

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 18:29:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618631.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_SRR618631 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618631_1.fastq.gz SRR618631_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 18:29:23 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618631.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,755,702
Mapped reads	21,751,332 / 95.59%
Unmapped reads	1,004,370 / 4.41%
Mapped paired reads	21,751,332 / 95.59%
Mapped reads, first in pair	11,048,802 / 48.55%
Mapped reads, second in pair	10,702,530 / 47.03%
Mapped reads, both in pair	21,216,516 / 93.24%
Mapped reads, singletons	534,816 / 2.35%
Secondary alignments	0
Supplementary alignments	61,388 / 0.27%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	3,784,835 / 16.63%
Duplication rate	15.45%
Clipped reads	4,864,598 / 21.38%

2.2. ACGT Content

Number/percentage of A's	553,713,507 / 27.06%
Number/percentage of C's	450,824,901 / 22.03%
Number/percentage of T's	559,491,909 / 27.34%
Number/percentage of G's	482,316,736 / 23.57%
Number/percentage of N's	51,913 / 0%

GC Percentage	45.6%
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2.3. Coverage

Mean	0.6615
Standard Deviation	2.5959

2.4. Mapping Quality

Mean Mapping Quality	53.67
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2.5. Insert size

Mean	67,275.07
Standard Deviation	2,602,160.34
P25/Median/P75	202 / 227 / 258

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	26,057,065
Insertions	368,457
Mapped reads with at least one insertion	1.67%
Deletions	1,038,799
Mapped reads with at least one deletion	4.66%
Homopolymer indels	53.11%

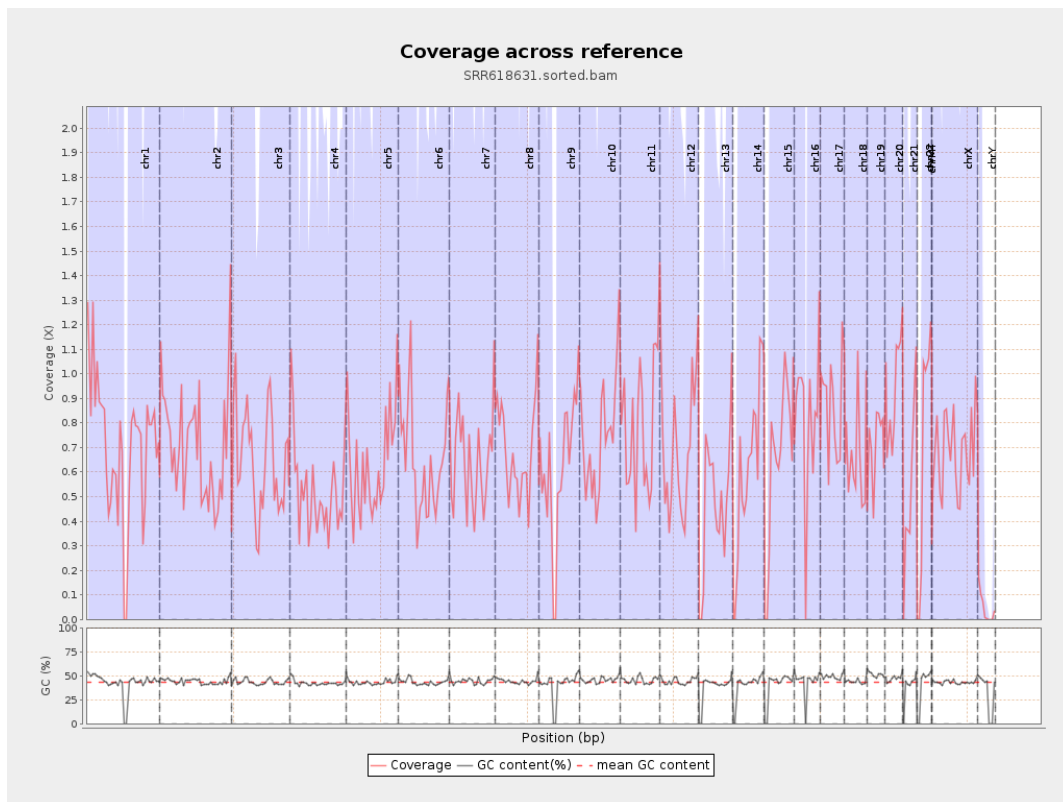
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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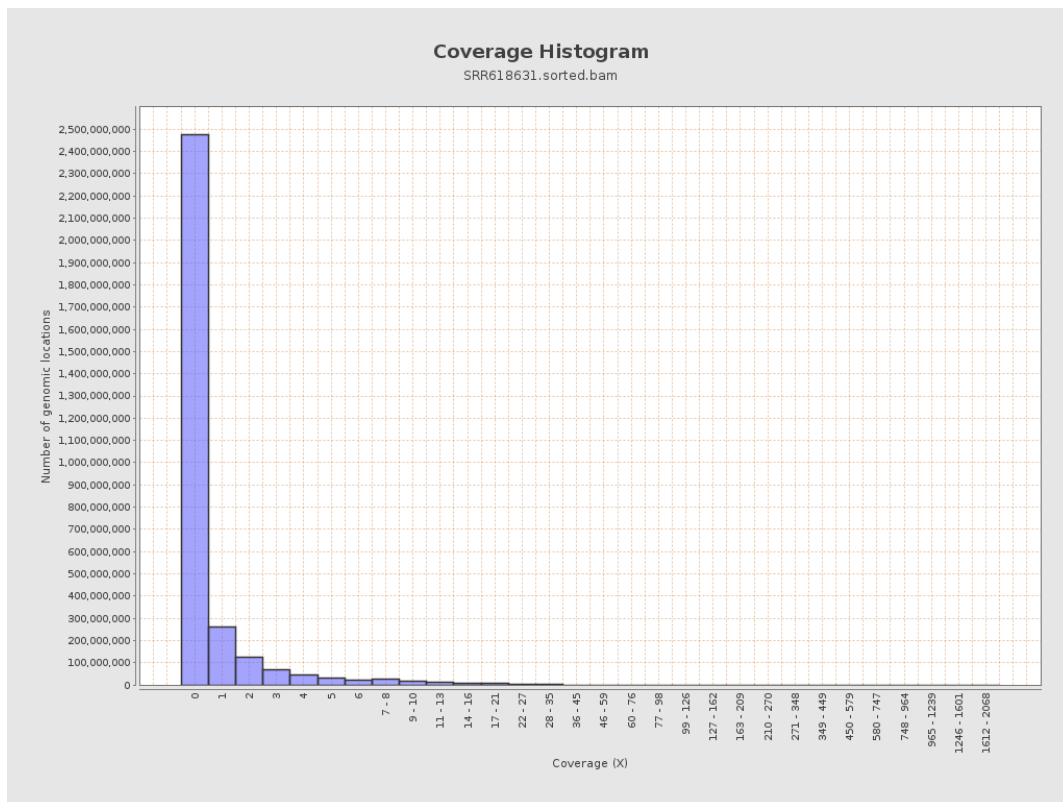
		bases	coverage	deviation
chr1	249250621	175127972	0.7026	2.8751
chr2	243199373	171745342	0.7062	2.9413
chr3	198022430	129349652	0.6532	2.2314
chr4	191154276	99602173	0.5211	2.0451
chr5	180915260	115477064	0.6383	2.186
chr6	171115067	111061913	0.649	2.2352
chr7	159138663	102880643	0.6465	2.2711
chr8	146364022	100189194	0.6845	2.4118
chr9	141213431	87778228	0.6216	2.808
chr10	135534747	101309759	0.7475	2.606
chr11	135006516	105315050	0.7801	2.8274
chr12	133851895	91808286	0.6859	2.445
chr13	115169878	54084748	0.4696	1.8484
chr14	107349540	64810507	0.6037	2.2563
chr15	102531392	66167436	0.6453	2.5389
chr16	90354753	73755441	0.8163	4.3857
chr17	81195210	71267988	0.8777	3.0872
chr18	78077248	52205322	0.6686	2.7443
chr19	59128983	42585517	0.7202	2.8315
chr20	63025520	58696969	0.9313	3.0472
chr21	48129895	26878285	0.5585	3.066
chr22	51304566	37307479	0.7272	2.8124
chrMT	16571	5028	0.3034	1.3102
chrX	155270560	105828700	0.6816	2.2644

chrY	59373566	2563680	0.0432	1.5596
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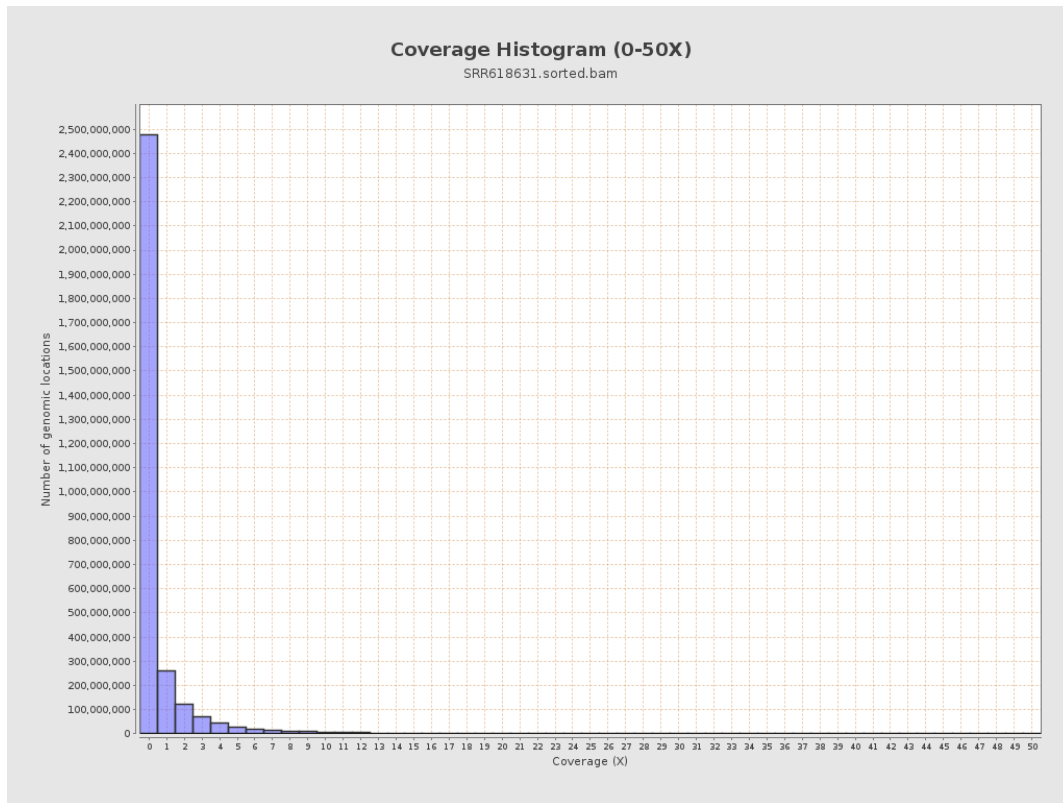
3. Results : Coverage across reference



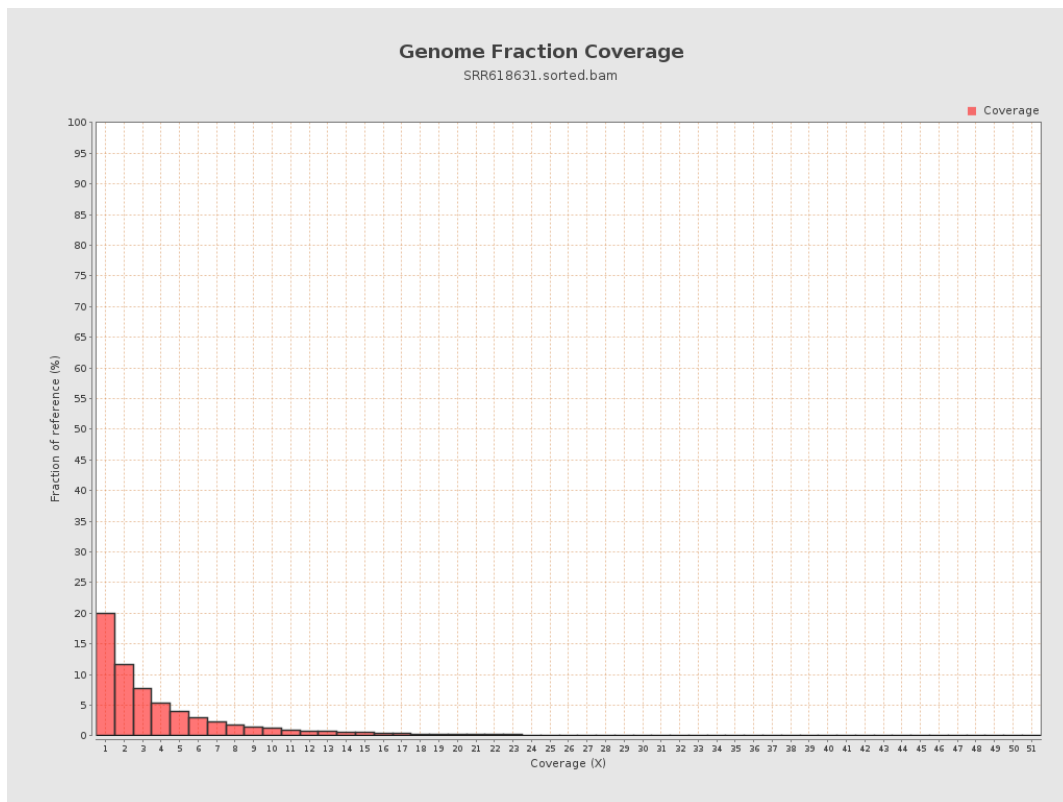
4. Results : Coverage Histogram



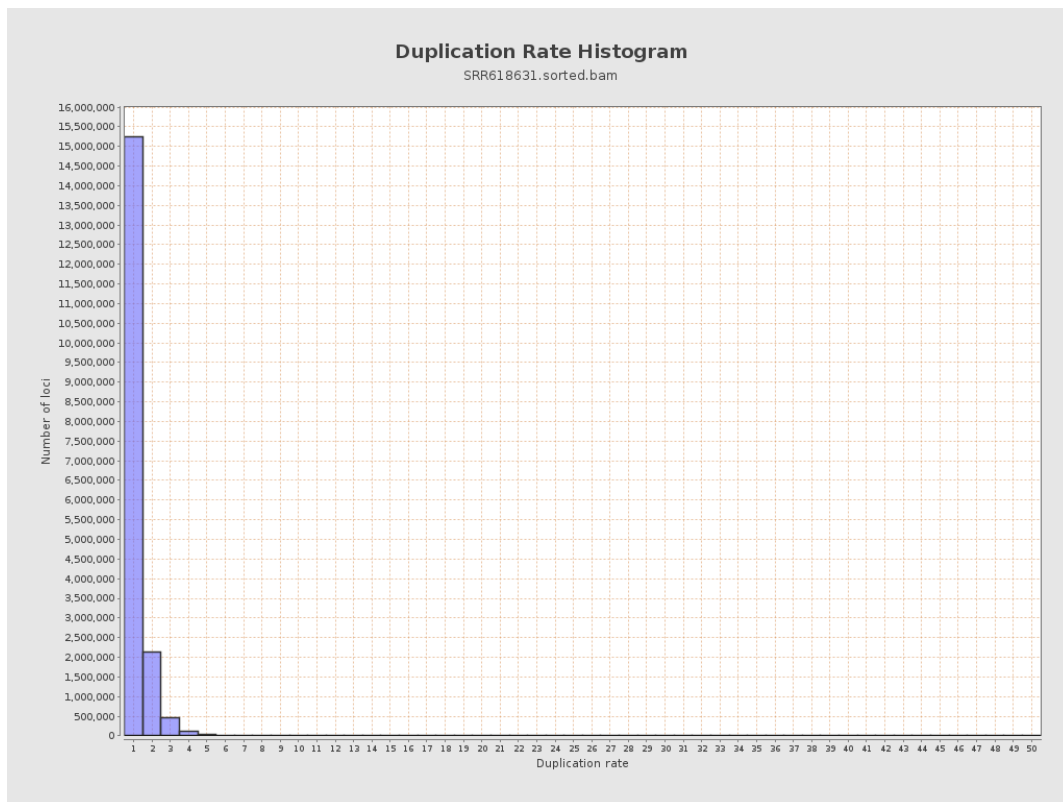
5. Results : Coverage Histogram (0-50X)



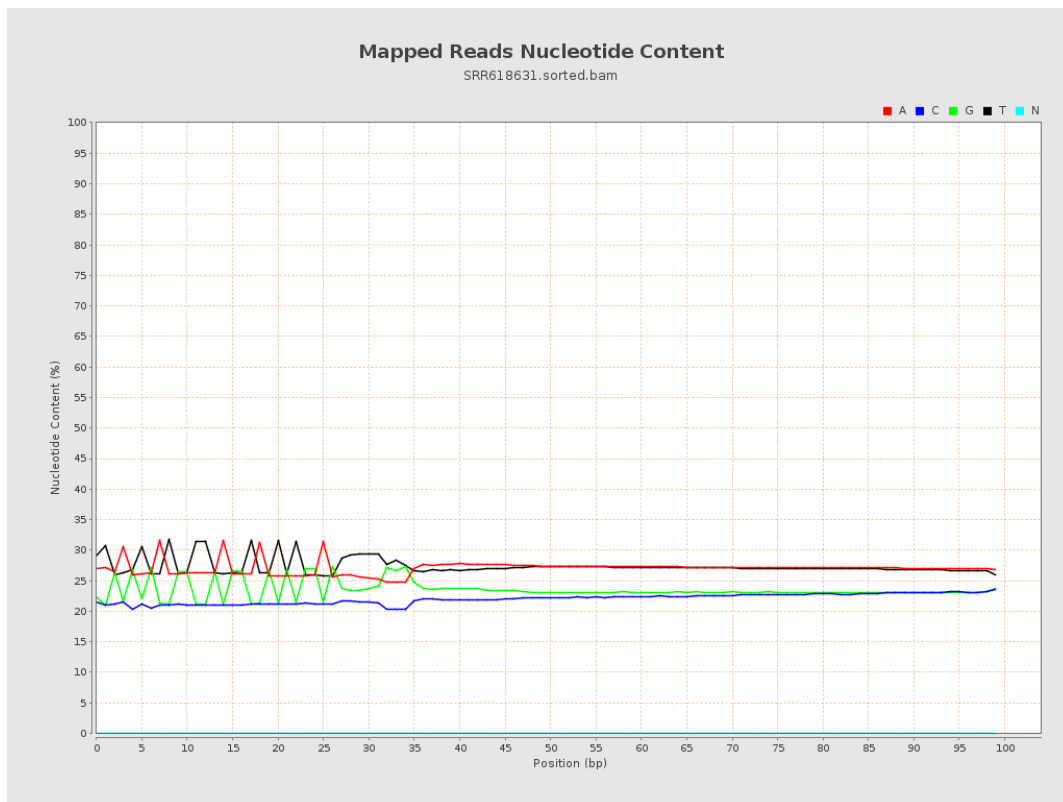
6. Results : Genome Fraction Coverage



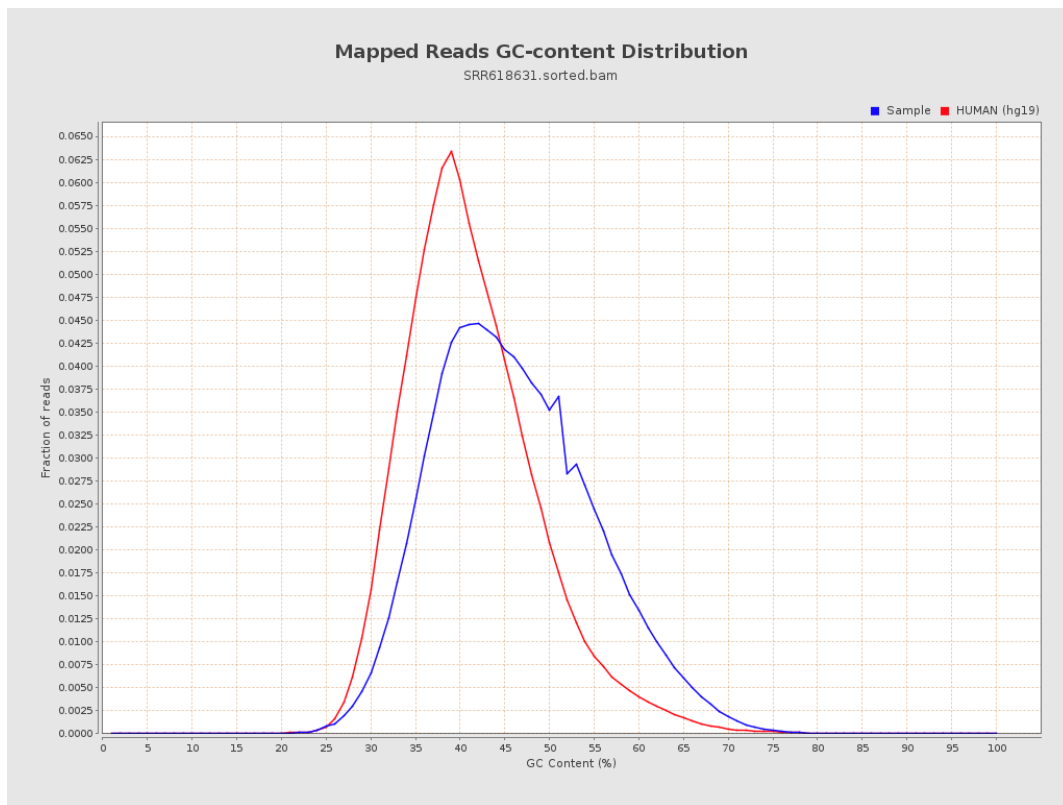
7. Results : Duplication Rate Histogram



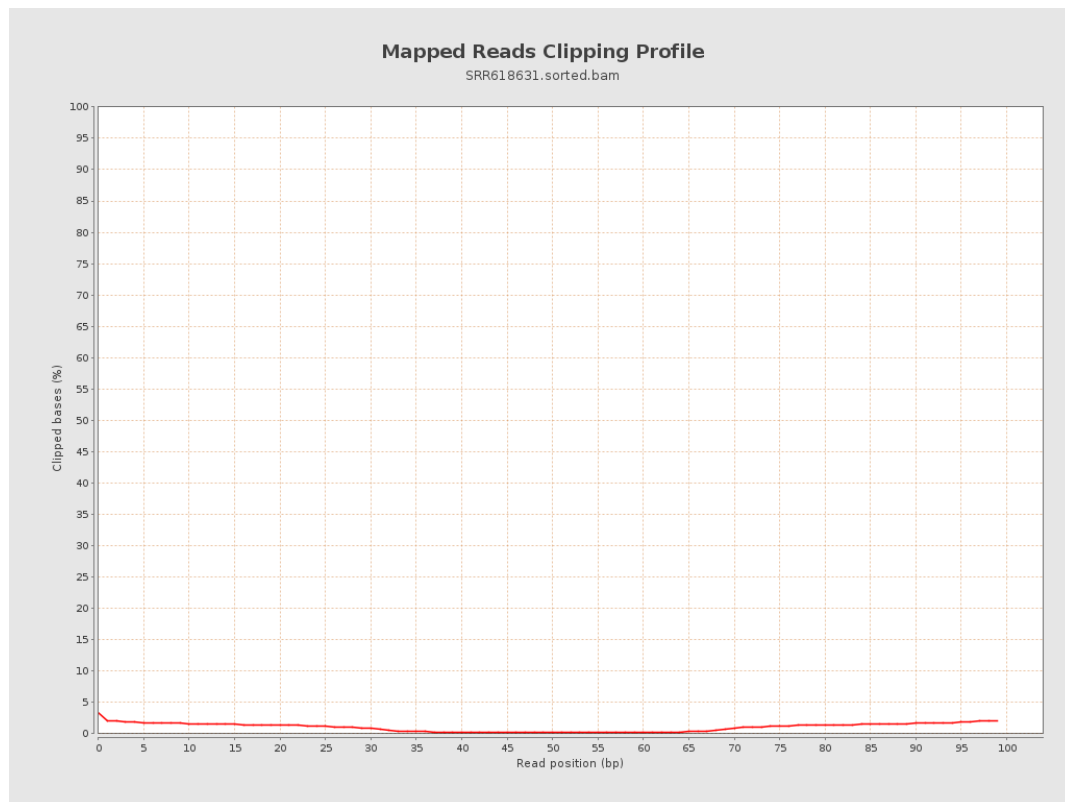
8. Results : Mapped Reads Nucleotide Content



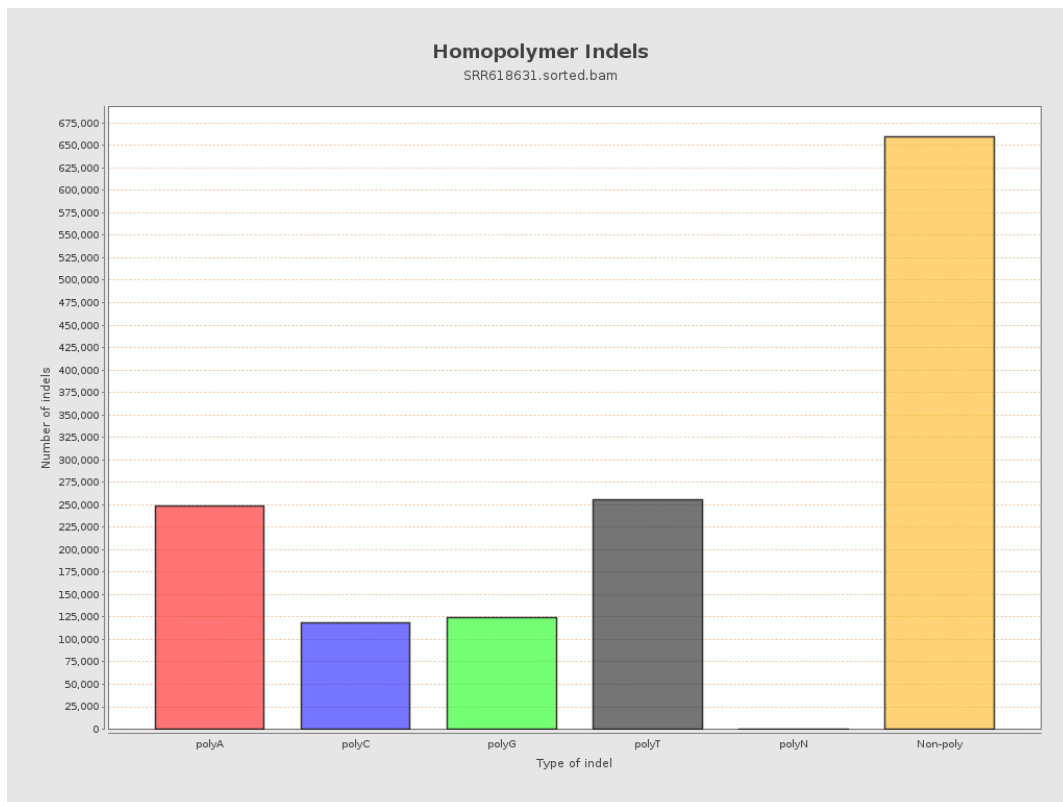
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



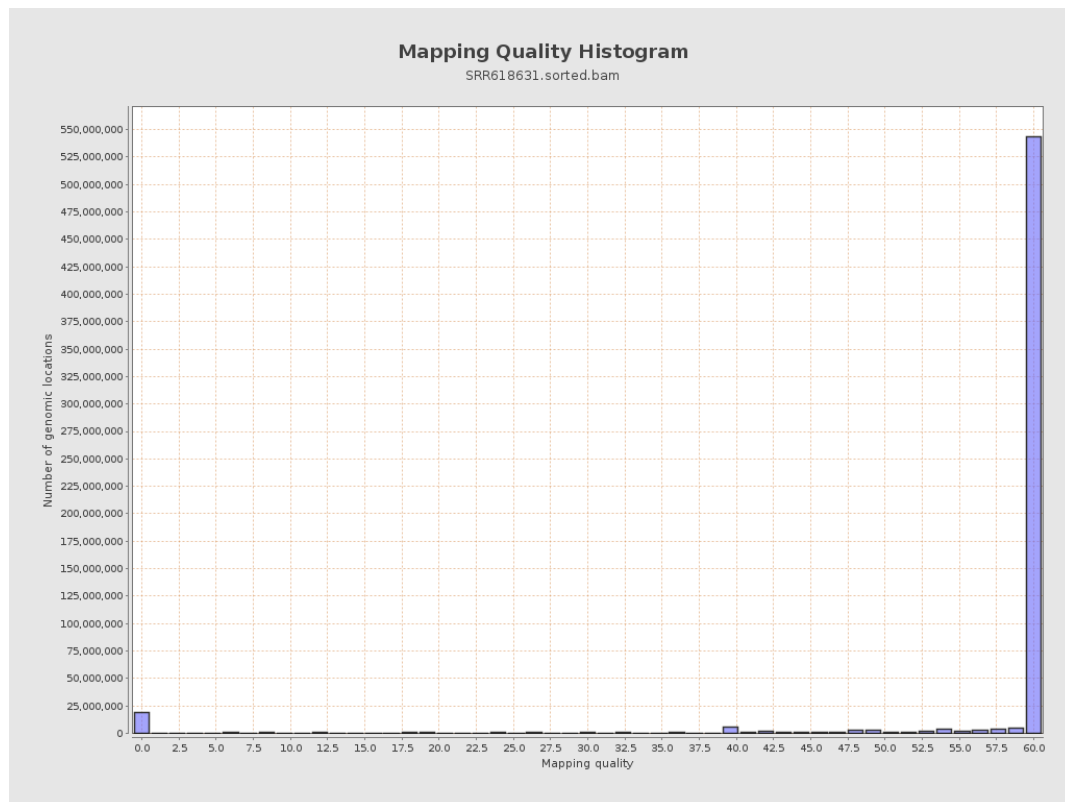
11. Results : Homopolymer Indels



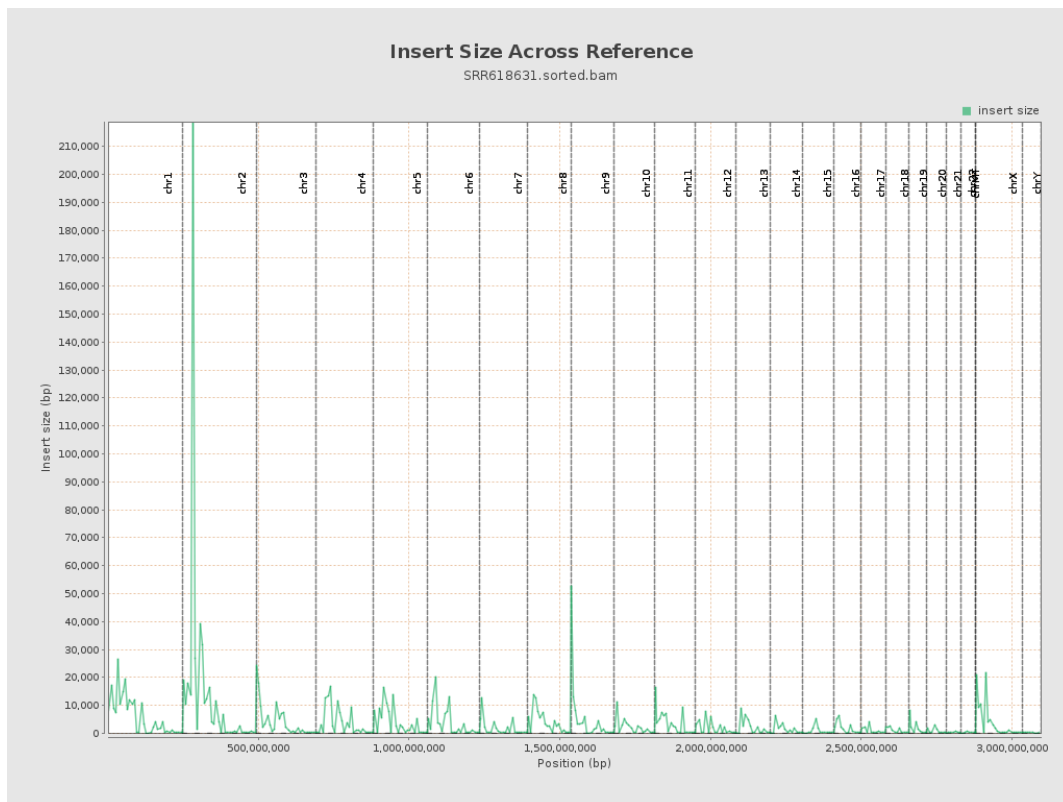
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

