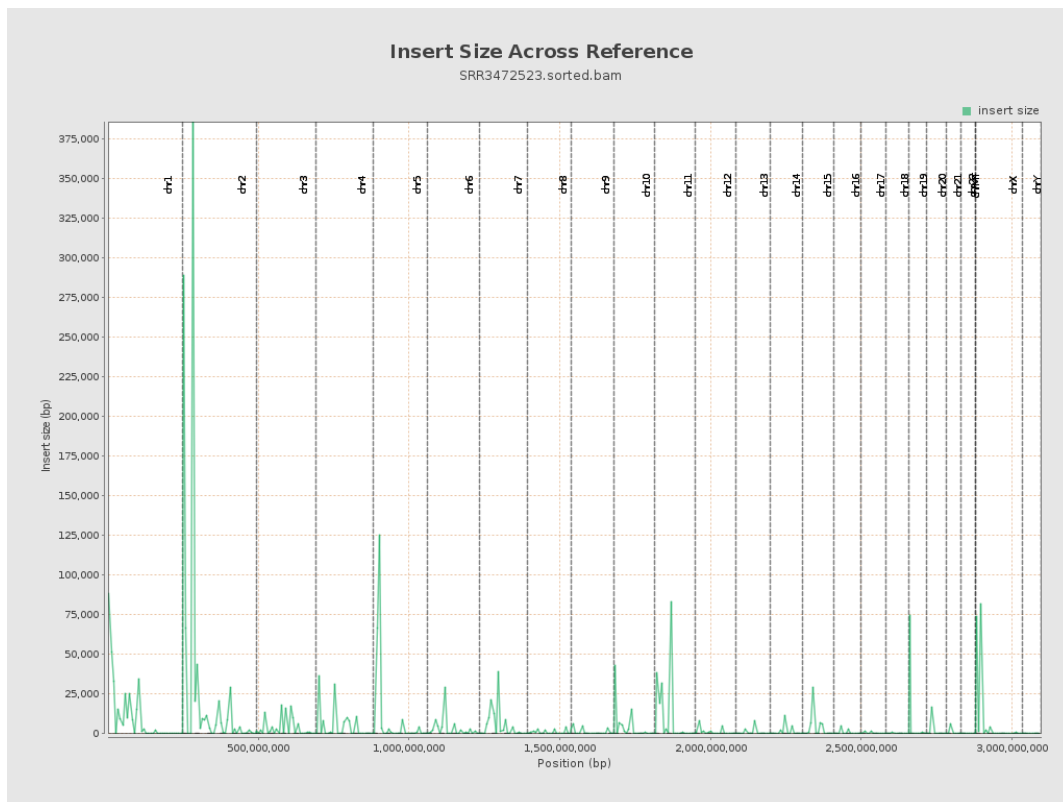
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

