

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 20:48:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174010.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_SRR10174010 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174010_1.fastq.gz SRR10174010_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 20:48:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174010.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,609,908
Mapped reads	4,476,801 / 97.11%
Unmapped reads	133,107 / 2.89%
Mapped paired reads	4,476,801 / 97.11%
Mapped reads, first in pair	2,242,714 / 48.65%
Mapped reads, second in pair	2,234,087 / 48.46%
Mapped reads, both in pair	4,386,944 / 95.16%
Mapped reads, singletons	89,857 / 1.95%
Secondary alignments	0
Supplementary alignments	473,268 / 10.27%
Read min/max/mean length	30 / 133 / 128.5
Duplicated reads (estimated)	3,394,150 / 73.63%
Duplication rate	63.56%
Clipped reads	2,053,333 / 44.54%

2.2. ACGT Content

Number/percentage of A's	159,121,741 / 30.26%
Number/percentage of C's	101,989,340 / 19.4%
Number/percentage of T's	158,729,559 / 30.19%
Number/percentage of G's	106,001,758 / 20.16%
Number/percentage of N's	6,325 / 0%

GC Percentage	39.55%
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2.3. Coverage

Mean	0.17
Standard Deviation	2.6085

2.4. Mapping Quality

Mean Mapping Quality	52.58
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2.5. Insert size

Mean	1,004,997.67
Standard Deviation	9,024,699.75
P25/Median/P75	144 / 202 / 293

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	5,633,681
Insertions	56,563
Mapped reads with at least one insertion	1.22%
Deletions	121,889
Mapped reads with at least one deletion	2.66%
Homopolymer indels	42.4%

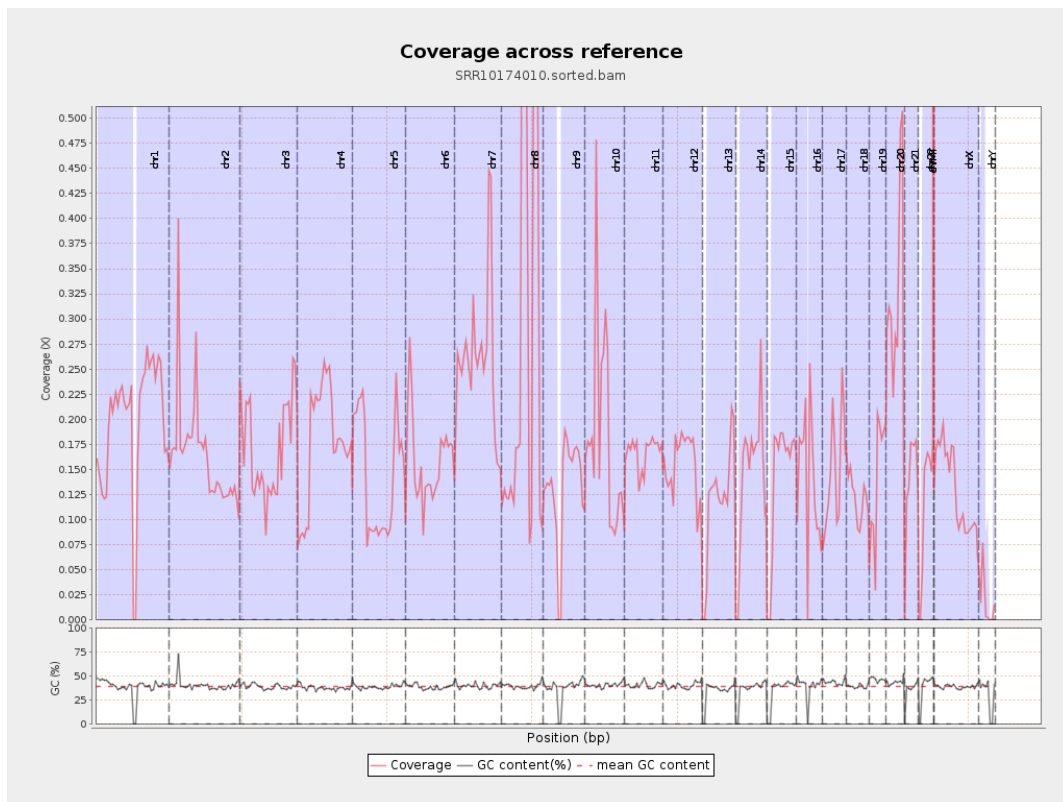
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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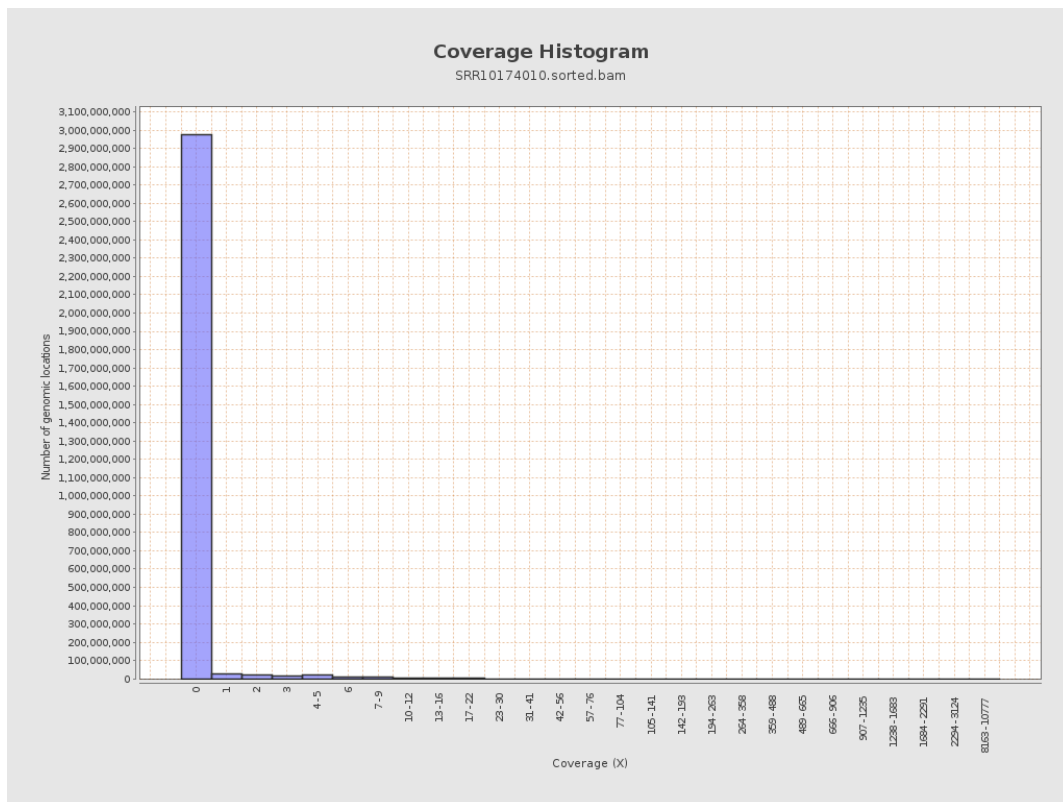
		bases	coverage	deviation
chr1	249250621	48990462	0.1966	1.5903
chr2	243199373	40029084	0.1646	7.5983
chr3	198022430	33867565	0.171	1.1544
chr4	191154276	33555025	0.1755	1.4798
chr5	180915260	25786254	0.1425	1.0468
chr6	171115067	26756709	0.1564	1.128
chr7	159138663	41811413	0.2627	2.6222
chr8	146364022	46919160	0.3206	1.9428
chr9	141213431	18651349	0.1321	1.307
chr10	135534747	24948258	0.1841	3.2969
chr11	135006516	22379008	0.1658	1.1745
chr12	133851895	20817850	0.1555	1.087
chr13	115169878	13641039	0.1184	0.9542
chr14	107349540	15546958	0.1448	1.0525
chr15	102531392	14612359	0.1425	1.0274
chr16	90354753	12383046	0.137	1.4231
chr17	81195210	12117259	0.1492	1.1739
chr18	78077248	9607786	0.1231	1.6079
chr19	59128983	8236521	0.1393	1.2943
chr20	63025520	20652808	0.3277	1.5941
chr21	48129895	6620291	0.1376	1.1221
chr22	51304566	5572758	0.1086	0.8624
chrMT	16571	1507218	90.9552	63.466
chrX	155270560	20066851	0.1292	0.9955

chrY	59373566	1074440	0.0181	0.764
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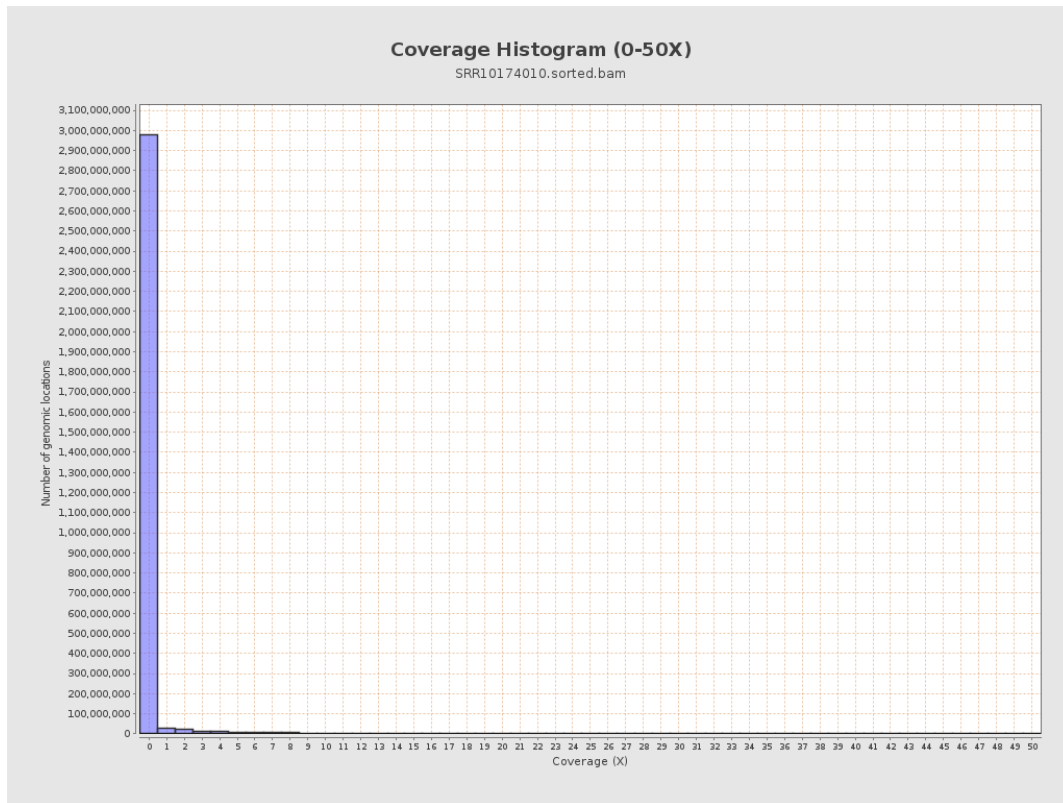
3. Results : Coverage across reference



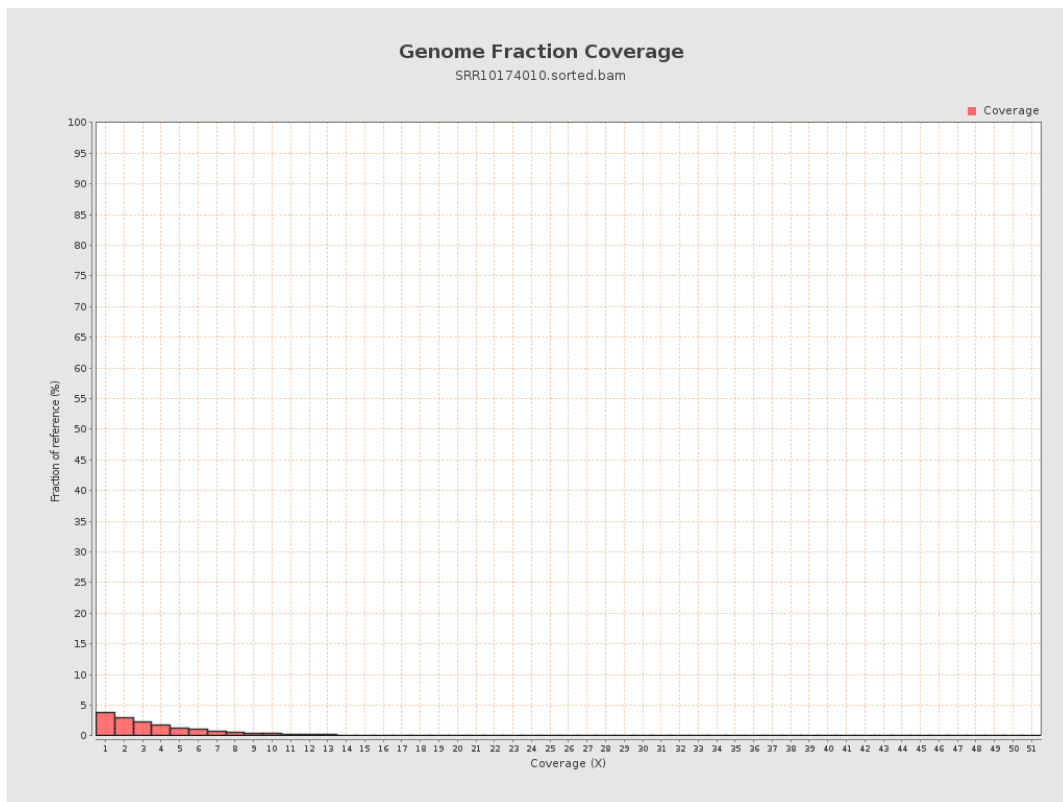
4. Results : Coverage Histogram



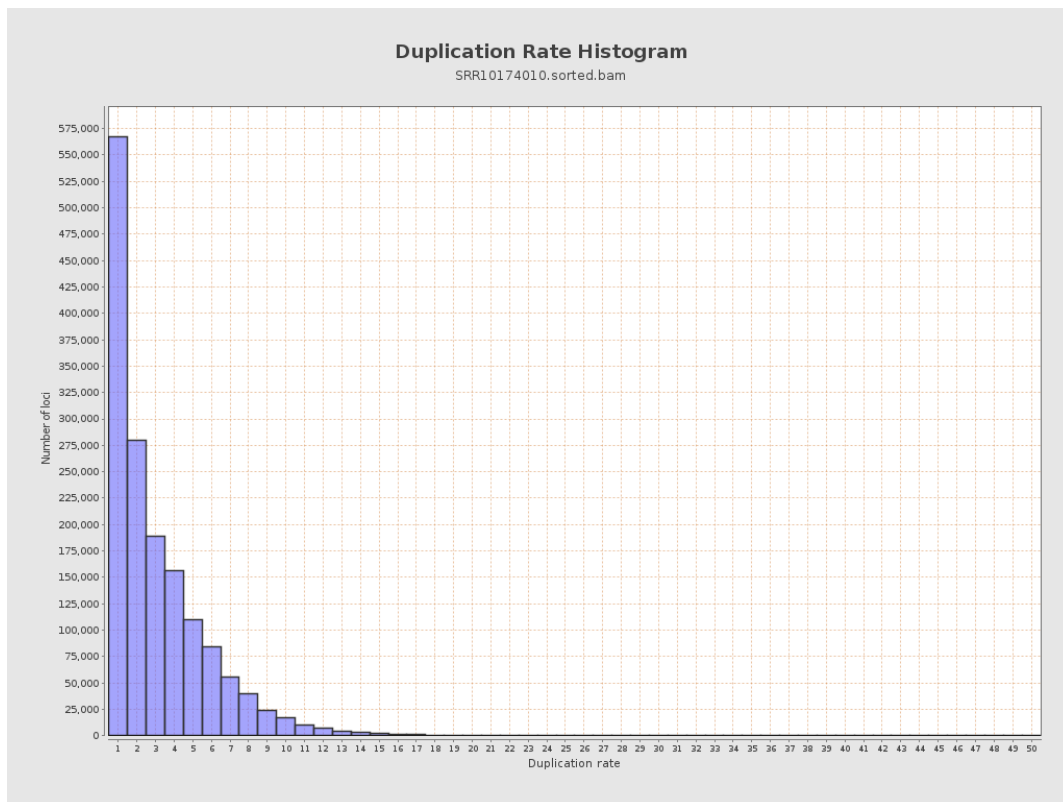
5. Results : Coverage Histogram (0-50X)



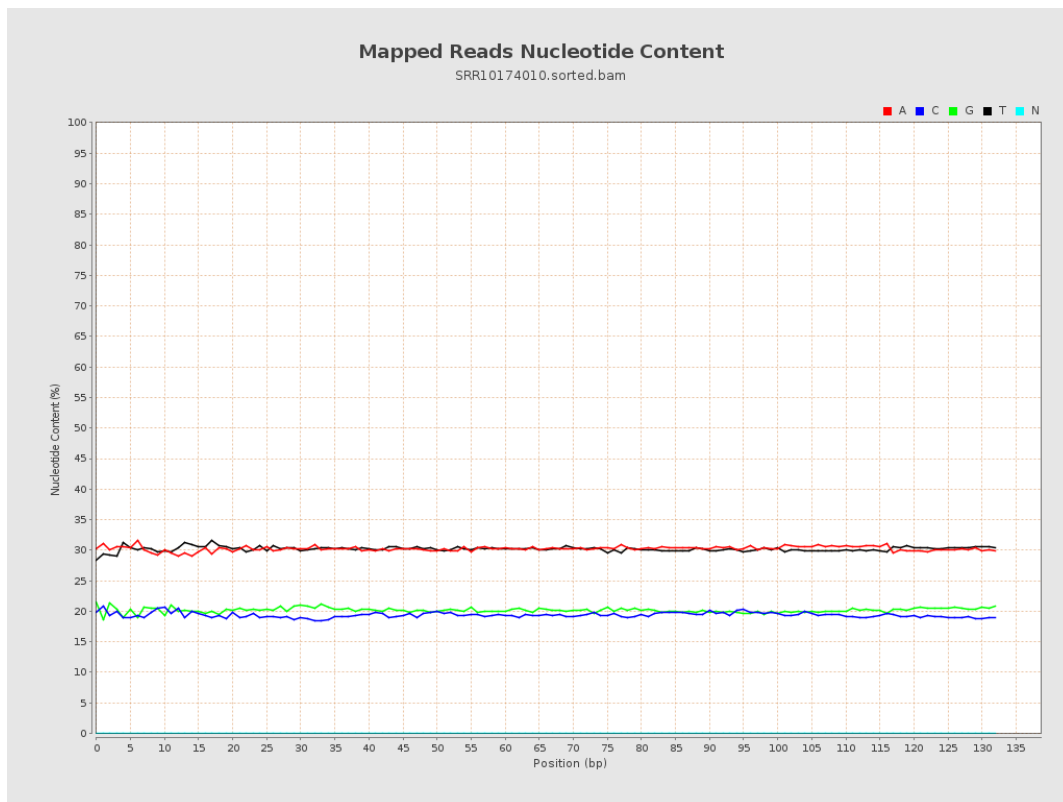
6. Results : Genome Fraction Coverage



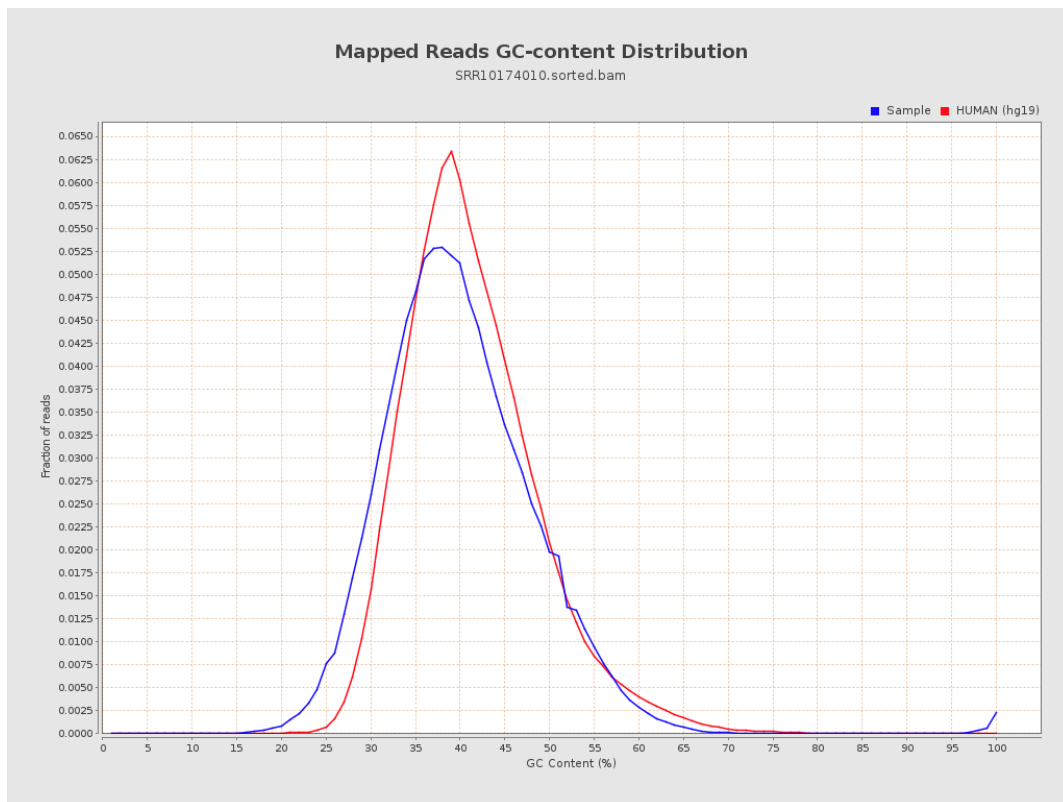
7. Results : Duplication Rate Histogram



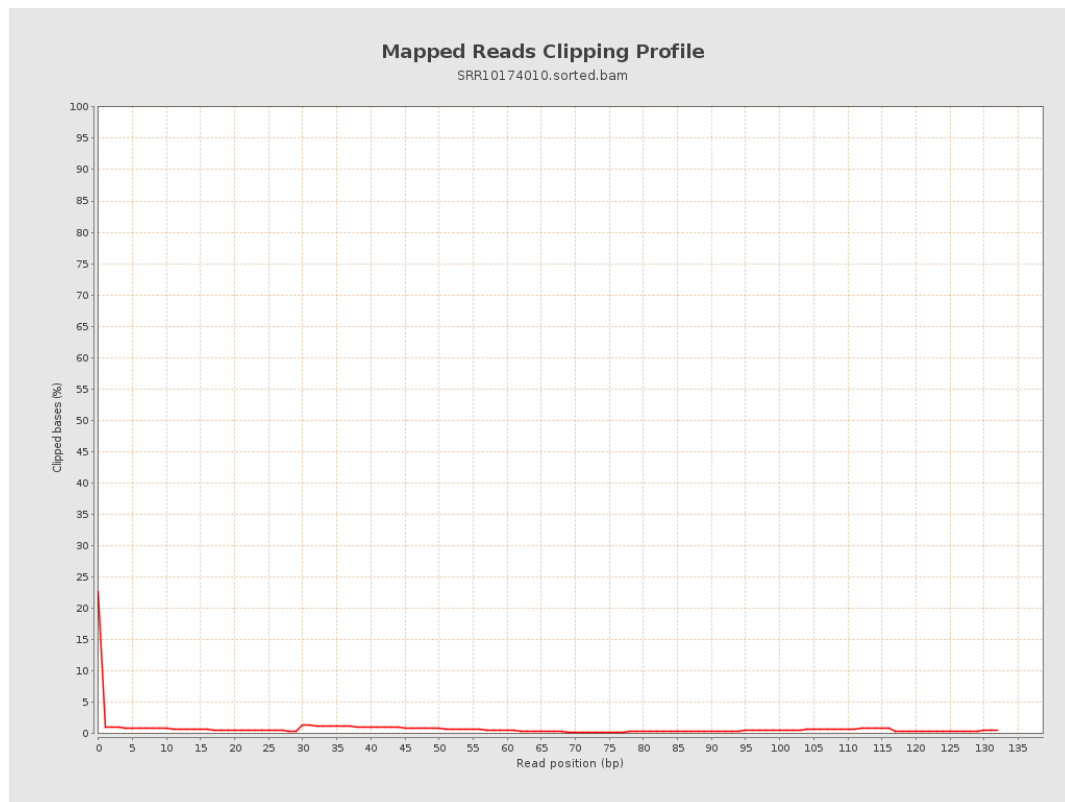
8. Results : Mapped Reads Nucleotide Content



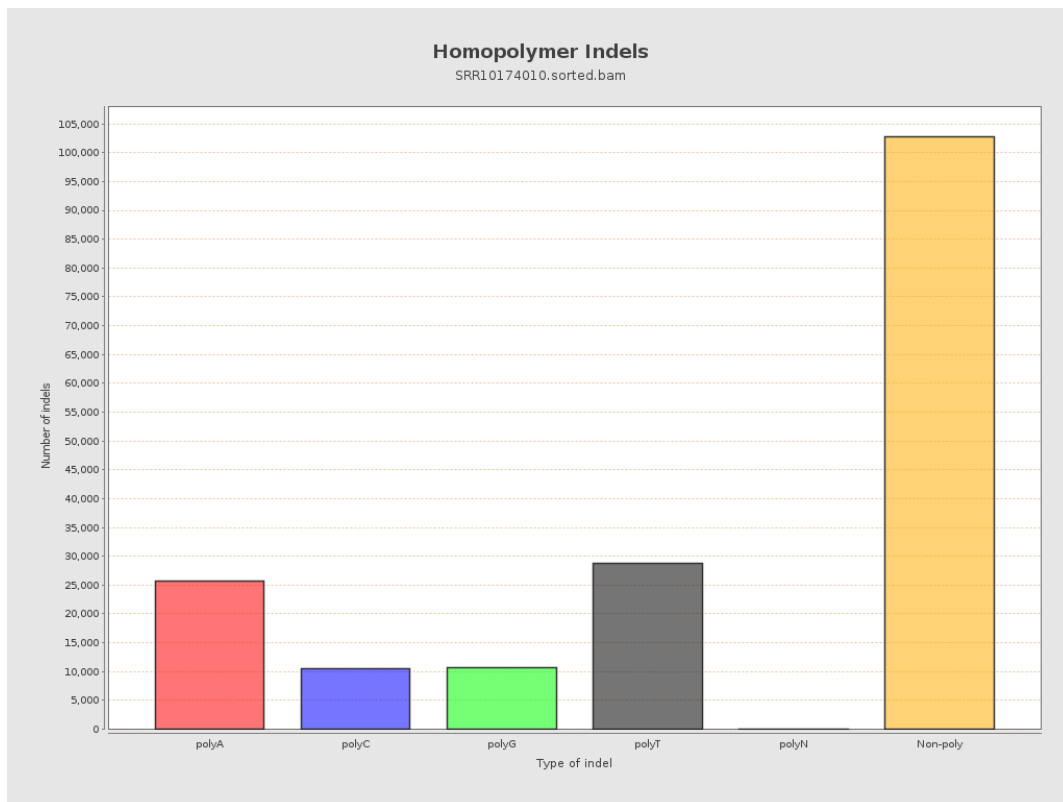
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



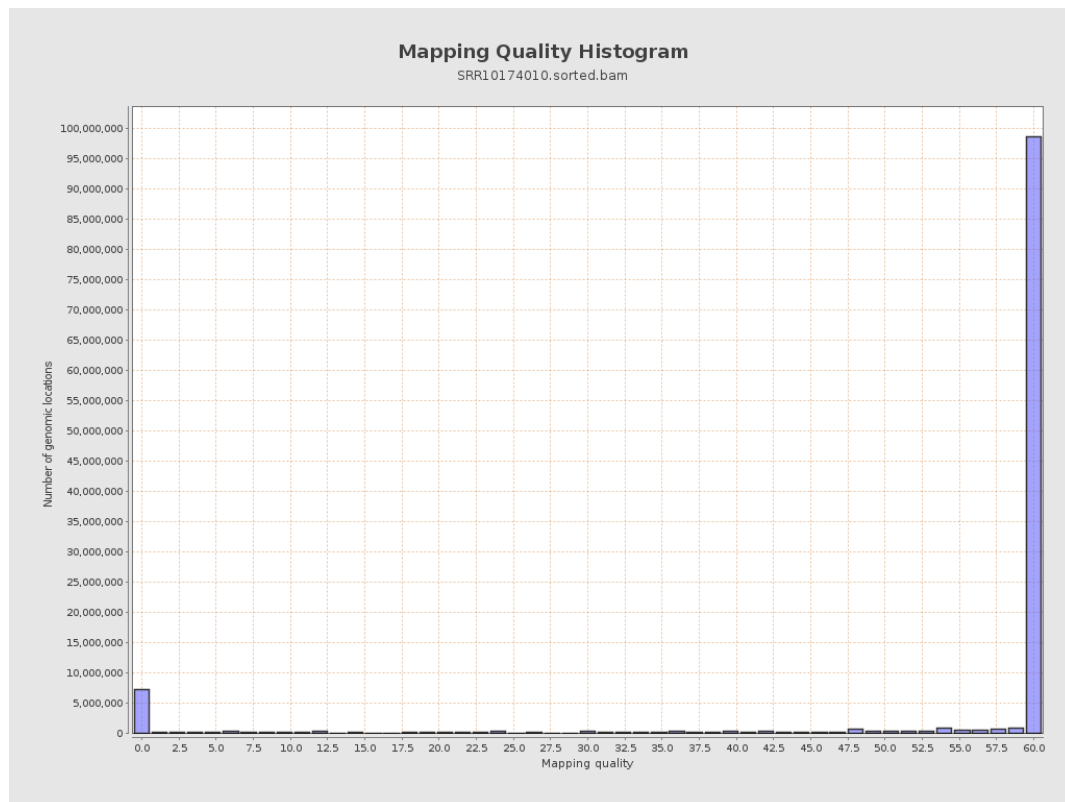
11. Results : Homopolymer Indels



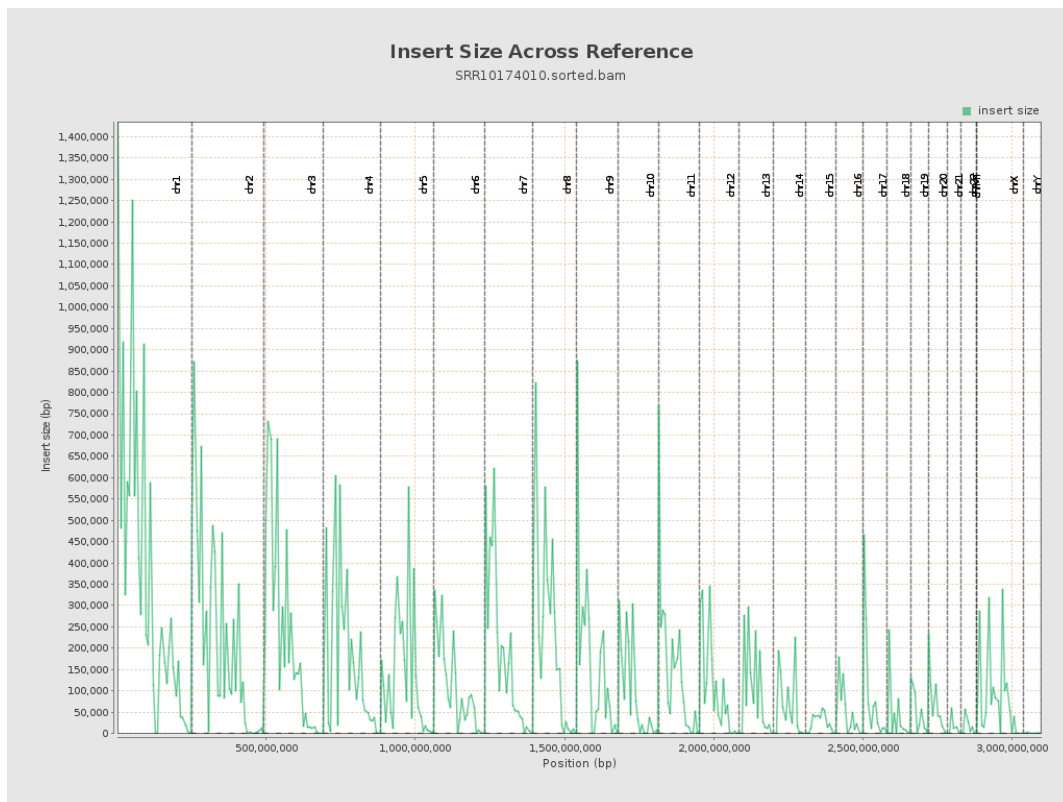
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

