

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 22:10:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630581.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_SRR630581 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630581_1.fastq.gz SRR630581_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 22:10:47 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630581.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	40,626,414
Mapped reads	40,071,135 / 98.63%
Unmapped reads	555,279 / 1.37%
Mapped paired reads	40,071,135 / 98.63%
Mapped reads, first in pair	20,140,031 / 49.57%
Mapped reads, second in pair	19,931,104 / 49.06%
Mapped reads, both in pair	39,792,436 / 97.95%
Mapped reads, singletons	278,699 / 0.69%
Secondary alignments	0
Supplementary alignments	69,240 / 0.17%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	3,504,801 / 8.63%
Duplication rate	7.39%
Clipped reads	5,018,107 / 12.35%

2.2. ACGT Content

Number/percentage of A's	1,097,100,275 / 28.02%
Number/percentage of C's	834,305,680 / 21.31%
Number/percentage of T's	1,104,124,345 / 28.2%
Number/percentage of G's	879,513,655 / 22.46%
Number/percentage of N's	586,309 / 0.01%

GC Percentage	43.77%
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2.3. Coverage

Mean	1.2657
Standard Deviation	4.5993

2.4. Mapping Quality

Mean Mapping Quality	53.98
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2.5. Insert size

Mean	33,341.86
Standard Deviation	1,877,982.72
P25/Median/P75	152 / 193 / 257

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	33,130,812
Insertions	635,677
Mapped reads with at least one insertion	1.56%
Deletions	1,949,822
Mapped reads with at least one deletion	4.74%
Homopolymer indels	54.29%

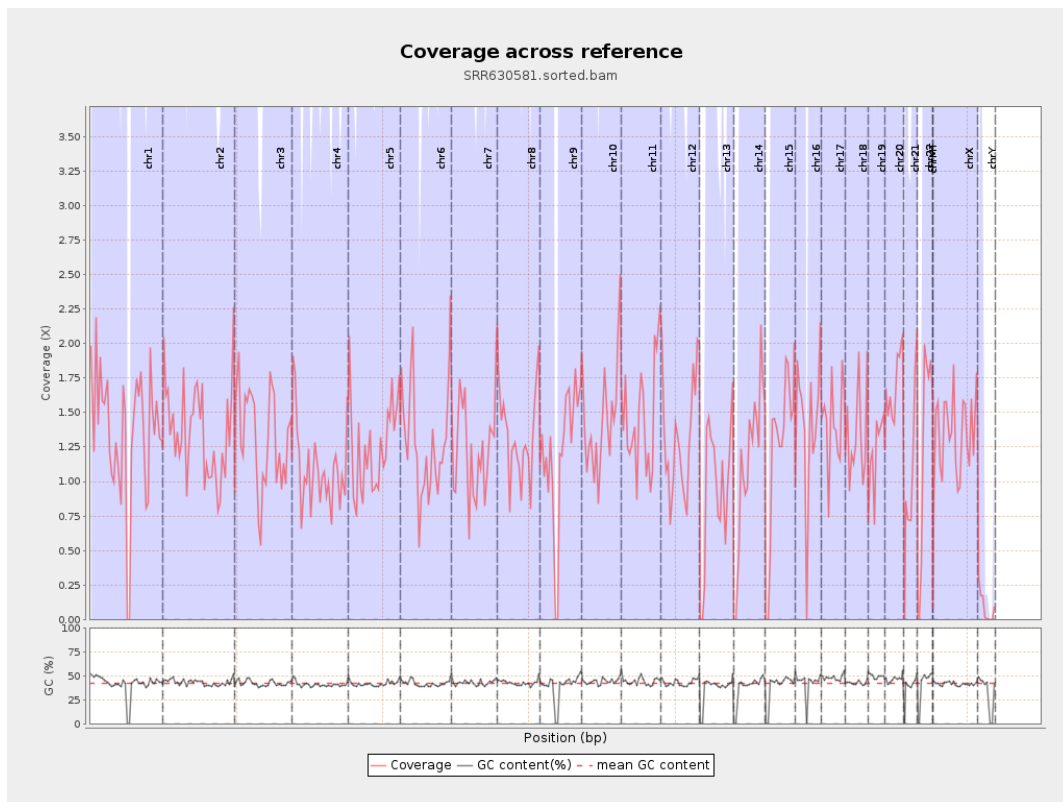
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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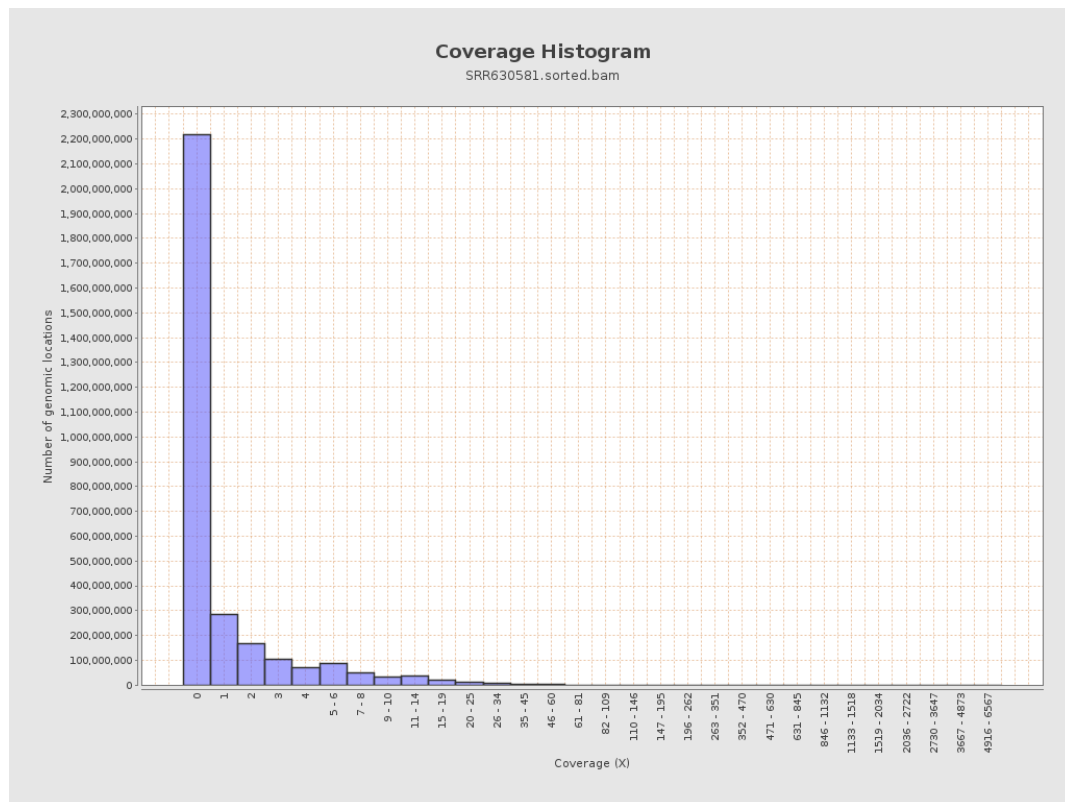
		bases	coverage	deviation
chr1	249250621	338109393	1.3565	5.8321
chr2	243199373	328308358	1.35	6.6487
chr3	198022430	259297595	1.3094	3.6932
chr4	191154276	208927235	1.093	3.5354
chr5	180915260	227761834	1.2589	3.582
chr6	171115067	217563724	1.2714	3.7797
chr7	159138663	196504434	1.2348	3.771
chr8	146364022	194019160	1.3256	3.9334
chr9	141213431	170797891	1.2095	5.6024
chr10	135534747	193717760	1.4293	4.148
chr11	135006516	196417623	1.4549	5.8369
chr12	133851895	177146837	1.3235	3.8368
chr13	115169878	108924709	0.9458	3.0572
chr14	107349540	121664316	1.1333	3.6924
chr15	102531392	125171687	1.2208	3.7694
chr16	90354753	126054675	1.3951	5.545
chr17	81195210	115180047	1.4186	4.4657
chr18	78077248	102198447	1.3089	5.4252
chr19	59128983	72048841	1.2185	4.6634
chr20	63025520	107515963	1.7059	4.8682
chr21	48129895	51474058	1.0695	5.2323
chr22	51304566	64423306	1.2557	4.2128
chrMT	16571	1164	0.0702	0.4638
chrX	155270560	209957146	1.3522	3.9745

chrY	59373566	5091286	0.0858	2.0587
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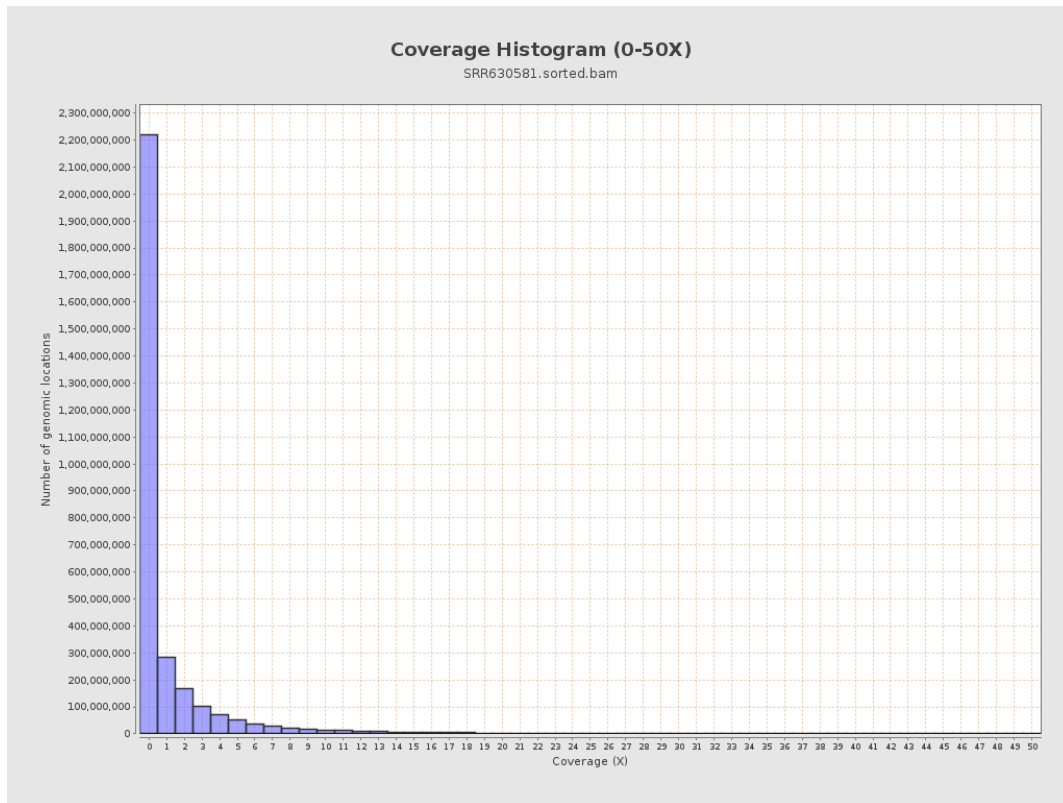
3. Results : Coverage across reference



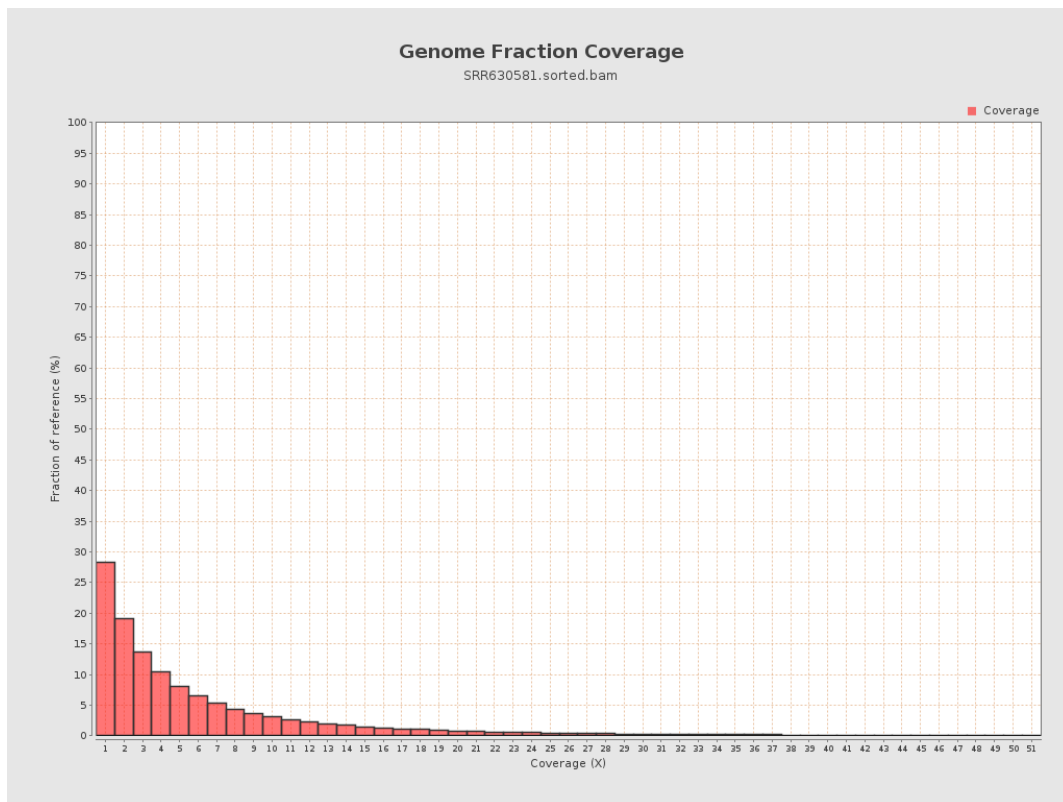
4. Results : Coverage Histogram



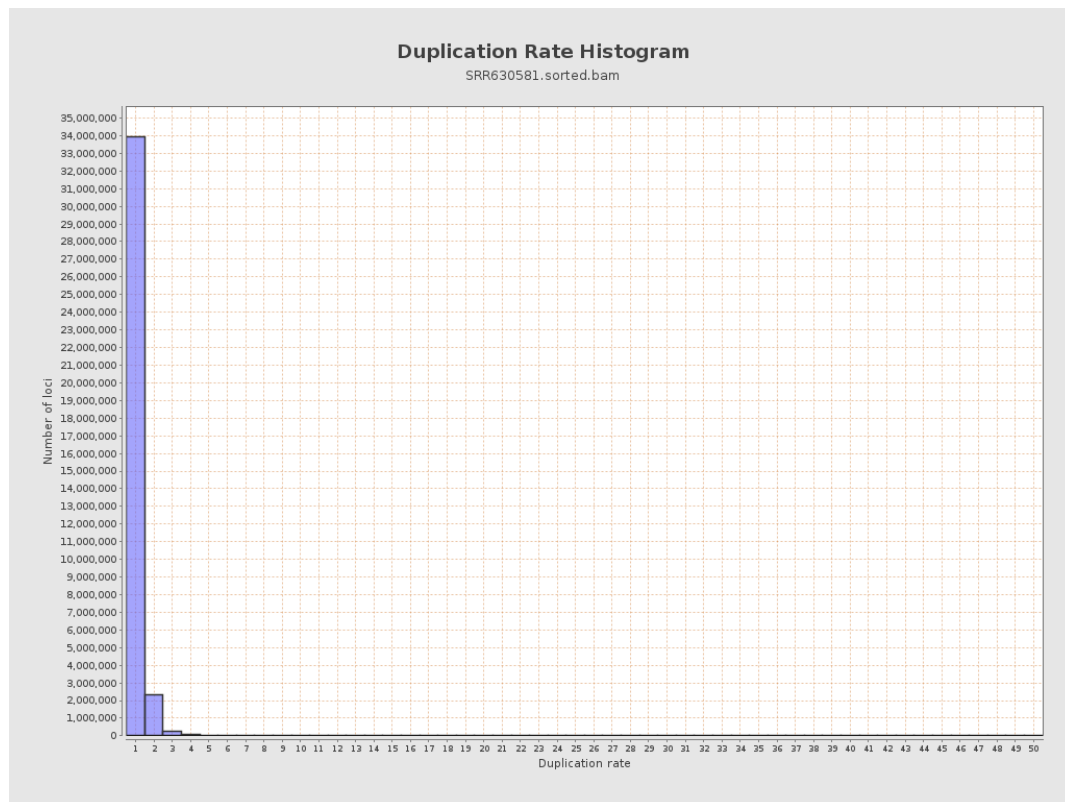
5. Results : Coverage Histogram (0-50X)



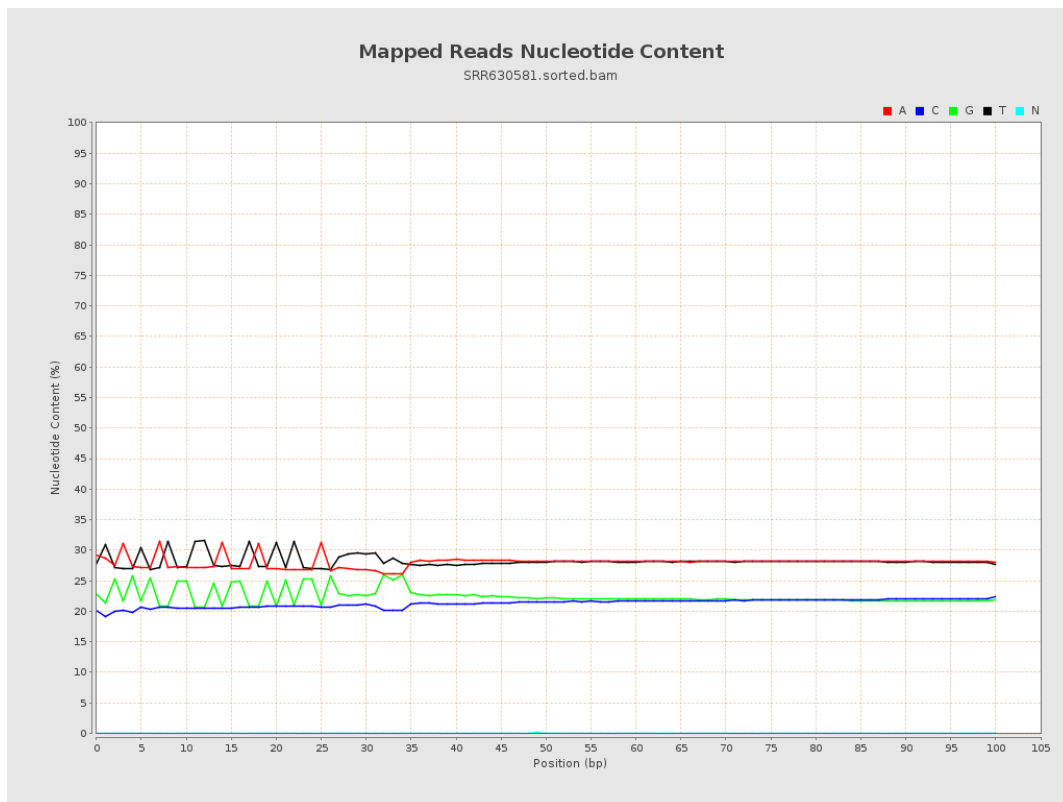
6. Results : Genome Fraction Coverage



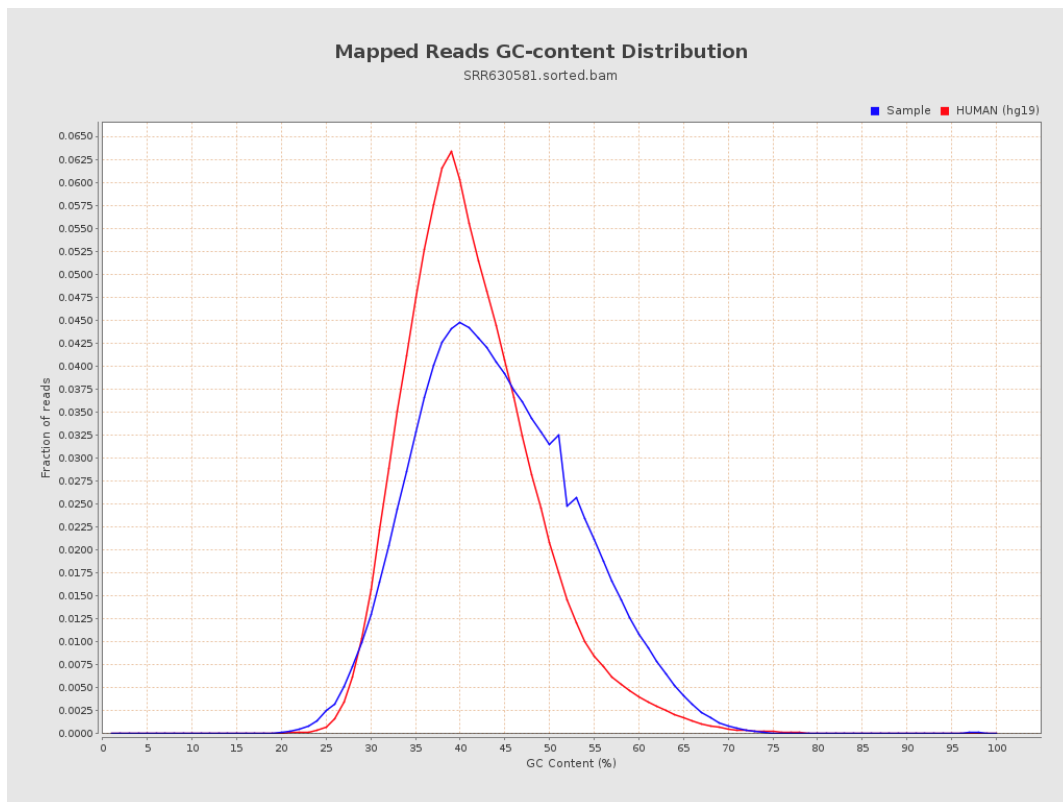
7. Results : Duplication Rate Histogram



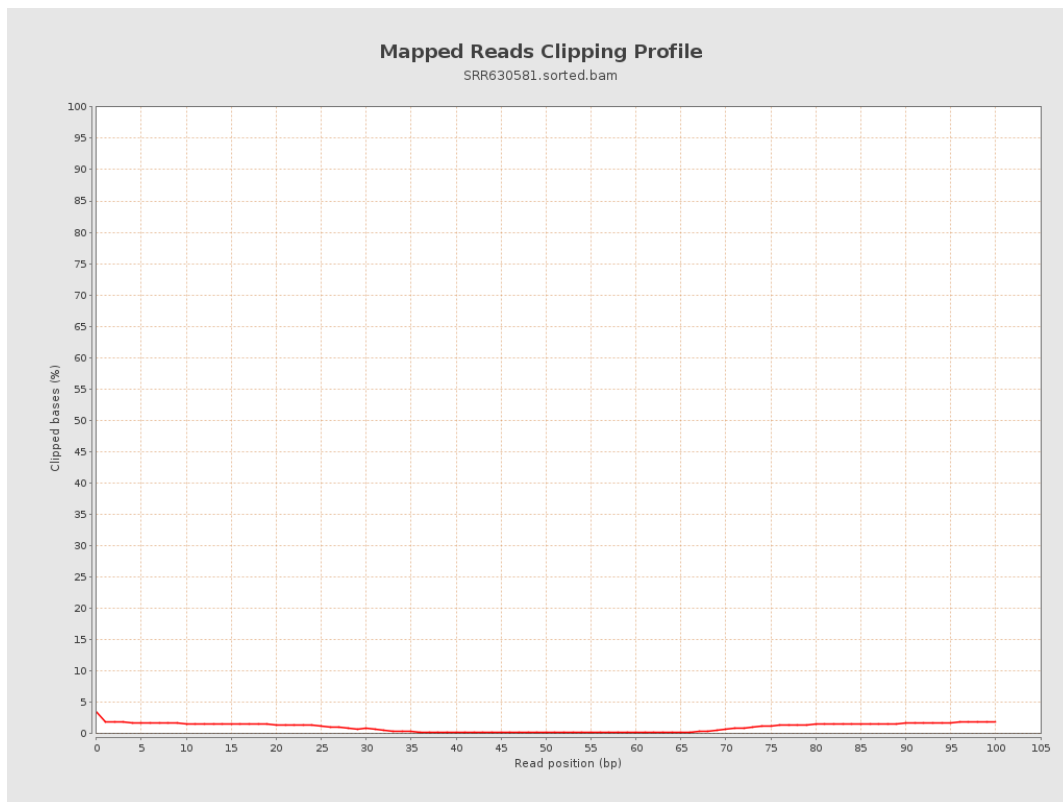
8. Results : Mapped Reads Nucleotide Content



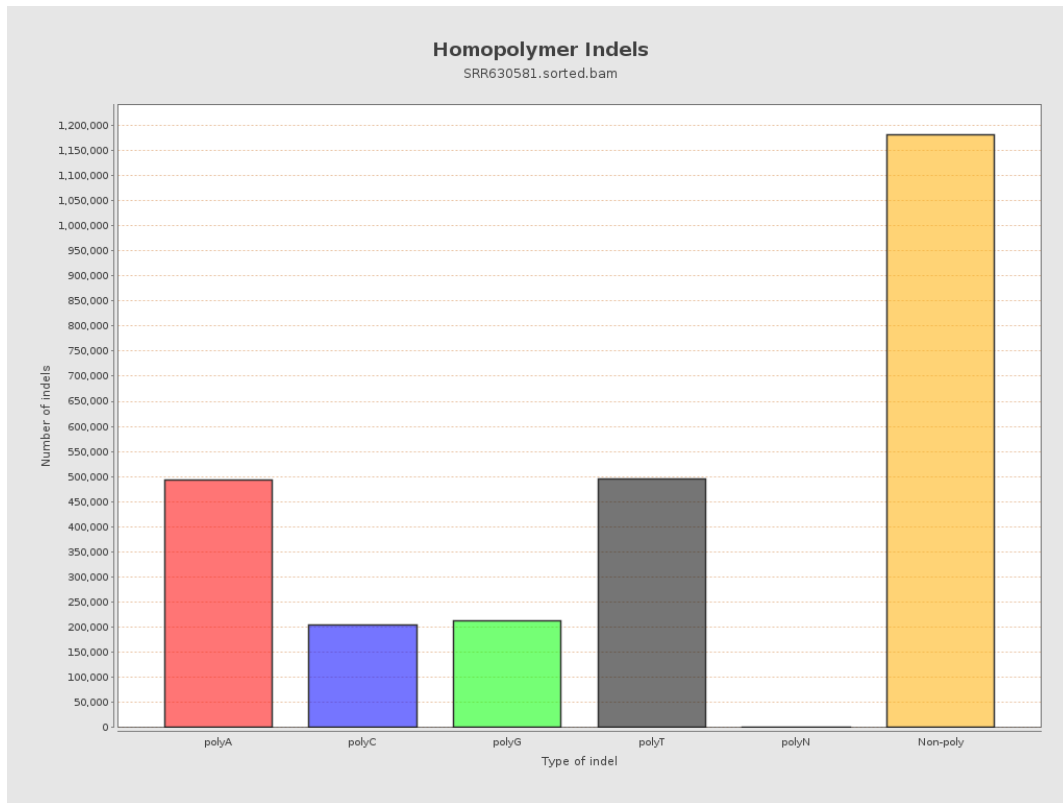
9. Results : Mapped Reads GC-content Distribution



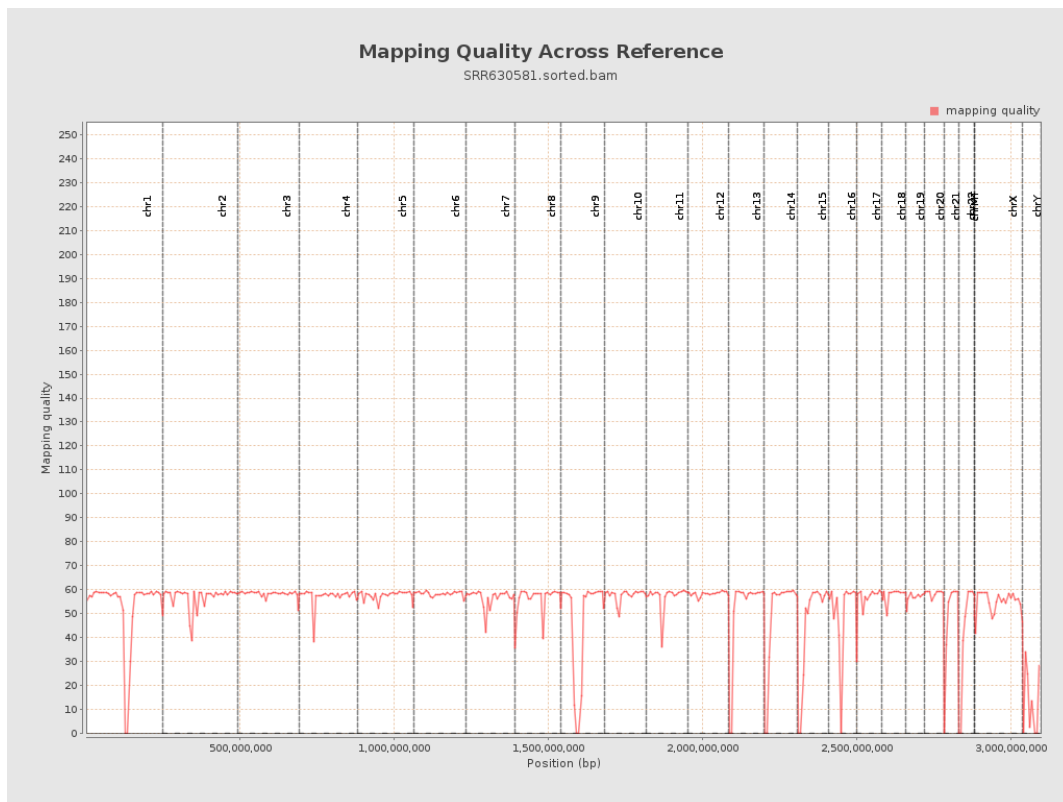
10. Results : Mapped Reads Clipping Profile



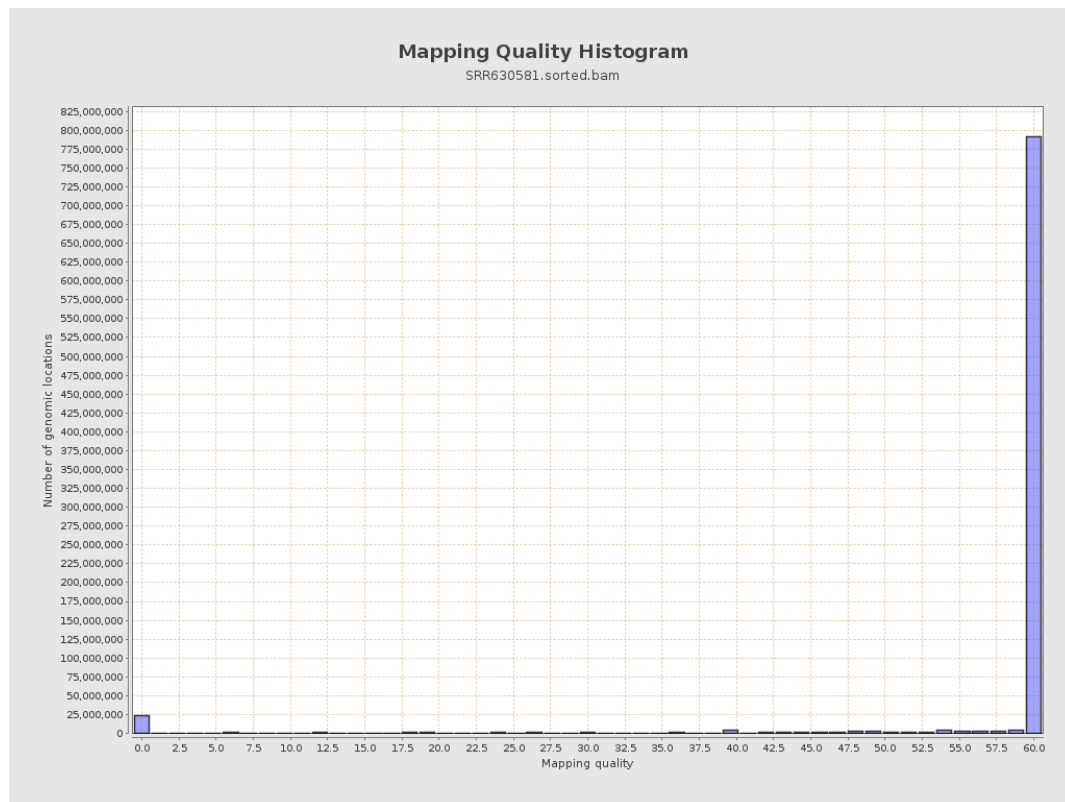
11. Results : Homopolymer Indels



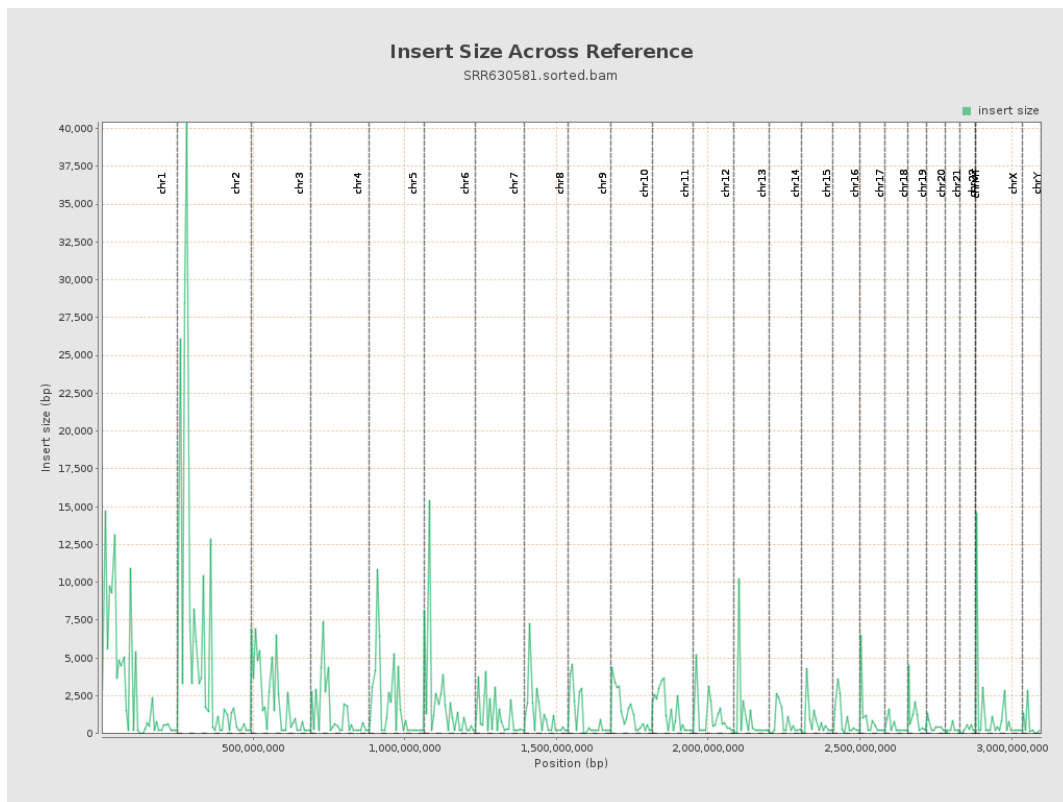
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

