Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:49:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472417.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_SRR3472417 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472417_1.fastq.gz SRR3472417_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:49:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472417.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,744,316
Mapped reads	19,591,061 / 99.22%
Unmapped reads	153,255 / 0.78%
Mapped paired reads	19,591,061 / 99.22%
Mapped reads, first in pair	9,827,003 / 49.77%
Mapped reads, second in pair	9,764,058 / 49.45%
Mapped reads, both in pair	19,494,914 / 98.74%
Mapped reads, singletons	96,147 / 0.49%
Secondary alignments	0
Supplementary alignments	72,554 / 0.37%
Read min/max/mean length	30 / 100 / 99.39
Duplicated reads (estimated)	12,245,317 / 62.02%
Duplication rate	47.23%
Clipped reads	1,384,401 / 7.01%

2.2. ACGT Content

Number/percentage of A's	519,793,335 / 27.06%
Number/percentage of C's	441,943,618 / 23.01%
Number/percentage of T's	520,347,367 / 27.09%
Number/percentage of G's	438,213,036 / 22.82%
Number/percentage of N's	241,061 / 0.01%

GC Percentage	45.83%

2.3. Coverage

Mean	0.6205
Standard Deviation	18.2571

2.4. Mapping Quality

Mean Mapping Quality	54.83

2.5. Insert size

Mean	16,809.47
Standard Deviation	1,263,696.64
P25/Median/P75	152 / 213 / 288

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	10,246,882
Insertions	110,500
Mapped reads with at least one insertion	0.56%
Deletions	100,476
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.35%

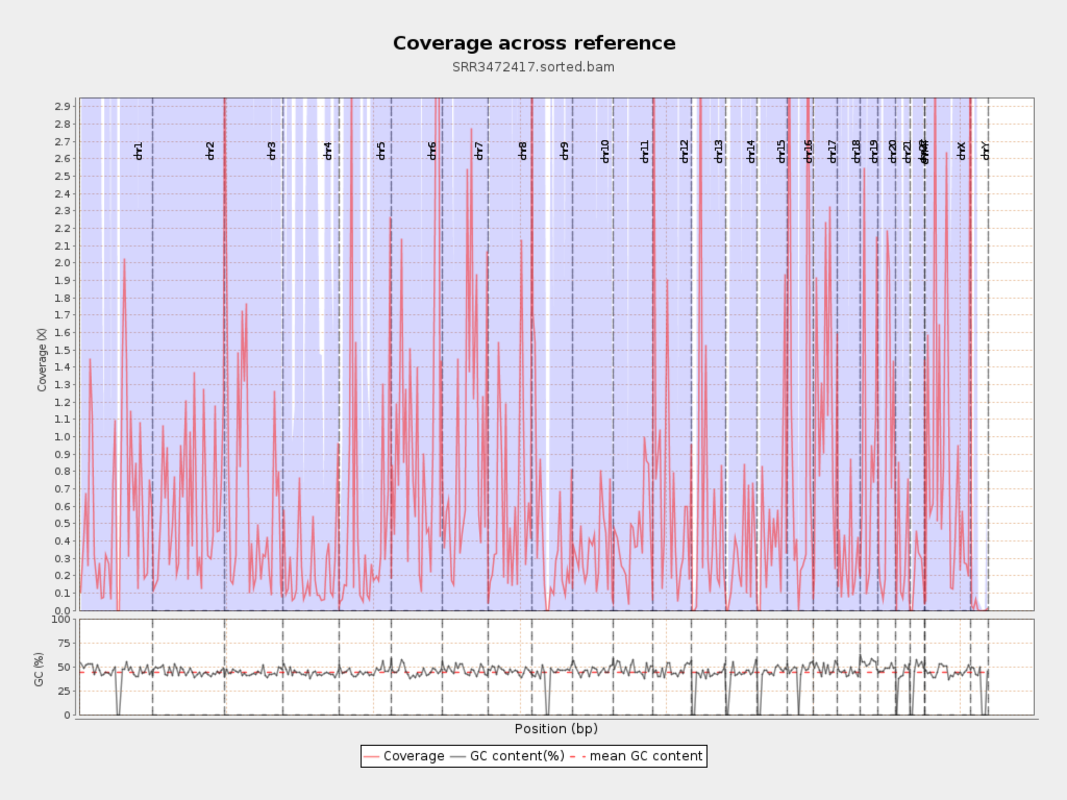
2.7. Chromosome stats

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

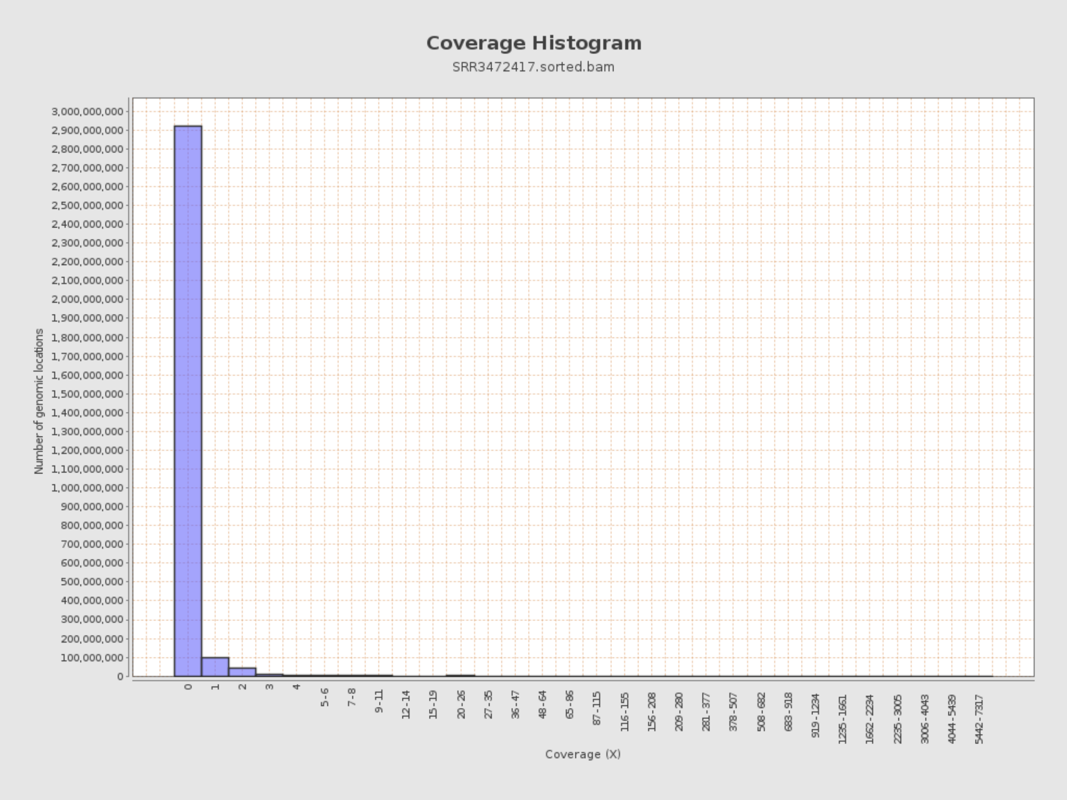
		bases	coverage	deviation
chr1	249250621	146608331	0.5882	16.5254
chr2	243199373	144760969	0.5952	16.3818
chr3	198022430	135539568	0.6845	15.1256
chr4	191154276	44304945	0.2318	6.9839
chr5	180915260	100117373	0.5534	24.2342
chr6	171115067	181146663	1.0586	26.6595
chr7	159138663	156257726	0.9819	27.1333
chr8	146364022	92071763	0.6291	16.8394
chr9	141213431	66149352	0.4684	11.3391
chr10	135534747	48524475	0.358	11.2694
chr11	135006516	59758845	0.4426	13.0323
chr12	133851895	99183841	0.741	17.3345
chr13	115169878	69843043	0.6064	21.1483
chr14	107349540	32885508	0.3063	10.5458
chr15	102531392	53696320	0.5237	15.7631
chr16	90354753	94359412	1.0443	27.6322
chr17	81195210	96689164	1.1908	27.9315
chr18	78077248	23498118	0.301	9.5326
chr19	59128983	53886836	0.9113	19.0036
chr20	63025520	54914332	0.8713	18.6341
chr21	48129895	15763282	0.3275	14.9833
chr22	51304566	11038229	0.2152	7.48
chrMT	16571	23920	1.4435	1.7577
chrX	155270560	139025914	0.8954	21.7

chrY	59373566	779870	0.0131	2.0558

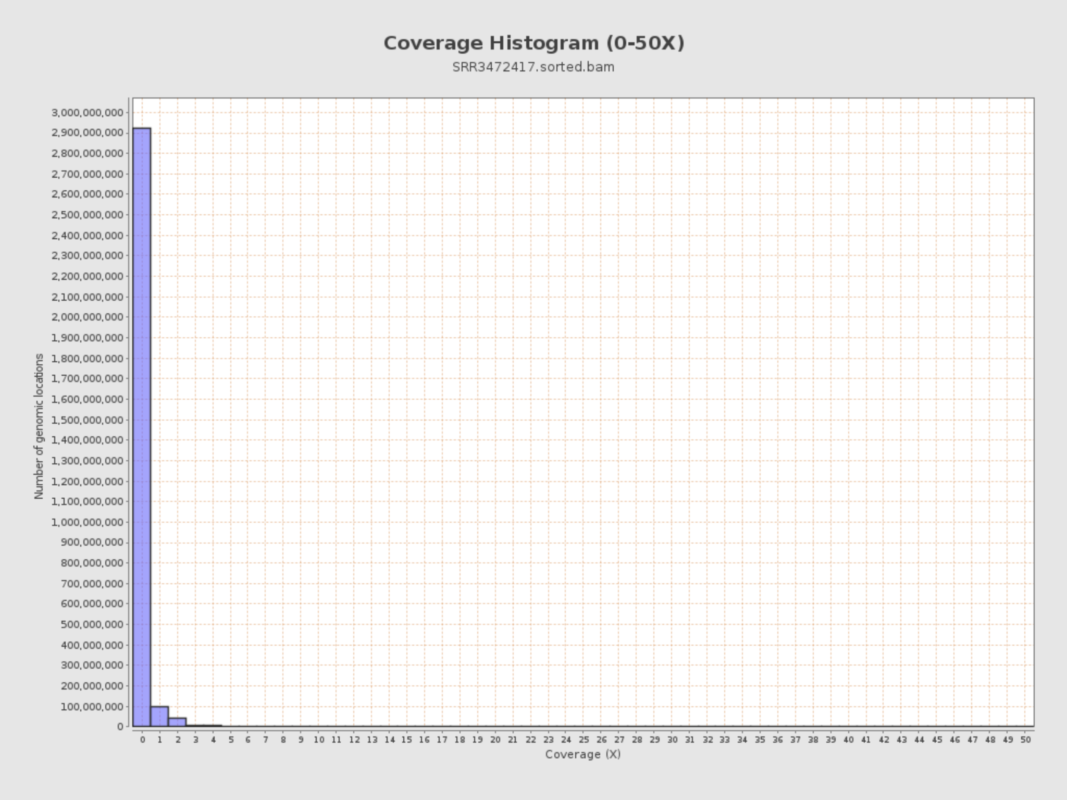
3. Results : Coverage across reference



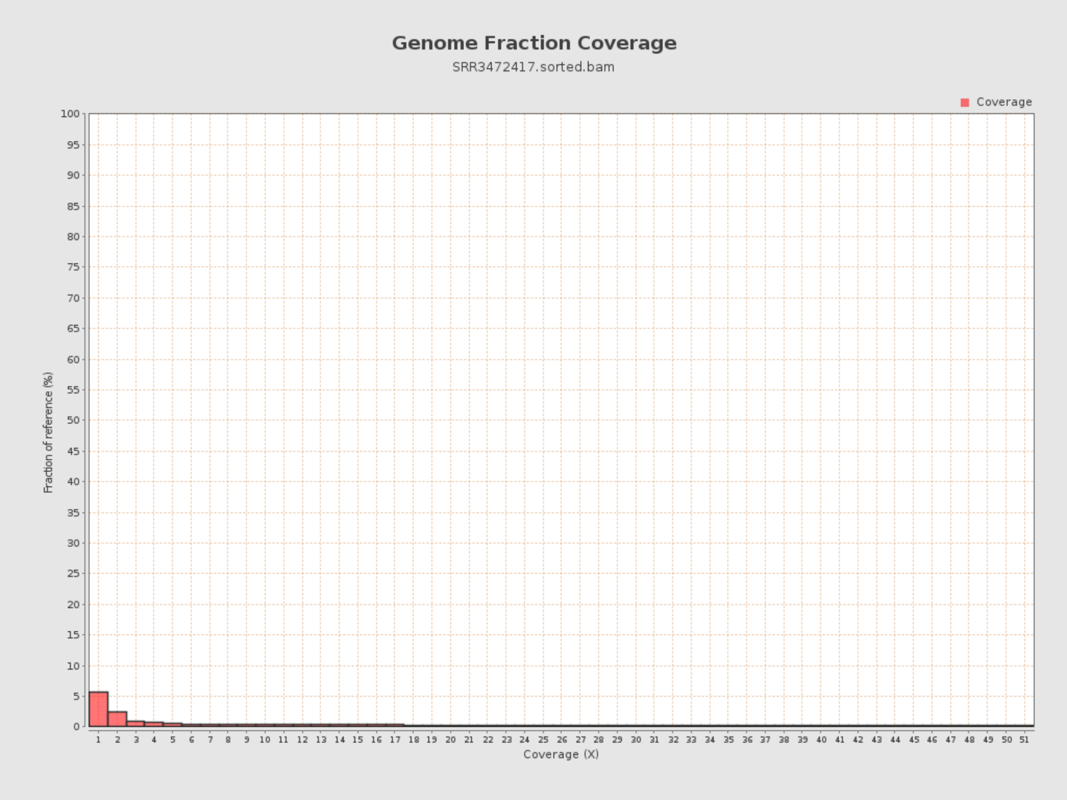
4. Results : Coverage Histogram



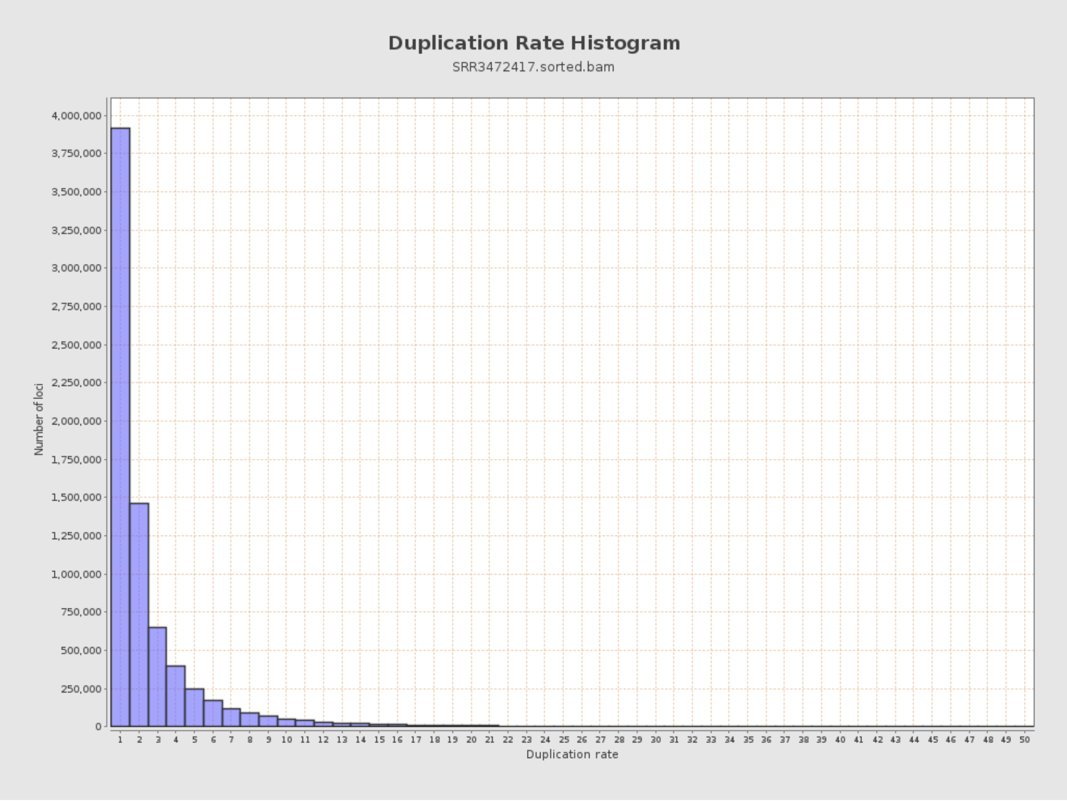
5. Results : Coverage Histogram (0-50X)



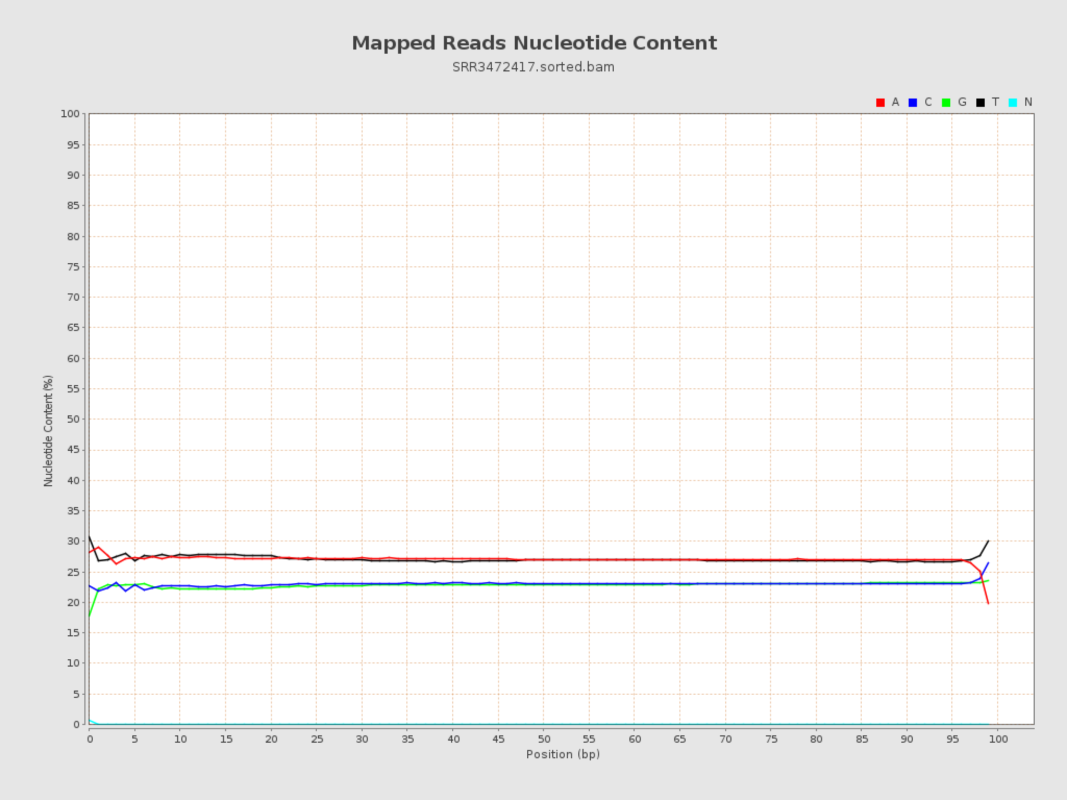
6. Results : Genome Fraction Coverage



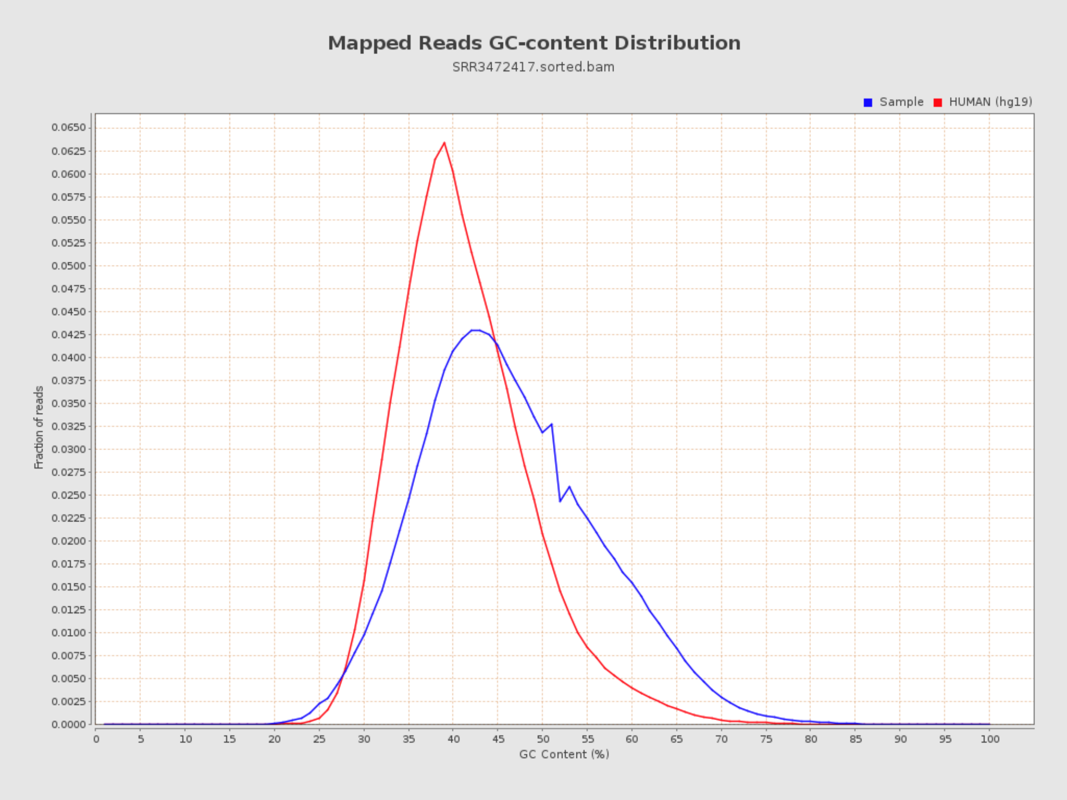
7. Results : Duplication Rate Histogram



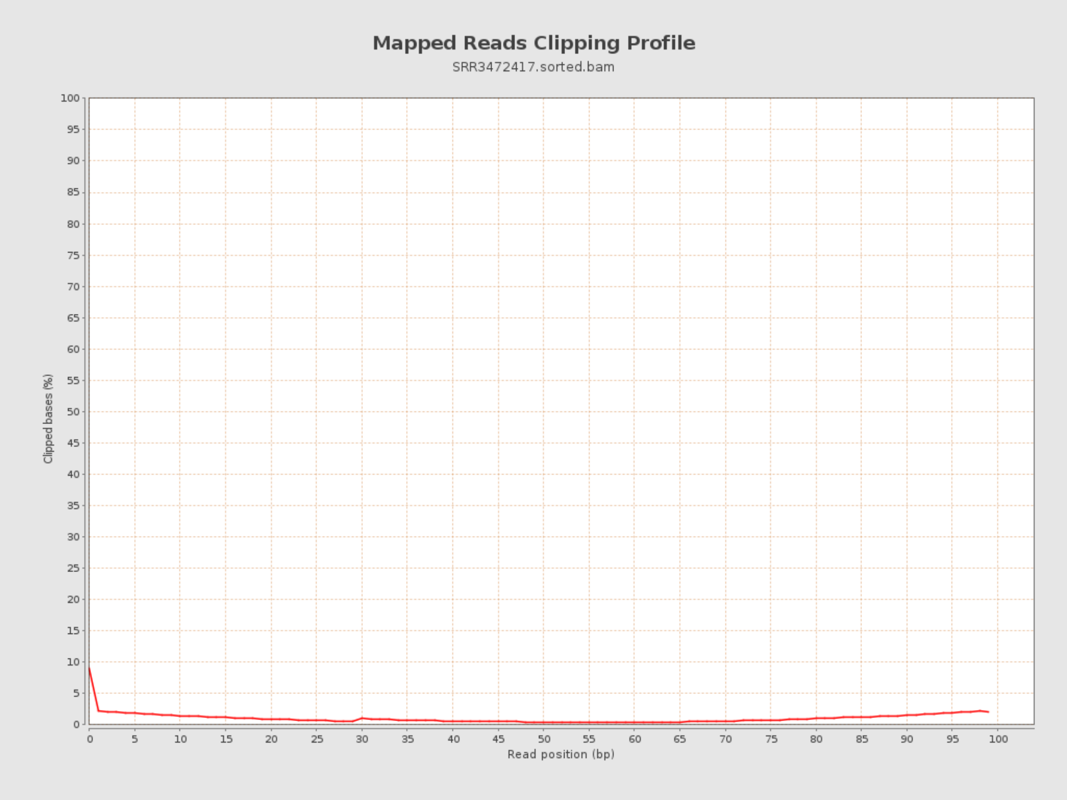
8. Results : Mapped Reads Nucleotide Content



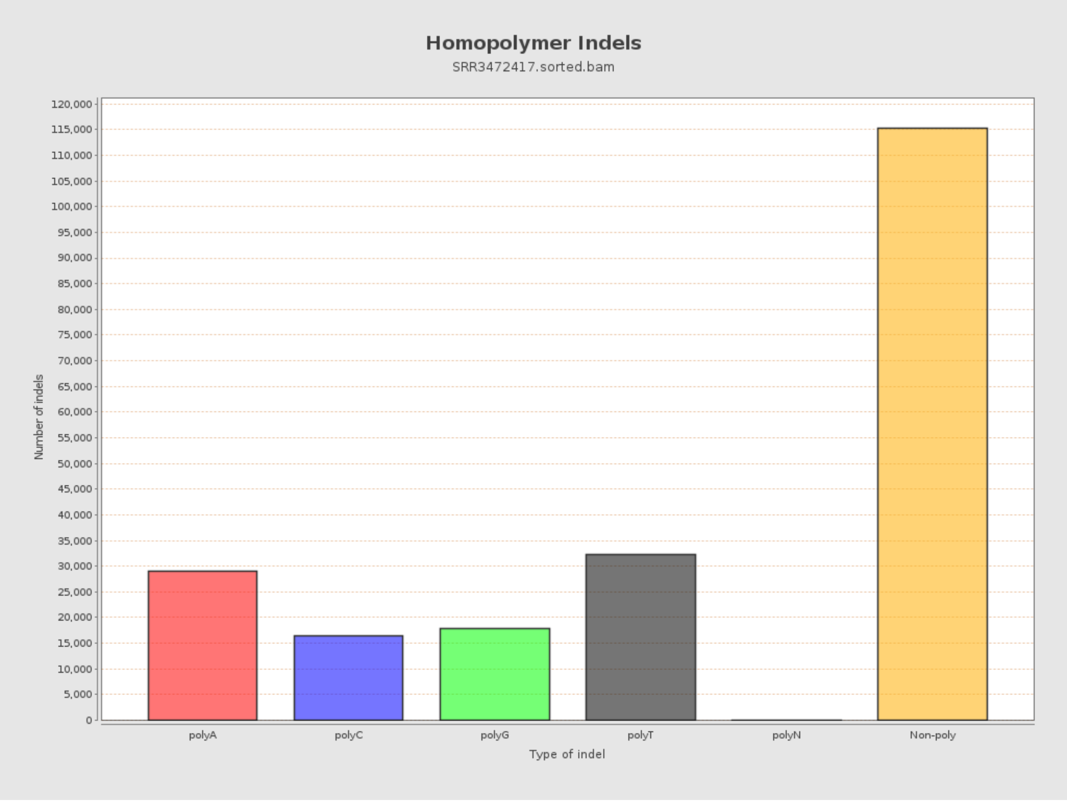
9. Results : Mapped Reads GC-content Distribution



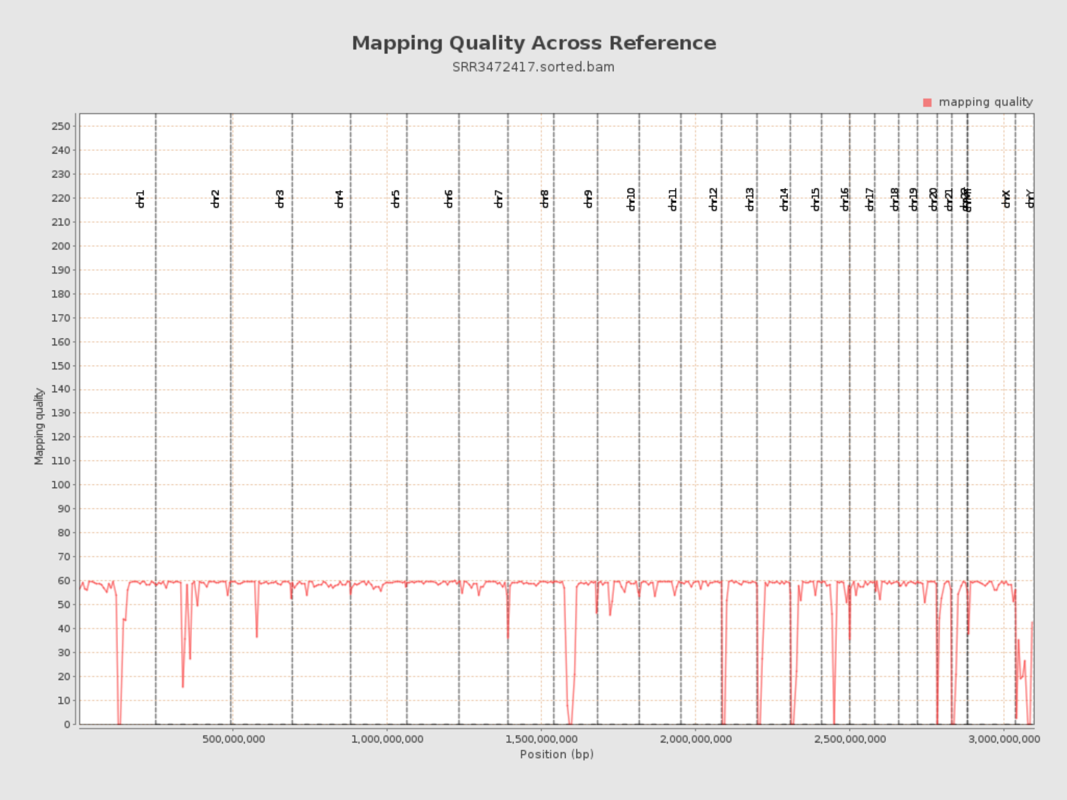
10. Results : Mapped Reads Clipping Profile



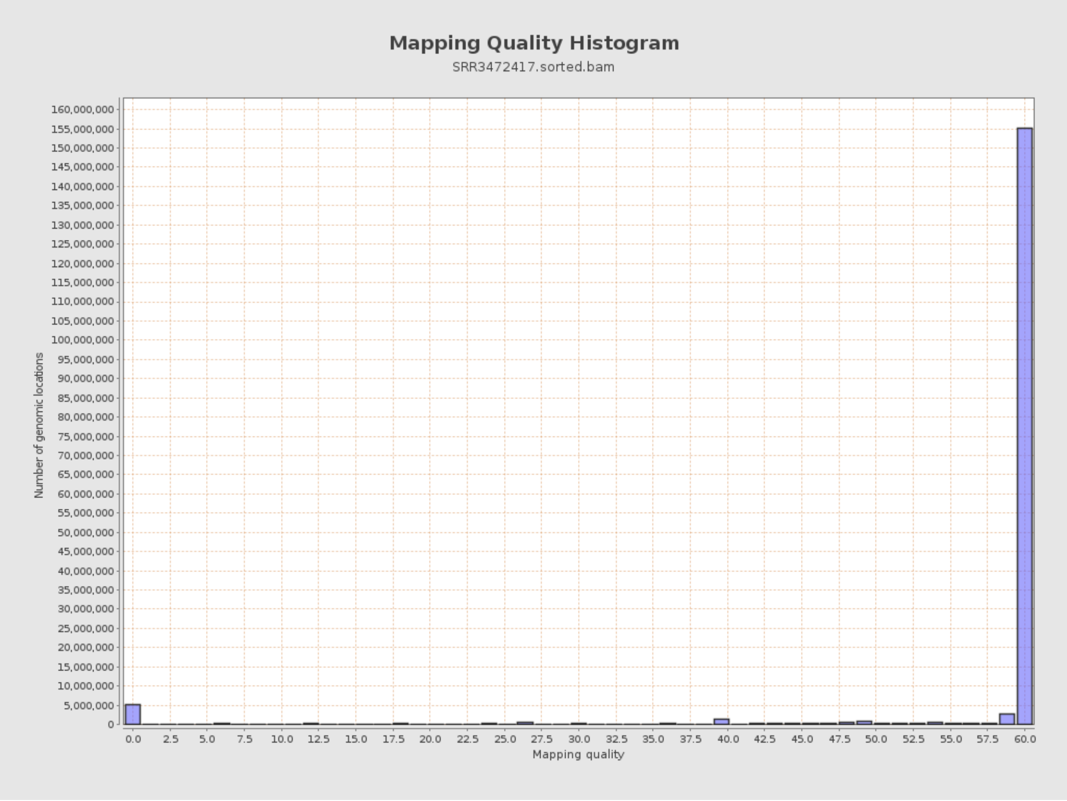
11. Results : Homopolymer Indels



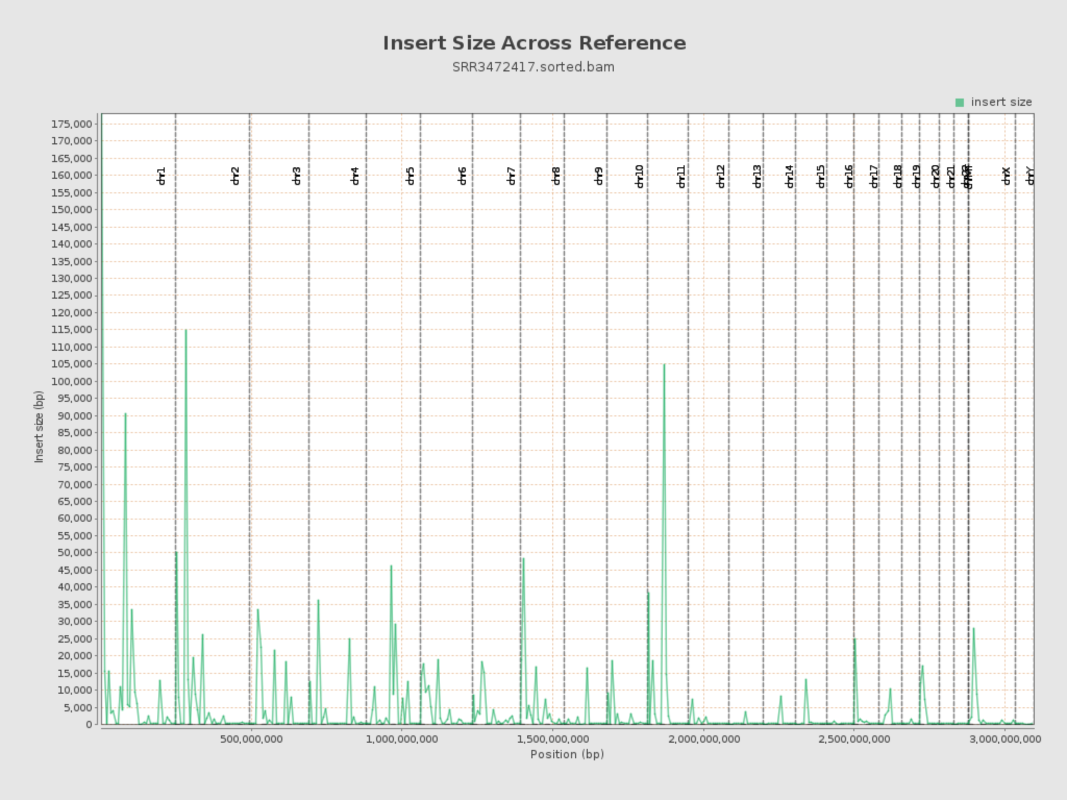
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram