Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 18:05:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006078.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_SRR1006078 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006078_1.fastq.gz SRR1006078_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 18:04:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,331,294
Mapped reads	12,106,828 / 84.48%
Unmapped reads	2,224,466 / 15.52%
Mapped paired reads	12,106,828 / 84.48%
Mapped reads, first in pair	6,168,272 / 43.04%
Mapped reads, second in pair	5,938,556 / 41.44%
Mapped reads, both in pair	10,714,560 / 74.76%
Mapped reads, singletons	1,392,268 / 9.71%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	2,154,226 / 15.03%
Duplication rate	15.8%
Clipped reads	1,164,419 / 8.13%

2.2. ACGT Content

Number/percentage of A's	124,013,441 / 26.6%
Number/percentage of C's	102,269,231 / 21.94%
Number/percentage of T's	129,636,805 / 27.81%
Number/percentage of G's	110,204,944 / 23.64%
Number/percentage of N's	18,819 / 0%
GC Percentage	45.58%

2.3. Coverage

Mean	0.1506
Standard Deviation	1.0233

2.4. Mapping Quality

Mean Mapping Quality	46.26

2.5. Insert size

Mean	93,035.3
Standard Deviation	2,989,297.28
P25/Median/P75	75 / 106 / 140

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	2,144,897
Insertions	16,147
Mapped reads with at least one insertion	0.13%
Deletions	40,163
Mapped reads with at least one deletion	0.33%
Homopolymer indels	45.26%

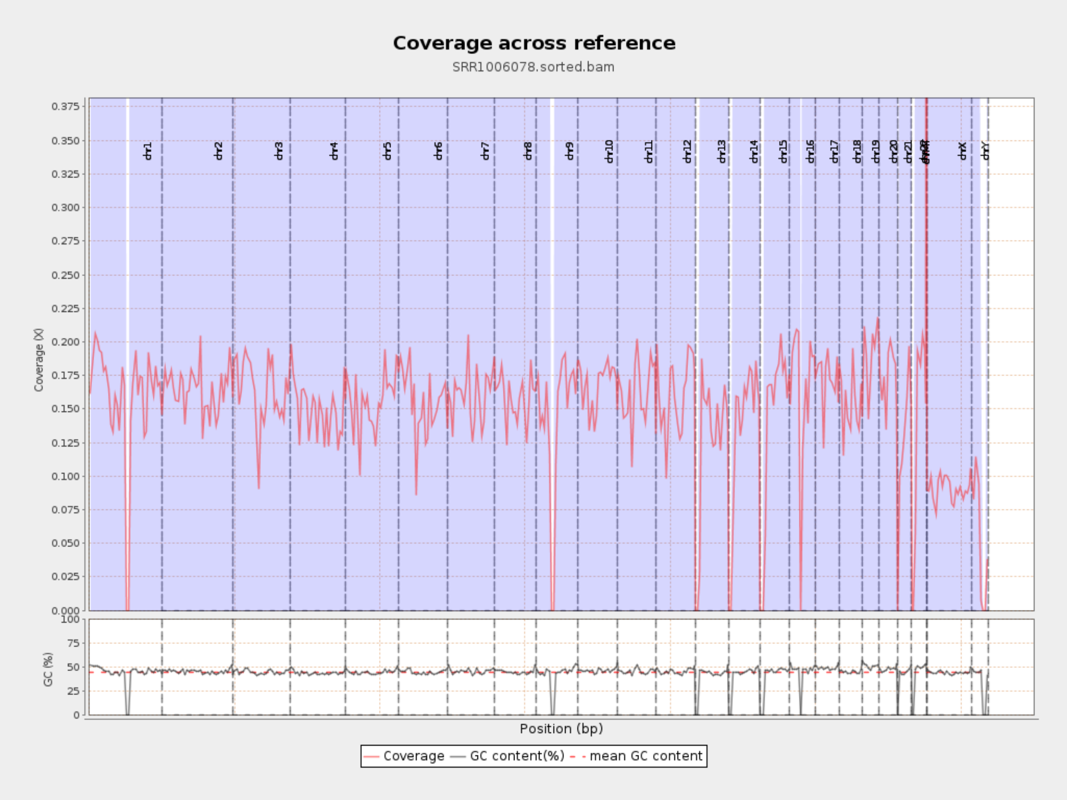
2.7. Chromosome stats

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

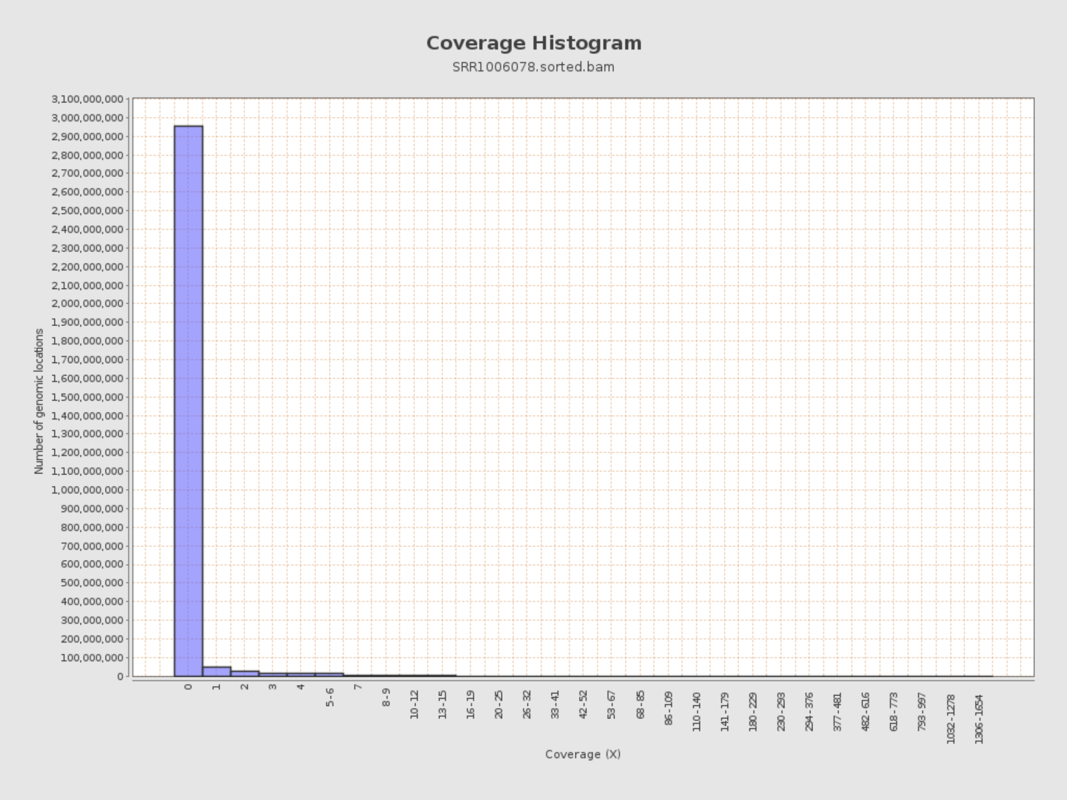
chr1	249250621	39379581	0.158	1.1275
chr2	243199373	40025658	0.1646	1.083
chr3	198022430	32394416	0.1636	0.9794
chr4	191154276	28464308	0.1489	0.9498
chr5	180915260	28053794	0.1551	0.9572
chr6	171115067	26700458	0.156	1.0889
chr7	159138663	25437355	0.1598	1.1611
chr8	146364022	23164774	0.1583	1.0706
chr9	141213431	20000124	0.1416	0.9363
chr10	135534747	22783576	0.1681	1.0265
chr11	135006516	21995867	0.1629	1.3417
chr12	133851895	21497753	0.1606	0.9748
chr13	115169878	14292467	0.1241	0.8596
chr14	107349540	14360301	0.1338	0.8948
chr15	102531392	14447302	0.1409	0.9294
chr16	90354753	14928959	0.1652	1.0257
chr17	81195210	14023973	0.1727	1.0779
chr18	78077248	11990083	0.1536	1.0737
chr19	59128983	11192179	0.1893	1.2843
chr20	63025520	11006082	0.1746	1.0419
chr21	48129895	6113032	0.127	0.9152
chr22	51304566	6763571	0.1318	0.9105
chrMT	16571	54873	3.3114	5.3977
chrX	155270560	14049211	0.0905	0.7284

chrY	59373566	3074324	0.0518	0.5323

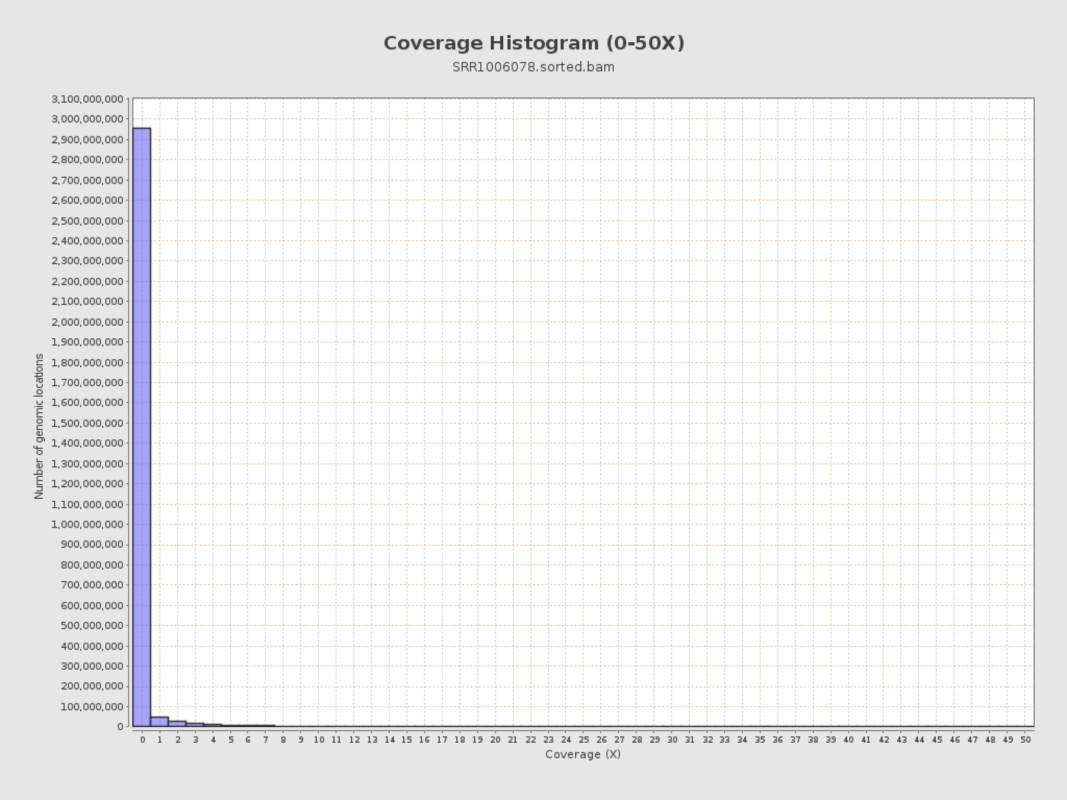
3. Results : Coverage across reference



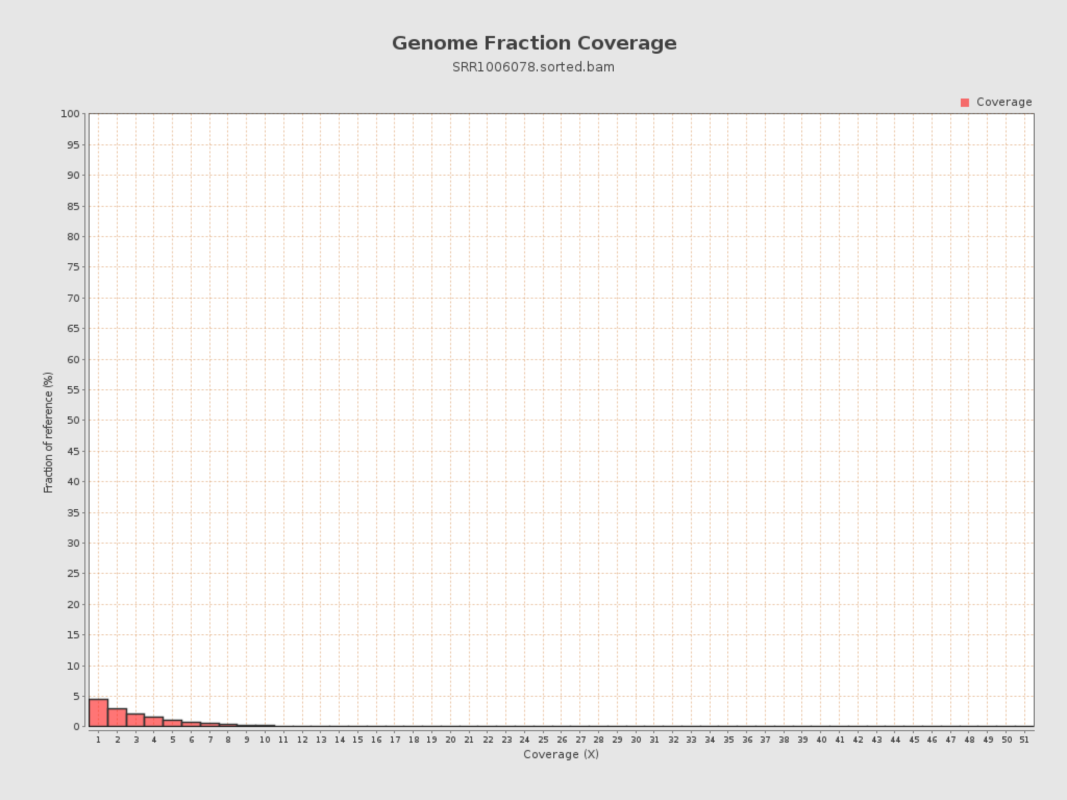
4. Results : Coverage Histogram



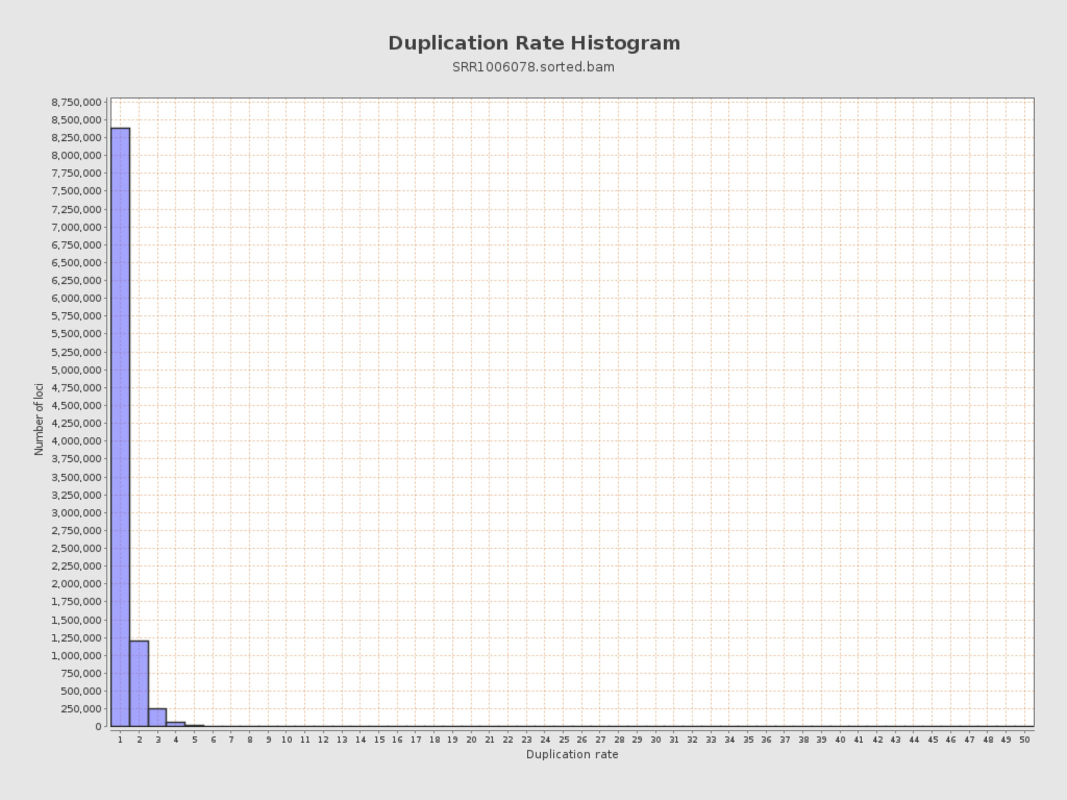
5. Results : Coverage Histogram (0-50X)



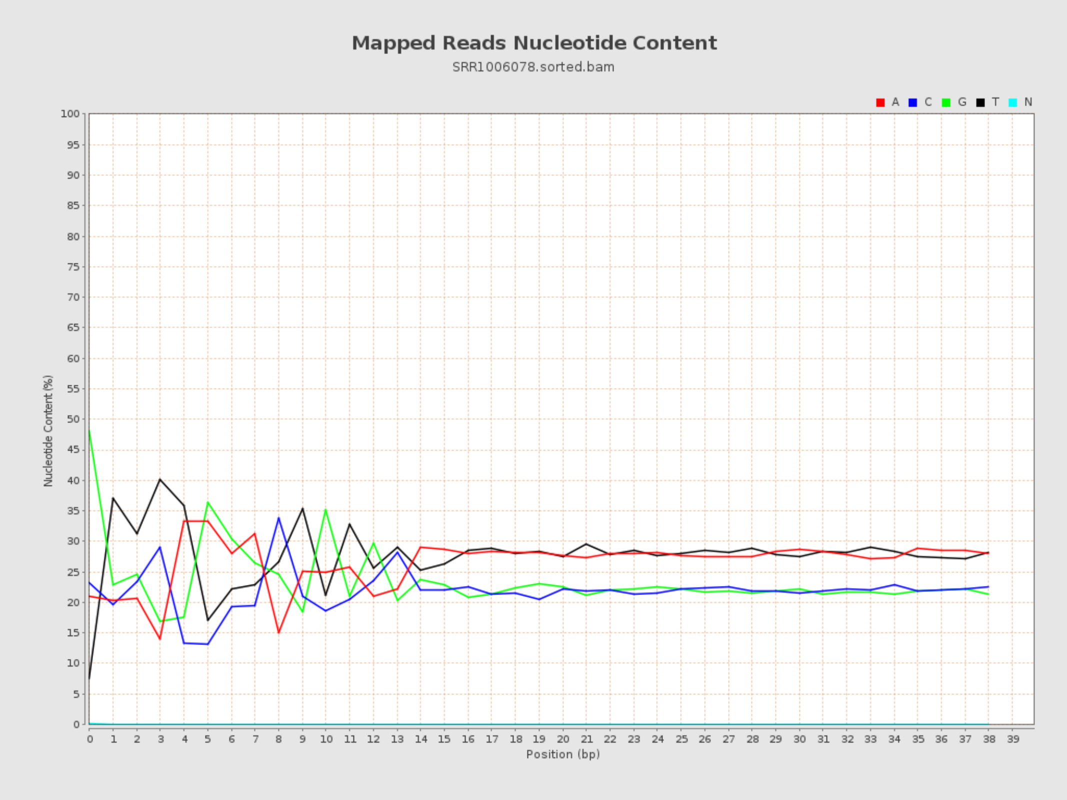
6. Results : Genome Fraction Coverage



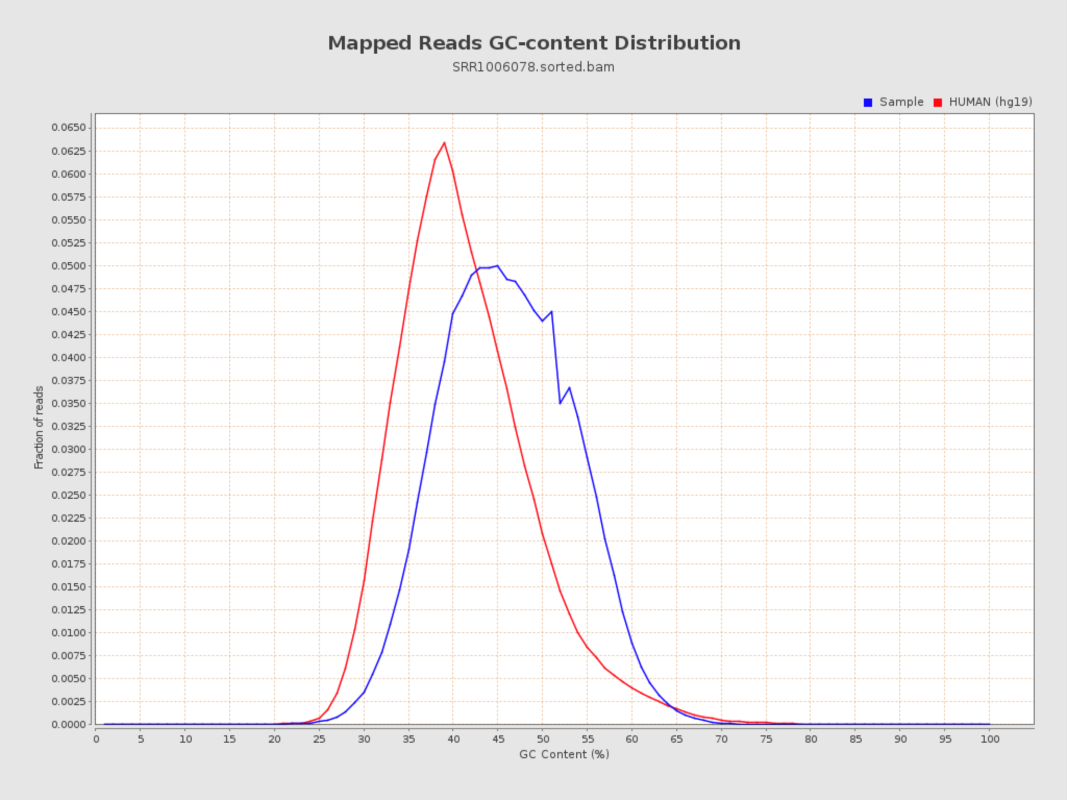
7. Results : Duplication Rate Histogram



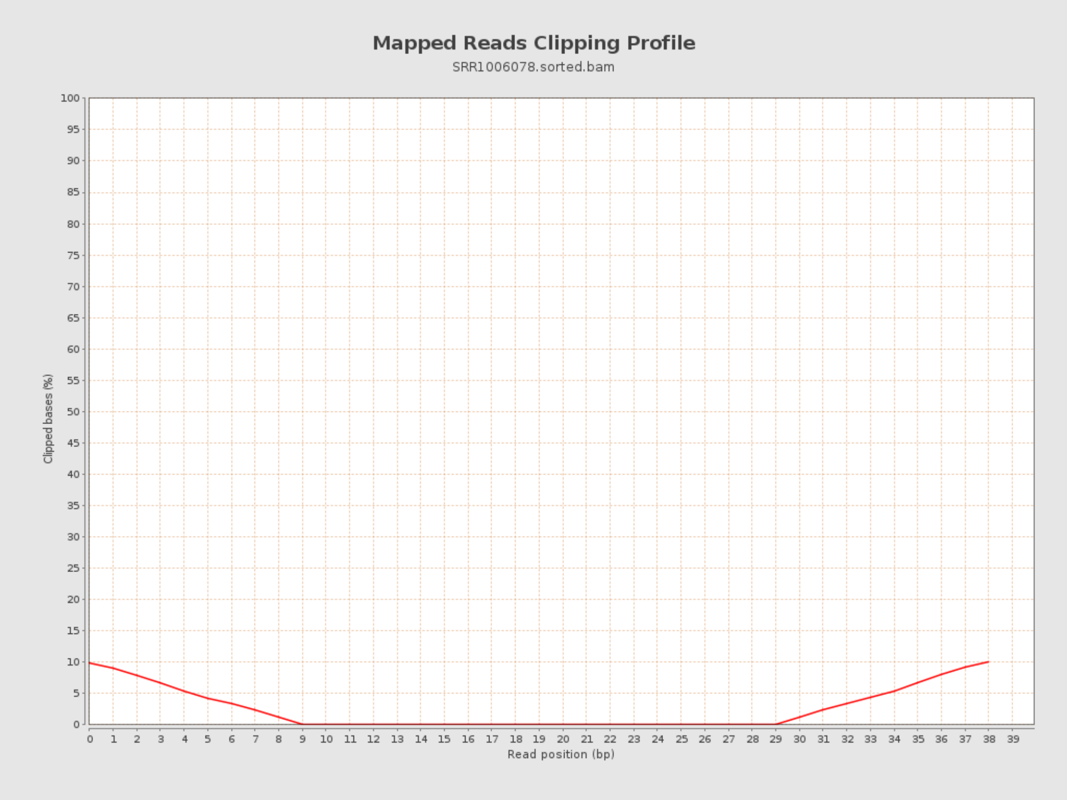
8. Results : Mapped Reads Nucleotide Content



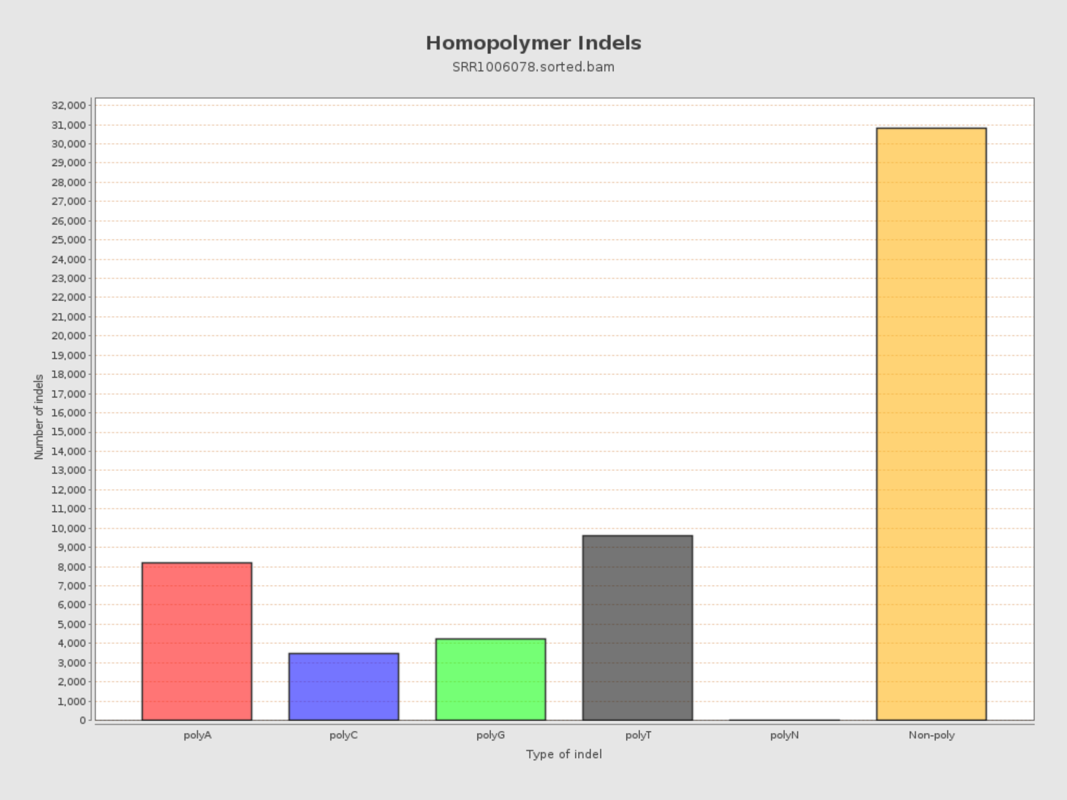
9. Results : Mapped Reads GC-content Distribution



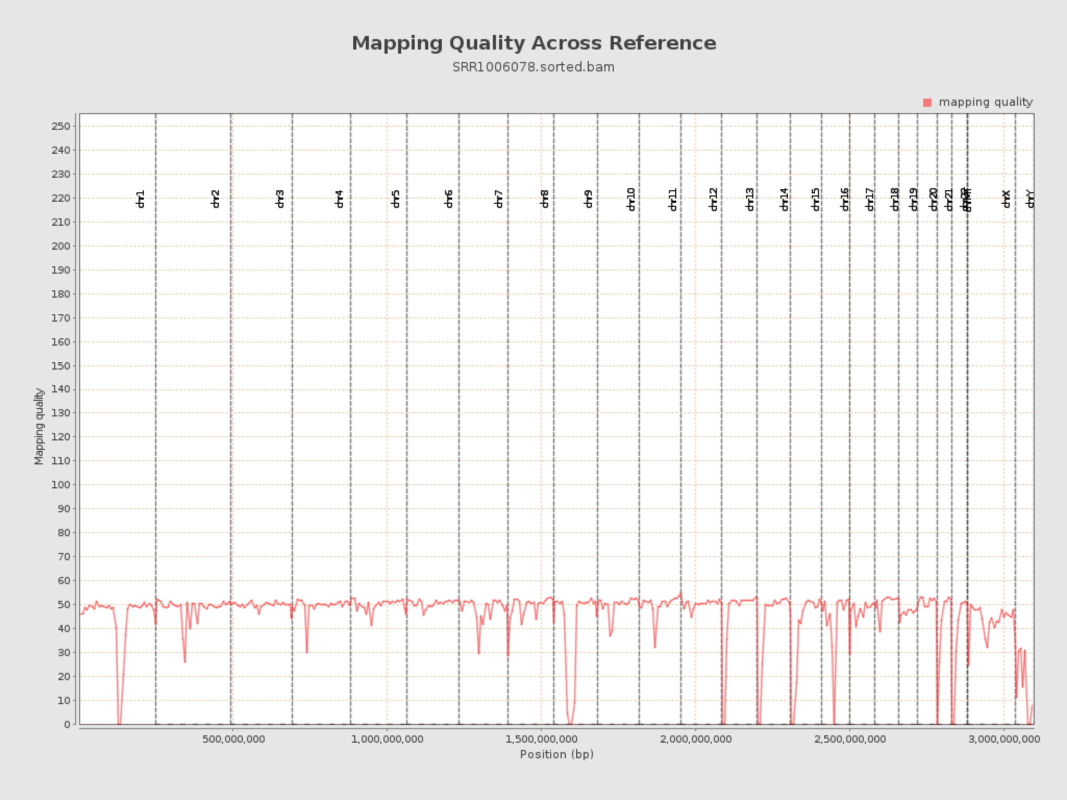
10. Results : Mapped Reads Clipping Profile



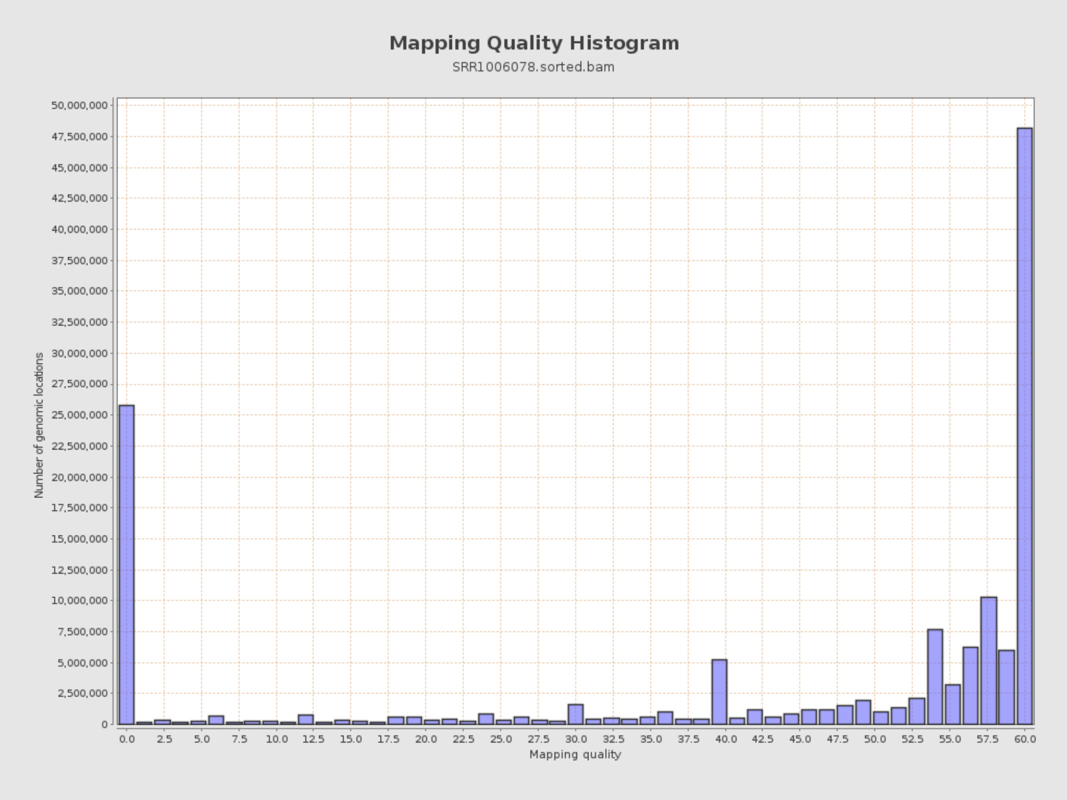
11. Results : Homopolymer Indels



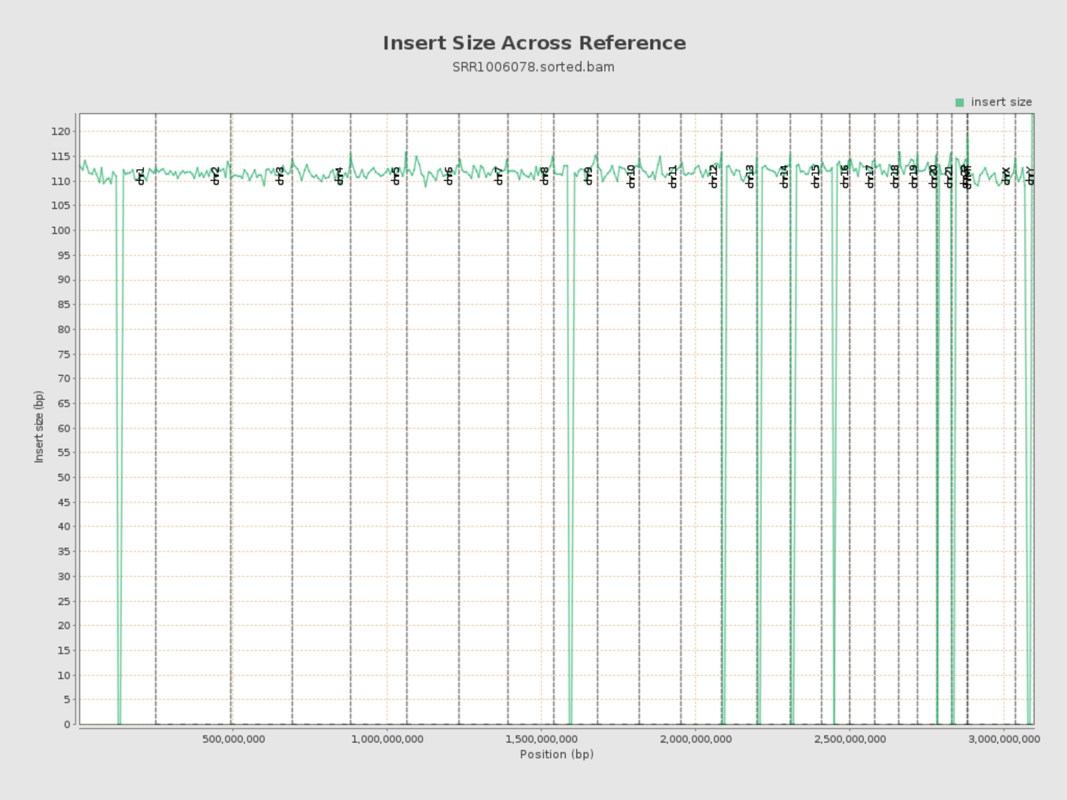
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram