

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:07:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472432.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_SRR3472432 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472432_1.fastq.gz SRR3472432_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:07:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472432.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,751,470
Mapped reads	18,572,091 / 99.04%
Unmapped reads	179,379 / 0.96%
Mapped paired reads	18,572,091 / 99.04%
Mapped reads, first in pair	9,309,457 / 49.65%
Mapped reads, second in pair	9,262,634 / 49.4%
Mapped reads, both in pair	18,476,090 / 98.53%
Mapped reads, singletons	96,001 / 0.51%
Secondary alignments	0
Supplementary alignments	66,463 / 0.35%
Read min/max/mean length	30 / 100 / 99.37
Duplicated reads (estimated)	11,947,316 / 63.71%
Duplication rate	48.32%
Clipped reads	1,432,684 / 7.64%

2.2. ACGT Content

Number/percentage of A's	492,766,660 / 27.09%
Number/percentage of C's	418,452,150 / 23.01%
Number/percentage of T's	492,662,447 / 27.09%
Number/percentage of G's	414,593,029 / 22.8%
Number/percentage of N's	236,159 / 0.01%

GC Percentage	45.8%
---------------	-------

2.3. Coverage

Mean	0.5876
Standard Deviation	18.9596

2.4. Mapping Quality

Mean Mapping Quality	54.61
----------------------	-------

2.5. Insert size

Mean	19,194.11
Standard Deviation	1,387,539.61
P25/Median/P75	148 / 206 / 278

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	10,104,765
Insertions	107,539
Mapped reads with at least one insertion	0.57%
Deletions	89,634
Mapped reads with at least one deletion	0.48%
Homopolymer indels	46.6%

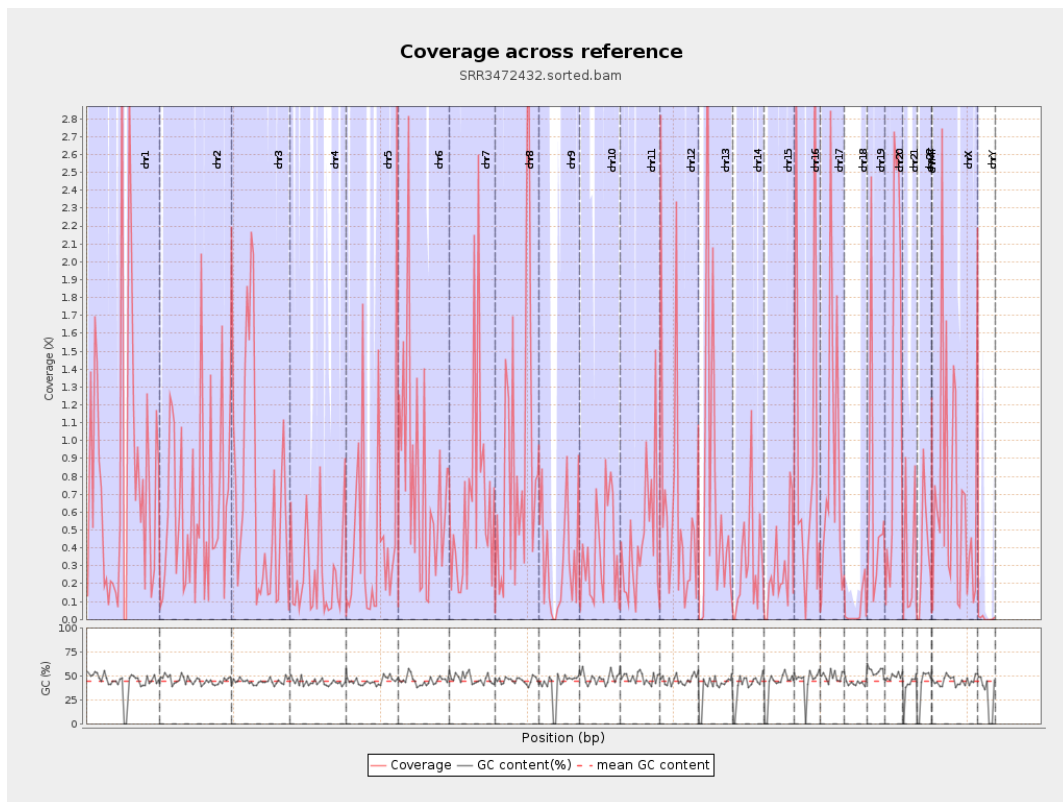
2.7. Chromosome stats

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

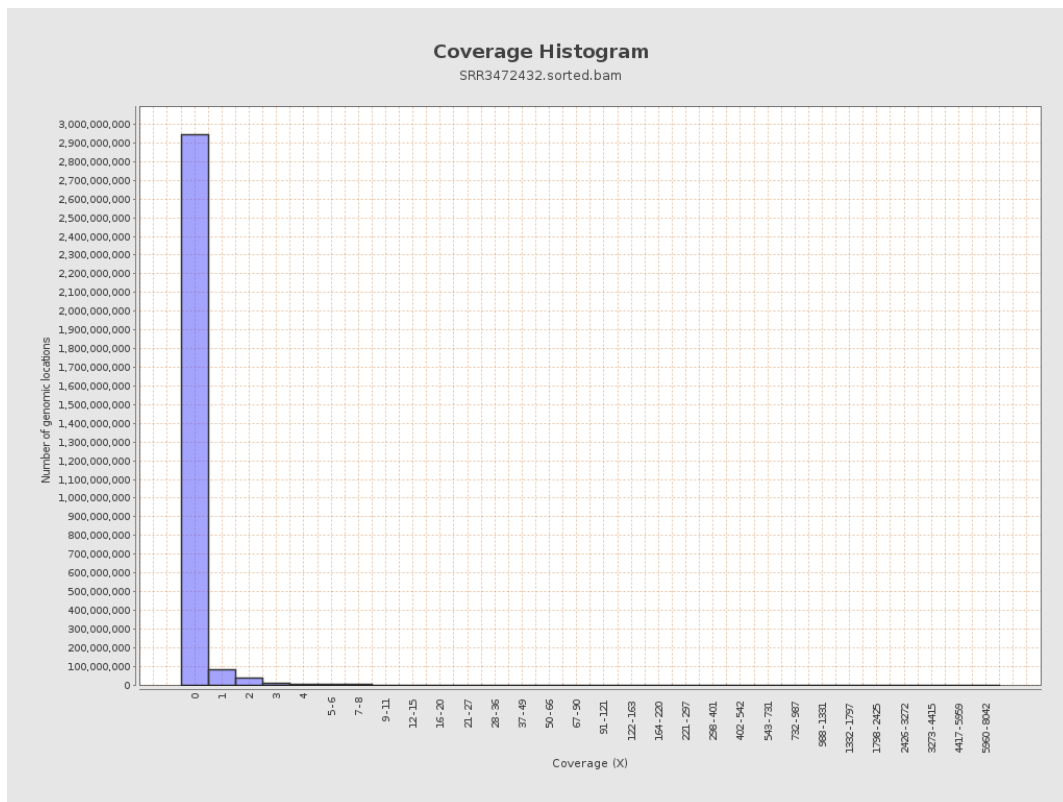
		bases	coverage	deviation
chr1	249250621	199603743	0.8008	24.2734
chr2	243199373	151827441	0.6243	18.4405
chr3	198022430	142305580	0.7186	17.3055
chr4	191154276	47910676	0.2506	8.7095
chr5	180915260	94627193	0.523	26.0512
chr6	171115067	130757760	0.7642	18.3004
chr7	159138663	107876364	0.6779	21.965
chr8	146364022	135261002	0.9241	22.7101
chr9	141213431	46600644	0.33	9.4593
chr10	135534747	50412576	0.372	16.6566
chr11	135006516	59663195	0.4419	14.2975
chr12	133851895	87025536	0.6502	17.5626
chr13	115169878	81617254	0.7087	27.3015
chr14	107349540	32301871	0.3009	8.9492
chr15	102531392	28328833	0.2763	8.5694
chr16	90354753	83675029	0.9261	25.0417
chr17	81195210	70596391	0.8695	20.8006
chr18	78077248	3880539	0.0497	2.897
chr19	59128983	38638908	0.6535	12.4533
chr20	63025520	85967815	1.364	31.641
chr21	48129895	16198723	0.3366	16.4615
chr22	51304566	19261484	0.3754	11.2296
chrMT	16571	20594	1.2428	1.5262
chrX	155270560	104155225	0.6708	21.4644

chrY	59373566	413189	0.007	0.6419
------	----------	--------	-------	--------

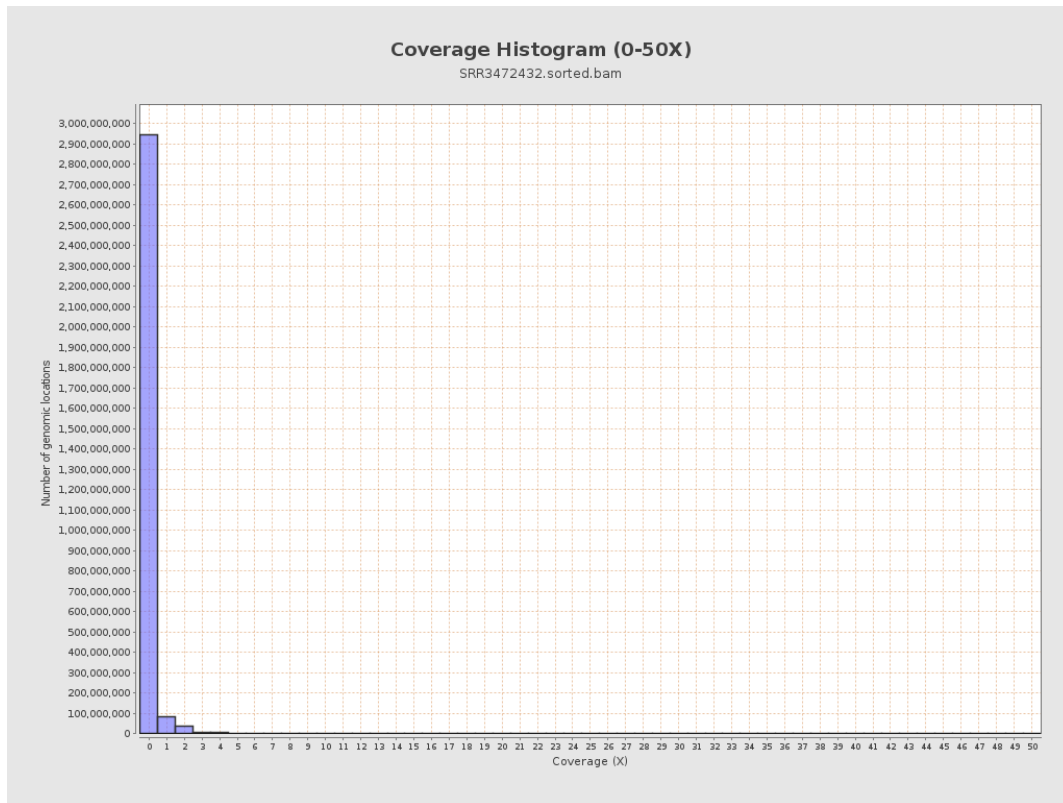
3. Results : Coverage across reference



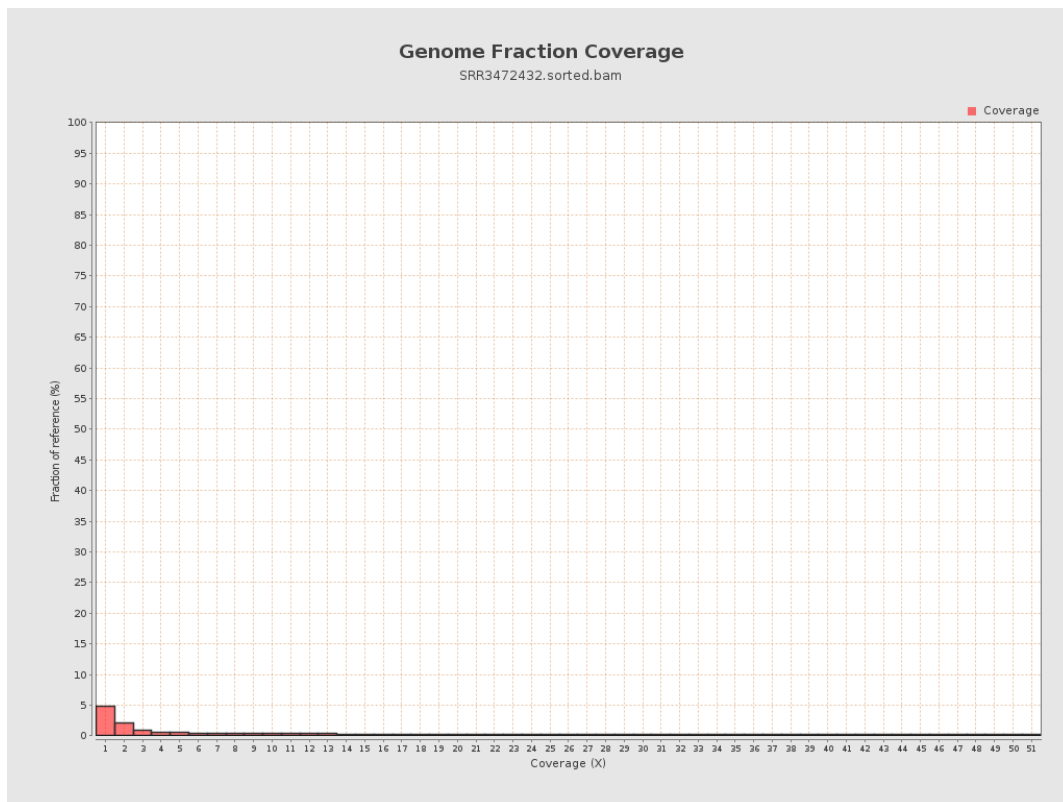
4. Results : Coverage Histogram



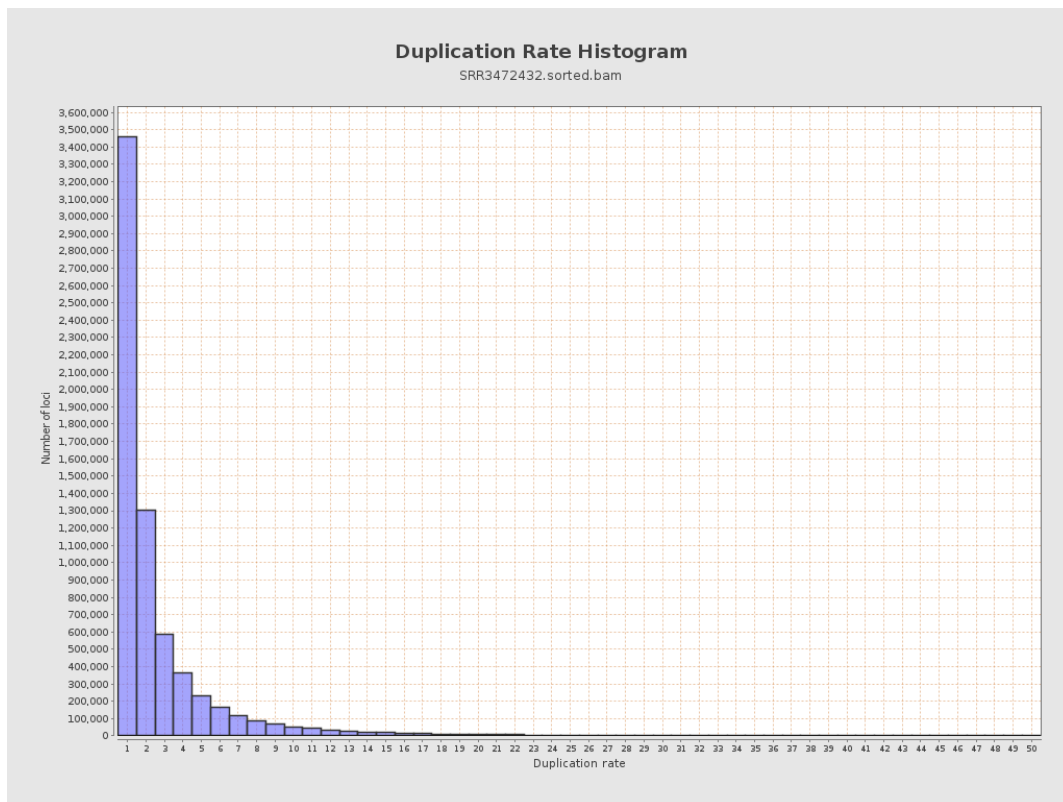
5. Results : Coverage Histogram (0-50X)



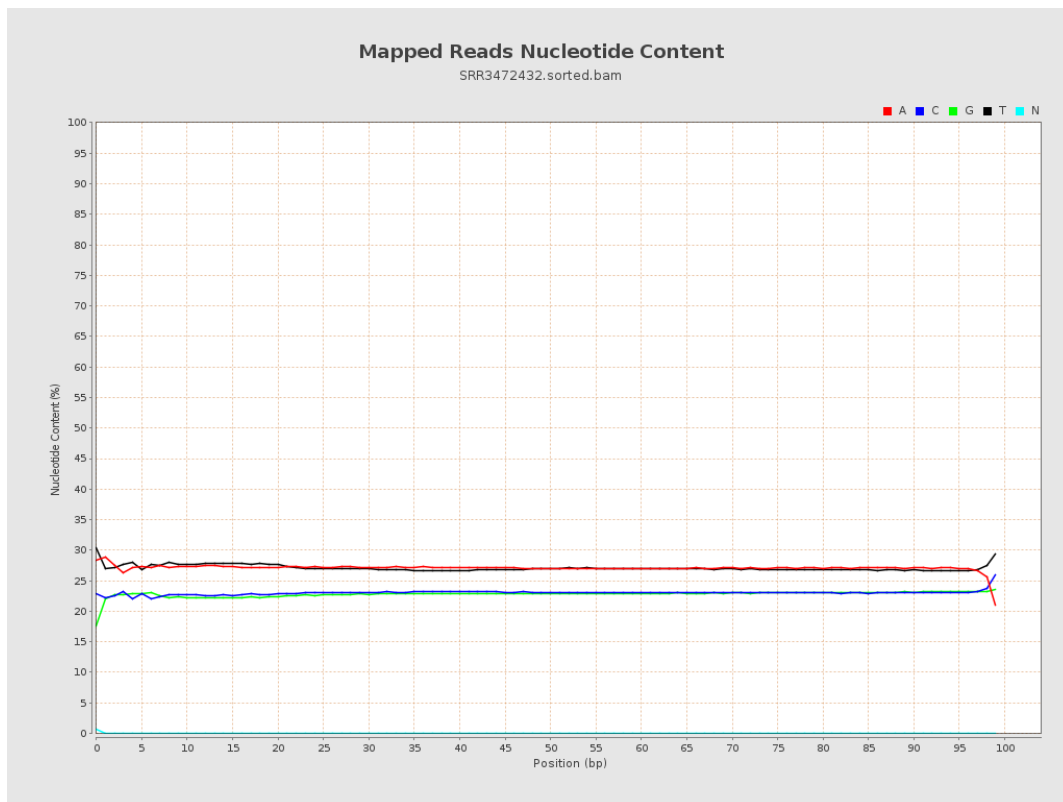
6. Results : Genome Fraction Coverage



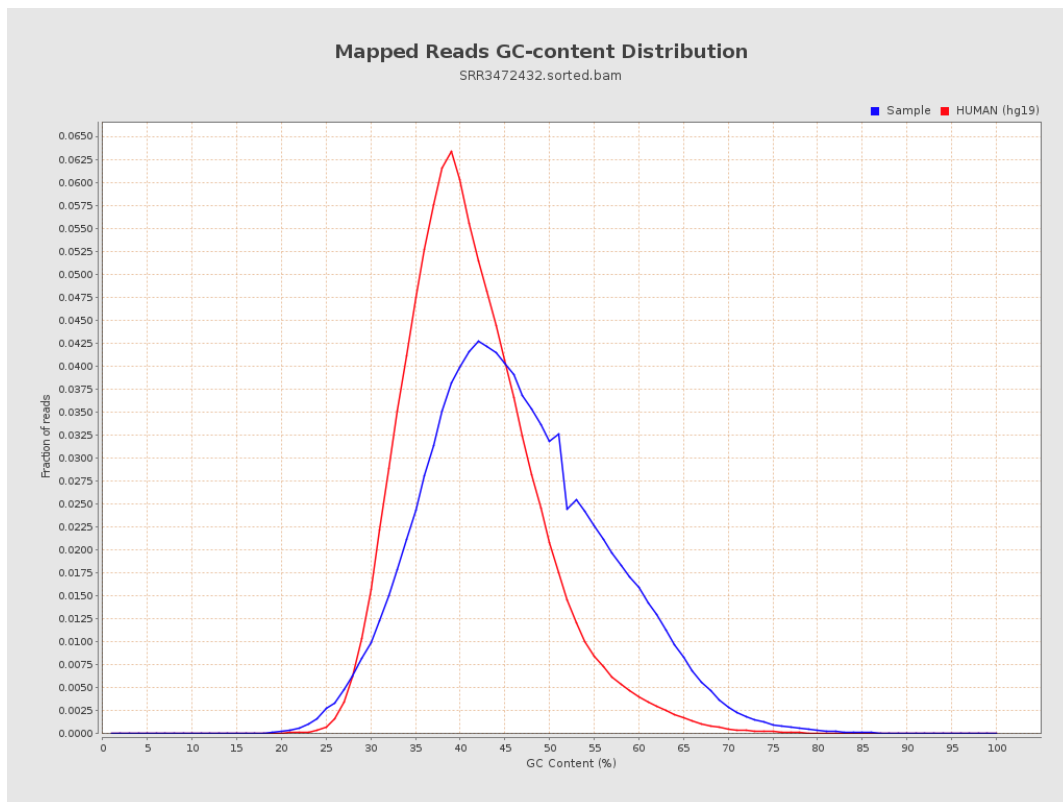
7. Results : Duplication Rate Histogram



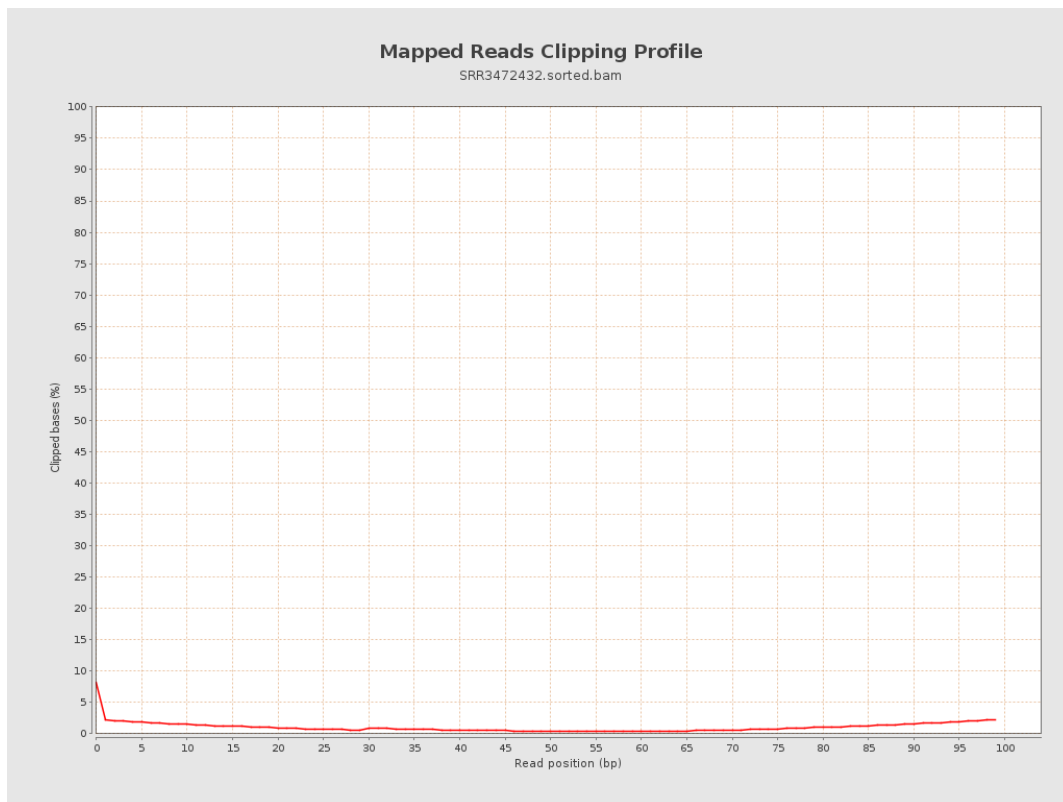
8. Results : Mapped Reads Nucleotide Content



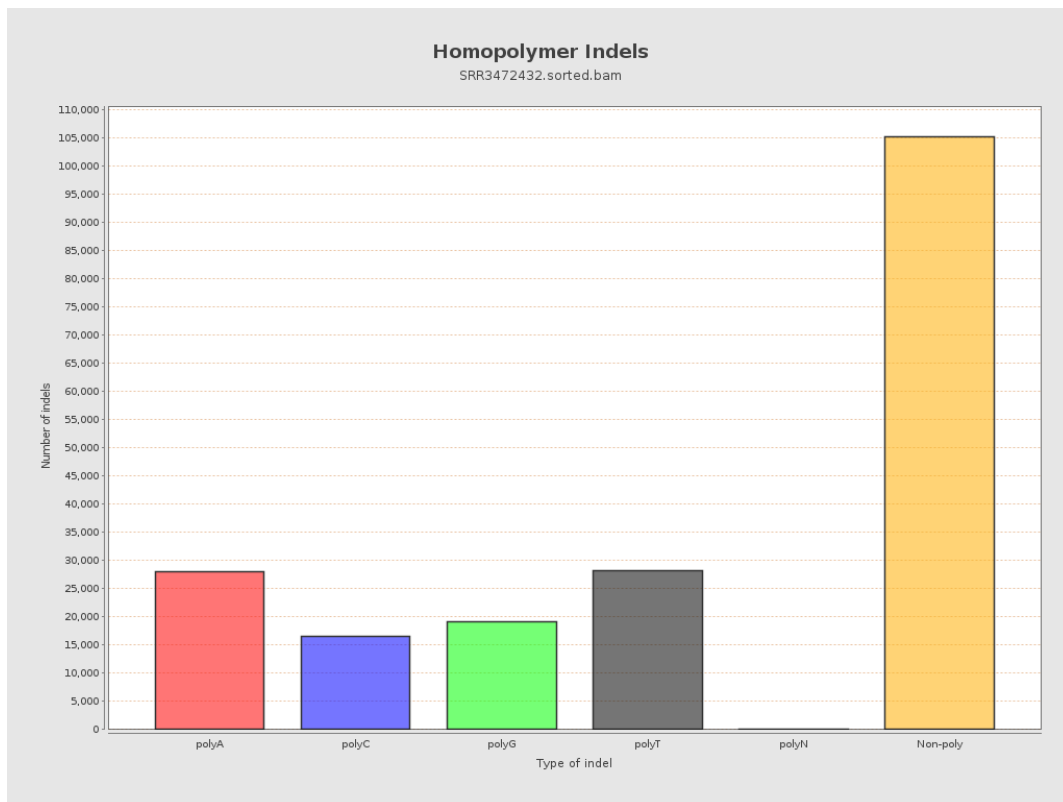
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



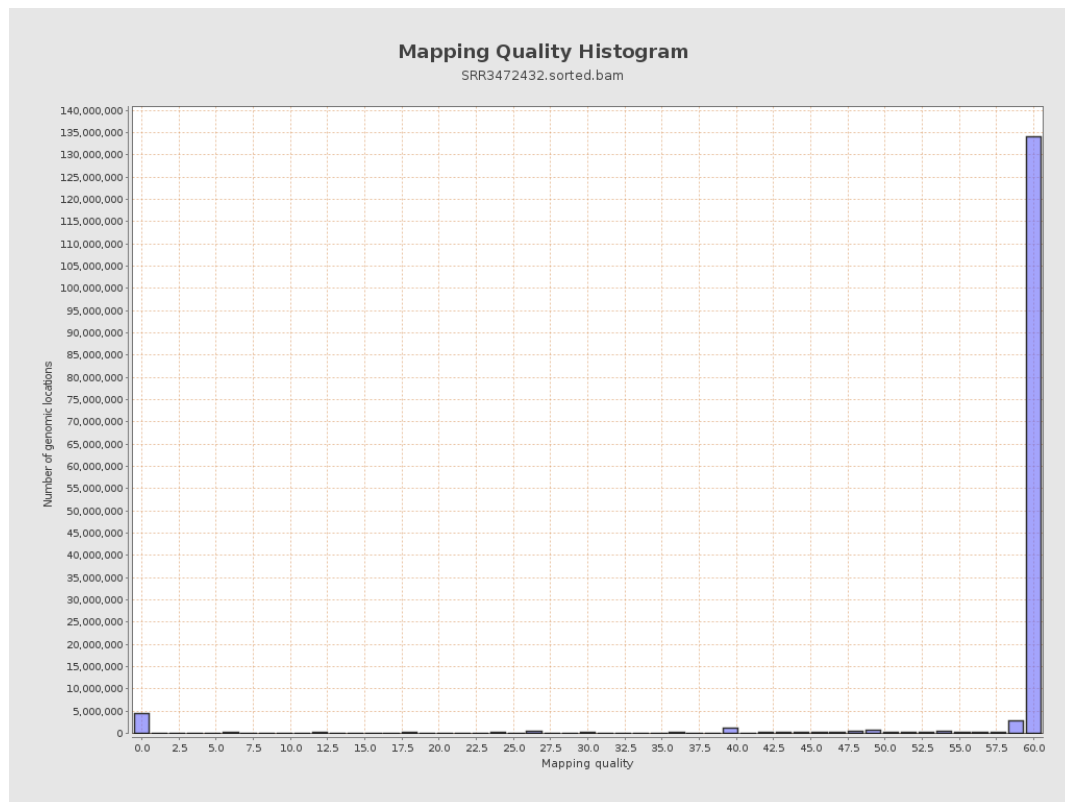
11. Results : Homopolymer Indels



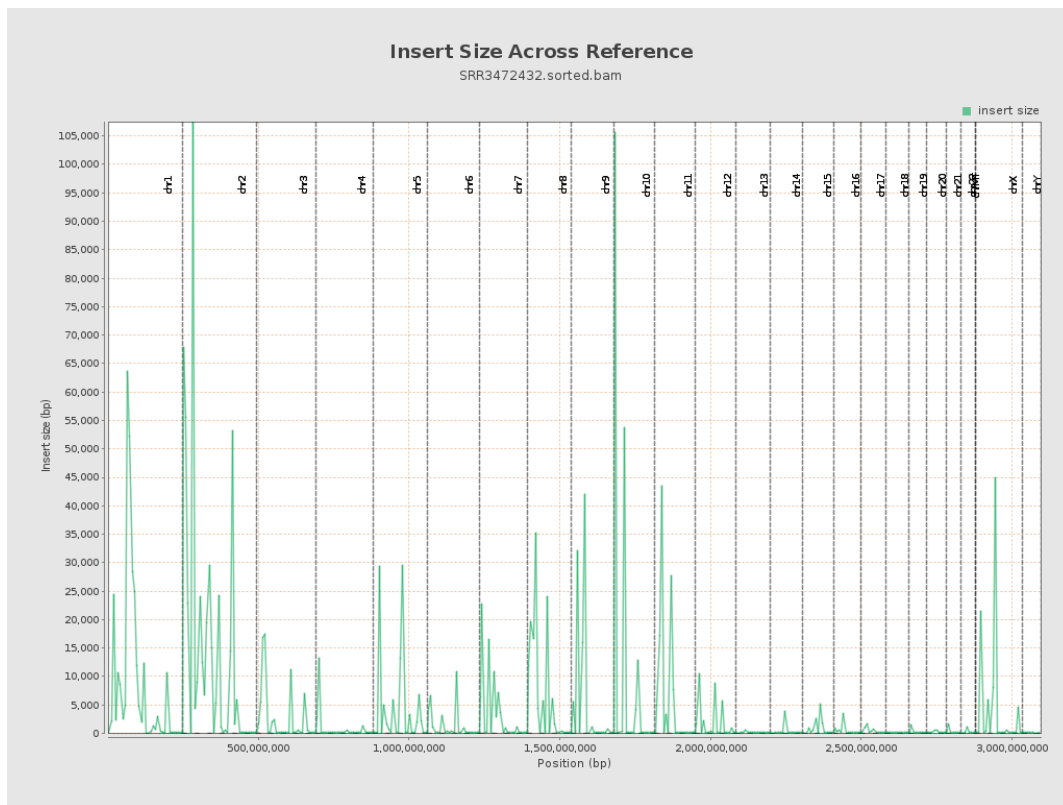
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

