Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 19:08:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006096.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_SRR1006096 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006096_1.fastq.gz SRR1006096_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 19:08:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006096.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,056,634
Mapped reads	7,851,931 / 86.7%
Unmapped reads	1,204,703 / 13.3%
Mapped paired reads	7,851,931 / 86.7%
Mapped reads, first in pair	3,993,678 / 44.1%
Mapped reads, second in pair	3,858,253 / 42.6%
Mapped reads, both in pair	7,078,570 / 78.16%
Mapped reads, singletons	773,361 / 8.54%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	531,080 / 5.86%
Duplication rate	6.09%
Clipped reads	676,626 / 7.47%

2.2. ACGT Content

Number/percentage of A's	82,323,098 / 27.17%
Number/percentage of C's	65,576,719 / 21.64%
Number/percentage of T's	85,076,382 / 28.08%
Number/percentage of G's	70,006,887 / 23.1%
Number/percentage of N's	12,268 / 0%
GC Percentage	44.75%

2.3. Coverage

Mean	0.0979
Standard Deviation	0.5501

2.4. Mapping Quality

Mean Mapping Quality	47.3

2.5. Insert size

Mean	68,518.41
Standard Deviation	2,545,223.82
P25/Median/P75	78 / 117 / 167

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	1,714,205
Insertions	10,032
Mapped reads with at least one insertion	0.13%
Deletions	26,135
Mapped reads with at least one deletion	0.33%
Homopolymer indels	45.67%

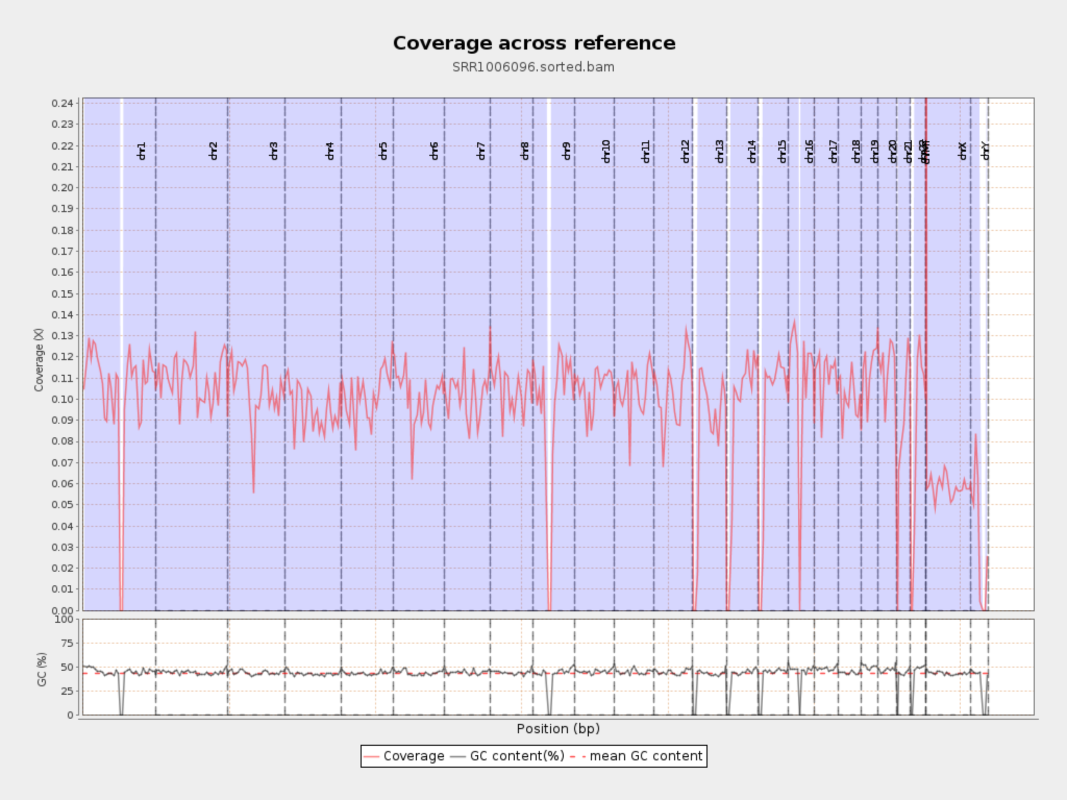
2.7. Chromosome stats

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

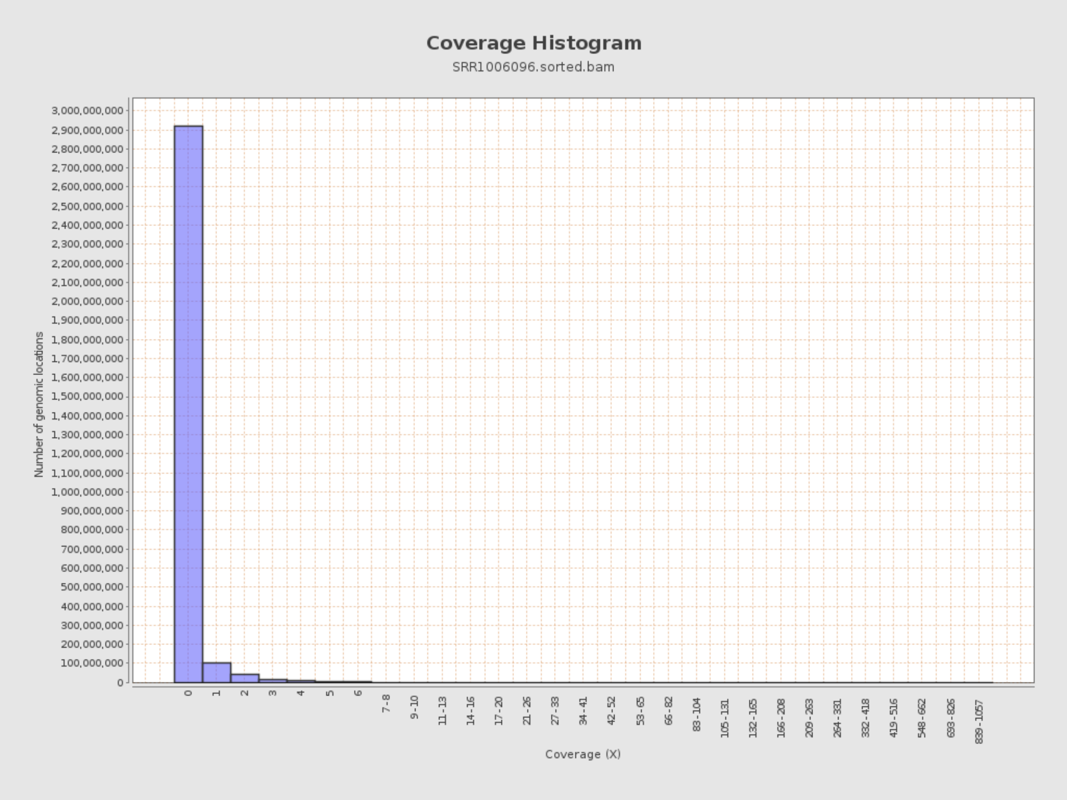
chr1	249250621	25817932	0.1036	0.6109
chr2	243199373	26678832	0.1097	0.5993
chr3	198022430	20674223	0.1044	0.4976
chr4	191154276	18296662	0.0957	0.4957
chr5	180915260	18582829	0.1027	0.4947
chr6	171115067	17215449	0.1006	0.5566
chr7	159138663	16263750	0.1022	0.6713
chr8	146364022	15306774	0.1046	0.5981
chr9	141213431	13187932	0.0934	0.5032
chr10	135534747	14278887	0.1054	0.5171
chr11	135006516	14045717	0.104	0.7626
chr12	133851895	13992500	0.1045	0.5018
chr13	115169878	9507545	0.0826	0.4453
chr14	107349540	9802984	0.0913	0.476
chr15	102531392	9266942	0.0904	0.4684
chr16	90354753	9659794	0.1069	0.5475
chr17	81195210	9115775	0.1123	0.5737
chr18	78077248	7836557	0.1004	0.6577
chr19	59128983	6726937	0.1138	0.6458
chr20	63025520	7238024	0.1148	0.5317
chr21	48129895	4219223	0.0877	0.5125
chr22	51304566	4167230	0.0812	0.4689
chrMT	16571	17626	1.0637	2.1363
chrX	155270560	9090712	0.0585	0.3959

chrY	59373566	2037425	0.0343	0.3189

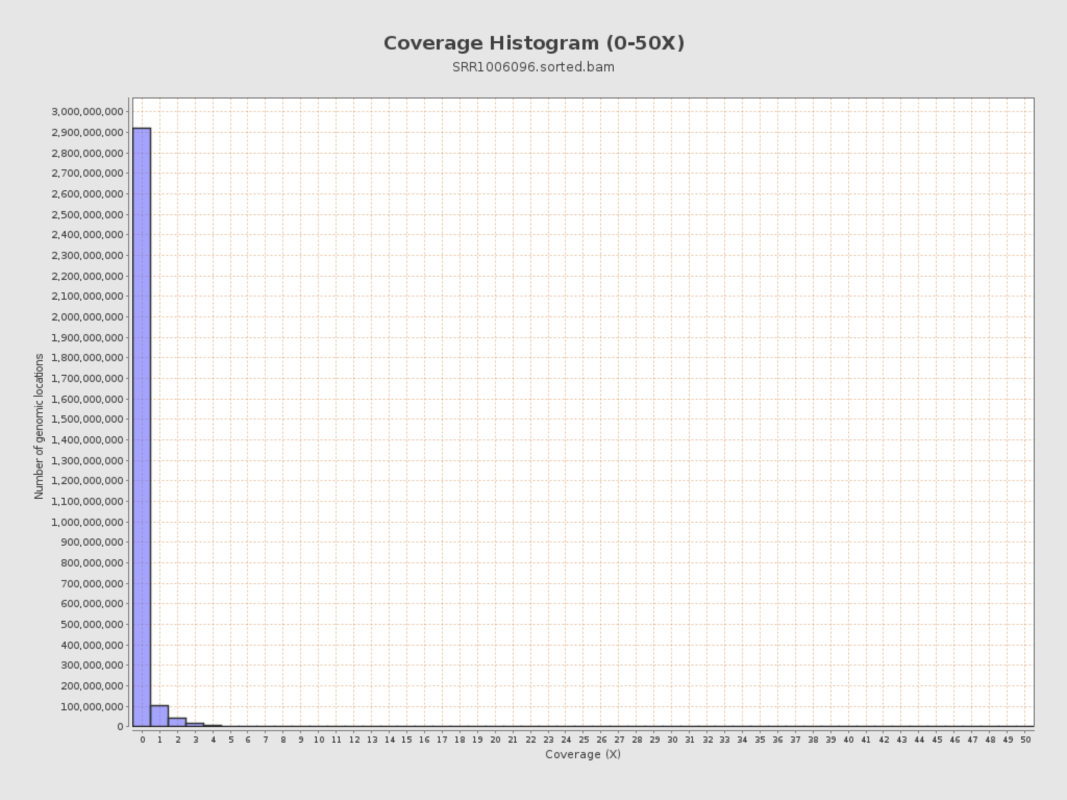
3. Results : Coverage across reference



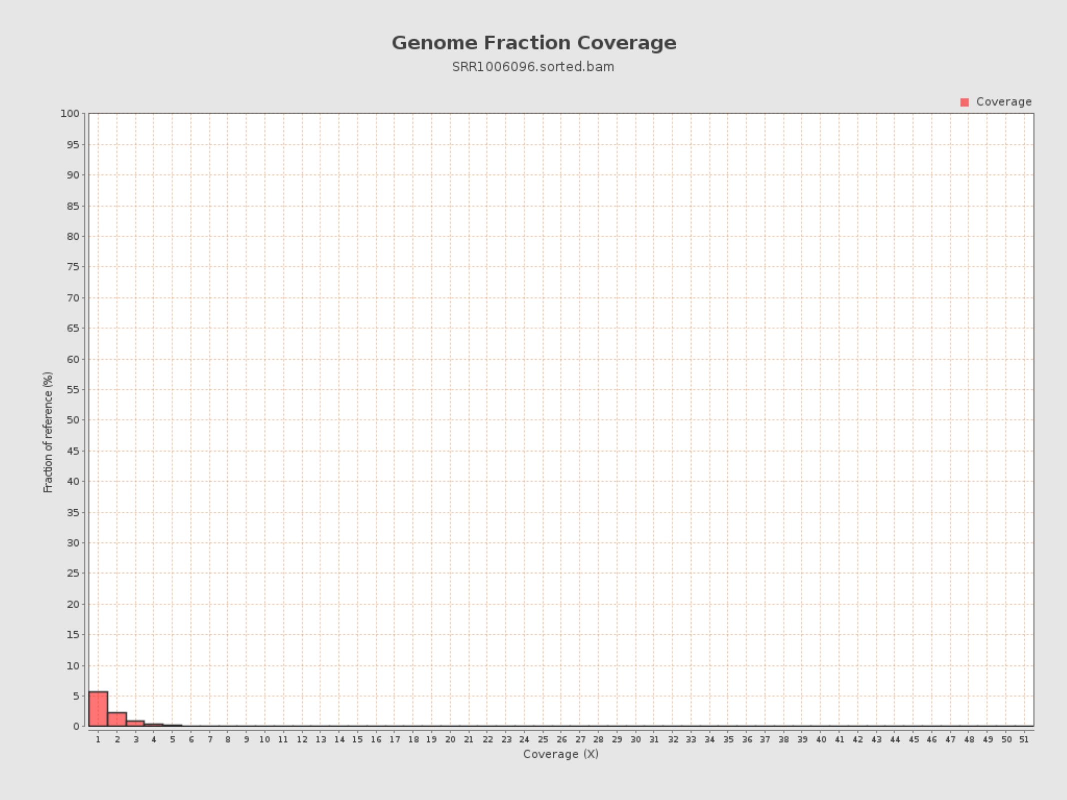
4. Results : Coverage Histogram



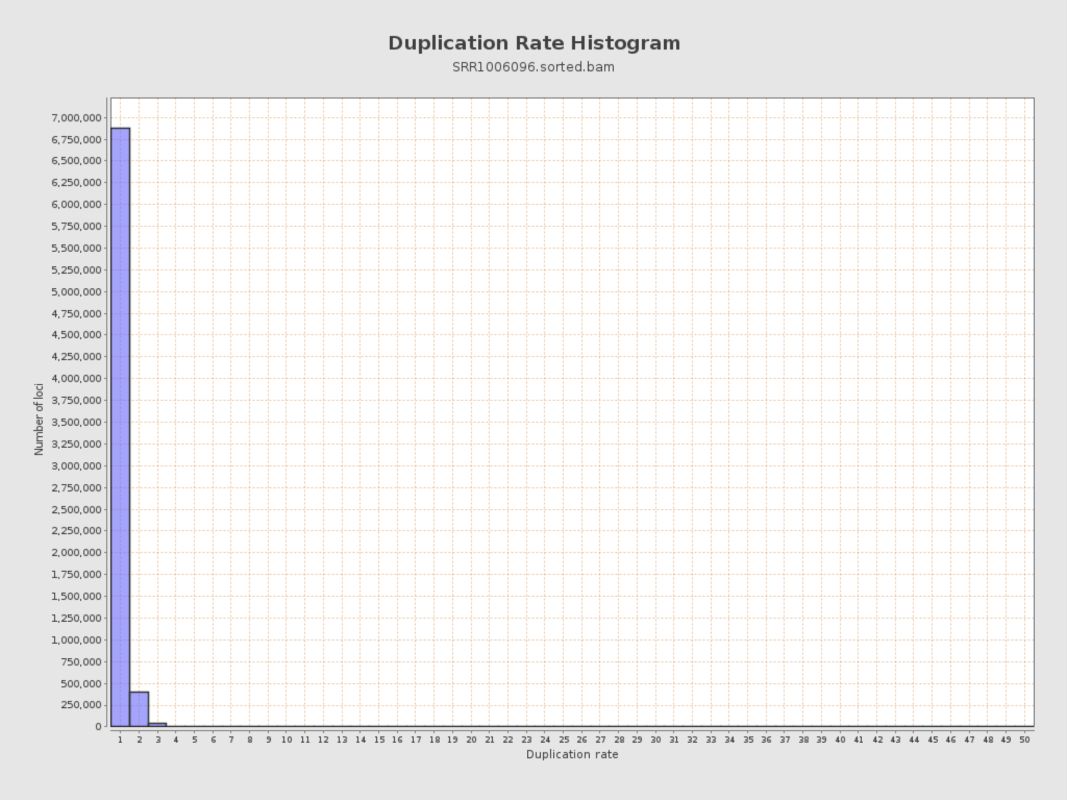
5. Results : Coverage Histogram (0-50X)



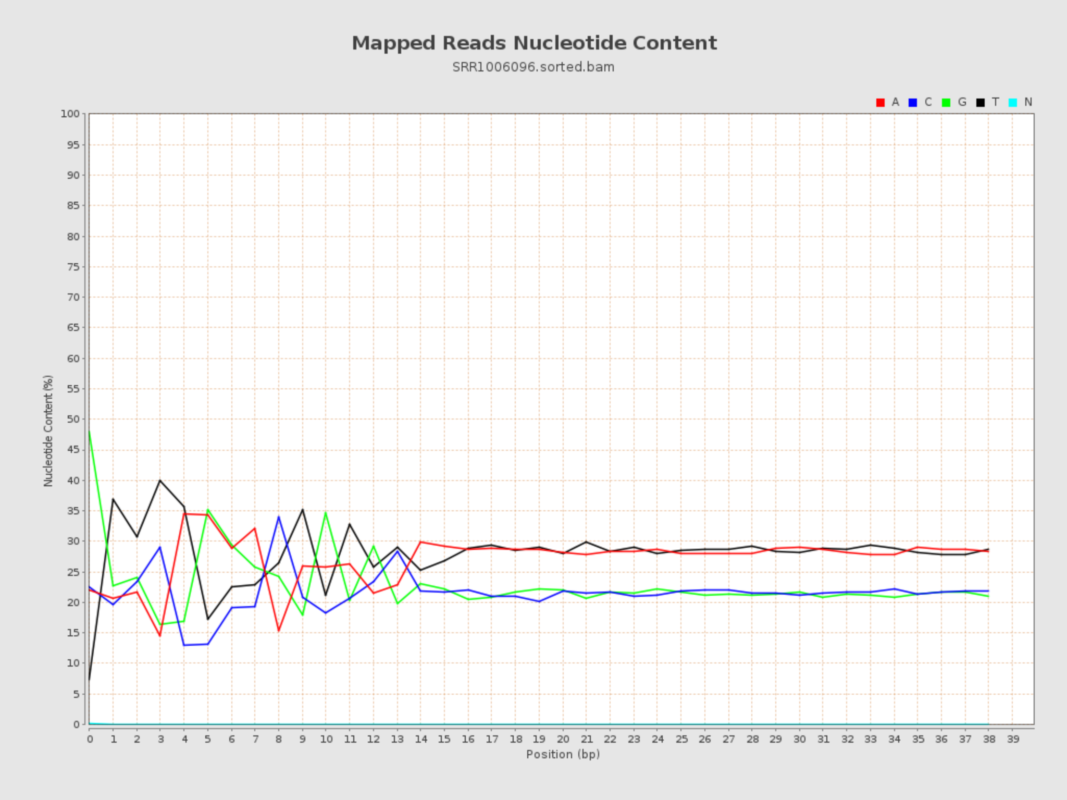
6. Results : Genome Fraction Coverage



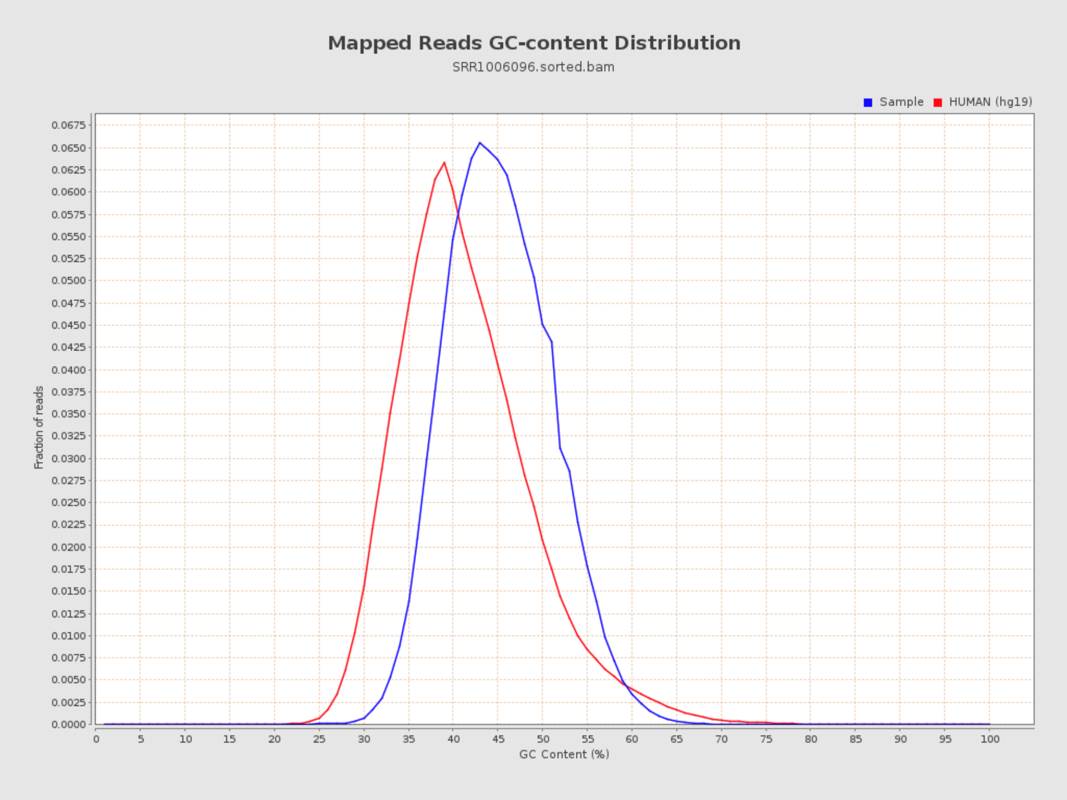
7. Results : Duplication Rate Histogram



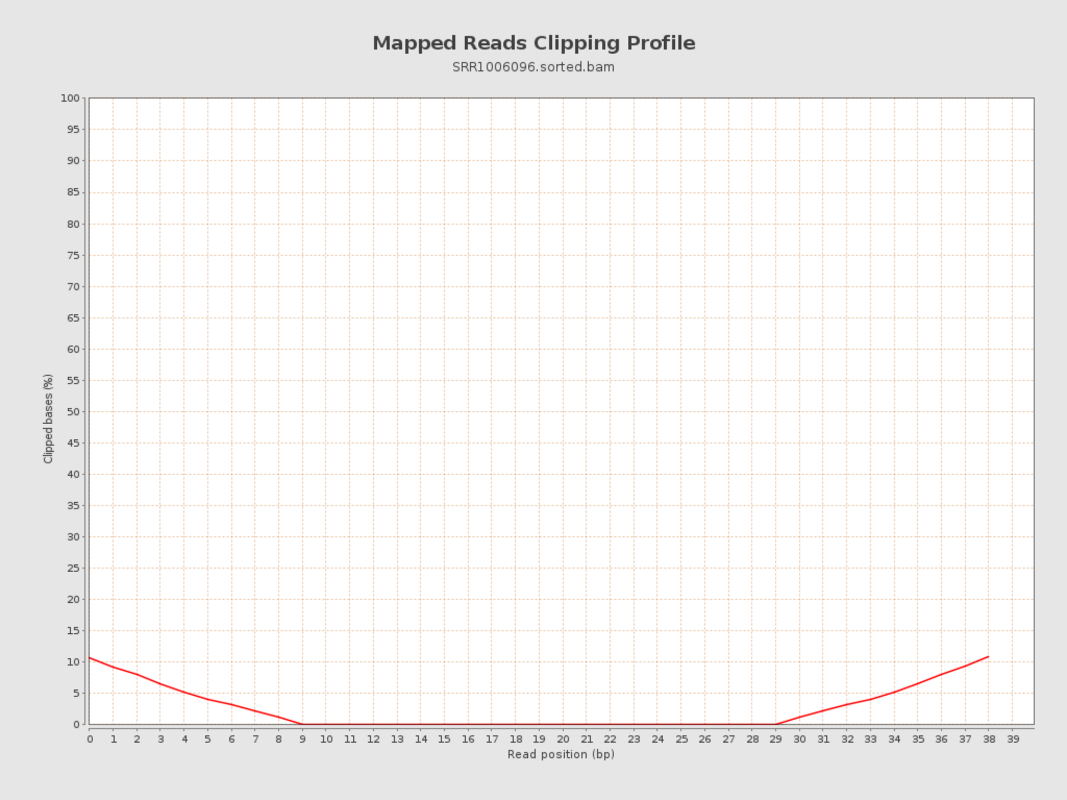
8. Results : Mapped Reads Nucleotide Content



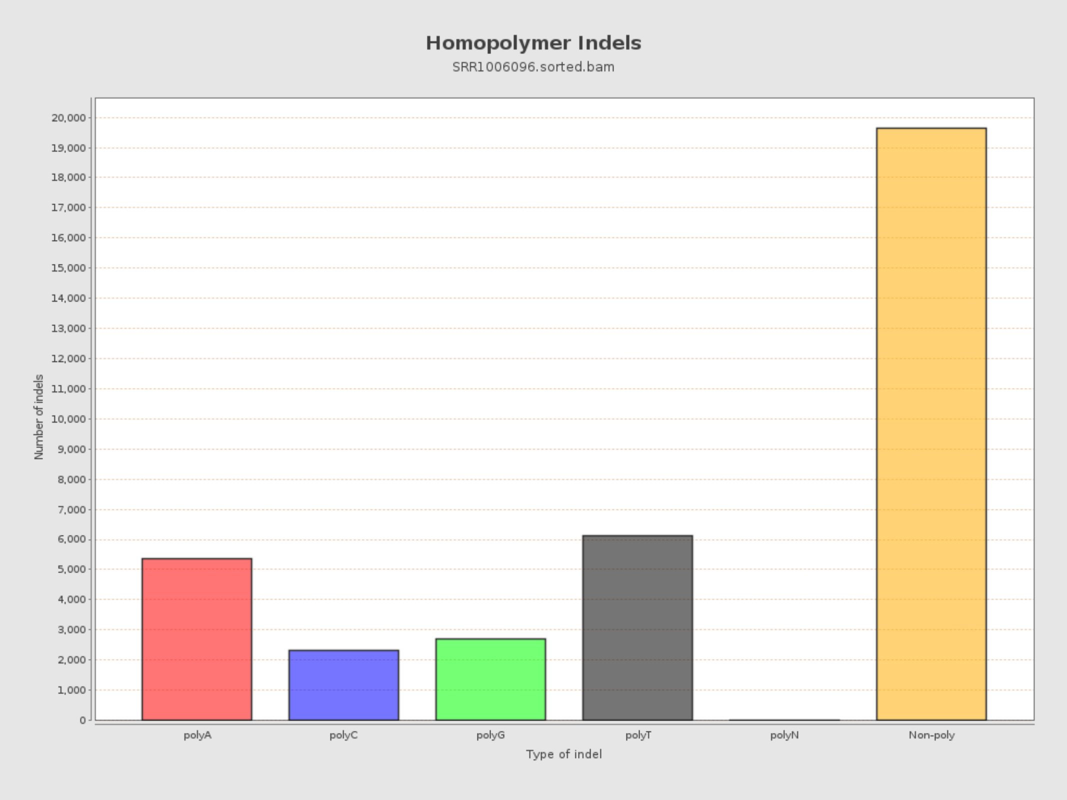
9. Results : Mapped Reads GC-content Distribution



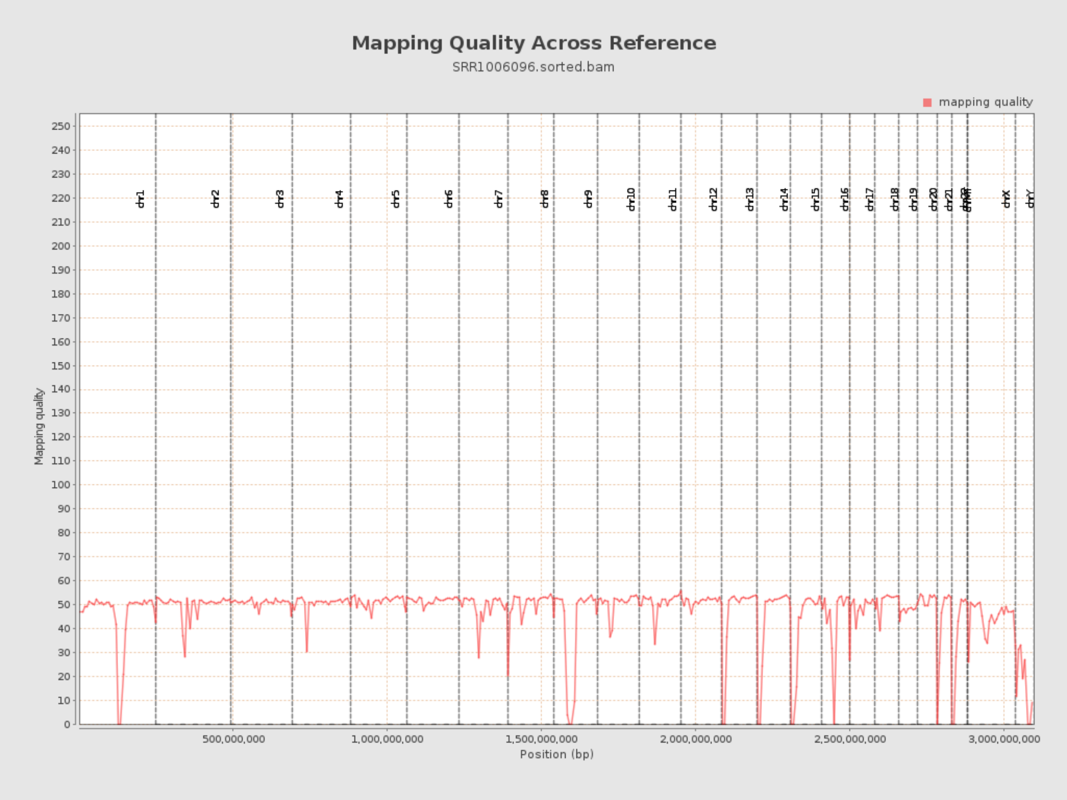
10. Results : Mapped Reads Clipping Profile



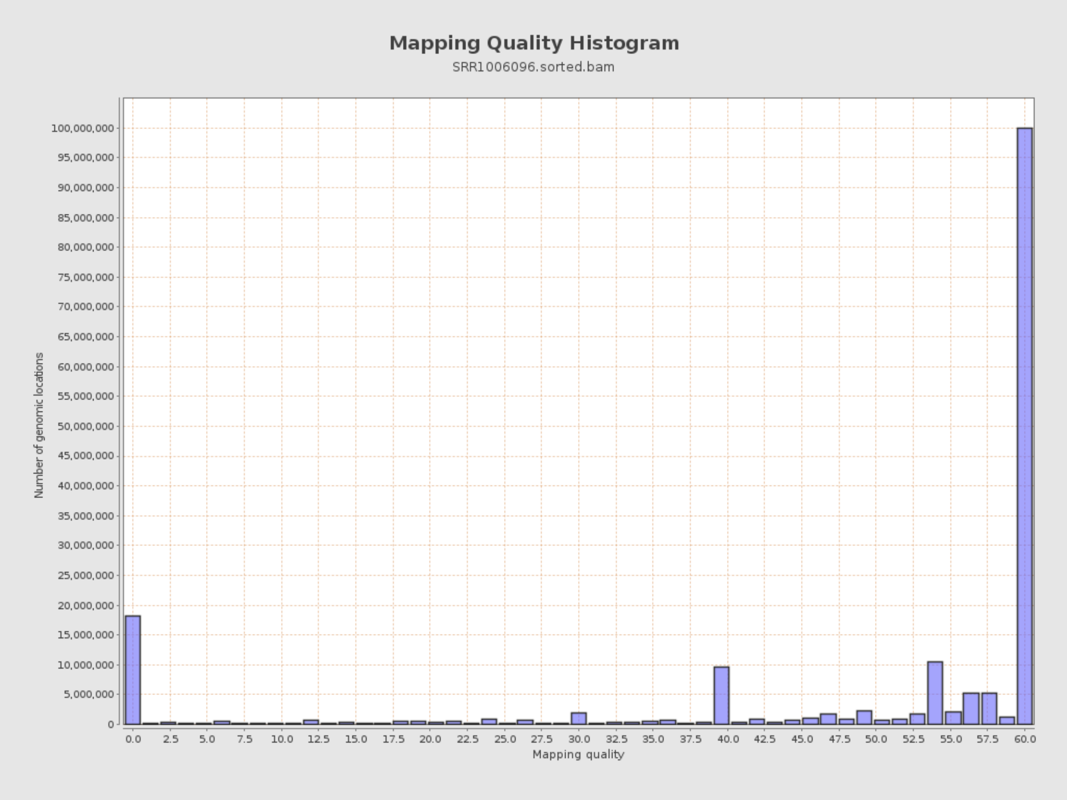
11. Results : Homopolymer Indels



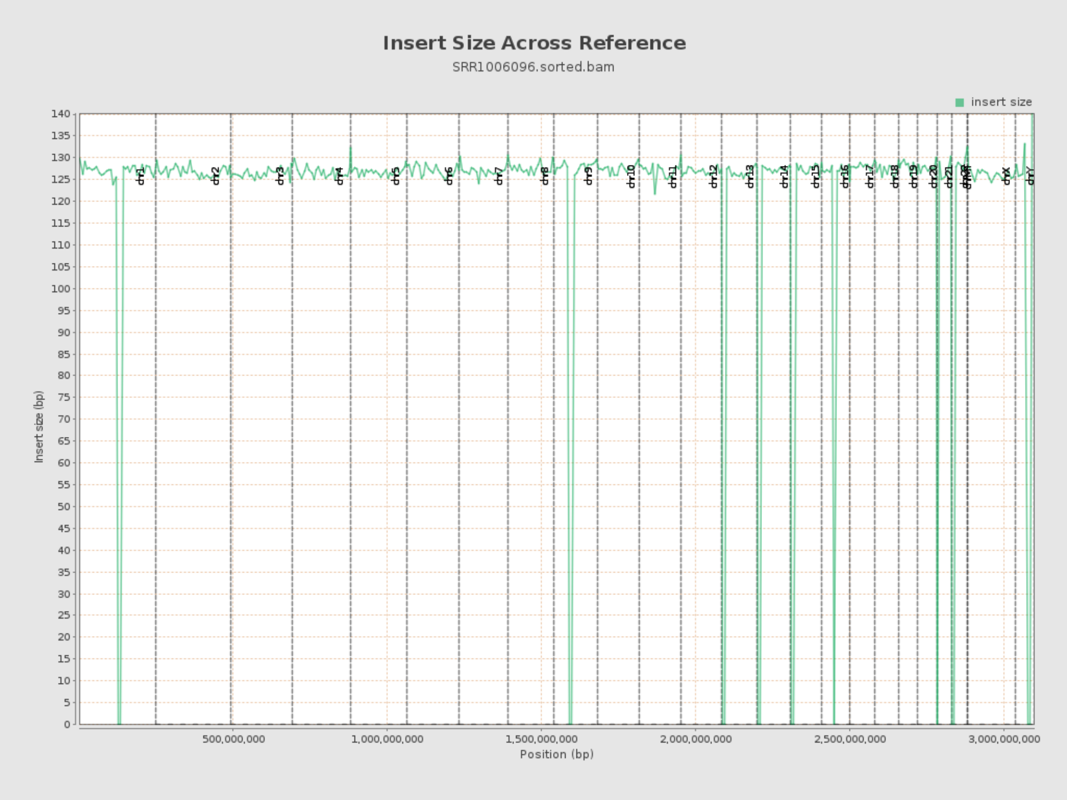
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram