

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:46:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173839.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_SRR10173839 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173839_1.fastq.gz SRR10173839_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:46:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173839.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,691,330
Mapped reads	3,595,546 / 97.41%
Unmapped reads	95,784 / 2.59%
Mapped paired reads	3,595,546 / 97.41%
Mapped reads, first in pair	1,803,538 / 48.86%
Mapped reads, second in pair	1,792,008 / 48.55%
Mapped reads, both in pair	3,531,482 / 95.67%
Mapped reads, singletons	64,064 / 1.74%
Secondary alignments	0
Supplementary alignments	355,776 / 9.64%
Read min/max/mean length	30 / 133 / 128.22
Duplicated reads (estimated)	2,777,351 / 75.24%
Duplication rate	63.97%
Clipped reads	1,603,744 / 43.45%

2.2. ACGT Content

Number/percentage of A's	127,615,142 / 30.27%
Number/percentage of C's	81,792,728 / 19.4%
Number/percentage of T's	127,285,696 / 30.19%
Number/percentage of G's	84,908,190 / 20.14%
Number/percentage of N's	4,859 / 0%

GC Percentage	39.54%
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2.3. Coverage

Mean	0.1363
Standard Deviation	2.1396

2.4. Mapping Quality

Mean Mapping Quality	52.72
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2.5. Insert size

Mean	902,221.47
Standard Deviation	8,652,102.93
P25/Median/P75	144 / 200 / 286

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	4,244,877
Insertions	43,635
Mapped reads with at least one insertion	1.17%
Deletions	94,801
Mapped reads with at least one deletion	2.57%
Homopolymer indels	42.78%

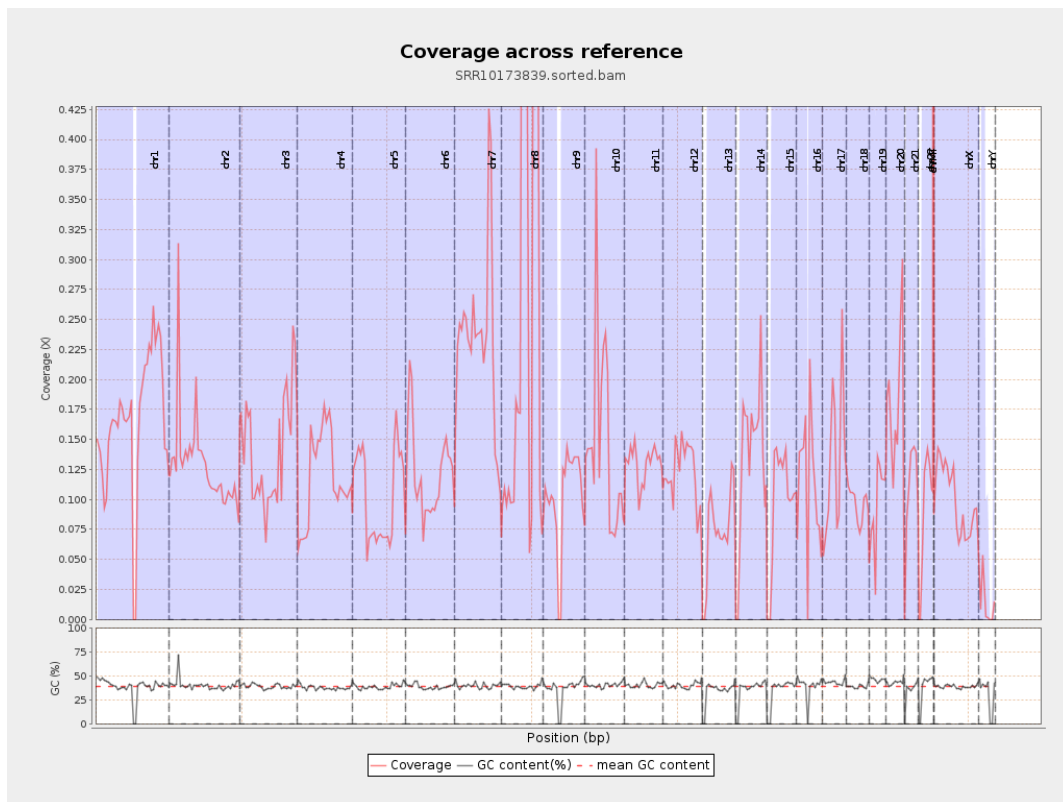
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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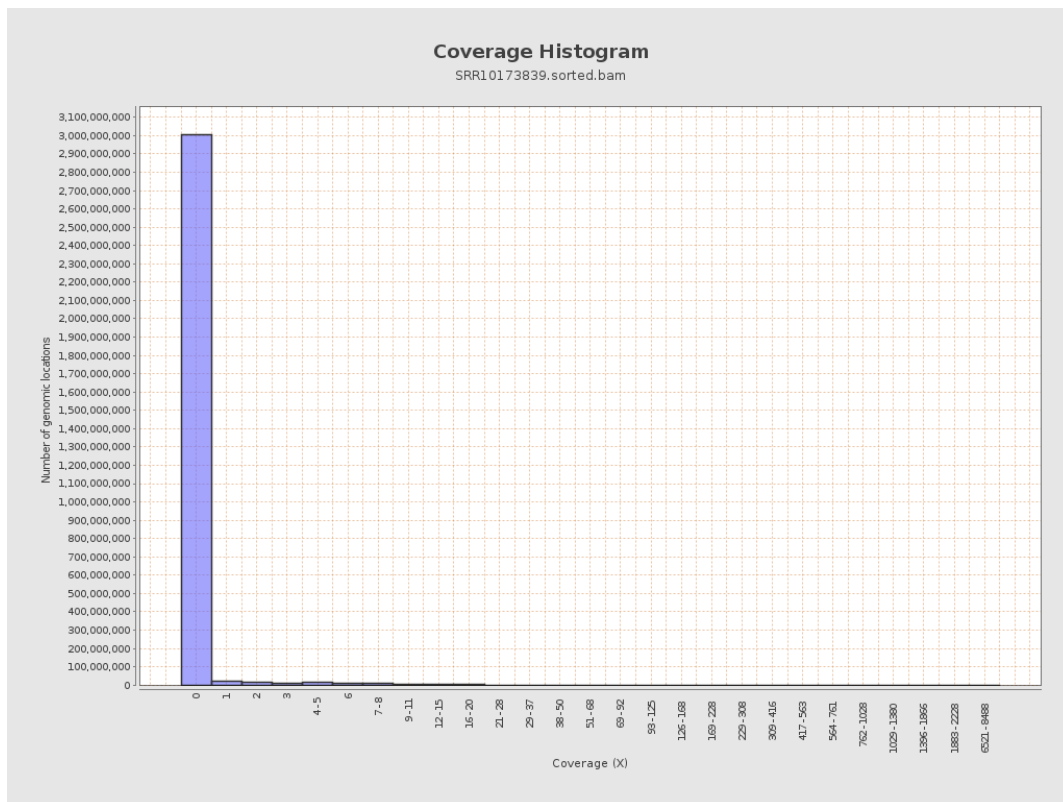
		bases	coverage	deviation
chr1	249250621	41181288	0.1652	1.3949
chr2	243199373	31436485	0.1293	5.9558
chr3	198022430	27800000	0.1404	1.0844
chr4	191154276	22501681	0.1177	1.2016
chr5	180915260	18432376	0.1019	0.9167
chr6	171115067	20486242	0.1197	1.0236
chr7	159138663	37623071	0.2364	2.2951
chr8	146364022	47959813	0.3277	1.9191
chr9	141213431	14566176	0.1032	1.1406
chr10	135534747	20082063	0.1482	2.9583
chr11	135006516	17505282	0.1297	1.0672
chr12	133851895	16544629	0.1236	1.014
chr13	115169878	8400381	0.0729	0.7766
chr14	107349540	14412828	0.1343	1.059
chr15	102531392	10120478	0.0987	0.8887
chr16	90354753	10148639	0.1123	1.2362
chr17	81195210	10720548	0.132	1.0997
chr18	78077248	7586271	0.0972	1.3488
chr19	59128983	5615460	0.095	1.0504
chr20	63025520	11549658	0.1833	1.2245
chr21	48129895	5204586	0.1081	0.9833
chr22	51304566	4514141	0.088	0.8081
chrMT	16571	1177039	71.0301	55.0312
chrX	155270560	15485820	0.0997	0.9075

chrY	59373566	787100	0.0133	0.6028
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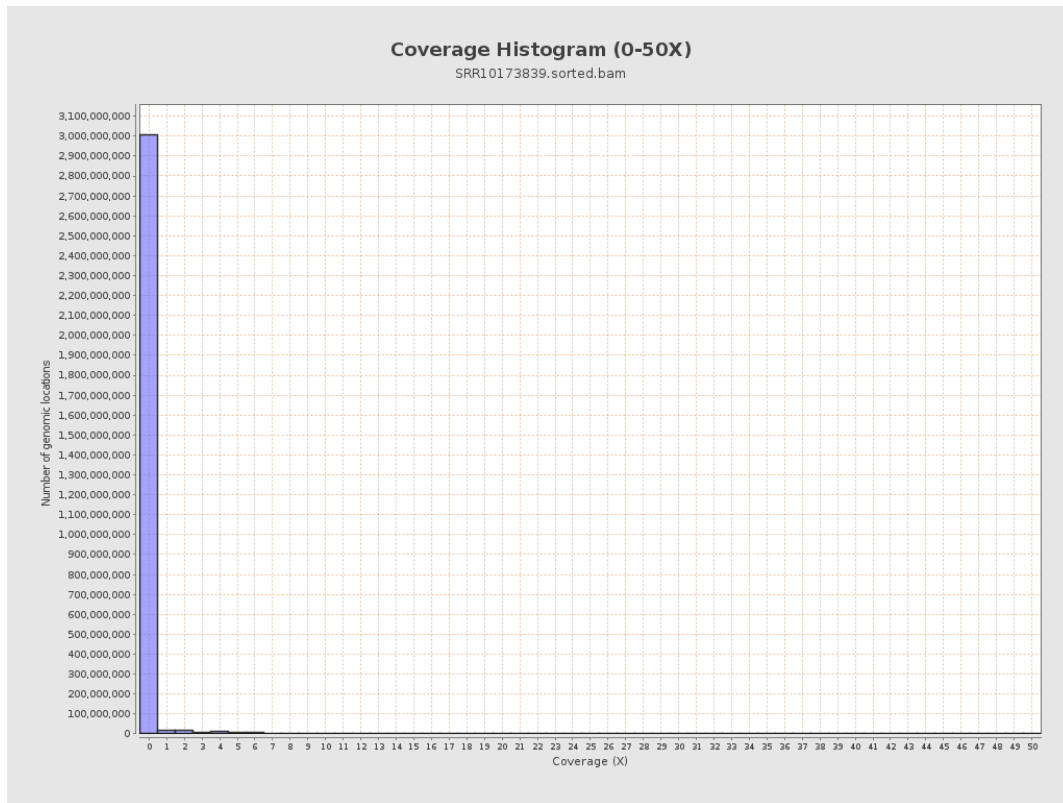
3. Results : Coverage across reference



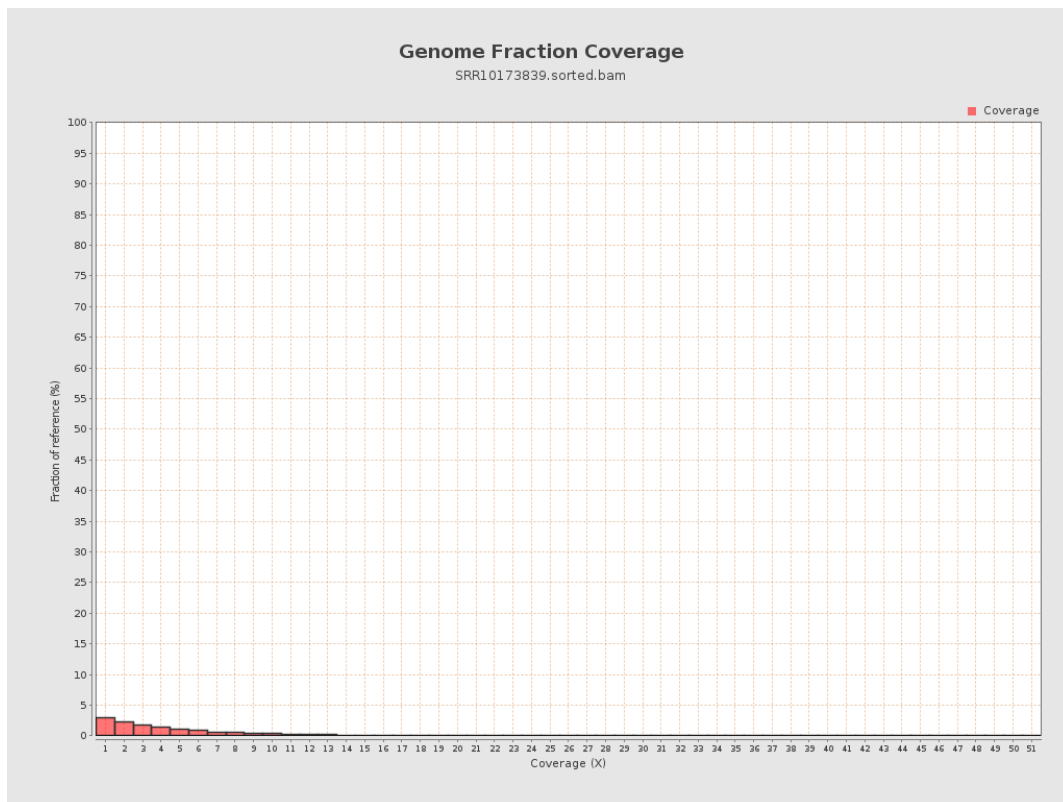
4. Results : Coverage Histogram



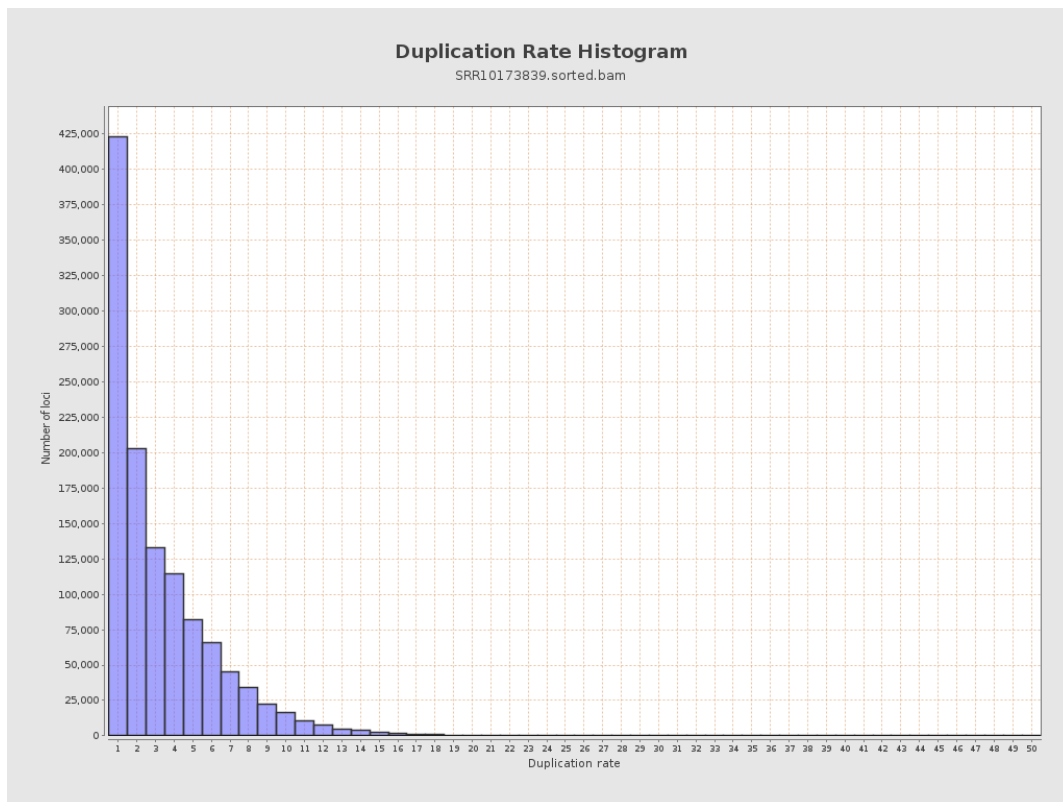
5. Results : Coverage Histogram (0-50X)



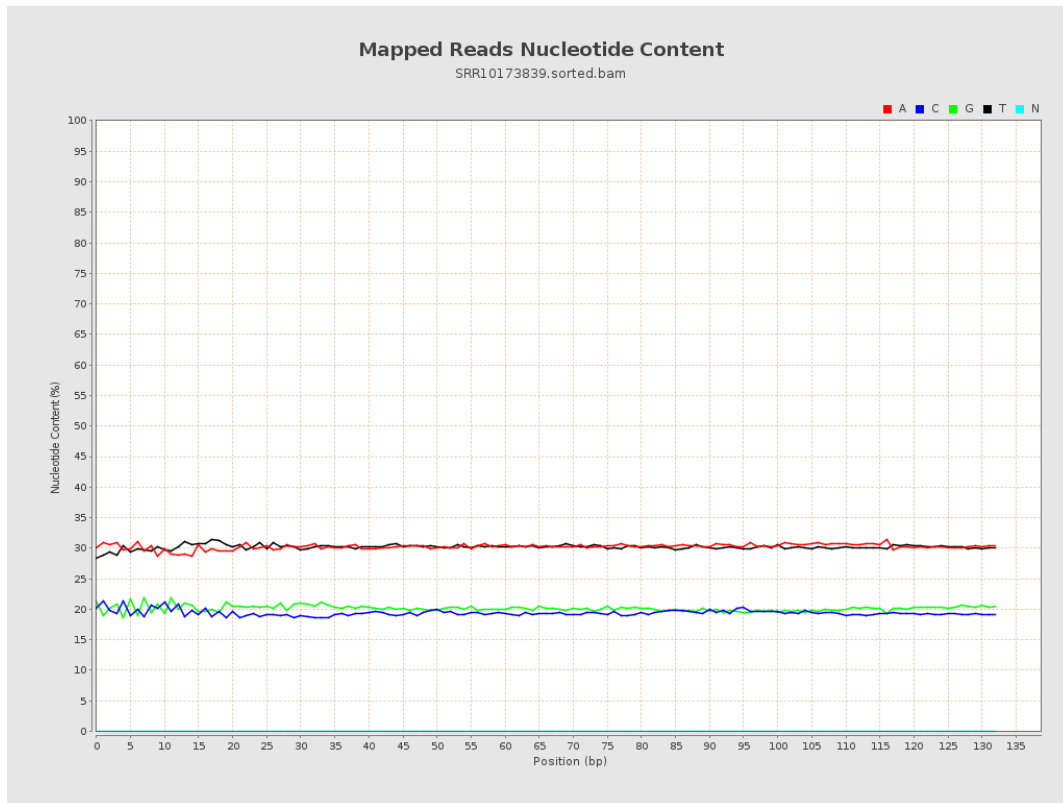
6. Results : Genome Fraction Coverage



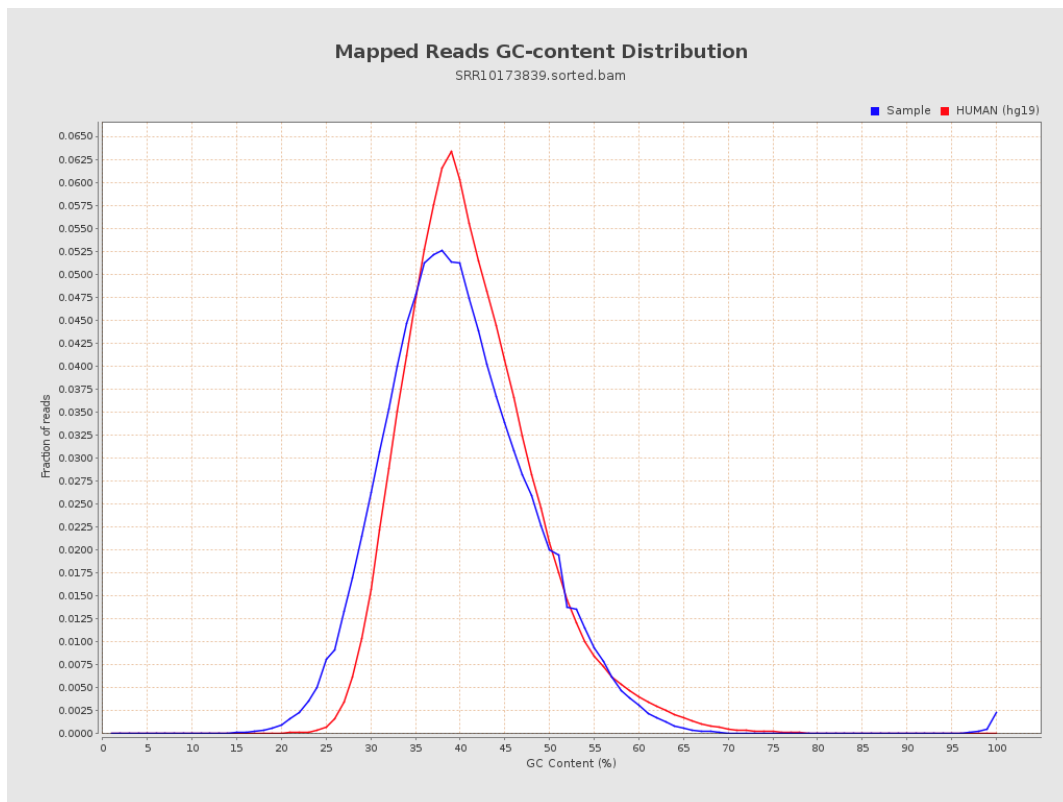
7. Results : Duplication Rate Histogram



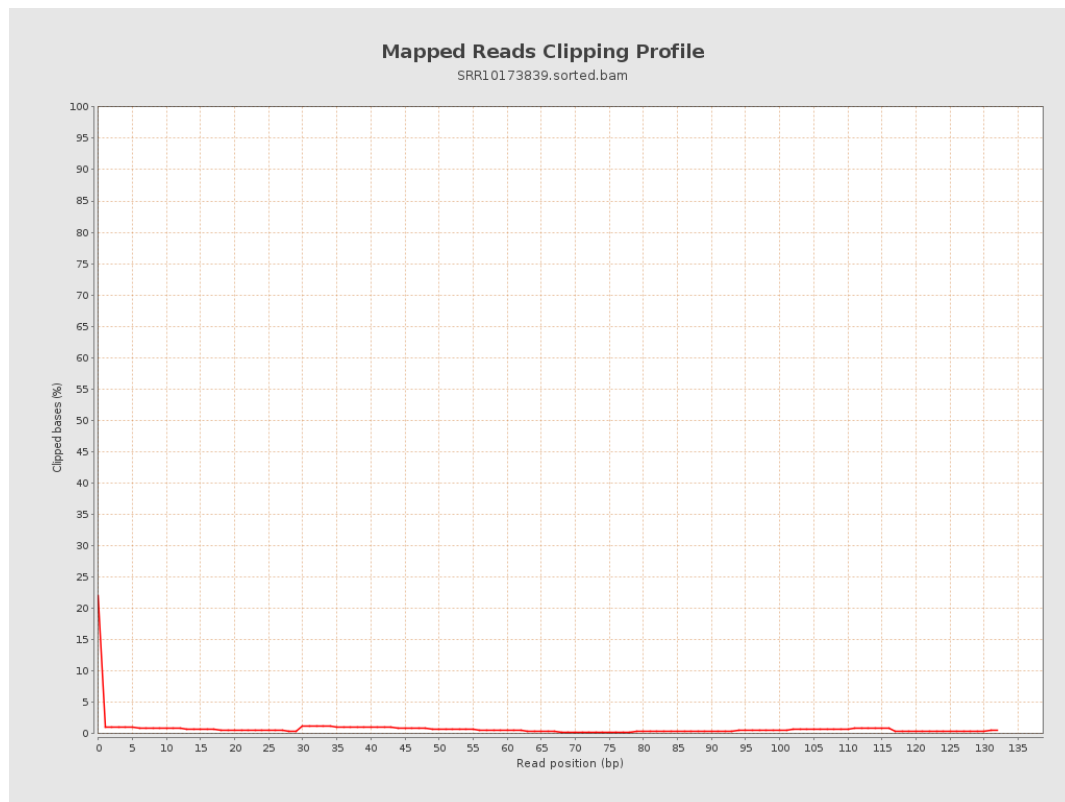
8. Results : Mapped Reads Nucleotide Content



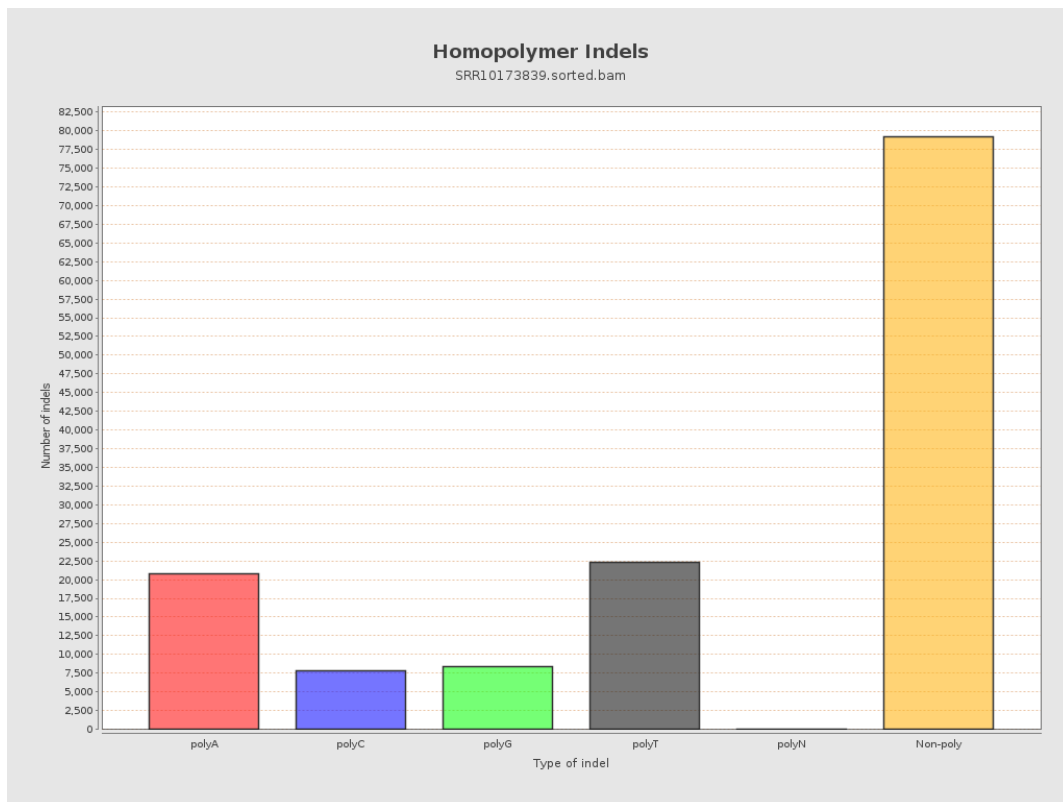
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



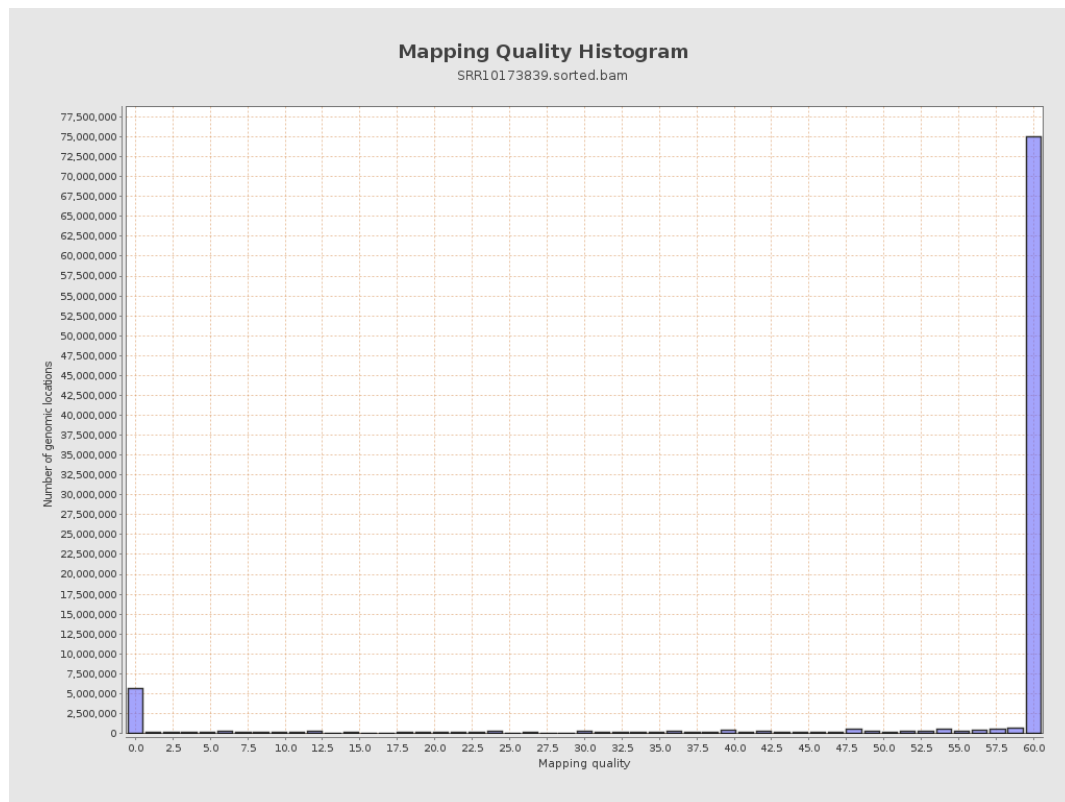
11. Results : Homopolymer Indels



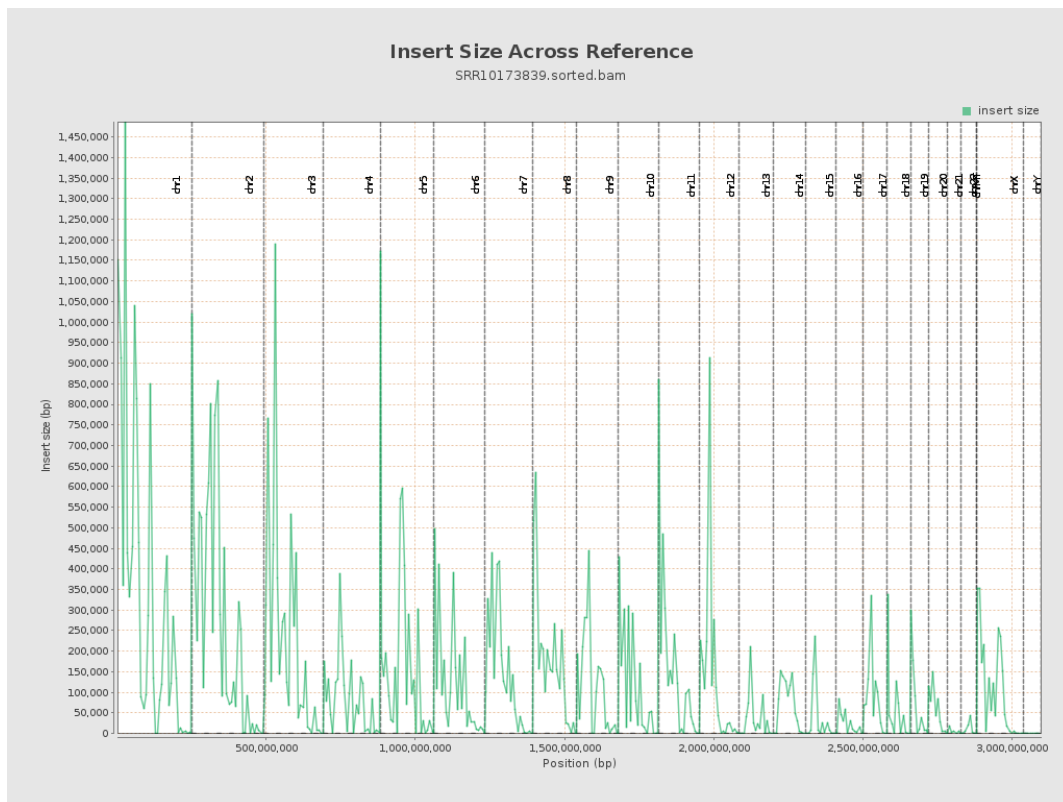
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

