

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/01 22:54:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438294.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_SRR8438294 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438294_1.fastq.gz SRR8438294_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 01 22:53:59 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438294.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	657,211,676
Mapped reads	654,856,490 / 99.64%
Unmapped reads	2,355,186 / 0.36%
Mapped paired reads	654,856,490 / 99.64%
Mapped reads, first in pair	327,621,246 / 49.85%
Mapped reads, second in pair	327,235,244 / 49.79%
Mapped reads, both in pair	653,120,456 / 99.38%
Mapped reads, singletons	1,736,034 / 0.26%
Secondary alignments	0
Supplementary alignments	10,928,532 / 1.66%
Read min/max/mean length	28 / 151 / 145.48
Duplicated reads (estimated)	269,986,945 / 41.08%
Duplication rate	38.51%
Clipped reads	117,897,439 / 17.94%

2.2. ACGT Content

Number/percentage of A's	28,554,097,904 / 30.24%
Number/percentage of C's	18,883,033,298 / 20%
Number/percentage of T's	27,209,466,848 / 28.81%
Number/percentage of G's	19,785,139,397 / 20.95%
Number/percentage of N's	706,429 / 0%

GC Percentage	40.95%
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2.3. Coverage

Mean	30.5131
Standard Deviation	106.3788

2.4. Mapping Quality

Mean Mapping Quality	55.06
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2.5. Insert size

Mean	38,597.4
Standard Deviation	1,906,485.02
P25/Median/P75	194 / 258 / 367

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	487,116,514
Insertions	11,999,288
Mapped reads with at least one insertion	1.8%
Deletions	10,714,016
Mapped reads with at least one deletion	1.61%
Homopolymer indels	48.44%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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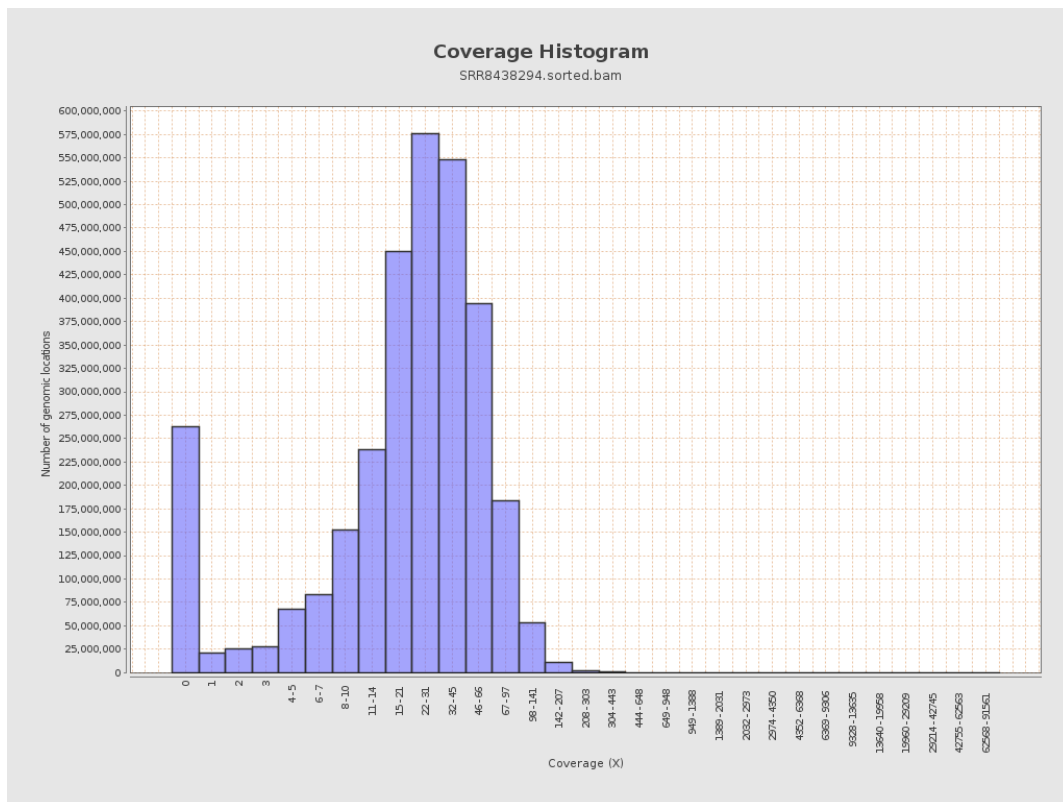
		bases	coverage	deviation
chr1	249250621	7800836952	31.2972	31.8908
chr2	243199373	8267042544	33.9929	95.331
chr3	198022430	6776718108	34.222	57.4804
chr4	191154276	6222482418	32.5521	24.5734
chr5	180915260	6082286700	33.6195	25.2121
chr6	171115067	5574596625	32.5781	26.0322
chr7	159138663	5093565959	32.0071	25.327
chr8	146364022	4921890568	33.6277	26.1354
chr9	141213431	4084829251	28.9266	31.0679
chr10	135534747	4489081358	33.1213	36.2262
chr11	135006516	4447172465	32.9404	26.5064
chr12	133851895	4469118195	33.3885	25.8788
chr13	115169878	3200978421	27.7935	25.1088
chr14	107349540	3002685452	27.9711	27.5285
chr15	102531392	2716231622	26.4917	27.097
chr16	90354753	2557695152	28.3073	49.5102
chr17	81195210	2434817785	29.9872	36.4803
chr18	78077248	2614118471	33.4812	27.0922
chr19	59128983	1498813837	25.3482	70.2734
chr20	63025520	2092326154	33.1981	29.1458
chr21	48129895	1203351545	25.0022	40.4009
chr22	51304566	1026228864	20.0027	26.4197
chrMT	16571	651854095	39,337.0403	15,572.0118
chrX	155270560	2752294919	17.7258	17.8851

chrY	59373566	478228524	8.0546	26.7887
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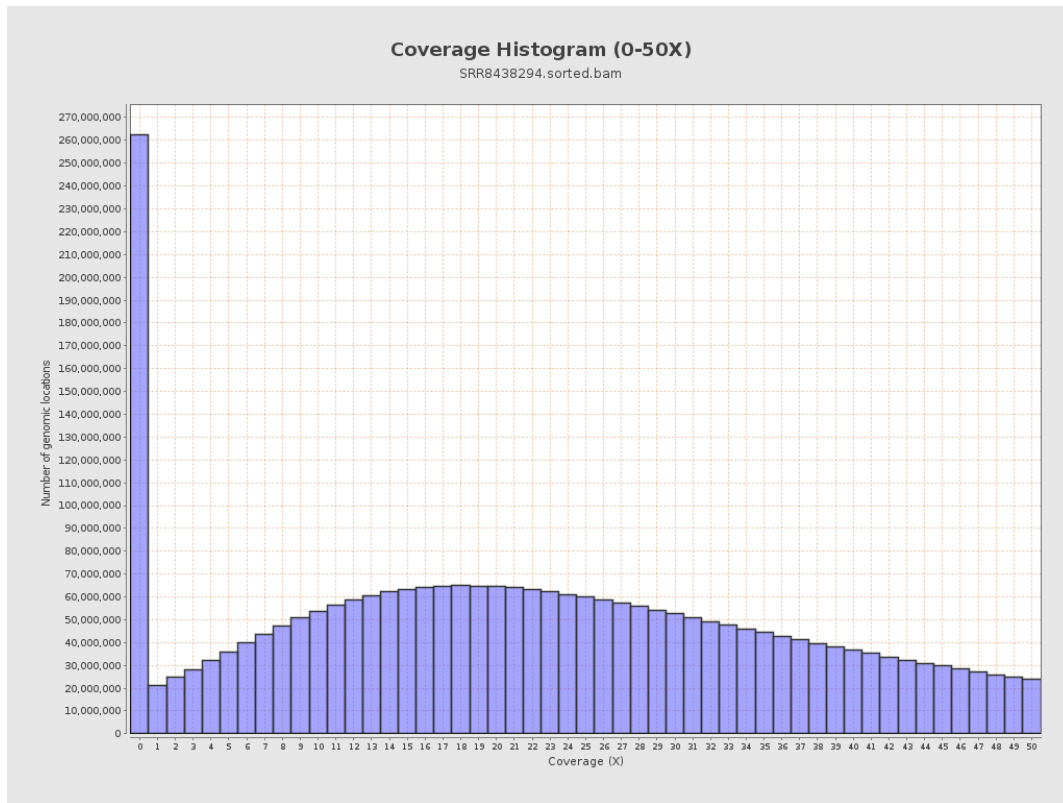
3. Results : Coverage across reference



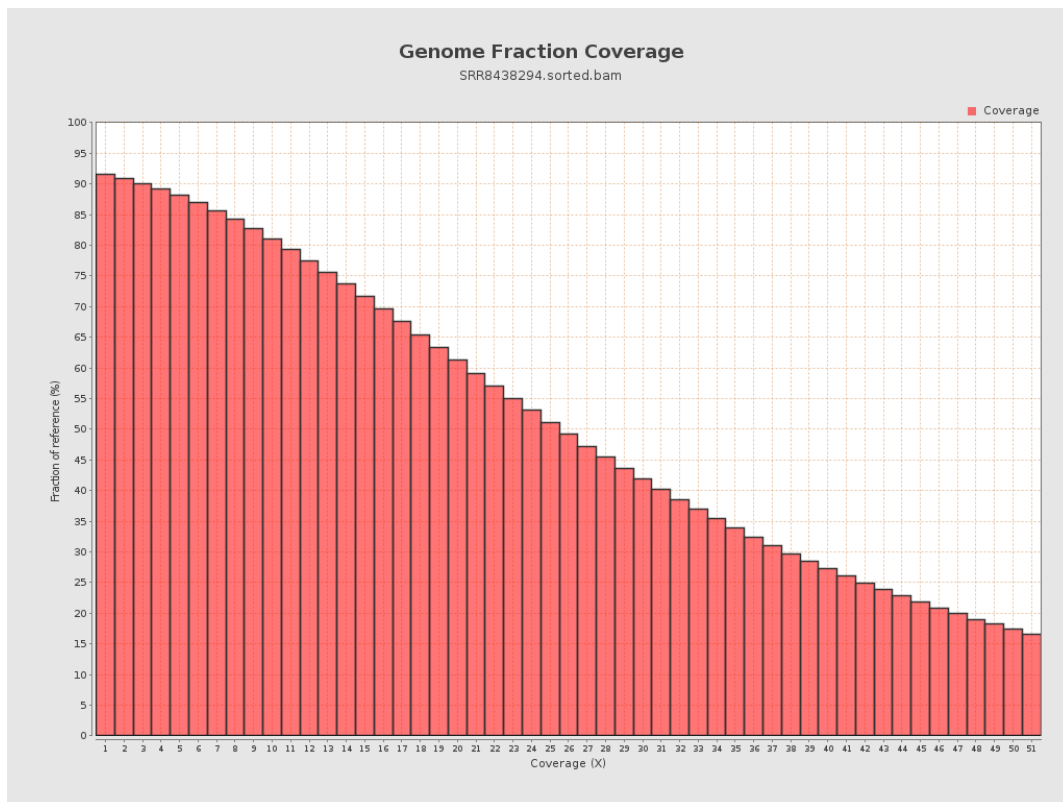
4. Results : Coverage Histogram



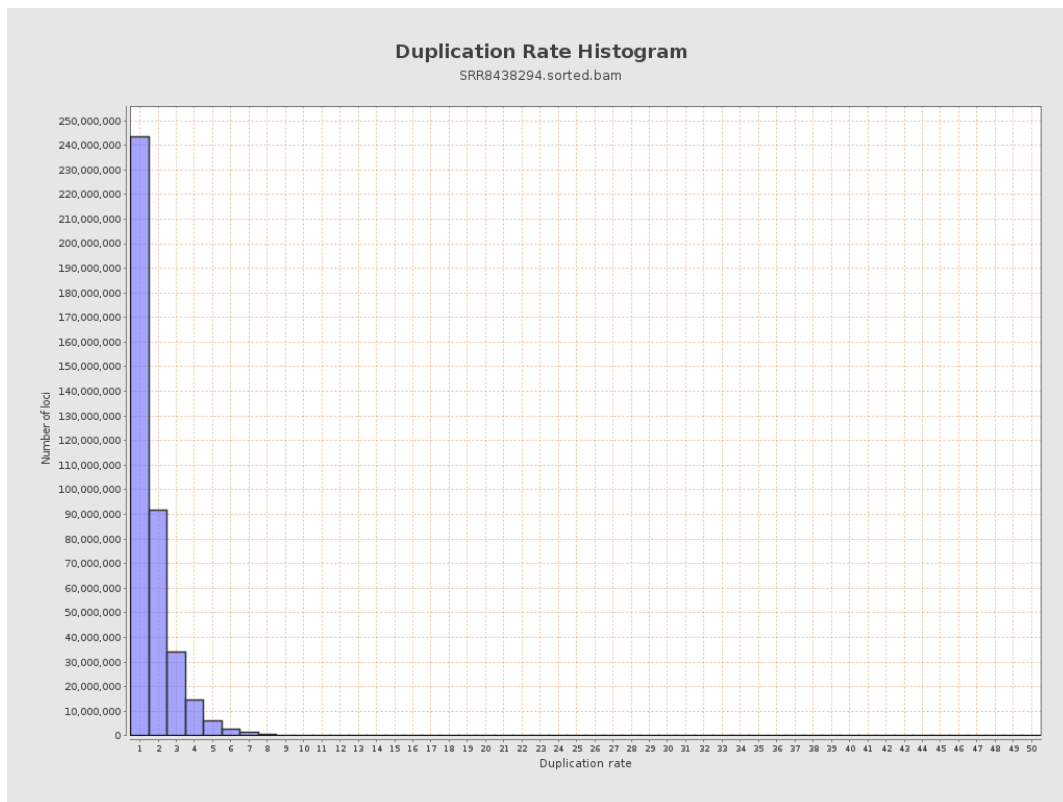
5. Results : Coverage Histogram (0-50X)



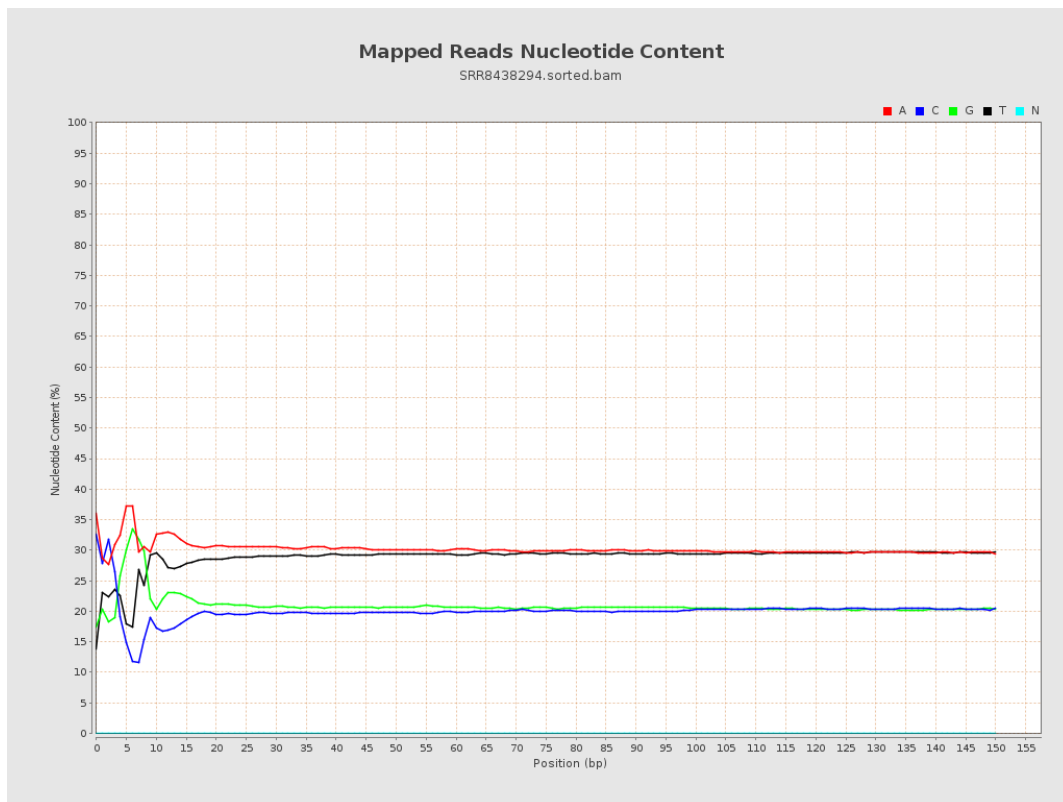
6. Results : Genome Fraction Coverage



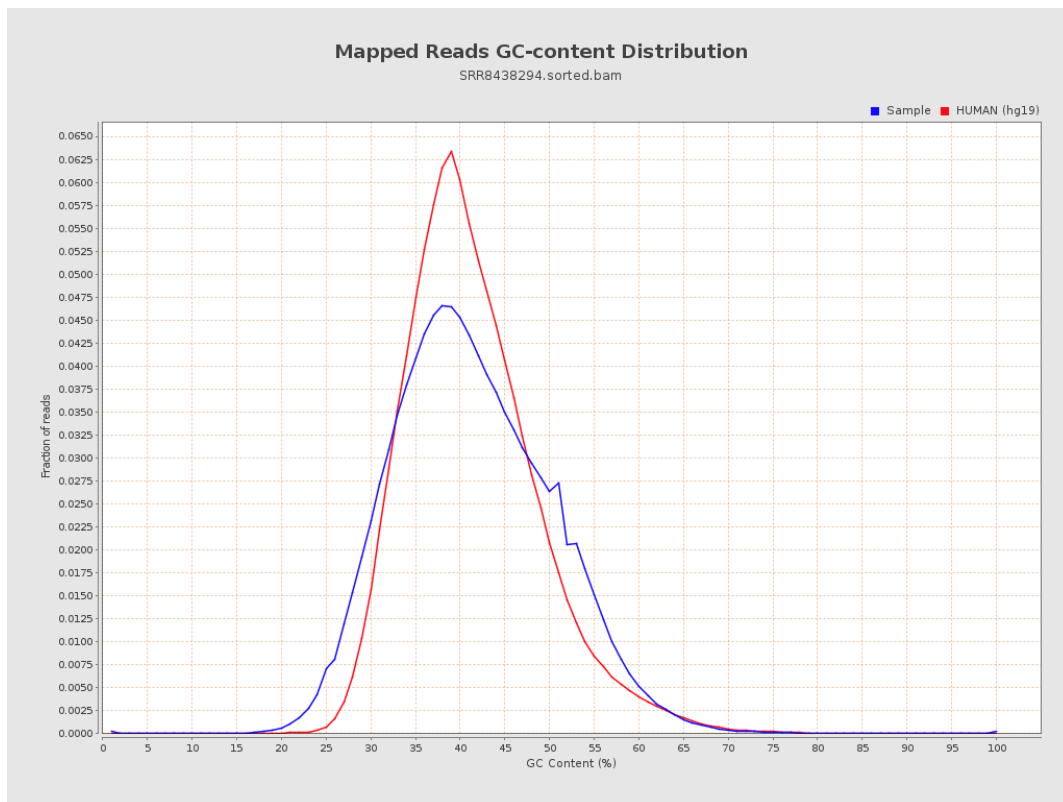
7. Results : Duplication Rate Histogram



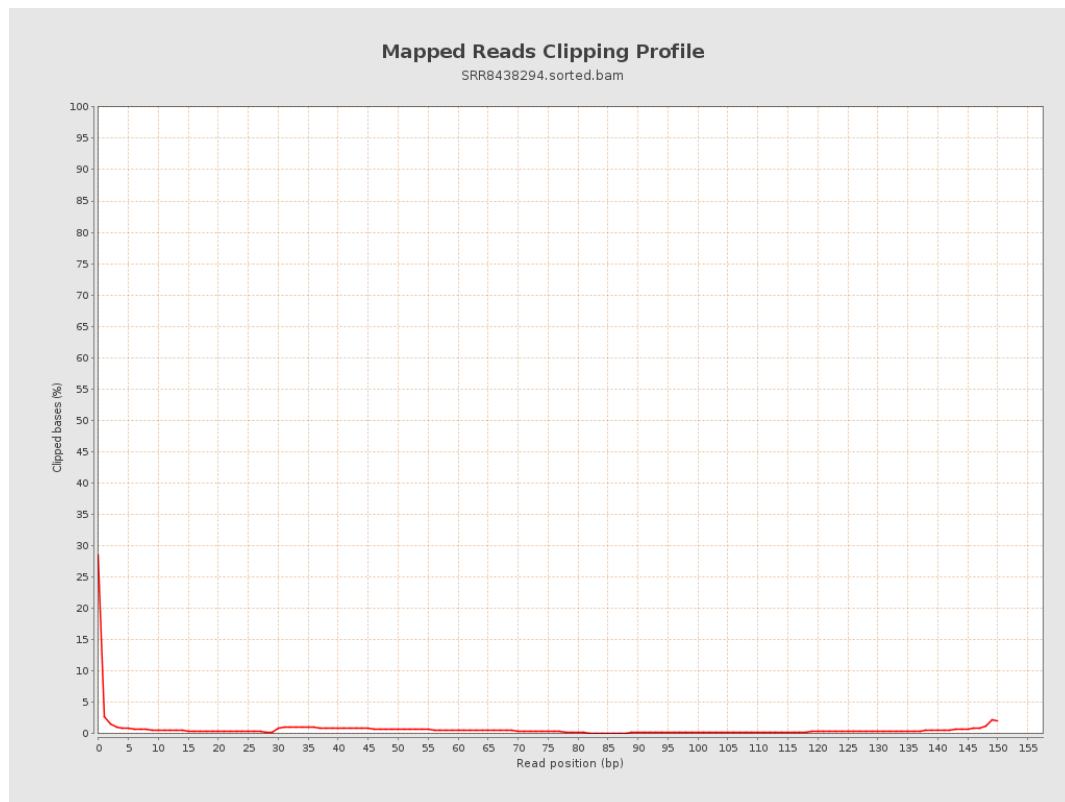
8. Results : Mapped Reads Nucleotide Content



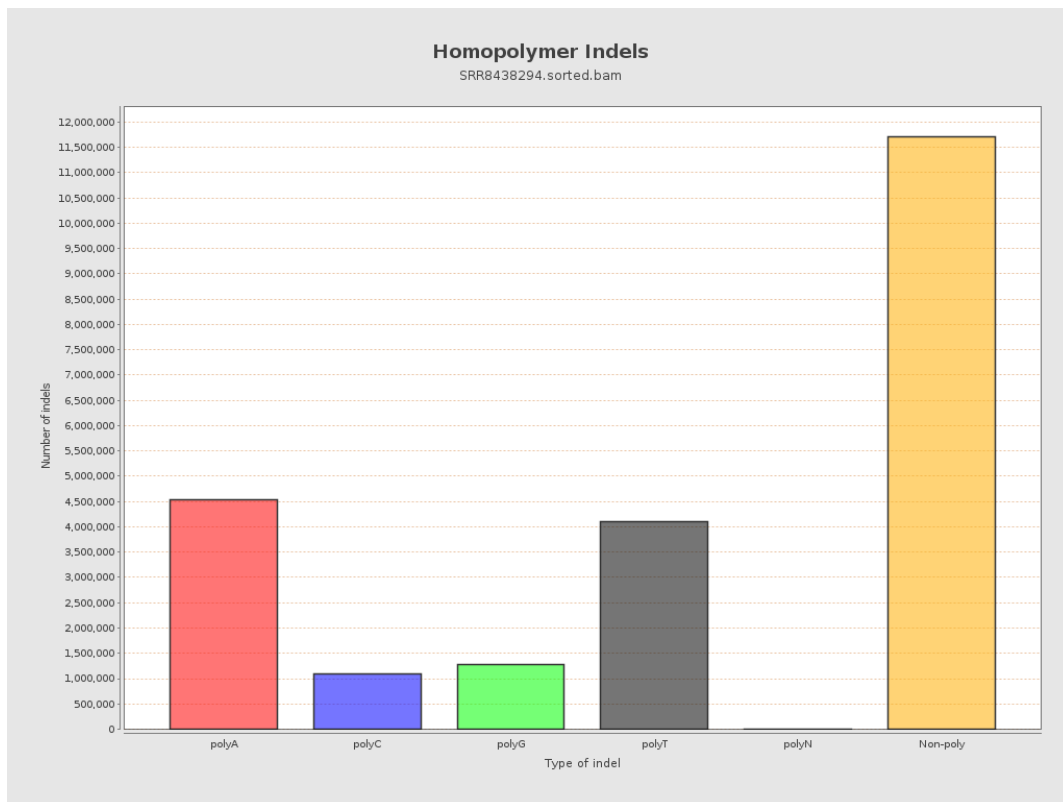
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



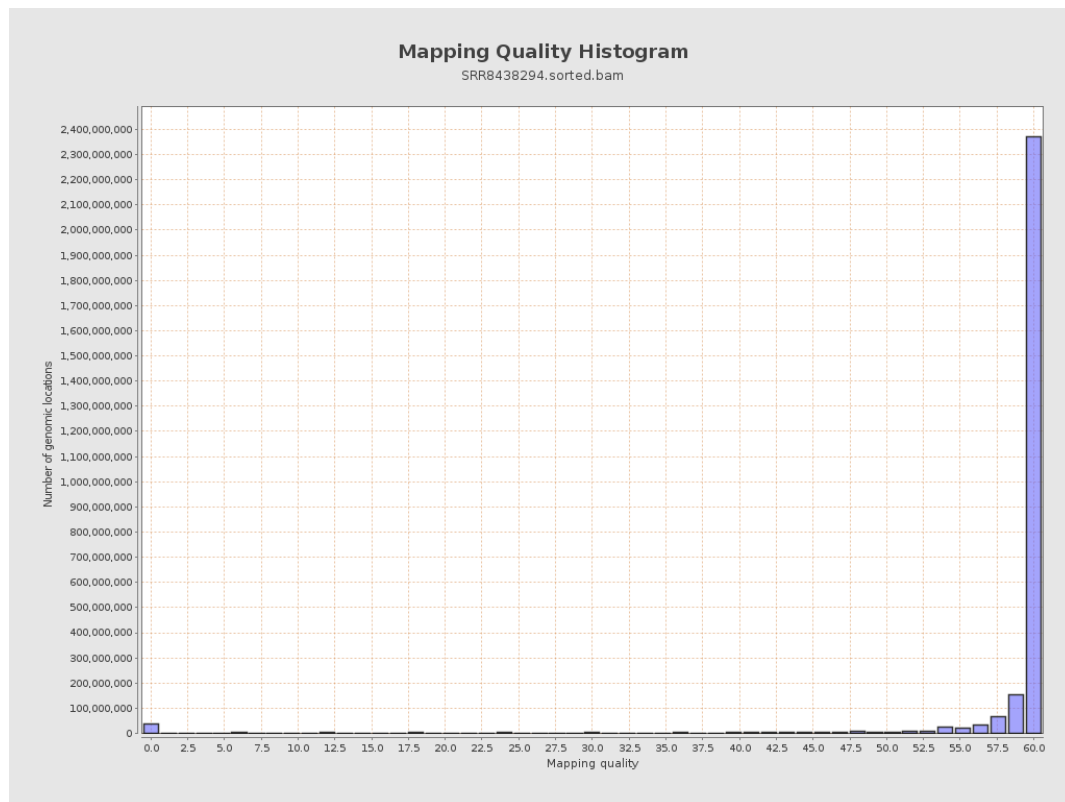
11. Results : Homopolymer Indels



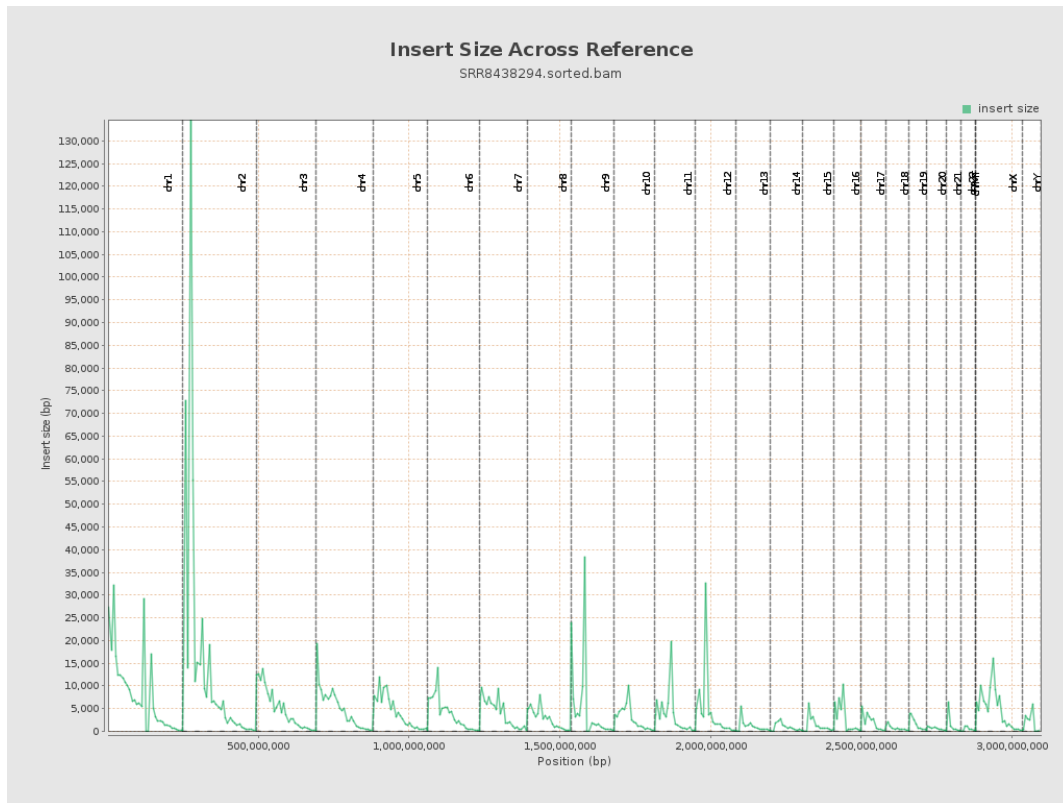
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

