Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 20:29:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472644.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_SRR3472644 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472644_1.fastq.gz SRR3472644_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 20:29:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472644.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,698,970
Mapped reads	9,615,790 / 99.14%
Unmapped reads	83,180 / 0.86%
Mapped paired reads	9,615,790 / 99.14%
Mapped reads, first in pair	4,814,293 / 49.64%
Mapped reads, second in pair	4,801,497 / 49.51%
Mapped reads, both in pair	9,564,072 / 98.61%
Mapped reads, singletons	51,718 / 0.53%
Secondary alignments	0
Supplementary alignments	49,136 / 0.51%
Read min/max/mean length	30 / 101 / 99.28
Duplicated reads (estimated)	6,376,742 / 65.75%
Duplication rate	42.93%
Clipped reads	624,785 / 6.44%

2.2. ACGT Content

Number/percentage of A's	259,259,561 / 27.51%
Number/percentage of C's	213,364,461 / 22.64%
Number/percentage of T's	260,099,774 / 27.6%
Number/percentage of G's	209,458,475 / 22.23%
Number/percentage of N's	122,181 / 0.01%

GC Percentage	44.87%

2.3. Coverage

Mean	0.3044
Standard Deviation	18.2946

2.4. Mapping Quality

Mean Mapping Quality	54.62

2.5. Insert size

Mean	21,500.76
Standard Deviation	1,435,704.67
P25/Median/P75	144 / 197 / 261

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	7,056,873
Insertions	60,061
Mapped reads with at least one insertion	0.62%
Deletions	58,084
Mapped reads with at least one deletion	0.58%
Homopolymer indels	45.81%

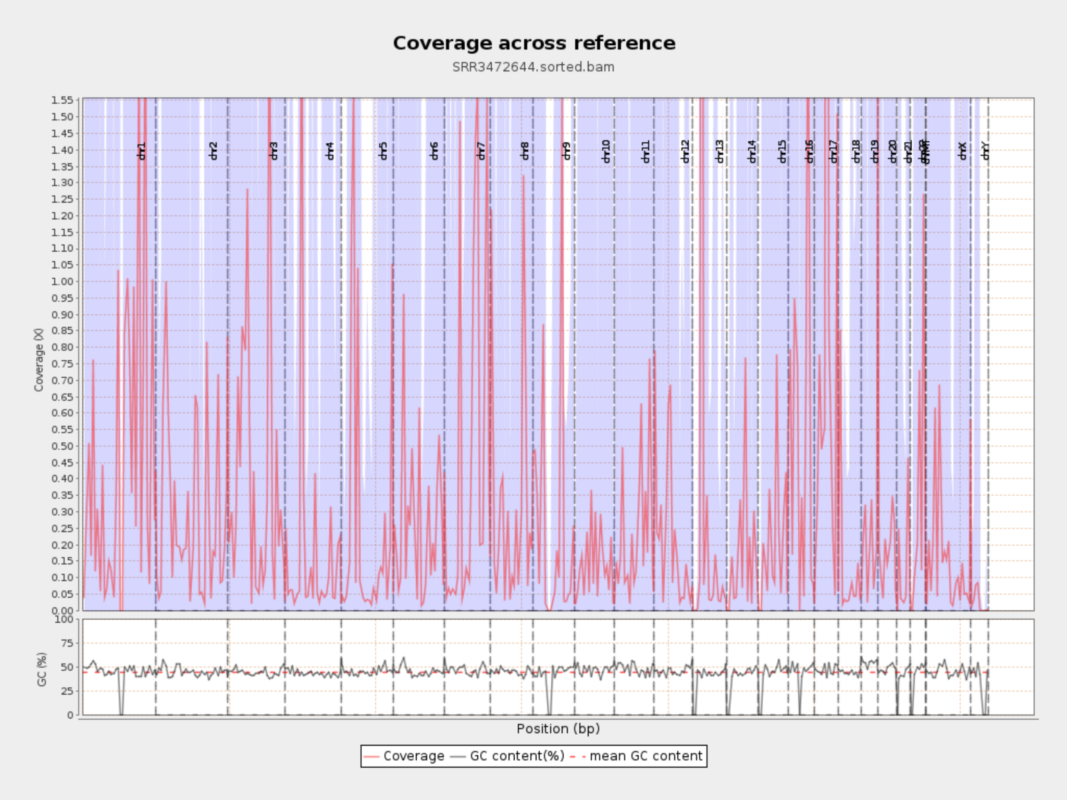
2.7. Chromosome stats

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

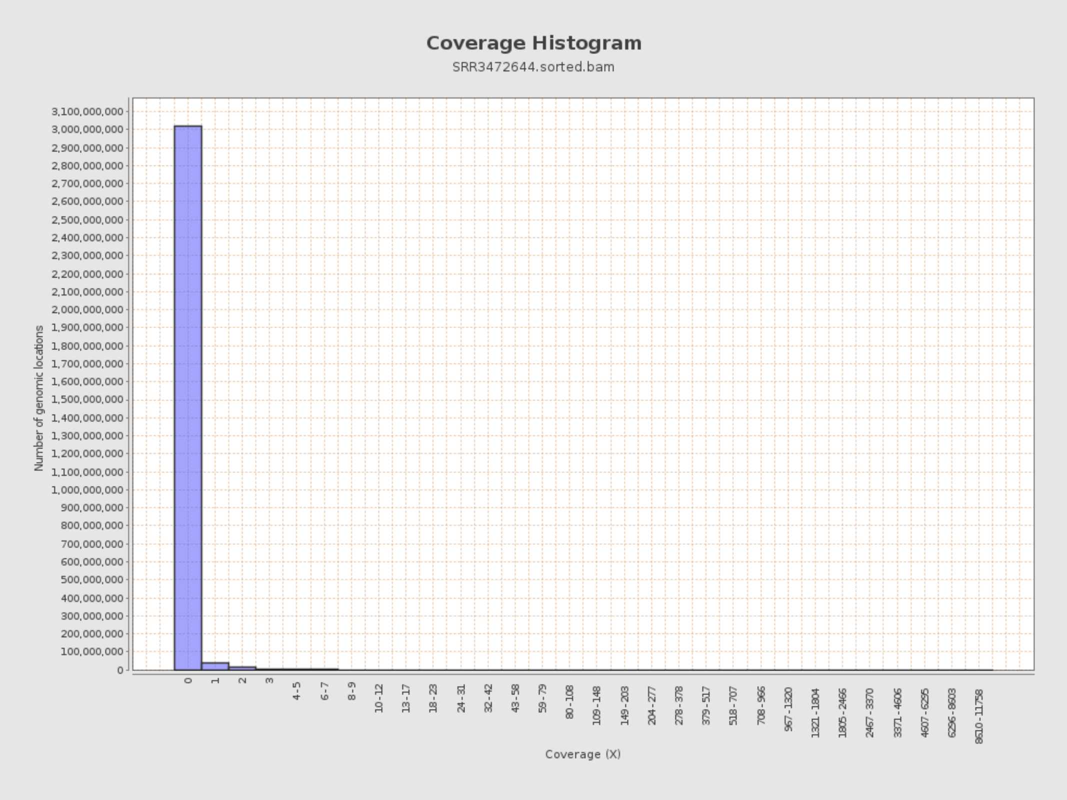
		bases	coverage	deviation
chr1	249250621	116871630	0.4689	23.4499
chr2	243199373	69970597	0.2877	14.6306
chr3	198022430	81565705	0.4119	17.9991
chr4	191154276	37127397	0.1942	13.4761
chr5	180915260	49812095	0.2753	16.6776
chr6	171115067	44351641	0.2592	10.0912
chr7	159138663	79444057	0.4992	30.2282
chr8	146364022	47576288	0.3251	16.7364
chr9	141213431	36140609	0.2559	17.7842
chr10	135534747	19501370	0.1439	6.7992
chr11	135006516	31725635	0.235	10.1906
chr12	133851895	31177570	0.2329	8.0722
chr13	115169878	38882881	0.3376	31.4522
chr14	107349540	18231810	0.1698	6.797
chr15	102531392	21611379	0.2108	13.786
chr16	90354753	48265308	0.5342	20.8025
chr17	81195210	82354899	1.0143	49.7021
chr18	78077248	10263648	0.1315	8.1756
chr19	59128983	13830319	0.2339	7.2073
chr20	63025520	11567089	0.1835	8.2579
chr21	48129895	6587514	0.1369	7.5407
chr22	51304566	18821635	0.3669	19.2856
chrMT	16571	3068	0.1851	0.5008
chrX	155270560	25151282	0.162	6.9876

chrY	59373566	1596403	0.0269	1.6778

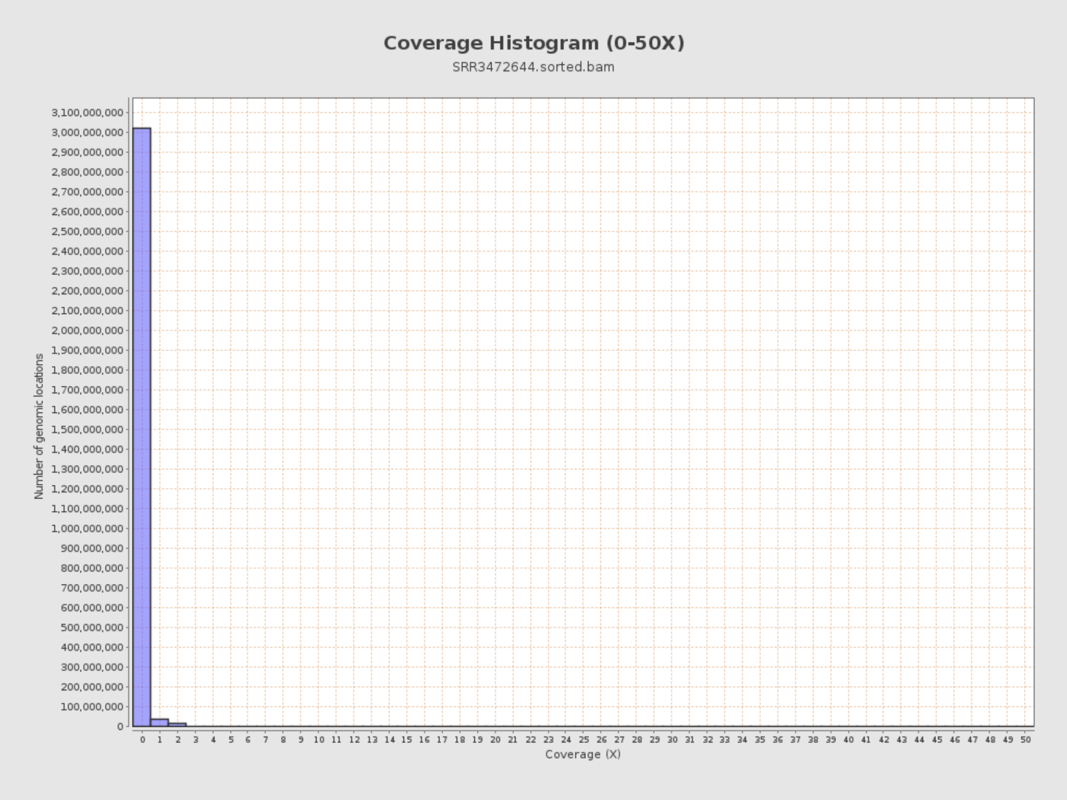
3. Results : Coverage across reference



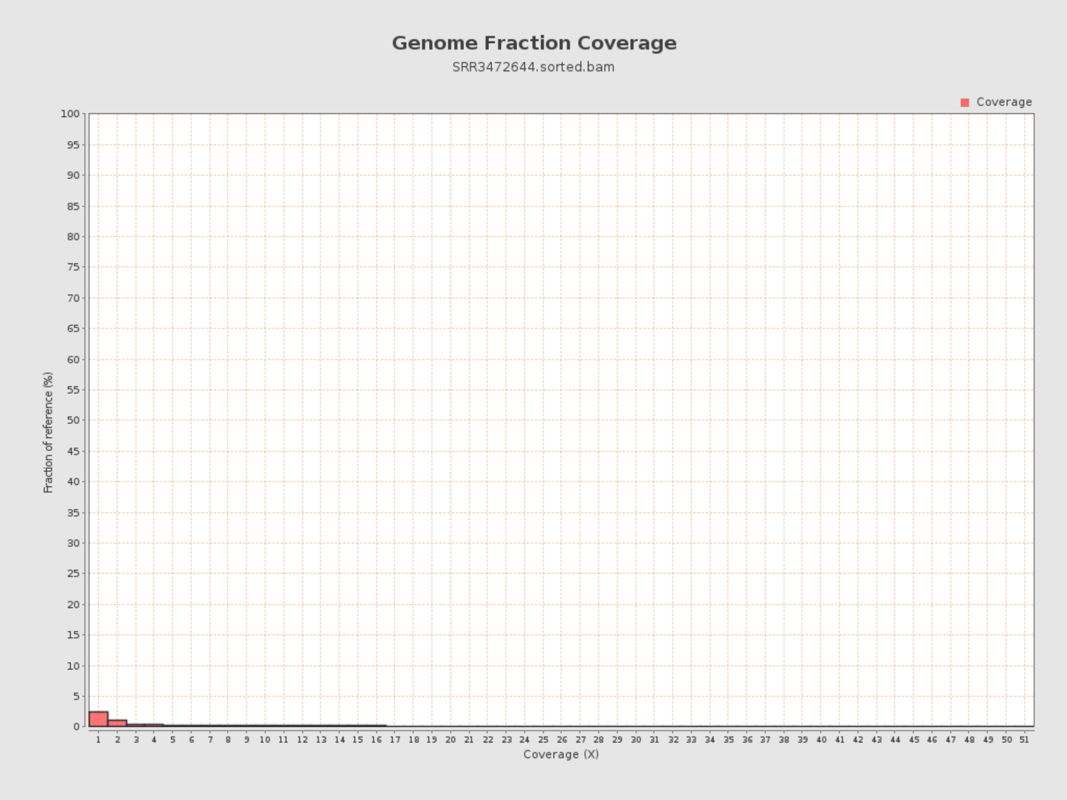
4. Results : Coverage Histogram



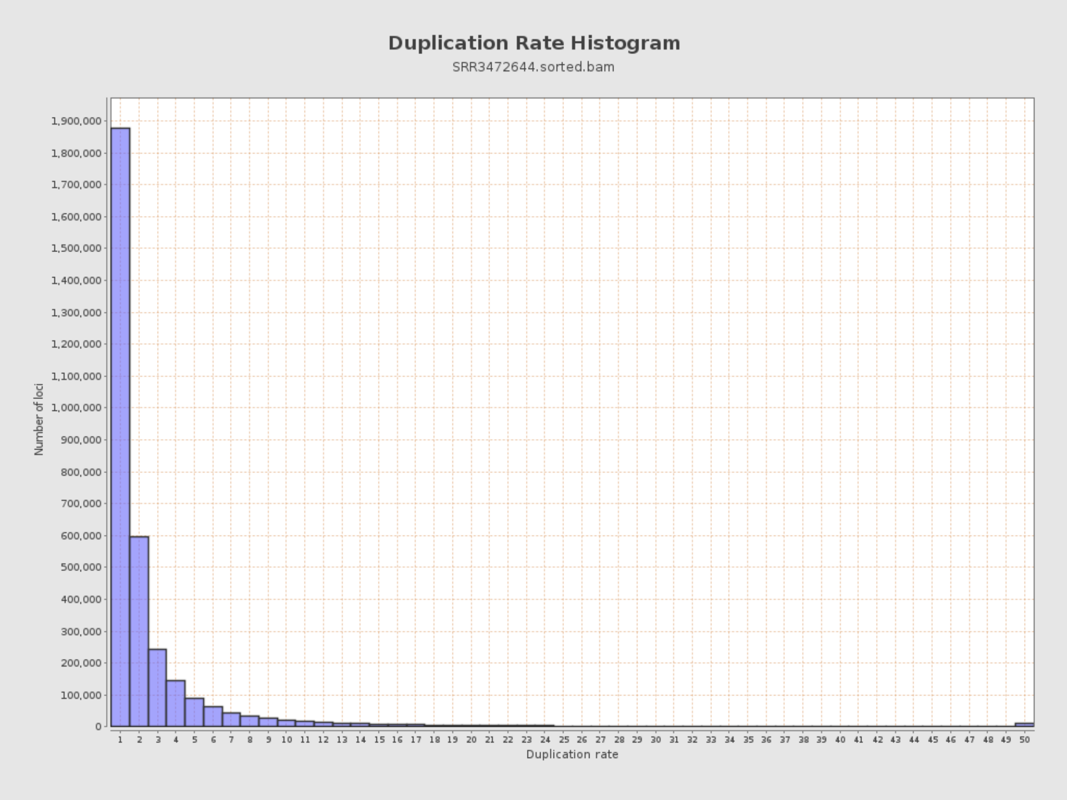
5. Results : Coverage Histogram (0-50X)



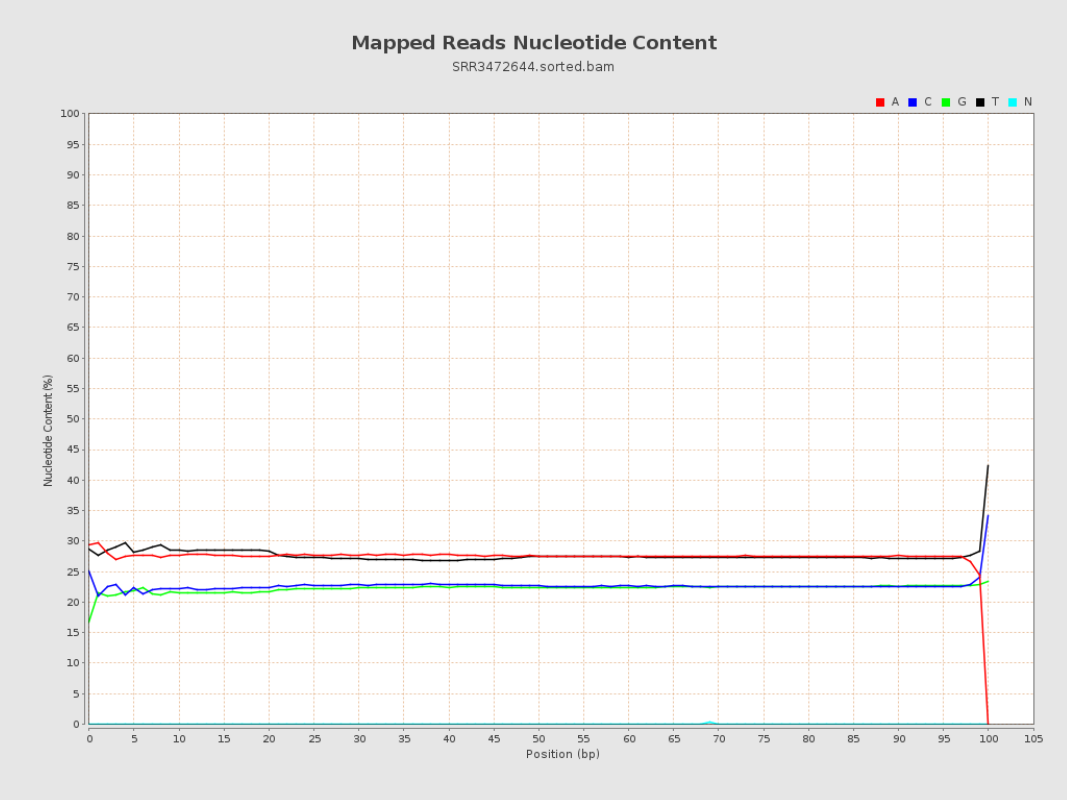
6. Results : Genome Fraction Coverage



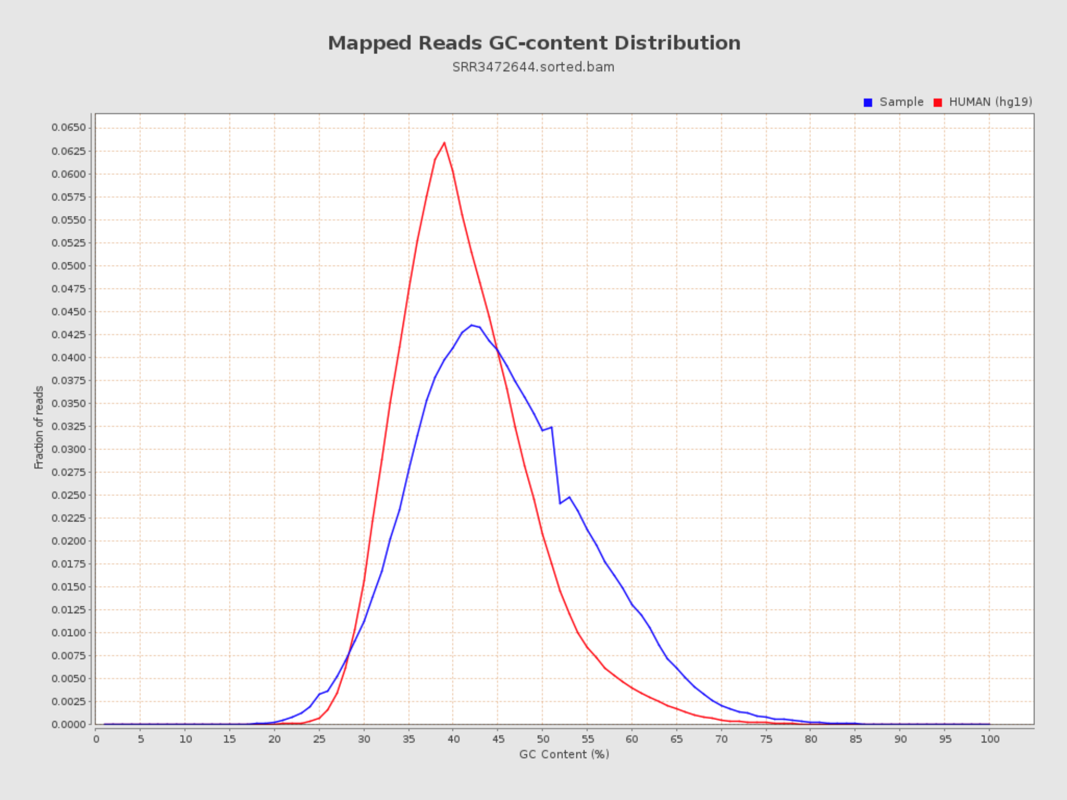
7. Results : Duplication Rate Histogram



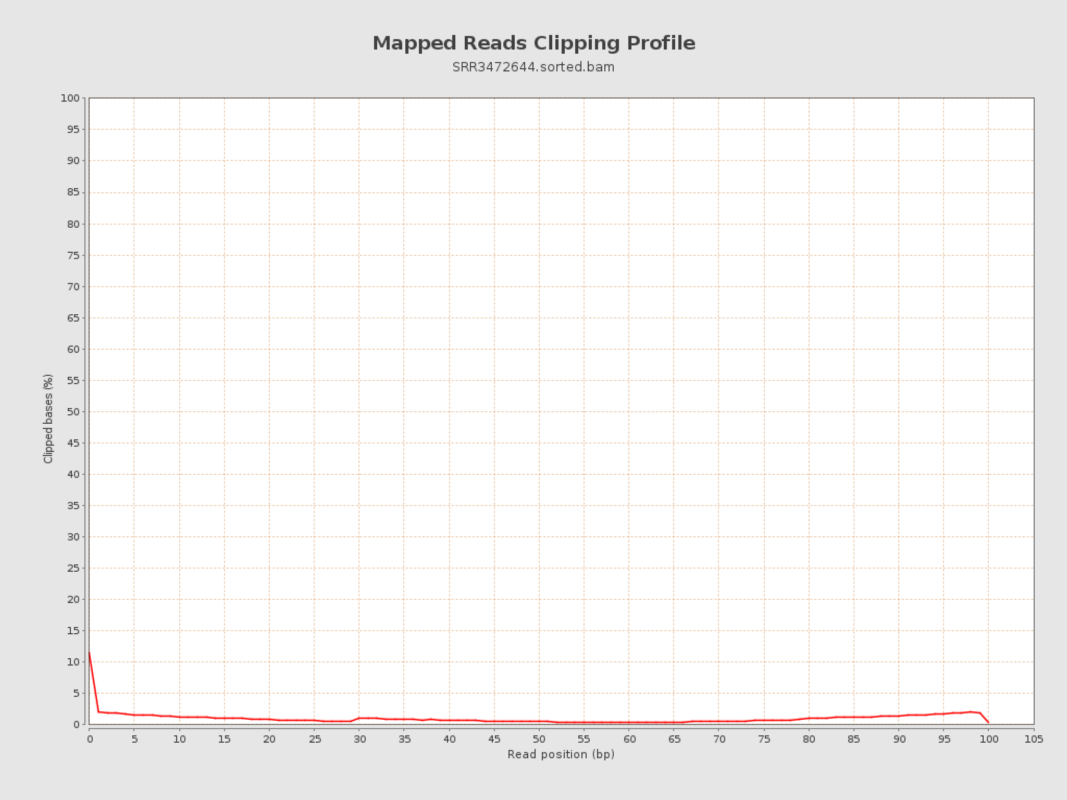
8. Results : Mapped Reads Nucleotide Content



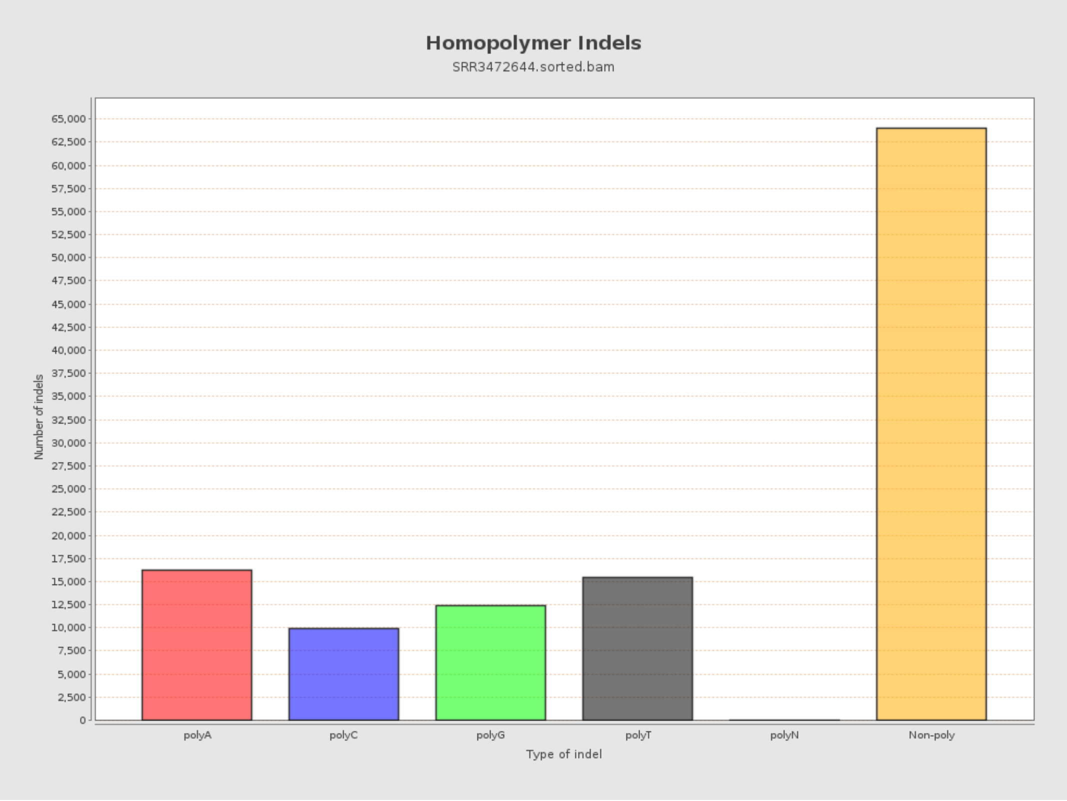
9. Results : Mapped Reads GC-content Distribution



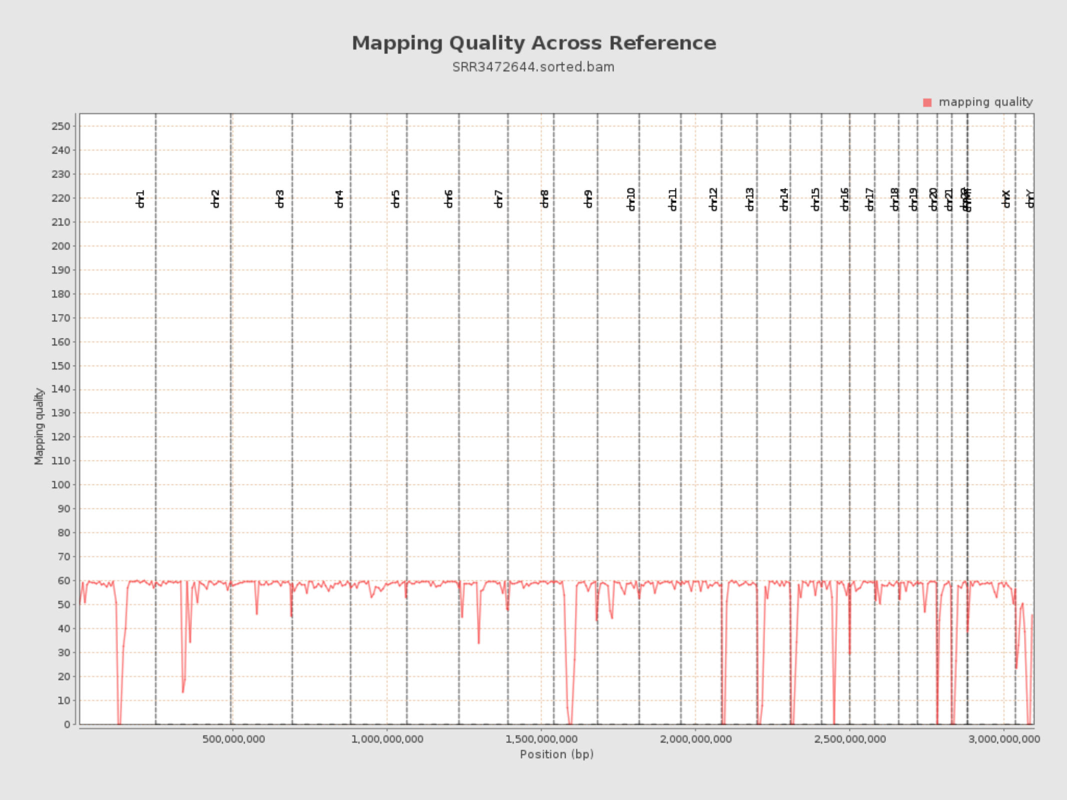
10. Results : Mapped Reads Clipping Profile



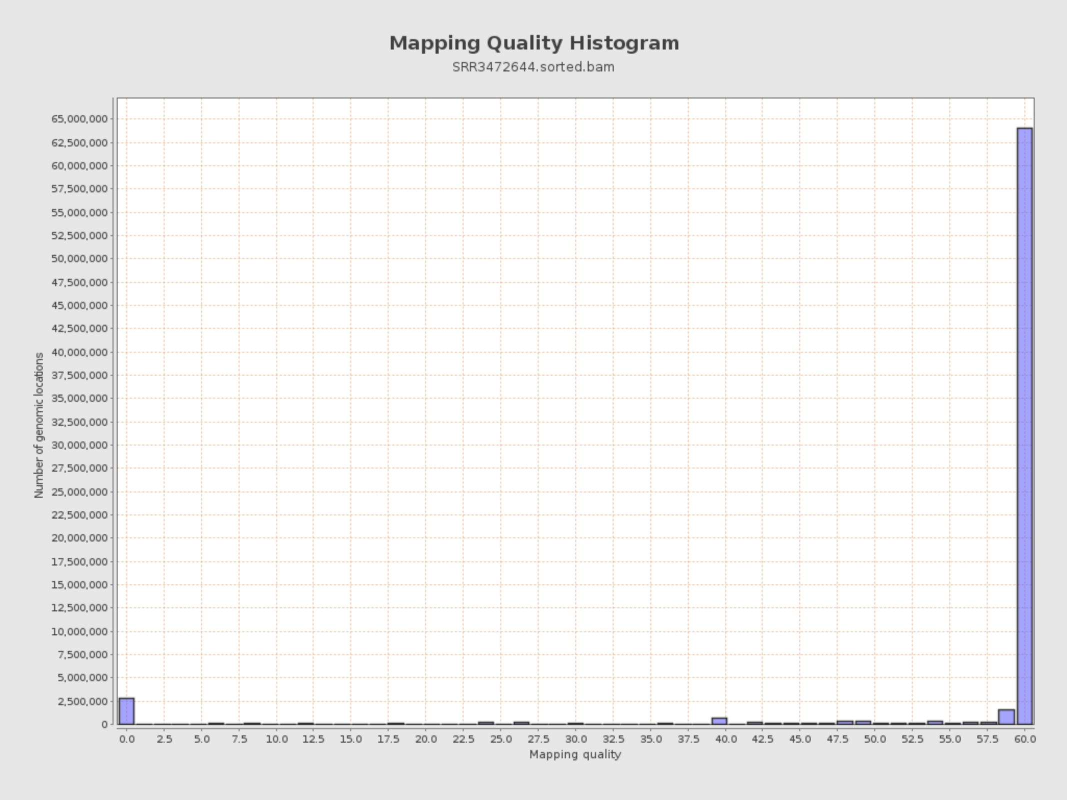
11. Results : Homopolymer Indels



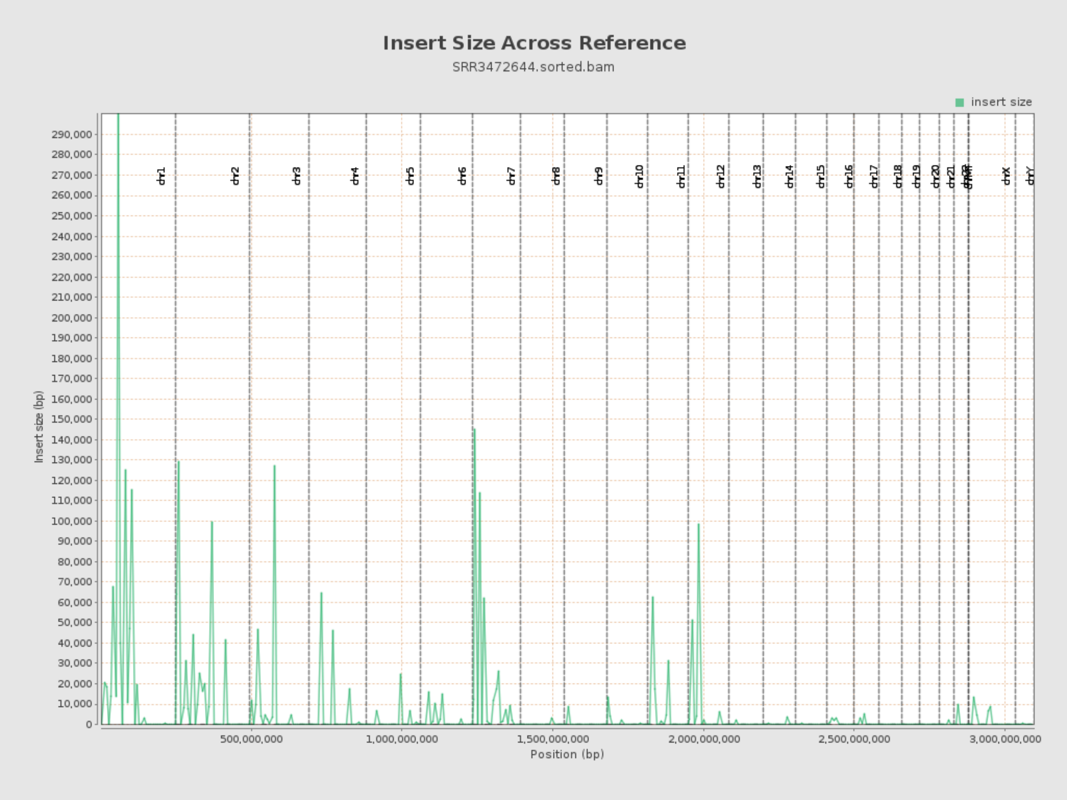
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram