

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 17:15:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618674.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_SRR618674 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618674_1.fastq.gz SRR618674_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 17:15:05 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618674.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	209,825,172
Mapped reads	203,234,848 / 96.86%
Unmapped reads	6,590,324 / 3.14%
Mapped paired reads	203,234,848 / 96.86%
Mapped reads, first in pair	101,585,984 / 48.41%
Mapped reads, second in pair	101,648,864 / 48.44%
Mapped reads, both in pair	200,452,356 / 95.53%
Mapped reads, singletons	2,782,492 / 1.33%
Secondary alignments	0
Supplementary alignments	514,340 / 0.25%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	29,309,868 / 13.97%
Duplication rate	10.47%
Clipped reads	29,235,885 / 13.93%

2.2. ACGT Content

Number/percentage of A's	5,750,638,249 / 29.25%
Number/percentage of C's	4,105,119,858 / 20.88%
Number/percentage of T's	5,723,286,737 / 29.11%
Number/percentage of G's	4,081,608,931 / 20.76%
Number/percentage of N's	1,154,992 / 0.01%

GC Percentage	41.64%
---------------	--------

2.3. Coverage

Mean	6.3531
Standard Deviation	60.3815

2.4. Mapping Quality

Mean Mapping Quality	53.6
----------------------	------

2.5. Insert size

Mean	38,030.29
Standard Deviation	1,872,417.09
P25/Median/P75	212 / 239 / 276

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	213,292,748
Insertions	2,237,627
Mapped reads with at least one insertion	1.07%
Deletions	2,465,448
Mapped reads with at least one deletion	1.18%
Homopolymer indels	41.11%

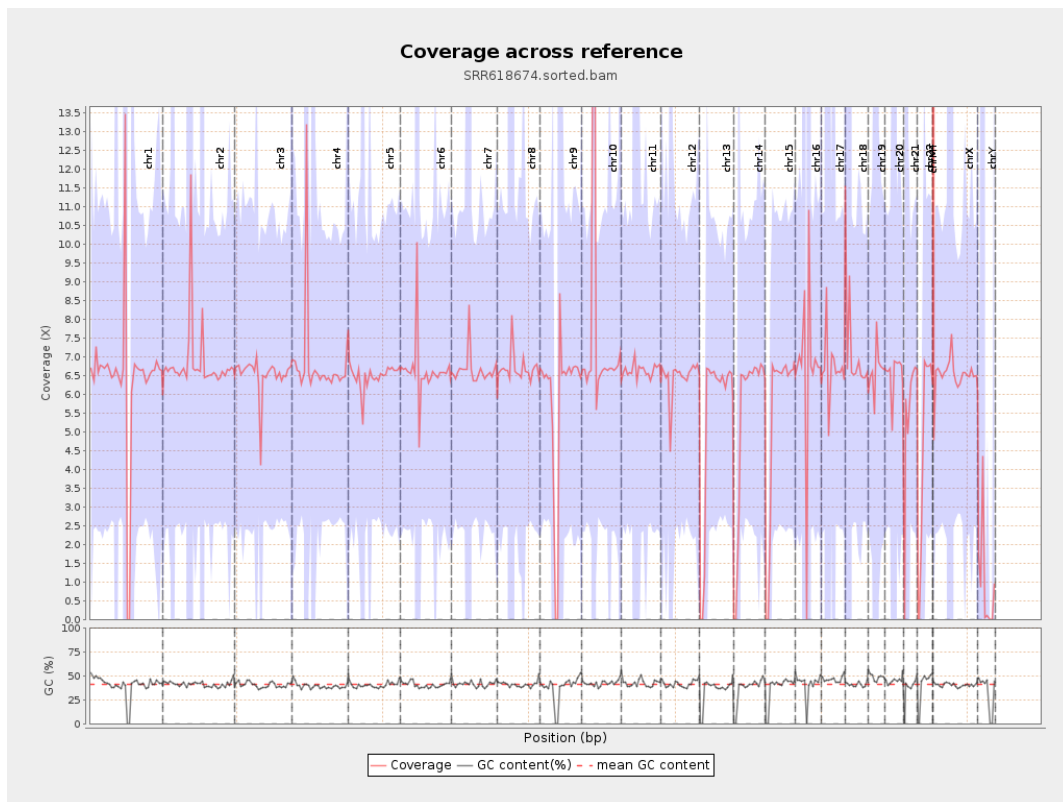
2.7. Chromosome stats

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

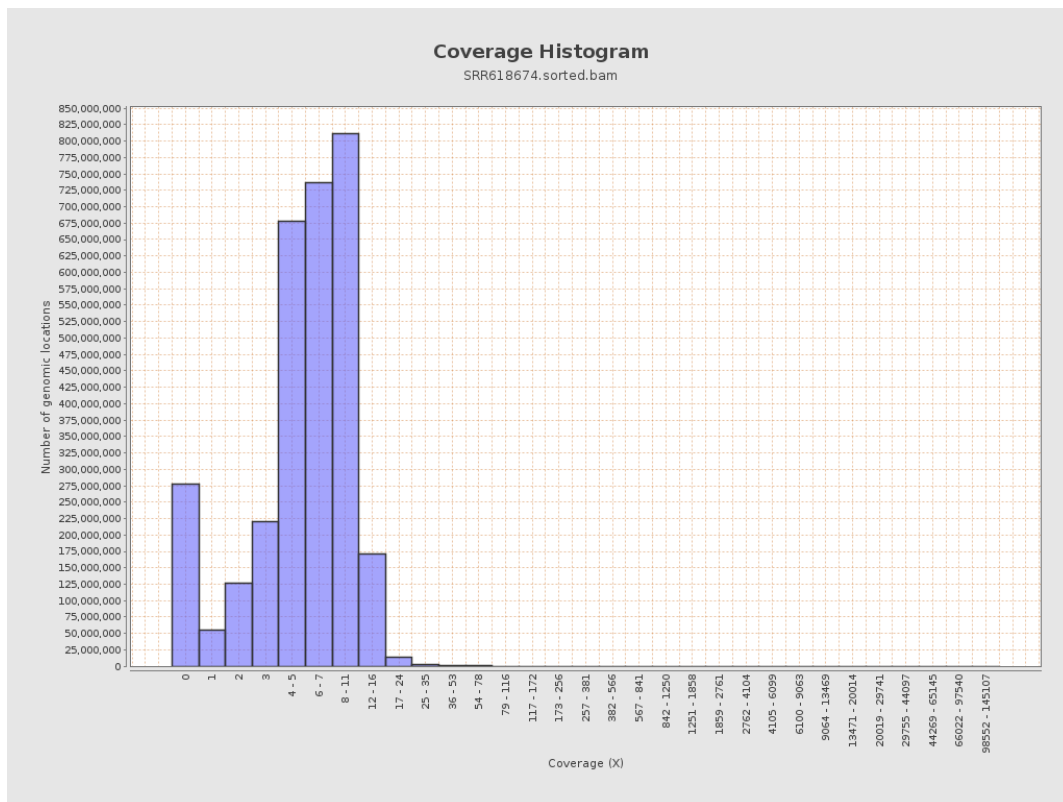
		bases	coverage	deviation
chr1	249250621	1598701157	6.414	151.2445
chr2	243199373	1662720563	6.8369	35.3659
chr3	198022430	1291821796	6.5236	4.4473
chr4	191154276	1302843689	6.8157	51.3624
chr5	180915260	1174162432	6.4901	5.1097
chr6	171115067	1133829237	6.6261	40.3208
chr7	159138663	1059719735	6.6591	45.3948
chr8	146364022	977977671	6.6818	37.2757
chr9	141213431	832030441	5.892	60.8596
chr10	135534747	1013399340	7.477	124.4437
chr11	135006516	895202083	6.6308	27.9273
chr12	133851895	866389535	6.4727	5.3891
chr13	115169878	624415696	5.4217	4.0528
chr14	107349540	589113959	5.4878	5.4252
chr15	102531392	553275751	5.3962	4.0816
chr16	90354753	606211310	6.7092	37.5683
chr17	81195210	546310181	6.7284	30.5744
chr18	78077248	550743994	7.0538	87.8668
chr19	59128983	393312182	6.6518	62.3705
chr20	63025520	411149811	6.5235	15.6029
chr21	48129895	268757796	5.584	18.4267
chr22	51304566	239844166	4.6749	4.8875
chrMT	16571	5839833	352.4128	41.9478
chrX	155270560	1011980438	6.5175	16.2903

chrY	59373566	57630375	0.9706	42.1715
------	----------	----------	--------	---------

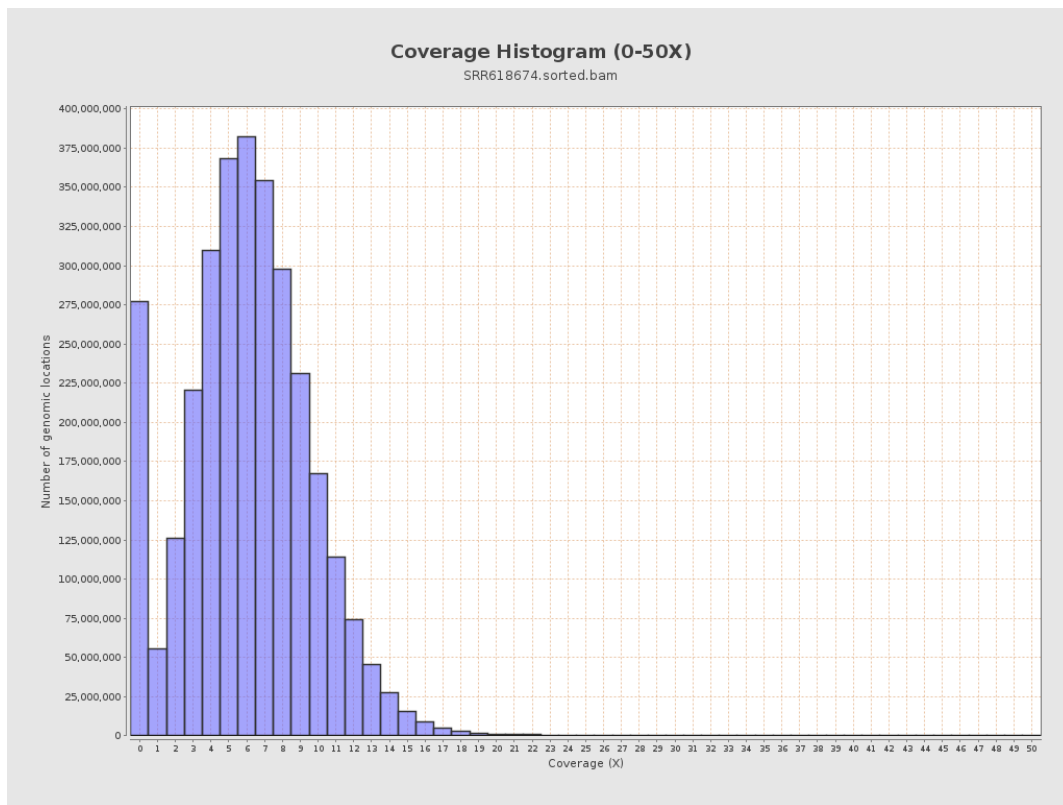
3. Results : Coverage across reference



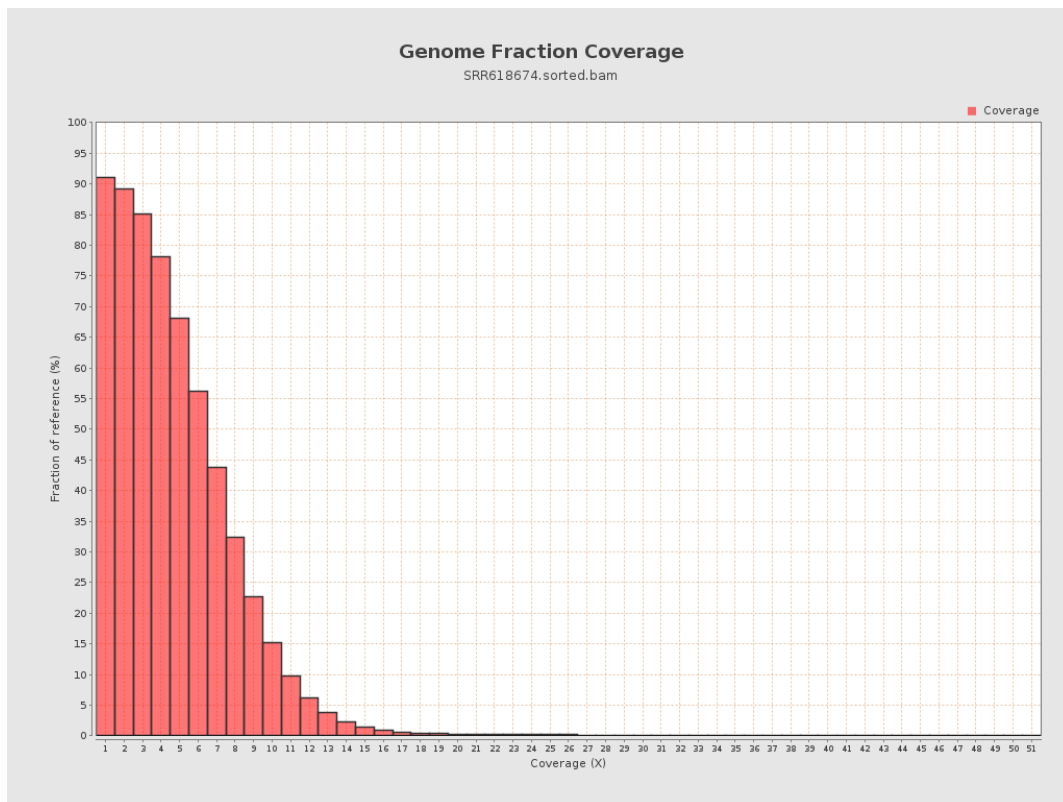
4. Results : Coverage Histogram



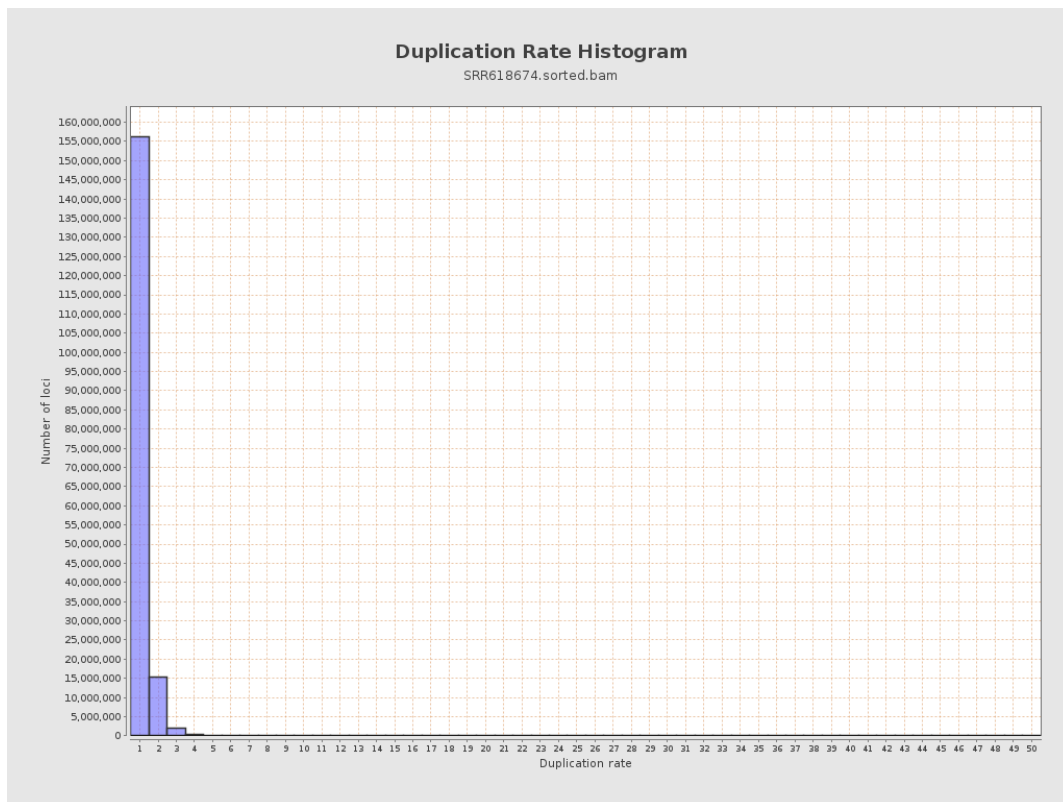
5. Results : Coverage Histogram (0-50X)



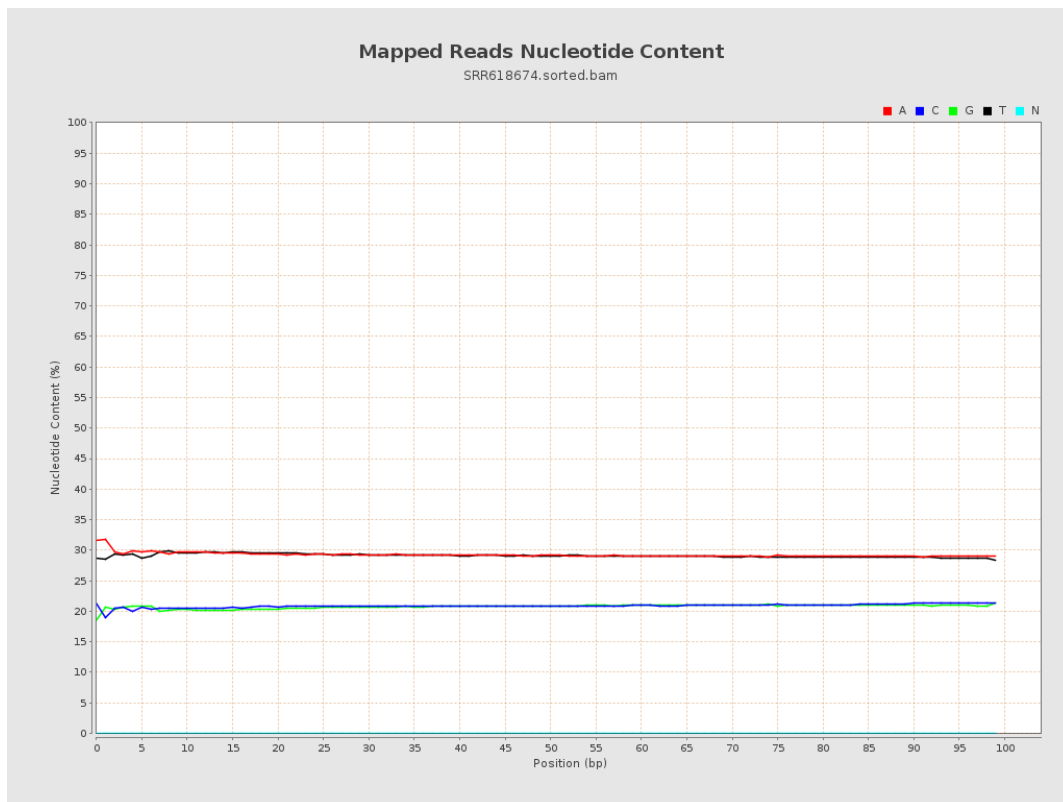
6. Results : Genome Fraction Coverage



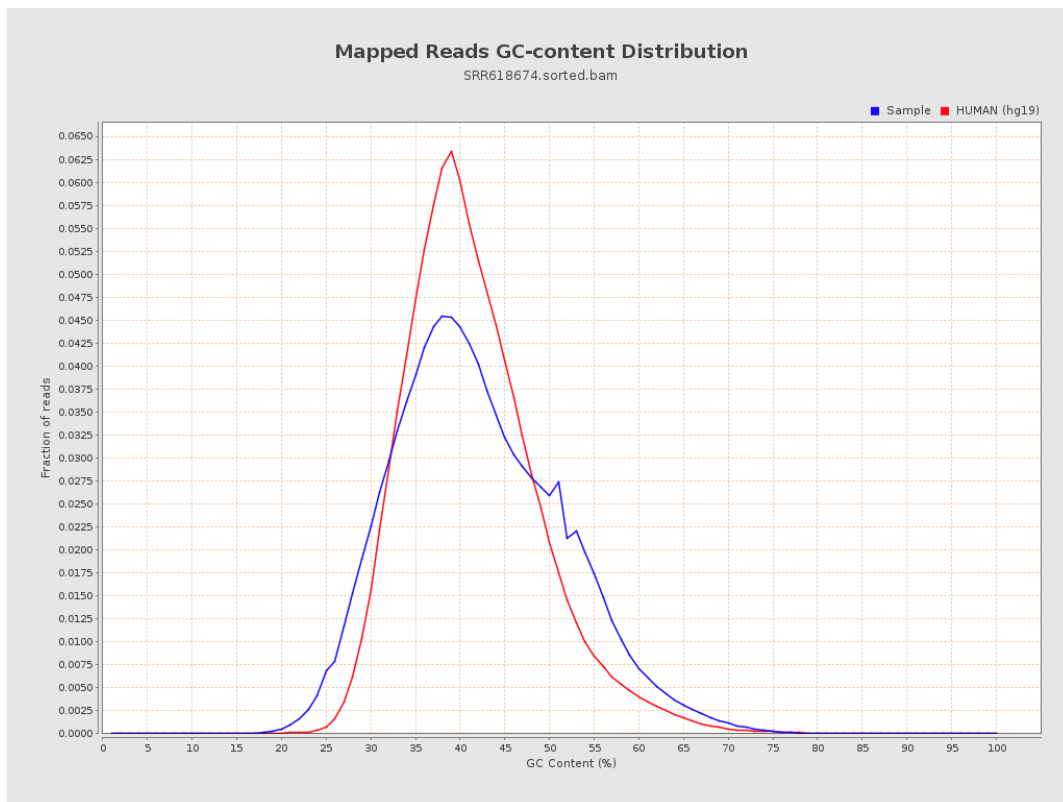
7. Results : Duplication Rate Histogram



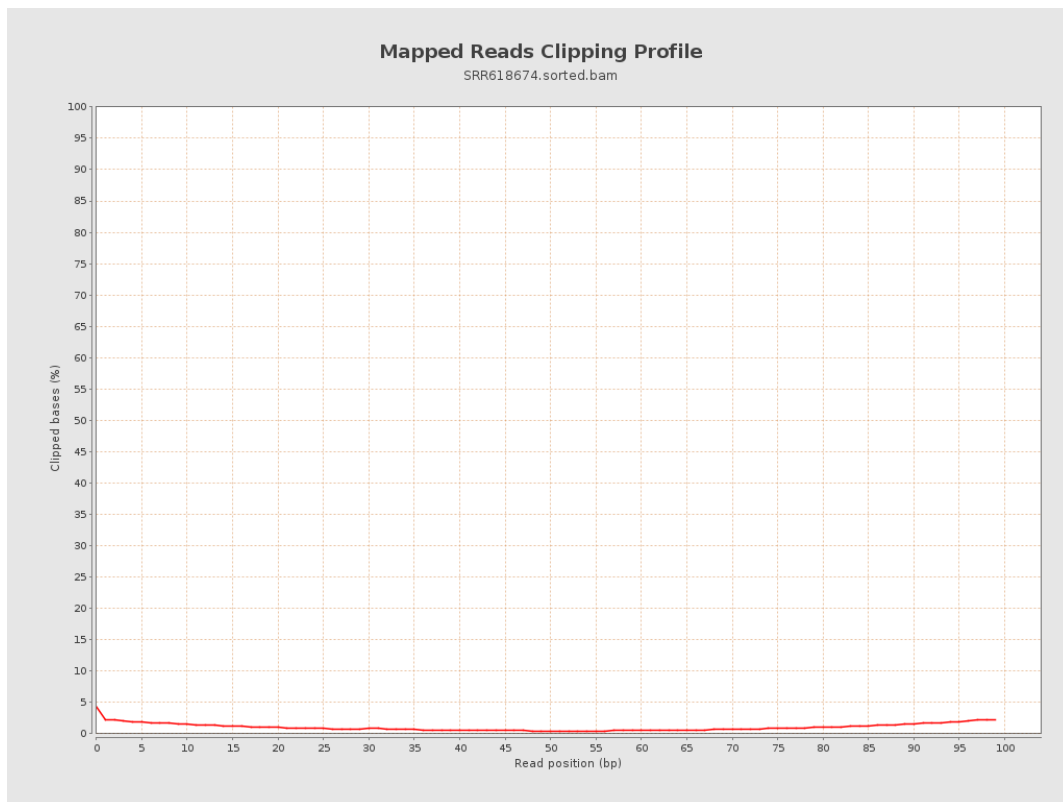
8. Results : Mapped Reads Nucleotide Content



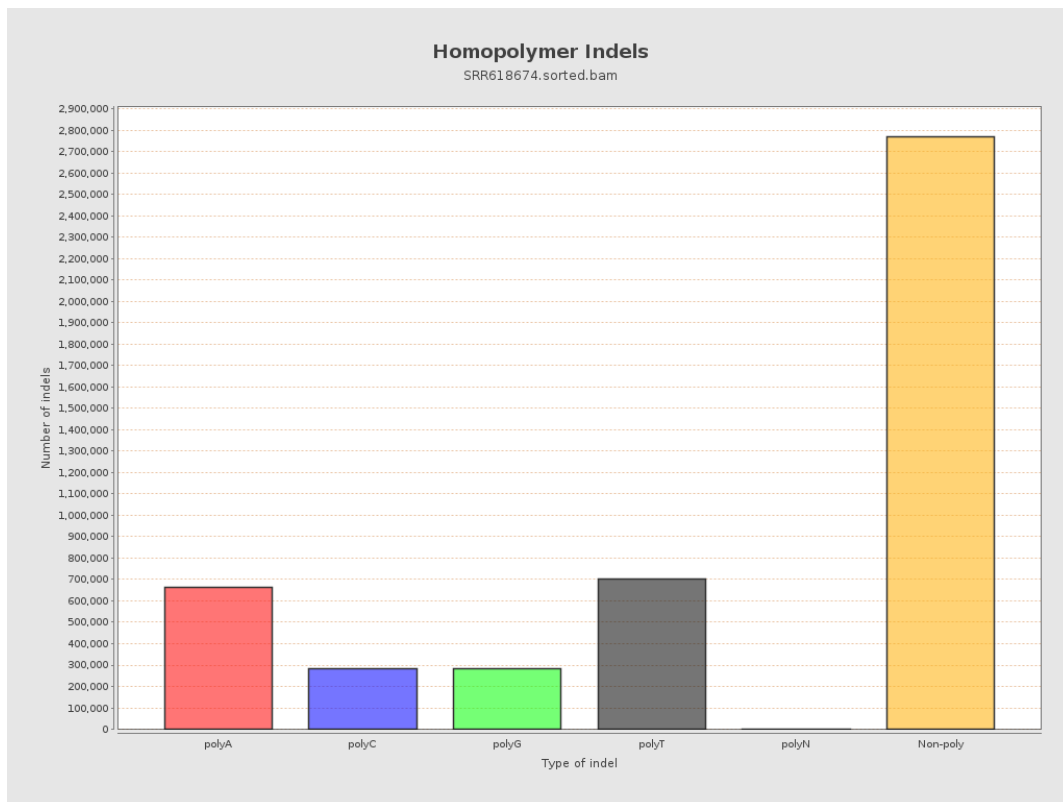
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



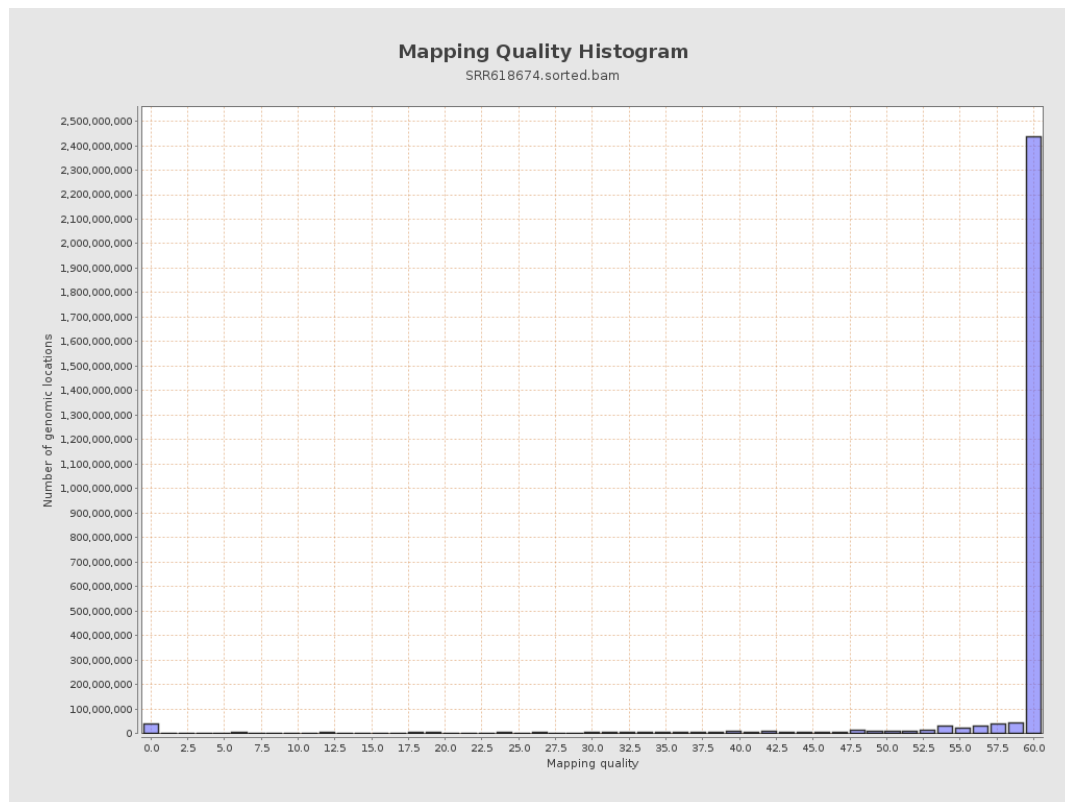
11. Results : Homopolymer Indels



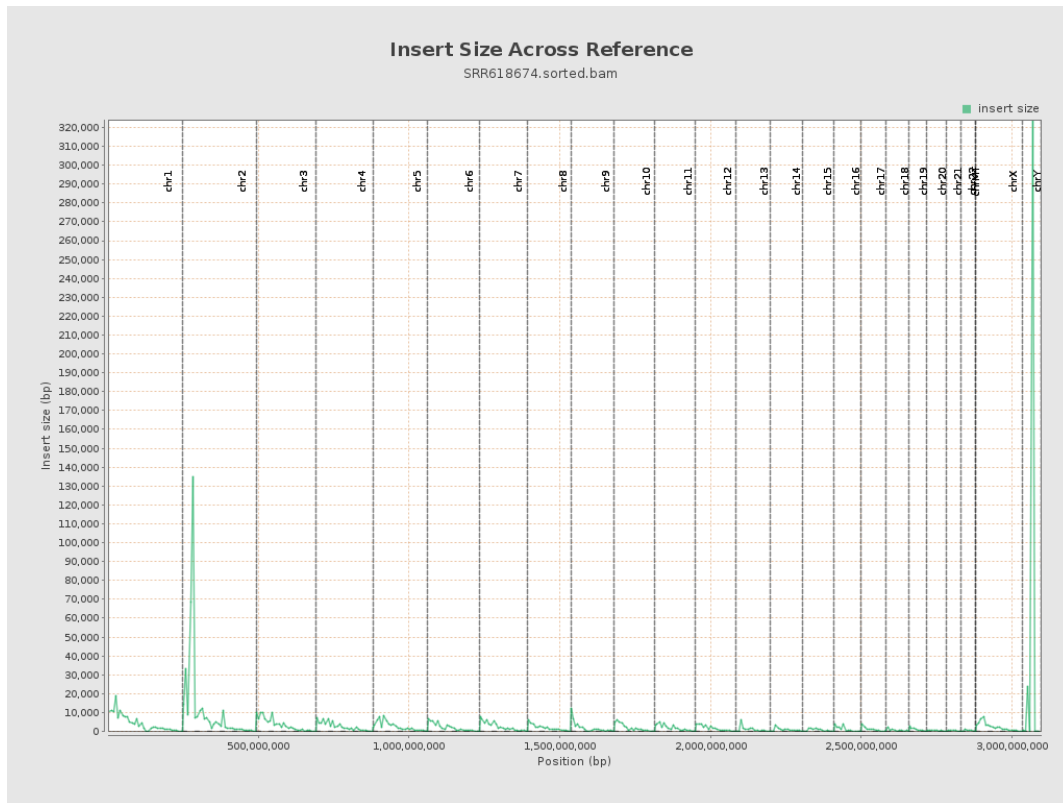
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

