Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 20:50:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472646.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_SRR3472646 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472646_1.fastq.gz SRR3472646_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 20:50:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472646.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,852,802
Mapped reads	8,754,415 / 98.89%
Unmapped reads	98,387 / 1.11%
Mapped paired reads	8,754,415 / 98.89%
Mapped reads, first in pair	4,380,624 / 49.48%
Mapped reads, second in pair	4,373,791 / 49.41%
Mapped reads, both in pair	8,695,308 / 98.22%
Mapped reads, singletons	59,107 / 0.67%
Secondary alignments	0
Supplementary alignments	48,079 / 0.54%
Read min/max/mean length	30 / 101 / 99.61
Duplicated reads (estimated)	5,800,428 / 65.52%
Duplication rate	41.55%
Clipped reads	564,281 / 6.37%

2.2. ACGT Content

Number/percentage of A's	231,373,097 / 26.87%
Number/percentage of C's	201,180,521 / 23.36%
Number/percentage of T's	230,720,730 / 26.79%
Number/percentage of G's	197,698,307 / 22.96%
Number/percentage of N's	108,726 / 0.01%

GC Percentage	46.32%

2.3. Coverage

Mean	0.2782
Standard Deviation	20.0937

2.4. Mapping Quality

Mean Mapping Quality	54.42

2.5. Insert size

Mean	20,830.83
Standard Deviation	1,450,867.89
P25/Median/P75	155 / 212 / 283

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	7,121,424
Insertions	53,738
Mapped reads with at least one insertion	0.61%
Deletions	42,867
Mapped reads with at least one deletion	0.48%
Homopolymer indels	46.8%

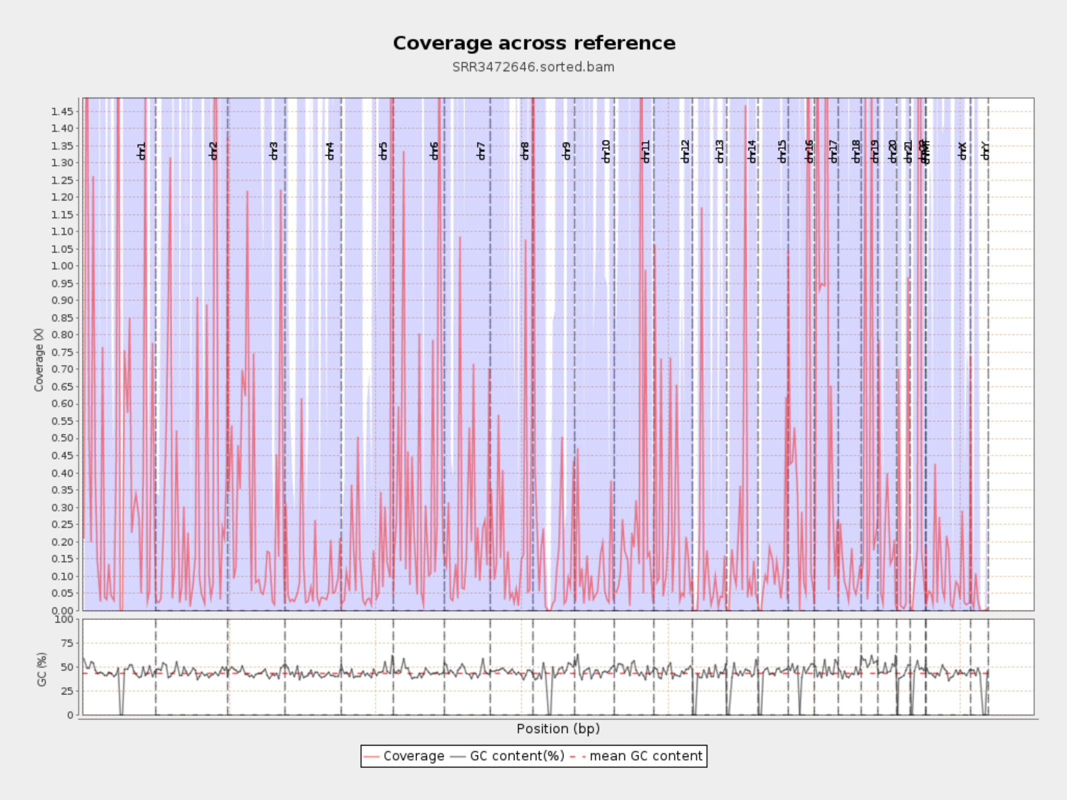
2.7. Chromosome stats

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

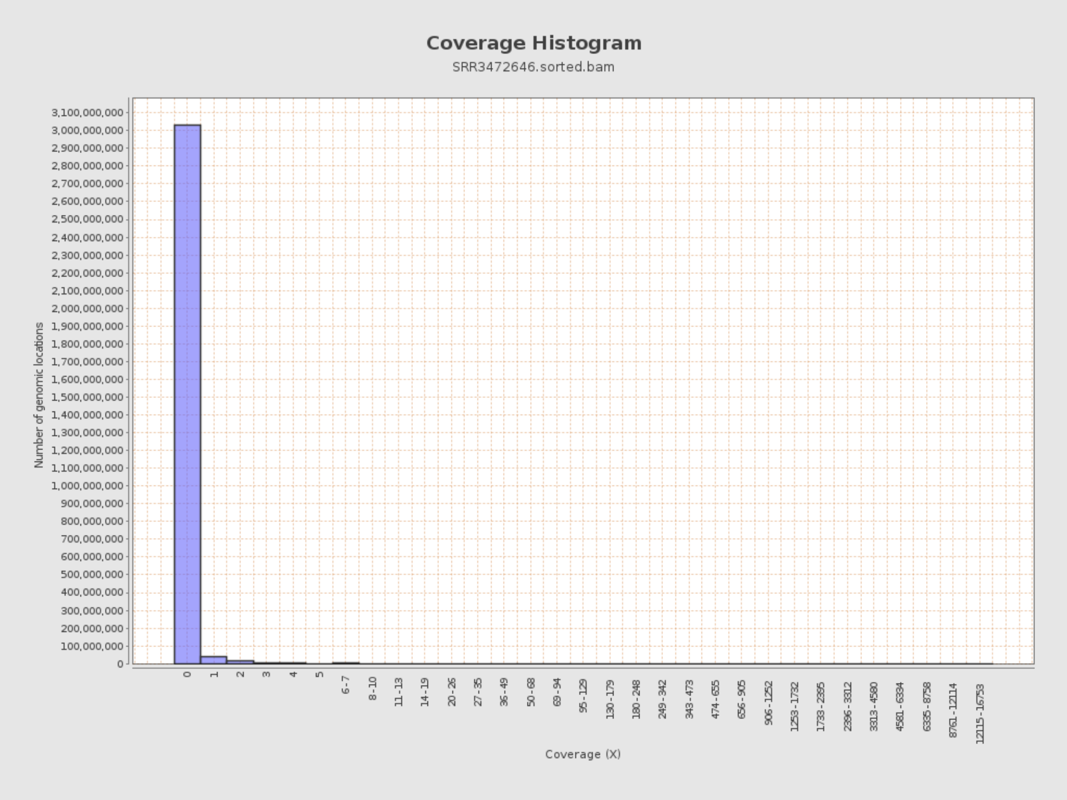
		bases	coverage	deviation
chr1	249250621	112062370	0.4496	27.1273
chr2	243199373	77911487	0.3204	23.6074
chr3	198022430	68323075	0.345	18.0588
chr4	191154276	19061915	0.0997	5.8295
chr5	180915260	57893005	0.32	37.7094
chr6	171115067	65407321	0.3822	17.4186
chr7	159138663	41149506	0.2586	12.7284
chr8	146364022	31928323	0.2181	12.3125
chr9	141213431	22908344	0.1622	6.5936
chr10	135534747	15418884	0.1138	8.3788
chr11	135006516	43029629	0.3187	17.733
chr12	133851895	34913225	0.2608	15.888
chr13	115169878	16234324	0.141	8.2893
chr14	107349540	21864328	0.2037	11.2672
chr15	102531392	13084976	0.1276	7.3795
chr16	90354753	39077726	0.4325	16.2172
chr17	81195210	66670054	0.8211	40.2595
chr18	78077248	8273367	0.106	5.2293
chr19	59128983	30098426	0.509	24.2583
chr20	63025520	13825632	0.2194	12.9664
chr21	48129895	13344414	0.2773	25.7591
chr22	51304566	30467860	0.5939	52.7053
chrMT	16571	3102	0.1872	0.5833
chrX	155270560	16872381	0.1087	6.2864

chrY	59373566	1357850	0.0229	1.5884

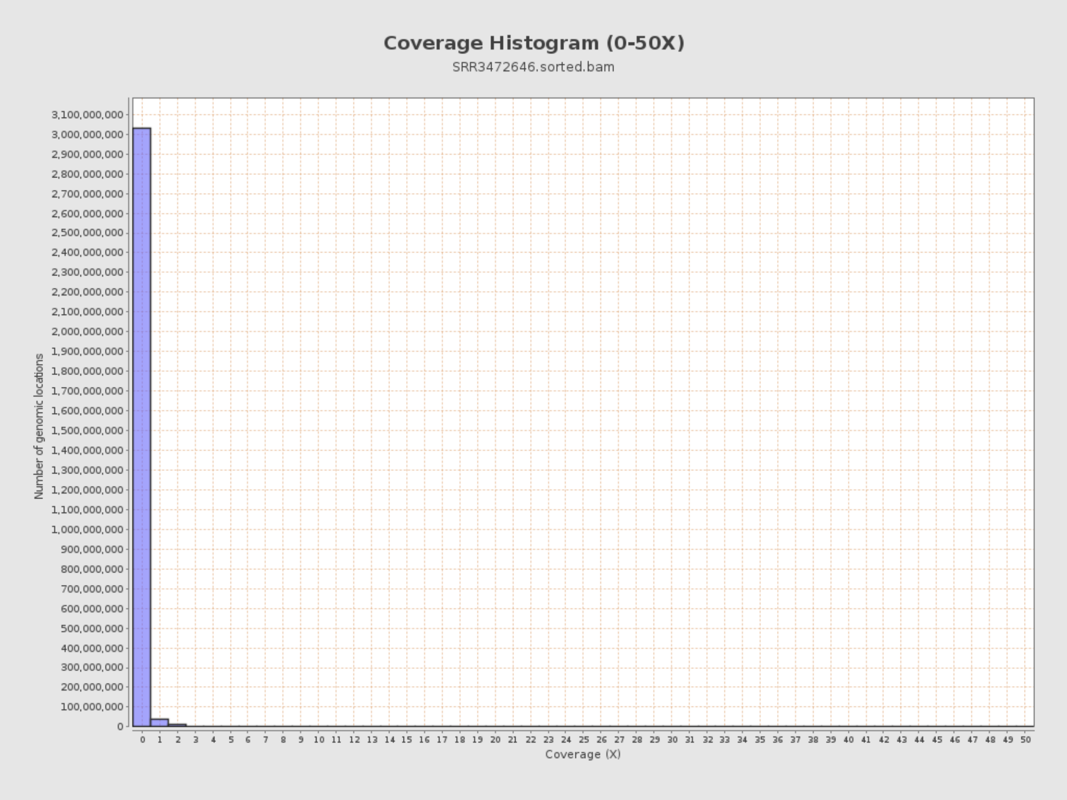
3. Results : Coverage across reference



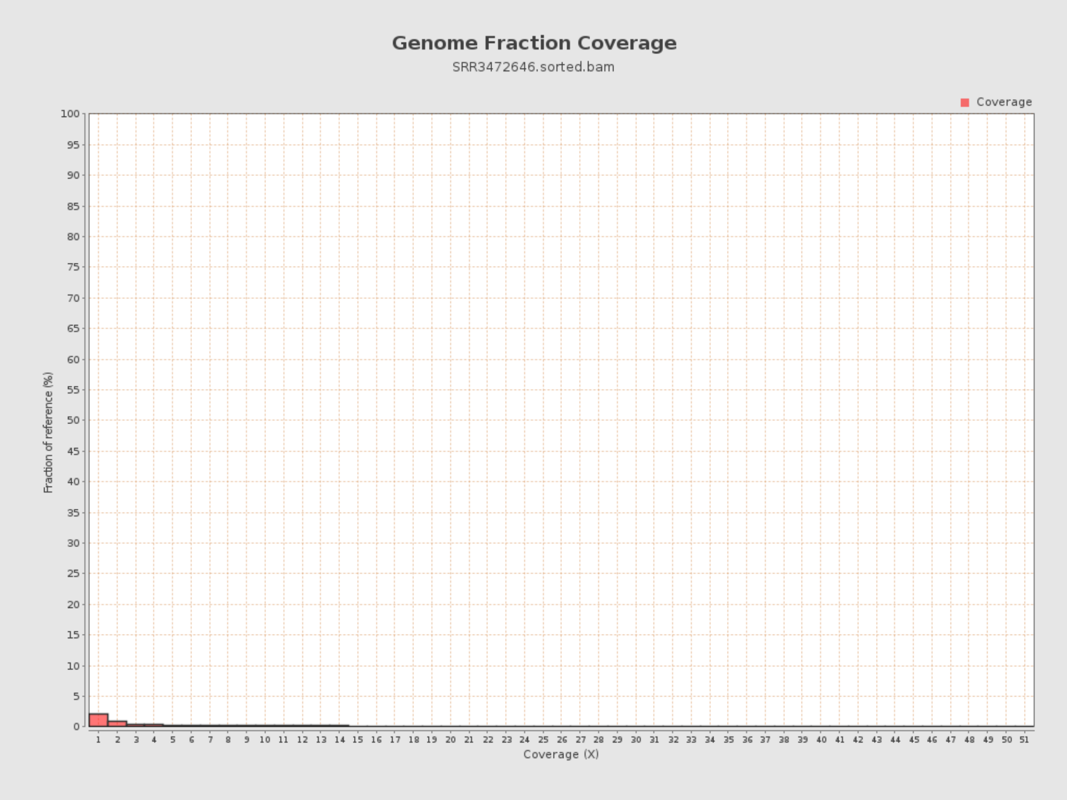
4. Results : Coverage Histogram



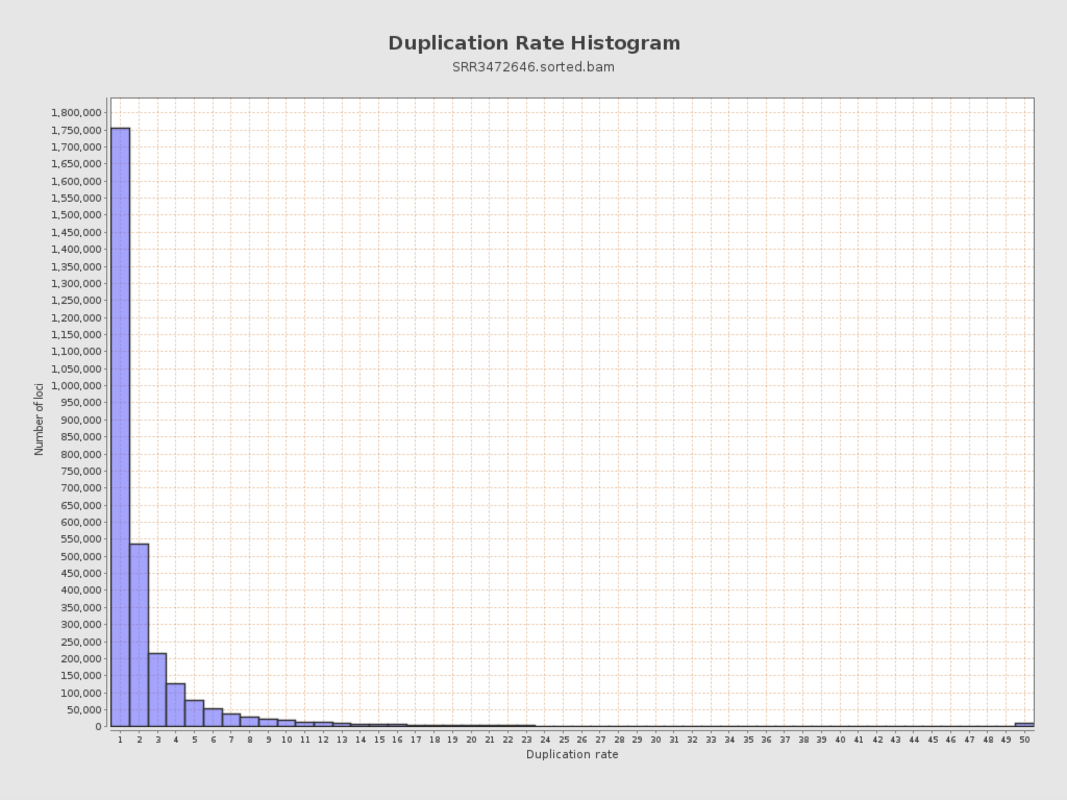
5. Results : Coverage Histogram (0-50X)



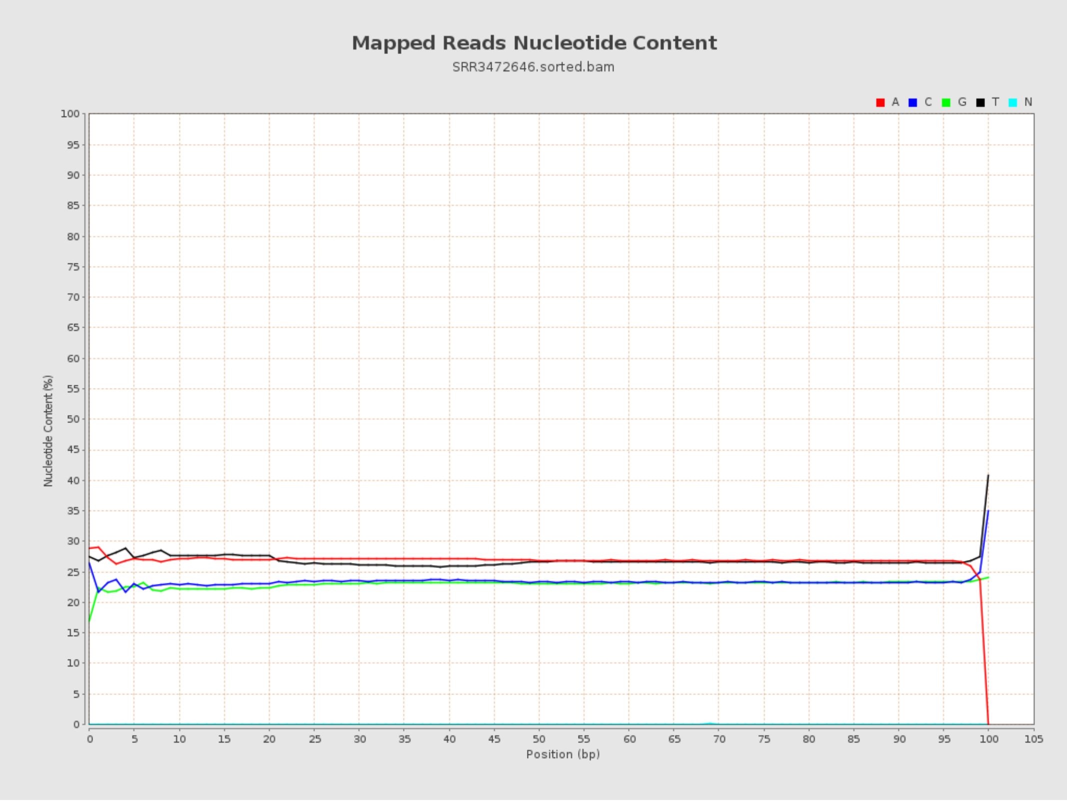
6. Results : Genome Fraction Coverage



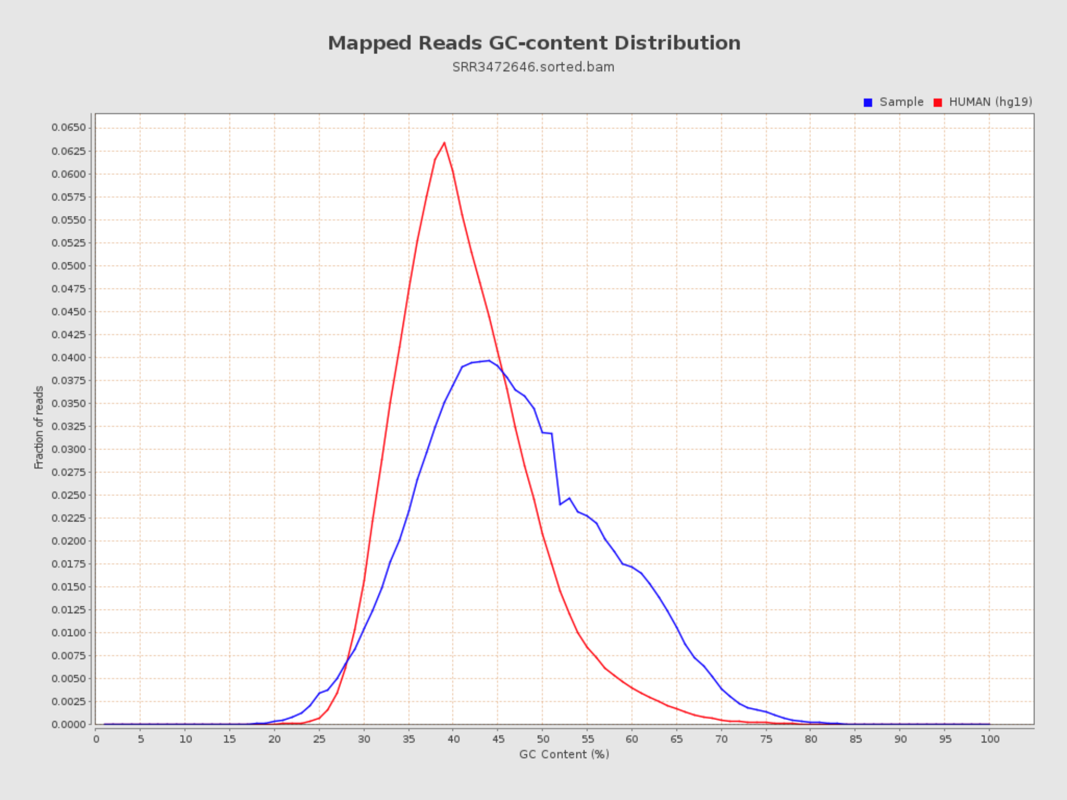
7. Results : Duplication Rate Histogram



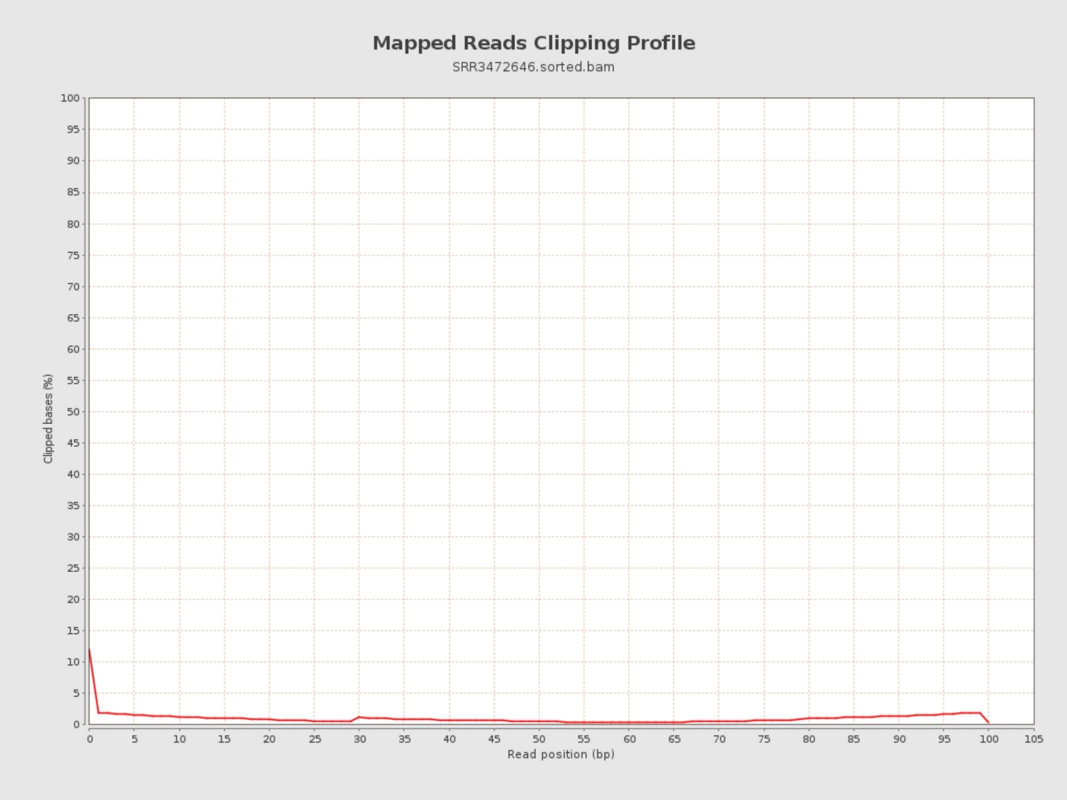
8. Results : Mapped Reads Nucleotide Content



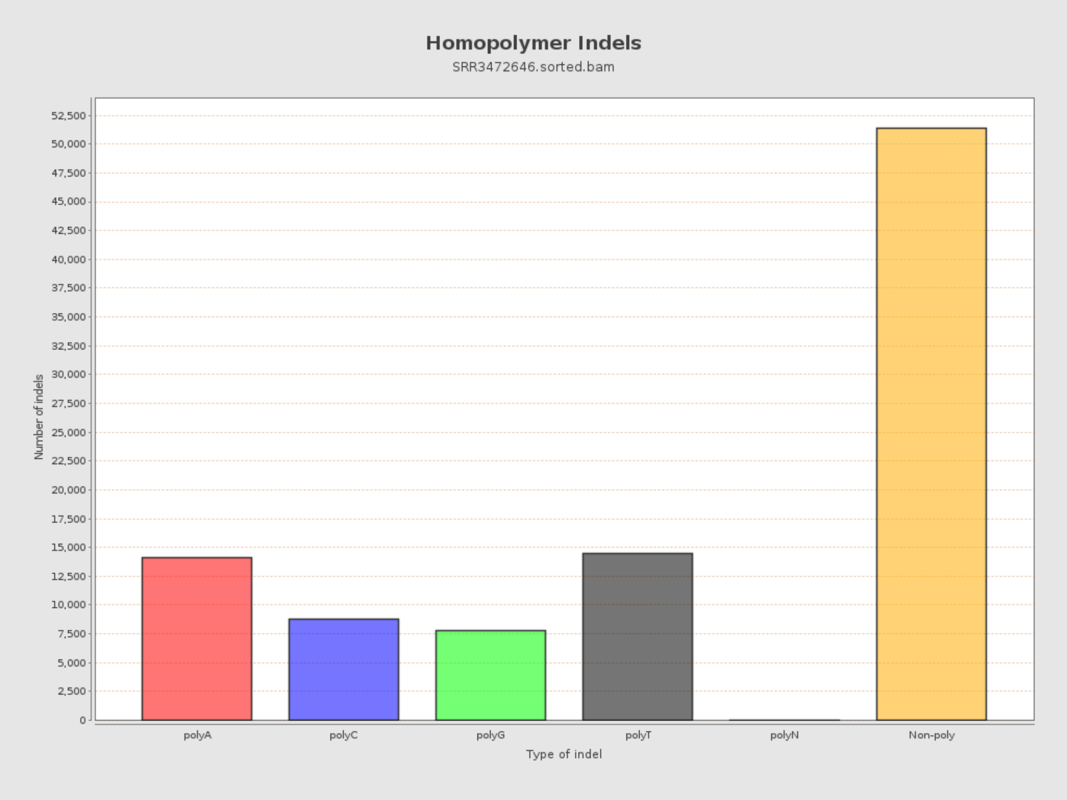
9. Results : Mapped Reads GC-content Distribution



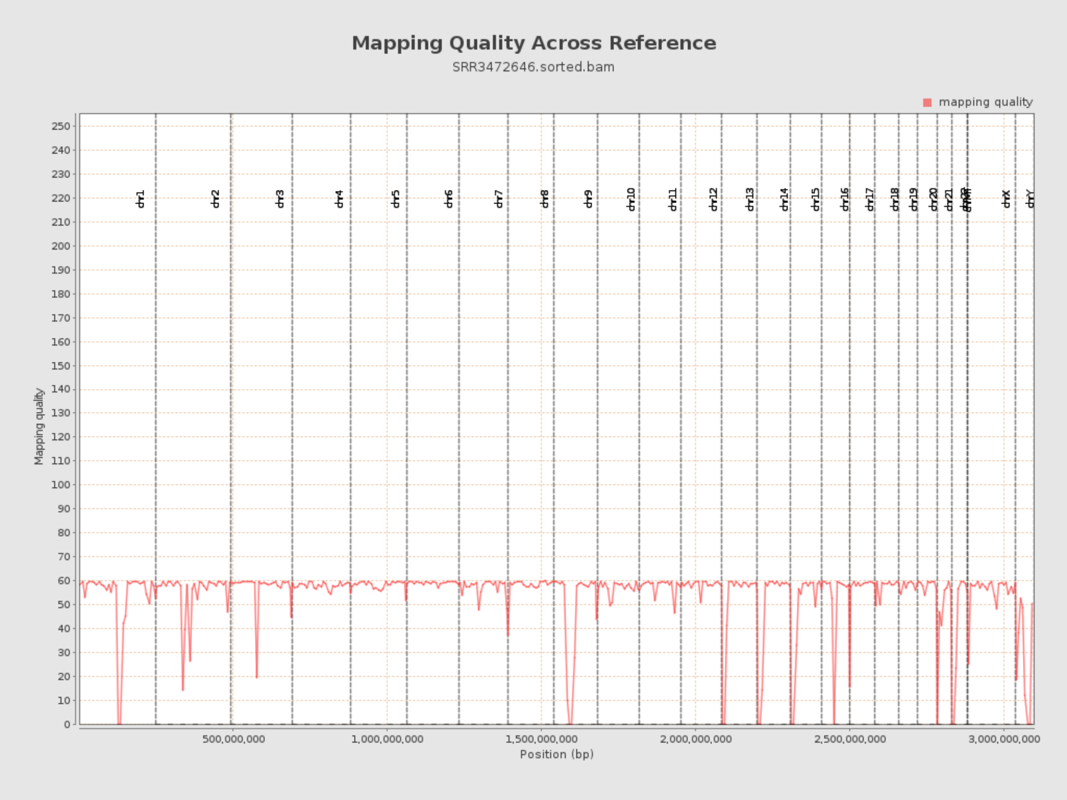
10. Results : Mapped Reads Clipping Profile



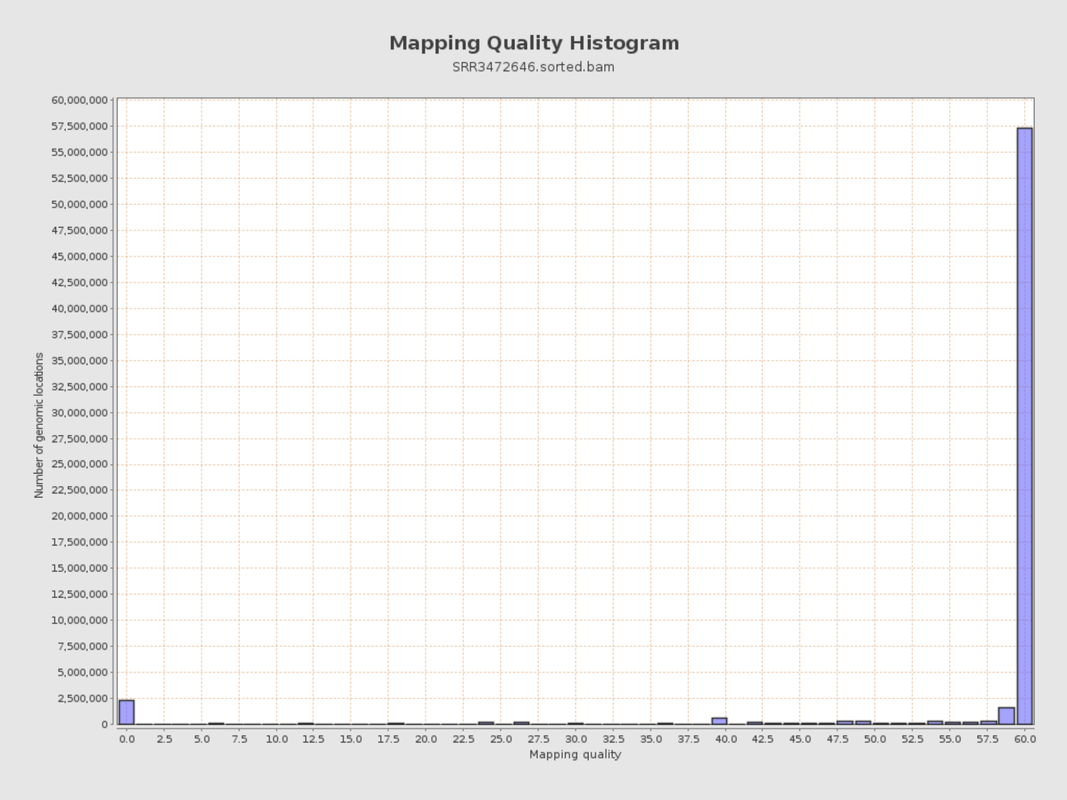
11. Results : Homopolymer Indels



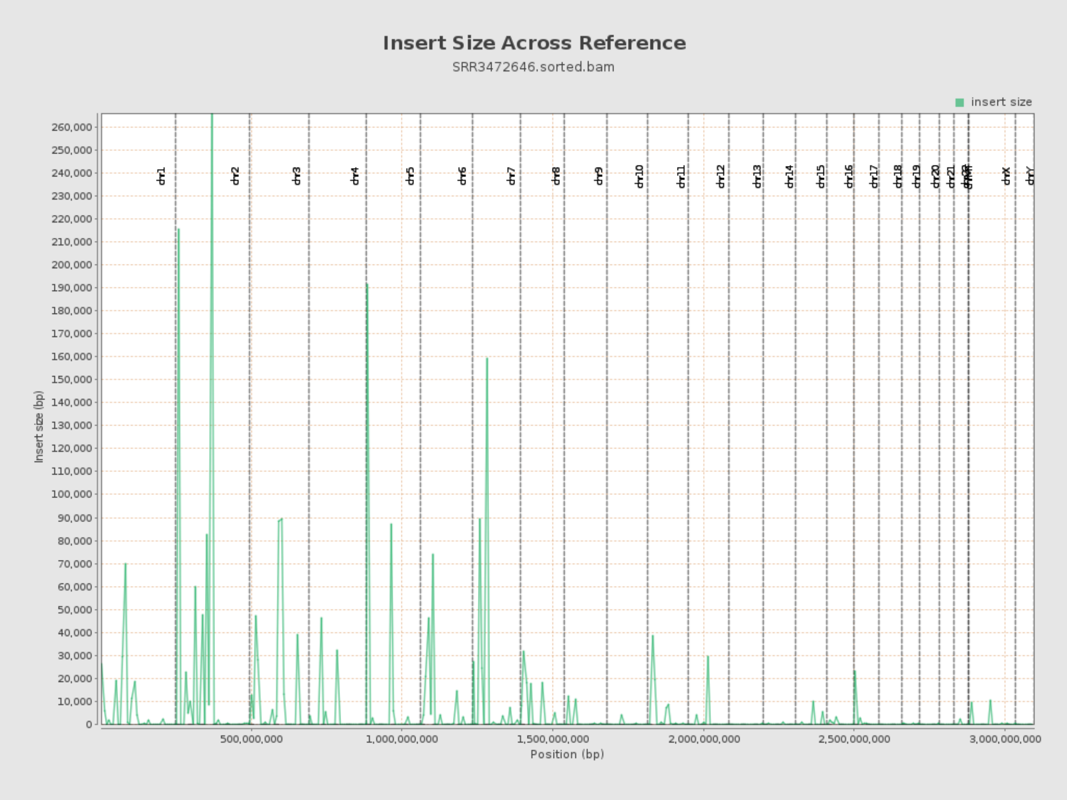
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram