Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 02:13:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124895.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_SRR3124895 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124895_1.fastq.gz SRR3124895_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 02:13:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124895.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,443,626
Mapped reads	4,371,881 / 98.39%
Unmapped reads	71,745 / 1.61%
Mapped paired reads	4,371,881 / 98.39%
Mapped reads, first in pair	2,190,430 / 49.29%
Mapped reads, second in pair	2,181,451 / 49.09%
Mapped reads, both in pair	4,351,324 / 97.92%
Mapped reads, singletons	20,557 / 0.46%
Secondary alignments	0
Supplementary alignments	21,924 / 0.49%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	333,618 / 7.51%
Duplication rate	4.71%
Clipped reads	2,159,975 / 48.61%

2.2. ACGT Content

Number/percentage of A's	106,893,259 / 28.06%
Number/percentage of C's	71,974,217 / 18.89%
Number/percentage of T's	112,407,916 / 29.5%
Number/percentage of G's	89,718,928 / 23.55%
Number/percentage of N's	11,428 / 0%

GC Percentage	42.44%

2.3. Coverage

Mean	0.1231
Standard Deviation	1.349

2.4. Mapping Quality

Mean Mapping Quality	52.78

2.5. Insert size

Mean	38,888.54
Standard Deviation	1,864,027.09
P25/Median/P75	143 / 190 / 261

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	2,794,486
Insertions	55,351
Mapped reads with at least one insertion	1.23%
Deletions	118,561
Mapped reads with at least one deletion	2.66%
Homopolymer indels	46.13%

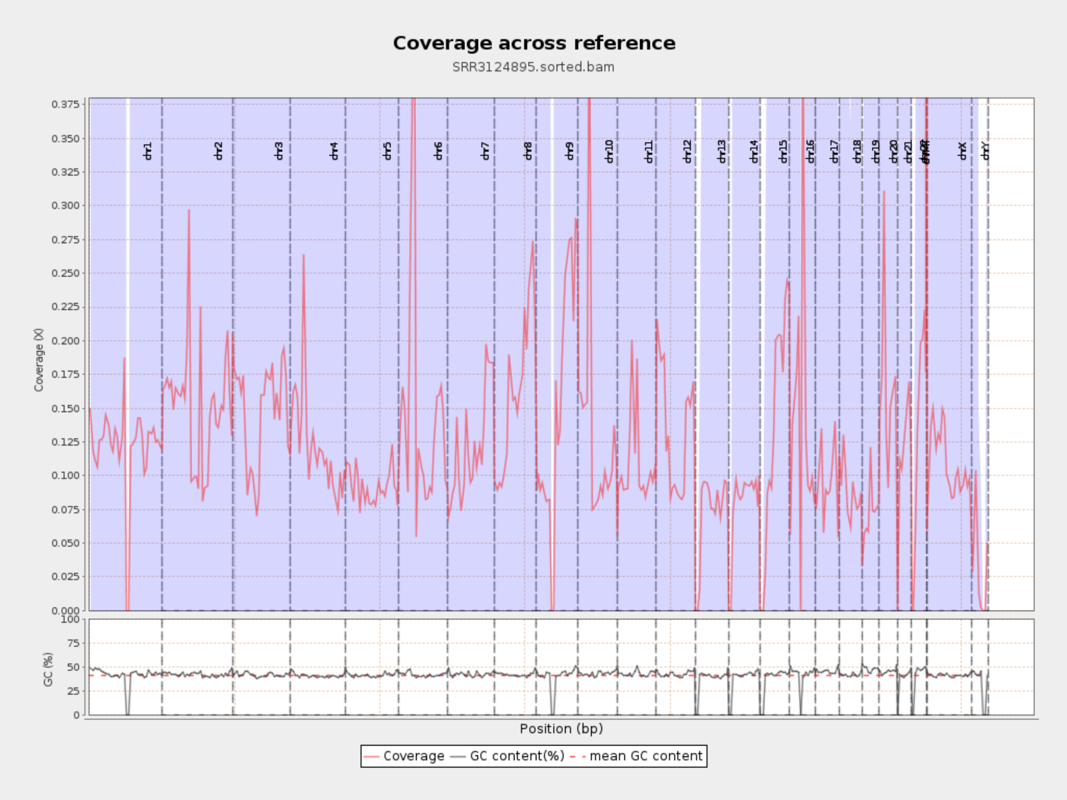
2.7. Chromosome stats

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

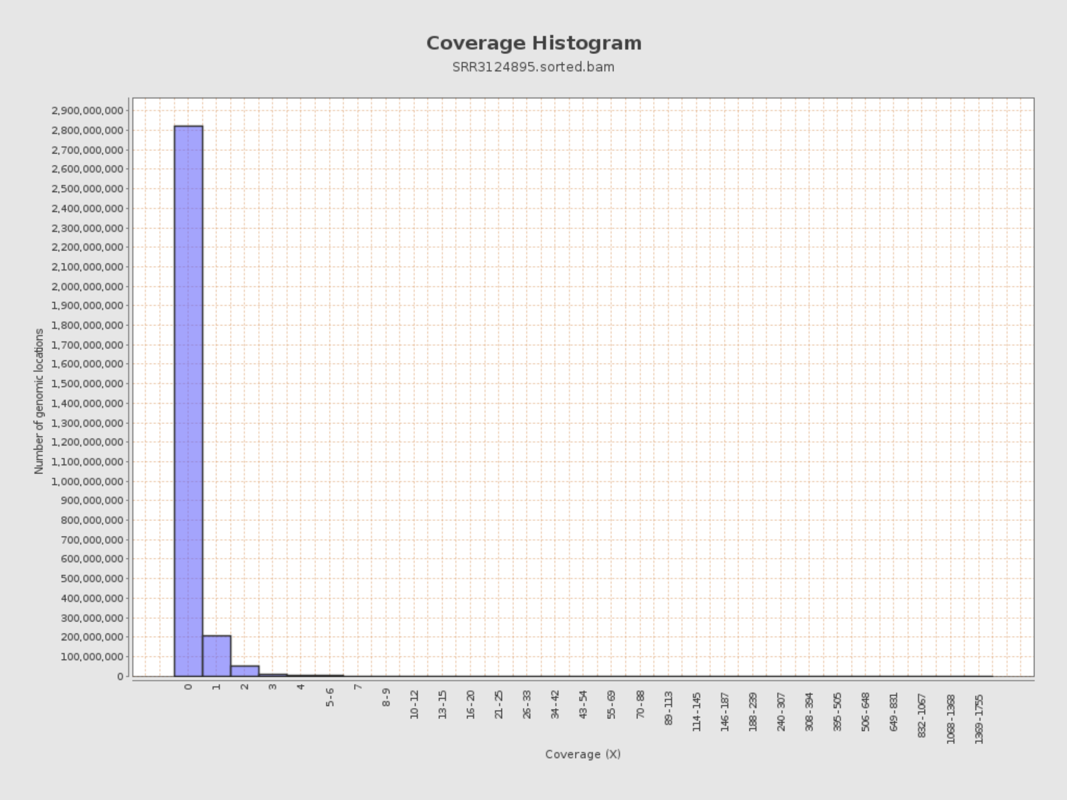
		bases	**coverage**	**deviation**
chr1	249250621	29987612	0.1203	1.1718
chr2	243199373	37166705	0.1528	1.652
chr3	198022430	29204067	0.1475	0.4924
chr4	191154276	23311240	0.1219	0.9701
chr5	180915260	16645965	0.092	0.4298
chr6	171115067	26241990	0.1534	2.9626
chr7	159138663	19429272	0.1221	1.0076
chr8	146364022	24192273	0.1653	0.6213
chr9	141213431	21386297	0.1514	1.4666
chr10	135534747	17904574	0.1321	2.787
chr11	135006516	14528968	0.1076	1.2201
chr12	133851895	17856895	0.1334	0.5159
chr13	115169878	8180027	0.071	0.325
chr14	107349540	8337535	0.0777	0.4258
chr15	102531392	13786370	0.1345	0.4736
chr16	90354753	12690687	0.1405	2.2158
chr17	81195210	7605643	0.0937	0.8444
chr18	78077248	7006212	0.0897	1.4772
chr19	59128983	4306796	0.0728	0.8288
chr20	63025520	10415704	0.1653	0.5792
chr21	48129895	5684012	0.1181	0.6813
chr22	51304566	6629474	0.1292	0.4874
chrMT	16571	122824	7.412	4.419
chrX	155270560	16744951	0.1078	0.6083

chrY	59373566	1851625	0.0312	1.6858

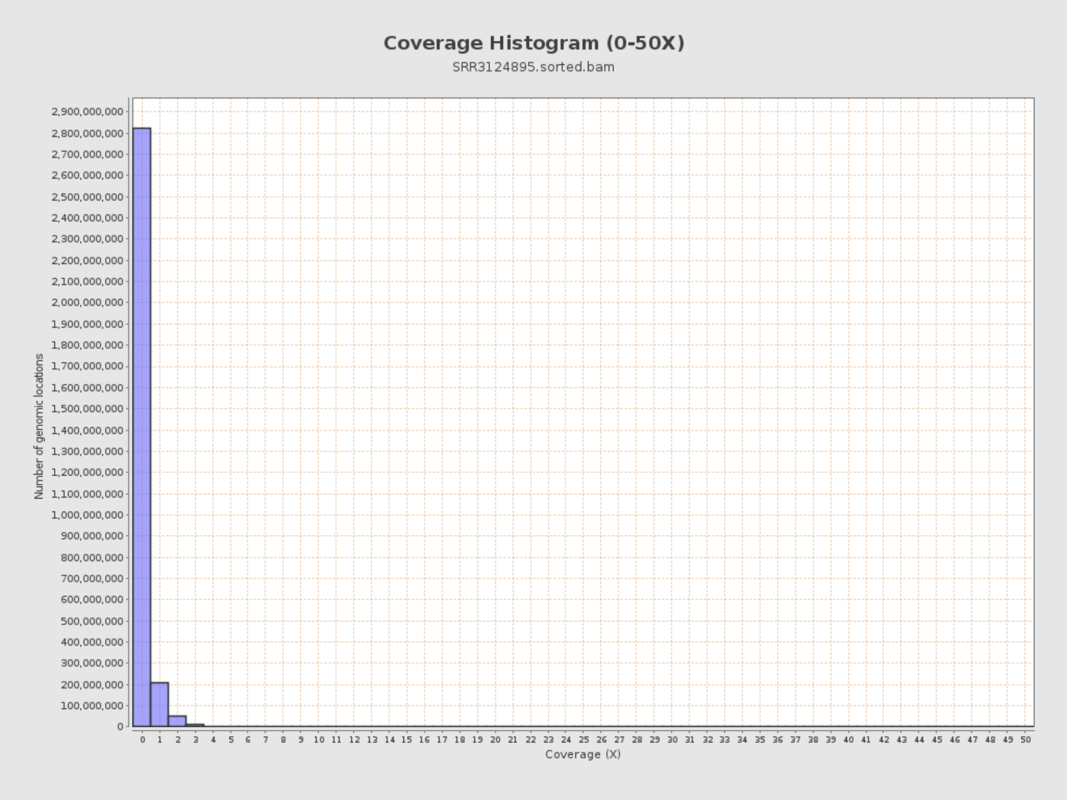
3. Results : Coverage across reference



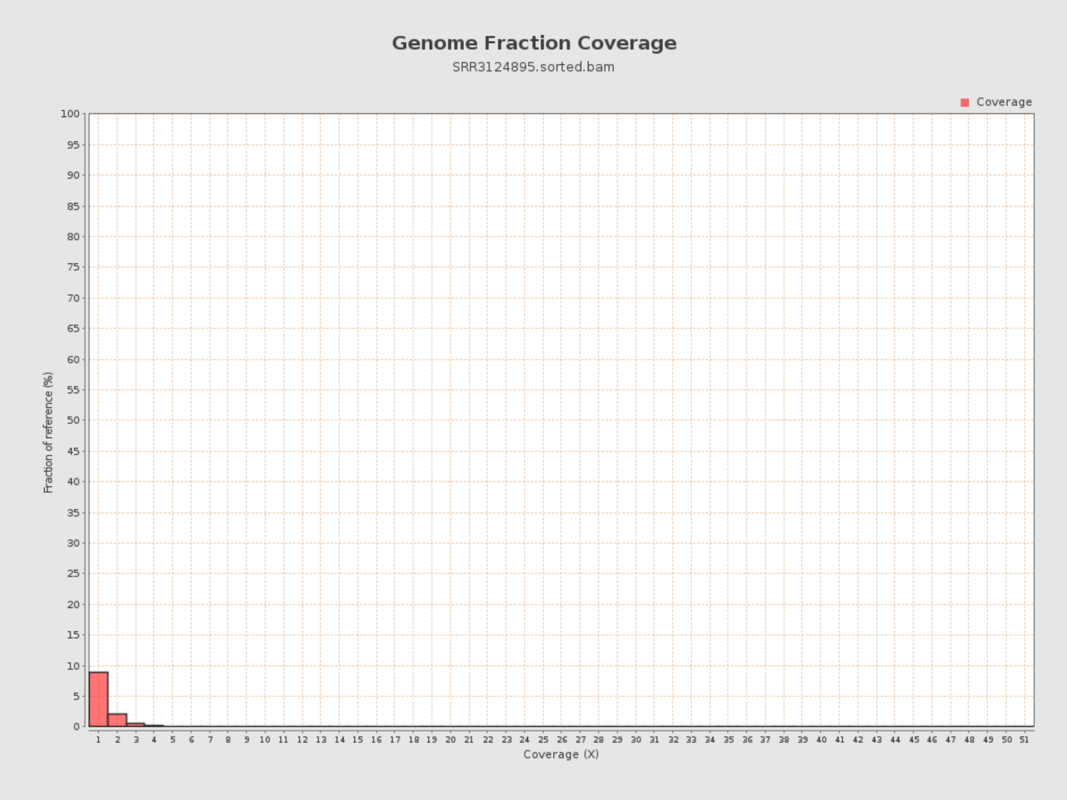
4. Results : Coverage Histogram



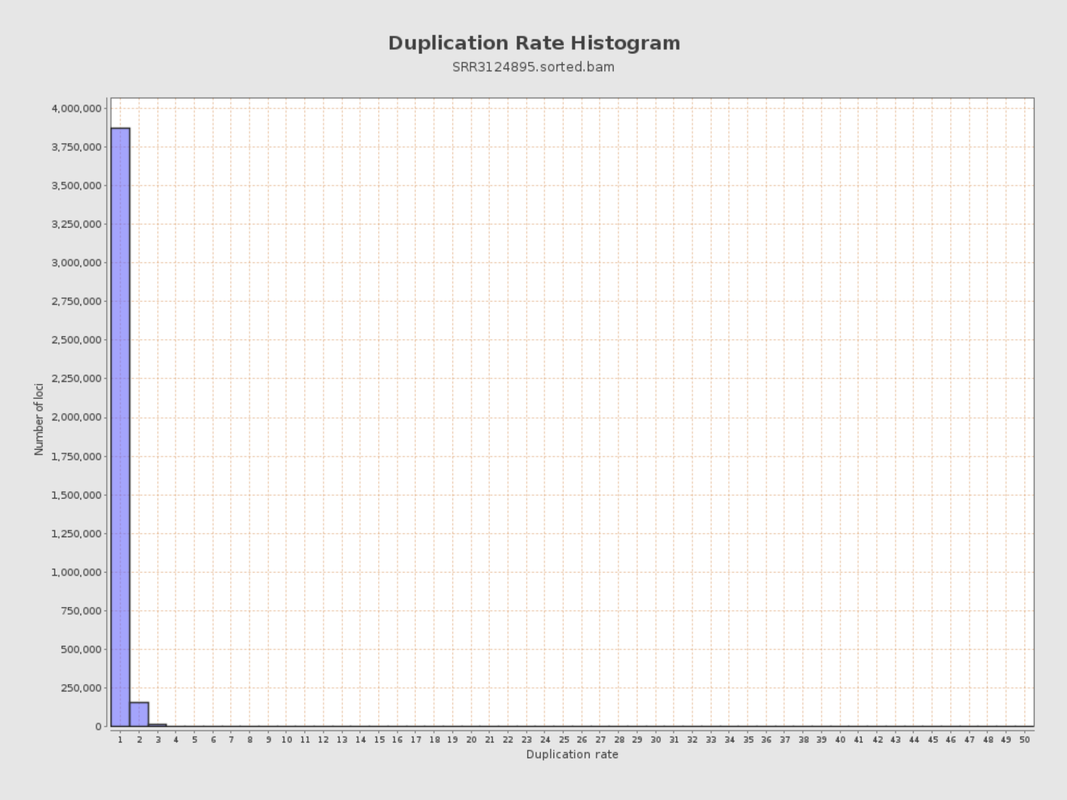
5. Results : Coverage Histogram (0-50X)



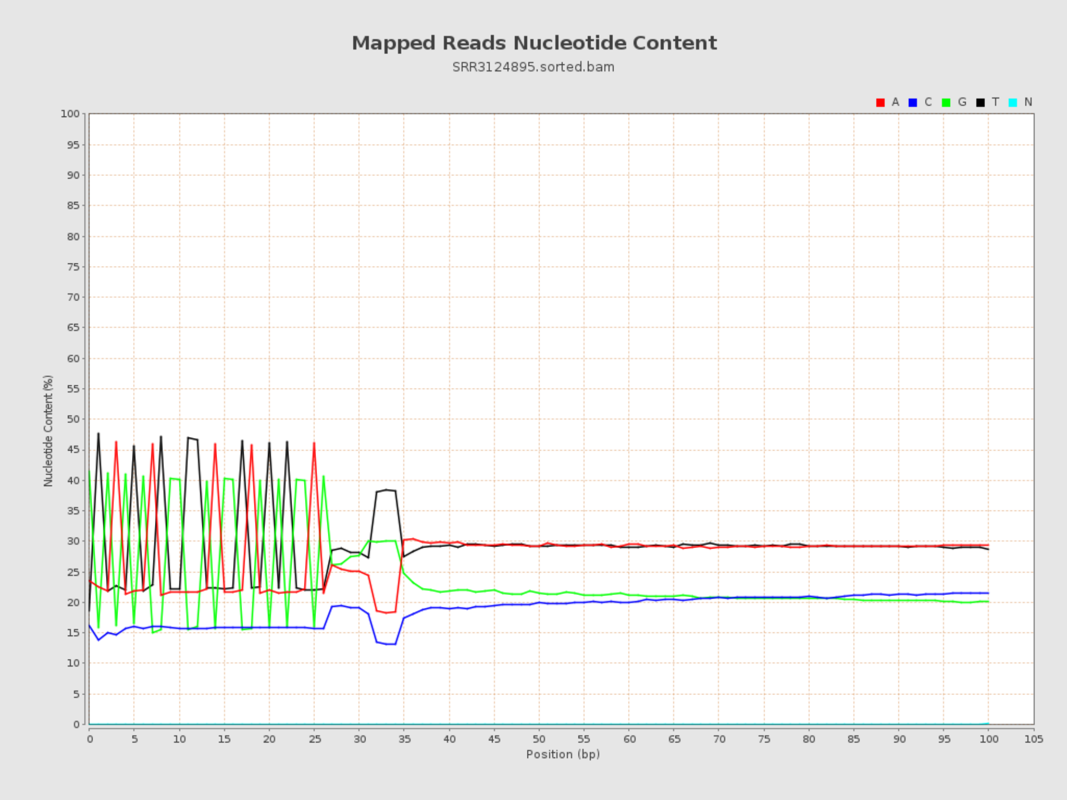
6. Results : Genome Fraction Coverage



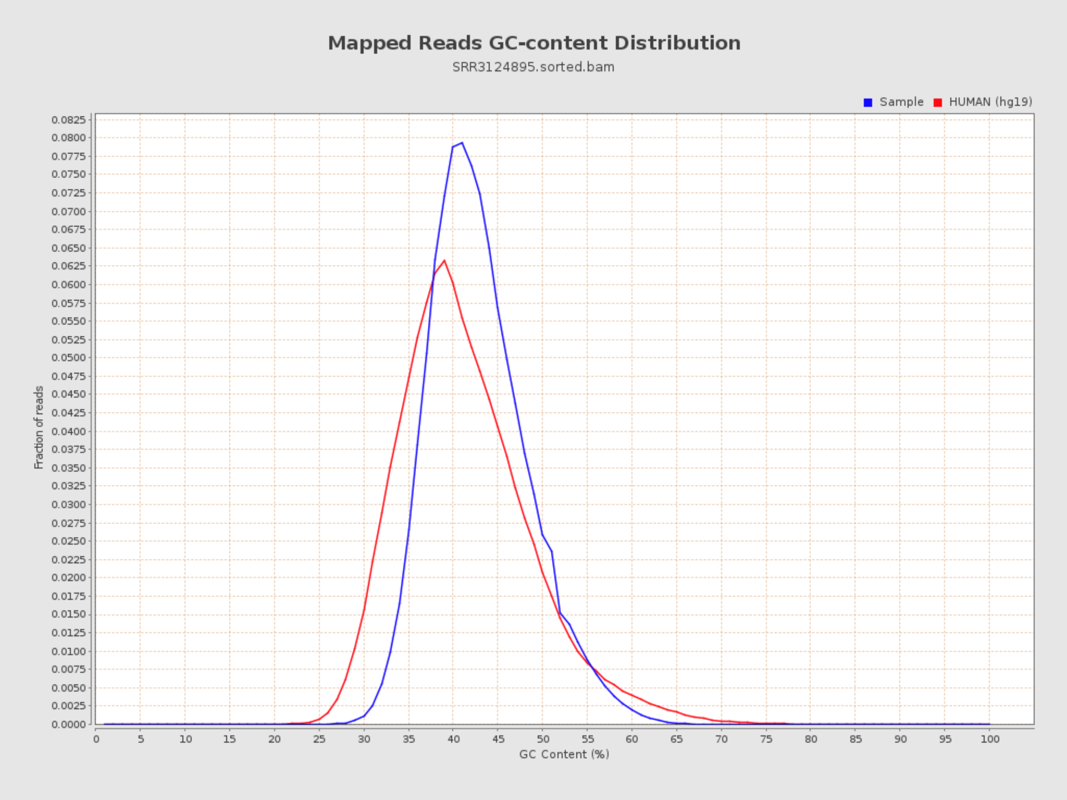
7. Results : Duplication Rate Histogram



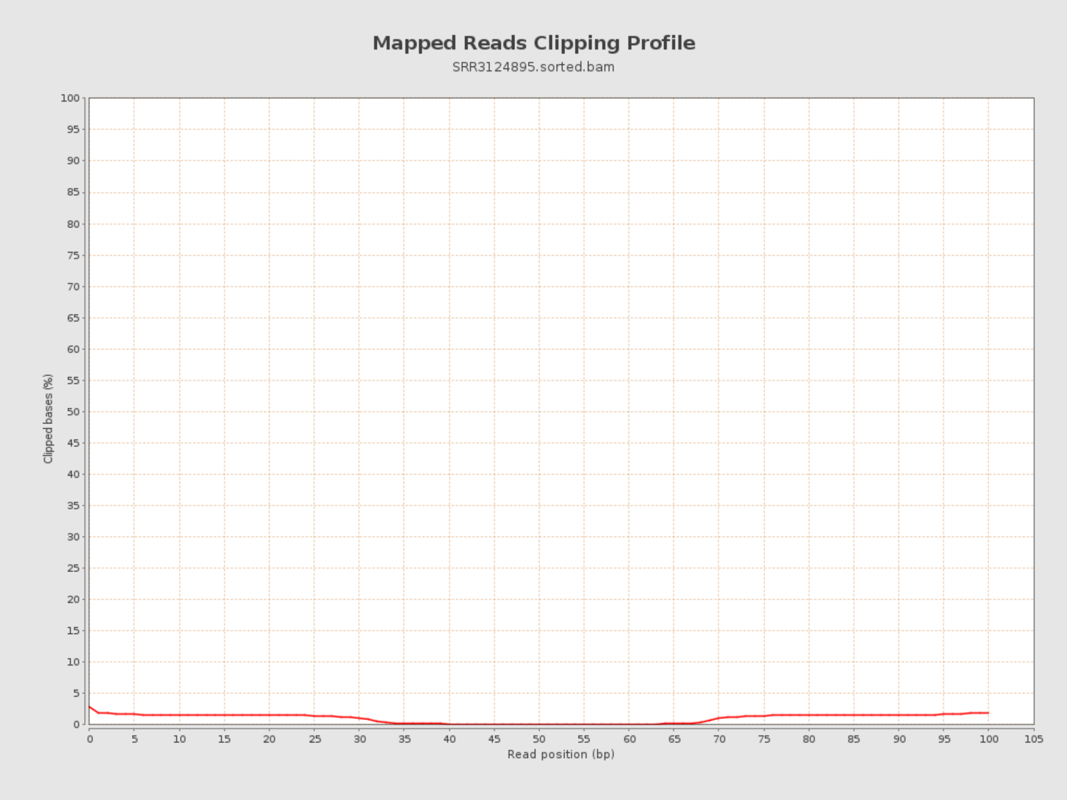
8. Results : Mapped Reads Nucleotide Content



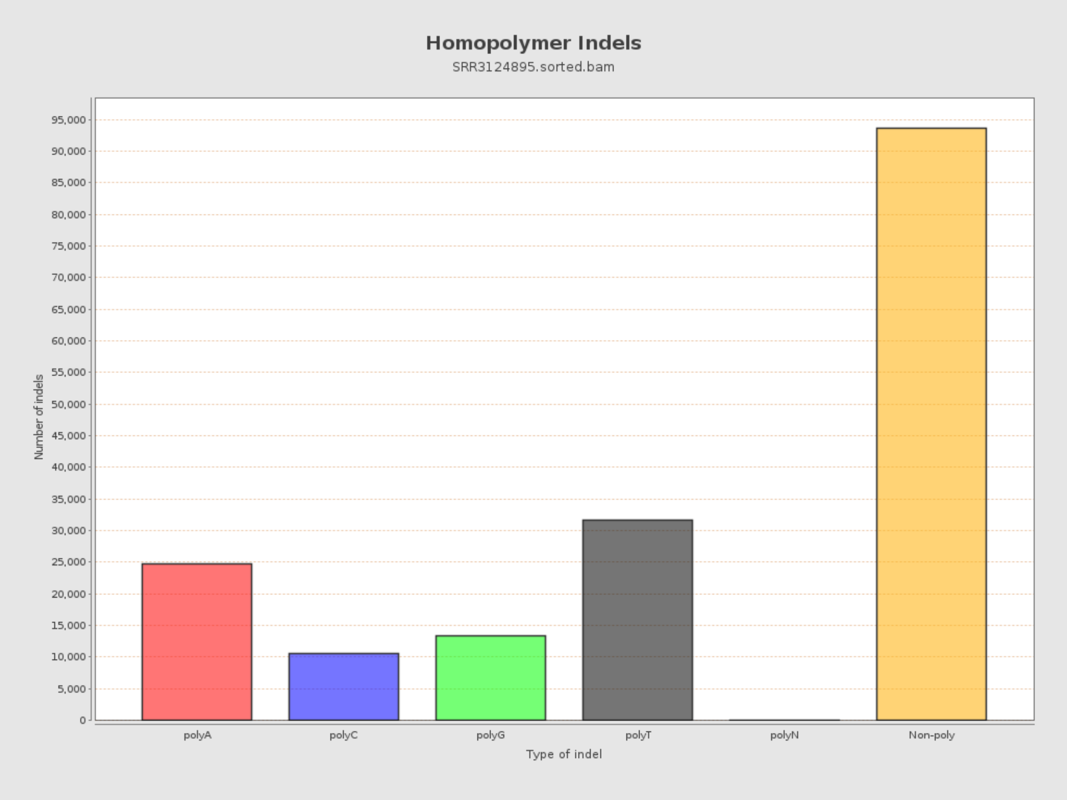
9. Results : Mapped Reads GC-content Distribution



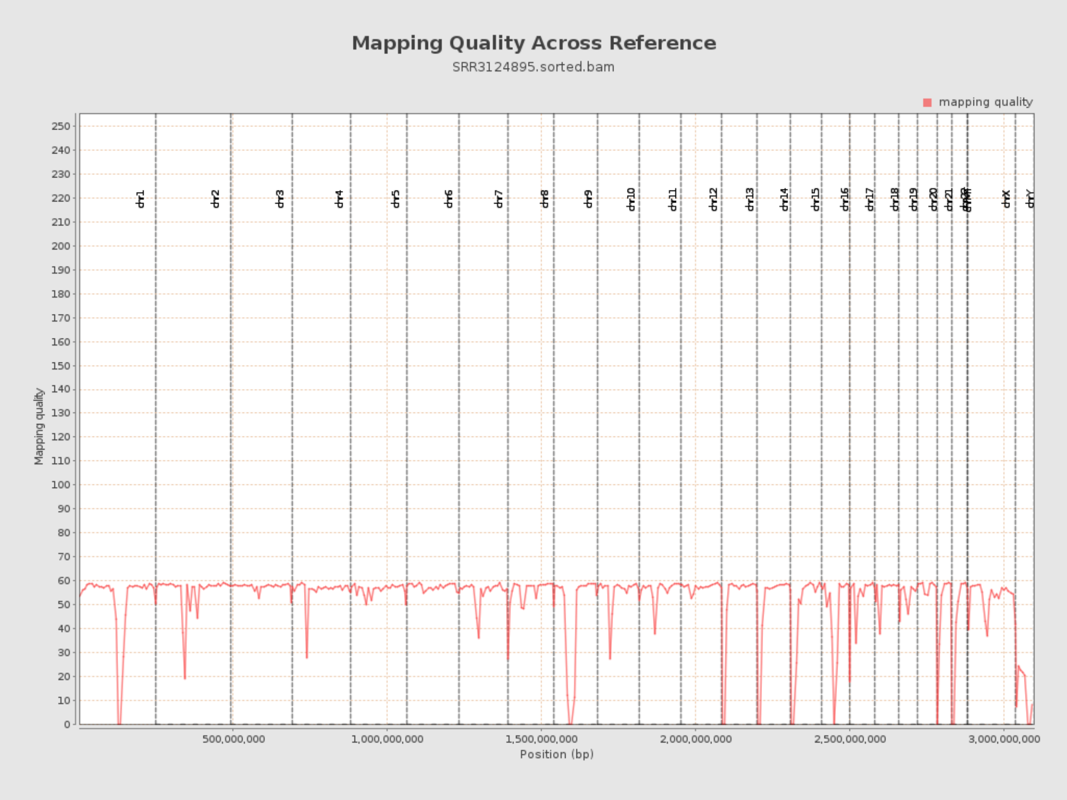
10. Results : Mapped Reads Clipping Profile



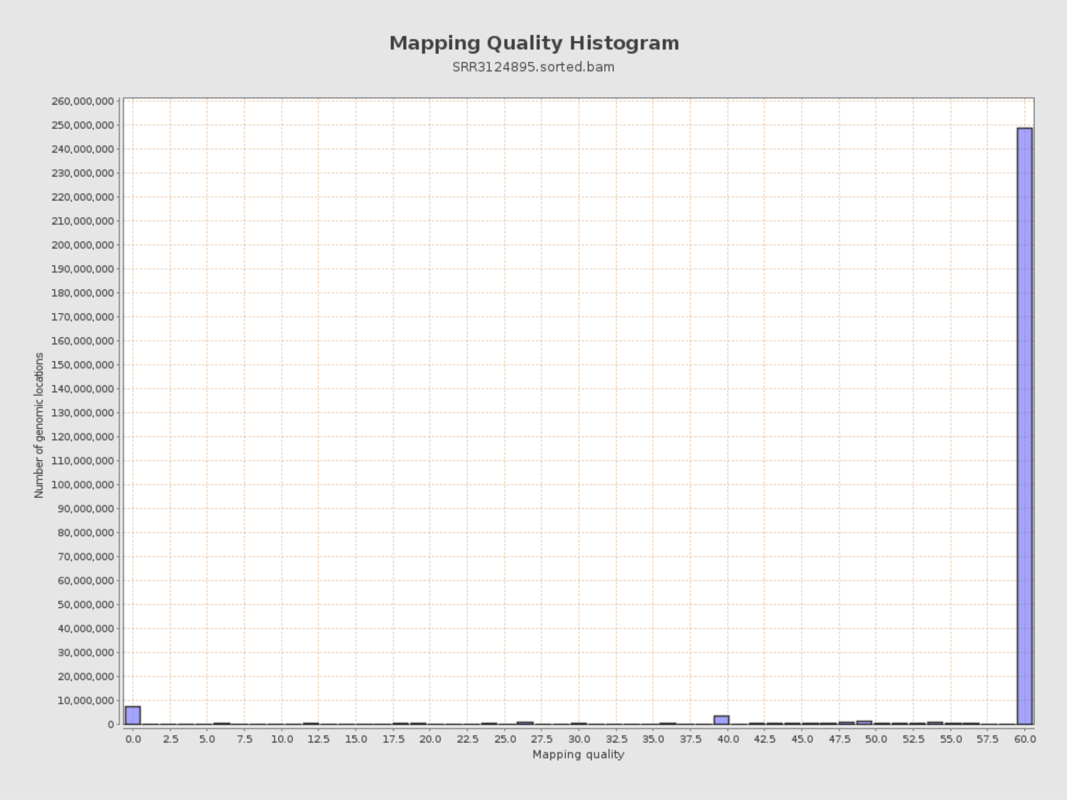
11. Results : Homopolymer Indels



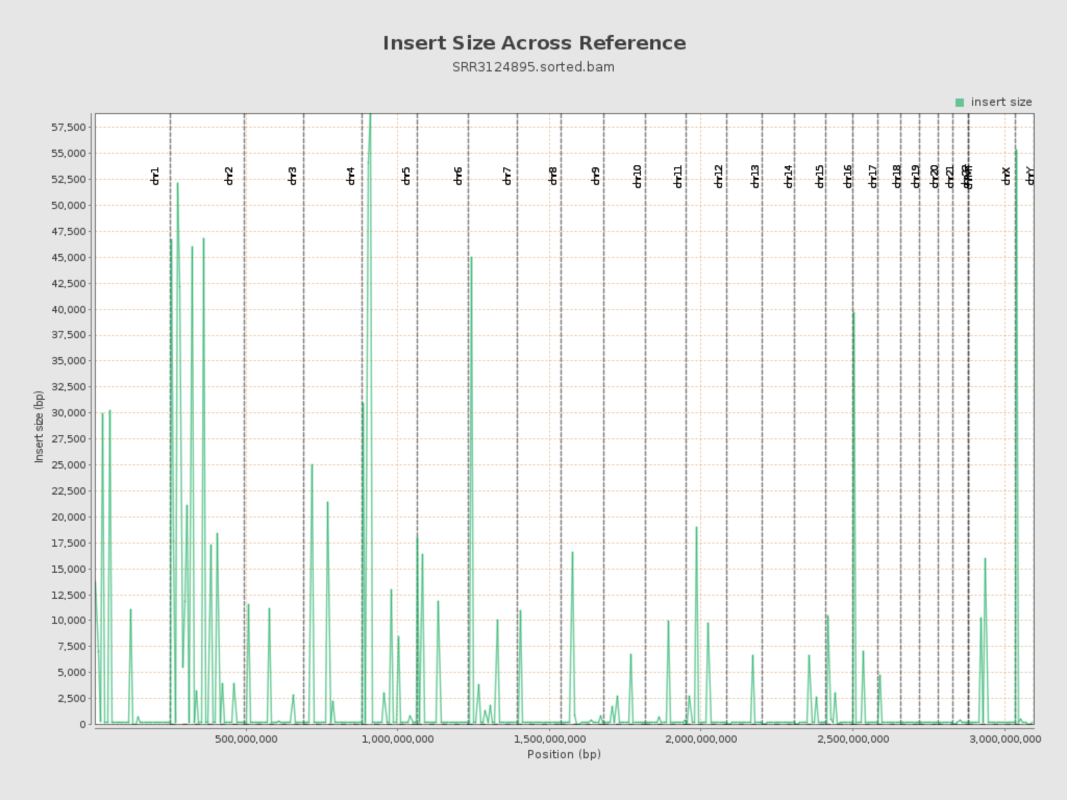
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram