Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:30:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472421.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_SRR3472421 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472421_1.fastq.gz SRR3472421_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:30:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472421.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,456,550
Mapped reads	32,087,014 / 98.86%
Unmapped reads	369,536 / 1.14%
Mapped paired reads	32,087,014 / 98.86%
Mapped reads, first in pair	16,146,565 / 49.75%
Mapped reads, second in pair	15,940,449 / 49.11%
Mapped reads, both in pair	31,824,452 / 98.05%
Mapped reads, singletons	262,562 / 0.81%
Secondary alignments	0
Supplementary alignments	45,380 / 0.14%
Read min/max/mean length	30 / 100 / 99.39
Duplicated reads (estimated)	20,023,302 / 61.69%
Duplication rate	51.49%
Clipped reads	1,657,464 / 5.11%

2.2. ACGT Content

Number/percentage of A's	887,126,901 / 28.12%
Number/percentage of C's	690,866,568 / 21.9%
Number/percentage of T's	892,427,210 / 28.29%
Number/percentage of G's	684,123,316 / 21.68%
Number/percentage of N's	421,708 / 0.01%

GC Percentage	43.58%

2.3. Coverage

Mean	1.0193
Standard Deviation	19.1404

2.4. Mapping Quality

Mean Mapping Quality	54.85

2.5. Insert size

Mean	45,447.51
Standard Deviation	2,144,334.87
P25/Median/P75	166 / 233 / 317

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	16,083,238
Insertions	155,290
Mapped reads with at least one insertion	0.48%
Deletions	194,326
Mapped reads with at least one deletion	0.6%
Homopolymer indels	45.64%

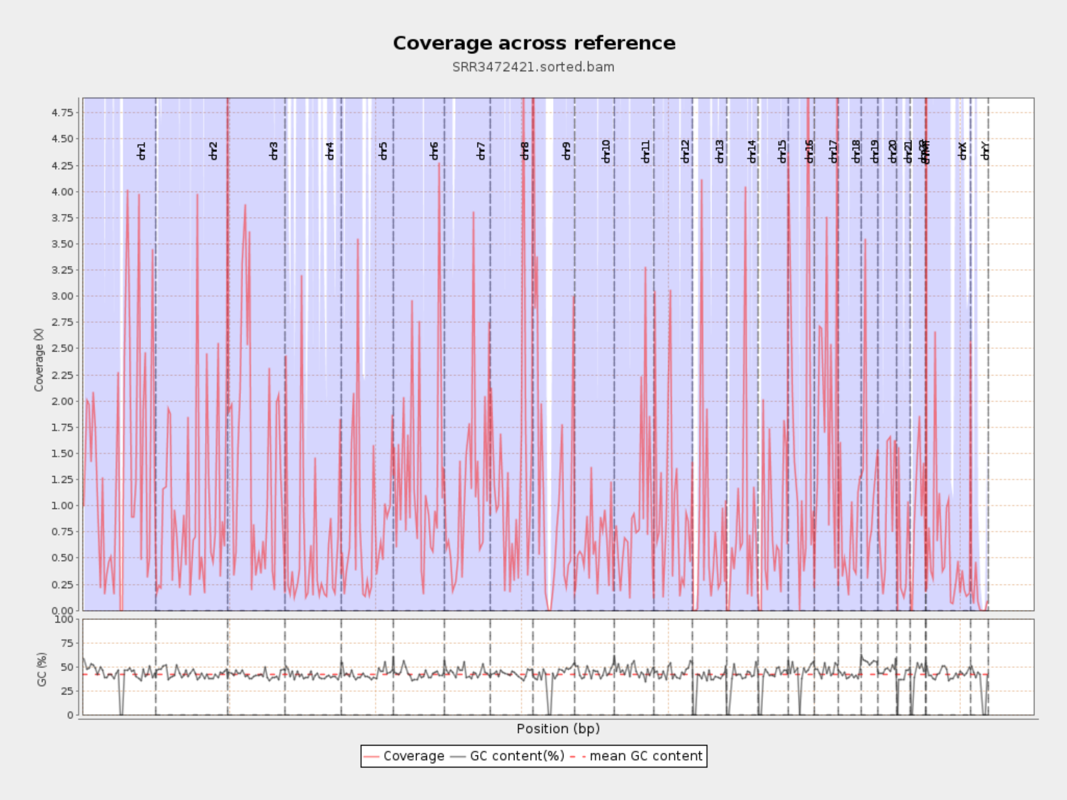
2.7. Chromosome stats

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

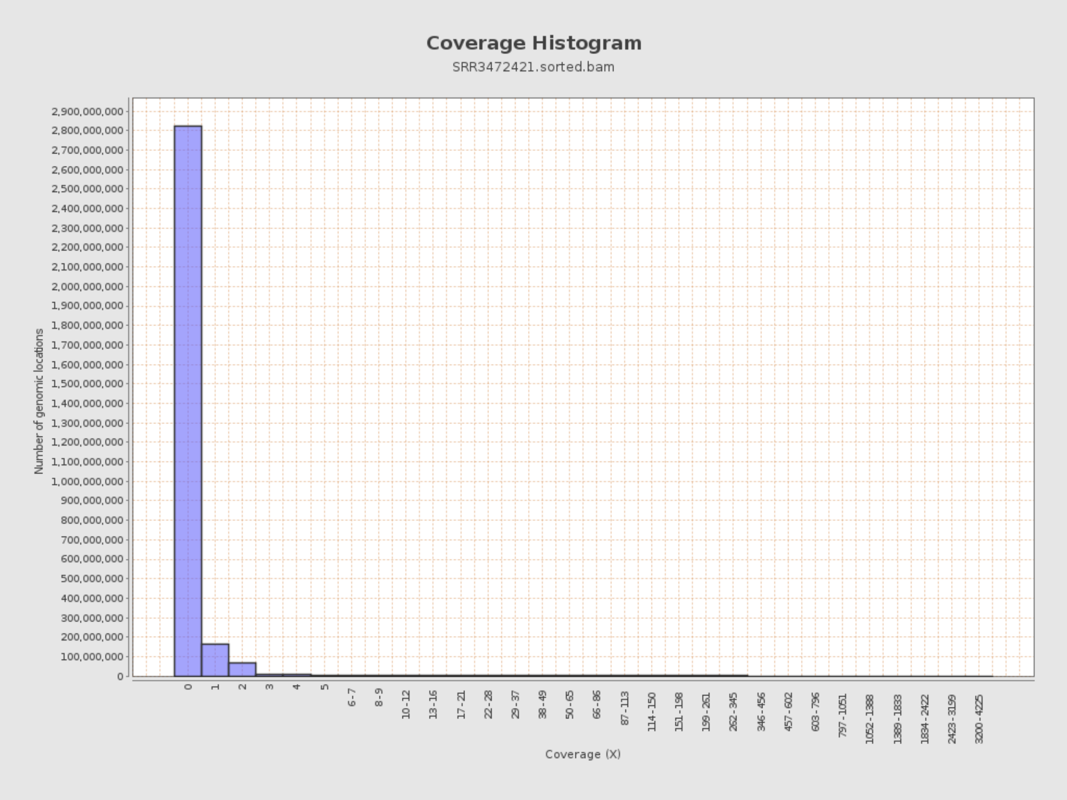
		bases	coverage	deviation
chr1	249250621	344726326	1.3831	23.2045
chr2	243199373	235025413	0.9664	19.6335
chr3	198022430	284488763	1.4366	21.7161
chr4	191154276	118759652	0.6213	15.0402
chr5	180915260	153452170	0.8482	17.1671
chr6	171115067	220052544	1.286	19.9317
chr7	159138663	185166809	1.1636	22.3819
chr8	146364022	179479248	1.2263	20.6383
chr9	141213431	151829959	1.0752	17.4941
chr10	135534747	85461536	0.6306	13.5262
chr11	135006516	126249988	0.9351	19.0091
chr12	133851895	139608812	1.043	16.5136
chr13	115169878	85592647	0.7432	18.7478
chr14	107349540	85437104	0.7959	16.0322
chr15	102531392	80284843	0.783	17.861
chr16	90354753	154256346	1.7072	29.4861
chr17	81195210	159714717	1.967	29.0704
chr18	78077248	52335747	0.6703	13.201
chr19	59128983	77992665	1.319	17.3066
chr20	63025520	60767192	0.9642	17.5774
chr21	48129895	26203990	0.5444	20.5047
chr22	51304566	50673007	0.9877	19.9679
chrMT	16571	720448	43.4764	10.9174
chrX	155270560	90498468	0.5828	8.9607

chrY	59373566	6646024	0.1119	3.0587

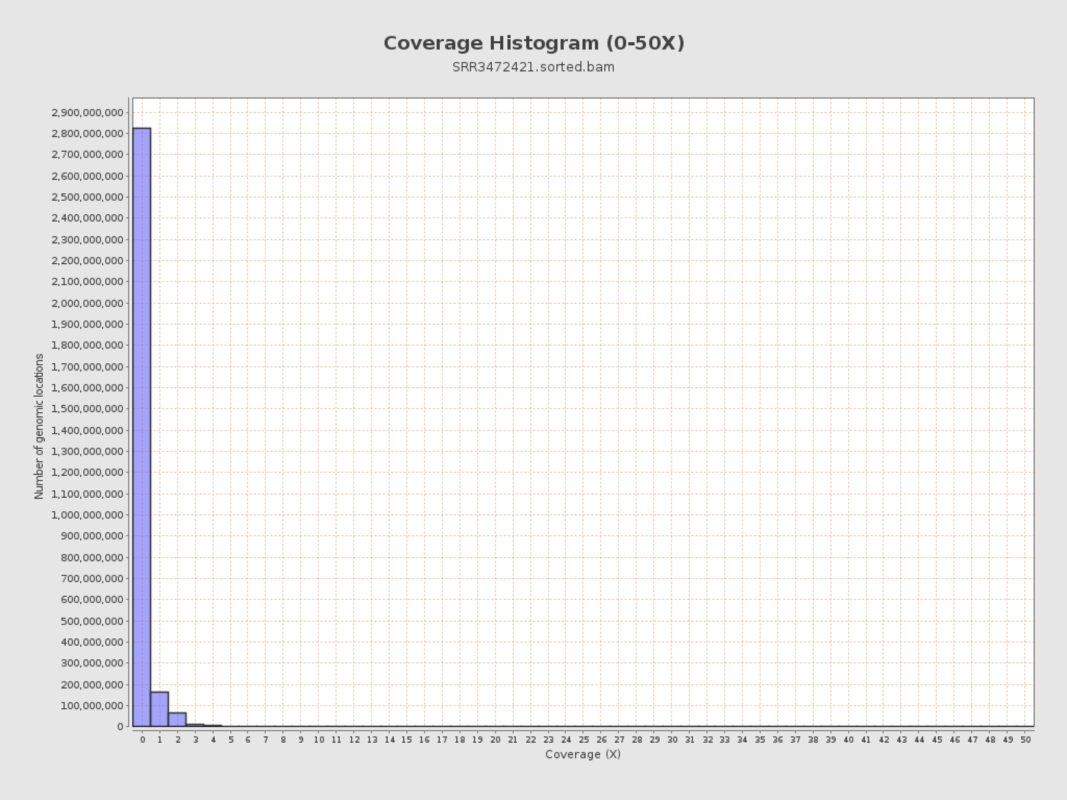
3. Results : Coverage across reference



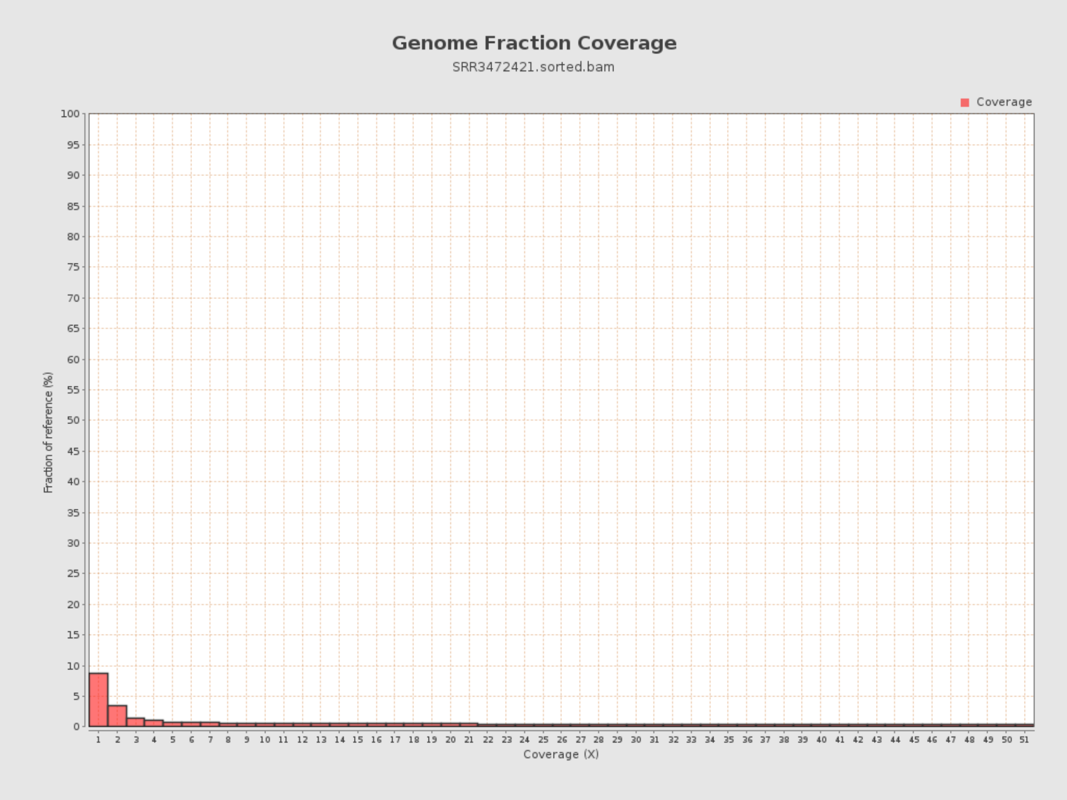
4. Results : Coverage Histogram



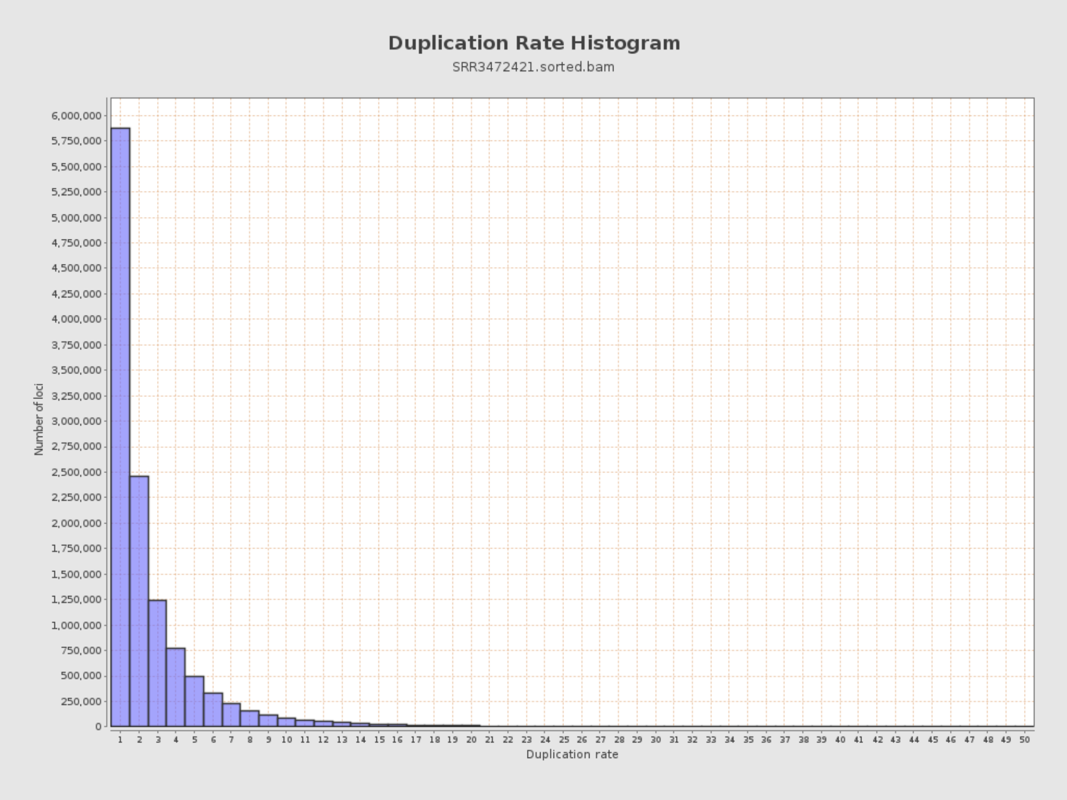
5. Results : Coverage Histogram (0-50X)



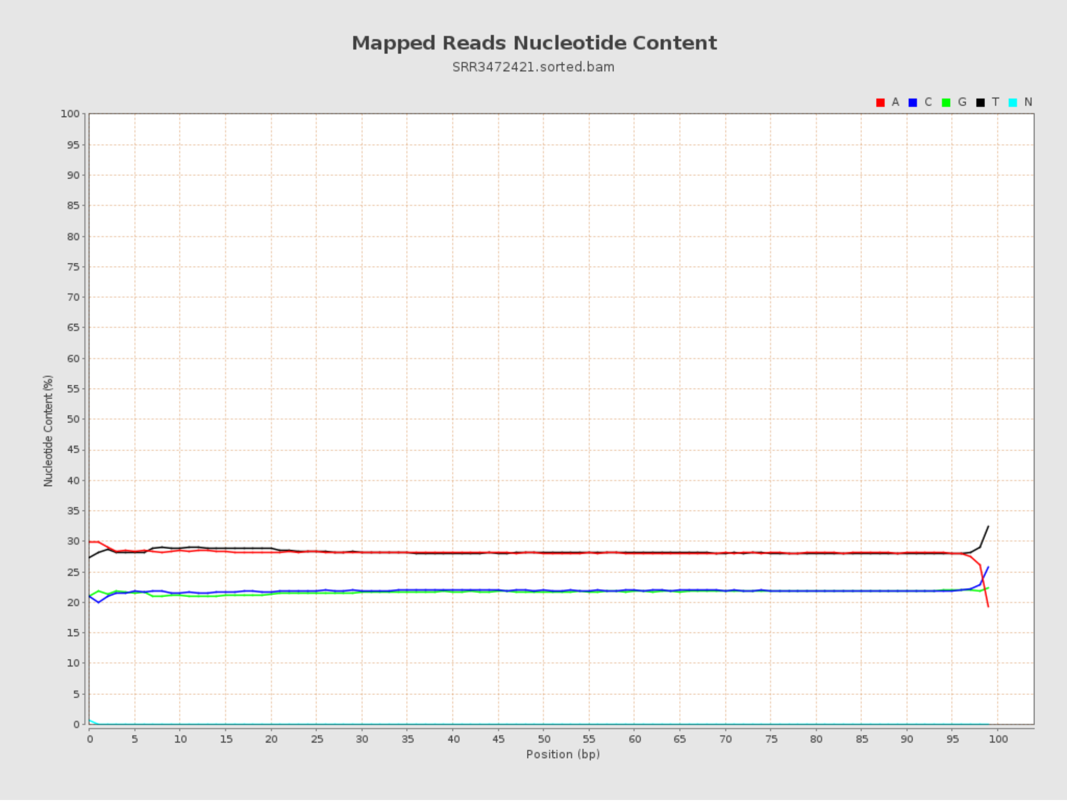
6. Results : Genome Fraction Coverage



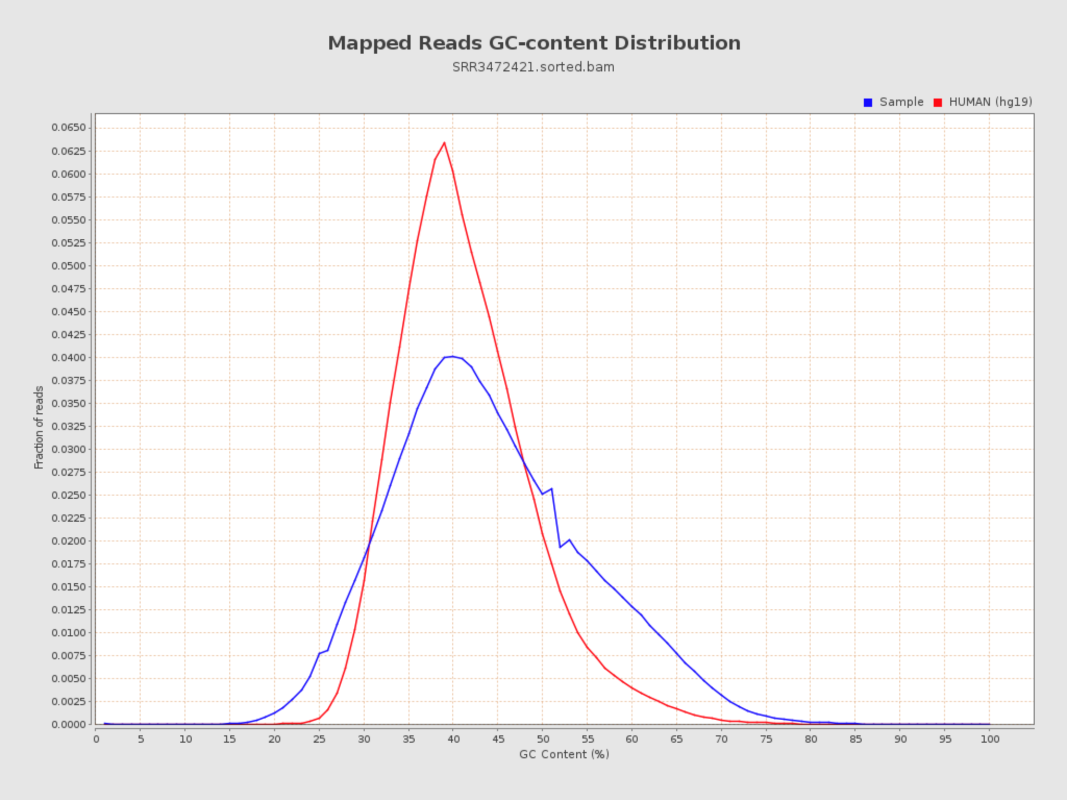
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

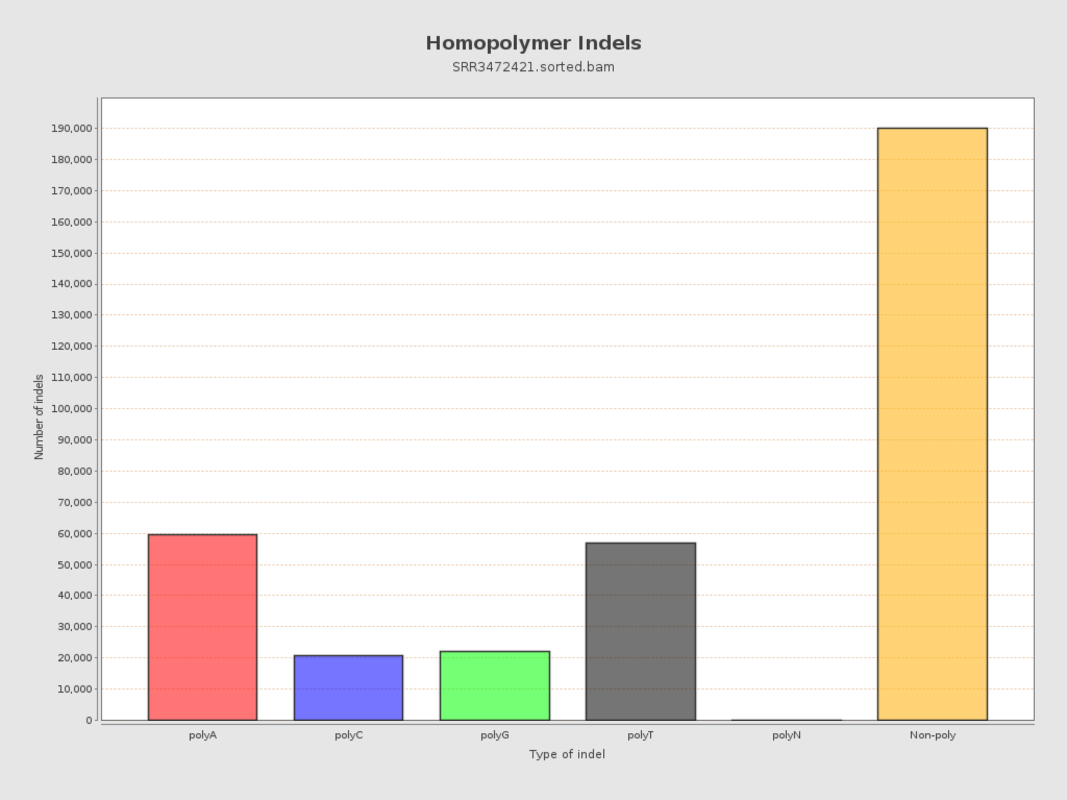


9. Results : Mapped Reads GC-content Distribution

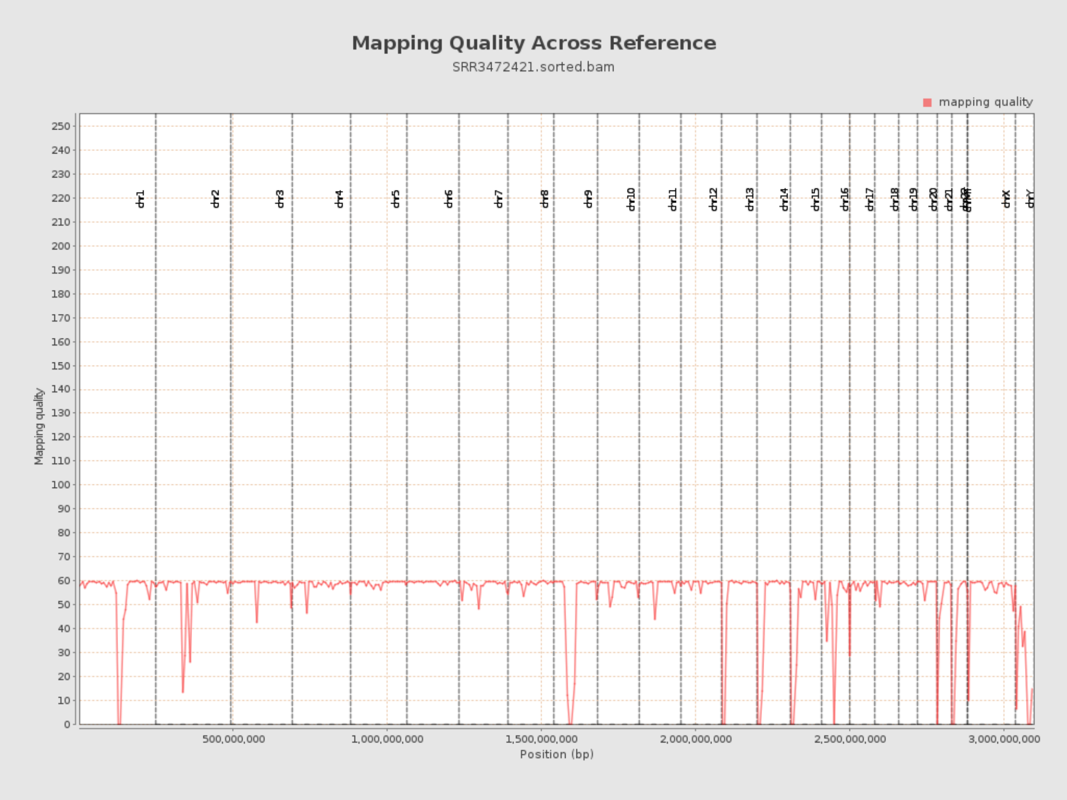


10. Results : Mapped Reads Clipping Profile

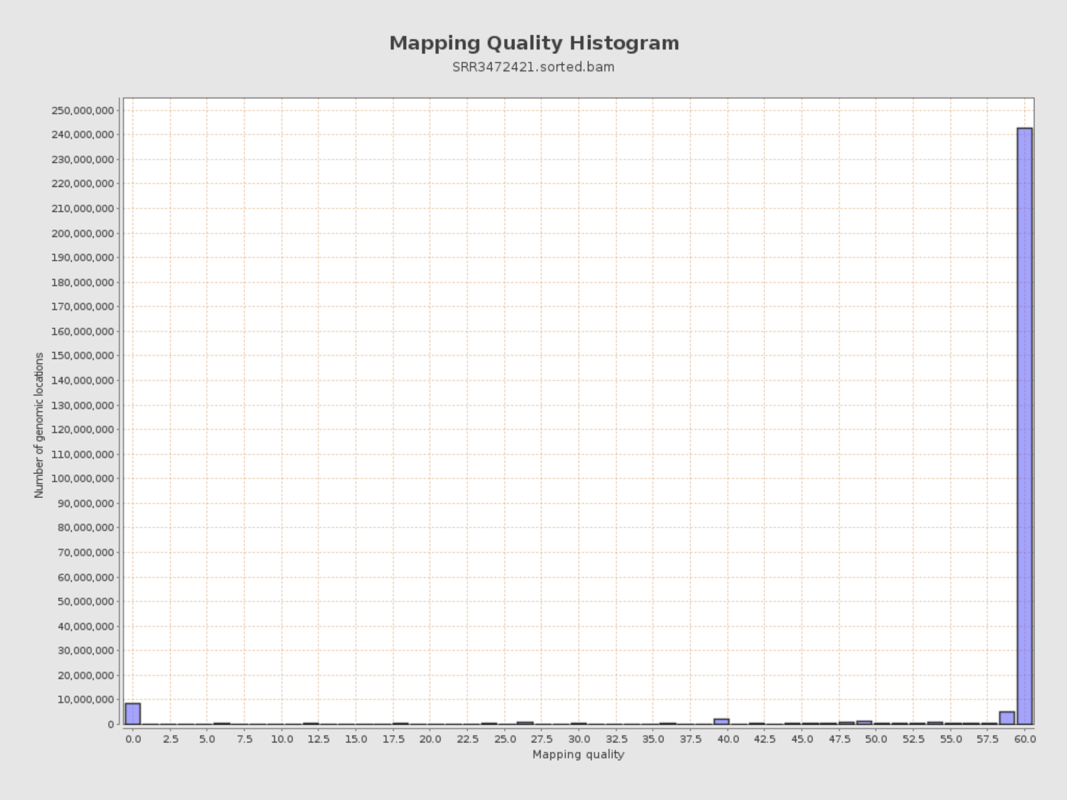
11. Results : Homopolymer Indels



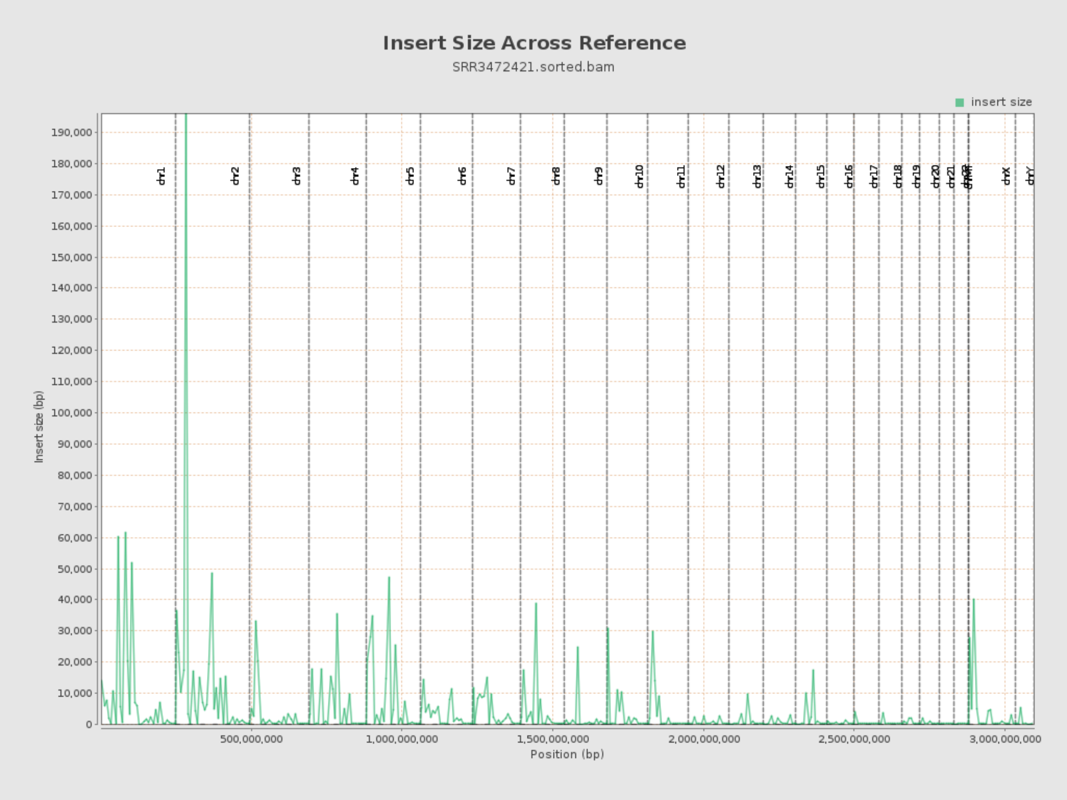
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram