

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/08 23:42:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124855.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_SRR3124855 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124855_1.fastq.gz SRR3124855_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 08 23:42:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124855.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	74,665,198
Mapped reads	68,450,221 / 91.68%
Unmapped reads	6,214,977 / 8.32%
Mapped paired reads	68,450,221 / 91.68%
Mapped reads, first in pair	35,253,107 / 47.21%
Mapped reads, second in pair	33,197,114 / 44.46%
Mapped reads, both in pair	65,604,178 / 87.86%
Mapped reads, singletons	2,846,043 / 3.81%
Secondary alignments	0
Supplementary alignments	2,204,549 / 2.95%
Read min/max/mean length	30 / 150 / 151.39
Duplicated reads (estimated)	22,705,181 / 30.41%
Duplication rate	20.37%
Clipped reads	41,030,269 / 54.95%

2.2. ACGT Content

Number/percentage of A's	2,563,078,430 / 28.9%
Number/percentage of C's	1,709,945,502 / 19.28%
Number/percentage of T's	2,619,156,659 / 29.53%
Number/percentage of G's	1,976,772,901 / 22.29%
Number/percentage of N's	148,653 / 0%

GC Percentage	41.57%
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2.3. Coverage

Mean	2.8676
Standard Deviation	39.2812

2.4. Mapping Quality

Mean Mapping Quality	53.05
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2.5. Insert size

Mean	186,412.4
Standard Deviation	4,102,100.63
P25/Median/P75	198 / 258 / 327

2.6. Mismatches and indels

General error rate	1.41%
Mismatches	118,536,678
Insertions	1,982,046
Mapped reads with at least one insertion	2.65%
Deletions	3,603,291
Mapped reads with at least one deletion	5%
Homopolymer indels	43.01%

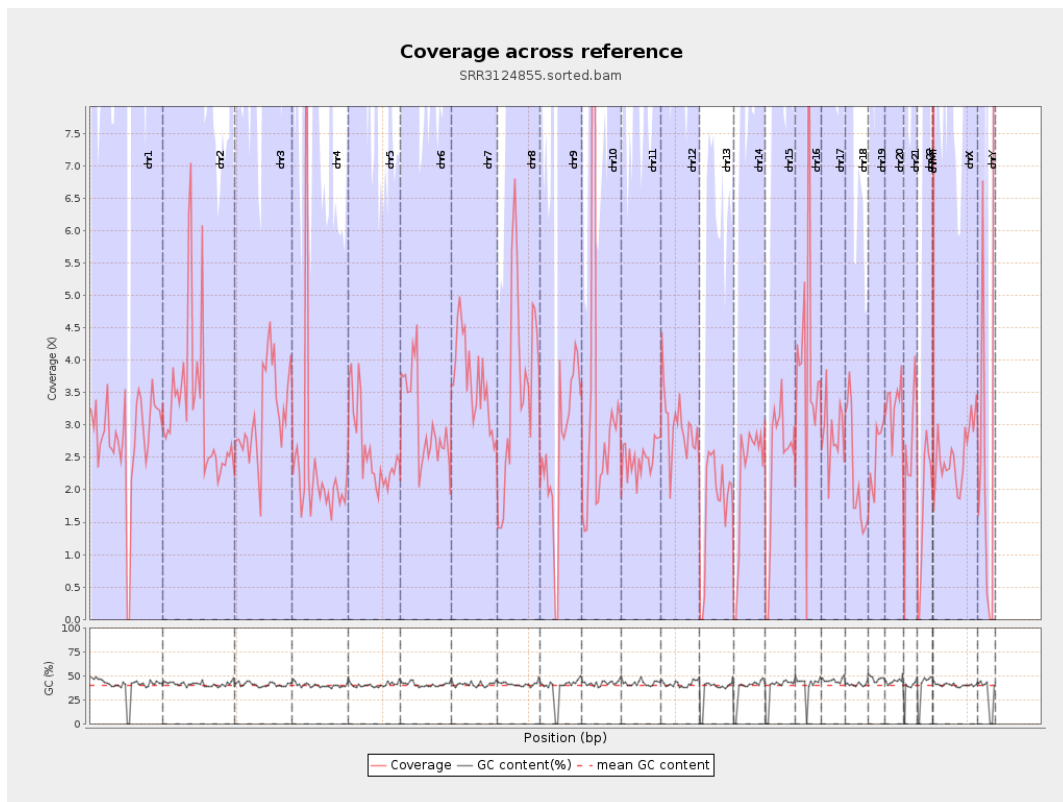
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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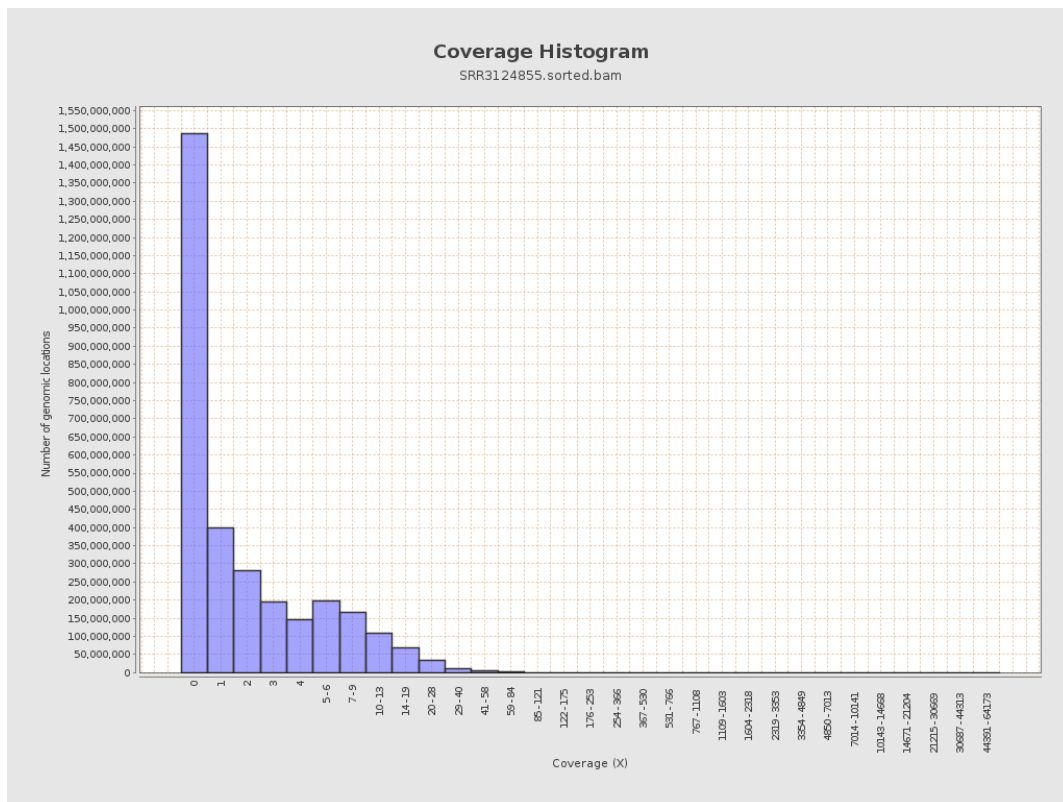
		bases	coverage	deviation
chr1	249250621	696310531	2.7936	19.6858
chr2	243199373	792573296	3.2589	48.4432
chr3	198022430	627355279	3.1681	6.3861
chr4	191154276	460181747	2.4074	60.1991
chr5	180915260	470774700	2.6022	6.6816
chr6	171115067	522715860	3.0548	11.2994
chr7	159138663	583704096	3.6679	22.0247
chr8	146364022	533519786	3.6452	9.8852
chr9	141213431	379258797	2.6857	33.4254
chr10	135534747	450190689	3.3216	122.4446
chr11	135006516	335126639	2.4823	9.836
chr12	133851895	402784403	3.0092	20.3461
chr13	115169878	205534287	1.7846	3.9227
chr14	107349540	238418356	2.221	6.0809
chr15	102531392	242970231	2.3697	9.4479
chr16	90354753	363107463	4.0187	58.8145
chr17	81195210	233587612	2.8769	22.8227
chr18	78077248	175293896	2.2451	30.849
chr19	59128983	149428817	2.5272	12.3946
chr20	63025520	209135792	3.3183	21.8512
chr21	48129895	127593842	2.651	29.2826
chr22	51304566	90609911	1.7661	6.7766
chrMT	16571	6742807	406.904	188.3611
chrX	155270560	394705064	2.542	7.39

chrY	59373566	185706540	3.1278	90.7937
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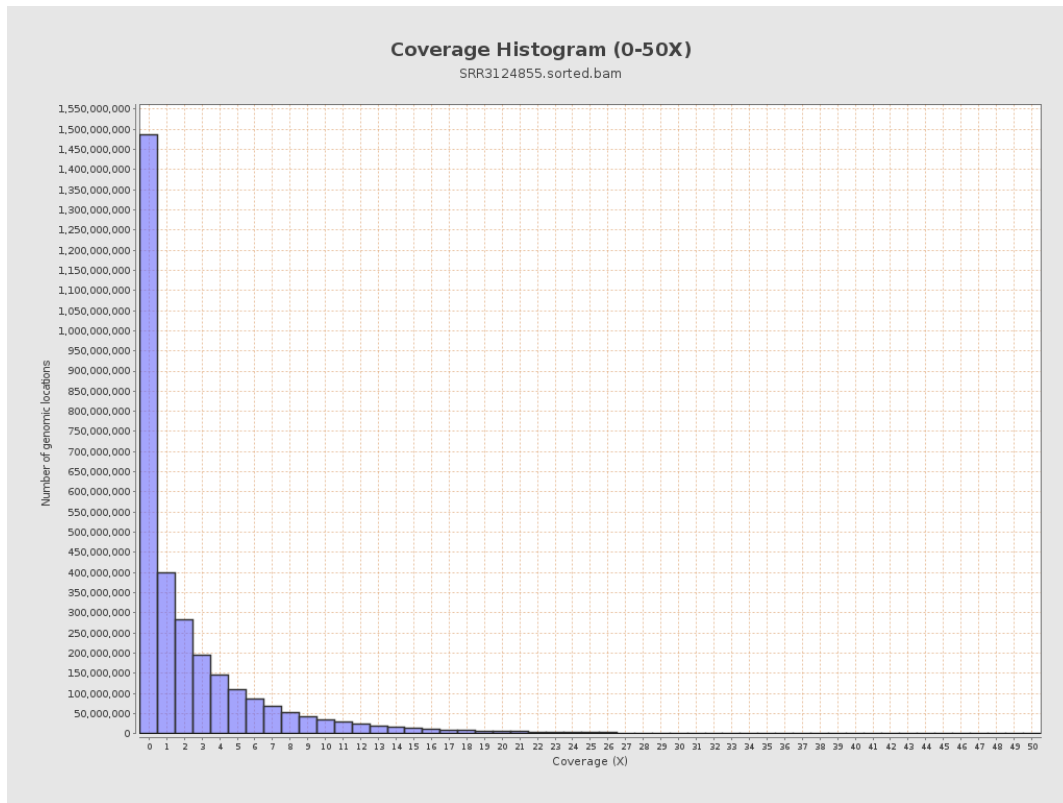
3. Results : Coverage across reference



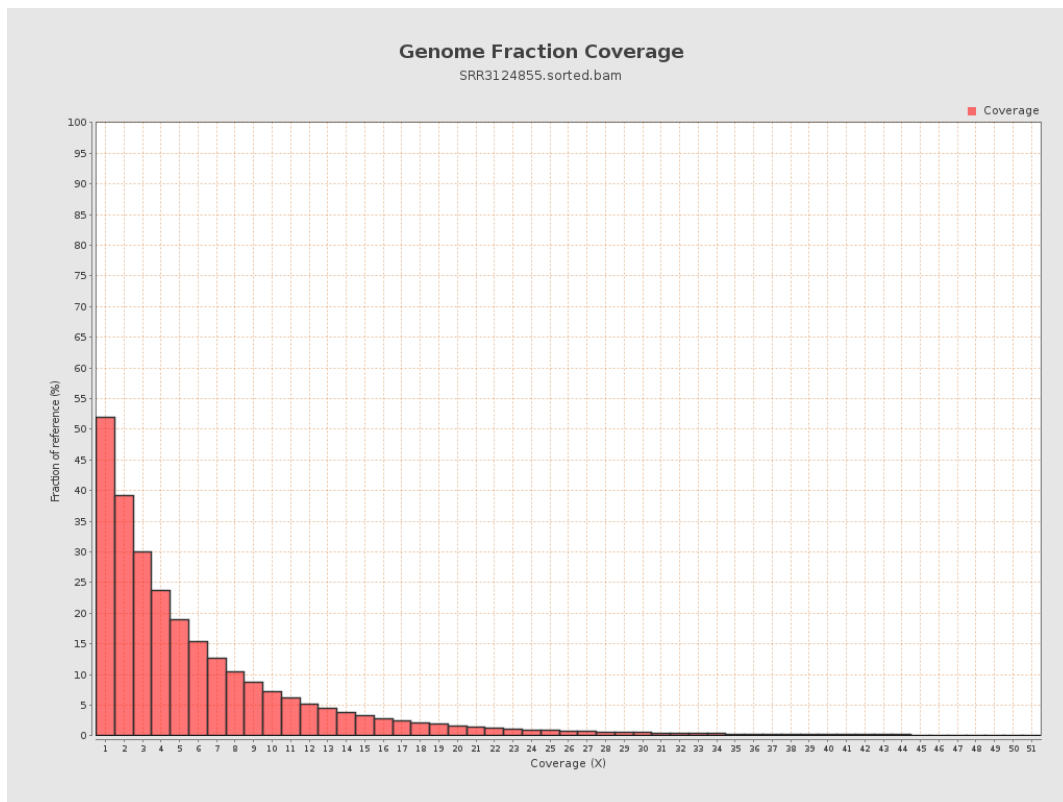
4. Results : Coverage Histogram



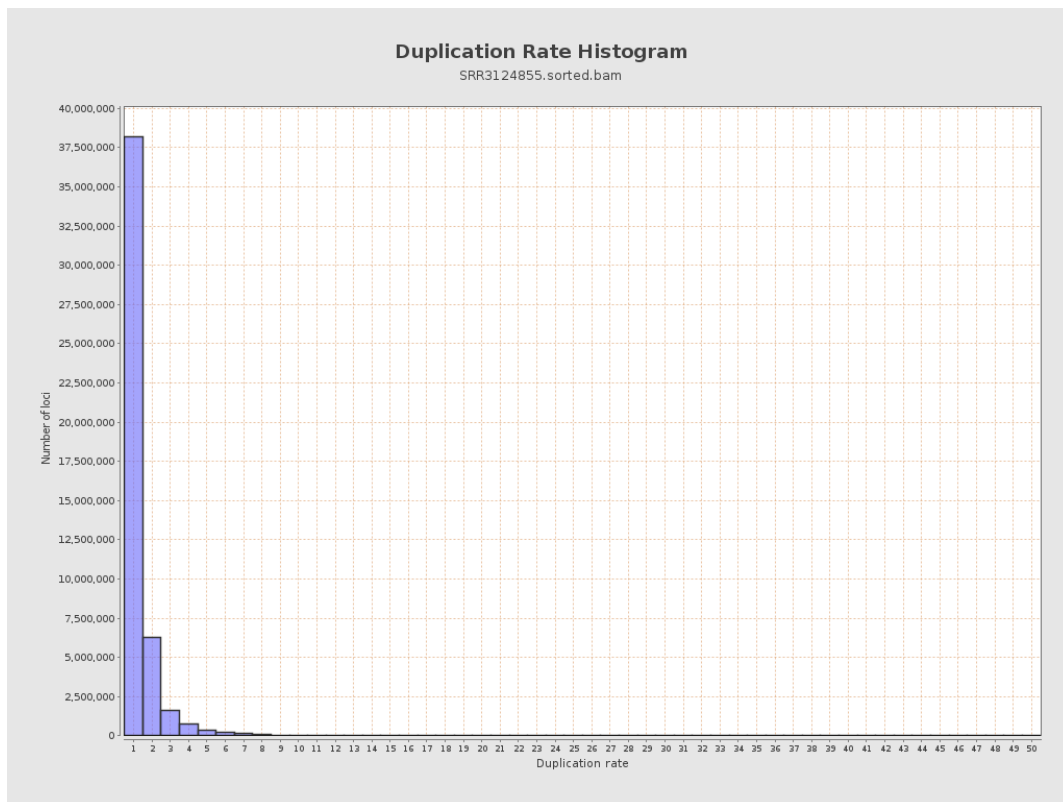
5. Results : Coverage Histogram (0-50X)



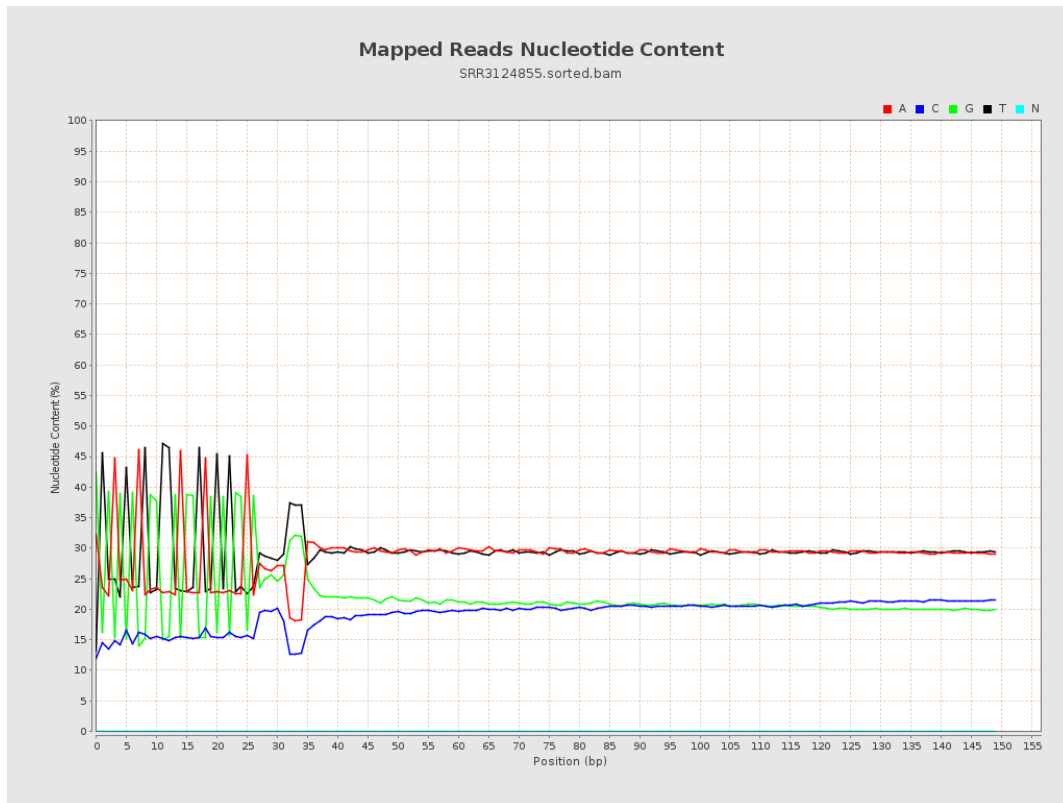
6. Results : Genome Fraction Coverage



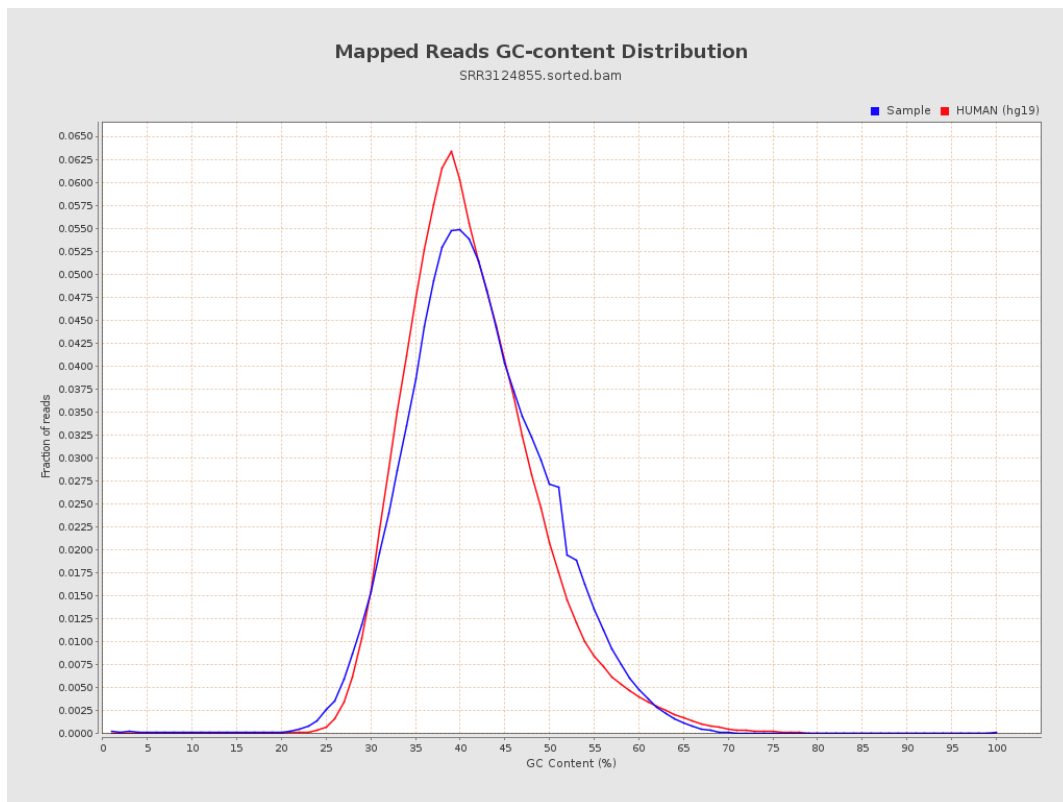
7. Results : Duplication Rate Histogram



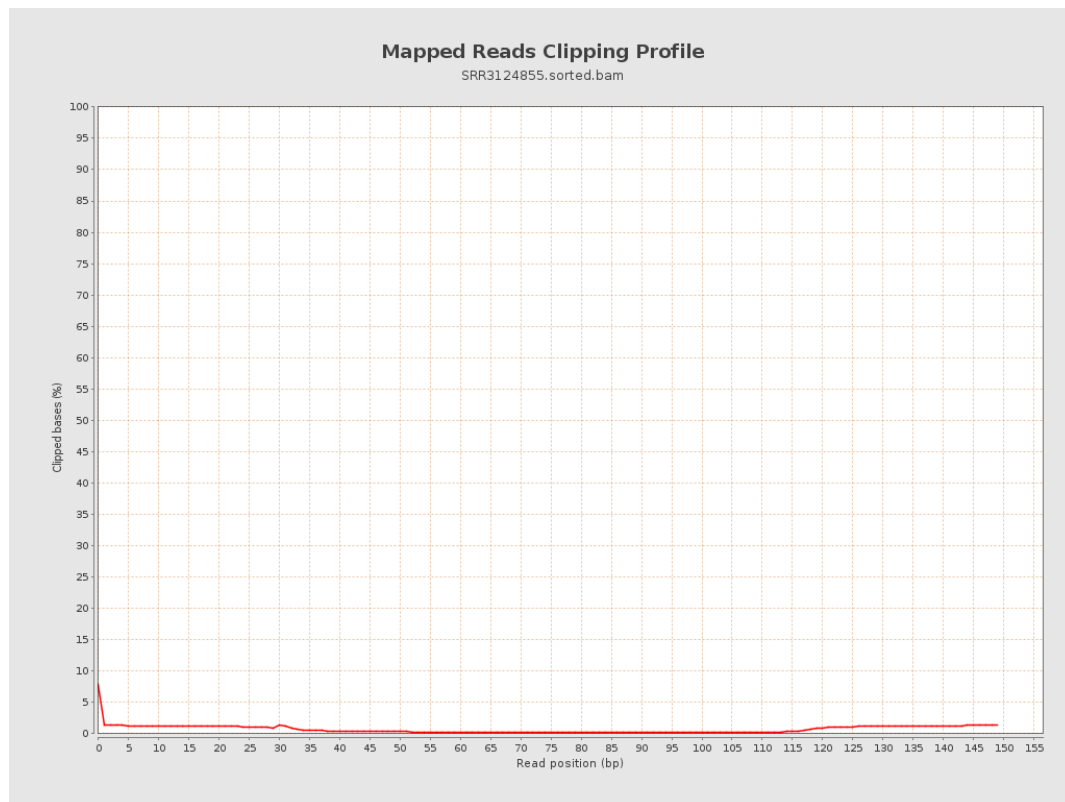
8. Results : Mapped Reads Nucleotide Content



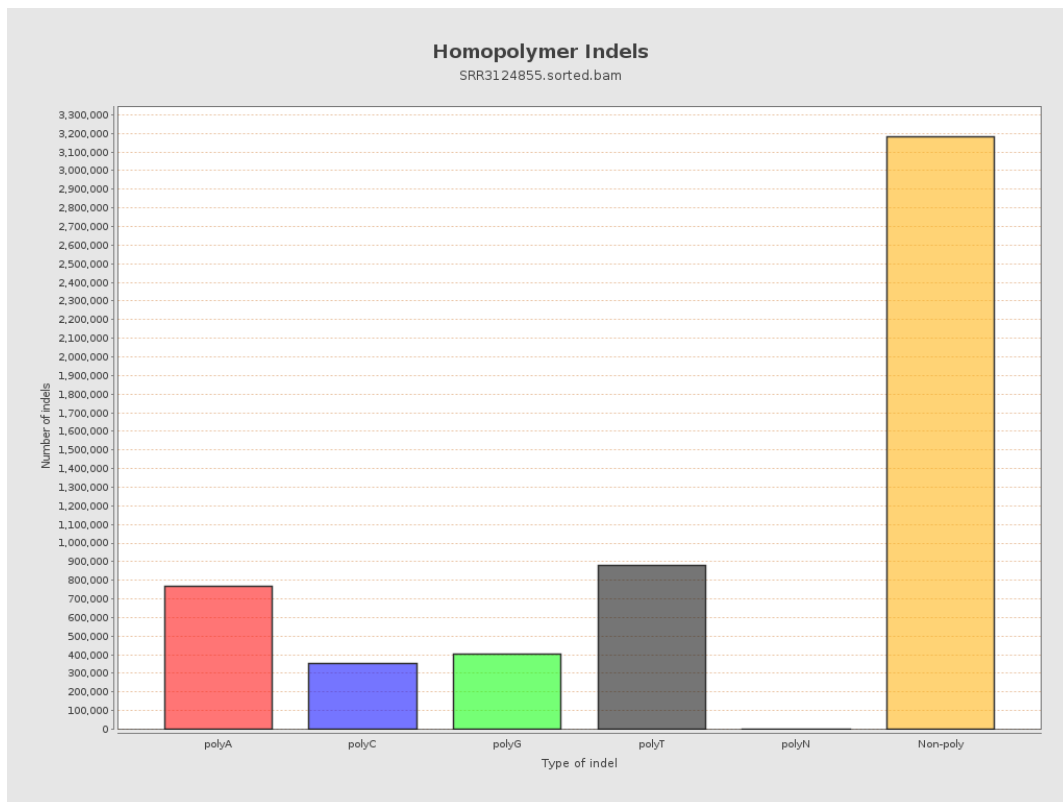
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



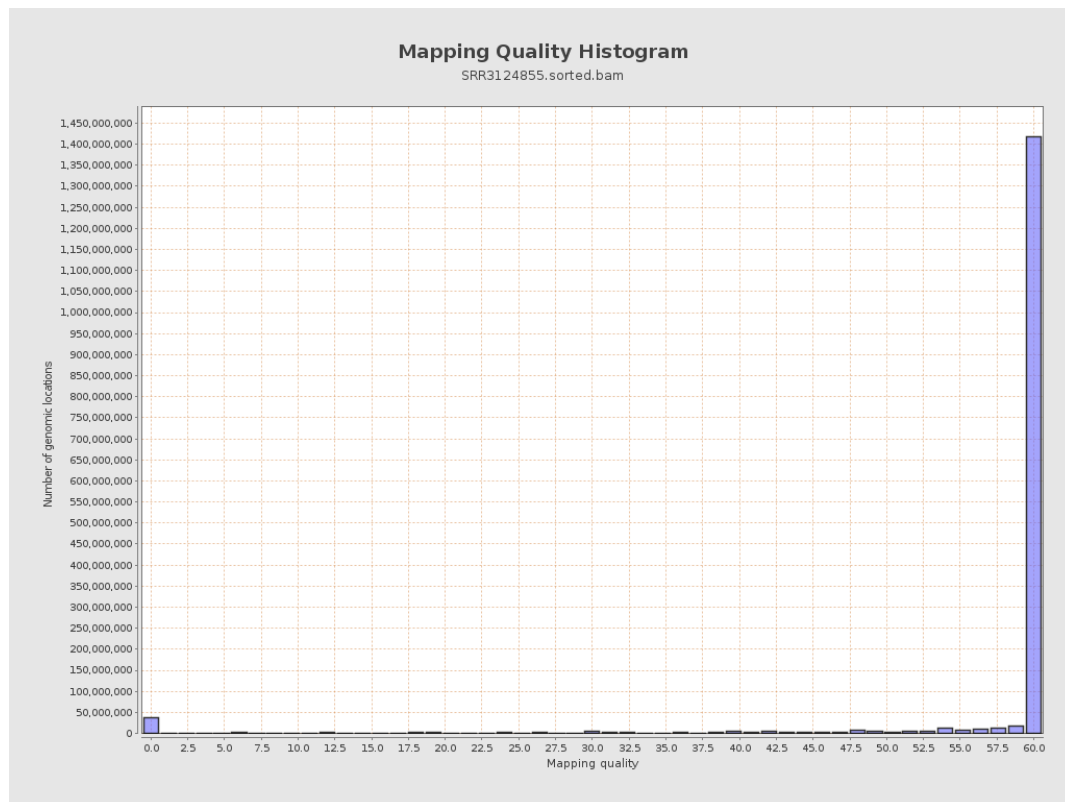
11. Results : Homopolymer Indels



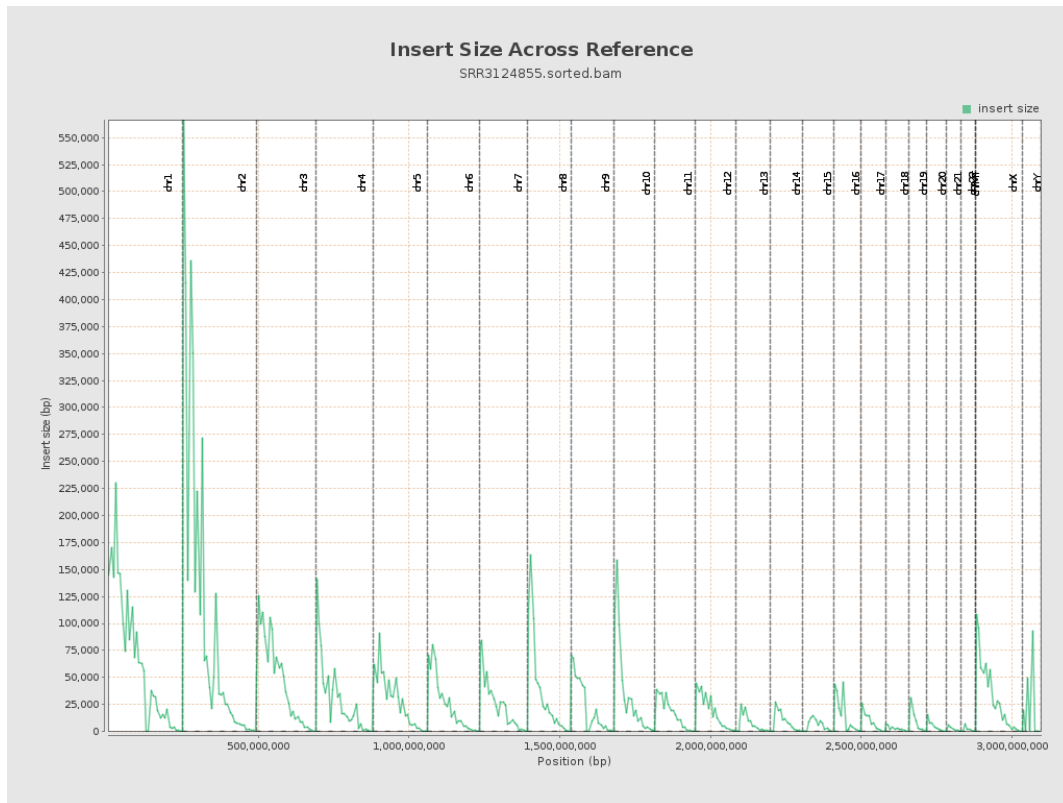
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

