Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 02:20:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124896.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_SRR3124896 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124896_1.fastq.gz SRR3124896_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 02:20:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124896.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,093,936
Mapped reads	4,020,590 / 98.21%
Unmapped reads	73,346 / 1.79%
Mapped paired reads	4,020,590 / 98.21%
Mapped reads, first in pair	2,014,712 / 49.21%
Mapped reads, second in pair	2,005,878 / 49%
Mapped reads, both in pair	4,003,460 / 97.79%
Mapped reads, singletons	17,130 / 0.42%
Secondary alignments	0
Supplementary alignments	18,695 / 0.46%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	318,196 / 7.77%
Duplication rate	5.78%
Clipped reads	1,974,488 / 48.23%

2.2. ACGT Content

Number/percentage of A's	97,160,181 / 27.99%
Number/percentage of C's	64,737,872 / 18.65%
Number/percentage of T's	103,134,411 / 29.71%
Number/percentage of G's	81,981,692 / 23.62%
Number/percentage of N's	130,926 / 0.04%

GC Percentage	42.26%

2.3. Coverage

Mean	0.1122
Standard Deviation	0.9378

2.4. Mapping Quality

Mean Mapping Quality	52.66

2.5. Insert size

Mean	34,744.39
Standard Deviation	1,751,640.51
P25/Median/P75	147 / 198 / 276

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	2,664,141
Insertions	51,766
Mapped reads with at least one insertion	1.25%
Deletions	124,436
Mapped reads with at least one deletion	3.03%
Homopolymer indels	46.87%

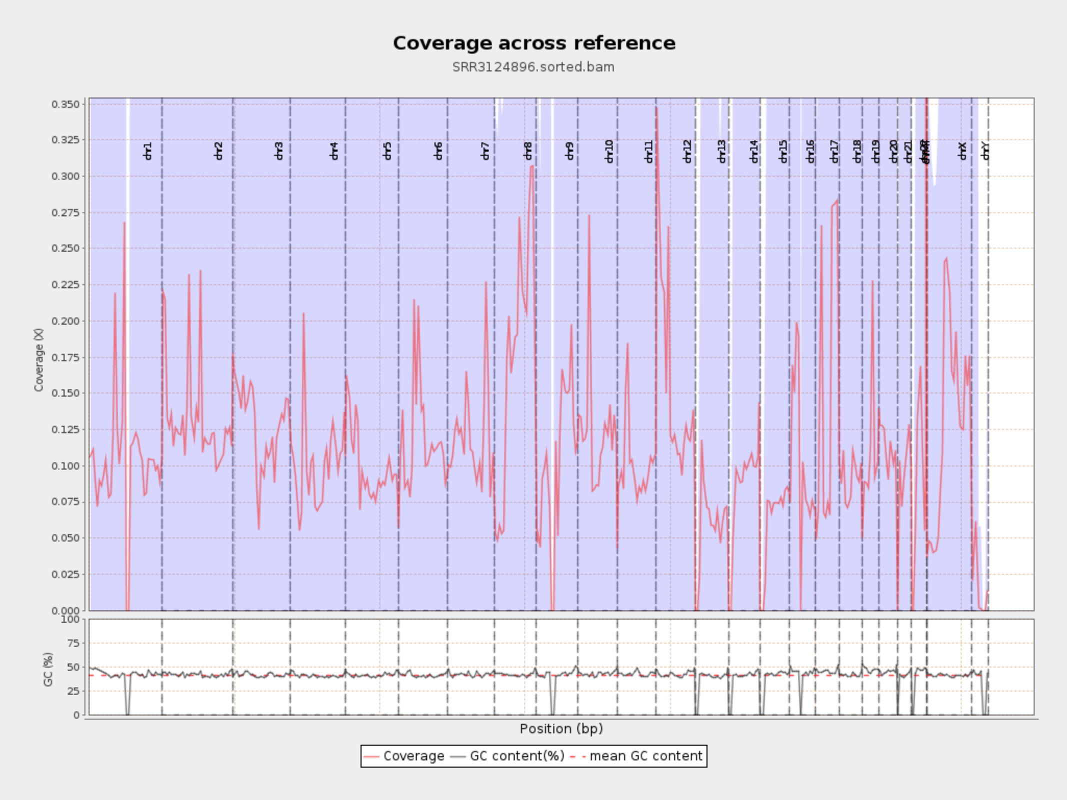
2.7. Chromosome stats

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

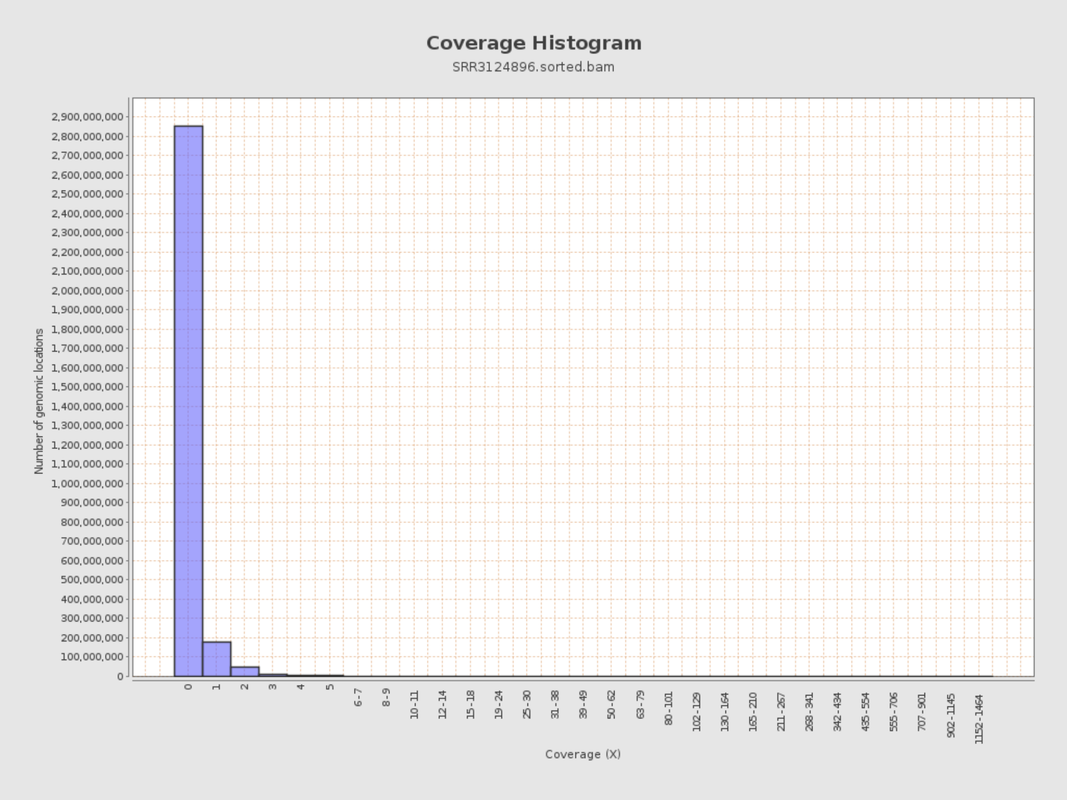
		bases	coverage	deviation
chr1	249250621	25866474	0.1038	1.0003
chr2	243199373	32513989	0.1337	1.4824
chr3	198022430	25400143	0.1283	0.467
chr4	191154276	19151130	0.1002	0.7268
chr5	180915260	18019075	0.0996	0.4353
chr6	171115067	20123249	0.1176	0.7851
chr7	159138663	19259944	0.121	1.1608
chr8	146364022	25672427	0.1754	0.8172
chr9	141213431	14237006	0.1008	1.2943
chr10	135534747	16727691	0.1234	1.4639
chr11	135006516	13499256	0.1	0.8854
chr12	133851895	21636692	0.1616	0.5514
chr13	115169878	6801952	0.0591	0.3113
chr14	107349540	8930015	0.0832	0.4088
chr15	102531392	6282053	0.0613	0.3182
chr16	90354753	9470543	0.1048	0.9492
chr17	81195210	12502187	0.154	1.6119
chr18	78077248	7167299	0.0918	1.1996
chr19	59128983	6619512	0.112	0.6317
chr20	63025520	6977869	0.1107	0.4925
chr21	48129895	4424159	0.0919	0.5212
chr22	51304566	4221012	0.0823	0.4064
chrMT	16571	578523	34.9118	22.2884
chrX	155270560	20284441	0.1306	0.5928

chrY	59373566	995593	0.0168	1.1519

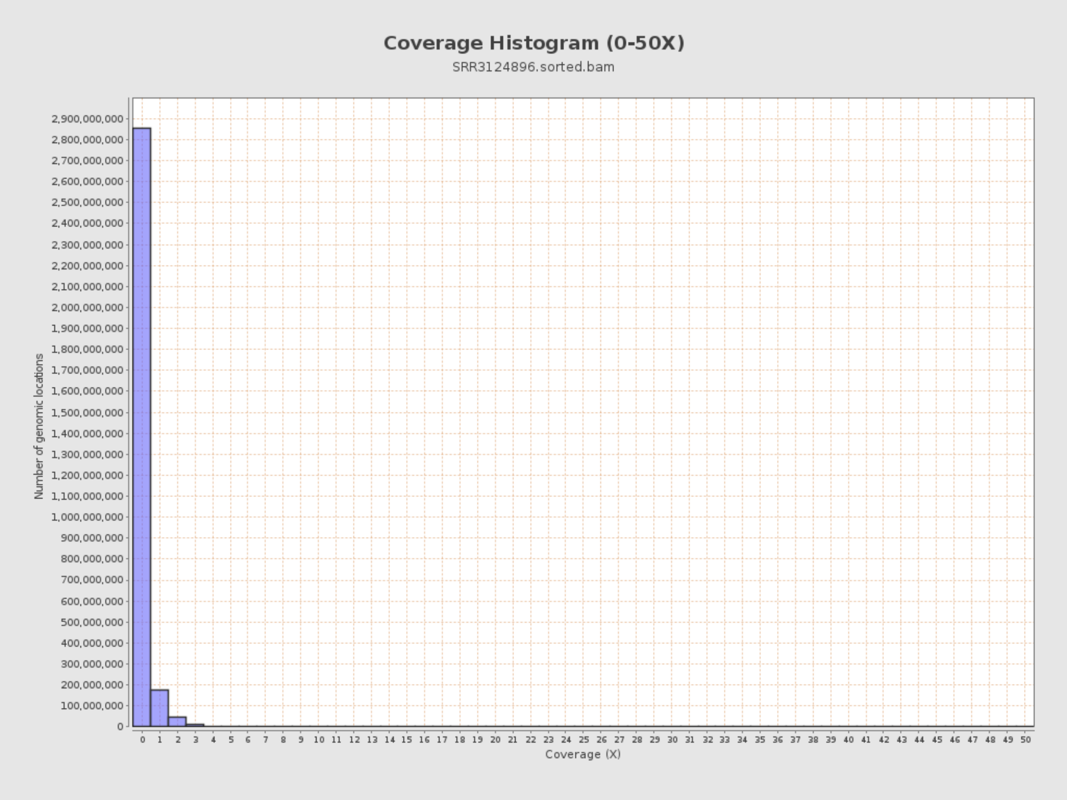
3. Results : Coverage across reference



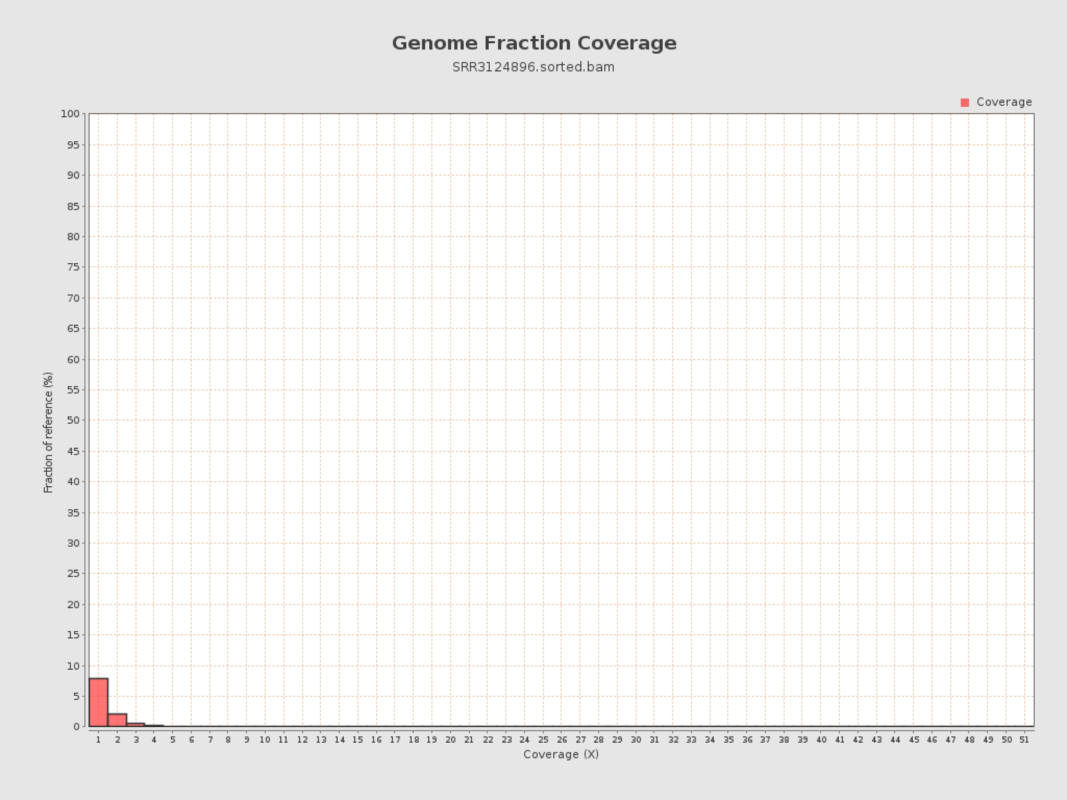
4. Results : Coverage Histogram



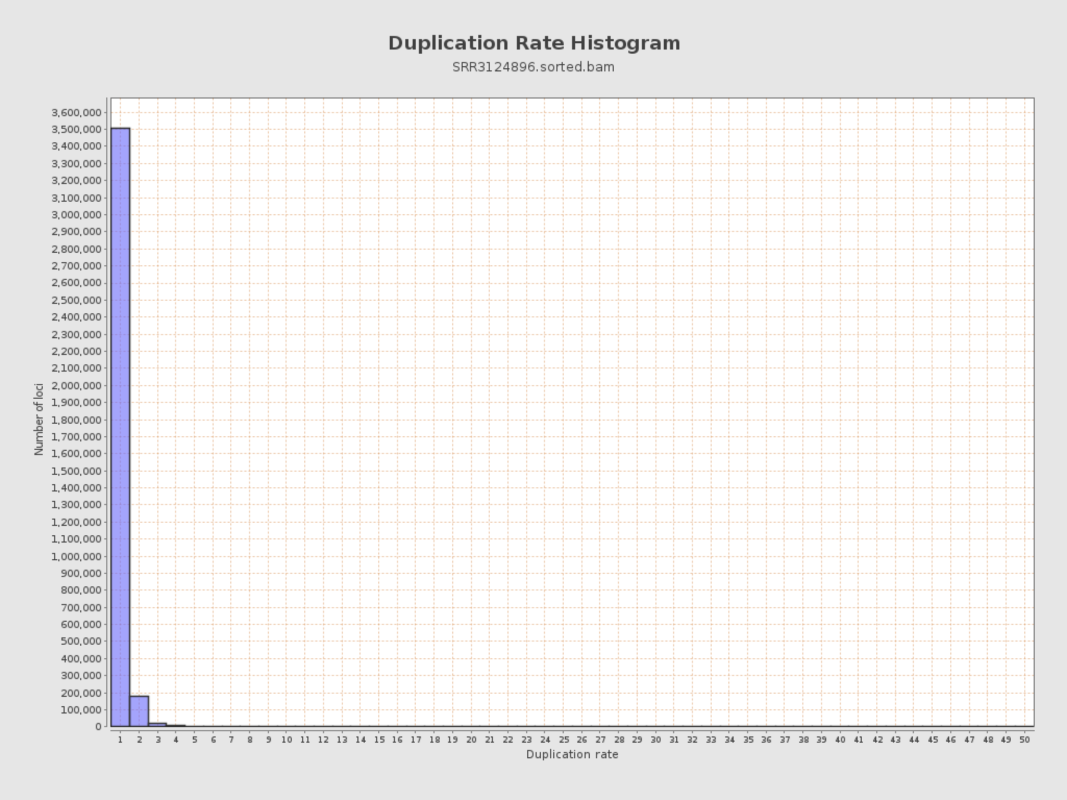
5. Results : Coverage Histogram (0-50X)



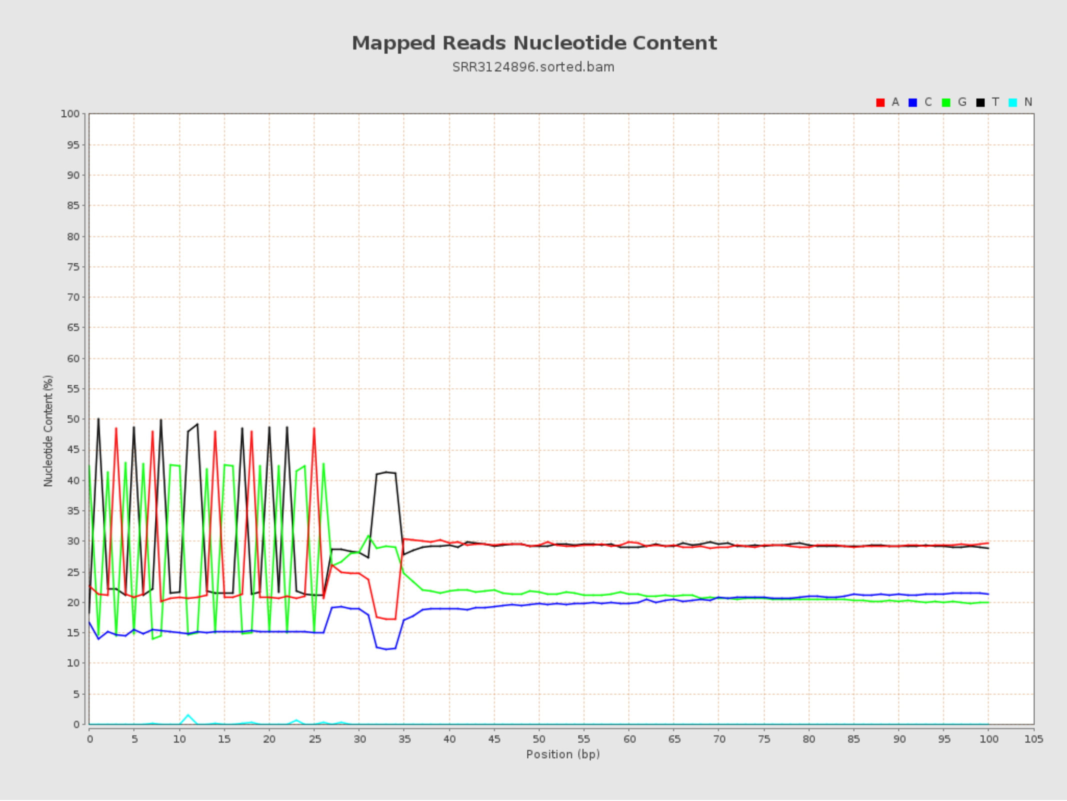
6. Results : Genome Fraction Coverage



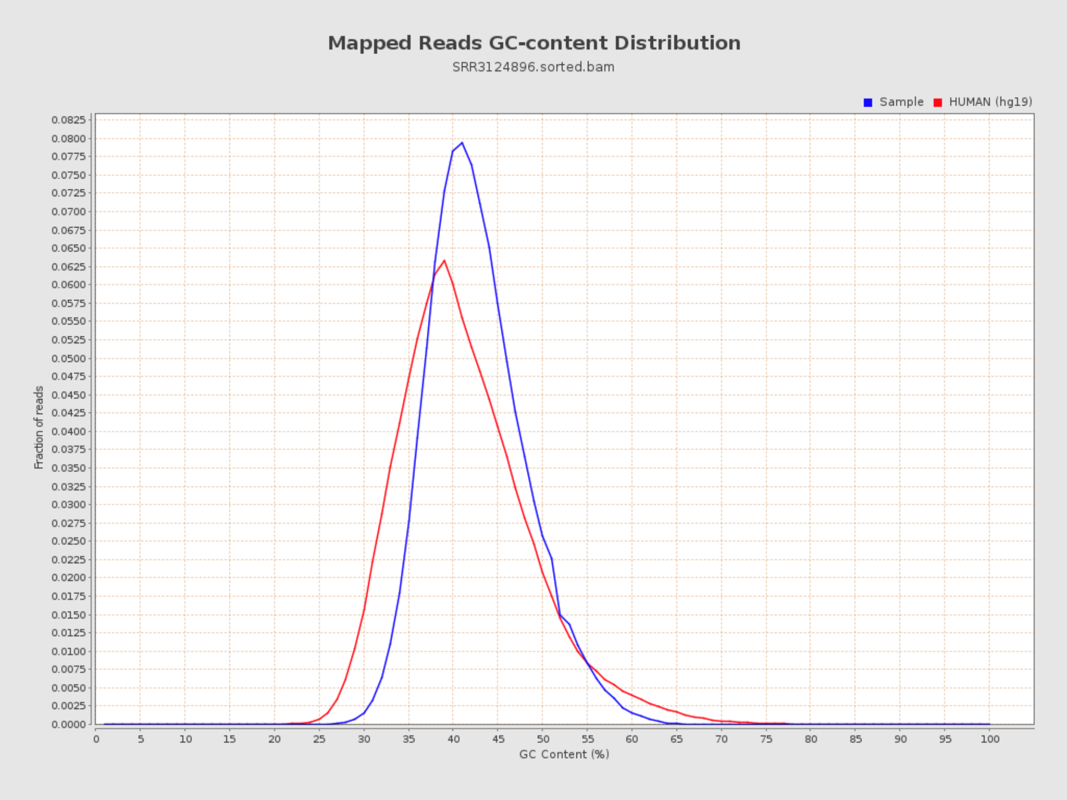
7. Results : Duplication Rate Histogram



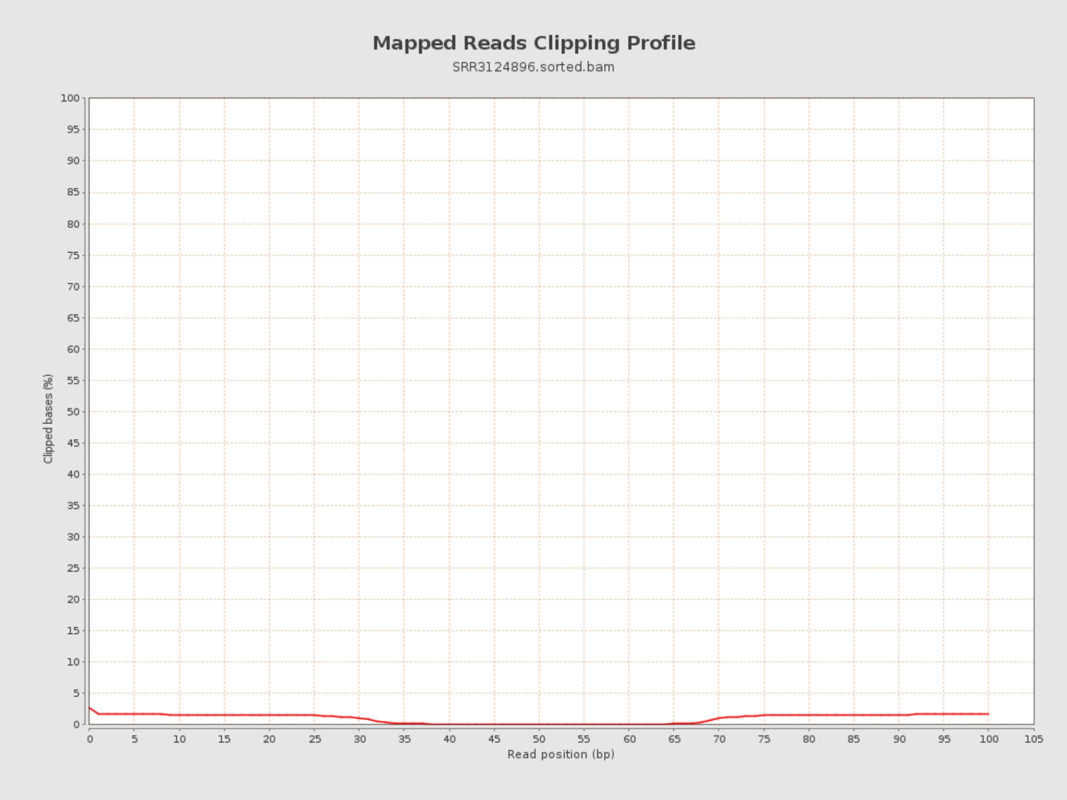
8. Results : Mapped Reads Nucleotide Content



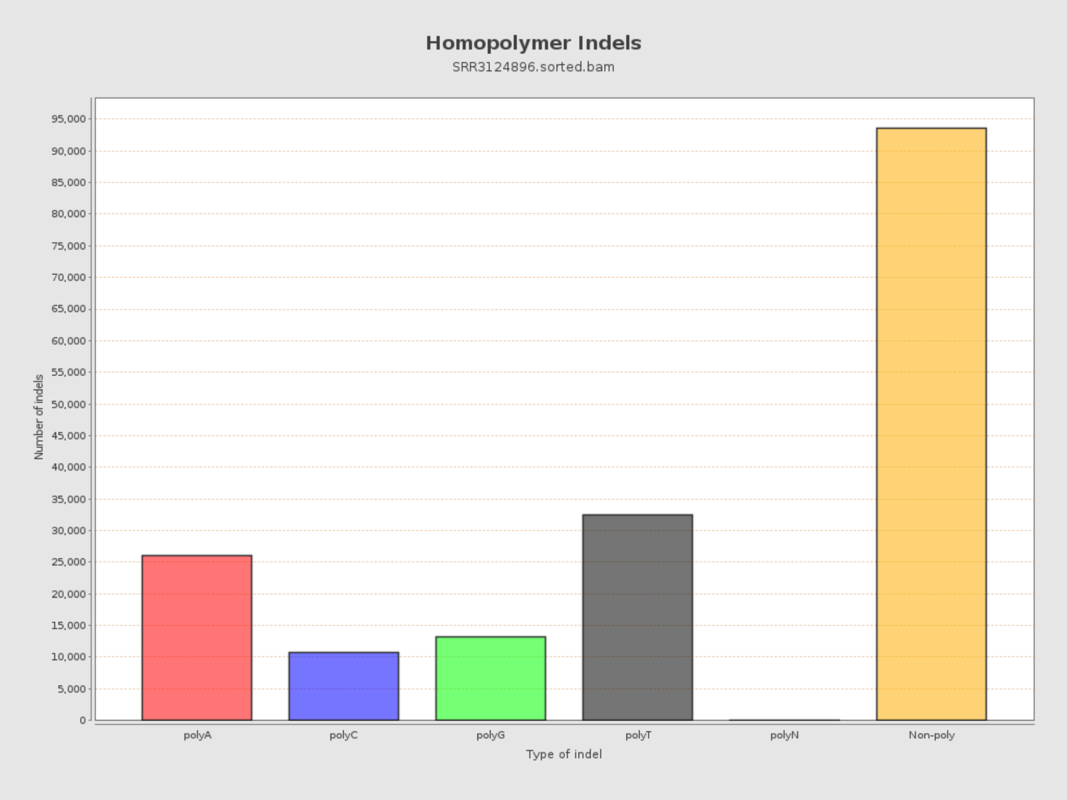
9. Results : Mapped Reads GC-content Distribution



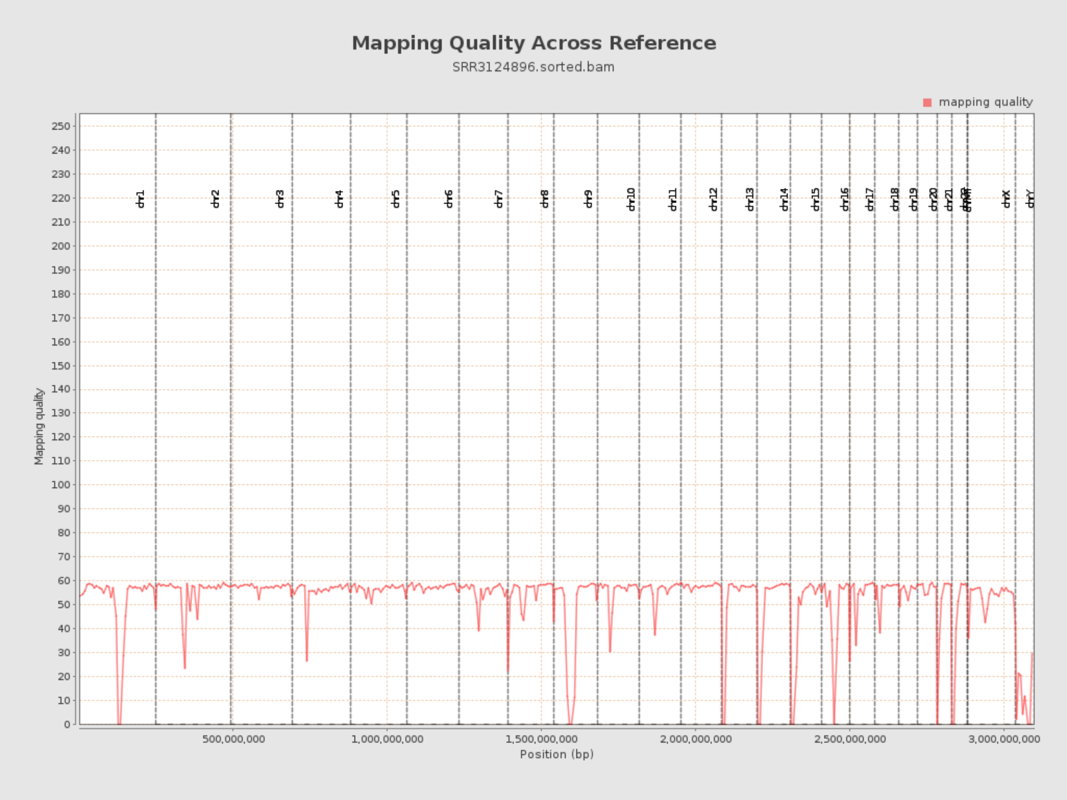
10. Results : Mapped Reads Clipping Profile



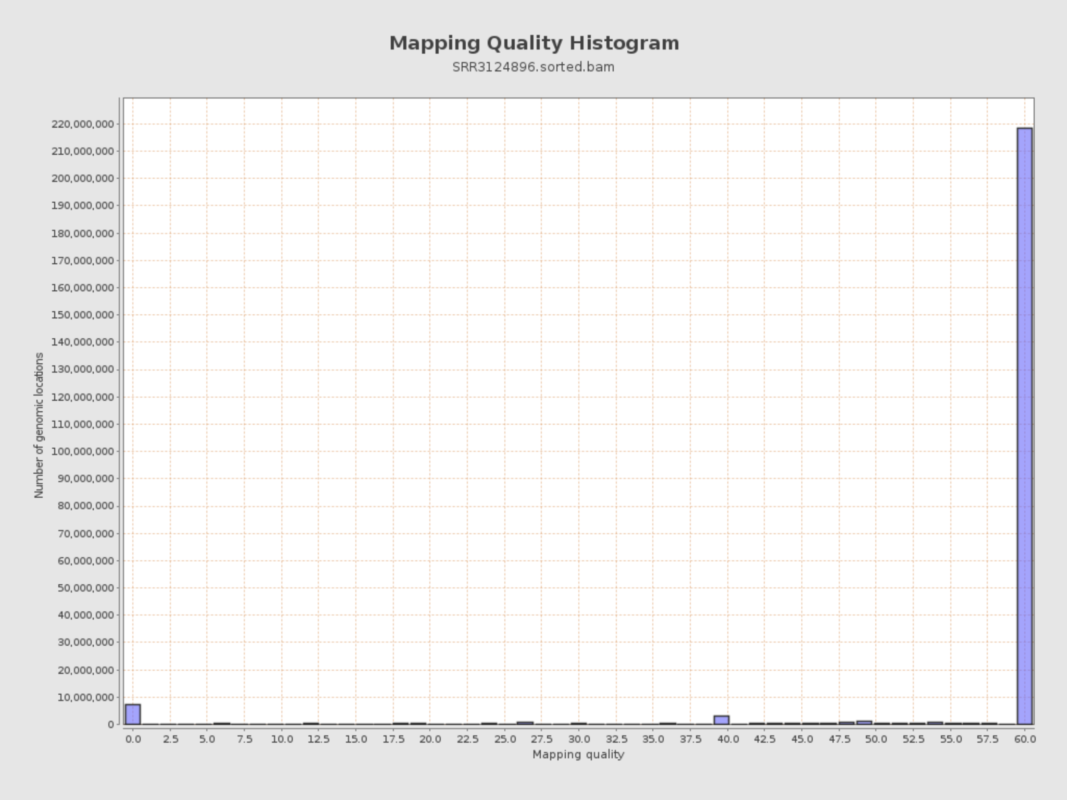
11. Results : Homopolymer Indels



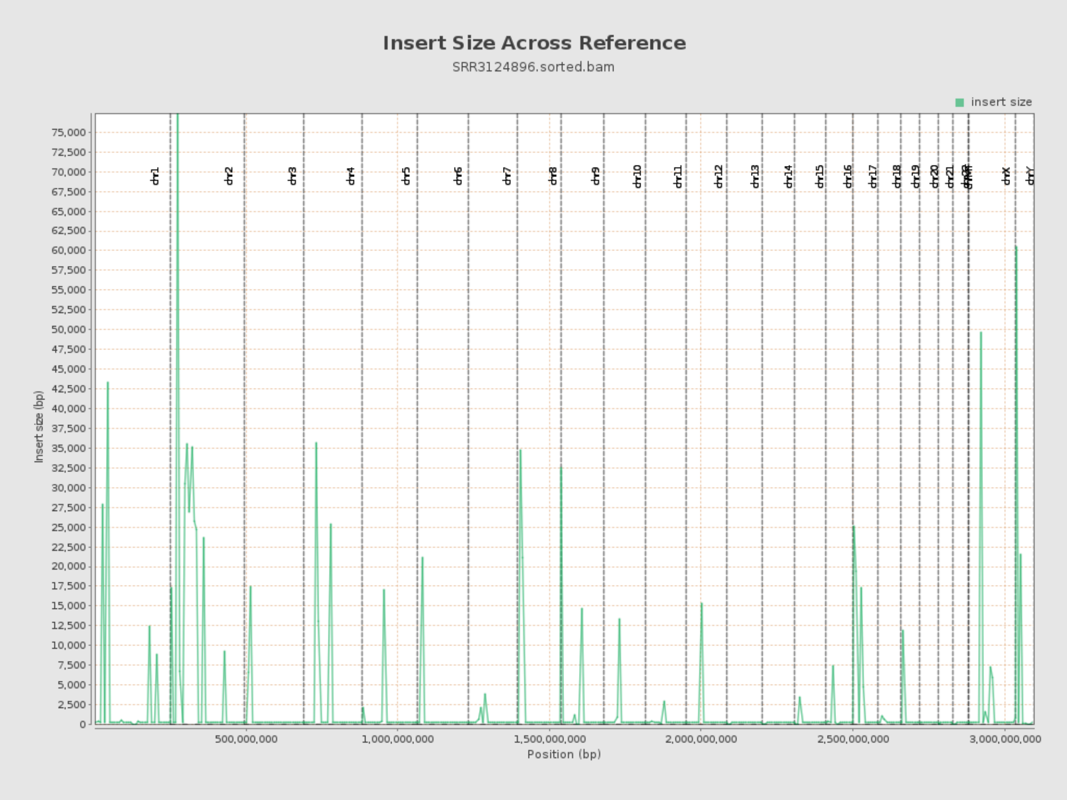
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram