Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 19:36:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006102.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_SRR1006102 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006102_1.fastq.gz SRR1006102_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 19:36:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006102.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,914,922
Mapped reads	9,717,537 / 89.03%
Unmapped reads	1,197,385 / 10.97%
Mapped paired reads	9,717,537 / 89.03%
Mapped reads, first in pair	4,924,052 / 45.11%
Mapped reads, second in pair	4,793,485 / 43.92%
Mapped reads, both in pair	8,993,152 / 82.39%
Mapped reads, singletons	724,385 / 6.64%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	611,084 / 5.6%
Duplication rate	5.56%
Clipped reads	689,099 / 6.31%

2.2. ACGT Content

Number/percentage of A's	103,158,296 / 27.46%
Number/percentage of C's	81,630,788 / 21.73%
Number/percentage of T's	105,737,879 / 28.14%
Number/percentage of G's	85,158,788 / 22.67%
Number/percentage of N's	15,321 / 0%
GC Percentage	44.39%

2.3. Coverage

Mean	0.1214
Standard Deviation	0.6579

2.4. Mapping Quality

Mean Mapping Quality	47.56

2.5. Insert size

Mean	54,005.3
Standard Deviation	2,233,237.98
P25/Median/P75	74 / 103 / 140

2.6. Mismatches and indels

General error rate	0.49%
Mismatches	1,836,898
Insertions	11,270
Mapped reads with at least one insertion	0.12%
Deletions	30,265
Mapped reads with at least one deletion	0.31%
Homopolymer indels	46.13%

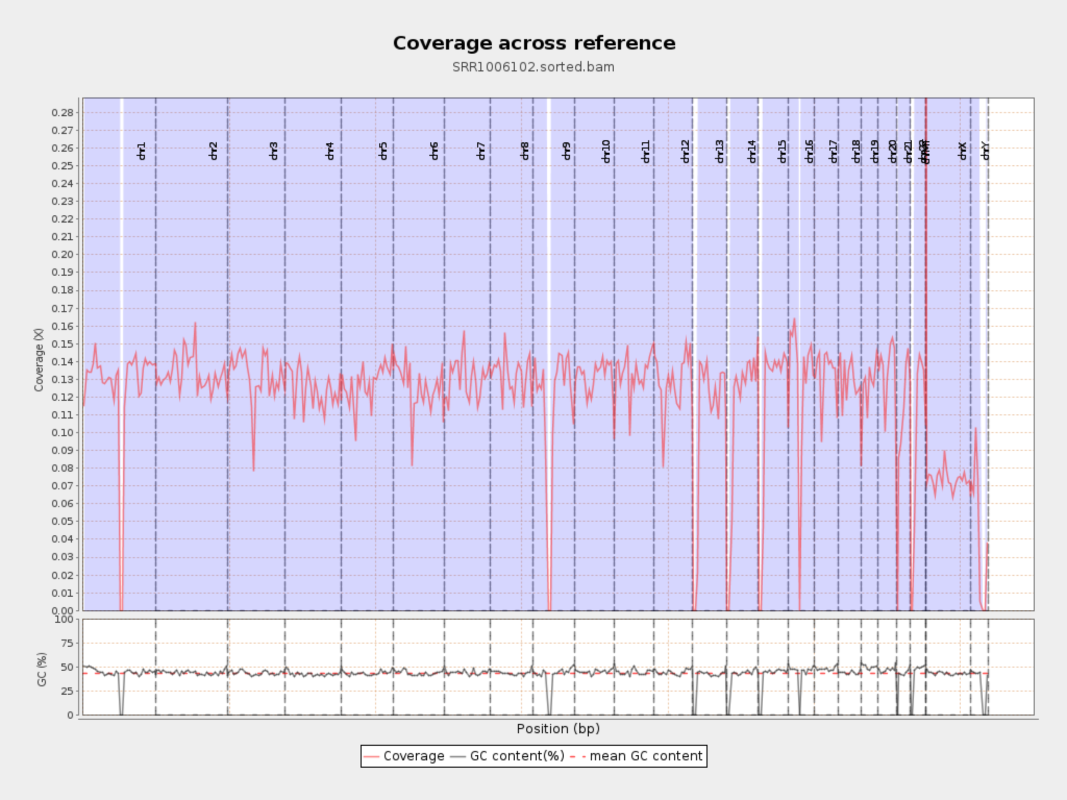
2.7. Chromosome stats

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

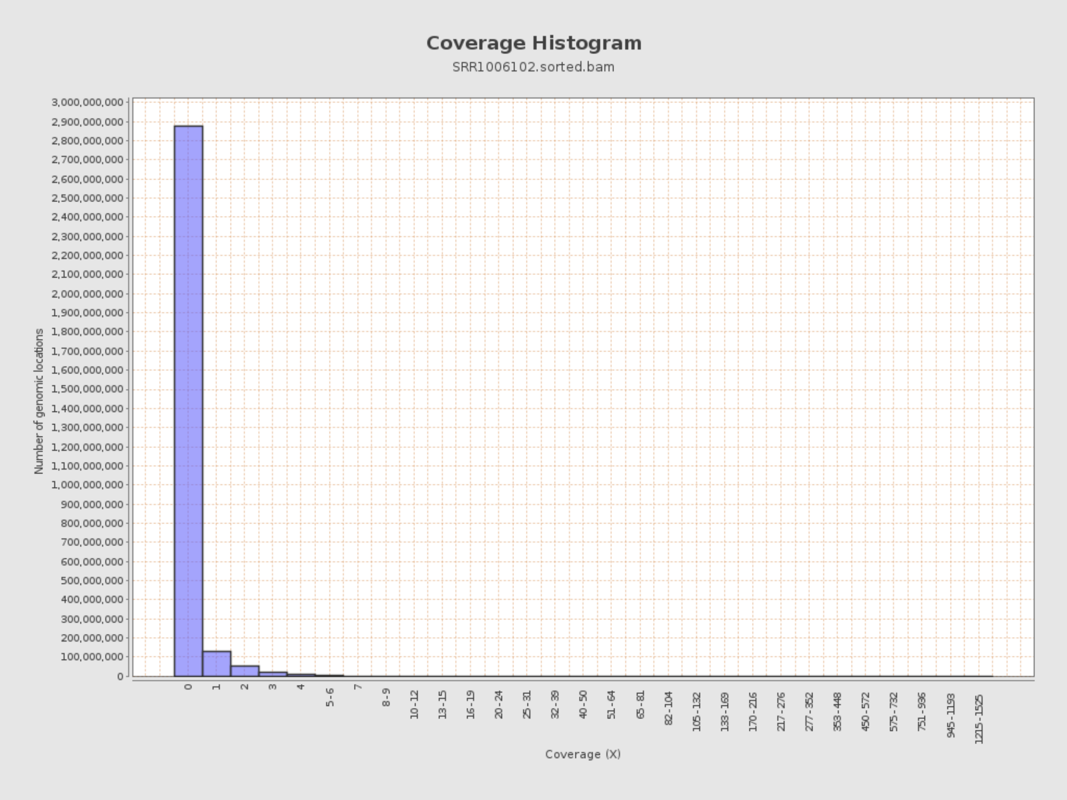
chr1	249250621	31218020	0.1252	0.7188
chr2	243199373	32467140	0.1335	0.6925
chr3	198022430	26058109	0.1316	0.5581
chr4	191154276	23965207	0.1254	0.57
chr5	180915260	23186737	0.1282	0.5562
chr6	171115067	21503400	0.1257	0.6004
chr7	159138663	20823386	0.1309	0.9428
chr8	146364022	19302521	0.1319	0.7759
chr9	141213431	16029589	0.1135	0.6148
chr10	135534747	17962691	0.1325	0.5941
chr11	135006516	17931016	0.1328	1.0024
chr12	133851895	17290993	0.1292	0.5598
chr13	115169878	12240183	0.1063	0.5079
chr14	107349540	11712366	0.1091	0.5357
chr15	102531392	11548317	0.1126	0.528
chr16	90354753	11401661	0.1262	0.597
chr17	81195210	10871387	0.1339	0.6592
chr18	78077248	10123679	0.1297	0.8924
chr19	59128983	7543285	0.1276	0.7541
chr20	63025520	8560124	0.1358	0.5869
chr21	48129895	5120858	0.1064	0.5644
chr22	51304566	4821220	0.094	0.5228
chrMT	16571	9612	0.58	1.1966
chrX	155270560	11460658	0.0738	0.4555

chrY	59373566	2587809	0.0436	0.3652

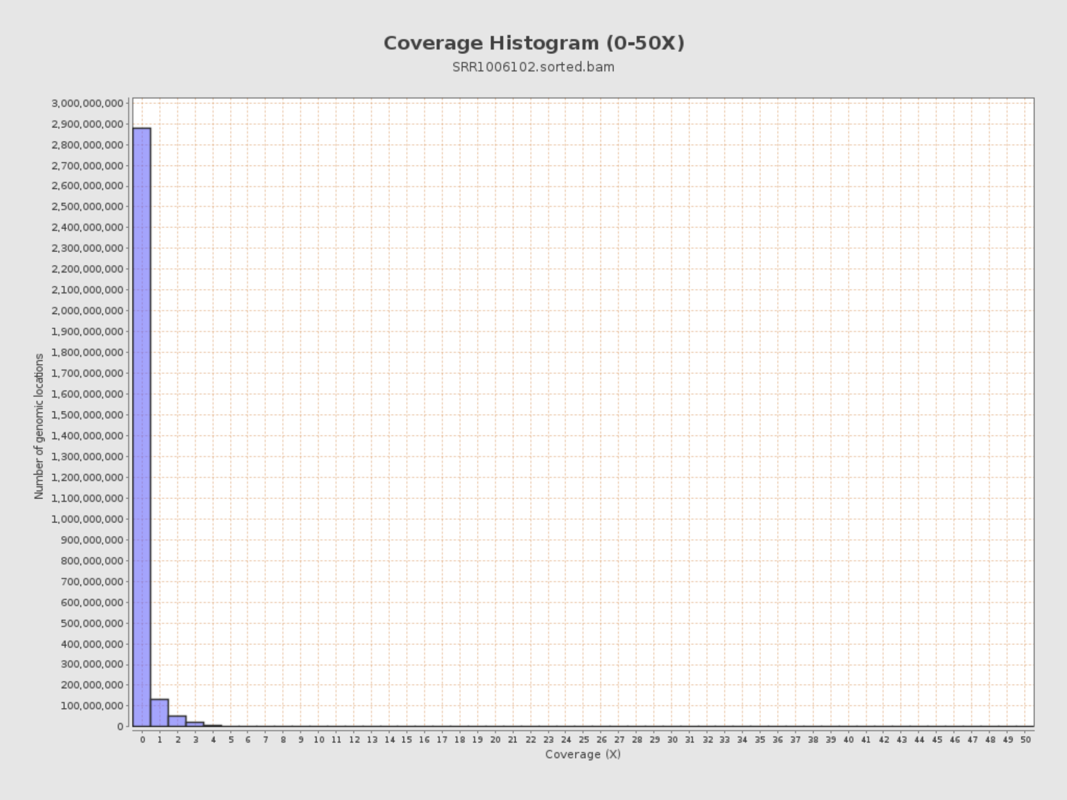
3. Results : Coverage across reference



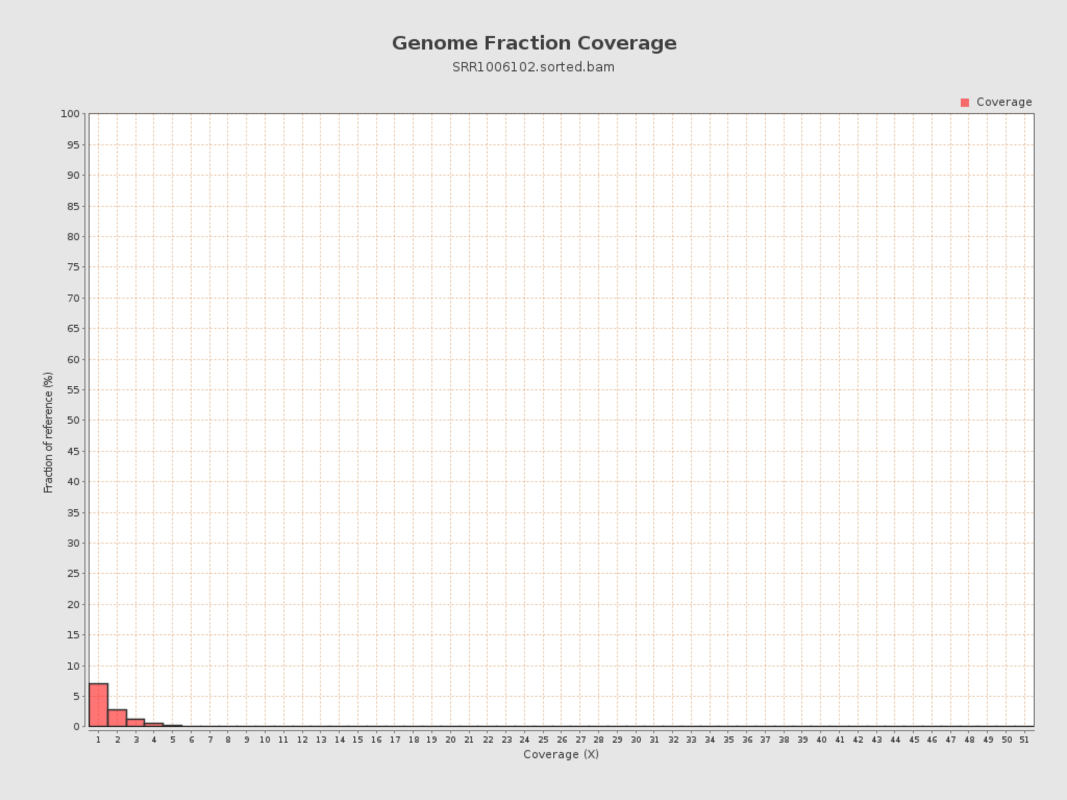
4. Results : Coverage Histogram



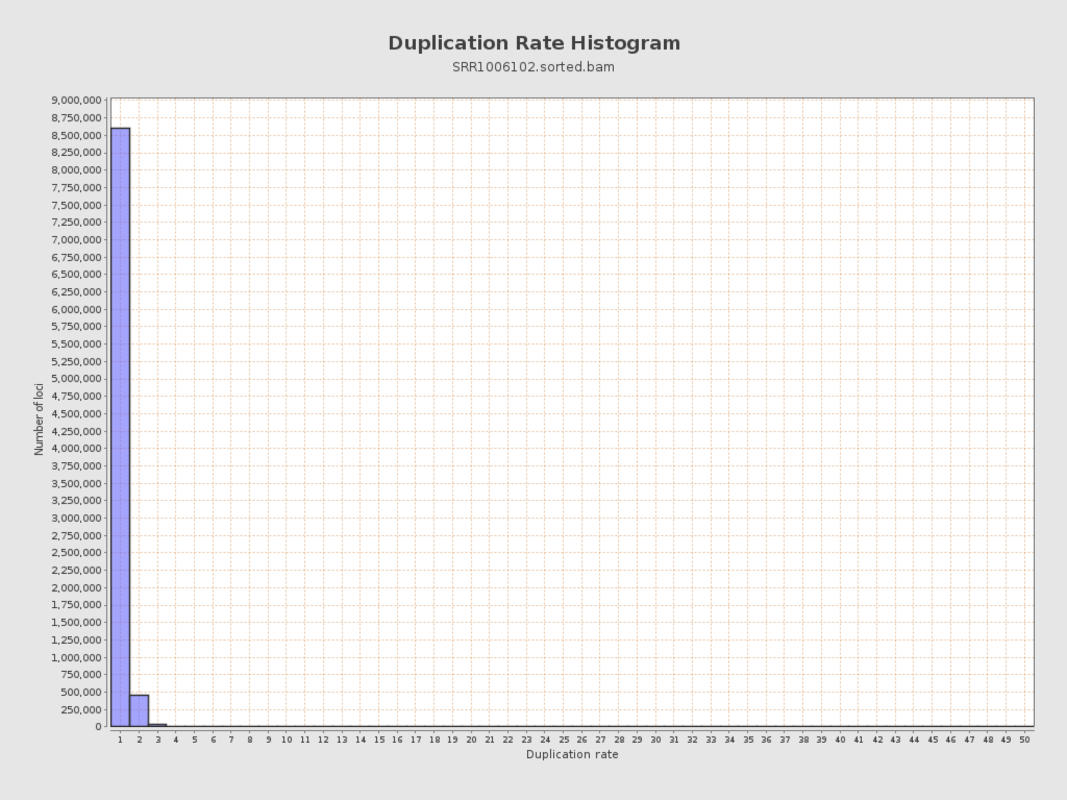
5. Results : Coverage Histogram (0-50X)



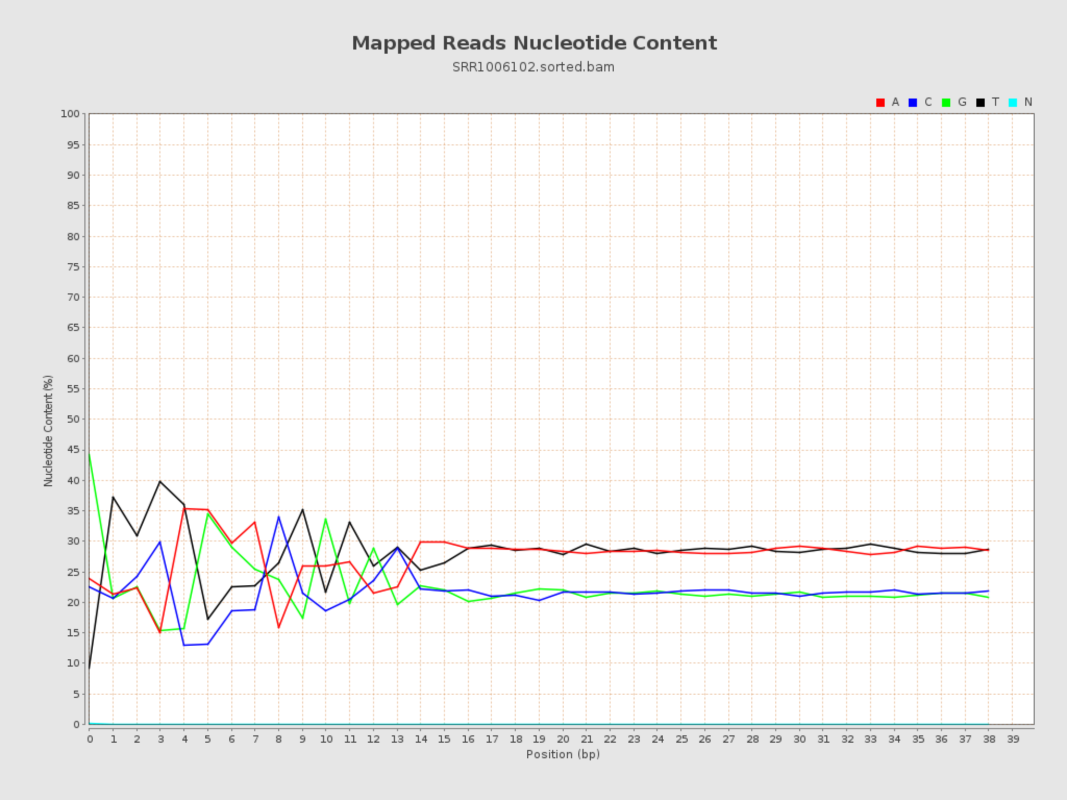
6. Results : Genome Fraction Coverage



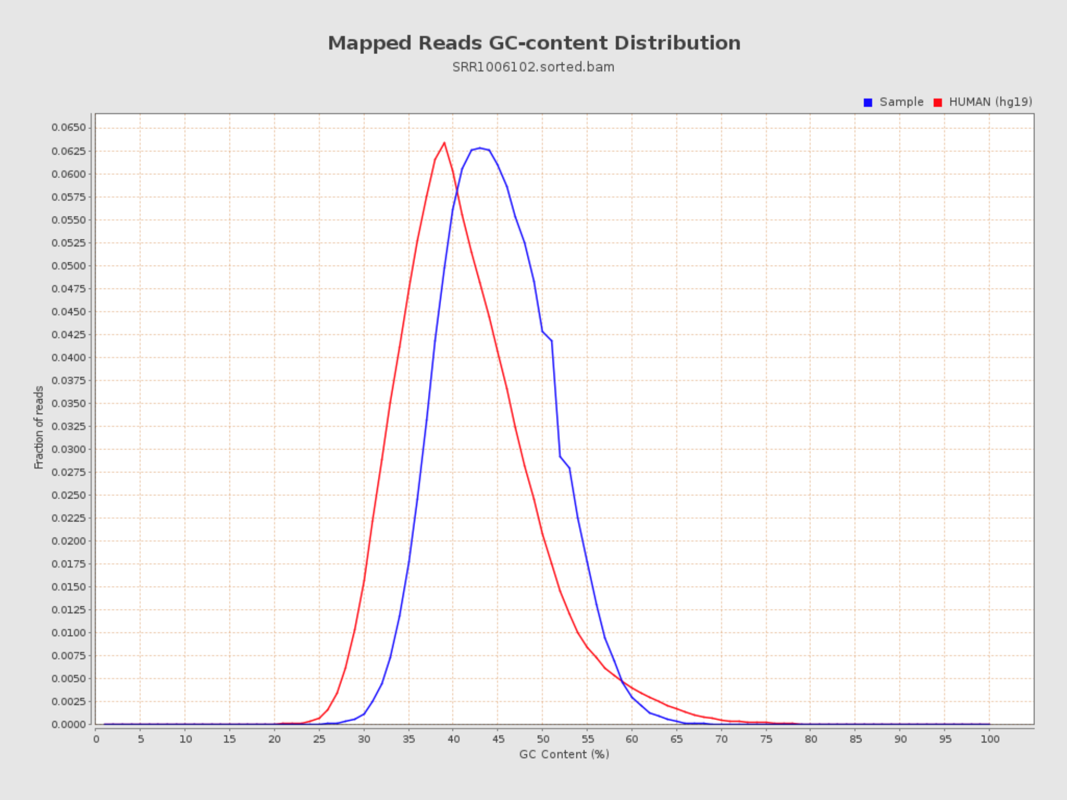
7. Results : Duplication Rate Histogram



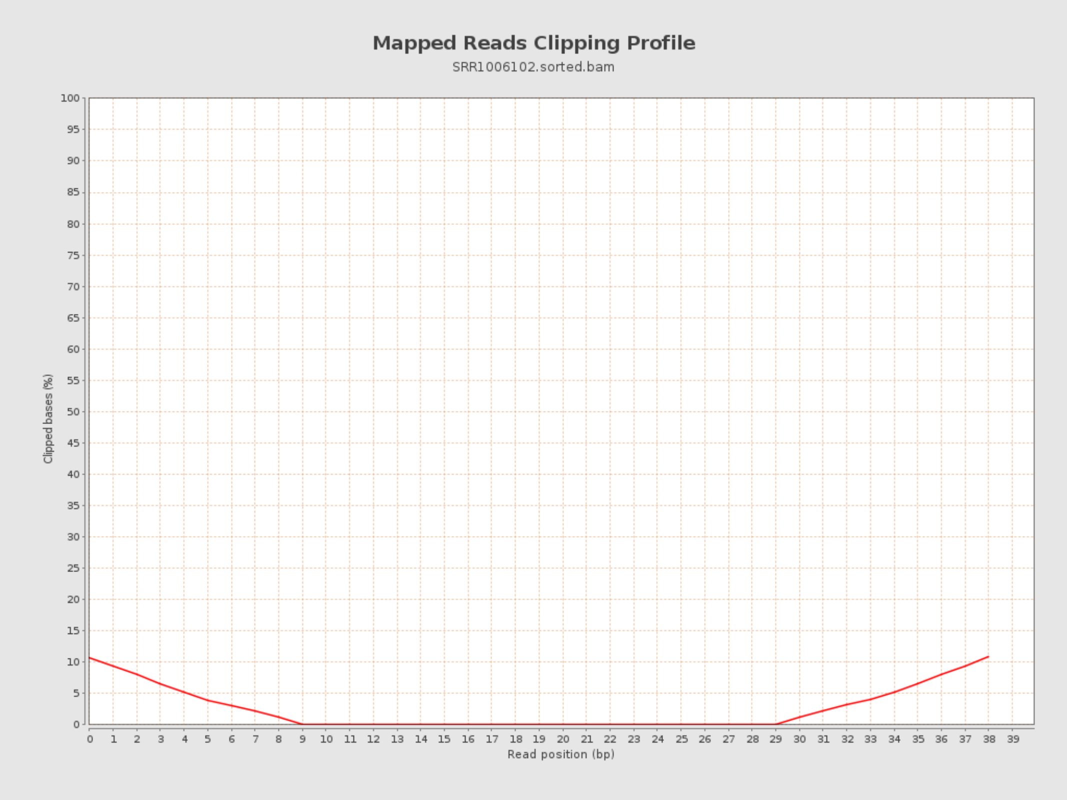
8. Results : Mapped Reads Nucleotide Content



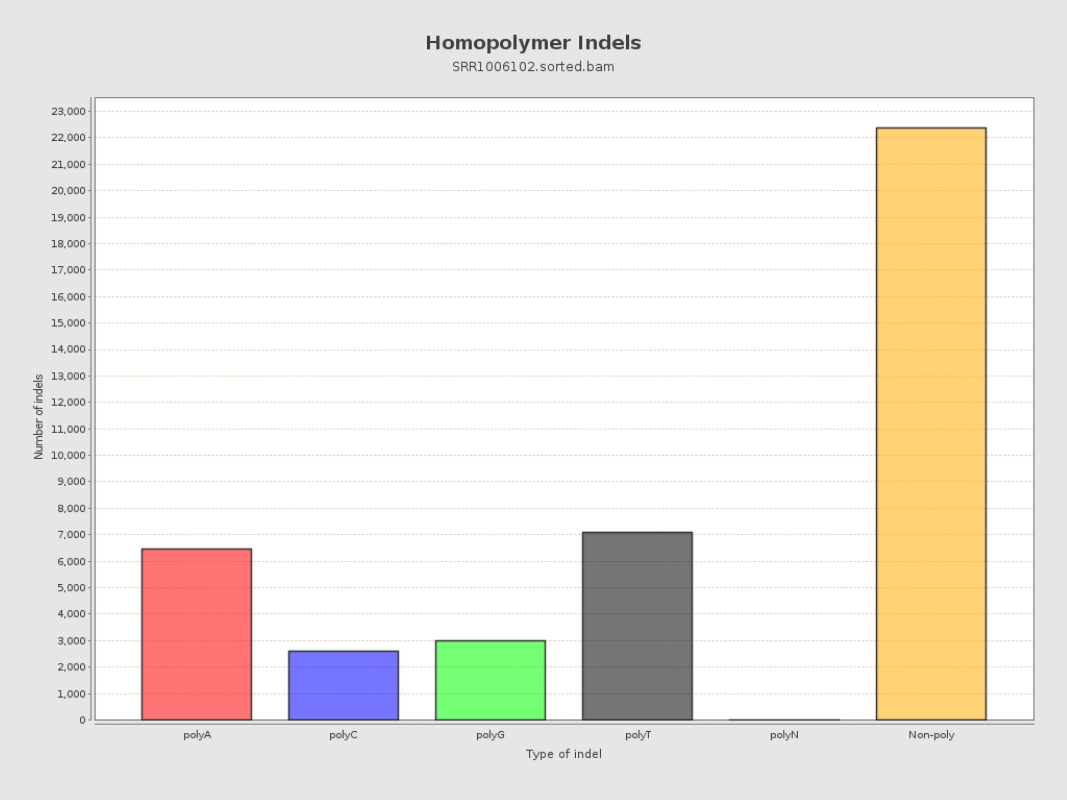
9. Results : Mapped Reads GC-content Distribution



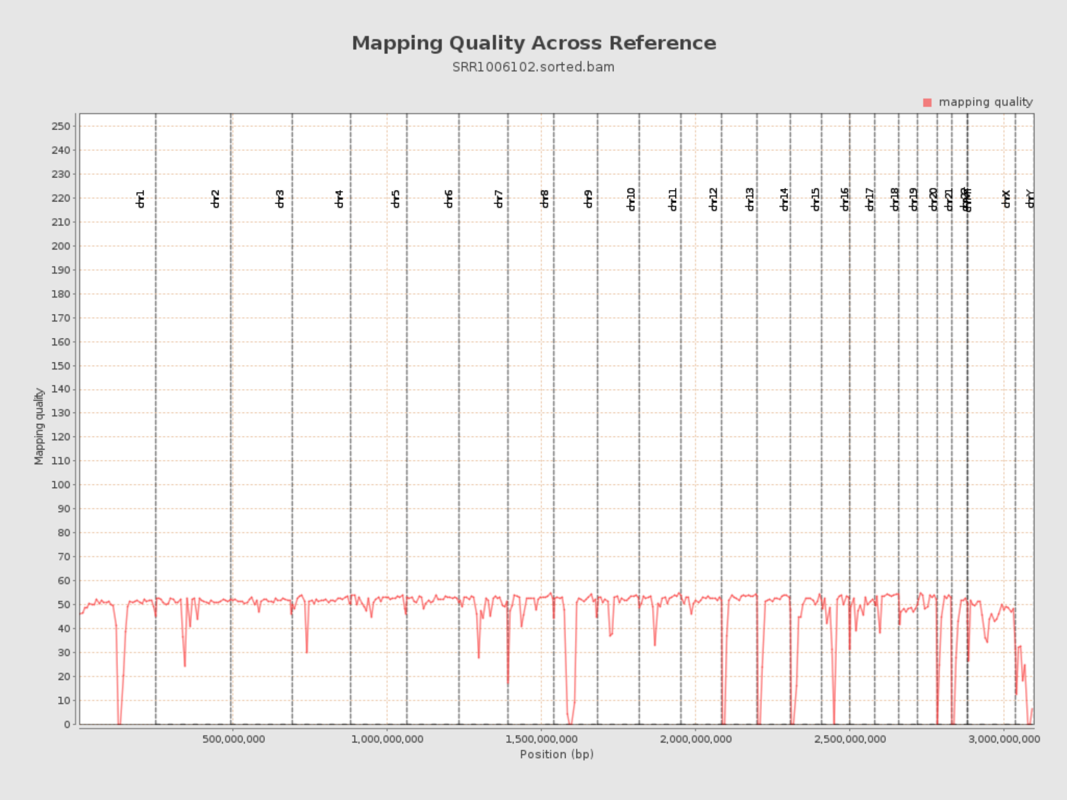
10. Results : Mapped Reads Clipping Profile



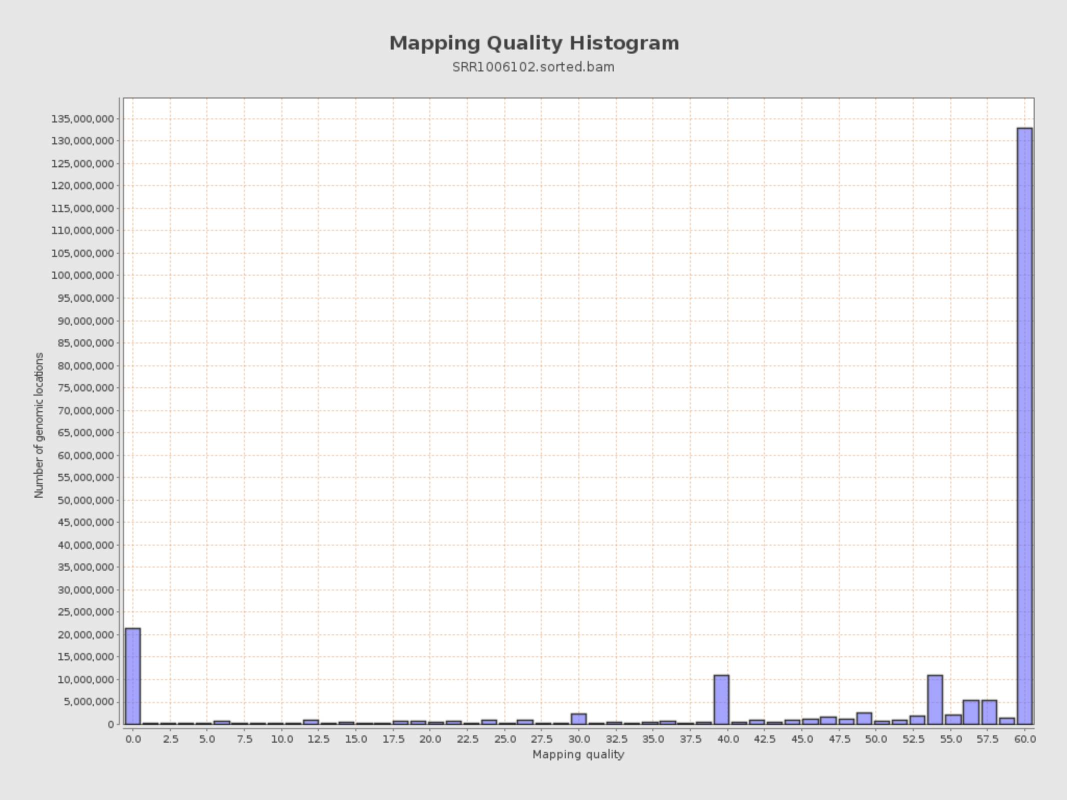
11. Results : Homopolymer Indels



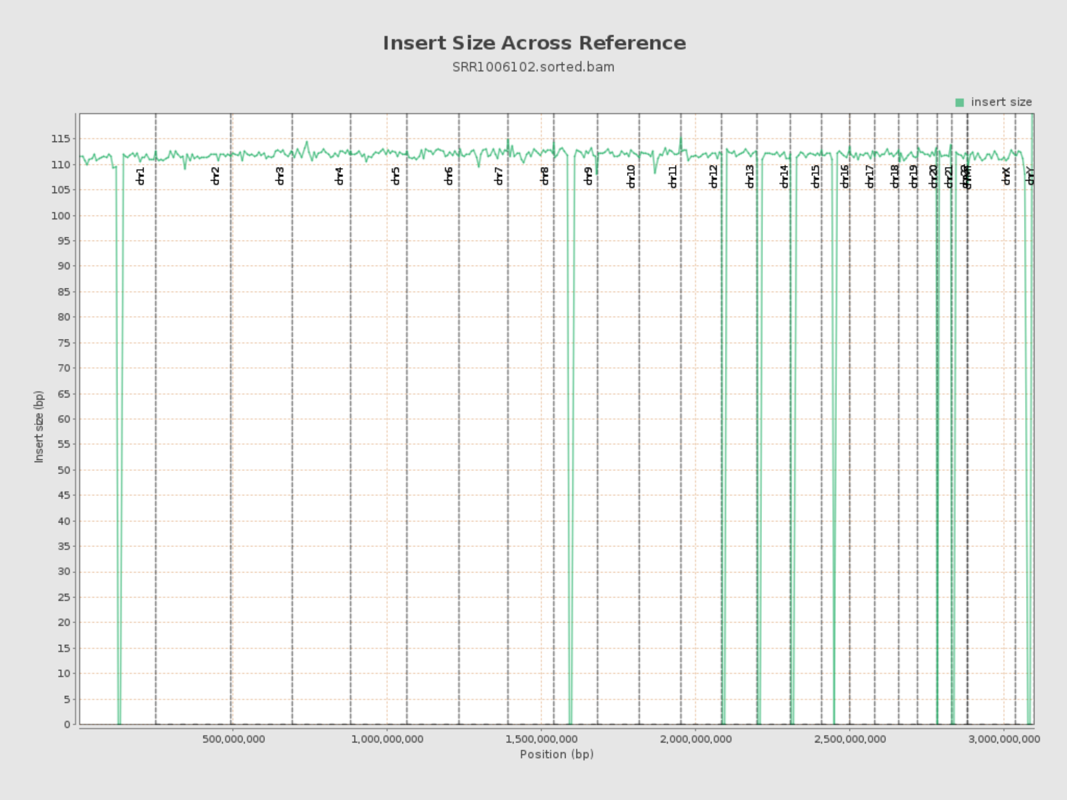
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram