

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 16:52:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006055.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_SRR1006055 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006055_1.fastq.gz SRR1006055_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 16:52:11 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,503,138
Mapped reads	3,956,649 / 87.86%
Unmapped reads	546,489 / 12.14%
Mapped paired reads	3,956,649 / 87.86%
Mapped reads, first in pair	2,009,726 / 44.63%
Mapped reads, second in pair	1,946,923 / 43.23%
Mapped reads, both in pair	3,647,238 / 80.99%
Mapped reads, singletons	309,411 / 6.87%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	181,954 / 4.04%
Duplication rate	4.22%
Clipped reads	342,088 / 7.6%

2.2. ACGT Content

Number/percentage of A's	39,423,127 / 25.82%
Number/percentage of C's	35,291,187 / 23.12%
Number/percentage of T's	40,853,431 / 26.76%
Number/percentage of G's	37,082,699 / 24.29%
Number/percentage of N's	7,024 / 0%
GC Percentage	47.41%

2.3. Coverage

Mean	0.0493
Standard Deviation	0.3318

2.4. Mapping Quality

Mean Mapping Quality	45.81
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2.5. Insert size

Mean	67,721.94
Standard Deviation	2,578,434.45
P25/Median/P75	63 / 91 / 123

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	703,390
Insertions	5,291
Mapped reads with at least one insertion	0.13%
Deletions	13,495
Mapped reads with at least one deletion	0.34%
Homopolymer indels	43.99%

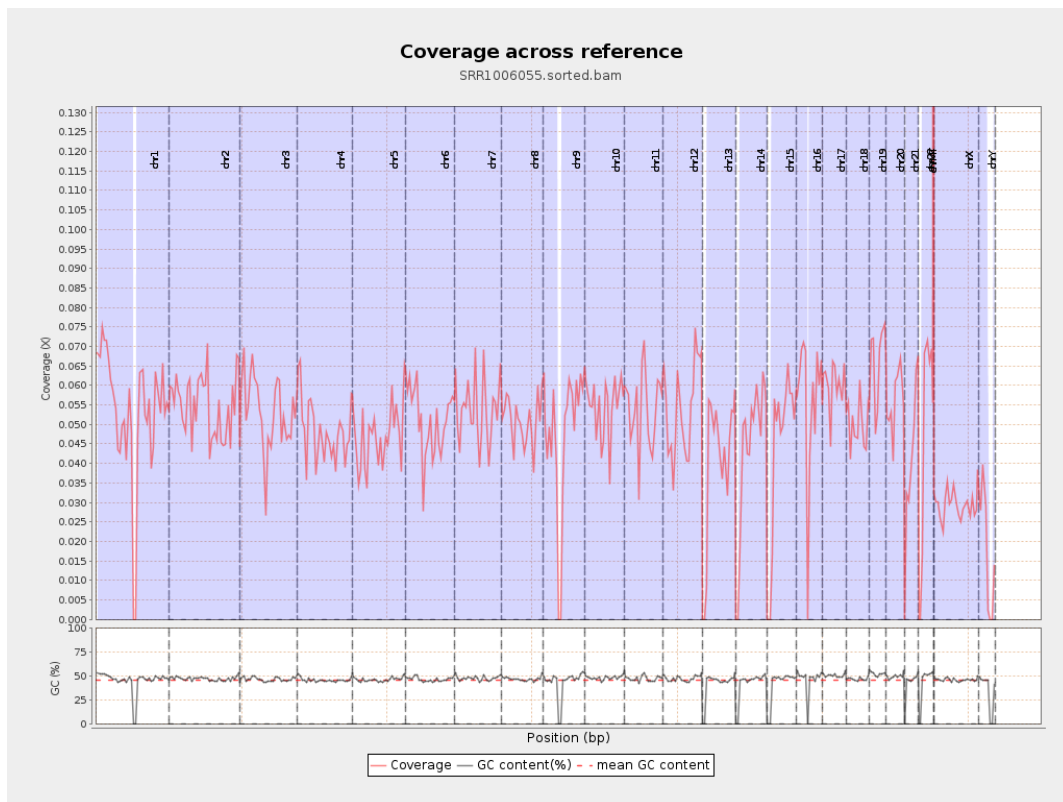
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

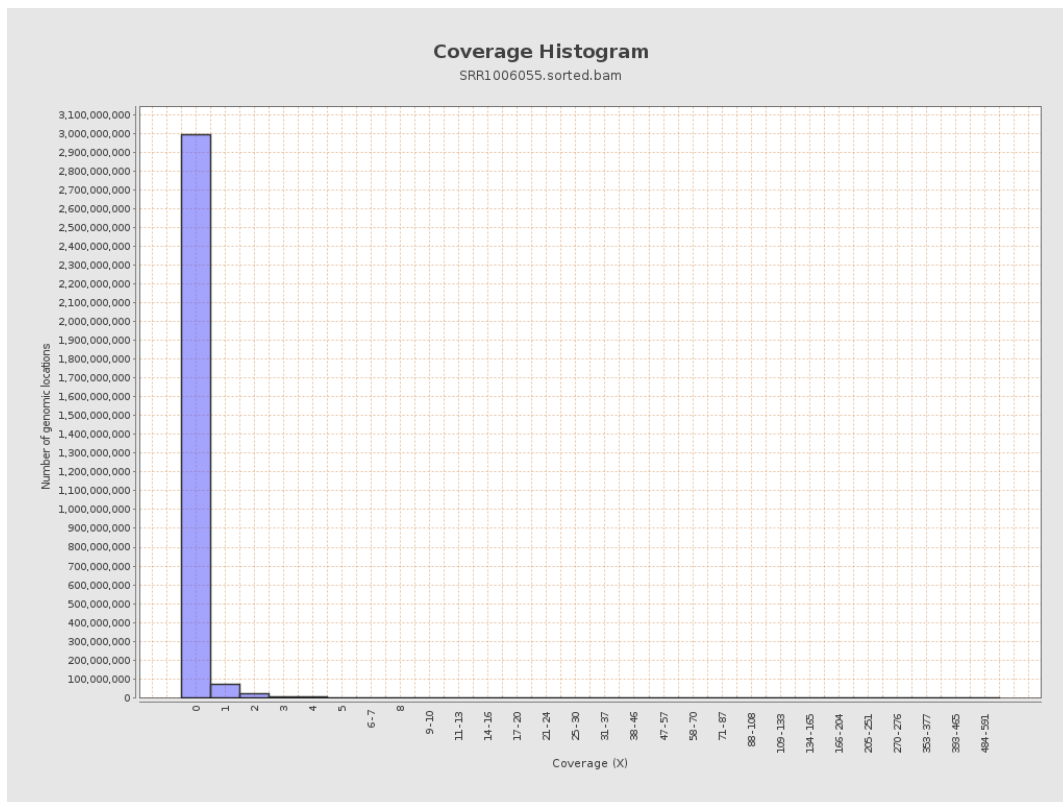
chr1	249250621	13200623	0.053	0.3396
chr2	243199373	13324729	0.0548	0.3725
chr3	198022430	10505630	0.0531	0.3187
chr4	191154276	9139713	0.0478	0.3123
chr5	180915260	8425291	0.0466	0.2979
chr6	171115067	8740009	0.0511	0.3344
chr7	159138663	8482560	0.0533	0.3687
chr8	146364022	7446974	0.0509	0.337
chr9	141213431	6521924	0.0462	0.3056
chr10	135534747	7369211	0.0544	0.3363
chr11	135006516	7288602	0.054	0.4384
chr12	133851895	7198933	0.0538	0.3227
chr13	115169878	4583370	0.0398	0.2815
chr14	107349540	4652199	0.0433	0.2945
chr15	102531392	4560321	0.0445	0.2949
chr16	90354753	5074452	0.0562	0.3663
chr17	81195210	4895312	0.0603	0.3561
chr18	78077248	3890556	0.0498	0.3295
chr19	59128983	3887392	0.0657	0.4173
chr20	63025520	3521525	0.0559	0.3339
chr21	48129895	1987121	0.0413	0.3112
chr22	51304566	2371361	0.0462	0.3434
chrMT	16571	15120	0.9124	1.4768
chrX	155270560	4558108	0.0294	0.2367

chrY	59373566	1033770	0.0174	0.2044
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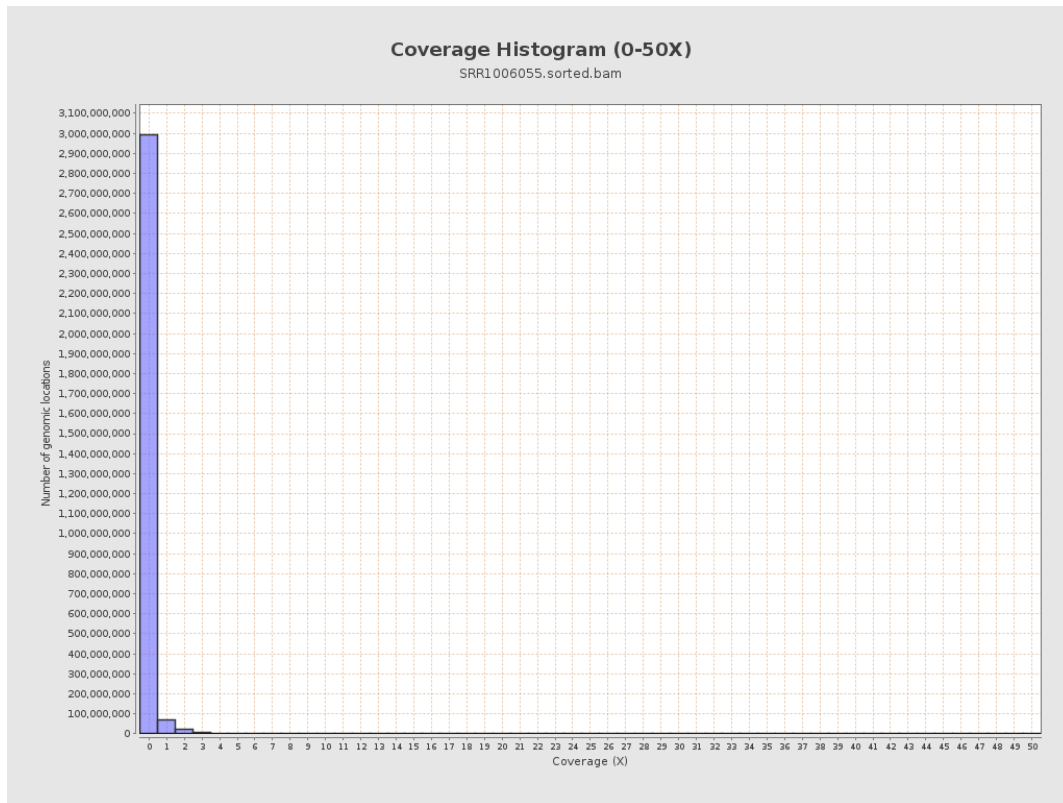
3. Results : Coverage across reference



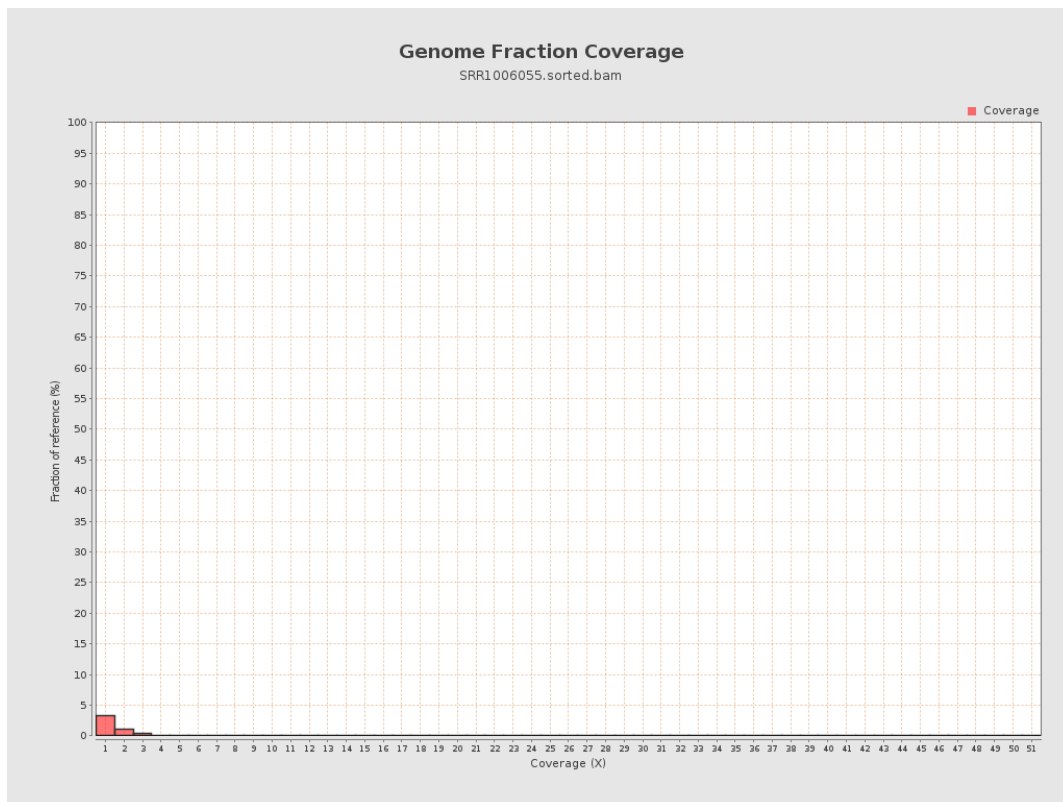
4. Results : Coverage Histogram



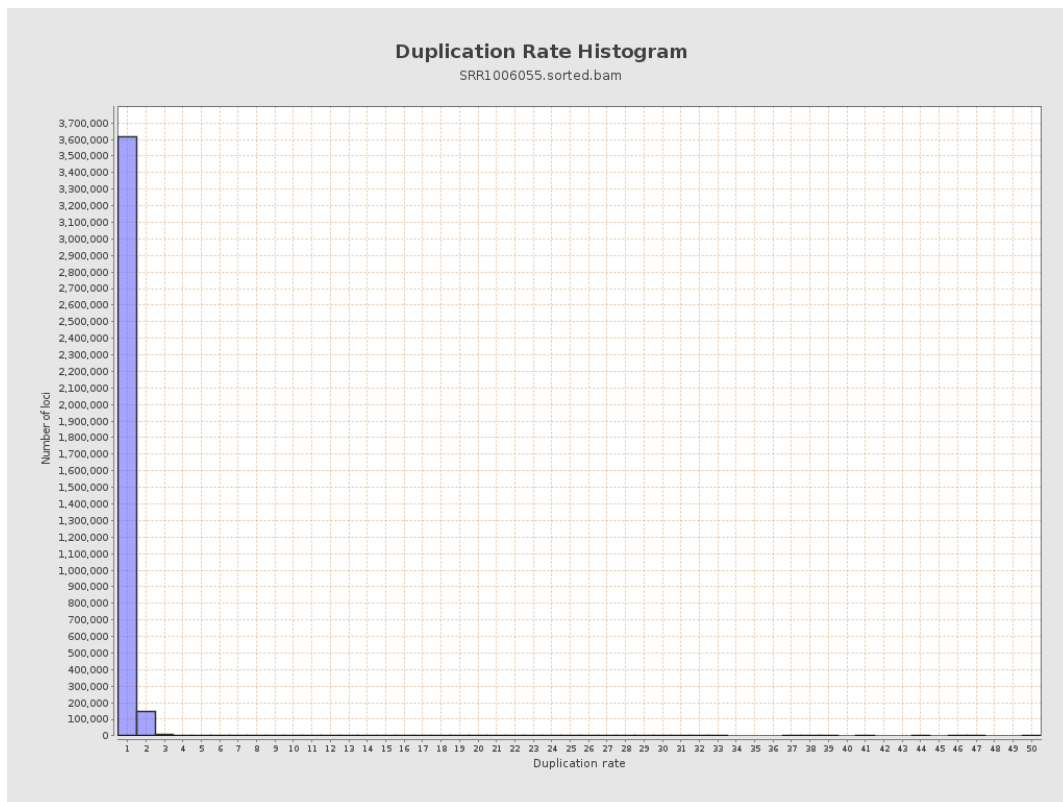
5. Results : Coverage Histogram (0-50X)



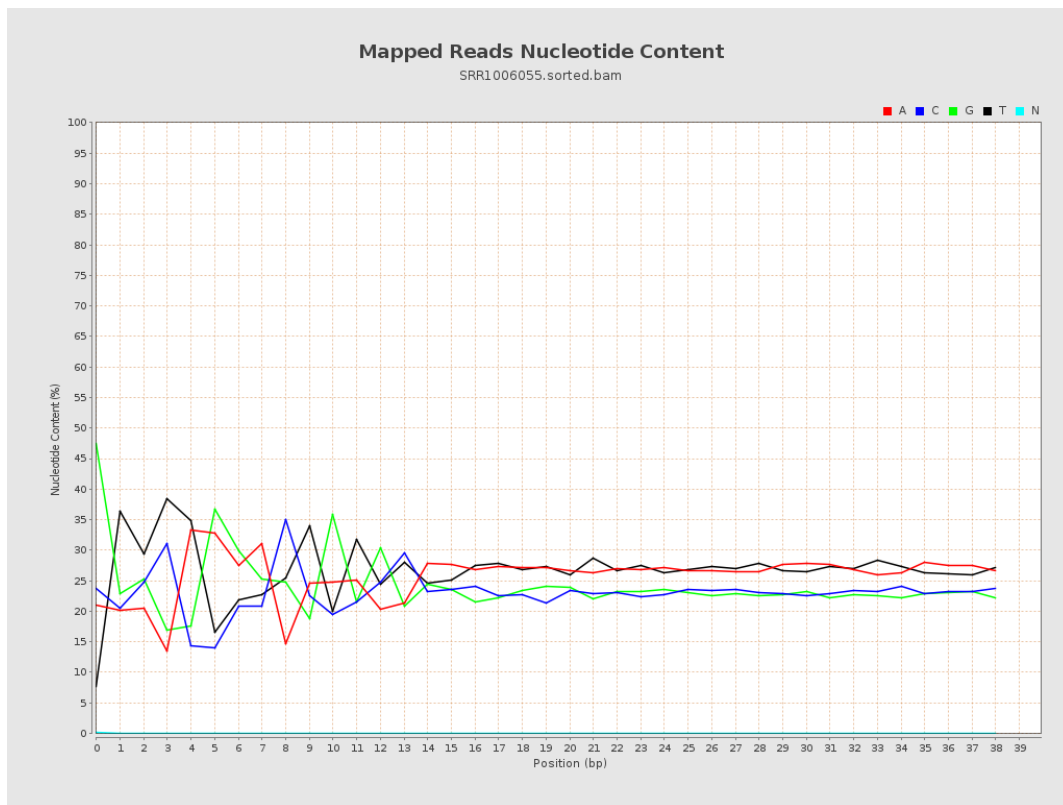
6. Results : Genome Fraction Coverage



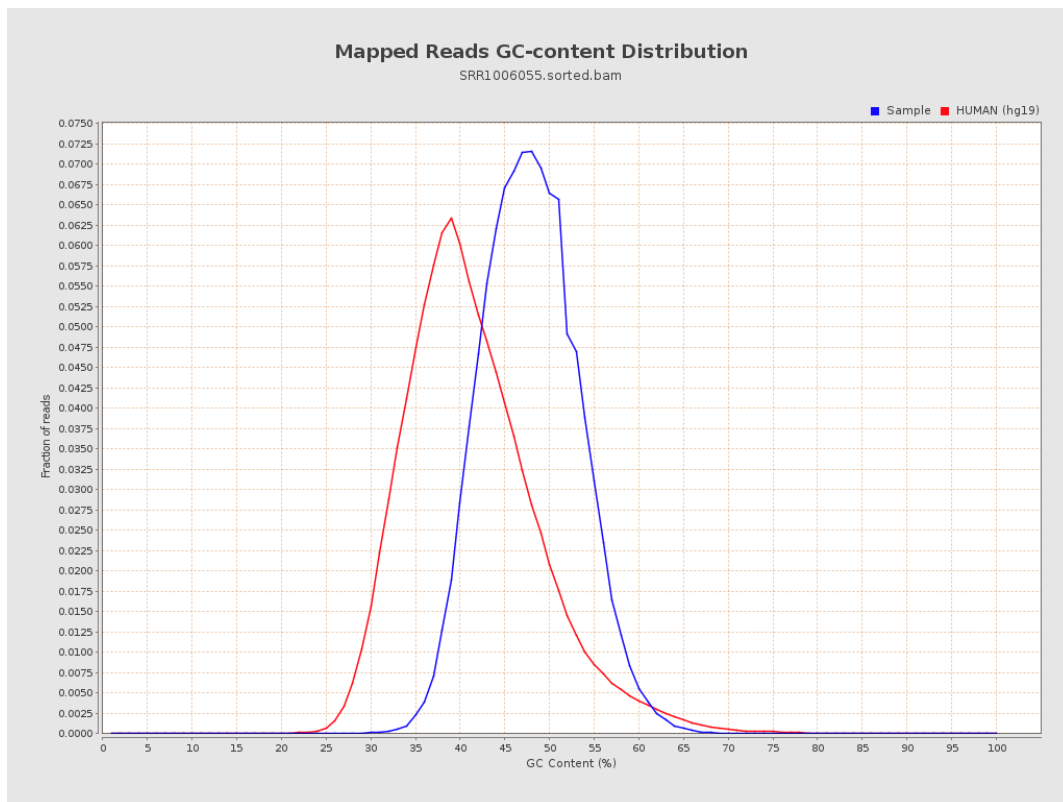
7. Results : Duplication Rate Histogram



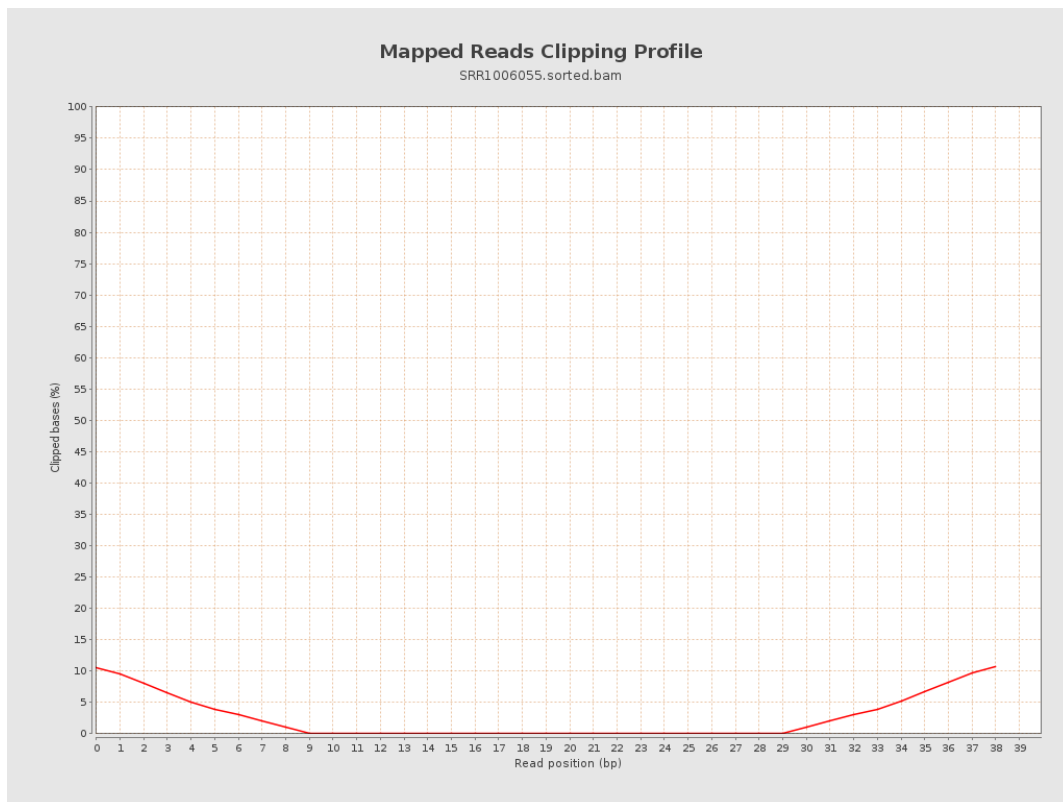
8. Results : Mapped Reads Nucleotide Content



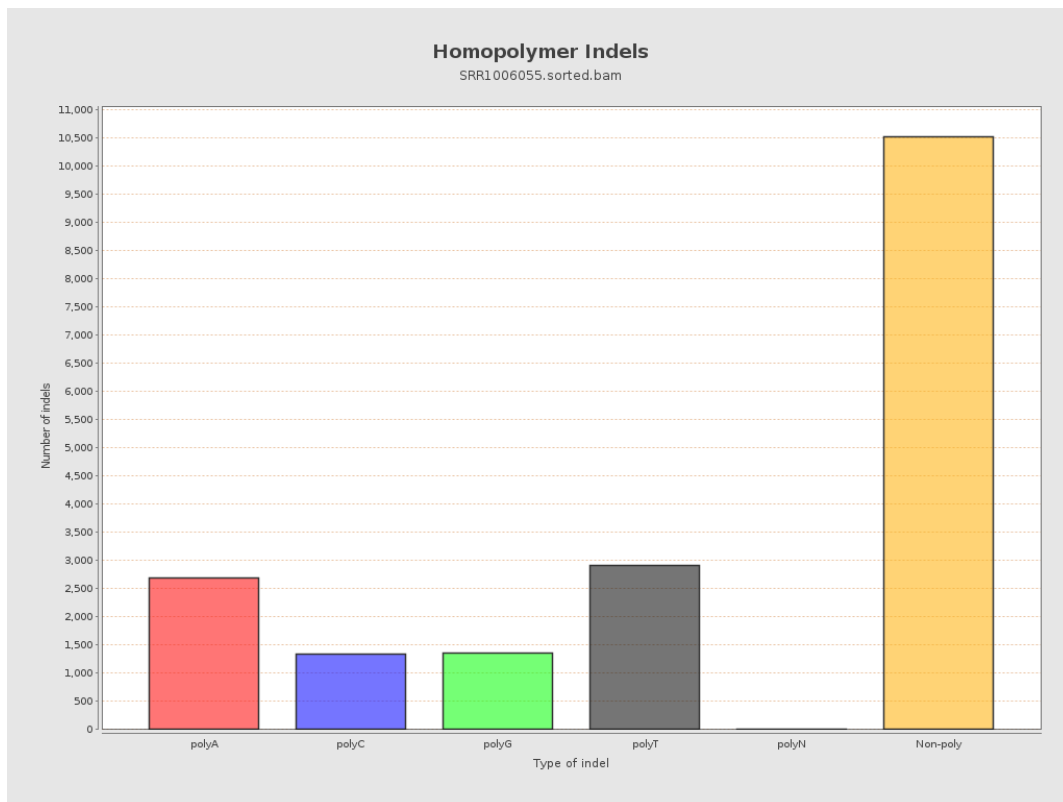
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



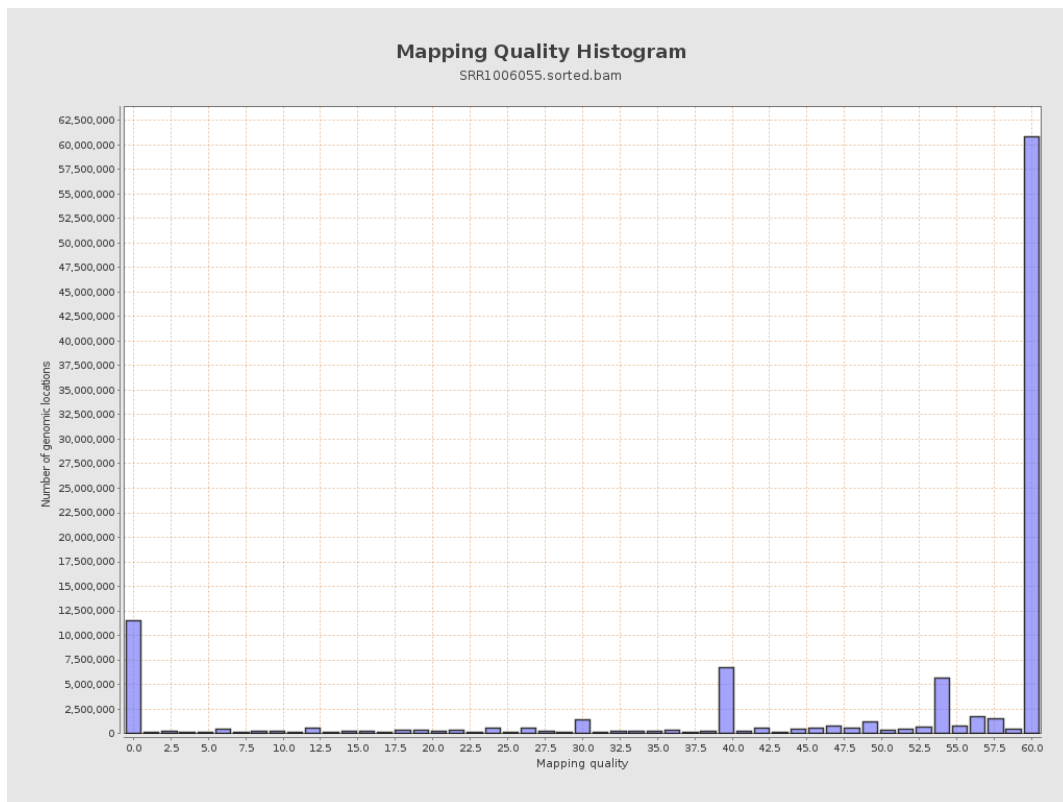
11. Results : Homopolymer Indels



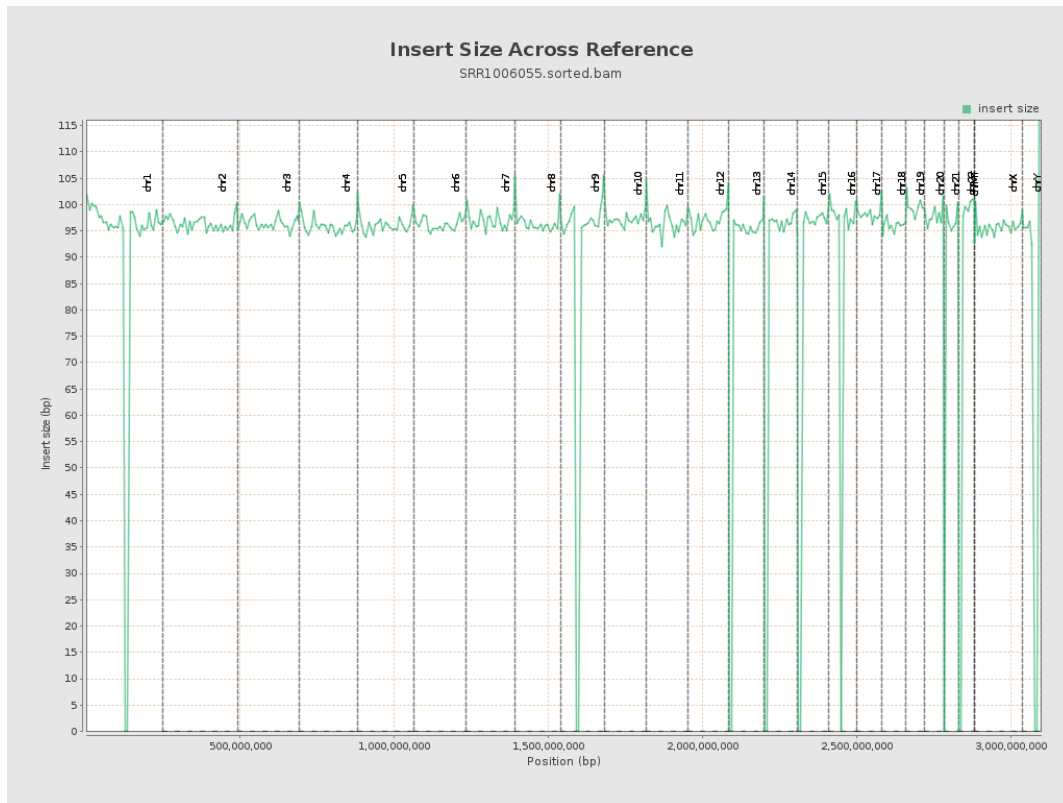
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

