Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:46:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472411.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_SRR3472411 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472411_1.fastq.gz SRR3472411_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:46:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472411.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,193,570
Mapped reads	19,961,104 / 98.85%
Unmapped reads	232,466 / 1.15%
Mapped paired reads	19,961,104 / 98.85%
Mapped reads, first in pair	10,030,488 / 49.67%
Mapped reads, second in pair	9,930,616 / 49.18%
Mapped reads, both in pair	19,806,864 / 98.09%
Mapped reads, singletons	154,240 / 0.76%
Secondary alignments	0
Supplementary alignments	74,007 / 0.37%
Read min/max/mean length	30 / 100 / 99.36
Duplicated reads (estimated)	12,870,612 / 63.74%
Duplication rate	48.8%
Clipped reads	1,440,123 / 7.13%

2.2. ACGT Content

Number/percentage of A's	524,073,510 / 26.8%
Number/percentage of C's	454,897,609 / 23.26%
Number/percentage of T's	524,853,304 / 26.84%
Number/percentage of G's	451,239,776 / 23.08%
Number/percentage of N's	247,261 / 0.01%

GC Percentage	46.34%

2.3. Coverage

Mean	0.6317
Standard Deviation	19.0633

2.4. Mapping Quality

Mean Mapping Quality	55.26

2.5. Insert size

Mean	19,166.04
Standard Deviation	1,380,855.31
P25/Median/P75	153 / 213 / 286

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	10,792,879
Insertions	108,243
Mapped reads with at least one insertion	0.53%
Deletions	93,201
Mapped reads with at least one deletion	0.46%
Homopolymer indels	44.76%

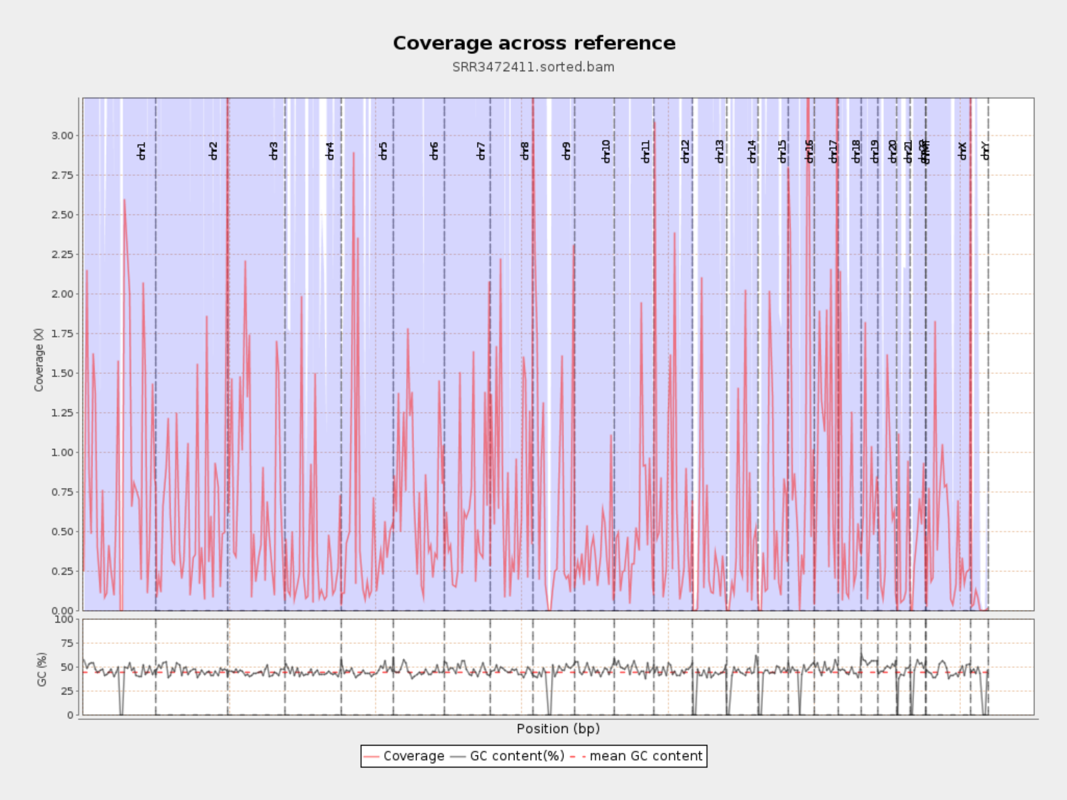
2.7. Chromosome stats

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

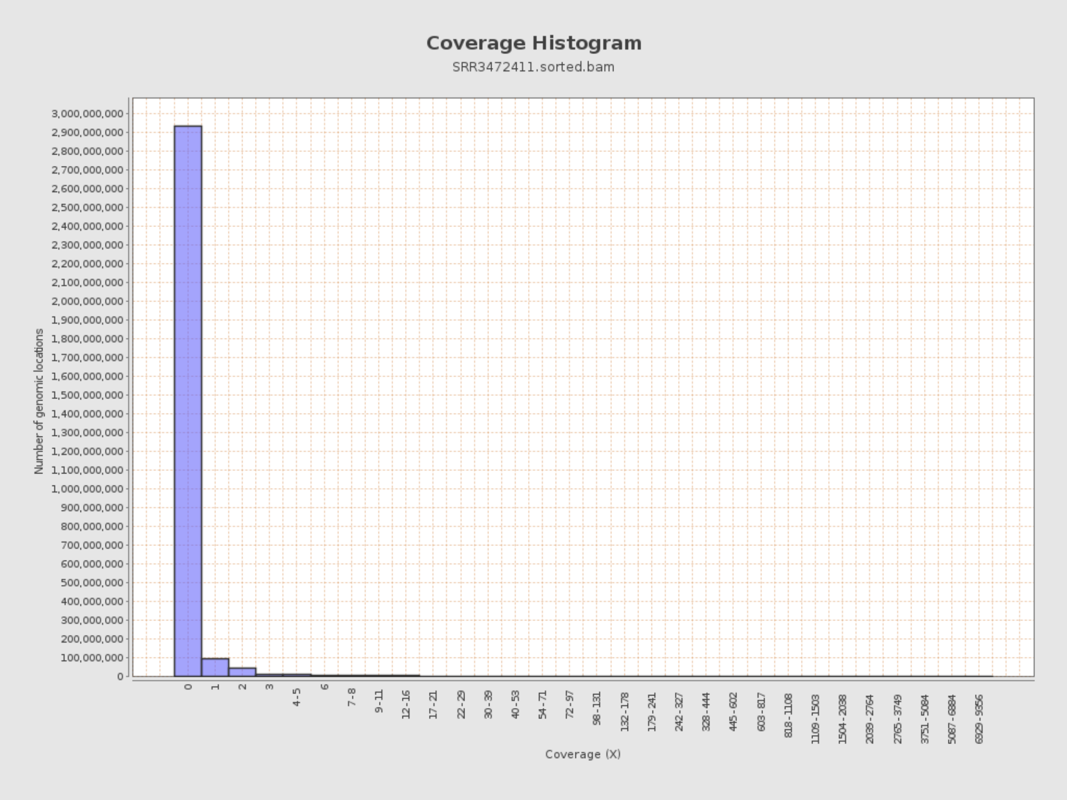
		bases	coverage	deviation
chr1	249250621	214441263	0.8603	23.8895
chr2	243199373	141143104	0.5804	17.1385
chr3	198022430	161472594	0.8154	19.4407
chr4	191154276	70224716	0.3674	14.7035
chr5	180915260	98512367	0.5445	16.8029
chr6	171115067	128638766	0.7518	19.5004
chr7	159138663	105091328	0.6604	18.3621
chr8	146364022	119507798	0.8165	23.3978
chr9	141213431	101895807	0.7216	21.2778
chr10	135534747	50336433	0.3714	12.0669
chr11	135006516	69167120	0.5123	15.6828
chr12	133851895	102343115	0.7646	21.941
chr13	115169878	42721899	0.3709	12.3124
chr14	107349540	50582953	0.4712	16.3899
chr15	102531392	51459717	0.5019	17.2343
chr16	90354753	103934460	1.1503	30.6513
chr17	81195210	97263707	1.1979	28.1095
chr18	78077248	41155337	0.5271	18.8142
chr19	59128983	43760291	0.7401	22.3596
chr20	63025520	36479700	0.5788	15.3427
chr21	48129895	18425231	0.3828	23.1197
chr22	51304566	23095532	0.4502	13.0933
chrMT	16571	7867	0.4747	0.9047
chrX	155270560	81696456	0.5262	14.1832

chrY	59373566	2189525	0.0369	1.7316

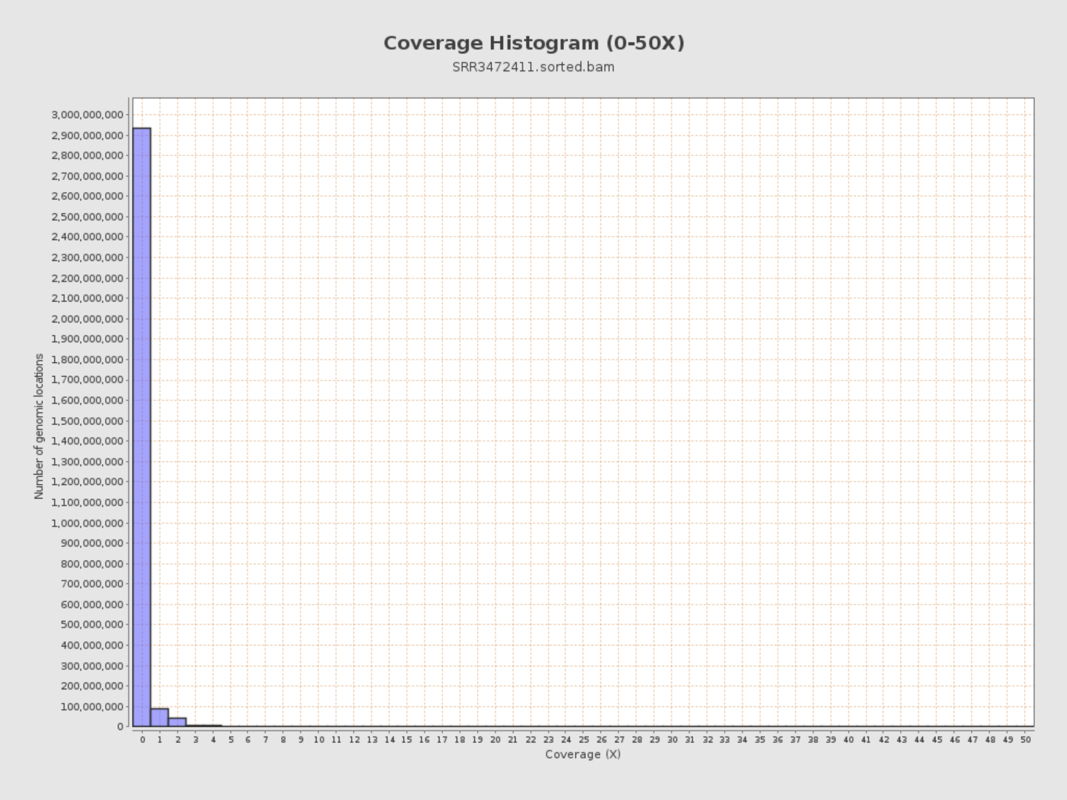
3. Results : Coverage across reference



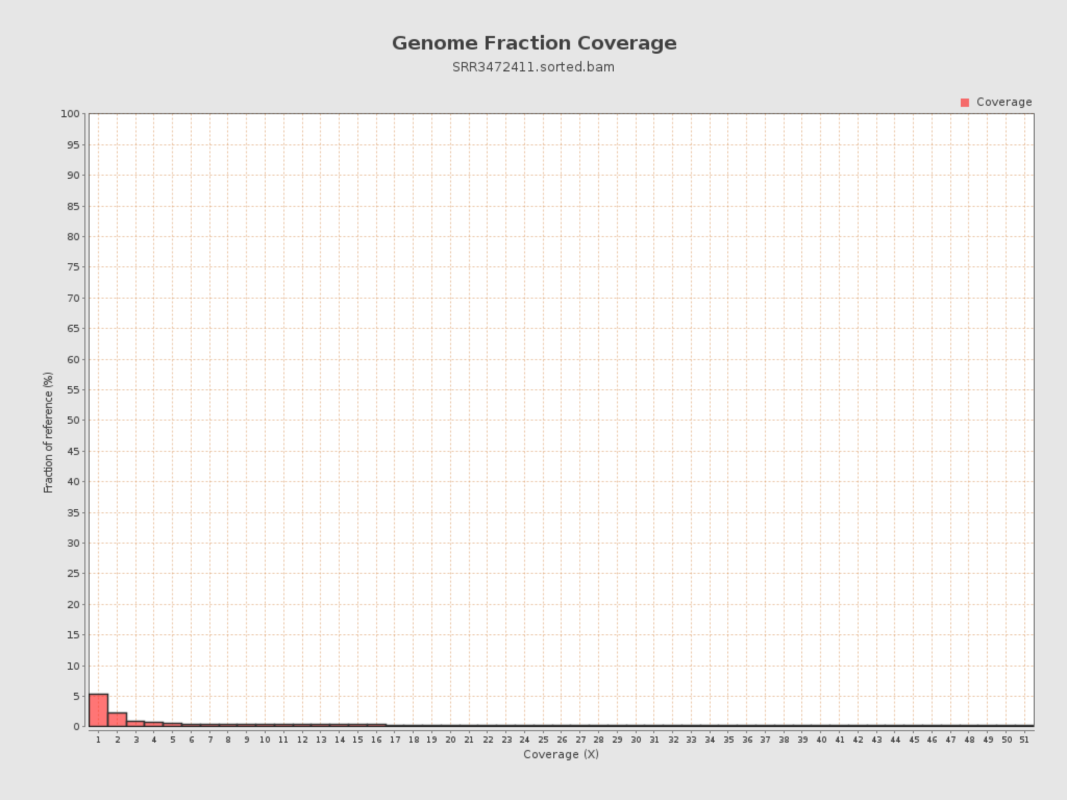
4. Results : Coverage Histogram



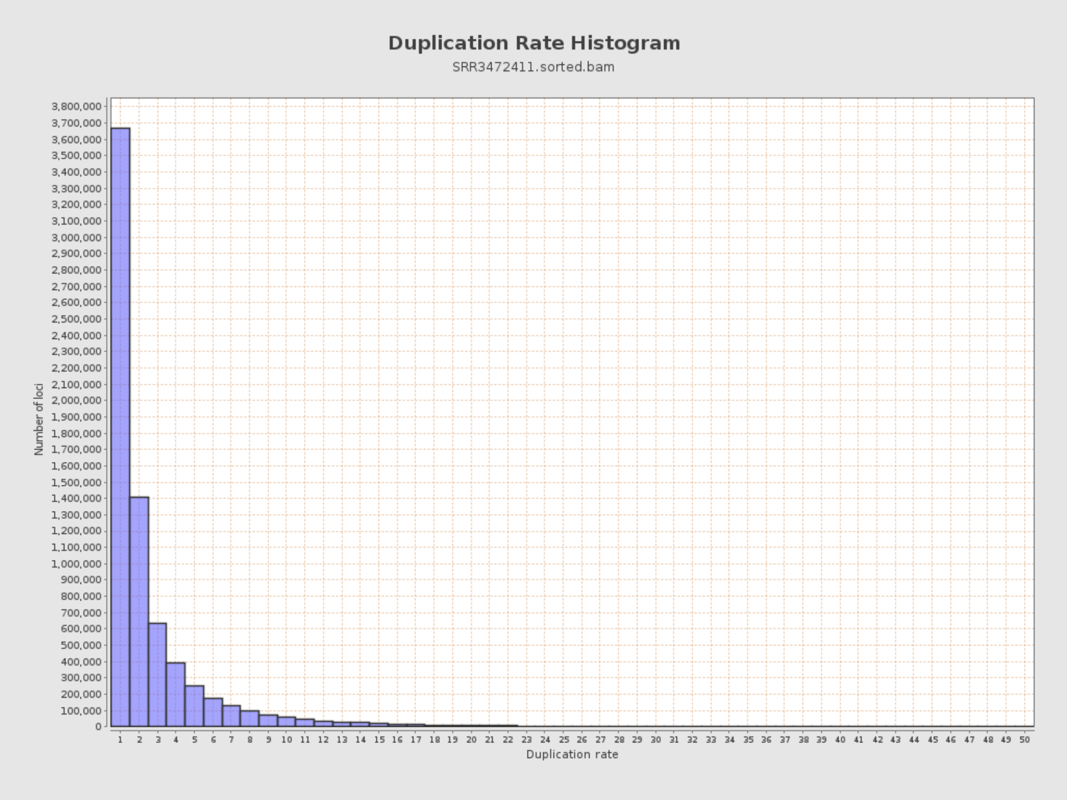
5. Results : Coverage Histogram (0-50X)



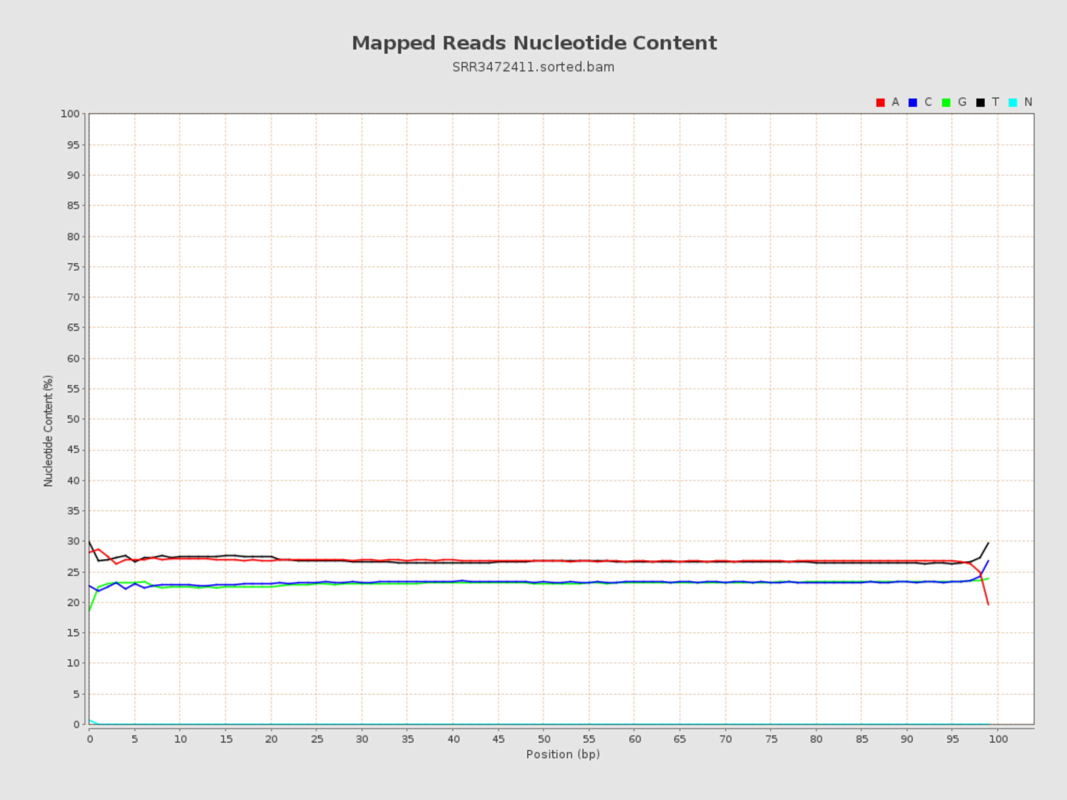
6. Results : Genome Fraction Coverage



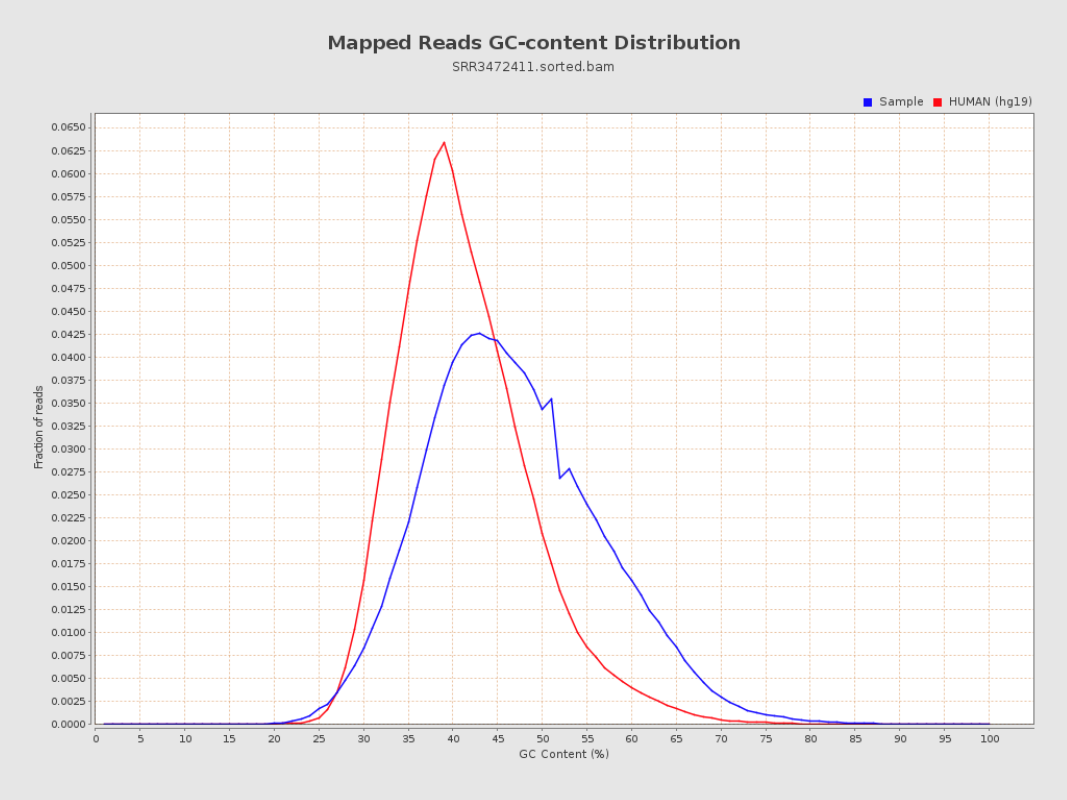
7. Results : Duplication Rate Histogram



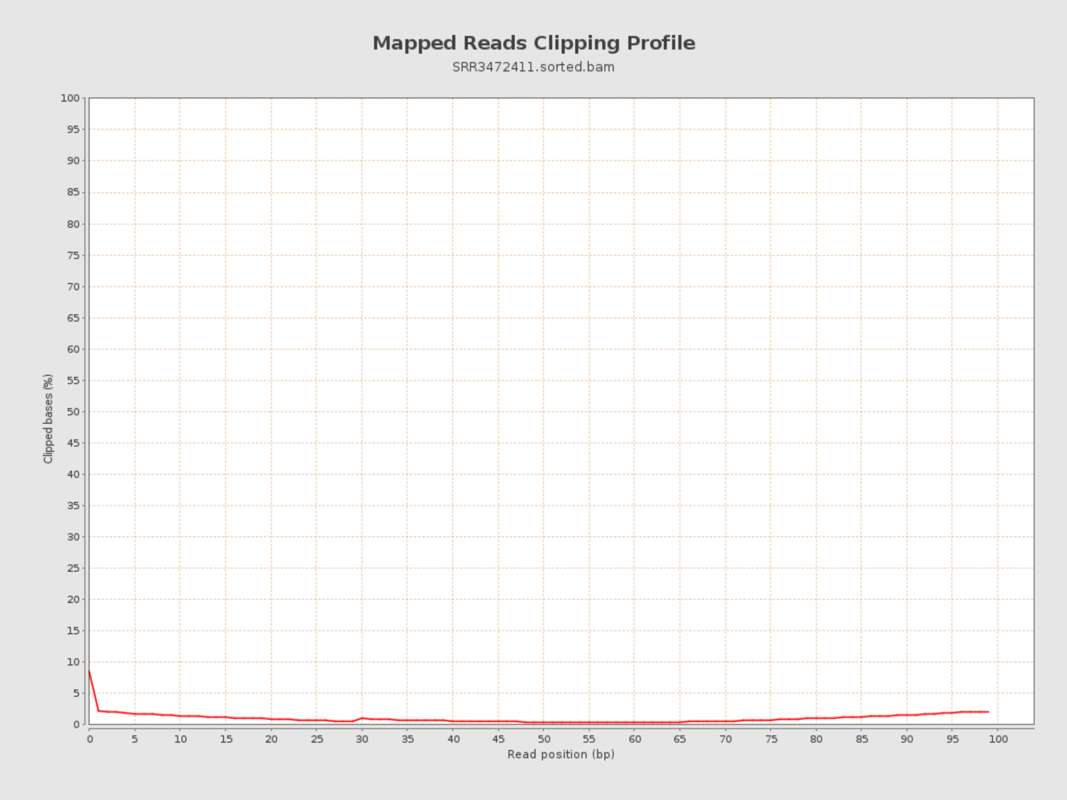
8. Results : Mapped Reads Nucleotide Content



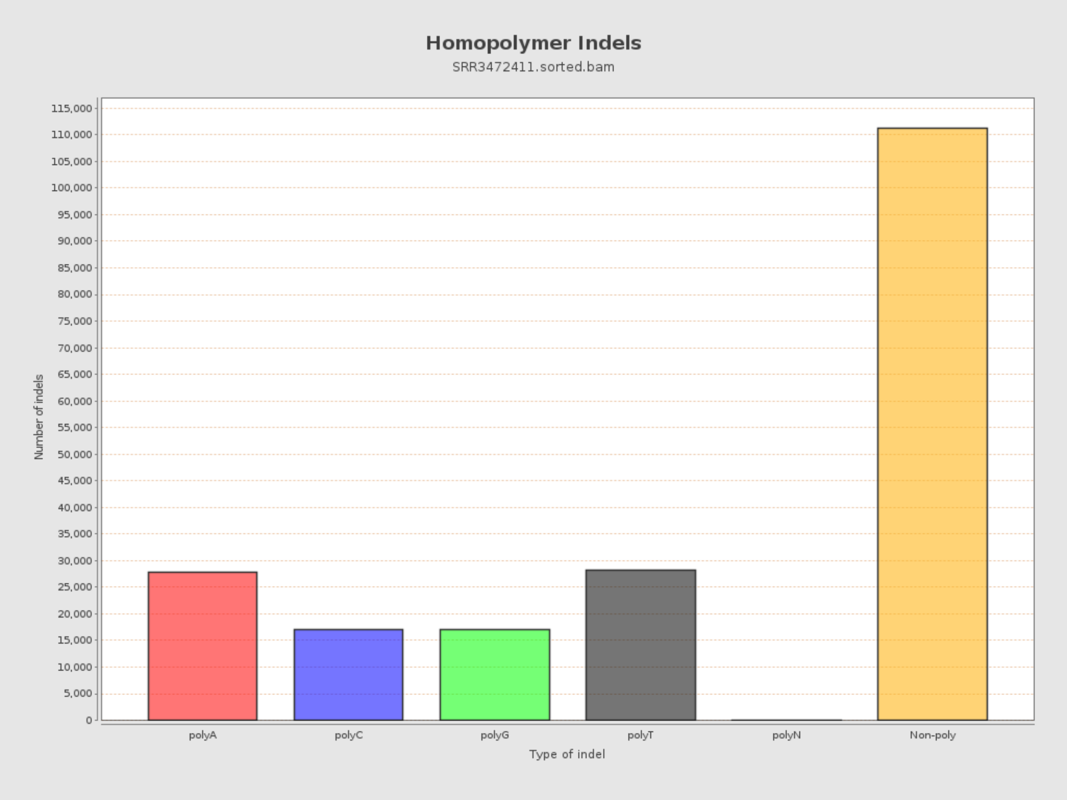
9. Results : Mapped Reads GC-content Distribution



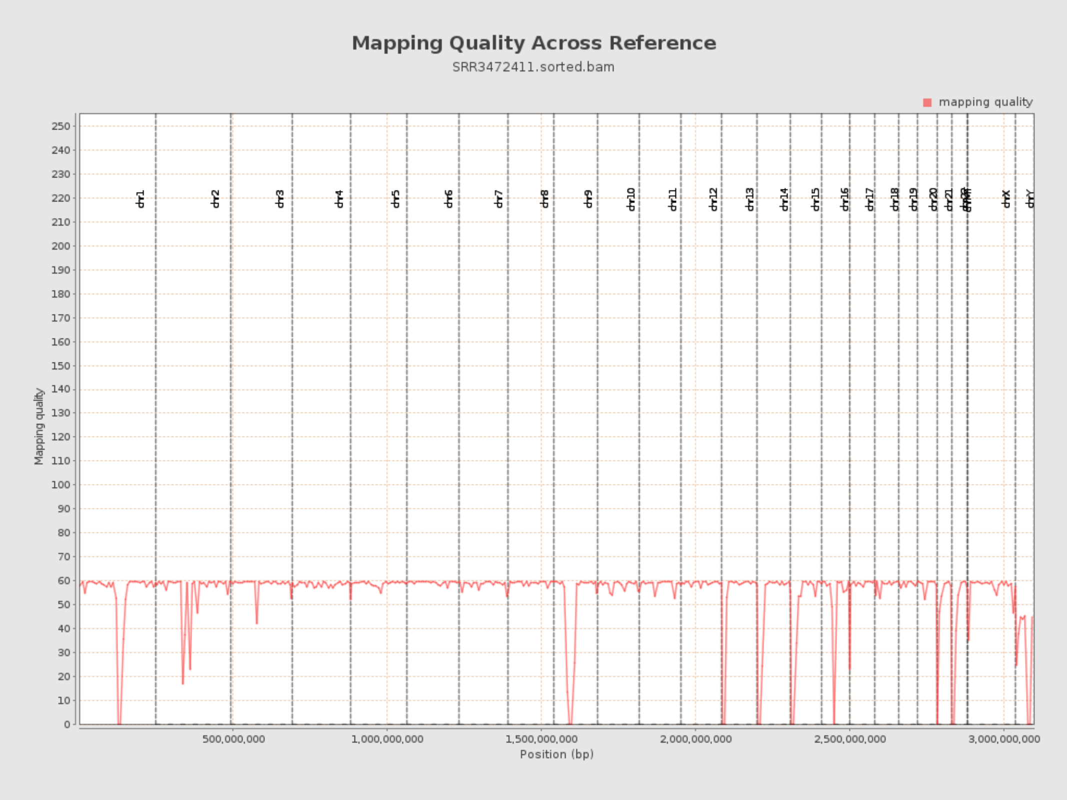
10. Results : Mapped Reads Clipping Profile



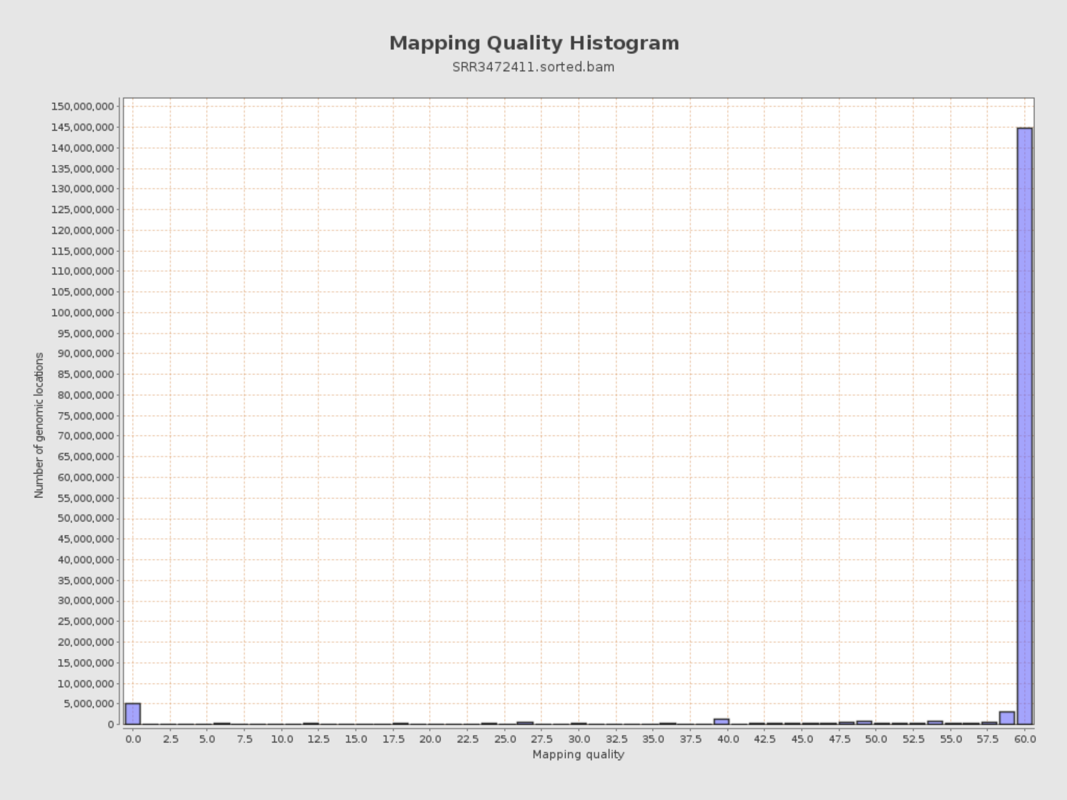
11. Results : Homopolymer Indels



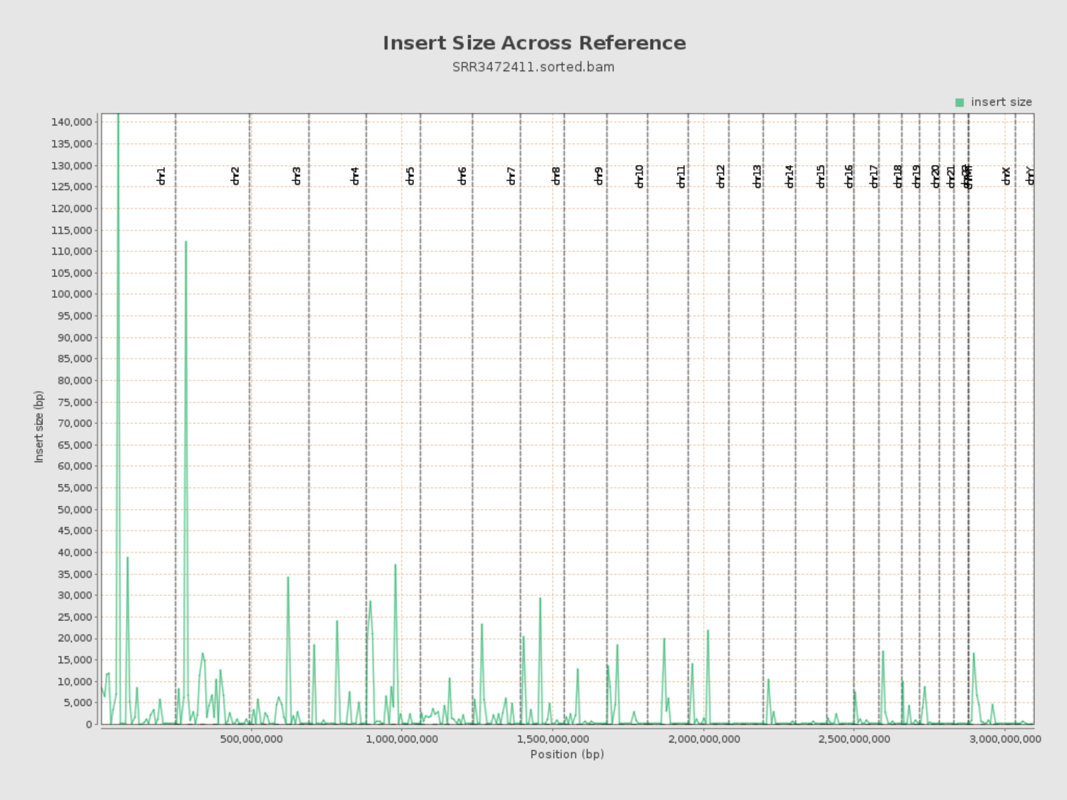
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram