

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 07:37:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174092.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_SRR10174092 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174092_1.fastq.gz SRR10174092_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 07:37:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174092.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,532,412
Mapped reads	2,490,655 / 98.35%
Unmapped reads	41,757 / 1.65%
Mapped paired reads	2,490,655 / 98.35%
Mapped reads, first in pair	1,244,619 / 49.15%
Mapped reads, second in pair	1,246,036 / 49.2%
Mapped reads, both in pair	2,464,708 / 97.33%
Mapped reads, singletons	25,947 / 1.02%
Secondary alignments	0
Supplementary alignments	268,361 / 10.6%
Read min/max/mean length	30 / 133 / 124.53
Duplicated reads (estimated)	1,977,679 / 78.09%
Duplication rate	66.81%
Clipped reads	1,083,933 / 42.8%

2.2. ACGT Content

Number/percentage of A's	85,703,800 / 29.97%
Number/percentage of C's	56,687,552 / 19.82%
Number/percentage of T's	84,977,165 / 29.71%
Number/percentage of G's	58,608,776 / 20.49%
Number/percentage of N's	2,288 / 0%

GC Percentage	40.32%
---------------	--------

2.3. Coverage

Mean	0.0924
Standard Deviation	1.7559

2.4. Mapping Quality

Mean Mapping Quality	52.99
----------------------	-------

2.5. Insert size

Mean	879,948.33
Standard Deviation	8,617,376.78
P25/Median/P75	111 / 158 / 236

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	2,240,148
Insertions	30,077
Mapped reads with at least one insertion	1.16%
Deletions	69,755
Mapped reads with at least one deletion	2.73%
Homopolymer indels	42.27%

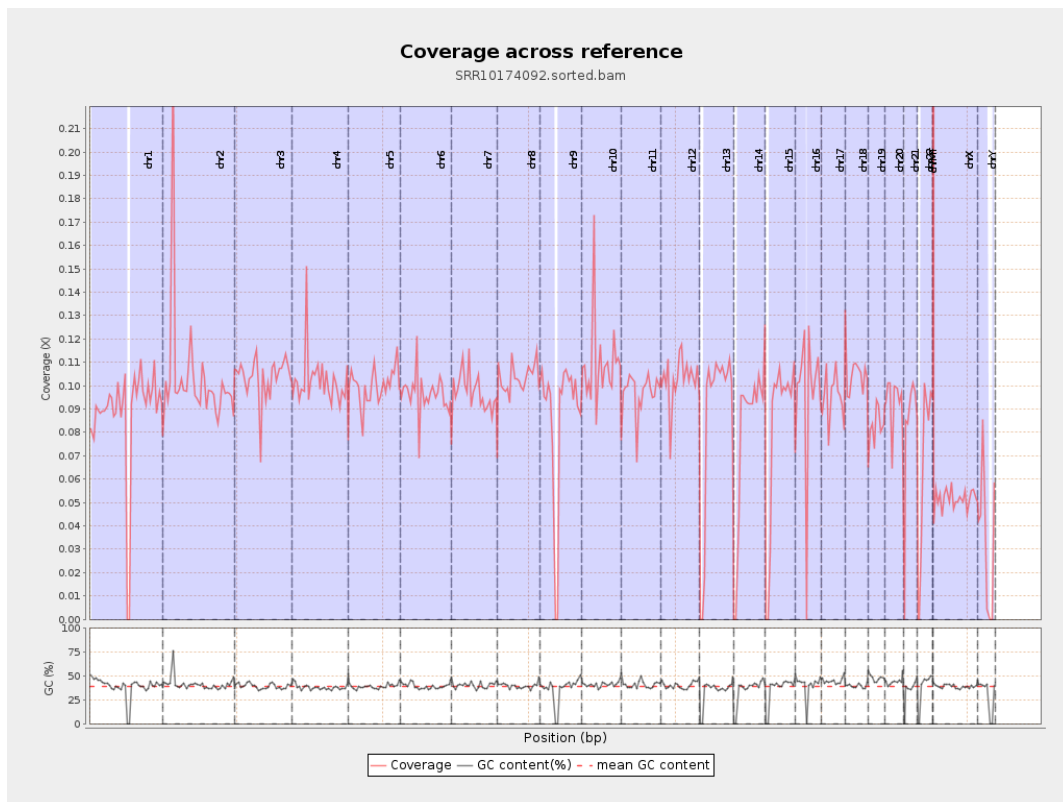
2.7. Chromosome stats

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

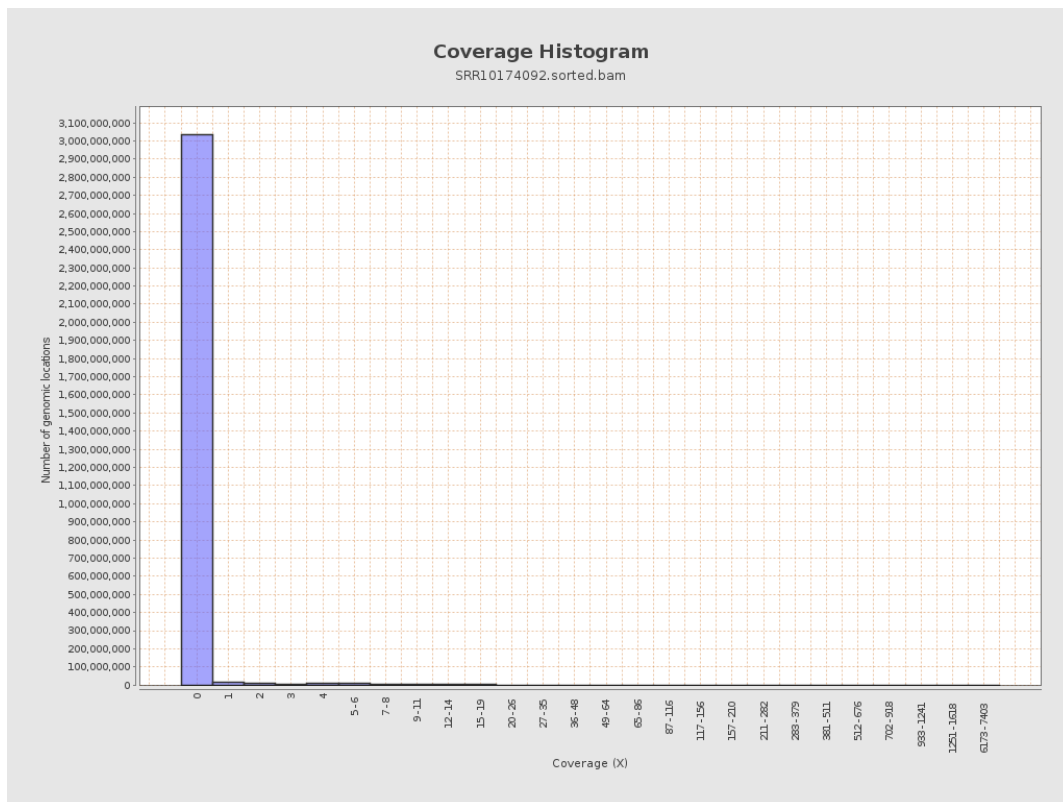
		bases	coverage	deviation
chr1	249250621	22019950	0.0883	1.0136
chr2	243199373	24974482	0.1027	5.2621
chr3	198022430	20542961	0.1037	0.9759
chr4	191154276	19531952	0.1022	1.0948
chr5	180915260	18062499	0.0998	0.9504
chr6	171115067	16526607	0.0966	0.993
chr7	159138663	15438930	0.097	1.0814
chr8	146364022	15131683	0.1034	1.2043
chr9	141213431	12253928	0.0868	1.0013
chr10	135534747	14764549	0.1089	1.2554
chr11	135006516	13089790	0.097	0.942
chr12	133851895	13799229	0.1031	0.9763
chr13	115169878	10043670	0.0872	0.9003
chr14	107349540	8615016	0.0803	0.8495
chr15	102531392	8271606	0.0807	0.8483
chr16	90354753	8651273	0.0957	1.0156
chr17	81195210	7783185	0.0959	0.9386
chr18	78077248	8167882	0.1046	1.1781
chr19	59128983	4919322	0.0832	0.8887
chr20	63025520	5850701	0.0928	0.9185
chr21	48129895	4019121	0.0835	0.9602
chr22	51304566	3357761	0.0654	0.8059
chrMT	16571	242633	14.642	19.4628
chrX	155270560	7987546	0.0514	0.6827

chrY	59373566	2101460	0.0354	0.6542
------	----------	---------	--------	--------

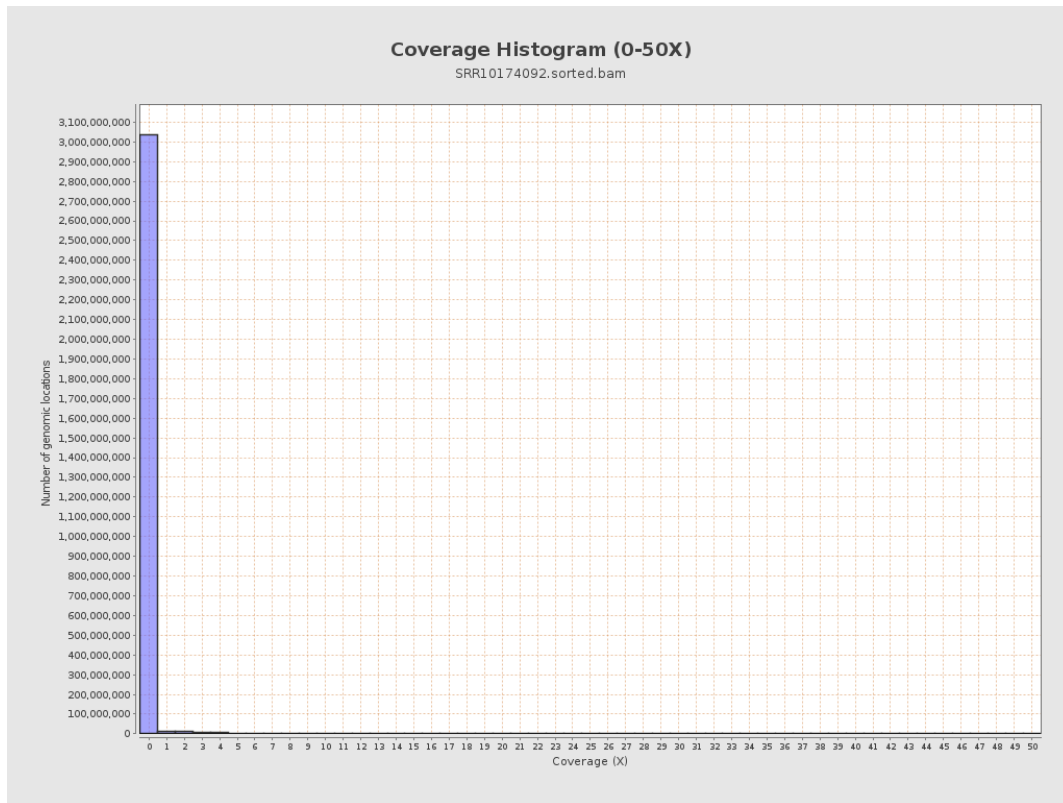
3. Results : Coverage across reference



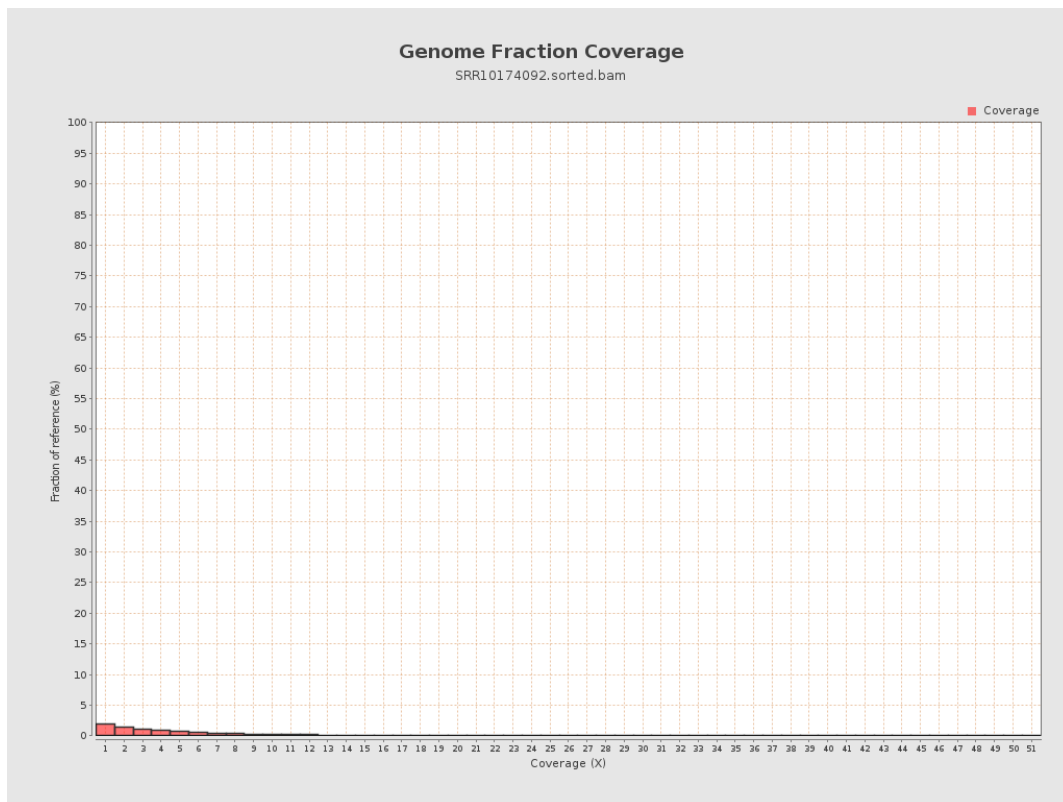
4. Results : Coverage Histogram



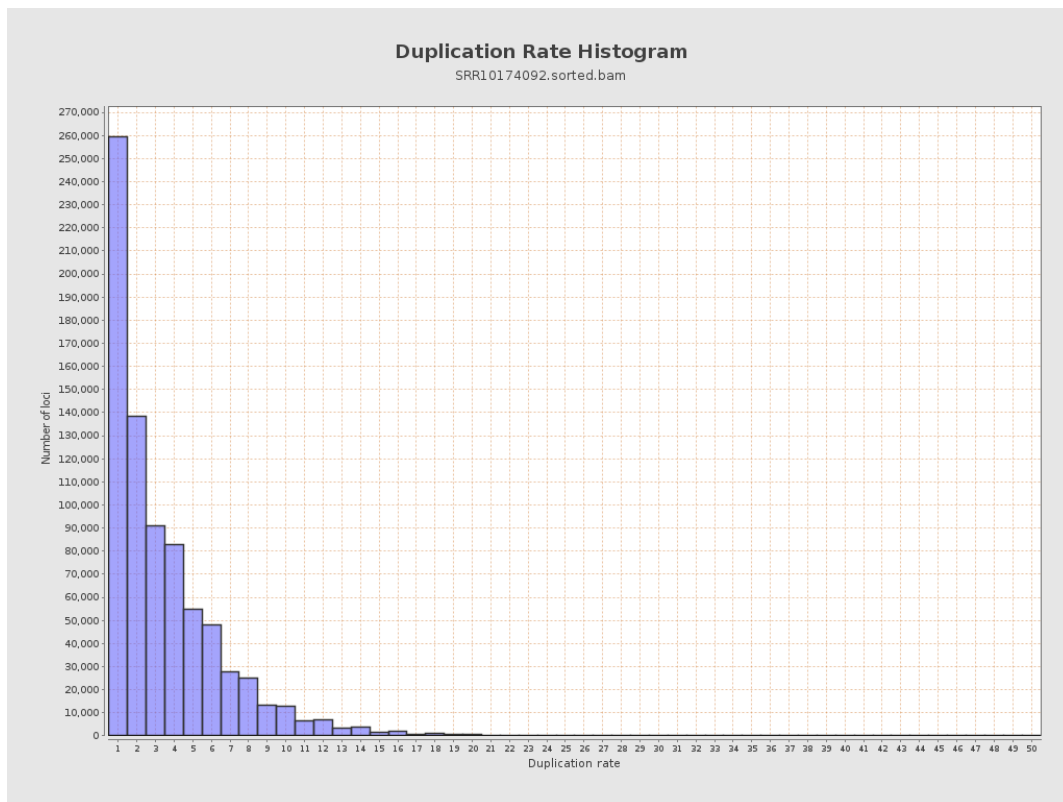
5. Results : Coverage Histogram (0-50X)



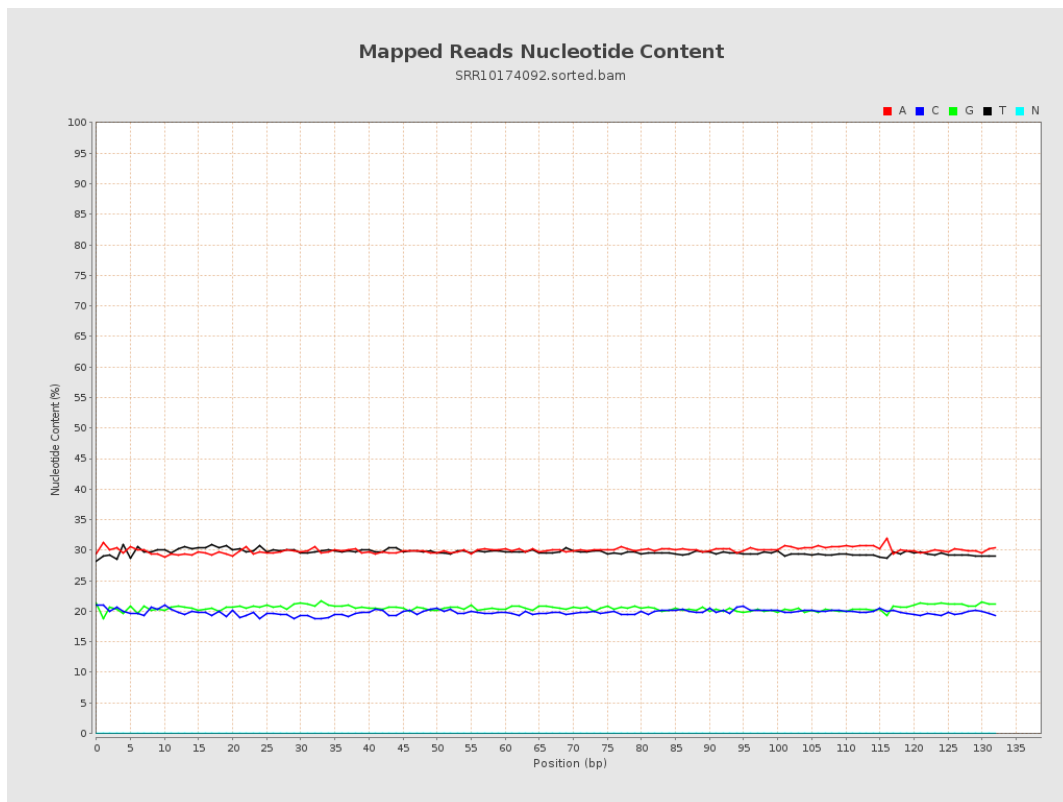
6. Results : Genome Fraction Coverage



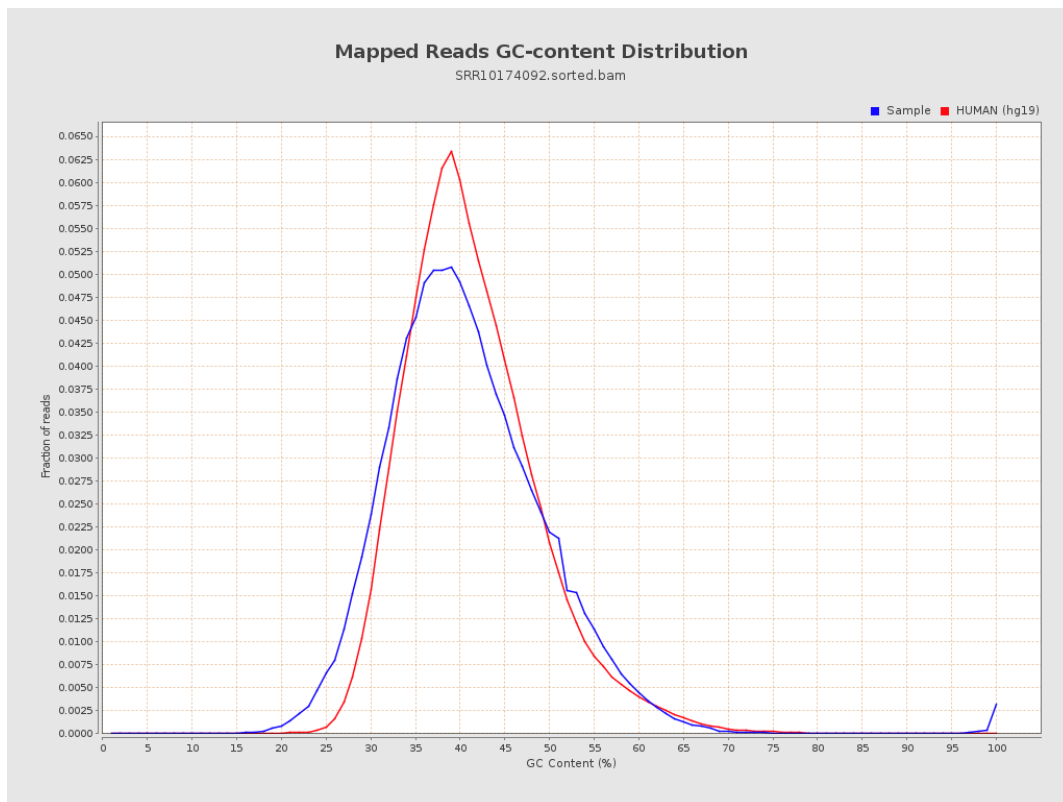
7. Results : Duplication Rate Histogram



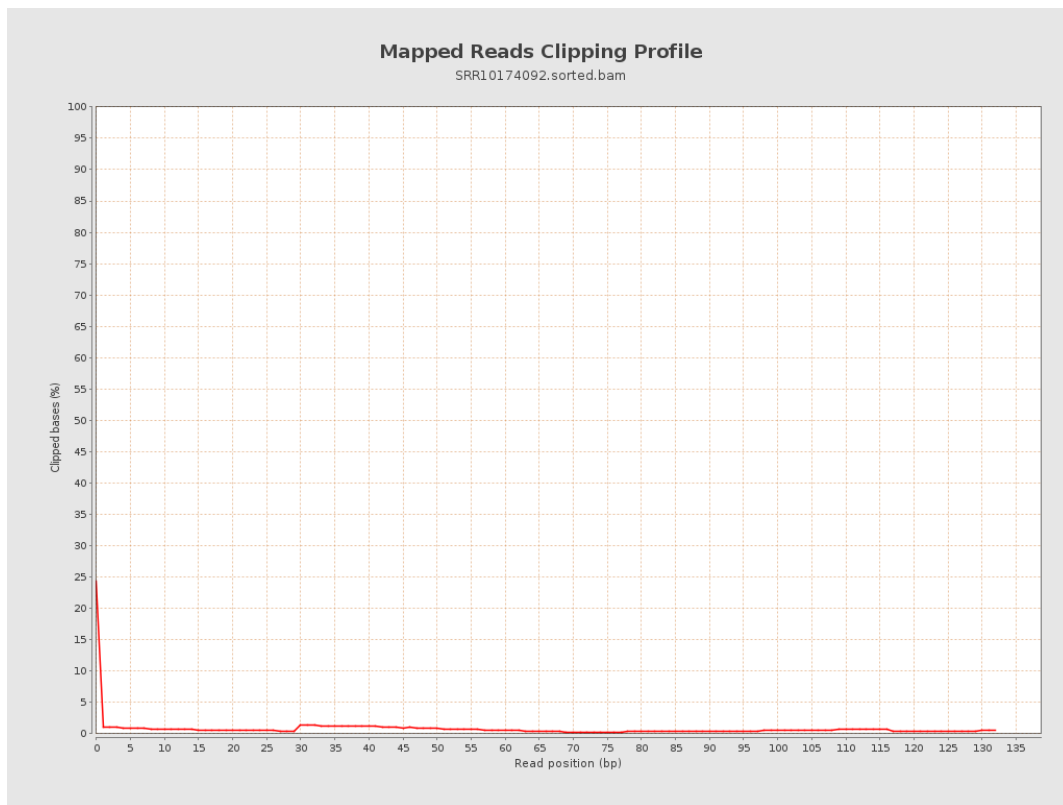
8. Results : Mapped Reads Nucleotide Content



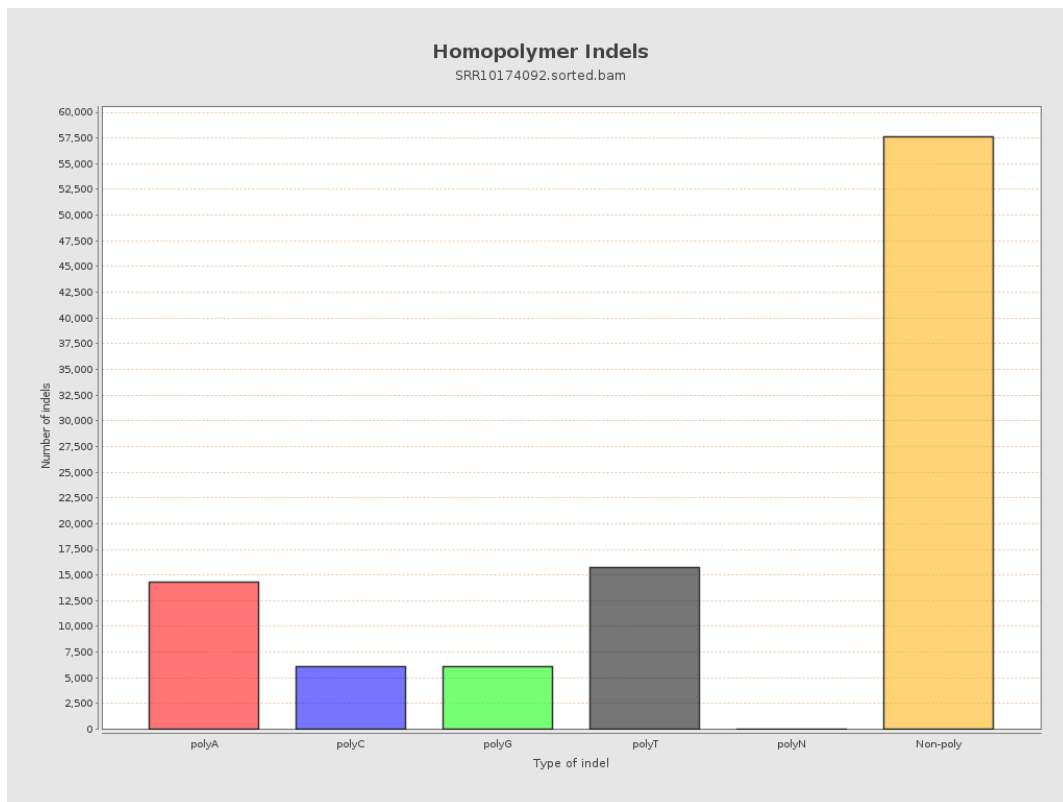
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



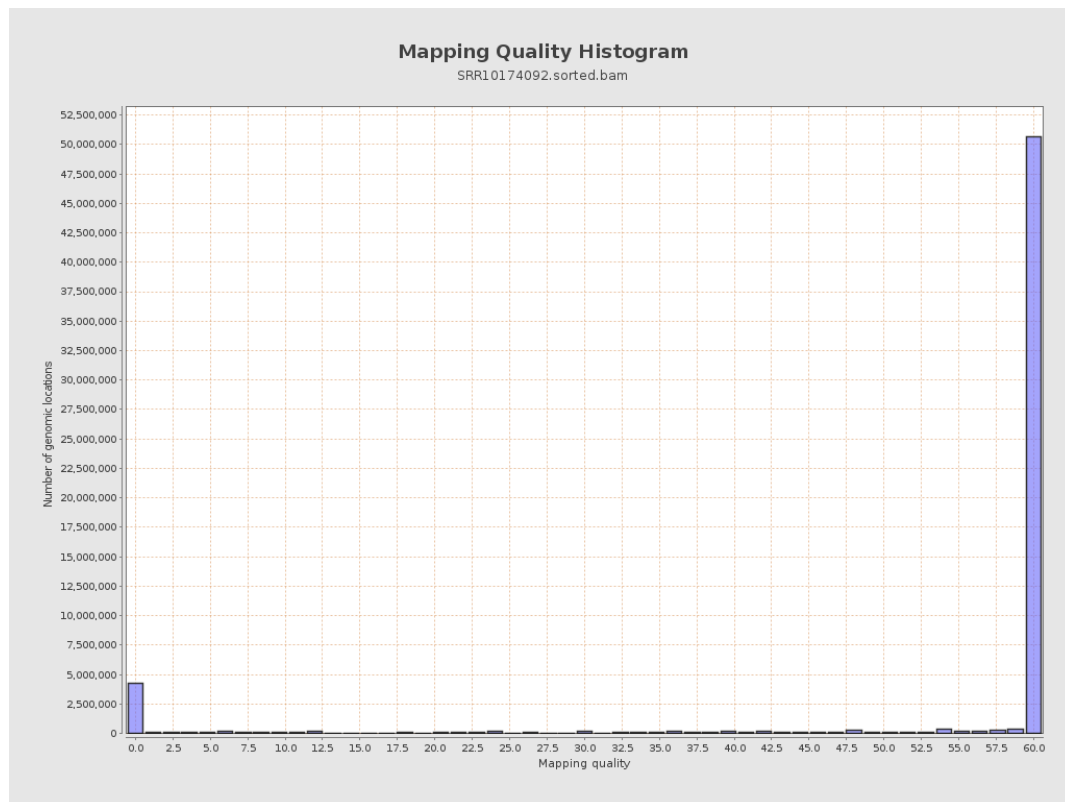
11. Results : Homopolymer Indels



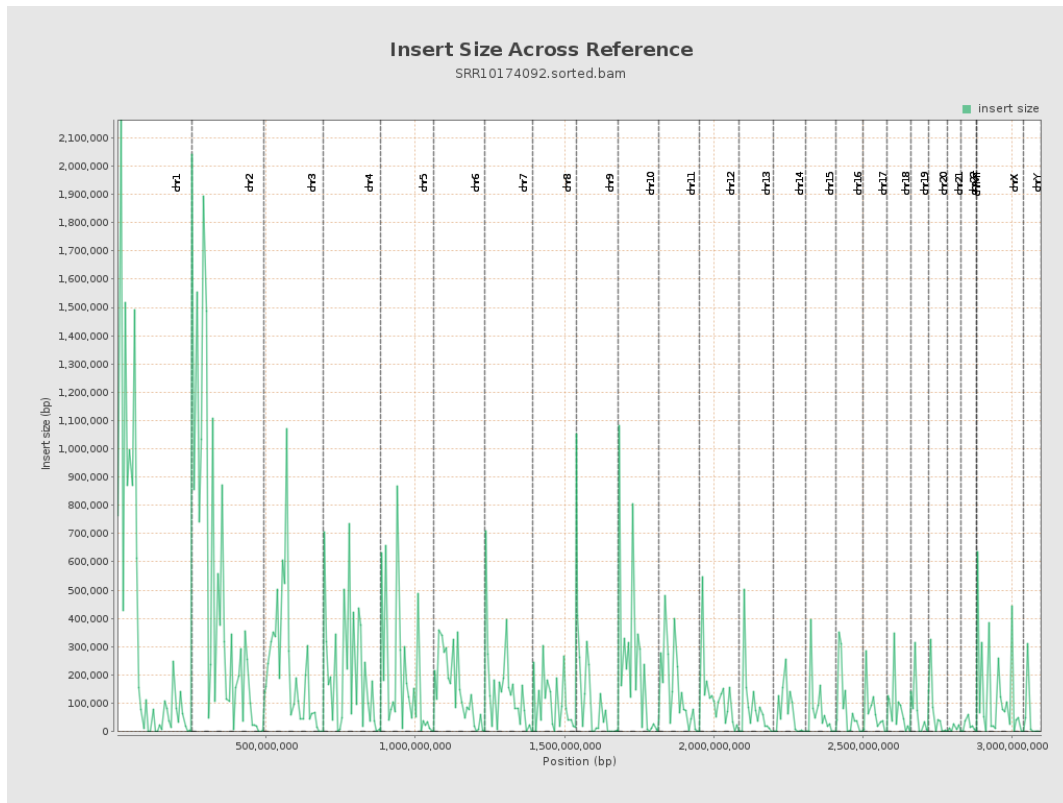
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

