Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 10:29:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472612.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_SRR3472612 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472612_1.fastq.gz SRR3472612_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 10:29:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472612.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,782,442
Mapped reads	14,674,596 / 99.27%
Unmapped reads	107,846 / 0.73%
Mapped paired reads	14,674,596 / 99.27%
Mapped reads, first in pair	7,353,109 / 49.74%
Mapped reads, second in pair	7,321,487 / 49.53%
Mapped reads, both in pair	14,604,262 / 98.79%
Mapped reads, singletons	70,334 / 0.48%
Secondary alignments	0
Supplementary alignments	67,059 / 0.45%
Read min/max/mean length	30 / 101 / 99.58
Duplicated reads (estimated)	9,610,554 / 65.01%
Duplication rate	49.23%
Clipped reads	1,016,245 / 6.87%

2.2. ACGT Content

Number/percentage of A's	381,549,274 / 26.46%
Number/percentage of C's	341,254,872 / 23.67%
Number/percentage of T's	382,698,951 / 26.54%
Number/percentage of G's	336,170,951 / 23.31%
Number/percentage of N's	255,152 / 0.02%

GC Percentage	46.98%

2.3. Coverage

Mean	0.4659
Standard Deviation	17.1192

2.4. Mapping Quality

Mean Mapping Quality	54.8

2.5. Insert size

Mean	19,655.49
Standard Deviation	1,380,048.27
P25/Median/P75	151 / 207 / 279

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	8,827,962
Insertions	85,929
Mapped reads with at least one insertion	0.58%
Deletions	85,877
Mapped reads with at least one deletion	0.57%
Homopolymer indels	43.82%

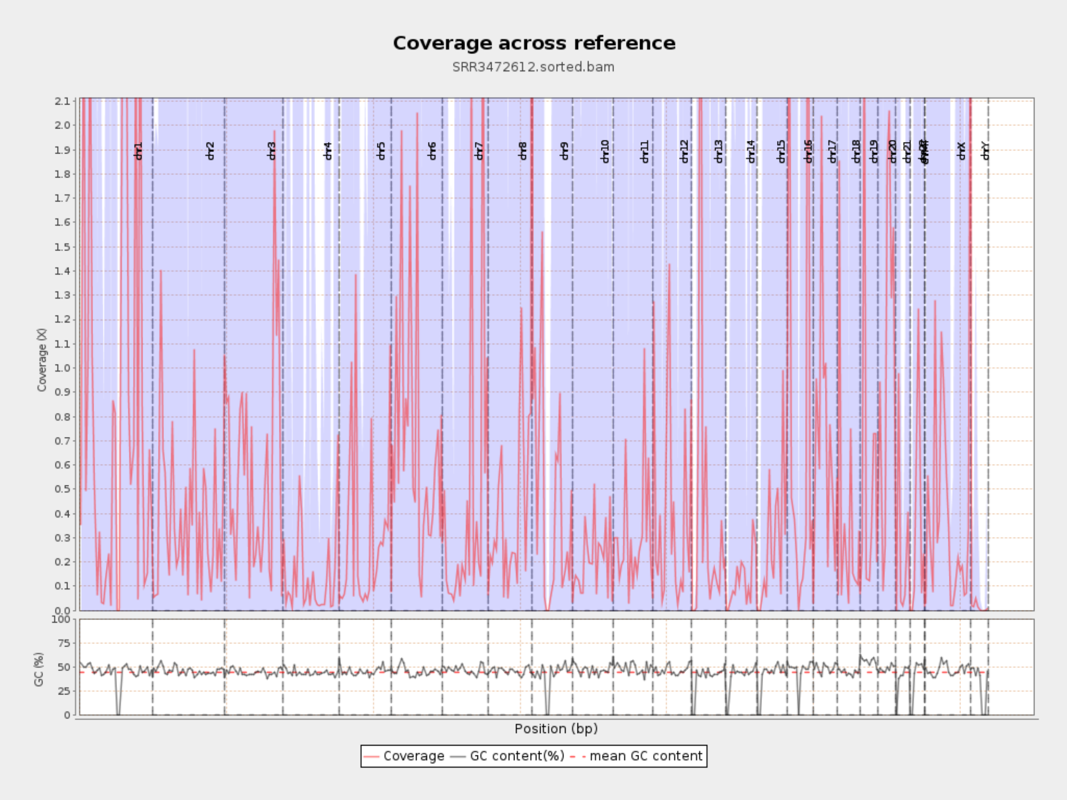
2.7. Chromosome stats

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

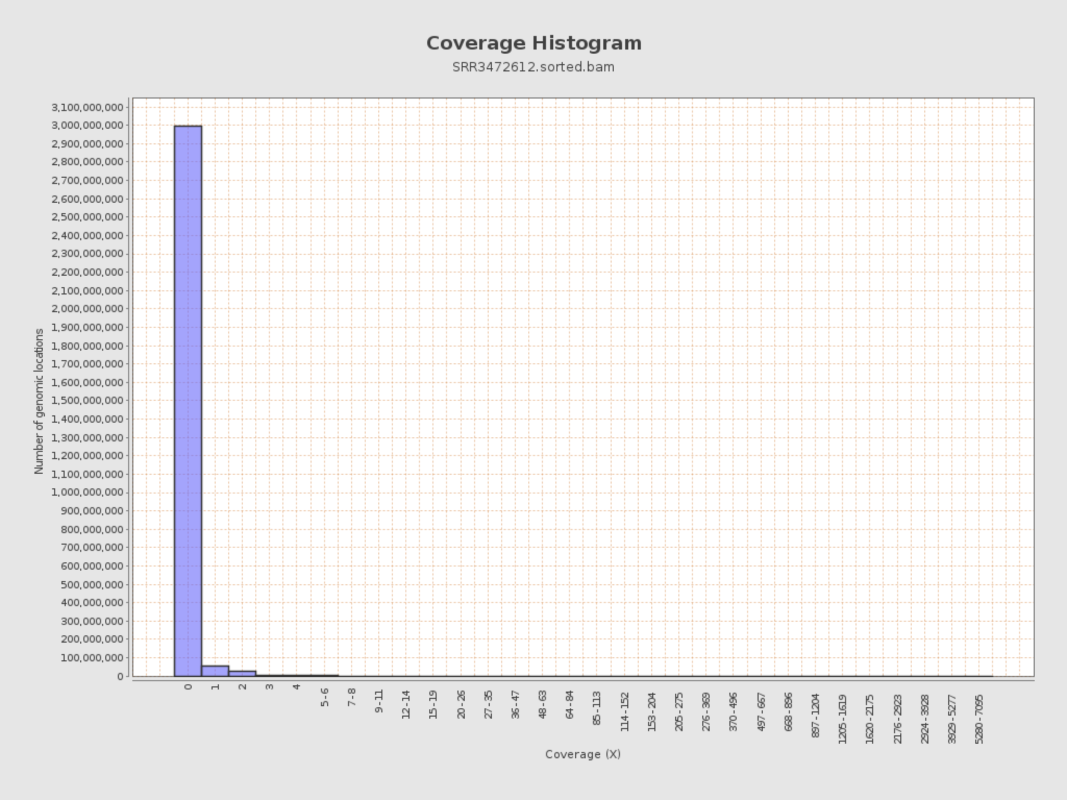
		bases	coverage	deviation
chr1	249250621	241071717	0.9672	29.0274
chr2	243199373	91089073	0.3745	13.9945
chr3	198022430	118054708	0.5962	18.7347
chr4	191154276	26929551	0.1409	8.2139
chr5	180915260	58068414	0.321	11.6661
chr6	171115067	121750316	0.7115	17.9208
chr7	159138663	76108992	0.4783	20.6995
chr8	146364022	60453369	0.413	13.2953
chr9	141213431	70939999	0.5024	16.9744
chr10	135534747	29584789	0.2183	8.7183
chr11	135006516	41959402	0.3108	11.7493
chr12	133851895	55108123	0.4117	11.4281
chr13	115169878	52074482	0.4522	20.7705
chr14	107349540	12835074	0.1196	3.9735
chr15	102531392	28329750	0.2763	11.0464
chr16	90354753	70311278	0.7782	23.5066
chr17	81195210	59193532	0.729	19.3345
chr18	78077248	29861347	0.3825	18.6915
chr19	59128983	37796838	0.6392	17.0987
chr20	63025520	67193467	1.0661	30.5975
chr21	48129895	12501412	0.2597	17.0016
chr22	51304566	17803239	0.347	12.9725
chrMT	16571	885	0.0534	0.3317
chrX	155270560	62283183	0.4011	15.2193

chrY	59373566	829824	0.014	0.596

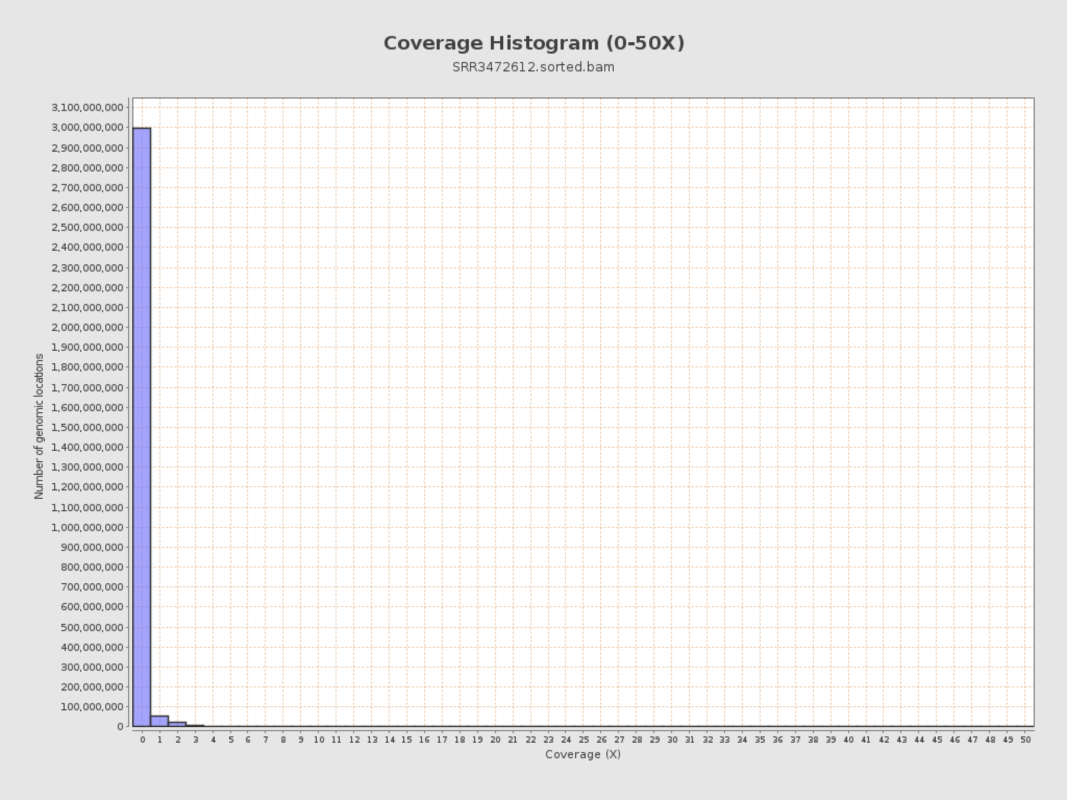
3. Results : Coverage across reference



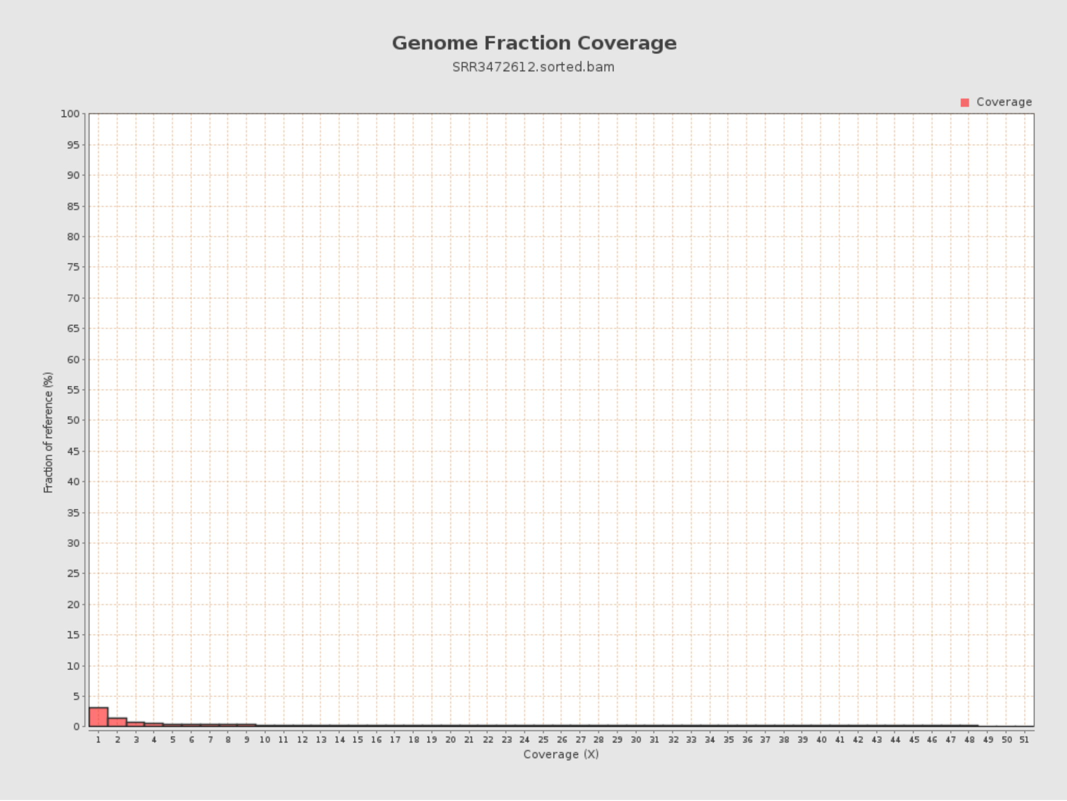
4. Results : Coverage Histogram



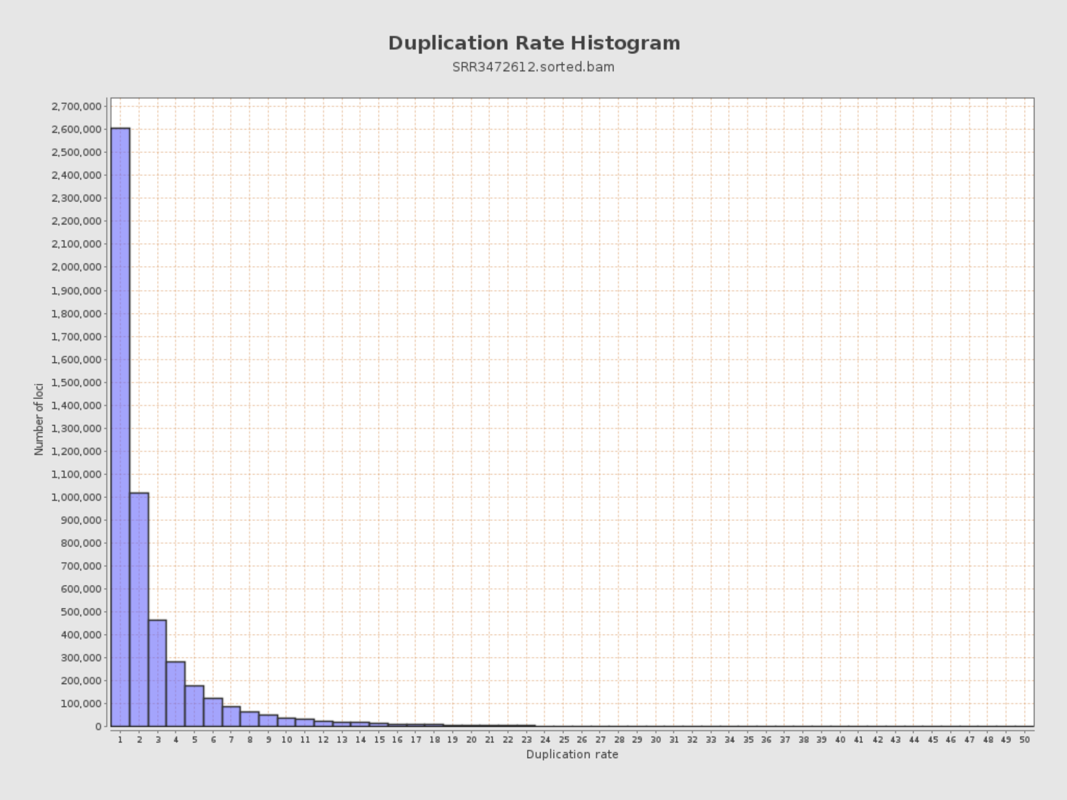
5. Results : Coverage Histogram (0-50X)



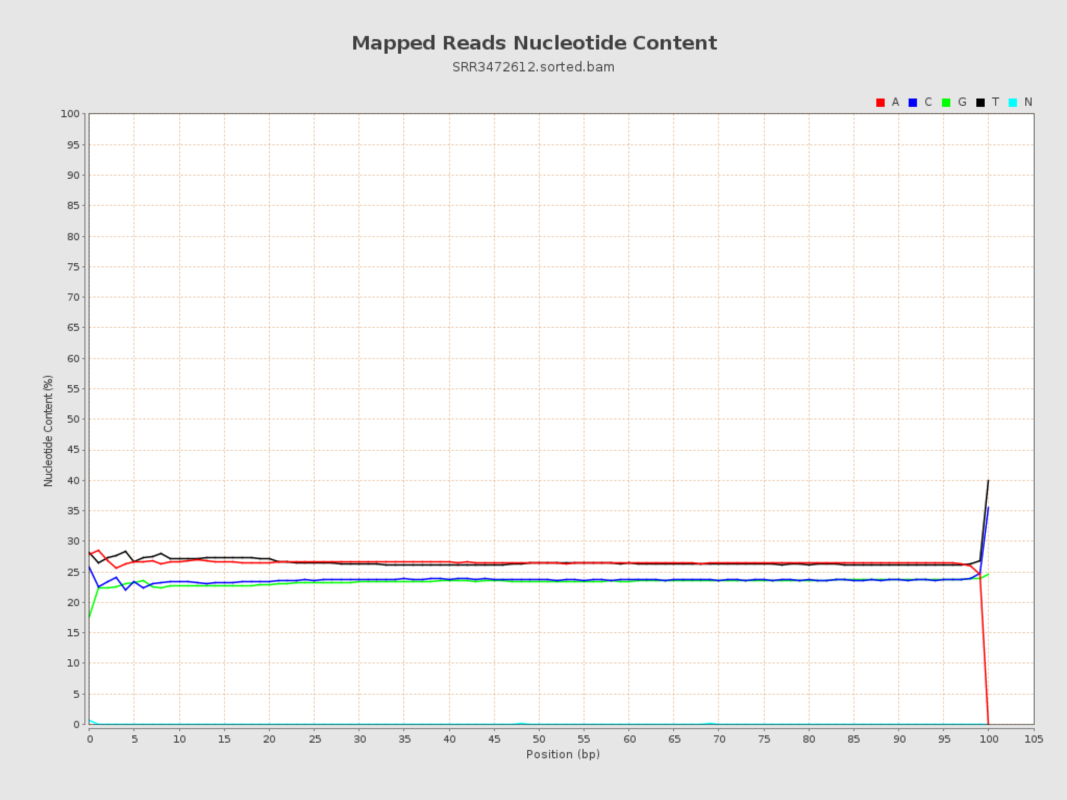
6. Results : Genome Fraction Coverage



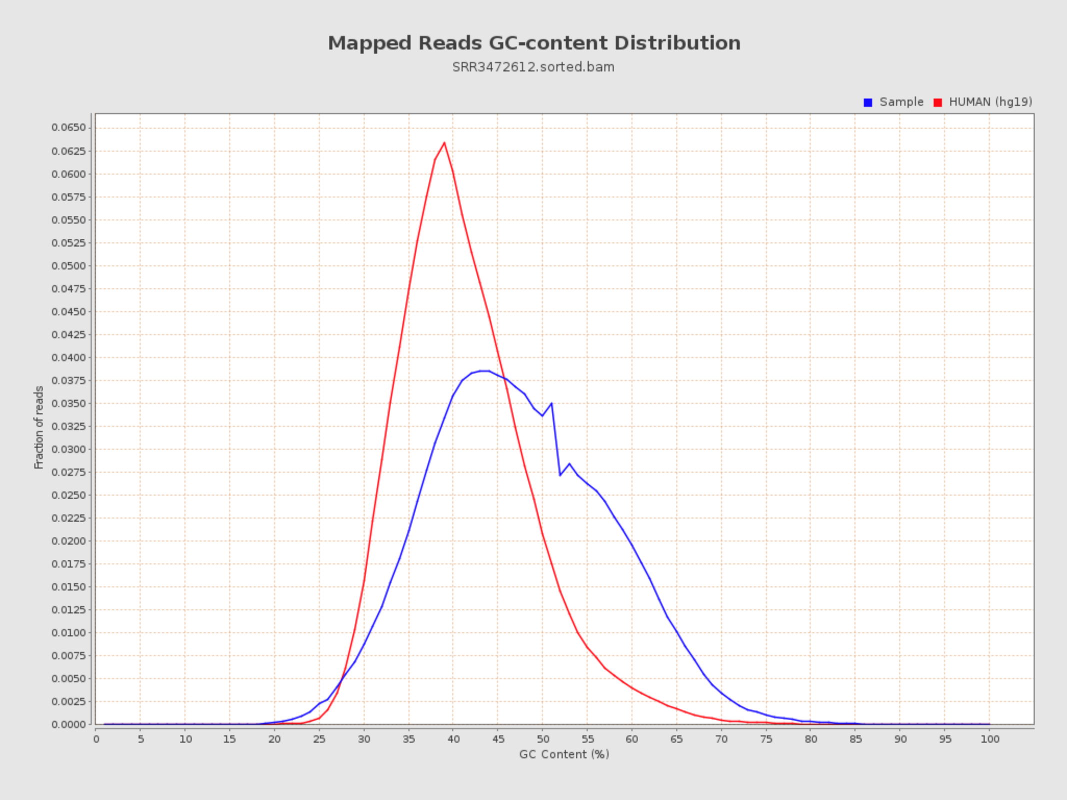
7. Results : Duplication Rate Histogram



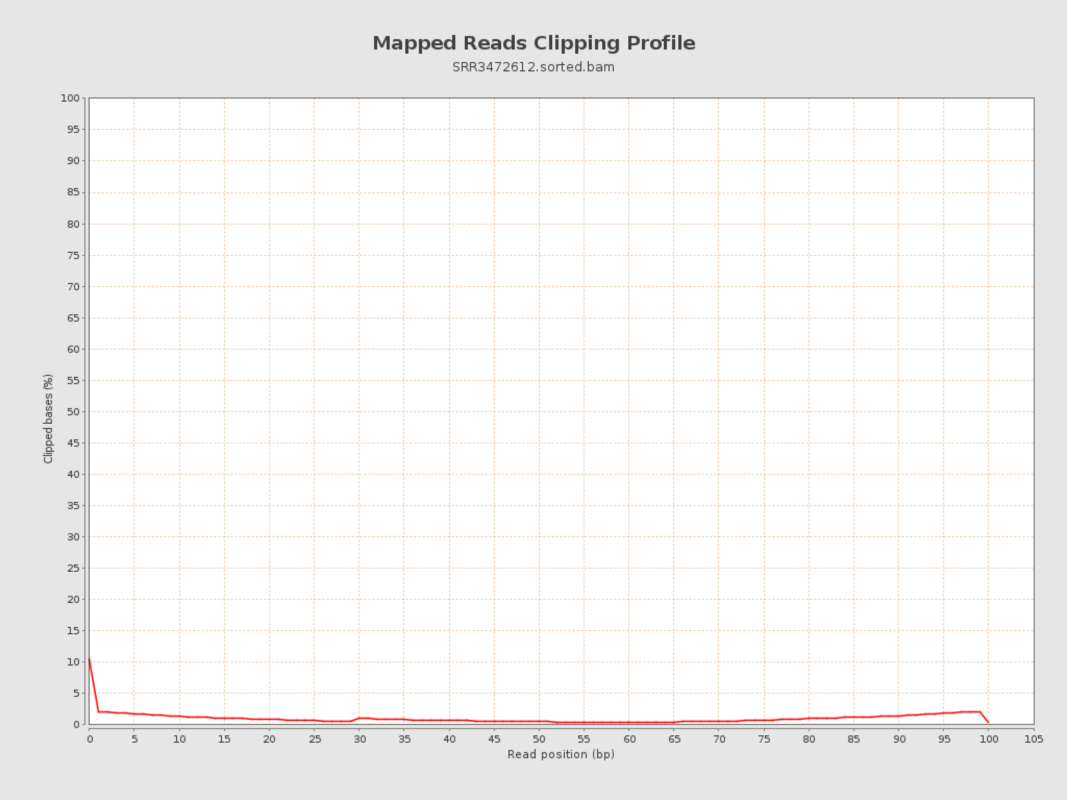
8. Results : Mapped Reads Nucleotide Content



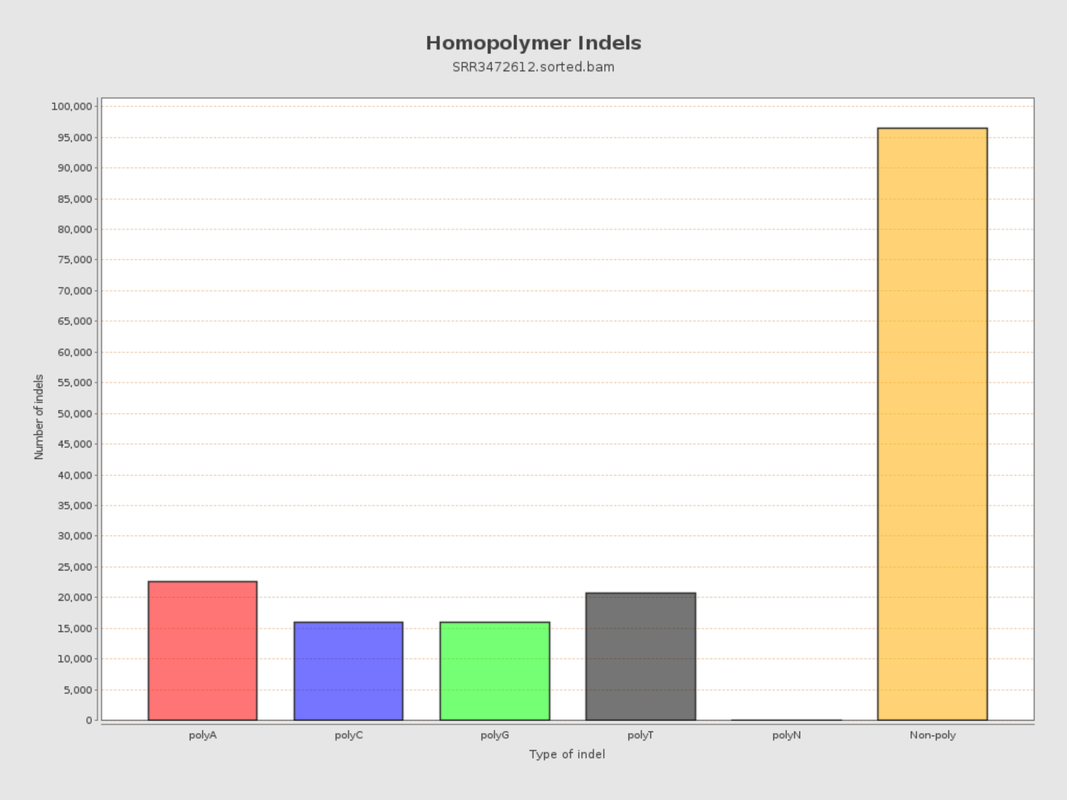
9. Results : Mapped Reads GC-content Distribution



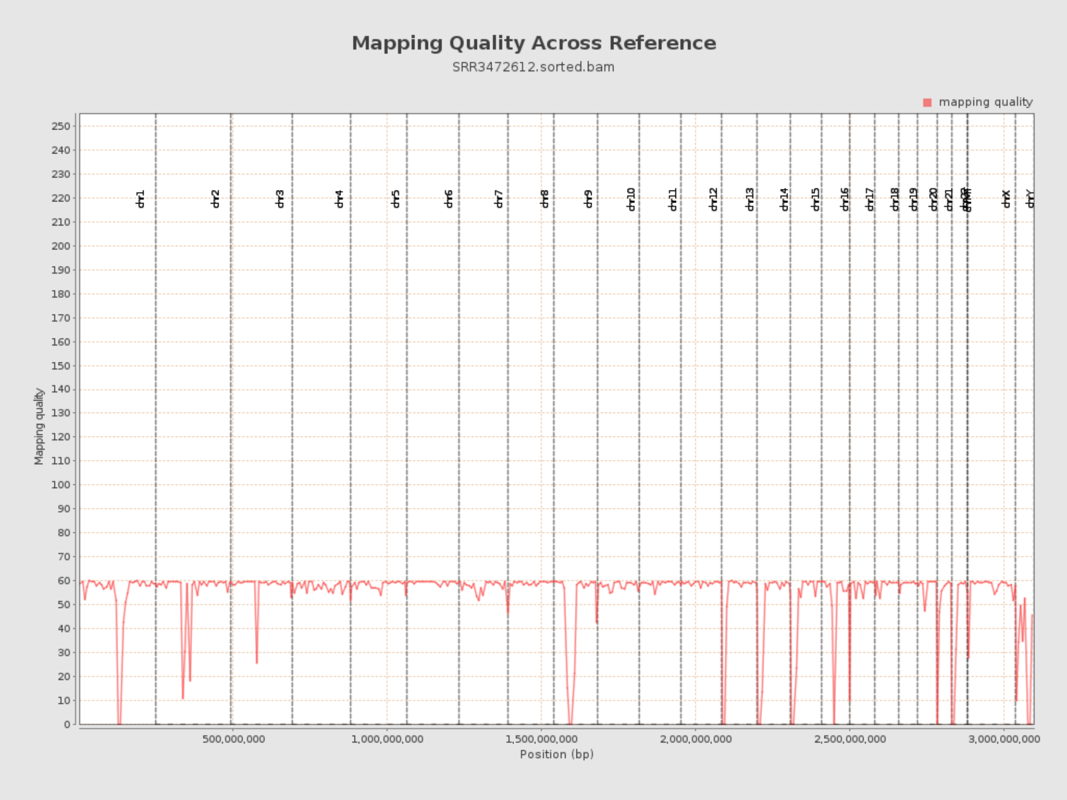
10. Results : Mapped Reads Clipping Profile



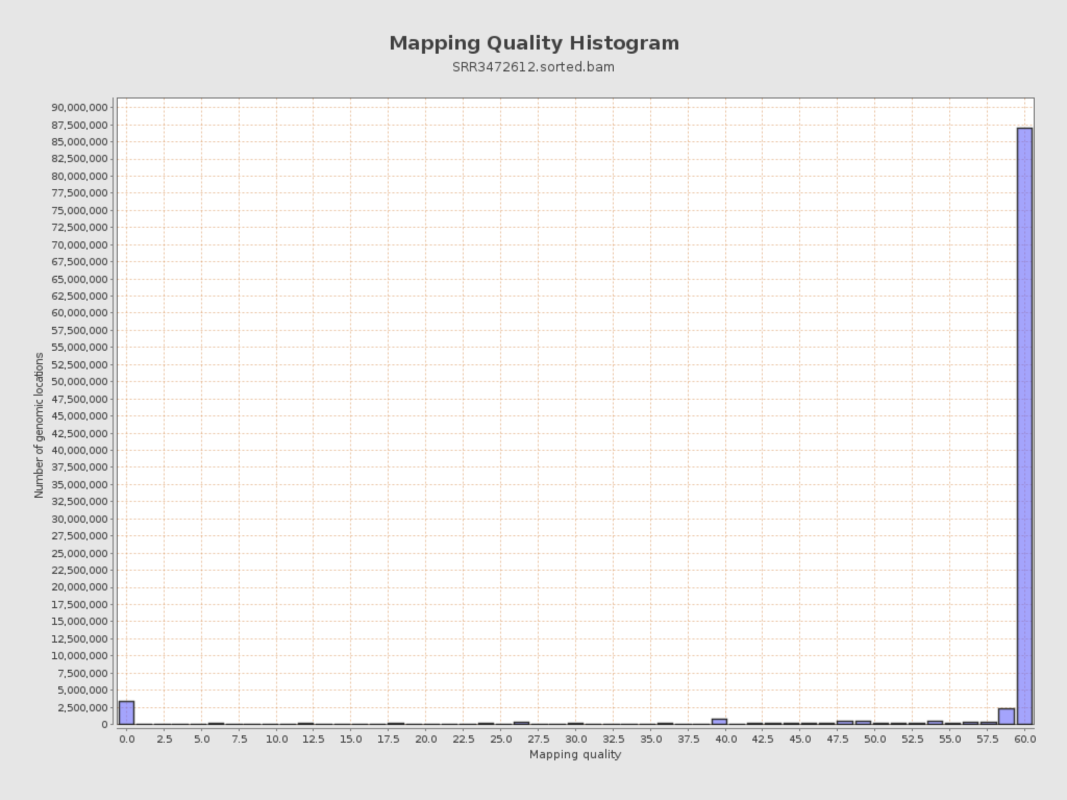
11. Results : Homopolymer Indels



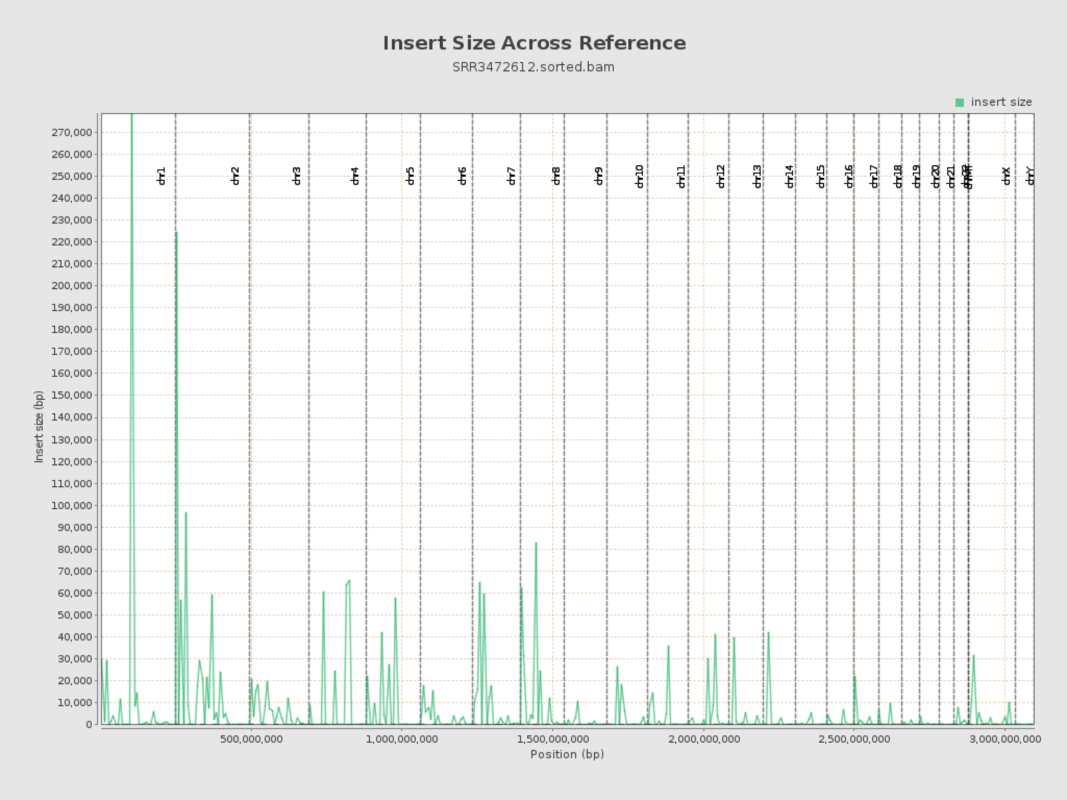
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram