Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 18:29:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006086.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_SRR1006086 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006086_1.fastq.gz SRR1006086_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 18:29:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,528,842
Mapped reads	4,746,674 / 85.85%
Unmapped reads	782,168 / 14.15%
Mapped paired reads	4,746,674 / 85.85%
Mapped reads, first in pair	2,399,372 / 43.4%
Mapped reads, second in pair	2,347,302 / 42.46%
Mapped reads, both in pair	4,368,210 / 79.01%
Mapped reads, singletons	378,464 / 6.85%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	200,909 / 3.63%
Duplication rate	3.83%
Clipped reads	385,601 / 6.97%

2.2. ACGT Content

Number/percentage of A's	48,457,925 / 26.44%
Number/percentage of C's	41,112,901 / 22.43%
Number/percentage of T's	50,147,333 / 27.36%
Number/percentage of G's	43,568,053 / 23.77%
Number/percentage of N's	7,632 / 0%
GC Percentage	46.2%

2.3. Coverage

Mean	0.0592
Standard Deviation	0.3536

2.4. Mapping Quality

Mean Mapping Quality	46.98

2.5. Insert size

Mean	63,503.43
Standard Deviation	2,474,500.94
P25/Median/P75	74 / 103 / 134

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	931,652
Insertions	5,956
Mapped reads with at least one insertion	0.13%
Deletions	15,565
Mapped reads with at least one deletion	0.33%
Homopolymer indels	44.08%

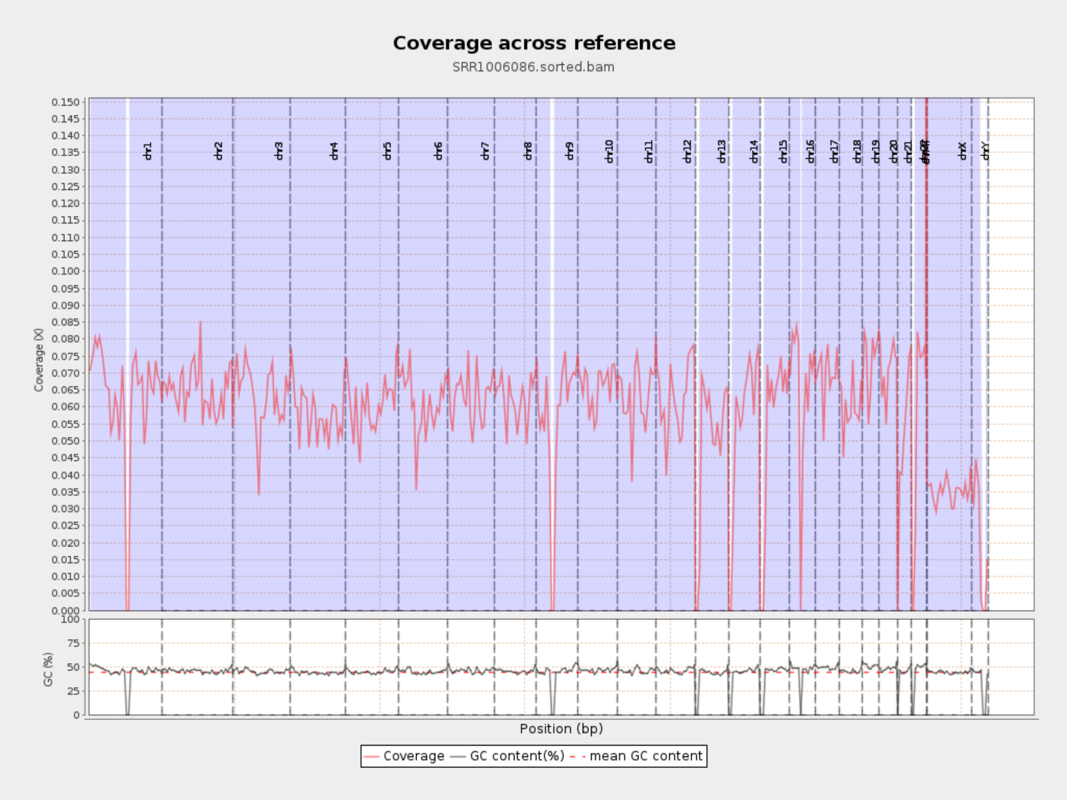
2.7. Chromosome stats

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

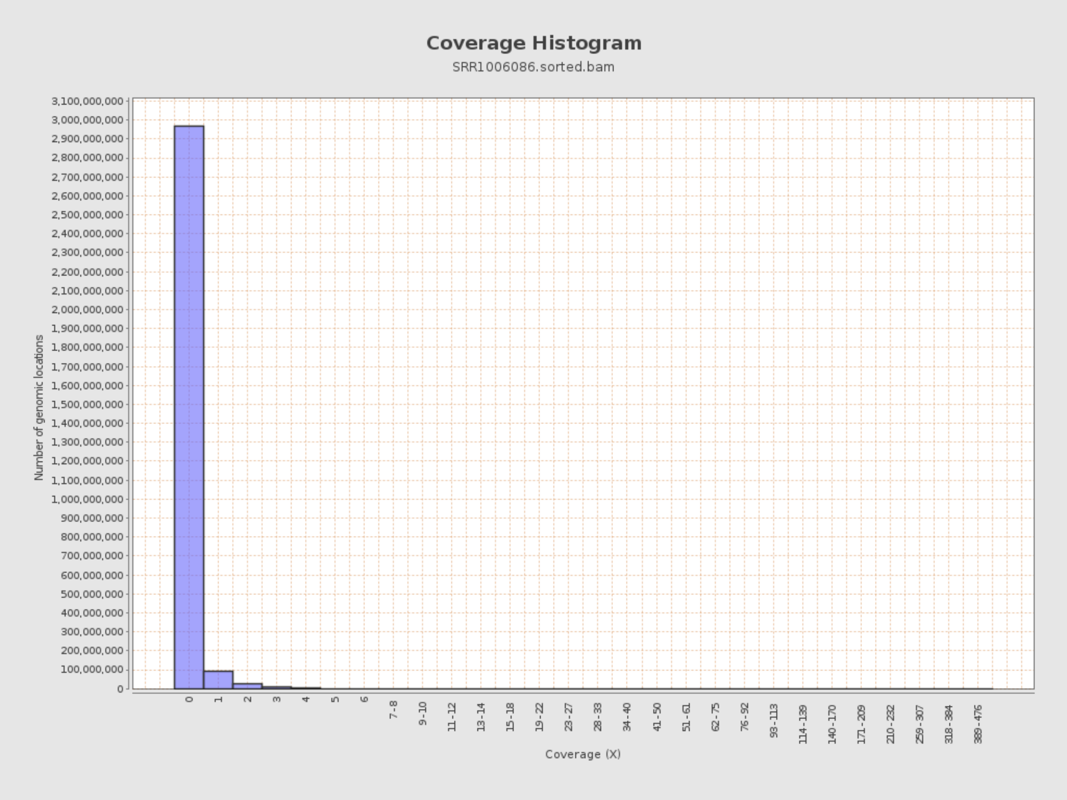
chr1	249250621	15627772	0.0627	0.3671
chr2	243199373	15837697	0.0651	0.3948
chr3	198022430	12538538	0.0633	0.3351
chr4	191154276	11077392	0.058	0.3317
chr5	180915260	10984116	0.0607	0.3283
chr6	171115067	10494526	0.0613	0.3473
chr7	159138663	9959608	0.0626	0.4102
chr8	146364022	9127030	0.0624	0.381
chr9	141213431	7770925	0.055	0.3306
chr10	135534747	8960967	0.0661	0.3561
chr11	135006516	8540450	0.0633	0.4261
chr12	133851895	8390997	0.0627	0.3353
chr13	115169878	5639767	0.049	0.2986
chr14	107349540	5832147	0.0543	0.3166
chr15	102531392	5580617	0.0544	0.3161
chr16	90354753	5962624	0.066	0.4025
chr17	81195210	5655639	0.0697	0.3708
chr18	78077248	4692548	0.0601	0.3761
chr19	59128983	4342841	0.0734	0.4169
chr20	63025520	4452515	0.0706	0.3692
chr21	48129895	2472053	0.0514	0.3441
chr22	51304566	2711917	0.0529	0.3508
chrMT	16571	19962	1.2046	1.787
chrX	155270560	5456596	0.0351	0.2511

chrY	59373566	1184651	0.02	0.2161

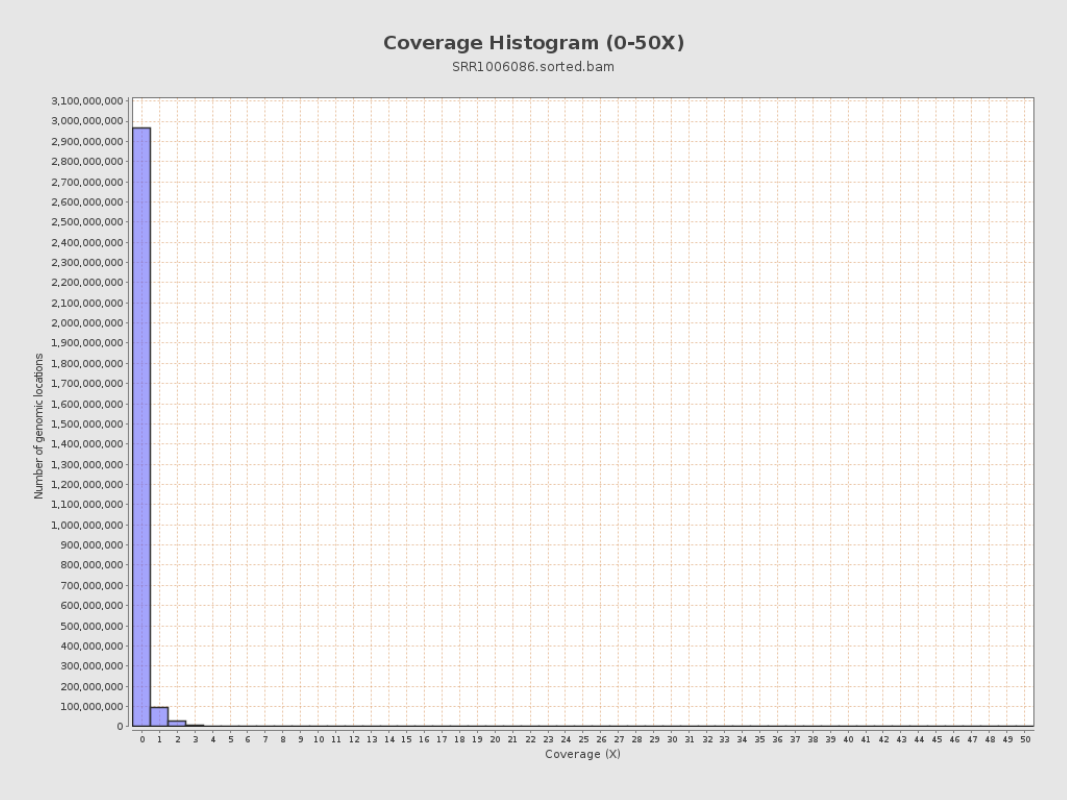
3. Results : Coverage across reference



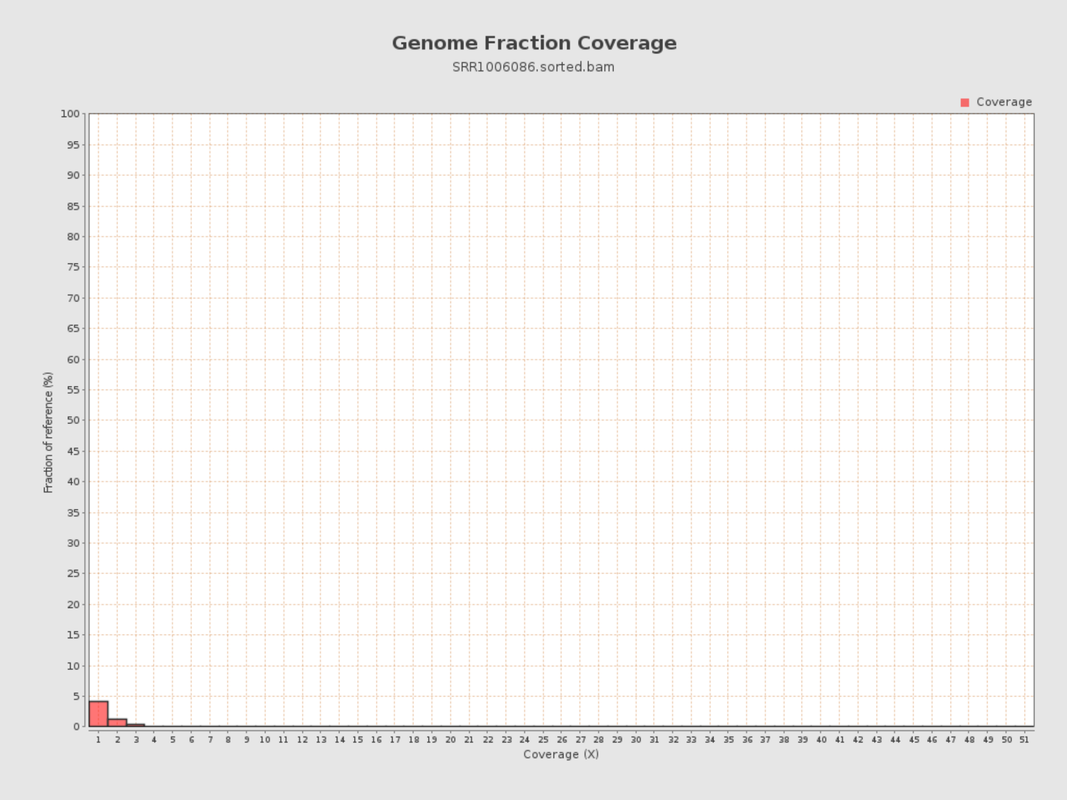
4. Results : Coverage Histogram



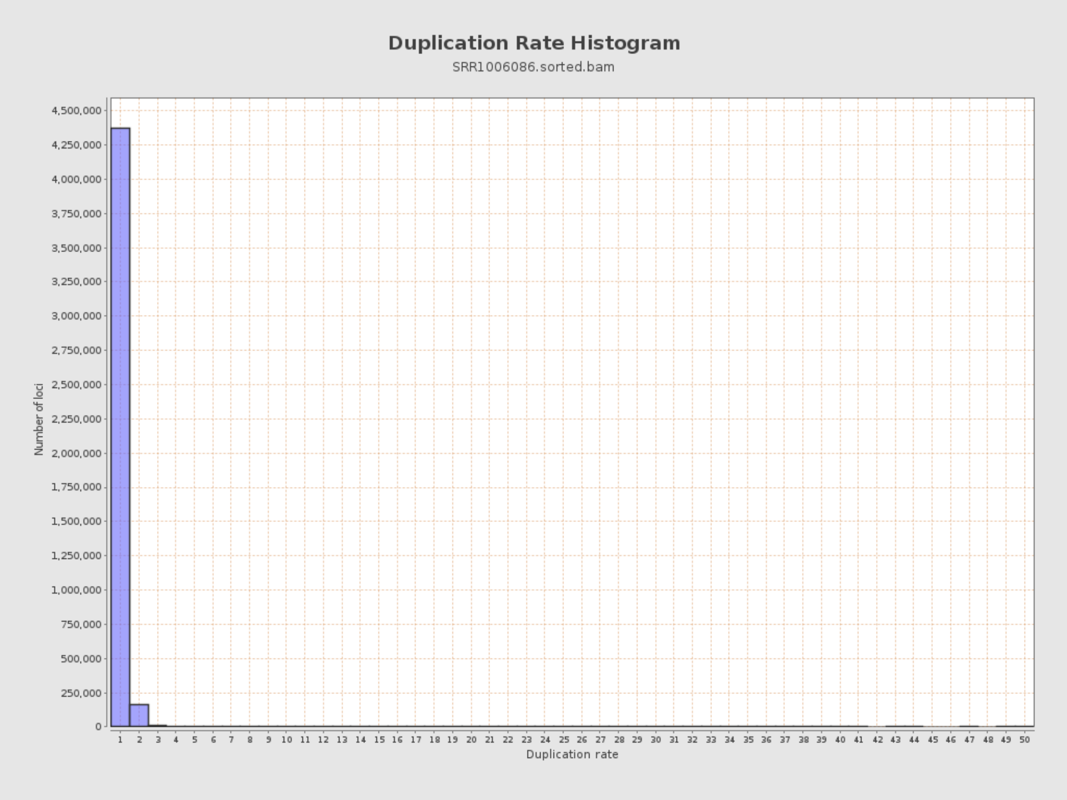
5. Results : Coverage Histogram (0-50X)



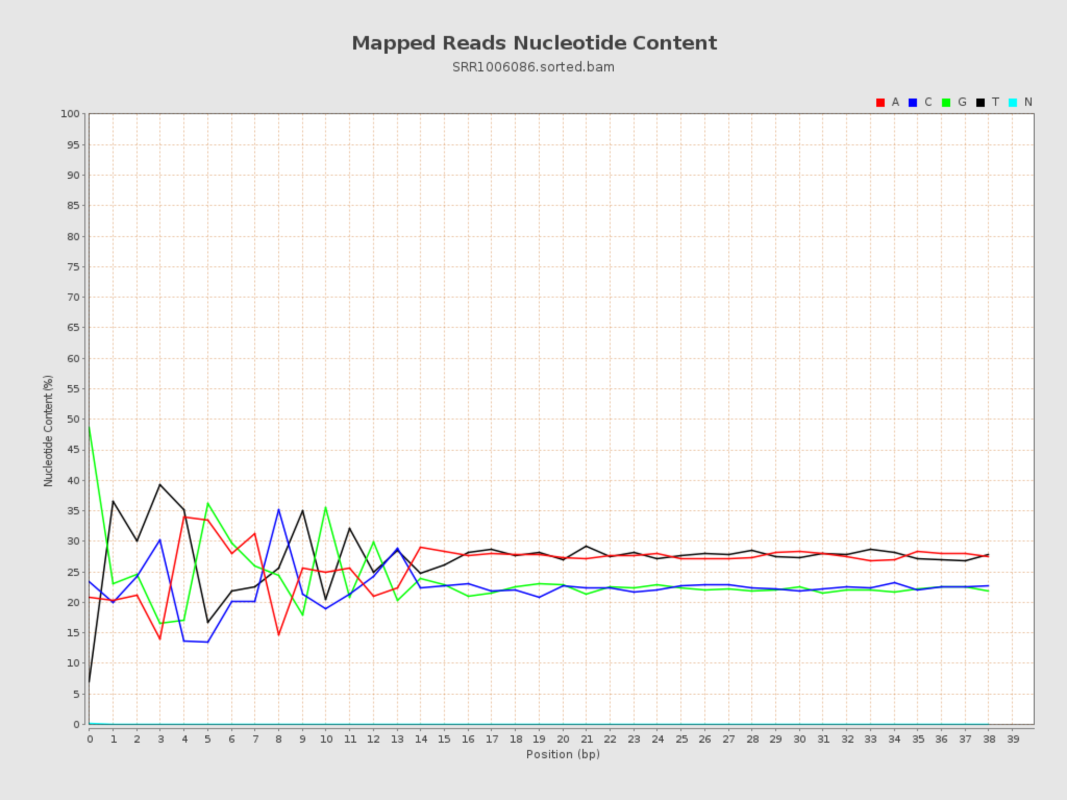
6. Results : Genome Fraction Coverage



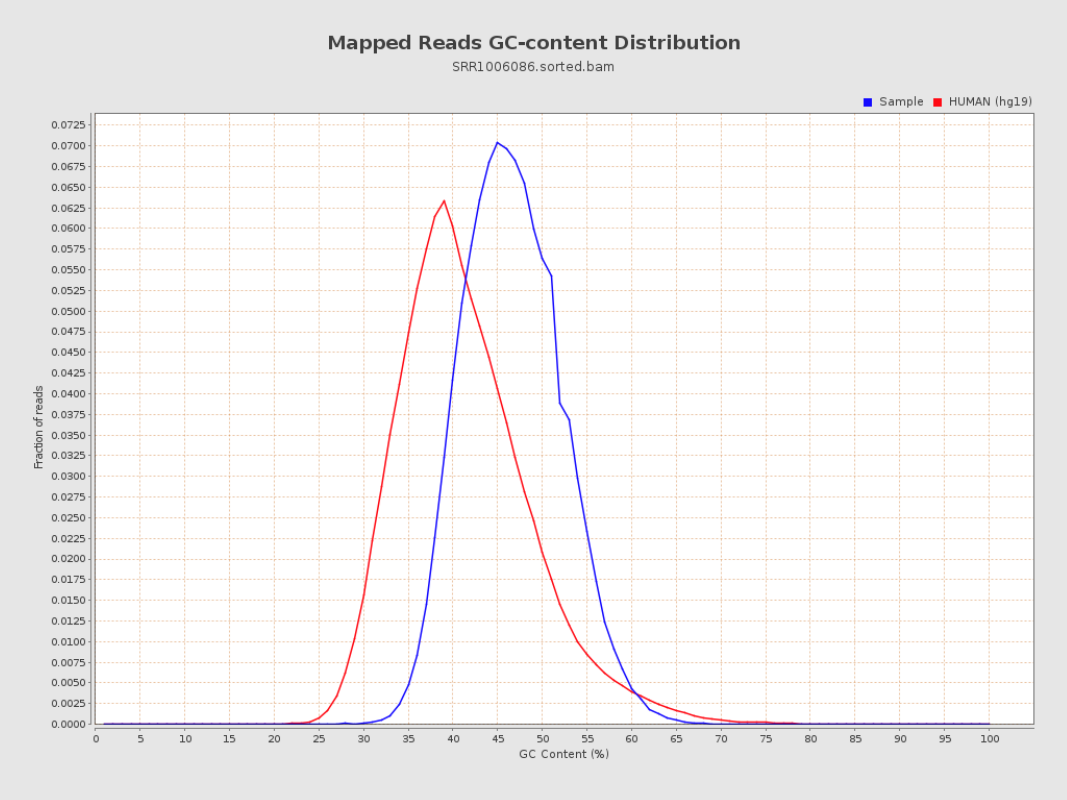
7. Results : Duplication Rate Histogram



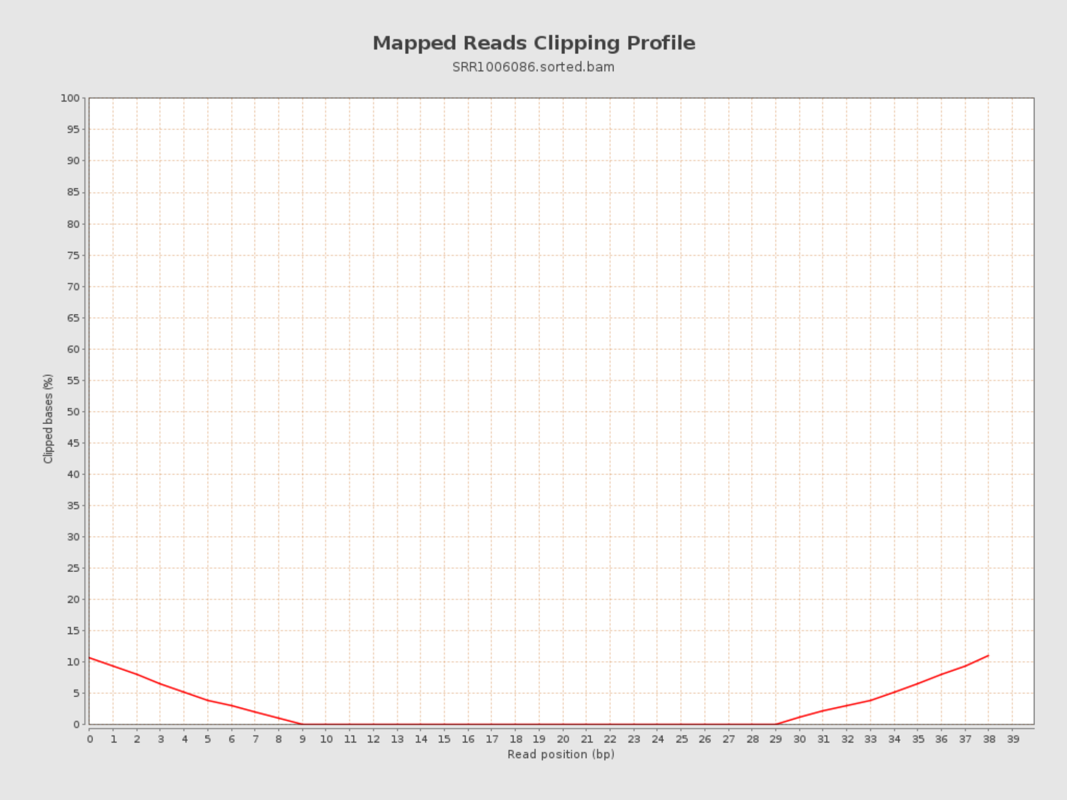
8. Results : Mapped Reads Nucleotide Content



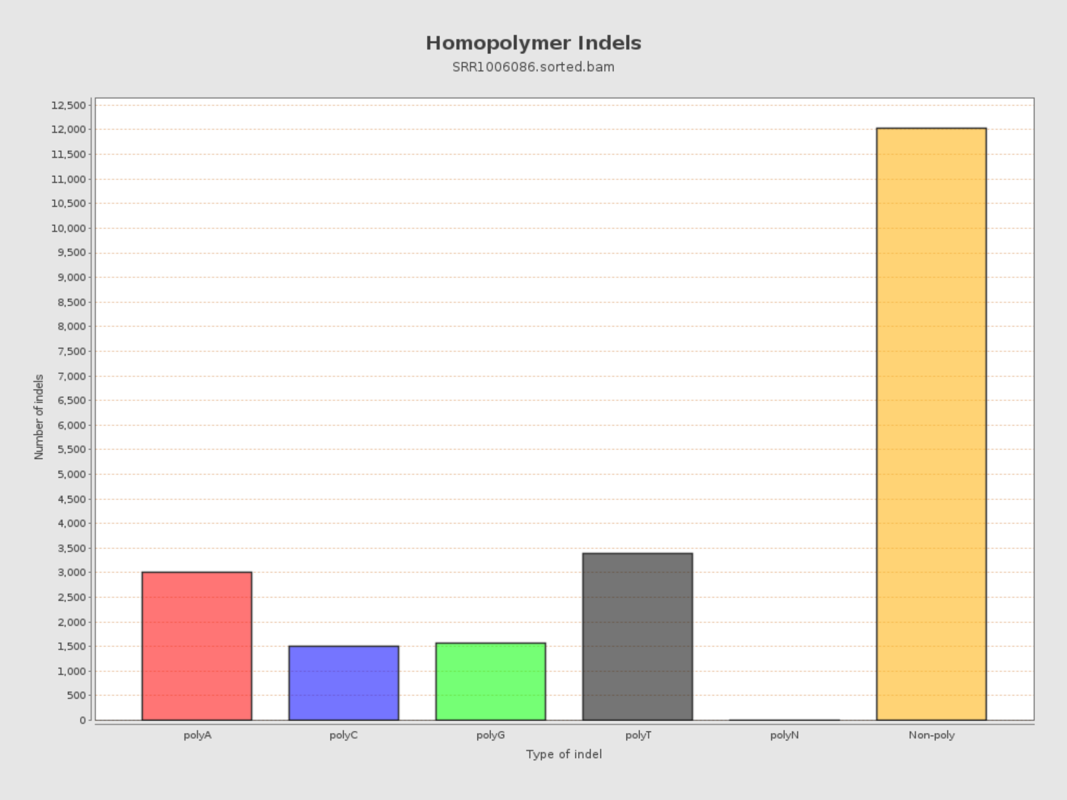
9. Results : Mapped Reads GC-content Distribution



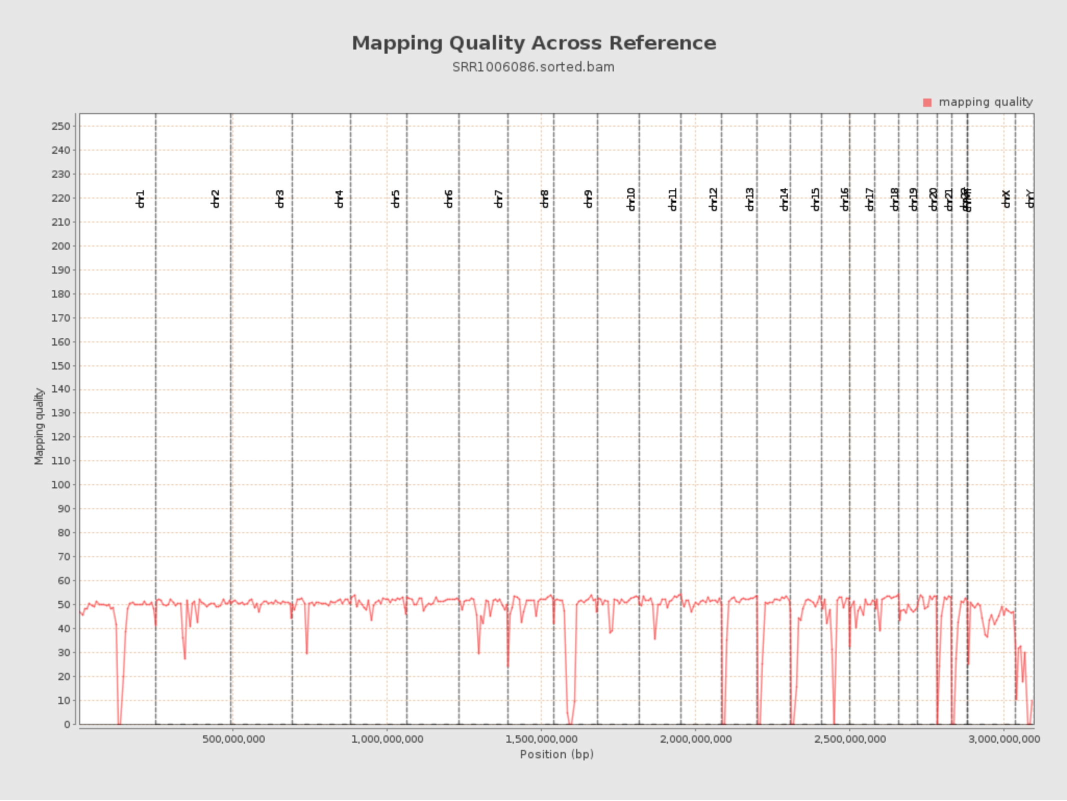
10. Results : Mapped Reads Clipping Profile



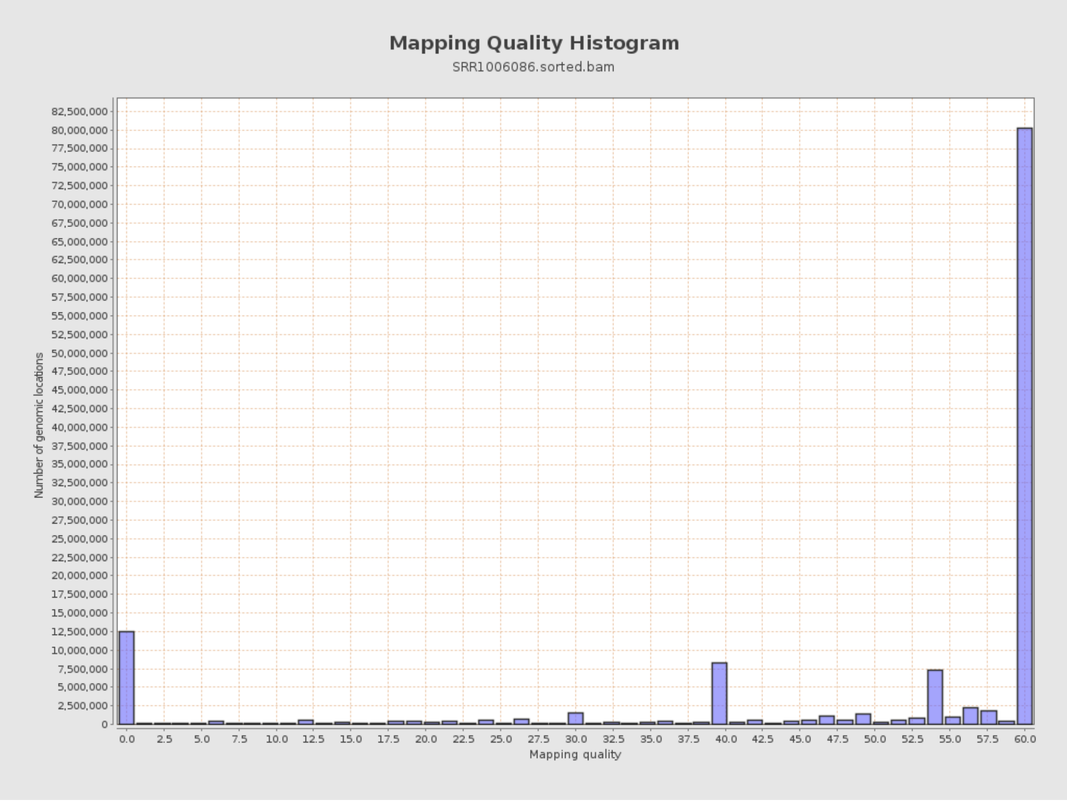
11. Results : Homopolymer Indels



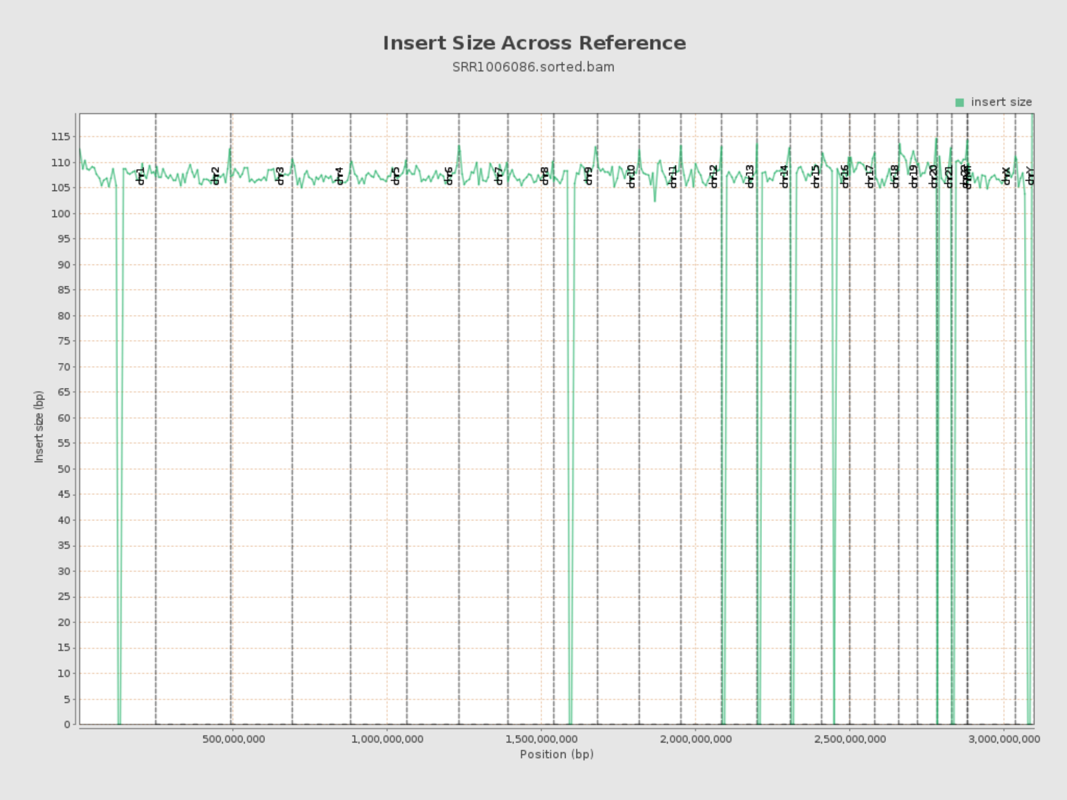
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram