Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 17:09:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472632.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_SRR3472632 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472632_1.fastq.gz SRR3472632_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 17:09:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472632.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,157,804
Mapped reads	15,040,408 / 99.23%
Unmapped reads	117,396 / 0.77%
Mapped paired reads	15,040,408 / 99.23%
Mapped reads, first in pair	7,543,755 / 49.77%
Mapped reads, second in pair	7,496,653 / 49.46%
Mapped reads, both in pair	14,959,320 / 98.69%
Mapped reads, singletons	81,088 / 0.53%
Secondary alignments	0
Supplementary alignments	68,160 / 0.45%
Read min/max/mean length	30 / 101 / 99.62
Duplicated reads (estimated)	9,799,077 / 64.65%
Duplication rate	48.26%
Clipped reads	1,016,163 / 6.7%

2.2. ACGT Content

Number/percentage of A's	395,790,665 / 26.77%
Number/percentage of C's	345,154,879 / 23.34%
Number/percentage of T's	397,925,828 / 26.91%
Number/percentage of G's	339,452,241 / 22.96%
Number/percentage of N's	265,945 / 0.02%

GC Percentage	46.3%

2.3. Coverage

Mean	0.4777
Standard Deviation	18.4469

2.4. Mapping Quality

Mean Mapping Quality	54.84

2.5. Insert size

Mean	21,459.64
Standard Deviation	1,413,547.01
P25/Median/P75	155 / 213 / 285

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	9,076,404
Insertions	90,481
Mapped reads with at least one insertion	0.59%
Deletions	90,968
Mapped reads with at least one deletion	0.6%
Homopolymer indels	47.86%

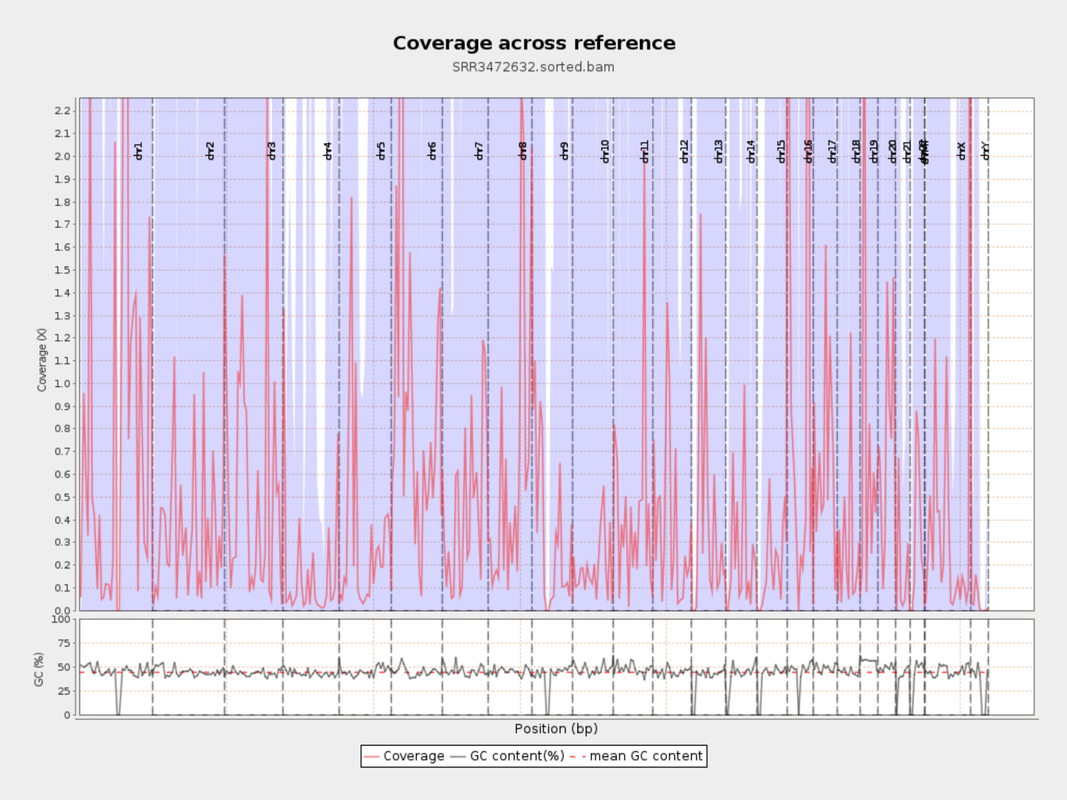
2.7. Chromosome stats

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

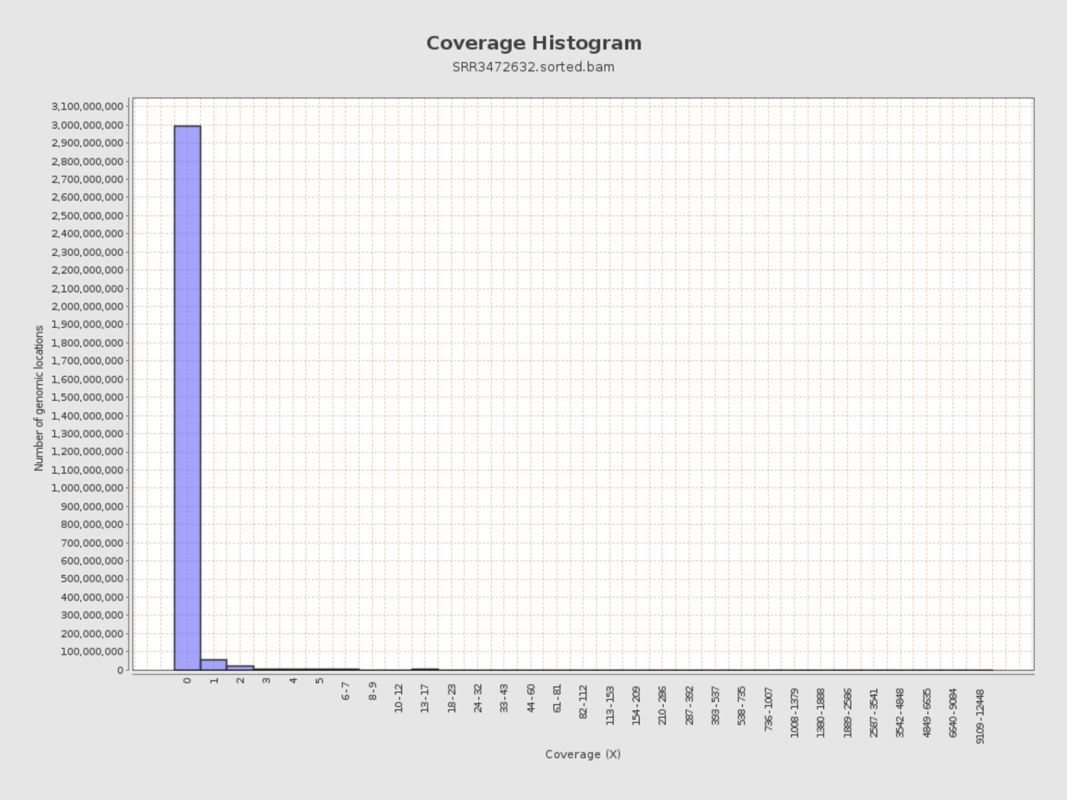
		bases	coverage	deviation
chr1	249250621	225091359	0.9031	30.5434
chr2	243199373	84919580	0.3492	13.0208
chr3	198022430	109680795	0.5539	19.3342
chr4	191154276	29755390	0.1557	7.1444
chr5	180915260	58864319	0.3254	13.0836
chr6	171115067	168847156	0.9867	33.2249
chr7	159138663	73272706	0.4604	17.5875
chr8	146364022	90920873	0.6212	21.9745
chr9	141213431	50777827	0.3596	9.5606
chr10	135534747	26393945	0.1947	8.081
chr11	135006516	59850325	0.4433	14.8544
chr12	133851895	50180420	0.3749	11.4195
chr13	115169878	45779092	0.3975	14.2632
chr14	107349540	25866270	0.241	8.5787
chr15	102531392	20578621	0.2007	7.8368
chr16	90354753	101790913	1.1266	35.6779
chr17	81195210	55250189	0.6805	16.2725
chr18	78077248	22607170	0.2895	15.903
chr19	59128983	46062811	0.779	22.5943
chr20	63025520	48388824	0.7678	20.6708
chr21	48129895	8640130	0.1795	11.6899
chr22	51304566	16722823	0.326	9.9087
chrMT	16571	1158	0.0699	0.2807
chrX	155270560	56279764	0.3625	12.331

chrY	59373566	2280417	0.0384	3.3542

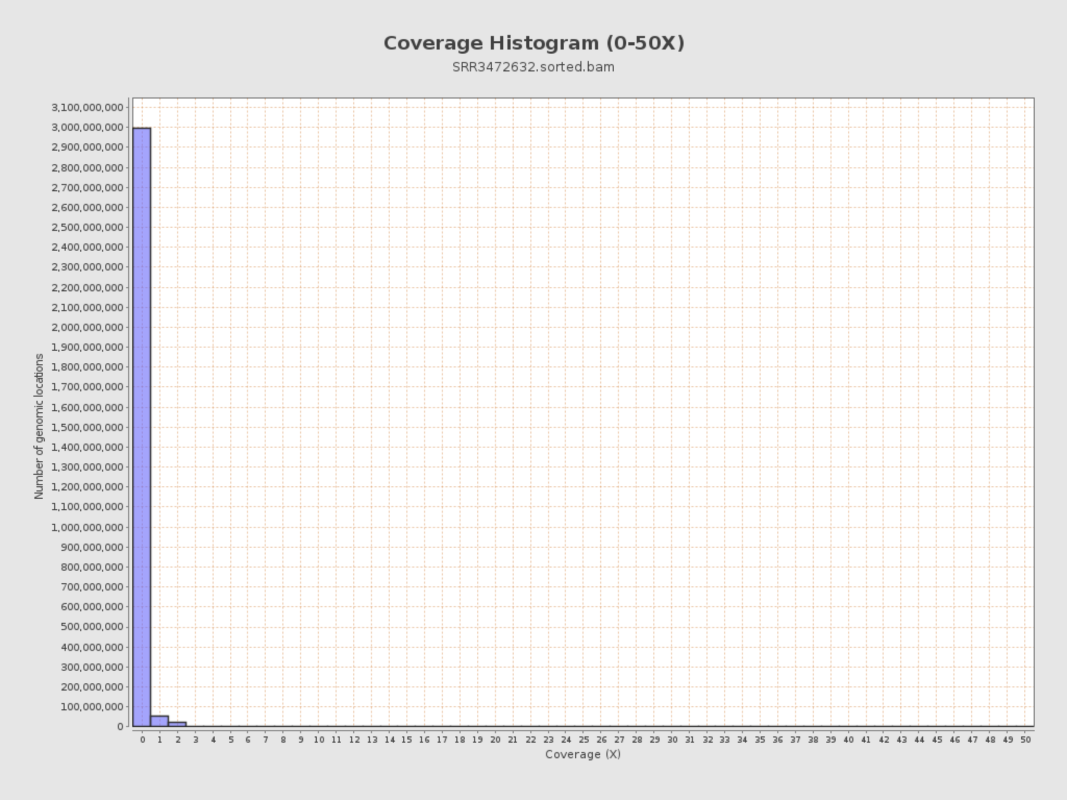
3. Results : Coverage across reference



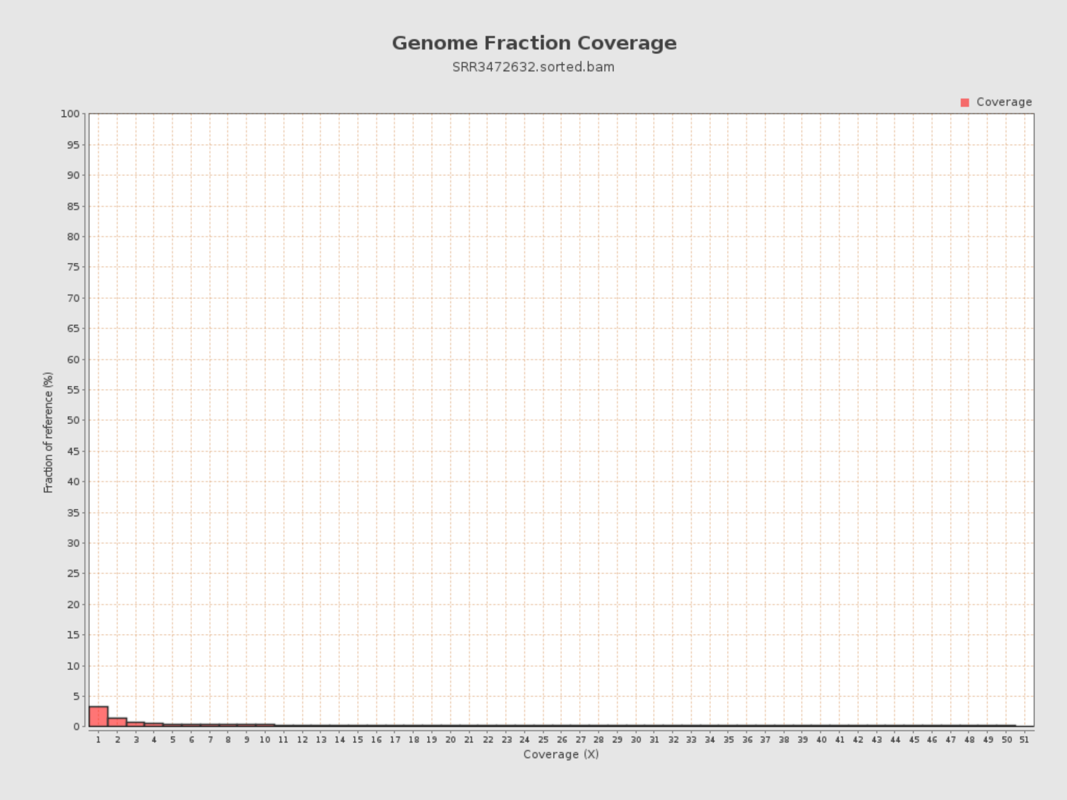
4. Results : Coverage Histogram



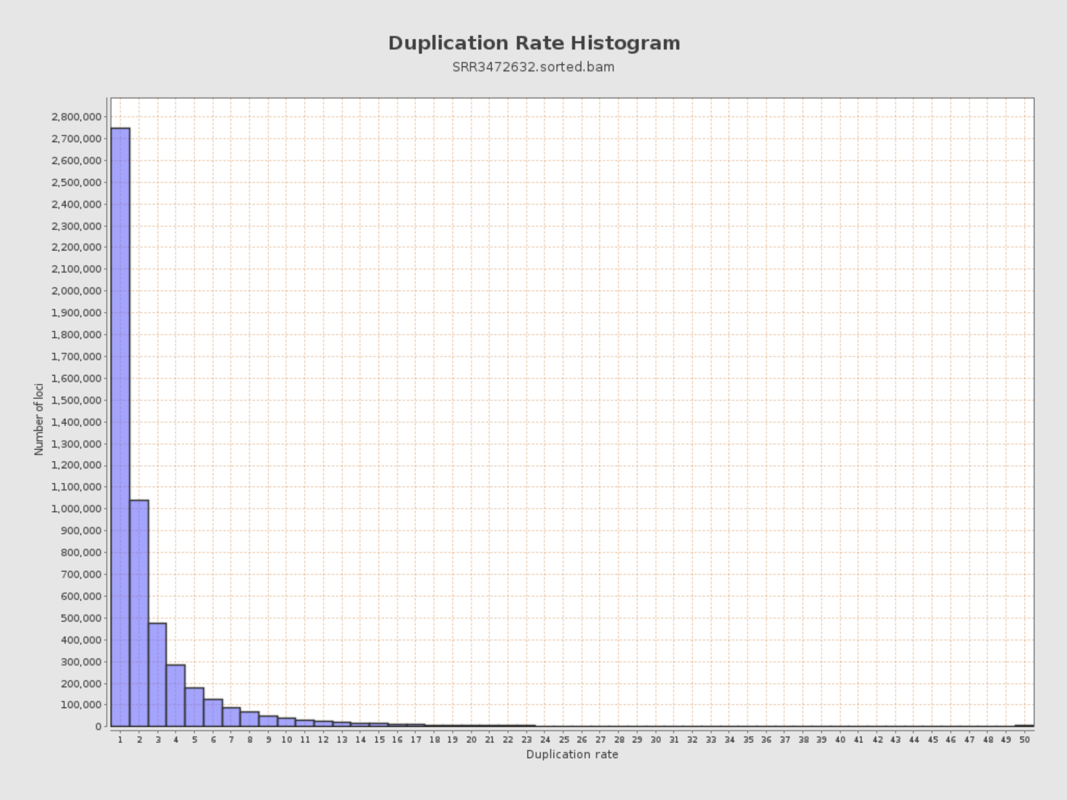
5. Results : Coverage Histogram (0-50X)



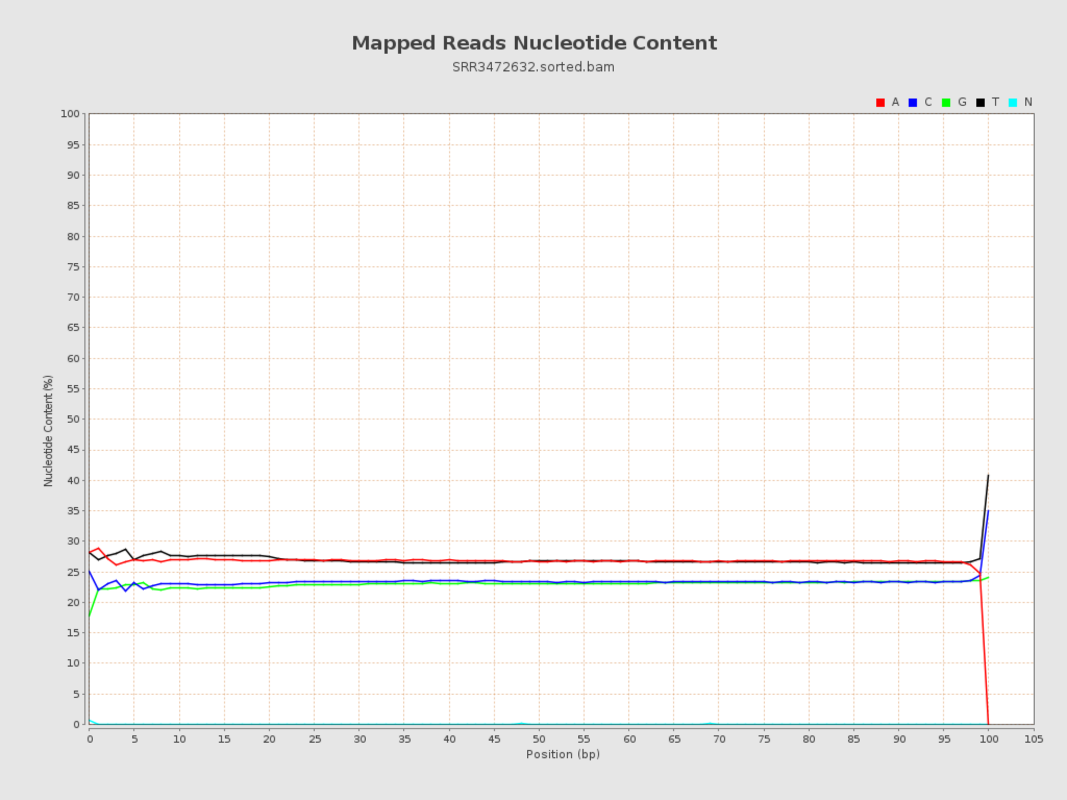
6. Results : Genome Fraction Coverage



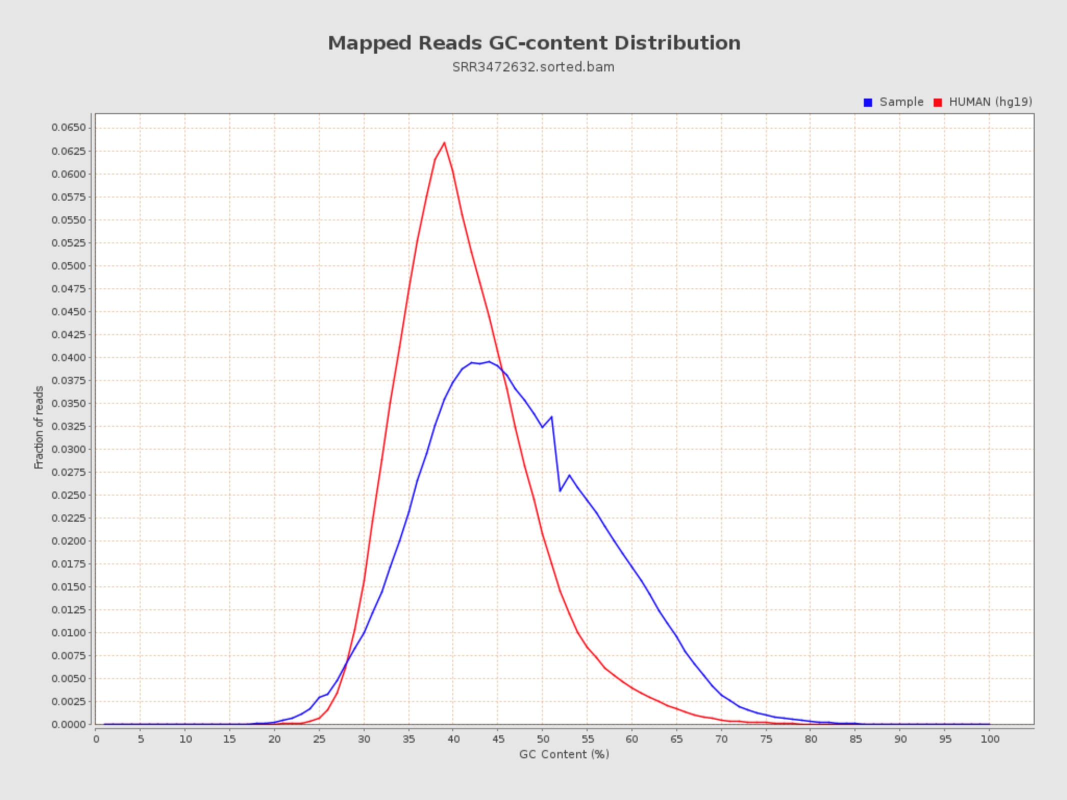
7. Results : Duplication Rate Histogram



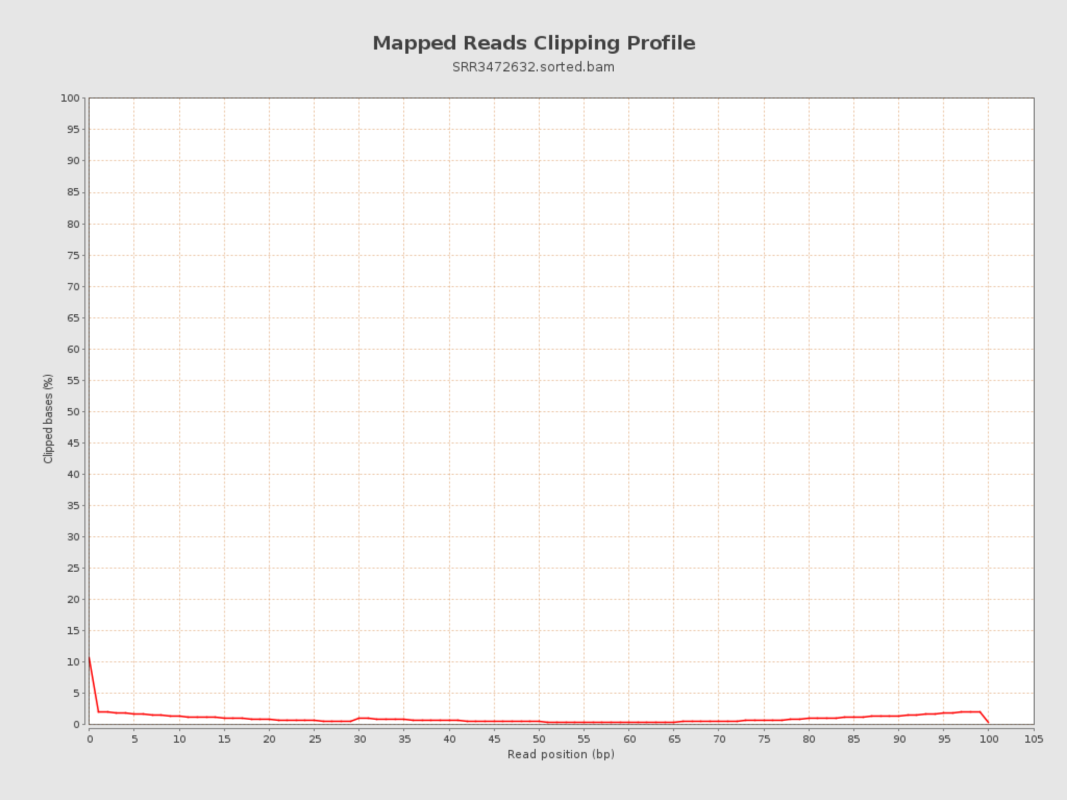
8. Results : Mapped Reads Nucleotide Content



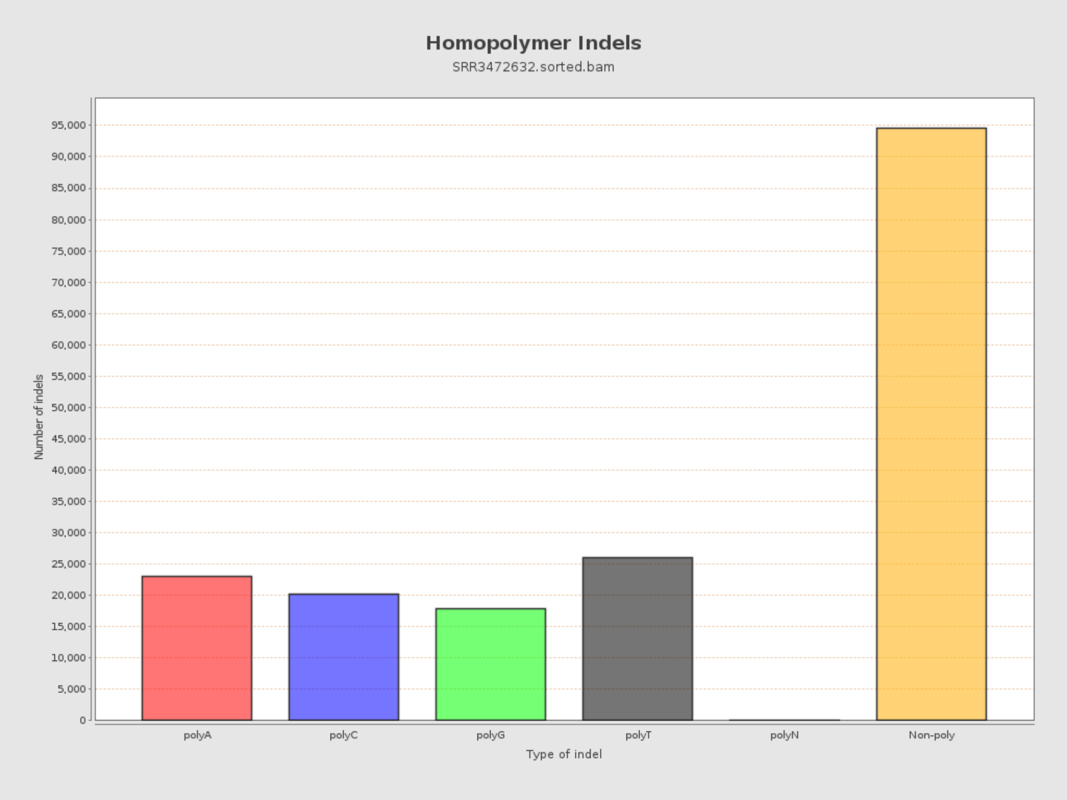
9. Results : Mapped Reads GC-content Distribution



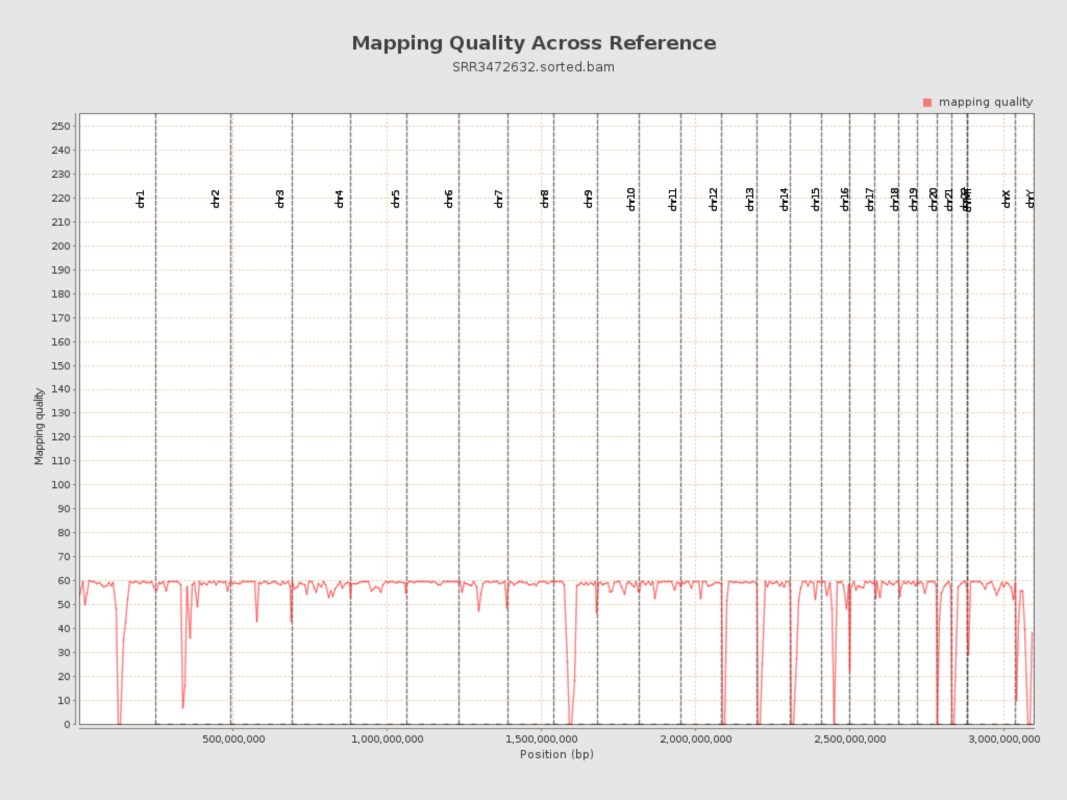
10. Results : Mapped Reads Clipping Profile



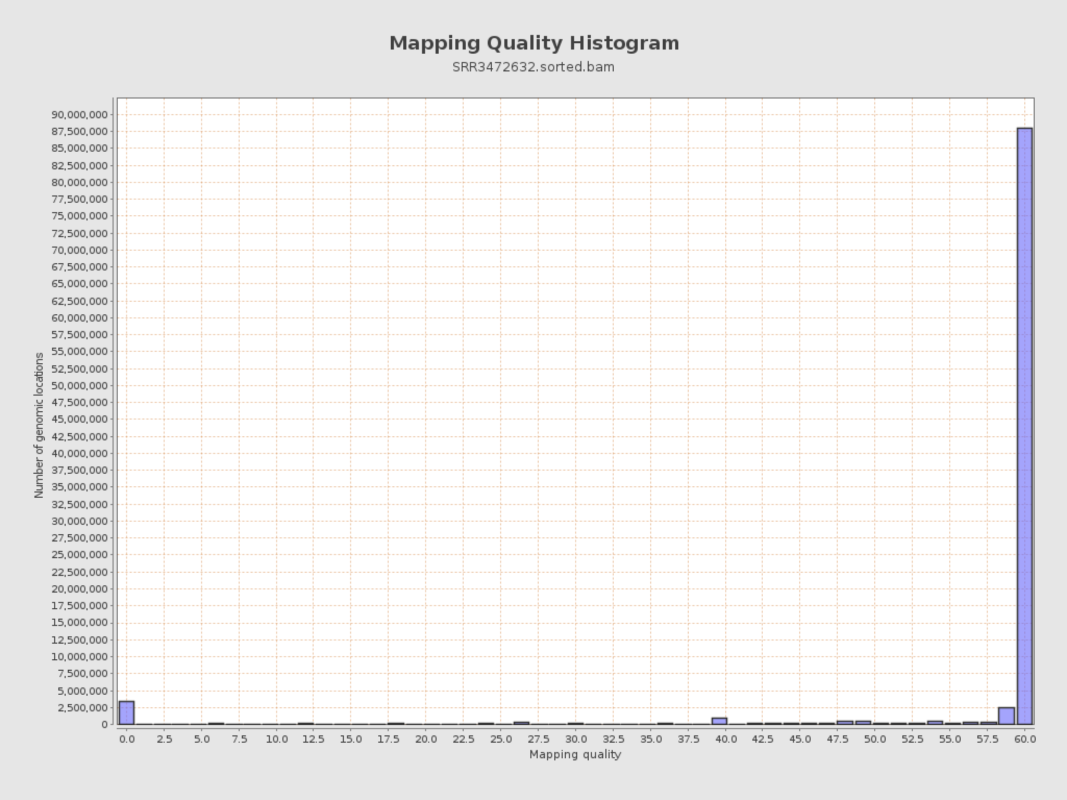
11. Results : Homopolymer Indels



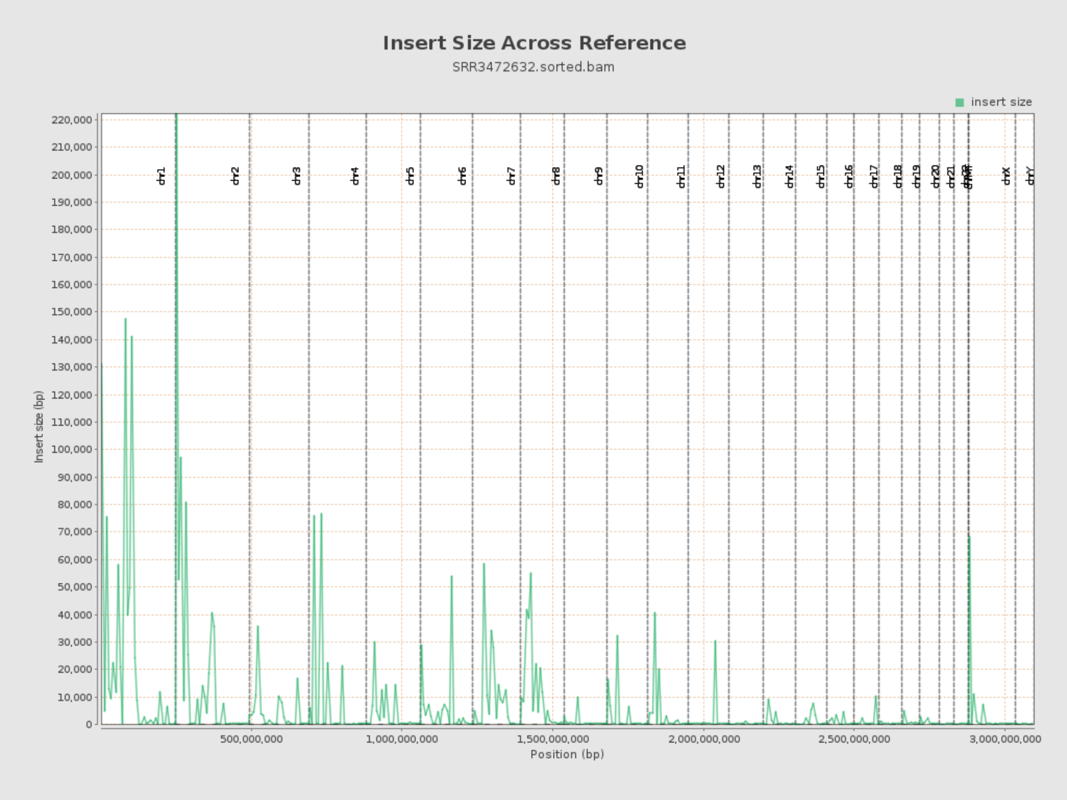
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram