Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 01:18:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617412.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_SRR617412 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617412_1.fastq.gz SRR617412_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 01:18:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617412.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,712,316 / 92.85%
Unmapped reads	2,287,684 / 7.15%
Mapped paired reads	29,712,316 / 92.85%
Mapped reads, first in pair	14,956,286 / 46.74%
Mapped reads, second in pair	14,756,030 / 46.11%
Mapped reads, both in pair	29,190,000 / 91.22%
Mapped reads, singletons	522,316 / 1.63%
Secondary alignments	0
Supplementary alignments	444,475 / 1.39%
Read min/max/mean length	30 / 100 / 100.58
Duplicated reads (estimated)	1,342,515 / 4.2%
Duplication rate	4.13%
Clipped reads	3,301,987 / 10.32%

2.2. ACGT Content

Number/percentage of A's	874,290,355 / 29.91%
Number/percentage of C's	586,218,344 / 20.05%
Number/percentage of T's	864,027,084 / 29.56%
Number/percentage of G's	597,858,973 / 20.45%
Number/percentage of N's	1,053,874 / 0.04%

GC Percentage	40.5%

2.3. Coverage

Mean	0.9446
Standard Deviation	2.8823

2.4. Mapping Quality

Mean Mapping Quality	53.89

2.5. Insert size

Mean	47,081.6
Standard Deviation	2,062,501.69
P25/Median/P75	169 / 207 / 266

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	33,992,181
Insertions	235,534
Mapped reads with at least one insertion	0.78%
Deletions	281,047
Mapped reads with at least one deletion	0.93%
Homopolymer indels	44.64%

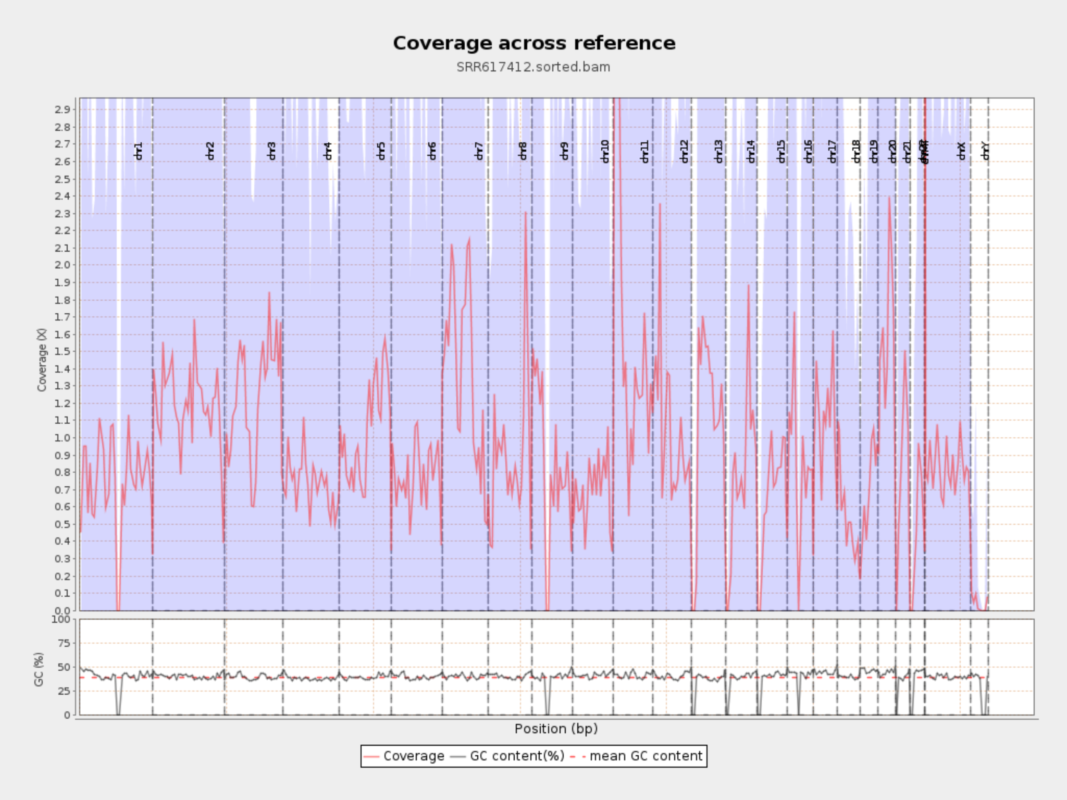
2.7. Chromosome stats

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

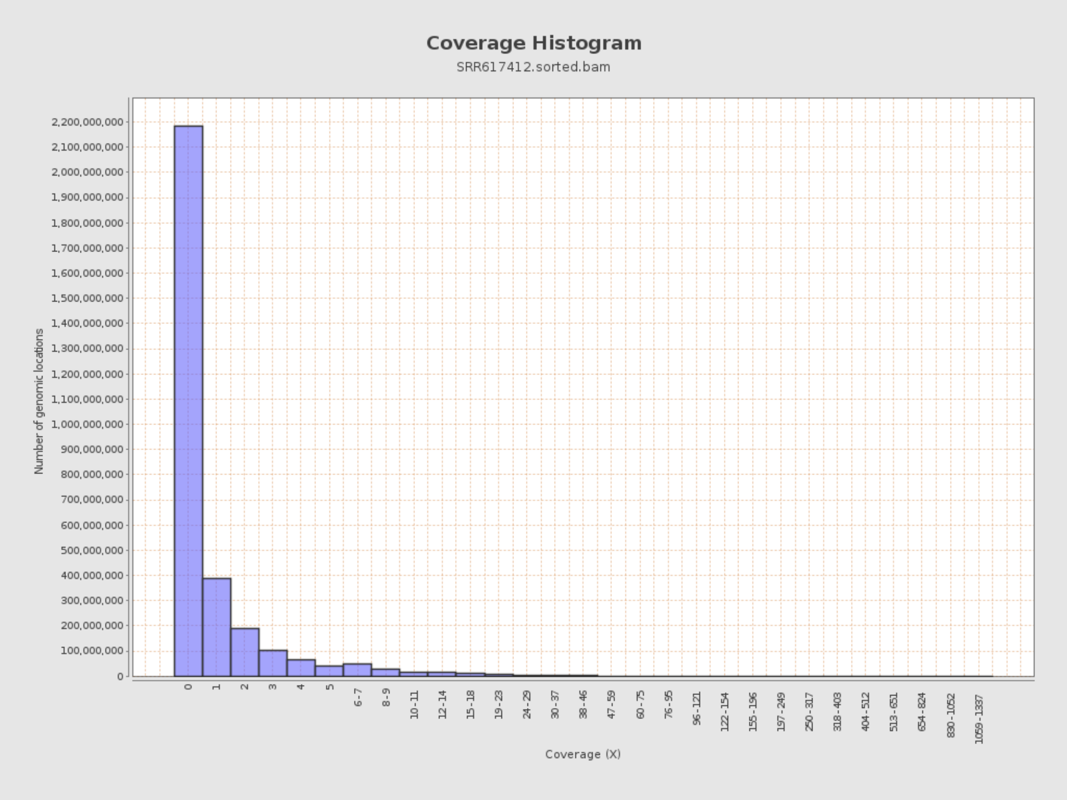
		bases	coverage	deviation
chr1	249250621	188020581	0.7543	2.7049
chr2	243199373	291929736	1.2004	3.0299
chr3	198022430	247212455	1.2484	3.3671
chr4	191154276	141108283	0.7382	2.2602
chr5	180915260	187780214	1.0379	2.8454
chr6	171115067	134495642	0.786	2.5663
chr7	159138663	218743309	1.3745	3.1939
chr8	146364022	129575052	0.8853	3.1961
chr9	141213431	117024900	0.8287	2.5823
chr10	135534747	93707683	0.6914	2.3713
chr11	135006516	217226220	1.609	3.7804
chr12	133851895	138898519	1.0377	2.7283
chr13	115169878	127360319	1.1058	2.7384
chr14	107349540	84854506	0.7905	2.8443
chr15	102531392	66926353	0.6527	2.3163
chr16	90354753	73167442	0.8098	3.273
chr17	81195210	89399291	1.101	3.6214
chr18	78077248	41942844	0.5372	1.9791
chr19	59128983	41218867	0.6971	2.2991
chr20	63025520	99100100	1.5724	4.6392
chr21	48129895	40126654	0.8337	2.5048
chr22	51304566	23305328	0.4543	2.0336
chrMT	16571	180371	10.8847	5.0173
chrX	155270560	128448561	0.8273	2.5296

chrY	59373566	2328546	0.0392	0.5609

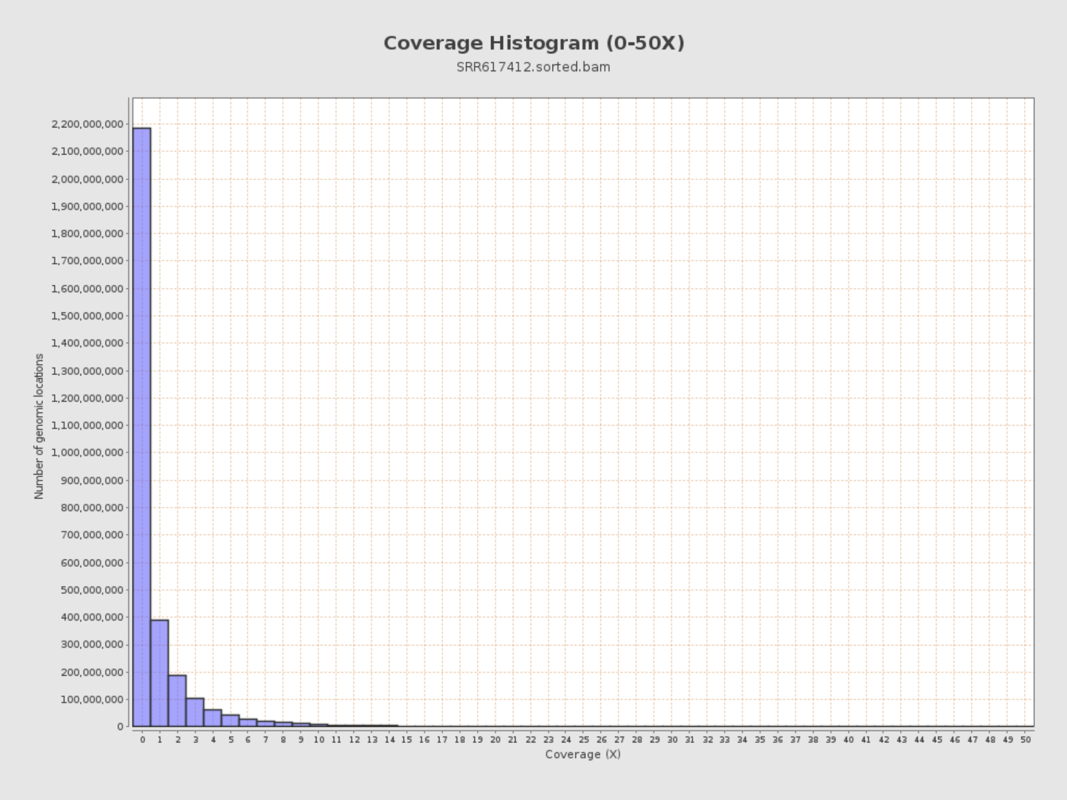
3. Results : Coverage across reference



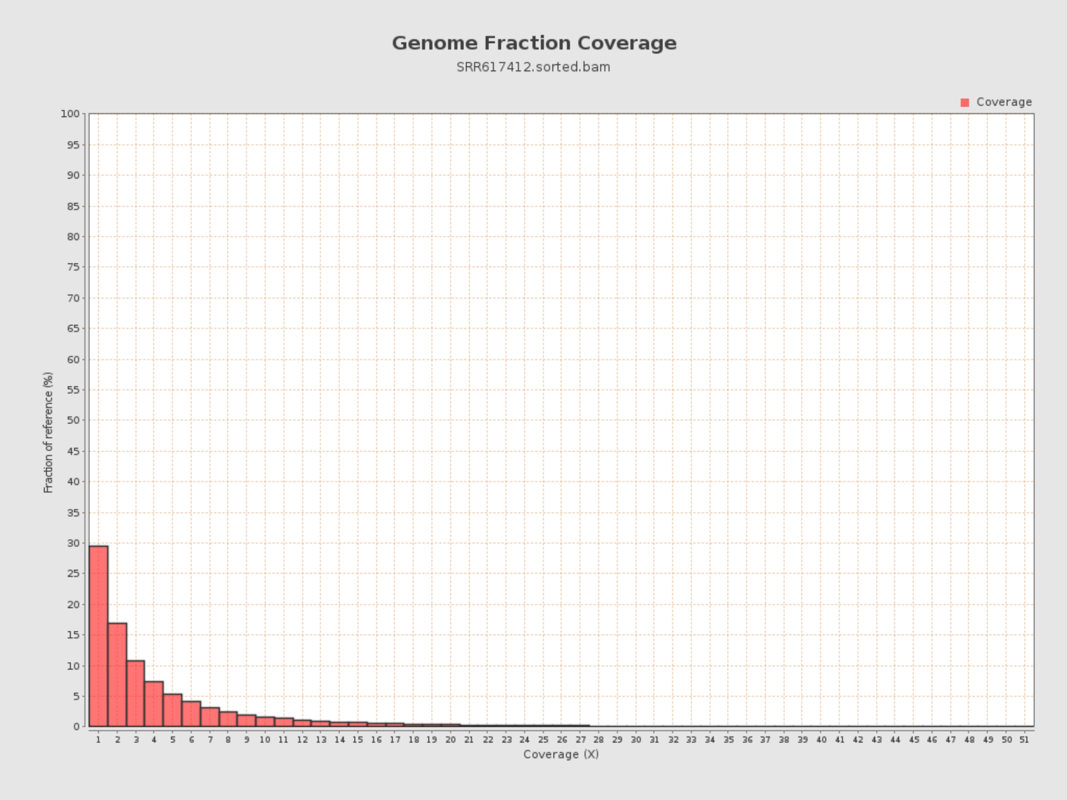
4. Results : Coverage Histogram



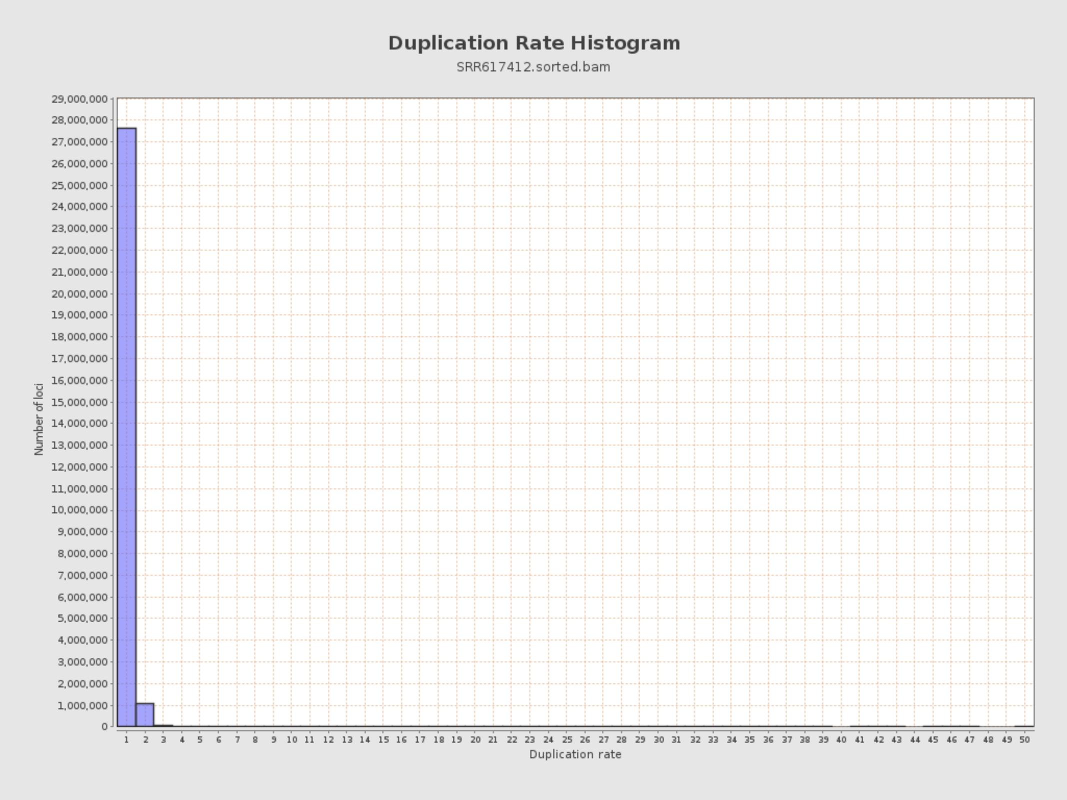
5. Results : Coverage Histogram (0-50X)



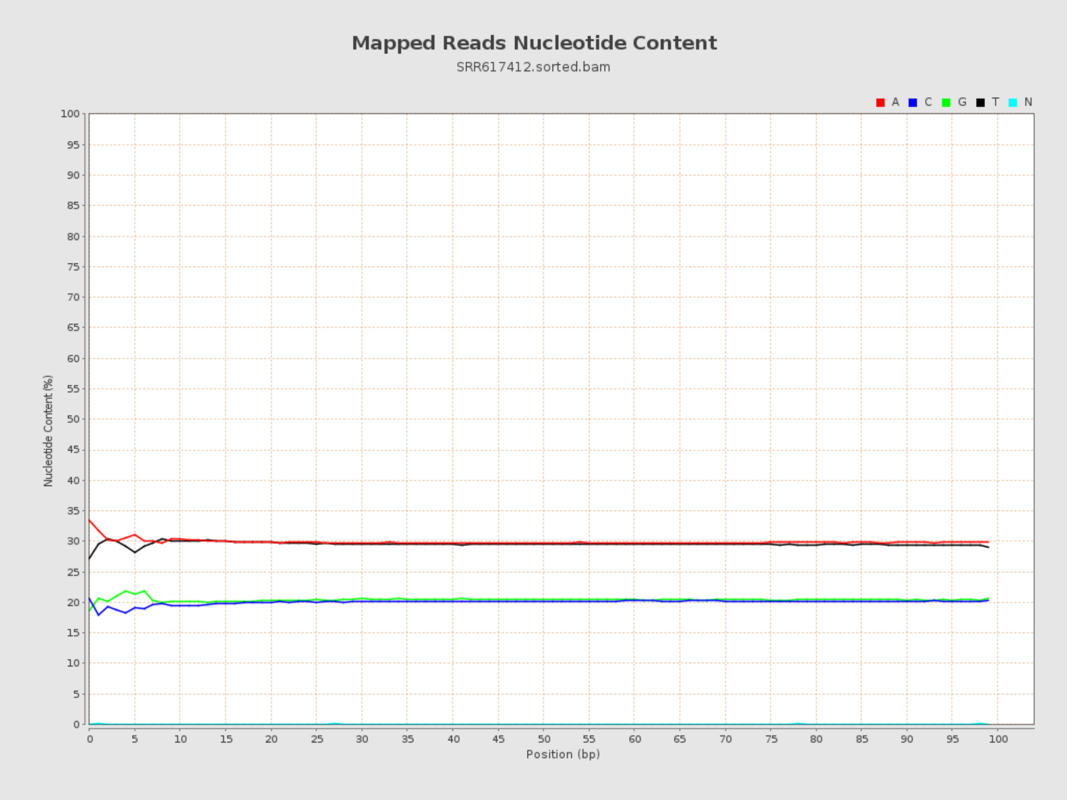
6. Results : Genome Fraction Coverage



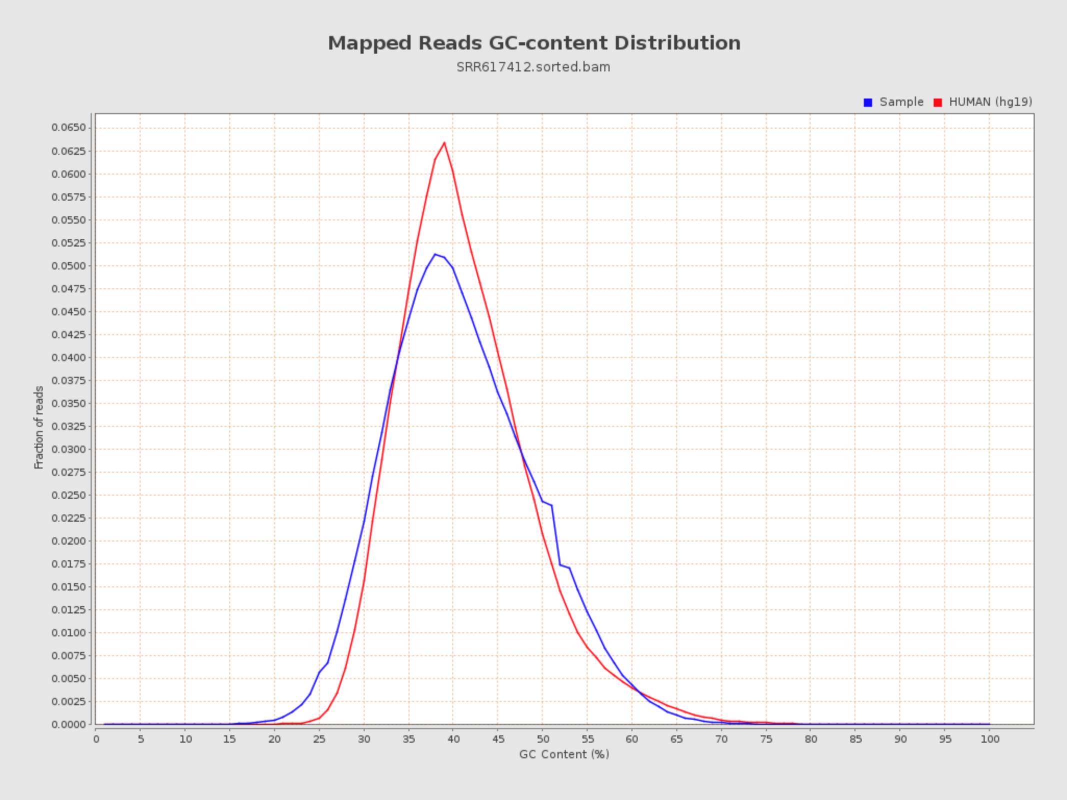
7. Results : Duplication Rate Histogram



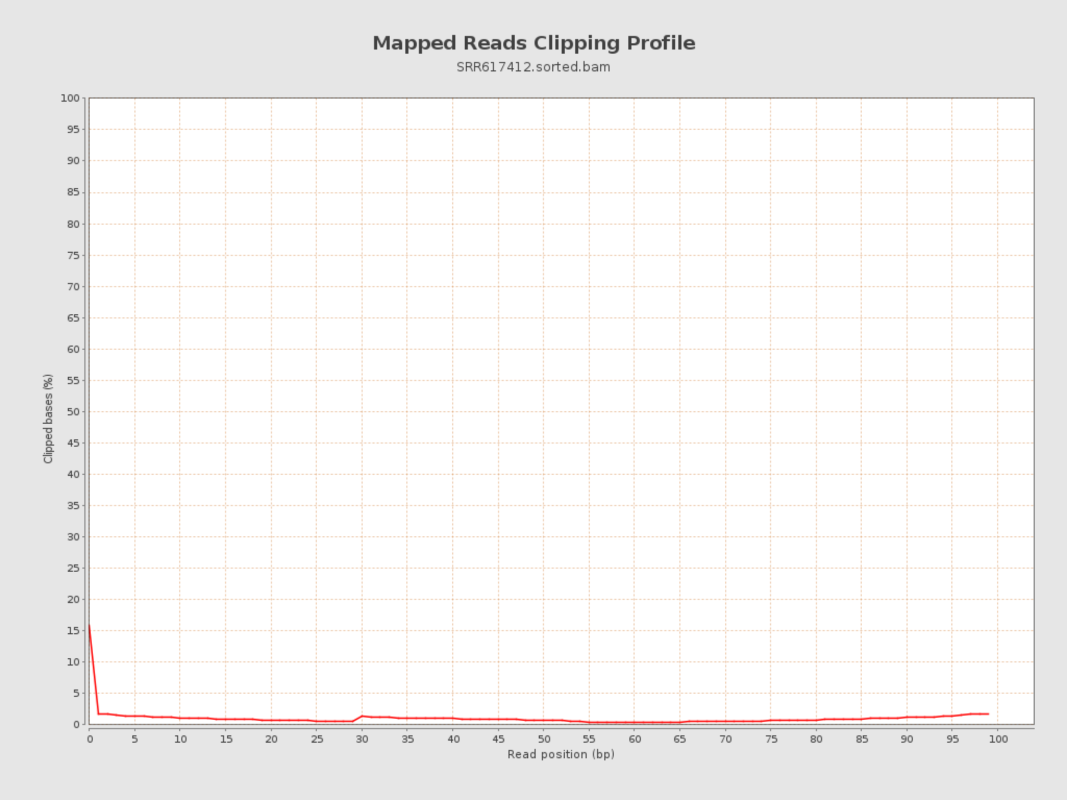
8. Results : Mapped Reads Nucleotide Content



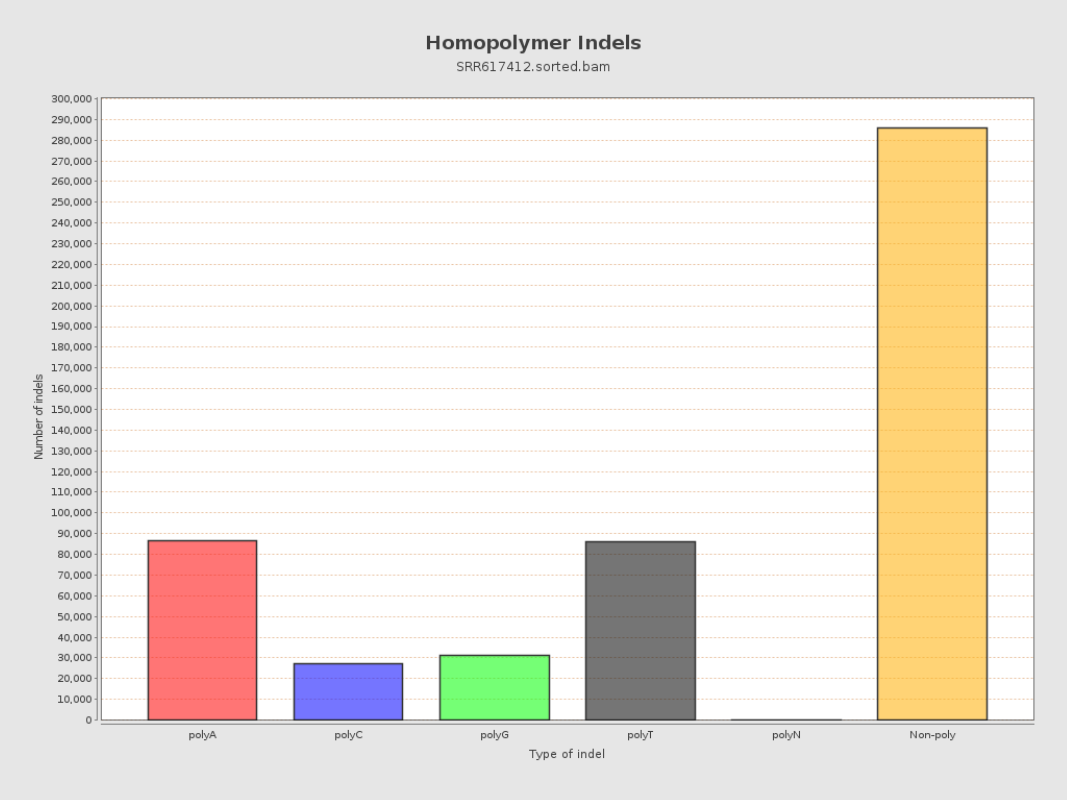
9. Results : Mapped Reads GC-content Distribution



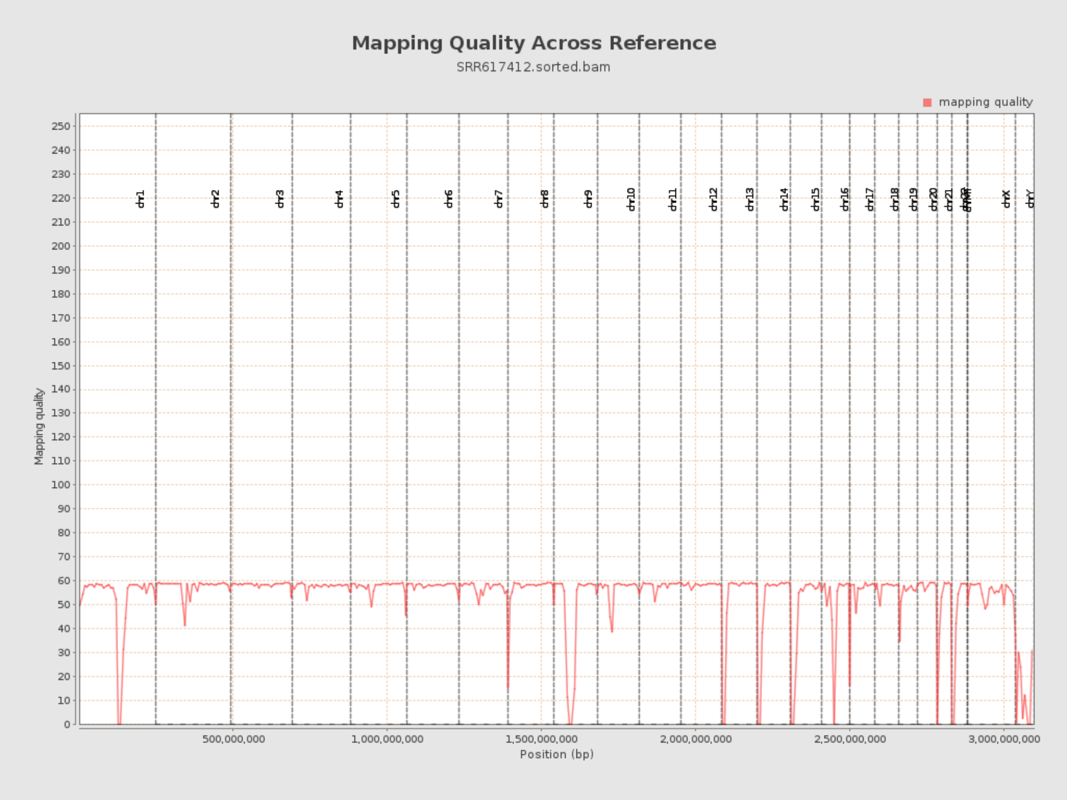
10. Results : Mapped Reads Clipping Profile



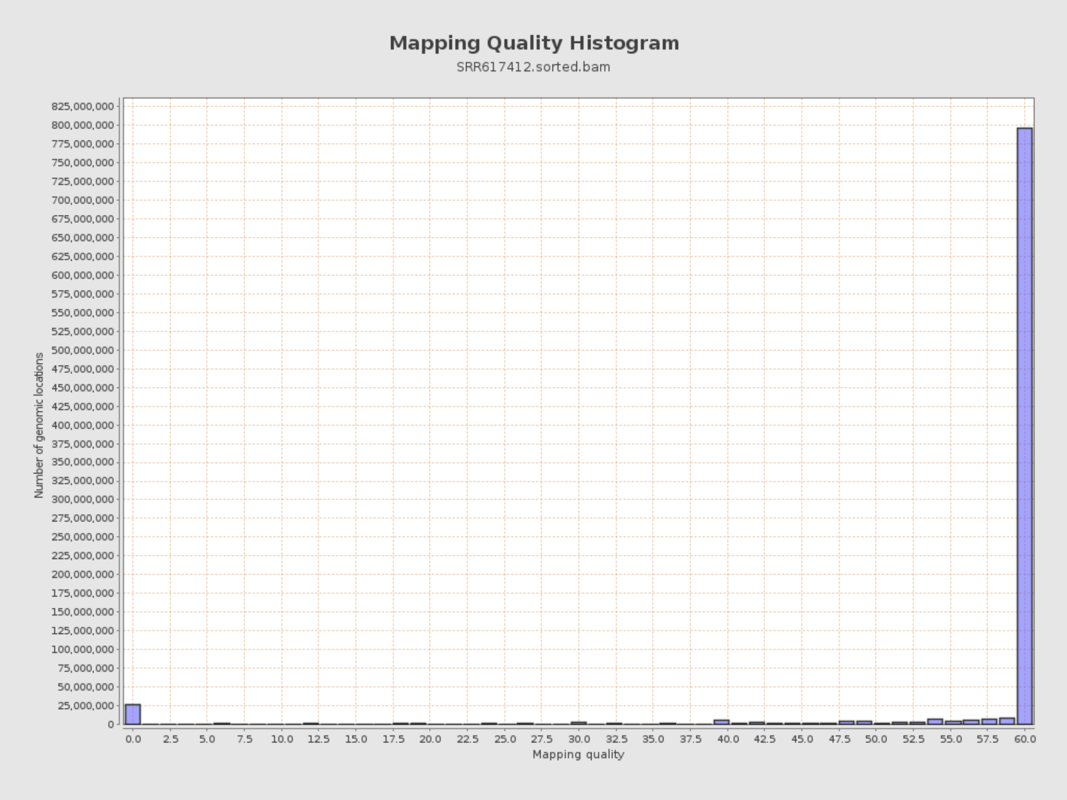
11. Results : Homopolymer Indels



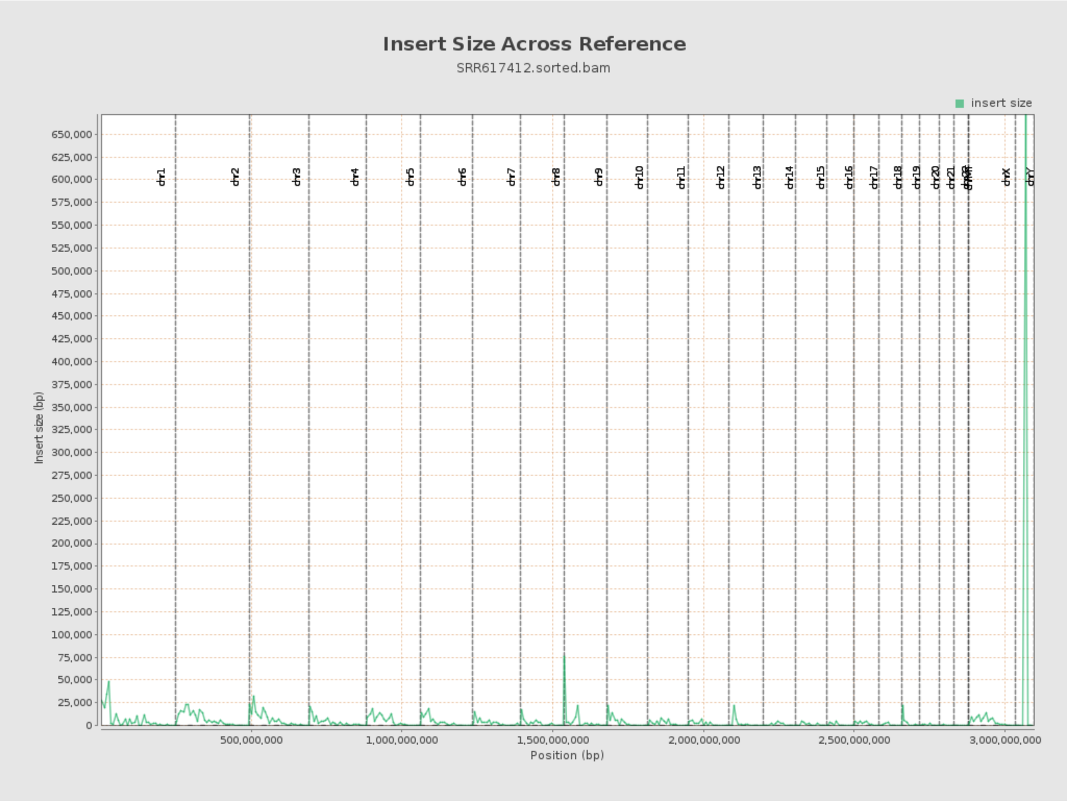
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram