

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 04:12:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926894.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_SRR926894 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926894_1.fastq.gz SRR926894_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 04:12:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926894.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,430,458
Mapped reads	29,489,802 / 96.91%
Unmapped reads	940,656 / 3.09%
Mapped paired reads	29,489,802 / 96.91%
Mapped reads, first in pair	14,744,127 / 48.45%
Mapped reads, second in pair	14,745,675 / 48.46%
Mapped reads, both in pair	29,121,330 / 95.7%
Mapped reads, singletons	368,472 / 1.21%
Secondary alignments	0
Supplementary alignments	906,077 / 2.98%
Read min/max/mean length	30 / 101 / 102.24
Duplicated reads (estimated)	2,885,356 / 9.48%
Duplication rate	7.76%
Clipped reads	12,633,326 / 41.52%

2.2. ACGT Content

Number/percentage of A's	745,828,134 / 27.79%
Number/percentage of C's	543,316,279 / 20.24%
Number/percentage of T's	754,705,522 / 28.12%
Number/percentage of G's	640,098,064 / 23.85%
Number/percentage of N's	307,500 / 0.01%

GC Percentage	44.09%
---------------	--------

2.3. Coverage

Mean	0.8678
Standard Deviation	3.0103

2.4. Mapping Quality

Mean Mapping Quality	52.55
----------------------	-------

2.5. Insert size

Mean	288,974.57
Standard Deviation	5,340,069.57
P25/Median/P75	134 / 171 / 224

2.6. Mismatches and indels

General error rate	1%
Mismatches	25,962,082
Insertions	455,930
Mapped reads with at least one insertion	1.52%
Deletions	1,433,626
Mapped reads with at least one deletion	4.74%
Homopolymer indels	51.86%

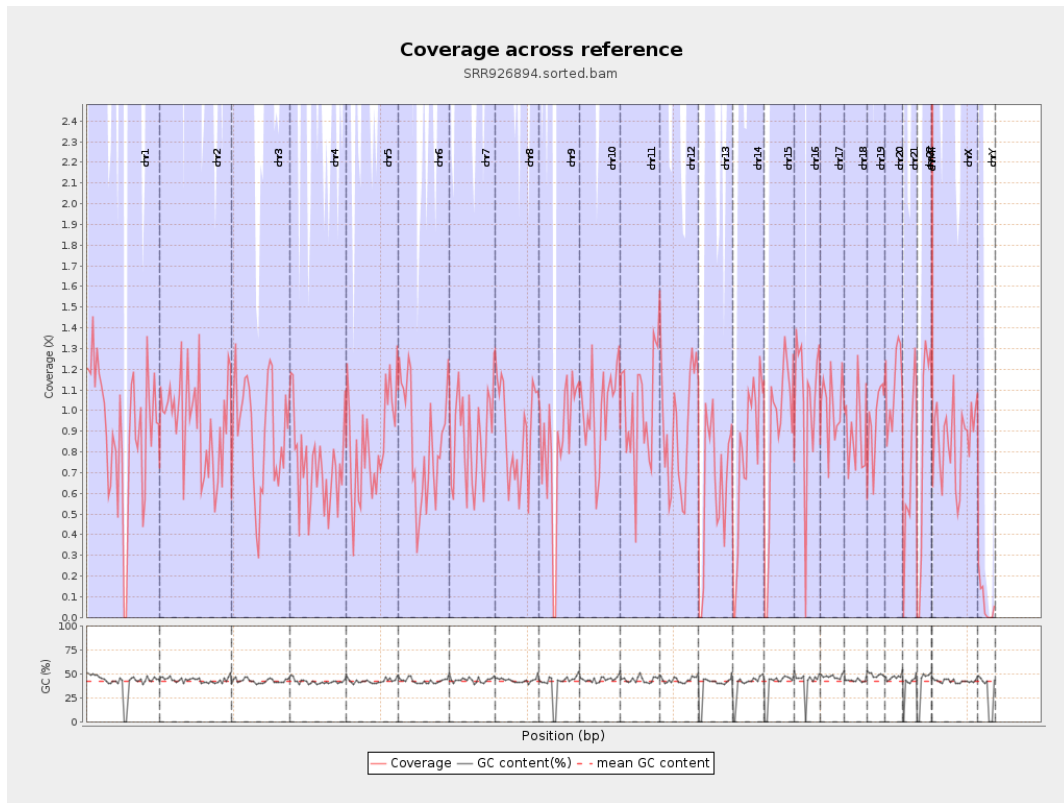
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

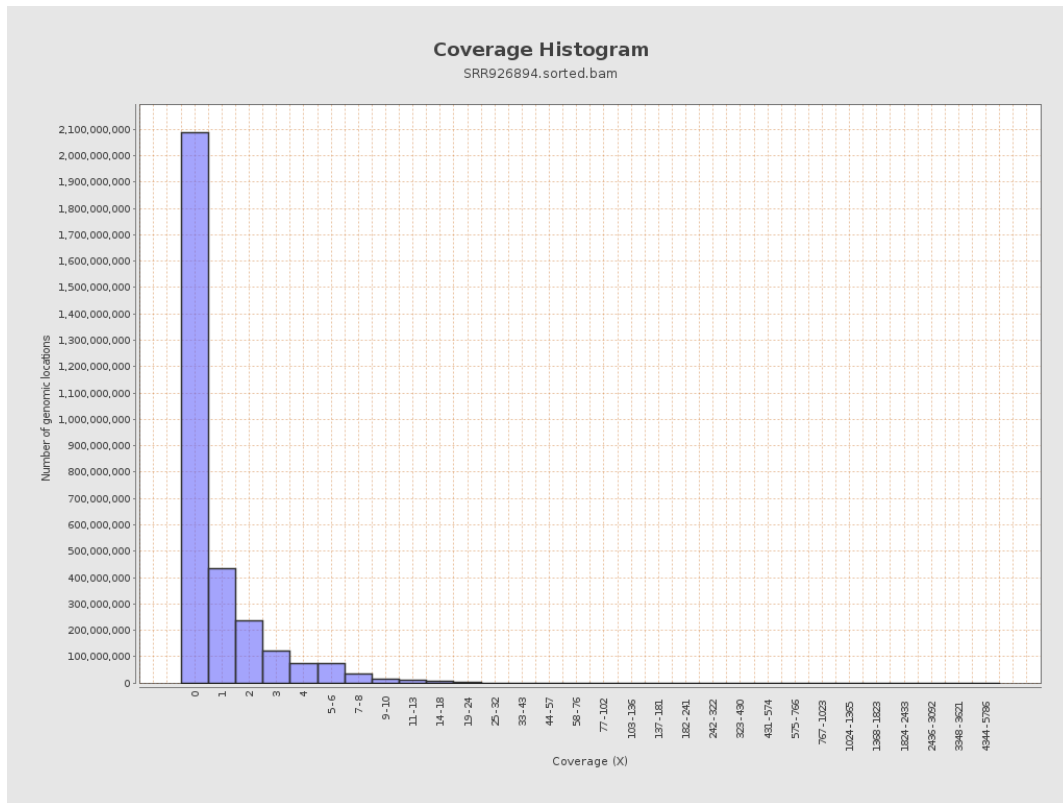
		bases	coverage	deviation
chr1	249250621	225129281	0.9032	2.6497
chr2	243199373	230406815	0.9474	5.3604
chr3	198022430	176787798	0.8928	1.9652
chr4	191154276	138714341	0.7257	2.1855
chr5	180915260	152514716	0.843	1.8751
chr6	171115067	144108636	0.8422	2.0153
chr7	159138663	137571645	0.8645	1.9803
chr8	146364022	129710039	0.8862	2.0789
chr9	141213431	118892375	0.8419	3.0141
chr10	135534747	137564209	1.015	6.718
chr11	135006516	135705259	1.0052	2.2576
chr12	133851895	121334802	0.9065	2.0492
chr13	115169878	72673296	0.631	1.6128
chr14	107349540	84430259	0.7865	1.8731
chr15	102531392	89374492	0.8717	2.0216
chr16	90354753	94485949	1.0457	4.4988
chr17	81195210	82728329	1.0189	2.2646
chr18	78077248	70441859	0.9022	2.558
chr19	59128983	57014659	0.9642	2.2743
chr20	63025520	70924266	1.1253	2.4004
chr21	48129895	35079374	0.7288	3.1419
chr22	51304566	43407877	0.8461	2.1915
chrMT	16571	1798335	108.523	67.9596
chrX	155270560	131448451	0.8466	1.9211

chrY	59373566	4136756	0.0697	2.0511
------	----------	---------	--------	--------

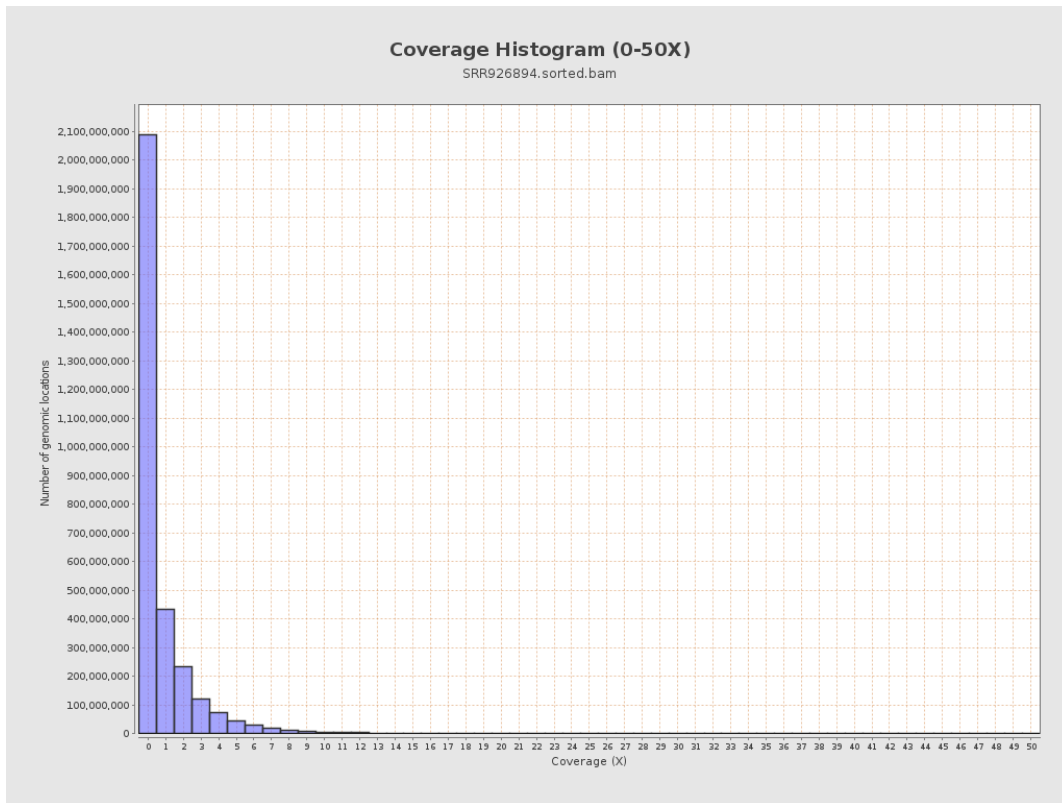
3. Results : Coverage across reference



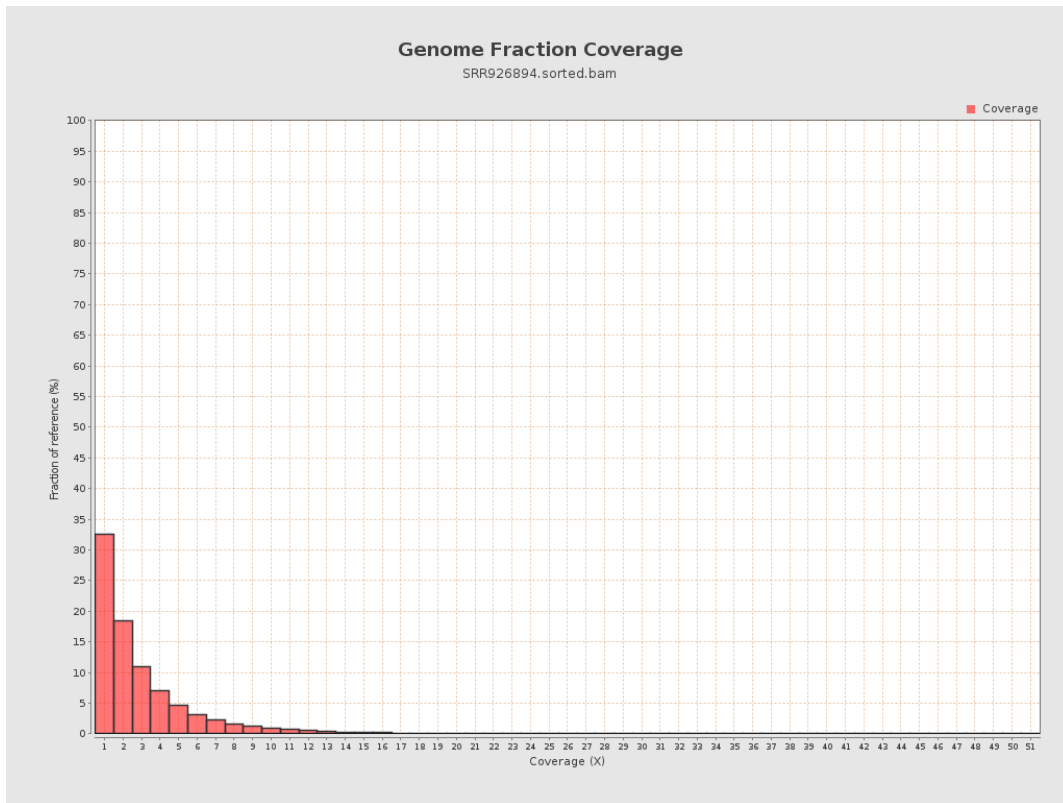
4. Results : Coverage Histogram



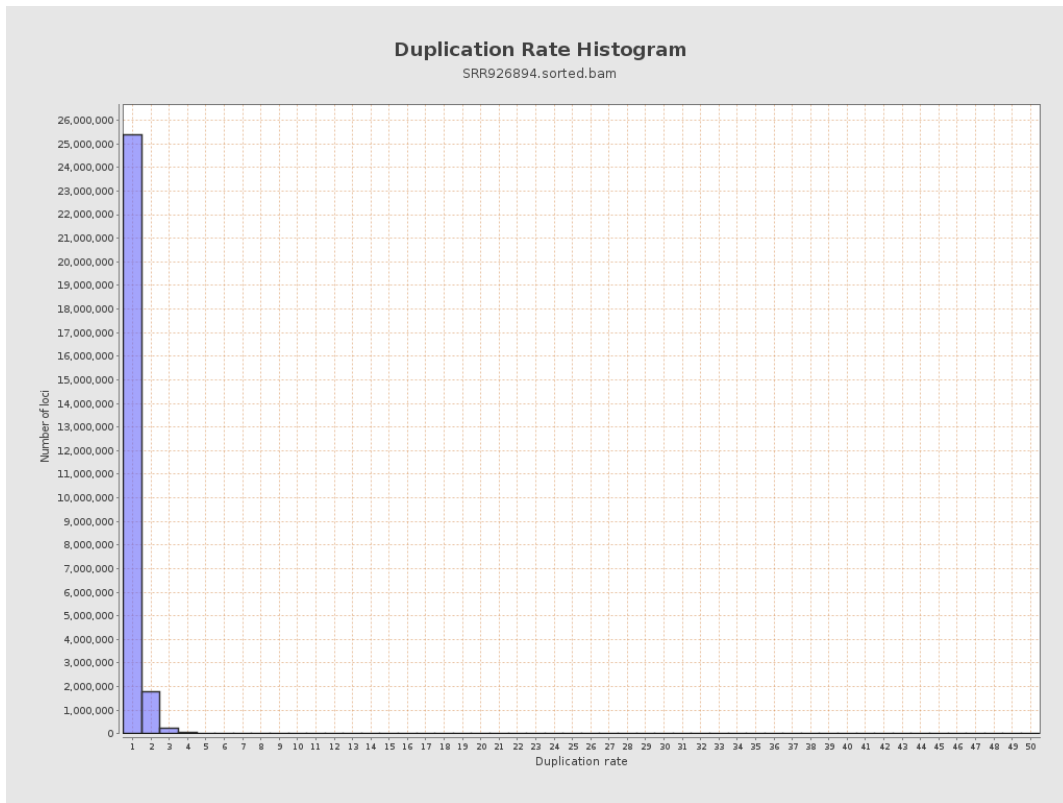
5. Results : Coverage Histogram (0-50X)



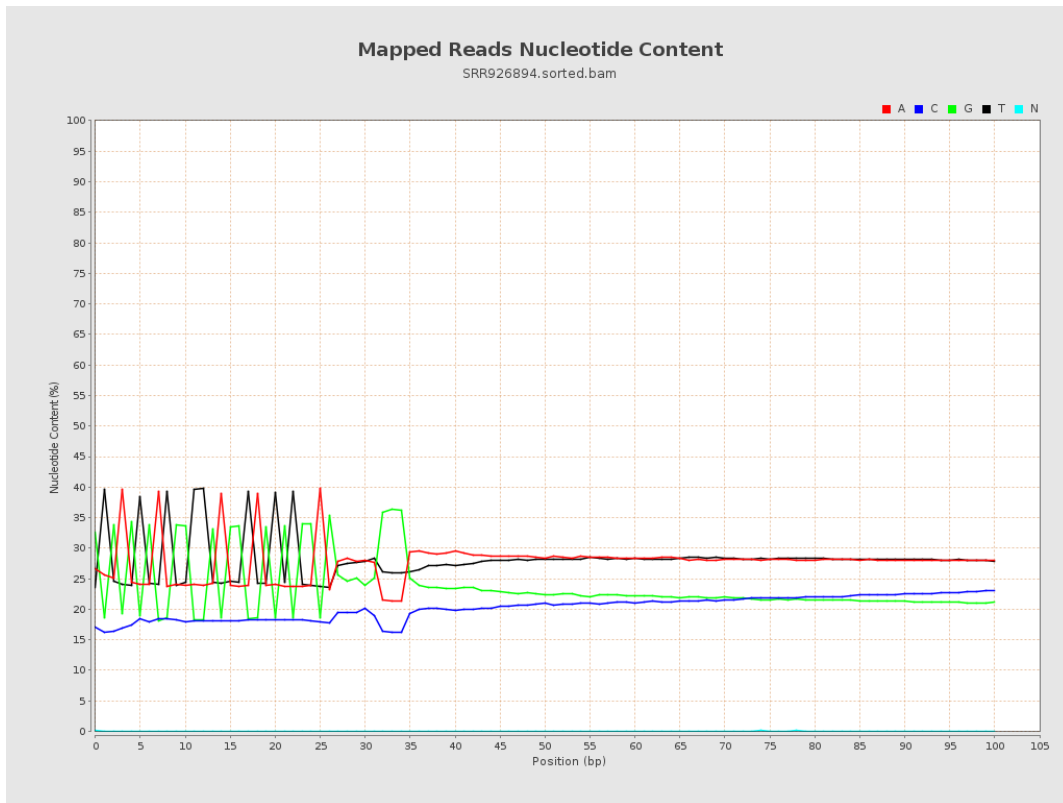
6. Results : Genome Fraction Coverage



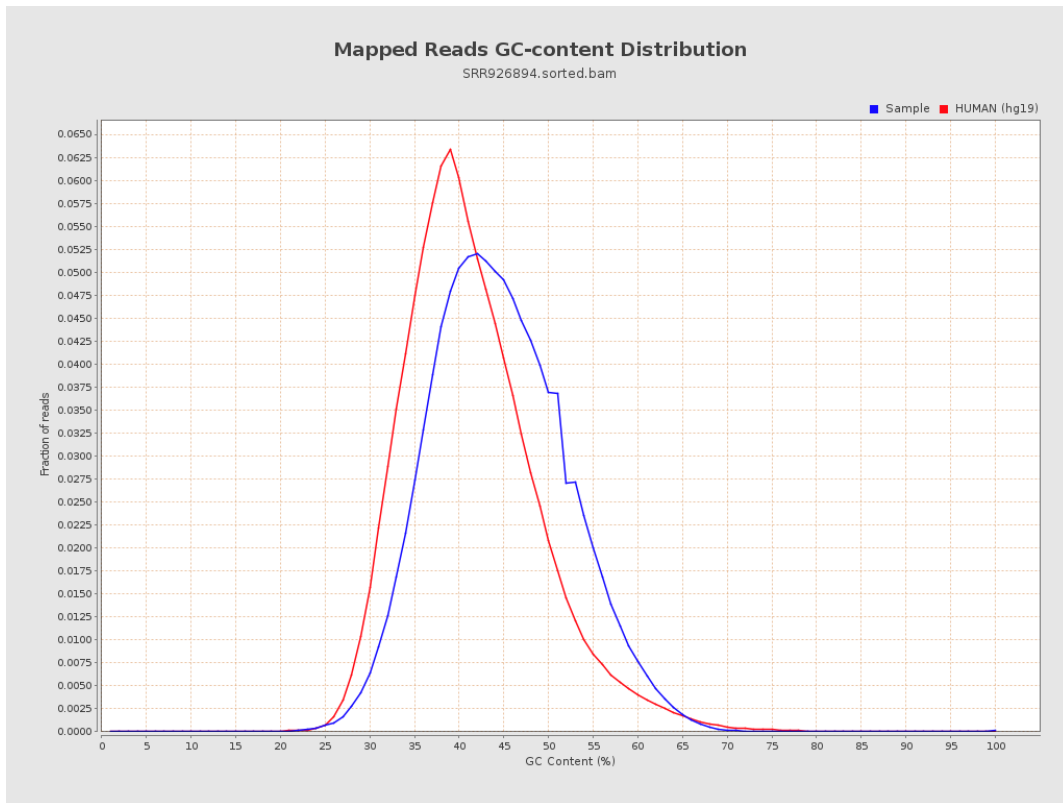
7. Results : Duplication Rate Histogram



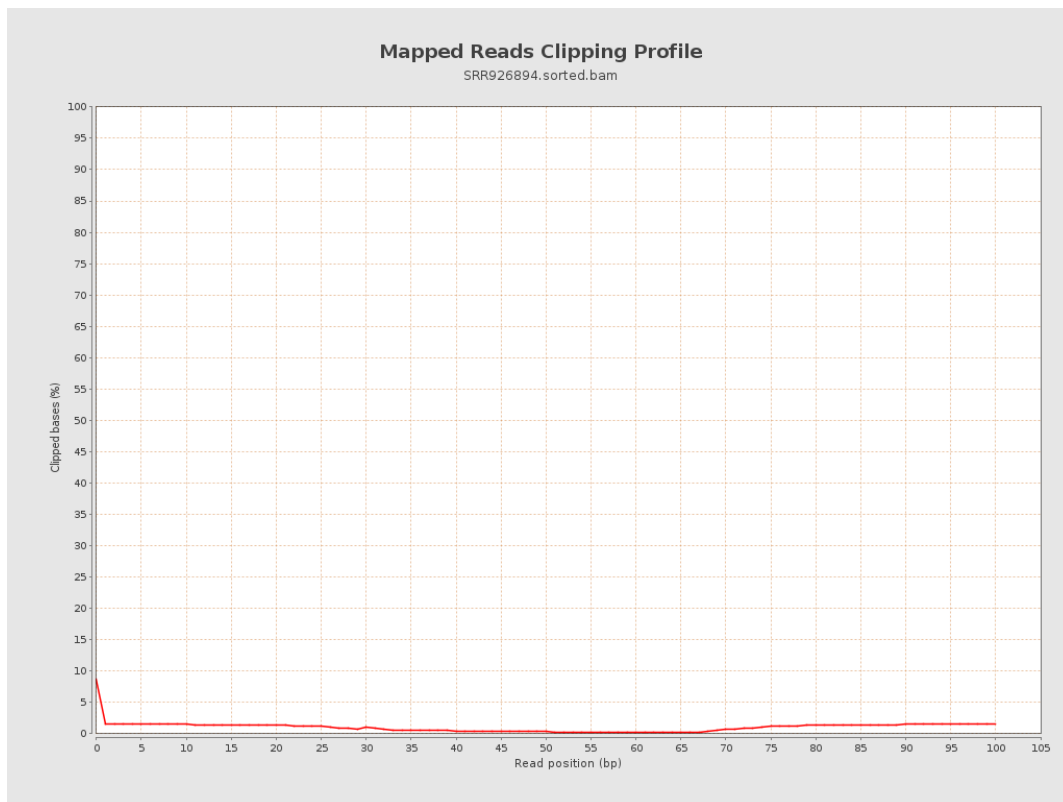
8. Results : Mapped Reads Nucleotide Content



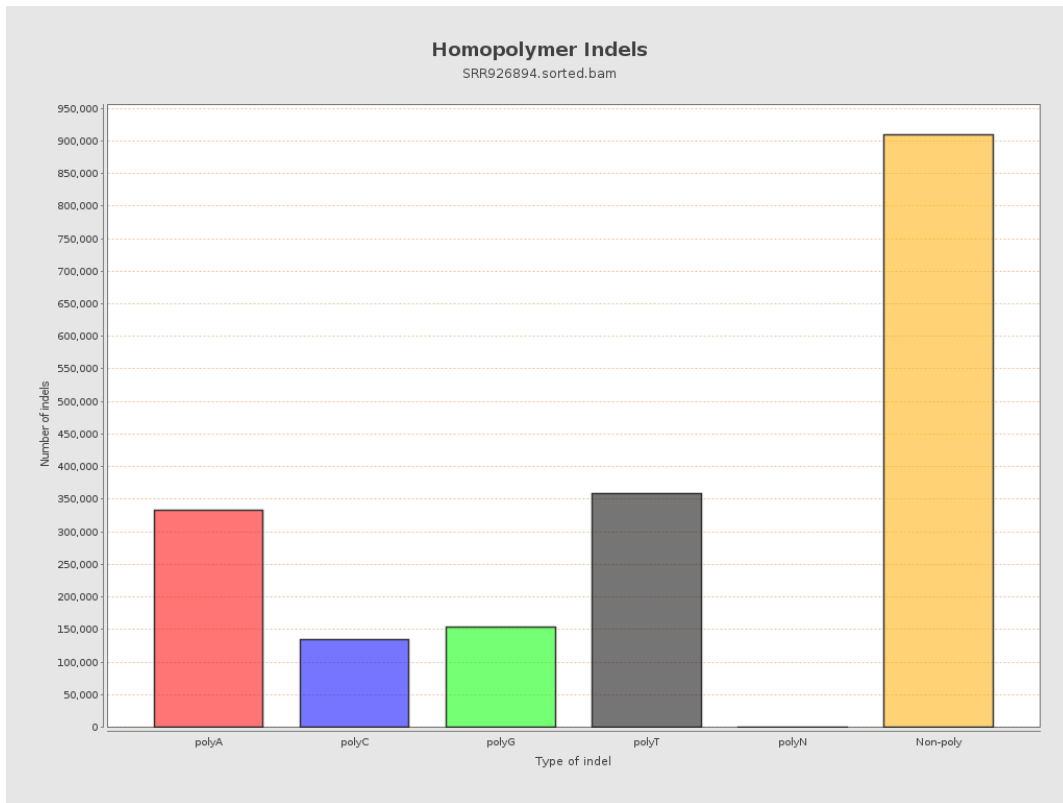
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



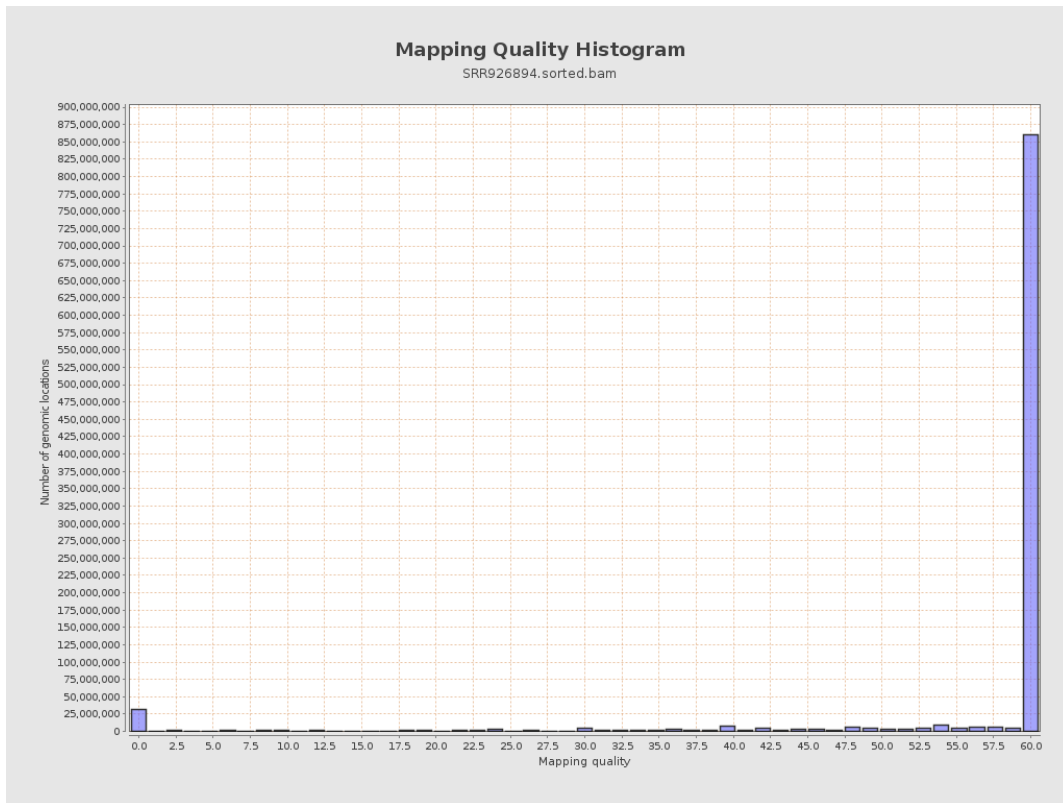
11. Results : Homopolymer Indels



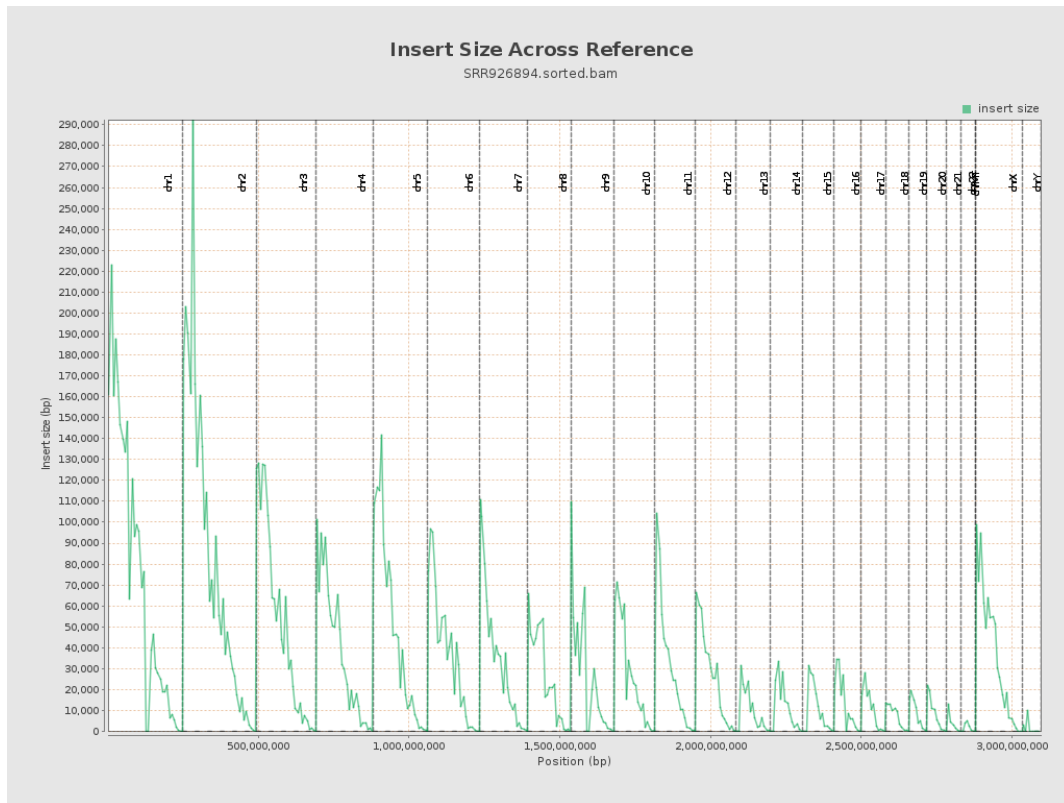
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

