Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 00:51:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472661.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_SRR3472661 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472661_1.fastq.gz SRR3472661_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 00:51:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472661.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,699,962
Mapped reads	18,534,029 / 99.11%
Unmapped reads	165,933 / 0.89%
Mapped paired reads	18,534,029 / 99.11%
Mapped reads, first in pair	9,291,708 / 49.69%
Mapped reads, second in pair	9,242,321 / 49.42%
Mapped reads, both in pair	18,427,822 / 98.54%
Mapped reads, singletons	106,207 / 0.57%
Secondary alignments	0
Supplementary alignments	117,950 / 0.63%
Read min/max/mean length	30 / 101 / 99.78
Duplicated reads (estimated)	13,080,851 / 69.95%
Duplication rate	49.14%
Clipped reads	1,286,129 / 6.88%

2.2. ACGT Content

Number/percentage of A's	496,916,285 / 27.23%
Number/percentage of C's	417,248,497 / 22.86%
Number/percentage of T's	499,219,430 / 27.35%
Number/percentage of G's	411,287,417 / 22.54%
Number/percentage of N's	345,805 / 0.02%

GC Percentage	45.4%

2.3. Coverage

Mean	0.5896
Standard Deviation	27.4053

2.4. Mapping Quality

Mean Mapping Quality	54.68

2.5. Insert size

Mean	25,205.71
Standard Deviation	1,578,601.11
P25/Median/P75	162 / 220 / 289

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	11,058,493
Insertions	112,633
Mapped reads with at least one insertion	0.6%
Deletions	99,436
Mapped reads with at least one deletion	0.53%
Homopolymer indels	47.53%

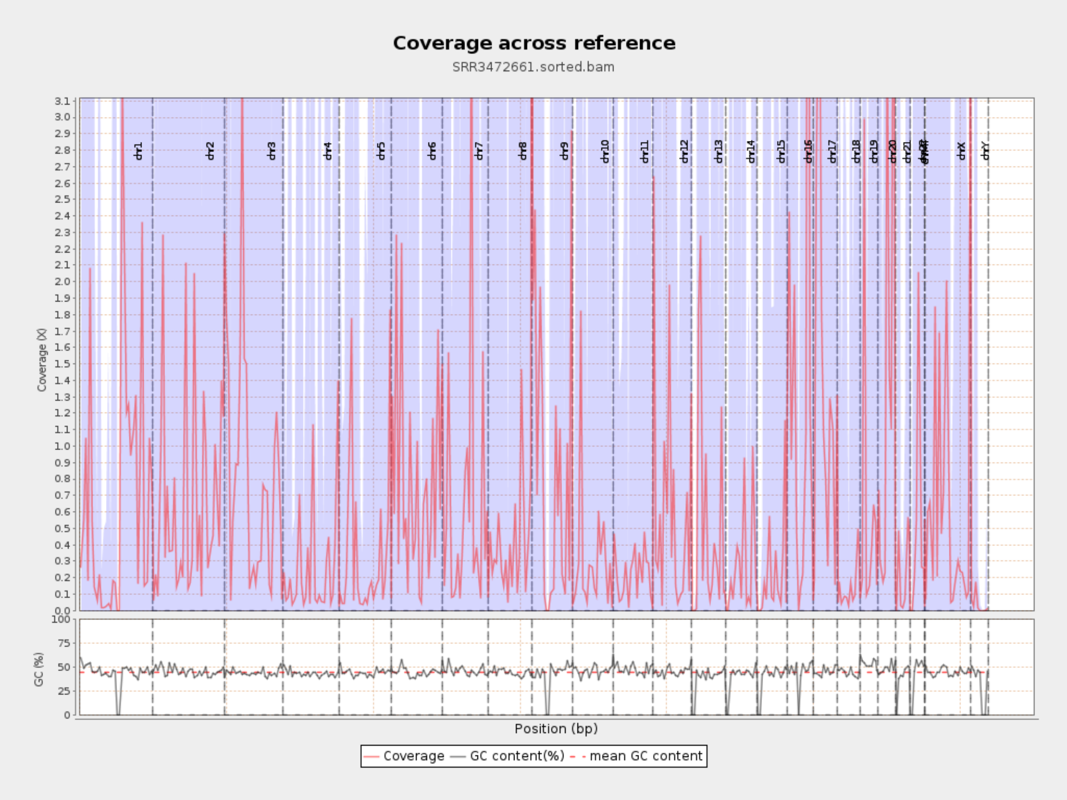
2.7. Chromosome stats

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

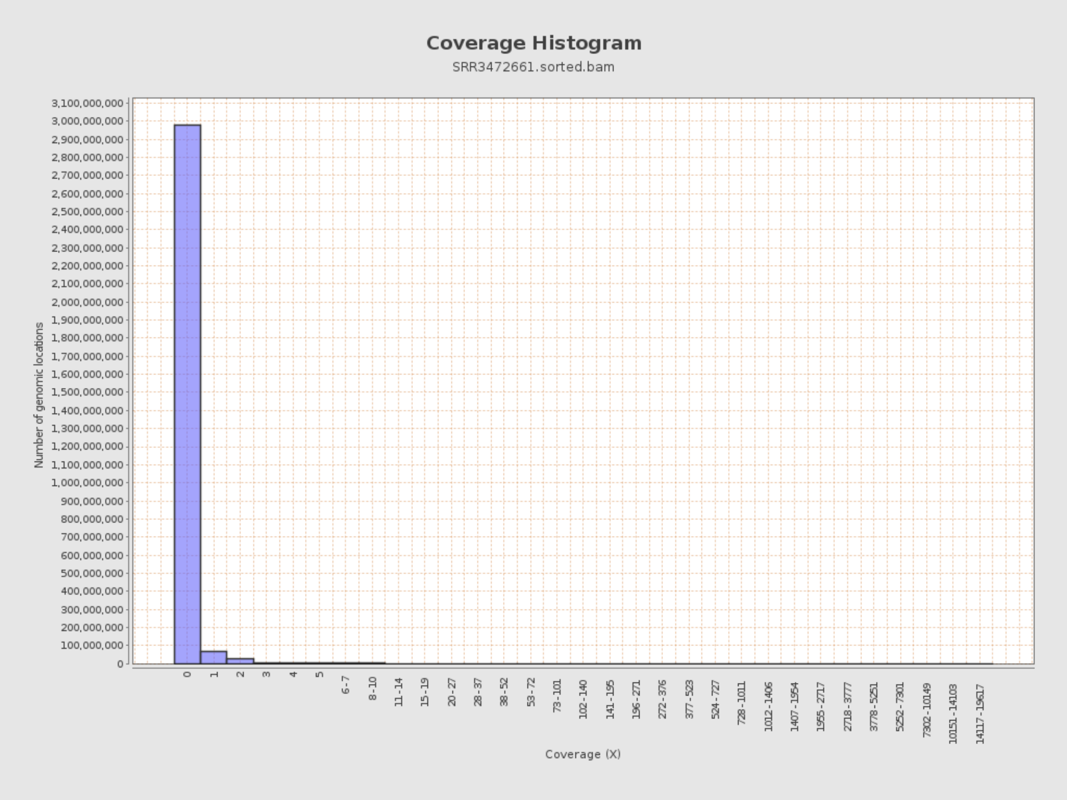
		bases	coverage	deviation
chr1	249250621	174712934	0.701	31.1046
chr2	243199373	158219914	0.6506	30.9656
chr3	198022430	169692095	0.8569	23.5511
chr4	191154276	47543795	0.2487	13.6376
chr5	180915260	64016742	0.3538	19.643
chr6	171115067	131313684	0.7674	22.4869
chr7	159138663	107407566	0.6749	28.0017
chr8	146364022	60290104	0.4119	16.5245
chr9	141213431	131352150	0.9302	27.4922
chr10	135534747	42338503	0.3124	25.4682
chr11	135006516	30988826	0.2295	8.3726
chr12	133851895	81703519	0.6104	22.9334
chr13	115169878	60147762	0.5223	23.3452
chr14	107349540	27477845	0.256	10.0441
chr15	102531392	23530921	0.2295	12.1526
chr16	90354753	124316241	1.3759	56.9808
chr17	81195210	110791658	1.3645	63.3782
chr18	78077248	11517662	0.1475	6.6691
chr19	59128983	39028837	0.6601	22.2151
chr20	63025520	96135225	1.5253	61.6206
chr21	48129895	11501256	0.239	12.6275
chr22	51304566	25743070	0.5018	29.5152
chrMT	16571	9183	0.5542	0.8738
chrX	155270560	93381287	0.6014	22.1345

chrY	59373566	2103548	0.0354	3.4997

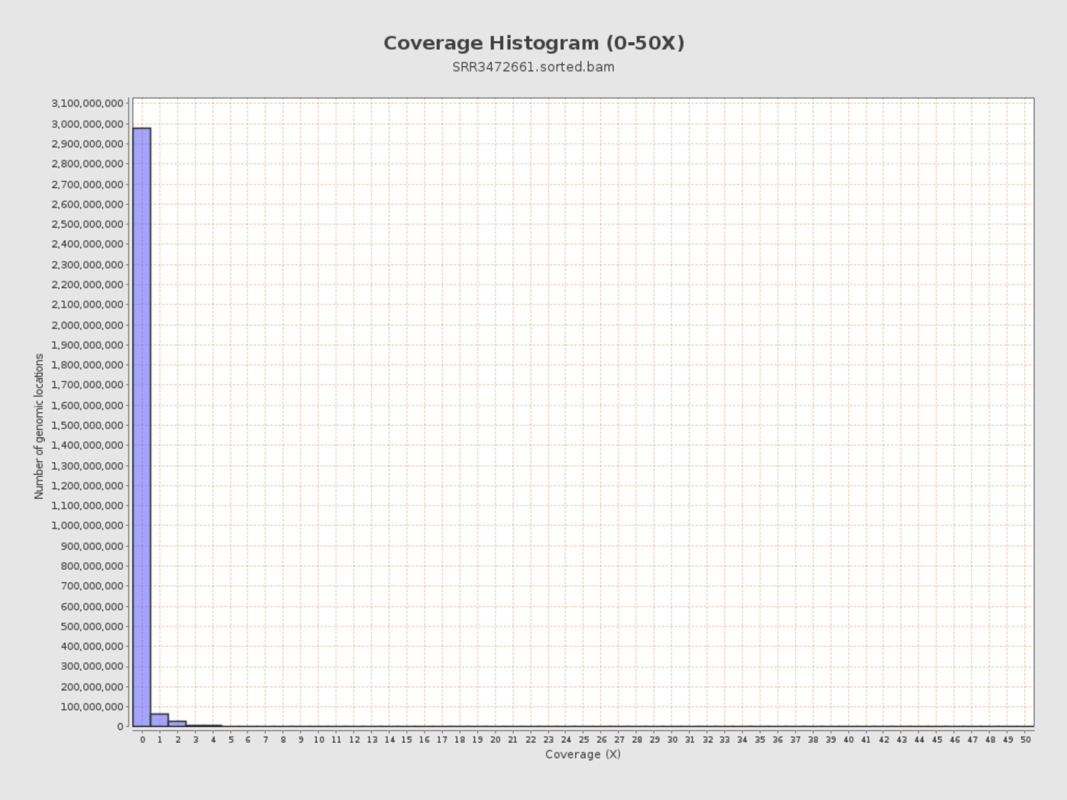
3. Results : Coverage across reference



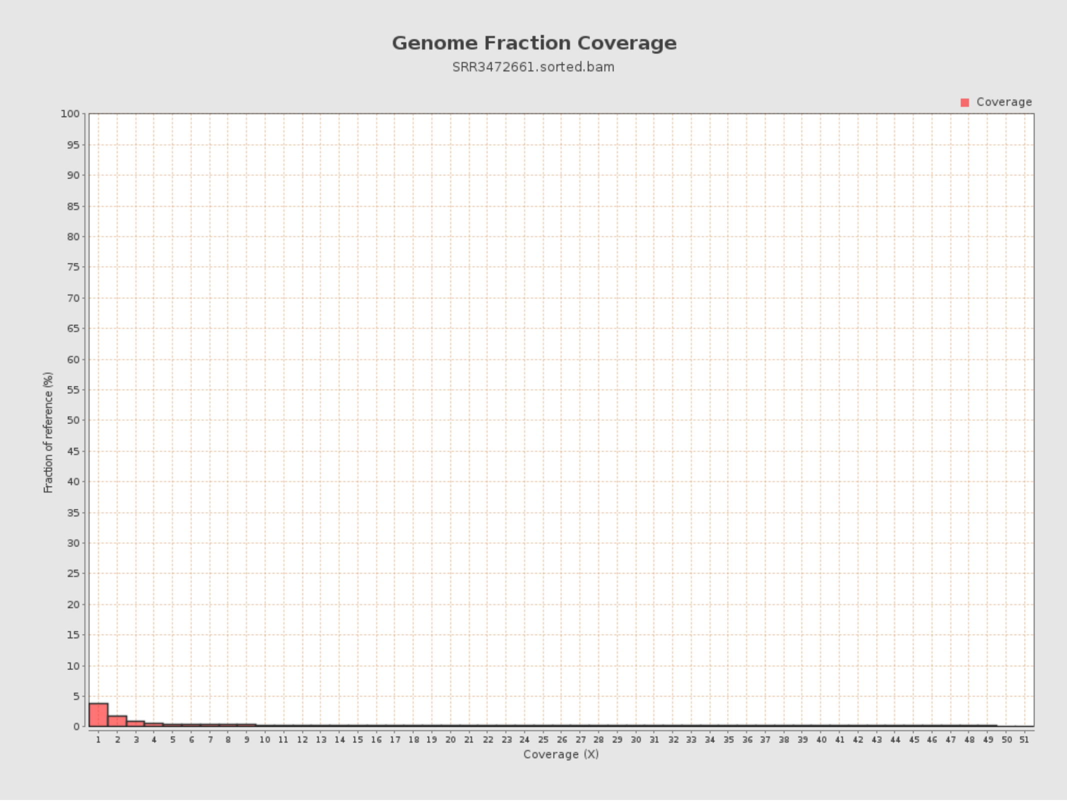
4. Results : Coverage Histogram



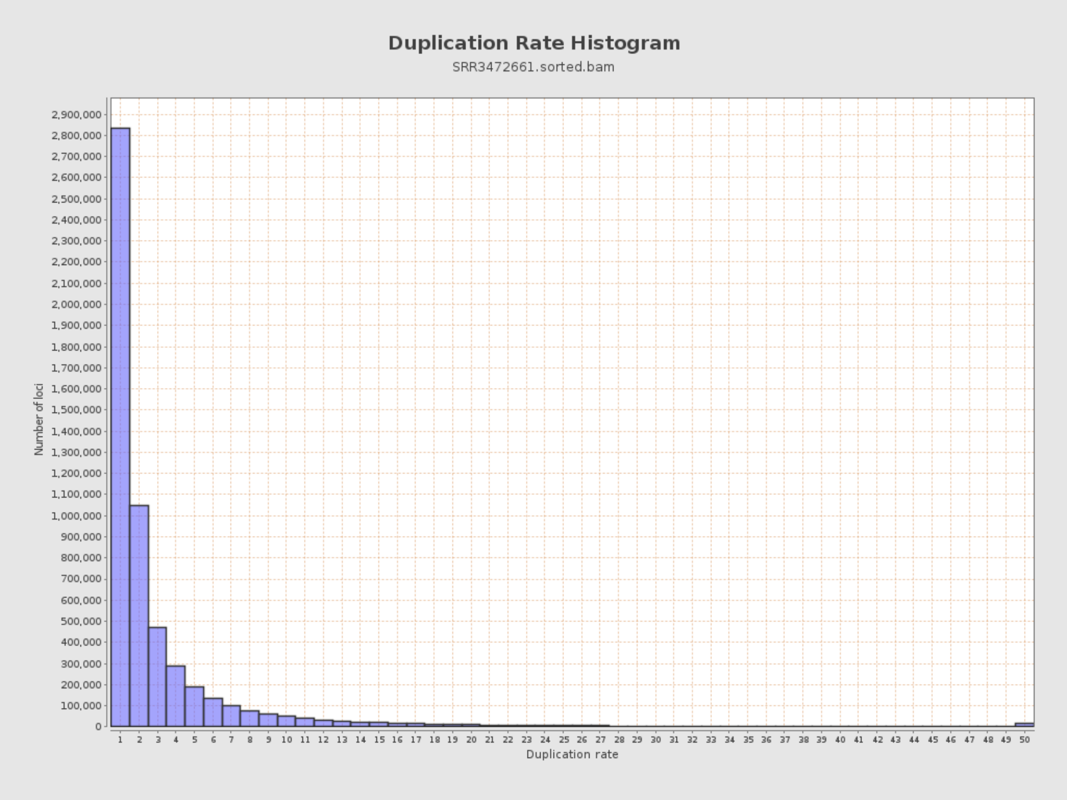
5. Results : Coverage Histogram (0-50X)



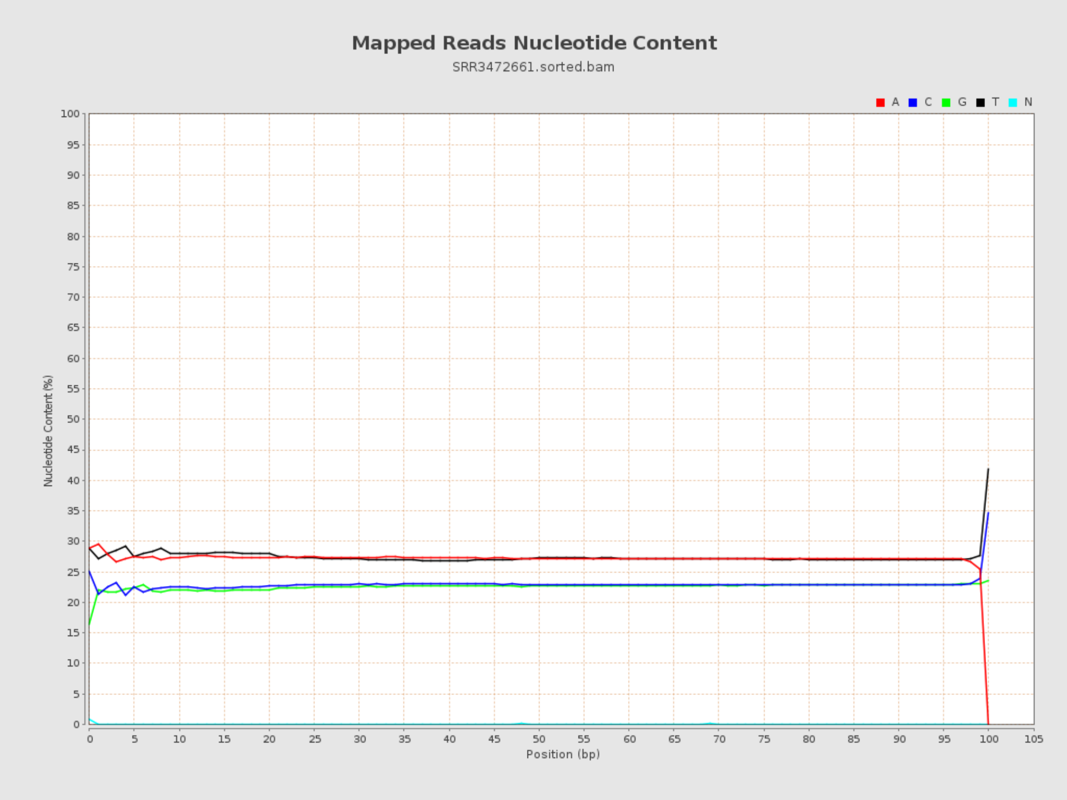
6. Results : Genome Fraction Coverage



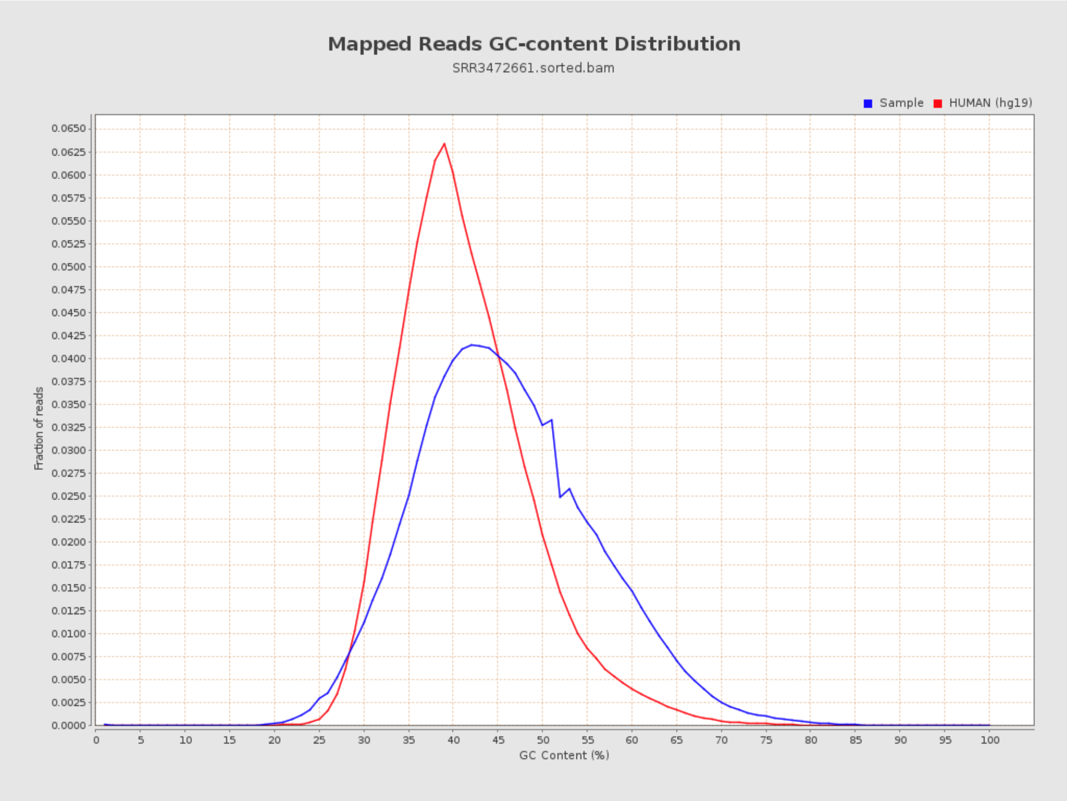
7. Results : Duplication Rate Histogram



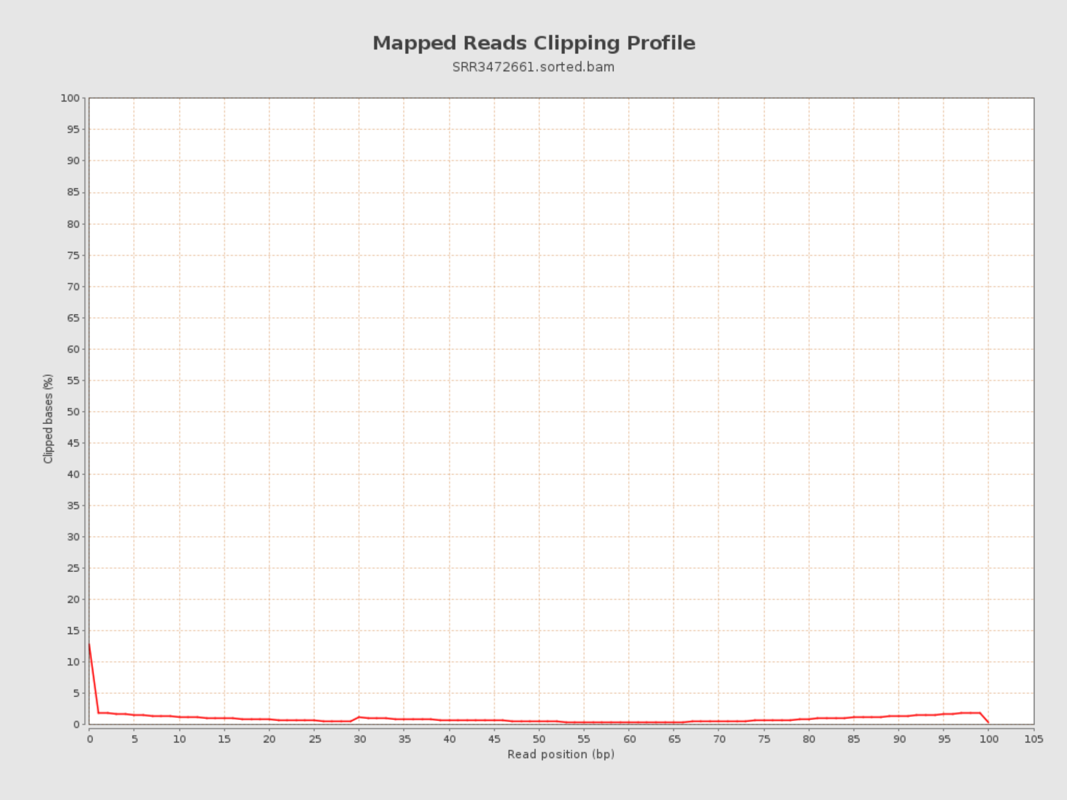
8. Results : Mapped Reads Nucleotide Content



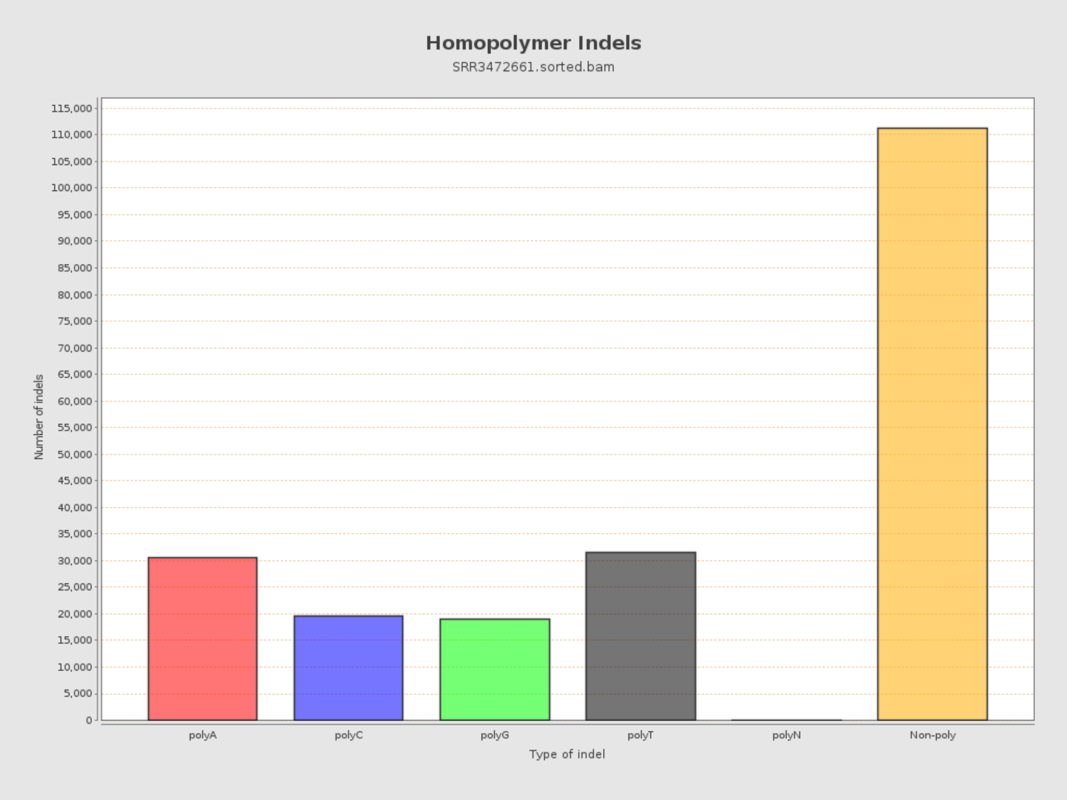
9. Results : Mapped Reads GC-content Distribution



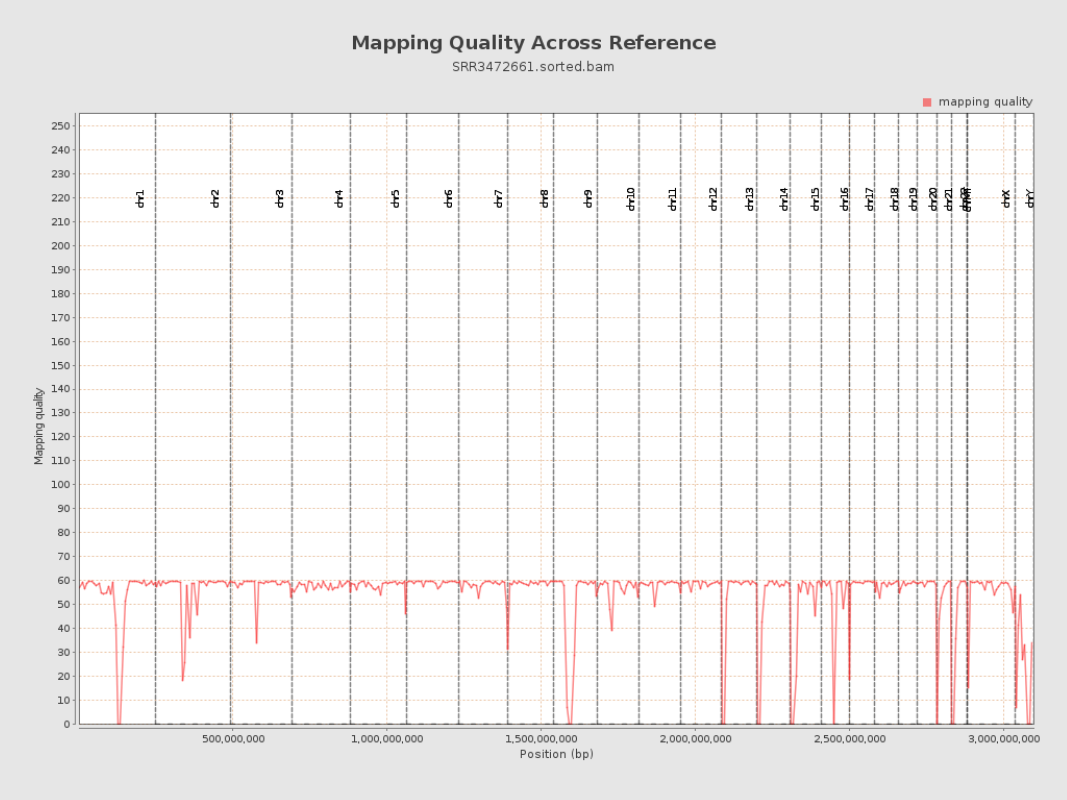
10. Results : Mapped Reads Clipping Profile



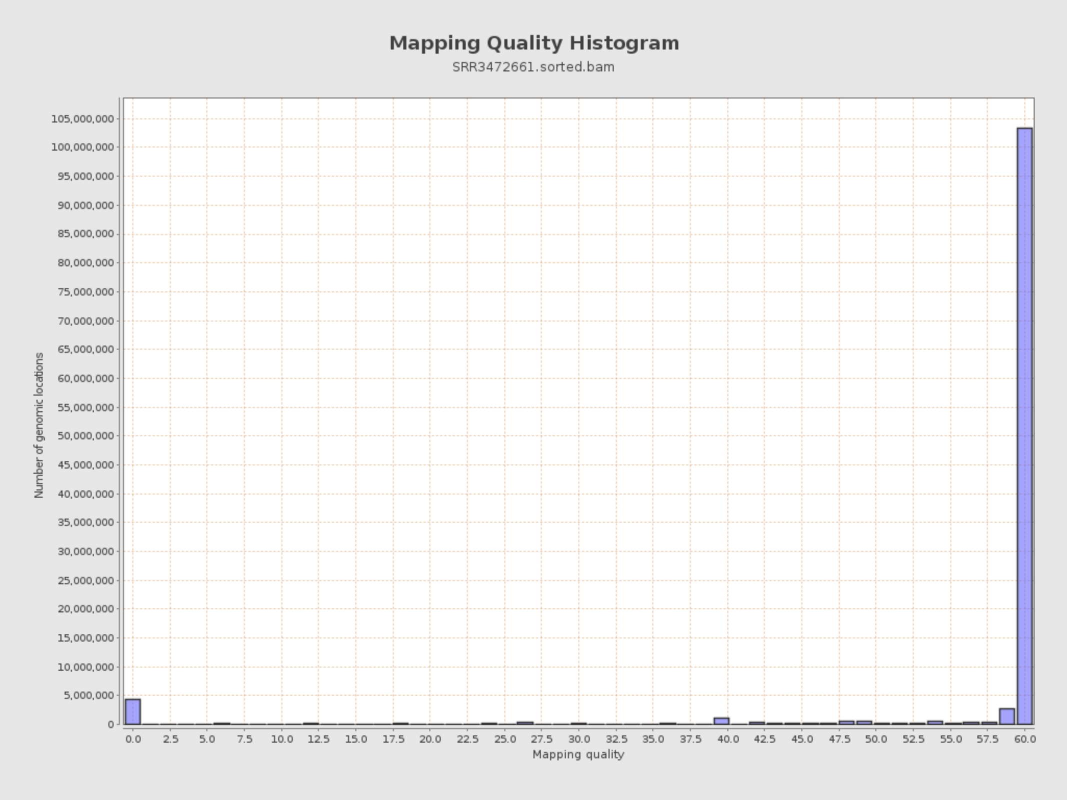
11. Results : Homopolymer Indels



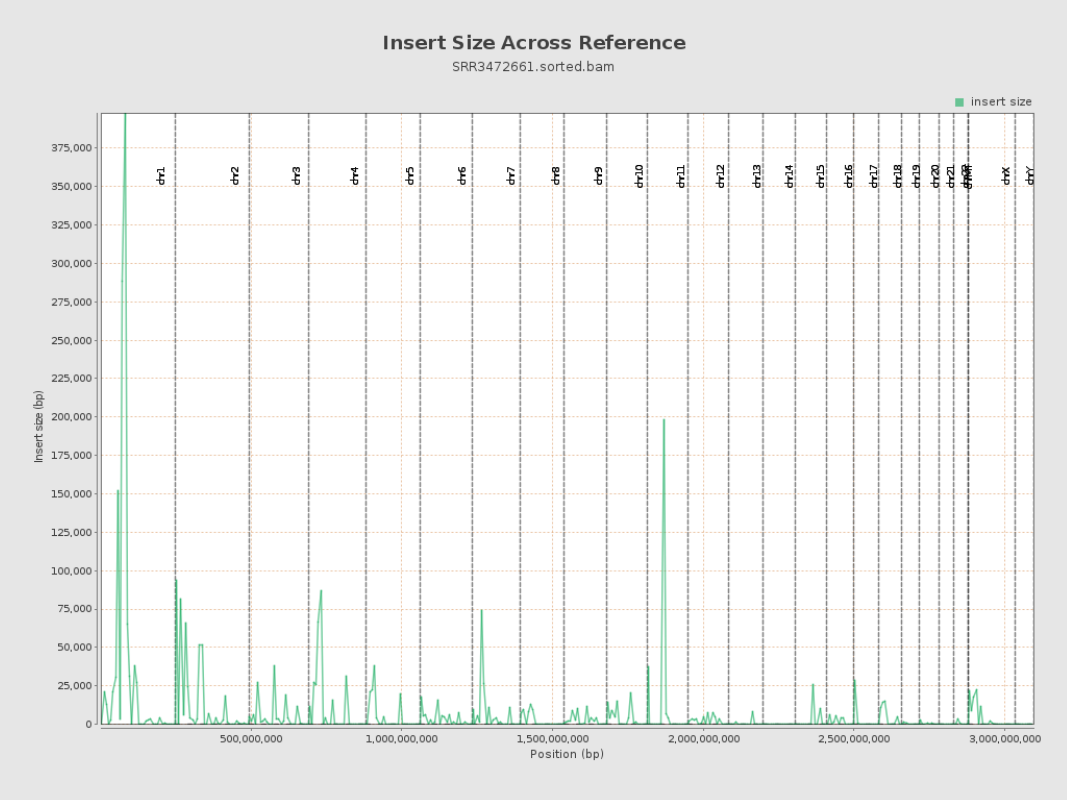
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram