

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 20:38:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006143.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_SRR1006143 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006143_1.fastq.gz SRR1006143_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 20:38:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006143.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,574,310
Mapped reads	14,578,270 / 87.96%
Unmapped reads	1,996,040 / 12.04%
Mapped paired reads	14,578,270 / 87.96%
Mapped reads, first in pair	7,403,355 / 44.67%
Mapped reads, second in pair	7,174,915 / 43.29%
Mapped reads, both in pair	13,328,216 / 80.41%
Mapped reads, singletons	1,250,054 / 7.54%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	1,145,266 / 6.91%
Duplication rate	6.95%
Clipped reads	1,115,645 / 6.73%

2.2. ACGT Content

Number/percentage of A's	154,223,599 / 27.39%
Number/percentage of C's	121,628,273 / 21.6%
Number/percentage of T's	159,059,870 / 28.25%
Number/percentage of G's	128,130,546 / 22.76%
Number/percentage of N's	22,343 / 0%
GC Percentage	44.36%

2.3. Coverage

Mean	0.1819
Standard Deviation	0.883

2.4. Mapping Quality

Mean Mapping Quality	47.42
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2.5. Insert size

Mean	60,998.42
Standard Deviation	2,408,374.89
P25/Median/P75	75 / 110 / 150

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	2,629,209
Insertions	18,075
Mapped reads with at least one insertion	0.12%
Deletions	49,669
Mapped reads with at least one deletion	0.34%
Homopolymer indels	46.43%

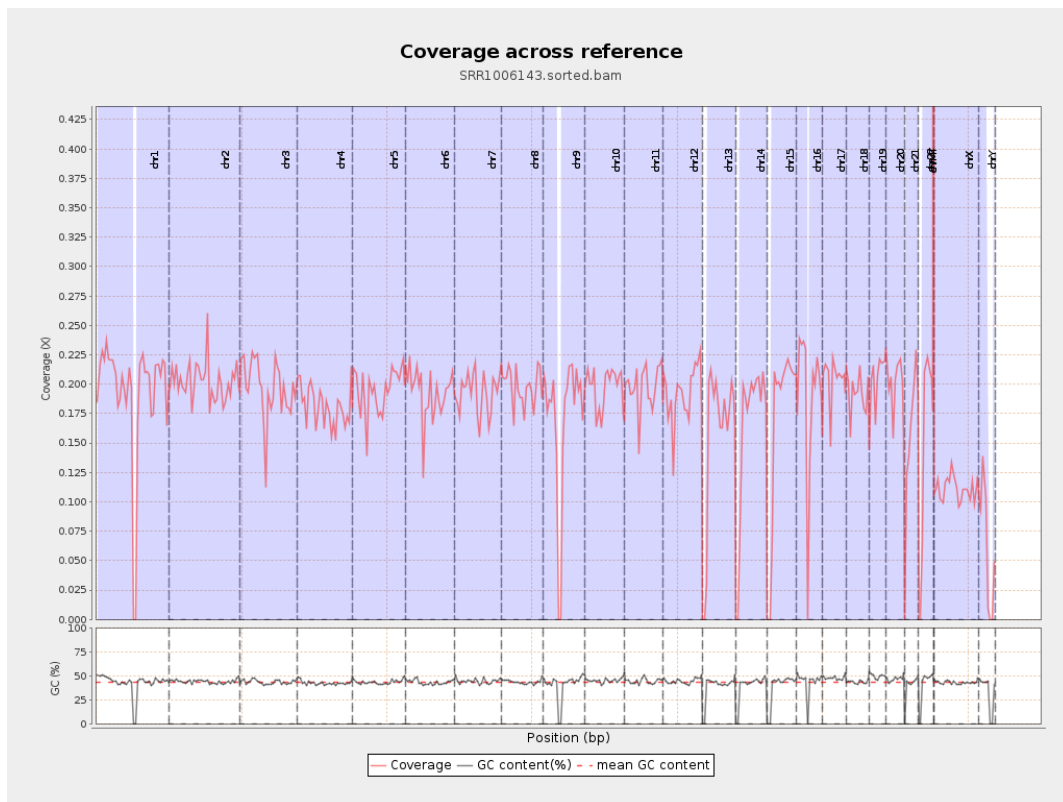
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

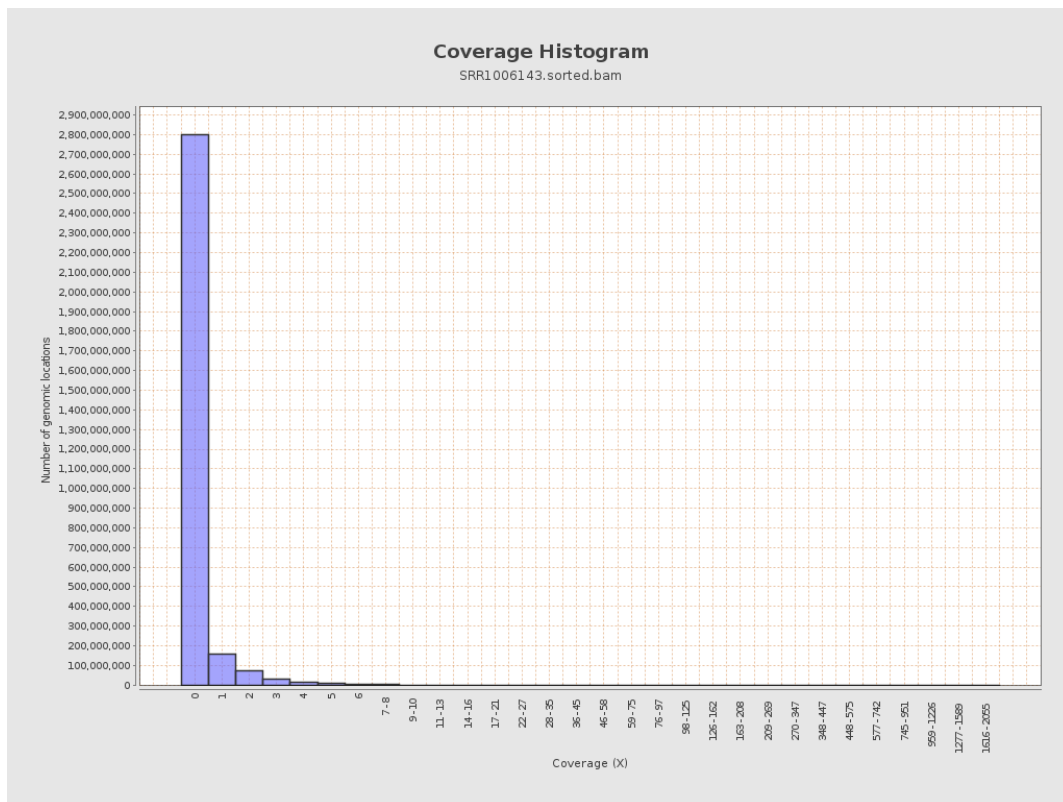
chr1	249250621	47940912	0.1923	0.9599
chr2	243199373	49218118	0.2024	0.9927
chr3	198022430	38886966	0.1964	0.7333
chr4	191154276	34515829	0.1806	0.7488
chr5	180915260	35209778	0.1946	0.732
chr6	171115067	33006169	0.1929	0.8413
chr7	159138663	30553369	0.192	1.2901
chr8	146364022	28893917	0.1974	0.9664
chr9	141213431	23769239	0.1683	0.8104
chr10	135534747	26837507	0.198	0.7858
chr11	135006516	26687476	0.1977	1.3488
chr12	133851895	25690179	0.1919	0.7297
chr13	115169878	17881728	0.1553	0.6605
chr14	107349540	17417156	0.1622	0.6962
chr15	102531392	17287156	0.1686	0.6973
chr16	90354753	17195502	0.1903	0.8589
chr17	81195210	16603738	0.2045	0.8783
chr18	78077248	14985713	0.1919	1.1937
chr19	59128983	12129723	0.2051	0.9894
chr20	63025520	12559048	0.1993	0.7584
chr21	48129895	7558964	0.1571	0.7659
chr22	51304566	7443259	0.1451	0.7135
chrMT	16571	44436	2.6816	3.7512
chrX	155270560	17265352	0.1112	0.615

chrY	59373566	3546460	0.0597	0.5041
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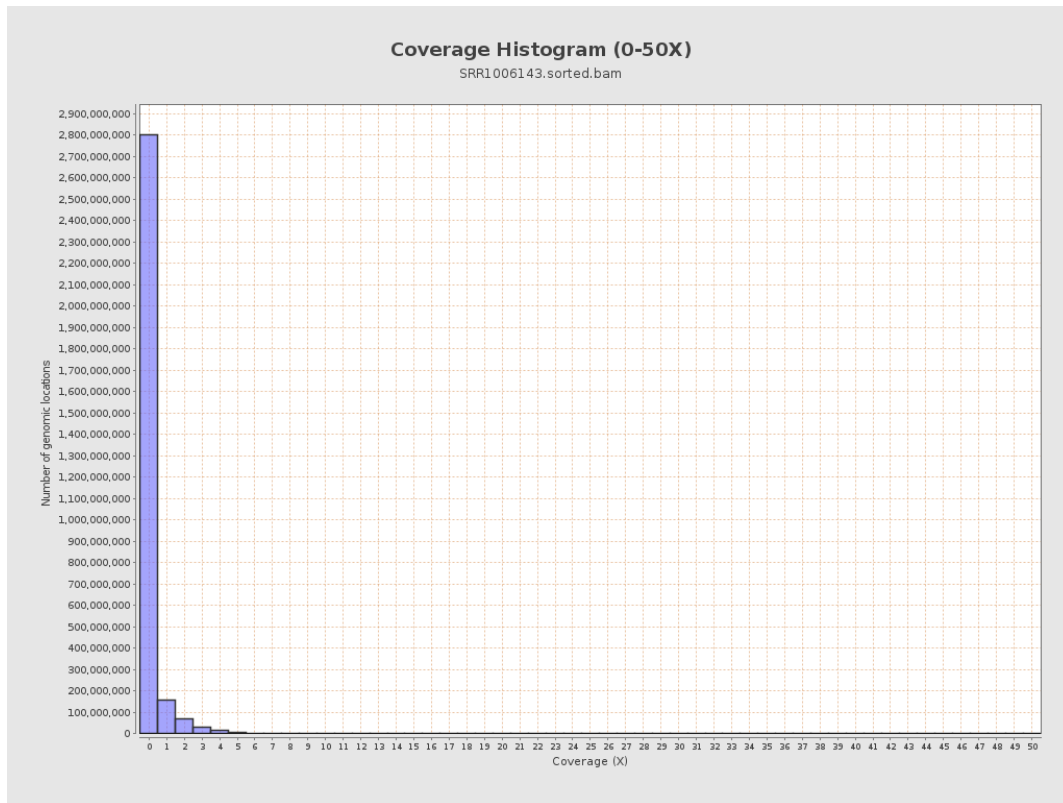
3. Results : Coverage across reference



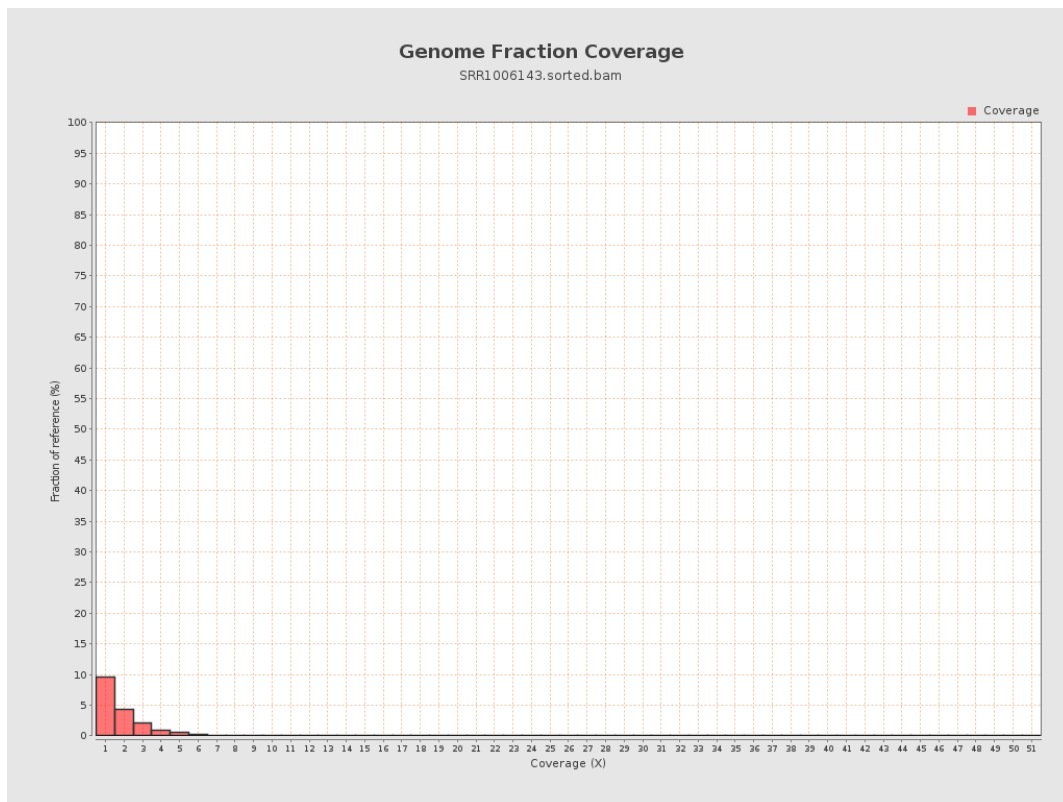
4. Results : Coverage Histogram



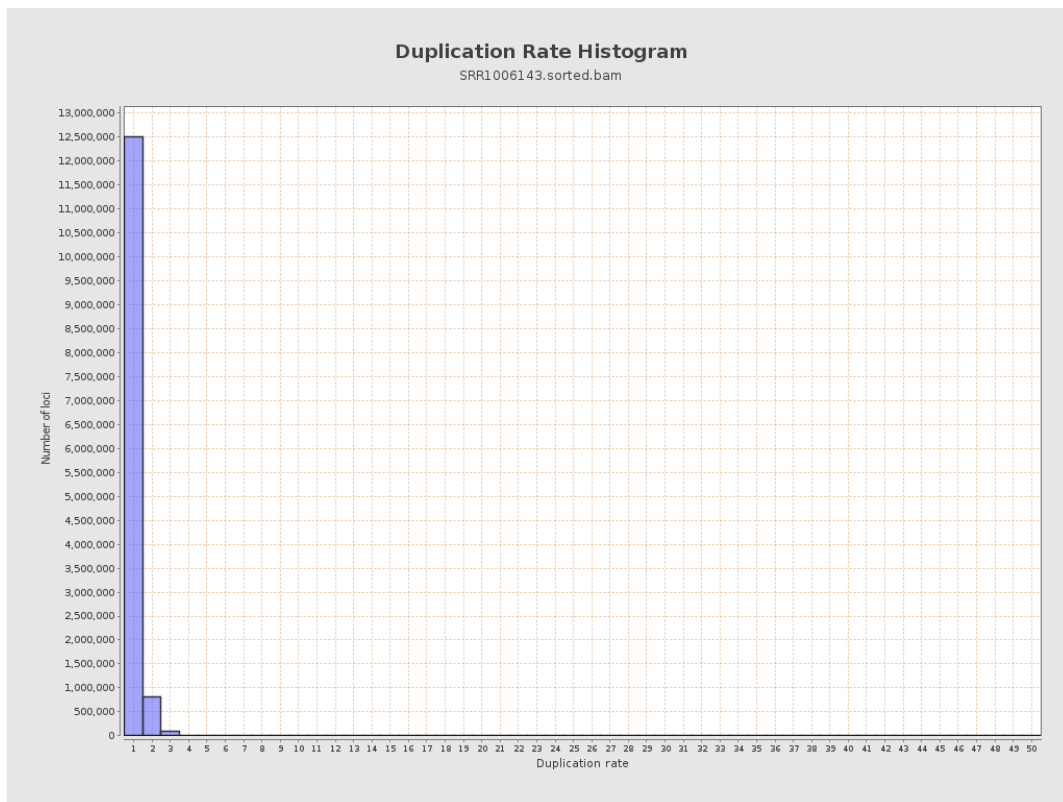
5. Results : Coverage Histogram (0-50X)



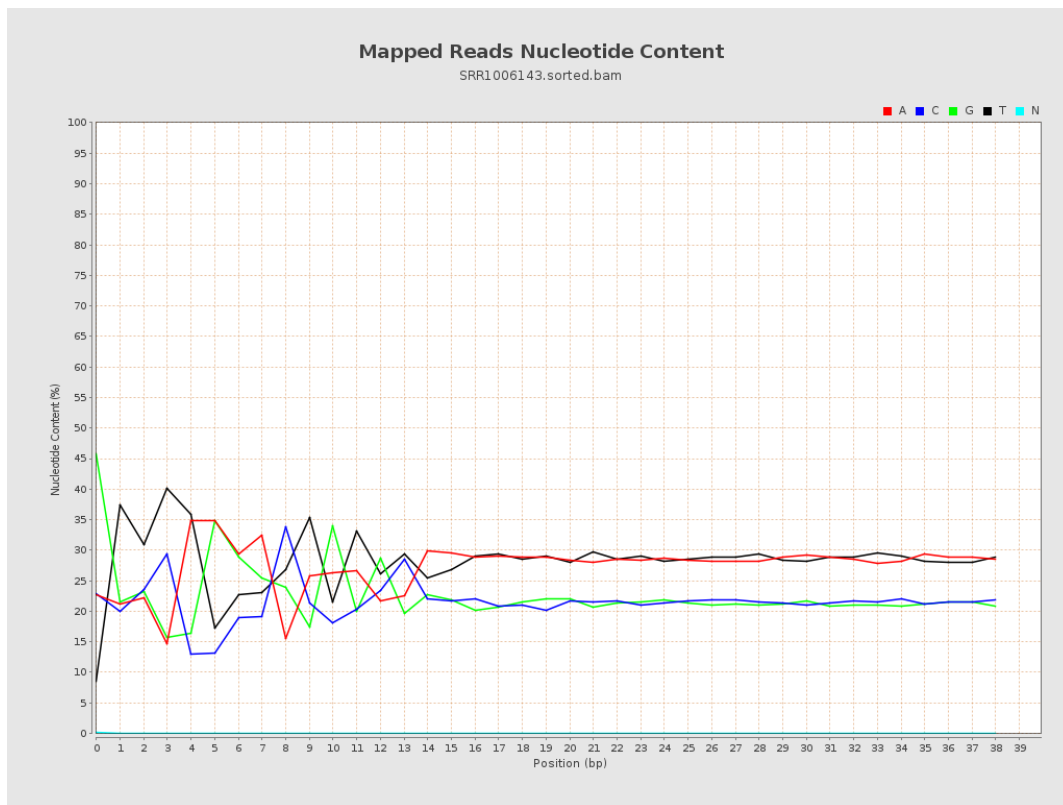
6. Results : Genome Fraction Coverage



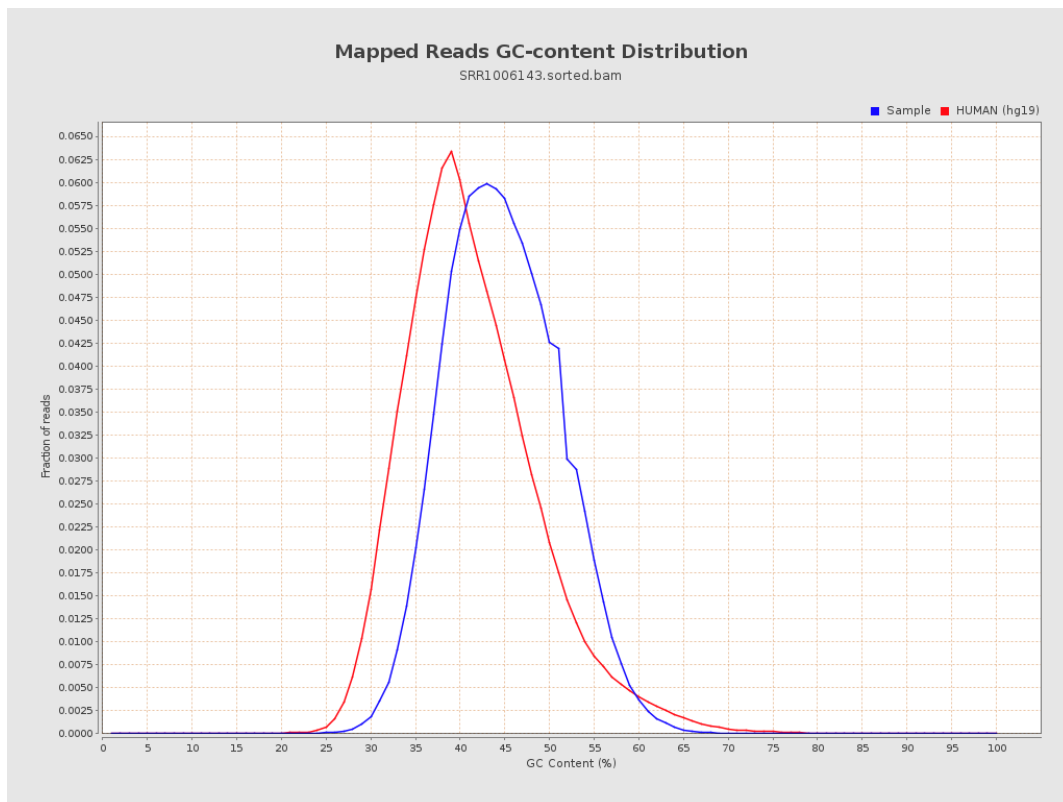
7. Results : Duplication Rate Histogram



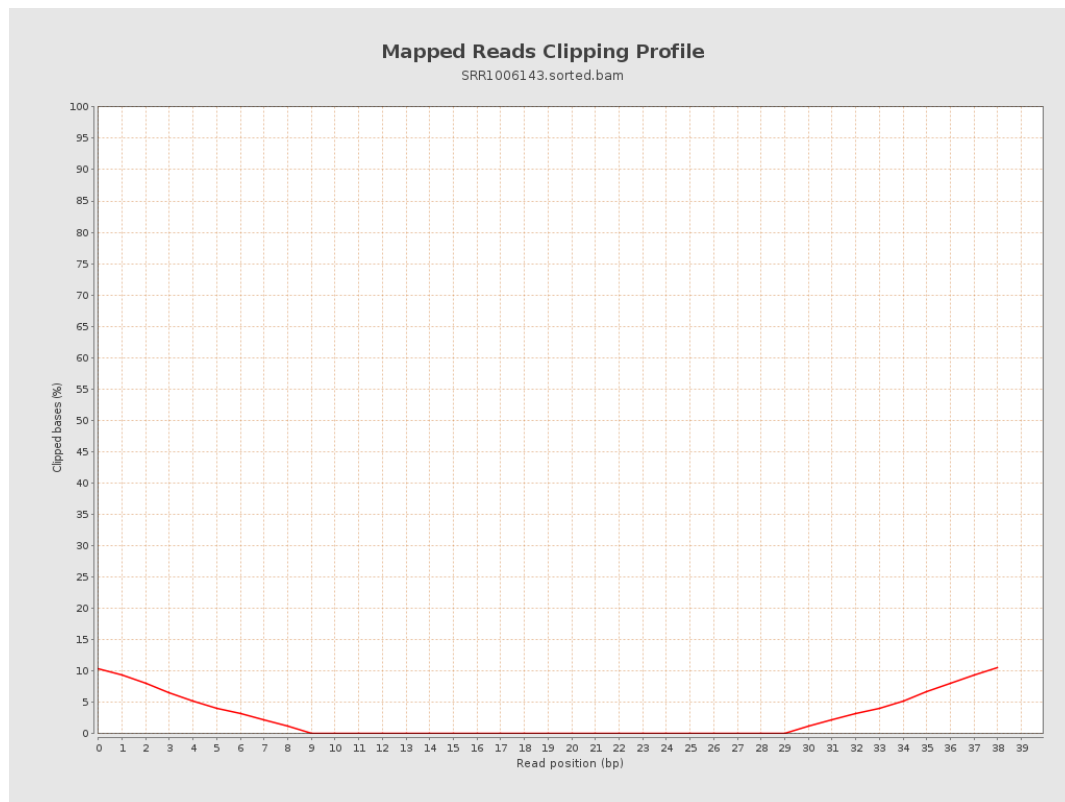
8. Results : Mapped Reads Nucleotide Content



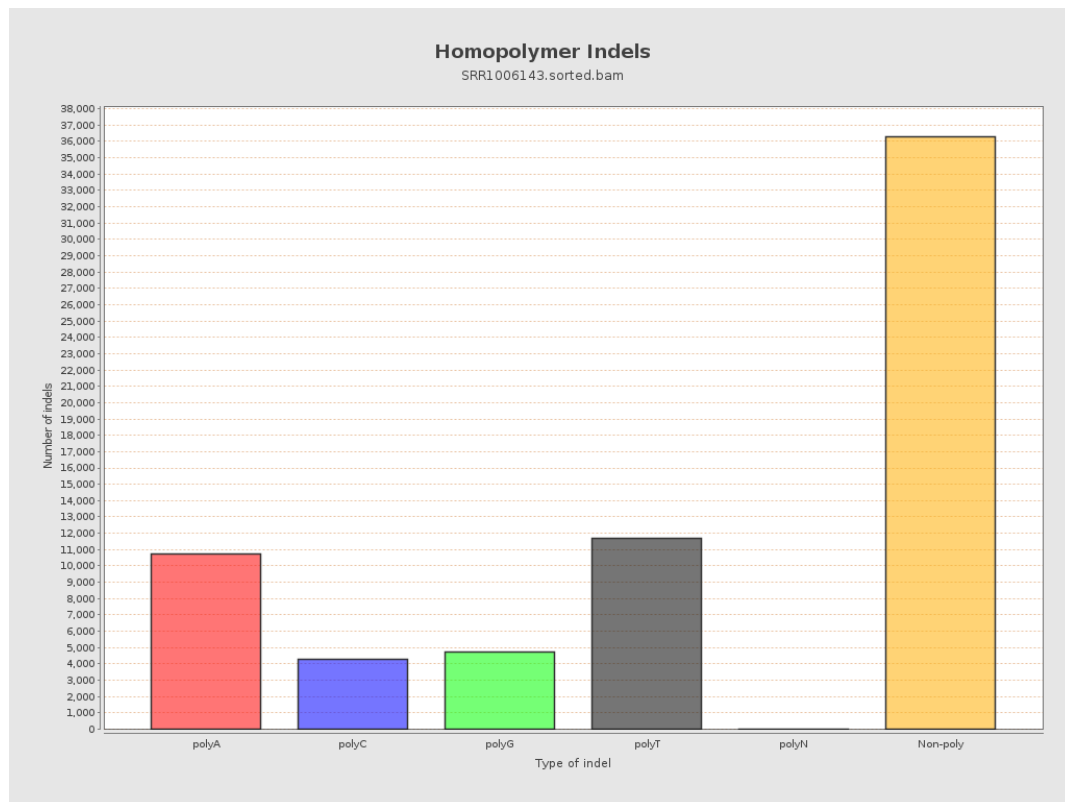
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



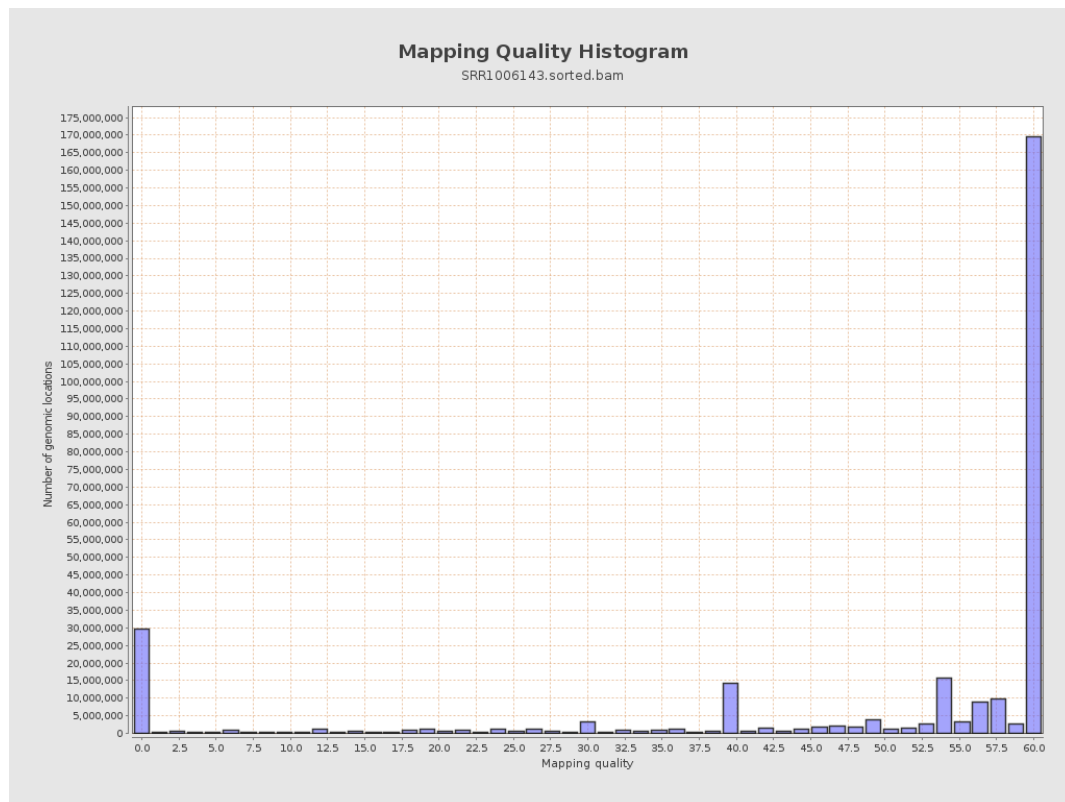
11. Results : Homopolymer Indels



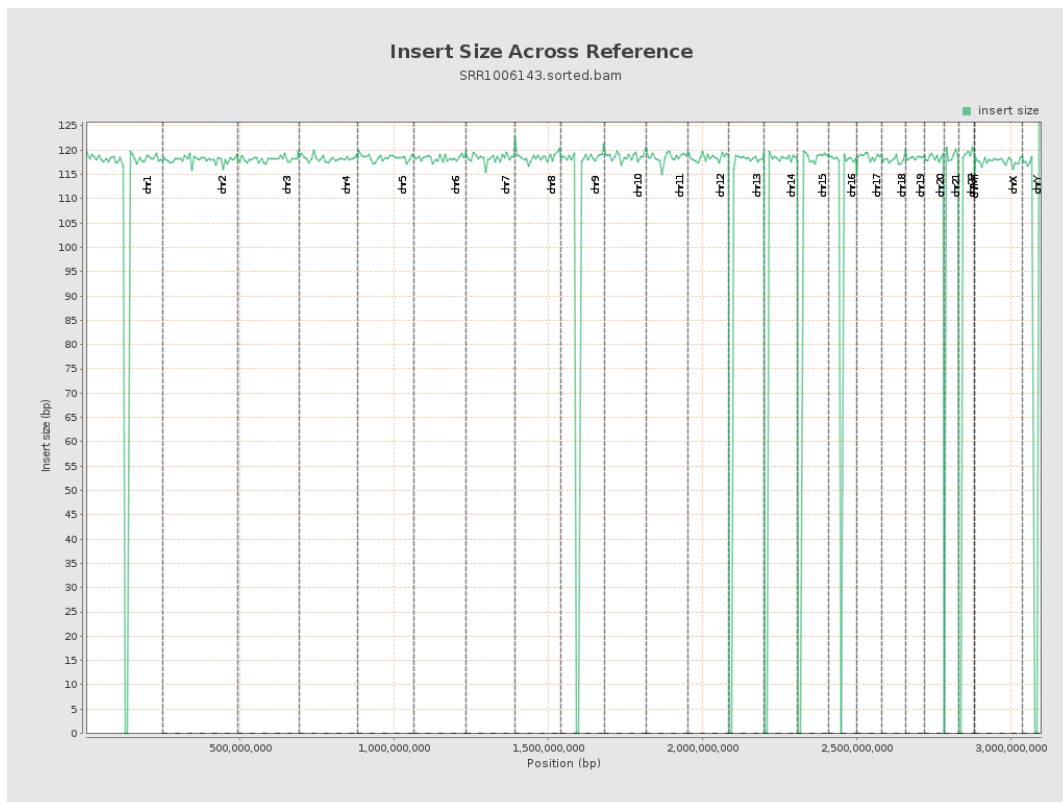
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

