Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 19:28:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006101.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_SRR1006101 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006101_1.fastq.gz SRR1006101_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 19:28:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006101.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,918,994
Mapped reads	6,884,362 / 86.93%
Unmapped reads	1,034,632 / 13.07%
Mapped paired reads	6,884,362 / 86.93%
Mapped reads, first in pair	3,504,076 / 44.25%
Mapped reads, second in pair	3,380,286 / 42.69%
Mapped reads, both in pair	6,221,970 / 78.57%
Mapped reads, singletons	662,392 / 8.36%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	508,054 / 6.42%
Duplication rate	6.71%
Clipped reads	609,484 / 7.7%

2.2. ACGT Content

Number/percentage of A's	71,288,282 / 26.85%
Number/percentage of C's	58,126,383 / 21.89%
Number/percentage of T's	73,798,762 / 27.8%
Number/percentage of G's	62,258,717 / 23.45%
Number/percentage of N's	9,996 / 0%
GC Percentage	45.35%

2.3. Coverage

Mean	0.0858
Standard Deviation	0.5243

2.4. Mapping Quality

Mean Mapping Quality	46.8

2.5. Insert size

Mean	70,670.68
Standard Deviation	2,605,504.46
P25/Median/P75	74 / 101 / 136

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	1,350,752
Insertions	8,784
Mapped reads with at least one insertion	0.13%
Deletions	23,045
Mapped reads with at least one deletion	0.33%
Homopolymer indels	45.2%

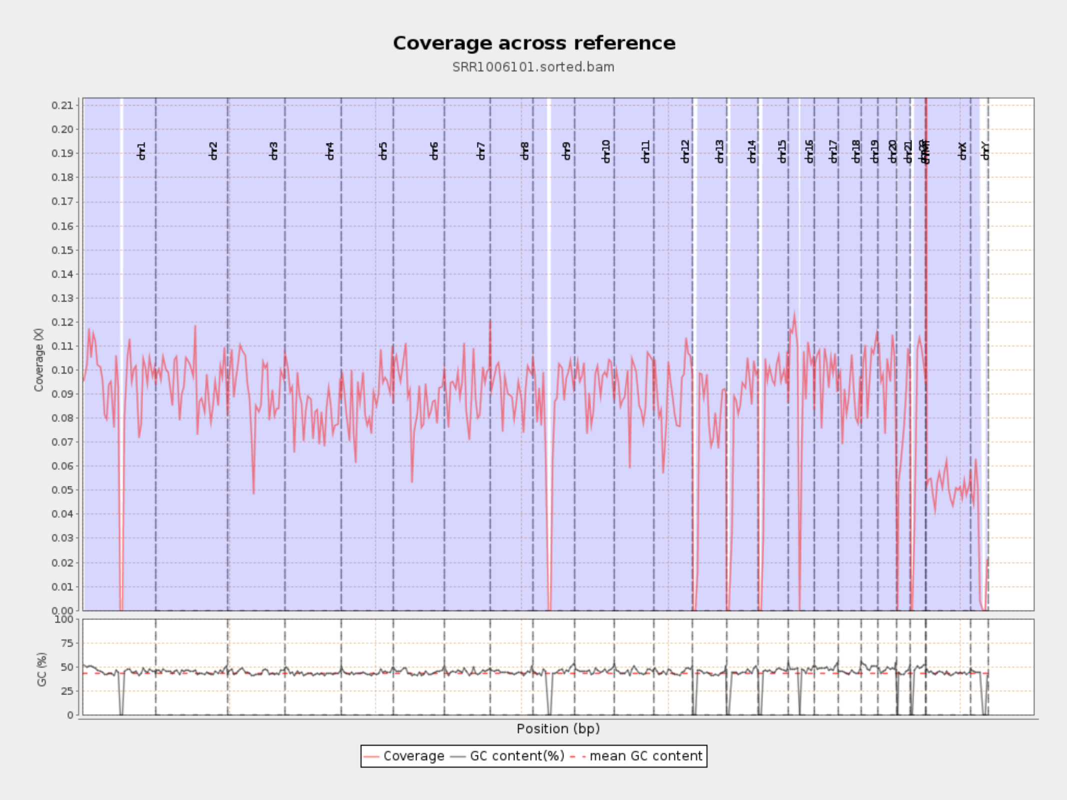
2.7. Chromosome stats

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

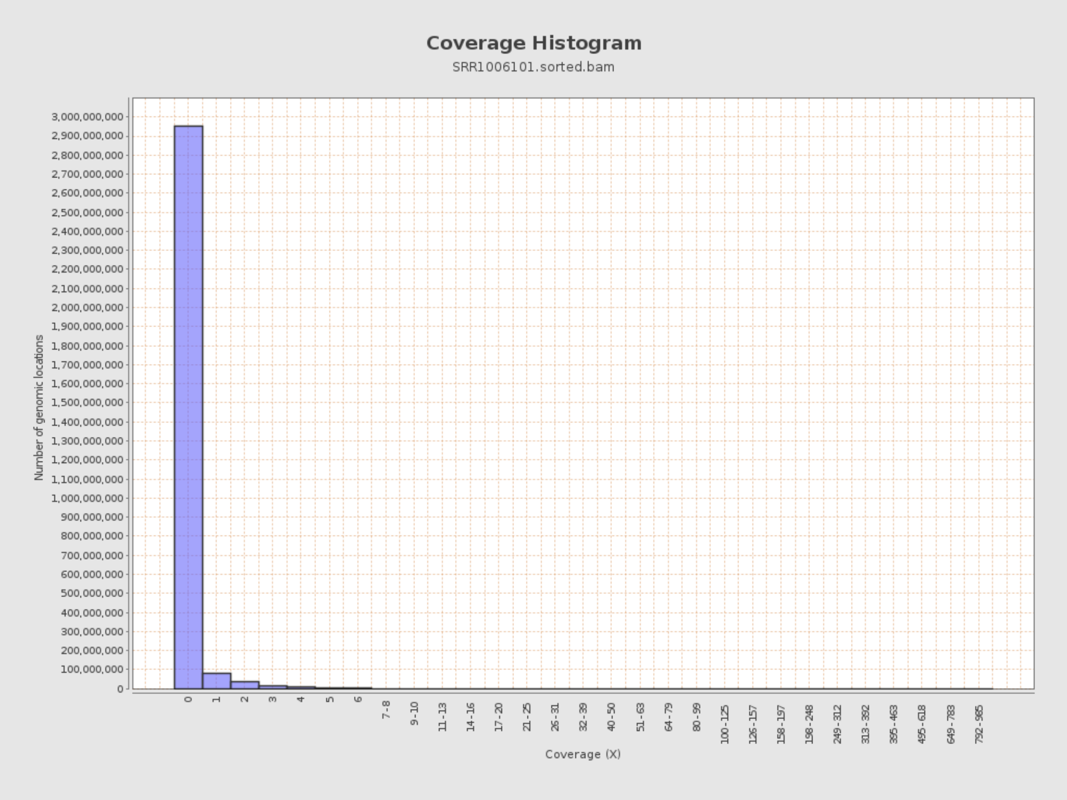
chr1	249250621	22771779	0.0914	0.5736
chr2	243199373	23089271	0.0949	0.5571
chr3	198022430	18181310	0.0918	0.4872
chr4	191154276	16053808	0.084	0.4822
chr5	180915260	15993992	0.0884	0.4791
chr6	171115067	15186849	0.0888	0.5558
chr7	159138663	14663656	0.0921	0.6274
chr8	146364022	13434944	0.0918	0.56
chr9	141213431	11303538	0.08	0.4796
chr10	135534747	12830852	0.0947	0.5119
chr11	135006516	12449698	0.0922	0.7315
chr12	133851895	12141540	0.0907	0.4878
chr13	115169878	8163406	0.0709	0.4317
chr14	107349540	8239946	0.0768	0.4545
chr15	102531392	8194639	0.0799	0.4624
chr16	90354753	8543294	0.0946	0.5262
chr17	81195210	8154317	0.1004	0.5547
chr18	78077248	6897752	0.0883	0.5546
chr19	59128983	6024507	0.1019	0.6065
chr20	63025520	6218186	0.0987	0.5184
chr21	48129895	3506651	0.0729	0.4706
chr22	51304566	3780692	0.0737	0.4654
chrMT	16571	21715	1.3104	2.1144
chrX	155270560	7989550	0.0515	0.3742

chrY	59373566	1675340	0.0282	0.2819

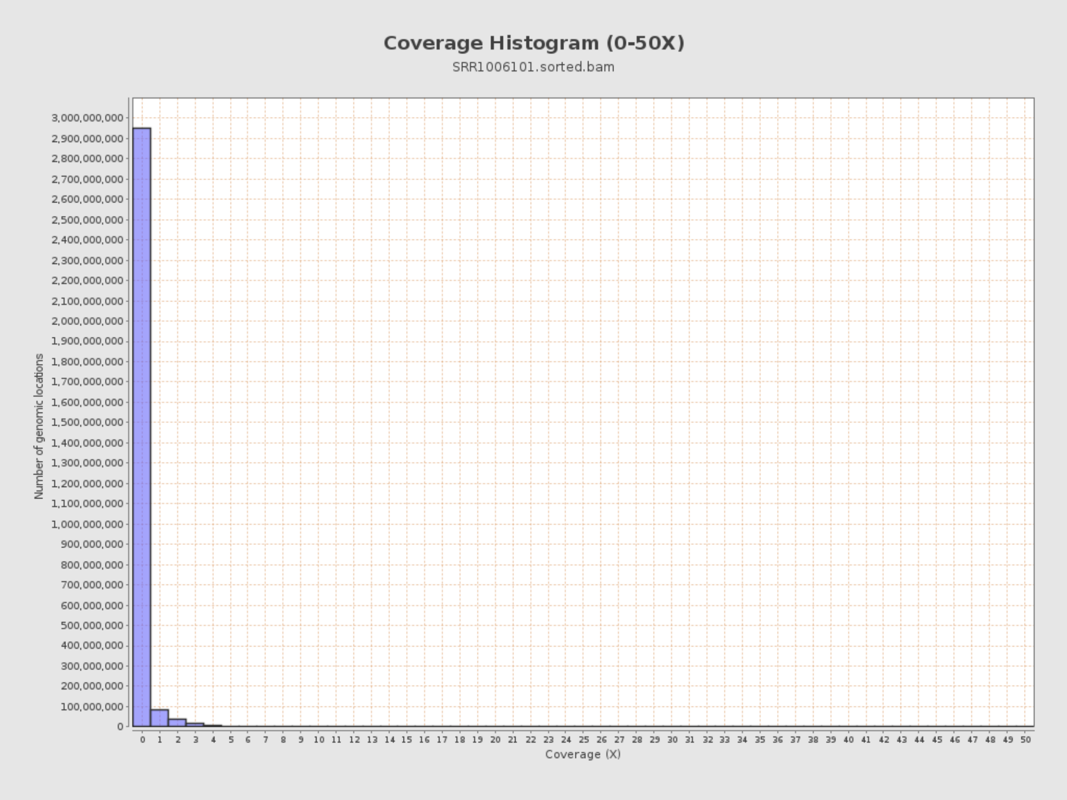
3. Results : Coverage across reference



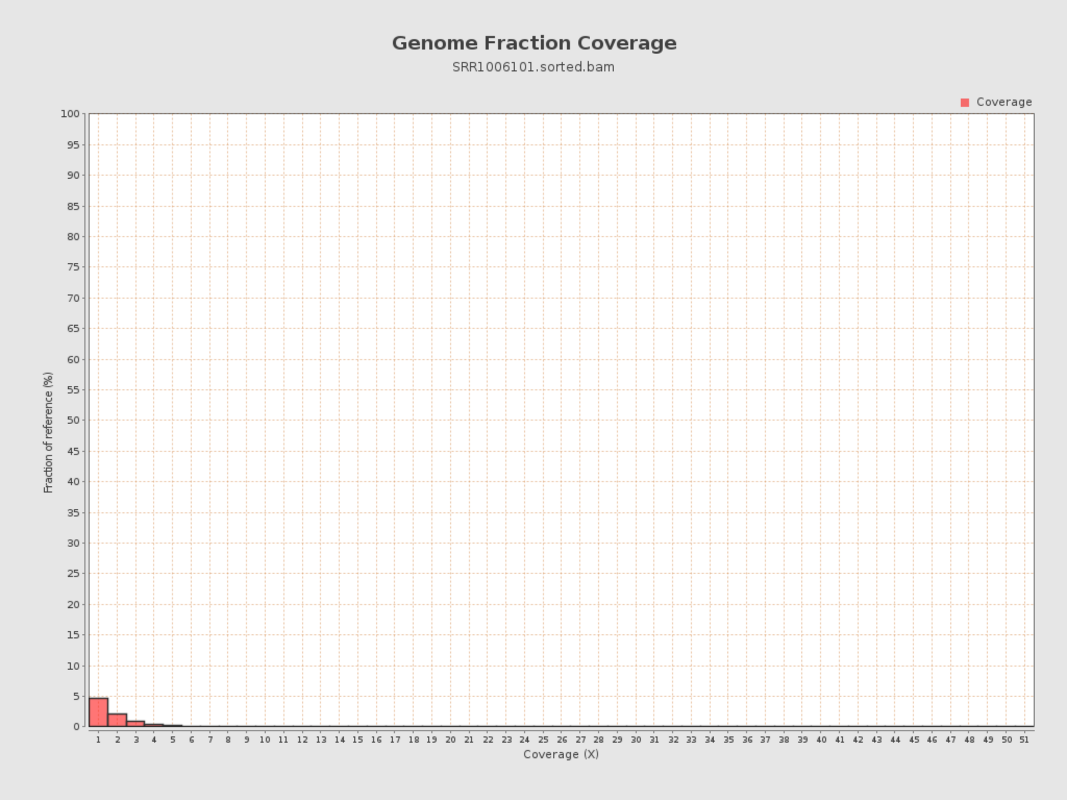
4. Results : Coverage Histogram



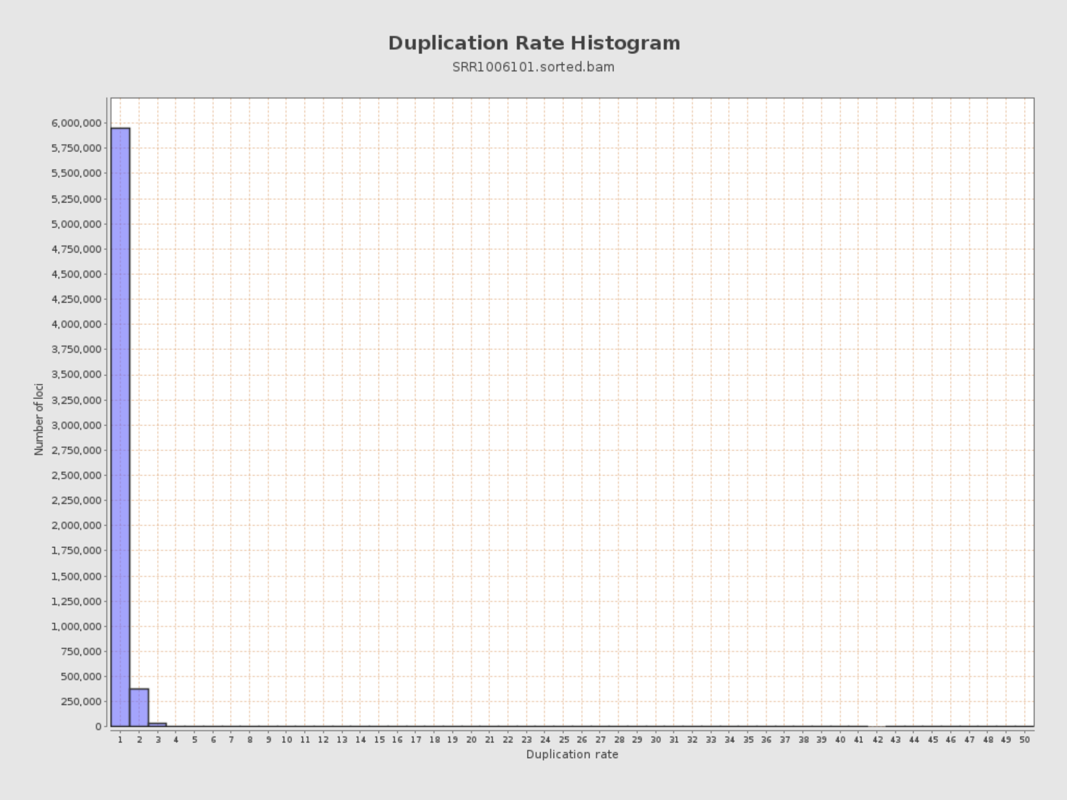
5. Results : Coverage Histogram (0-50X)



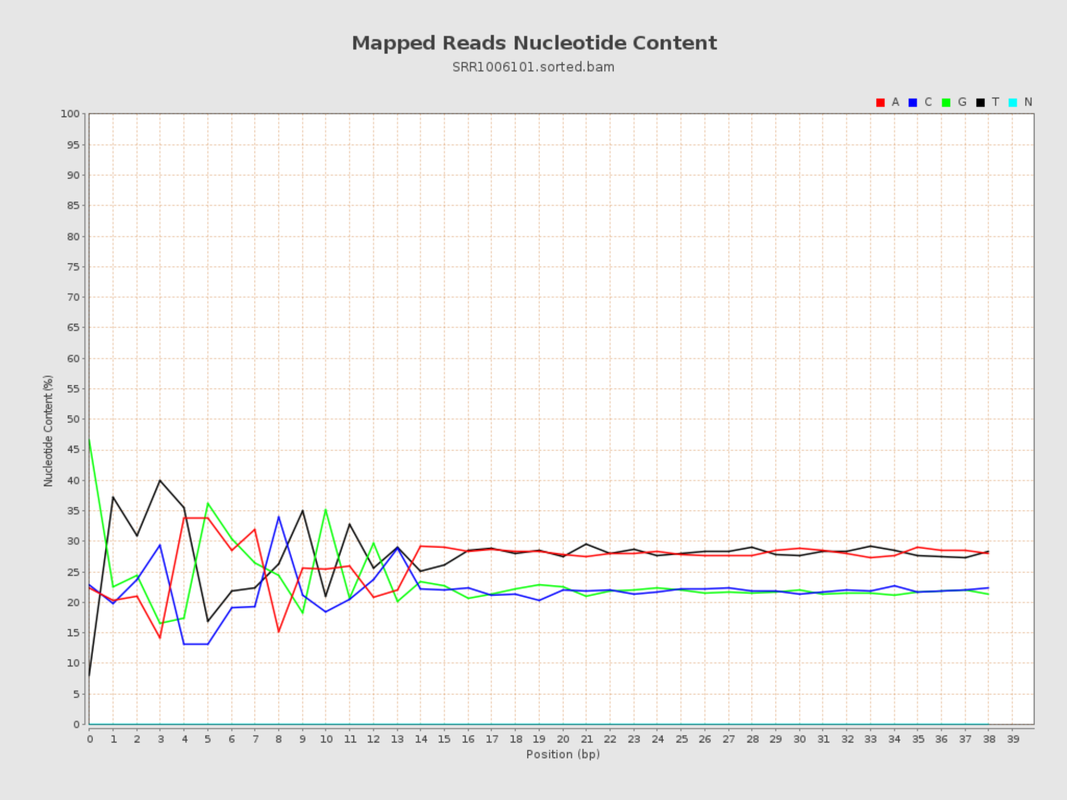
6. Results : Genome Fraction Coverage



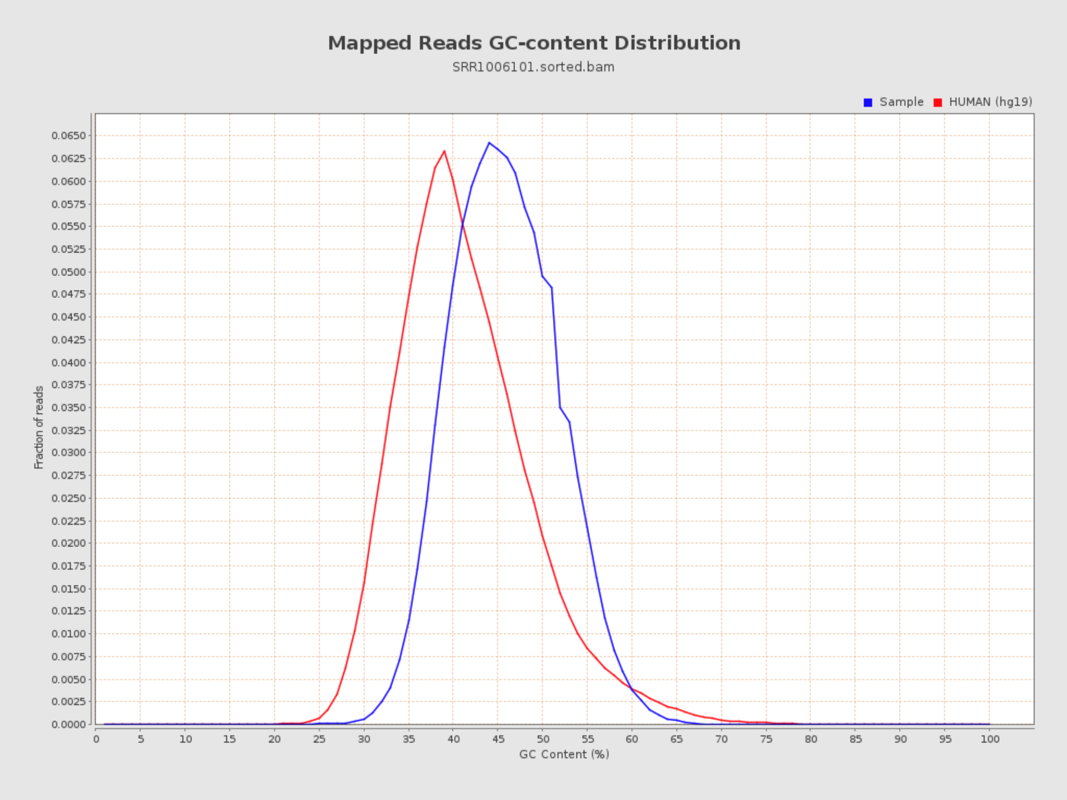
7. Results : Duplication Rate Histogram



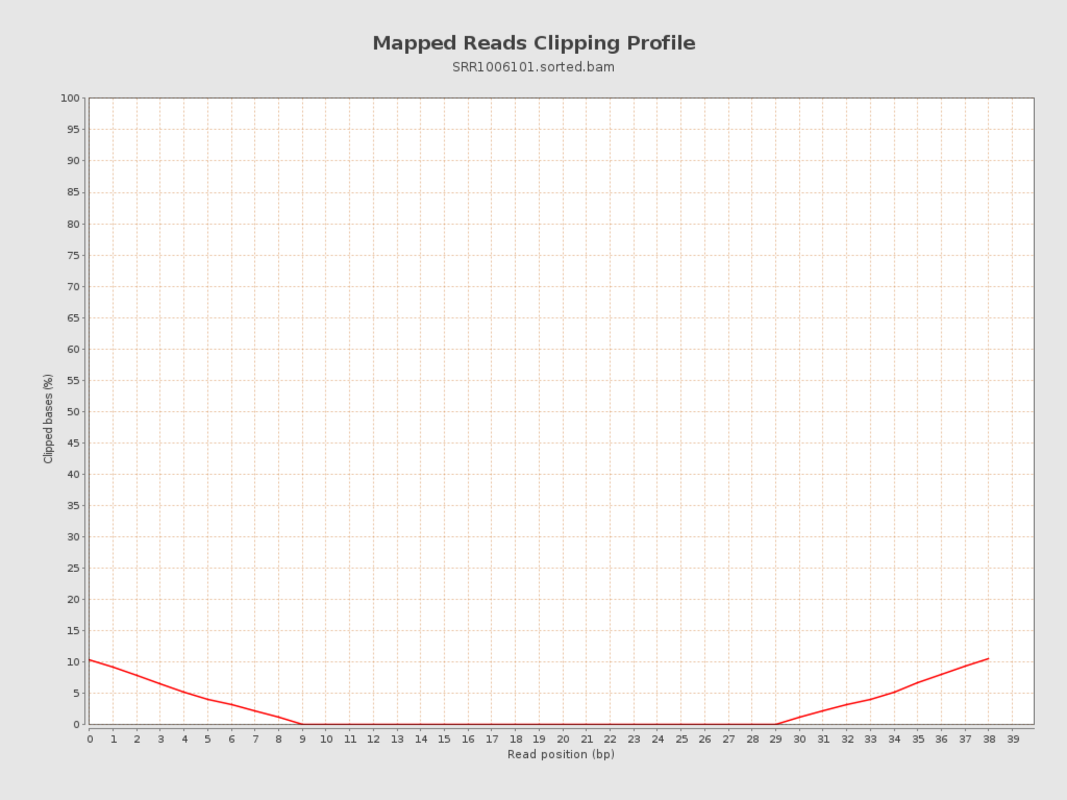
8. Results : Mapped Reads Nucleotide Content



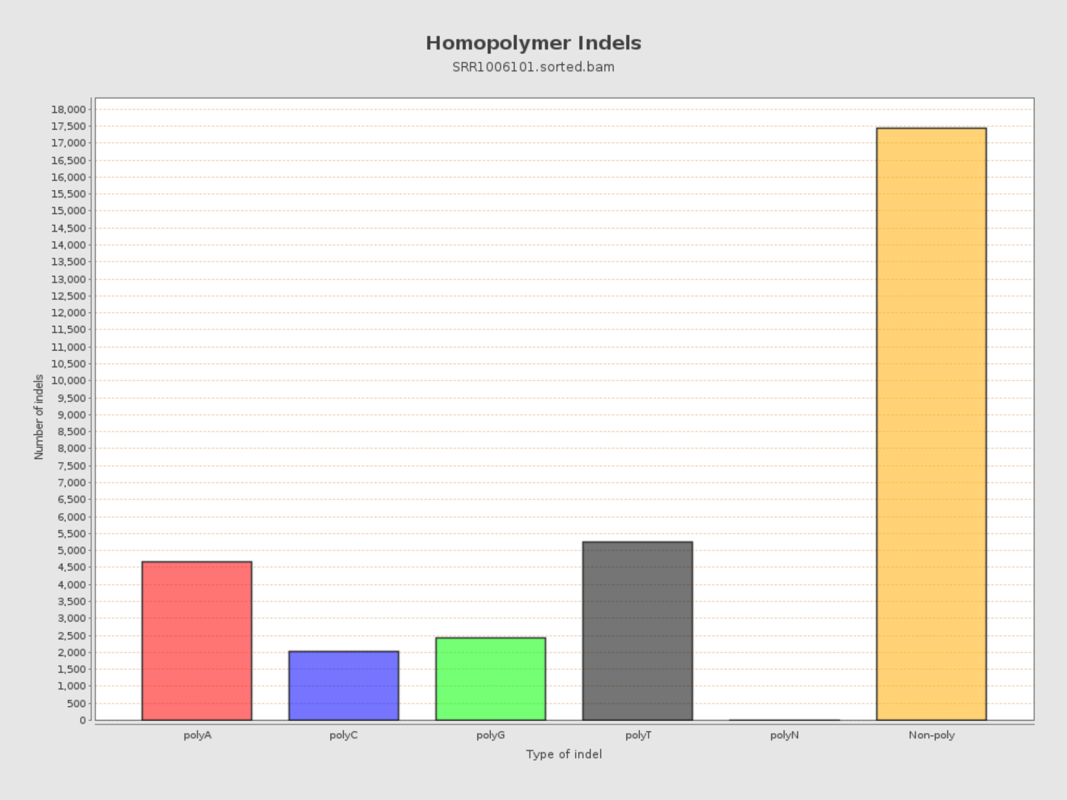
9. Results : Mapped Reads GC-content Distribution



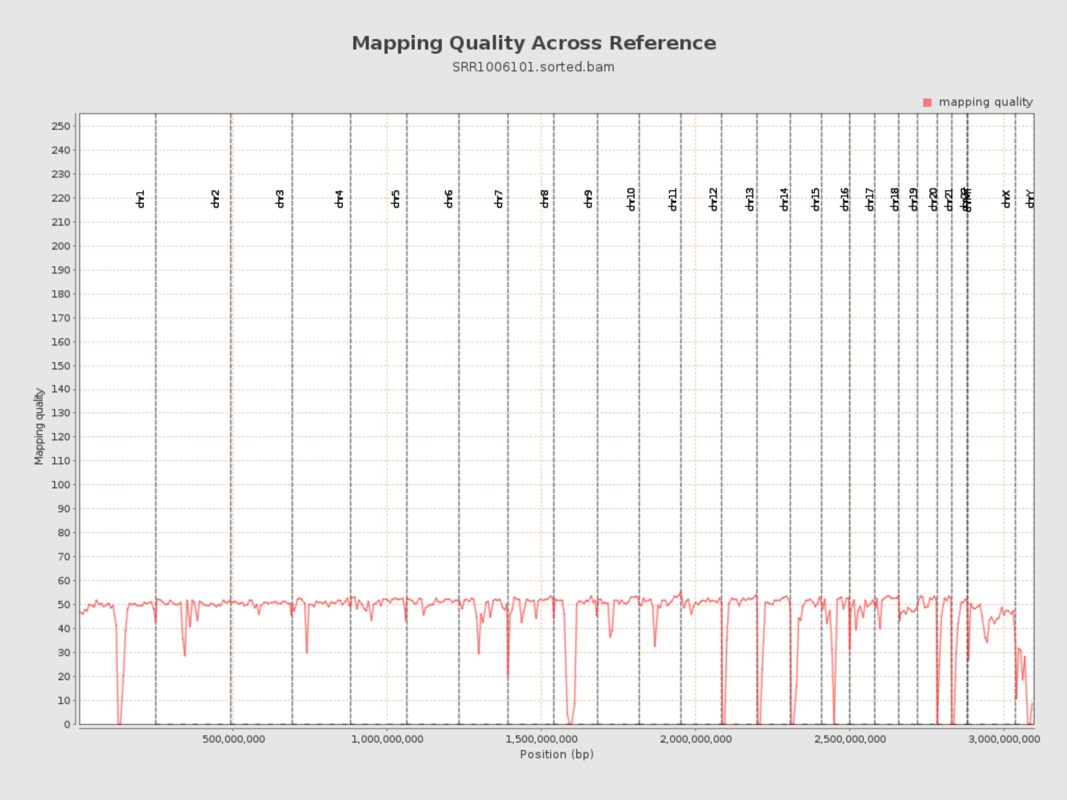
10. Results : Mapped Reads Clipping Profile



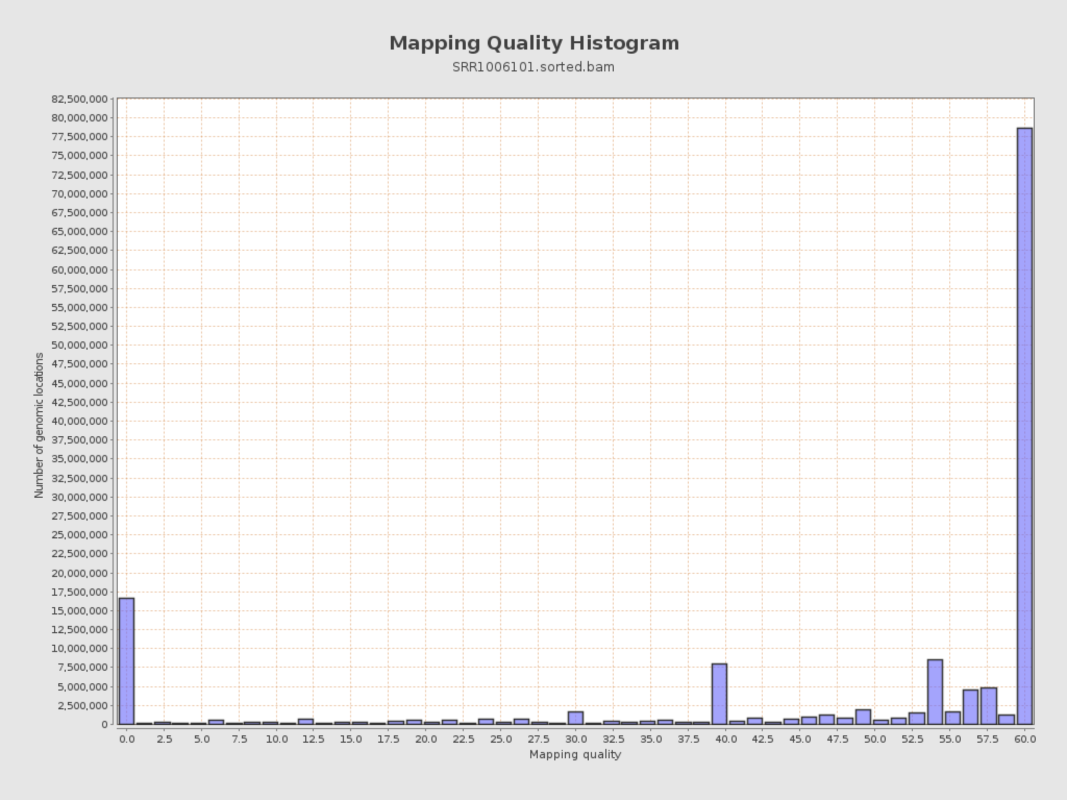
11. Results : Homopolymer Indels



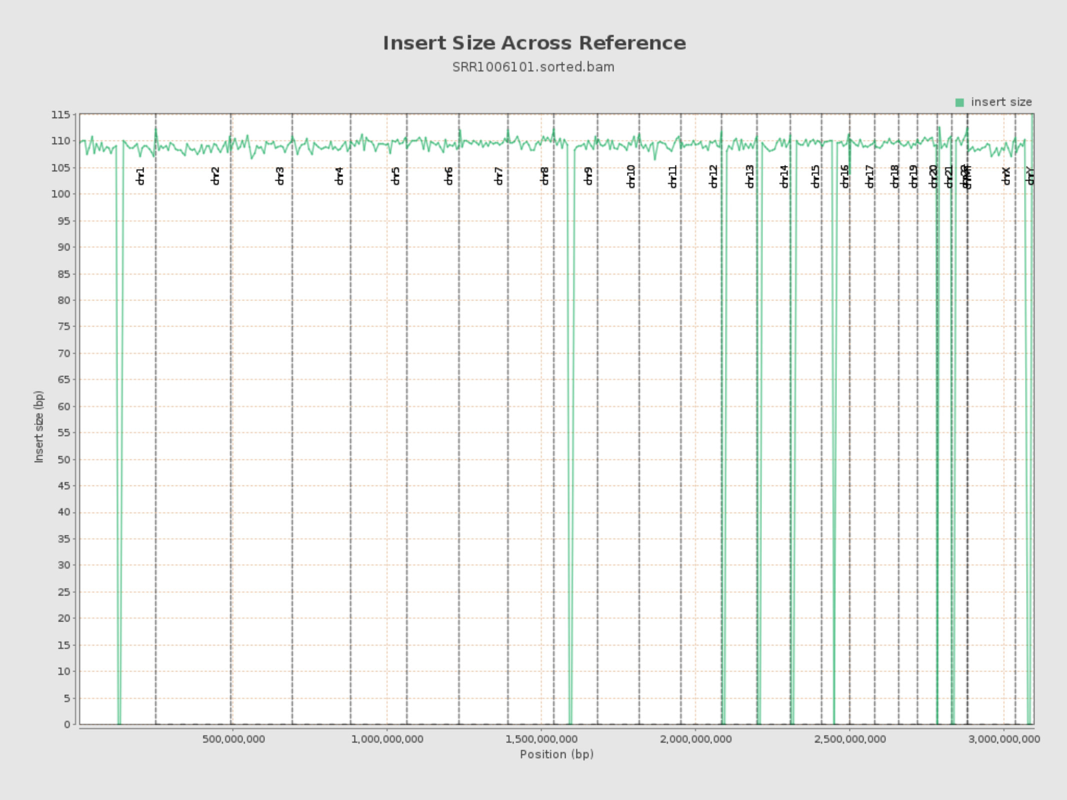
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram