Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 10:59:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472767.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_SRR3472767 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472767_1.fastq.gz SRR3472767_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 10:59:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472767.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,422,146
Mapped reads	15,216,361 / 98.67%
Unmapped reads	205,785 / 1.33%
Mapped paired reads	15,216,361 / 98.67%
Mapped reads, first in pair	7,658,776 / 49.66%
Mapped reads, second in pair	7,557,585 / 49%
Mapped reads, both in pair	15,080,736 / 97.79%
Mapped reads, singletons	135,625 / 0.88%
Secondary alignments	0
Supplementary alignments	51,608 / 0.33%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	9,300,452 / 60.31%
Duplication rate	47.24%
Clipped reads	1,155,460 / 7.49%

2.2. ACGT Content

Number/percentage of A's	419,458,580 / 27.97%
Number/percentage of C's	332,092,394 / 22.15%
Number/percentage of T's	417,305,594 / 27.83%
Number/percentage of G's	330,268,391 / 22.03%
Number/percentage of N's	291,263 / 0.02%

GC Percentage	44.17%

2.3. Coverage

Mean	0.4844
Standard Deviation	15.6527

2.4. Mapping Quality

Mean Mapping Quality	55.24

2.5. Insert size

Mean	24,854.39
Standard Deviation	1,573,265.93
P25/Median/P75	180 / 252 / 339

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	9,662,687
Insertions	92,599
Mapped reads with at least one insertion	0.6%
Deletions	90,925
Mapped reads with at least one deletion	0.59%
Homopolymer indels	44.97%

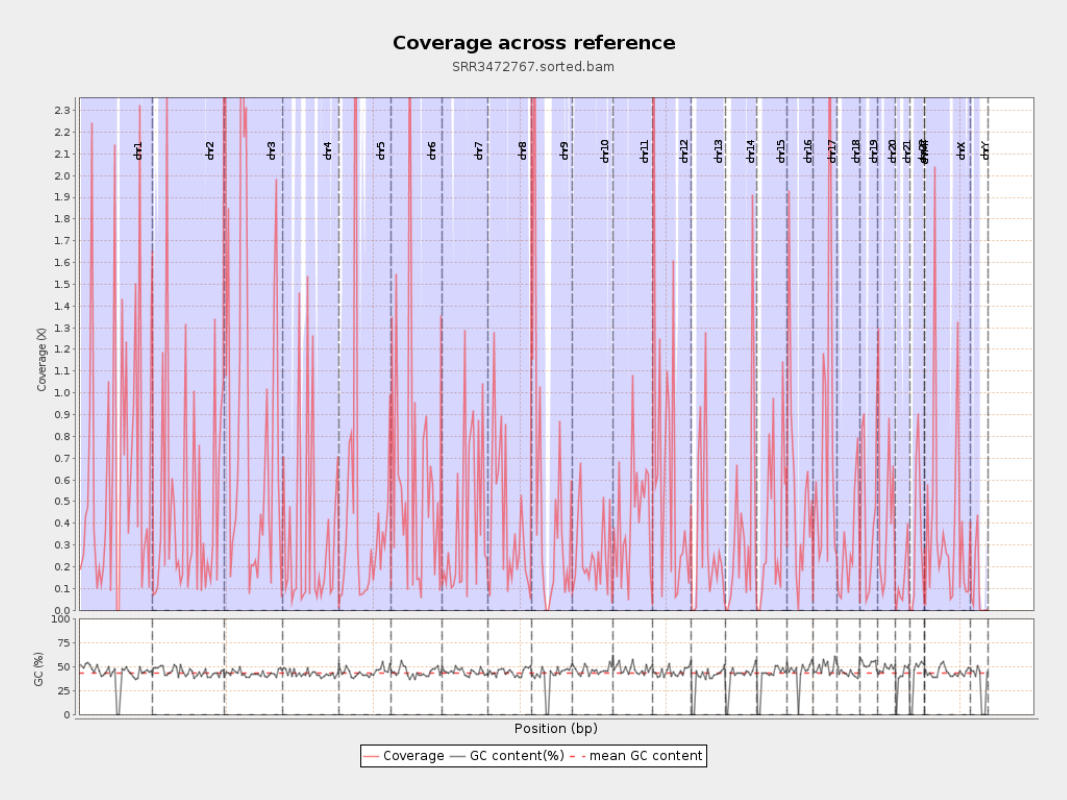
2.7. Chromosome stats

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

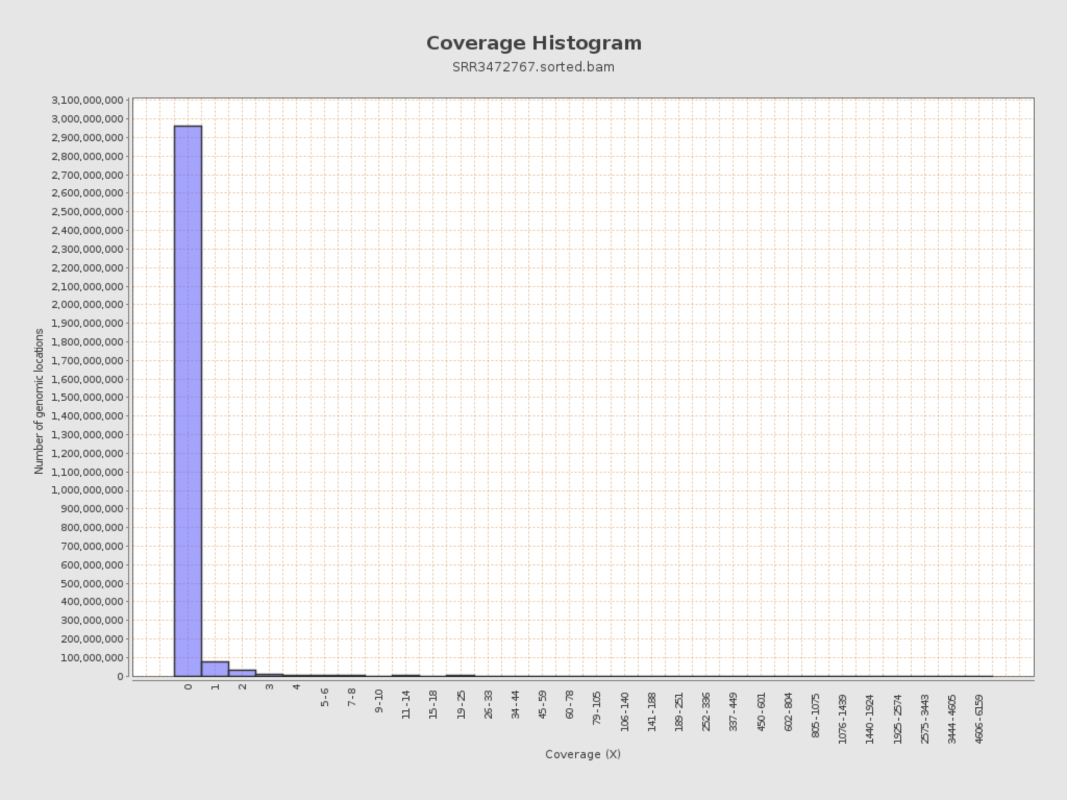
		bases	coverage	deviation
chr1	249250621	169497115	0.68	20.8053
chr2	243199373	116849702	0.4805	19.8577
chr3	198022430	186801550	0.9433	20.7304
chr4	191154276	65905931	0.3448	15.7521
chr5	180915260	81900820	0.4527	13.6877
chr6	171115067	108512437	0.6341	16.5928
chr7	159138663	66928185	0.4206	11.8594
chr8	146364022	59202247	0.4045	11.3656
chr9	141213431	72431751	0.5129	13.1852
chr10	135534747	34585034	0.2552	7.6974
chr11	135006516	58956714	0.4367	16.3607
chr12	133851895	87949155	0.6571	20.1576
chr13	115169878	36141800	0.3138	12.5716
chr14	107349540	36707829	0.3419	16.5539
chr15	102531392	40455219	0.3946	12.7191
chr16	90354753	48821813	0.5403	15.308
chr17	81195210	62543783	0.7703	20.6257
chr18	78077248	23046891	0.2952	10.2224
chr19	59128983	24913103	0.4213	9.3788
chr20	63025520	29219403	0.4636	12.2422
chr21	48129895	6399861	0.133	4.7656
chr22	51304566	16066017	0.3131	10.1594
chrMT	16571	4733	0.2856	0.935
chrX	155270560	59583327	0.3837	12.7044

chrY	59373566	6216387	0.1047	6.4444

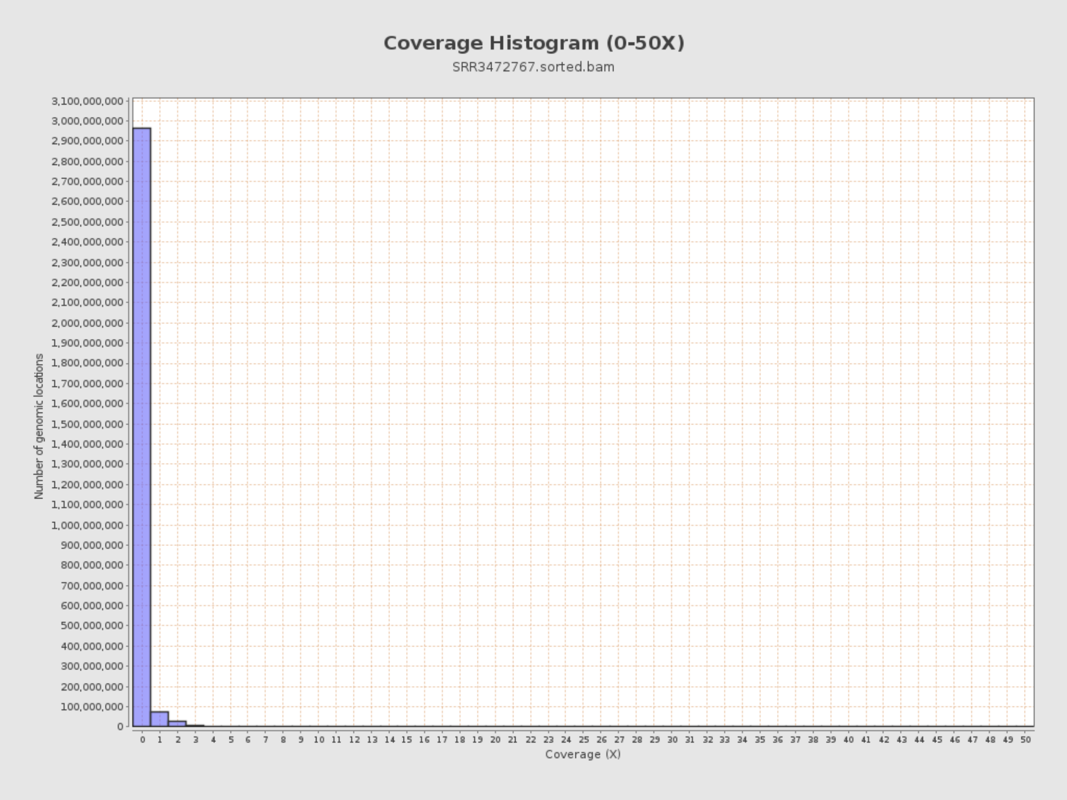
3. Results : Coverage across reference



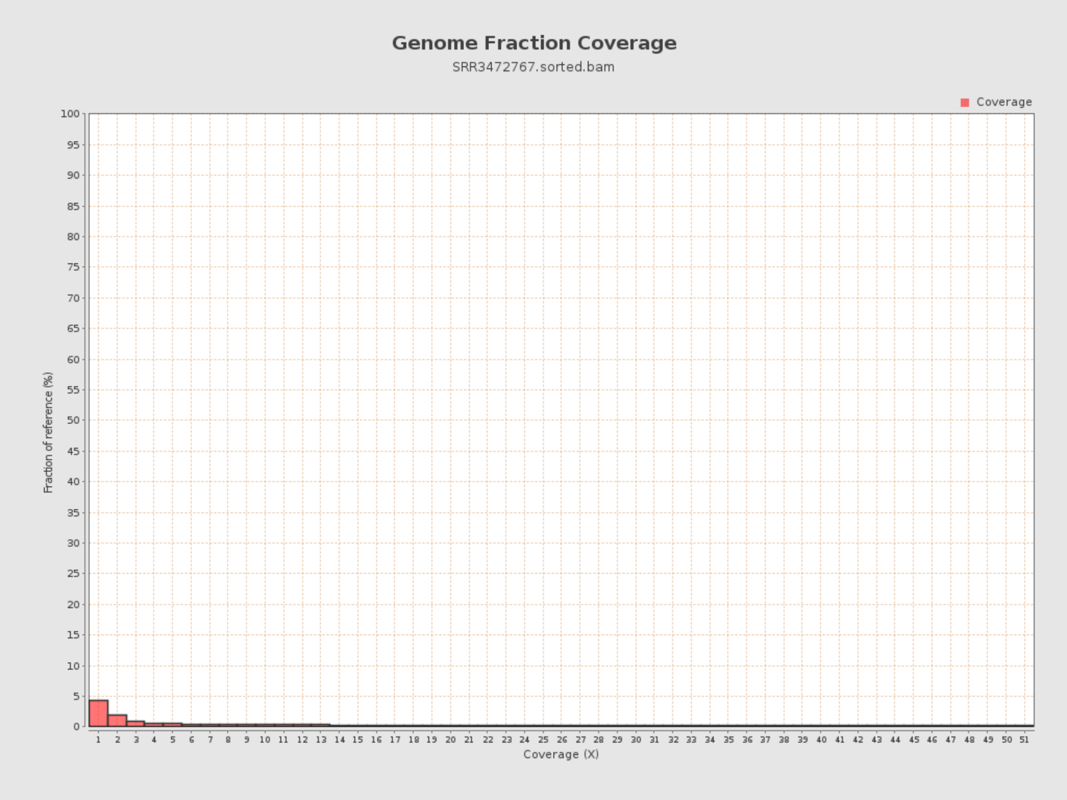
4. Results : Coverage Histogram



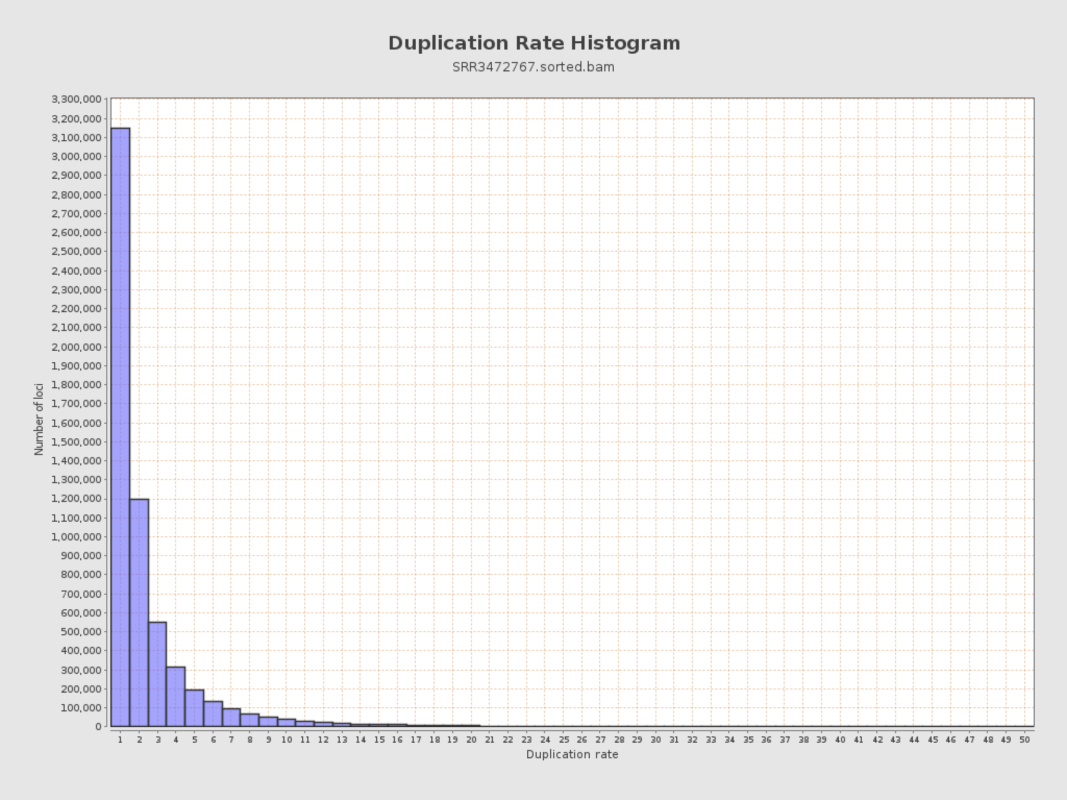
5. Results : Coverage Histogram (0-50X)



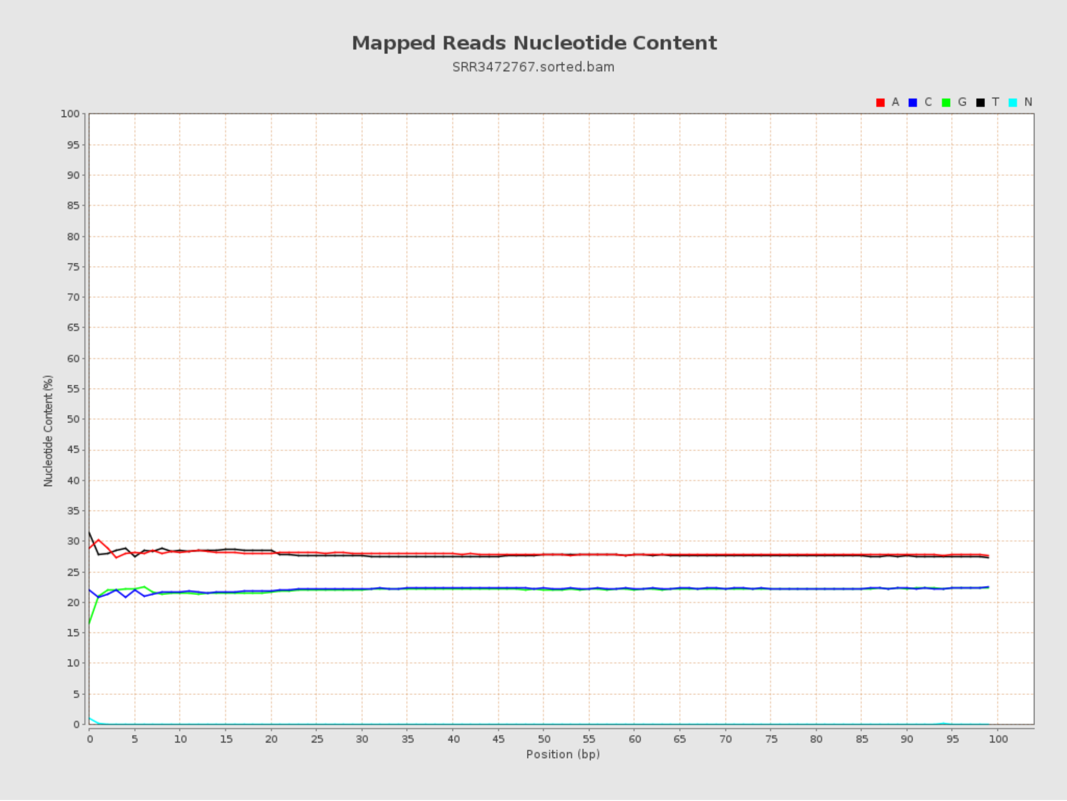
6. Results : Genome Fraction Coverage



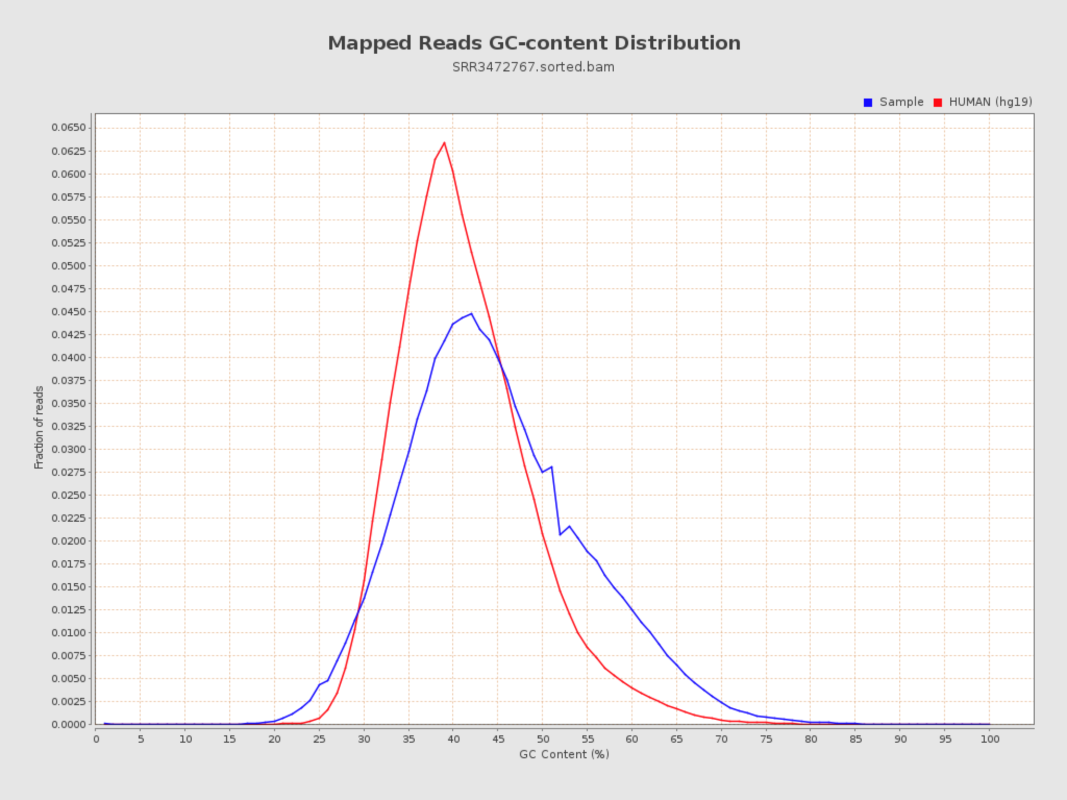
7. Results : Duplication Rate Histogram



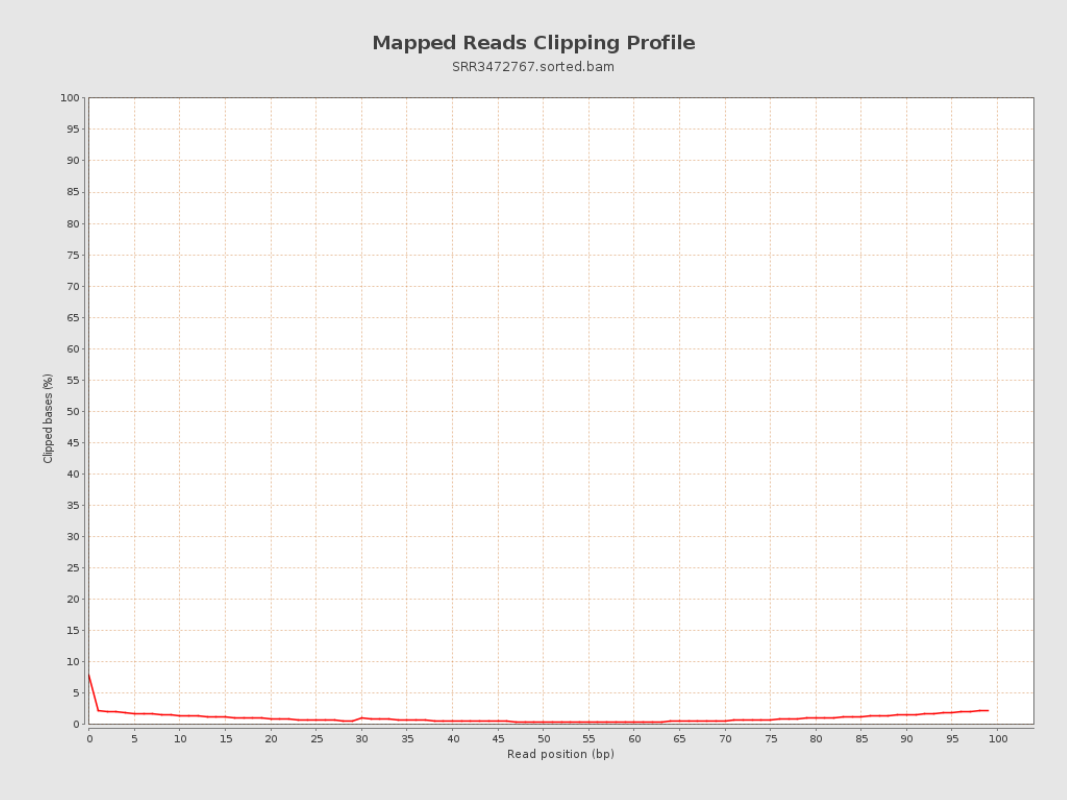
8. Results : Mapped Reads Nucleotide Content



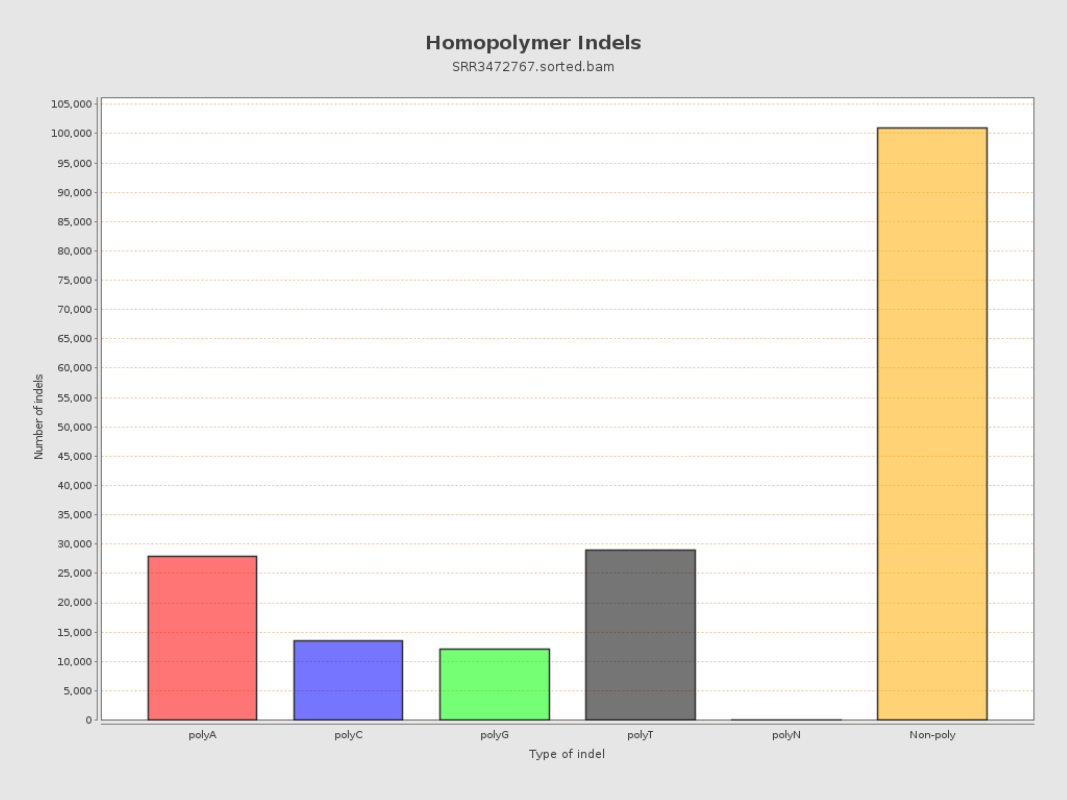
9. Results : Mapped Reads GC-content Distribution



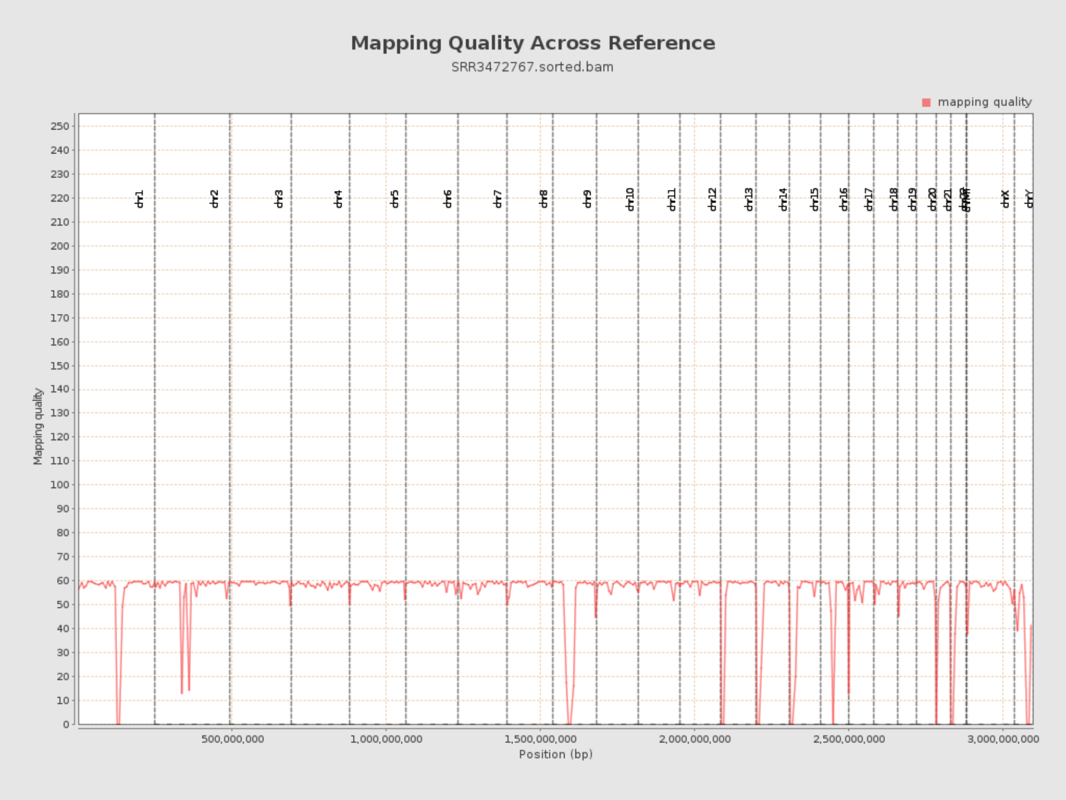
10. Results : Mapped Reads Clipping Profile



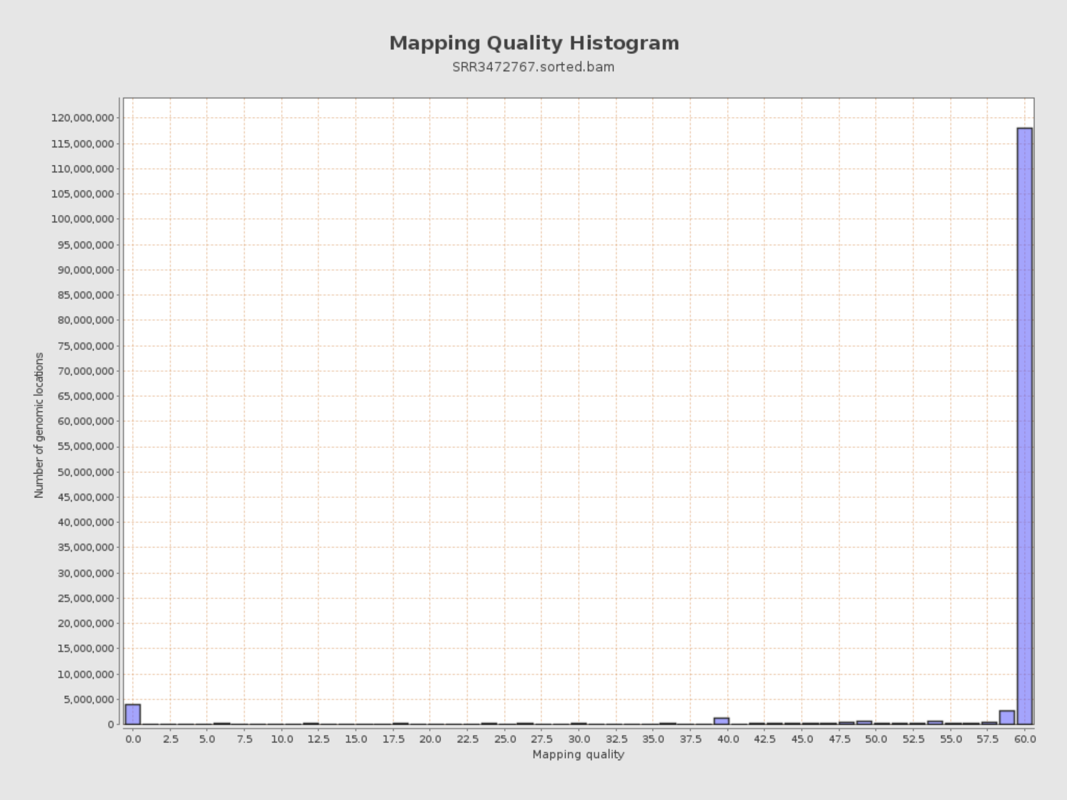
11. Results : Homopolymer Indels



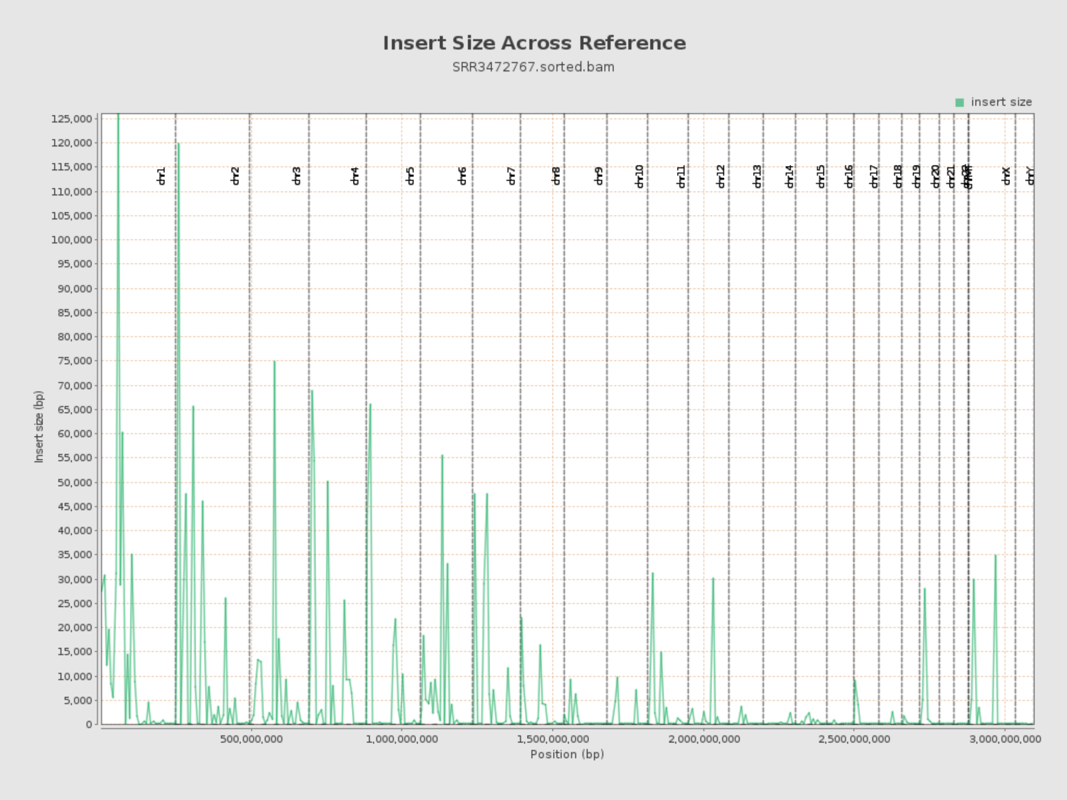
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram