Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 01:11:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006396.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_SRR1006396 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006396_1.fastq.gz SRR1006396_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 01:11:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006396.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,423,000
Mapped reads	5,046,401 / 78.57%
Unmapped reads	1,376,599 / 21.43%
Mapped paired reads	5,046,401 / 78.57%
Mapped reads, first in pair	2,556,704 / 39.81%
Mapped reads, second in pair	2,489,697 / 38.76%
Mapped reads, both in pair	4,642,242 / 72.28%
Mapped reads, singletons	404,159 / 6.29%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	190,763 / 2.97%
Duplication rate	3.23%
Clipped reads	260,789 / 4.06%

2.2. ACGT Content

Number/percentage of A's	55,300,387 / 28.29%
Number/percentage of C's	41,646,845 / 21.31%
Number/percentage of T's	55,693,850 / 28.49%
Number/percentage of G's	42,808,830 / 21.9%
Number/percentage of N's	8,403 / 0%
GC Percentage	43.21%

2.3. Coverage

Mean	0.0631
Standard Deviation	0.3905

2.4. Mapping Quality

Mean Mapping Quality	48.5

2.5. Insert size

Mean	67,261.69
Standard Deviation	2,467,249.33
P25/Median/P75	113 / 145 / 194

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	711,258
Insertions	5,230
Mapped reads with at least one insertion	0.1%
Deletions	17,498
Mapped reads with at least one deletion	0.35%
Homopolymer indels	43.84%

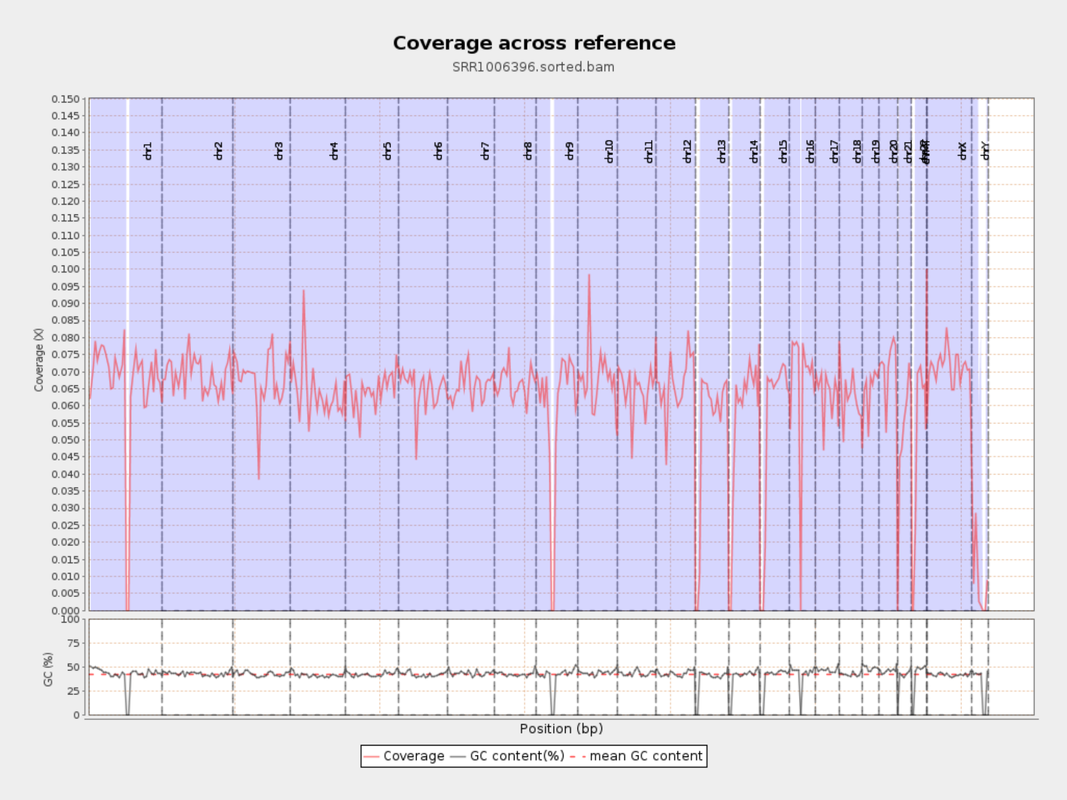
2.7. Chromosome stats

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

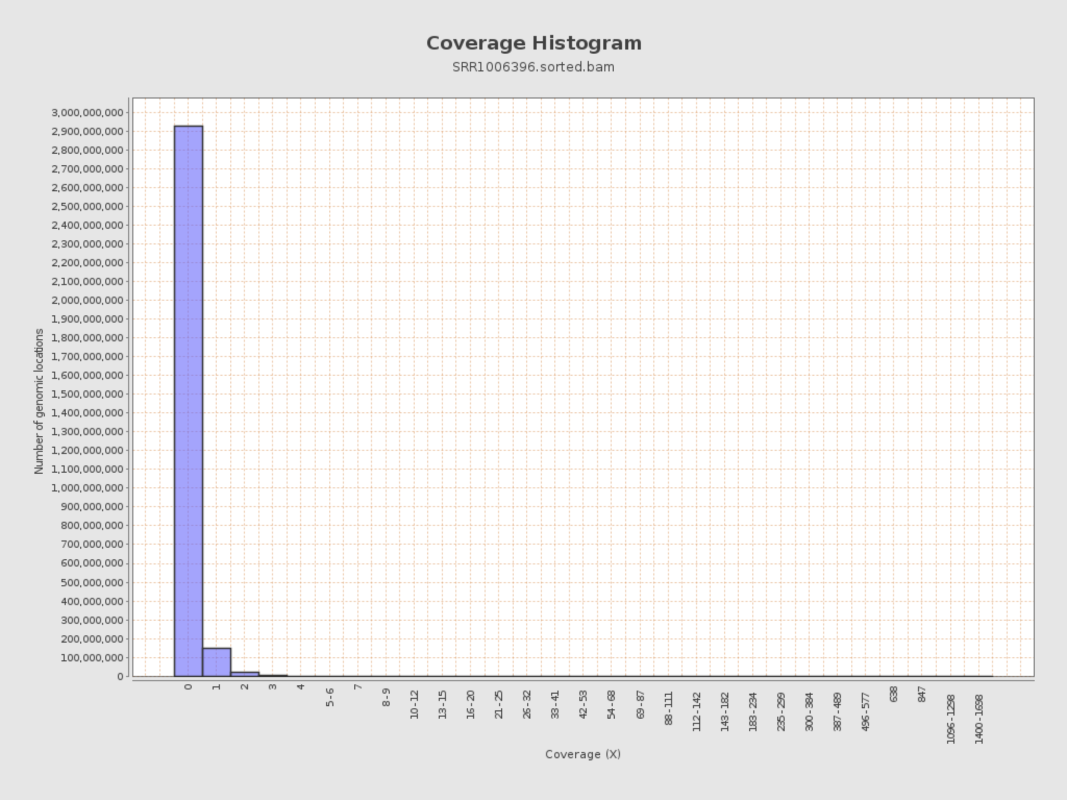
chr1	249250621	16494044	0.0662	0.5088
chr2	243199373	16829499	0.0692	0.3741
chr3	198022430	13420674	0.0678	0.2912
chr4	191154276	12200532	0.0638	0.318
chr5	180915260	11698089	0.0647	0.3144
chr6	171115067	11162496	0.0652	0.3148
chr7	159138663	10472792	0.0658	0.4207
chr8	146364022	9740163	0.0665	0.878
chr9	141213431	8183851	0.058	0.3034
chr10	135534747	9270018	0.0684	0.4133
chr11	135006516	8719829	0.0646	0.3328
chr12	133851895	8897201	0.0665	0.2901
chr13	115169878	6040710	0.0525	0.2555
chr14	107349540	5910993	0.0551	0.2764
chr15	102531392	5617313	0.0548	0.2624
chr16	90354753	6016064	0.0666	0.353
chr17	81195210	5152592	0.0635	0.2944
chr18	78077248	4900062	0.0628	0.4585
chr19	59128983	3817216	0.0646	0.3978
chr20	63025520	4489871	0.0712	0.312
chr21	48129895	2503454	0.052	0.2935
chr22	51304566	2403483	0.0468	0.246
chrMT	16571	1661	0.1002	0.3336
chrX	155270560	11019690	0.071	0.3166

chrY	59373566	519475	0.0087	0.2281

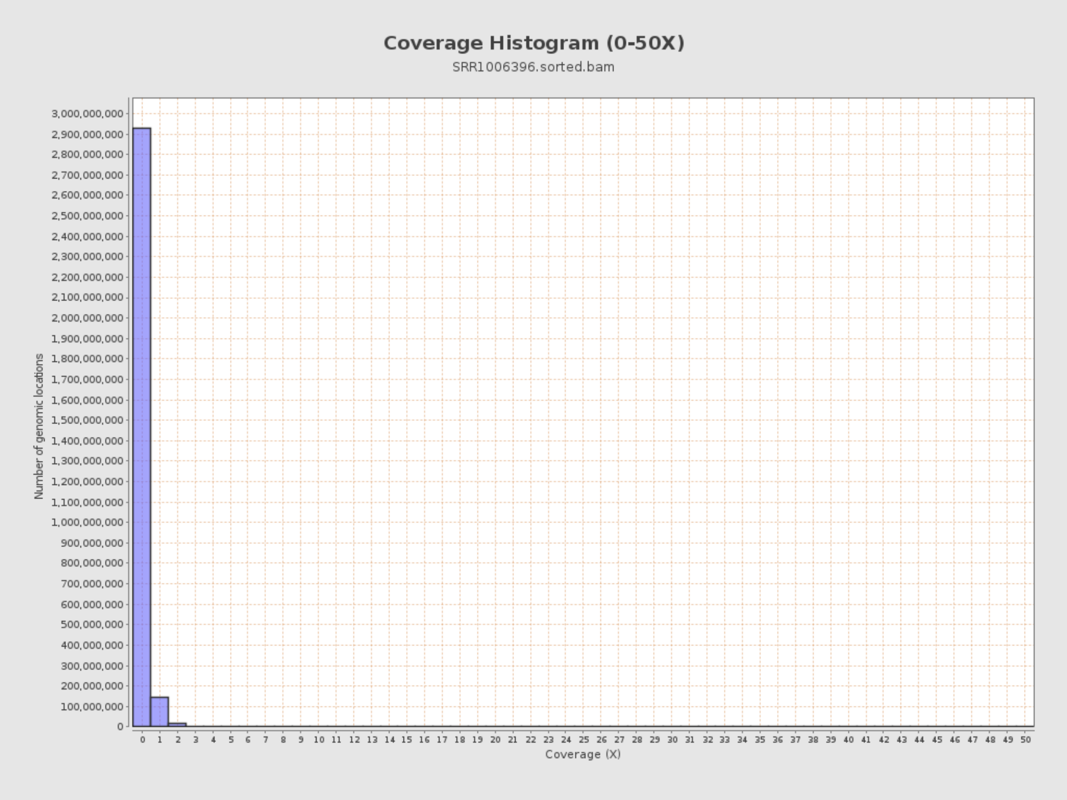
3. Results : Coverage across reference



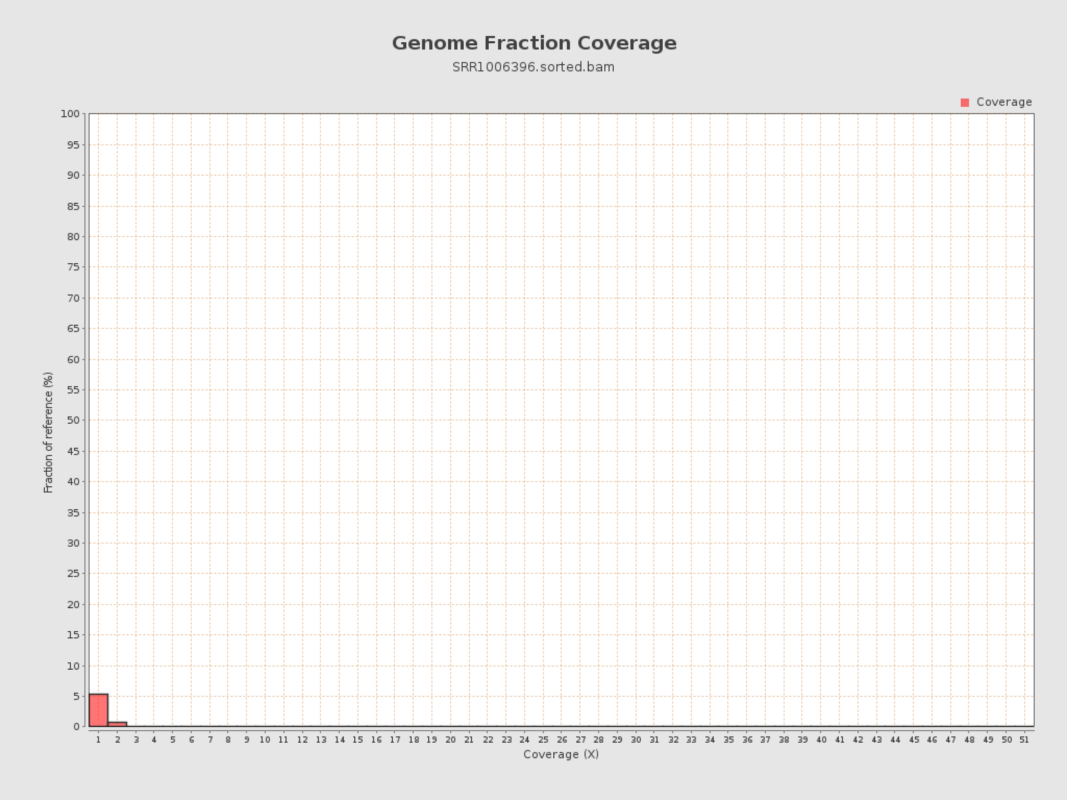
4. Results : Coverage Histogram



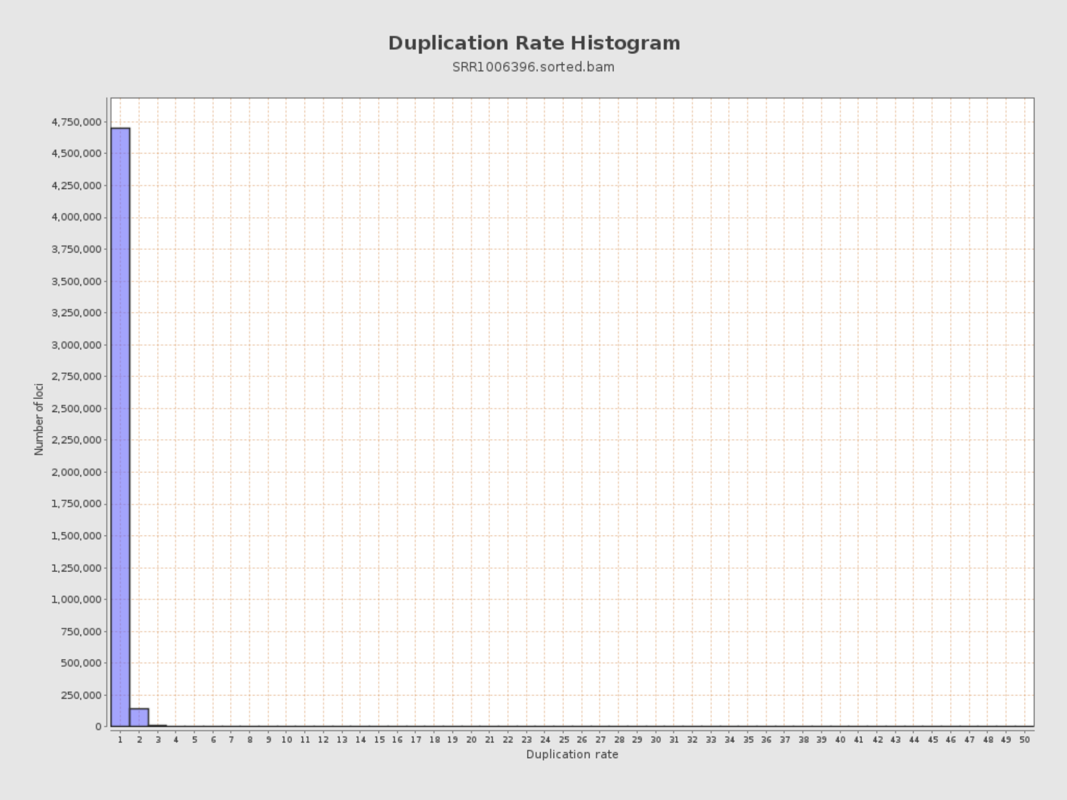
5. Results : Coverage Histogram (0-50X)



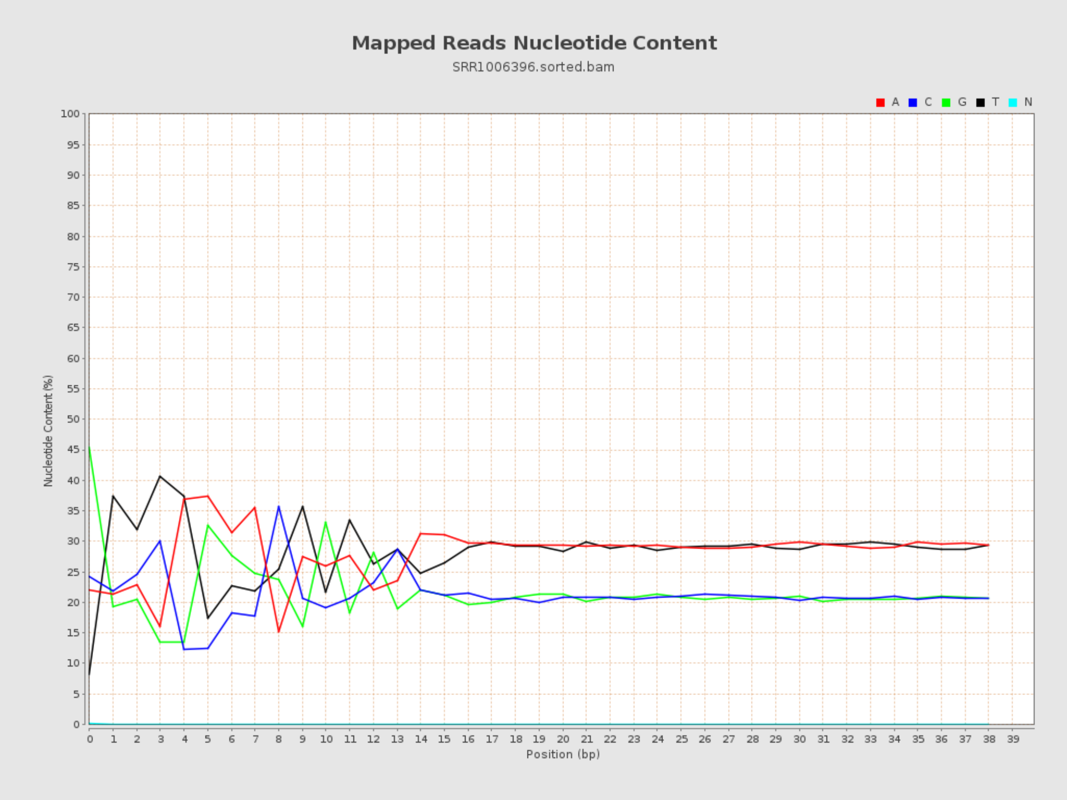
6. Results : Genome Fraction Coverage



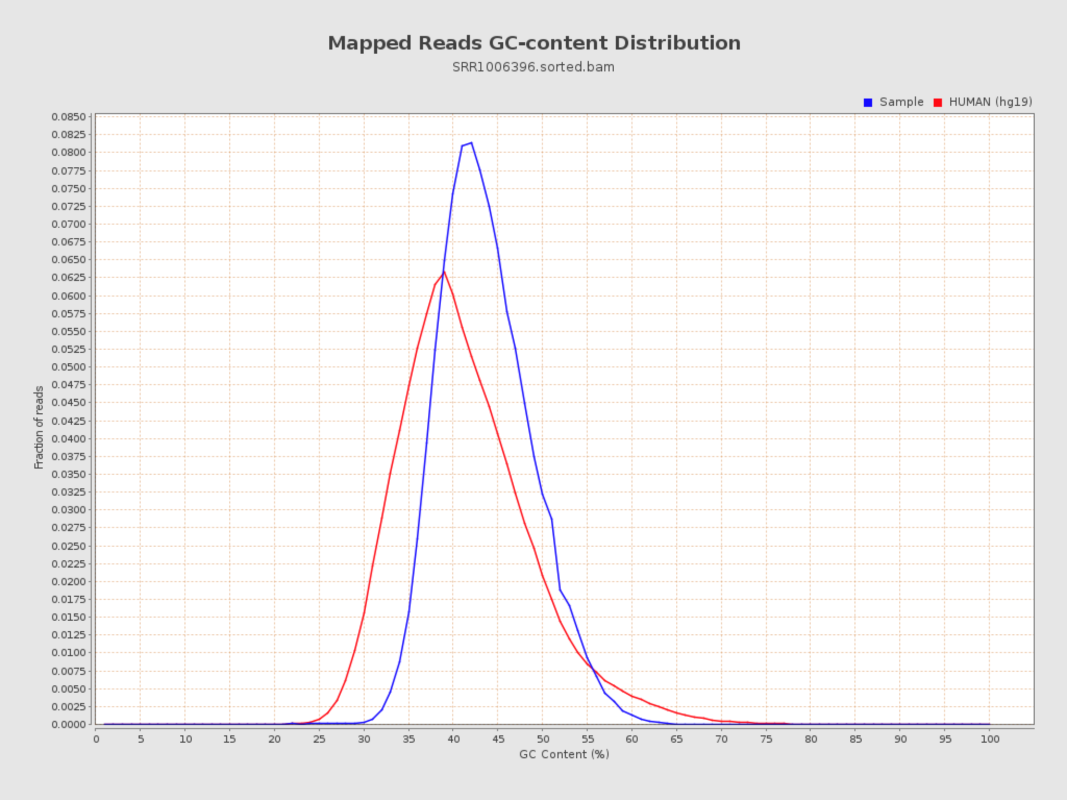
7. Results : Duplication Rate Histogram



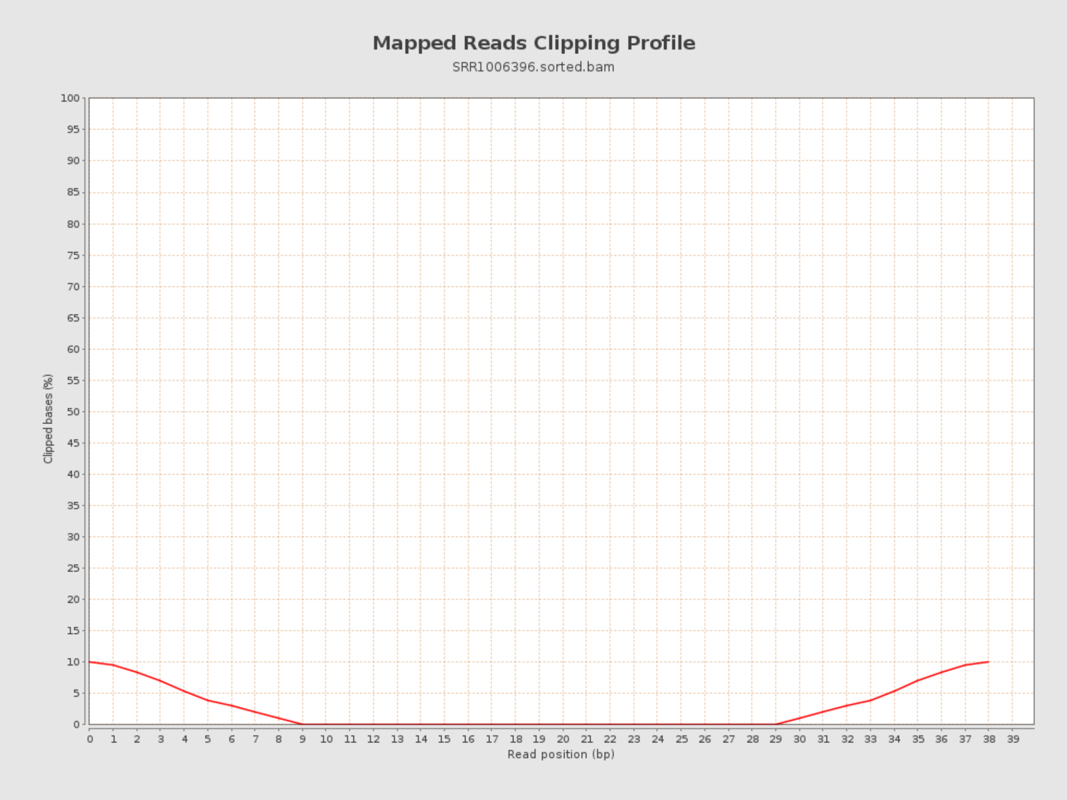
8. Results : Mapped Reads Nucleotide Content



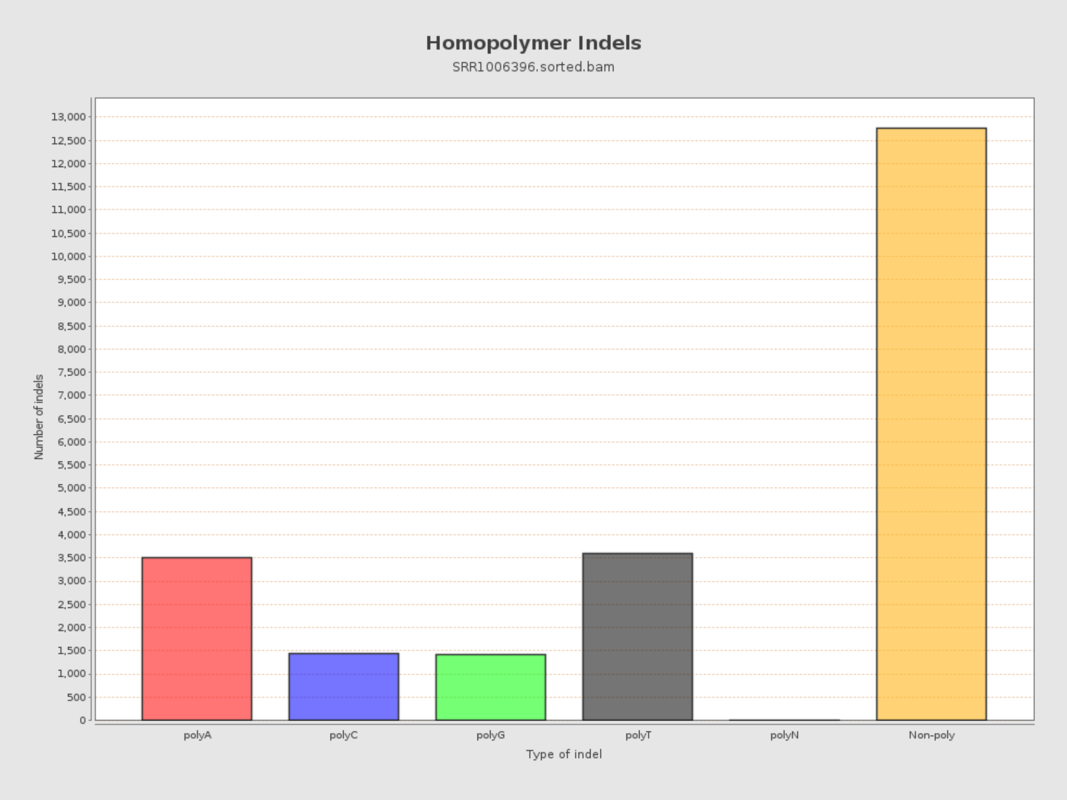
9. Results : Mapped Reads GC-content Distribution



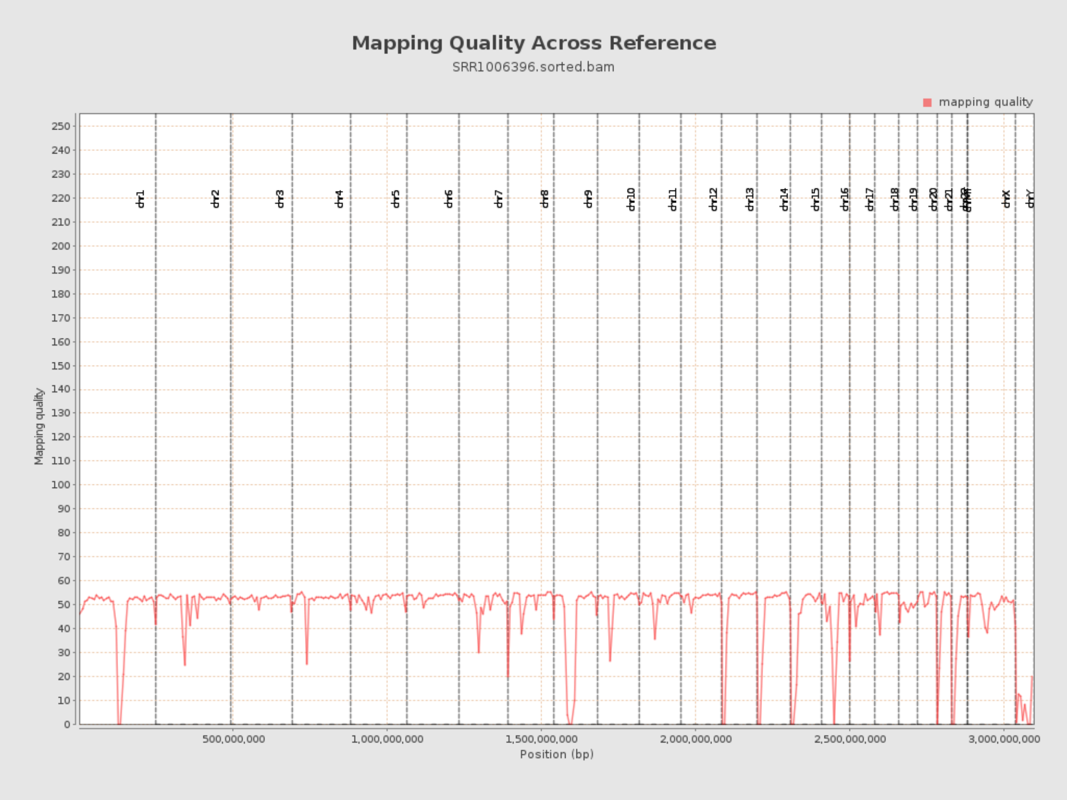
10. Results : Mapped Reads Clipping Profile



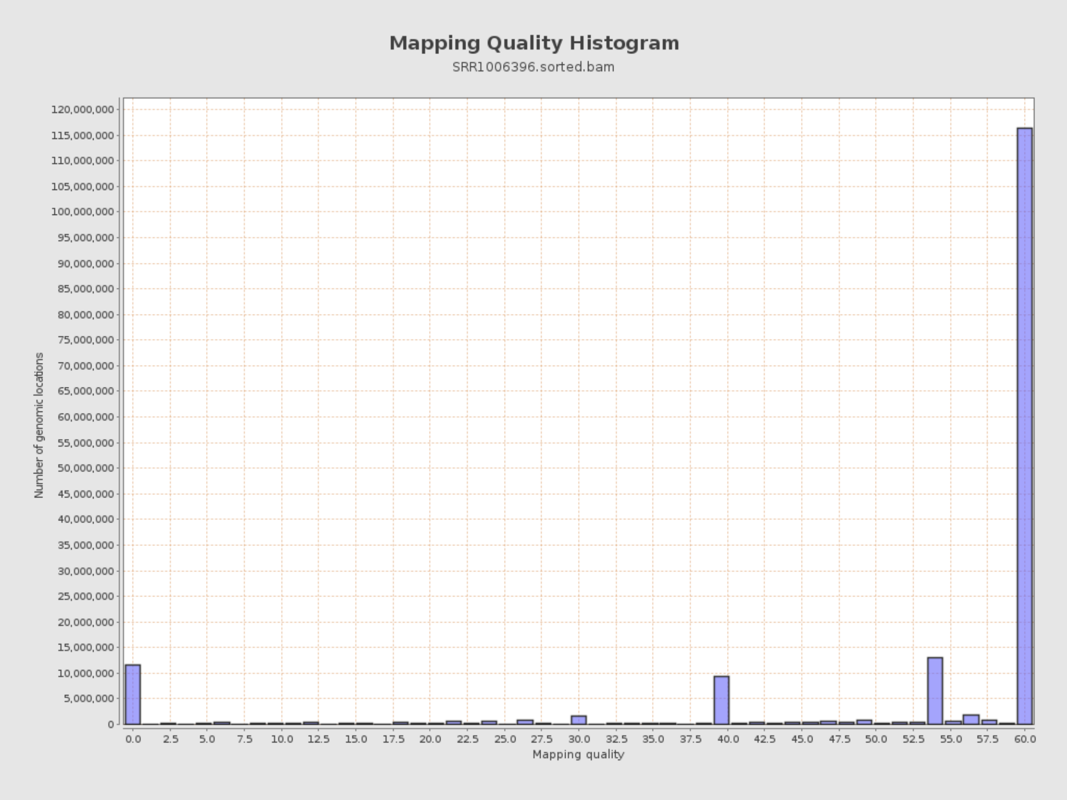
11. Results : Homopolymer Indels



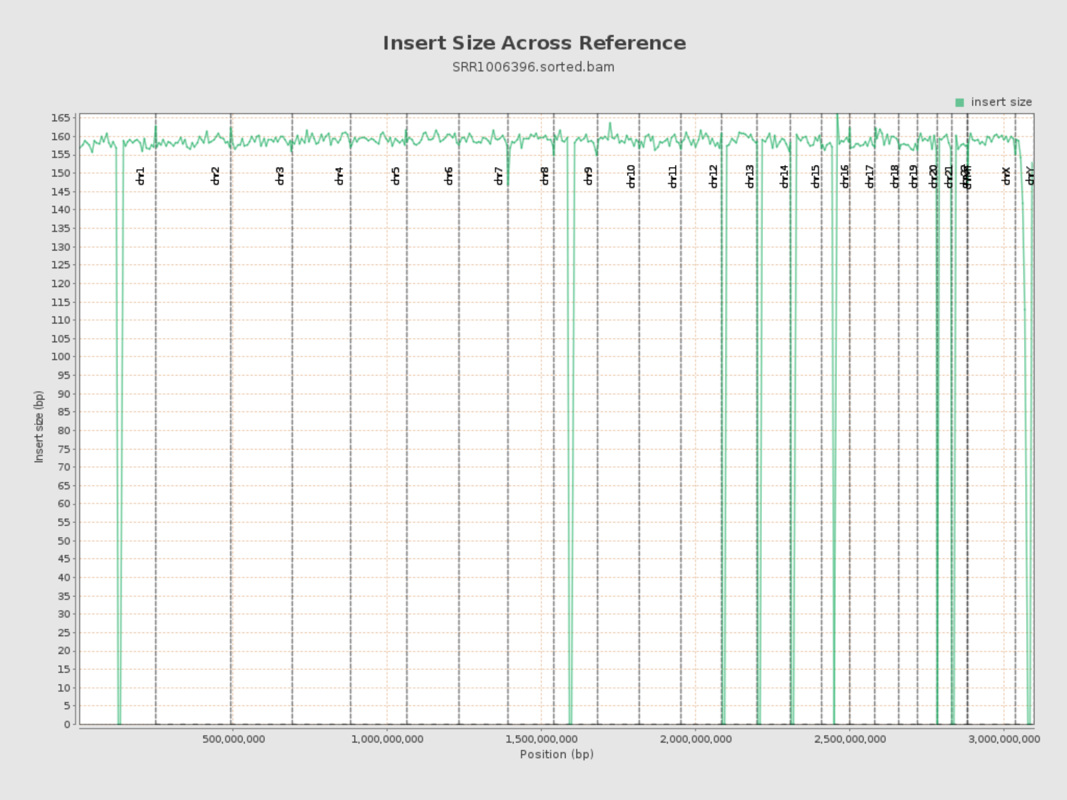
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram