Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 01:25:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006399.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_SRR1006399 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006399_1.fastq.gz SRR1006399_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 01:25:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006399.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,838,280
Mapped reads	4,233,433 / 87.5%
Unmapped reads	604,847 / 12.5%
Mapped paired reads	4,233,433 / 87.5%
Mapped reads, first in pair	2,119,849 / 43.81%
Mapped reads, second in pair	2,113,584 / 43.68%
Mapped reads, both in pair	3,894,450 / 80.49%
Mapped reads, singletons	338,983 / 7.01%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	108,551 / 2.24%
Duplication rate	2.04%
Clipped reads	236,724 / 4.89%

2.2. ACGT Content

Number/percentage of A's	45,721,926 / 27.9%
Number/percentage of C's	35,324,046 / 21.56%
Number/percentage of T's	46,298,584 / 28.26%
Number/percentage of G's	36,500,567 / 22.28%
Number/percentage of N's	6,726 / 0%
GC Percentage	43.84%

2.3. Coverage

Mean	0.0529
Standard Deviation	0.3448

2.4. Mapping Quality

Mean Mapping Quality	48.05

2.5. Insert size

Mean	69,564.61
Standard Deviation	2,502,083.27
P25/Median/P75	92 / 125 / 175

2.6. Mismatches and indels

General error rate	0.31%
Mismatches	504,028
Insertions	4,600
Mapped reads with at least one insertion	0.11%
Deletions	15,734
Mapped reads with at least one deletion	0.37%
Homopolymer indels	44.03%

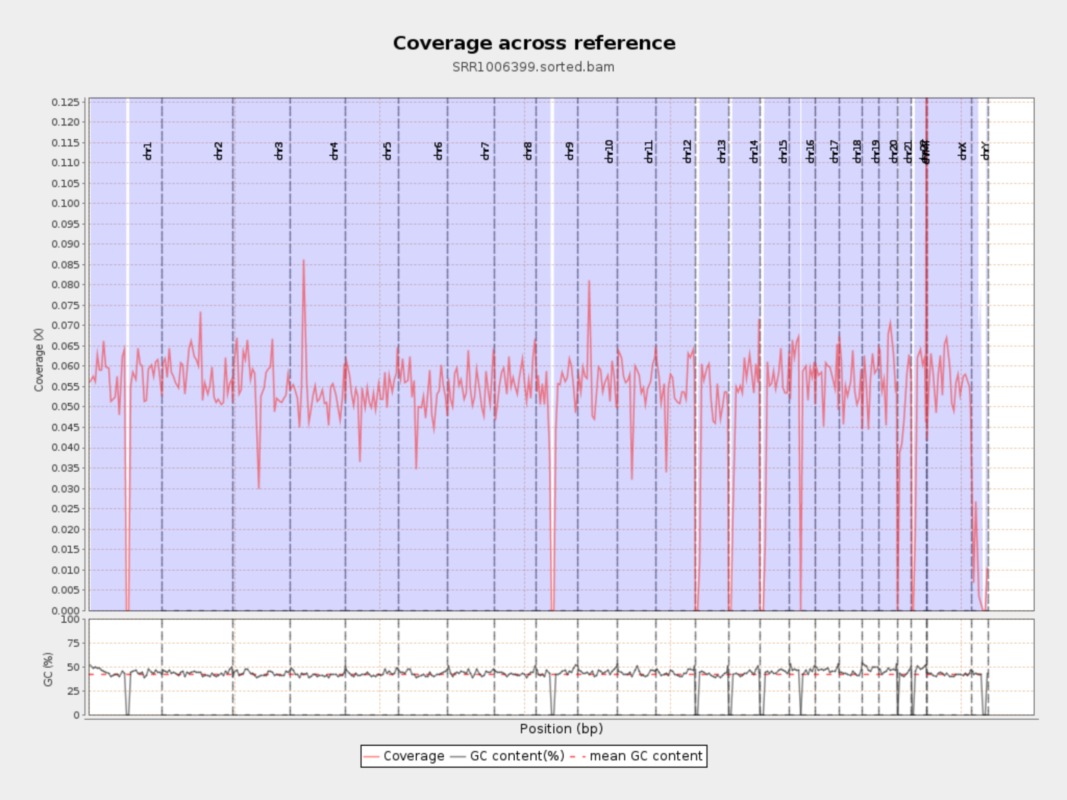
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

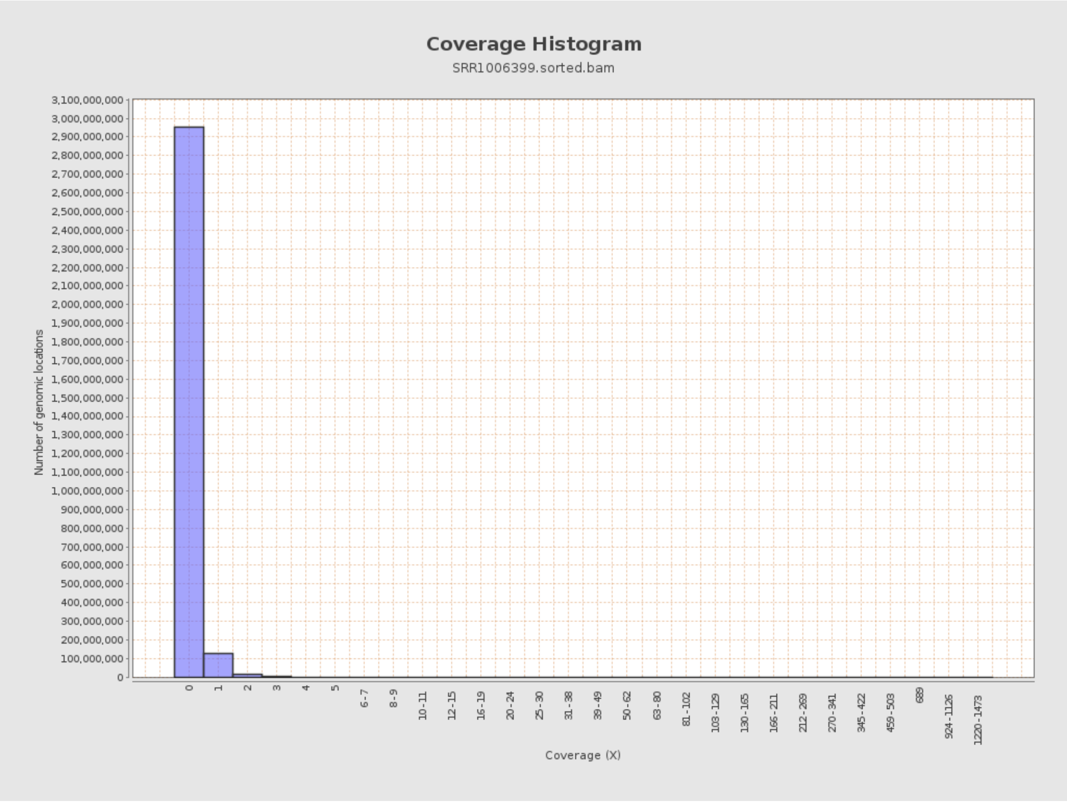
chr1	249250621	13557698	0.0544	0.44
chr2	243199373	14091551	0.0579	0.3245
chr3	198022430	11028455	0.0557	0.2627
chr4	191154276	10236616	0.0536	0.294
chr5	180915260	9657244	0.0534	0.2583
chr6	171115067	9125329	0.0533	0.2764
chr7	159138663	8736551	0.0549	0.3468
chr8	146364022	8249455	0.0564	0.7629
chr9	141213431	6814025	0.0483	0.279
chr10	135534747	7712802	0.0569	0.3623
chr11	135006516	7576457	0.0561	0.2979
chr12	133851895	7351329	0.0549	0.2635
chr13	115169878	5161579	0.0448	0.2371
chr14	107349540	5115599	0.0477	0.3
chr15	102531392	4725525	0.0461	0.2399
chr16	90354753	4997113	0.0553	0.3116
chr17	81195210	4675078	0.0576	0.2766
chr18	78077248	4337961	0.0556	0.4104
chr19	59128983	3364906	0.0569	0.3572
chr20	63025520	3731389	0.0592	0.2952
chr21	48129895	2191926	0.0455	0.2661
chr22	51304566	2171544	0.0423	0.2397
chrMT	16571	3747	0.2261	0.8962
chrX	155270560	8765626	0.0565	0.279

chrY	59373566	493518	0.0083	0.2096

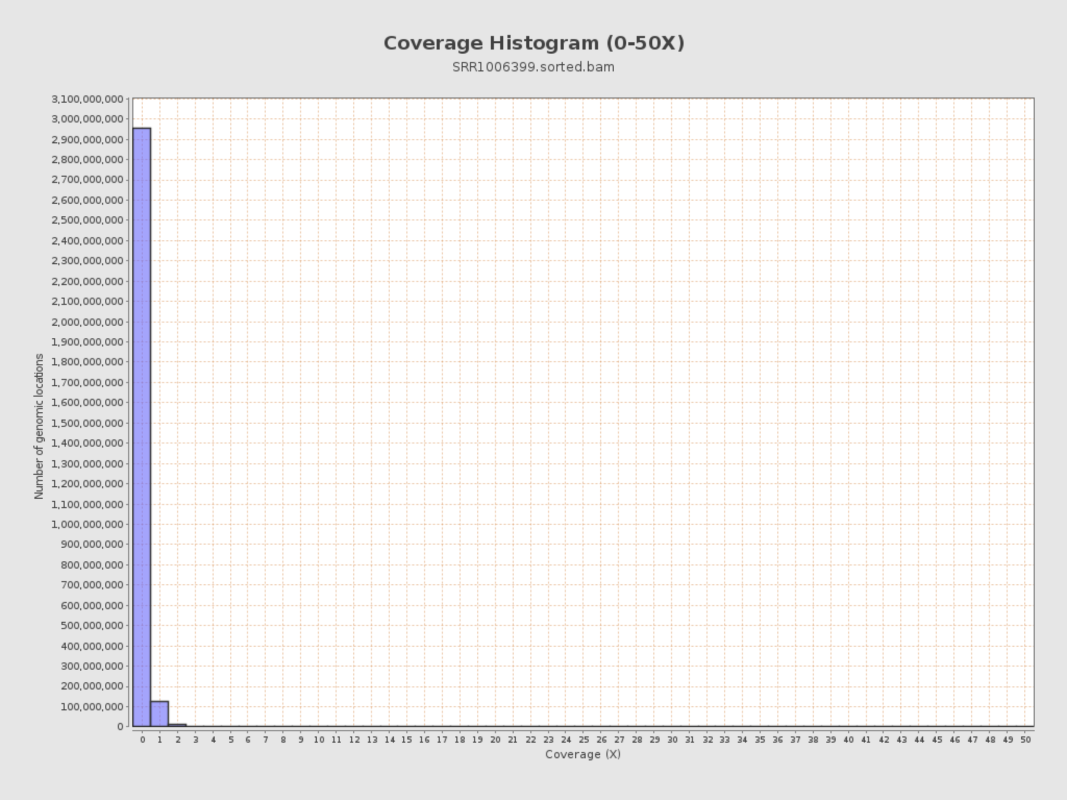
3. Results : Coverage across reference



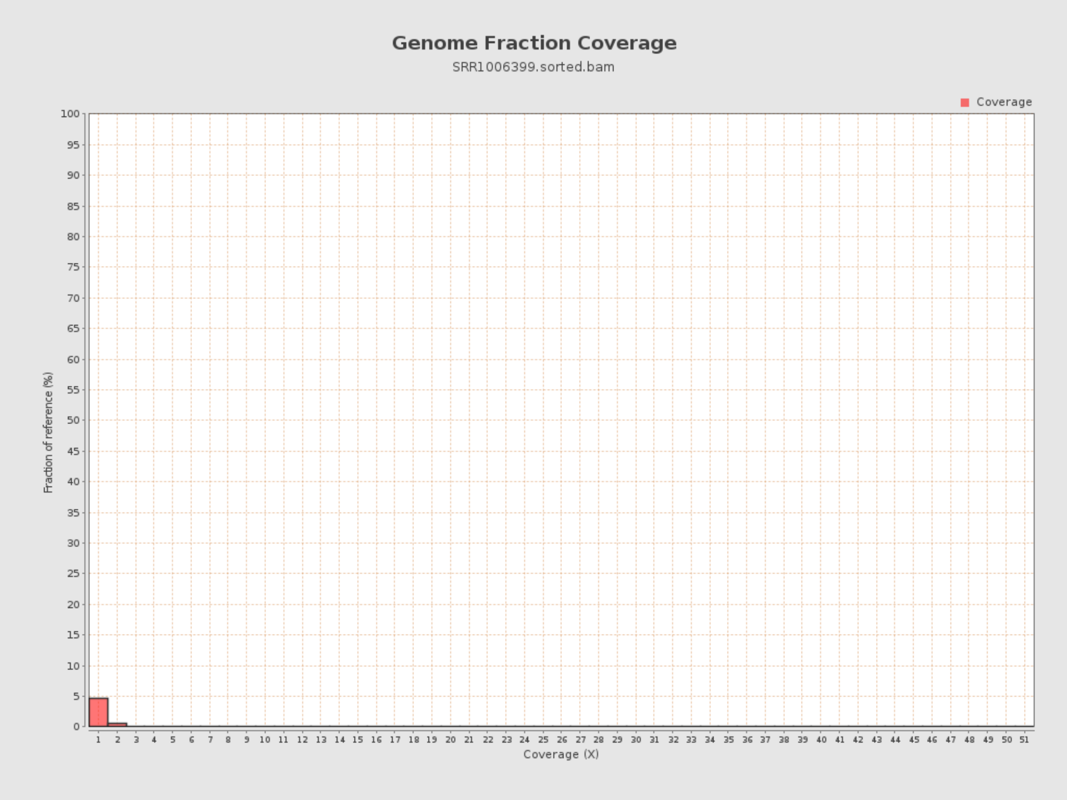
4. Results : Coverage Histogram



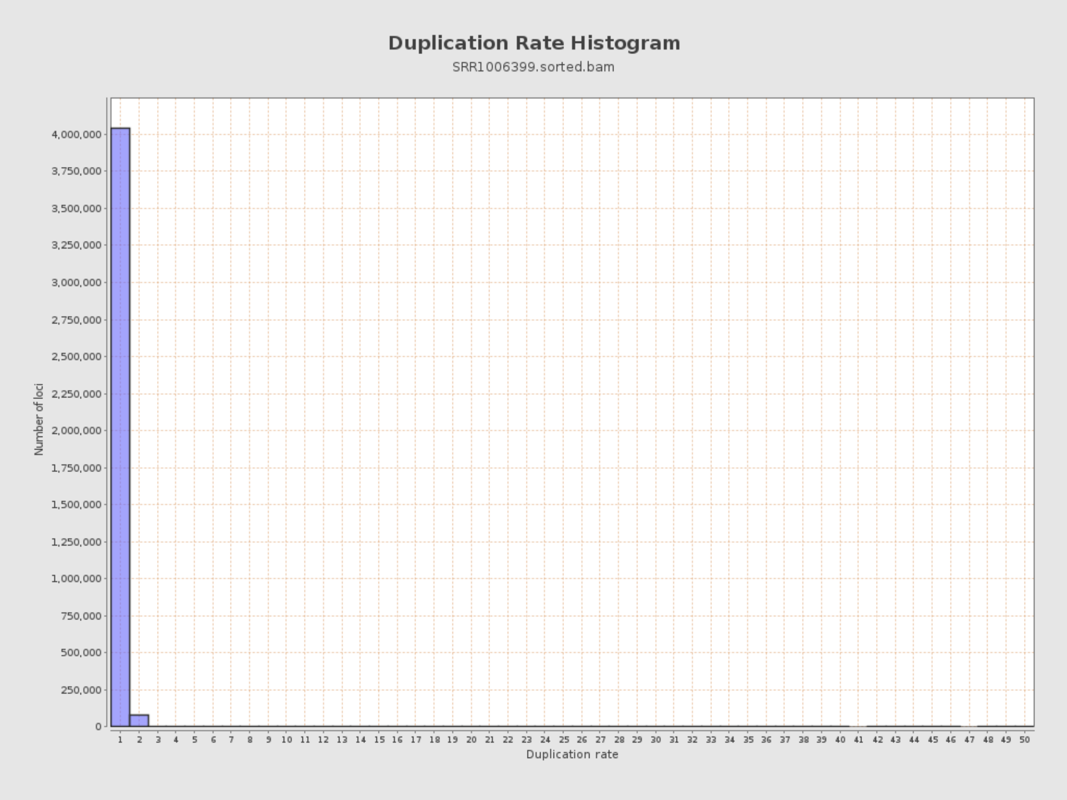
5. Results : Coverage Histogram (0-50X)



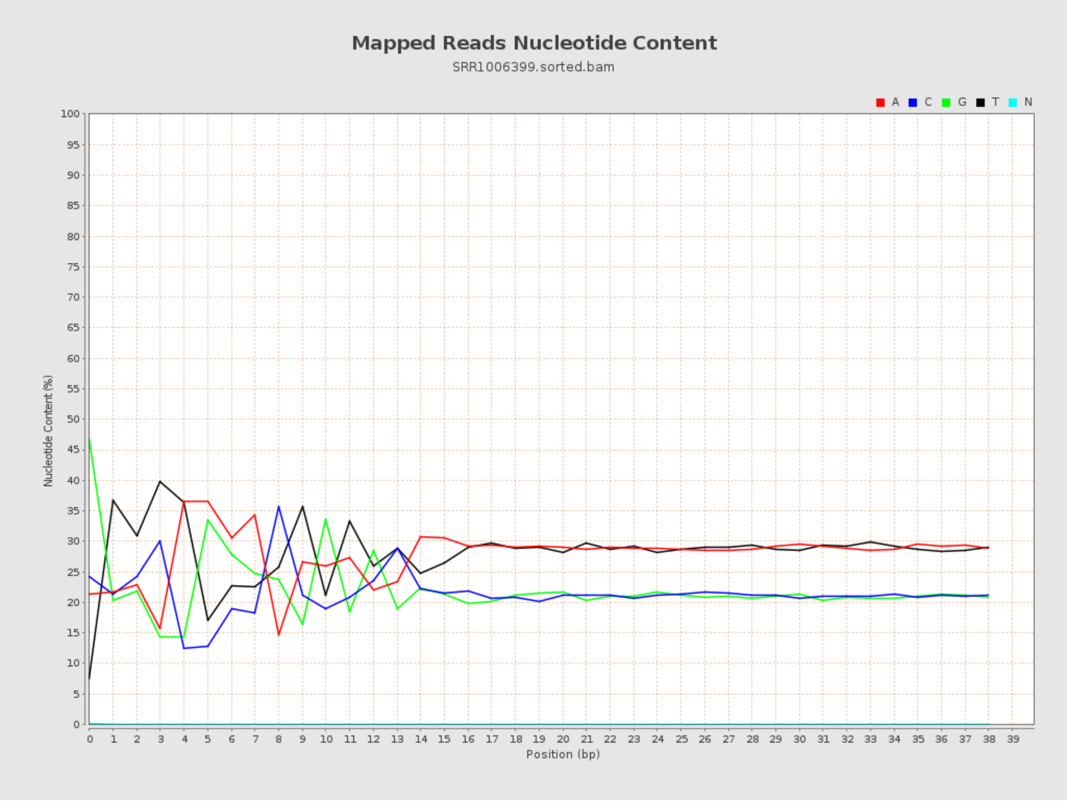
6. Results : Genome Fraction Coverage



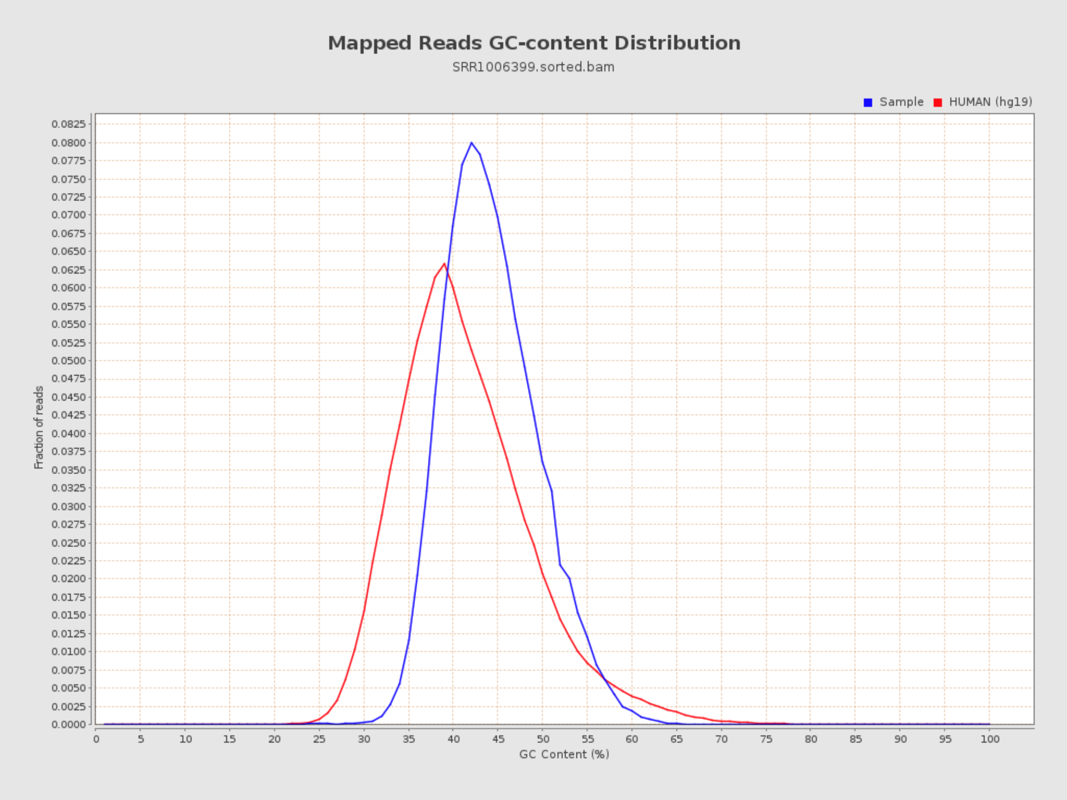
7. Results : Duplication Rate Histogram



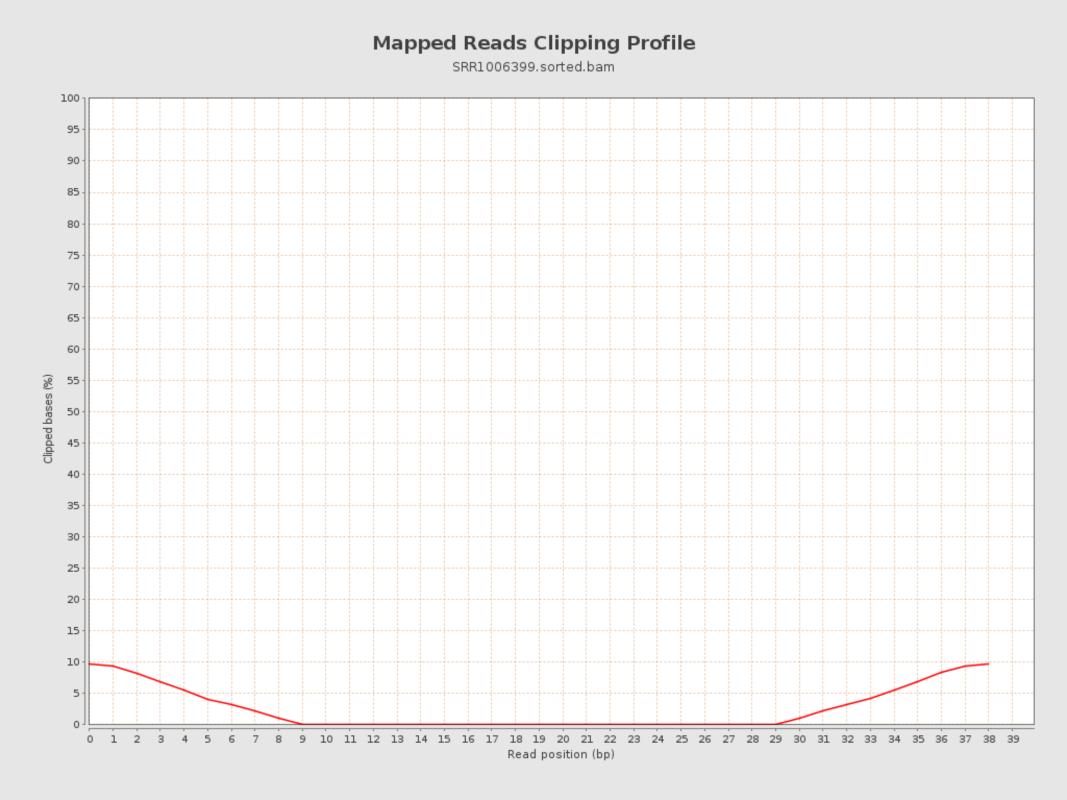
8. Results : Mapped Reads Nucleotide Content



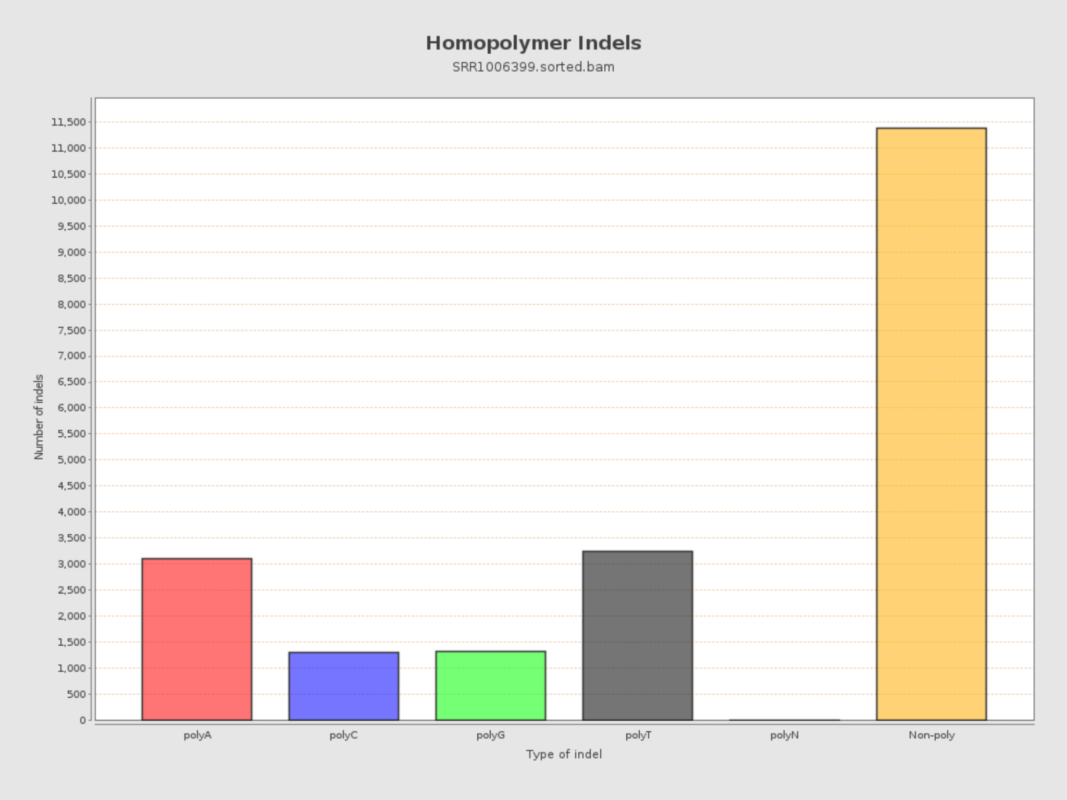
9. Results : Mapped Reads GC-content Distribution



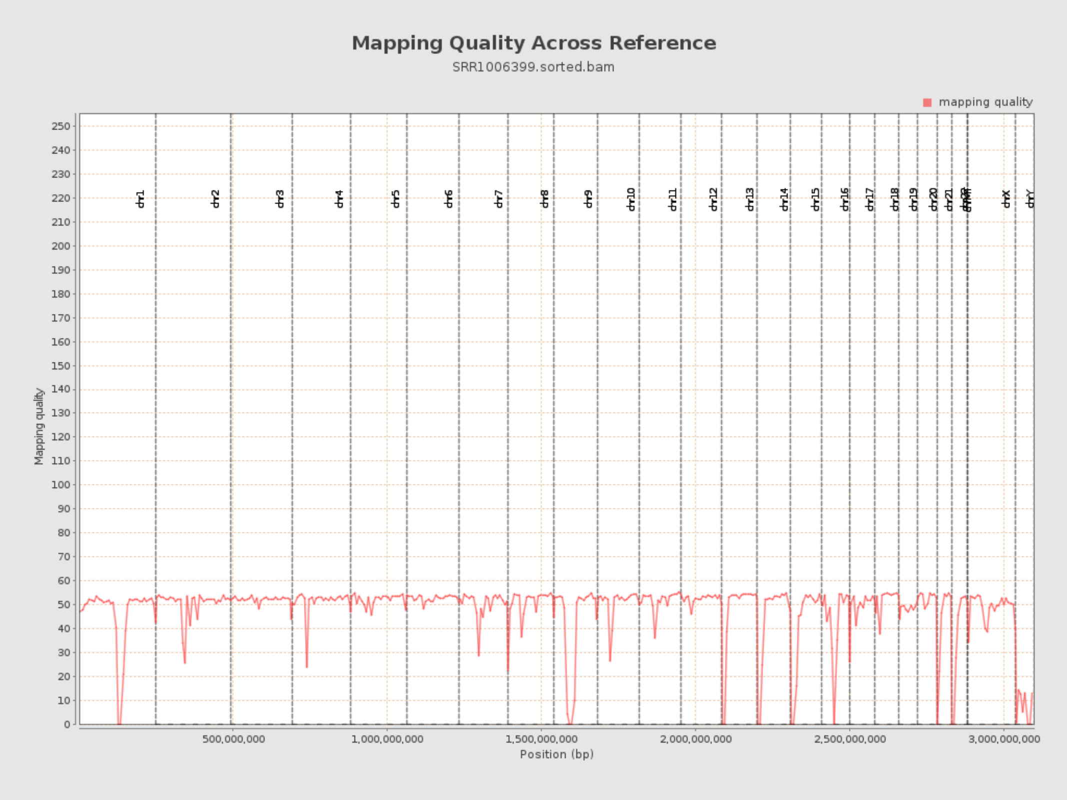
10. Results : Mapped Reads Clipping Profile



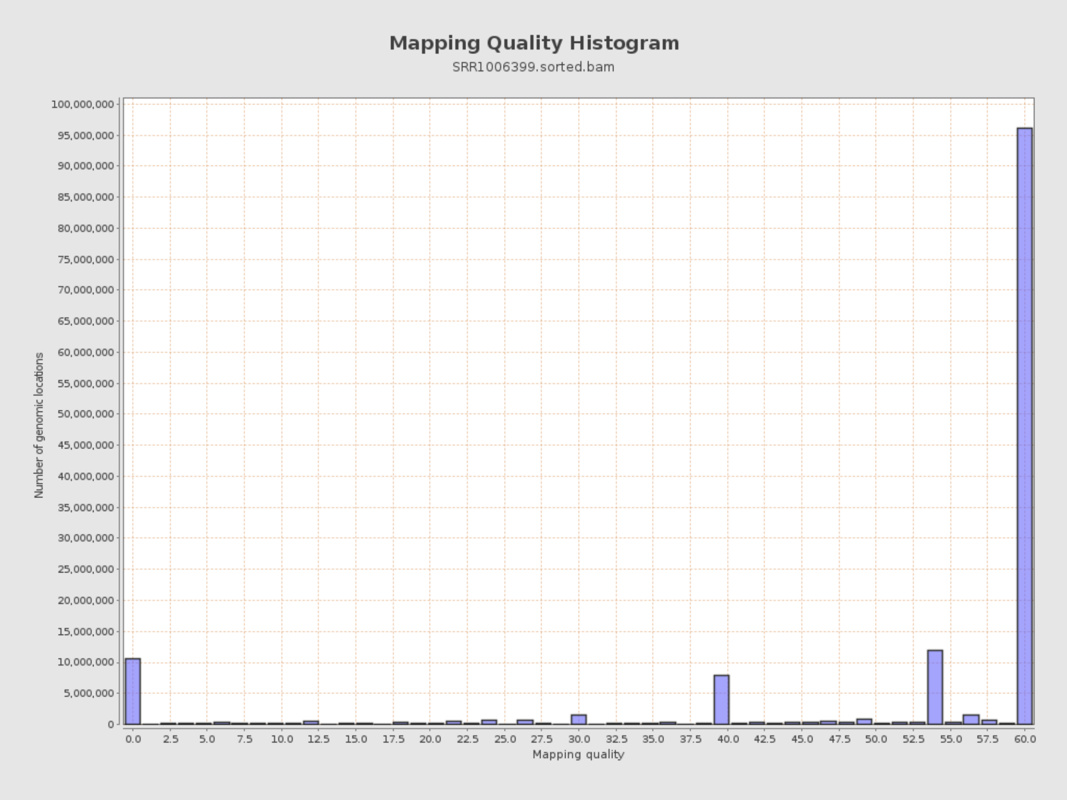
11. Results : Homopolymer Indels



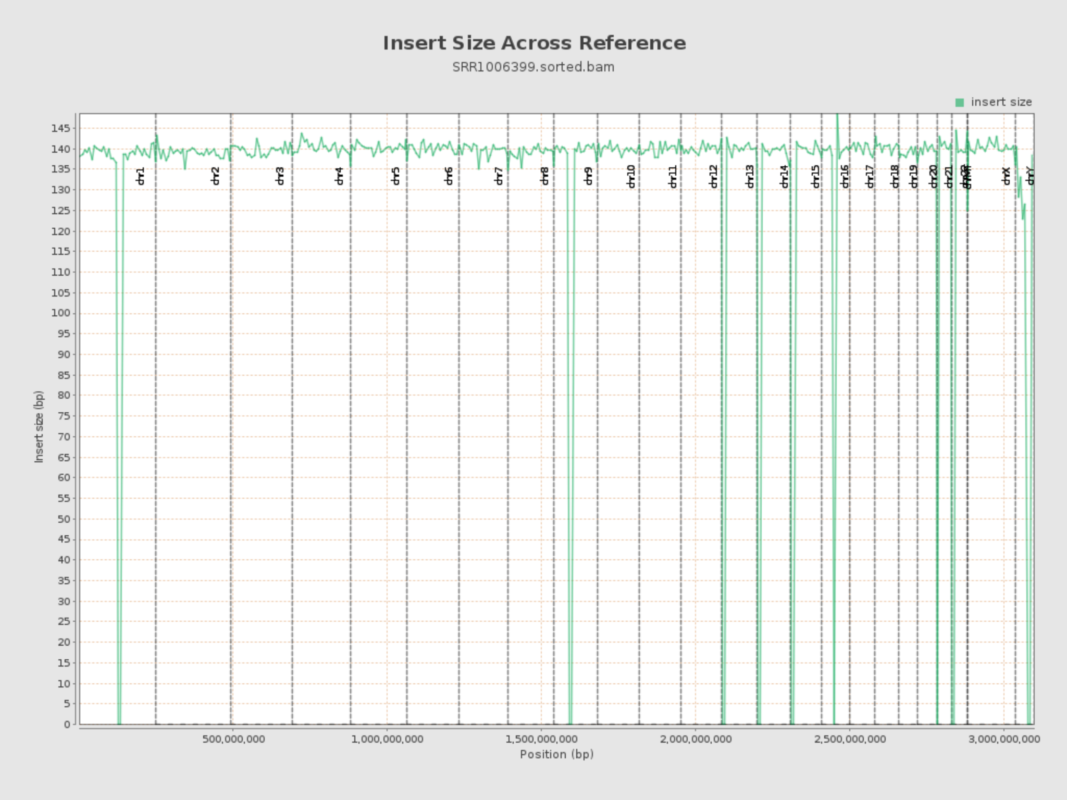
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram