Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 15:58:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472781.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_SRR3472781 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472781_1.fastq.gz SRR3472781_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 15:58:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472781.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,734,862
Mapped reads	12,585,527 / 98.83%
Unmapped reads	149,335 / 1.17%
Mapped paired reads	12,585,527 / 98.83%
Mapped reads, first in pair	6,327,197 / 49.68%
Mapped reads, second in pair	6,258,330 / 49.14%
Mapped reads, both in pair	12,487,628 / 98.06%
Mapped reads, singletons	97,899 / 0.77%
Secondary alignments	0
Supplementary alignments	47,575 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	7,620,749 / 59.84%
Duplication rate	46%
Clipped reads	1,073,821 / 8.43%

2.2. ACGT Content

Number/percentage of A's	340,539,189 / 27.51%
Number/percentage of C's	280,239,739 / 22.64%
Number/percentage of T's	338,393,034 / 27.34%
Number/percentage of G's	278,482,495 / 22.5%
Number/percentage of N's	239,086 / 0.02%

GC Percentage	45.13%

2.3. Coverage

Mean	0.3999
Standard Deviation	14.1455

2.4. Mapping Quality

Mean Mapping Quality	55.03

2.5. Insert size

Mean	27,311.07
Standard Deviation	1,622,164.91
P25/Median/P75	171 / 242 / 329

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	7,781,824
Insertions	77,332
Mapped reads with at least one insertion	0.61%
Deletions	68,116
Mapped reads with at least one deletion	0.53%
Homopolymer indels	43.83%

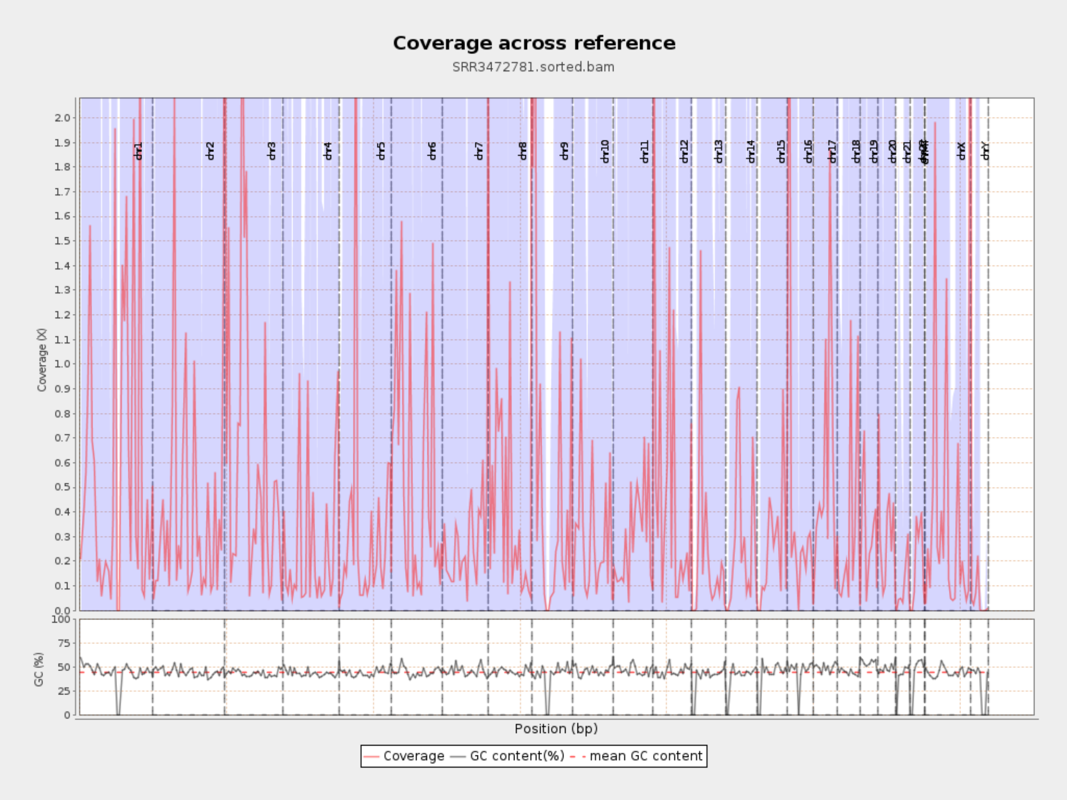
2.7. Chromosome stats

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

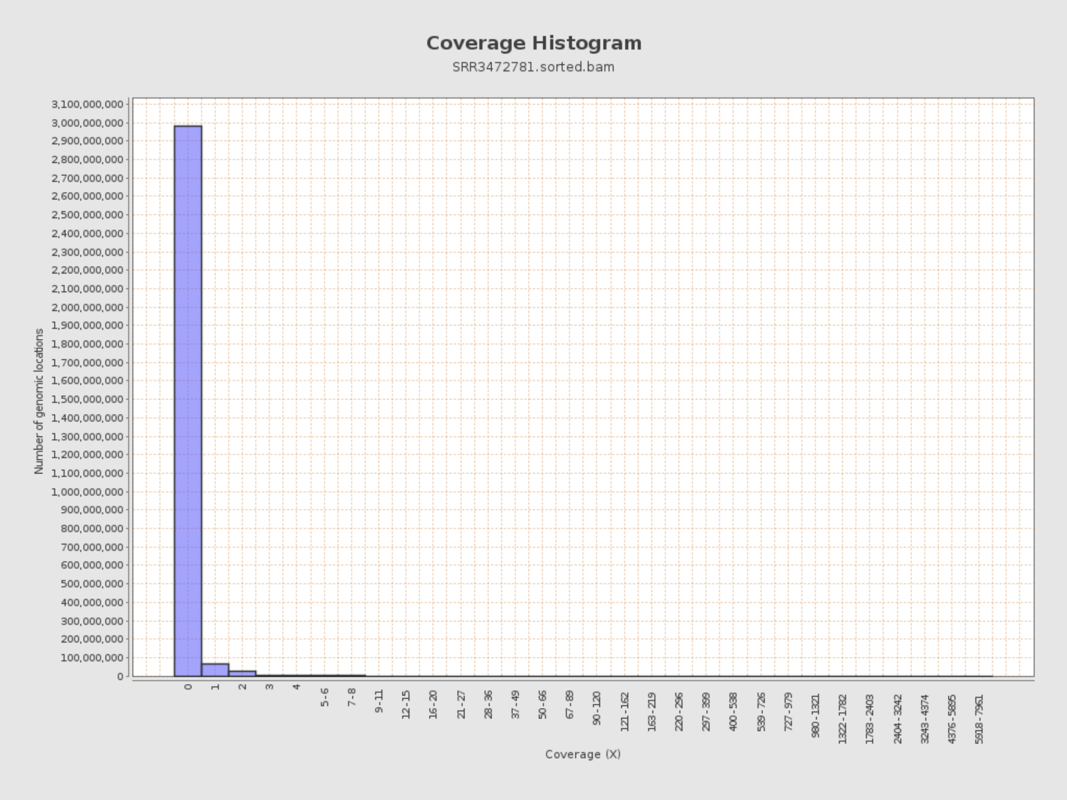
		bases	coverage	deviation
chr1	249250621	150071490	0.6021	22.6484
chr2	243199373	92420266	0.38	13.9944
chr3	198022430	130855975	0.6608	17.4353
chr4	191154276	48864216	0.2556	10.8882
chr5	180915260	60768050	0.3359	11.3211
chr6	171115067	94273930	0.5509	16.684
chr7	159138663	43150461	0.2712	9.6301
chr8	146364022	55547001	0.3795	13.6473
chr9	141213431	85055297	0.6023	17.7842
chr10	135534747	40598035	0.2995	14.2402
chr11	135006516	41070498	0.3042	10.4634
chr12	133851895	72265147	0.5399	15.7219
chr13	115169878	26975072	0.2342	9.938
chr14	107349540	29925214	0.2788	10.2409
chr15	102531392	27521756	0.2684	9.5721
chr16	90354753	44054988	0.4876	15.1213
chr17	81195210	45201575	0.5567	14.4845
chr18	78077248	26923622	0.3448	16.0052
chr19	59128983	19754105	0.3341	6.8115
chr20	63025520	20370883	0.3232	10.5079
chr21	48129895	4841463	0.1006	3.5526
chr22	51304566	9585607	0.1868	5.1234
chrMT	16571	1789	0.108	0.3791
chrX	155270560	65198310	0.4199	13.0296

chrY	59373566	2771564	0.0467	2.7111

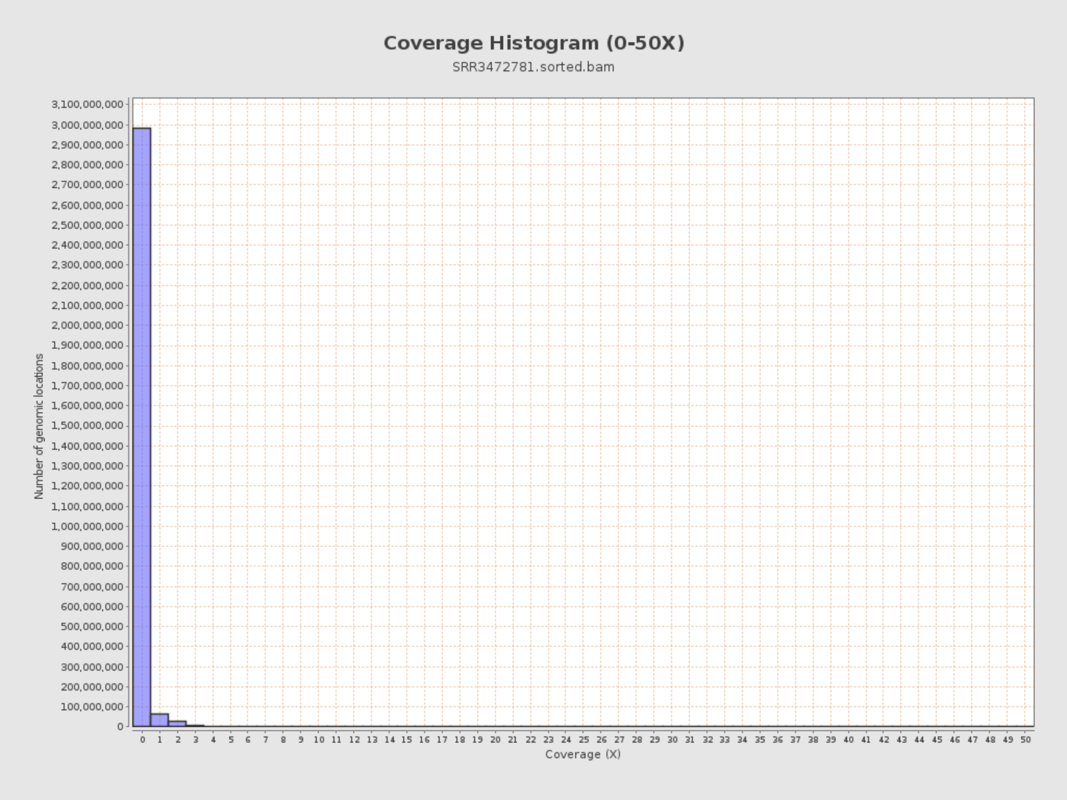
3. Results : Coverage across reference



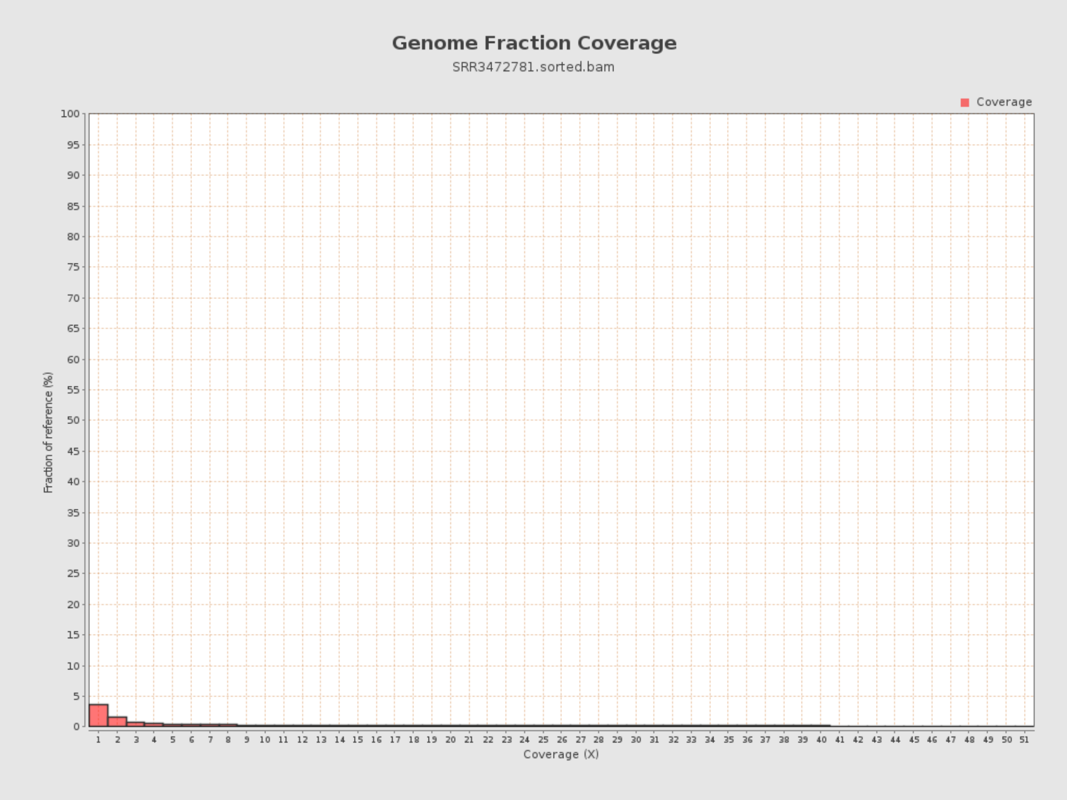
4. Results : Coverage Histogram



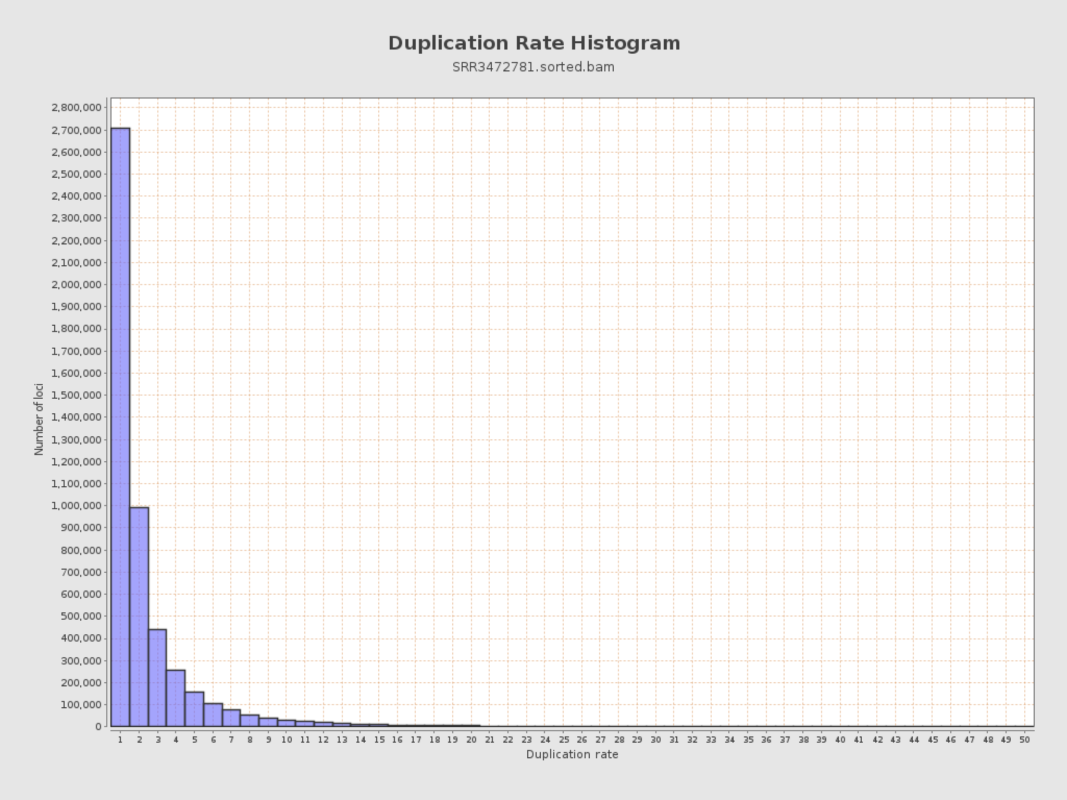
5. Results : Coverage Histogram (0-50X)



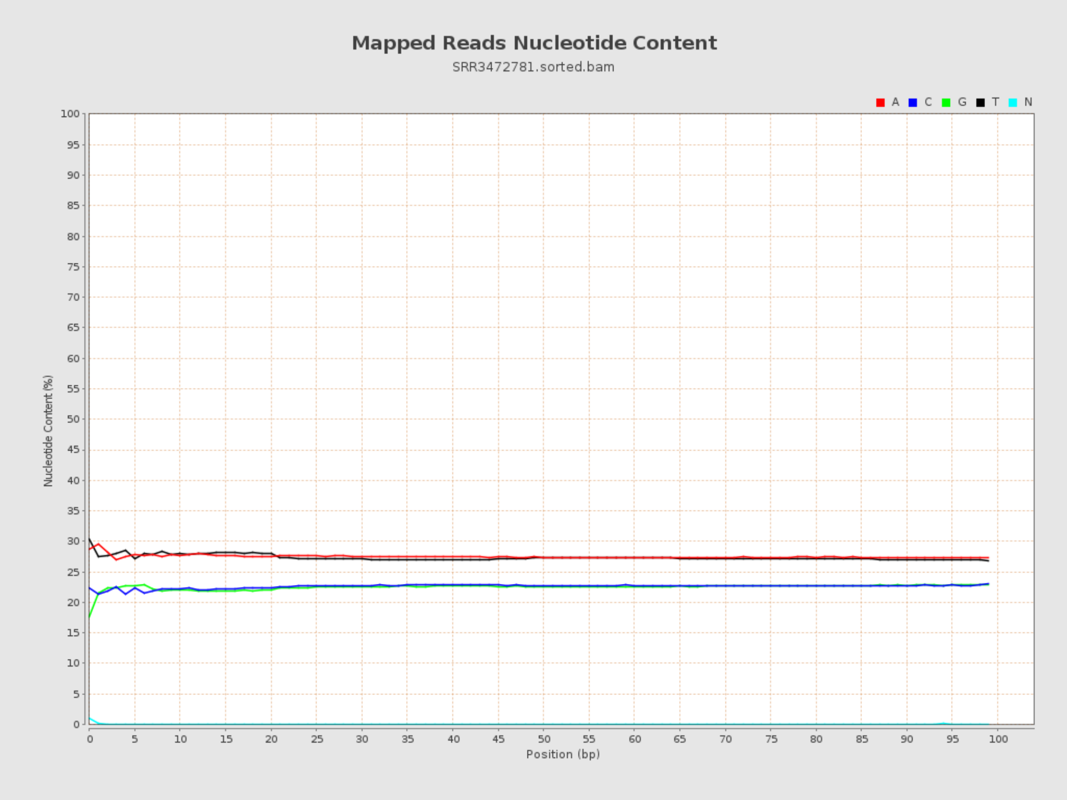
6. Results : Genome Fraction Coverage



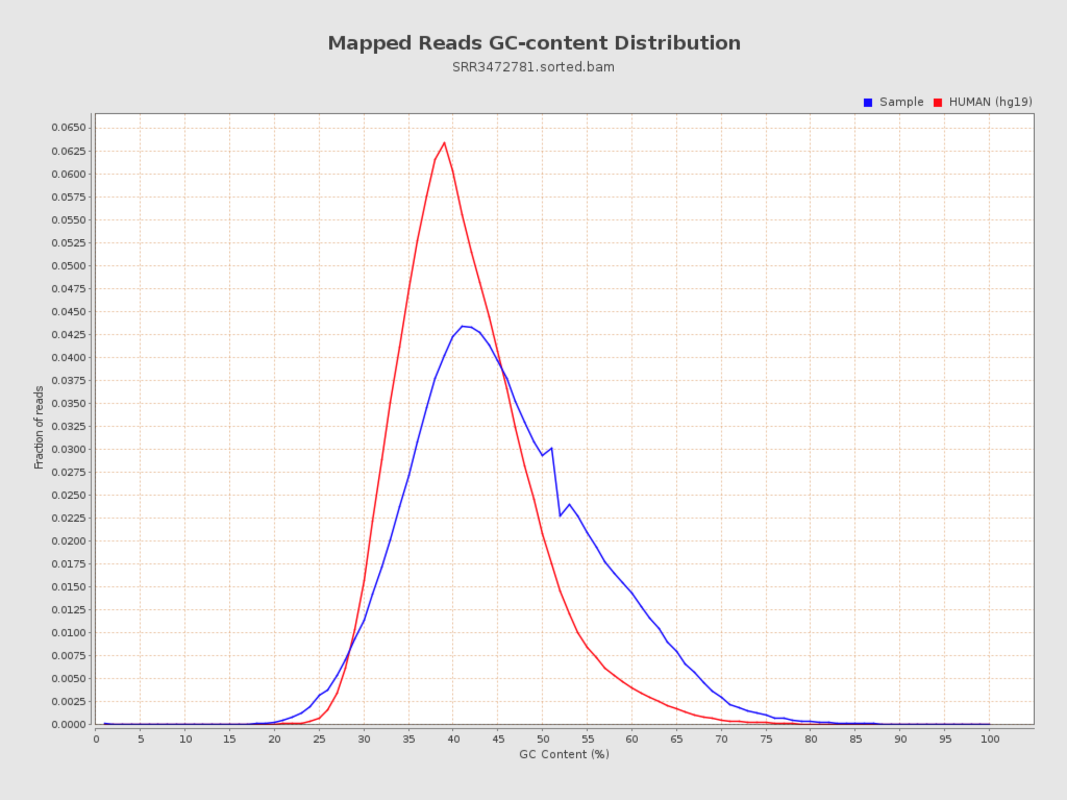
7. Results : Duplication Rate Histogram



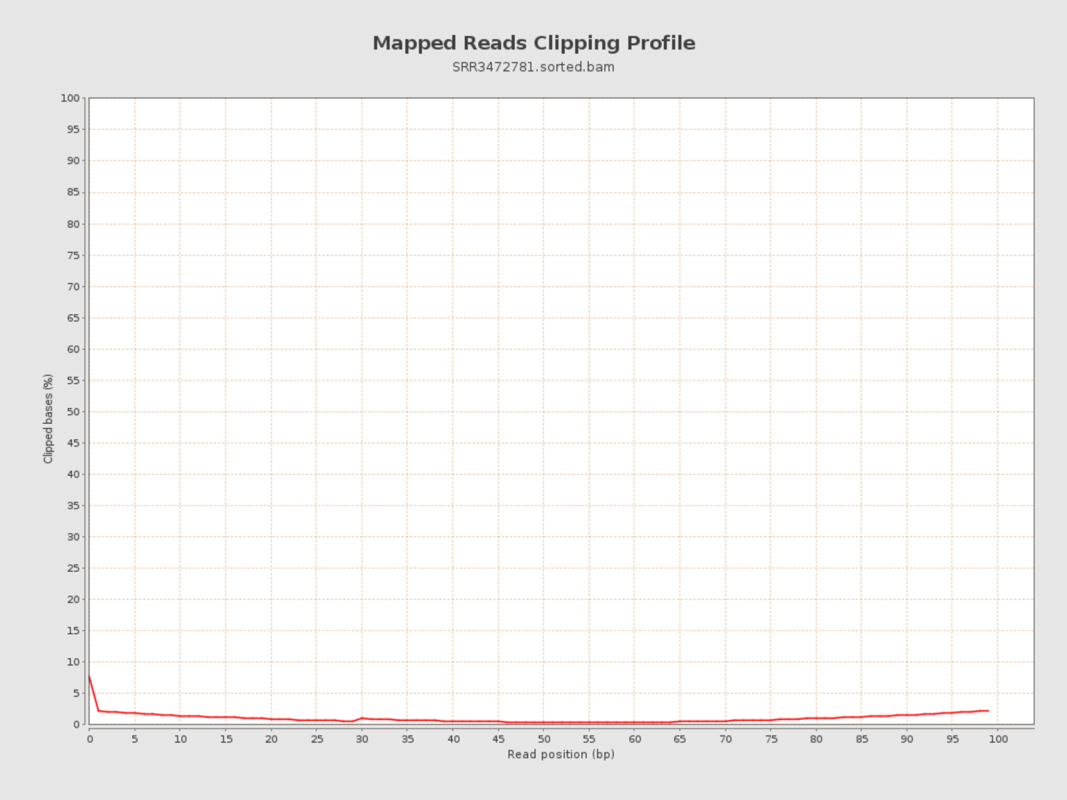
8. Results : Mapped Reads Nucleotide Content



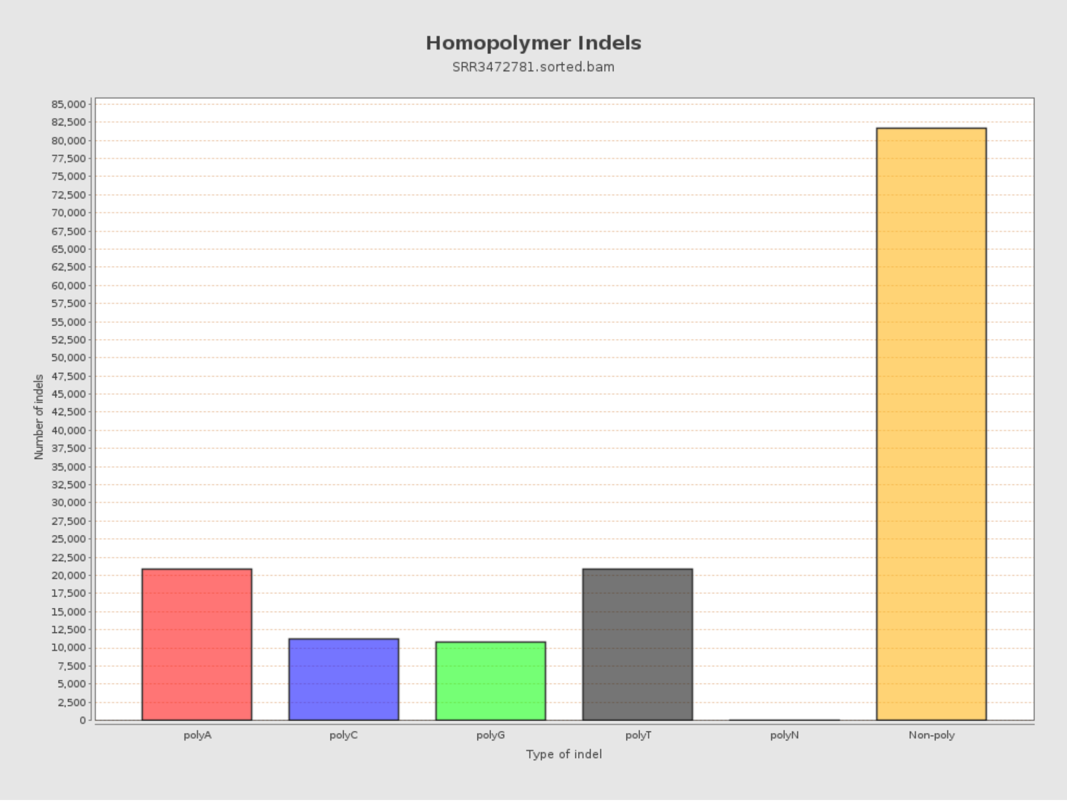
9. Results : Mapped Reads GC-content Distribution



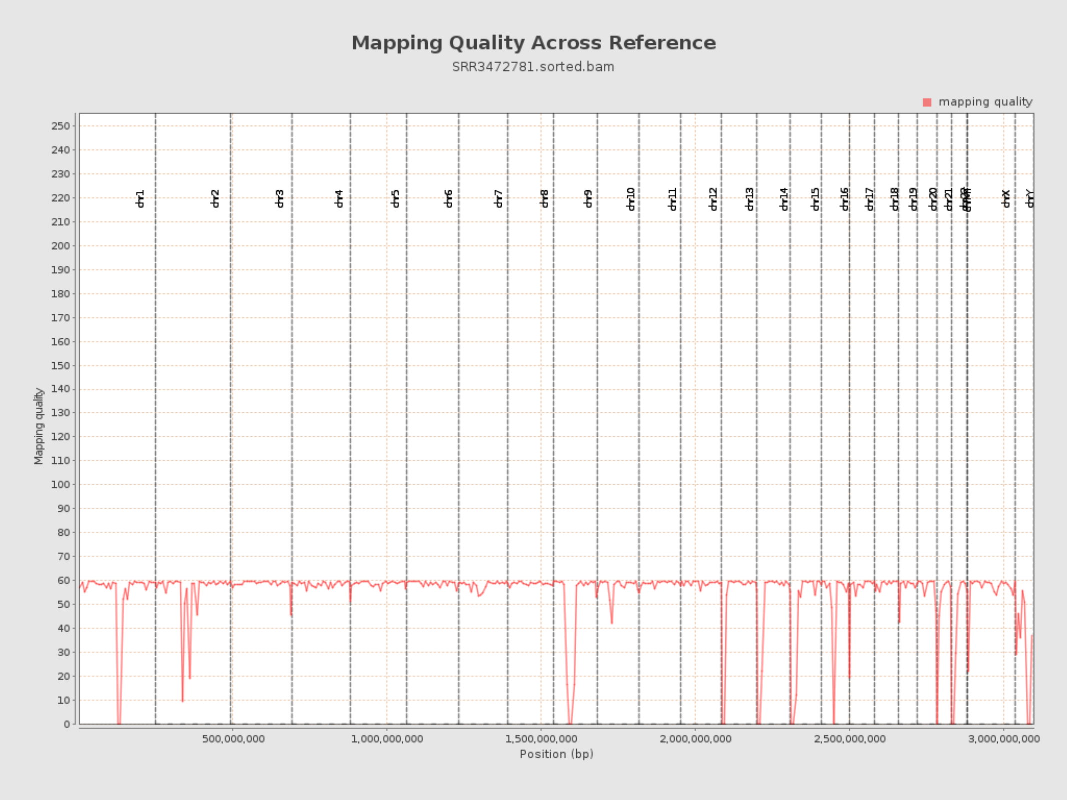
10. Results : Mapped Reads Clipping Profile



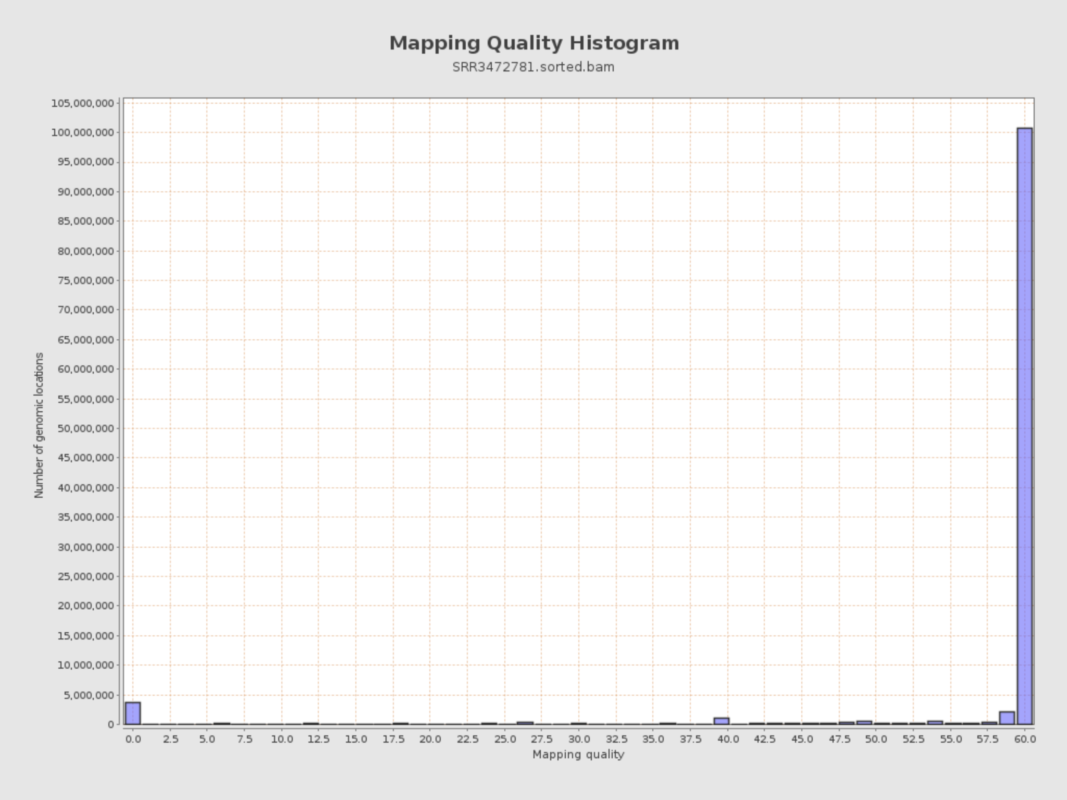
11. Results : Homopolymer Indels



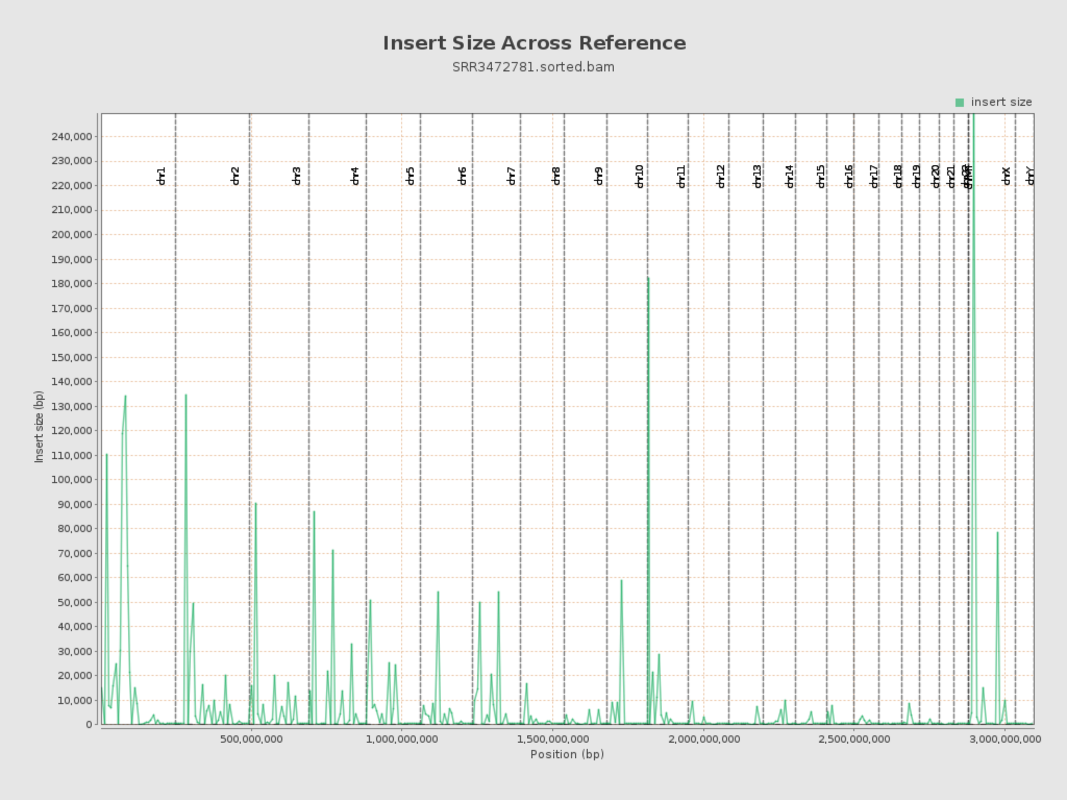
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram