

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:26:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472436.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_SRR3472436 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472436_1.fastq.gz SRR3472436_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:26:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472436.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,819,380
Mapped reads	18,628,313 / 98.98%
Unmapped reads	191,067 / 1.02%
Mapped paired reads	18,628,313 / 98.98%
Mapped reads, first in pair	9,350,412 / 49.69%
Mapped reads, second in pair	9,277,901 / 49.3%
Mapped reads, both in pair	18,518,172 / 98.4%
Mapped reads, singletons	110,141 / 0.59%
Secondary alignments	0
Supplementary alignments	77,630 / 0.41%
Read min/max/mean length	30 / 100 / 99.36
Duplicated reads (estimated)	11,971,333 / 63.61%
Duplication rate	47.24%
Clipped reads	1,277,976 / 6.79%

2.2. ACGT Content

Number/percentage of A's	510,365,848 / 27.93%
Number/percentage of C's	404,835,220 / 22.15%
Number/percentage of T's	510,059,299 / 27.91%
Number/percentage of G's	401,871,218 / 21.99%
Number/percentage of N's	226,560 / 0.01%

GC Percentage	44.15%
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2.3. Coverage

Mean	0.5904
Standard Deviation	20.8822

2.4. Mapping Quality

Mean Mapping Quality	54.73
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2.5. Insert size

Mean	19,189.24
Standard Deviation	1,334,011.3
P25/Median/P75	162 / 227 / 307

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	10,462,760
Insertions	119,859
Mapped reads with at least one insertion	0.64%
Deletions	96,414
Mapped reads with at least one deletion	0.51%
Homopolymer indels	46.84%

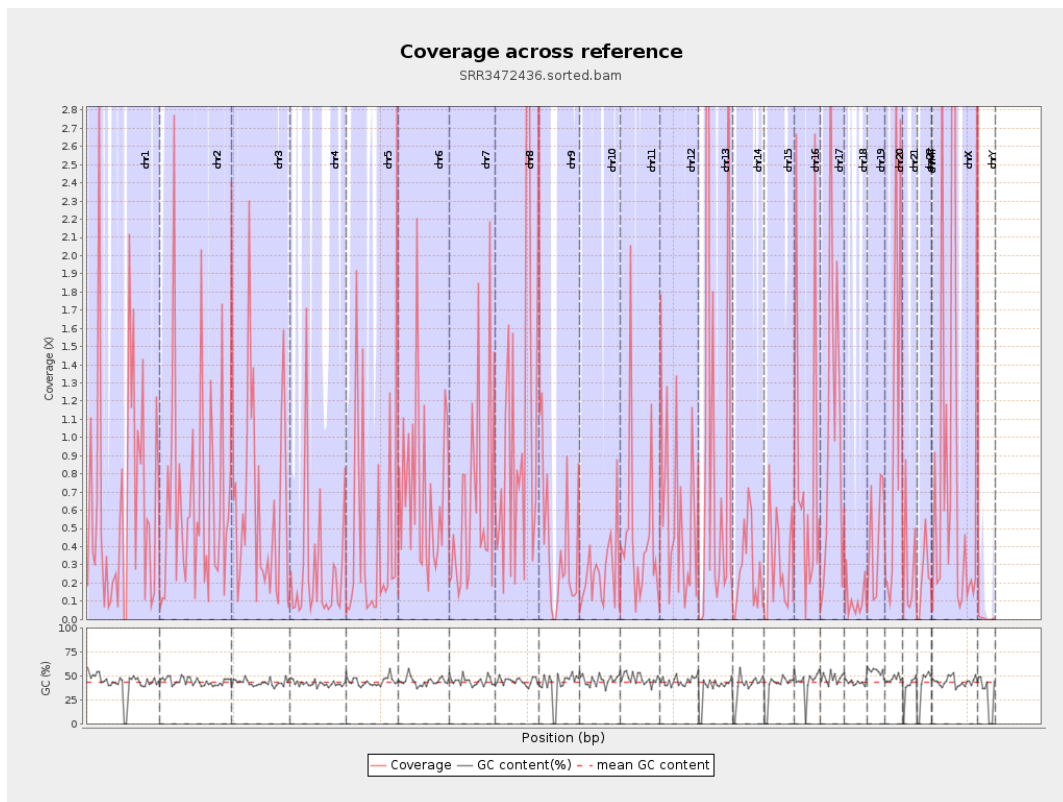
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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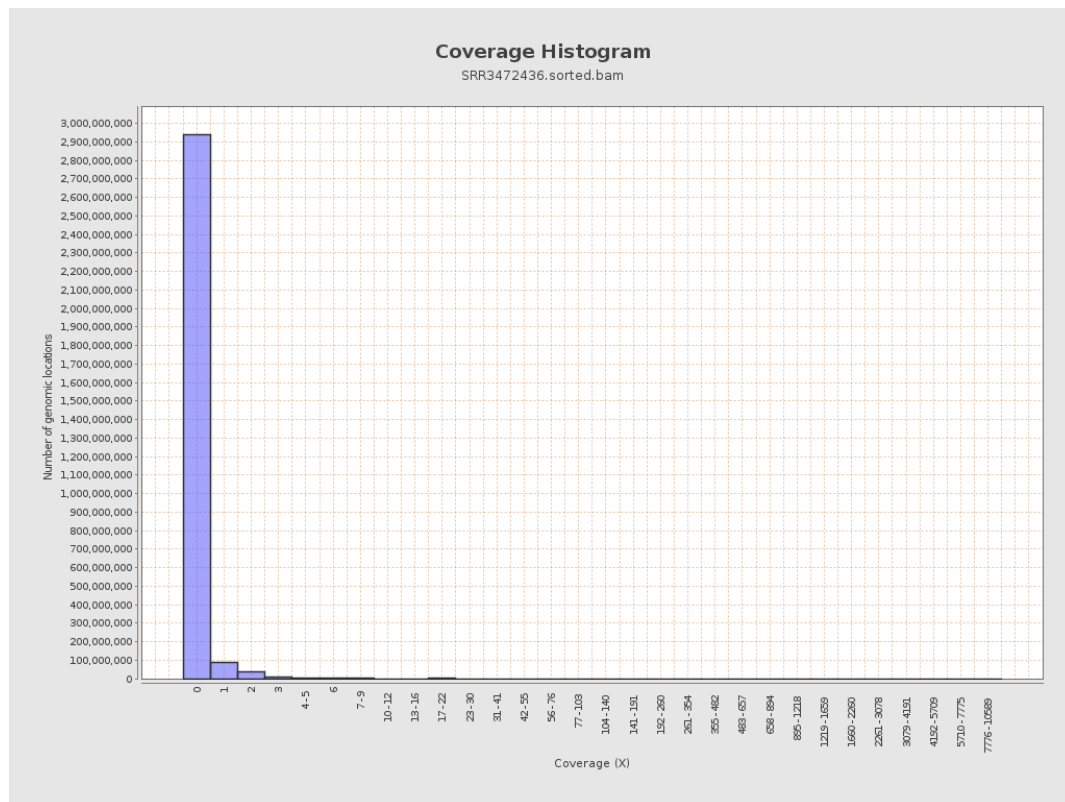
		bases	coverage	deviation
chr1	249250621	158470608	0.6358	20.4537
chr2	243199373	157948815	0.6495	21.8503
chr3	198022430	128865796	0.6508	15.5581
chr4	191154276	49529721	0.2591	8.8853
chr5	180915260	91996567	0.5085	23.073
chr6	171115067	121866759	0.7122	15.862
chr7	159138663	103159085	0.6482	20.1848
chr8	146364022	161286378	1.102	25.8872
chr9	141213431	59801345	0.4235	10.8823
chr10	135534747	35686850	0.2633	10.5797
chr11	135006516	61753450	0.4574	20.2798
chr12	133851895	81063699	0.6056	14.7732
chr13	115169878	120859083	1.0494	45.0197
chr14	107349540	28455898	0.2651	7.9021
chr15	102531392	32919383	0.3211	11.298
chr16	90354753	74308426	0.8224	19.5732
chr17	81195210	87581182	1.0786	27.0479
chr18	78077248	8549238	0.1095	3.3457
chr19	59128983	27692840	0.4683	13.2677
chr20	63025520	68773245	1.0912	35.0557
chr21	48129895	13226824	0.2748	12.519
chr22	51304566	11827942	0.2305	6.8116
chrMT	16571	1704	0.1028	0.4218
chrX	155270560	141586884	0.9119	36.0206

chrY	59373566	376245	0.0063	0.3756
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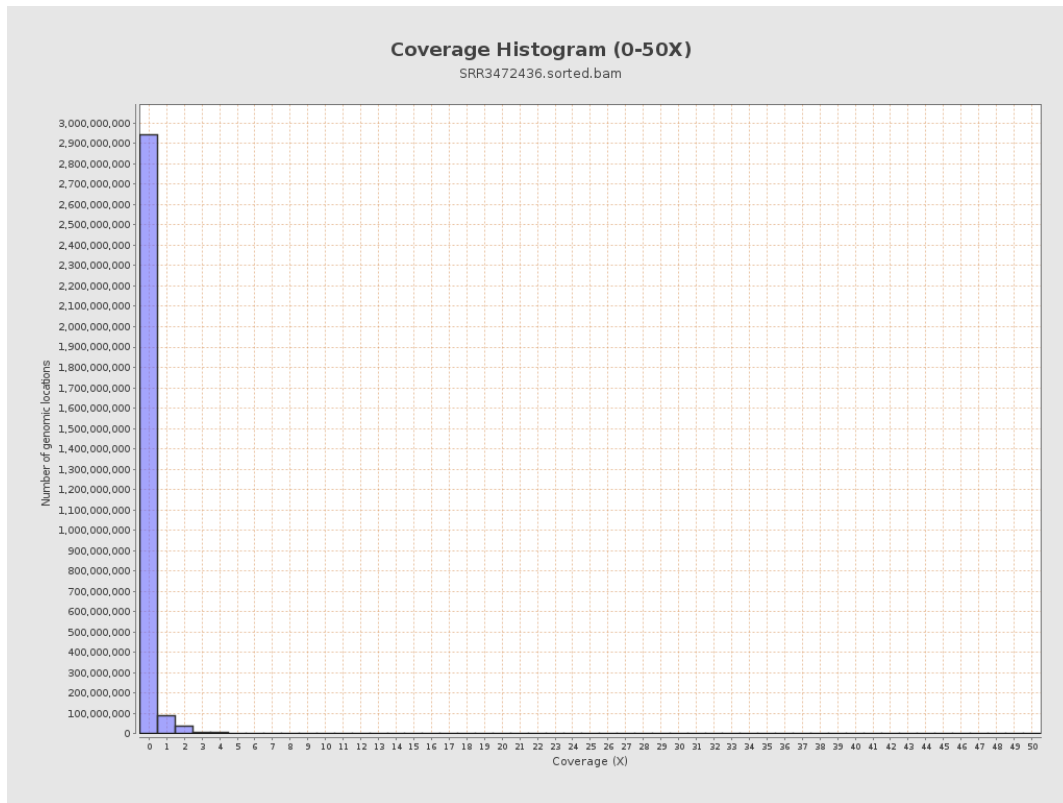
3. Results : Coverage across reference



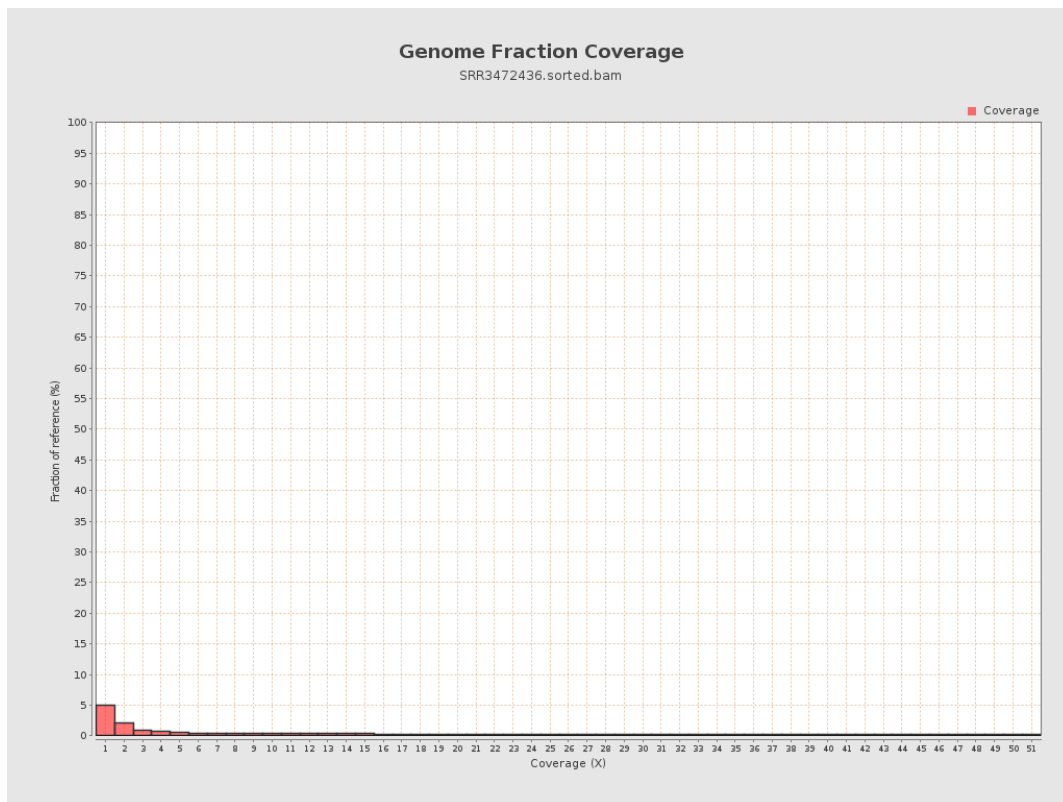
4. Results : Coverage Histogram



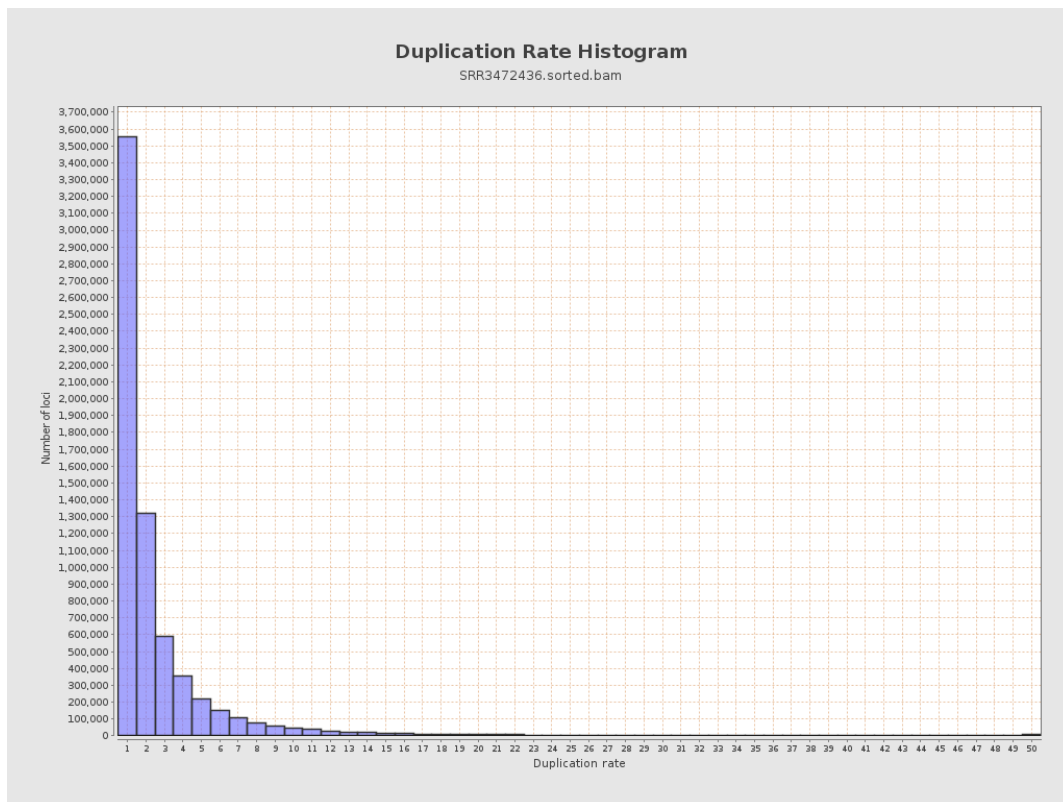
5. Results : Coverage Histogram (0-50X)



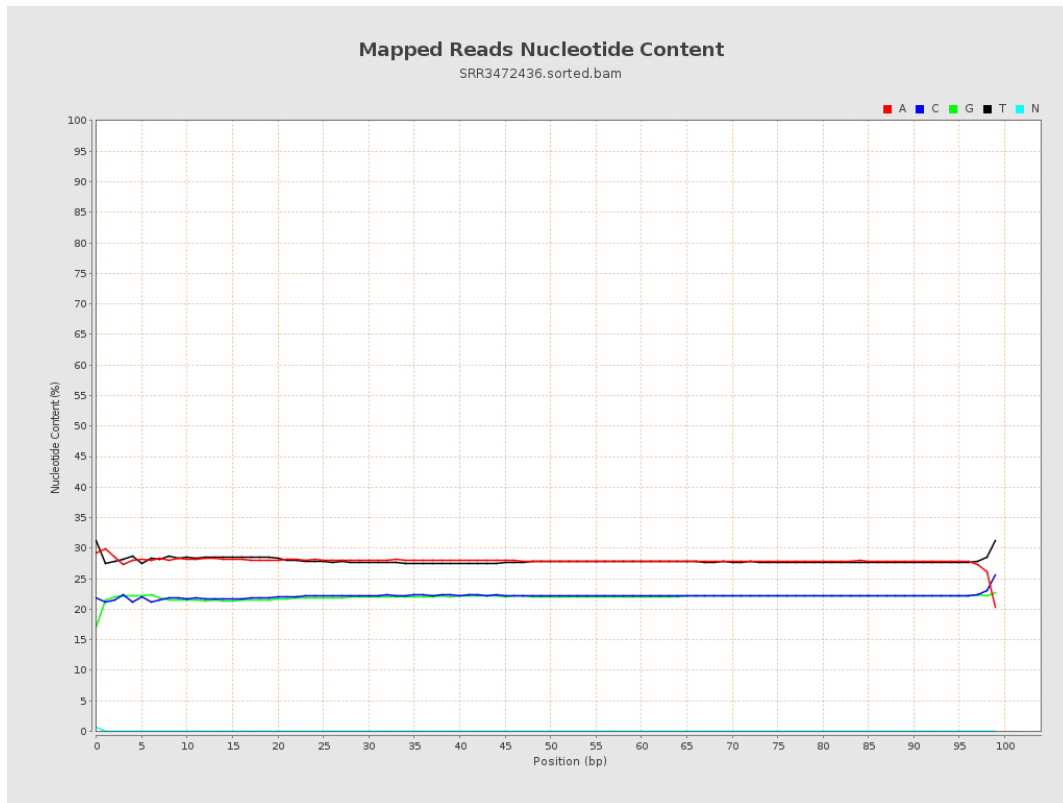
6. Results : Genome Fraction Coverage



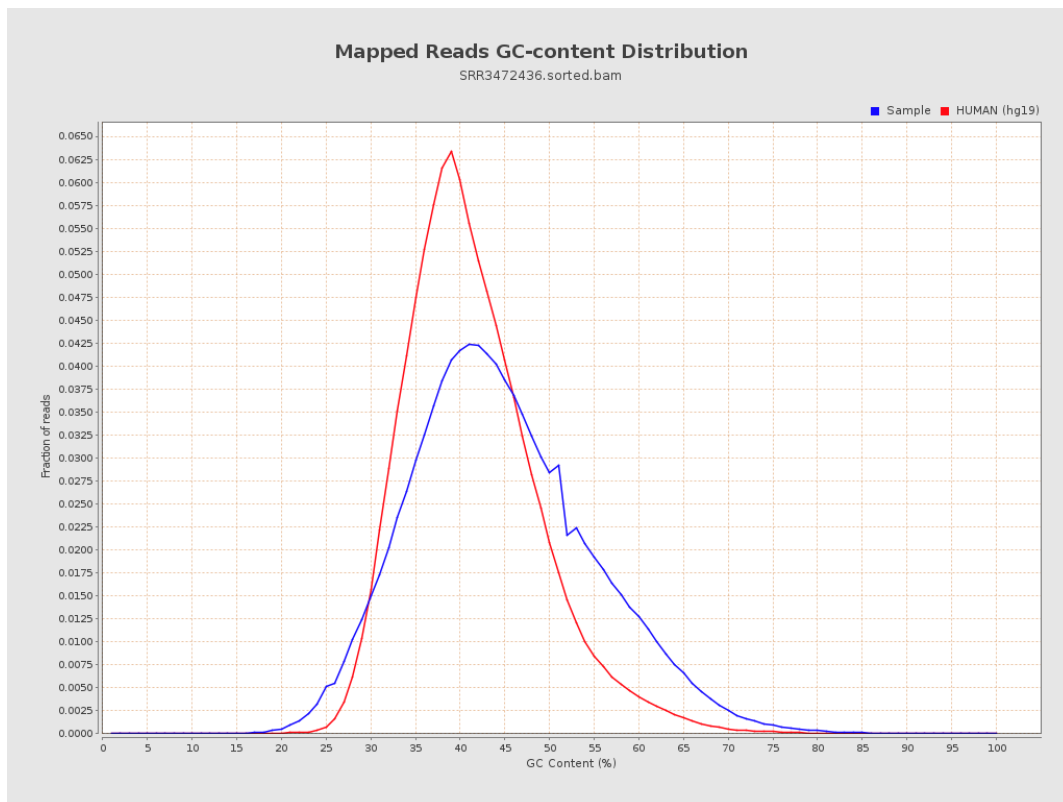
7. Results : Duplication Rate Histogram



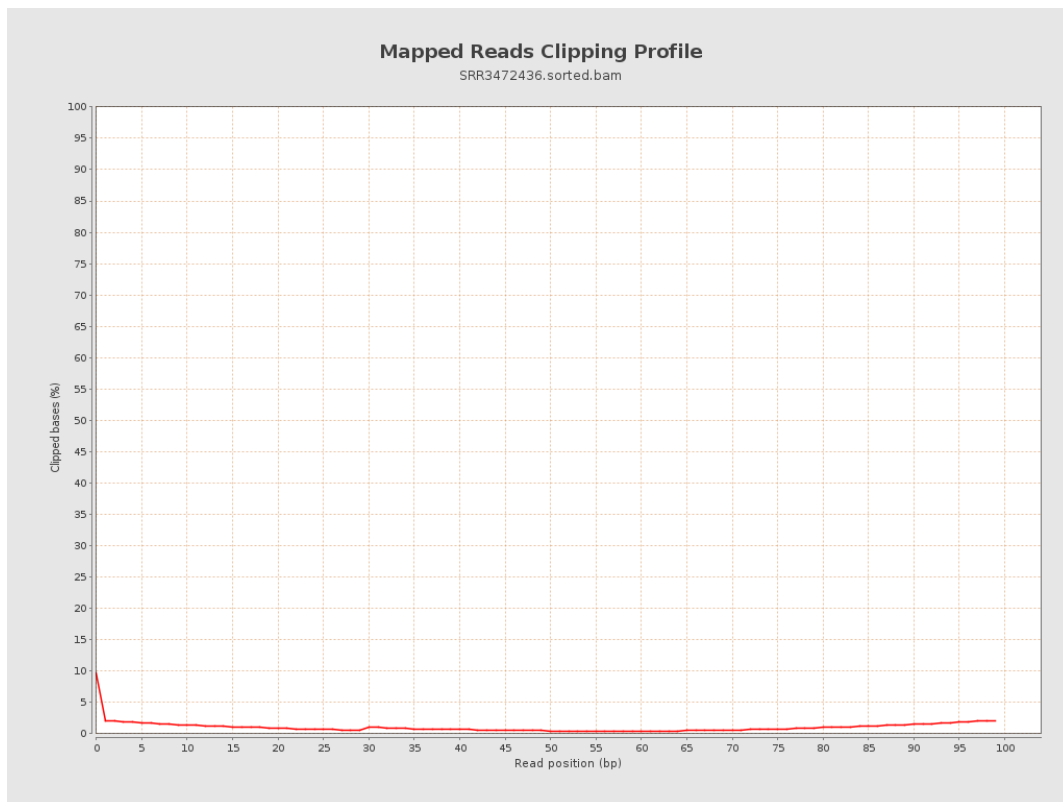
8. Results : Mapped Reads Nucleotide Content



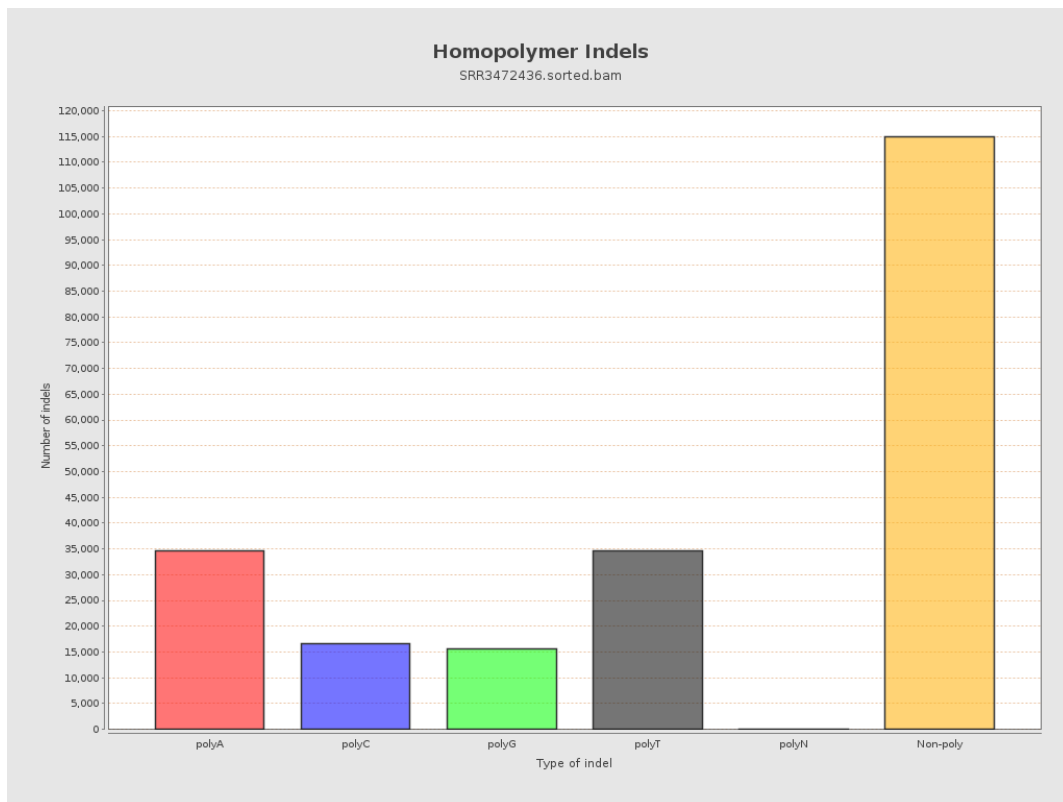
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



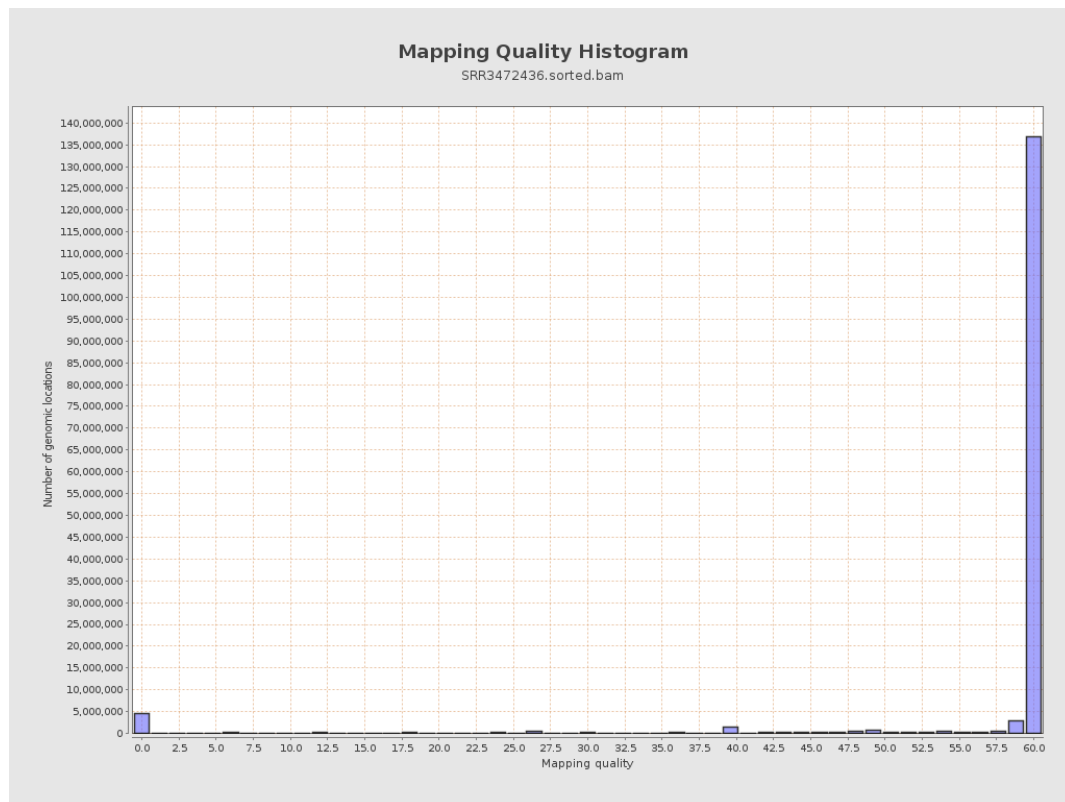
11. Results : Homopolymer Indels



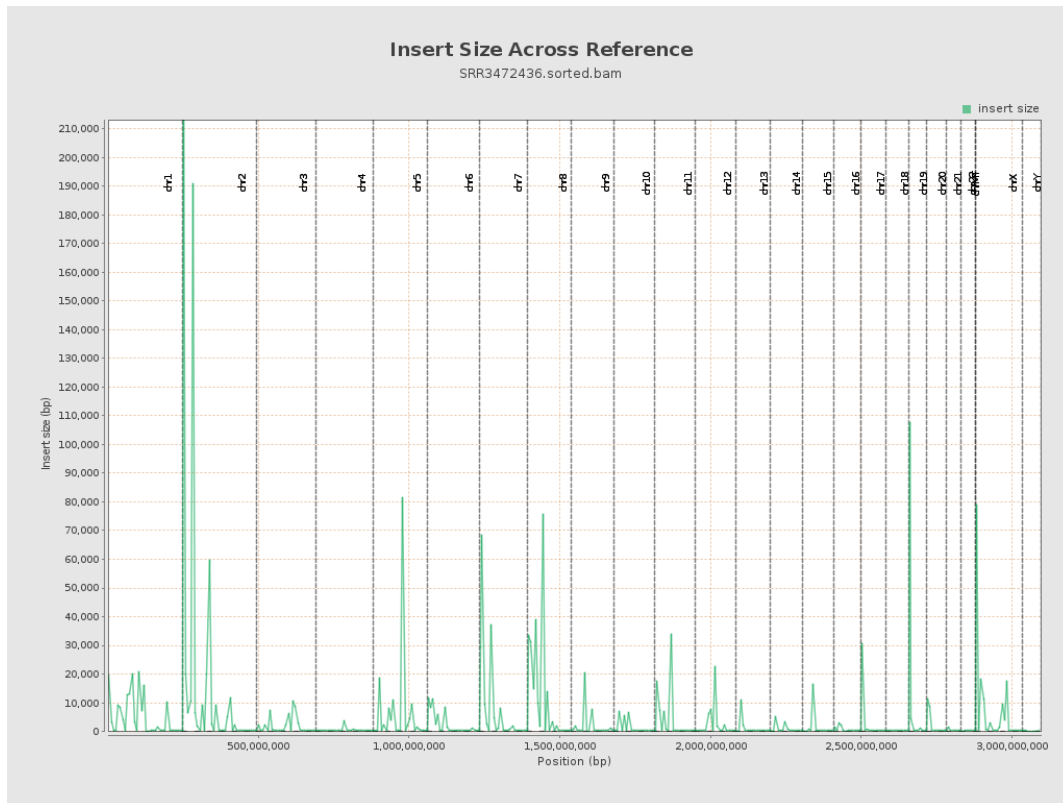
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

