

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 22:37:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926999.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_SRR926999 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926999_1.fastq.gz SRR926999_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 22:37:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926999.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	38,018,954
Mapped reads	37,409,158 / 98.4%
Unmapped reads	609,796 / 1.6%
Mapped paired reads	37,409,158 / 98.4%
Mapped reads, first in pair	18,765,069 / 49.36%
Mapped reads, second in pair	18,644,089 / 49.04%
Mapped reads, both in pair	37,035,456 / 97.41%
Mapped reads, singletons	373,702 / 0.98%
Secondary alignments	0
Supplementary alignments	400,086 / 1.05%
Read min/max/mean length	30 / 101 / 101.43
Duplicated reads (estimated)	3,328,830 / 8.76%
Duplication rate	7.03%
Clipped reads	9,666,669 / 25.43%

2.2. ACGT Content

Number/percentage of A's	1,017,531,911 / 28.82%
Number/percentage of C's	697,753,494 / 19.77%
Number/percentage of T's	1,032,266,603 / 29.24%
Number/percentage of G's	782,287,396 / 22.16%
Number/percentage of N's	392,141 / 0.01%

GC Percentage	41.92%
---------------	--------

2.3. Coverage

Mean	1.1412
Standard Deviation	4.4217

2.4. Mapping Quality

Mean Mapping Quality	52.18
----------------------	-------

2.5. Insert size

Mean	100,445.59
Standard Deviation	3,103,194.38
P25/Median/P75	153 / 199 / 265

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	32,111,164
Insertions	583,367
Mapped reads with at least one insertion	1.53%
Deletions	1,919,389
Mapped reads with at least one deletion	4.99%
Homopolymer indels	53.12%

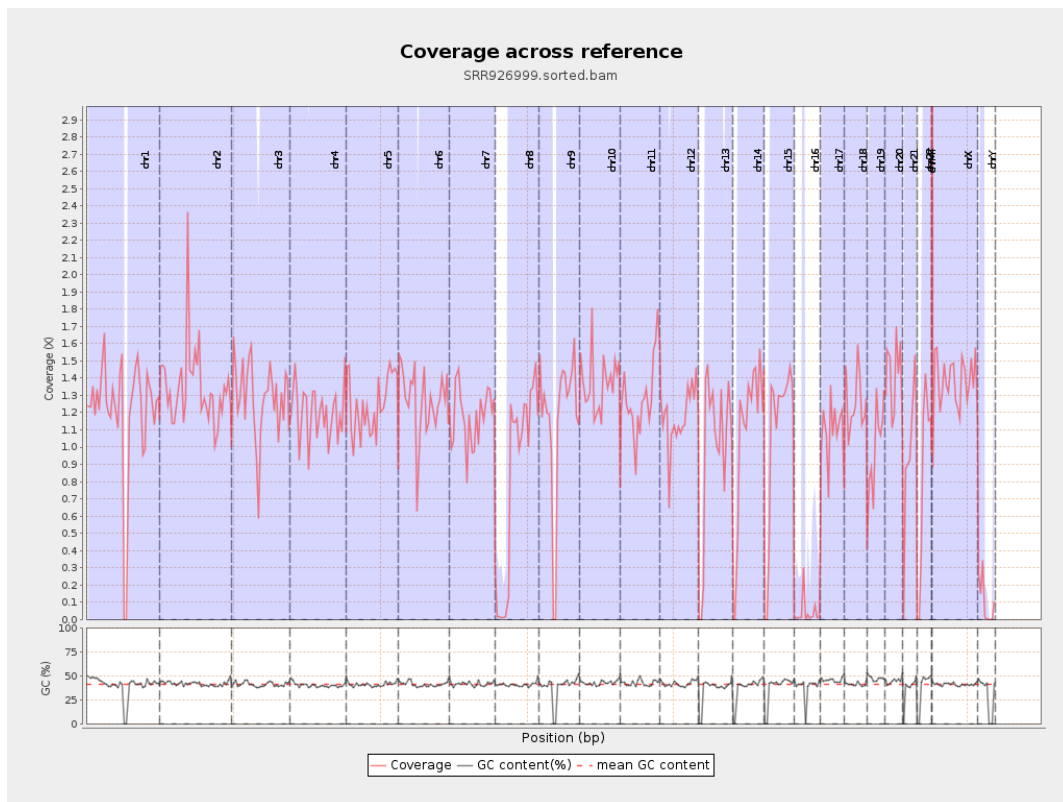
2.7. Chromosome stats

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

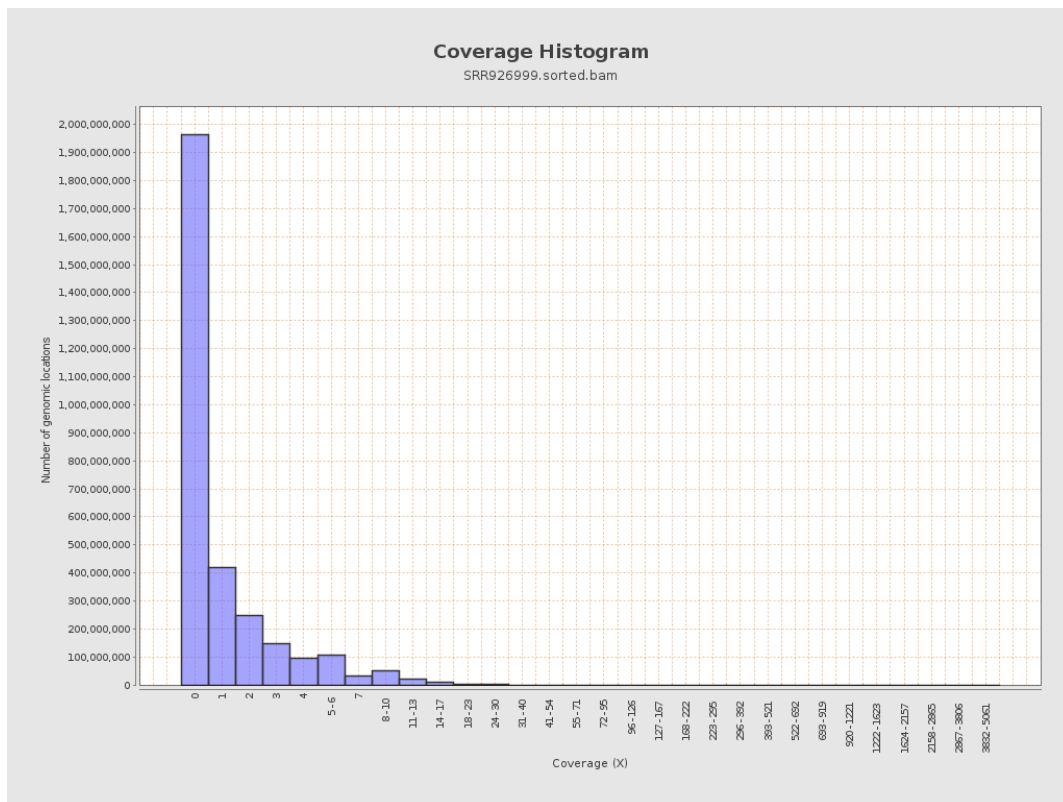
		bases	coverage	deviation
chr1	249250621	301728480	1.2105	6.1847
chr2	243199373	327555058	1.3469	7.9996
chr3	198022430	254876723	1.2871	2.4658
chr4	191154276	228985745	1.1979	3.7093
chr5	180915260	225497165	1.2464	2.3967
chr6	171115067	217992640	1.274	3.5755
chr7	159138663	187155165	1.1761	3.4023
chr8	146364022	121444206	0.8297	2.5245
chr9	141213431	163497006	1.1578	5.9937
chr10	135534747	186104126	1.3731	7.3756
chr11	135006516	172387216	1.2769	4.2803
chr12	133851895	157486521	1.1766	2.4215
chr13	115169878	113893694	0.9889	2.1549
chr14	107349540	115347891	1.0745	2.3623
chr15	102531392	109220439	1.0652	2.3572
chr16	90354753	4081670	0.0452	1.8829
chr17	81195210	88435747	1.0892	3.1535
chr18	78077248	99698472	1.2769	5.5409
chr19	59128983	58217832	0.9846	3.6409
chr20	63025520	89119947	1.414	2.8592
chr21	48129895	47845050	0.9941	3.6949
chr22	51304566	43226803	0.8426	2.1571
chrMT	16571	225562	13.6119	10.9643
chrX	155270560	212820417	1.3706	3.0604

chrY	59373566	6100441	0.1027	3.5813
------	----------	---------	--------	--------

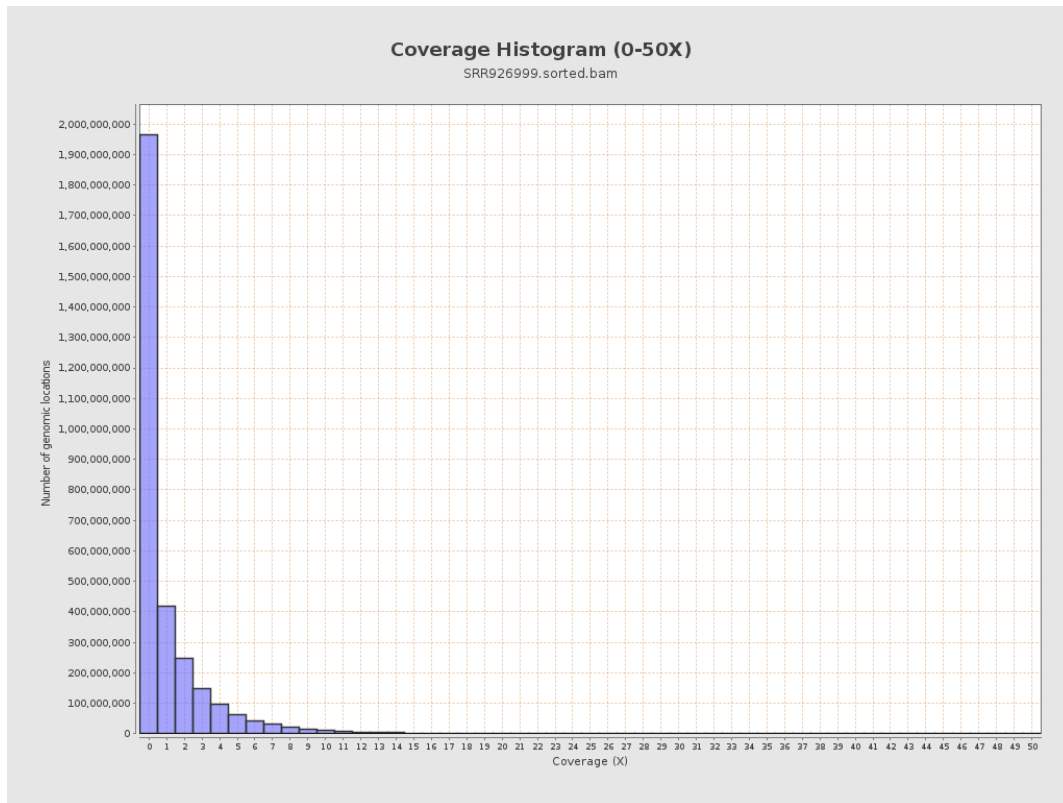
3. Results : Coverage across reference



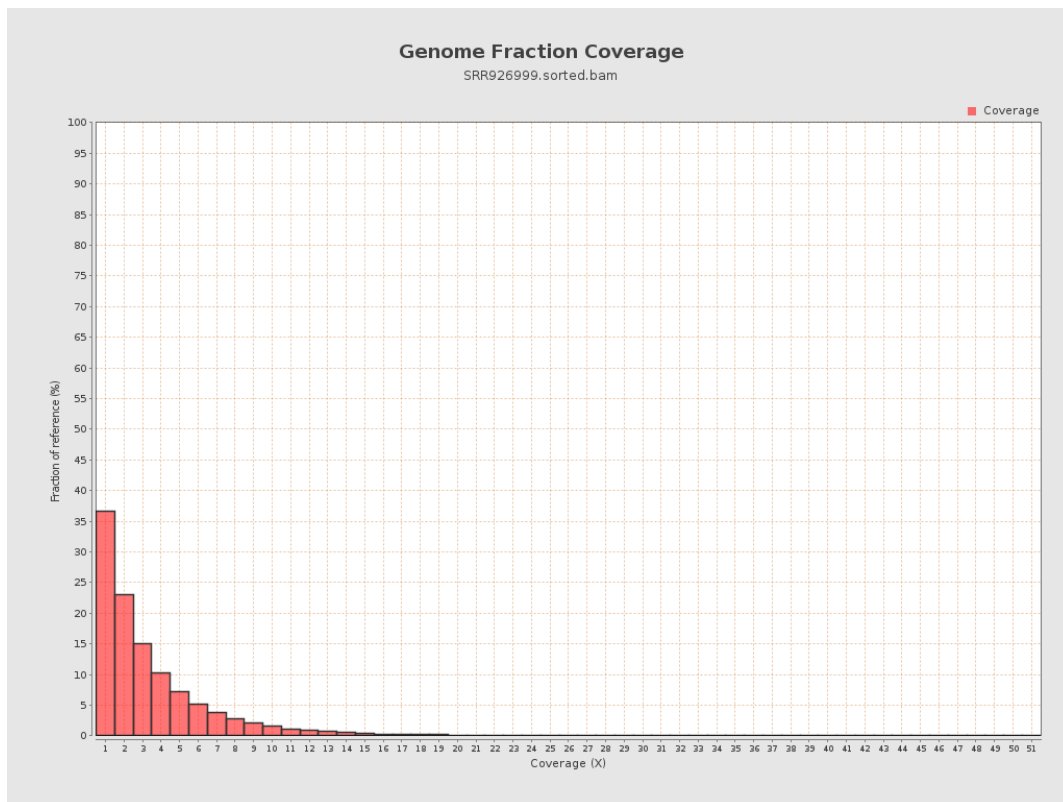
4. Results : Coverage Histogram



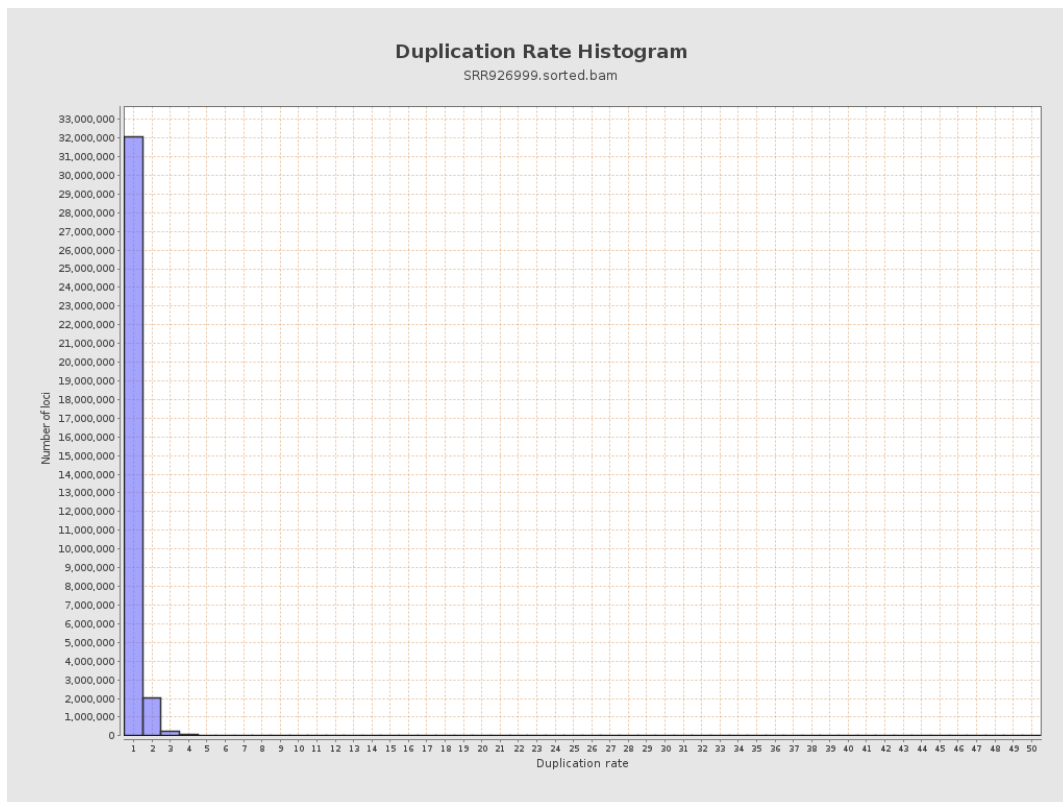
5. Results : Coverage Histogram (0-50X)



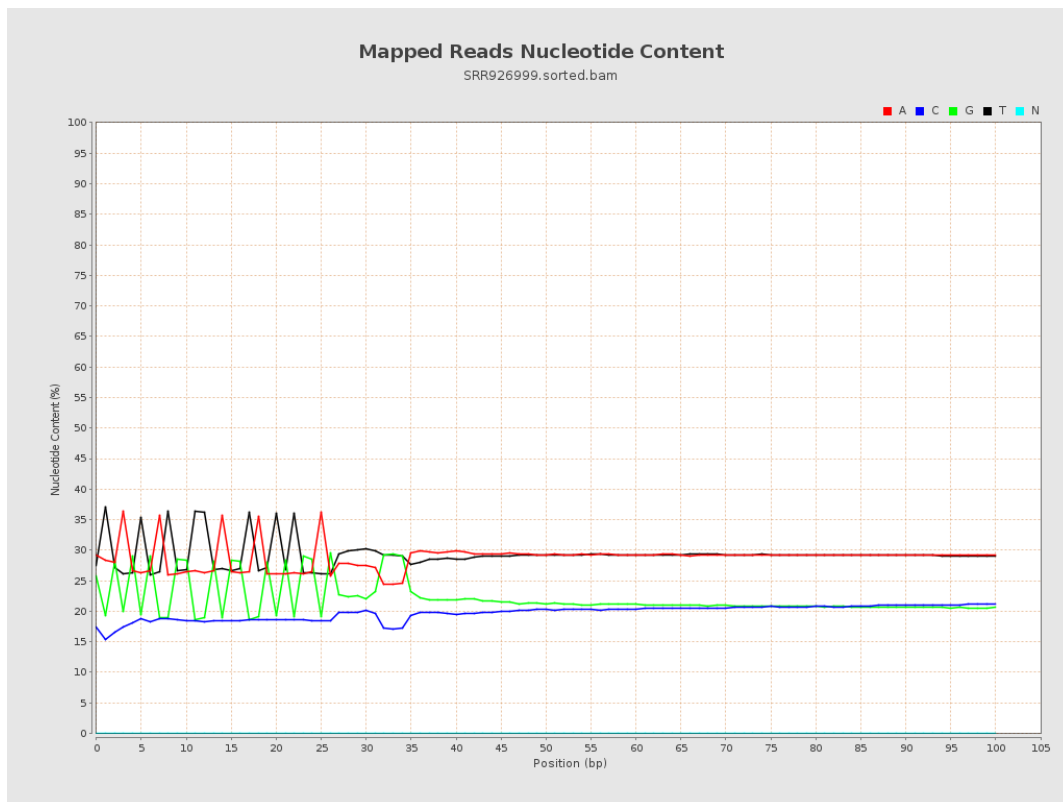
6. Results : Genome Fraction Coverage



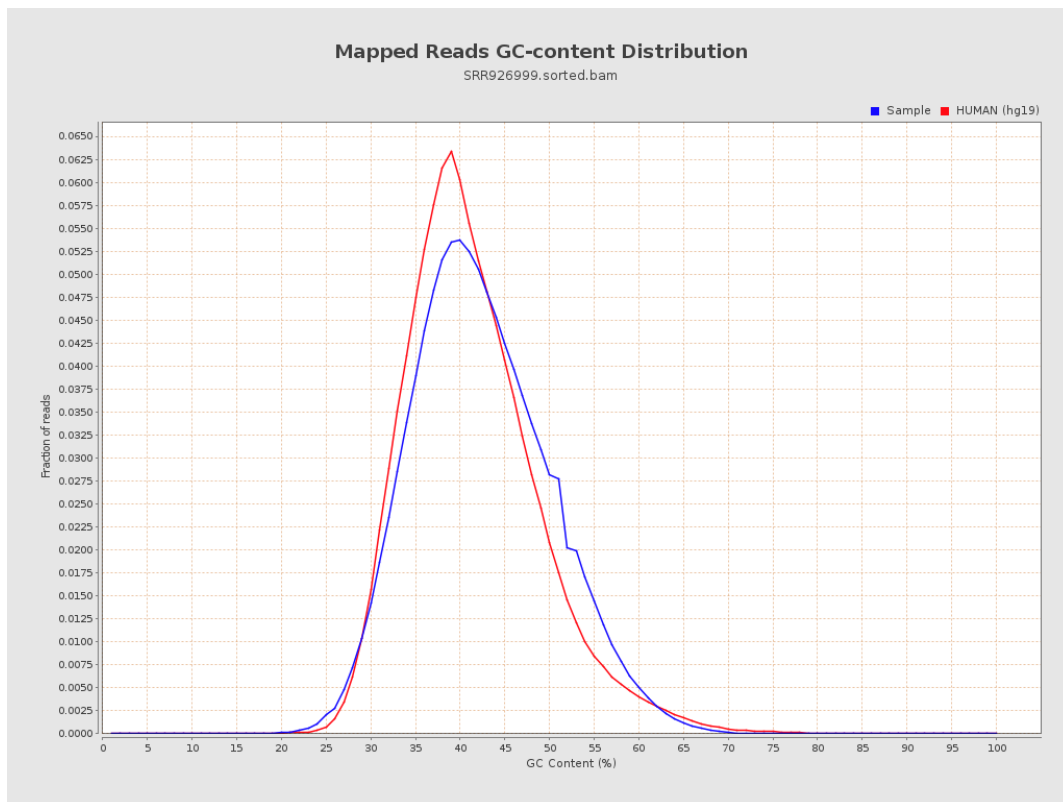
7. Results : Duplication Rate Histogram



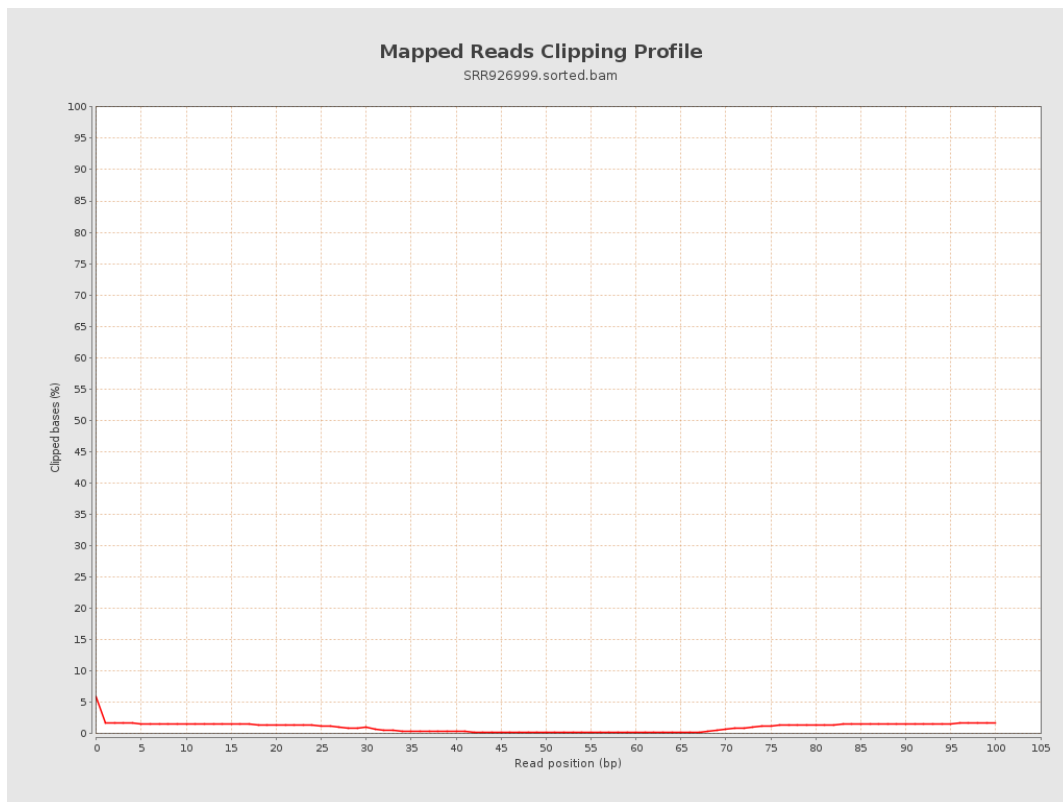
8. Results : Mapped Reads Nucleotide Content



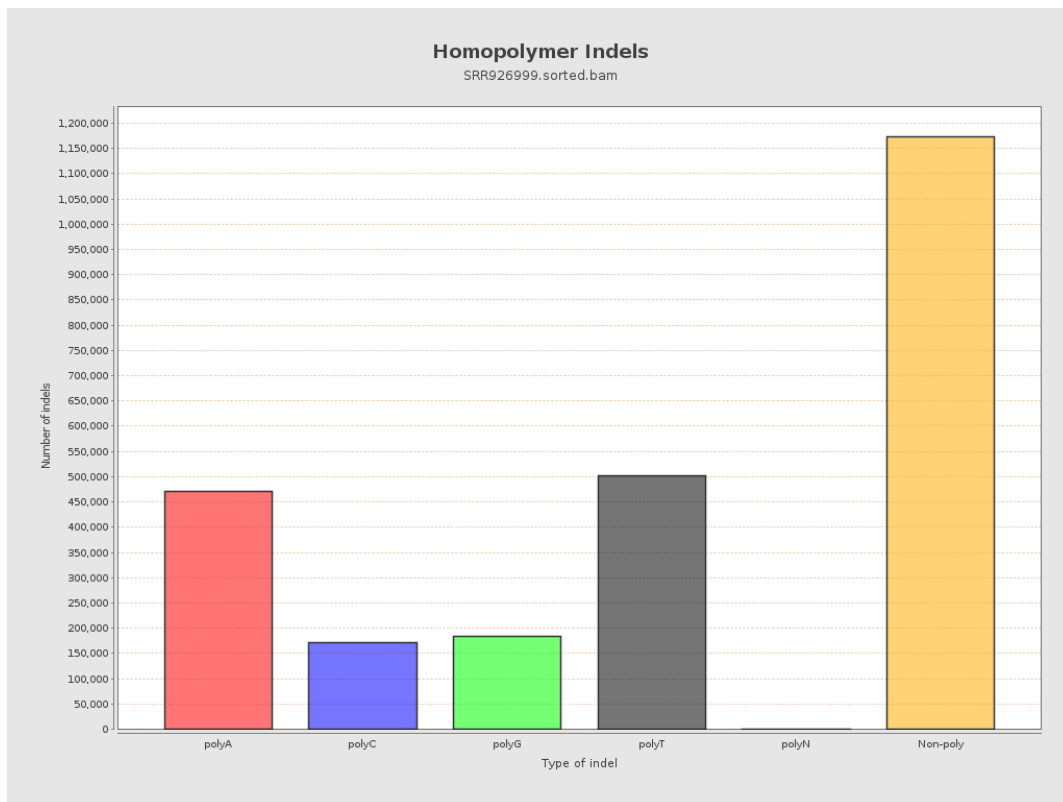
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



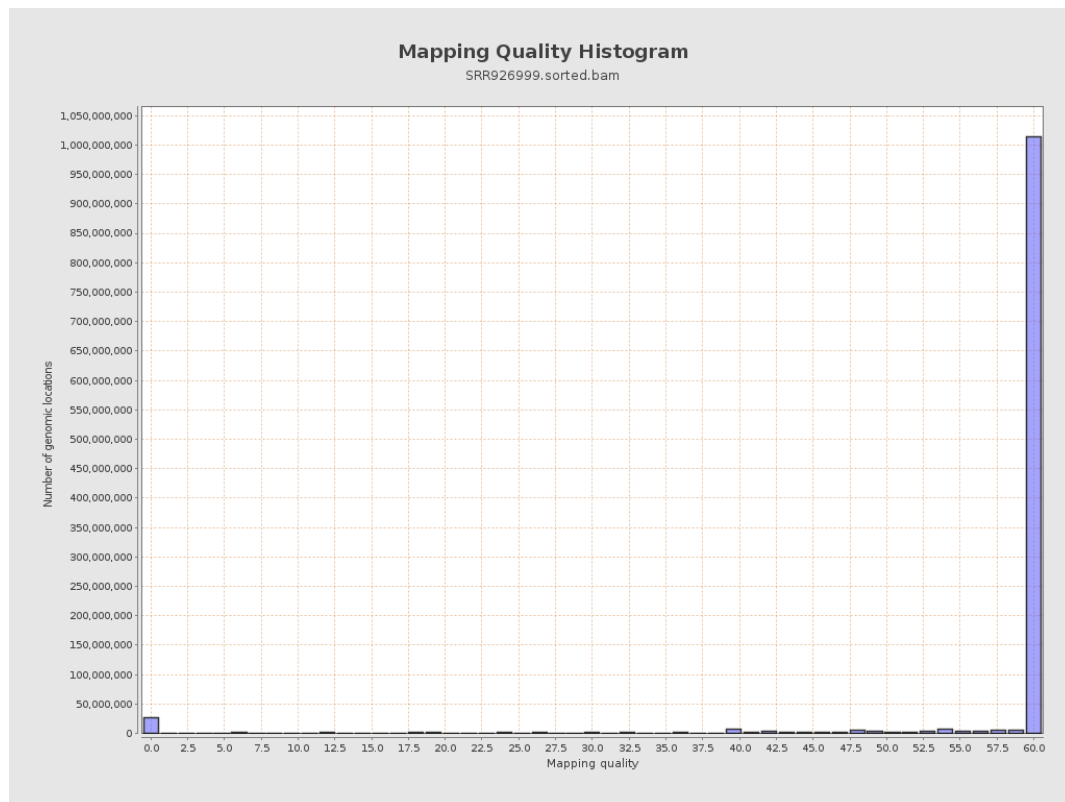
11. Results : Homopolymer Indels



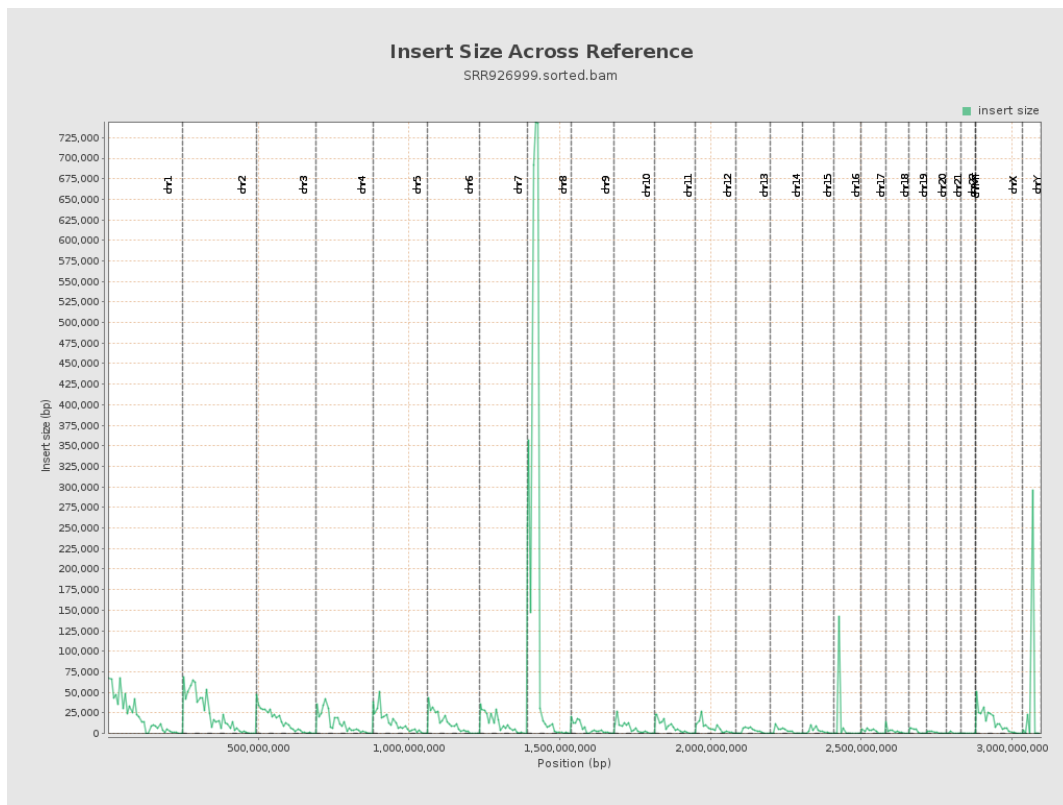
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

