Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:04:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006411.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_SRR1006411 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006411_1.fastq.gz SRR1006411_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:04:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006411.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,015,608
Mapped reads	5,326,227 / 59.08%
Unmapped reads	3,689,381 / 40.92%
Mapped paired reads	5,326,227 / 59.08%
Mapped reads, first in pair	2,687,814 / 29.81%
Mapped reads, second in pair	2,638,413 / 29.26%
Mapped reads, both in pair	4,770,642 / 52.92%
Mapped reads, singletons	555,585 / 6.16%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	209,384 / 2.32%
Duplication rate	3.31%
Clipped reads	317,209 / 3.52%

2.2. ACGT Content

Number/percentage of A's	57,544,513 / 27.93%
Number/percentage of C's	44,186,553 / 21.45%
Number/percentage of T's	58,631,821 / 28.46%
Number/percentage of G's	45,653,186 / 22.16%
Number/percentage of N's	8,885 / 0%
GC Percentage	43.61%

2.3. Coverage

Mean	0.0666
Standard Deviation	0.4411

2.4. Mapping Quality

Mean Mapping Quality	47.83

2.5. Insert size

Mean	85,764.89
Standard Deviation	2,797,771.65
P25/Median/P75	117 / 152 / 203

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	706,493
Insertions	5,946
Mapped reads with at least one insertion	0.11%
Deletions	19,512
Mapped reads with at least one deletion	0.37%
Homopolymer indels	43.09%

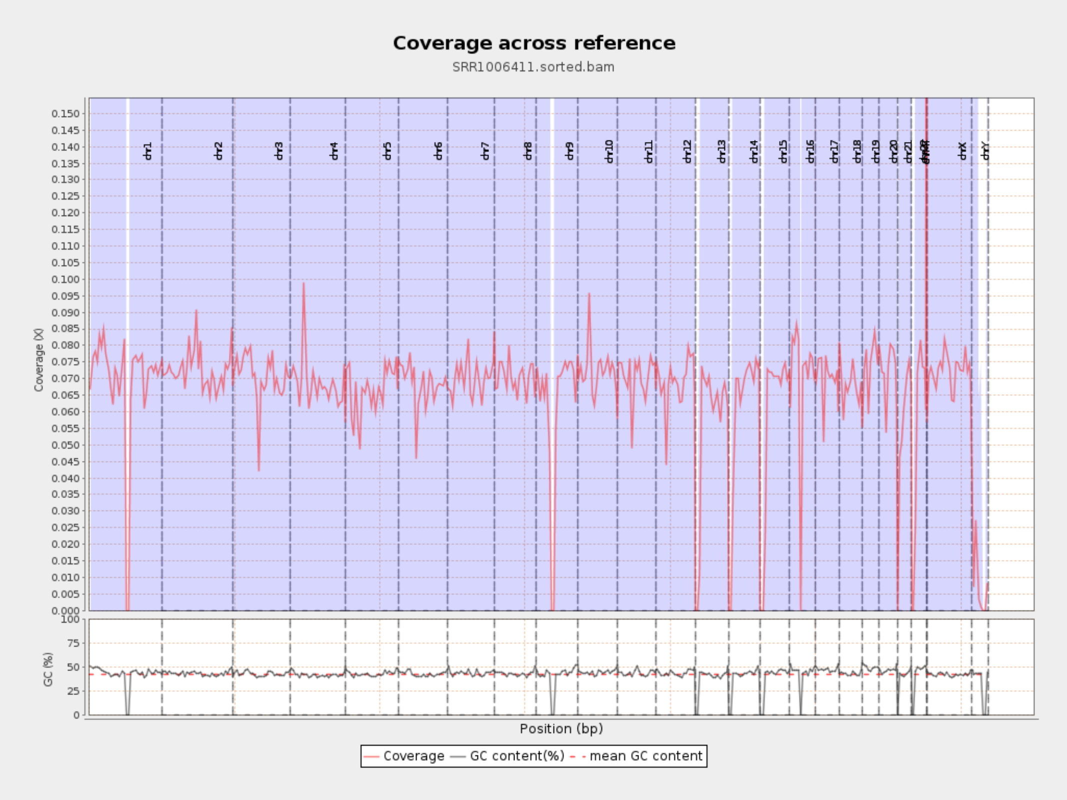
2.7. Chromosome stats

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

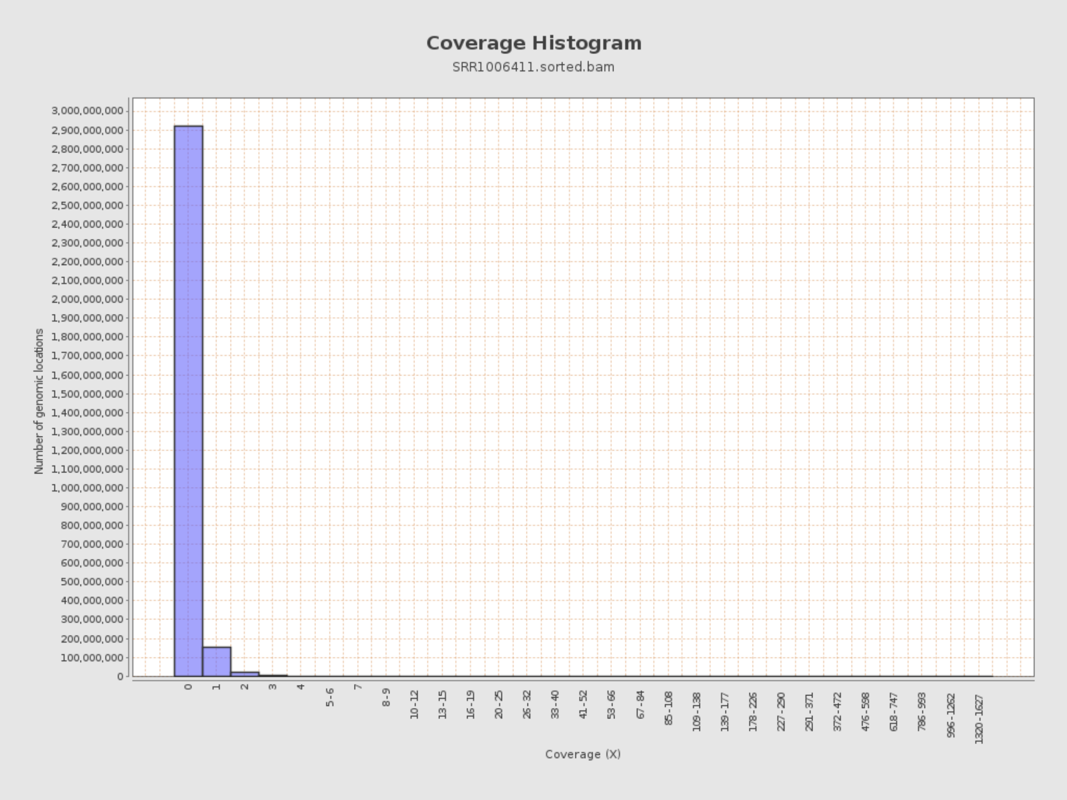
chr1	249250621	17130450	0.0687	0.5272
chr2	243199373	17654266	0.0726	0.5865
chr3	198022430	13968921	0.0705	0.3
chr4	191154276	13131810	0.0687	0.3297
chr5	180915260	11999596	0.0663	0.6517
chr6	171115067	11719808	0.0685	0.3751
chr7	159138663	11122267	0.0699	0.4262
chr8	146364022	10278740	0.0702	0.8482
chr9	141213431	8573871	0.0607	0.3159
chr10	135534747	9828635	0.0725	0.3982
chr11	135006516	9482663	0.0702	0.3559
chr12	133851895	9235382	0.069	0.2999
chr13	115169878	6341331	0.0551	0.2647
chr14	107349540	6351481	0.0592	0.3407
chr15	102531392	5915289	0.0577	0.2723
chr16	90354753	6314585	0.0699	0.3487
chr17	81195210	5683834	0.07	0.321
chr18	78077248	5314316	0.0681	0.4927
chr19	59128983	4384649	0.0742	0.413
chr20	63025520	4540611	0.072	0.3156
chr21	48129895	2702739	0.0562	0.322
chr22	51304566	2640154	0.0515	0.2616
chrMT	16571	9808	0.5919	0.9012
chrX	155270560	11217547	0.0722	0.3311

chrY	59373566	508313	0.0086	0.1972

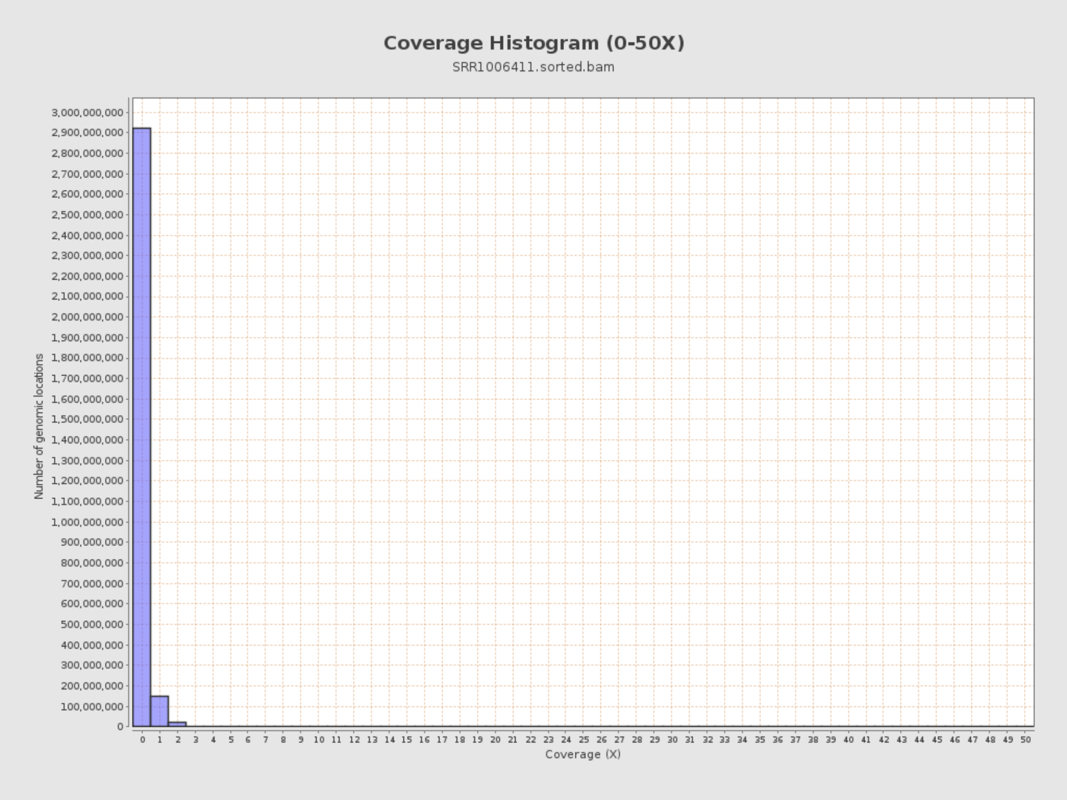
3. Results : Coverage across reference



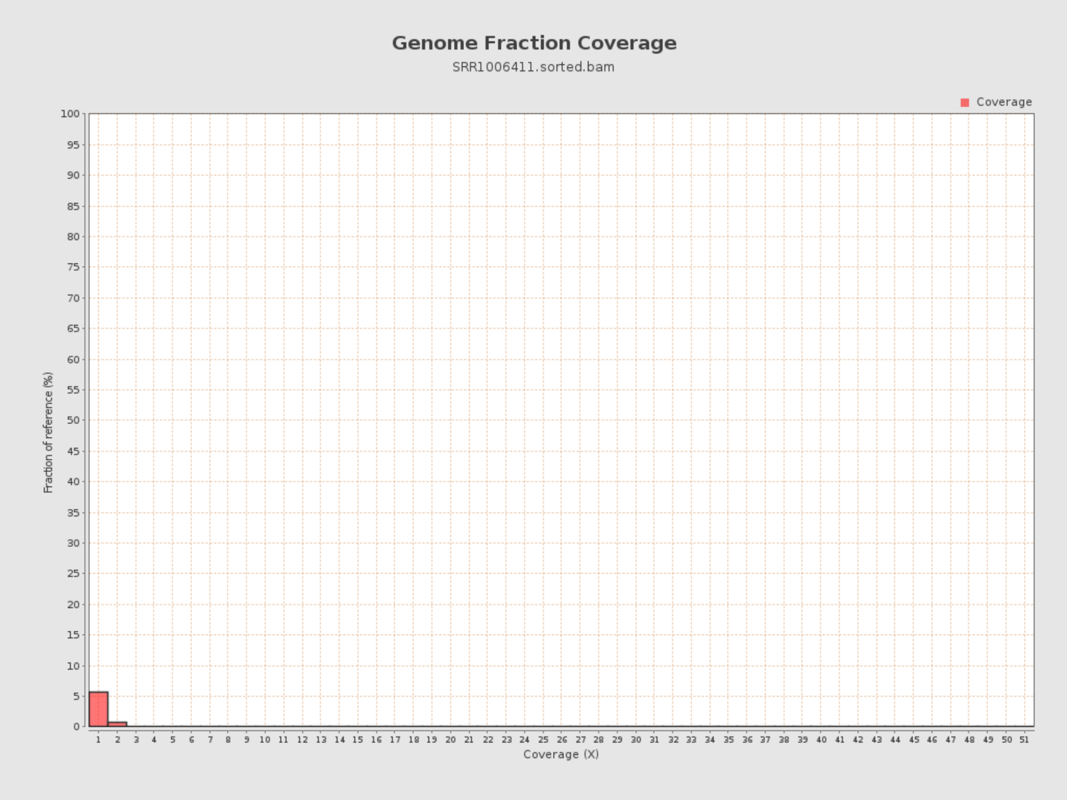
4. Results : Coverage Histogram



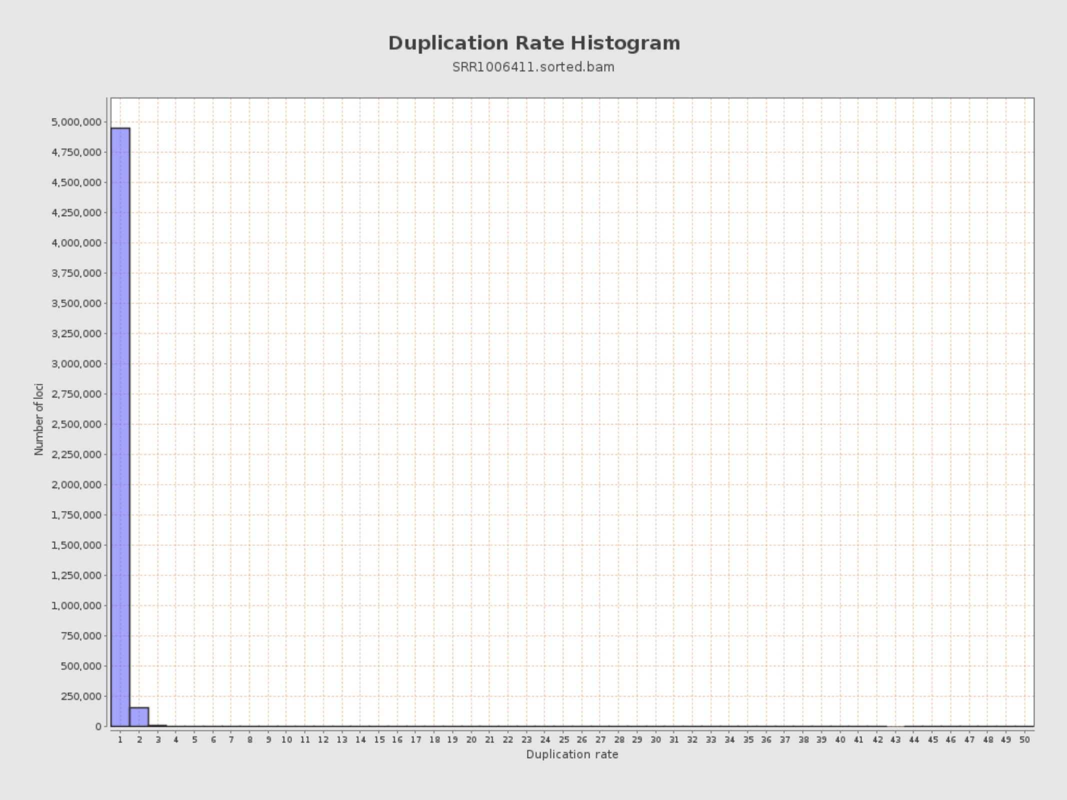
5. Results : Coverage Histogram (0-50X)



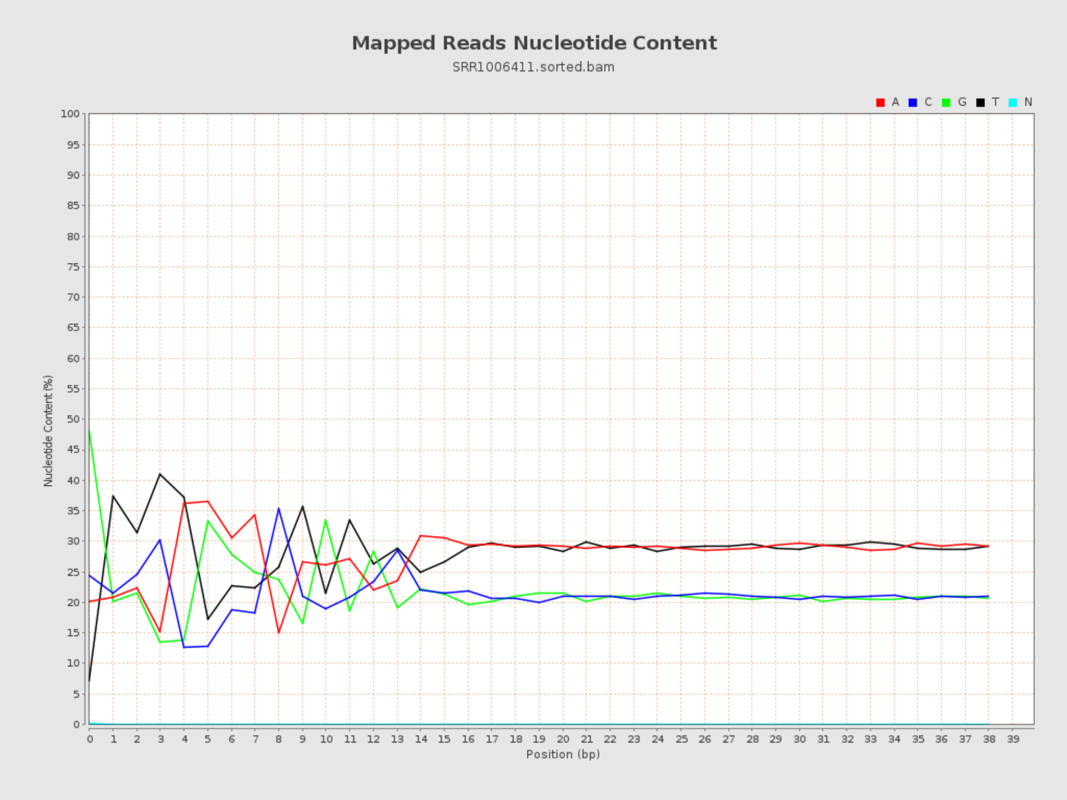
6. Results : Genome Fraction Coverage



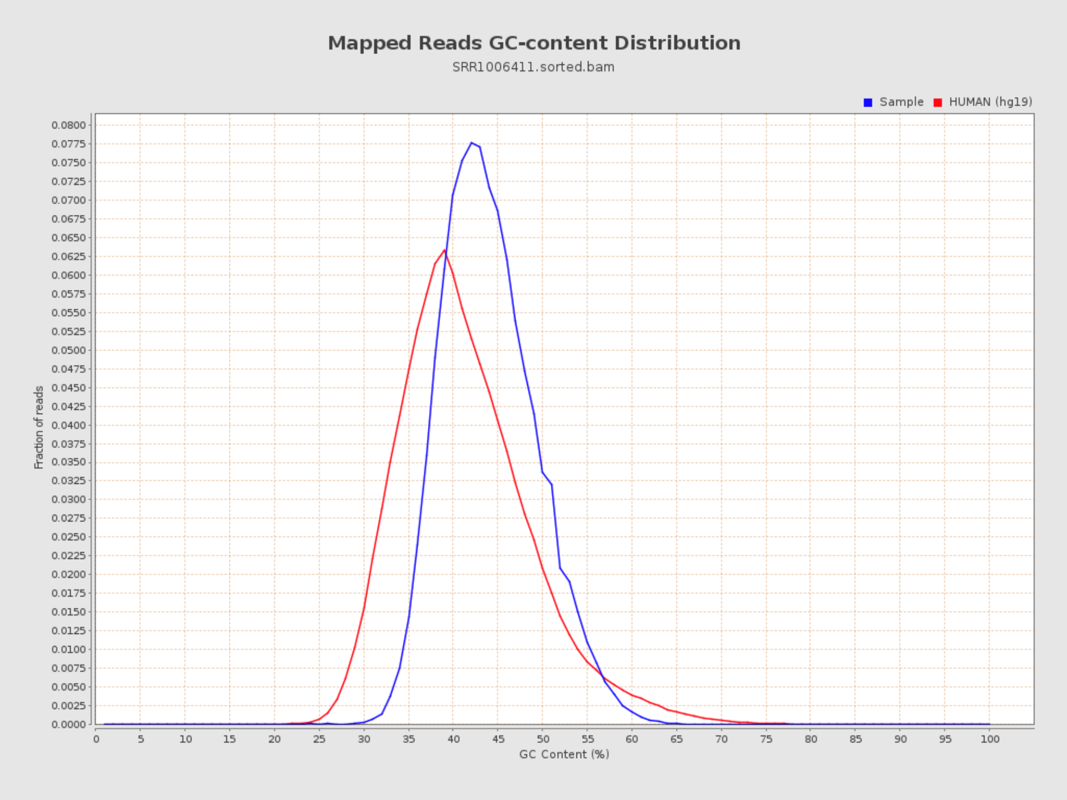
7. Results : Duplication Rate Histogram



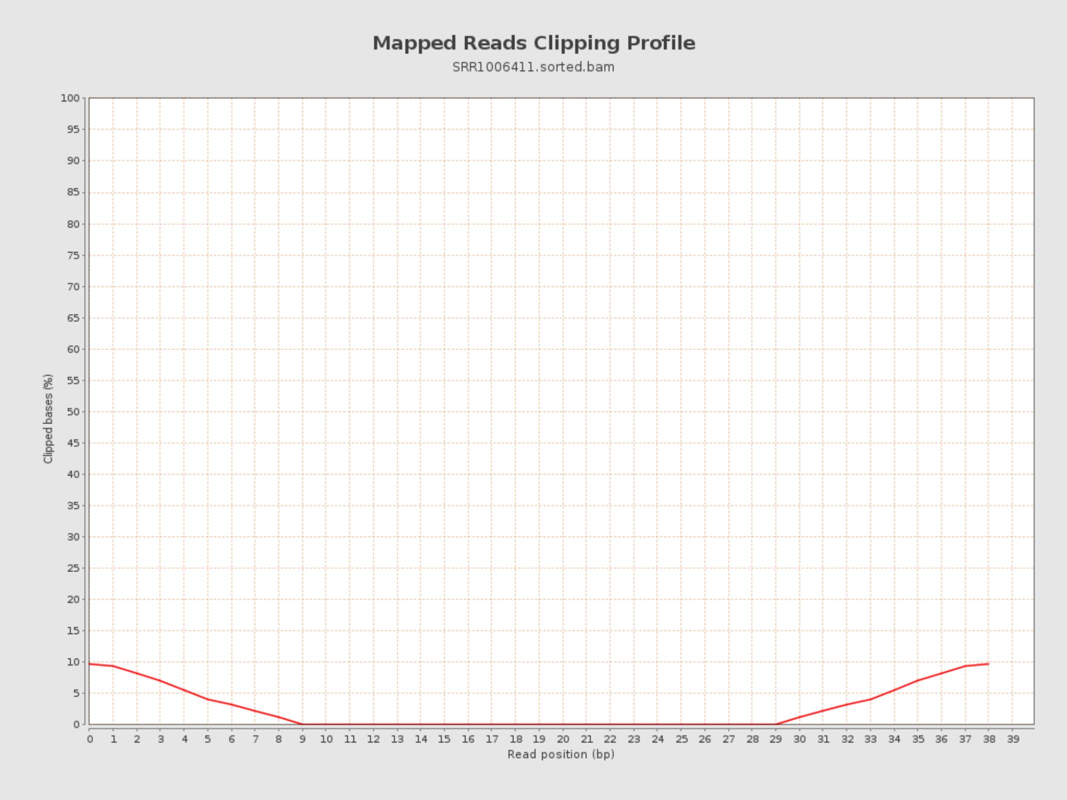
8. Results : Mapped Reads Nucleotide Content



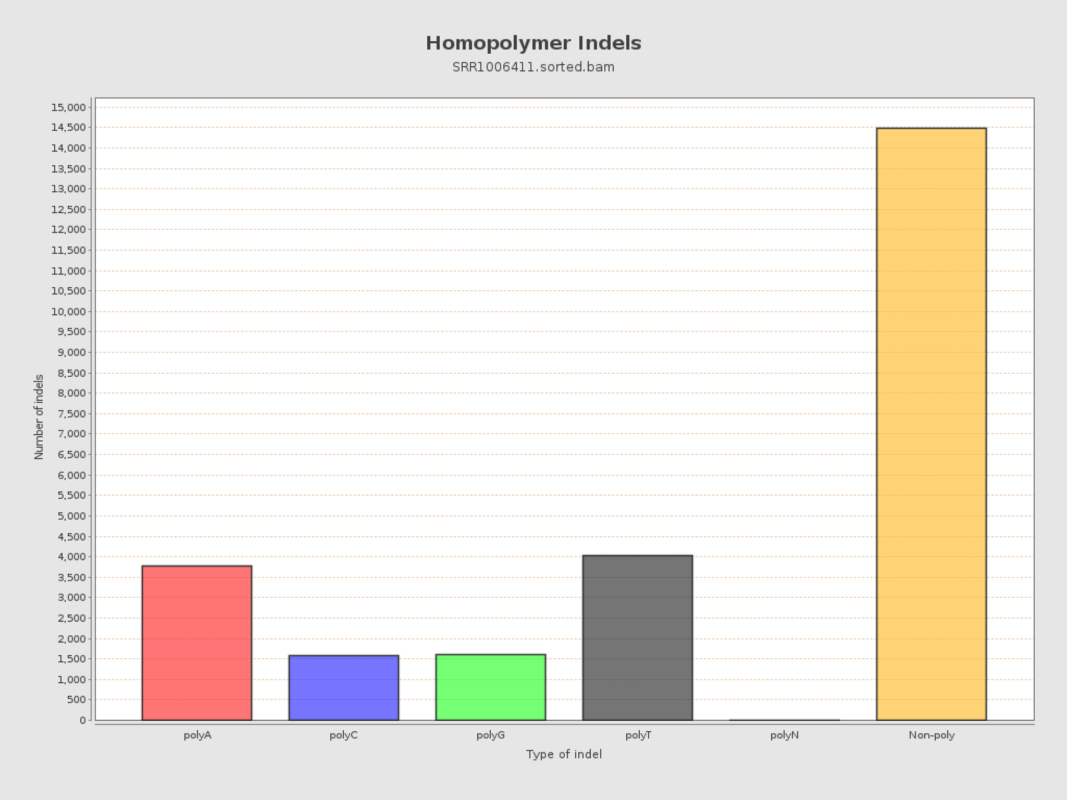
9. Results : Mapped Reads GC-content Distribution



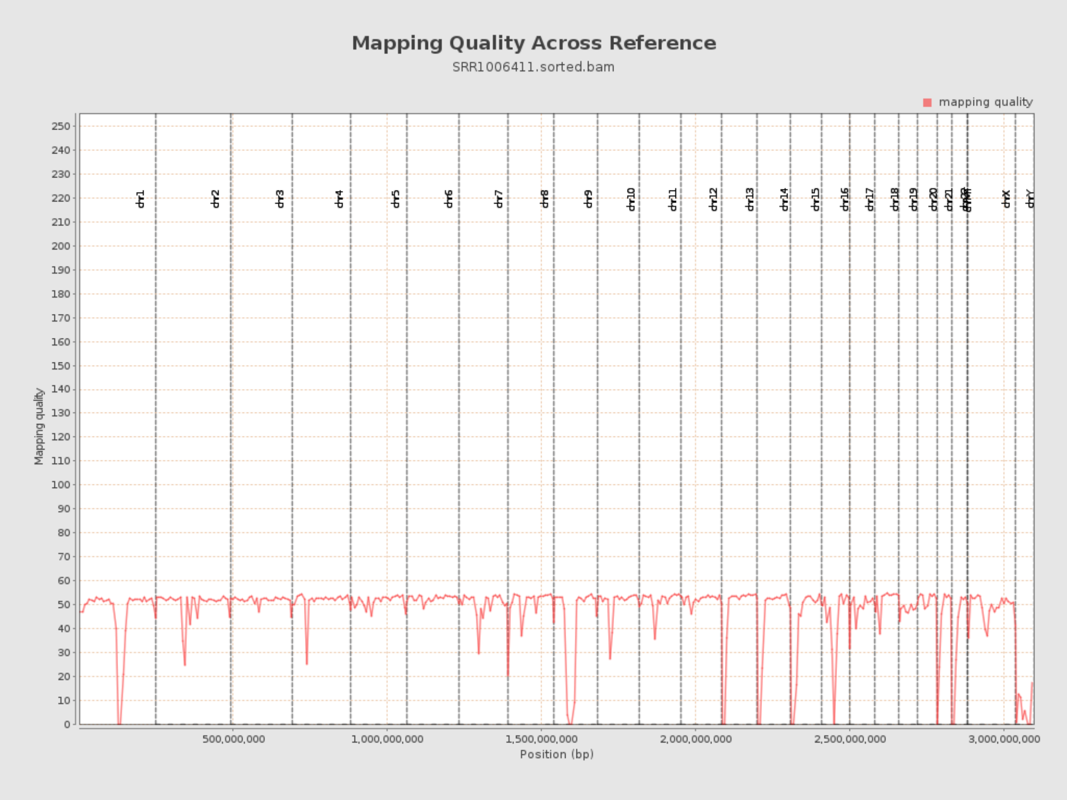
10. Results : Mapped Reads Clipping Profile



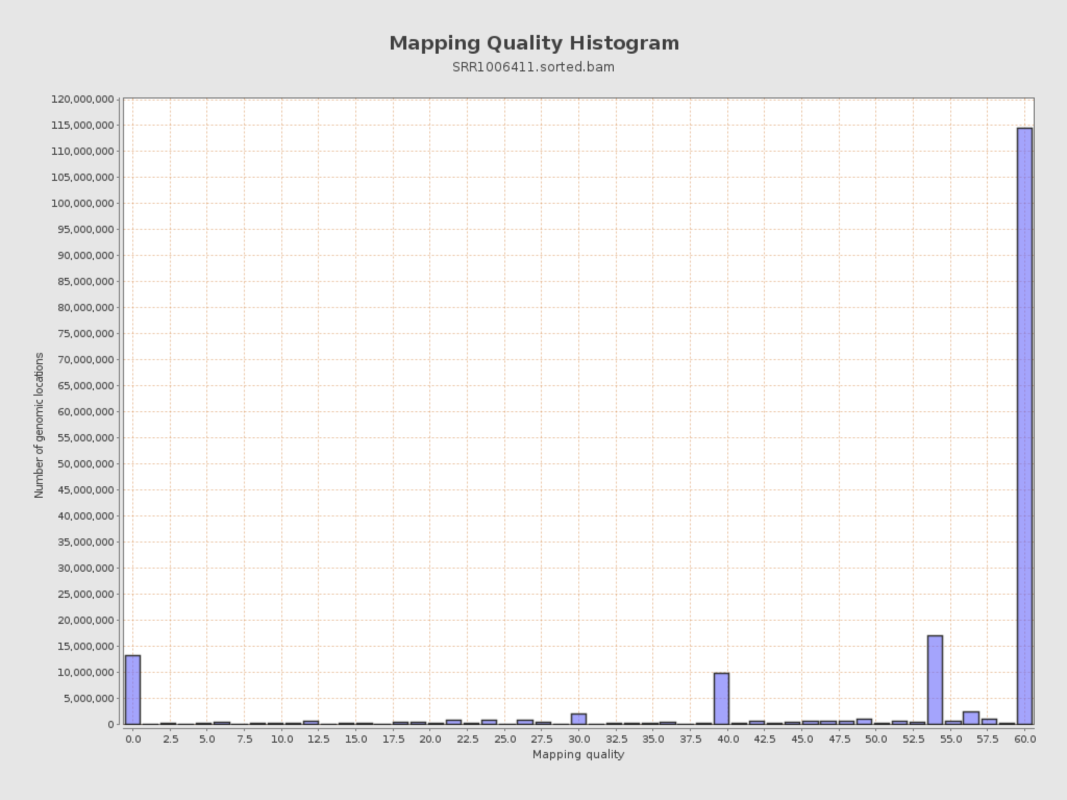
11. Results : Homopolymer Indels



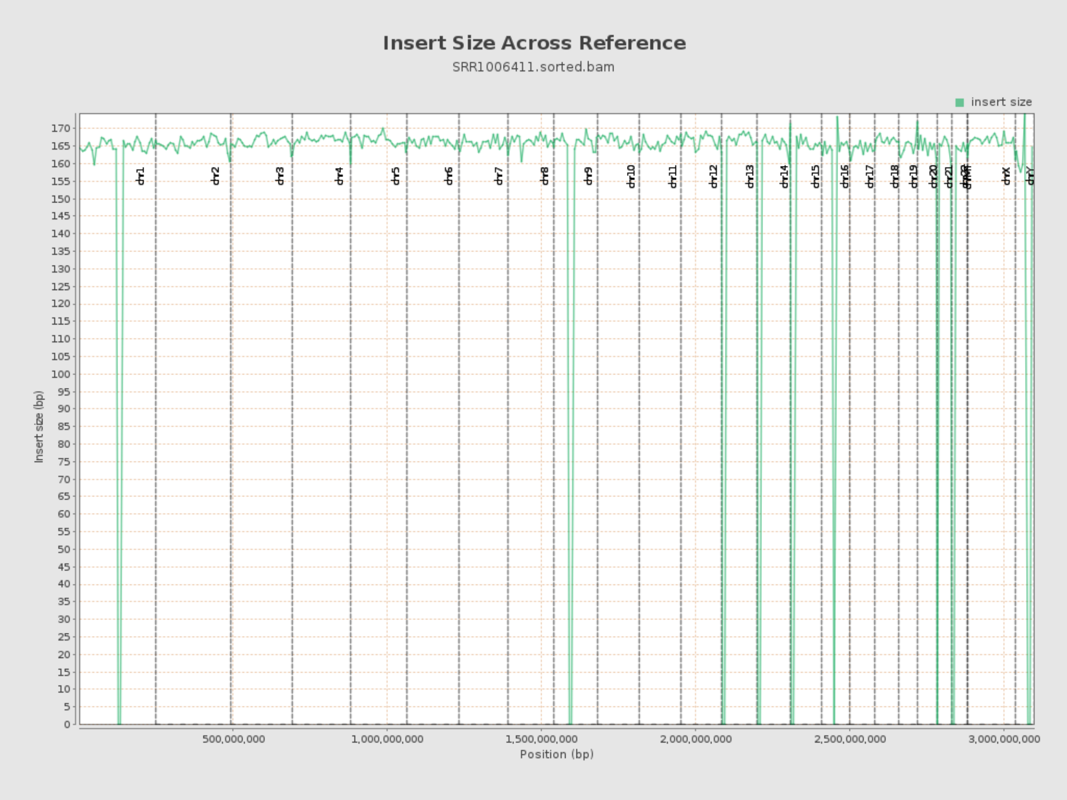
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram