Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 20:19:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472723.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_SRR3472723 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472723_1.fastq.gz SRR3472723_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 20:19:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472723.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,666,124
Mapped reads	10,566,541 / 99.07%
Unmapped reads	99,583 / 0.93%
Mapped paired reads	10,566,541 / 99.07%
Mapped reads, first in pair	5,306,017 / 49.75%
Mapped reads, second in pair	5,260,524 / 49.32%
Mapped reads, both in pair	10,499,280 / 98.44%
Mapped reads, singletons	67,261 / 0.63%
Secondary alignments	0
Supplementary alignments	42,027 / 0.39%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	7,435,417 / 69.71%
Duplication rate	45.91%
Clipped reads	854,696 / 8.01%

2.2. ACGT Content

Number/percentage of A's	304,142,085 / 29.22%
Number/percentage of C's	217,426,292 / 20.89%
Number/percentage of T's	302,416,082 / 29.06%
Number/percentage of G's	216,652,188 / 20.82%
Number/percentage of N's	203,069 / 0.02%

GC Percentage	41.7%

2.3. Coverage

Mean	0.3363
Standard Deviation	20.5284

2.4. Mapping Quality

Mean Mapping Quality	54.55

2.5. Insert size

Mean	28,803.3
Standard Deviation	1,677,274
P25/Median/P75	171 / 239 / 321

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	6,149,418
Insertions	73,536
Mapped reads with at least one insertion	0.68%
Deletions	62,140
Mapped reads with at least one deletion	0.58%
Homopolymer indels	42.28%

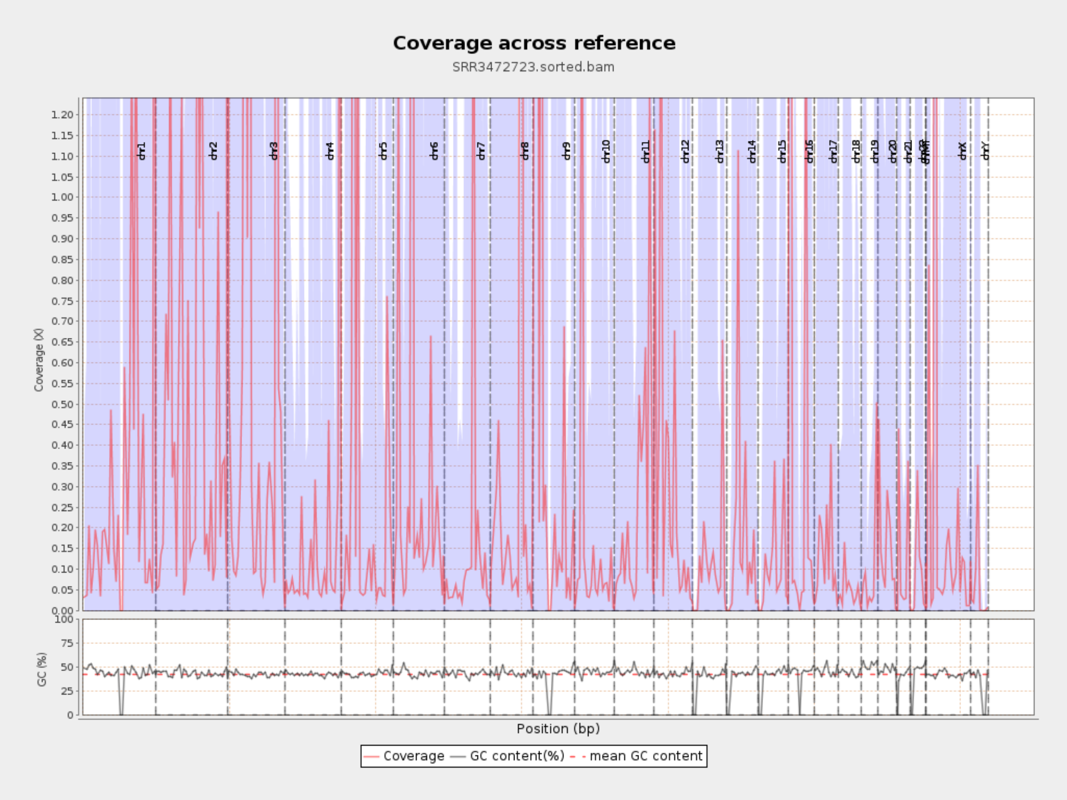
2.7. Chromosome stats

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

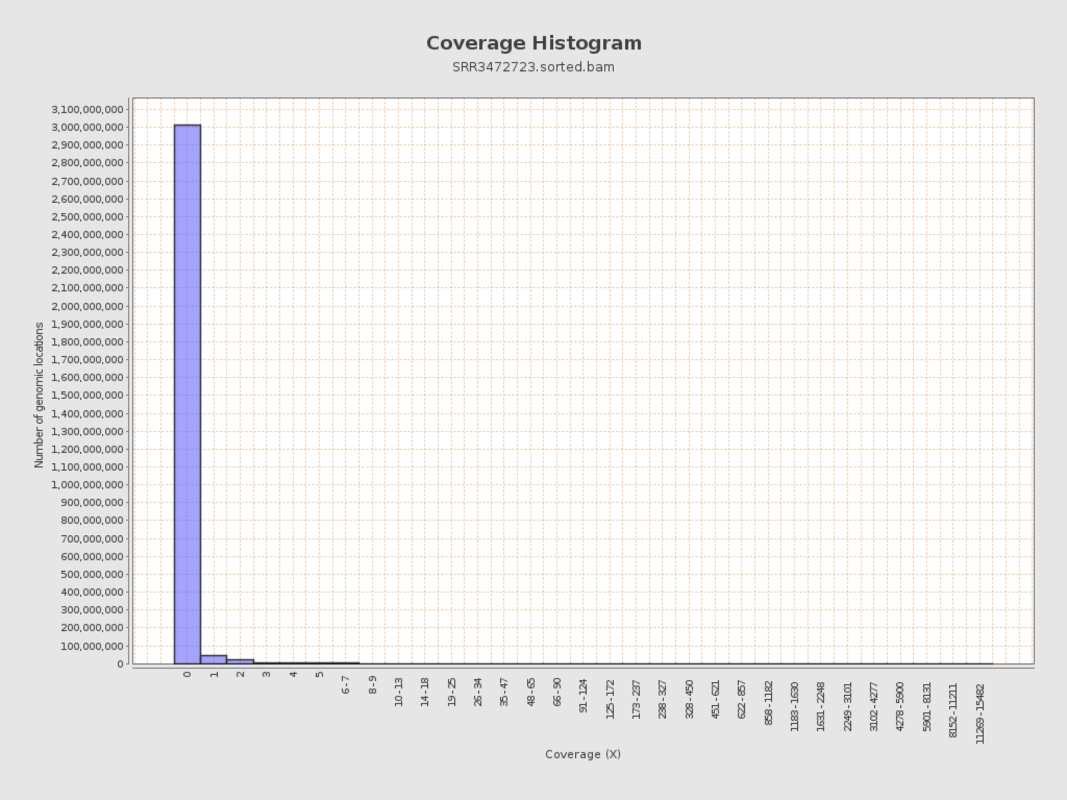
		bases	coverage	deviation
chr1	249250621	89637728	0.3596	25.8005
chr2	243199373	115501898	0.4749	21.8144
chr3	198022430	154767939	0.7816	28.2409
chr4	191154276	38919271	0.2036	14.2286
chr5	180915260	70865513	0.3917	24.0347
chr6	171115067	84497129	0.4938	23.413
chr7	159138663	26439045	0.1661	18.5206
chr8	146364022	60527042	0.4135	30.6255
chr9	141213431	91888279	0.6507	24.4517
chr10	135534747	23330073	0.1721	22.0897
chr11	135006516	33310103	0.2467	11.7466
chr12	133851895	46071378	0.3442	16.3464
chr13	115169878	13529443	0.1175	12.6222
chr14	107349540	20352199	0.1896	11.4214
chr15	102531392	11048342	0.1078	7.5503
chr16	90354753	59730679	0.6611	32.7127
chr17	81195210	11267687	0.1388	6.2948
chr18	78077248	3965822	0.0508	1.785
chr19	59128983	6056147	0.1024	6.4894
chr20	63025520	9783322	0.1552	7.119
chr21	48129895	6977714	0.145	15.8528
chr22	51304566	4594175	0.0895	4.0022
chrMT	16571	1931	0.1165	0.5579
chrX	155270560	54078435	0.3483	21.6044

chrY	59373566	3858666	0.065	5.2068

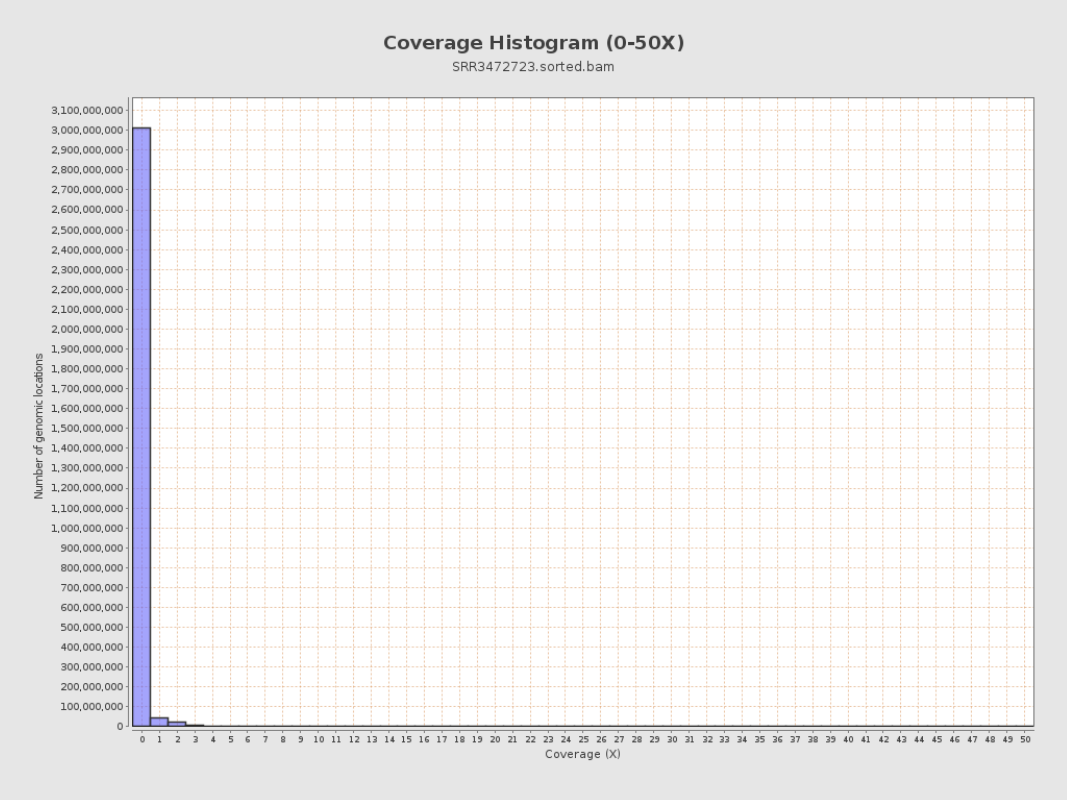
3. Results : Coverage across reference



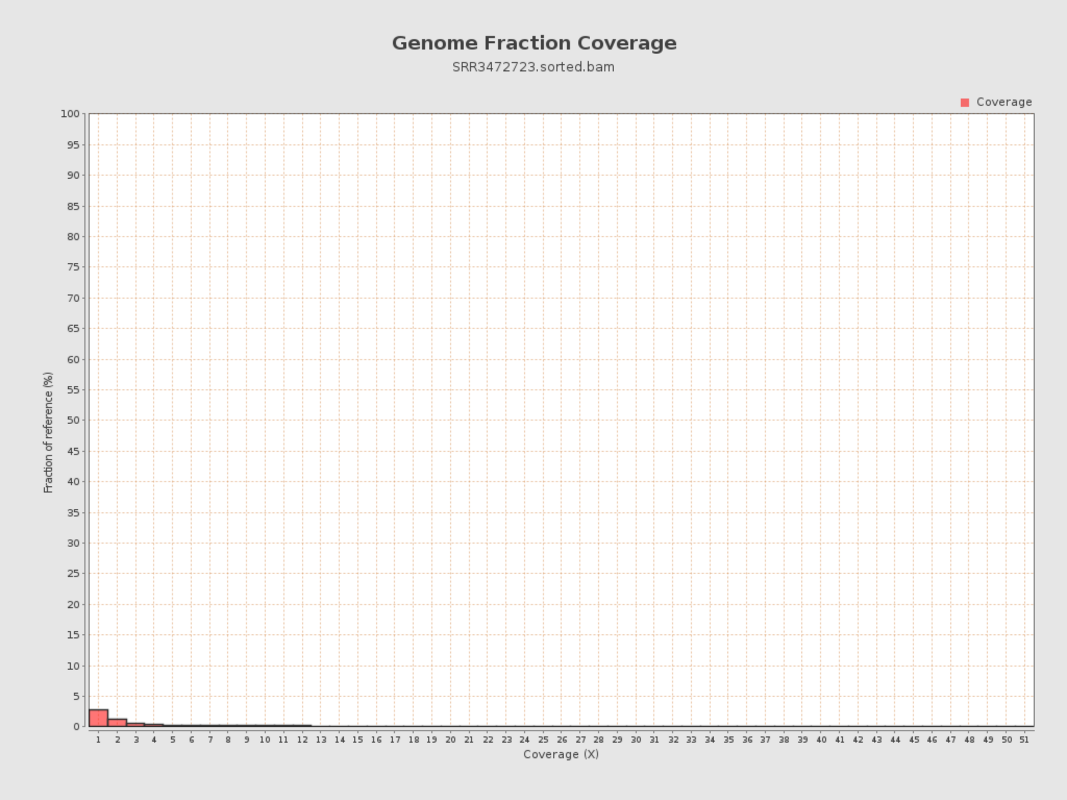
4. Results : Coverage Histogram



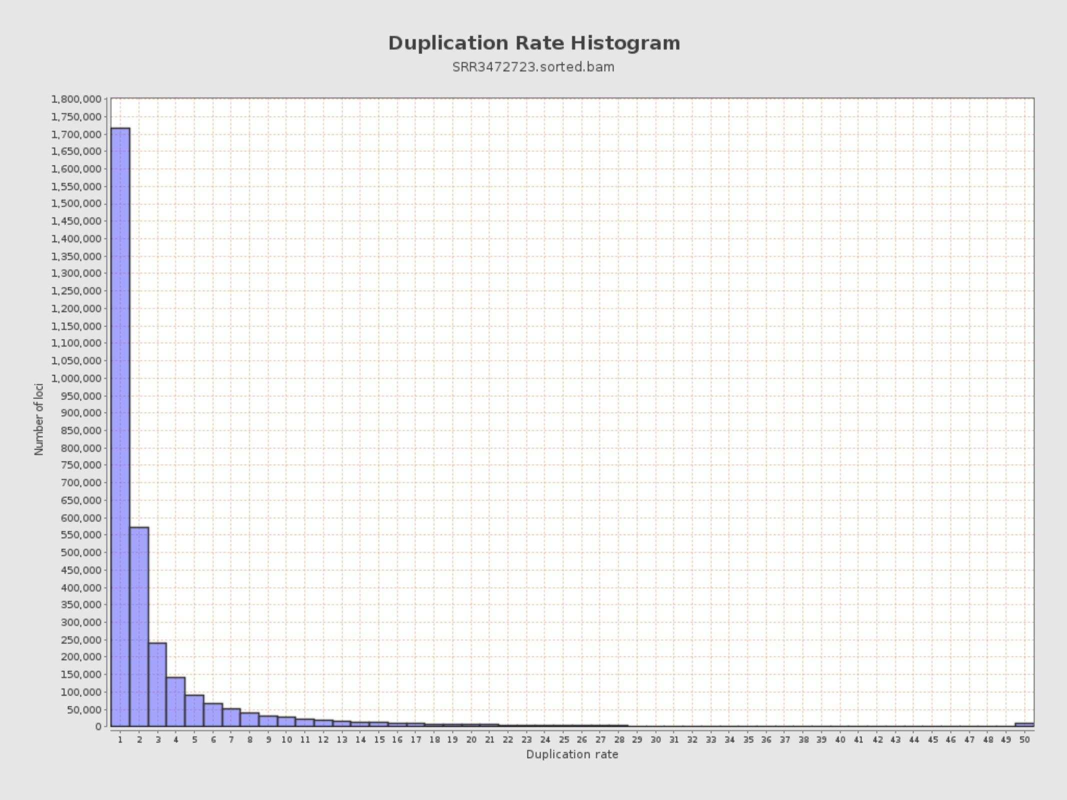
5. Results : Coverage Histogram (0-50X)



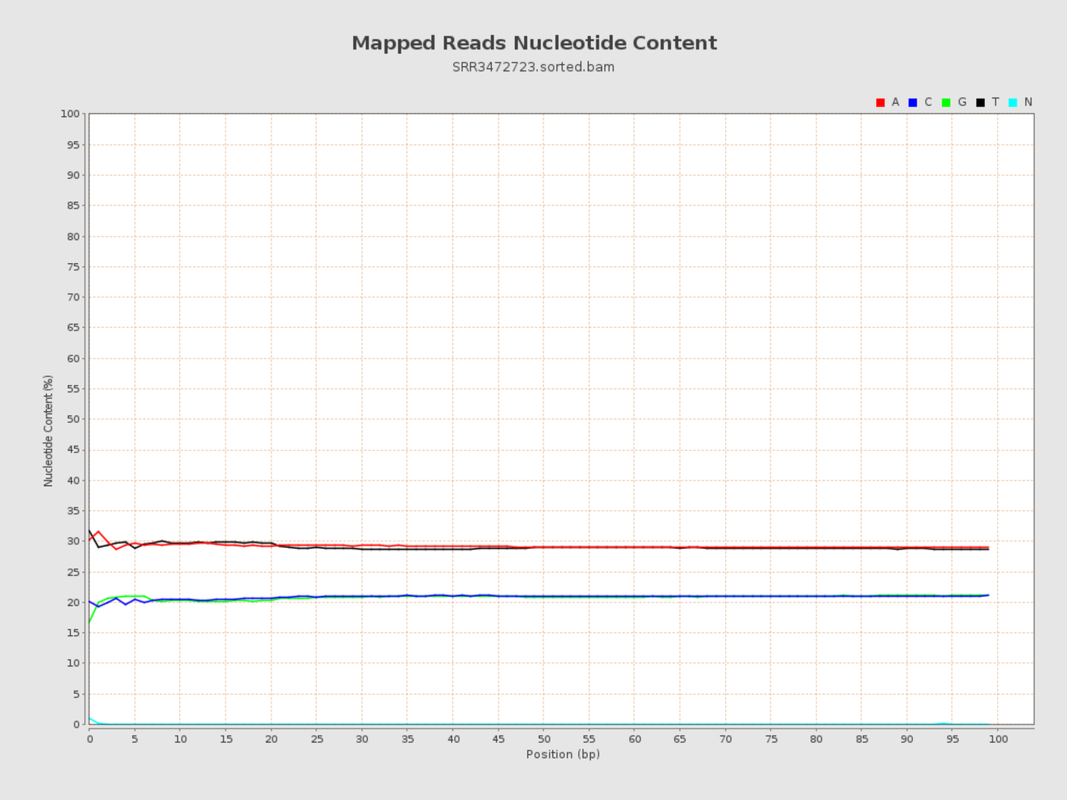
6. Results : Genome Fraction Coverage



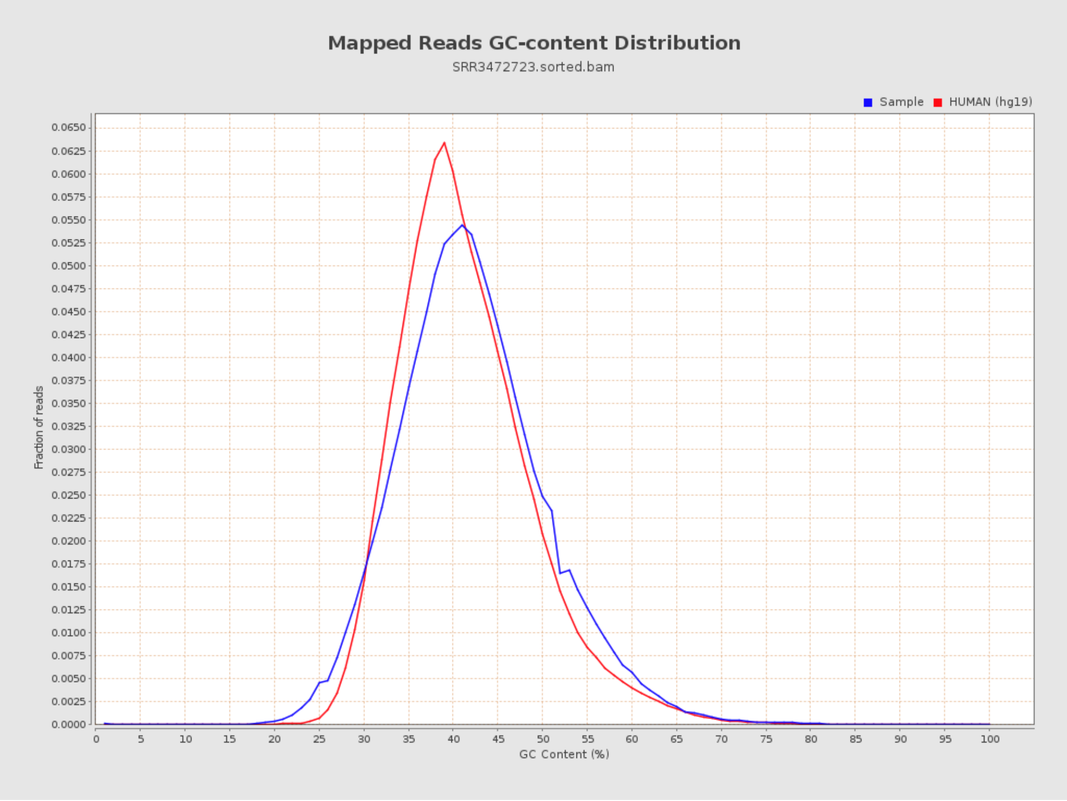
7. Results : Duplication Rate Histogram



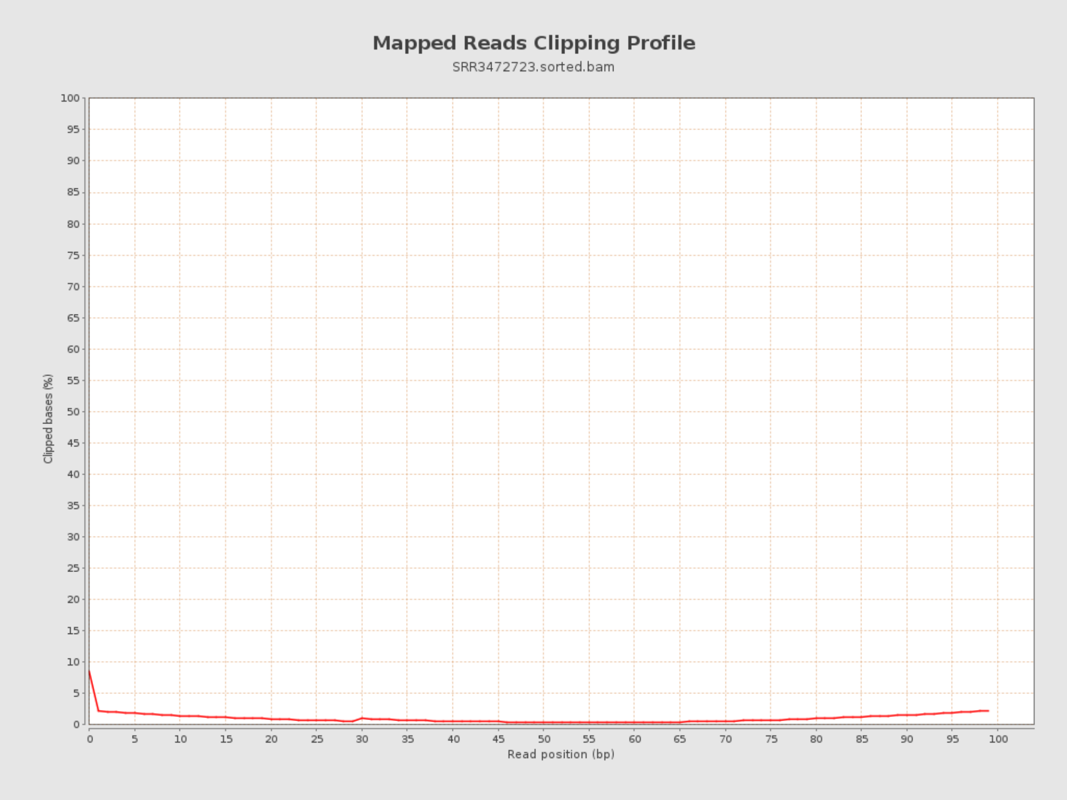
8. Results : Mapped Reads Nucleotide Content



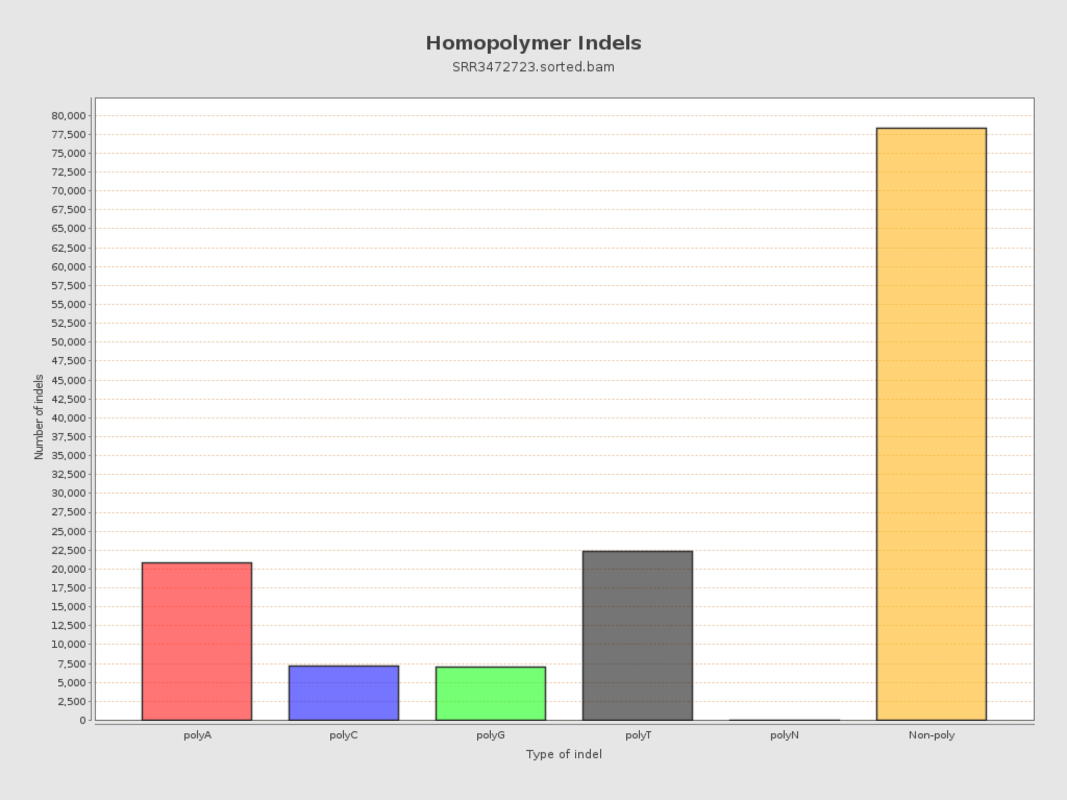
9. Results : Mapped Reads GC-content Distribution



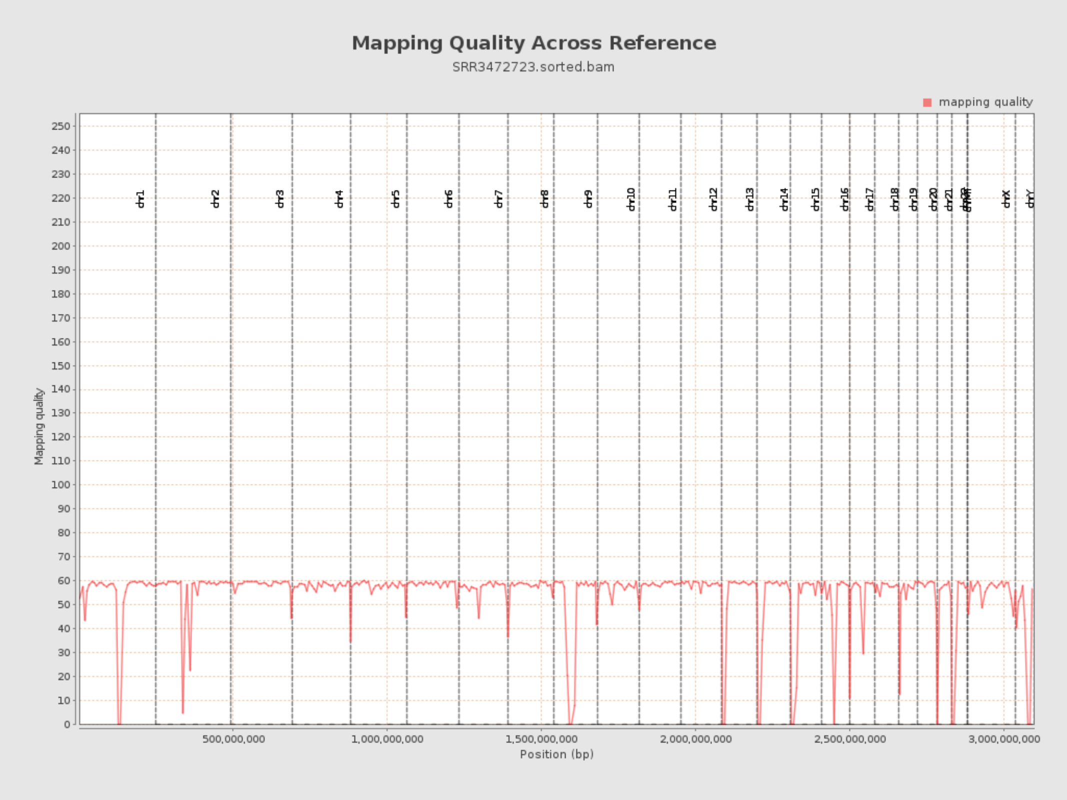
10. Results : Mapped Reads Clipping Profile



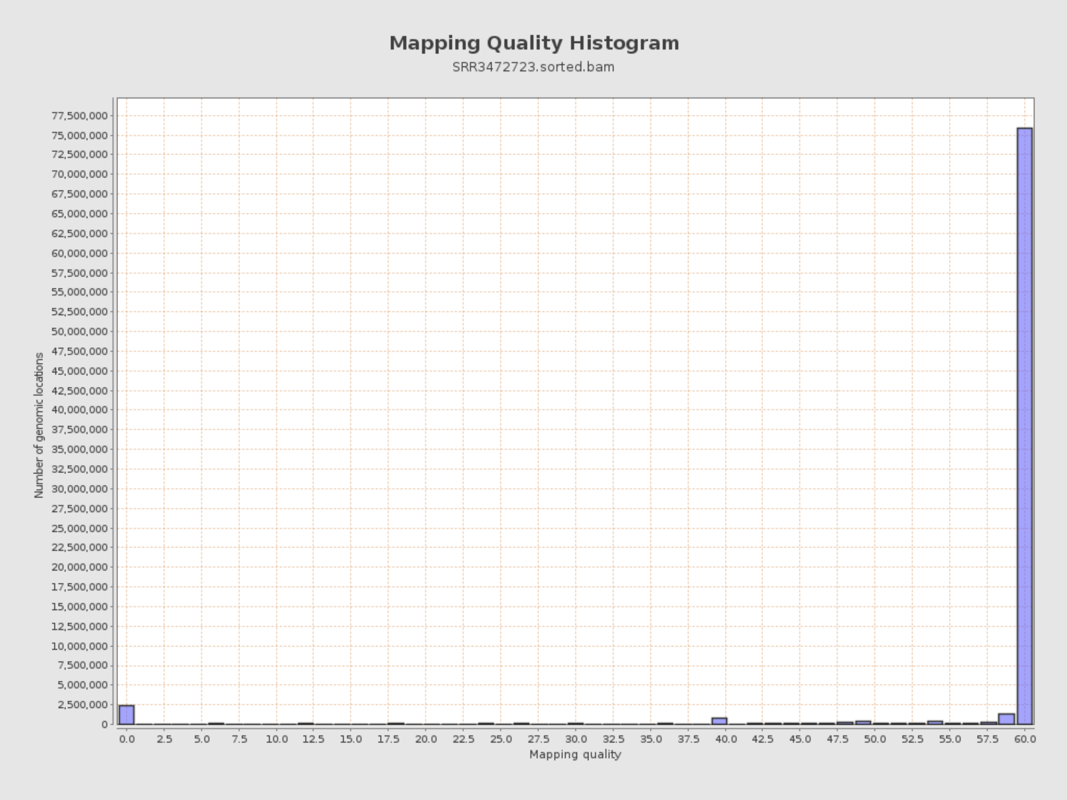
11. Results : Homopolymer Indels



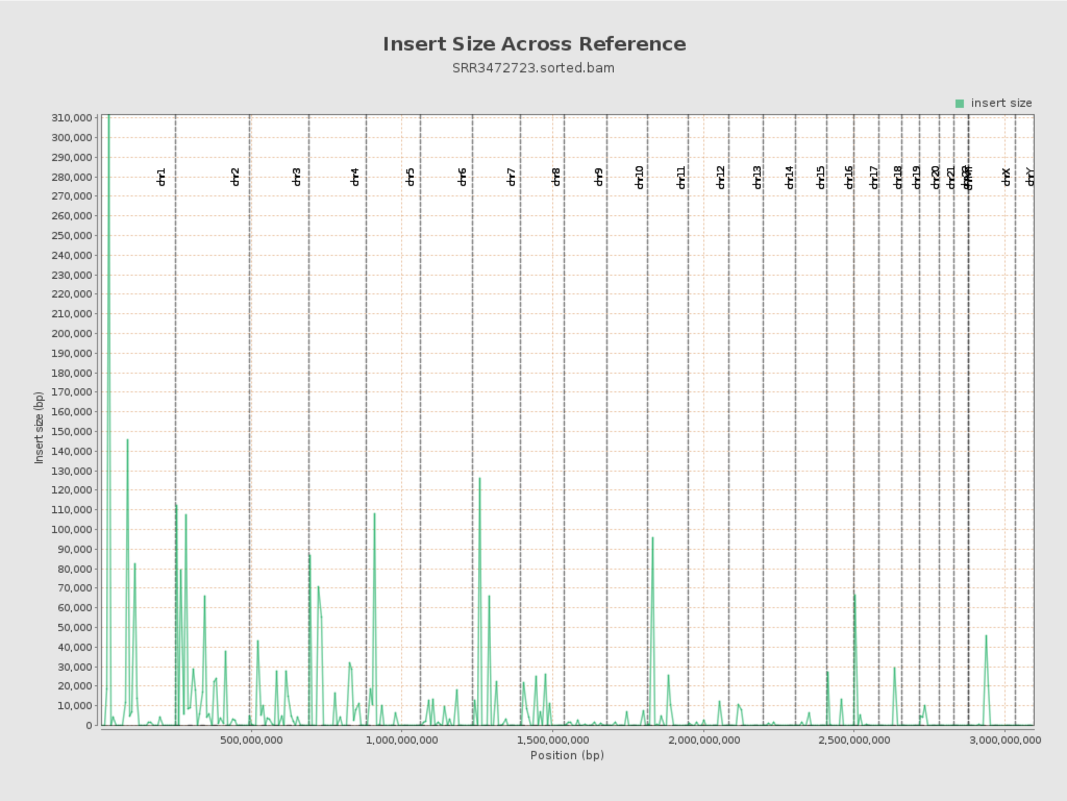
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram