

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 00:20:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006255.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_SRR1006255 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006255_1.fastq.gz SRR1006255_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 00:20:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,306,982
Mapped reads	2,507,295 / 75.82%
Unmapped reads	799,687 / 24.18%
Mapped paired reads	2,507,295 / 75.82%
Mapped reads, first in pair	1,264,281 / 38.23%
Mapped reads, second in pair	1,243,014 / 37.59%
Mapped reads, both in pair	2,318,570 / 70.11%
Mapped reads, singletons	188,725 / 5.71%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	76,121 / 2.3%
Duplication rate	2.76%
Clipped reads	173,732 / 5.25%

2.2. ACGT Content

Number/percentage of A's	26,266,133 / 27.11%
Number/percentage of C's	21,661,232 / 22.36%
Number/percentage of T's	26,806,732 / 27.67%
Number/percentage of G's	22,152,057 / 22.86%
Number/percentage of N's	3,988 / 0%
GC Percentage	45.22%

2.3. Coverage

Mean	0.0313
Standard Deviation	0.2196

2.4. Mapping Quality

Mean Mapping Quality	47.42
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2.5. Insert size

Mean	82,966
Standard Deviation	2,800,506.46
P25/Median/P75	99 / 130 / 164

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	389,877
Insertions	2,668
Mapped reads with at least one insertion	0.11%
Deletions	9,112
Mapped reads with at least one deletion	0.36%
Homopolymer indels	42.72%

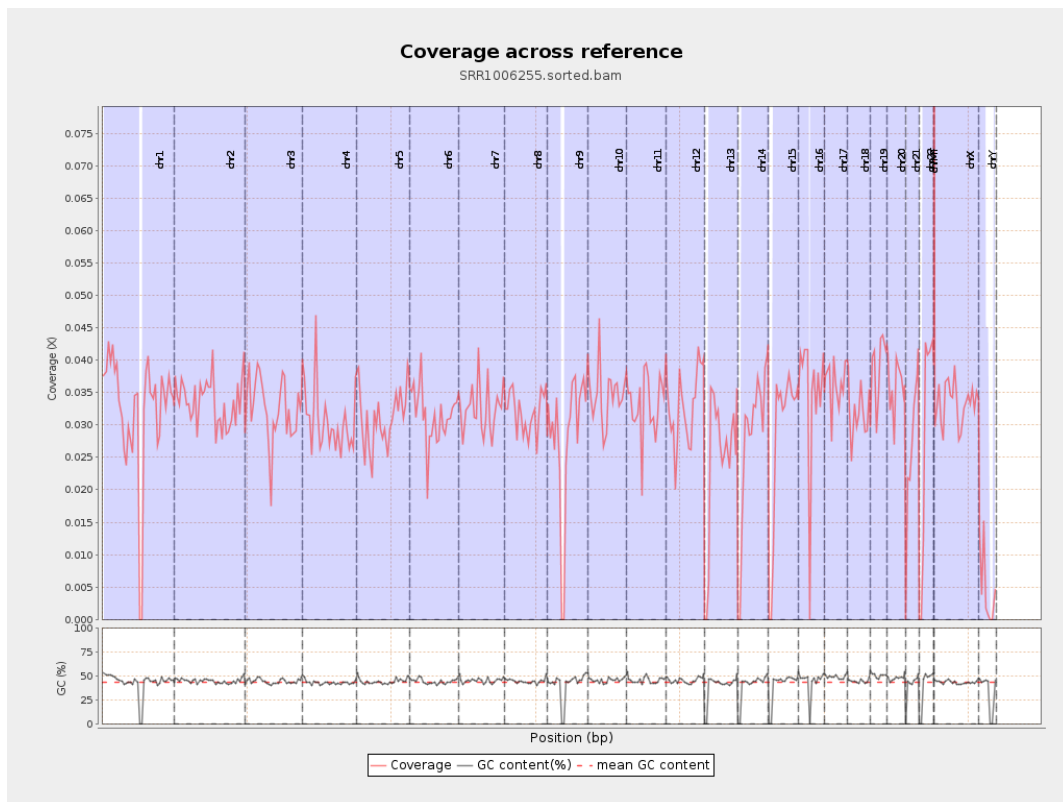
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

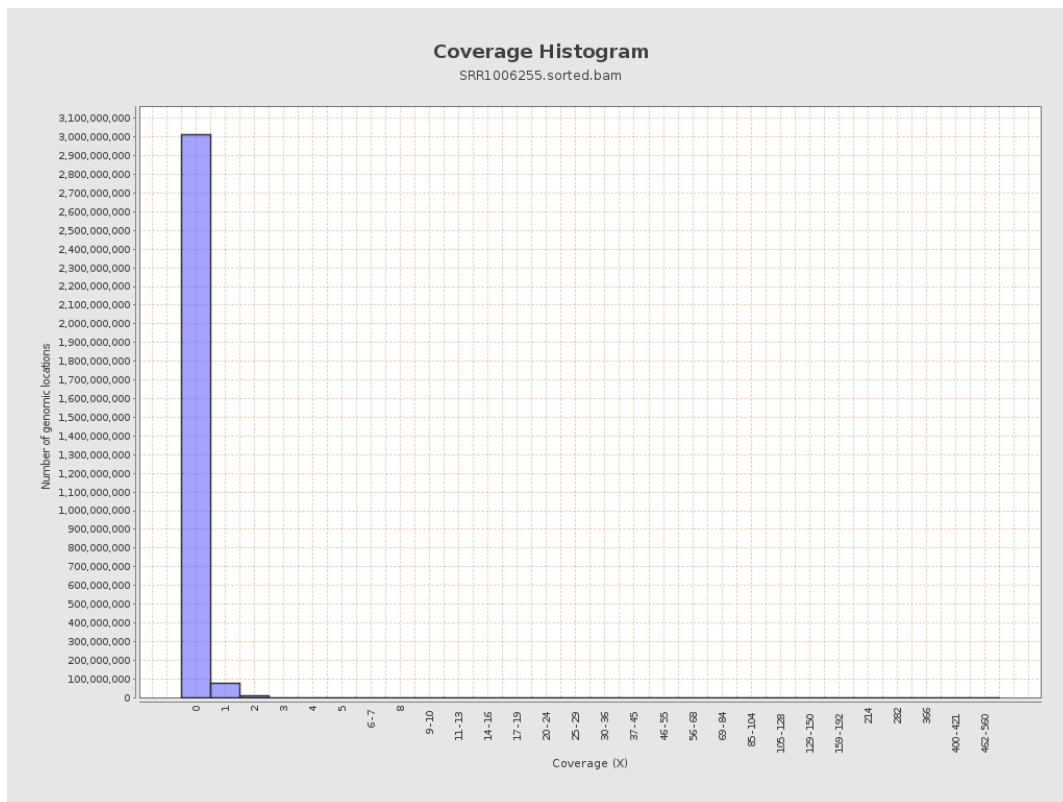
chr1	249250621	8032968	0.0322	0.2477
chr2	243199373	8153099	0.0335	0.2217
chr3	198022430	6444645	0.0325	0.1984
chr4	191154276	5866207	0.0307	0.2067
chr5	180915260	5624509	0.0311	0.199
chr6	171115067	5397909	0.0315	0.202
chr7	159138663	5176428	0.0325	0.2277
chr8	146364022	4668728	0.0319	0.3381
chr9	141213431	3956392	0.028	0.1928
chr10	135534747	4710180	0.0348	0.2451
chr11	135006516	4488148	0.0332	0.21
chr12	133851895	4363545	0.0326	0.1996
chr13	115169878	2811559	0.0244	0.1739
chr14	107349540	2989494	0.0278	0.2061
chr15	102531392	2869282	0.028	0.1841
chr16	90354753	3129359	0.0346	0.221
chr17	81195210	2968528	0.0366	0.2154
chr18	78077248	2470910	0.0316	0.2437
chr19	59128983	2296793	0.0388	0.247
chr20	63025520	2253820	0.0358	0.2133
chr21	48129895	1297160	0.027	0.1986
chr22	51304566	1473899	0.0287	0.1949
chrMT	16571	2370	0.143	0.5626
chrX	155270560	5184343	0.0334	0.2055

chrY	59373566	272127	0.0046	0.1258
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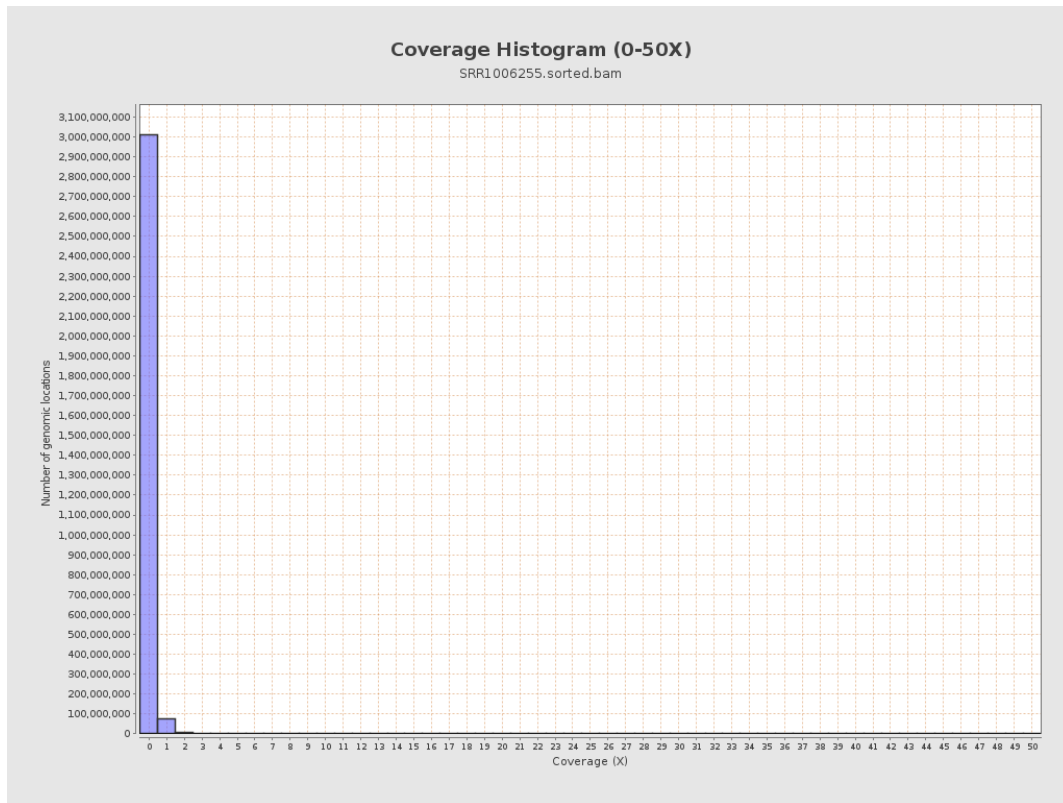
3. Results : Coverage across reference



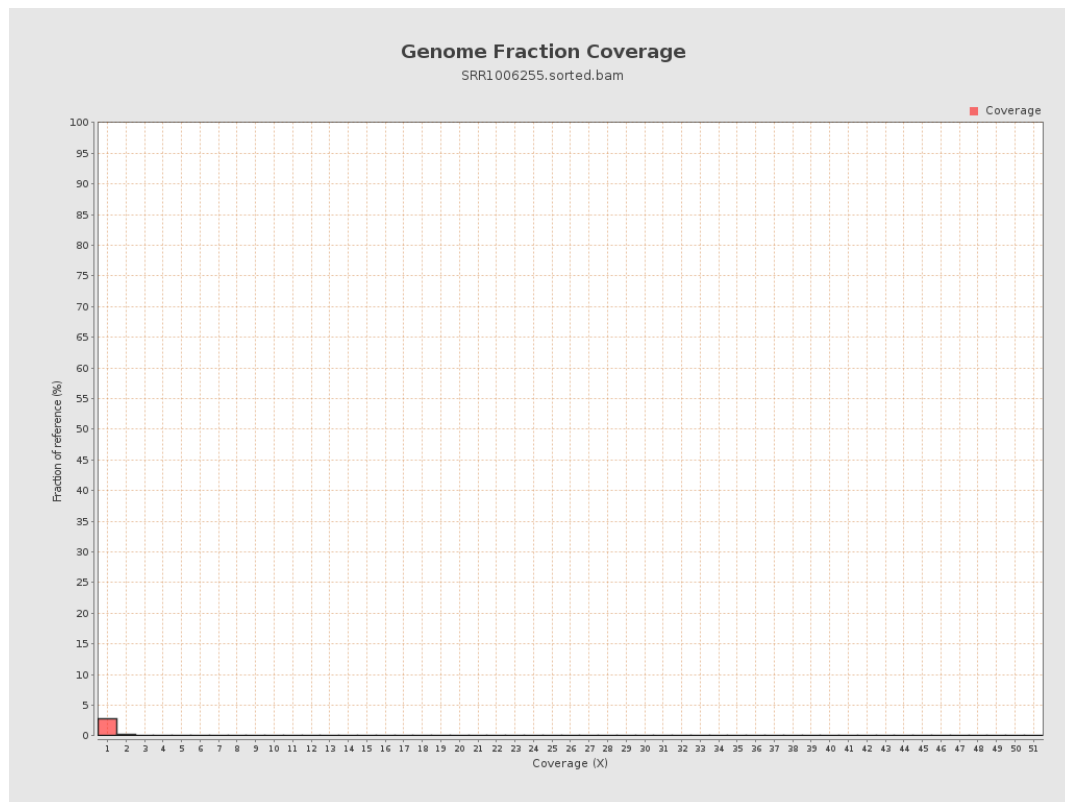
4. Results : Coverage Histogram



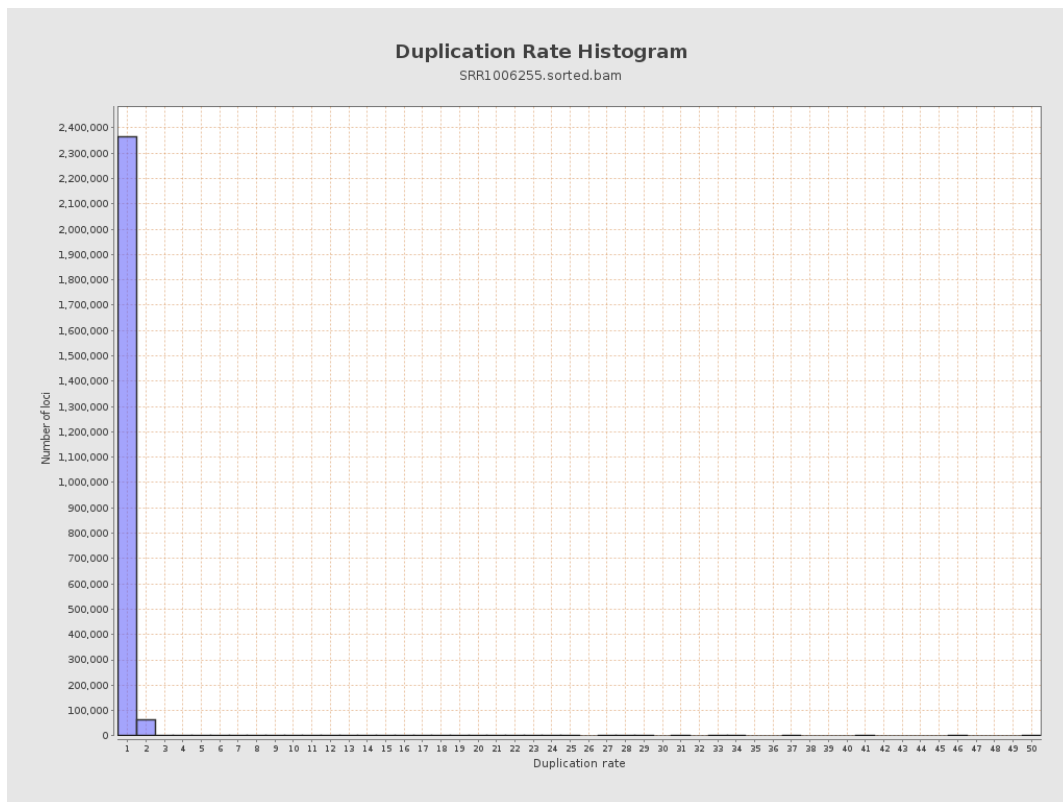
5. Results : Coverage Histogram (0-50X)



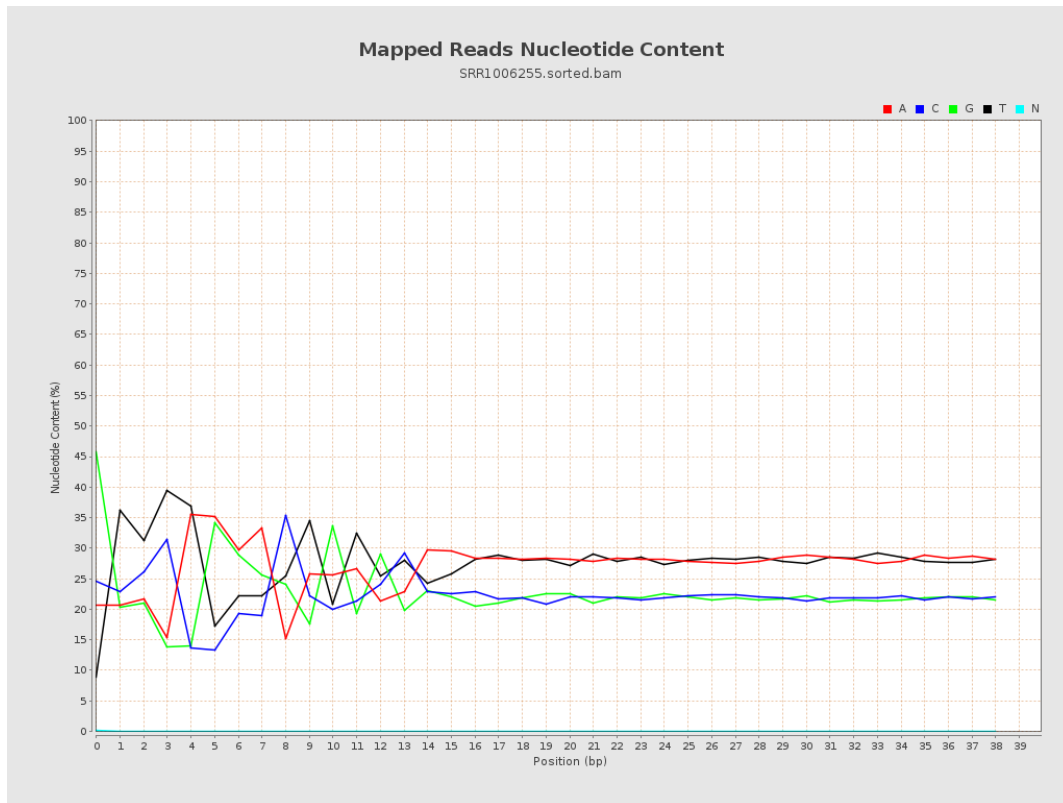
6. Results : Genome Fraction Coverage



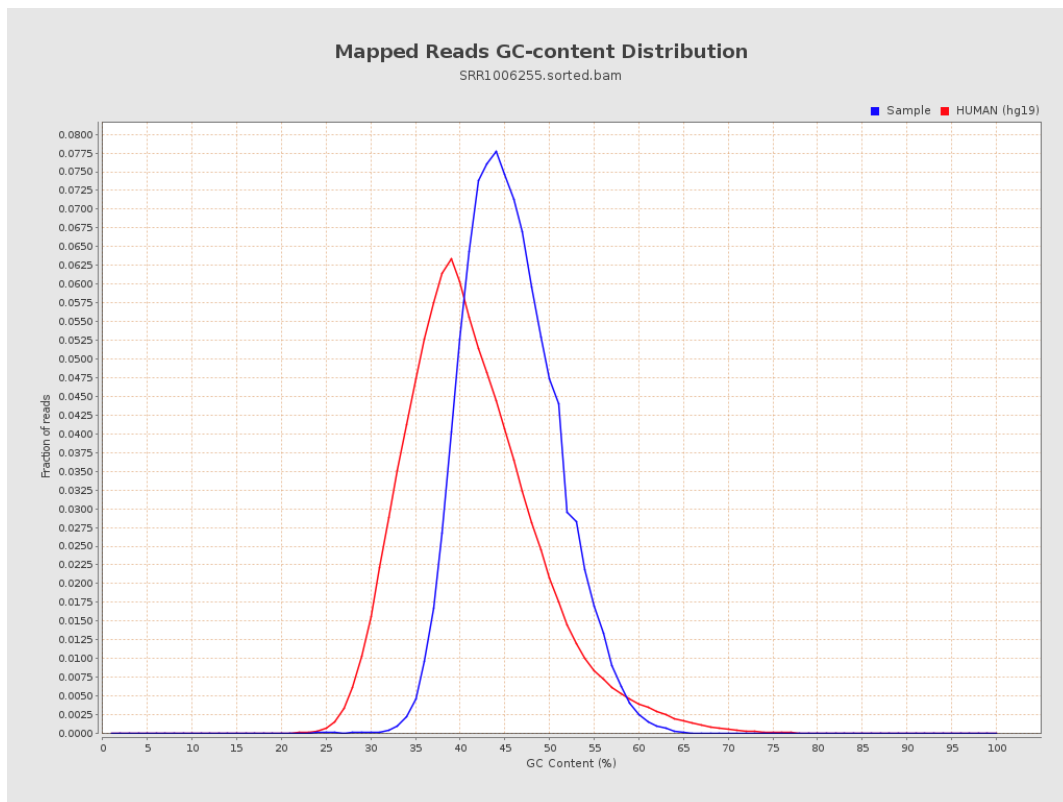
7. Results : Duplication Rate Histogram



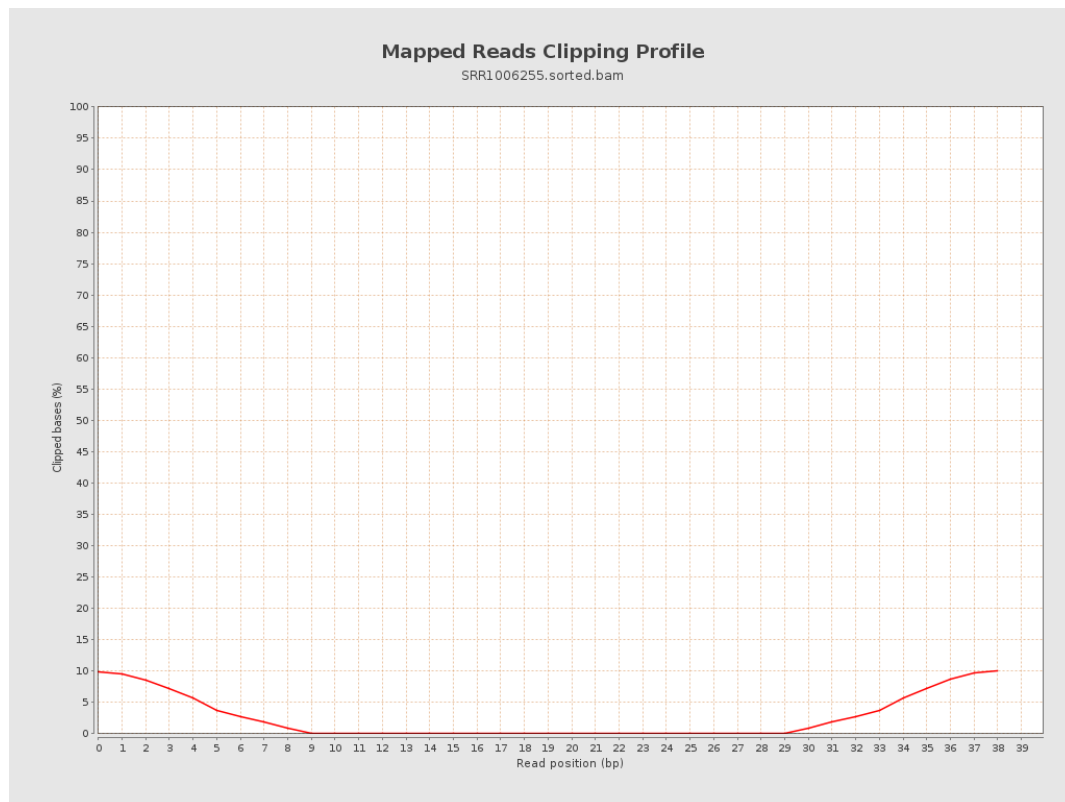
8. Results : Mapped Reads Nucleotide Content



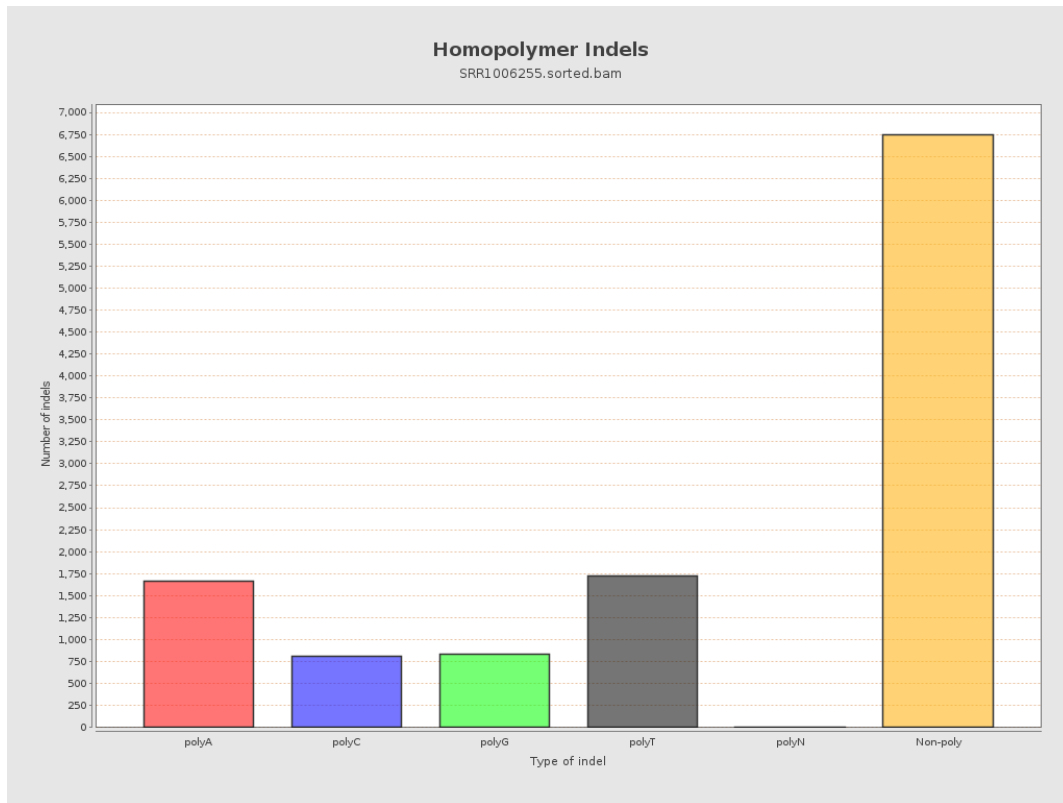
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



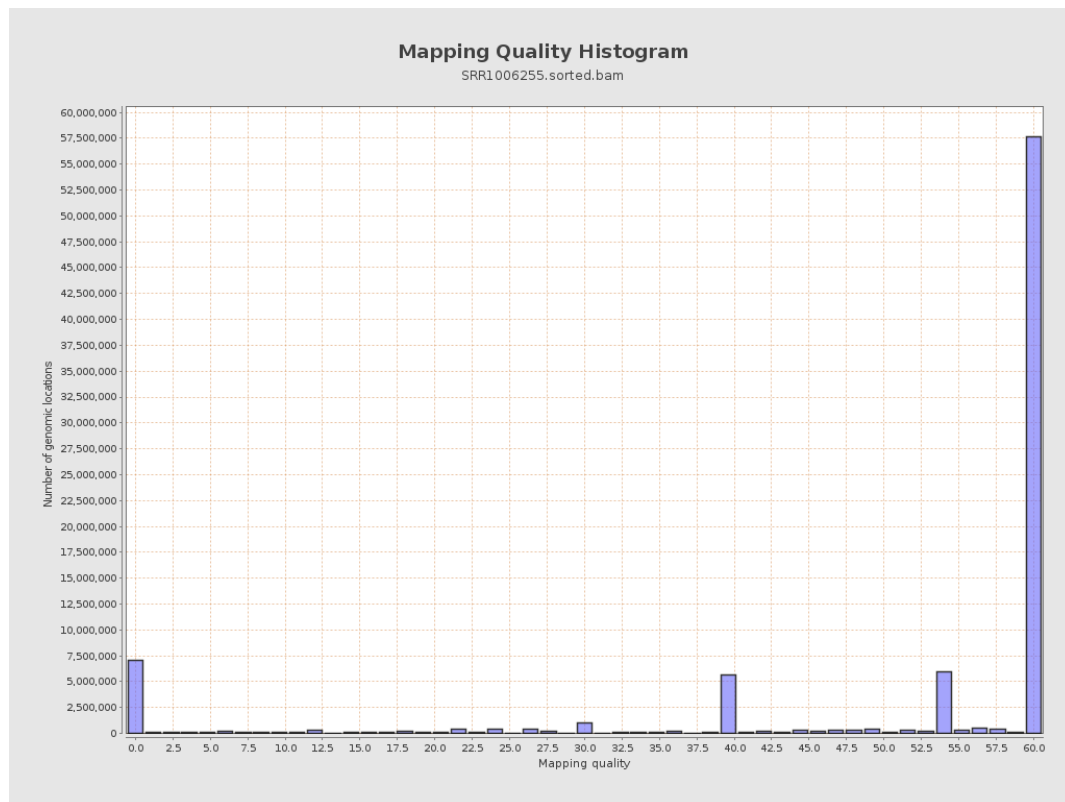
11. Results : Homopolymer Indels



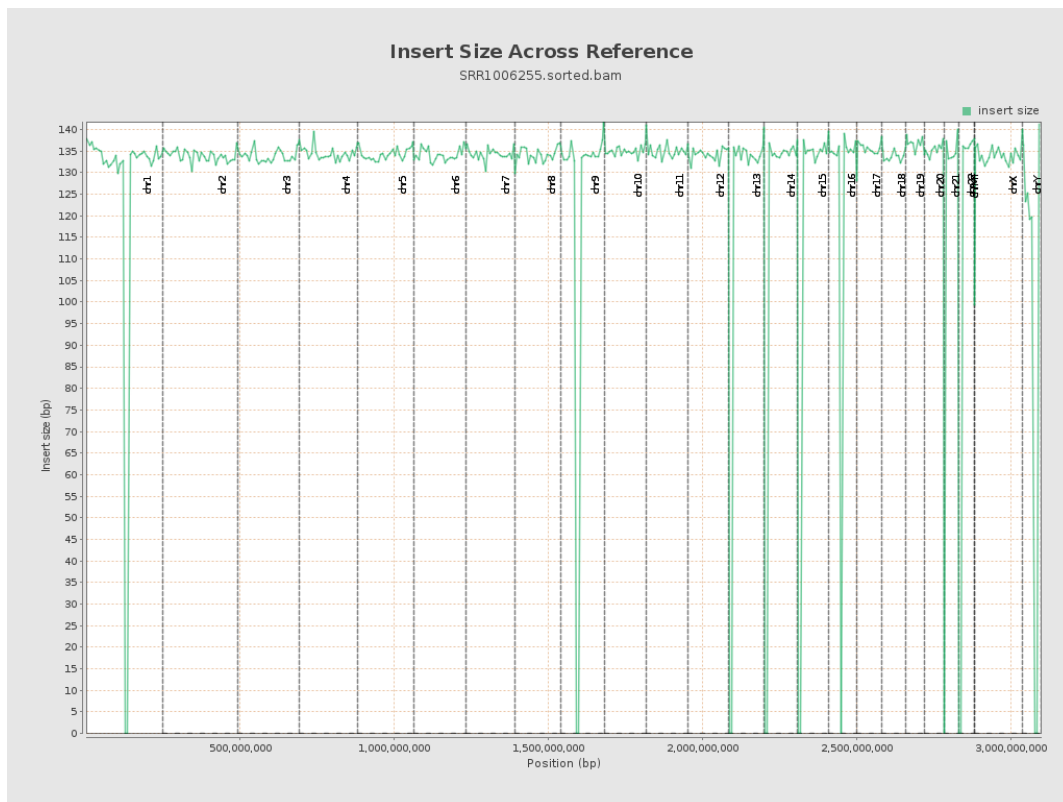
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

