

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 05:27:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472548.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_SRR3472548 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472548_1.fastq.gz SRR3472548_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 05:27:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472548.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,916,194
Mapped reads	9,764,895 / 98.47%
Unmapped reads	151,299 / 1.53%
Mapped paired reads	9,764,895 / 98.47%
Mapped reads, first in pair	4,899,175 / 49.41%
Mapped reads, second in pair	4,865,720 / 49.07%
Mapped reads, both in pair	9,689,310 / 97.71%
Mapped reads, singletons	75,585 / 0.76%
Secondary alignments	0
Supplementary alignments	45,626 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	7,742,498 / 78.08%
Duplication rate	32.79%
Clipped reads	856,373 / 8.64%

2.2. ACGT Content

Number/percentage of A's	279,842,821 / 29.18%
Number/percentage of C's	201,750,851 / 21.03%
Number/percentage of T's	276,700,630 / 28.85%
Number/percentage of G's	200,692,774 / 20.92%
Number/percentage of N's	148,564 / 0.02%

GC Percentage	41.96%
---------------	--------

2.3. Coverage

Mean	0.3099
Standard Deviation	58.764

2.4. Mapping Quality

Mean Mapping Quality	49.95
----------------------	-------

2.5. Insert size

Mean	35,839.19
Standard Deviation	1,831,006.17
P25/Median/P75	170 / 237 / 322

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	5,674,878
Insertions	49,529
Mapped reads with at least one insertion	0.5%
Deletions	56,747
Mapped reads with at least one deletion	0.58%
Homopolymer indels	48.67%

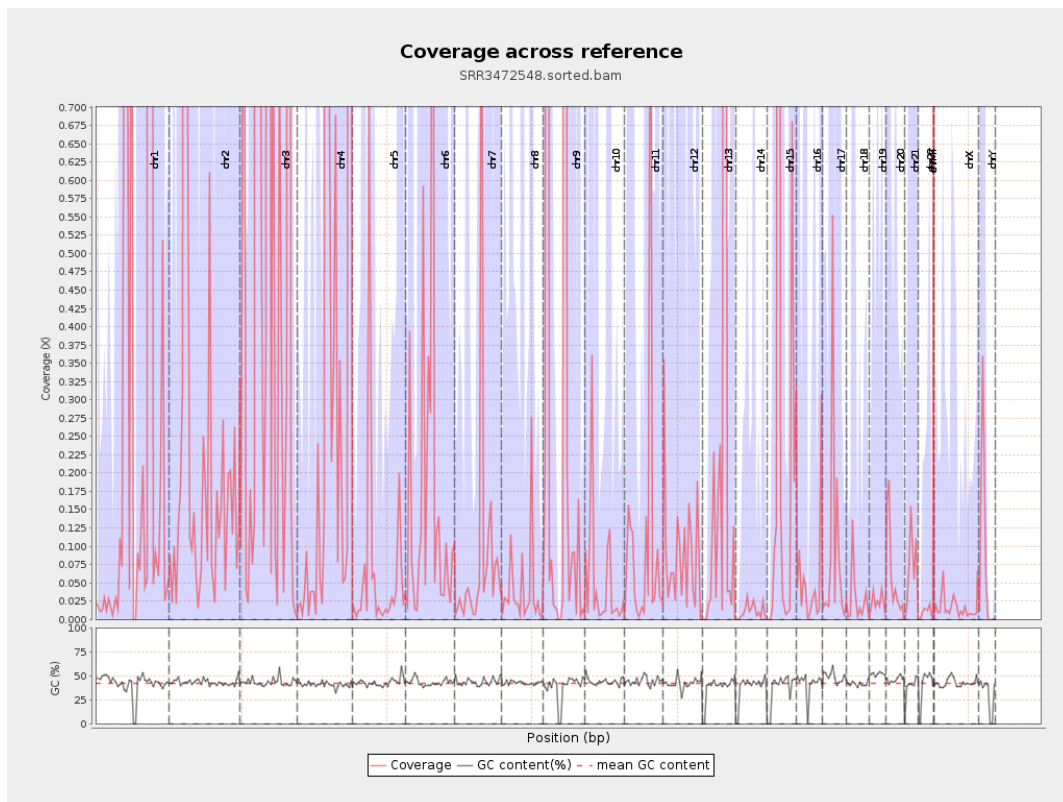
2.7. Chromosome stats

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

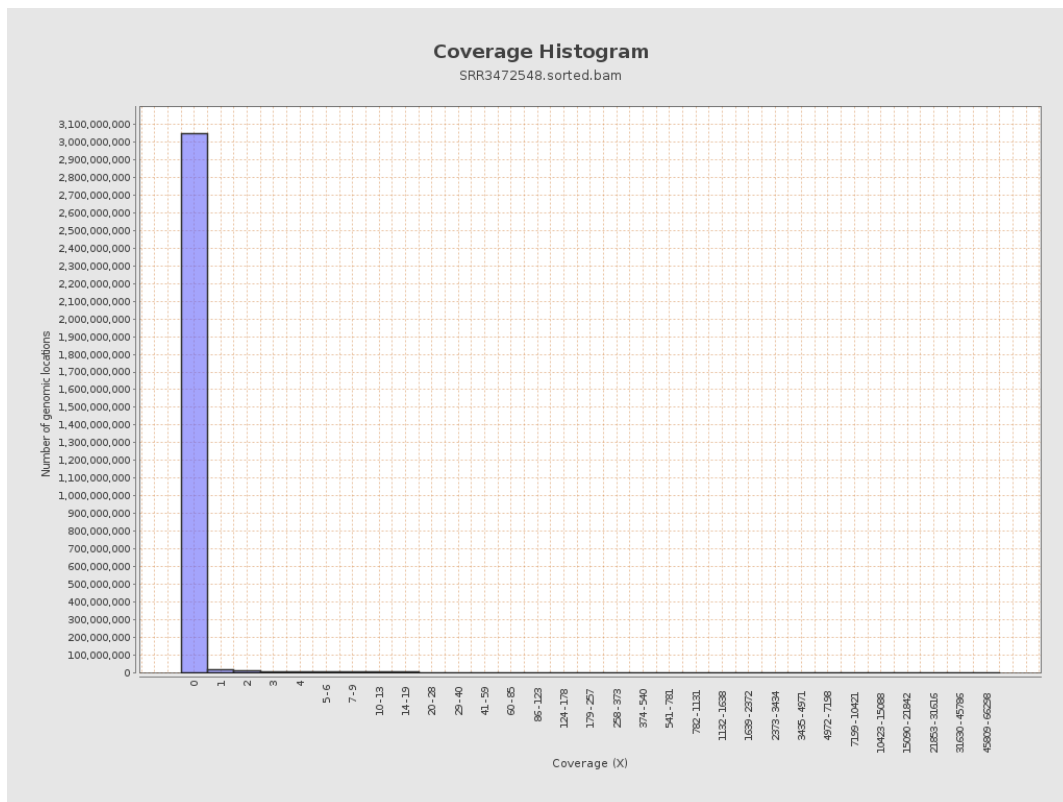
		bases	coverage	deviation
chr1	249250621	148371220	0.5953	107.9281
chr2	243199373	79876711	0.3284	51.9287
chr3	198022430	288697698	1.4579	137.1328
chr4	191154276	100237176	0.5244	50.4726
chr5	180915260	11434654	0.0632	8.7811
chr6	171115067	31367666	0.1833	23.9058
chr7	159138663	14964306	0.094	1.5641
chr8	146364022	5854671	0.04	4.257
chr9	141213431	141877148	1.0047	124.6663
chr10	135534747	7367357	0.0544	1.782
chr11	135006516	15202465	0.1126	10.8922
chr12	133851895	11999351	0.0896	2.76
chr13	115169878	29947160	0.26	48.5202
chr14	107349540	1227877	0.0114	0.4034
chr15	102531392	40121162	0.3913	55.1214
chr16	90354753	5027923	0.0556	1.3885
chr17	81195210	7835271	0.0965	6.2211
chr18	78077248	2255860	0.0289	0.5487
chr19	59128983	1377080	0.0233	0.5118
chr20	63025520	3790766	0.0601	1.7921
chr21	48129895	3113418	0.0647	3.7388
chr22	51304566	488151	0.0095	0.2864
chrMT	16571	24187	1.4596	1.7586
chrX	155270560	2381623	0.0153	0.3315

chrY	59373566	4414013	0.0743	9.7928
------	----------	---------	--------	--------

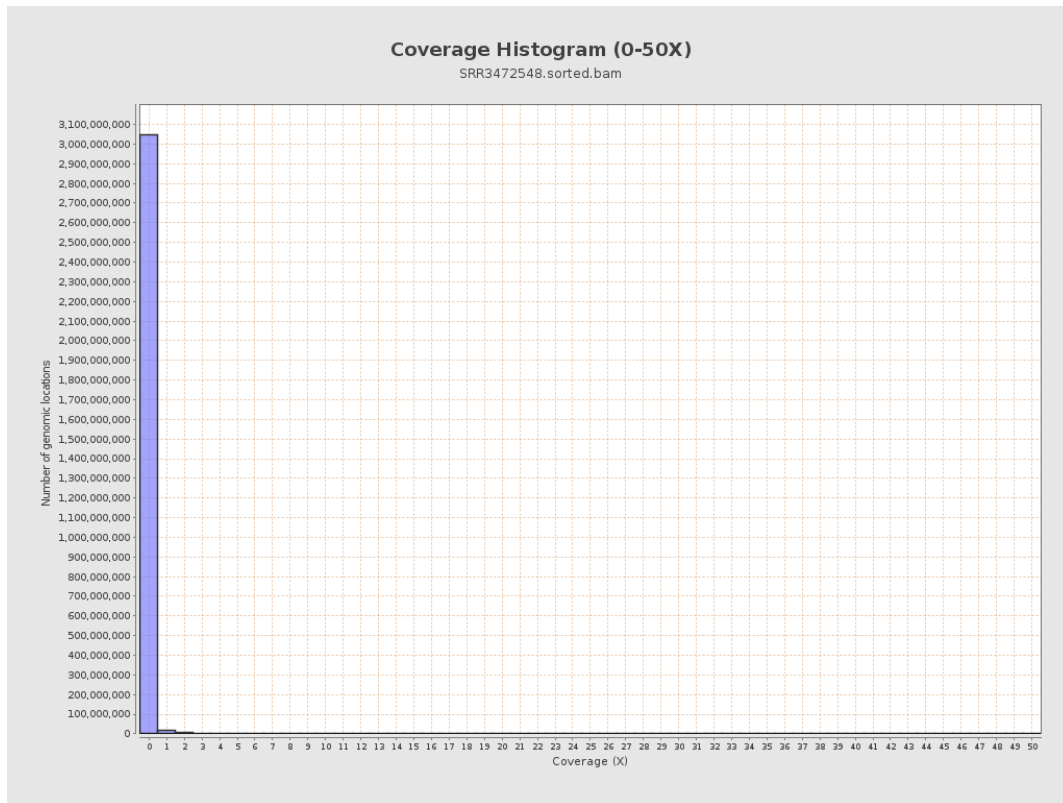
3. Results : Coverage across reference



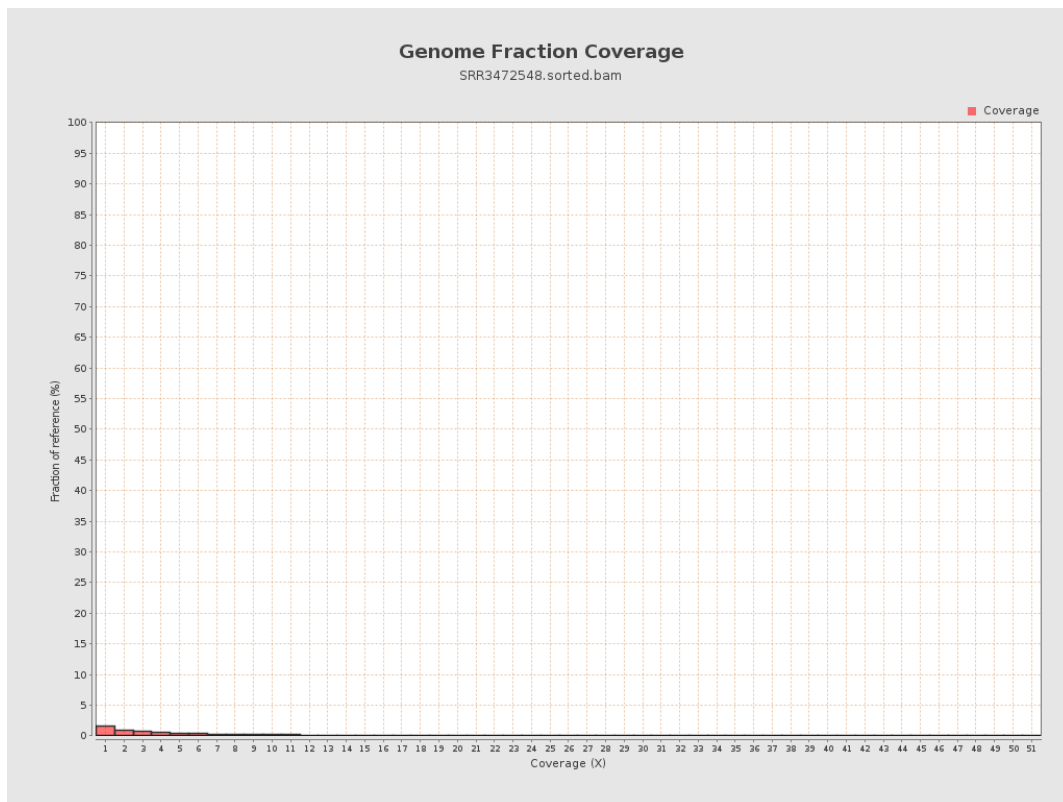
4. Results : Coverage Histogram



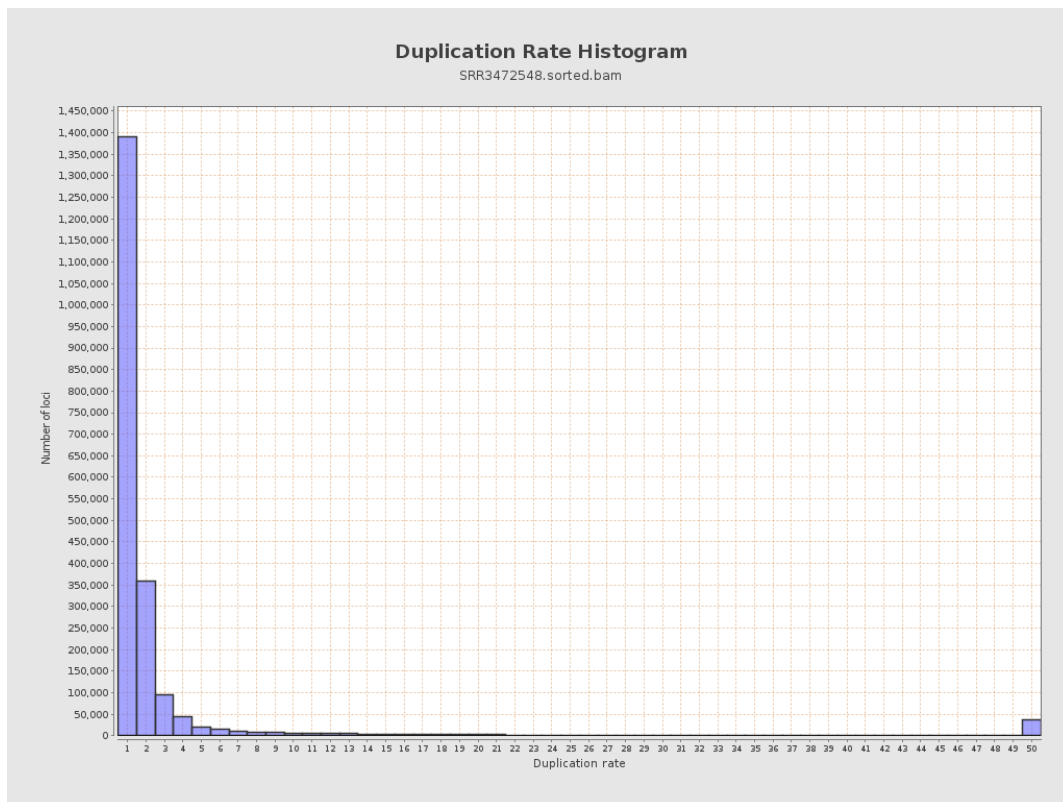
5. Results : Coverage Histogram (0-50X)



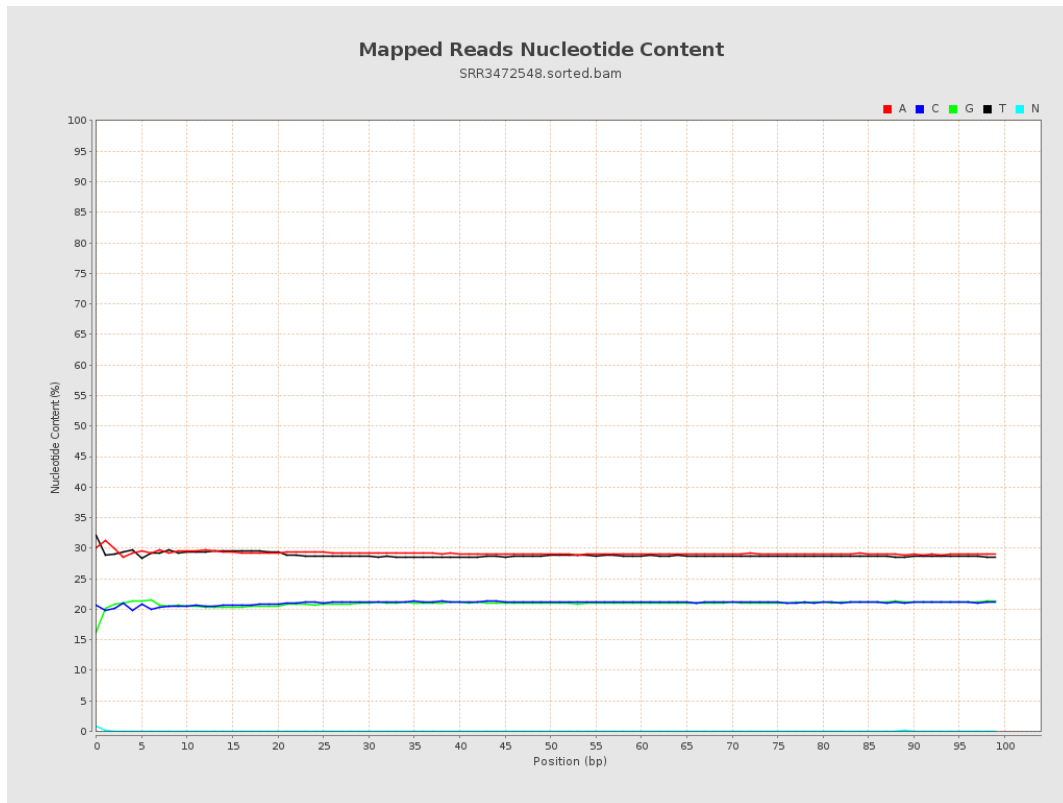
6. Results : Genome Fraction Coverage



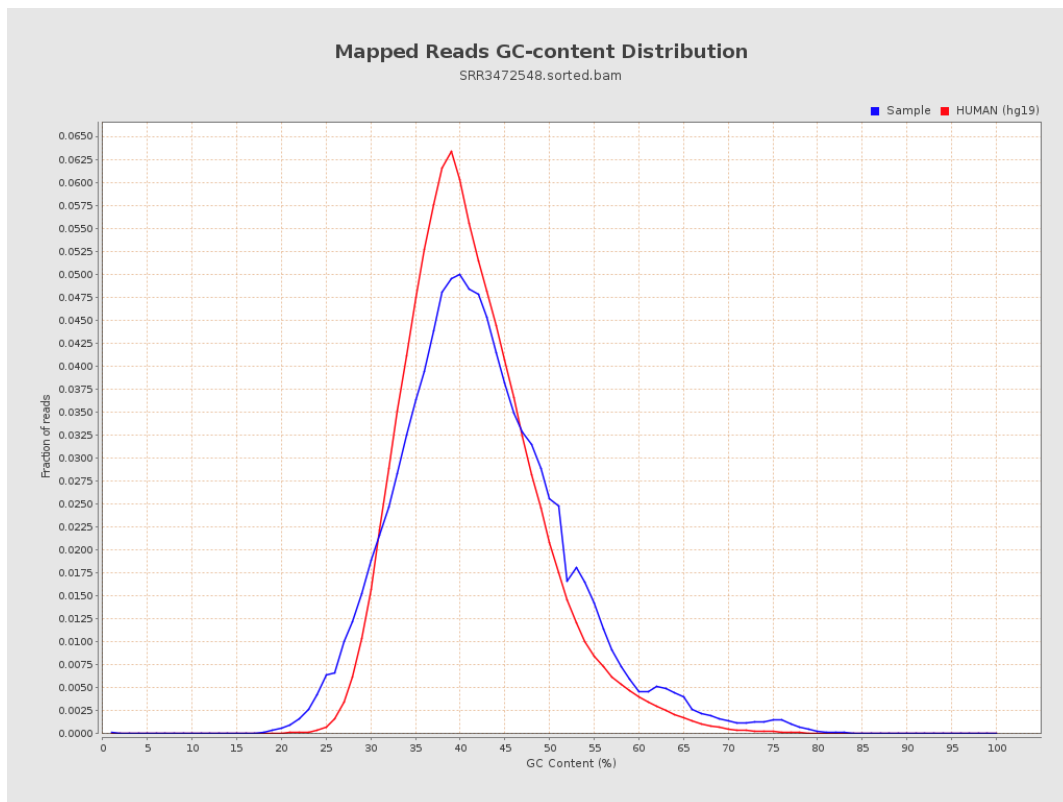
7. Results : Duplication Rate Histogram



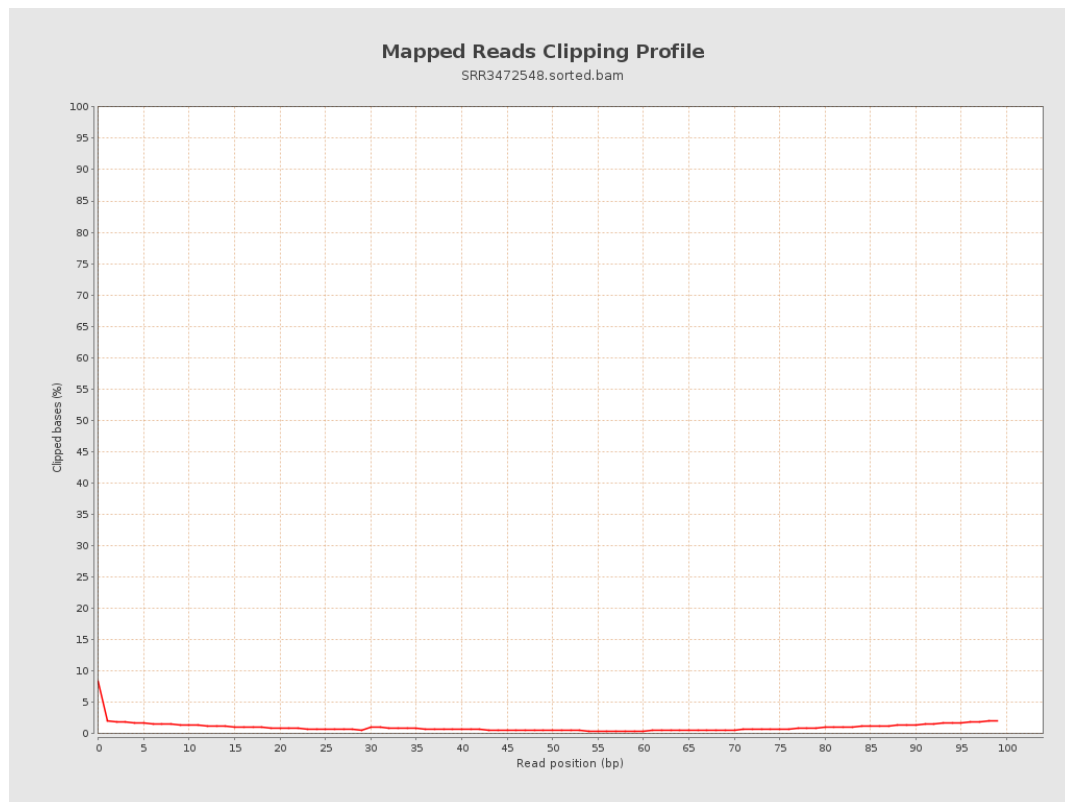
8. Results : Mapped Reads Nucleotide Content



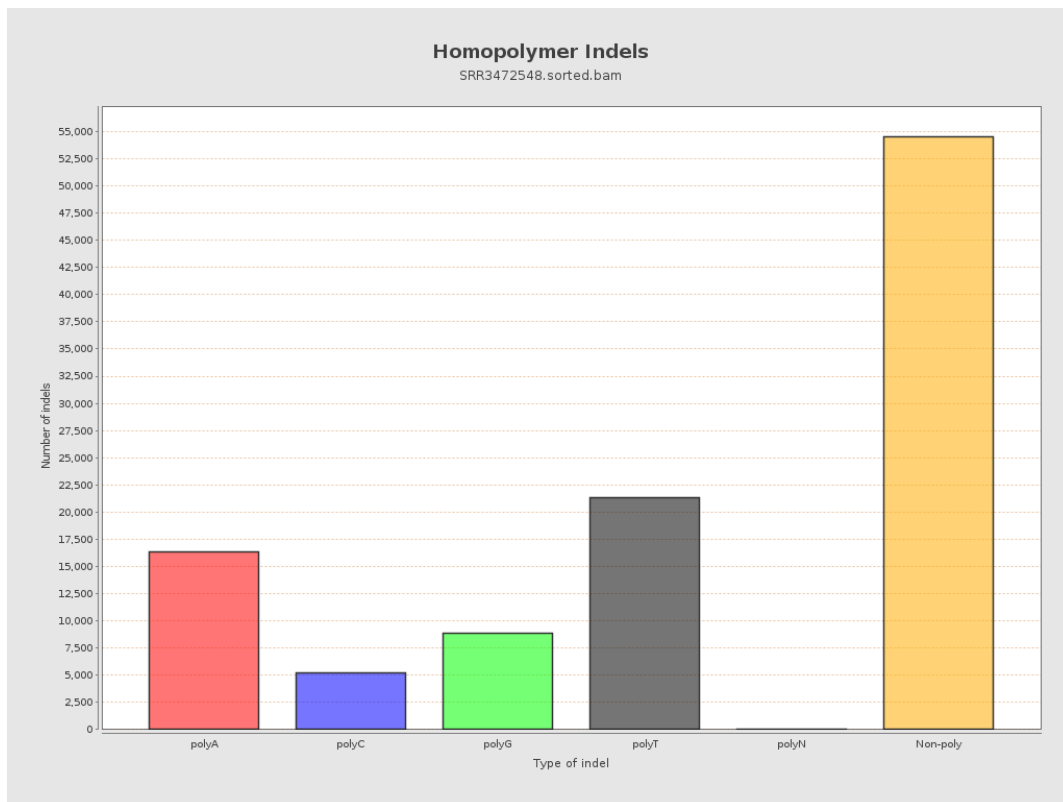
9. Results : Mapped Reads GC-content Distribution



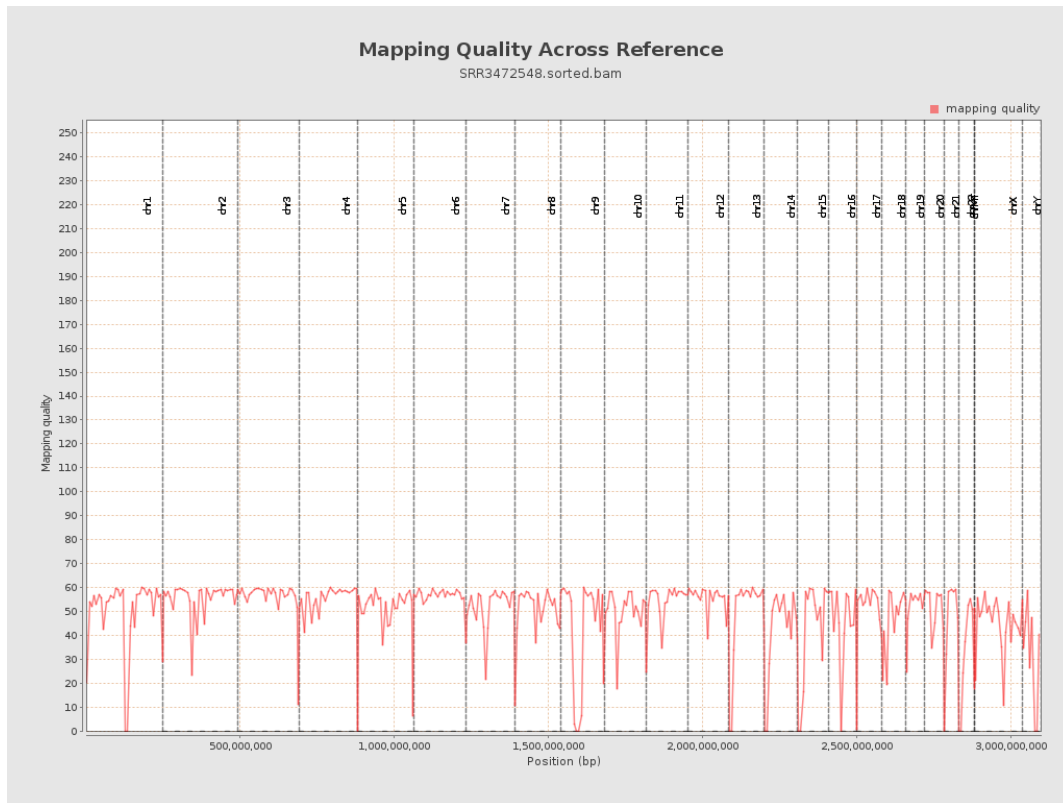
10. Results : Mapped Reads Clipping Profile



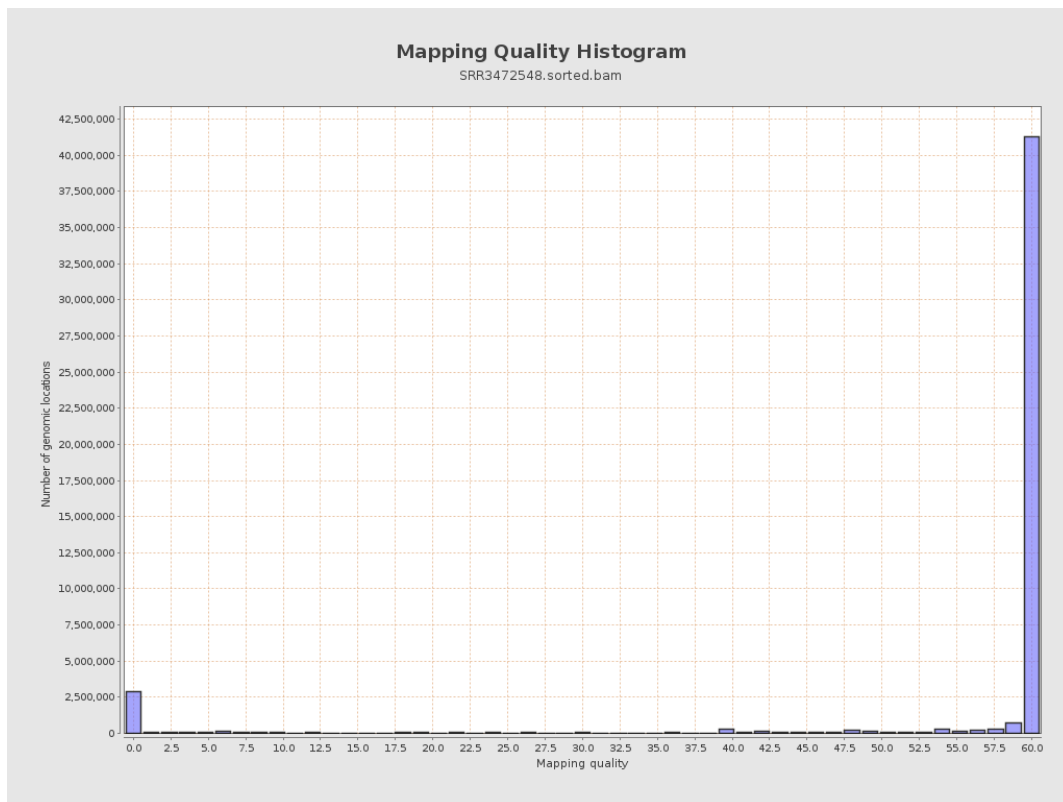
11. Results : Homopolymer Indels



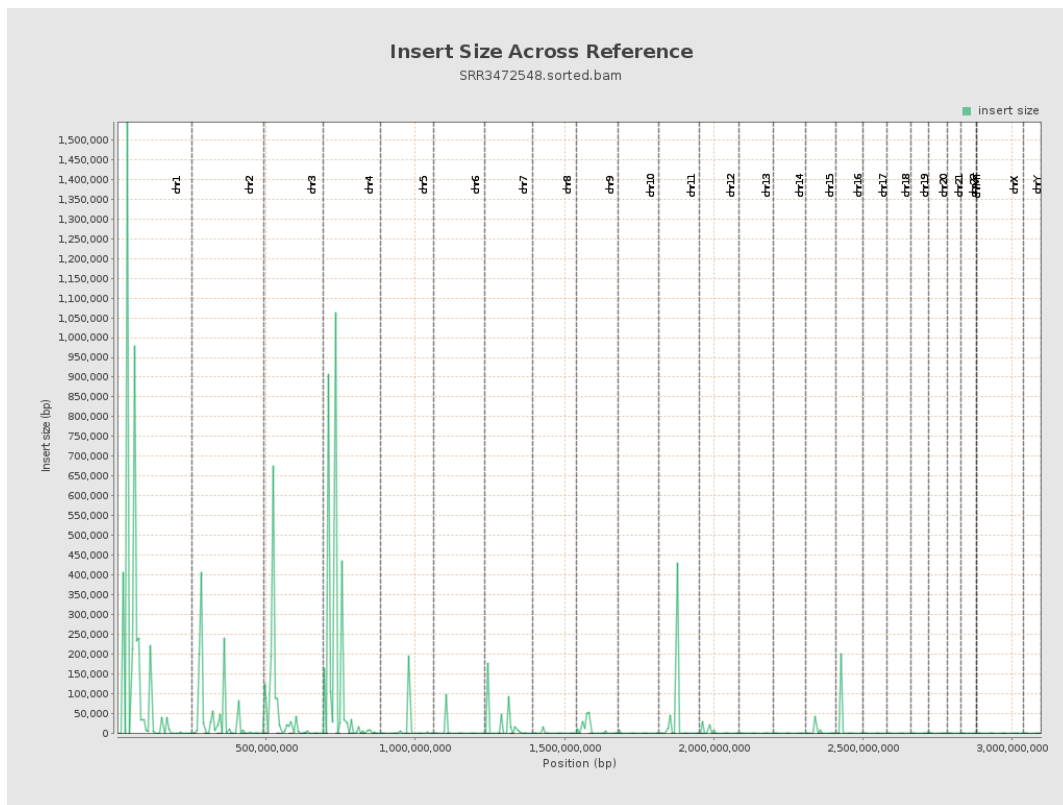
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

