Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 01:44:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472664.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_SRR3472664 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472664_1.fastq.gz SRR3472664_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 01:44:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472664.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,231,644
Mapped reads	18,106,771 / 99.32%
Unmapped reads	124,873 / 0.68%
Mapped paired reads	18,106,771 / 99.32%
Mapped reads, first in pair	9,071,975 / 49.76%
Mapped reads, second in pair	9,034,796 / 49.56%
Mapped reads, both in pair	18,025,988 / 98.87%
Mapped reads, singletons	80,783 / 0.44%
Secondary alignments	0
Supplementary alignments	113,441 / 0.62%
Read min/max/mean length	30 / 101 / 99.76
Duplicated reads (estimated)	13,060,393 / 71.64%
Duplication rate	50.14%
Clipped reads	1,335,971 / 7.33%

2.2. ACGT Content

Number/percentage of A's	483,175,600 / 27.12%
Number/percentage of C's	409,508,205 / 22.99%
Number/percentage of T's	483,488,106 / 27.14%
Number/percentage of G's	404,944,479 / 22.73%
Number/percentage of N's	343,583 / 0.02%

GC Percentage	45.72%

2.3. Coverage

Mean	0.5755
Standard Deviation	29.3985

2.4. Mapping Quality

Mean Mapping Quality	54.73

2.5. Insert size

Mean	22,093.29
Standard Deviation	1,462,872.6
P25/Median/P75	151 / 206 / 275

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	10,114,587
Insertions	115,098
Mapped reads with at least one insertion	0.63%
Deletions	98,625
Mapped reads with at least one deletion	0.54%
Homopolymer indels	46.87%

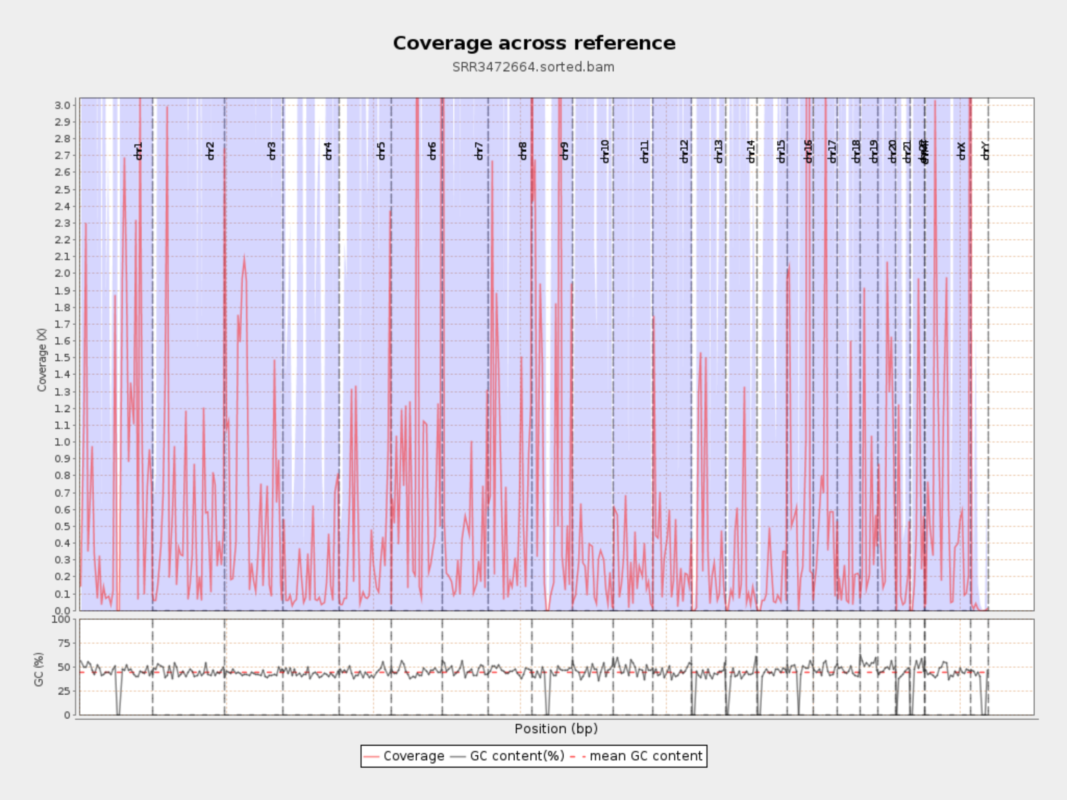
2.7. Chromosome stats

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

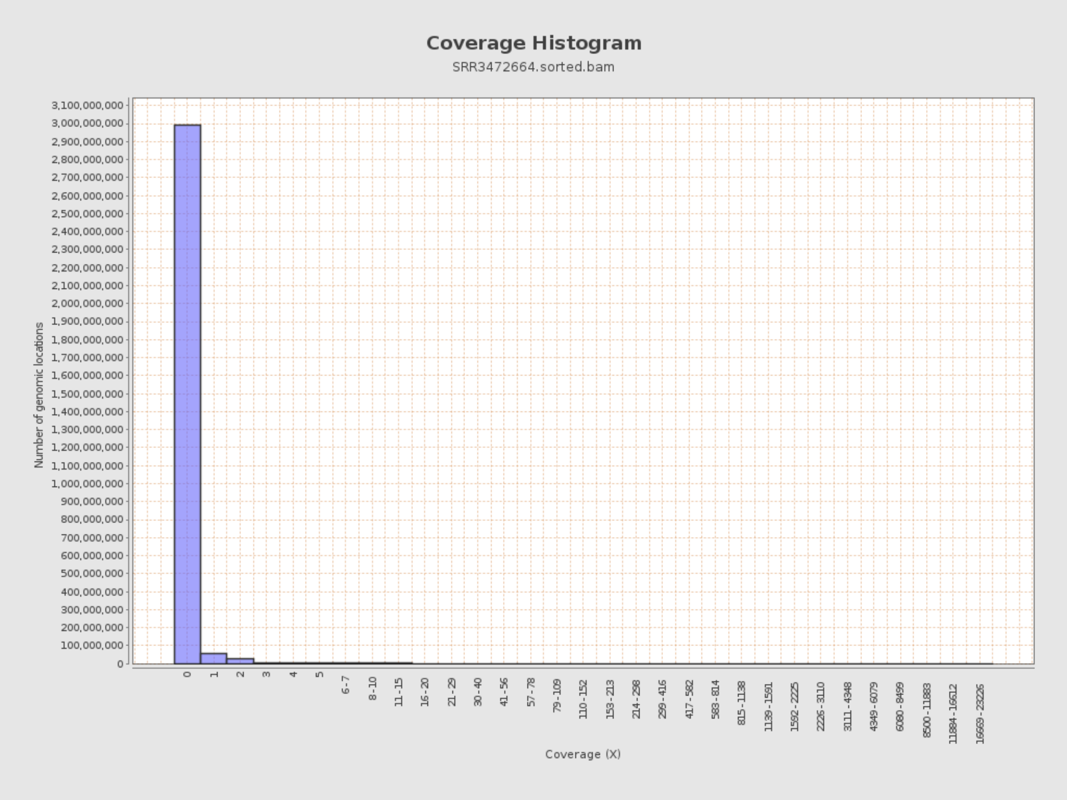
		bases	coverage	deviation
chr1	249250621	213423532	0.8563	34.8347
chr2	243199373	129920079	0.5342	24.9841
chr3	198022430	153974638	0.7776	23.8122
chr4	191154276	39193667	0.205	11.3519
chr5	180915260	77726221	0.4296	21.7349
chr6	171115067	146112244	0.8539	32.1633
chr7	159138663	97059107	0.6099	43.5483
chr8	146364022	108151344	0.7389	38.3689
chr9	141213431	157909197	1.1182	54.0149
chr10	135534747	30907991	0.228	12.1695
chr11	135006516	35322657	0.2616	12.517
chr12	133851895	50110585	0.3744	15.235
chr13	115169878	48379617	0.4201	19.3314
chr14	107349540	24958904	0.2325	12.6617
chr15	102531392	14891839	0.1452	5.628
chr16	90354753	118165247	1.3078	62.5436
chr17	81195210	58593447	0.7216	33.9582
chr18	78077248	22214563	0.2845	22.648
chr19	59128983	34545662	0.5842	22.8747
chr20	63025520	58275679	0.9246	31.7423
chr21	48129895	15058632	0.3129	23.2037
chr22	51304566	26266190	0.512	21.533
chrMT	16571	5624	0.3394	0.8613
chrX	155270560	119774020	0.7714	28.3958

chrY	59373566	757550	0.0128	0.9219

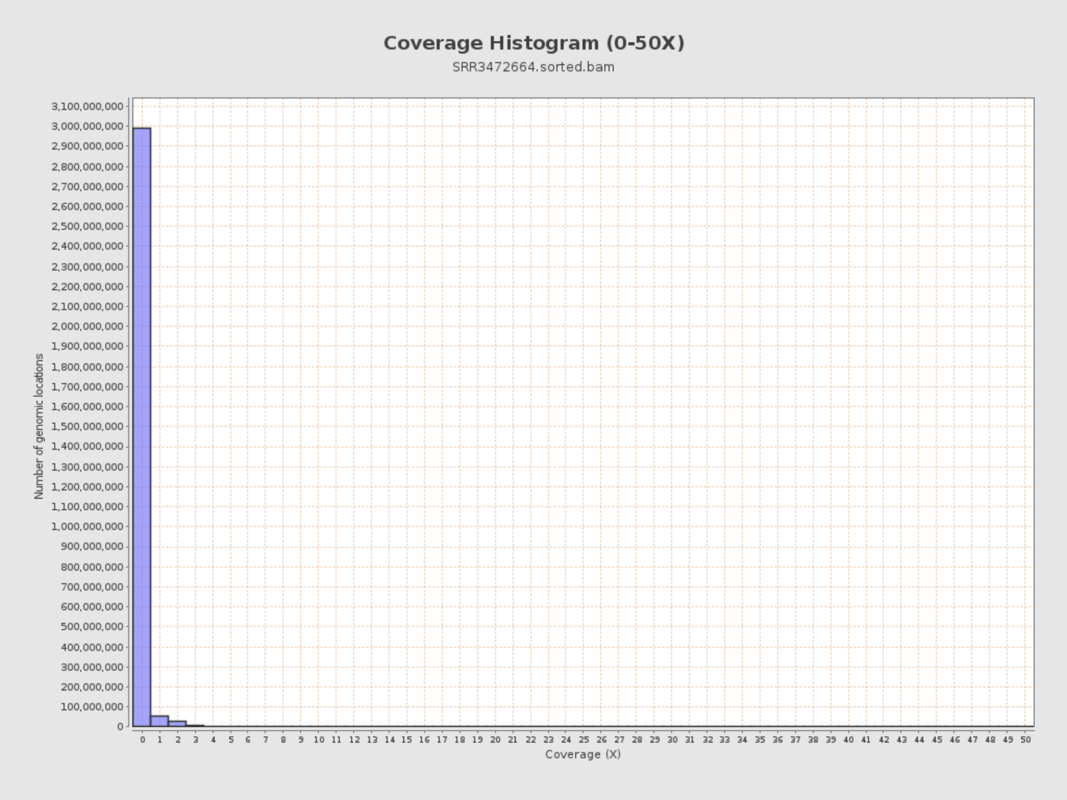
3. Results : Coverage across reference



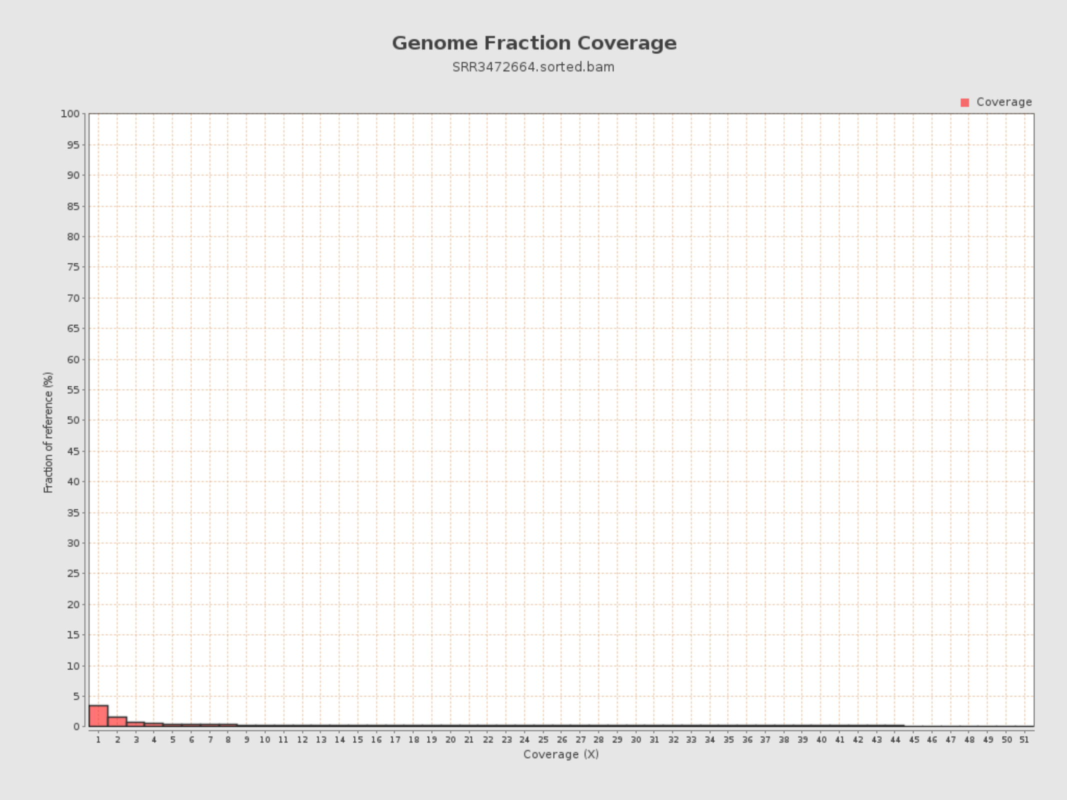
4. Results : Coverage Histogram



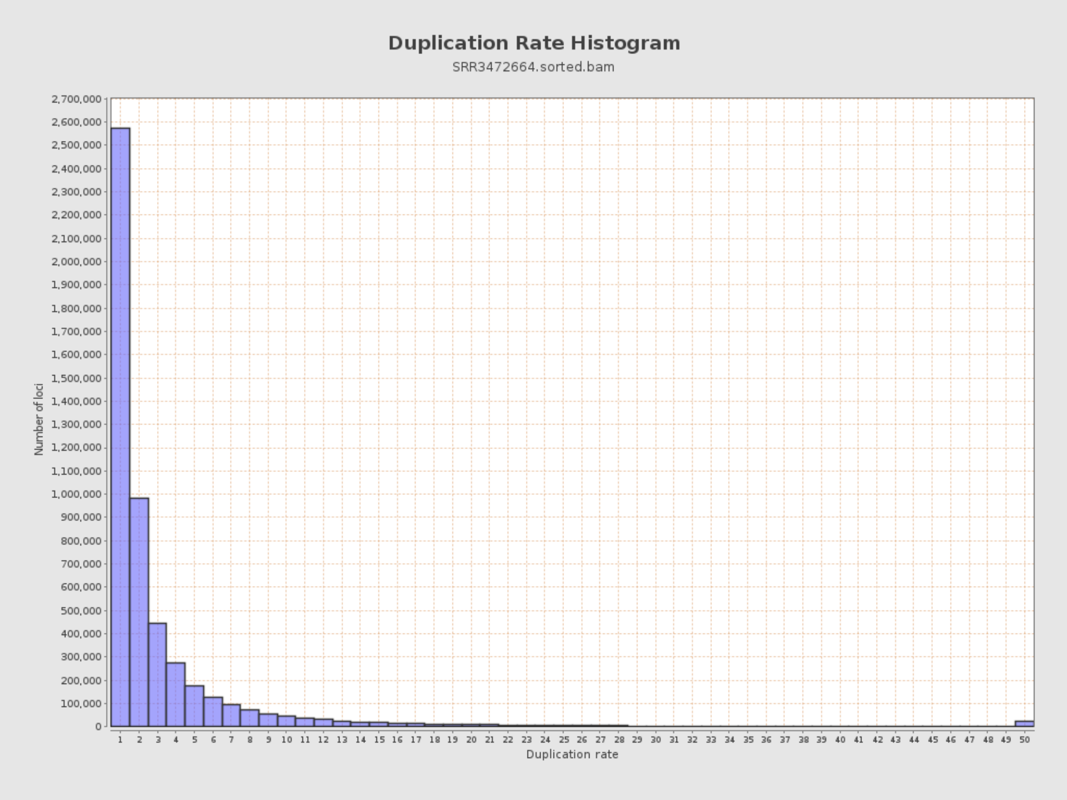
5. Results : Coverage Histogram (0-50X)



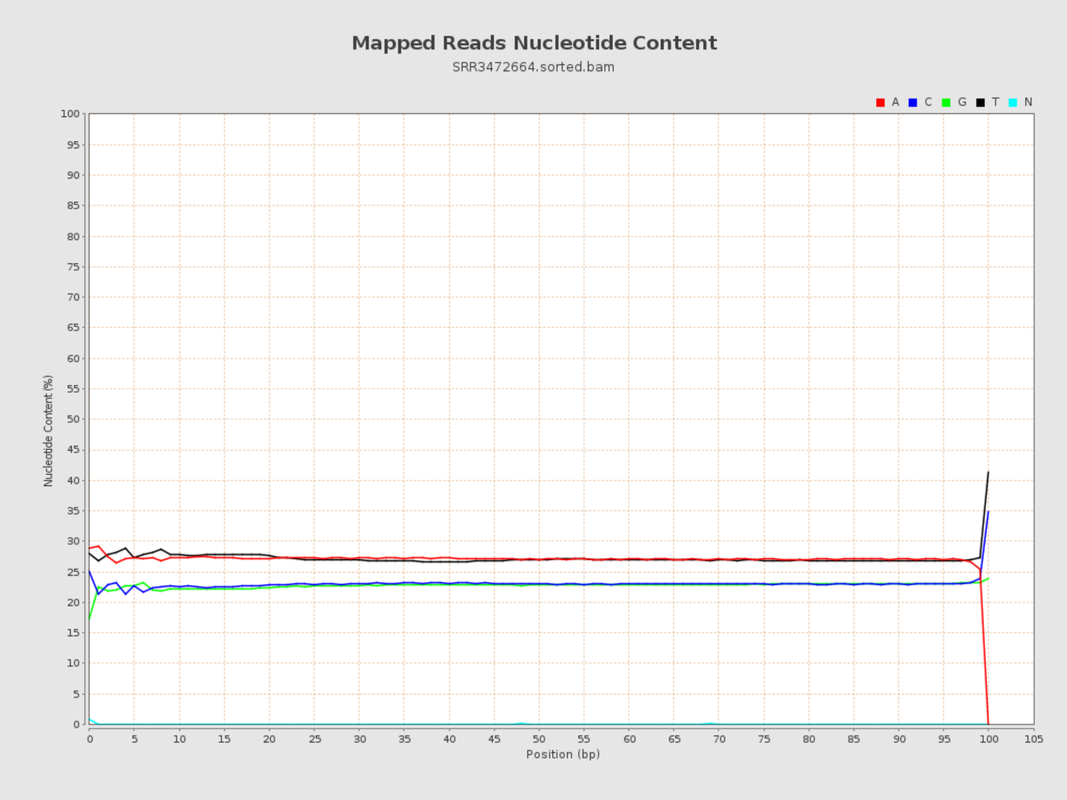
6. Results : Genome Fraction Coverage



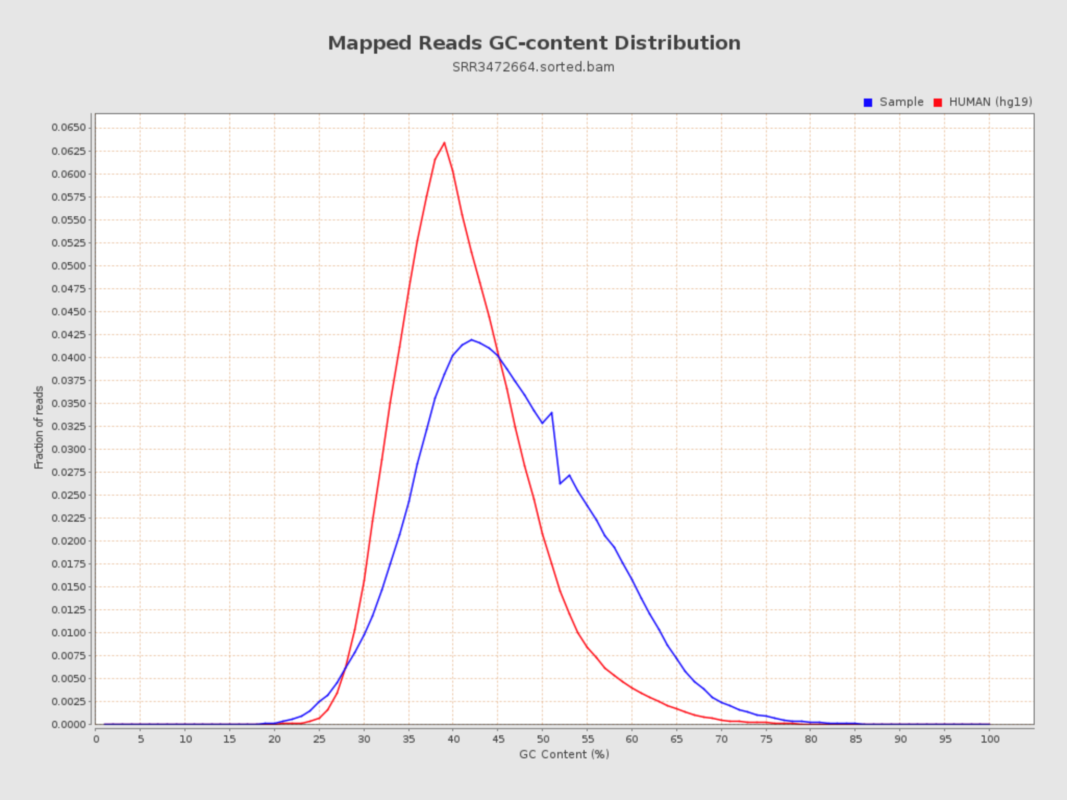
7. Results : Duplication Rate Histogram



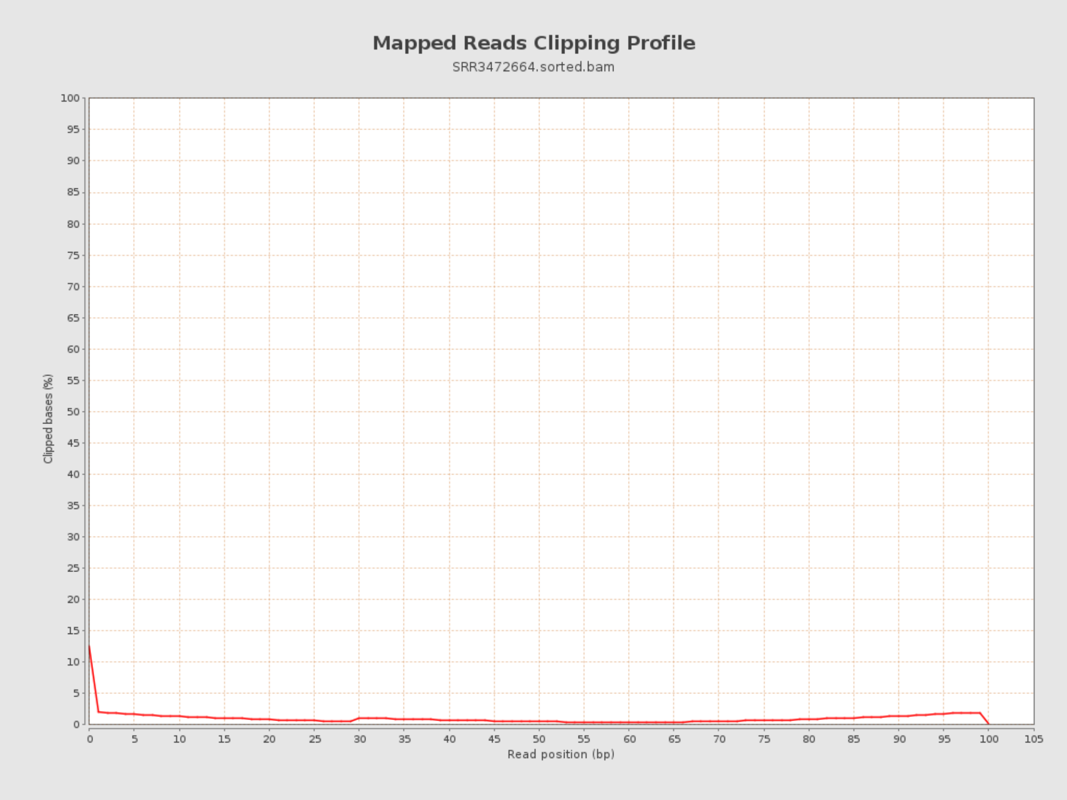
8. Results : Mapped Reads Nucleotide Content



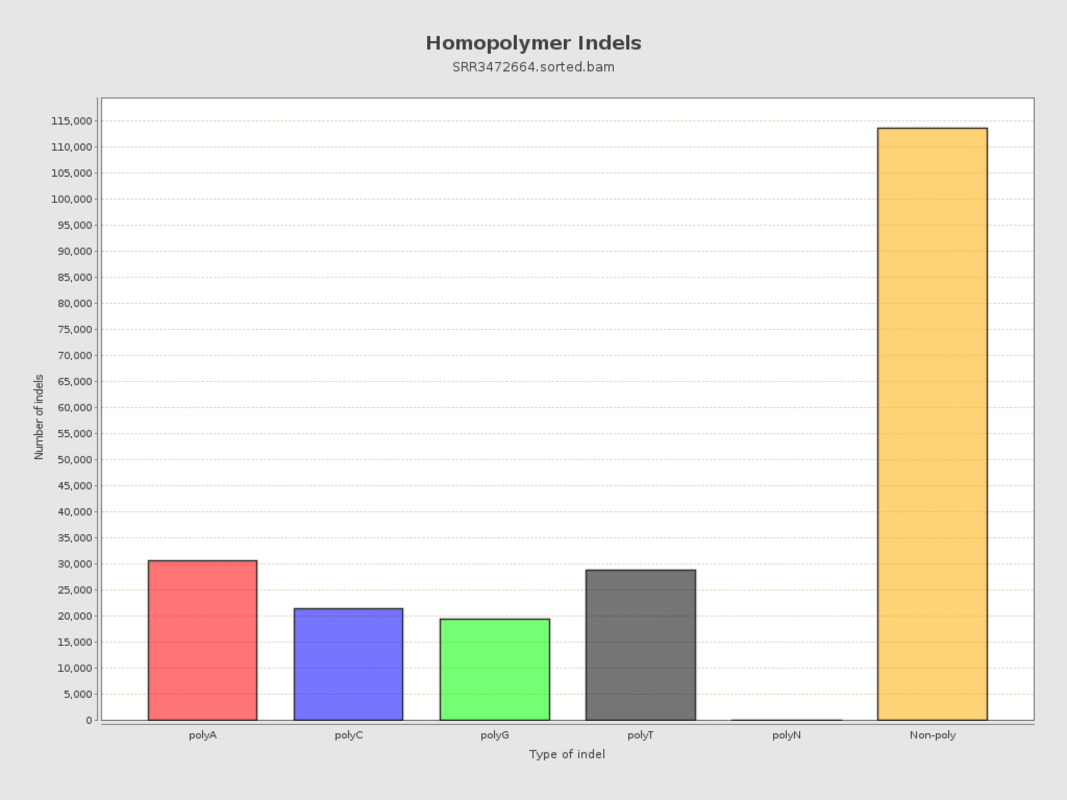
9. Results : Mapped Reads GC-content Distribution



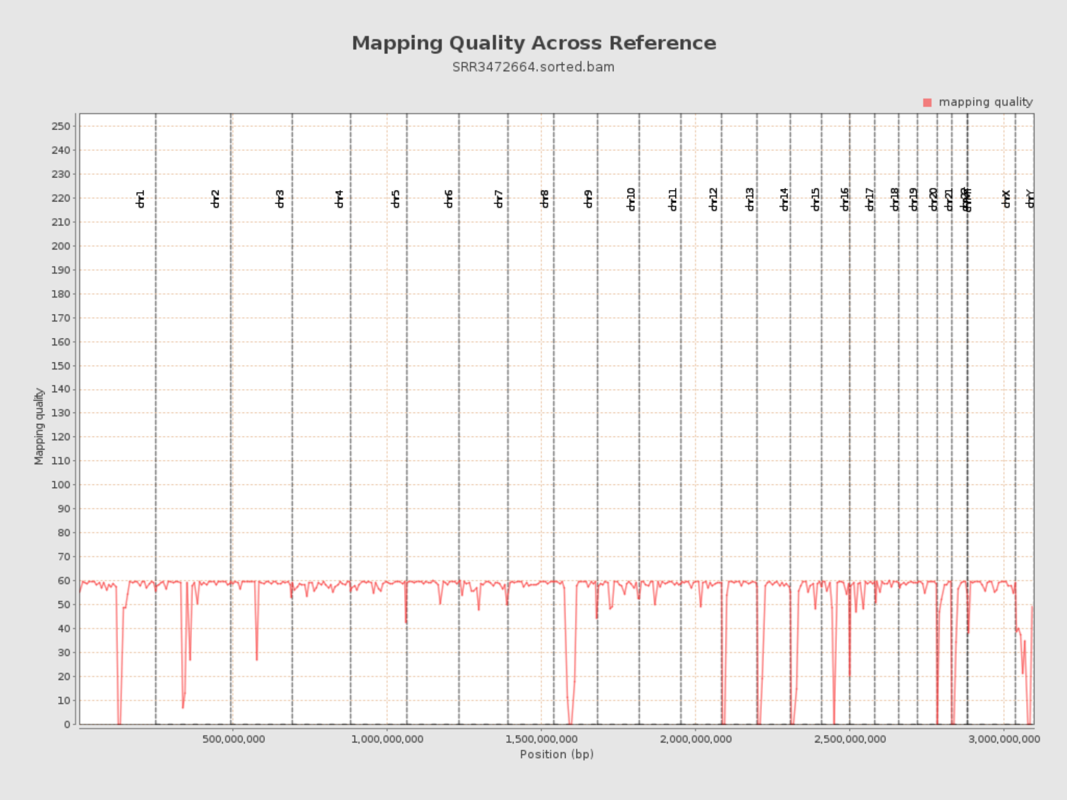
10. Results : Mapped Reads Clipping Profile



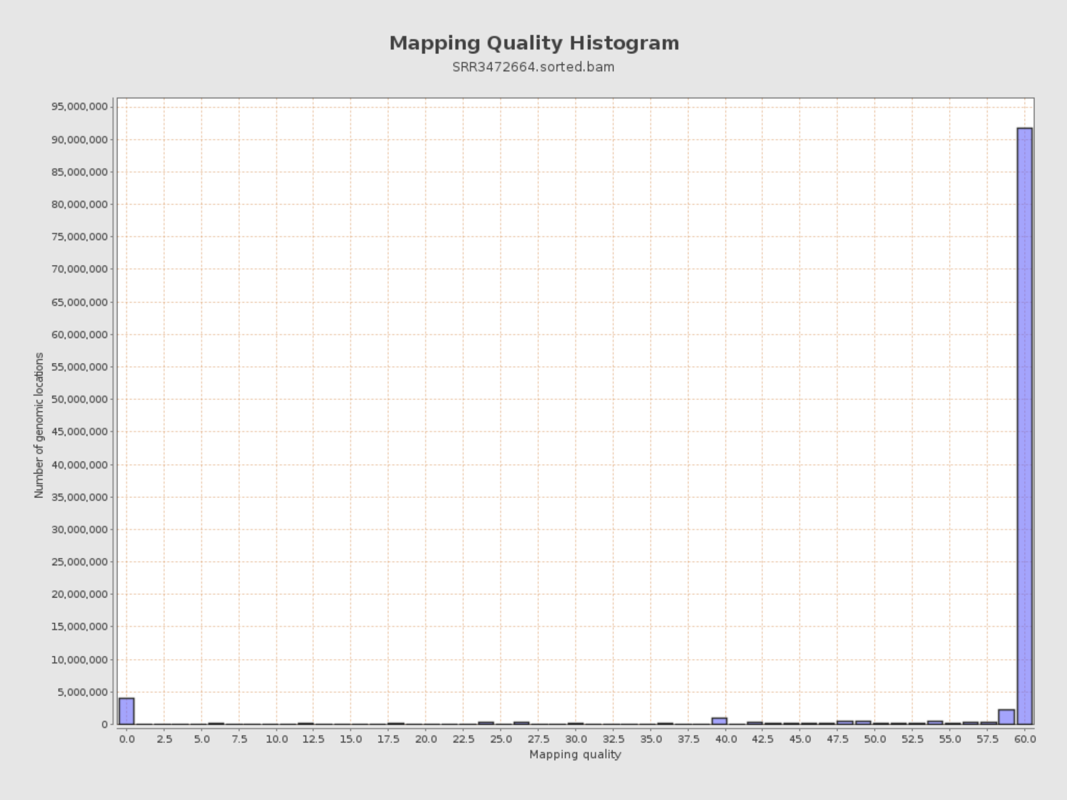
11. Results : Homopolymer Indels



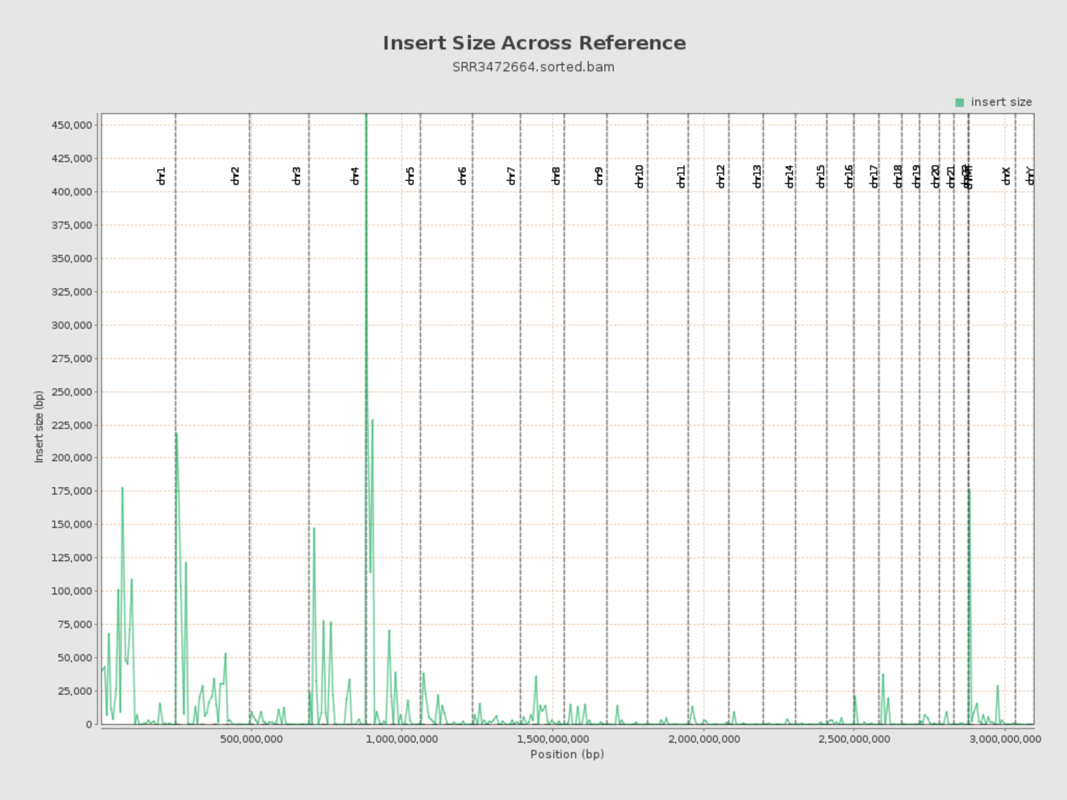
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram