Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:27:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472554.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_SRR3472554 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472554_1.fastq.gz SRR3472554_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:27:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472554.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,390,276
Mapped reads	12,152,396 / 98.08%
Unmapped reads	237,880 / 1.92%
Mapped paired reads	12,152,396 / 98.08%
Mapped reads, first in pair	6,095,696 / 49.2%
Mapped reads, second in pair	6,056,700 / 48.88%
Mapped reads, both in pair	12,052,134 / 97.27%
Mapped reads, singletons	100,262 / 0.81%
Secondary alignments	0
Supplementary alignments	55,544 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	7,029,991 / 56.74%
Duplication rate	44.95%
Clipped reads	1,245,502 / 10.05%

2.2. ACGT Content

Number/percentage of A's	327,652,545 / 27.56%
Number/percentage of C's	268,556,595 / 22.59%
Number/percentage of T's	324,955,218 / 27.33%
Number/percentage of G's	267,533,032 / 22.5%
Number/percentage of N's	182,484 / 0.02%

GC Percentage	45.09%

2.3. Coverage

Mean	0.3841
Standard Deviation	12.616

2.4. Mapping Quality

Mean Mapping Quality	54.93

2.5. Insert size

Mean	38,628.41
Standard Deviation	1,936,356.35
P25/Median/P75	163 / 231 / 316

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	7,236,848
Insertions	64,083
Mapped reads with at least one insertion	0.52%
Deletions	59,189
Mapped reads with at least one deletion	0.48%
Homopolymer indels	44.7%

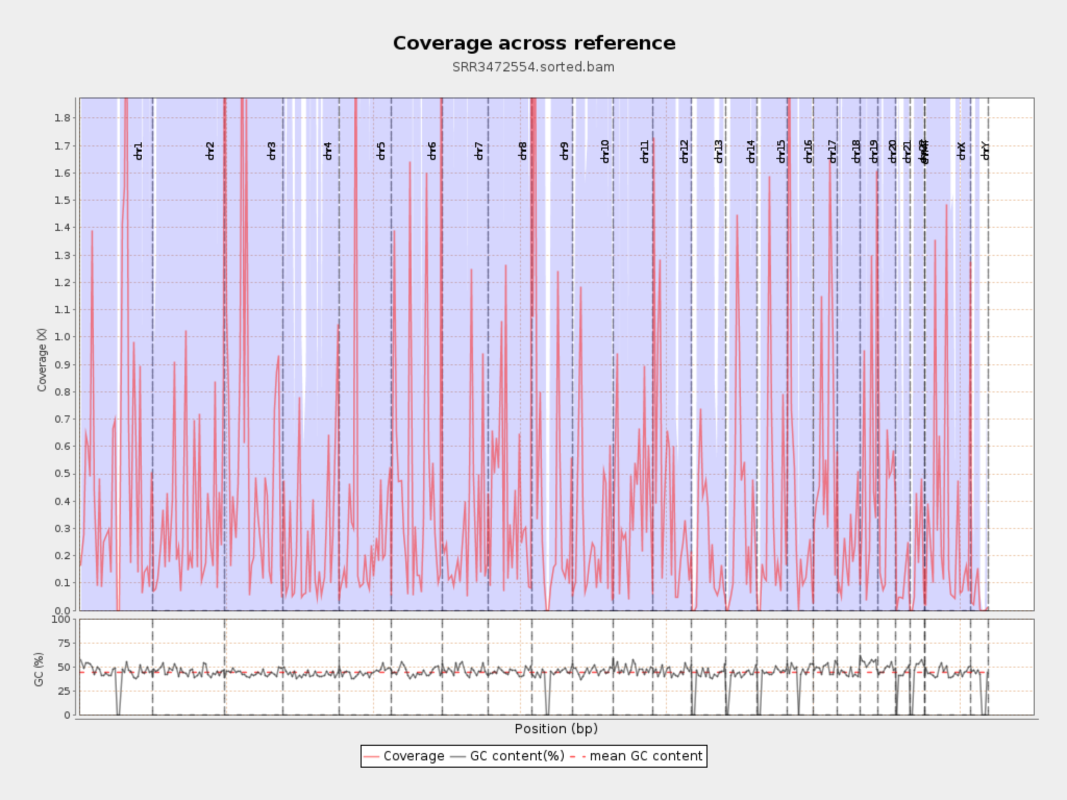
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

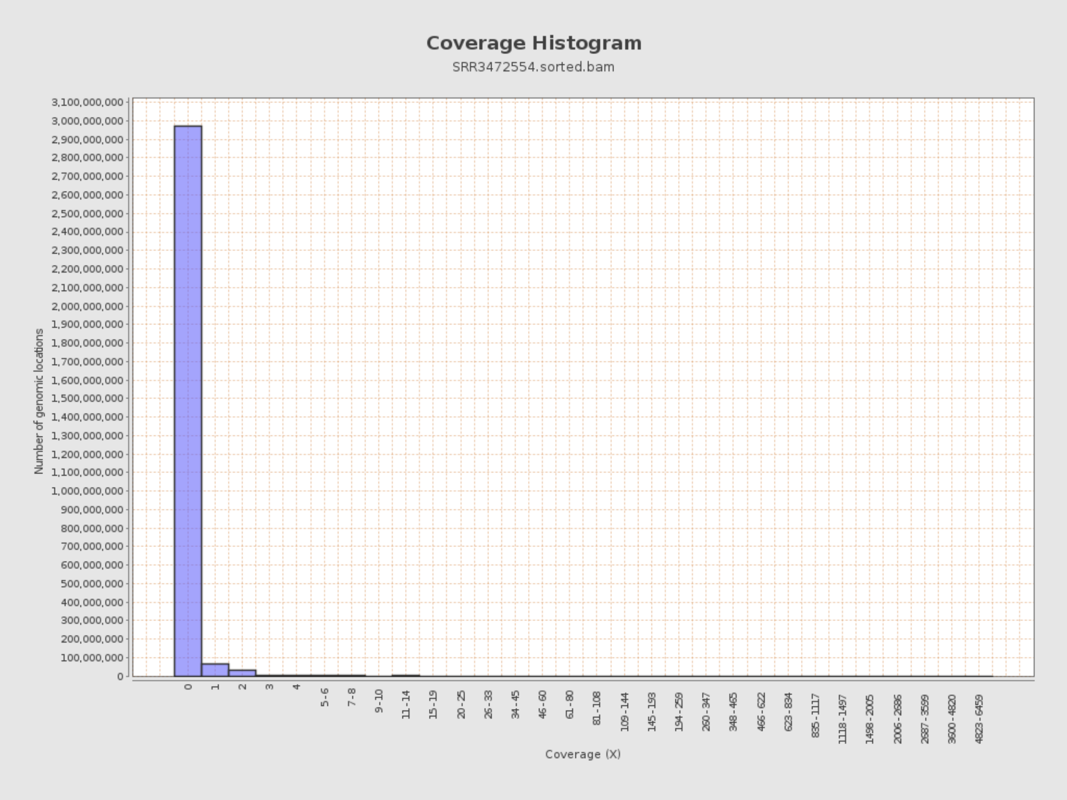
		bases	coverage	deviation
chr1	249250621	130539298	0.5237	14.5523
chr2	243199373	78550566	0.323	11.3383
chr3	198022430	119527619	0.6036	13.9559
chr4	191154276	48984420	0.2563	9.3219
chr5	180915260	57344444	0.317	9.6817
chr6	171115067	86586911	0.506	16.8971
chr7	159138663	47897202	0.301	8.4969
chr8	146364022	58850669	0.4021	13.0846
chr9	141213431	70798837	0.5014	13.2003
chr10	135534747	41138105	0.3035	15.6417
chr11	135006516	55116450	0.4083	13.0979
chr12	133851895	62188907	0.4646	16.6965
chr13	115169878	25955032	0.2254	8.2241
chr14	107349540	40491000	0.3772	12.6325
chr15	102531392	35206033	0.3434	12.1575
chr16	90354753	38638814	0.4276	11.8488
chr17	81195210	50856243	0.6263	16.2034
chr18	78077248	16363597	0.2096	7.111
chr19	59128983	31611783	0.5346	22.1719
chr20	63025520	25345482	0.4021	11.0815
chr21	48129895	4362893	0.0906	3.1683
chr22	51304566	9426596	0.1837	5.6456
chrMT	16571	2547	0.1537	0.5831
chrX	155270560	50870743	0.3276	10.0338

chrY	59373566	2374333	0.04	2.0626

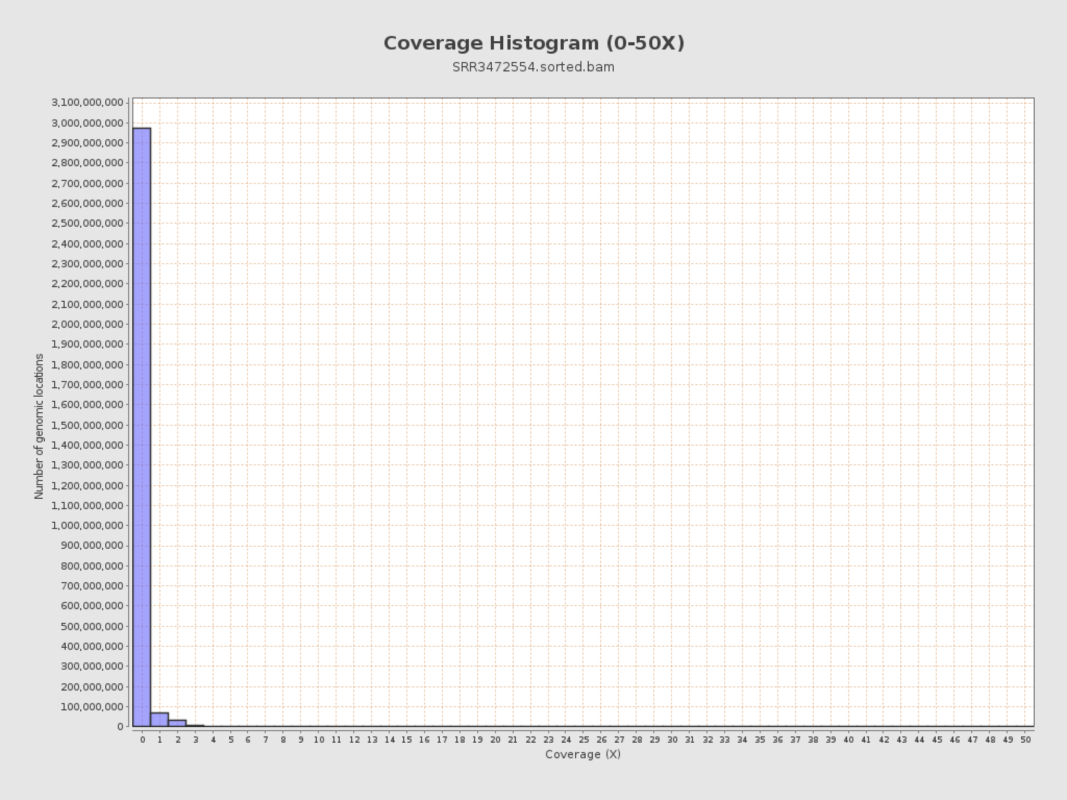
3. Results : Coverage across reference



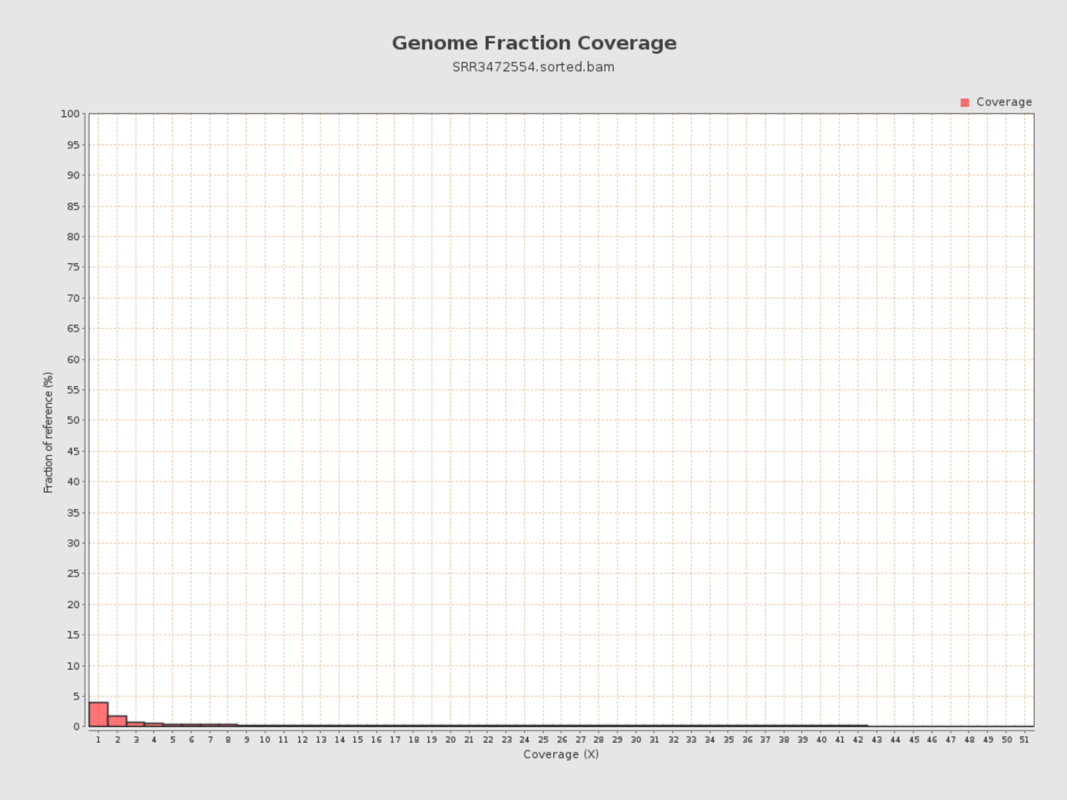
4. Results : Coverage Histogram



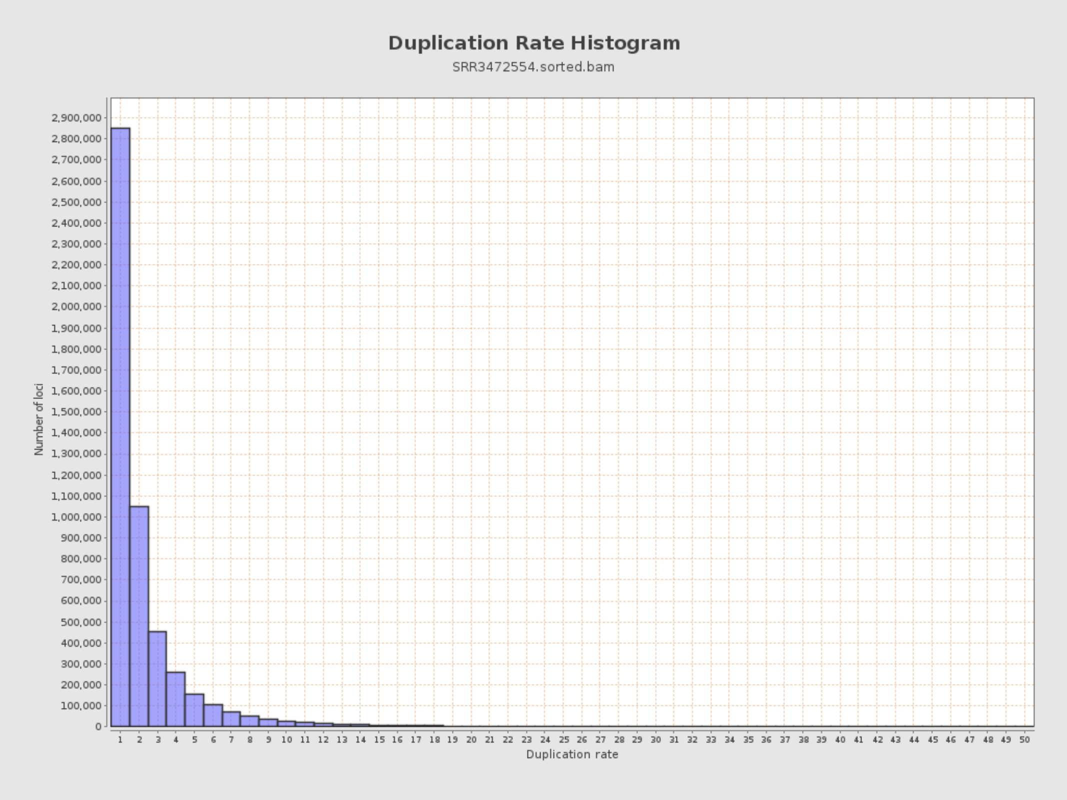
5. Results : Coverage Histogram (0-50X)



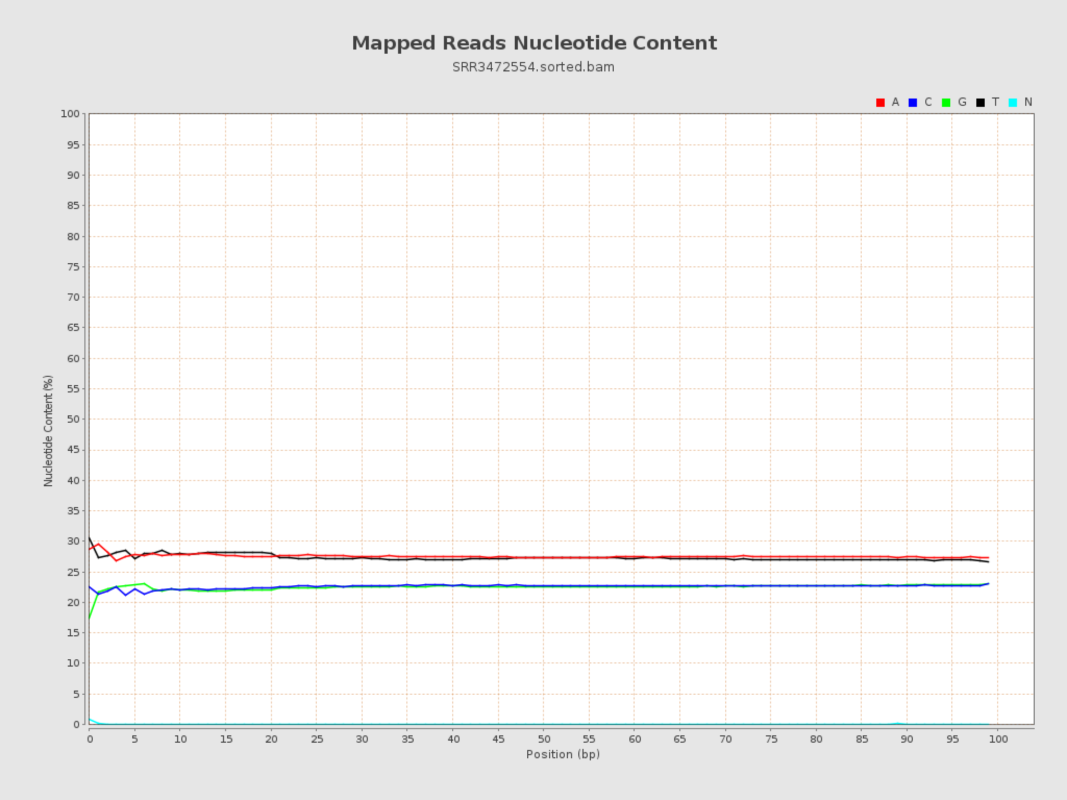
6. Results : Genome Fraction Coverage



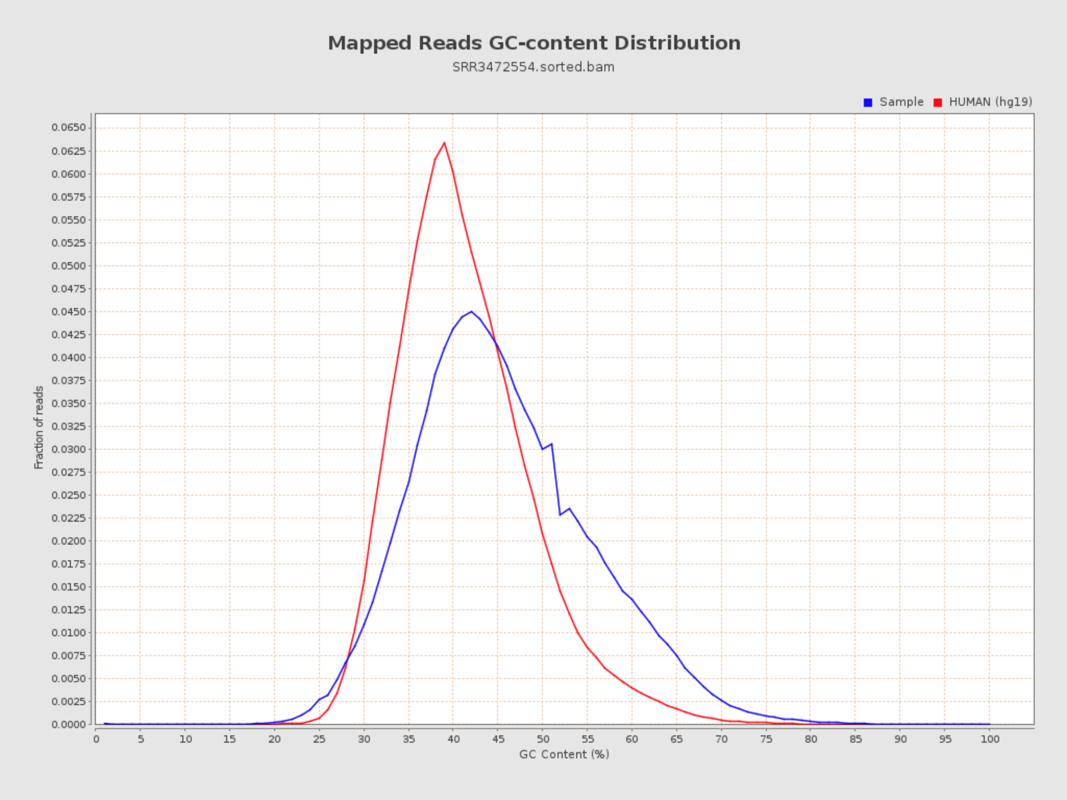
7. Results : Duplication Rate Histogram



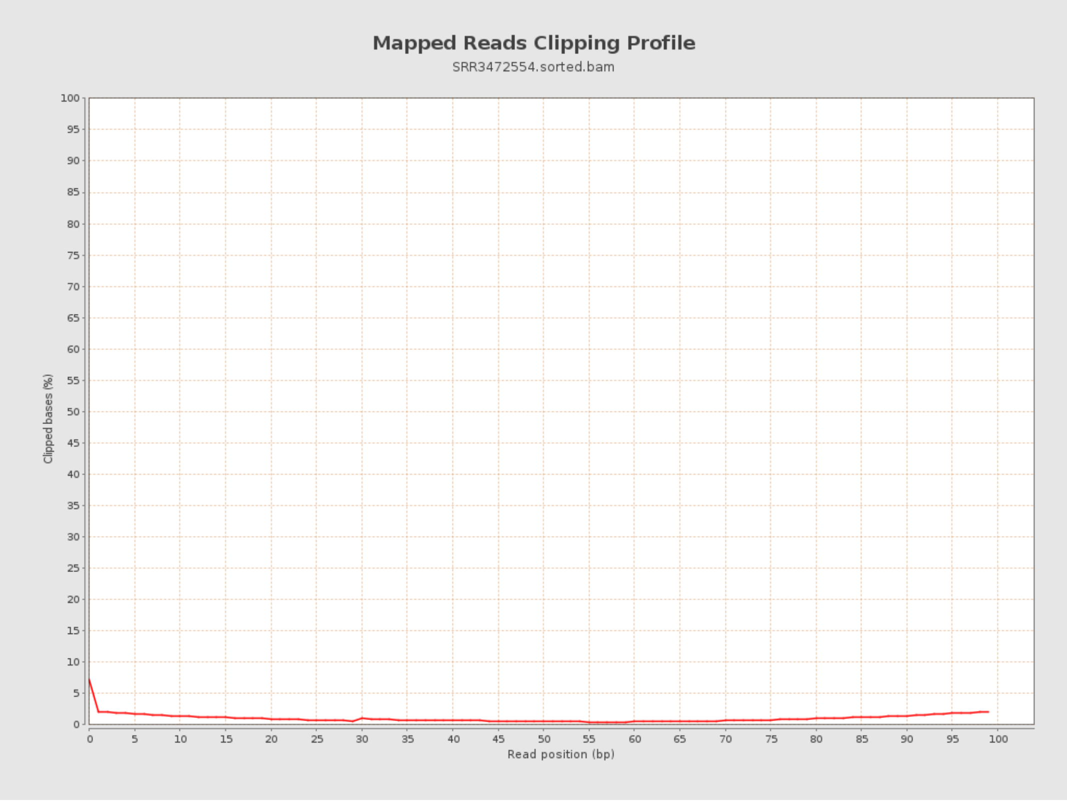
8. Results : Mapped Reads Nucleotide Content



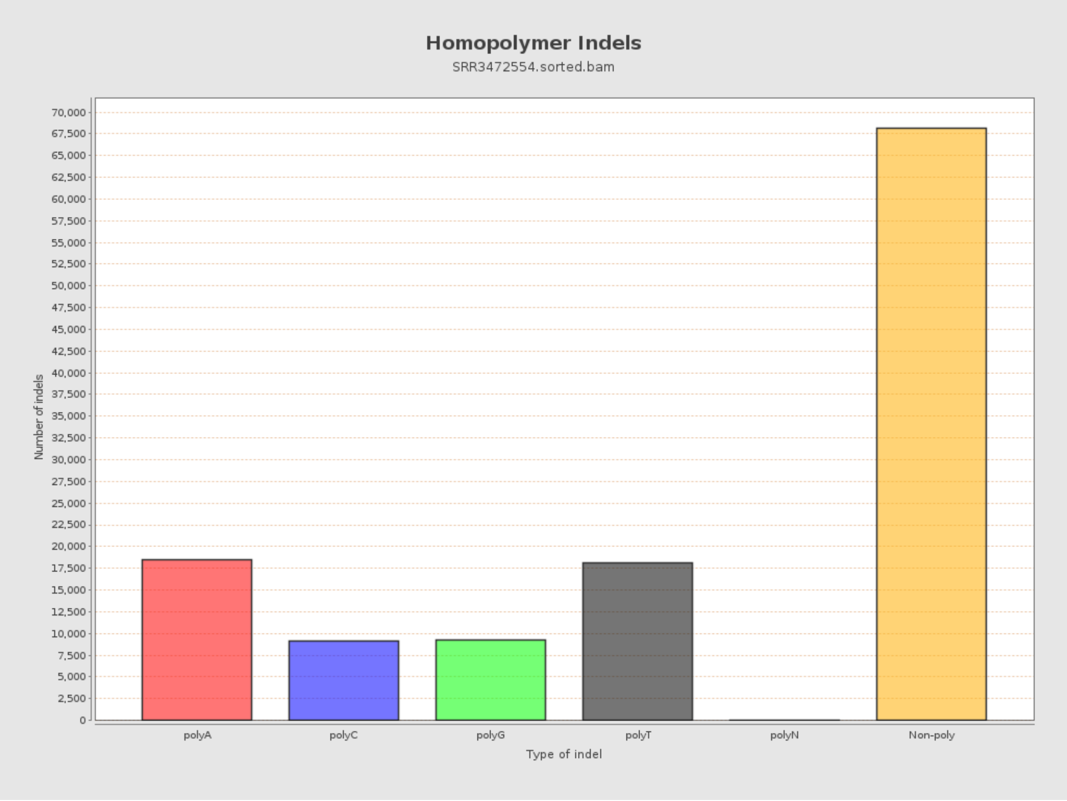
9. Results : Mapped Reads GC-content Distribution



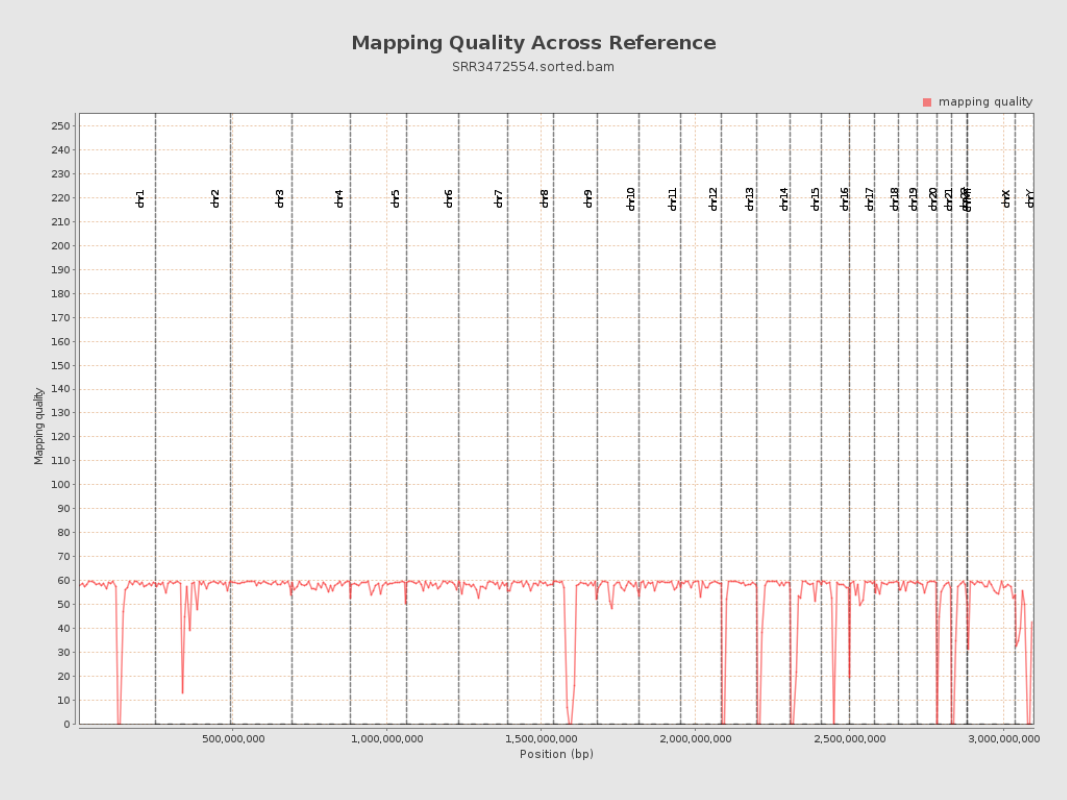
10. Results : Mapped Reads Clipping Profile



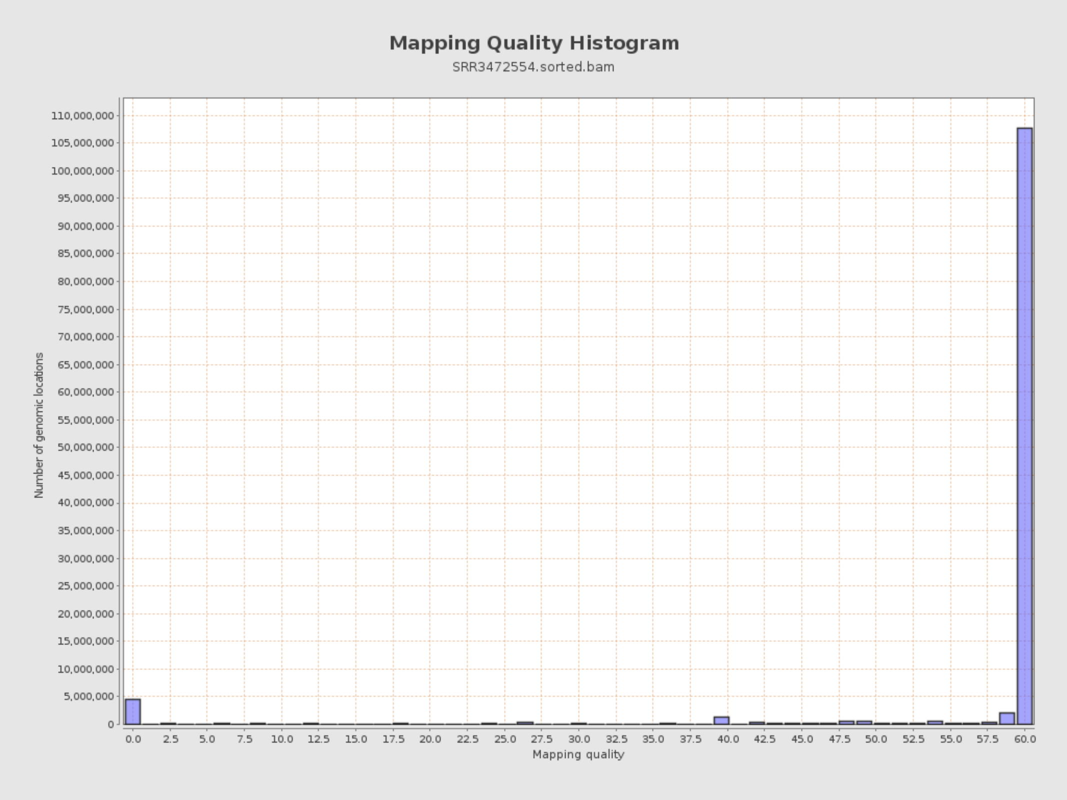
11. Results : Homopolymer Indels



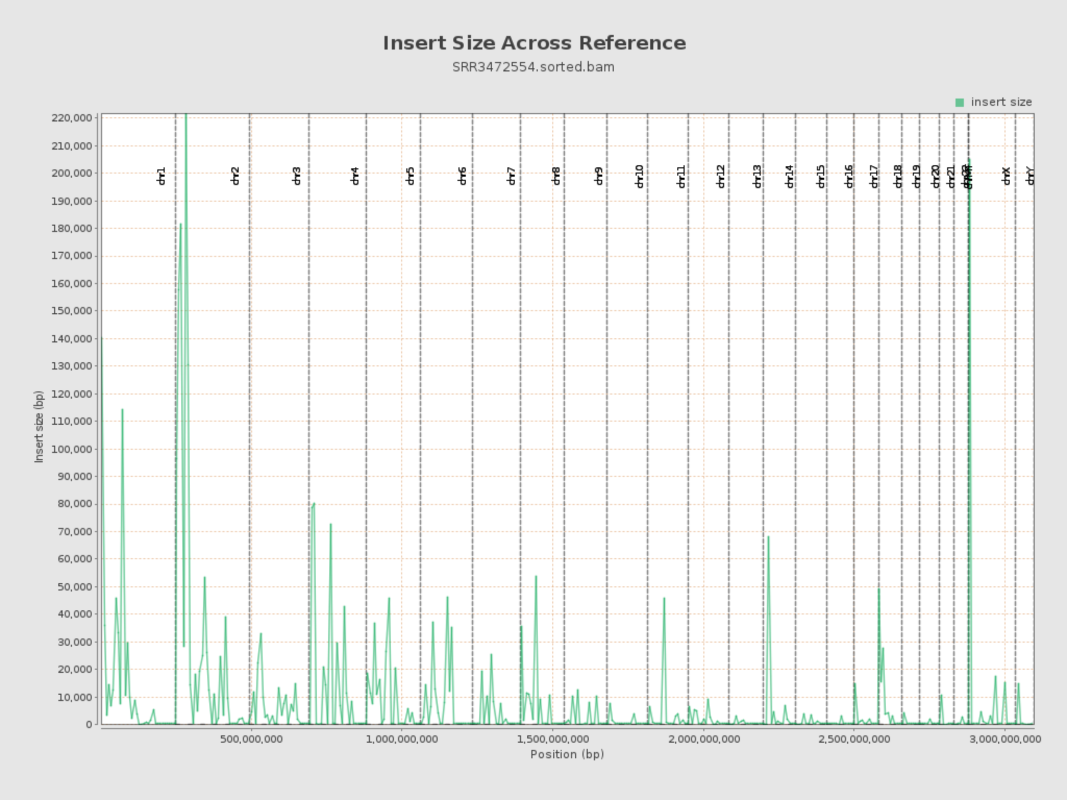
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram