

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 23:41:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006205.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_SRR1006205 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006205_1.fastq.gz SRR1006205_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 23:41:29 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006205.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,126,044
Mapped reads	2,256,281 / 72.18%
Unmapped reads	869,763 / 27.82%
Mapped paired reads	2,256,281 / 72.18%
Mapped reads, first in pair	1,130,937 / 36.18%
Mapped reads, second in pair	1,125,344 / 36%
Mapped reads, both in pair	2,074,696 / 66.37%
Mapped reads, singletons	181,585 / 5.81%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	55,456 / 1.77%
Duplication rate	2.08%
Clipped reads	133,730 / 4.28%

2.2. ACGT Content

Number/percentage of A's	23,926,695 / 27.41%
Number/percentage of C's	19,112,447 / 21.89%
Number/percentage of T's	24,439,115 / 27.99%
Number/percentage of G's	19,819,452 / 22.7%
Number/percentage of N's	4,337 / 0%
GC Percentage	44.59%

2.3. Coverage

Mean	0.0282
Standard Deviation	0.2156

2.4. Mapping Quality

Mean Mapping Quality	47.8
----------------------	------

2.5. Insert size

Mean	57,504.61
Standard Deviation	2,330,578.85
P25/Median/P75	74 / 112 / 153

2.6. Mismatches and indels

General error rate	0.29%
Mismatches	253,983
Insertions	2,818
Mapped reads with at least one insertion	0.12%
Deletions	8,603
Mapped reads with at least one deletion	0.38%
Homopolymer indels	43.53%

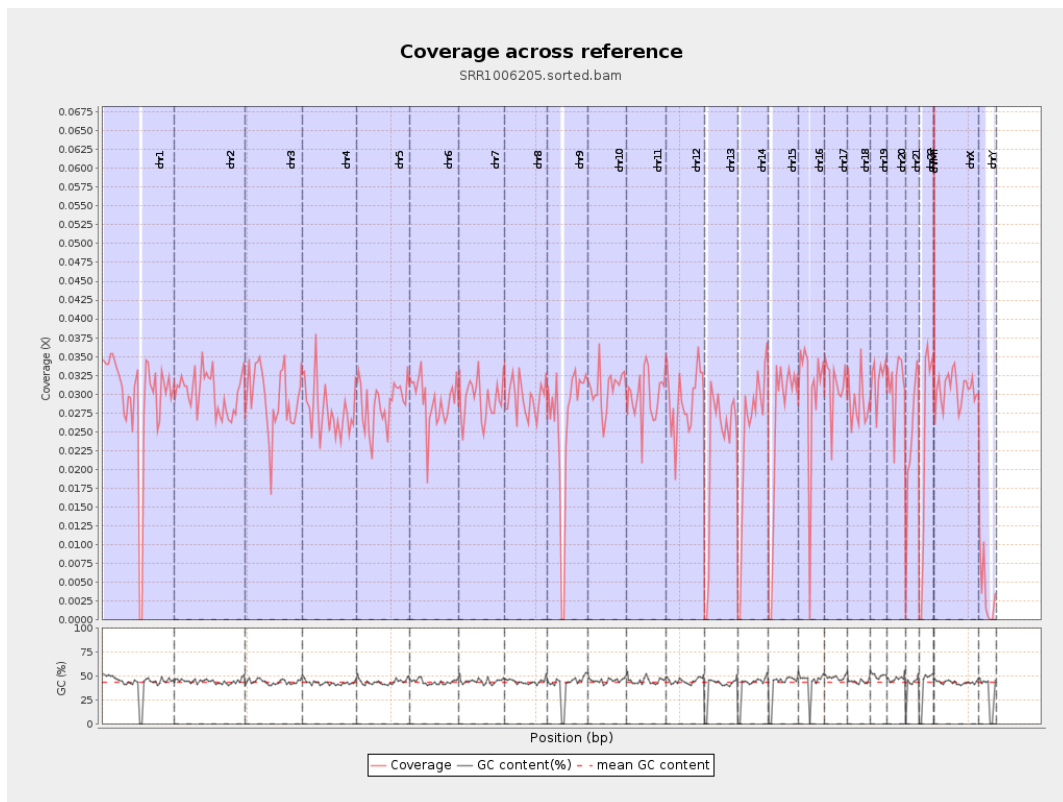
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

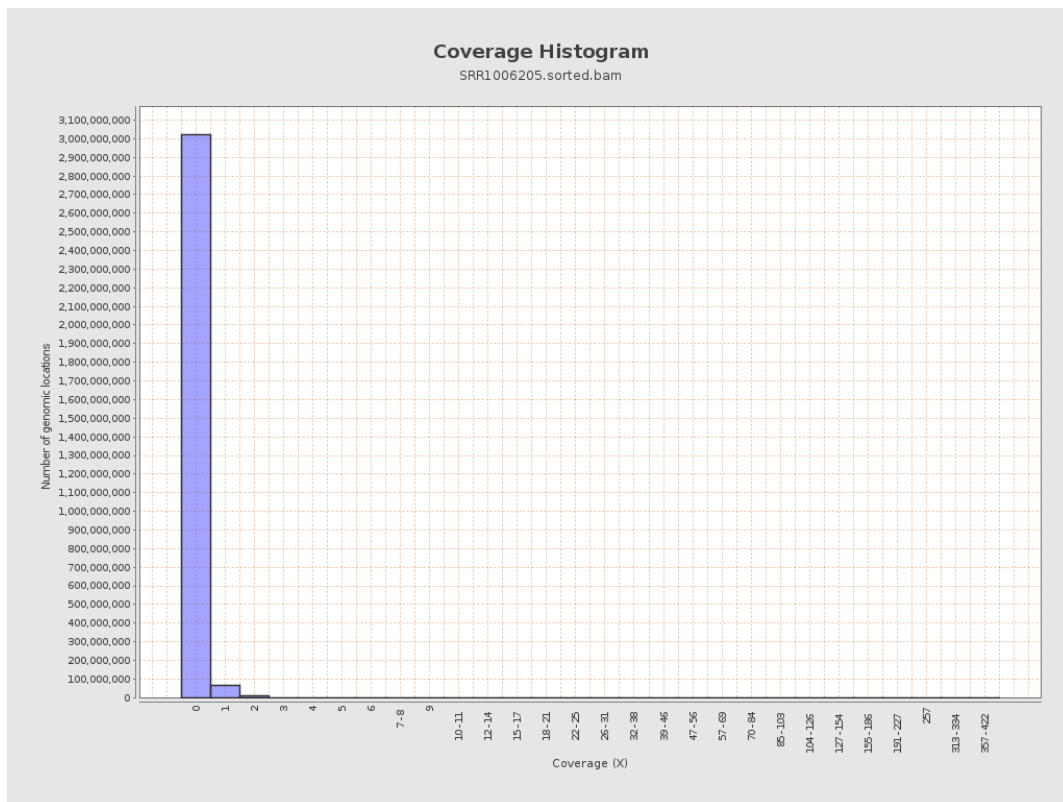
chr1	249250621	7293325	0.0293	0.2528
chr2	243199373	7342414	0.0302	0.2322
chr3	198022430	5825785	0.0294	0.1907
chr4	191154276	5328152	0.0279	0.1937
chr5	180915260	5206352	0.0288	0.2108
chr6	171115067	4967552	0.029	0.199
chr7	159138663	4658192	0.0293	0.2312
chr8	146364022	4305355	0.0294	0.2846
chr9	141213431	3683214	0.0261	0.1936
chr10	135534747	4164273	0.0307	0.2184
chr11	135006516	4022895	0.0298	0.2084
chr12	133851895	3882984	0.029	0.1899
chr13	115169878	2634082	0.0229	0.1679
chr14	107349540	2673275	0.0249	0.2697
chr15	102531392	2633052	0.0257	0.1784
chr16	90354753	2720208	0.0301	0.2067
chr17	81195210	2524492	0.0311	0.2011
chr18	78077248	2252033	0.0288	0.2471
chr19	59128983	1888761	0.0319	0.2328
chr20	63025520	1968512	0.0312	0.1997
chr21	48129895	1163077	0.0242	0.2119
chr22	51304566	1215866	0.0237	0.1929
chrMT	16571	1512	0.0912	0.381
chrX	155270560	4749683	0.0306	0.201

chrY	59373566	208431	0.0035	0.0939
------	----------	--------	--------	--------

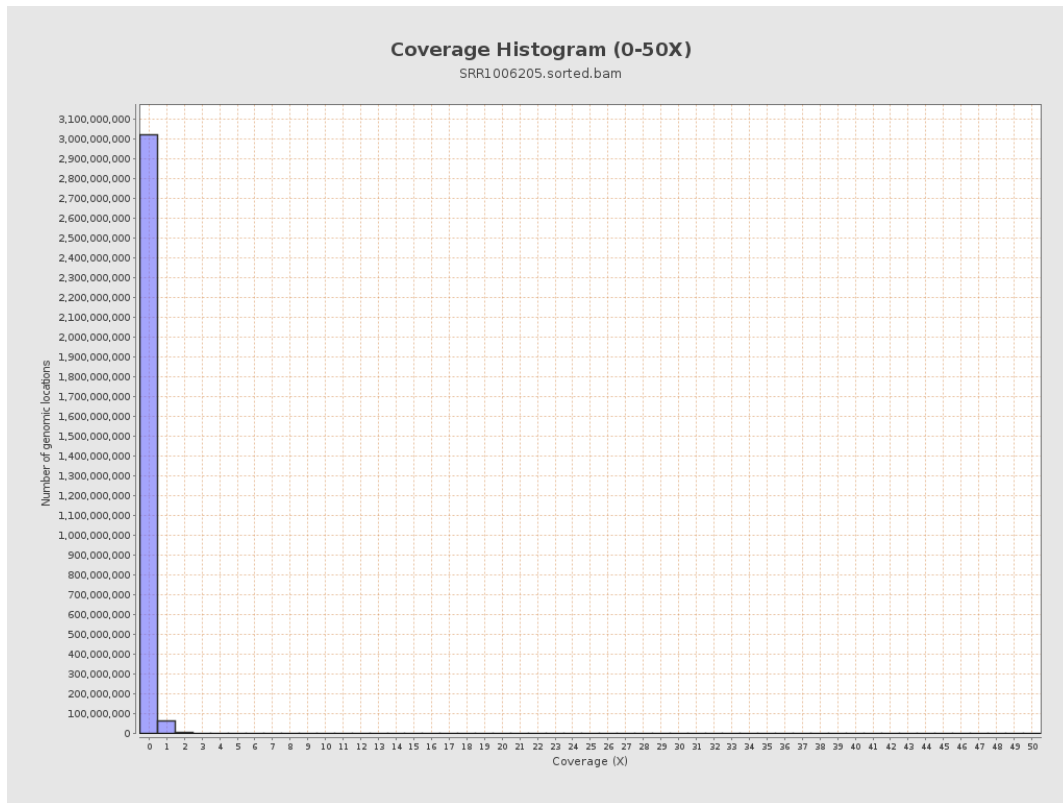
3. Results : Coverage across reference



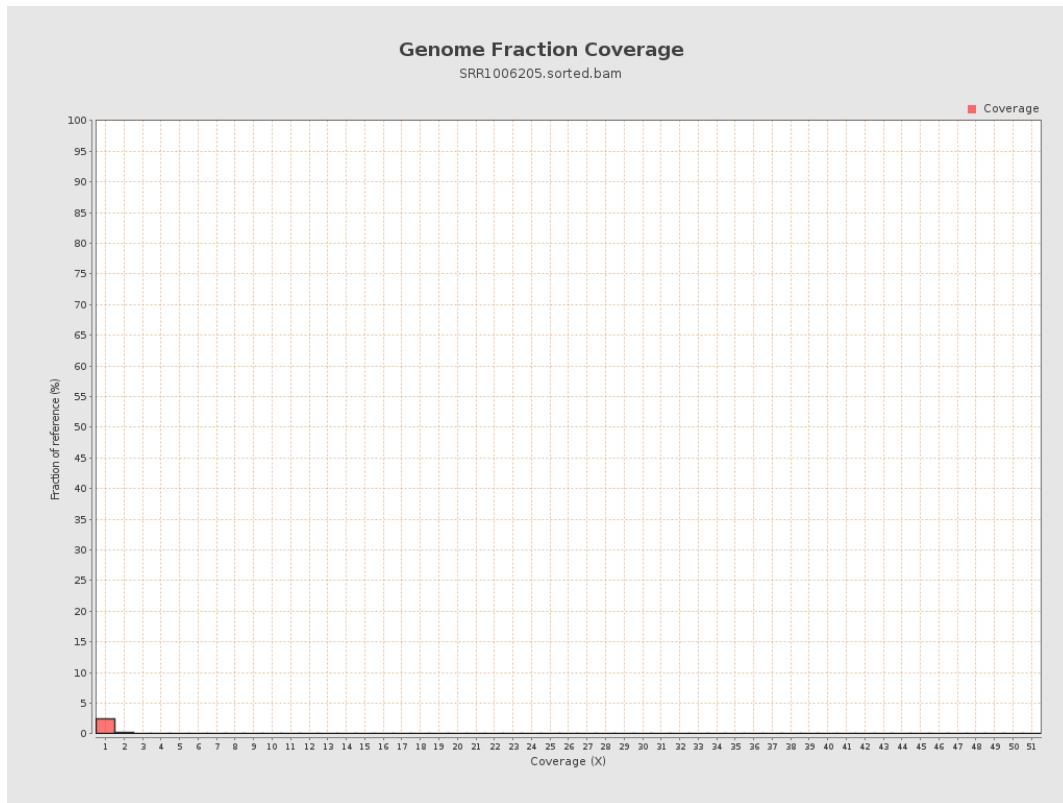
4. Results : Coverage Histogram



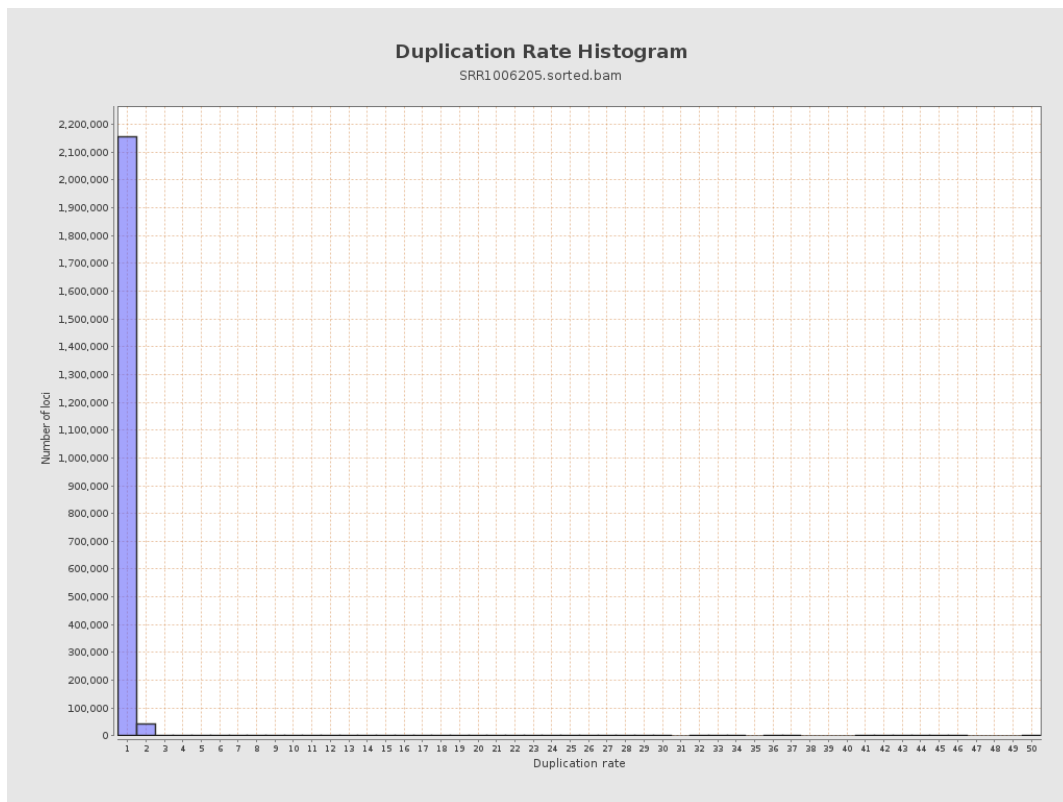
5. Results : Coverage Histogram (0-50X)



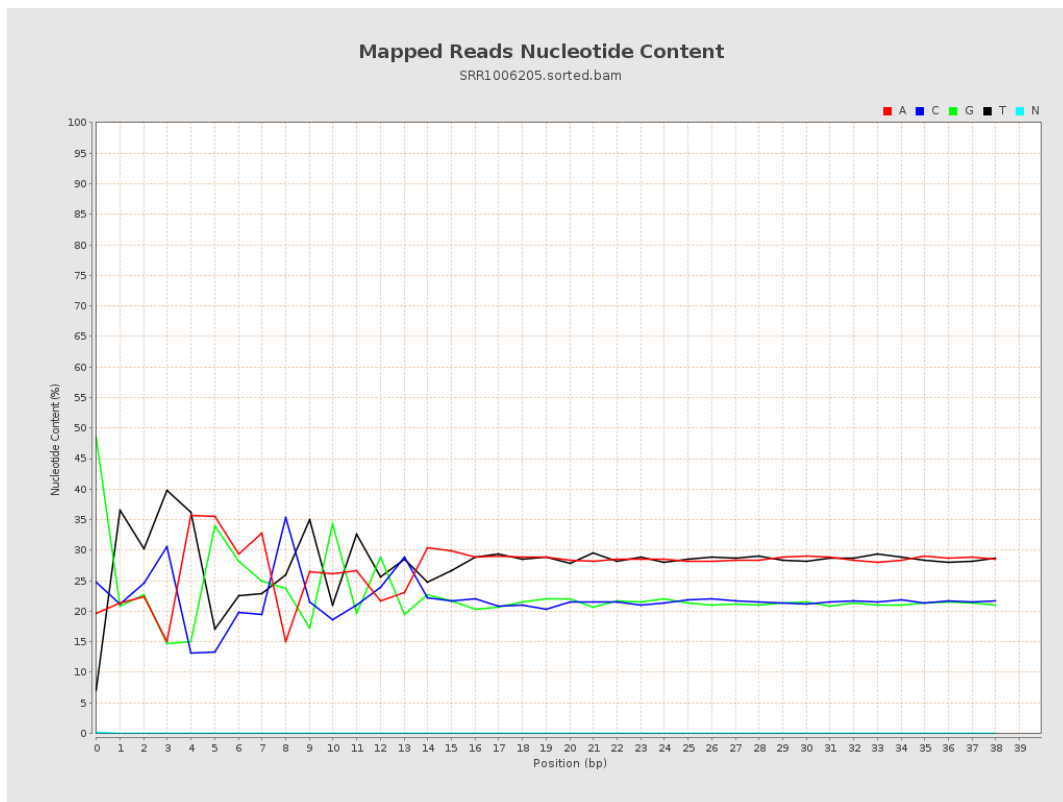
6. Results : Genome Fraction Coverage



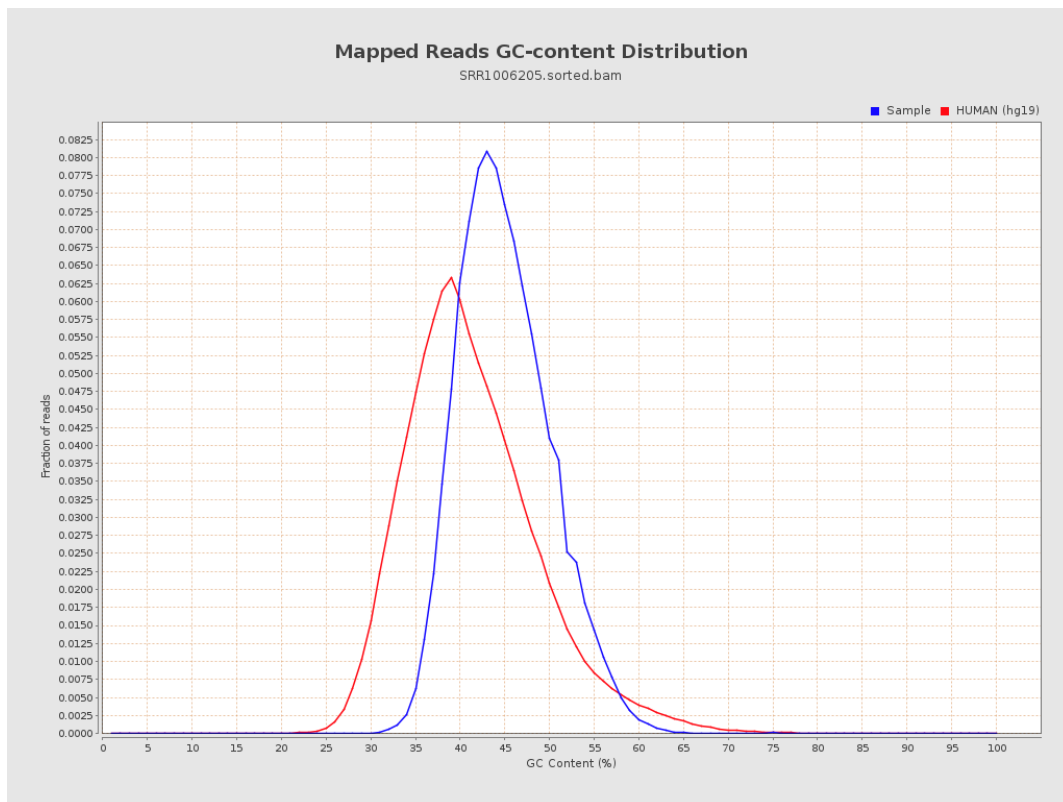
7. Results : Duplication Rate Histogram



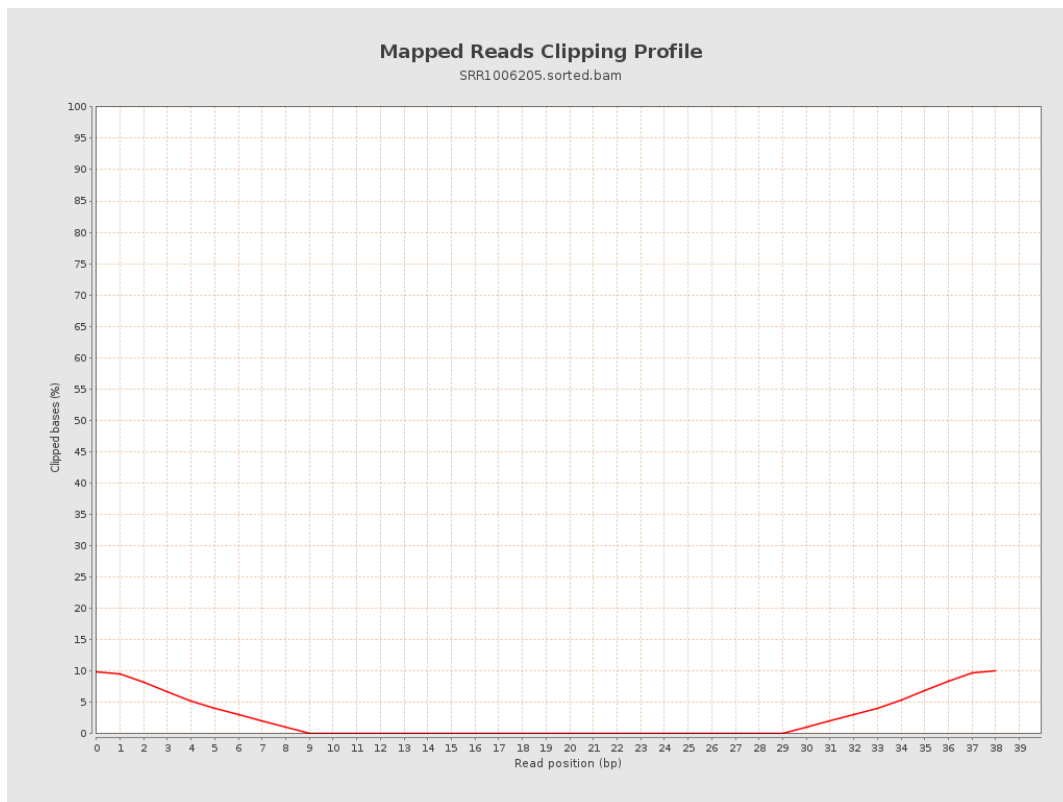
8. Results : Mapped Reads Nucleotide Content



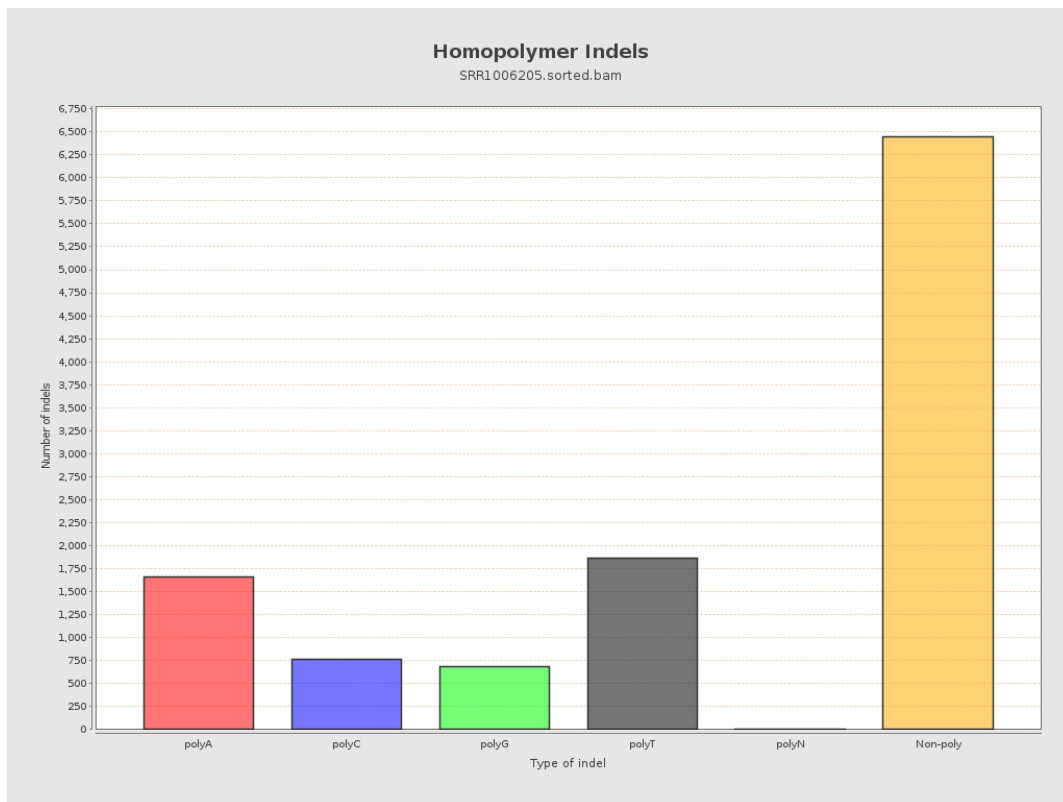
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



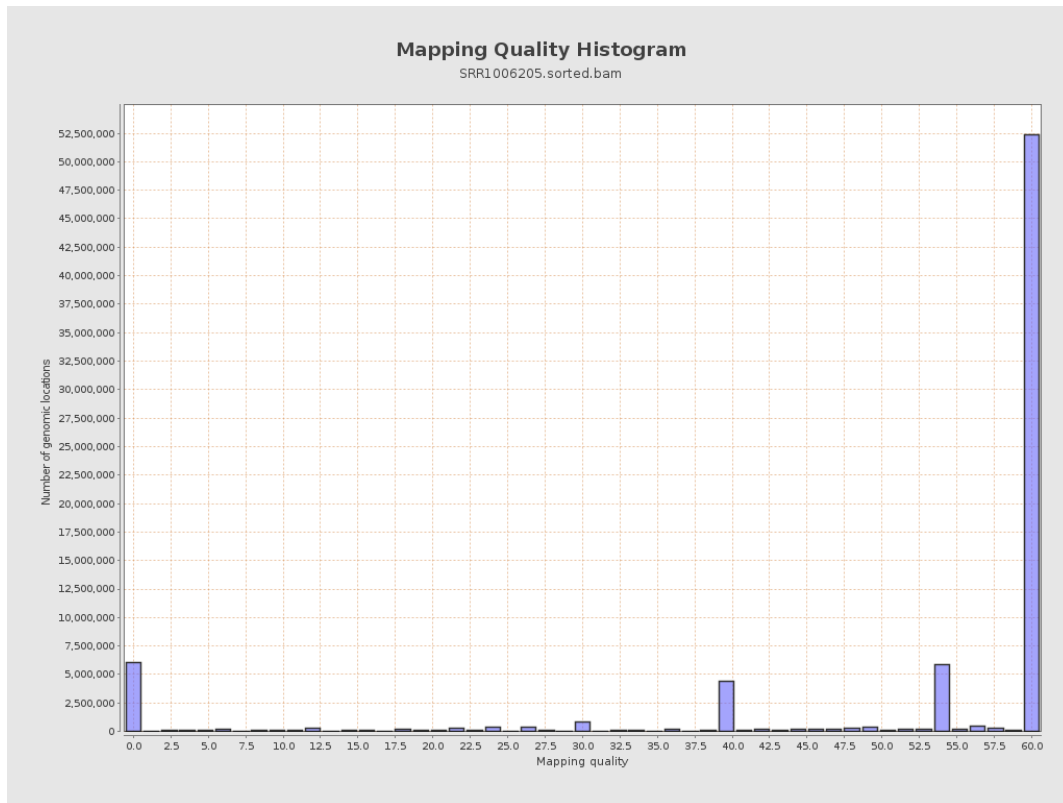
11. Results : Homopolymer Indels



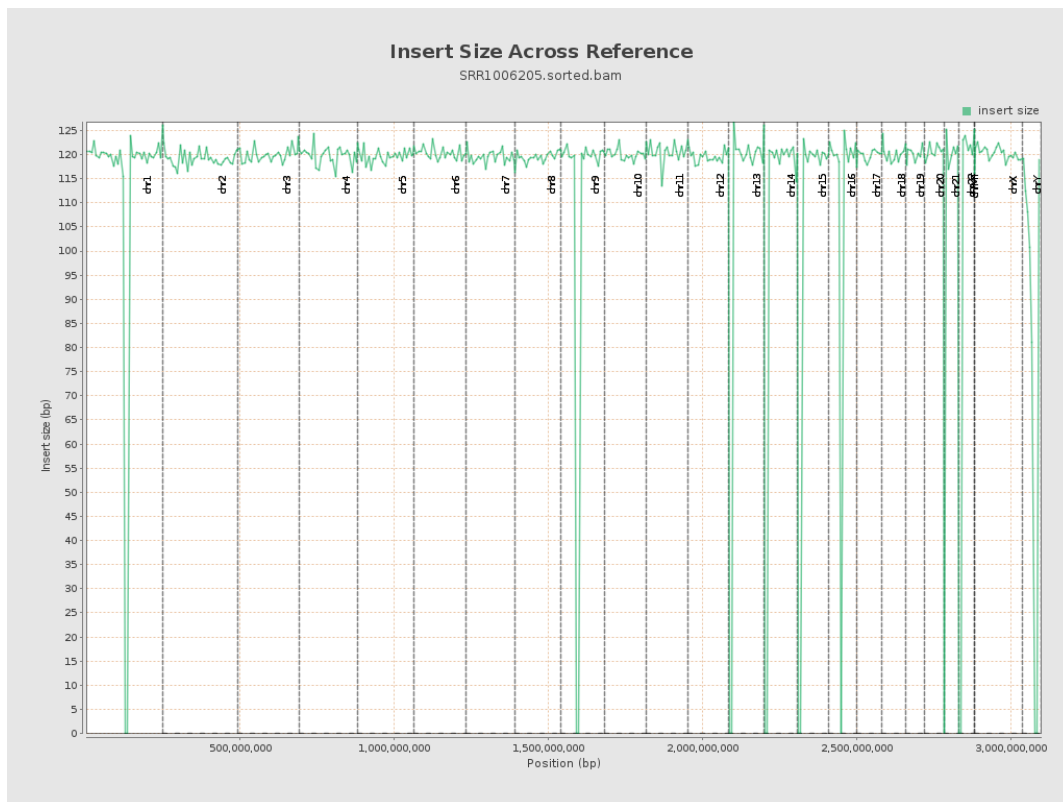
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

