

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 03:24:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1039846.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_SRR1039846 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1039846_1.fastq.gz SRR1039846_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 03:24:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1039846.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,030,984
Mapped reads	8,600,919 / 85.74%
Unmapped reads	1,430,065 / 14.26%
Mapped paired reads	8,600,919 / 85.74%
Mapped reads, first in pair	4,364,057 / 43.51%
Mapped reads, second in pair	4,236,862 / 42.24%
Mapped reads, both in pair	7,726,638 / 77.03%
Mapped reads, singletons	874,281 / 8.72%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	1,187,795 / 11.84%
Duplication rate	12.35%
Clipped reads	885,431 / 8.83%

2.2. ACGT Content

Number/percentage of A's	85,708,800 / 25.89%
Number/percentage of C's	75,418,220 / 22.78%
Number/percentage of T's	89,199,724 / 26.94%
Number/percentage of G's	80,738,820 / 24.39%
Number/percentage of N's	13,020 / 0%
GC Percentage	47.17%

2.3. Coverage

Mean	0.107
Standard Deviation	0.7432

2.4. Mapping Quality

Mean Mapping Quality	45.46
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2.5. Insert size

Mean	87,296.87
Standard Deviation	2,872,518.24
P25/Median/P75	68 / 92 / 120

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	1,804,884
Insertions	11,164
Mapped reads with at least one insertion	0.13%
Deletions	26,728
Mapped reads with at least one deletion	0.31%
Homopolymer indels	43.65%

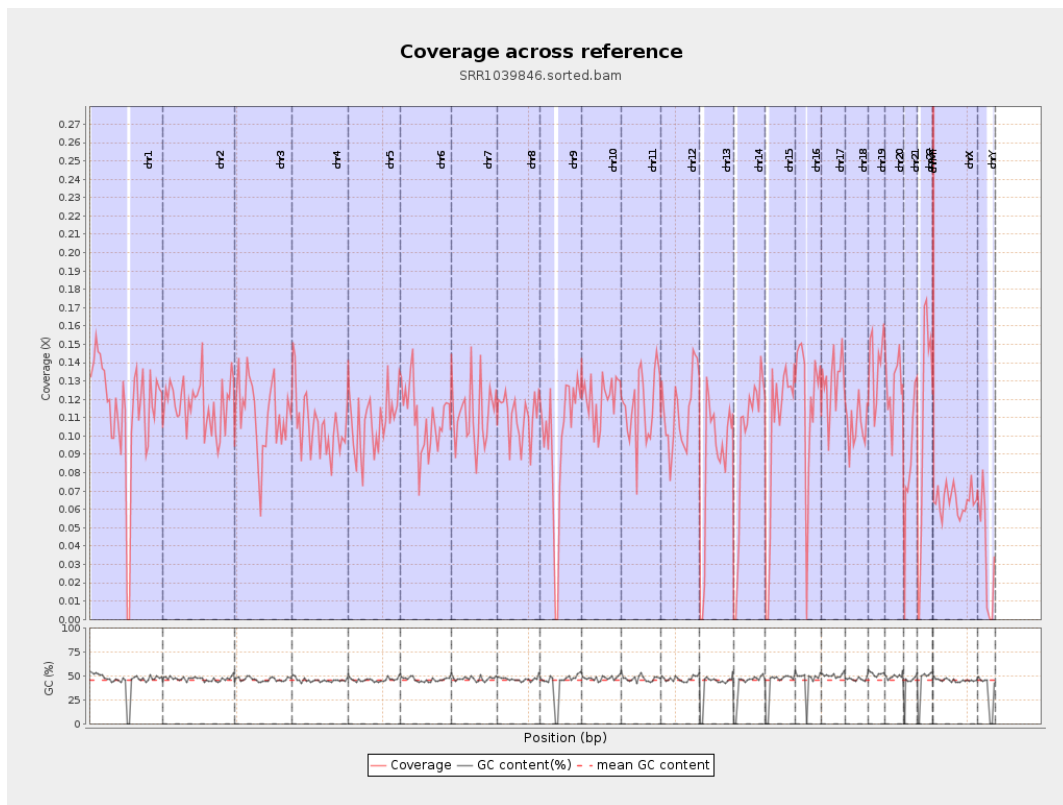
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

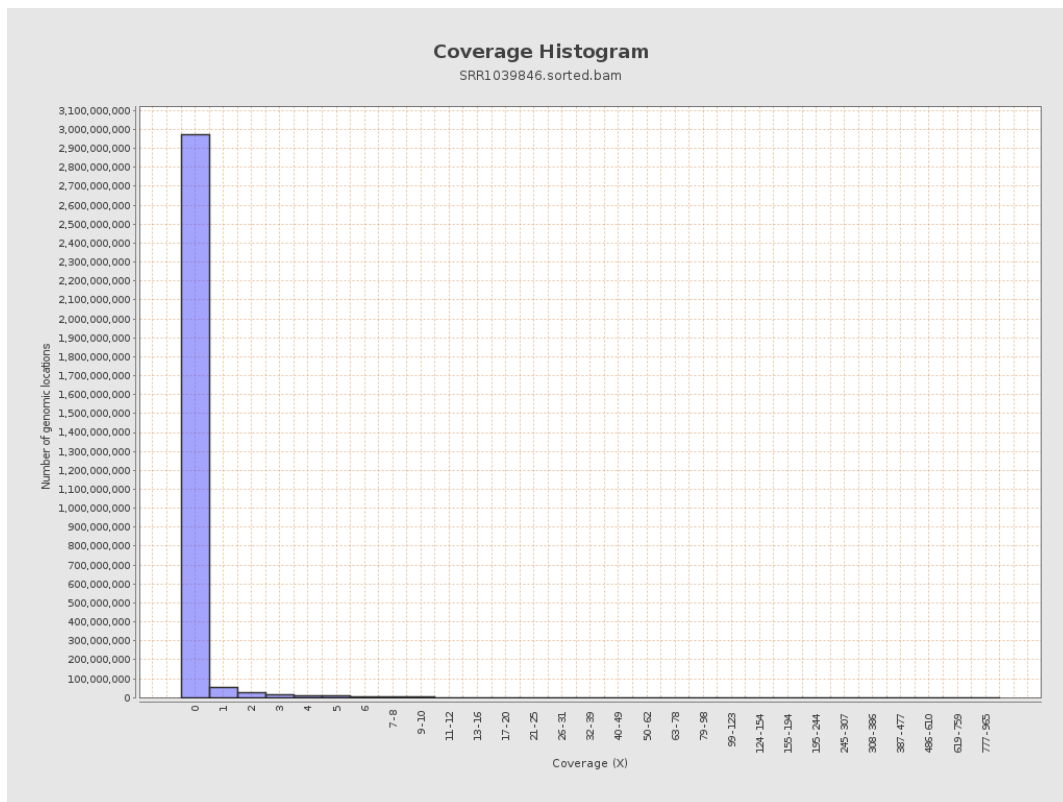
chr1	249250621	28448771	0.1141	0.8239
chr2	243199373	28492776	0.1172	0.7947
chr3	198022430	22038710	0.1113	0.7039
chr4	191154276	20192679	0.1056	0.6998
chr5	180915260	19523303	0.1079	0.6939
chr6	171115067	18673955	0.1091	0.7618
chr7	159138663	17837548	0.1121	0.7903
chr8	146364022	16151548	0.1104	0.7913
chr9	141213431	13789361	0.0976	0.6663
chr10	135534747	16273184	0.1201	0.7662
chr11	135006516	15637337	0.1158	0.8971
chr12	133851895	15196225	0.1135	0.7168
chr13	115169878	9981545	0.0867	0.6276
chr14	107349540	10540979	0.0982	0.6755
chr15	102531392	10362841	0.1011	0.688
chr16	90354753	10771709	0.1192	0.782
chr17	81195210	10611673	0.1307	0.811
chr18	78077248	8199686	0.105	0.7437
chr19	59128983	8239585	0.1393	0.9868
chr20	63025520	7940854	0.126	0.781
chr21	48129895	4261258	0.0885	0.6671
chr22	51304566	5624556	0.1096	0.7574
chrMT	16571	84823	5.1188	8.7307
chrX	155270560	10079853	0.0649	0.5311

chrY	59373566	2157429	0.0363	0.4193
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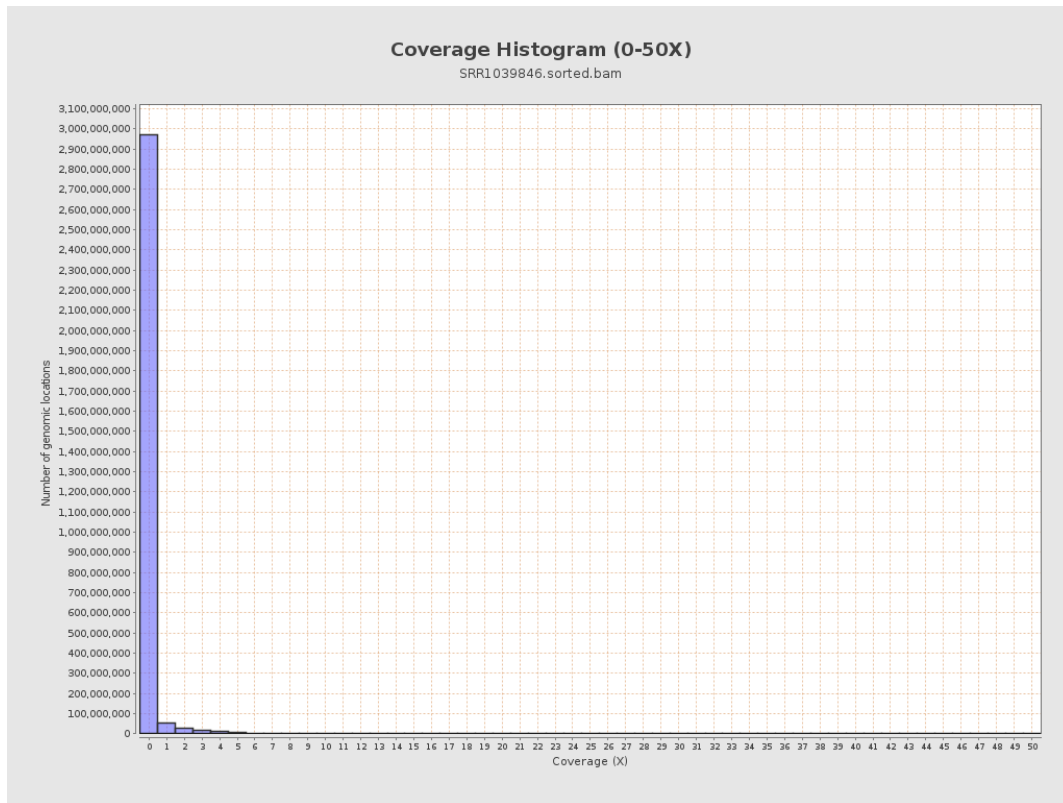
3. Results : Coverage across reference



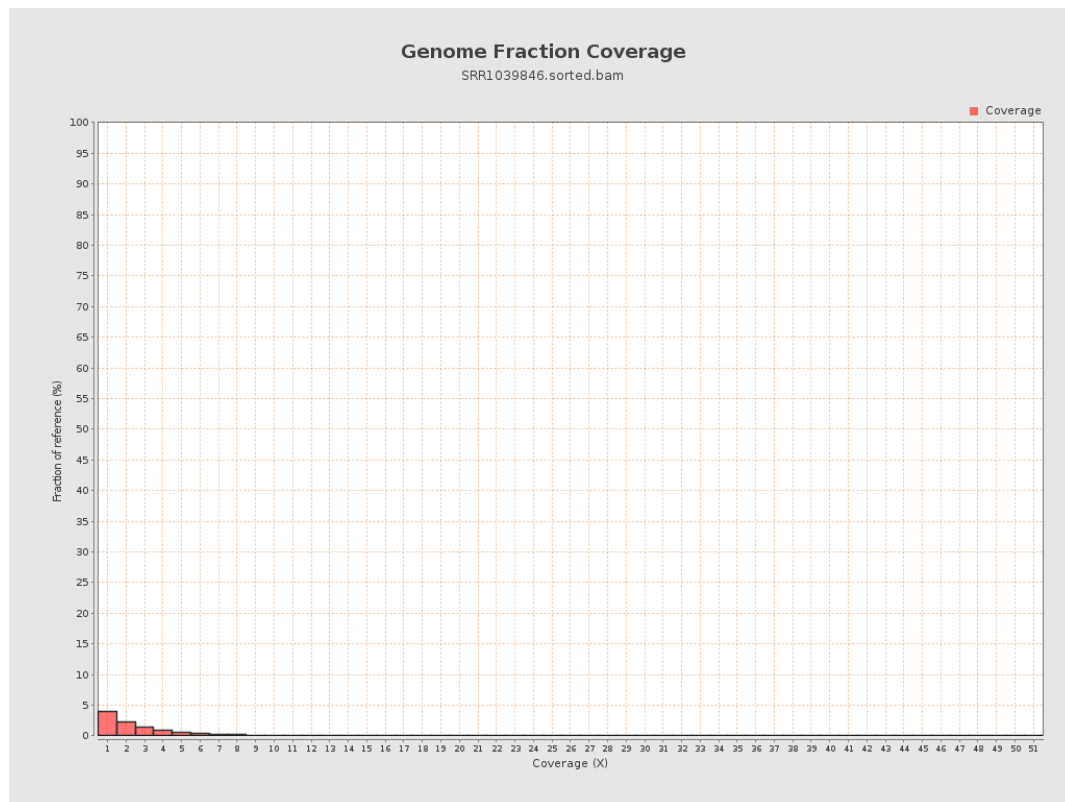
4. Results : Coverage Histogram



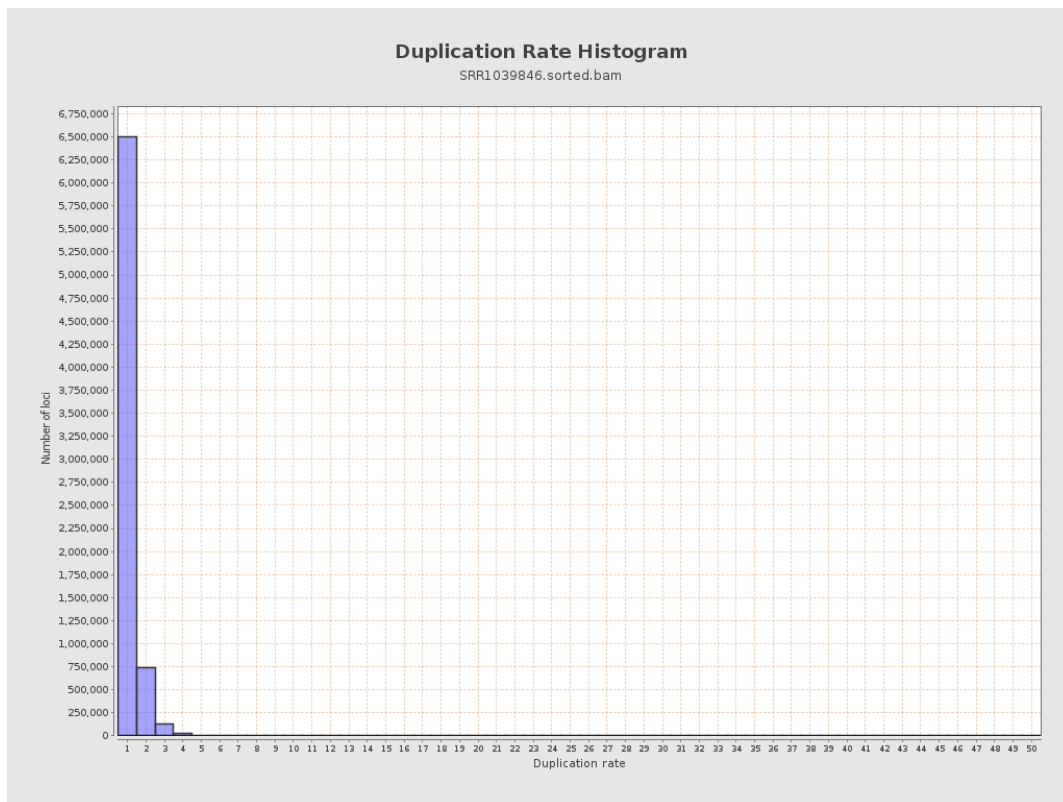
5. Results : Coverage Histogram (0-50X)



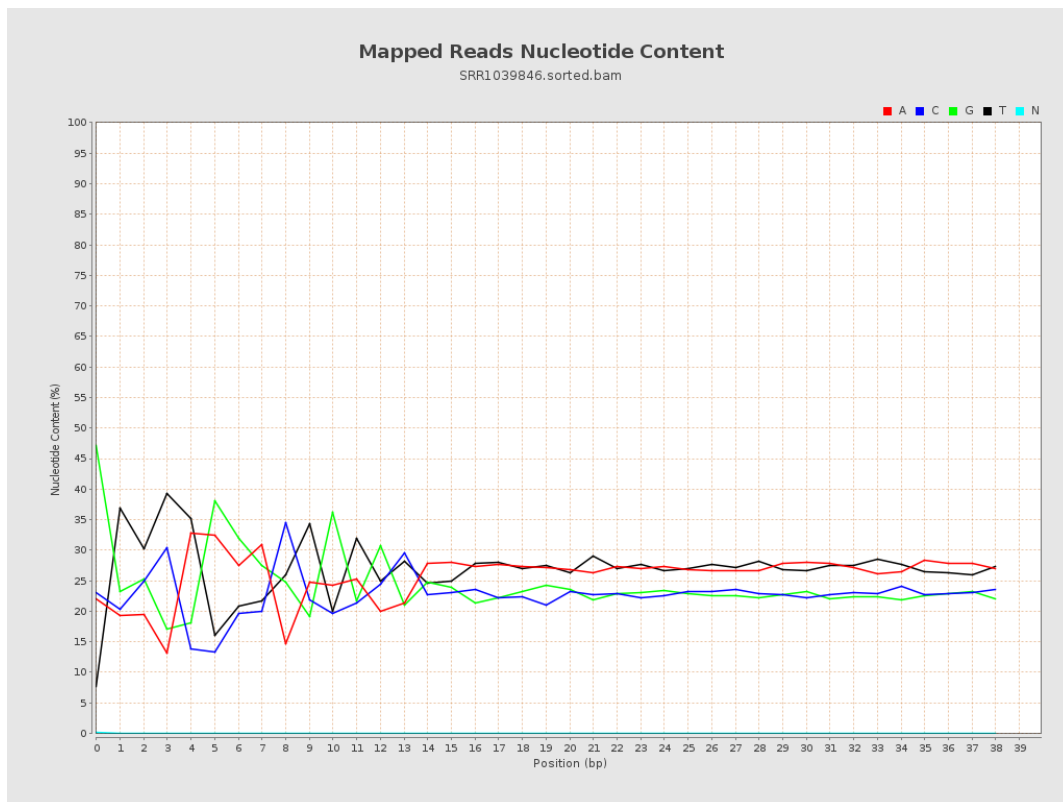
6. Results : Genome Fraction Coverage



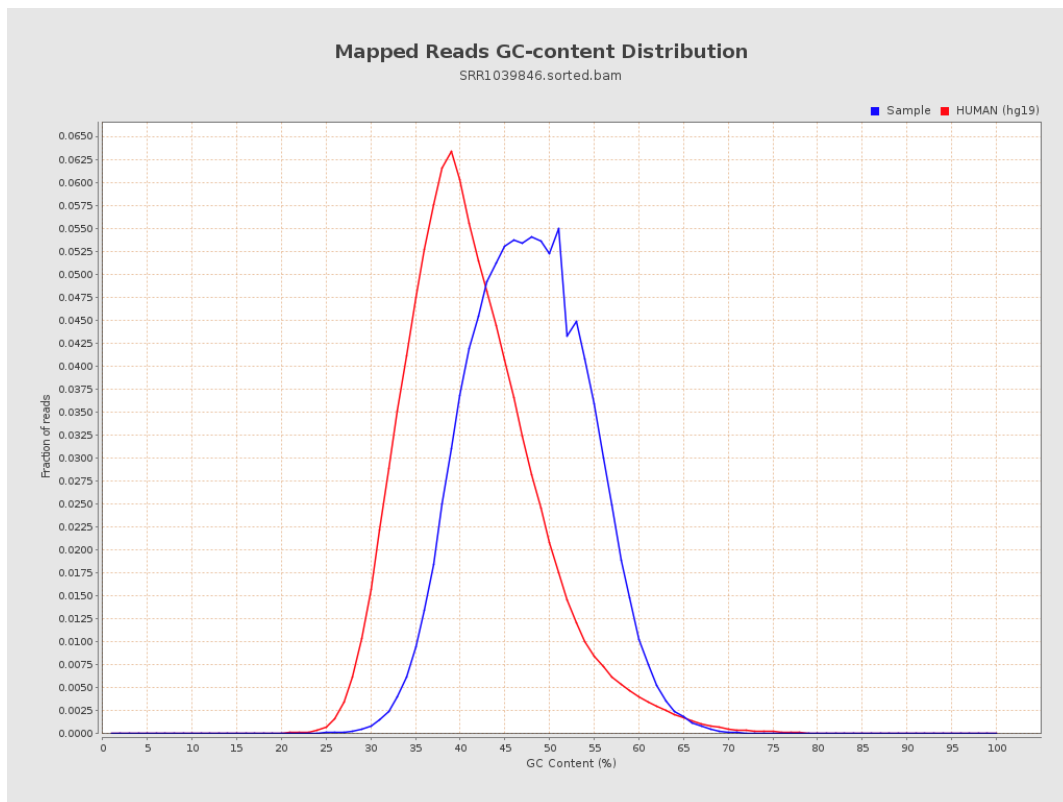
7. Results : Duplication Rate Histogram



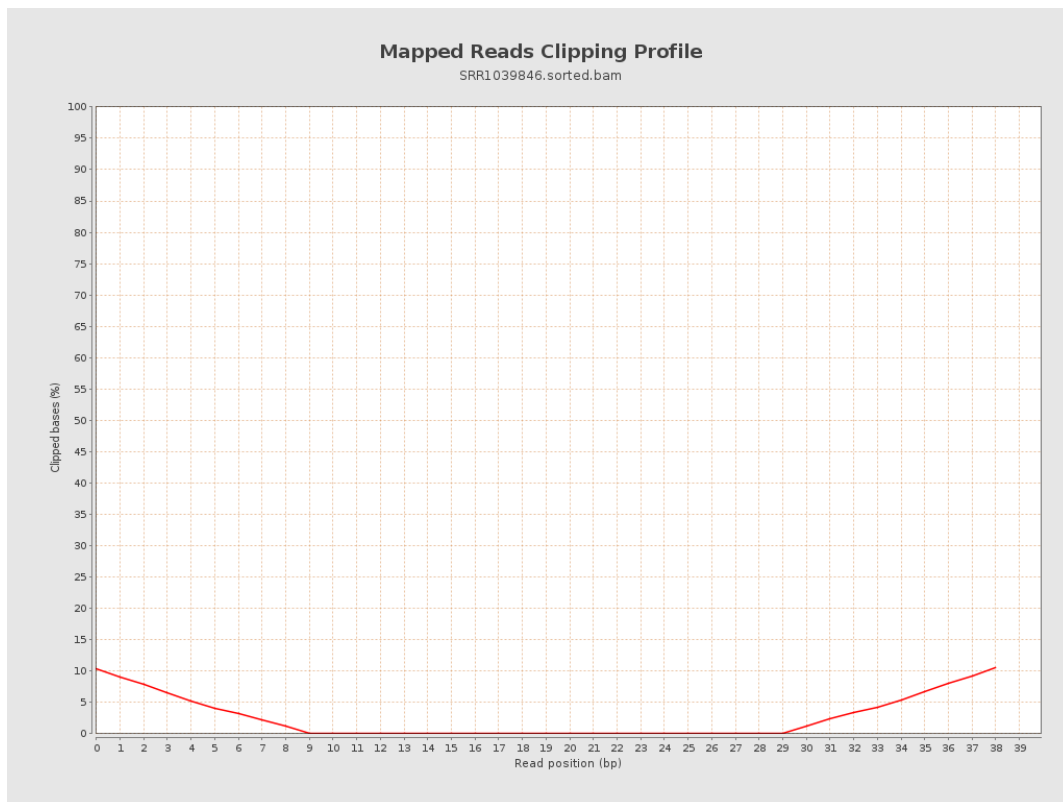
8. Results : Mapped Reads Nucleotide Content



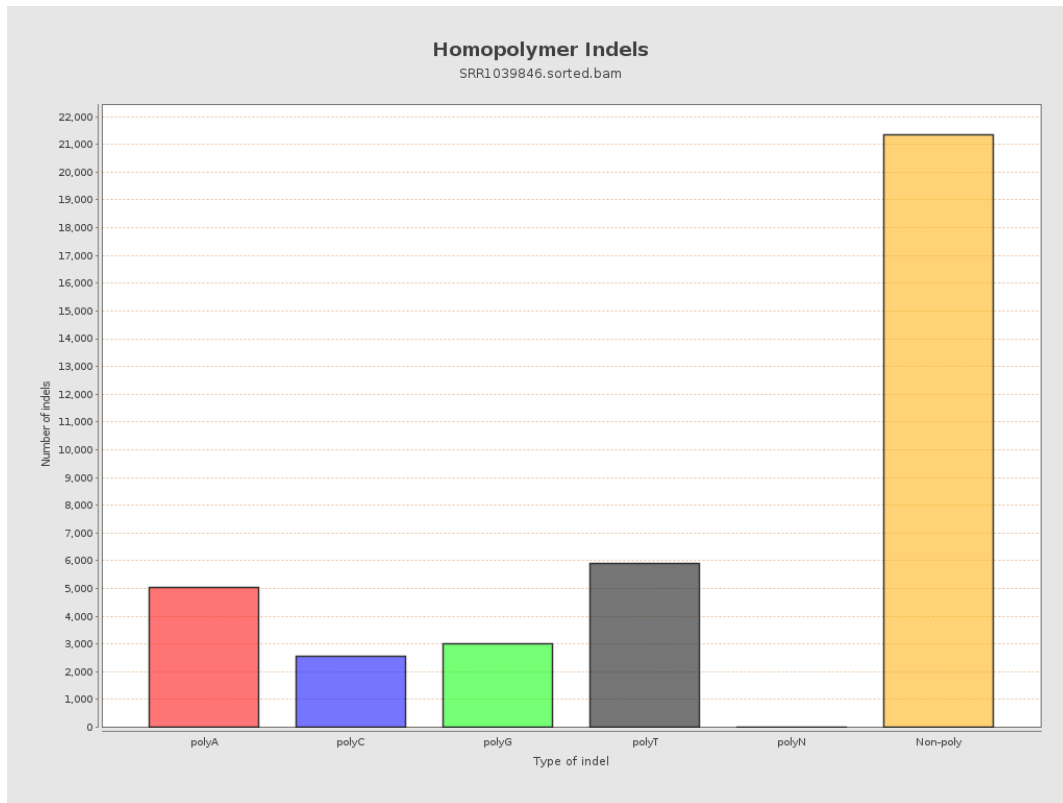
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



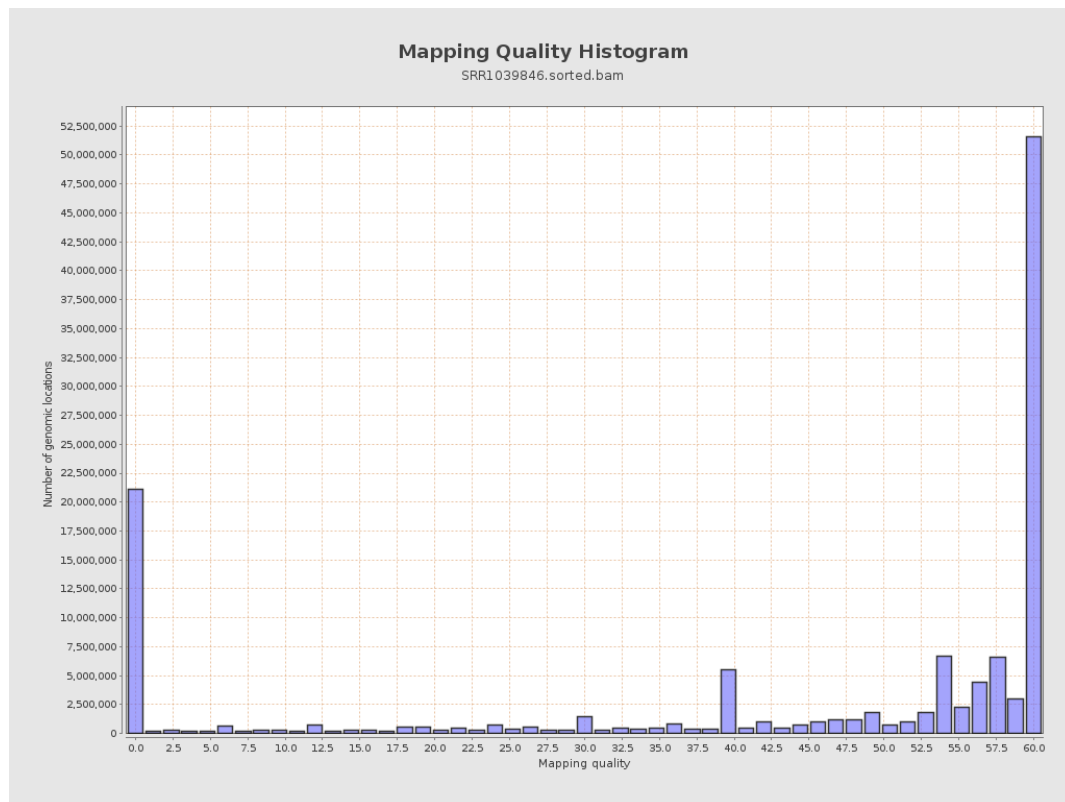
11. Results : Homopolymer Indels



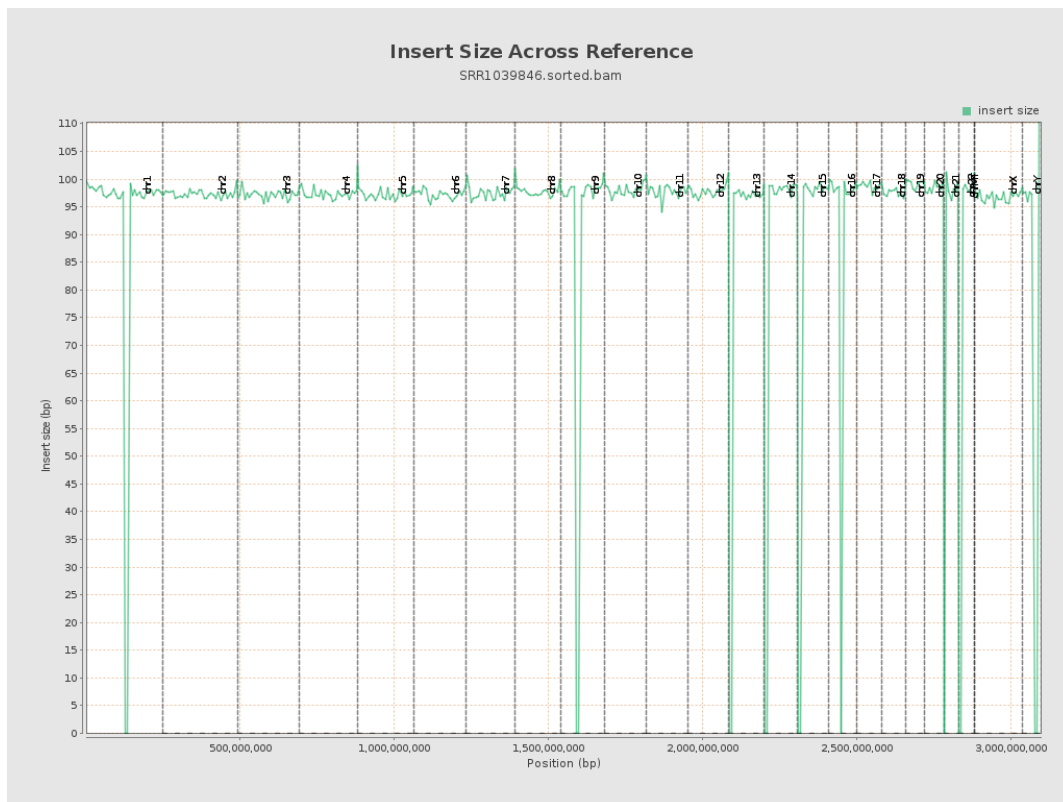
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

