

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 02:17:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472666.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_SRR3472666 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472666_1.fastq.gz SRR3472666_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 02:17:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472666.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,688,888
Mapped reads	16,489,450 / 98.8%
Unmapped reads	199,438 / 1.2%
Mapped paired reads	16,489,450 / 98.8%
Mapped reads, first in pair	8,277,578 / 49.6%
Mapped reads, second in pair	8,211,872 / 49.21%
Mapped reads, both in pair	16,363,670 / 98.05%
Mapped reads, singletons	125,780 / 0.75%
Secondary alignments	0
Supplementary alignments	93,530 / 0.56%
Read min/max/mean length	30 / 101 / 99.68
Duplicated reads (estimated)	11,388,343 / 68.24%
Duplication rate	49.71%
Clipped reads	1,304,394 / 7.82%

2.2. ACGT Content

Number/percentage of A's	432,298,767 / 26.71%
Number/percentage of C's	378,769,390 / 23.41%
Number/percentage of T's	432,567,103 / 26.73%
Number/percentage of G's	374,326,107 / 23.13%
Number/percentage of N's	316,393 / 0.02%

GC Percentage	46.54%
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2.3. Coverage

Mean	0.5228
Standard Deviation	22.5843

2.4. Mapping Quality

Mean Mapping Quality	54.97
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2.5. Insert size

Mean	24,706.33
Standard Deviation	1,539,790.09
P25/Median/P75	150 / 205 / 273

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	10,032,500
Insertions	101,693
Mapped reads with at least one insertion	0.61%
Deletions	92,302
Mapped reads with at least one deletion	0.55%
Homopolymer indels	44.49%

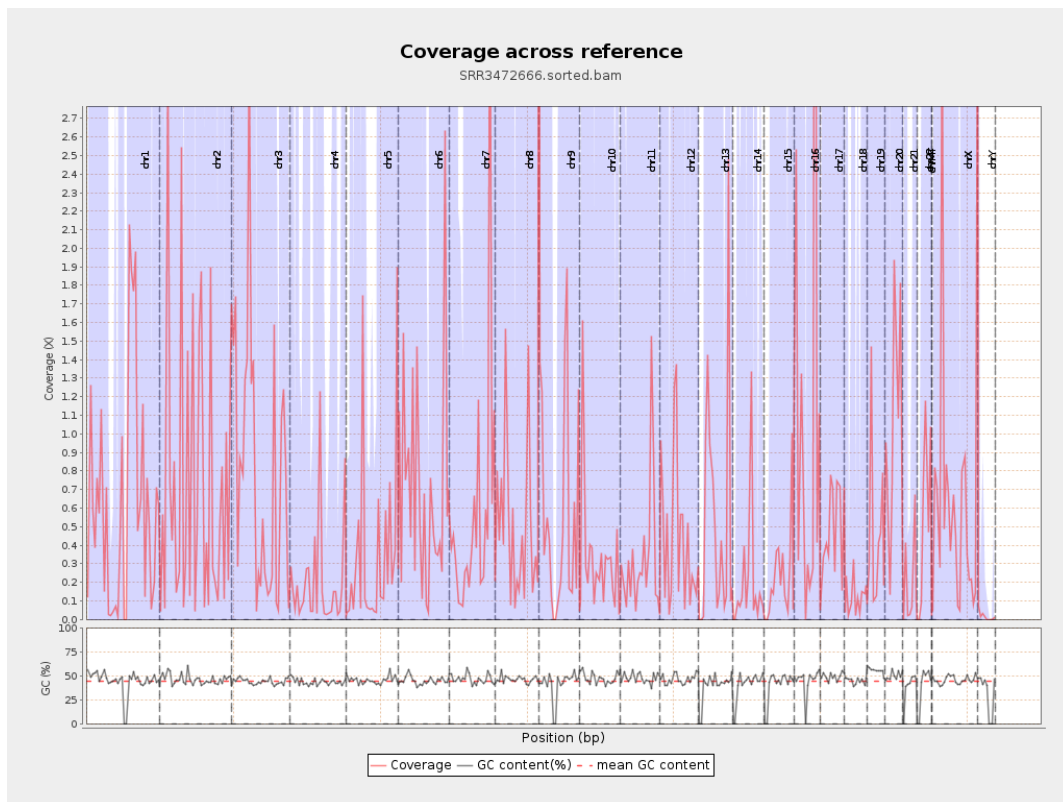
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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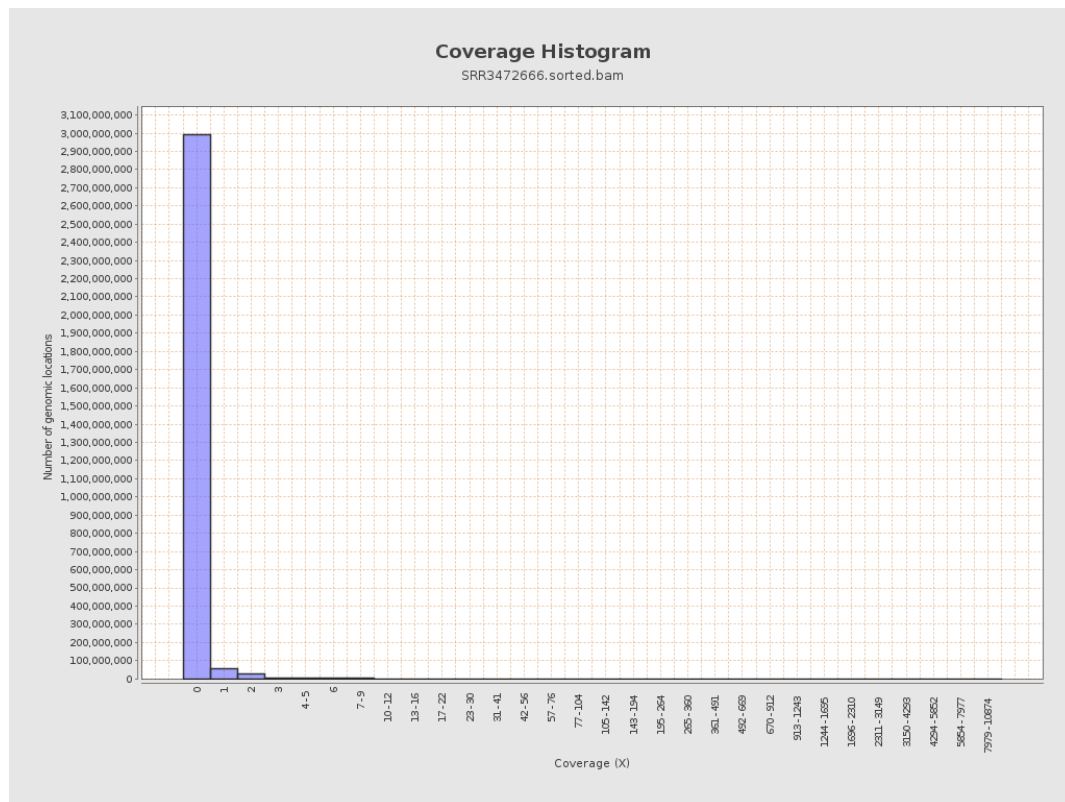
		bases	coverage	deviation
chr1	249250621	157760512	0.6329	23.0352
chr2	243199373	176831969	0.7271	36.8673
chr3	198022430	163805760	0.8272	24.1181
chr4	191154276	36806507	0.1925	11.5066
chr5	180915260	64495167	0.3565	20.4103
chr6	171115067	117508329	0.6867	21.1402
chr7	159138663	93323803	0.5864	23.2796
chr8	146364022	74710472	0.5104	19.283
chr9	141213431	87635548	0.6206	22.5975
chr10	135534747	44073277	0.3252	16.6413
chr11	135006516	45525152	0.3372	15.6806
chr12	133851895	59053982	0.4412	17.392
chr13	115169878	62326841	0.5412	31.6002
chr14	107349540	21099277	0.1965	10.2695
chr15	102531392	24419321	0.2382	12.707
chr16	90354753	107408306	1.1887	43.3647
chr17	81195210	38584812	0.4752	14.1219
chr18	78077248	9782541	0.1253	6.0684
chr19	59128983	28978267	0.4901	12.323
chr20	63025520	68405453	1.0854	29.5653
chr21	48129895	9881577	0.2053	13.4381
chr22	51304566	27257896	0.5313	21.0183
chrMT	16571	4574	0.276	0.7447
chrX	155270560	97899173	0.6305	21.5705

chrY	59373566	932478	0.0157	1.282
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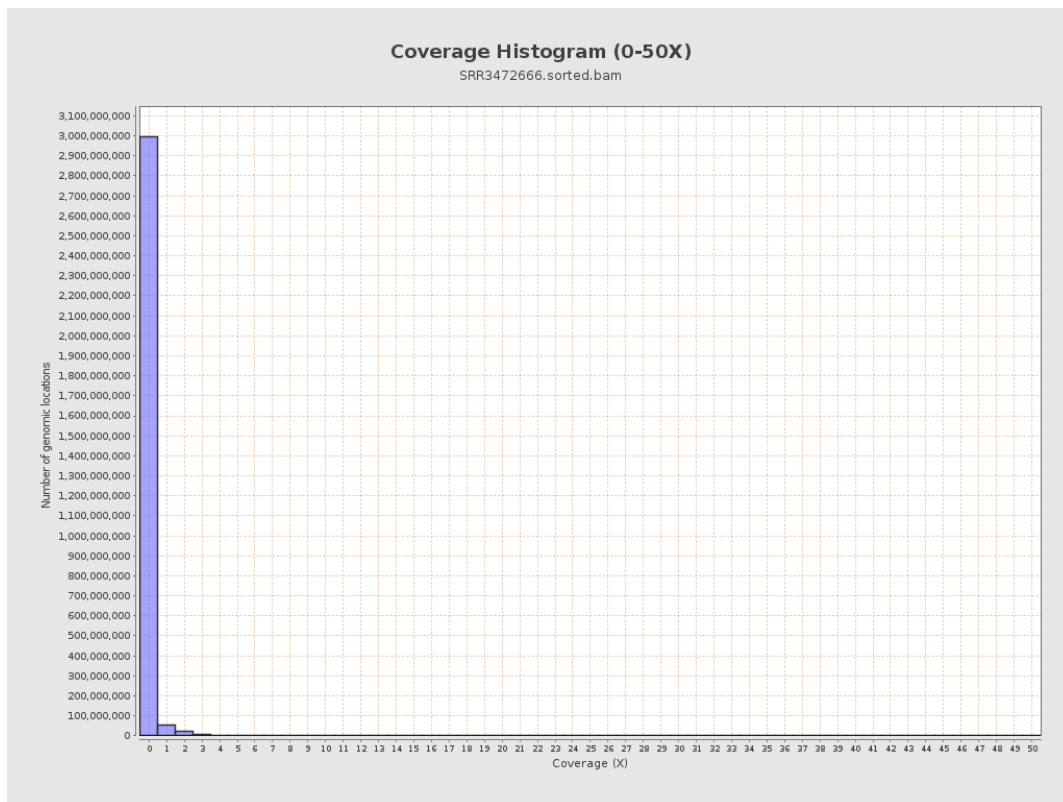
3. Results : Coverage across reference



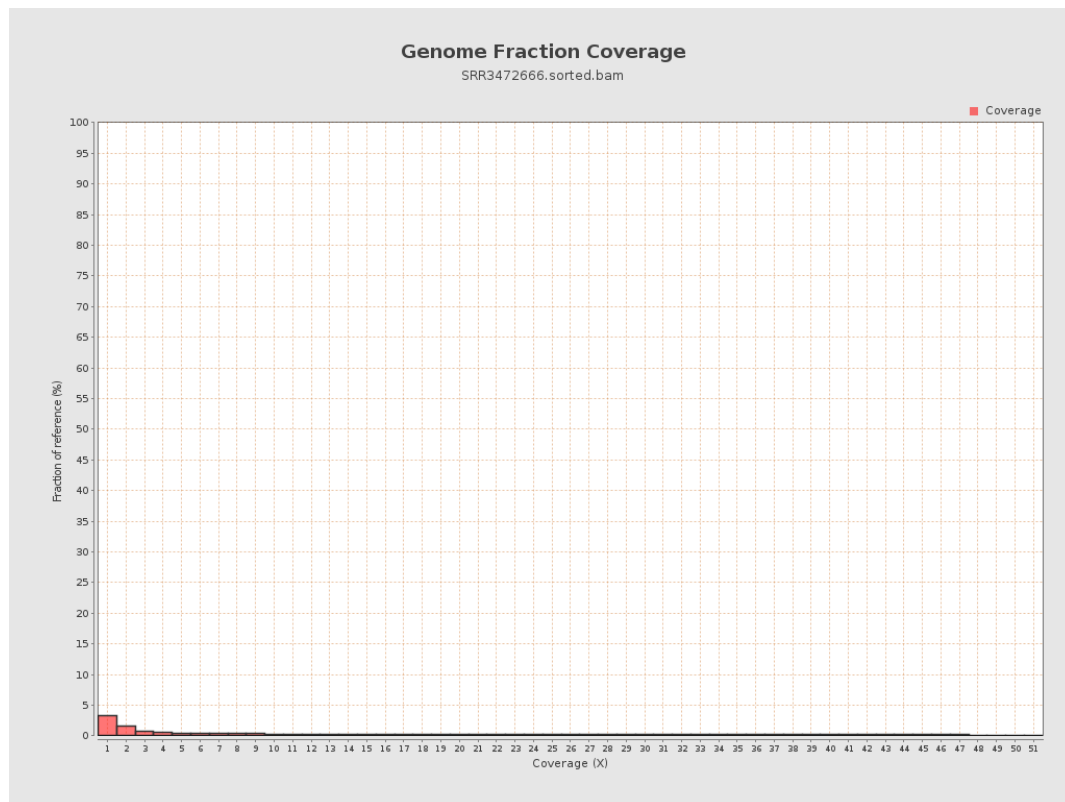
4. Results : Coverage Histogram



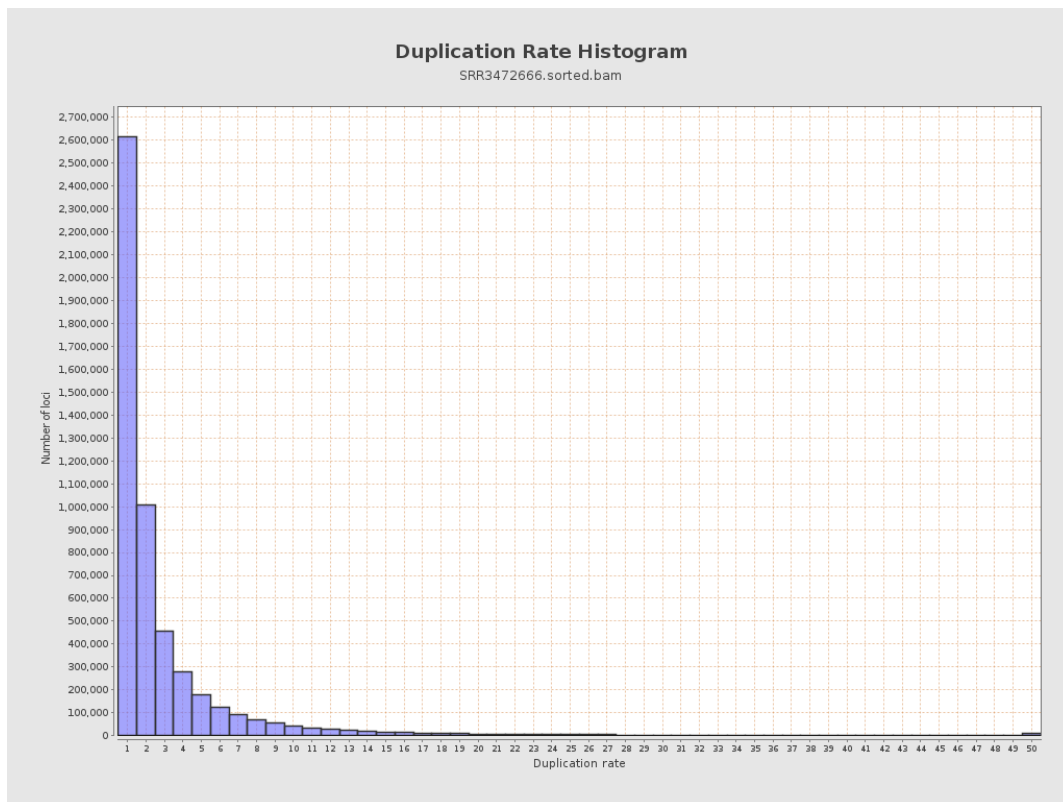
5. Results : Coverage Histogram (0-50X)



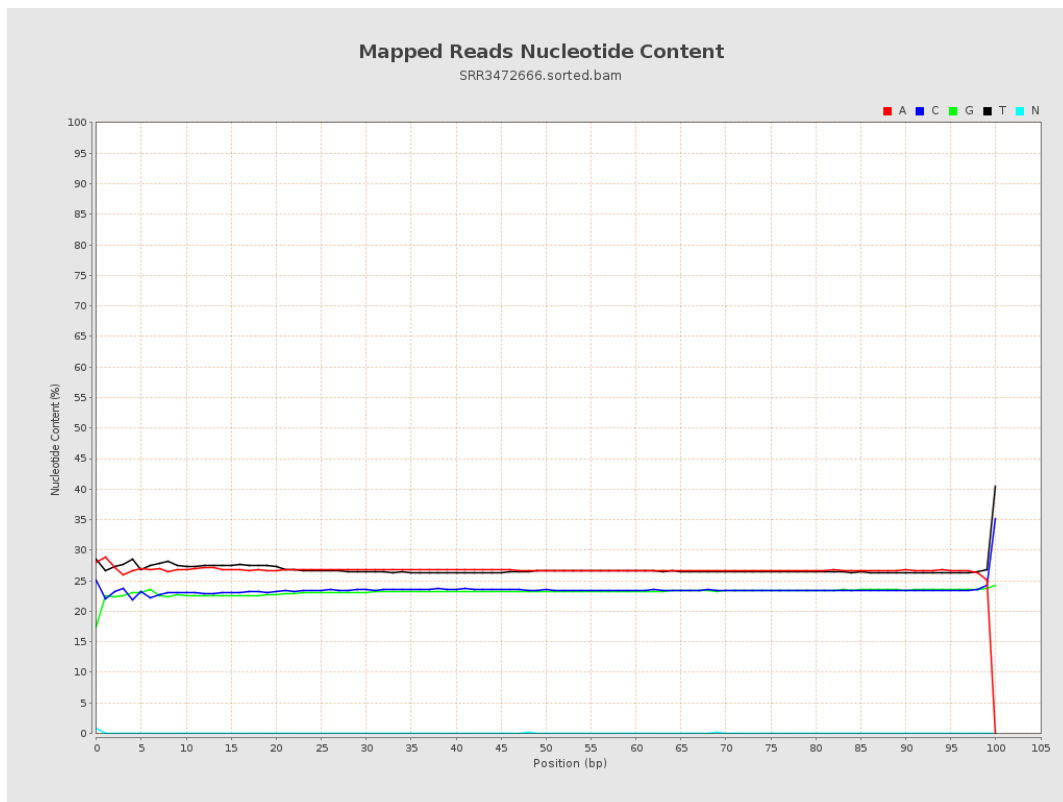
6. Results : Genome Fraction Coverage



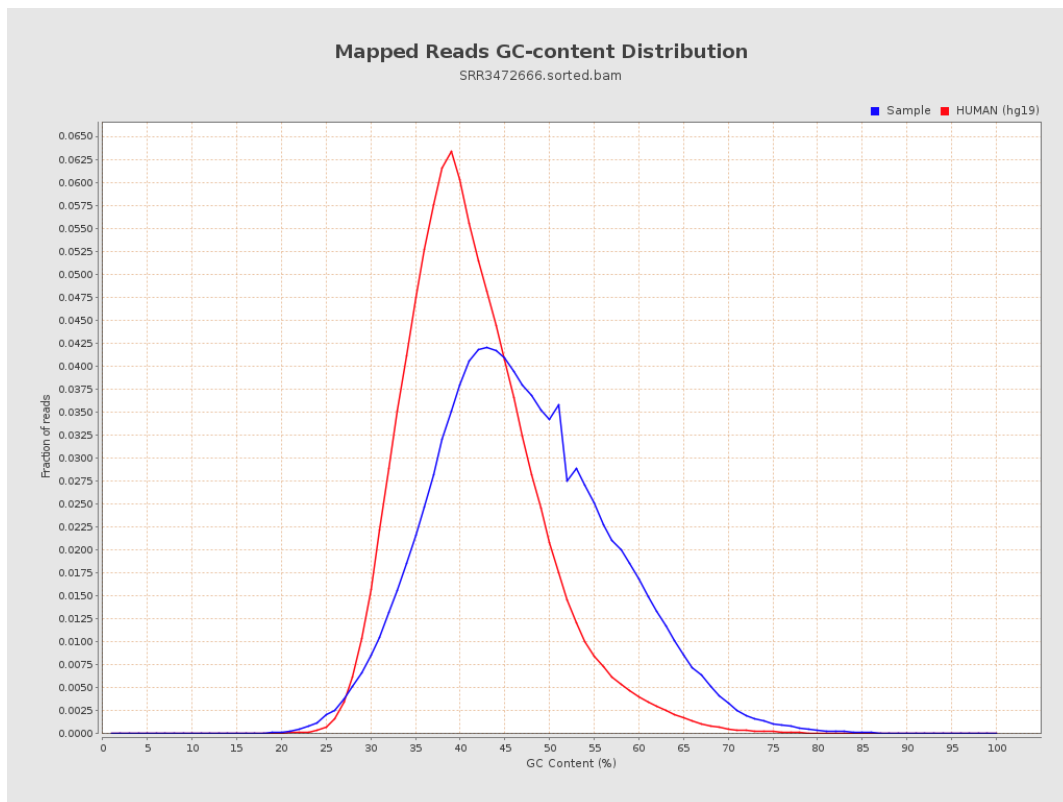
7. Results : Duplication Rate Histogram



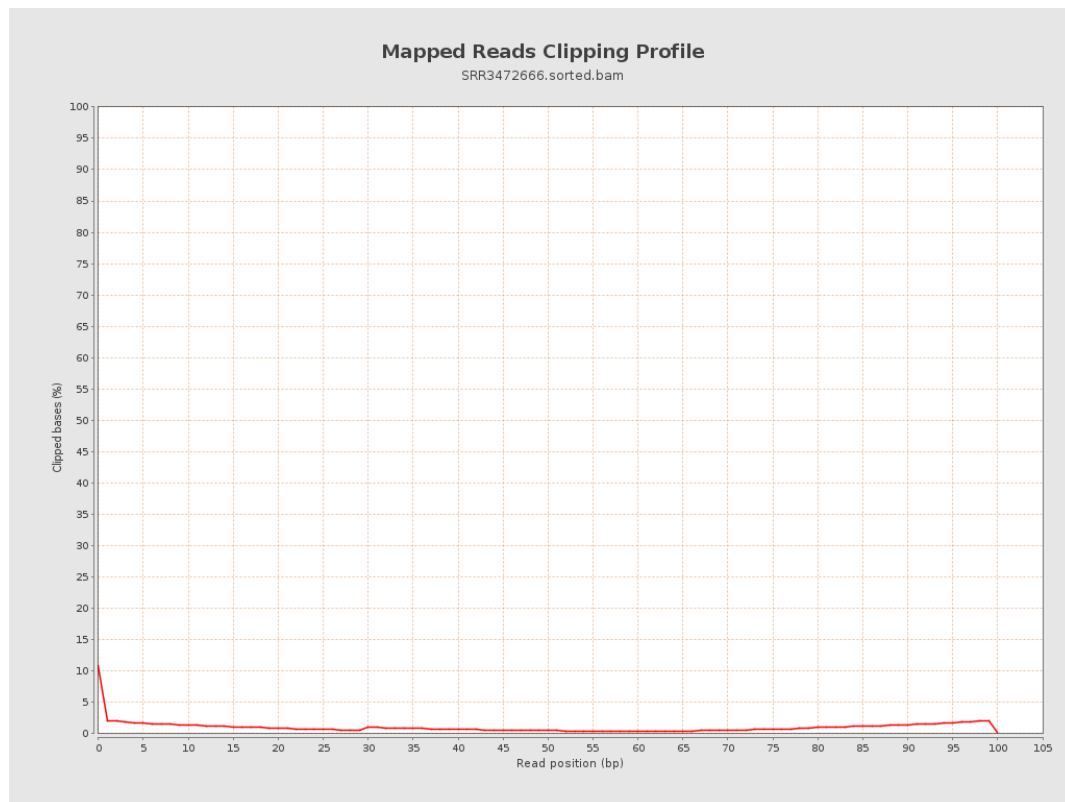
8. Results : Mapped Reads Nucleotide Content



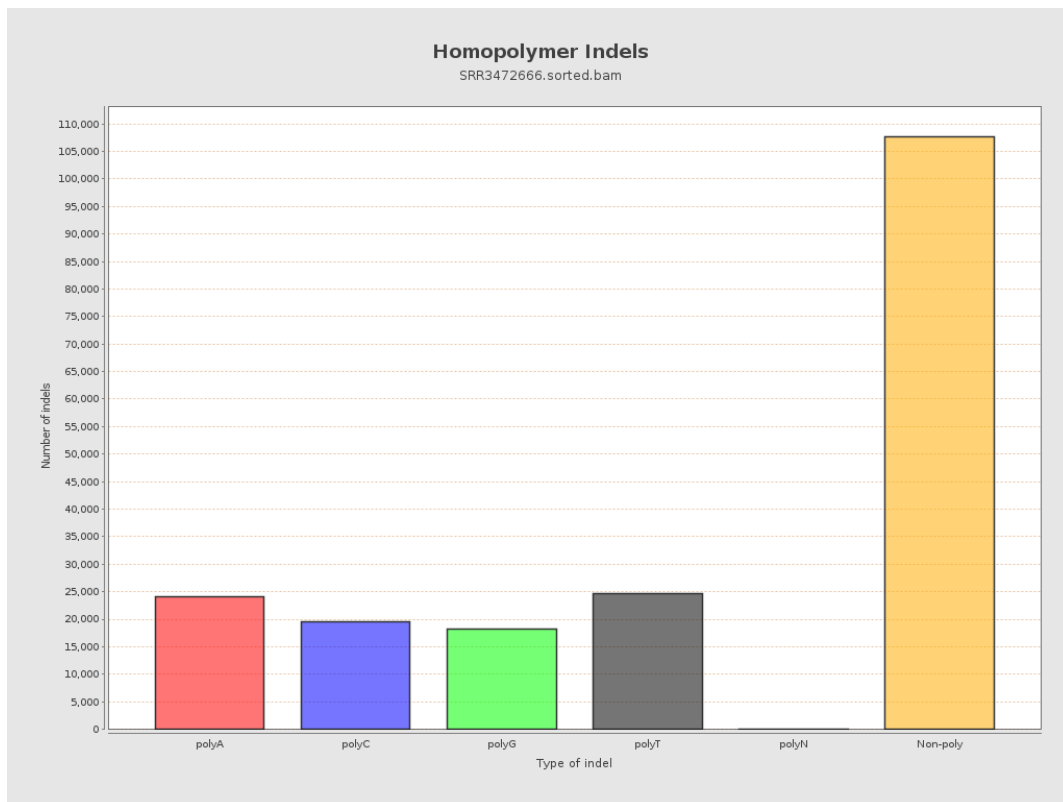
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



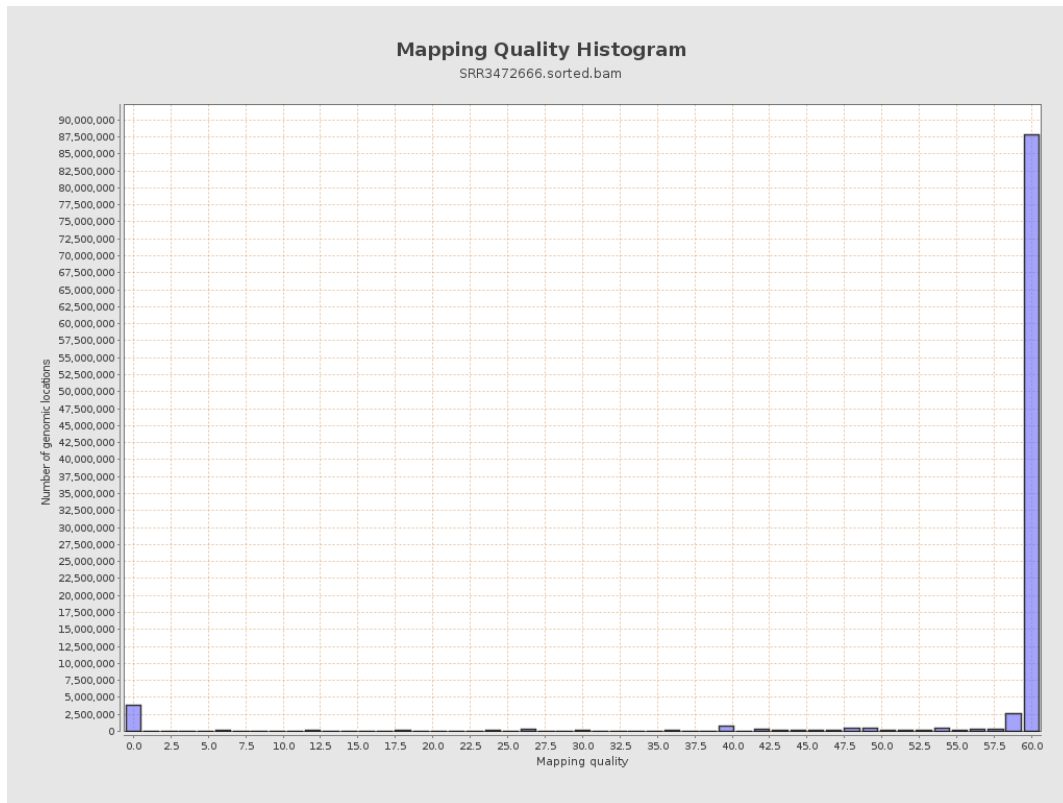
11. Results : Homopolymer Indels



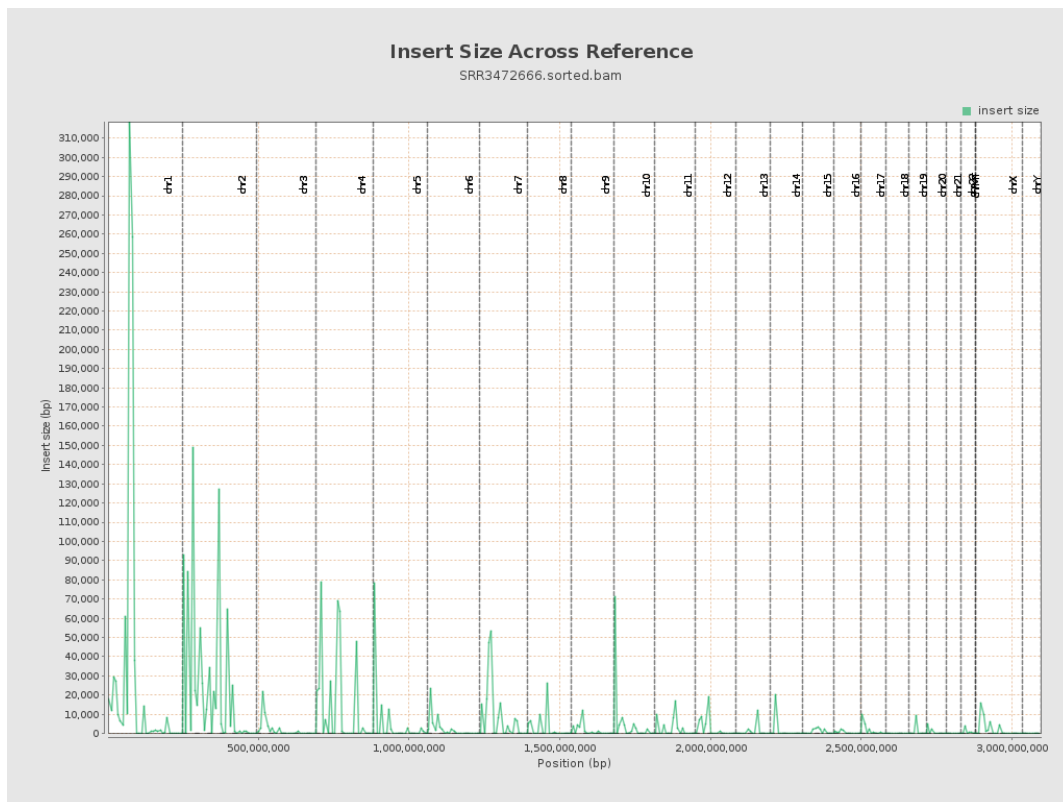
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

