Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 13:07:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124982.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_SRR3124982 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124982_1.fastq.gz SRR3124982_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 13:07:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124982.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,897,572
Mapped reads	5,793,969 / 98.24%
Unmapped reads	103,603 / 1.76%
Mapped paired reads	5,793,969 / 98.24%
Mapped reads, first in pair	2,903,647 / 49.23%
Mapped reads, second in pair	2,890,322 / 49.01%
Mapped reads, both in pair	5,763,572 / 97.73%
Mapped reads, singletons	30,397 / 0.52%
Secondary alignments	0
Supplementary alignments	58,994 / 1%
Read min/max/mean length	30 / 101 / 101.4
Duplicated reads (estimated)	653,684 / 11.08%
Duplication rate	7.49%
Clipped reads	3,166,325 / 53.69%

2.2. ACGT Content

Number/percentage of A's	141,856,257 / 28.64%
Number/percentage of C's	91,147,363 / 18.4%
Number/percentage of T's	150,042,485 / 30.3%
Number/percentage of G's	112,194,189 / 22.65%
Number/percentage of N's	5,248 / 0%

GC Percentage	41.06%

2.3. Coverage

Mean	0.1601
Standard Deviation	2.1137

2.4. Mapping Quality

Mean Mapping Quality	52.36

2.5. Insert size

Mean	95,421.96
Standard Deviation	2,900,358.72
P25/Median/P75	132 / 178 / 242

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	3,805,929
Insertions	78,593
Mapped reads with at least one insertion	1.31%
Deletions	158,611
Mapped reads with at least one deletion	2.67%
Homopolymer indels	45.69%

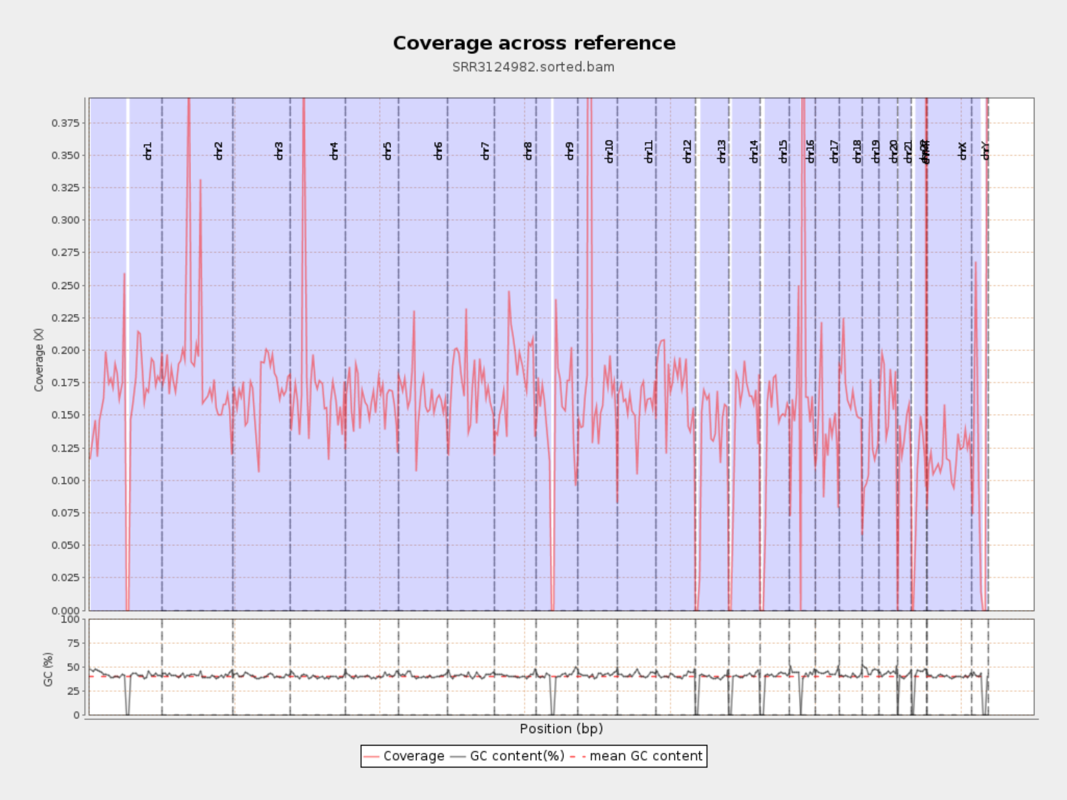
2.7. Chromosome stats

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

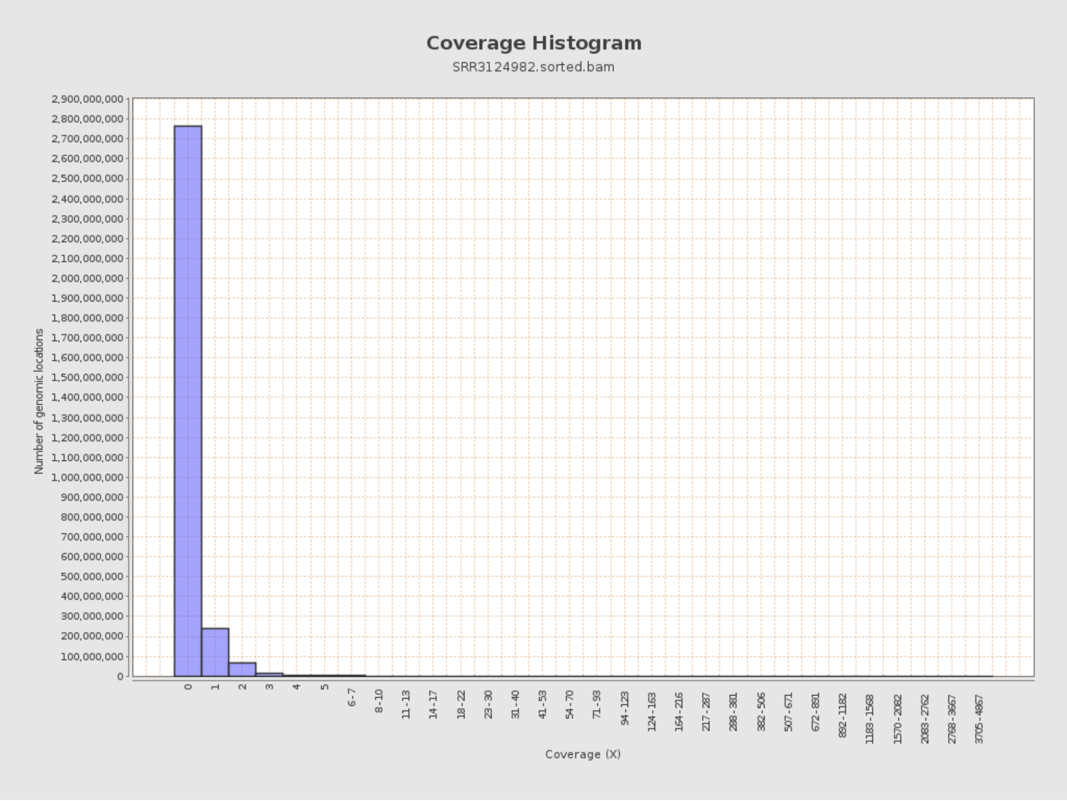
		bases	coverage	deviation
chr1	249250621	40450303	0.1623	1.6118
chr2	243199373	46489588	0.1912	2.5363
chr3	198022430	33433452	0.1688	0.6197
chr4	191154276	32825167	0.1717	1.6675
chr5	180915260	29258815	0.1617	0.5751
chr6	171115067	28100406	0.1642	0.894
chr7	159138663	27721995	0.1742	1.4469
chr8	146364022	26385579	0.1803	0.7921
chr9	141213431	20573725	0.1457	2.1
chr10	135534747	27996333	0.2066	7.2062
chr11	135006516	21210581	0.1571	1.0613
chr12	133851895	23465115	0.1753	0.5686
chr13	115169878	14272243	0.1239	0.4631
chr14	107349540	14951031	0.1393	0.6313
chr15	102531392	13339934	0.1301	0.4969
chr16	90354753	16558493	0.1833	3.3023
chr17	81195210	11012475	0.1356	1.6002
chr18	78077248	13187697	0.1689	2.2533
chr19	59128983	6992001	0.1182	0.9699
chr20	63025520	10416978	0.1653	0.7333
chr21	48129895	5932611	0.1233	0.8523
chr22	51304566	4558965	0.0889	0.4745
chrMT	16571	352373	21.2644	12.4202
chrX	155270560	18206408	0.1173	0.7102

chrY	59373566	7851638	0.1322	3.2418

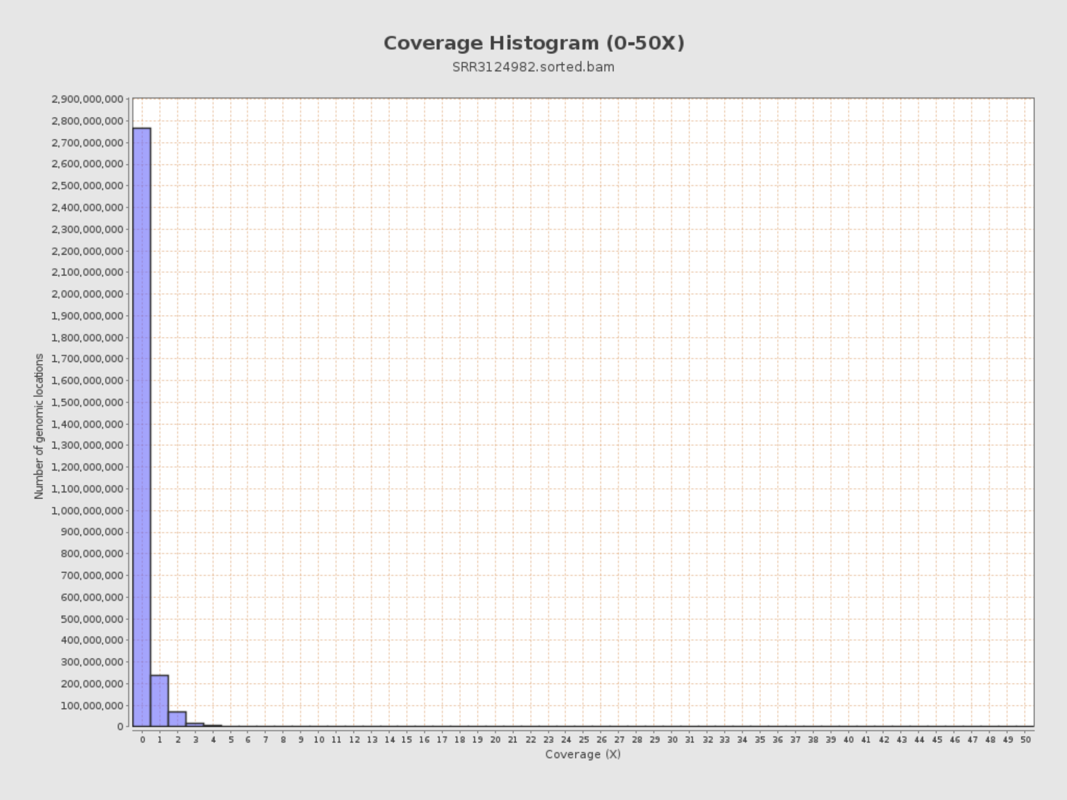
3. Results : Coverage across reference



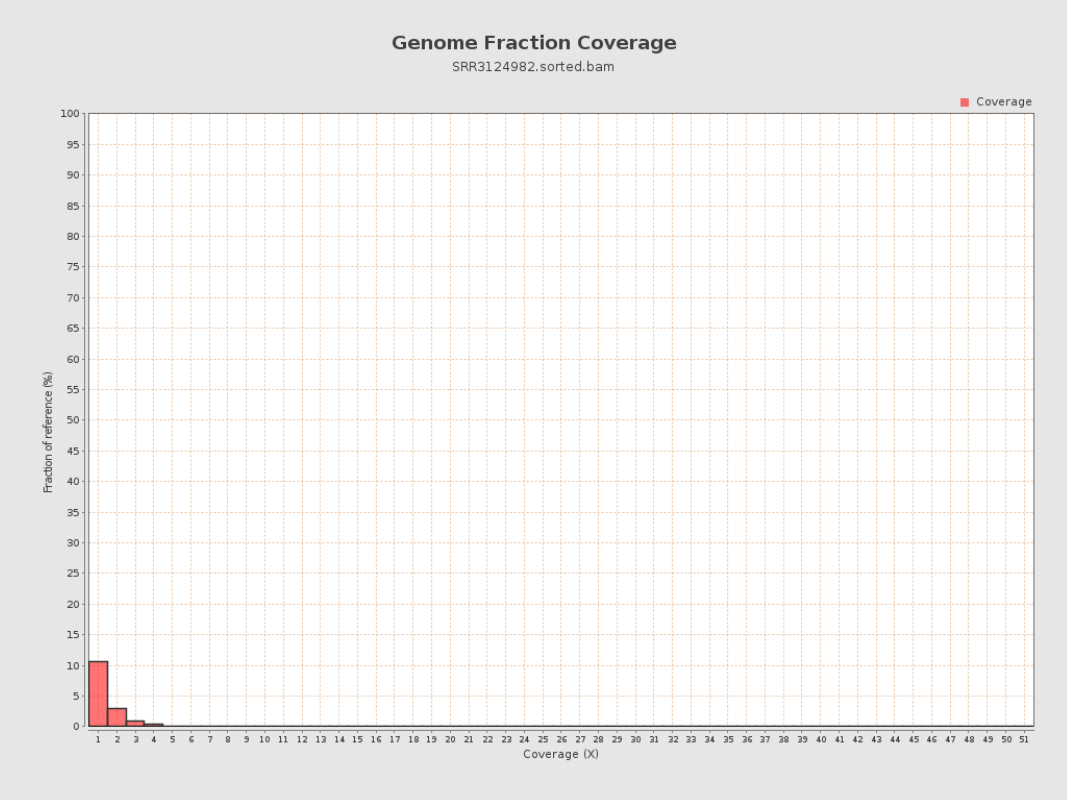
4. Results : Coverage Histogram



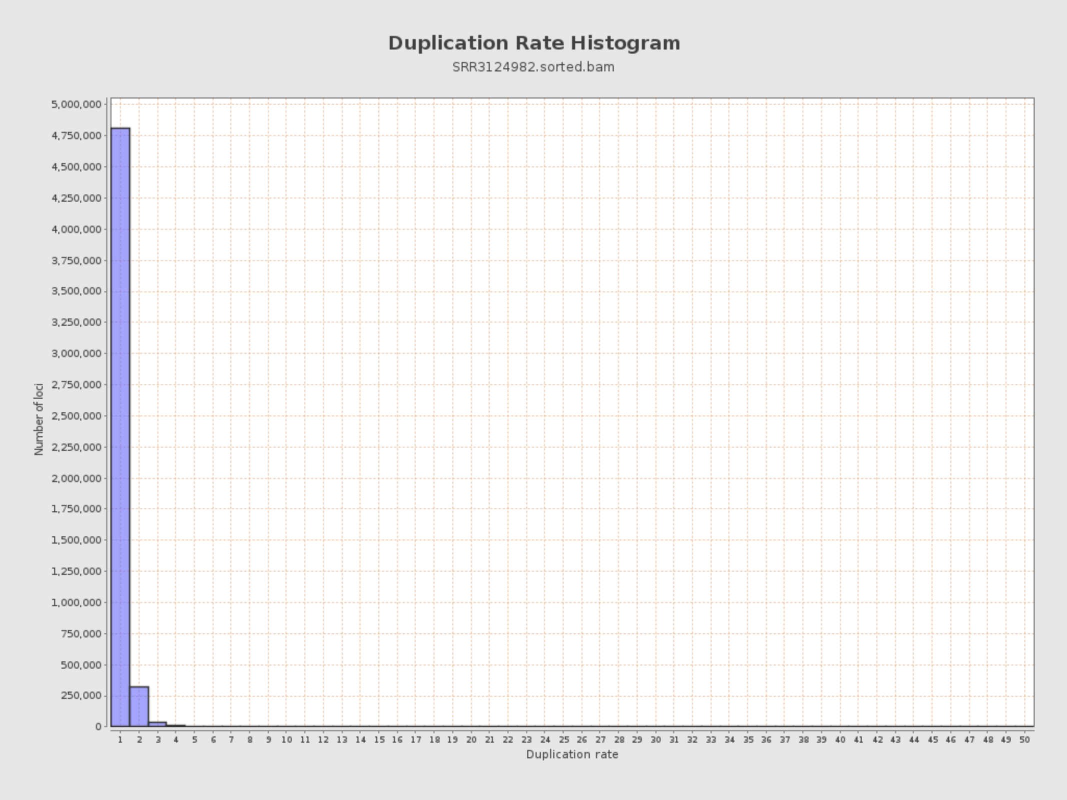
5. Results : Coverage Histogram (0-50X)



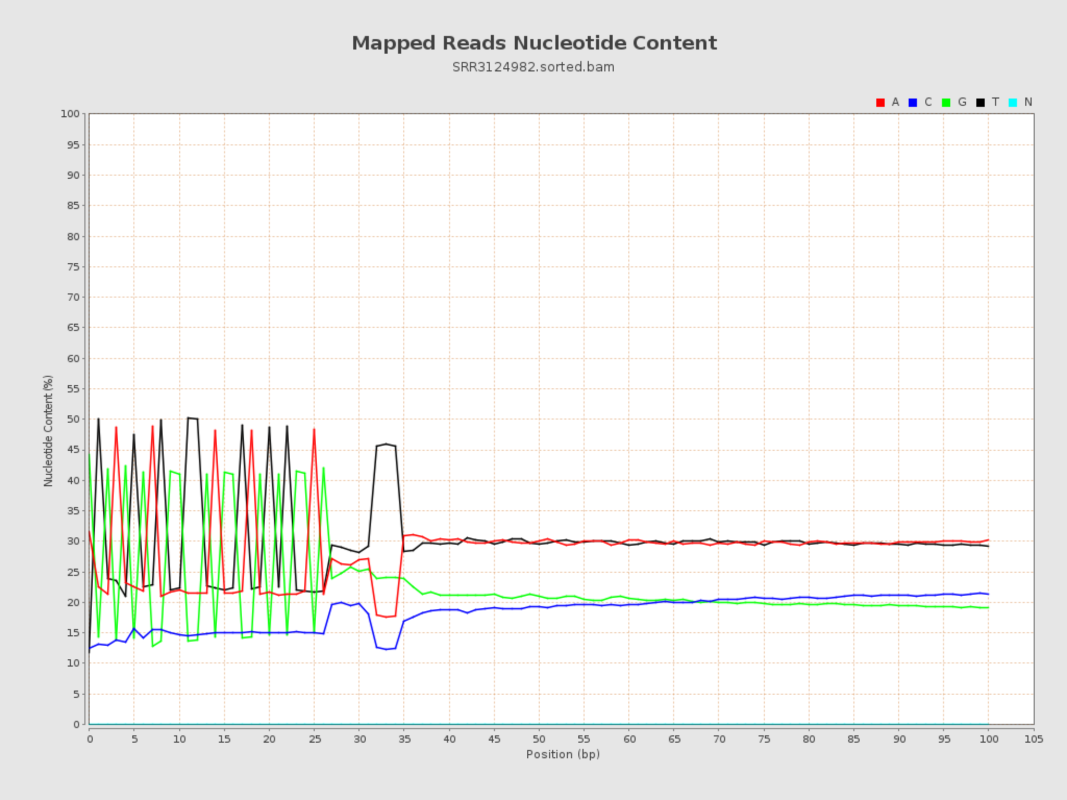
6. Results : Genome Fraction Coverage



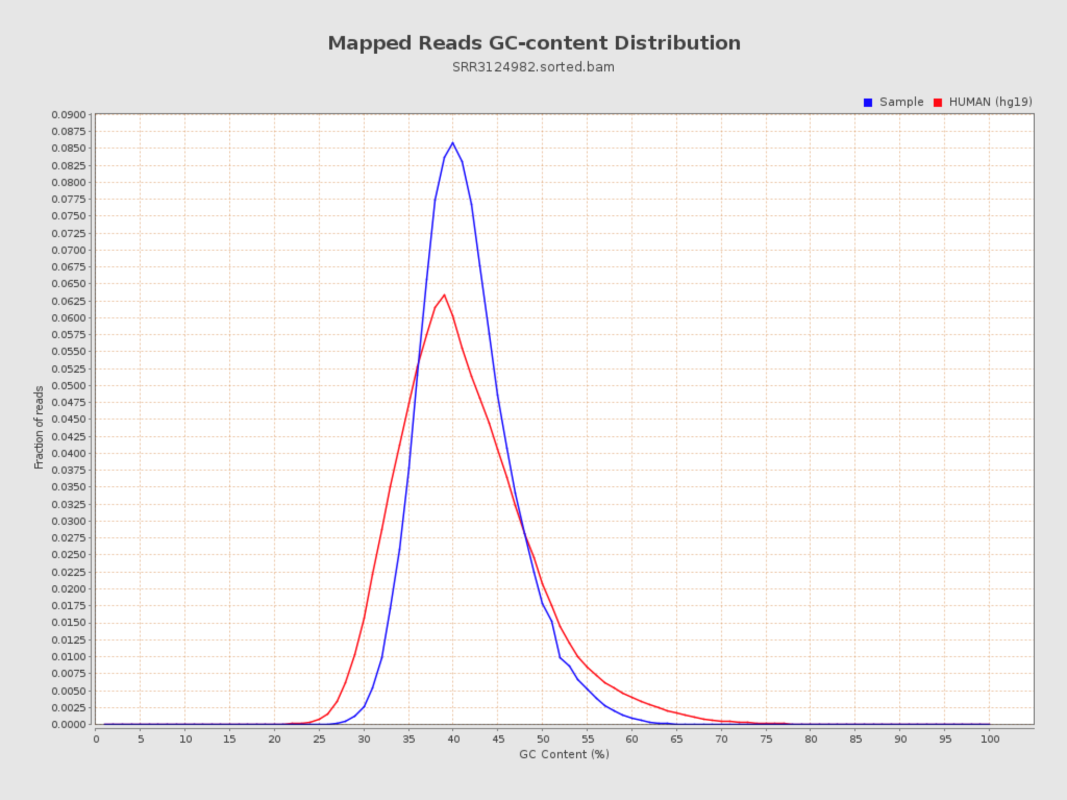
7. Results : Duplication Rate Histogram



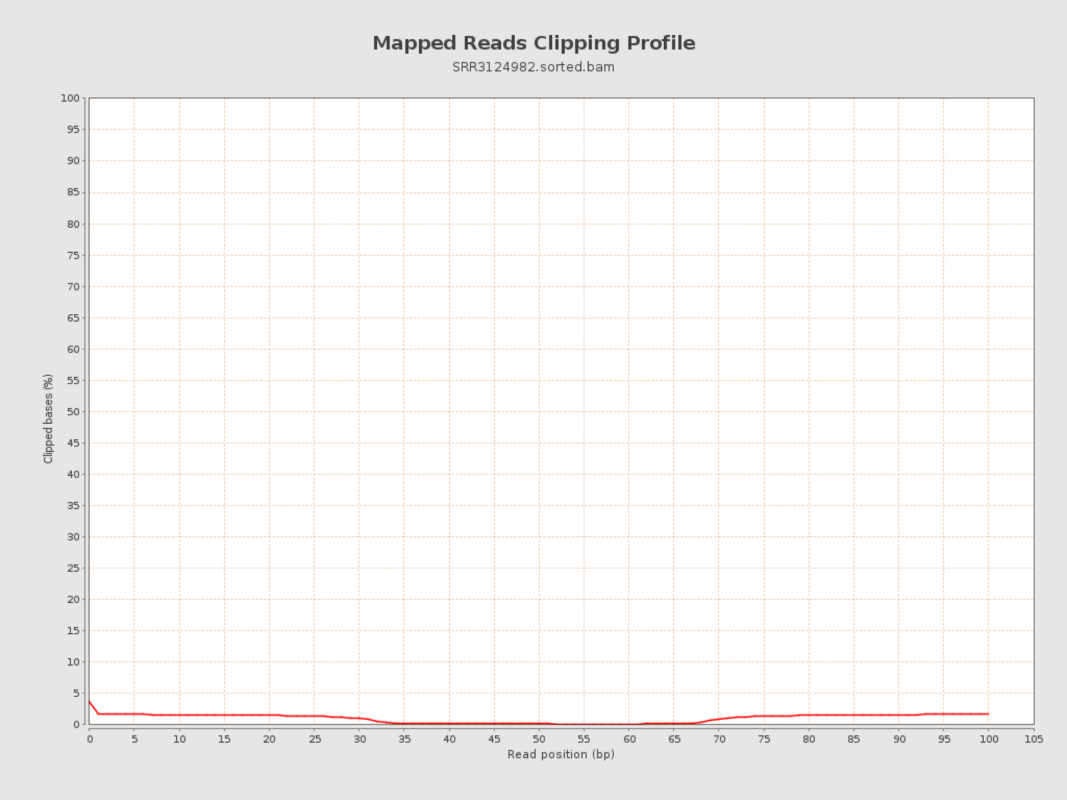
8. Results : Mapped Reads Nucleotide Content



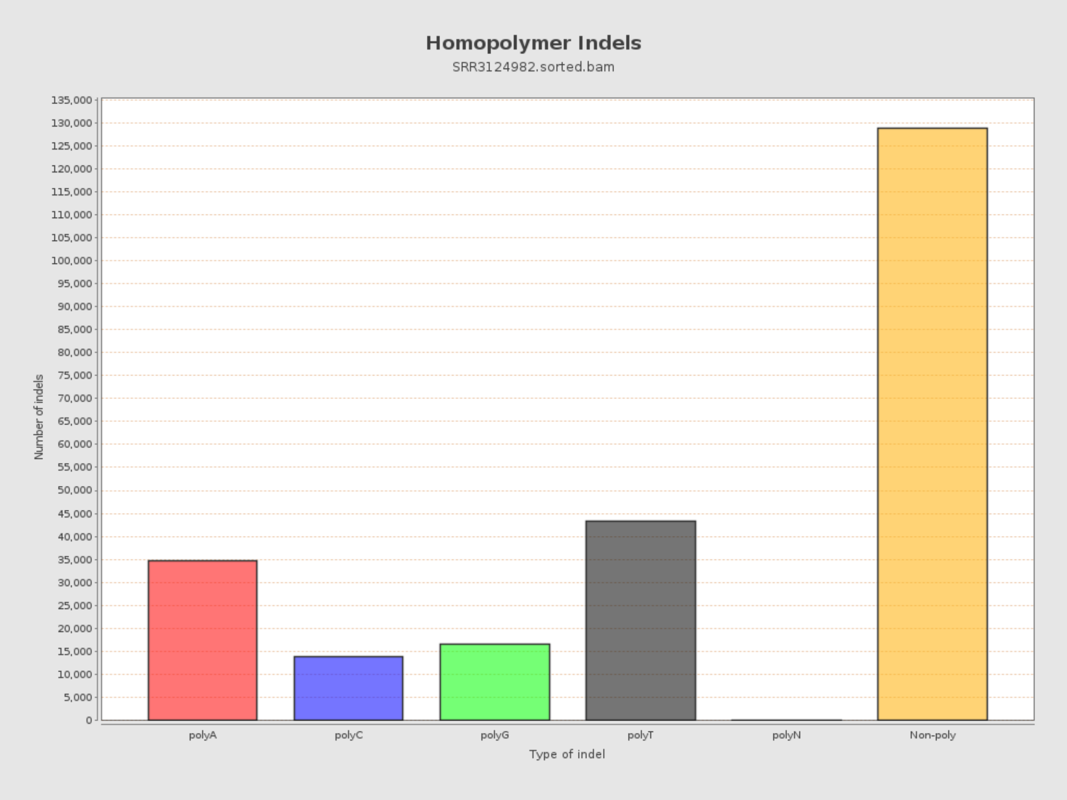
9. Results : Mapped Reads GC-content Distribution



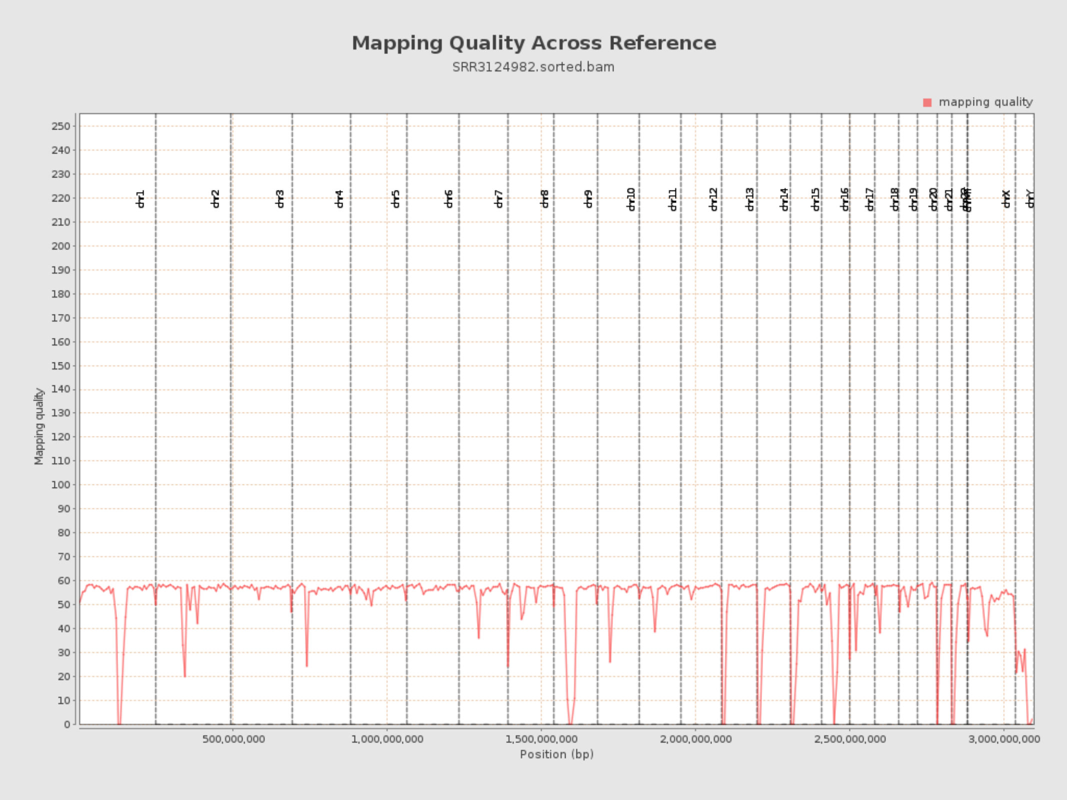
10. Results : Mapped Reads Clipping Profile



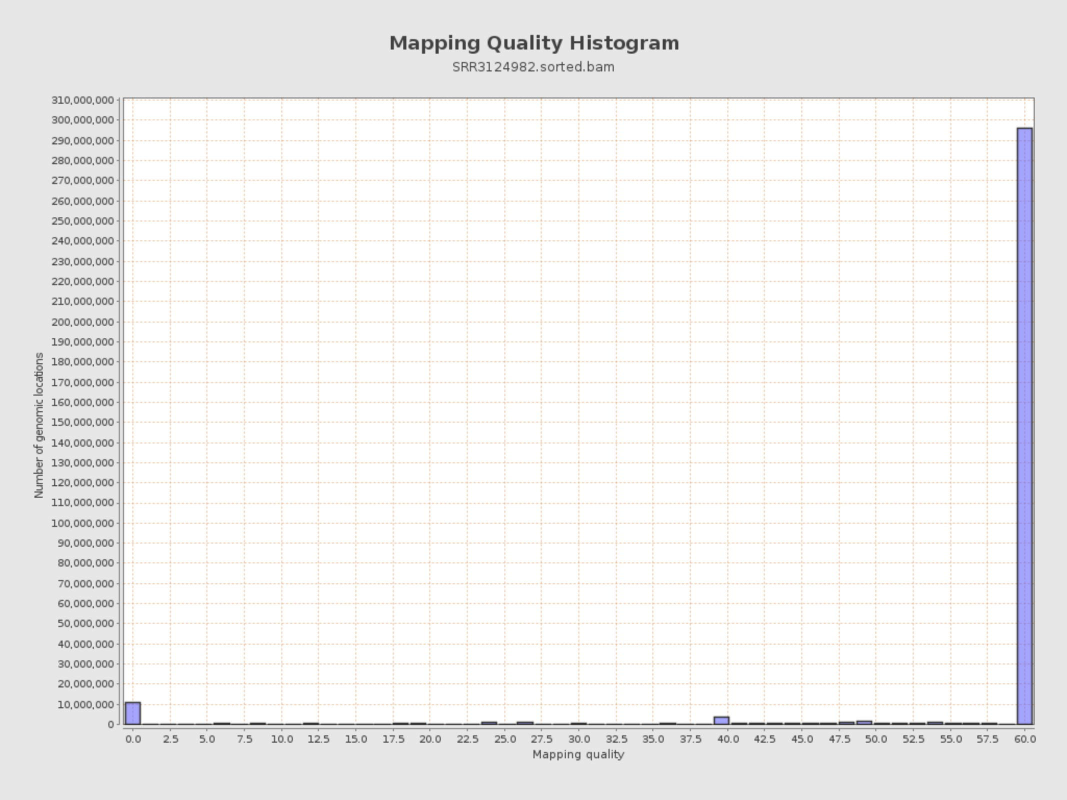
11. Results : Homopolymer Indels



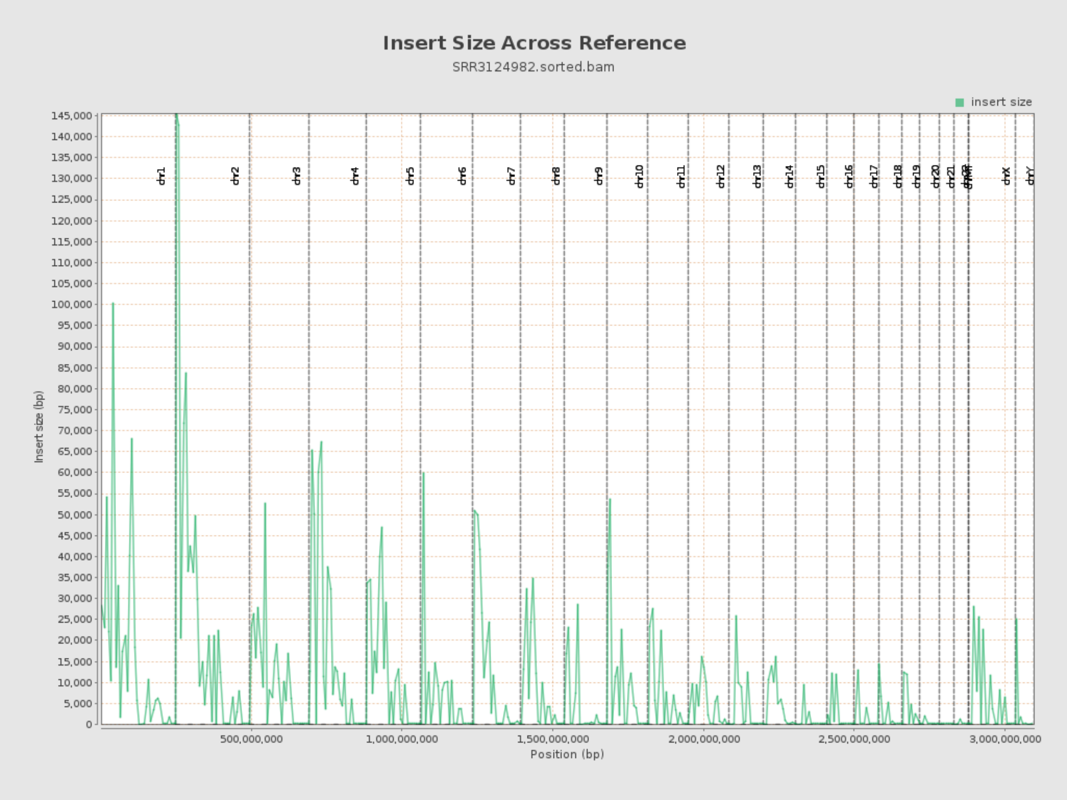
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram