

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:56:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472453.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_SRR3472453 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472453_1.fastq.gz SRR3472453_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:56:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472453.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,406,166
Mapped reads	13,271,829 / 99%
Unmapped reads	134,337 / 1%
Mapped paired reads	13,271,829 / 99%
Mapped reads, first in pair	6,655,963 / 49.65%
Mapped reads, second in pair	6,615,866 / 49.35%
Mapped reads, both in pair	13,213,268 / 98.56%
Mapped reads, singletons	58,561 / 0.44%
Secondary alignments	0
Supplementary alignments	48,029 / 0.36%
Read min/max/mean length	30 / 100 / 98.95
Duplicated reads (estimated)	8,473,387 / 63.21%
Duplication rate	46.61%
Clipped reads	1,035,761 / 7.73%

2.2. ACGT Content

Number/percentage of A's	342,826,247 / 26.49%
Number/percentage of C's	305,478,143 / 23.6%
Number/percentage of T's	344,628,120 / 26.63%
Number/percentage of G's	301,063,739 / 23.26%
Number/percentage of N's	173,456 / 0.01%

GC Percentage	46.87%
---------------	--------

2.3. Coverage

Mean	0.4181
Standard Deviation	16.27

2.4. Mapping Quality

Mean Mapping Quality	54.46
----------------------	-------

2.5. Insert size

Mean	18,470.88
Standard Deviation	1,404,029.43
P25/Median/P75	140 / 195 / 264

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	5,785,581
Insertions	72,828
Mapped reads with at least one insertion	0.54%
Deletions	59,371
Mapped reads with at least one deletion	0.44%
Homopolymer indels	45.38%

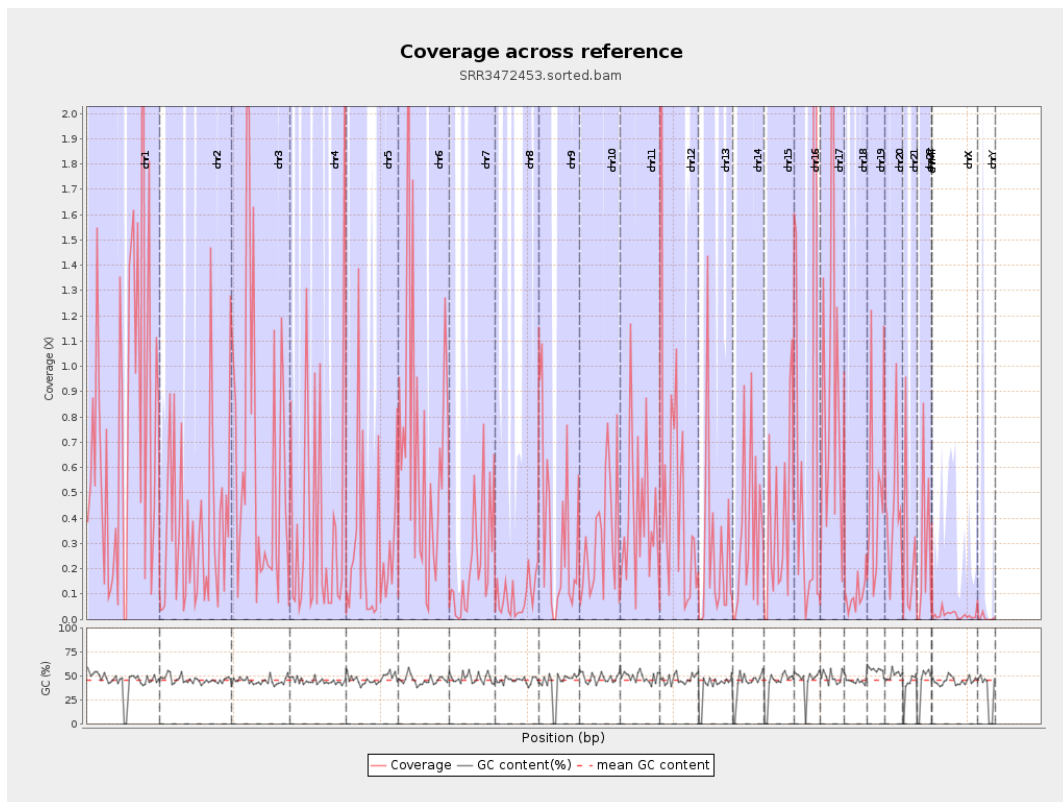
2.7. Chromosome stats

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

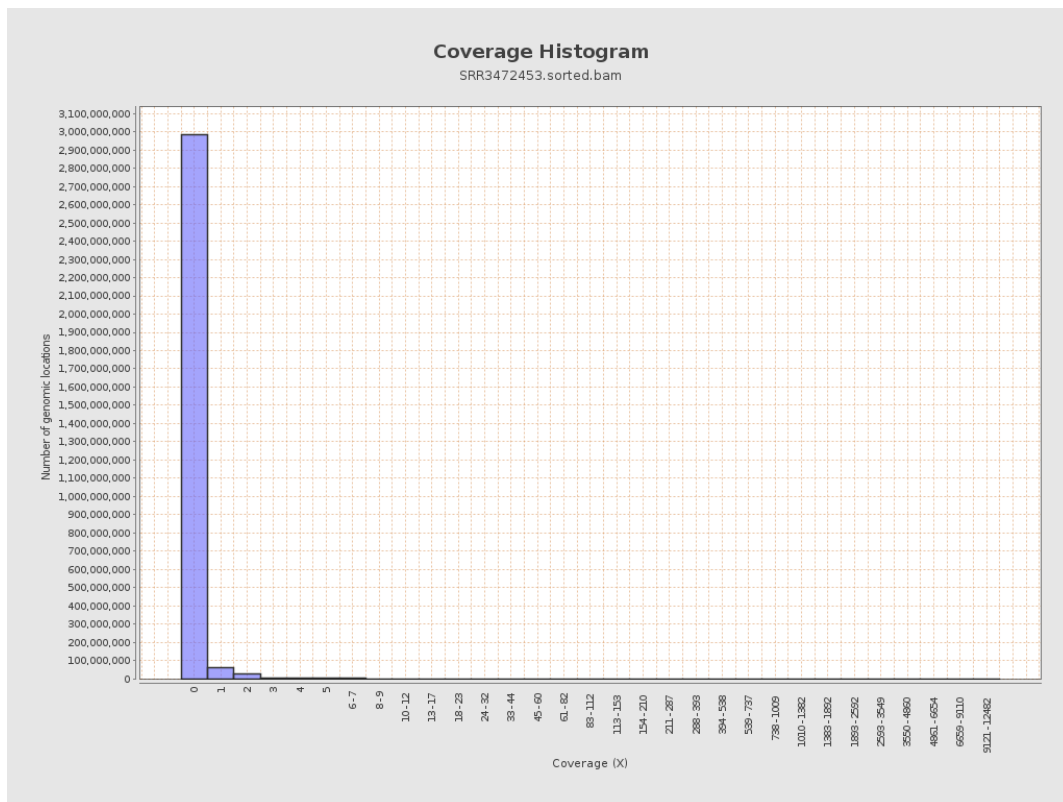
		bases	coverage	deviation
chr1	249250621	200006966	0.8024	25.7599
chr2	243199373	89878391	0.3696	12.9772
chr3	198022430	127550485	0.6441	16.6246
chr4	191154276	74148704	0.3879	15.5845
chr5	180915260	50876670	0.2812	12.3844
chr6	171115067	115973201	0.6777	25.062
chr7	159138663	36346020	0.2284	9.7381
chr8	146364022	13347623	0.0912	3.2047
chr9	141213431	48024087	0.3401	11.2118
chr10	135534747	42508030	0.3136	10.988
chr11	135006516	56161967	0.416	14.3859
chr12	133851895	80483433	0.6013	17.8972
chr13	115169878	30057443	0.261	10.1457
chr14	107349540	36012772	0.3355	12.0379
chr15	102531392	39774277	0.3879	13.9377
chr16	90354753	82121170	0.9089	37.4576
chr17	81195210	78238691	0.9636	24.228
chr18	78077248	7676042	0.0983	3.1266
chr19	59128983	29174456	0.4934	11.3282
chr20	63025520	27159478	0.4309	11.1888
chr21	48129895	12437521	0.2584	15.888
chr22	51304566	13327733	0.2598	9.6866
chrMT	16571	6303	0.3804	0.8311
chrX	155270560	2663138	0.0172	0.3986

chrY	59373566	371909	0.0063	0.7589
------	----------	--------	--------	--------

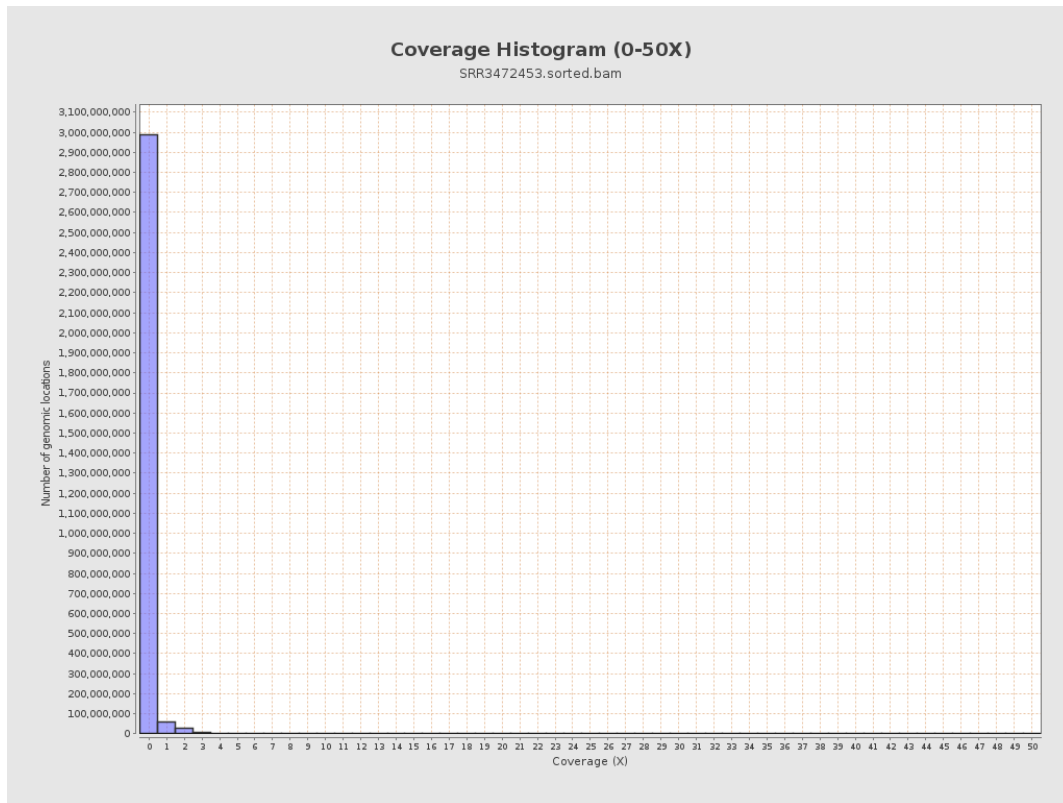
3. Results : Coverage across reference



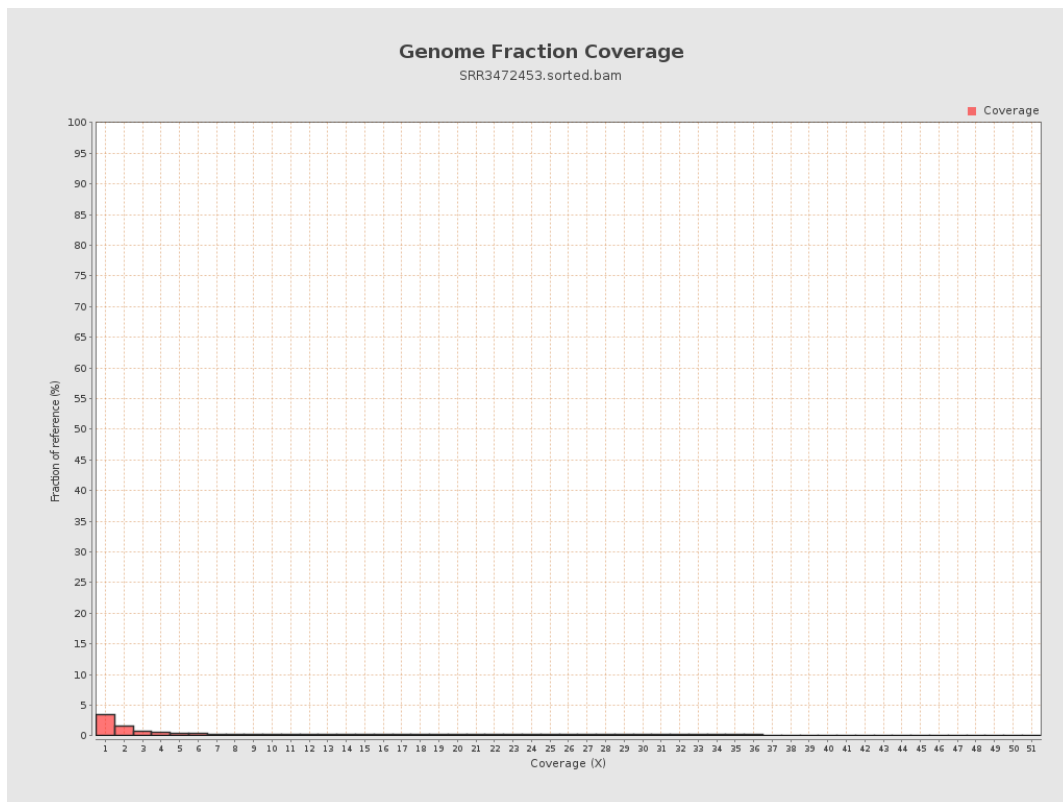
4. Results : Coverage Histogram



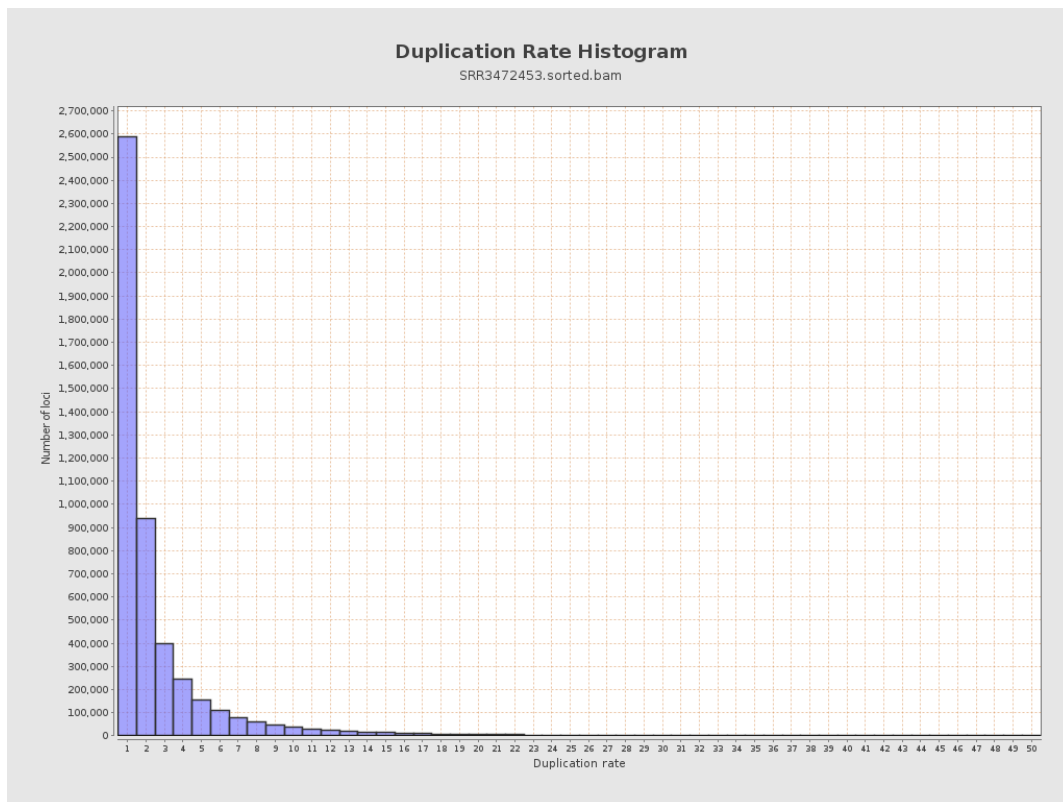
5. Results : Coverage Histogram (0-50X)



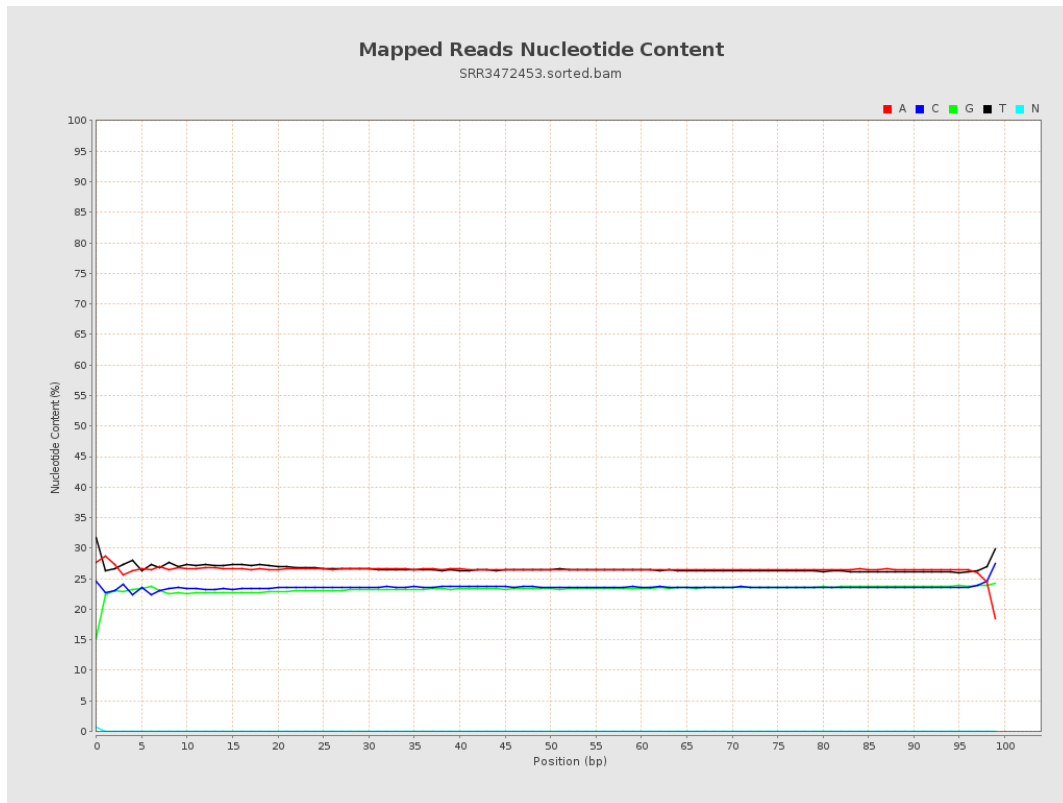
6. Results : Genome Fraction Coverage



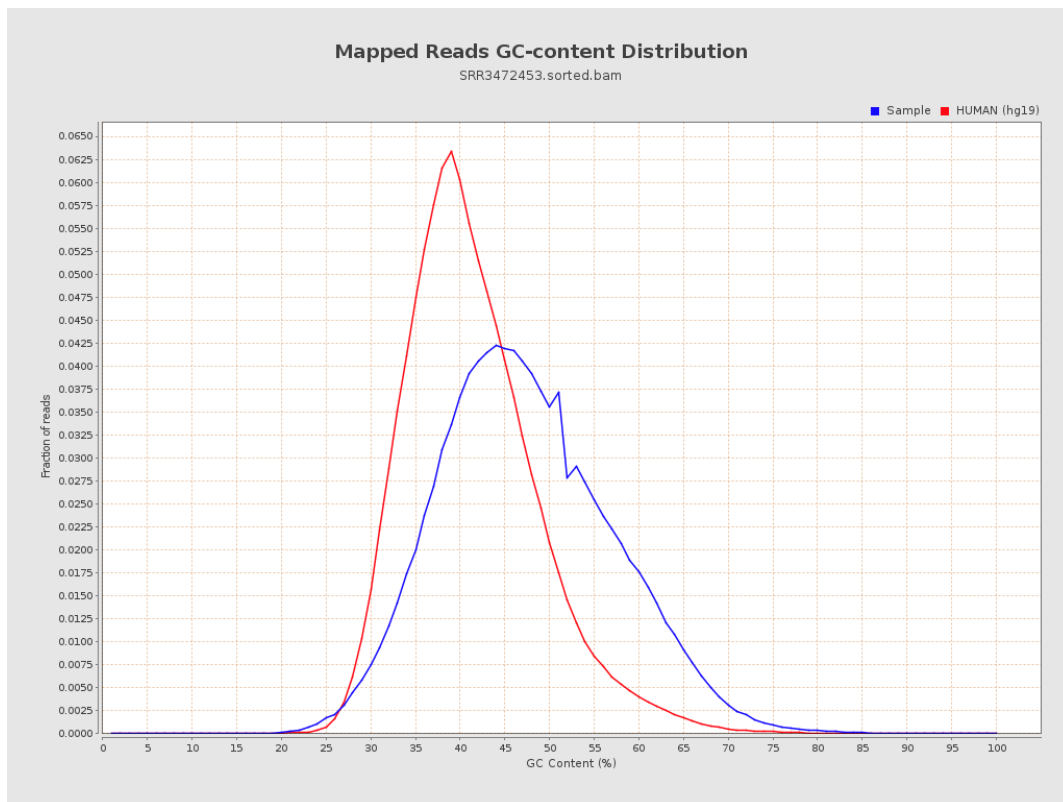
7. Results : Duplication Rate Histogram



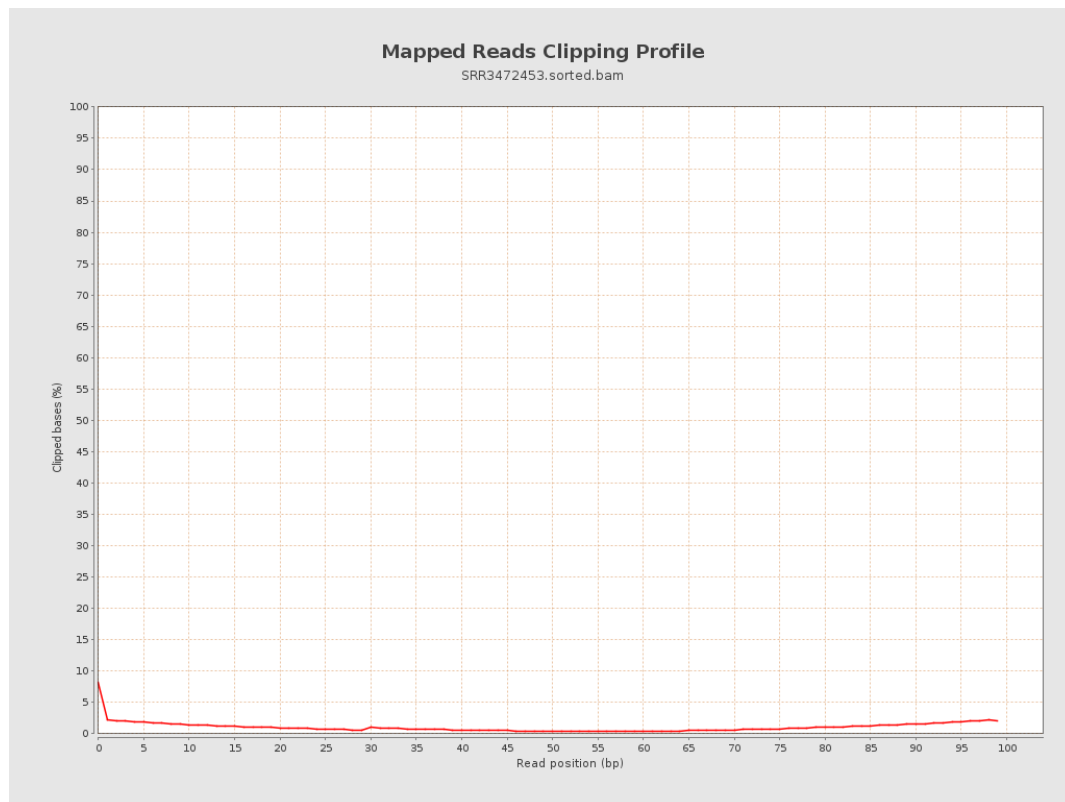
8. Results : Mapped Reads Nucleotide Content



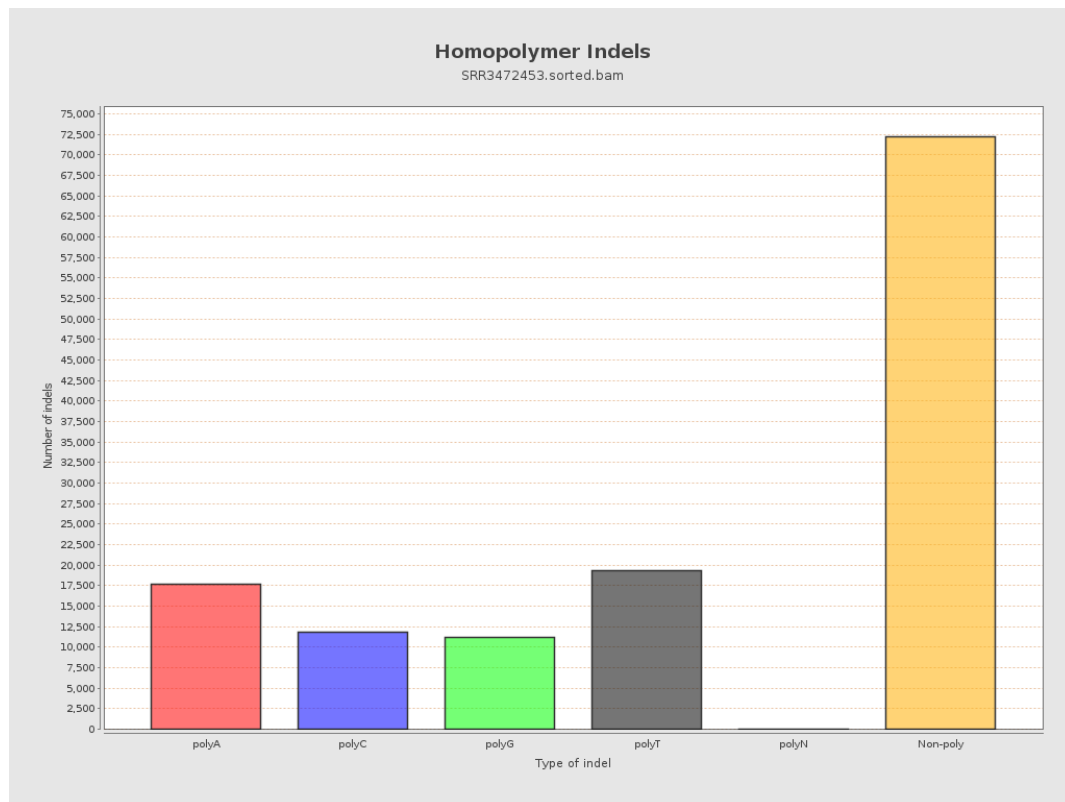
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



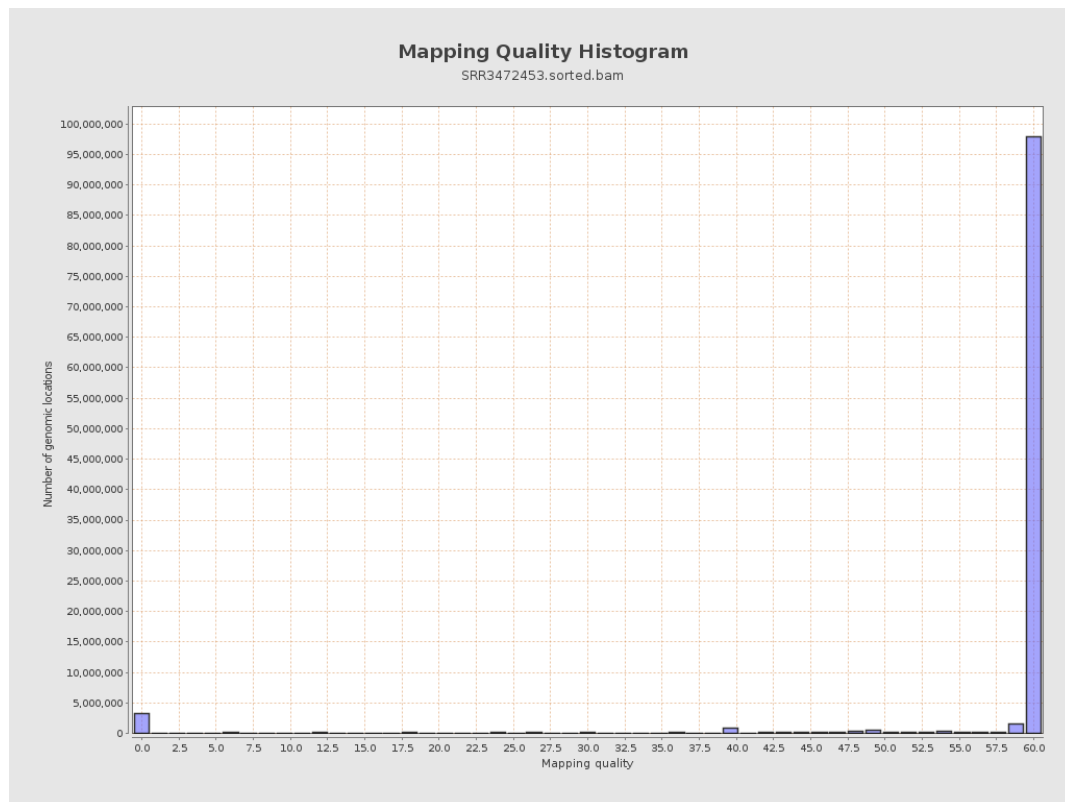
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

