Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 18:14:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006081.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_SRR1006081 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006081_1.fastq.gz SRR1006081_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 18:14:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,796,622
Mapped reads	6,877,961 / 88.22%
Unmapped reads	918,661 / 11.78%
Mapped paired reads	6,877,961 / 88.22%
Mapped reads, first in pair	3,477,100 / 44.6%
Mapped reads, second in pair	3,400,861 / 43.62%
Mapped reads, both in pair	6,299,624 / 80.8%
Mapped reads, singletons	578,337 / 7.42%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	435,288 / 5.58%
Duplication rate	5.71%
Clipped reads	591,583 / 7.59%

2.2. ACGT Content

Number/percentage of A's	70,340,142 / 26.51%
Number/percentage of C's	59,138,496 / 22.29%
Number/percentage of T's	72,949,534 / 27.49%
Number/percentage of G's	62,926,984 / 23.71%
Number/percentage of N's	11,388 / 0%
GC Percentage	46%

2.3. Coverage

Mean	0.0857
Standard Deviation	0.5

2.4. Mapping Quality

Mean Mapping Quality	46.9

2.5. Insert size

Mean	67,421.51
Standard Deviation	2,524,137.67
P25/Median/P75	73 / 107 / 145

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	1,359,478
Insertions	8,794
Mapped reads with at least one insertion	0.13%
Deletions	22,093
Mapped reads with at least one deletion	0.32%
Homopolymer indels	44.88%

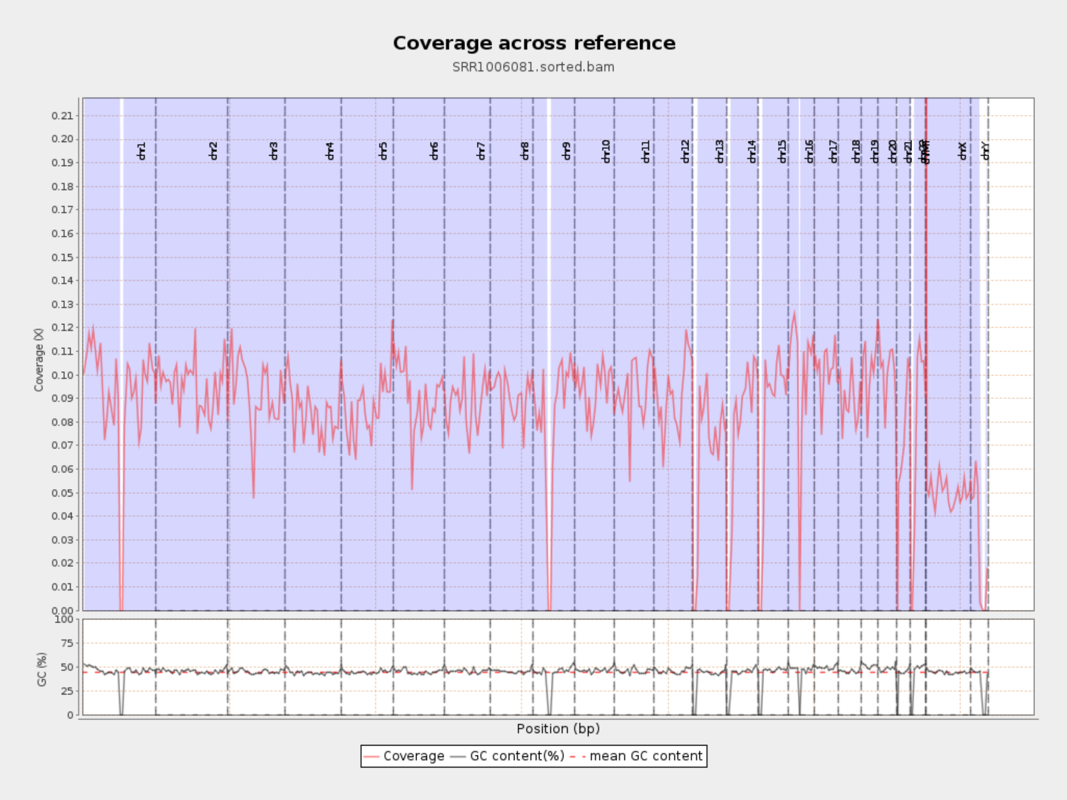
2.7. Chromosome stats

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

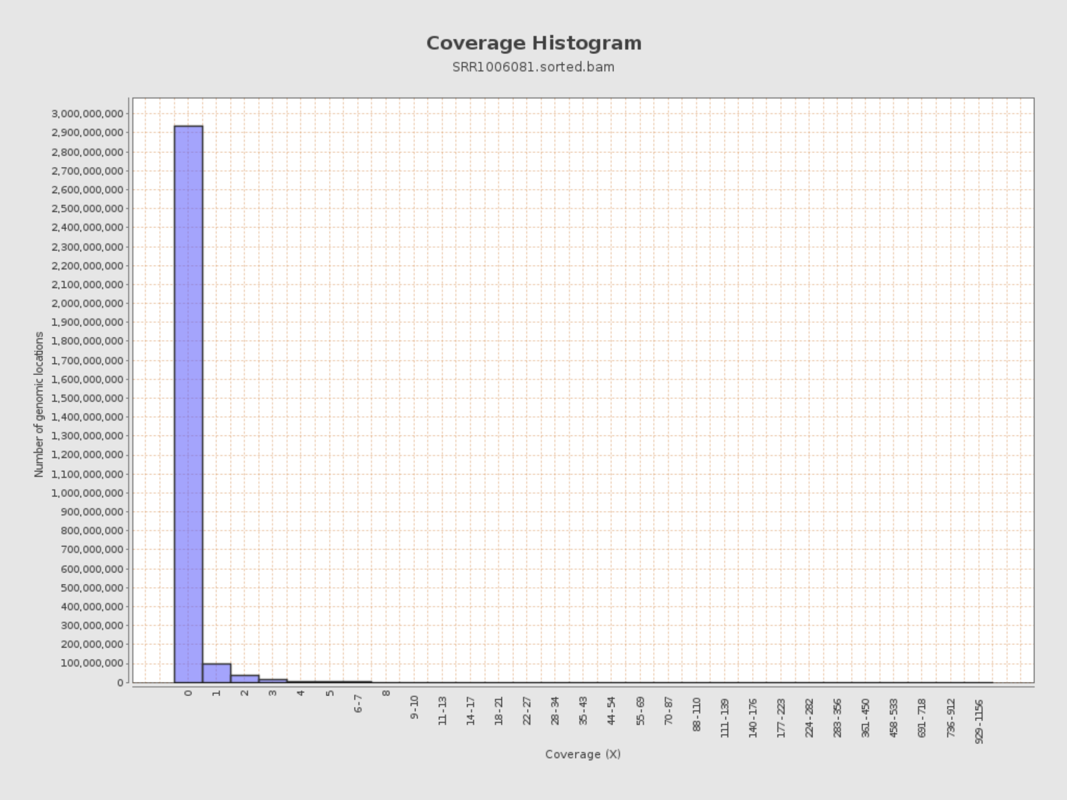
chr1	249250621	22777851	0.0914	0.5324
chr2	243199373	23242908	0.0956	0.5359
chr3	198022430	18199831	0.0919	0.4548
chr4	191154276	16115041	0.0843	0.4491
chr5	180915260	15769010	0.0872	0.4432
chr6	171115067	15474903	0.0904	0.4999
chr7	159138663	14170358	0.089	0.6168
chr8	146364022	13282334	0.0907	0.5317
chr9	141213431	11283744	0.0799	0.4574
chr10	135534747	12724088	0.0939	0.475
chr11	135006516	12532058	0.0928	0.7563
chr12	133851895	12359821	0.0923	0.4598
chr13	115169878	7676348	0.0667	0.3883
chr14	107349540	8181093	0.0762	0.4233
chr15	102531392	8206586	0.08	0.434
chr16	90354753	8907054	0.0986	0.5175
chr17	81195210	8345827	0.1028	0.5293
chr18	78077248	6952223	0.089	0.552
chr19	59128983	6031856	0.102	0.6077
chr20	63025520	6459652	0.1025	0.4956
chr21	48129895	3424358	0.0711	0.4409
chr22	51304566	3789571	0.0739	0.4562
chrMT	16571	25797	1.5568	2.4593
chrX	155270560	7780676	0.0501	0.3475

chrY	59373566	1681491	0.0283	0.2736

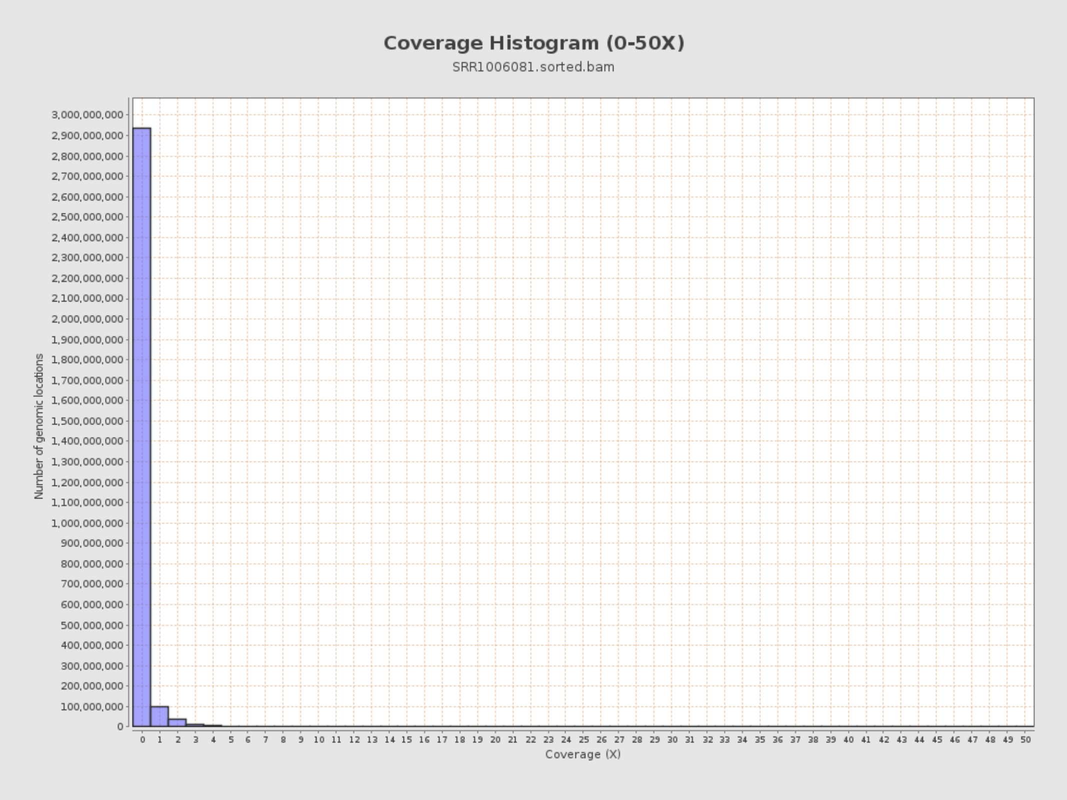
3. Results : Coverage across reference



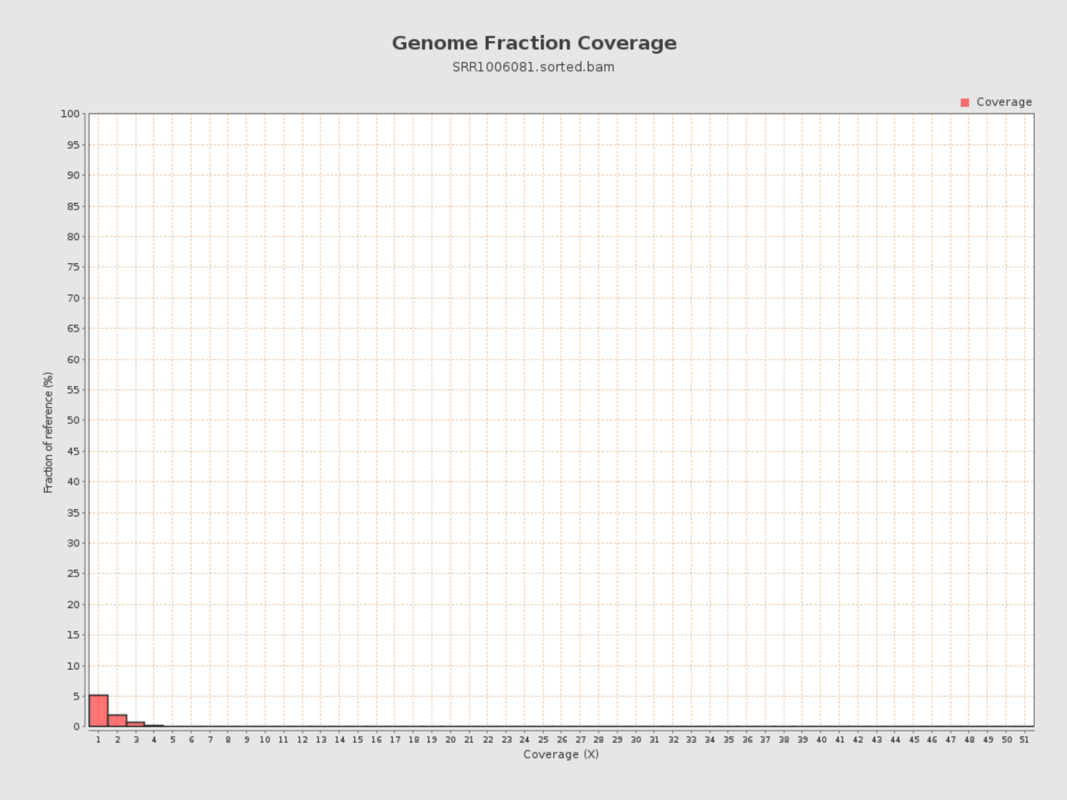
4. Results : Coverage Histogram



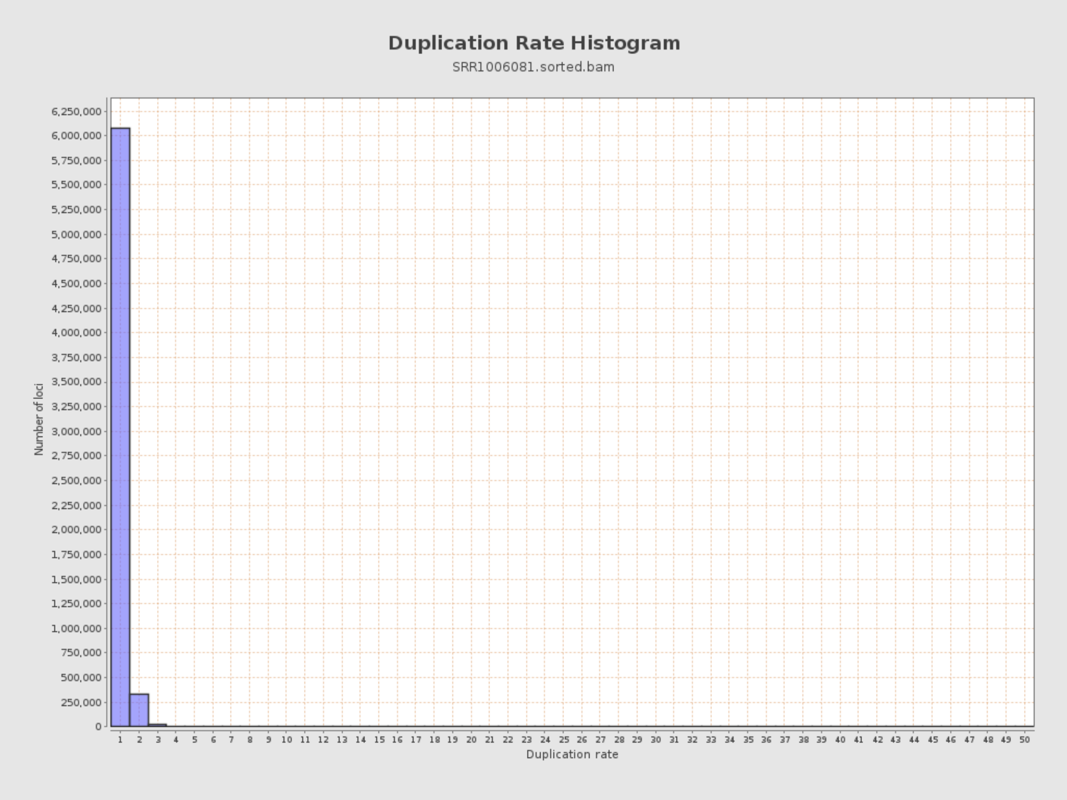
5. Results : Coverage Histogram (0-50X)



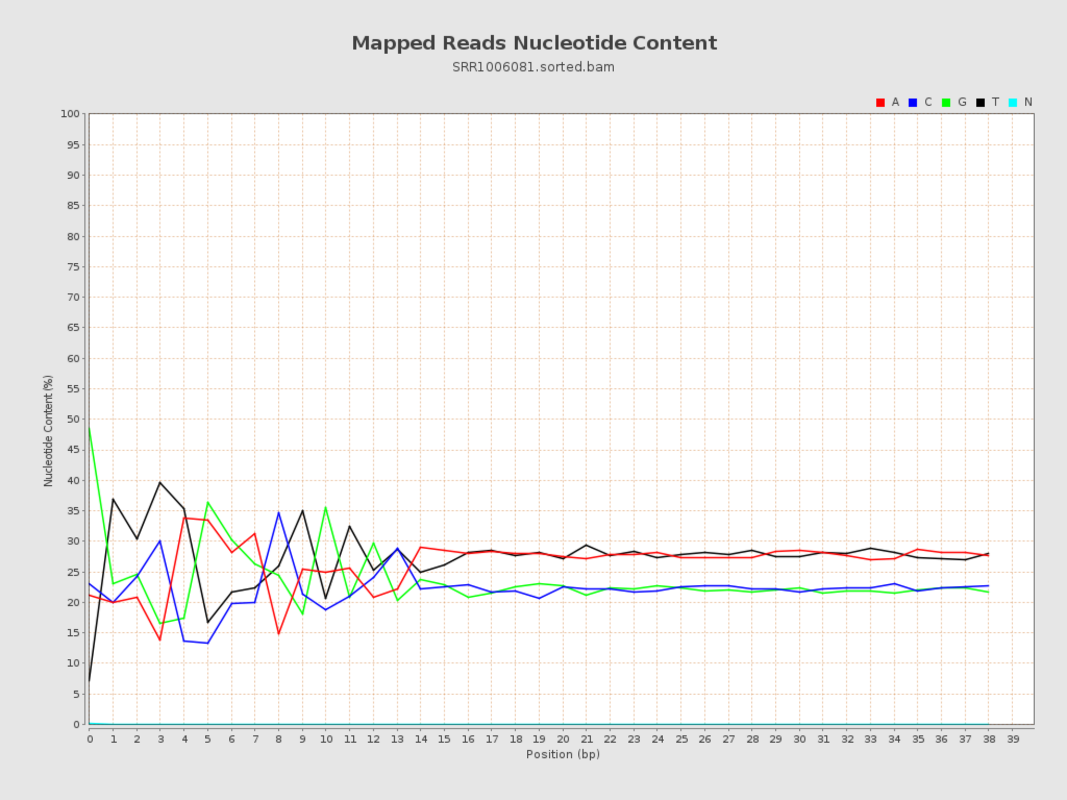
6. Results : Genome Fraction Coverage



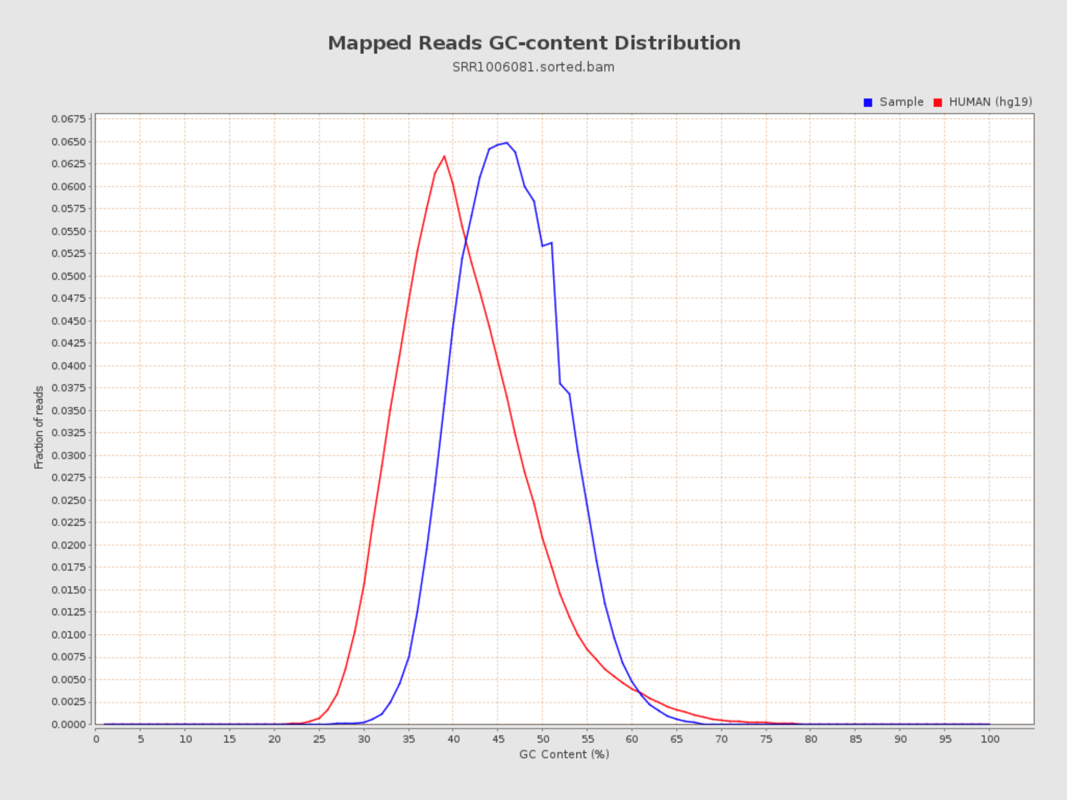
7. Results : Duplication Rate Histogram



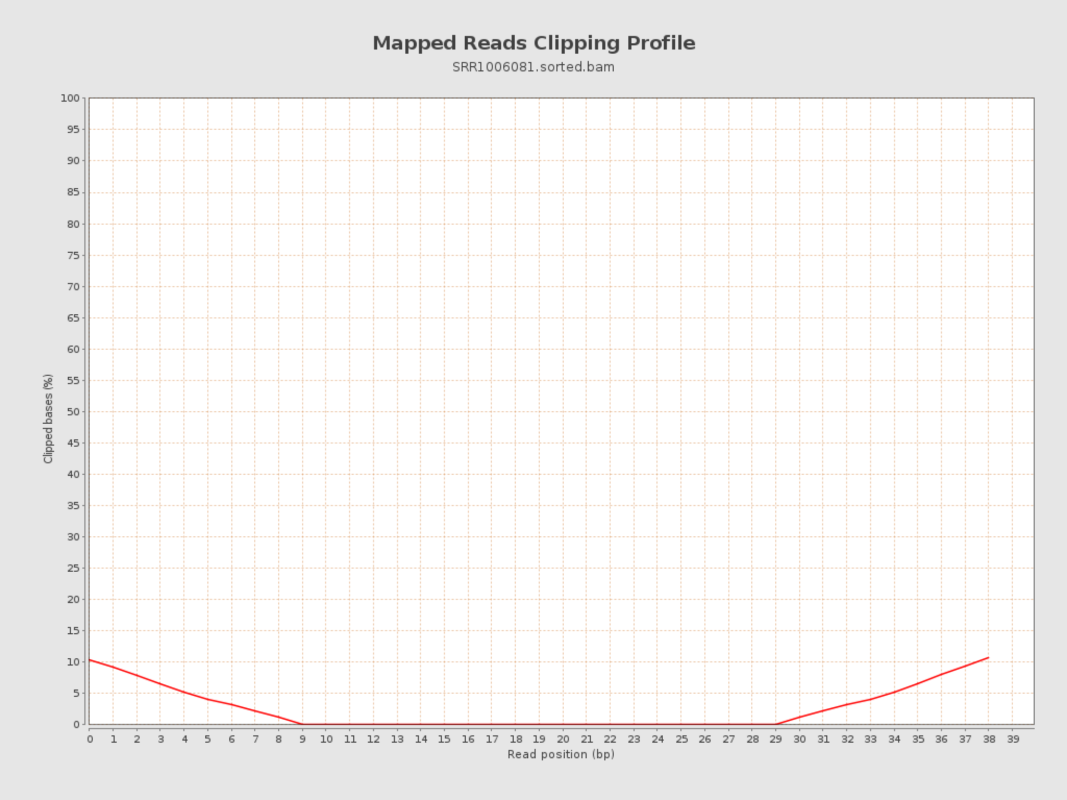
8. Results : Mapped Reads Nucleotide Content



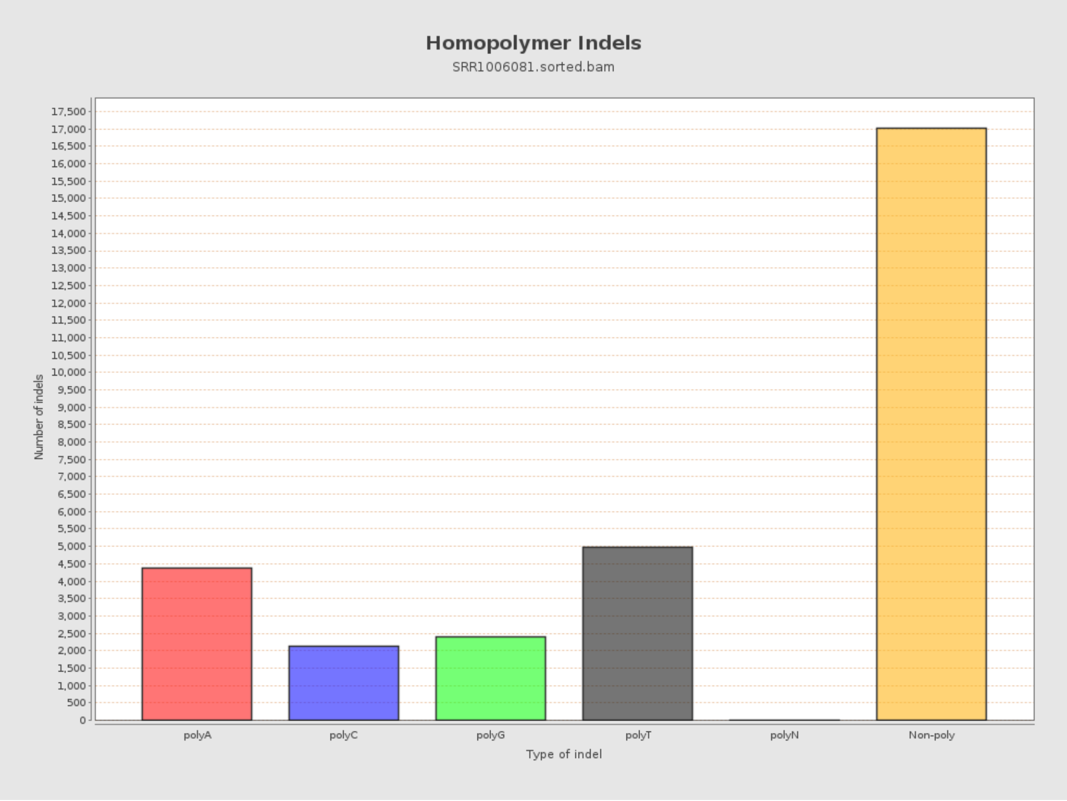
9. Results : Mapped Reads GC-content Distribution



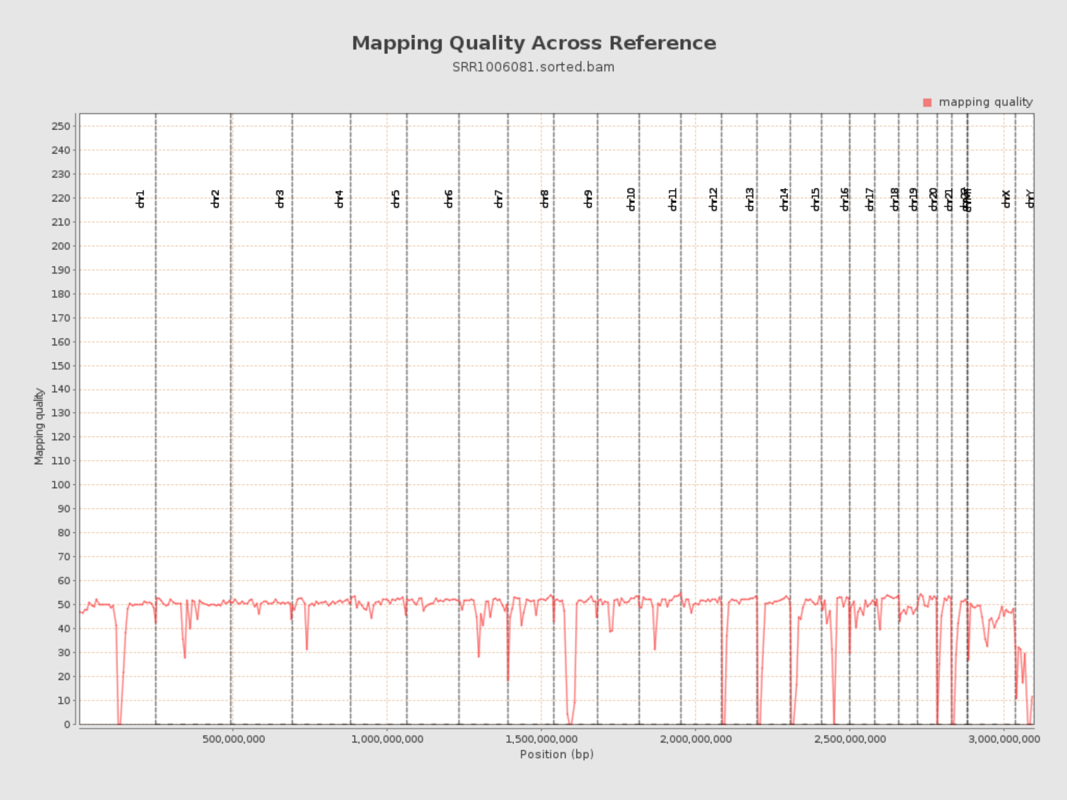
10. Results : Mapped Reads Clipping Profile



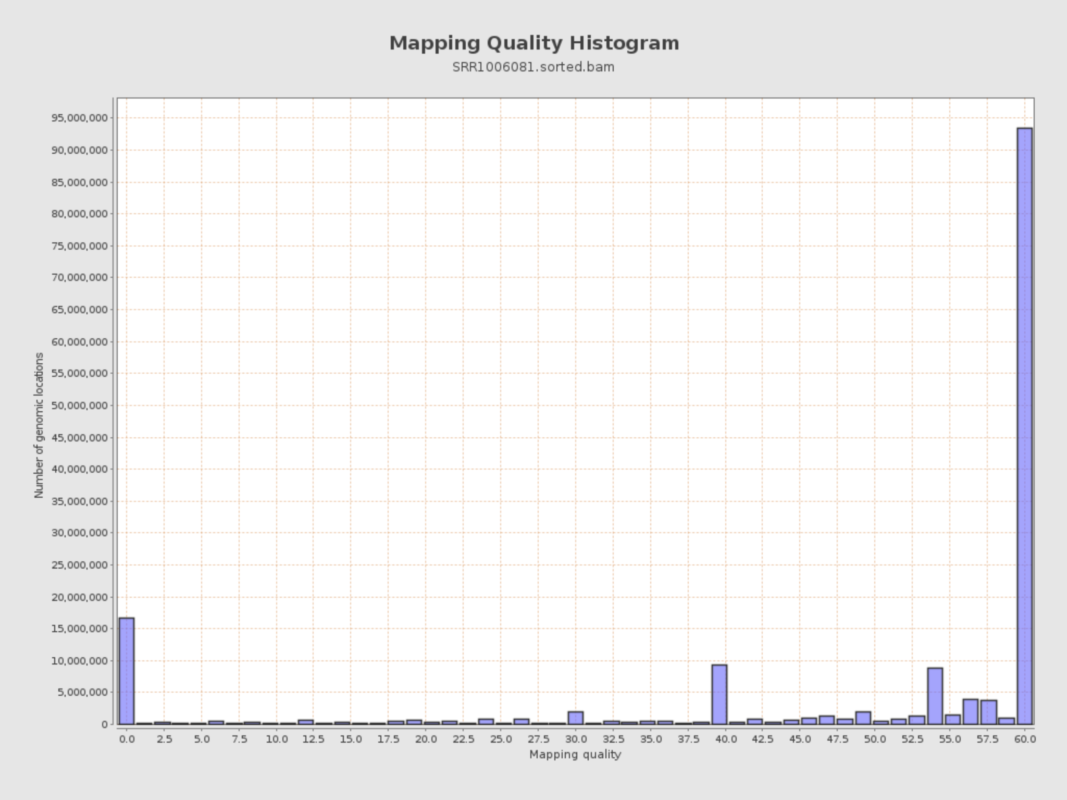
11. Results : Homopolymer Indels



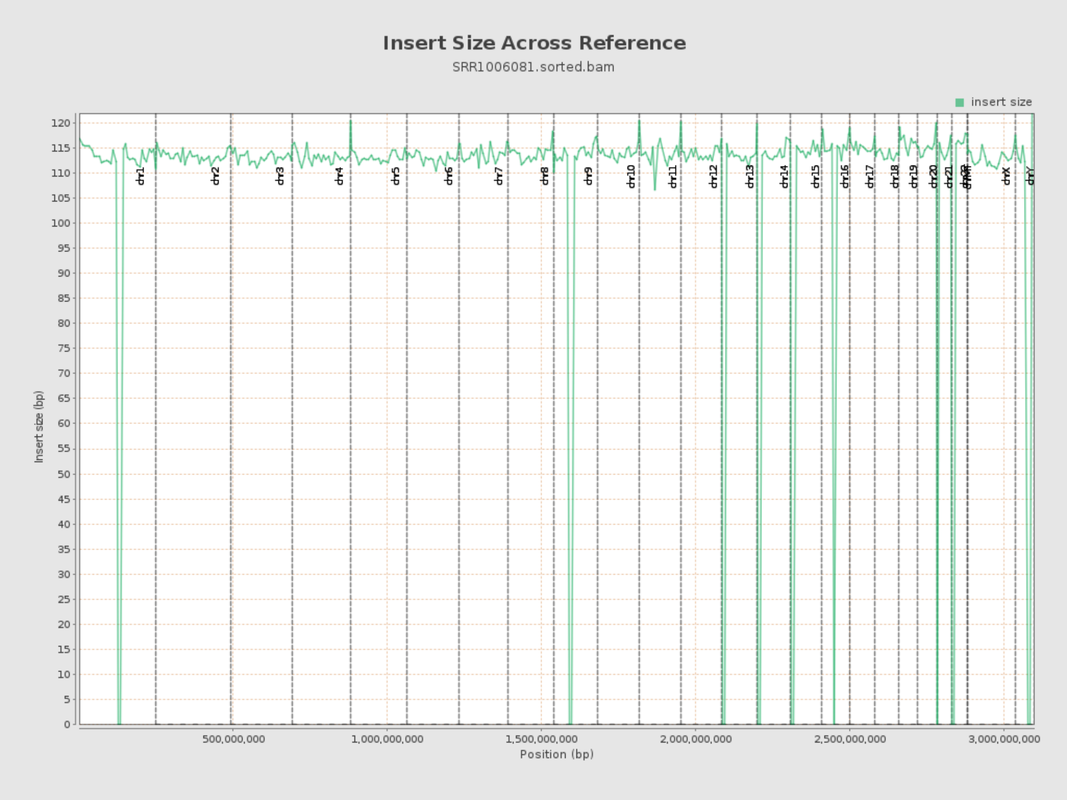
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram