

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:00:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472500.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_SRR3472500 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472500_1.fastq.gz SRR3472500_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:00:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472500.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,151,610
Mapped reads	13,936,649 / 98.48%
Unmapped reads	214,961 / 1.52%
Mapped paired reads	13,936,649 / 98.48%
Mapped reads, first in pair	6,991,257 / 49.4%
Mapped reads, second in pair	6,945,392 / 49.08%
Mapped reads, both in pair	13,840,004 / 97.8%
Mapped reads, singletons	96,645 / 0.68%
Secondary alignments	0
Supplementary alignments	58,892 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	9,427,281 / 66.62%
Duplication rate	43.94%
Clipped reads	1,256,567 / 8.88%

2.2. ACGT Content

Number/percentage of A's	384,164,661 / 28.06%
Number/percentage of C's	302,878,043 / 22.12%
Number/percentage of T's	381,796,897 / 27.89%
Number/percentage of G's	299,960,110 / 21.91%
Number/percentage of N's	213,203 / 0.02%

GC Percentage	44.03%
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2.3. Coverage

Mean	0.4423
Standard Deviation	21.6478

2.4. Mapping Quality

Mean Mapping Quality	54.32
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2.5. Insert size

Mean	28,900.5
Standard Deviation	1,643,611.77
P25/Median/P75	161 / 224 / 304

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	8,094,350
Insertions	73,816
Mapped reads with at least one insertion	0.53%
Deletions	73,090
Mapped reads with at least one deletion	0.52%
Homopolymer indels	43.5%

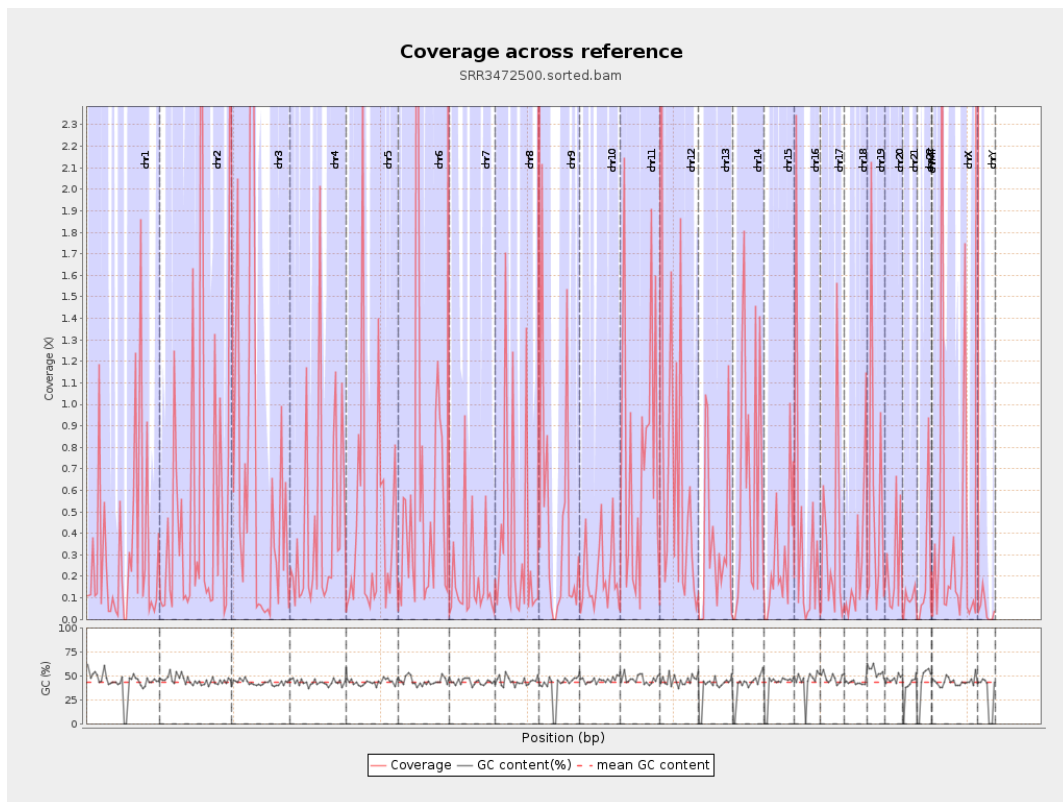
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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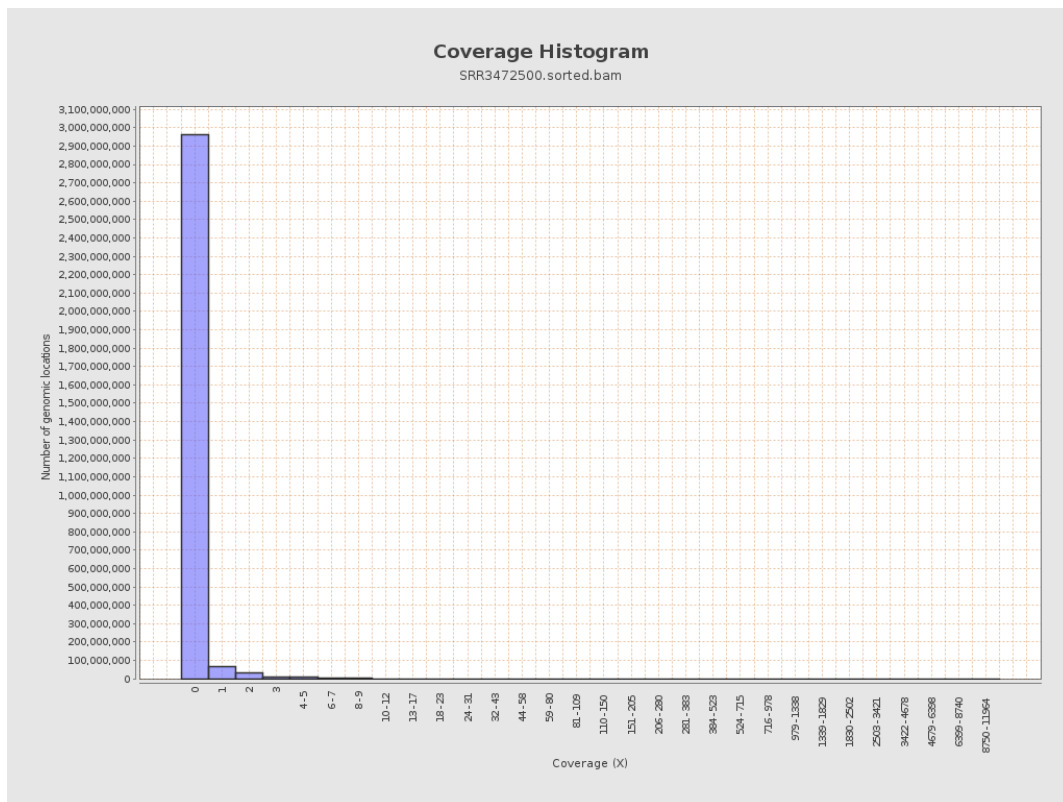
		bases	coverage	deviation
chr1	249250621	78361388	0.3144	18.2752
chr2	243199373	131567393	0.541	27.1772
chr3	198022430	142869710	0.7215	29.9536
chr4	191154276	80187811	0.4195	18.3291
chr5	180915260	77507063	0.4284	18.3882
chr6	171115067	113364907	0.6625	24.8117
chr7	159138663	30177839	0.1896	14.0145
chr8	146364022	51710776	0.3533	19.2859
chr9	141213431	64381446	0.4559	17.4214
chr10	135534747	27570959	0.2034	8.6824
chr11	135006516	100719876	0.746	26.8001
chr12	133851895	103686573	0.7746	35.7113
chr13	115169878	41980513	0.3645	15.7575
chr14	107349540	67482412	0.6286	32.0343
chr15	102531392	27807070	0.2712	10.3596
chr16	90354753	33086285	0.3662	24.6854
chr17	81195210	25459547	0.3136	12.4223
chr18	78077248	21660427	0.2774	12.5285
chr19	59128983	35322858	0.5974	22.1291
chr20	63025520	15654659	0.2484	9.8847
chr21	48129895	4704309	0.0977	4.7961
chr22	51304566	9901023	0.193	11.783
chrMT	16571	3709	0.2238	0.6473
chrX	155270560	80952568	0.5214	25.3557

chrY	59373566	3078742	0.0519	1.4729
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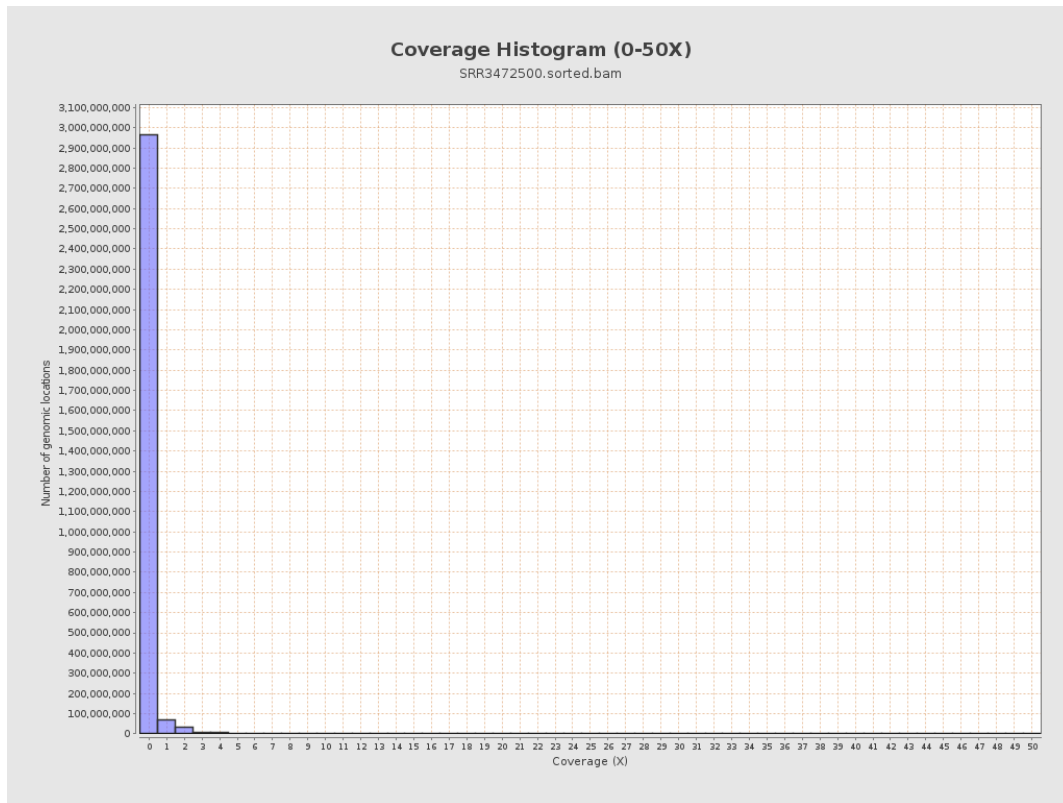
3. Results : Coverage across reference



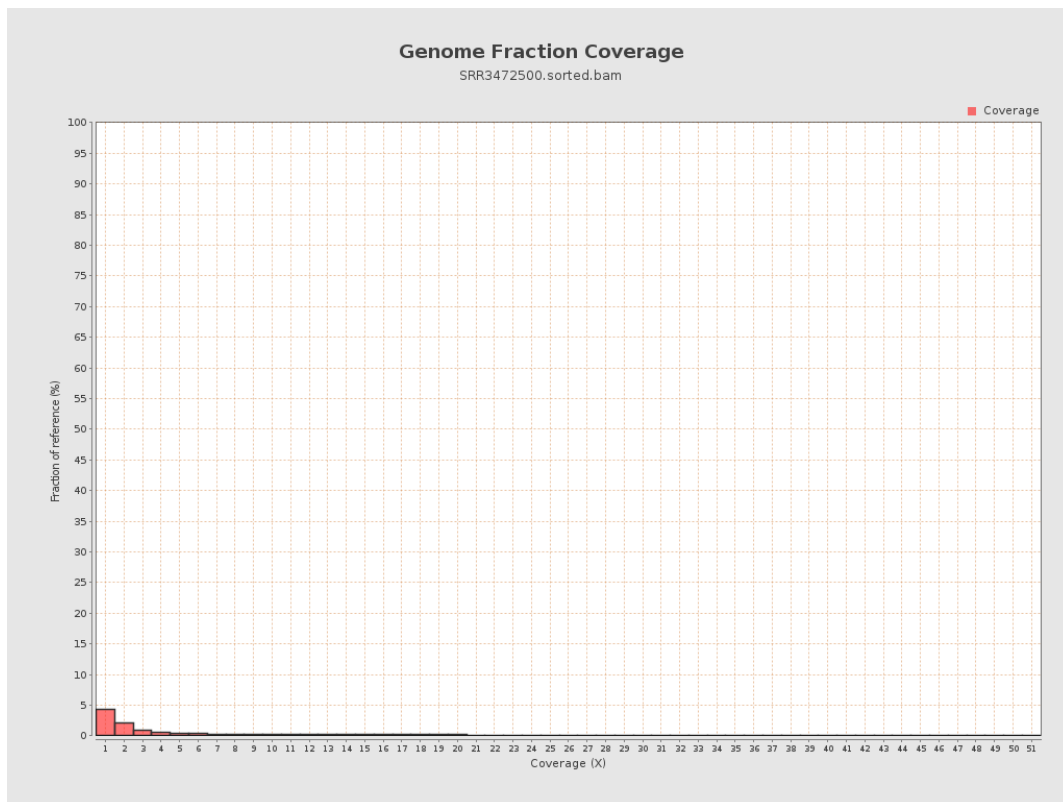
4. Results : Coverage Histogram



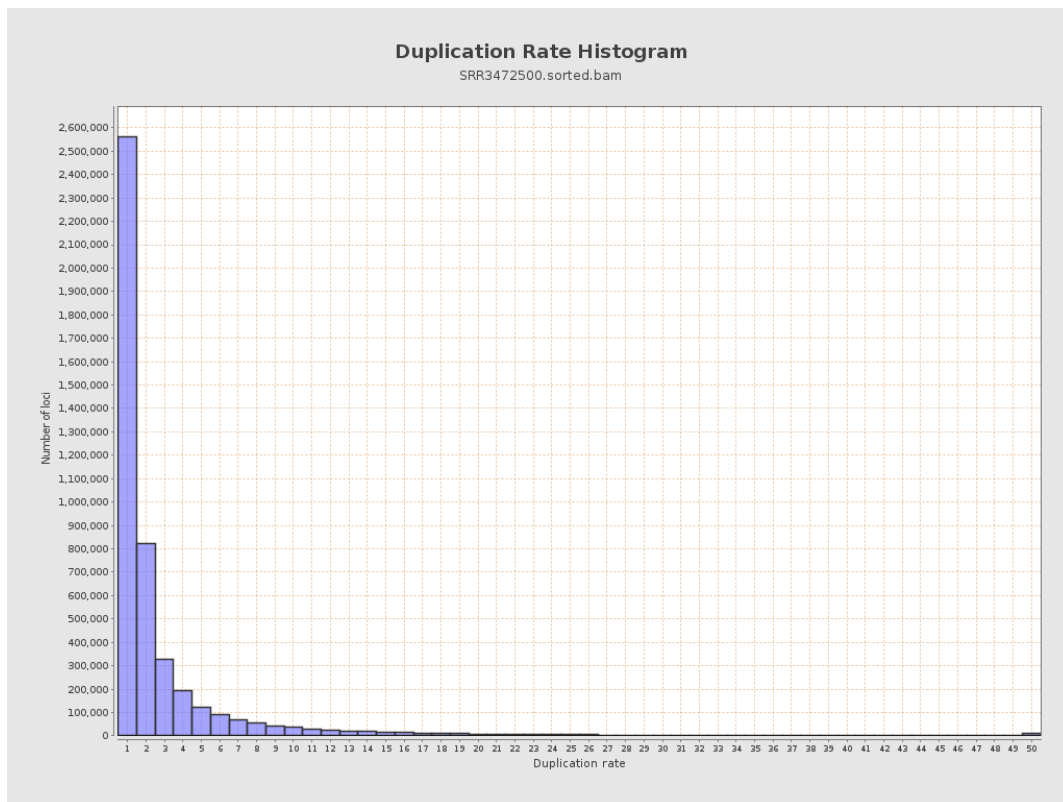
5. Results : Coverage Histogram (0-50X)



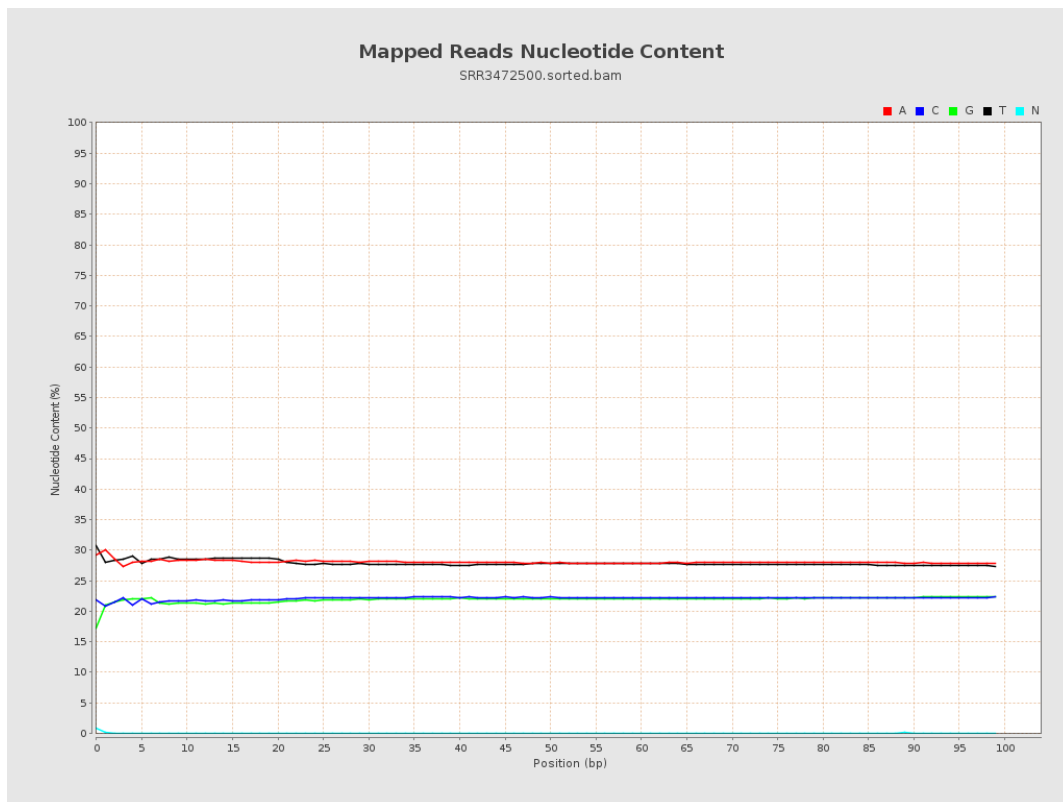
6. Results : Genome Fraction Coverage



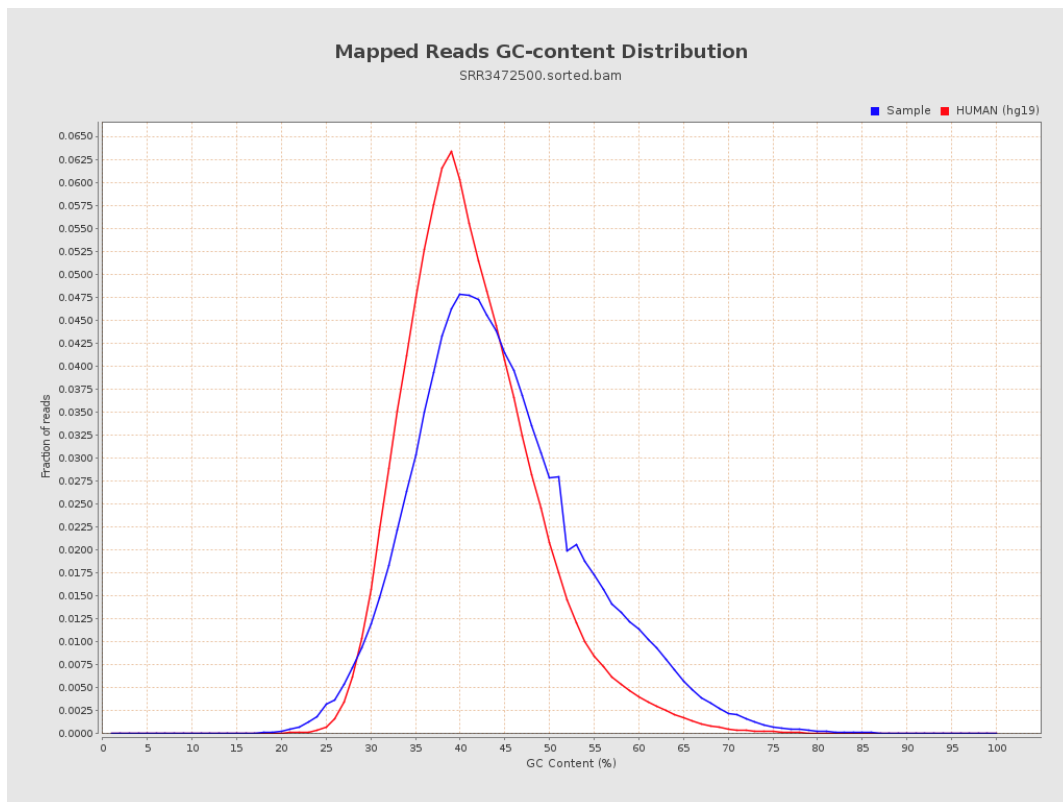
7. Results : Duplication Rate Histogram



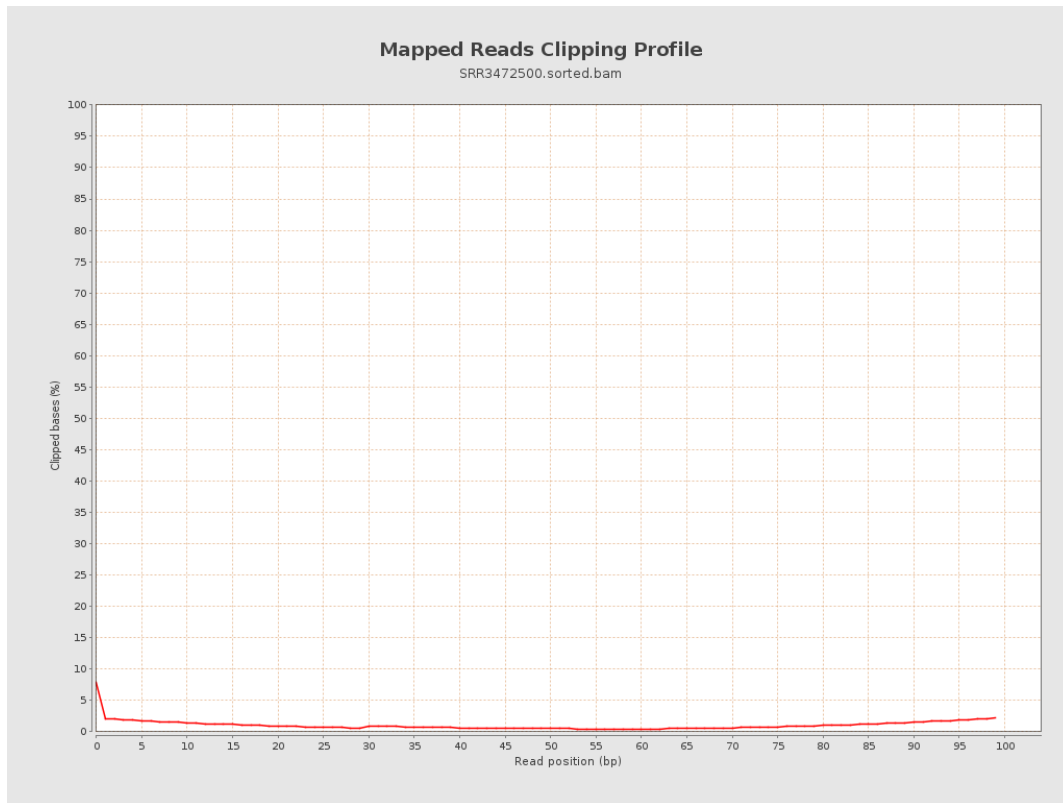
8. Results : Mapped Reads Nucleotide Content



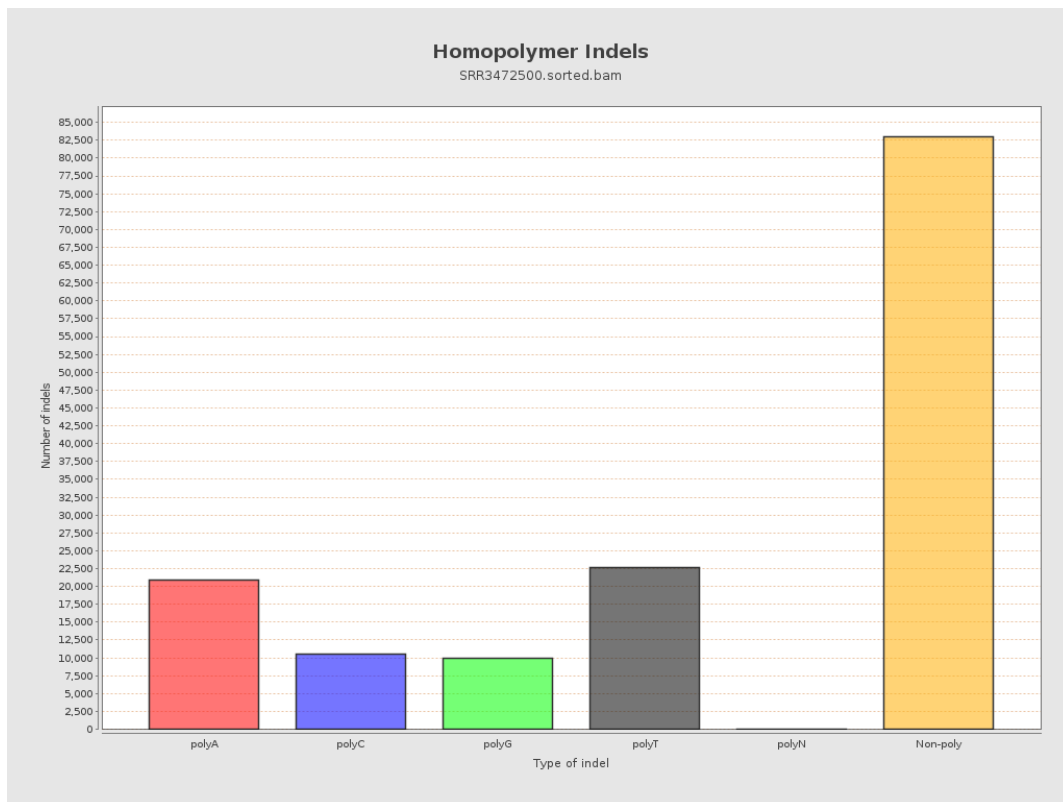
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



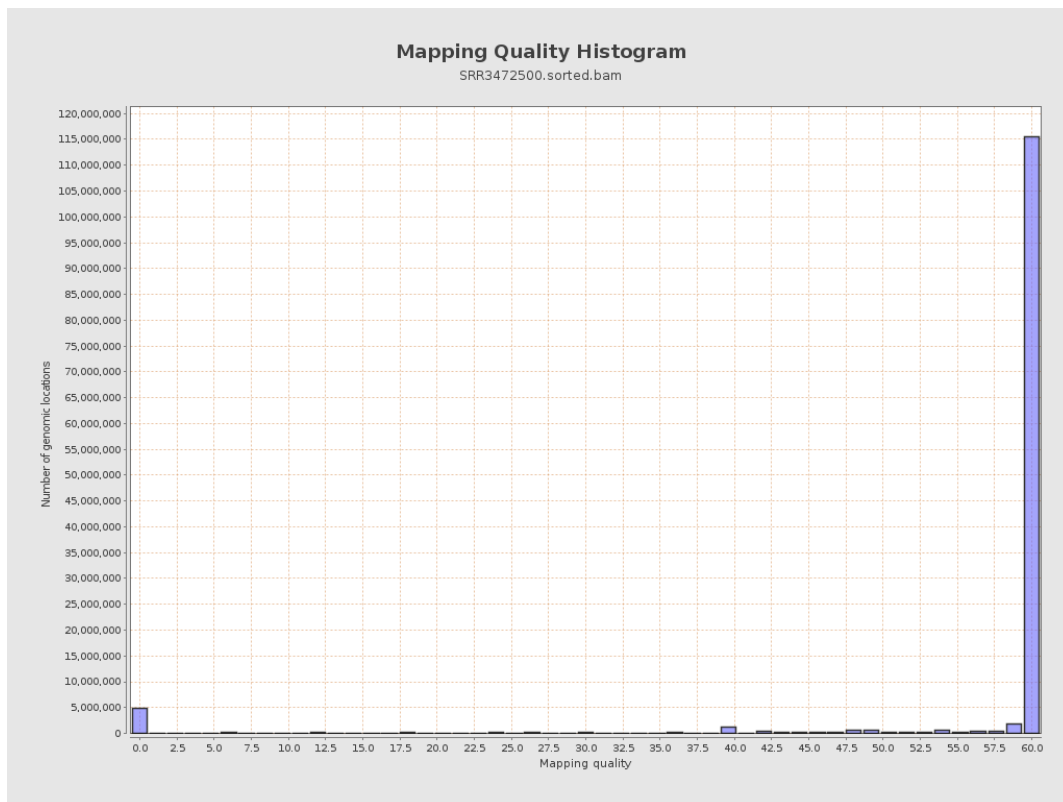
11. Results : Homopolymer Indels



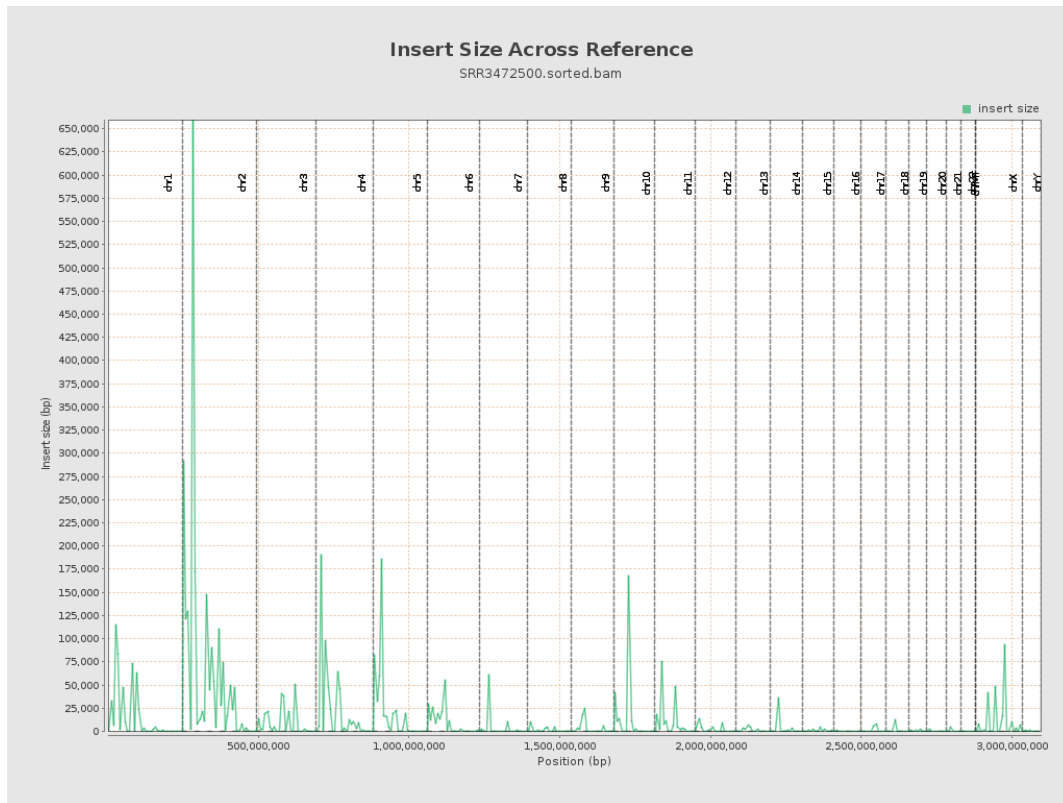
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

