

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 00:46:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006383.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_SRR1006383 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006383_1.fastq.gz SRR1006383_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 00:46:29 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006383.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,920,688
Mapped reads	4,343,620 / 88.27%
Unmapped reads	577,068 / 11.73%
Mapped paired reads	4,343,620 / 88.27%
Mapped reads, first in pair	2,205,283 / 44.82%
Mapped reads, second in pair	2,138,337 / 43.46%
Mapped reads, both in pair	3,984,328 / 80.97%
Mapped reads, singletons	359,292 / 7.3%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	144,870 / 2.94%
Duplication rate	2.89%
Clipped reads	230,031 / 4.67%

2.2. ACGT Content

Number/percentage of A's	46,874,607 / 27.87%
Number/percentage of C's	36,295,728 / 21.58%
Number/percentage of T's	47,513,213 / 28.25%
Number/percentage of G's	37,526,776 / 22.31%
Number/percentage of N's	7,170 / 0%
GC Percentage	43.89%

2.3. Coverage

Mean	0.0543
Standard Deviation	0.3314

2.4. Mapping Quality

Mean Mapping Quality	48.37
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2.5. Insert size

Mean	72,612.46
Standard Deviation	2,570,802.37
P25/Median/P75	122 / 159 / 213

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	621,532
Insertions	4,585
Mapped reads with at least one insertion	0.11%
Deletions	15,225
Mapped reads with at least one deletion	0.35%
Homopolymer indels	44.28%

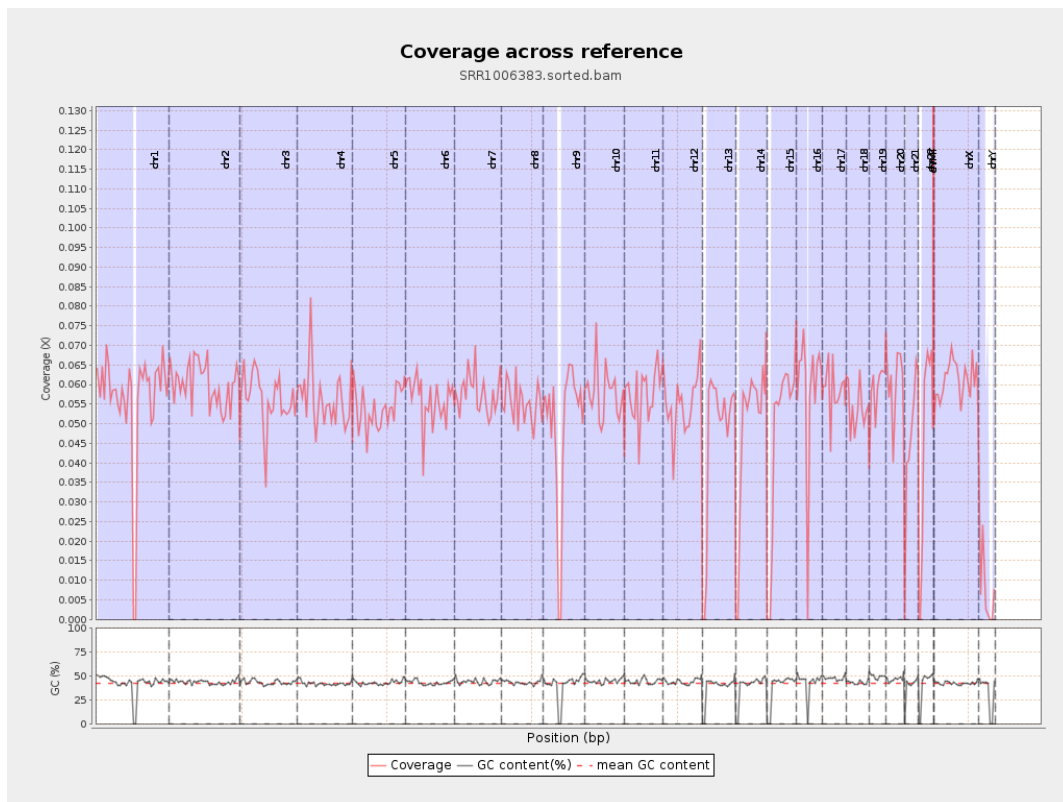
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

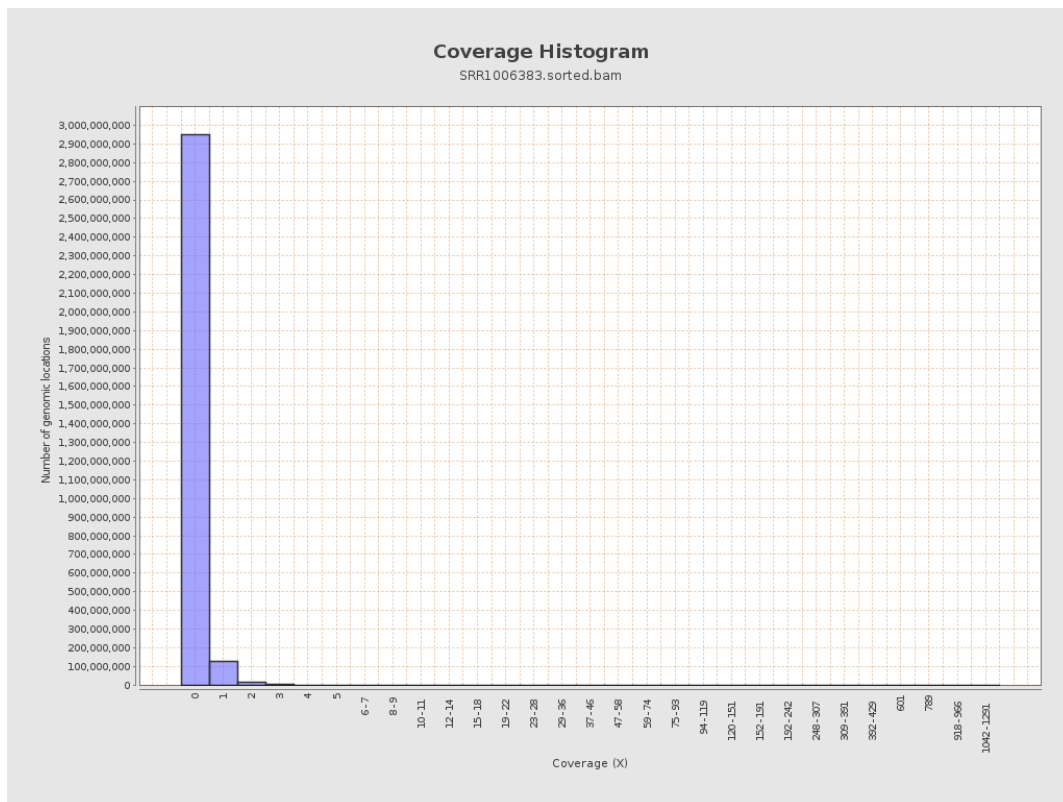
chr1	249250621	13993537	0.0561	0.4204
chr2	243199373	14639522	0.0602	0.3188
chr3	198022430	11106390	0.0561	0.2643
chr4	191154276	10757798	0.0563	0.2928
chr5	180915260	9725577	0.0538	0.2591
chr6	171115067	9596386	0.0561	0.2818
chr7	159138663	9170245	0.0576	0.3485
chr8	146364022	8062178	0.0551	0.6781
chr9	141213431	6916118	0.049	0.2722
chr10	135534747	7817551	0.0577	0.3383
chr11	135006516	7746311	0.0574	0.3009
chr12	133851895	7320672	0.0547	0.2641
chr13	115169878	5335224	0.0463	0.2428
chr14	107349540	5183000	0.0483	0.2553
chr15	102531392	4887010	0.0477	0.2449
chr16	90354753	5296586	0.0586	0.3019
chr17	81195210	4747267	0.0585	0.2835
chr18	78077248	4212868	0.054	0.3932
chr19	59128983	3499944	0.0592	0.3445
chr20	63025520	3737340	0.0593	0.2797
chr21	48129895	2239149	0.0465	0.2743
chr22	51304566	2295056	0.0447	0.2442
chrMT	16571	4605	0.2779	0.6306
chrX	155270560	9489691	0.0611	0.2925

chrY	59373566	457895	0.0077	0.1899
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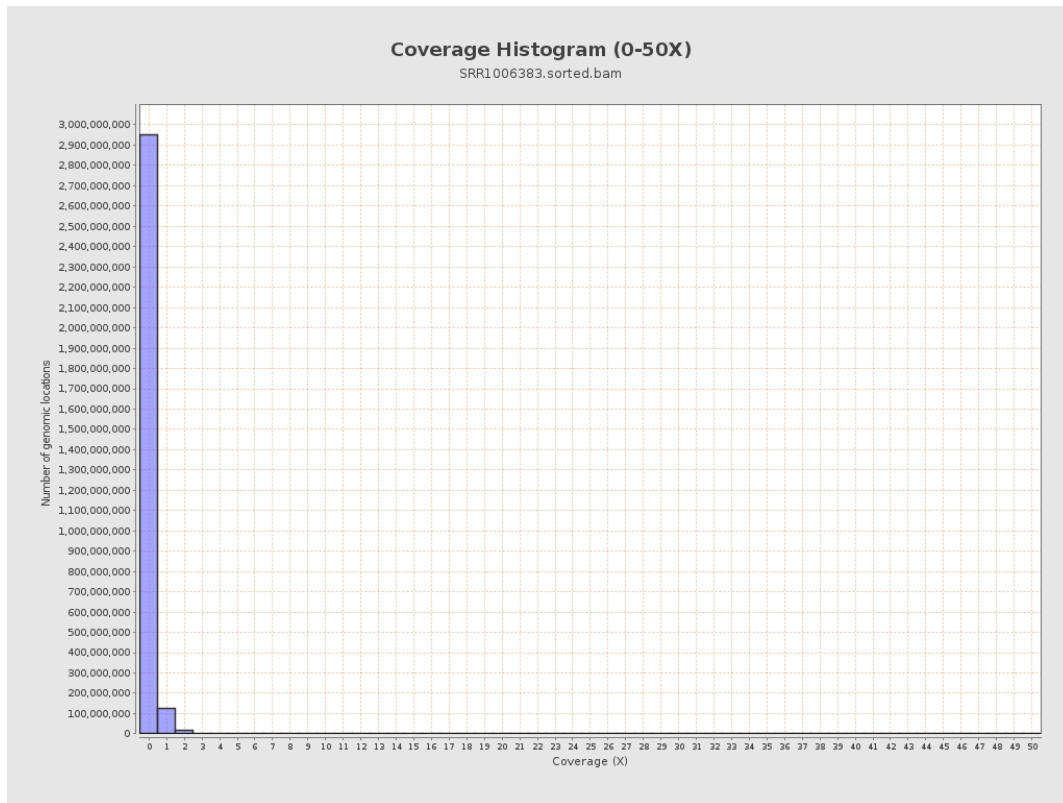
3. Results : Coverage across reference



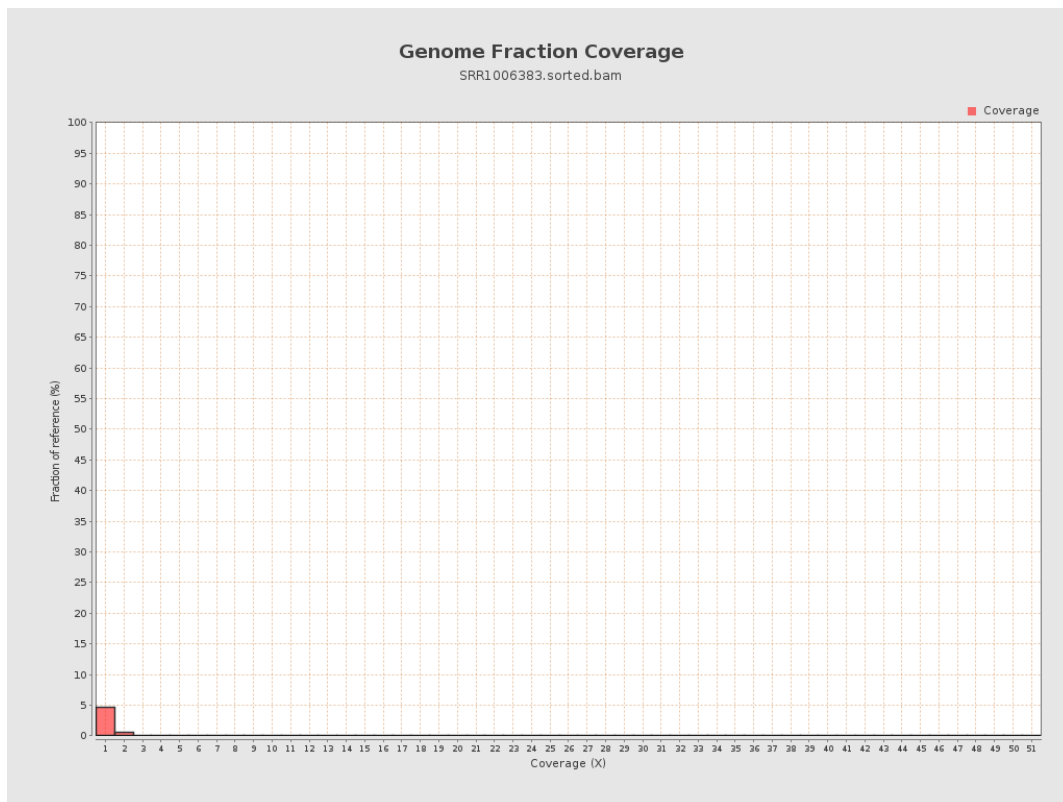
4. Results : Coverage Histogram



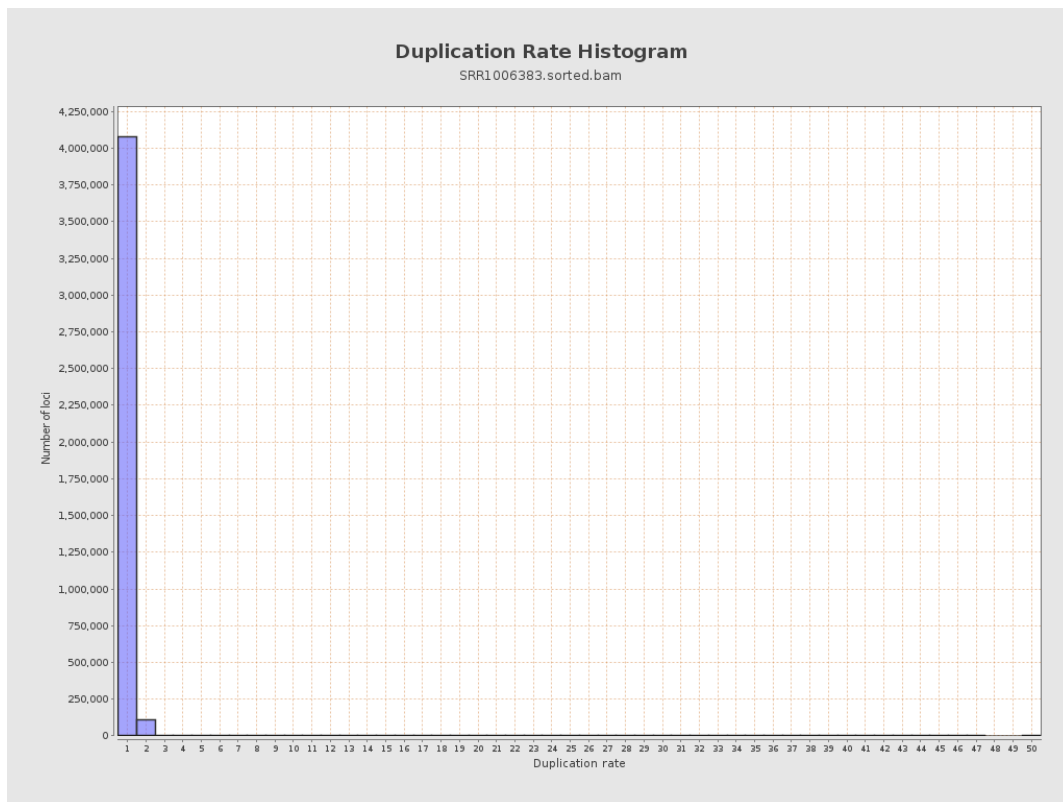
5. Results : Coverage Histogram (0-50X)



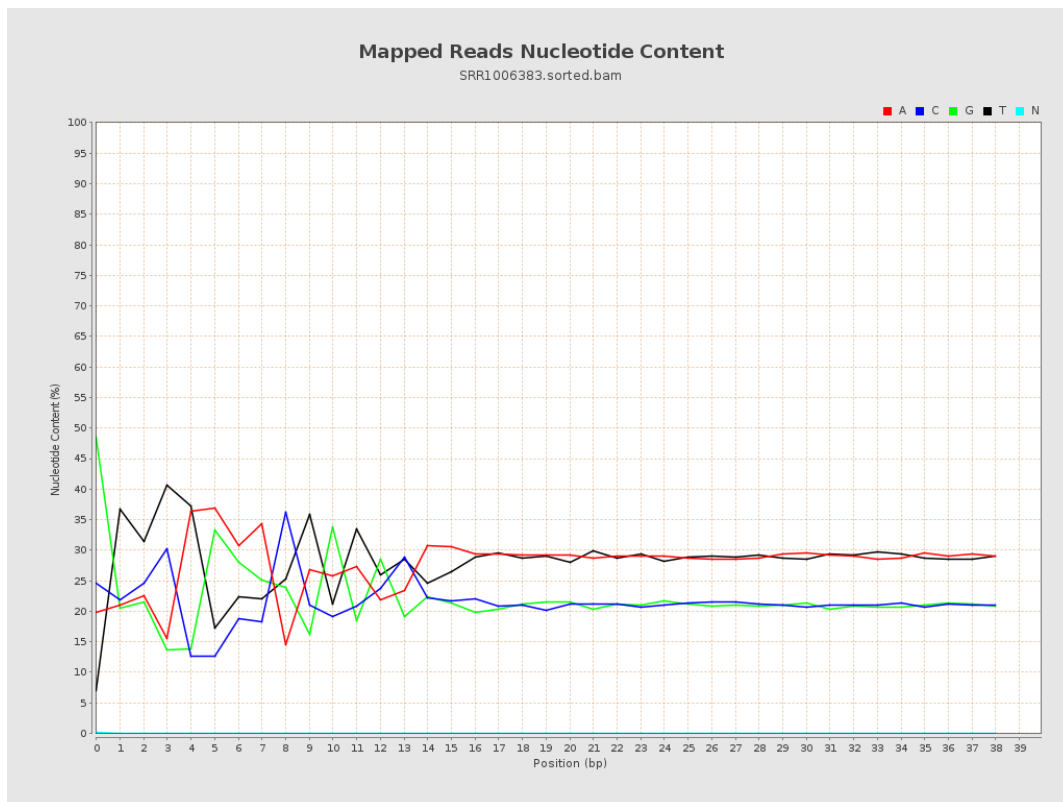
6. Results : Genome Fraction Coverage



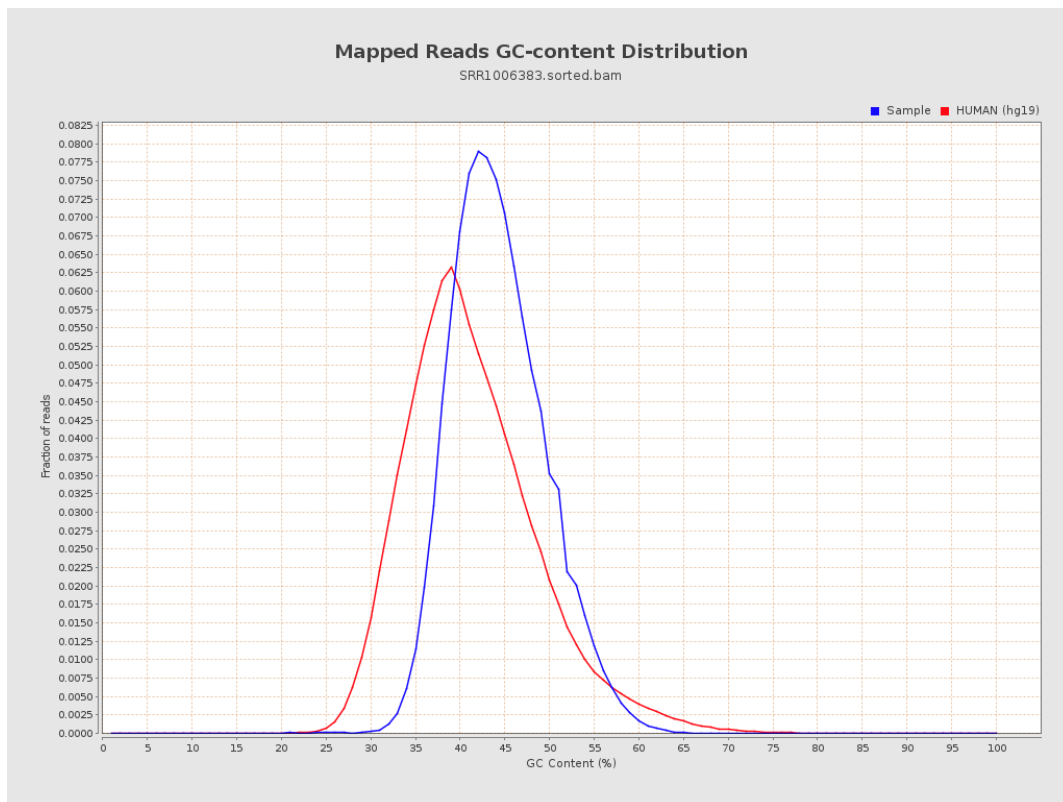
7. Results : Duplication Rate Histogram



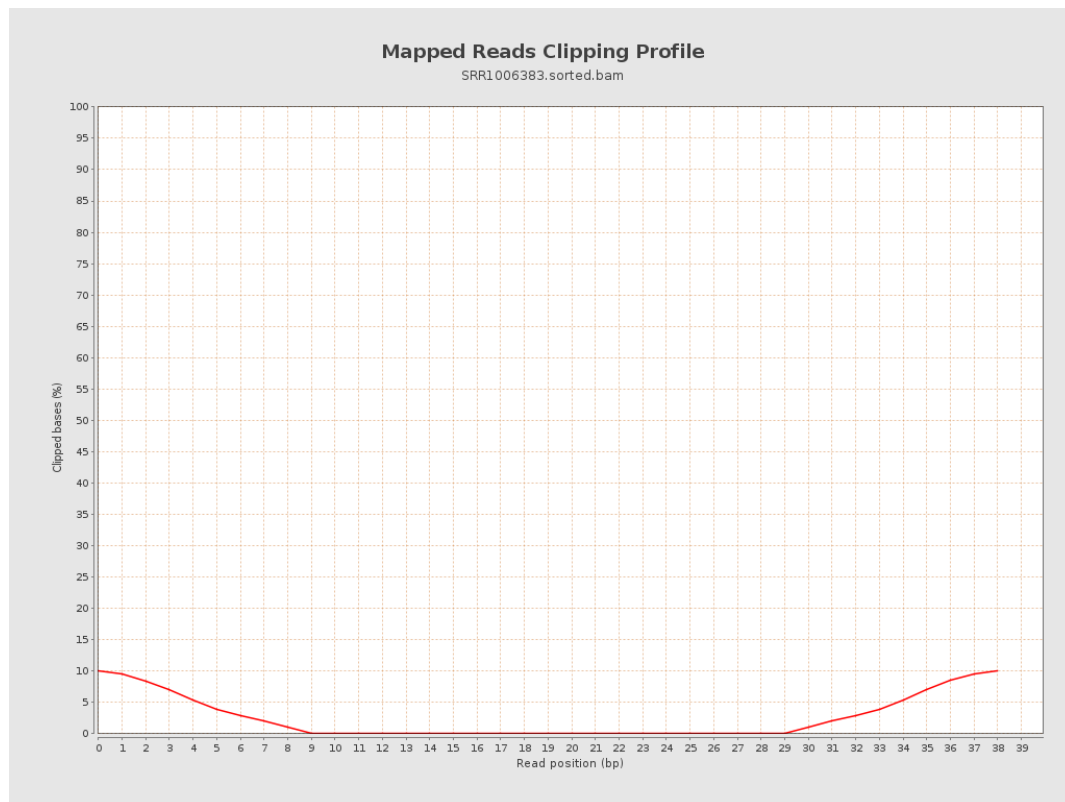
8. Results : Mapped Reads Nucleotide Content



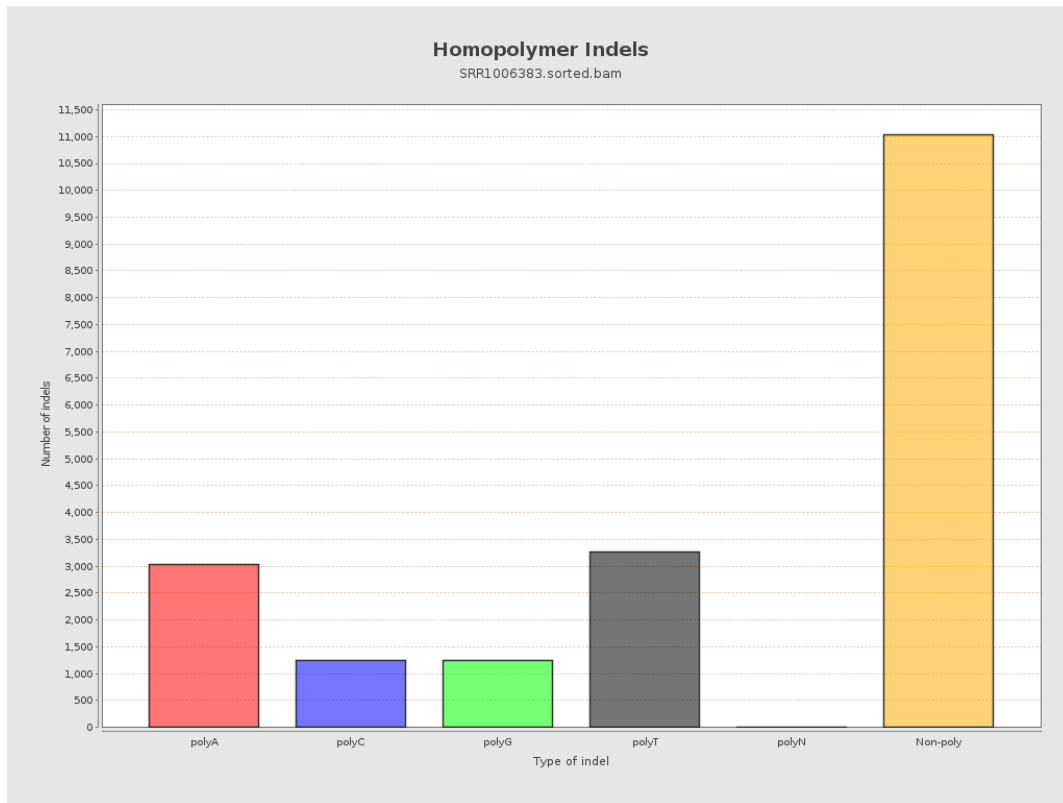
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



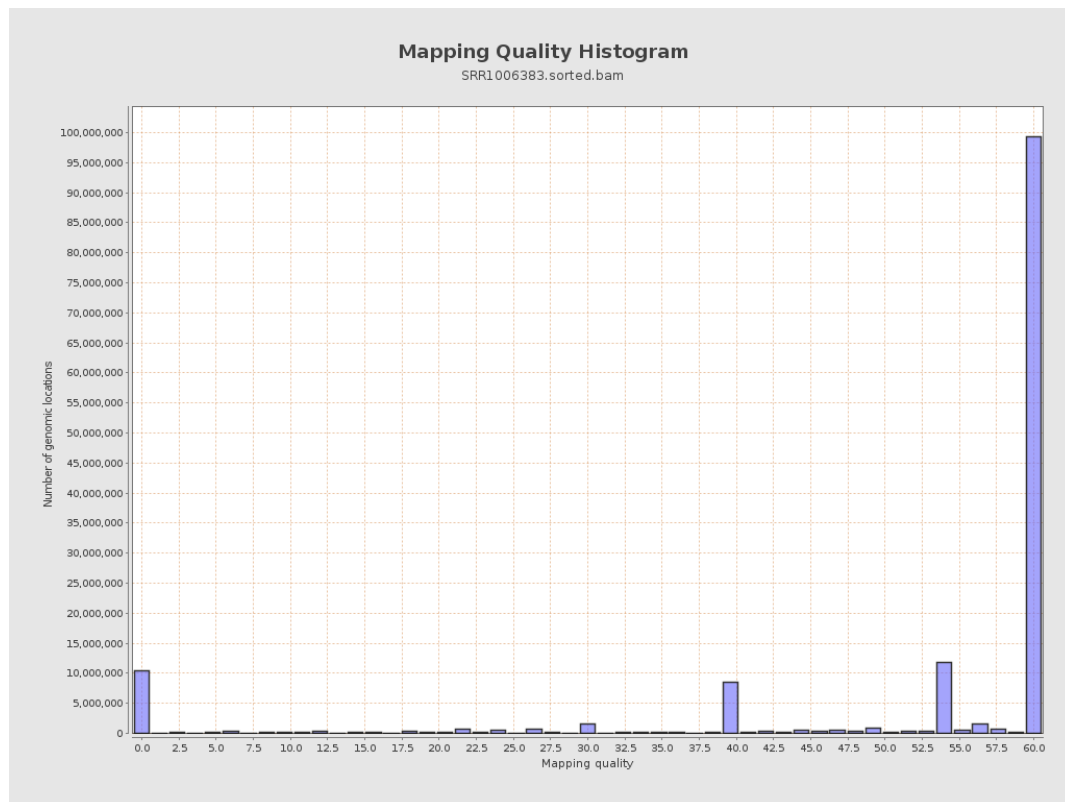
11. Results : Homopolymer Indels



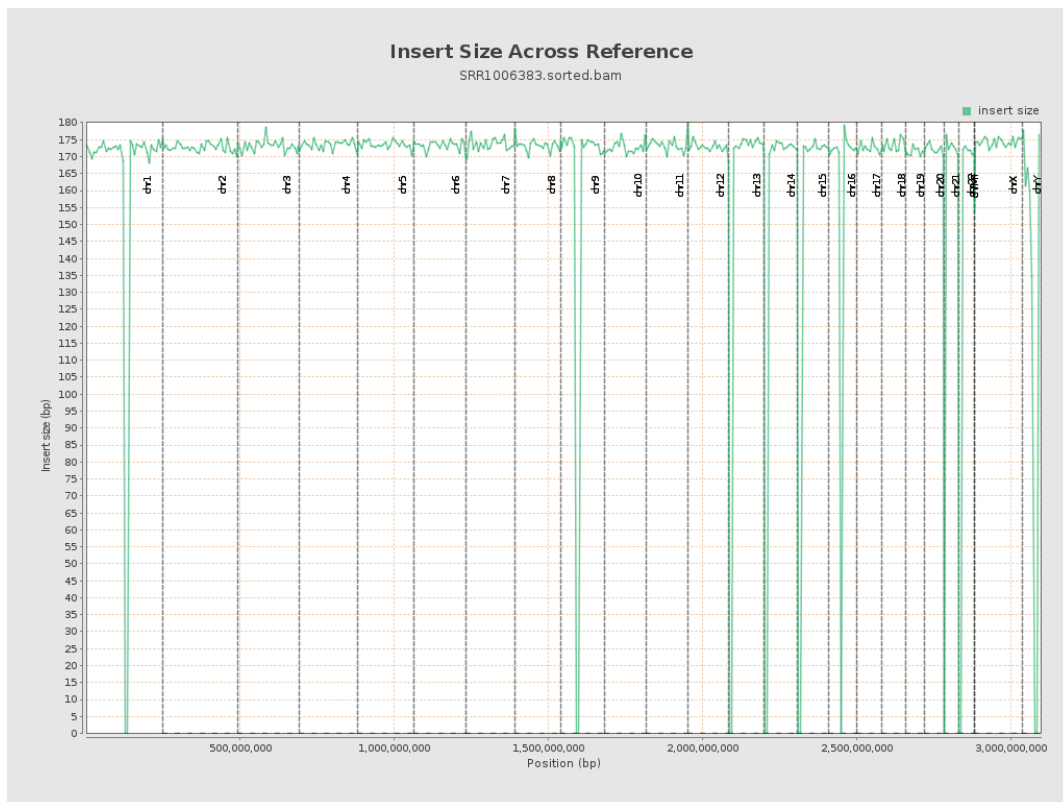
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

