

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 15:02:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472706.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_SRR3472706 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472706_1.fastq.gz SRR3472706_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 15:02:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472706.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,190,544
Mapped reads	9,090,218 / 98.91%
Unmapped reads	100,326 / 1.09%
Mapped paired reads	9,090,218 / 98.91%
Mapped reads, first in pair	4,566,381 / 49.69%
Mapped reads, second in pair	4,523,837 / 49.22%
Mapped reads, both in pair	9,029,444 / 98.25%
Mapped reads, singletons	60,774 / 0.66%
Secondary alignments	0
Supplementary alignments	28,464 / 0.31%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	5,073,750 / 55.21%
Duplication rate	44.67%
Clipped reads	1,013,120 / 11.02%

2.2. ACGT Content

Number/percentage of A's	237,581,331 / 26.74%
Number/percentage of C's	208,308,545 / 23.44%
Number/percentage of T's	235,719,237 / 26.53%
Number/percentage of G's	206,820,192 / 23.27%
Number/percentage of N's	172,185 / 0.02%

GC Percentage	46.72%
---------------	--------

2.3. Coverage

Mean	0.2871
Standard Deviation	9.8602

2.4. Mapping Quality

Mean Mapping Quality	55.21
----------------------	-------

2.5. Insert size

Mean	17,428.74
Standard Deviation	1,309,060.63
P25/Median/P75	145 / 202 / 275

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	5,340,256
Insertions	49,349
Mapped reads with at least one insertion	0.54%
Deletions	46,294
Mapped reads with at least one deletion	0.5%
Homopolymer indels	43.37%

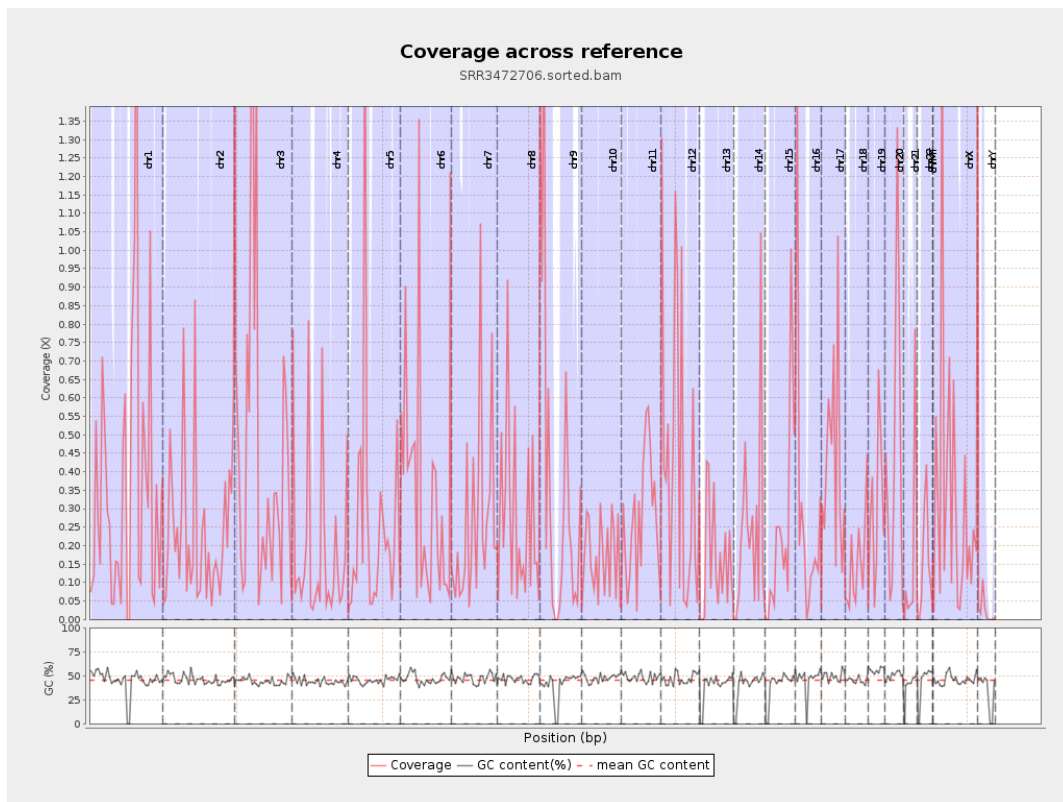
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

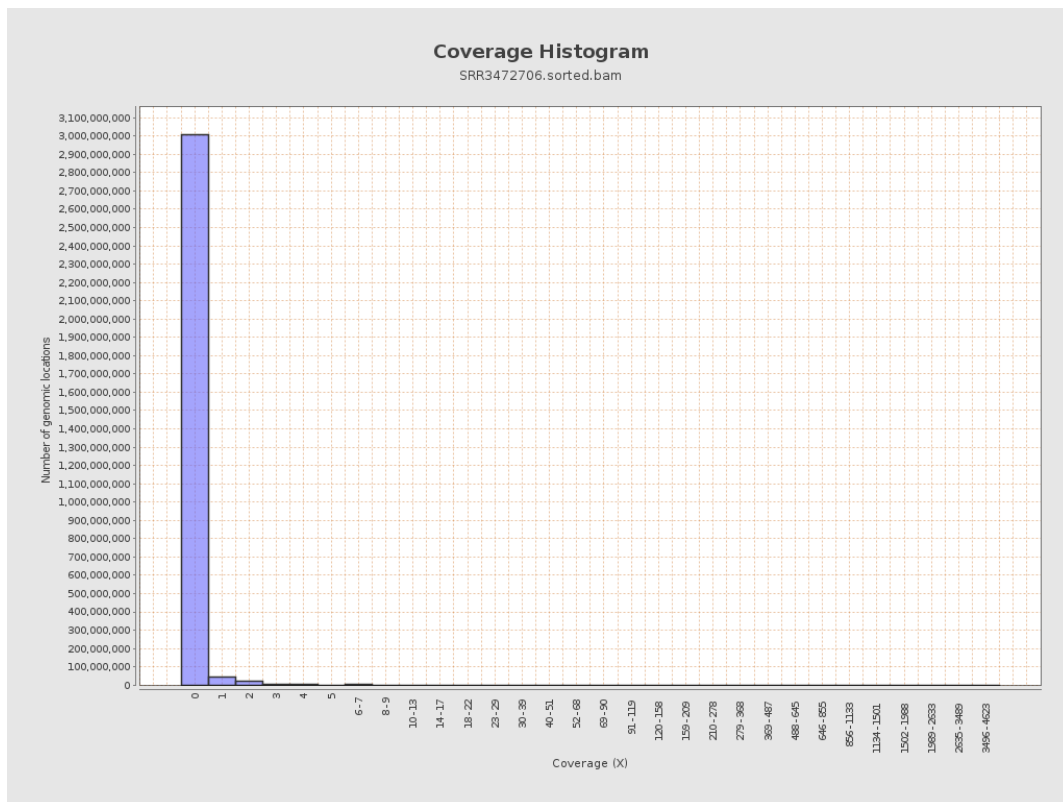
		bases	coverage	deviation
chr1	249250621	90885068	0.3646	13.6473
chr2	243199373	57040921	0.2345	7.1881
chr3	198022430	92361887	0.4664	11.0113
chr4	191154276	36668548	0.1918	8.8811
chr5	180915260	46776584	0.2586	8.7198
chr6	171115067	58548432	0.3422	10.5348
chr7	159138663	42220578	0.2653	8.2908
chr8	146364022	38886667	0.2657	10.7389
chr9	141213431	47171414	0.334	8.7143
chr10	135534747	23782230	0.1755	6.1232
chr11	135006516	36815329	0.2727	9.147
chr12	133851895	58801432	0.4393	13.6579
chr13	115169878	18257823	0.1585	6.095
chr14	107349540	26023278	0.2424	10.268
chr15	102531392	24360959	0.2376	8.2479
chr16	90354753	26319874	0.2913	8.2445
chr17	81195210	35155788	0.433	10.8078
chr18	78077248	11598998	0.1486	5.0303
chr19	59128983	18182641	0.3075	8.4188
chr20	63025520	27097042	0.4299	18.213
chr21	48129895	7946395	0.1651	8.5207
chr22	51304566	8001499	0.156	4.2698
chrMT	16571	2748	0.1658	0.578
chrX	155270560	54366877	0.3501	11.485

chrY	59373566	1436790	0.0242	0.9599
------	----------	---------	--------	--------

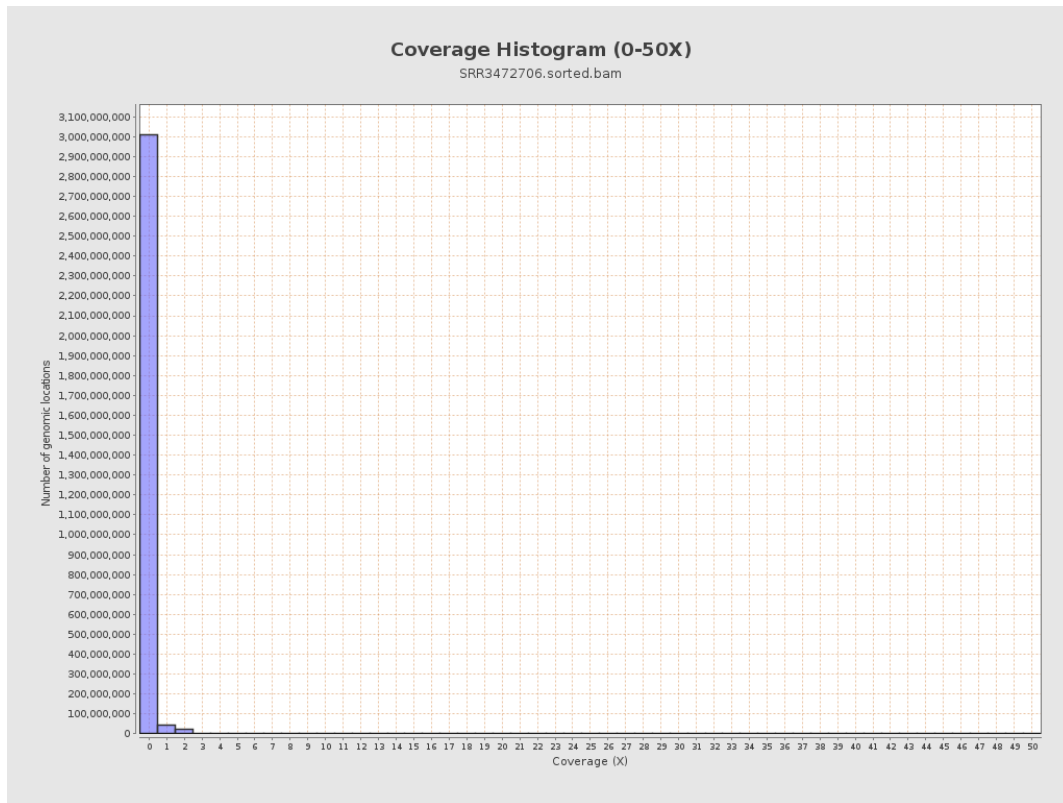
3. Results : Coverage across reference



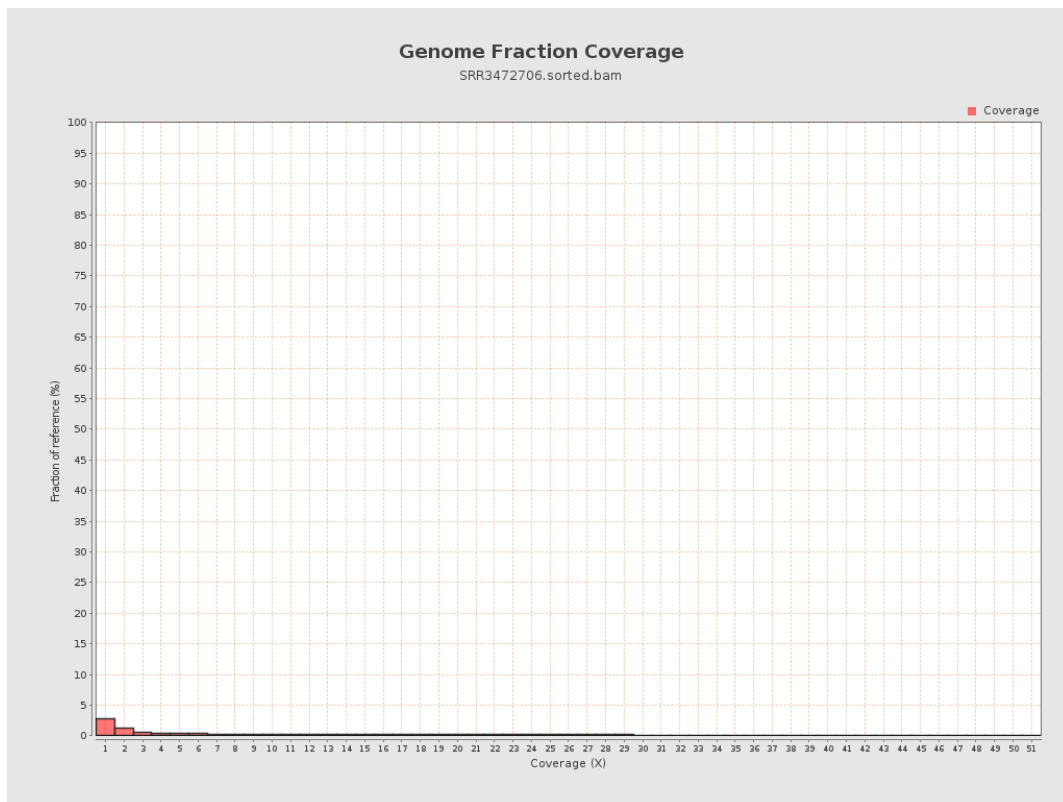
4. Results : Coverage Histogram



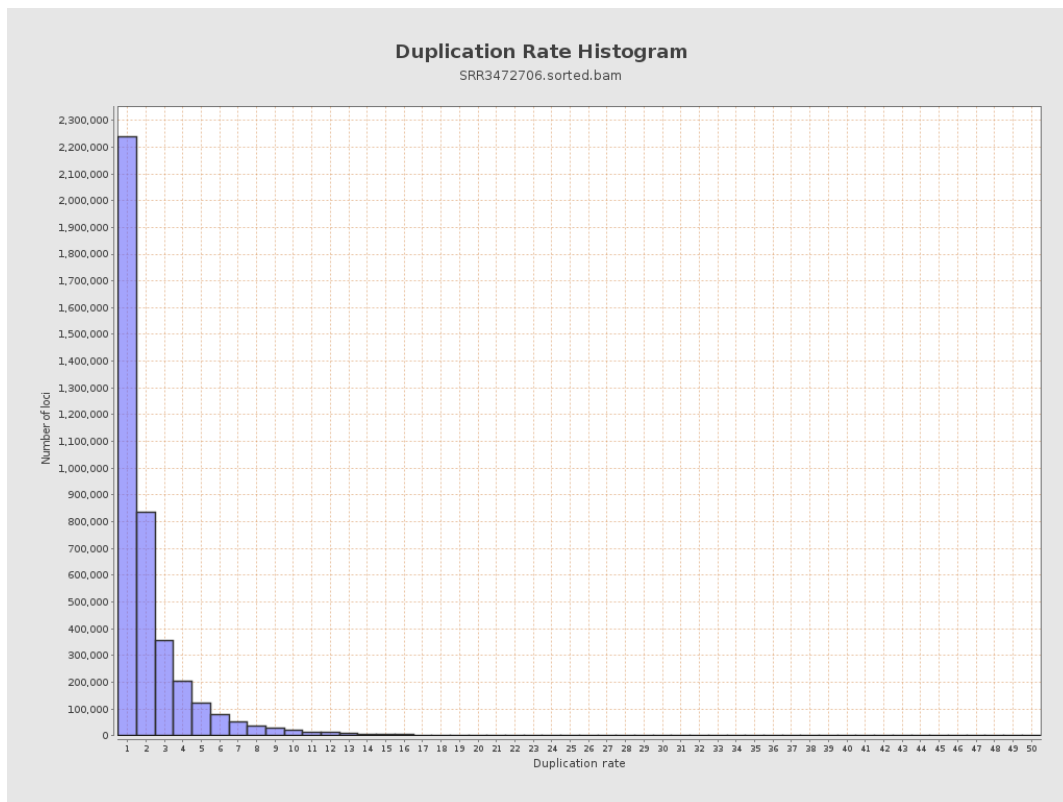
5. Results : Coverage Histogram (0-50X)



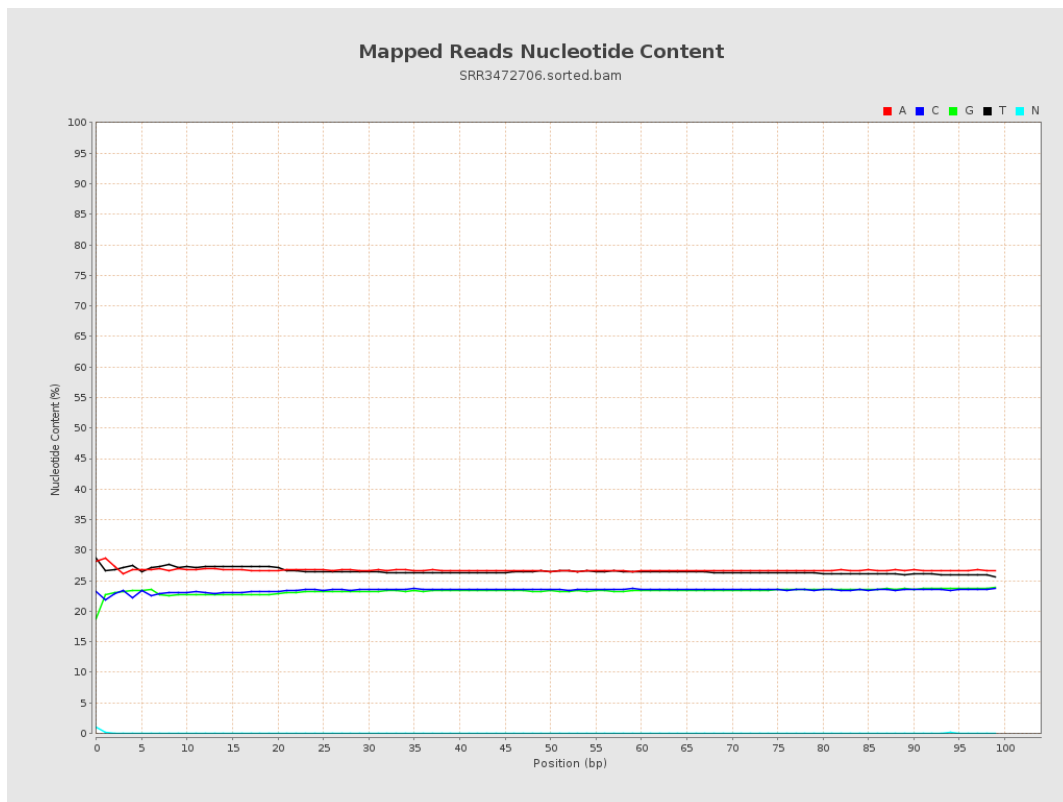
6. Results : Genome Fraction Coverage



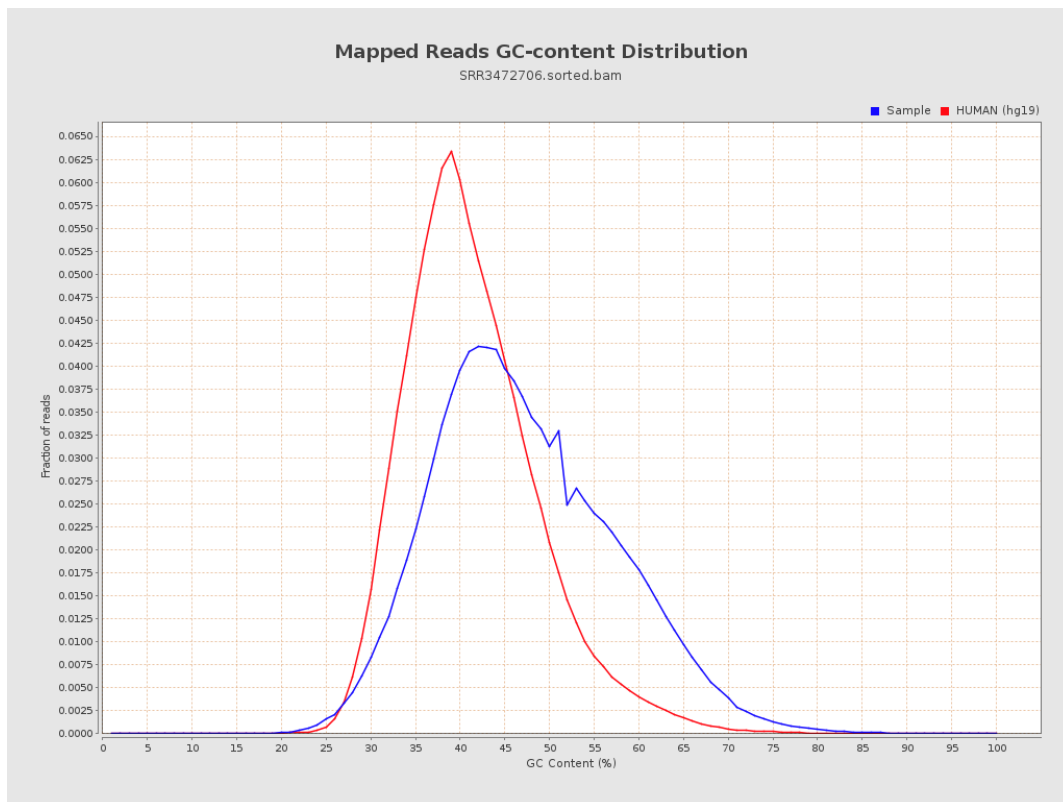
7. Results : Duplication Rate Histogram



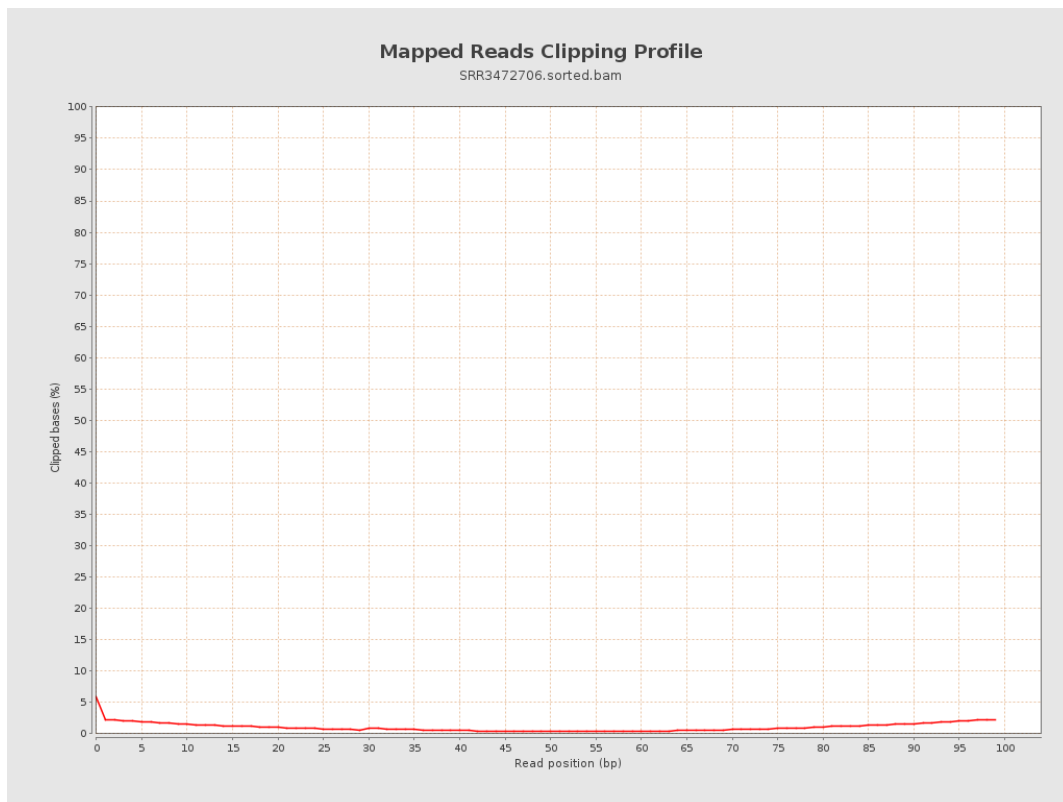
8. Results : Mapped Reads Nucleotide Content



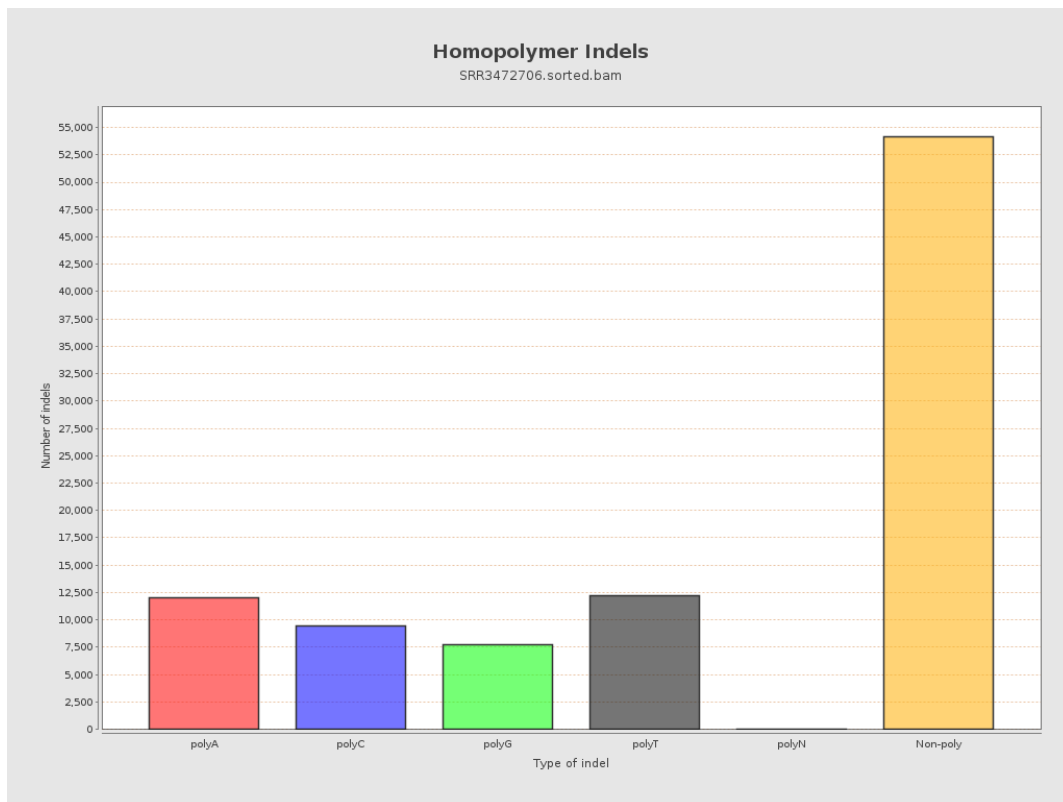
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



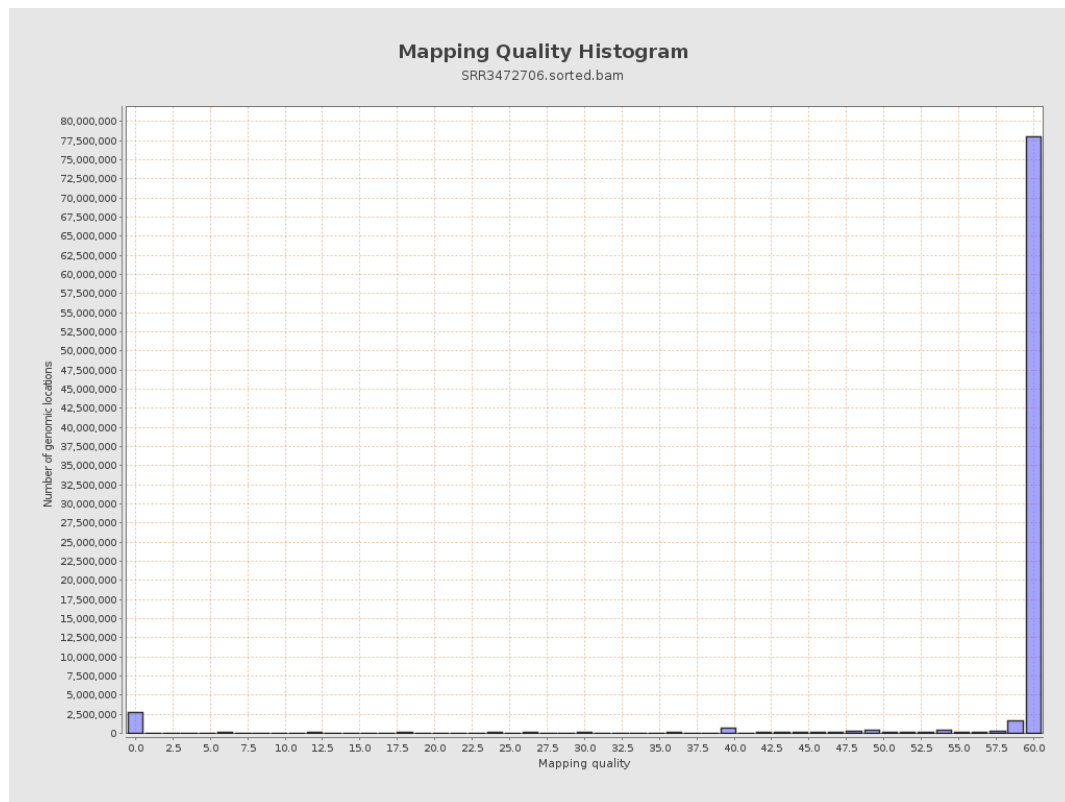
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

