Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 15:23:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006036.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_SRR1006036 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006036_1.fastq.gz SRR1006036_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 15:23:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006036.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,759,904
Mapped reads	9,553,874 / 74.87%
Unmapped reads	3,206,030 / 25.13%
Mapped paired reads	9,553,874 / 74.87%
Mapped reads, first in pair	4,793,412 / 37.57%
Mapped reads, second in pair	4,760,462 / 37.31%
Mapped reads, both in pair	8,554,190 / 67.04%
Mapped reads, singletons	999,684 / 7.83%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	350,137 / 2.74%
Duplication rate	3.07%
Clipped reads	697,904 / 5.47%

2.2. ACGT Content

Number/percentage of A's	106,788,088 / 28.92%
Number/percentage of C's	76,949,074 / 20.84%
Number/percentage of T's	107,236,779 / 29.04%
Number/percentage of G's	78,259,250 / 21.19%
Number/percentage of N's	45,168 / 0.01%
GC Percentage	42.03%

2.3. Coverage

Mean	0.1193
Standard Deviation	0.6086

2.4. Mapping Quality

Mean Mapping Quality	47.42

2.5. Insert size

Mean	70,384.69
Standard Deviation	2,523,774.4
P25/Median/P75	71 / 101 / 147

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	2,088,057
Insertions	10,746
Mapped reads with at least one insertion	0.11%
Deletions	33,531
Mapped reads with at least one deletion	0.35%
Homopolymer indels	45.36%

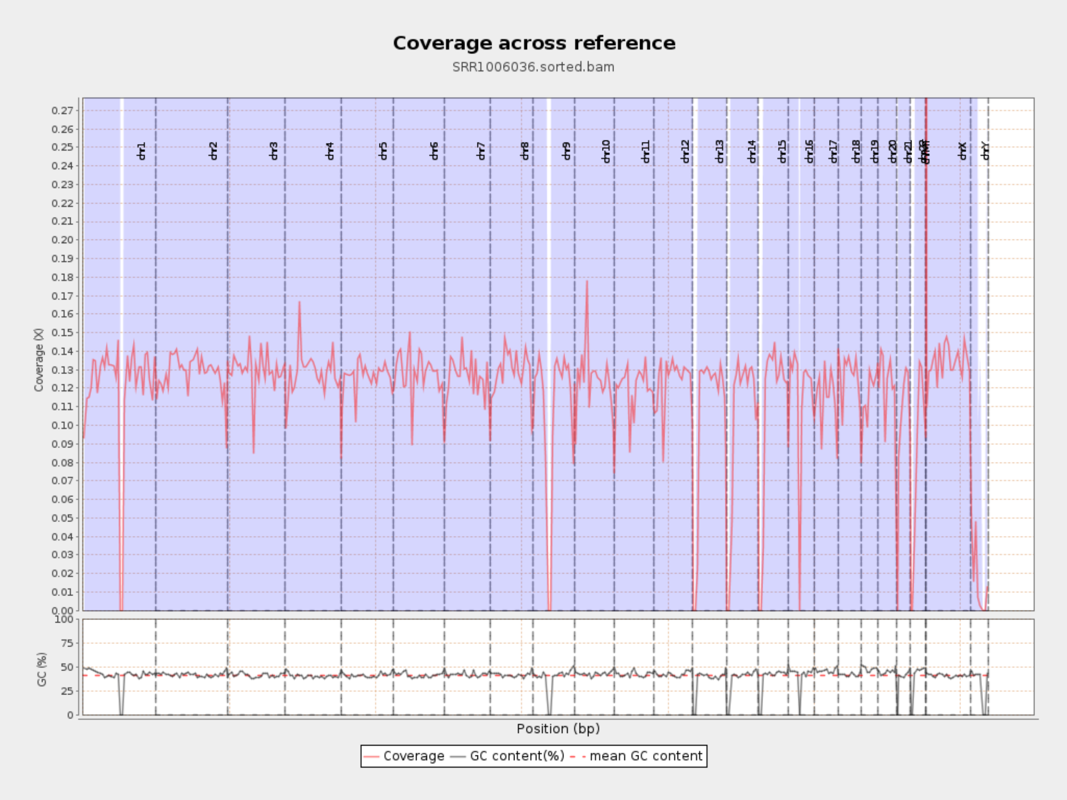
2.7. Chromosome stats

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

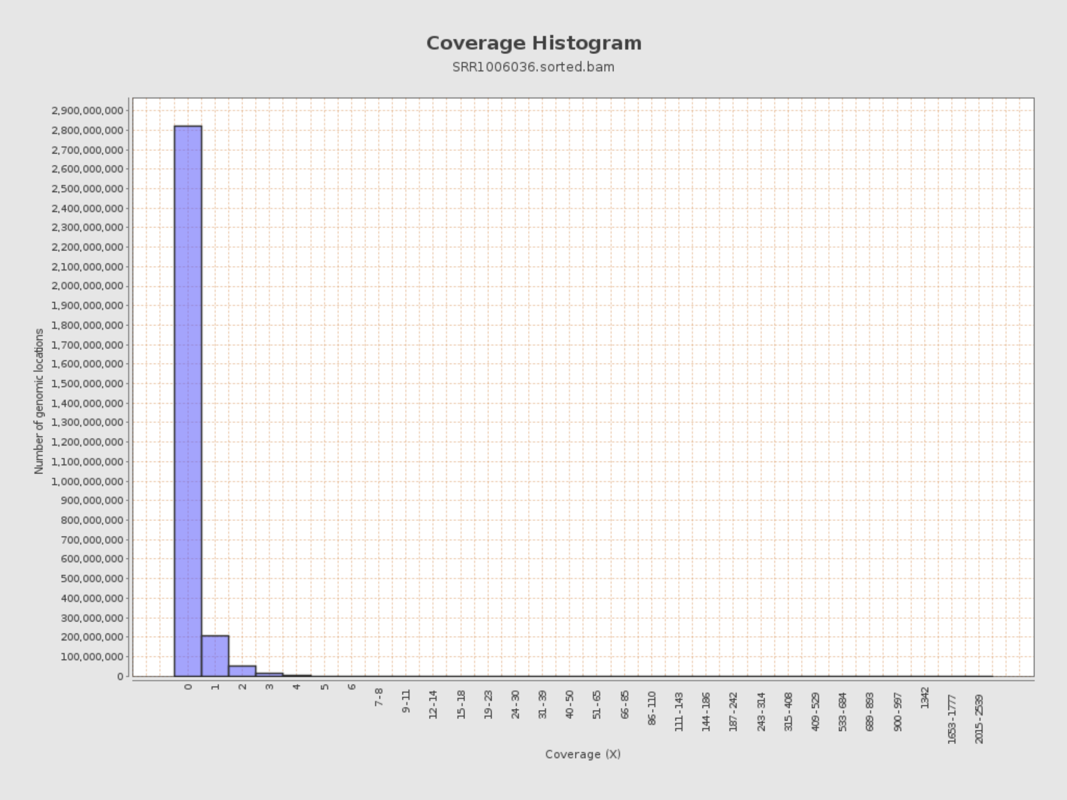
chr1	249250621	30006153	0.1204	0.8263
chr2	243199373	31287123	0.1286	0.5541
chr3	198022430	25725873	0.1299	0.4537
chr4	191154276	24638032	0.1289	0.5053
chr5	180915260	22820035	0.1261	0.4471
chr6	171115067	21997843	0.1286	0.5591
chr7	159138663	20000594	0.1257	0.7134
chr8	146364022	18956191	0.1295	1.3194
chr9	141213431	15257496	0.108	0.4642
chr10	135534747	16976817	0.1253	0.6891
chr11	135006516	16150072	0.1196	0.4808
chr12	133851895	16636200	0.1243	0.448
chr13	115169878	12116714	0.1052	0.4072
chr14	107349540	11140885	0.1038	0.4272
chr15	102531392	10797708	0.1053	0.409
chr16	90354753	10257978	0.1135	0.4914
chr17	81195210	9382936	0.1156	0.4446
chr18	78077248	9929427	0.1272	0.6809
chr19	59128983	6889014	0.1165	0.7038
chr20	63025520	7666110	0.1216	0.4583
chr21	48129895	4841661	0.1006	0.4425
chr22	51304566	4152589	0.0809	0.3647
chrMT	16571	69487	4.1933	3.8788
chrX	155270560	20709162	0.1334	0.4898

chrY	59373566	915846	0.0154	0.3259

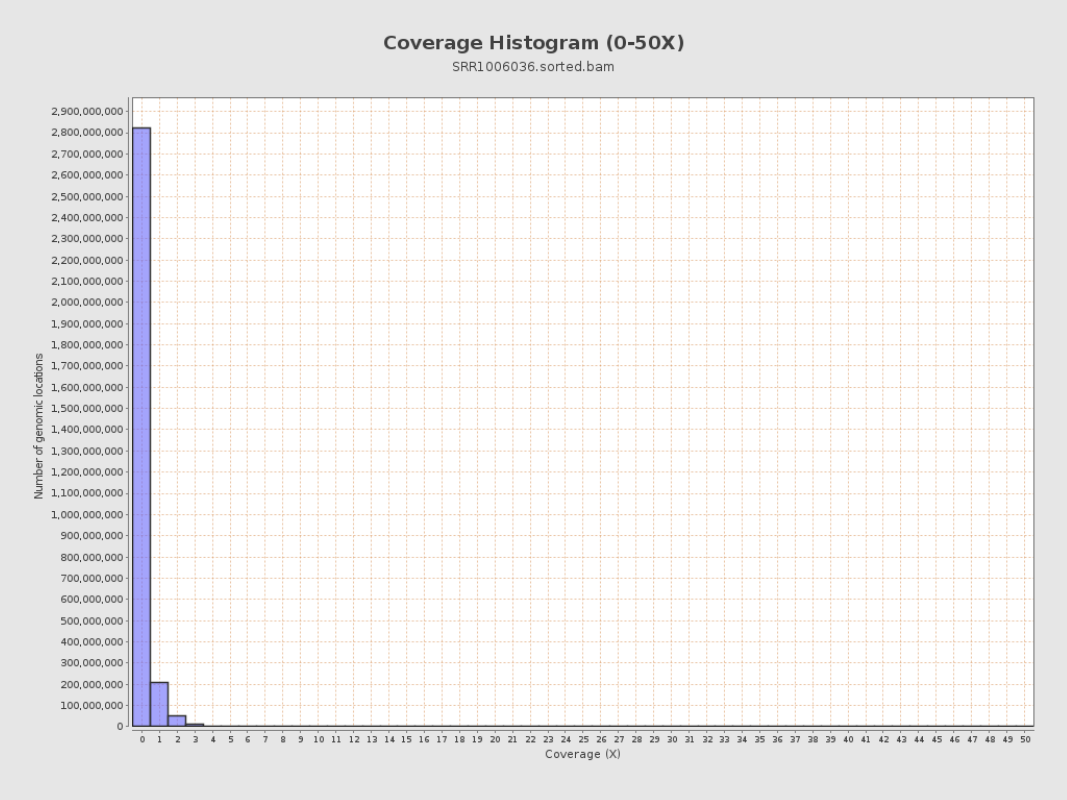
3. Results : Coverage across reference



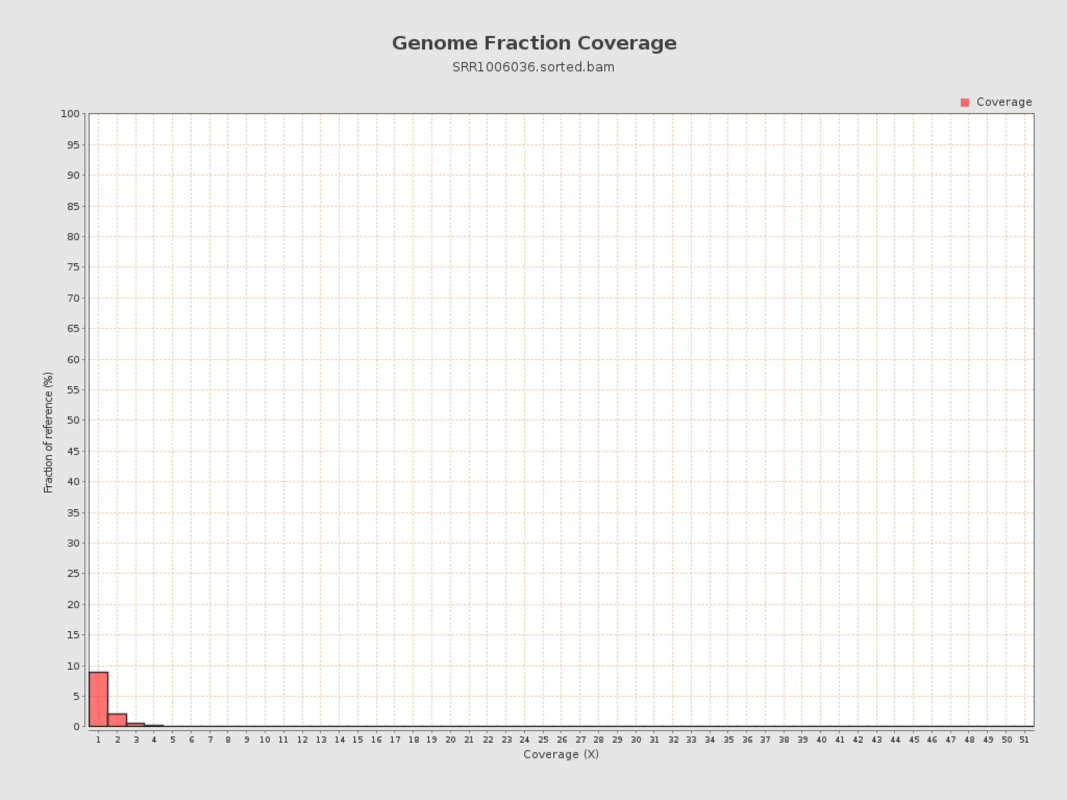
4. Results : Coverage Histogram



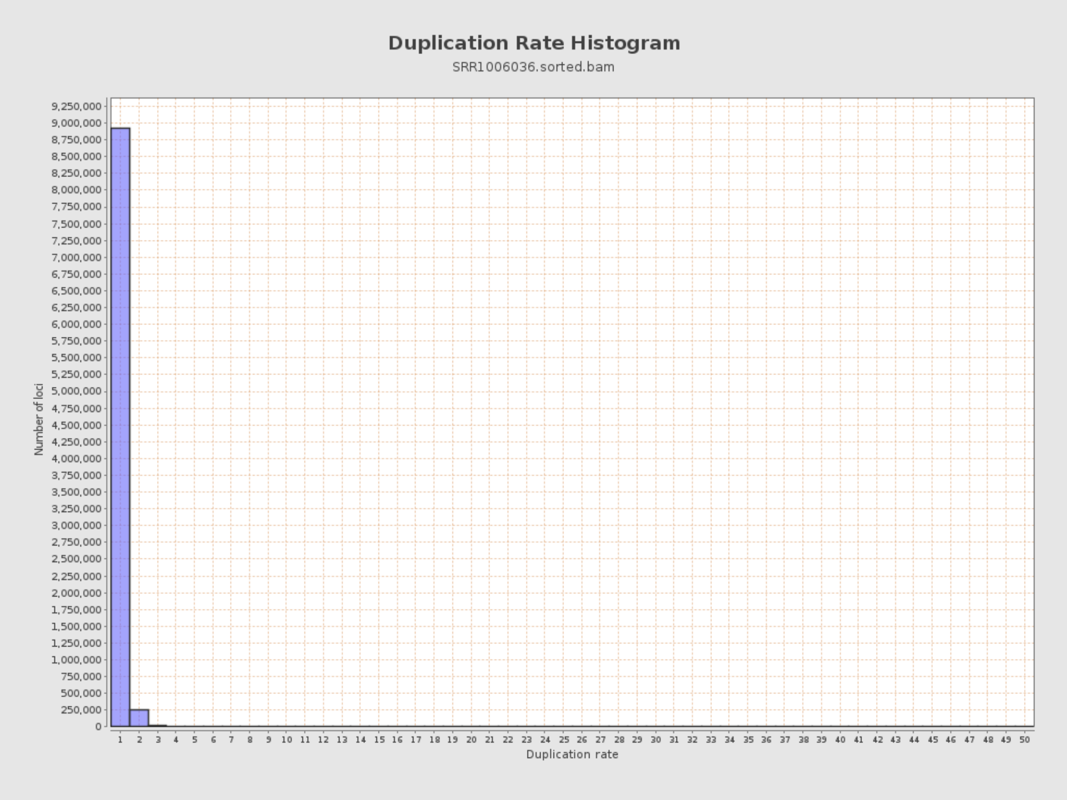
5. Results : Coverage Histogram (0-50X)



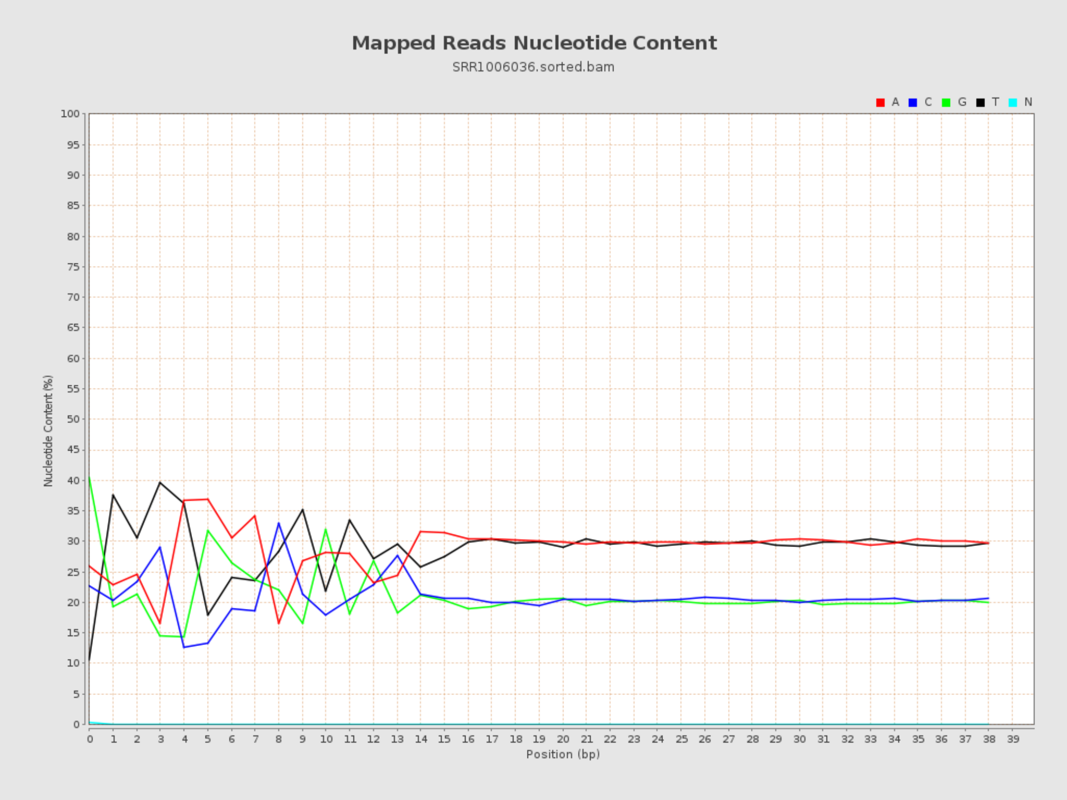
6. Results : Genome Fraction Coverage



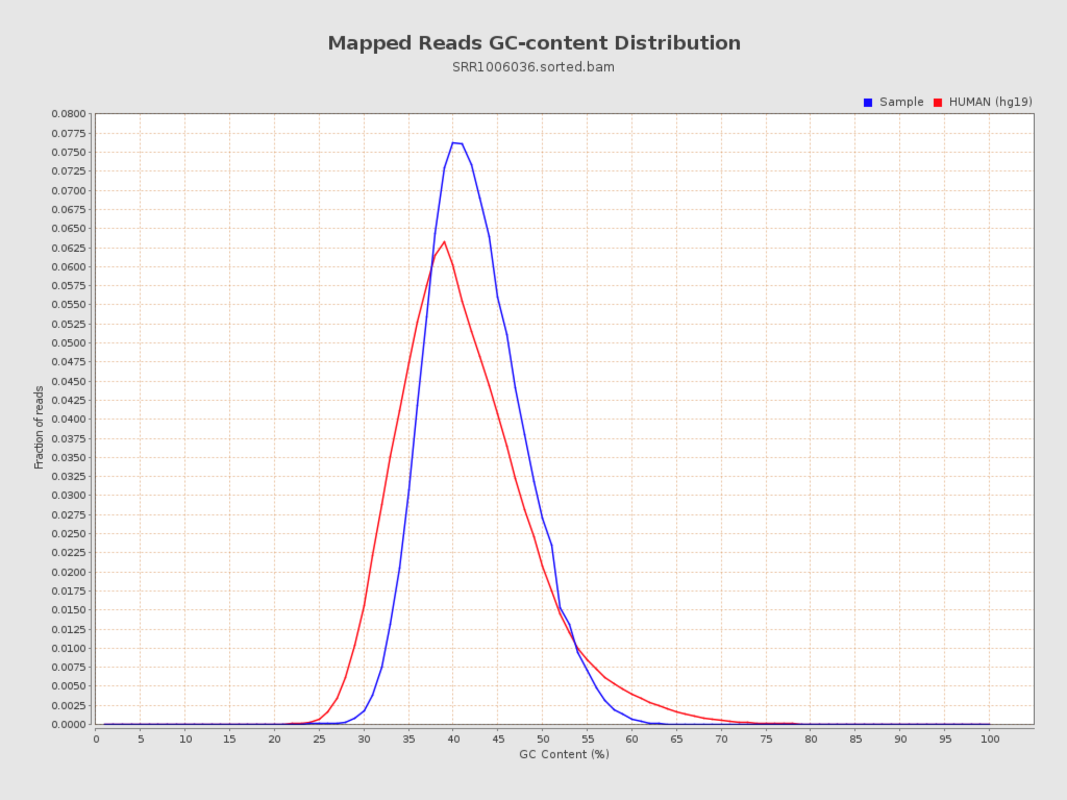
7. Results : Duplication Rate Histogram



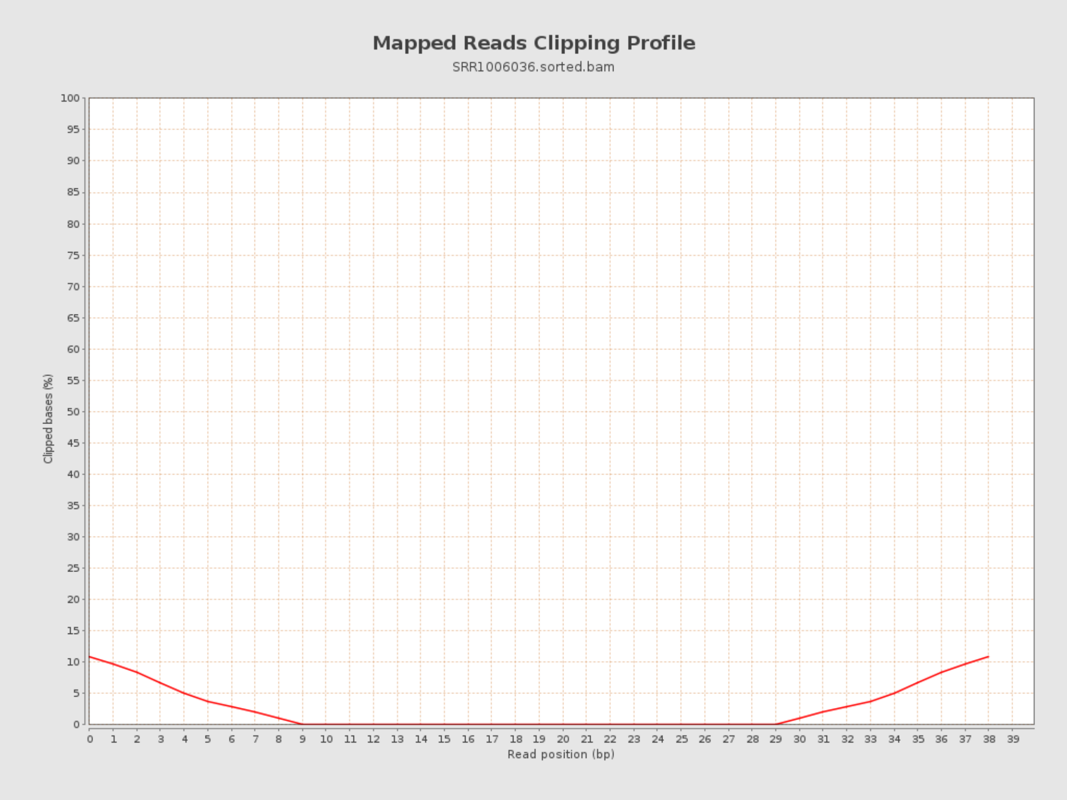
8. Results : Mapped Reads Nucleotide Content



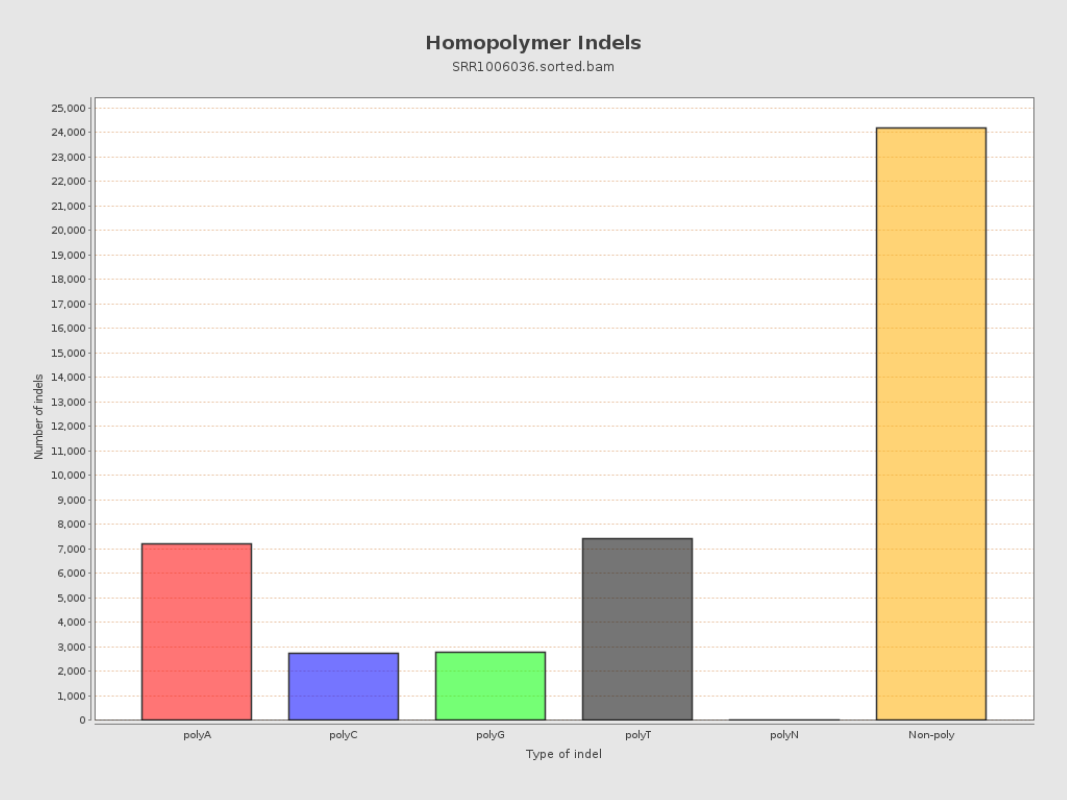
9. Results : Mapped Reads GC-content Distribution



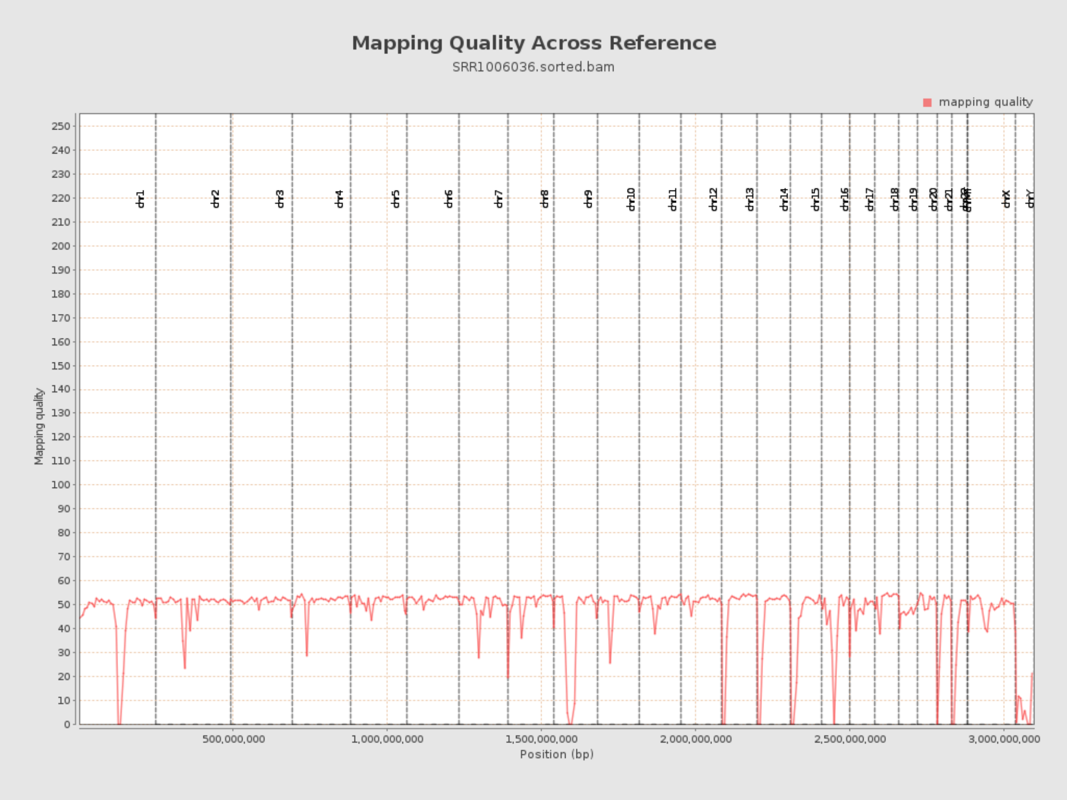
10. Results : Mapped Reads Clipping Profile



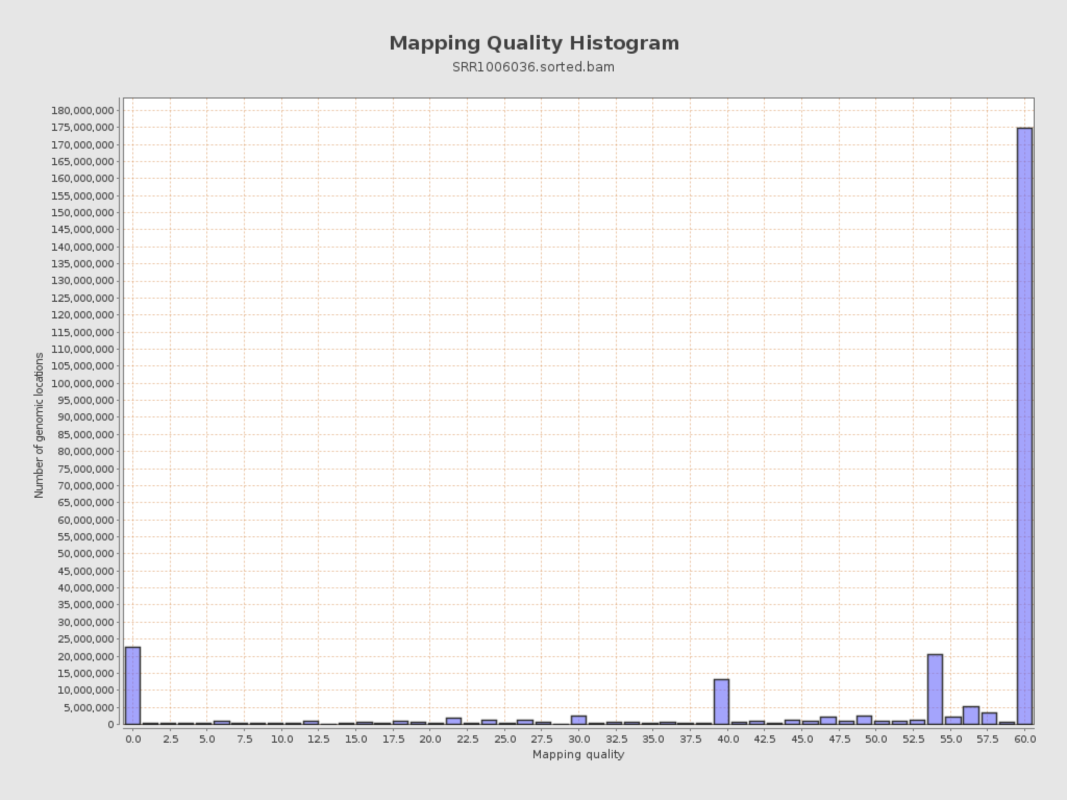
11. Results : Homopolymer Indels



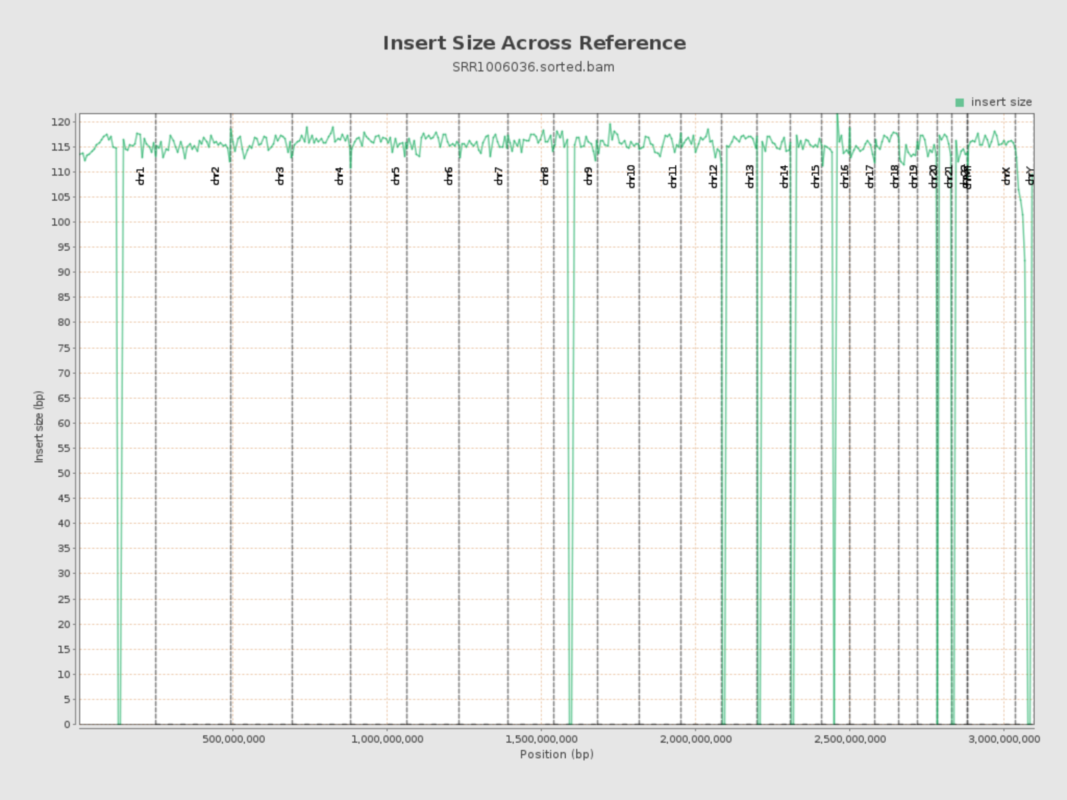
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram