Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 07:19:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617421.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_SRR617421 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617421_1.fastq.gz SRR617421_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 07:19:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617421.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	27,423,783 / 85.7%
Unmapped reads	4,576,217 / 14.3%
Mapped paired reads	27,423,783 / 85.7%
Mapped reads, first in pair	14,392,501 / 44.98%
Mapped reads, second in pair	13,031,282 / 40.72%
Mapped reads, both in pair	25,785,654 / 80.58%
Mapped reads, singletons	1,638,129 / 5.12%
Secondary alignments	0
Supplementary alignments	394,403 / 1.23%
Read min/max/mean length	30 / 100 / 100.51
Duplicated reads (estimated)	1,163,531 / 3.64%
Duplication rate	3.84%
Clipped reads	4,222,853 / 13.2%

2.2. ACGT Content

Number/percentage of A's	796,160,389 / 29.89%
Number/percentage of C's	533,830,283 / 20.04%
Number/percentage of T's	788,320,250 / 29.59%
Number/percentage of G's	545,182,291 / 20.47%
Number/percentage of N's	255,712 / 0.01%

GC Percentage	40.51%

2.3. Coverage

Mean	0.8607
Standard Deviation	2.6448

2.4. Mapping Quality

Mean Mapping Quality	53.49

2.5. Insert size

Mean	56,923.16
Standard Deviation	2,274,432.09
P25/Median/P75	167 / 204 / 261

2.6. Mismatches and indels

General error rate	1.63%
Mismatches	43,089,407
Insertions	224,828
Mapped reads with at least one insertion	0.81%
Deletions	260,660
Mapped reads with at least one deletion	0.93%
Homopolymer indels	43.71%

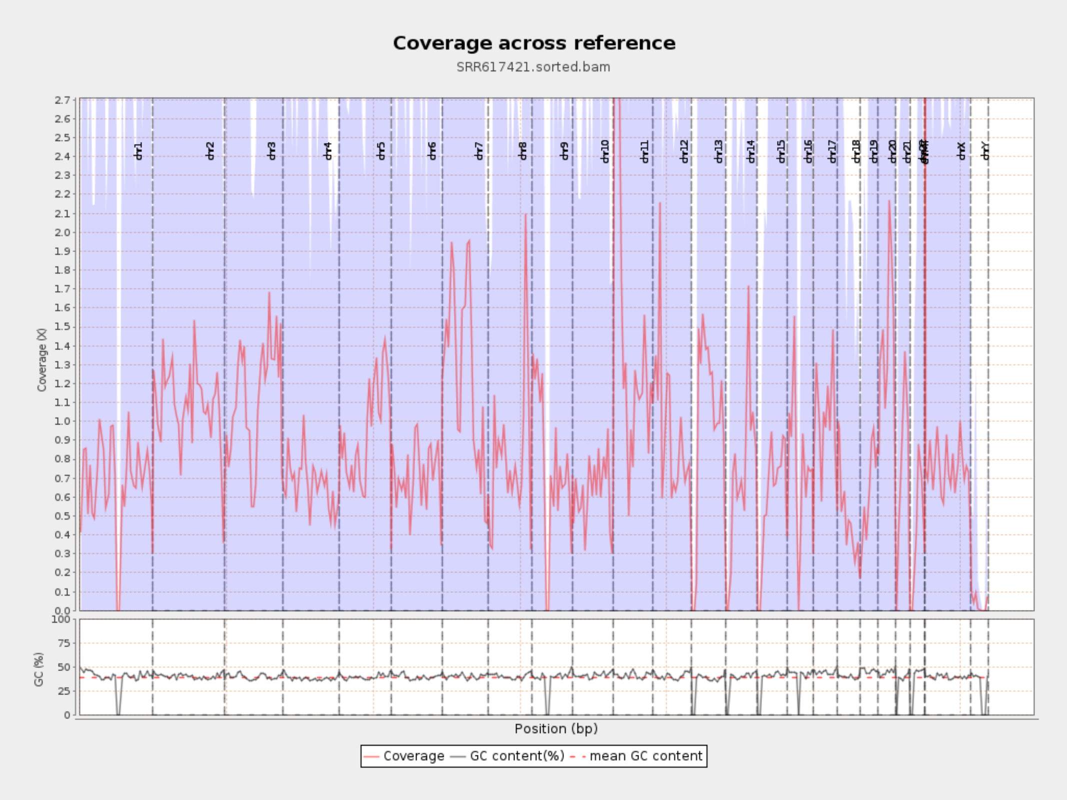
2.7. Chromosome stats

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

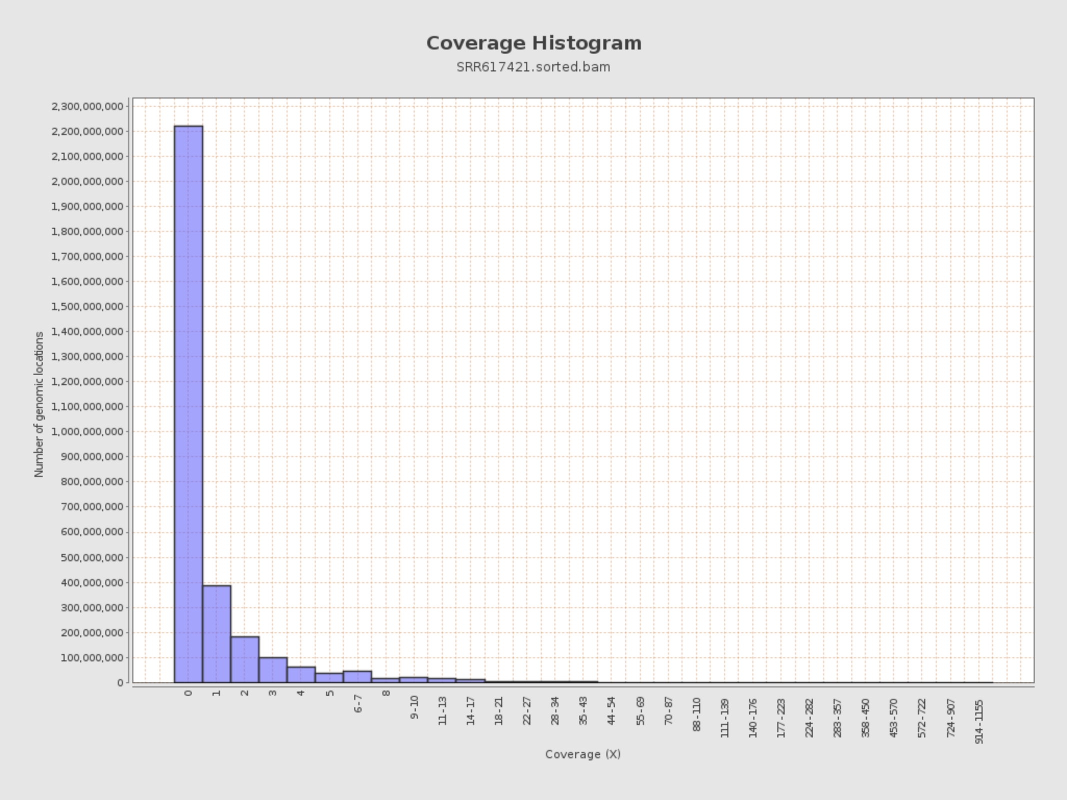
		bases	coverage	deviation
chr1	249250621	171010467	0.6861	2.4786
chr2	243199373	266186121	1.0945	2.8249
chr3	198022430	225379216	1.1381	3.0854
chr4	191154276	128946026	0.6746	2.0886
chr5	180915260	171356635	0.9472	2.613
chr6	171115067	122612512	0.7166	2.3602
chr7	159138663	199762554	1.2553	2.9481
chr8	146364022	118092192	0.8068	2.9133
chr9	141213431	106382041	0.7533	2.3437
chr10	135534747	85403923	0.6301	2.1769
chr11	135006516	197274699	1.4612	3.458
chr12	133851895	126662084	0.9463	2.5277
chr13	115169878	116254615	1.0094	2.5349
chr14	107349540	77118223	0.7184	2.6022
chr15	102531392	60883649	0.5938	2.1633
chr16	90354753	66482084	0.7358	2.9667
chr17	81195210	81281610	1.0011	3.2569
chr18	78077248	38429020	0.4922	1.817
chr19	59128983	37390965	0.6324	2.0675
chr20	63025520	89868645	1.4259	4.2221
chr21	48129895	36564009	0.7597	2.2956
chr22	51304566	21146025	0.4122	1.8607
chrMT	16571	158239	9.5492	4.8368
chrX	155270560	117531115	0.7569	2.3267

chrY	59373566	2154290	0.0363	0.5586

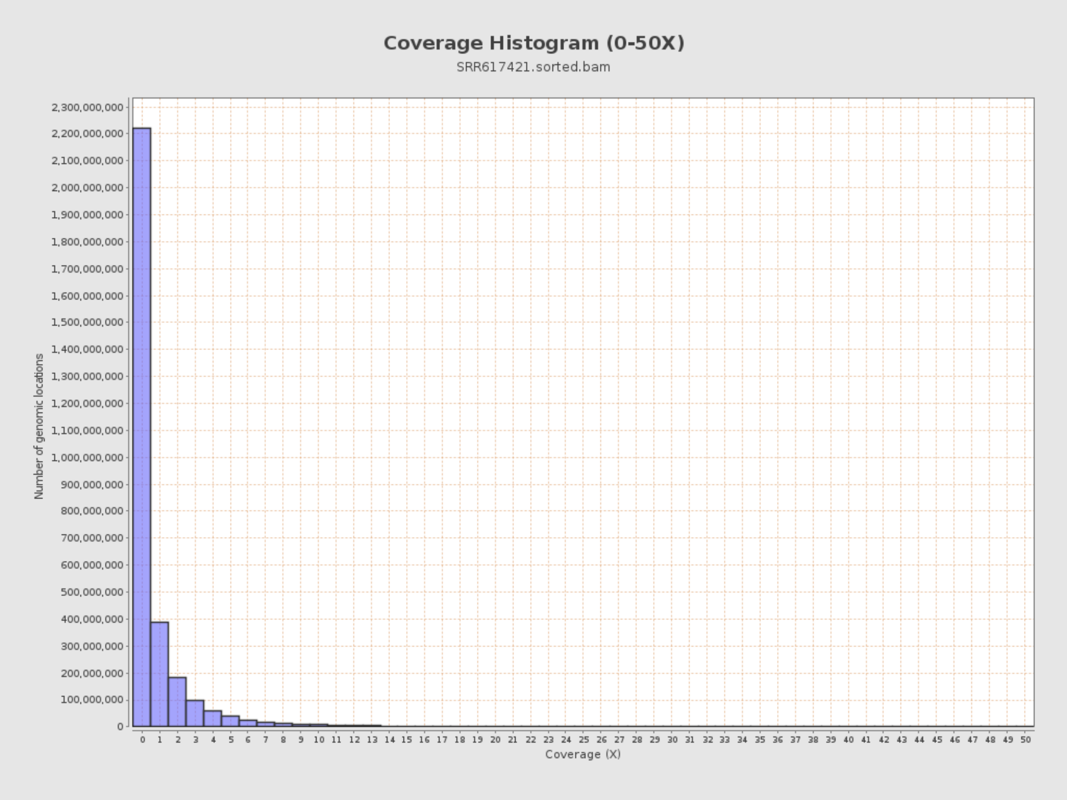
3. Results : Coverage across reference



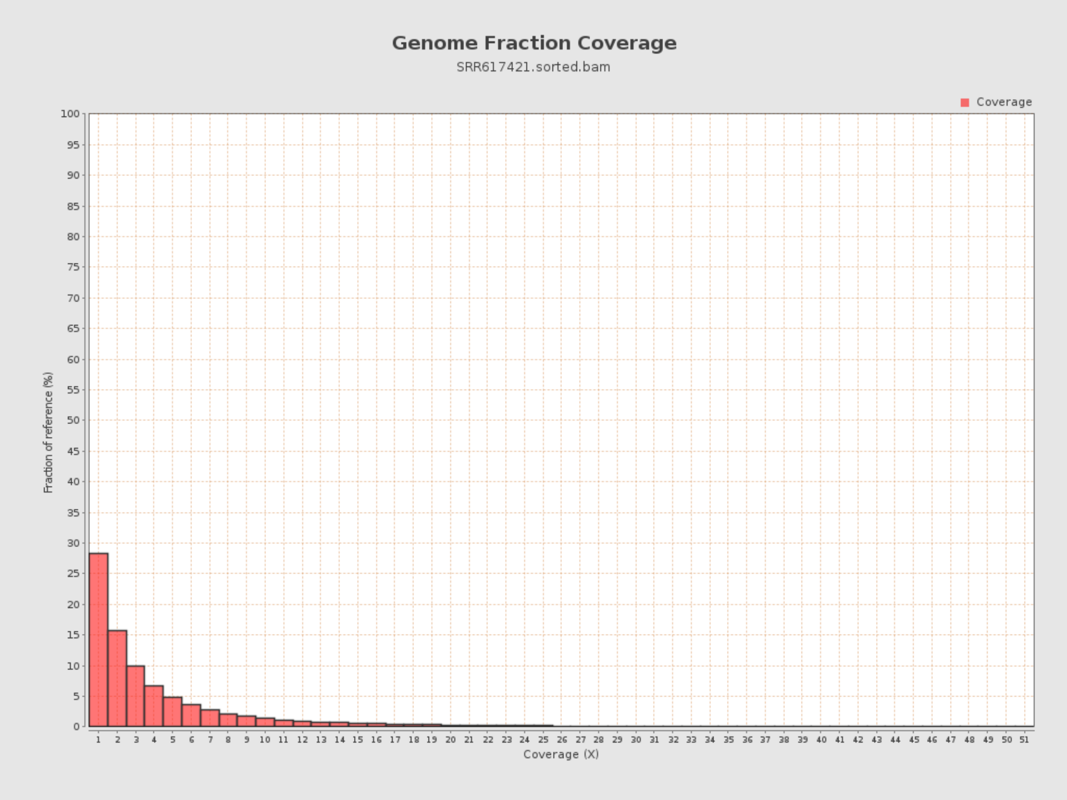
4. Results : Coverage Histogram



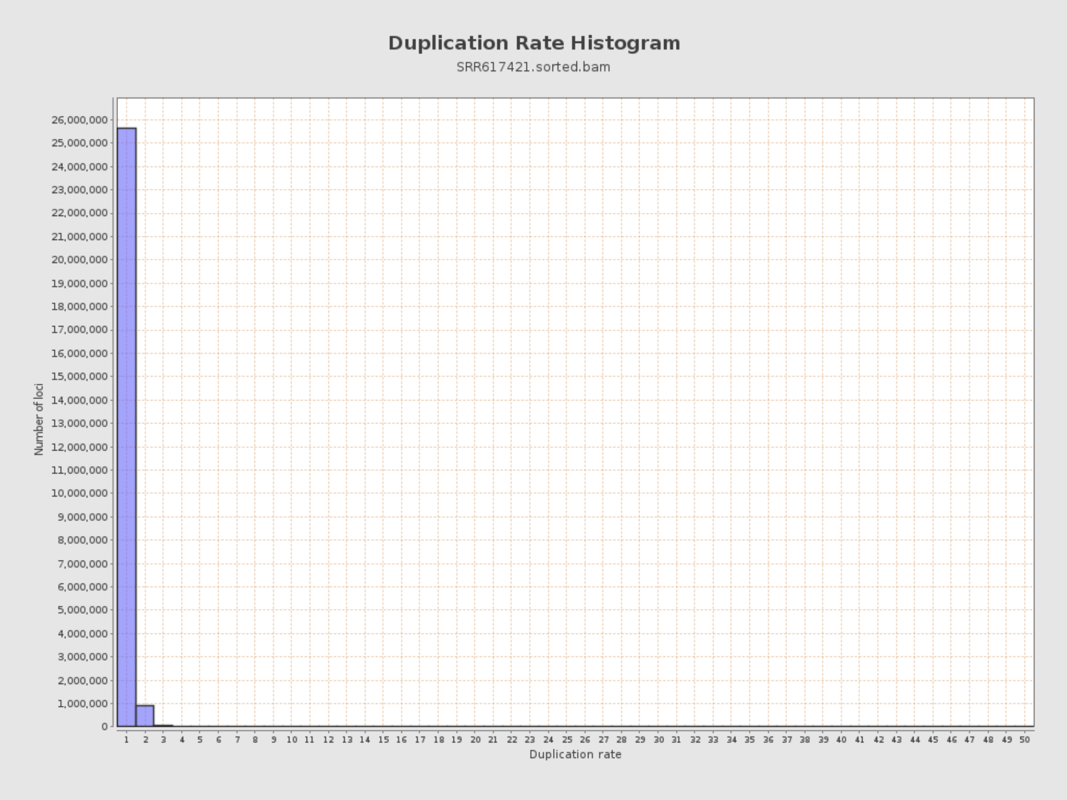
5. Results : Coverage Histogram (0-50X)



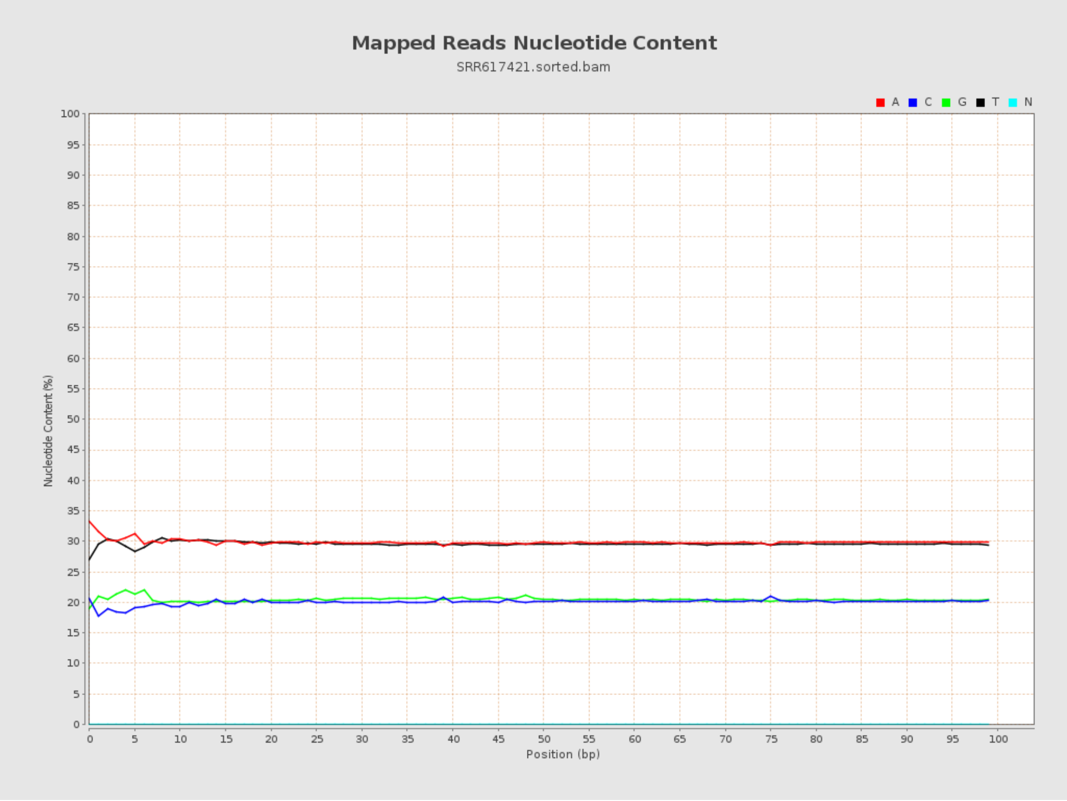
6. Results : Genome Fraction Coverage



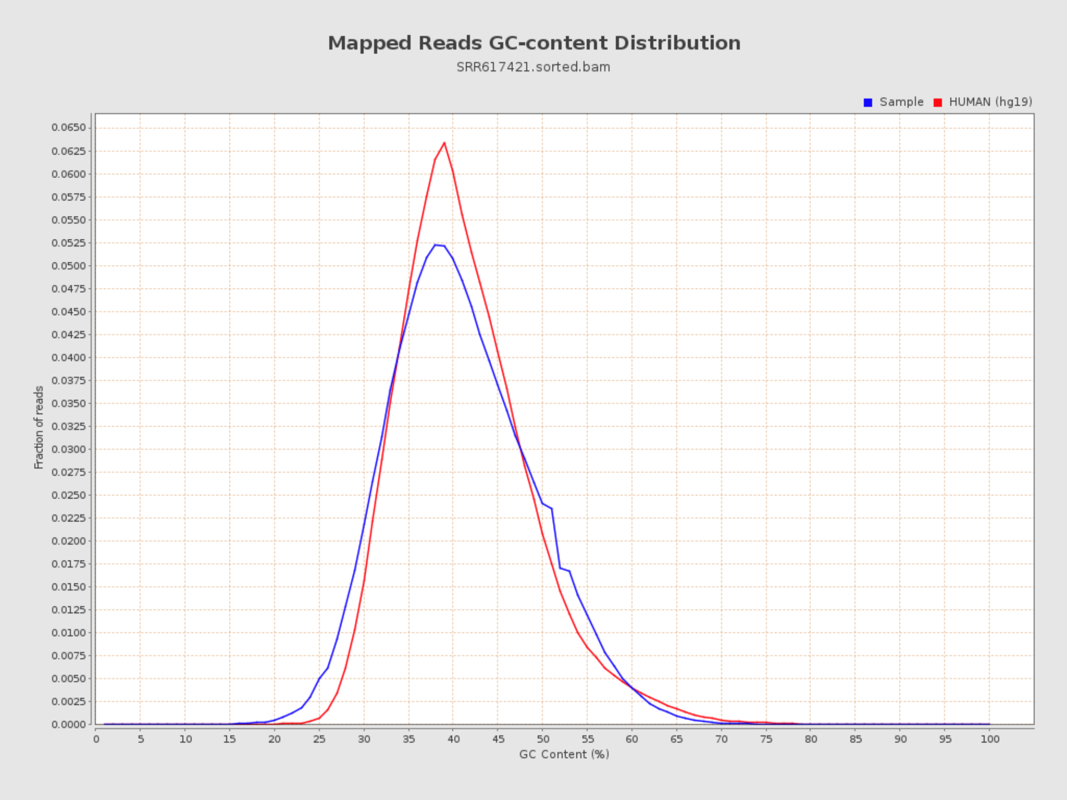
7. Results : Duplication Rate Histogram



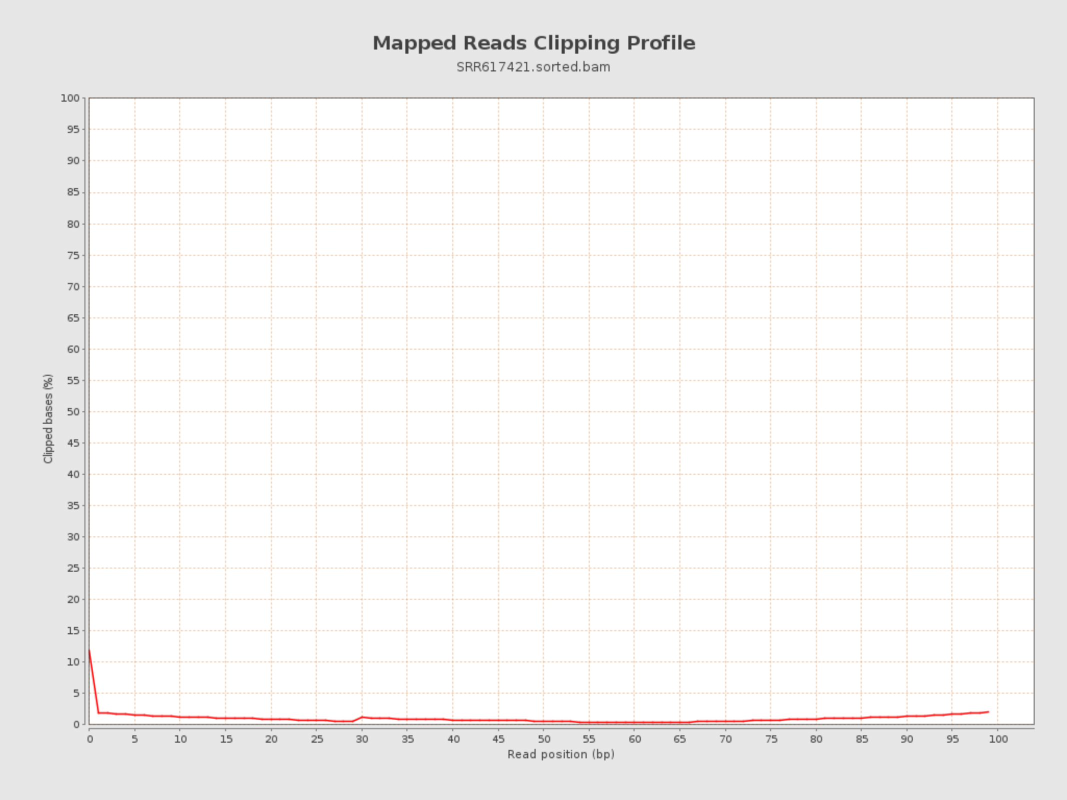
8. Results : Mapped Reads Nucleotide Content



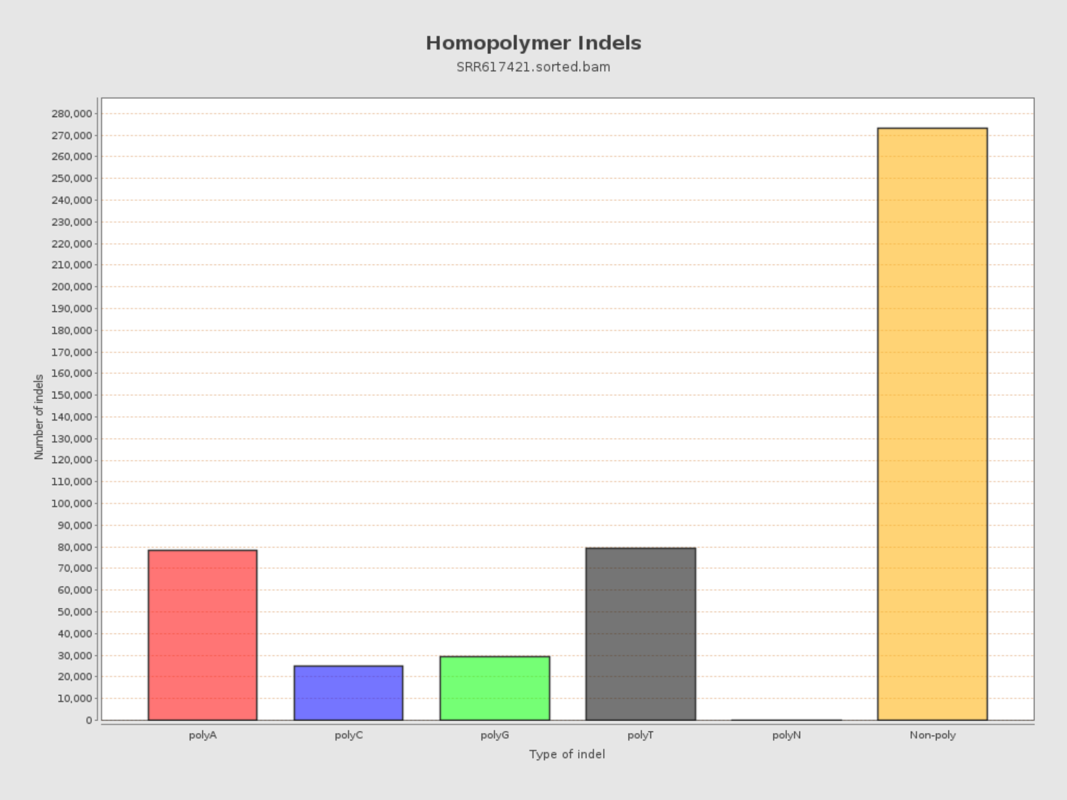
9. Results : Mapped Reads GC-content Distribution



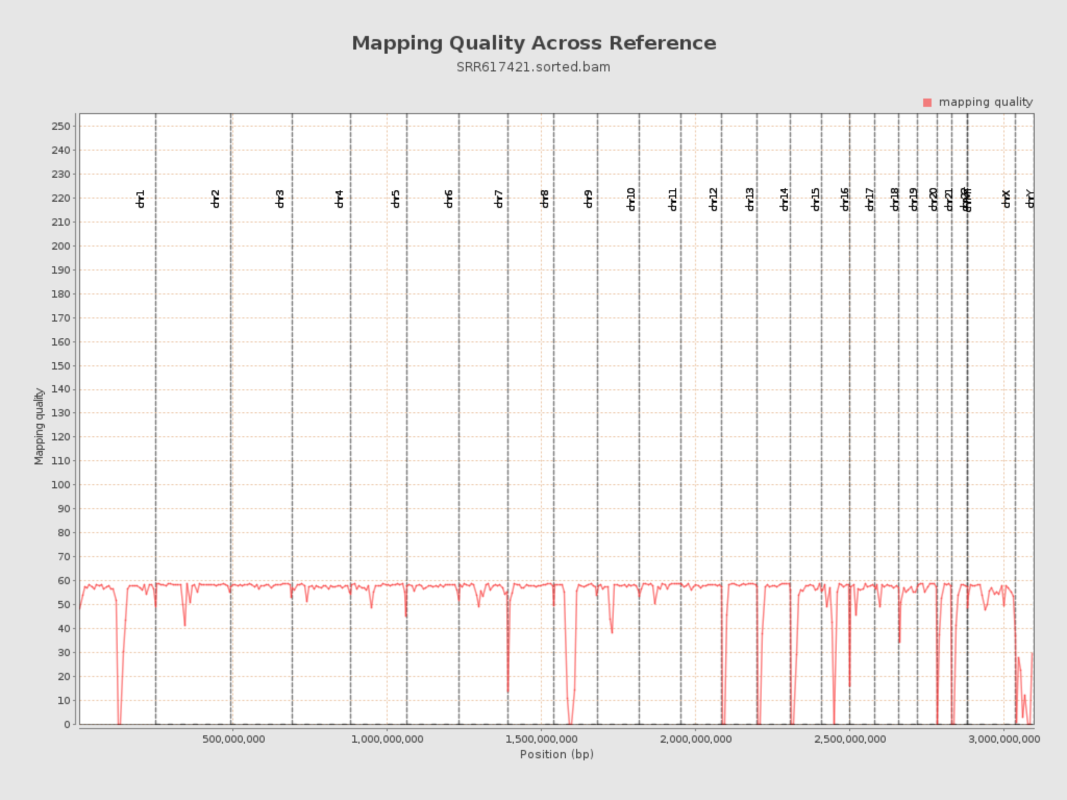
10. Results : Mapped Reads Clipping Profile



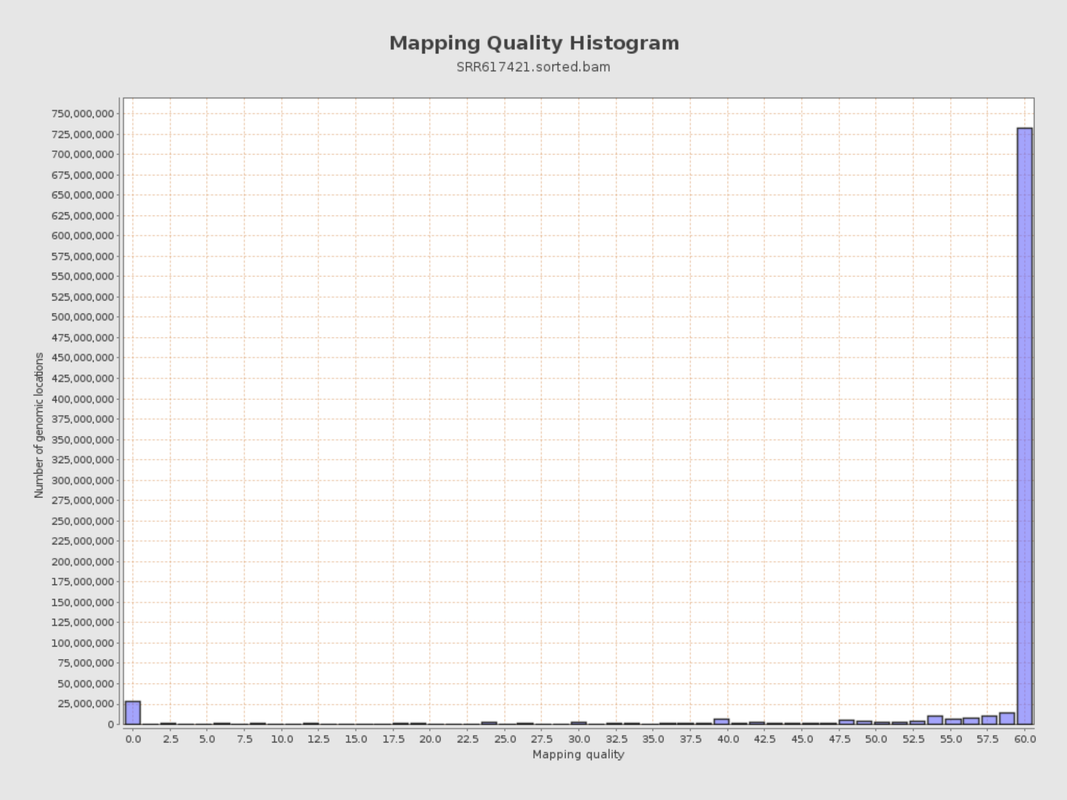
11. Results : Homopolymer Indels



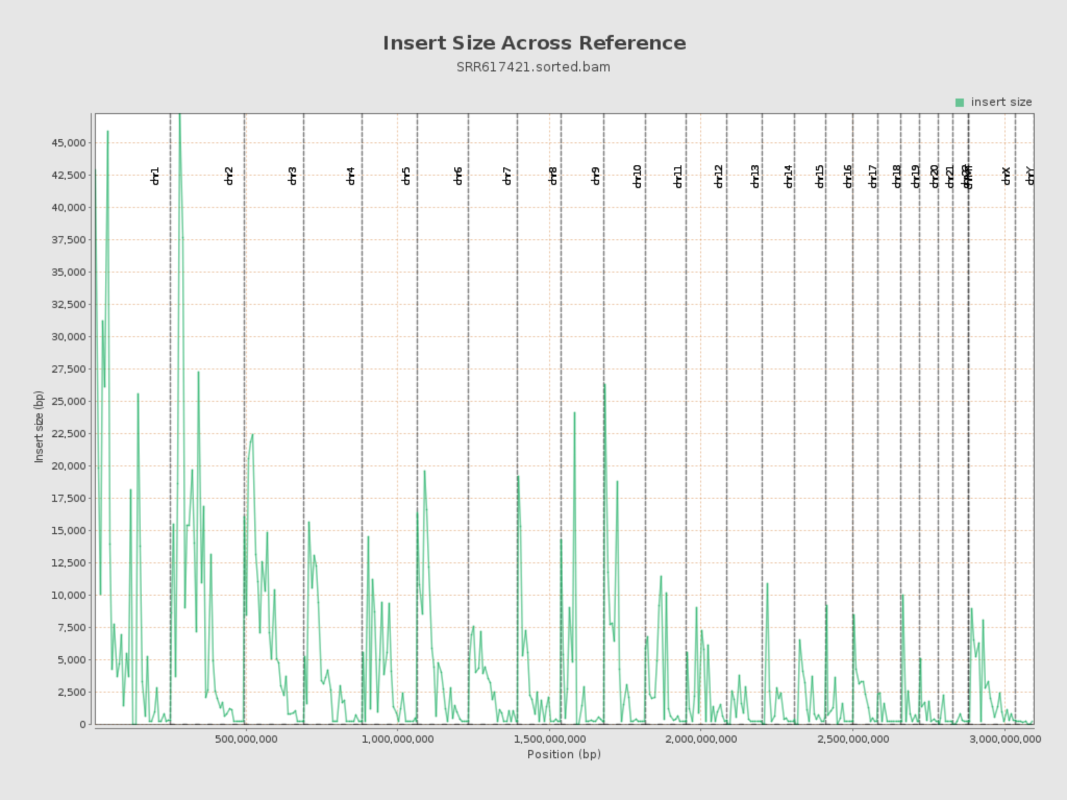
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram