Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:28:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472419.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_SRR3472419 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472419_1.fastq.gz SRR3472419_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:28:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472419.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,758,788
Mapped reads	20,572,785 / 99.1%
Unmapped reads	186,003 / 0.9%
Mapped paired reads	20,572,785 / 99.1%
Mapped reads, first in pair	10,331,311 / 49.77%
Mapped reads, second in pair	10,241,474 / 49.34%
Mapped reads, both in pair	20,439,666 / 98.46%
Mapped reads, singletons	133,119 / 0.64%
Secondary alignments	0
Supplementary alignments	88,282 / 0.43%
Read min/max/mean length	30 / 100 / 99.57
Duplicated reads (estimated)	12,989,853 / 62.58%
Duplication rate	46.95%
Clipped reads	1,327,678 / 6.4%

2.2. ACGT Content

Number/percentage of A's	556,920,452 / 27.53%
Number/percentage of C's	455,938,102 / 22.54%
Number/percentage of T's	558,447,002 / 27.61%
Number/percentage of G's	451,270,520 / 22.31%
Number/percentage of N's	247,534 / 0.01%

GC Percentage	44.85%

2.3. Coverage

Mean	0.6535
Standard Deviation	19.6837

2.4. Mapping Quality

Mean Mapping Quality	54.97

2.5. Insert size

Mean	22,912.23
Standard Deviation	1,442,252.97
P25/Median/P75	171 / 240 / 324

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	11,962,575
Insertions	123,921
Mapped reads with at least one insertion	0.6%
Deletions	113,050
Mapped reads with at least one deletion	0.54%
Homopolymer indels	47.22%

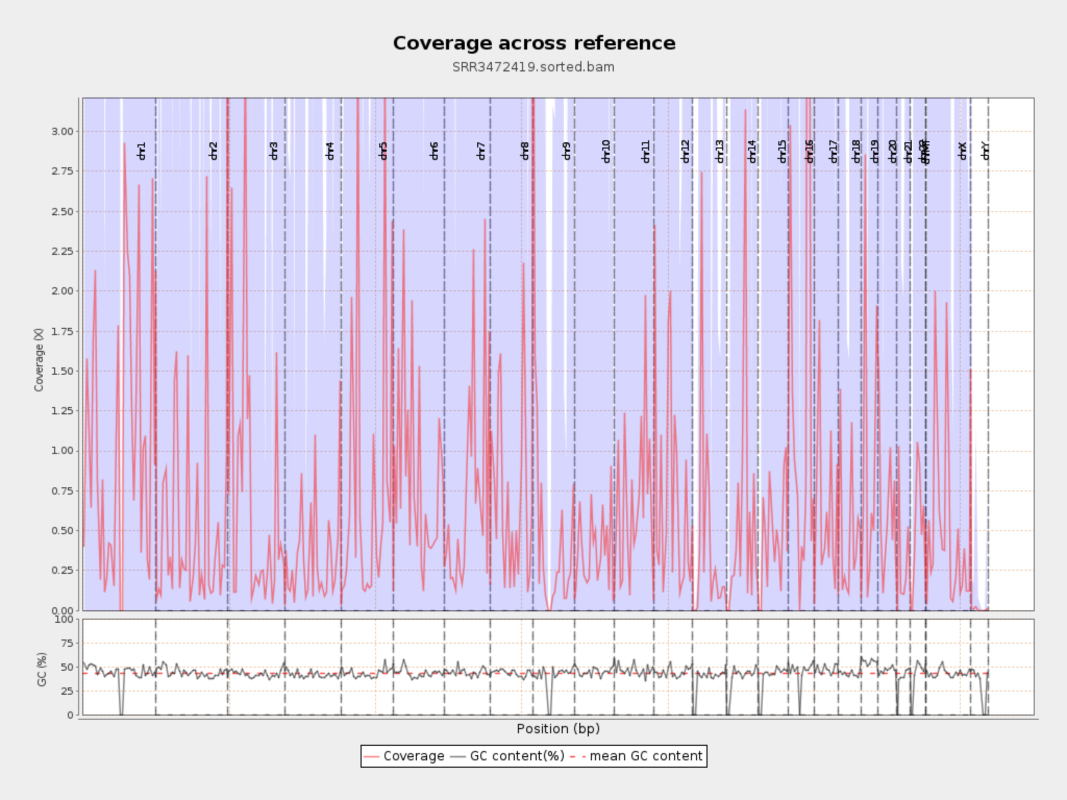
2.7. Chromosome stats

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

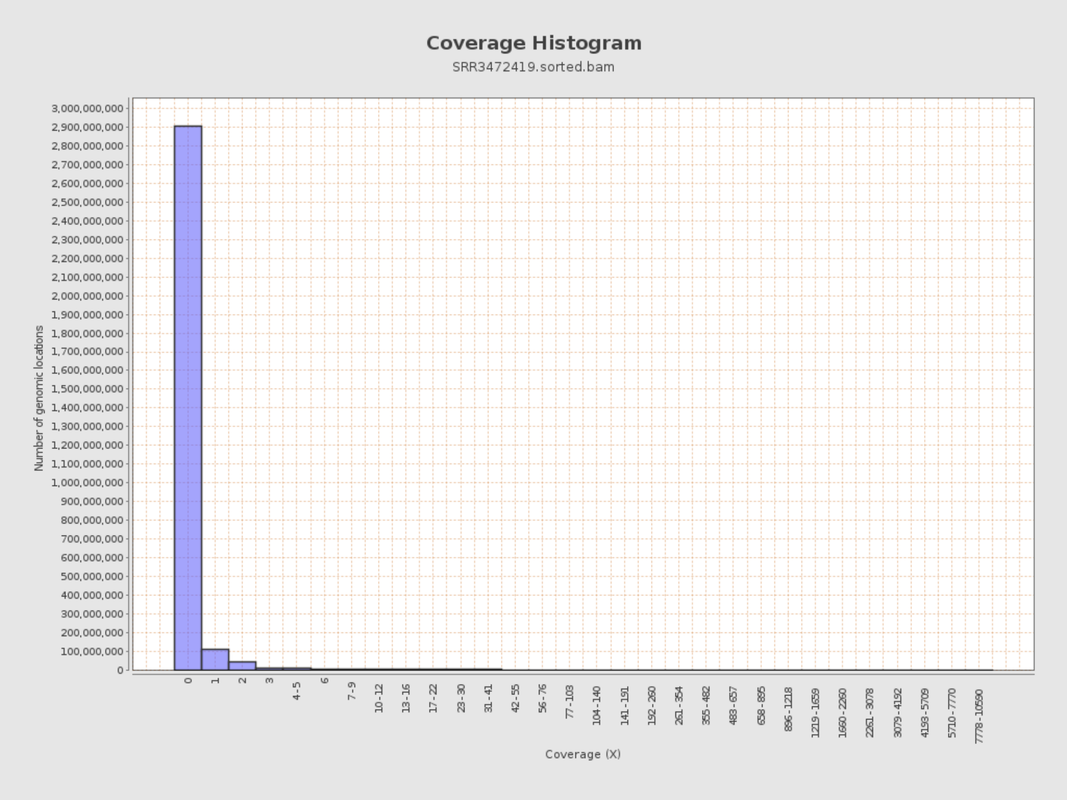
		bases	coverage	deviation
chr1	249250621	261065877	1.0474	26.5509
chr2	243199373	120608953	0.4959	15.6218
chr3	198022430	150531664	0.7602	20.1191
chr4	191154276	67988275	0.3557	10.2994
chr5	180915260	150910518	0.8342	27.4249
chr6	171115067	143532541	0.8388	19.6891
chr7	159138663	117970232	0.7413	20.642
chr8	146364022	104938191	0.717	18.3877
chr9	141213431	58149189	0.4118	12.1285
chr10	135534747	53476895	0.3946	10.7953
chr11	135006516	92602084	0.6859	17.9378
chr12	133851895	100464798	0.7506	20.9518
chr13	115169878	48369631	0.42	17.952
chr14	107349540	60797186	0.5663	15.9626
chr15	102531392	47533003	0.4636	12.9418
chr16	90354753	131106005	1.451	43.4242
chr17	81195210	53797733	0.6626	19.5464
chr18	78077248	36280489	0.4647	13.5095
chr19	59128983	56363750	0.9532	24.162
chr20	63025520	38428215	0.6097	14.5749
chr21	48129895	16058754	0.3337	16.473
chr22	51304566	26686444	0.5202	13.3968
chrMT	16571	8971	0.5414	0.9325
chrX	155270560	85013588	0.5475	15.5975

chrY	59373566	428098	0.0072	0.4833

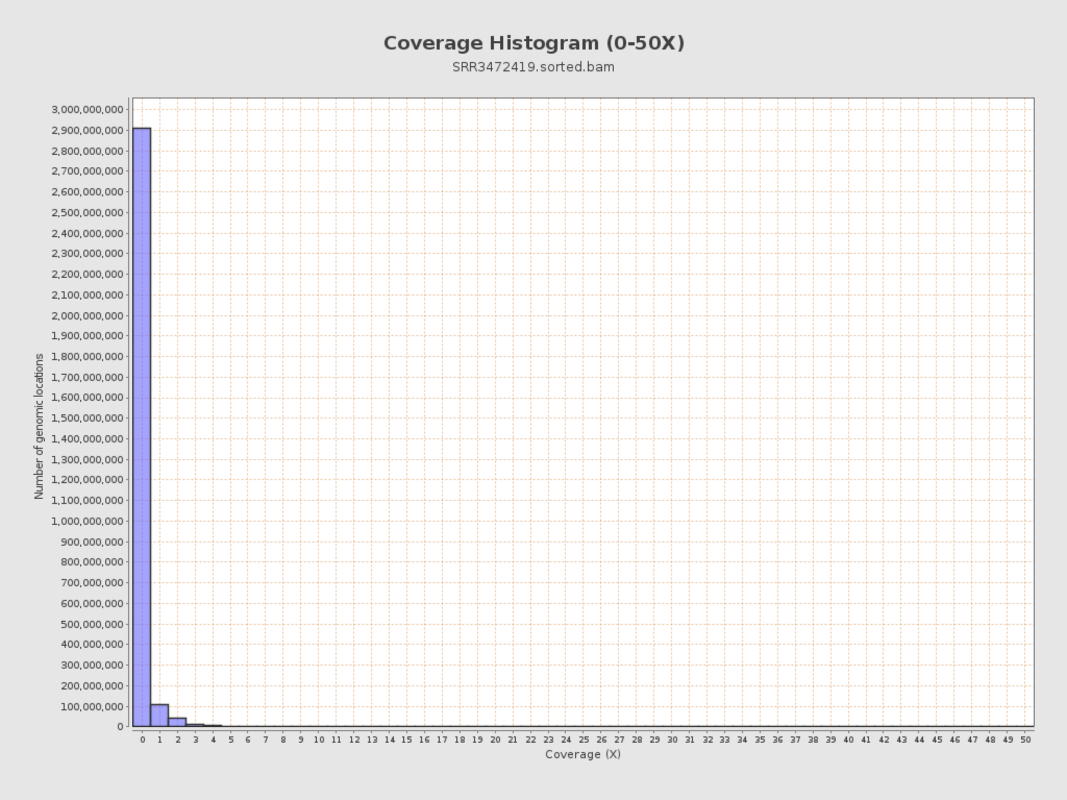
3. Results : Coverage across reference



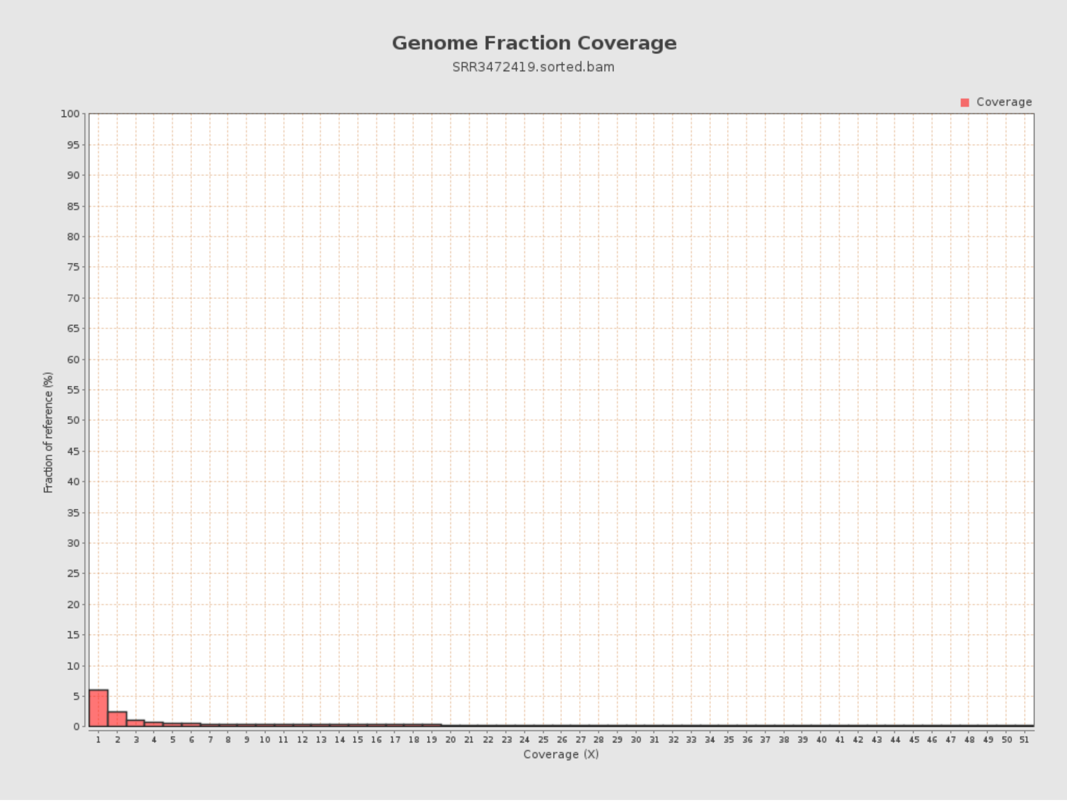
4. Results : Coverage Histogram



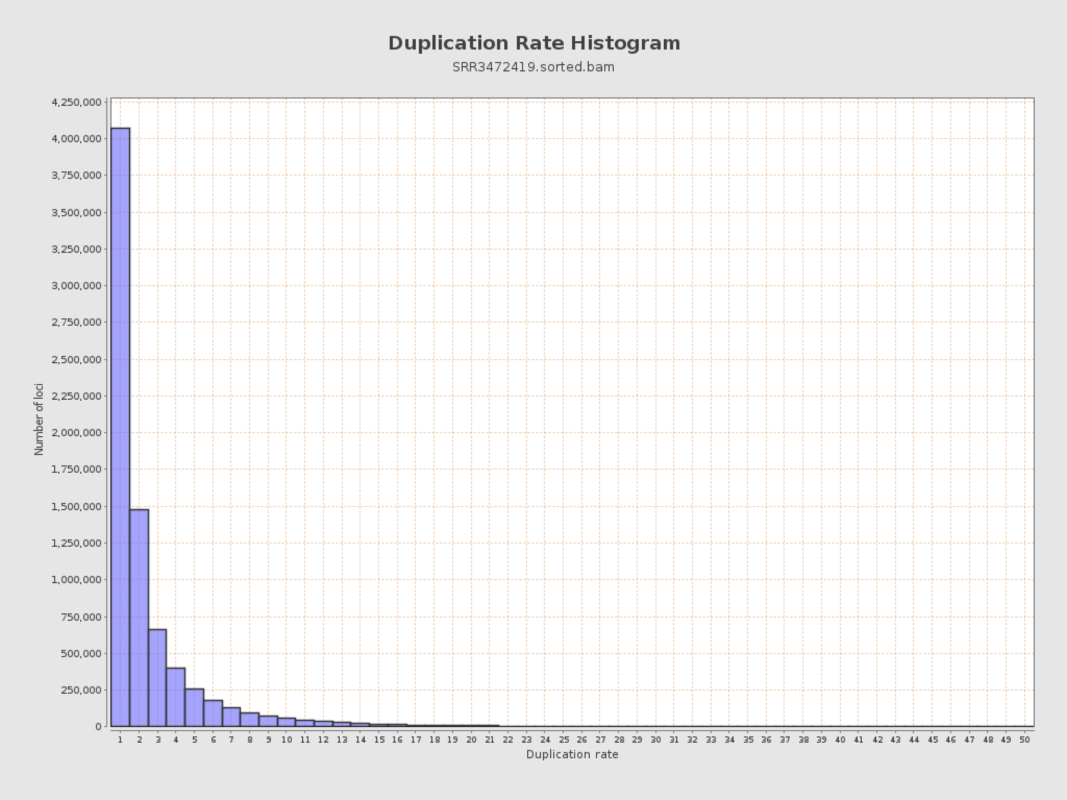
5. Results : Coverage Histogram (0-50X)



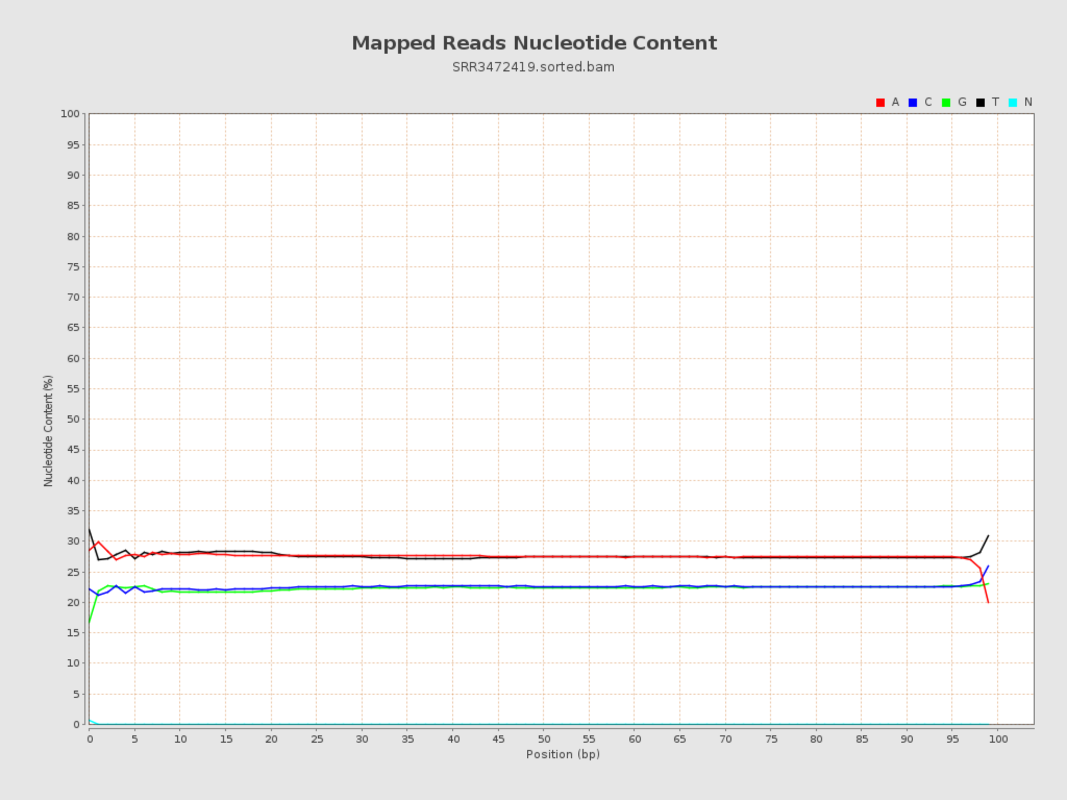
6. Results : Genome Fraction Coverage



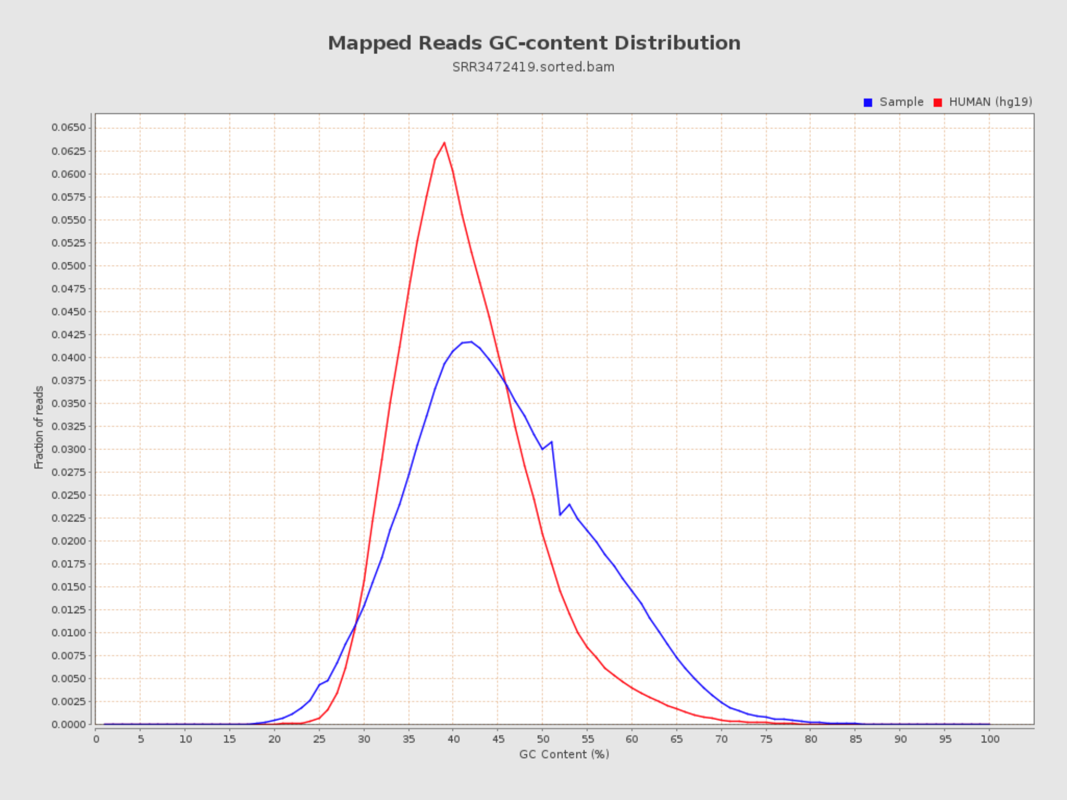
7. Results : Duplication Rate Histogram



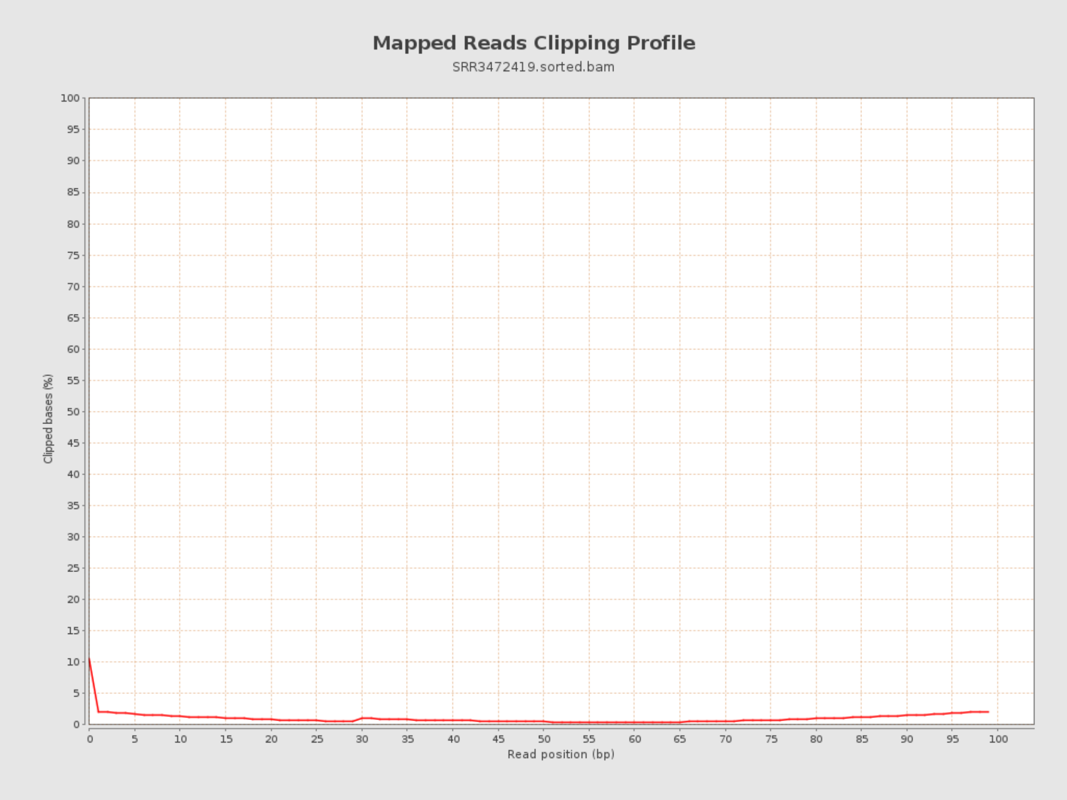
8. Results : Mapped Reads Nucleotide Content



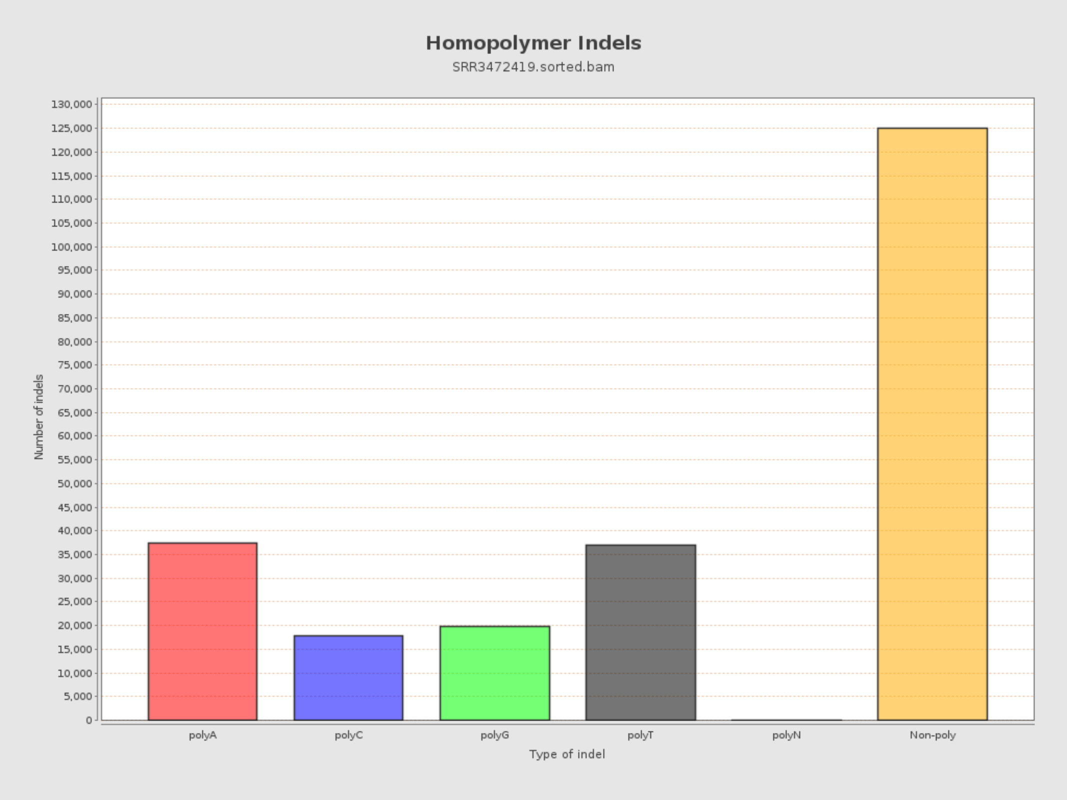
9. Results : Mapped Reads GC-content Distribution



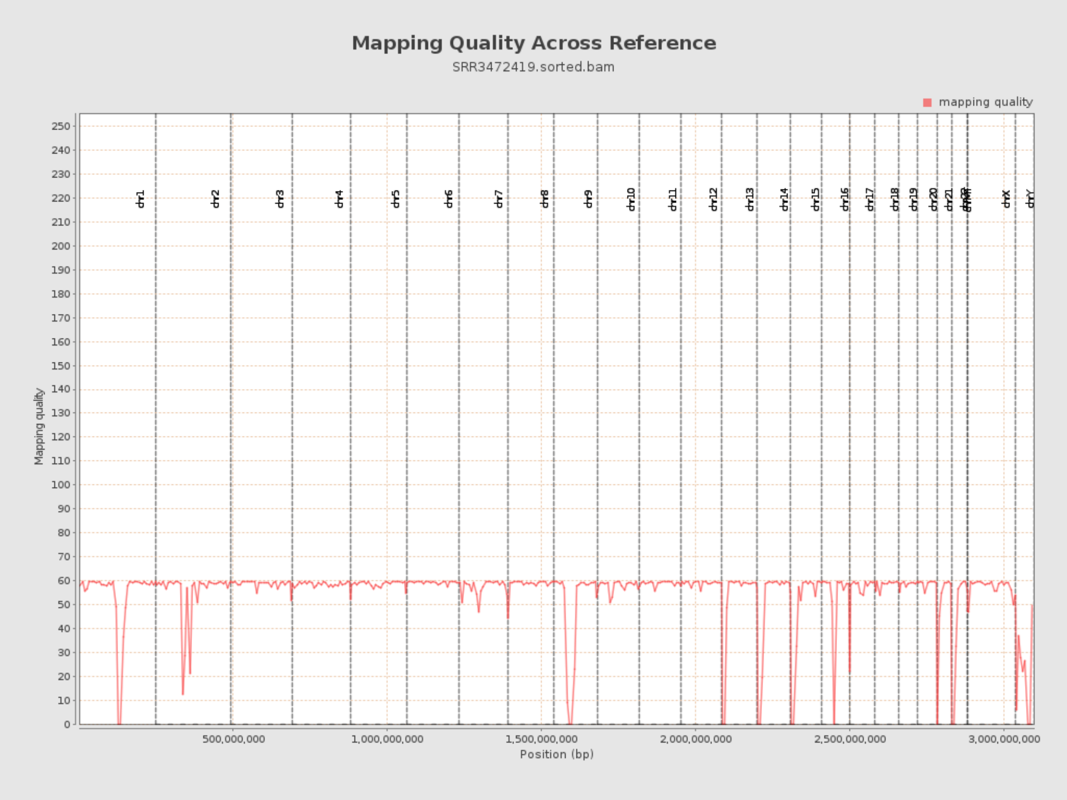
10. Results : Mapped Reads Clipping Profile



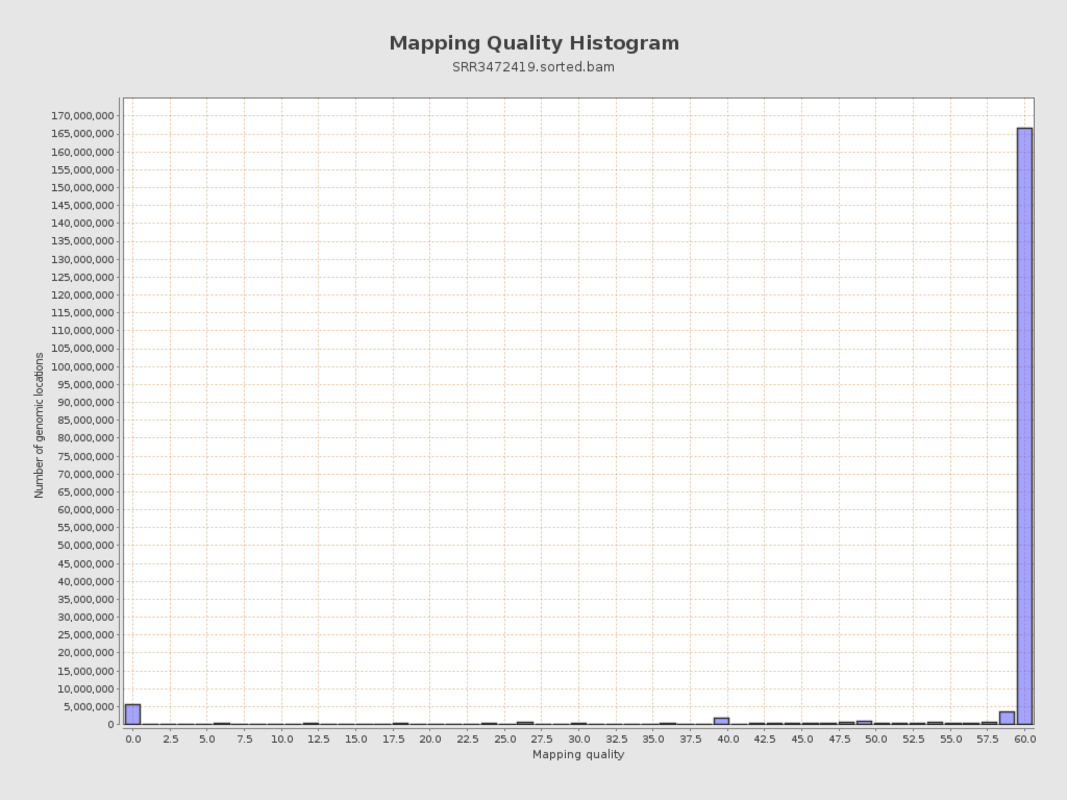
11. Results : Homopolymer Indels



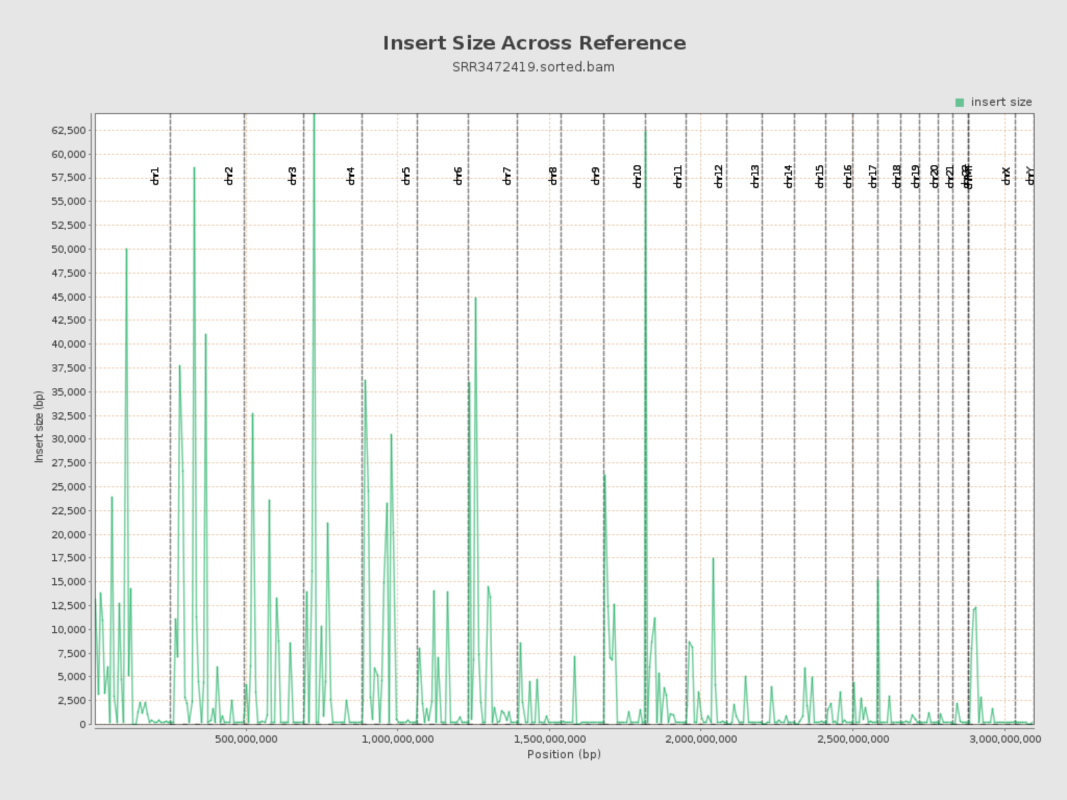
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram