Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 08:54:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472608.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_SRR3472608 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472608_1.fastq.gz SRR3472608_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 08:54:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472608.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,940,304
Mapped reads	14,830,522 / 99.27%
Unmapped reads	109,782 / 0.73%
Mapped paired reads	14,830,522 / 99.27%
Mapped reads, first in pair	7,435,896 / 49.77%
Mapped reads, second in pair	7,394,626 / 49.49%
Mapped reads, both in pair	14,759,558 / 98.79%
Mapped reads, singletons	70,964 / 0.47%
Secondary alignments	0
Supplementary alignments	70,921 / 0.47%
Read min/max/mean length	30 / 101 / 99.59
Duplicated reads (estimated)	9,904,298 / 66.29%
Duplication rate	49.13%
Clipped reads	1,059,482 / 7.09%

2.2. ACGT Content

Number/percentage of A's	391,664,822 / 26.88%
Number/percentage of C's	338,632,784 / 23.24%
Number/percentage of T's	392,166,092 / 26.92%
Number/percentage of G's	334,225,666 / 22.94%
Number/percentage of N's	271,765 / 0.02%

GC Percentage	46.18%

2.3. Coverage

Mean	0.4707
Standard Deviation	19.2138

2.4. Mapping Quality

Mean Mapping Quality	54.76

2.5. Insert size

Mean	21,126.13
Standard Deviation	1,470,302.39
P25/Median/P75	148 / 204 / 275

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	8,496,896
Insertions	82,228
Mapped reads with at least one insertion	0.55%
Deletions	78,121
Mapped reads with at least one deletion	0.52%
Homopolymer indels	44.93%

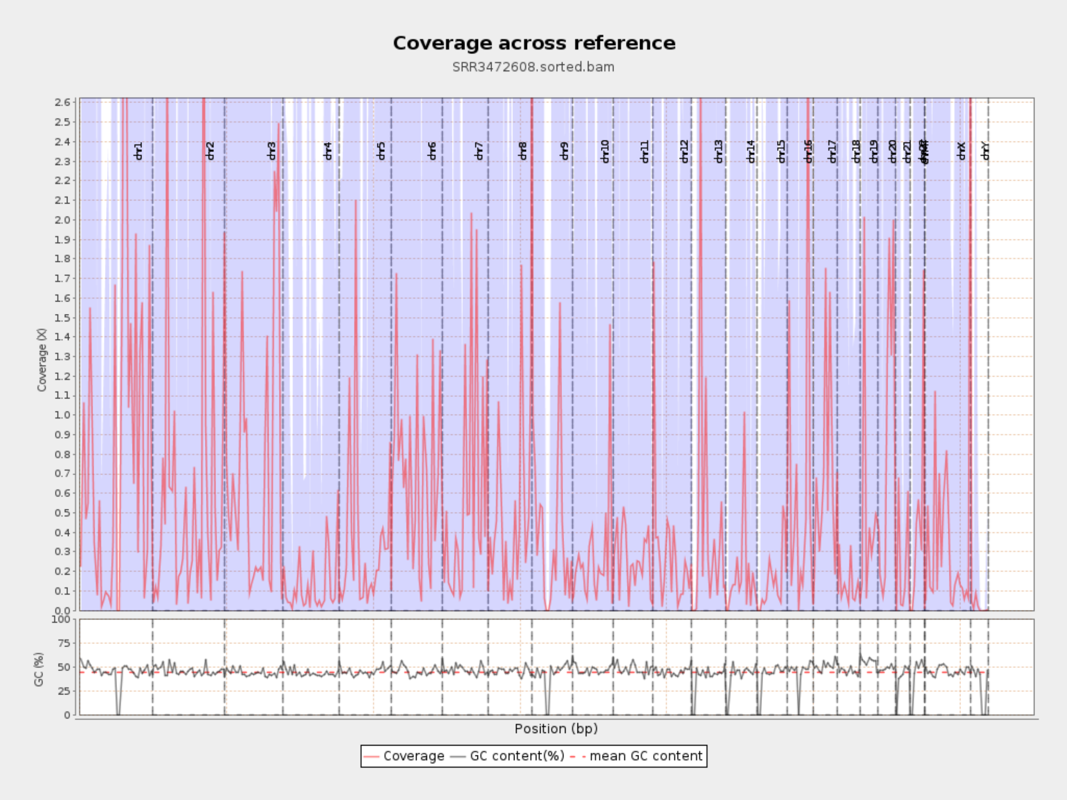
2.7. Chromosome stats

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

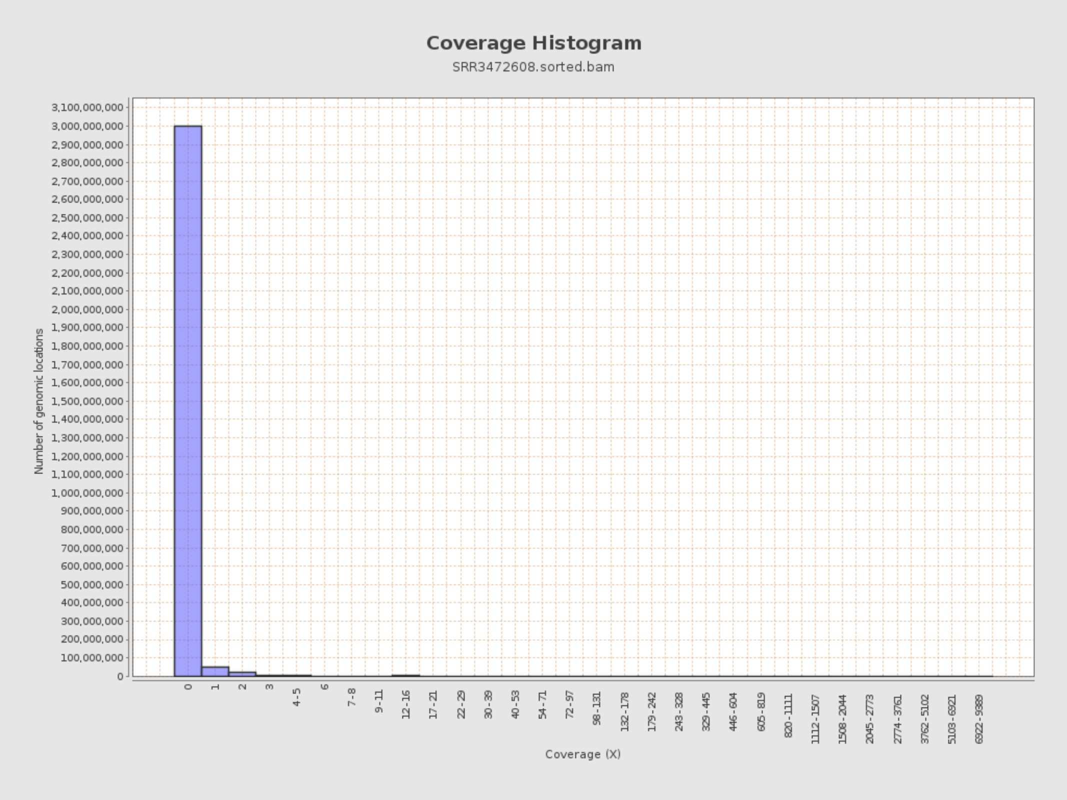
		bases	coverage	deviation
chr1	249250621	222061621	0.8909	26.5452
chr2	243199373	145842253	0.5997	31.1956
chr3	198022430	148218004	0.7485	25.7535
chr4	191154276	24705985	0.1292	6.6525
chr5	180915260	64490709	0.3565	12.1982
chr6	171115067	122603933	0.7165	20.0211
chr7	159138663	93356634	0.5866	26.3288
chr8	146364022	70540872	0.482	17.3251
chr9	141213431	59568292	0.4218	14.0066
chr10	135534747	36968923	0.2728	12.5471
chr11	135006516	36493908	0.2703	11.0764
chr12	133851895	41276984	0.3084	11.2512
chr13	115169878	51449332	0.4467	17.7317
chr14	107349540	19135038	0.1782	7.003
chr15	102531392	16407607	0.16	7.9842
chr16	90354753	60010194	0.6642	25.2237
chr17	81195210	56314314	0.6936	20.3288
chr18	78077248	10592933	0.1357	4.8881
chr19	59128983	30585422	0.5173	14.8563
chr20	63025520	56408693	0.895	27.3185
chr21	48129895	11758498	0.2443	13.5915
chr22	51304566	24724922	0.4819	24.6454
chrMT	16571	2211	0.1334	0.4592
chrX	155270560	52401190	0.3375	10.4999

chrY	59373566	1248190	0.021	1.1395

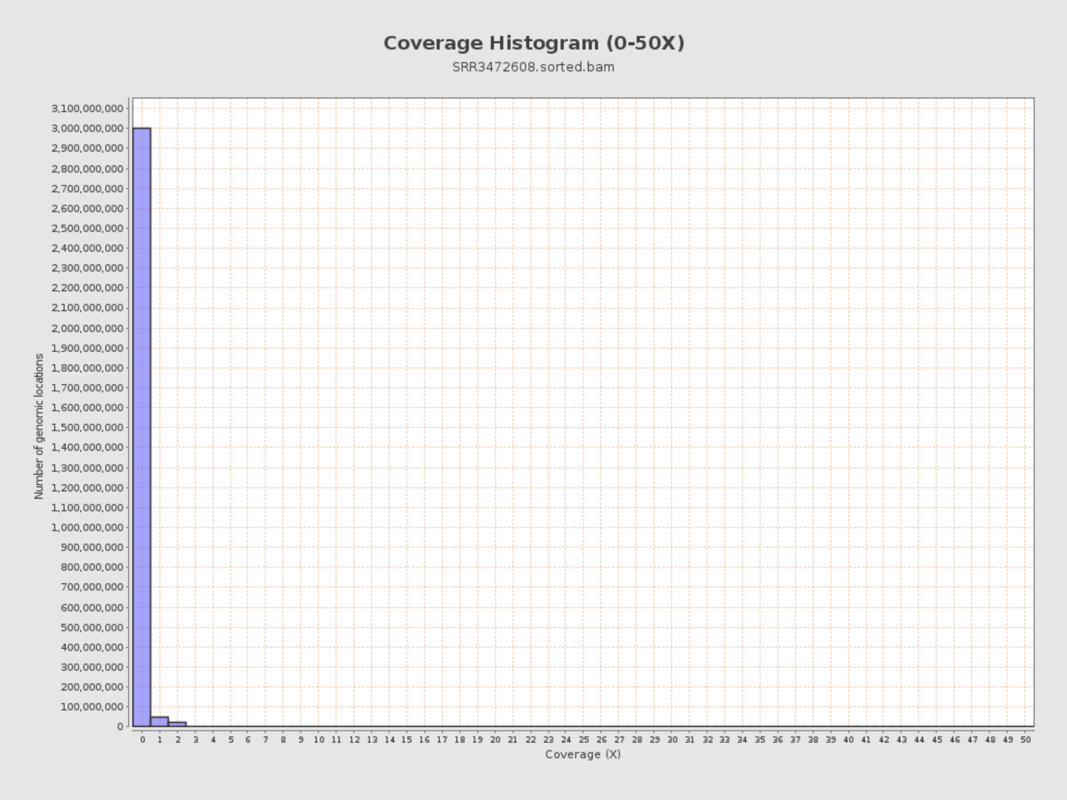
3. Results : Coverage across reference



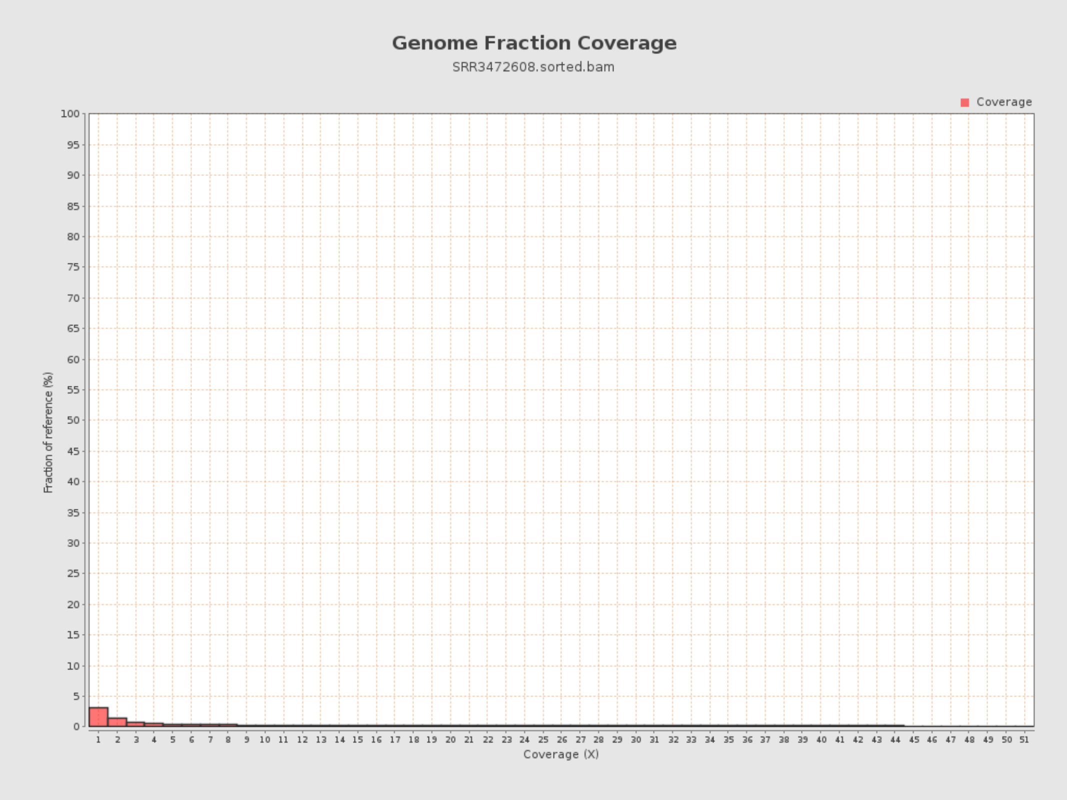
4. Results : Coverage Histogram



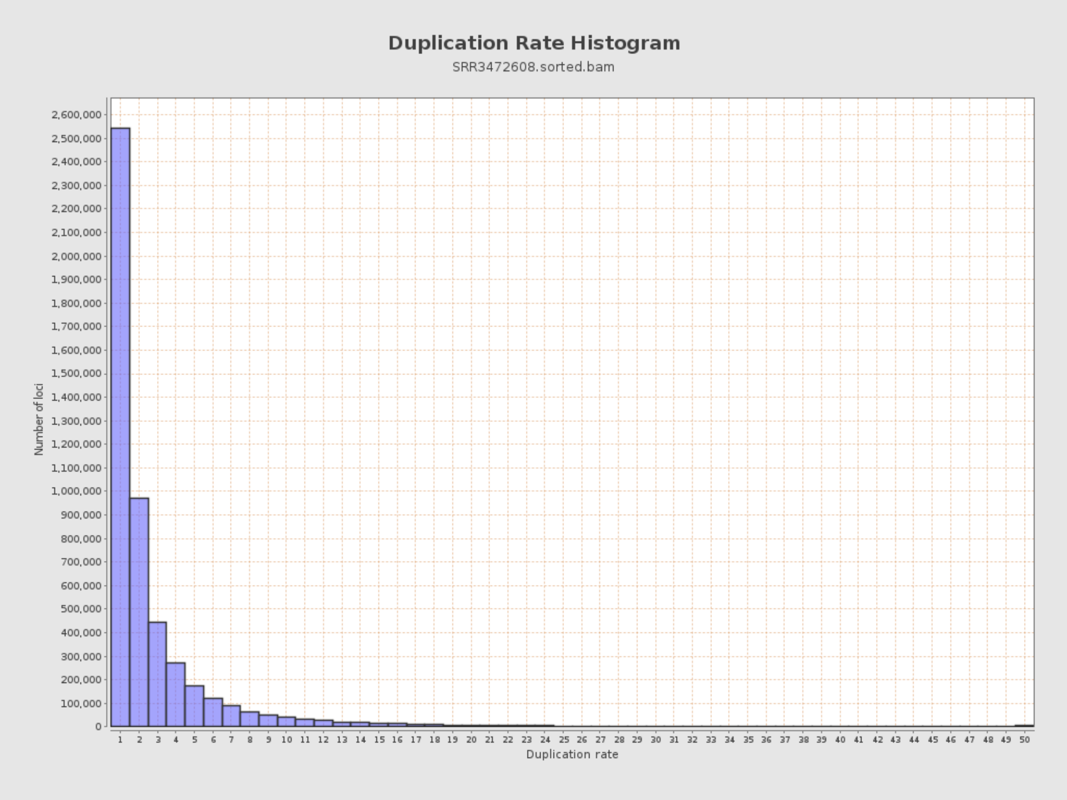
5. Results : Coverage Histogram (0-50X)



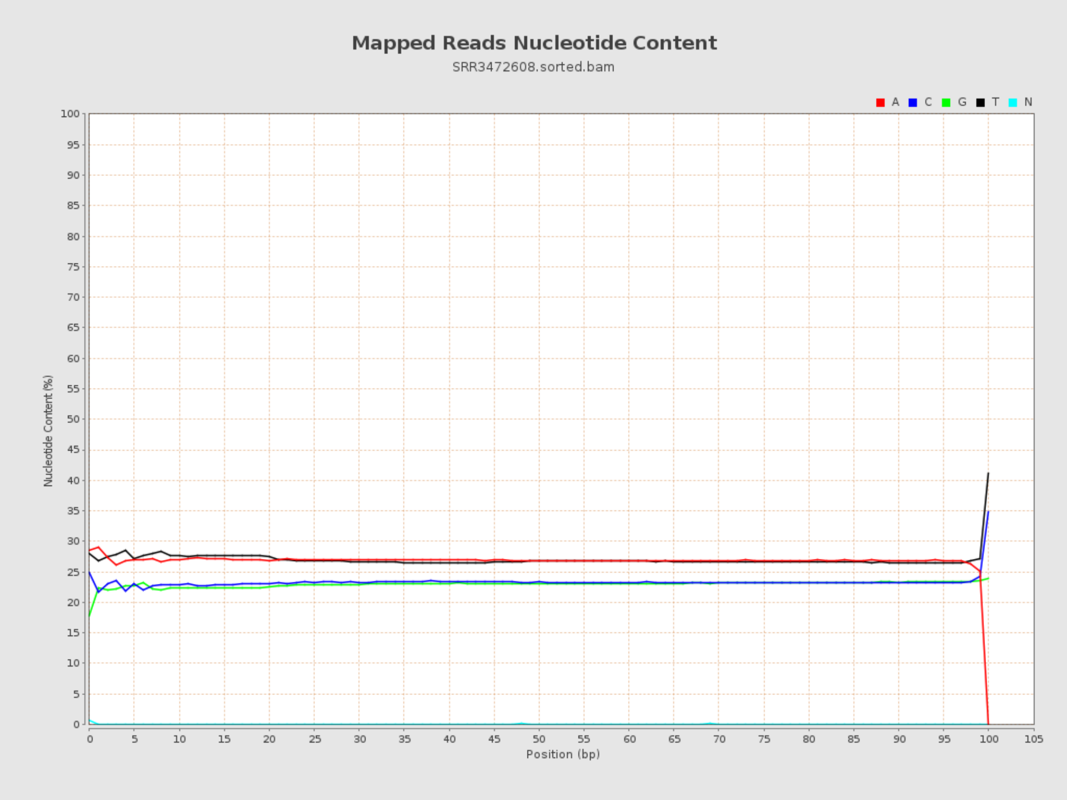
6. Results : Genome Fraction Coverage



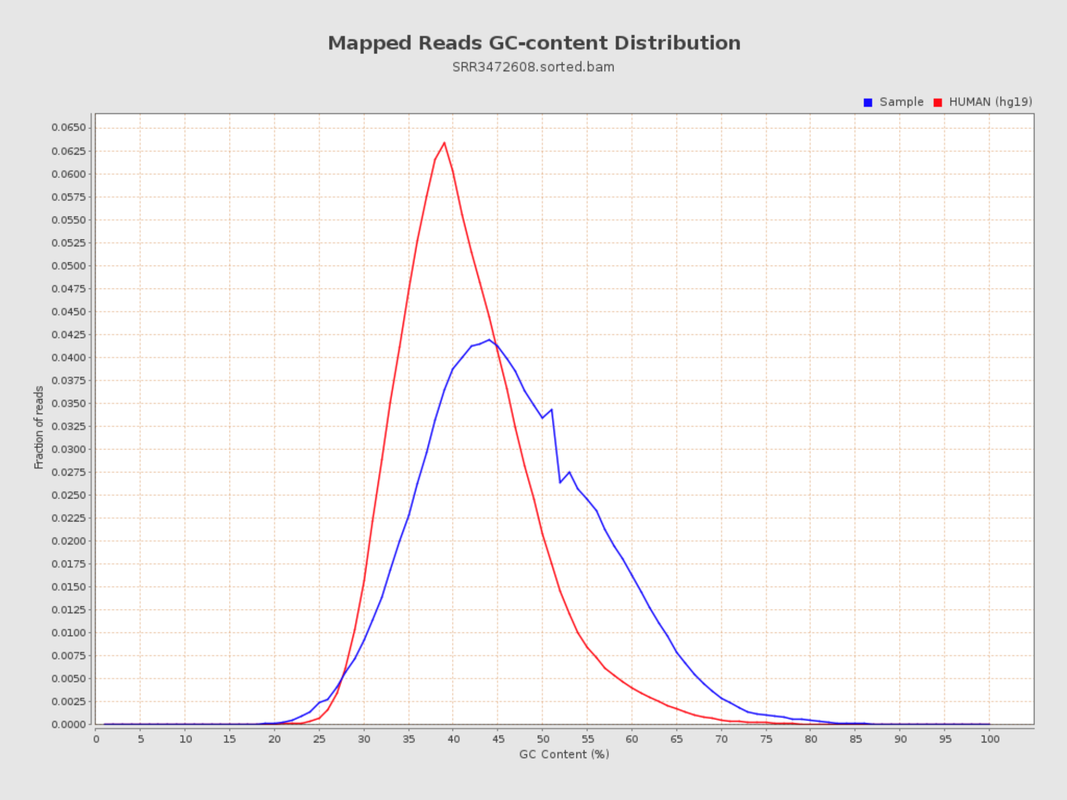
7. Results : Duplication Rate Histogram



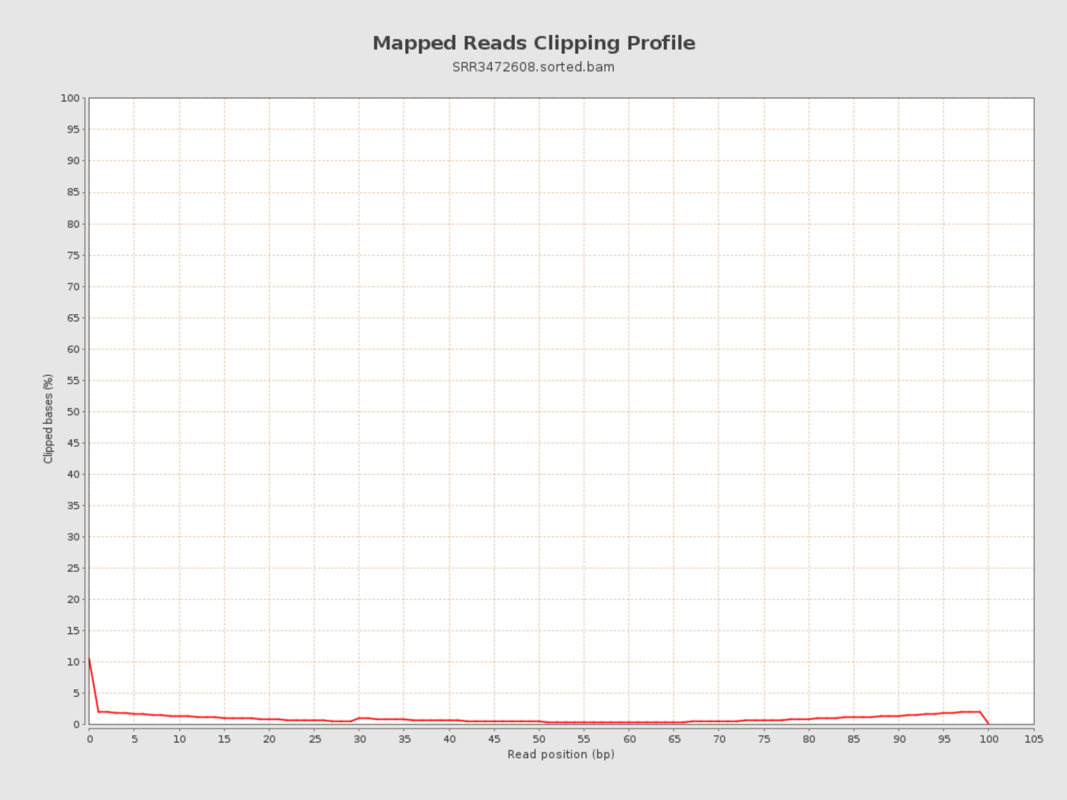
8. Results : Mapped Reads Nucleotide Content



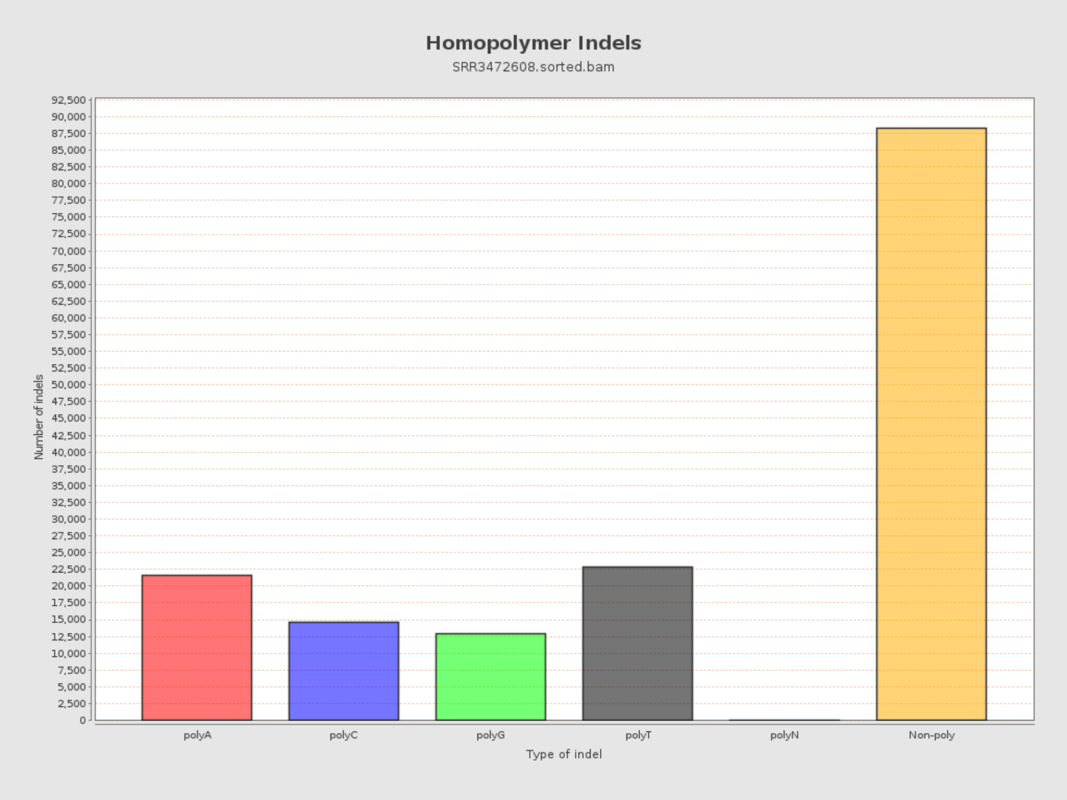
9. Results : Mapped Reads GC-content Distribution



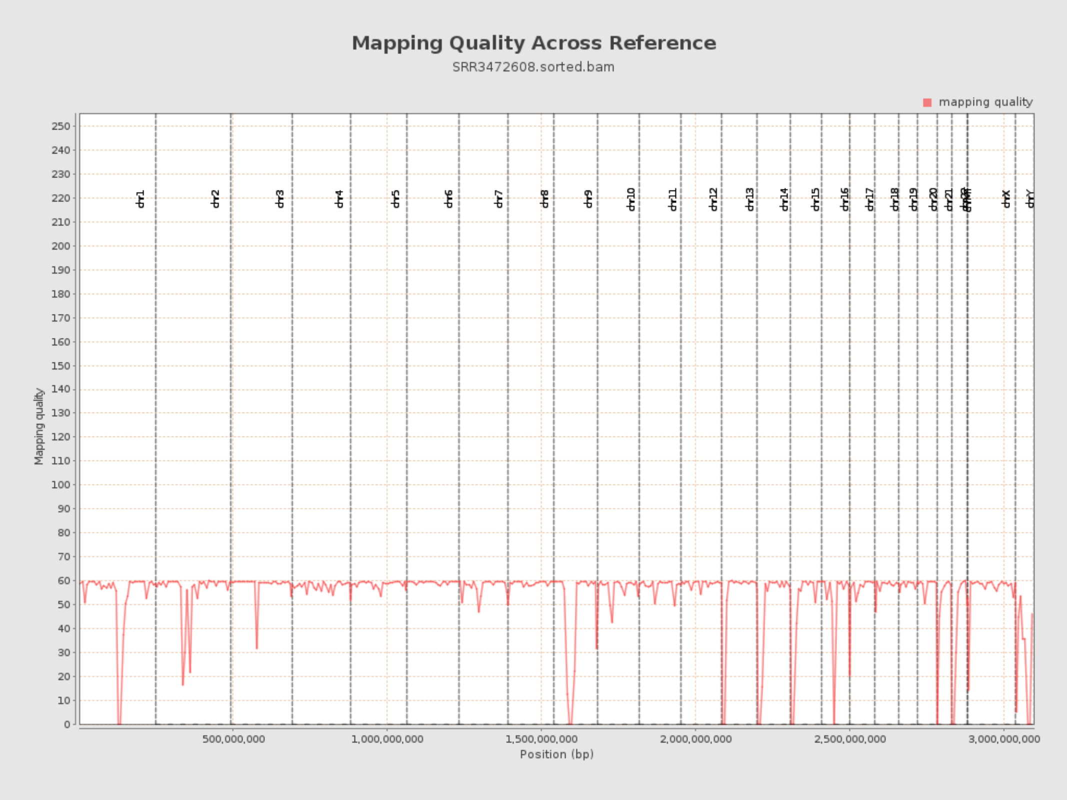
10. Results : Mapped Reads Clipping Profile



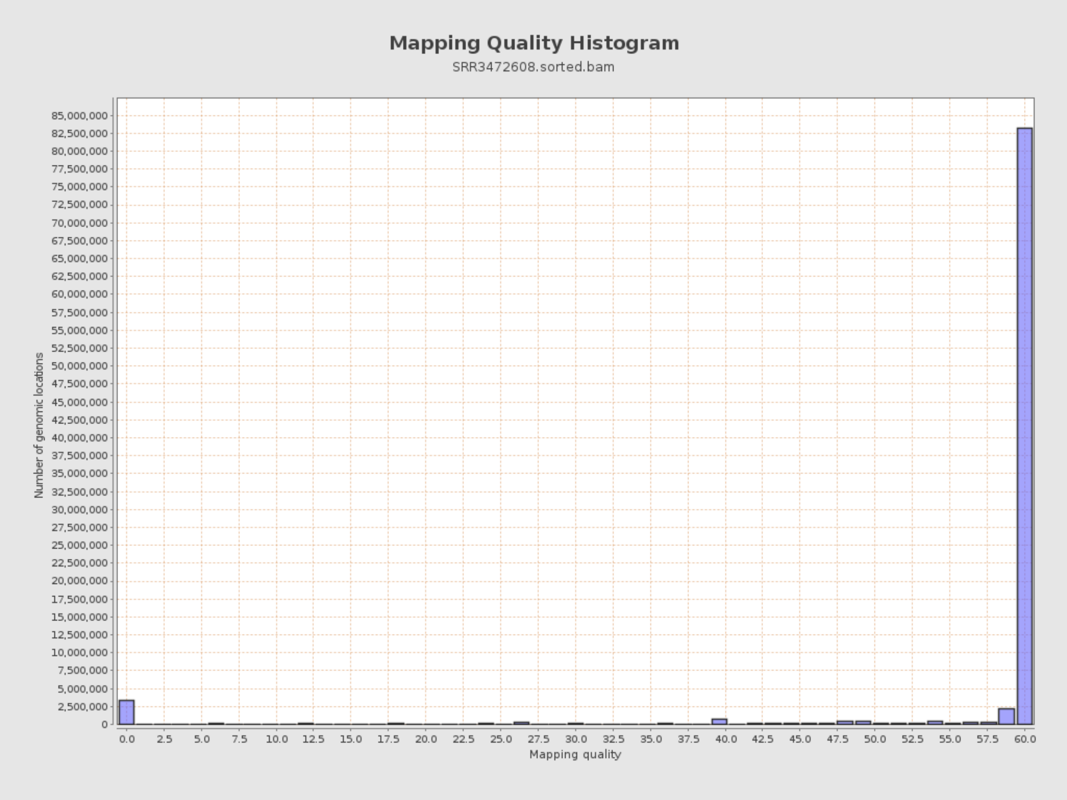
11. Results : Homopolymer Indels



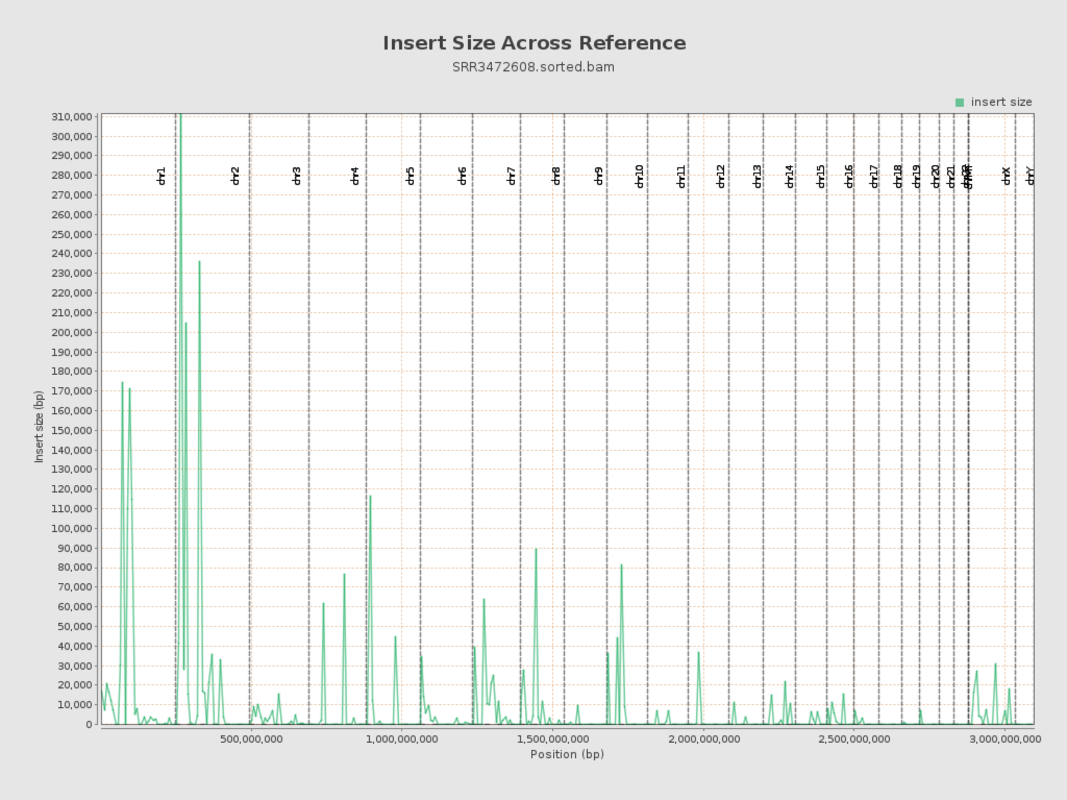
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram