Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:12:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472469.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_SRR3472469 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472469_1.fastq.gz SRR3472469_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:12:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472469.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,725,020
Mapped reads	28,416,494 / 98.93%
Unmapped reads	308,526 / 1.07%
Mapped paired reads	28,416,494 / 98.93%
Mapped reads, first in pair	14,297,539 / 49.77%
Mapped reads, second in pair	14,118,955 / 49.15%
Mapped reads, both in pair	28,193,678 / 98.15%
Mapped reads, singletons	222,816 / 0.78%
Secondary alignments	0
Supplementary alignments	41,177 / 0.14%
Read min/max/mean length	30 / 100 / 99.52
Duplicated reads (estimated)	17,487,972 / 60.88%
Duplication rate	50.72%
Clipped reads	1,232,735 / 4.29%

2.2. ACGT Content

Number/percentage of A's	786,842,251 / 28.07%
Number/percentage of C's	613,741,544 / 21.89%
Number/percentage of T's	793,072,523 / 28.29%
Number/percentage of G's	609,222,511 / 21.73%
Number/percentage of N's	372,471 / 0.01%

GC Percentage	43.63%

2.3. Coverage

Mean	0.9057
Standard Deviation	17.3484

2.4. Mapping Quality

Mean Mapping Quality	54.86

2.5. Insert size

Mean	47,996.2
Standard Deviation	2,190,993.13
P25/Median/P75	172 / 237 / 318

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	14,192,745
Insertions	138,157
Mapped reads with at least one insertion	0.48%
Deletions	170,189
Mapped reads with at least one deletion	0.59%
Homopolymer indels	46.1%

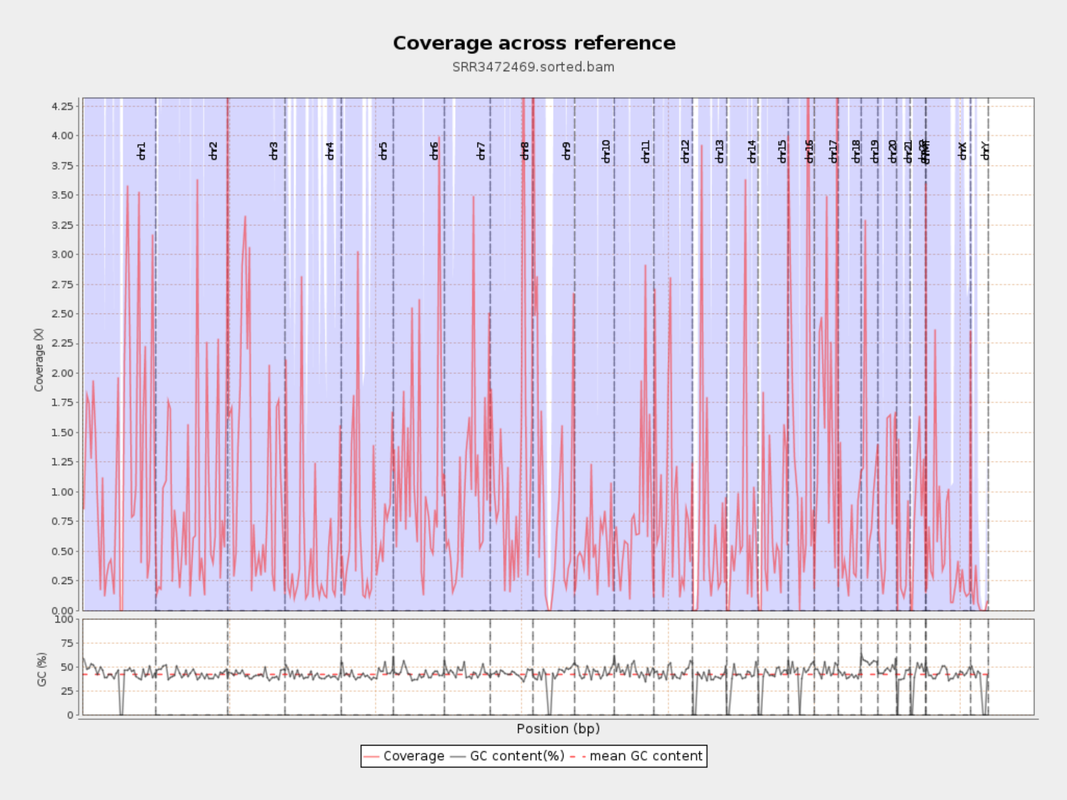
2.7. Chromosome stats

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

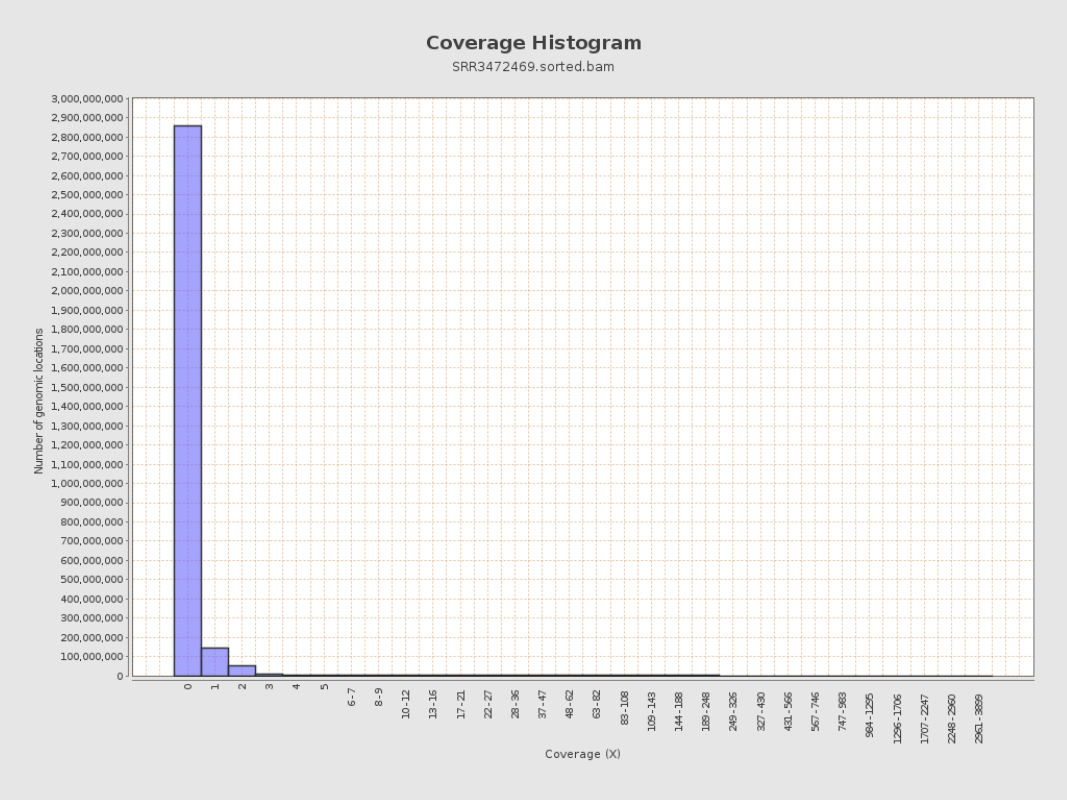
		bases	coverage	deviation
chr1	249250621	304477183	1.2216	20.8153
chr2	243199373	209636888	0.862	17.8178
chr3	198022430	246227568	1.2434	19.1451
chr4	191154276	101863674	0.5329	13.2001
chr5	180915260	133232035	0.7364	15.2173
chr6	171115067	197080459	1.1517	18.1867
chr7	159138663	166509641	1.0463	20.4295
chr8	146364022	165579855	1.1313	19.4534
chr9	141213431	130892366	0.9269	15.4215
chr10	135534747	73972663	0.5458	11.9658
chr11	135006516	109590062	0.8117	16.7671
chr12	133851895	124313517	0.9287	14.9663
chr13	115169878	79463480	0.69	17.7739
chr14	107349540	74860446	0.6974	14.3401
chr15	102531392	69876131	0.6815	15.9474
chr16	90354753	140675889	1.5569	27.3131
chr17	81195210	144159772	1.7755	26.5168
chr18	78077248	44396696	0.5686	11.4489
chr19	59128983	70944953	1.1998	15.8812
chr20	63025520	59245740	0.94	17.5495
chr21	48129895	23663562	0.4917	19.0502
chr22	51304566	45105794	0.8792	18.0924
chrMT	16571	59593	3.5962	2.3817
chrX	155270560	82298872	0.53	8.3391

chrY	59373566	5530235	0.0931	2.6573

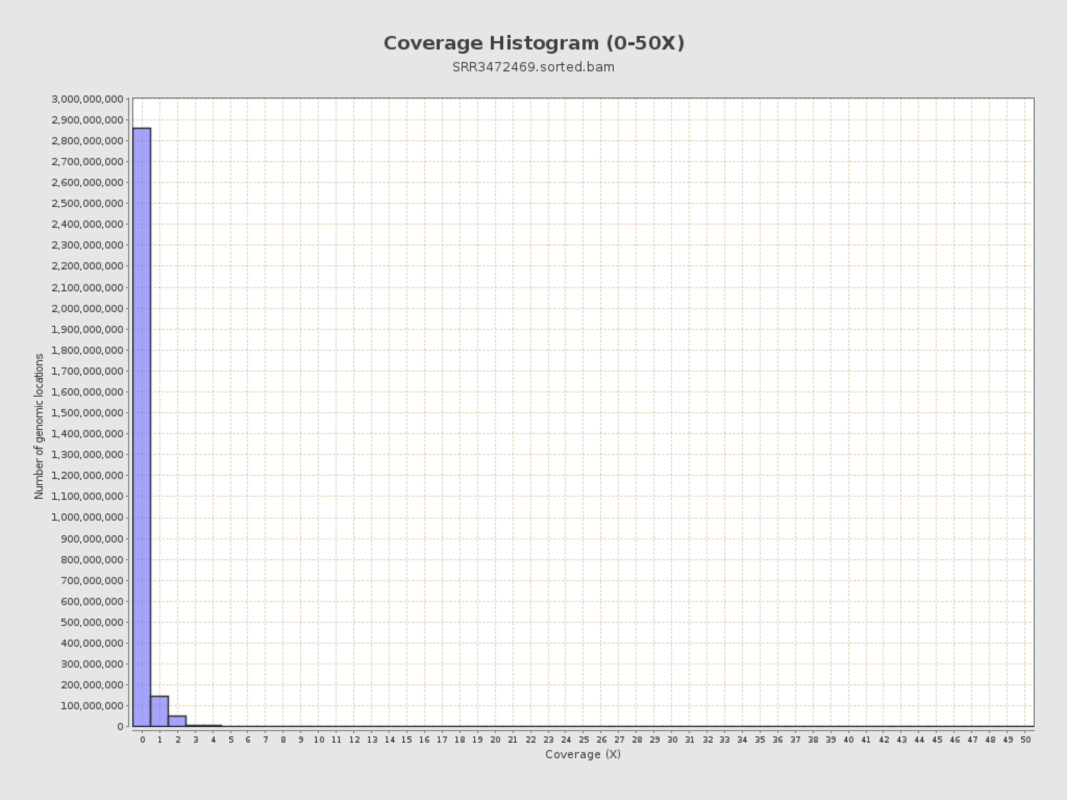
3. Results : Coverage across reference



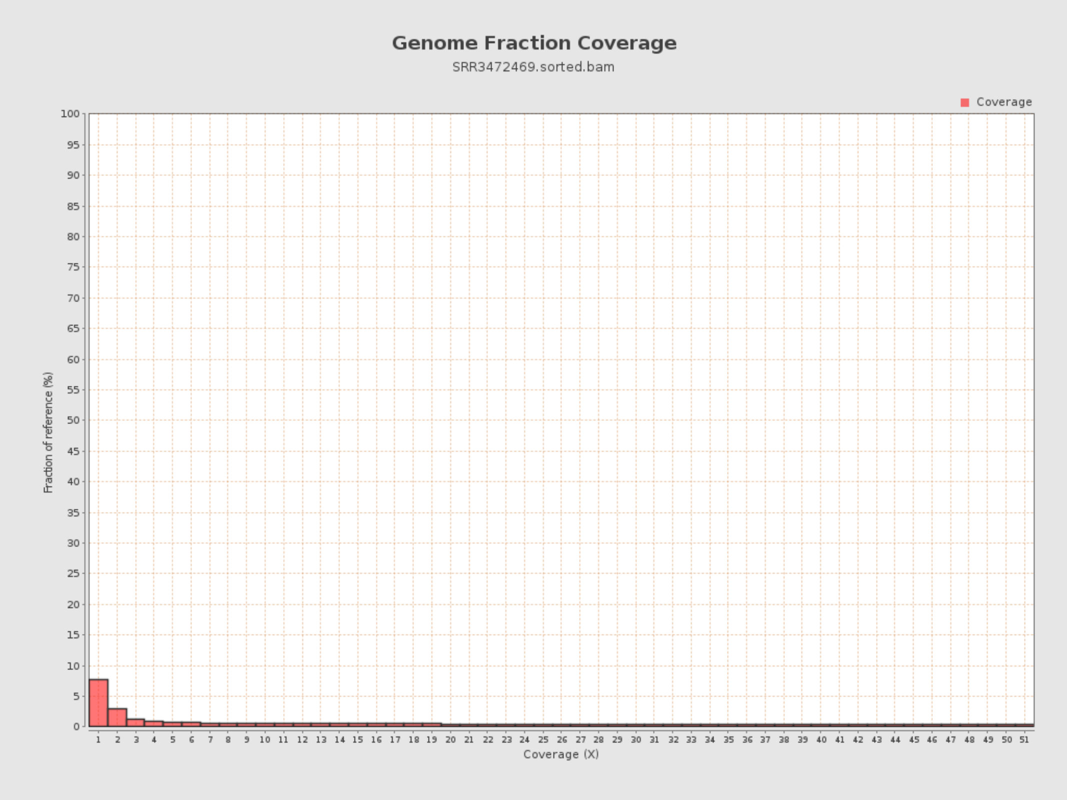
4. Results : Coverage Histogram



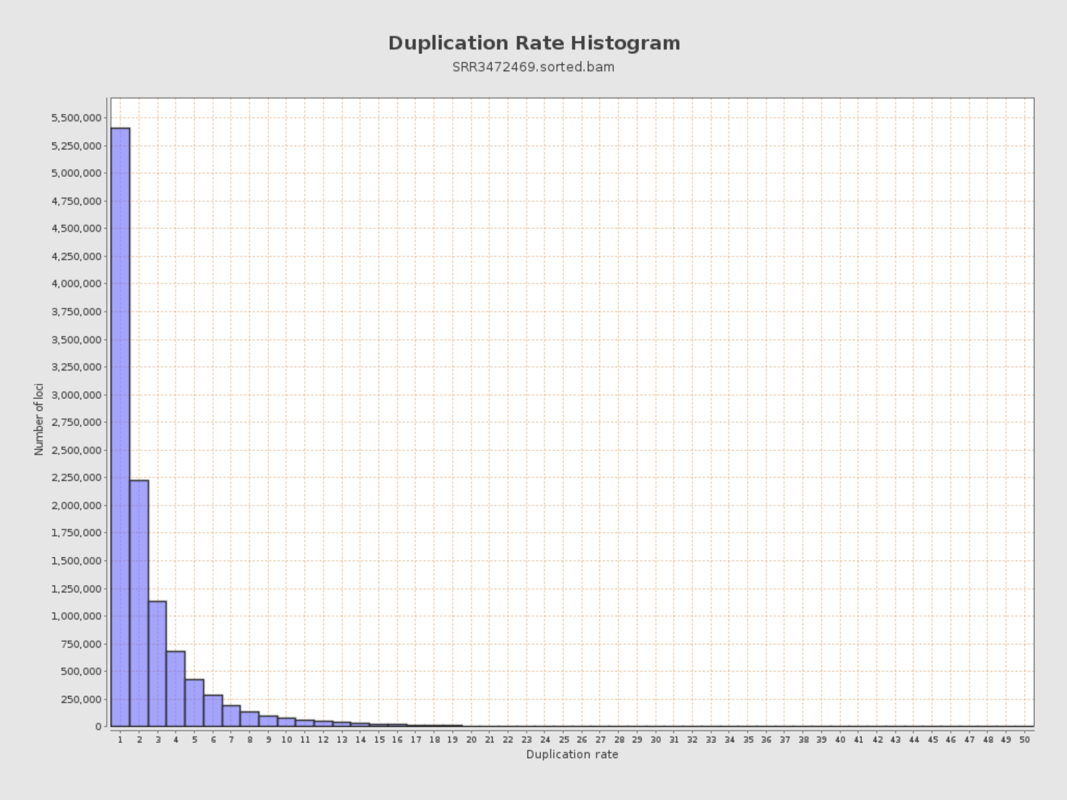
5. Results : Coverage Histogram (0-50X)



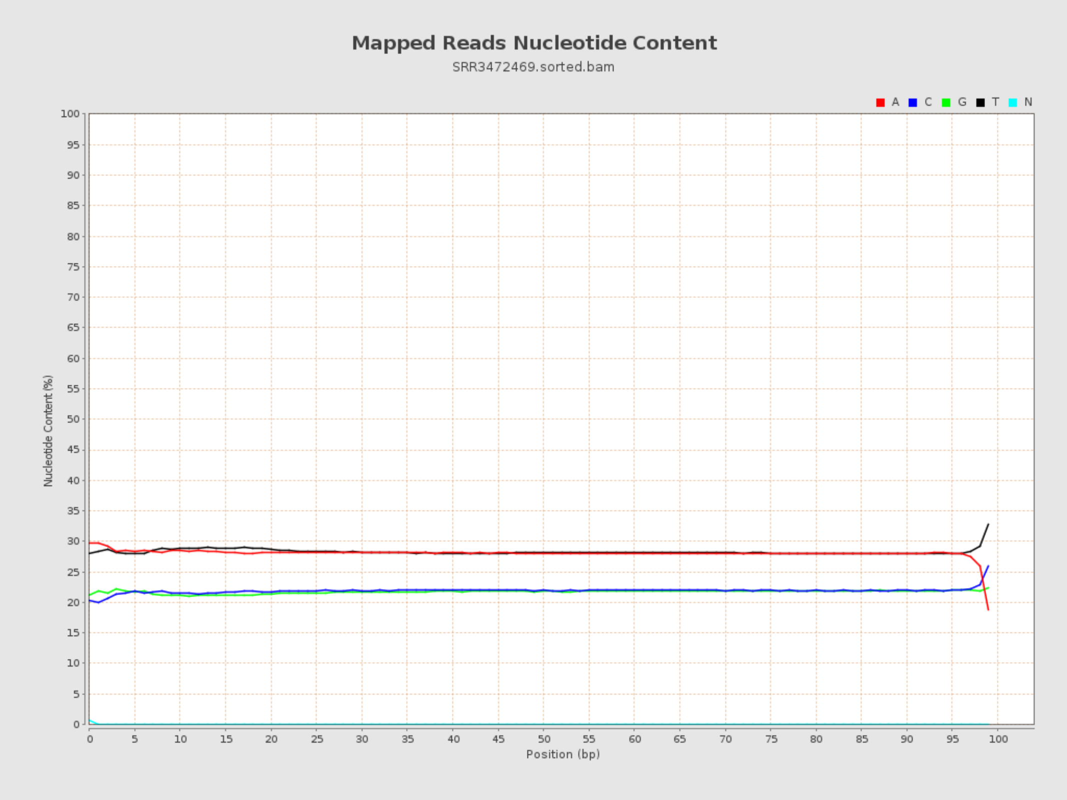
6. Results : Genome Fraction Coverage



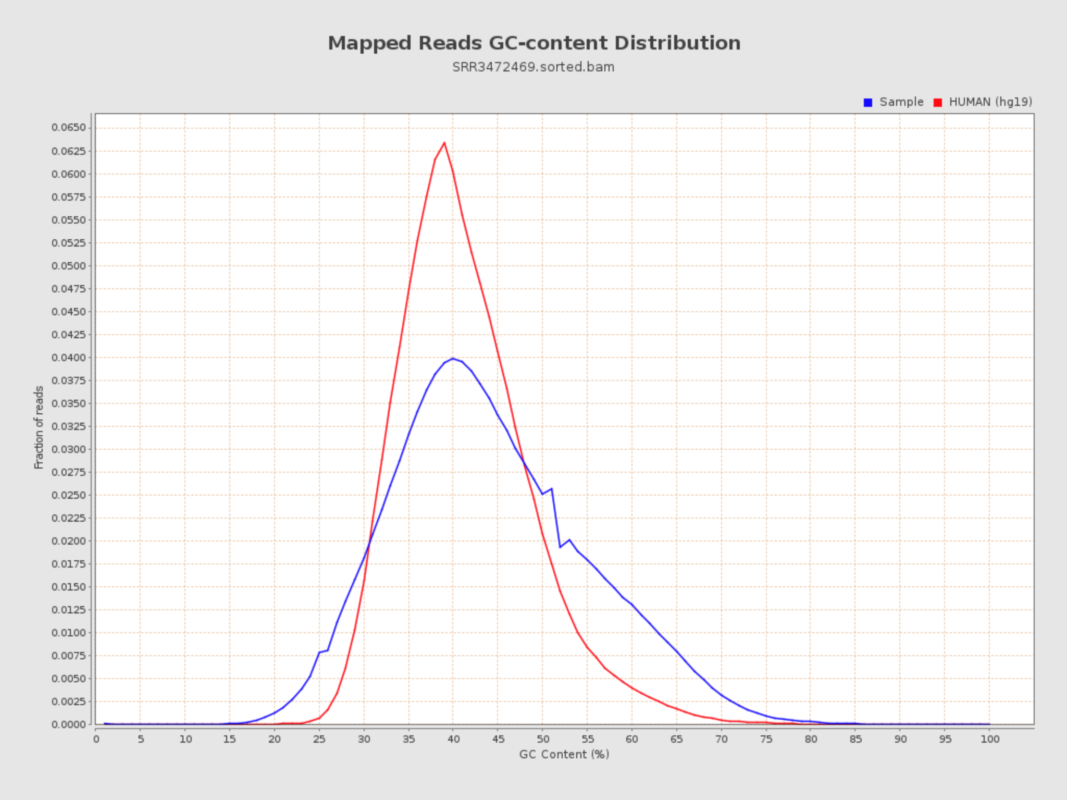
7. Results : Duplication Rate Histogram



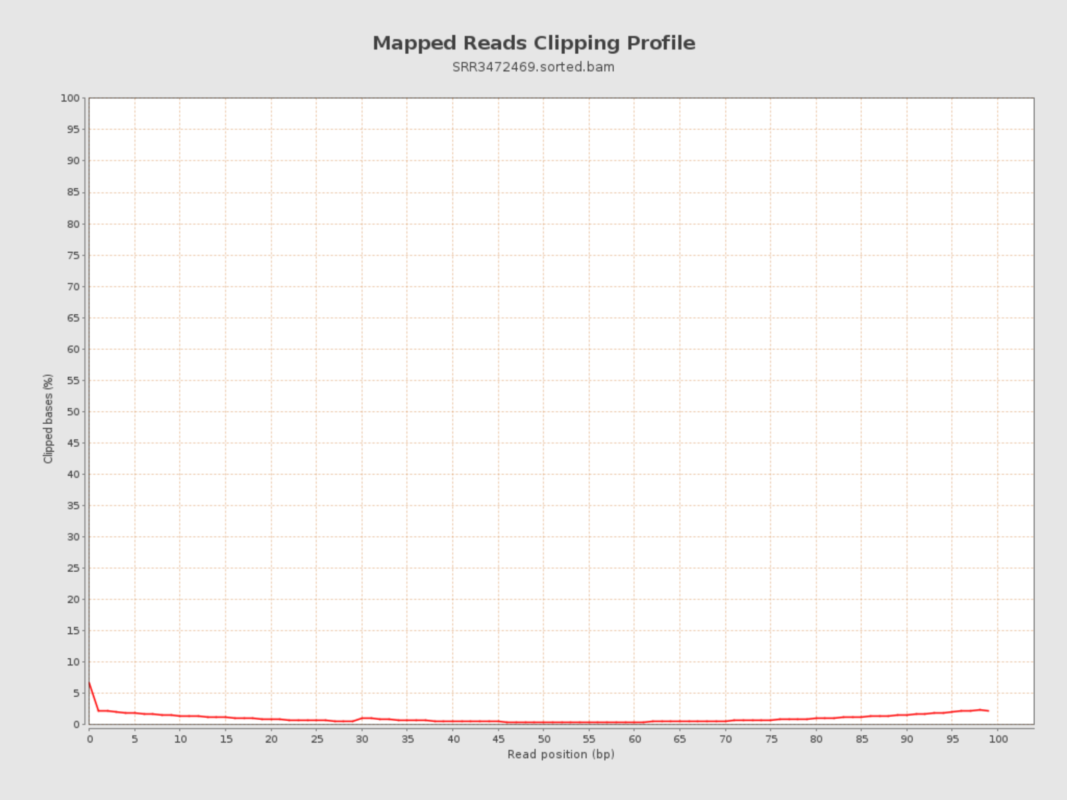
8. Results : Mapped Reads Nucleotide Content



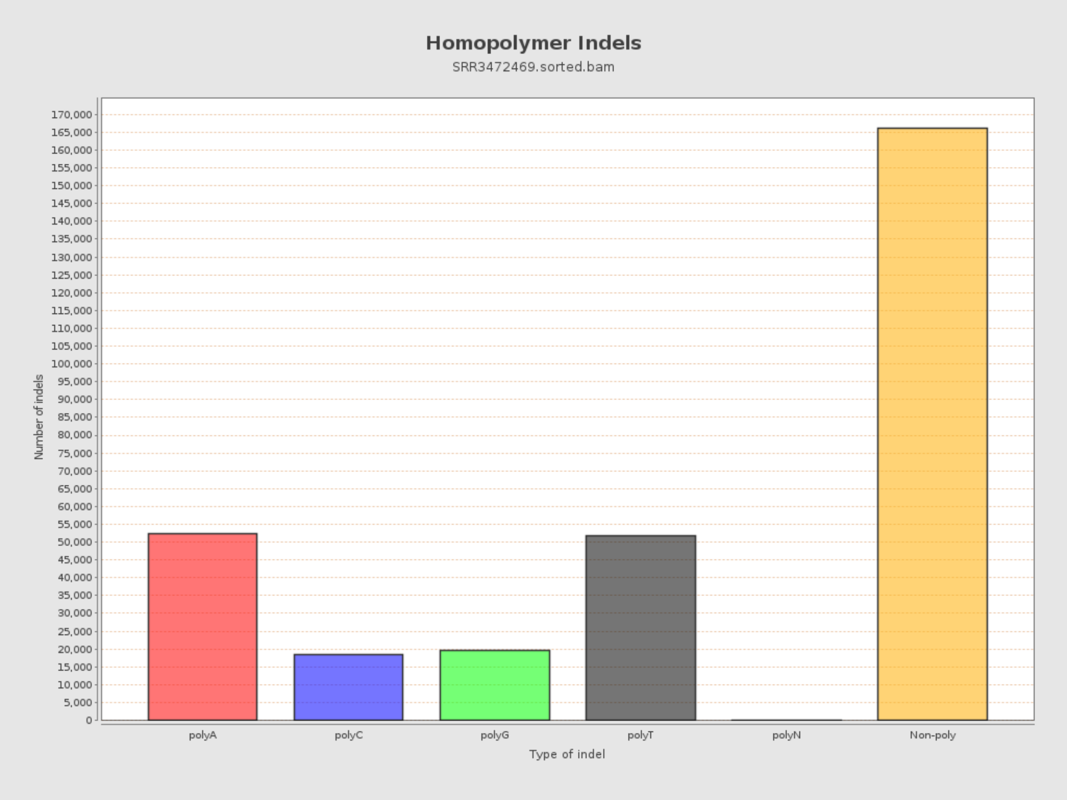
9. Results : Mapped Reads GC-content Distribution



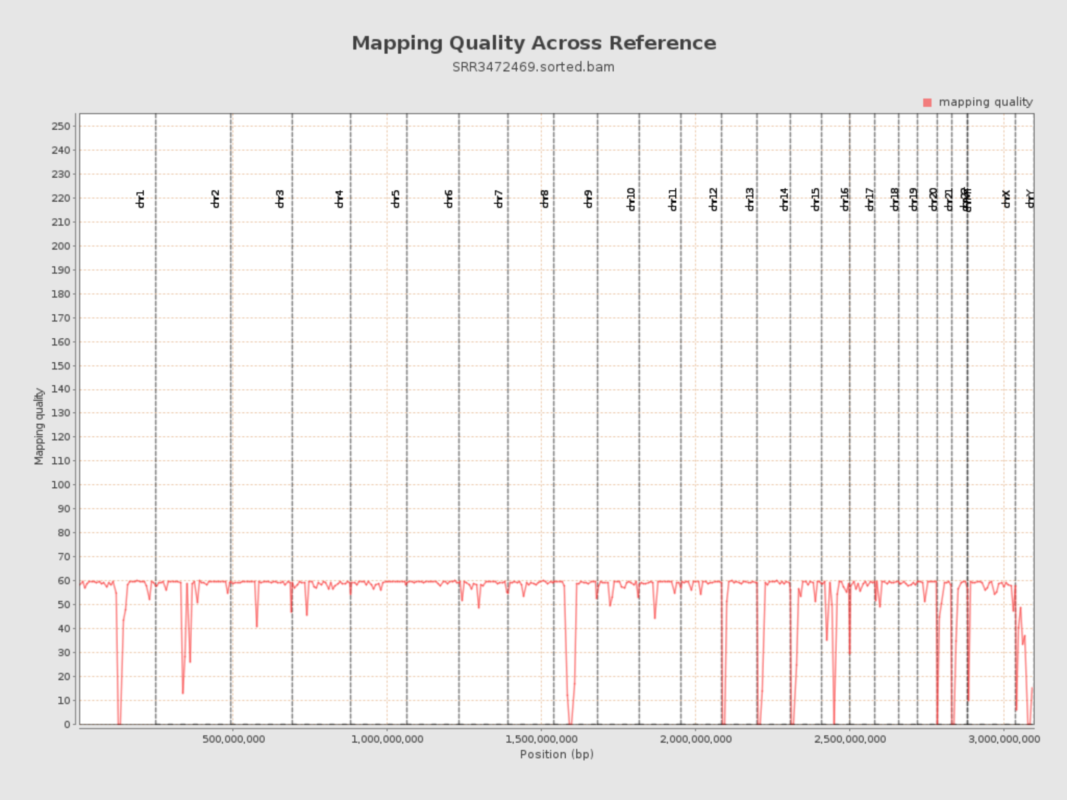
10. Results : Mapped Reads Clipping Profile



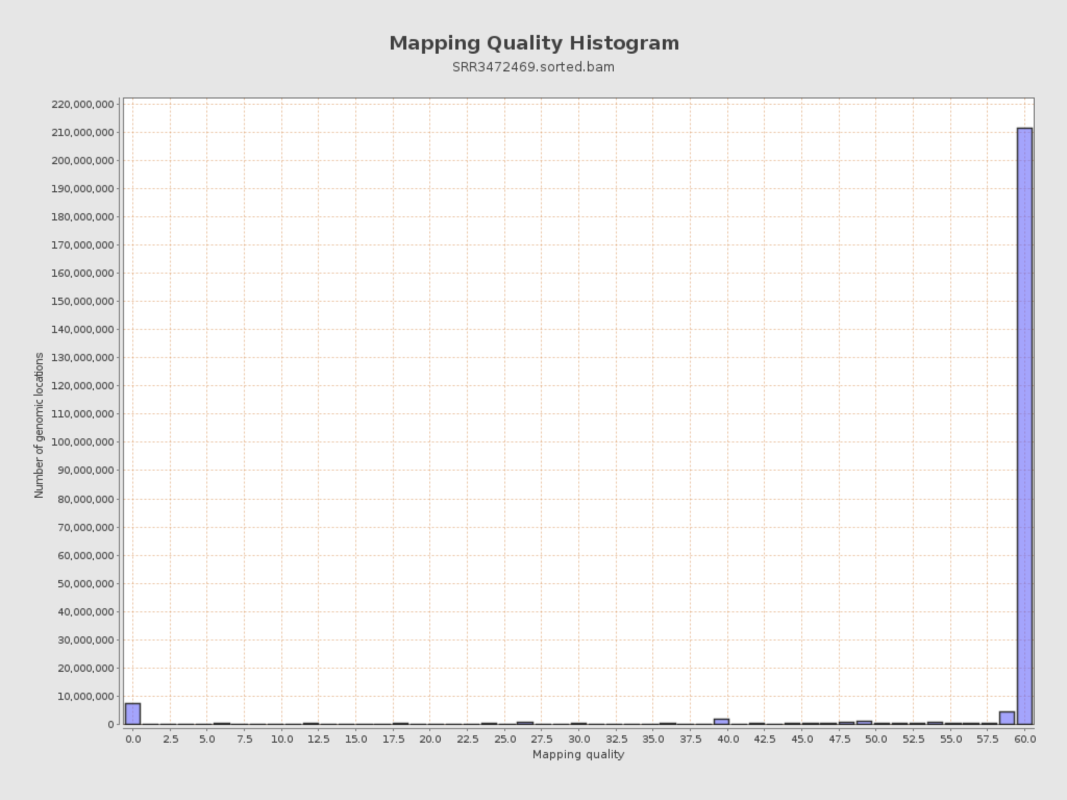
11. Results : Homopolymer Indels



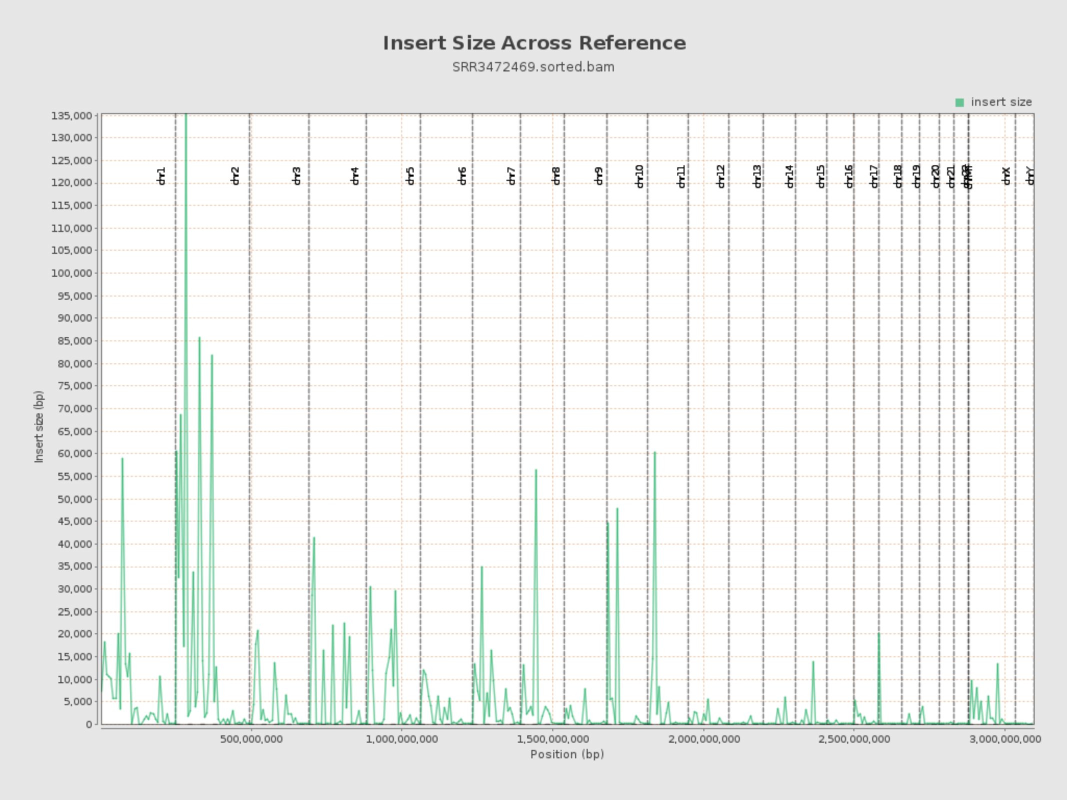
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram