Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:08:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472418.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_SRR3472418 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472418_1.fastq.gz SRR3472418_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:08:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472418.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,359,594
Mapped reads	18,203,419 / 99.15%
Unmapped reads	156,175 / 0.85%
Mapped paired reads	18,203,419 / 99.15%
Mapped reads, first in pair	9,137,266 / 49.77%
Mapped reads, second in pair	9,066,153 / 49.38%
Mapped reads, both in pair	18,100,990 / 98.59%
Mapped reads, singletons	102,429 / 0.56%
Secondary alignments	0
Supplementary alignments	75,373 / 0.41%
Read min/max/mean length	30 / 100 / 99.42
Duplicated reads (estimated)	11,448,531 / 62.36%
Duplication rate	46.86%
Clipped reads	1,158,313 / 6.31%

2.2. ACGT Content

Number/percentage of A's	491,766,315 / 27.51%
Number/percentage of C's	403,210,960 / 22.55%
Number/percentage of T's	493,570,598 / 27.61%
Number/percentage of G's	398,978,715 / 22.32%
Number/percentage of N's	214,057 / 0.01%

GC Percentage	44.87%

2.3. Coverage

Mean	0.5776
Standard Deviation	17.9513

2.4. Mapping Quality

Mean Mapping Quality	55.13

2.5. Insert size

Mean	22,597.6
Standard Deviation	1,502,172.18
P25/Median/P75	164 / 229 / 310

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	9,566,742
Insertions	105,493
Mapped reads with at least one insertion	0.57%
Deletions	89,950
Mapped reads with at least one deletion	0.49%
Homopolymer indels	46.42%

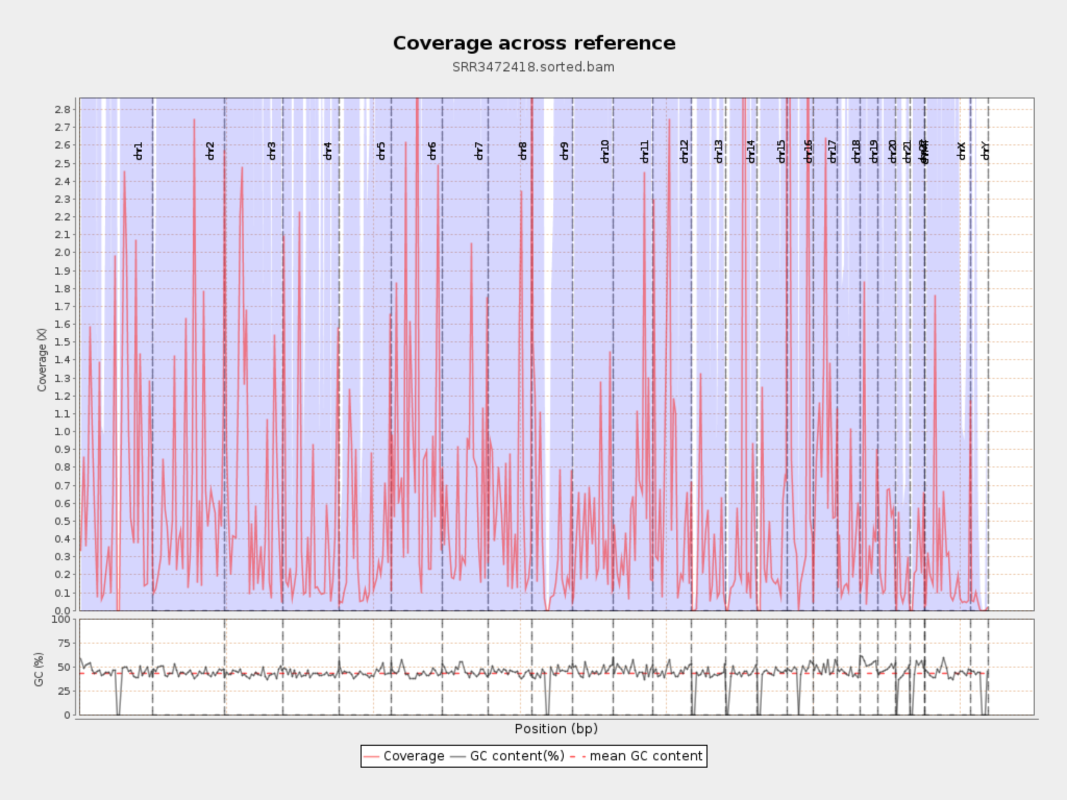
2.7. Chromosome stats

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

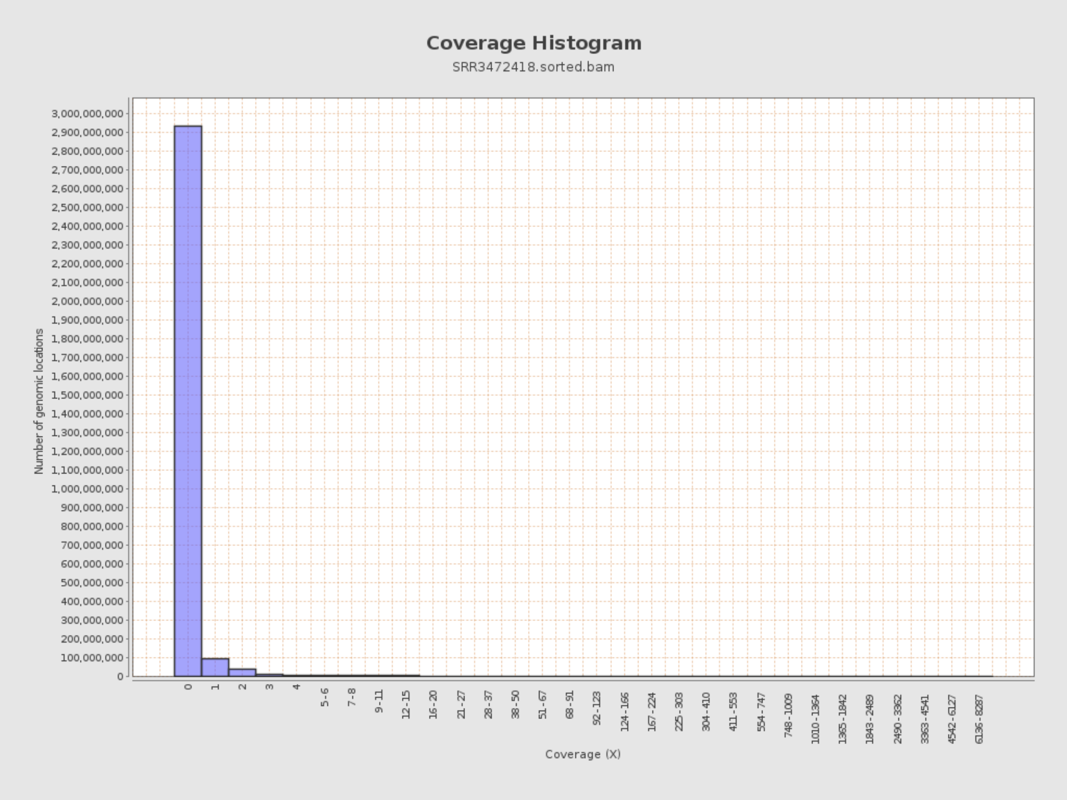
		bases	coverage	deviation
chr1	249250621	197027889	0.7905	20.6444
chr2	243199373	149071395	0.613	18.4573
chr3	198022430	146772981	0.7412	17.7891
chr4	191154276	80144309	0.4193	14.6944
chr5	180915260	69325133	0.3832	13.6614
chr6	171115067	170785469	0.9981	27.7103
chr7	159138663	103182589	0.6484	18.3743
chr8	146364022	93026781	0.6356	17.418
chr9	141213431	59397273	0.4206	10.8243
chr10	135534747	63170148	0.4661	16.2972
chr11	135006516	79751110	0.5907	17.9828
chr12	133851895	104962339	0.7842	18.2459
chr13	115169878	35715023	0.3101	9.8373
chr14	107349540	63066619	0.5875	29.3624
chr15	102531392	35198388	0.3433	11.3575
chr16	90354753	104921590	1.1612	30.9265
chr17	81195210	82864649	1.0206	23.6933
chr18	78077248	26601816	0.3407	12.7828
chr19	59128983	28700089	0.4854	12.4045
chr20	63025520	25599957	0.4062	9.5852
chr21	48129895	8609214	0.1789	8.248
chr22	51304566	14601040	0.2846	9.5653
chrMT	16571	4399	0.2655	0.626
chrX	155270560	43446480	0.2798	10.0386

chrY	59373566	2013932	0.0339	1.5674

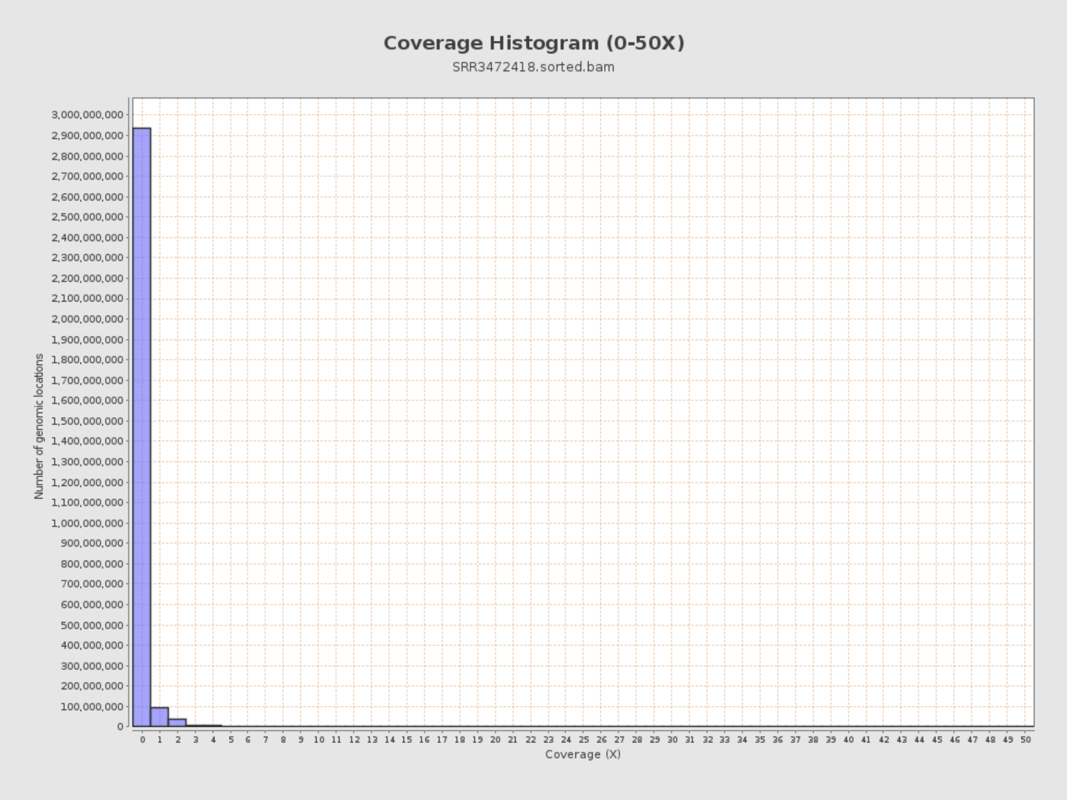
3. Results : Coverage across reference



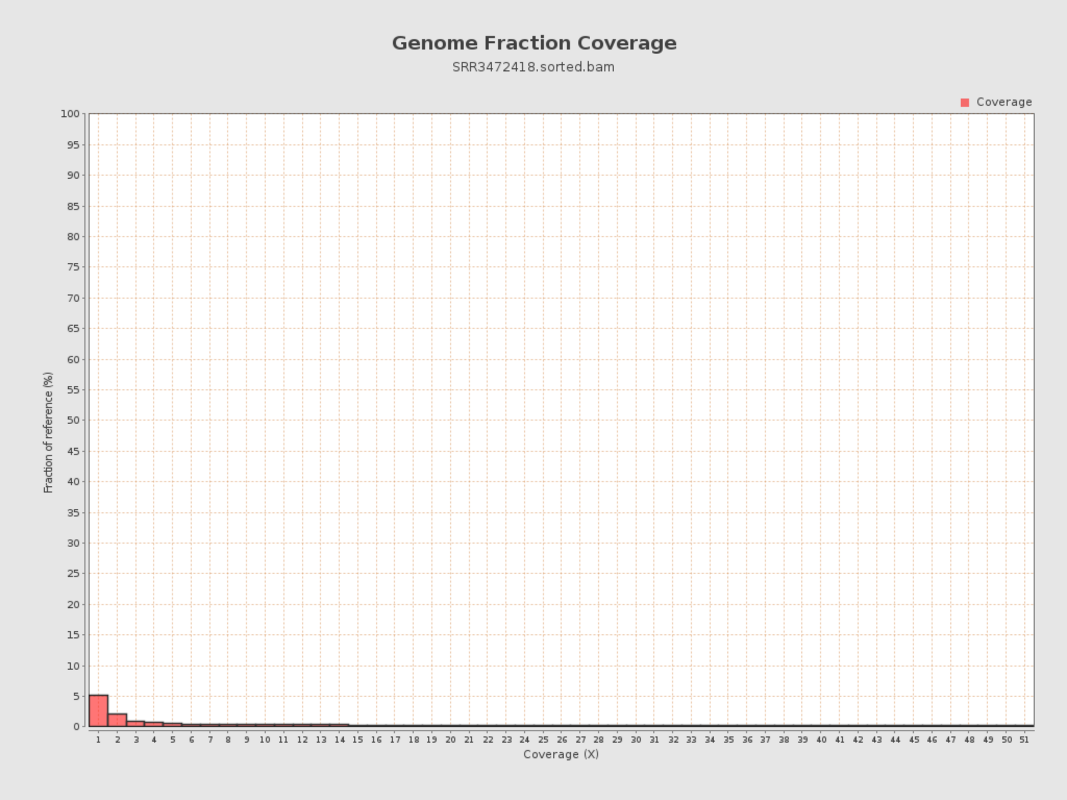
4. Results : Coverage Histogram



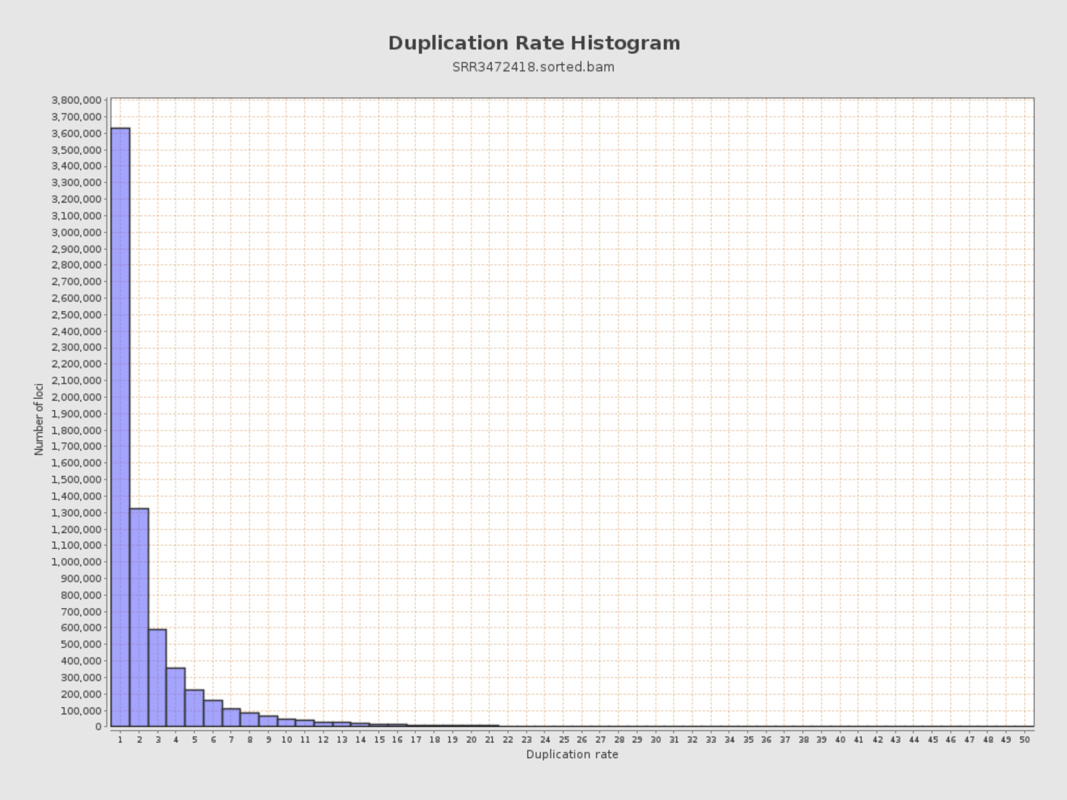
5. Results : Coverage Histogram (0-50X)



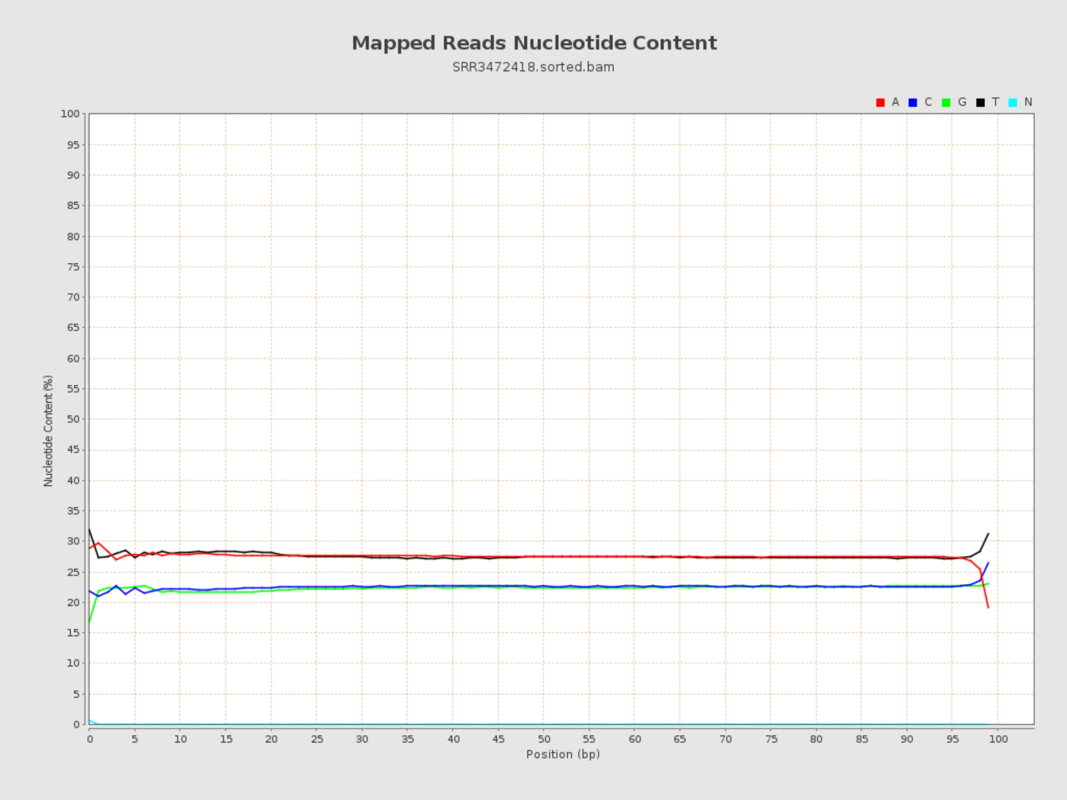
6. Results : Genome Fraction Coverage



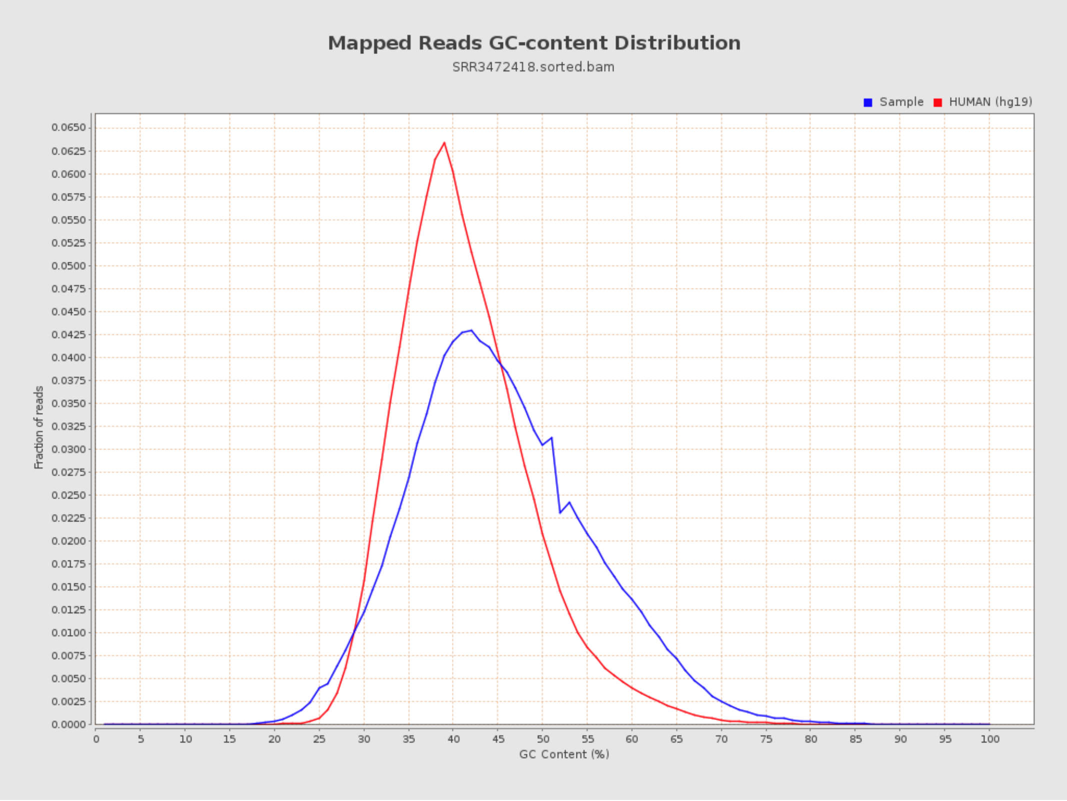
7. Results : Duplication Rate Histogram



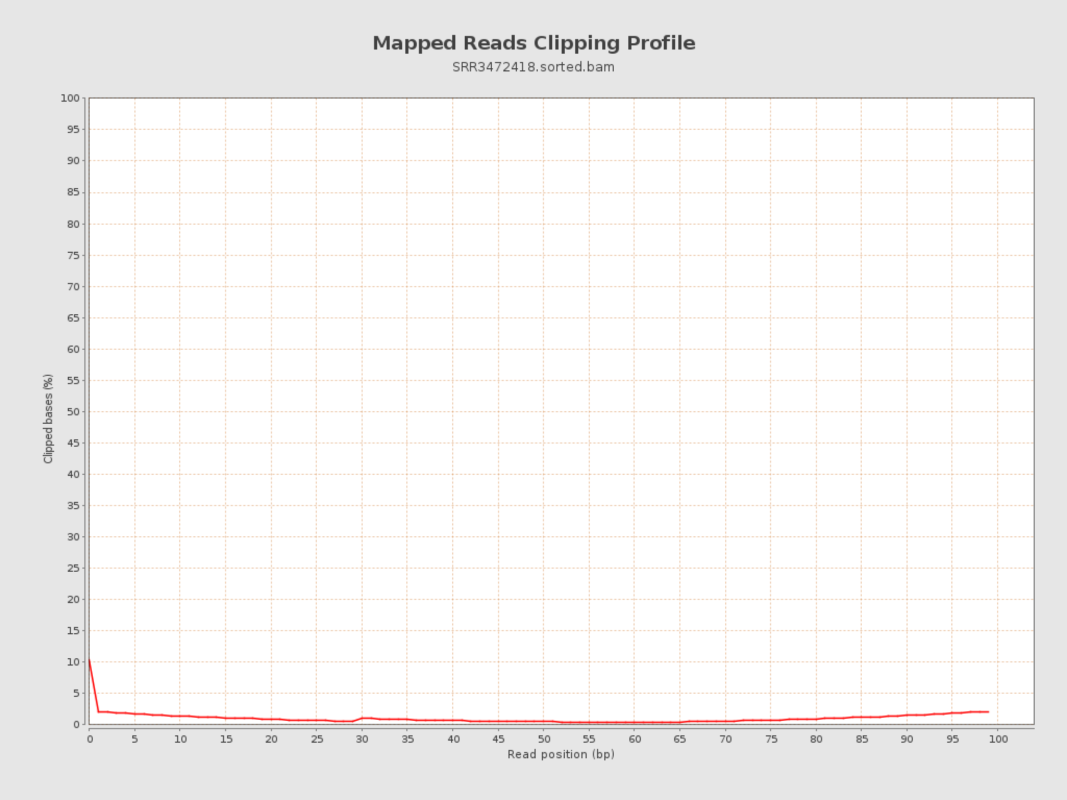
8. Results : Mapped Reads Nucleotide Content



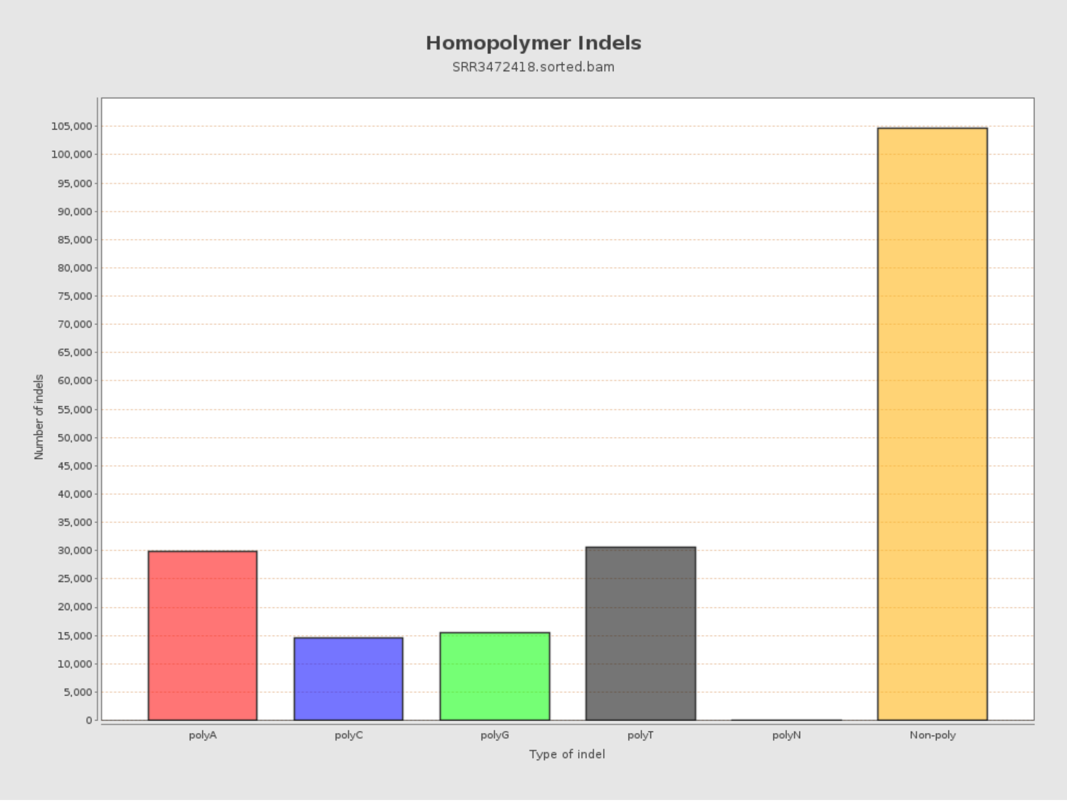
9. Results : Mapped Reads GC-content Distribution



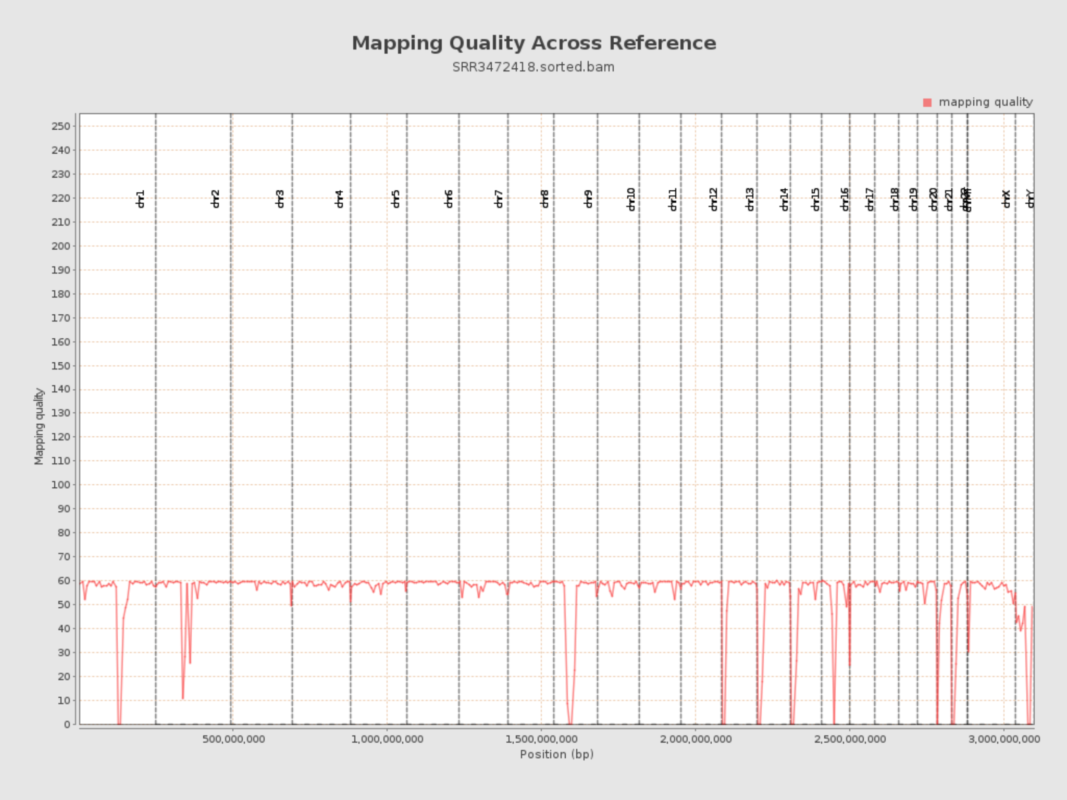
10. Results : Mapped Reads Clipping Profile



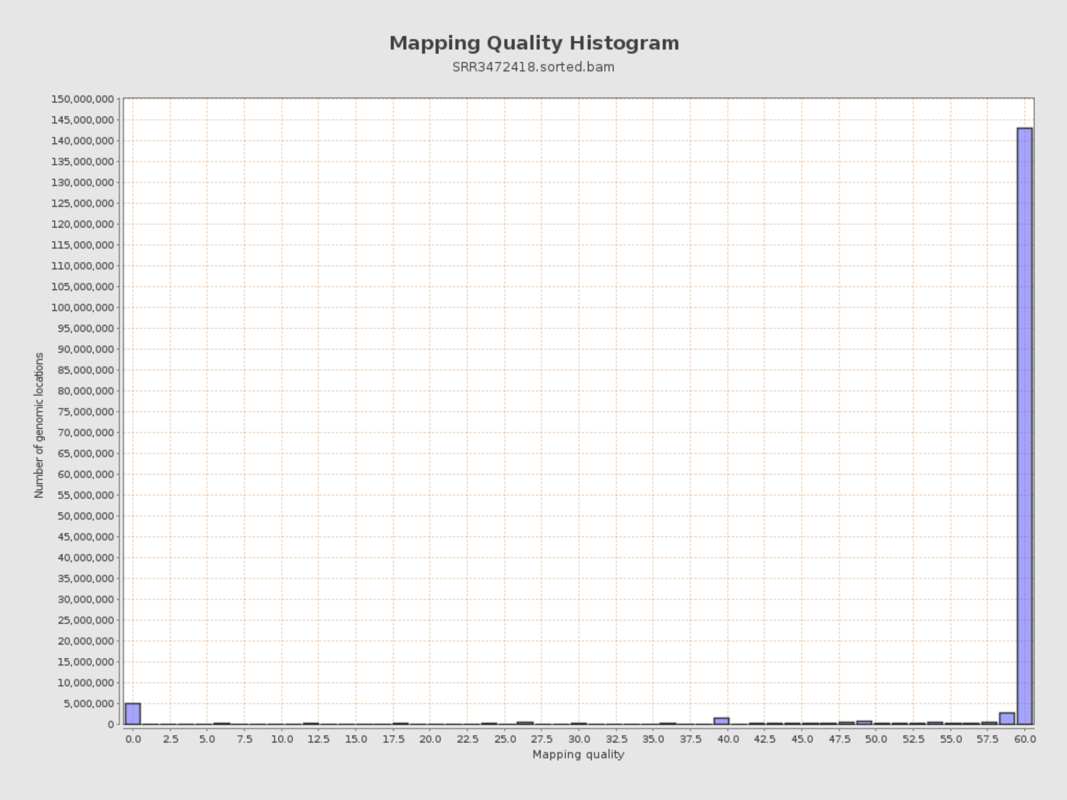
11. Results : Homopolymer Indels



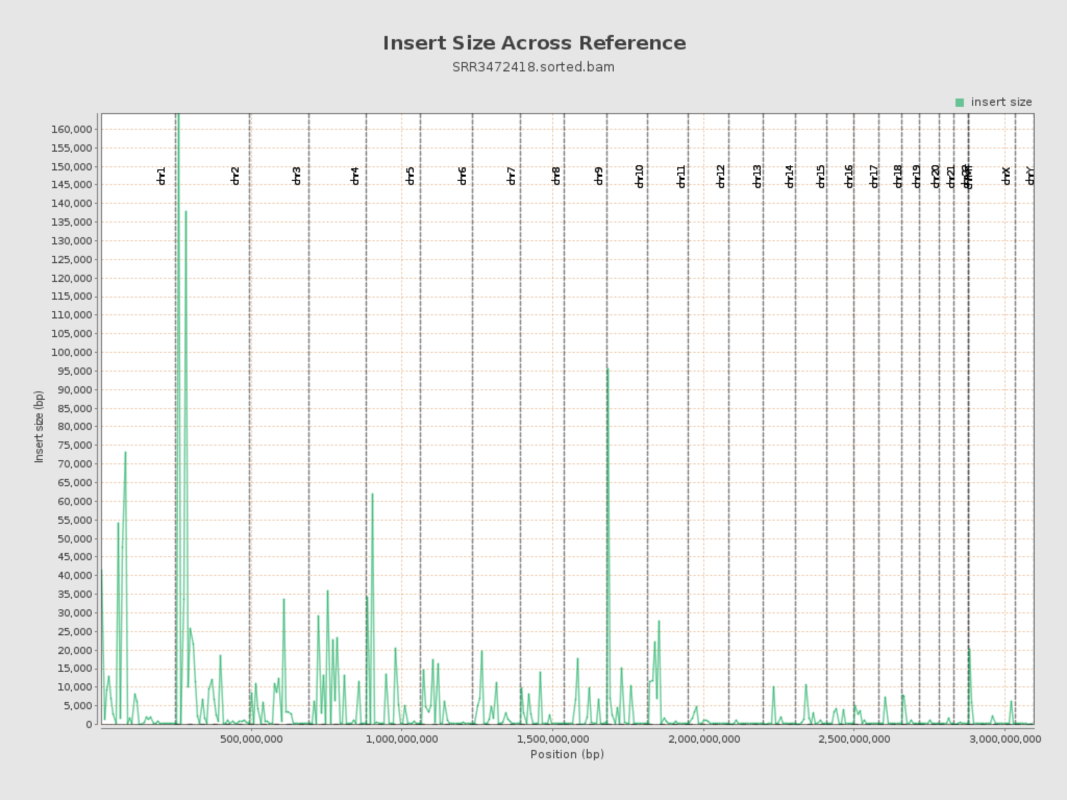
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram