Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 05:45:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124922.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_SRR3124922 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124922_1.fastq.gz SRR3124922_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 05:45:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124922.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,308,364
Mapped reads	4,234,455 / 98.28%
Unmapped reads	73,909 / 1.72%
Mapped paired reads	4,234,455 / 98.28%
Mapped reads, first in pair	2,120,620 / 49.22%
Mapped reads, second in pair	2,113,835 / 49.06%
Mapped reads, both in pair	4,220,518 / 97.96%
Mapped reads, singletons	13,937 / 0.32%
Secondary alignments	0
Supplementary alignments	16,178 / 0.38%
Read min/max/mean length	30 / 101 / 101.15
Duplicated reads (estimated)	303,409 / 7.04%
Duplication rate	5.23%
Clipped reads	2,019,493 / 46.87%

2.2. ACGT Content

Number/percentage of A's	103,660,479 / 28.23%
Number/percentage of C's	67,884,929 / 18.49%
Number/percentage of T's	109,254,638 / 29.75%
Number/percentage of G's	86,412,527 / 23.53%
Number/percentage of N's	4,779 / 0%

GC Percentage	42.02%

2.3. Coverage

Mean	0.1187
Standard Deviation	0.9794

2.4. Mapping Quality

Mean Mapping Quality	52.91

2.5. Insert size

Mean	28,236.88
Standard Deviation	1,543,744.43
P25/Median/P75	148 / 197 / 272

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	2,561,431
Insertions	48,733
Mapped reads with at least one insertion	1.12%
Deletions	115,756
Mapped reads with at least one deletion	2.68%
Homopolymer indels	47.92%

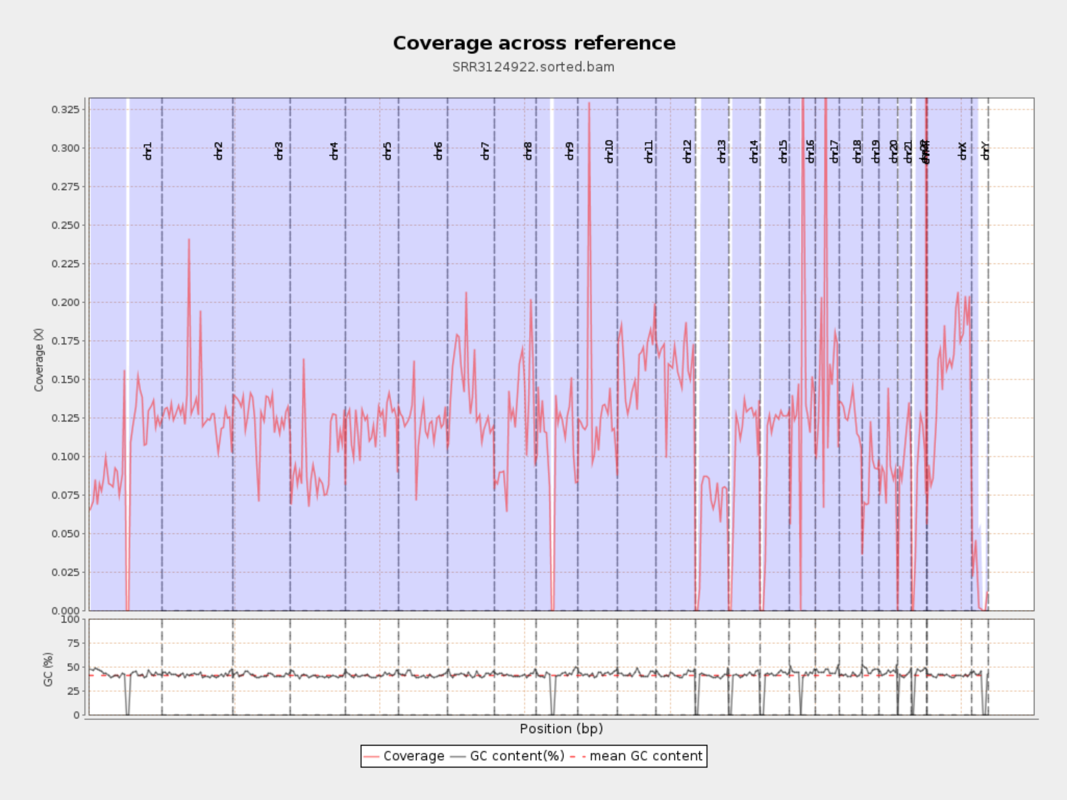
2.7. Chromosome stats

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

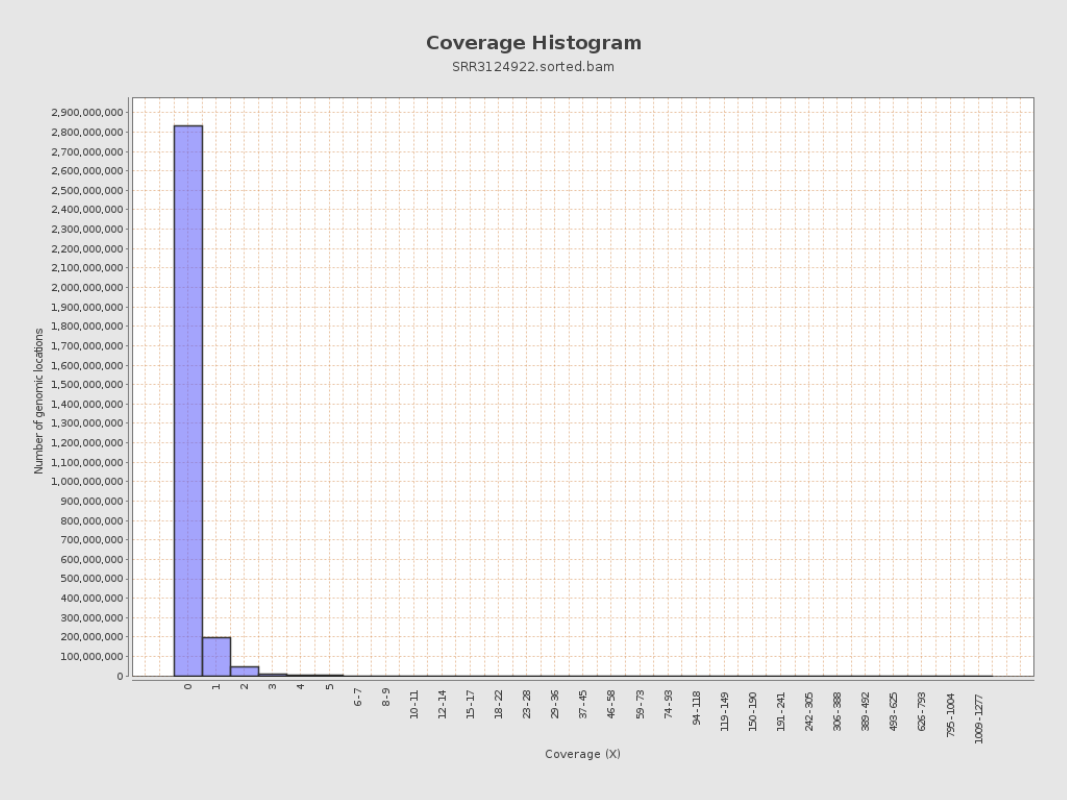
		bases	coverage	deviation
chr1	249250621	24585066	0.0986	1.0787
chr2	243199373	31964557	0.1314	1.1321
chr3	198022430	24982673	0.1262	0.4516
chr4	191154276	18341743	0.096	0.6416
chr5	180915260	21867881	0.1209	0.4505
chr6	171115067	20863262	0.1219	0.6441
chr7	159138663	22686902	0.1426	1.6777
chr8	146364022	17951709	0.1227	0.5152
chr9	141213431	15084088	0.1068	1.0299
chr10	135534747	17766637	0.1311	1.8389
chr11	135006516	21458107	0.1589	0.8938
chr12	133851895	21201591	0.1584	0.5142
chr13	115169878	7398311	0.0642	0.3119
chr14	107349540	11029611	0.1027	0.4418
chr15	102531392	10255540	0.1	0.4042
chr16	90354753	12545162	0.1388	1.9666
chr17	81195210	13269427	0.1634	1.7027
chr18	78077248	9890087	0.1267	1.2085
chr19	59128983	5050504	0.0854	0.6337
chr20	63025520	5741784	0.0911	0.4142
chr21	48129895	4597394	0.0955	0.4887
chr22	51304566	3852257	0.0751	0.3625
chrMT	16571	63385	3.8251	2.9317
chrX	155270560	24147450	0.1555	0.6448

chrY	59373566	815073	0.0137	0.7678

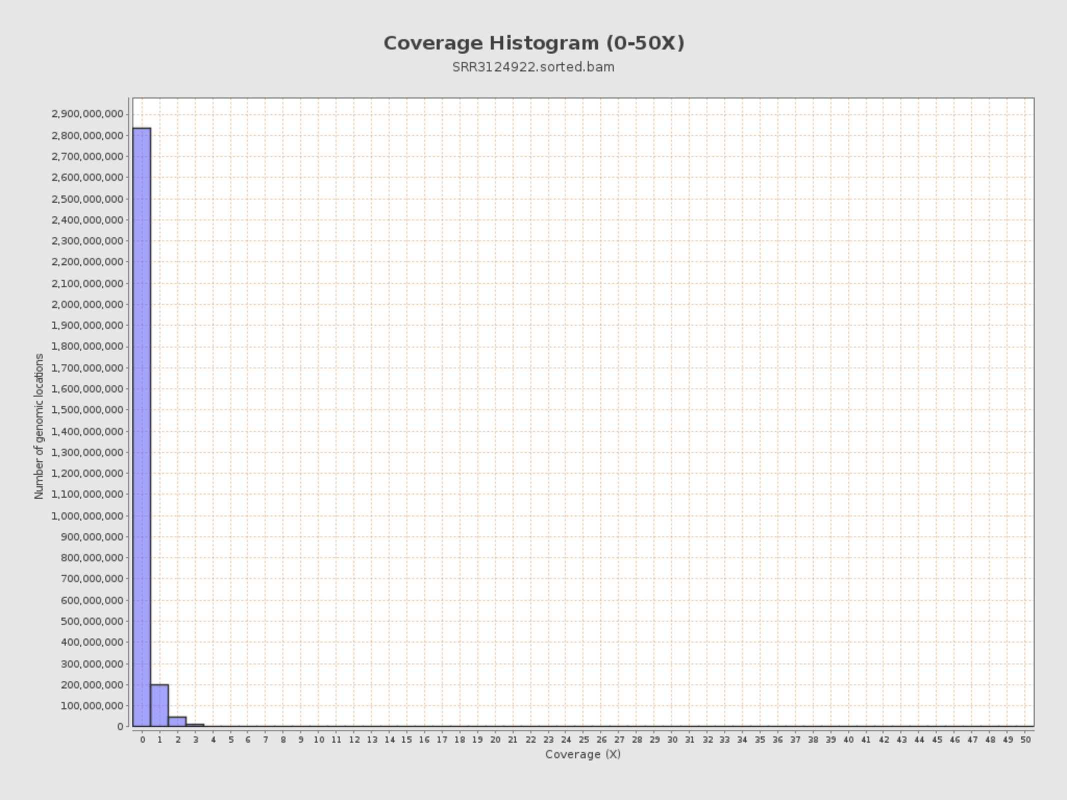
3. Results : Coverage across reference



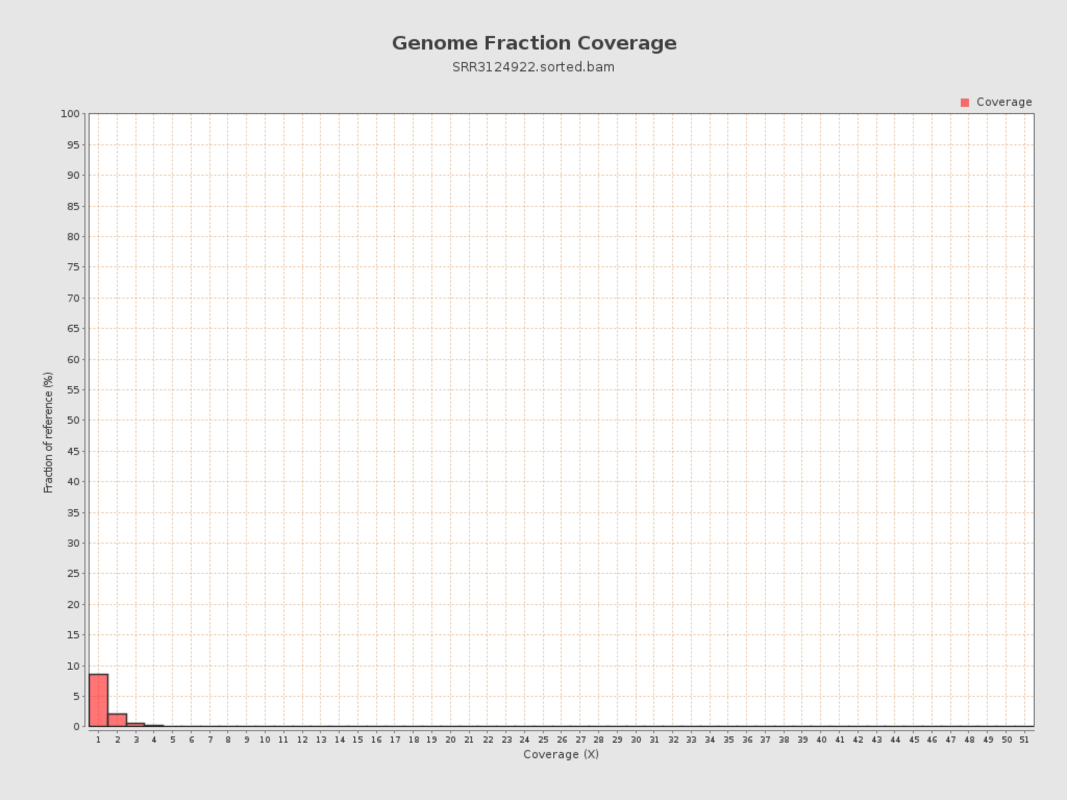
4. Results : Coverage Histogram



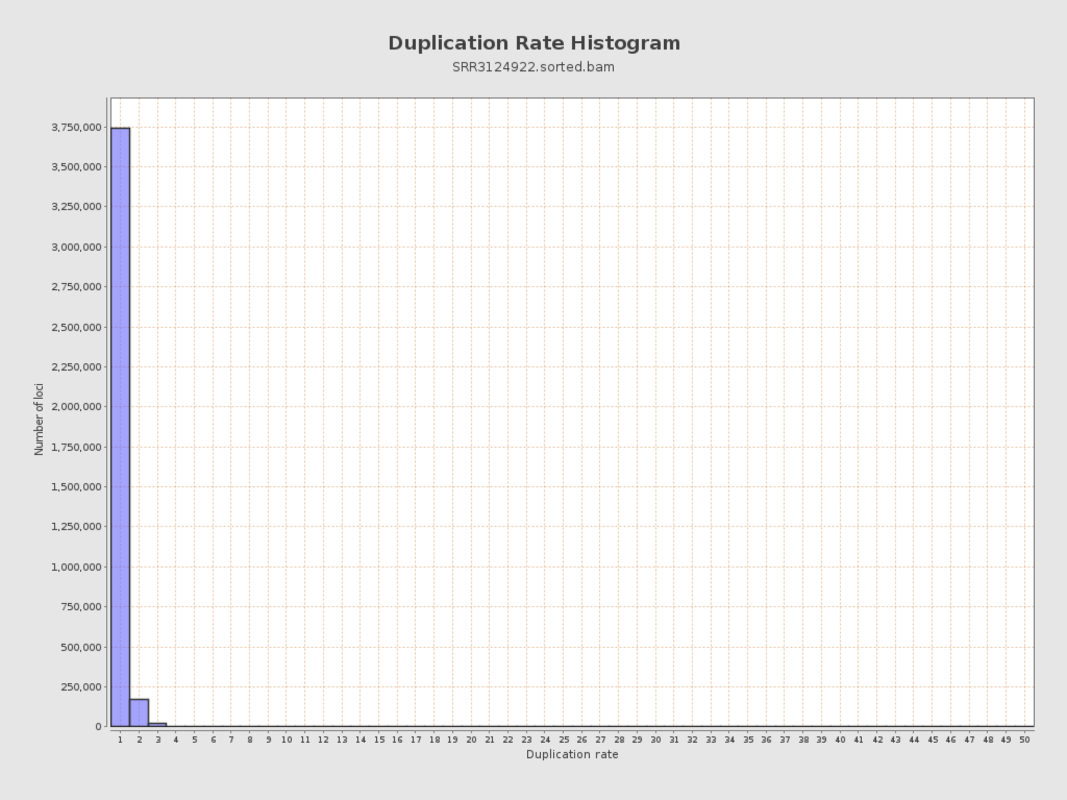
5. Results : Coverage Histogram (0-50X)



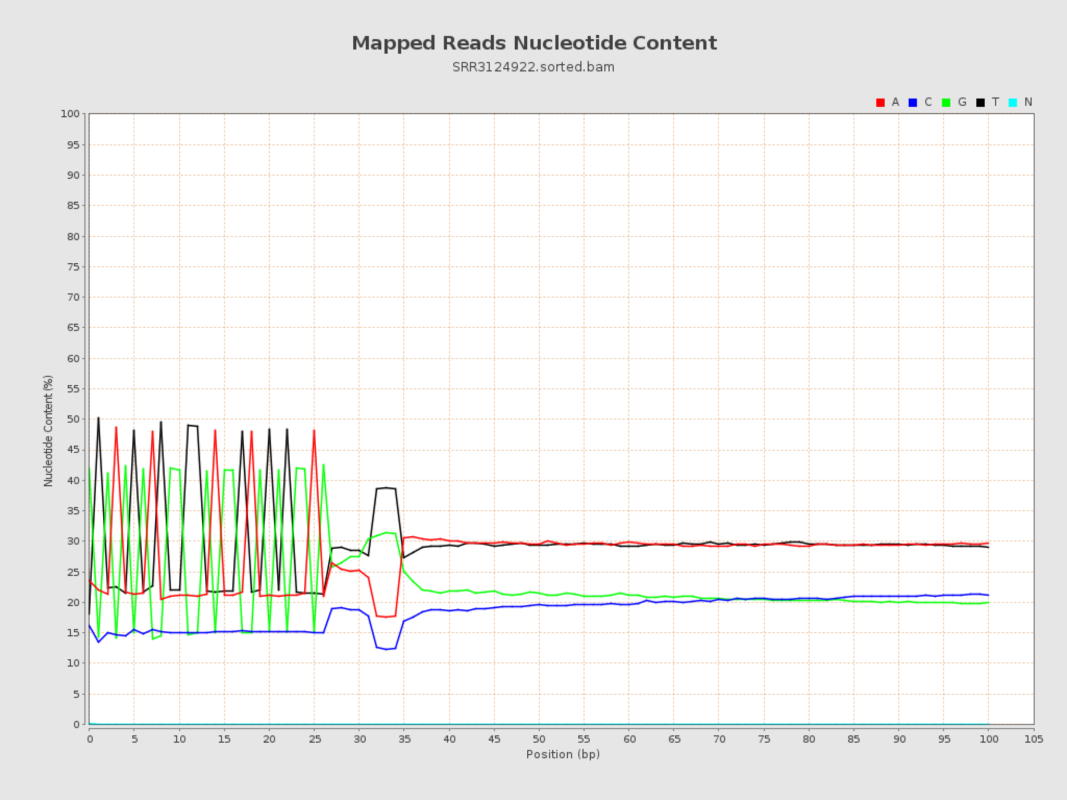
6. Results : Genome Fraction Coverage



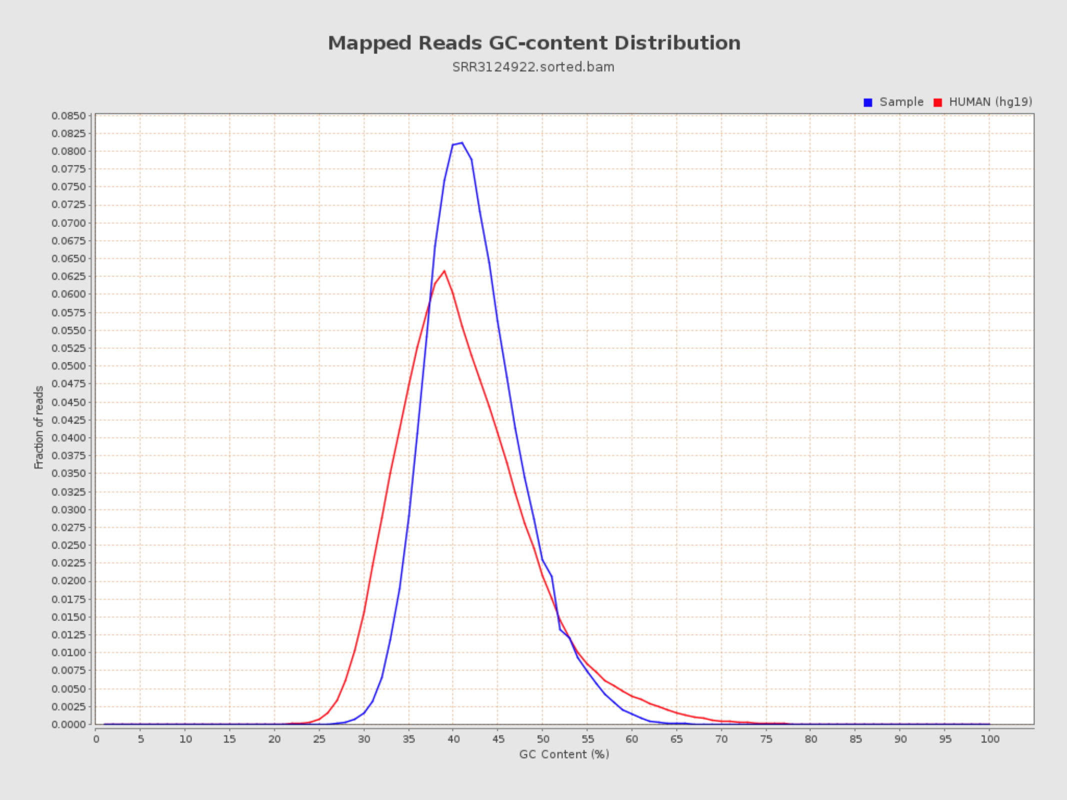
7. Results : Duplication Rate Histogram



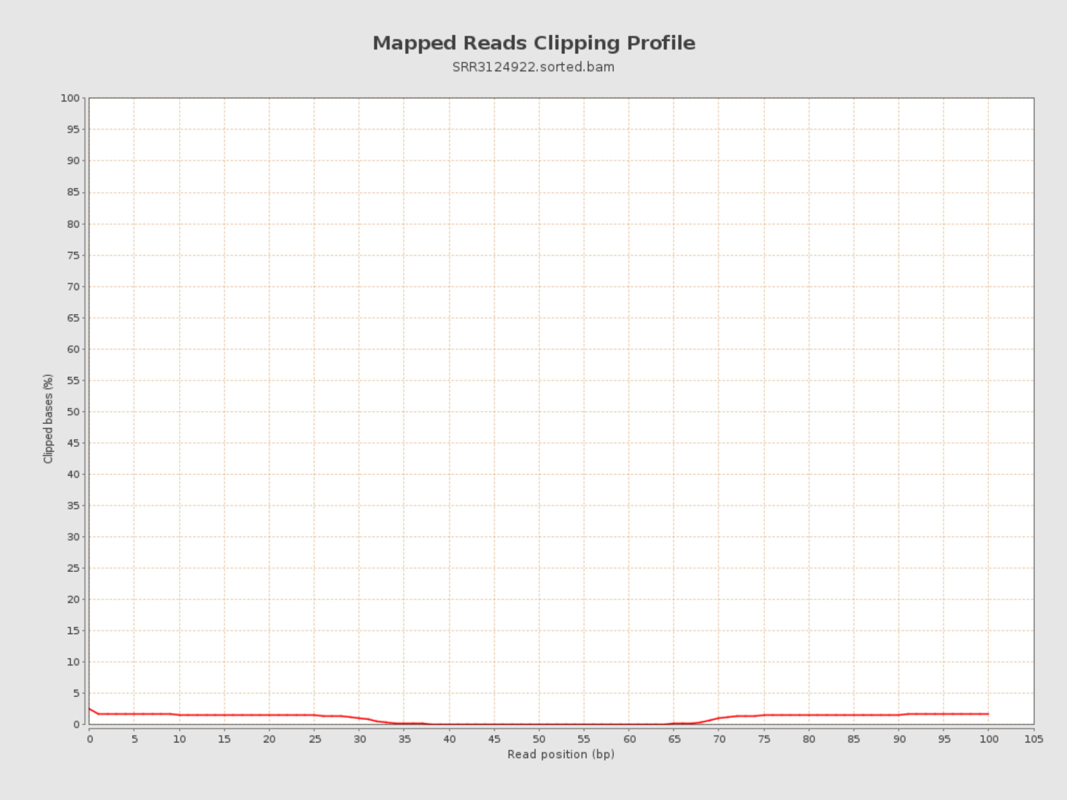
8. Results : Mapped Reads Nucleotide Content



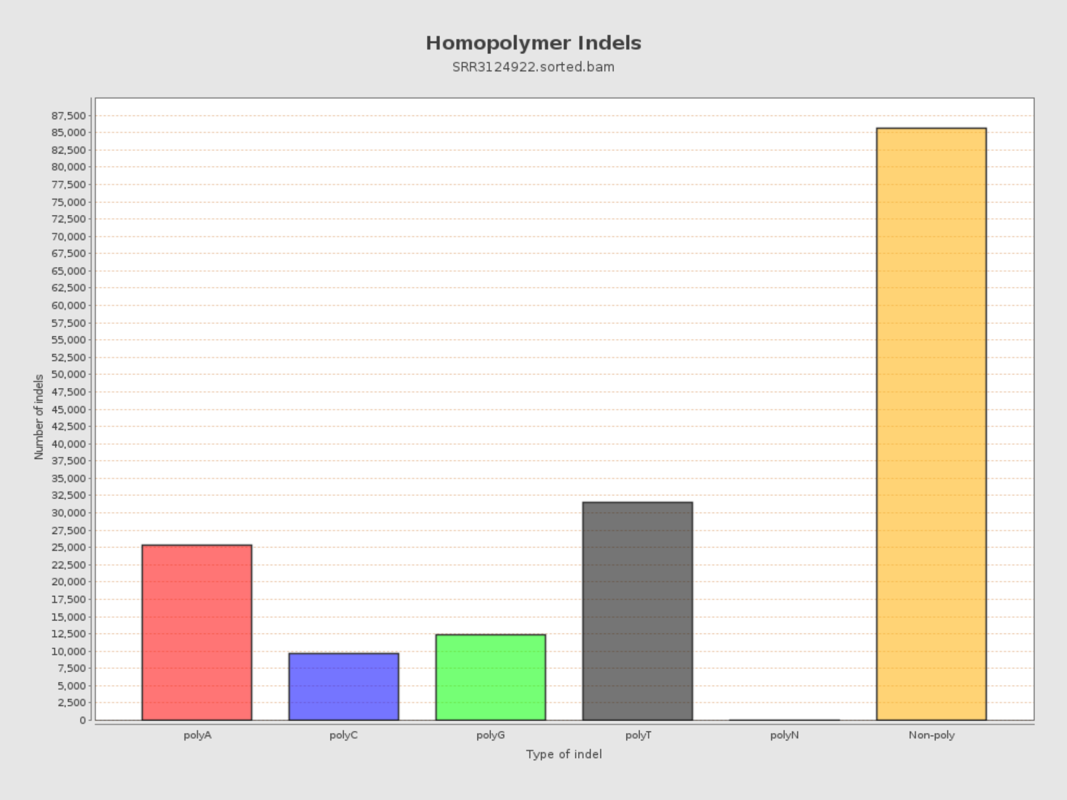
9. Results : Mapped Reads GC-content Distribution



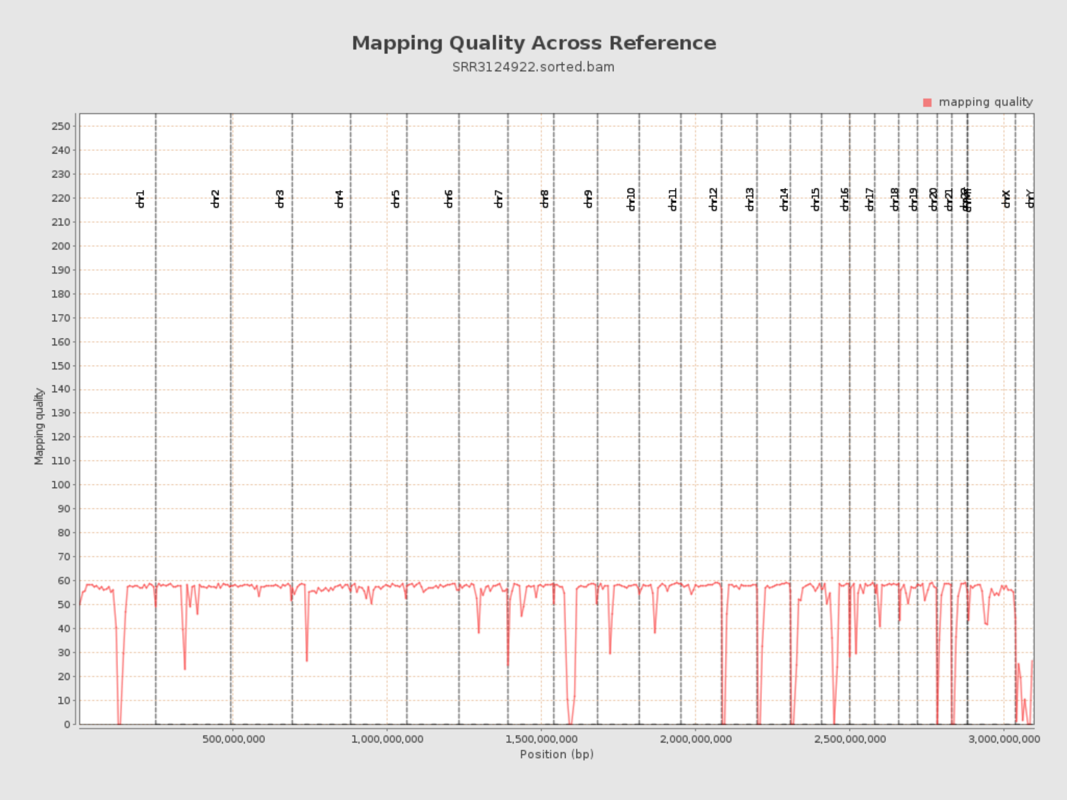
10. Results : Mapped Reads Clipping Profile



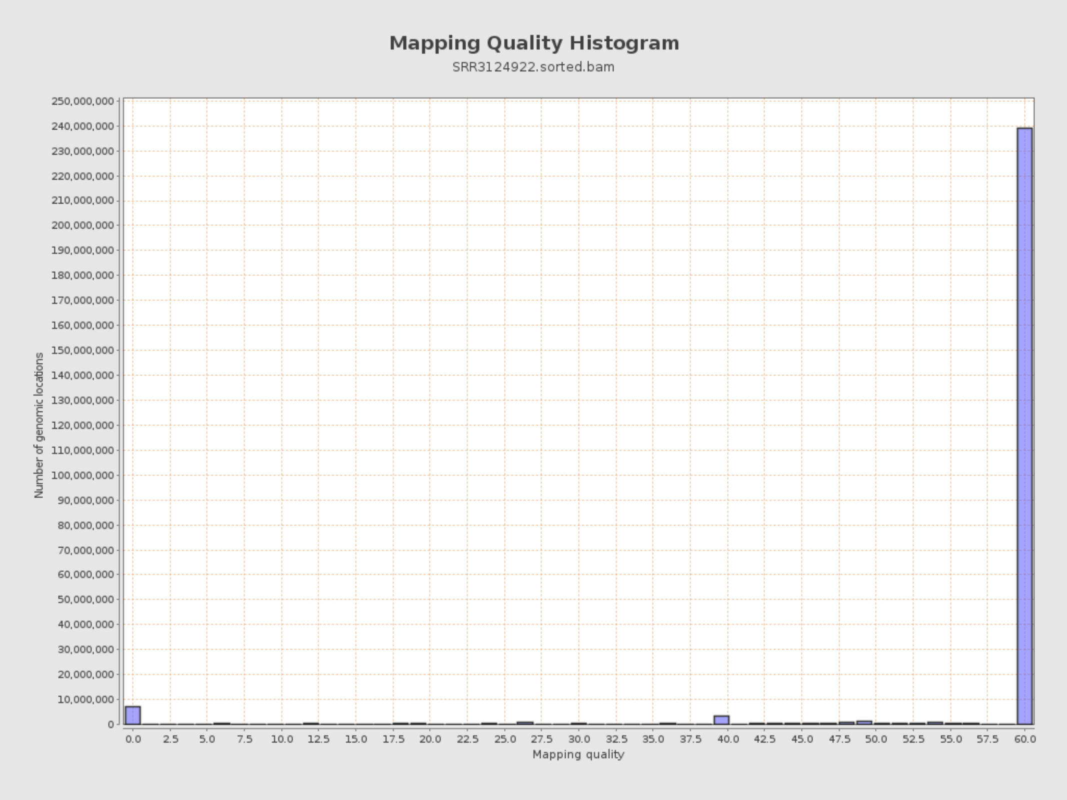
11. Results : Homopolymer Indels



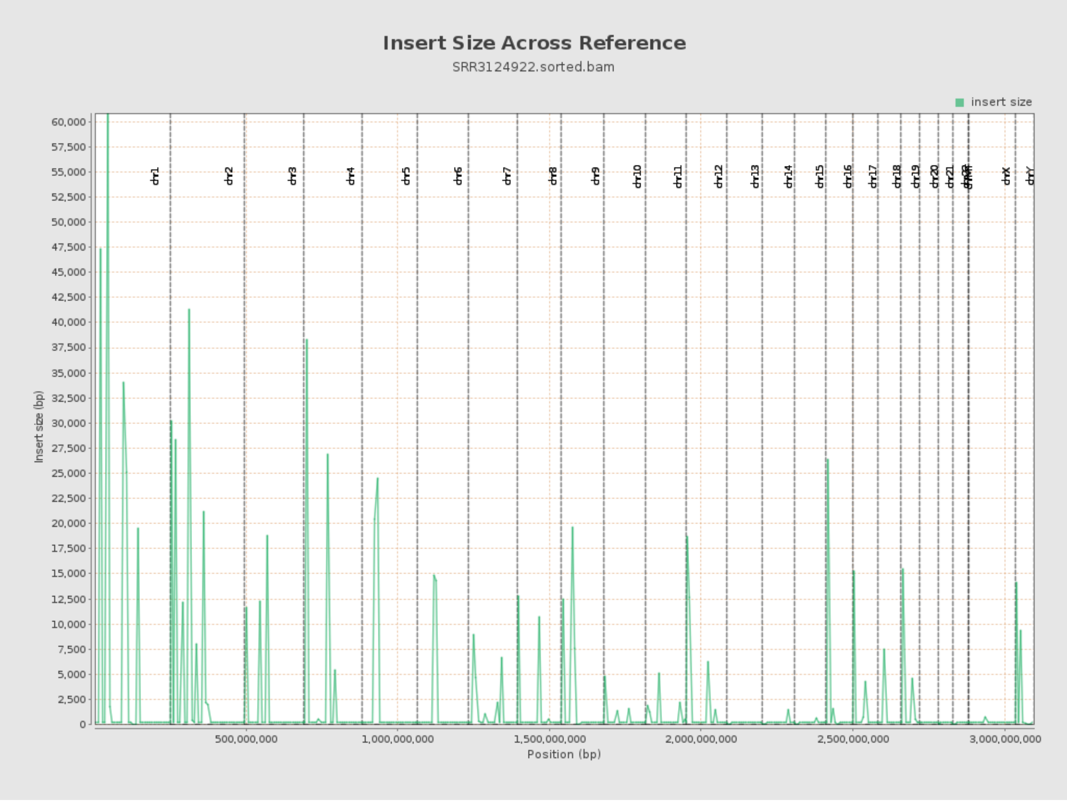
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram