

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 21:05:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174012.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_SRR10174012 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174012_1.fastq.gz SRR10174012_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 21:05:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174012.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,522,478
Mapped reads	6,379,593 / 97.81%
Unmapped reads	142,885 / 2.19%
Mapped paired reads	6,379,593 / 97.81%
Mapped reads, first in pair	3,190,416 / 48.91%
Mapped reads, second in pair	3,189,177 / 48.9%
Mapped reads, both in pair	6,284,596 / 96.35%
Mapped reads, singletons	94,997 / 1.46%
Secondary alignments	0
Supplementary alignments	601,776 / 9.23%
Read min/max/mean length	30 / 133 / 127.54
Duplicated reads (estimated)	5,100,260 / 78.2%
Duplication rate	67.33%
Clipped reads	2,414,948 / 37.03%

2.2. ACGT Content

Number/percentage of A's	228,354,084 / 30.28%
Number/percentage of C's	146,715,549 / 19.46%
Number/percentage of T's	227,508,521 / 30.17%
Number/percentage of G's	151,431,772 / 20.08%
Number/percentage of N's	9,151 / 0%

GC Percentage	39.54%
---------------	--------

2.3. Coverage

Mean	0.2437
Standard Deviation	3.5959

2.4. Mapping Quality

Mean Mapping Quality	52.83
----------------------	-------

2.5. Insert size

Mean	841,280.9
Standard Deviation	8,272,292.84
P25/Median/P75	141 / 196 / 280

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	7,266,493
Insertions	77,411
Mapped reads with at least one insertion	1.17%
Deletions	168,836
Mapped reads with at least one deletion	2.58%
Homopolymer indels	43.1%

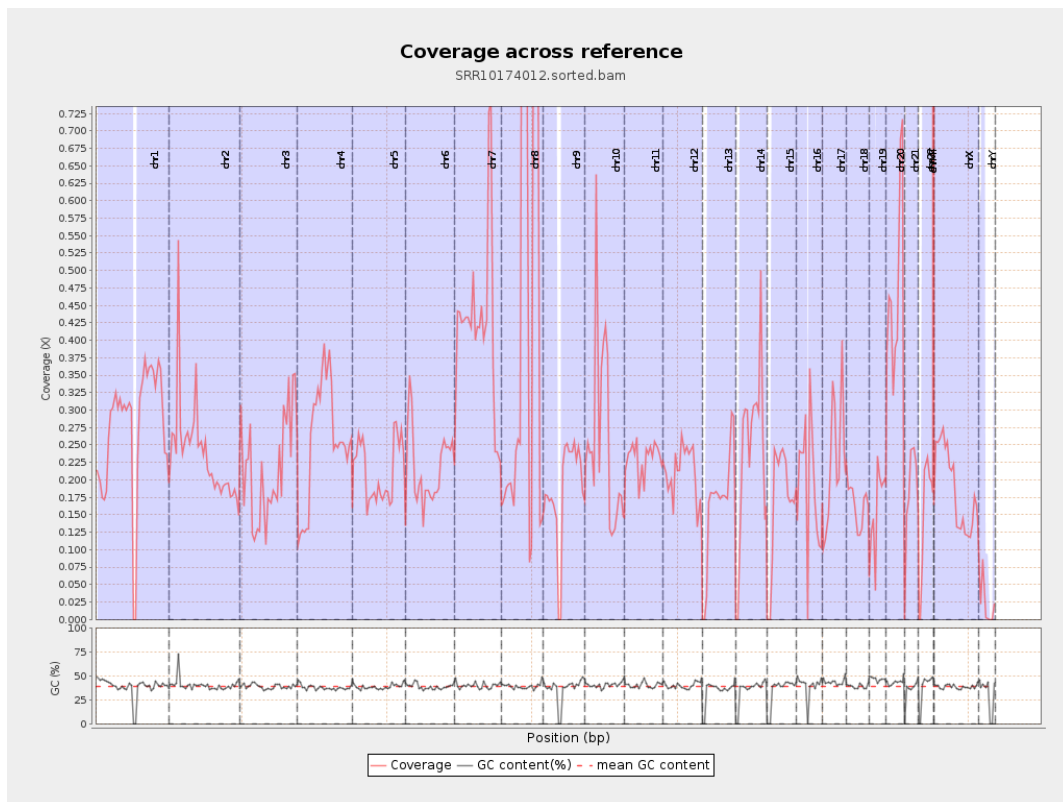
2.7. Chromosome stats

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

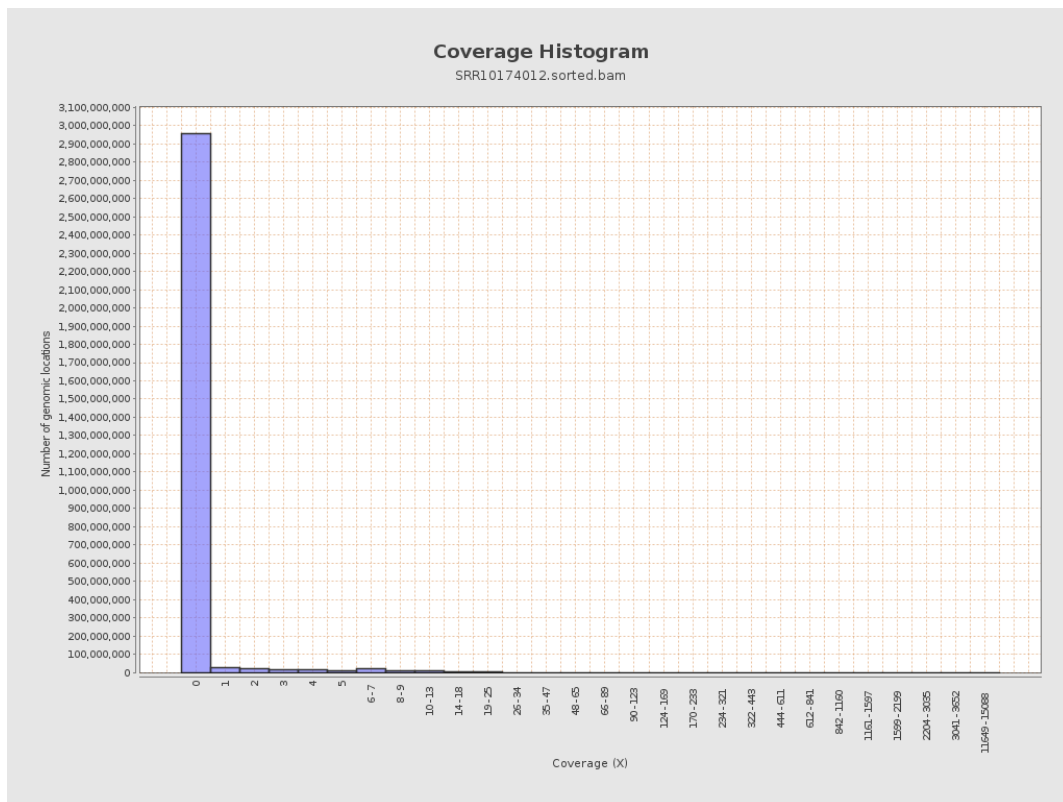
		bases	coverage	deviation
chr1	249250621	68464086	0.2747	1.952
chr2	243199373	57706902	0.2373	10.5678
chr3	198022430	42734660	0.2158	1.4089
chr4	191154276	48670907	0.2546	1.9025
chr5	180915260	38491621	0.2128	1.389
chr6	171115067	36887401	0.2156	1.4539
chr7	159138663	67726376	0.4256	4.049
chr8	146364022	74989399	0.5123	2.6637
chr9	141213431	26263743	0.186	1.6875
chr10	135534747	34954040	0.2579	4.5797
chr11	135006516	31032847	0.2299	1.4958
chr12	133851895	28253326	0.2111	1.3864
chr13	115169878	19295697	0.1675	1.2517
chr14	107349540	25839921	0.2407	1.5022
chr15	102531392	17420052	0.1699	1.2307
chr16	90354753	17129210	0.1896	1.8952
chr17	81195210	18534951	0.2283	1.5926
chr18	78077248	12845566	0.1645	2.1039
chr19	59128983	9422288	0.1594	1.5561
chr20	63025520	29429672	0.4669	2.1005
chr21	48129895	8782835	0.1825	1.3934
chr22	51304566	7562658	0.1474	1.1131
chrMT	16571	1736563	104.7953	82.9208
chrX	155270560	28937612	0.1864	1.3175

chrY	59373566	1337145	0.0225	0.8963
------	----------	---------	--------	--------

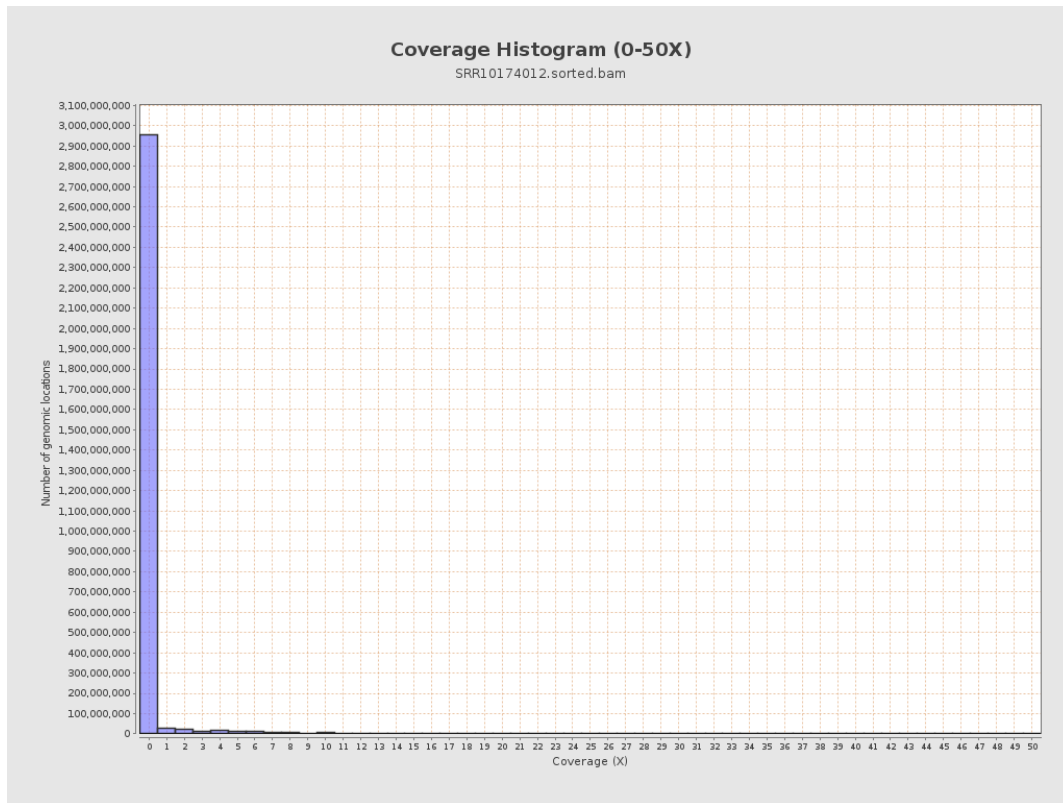
3. Results : Coverage across reference



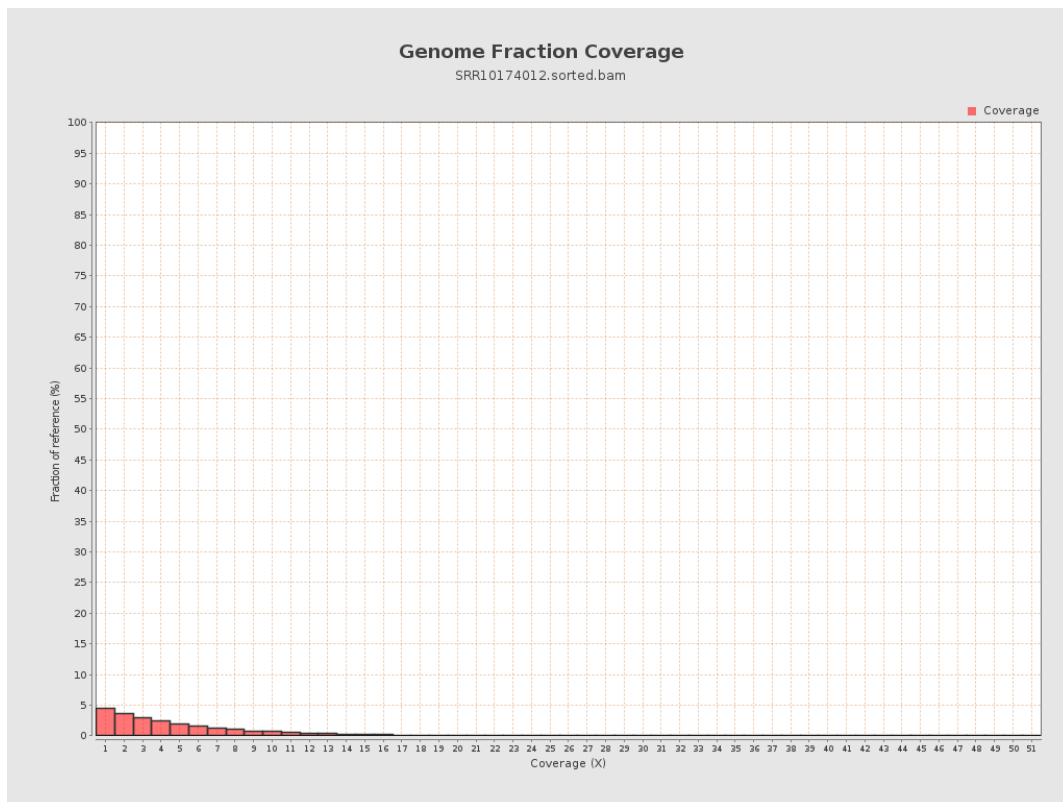
4. Results : Coverage Histogram



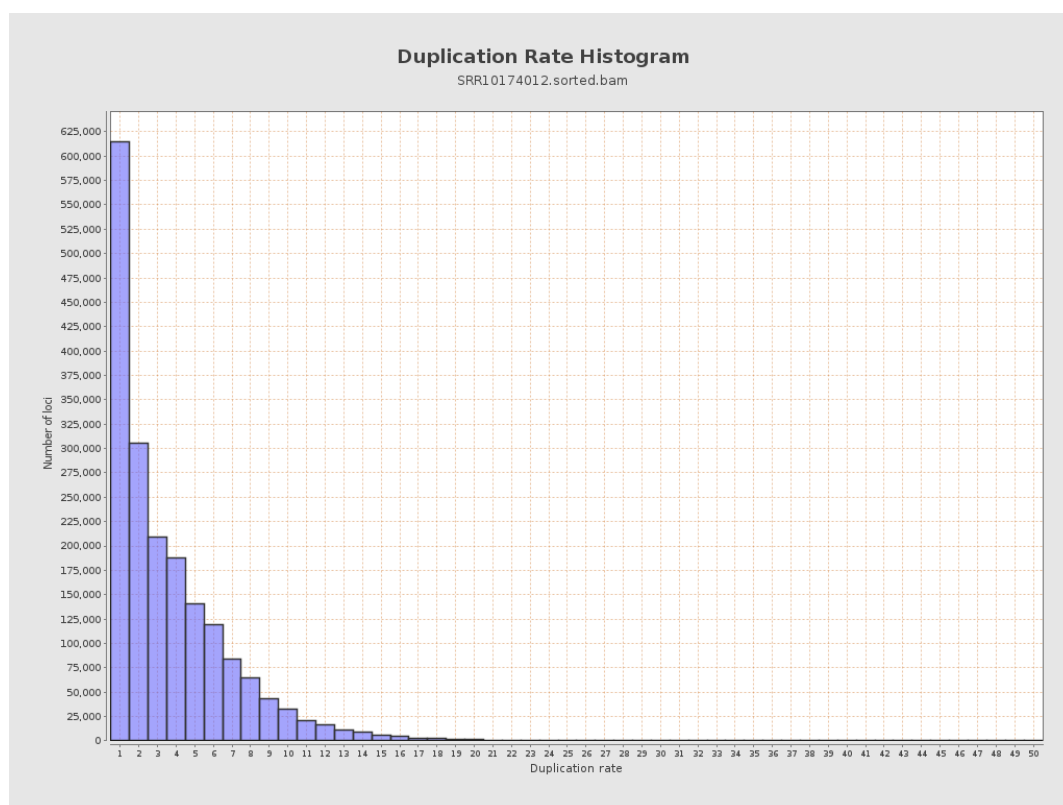
5. Results : Coverage Histogram (0-50X)



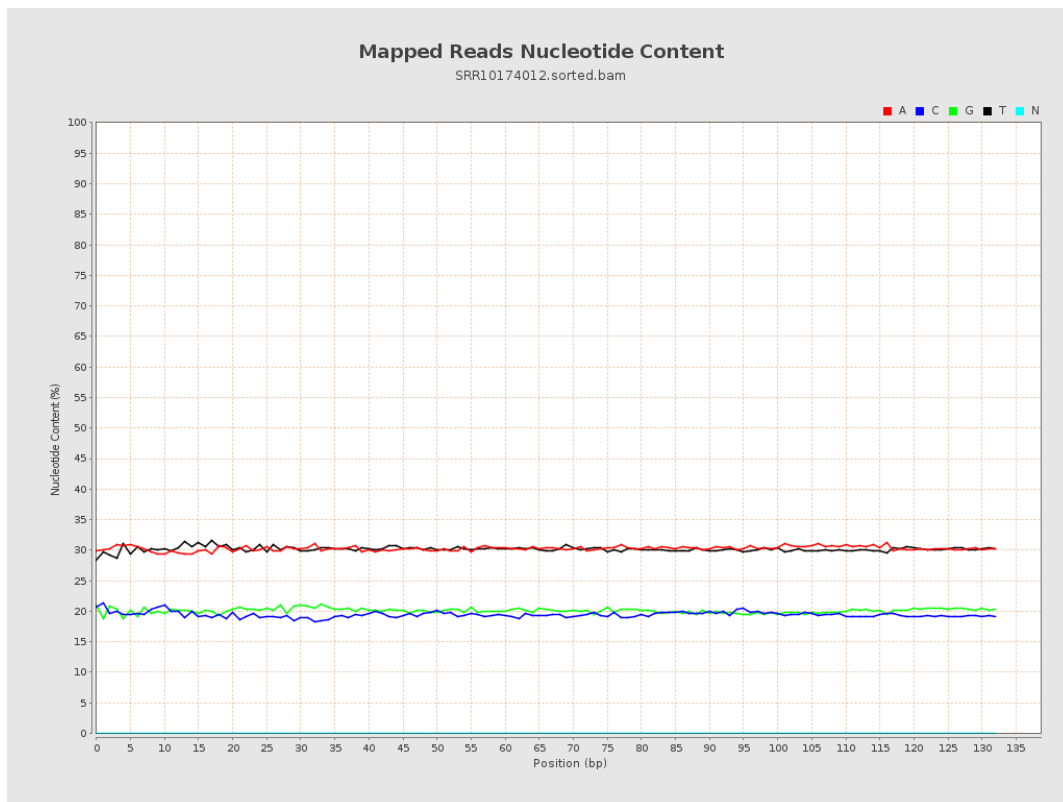
6. Results : Genome Fraction Coverage



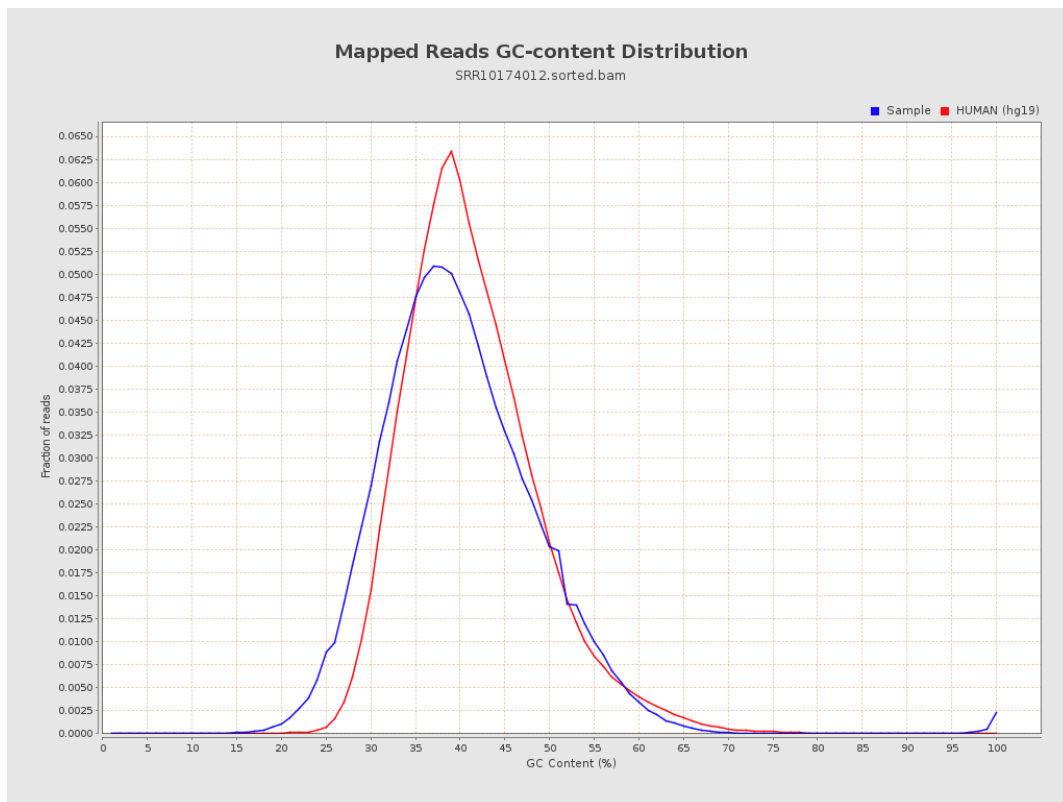
7. Results : Duplication Rate Histogram



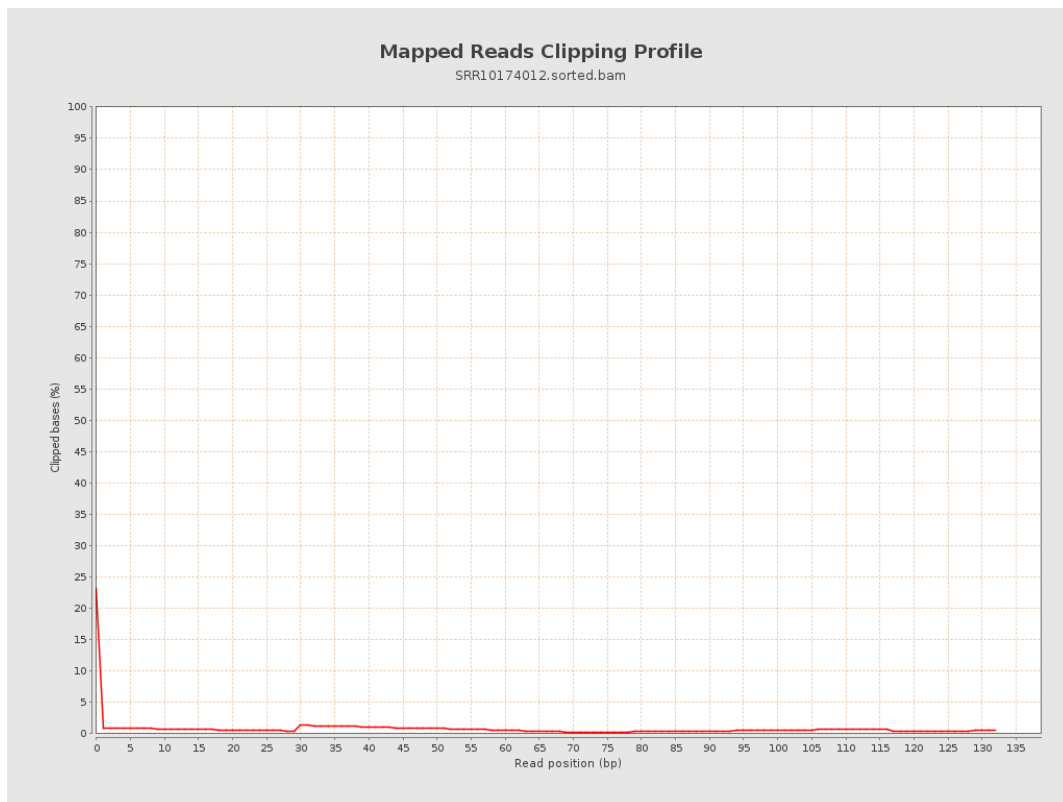
8. Results : Mapped Reads Nucleotide Content



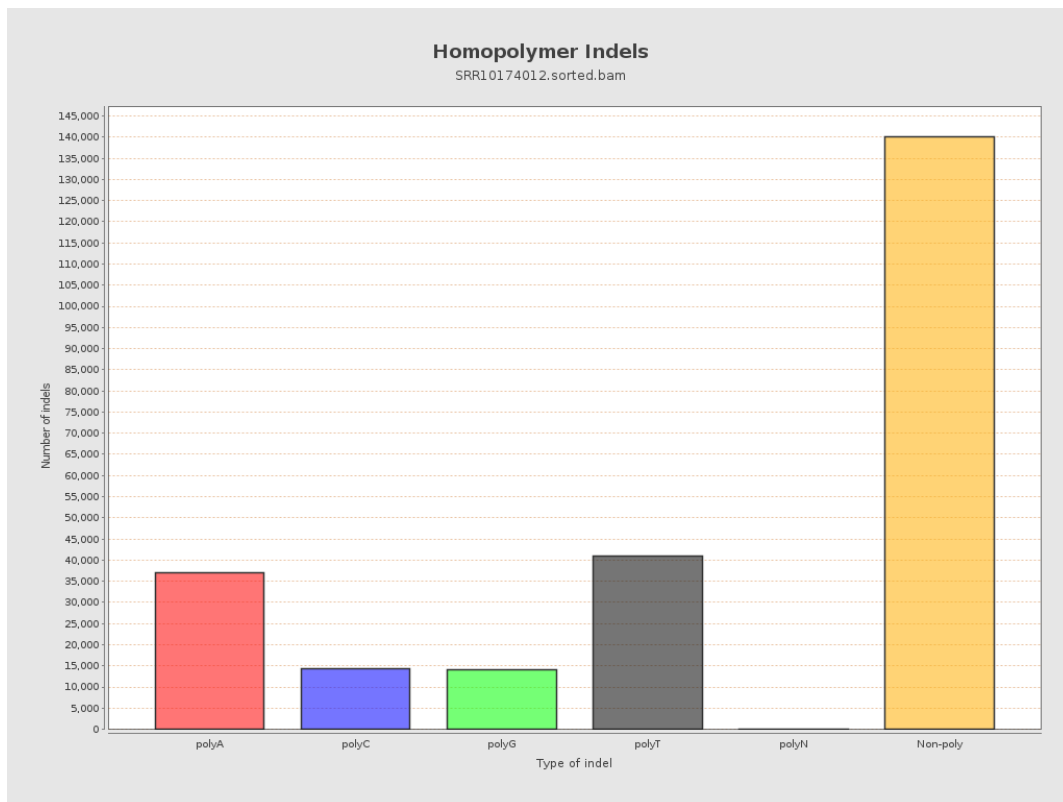
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



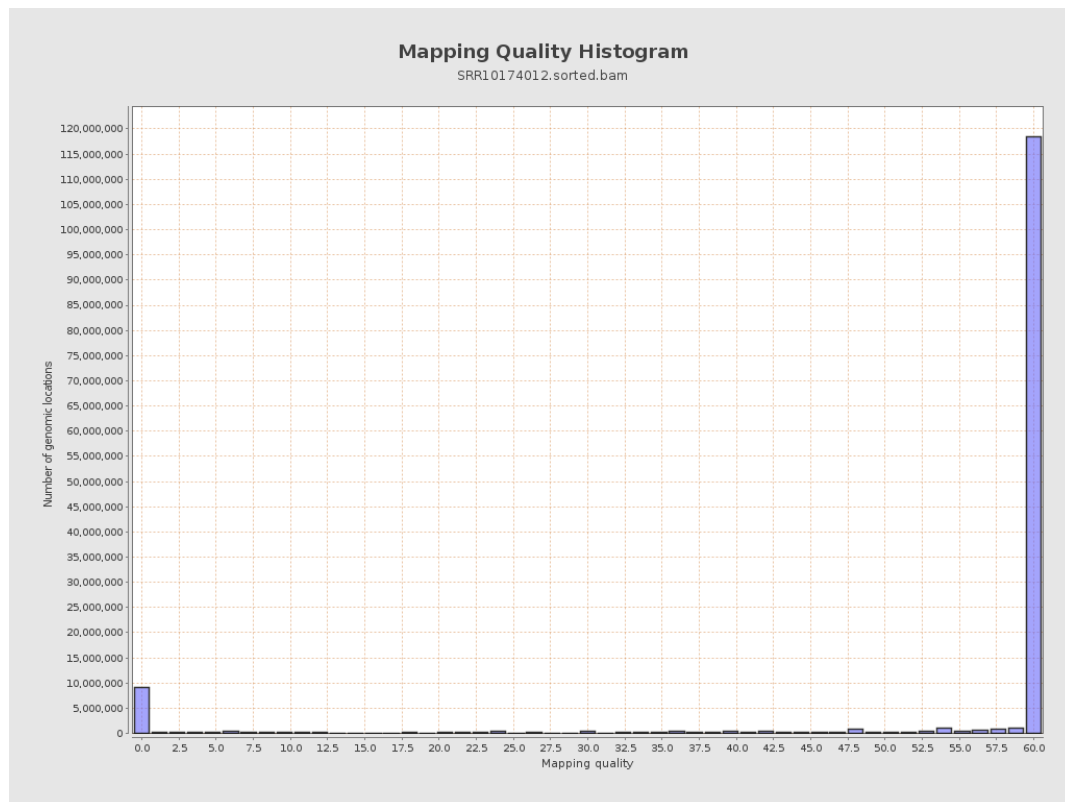
11. Results : Homopolymer Indels



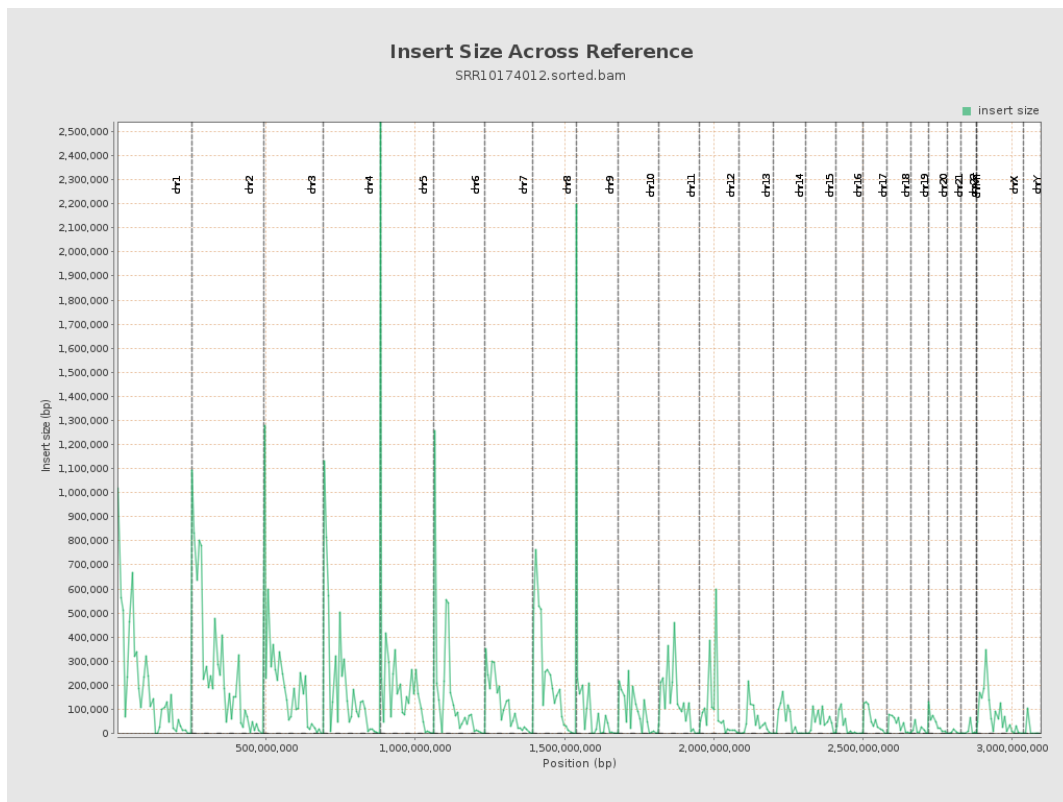
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

