

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 23:57:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174039.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_SRR10174039 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174039_1.fastq.gz SRR10174039_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 23:57:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174039.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,885,004
Mapped reads	2,819,452 / 97.73%
Unmapped reads	65,552 / 2.27%
Mapped paired reads	2,819,452 / 97.73%
Mapped reads, first in pair	1,410,122 / 48.88%
Mapped reads, second in pair	1,409,330 / 48.85%
Mapped reads, both in pair	2,777,380 / 96.27%
Mapped reads, singletons	42,072 / 1.46%
Secondary alignments	0
Supplementary alignments	286,617 / 9.93%
Read min/max/mean length	30 / 133 / 127.76
Duplicated reads (estimated)	2,083,807 / 72.23%
Duplication rate	62.66%
Clipped reads	1,134,540 / 39.33%

2.2. ACGT Content

Number/percentage of A's	100,904,582 / 30.35%
Number/percentage of C's	64,463,433 / 19.39%
Number/percentage of T's	100,589,348 / 30.25%
Number/percentage of G's	66,530,498 / 20.01%
Number/percentage of N's	4,272 / 0%

GC Percentage	39.4%
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2.3. Coverage

Mean	0.1075
Standard Deviation	1.7105

2.4. Mapping Quality

Mean Mapping Quality	52.71
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2.5. Insert size

Mean	825,297.23
Standard Deviation	8,389,364.42
P25/Median/P75	138 / 192 / 276

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	3,383,070
Insertions	35,125
Mapped reads with at least one insertion	1.2%
Deletions	80,098
Mapped reads with at least one deletion	2.77%
Homopolymer indels	42.72%

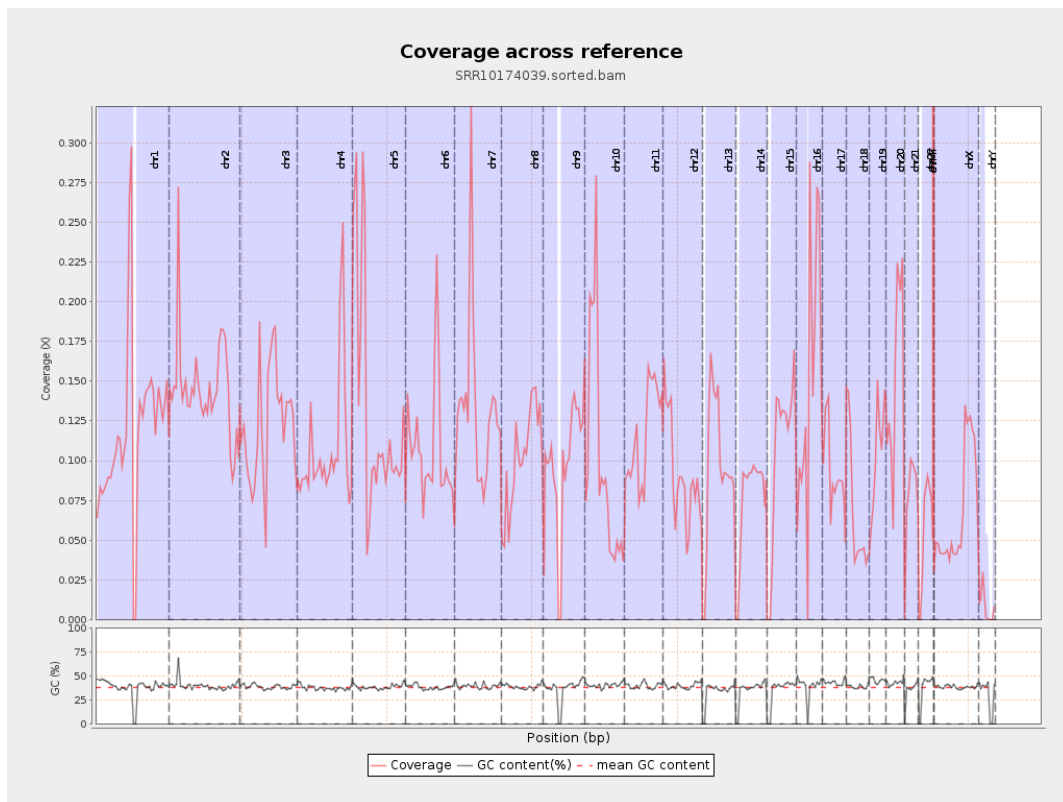
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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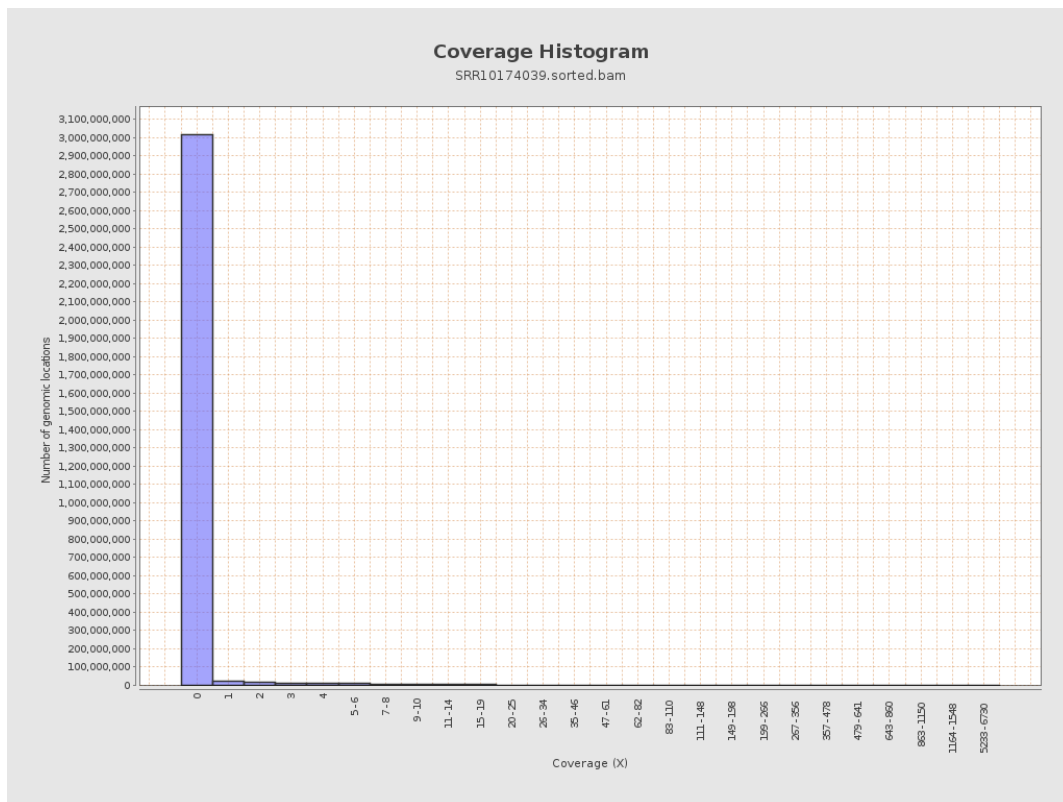
		bases	coverage	deviation
chr1	249250621	29587025	0.1187	1.4353
chr2	243199373	35271547	0.145	4.766
chr3	198022430	24330101	0.1229	0.9597
chr4	191154276	20165305	0.1055	1.001
chr5	180915260	23686924	0.1309	0.9949
chr6	171115067	18522756	0.1082	0.9163
chr7	159138663	21053449	0.1323	1.5961
chr8	146364022	15020285	0.1026	0.9859
chr9	141213431	13801479	0.0977	0.9904
chr10	135534747	13441019	0.0992	1.7084
chr11	135006516	15667653	0.1161	0.9415
chr12	133851895	12079338	0.0902	0.8213
chr13	115169878	10889993	0.0946	0.8493
chr14	107349540	8043856	0.0749	0.7485
chr15	102531392	10744617	0.1048	0.8681
chr16	90354753	13546798	0.1499	1.4506
chr17	81195210	7372042	0.0908	0.8946
chr18	78077248	5210351	0.0667	1.1368
chr19	59128983	6224194	0.1053	1.5426
chr20	63025520	9588268	0.1521	1.0425
chr21	48129895	3701162	0.0769	0.7784
chr22	51304566	2828323	0.0551	0.6067
chrMT	16571	1037265	62.5952	53.6246
chrX	155270560	10416873	0.0671	0.698

chrY	59373566	462384	0.0078	0.3549
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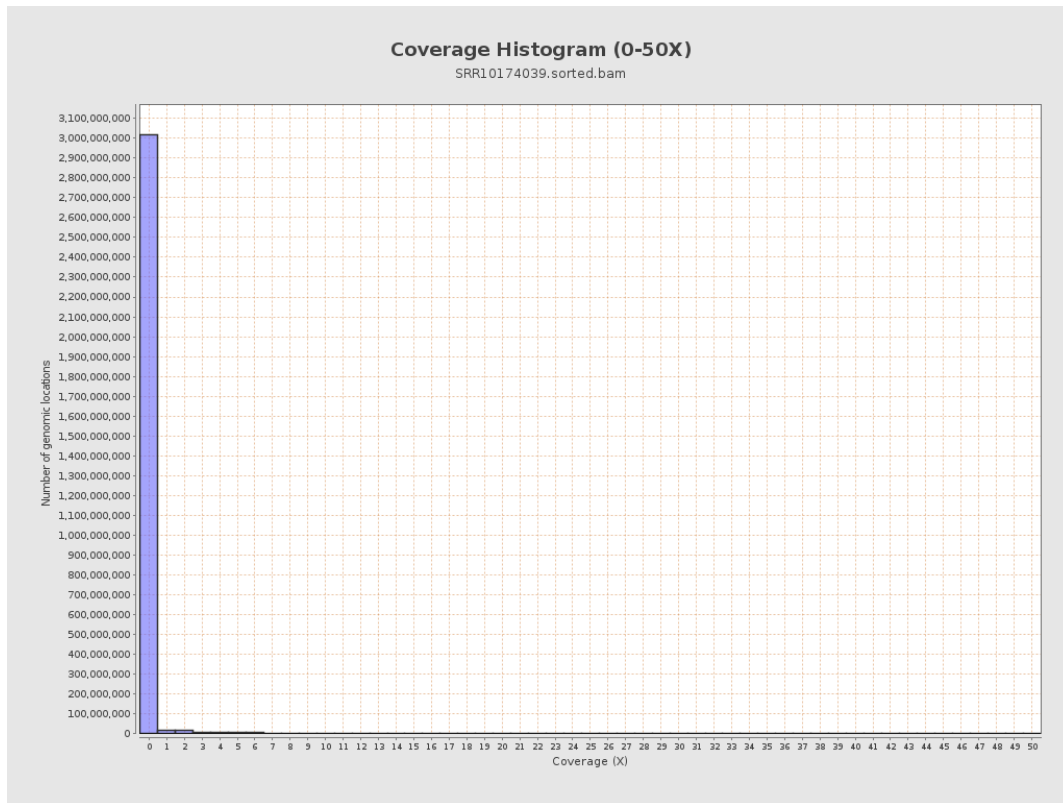
3. Results : Coverage across reference



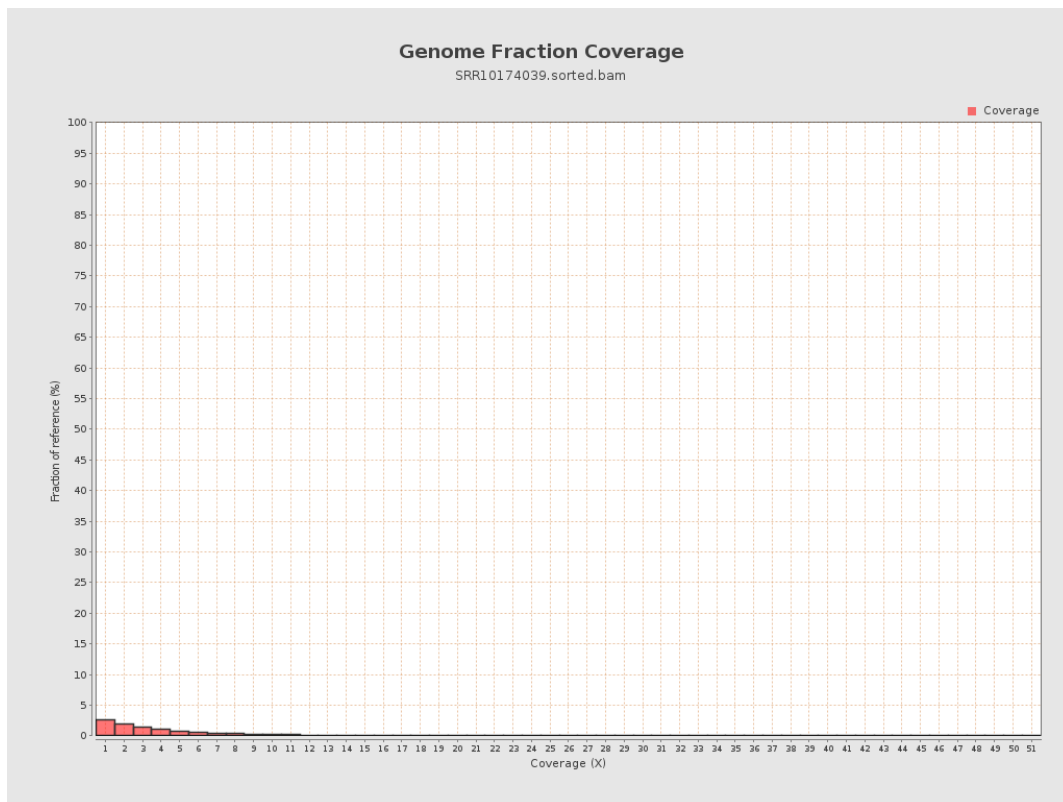
4. Results : Coverage Histogram



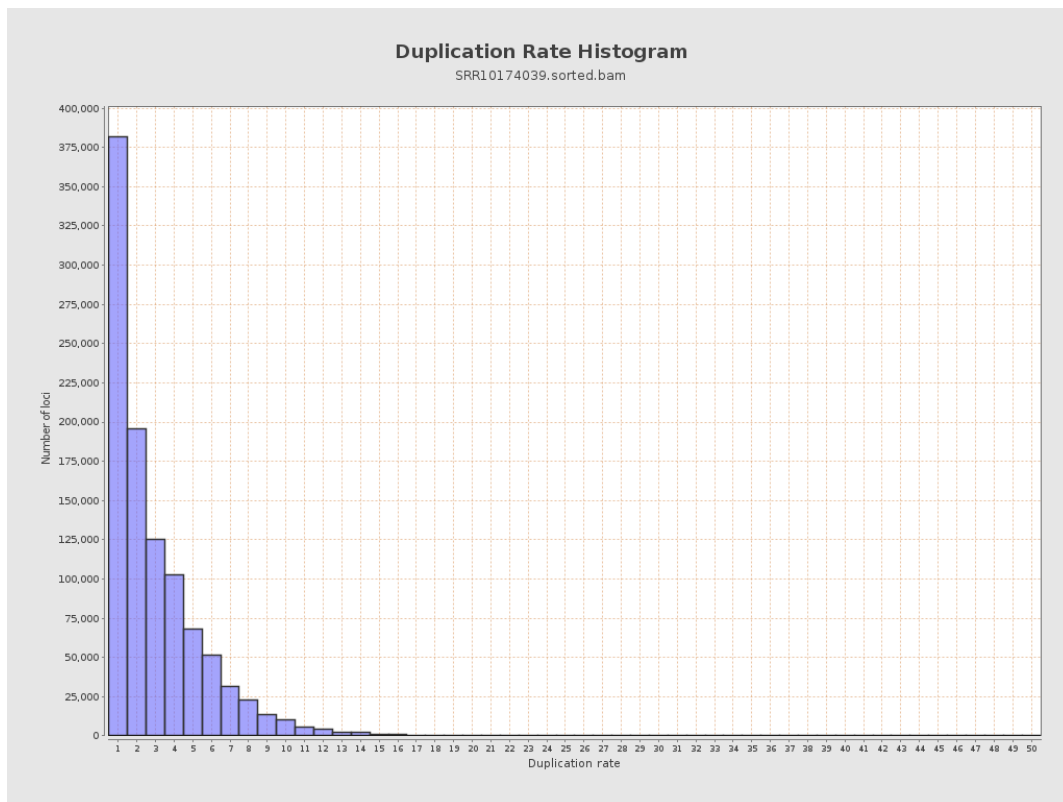
5. Results : Coverage Histogram (0-50X)



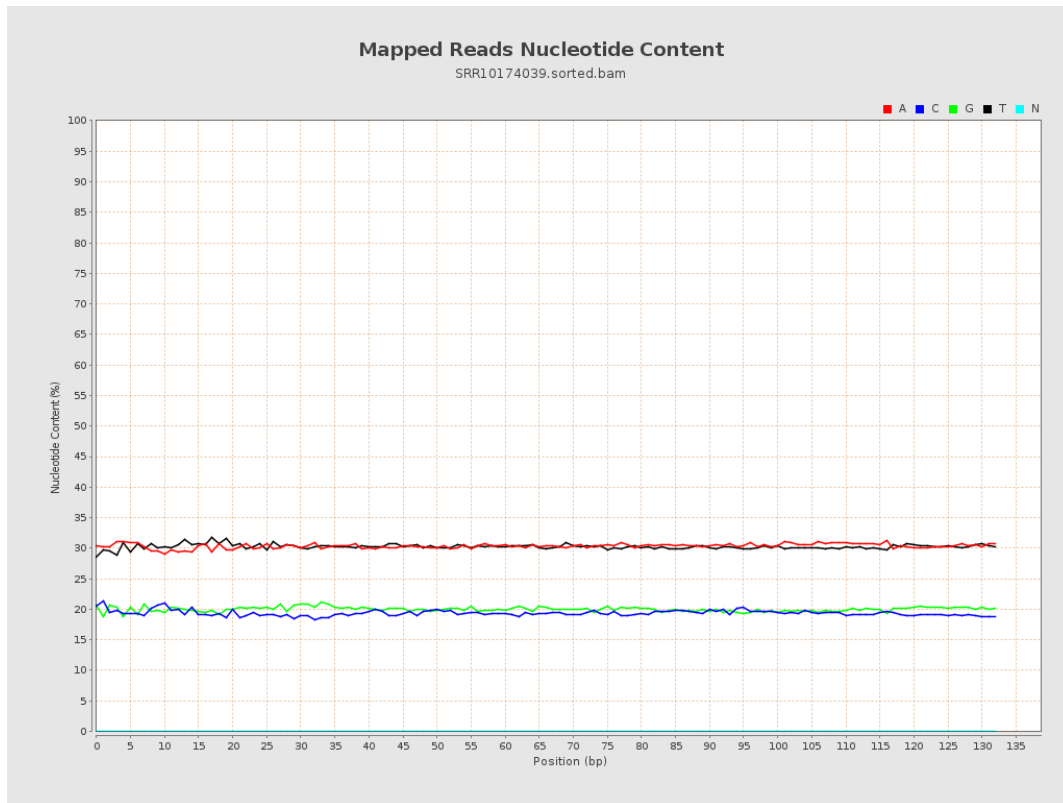
6. Results : Genome Fraction Coverage



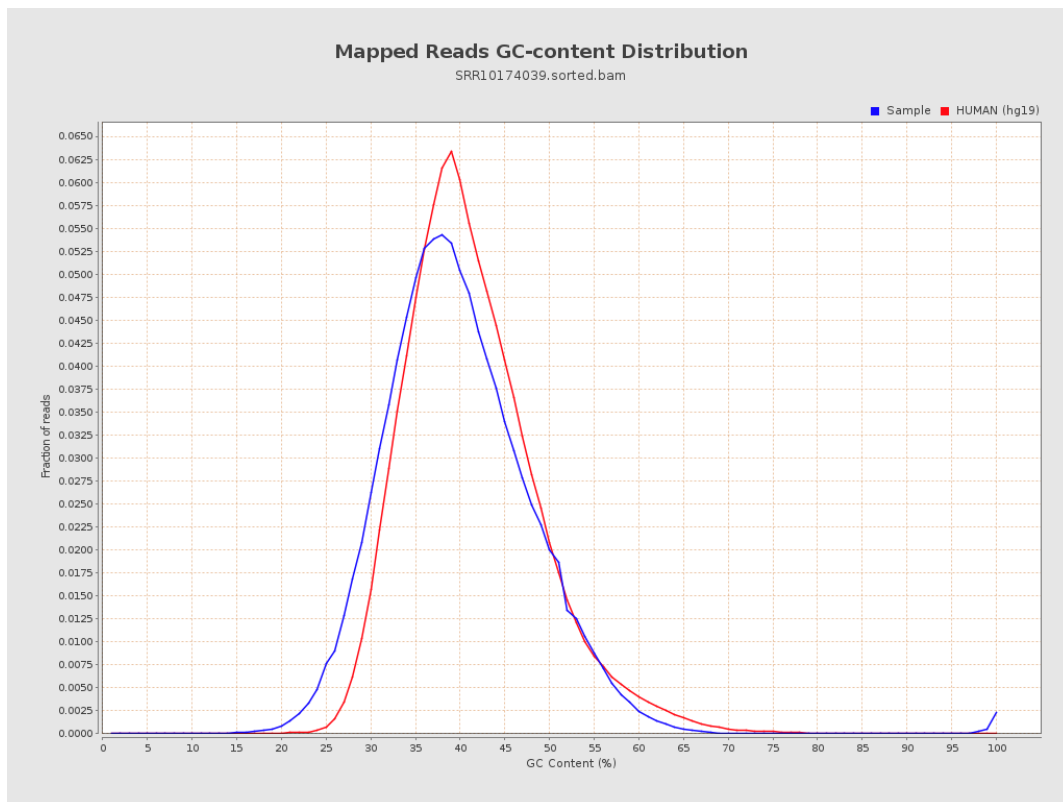
7. Results : Duplication Rate Histogram



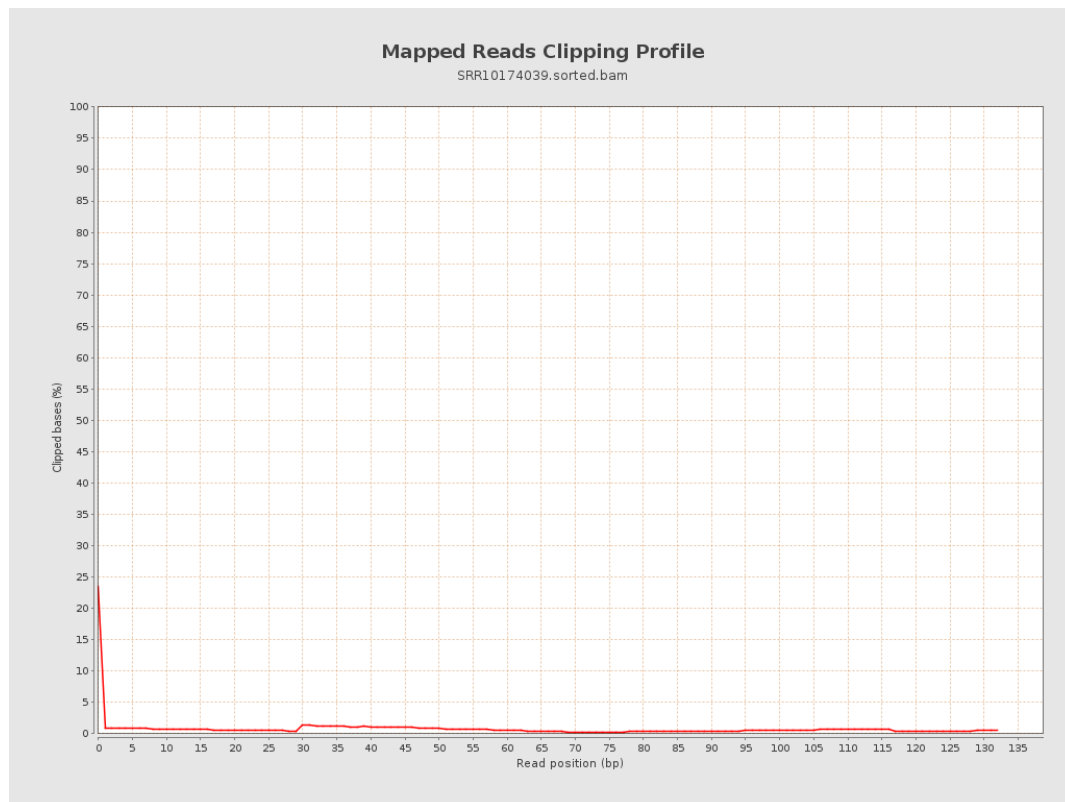
8. Results : Mapped Reads Nucleotide Content



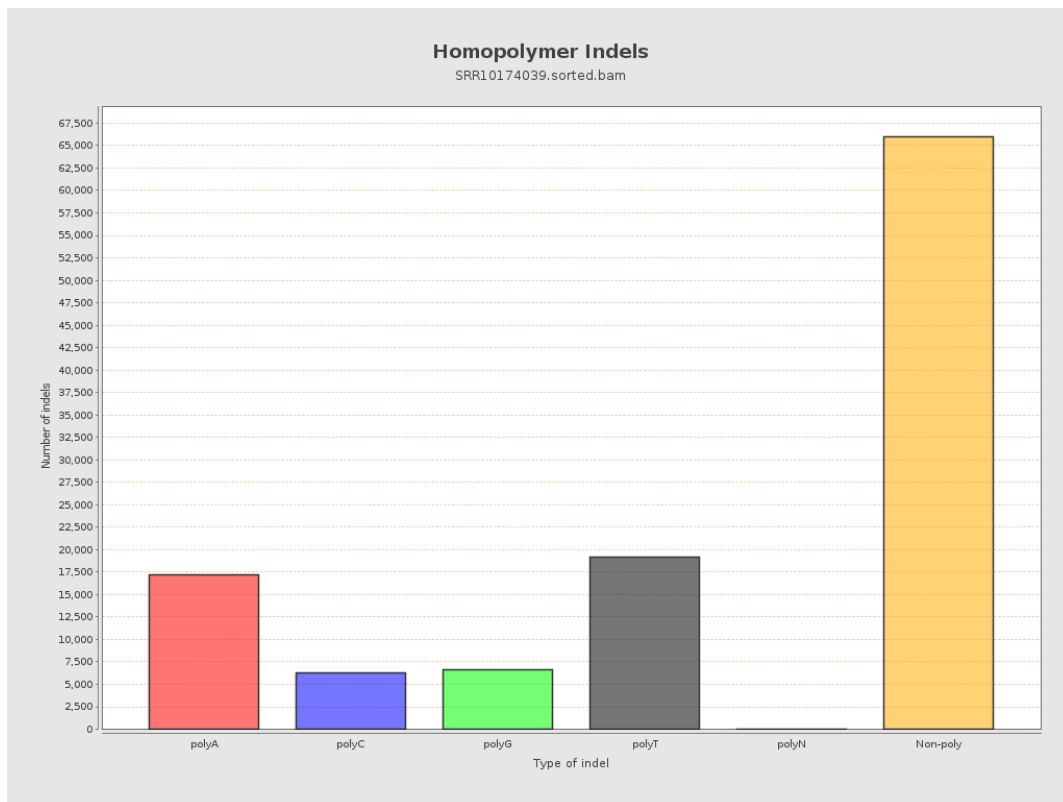
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



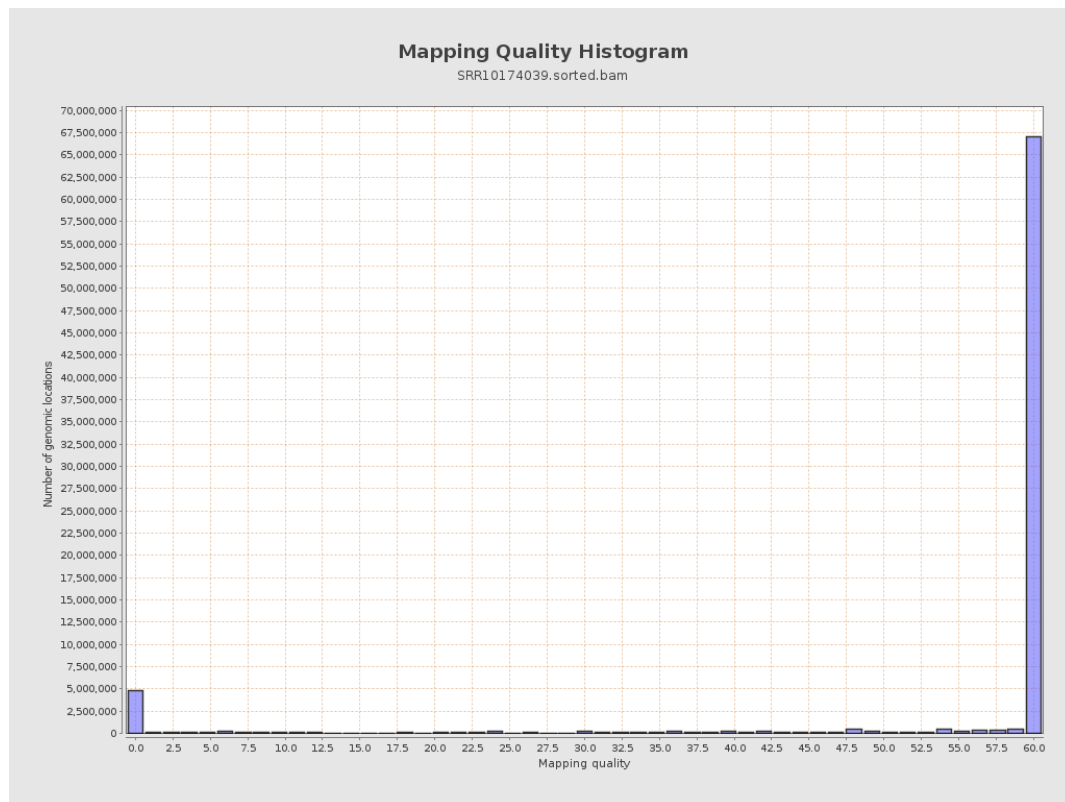
11. Results : Homopolymer Indels



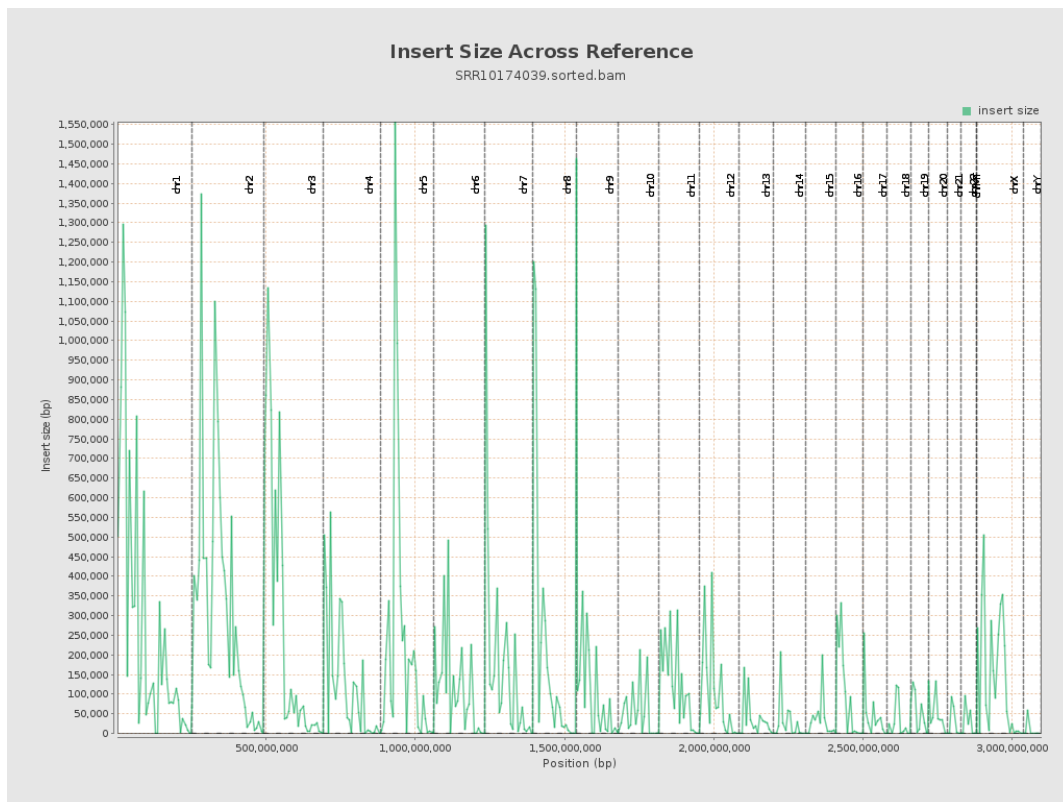
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

