Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:14:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472412.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_SRR3472412 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472412_1.fastq.gz SRR3472412_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:14:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472412.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,608,334
Mapped reads	19,480,875 / 99.35%
Unmapped reads	127,459 / 0.65%
Mapped paired reads	19,480,875 / 99.35%
Mapped reads, first in pair	9,765,859 / 49.8%
Mapped reads, second in pair	9,715,016 / 49.55%
Mapped reads, both in pair	19,401,400 / 98.94%
Mapped reads, singletons	79,475 / 0.41%
Secondary alignments	0
Supplementary alignments	68,504 / 0.35%
Read min/max/mean length	30 / 100 / 99.37
Duplicated reads (estimated)	12,572,921 / 64.12%
Duplication rate	48.13%
Clipped reads	1,366,548 / 6.97%

2.2. ACGT Content

Number/percentage of A's	509,430,835 / 26.67%
Number/percentage of C's	447,056,941 / 23.41%
Number/percentage of T's	510,647,443 / 26.73%
Number/percentage of G's	442,714,125 / 23.18%
Number/percentage of N's	238,605 / 0.01%

GC Percentage	46.58%

2.3. Coverage

Mean	0.6171
Standard Deviation	20.2286

2.4. Mapping Quality

Mean Mapping Quality	55.25

2.5. Insert size

Mean	16,853.97
Standard Deviation	1,314,566.48
P25/Median/P75	149 / 205 / 275

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	9,593,884
Insertions	108,915
Mapped reads with at least one insertion	0.55%
Deletions	88,303
Mapped reads with at least one deletion	0.45%
Homopolymer indels	45.34%

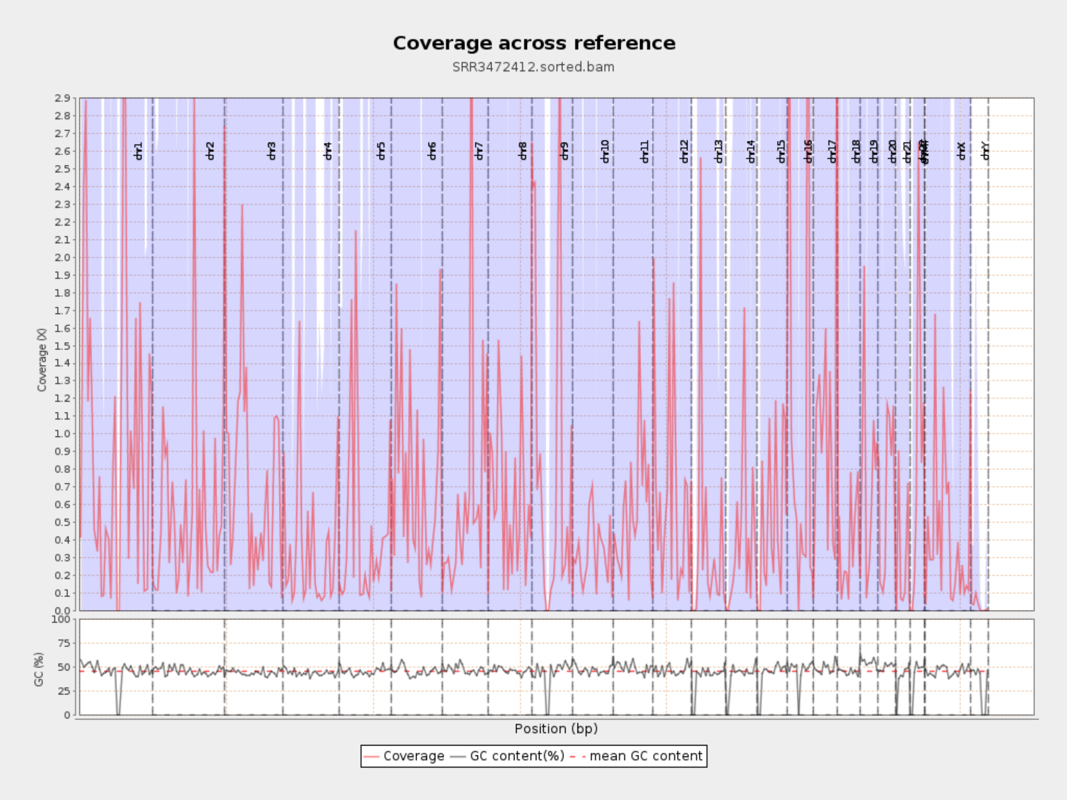
2.7. Chromosome stats

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

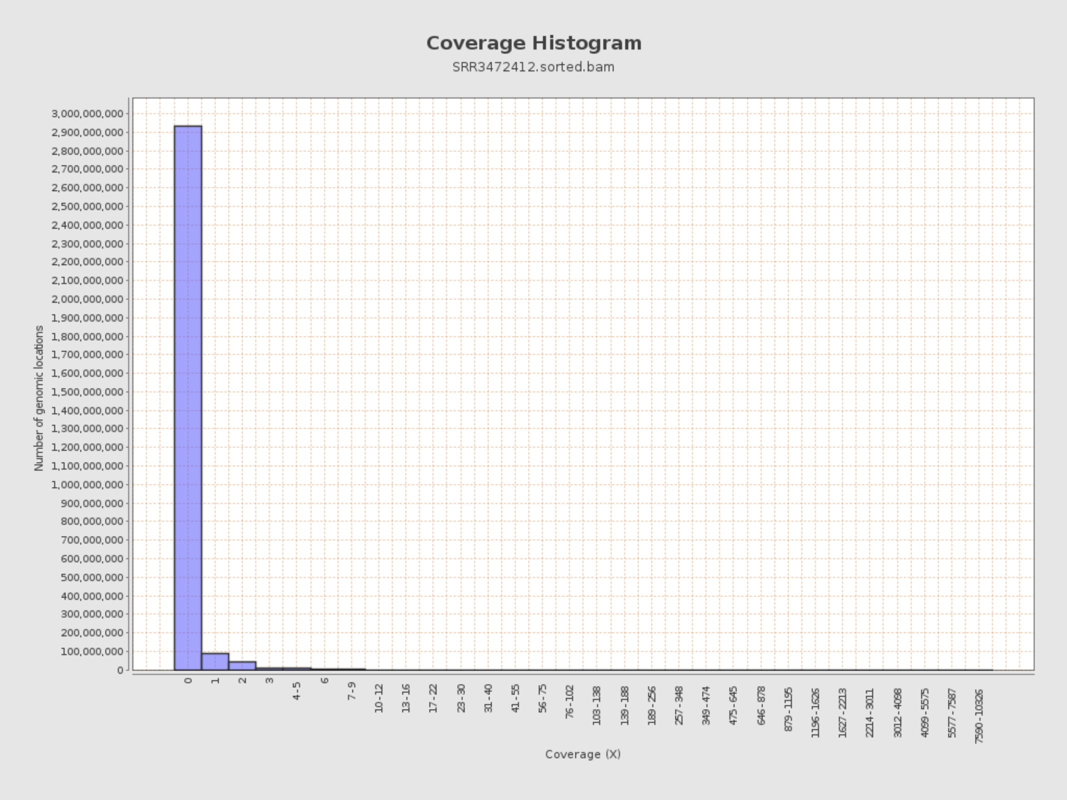
		bases	coverage	deviation
chr1	249250621	244844307	0.9823	29.5771
chr2	243199373	129889289	0.5341	19.474
chr3	198022430	149018859	0.7525	17.6899
chr4	191154276	65918241	0.3448	11.3746
chr5	180915260	87270984	0.4824	15.471
chr6	171115067	124899247	0.7299	20.7196
chr7	159138663	110216494	0.6926	23.1644
chr8	146364022	94741876	0.6473	19.0616
chr9	141213431	121033106	0.8571	28.242
chr10	135534747	44315267	0.327	10.1225
chr11	135006516	77195997	0.5718	14.5536
chr12	133851895	91196552	0.6813	18.9017
chr13	115169878	44031229	0.3823	19.7691
chr14	107349540	40790062	0.38	11.1076
chr15	102531392	54166544	0.5283	23.8164
chr16	90354753	104658120	1.1583	29.8204
chr17	81195210	85761032	1.0562	26.5815
chr18	78077248	28829066	0.3692	11.8965
chr19	59128983	46412400	0.7849	17.4329
chr20	63025520	42307035	0.6713	17.8088
chr21	48129895	14791672	0.3073	16.5346
chr22	51304566	42219372	0.8229	30.3977
chrMT	16571	2556	0.1542	0.4187
chrX	155270560	64121930	0.413	17.5039

chrY	59373566	1678050	0.0283	0.8176

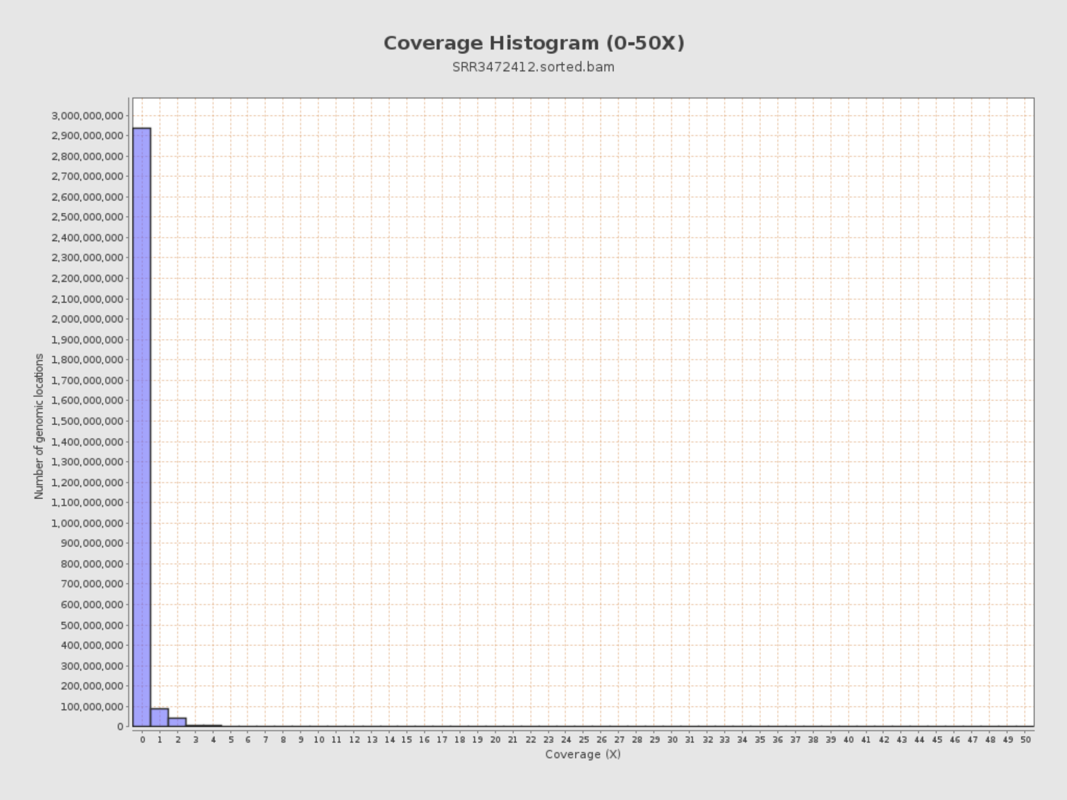
3. Results : Coverage across reference



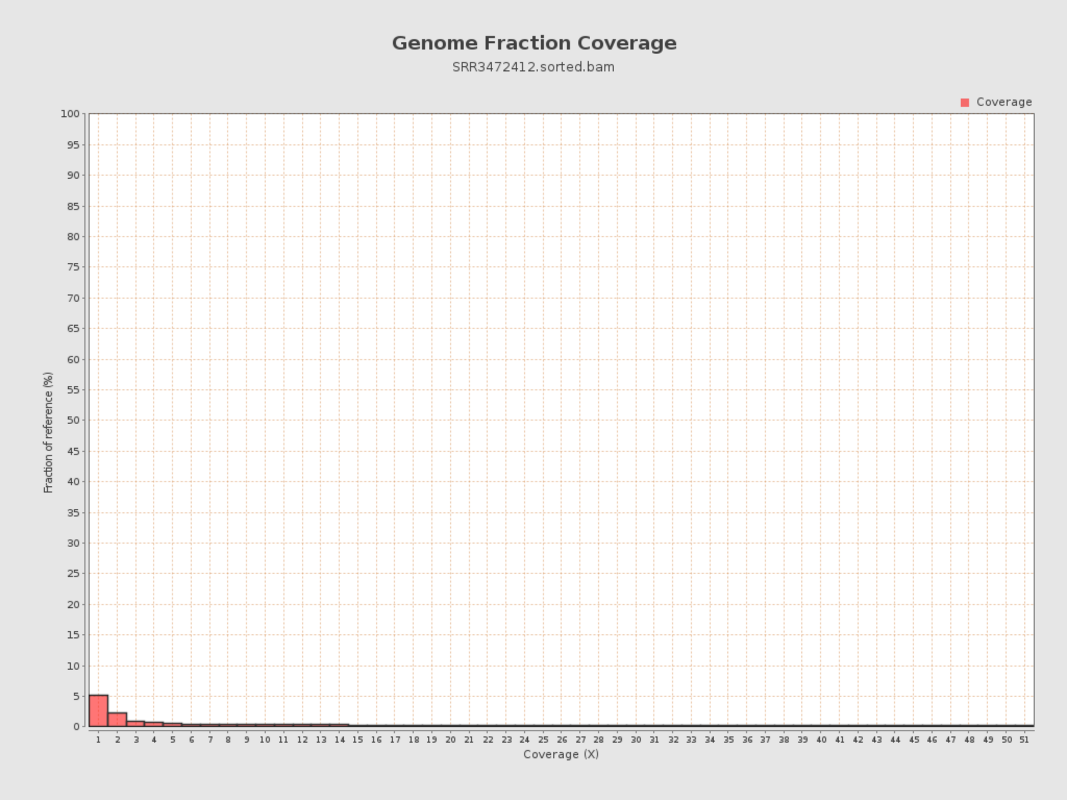
4. Results : Coverage Histogram



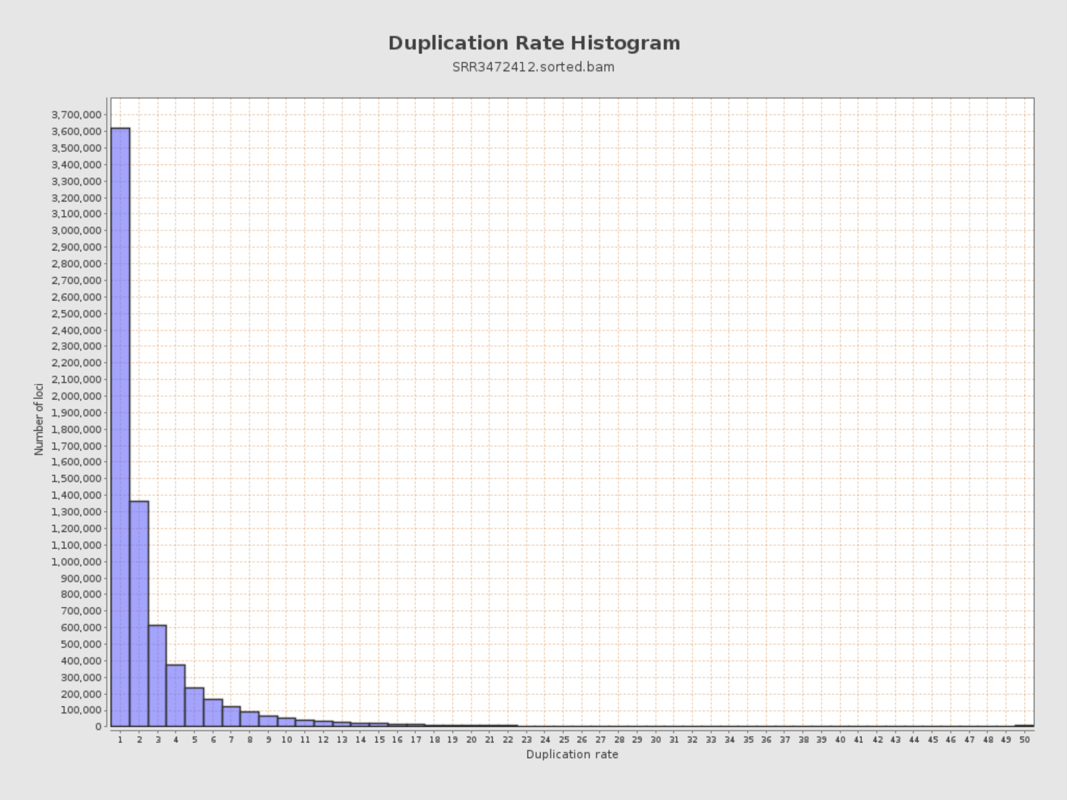
5. Results : Coverage Histogram (0-50X)



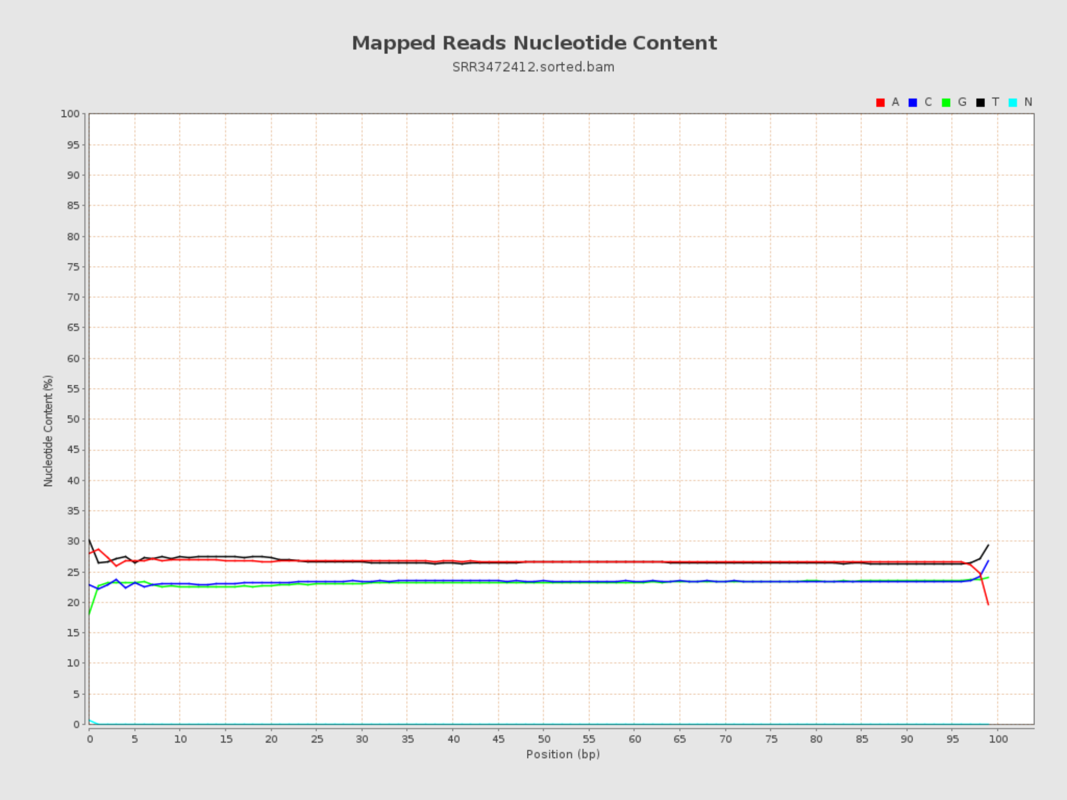
6. Results : Genome Fraction Coverage



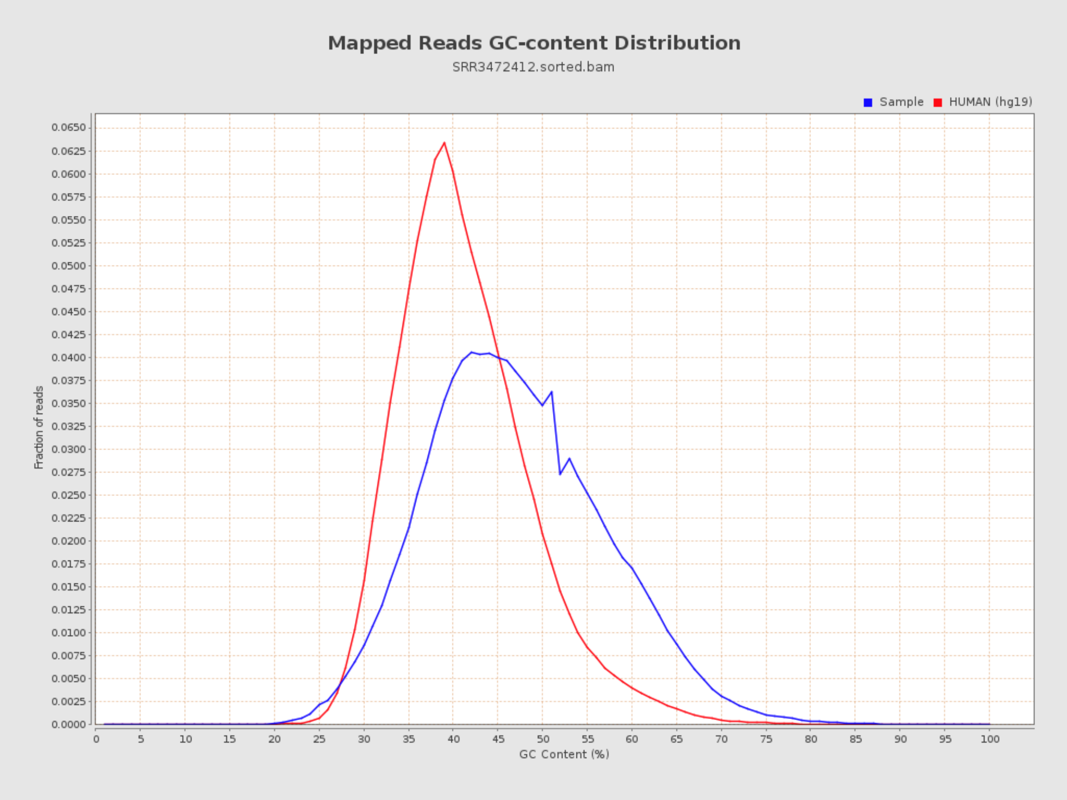
7. Results : Duplication Rate Histogram



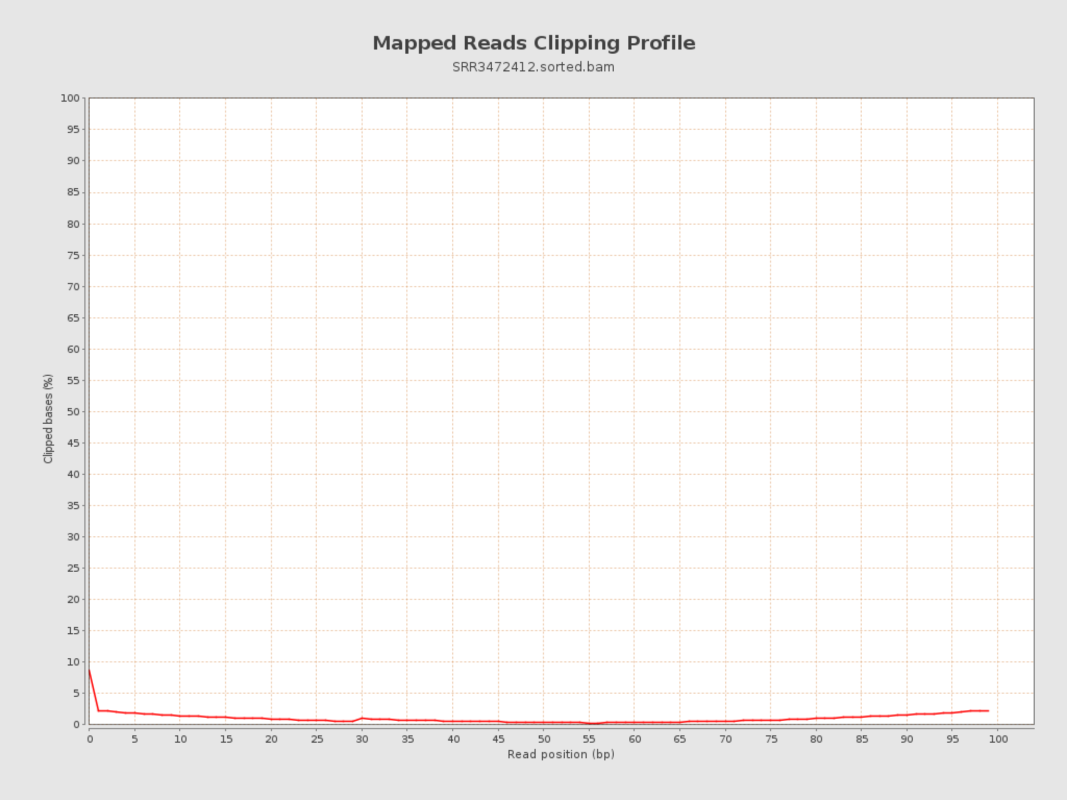
8. Results : Mapped Reads Nucleotide Content



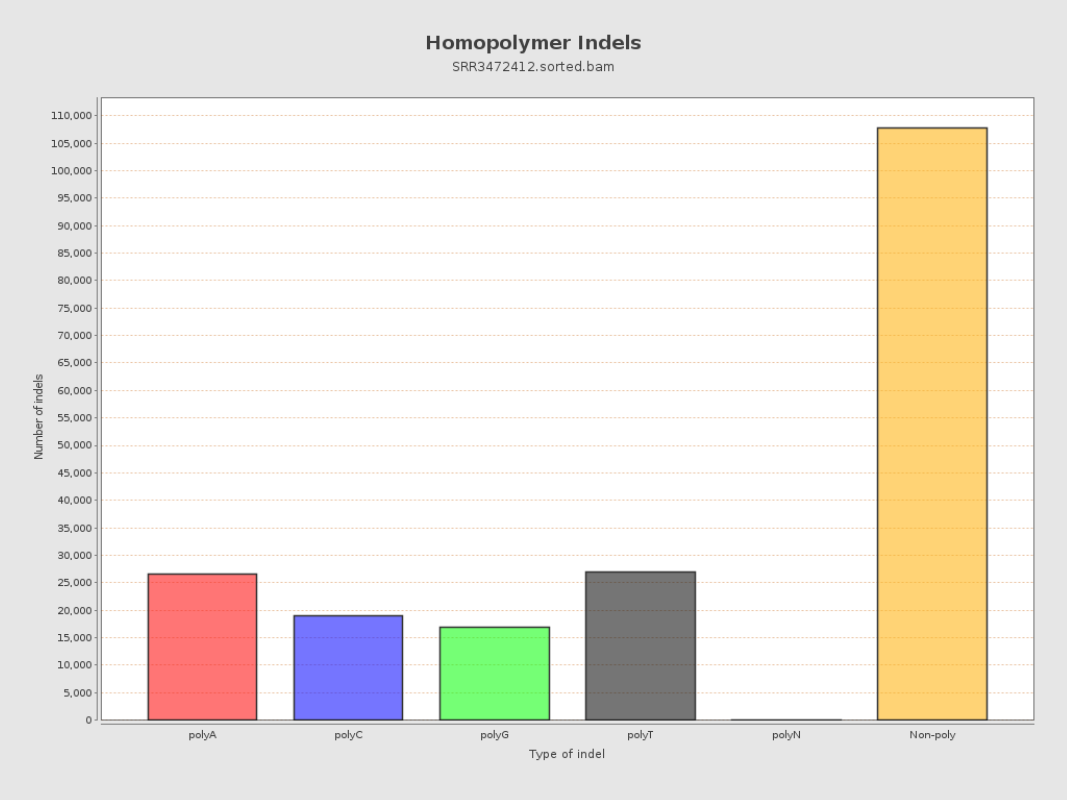
9. Results : Mapped Reads GC-content Distribution



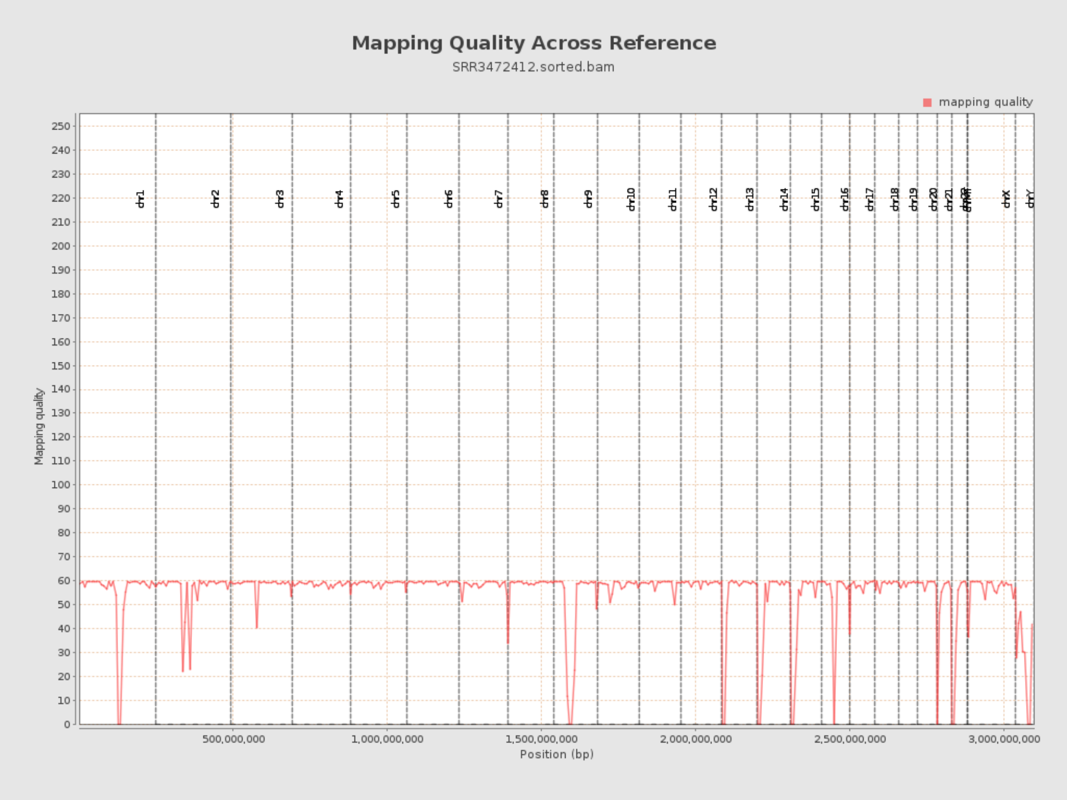
10. Results : Mapped Reads Clipping Profile



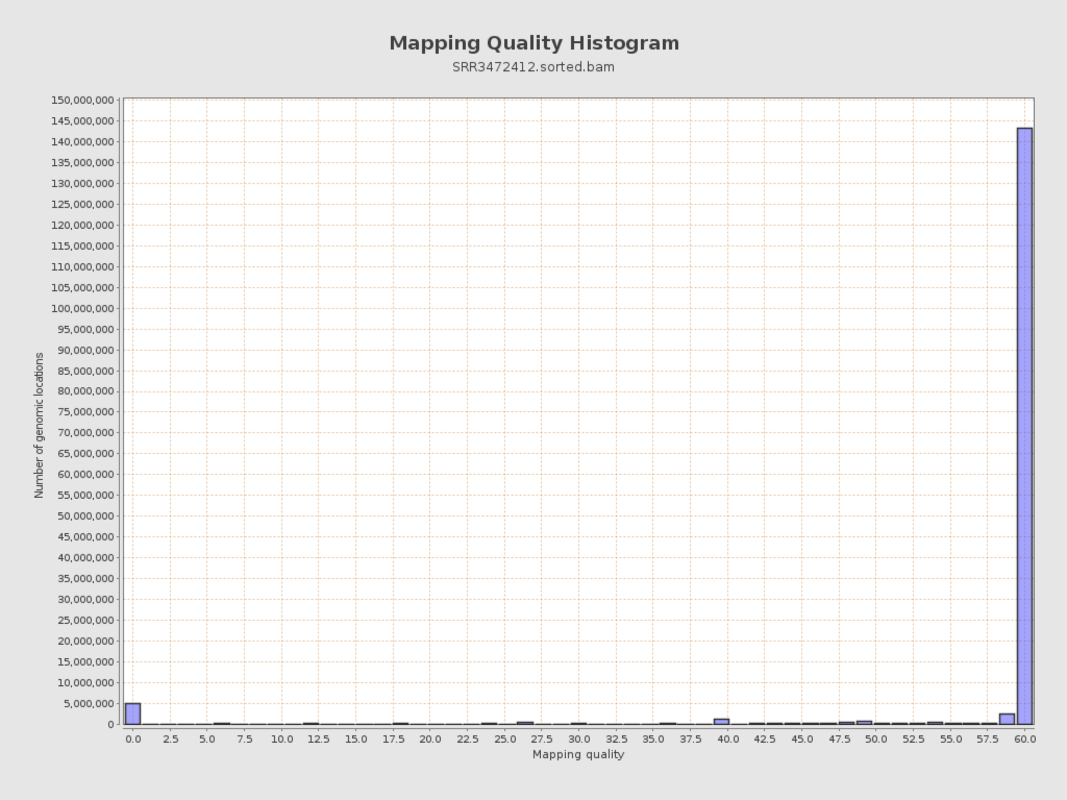
11. Results : Homopolymer Indels



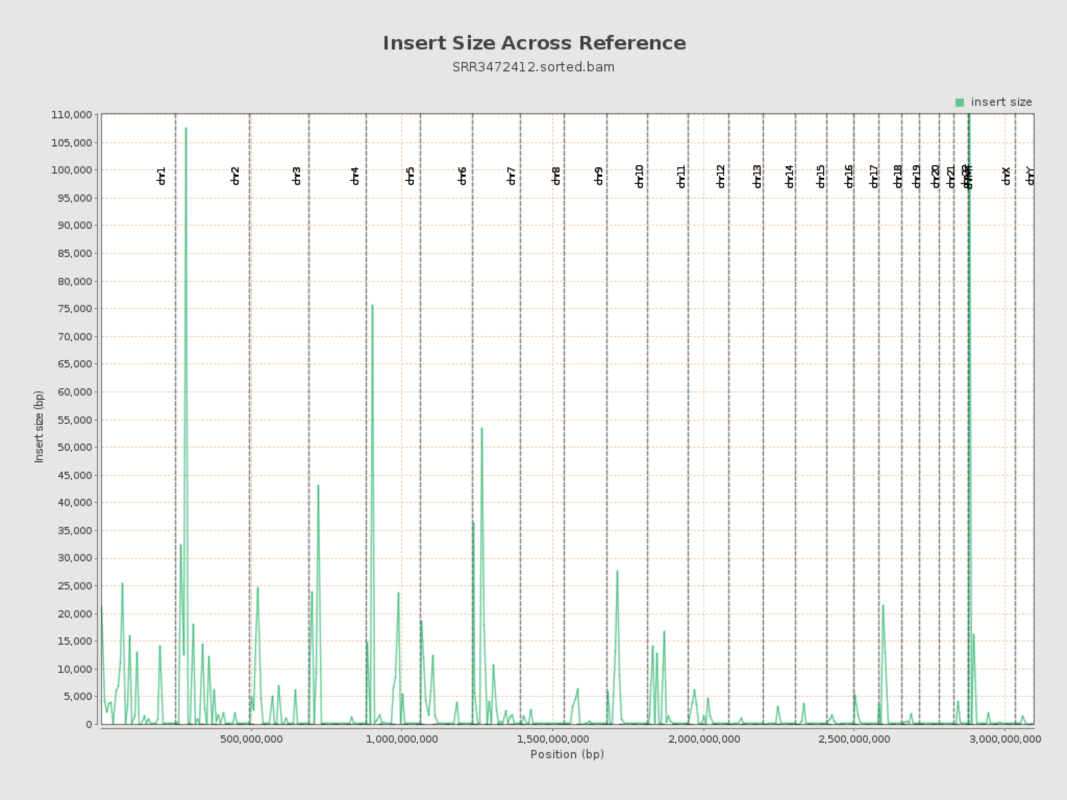
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram