

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/05 03:17:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960895.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_SRR960895 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960895_1.fastq.gz SRR960895_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 05 03:17:38 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960895.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	221,315,980
Mapped reads	217,350,267 / 98.21%
Unmapped reads	3,965,713 / 1.79%
Mapped paired reads	217,350,267 / 98.21%
Mapped reads, first in pair	109,010,315 / 49.26%
Mapped reads, second in pair	108,339,952 / 48.95%
Mapped reads, both in pair	215,897,206 / 97.55%
Mapped reads, singletons	1,453,061 / 0.66%
Secondary alignments	0
Supplementary alignments	368,740 / 0.17%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	30,614,984 / 13.83%
Duplication rate	9.44%
Clipped reads	37,949,577 / 17.15%

2.2. ACGT Content

Number/percentage of A's	6,476,894,265 / 30.52%
Number/percentage of C's	4,145,530,854 / 19.53%
Number/percentage of T's	6,469,410,016 / 30.48%
Number/percentage of G's	4,129,448,192 / 19.46%
Number/percentage of N's	3,132,890 / 0.01%

GC Percentage	38.99%
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2.3. Coverage

Mean	6.8581
Standard Deviation	91.8602

2.4. Mapping Quality

Mean Mapping Quality	53.6
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2.5. Insert size

Mean	15,239.15
Standard Deviation	1,152,644.84
P25/Median/P75	136 / 164 / 192

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	289,132,095
Insertions	2,646,980
Mapped reads with at least one insertion	1.19%
Deletions	2,709,944
Mapped reads with at least one deletion	1.21%
Homopolymer indels	39.93%

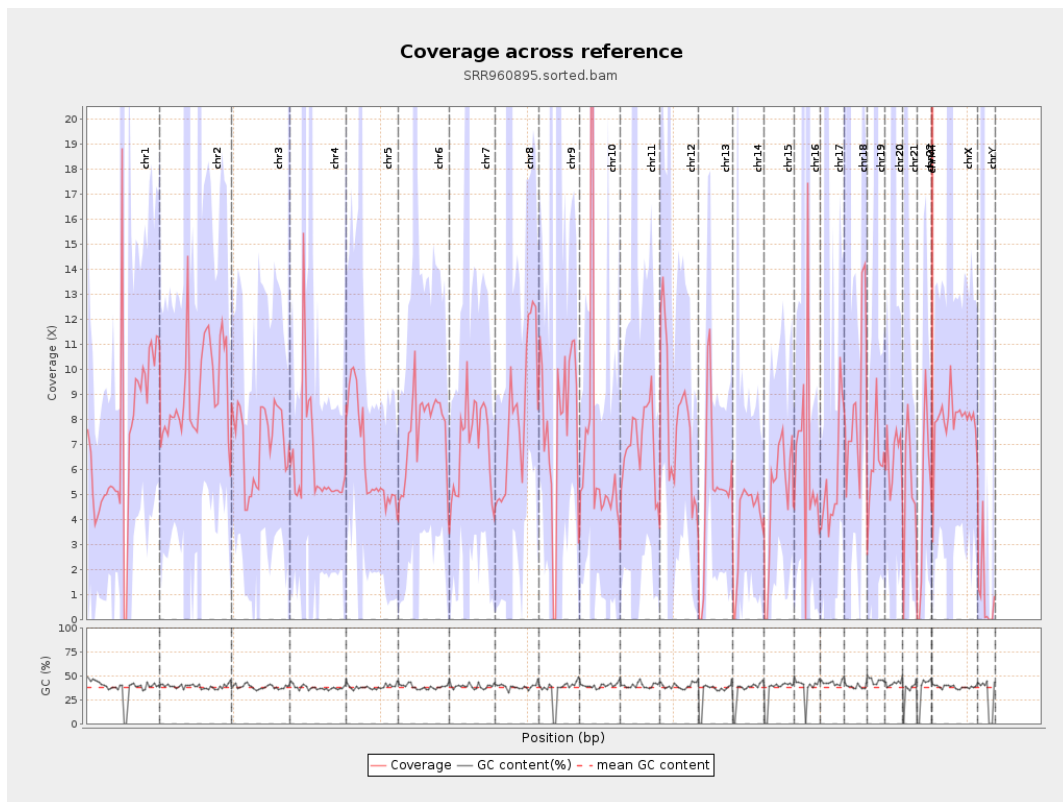
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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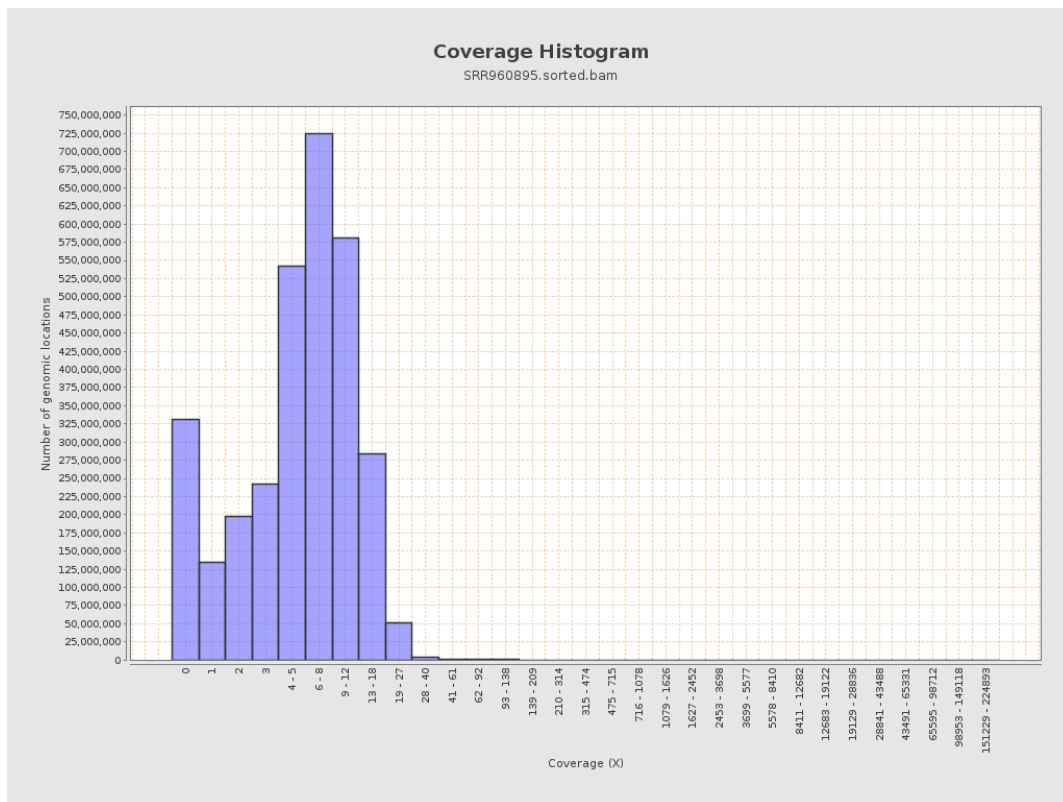
		bases	coverage	deviation
chr1	249250621	1799676487	7.2203	229.8374
chr2	243199373	2232022714	9.1777	48.9168
chr3	198022430	1396398856	7.0517	13.818
chr4	191154276	1181875904	6.1828	72.5679
chr5	180915260	1148677616	6.3493	8.0061
chr6	171115067	1301304713	7.6049	27.2002
chr7	159138663	1101358949	6.9208	58.4079
chr8	146364022	1212665947	8.2853	91.8622
chr9	141213431	1074353632	7.608	74.4623
chr10	135534747	941488556	6.9465	214.9226
chr11	135006516	941102285	6.9708	35.4079
chr12	133851895	1073807962	8.0224	7.6812
chr13	115169878	597313761	5.1864	4.6313
chr14	107349540	422175202	3.9327	6.7702
chr15	102531392	519117578	5.063	4.5587
chr16	90354753	574894483	6.3626	84.054
chr17	81195210	452102271	5.5681	23.6965
chr18	78077248	670011396	8.5814	78.1896
chr19	59128983	368838554	6.2379	101.1818
chr20	63025520	410808783	6.5181	21.2589
chr21	48129895	265473173	5.5158	29.6052
chr22	51304566	244183929	4.7595	6.0815
chrMT	16571	8426348	508.4997	110.8611
chrX	155270560	1234192890	7.9487	25.1569

chrY	59373566	58280673	0.9816	62.8175
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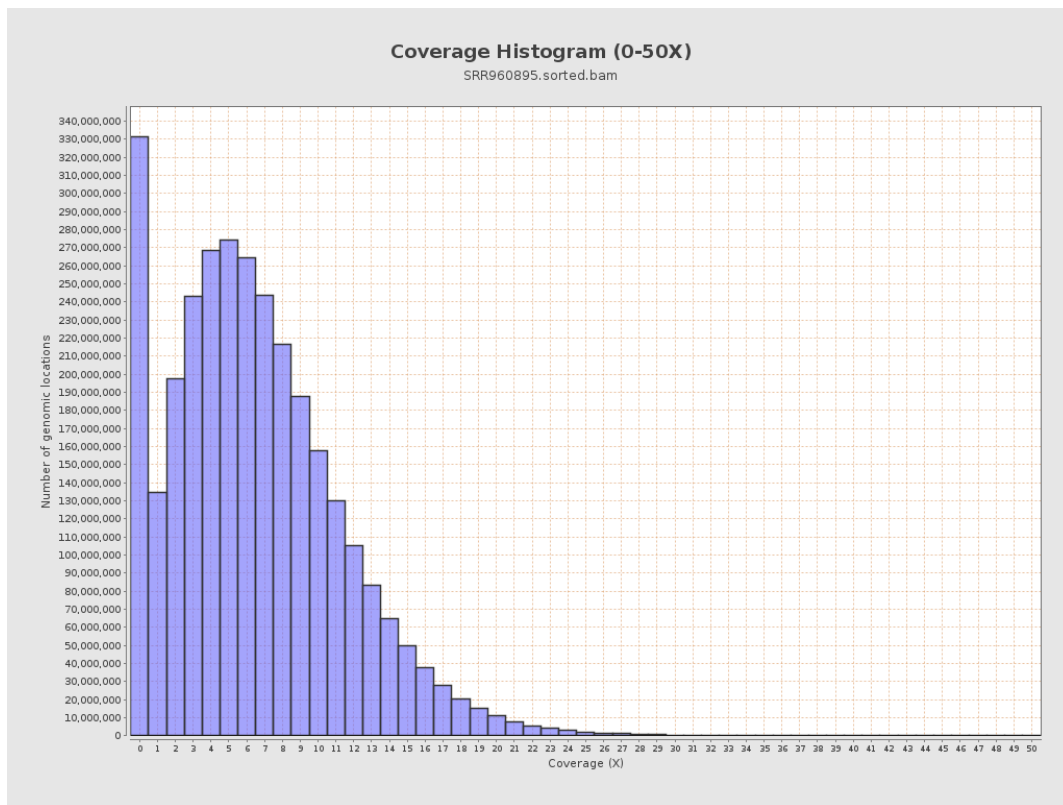
3. Results : Coverage across reference



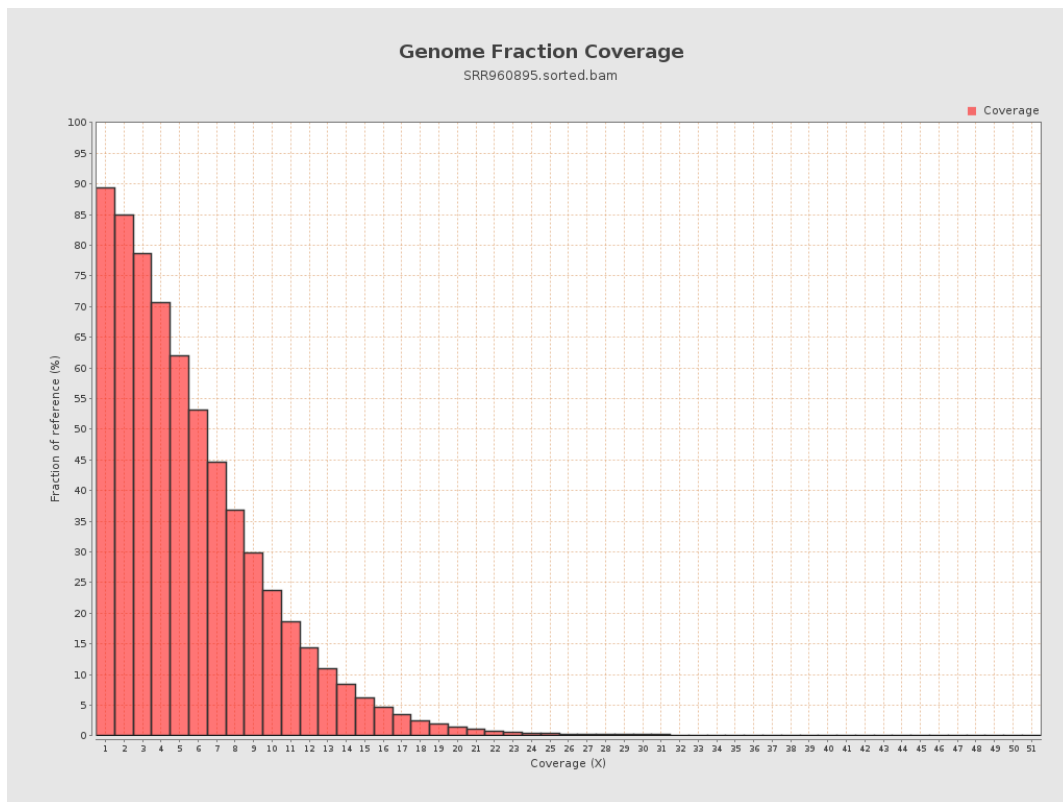
4. Results : Coverage Histogram



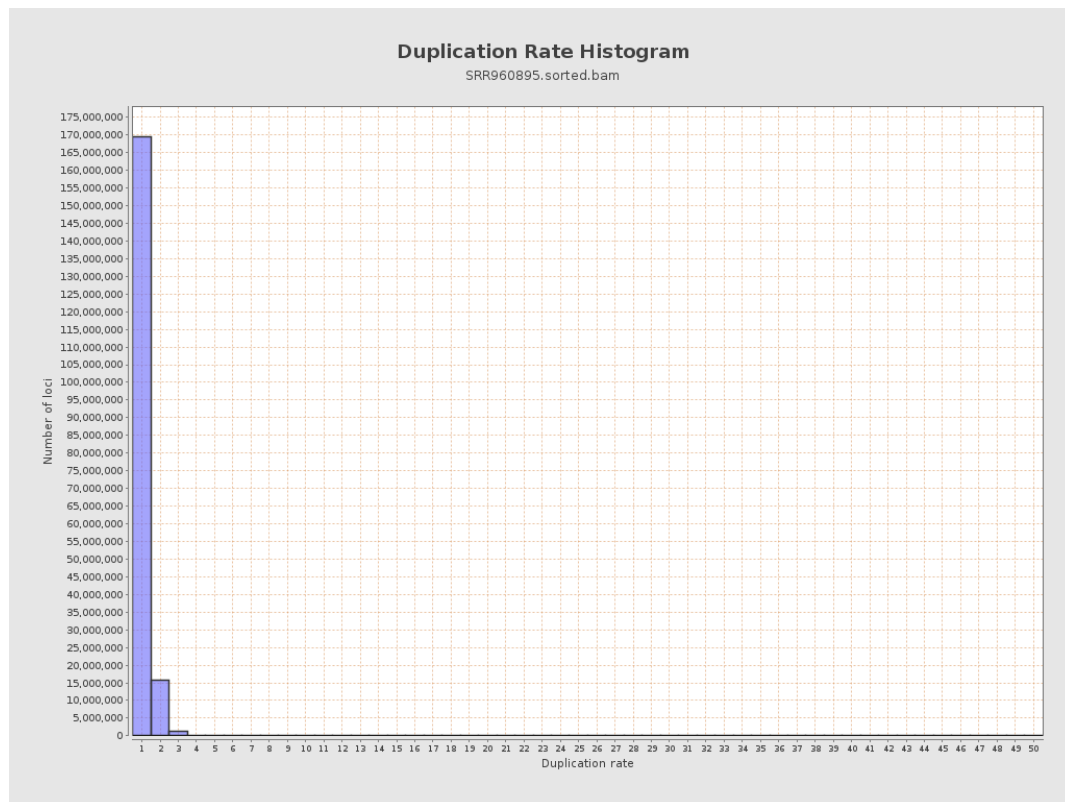
5. Results : Coverage Histogram (0-50X)



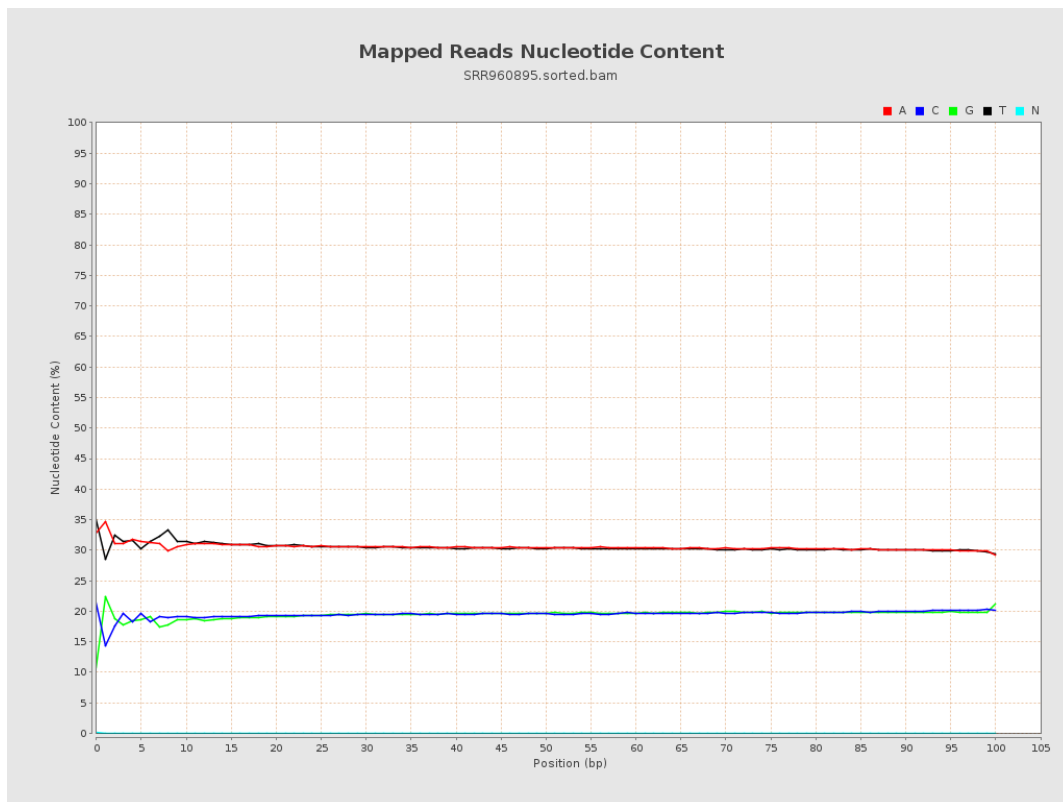
6. Results : Genome Fraction Coverage



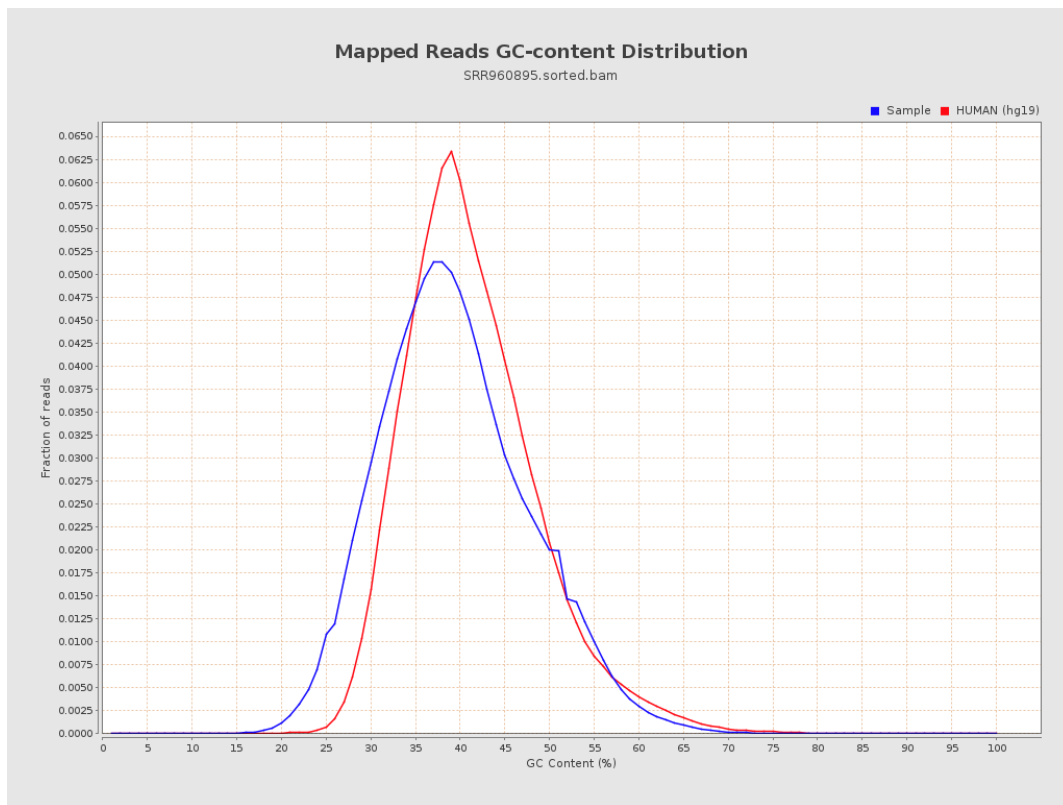
7. Results : Duplication Rate Histogram



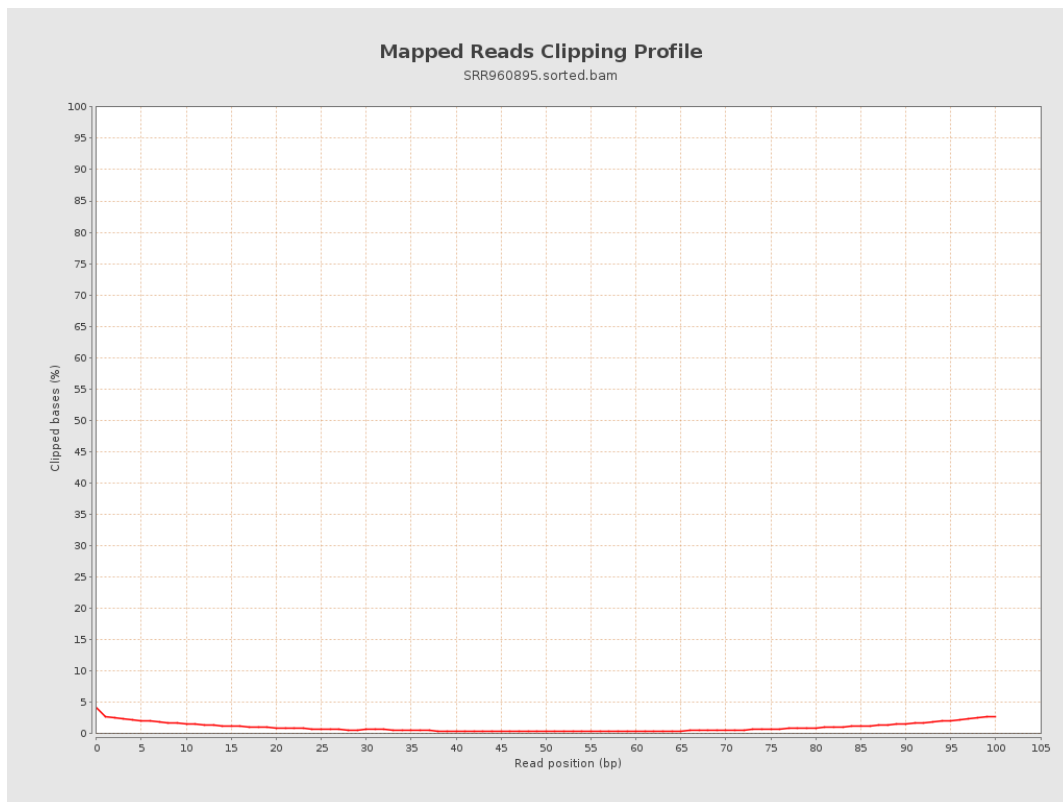
8. Results : Mapped Reads Nucleotide Content



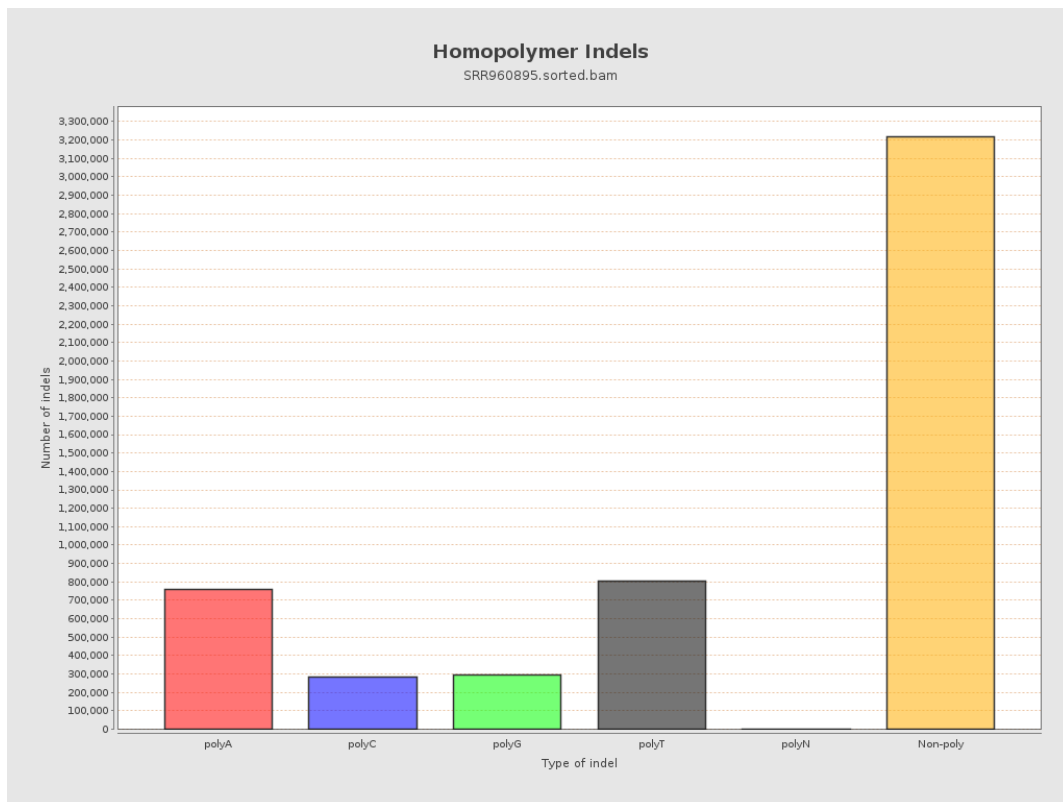
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



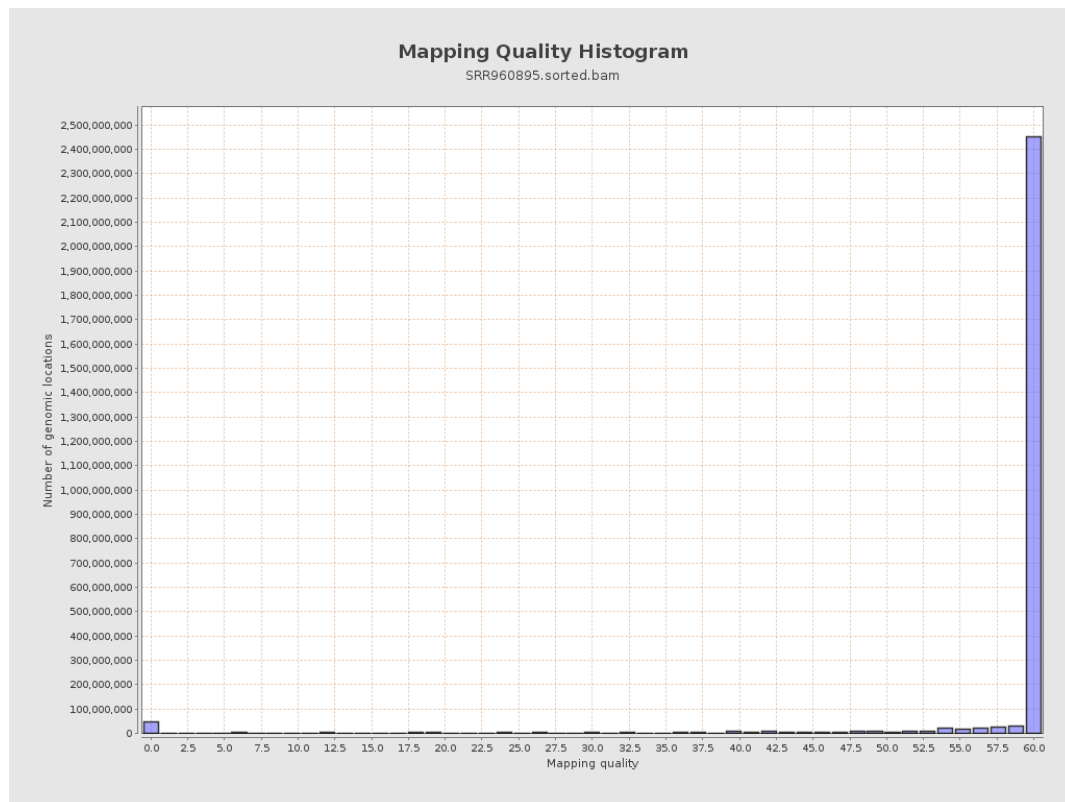
11. Results : Homopolymer Indels



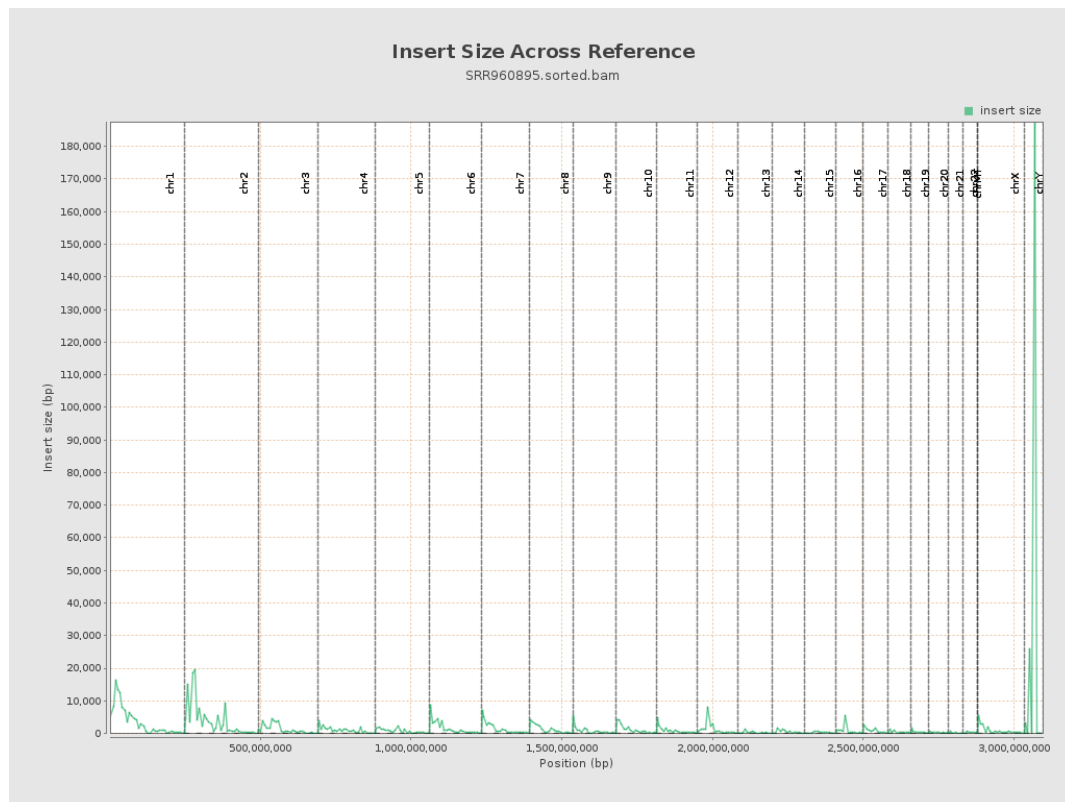
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

