Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 06:18:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926898.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_SRR926898 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926898_1.fastq.gz SRR926898_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 06:18:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926898.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,409,418
Mapped reads	31,318,145 / 93.74%
Unmapped reads	2,091,273 / 6.26%
Mapped paired reads	31,318,145 / 93.74%
Mapped reads, first in pair	15,736,141 / 47.1%
Mapped reads, second in pair	15,582,004 / 46.64%
Mapped reads, both in pair	31,025,884 / 92.87%
Mapped reads, singletons	292,261 / 0.87%
Secondary alignments	0
Supplementary alignments	175,460 / 0.53%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	2,228,227 / 6.67%
Duplication rate	5.56%
Clipped reads	7,838,212 / 23.46%

2.2. ACGT Content

Number/percentage of A's	838,033,391 / 28.44%
Number/percentage of C's	590,632,014 / 20.04%
Number/percentage of T's	842,915,979 / 28.6%
Number/percentage of G's	675,278,741 / 22.91%
Number/percentage of N's	281,013 / 0.01%

GC Percentage	42.95%

2.3. Coverage

Mean	0.9527
Standard Deviation	3.8194

2.4. Mapping Quality

Mean Mapping Quality	53.64

2.5. Insert size

Mean	81,387.5
Standard Deviation	2,811,854.56
P25/Median/P75	186 / 233 / 295

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	30,592,927
Insertions	464,805
Mapped reads with at least one insertion	1.46%
Deletions	1,608,568
Mapped reads with at least one deletion	5%
Homopolymer indels	53.17%

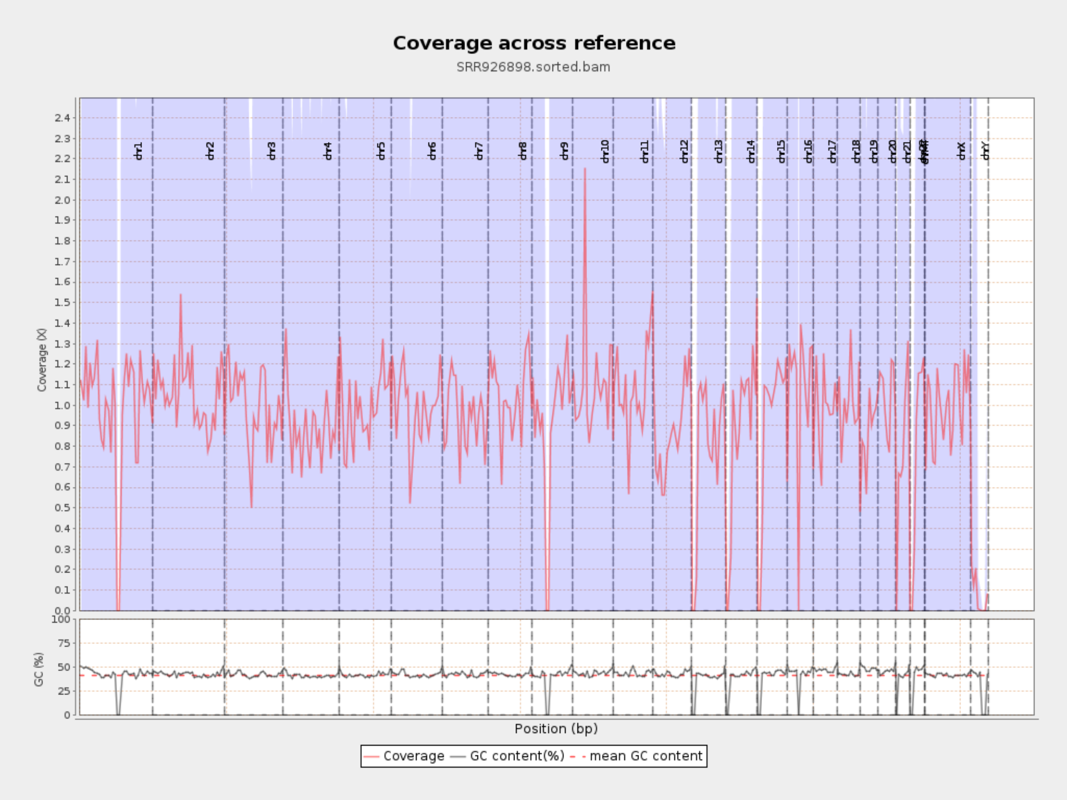
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

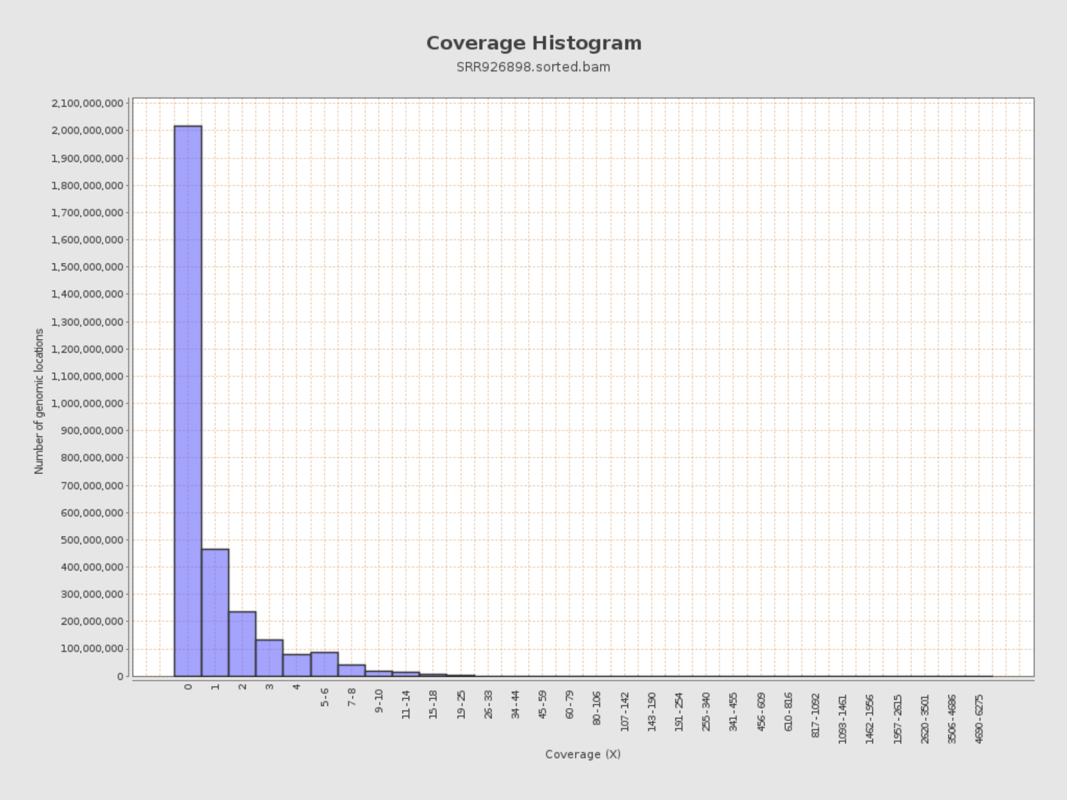
		bases	**coverage**	**deviation**
chr1	249250621	245283769	0.9841	3.6167
chr2	243199373	258636231	1.0635	4.4311
chr3	198022430	196757401	0.9936	2.0594
chr4	191154276	172579481	0.9028	2.1547
chr5	180915260	180554441	0.998	2.0187
chr6	171115067	170274773	0.9951	2.5682
chr7	159138663	149955943	0.9423	2.2134
chr8	146364022	154012687	1.0523	2.2307
chr9	141213431	128908786	0.9129	3.1969
chr10	135534747	150898057	1.1134	12.9107
chr11	135006516	144424350	1.0698	2.5601
chr12	133851895	117296886	0.8763	1.9905
chr13	115169878	89959294	0.7811	1.7853
chr14	107349540	90044082	0.8388	1.9142
chr15	102531392	91667237	0.894	2.0636
chr16	90354753	96717663	1.0704	4.5491
chr17	81195210	79818797	0.983	2.3534
chr18	78077248	79939032	1.0238	3.2498
chr19	59128983	50837595	0.8598	2.4595
chr20	63025520	65606326	1.0409	2.3289
chr21	48129895	37752065	0.7844	2.7758
chr22	51304566	38844047	0.7571	1.9884
chrMT	16571	17706	1.0685	1.3951
chrX	155270560	154198474	0.9931	2.1311

chrY	59373566	4414831	0.0744	1.7595

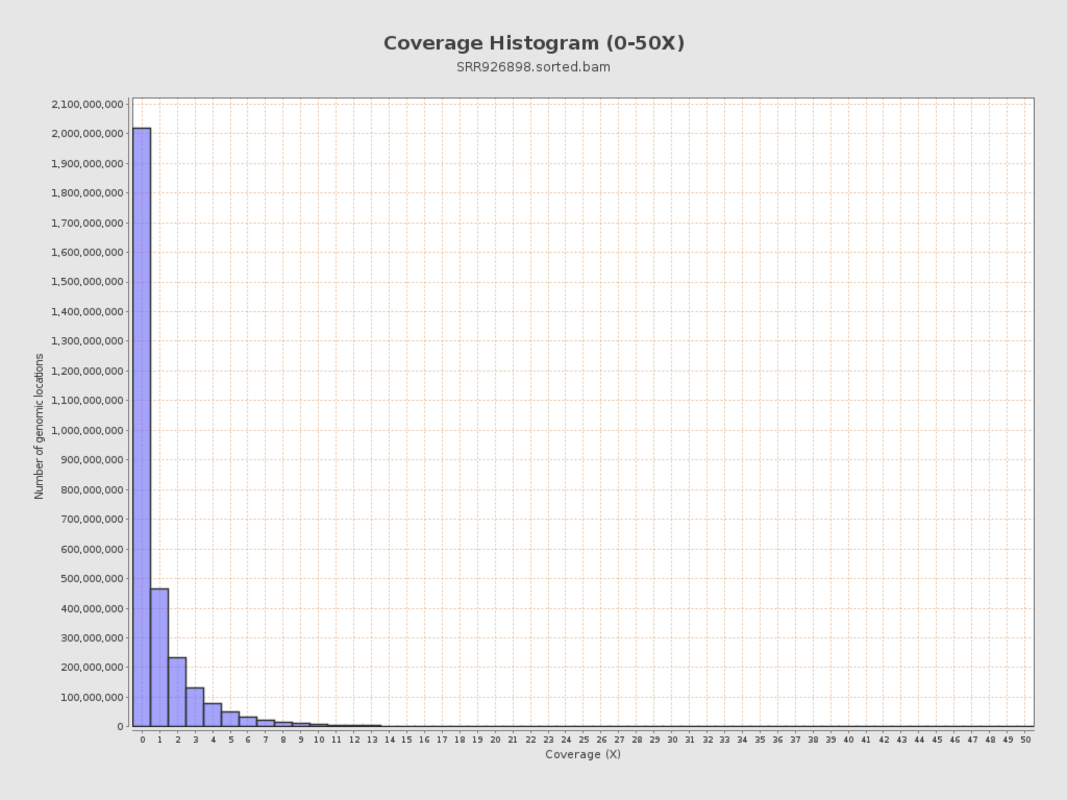
3. Results : Coverage across reference



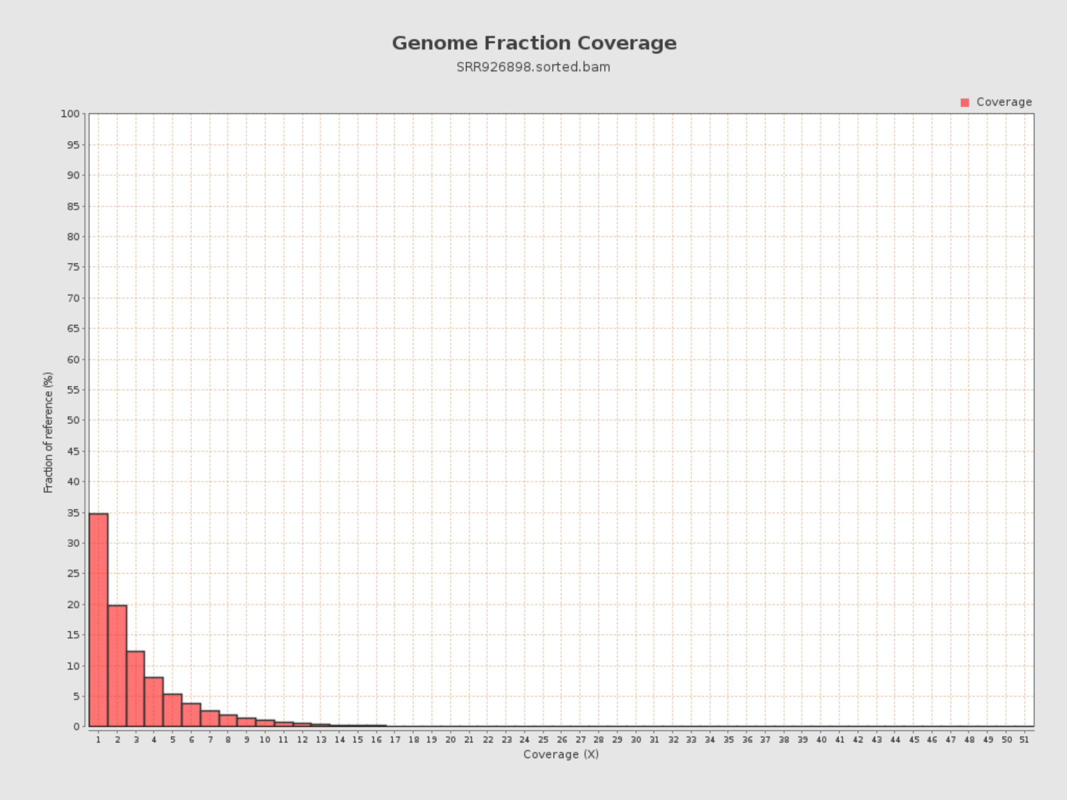
4. Results : Coverage Histogram



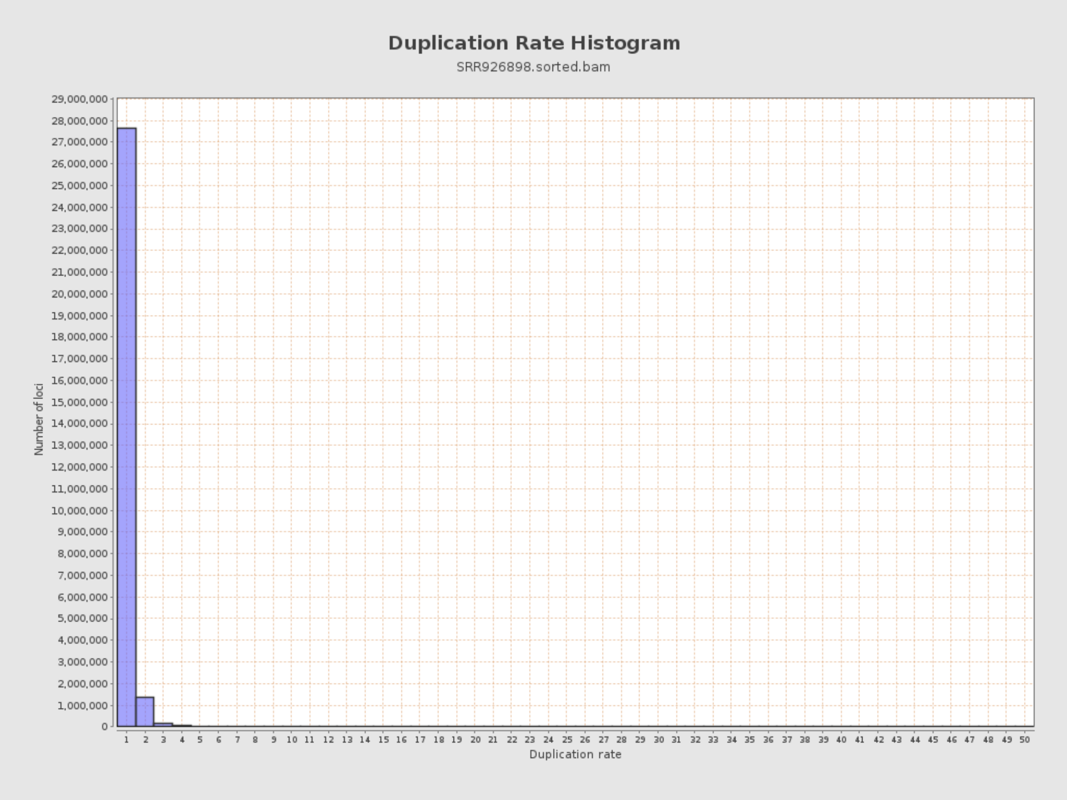
5. Results : Coverage Histogram (0-50X)



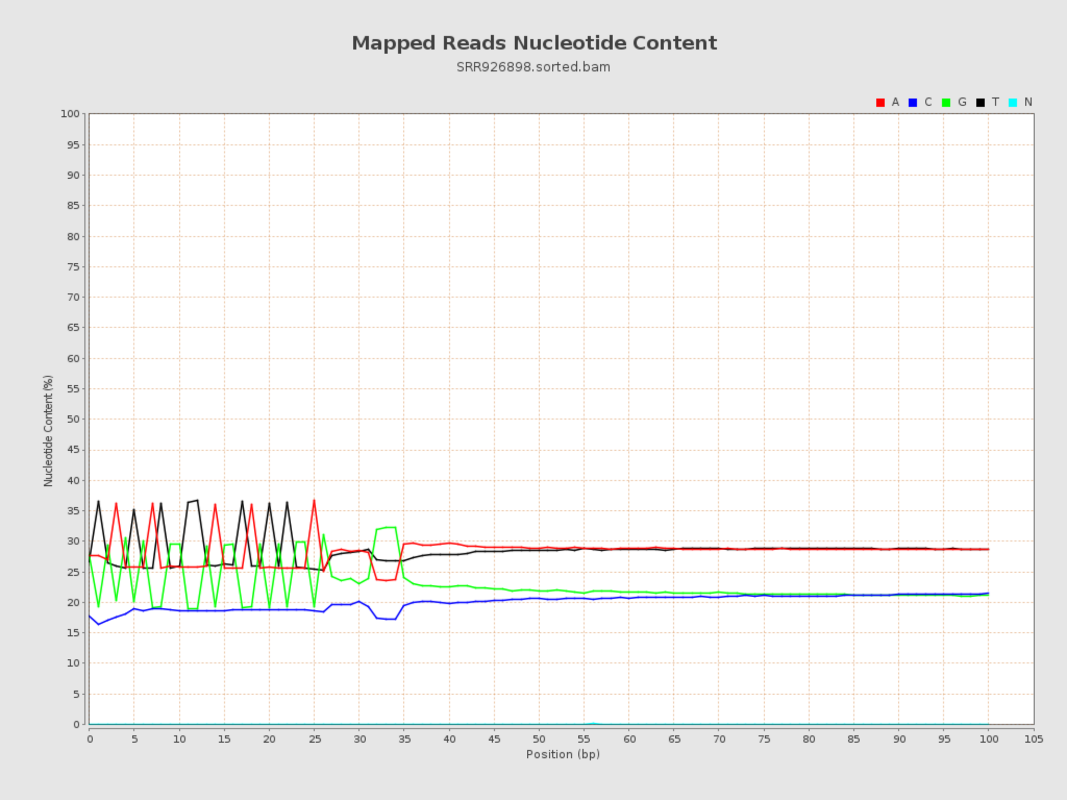
6. Results : Genome Fraction Coverage



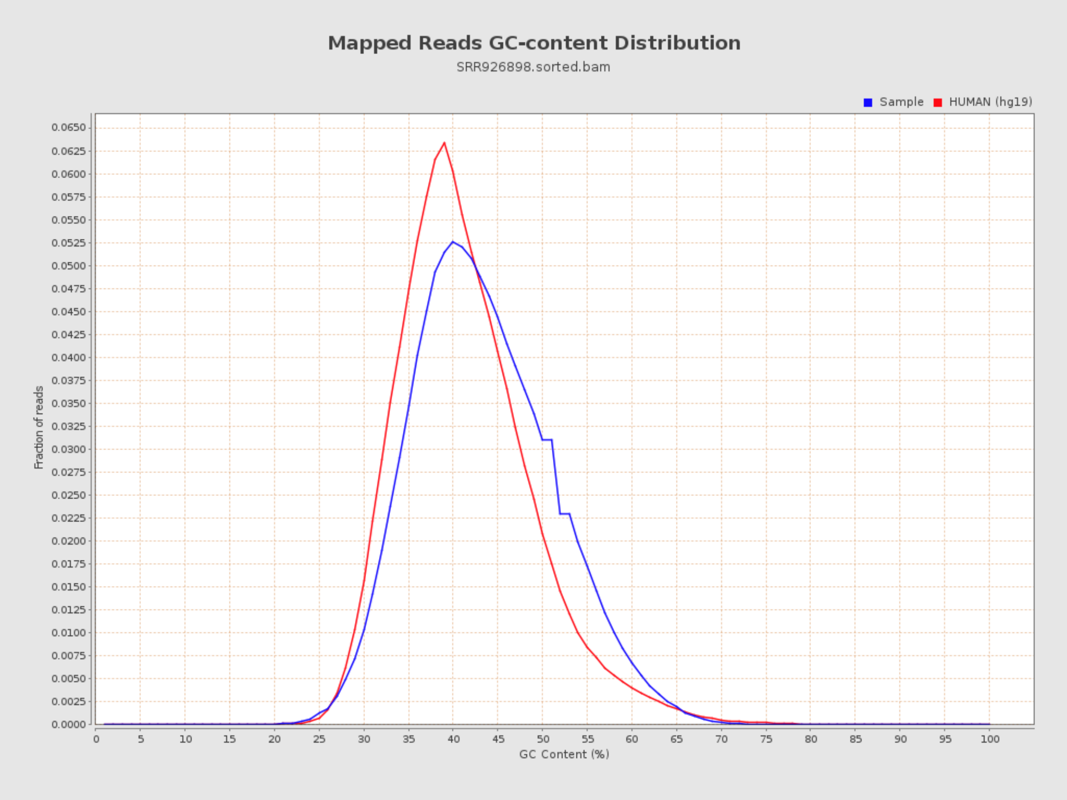
7. Results : Duplication Rate Histogram



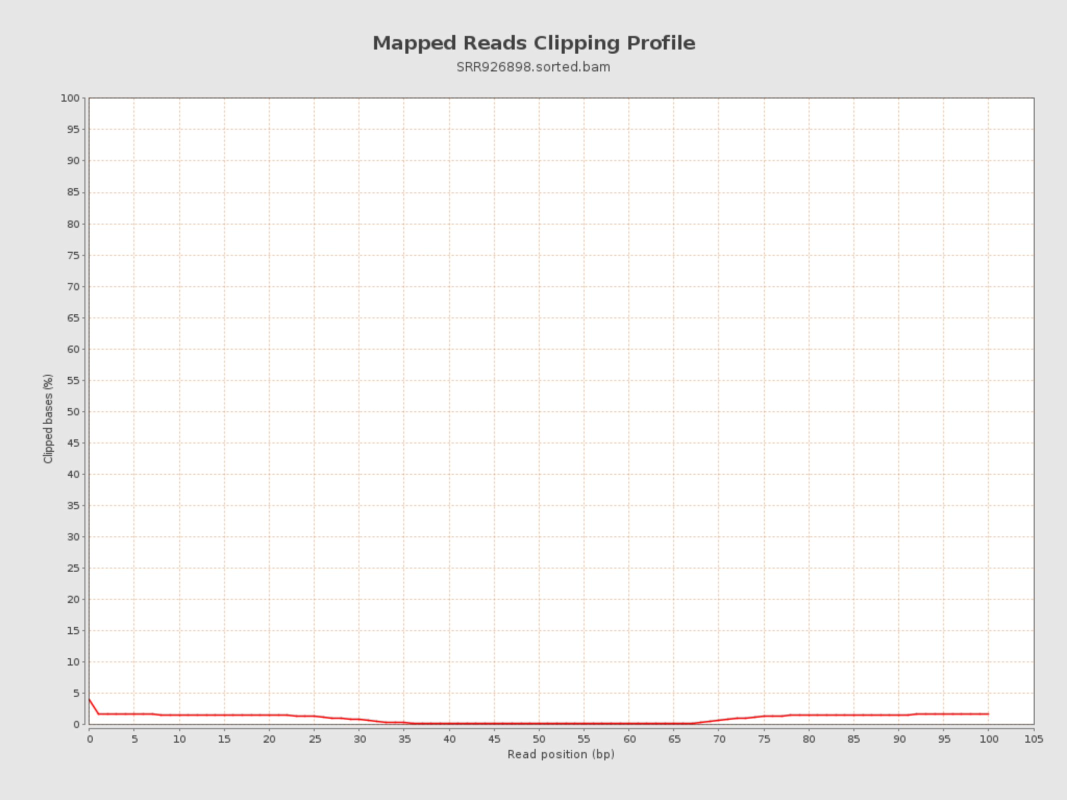
8. Results : Mapped Reads Nucleotide Content



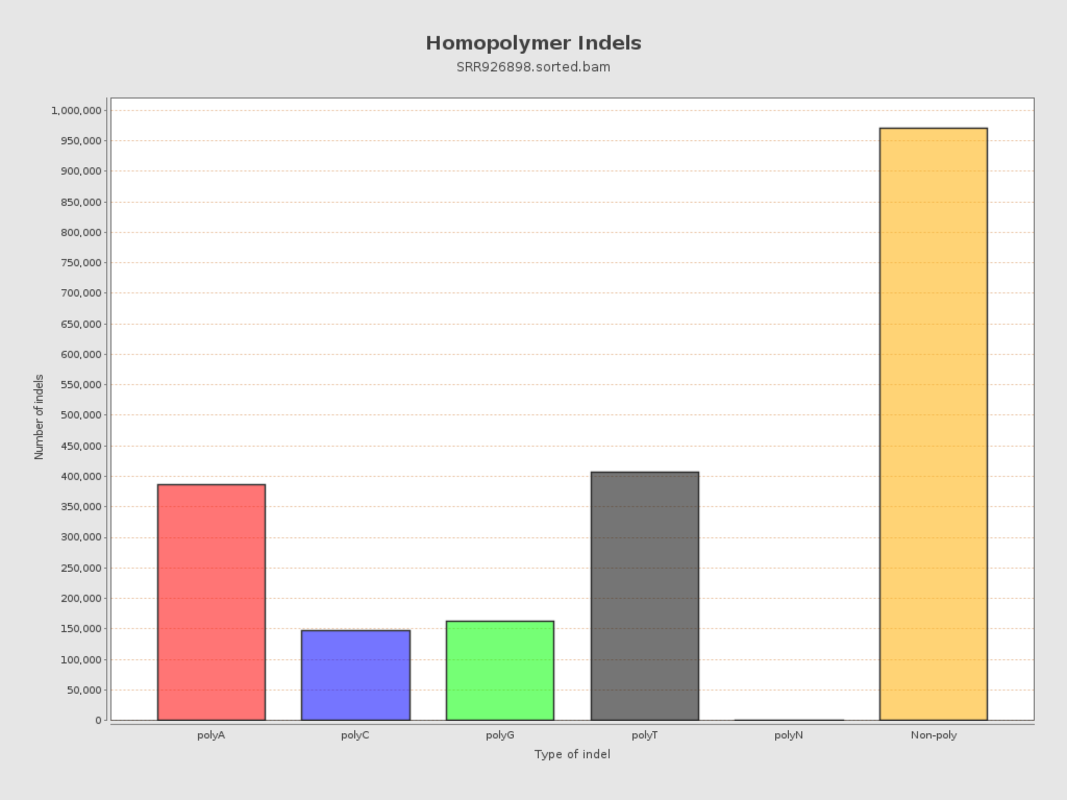
9. Results : Mapped Reads GC-content Distribution



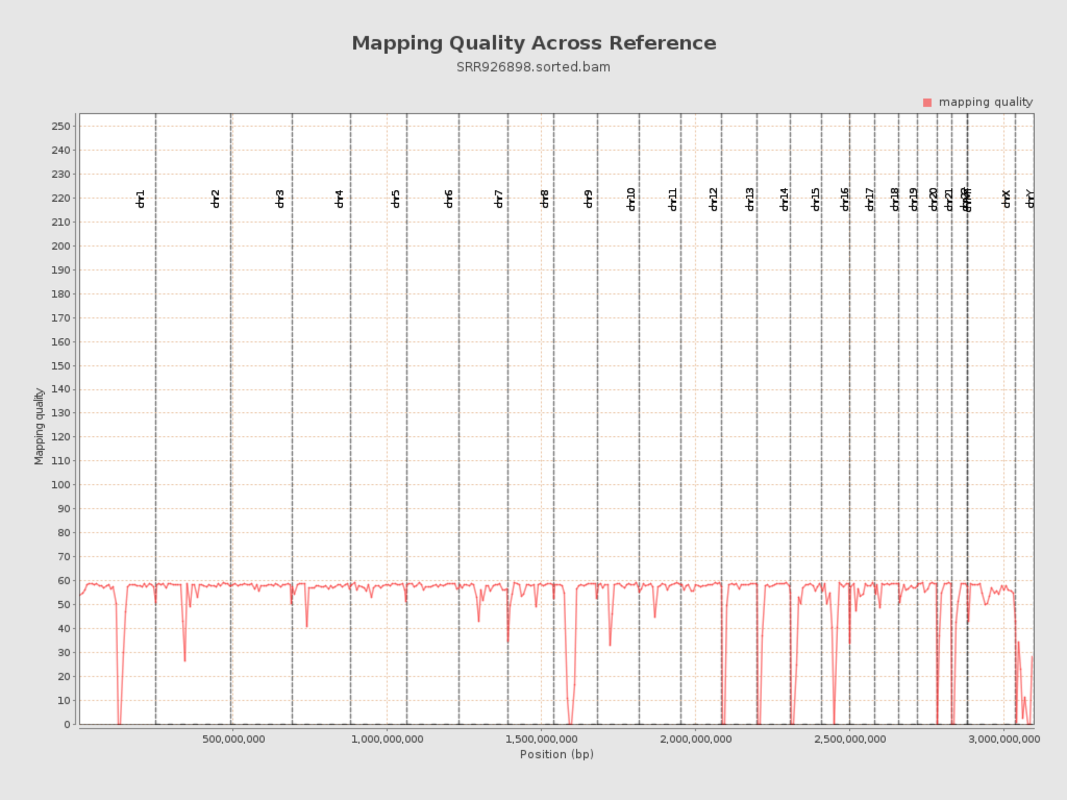
10. Results : Mapped Reads Clipping Profile



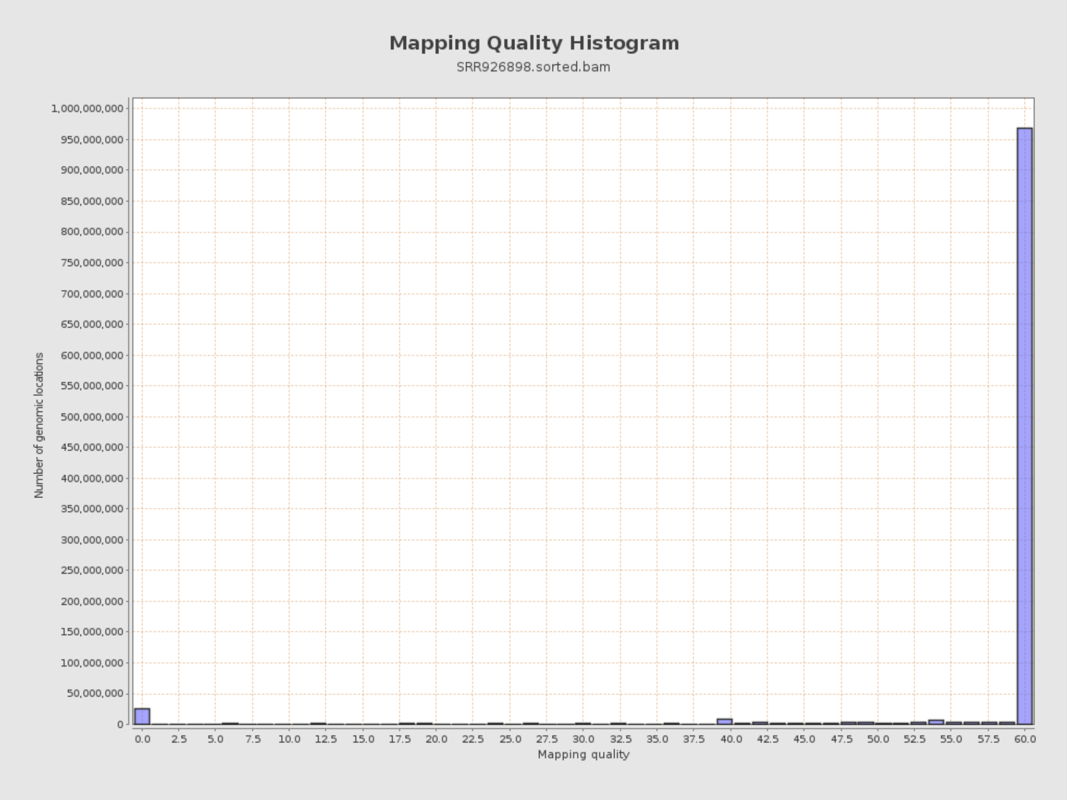
11. Results : Homopolymer Indels



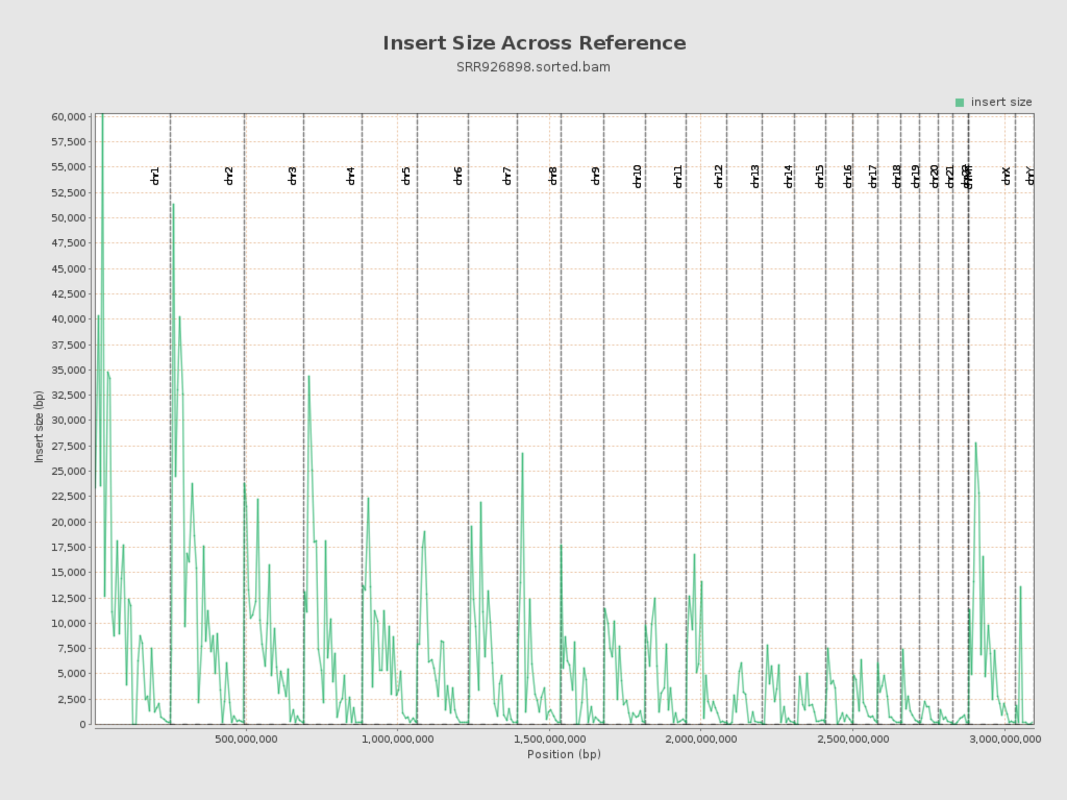
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram