

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:28:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472396.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_SRR3472396 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472396_1.fastq.gz SRR3472396_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:28:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472396.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,433,458
Mapped reads	16,286,831 / 99.11%
Unmapped reads	146,627 / 0.89%
Mapped paired reads	16,286,831 / 99.11%
Mapped reads, first in pair	8,169,798 / 49.71%
Mapped reads, second in pair	8,117,033 / 49.39%
Mapped reads, both in pair	16,196,328 / 98.56%
Mapped reads, singletons	90,503 / 0.55%
Secondary alignments	0
Supplementary alignments	65,531 / 0.4%
Read min/max/mean length	30 / 100 / 99.42
Duplicated reads (estimated)	9,716,146 / 59.12%
Duplication rate	46.11%
Clipped reads	1,129,464 / 6.87%

2.2. ACGT Content

Number/percentage of A's	430,276,971 / 26.92%
Number/percentage of C's	370,080,580 / 23.16%
Number/percentage of T's	430,628,910 / 26.95%
Number/percentage of G's	366,918,944 / 22.96%
Number/percentage of N's	192,823 / 0.01%

GC Percentage	46.12%
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2.3. Coverage

Mean	0.5163
Standard Deviation	15.0292

2.4. Mapping Quality

Mean Mapping Quality	54.76
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2.5. Insert size

Mean	19,380.51
Standard Deviation	1,350,756.82
P25/Median/P75	158 / 220 / 295

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	8,913,024
Insertions	91,621
Mapped reads with at least one insertion	0.56%
Deletions	80,522
Mapped reads with at least one deletion	0.49%
Homopolymer indels	45.27%

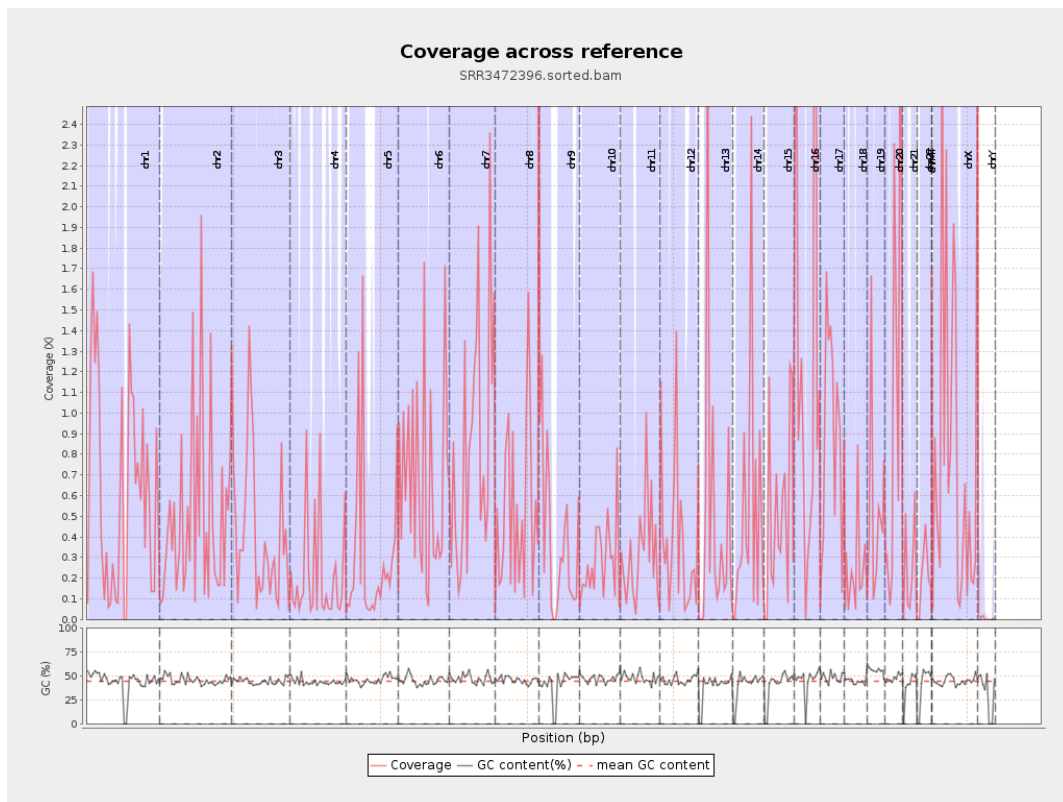
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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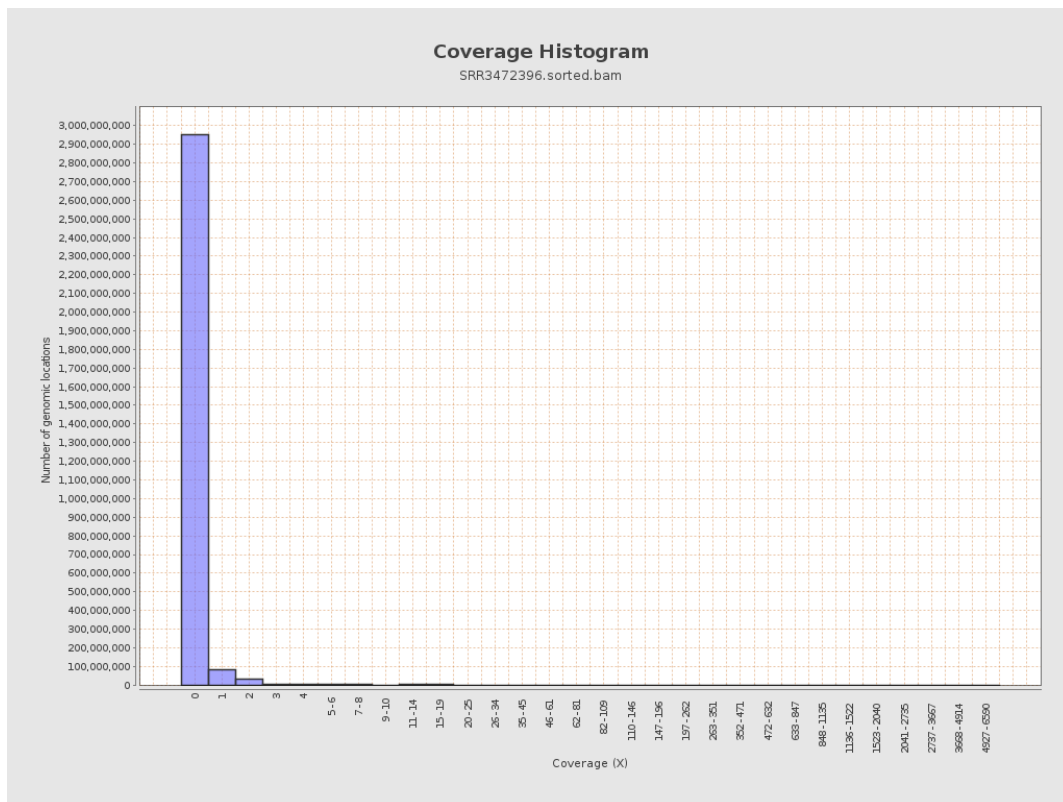
		bases	coverage	deviation
chr1	249250621	156161109	0.6265	18.0878
chr2	243199373	119448752	0.4912	13.831
chr3	198022430	86243306	0.4355	9.2183
chr4	191154276	40026961	0.2094	8.8965
chr5	180915260	56628688	0.313	9.5548
chr6	171115067	113807088	0.6651	14.5064
chr7	159138663	136985181	0.8608	21.43
chr8	146364022	79022271	0.5399	11.9917
chr9	141213431	56594994	0.4008	10.08
chr10	135534747	38824545	0.2865	8.9269
chr11	135006516	43040189	0.3188	9.6815
chr12	133851895	51915049	0.3879	10.0857
chr13	115169878	56071456	0.4869	17.0403
chr14	107349540	52904325	0.4928	16.215
chr15	102531392	53406869	0.5209	17.111
chr16	90354753	118984160	1.3169	29.5093
chr17	81195210	73444586	0.9045	19.9157
chr18	78077248	19443818	0.249	8.8905
chr19	59128983	31665006	0.5355	9.792
chr20	63025520	68161558	1.0815	31.6099
chr21	48129895	11593653	0.2409	10.4981
chr22	51304566	10276045	0.2003	4.8884
chrMT	16571	28091	1.6952	1.8573
chrX	155270560	123222683	0.7936	19.1621

chrY	59373566	393275	0.0066	0.5003
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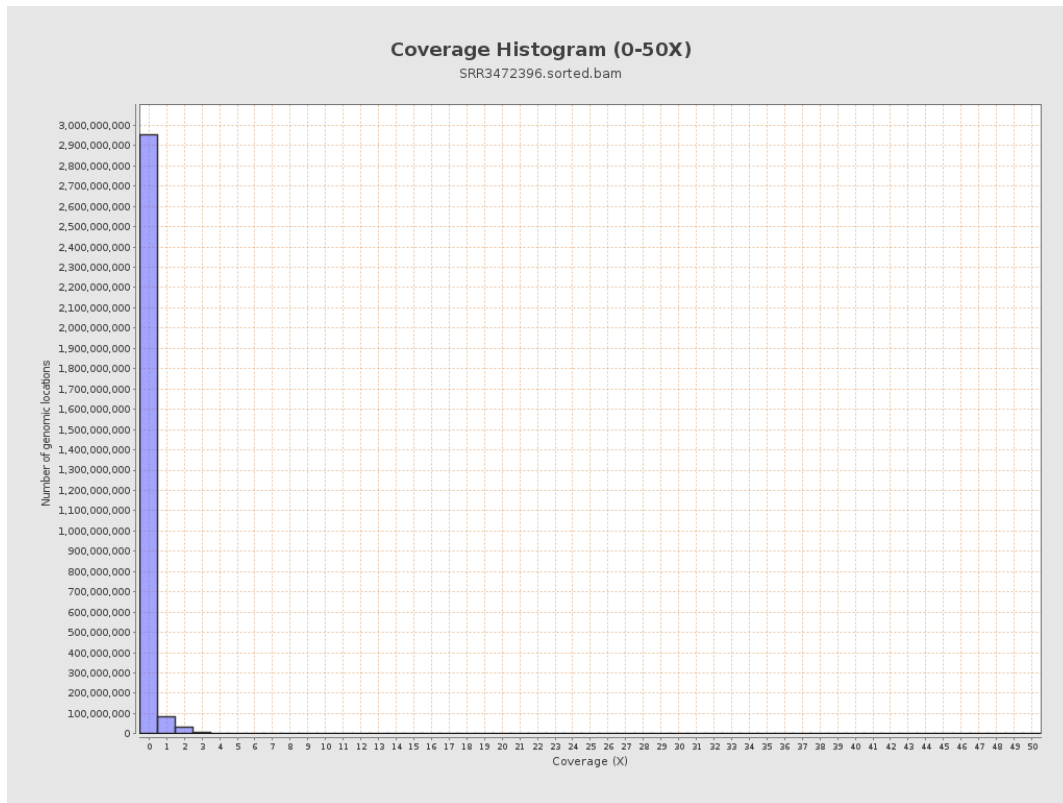
3. Results : Coverage across reference



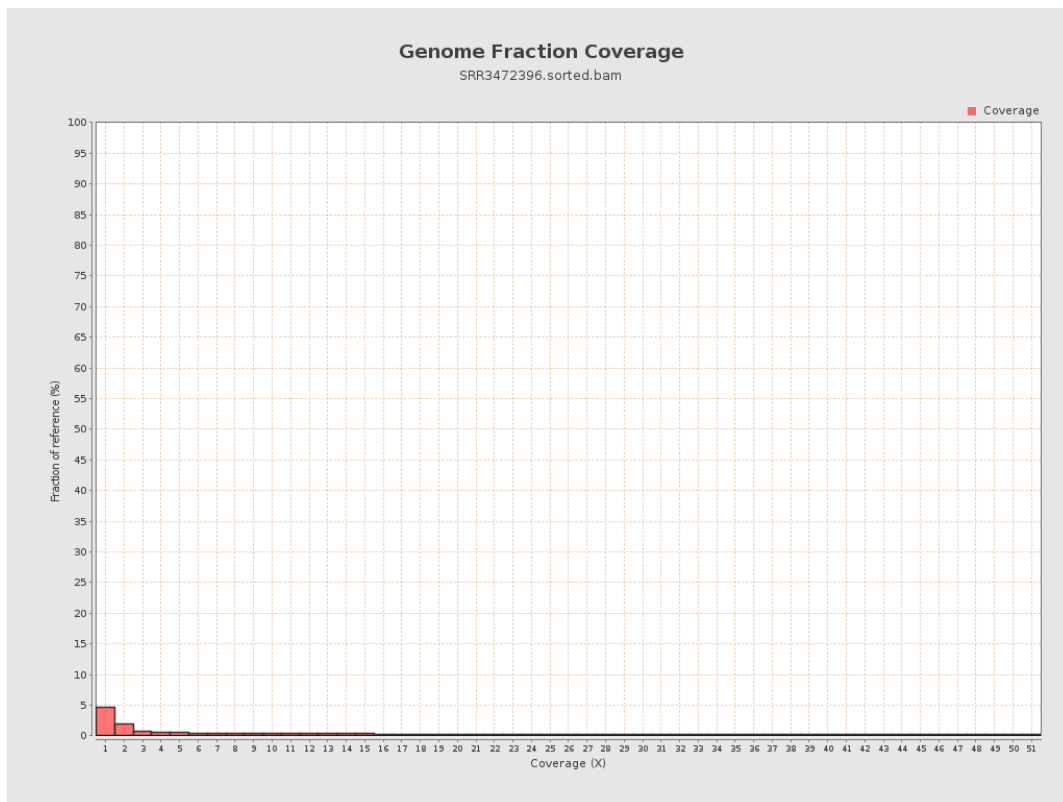
4. Results : Coverage Histogram



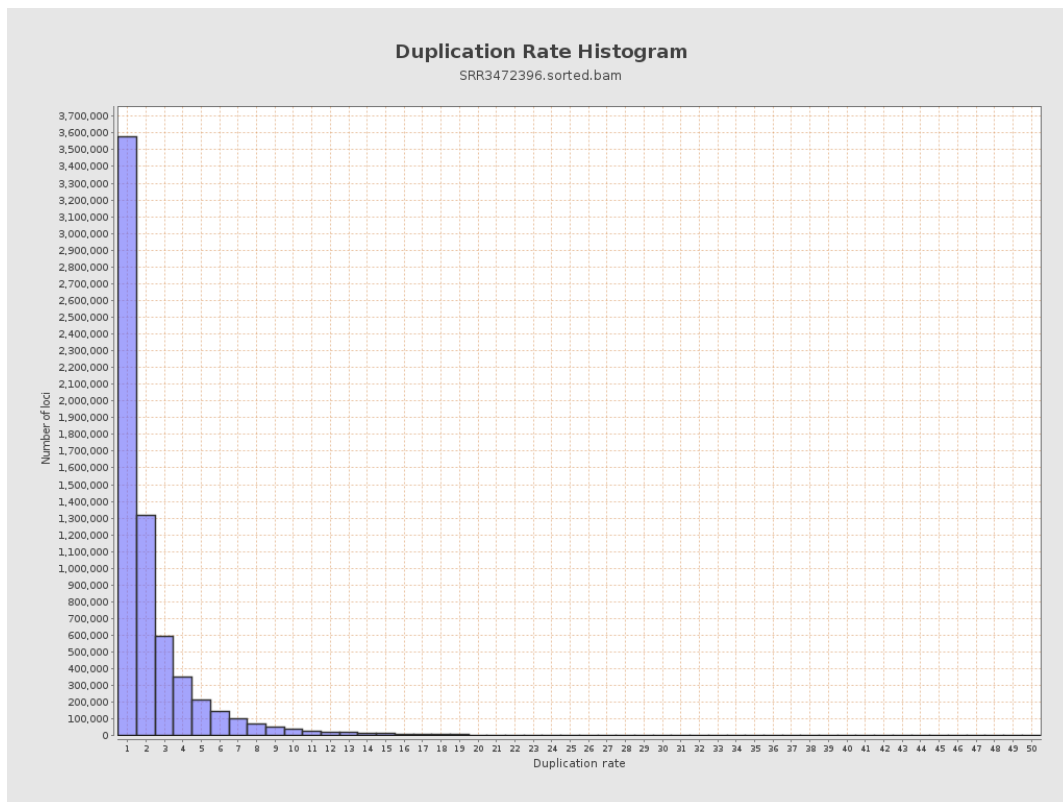
5. Results : Coverage Histogram (0-50X)



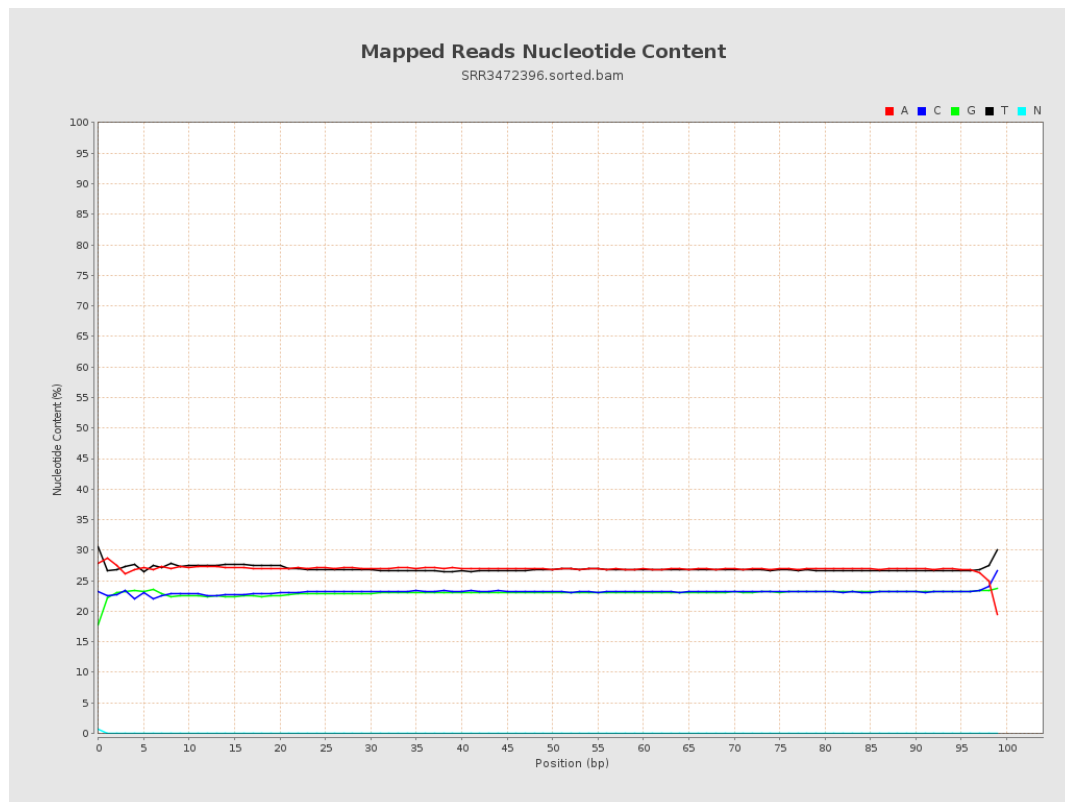
6. Results : Genome Fraction Coverage



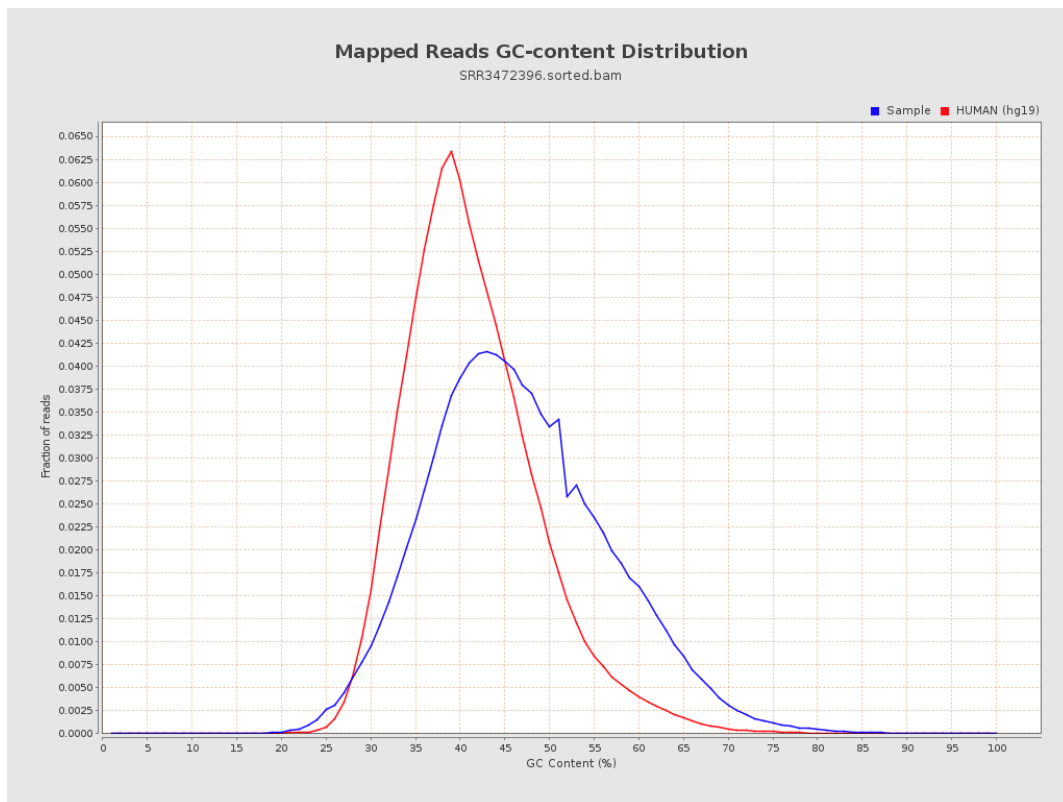
7. Results : Duplication Rate Histogram



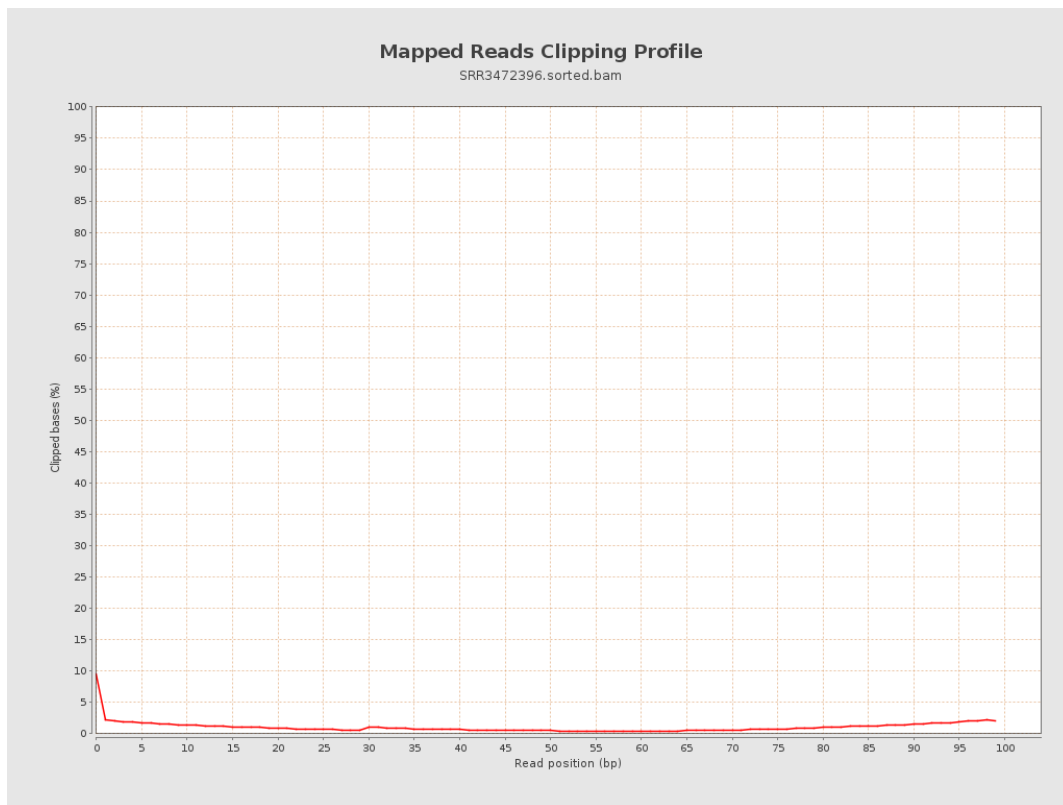
8. Results : Mapped Reads Nucleotide Content



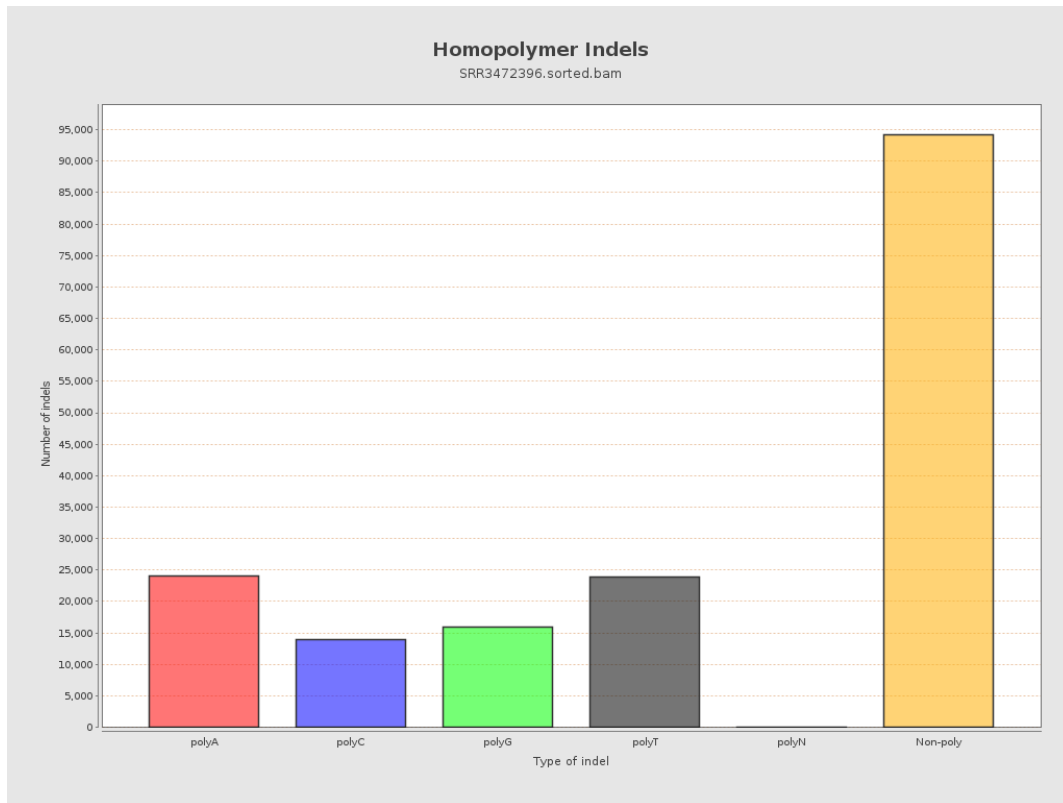
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



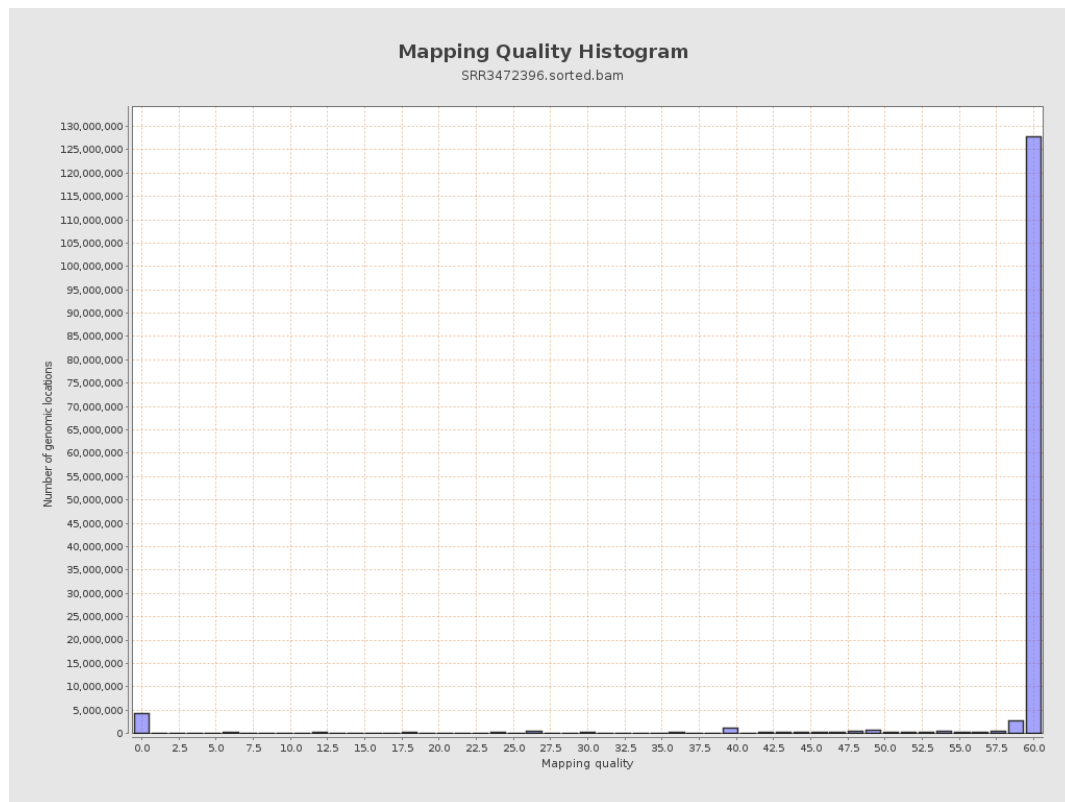
11. Results : Homopolymer Indels



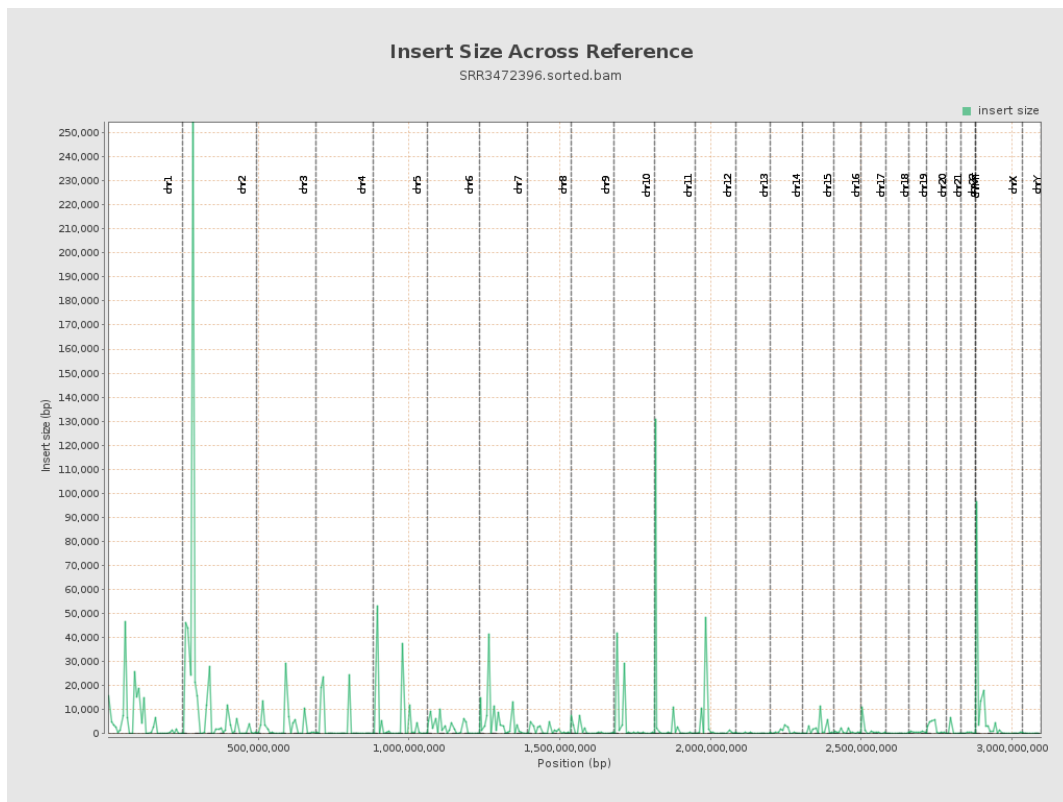
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

